Full wwPDB EM Validation Report

Nov 27, 2025 – 12:05 AM EST

PDB ID	:	9Y9Z / pdb_00009y9z
EMDB ID	:	EMD-72715
Title	:	Cryo-EM structure of conoid fiber from Toxoplasma gondii (24-nm repeat)
Authors	:	Zeng, J.; Zhang, R.
Deposited on	:	2025-09-15
Resolution	:	3.14 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

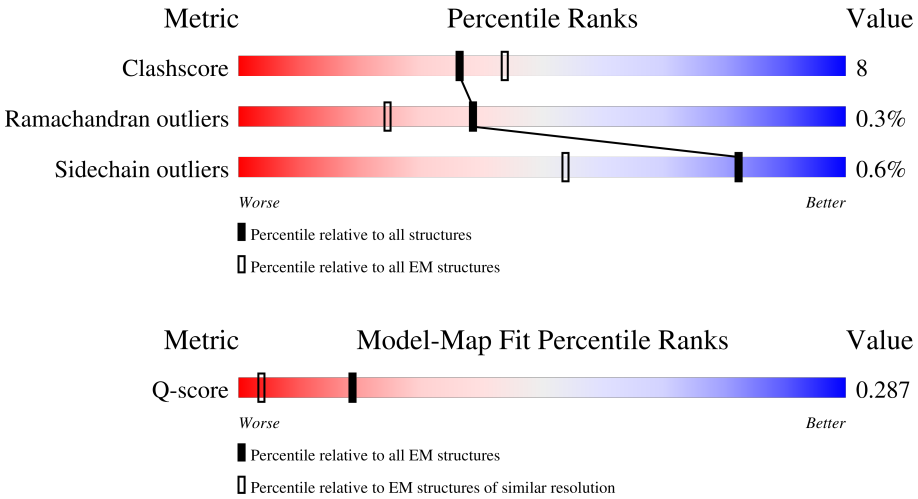
EMDB validation analysis	:	0.0.1.dev129
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.46

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.14 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	14483 (2.64 - 3.64)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	954	10% · 88%
1	2	954	8% · 88%
1	A	954	26% 5% 69%
1	B	954	21% · 75%

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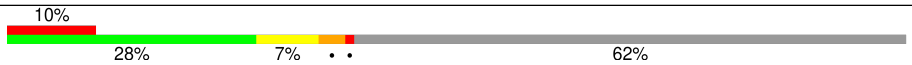
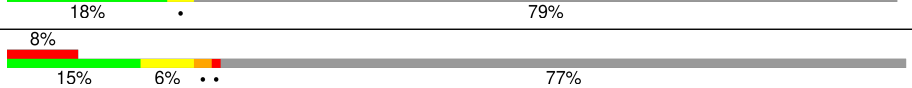
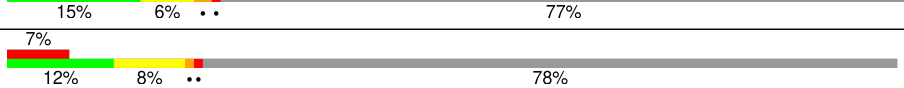
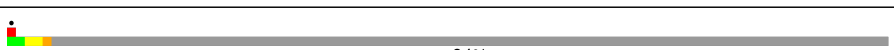
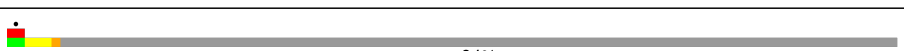
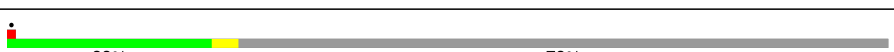
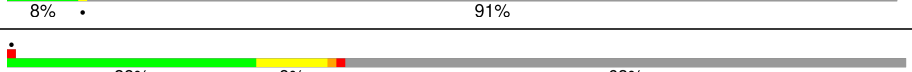
Mol	Chain	Length	Quality of chain
1	C	954	
1	D	954	
1	E	954	
1	F	954	
1	G	954	
1	H	954	
1	I	954	
1	J	954	
1	K	954	
1	L	954	
1	M	954	
1	N	954	
1	O	954	
1	P	954	
1	Q	954	
1	R	954	
1	S	954	
1	T	954	
1	U	954	
1	V	954	
1	W	954	
1	X	954	
1	Y	954	
1	Z	954	
1	a	954	

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Mol	Chain	Length	Quality of chain
1	b	954	8% 91%
1	c	954	25% 8% 62%
1	d	954	22% 74%
1	e	954	7% 91%
1	f	954	7% 8% 80%
1	g	954	9% 90%
1	h	954	8% 90%
1	i	954	7% 90%
1	j	954	8% 90%
1	k	954	9% 90%
1	l	954	8% 90%
1	m	954	8% 90%
1	n	954	8% 91%
1	o	954	7% 91%
1	p	954	7% 91%
1	q	954	7% 91%
1	r	954	7% 91%
1	s	954	5% 8% 91%
1	t	954	6% 7% 91%
1	u	954	9% 88%
1	v	954	10% 88%
1	w	954	10% 88%
1	x	954	9% 88%
1	y	954	9% 88%
1	z	954	10% 88%

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Mol	Chain	Length	Quality of chain
2	10	410	21% 35% 7% 57%
2	11	410	17% 37% 7% 57%
2	12	410	17% 30% 12% 57%
2	13	410	14% 38% 6% 57%
2	14	410	19% 35% 7% 57%
2	15	410	7% 19% 79%
2	16	410	10% 19% 5% 76%
2	3	410	13% 35% 8% 57%
2	4	410	17% 35% 7% 57%
2	5	410	14% 37% 6% 57%
2	6	410	18% 32% 10% 57%
2	7	410	12% 37% 6% 57%
2	8	410	16% 32% 10% 57%
2	9	410	19% 34% 9% 57%
3	1A	453	6% 67% 27% 6%
3	1C	453	74% 21% 6%
3	1E	453	68% 26% 6%
3	1G	453	77% 17% 6%
3	1I	453	79% 15% 6%
3	1K	453	77% 17% 6%
3	1M	453	67% 27% 6%
3	2A	453	71% 24% 6%
3	2C	453	74% 20% 6%
3	2E	453	72% 21% 6%
3	2G	453	77% 17% 6%

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Mol	Chain	Length	Quality of chain
3	2I	453	75% 19% 6%
3	2K	453	77% 17% 6%
3	2M	453	75% 19% 6%
3	3A	453	66% 28% 6%
3	3C	453	72% 22% 6%
3	3E	453	78% 16% 6%
3	3G	453	83% 11% 6%
3	3I	453	79% 15% 6%
3	3K	453	77% 17% 6%
3	3M	453	72% 23% 6%
3	4A	453	70% 24% 6%
3	4C	453	76% 18% 6%
3	4E	453	78% 16% 6%
3	4G	453	78% 17% 6%
3	4I	453	81% 14% 6%
3	4K	453	80% 14% 6%
3	4M	453	68% 26% 6%
3	5A	453	70% 24% 6%
3	5C	453	72% 22% 6%
3	5E	453	79% 15% 6%
3	5G	453	81% 13% 6%
3	5I	453	79% 16% 6%
3	5K	453	82% 12% 6%
3	5M	453	76% 18% 6%
3	6A	453	76% 19% 6%

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Mol	Chain	Length	Quality of chain
3	6C	453	77% 17% 6%
3	6E	453	78% 16% 6%
3	6G	453	83% 12% 6%
3	6I	453	79% 16% 6%
3	6K	453	80% 15% 6%
3	6M	453	66% 29% 6%
3	7A	453	80% 15% 6%
3	7C	453	74% 20% 6%
3	7E	453	75% 19% 6%
3	7G	453	78% 17% 6%
3	7I	453	77% 17% 6%
3	7K	453	73% 22% 6%
3	7M	453	71% 23% 6%
3	8A	453	6% 75% 19% 6%
3	8C	453	76% 17% 6%
3	8E	453	74% 21% 6%
3	8G	453	79% 16% 6%
3	8I	453	76% 19% 6%
3	8K	453	69% 25% 6%
3	8M	453	5% 76% 18% 6%
3	9A	453	28% 75% 20% 6%
3	9C	453	18% 76% 18% 6%
3	9E	453	9% 75% 20% 6%
3	9G	453	75% 19% 6%
3	9I	453	9% 72% 22% 6%

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Mol	Chain	Length	Quality of chain
3	9K	453	19% 76% 18% 6%
3	9M	453	36% 82% 13% 6%
4	1B	449	69% 25% 5%
4	1D	449	71% 23% 5%
4	1F	449	72% 23% 5%
4	1H	449	75% 20% 5%
4	1J	449	75% 20% 5%
4	1L	449	74% 20% 5%
4	1N	449	77% 18% 5%
4	2B	449	69% 25% 5%
4	2D	449	72% 22% 5%
4	2F	449	75% 19% 5%
4	2H	449	80% 15% 5%
4	2J	449	75% 20% 5%
4	2L	449	74% 20% 5%
4	3B	449	65% 29% 5%
4	3D	449	73% 22% 5%
4	3F	449	73% 21% 5%
4	3H	449	80% 14% 5%
4	3J	449	77% 18% 5%
4	3L	449	75% 20% 5%
4	4B	449	69% 25% 5%
4	4D	449	78% 17% 5%
4	4F	449	81% 13% 5%
4	4H	449	80% 14% 5%

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Mol	Chain	Length	Quality of chain
4	4J	449	81% 14% 5%
4	4L	449	76% 19% 5%
4	5B	449	67% 28% • 5%
4	5D	449	78% 16% 5%
4	5F	449	80% 14% 5%
4	5H	449	78% 17% 5%
4	5J	449	78% 17% 5%
4	5L	449	78% 16% 5%
4	5N	449	71% 23% • 5%
4	6B	449	75% 20% 5%
4	6D	449	75% 20% 5%
4	6F	449	79% 16% 5%
4	6H	449	73% 22% 5%
4	6J	449	73% 22% 5%
4	6L	449	76% 19% 5%
4	6N	449	• 69% 26% 5%
4	7B	449	67% 27% • 5%
4	7D	449	73% 22% • 5%
4	7F	449	75% 20% 5%
4	7H	449	73% 22% 5%
4	7J	449	70% 25% 5%
4	7L	449	69% 26% 5%
4	8B	449	• 72% 22% 5%
4	8D	449	77% 18% 5%
4	8F	449	69% 25% • 5%

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Mol	Chain	Length	Quality of chain
4	8H	449	77% 18% 5%
4	8J	449	68% 26% 5%
4	8L	449	66% 29% 5%
4	9B	449	13% 69% 25% 5%
4	9D	449	18% 77% 18% 5%
4	9F	449	68% 26% 5%
4	9H	449	73% 21% 5%
4	9J	449	19% 73% 21% 5%
4	9L	449	20% 78% 17% 5%
5	20	263	70% 15% 14%
5	21	263	68% 17% 14%
5	22	263	69% 16% 14%
5	23	263	5% 73% 12% 14%
5	24	263	5% 65% 20% 14%
5	25	263	5% 65% 19% 14%
5	26	263	68% 17% 14%
5	27	263	6% 63% 22% 14%
5	28	263	7% 71% 14% 14%
5	29	263	5% 64% 21% 14%
5	30	263	71% 15% 14%
5	31	263	7% 62% 22% 14%
5	32	263	8% 70% 16% 14%
5	33	263	35% 48% 14% 37%
5	35	263	29% 62% 20% 17%
5	36	263	27% 70% 11% 19%

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Mol	Chain	Length	Quality of chain
5	37	263	29% 71% 11% 17%
5	38	263	32% 68% 13% 19%
5	39	263	37% 66% 16% 17%
5	40	263	36% 66% 15% 19%
5	42	263	67% 71% 10% 19%
5	43	263	33% 68% 14% 17%
5	44	263	32% 68% 13% 19%
5	45	263	32% 73% 10% 17%
5	46	263	45% 70% 11% 19%
5	47	263	48% 68% 14% 17%
5	48	263	77% 72% 9% 19%
5	49	263	7% 67% 21% 13%
5	50	263	8% 68% 21% 11%
5	51	263	8% 65% 22% 13%
5	52	263	10% 67% 22% 11%
5	53	263	11% 64% 24% 13%
5	54	263	13% 72% 17% 11%
5	55	263	10% 68% 19% 13%
5	56	263	10% 71% 18% 11%
5	57	263	10% 68% 19% 13%
5	58	263	14% 72% 16% 11%
5	59	263	40% 70% 17% 13%
5	60	263	15% 69% 19% 11%
5	61	263	16% 63% 24% 13%
5	62	263	36% 67% 22% 11%

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Mol	Chain	Length	Quality of chain
6	63	1010	52% 9% 38%
6	64	1010	52% 9% 38%
6	65	1010	51% 9% 38%
6	66	1010	50% 10% 38%
6	67	1010	10% 50% 11% 38%
6	68	1010	50% 10% 38%
6	69	1010	50% 11% 38%
7	71	416	6% 34% 7% 59%
7	72	416	8% 33% 7% 59%
7	73	416	8% 33% 8% 59%
7	75	416	6% 32% 8% 59%
7	76	416	8% 34% 7% 59%
7	77	416	8% 31% 10% 59%
7	78	416	33% 8% 59%
7	79	416	36% 5% 59%
7	80	416	34% 7% 59%
7	82	416	32% 9% 59%
7	83	416	31% 10% 59%
7	84	416	32% 8% 59%
7	85	416	35% 6% 59%
7	86	416	5% 34% 7% 59%
7	87	416	5% 31% 10% 59%
7	89	416	32% 8% 59%
7	90	416	32% 9% 59%
7	91	416	6% 32% 8% 59%

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Mol	Chain	Length	Quality of chain
7	92	416	33% 33% 8% 59%
7	93	416	37% 34% 6% 59%
7	94	416	36% 34% 7% 59%
7	95	416	37% 36% 5% 59%
7	96	416	25% 31% 10% 59%
7	97	416	37% 34% 6% 59%
8	A1	502	54% 11% 35%
8	A2	502	53% 12% 35%
8	A3	502	37% 9% 54%
8	A4	502	23% 5% 72%
8	A5	502	57% 8% 35%
8	A6	502	56% 9% 35%
8	A7	502	54% 11% 35%
8	A8	502	55% 10% 35%
8	A9	502	22% 75%
9	B1	556	41% 5% 54%
9	B2	556	39% 7% 54%
9	B3	556	42% 5% 54%
9	B4	556	40% 6% 54%
9	B5	556	38% 8% 54%
9	B6	556	38% 8% 54%
9	B7	556	37% 9% 54%
10	C0	582	10% 27% 68%
10	C6	582	10% 25% 7% 68%
10	C7	582	9% 25% 7% 68%

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Mol	Chain	Length	Quality of chain
10	C8	582	11% 24% 8% 68%
10	C9	582	10% 25% 7% 68%
10	D0	582	40% 6% 53%
10	D1	582	10% 25% 6% 68%
10	D2	582	10% 25% 6% 68%
10	D3	582	19% 41% 5% 53%
10	D4	582	19% 42% 5% 53%
10	D5	582	18% 40% 7% 53%
10	D6	582	25% 39% 7% 53%
10	D7	582	16% 40% 7% 53%
10	D8	582	18% 39% 7% 53%
10	D9	582	20% 38% 9% 53%
10	E0	582	41% 5% 53%
10	E1	582	39% 7% 53%
10	E2	582	36% 10% 53%
10	E3	582	16% 38% 8% 53%
10	E4	582	38% 8% 53%
10	E5	582	41% 6% 53%
10	E6	582	36% 10% 53%
10	E7	582	40% 7% 53%
10	E8	582	39% 8% 53%
10	E9	582	40% 39% 8% 53%
10	F1	582	40% 6% 53%
10	F2	582	38% 9% 53%
10	F3	582	38% 8% 53%

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Mol	Chain	Length	Quality of chain
11	C1	351	8% 91%
11	C2	351	8% 91%
11	C3	351	7% 91%
11	C4	351	8% 92%
11	C5	351	6% 91%
12	F0	783	10% 86%
12	F5	783	10% 87%
12	F6	783	9% 86%
12	F7	783	9% 87%
12	F8	783	11% 86%
12	F9	783	10% 87%
12	G0	783	6% 94%
12	G1	783	9% 87%
12	G2	783	9% 86%
12	G3	783	10% 87%
12	G4	783	10% 86%
12	G5	783	9% 87%
12	G6	783	10% 86%
12	G7	783	10% 87%
12	G8	783	10% 86%
12	G9	783	5% 94%
12	H0	783	97%
12	H1	783	97%
12	H2	783	5% 94%
12	H3	783	6% 94%

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Mol	Chain	Length	Quality of chain
12	H4	783	97%
12	H5	783	5% 94%
12	H6	783	6% 94%
12	H7	783	97%
12	H8	783	5% 94%
12	H9	783	6% 94%
12	I1	783	5% 94%
12	I2	783	6% 94%
12	I3	783	97%
12	I4	783	5% 94%
12	I5	783	94%
12	I6	783	97%
12	I7	783	5% 94%
12	I8	783	6% 94%
12	I9	783	97%
13	J1	871	10% 28% 8% 65%
13	J2	871	11% 27% 8% 65%
13	J3	871	11% 29% 7% 65%
13	J4	871	21% 30% 6% 65%
13	J5	871	12% 29% 7% 65%
13	J6	871	14% 28% 7% 65%
13	J7	871	30% 31% 65%
14	K0	256	63% 11% 26%
14	K1	256	64% 10% 26%
14	K2	256	66% 7% 26%

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Mol	Chain	Length	Quality of chain
14	K3	256	63% 11% 26%
14	K4	256	58% 16% 26%
14	K5	256	64% 10% 26%
14	K6	256	62% 11% 26%
14	K7	256	68% 6% 26%
14	K8	256	64% 9% 26%
14	K9	256	67% 7% 26%
14	L0	256	60% 14% 26%
14	L1	256	60% 14% 26%
14	L2	256	65% 9% 26%
14	L3	256	55% 19% 26%
14	L4	256	42% 10% 48%
14	L5	256	62% 12% 26%
14	L6	256	62% 12% 26%
14	L7	256	61% 12% 26%
14	L8	256	62% 12% 26%
14	L9	256	59% 15% 26%
14	M1	256	38% 10% 51%
14	M2	256	6% 61% 13% 26%
14	M3	256	7% 56% 18% 26%
14	M4	256	11% 60% 14% 26%
14	M5	256	13% 58% 16% 26%
14	M6	256	7% 62% 11% 26%
14	M7	256	10% 54% 20% 26%

2 Entry composition (i)

There are 17 unique types of molecules in this entry. The entry contains 806376 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CF2, TGME49_258090.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	294	Total	C	N	O	S	0	0
			2425	1459	480	479	7		
1	B	241	Total	C	N	O	S	0	0
			1998	1212	394	385	7		
1	C	148	Total	C	N	O	S	0	0
			1232	751	239	237	5		
1	D	118	Total	C	N	O	S	0	0
			993	597	197	195	4		
1	E	269	Total	C	N	O	S	0	0
			2215	1345	439	424	7		
1	F	299	Total	C	N	O	S	0	0
			2469	1484	491	487	7		
1	G	170	Total	C	N	O	S	0	0
			1403	857	272	269	5		
1	H	114	Total	C	N	O	S	0	0
			959	578	192	185	4		
1	I	362	Total	C	N	O	S	0	0
			3014	1819	603	582	10		
1	J	356	Total	C	N	O	S	0	0
			2963	1787	593	572	11		
1	K	197	Total	C	N	O	S	0	0
			1637	990	325	317	5		
1	L	202	Total	C	N	O	S	0	0
			1678	1015	330	327	6		
1	M	215	Total	C	N	O	S	0	0
			1786	1077	356	347	6		
1	N	208	Total	C	N	O	S	0	0
			1723	1038	345	334	6		
1	O	57	Total	C	N	O	S	0	0
			465	280	92	90	3		
1	P	54	Total	C	N	O	S	0	0
			444	265	89	87	3		
1	Q	346	Total	C	N	O	S	0	0
			2876	1740	572	554	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	254	Total	C	N	O	S	0	0
			2096	1265	420	405	6		
1	S	177	Total	C	N	O	S	0	0
			1468	889	289	285	5		
1	T	77	Total	C	N	O	S	0	0
			647	394	126	123	4		
1	U	372	Total	C	N	O	S	0	0
			3096	1864	617	604	11		
1	V	258	Total	C	N	O	S	0	0
			2121	1278	424	413	6		
1	W	198	Total	C	N	O	S	0	0
			1649	996	326	321	6		
1	X	90	Total	C	N	O	S	0	0
			749	456	149	140	4		
1	Y	356	Total	C	N	O	S	0	0
			2959	1788	593	569	9		
1	Z	243	Total	C	N	O	S	0	0
			2017	1217	406	388	6		
1	1	112	Total	C	N	O	S	0	0
			881	542	170	167	2		
1	2	112	Total	C	N	O	S	0	0
			881	542	170	167	2		
1	a	187	Total	C	N	O	S	0	0
			1559	941	315	298	5		
1	b	85	Total	C	N	O	S	0	0
			731	440	146	141	4		
1	c	359	Total	C	N	O	S	0	0
			2988	1800	600	579	9		
1	d	248	Total	C	N	O	S	0	0
			2057	1241	411	398	7		
1	e	85	Total	C	N	O	S	0	0
			725	436	142	142	5		
1	f	190	Total	C	N	O	S	0	0
			1586	949	322	310	5		
1	g	100	Total	C	N	O	S	0	0
			729	438	143	140	8		
1	h	100	Total	C	N	O	S	0	0
			729	438	143	140	8		
1	i	100	Total	C	N	O	S	0	0
			729	438	143	140	8		
1	j	100	Total	C	N	O	S	0	0
			729	438	143	140	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	k	100	Total	C	N	O	S	0	0
			729	438	143	140	8		
1	l	100	Total	C	N	O	S	0	0
			729	438	143	140	8		
1	m	100	Total	C	N	O	S	0	0
			729	438	143	140	8		
1	n	88	Total	C	N	O	S	0	0
			699	428	140	130	1		
1	o	88	Total	C	N	O	S	0	0
			699	428	140	130	1		
1	p	88	Total	C	N	O	S	0	0
			699	428	140	130	1		
1	q	88	Total	C	N	O	S	0	0
			699	428	140	130	1		
1	r	88	Total	C	N	O	S	0	0
			699	428	140	130	1		
1	s	88	Total	C	N	O	S	0	0
			699	428	140	130	1		
1	t	88	Total	C	N	O	S	0	0
			699	428	140	130	1		
1	u	112	Total	C	N	O	S	0	0
			881	542	170	167	2		
1	v	112	Total	C	N	O	S	0	0
			881	542	170	167	2		
1	w	112	Total	C	N	O	S	0	0
			881	542	170	167	2		
1	x	112	Total	C	N	O	S	0	0
			881	542	170	167	2		
1	y	112	Total	C	N	O	S	0	0
			881	542	170	167	2		
1	z	112	Total	C	N	O	S	0	0
			881	542	170	167	2		

- Molecule 2 is a protein called CF1, TGME49_222350.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	10	175	Total	C	N	O	S	0	0
			1493	913	298	275	7		
2	11	177	Total	C	N	O	S	0	0
			1512	925	303	277	7		
2	12	175	Total	C	N	O	S	0	0
			1493	913	298	275	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	13	177	Total	C	N	O	S	0	0
			1512	925	303	277	7		
2	14	175	Total	C	N	O	S	0	0
			1493	913	298	275	7		
2	15	88	Total	C	N	O	S	0	0
			764	473	155	133	3		
2	16	97	Total	C	N	O	S	0	0
			834	516	167	147	4		
2	3	177	Total	C	N	O	S	0	0
			1512	925	303	277	7		
2	4	175	Total	C	N	O	S	0	0
			1493	913	298	275	7		
2	5	177	Total	C	N	O	S	0	0
			1512	925	303	277	7		
2	6	175	Total	C	N	O	S	0	0
			1493	913	298	275	7		
2	7	177	Total	C	N	O	S	0	0
			1512	925	303	277	7		
2	8	175	Total	C	N	O	S	0	0
			1493	913	298	275	7		
2	9	177	Total	C	N	O	S	0	0
			1512	925	303	277	7		

- Molecule 3 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	1C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	1E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	1G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	1I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	1K	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	1M	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	2A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	2C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	2E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	2G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	2I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	2K	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	2M	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	3A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	3C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	3E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	3G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	3I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	3K	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	3M	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	4A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	4C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	4E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	4G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	4I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	4K	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	4M	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	5A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	5C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	5E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	5G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	5I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	5K	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	5M	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	6A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	6C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	6E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	6G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	6I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	6K	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	6M	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	7A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	7C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	7E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	7G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	7I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	7K	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	7M	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	8A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	8C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	8E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	8G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	8I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	8K	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	8M	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	9A	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	9C	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	9E	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	9G	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	9I	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	9K	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		
3	9M	428	Total	C	N	O	S	0	0
			3325	2105	569	625	26		

- Molecule 4 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	1D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	1F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	1H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	1J	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	1L	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	1N	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	2B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	2D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	2F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	2H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	2J	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	2L	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	3B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	3D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	3F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	3H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	3J	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	3L	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	4B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	4D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	4F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	4H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	4J	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	4L	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	5B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	5D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	5F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	5H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	5J	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	5L	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	5N	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	6B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	6D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	6F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	6H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	6J	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	6L	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	6N	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	7B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	7D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	7F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	7H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	7J	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	7L	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	8B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	8D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	8F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	8H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	8J	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	8L	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	9B	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	9D	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	9F	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	9H	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	9J	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		
4	9L	426	Total	C	N	O	S	0	0
			3331	2094	569	641	27		

- Molecule 5 is a protein called Spindle assembly abnormal protein 6 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	20	225	Total	C	N	O	S	0	0
			1814	1144	318	339	13		
5	21	225	Total	C	N	O	S	0	0
			1815	1146	318	339	12		
5	22	225	Total	C	N	O	S	0	0
			1814	1144	318	339	13		
5	23	225	Total	C	N	O	S	0	0
			1815	1146	318	339	12		
5	24	225	Total	C	N	O	S	0	0
			1814	1144	318	339	13		
5	25	225	Total	C	N	O	S	0	0
			1815	1146	318	339	12		
5	26	225	Total	C	N	O	S	0	0
			1814	1144	318	339	13		
5	27	225	Total	C	N	O	S	0	0
			1815	1146	318	339	12		
5	28	225	Total	C	N	O	S	0	0
			1814	1144	318	339	13		
5	29	225	Total	C	N	O	S	0	0
			1815	1146	318	339	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	30	225	Total	C	N	O	S	0	0
			1814	1144	318	339	13		
5	31	225	Total	C	N	O	S	0	0
			1815	1146	318	339	12		
5	32	225	Total	C	N	O	S	0	0
			1814	1144	318	339	13		
5	33	165	Total	C	N	O	S	0	0
			1321	836	220	255	10		
5	35	217	Total	C	N	O	S	0	0
			1744	1106	301	325	12		
5	36	213	Total	C	N	O	S	0	0
			1723	1090	304	317	12		
5	37	217	Total	C	N	O	S	0	0
			1744	1106	301	325	12		
5	38	213	Total	C	N	O	S	0	0
			1723	1090	304	317	12		
5	39	217	Total	C	N	O	S	0	0
			1744	1106	301	325	12		
5	40	213	Total	C	N	O	S	0	0
			1723	1090	304	317	12		
5	42	213	Total	C	N	O	S	0	0
			1723	1090	304	317	12		
5	43	217	Total	C	N	O	S	0	0
			1744	1106	301	325	12		
5	44	213	Total	C	N	O	S	0	0
			1723	1090	304	317	12		
5	45	217	Total	C	N	O	S	0	0
			1744	1106	301	325	12		
5	46	213	Total	C	N	O	S	0	0
			1723	1090	304	317	12		
5	47	217	Total	C	N	O	S	0	0
			1744	1106	301	325	12		
5	48	213	Total	C	N	O	S	0	0
			1723	1090	304	317	12		
5	49	230	Total	C	N	O	S	0	0
			1841	1161	323	344	13		
5	50	233	Total	C	N	O	S	0	0
			1853	1166	326	348	13		
5	51	230	Total	C	N	O	S	0	0
			1841	1161	323	344	13		
5	52	233	Total	C	N	O	S	0	0
			1853	1166	326	348	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	53	230	Total	C	N	O	S	0	0
			1841	1161	323	344	13		
5	54	233	Total	C	N	O	S	0	0
			1853	1166	326	348	13		
5	55	230	Total	C	N	O	S	0	0
			1841	1161	323	344	13		
5	56	233	Total	C	N	O	S	0	0
			1853	1166	326	348	13		
5	57	230	Total	C	N	O	S	0	0
			1841	1161	323	344	13		
5	58	233	Total	C	N	O	S	0	0
			1853	1166	326	348	13		
5	59	230	Total	C	N	O	S	0	0
			1841	1161	323	344	13		
5	60	233	Total	C	N	O	S	0	0
			1853	1166	326	348	13		
5	61	230	Total	C	N	O	S	0	0
			1841	1161	323	344	13		
5	62	233	Total	C	N	O	S	0	0
			1853	1166	326	348	13		

- Molecule 6 is a protein called CIP3, TGME49_225020.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	63	623	Total	C	N	O	S	0	0
			5055	3170	940	928	17		
6	64	623	Total	C	N	O	S	0	0
			5055	3170	940	928	17		
6	65	623	Total	C	N	O	S	0	0
			5055	3170	940	928	17		
6	66	623	Total	C	N	O	S	0	0
			5055	3170	940	928	17		
6	67	623	Total	C	N	O	S	0	0
			5055	3170	940	928	17		
6	68	623	Total	C	N	O	S	0	0
			5055	3170	940	928	17		
6	69	623	Total	C	N	O	S	0	0
			5055	3170	940	928	17		

- Molecule 7 is a protein called CF6, TGME49_245640.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	71	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	72	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	73	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	75	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	76	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	77	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	78	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	79	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	80	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	82	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	83	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	84	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	85	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	86	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	87	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	89	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	90	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	91	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	92	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	93	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	94	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	95	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	96	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		
7	97	170	Total	C	N	O	S	0	0
			1382	881	251	243	7		

- Molecule 8 is a protein called CF4, TGME49_246720.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A1	325	Total	C	N	O	S	0	0
			2582	1631	455	482	14		
8	A2	325	Total	C	N	O	S	0	0
			2582	1631	455	482	14		
8	A3	232	Total	C	N	O	S	0	0
			1844	1157	327	347	13		
8	A4	142	Total	C	N	O	S	0	0
			1016	628	183	199	6		
8	A5	325	Total	C	N	O	S	0	0
			2582	1631	455	482	14		
8	A6	325	Total	C	N	O	S	0	0
			2582	1631	455	482	14		
8	A7	325	Total	C	N	O	S	0	0
			2582	1631	455	482	14		
8	A8	325	Total	C	N	O	S	0	0
			2582	1631	455	482	14		
8	A9	128	Total	C	N	O	S	0	0
			1020	658	178	183	1		

- Molecule 9 is a protein called CF3, TGME49_255895.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B1	257	Total	C	N	O	S	0	0
			2055	1287	388	369	11		
9	B2	257	Total	C	N	O	S	0	0
			2055	1287	388	369	11		
9	B3	257	Total	C	N	O	S	0	0
			2055	1287	388	369	11		
9	B4	257	Total	C	N	O	S	0	0
			2055	1287	388	369	11		
9	B5	257	Total	C	N	O	S	0	0
			2055	1287	388	369	11		
9	B6	257	Total	C	N	O	S	0	0
			2055	1287	388	369	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	B7	257	Total	C	N	O	S	0	0
			2055	1287	388	369	11		

- Molecule 10 is a protein called CPH1, TGME49_266630.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C0	184	Total	C	N	O	S	0	0
			1471	938	257	261	15		
10	C6	184	Total	C	N	O	S	0	0
			1471	938	257	261	15		
10	C7	184	Total	C	N	O	S	0	0
			1471	938	257	261	15		
10	C8	184	Total	C	N	O	S	0	0
			1471	938	257	261	15		
10	C9	184	Total	C	N	O	S	0	0
			1471	938	257	261	15		
10	D0	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	D1	184	Total	C	N	O	S	0	0
			1471	938	257	261	15		
10	D2	184	Total	C	N	O	S	0	0
			1471	938	257	261	15		
10	D3	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	D4	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	D5	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	D6	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	D7	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	D8	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	D9	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	E0	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	E1	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	E2	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	E3	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	E4	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	E5	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	E6	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	E7	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	E8	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	E9	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	F1	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	F2	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		
10	F3	272	Total	C	N	O	S	0	0
			2197	1400	389	390	18		

- Molecule 11 is a protein called Microtubule associated protein SPM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C1	30	Total	C	N	O	S	0	0
			237	155	38	43	1		
11	C2	30	Total	C	N	O		0	0
			238	158	36	44			
11	C3	30	Total	C	N	O		0	0
			242	159	39	44			
11	C4	27	Total	C	N	O		0	0
			214	140	35	39			
11	C5	30	Total	C	N	O		0	0
			239	158	38	43			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C1	93	ARG	PRO	conflict	UNP A0A7J6K285
C2	93	ARG	PRO	conflict	UNP A0A7J6K285
C3	93	ARG	PRO	conflict	UNP A0A7J6K285
C4	93	ARG	PRO	conflict	UNP A0A7J6K285
C5	93	ARG	PRO	conflict	UNP A0A7J6K285

- Molecule 12 is a protein called PRP, TGME49_291880.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F0	107	Total	C	N	O	S	0	0
			883	576	150	153	4		
12	F5	102	Total	C	N	O	S	0	0
			847	554	142	148	3		
12	F6	107	Total	C	N	O	S	0	0
			883	576	150	153	4		
12	F7	102	Total	C	N	O	S	0	0
			847	554	142	148	3		
12	F8	107	Total	C	N	O	S	0	0
			883	576	150	153	4		
12	F9	102	Total	C	N	O	S	0	0
			847	554	142	148	3		
12	G0	50	Total	C	N	O		0	0
			412	253	82	77			
12	G1	102	Total	C	N	O	S	0	0
			847	554	142	148	3		
12	G2	107	Total	C	N	O	S	0	0
			883	576	150	153	4		
12	G3	102	Total	C	N	O	S	0	0
			847	554	142	148	3		
12	G4	107	Total	C	N	O	S	0	0
			883	576	150	153	4		
12	G5	102	Total	C	N	O	S	0	0
			847	554	142	148	3		
12	G6	107	Total	C	N	O	S	0	0
			883	576	150	153	4		
12	G7	102	Total	C	N	O	S	0	0
			847	554	142	148	3		
12	G8	107	Total	C	N	O	S	0	0
			883	576	150	153	4		
12	G9	44	Total	C	N	O		0	0
			365	222	73	70			
12	H0	24	Total	C	N	O		0	0
			184	114	30	40			
12	H1	24	Total	C	N	O		0	0
			184	114	30	40			
12	H2	44	Total	C	N	O		0	0
			365	222	73	70			
12	H3	50	Total	C	N	O		0	0
			412	253	82	77			
12	H4	24	Total	C	N	O		0	0
			184	114	30	40			

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	H5	44	Total	C	N	O		0	0
			365	222	73	70			
12	H6	50	Total	C	N	O		0	0
			412	253	82	77			
12	H7	24	Total	C	N	O		0	0
			184	114	30	40			
12	H8	44	Total	C	N	O		0	0
			365	222	73	70			
12	H9	50	Total	C	N	O		0	0
			412	253	82	77			
12	I1	44	Total	C	N	O		0	0
			365	222	73	70			
12	I2	50	Total	C	N	O		0	0
			412	253	82	77			
12	I3	24	Total	C	N	O		0	0
			184	114	30	40			
12	I4	44	Total	C	N	O		0	0
			365	222	73	70			
12	I5	50	Total	C	N	O		0	0
			412	253	82	77			
12	I6	24	Total	C	N	O		0	0
			184	114	30	40			
12	I7	44	Total	C	N	O		0	0
			365	222	73	70			
12	I8	50	Total	C	N	O		0	0
			412	253	82	77			
12	I9	24	Total	C	N	O		0	0
			184	114	30	40			

- Molecule 13 is a protein called CF5, TGME49_297180.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J1	308	Total	C	N	O	S	0	0
			2488	1572	457	452	7		
13	J2	308	Total	C	N	O	S	0	0
			2488	1572	457	452	7		
13	J3	308	Total	C	N	O	S	0	0
			2488	1572	457	452	7		
13	J4	308	Total	C	N	O	S	0	0
			2488	1572	457	452	7		
13	J5	308	Total	C	N	O	S	0	0
			2488	1572	457	452	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	J6	308	Total	C	N	O	S	0	0
			2488	1572	457	452	7		
13	J7	308	Total	C	N	O	S	0	0
			2488	1572	457	452	7		

- Molecule 14 is a protein called DCX, TGME49_256030.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K0	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	K1	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	K2	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	K3	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	K4	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	K5	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	K6	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	K7	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	K8	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	K9	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	L0	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	L1	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	L2	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	L3	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	L4	132	Total	C	N	O	S	0	0
			1073	696	185	189	3		
14	L5	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	L6	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		

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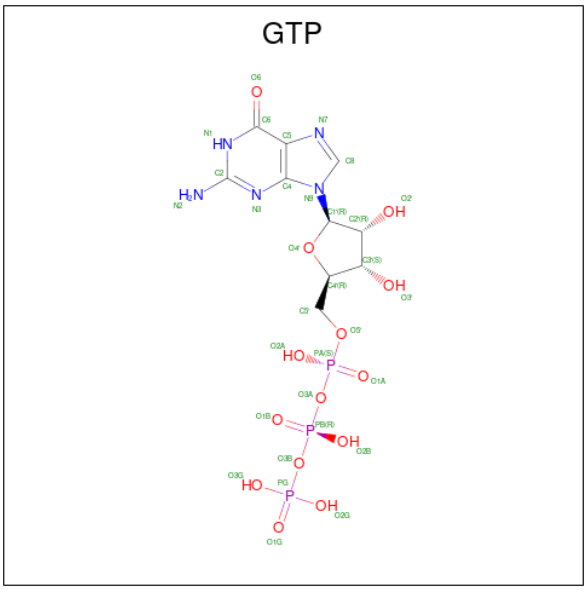
Mol	Chain	Residues	Atoms					AltConf	Trace
14	L7	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	L8	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	L9	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	M1	125	Total	C	N	O	S	0	0
			1011	656	170	182	3		
14	M2	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	M3	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	M4	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	M5	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	M6	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		
14	M7	189	Total	C	N	O	S	0	0
			1537	983	269	281	4		

- Molecule 15 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
15	1A	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
15	1C	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	1E	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	1G	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	1I	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	1K	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	1M	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	2A	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	2C	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	2E	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	2G	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	2I	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	2K	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	2M	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	3A	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	3C	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	3E	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	3G	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	3I	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	3K	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	3M	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	4A	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
15	4C	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	4E	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	4G	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	4I	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	4K	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	4M	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	5A	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	5C	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	5E	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	5G	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	5I	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	5K	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	5M	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	6A	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	6C	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	6E	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	6G	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	6I	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	6K	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	6N	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	7A	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
15	7C	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	7E	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	7G	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	7I	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	7K	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	7M	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	8A	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	8C	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	8E	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	8G	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	8I	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	8K	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	8M	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	9A	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	9C	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	9E	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	9G	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	9I	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	9K	1	Total	C	N	O	P	0
			32	10	5	14	3	
15	9M	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
16	1A	1	Total Mg 1 1	0
16	1C	1	Total Mg 1 1	0
16	1E	1	Total Mg 1 1	0
16	1G	1	Total Mg 1 1	0
16	1I	1	Total Mg 1 1	0
16	1K	1	Total Mg 1 1	0
16	2A	1	Total Mg 1 1	0
16	2C	1	Total Mg 1 1	0
16	2E	1	Total Mg 1 1	0
16	2G	1	Total Mg 1 1	0
16	2I	1	Total Mg 1 1	0
16	2K	1	Total Mg 1 1	0
16	3A	1	Total Mg 1 1	0
16	3C	1	Total Mg 1 1	0
16	3E	1	Total Mg 1 1	0
16	3G	1	Total Mg 1 1	0
16	3I	1	Total Mg 1 1	0
16	3K	1	Total Mg 1 1	0
16	4A	1	Total Mg 1 1	0
16	4C	1	Total Mg 1 1	0
16	4E	1	Total Mg 1 1	0
16	4G	1	Total Mg 1 1	0

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Mol	Chain	Residues	Atoms	AltConf
16	4I	1	Total Mg 1 1	0
16	4K	1	Total Mg 1 1	0
16	5A	1	Total Mg 1 1	0
16	5C	1	Total Mg 1 1	0
16	5E	1	Total Mg 1 1	0
16	5G	1	Total Mg 1 1	0
16	5I	1	Total Mg 1 1	0
16	5K	1	Total Mg 1 1	0
16	6A	1	Total Mg 1 1	0
16	6C	1	Total Mg 1 1	0
16	6E	1	Total Mg 1 1	0
16	6G	1	Total Mg 1 1	0
16	6I	1	Total Mg 1 1	0
16	6K	1	Total Mg 1 1	0
16	7B	1	Total Mg 1 1	0
16	7C	1	Total Mg 1 1	0
16	7E	1	Total Mg 1 1	0
16	7G	1	Total Mg 1 1	0
16	7I	1	Total Mg 1 1	0
16	7K	1	Total Mg 1 1	0
16	8A	1	Total Mg 1 1	0

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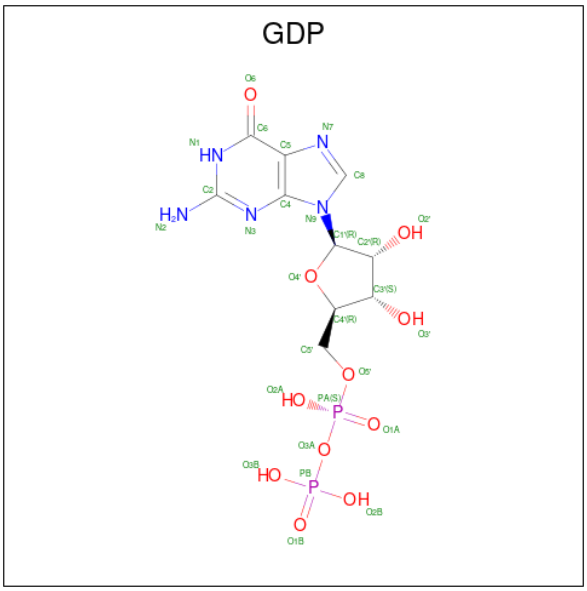
Mol	Chain	Residues	Atoms	AltConf
16	8C	1	Total Mg 1 1	0
16	8E	1	Total Mg 1 1	0
16	8G	1	Total Mg 1 1	0
16	8I	1	Total Mg 1 1	0
16	8K	1	Total Mg 1 1	0
16	9A	1	Total Mg 1 1	0
16	9C	1	Total Mg 1 1	0
16	9E	1	Total Mg 1 1	0
16	9G	1	Total Mg 1 1	0
16	9I	1	Total Mg 1 1	0
16	9K	1	Total Mg 1 1	0

- Molecule 17 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
17	1B	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	1D	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	1F	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	1H	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	1J	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	1L	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	1N	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	2B	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	2D	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	2F	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	2H	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	2J	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	2L	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	3B	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	3D	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	3F	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	3H	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	3J	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	3L	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	4B	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	4D	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	4F	1	Total	C	N	O	P	0
			28	10	5	11	2	

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Mol	Chain	Residues	Atoms					AltConf
17	4H	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	4J	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	4L	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	5B	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	5D	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	5F	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	5H	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	5J	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	5L	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	5N	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	6B	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	6D	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	6F	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	6H	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	6J	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	6L	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	6N	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	7B	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	7D	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	7F	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	7H	1	Total	C	N	O	P	0
			28	10	5	11	2	

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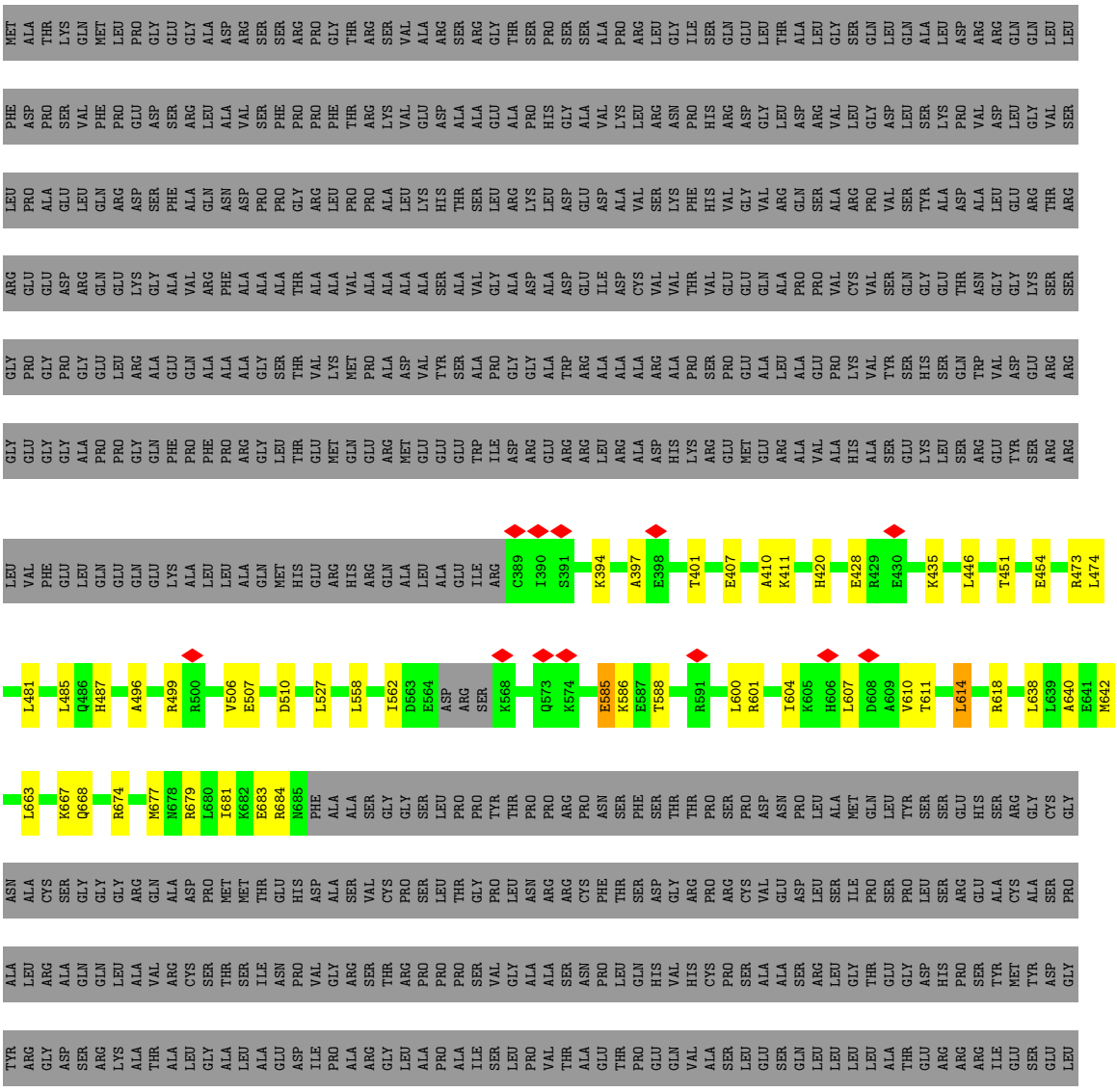
Mol	Chain	Residues	Atoms					AltConf
17	7J	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	7L	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	8B	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	8D	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	8F	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	8H	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	8J	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	8L	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	9B	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	9D	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	9F	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	9H	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	9J	1	Total	C	N	O	P	0
			28	10	5	11	2	
17	9L	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

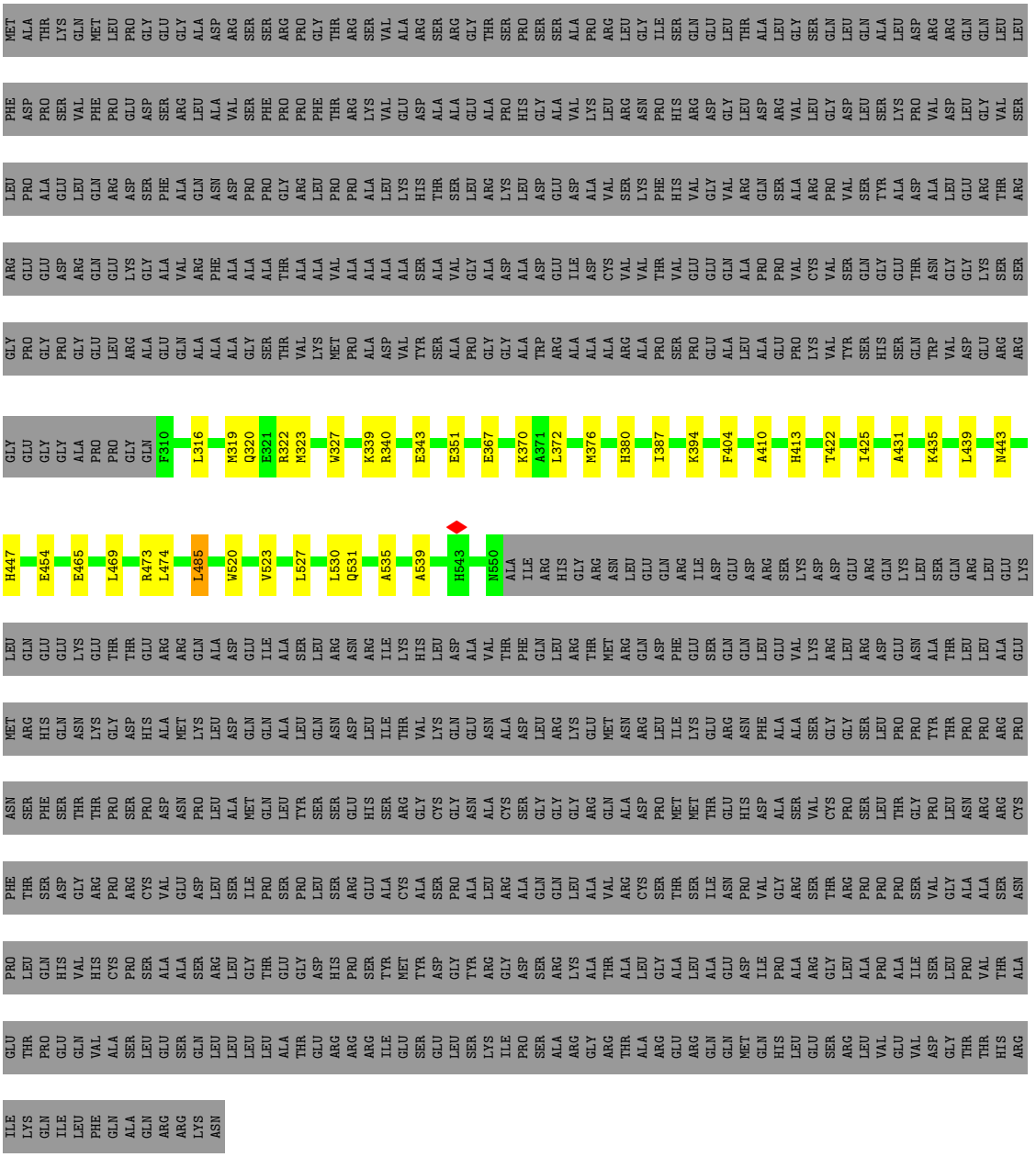
- Molecule 1: CF2, TGME49_258090

Chain A:



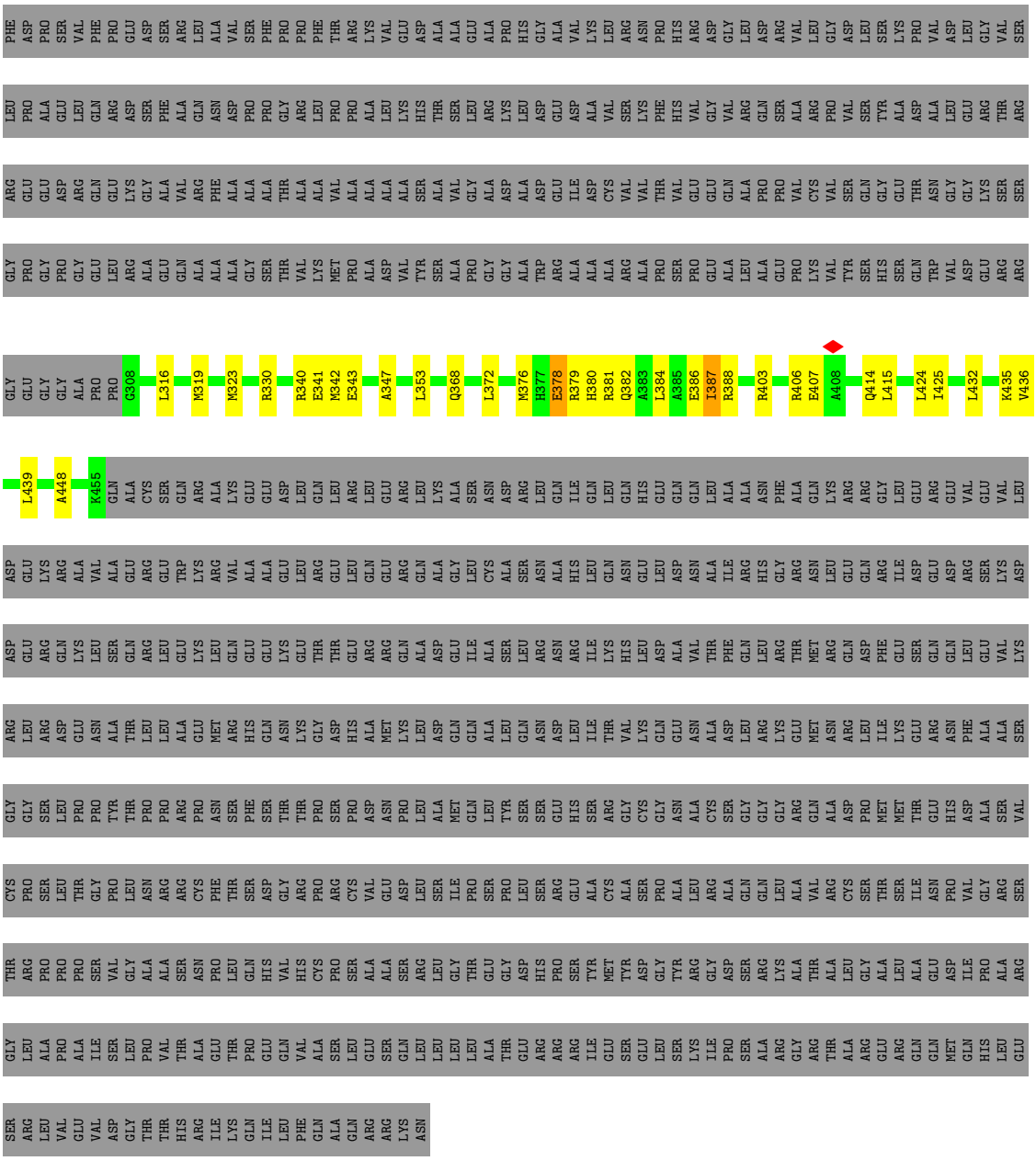
• Molecule 1: CF2, TGME49_258090

Chain B:



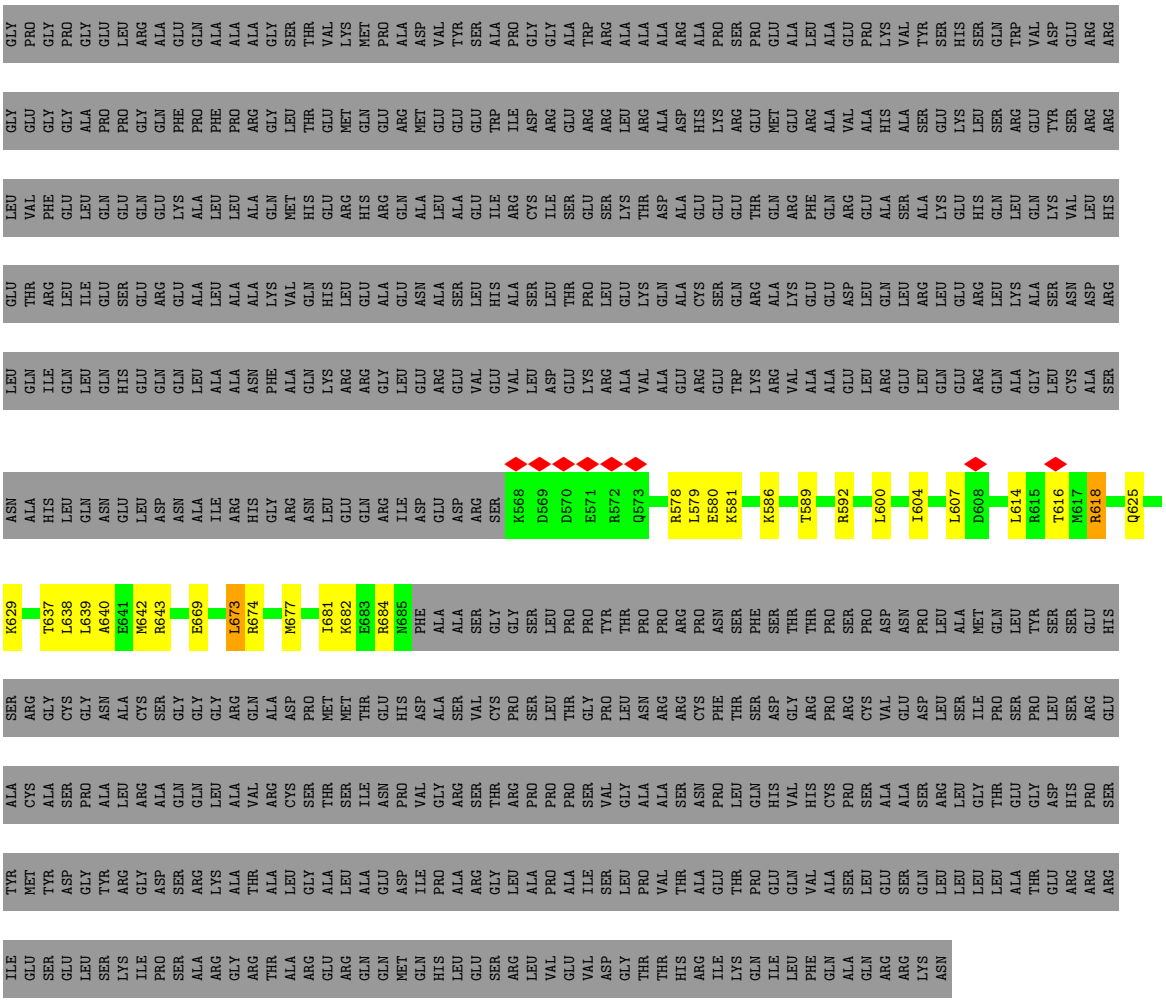
• Molecule 1: CF2, TGME49_258090

Chain C:



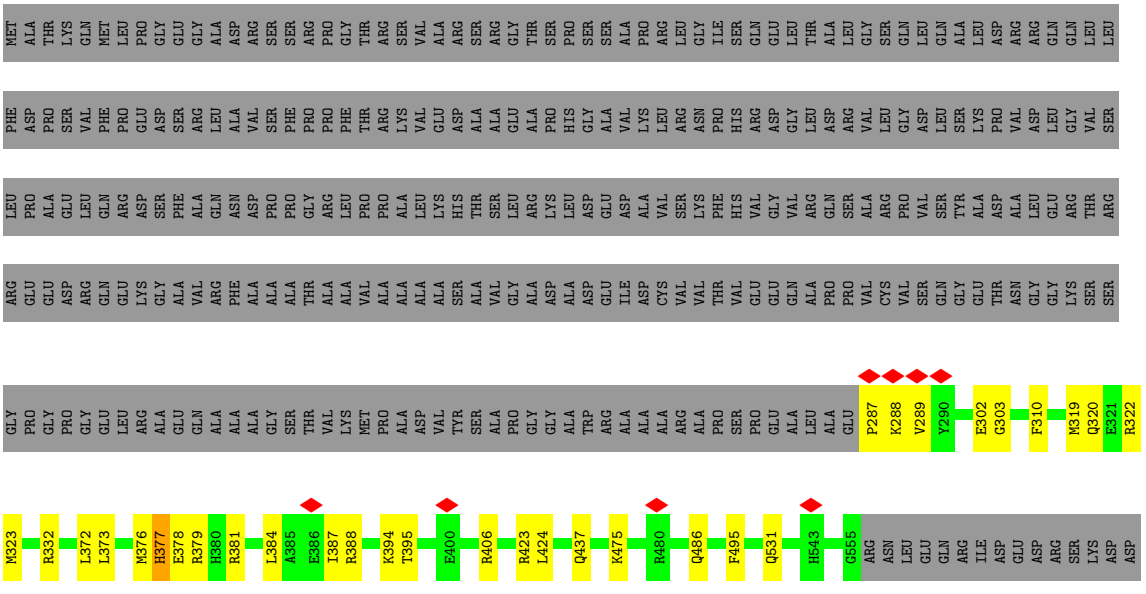
• Molecule 1: CF2, TGME49_258090

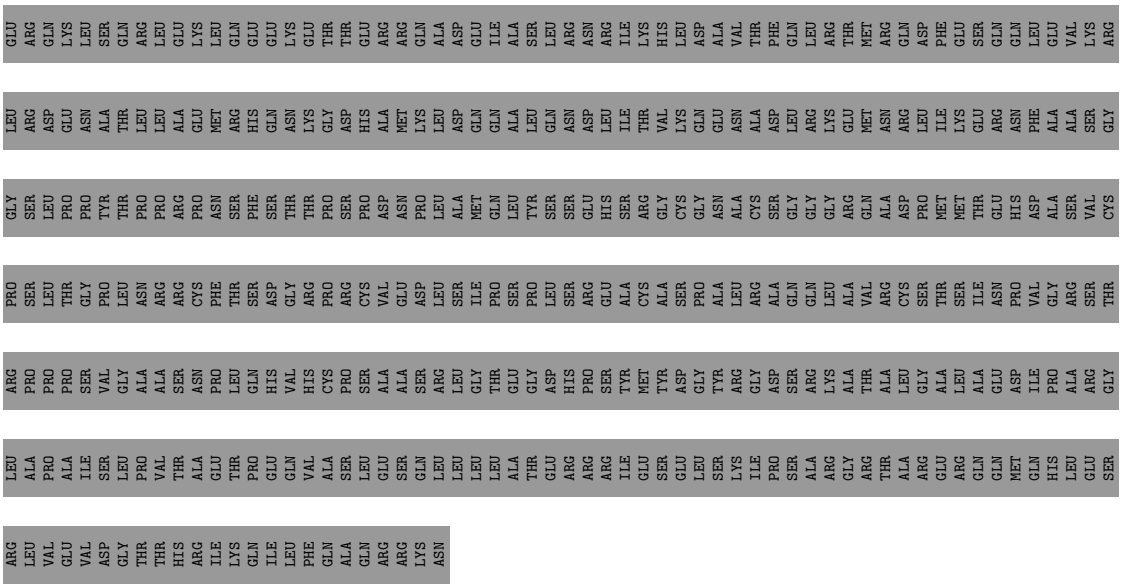
Chain D:



• Molecule 1: CF2, TGME49_258090

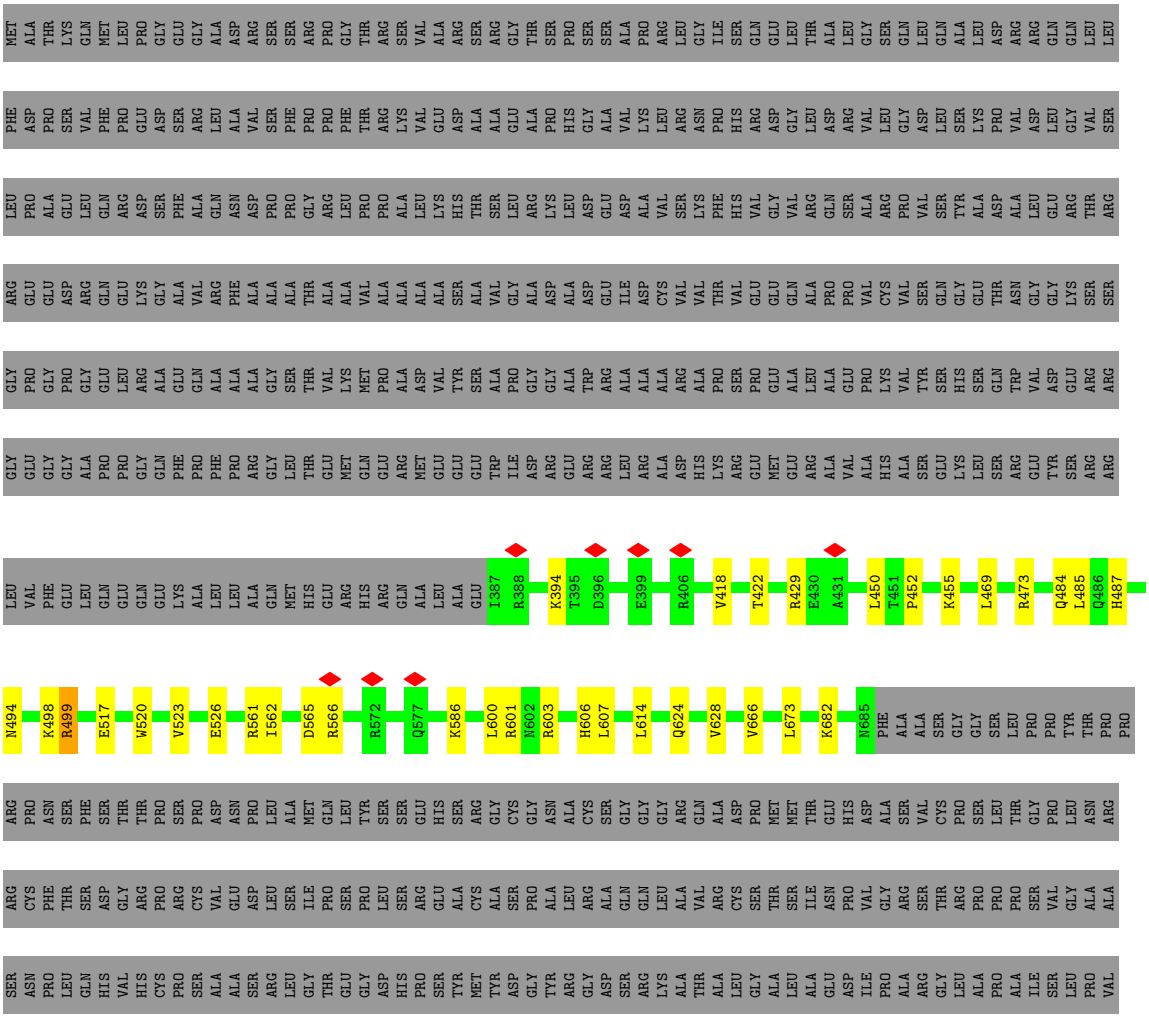
Chain E:

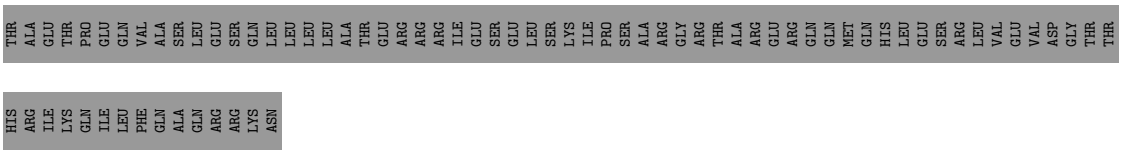




• Molecule 1: CF2, TGME49_258090

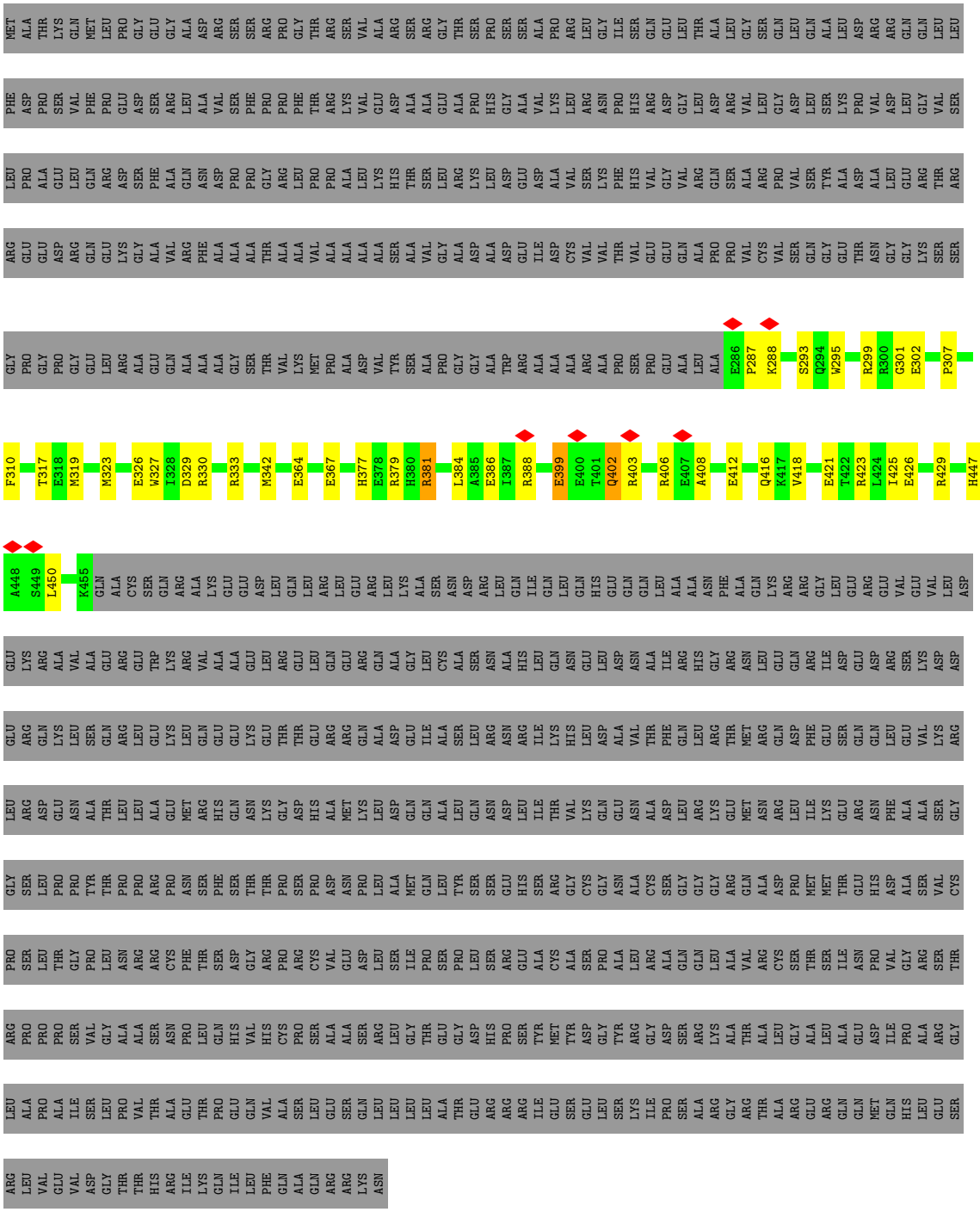
Chain F:





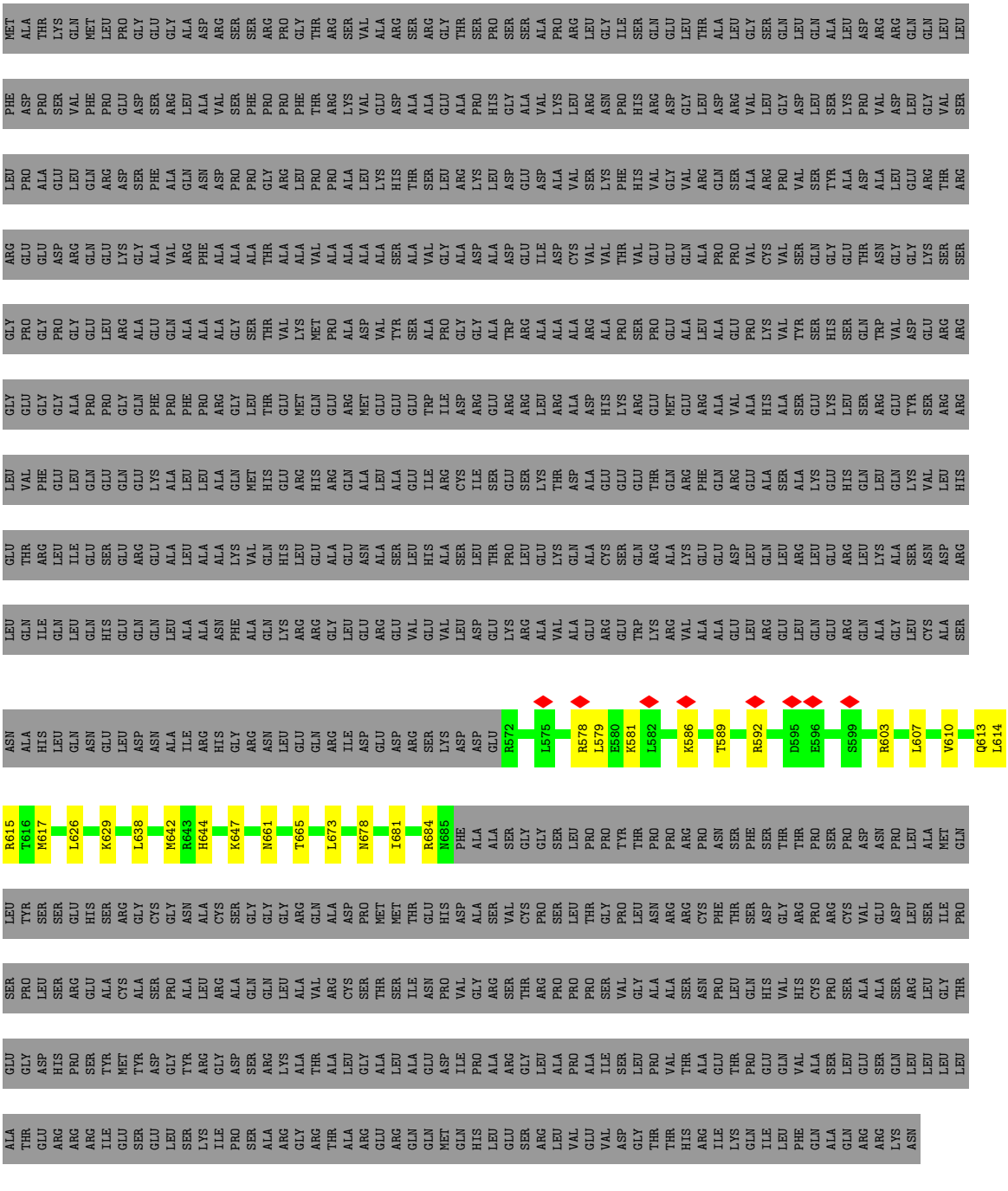
• Molecule 1: CF2, TGME49_258090

Chain G:



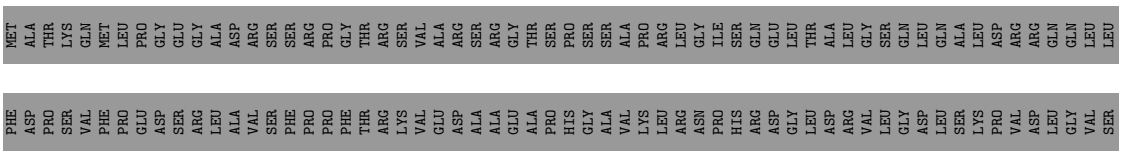
• Molecule 1: CF2, TGME49_258090

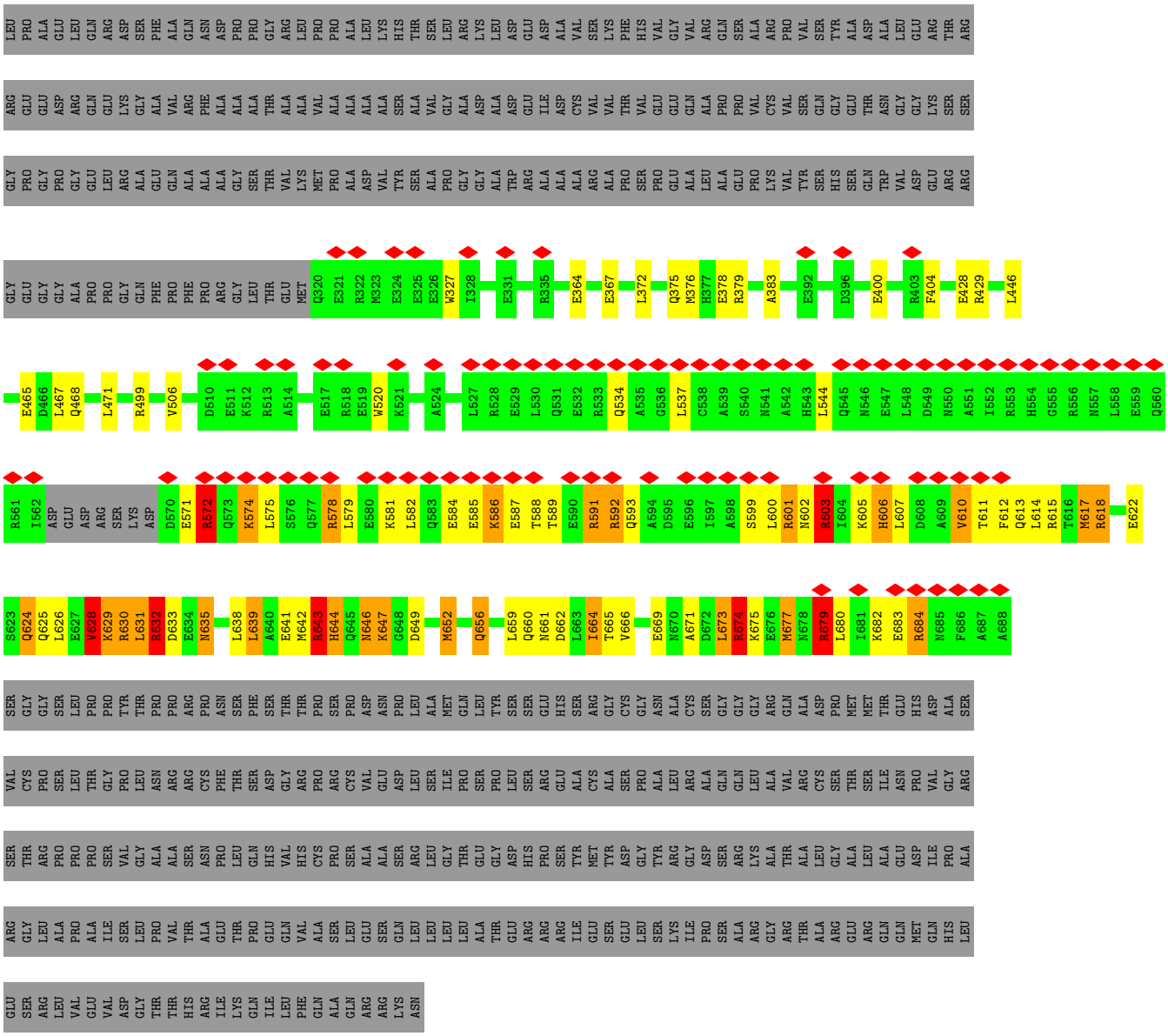
Chain H:



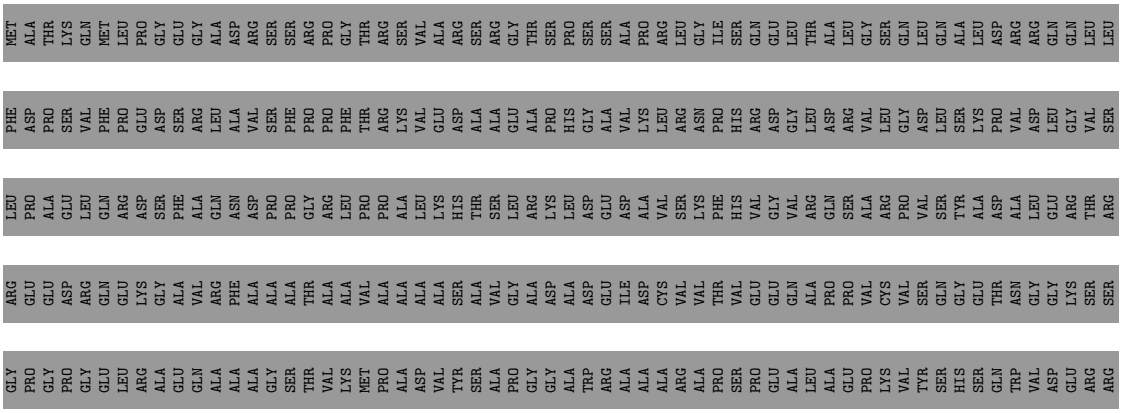
• Molecule 1: CF2, TGME49_258090

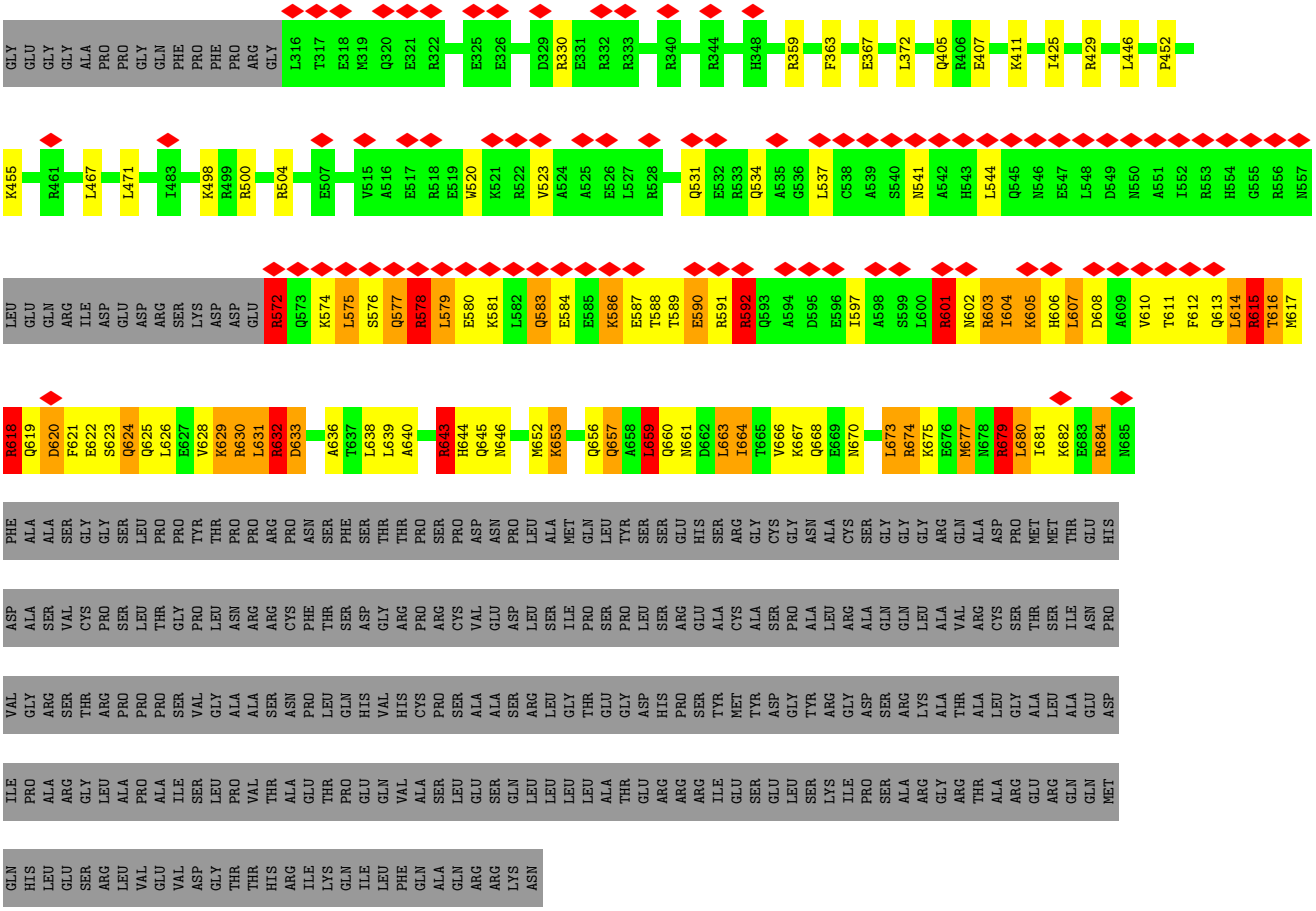
Chain I:





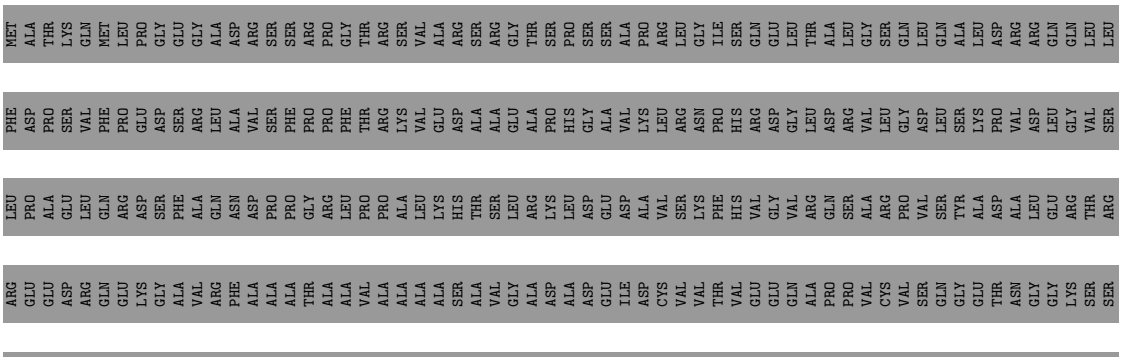
• Molecule 1: CF2, TGME49_258090

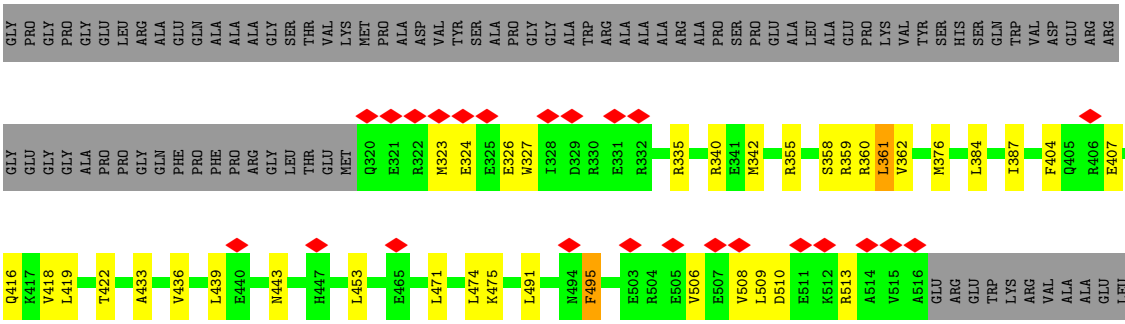




• Molecule 1: CF2, TGME49_258090

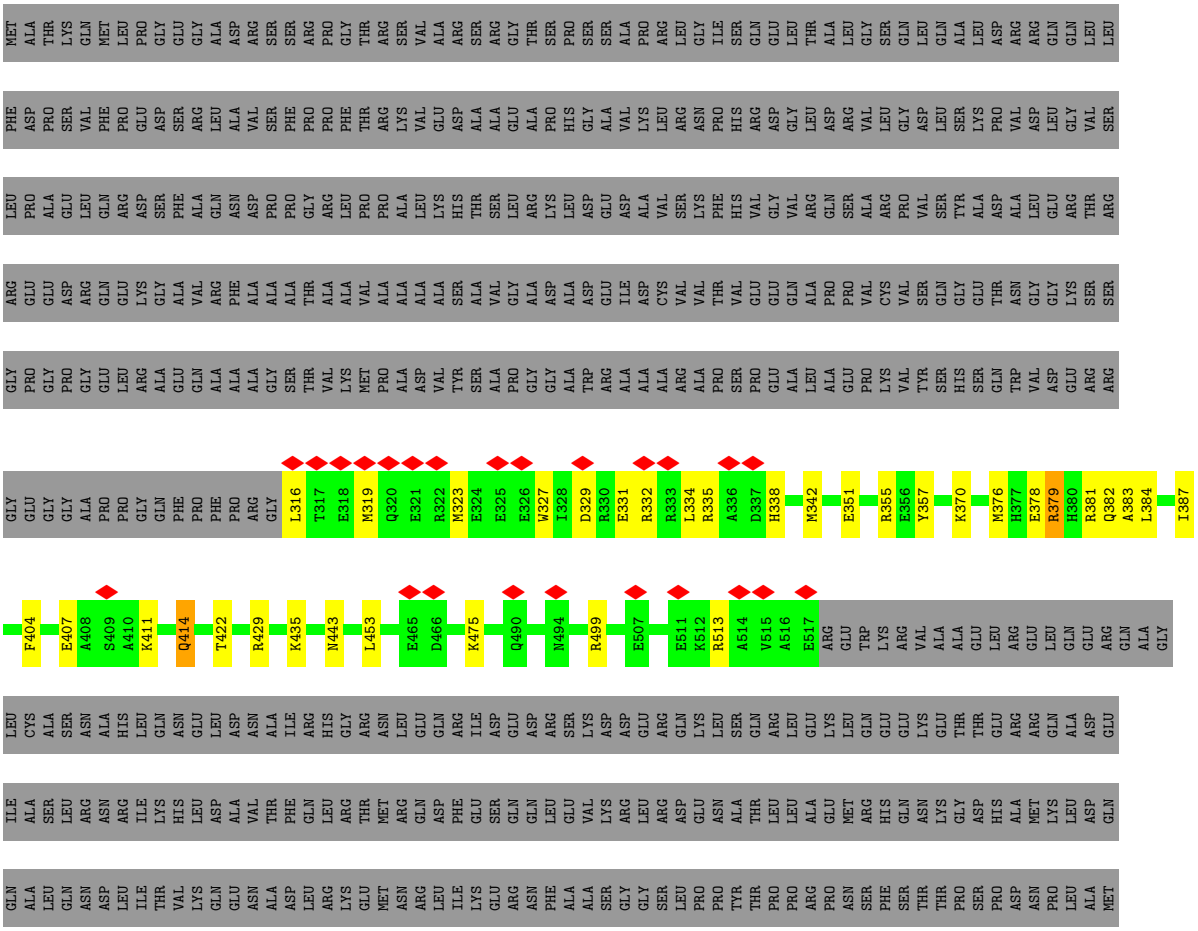
Chain K:

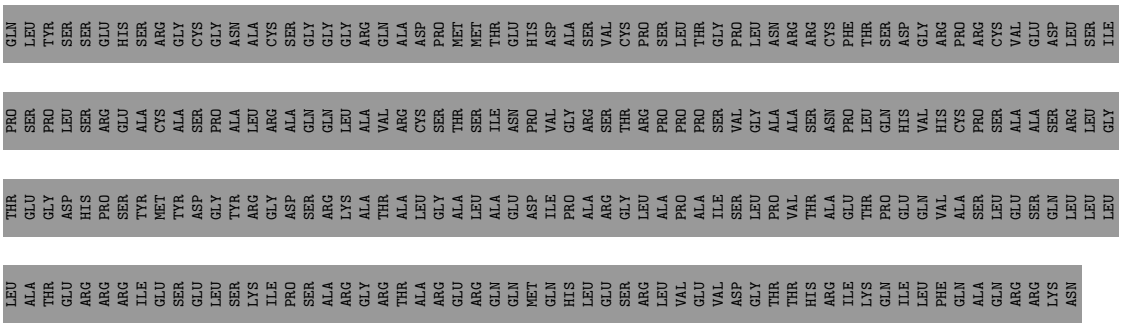




• Molecule 1: CF2, TGME49_258090

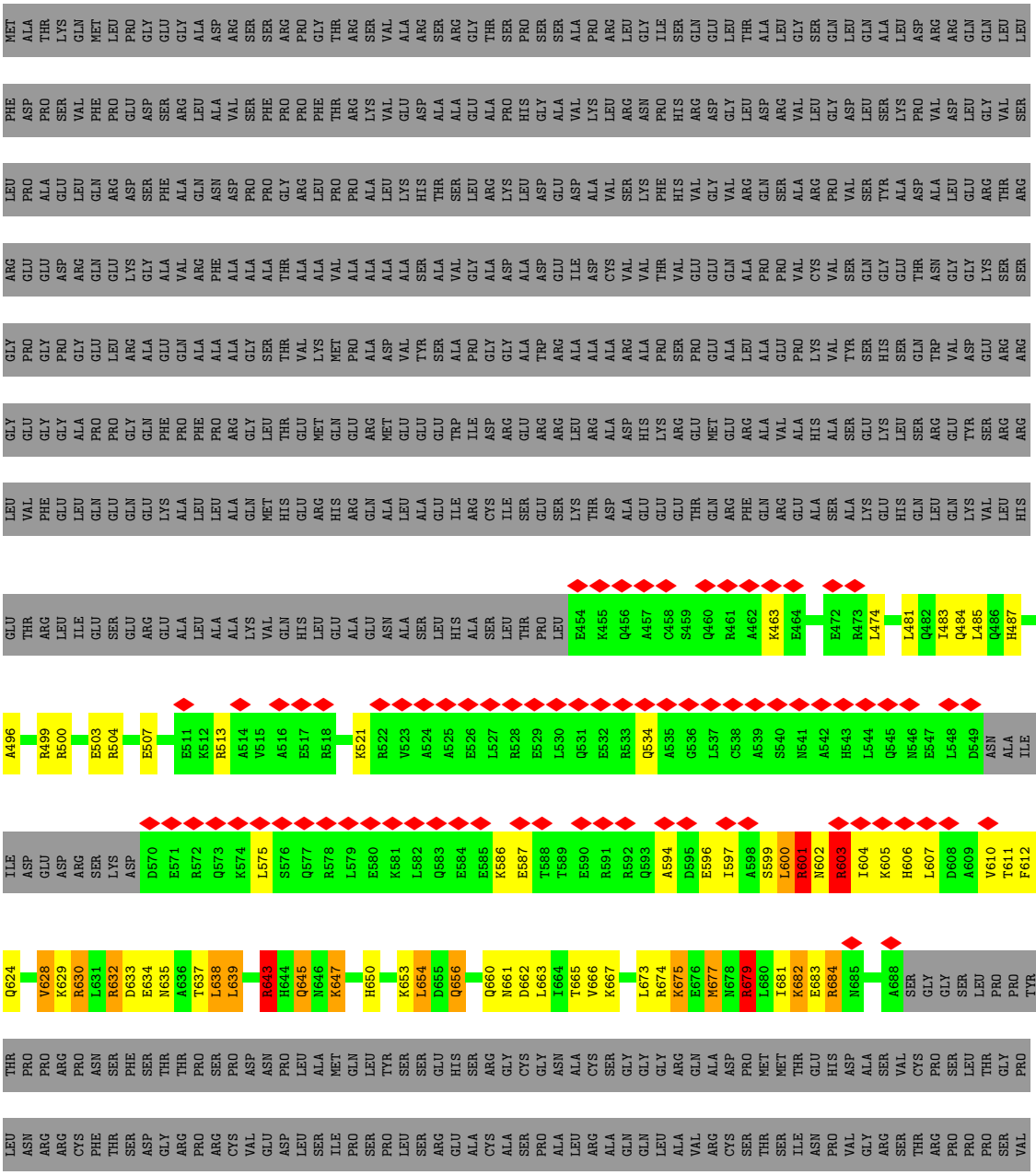
Chain L:

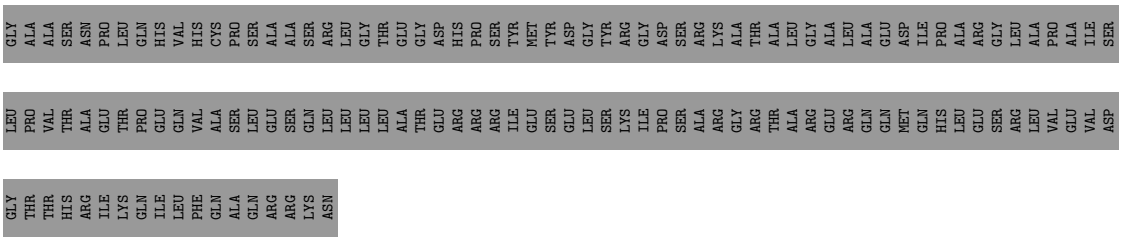


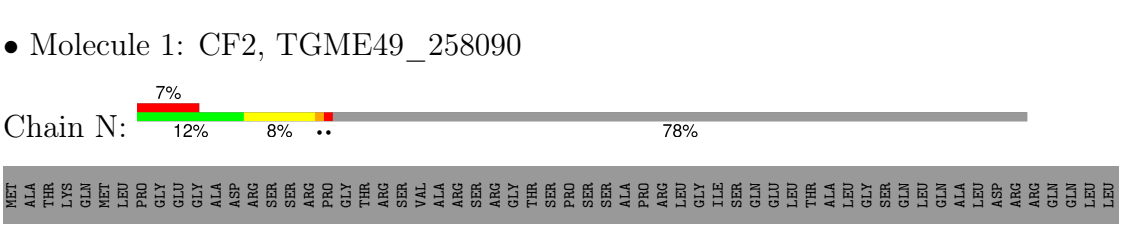


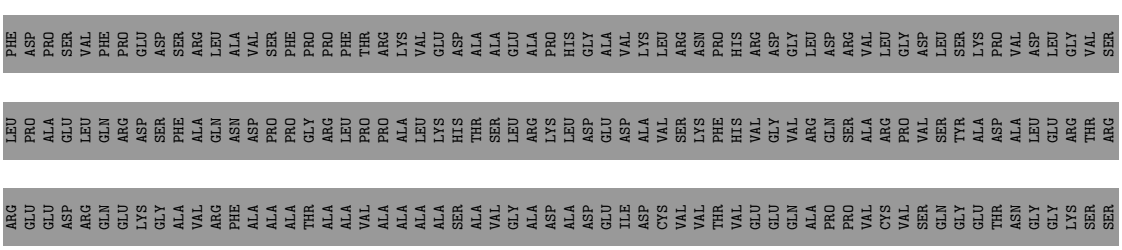
• Molecule 1: CF2, TGME49_258090

Chain M:



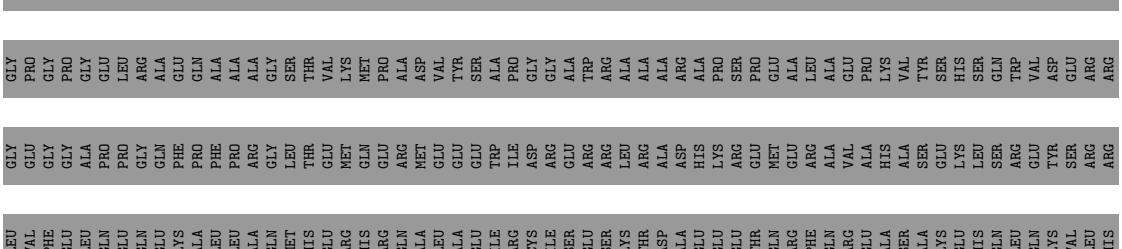


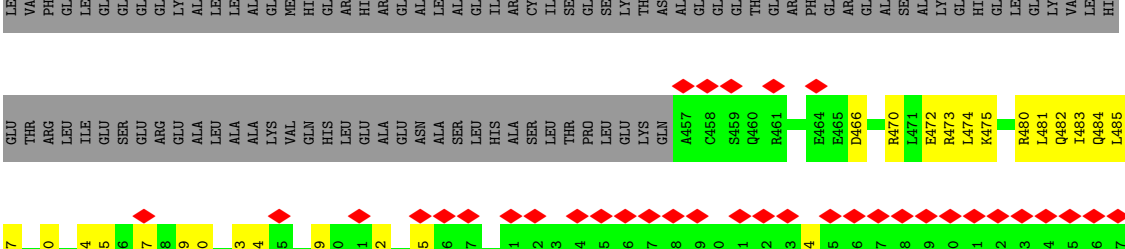


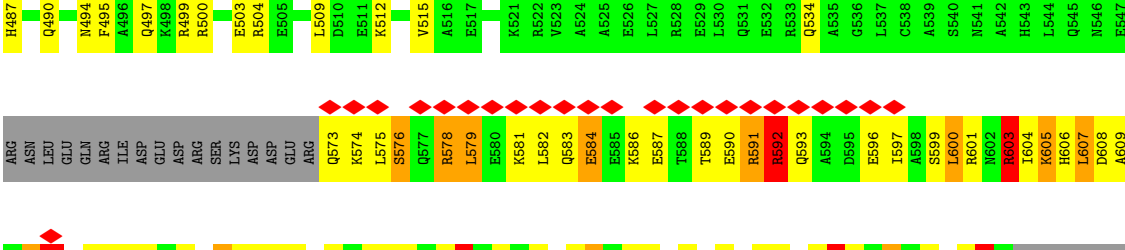


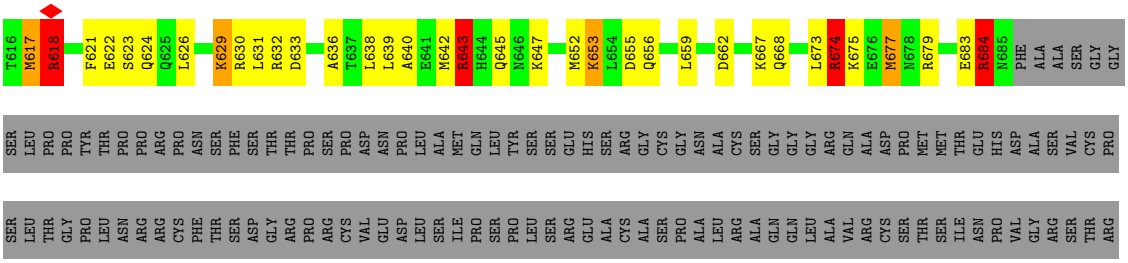
• Molecule 1: CF2, TGME49_258090

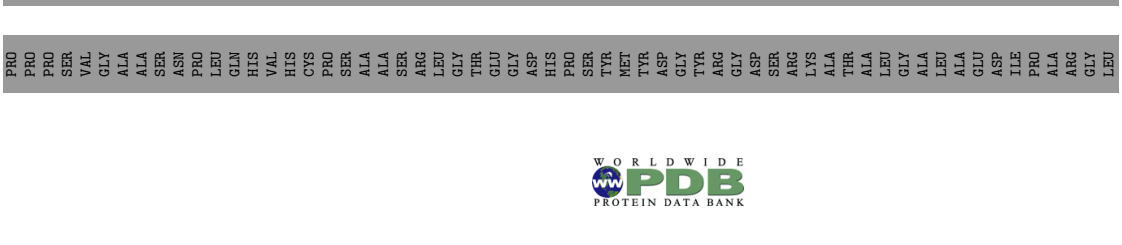
Chain N:

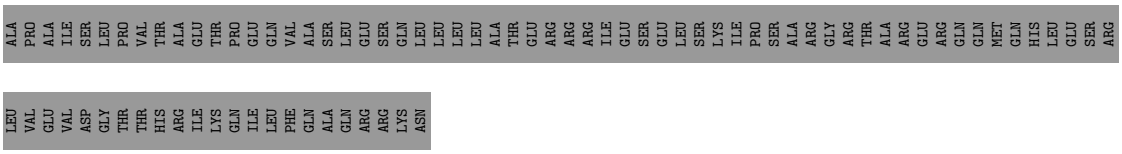






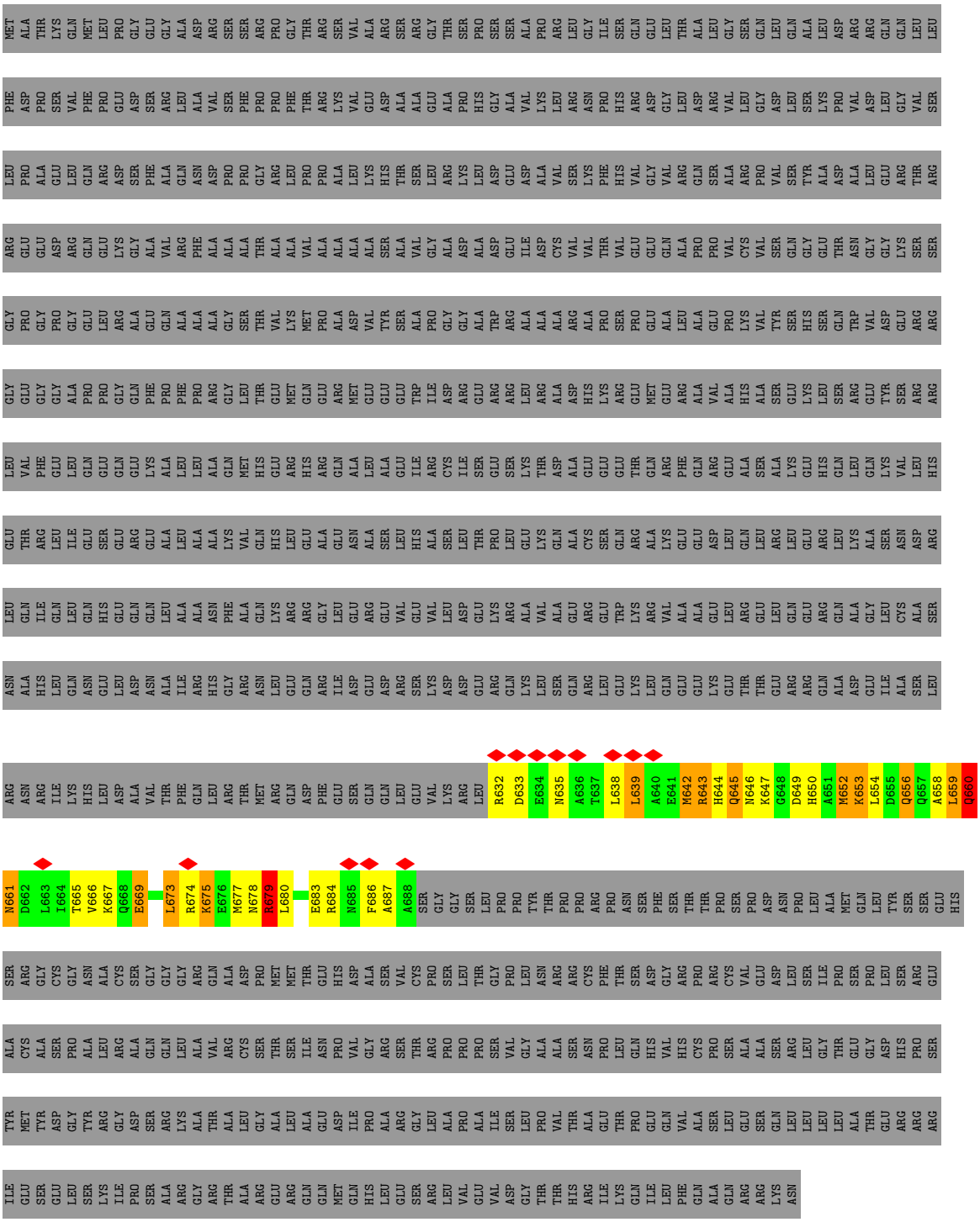






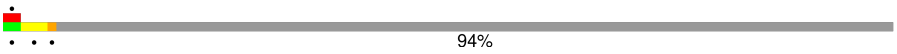
• Molecule 1: CF2, TGME49_258090

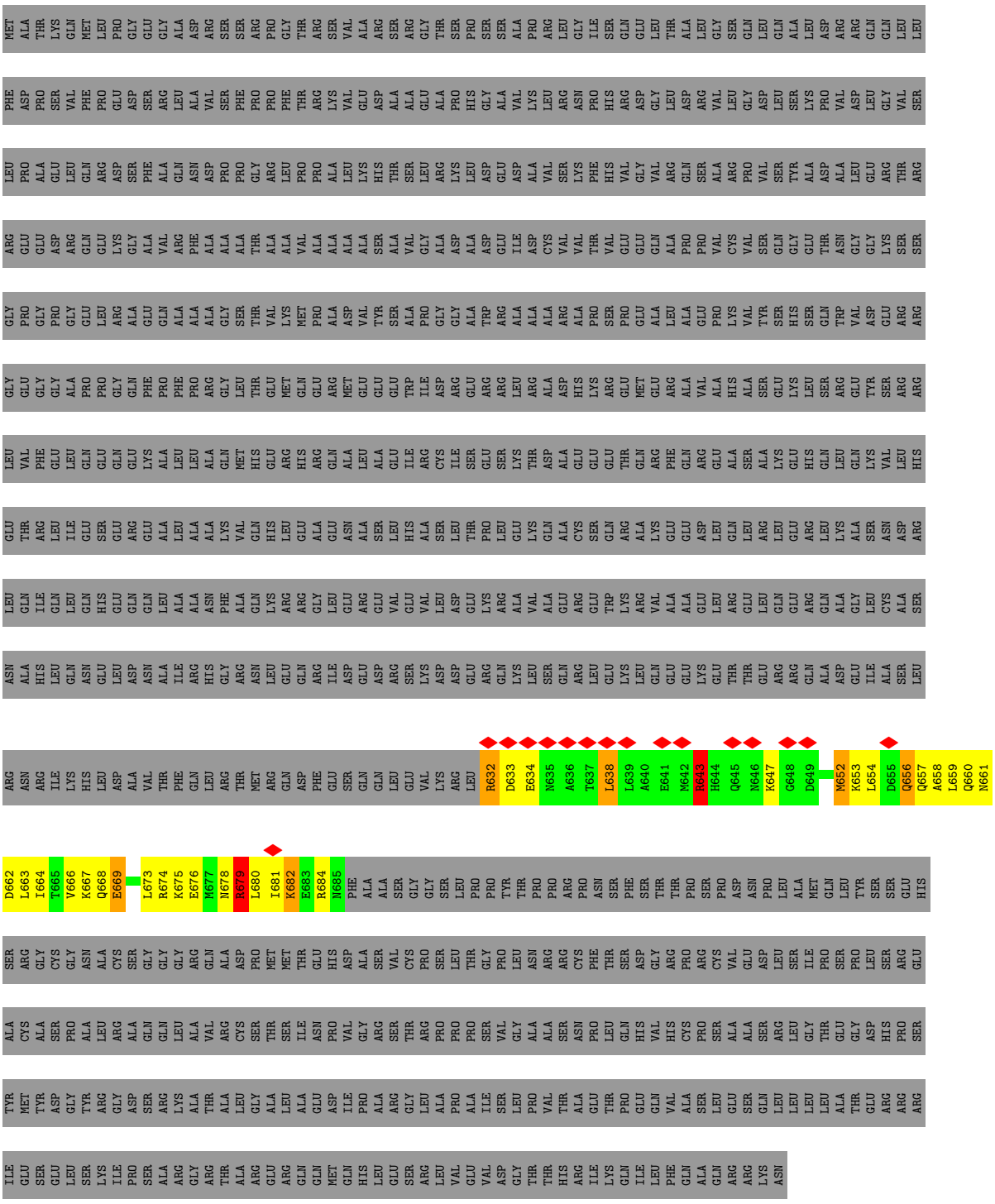
Chain O: 94%



• Molecule 1: CF2, TGME49_258090

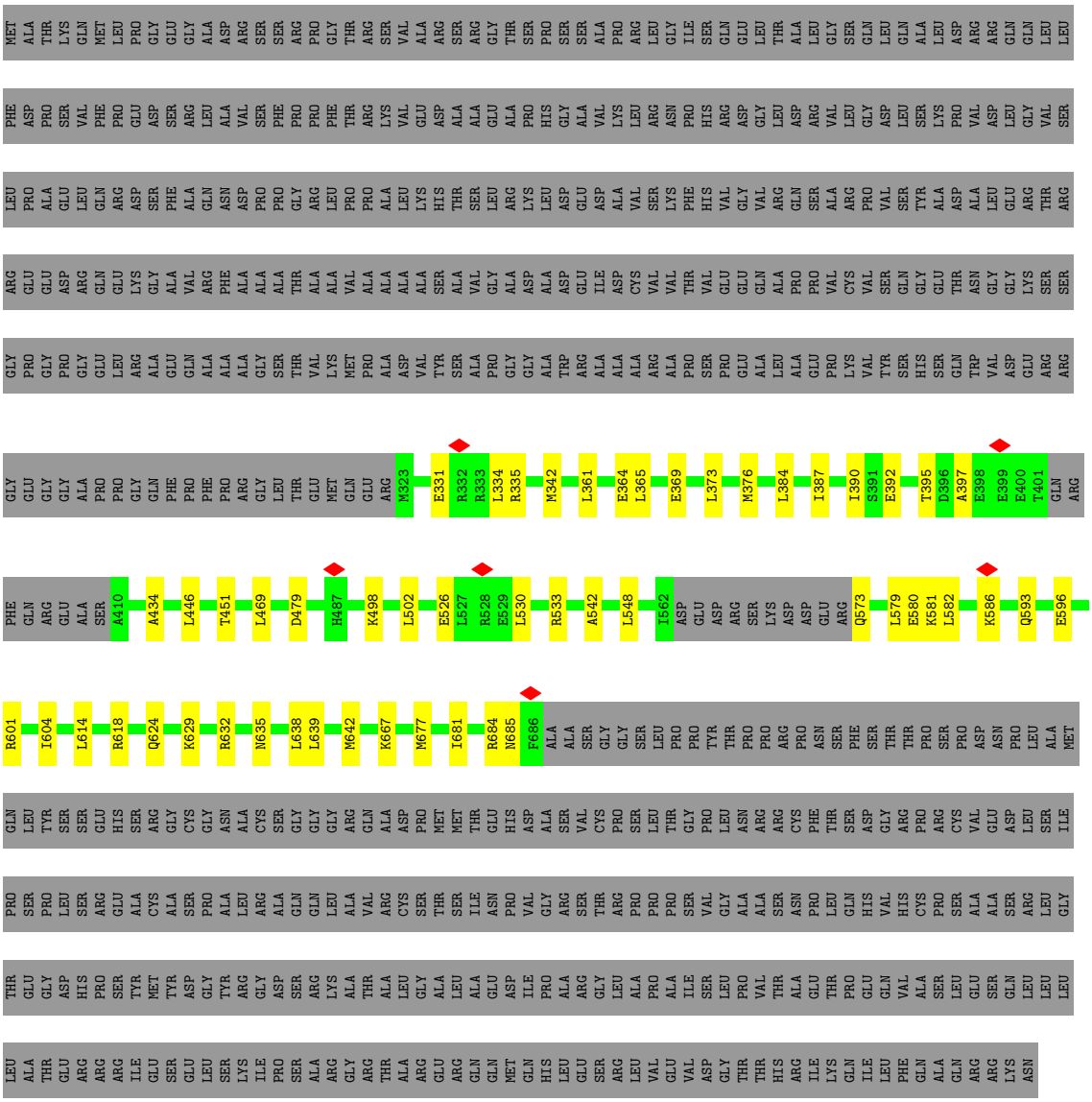
Chain P:





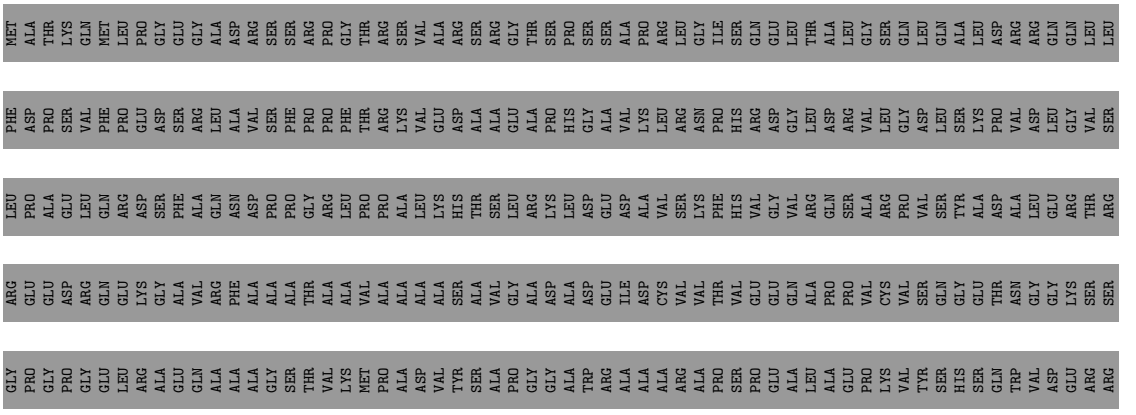
• Molecule 1: CF2, TGME49_258090

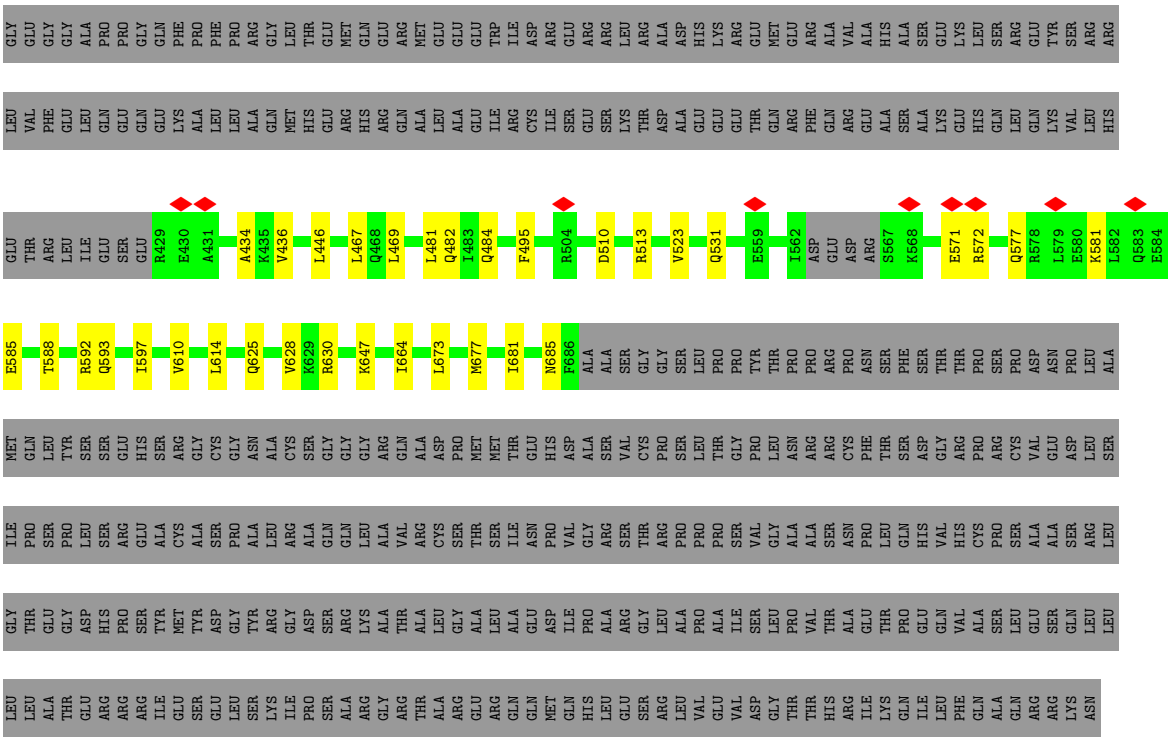
Chain Q:



• Molecule 1: CF2, TGME49_258090

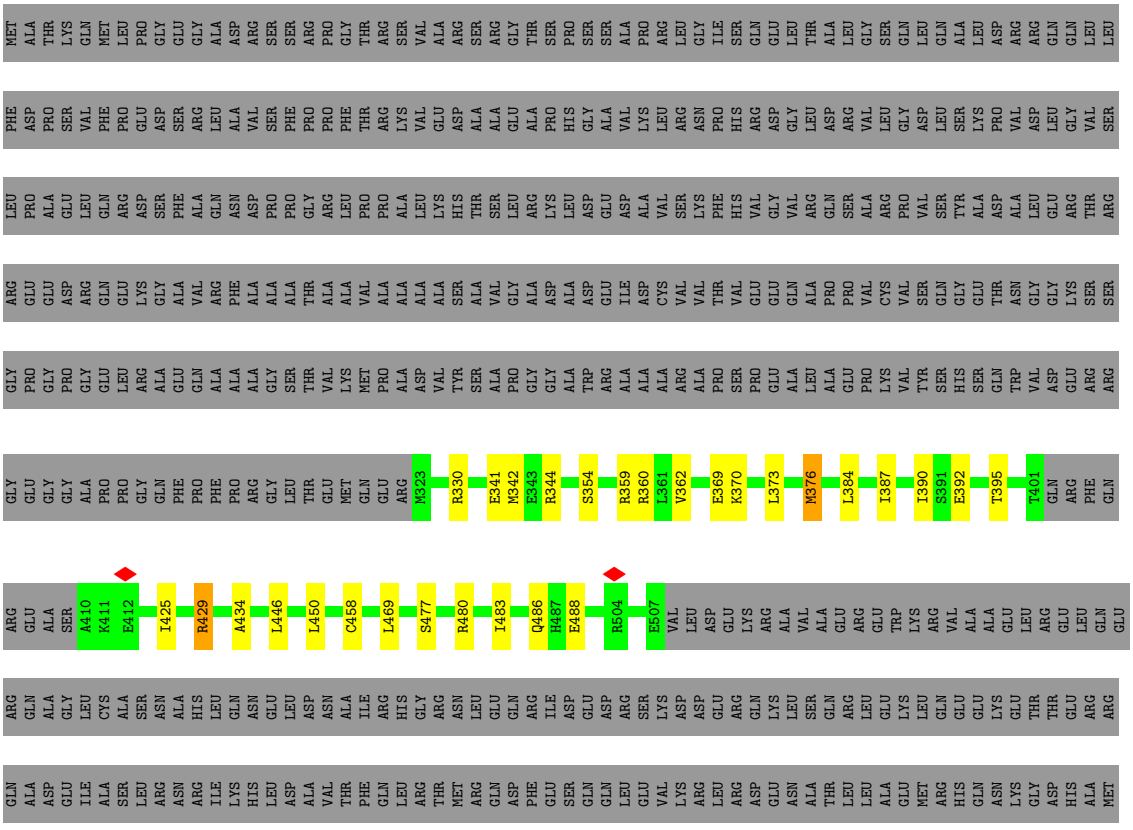
Chain R:

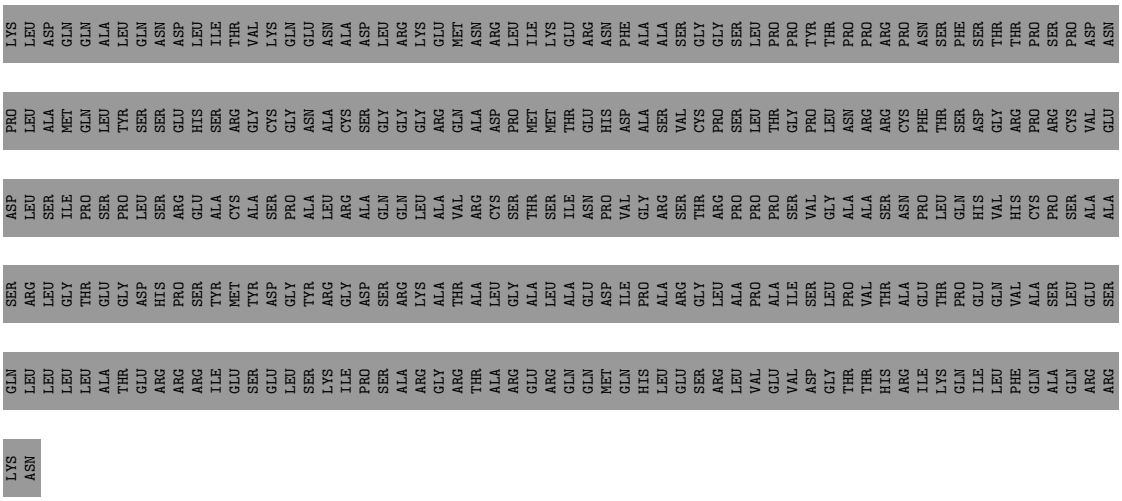




• Molecule 1: CF2, TGME49_258090

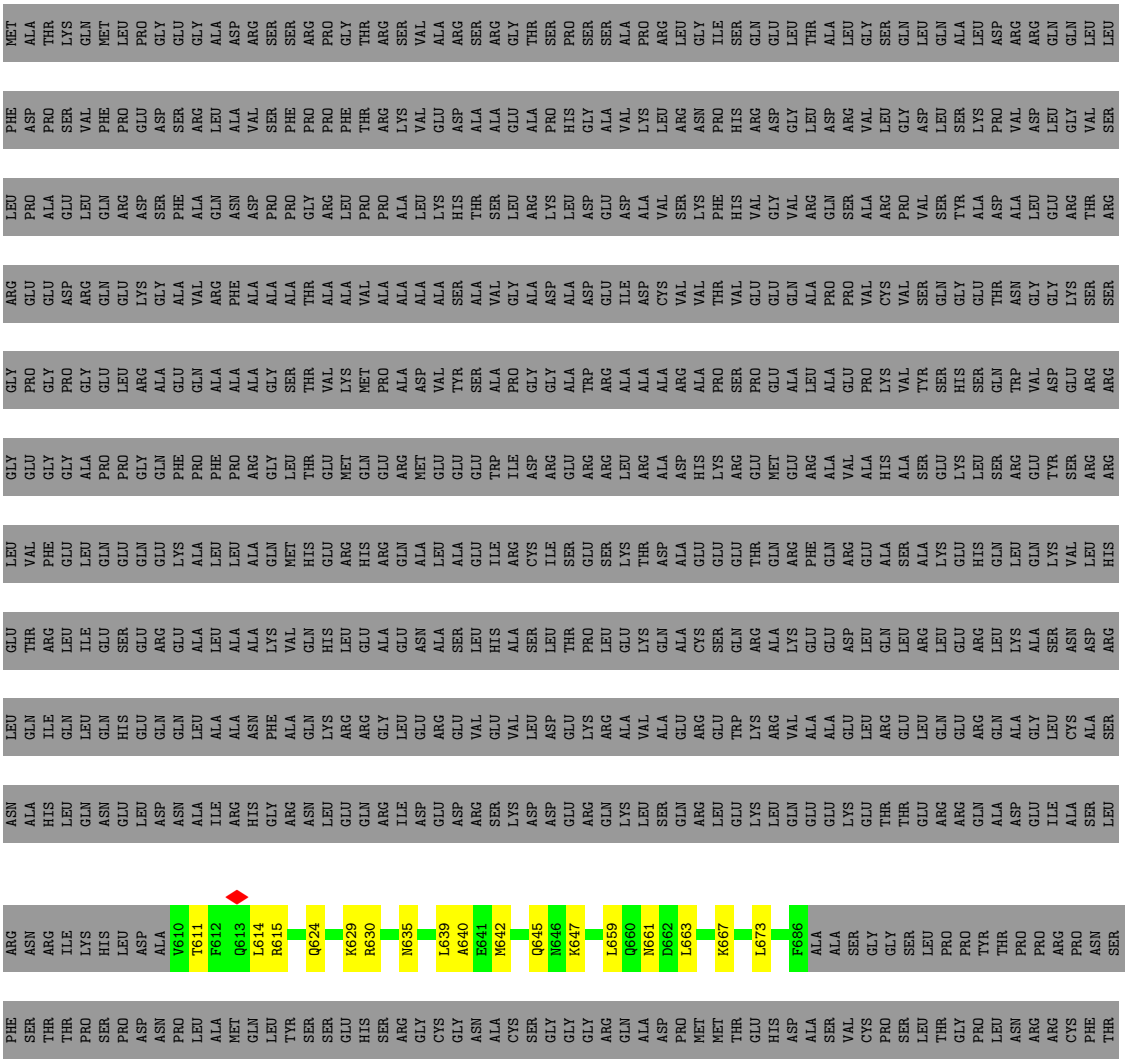
Chain S:

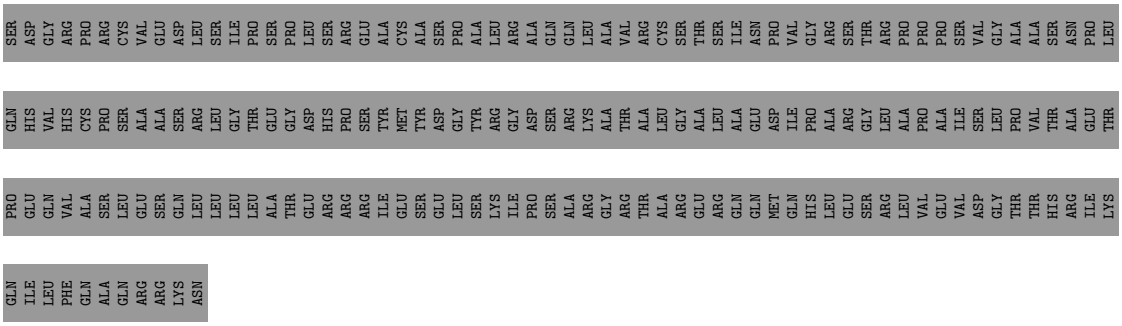




- Molecule 1: CF2, TGME49_258090

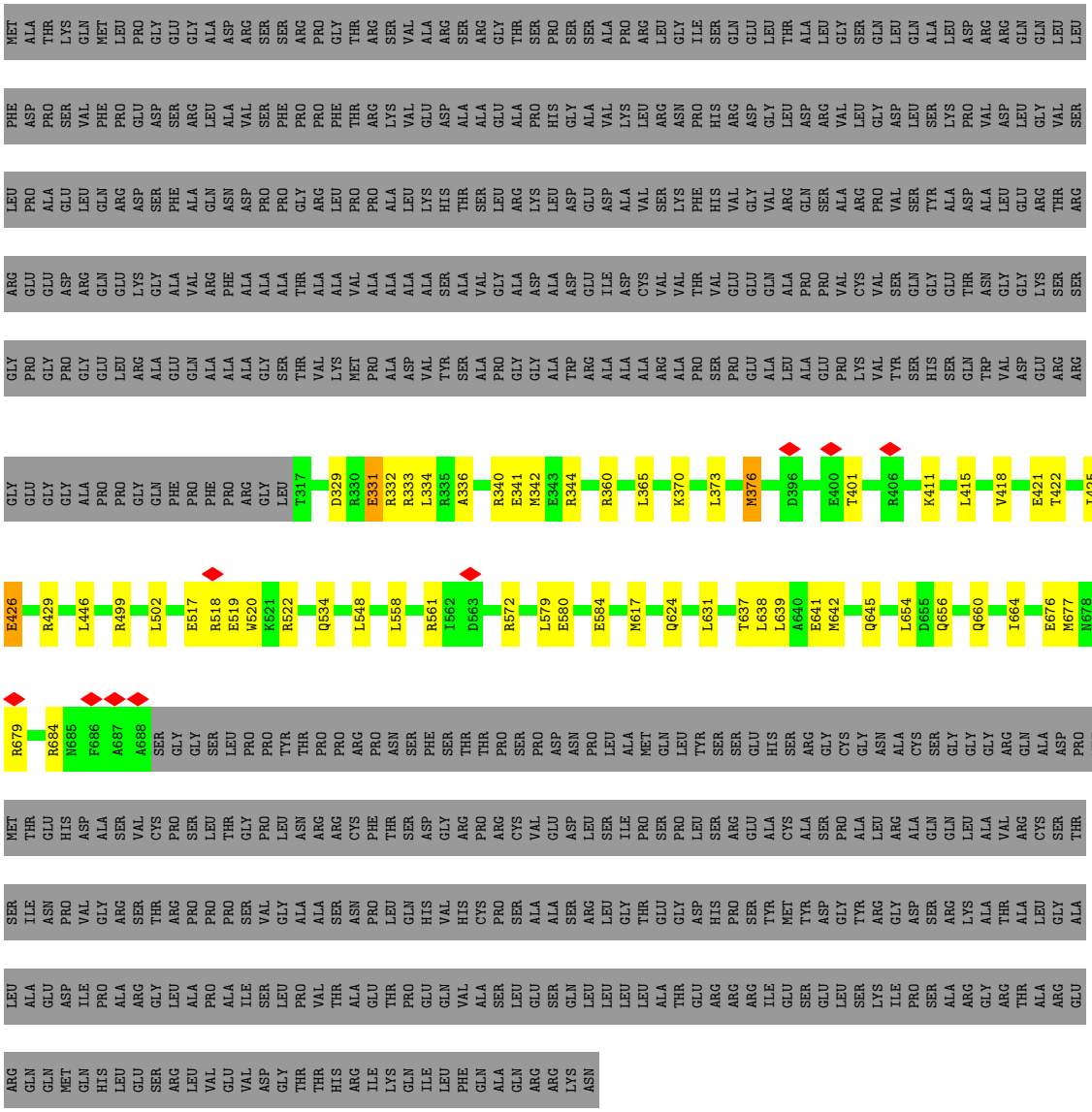
Chain T: 6% 92%





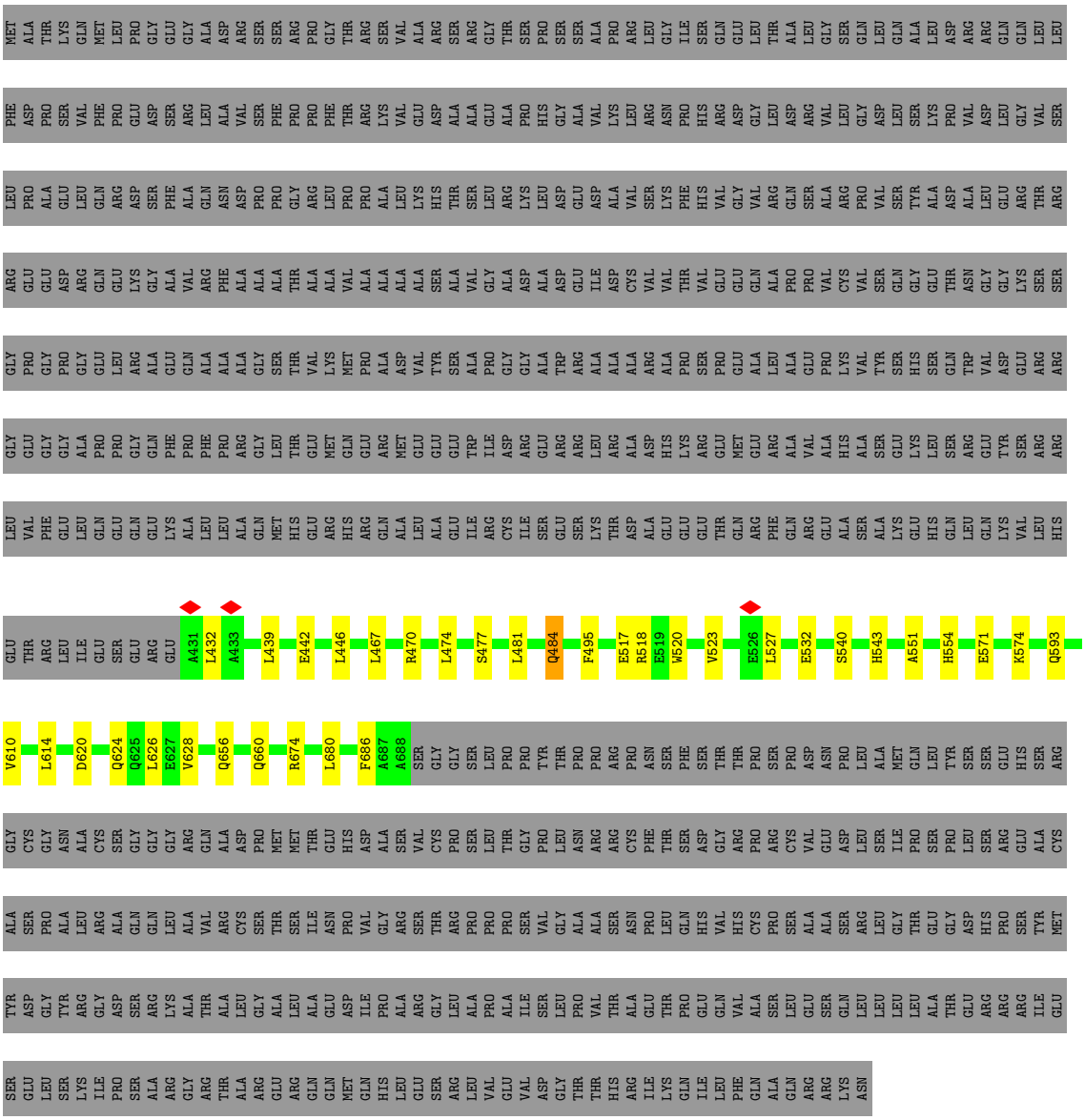
• Molecule 1: CF2, TGME49_258090

Chain U:



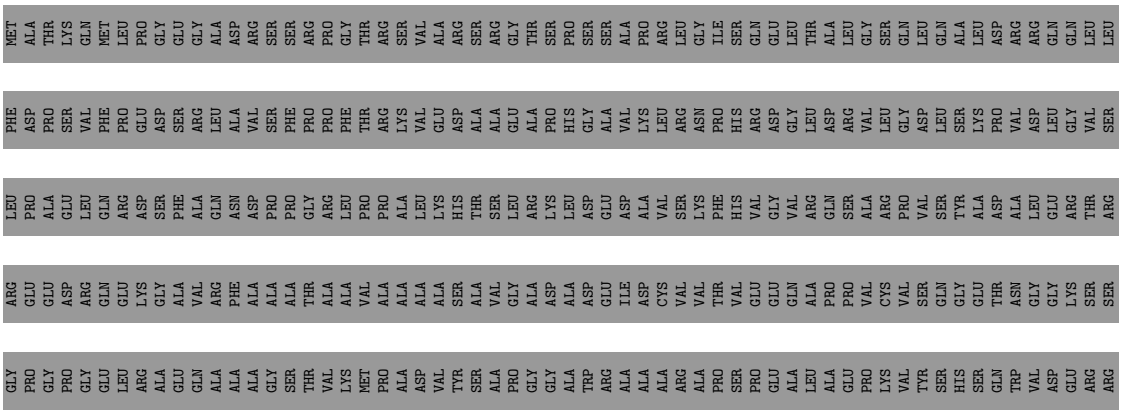
• Molecule 1: CF2, TGME49_258090

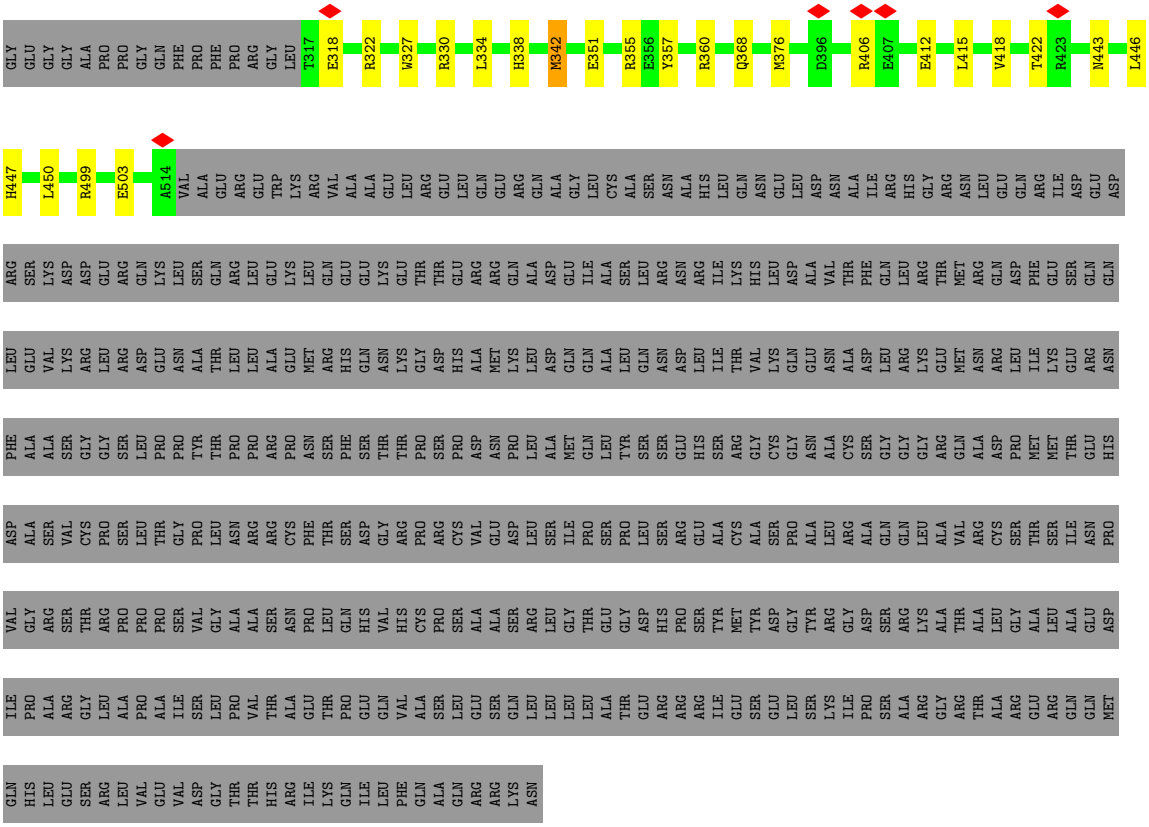
Chain V:



• Molecule 1: CF2, TGME49_258090

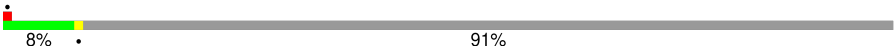
Chain W:

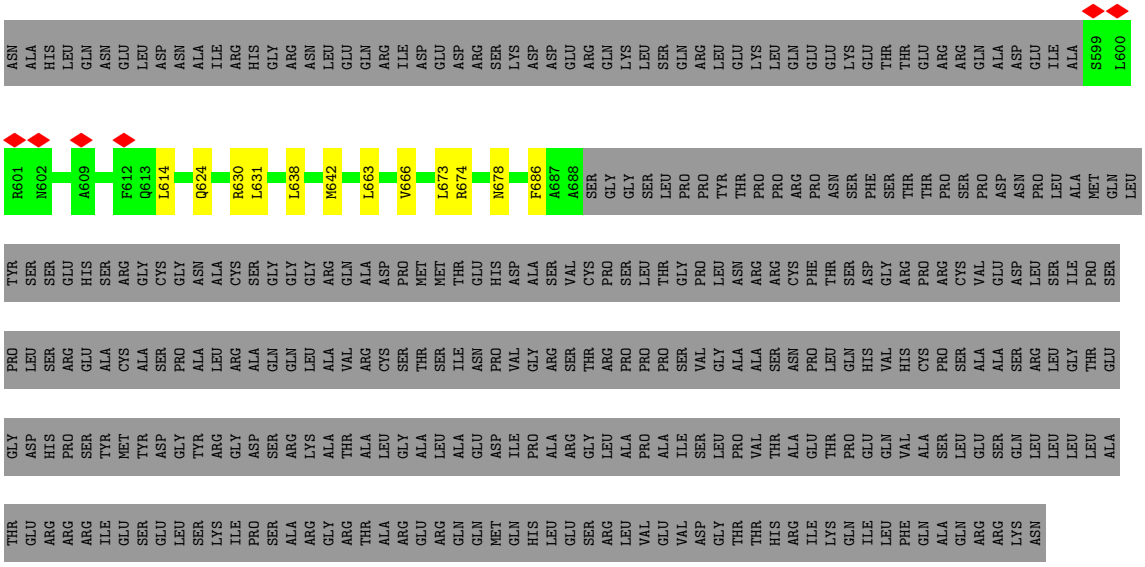




• Molecule 1: CF2, TGME49_258090

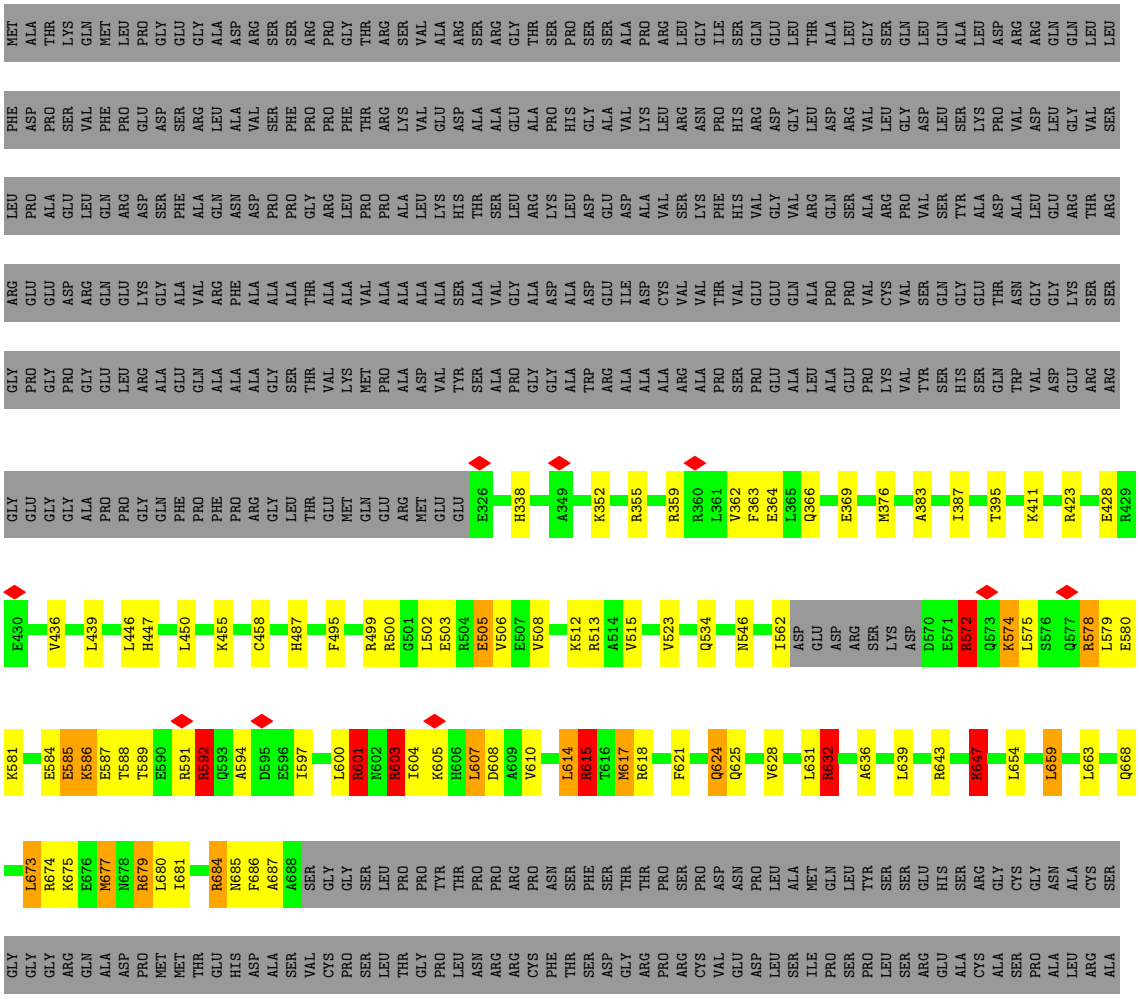
Chain X:

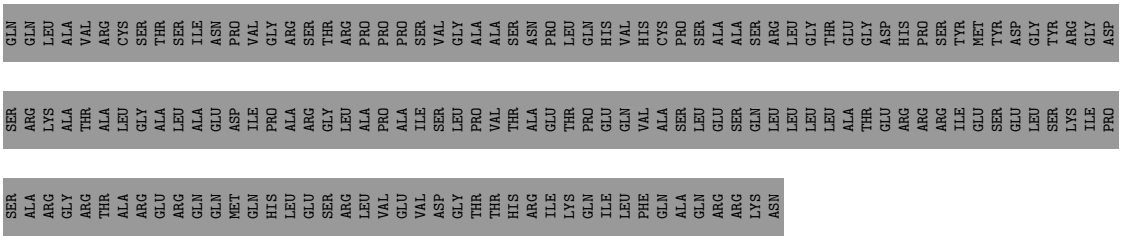




• Molecule 1: CF2, TGME49_258090

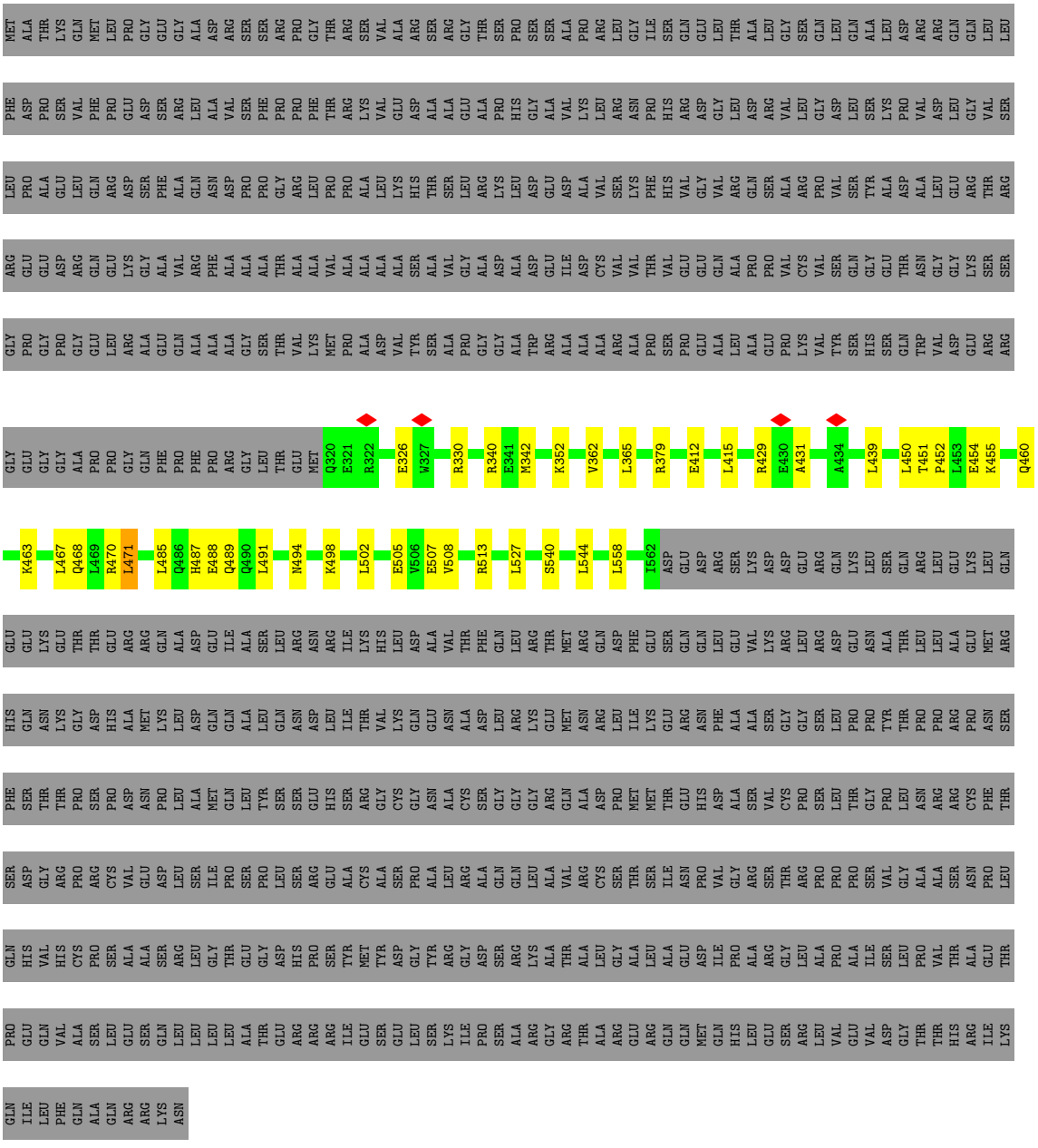
Chain Y:





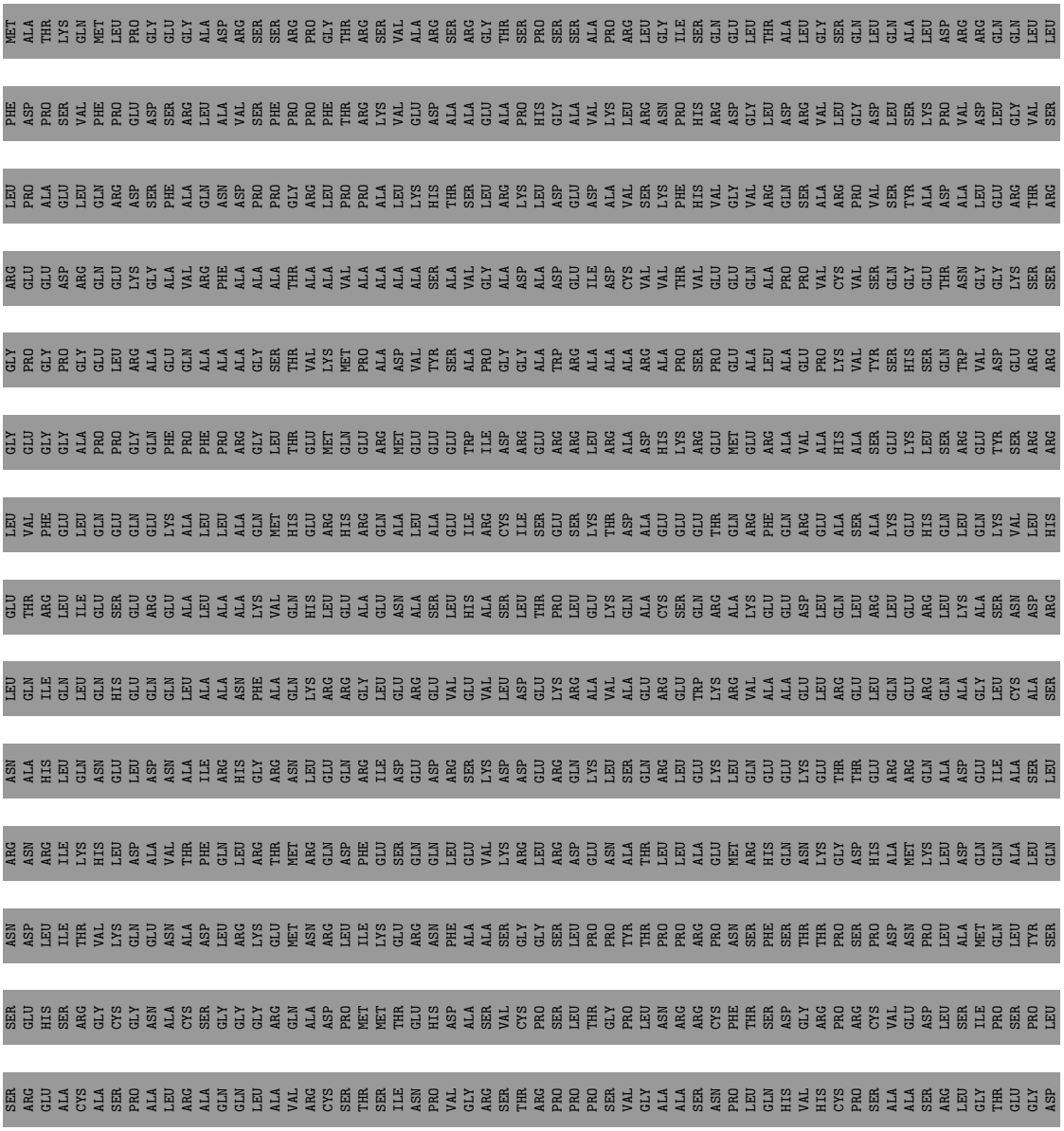
• Molecule 1: CF2, TGME49_258090

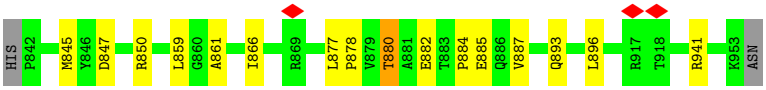
Chain Z:



• Molecule 1: CF2, TGME49_258090

Chain 1:





• Molecule 1: CF2, TGME49_258090

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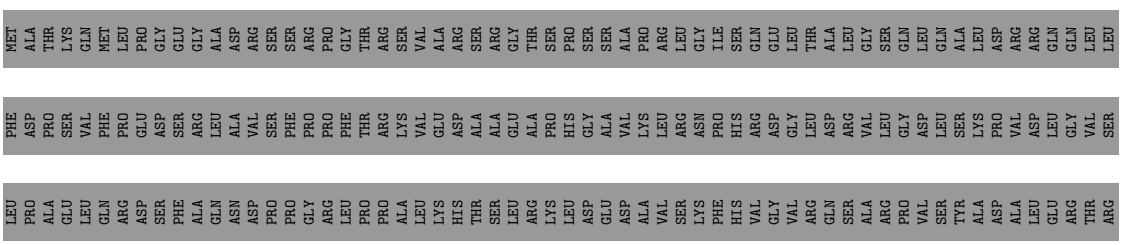
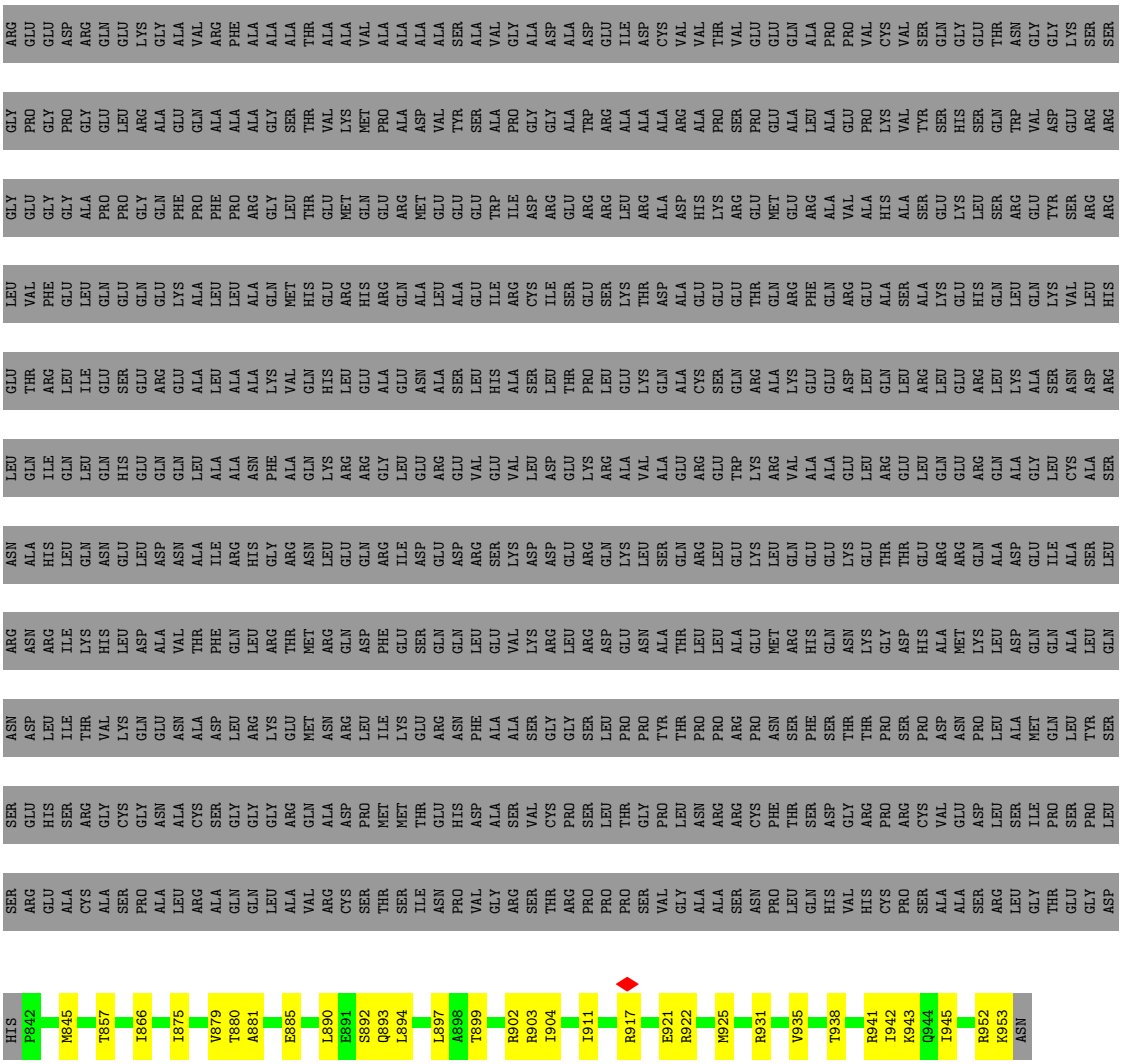
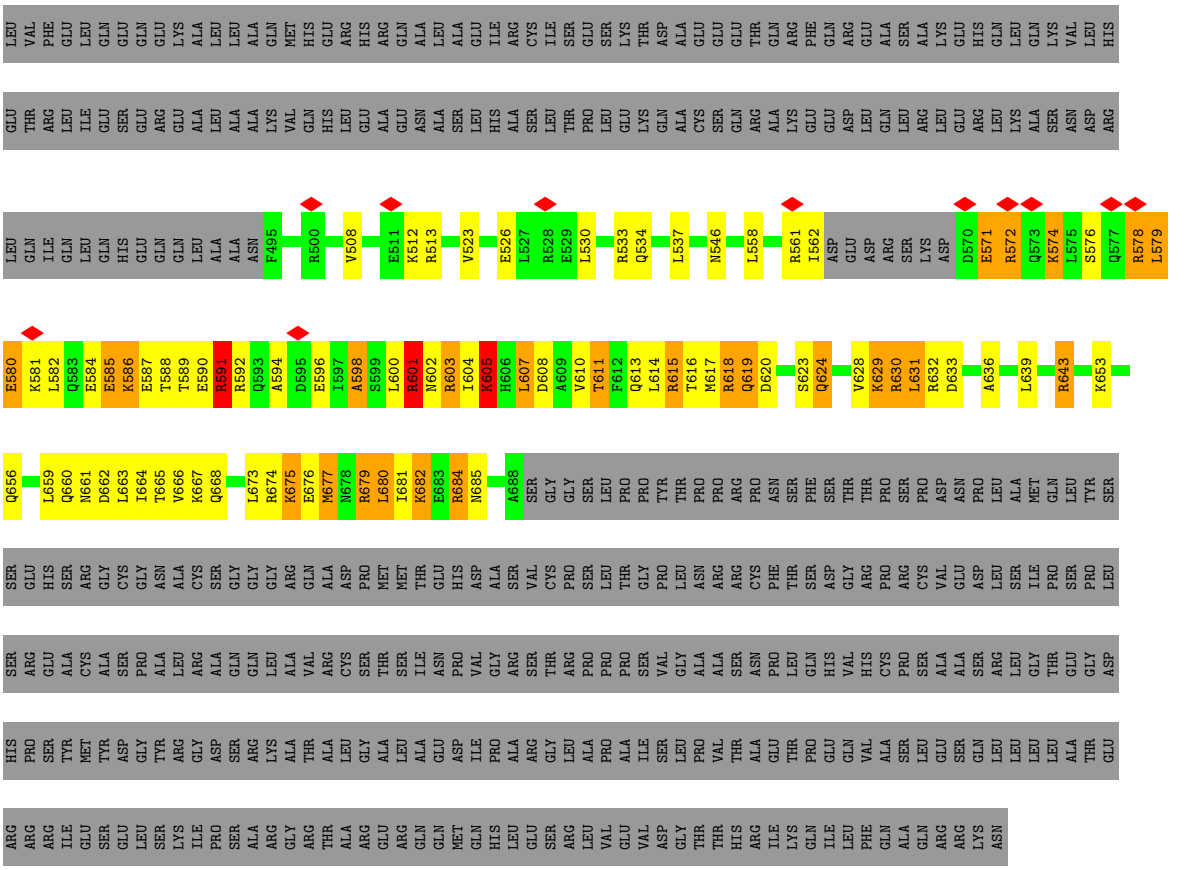




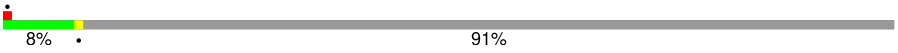
• Molecule 1: CF2, TGME49_258090

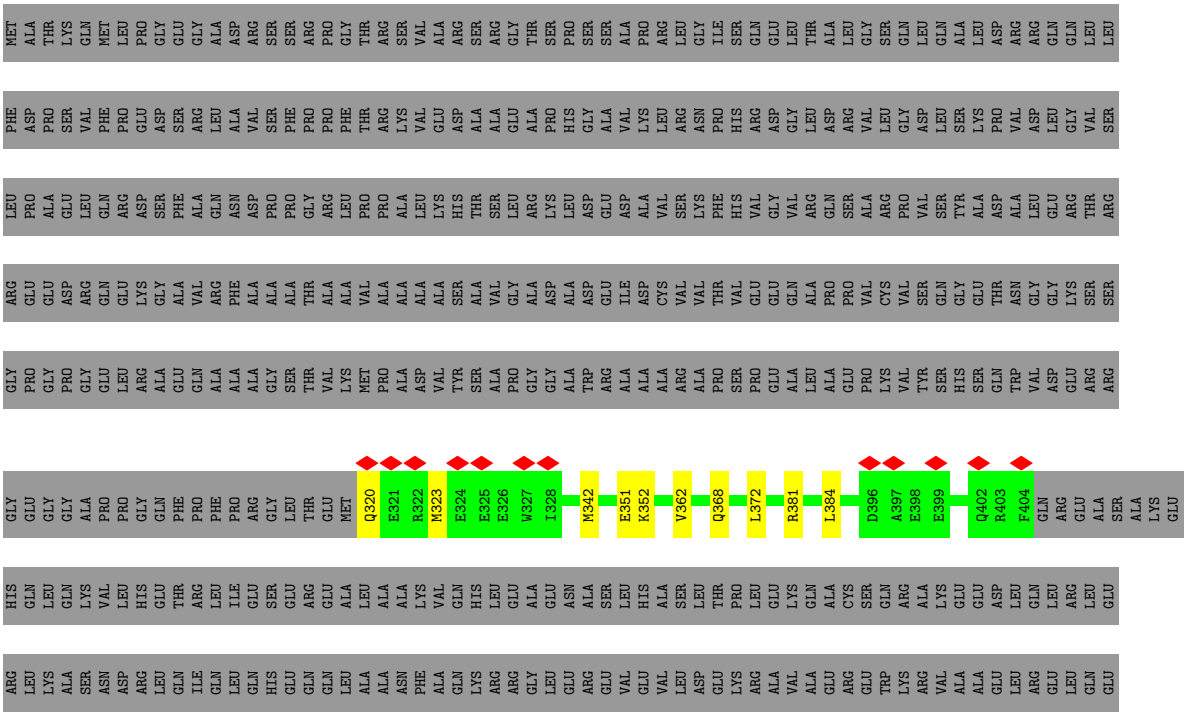
Chain a:



• Molecule 1: CF2, TGME49_258090

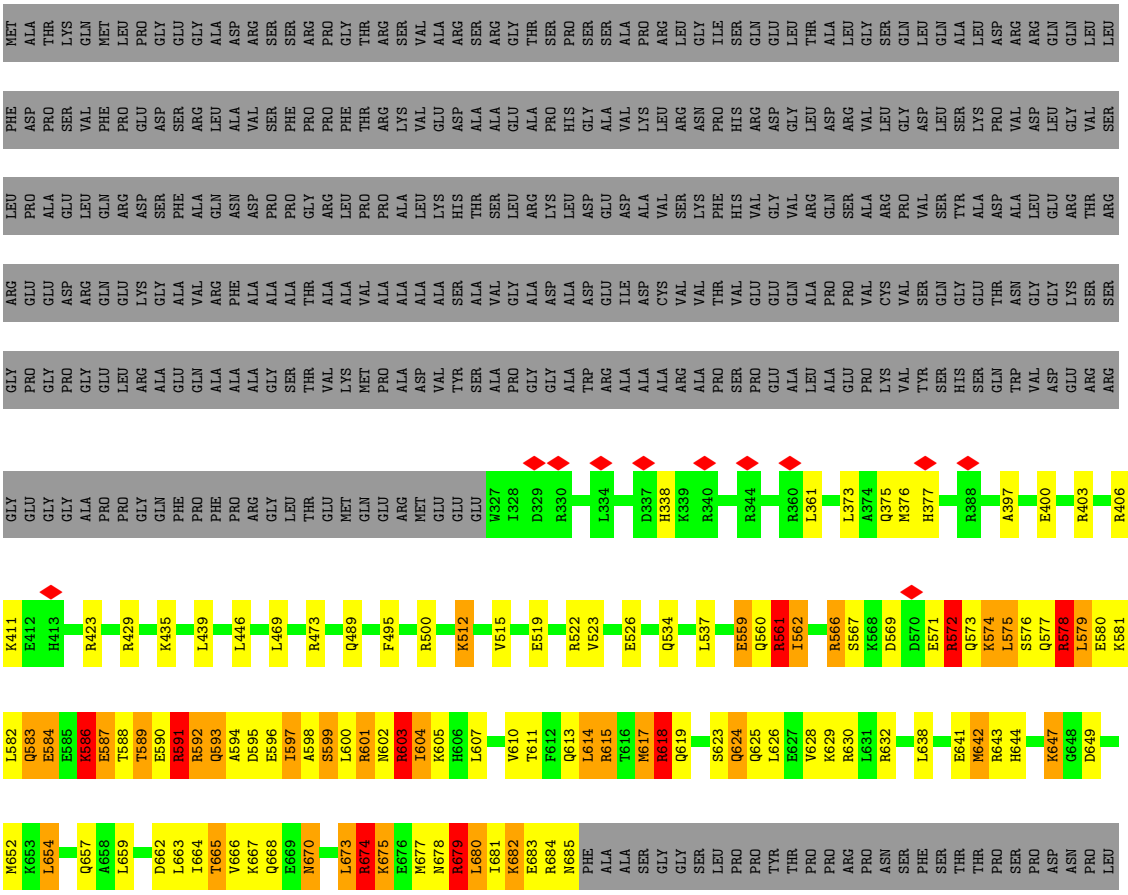
Chain b:

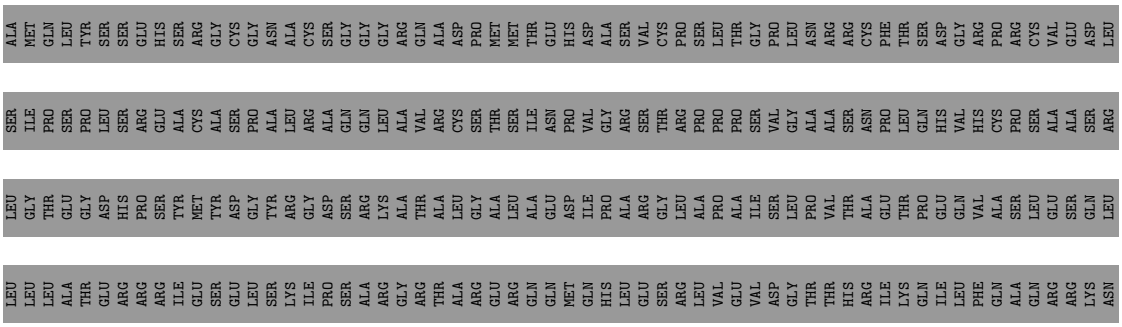




• Molecule 1: CF2, TGME49_258090

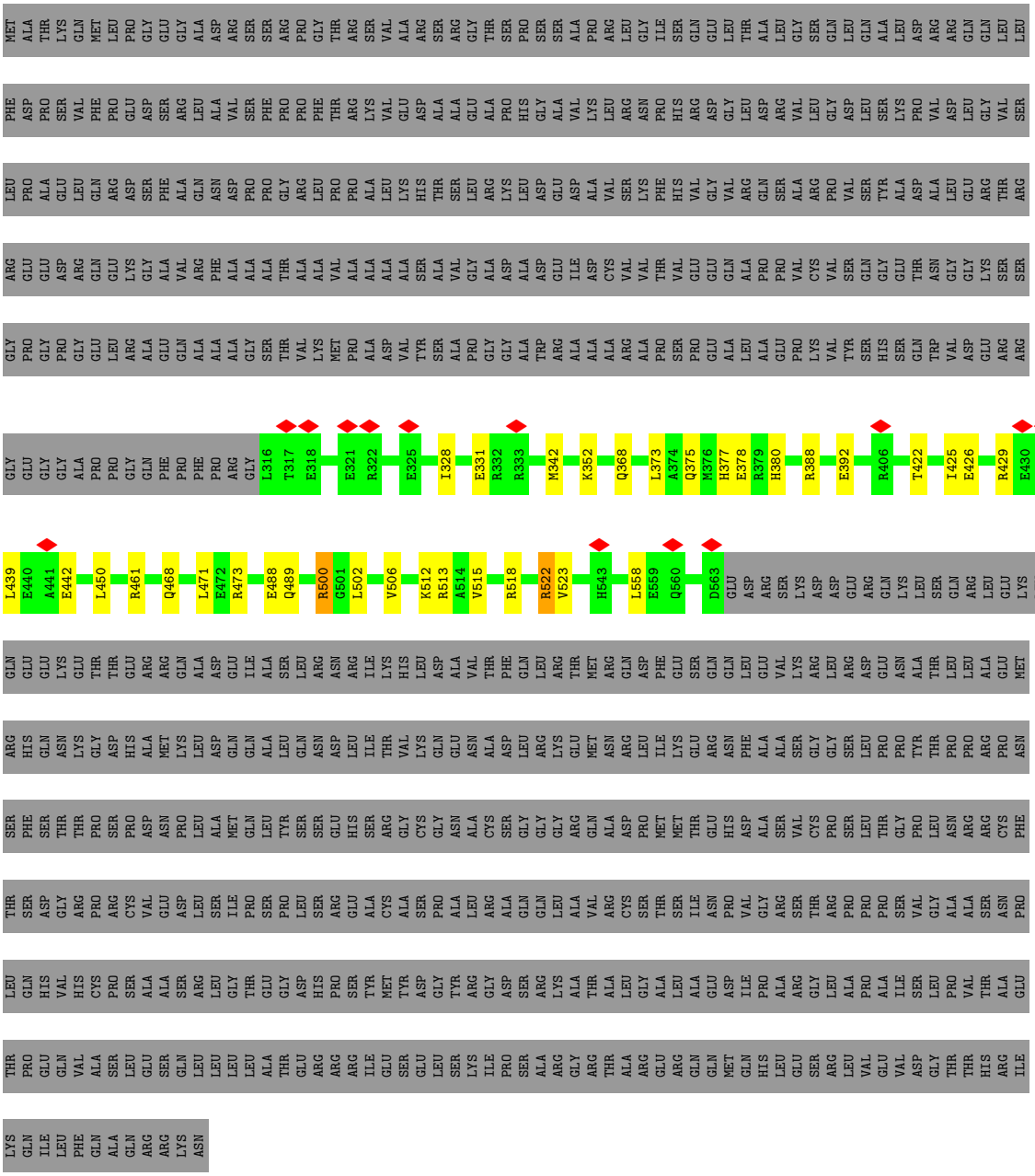
Chain c:





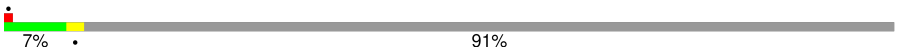
• Molecule 1: CF2, TGME49_258090

Chain d:



• Molecule 1: CF2, TGME49_258090

Chain e:



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PHE ASP PRO SER VAL PHE PRO GLU ASP SER ARG LEU ALA VAL SER PHE PRO PRO PHE THR ARG LYS VAL GLU ASP ALA ALA GLU ALA PRO HIS GLY ALA VAL LYS LEU ARG ASN PRO HIS ARG ASP GLY LEU ASP ARG VAL LEU GLY ASP LEU SER LYS PRO VAL ASP LEU GLY VAL SER
LEU PRO ALA GLU LEU GLN ARG ASP SER PHE ALA GLN ASN ASP PRO PRO GLY ARG LEU PRO PRO ALA LEU LYS HIS THR SER LEU ARG LYS LEU ASP GLU ASP ALA VAL SER LYS PHE HIS VAL GLY VAL ARG GLN SER ALA ARG PRO VAL SER TYR ALA ASP ALA LEU GLU ARG THR ARG
ARG GLU GLU ASP ARG GLN GLU LYS GLY ALA VAL ARG PHE ALA ALA ALA ALA THR ALA ALA VAL ALA ALA ALA ALA SER ALA VAL GLY ALA GLU ASP ALA ASP GLU ILE ASP CYS VAL SER VAL THR VAL GLU GLU GLN ALA PRO PRO VAL CYS VAL SER GLN GLY GLU THR ASN GLY GLY LYS SER SER
GLY PRO GLY PRO GLY GLU LEU ARG ALA GLU GLN ALA ALA ALA GLY SER THR VAL LYS MET PRO ALA ASP VAL TYR SER ALA PRO GLY GLY ALA TRP ARG ALA ALA ALA ARG ALA PRO SER PRO GLU ALA LEU ALA GLU PRO LYS VAL TYR SER HIS SER GLN TRP VAL ASP GLU ARG ARG

GLY GLU GLY GLY ALA PRO PRO GLY GLN PHE PRO PHE PRO ARG GLY L316 T317 E318 E321 R322 R332 H338 M342 E356 R359 L365 Q366 E367 Q375 M376 H377 E378 R379 H380 R381 R388 E392 T395 E398 E399 E400 THR GLN ARG PHE GLN ARG GLU

ALA SER ALA LYS GLU HIS GLN LEU GLN LYS VAL LEU HIS GLU GLU THR ARG LEU ILE GLU SER GLU ARG GLU ALA LEU ALA ALA LYS VAL GLN HIS LEU GLU GLU ALA GLU ASN ALA SER LEU HIS ALA SER LEU THR PRO LEU GLU GLU LYS GLN ALA CYS SER GLN GLU ALA GLU ASP LEU
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PRO SER PRO ASP ASN PRO LEU ALA MET GLN LEU TYR SER SER GLU HIS SER ARG GLY CYS GLY ASN ALA CYS SER GLY GLY GLY GLY ARG GLN ALA ASP PRO MET MET THR GLU HIS ASP ALA ALA SER VAL CYS PRO SER LEU THR GLY PRO LEU ASN ARG ARG CYS PHE THR SER ASP GLY ARG
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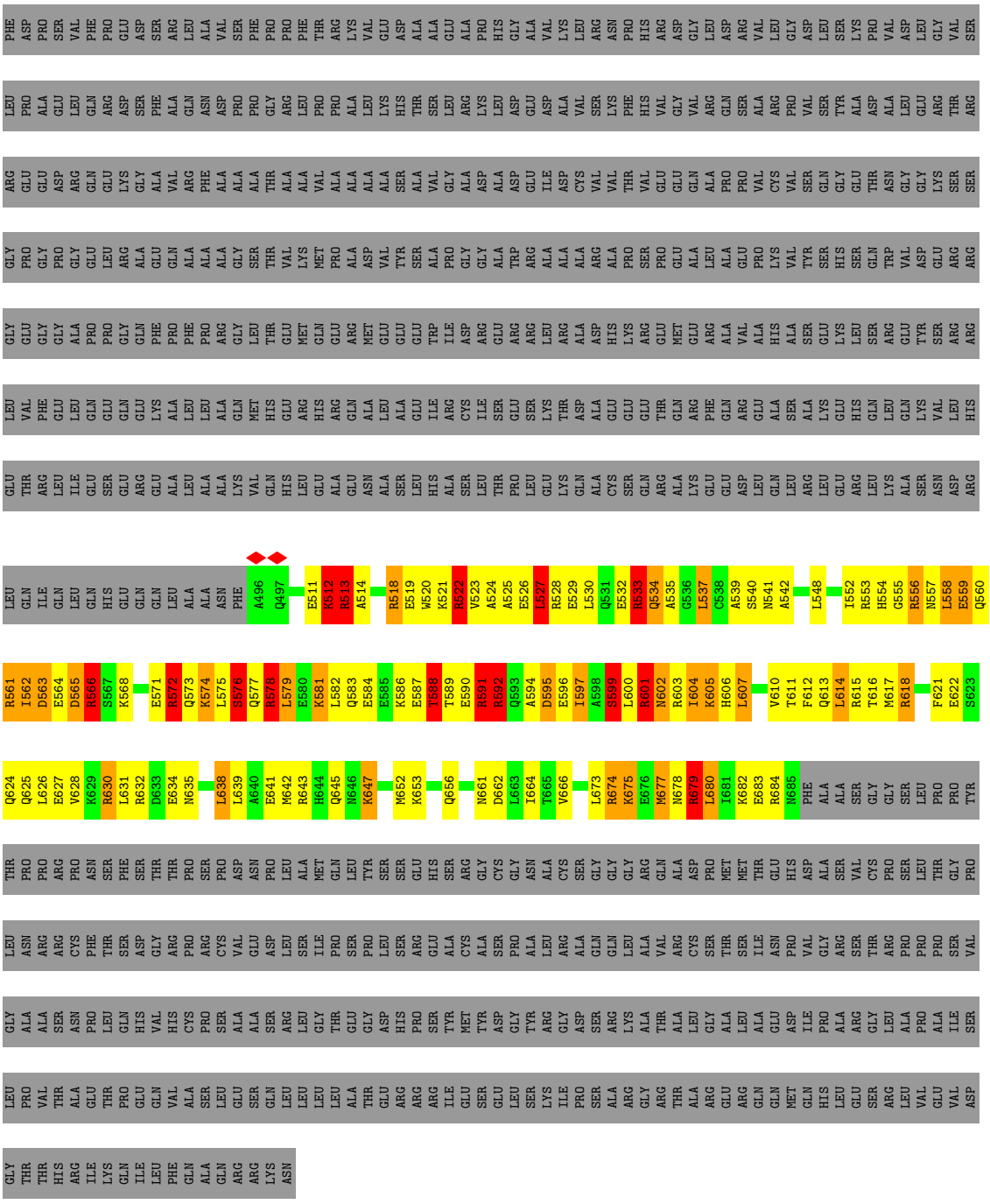
GLN ALA GLN ARG ARG LYS ASN

• Molecule 1: CF2, TGME49_258090

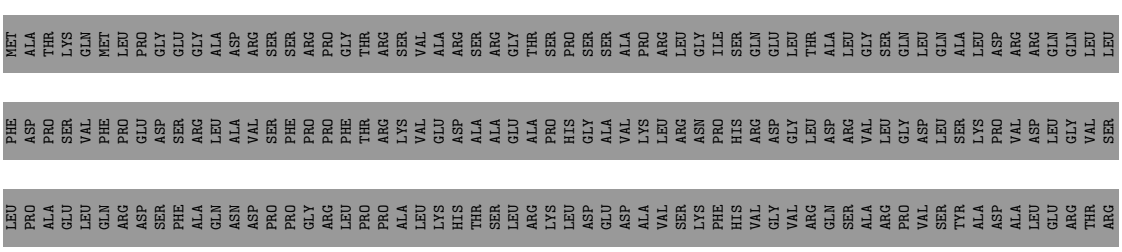
Chain f:

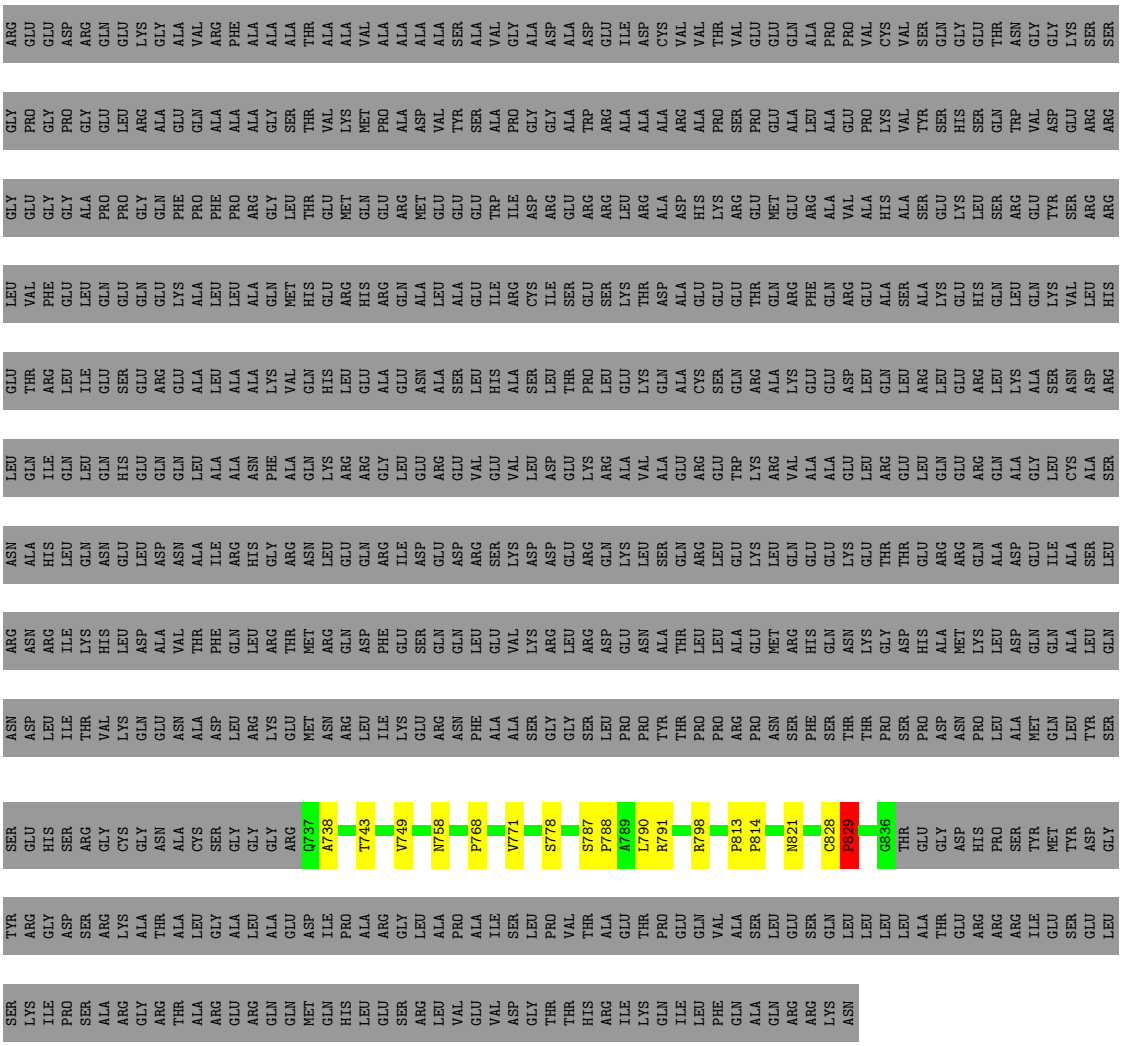
MET ALA THR LYS GLN MET LEU PRO GLY GLU GLY ALA ASP ARG SER SER ARG PRO GLY THR ARG SER VAL ALA ARG SER ARG GLY THR SER PRO SER SER ALA PRO ARG LEU GLY ILE SER GLN GLU LEU THR ALA LEU GLY SER GLN LEU GLN ALA LEU ASP ARG ARG GLN GLN LEU LEU



• Molecule 1: CF2, TGME49_258090

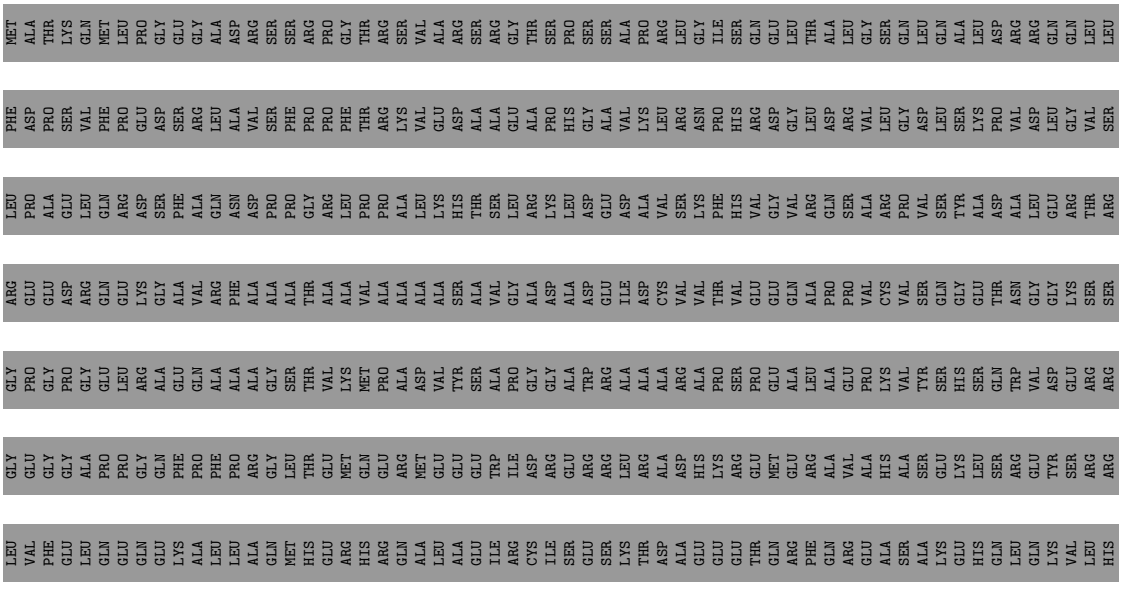
Chain g:

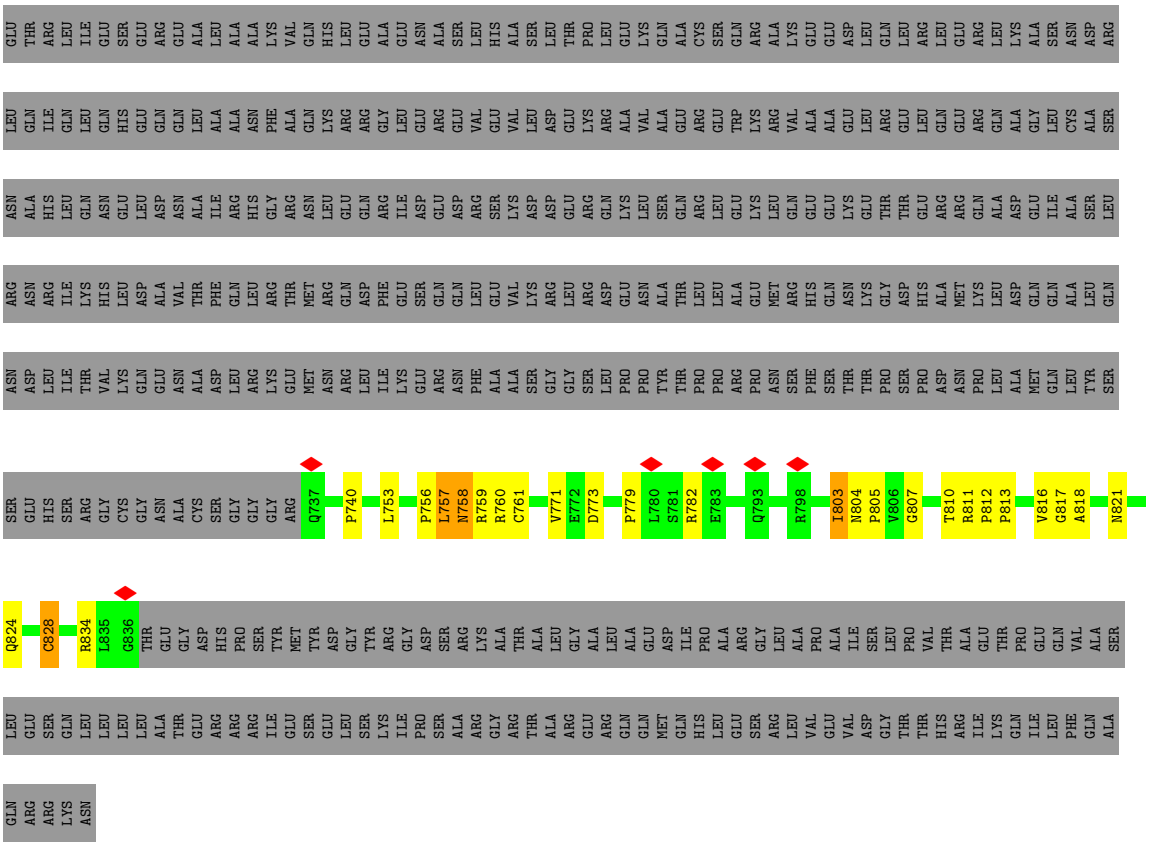




• Molecule 1: CF2, TGME49_258090

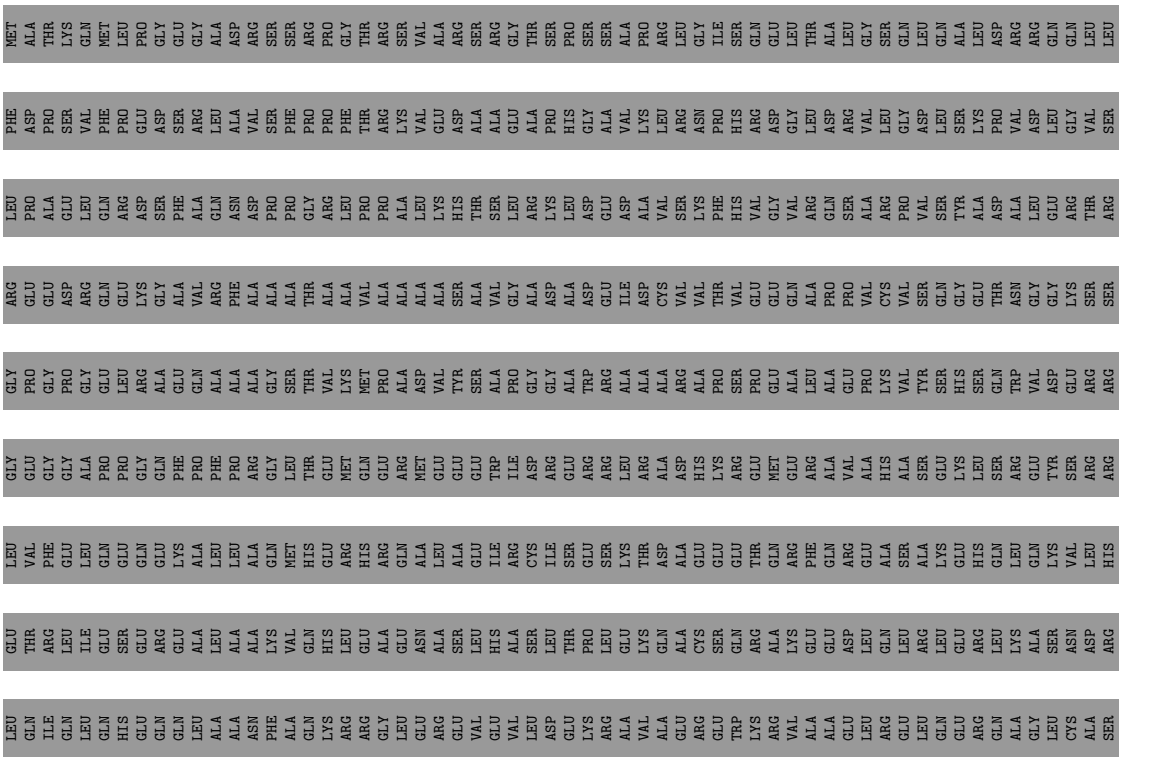
Chain h:

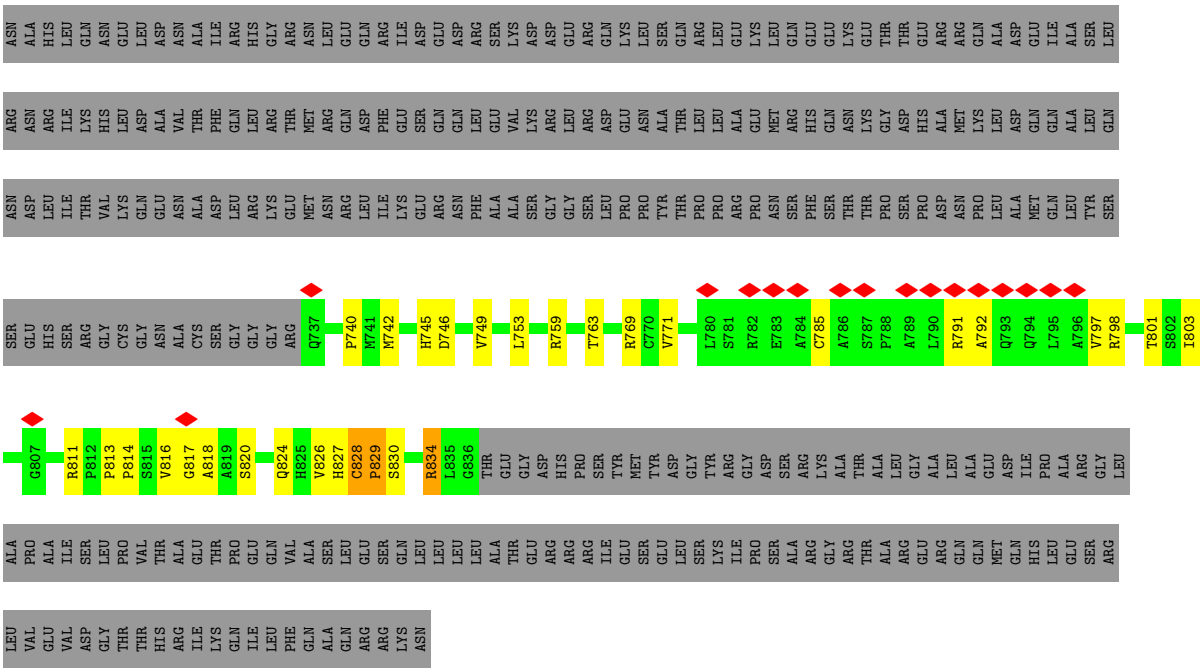




• Molecule 1: CF2, TGME49_258090

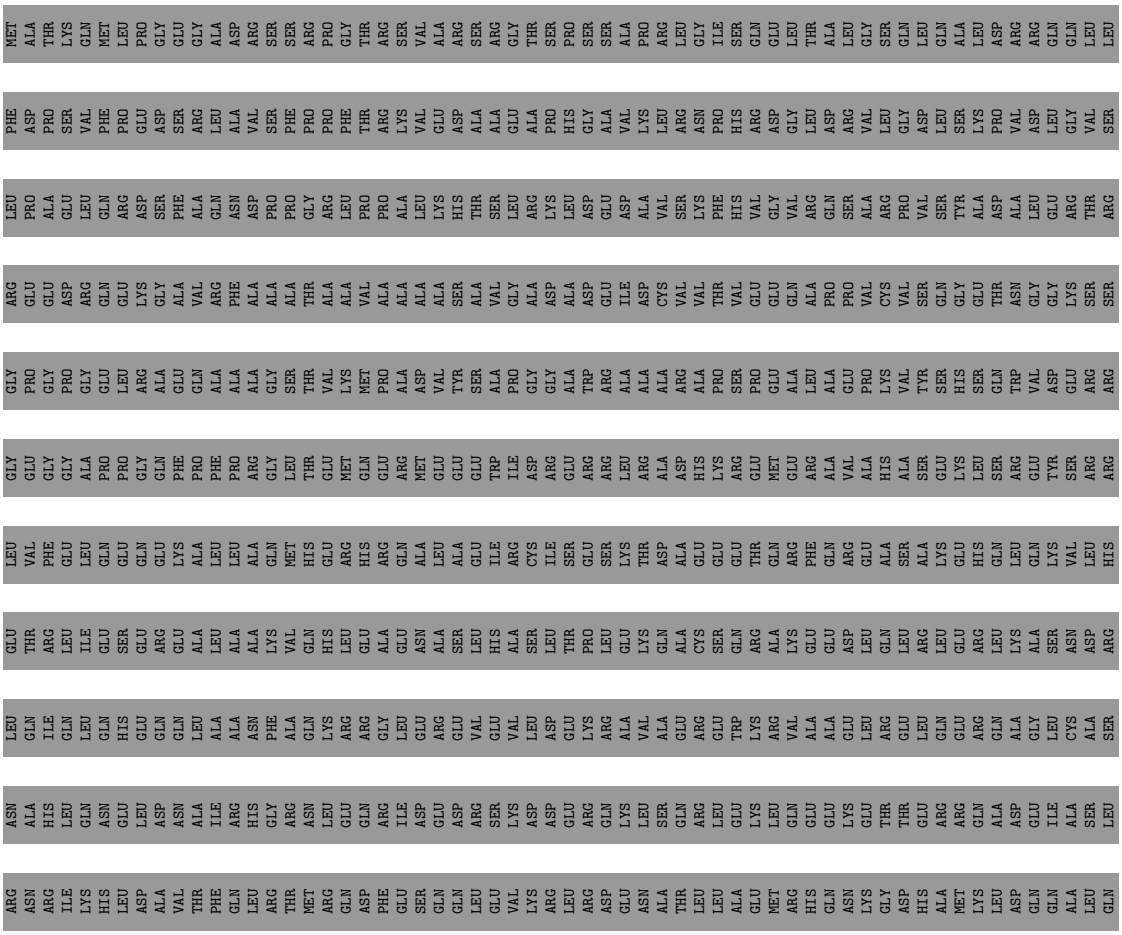
Chain i:

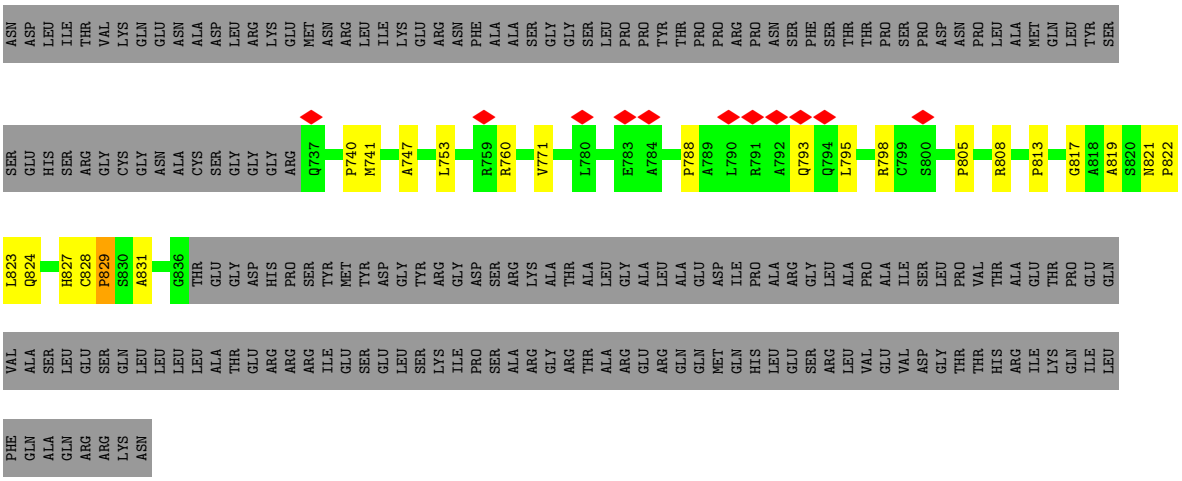




• Molecule 1: CF2, TGME49_258090

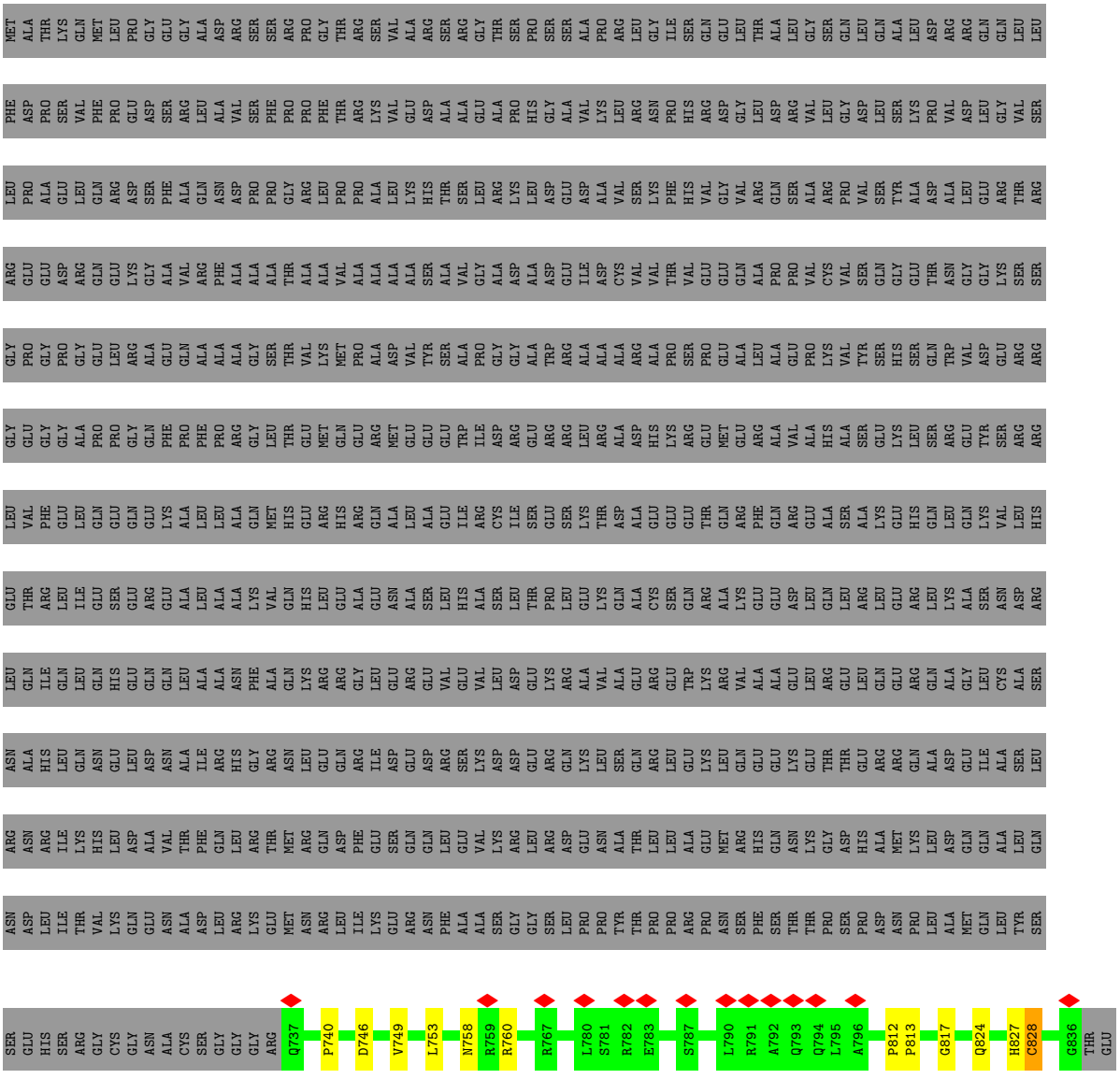
Chain j:

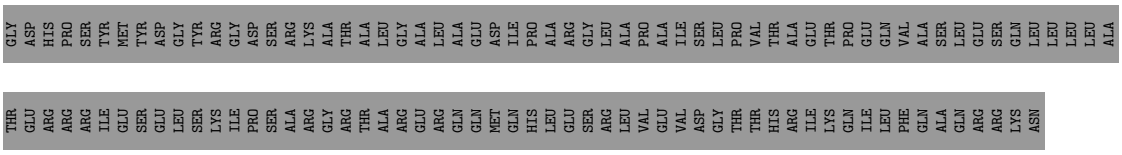




• Molecule 1: CF2, TGME49_258090

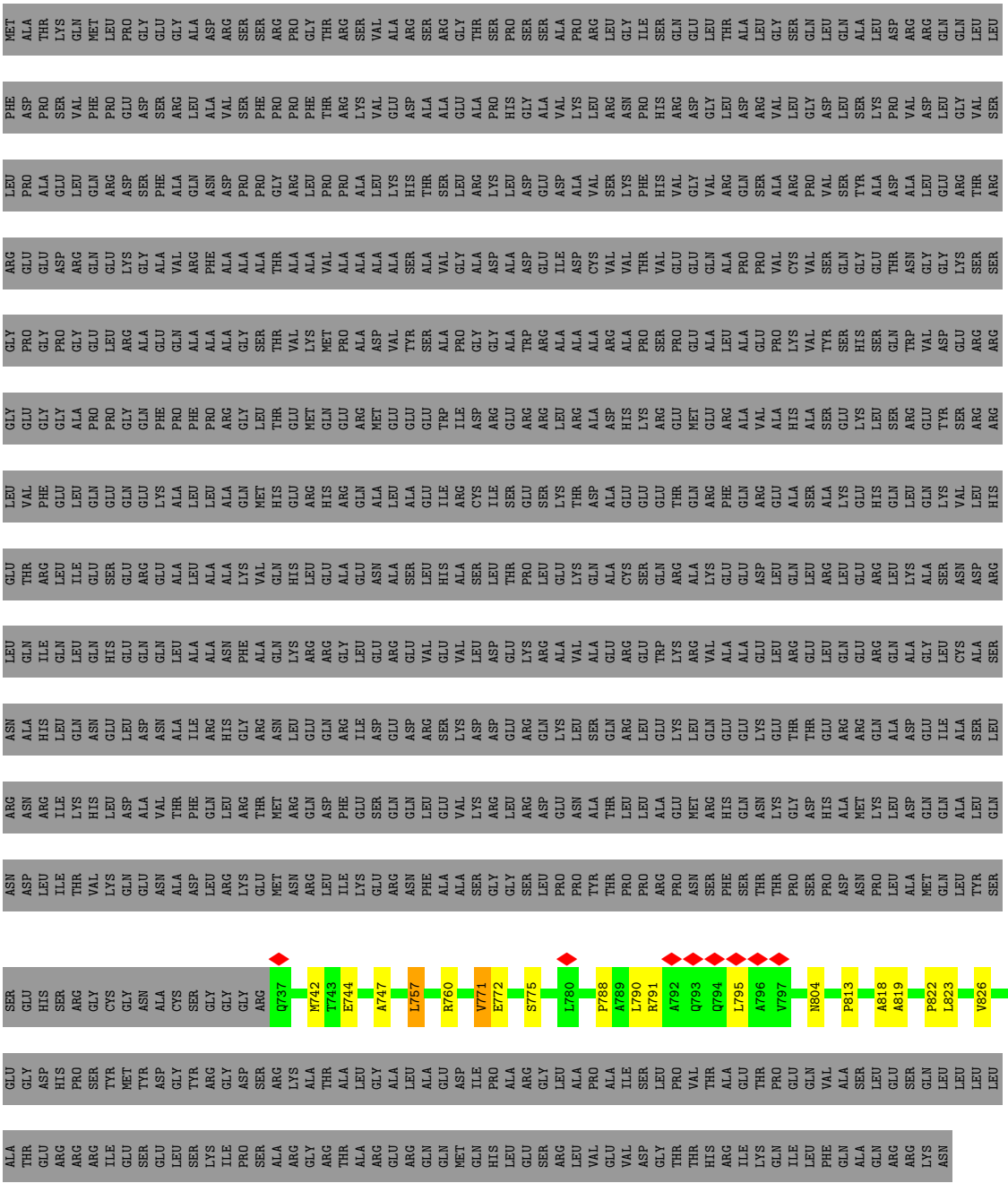
Chain k:





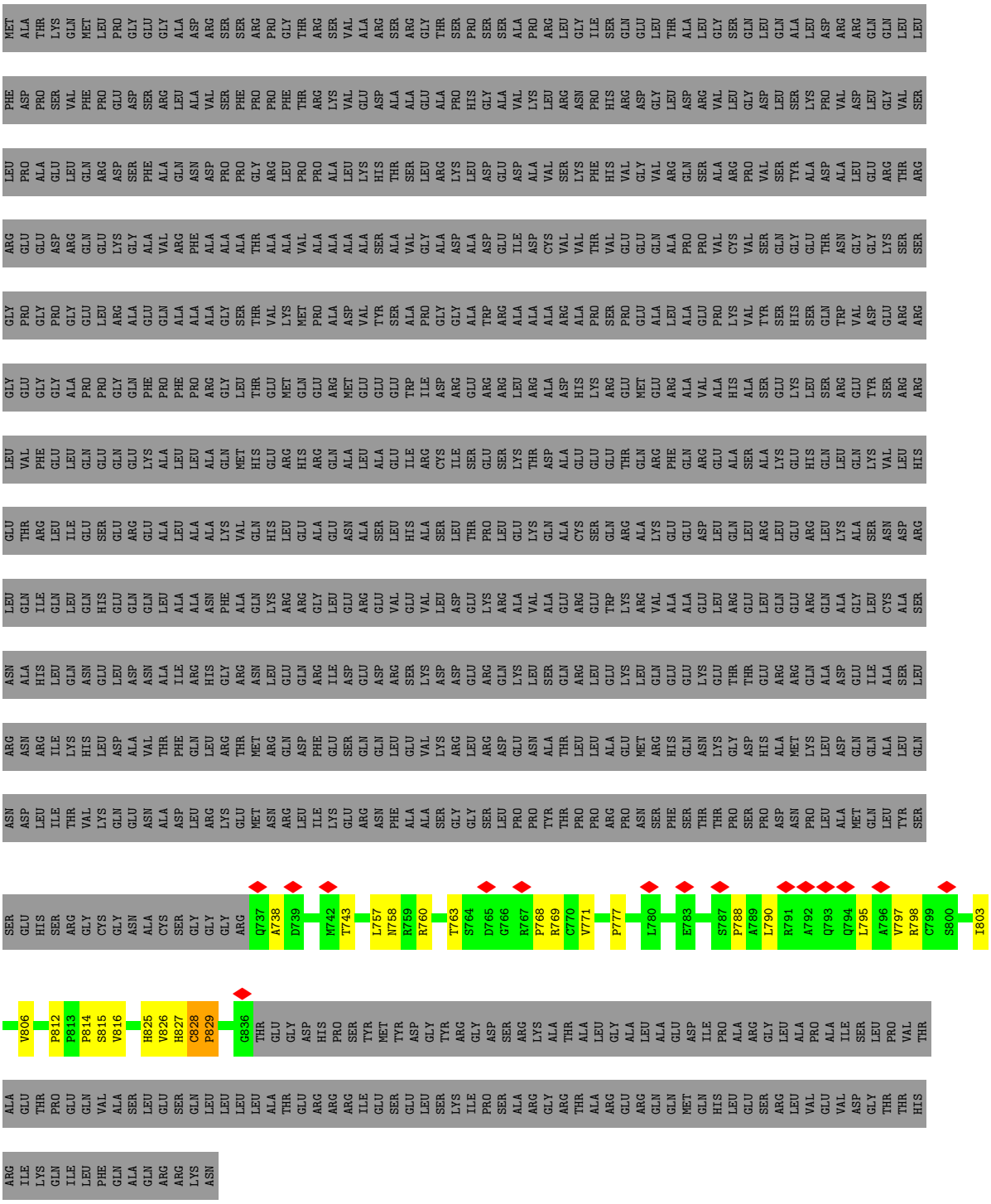
• Molecule 1: CF2, TGME49_258090

Chain l:



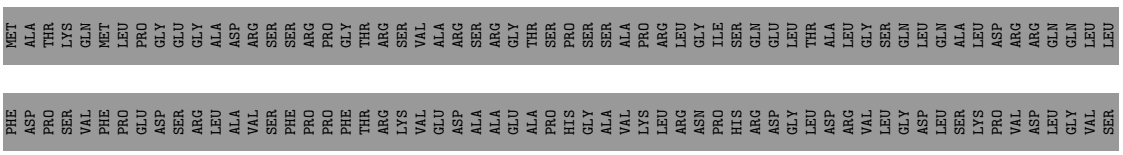
• Molecule 1: CF2, TGME49_258090

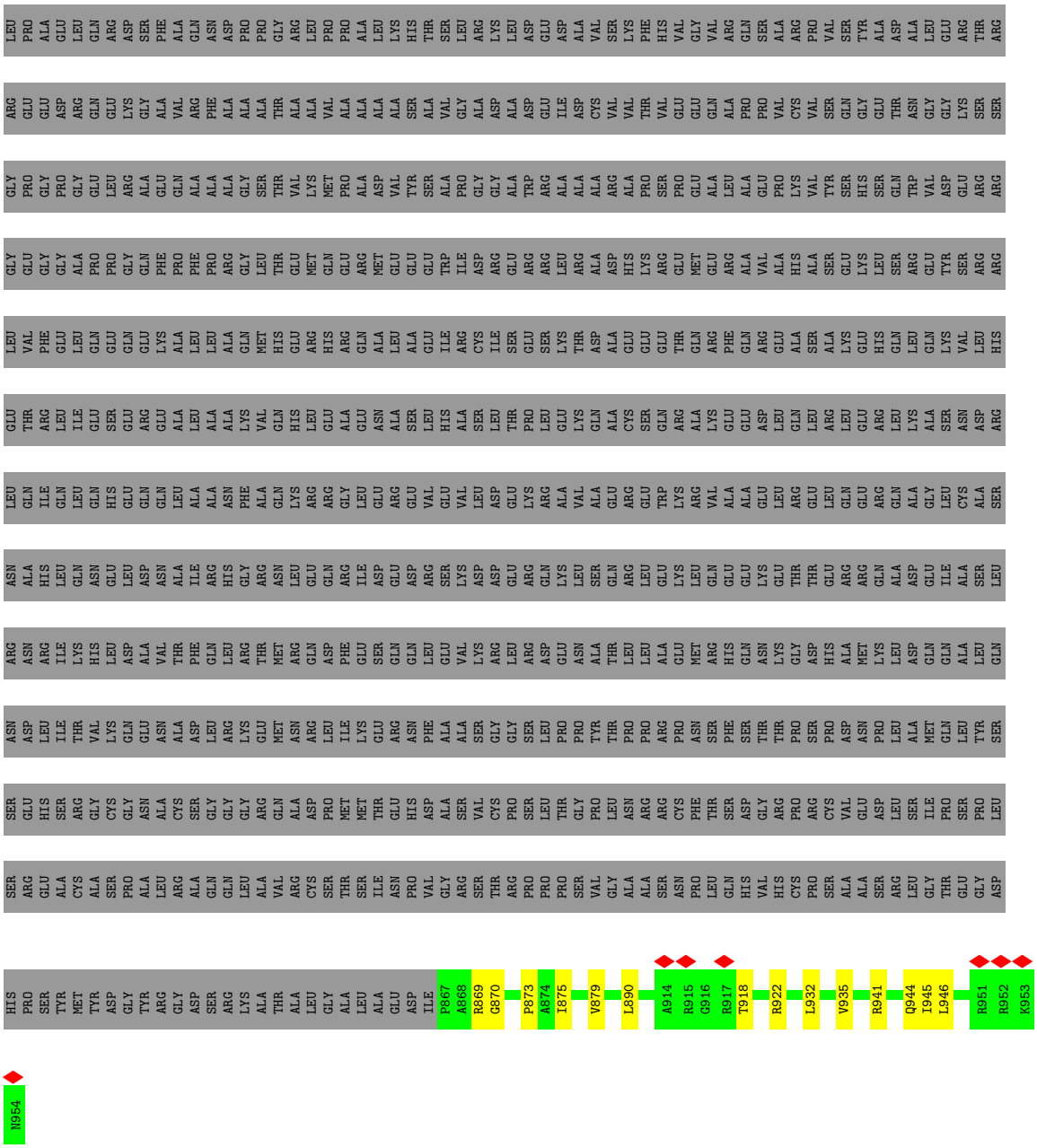
Chain m:



• Molecule 1: CF2, TGME49_258090

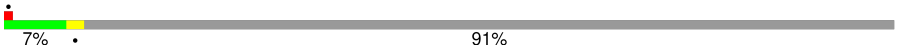
Chain n:

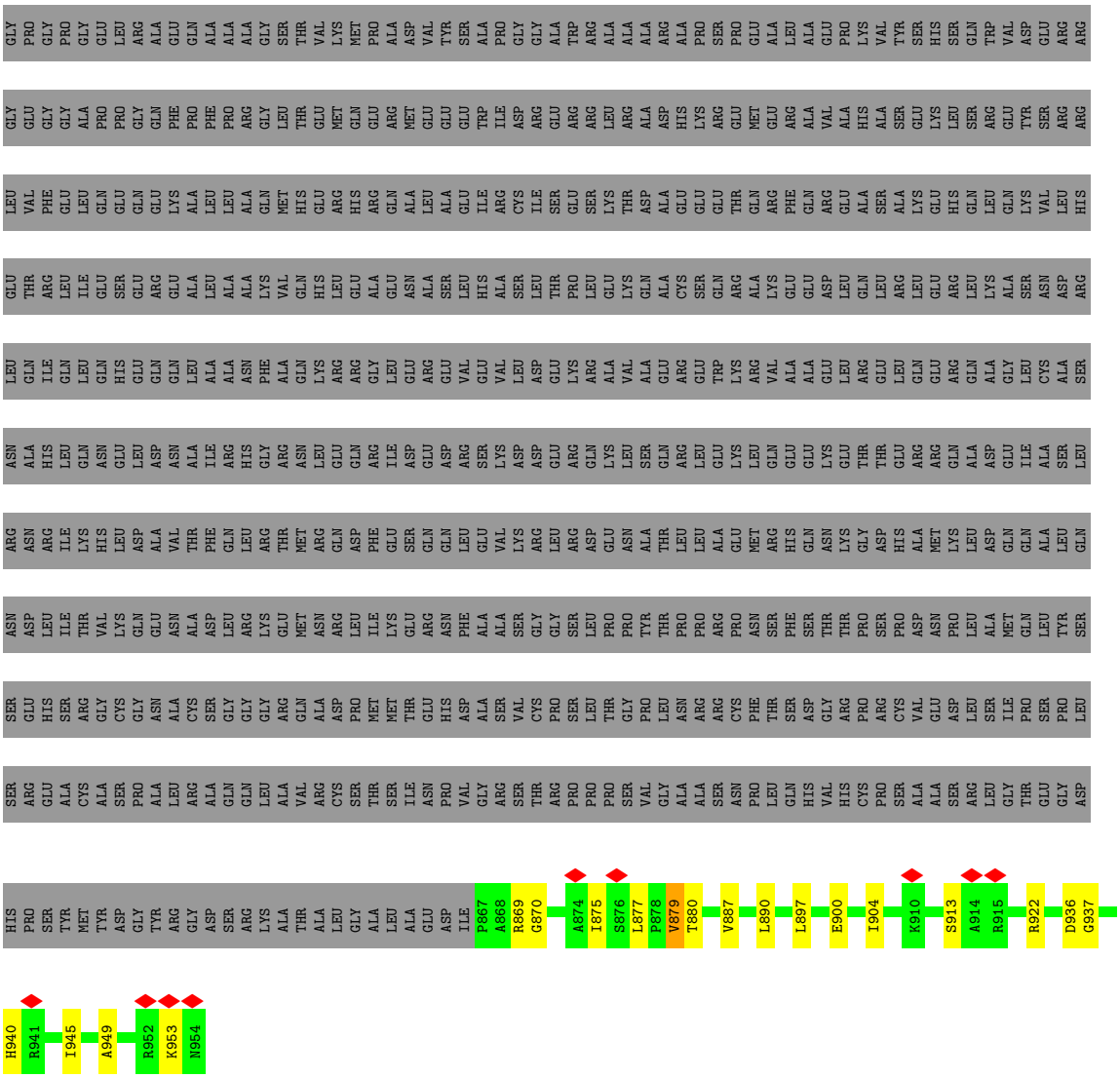




• Molecule 1: CF2, TGME49_258090

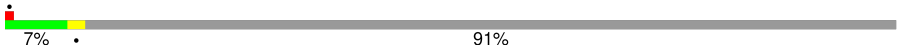
Chain o:

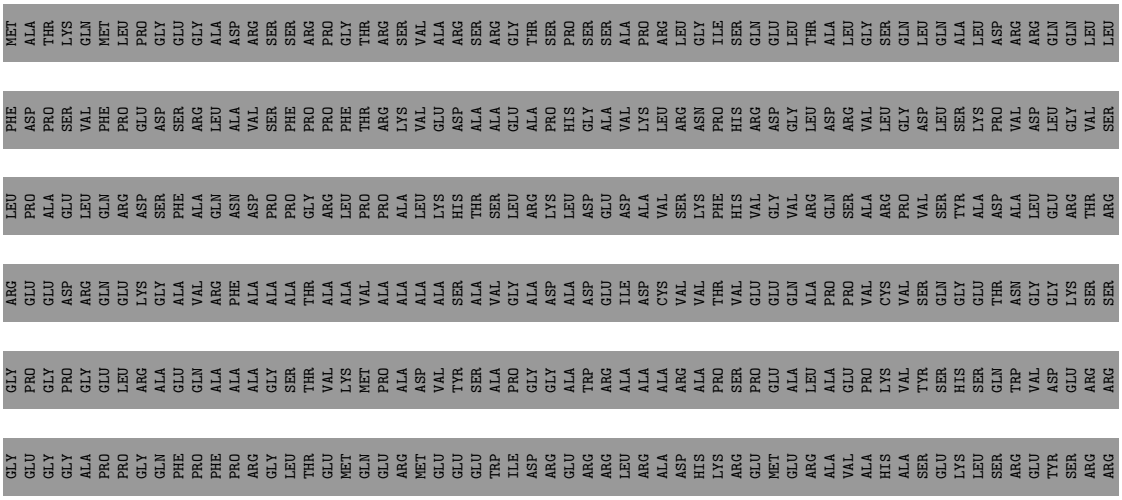


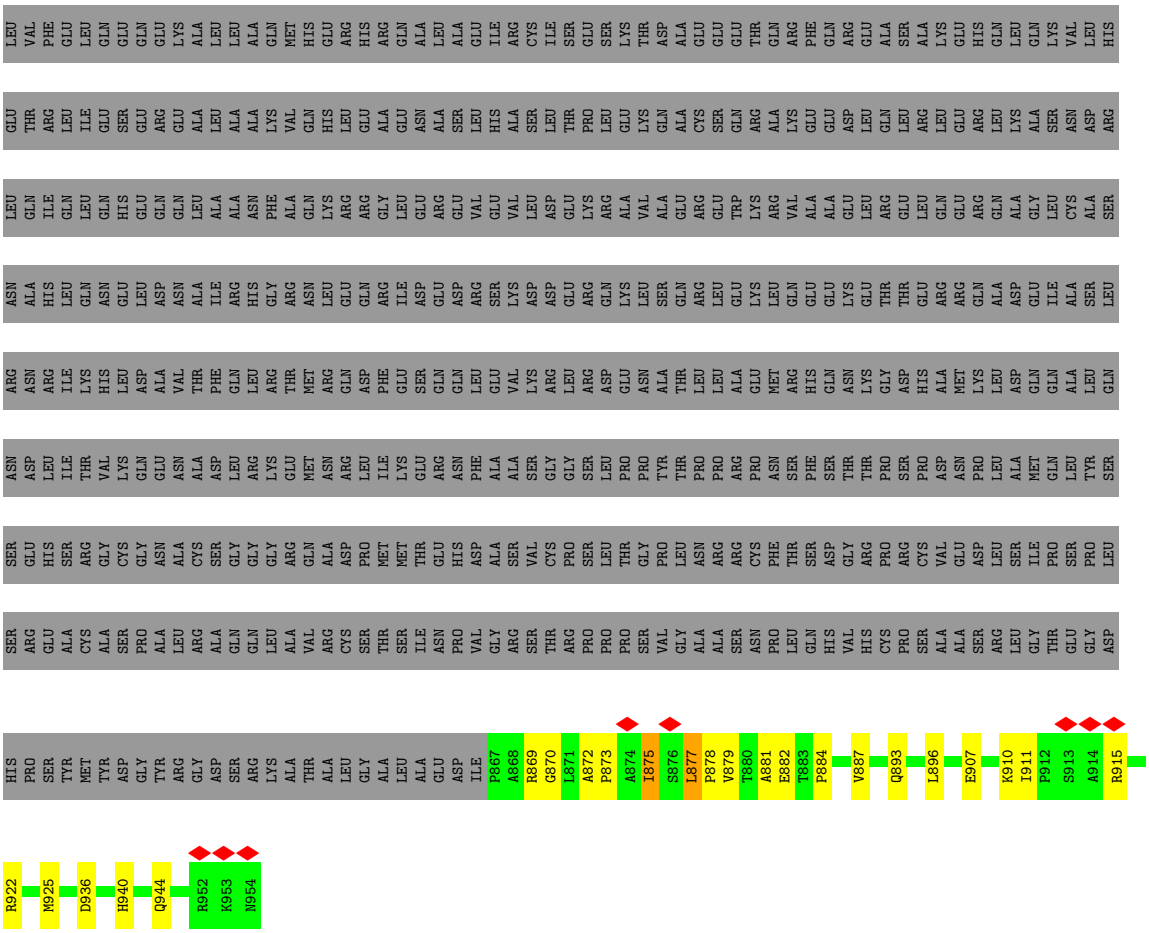


• Molecule 1: CF2, TGME49_258090

Chain p:

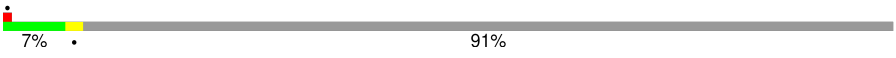


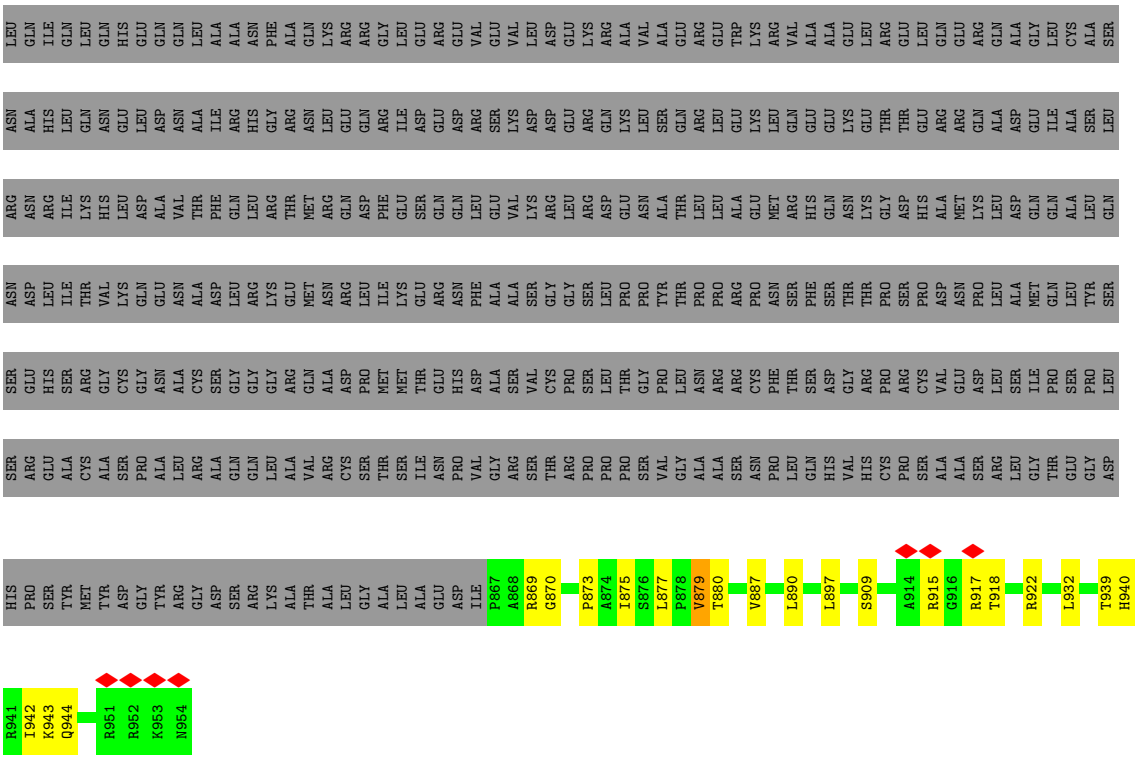




- Molecule 1: CF2, TGME49_258090

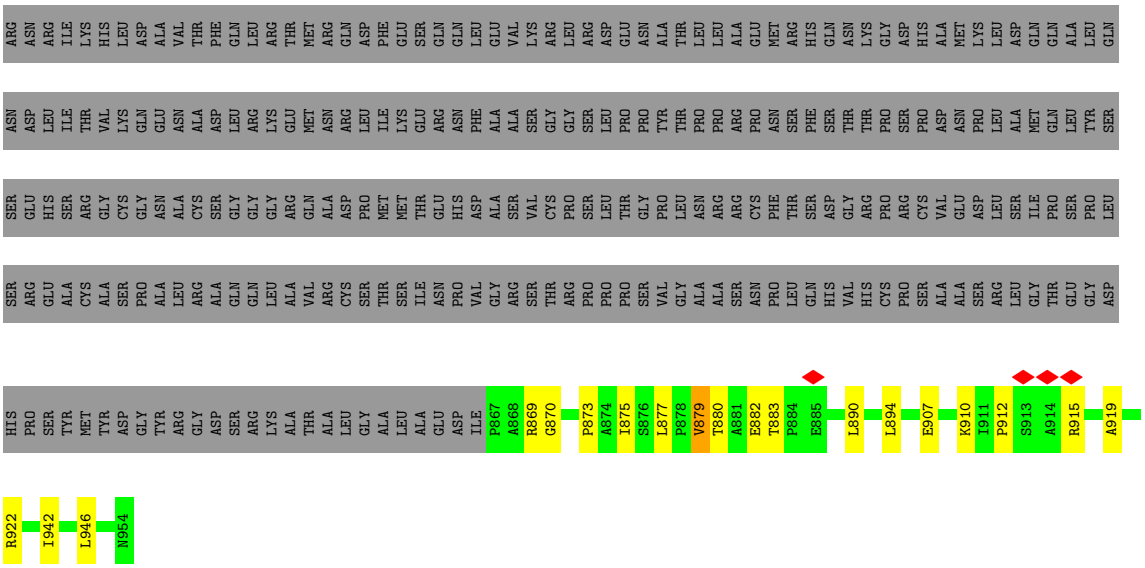
Chain q:



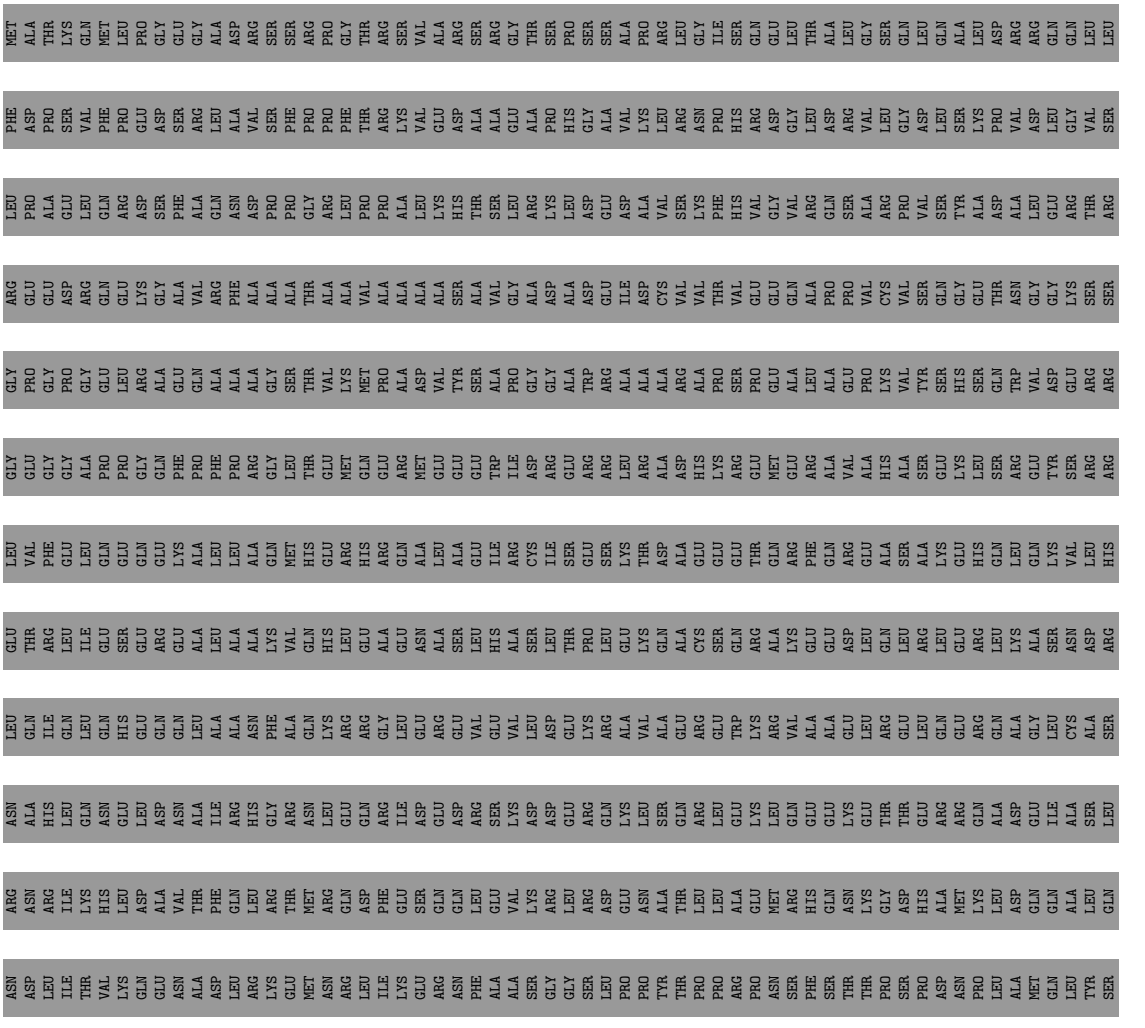


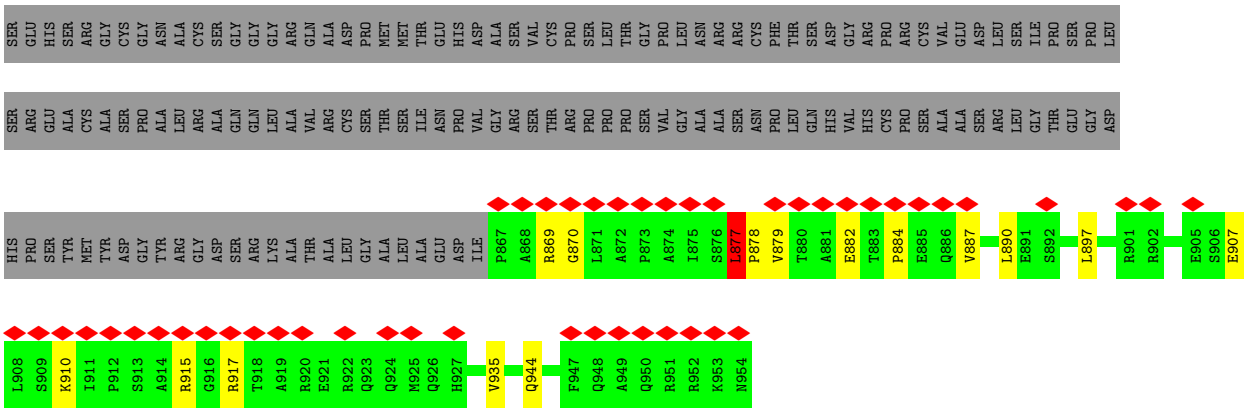
• Molecule 1: CF2, TGME49_258090

Chain r: 7% 91%

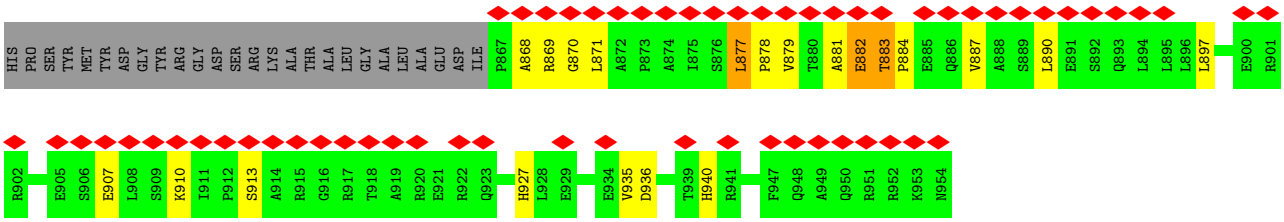


• Molecule 1: CF2, TGME49_258090



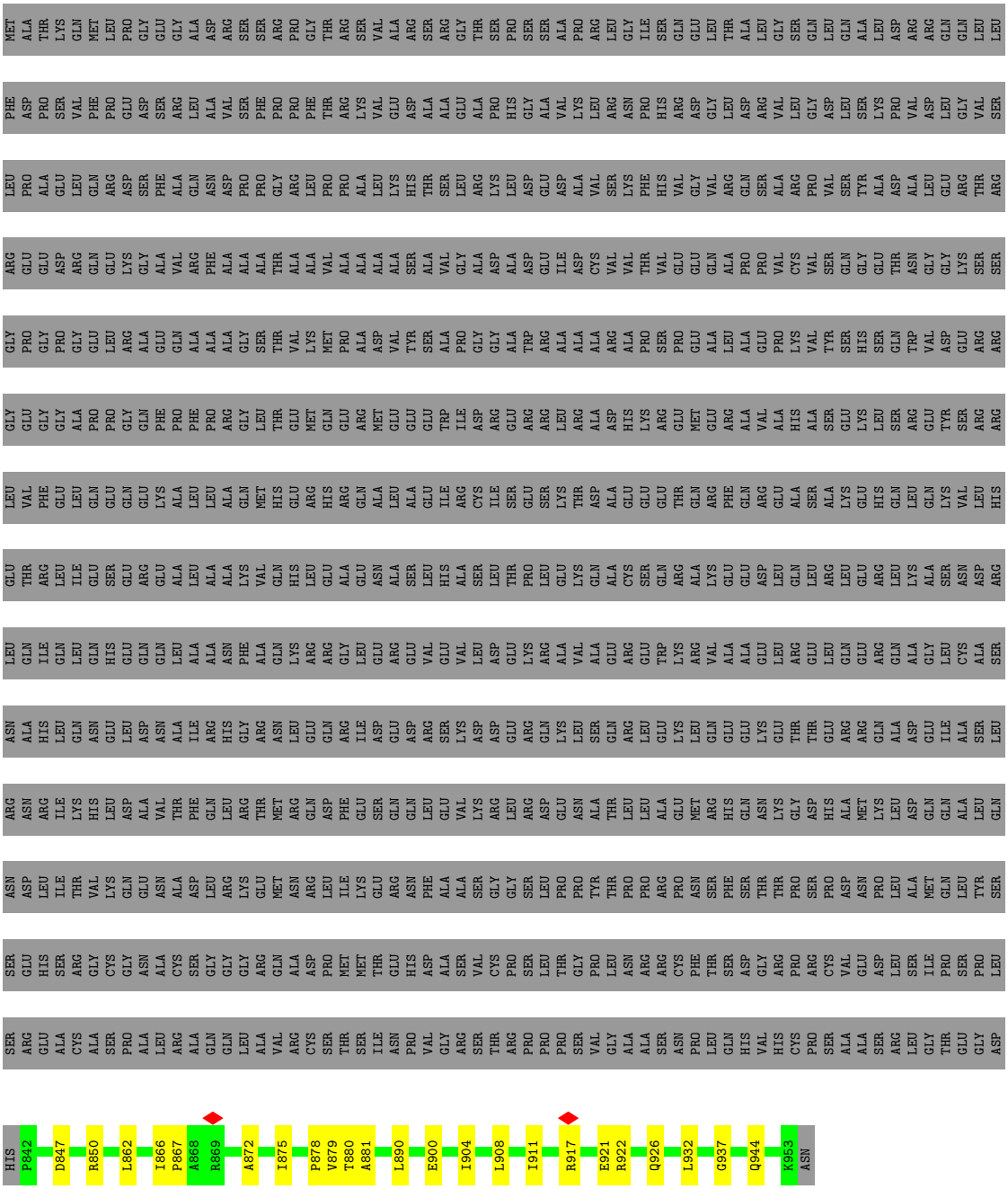


• Molecule 1: CF2, TGME49_258090



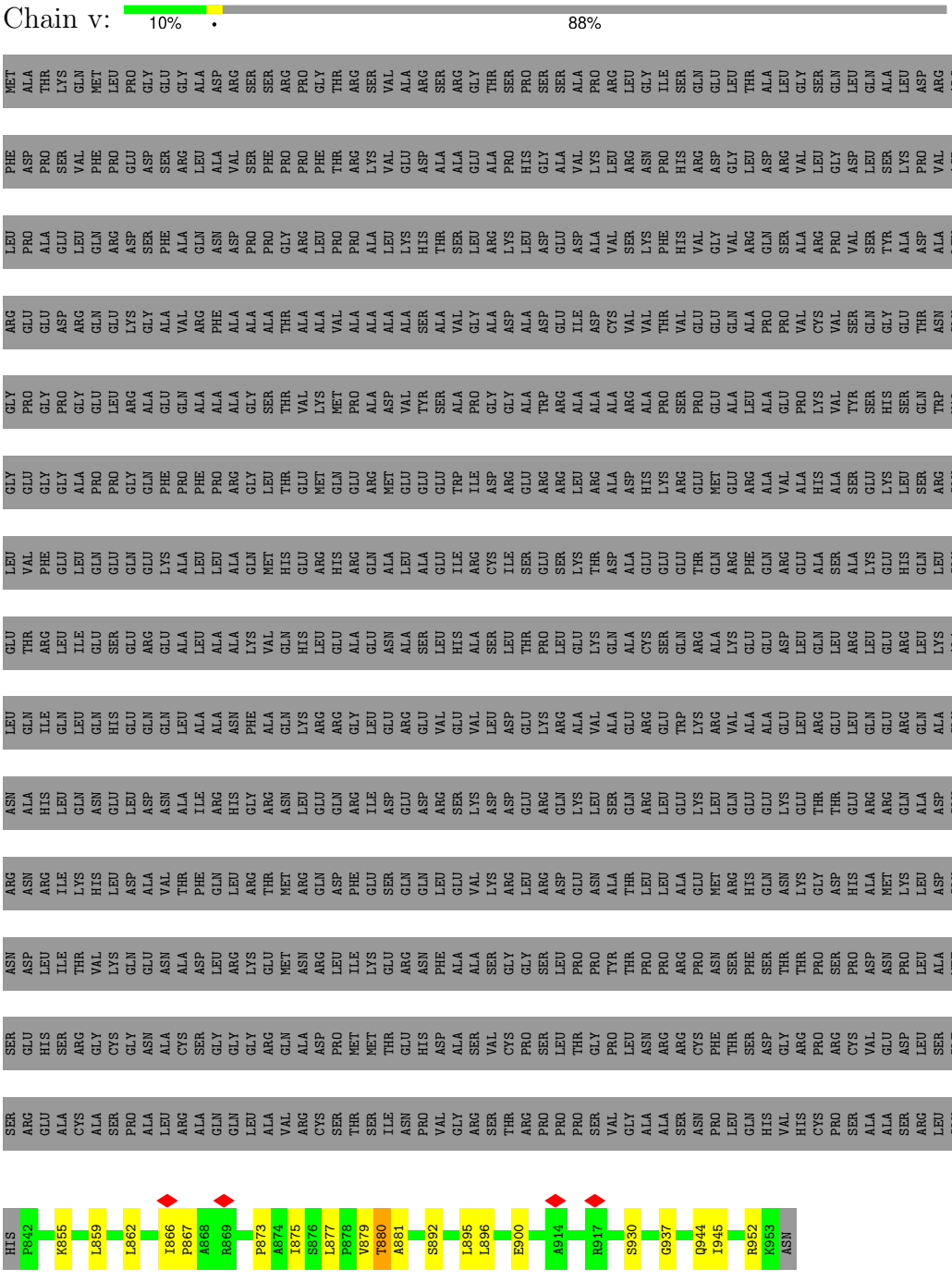
• Molecule 1: CF2, TGME49_258090

Chain u:



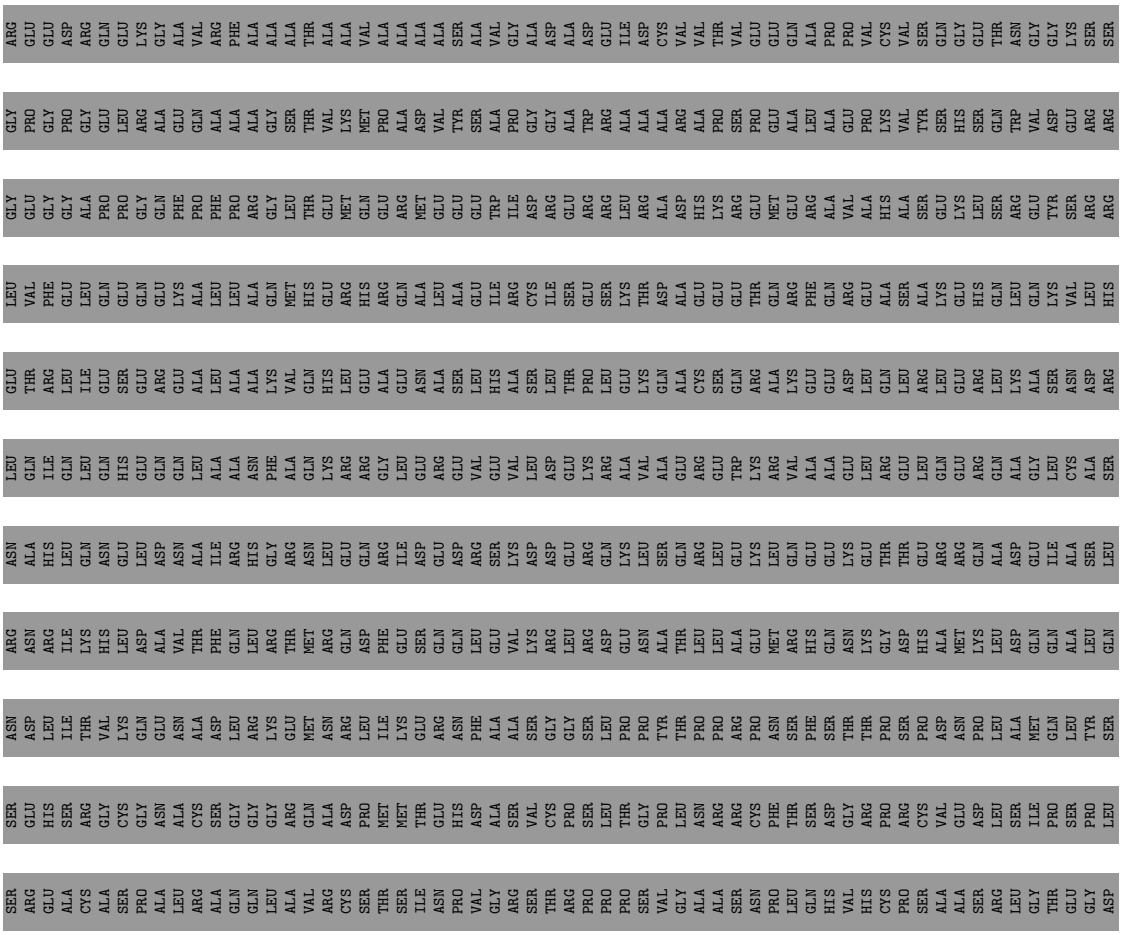
• Molecule 1: CF2, TGME49_258090

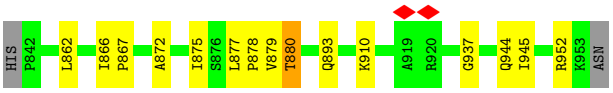
Chain v:



• Molecule 1: CF2, TGME49_258090

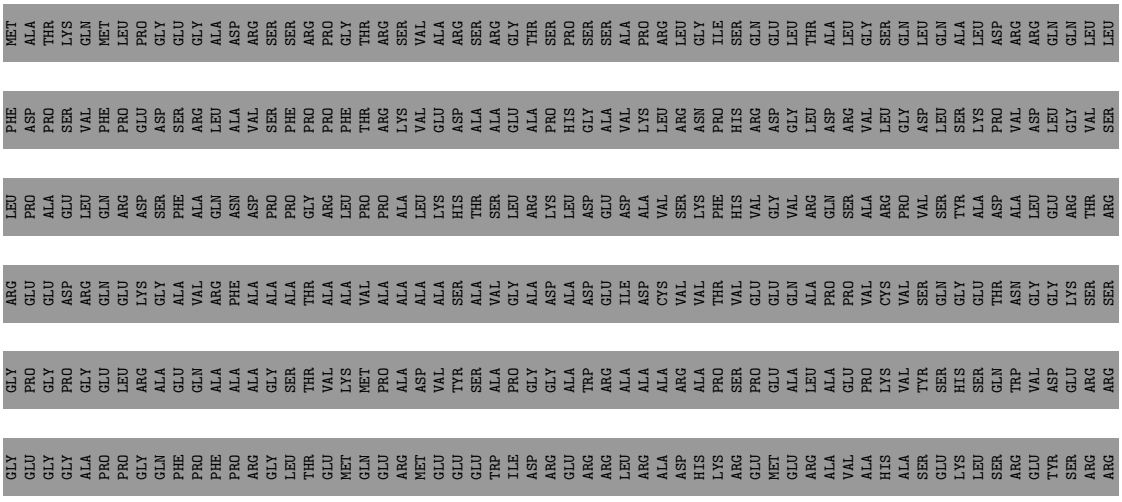
Chain w:

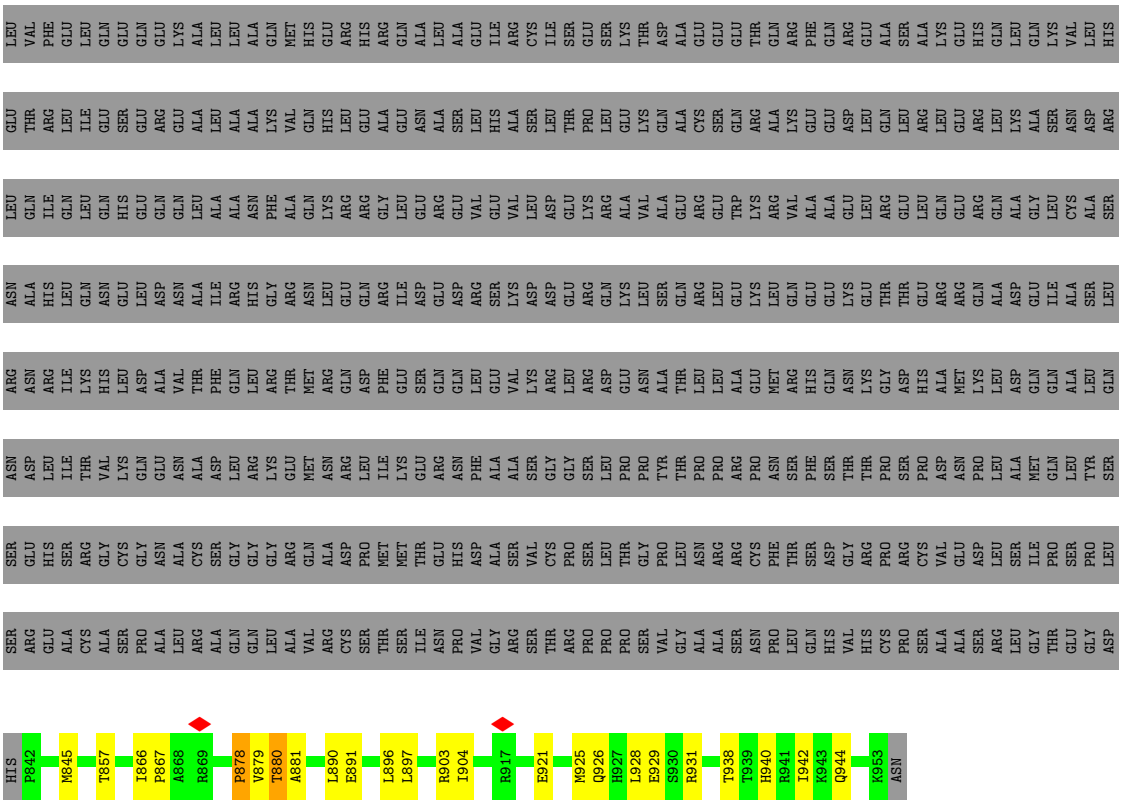




• Molecule 1: CF2, TGME49_258090

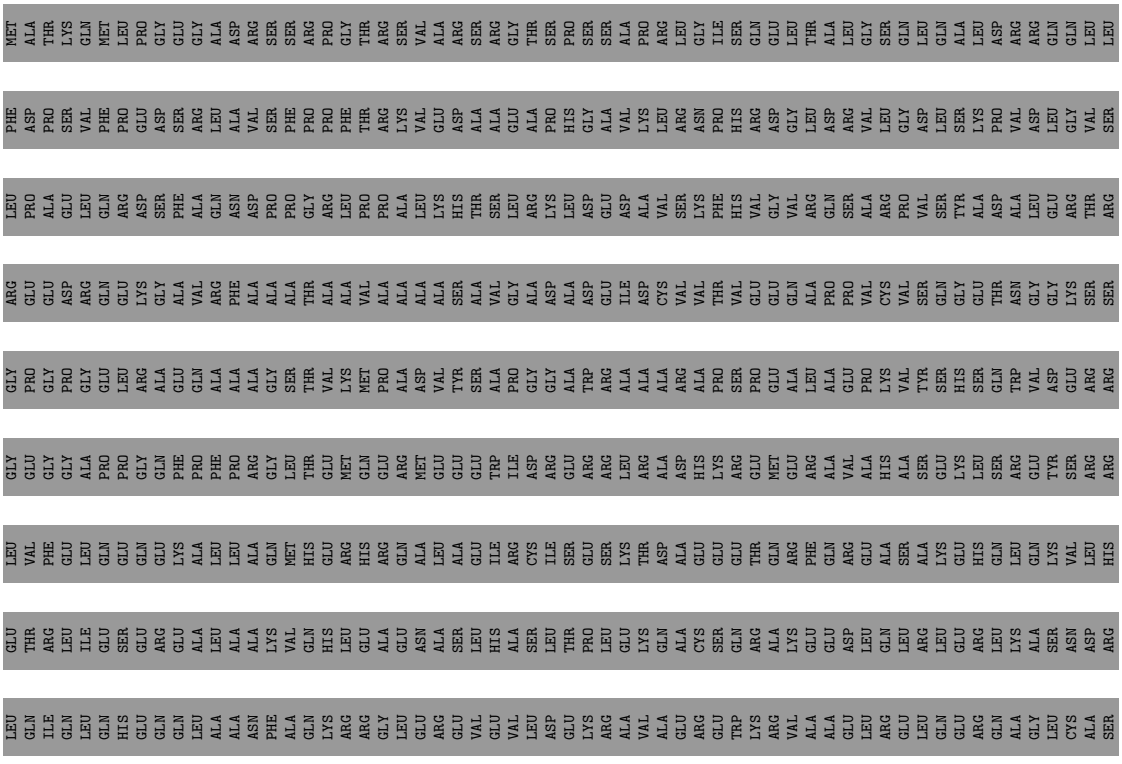
Chain x: 9% 88%

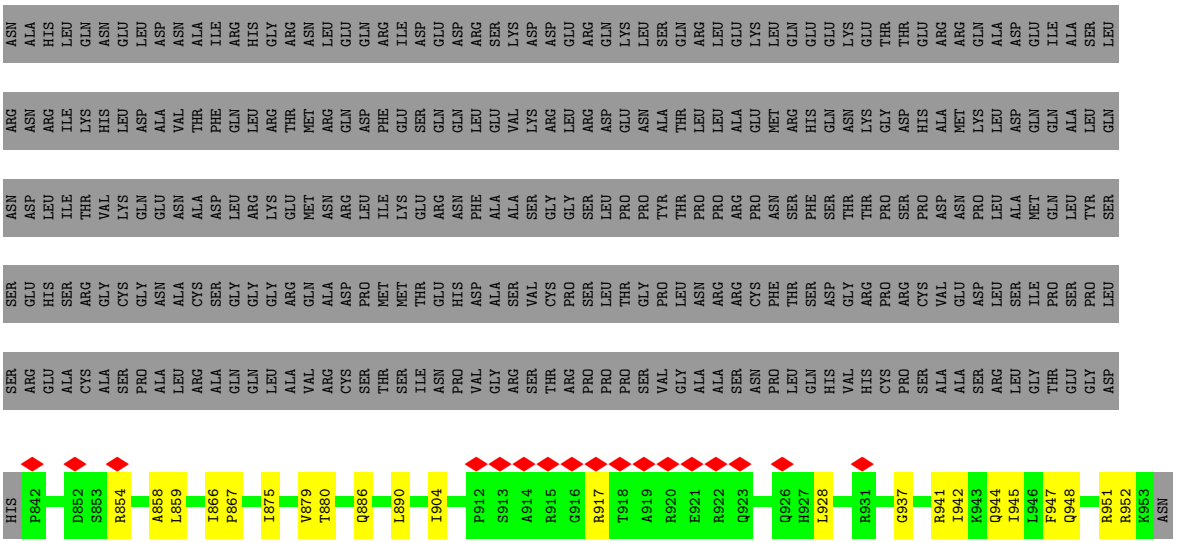




• Molecule 1: CF2, TGME49_258090

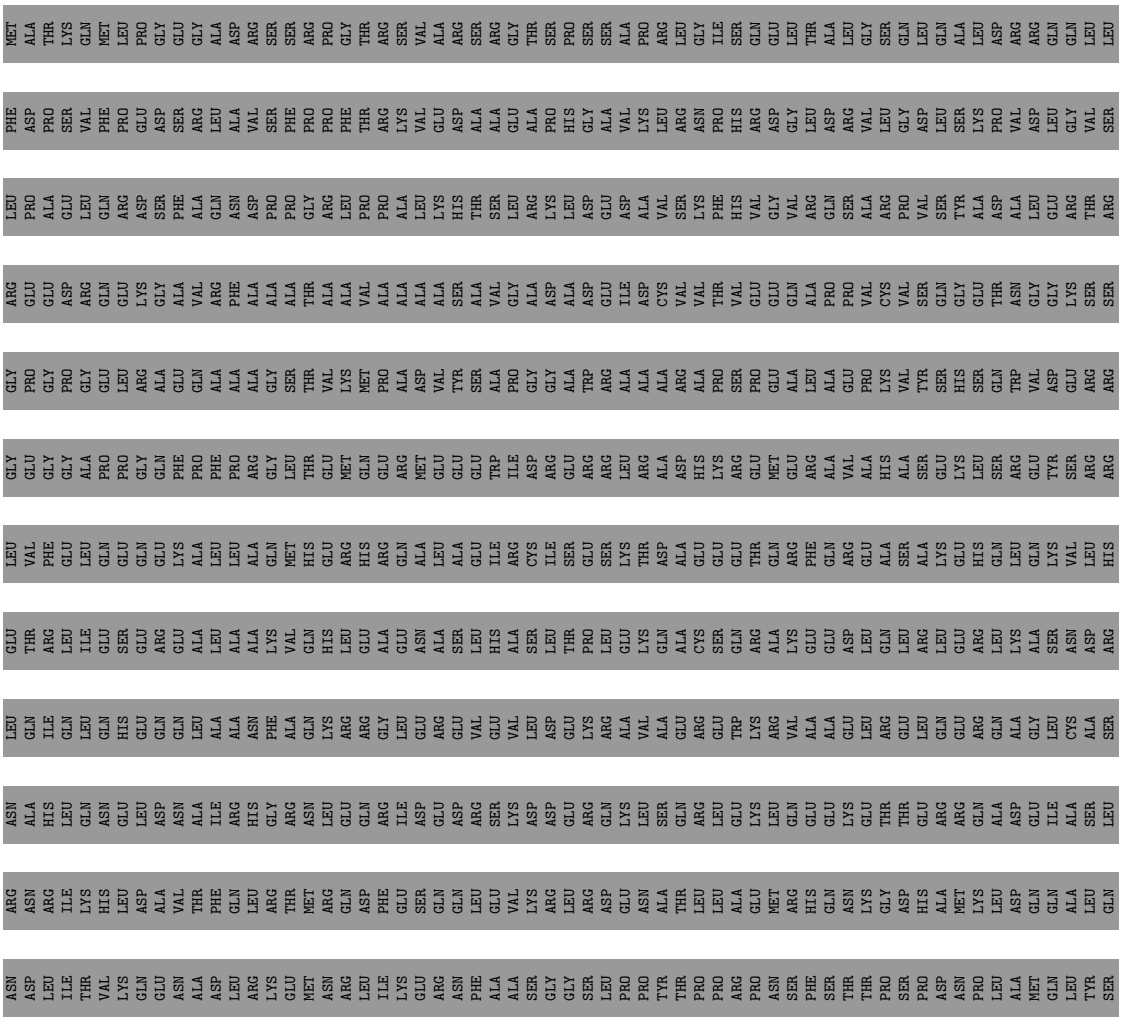
Chain y:

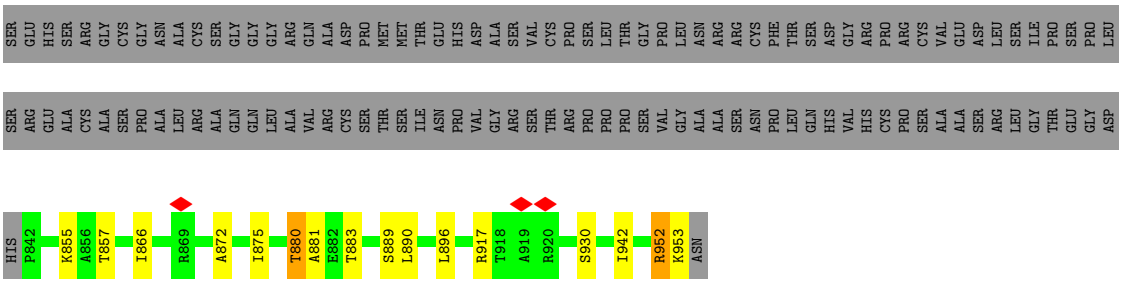




- Molecule 1: CF2, TGME49_258090

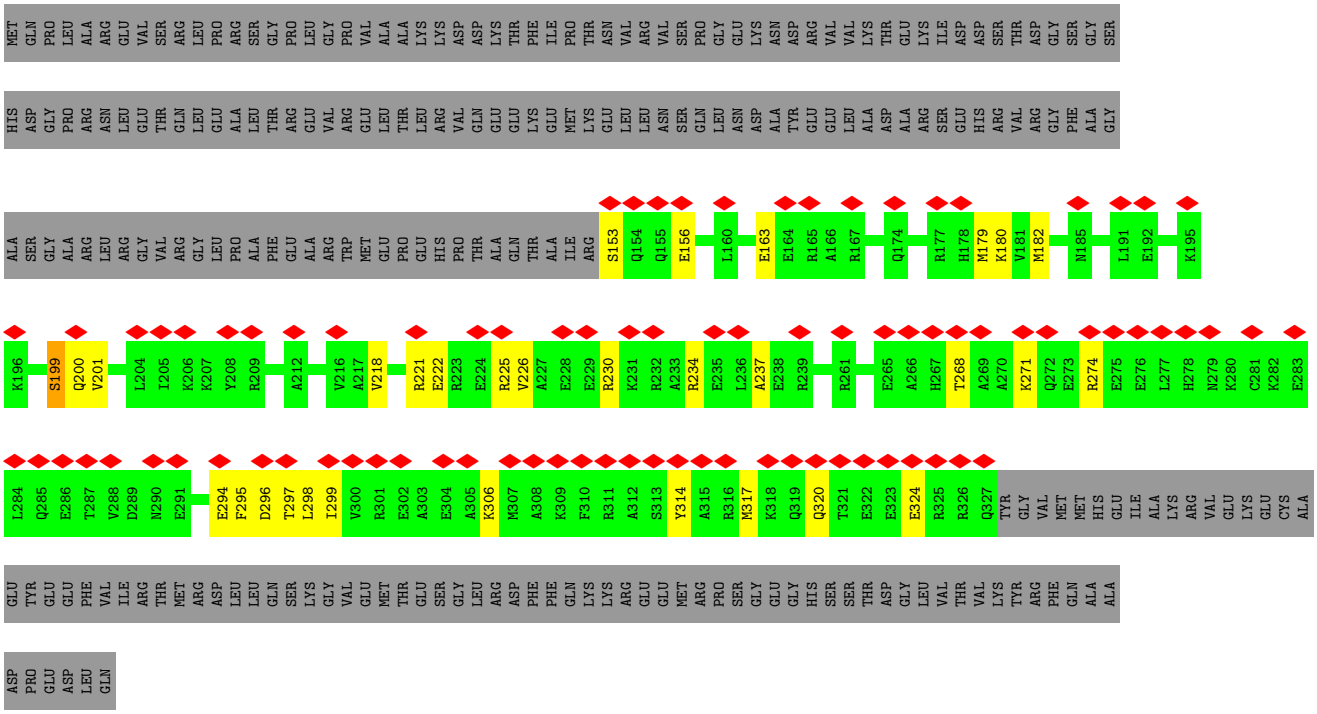
Chain z:





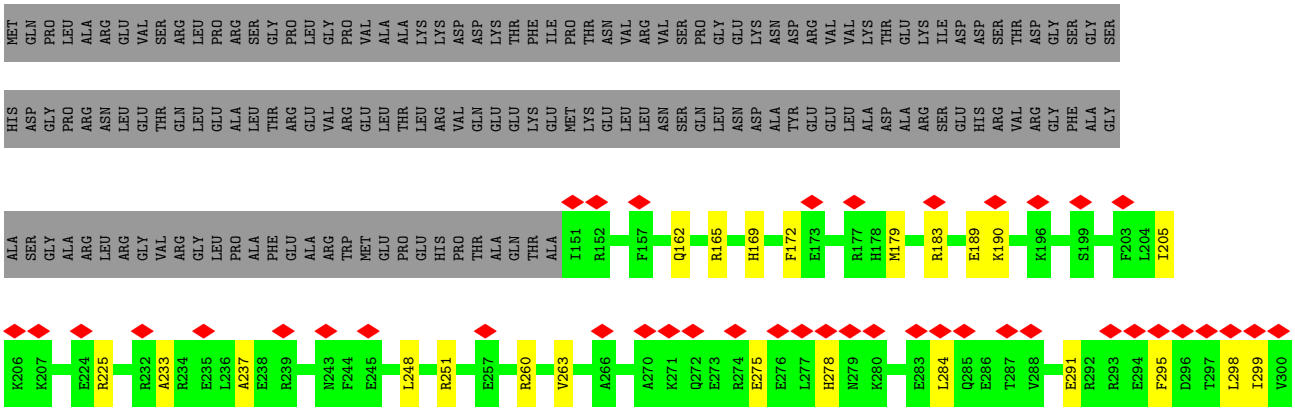
• Molecule 2: CF1, TGME49_222350

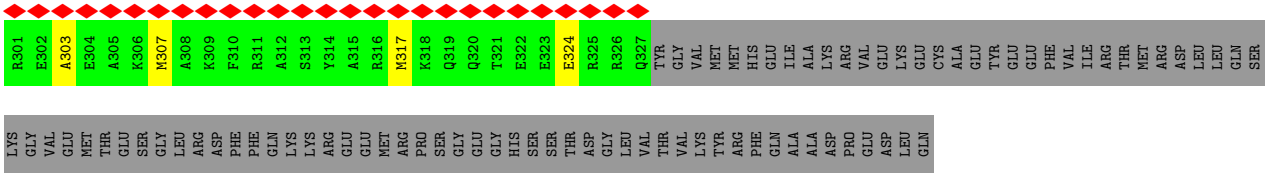
Chain 10:



• Molecule 2: CF1, TGME49_222350

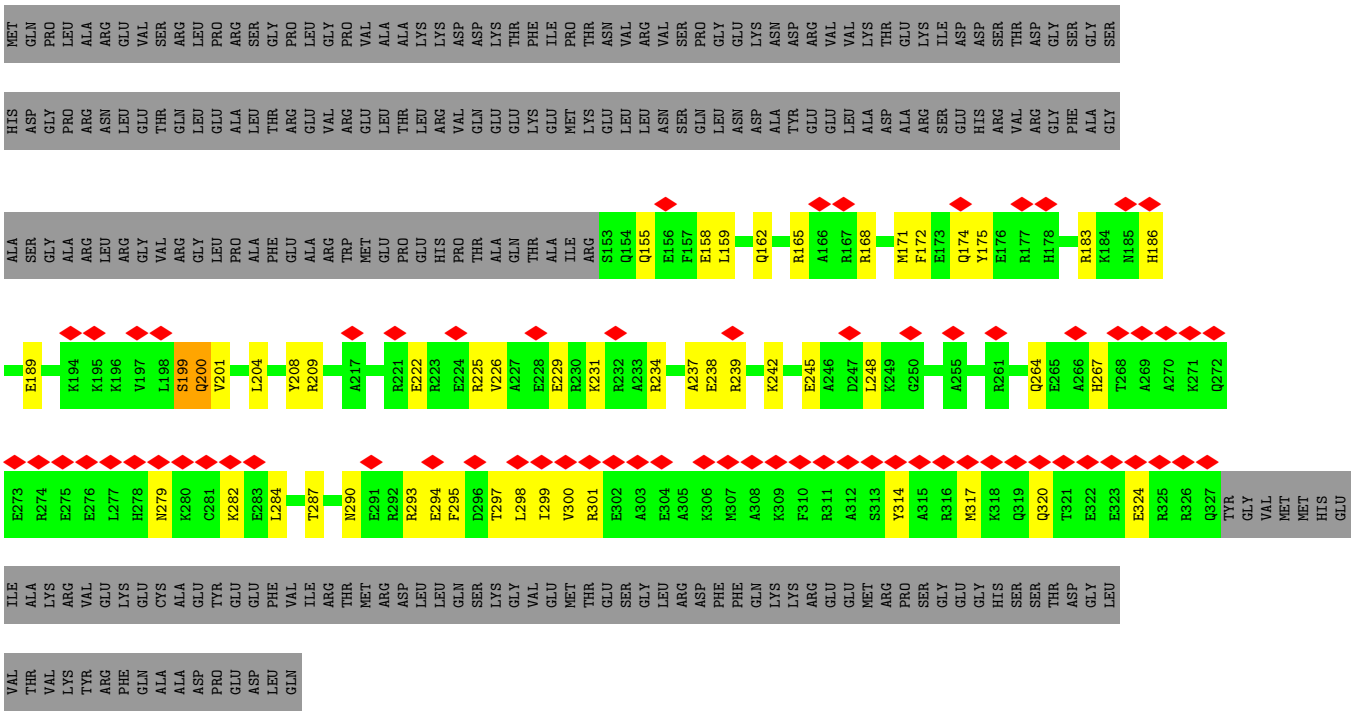
Chain 11:





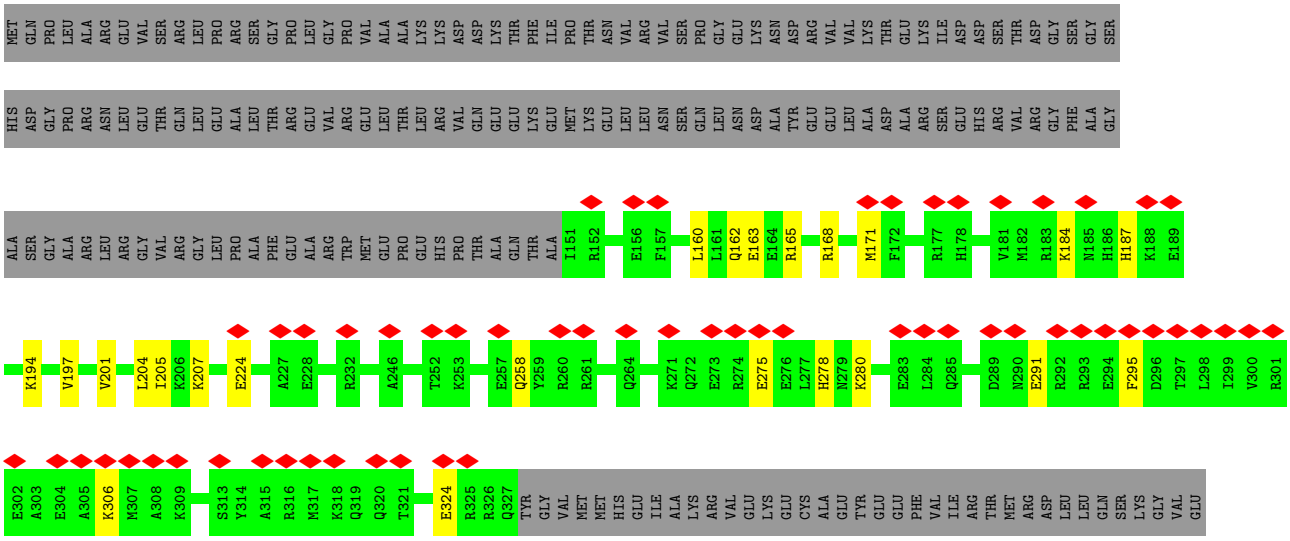
• Molecule 2: CF1, TGME49_222350

Chain 12:



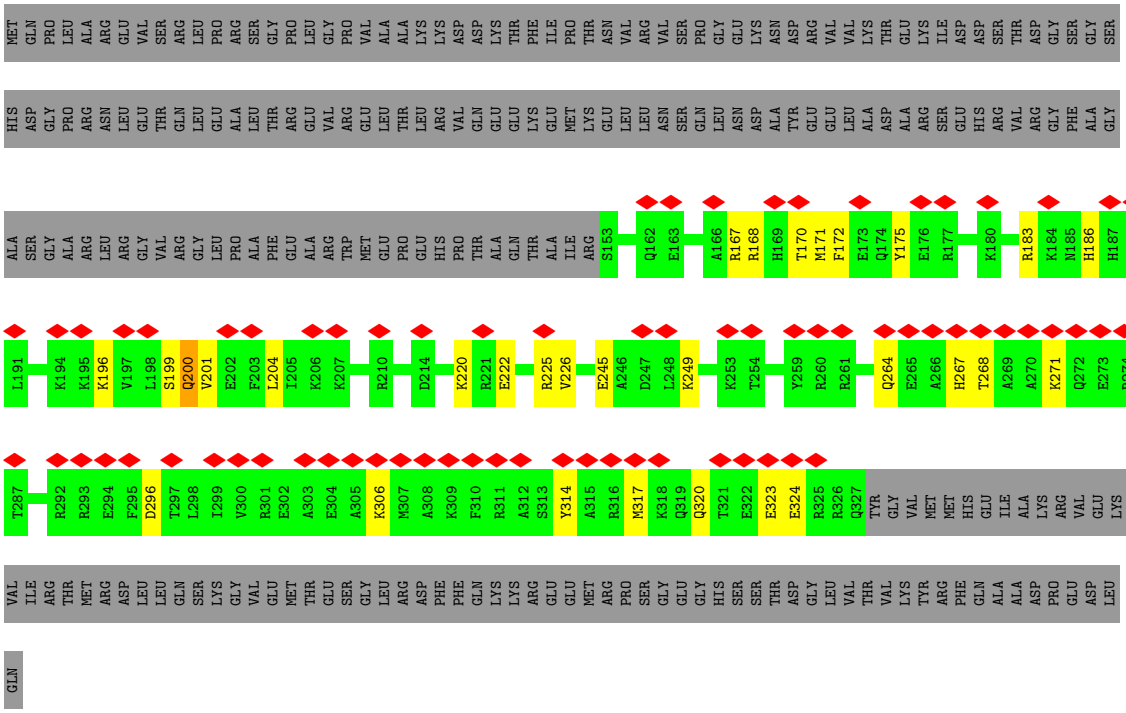
• Molecule 2: CF1, TGME49_222350

Chain 13:



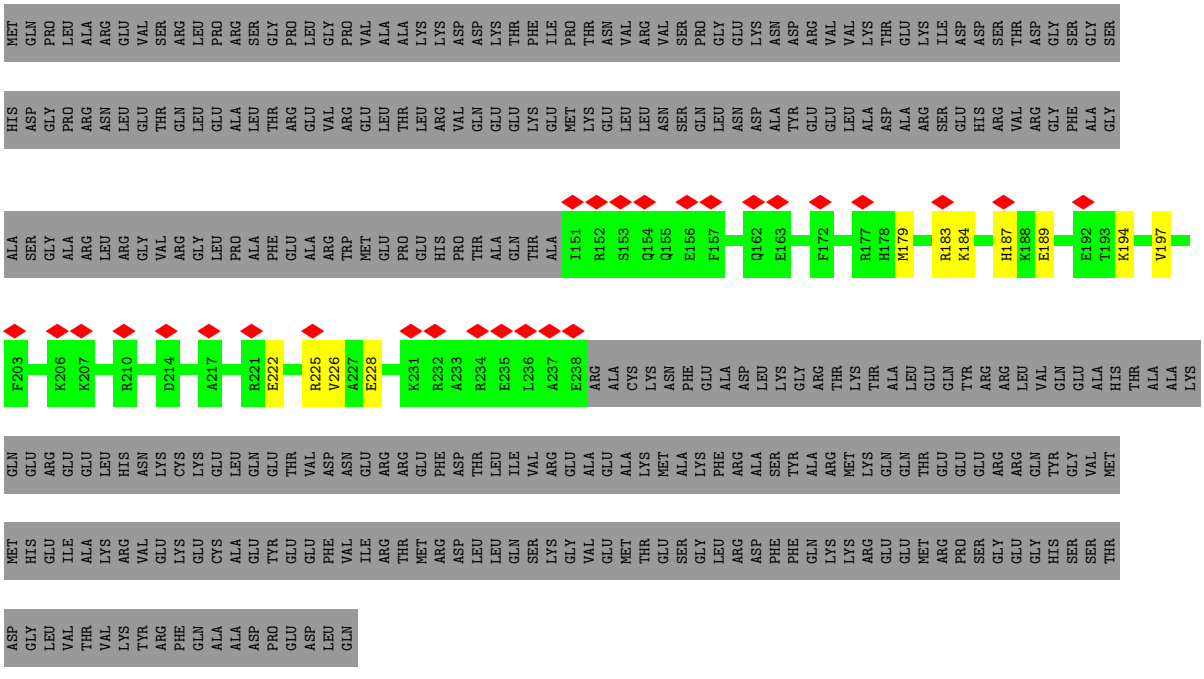
• Molecule 2: CF1, TGME49_222350

Chain 14:



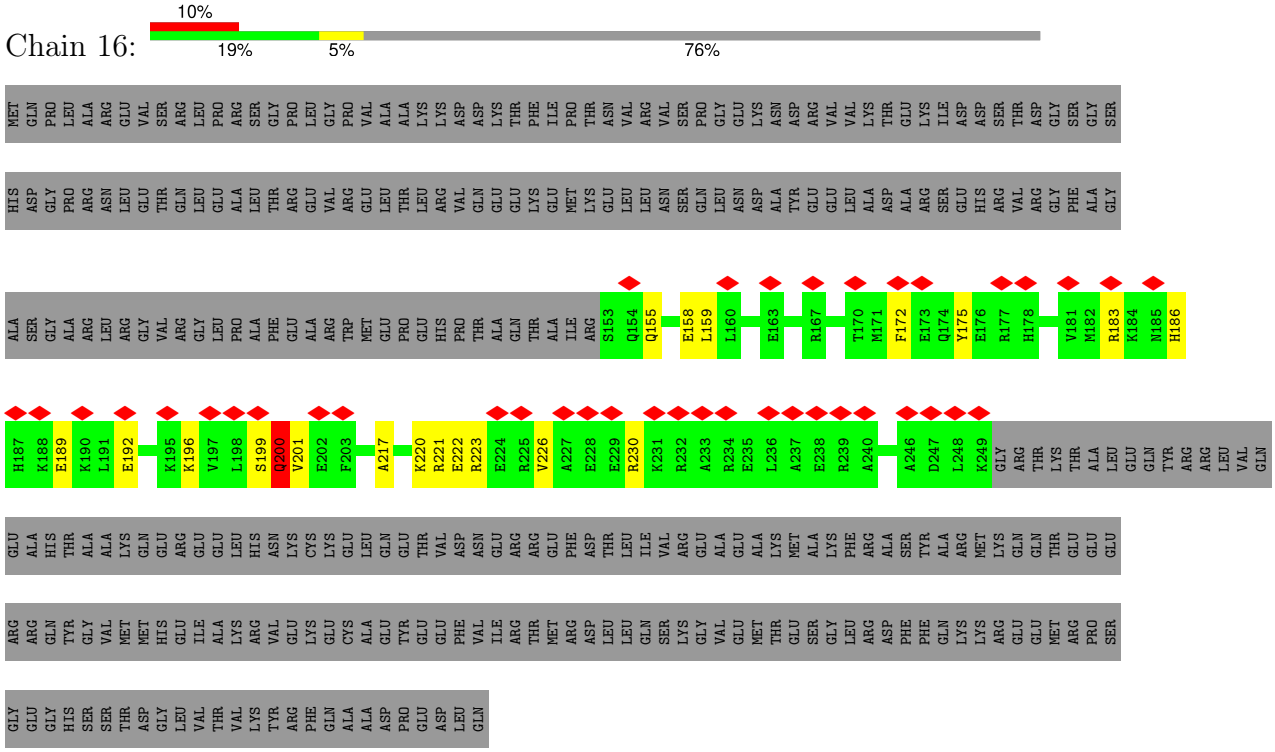
• Molecule 2: CF1, TGME49_222350

Chain 15:



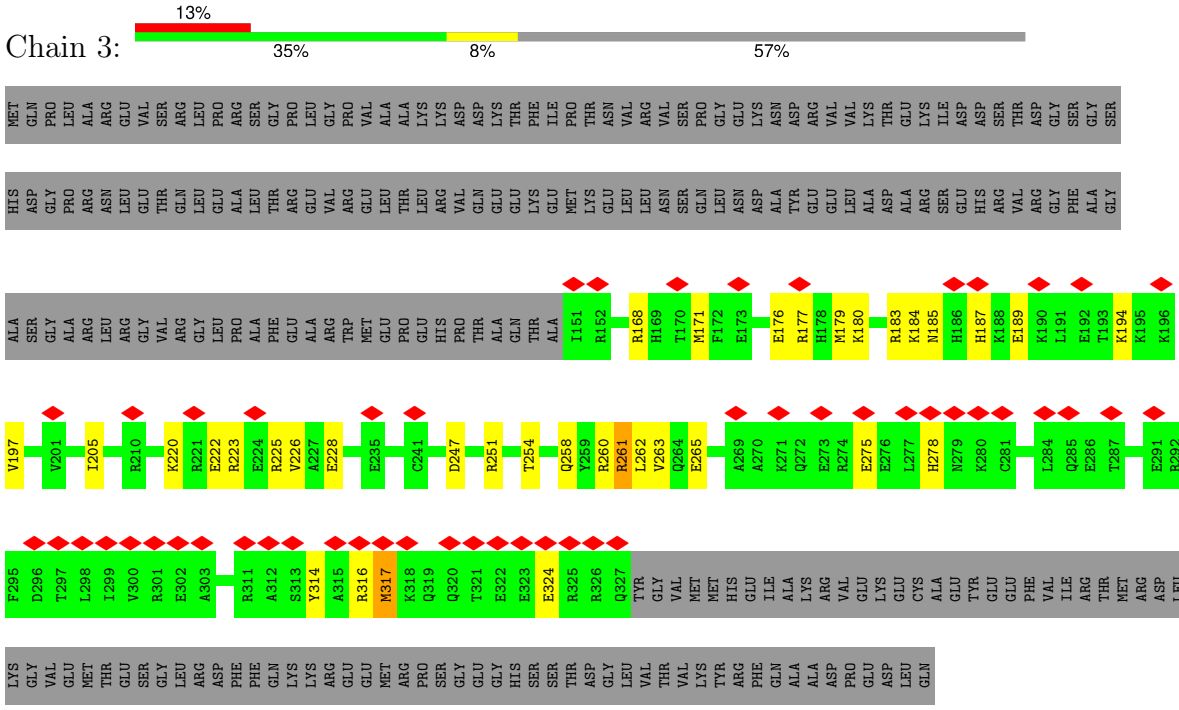
• Molecule 2: CF1, TGME49_222350

Chain 16:



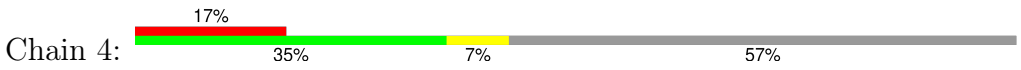
• Molecule 2: CF1, TGME49_222350

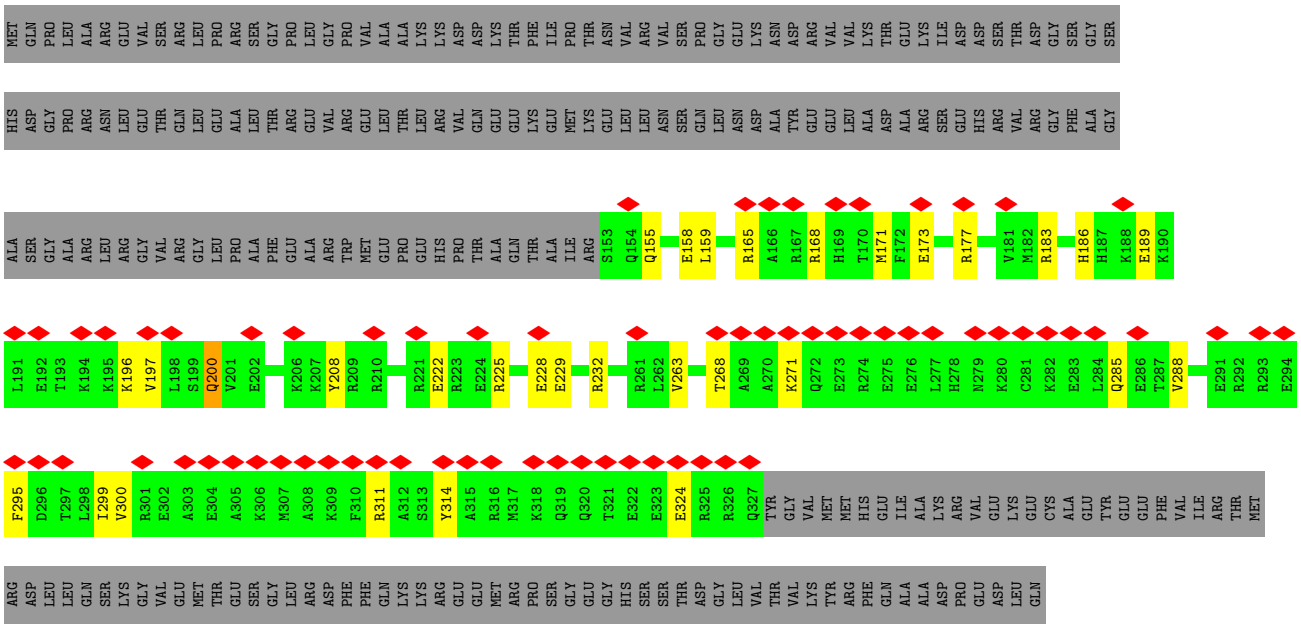
Chain 3:



• Molecule 2: CF1, TGME49_222350

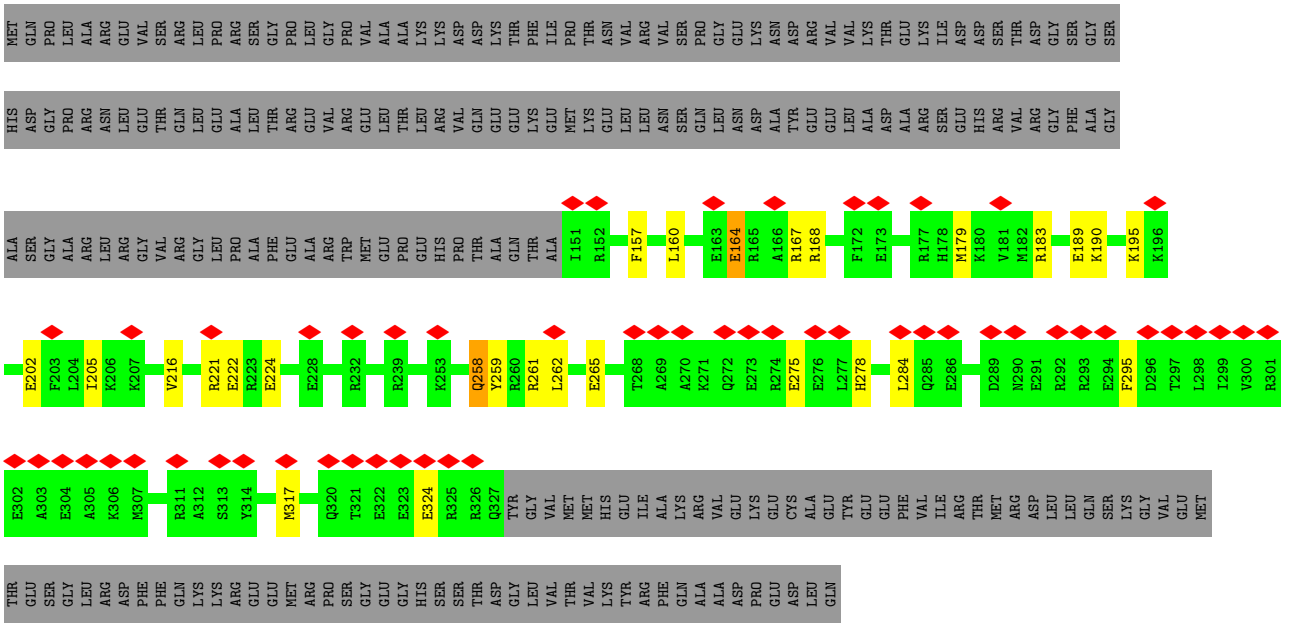
Chain 4:





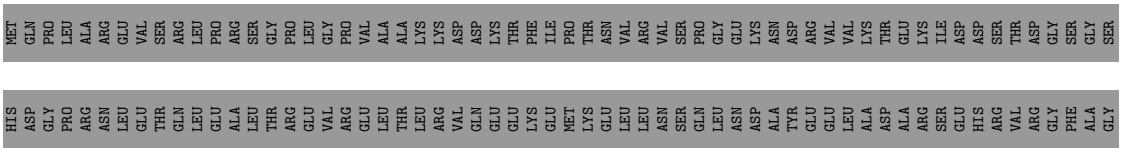
• Molecule 2: CF1, TGME49_222350

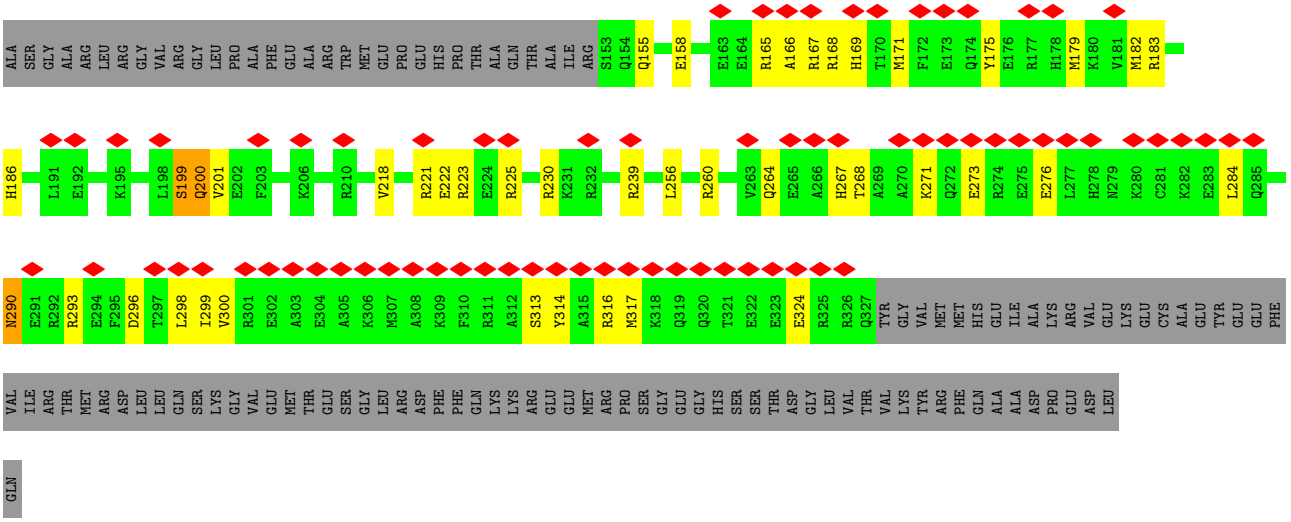
Chain 5:

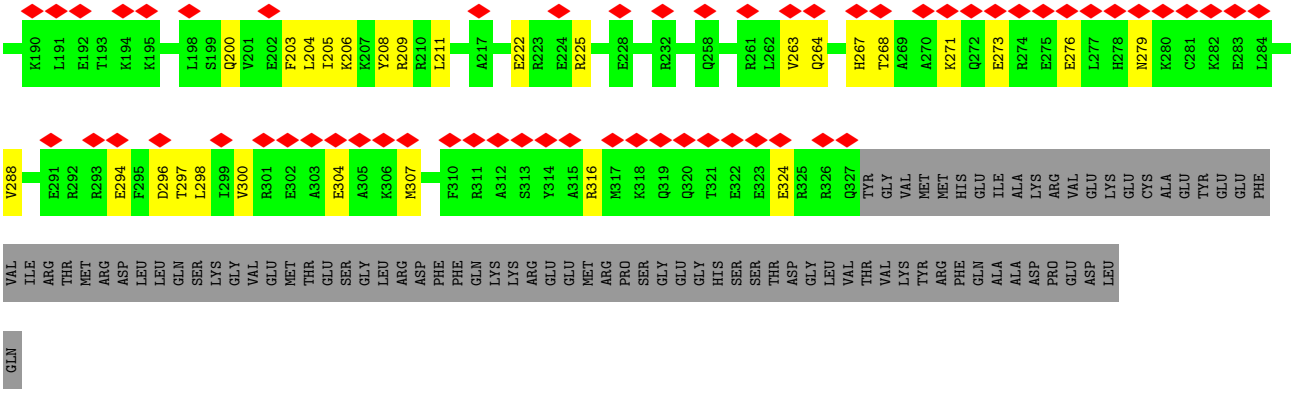


• Molecule 2: CF1, TGME49_222350

Chain 6:

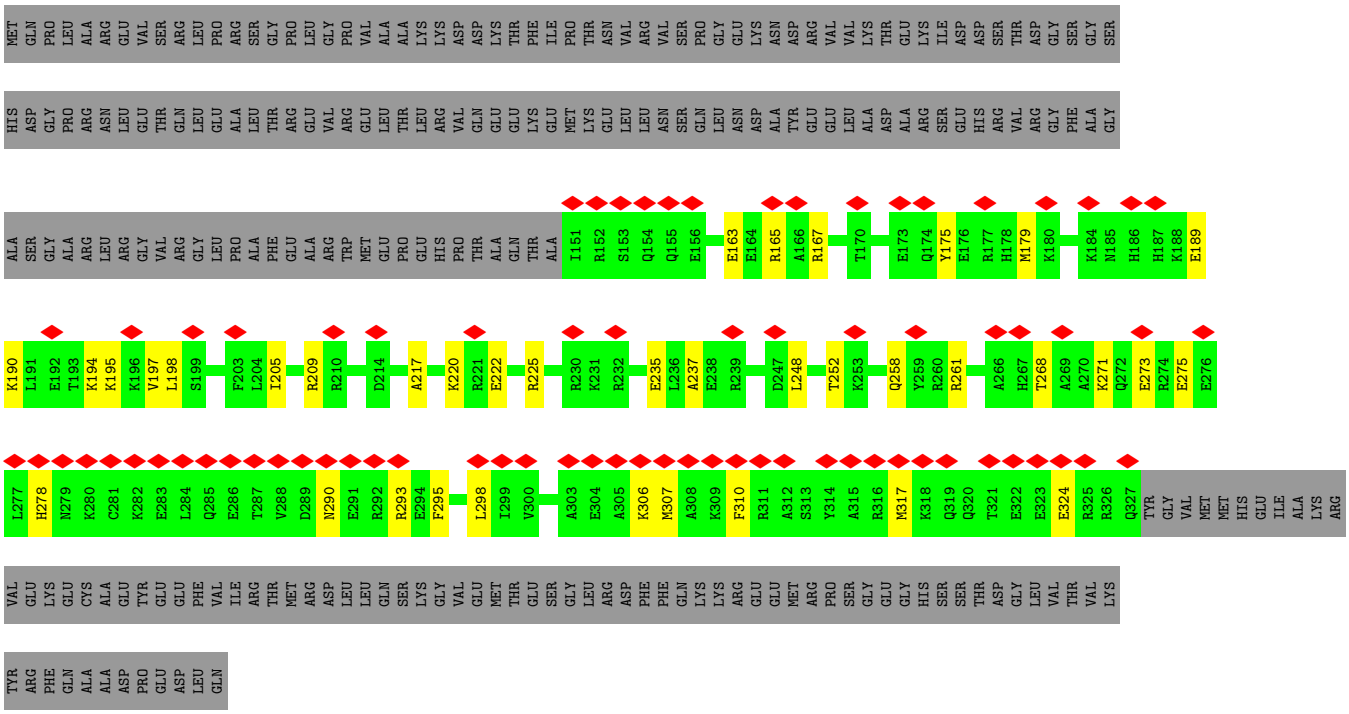






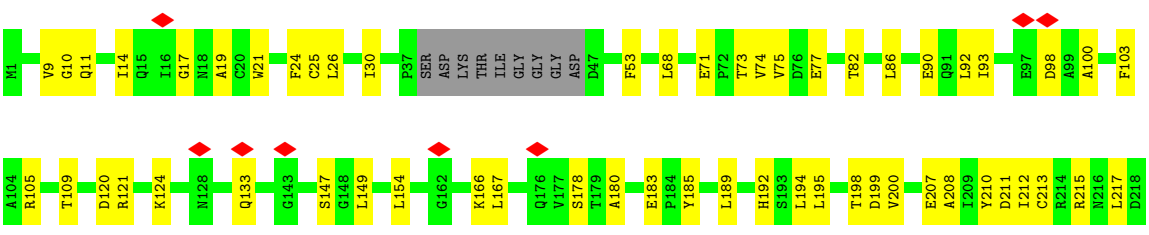
• Molecule 2: CF1, TGME49_222350

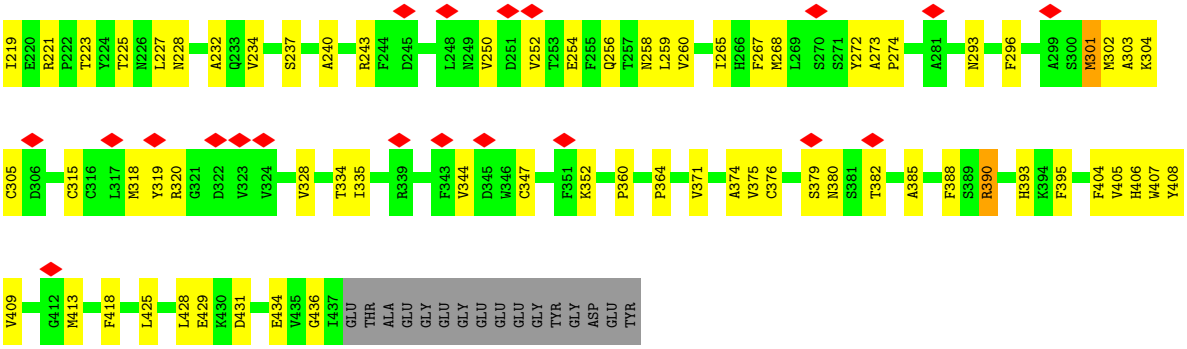
Chain 9:



• Molecule 3: Tubulin alpha chain

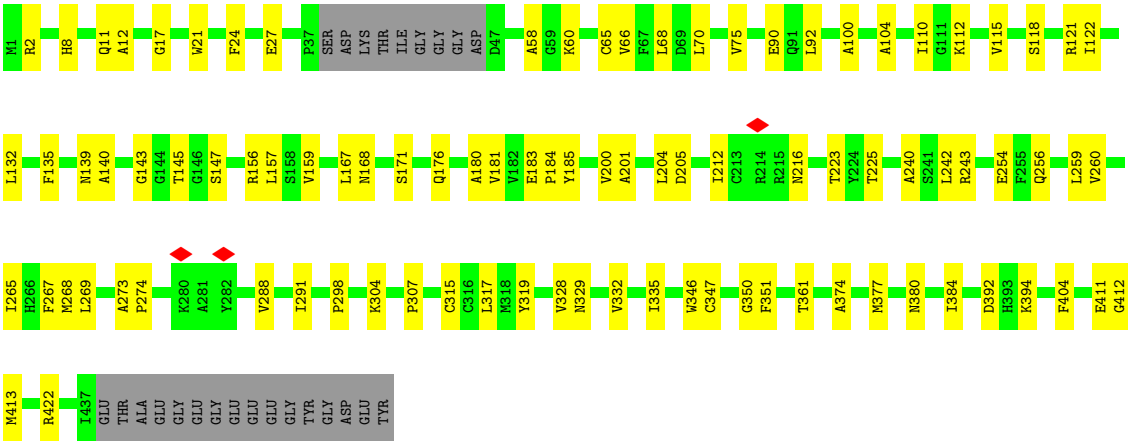
Chain 1A:





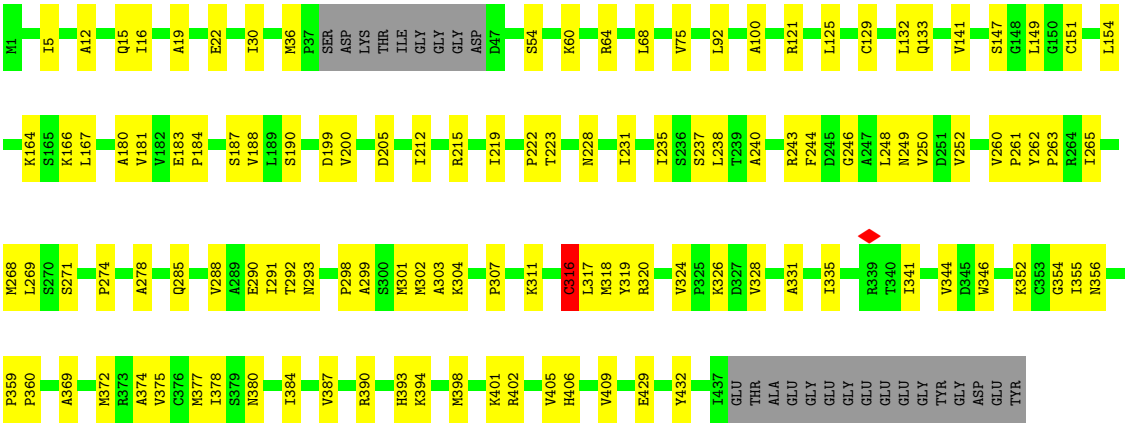
• Molecule 3: Tubulin alpha chain

Chain 1C:



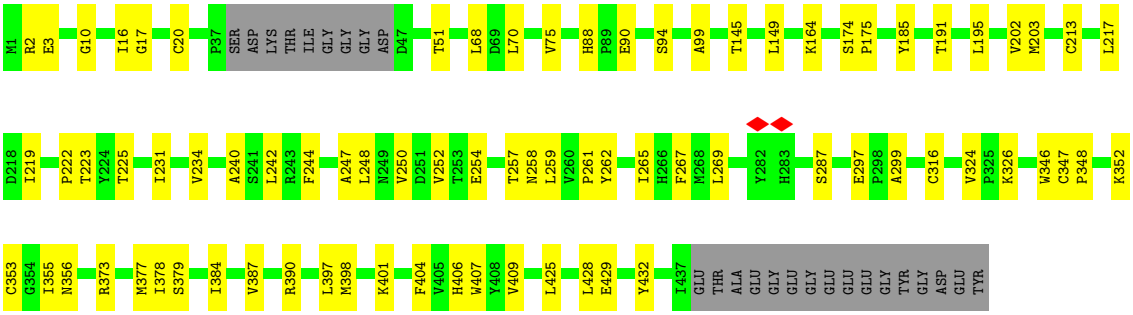
• Molecule 3: Tubulin alpha chain

Chain 1E:



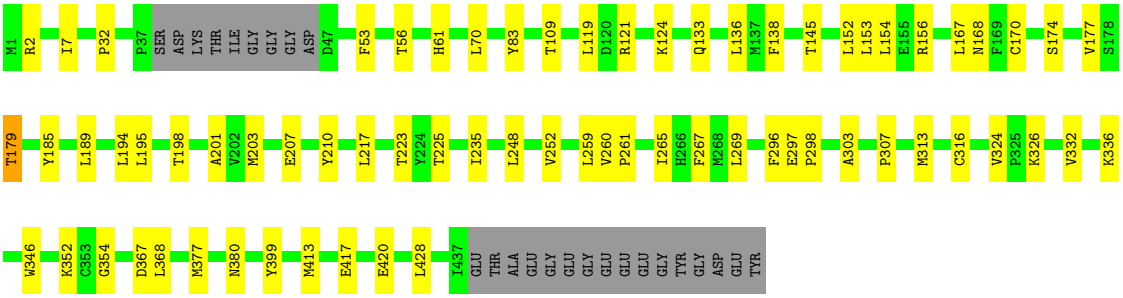
• Molecule 3: Tubulin alpha chain

Chain 1G:



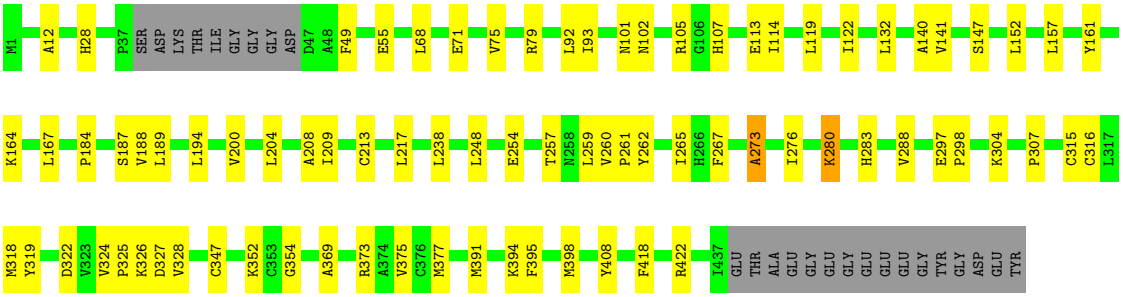
• Molecule 3: Tubulin alpha chain

Chain 1I:



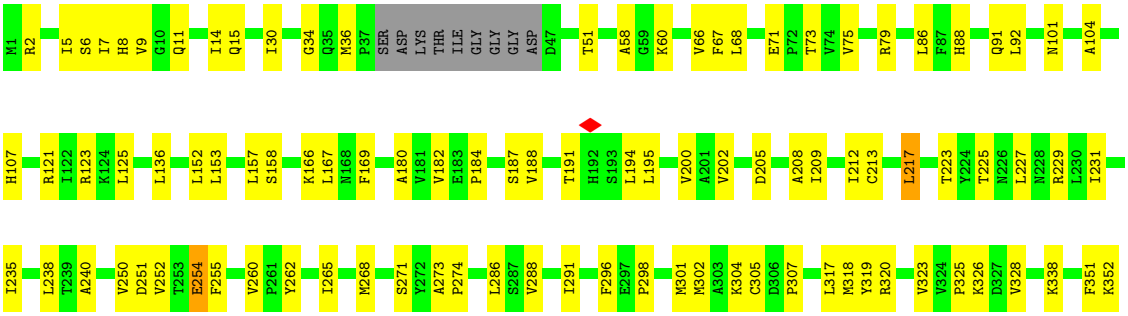
• Molecule 3: Tubulin alpha chain

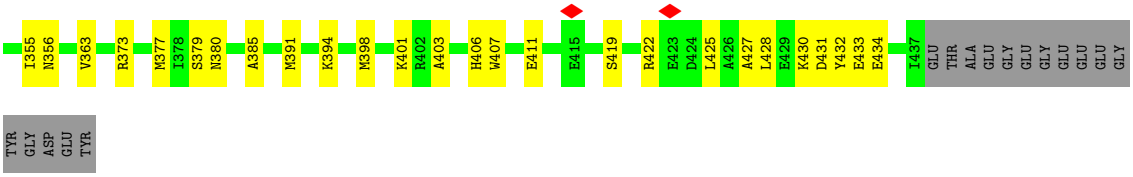
Chain 1K:



• Molecule 3: Tubulin alpha chain

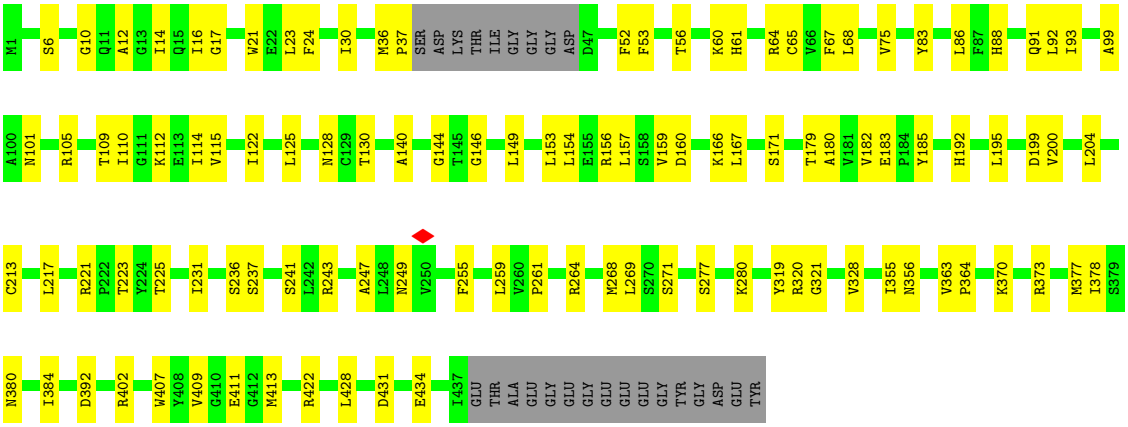
Chain 1M:





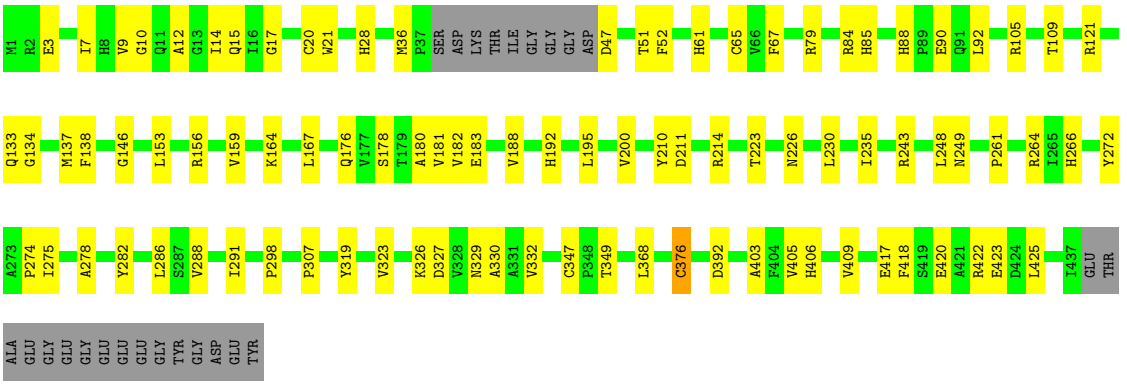
• Molecule 3: Tubulin alpha chain

Chain 2A:



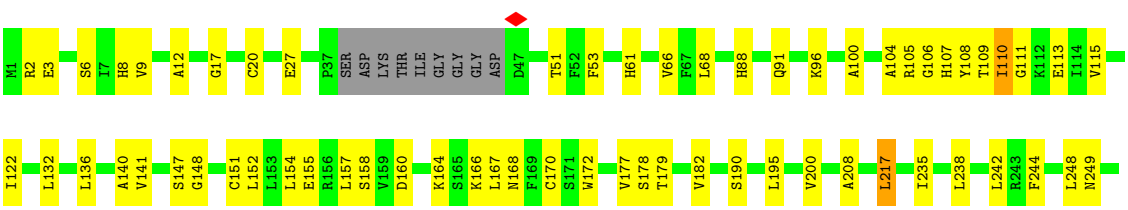
• Molecule 3: Tubulin alpha chain

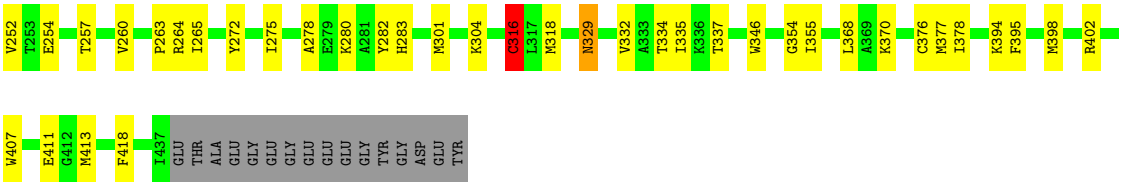
Chain 2C:



• Molecule 3: Tubulin alpha chain

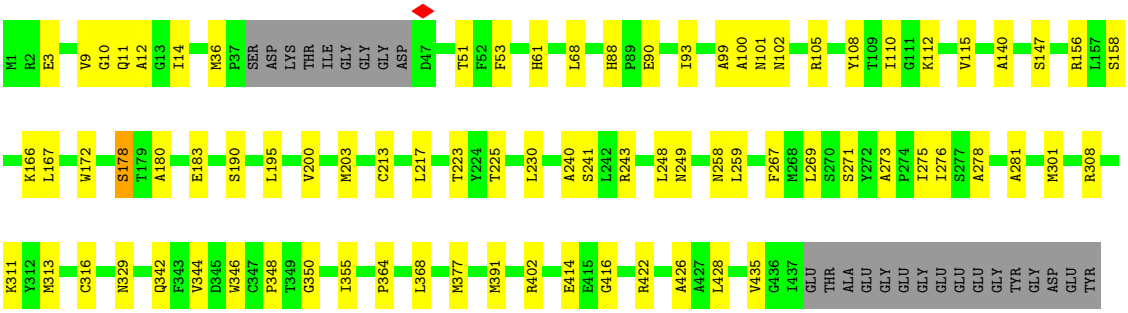
Chain 2E:





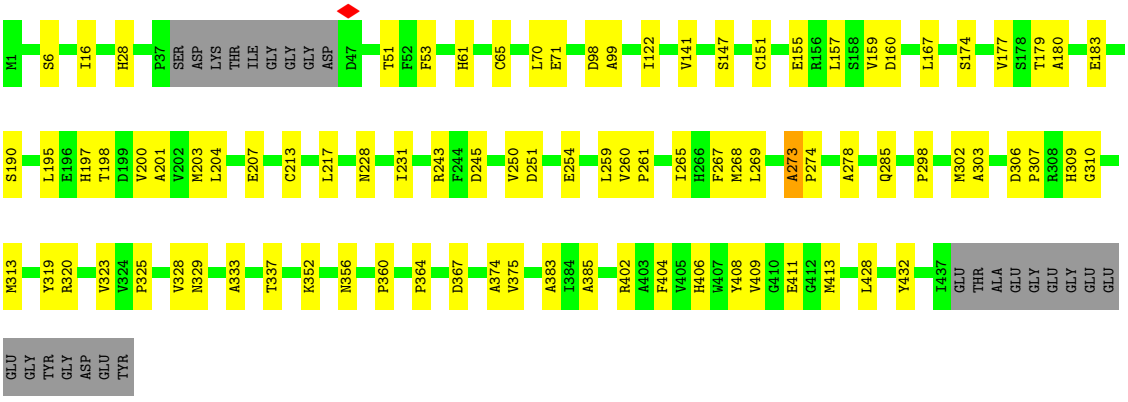
• Molecule 3: Tubulin alpha chain

Chain 2G:



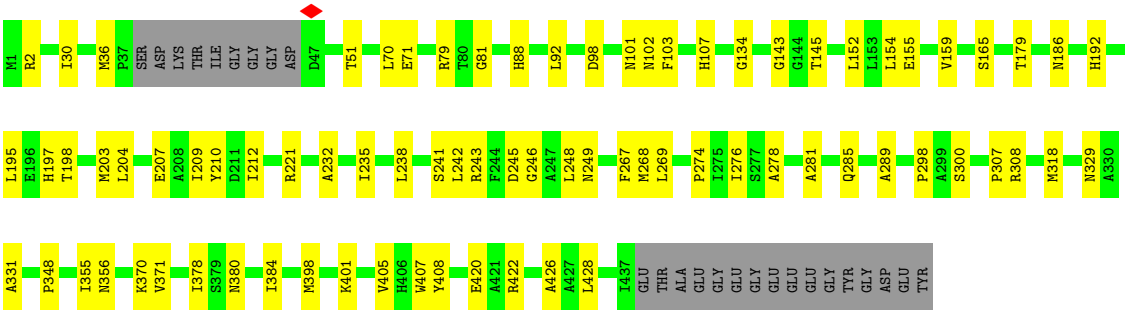
• Molecule 3: Tubulin alpha chain

Chain 2I:



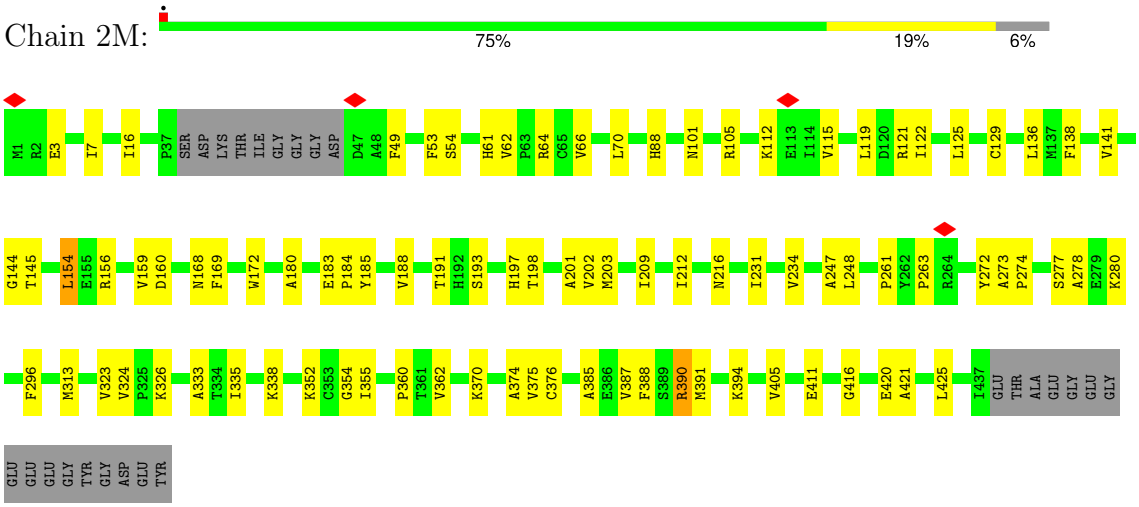
• Molecule 3: Tubulin alpha chain

Chain 2K:



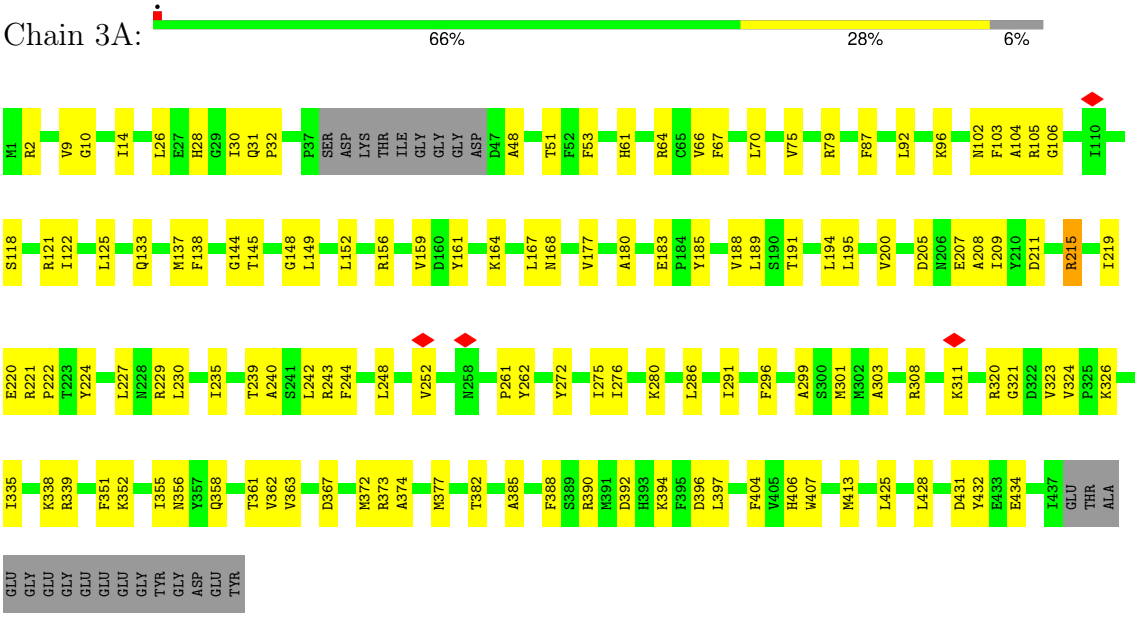
• Molecule 3: Tubulin alpha chain

Chain 2M:



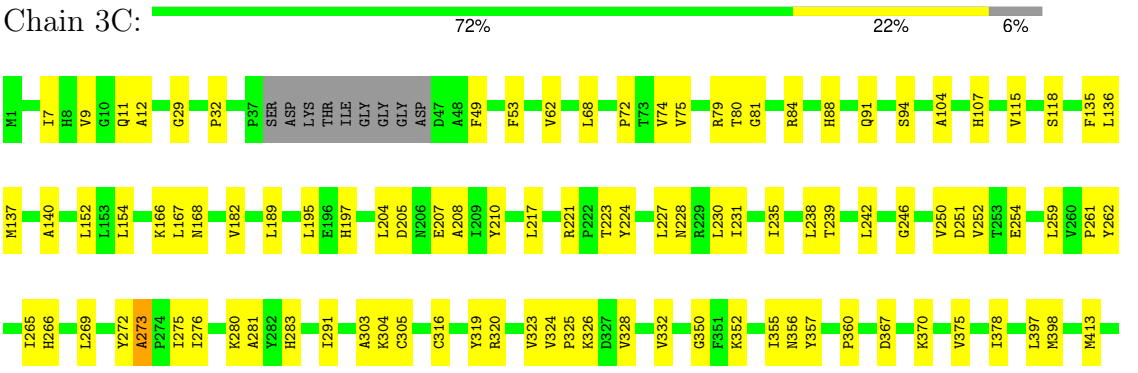
• Molecule 3: Tubulin alpha chain

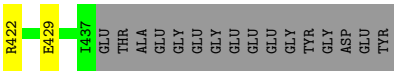
Chain 3A:



• Molecule 3: Tubulin alpha chain

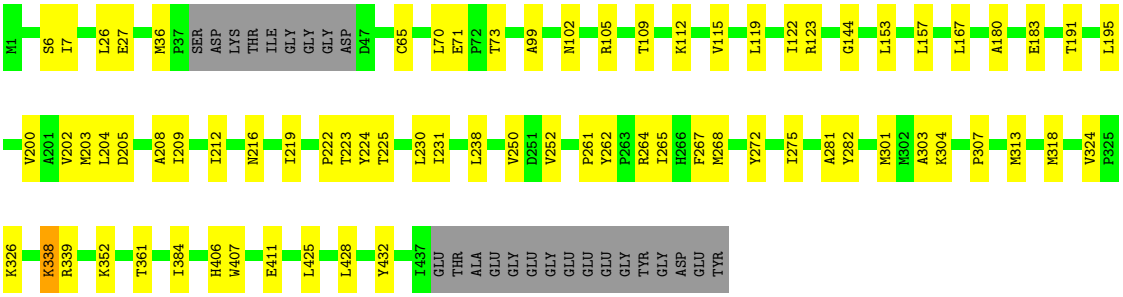
Chain 3C:





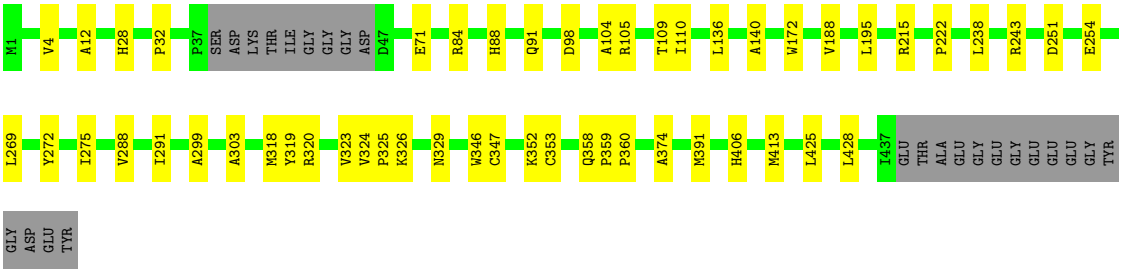
• Molecule 3: Tubulin alpha chain

Chain 3E:



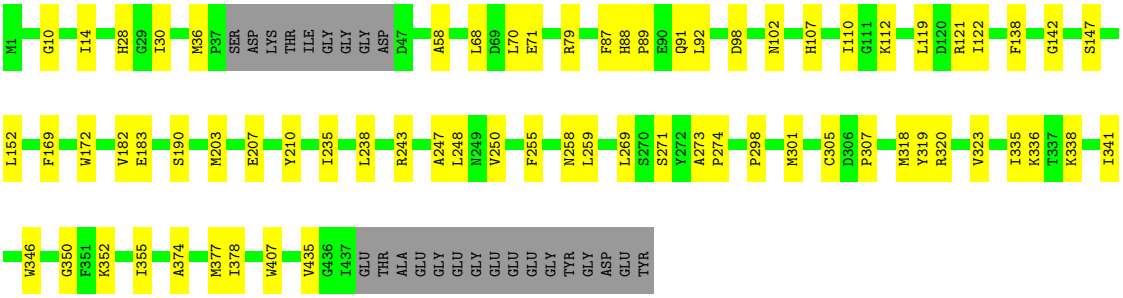
• Molecule 3: Tubulin alpha chain

Chain 3G:



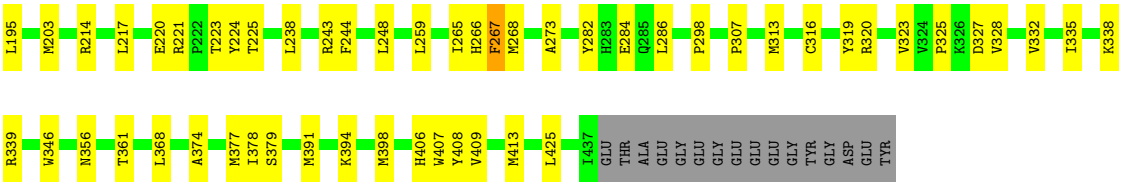
• Molecule 3: Tubulin alpha chain

Chain 3I:



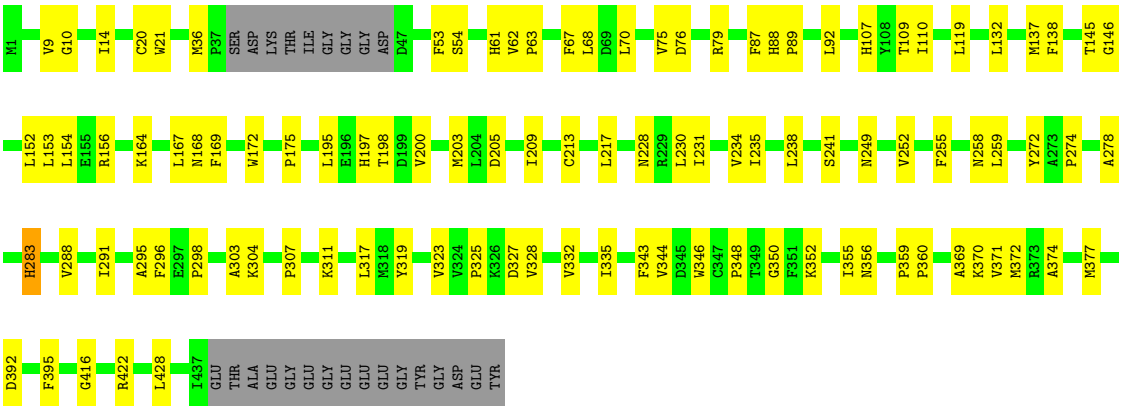
• Molecule 3: Tubulin alpha chain

Chain 3K:



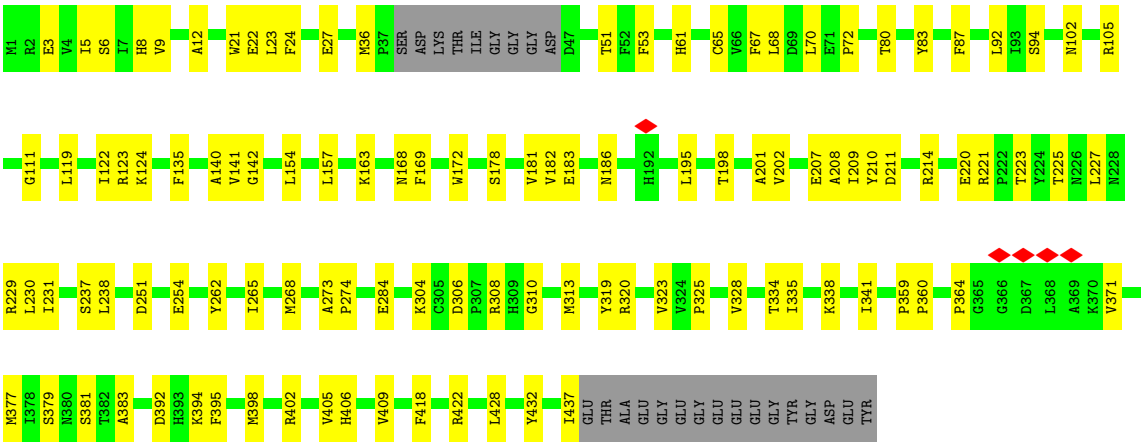
• Molecule 3: Tubulin alpha chain

Chain 3M:



• Molecule 3: Tubulin alpha chain

Chain 4A:

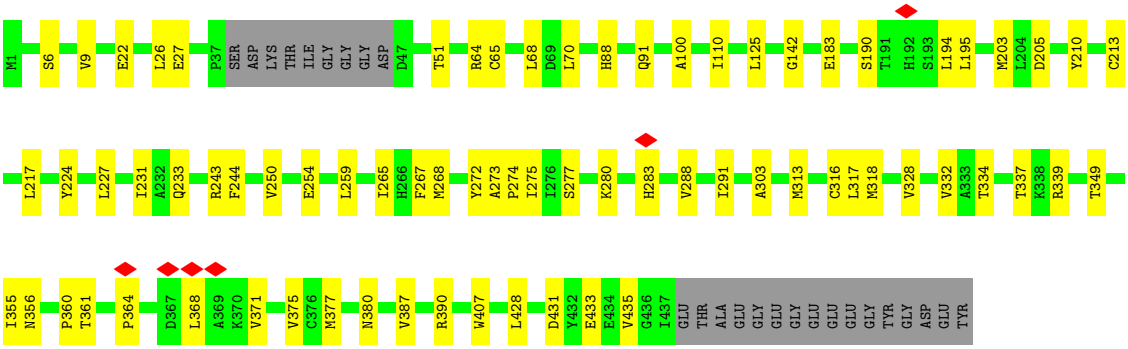


• Molecule 3: Tubulin alpha chain

Chain 4C:

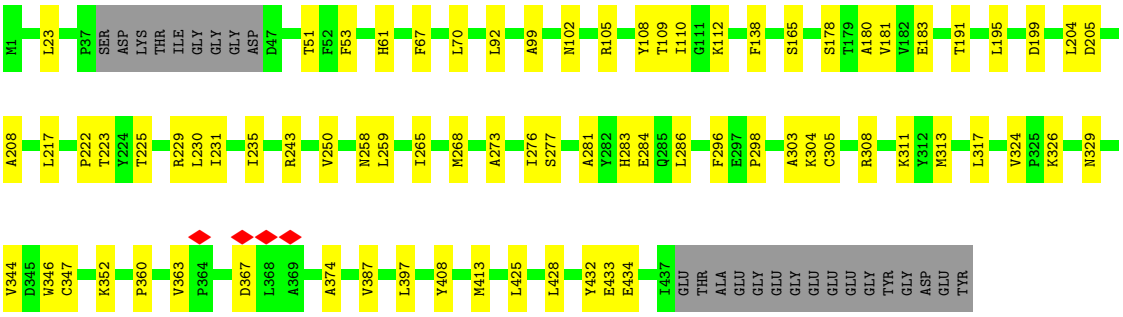
• Molecule 3: Tubulin alpha chain

Chain 4E:



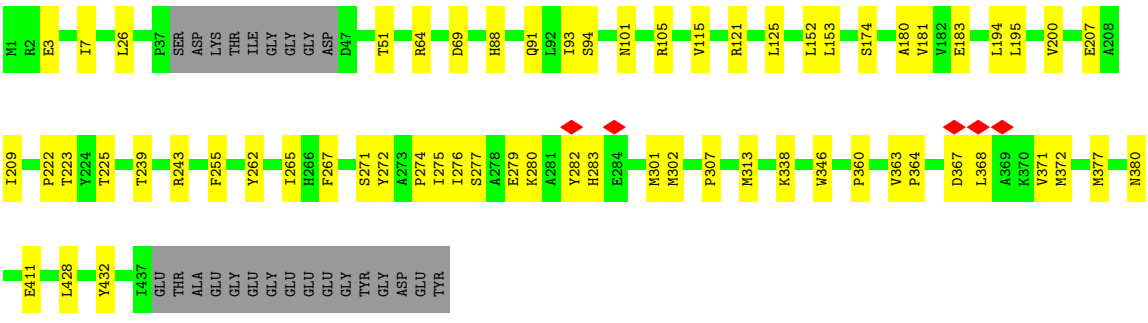
• Molecule 3: Tubulin alpha chain

Chain 4G:



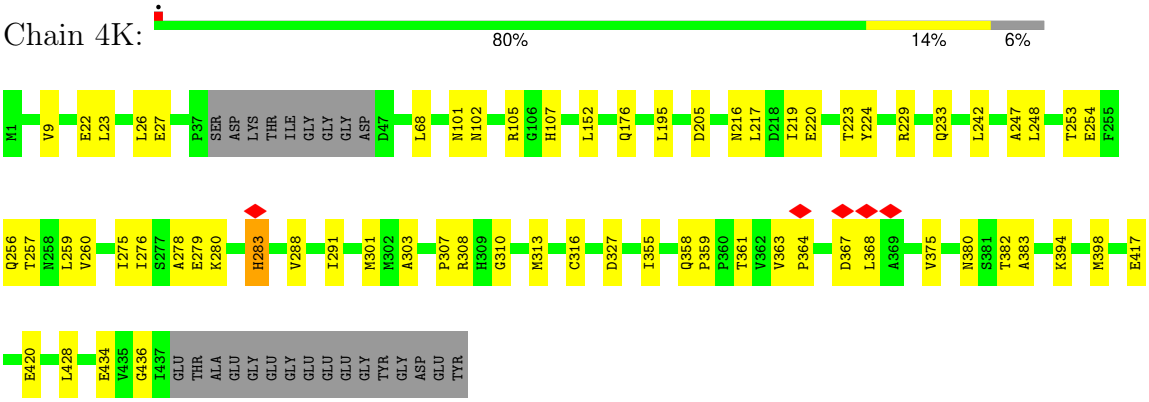
• Molecule 3: Tubulin alpha chain

Chain 4I:



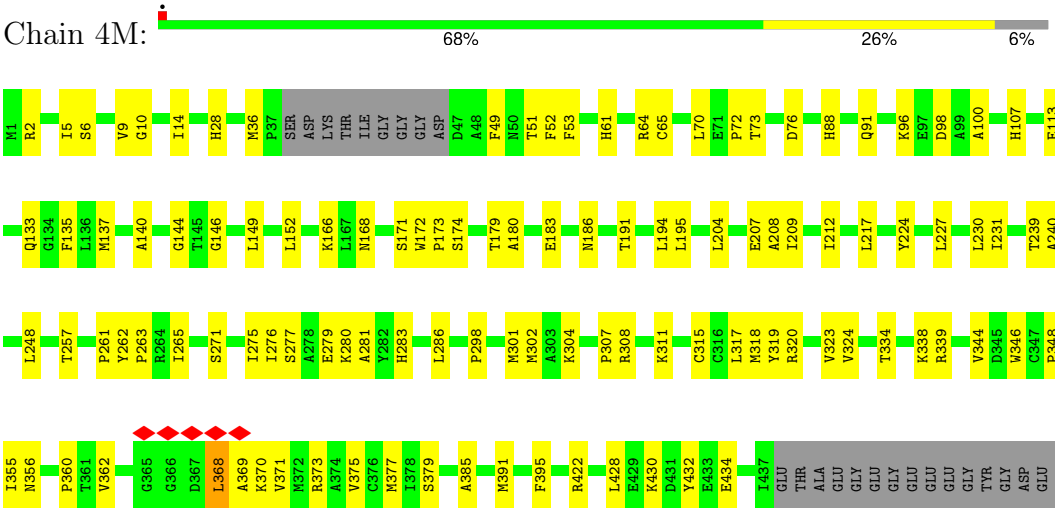
• Molecule 3: Tubulin alpha chain

Chain 4K:



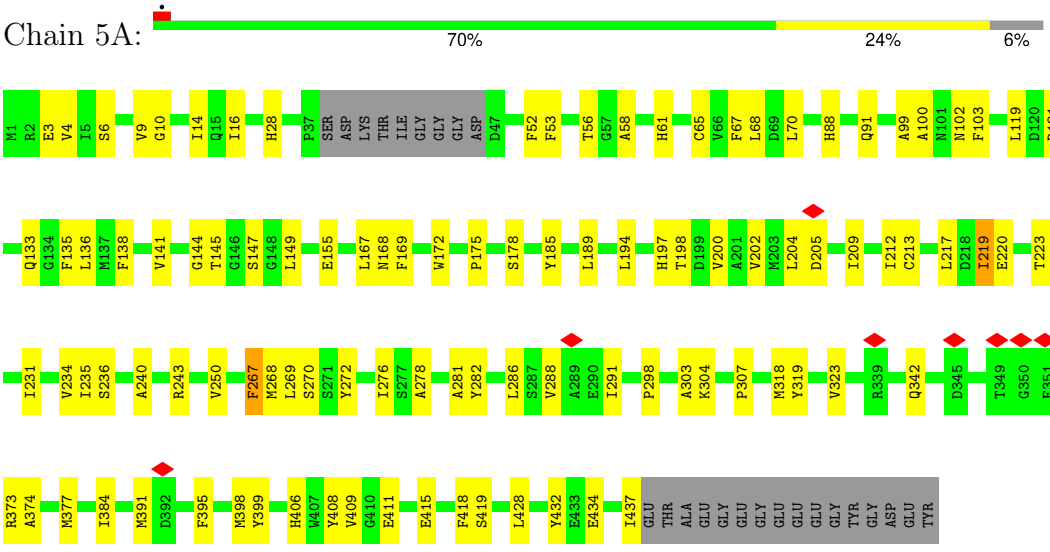
• Molecule 3: Tubulin alpha chain

Chain 4M:



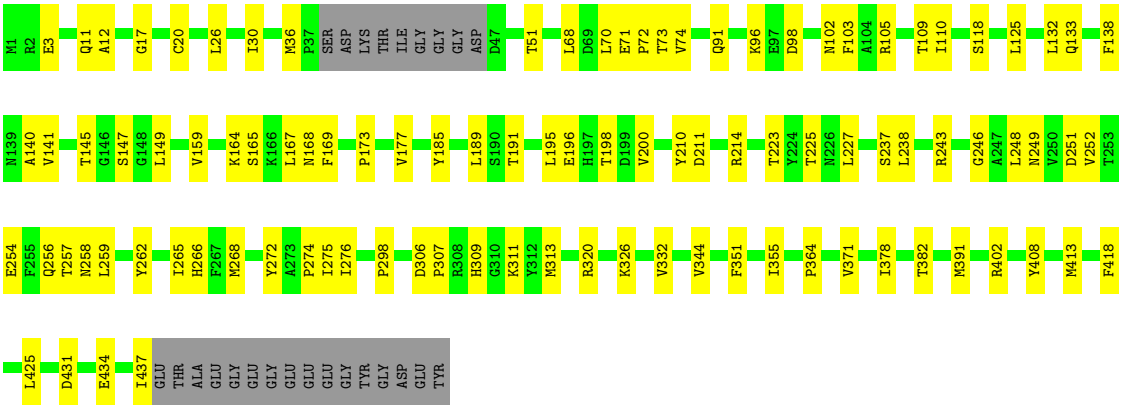
• Molecule 3: Tubulin alpha chain

Chain 5A:



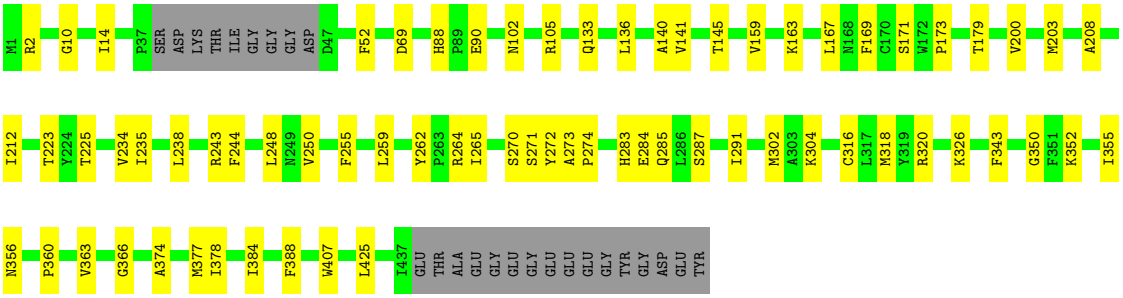
• Molecule 3: Tubulin alpha chain

Chain 5C:



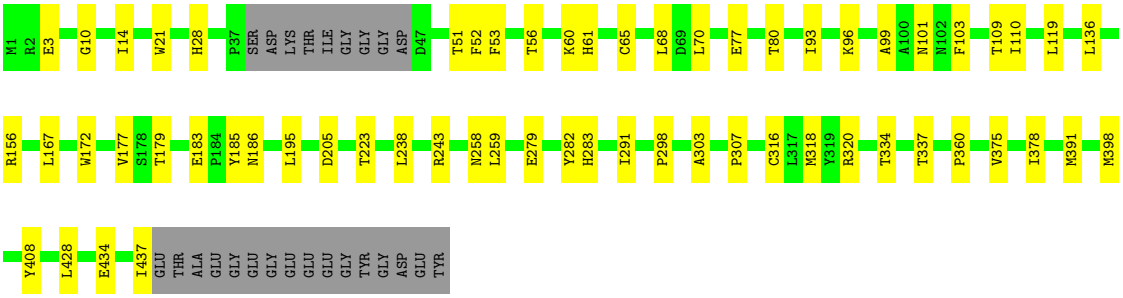
• Molecule 3: Tubulin alpha chain

Chain 5E:



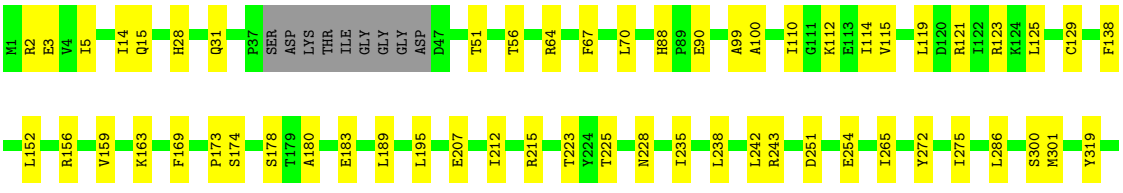
• Molecule 3: Tubulin alpha chain

Chain 5G:



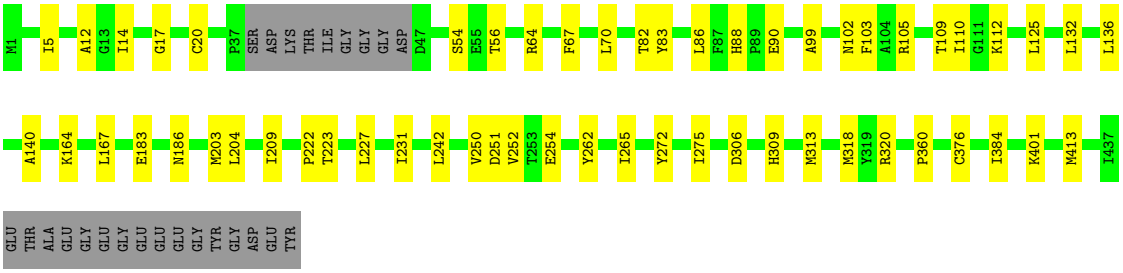
• Molecule 3: Tubulin alpha chain

Chain 5I:



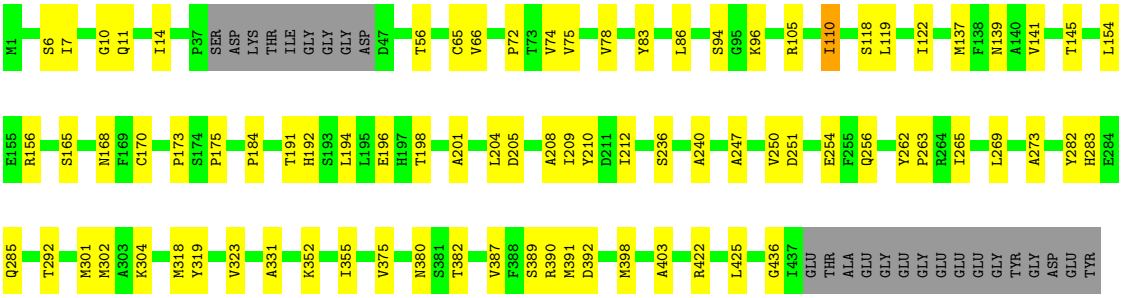
• Molecule 3: Tubulin alpha chain

Chain 5K:



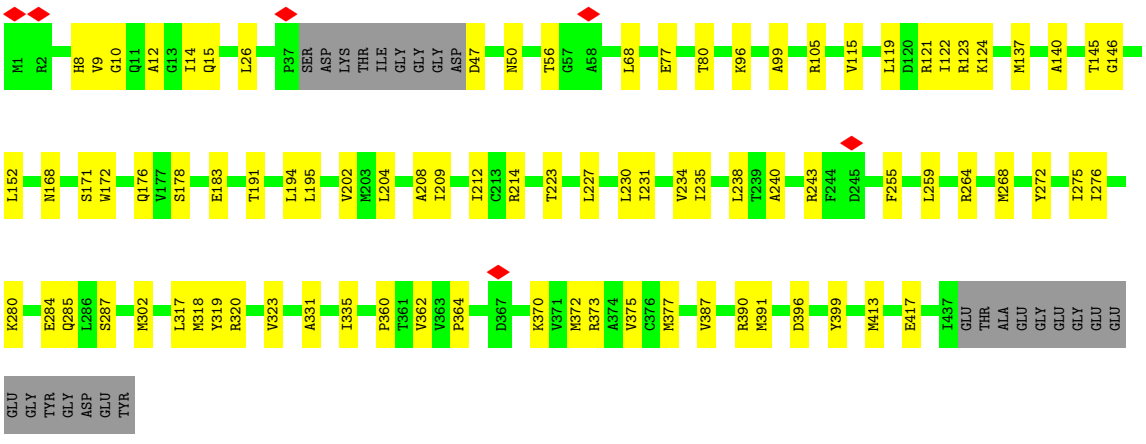
• Molecule 3: Tubulin alpha chain

Chain 5M:



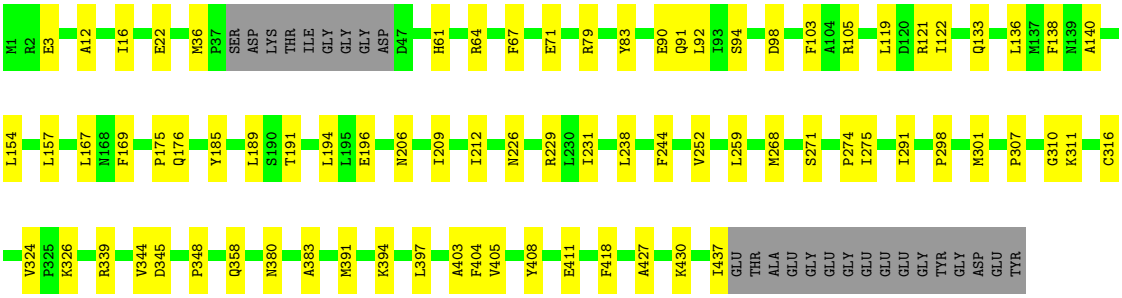
• Molecule 3: Tubulin alpha chain

Chain 6A:



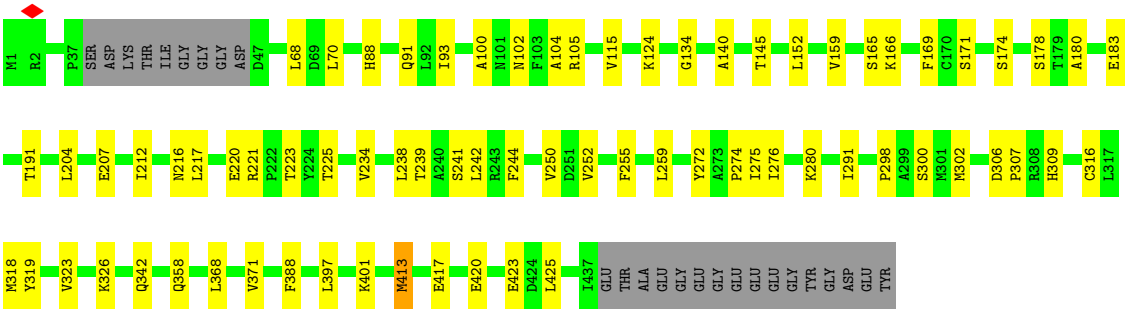
• Molecule 3: Tubulin alpha chain

Chain 6C:



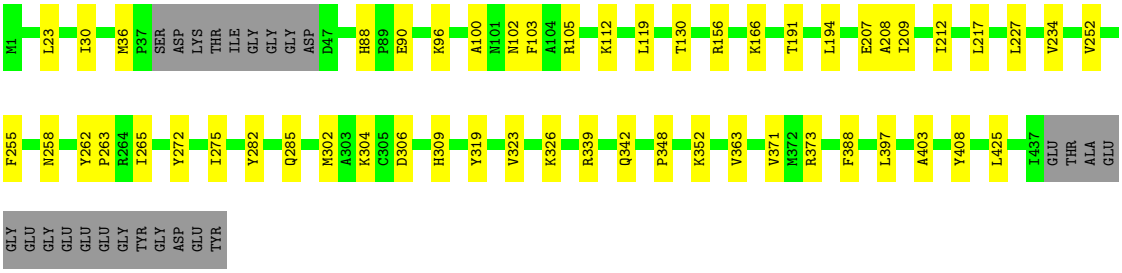
• Molecule 3: Tubulin alpha chain

Chain 6E:



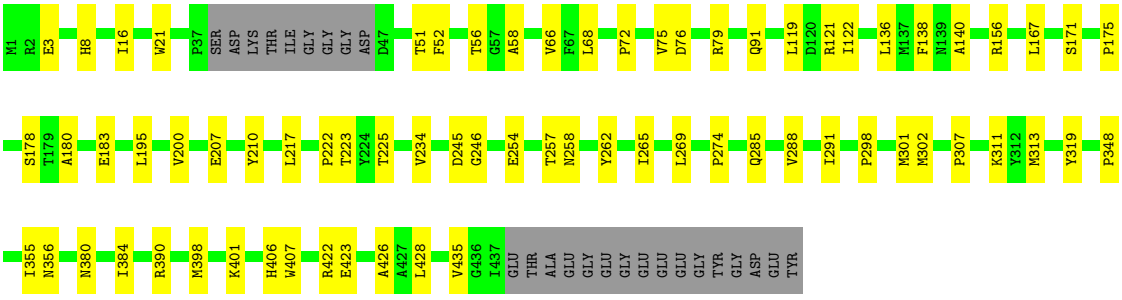
• Molecule 3: Tubulin alpha chain

Chain 6G:



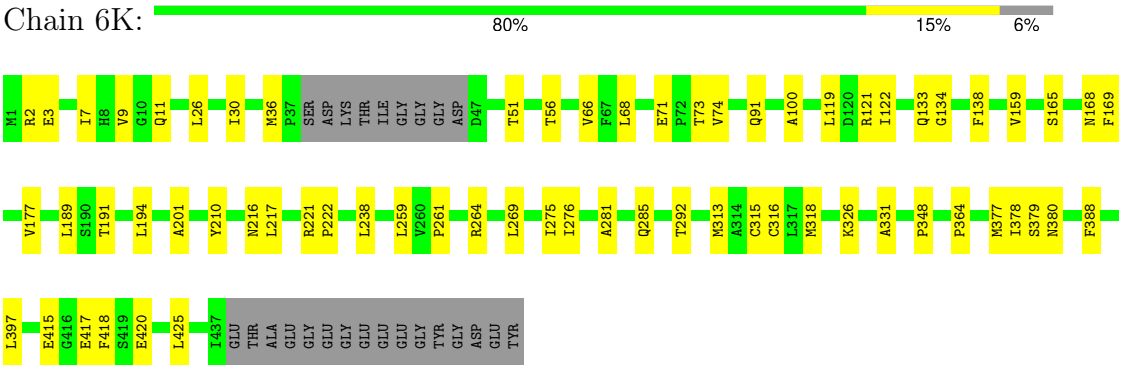
• Molecule 3: Tubulin alpha chain

Chain 6I:



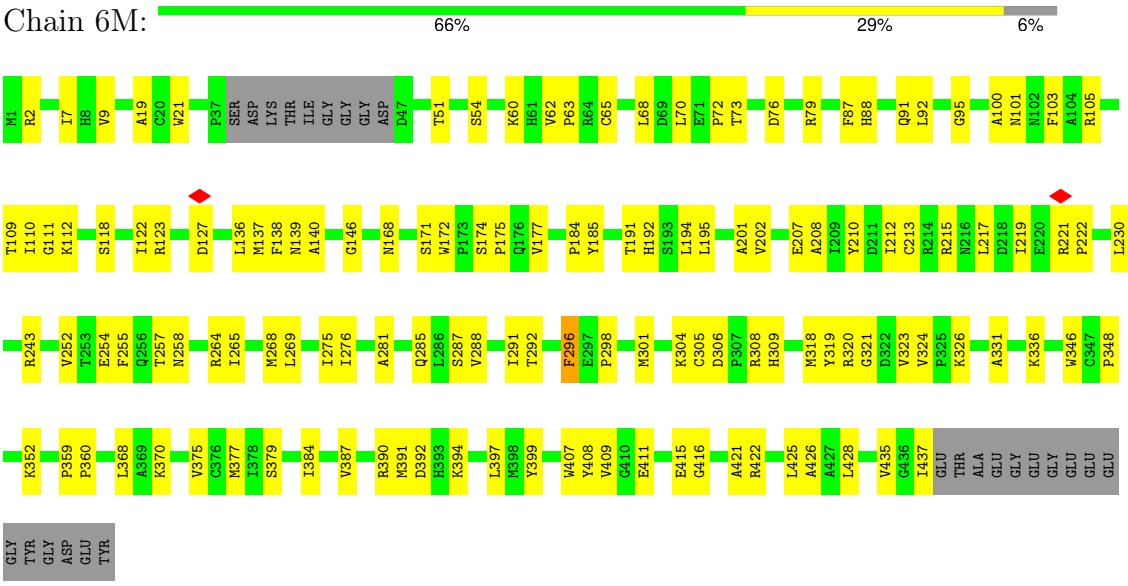
• Molecule 3: Tubulin alpha chain

Chain 6K:



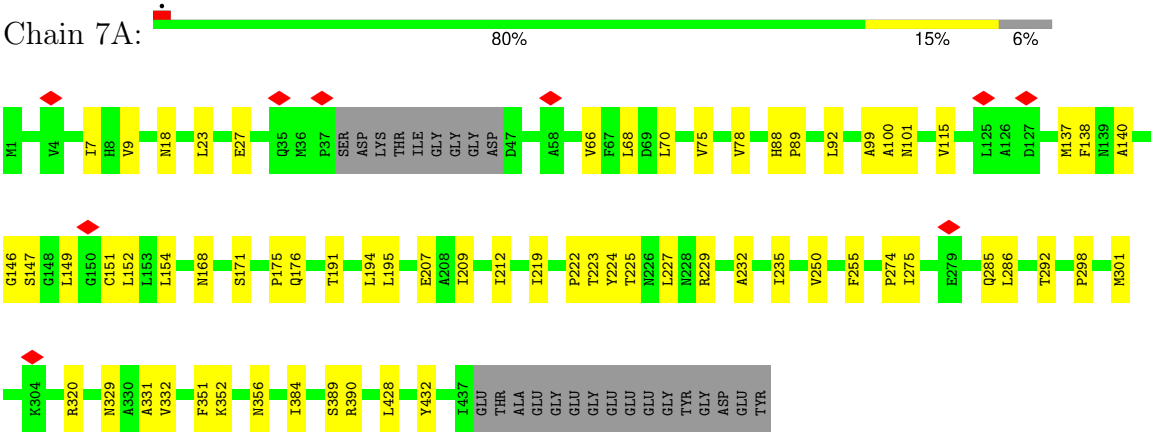
• Molecule 3: Tubulin alpha chain

Chain 6M:



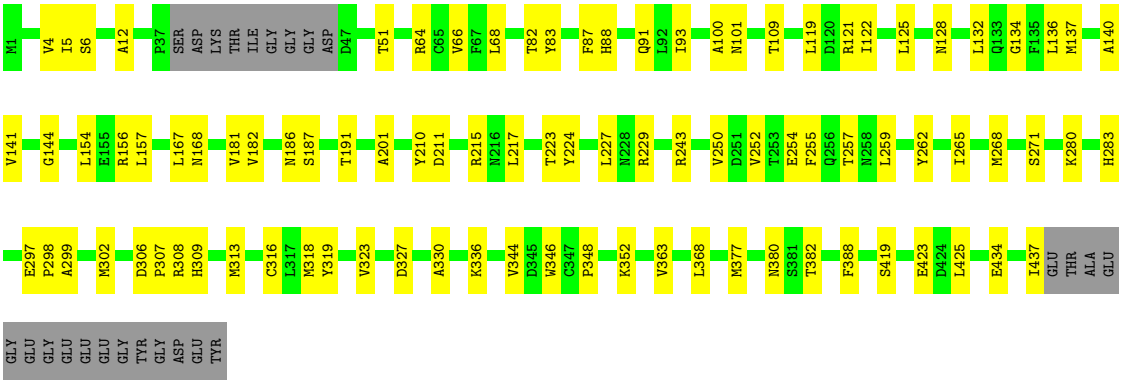
• Molecule 3: Tubulin alpha chain

Chain 7A:



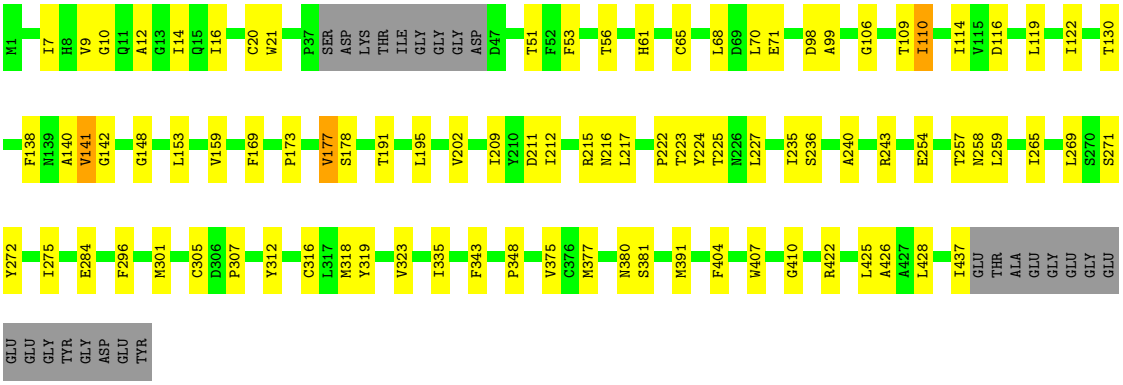
• Molecule 3: Tubulin alpha chain

Chain 7C:



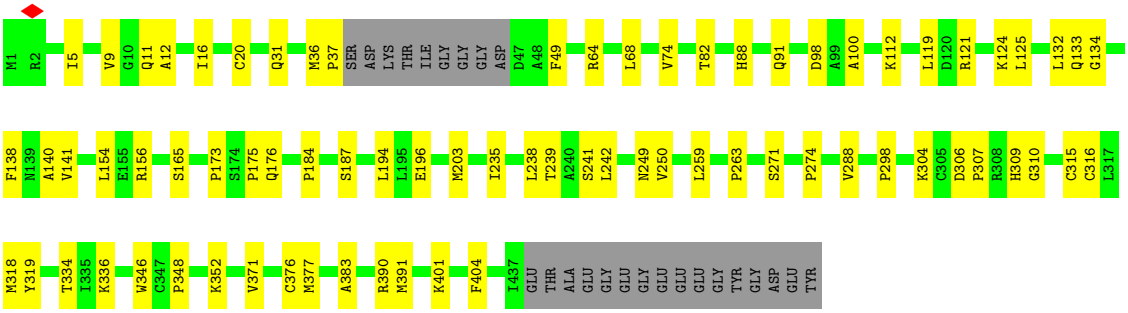
• Molecule 3: Tubulin alpha chain

Chain 7E:



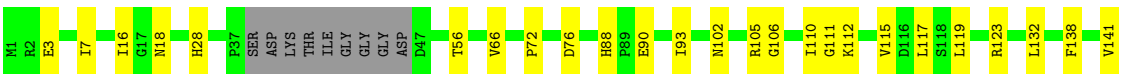
• Molecule 3: Tubulin alpha chain

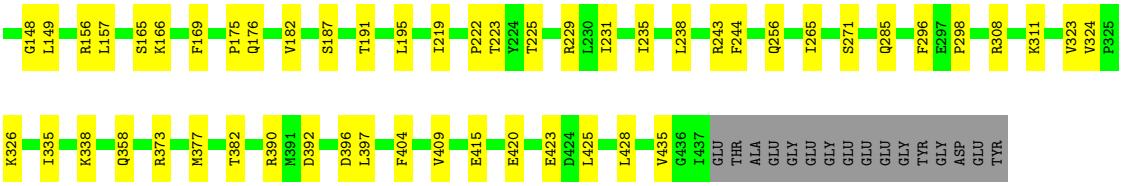
Chain 7G:



• Molecule 3: Tubulin alpha chain

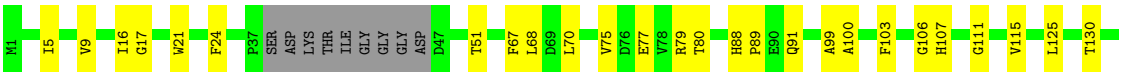
Chain 7I:

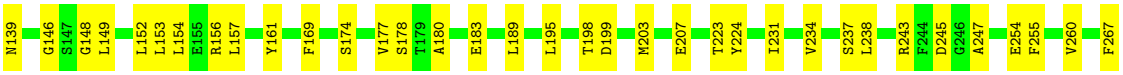


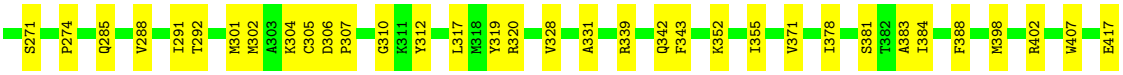


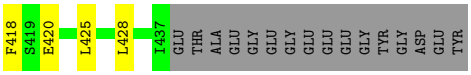
• Molecule 3: Tubulin alpha chain

Chain 7K:



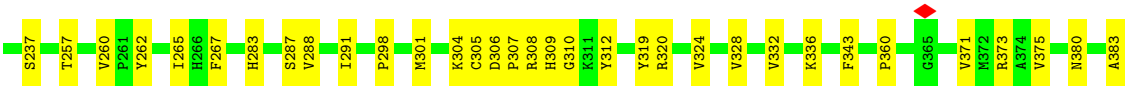


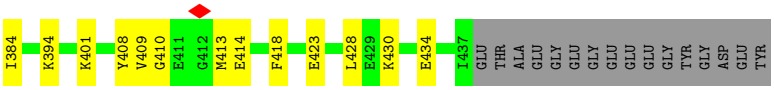




• Molecule 3: Tubulin alpha chain

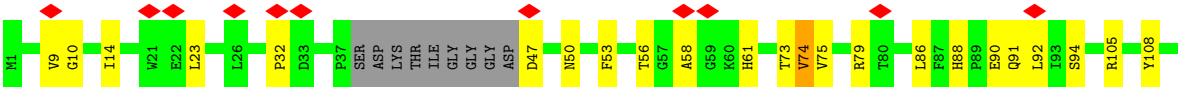
Chain 7M:

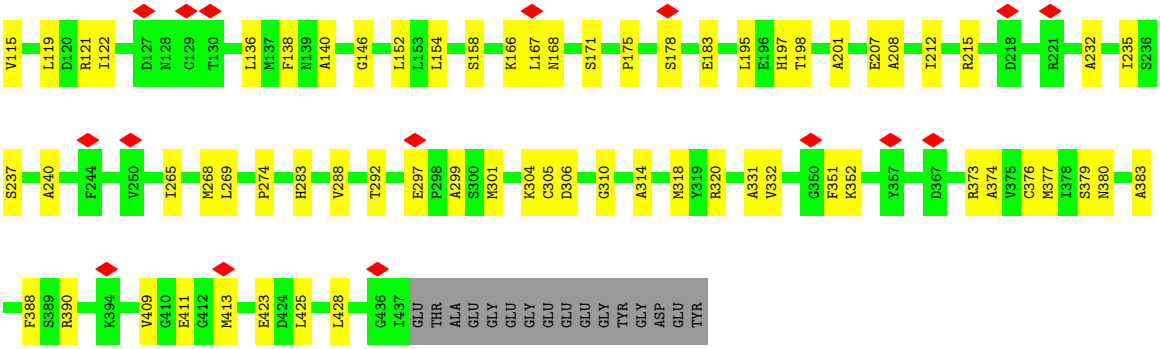




• Molecule 3: Tubulin alpha chain

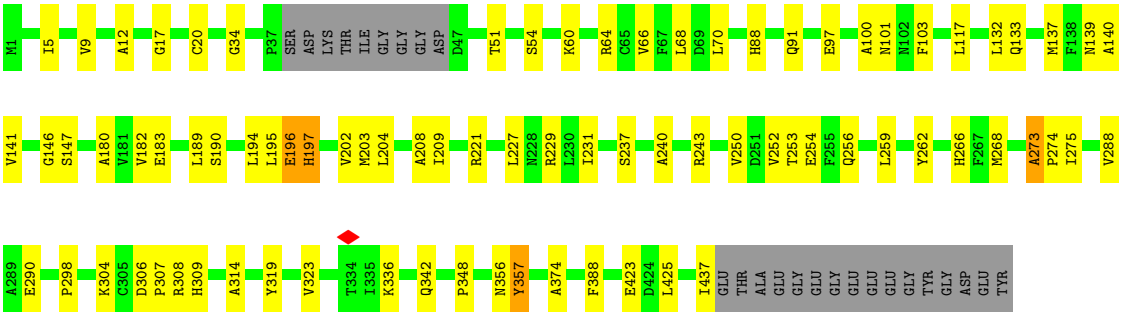
Chain 8A:





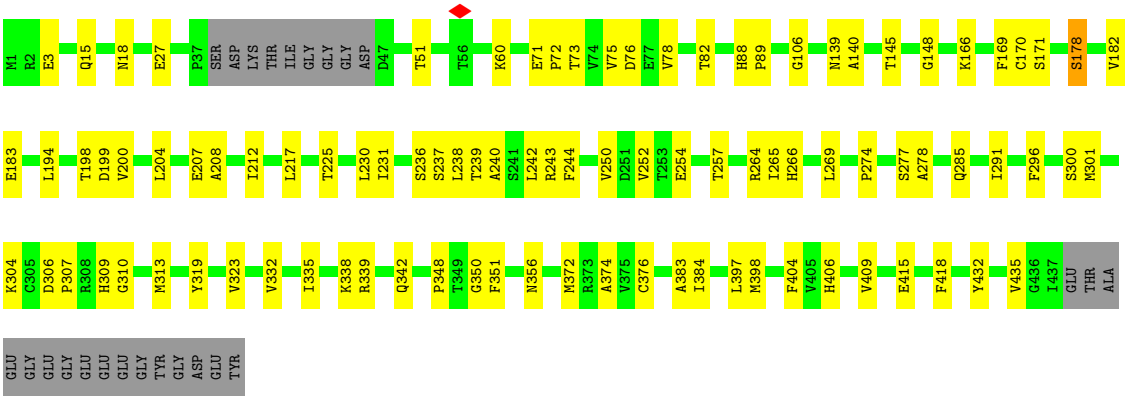
• Molecule 3: Tubulin alpha chain

Chain 8C:



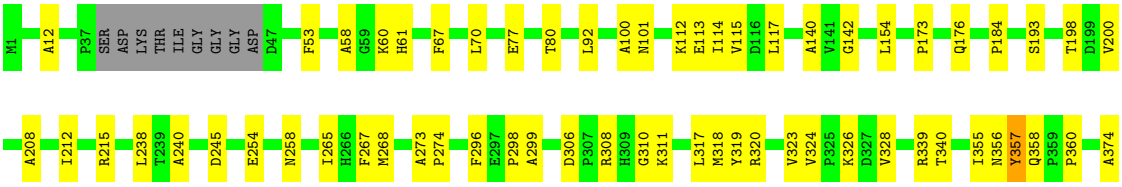
• Molecule 3: Tubulin alpha chain

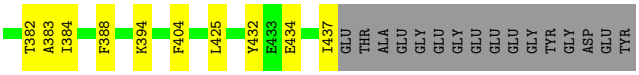
Chain 8E:



• Molecule 3: Tubulin alpha chain

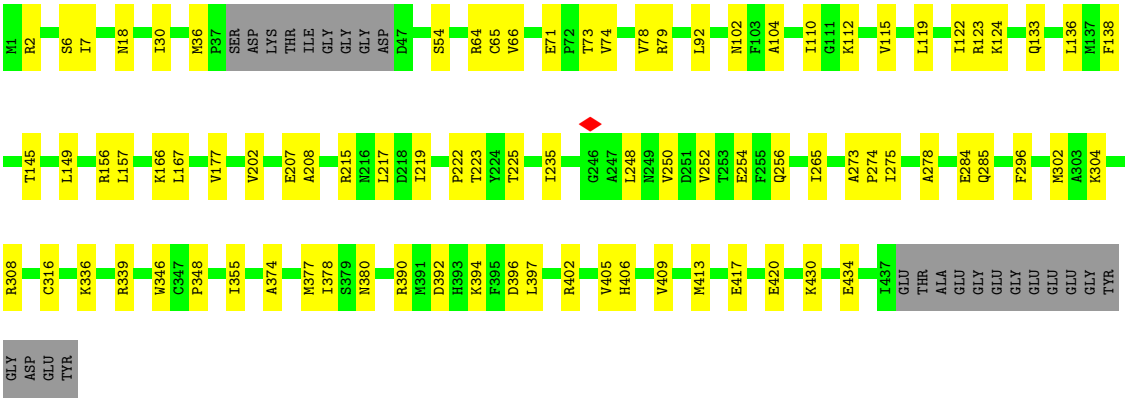
Chain 8G:





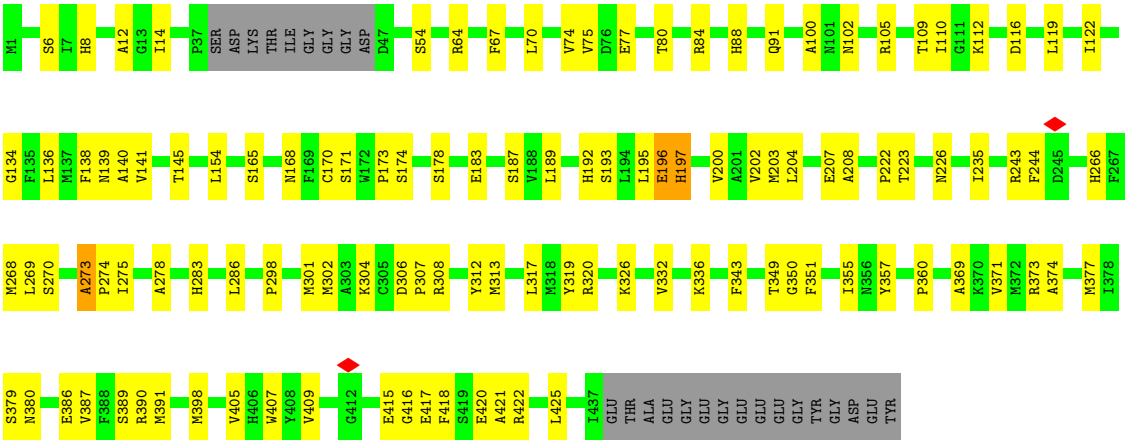
• Molecule 3: Tubulin alpha chain

Chain 8I:



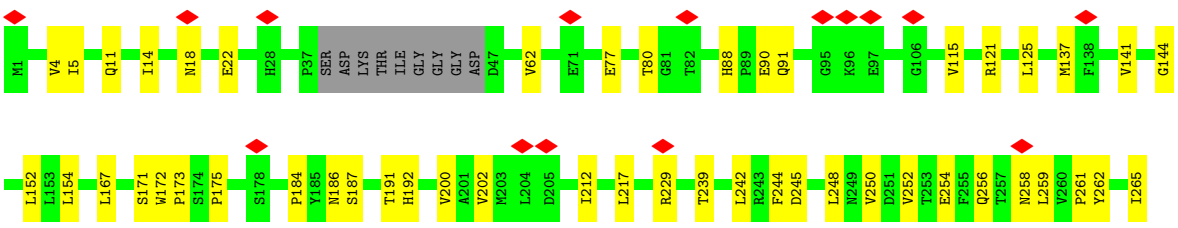
• Molecule 3: Tubulin alpha chain

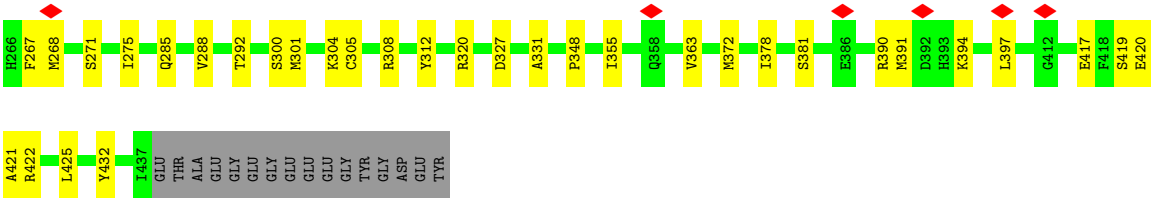
Chain 8K:



• Molecule 3: Tubulin alpha chain

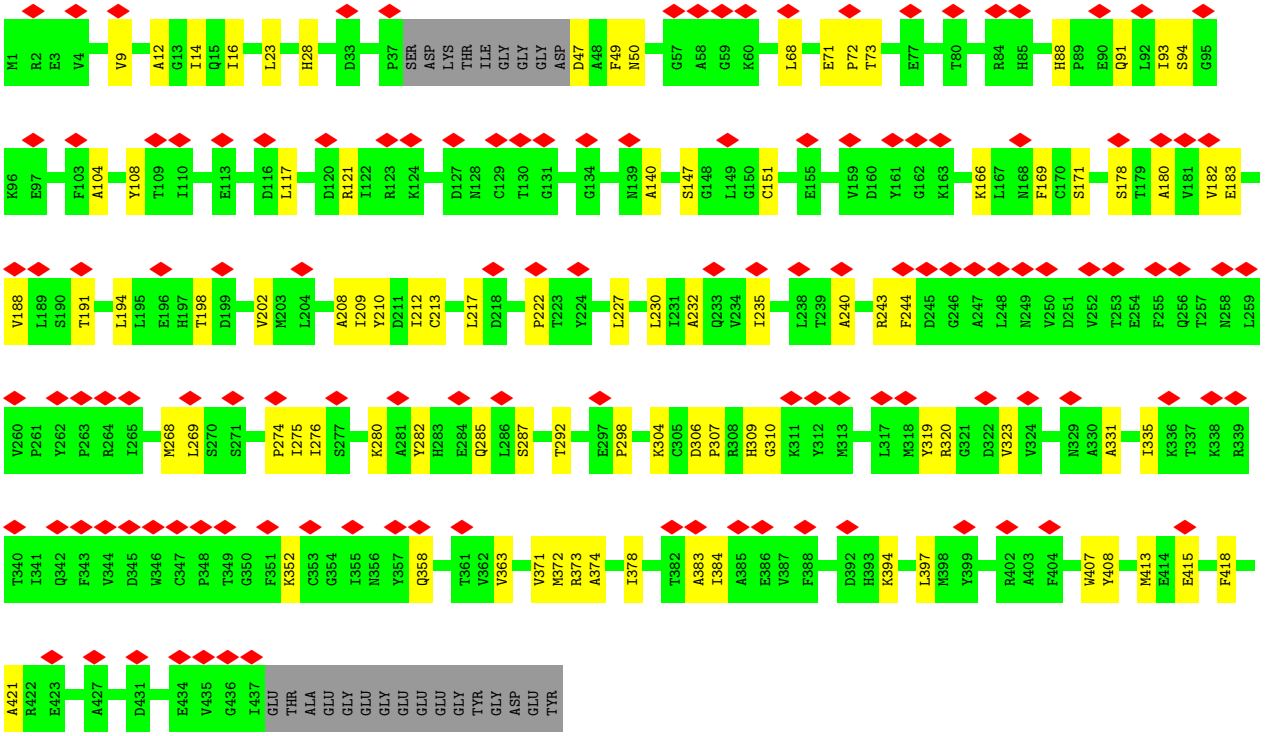
Chain 8M:





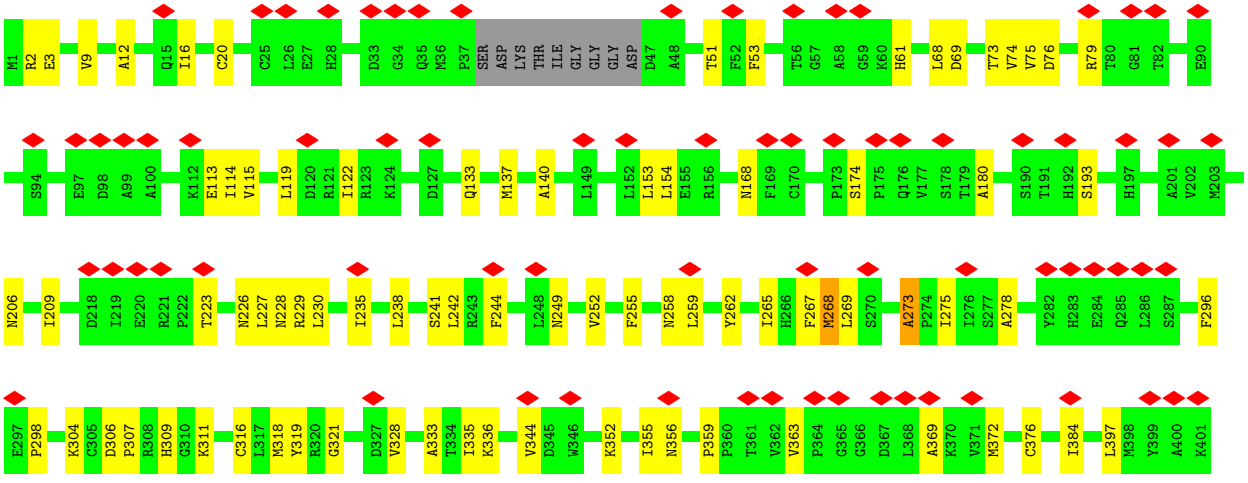
• Molecule 3: Tubulin alpha chain

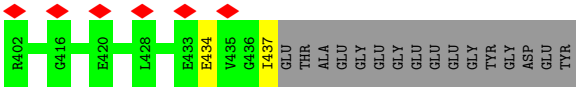
Chain 9A:



• Molecule 3: Tubulin alpha chain

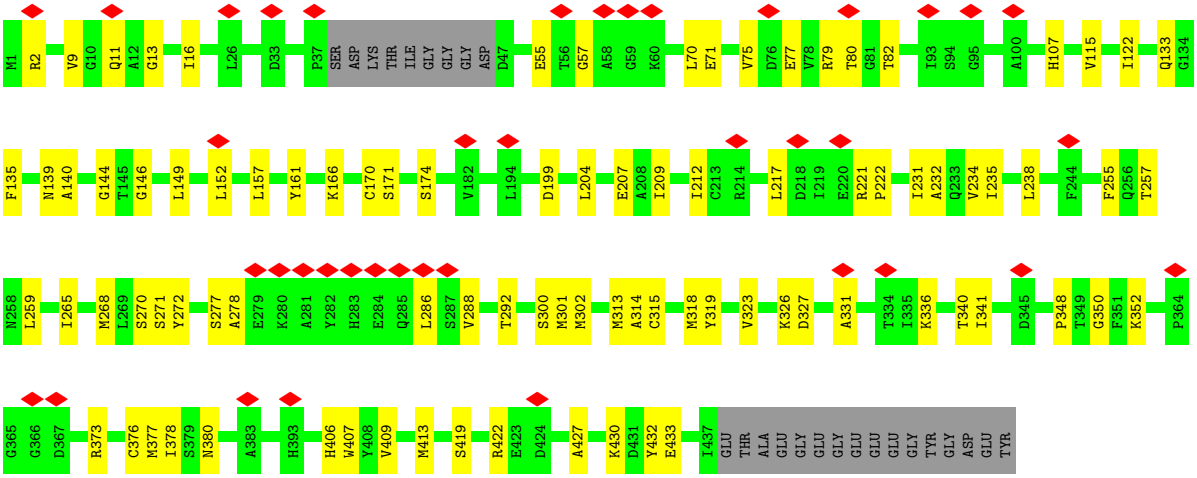
Chain 9C:





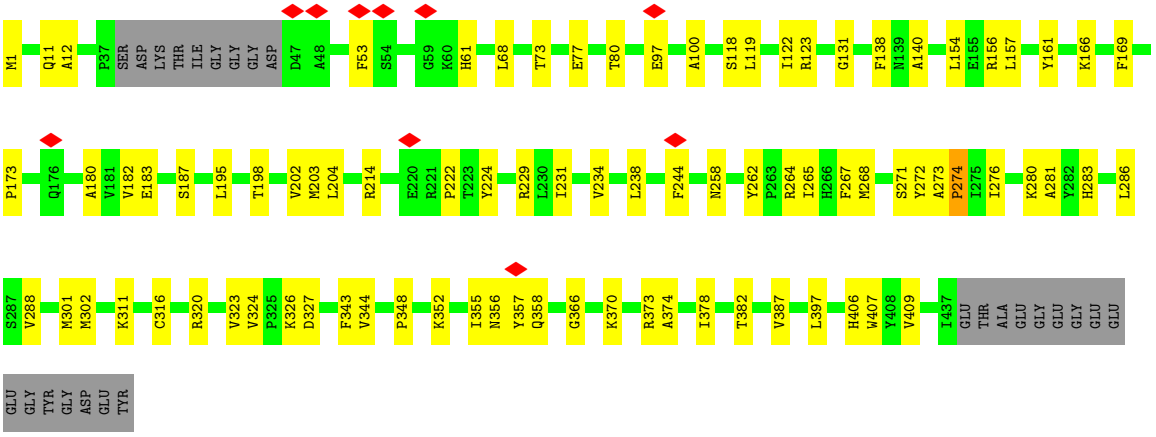
• Molecule 3: Tubulin alpha chain

Chain 9E:



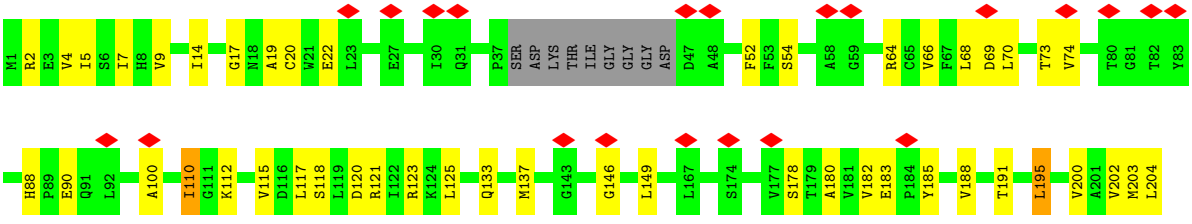
• Molecule 3: Tubulin alpha chain

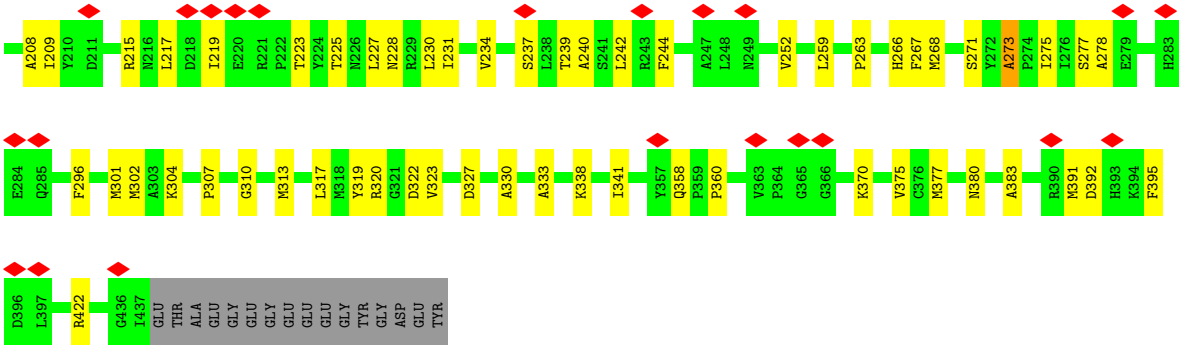
Chain 9G:



• Molecule 3: Tubulin alpha chain

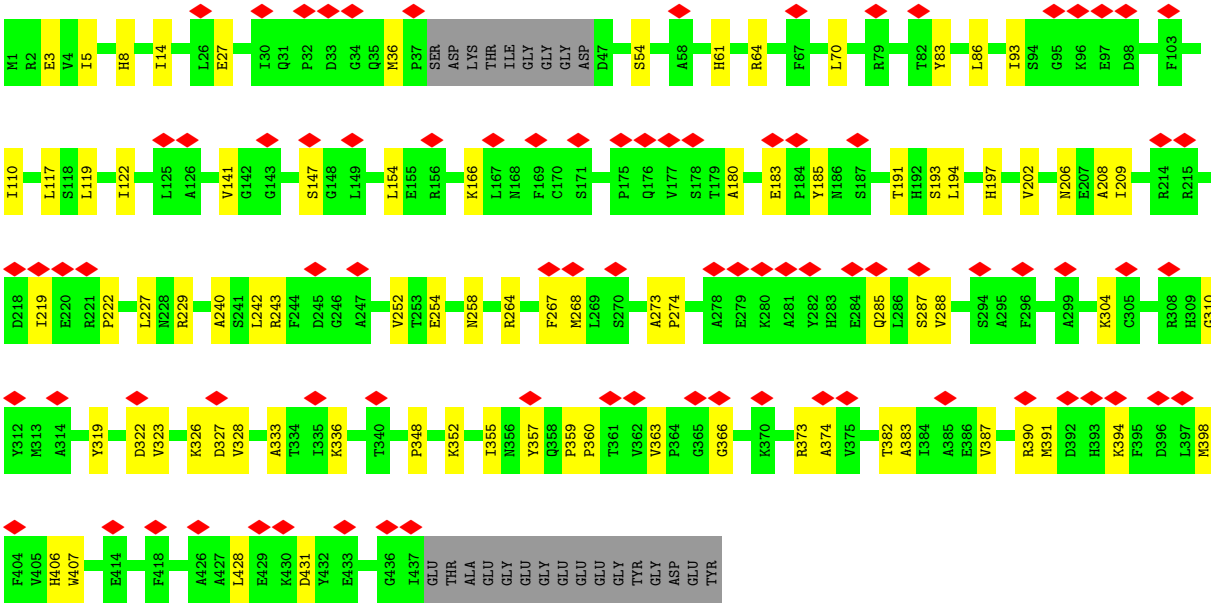
Chain 9I:





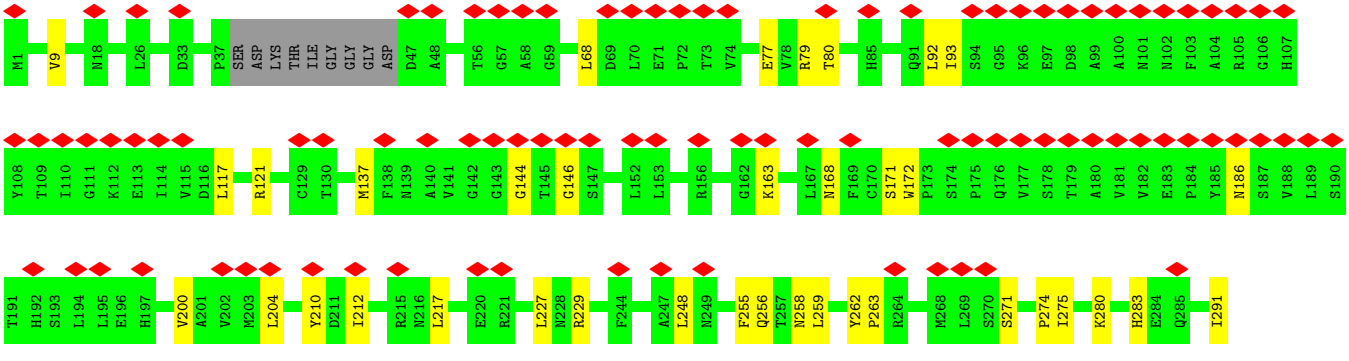
• Molecule 3: Tubulin alpha chain

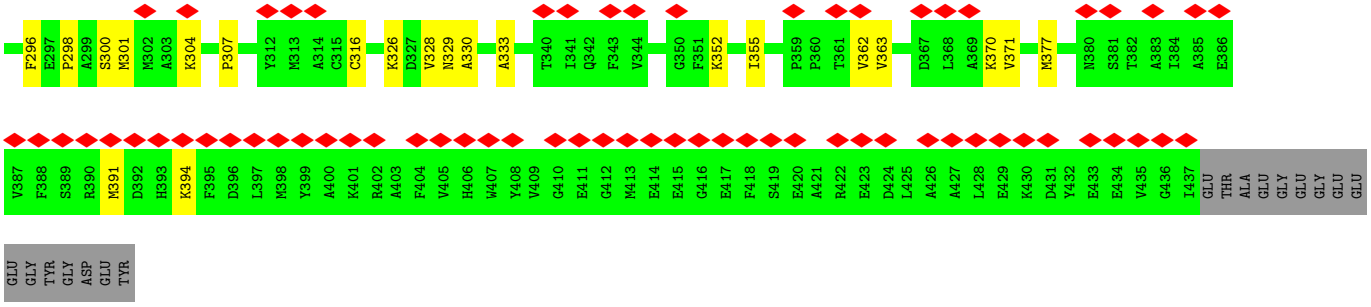
Chain 9K:



• Molecule 3: Tubulin alpha chain

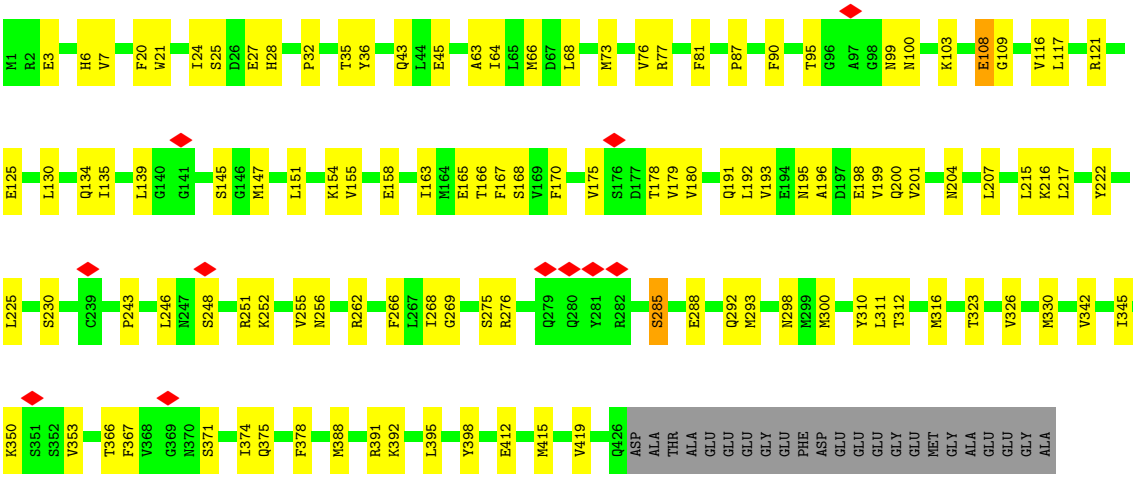
Chain 9M:





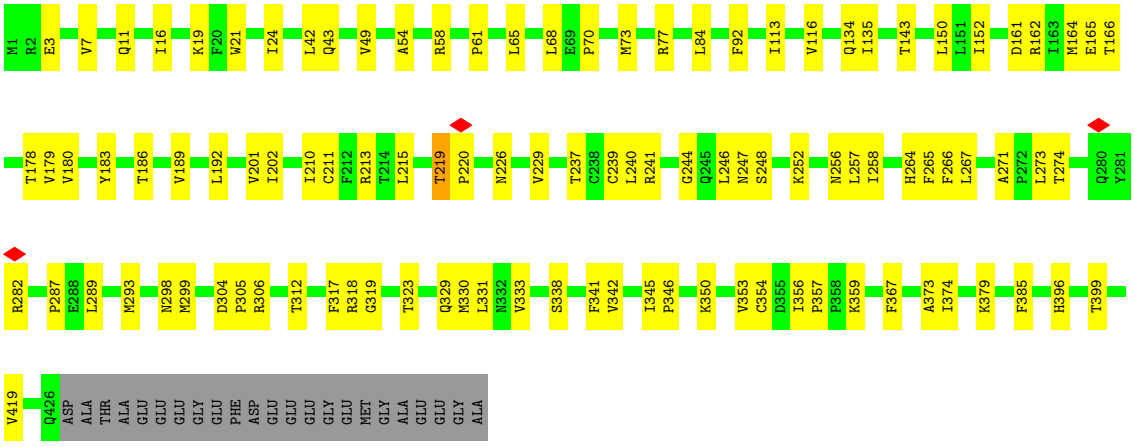
• Molecule 4: Tubulin beta chain

Chain 1B:



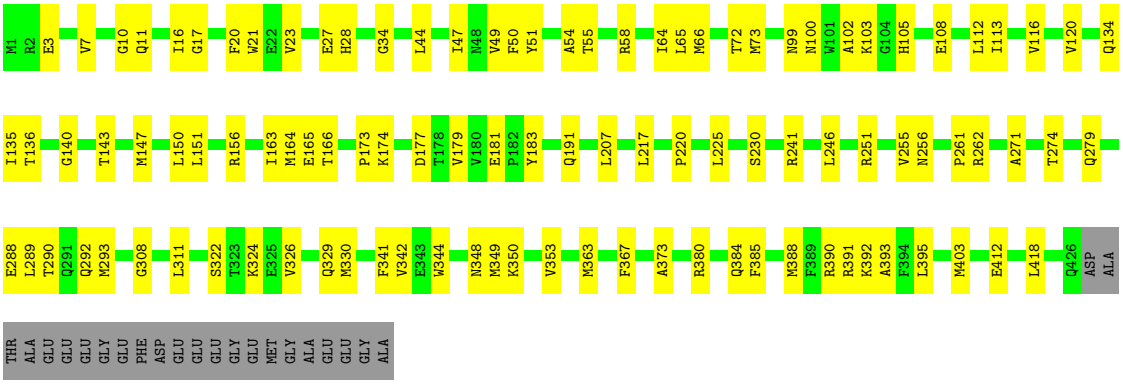
• Molecule 4: Tubulin beta chain

Chain 1D:



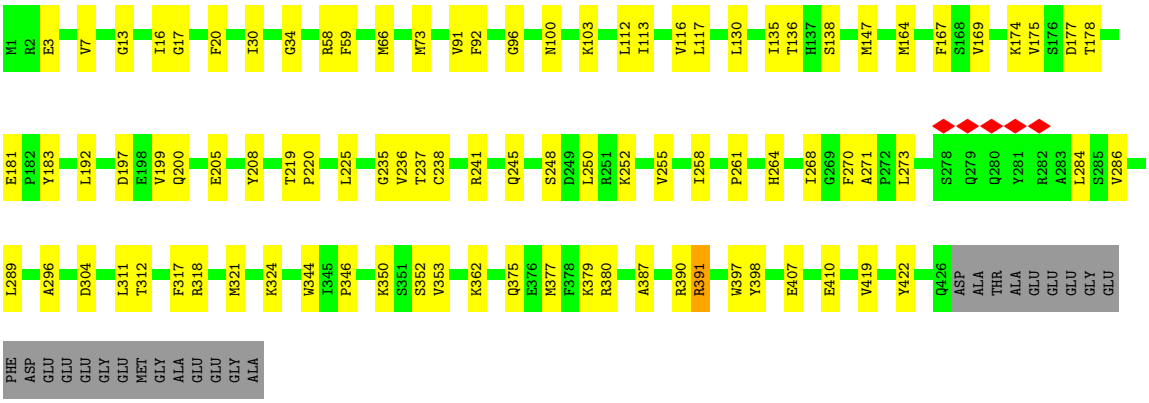
• Molecule 4: Tubulin beta chain

Chain 1F:



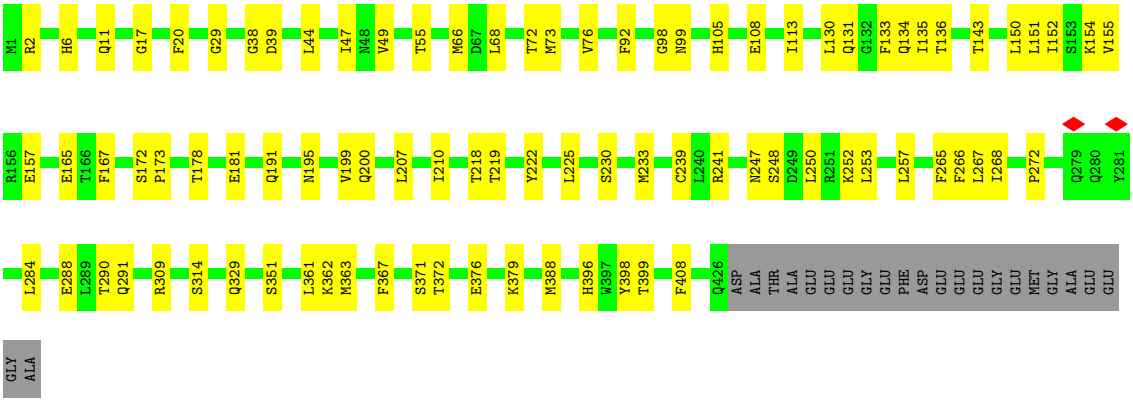
• Molecule 4: Tubulin beta chain

Chain 1H:



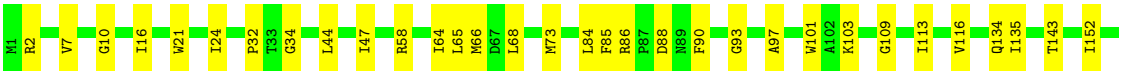
• Molecule 4: Tubulin beta chain

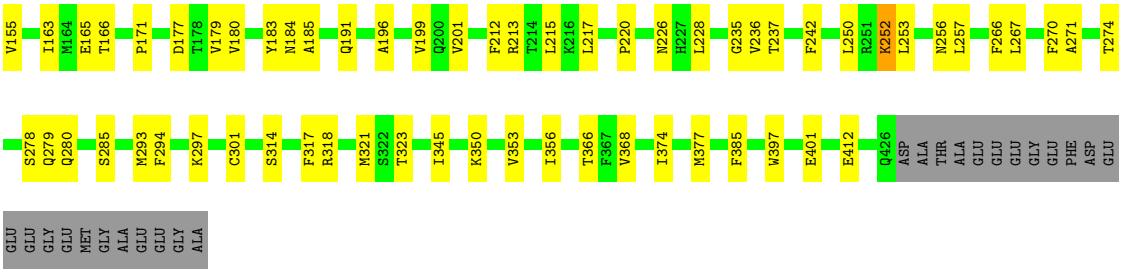
Chain 1J:



• Molecule 4: Tubulin beta chain

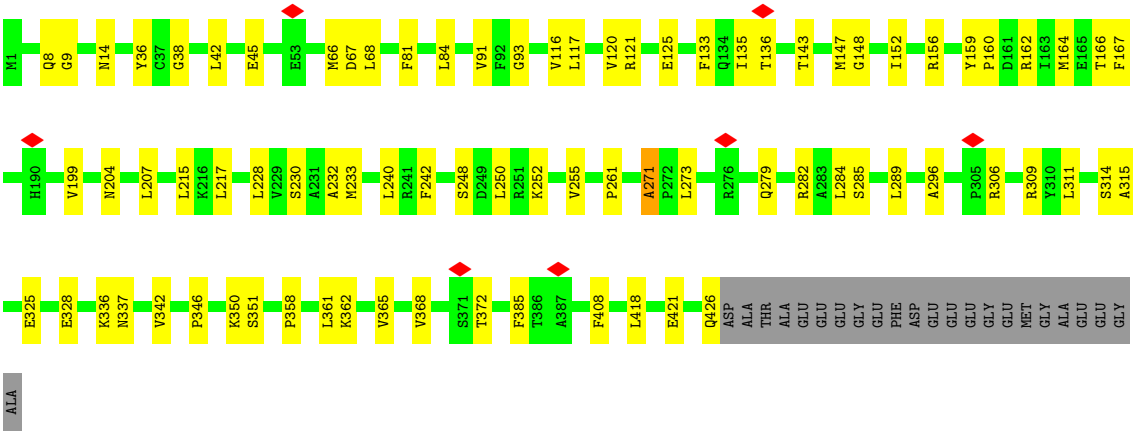
Chain 1L:





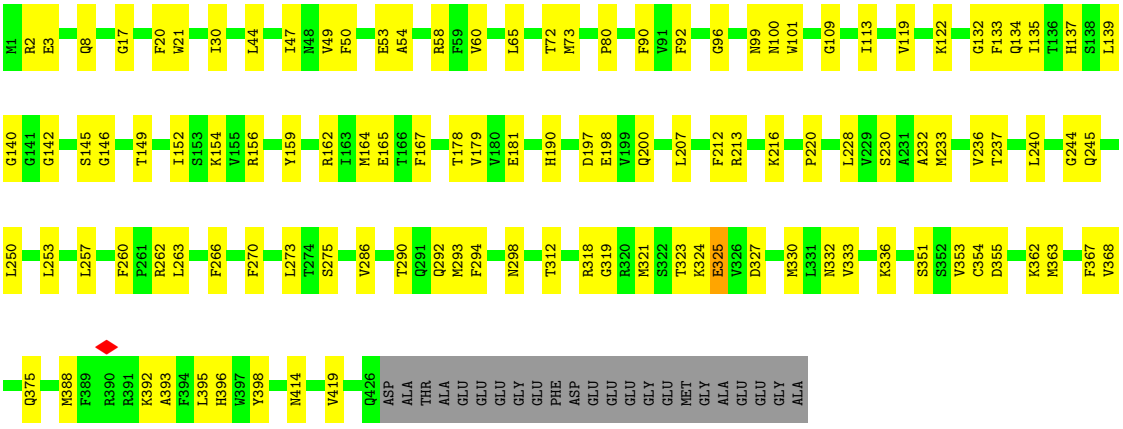
• Molecule 4: Tubulin beta chain

Chain 1N:



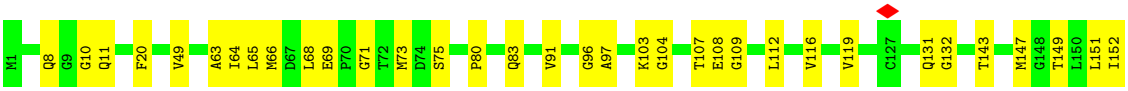
• Molecule 4: Tubulin beta chain

Chain 2B:



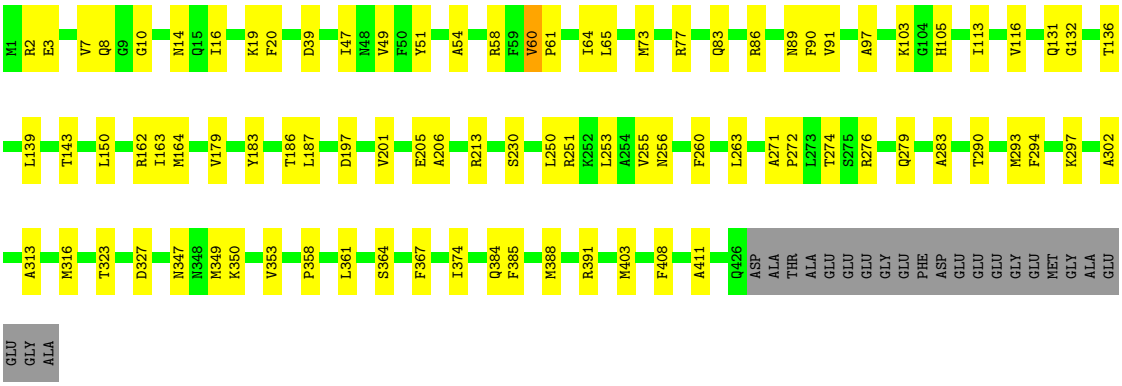
• Molecule 4: Tubulin beta chain

Chain 2D:



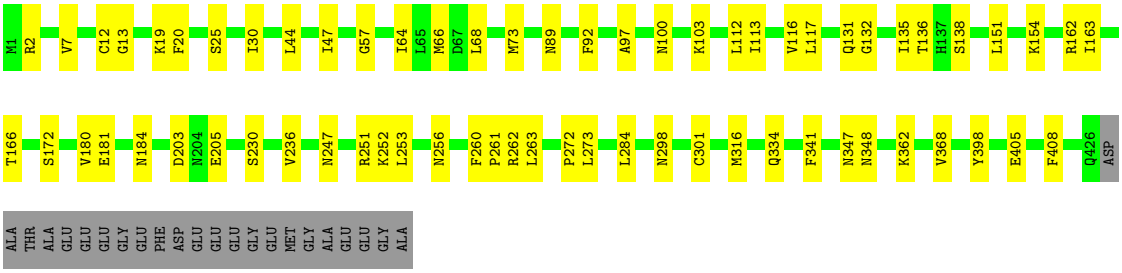
• Molecule 4: Tubulin beta chain

Chain 2F:



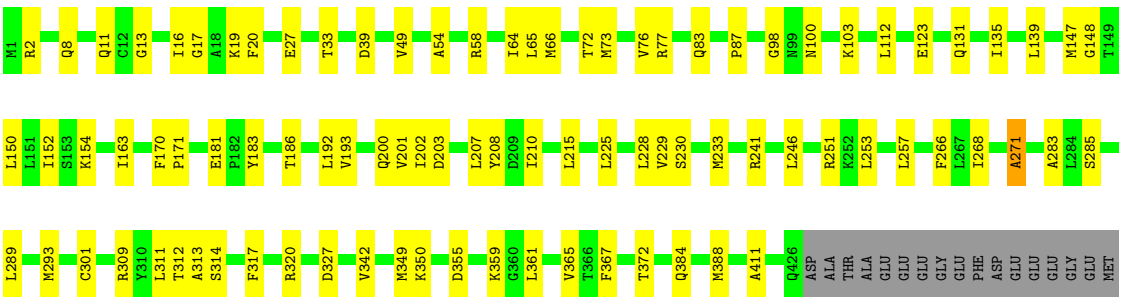
• Molecule 4: Tubulin beta chain

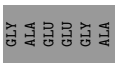
Chain 2H:



• Molecule 4: Tubulin beta chain

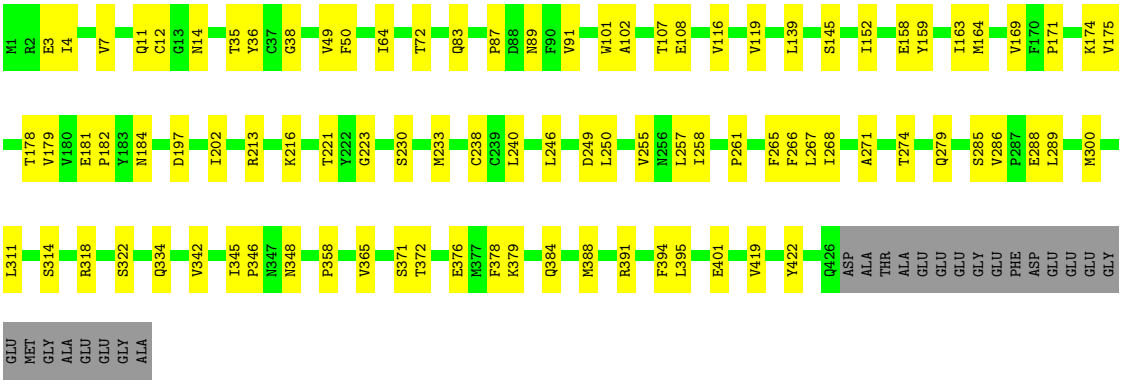
Chain 2J:





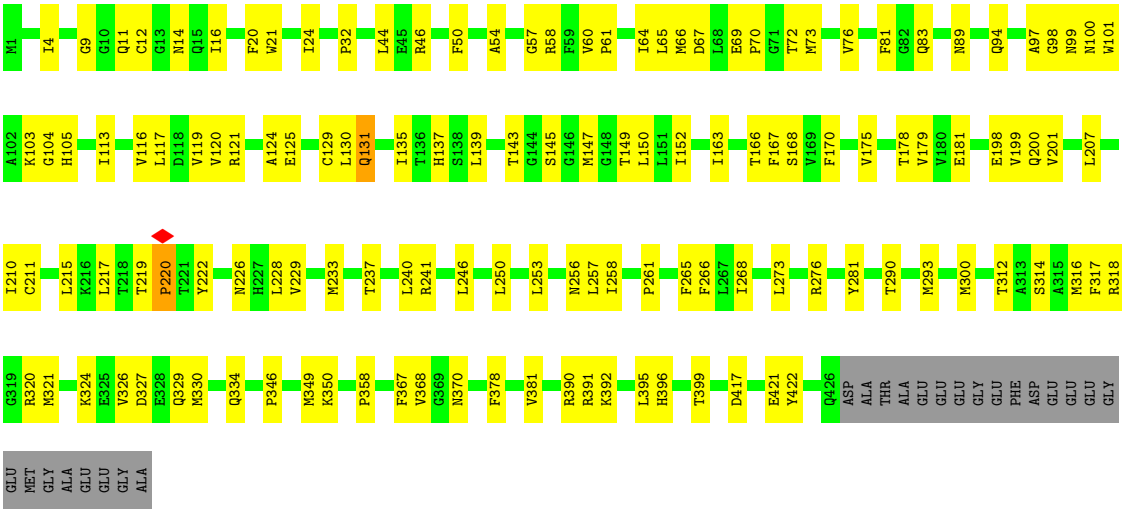
• Molecule 4: Tubulin beta chain

Chain 2L:



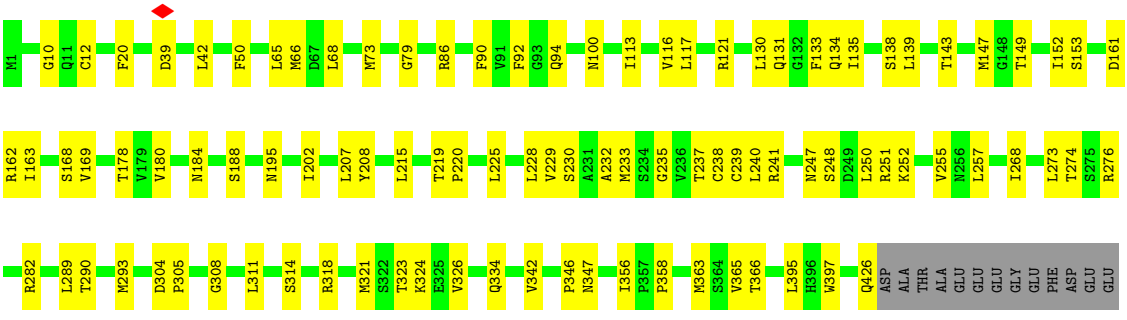
• Molecule 4: Tubulin beta chain

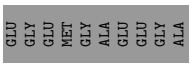
Chain 3B:



• Molecule 4: Tubulin beta chain

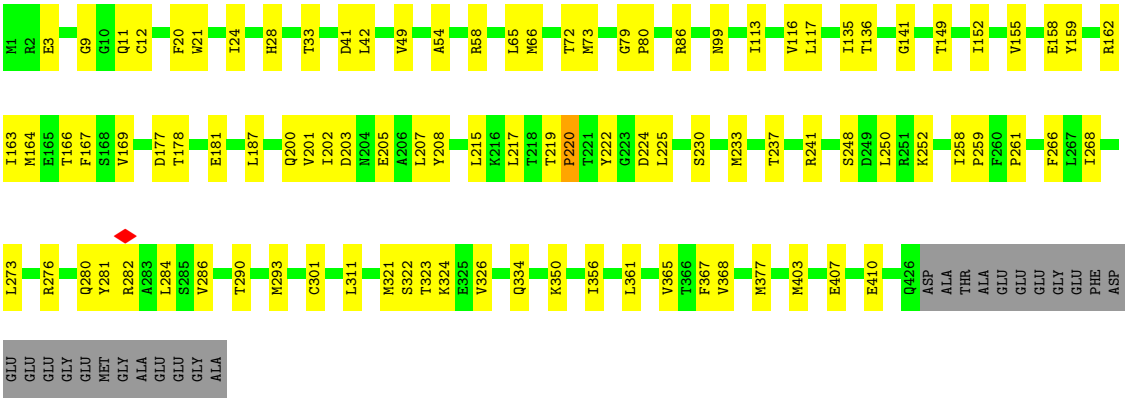
Chain 3D:





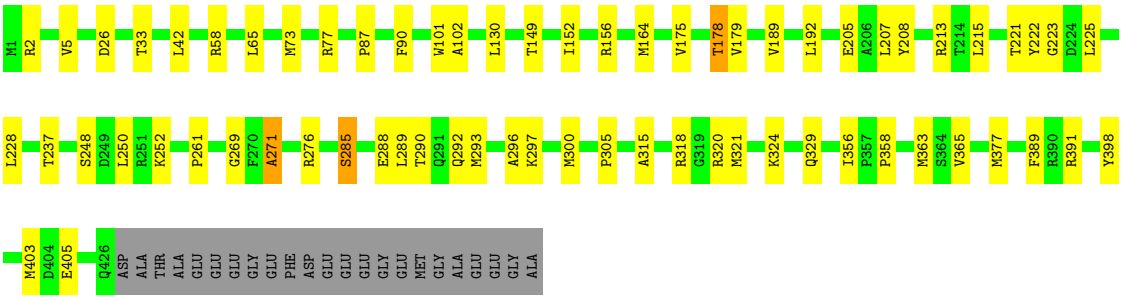
• Molecule 4: Tubulin beta chain

Chain 3F:



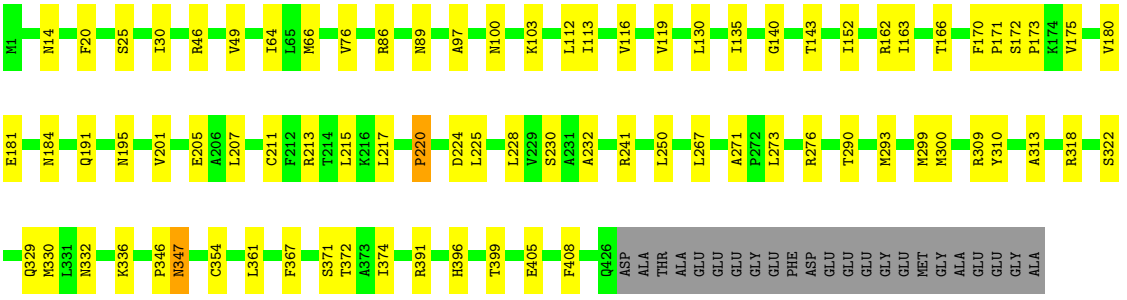
• Molecule 4: Tubulin beta chain

Chain 3H:



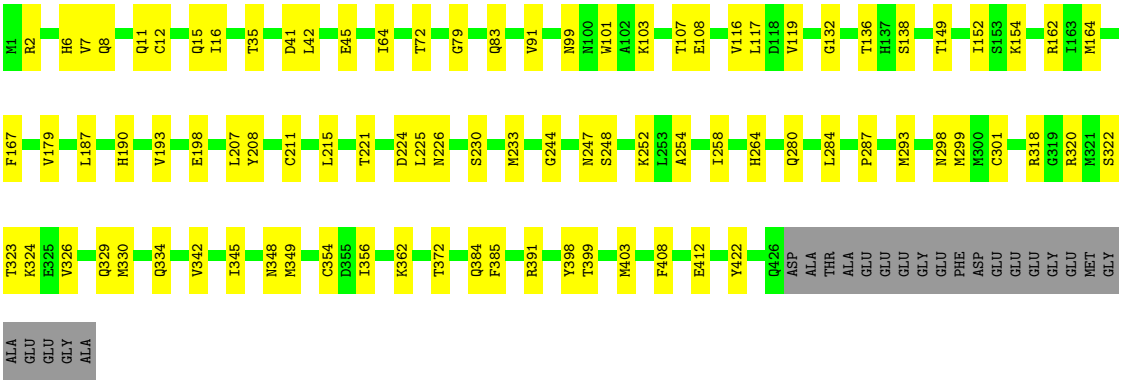
• Molecule 4: Tubulin beta chain

Chain 3J:



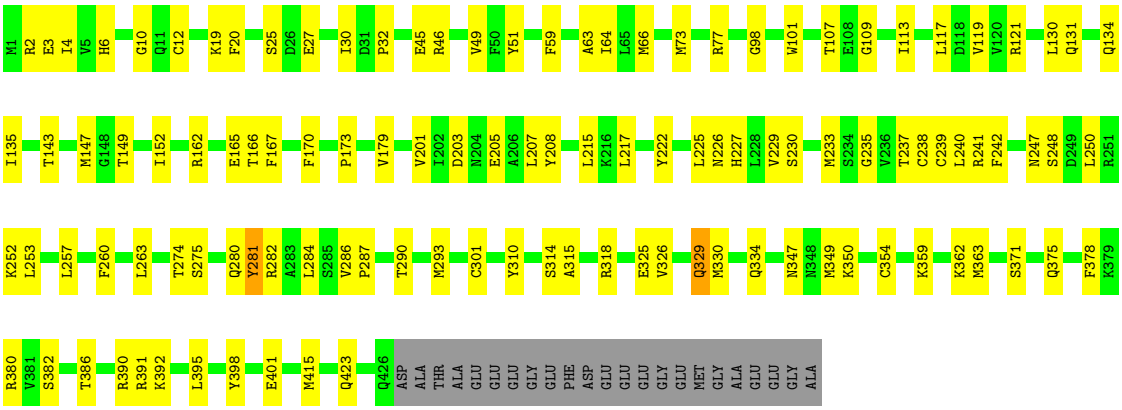
• Molecule 4: Tubulin beta chain

Chain 3L:



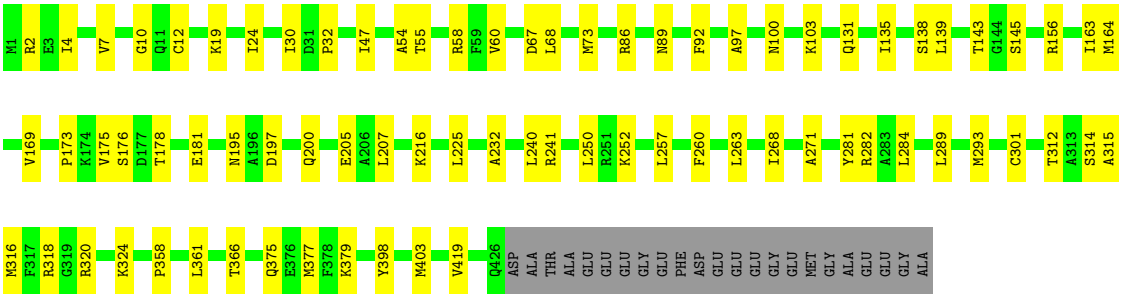
• Molecule 4: Tubulin beta chain

Chain 4B:



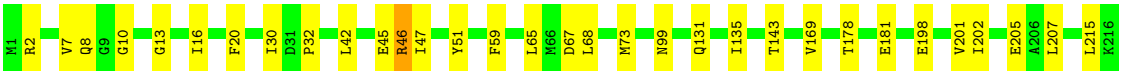
• Molecule 4: Tubulin beta chain

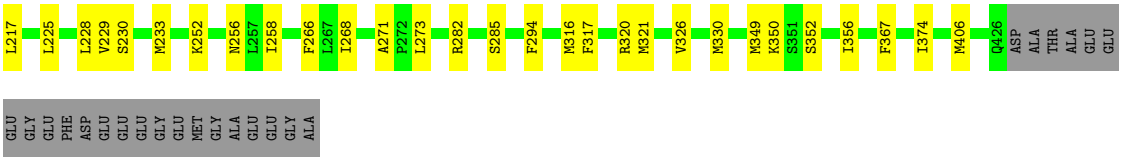
Chain 4D:



• Molecule 4: Tubulin beta chain

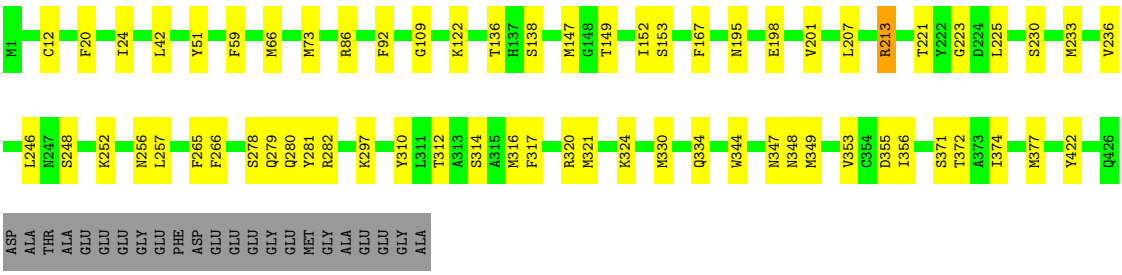
Chain 4F:





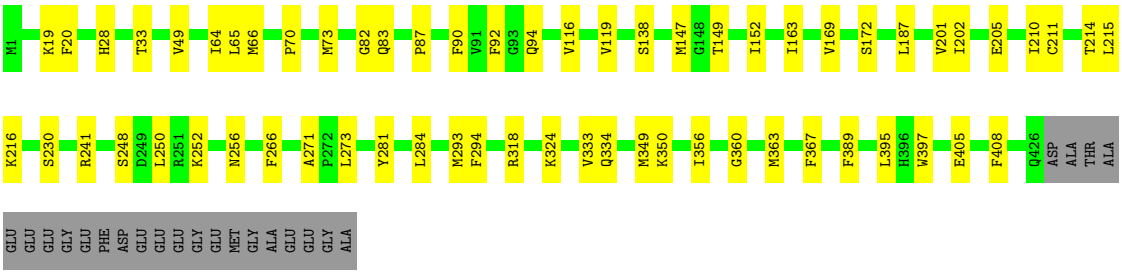
• Molecule 4: Tubulin beta chain

Chain 4H:



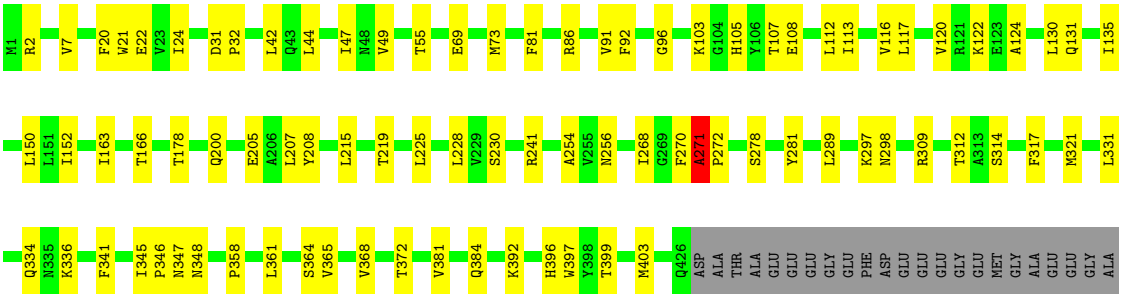
• Molecule 4: Tubulin beta chain

Chain 4J:



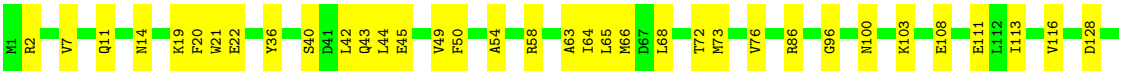
• Molecule 4: Tubulin beta chain

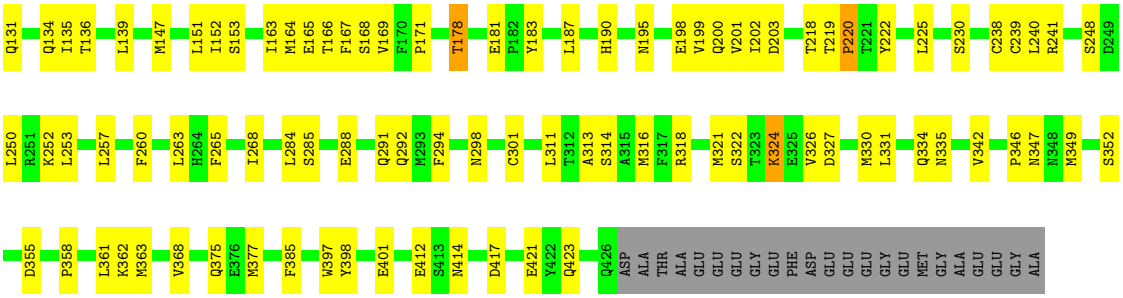
Chain 4L:



• Molecule 4: Tubulin beta chain

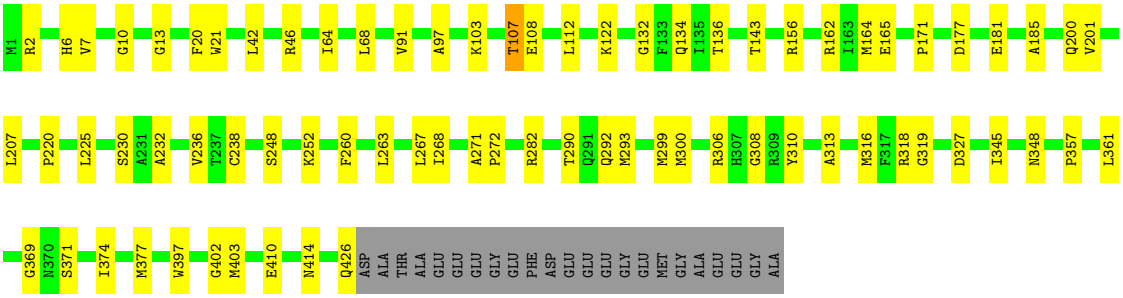
Chain 5B:





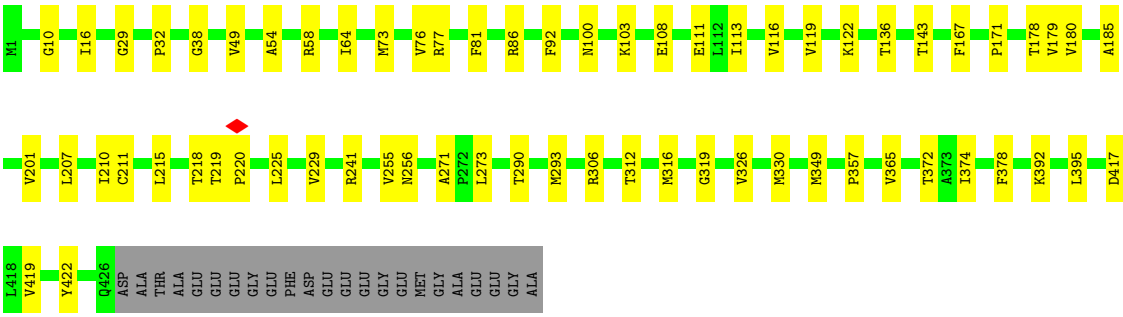
• Molecule 4: Tubulin beta chain

Chain 5D:



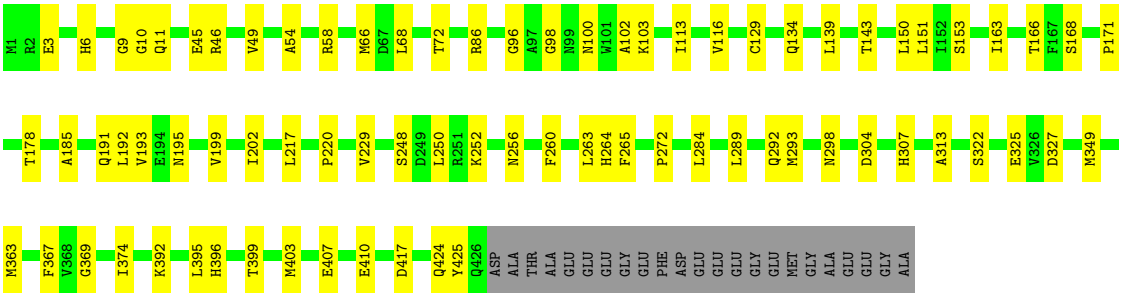
• Molecule 4: Tubulin beta chain

Chain 5F:



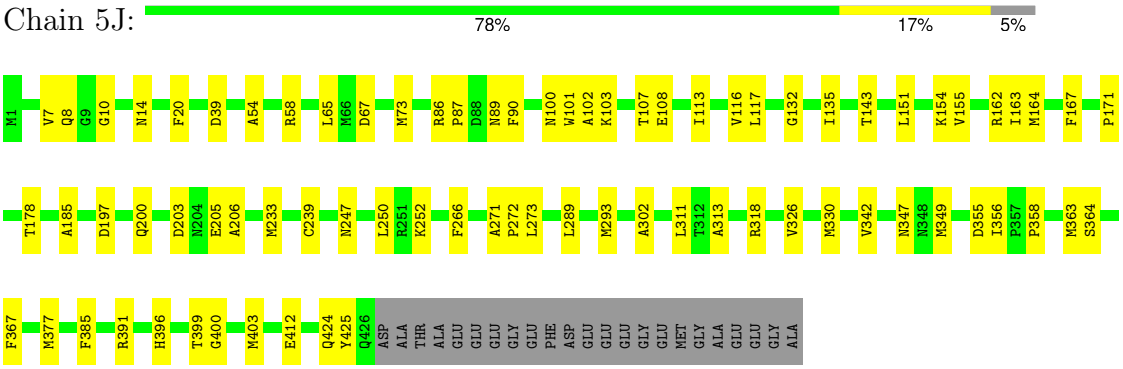
• Molecule 4: Tubulin beta chain

Chain 5H:



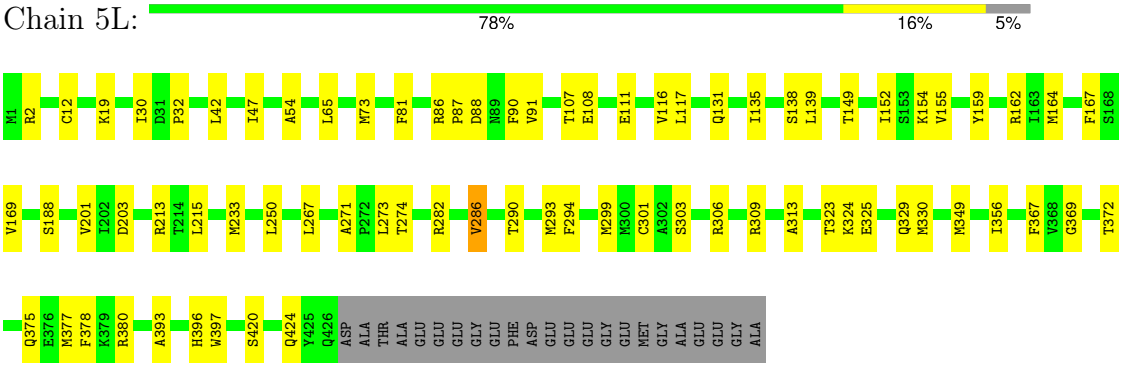
• Molecule 4: Tubulin beta chain

Chain 5J:



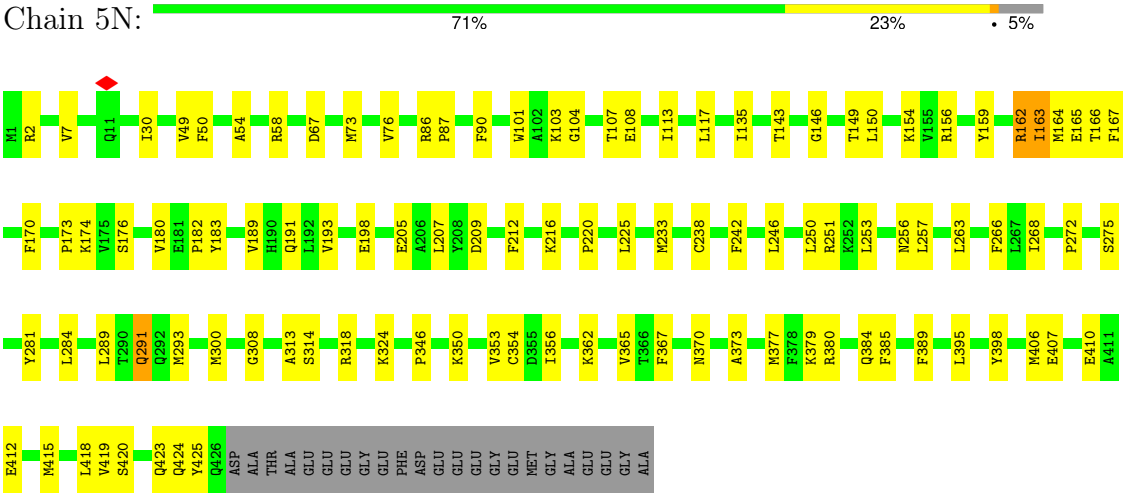
• Molecule 4: Tubulin beta chain

Chain 5L:



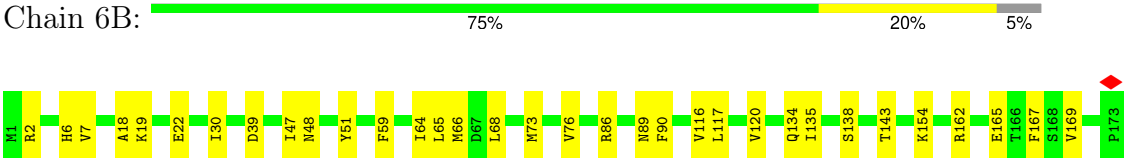
• Molecule 4: Tubulin beta chain

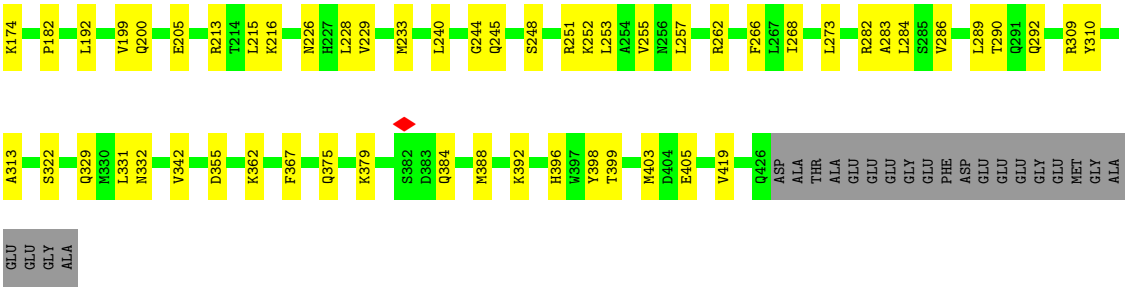
Chain 5N:



• Molecule 4: Tubulin beta chain

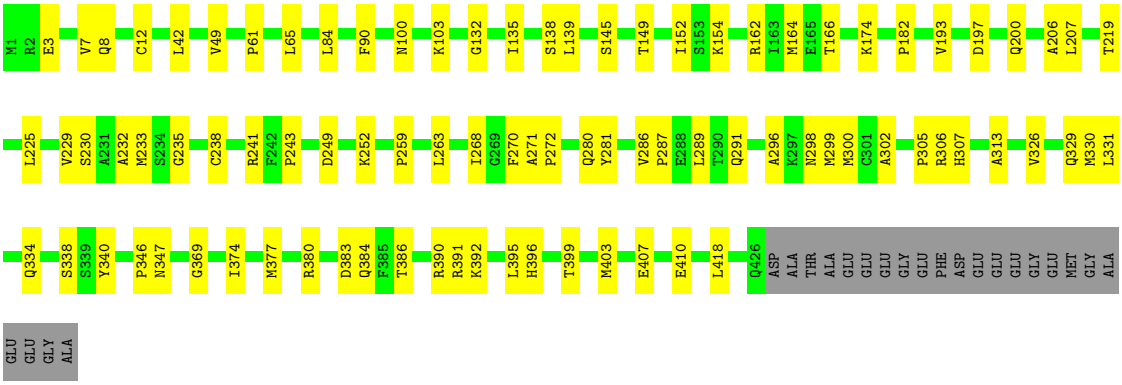
Chain 6B:





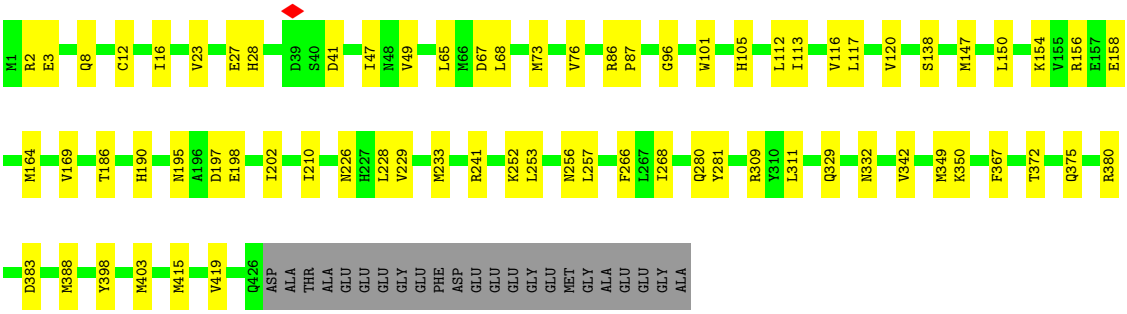
• Molecule 4: Tubulin beta chain

Chain 6D:



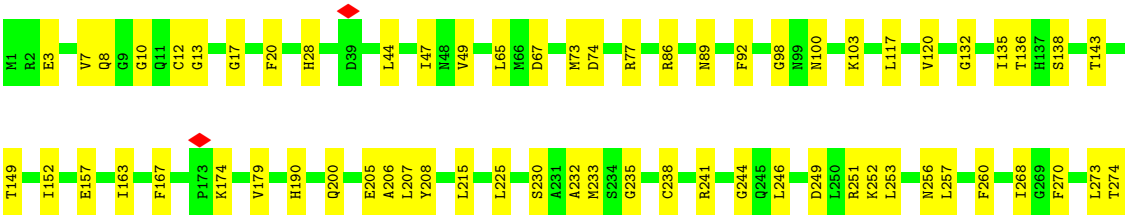
• Molecule 4: Tubulin beta chain

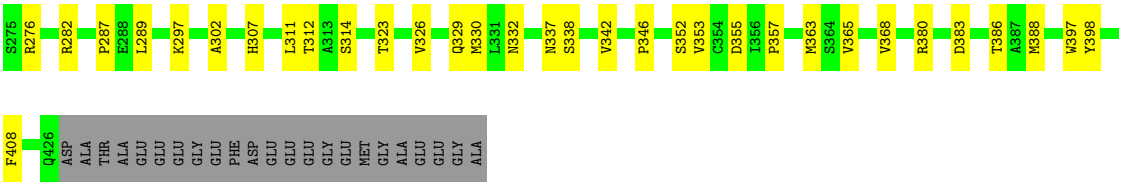
Chain 6F:



• Molecule 4: Tubulin beta chain

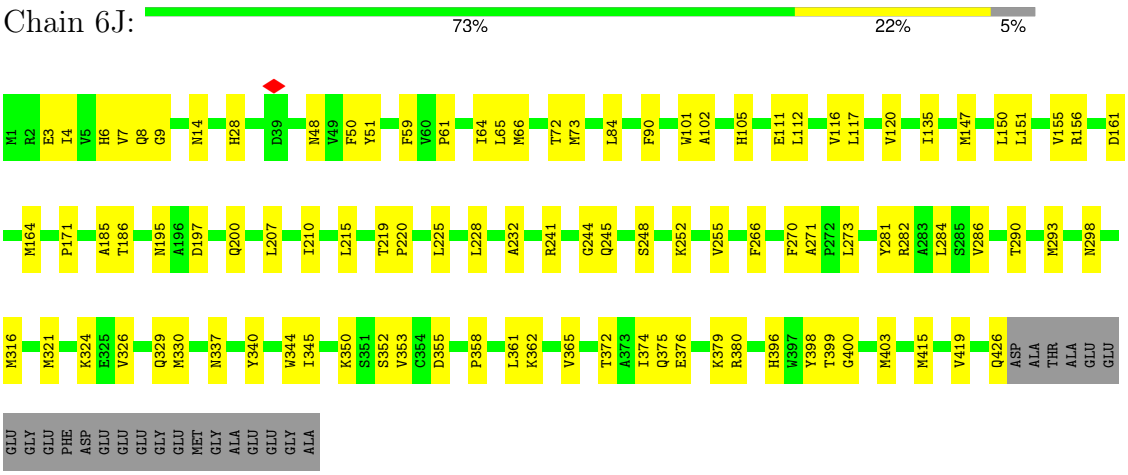
Chain 6H:





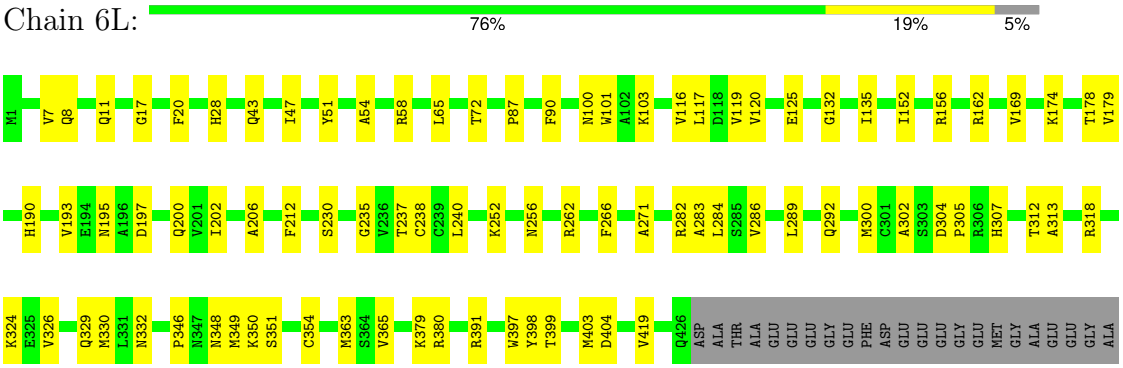
• Molecule 4: Tubulin beta chain

Chain 6J:



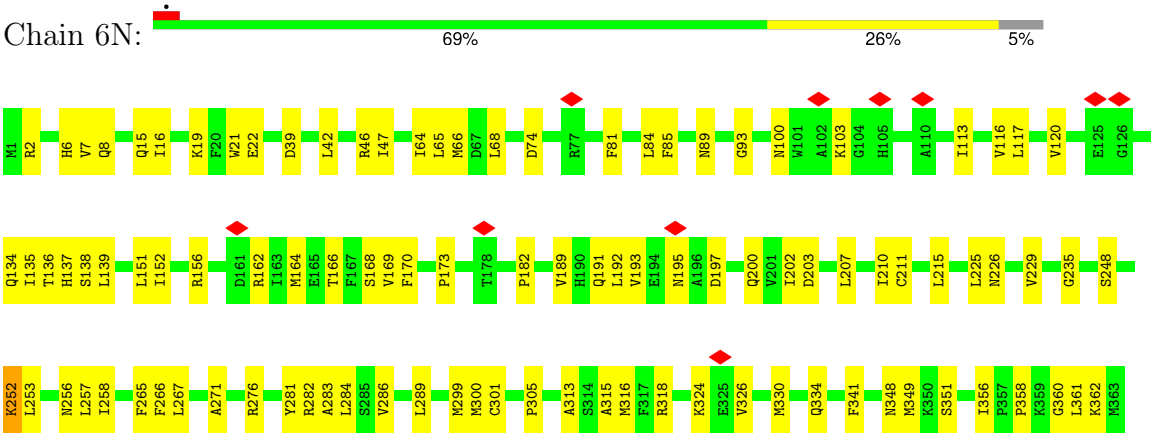
• Molecule 4: Tubulin beta chain

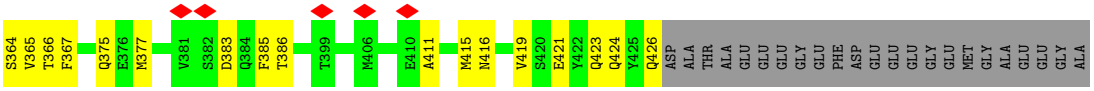
Chain 6L:



• Molecule 4: Tubulin beta chain

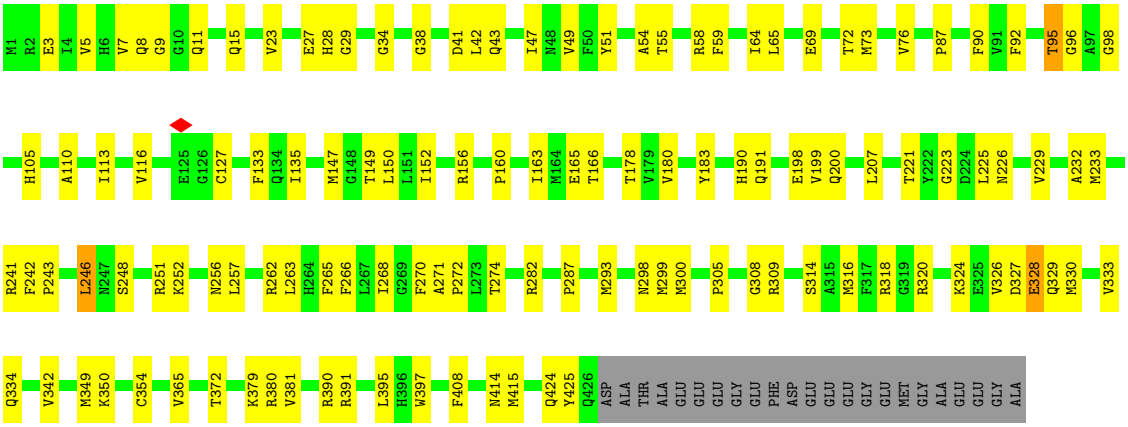
Chain 6N:





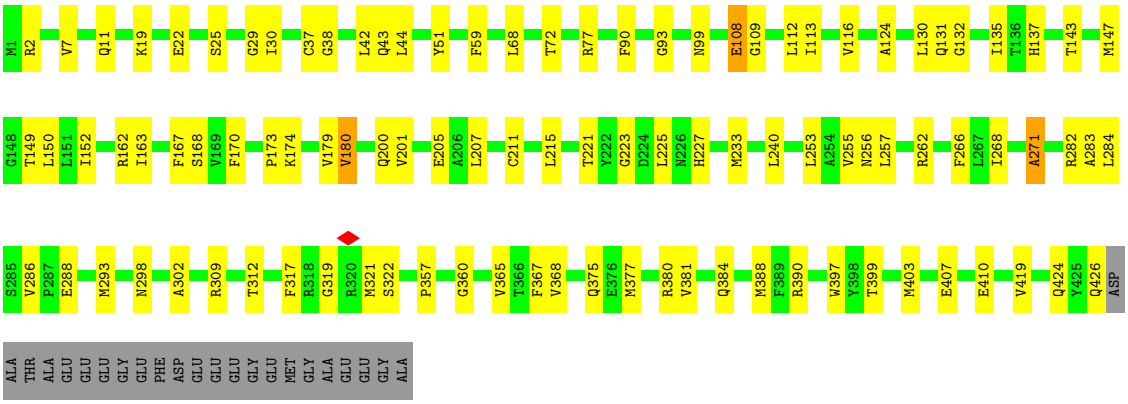
• Molecule 4: Tubulin beta chain

Chain 7B:



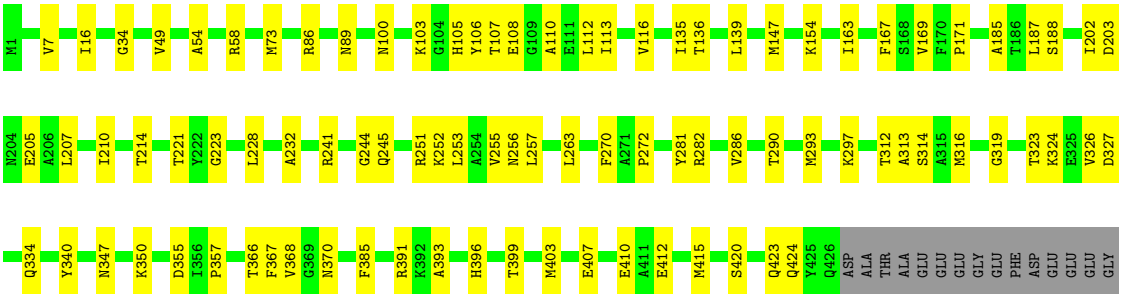
• Molecule 4: Tubulin beta chain

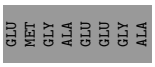
Chain 7D:



• Molecule 4: Tubulin beta chain

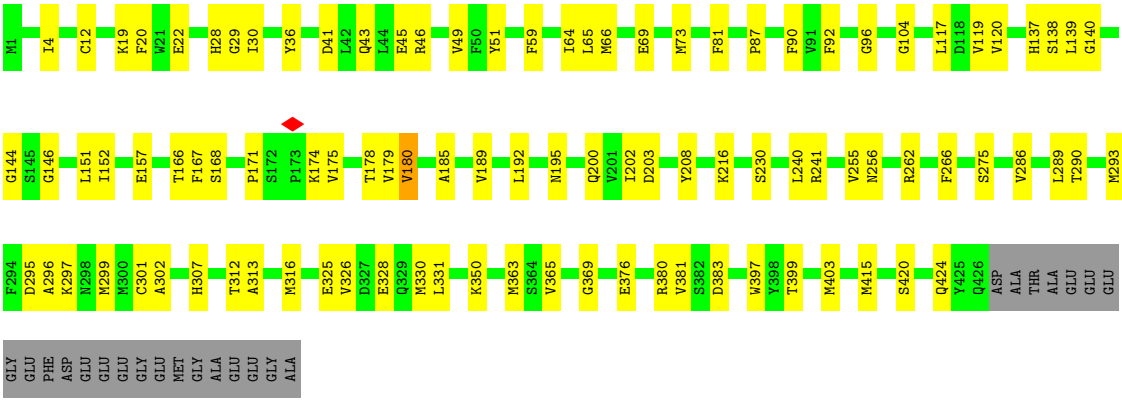
Chain 7F:





• Molecule 4: Tubulin beta chain

Chain 7H:

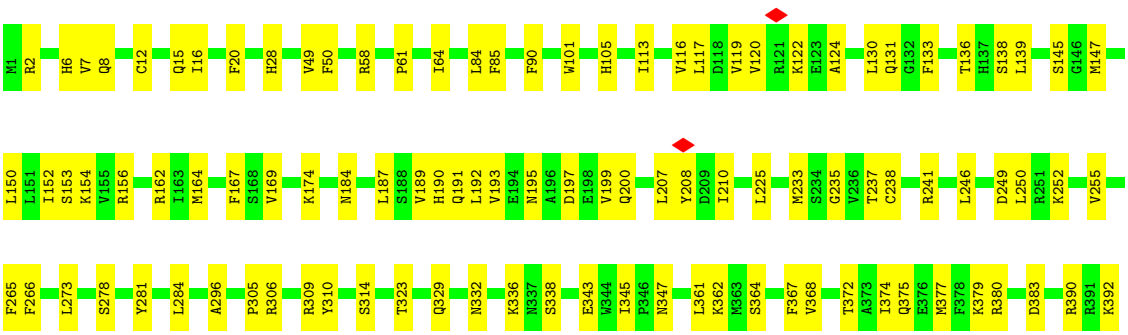


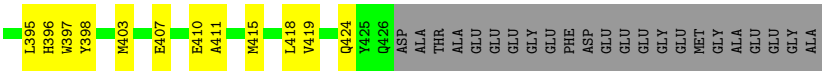
• Molecule 4: Tubulin beta chain

Chain 7J:

• Molecule 4: Tubulin beta chain

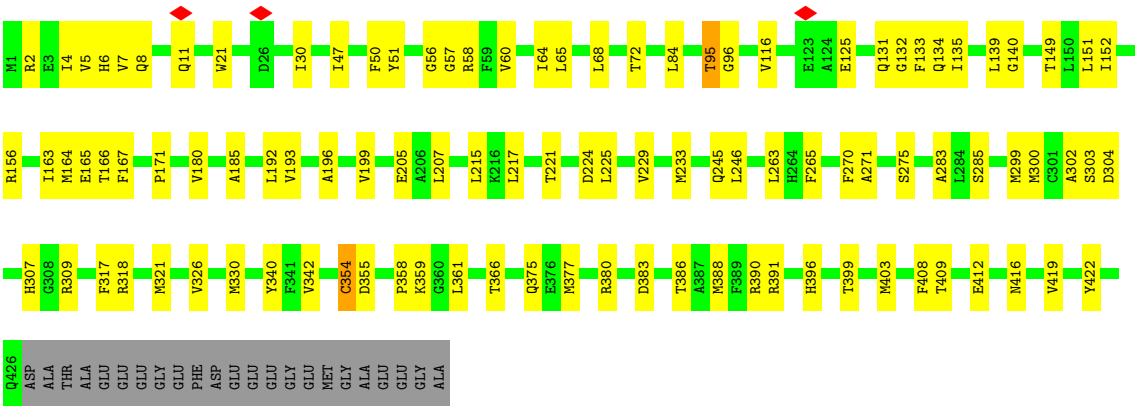
Chain 7L:





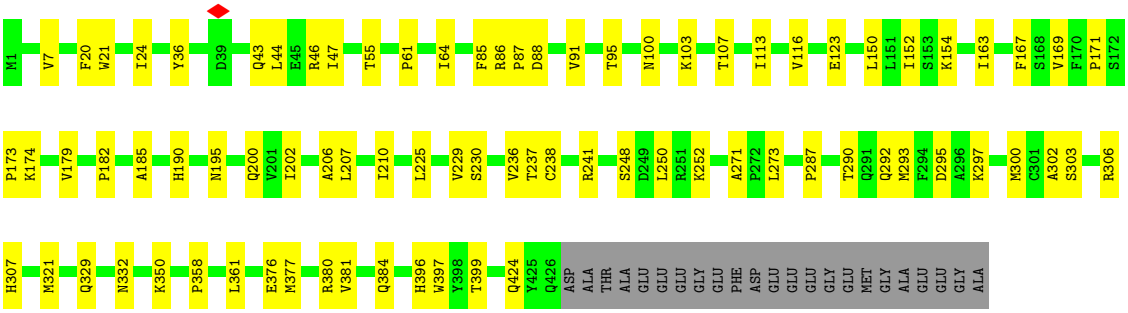
• Molecule 4: Tubulin beta chain

Chain 8B:



• Molecule 4: Tubulin beta chain

Chain 8D:

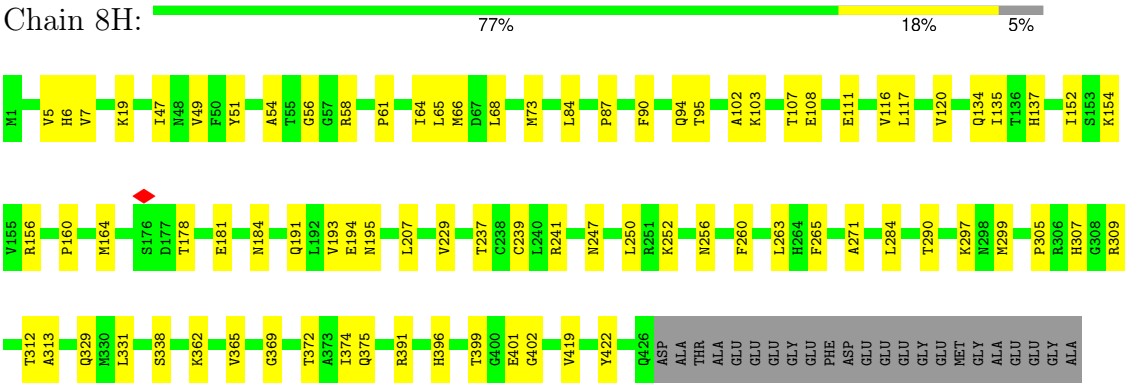


• Molecule 4: Tubulin beta chain

Chain 8F:

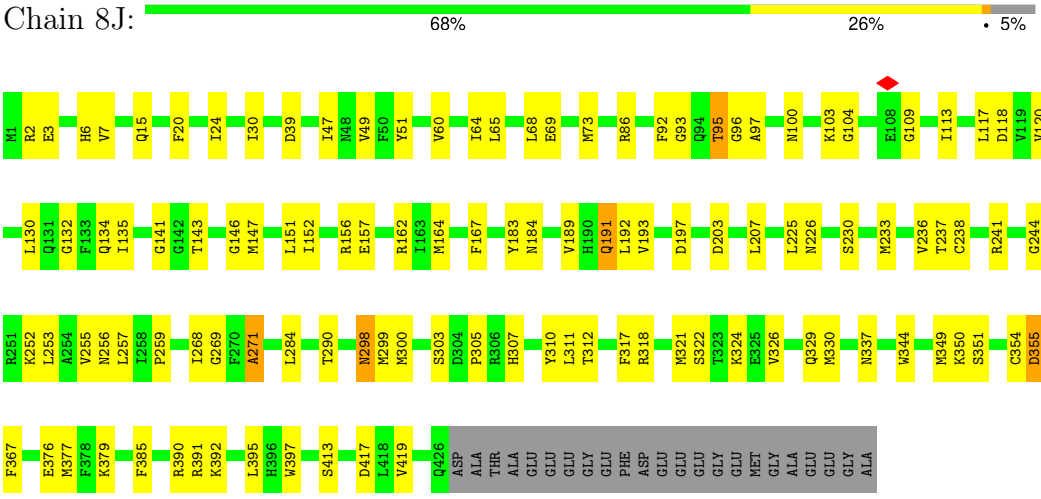
• Molecule 4: Tubulin beta chain

Chain 8H:



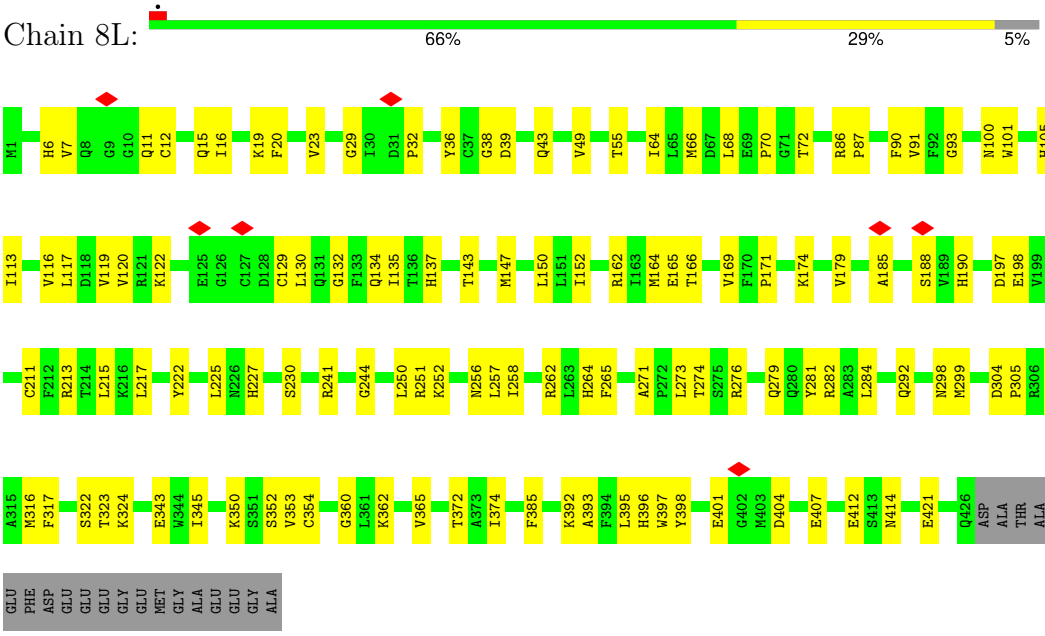
• Molecule 4: Tubulin beta chain

Chain 8J:



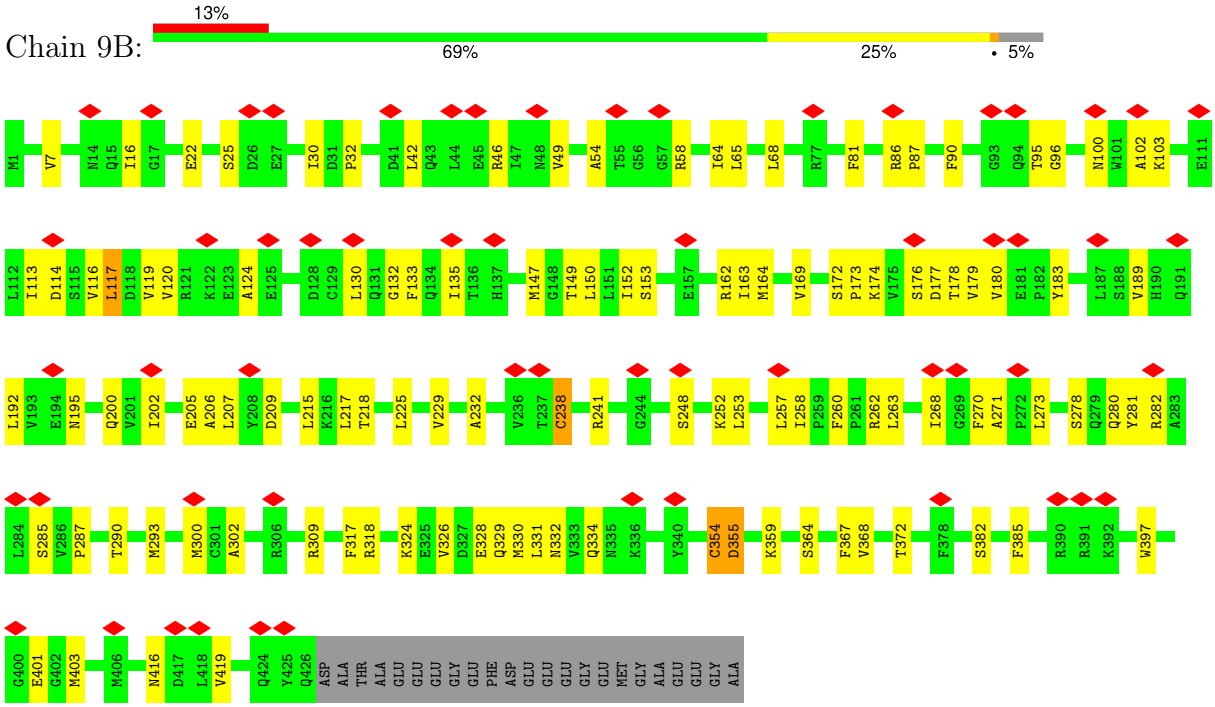
• Molecule 4: Tubulin beta chain

Chain 8L:



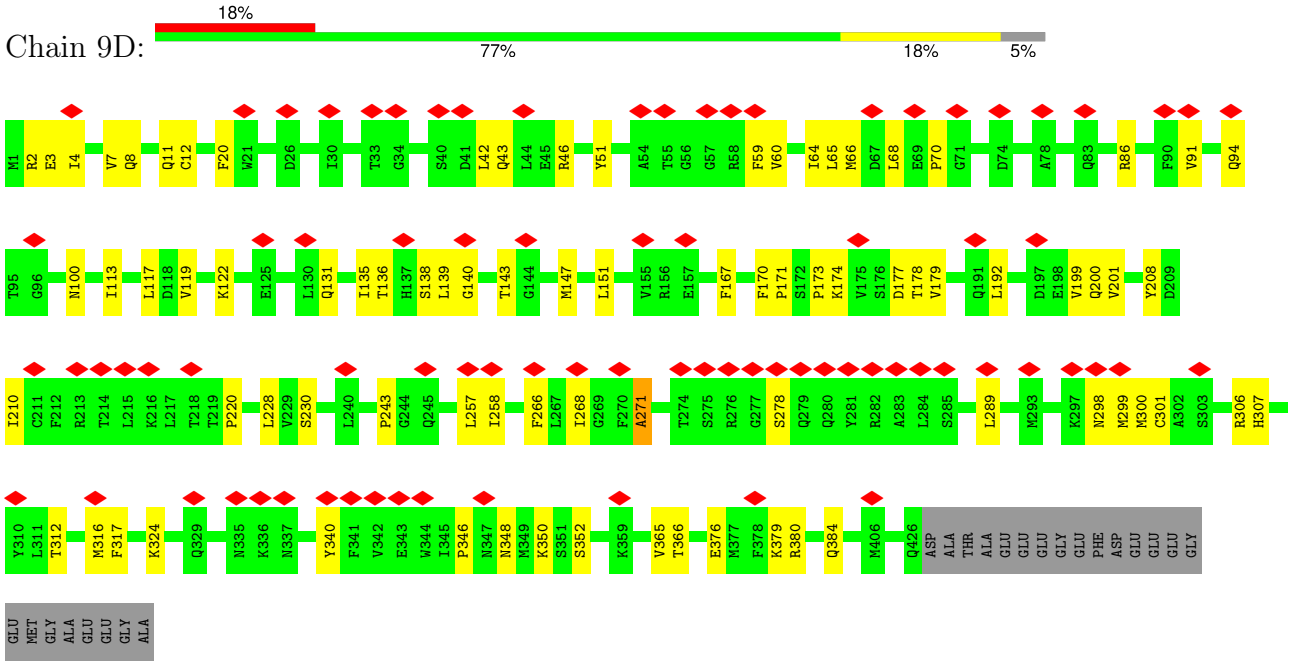
• Molecule 4: Tubulin beta chain

Chain 9B:



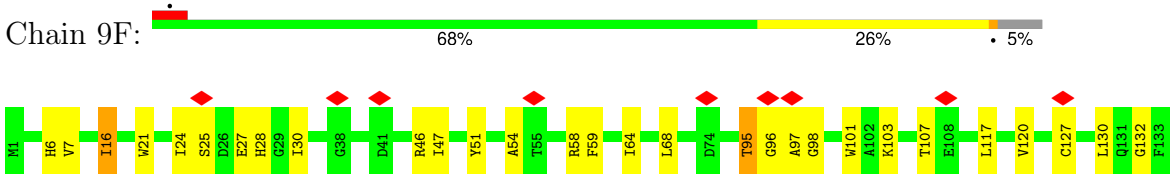
• Molecule 4: Tubulin beta chain

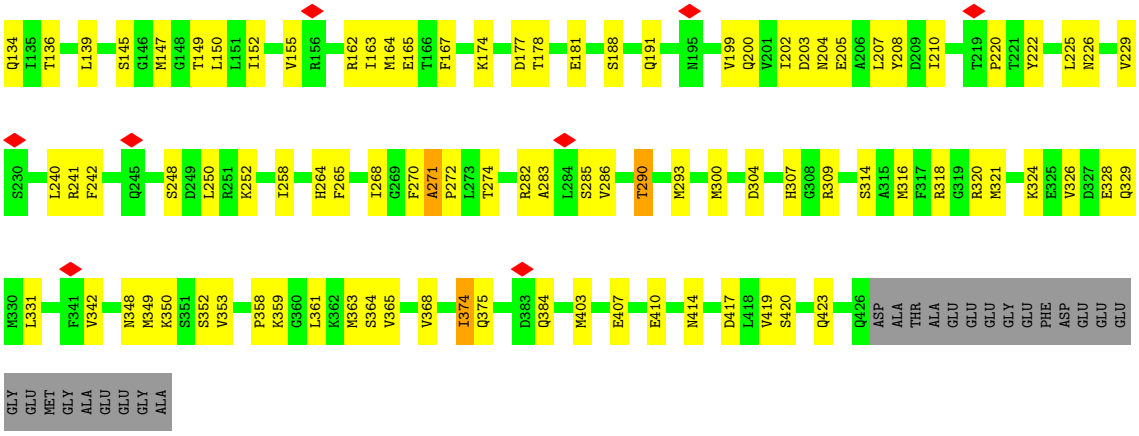
Chain 9D:



• Molecule 4: Tubulin beta chain

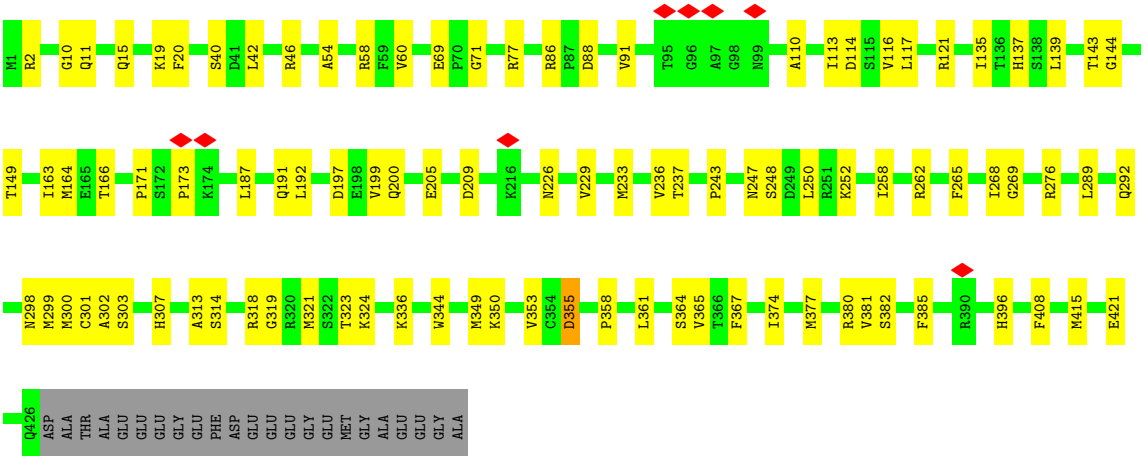
Chain 9F:





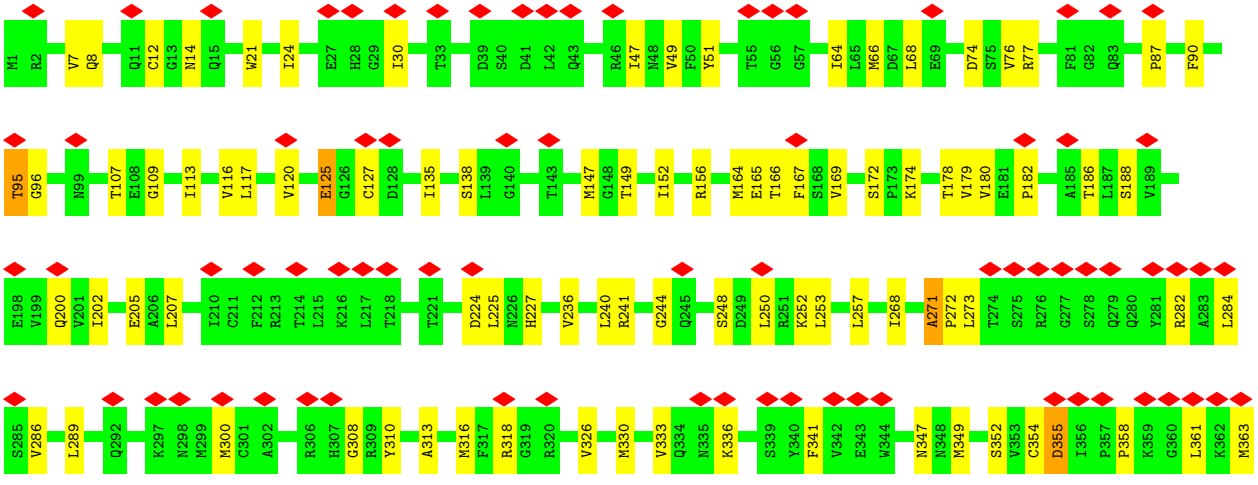
• Molecule 4: Tubulin beta chain

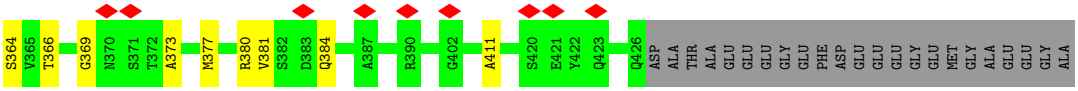
Chain 9H:



• Molecule 4: Tubulin beta chain

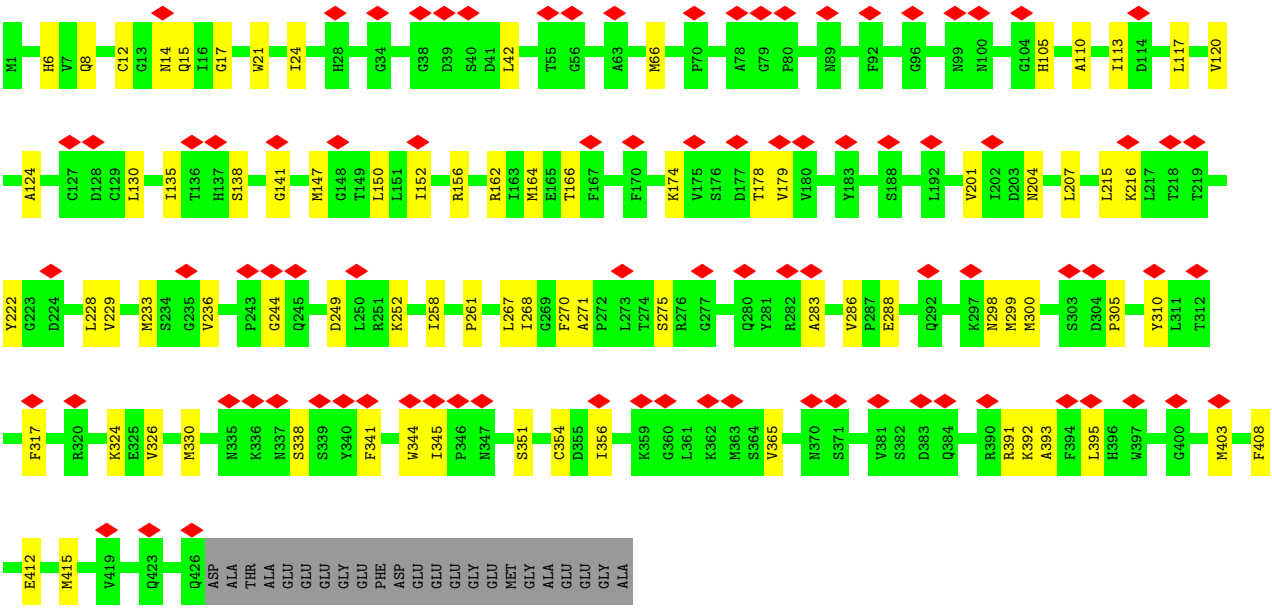
Chain 9J:





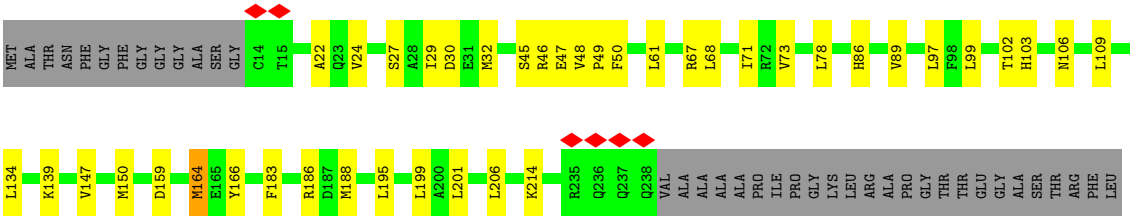
• Molecule 4: Tubulin beta chain

Chain 9L:



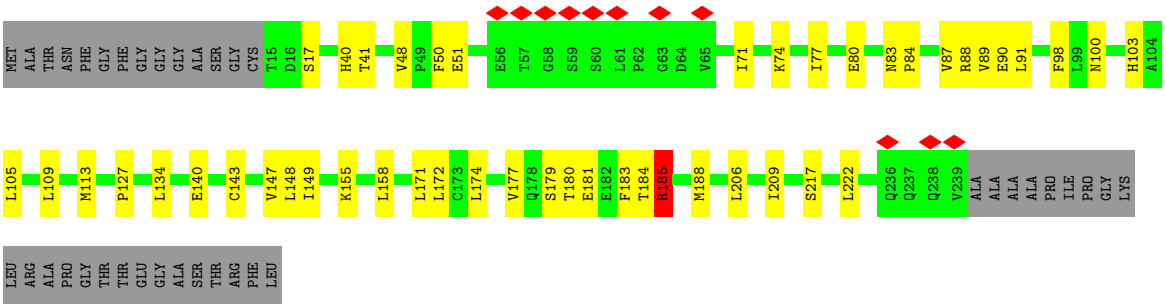
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 20:



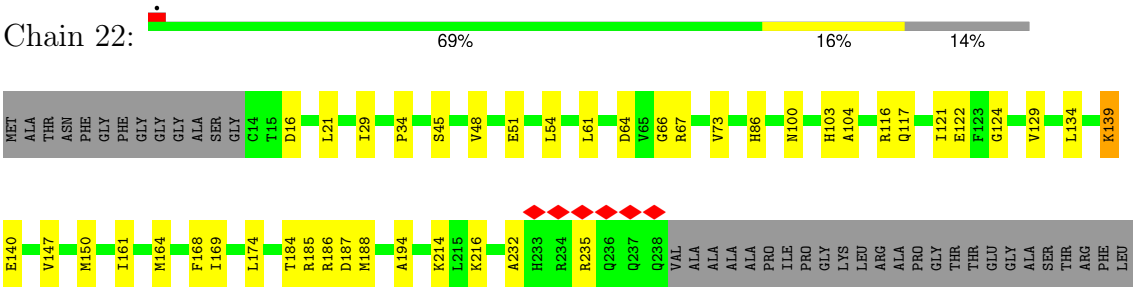
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 21:



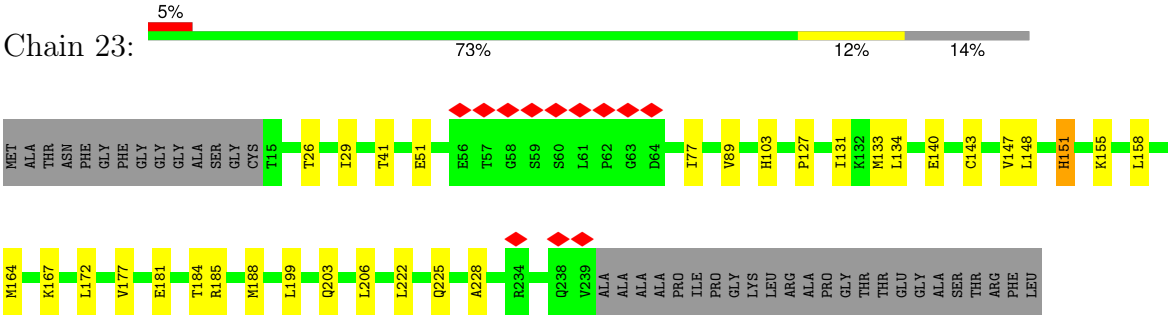
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 22:



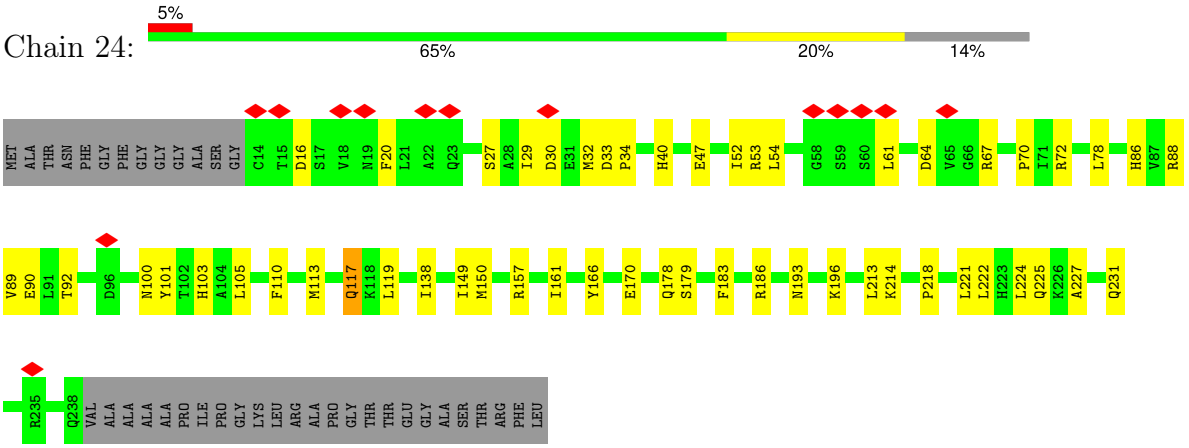
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 23:



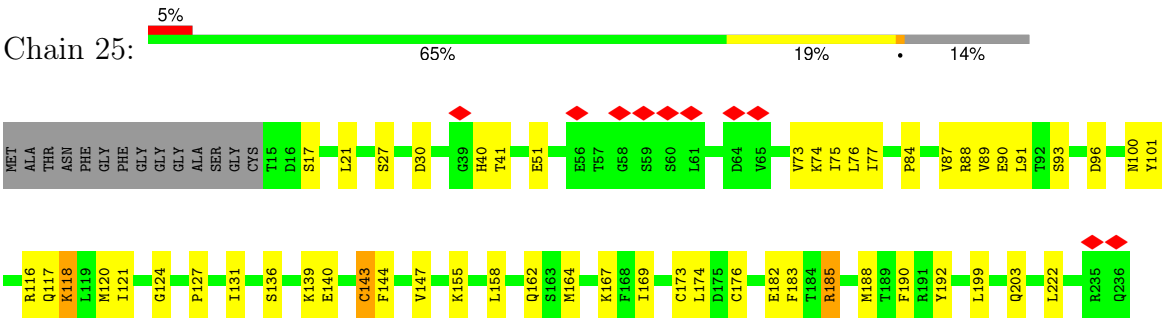
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

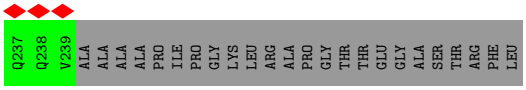
Chain 24:



• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

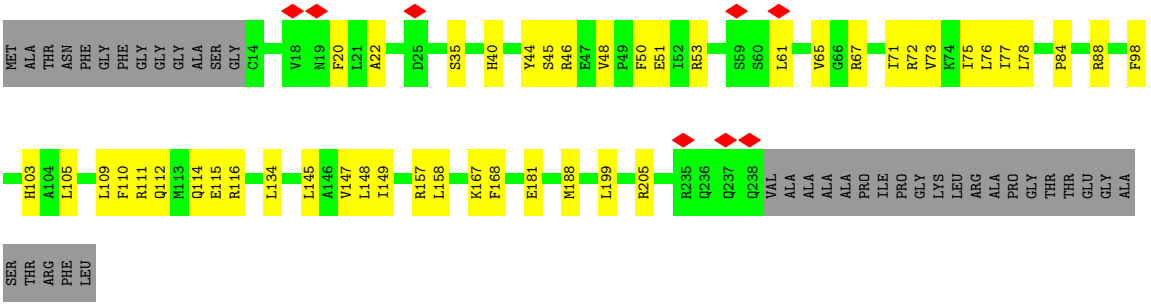
Chain 25:





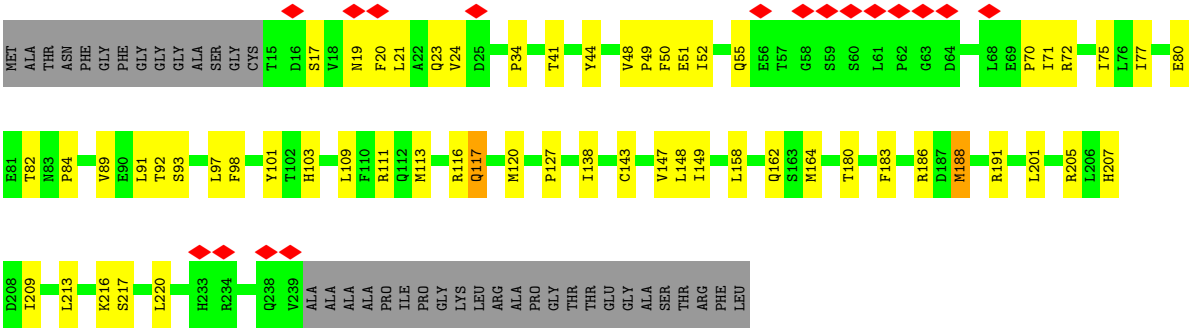
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 26:



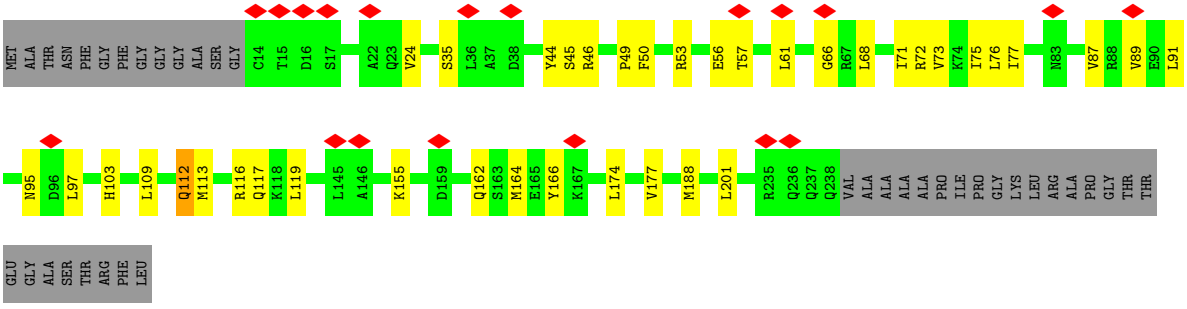
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 27:



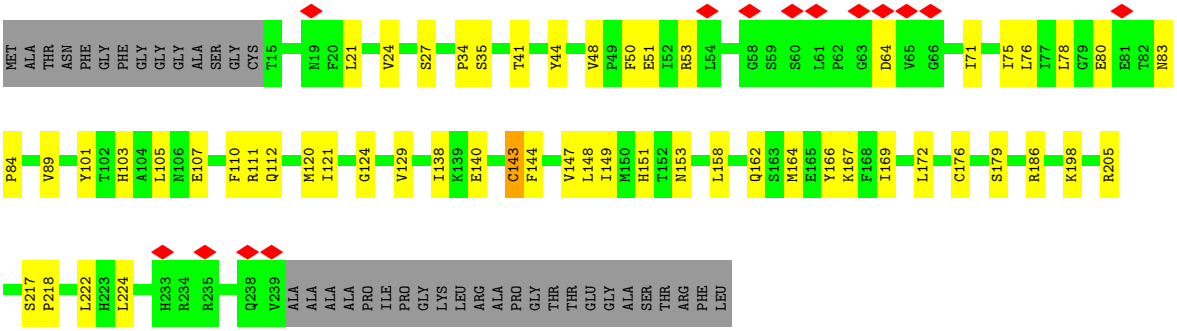
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 28:



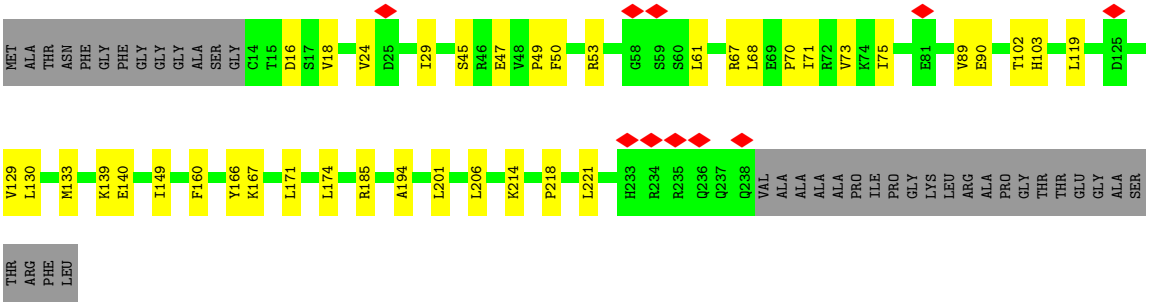
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 29:



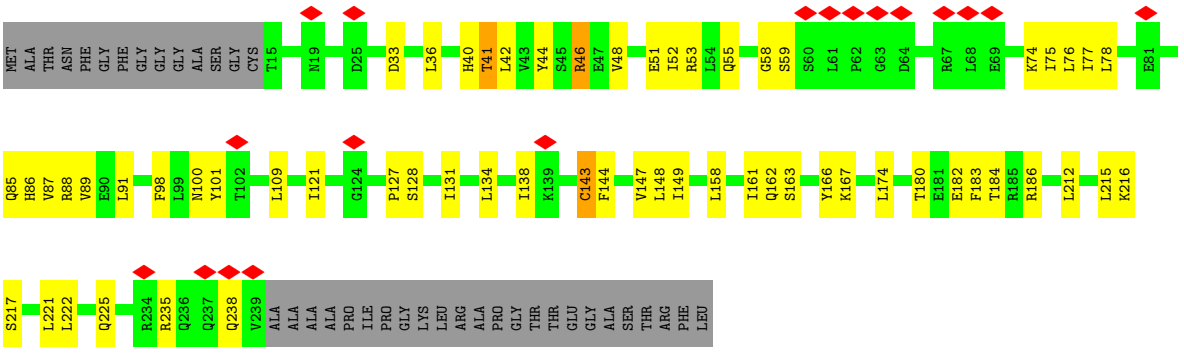
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 30:



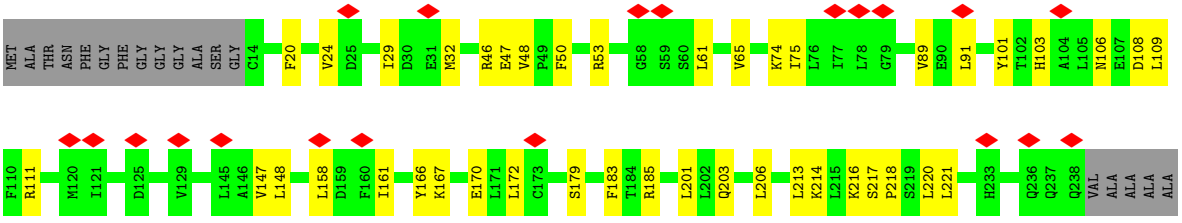
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 31:



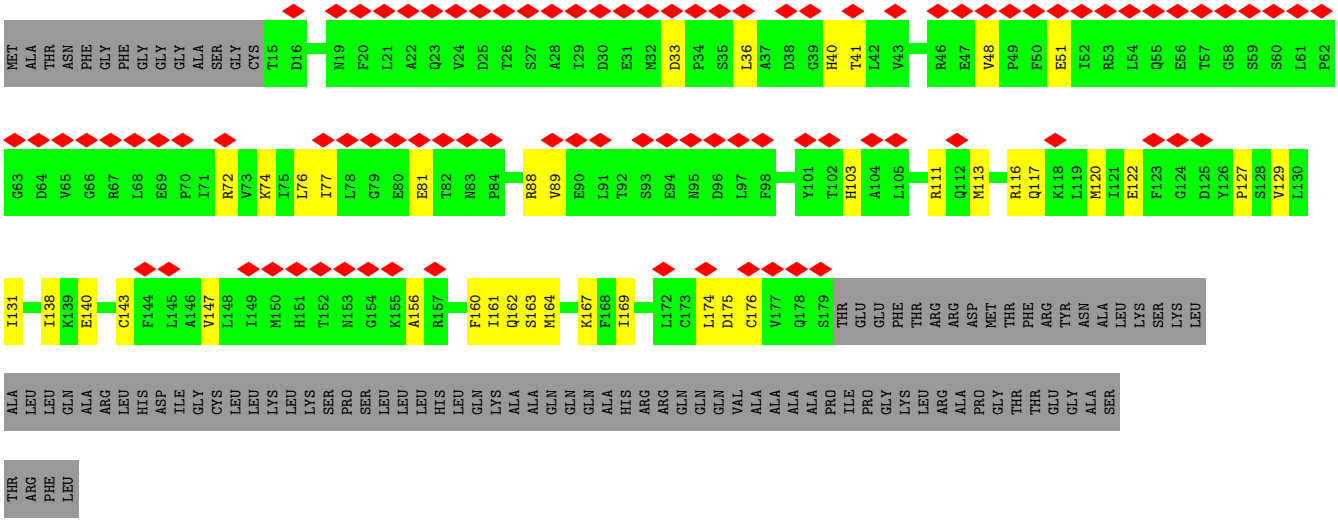
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 32:



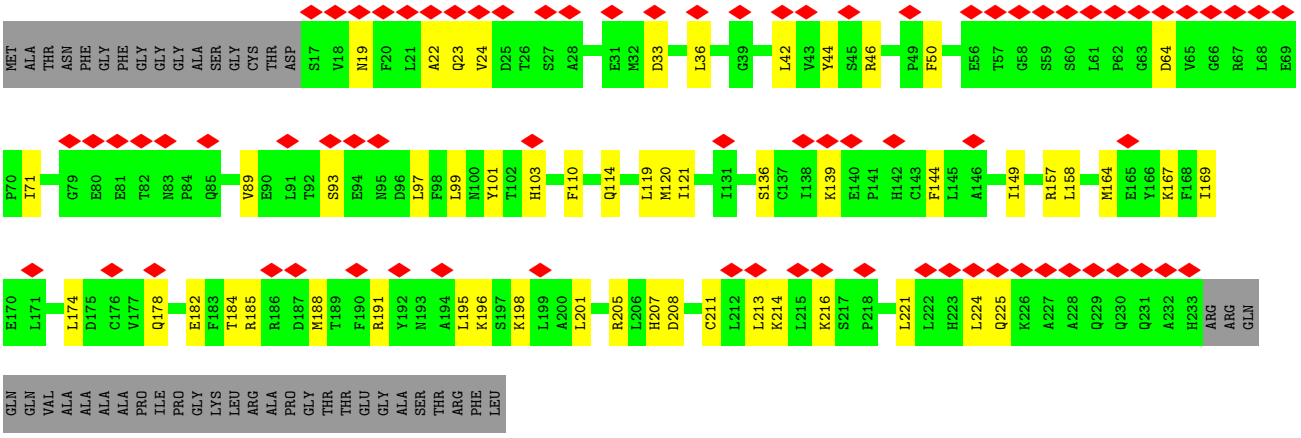
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 33:



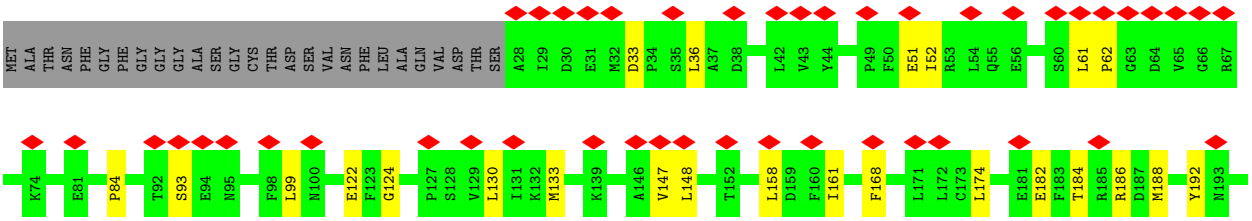
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

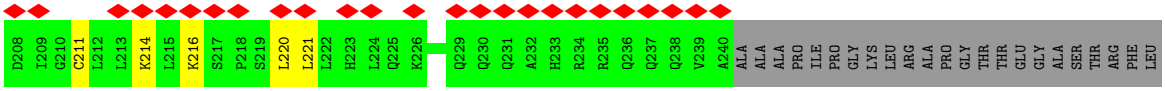
Chain 35:



• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

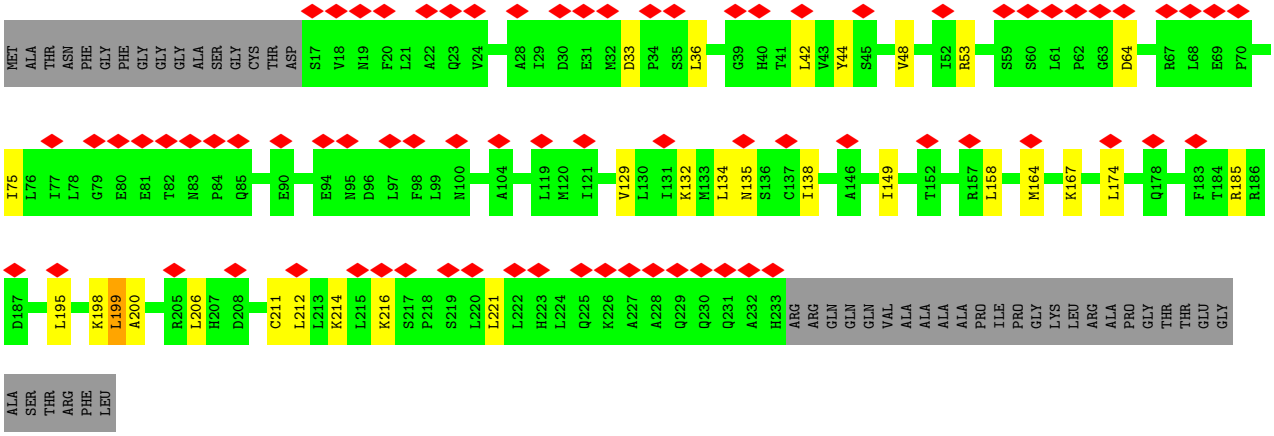
Chain 36:





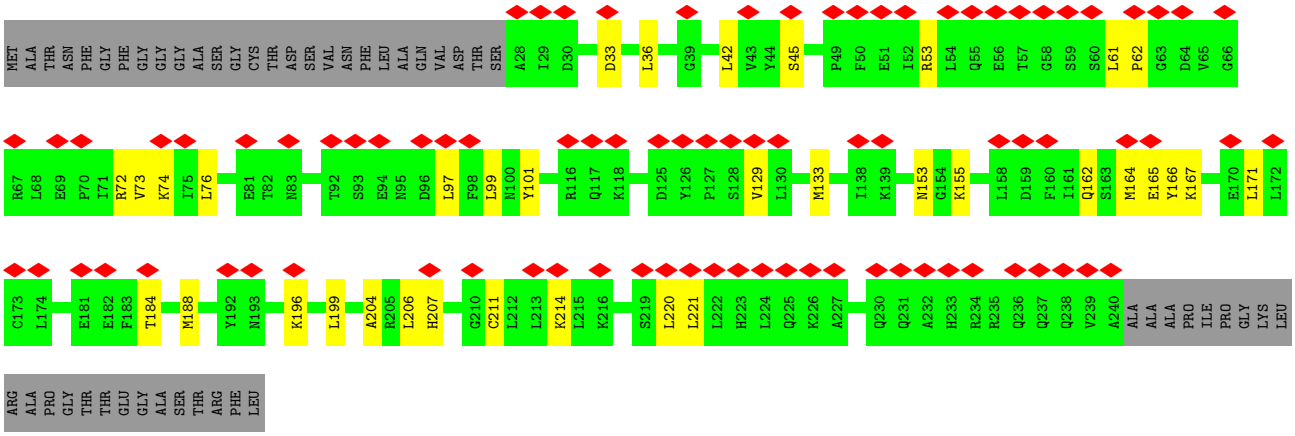
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 37:



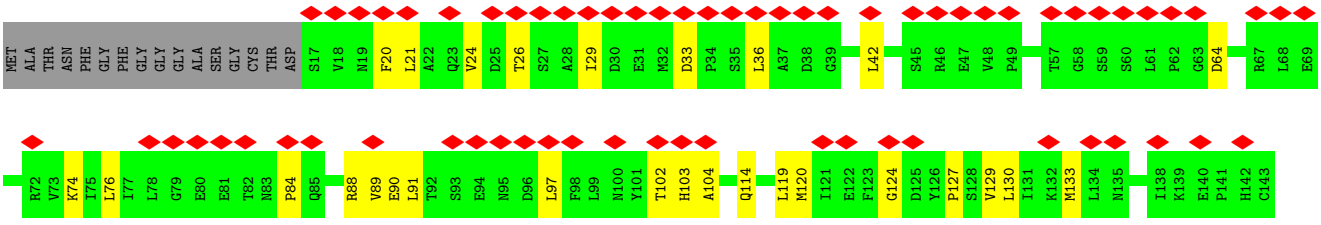
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

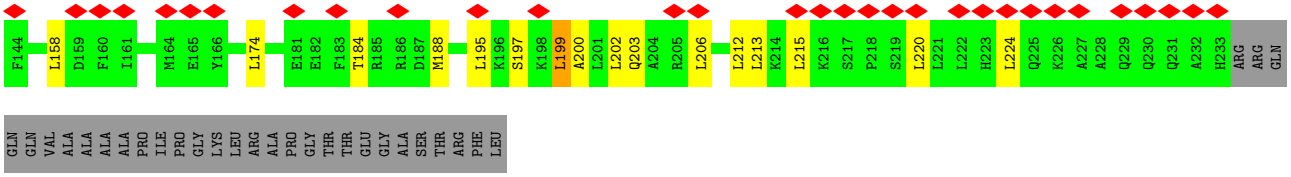
Chain 38:



• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

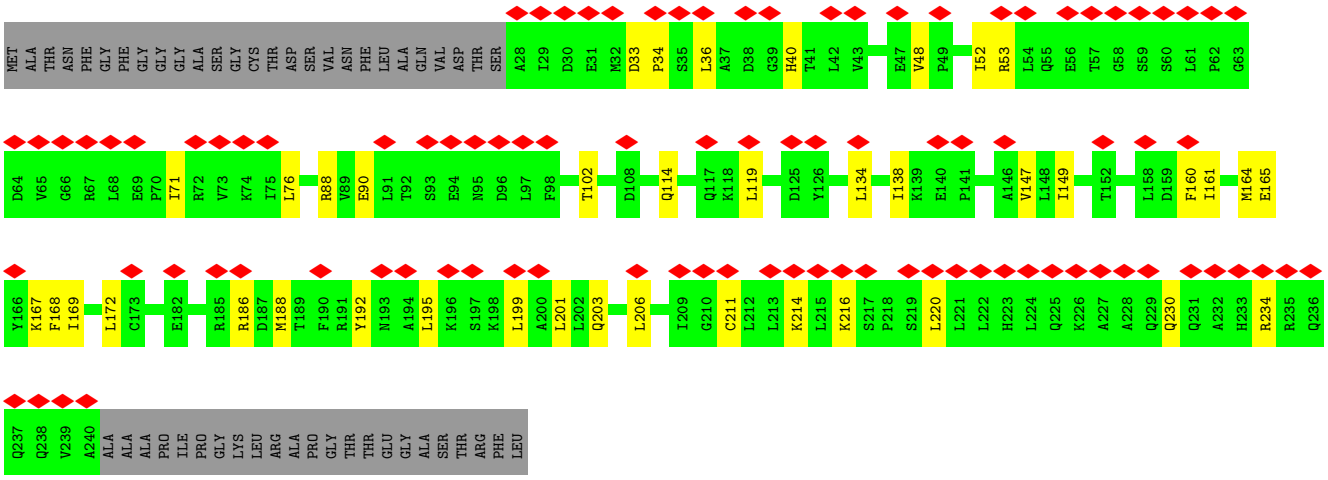
Chain 39:





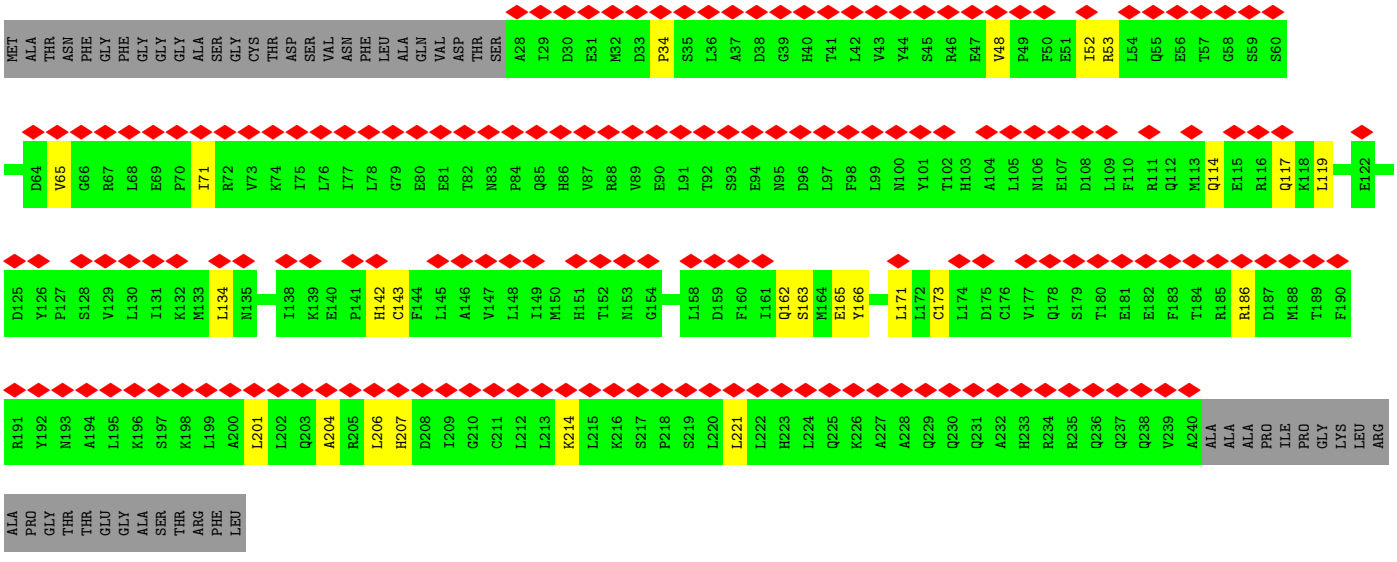
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 40:



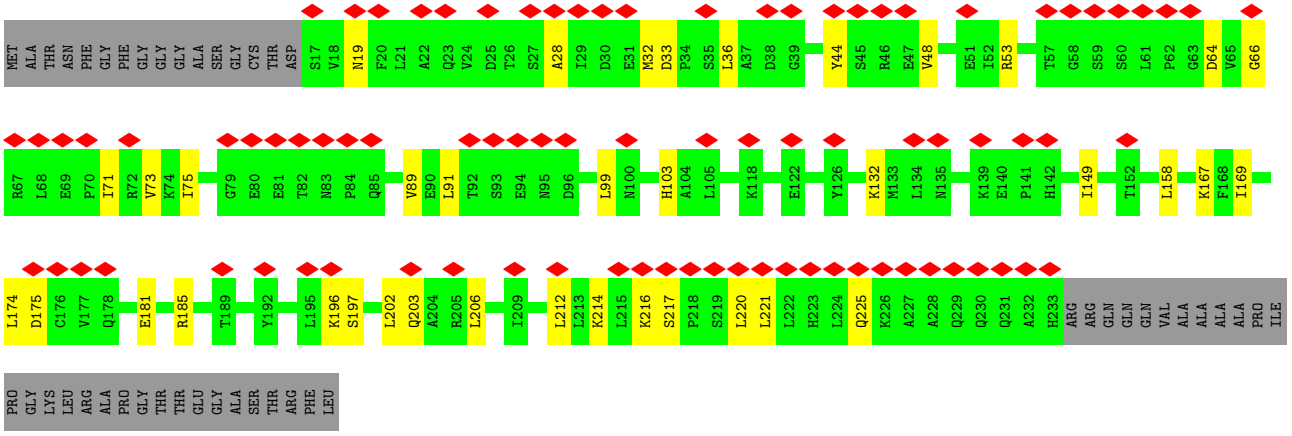
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 42:



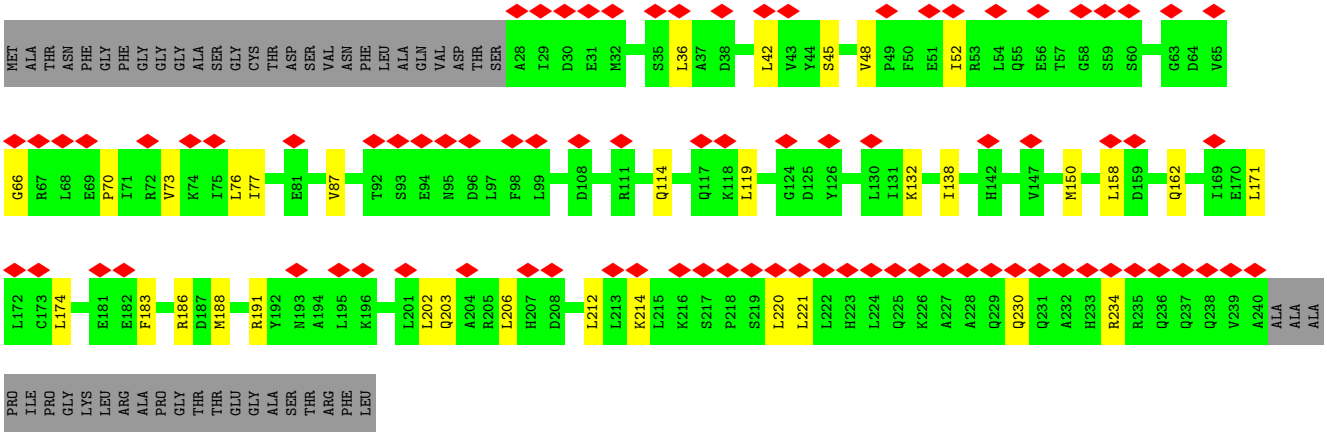
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 43:



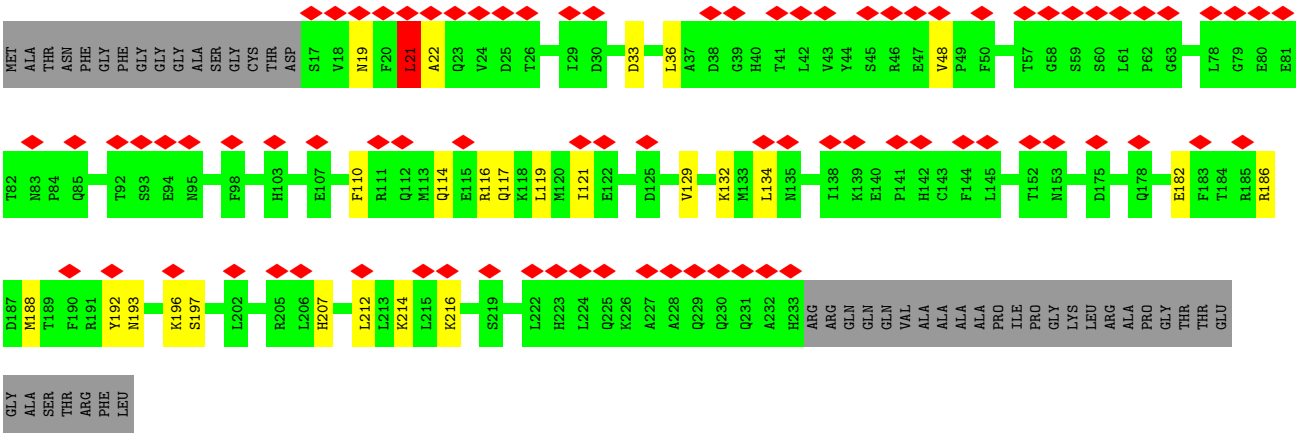
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 44:



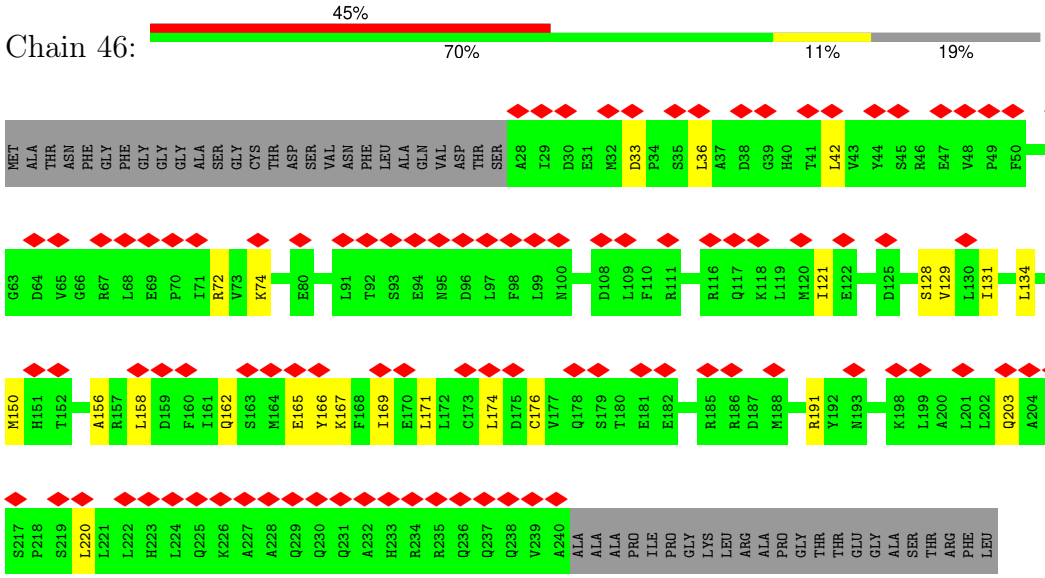
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 45:



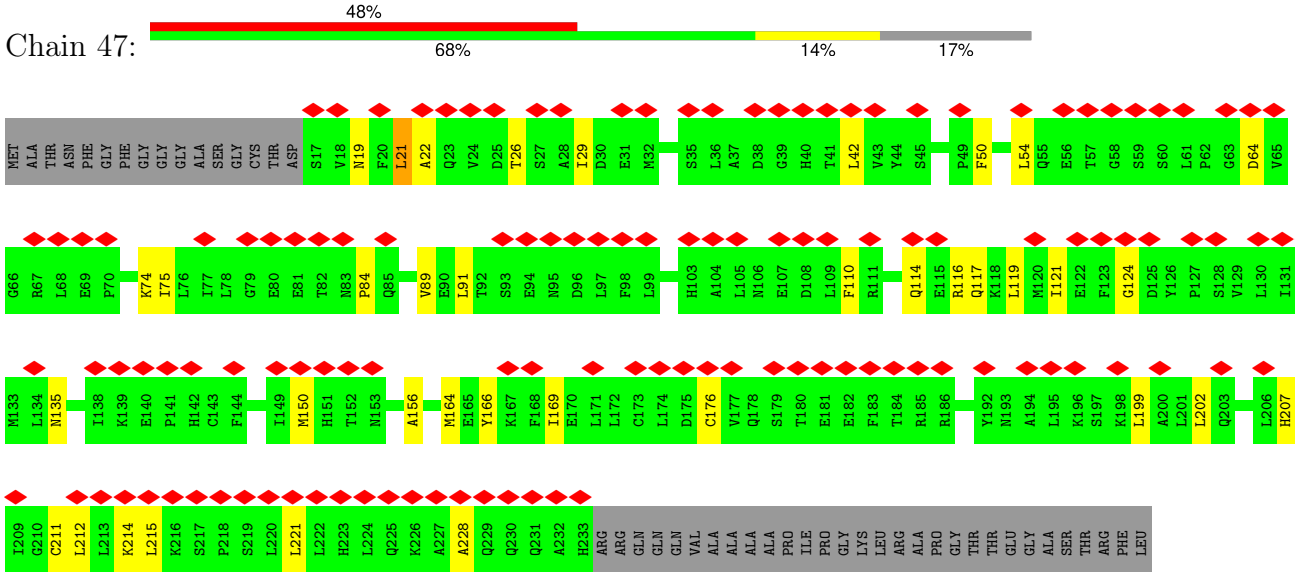
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 46:



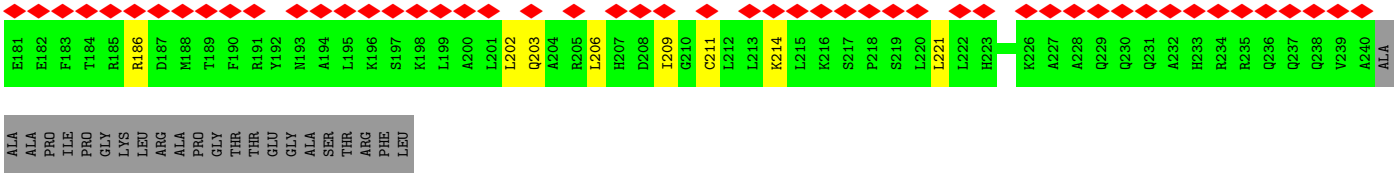
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 47:



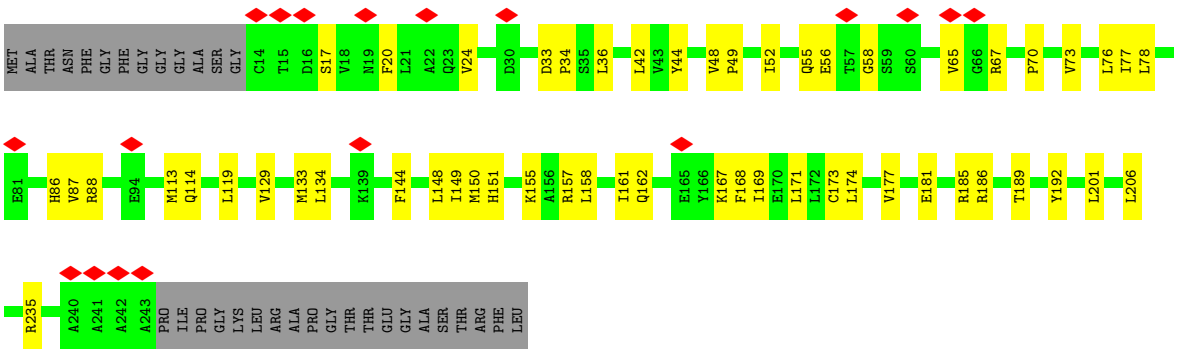
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 48:



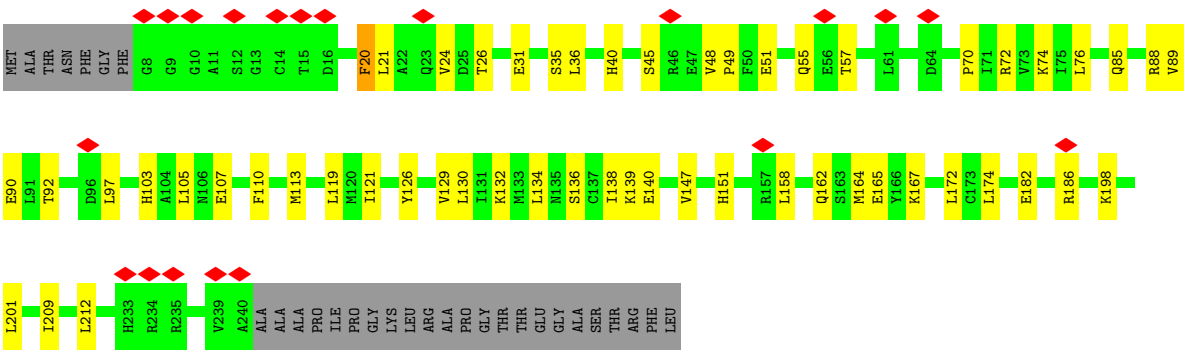
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 49:



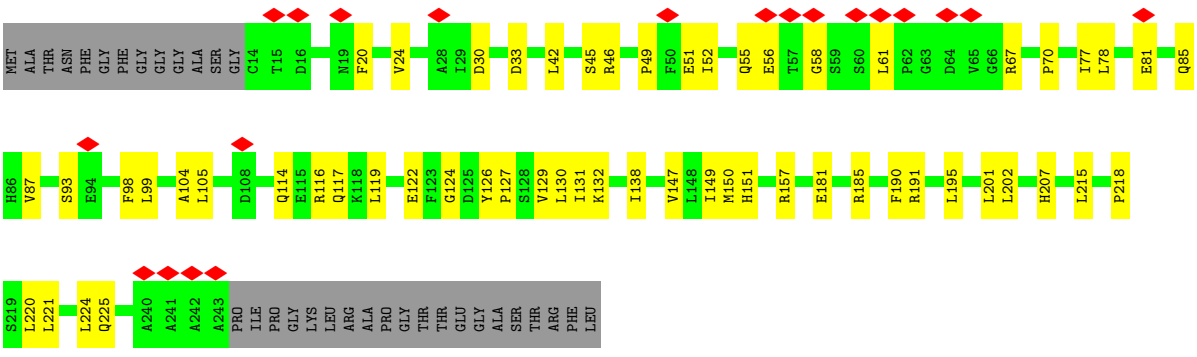
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 50:



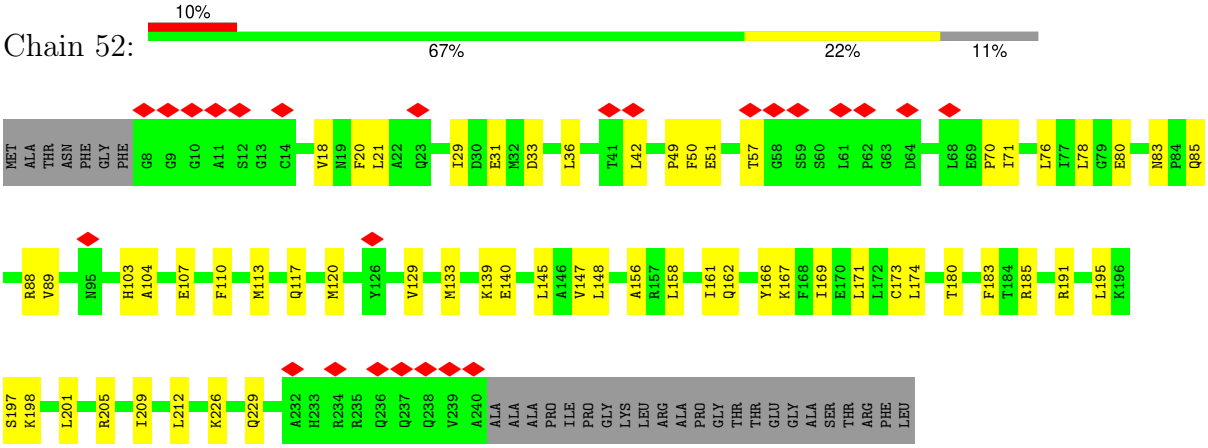
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 51:



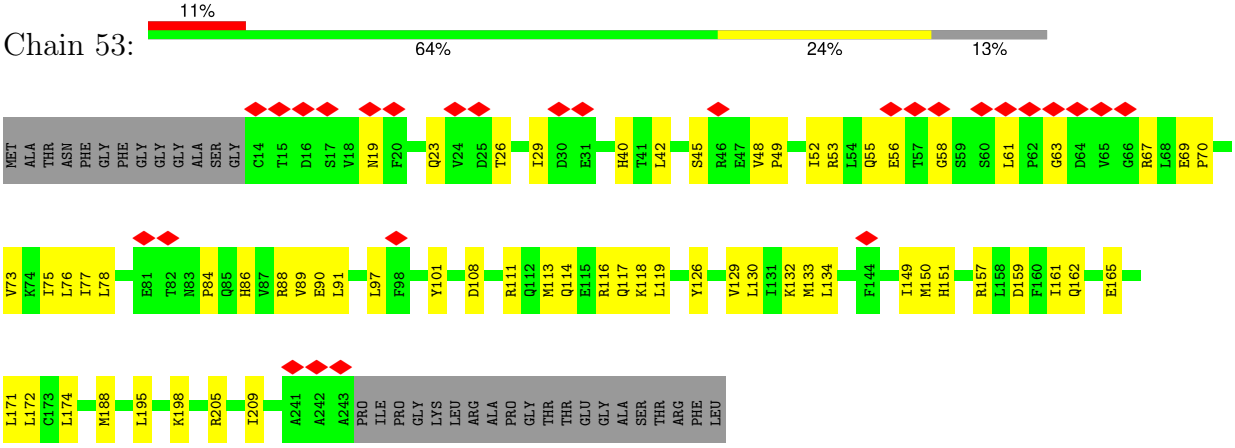
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 52:



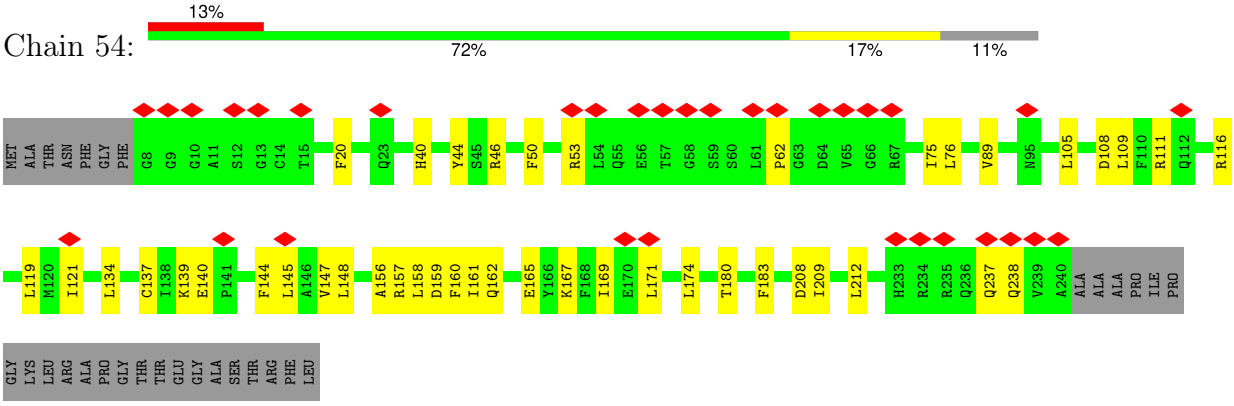
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 53:



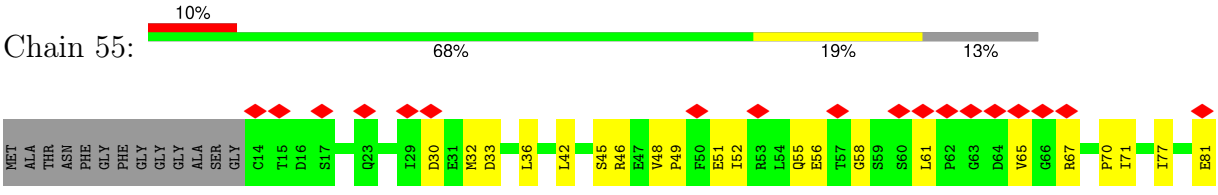
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

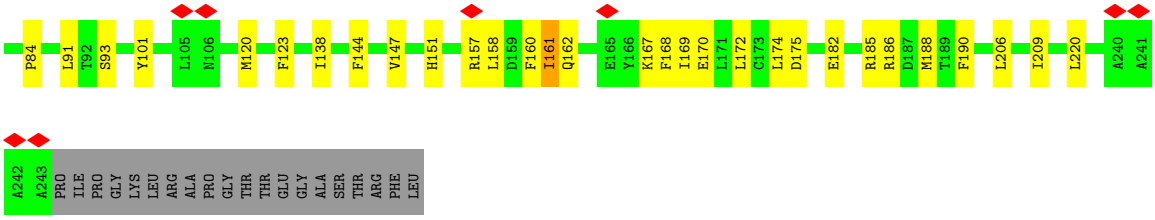
Chain 54:



• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

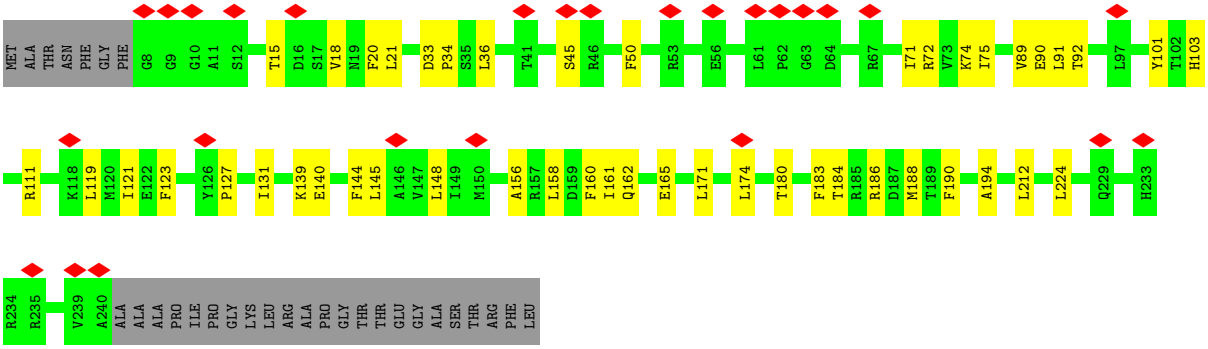
Chain 55:





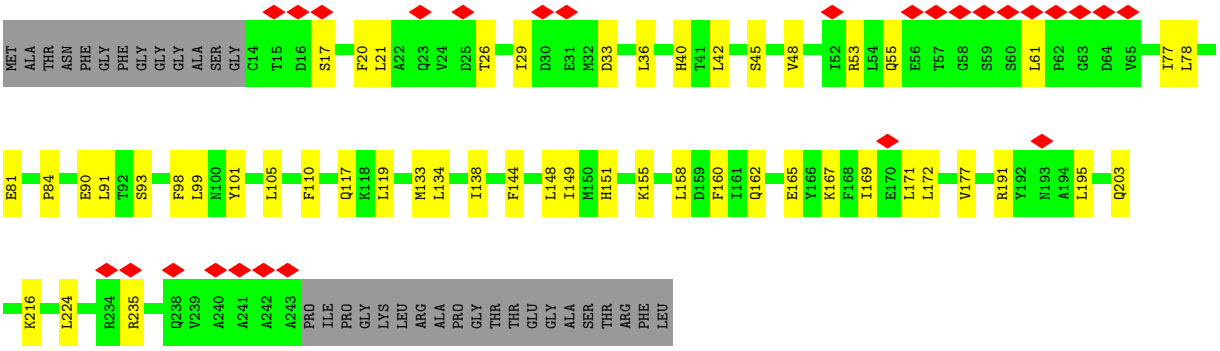
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 56:



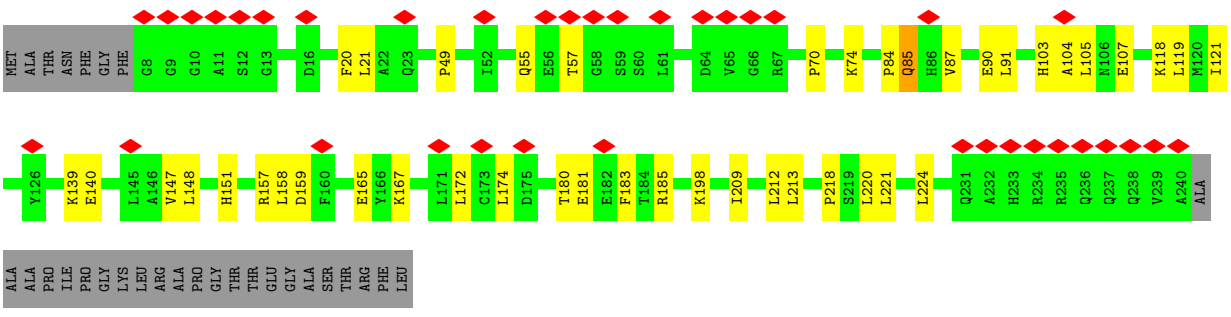
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 57:



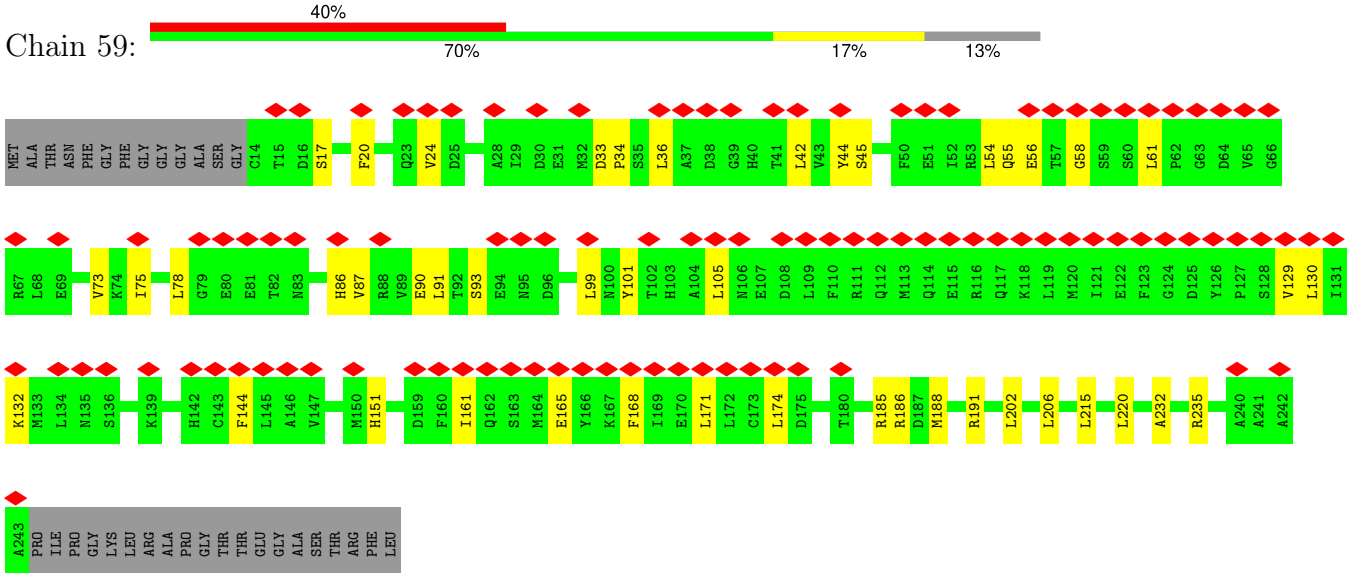
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 58:



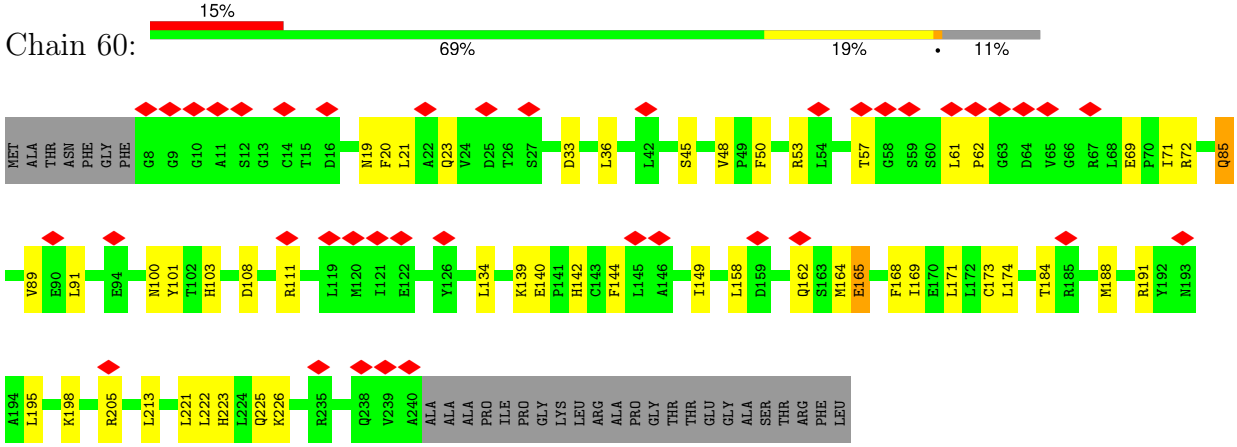
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 59:



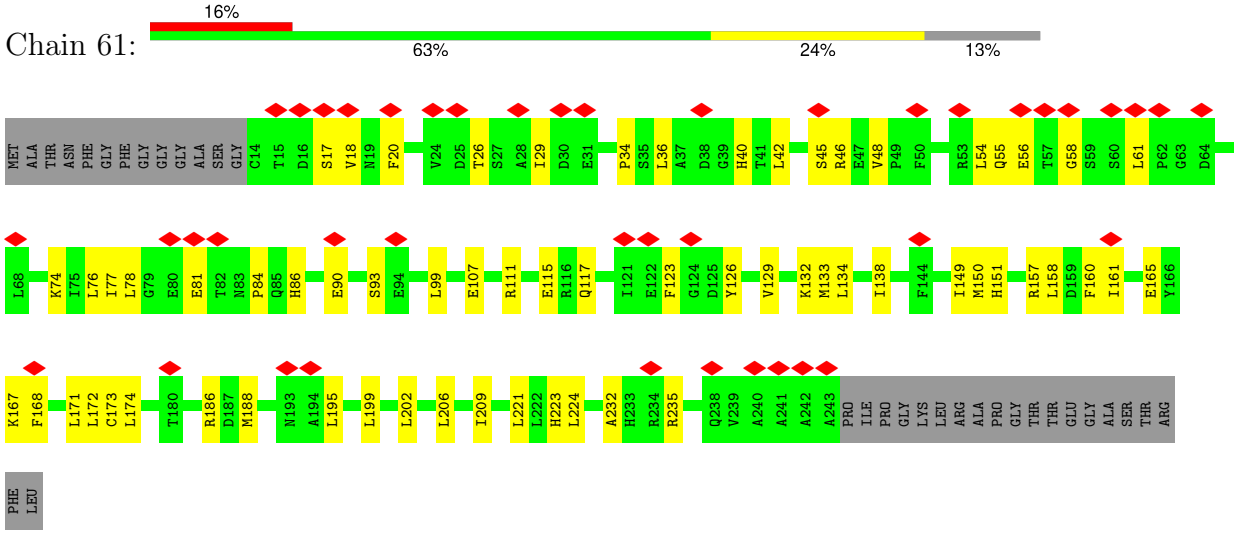
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 60:



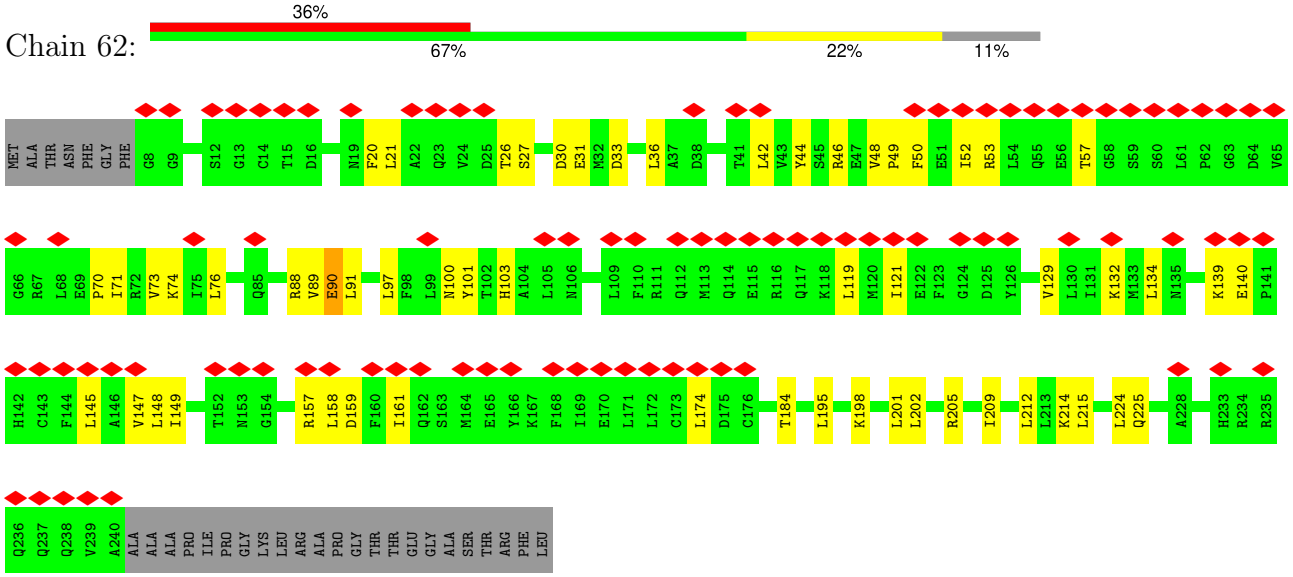
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

Chain 61:



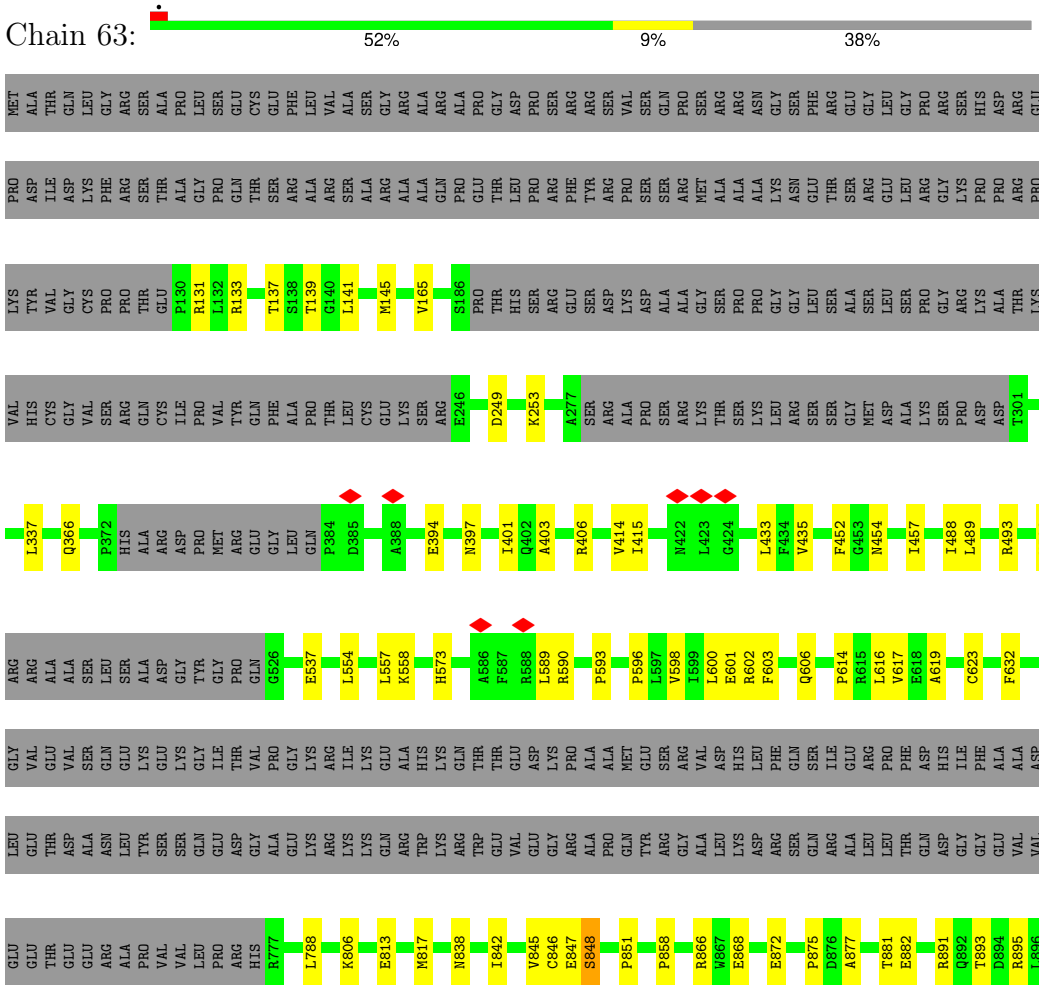
• Molecule 5: Spindle assembly abnormal protein 6 N-terminal domain-containing protein

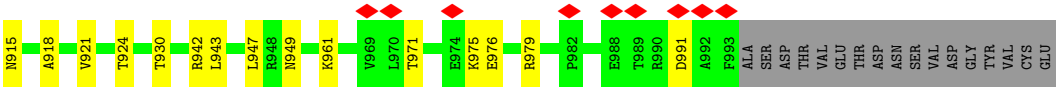
Chain 62:



• Molecule 6: CIP3, TGME49_225020

Chain 63:





• Molecule 6: CIP3, TGME49_225020

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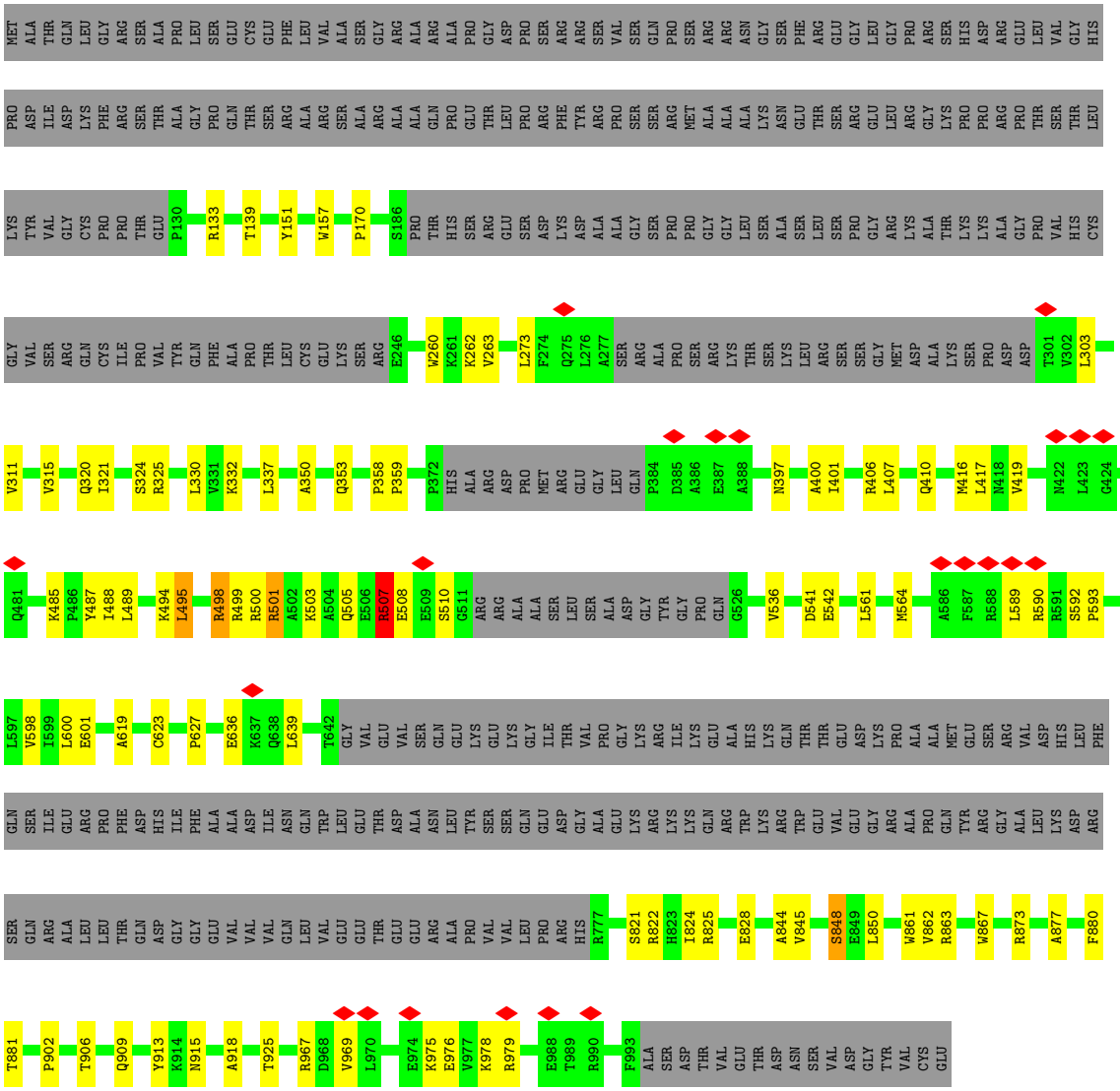
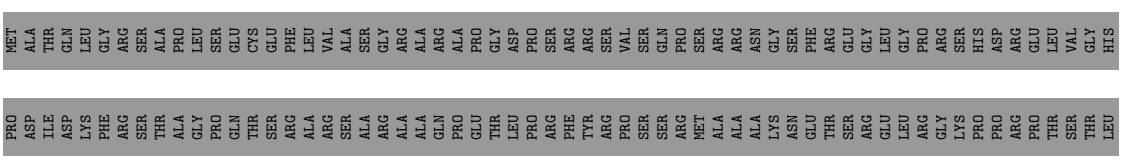
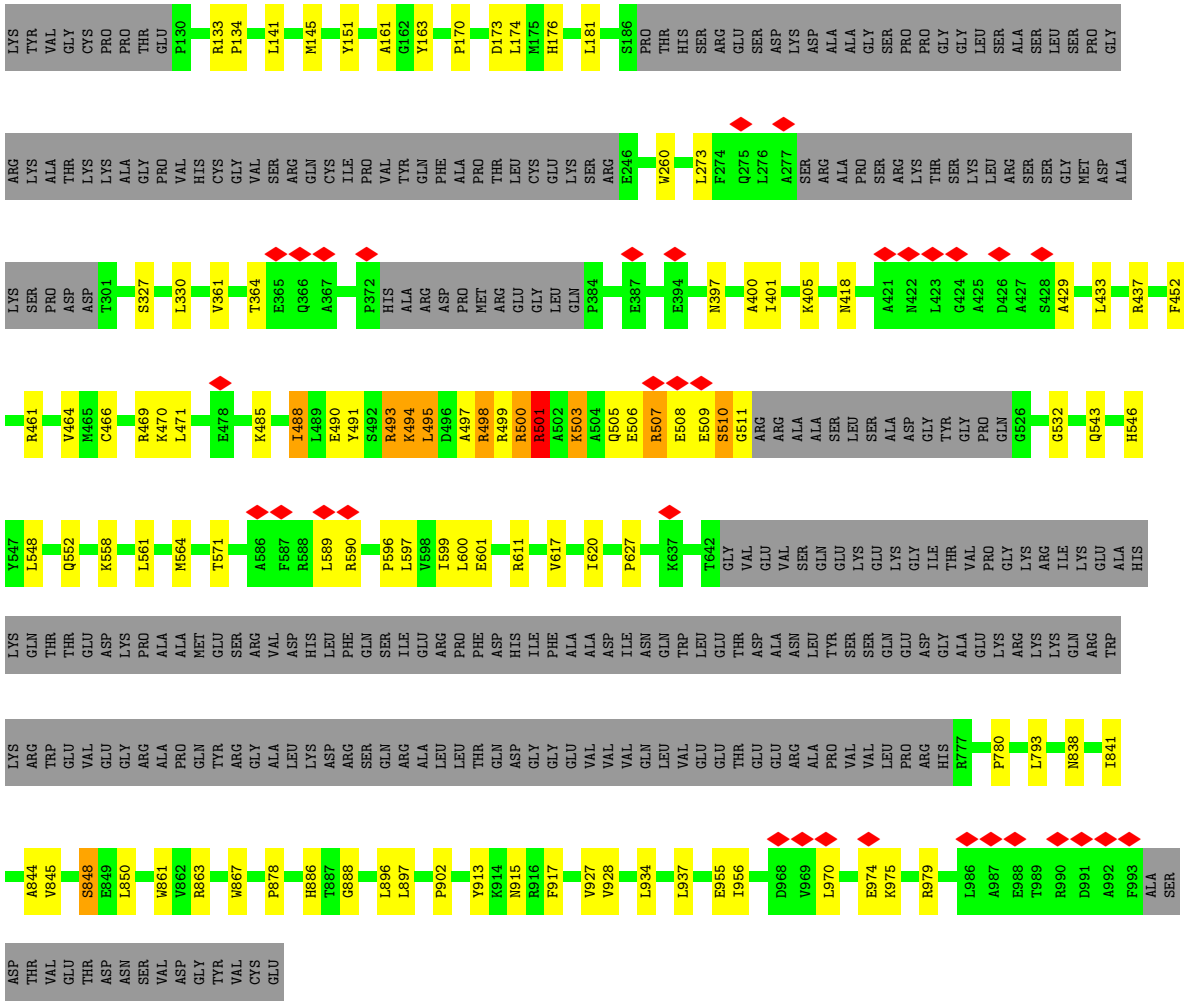


• Molecule 6: CIP3, TGME49_225020

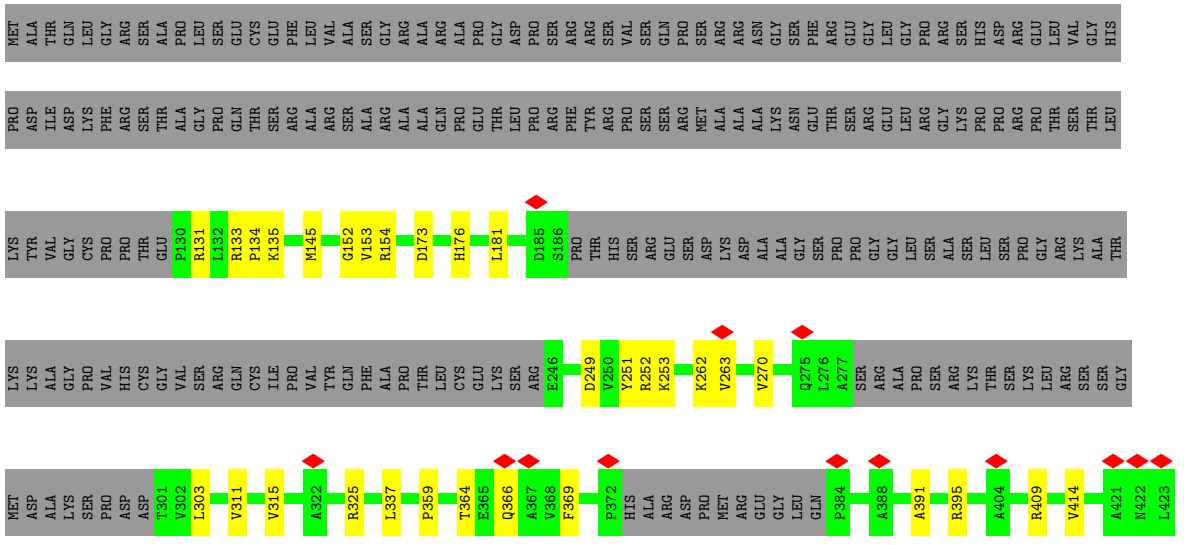
Chain 65:

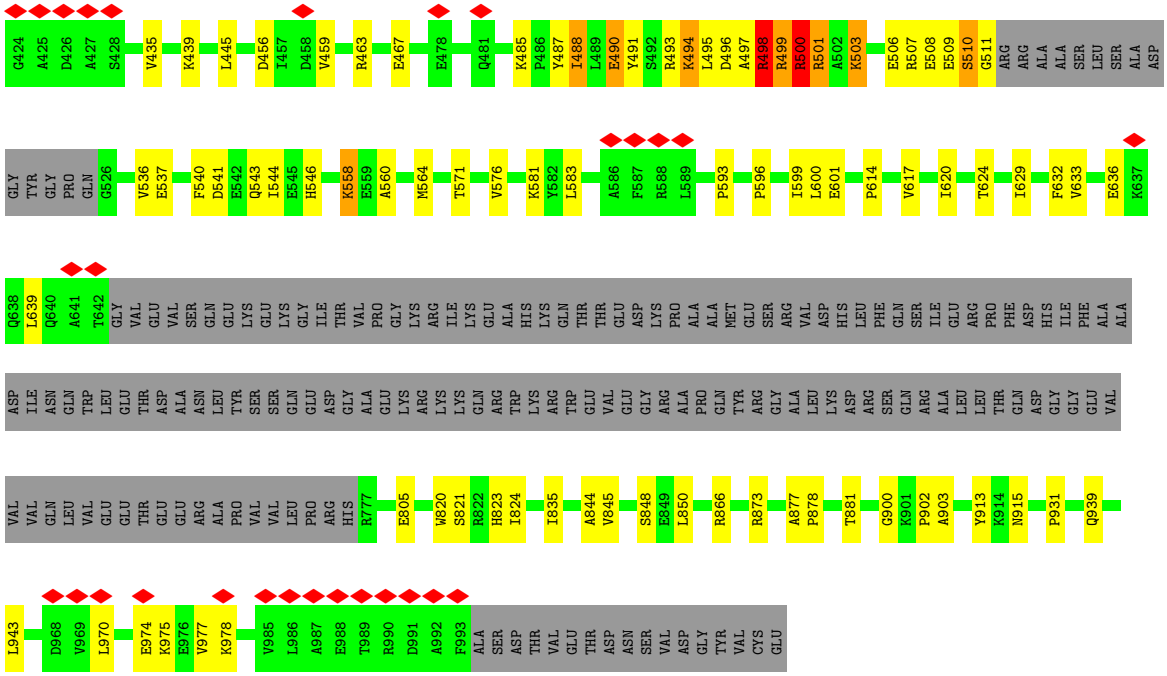




• Molecule 6: CIP3, TGME49_225020

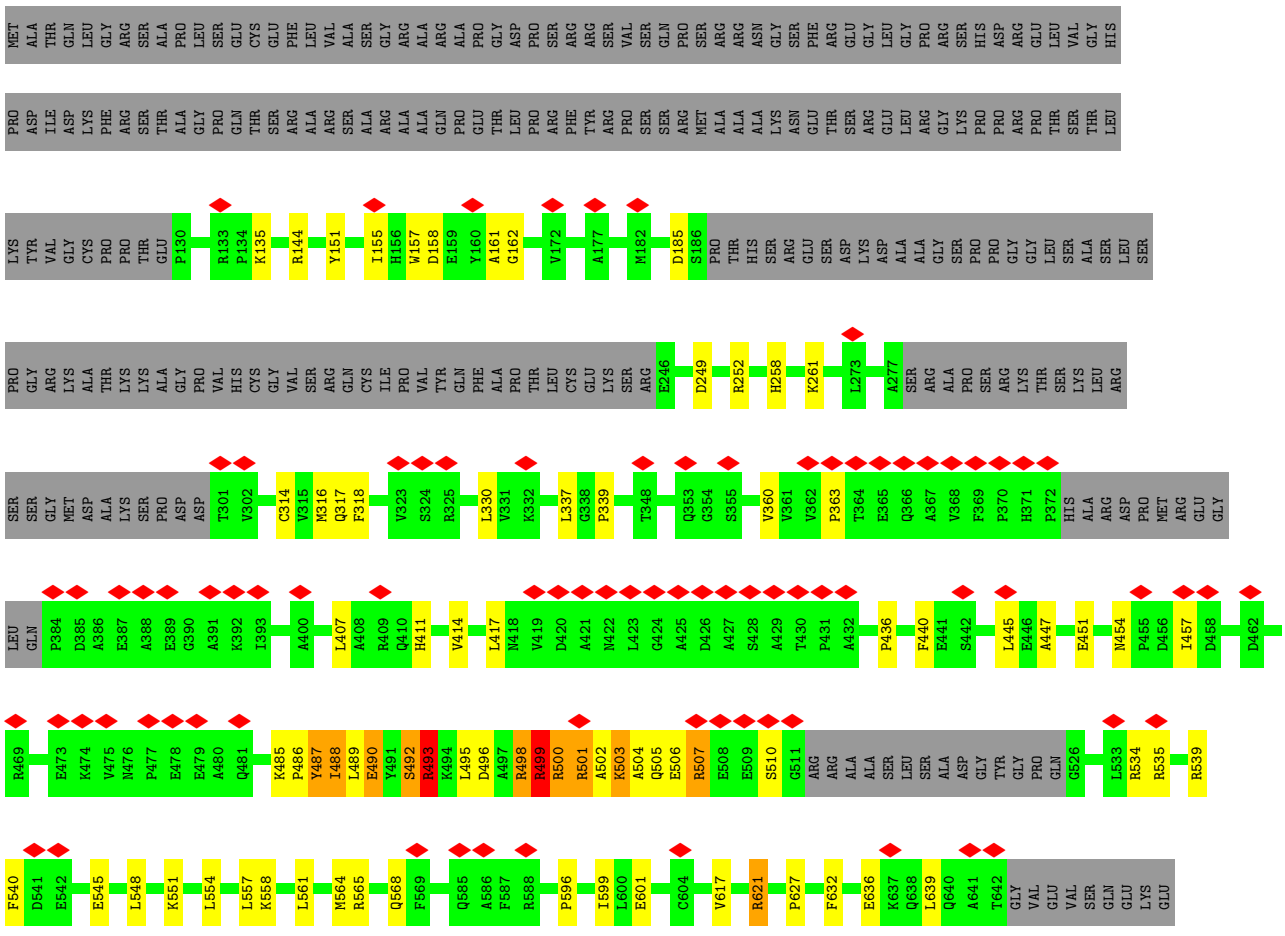
Chain 66:

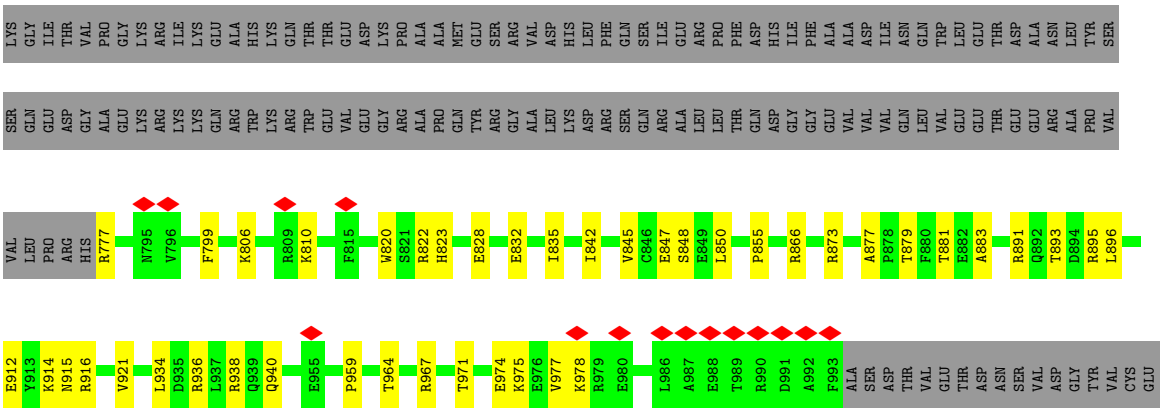


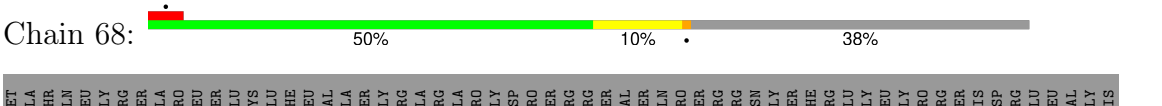


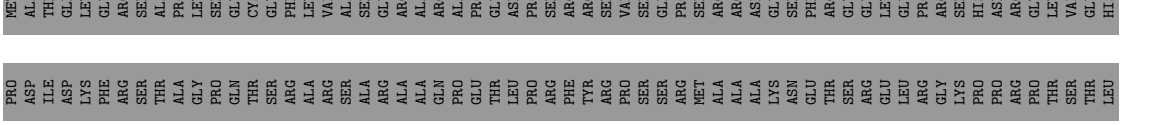
• Molecule 6: CIP3, TGME49_225020

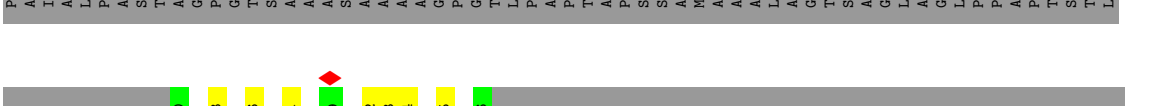
Chain 67:

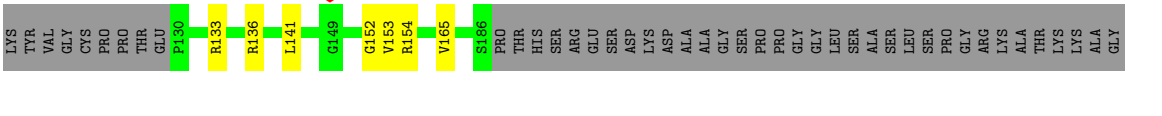


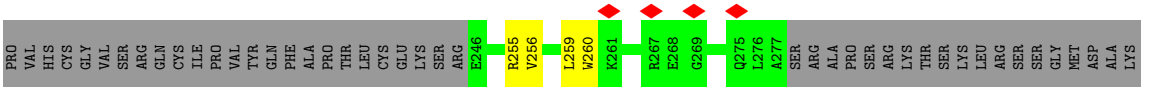


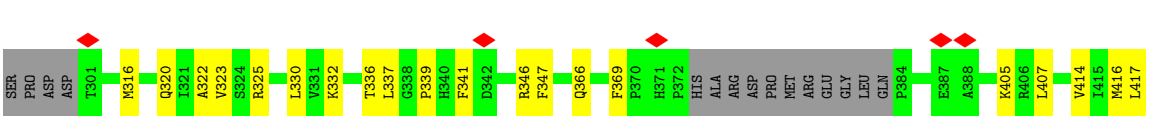


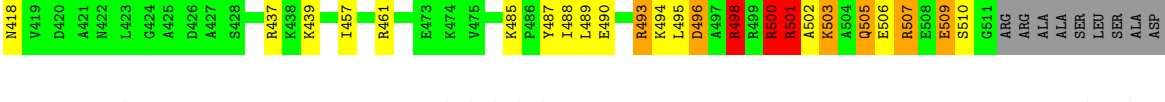


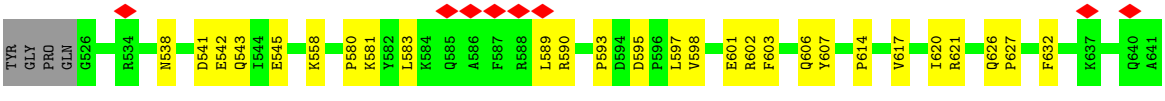


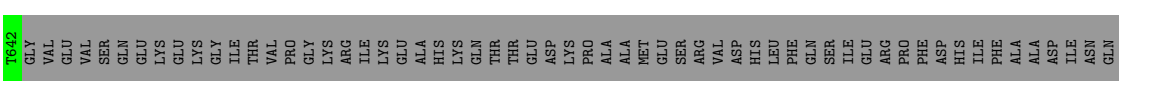


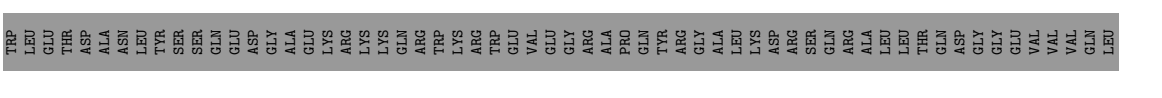


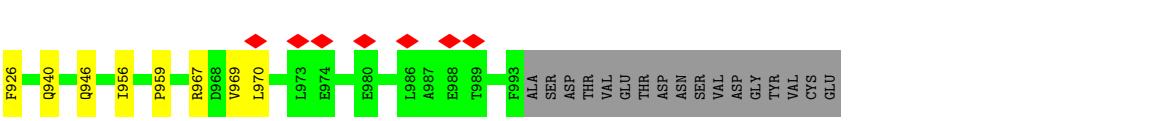










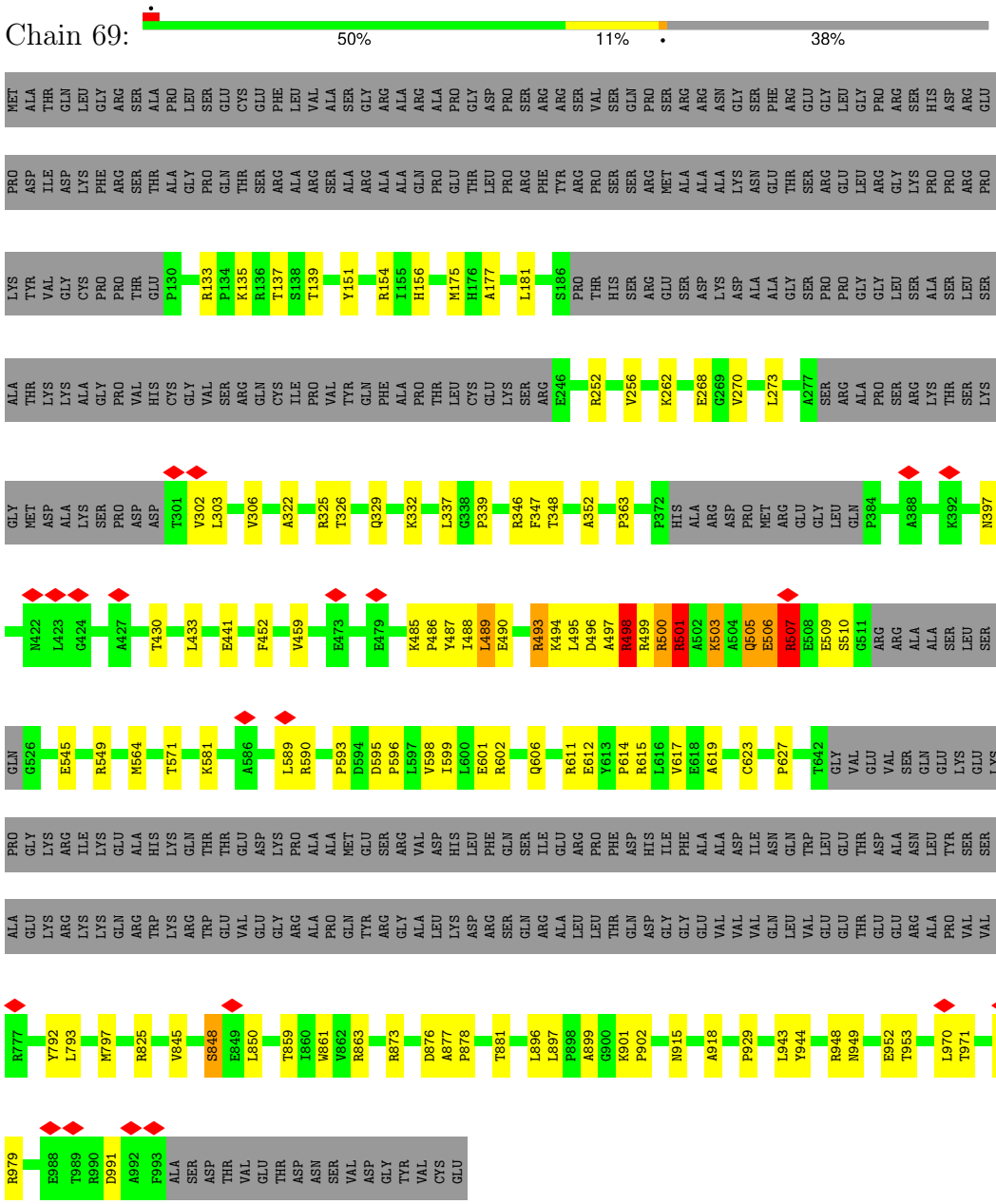


• Molecule 6: CIP3, TGME49_225020

Chain 68:

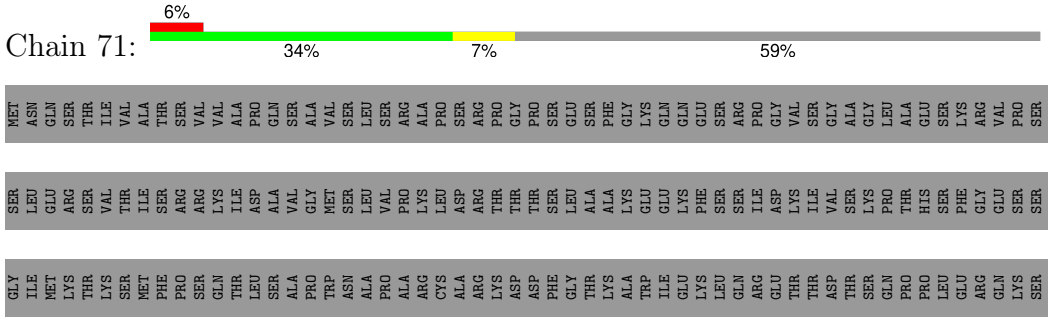
• Molecule 6: CIP3, TGME49_225020

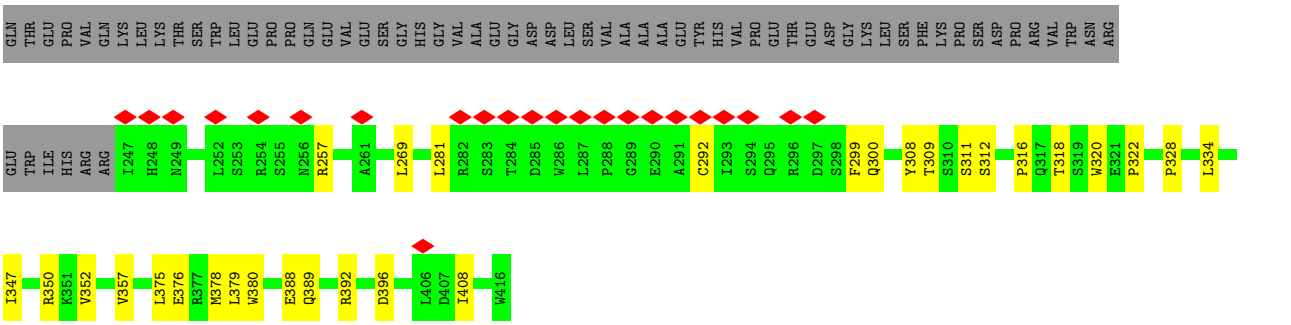
Chain 69:



• Molecule 7: CF6, TGME49_245640

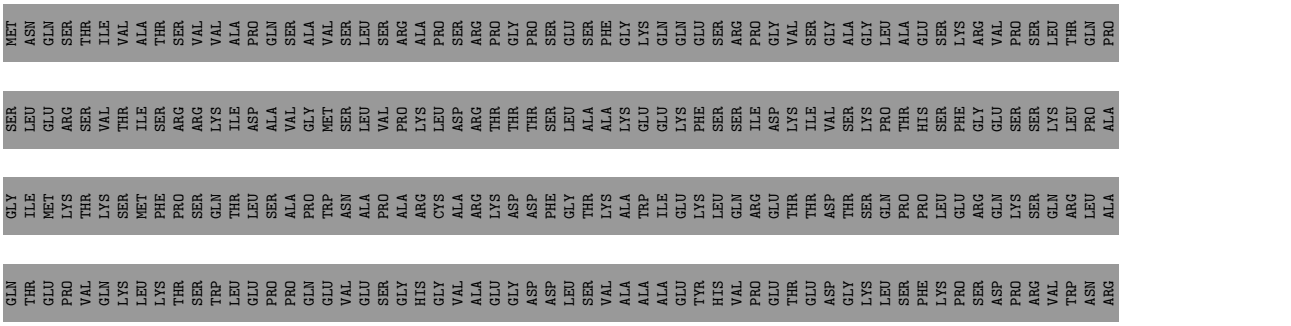
Chain 71:

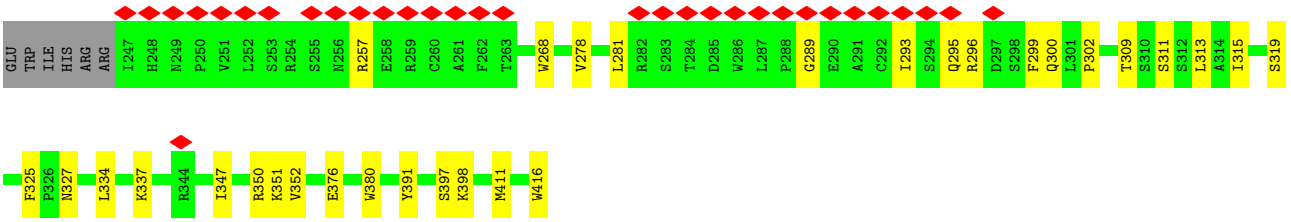




• Molecule 7: CF6, TGME49_245640

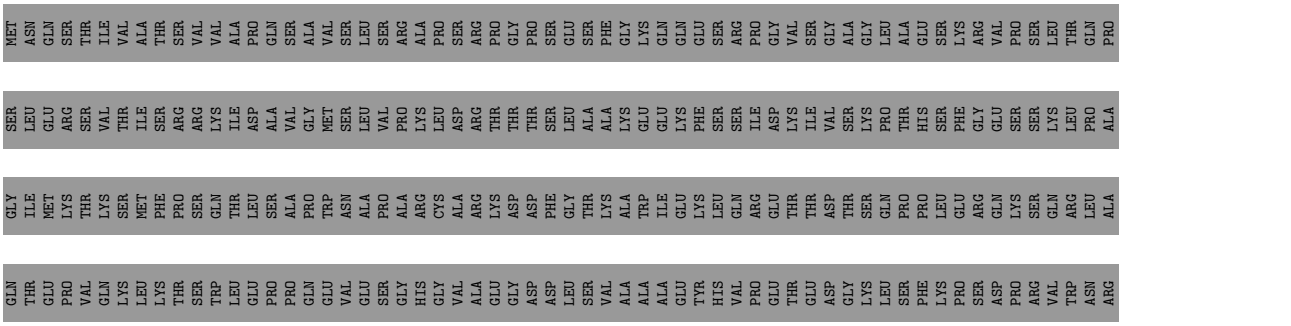
Chain 72:

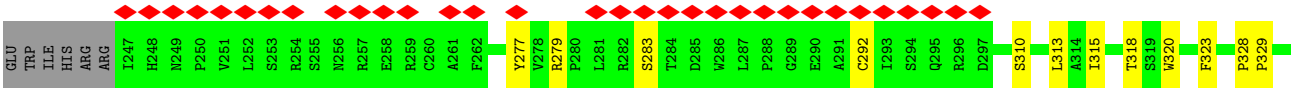




• Molecule 7: CF6, TGME49_245640

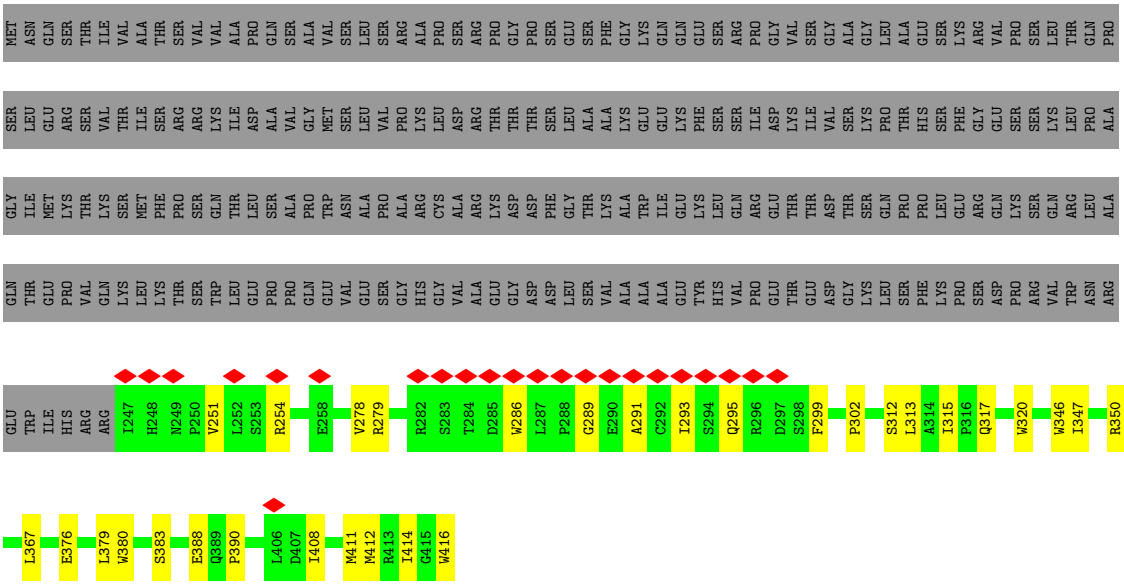
Chain 73:





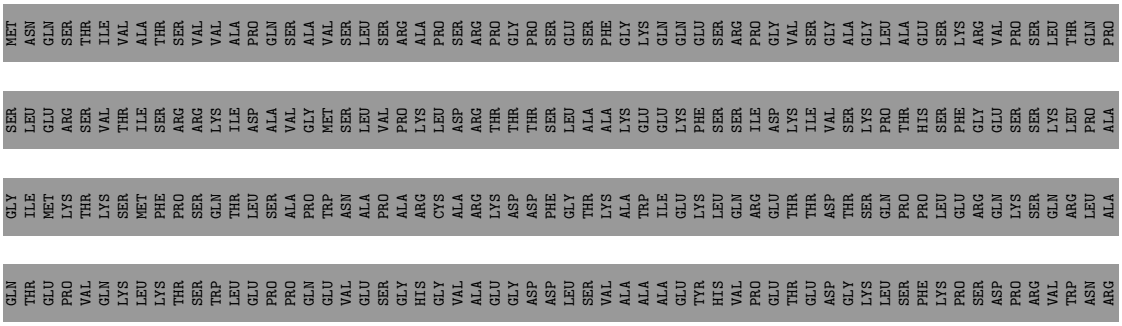
• Molecule 7: CF6, TGME49_245640

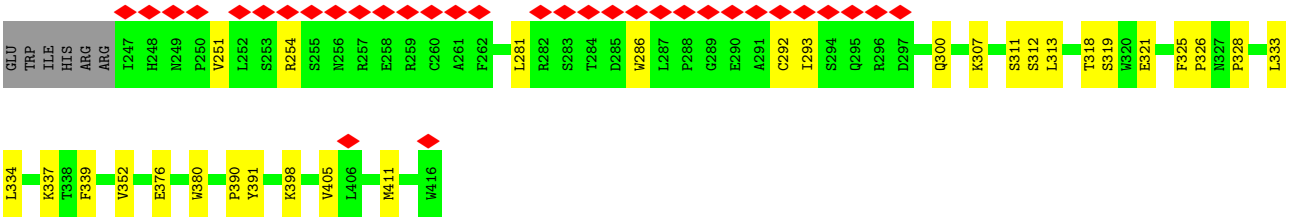
Chain 75:



• Molecule 7: CF6, TGME49_245640

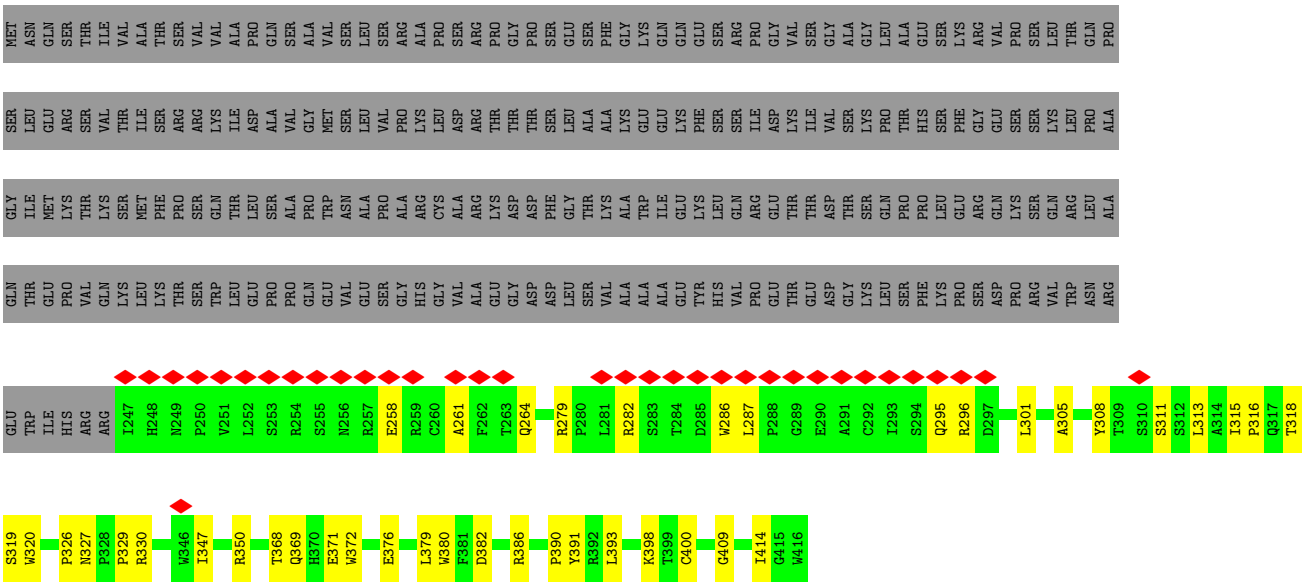
Chain 76:





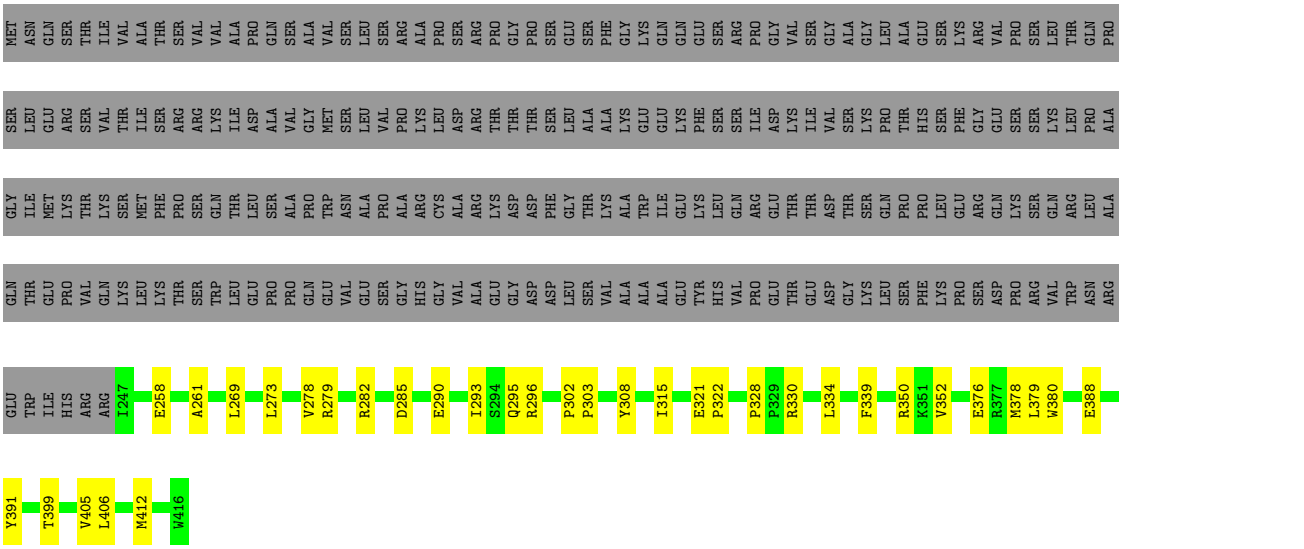
• Molecule 7: CF6, TGME49_245640

Chain 77:



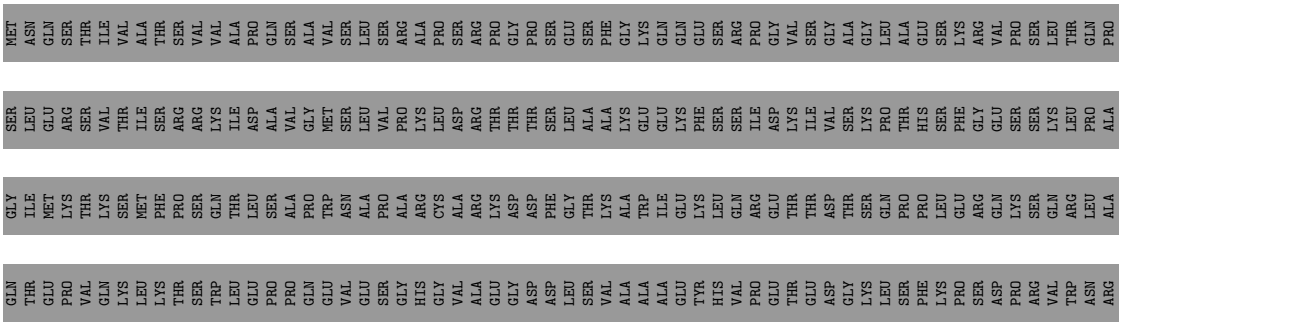
• Molecule 7: CF6, TGME49_245640

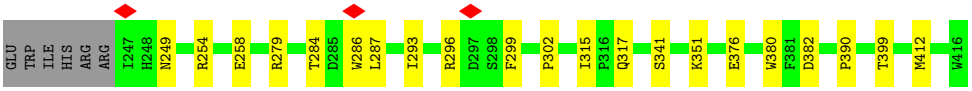
Chain 78:



• Molecule 7: CF6, TGME49_245640

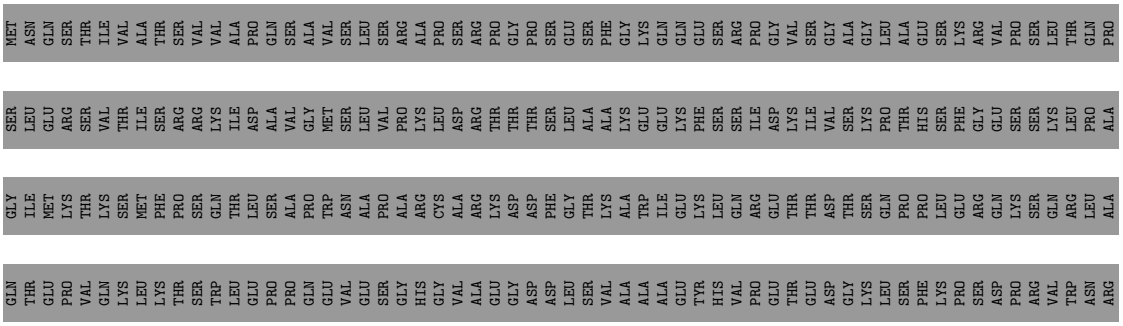
Chain 79:

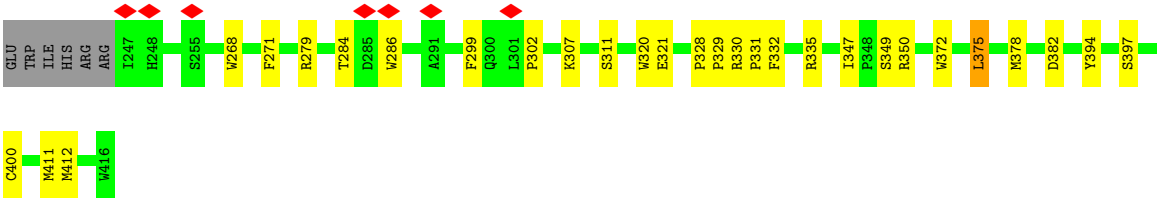




• Molecule 7: CF6, TGME49_245640

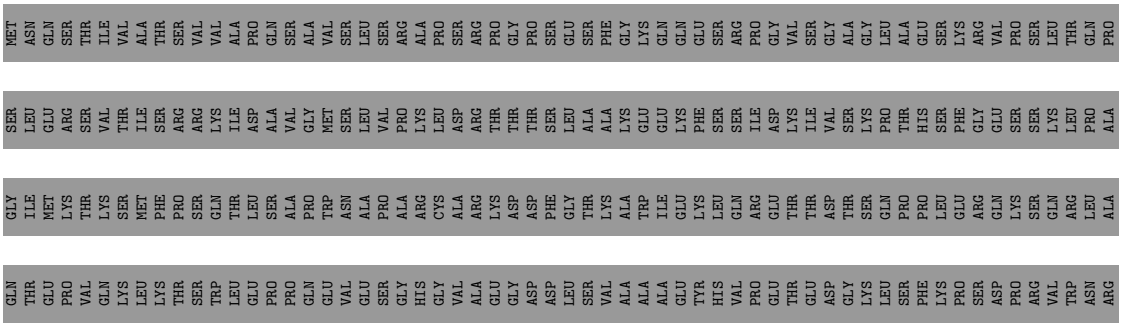
Chain 80:

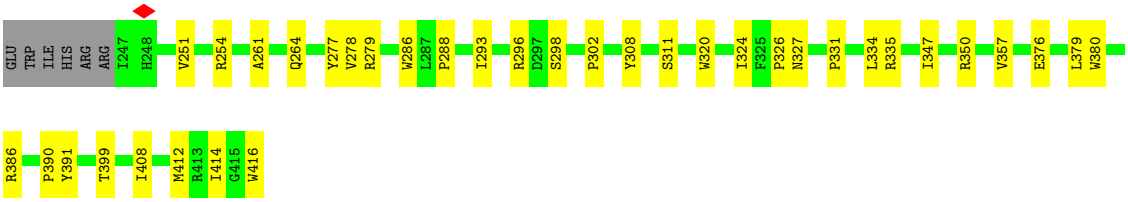




• Molecule 7: CF6, TGME49_245640

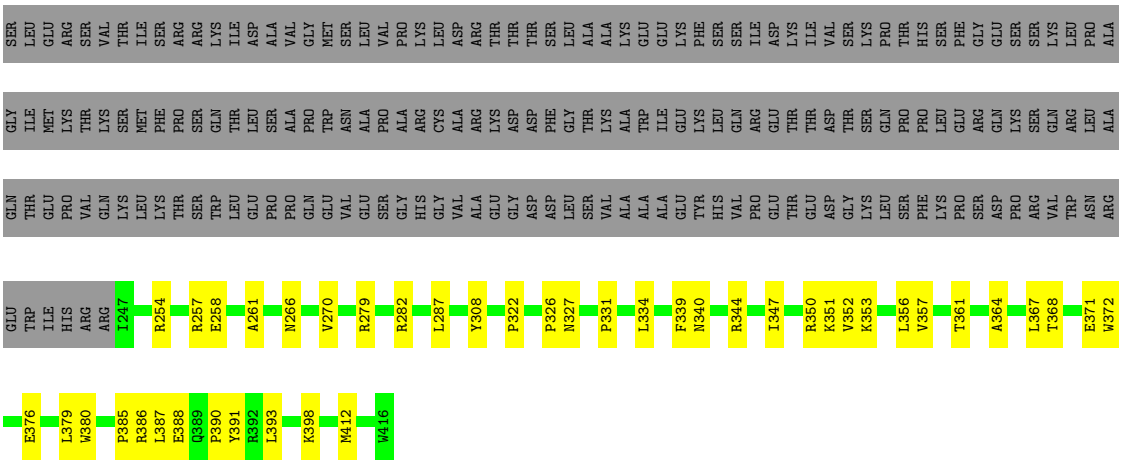
Chain 82:





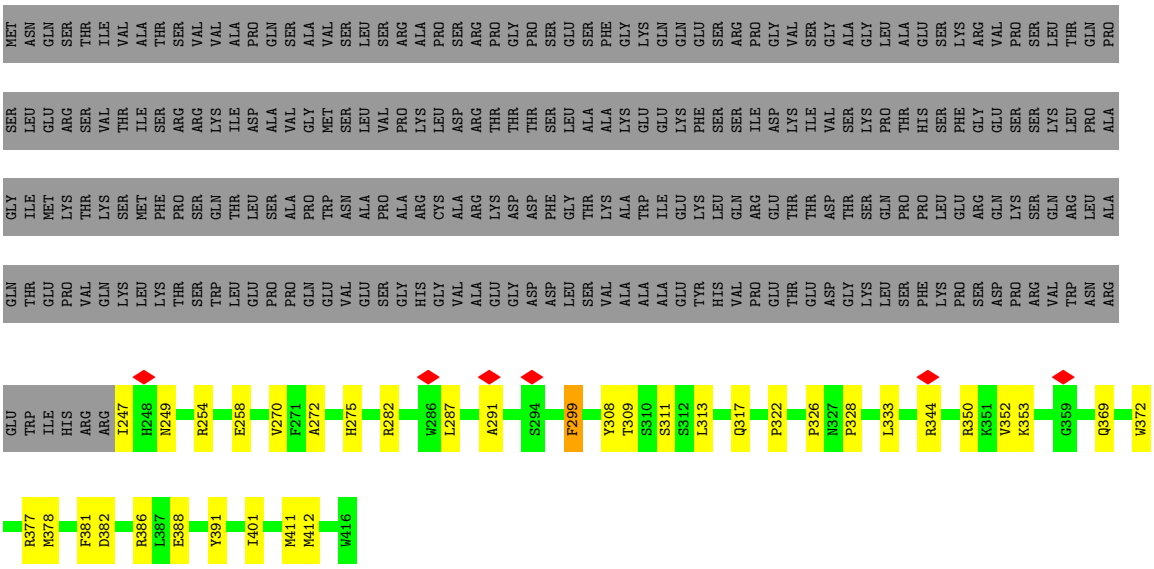
• Molecule 7: CF6, TGME49_245640

Chain 83:



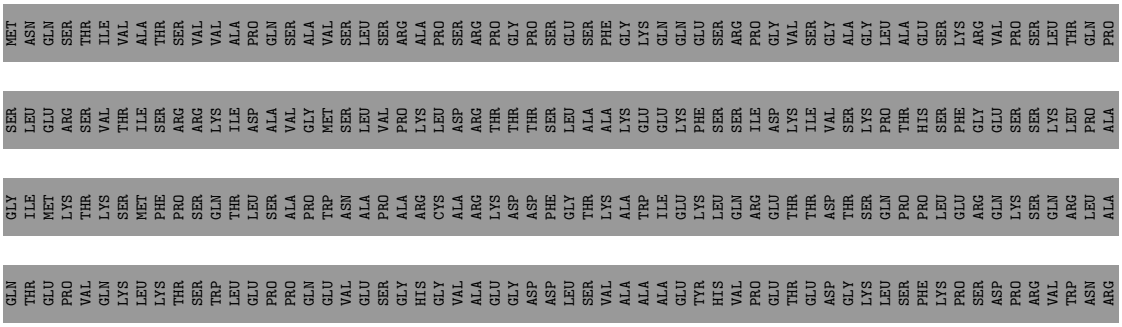
• Molecule 7: CF6, TGME49_245640

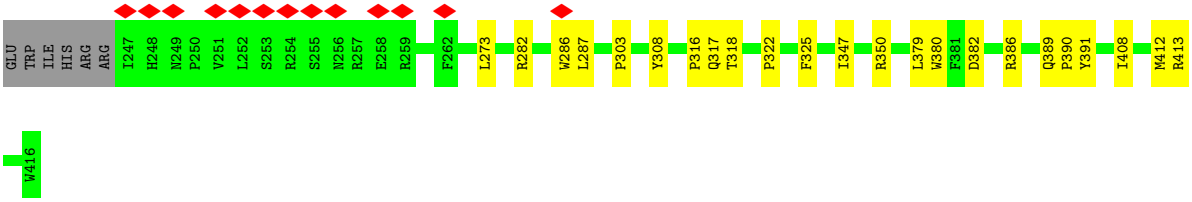
Chain 84:



• Molecule 7: CF6, TGME49_245640

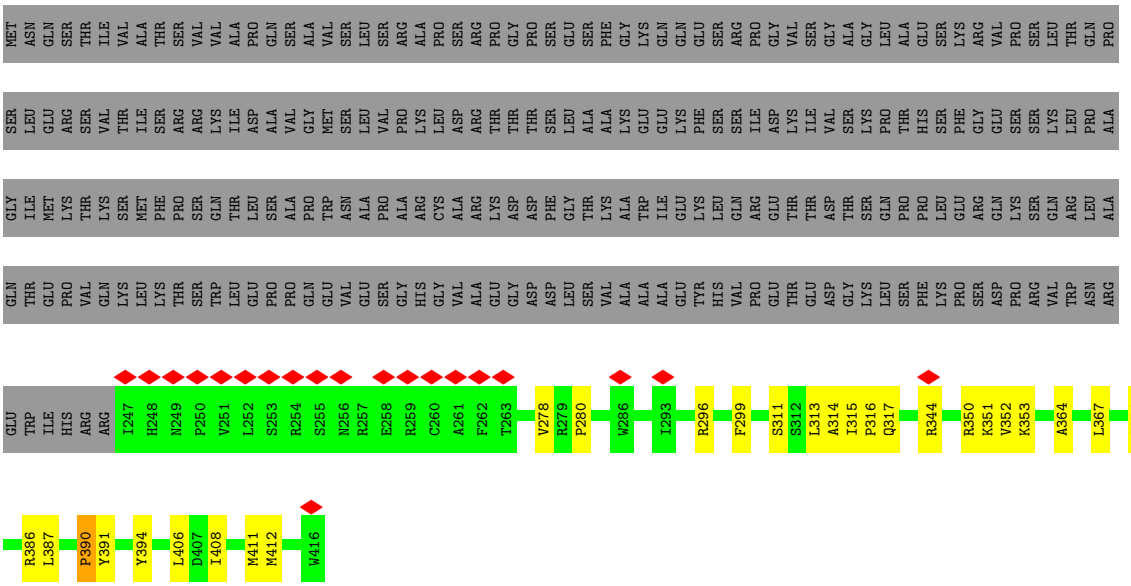
Chain 85:





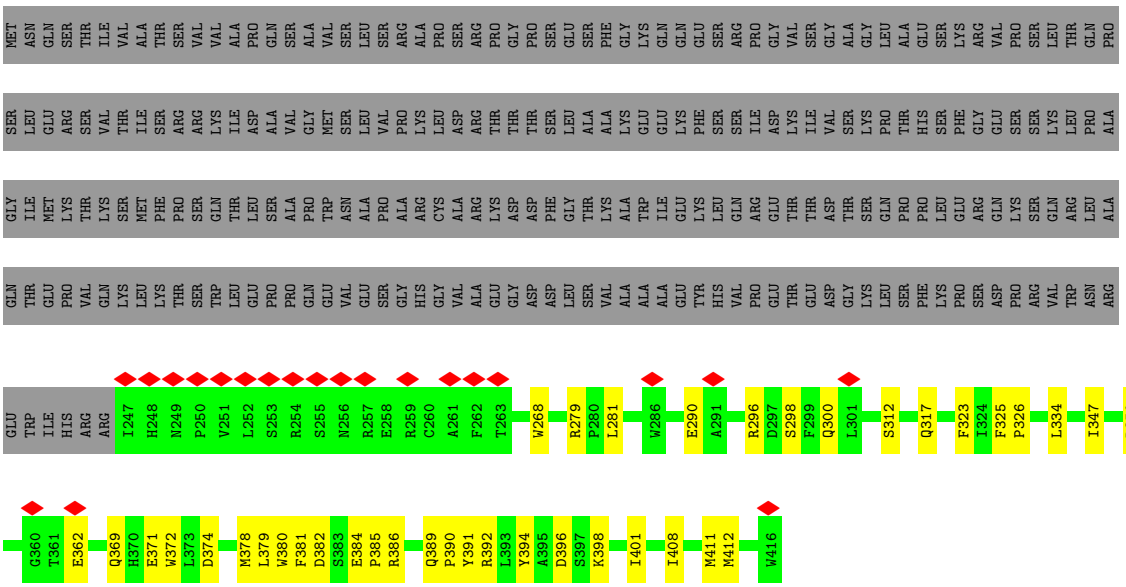
• Molecule 7: CF6, TGME49_245640

Chain 86:



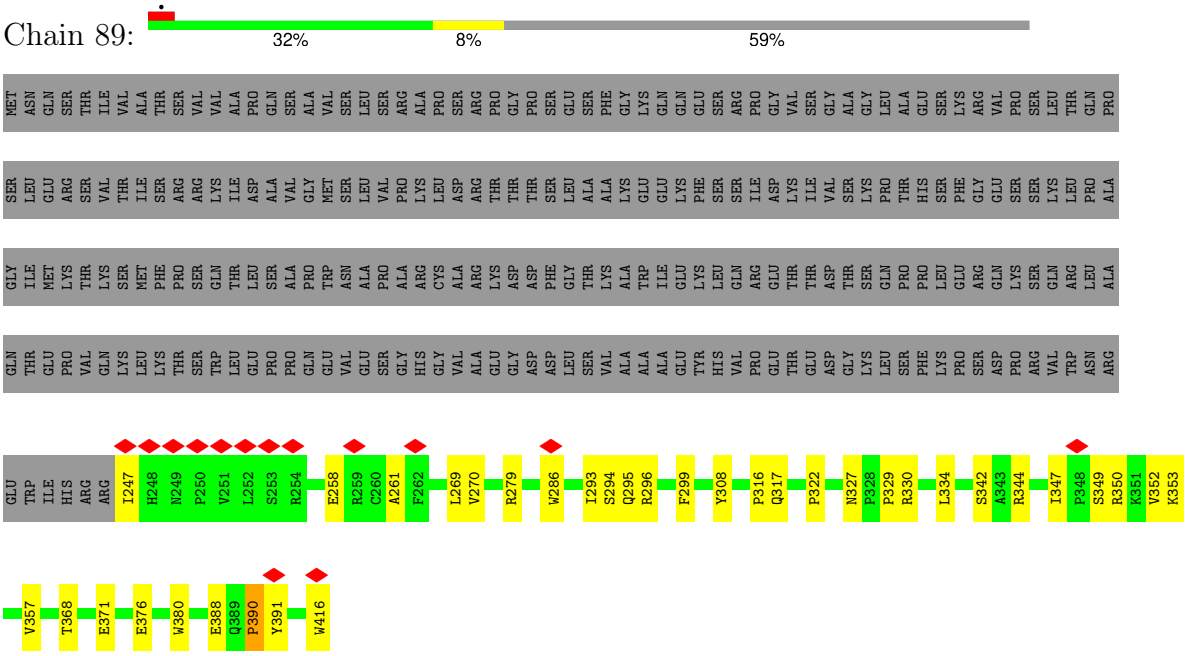
• Molecule 7: CF6, TGME49_245640

Chain 87:



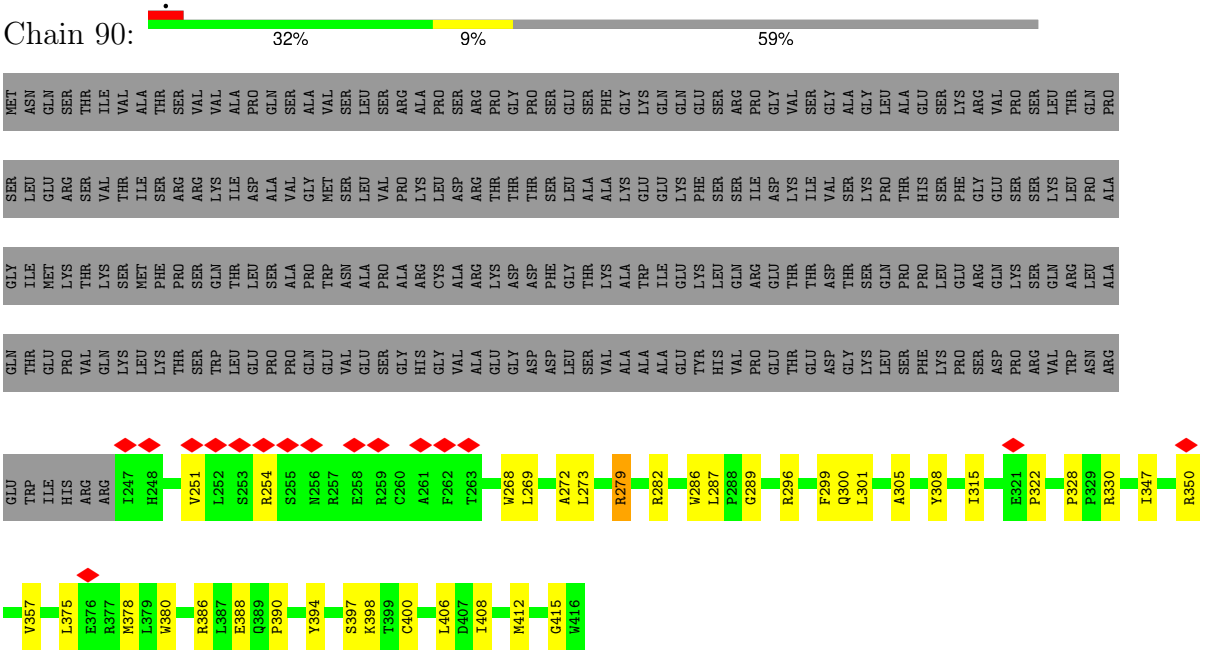
• Molecule 7: CF6, TGME49_245640

Chain 89:



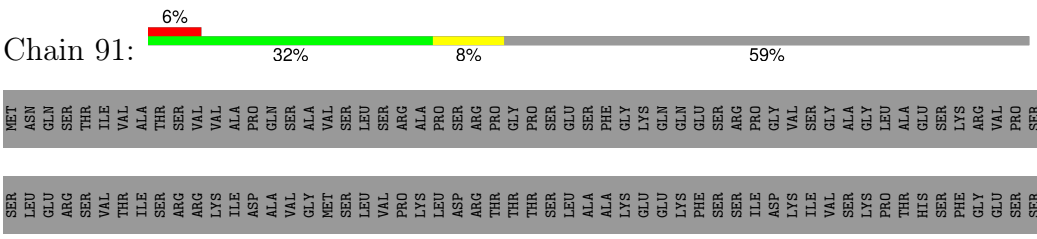
• Molecule 7: CF6, TGME49_245640

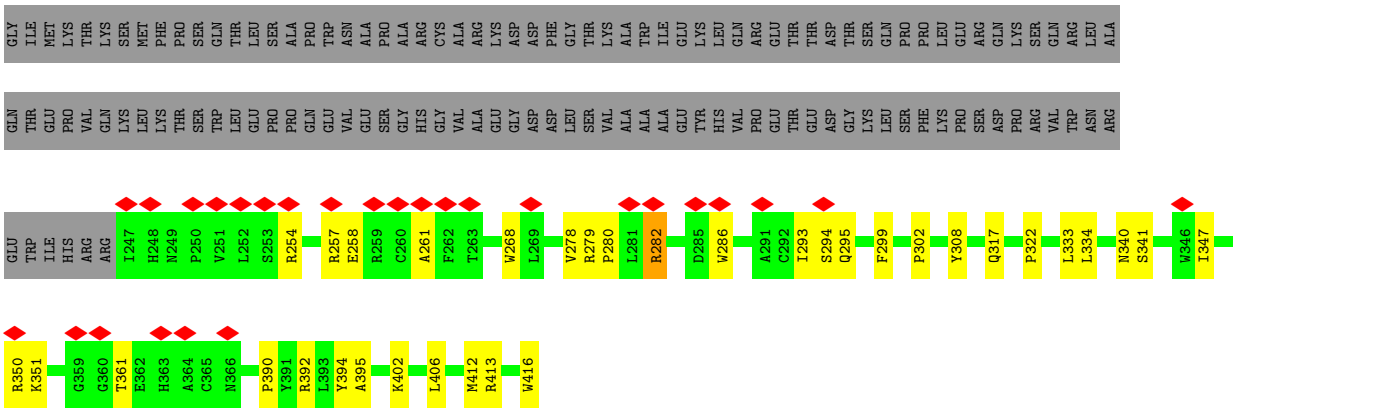
Chain 90:



• Molecule 7: CF6, TGME49_245640

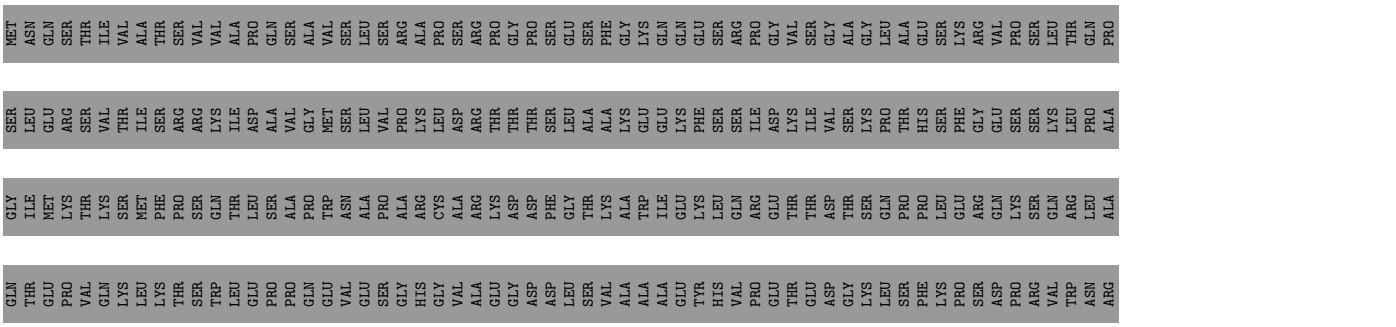
Chain 91:

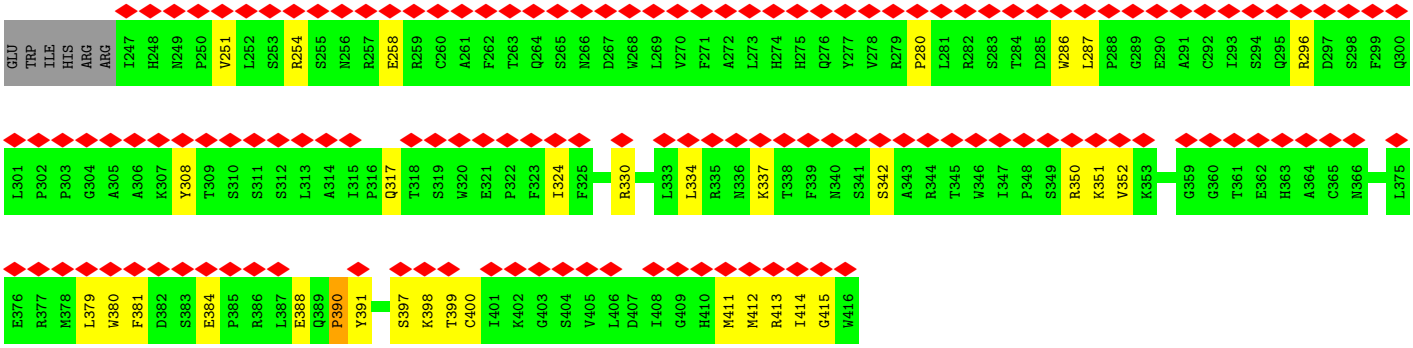




• Molecule 7: CF6, TGME49_245640

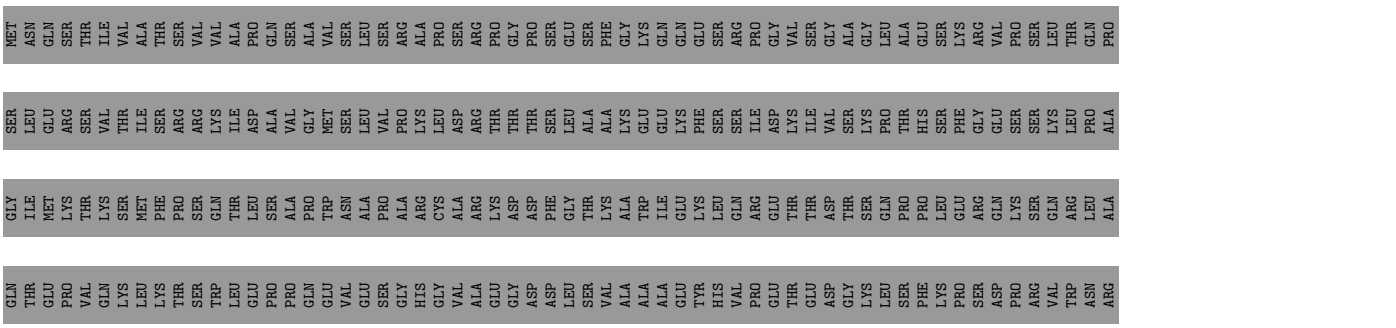
Chain 92:

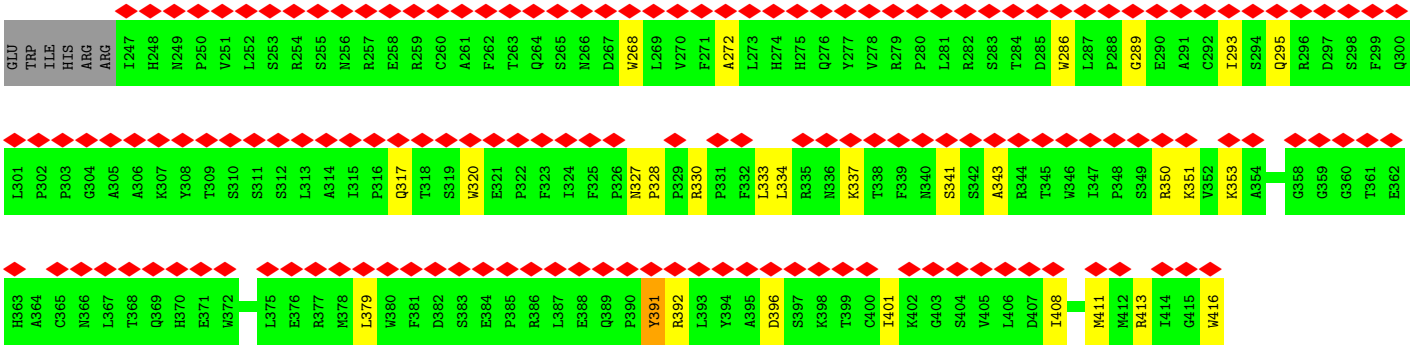




• Molecule 7: CF6, TGME49_245640

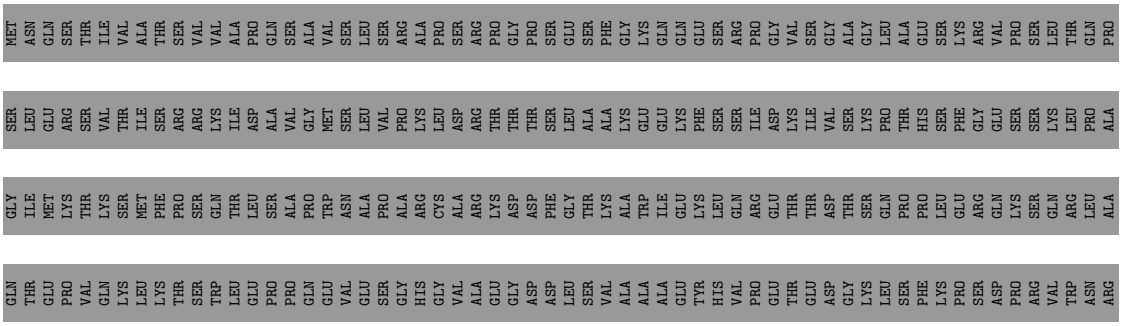
Chain 93:

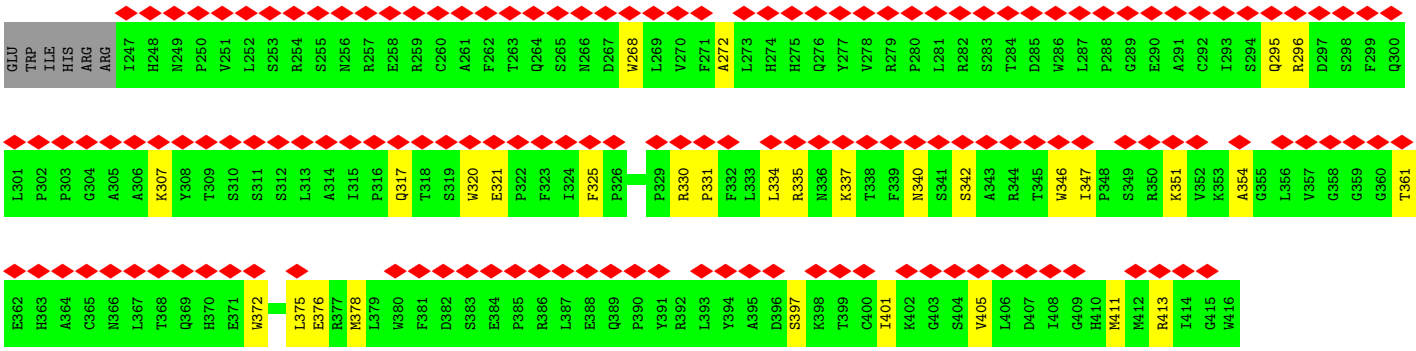




• Molecule 7: CF6, TGME49_245640

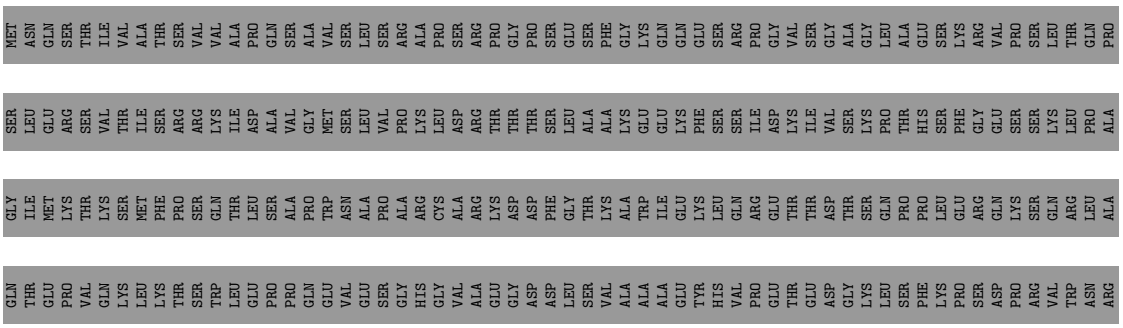
Chain 94:

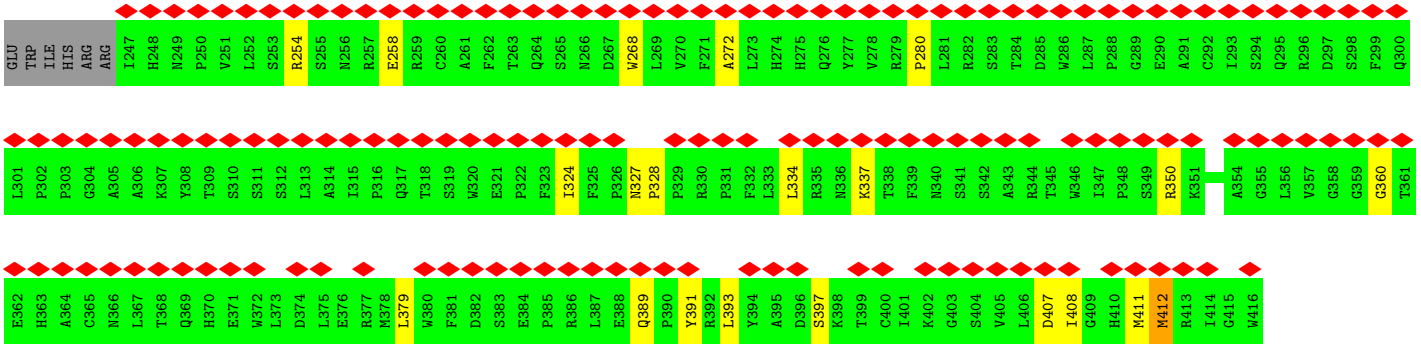




• Molecule 7: CF6, TGME49_245640

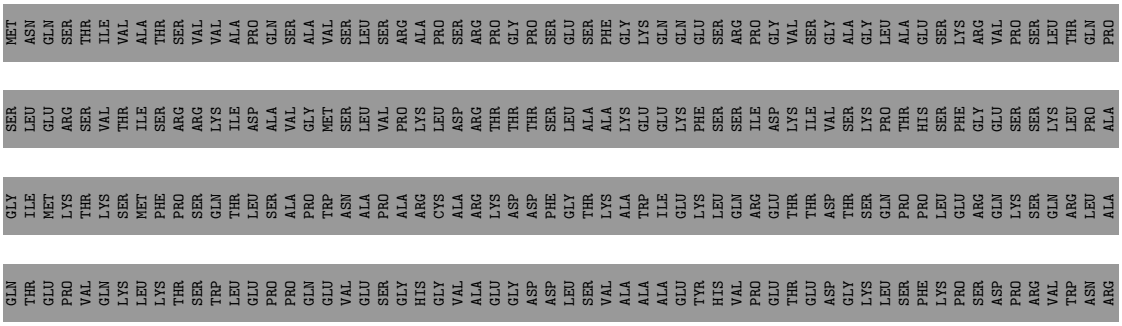
Chain 95:

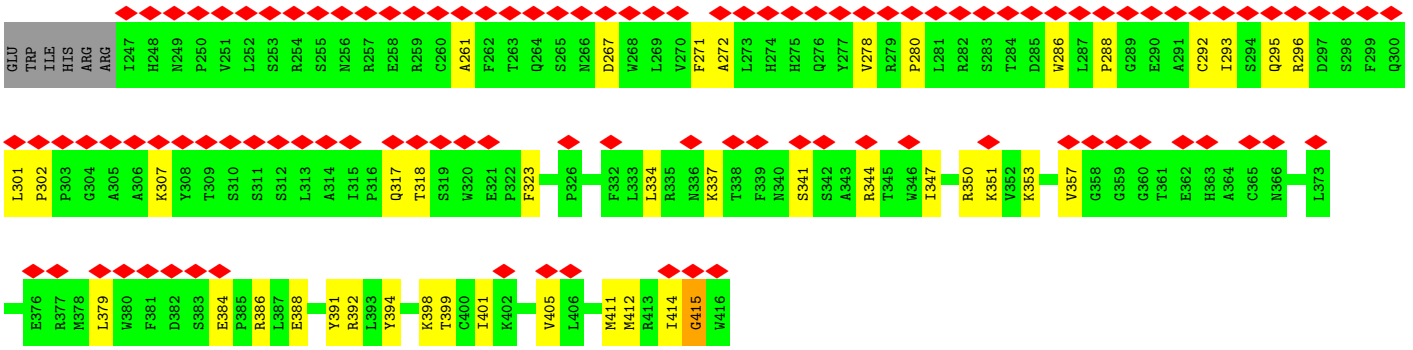




• Molecule 7: CF6, TGME49_245640

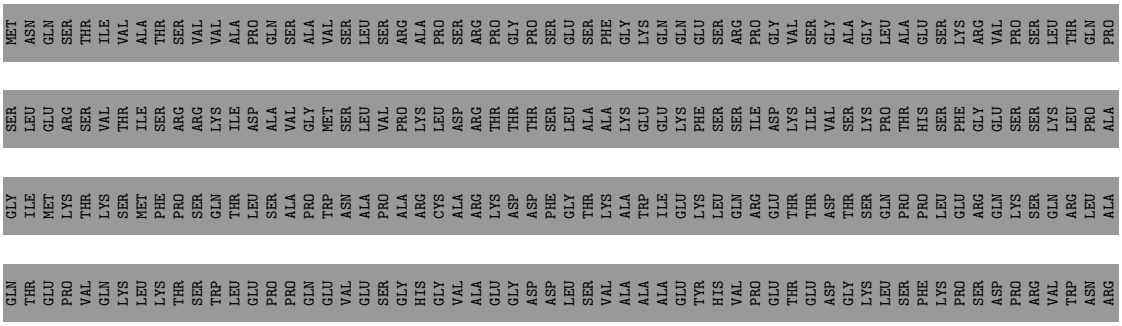
Chain 96:

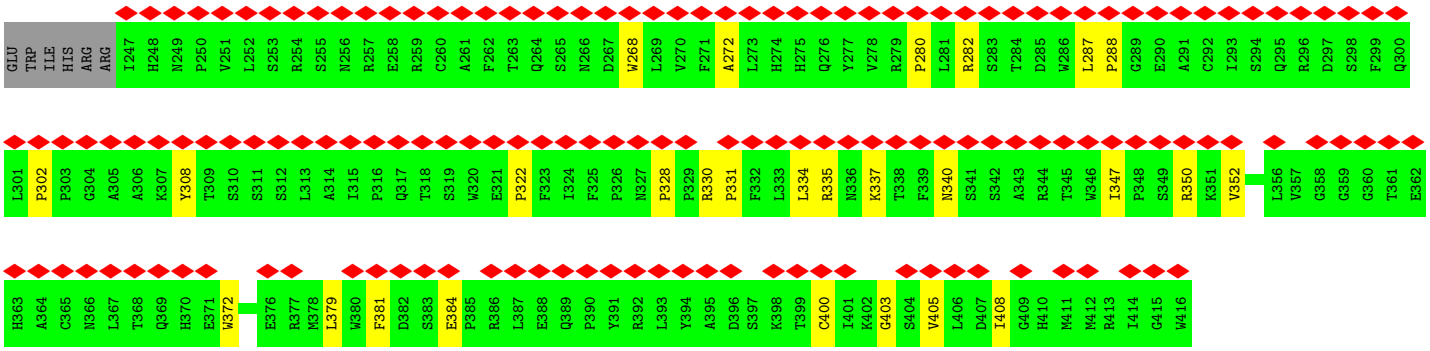




• Molecule 7: CF6, TGME49_245640

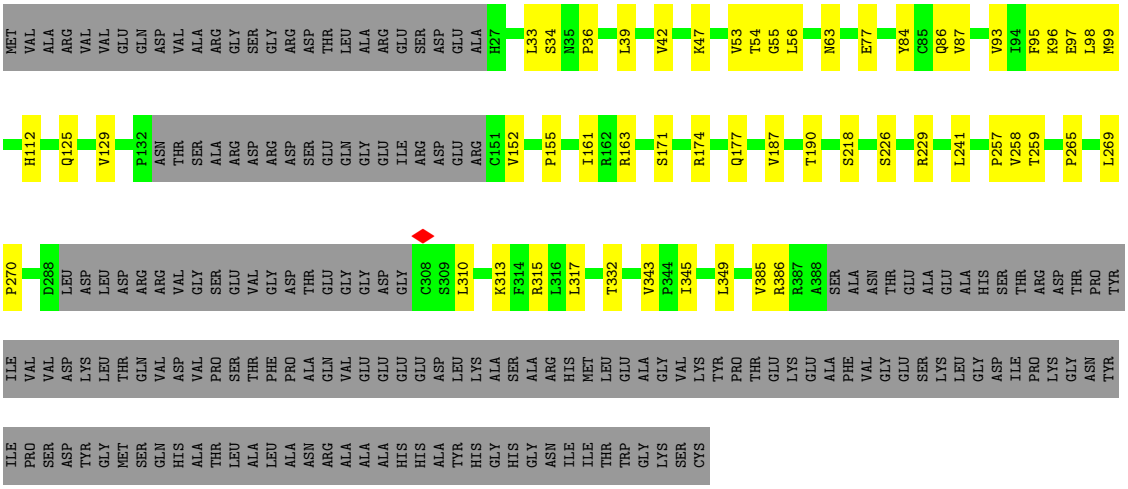
Chain 97:





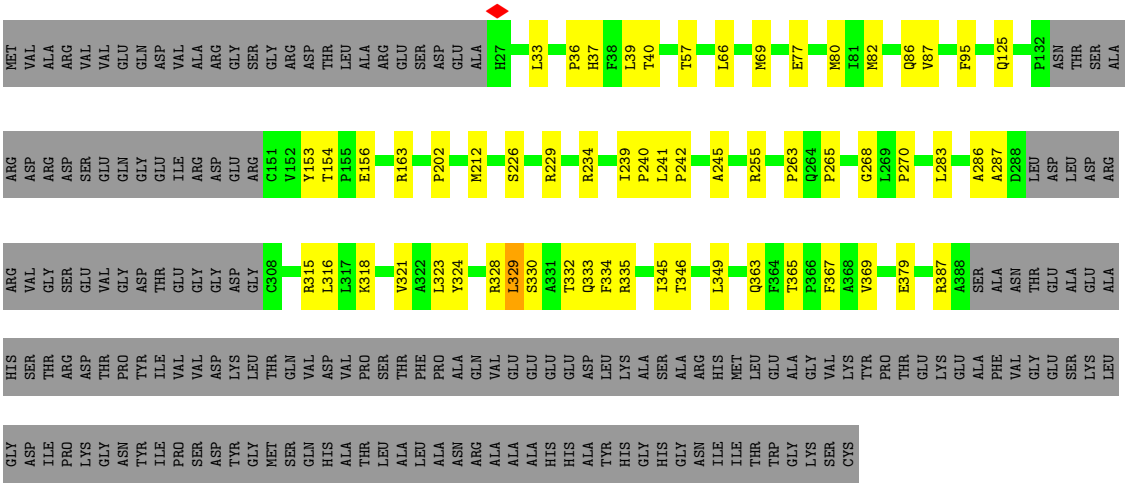
• Molecule 8: CF4, TGME49_246720

Chain A1:



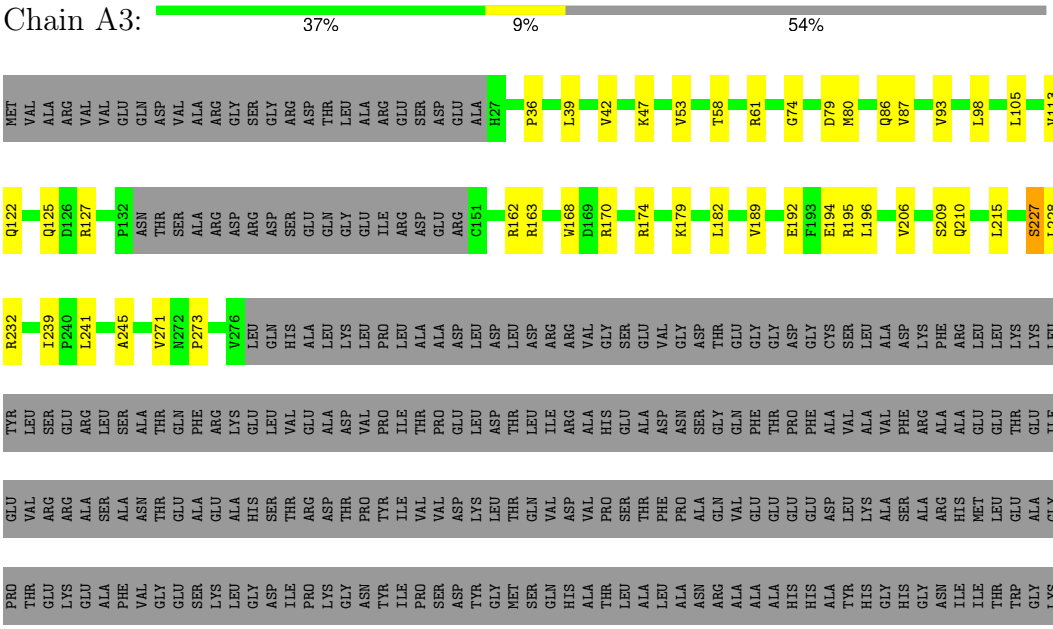
• Molecule 8: CF4, TGME49_246720

Chain A2:



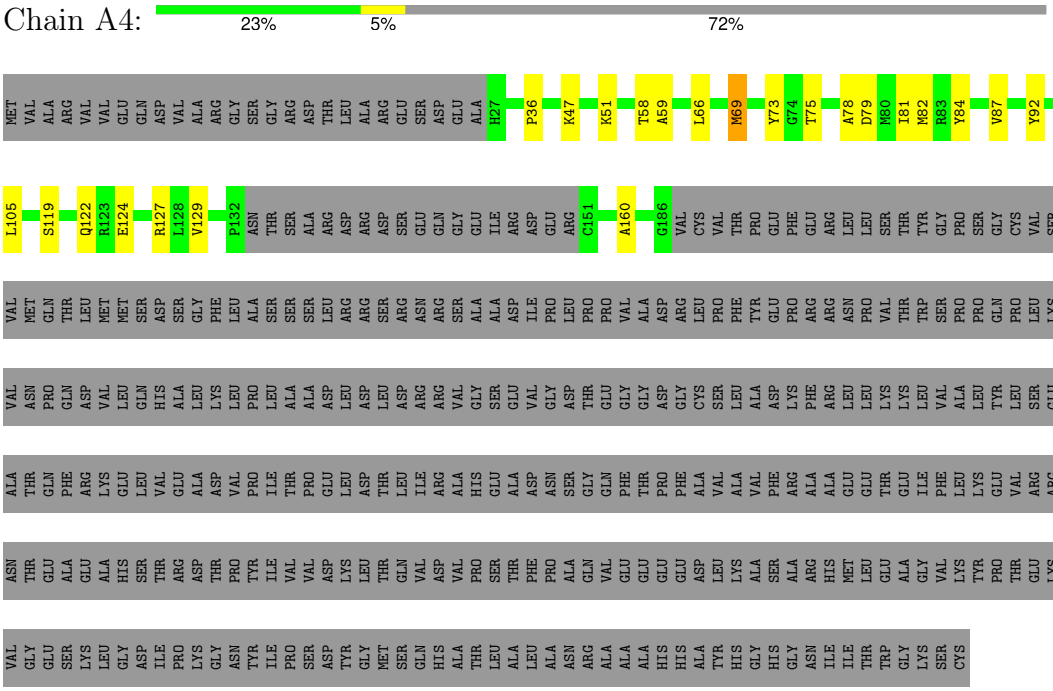
• Molecule 8: CF4, TGME49_246720

Chain A3:



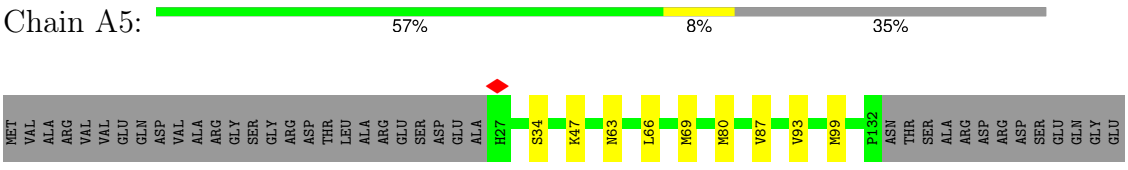
• Molecule 8: CF4, TGME49_246720

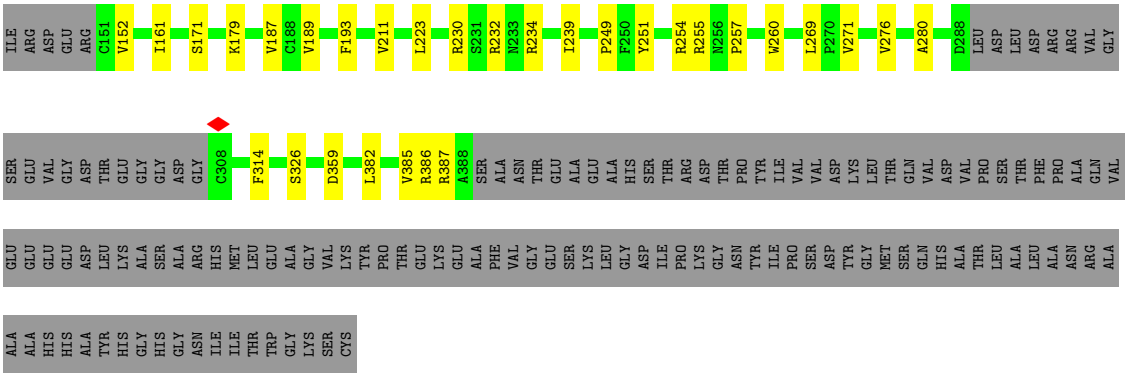
Chain A4:



• Molecule 8: CF4, TGME49_246720

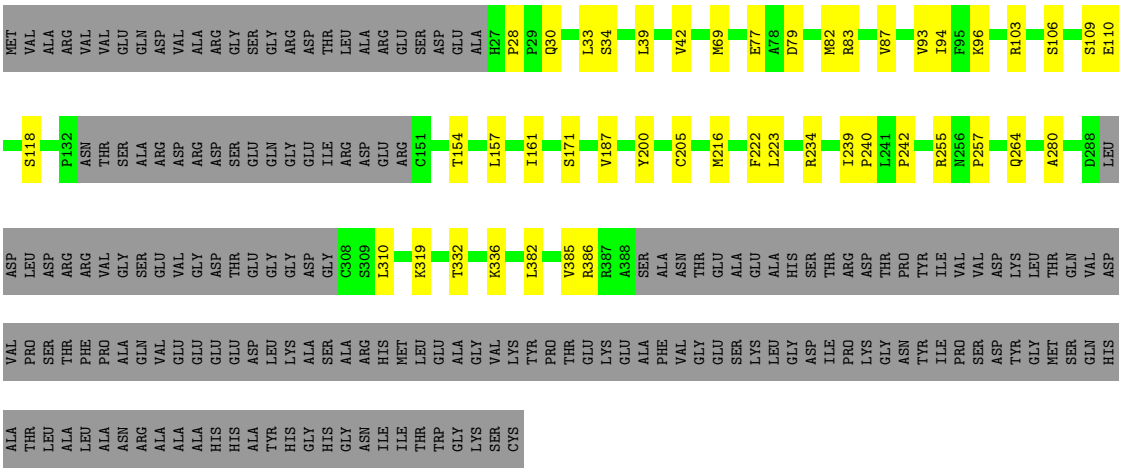
Chain A5:





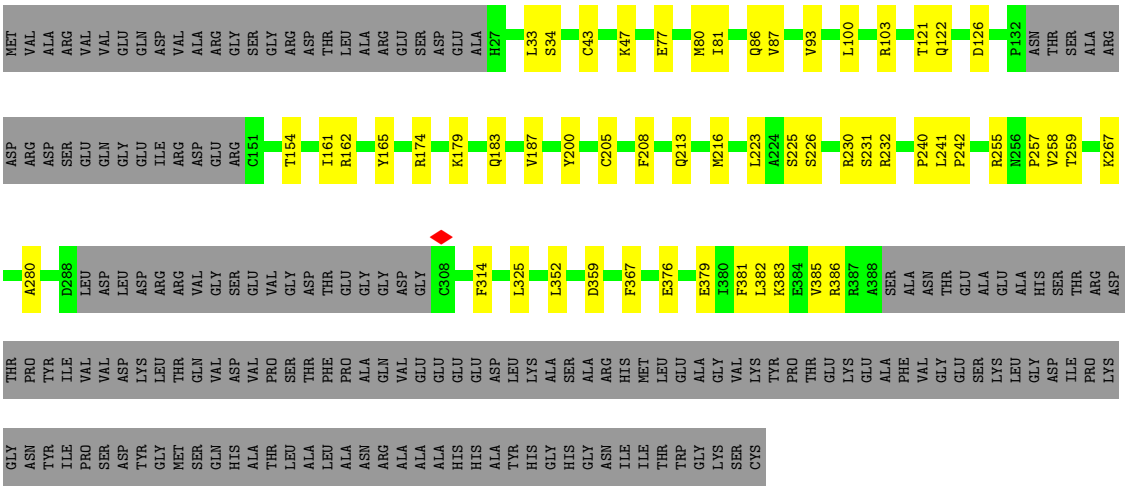
• Molecule 8: CF4, TGME49_246720

Chain A6:



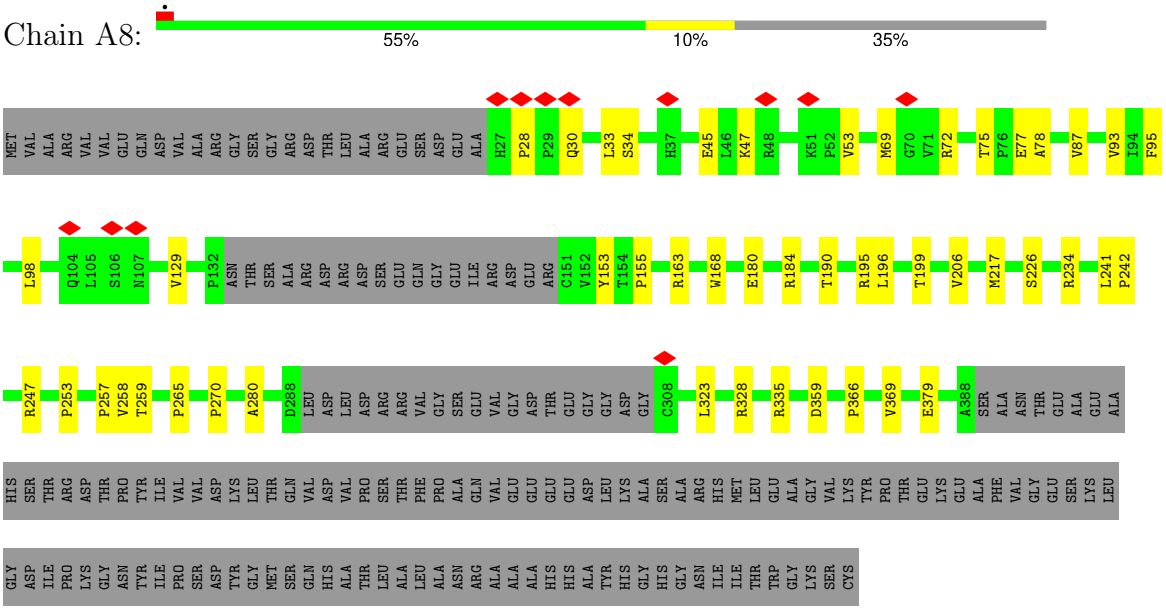
• Molecule 8: CF4, TGME49_246720

Chain A7:



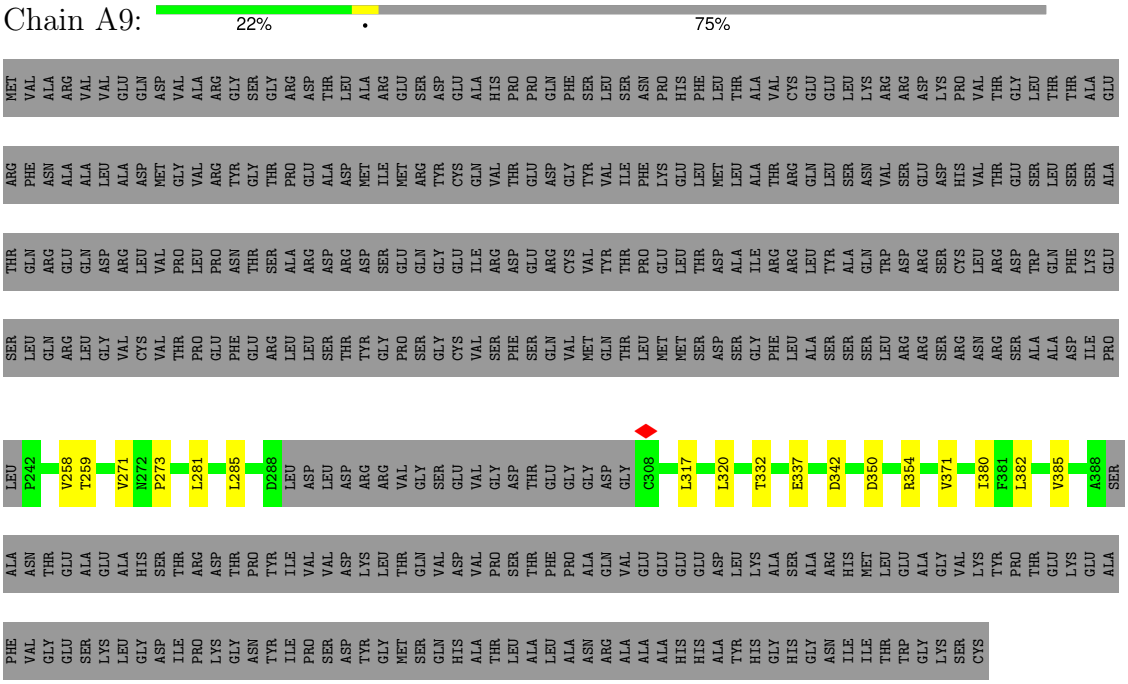
• Molecule 8: CF4, TGME49_246720

Chain A8:



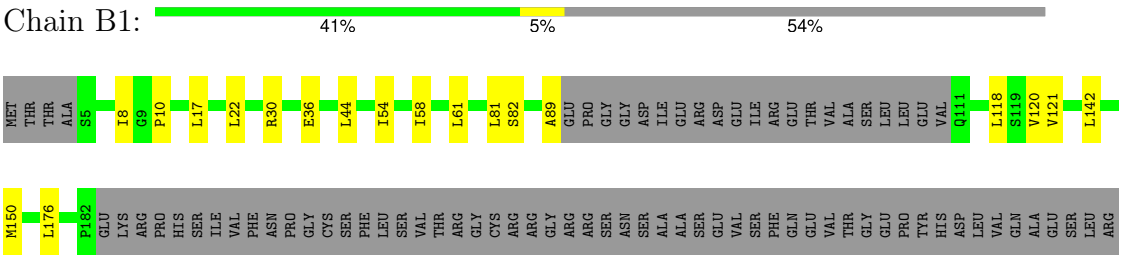
• Molecule 8: CF4, TGME49_246720

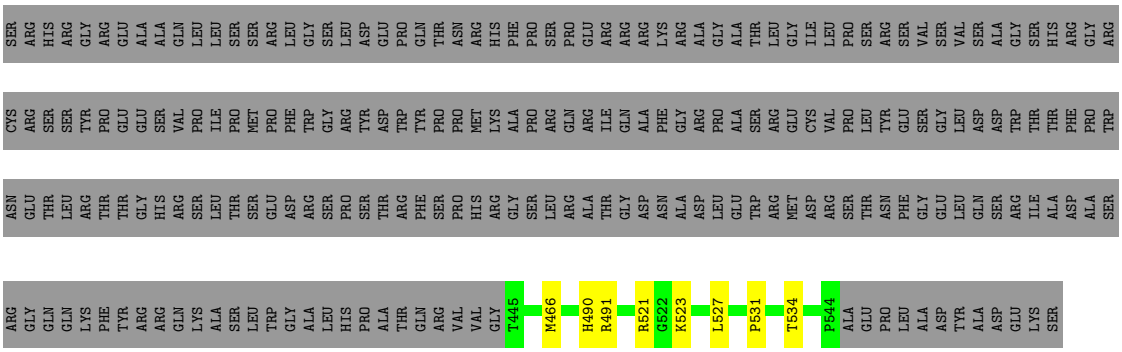
Chain A9:



• Molecule 9: CF3, TGME49_255895

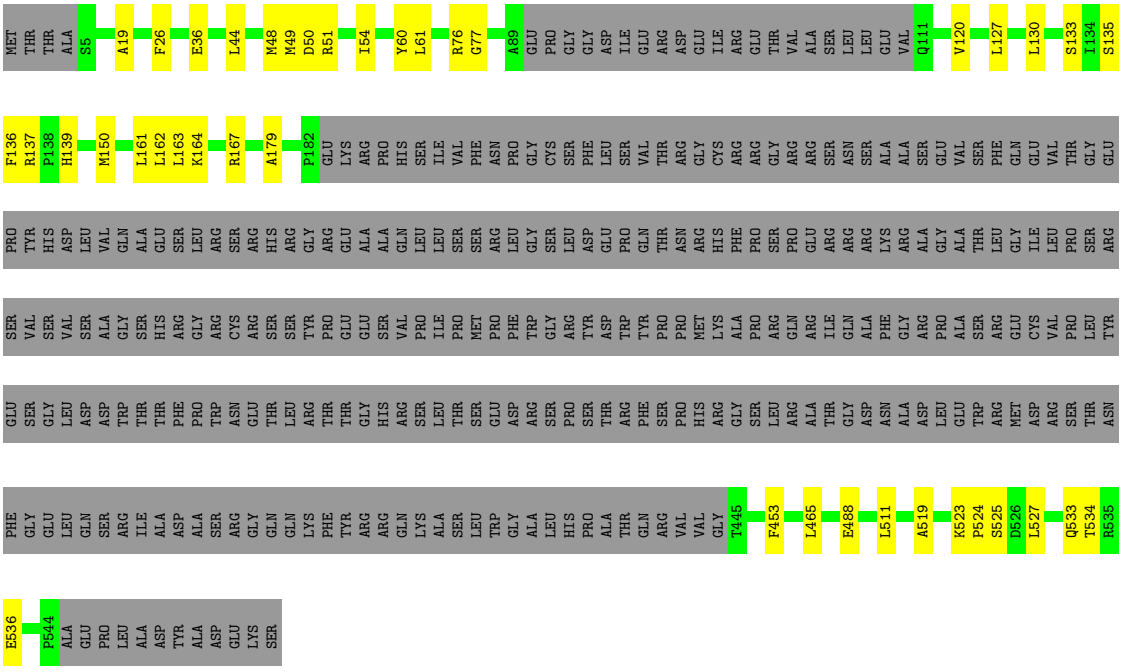
Chain B1:





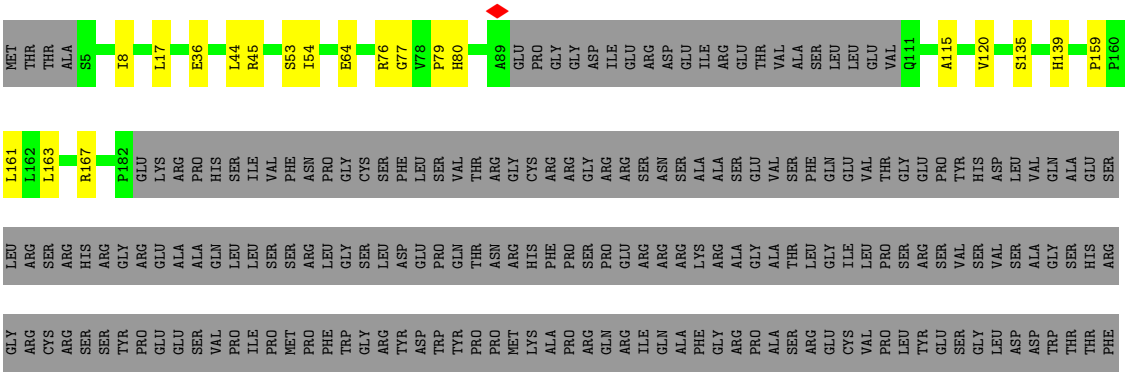
• Molecule 9: CF3, TGME49_255895

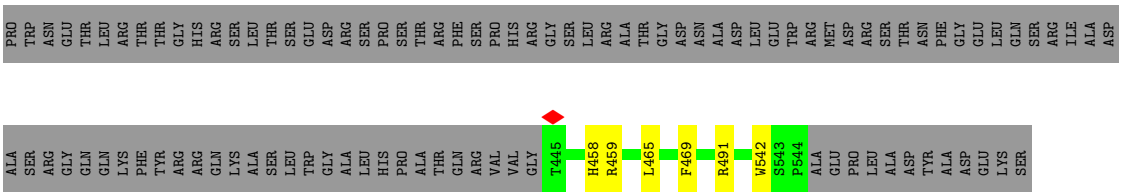
Chain B2:



• Molecule 9: CF3, TGME49_255895

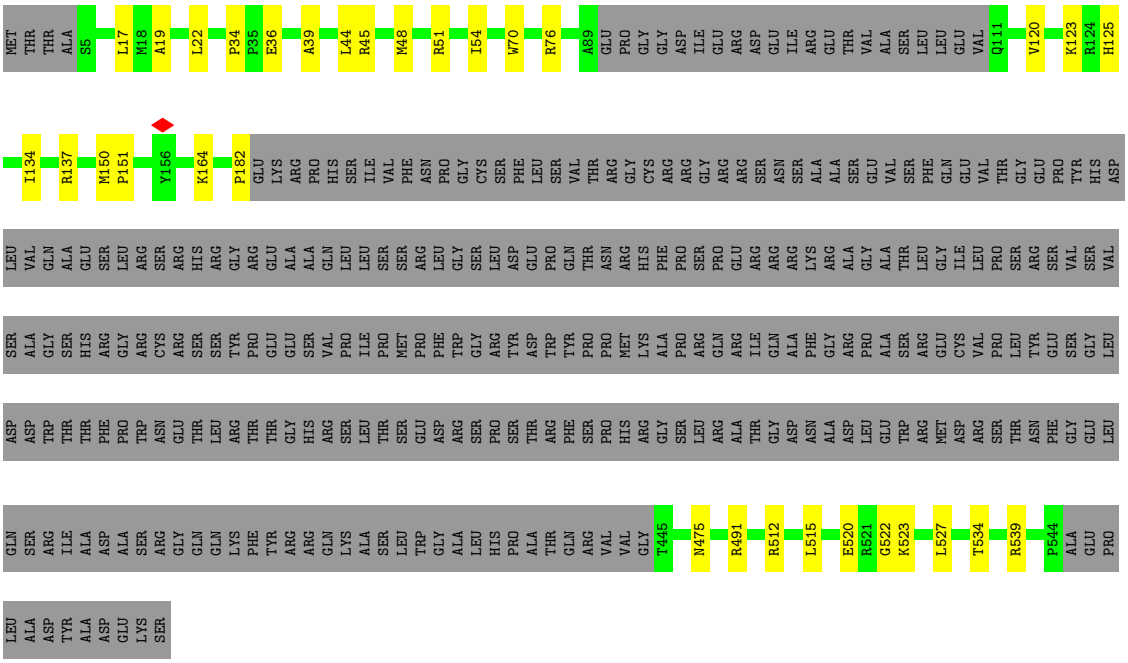
Chain B3:





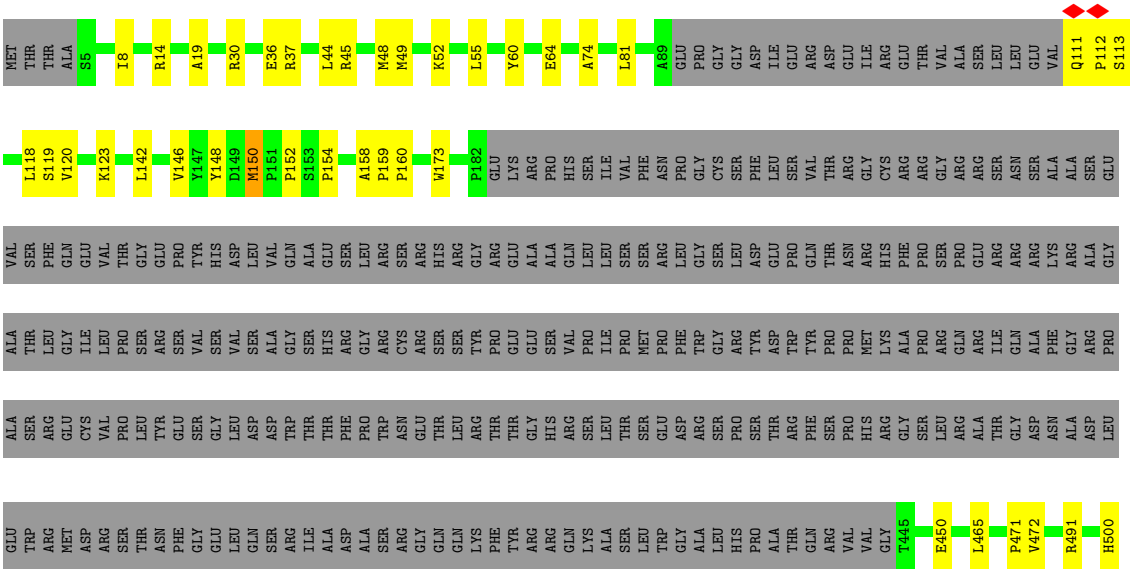
• Molecule 9: CF3, TGME49_255895

Chain B4:



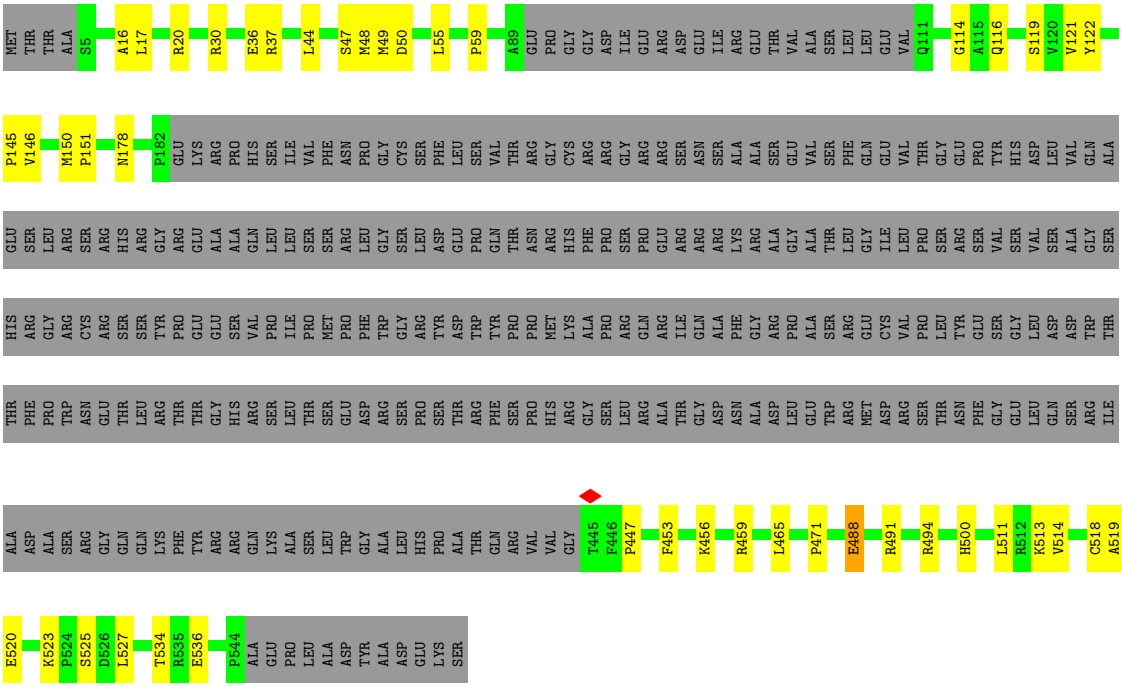
• Molecule 9: CF3, TGME49_255895

Chain B5:



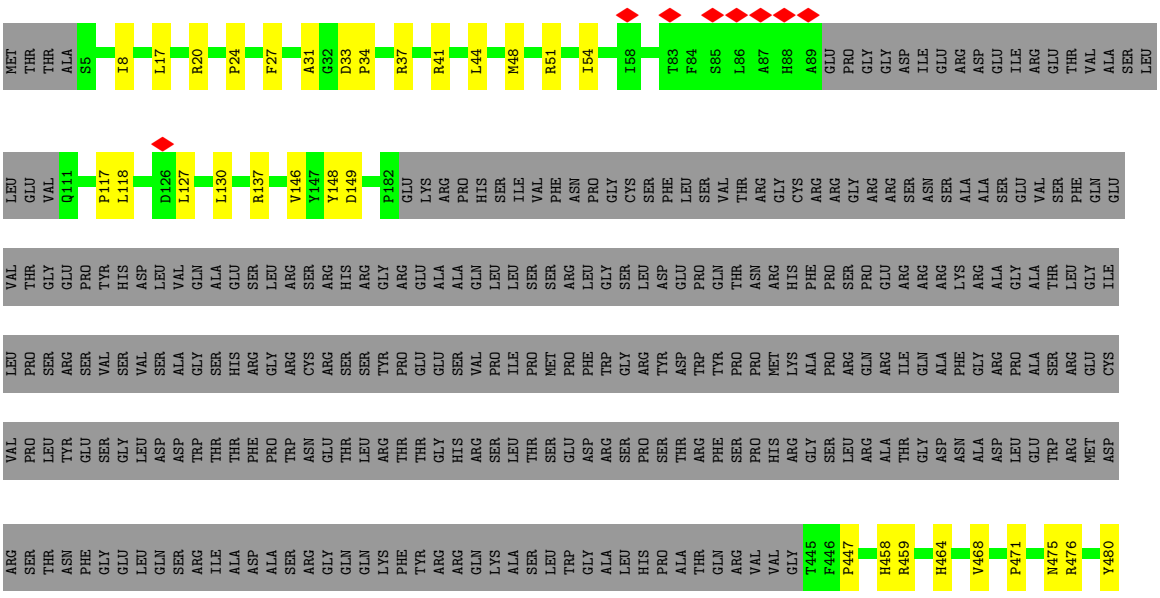
• Molecule 9: CF3, TGME49_255895

Chain B6:



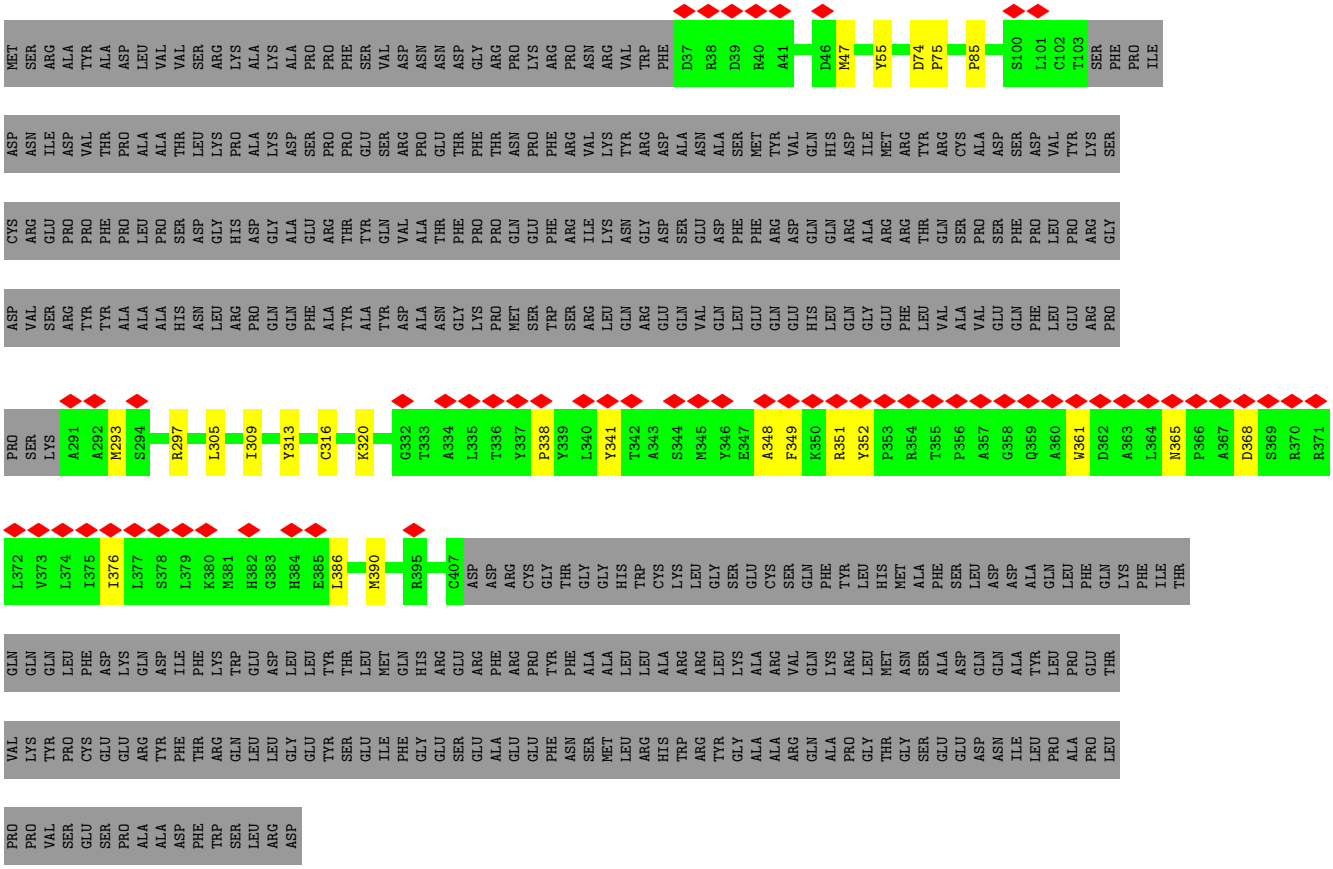
• Molecule 9: CF3, TGME49_255895

Chain B7:



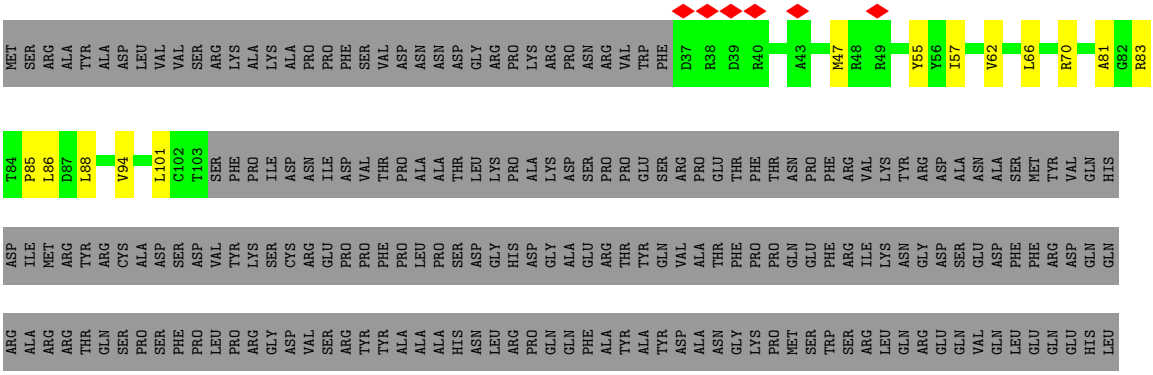
• Molecule 10: CPH1, TGME49_266630

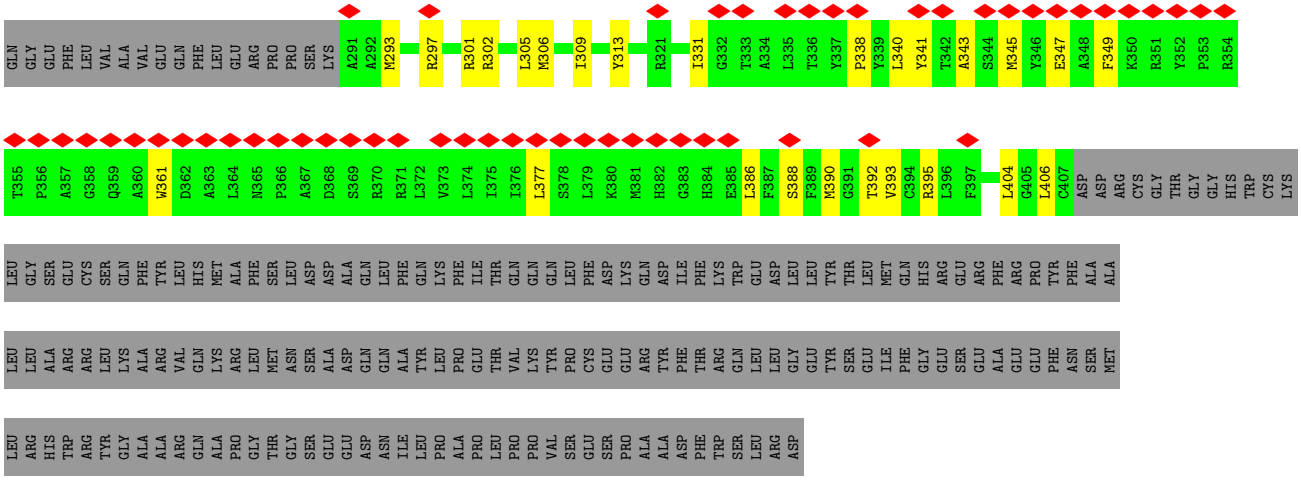
Chain C0:



• Molecule 10: CPH1, TGME49_266630

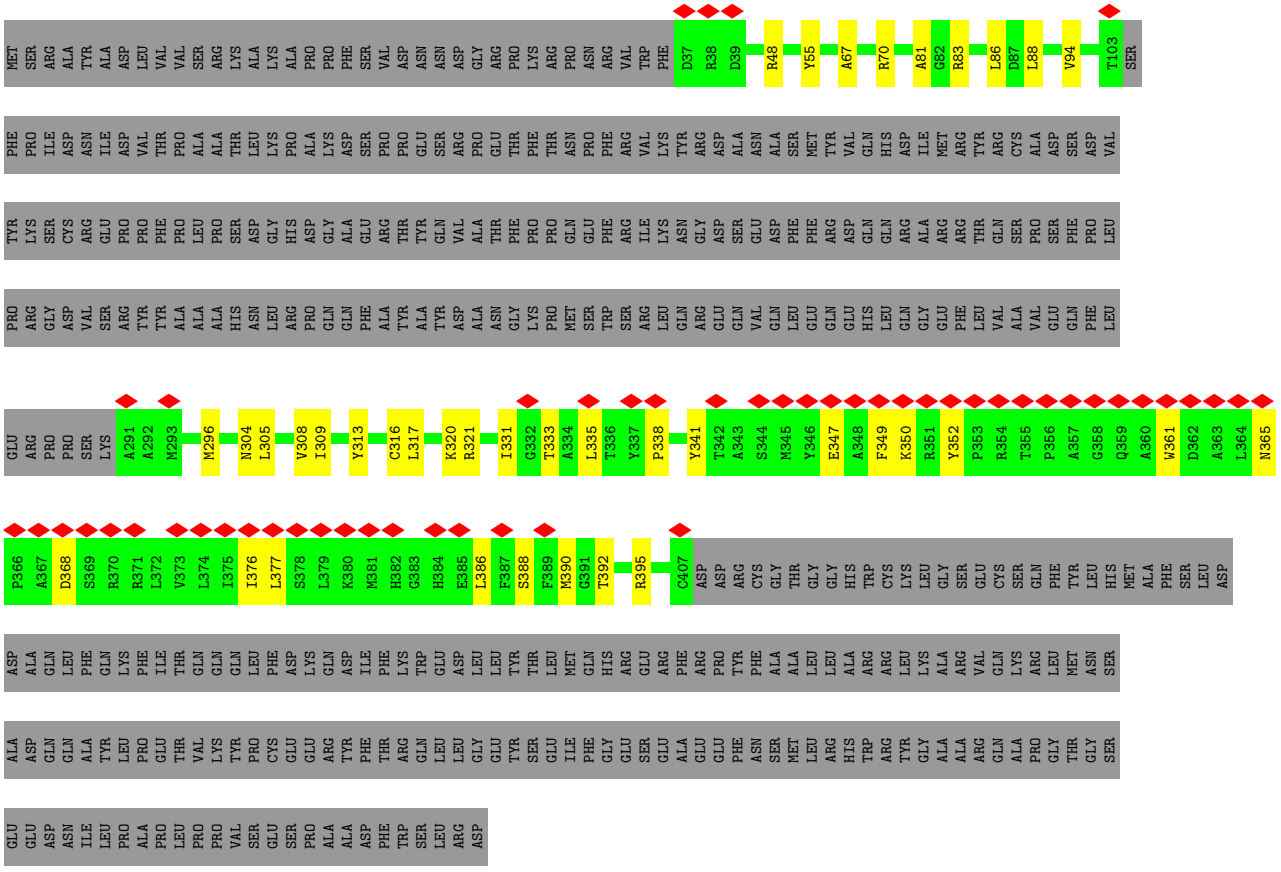
Chain C6:





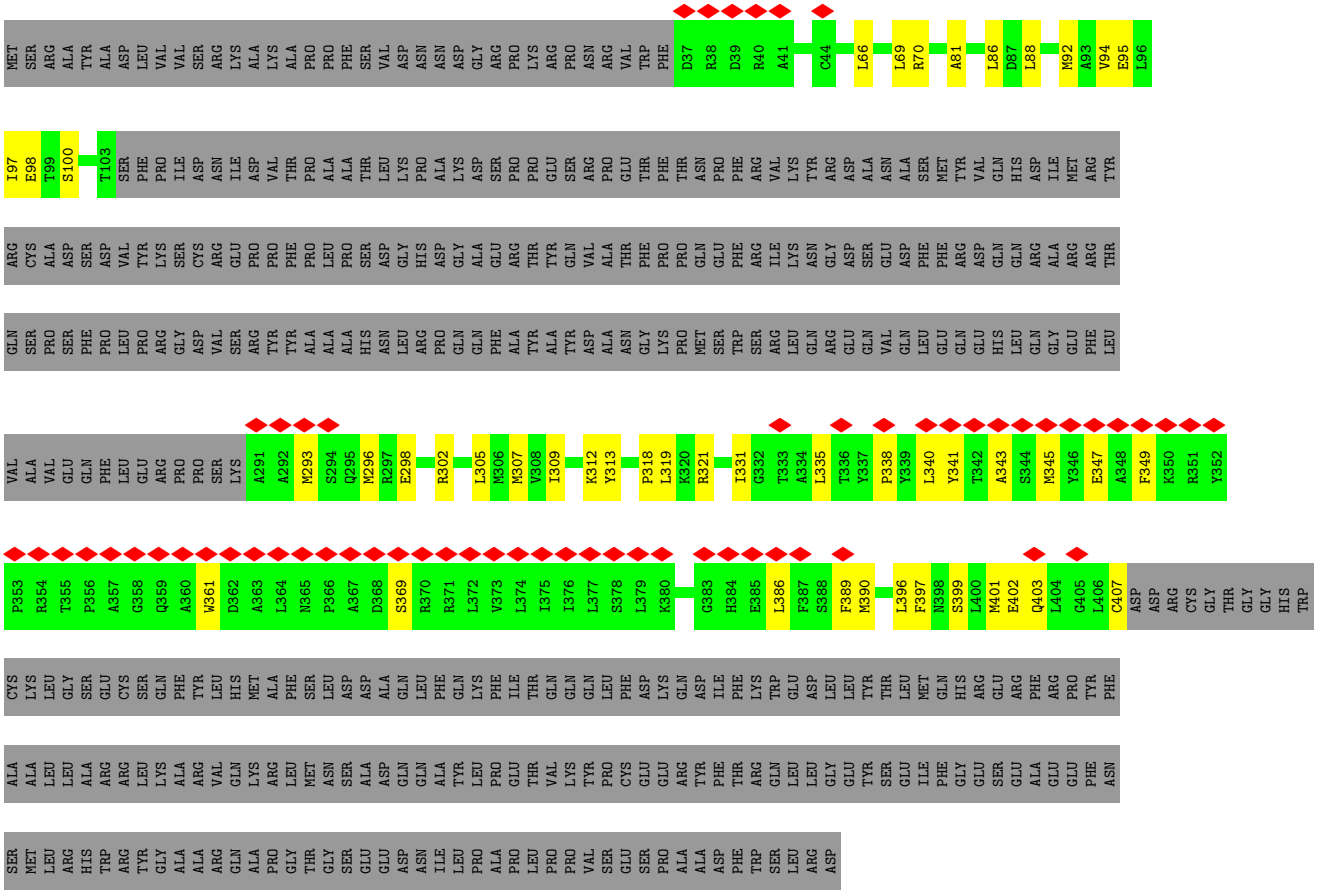
• Molecule 10: CPH1, TGME49_266630

Chain C7:



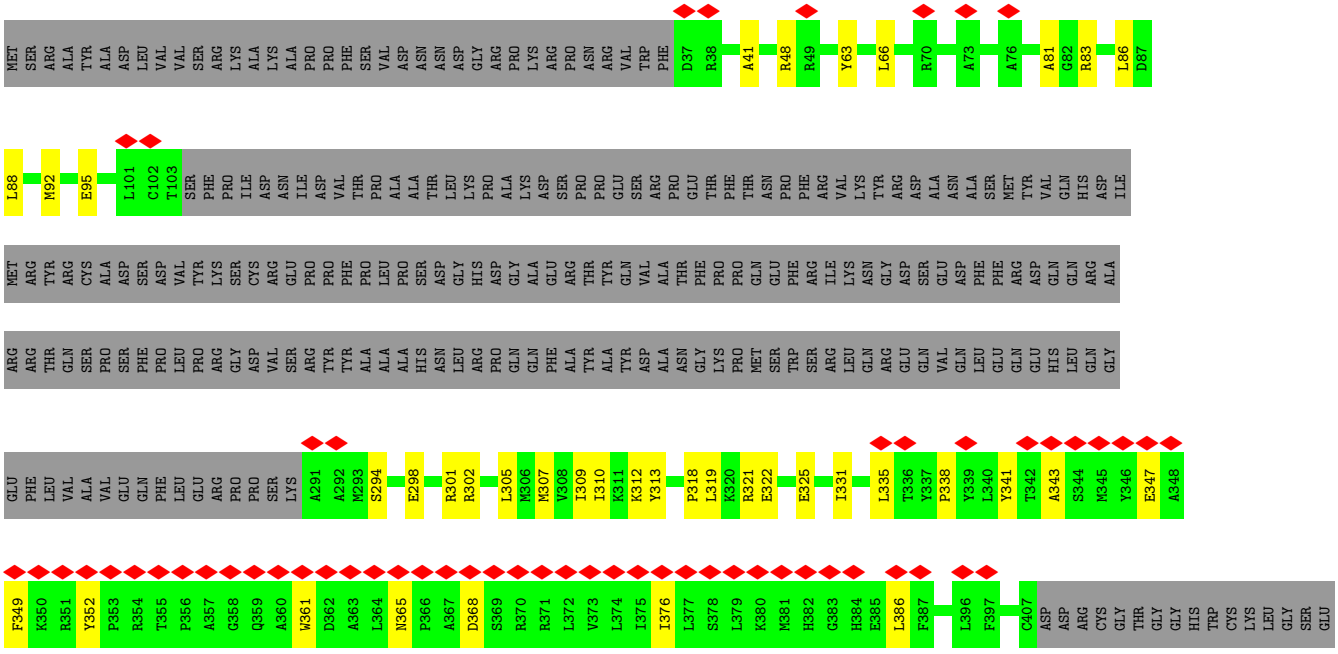
• Molecule 10: CPH1, TGME49_266630

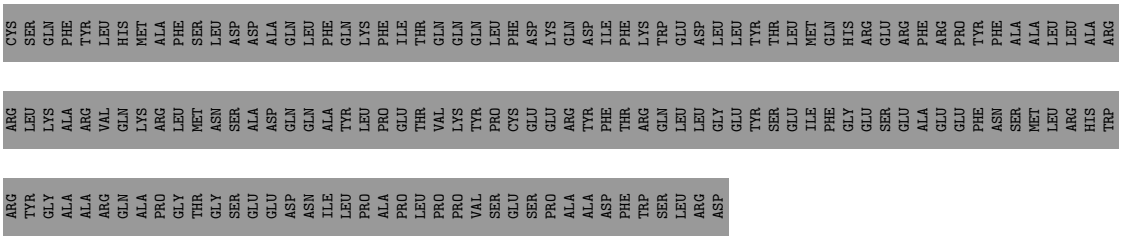
Chain C8:



• Molecule 10: CPH1, TGME49_266630

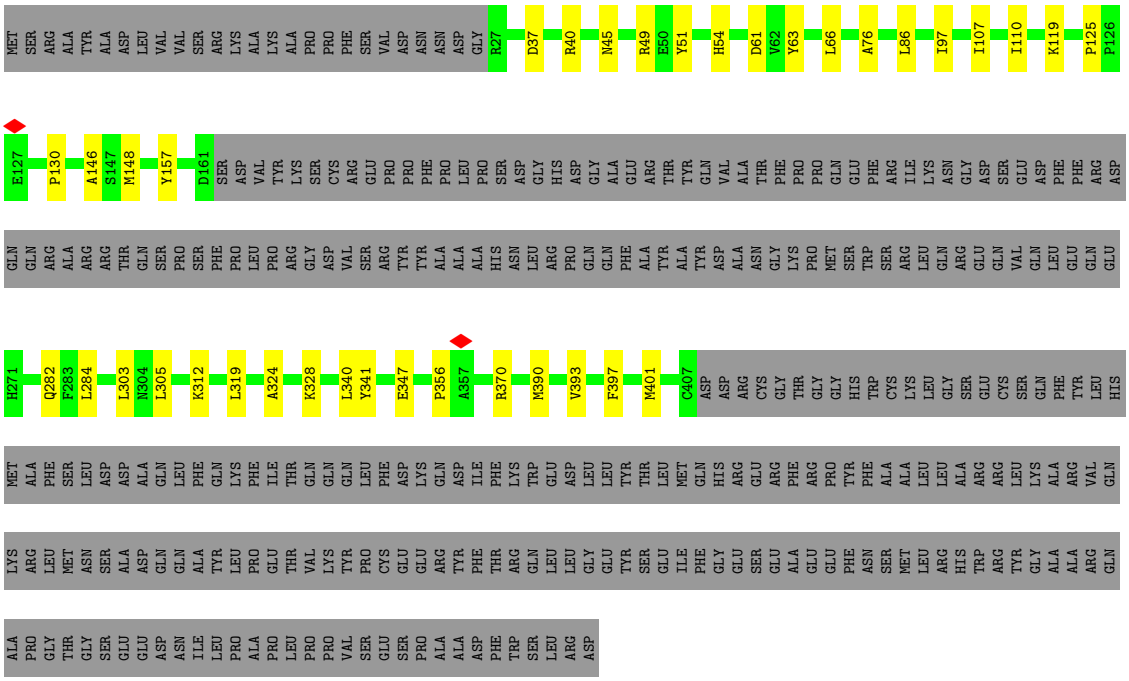
Chain C9:





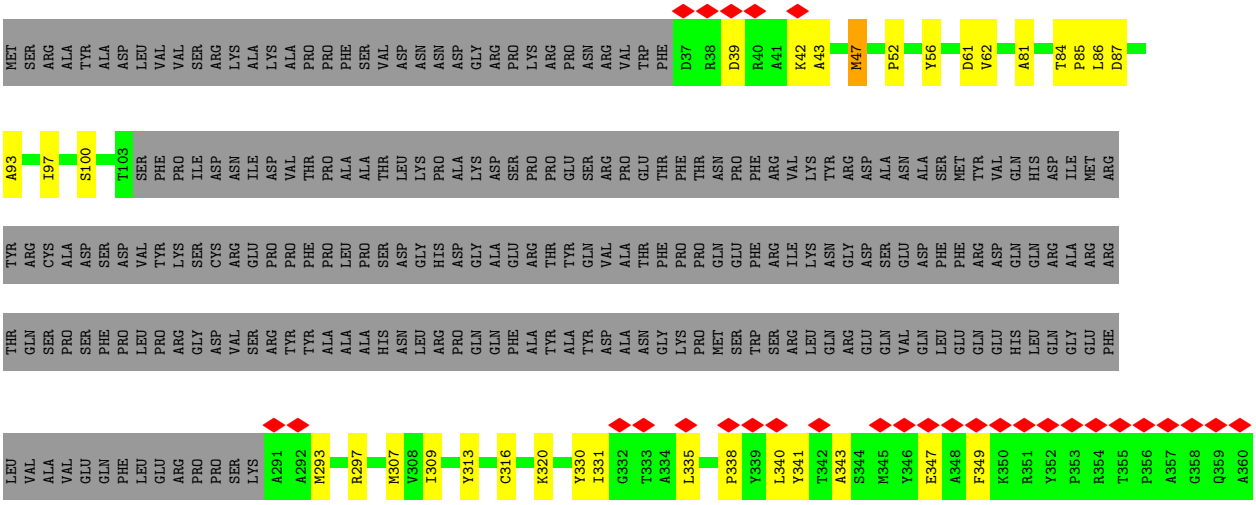
• Molecule 10: CPH1, TGME49_266630

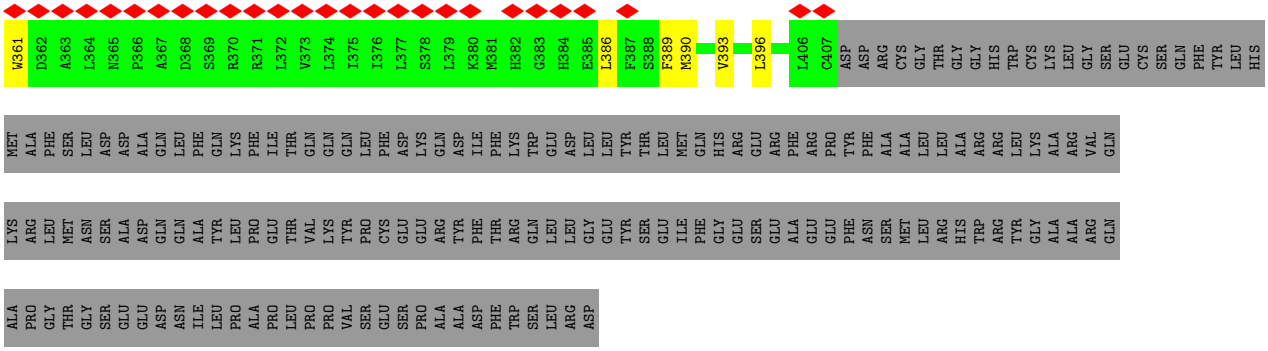
Chain D0:



• Molecule 10: CPH1, TGME49_266630

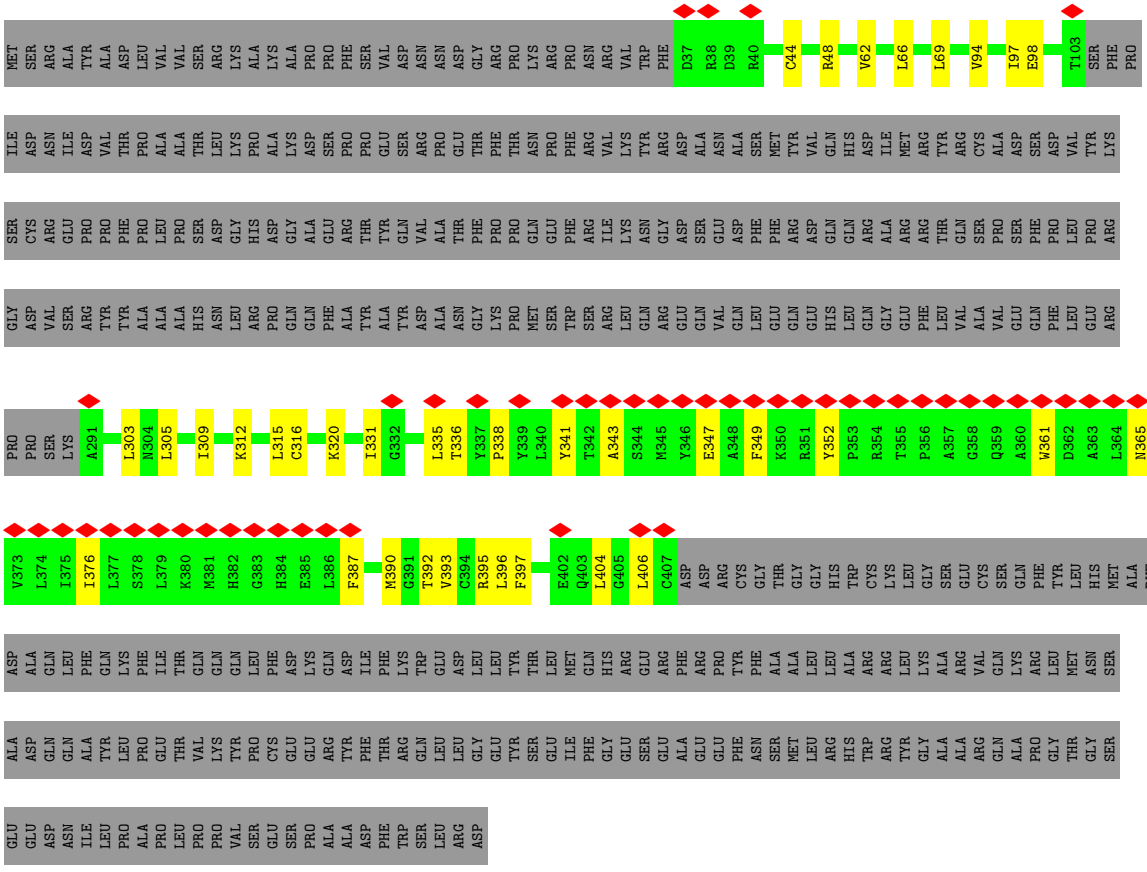
Chain D1:





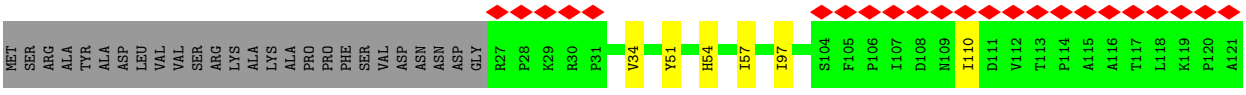
• Molecule 10: CPH1, TGME49_266630

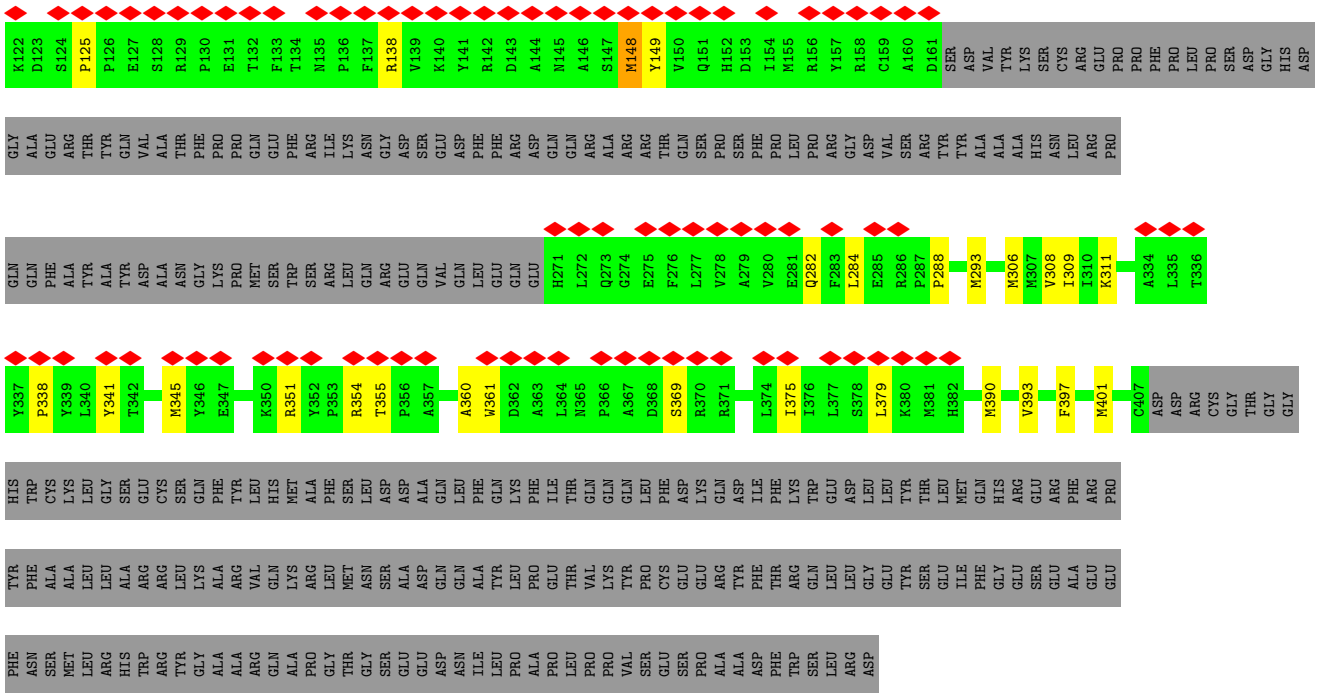
Chain D2:



• Molecule 10: CPH1, TGME49_266630

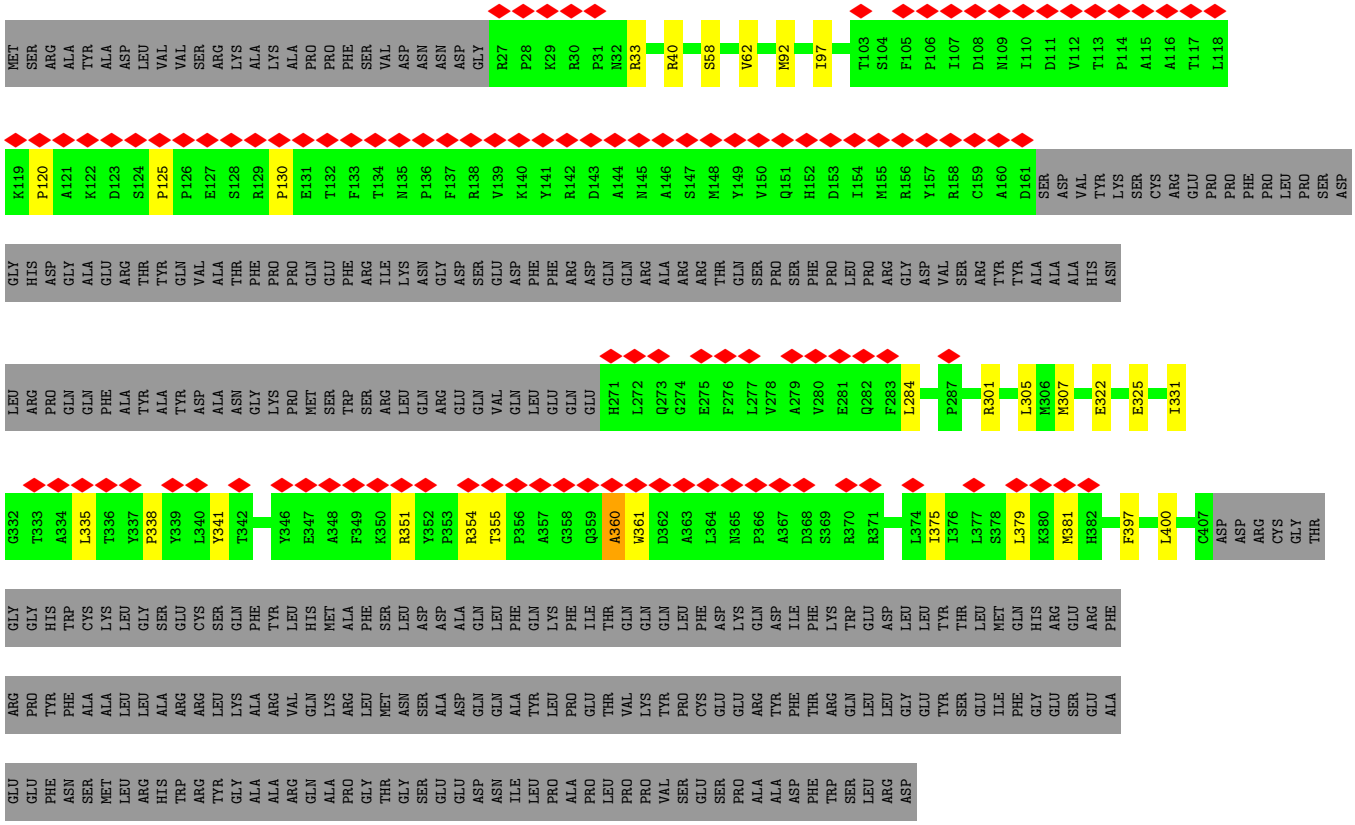
Chain D3:





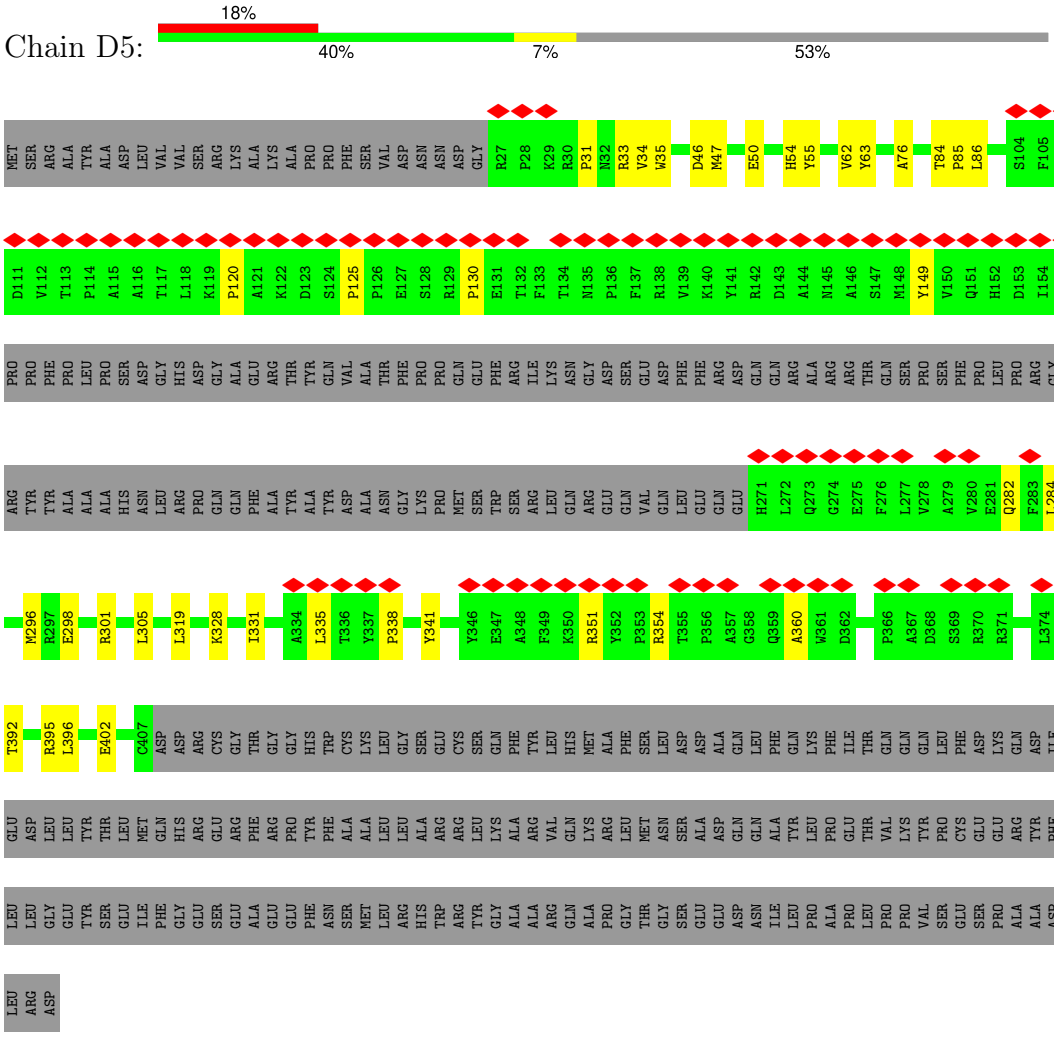
• Molecule 10: CPH1, TGME49_266630

Chain D4:



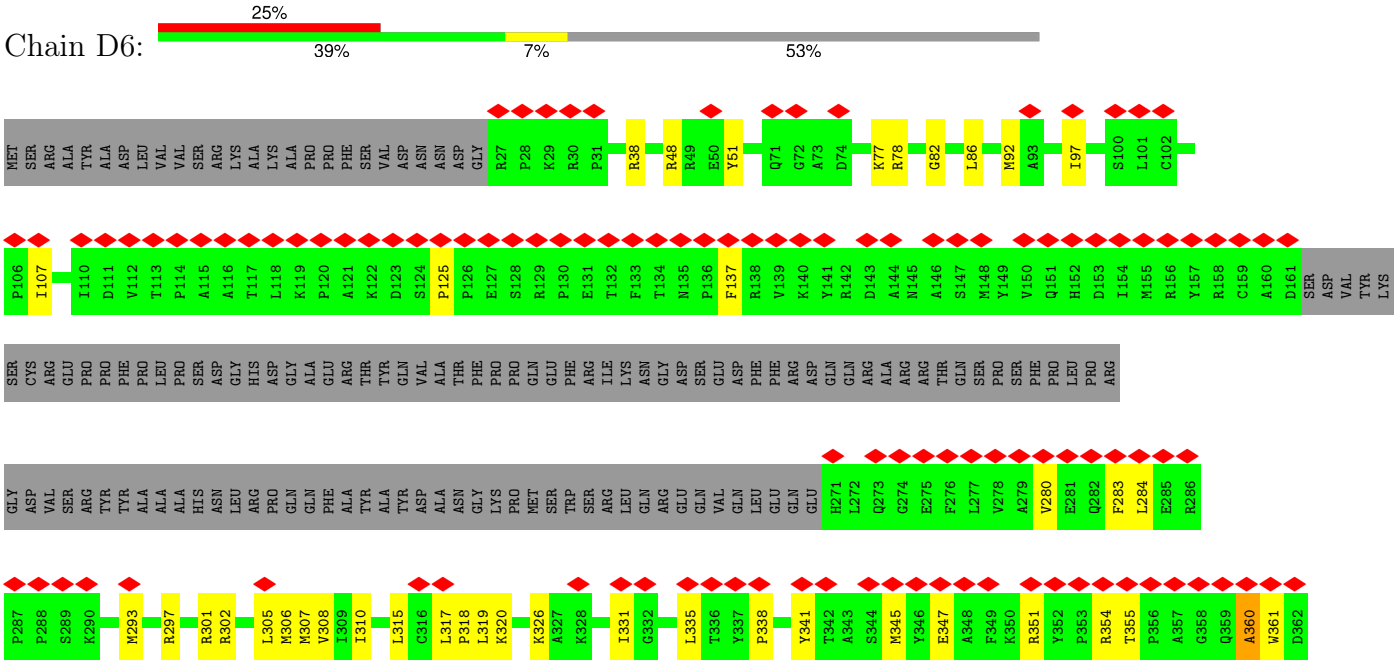
• Molecule 10: CPH1, TGME49_266630

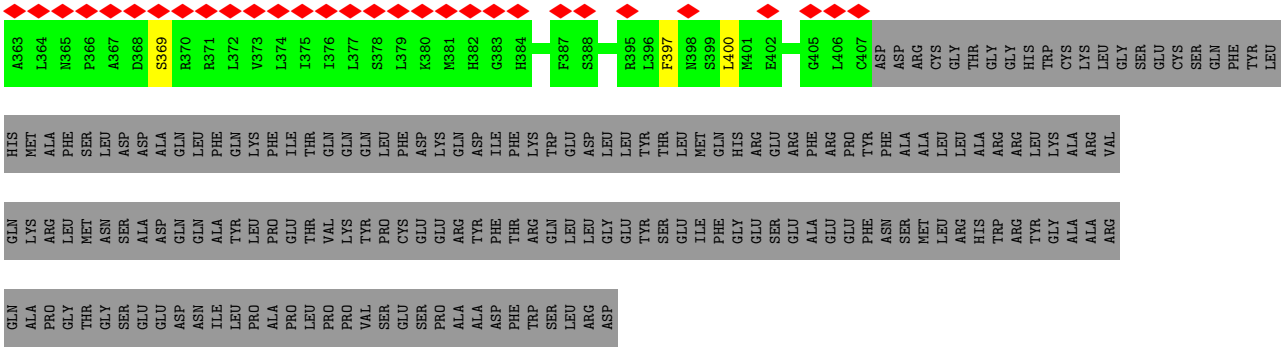
Chain D5:



• Molecule 10: CPH1, TGME49_266630

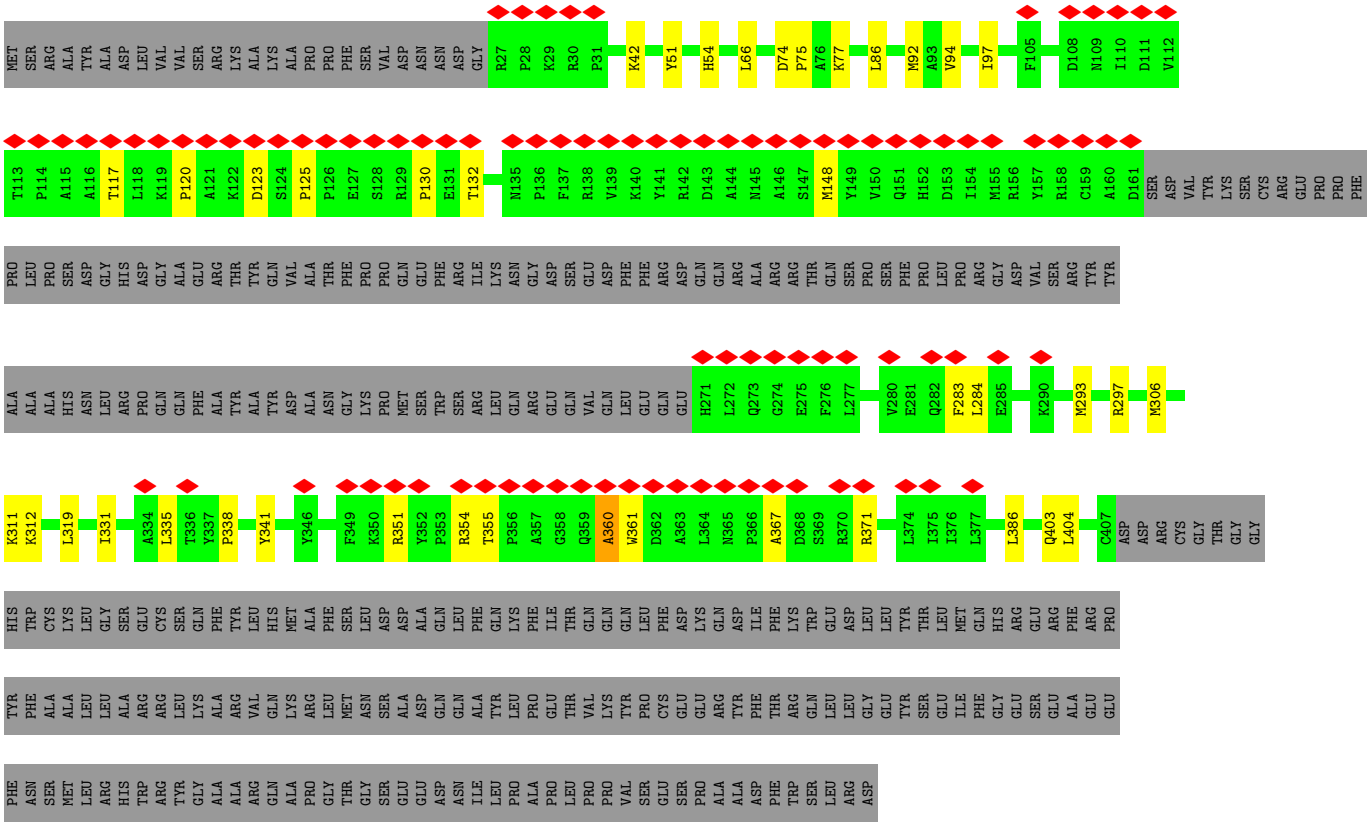
Chain D6:





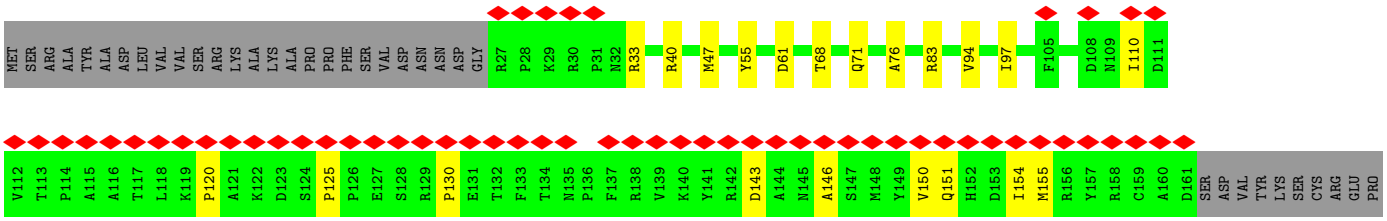
• Molecule 10: CPH1, TGME49_266630

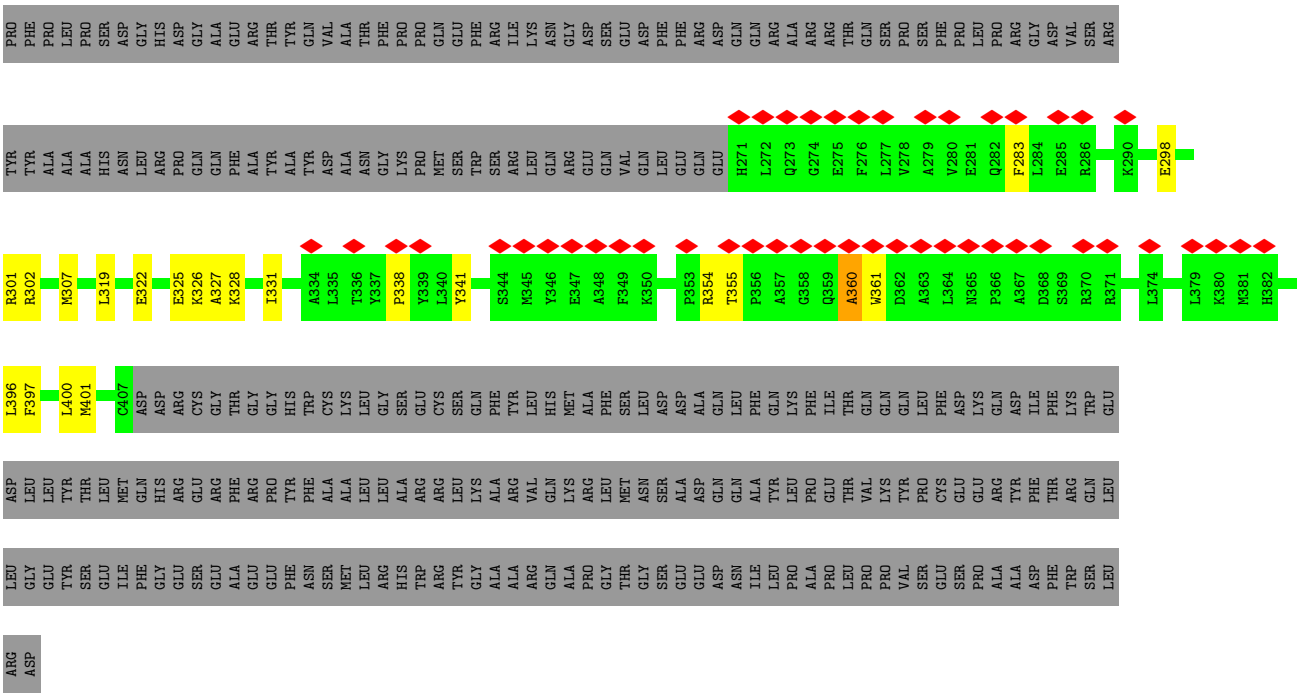
Chain D7:



• Molecule 10: CPH1, TGME49_266630

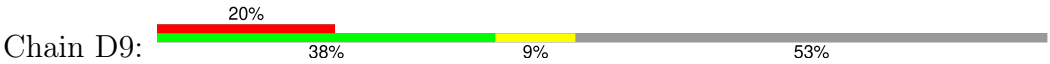
Chain D8:

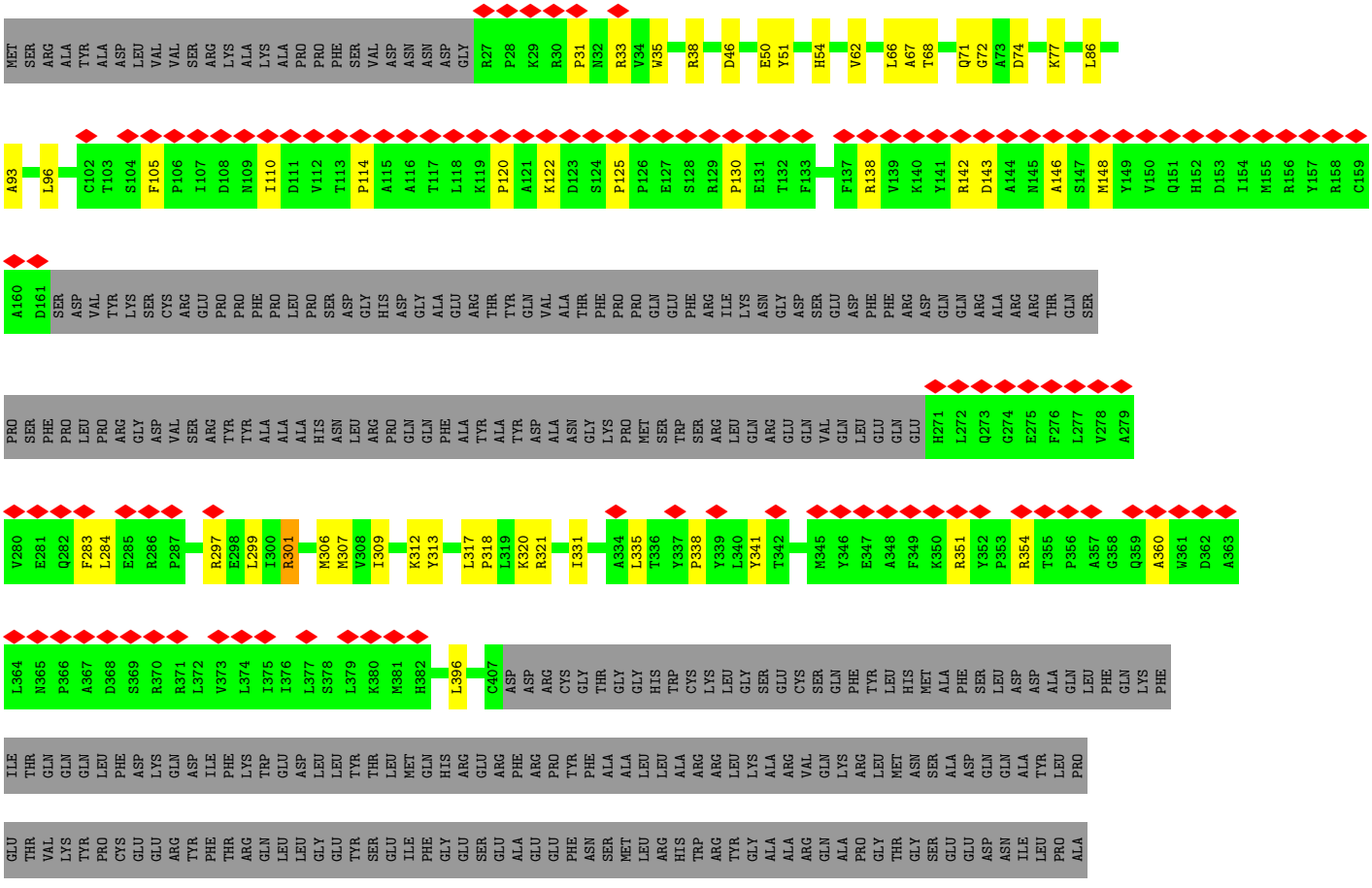




• Molecule 10: CPH1, TGME49_266630

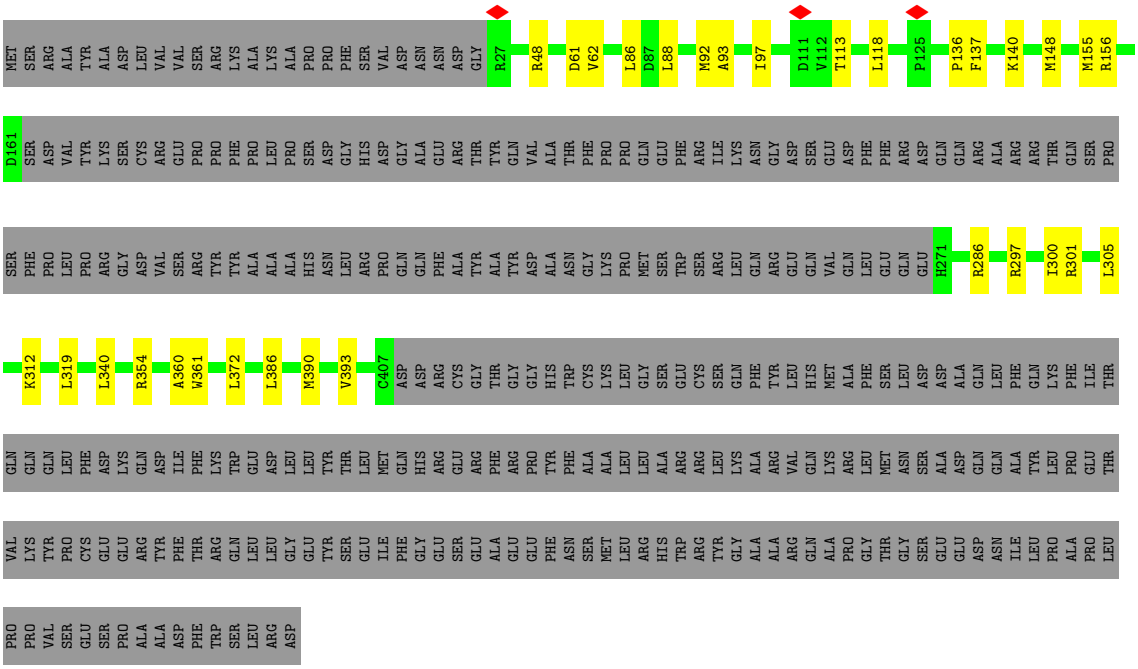
Chain D9:





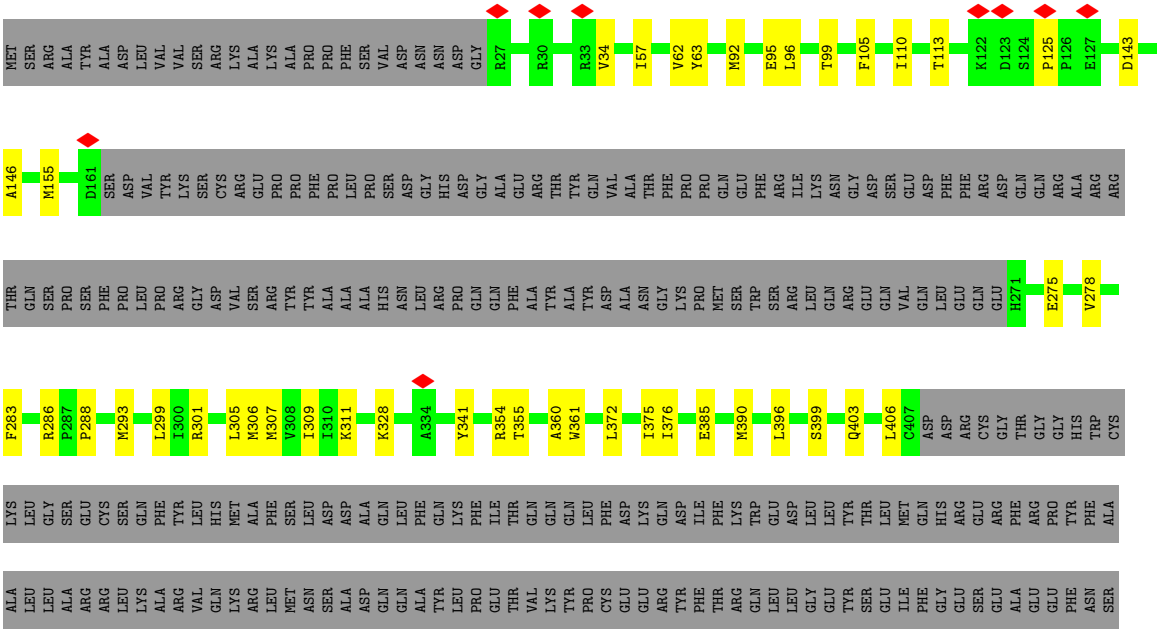
• Molecule 10: CPH1, TGME49_266630

Chain E0:



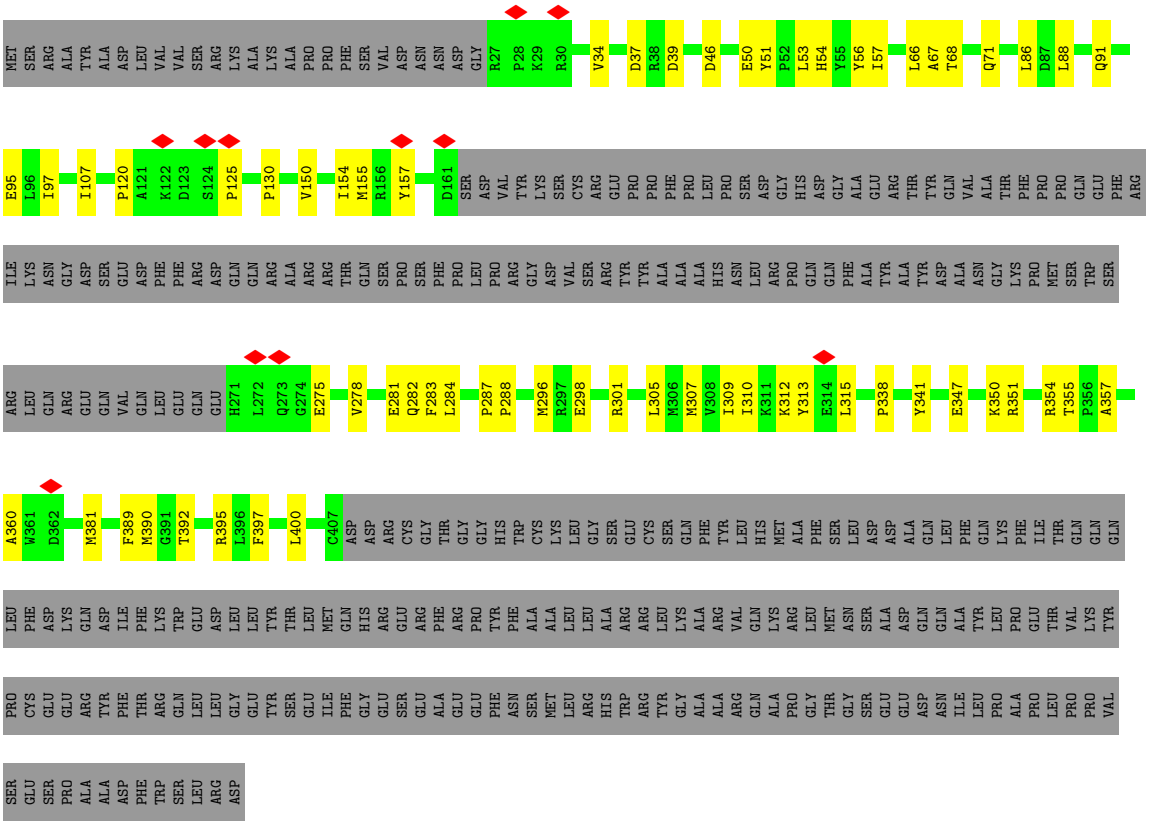
• Molecule 10: CPH1, TGME49_266630

Chain E1:



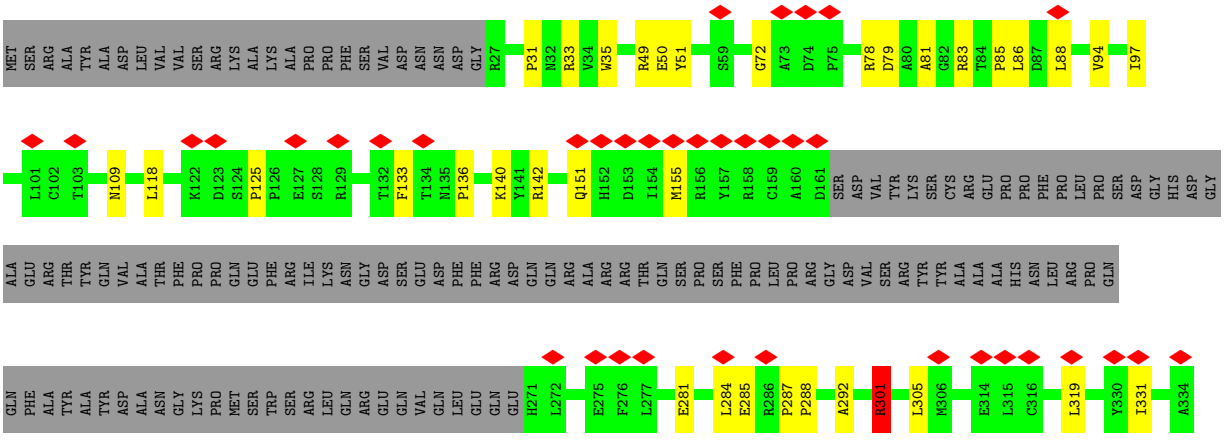
• Molecule 10: CPH1, TGME49_266630

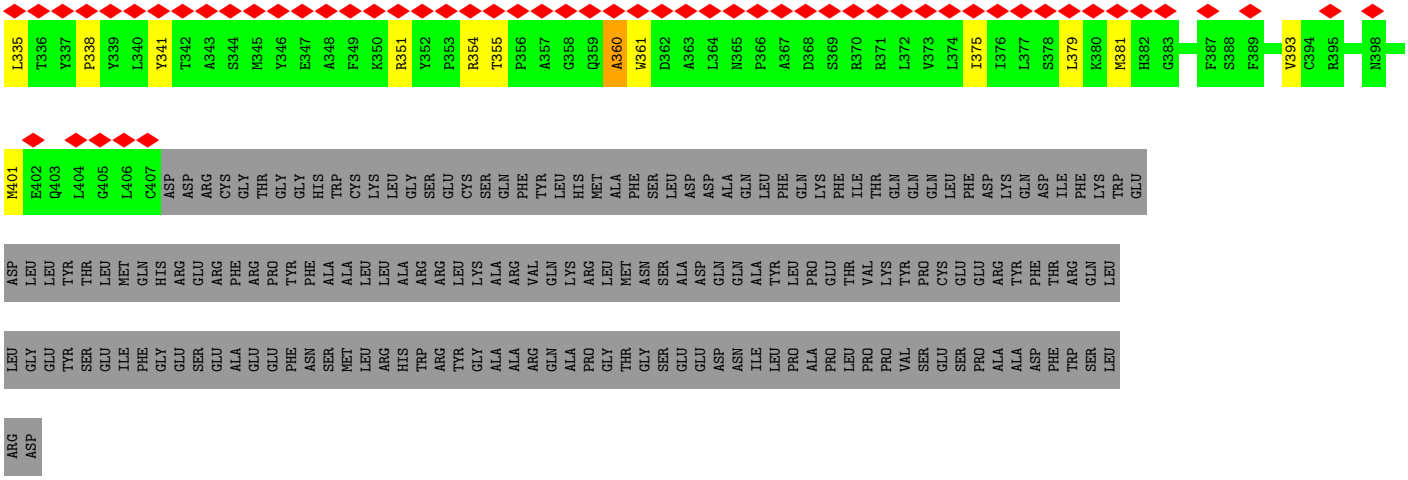
Chain E2:



• Molecule 10: CPH1, TGME49_266630

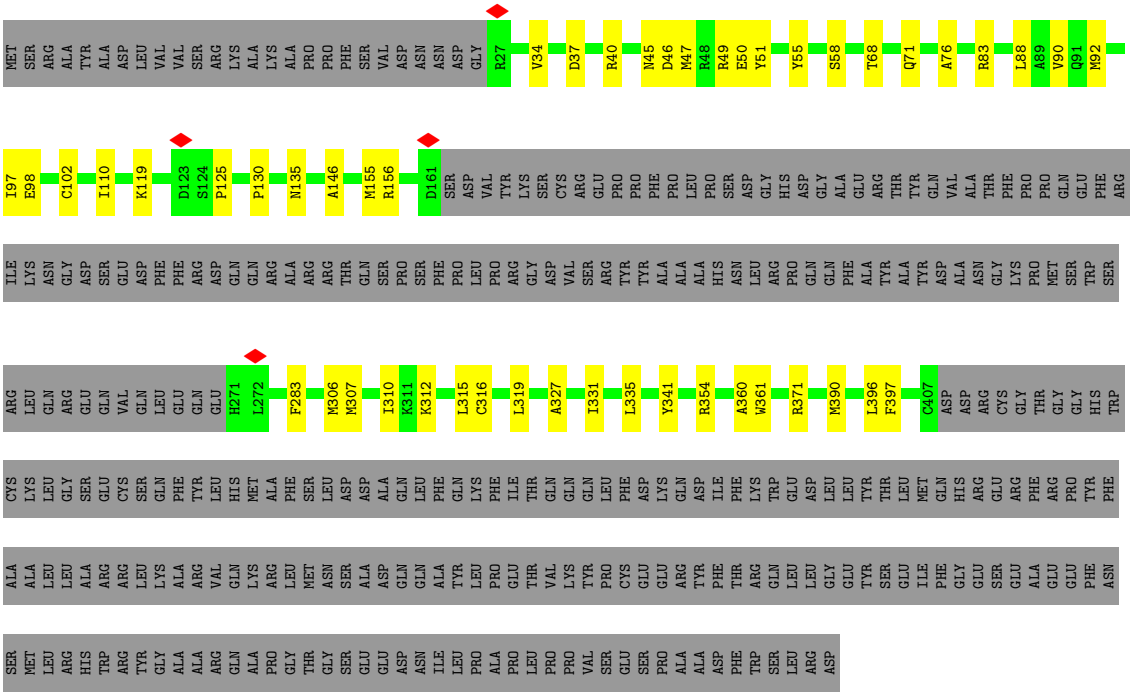
Chain E3:





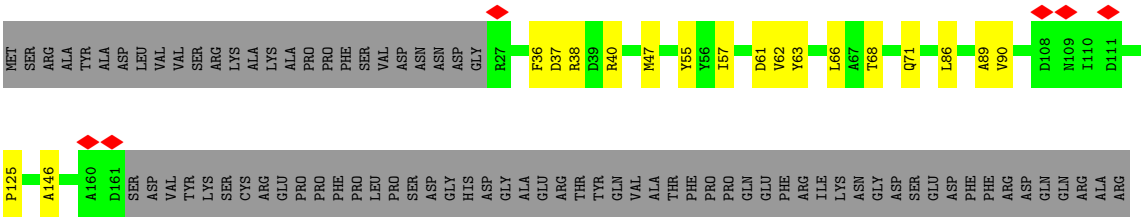
• Molecule 10: CPH1, TGME49_266630

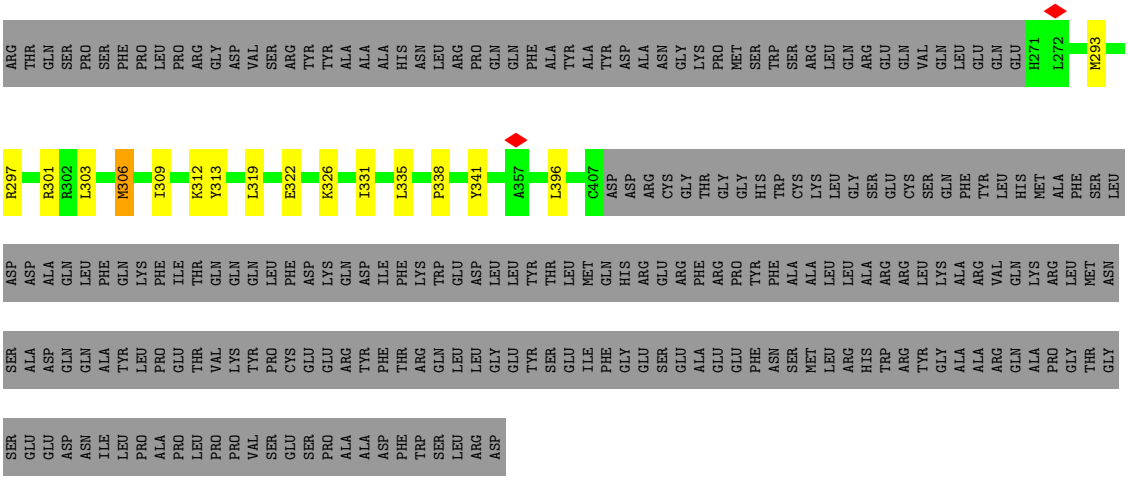
Chain E4:



• Molecule 10: CPH1, TGME49_266630

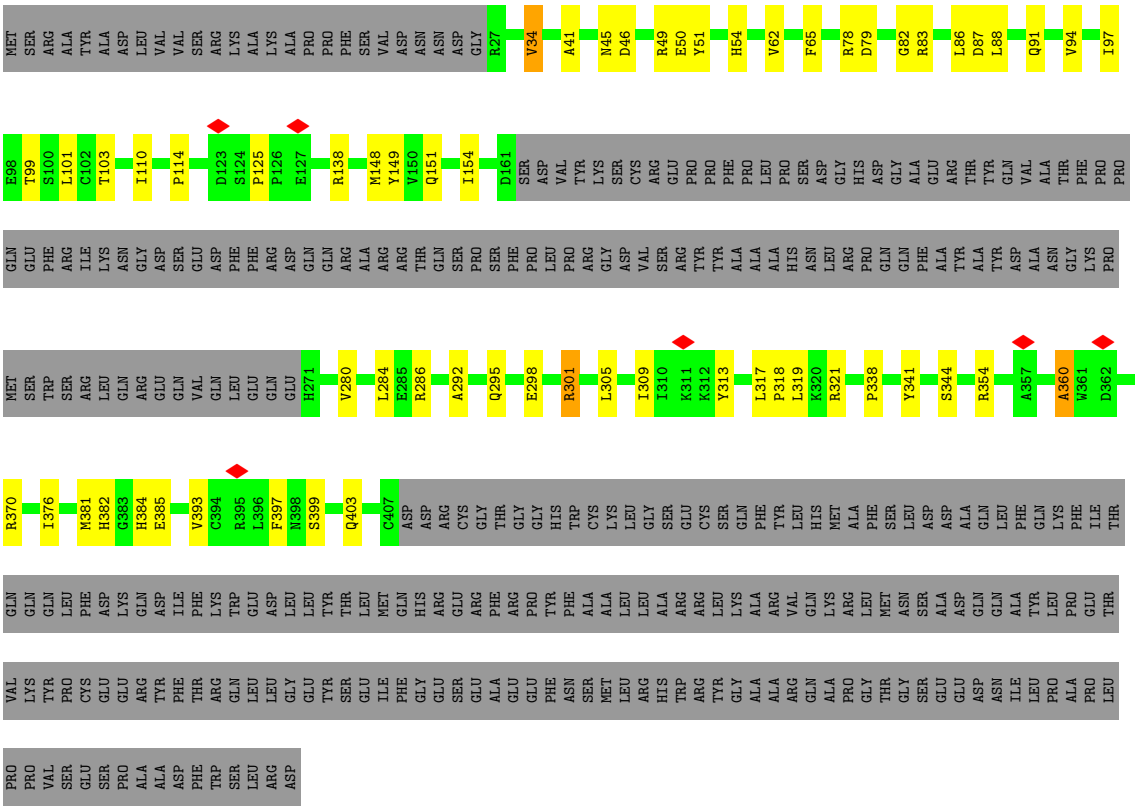
Chain E5:





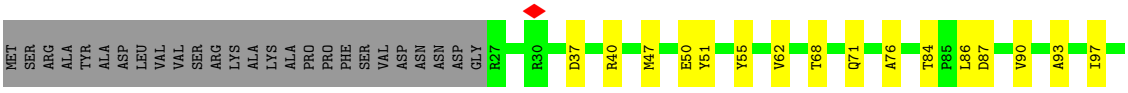
• Molecule 10: CPH1, TGME49_266630

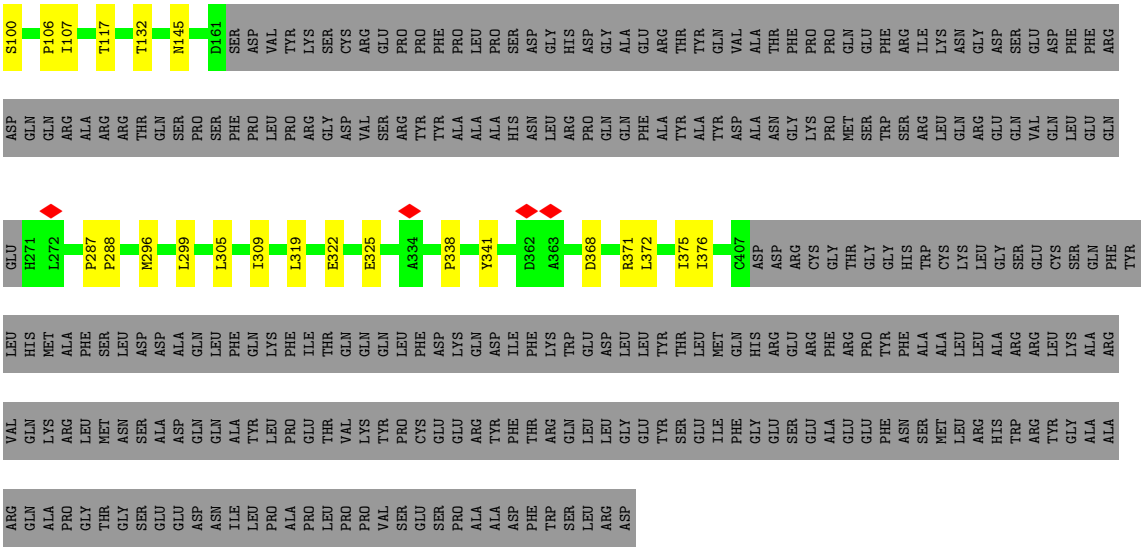
Chain E6:



• Molecule 10: CPH1, TGME49_266630

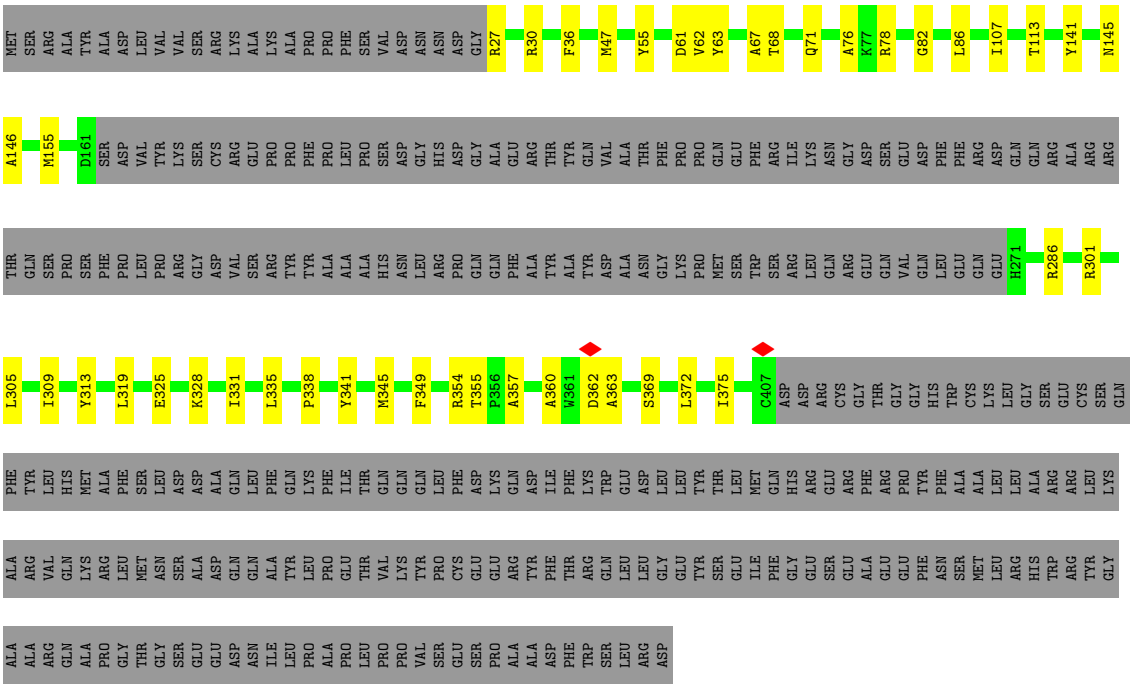
Chain E7:





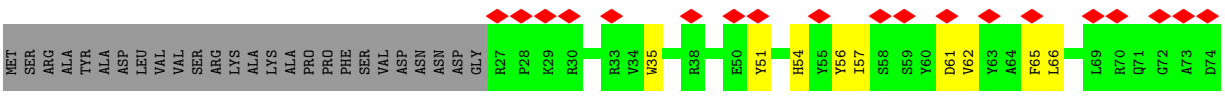
• Molecule 10: CPH1, TGME49_266630

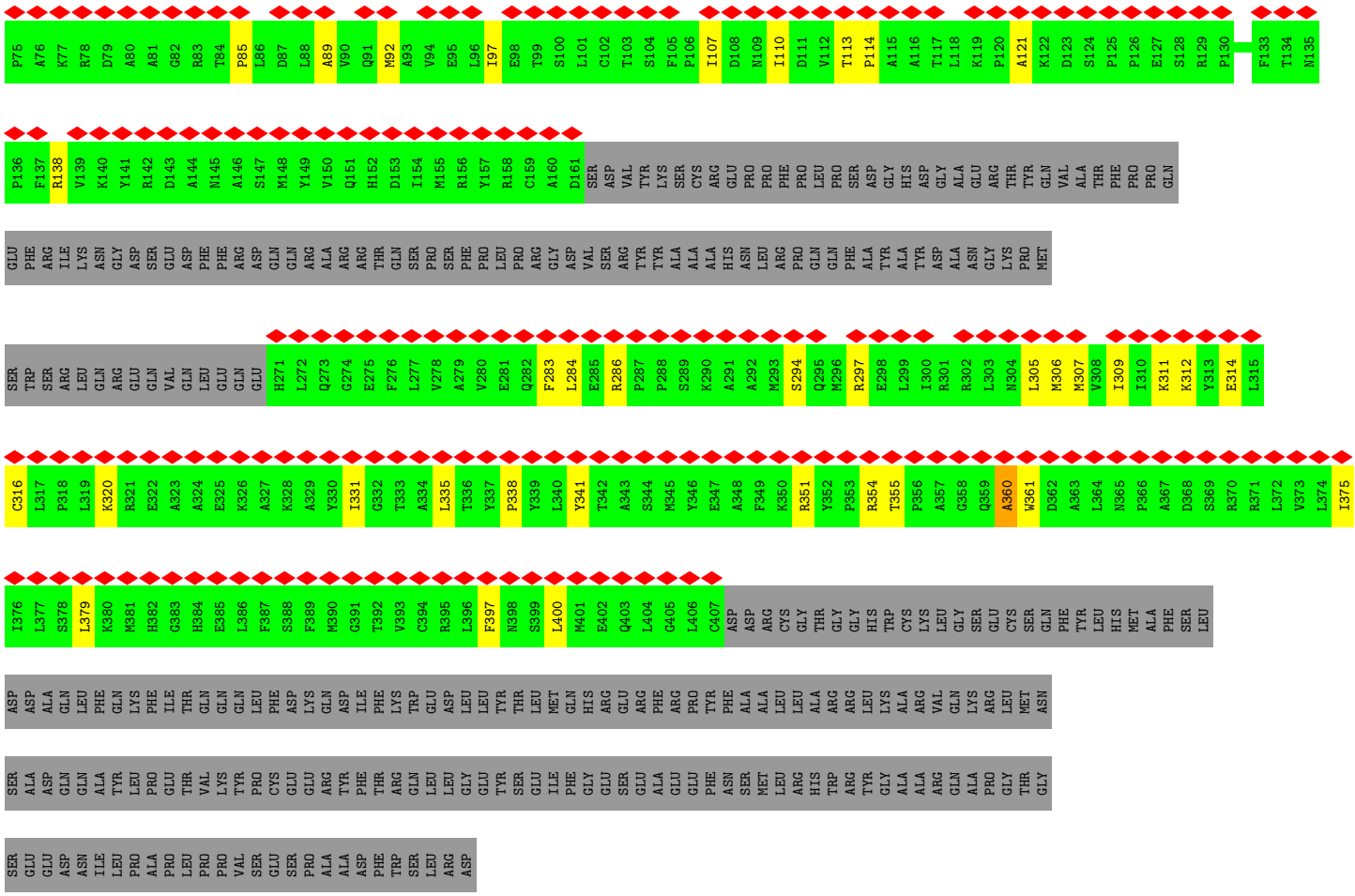
Chain E8:



• Molecule 10: CPH1, TGME49_266630

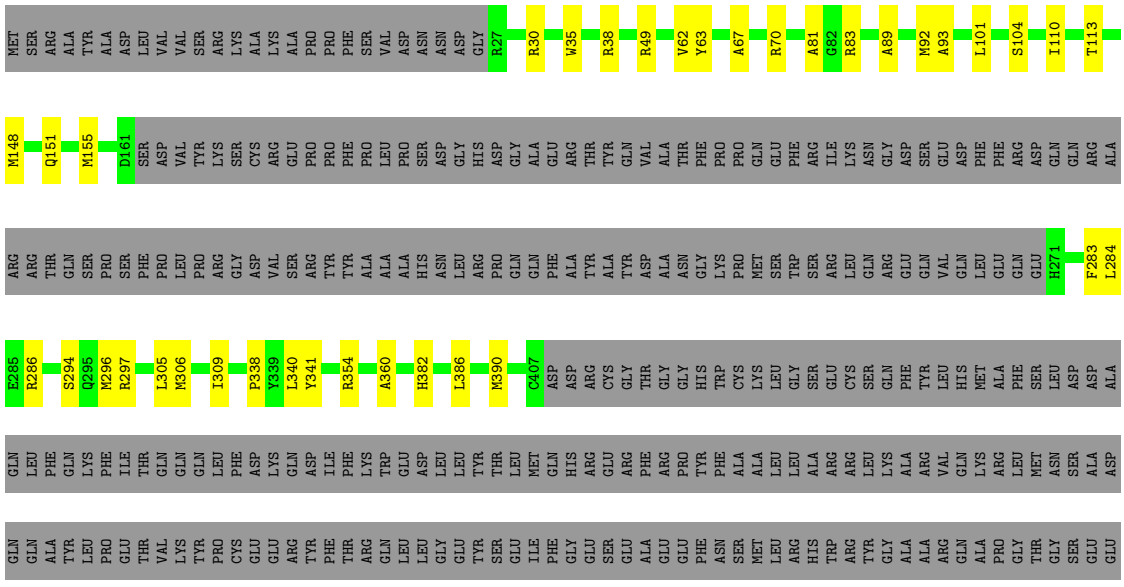
Chain E9:





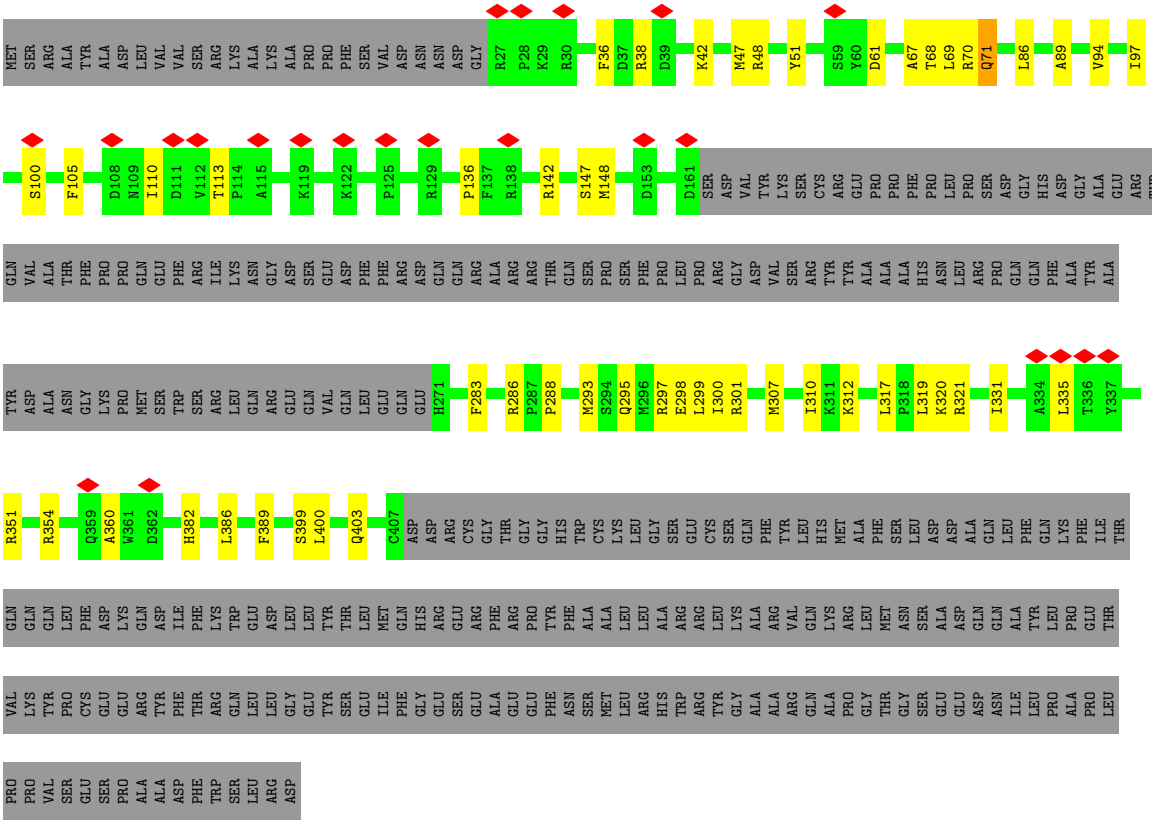
• Molecule 10: CPH1, TGME49_266630

Chain F1:



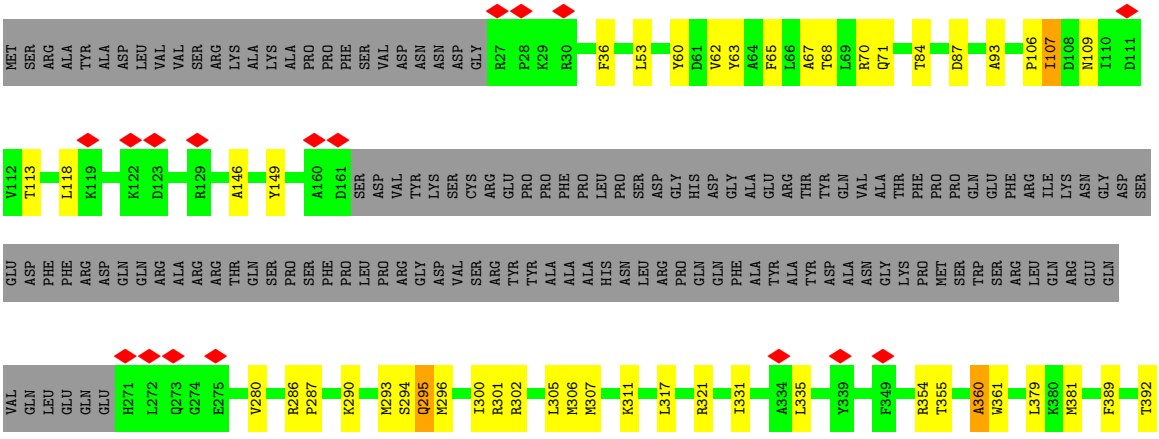
• Molecule 10: CPH1, TGME49_266630

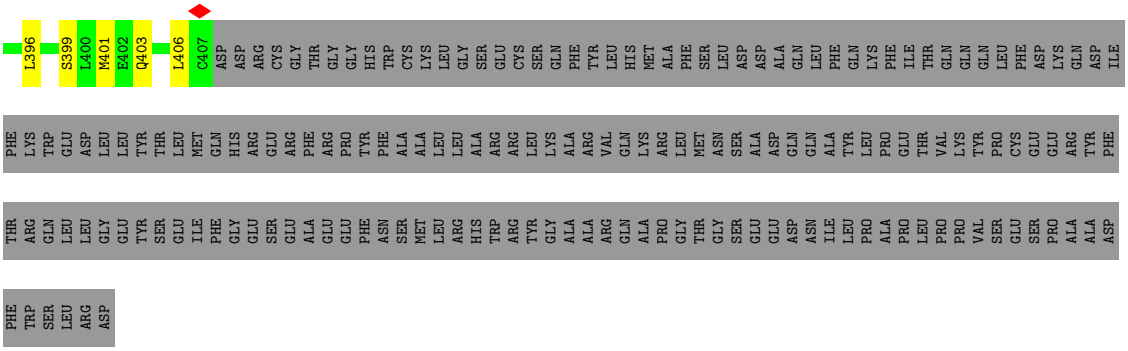
Chain F2:



• Molecule 10: CPH1, TGME49_266630

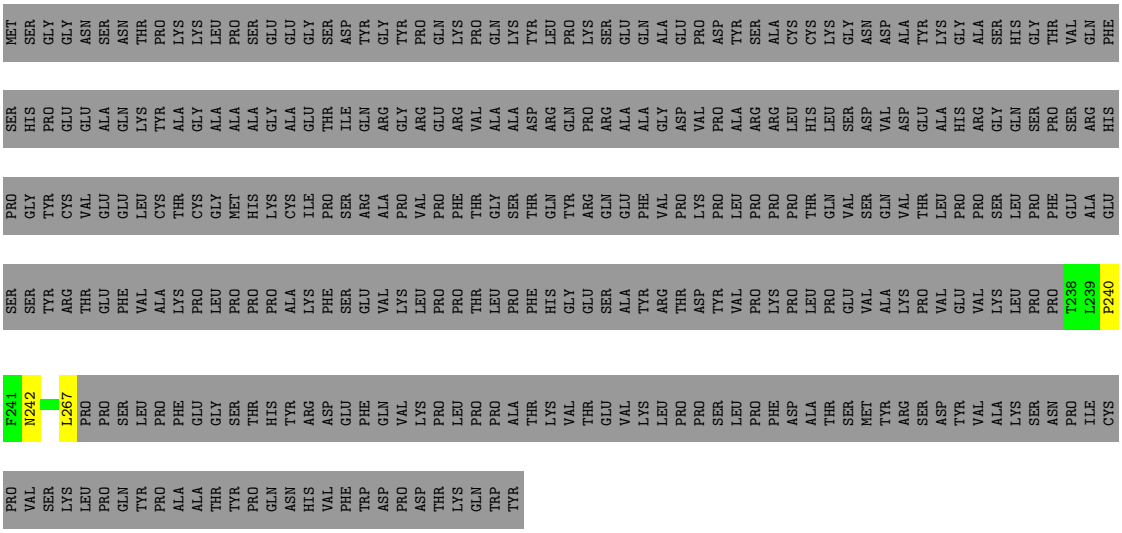
Chain F3:





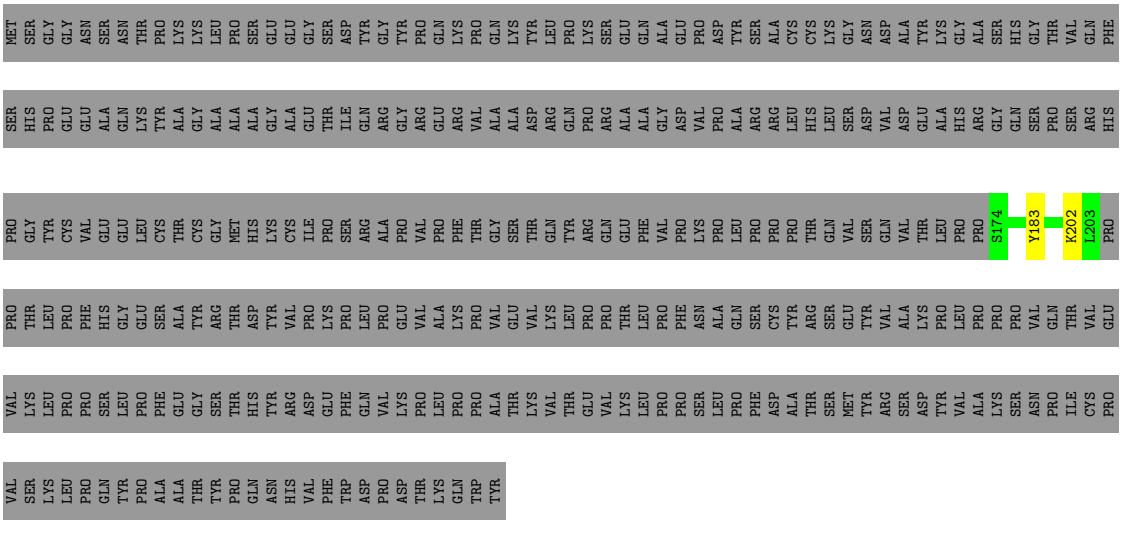
• Molecule 11: Microtubule associated protein SPM1

Chain C1:



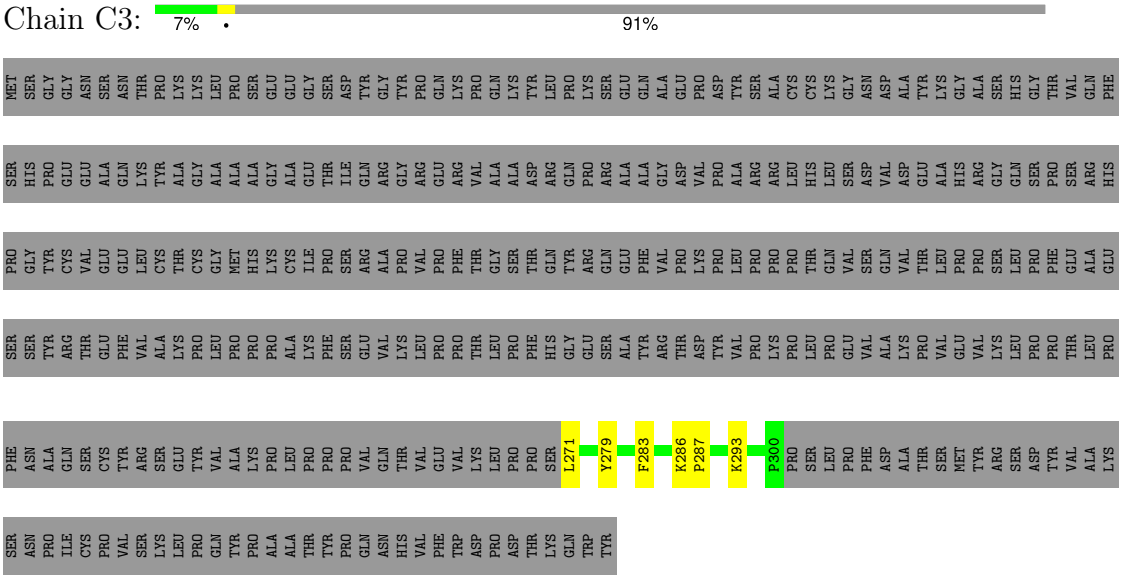
• Molecule 11: Microtubule associated protein SPM1

Chain C2:



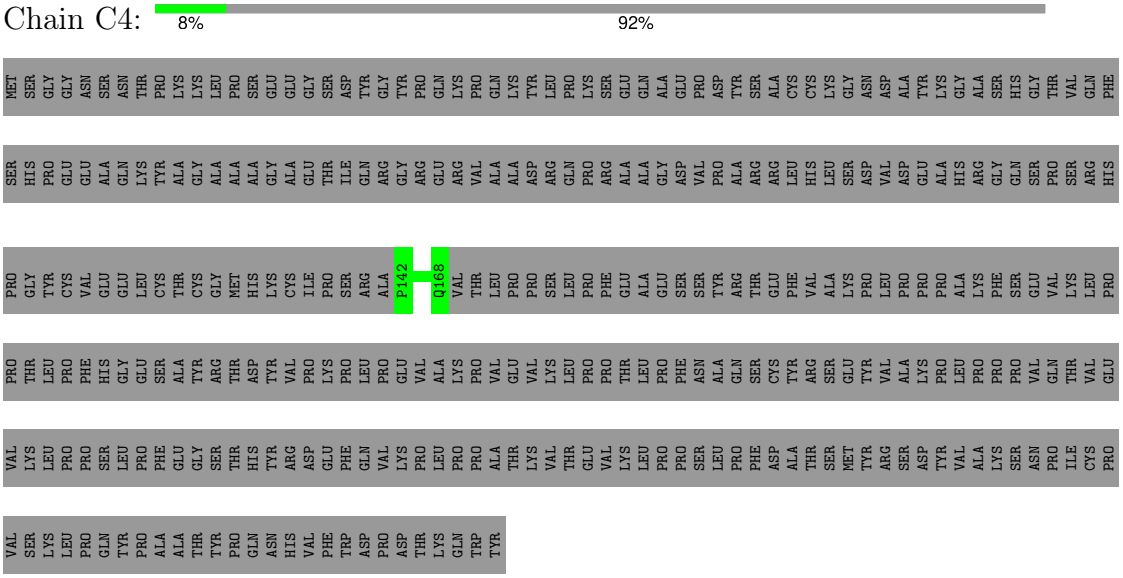
• Molecule 11: Microtubule associated protein SPM1

Chain C3:



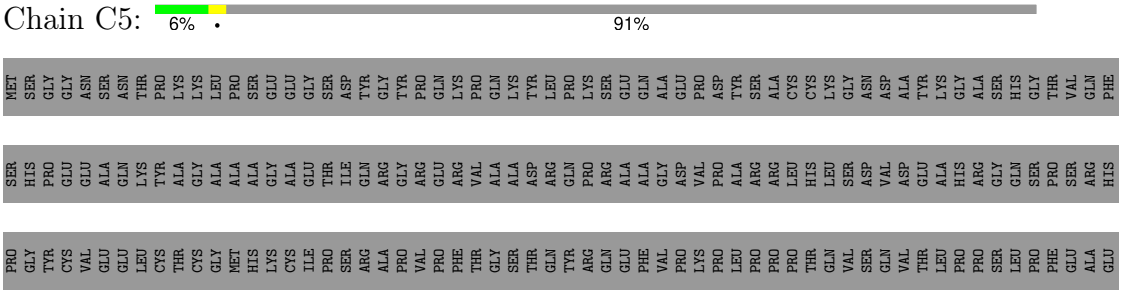
• Molecule 11: Microtubule associated protein SPM1

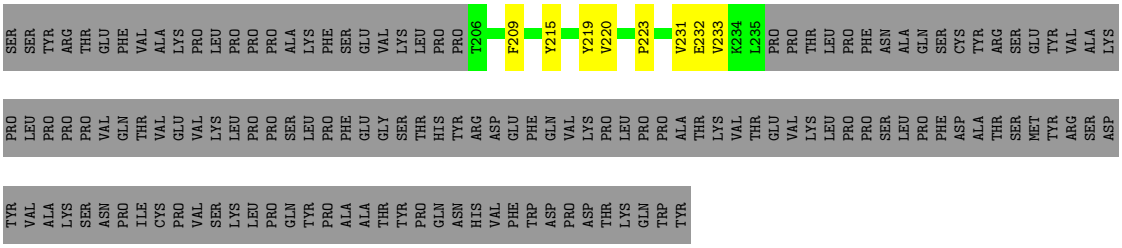
Chain C4:



• Molecule 11: Microtubule associated protein SPM1

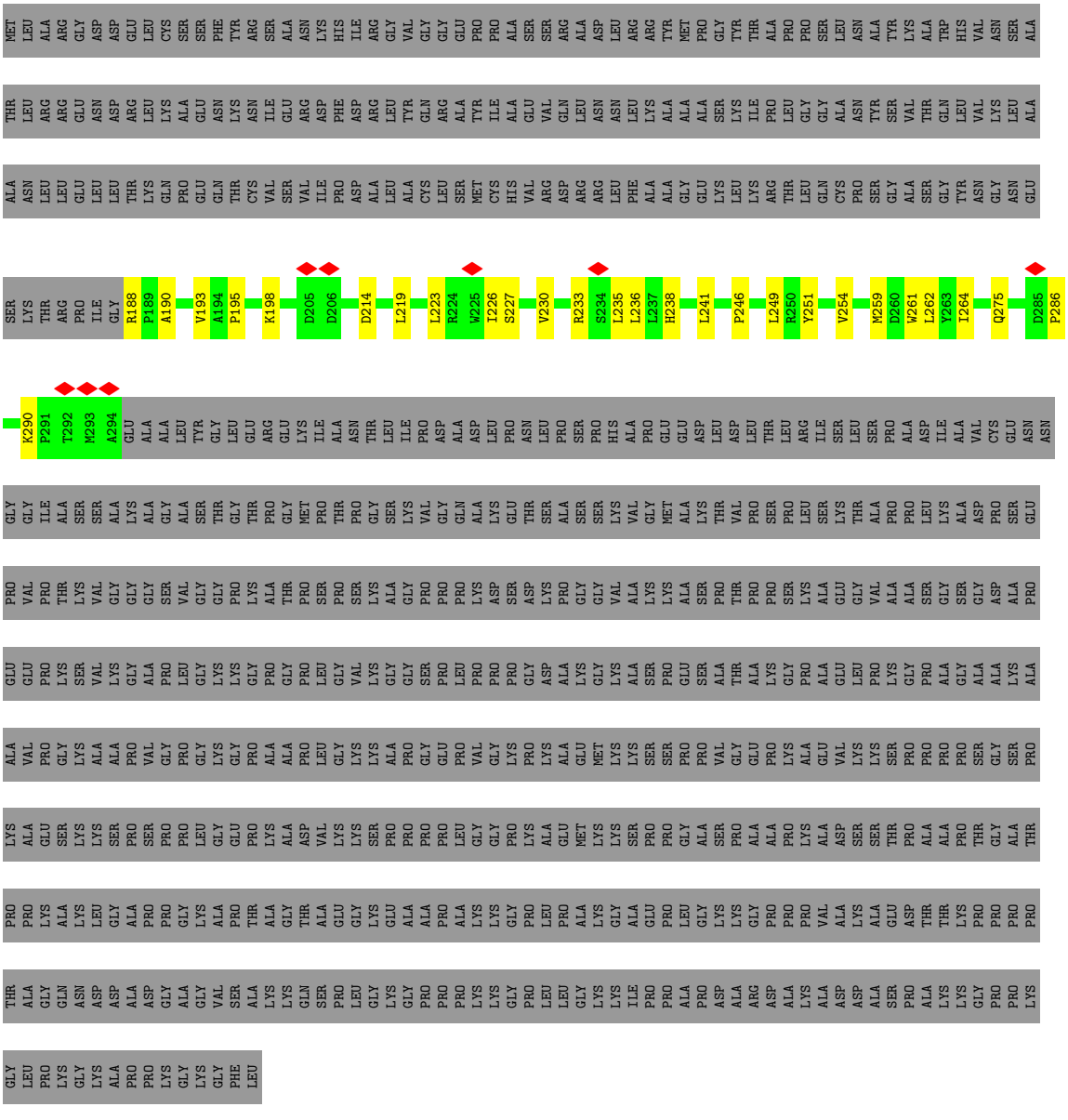
Chain C5:





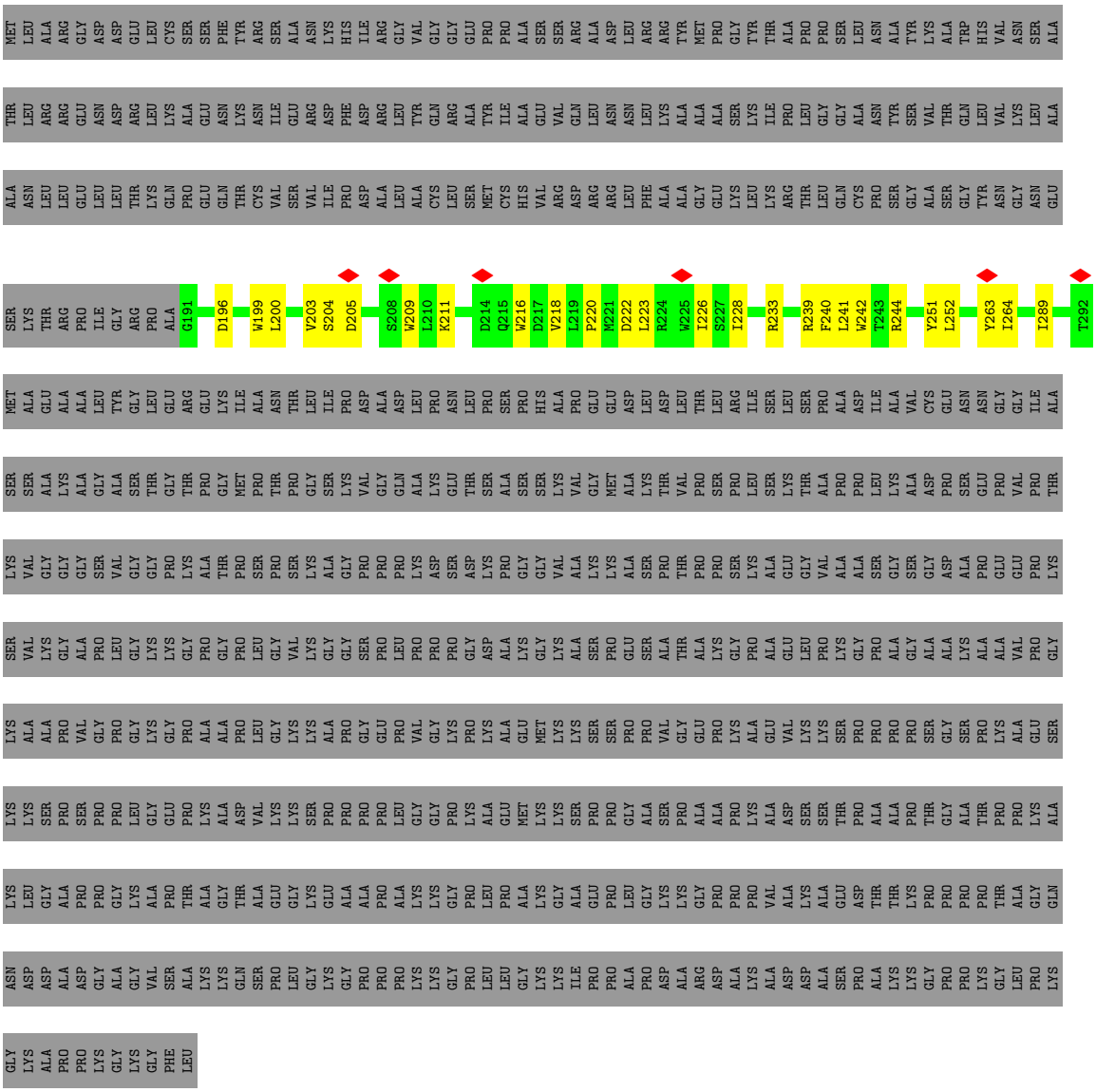
• Molecule 12: PRP, TGME49_291880

Chain F0:



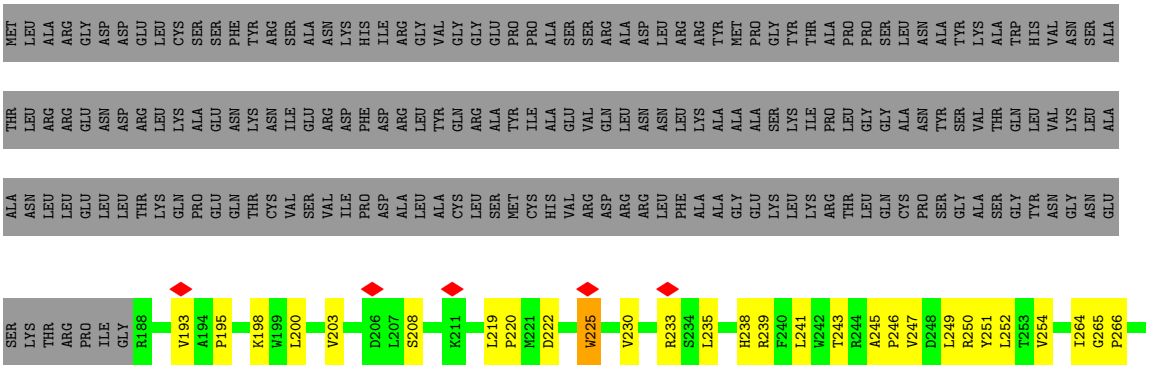
• Molecule 12: PRP, TGME49_291880

Chain F5:



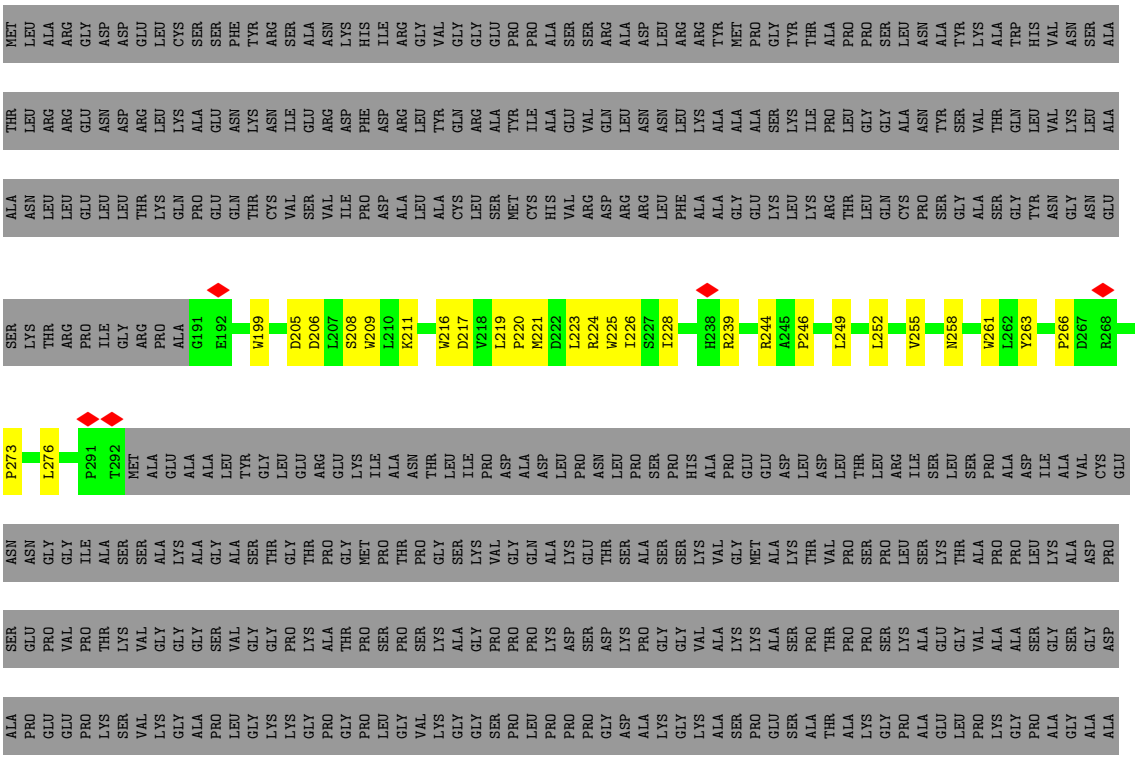
• Molecule 12: PRP, TGME49_291880

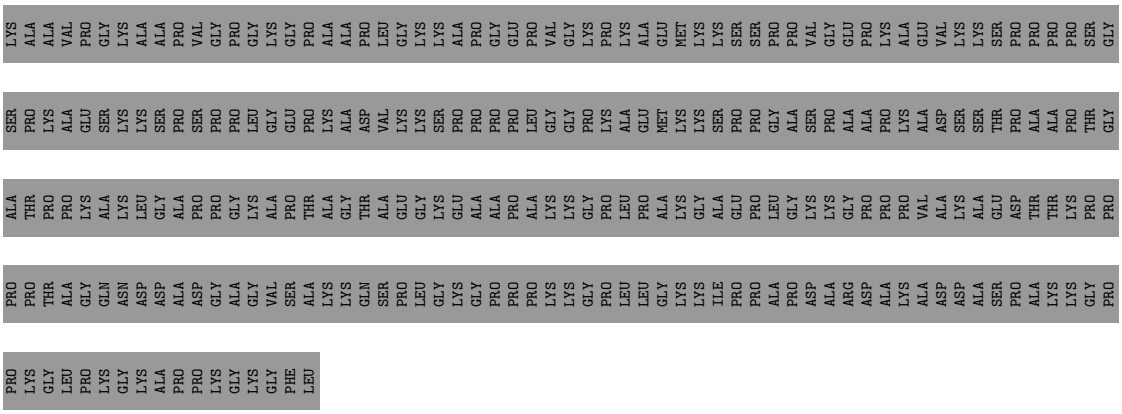
Chain F6:



• Molecule 12: PRP, TGME49_291880

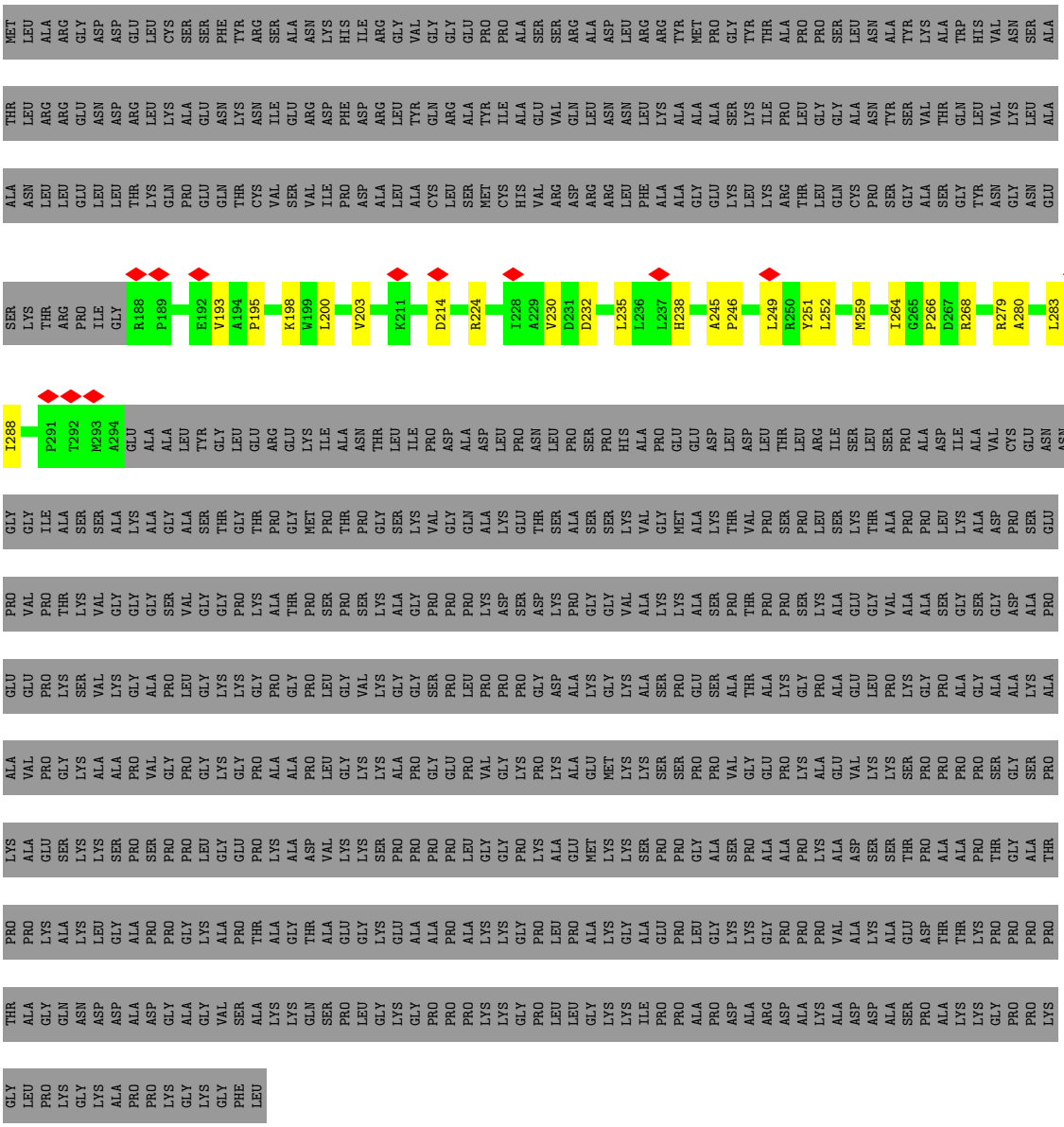
Chain F7:





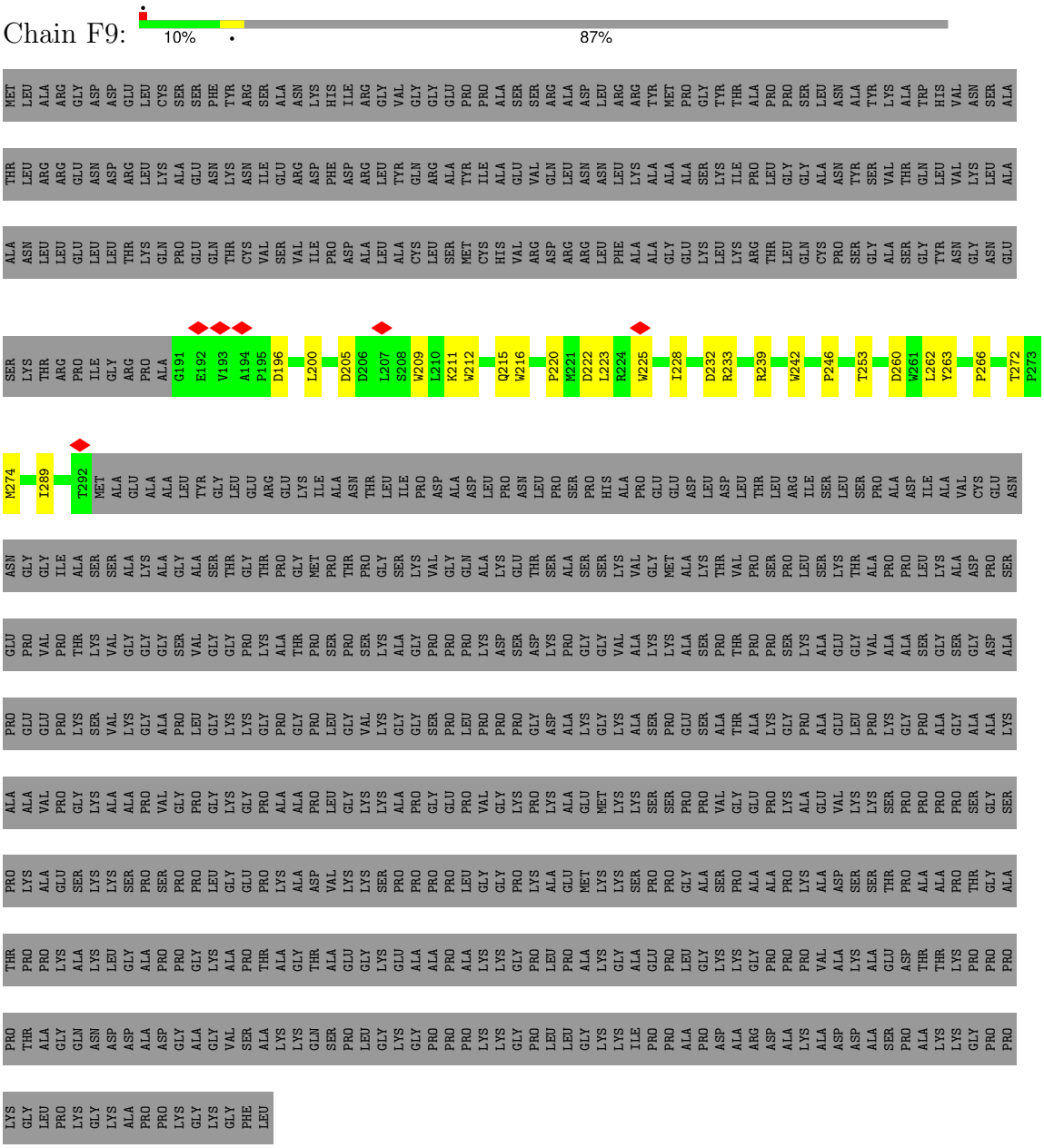
• Molecule 12: PRP, TGME49_291880

Chain F8:



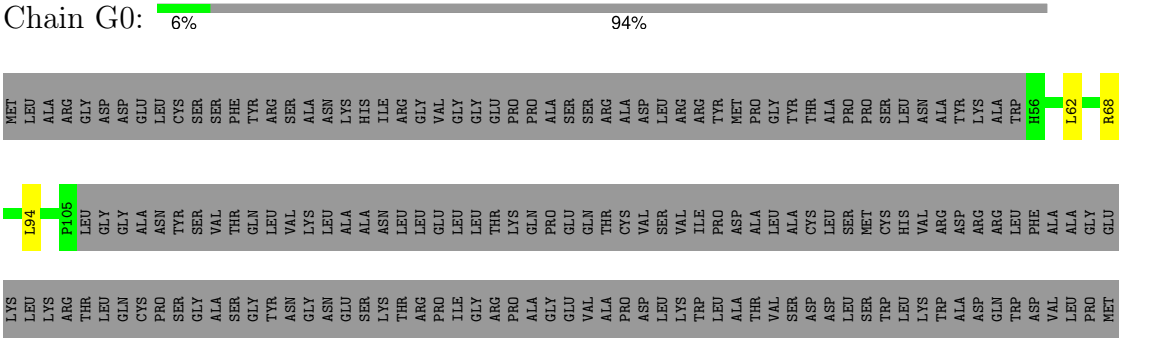
• Molecule 12: PRP, TGME49_291880

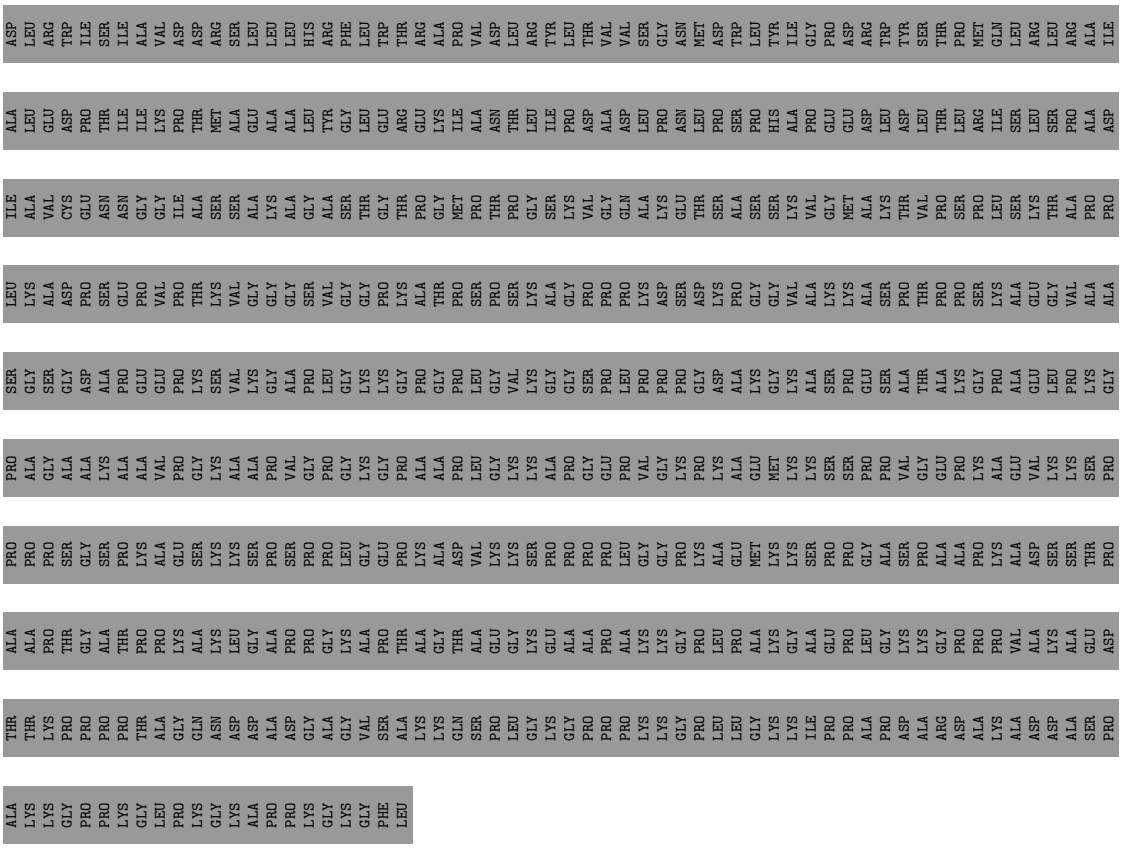
Chain F9:



• Molecule 12: PRP, TGME49_291880

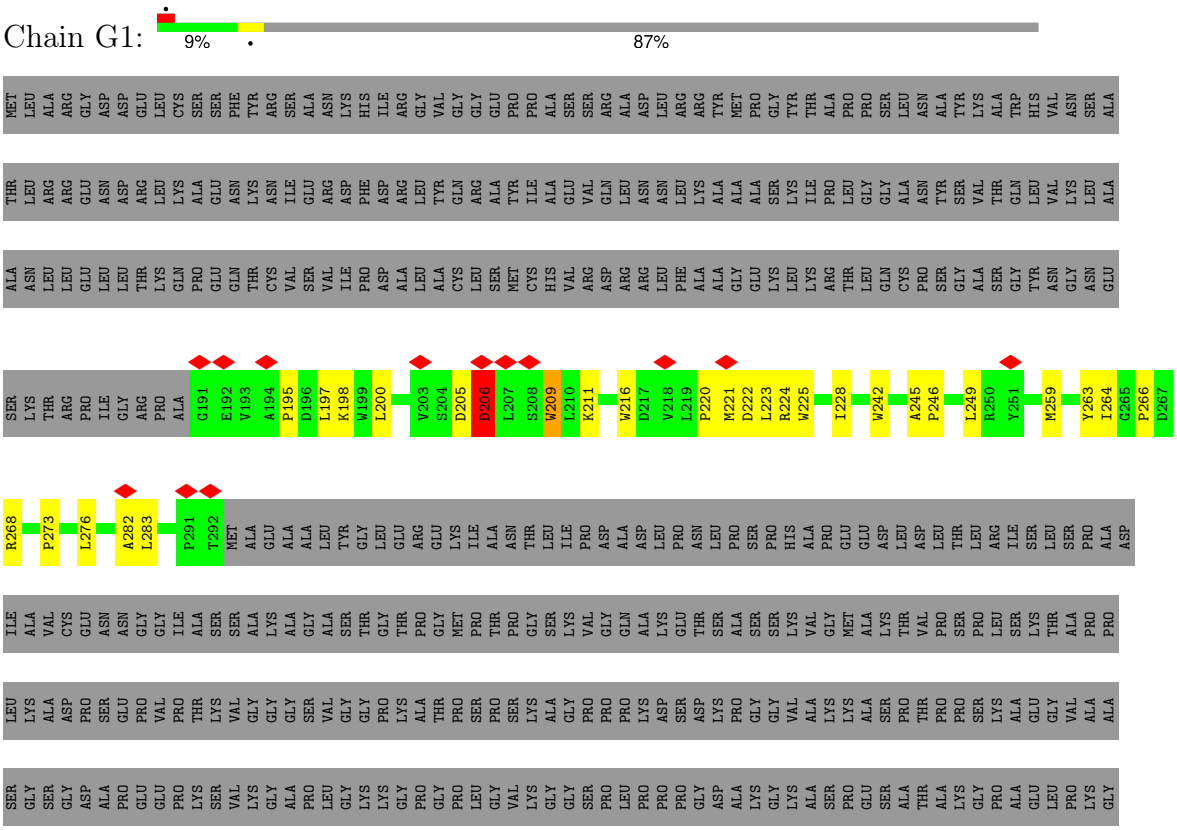
Chain G0:

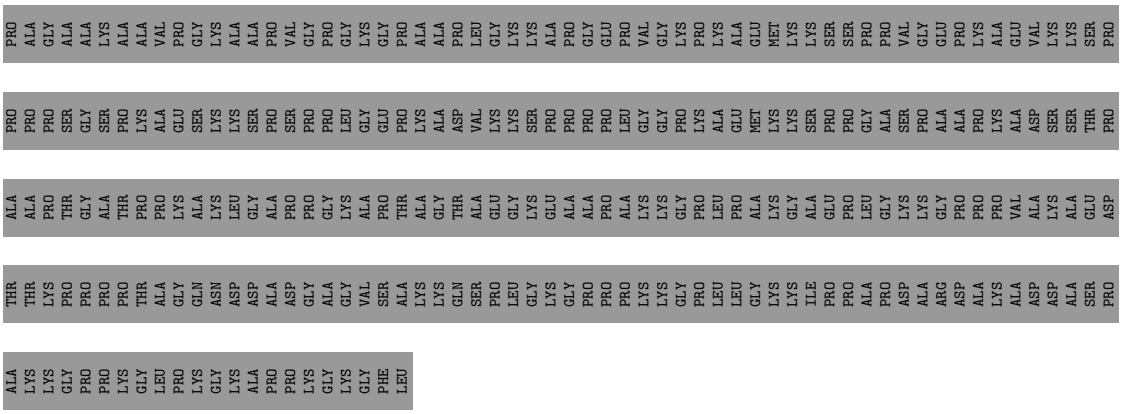




• Molecule 12: PRP, TGME49_291880

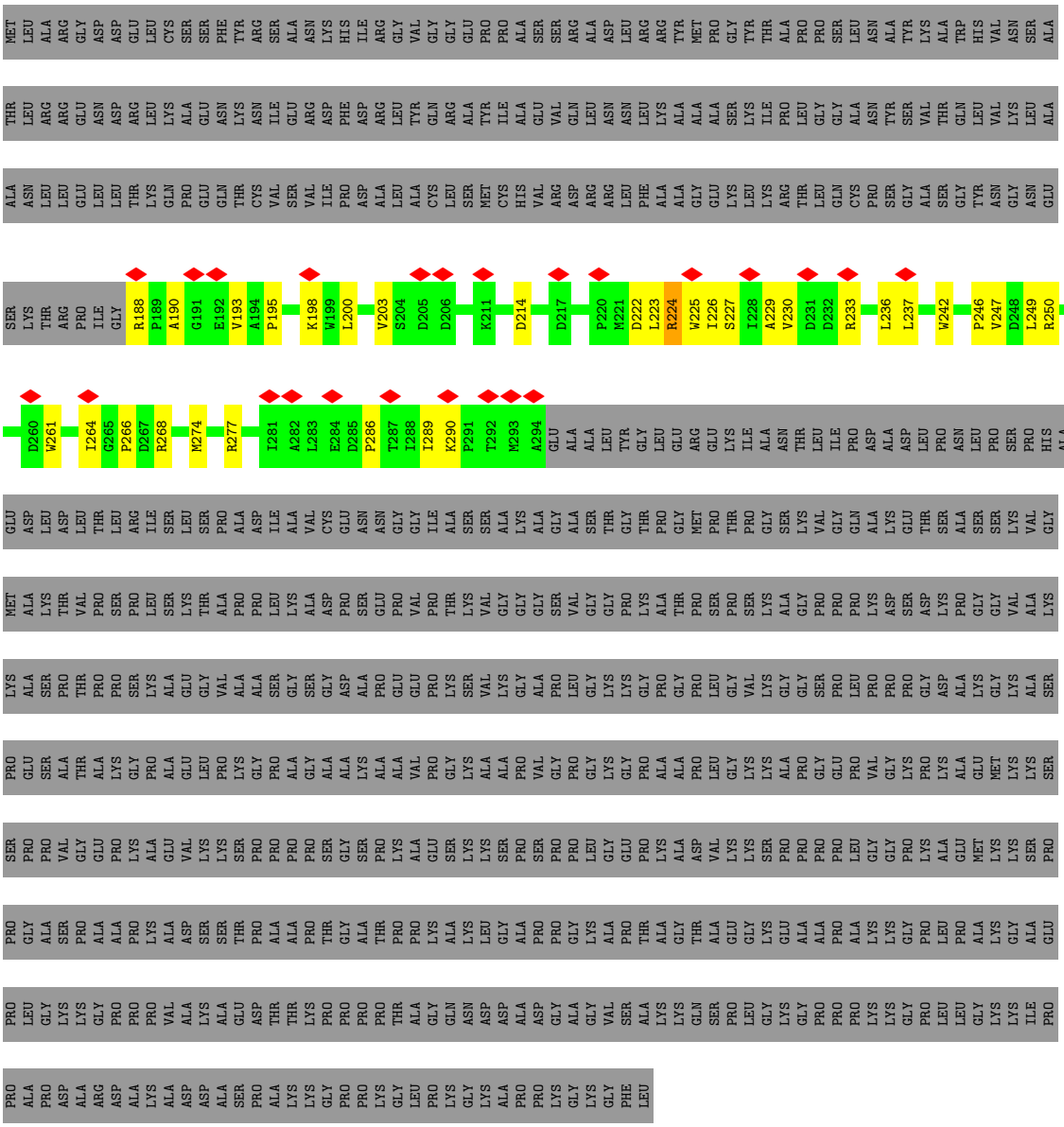
Chain G1:





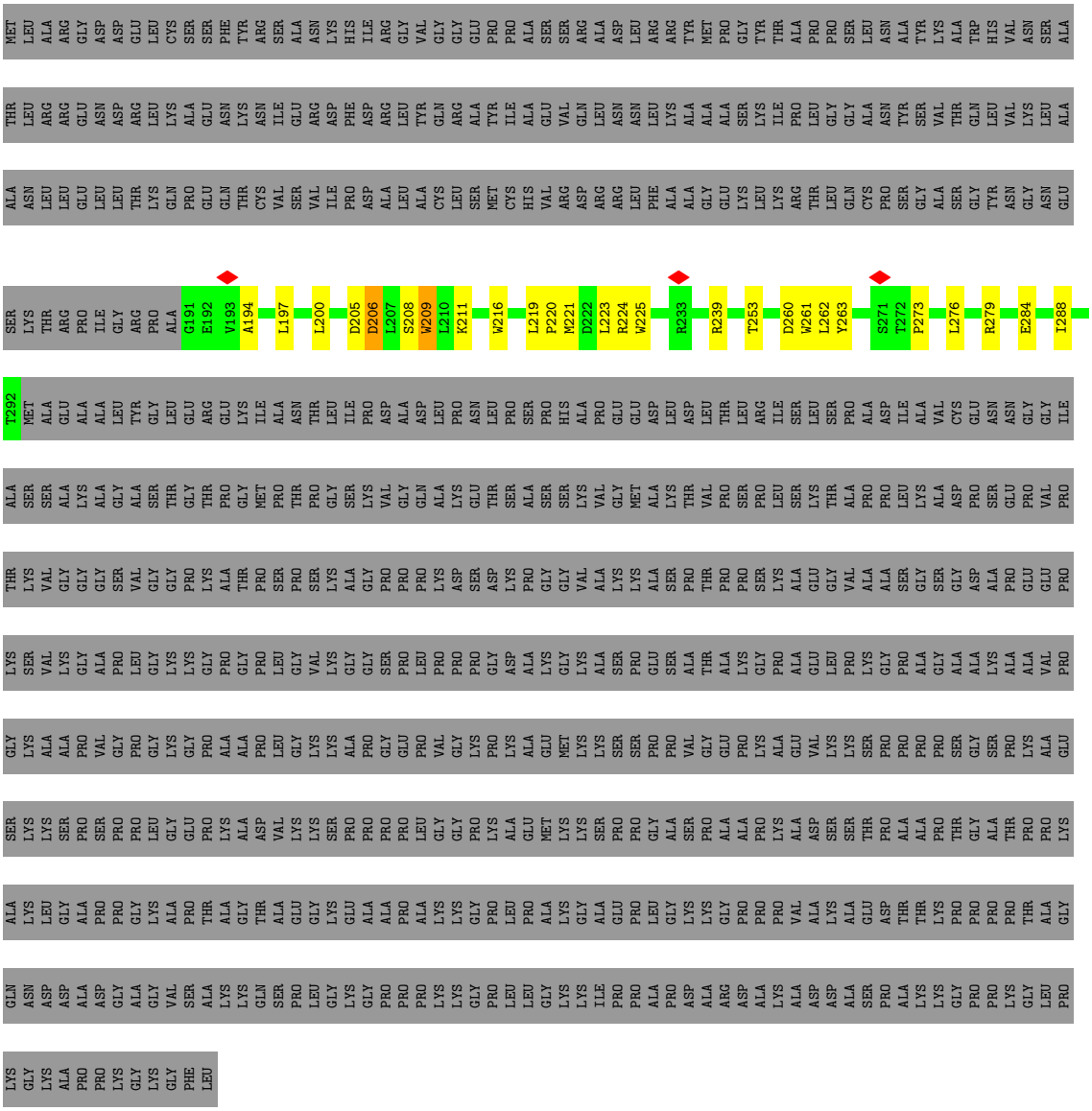
• Molecule 12: PRP, TGME49_291880

Chain G2:



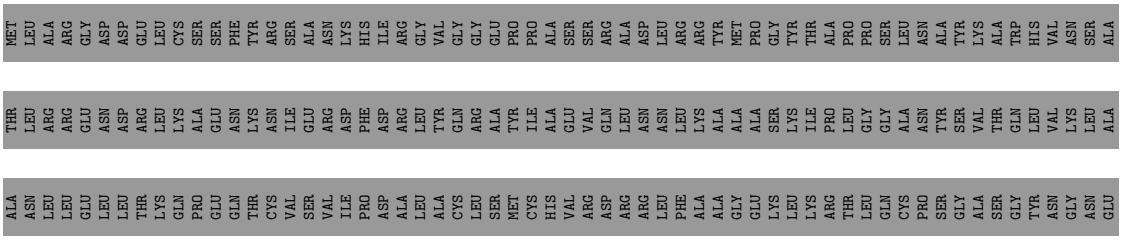
• Molecule 12: PRP, TGME49_291880

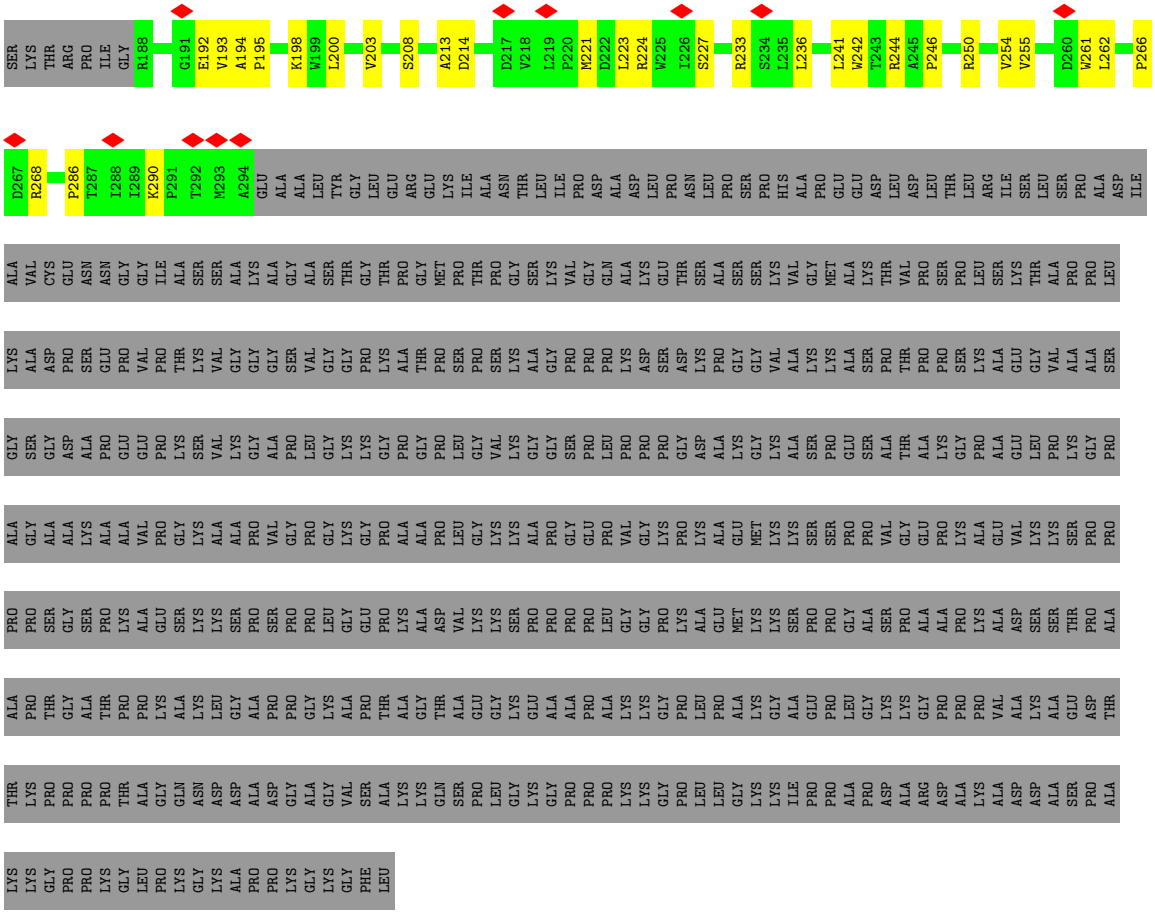
Chain G3:



• Molecule 12: PRP, TGME49_291880

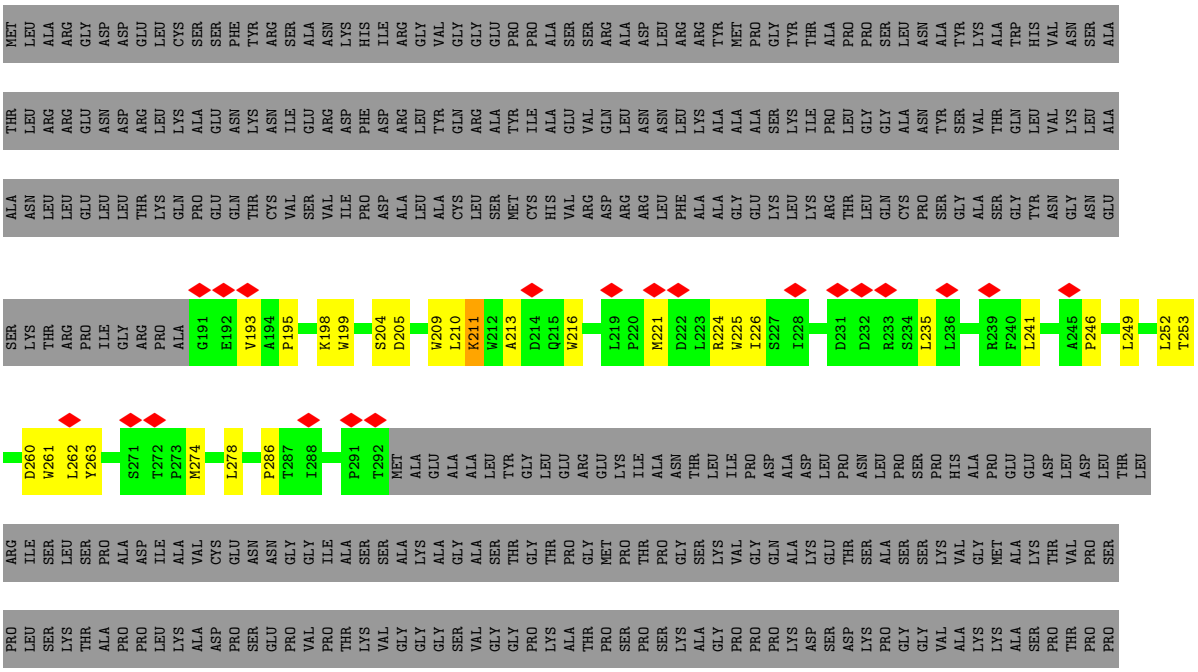
Chain G4:

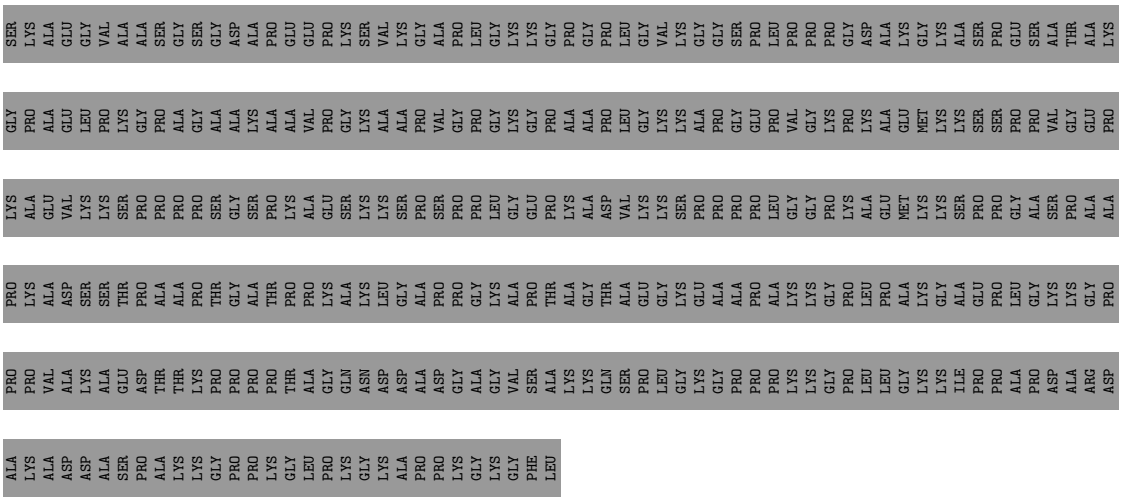




• Molecule 12: PRP, TGME49_291880

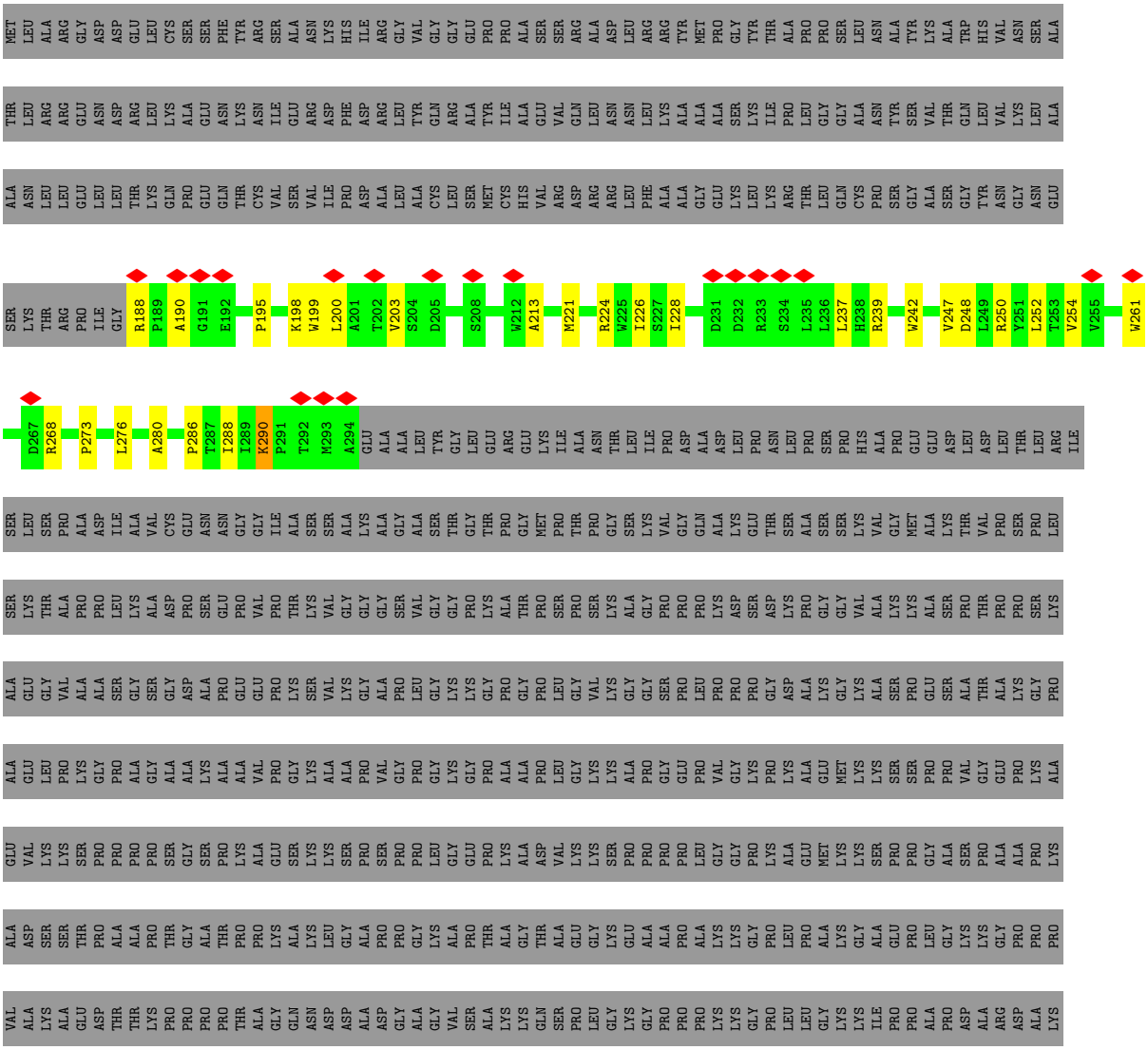
Chain G5:





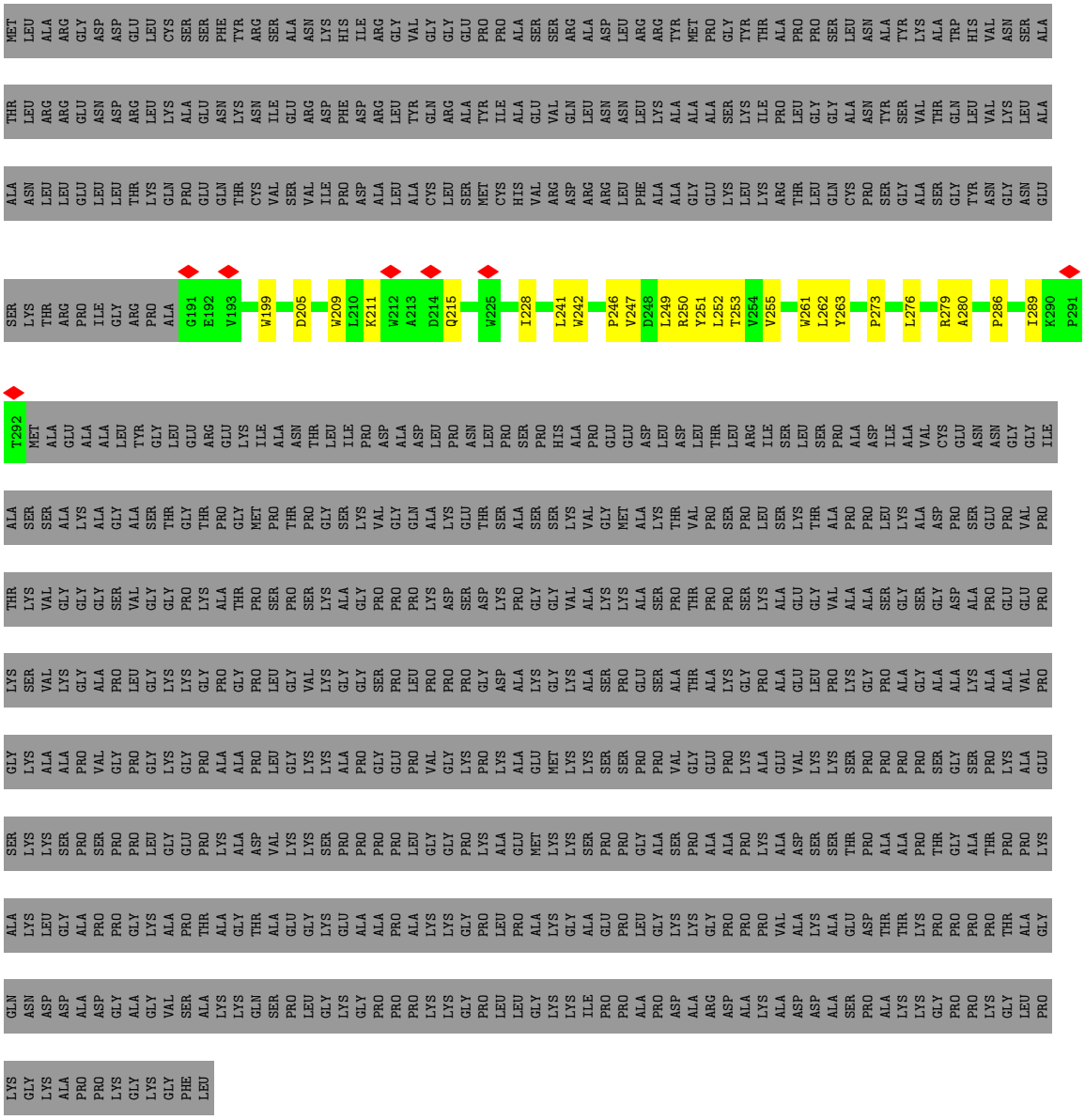
• Molecule 12: PRP, TGME49_291880

Chain G6:



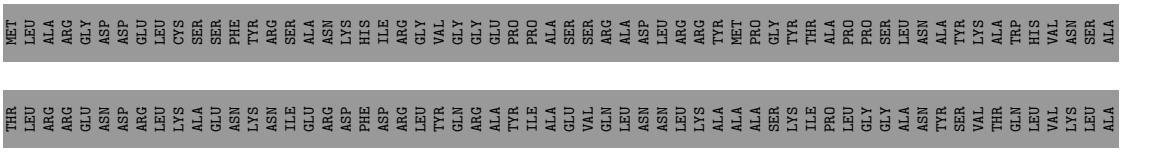
• Molecule 12: PRP, TGME49_291880

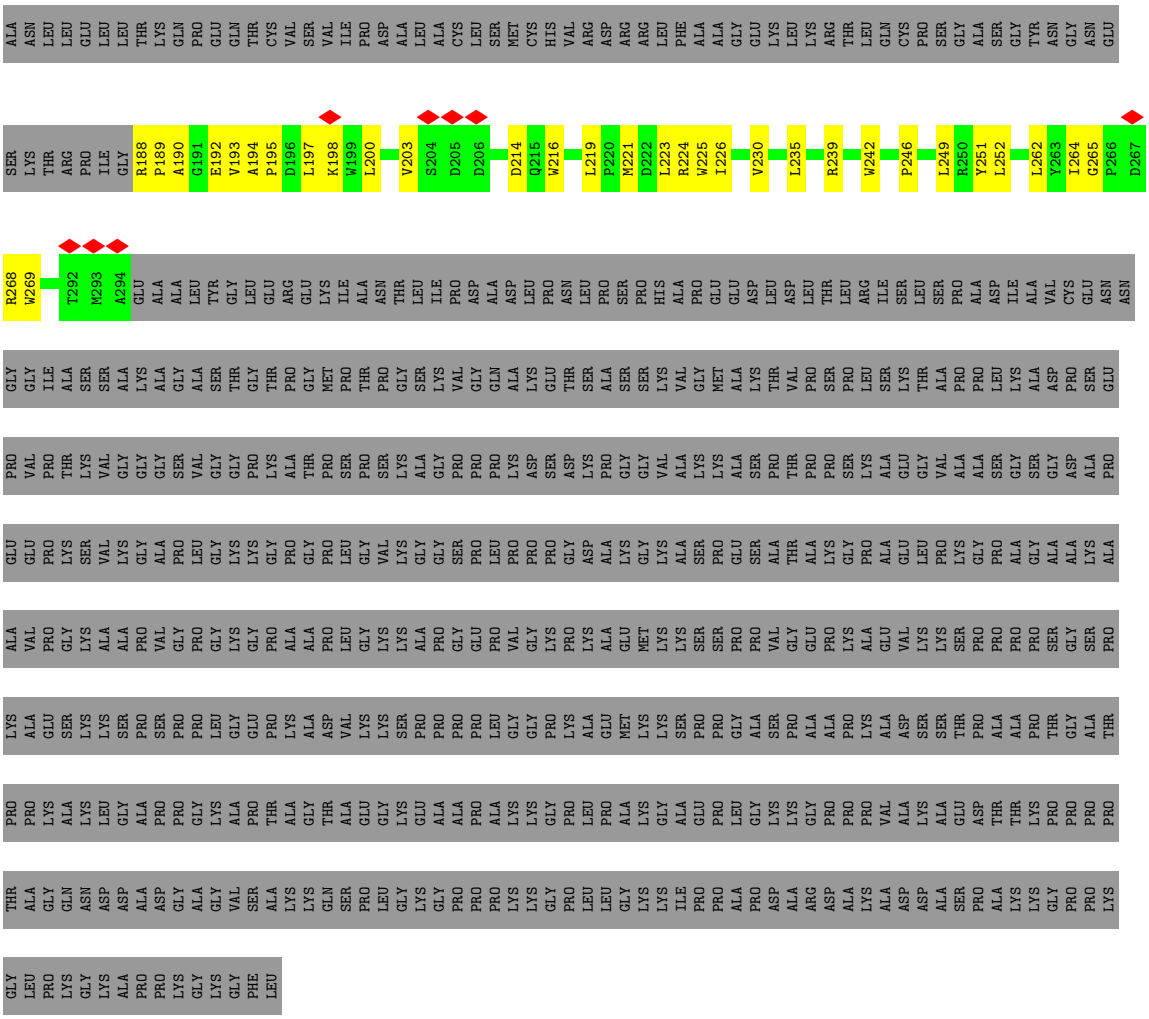
Chain G7:



• Molecule 12: PRP, TGME49_291880

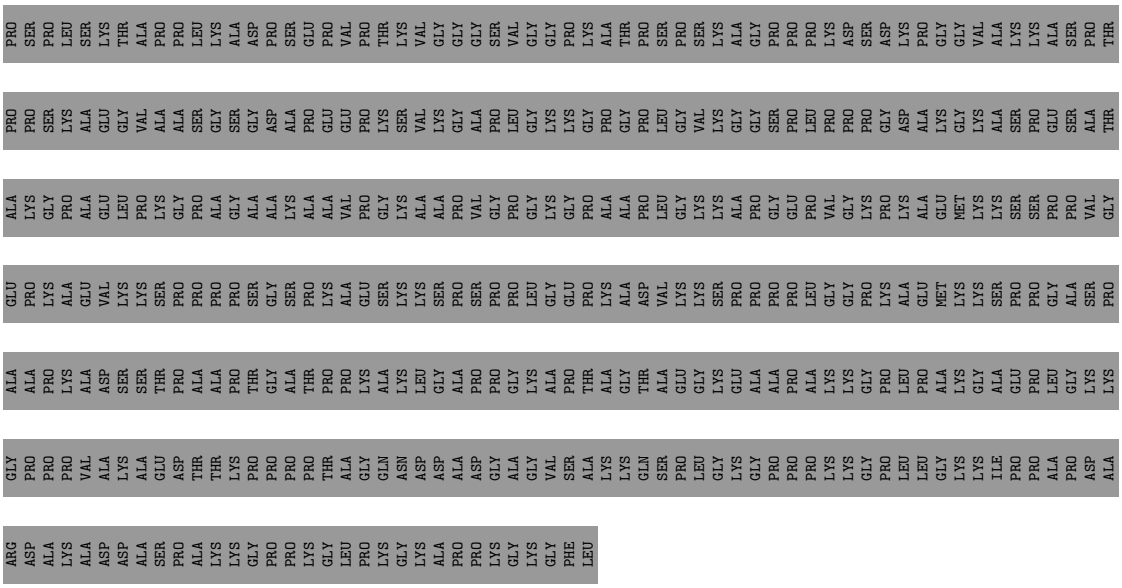
Chain G8:





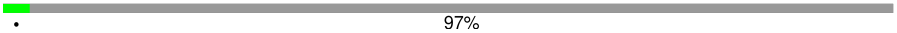
• Molecule 12: PRP, TGME49_291880

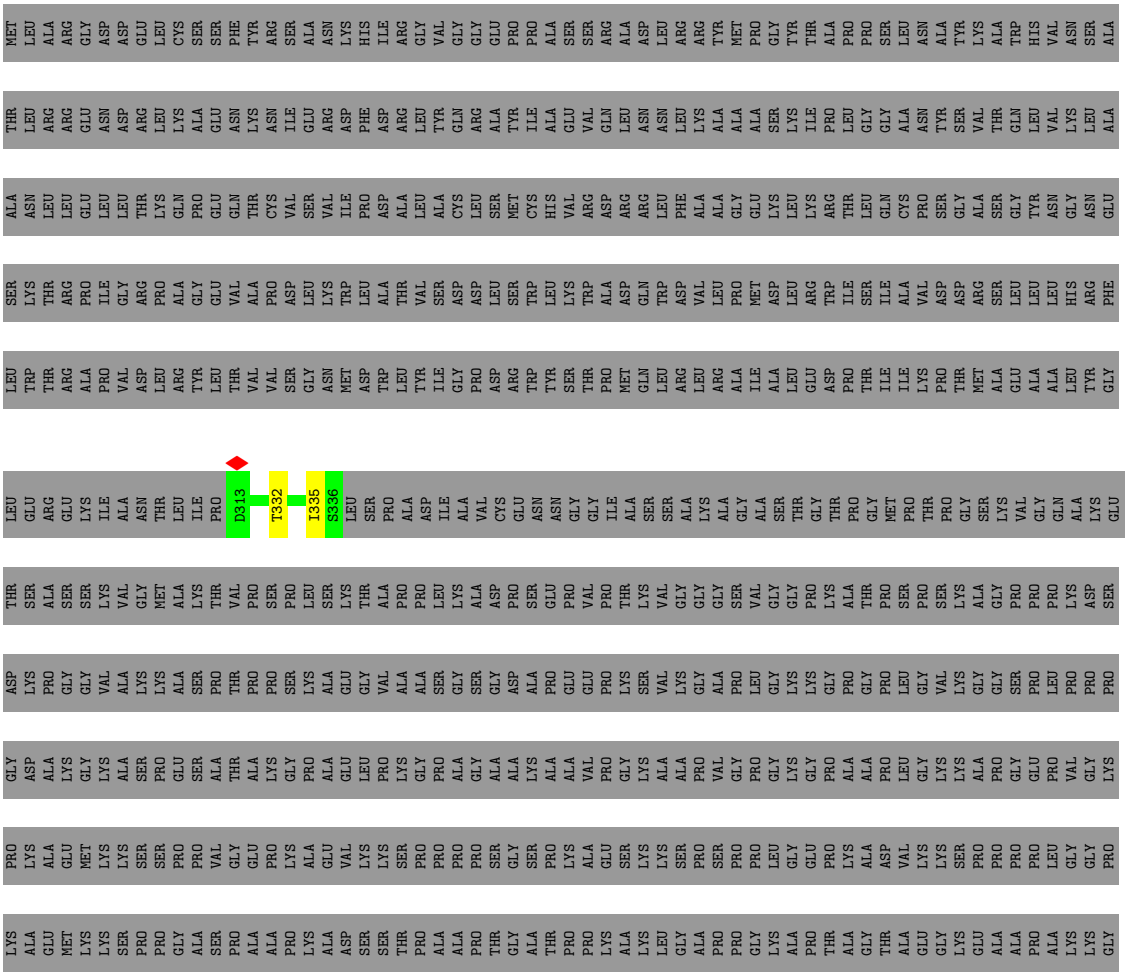
Chain G9:

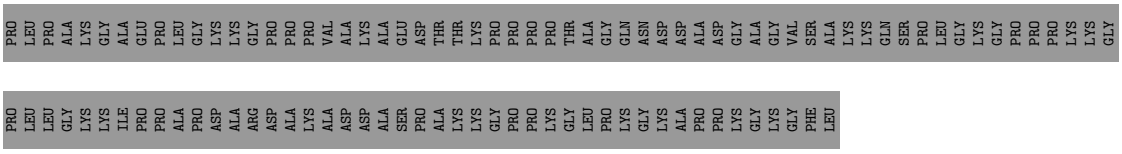


• Molecule 12: PRP, TGME49_291880

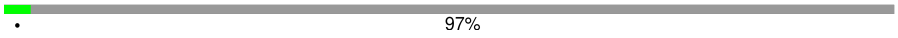
Chain H0:

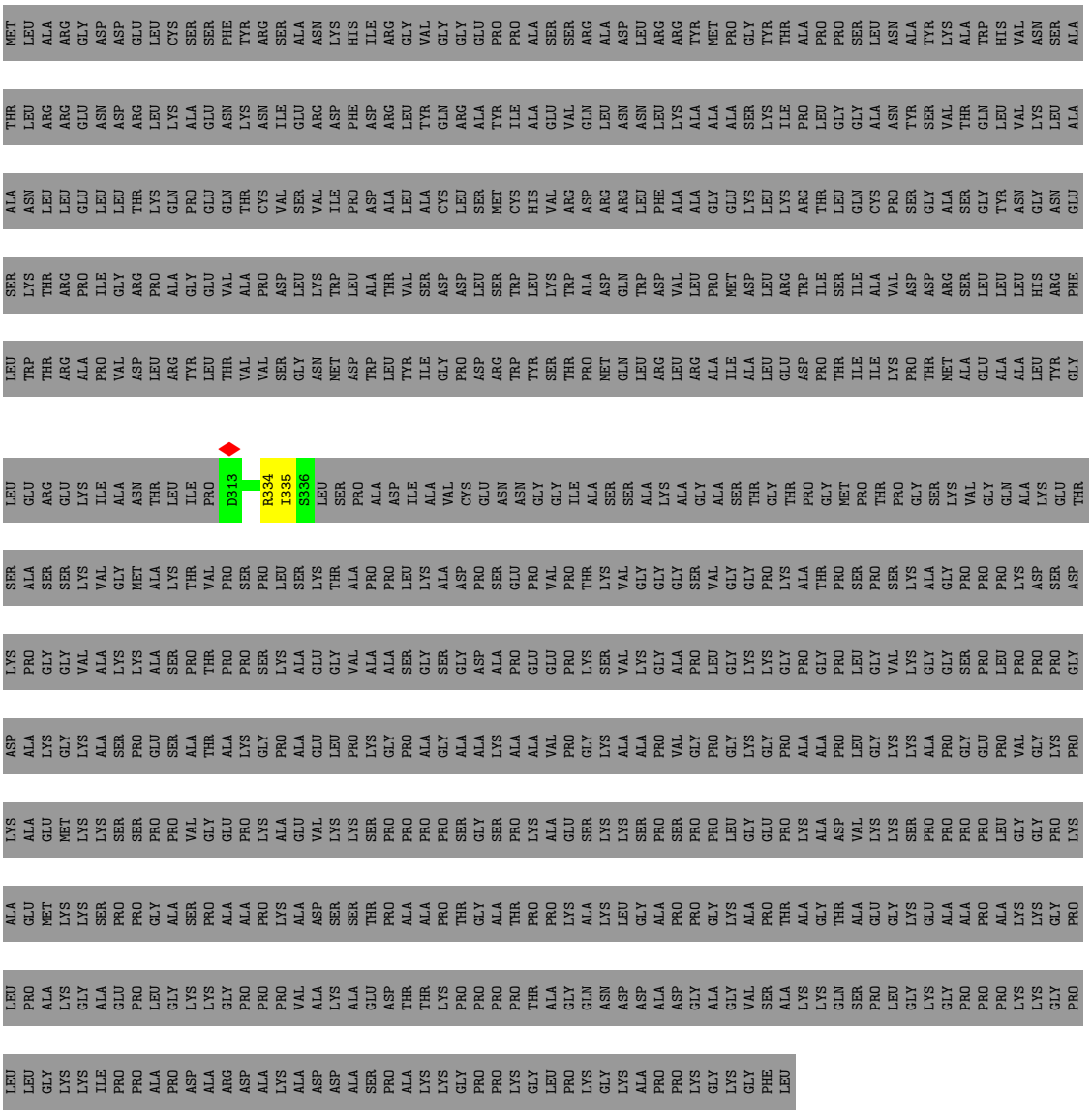




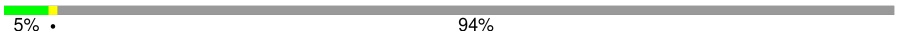


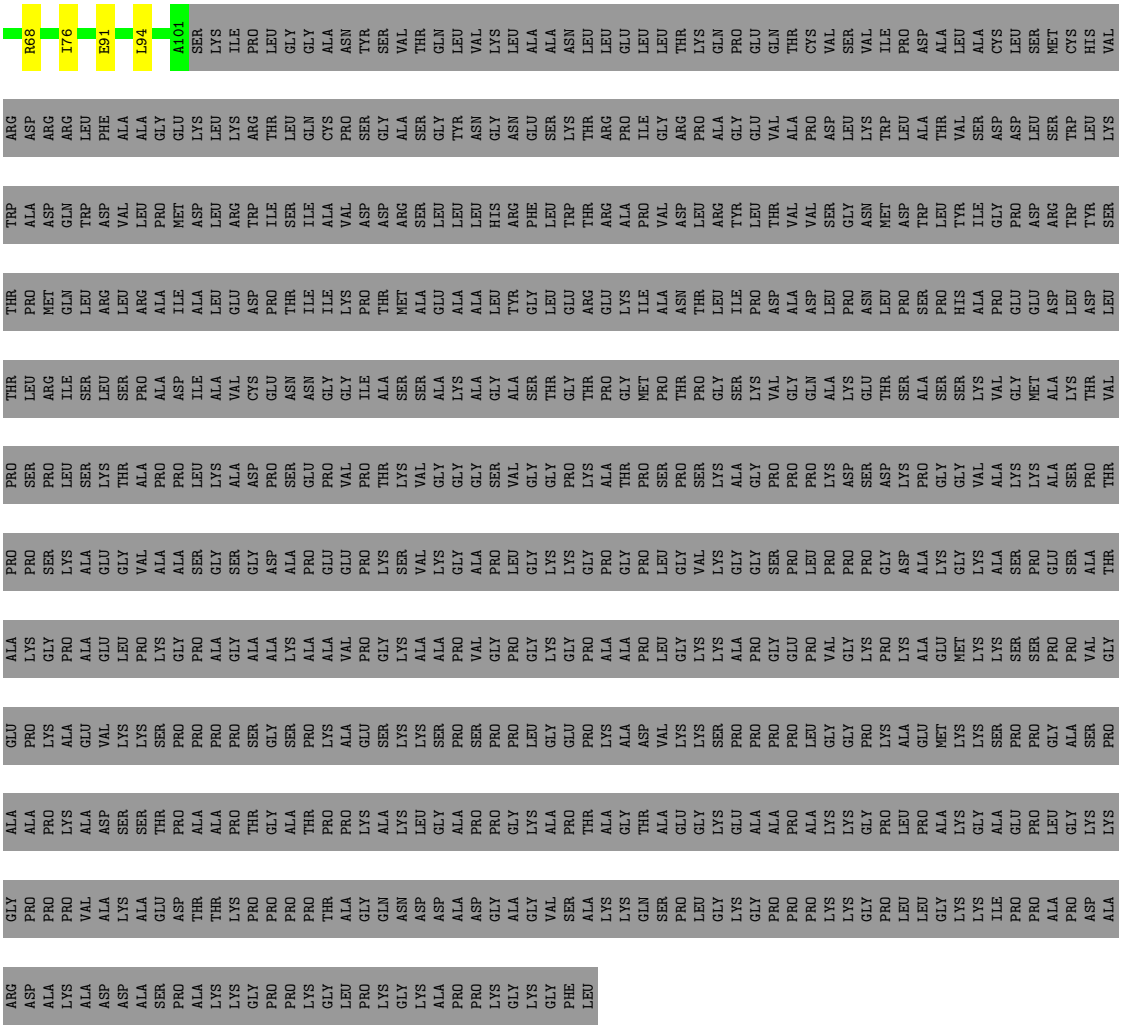
• Molecule 12: PRP, TGME49_291880

Chain H1: 



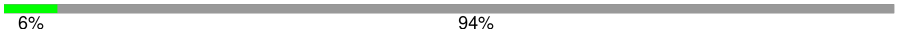
• Molecule 12: PRP, TGME49_291880

Chain H2: 



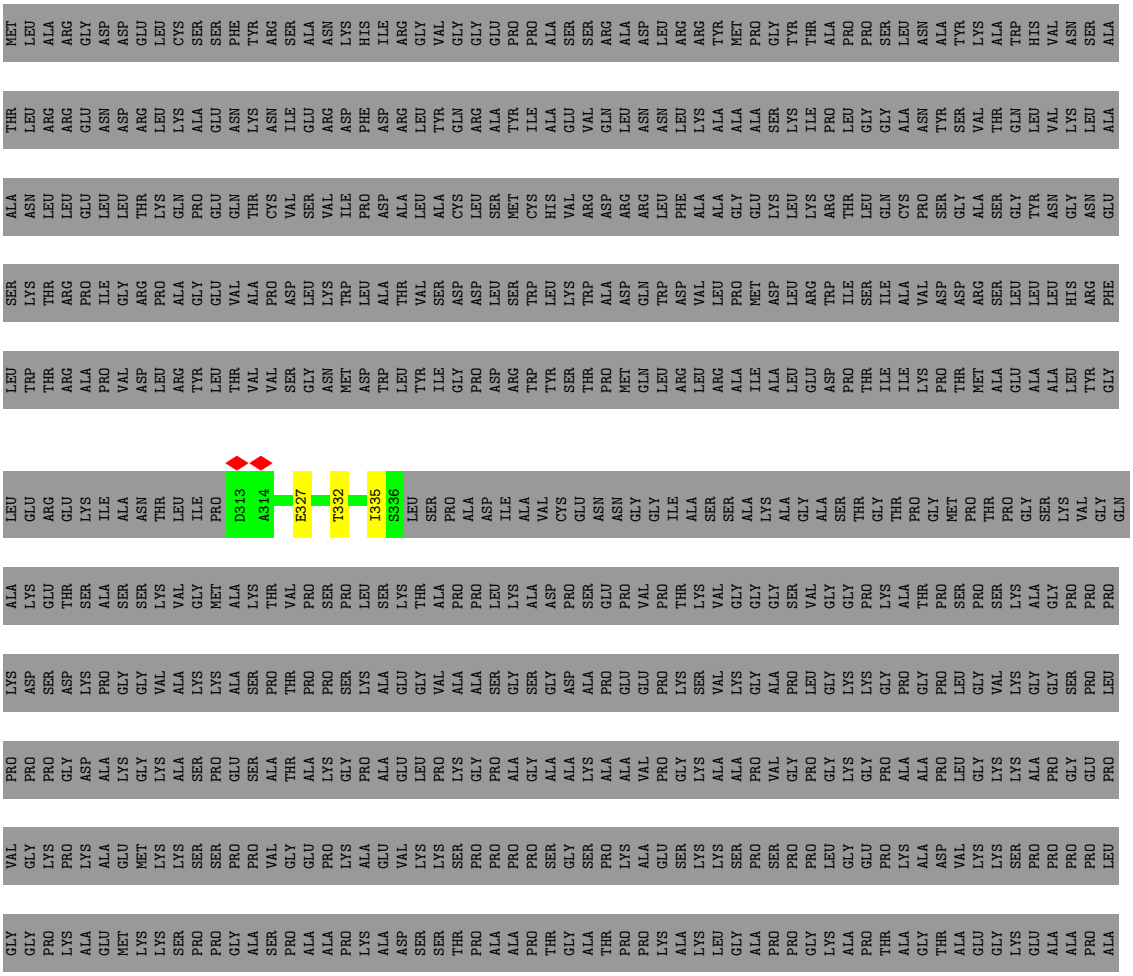
• Molecule 12: PRP, TGME49_291880

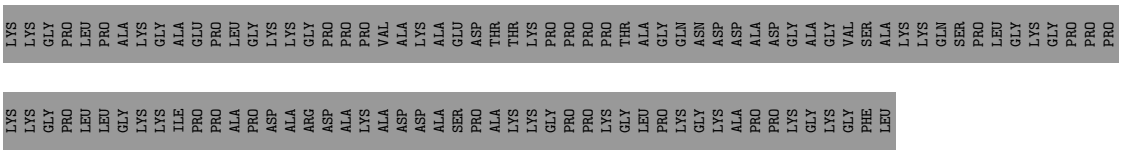
Chain H3:



• Molecule 12: PRP, TGME49_291880

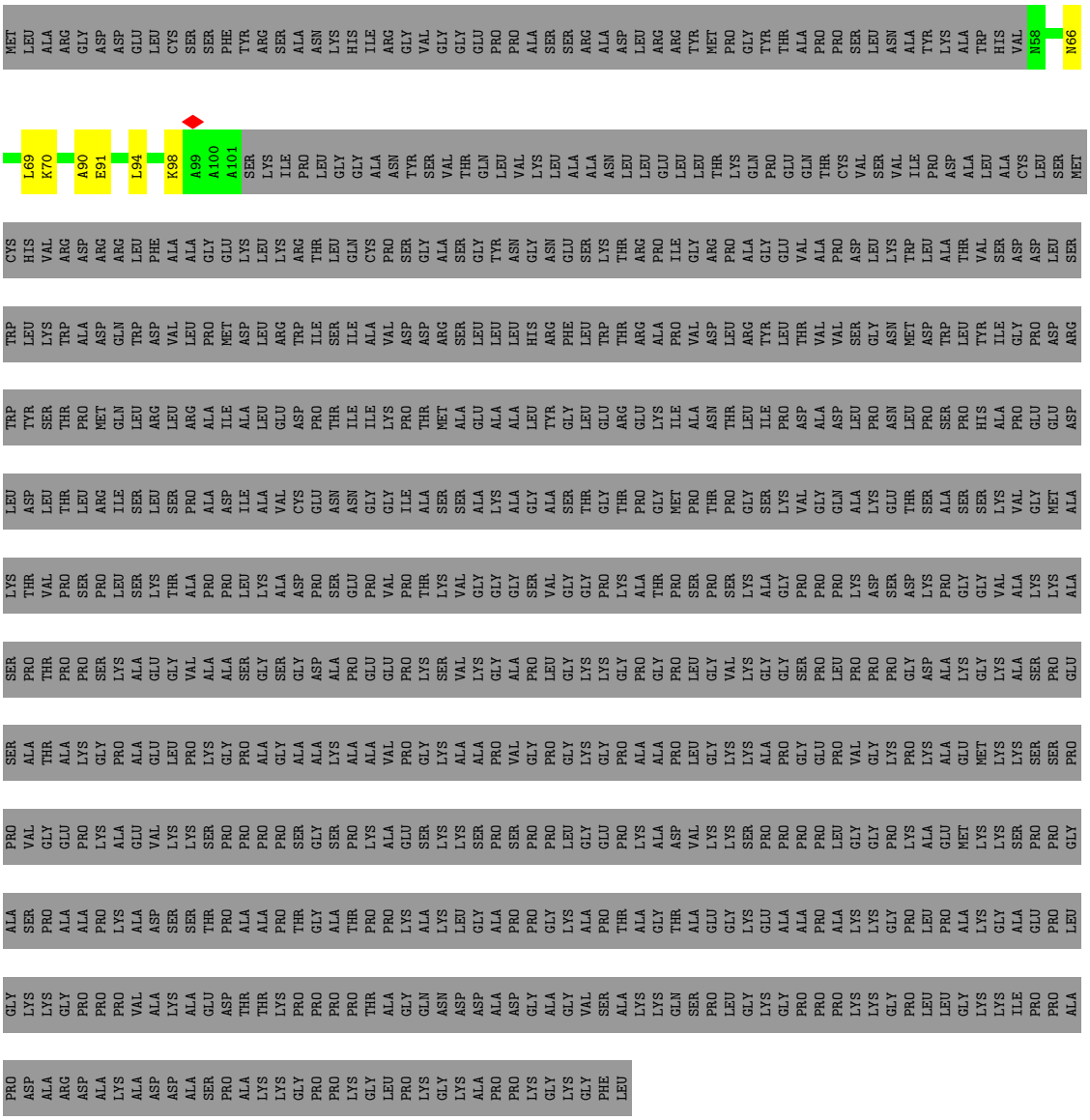
Chain H4:





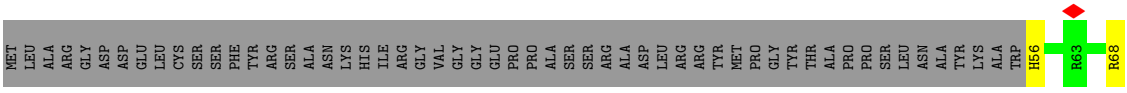
• Molecule 12: PRP, TGME49_291880

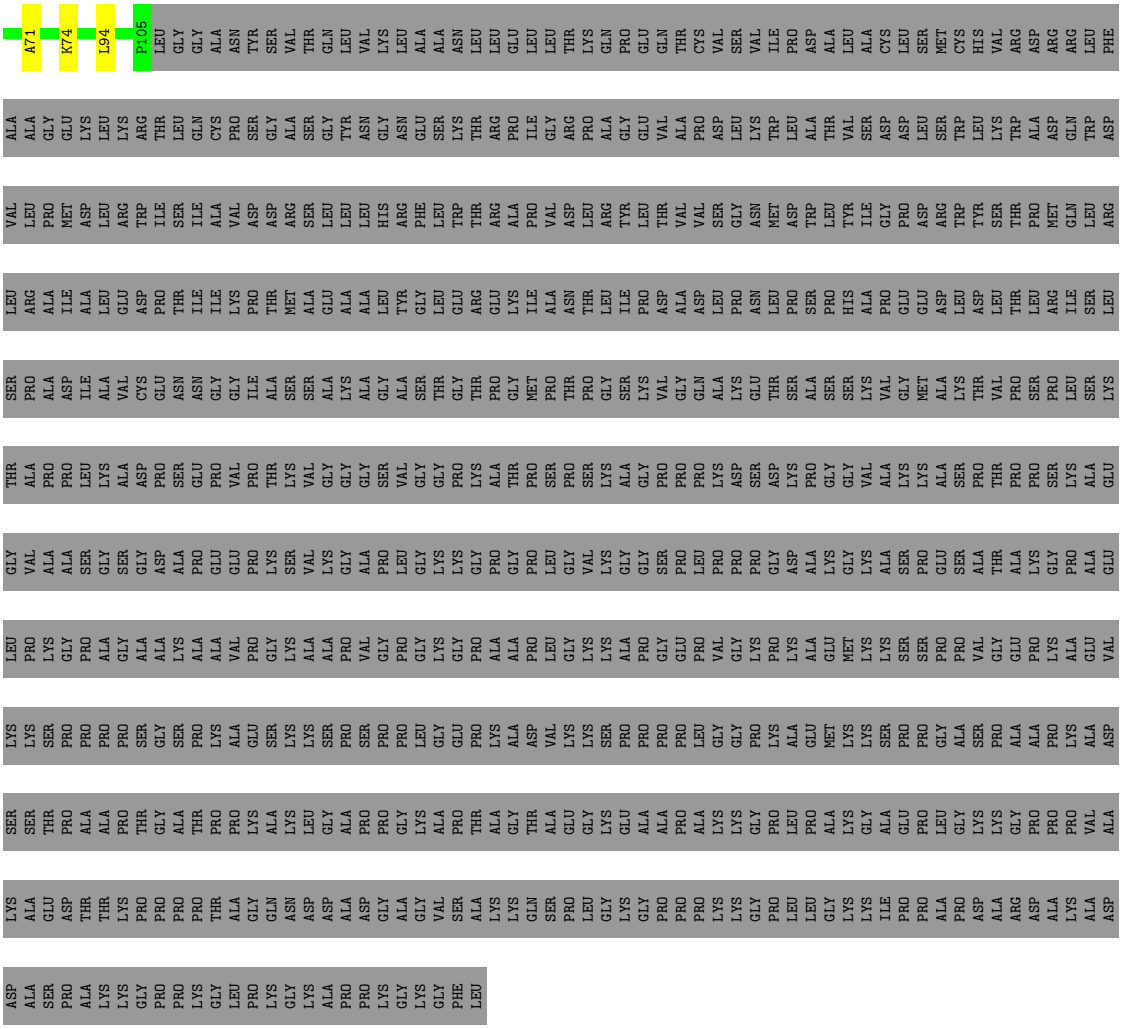
Chain H5: 5% 94%



• Molecule 12: PRP, TGME49_291880

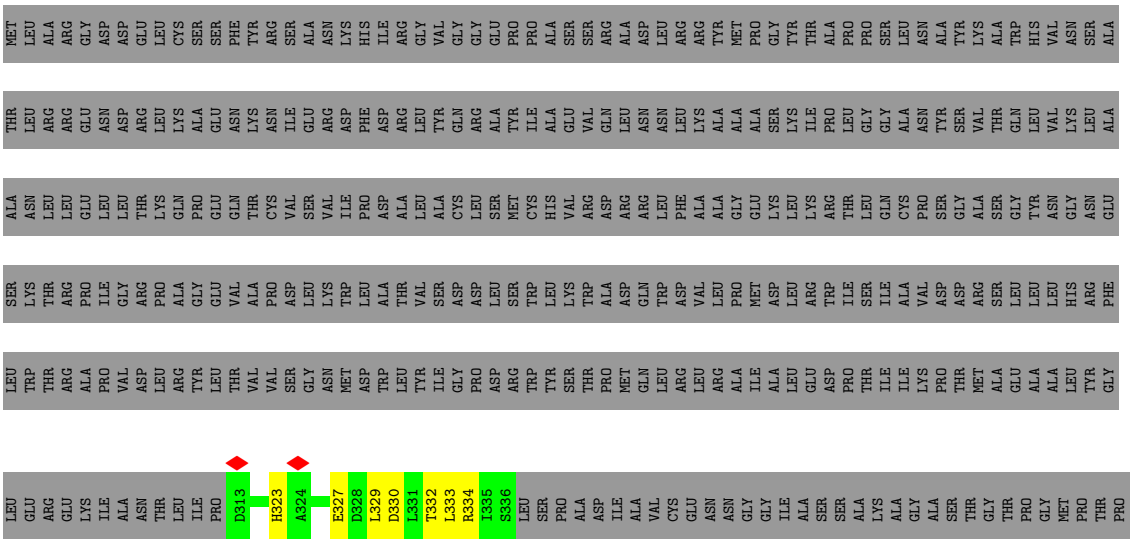
Chain H6: 6% 94%

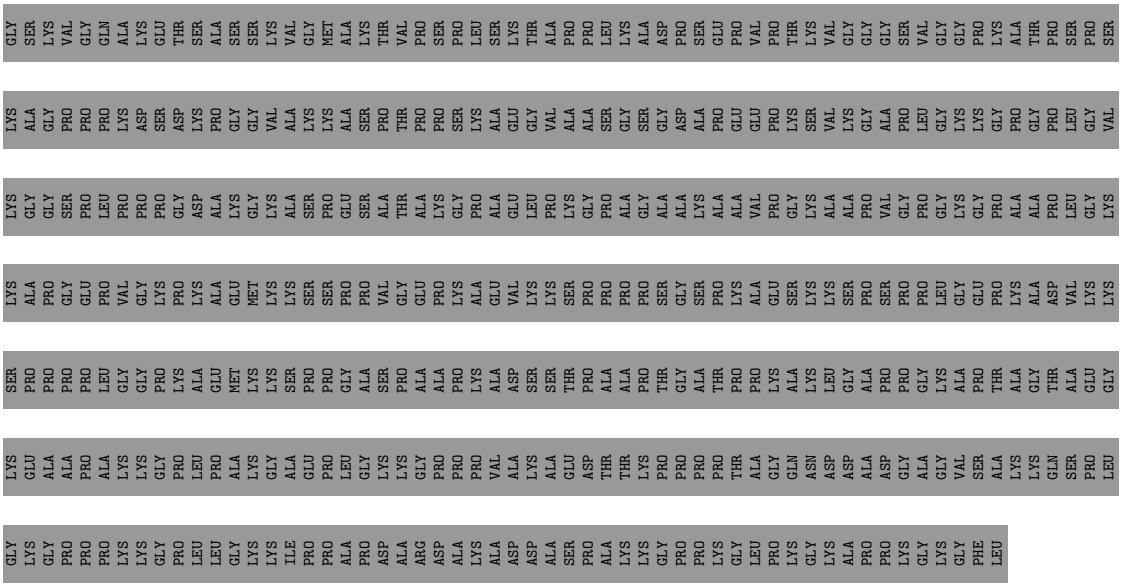




• Molecule 12: PRP, TGME49_291880

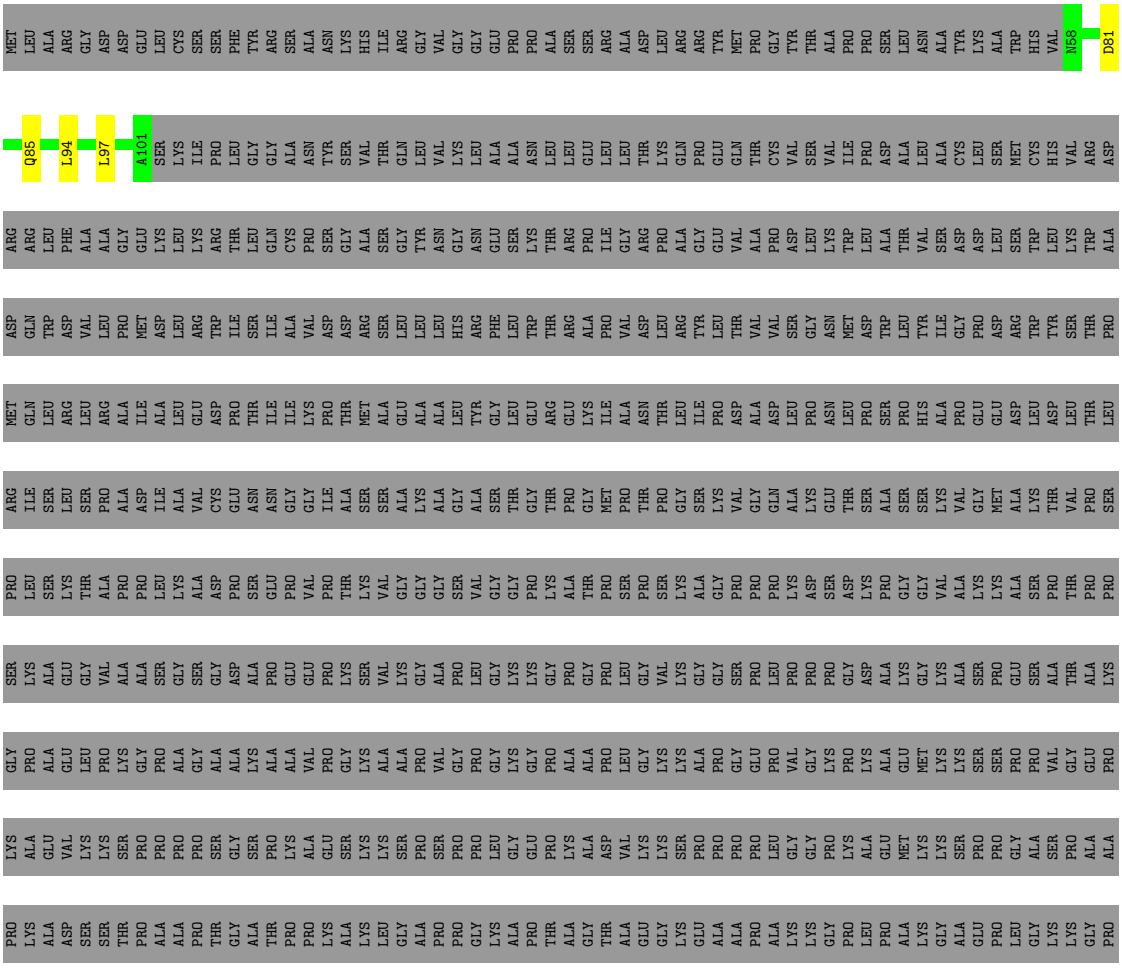
Chain H7:

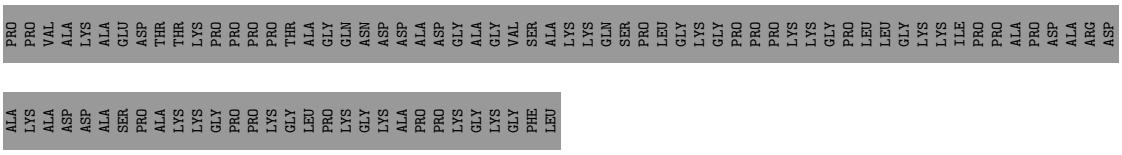




• Molecule 12: PRP, TGME49_291880

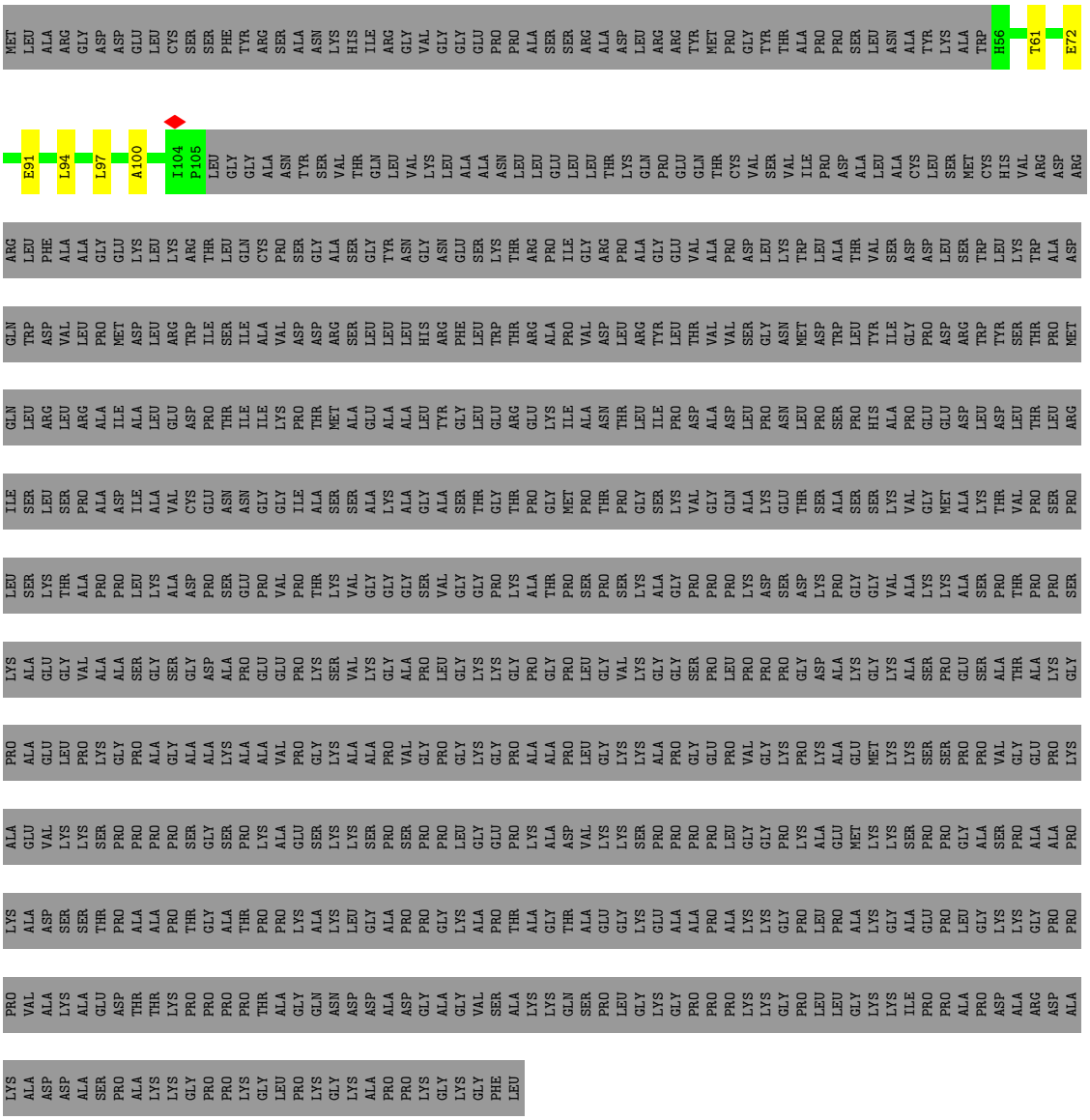
Chain H8: 5% 94%





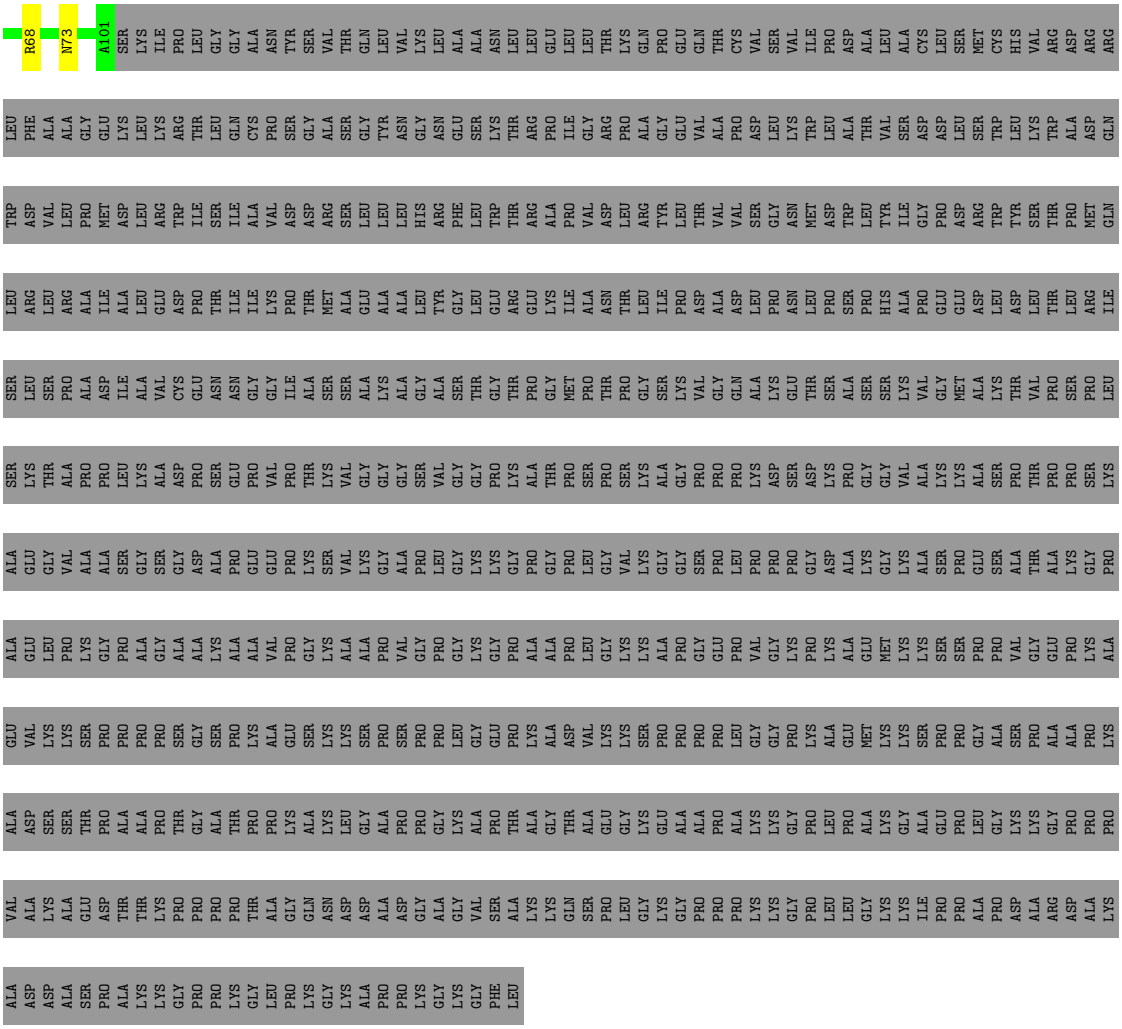
• Molecule 12: PRP, TGME49_291880

Chain H9: 6% 94%



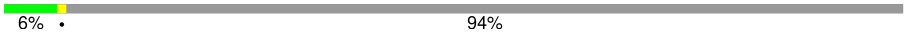
• Molecule 12: PRP, TGME49_291880

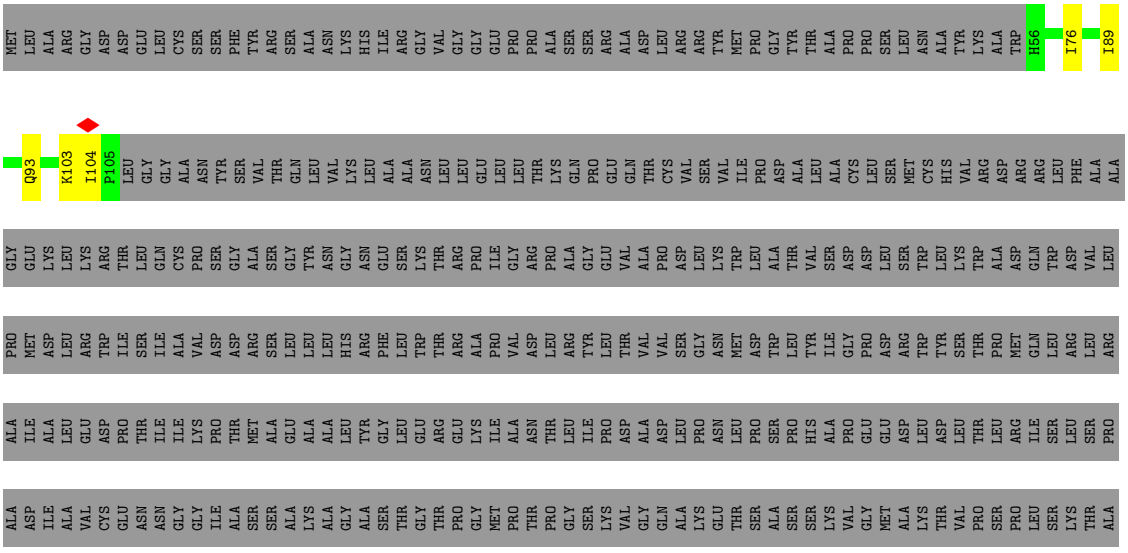
Chain I1: 5% 94%

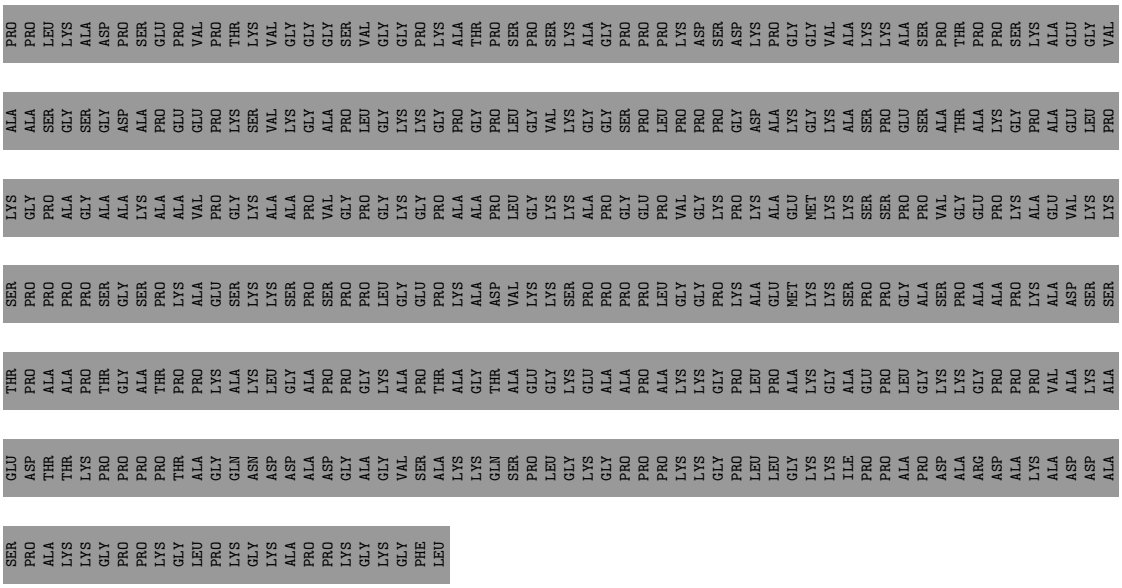


• Molecule 12: PRP, TGME49_291880

Chain I2:

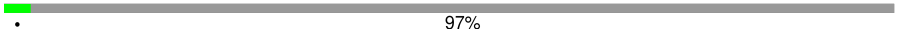


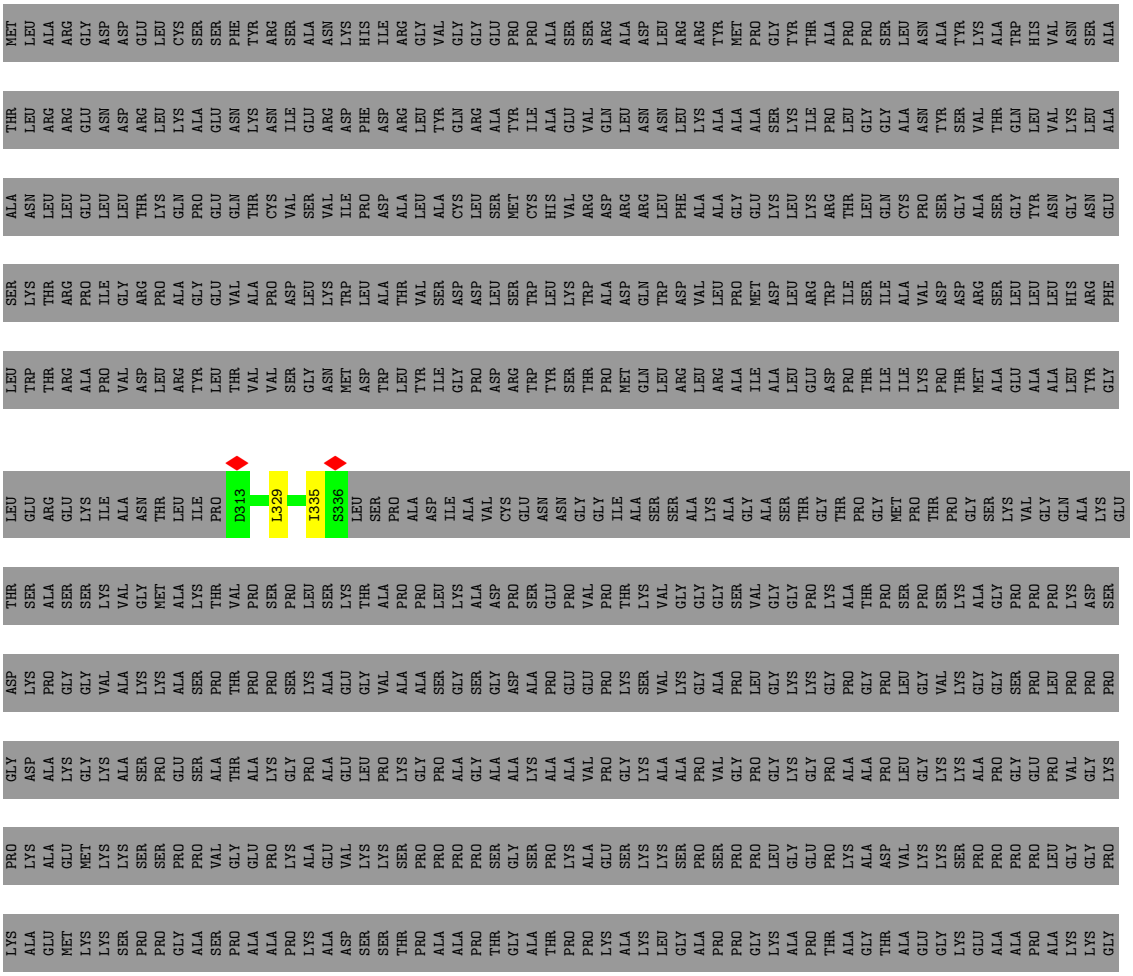


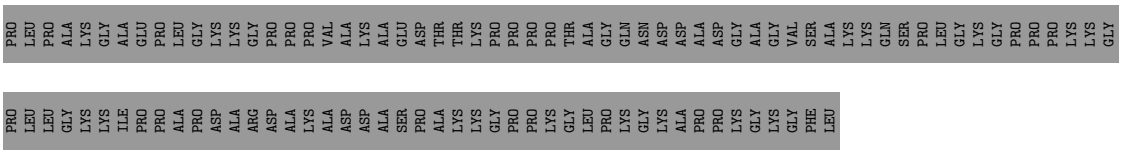


• Molecule 12: PRP, TGME49_291880

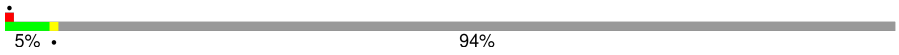
Chain I3:

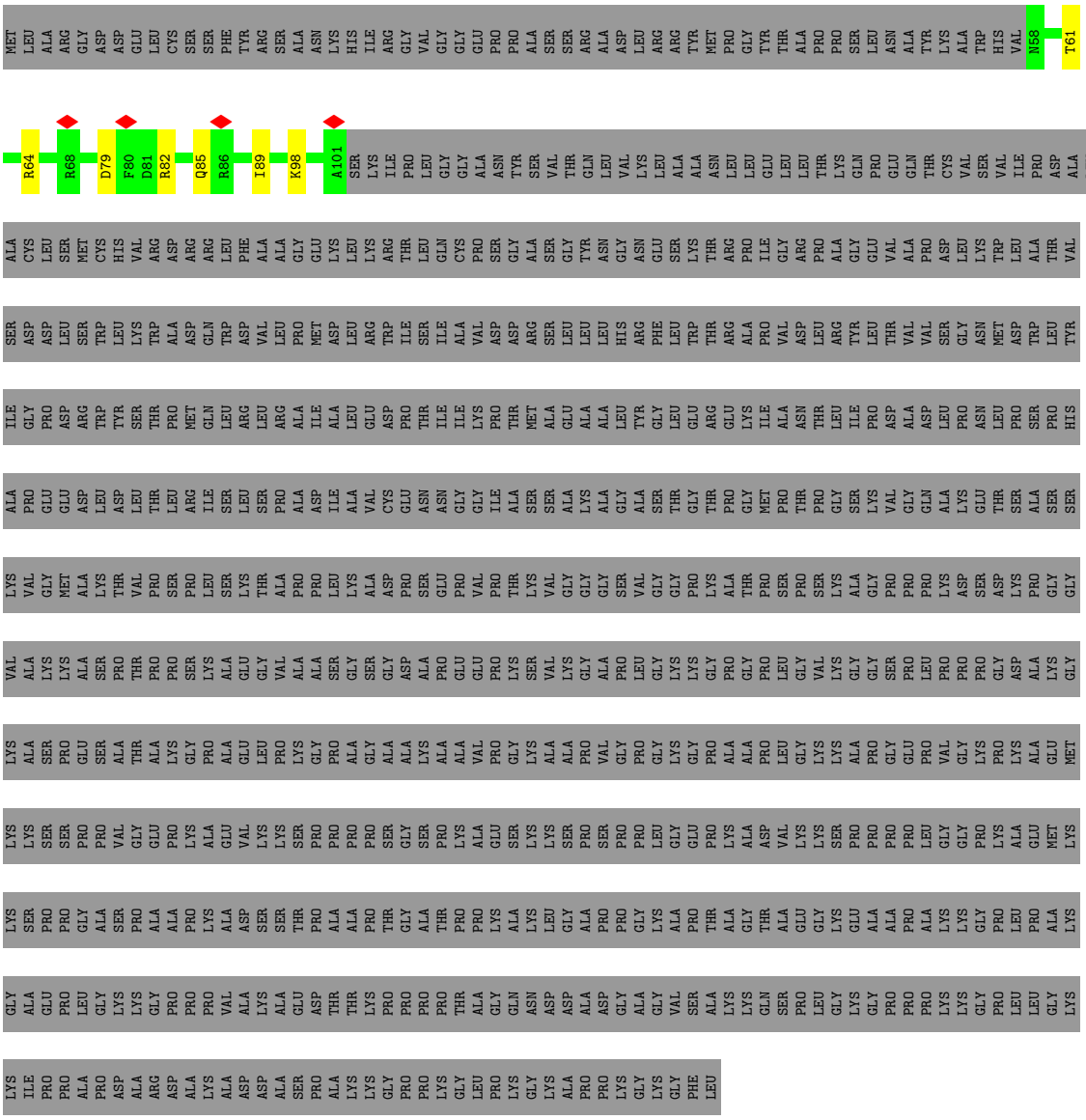




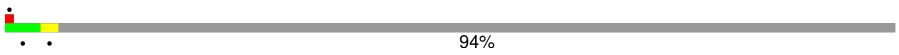


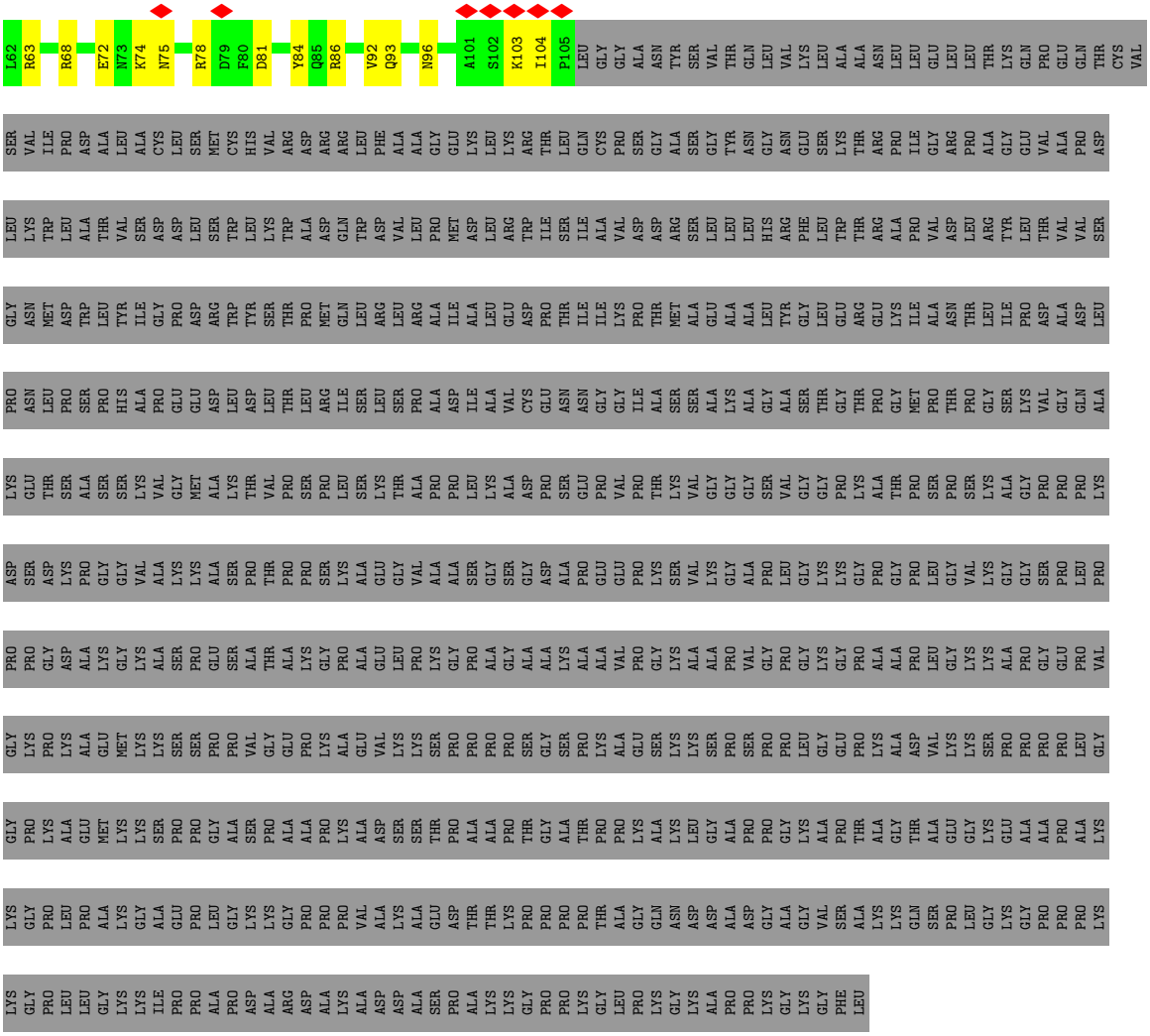
• Molecule 12: PRP, TGME49_291880

Chain I4: 



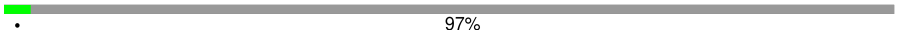
• Molecule 12: PRP, TGME49_291880

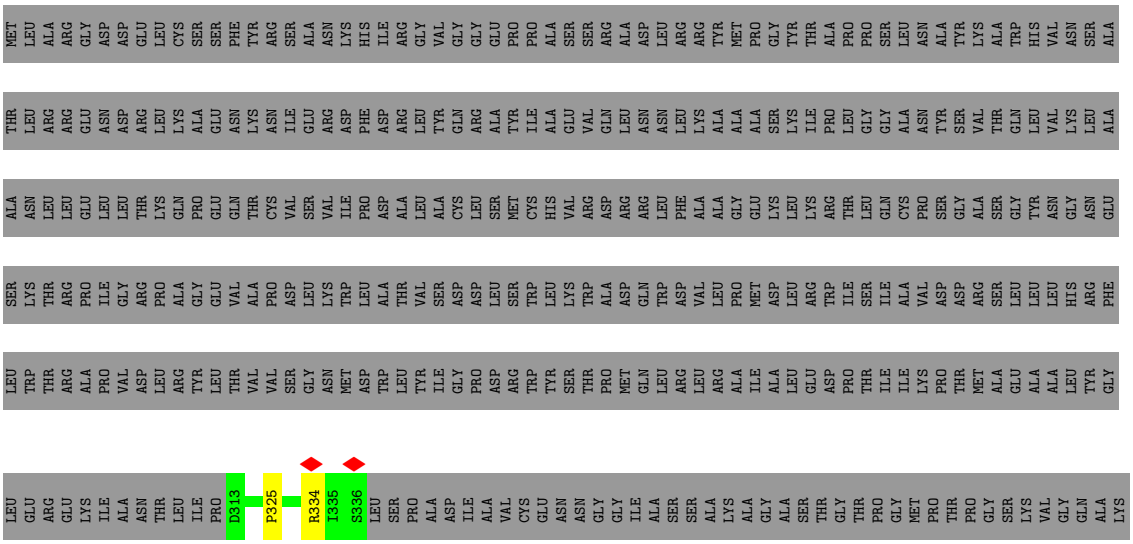
Chain I5: 

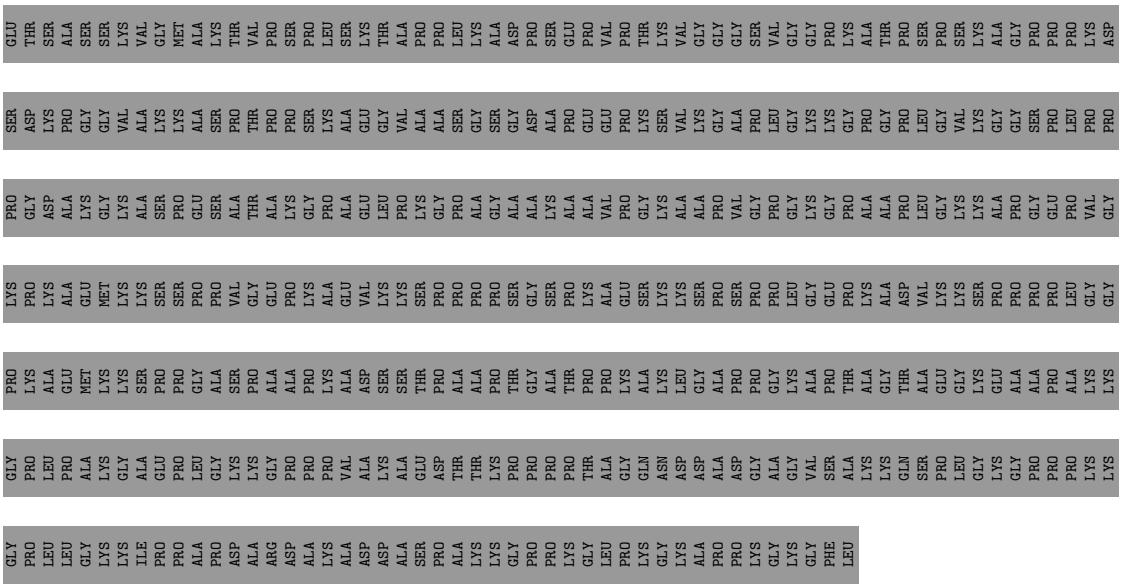


• Molecule 12: PRP, TGME49_291880

Chain I6:

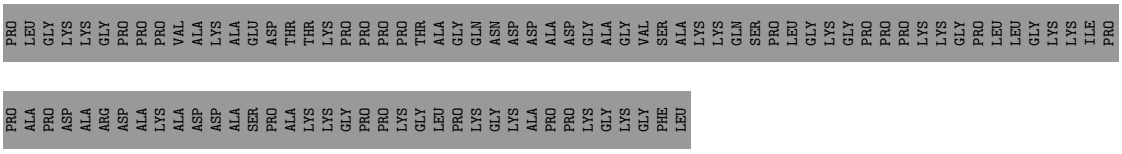






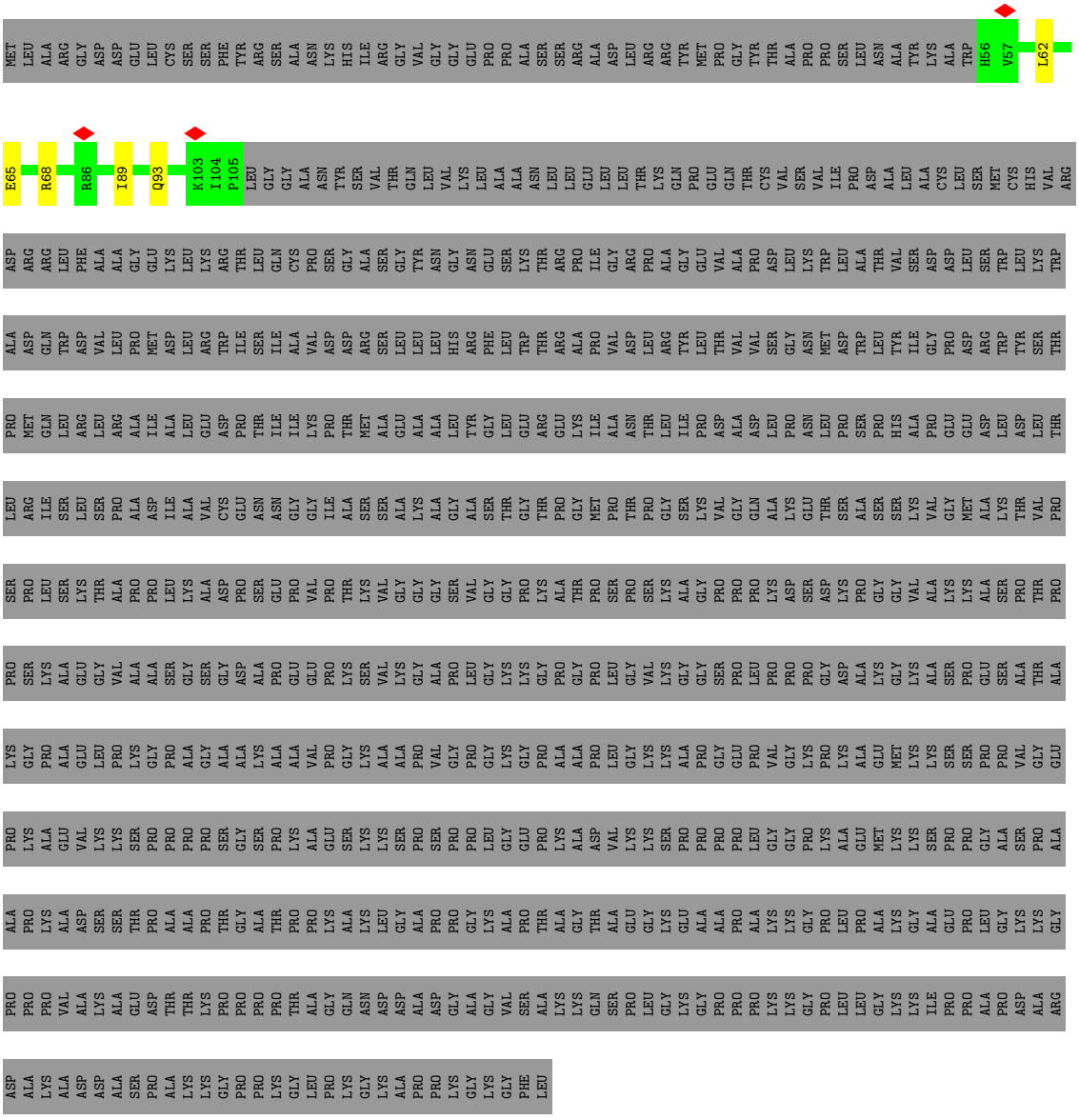
• Molecule 12: PRP, TGME49_291880

Chain I7: 5% 94%



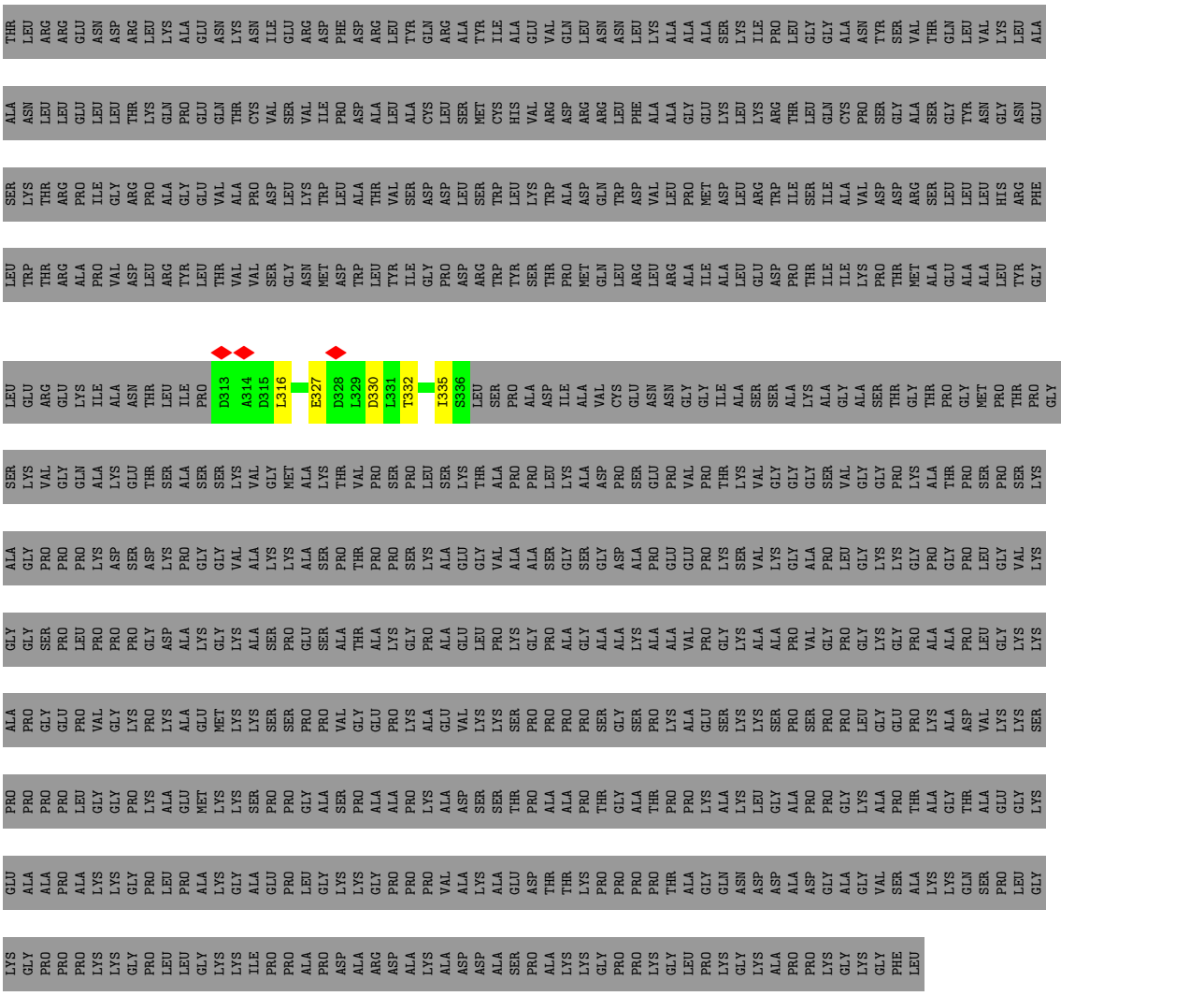
• Molecule 12: PRP, TGME49_291880

Chain I8: 6% 94%



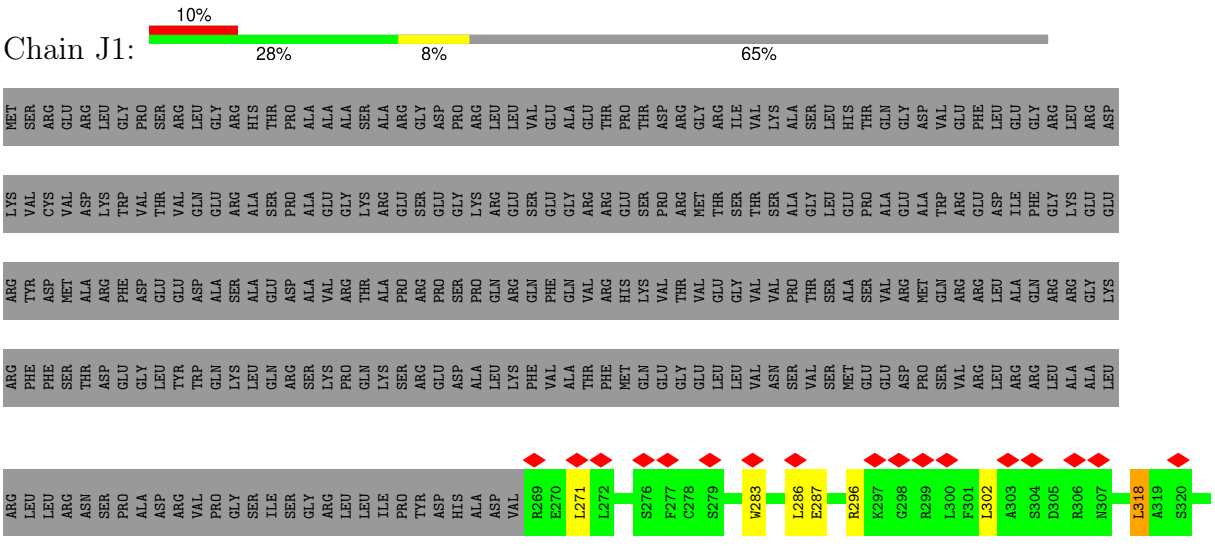
• Molecule 12: PRP, TGME49_291880

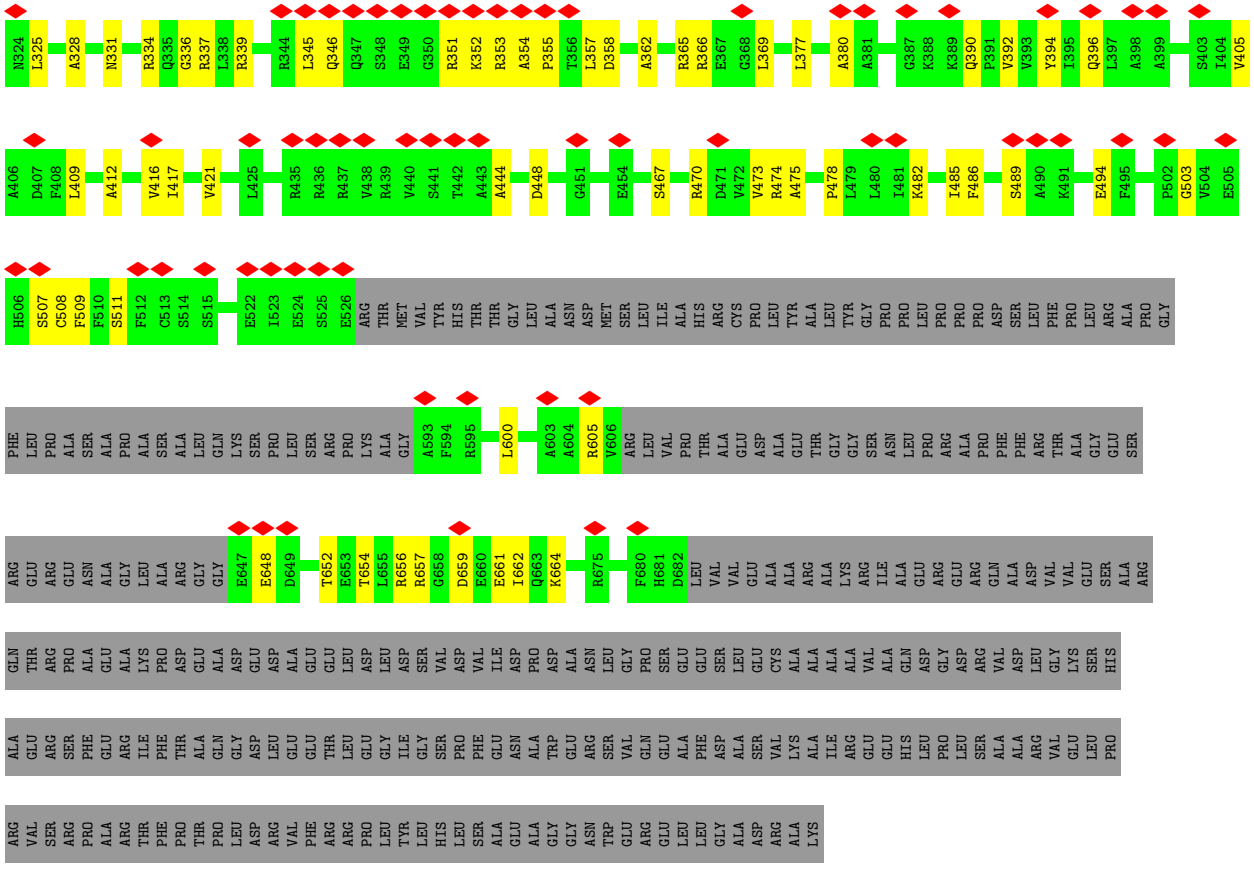
Chain I9: 97%



• Molecule 13: CF5, TGME49_297180

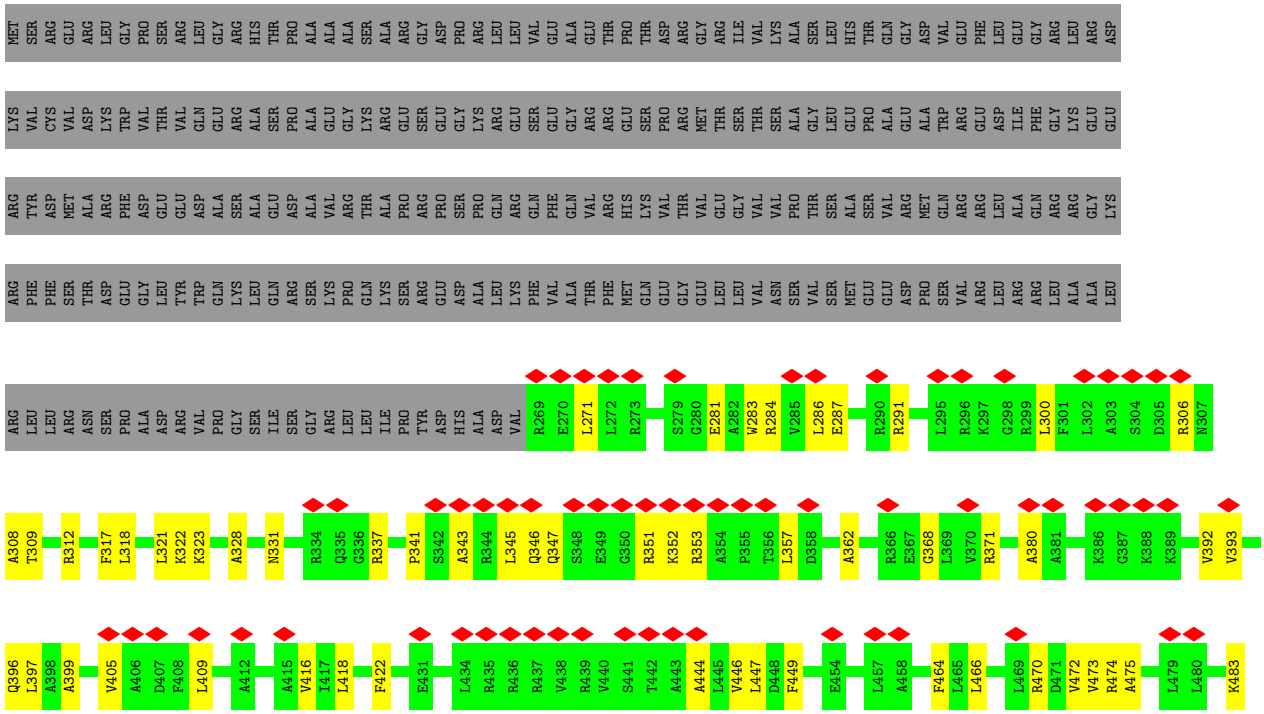
Chain J1:

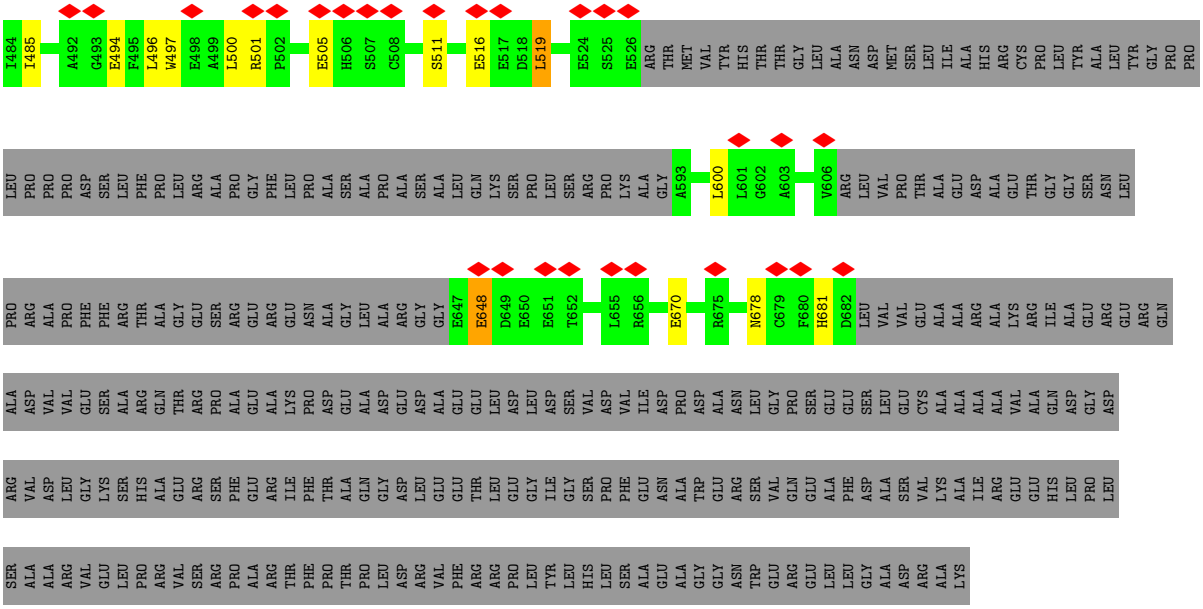




• Molecule 13: CF5, TGME49_297180

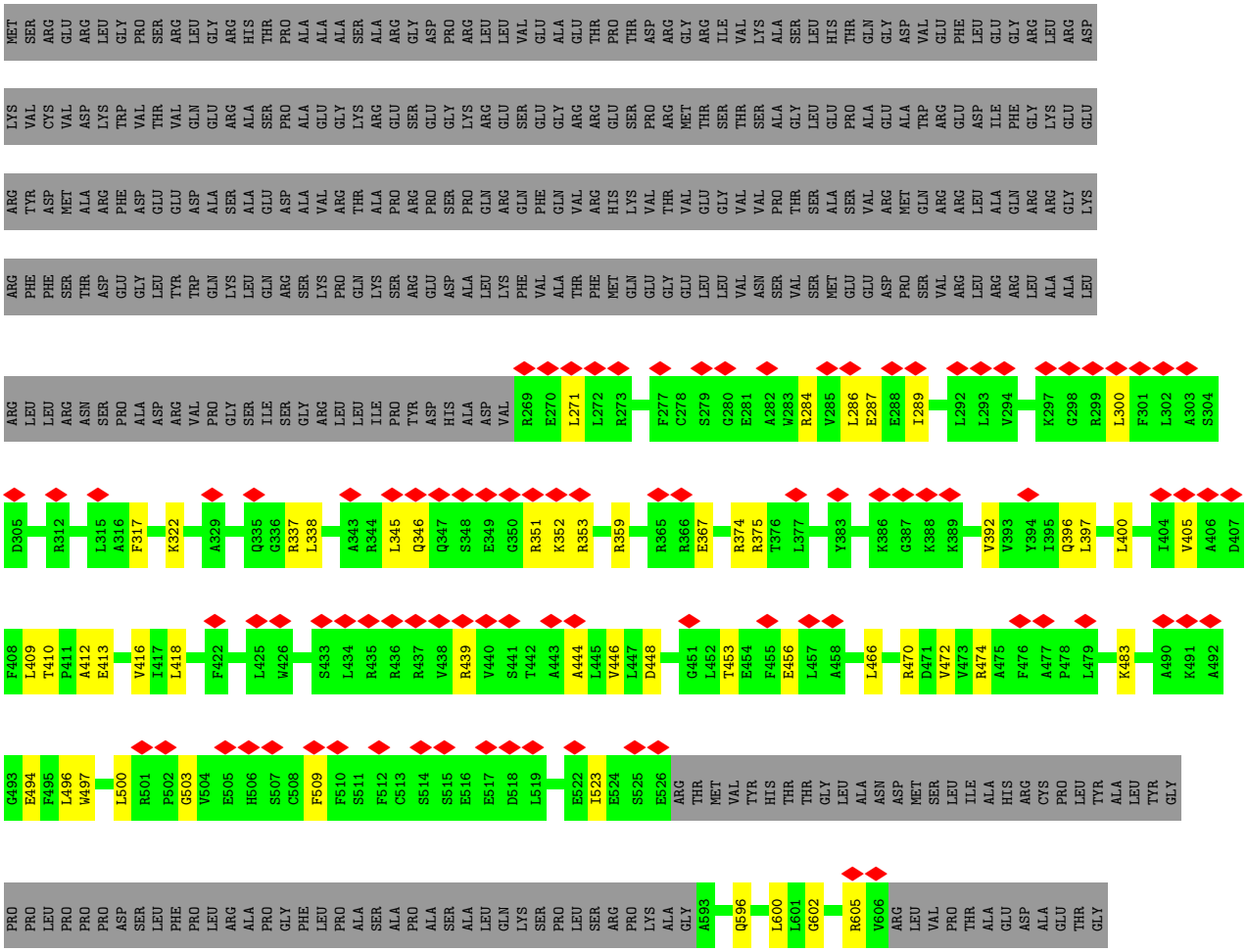
Chain J2:

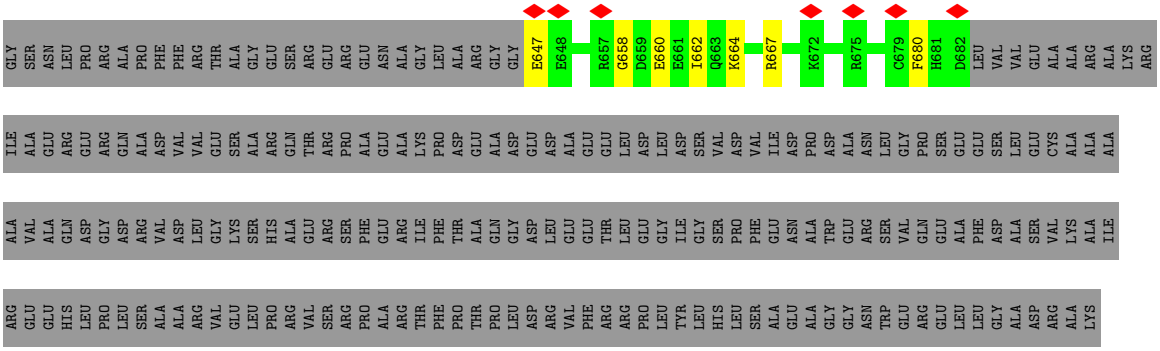




• Molecule 13: CF5, TGME49_297180

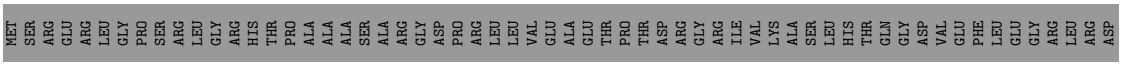
Chain J3:

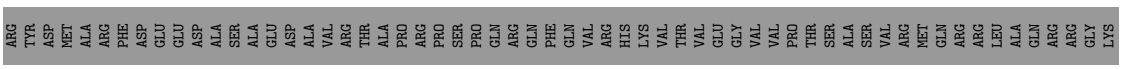


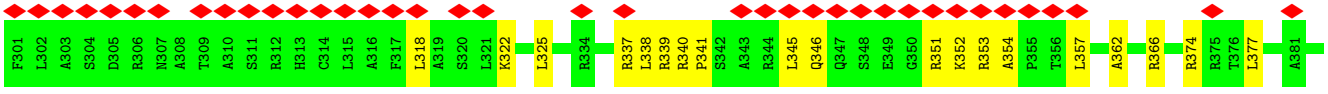


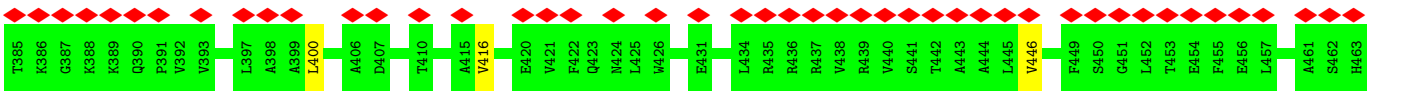
• Molecule 13: CF5, TGME49_297180

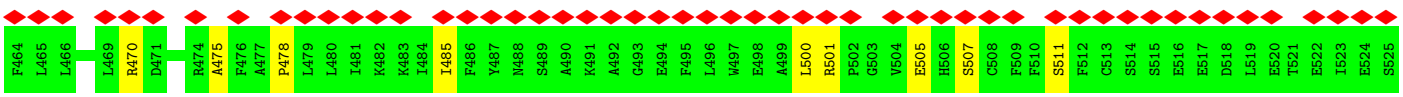
Chain J4:

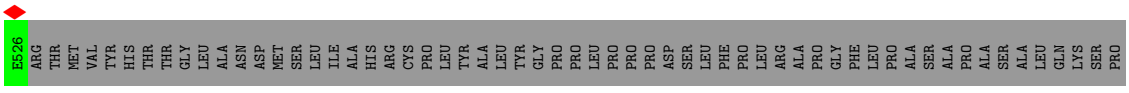


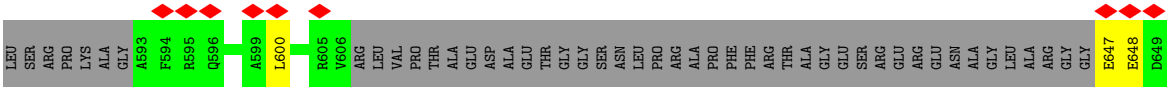


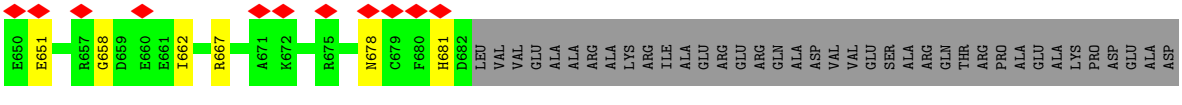


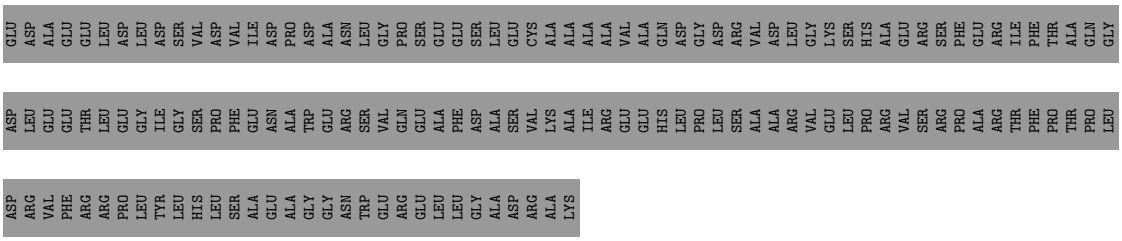






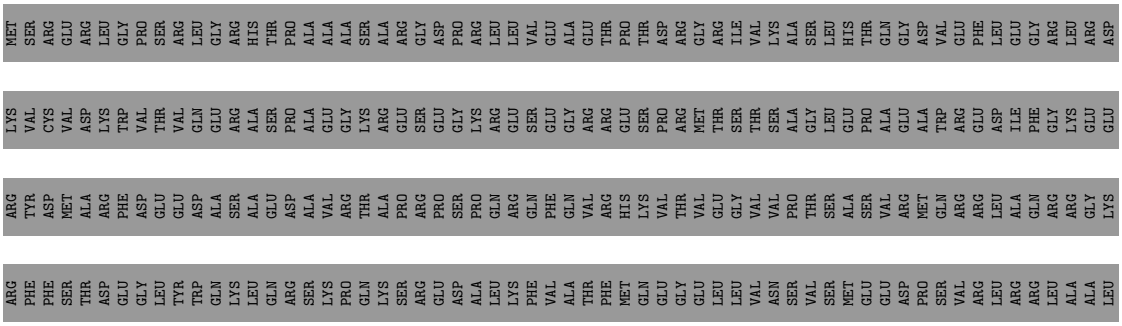


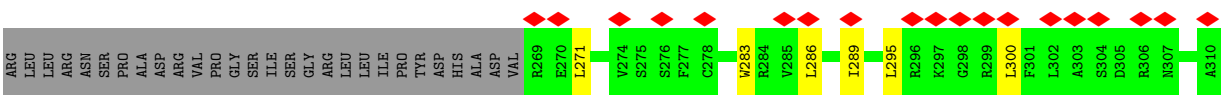


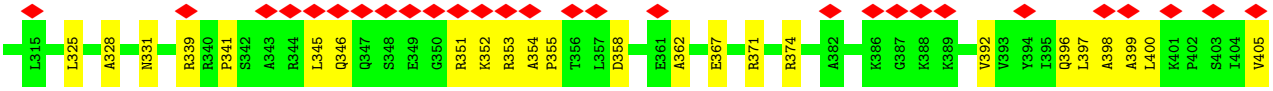


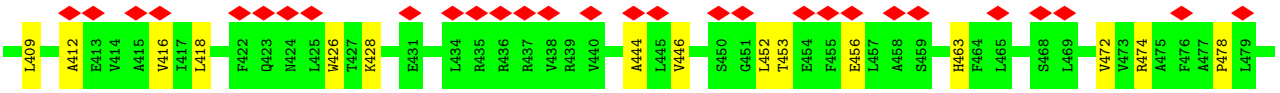
• Molecule 13: CF5, TGME49_297180

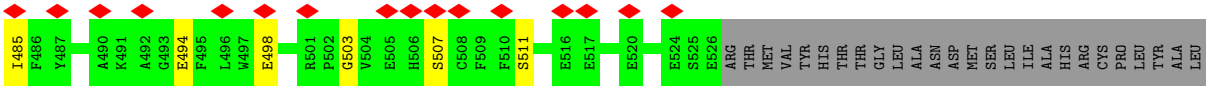
Chain J5:

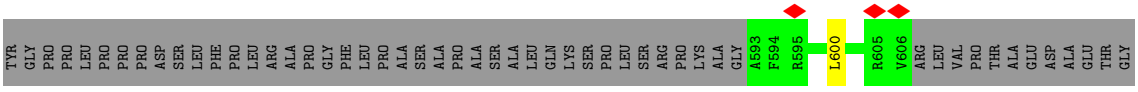


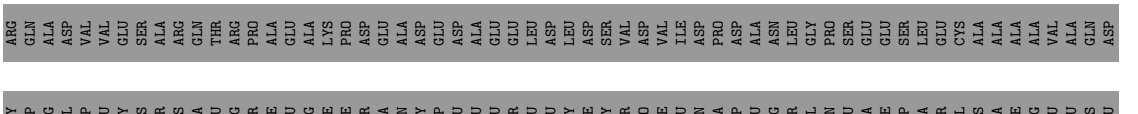


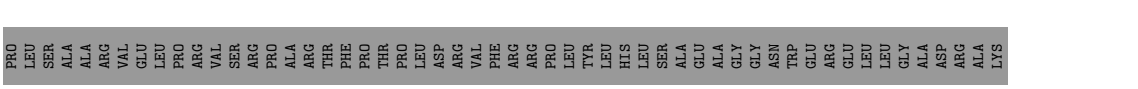






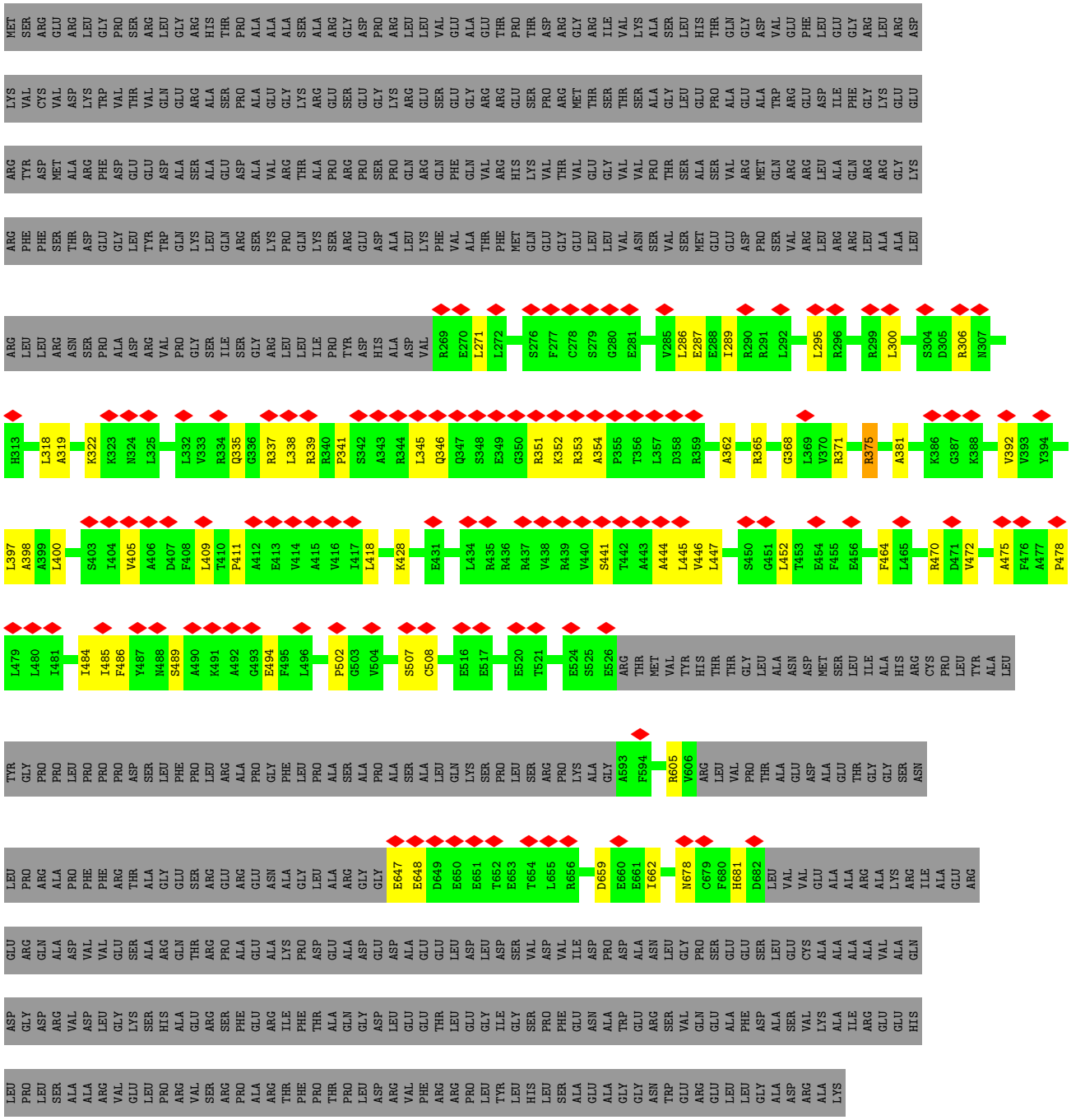






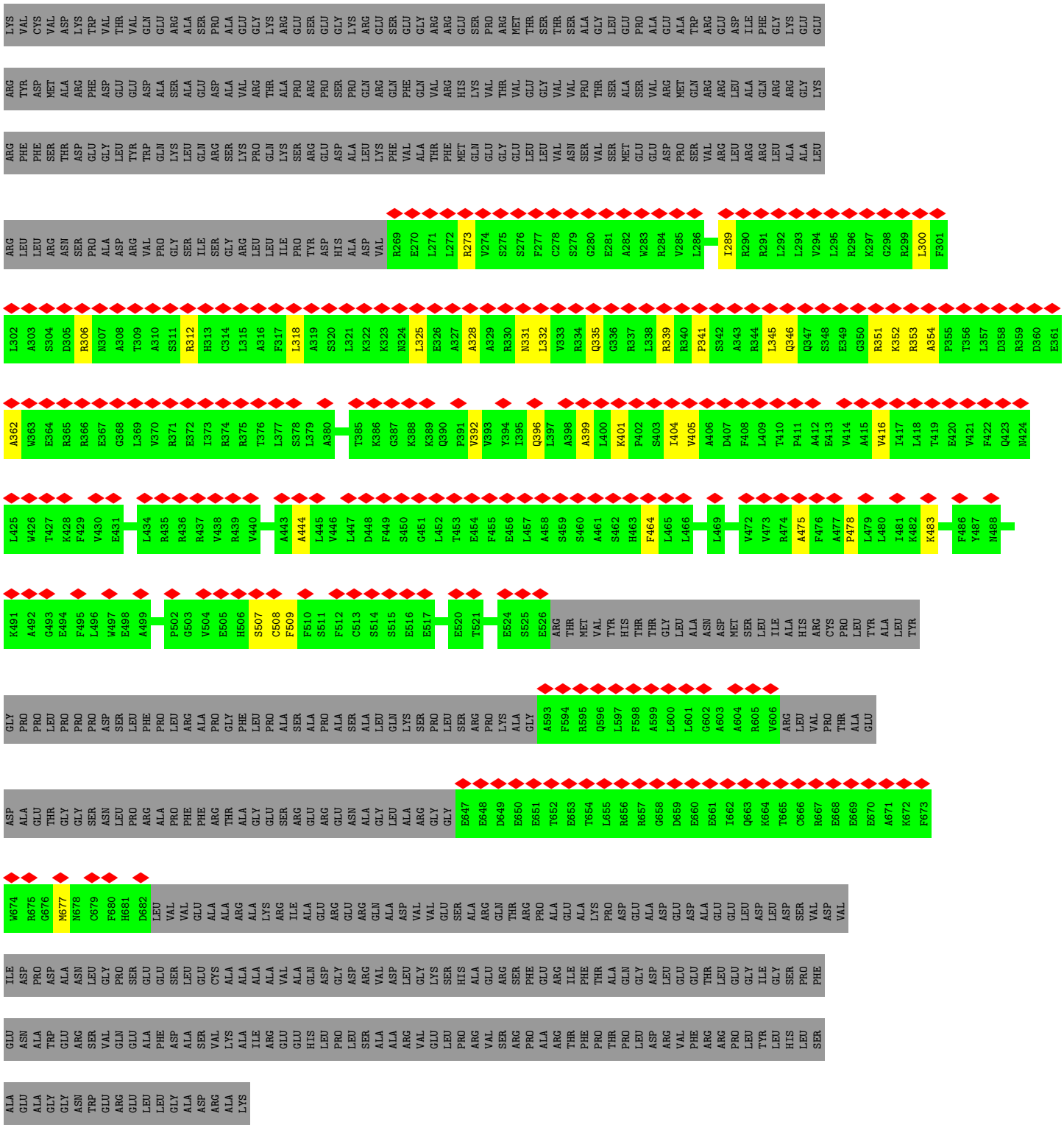
• Molecule 13: CF5, TGME49_297180

Chain J6:



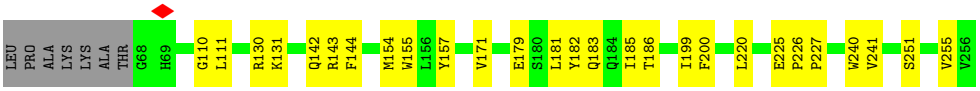
• Molecule 13: CF5, TGME49_297180

Chain J7:



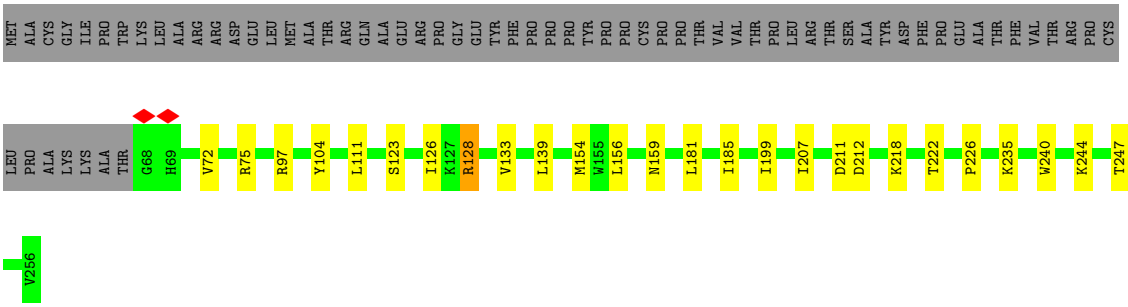
• Molecule 14: DCX, TGME49_256030

Chain K0:



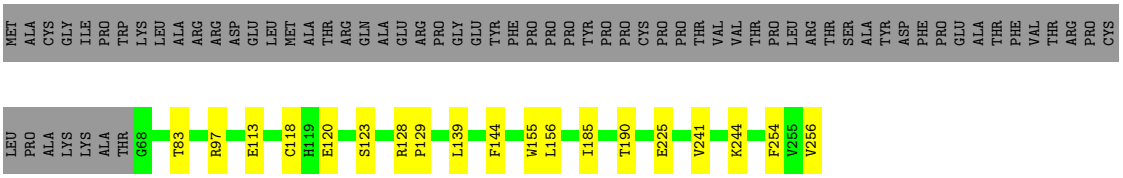
• Molecule 14: DCX, TGME49_256030

Chain K1:



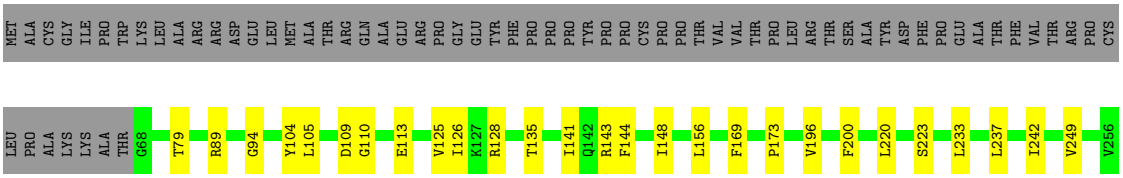
• Molecule 14: DCX, TGME49_256030

Chain K2:



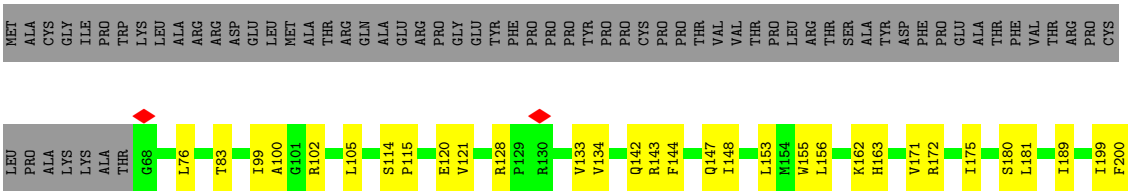
• Molecule 14: DCX, TGME49_256030

Chain K3:



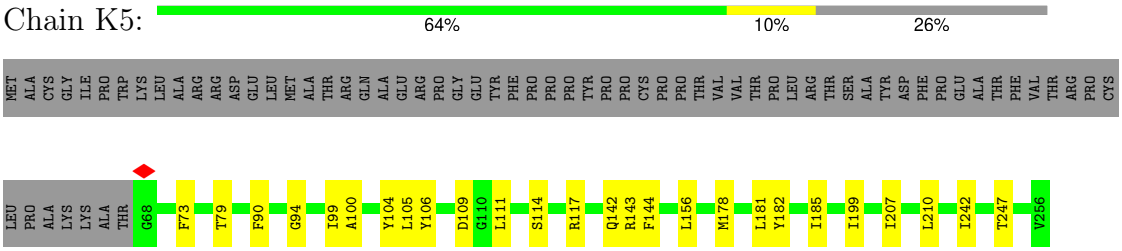
• Molecule 14: DCX, TGME49_256030

Chain K4:



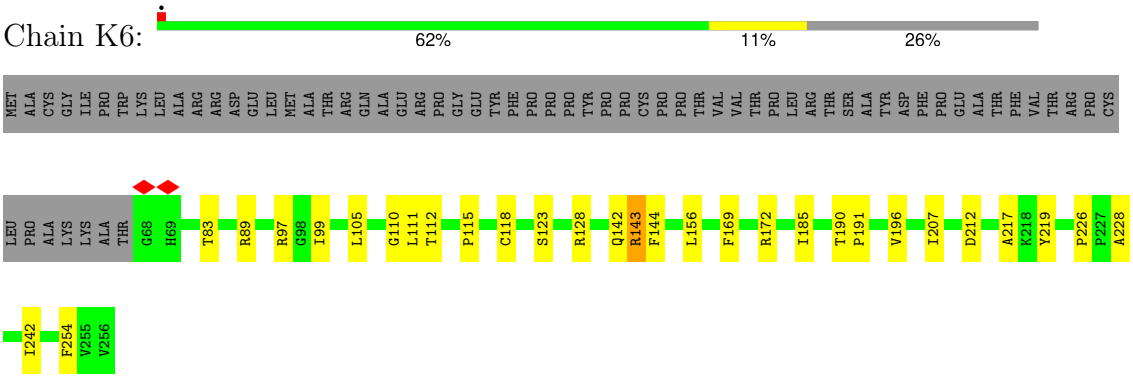
• Molecule 14: DCX, TGME49_256030

Chain K5:



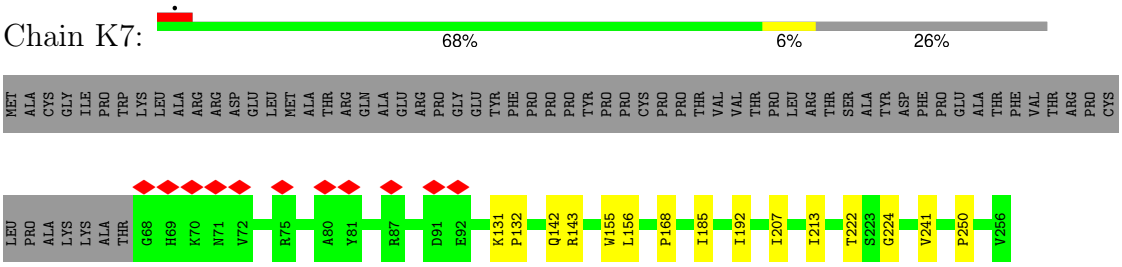
• Molecule 14: DCX, TGME49_256030

Chain K6:



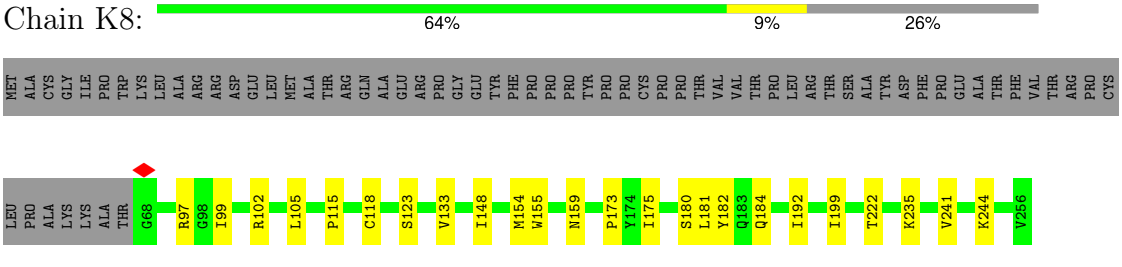
• Molecule 14: DCX, TGME49_256030

Chain K7:



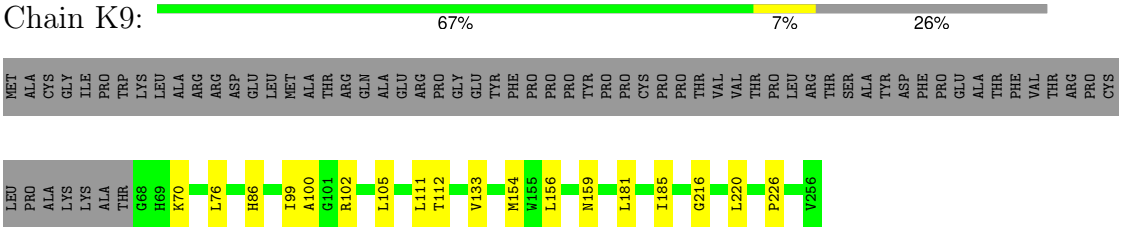
• Molecule 14: DCX, TGME49_256030

Chain K8:



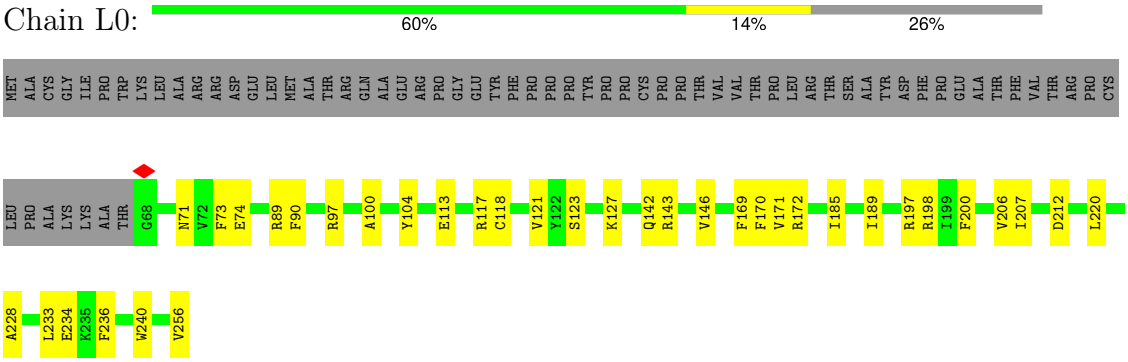
• Molecule 14: DCX, TGME49_256030

Chain K9:



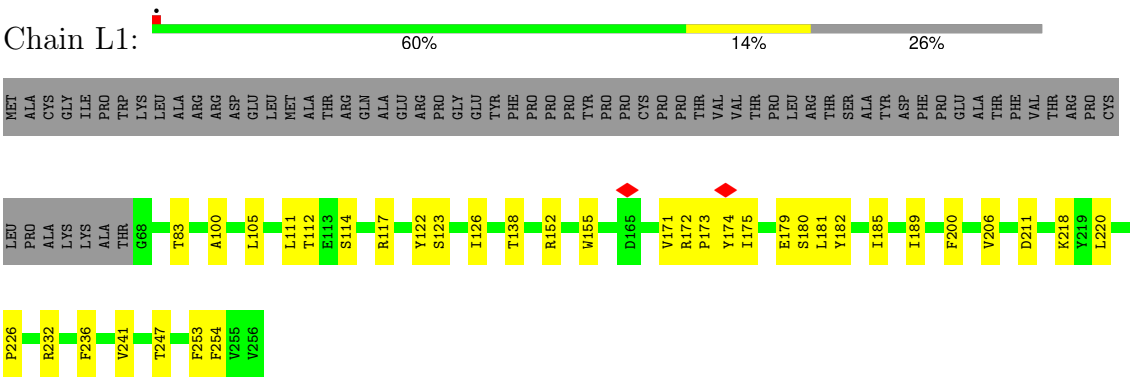
• Molecule 14: DCX, TGME49_256030

Chain L0:



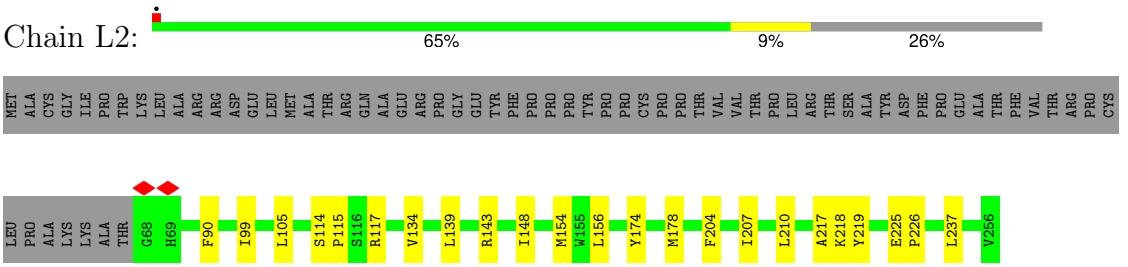
• Molecule 14: DCX, TGME49_256030

Chain L1:



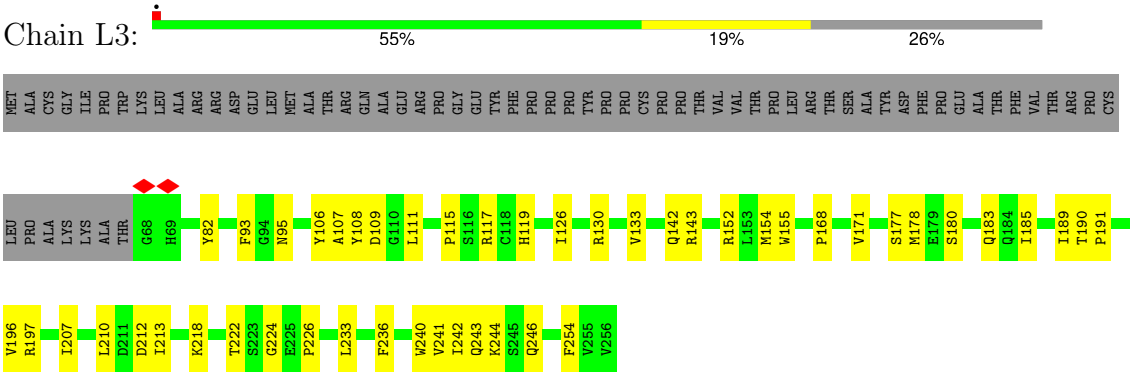
• Molecule 14: DCX, TGME49_256030

Chain L2:



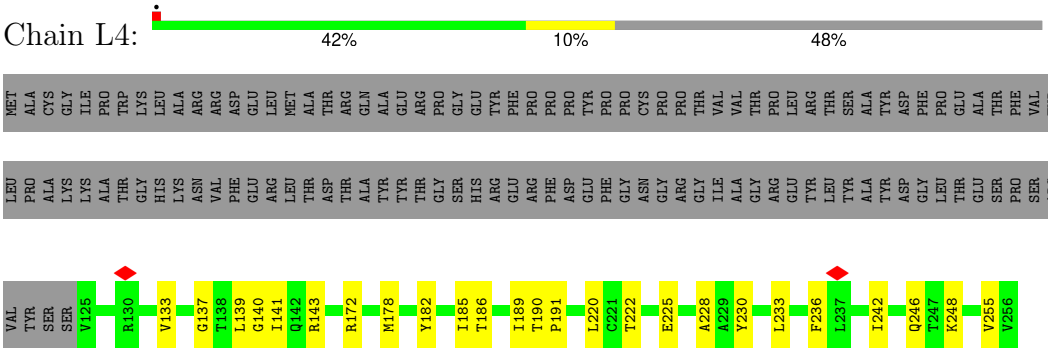
• Molecule 14: DCX, TGME49_256030

Chain L3:



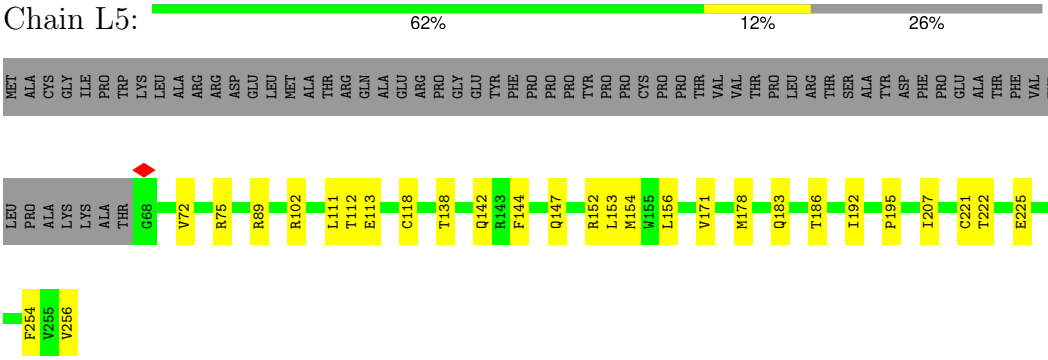
• Molecule 14: DCX, TGME49_256030

Chain L4:



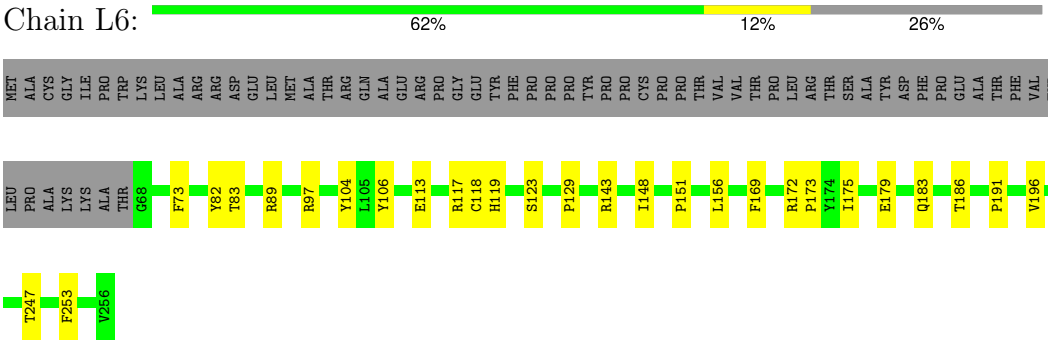
• Molecule 14: DCX, TGME49_256030

Chain L5:



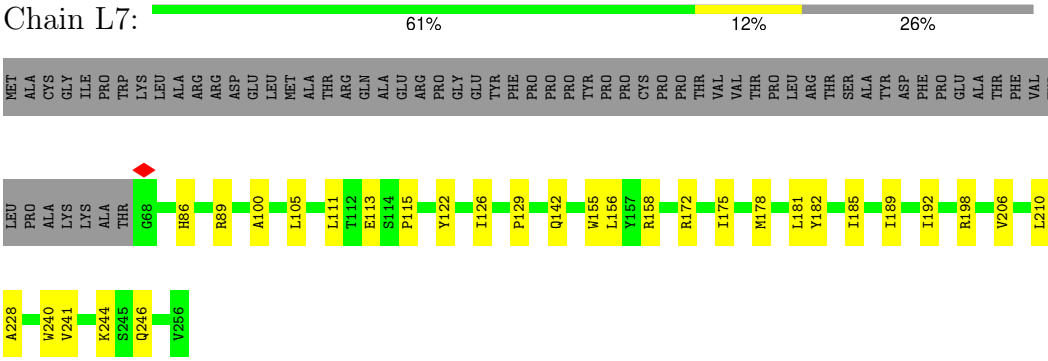
• Molecule 14: DCX, TGME49_256030

Chain L6:



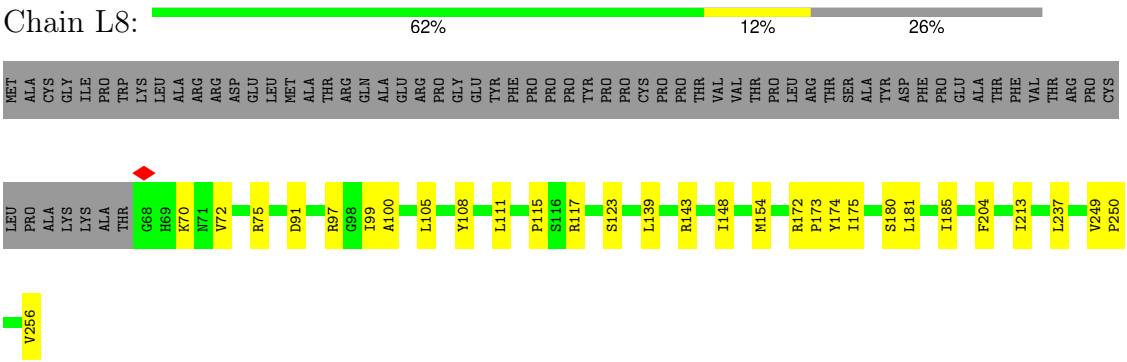
• Molecule 14: DCX, TGME49_256030

Chain L7:



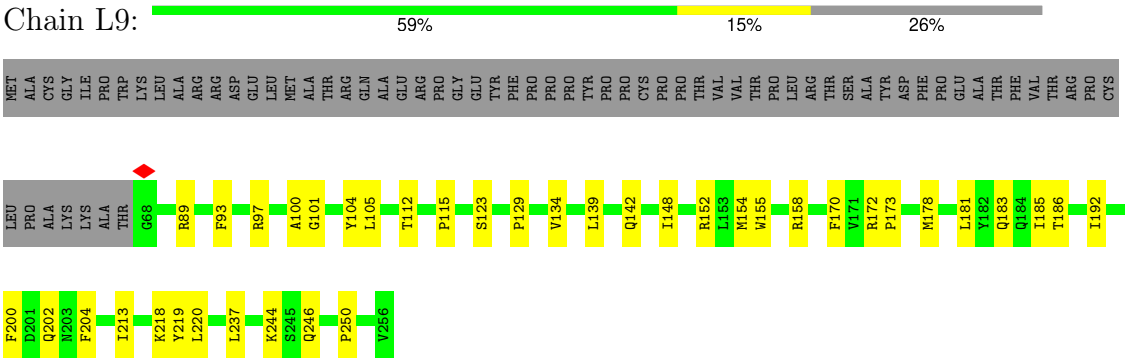
• Molecule 14: DCX, TGME49_256030

Chain L8:



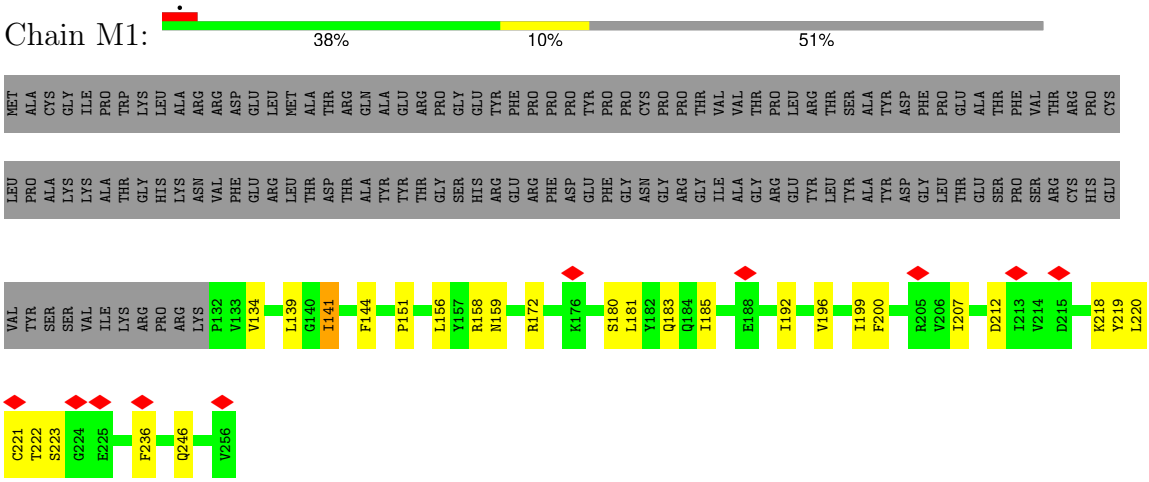
• Molecule 14: DCX, TGME49_256030

Chain L9:



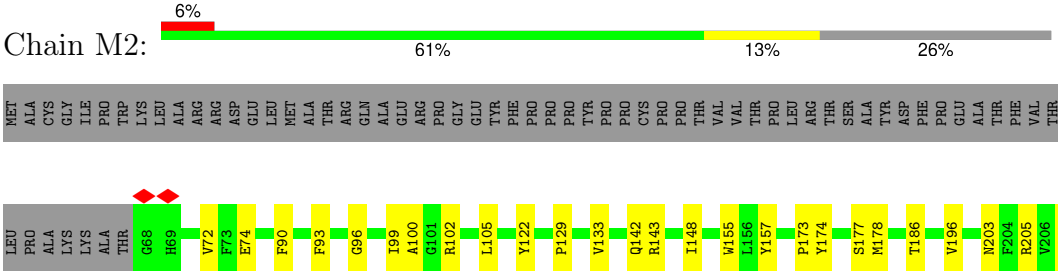
• Molecule 14: DCX, TGME49_256030

Chain M1:



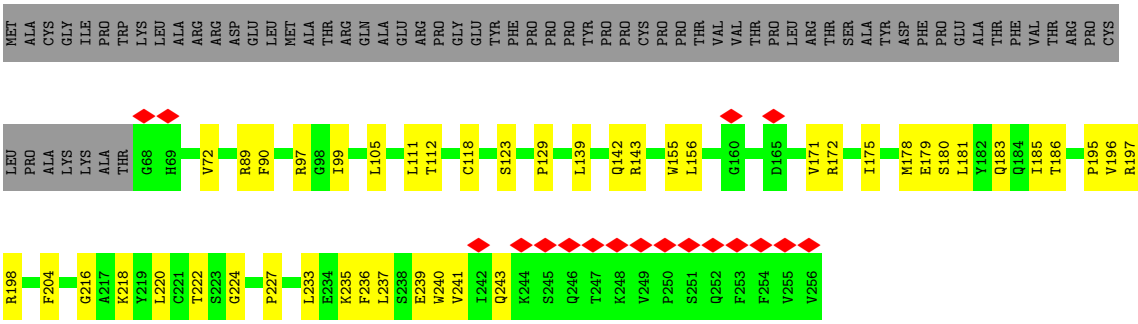
• Molecule 14: DCX, TGME49_256030

Chain M2:



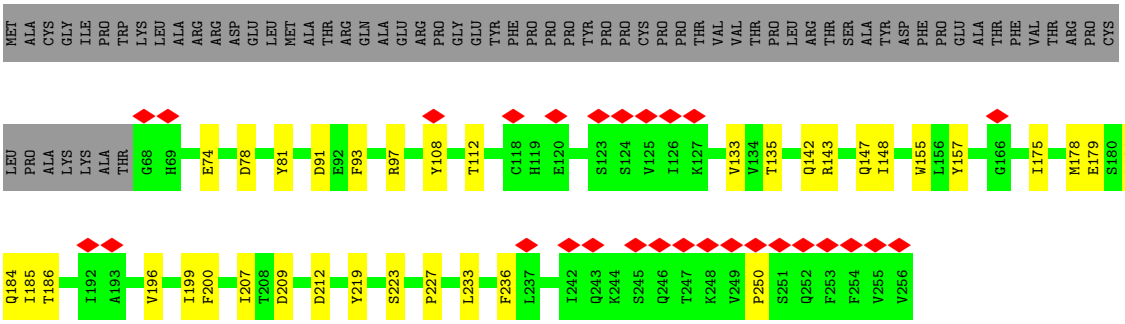
• Molecule 14: DCX, TGME49_256030

Chain M3:



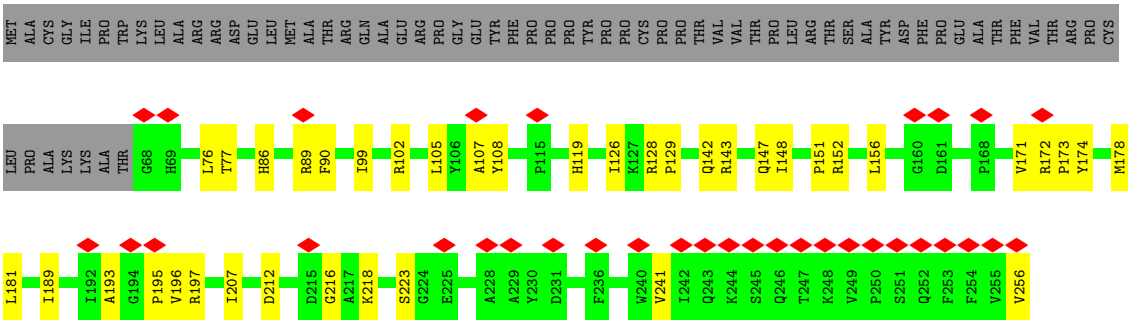
• Molecule 14: DCX, TGME49_256030

Chain M4:



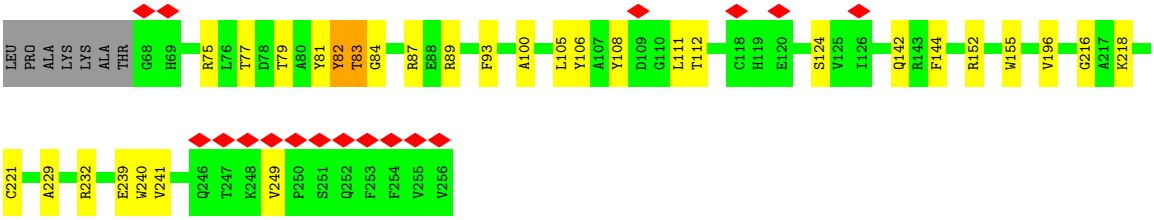
• Molecule 14: DCX, TGME49_256030

Chain M5:



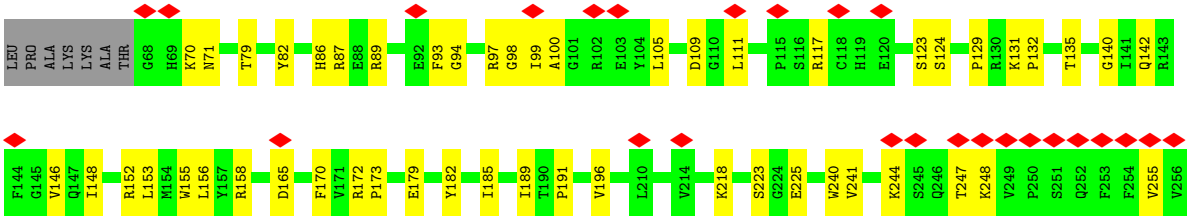
• Molecule 14: DCX, TGME49_256030

Chain M6:



• Molecule 14: DCX, TGME49_256030

Chain M7:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	95409	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.352	Depositor
Minimum map value	-0.059	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	686.08, 686.08, 686.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, GDP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1	0.28	0/892	0.73	0/1200
1	2	0.30	0/892	0.81	0/1200
1	A	0.29	0/2440	0.65	2/3258 (0.1%)
1	B	0.34	1/2020 (0.0%)	0.68	2/2701 (0.1%)
1	C	0.44	0/1249	0.79	2/1669 (0.1%)
1	D	0.37	0/997	0.89	7/1326 (0.5%)
1	E	0.30	0/2245	0.65	0/3005
1	F	0.29	0/2485	0.65	0/3319
1	G	0.39	0/1427	0.90	9/1912 (0.5%)
1	H	0.32	0/963	0.67	0/1281
1	I	0.60	0/3038	0.88	1/4054 (0.0%)
1	J	0.64	0/2986	0.97	5/3984 (0.1%)
1	K	0.31	0/1652	0.74	5/2205 (0.2%)
1	L	0.30	0/1693	0.71	0/2260
1	M	0.71	0/1795	1.03	3/2392 (0.1%)
1	N	0.77	0/1731	1.07	1/2308 (0.0%)
1	O	0.96	0/467	1.29	1/622 (0.2%)
1	P	0.94	0/445	1.35	1/592 (0.2%)
1	Q	0.28	0/2898	0.61	0/3867
1	R	0.29	0/2109	0.65	0/2815
1	S	0.29	0/1481	0.73	4/1976 (0.2%)
1	T	0.23	0/651	0.64	0/867
1	U	0.28	0/3121	0.68	8/4165 (0.2%)
1	V	0.26	0/2135	0.60	0/2852
1	W	0.25	0/1664	0.56	2/2220 (0.1%)
1	X	0.28	0/754	0.60	0/1005
1	Y	0.67	1/2983 (0.0%)	0.96	3/3982 (0.1%)
1	Z	0.35	0/2036	0.74	2/2720 (0.1%)
1	a	0.90	3/1568 (0.2%)	1.15	1/2089 (0.0%)
1	b	0.29	0/739	0.62	0/982
1	c	0.75	2/3012 (0.1%)	0.97	4/4021 (0.1%)
1	d	0.34	0/2076	0.73	1/2774 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	e	0.29	0/732	0.77	1/973 (0.1%)
1	f	1.16	5/1594 (0.3%)	1.38	9/2124 (0.4%)
1	g	0.25	0/745	0.71	2/1017 (0.2%)
1	h	0.31	0/745	0.89	2/1017 (0.2%)
1	i	0.30	0/745	0.77	0/1017
1	j	0.31	0/745	0.82	2/1017 (0.2%)
1	k	0.25	0/745	0.74	0/1017
1	l	0.26	0/745	0.83	0/1017
1	m	0.28	0/745	0.81	2/1017 (0.2%)
1	n	0.26	0/706	0.63	0/949
1	o	0.27	0/706	0.76	0/949
1	p	0.27	0/706	0.70	2/949 (0.2%)
1	q	0.30	0/706	0.76	0/949
1	r	0.32	0/706	0.73	0/949
1	s	0.31	1/706 (0.1%)	0.59	0/949
1	t	0.23	0/706	0.59	0/949
1	u	0.24	0/892	0.62	0/1200
1	v	0.21	0/892	0.56	1/1200 (0.1%)
1	w	0.29	0/892	0.69	0/1200
1	x	0.29	0/892	0.74	1/1200 (0.1%)
1	y	0.22	0/892	0.66	1/1200 (0.1%)
1	z	0.23	0/892	0.64	1/1200 (0.1%)
2	10	0.25	0/1508	0.63	2/1999 (0.1%)
2	11	0.28	0/1527	0.69	0/2024
2	12	0.30	0/1508	0.83	4/1999 (0.2%)
2	13	0.29	0/1527	0.71	4/2024 (0.2%)
2	14	0.28	0/1508	0.67	0/1999
2	15	0.27	0/772	0.63	2/1020 (0.2%)
2	16	0.29	0/843	0.83	4/1114 (0.4%)
2	3	0.30	0/1527	0.75	5/2024 (0.2%)
2	4	0.28	0/1508	0.68	0/1999
2	5	0.33	0/1527	0.81	3/2024 (0.1%)
2	6	0.35	0/1508	0.90	5/1999 (0.3%)
2	7	0.28	0/1527	0.68	3/2024 (0.1%)
2	8	0.29	0/1508	0.73	1/1999 (0.1%)
2	9	0.29	0/1527	0.70	2/2024 (0.1%)
3	1A	0.27	0/3398	0.66	1/4606 (0.0%)
3	1C	0.24	0/3398	0.61	0/4606
3	1E	0.25	0/3398	0.66	1/4606 (0.0%)
3	1G	0.21	0/3398	0.55	0/4606
3	1I	0.23	0/3398	0.56	0/4606
3	1K	0.22	0/3398	0.55	0/4606
3	1M	0.29	0/3398	0.78	8/4606 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
3	2A	0.29	0/3398	0.74	2/4606 (0.0%)
3	2C	0.23	0/3398	0.58	1/4606 (0.0%)
3	2E	0.28	0/3398	0.74	4/4606 (0.1%)
3	2G	0.19	0/3398	0.51	2/4606 (0.0%)
3	2I	0.22	0/3398	0.56	0/4606
3	2K	0.22	0/3398	0.53	0/4606
3	2M	0.27	0/3398	0.68	2/4606 (0.0%)
3	3A	0.29	0/3398	0.75	1/4606 (0.0%)
3	3C	0.22	0/3398	0.56	0/4606
3	3E	0.22	0/3398	0.57	2/4606 (0.0%)
3	3G	0.18	0/3398	0.46	0/4606
3	3I	0.21	0/3398	0.56	3/4606 (0.1%)
3	3K	0.21	0/3398	0.54	0/4606
3	3M	0.26	0/3398	0.63	2/4606 (0.0%)
3	4A	0.24	0/3398	0.62	2/4606 (0.0%)
3	4C	0.22	0/3398	0.56	0/4606
3	4E	0.24	0/3398	0.60	0/4606
3	4G	0.20	0/3398	0.52	0/4606
3	4I	0.22	0/3398	0.56	0/4606
3	4K	0.22	0/3398	0.56	0/4606
3	4M	0.27	0/3398	0.70	2/4606 (0.0%)
3	5A	0.26	0/3398	0.69	2/4606 (0.0%)
3	5C	0.20	0/3398	0.52	0/4606
3	5E	0.20	0/3398	0.51	0/4606
3	5G	0.19	0/3398	0.47	0/4606
3	5I	0.20	0/3398	0.52	0/4606
3	5K	0.19	0/3398	0.49	0/4606
3	5M	0.26	0/3398	0.72	2/4606 (0.0%)
3	6A	0.23	0/3398	0.60	0/4606
3	6C	0.22	0/3398	0.58	0/4606
3	6E	0.22	0/3398	0.57	2/4606 (0.0%)
3	6G	0.22	0/3398	0.52	2/4606 (0.0%)
3	6I	0.22	0/3398	0.55	3/4606 (0.1%)
3	6K	0.22	0/3398	0.53	2/4606 (0.0%)
3	6M	0.25	0/3398	0.67	3/4606 (0.1%)
3	7A	0.23	0/3398	0.59	0/4606
3	7C	0.22	0/3398	0.59	0/4606
3	7E	0.26	0/3398	0.63	0/4606
3	7G	0.21	0/3398	0.55	0/4606
3	7I	0.23	0/3398	0.57	0/4606
3	7K	0.22	0/3398	0.58	0/4606
3	7M	0.26	0/3398	0.69	1/4606 (0.0%)
3	8A	0.23	0/3398	0.58	2/4606 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
3	8C	0.23	0/3398	0.62	1/4606 (0.0%)
3	8E	0.26	0/3398	0.65	4/4606 (0.1%)
3	8G	0.22	0/3398	0.57	1/4606 (0.0%)
3	8I	0.24	0/3398	0.66	2/4606 (0.0%)
3	8K	0.25	0/3398	0.66	3/4606 (0.1%)
3	8M	0.22	0/3398	0.62	2/4606 (0.0%)
3	9A	0.19	0/3398	0.49	1/4606 (0.0%)
3	9C	0.19	0/3398	0.52	1/4606 (0.0%)
3	9E	0.23	0/3398	0.58	1/4606 (0.0%)
3	9G	0.21	0/3398	0.61	1/4606 (0.0%)
3	9I	0.26	0/3398	0.69	4/4606 (0.1%)
3	9K	0.21	0/3398	0.59	1/4606 (0.0%)
3	9M	0.19	0/3398	0.53	0/4606
4	1B	0.26	0/3404	0.68	3/4606 (0.1%)
4	1D	0.24	0/3404	0.64	0/4606
4	1F	0.23	0/3404	0.61	0/4606
4	1H	0.22	0/3404	0.60	3/4606 (0.1%)
4	1J	0.24	0/3404	0.63	0/4606
4	1L	0.23	0/3404	0.63	3/4606 (0.1%)
4	1N	0.25	0/3404	0.69	2/4606 (0.0%)
4	2B	0.27	0/3404	0.70	1/4606 (0.0%)
4	2D	0.24	0/3404	0.63	2/4606 (0.0%)
4	2F	0.23	0/3404	0.60	0/4606
4	2H	0.20	0/3404	0.50	1/4606 (0.0%)
4	2J	0.24	0/3404	0.61	2/4606 (0.0%)
4	2L	0.22	0/3404	0.61	1/4606 (0.0%)
4	3B	0.27	0/3404	0.72	2/4606 (0.0%)
4	3D	0.21	0/3404	0.54	0/4606
4	3F	0.24	0/3404	0.55	0/4606
4	3H	0.20	0/3404	0.54	2/4606 (0.0%)
4	3J	0.23	0/3404	0.60	0/4606
4	3L	0.22	0/3404	0.56	1/4606 (0.0%)
4	4B	0.25	0/3404	0.65	1/4606 (0.0%)
4	4D	0.18	0/3404	0.50	0/4606
4	4F	0.24	0/3404	0.58	2/4606 (0.0%)
4	4H	0.19	0/3404	0.52	2/4606 (0.0%)
4	4J	0.25	0/3404	0.61	0/4606
4	4L	0.23	0/3404	0.61	3/4606 (0.1%)
4	5B	0.30	0/3404	0.74	3/4606 (0.1%)
4	5D	0.21	0/3404	0.55	3/4606 (0.1%)
4	5F	0.21	0/3404	0.55	0/4606
4	5H	0.18	0/3404	0.47	0/4606
4	5J	0.23	0/3404	0.60	0/4606

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
4	5L	0.23	1/3404 (0.0%)	0.52	1/4606 (0.0%)
4	5N	0.28	0/3404	0.76	6/4606 (0.1%)
4	6B	0.26	0/3404	0.70	0/4606
4	6D	0.22	0/3404	0.55	0/4606
4	6F	0.22	0/3404	0.57	0/4606
4	6H	0.21	0/3404	0.53	0/4606
4	6J	0.25	0/3404	0.61	1/4606 (0.0%)
4	6L	0.22	0/3404	0.59	0/4606
4	6N	0.27	0/3404	0.66	1/4606 (0.0%)
4	7B	0.29	0/3404	0.75	7/4606 (0.2%)
4	7D	0.24	0/3404	0.64	0/4606
4	7F	0.24	0/3404	0.64	1/4606 (0.0%)
4	7H	0.22	0/3404	0.56	0/4606
4	7J	0.27	0/3404	0.68	2/4606 (0.0%)
4	7L	0.25	0/3404	0.66	0/4606
4	8B	0.27	0/3404	0.71	5/4606 (0.1%)
4	8D	0.26	0/3404	0.64	0/4606
4	8F	0.26	0/3404	0.69	1/4606 (0.0%)
4	8H	0.23	0/3404	0.59	0/4606
4	8J	0.25	0/3404	0.68	1/4606 (0.0%)
4	8L	0.24	0/3404	0.66	0/4606
4	9B	0.31	0/3404	0.72	7/4606 (0.2%)
4	9D	0.21	0/3404	0.59	2/4606 (0.0%)
4	9F	0.25	0/3404	0.67	9/4606 (0.2%)
4	9H	0.23	0/3404	0.62	2/4606 (0.0%)
4	9J	0.25	0/3404	0.65	2/4606 (0.0%)
4	9L	0.22	0/3404	0.56	0/4606
5	20	0.29	0/1844	0.74	0/2487
5	21	0.26	0/1845	0.74	3/2489 (0.1%)
5	22	0.26	0/1844	0.67	1/2487 (0.0%)
5	23	0.25	0/1845	0.70	0/2489
5	24	0.29	0/1844	0.78	0/2487
5	25	0.29	0/1845	0.75	3/2489 (0.1%)
5	26	0.27	0/1844	0.74	1/2487 (0.0%)
5	27	0.28	0/1845	0.71	1/2489 (0.0%)
5	28	0.27	0/1844	0.71	1/2487 (0.0%)
5	29	0.26	0/1845	0.67	0/2489
5	30	0.25	0/1844	0.67	0/2487
5	31	0.27	0/1845	0.70	0/2489
5	32	0.27	0/1844	0.71	0/2487
5	33	0.19	0/1344	0.58	0/1818
5	35	0.21	0/1774	0.51	0/2394
5	36	0.21	0/1752	0.51	0/2361

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
5	37	0.23	0/1774	0.62	2/2394 (0.1%)
5	38	0.21	0/1752	0.51	0/2361
5	39	0.20	0/1774	0.58	3/2394 (0.1%)
5	40	0.21	0/1752	0.48	0/2361
5	42	0.17	0/1752	0.38	0/2361
5	43	0.20	0/1774	0.52	0/2394
5	44	0.21	0/1752	0.44	0/2361
5	45	0.21	0/1774	0.54	2/2394 (0.1%)
5	46	0.18	0/1752	0.39	0/2361
5	47	0.17	0/1774	0.47	1/2394 (0.0%)
5	48	0.17	0/1752	0.34	0/2361
5	49	0.25	0/1871	0.64	0/2525
5	50	0.25	0/1883	0.70	0/2539
5	51	0.25	0/1871	0.65	0/2525
5	52	0.22	0/1883	0.64	0/2539
5	53	0.25	0/1871	0.65	0/2525
5	54	0.27	0/1883	0.67	3/2539 (0.1%)
5	55	0.24	0/1871	0.65	1/2525 (0.0%)
5	56	0.27	0/1883	0.70	1/2539 (0.0%)
5	57	0.24	0/1871	0.63	0/2525
5	58	0.23	0/1883	0.62	3/2539 (0.1%)
5	59	0.23	0/1871	0.63	0/2525
5	60	0.24	0/1883	0.68	1/2539 (0.0%)
5	61	0.24	0/1871	0.64	1/2525 (0.0%)
5	62	0.23	0/1883	0.59	0/2539
6	63	0.22	0/5165	0.60	1/6980 (0.0%)
6	64	0.29	0/5165	0.61	0/6980
6	65	0.29	0/5165	0.62	0/6980
6	66	0.30	0/5165	0.65	1/6980 (0.0%)
6	67	0.33	1/5165 (0.0%)	0.69	5/6980 (0.1%)
6	68	0.32	0/5165	0.70	1/6980 (0.0%)
6	69	0.31	0/5165	0.67	0/6980
7	71	0.20	0/1427	0.51	0/1942
7	72	0.20	0/1427	0.55	0/1942
7	73	0.25	0/1427	0.66	0/1942
7	75	0.20	0/1427	0.58	2/1942 (0.1%)
7	76	0.20	0/1427	0.52	0/1942
7	77	0.22	0/1427	0.62	4/1942 (0.2%)
7	78	0.22	0/1427	0.55	0/1942
7	79	0.31	1/1427 (0.1%)	0.57	1/1942 (0.1%)
7	80	0.25	0/1427	0.63	1/1942 (0.1%)
7	82	0.21	0/1427	0.50	0/1942
7	83	0.22	0/1427	0.59	0/1942

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
7	84	0.23	0/1427	0.60	0/1942
7	85	0.27	0/1427	0.63	0/1942
7	86	0.24	0/1427	0.67	2/1942 (0.1%)
7	87	0.28	0/1427	0.69	0/1942
7	89	0.27	0/1427	0.61	0/1942
7	90	0.28	0/1427	0.64	0/1942
7	91	0.23	0/1427	0.60	0/1942
7	92	0.23	0/1427	0.60	0/1942
7	93	0.19	0/1427	0.52	0/1942
7	94	0.19	0/1427	0.48	0/1942
7	95	0.20	0/1427	0.53	1/1942 (0.1%)
7	96	0.19	0/1427	0.52	0/1942
7	97	0.31	1/1427 (0.1%)	0.52	1/1942 (0.1%)
8	A1	0.19	0/2638	0.48	0/3582
8	A2	0.22	0/2638	0.59	1/3582 (0.0%)
8	A3	0.23	0/1888	0.59	1/2568 (0.0%)
8	A4	0.27	0/1031	0.77	1/1404 (0.1%)
8	A5	0.20	0/2638	0.49	0/3582
8	A6	0.21	0/2638	0.52	0/3582
8	A7	0.25	0/2638	0.55	0/3582
8	A8	0.22	0/2638	0.49	0/3582
8	A9	0.18	0/1045	0.45	0/1423
9	B1	0.22	0/2119	0.58	0/2878
9	B2	0.21	0/2119	0.54	3/2878 (0.1%)
9	B3	0.20	0/2119	0.54	0/2878
9	B4	0.22	0/2119	0.55	0/2878
9	B5	0.24	0/2119	0.64	1/2878 (0.0%)
9	B6	0.29	1/2119 (0.0%)	0.65	2/2878 (0.1%)
9	B7	0.25	0/2119	0.66	1/2878 (0.0%)
10	C0	0.22	0/1499	0.56	0/2021
10	C6	0.21	0/1499	0.57	0/2021
10	C7	0.25	0/1499	0.63	1/2021 (0.0%)
10	C8	0.27	0/1499	0.66	0/2021
10	C9	0.25	0/1499	0.68	0/2021
10	D0	0.21	0/2249	0.54	0/3042
10	D1	0.25	0/1499	0.62	0/2021
10	D2	0.25	0/1499	0.67	1/2021 (0.0%)
10	D3	0.21	0/2249	0.53	0/3042
10	D4	0.20	0/2249	0.53	0/3042
10	D5	0.23	0/2249	0.59	1/3042 (0.0%)
10	D6	0.22	0/2249	0.53	0/3042
10	D7	0.22	0/2249	0.58	0/3042
10	D8	0.23	0/2249	0.59	0/3042

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
10	D9	0.24	0/2249	0.60	0/3042
10	E0	0.22	0/2249	0.56	0/3042
10	E1	0.22	0/2249	0.54	1/3042 (0.0%)
10	E2	0.26	0/2249	0.68	3/3042 (0.1%)
10	E3	0.23	0/2249	0.59	1/3042 (0.0%)
10	E4	0.24	0/2249	0.60	0/3042
10	E5	0.27	0/2249	0.59	1/3042 (0.0%)
10	E6	0.25	0/2249	0.61	1/3042 (0.0%)
10	E7	0.24	0/2249	0.63	1/3042 (0.0%)
10	E8	0.23	0/2249	0.61	1/3042 (0.0%)
10	E9	0.21	0/2249	0.57	3/3042 (0.1%)
10	F1	0.23	0/2249	0.57	0/3042
10	F2	0.28	0/2249	0.69	3/3042 (0.1%)
10	F3	0.26	0/2249	0.66	4/3042 (0.1%)
11	C1	0.29	0/244	0.42	0/335
11	C2	0.12	0/246	0.36	0/334
11	C3	0.22	0/250	0.58	0/341
11	C4	0.30	0/223	0.51	0/307
11	C5	0.18	0/247	0.55	0/338
12	F0	0.25	0/911	0.69	0/1250
12	F5	0.27	0/874	0.83	0/1200
12	F6	0.26	0/911	0.66	1/1250 (0.1%)
12	F7	0.25	0/874	0.73	1/1200 (0.1%)
12	F8	0.23	0/911	0.60	0/1250
12	F9	0.24	0/874	0.65	0/1200
12	G0	0.21	0/416	0.48	0/558
12	G1	0.24	0/874	0.70	0/1200
12	G2	0.26	0/911	0.71	0/1250
12	G3	0.24	0/874	0.71	0/1200
12	G4	0.24	0/911	0.66	2/1250 (0.2%)
12	G5	0.27	0/874	0.71	2/1200 (0.2%)
12	G6	0.27	0/911	0.70	1/1250 (0.1%)
12	G7	0.27	0/874	0.76	1/1200 (0.1%)
12	G8	0.23	0/911	0.64	1/1250 (0.1%)
12	G9	0.25	0/367	0.71	1/491 (0.2%)
12	H0	0.25	0/188	0.55	0/259
12	H1	0.24	0/188	0.68	0/259
12	H2	0.24	0/367	0.67	1/491 (0.2%)
12	H3	0.23	0/416	0.50	0/558
12	H4	0.21	0/188	0.50	0/259
12	H5	0.26	0/367	0.71	0/491
12	H6	0.25	0/416	0.57	0/558
12	H7	0.23	0/188	0.74	0/259

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
12	H8	0.19	0/367	0.36	0/491
12	H9	0.31	0/416	0.75	1/558 (0.2%)
12	I1	0.31	0/367	0.81	1/491 (0.2%)
12	I2	0.23	0/416	0.56	0/558
12	I3	0.21	0/188	0.60	0/259
12	I4	0.27	0/367	0.69	0/491
12	I5	0.32	0/416	0.78	0/558
12	I6	0.23	0/188	0.64	0/259
12	I7	0.24	0/367	0.64	0/491
12	I8	0.23	0/416	0.54	0/558
12	I9	0.21	0/188	0.56	0/259
13	J1	0.21	0/2529	0.54	1/3401 (0.0%)
13	J2	0.22	0/2529	0.56	2/3401 (0.1%)
13	J3	0.22	0/2529	0.51	0/3401
13	J4	0.20	0/2529	0.50	0/3401
13	J5	0.23	0/2529	0.56	2/3401 (0.1%)
13	J6	0.20	0/2529	0.51	1/3401 (0.0%)
13	J7	0.16	0/2529	0.40	0/3401
14	K0	0.22	0/1579	0.61	0/2139
14	K1	0.21	0/1579	0.50	0/2139
14	K2	0.19	0/1579	0.48	0/2139
14	K3	0.23	0/1579	0.61	0/2139
14	K4	0.21	0/1579	0.57	0/2139
14	K5	0.21	0/1579	0.52	0/2139
14	K6	0.22	0/1579	0.54	0/2139
14	K7	0.19	0/1579	0.47	0/2139
14	K8	0.19	0/1579	0.48	0/2139
14	K9	0.19	0/1579	0.47	0/2139
14	L0	0.22	0/1579	0.57	1/2139 (0.0%)
14	L1	0.24	0/1579	0.62	0/2139
14	L2	0.18	0/1579	0.46	0/2139
14	L3	0.22	0/1579	0.57	0/2139
14	L4	0.20	0/1102	0.55	0/1496
14	L5	0.19	0/1579	0.50	0/2139
14	L6	0.20	0/1579	0.52	0/2139
14	L7	0.22	0/1579	0.59	0/2139
14	L8	0.22	0/1579	0.58	0/2139
14	L9	0.22	0/1579	0.54	0/2139
14	M1	0.23	0/1039	0.64	1/1412 (0.1%)
14	M2	0.21	0/1579	0.52	0/2139
14	M3	0.22	0/1579	0.54	0/2139
14	M4	0.20	0/1579	0.53	0/2139
14	M5	0.22	0/1579	0.58	0/2139

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
14	M6	0.20	0/1579	0.54	0/2139
14	M7	0.22	0/1579	0.60	2/2139 (0.1%)
All	All	0.27	18/819485 (0.0%)	0.63	385/1107855 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	2
1	2	0	1
1	C	0	3
1	F	0	1
1	G	0	1
1	I	0	13
1	J	0	12
1	L	0	2
1	M	0	9
1	N	0	12
1	O	0	4
1	P	0	5
1	S	0	1
1	Y	0	12
1	Z	0	1
1	a	0	13
1	c	0	13
1	d	0	1
1	f	0	21
1	g	0	1
1	h	0	2
1	i	0	2
1	j	0	1
1	k	0	1
1	l	0	2
1	m	0	2
1	p	0	1
1	u	0	1
1	v	0	2
1	w	0	2
1	x	0	1
1	y	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	z	0	1
2	3	0	1
3	1A	0	3
3	1E	0	1
3	1G	0	1
3	1K	0	2
3	1M	0	1
3	2C	0	1
3	2E	0	1
3	2G	0	1
3	2I	0	2
3	2M	0	1
3	3A	0	2
3	3C	0	1
3	3E	0	1
3	3I	0	1
3	3K	0	2
3	4A	0	2
3	4C	0	1
3	4E	0	1
3	4G	0	1
3	4K	0	1
3	5A	0	1
3	5E	0	1
3	5M	0	3
3	6C	0	1
3	6G	0	1
3	7E	0	2
3	8C	0	5
3	8G	0	2
3	8I	0	2
3	8K	0	4
3	8M	0	1
3	9C	0	2
3	9E	0	1
3	9G	0	3
3	9I	0	3
3	9K	0	2
4	1B	0	1
4	1D	0	2
4	1H	0	2
4	1L	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
4	1N	0	1
4	2F	0	2
4	2J	0	1
4	2L	0	2
4	3H	0	1
4	3J	0	1
4	4B	0	2
4	4D	0	1
4	4F	0	2
4	4H	0	2
4	4J	0	2
4	4L	0	1
4	5D	0	2
4	5F	0	1
4	5J	0	1
4	5L	0	1
4	6H	0	1
4	7B	0	2
4	7D	0	1
4	7H	0	1
4	8B	0	1
4	8D	0	1
4	8F	0	1
4	8J	0	2
4	8L	0	1
4	9B	0	2
4	9D	0	2
4	9F	0	4
4	9J	0	2
5	20	0	1
5	21	0	2
5	22	0	1
5	23	0	2
5	24	0	1
5	25	0	2
5	27	0	2
5	29	0	2
5	31	0	3
5	33	0	1
5	50	0	1
6	63	0	1
6	64	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	65	0	6
6	66	0	6
6	67	0	6
6	68	0	7
6	69	0	5
7	72	0	1
7	79	0	1
7	84	0	1
7	87	0	1
7	89	0	2
7	90	0	3
7	91	0	1
7	92	0	3
7	93	0	2
7	95	0	2
7	96	0	1
7	97	0	1
8	A1	0	1
8	A3	0	1
8	A4	0	1
8	A5	0	1
8	A6	0	1
8	A7	0	1
8	A8	0	1
9	B5	0	1
9	B6	0	1
9	B7	0	2
10	D0	0	1
10	D1	0	2
10	D3	0	2
10	D4	0	2
10	D5	0	1
10	D6	0	2
10	D7	0	2
10	D8	0	2
10	D9	0	3
10	E1	0	1
10	E2	0	1
10	E3	0	3
10	E4	0	1
10	E5	0	1
10	E6	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	E8	0	2
10	E9	0	2
10	F2	0	1
10	F3	0	2
12	F5	0	1
12	F7	0	1
12	F9	0	1
12	G1	0	2
12	G2	0	1
12	G3	0	2
12	G5	0	1
12	G7	0	1
13	J6	0	1
14	K1	0	1
14	K3	0	1
14	K4	0	1
14	K6	0	1
14	M4	0	1
All	All	0	393

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	67	855	PRO	CA-C	-9.07	1.46	1.51
7	97	302	PRO	CA-C	-8.48	1.46	1.52
7	79	302	PRO	CA-C	-8.25	1.47	1.51
9	B6	151	PRO	CA-C	6.89	1.56	1.52
4	5L	286	VAL	CA-CB	-6.63	1.49	1.53
1	f	532	GLU	C-O	6.63	1.31	1.24
1	c	619	GLN	C-O	6.48	1.31	1.24
1	f	599	SER	C-O	6.21	1.31	1.24
1	B	319	MET	N-CA	-5.94	1.39	1.46
1	a	608	ASP	C-O	5.84	1.31	1.24
1	Y	608	ASP	C-O	5.79	1.31	1.24
1	f	626	LEU	C-O	5.74	1.30	1.24
1	f	588	THR	C-O	5.66	1.30	1.24
1	a	605	LYS	C-O	5.61	1.30	1.24
1	c	623	SER	C-O	5.50	1.30	1.24
1	a	598	ALA	C-O	5.06	1.30	1.24
1	s	877	LEU	C-N	5.05	1.39	1.34
1	f	622	GLU	C-O	5.01	1.29	1.24

All (385) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	5N	30	ILE	CA-C-N	10.00	139.95	120.94
4	5N	30	ILE	C-N-CA	10.00	139.95	120.94
1	K	361	LEU	CA-CB-CG	8.38	145.63	116.30
4	5B	324	LYS	CG-CD-CE	-8.28	92.26	111.30
1	J	618	ARG	N-CA-C	-8.18	102.44	111.36
1	J	659	LEU	N-CA-CB	-8.01	96.95	110.49
4	6J	374	ILE	N-CA-C	-7.99	104.92	112.83
4	7B	233	MET	CA-CB-CG	7.92	129.94	114.10
2	6	200	GLN	CA-C-N	7.85	129.82	121.97
2	6	200	GLN	C-N-CA	7.85	129.82	121.97
4	9F	374	ILE	N-CA-C	-7.85	105.67	113.20
2	12	200	GLN	CA-C-N	7.76	129.74	121.97
2	12	200	GLN	C-N-CA	7.76	129.74	121.97
6	66	558	LYS	CB-CG-CD	-7.75	93.46	111.30
1	D	616	THR	CA-C-N	-7.70	110.34	122.65
1	D	616	THR	C-N-CA	-7.70	110.34	122.65
5	22	67	ARG	CB-CG-CD	-7.55	93.93	111.30
10	E5	306	MET	CB-CG-SD	-7.41	90.47	112.70
9	B6	151	PRO	O-C-N	7.38	124.62	121.15
4	4F	285	SER	CA-C-N	7.23	124.80	120.24
4	4F	285	SER	C-N-CA	7.23	124.80	120.24
4	9F	16	ILE	N-CA-C	-7.13	105.68	111.81
4	7J	40	SER	CA-C-N	7.12	139.05	126.45
4	7J	40	SER	C-N-CA	7.12	139.05	126.45
4	8B	285	SER	CA-C-N	6.99	124.65	120.24
4	8B	285	SER	C-N-CA	6.99	124.65	120.24
10	E8	107	ILE	N-CA-C	-6.95	106.45	113.47
3	2E	217	LEU	CA-C-N	6.86	133.31	122.61
3	2E	217	LEU	C-N-CA	6.86	133.31	122.61
4	1B	285	SER	CA-C-N	6.83	124.54	120.24
4	1B	285	SER	C-N-CA	6.83	124.54	120.24
10	E9	107	ILE	N-CA-C	-6.81	106.17	112.43
3	1M	433	GLU	CA-CB-CG	6.79	127.69	114.10
2	7	317	MET	CB-CG-SD	6.78	133.04	112.70
14	M1	141	ILE	N-CA-C	-6.73	106.23	112.96
4	7B	293	MET	CB-CG-SD	-6.72	92.53	112.70
4	7B	233	MET	CB-CG-SD	6.71	132.84	112.70
3	3A	275	ILE	N-CA-C	-6.64	104.84	111.88
1	m	829	PRO	CA-C-N	6.54	134.03	121.54
1	m	829	PRO	C-N-CA	6.54	134.03	121.54
12	G7	215	GLN	CA-CB-CG	6.50	127.10	114.10
7	97	302	PRO	O-C-N	-6.49	118.10	121.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	381	ARG	CB-CG-CD	-6.46	96.43	111.30
3	2E	316	CYS	CA-CB-SG	6.45	129.23	114.40
4	6N	252	LYS	CB-CG-CD	6.44	126.12	111.30
12	F7	209	TRP	CB-CA-C	-6.43	108.48	117.23
1	d	522	ARG	CG-CD-NE	-6.43	97.85	112.00
3	1M	254	GLU	CA-CB-CG	6.42	126.95	114.10
6	67	855	PRO	O-C-N	-6.42	118.36	121.31
8	A4	69	MET	CA-CB-CG	6.36	126.83	114.10
1	O	660	GLN	N-CA-C	-6.30	104.51	111.82
2	5	164	GLU	N-CA-CB	6.25	119.96	110.28
2	13	224	GLU	CA-C-N	-6.24	110.46	122.06
2	13	224	GLU	C-N-CA	-6.24	110.46	122.06
1	S	376	MET	CB-CG-SD	6.19	131.26	112.70
1	y	952	ARG	CB-CA-C	-6.18	109.43	116.54
10	F3	107	ILE	N-CA-C	-6.18	105.62	113.22
3	6E	413	MET	CB-CG-SD	-6.18	94.17	112.70
4	1L	252	LYS	CB-CG-CD	6.17	125.48	111.30
3	8A	74	VAL	N-CA-C	-6.16	107.49	113.53
2	12	199	SER	CA-C-N	6.13	133.24	121.54
2	12	199	SER	C-N-CA	6.13	133.24	121.54
5	55	161	ILE	CG1-CB-CG2	-6.12	92.35	110.70
3	3I	182	VAL	N-CA-C	-6.12	106.54	112.29
1	Y	647	LYS	N-CA-C	-6.11	104.54	111.07
7	75	383	SER	CA-C-N	6.10	144.76	121.95
7	75	383	SER	C-N-CA	6.10	144.76	121.95
4	2D	356	ILE	N-CA-C	6.08	113.90	107.76
7	79	302	PRO	O-C-N	-6.07	118.52	121.31
7	95	360	GLY	N-CA-C	6.03	117.22	111.67
4	1L	285	SER	CA-C-N	6.02	125.14	120.33
4	1L	285	SER	C-N-CA	6.02	125.14	120.33
5	25	185	ARG	CB-CG-CD	6.02	125.14	111.30
5	60	85	GLN	CA-CB-CG	6.01	126.13	114.10
3	6I	423	GLU	N-CA-CB	6.01	120.20	110.40
4	9B	117	LEU	CA-CB-CG	6.01	137.32	116.30
1	K	342	MET	CA-CB-CG	6.00	126.10	114.10
4	5B	324	LYS	CB-CG-CD	5.96	125.00	111.30
3	8I	73	THR	CA-C-N	5.95	132.68	121.97
3	8I	73	THR	C-N-CA	5.95	132.68	121.97
10	E7	107	ILE	N-CA-C	-5.94	107.20	112.90
2	16	200	GLN	CA-C-N	5.94	131.03	121.95
2	16	200	GLN	C-N-CA	5.94	131.03	121.95
10	E2	281	GLU	CA-C-N	-5.93	111.02	122.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	E2	281	GLU	C-N-CA	-5.93	111.02	122.06
13	J2	318	LEU	CA-CB-CG	5.92	137.00	116.30
4	4L	271	ALA	N-CA-C	5.91	119.90	110.73
3	9I	73	THR	CA-C-N	5.90	132.60	121.97
3	9I	73	THR	C-N-CA	5.90	132.60	121.97
1	z	952	ARG	CB-CA-C	-5.90	109.75	116.54
1	f	576	SER	N-CA-C	-5.87	104.88	111.28
1	G	416	GLN	CA-CB-CG	5.87	125.84	114.10
4	4H	279	GLN	CA-C-N	5.87	132.75	121.54
4	4H	279	GLN	C-N-CA	5.87	132.75	121.54
1	G	287	PRO	CA-C-N	5.84	132.70	121.54
1	G	287	PRO	C-N-CA	5.84	132.70	121.54
1	K	360	ARG	CG-CD-NE	5.84	124.85	112.00
10	D2	98	GLU	N-CA-CB	5.84	119.29	110.30
10	F3	295	GLN	N-CA-CB	5.83	120.08	110.39
4	2D	320	ARG	CB-CG-CD	5.83	124.70	111.30
4	2L	395	LEU	CA-CB-CG	5.83	136.69	116.30
4	5D	177	ASP	CA-C-N	5.81	132.64	121.54
4	5D	177	ASP	C-N-CA	5.81	132.64	121.54
2	6	230	ARG	CB-CG-CD	5.80	124.64	111.30
4	9B	238	CYS	CA-CB-SG	5.80	127.74	114.40
12	H9	91	GLU	N-CA-CB	5.79	118.72	110.16
5	25	185	ARG	CA-CB-CG	5.78	125.66	114.10
3	1M	433	GLU	N-CA-CB	5.77	120.10	110.41
4	9B	354	CYS	CA-C-N	5.77	132.55	121.54
4	9B	354	CYS	C-N-CA	5.77	132.55	121.54
4	8B	354	CYS	CA-C-N	5.76	132.54	121.54
4	8B	354	CYS	C-N-CA	5.76	132.54	121.54
1	U	425	ILE	CA-C-N	-5.74	111.09	121.14
1	U	425	ILE	C-N-CA	-5.74	111.09	121.14
13	J6	375	ARG	CB-CG-CD	5.73	124.47	111.30
3	1M	205	ASP	CB-CA-C	5.72	120.35	110.45
1	f	683	GLU	CB-CA-C	5.72	121.22	110.63
3	8C	357	TYR	CA-CB-CG	5.72	124.20	113.90
1	M	507	GLU	N-CA-CB	5.72	118.62	110.16
4	5N	162	ARG	CA-C-N	5.70	132.24	121.97
4	5N	162	ARG	C-N-CA	5.70	132.24	121.97
3	7M	423	GLU	N-CA-CB	5.70	119.69	110.40
1	D	618	ARG	CA-CB-CG	5.70	125.49	114.10
4	3B	20	PHE	CA-C-N	-5.69	111.48	122.06
4	3B	20	PHE	C-N-CA	-5.69	111.48	122.06
2	9	235	GLU	N-CA-CB	5.69	119.09	110.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	1B	108	GLU	CA-CB-CG	5.69	125.47	114.10
1	Z	471	LEU	CA-CB-CG	5.68	136.20	116.30
4	9F	285	SER	CA-C-N	5.68	123.82	120.24
4	9F	285	SER	C-N-CA	5.68	123.82	120.24
1	a	608	ASP	N-CA-C	-5.67	105.18	111.36
3	6E	423	GLU	N-CA-CB	5.66	119.92	110.41
4	5D	42	LEU	CA-CB-CG	5.65	136.09	116.30
3	9I	195	LEU	CA-C-N	-5.65	111.97	122.09
3	9I	195	LEU	C-N-CA	-5.65	111.97	122.09
9	B6	488	GLU	N-CA-CB	5.64	118.90	110.22
10	E2	282	GLN	N-CA-CB	5.64	119.31	110.46
2	5	164	GLU	CA-CB-CG	5.63	125.37	114.10
5	21	113	MET	CA-C-N	-5.63	111.29	121.14
5	21	113	MET	C-N-CA	-5.63	111.29	121.14
4	2B	325	GLU	N-CA-CB	5.62	118.38	110.12
3	8M	171	SER	CA-C-N	5.62	131.62	120.94
3	8M	171	SER	C-N-CA	5.62	131.62	120.94
4	2H	398	TYR	N-CA-C	-5.62	105.71	113.18
9	B2	488	GLU	N-CA-CB	5.62	118.99	110.28
1	f	512	LYS	CB-CA-C	-5.61	101.61	110.86
1	P	669	GLU	N-CA-C	-5.60	105.18	111.28
1	U	421	GLU	N-CA-CB	5.59	118.34	110.12
3	9A	182	VAL	N-CA-C	-5.59	107.04	112.29
12	G6	290	LYS	CA-CB-CG	5.58	125.26	114.10
3	5A	219	ILE	CA-C-N	5.58	132.19	121.54
3	5A	219	ILE	C-N-CA	5.58	132.19	121.54
6	63	394	GLU	N-CA-CB	5.57	119.47	110.40
1	U	426	GLU	N-CA-CB	5.56	119.47	110.40
8	A2	329	LEU	CA-CB-CG	5.56	135.77	116.30
1	U	331	GLU	CA-C-N	-5.55	111.89	121.66
1	U	331	GLU	C-N-CA	-5.55	111.89	121.66
3	2A	109	THR	CA-C-N	5.55	131.95	121.97
3	2A	109	THR	C-N-CA	5.55	131.95	121.97
10	E3	301	ARG	CA-CB-CG	5.54	125.18	114.10
2	3	261	ARG	CA-CB-CG	5.53	125.17	114.10
1	e	367	GLU	N-CA-CB	5.53	119.71	110.41
4	9D	177	ASP	CA-C-N	5.53	132.10	121.54
4	9D	177	ASP	C-N-CA	5.53	132.10	121.54
4	9F	290	THR	CA-C-N	-5.52	110.89	121.94
4	9F	290	THR	C-N-CA	-5.52	110.89	121.94
3	1M	217	LEU	CA-C-N	5.52	132.09	121.54
3	1M	217	LEU	C-N-CA	5.52	132.09	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
13	J5	660	GLU	N-CA-CB	5.52	118.72	110.22
1	S	376	MET	CA-CB-CG	5.52	125.14	114.10
1	f	532	GLU	N-CA-CB	-5.51	101.87	109.91
4	1H	270	PHE	CA-C-N	-5.50	116.67	122.28
4	1H	270	PHE	C-N-CA	-5.50	116.67	122.28
2	15	189	GLU	CA-C-N	5.49	130.37	122.40
2	15	189	GLU	C-N-CA	5.49	130.37	122.40
3	8A	423	GLU	N-CA-CB	5.49	118.80	110.28
3	6M	296	PHE	CA-C-N	-5.49	105.38	120.97
3	6M	296	PHE	C-N-CA	-5.49	105.38	120.97
4	1N	232	ALA	CA-C-N	-5.48	112.45	122.38
4	1N	232	ALA	C-N-CA	-5.48	112.45	122.38
1	D	677	MET	N-CA-C	5.47	117.24	111.28
4	5B	324	LYS	CA-CB-CG	-5.47	103.16	114.10
1	G	402	GLN	CA-CB-CG	5.46	125.02	114.10
1	S	488	GLU	CA-C-N	-5.46	111.59	121.14
1	S	488	GLU	C-N-CA	-5.46	111.59	121.14
1	Z	439	LEU	CA-CB-CG	5.46	135.41	116.30
3	6K	217	LEU	CA-C-N	5.46	131.97	121.54
3	6K	217	LEU	C-N-CA	5.46	131.97	121.54
5	45	188	MET	CB-CG-SD	5.45	129.06	112.70
4	8B	180	VAL	N-CA-C	-5.44	107.07	111.91
3	9C	268	MET	CB-CA-C	5.44	119.05	109.80
2	16	222	GLU	CA-C-N	-5.43	111.64	121.14
2	16	222	GLU	C-N-CA	-5.43	111.64	121.14
1	N	609	ALA	N-CA-C	-5.42	105.47	111.71
4	7F	108	GLU	N-CA-C	-5.42	107.67	114.56
1	U	376	MET	CA-CB-CG	5.41	124.92	114.10
1	v	880	THR	CB-CA-C	-5.41	109.36	115.79
3	3M	109	THR	CA-C-N	5.41	131.70	121.97
3	3M	109	THR	C-N-CA	5.41	131.70	121.97
8	A3	227	SER	N-CA-C	5.40	119.35	112.87
12	G4	213	ALA	CA-C-N	5.40	131.86	121.54
12	G4	213	ALA	C-N-CA	5.40	131.86	121.54
4	9J	125	GLU	CA-CB-CG	5.40	124.90	114.10
12	G5	204	SER	CA-C-N	5.38	131.82	121.54
12	G5	204	SER	C-N-CA	5.38	131.82	121.54
2	3	317	MET	CB-CG-SD	5.38	128.83	112.70
1	J	367	GLU	N-CA-CB	5.38	118.58	110.30
7	86	316	PRO	CA-C-N	-5.38	113.73	122.65
7	86	316	PRO	C-N-CA	-5.38	113.73	122.65
4	8F	271	ALA	N-CA-C	5.37	121.68	109.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	2M	154	LEU	CA-CB-CG	5.37	135.09	116.30
10	E6	34	VAL	N-CA-C	-5.36	108.27	113.53
7	77	326	PRO	CA-C-N	5.36	128.28	120.51
7	77	326	PRO	C-N-CA	5.36	128.28	120.51
4	4L	270	PHE	CA-C-N	-5.36	116.81	122.28
4	4L	270	PHE	C-N-CA	-5.36	116.81	122.28
1	G	399	GLU	N-CA-CB	5.35	119.12	110.40
3	3E	281	ALA	CA-C-N	5.35	131.76	121.54
3	3E	281	ALA	C-N-CA	5.35	131.76	121.54
2	6	199	SER	CA-C-N	5.35	131.76	121.54
2	6	199	SER	C-N-CA	5.35	131.76	121.54
5	58	84	PRO	CA-C-N	5.35	131.76	121.54
5	58	84	PRO	C-N-CA	5.35	131.76	121.54
1	c	512	LYS	CB-CA-C	5.35	119.99	109.72
3	1A	302	MET	CA-CB-CG	5.35	124.80	114.10
4	4B	329	GLN	N-CA-CB	5.35	119.12	110.40
1	C	319	MET	CB-CG-SD	5.34	128.73	112.70
3	8G	357	TYR	CA-CB-CG	5.34	123.52	113.90
4	9F	270	PHE	CA-C-N	-5.34	117.40	122.37
4	9F	270	PHE	C-N-CA	-5.34	117.40	122.37
1	D	677	MET	CG-SD-CE	5.34	112.64	100.90
10	F2	71	GLN	CA-CB-CG	5.33	124.76	114.10
13	J5	663	GLN	N-CA-CB	5.33	119.09	110.40
3	2M	390	ARG	CA-CB-CG	5.33	124.75	114.10
1	M	628	VAL	N-CA-CB	5.33	116.42	110.51
4	3L	349	MET	CB-CG-SD	-5.32	96.73	112.70
3	4M	72	PRO	CA-C-N	5.31	131.69	121.54
3	4M	72	PRO	C-N-CA	5.31	131.69	121.54
3	8K	350	GLY	CA-C-N	5.31	130.48	122.67
3	8K	350	GLY	C-N-CA	5.31	130.48	122.67
1	G	425	ILE	CA-C-N	-5.31	111.22	121.58
1	G	425	ILE	C-N-CA	-5.31	111.22	121.58
12	G9	65	GLU	N-CA-CB	5.29	118.48	110.28
1	x	891	GLU	N-CA-CB	5.29	118.48	110.28
1	A	614	LEU	CA-CB-CG	5.29	134.82	116.30
5	37	199	LEU	CA-C-N	-5.29	112.80	122.38
5	37	199	LEU	C-N-CA	-5.29	112.80	122.38
4	5N	180	VAL	CA-C-N	5.29	129.93	121.62
4	5N	180	VAL	C-N-CA	5.29	129.93	121.62
7	77	329	PRO	CA-C-N	5.29	126.70	120.09
7	77	329	PRO	C-N-CA	5.29	126.70	120.09
1	h	757	LEU	CA-C-N	5.29	131.64	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	h	757	LEU	C-N-CA	5.29	131.64	121.54
2	5	258	GLN	N-CA-CB	5.27	119.14	110.39
4	7B	246	LEU	CA-CB-CG	5.27	134.75	116.30
7	80	375	LEU	CA-CB-CG	5.27	134.73	116.30
1	C	378	GLU	N-CA-CB	5.26	117.95	110.16
1	c	512	LYS	CA-CB-CG	5.26	124.63	114.10
6	67	847	GLU	CA-C-N	5.26	131.59	121.54
6	67	847	GLU	C-N-CA	5.26	131.59	121.54
4	9B	22	GLU	N-CA-CB	5.26	117.95	110.16
2	7	186	HIS	CA-C-N	-5.26	112.87	122.38
2	7	186	HIS	C-N-CA	-5.26	112.87	122.38
1	A	585	GLU	N-CA-CB	5.25	118.42	110.28
1	c	586	LYS	N-CA-C	-5.25	106.13	112.54
3	8E	27	GLU	N-CA-CB	5.24	117.67	110.07
4	9H	40	SER	CA-C-N	5.24	129.78	122.08
4	9H	40	SER	C-N-CA	5.24	129.78	122.08
4	7B	328	GLU	CA-C-N	-5.23	113.21	122.26
4	7B	328	GLU	C-N-CA	-5.23	113.21	122.26
9	B5	45	ARG	CA-CB-CG	5.23	124.57	114.10
5	26	181	GLU	CA-CB-CG	5.22	124.55	114.10
1	g	829	PRO	CA-C-N	5.22	131.52	121.54
1	g	829	PRO	C-N-CA	5.22	131.52	121.54
1	D	580	GLU	N-CA-CB	5.22	117.89	110.16
3	8E	397	LEU	CA-CB-CG	5.22	134.56	116.30
13	J2	519	LEU	CA-CB-CG	5.22	134.56	116.30
2	13	224	GLU	N-CA-CB	5.21	117.88	110.16
4	7B	293	MET	CA-CB-CG	5.21	124.52	114.10
4	9B	355	ASP	CA-C-N	-5.21	118.25	123.04
4	9B	355	ASP	C-N-CA	-5.21	118.25	123.04
5	39	20	PHE	CA-C-N	5.21	131.49	121.54
5	39	20	PHE	C-N-CA	5.21	131.49	121.54
1	D	673	LEU	CA-CB-CG	5.21	134.52	116.30
4	3H	285	SER	CA-C-N	5.21	123.52	120.24
4	3H	285	SER	C-N-CA	5.21	123.52	120.24
1	Y	608	ASP	N-CA-C	-5.21	105.69	111.36
1	J	405	GLN	CA-CB-CG	5.20	124.51	114.10
10	F2	300	ILE	CA-C-N	5.20	127.20	120.44
10	F2	300	ILE	C-N-CA	5.20	127.20	120.44
14	L0	71	ASN	CB-CA-C	-5.20	109.60	115.79
3	9E	144	GLY	N-CA-C	5.20	114.94	110.21
3	1E	316	CYS	CA-CB-SG	5.19	126.34	114.40
1	f	595	ASP	CA-CB-CG	5.19	117.79	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	1H	311	LEU	CB-CA-C	-5.19	110.57	116.54
4	2J	193	VAL	N-CA-C	-5.19	106.02	113.07
4	2J	271	ALA	N-CA-C	5.19	121.27	109.81
3	2C	376	CYS	CA-CB-SG	5.18	126.32	114.40
5	39	199	LEU	CA-CB-CG	5.18	134.43	116.30
1	B	319	MET	CA-CB-CG	5.18	124.45	114.10
5	27	188	MET	CB-CG-SD	5.17	128.22	112.70
4	9J	271	ALA	N-CA-C	5.17	118.75	110.73
1	f	527	LEU	N-CA-C	-5.17	105.64	111.28
1	c	654	LEU	N-CA-C	-5.16	105.65	111.28
1	K	495	PHE	N-CA-CB	-5.16	102.59	110.07
3	5M	173	PRO	CA-C-N	5.16	129.28	121.03
3	5M	173	PRO	C-N-CA	5.16	129.28	121.03
1	j	829	PRO	CA-C-N	5.15	131.38	121.54
1	j	829	PRO	C-N-CA	5.15	131.38	121.54
3	3I	87	PHE	CA-C-N	5.15	131.60	122.48
3	3I	87	PHE	C-N-CA	5.15	131.60	122.48
5	21	185	ARG	CA-CB-CG	5.14	124.38	114.10
4	8J	271	ALA	N-CA-C	5.14	121.17	109.81
2	3	316	ARG	CA-C-N	-5.14	112.15	121.14
2	3	316	ARG	C-N-CA	-5.14	112.15	121.14
1	B	485	LEU	CA-CB-CG	5.13	134.27	116.30
5	58	85	GLN	CA-CB-CG	5.13	124.37	114.10
3	8K	357	TYR	CA-CB-CG	5.13	123.14	113.90
3	9K	357	TYR	CA-CB-CG	5.13	123.14	113.90
12	I1	65	GLU	N-CA-CB	5.13	118.24	110.28
2	3	258	GLN	N-CA-CB	5.13	118.91	110.39
4	9F	271	ALA	N-CA-C	5.13	116.15	108.76
13	J1	318	LEU	CA-CB-CG	5.12	134.23	116.30
4	5L	139	LEU	CA-CB-CG	5.12	134.22	116.30
2	9	222	GLU	N-CA-CB	5.12	118.22	110.28
3	2G	178	SER	CA-C-N	5.12	129.60	122.08
3	2G	178	SER	C-N-CA	5.12	129.60	122.08
1	M	587	GLU	N-CA-CB	5.12	118.21	110.28
6	67	545	GLU	N-CA-CB	5.12	118.21	110.28
3	8E	178	SER	CA-C-N	5.12	131.31	121.54
3	8E	178	SER	C-N-CA	5.12	131.31	121.54
3	9G	182	VAL	N-CA-C	-5.12	107.48	112.29
1	U	331	GLU	CB-CG-CD	5.11	121.29	112.60
9	B7	488	GLU	N-CA-CB	5.11	118.99	110.41
10	D5	402	GLU	N-CA-CB	5.11	117.72	110.16
3	2E	182	VAL	N-CA-C	-5.11	107.49	112.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	28	112	GLN	CA-CB-CG	5.10	124.31	114.10
1	p	881	ALA	CA-C-N	5.10	131.29	121.54
1	p	881	ALA	C-N-CA	5.10	131.29	121.54
5	54	238	GLN	N-CA-CB	5.10	118.72	110.40
3	1M	15	GLN	CA-CB-CG	5.10	124.30	114.10
2	10	199	SER	CA-C-N	5.10	131.28	121.54
2	10	199	SER	C-N-CA	5.10	131.28	121.54
5	47	21	LEU	CA-CB-CG	5.10	134.14	116.30
12	H2	65	GLU	N-CA-CB	5.09	118.16	110.28
1	W	376	MET	N-CA-C	5.08	117.22	111.02
5	56	15	THR	N-CA-C	-5.08	108.35	114.75
5	61	115	GLU	N-CA-CB	5.08	118.95	110.41
1	J	405	GLN	N-CA-CB	5.08	117.58	110.12
3	6G	217	LEU	CA-C-N	5.08	131.24	121.54
3	6G	217	LEU	C-N-CA	5.08	131.24	121.54
1	I	628	VAL	N-CA-CB	5.08	116.14	110.51
3	6I	217	LEU	CA-C-N	5.07	131.23	121.54
3	6I	217	LEU	C-N-CA	5.07	131.23	121.54
1	f	558	LEU	N-CA-CB	-5.07	101.92	110.49
2	13	258	GLN	N-CA-CB	5.07	118.66	110.40
10	C7	296	MET	CA-CB-CG	5.06	124.22	114.10
5	25	118	LYS	CA-CB-CG	5.06	124.22	114.10
2	8	173	GLU	N-CA-CB	5.06	118.91	110.41
1	W	342	MET	CB-CG-SD	5.06	127.87	112.70
6	67	895	ARG	CB-CG-CD	5.06	122.93	111.30
10	F3	294	SER	CA-C-N	-5.06	112.28	120.72
10	F3	294	SER	C-N-CA	-5.06	112.28	120.72
5	54	237	GLN	CA-C-N	-5.05	112.29	121.14
5	54	237	GLN	C-N-CA	-5.05	112.29	121.14
1	K	439	LEU	CA-CB-CG	5.05	133.96	116.30
10	E1	293	MET	CB-CG-SD	5.05	127.84	112.70
6	68	405	LYS	CA-CB-CG	5.04	124.19	114.10
1	f	524	ALA	N-CA-C	-5.04	106.63	112.89
9	B2	77	GLY	CA-C-N	5.04	123.42	120.24
9	B2	77	GLY	C-N-CA	5.04	123.42	120.24
10	E9	61	ASP	CA-C-N	5.03	127.62	120.53
10	E9	61	ASP	C-N-CA	5.03	127.62	120.53
1	G	426	GLU	N-CA-CB	5.03	118.86	110.41
3	4A	274	PRO	CA-C-N	5.03	131.02	121.97
3	4A	274	PRO	C-N-CA	5.03	131.02	121.97
3	1M	15	GLN	N-CA-CB	5.03	118.59	110.40
12	G8	221	MET	CA-CB-CG	5.02	124.14	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	45	21	LEU	CA-CB-CG	5.02	133.87	116.30
1	Y	505	GLU	N-CA-CB	5.01	118.05	110.28
3	6M	254	GLU	CA-CB-CG	5.01	124.13	114.10
14	M7	70	LYS	CA-C-N	5.01	131.12	121.54
14	M7	70	LYS	C-N-CA	5.01	131.12	121.54
12	F6	225	TRP	CA-CB-CG	5.01	123.11	113.60
1	f	548	LEU	N-CA-C	-5.00	105.91	111.36

There are no chirality outliers.

All (393) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	866	ILE	Peptide
1	1	877	LEU	Peptide
3	1A	273	ALA	Peptide
3	1A	301	MET	Peptide
3	1A	390	ARG	Sidechain
4	1B	323	THR	Peptide
4	1D	219	THR	Peptide
4	1D	271	ALA	Peptide
3	1E	316	CYS	Peptide
3	1G	324	VAL	Peptide
4	1H	271	ALA	Peptide
4	1H	391	ARG	Peptide
3	1K	273	ALA	Peptide
3	1K	280	LYS	Peptide
4	1L	271	ALA	Peptide
3	1M	273	ALA	Peptide
4	1N	271	ALA	Peptide
1	2	866	ILE	Peptide
5	20	164	MET	Peptide
5	21	185	ARG	Sidechain
5	21	41	THR	Peptide
5	22	139	LYS	Peptide
5	23	151	HIS	Peptide
5	23	41	THR	Peptide
5	24	117	GLN	Peptide
5	25	143	CYS	Peptide
5	25	41	THR	Peptide
5	27	143	CYS	Peptide
5	27	41	THR	Peptide
5	29	143	CYS	Peptide

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Mol	Chain	Res	Type	Group
5	29	41	THR	Peptide
3	2C	376	CYS	Peptide
3	2E	316	CYS	Peptide
4	2F	271	ALA	Peptide
4	2F	60	VAL	Peptide
3	2G	273	ALA	Peptide
3	2I	273	ALA	Peptide
3	2I	411	GLU	Peptide
4	2J	271	ALA	Peptide
4	2L	107	THR	Peptide
4	2L	271	ALA	Peptide
3	2M	273	ALA	Peptide
2	3	168	ARG	Sidechain
5	31	143	CYS	Peptide
5	31	41	THR	Peptide
5	31	46	ARG	Sidechain
5	33	41	THR	Peptide
3	3A	215	ARG	Sidechain
3	3A	262	TYR	Peptide
3	3C	273	ALA	Peptide
3	3E	338	LYS	Peptide
4	3H	271	ALA	Peptide
3	3I	273	ALA	Peptide
4	3J	271	ALA	Peptide
3	3K	267	PHE	Peptide
3	3K	273	ALA	Peptide
3	4A	273	ALA	Peptide
3	4A	284	GLU	Peptide
4	4B	281	TYR	Peptide
4	4B	282	ARG	Sidechain
3	4C	281	ALA	Peptide
4	4D	271	ALA	Peptide
3	4E	273	ALA	Peptide
4	4F	271	ALA	Peptide
4	4F	46	ARG	Sidechain
3	4G	273	ALA	Peptide
4	4H	213	ARG	Sidechain
4	4H	355	ASP	Peptide
4	4J	271	ALA	Peptide
4	4J	281	TYR	Peptide
3	4K	283	HIS	Peptide
4	4L	271	ALA	Peptide

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Mol	Chain	Res	Type	Group
5	50	20	PHE	Peptide
3	5A	267	PHE	Peptide
4	5D	107	THR	Peptide
4	5D	271	ALA	Peptide
3	5E	273	ALA	Peptide
4	5F	271	ALA	Peptide
4	5J	271	ALA	Peptide
4	5L	271	ALA	Peptide
3	5M	110	ILE	Peptide
3	5M	192	HIS	Peptide
3	5M	273	ALA	Peptide
6	63	851	PRO	Peptide
6	64	498	ARG	Sidechain
6	64	499	ARG	Sidechain
6	64	500	ARG	Sidechain
6	64	501	ARG	Sidechain
6	64	507	ARG	Sidechain
6	65	493	ARG	Sidechain
6	65	498	ARG	Sidechain
6	65	499	ARG	Sidechain
6	65	500	ARG	Sidechain
6	65	501	ARG	Sidechain
6	65	507	ARG	Sidechain
6	66	493	ARG	Sidechain
6	66	498	ARG	Sidechain
6	66	500	ARG	Sidechain
6	66	507	ARG	Sidechain
6	66	624	THR	Peptide
6	66	915	ASN	Peptide
6	67	493	ARG	Sidechain
6	67	499	ARG	Sidechain
6	67	500	ARG	Sidechain
6	67	501	ARG	Sidechain
6	67	507	ARG	Sidechain
6	67	621	ARG	Sidechain
6	68	493	ARG	Sidechain
6	68	498	ARG	Sidechain
6	68	500	ARG	Sidechain
6	68	501	ARG	Sidechain
6	68	507	ARG	Sidechain
6	68	828	GLU	Peptide
6	68	874	GLY	Peptide

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Mol	Chain	Res	Type	Group
6	69	493	ARG	Sidechain
6	69	498	ARG	Sidechain
6	69	500	ARG	Sidechain
6	69	501	ARG	Sidechain
6	69	507	ARG	Sidechain
3	6C	90	GLU	Peptide
3	6G	100	ALA	Peptide
4	6H	157	GLU	Peptide
7	72	411	MET	Peptide
7	79	299	PHE	Peptide
4	7B	271	ALA	Peptide
4	7B	298	ASN	Peptide
4	7D	271	ALA	Peptide
3	7E	110	ILE	Peptide
3	7E	284	GLU	Peptide
4	7H	137	HIS	Peptide
7	84	299	PHE	Peptide
7	87	389	GLN	Peptide
7	89	299	PHE	Peptide
7	89	388	GLU	Peptide
4	8B	271	ALA	Peptide
3	8C	196	GLU	Peptide
3	8C	229	ARG	Sidechain
3	8C	273	ALA	Peptide
3	8C	356	ASN	Peptide
3	8C	357	TYR	Peptide
4	8D	271	ALA	Peptide
4	8F	271	ALA	Peptide
3	8G	273	ALA	Peptide
3	8G	357	TYR	Peptide
3	8I	110	ILE	Peptide
3	8I	273	ALA	Peptide
4	8J	157	GLU	Peptide
4	8J	271	ALA	Peptide
3	8K	196	GLU	Peptide
3	8K	273	ALA	Peptide
3	8K	349	THR	Peptide
3	8K	391	MET	Peptide
4	8L	70	PRO	Peptide
3	8M	267	PHE	Peptide
7	90	279	ARG	Peptide
7	90	299	PHE	Peptide

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Mol	Chain	Res	Type	Group
7	90	388	GLU	Peptide
7	91	282	ARG	Peptide
7	92	390	PRO	Peptide
7	92	391	TYR	Peptide
7	92	413	ARG	Peptide
7	93	289	GLY	Peptide
7	93	391	TYR	Peptide
7	95	389	GLN	Peptide
7	95	412	MET	Peptide
7	96	415	GLY	Peptide
7	97	400	CYS	Peptide
4	9B	238	CYS	Peptide
4	9B	271	ALA	Peptide
3	9C	268	MET	Peptide
3	9C	273	ALA	Peptide
4	9D	11	GLN	Peptide
4	9D	271	ALA	Peptide
3	9E	221	ARG	Sidechain
4	9F	107	THR	Peptide
4	9F	271	ALA	Peptide
4	9F	320	ARG	Peptide
4	9F	365	VAL	Peptide
3	9G	273	ALA	Peptide
3	9G	356	ASN	Peptide
3	9G	357	TYR	Peptide
3	9I	110	ILE	Peptide
3	9I	219	ILE	Peptide
3	9I	273	ALA	Peptide
4	9J	107	THR	Peptide
4	9J	271	ALA	Peptide
3	9K	254	GLU	Peptide
3	9K	273	ALA	Peptide
8	A1	34	SER	Peptide
8	A3	228	LEU	Peptide
8	A4	51	LYS	Peptide
8	A5	34	SER	Peptide
8	A6	34	SER	Peptide
8	A7	34	SER	Peptide
8	A8	34	SER	Peptide
9	B5	150	MET	Peptide
9	B6	47	SER	Peptide
9	B7	148	TYR	Peptide

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Mol	Chain	Res	Type	Group
9	B7	464	HIS	Peptide
1	C	316	LEU	Peptide
1	C	379	ARG	Sidechain
1	C	387	ILE	Peptide
10	D0	125	PRO	Peptide
10	D1	330	TYR	Peptide
10	D1	47	MET	Peptide
10	D3	125	PRO	Peptide
10	D3	148	MET	Peptide
10	D4	125	PRO	Peptide
10	D4	360	ALA	Peptide
10	D5	125	PRO	Peptide
10	D6	125	PRO	Peptide
10	D6	360	ALA	Peptide
10	D7	125	PRO	Peptide
10	D7	360	ALA	Peptide
10	D8	125	PRO	Peptide
10	D8	360	ALA	Peptide
10	D9	125	PRO	Peptide
10	D9	301	ARG	Sidechain
10	D9	38	ARG	Sidechain
10	E1	125	PRO	Peptide
10	E2	125	PRO	Peptide
10	E3	125	PRO	Peptide
10	E3	301	ARG	Sidechain
10	E3	360	ALA	Peptide
10	E4	125	PRO	Peptide
10	E5	125	PRO	Peptide
10	E6	125	PRO	Peptide
10	E6	301	ARG	Sidechain
10	E6	360	ALA	Peptide
10	E8	36	PHE	Peptide
10	E8	362	ASP	Peptide
10	E9	35	TRP	Peptide
10	E9	360	ALA	Peptide
1	F	499	ARG	Sidechain
10	F2	147	SER	Peptide
10	F3	36	PHE	Peptide
10	F3	360	ALA	Peptide
12	F5	205	ASP	Peptide
12	F7	205	ASP	Peptide
12	F9	205	ASP	Peptide

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Mol	Chain	Res	Type	Group
1	G	429	ARG	Sidechain
12	G1	205	ASP	Peptide
12	G1	206	ASP	Peptide
12	G2	224	ARG	Sidechain
12	G3	205	ASP	Peptide
12	G3	208	SER	Peptide
12	G5	205	ASP	Peptide
12	G7	205	ASP	Peptide
1	I	572	ARG	Sidechain
1	I	578	ARG	Sidechain
1	I	591	ARG	Sidechain
1	I	592	ARG	Sidechain
1	I	601	ARG	Sidechain
1	I	603	ARG	Sidechain
1	I	618	ARG	Sidechain
1	I	630	ARG	Sidechain
1	I	632	ARG	Sidechain
1	I	643	ARG	Sidechain
1	I	674	ARG	Sidechain
1	I	679	ARG	Sidechain
1	I	684	ARG	Sidechain
1	J	572	ARG	Sidechain
1	J	578	ARG	Sidechain
1	J	591	ARG	Sidechain
1	J	592	ARG	Sidechain
1	J	601	ARG	Sidechain
1	J	603	ARG	Sidechain
1	J	615	ARG	Sidechain
1	J	618	ARG	Sidechain
1	J	632	ARG	Sidechain
1	J	643	ARG	Sidechain
1	J	679	ARG	Sidechain
1	J	684	ARG	Sidechain
13	J6	375	ARG	Sidechain
14	K1	128	ARG	Sidechain
14	K3	128	ARG	Peptide
14	K4	128	ARG	Peptide
14	K6	143	ARG	Peptide
1	L	379	ARG	Sidechain
1	L	499	ARG	Sidechain
1	M	601	ARG	Sidechain
1	M	603	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	M	615	ARG	Sidechain
1	M	618	ARG	Sidechain
1	M	630	ARG	Sidechain
1	M	632	ARG	Sidechain
1	M	643	ARG	Sidechain
1	M	674	ARG	Sidechain
1	M	679	ARG	Sidechain
14	M4	179	GLU	Peptide
1	N	578	ARG	Sidechain
1	N	591	ARG	Sidechain
1	N	592	ARG	Sidechain
1	N	601	ARG	Sidechain
1	N	603	ARG	Sidechain
1	N	615	ARG	Sidechain
1	N	618	ARG	Sidechain
1	N	632	ARG	Sidechain
1	N	643	ARG	Sidechain
1	N	674	ARG	Sidechain
1	N	679	ARG	Sidechain
1	N	684	ARG	Sidechain
1	O	643	ARG	Sidechain
1	O	674	ARG	Sidechain
1	O	679	ARG	Sidechain
1	O	684	ARG	Sidechain
1	P	632	ARG	Sidechain
1	P	643	ARG	Sidechain
1	P	674	ARG	Sidechain
1	P	679	ARG	Sidechain
1	P	684	ARG	Sidechain
1	S	429	ARG	Sidechain
1	Y	572	ARG	Sidechain
1	Y	578	ARG	Sidechain
1	Y	591	ARG	Sidechain
1	Y	592	ARG	Sidechain
1	Y	601	ARG	Sidechain
1	Y	603	ARG	Sidechain
1	Y	615	ARG	Sidechain
1	Y	618	ARG	Sidechain
1	Y	632	ARG	Sidechain
1	Y	674	ARG	Sidechain
1	Y	679	ARG	Sidechain
1	Y	684	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	Z	379	ARG	Sidechain
1	a	572	ARG	Sidechain
1	a	578	ARG	Sidechain
1	a	591	ARG	Sidechain
1	a	601	ARG	Sidechain
1	a	603	ARG	Sidechain
1	a	615	ARG	Sidechain
1	a	618	ARG	Sidechain
1	a	630	ARG	Sidechain
1	a	632	ARG	Sidechain
1	a	643	ARG	Sidechain
1	a	674	ARG	Sidechain
1	a	679	ARG	Sidechain
1	a	684	ARG	Sidechain
1	c	561	ARG	Sidechain
1	c	566	ARG	Sidechain
1	c	572	ARG	Sidechain
1	c	578	ARG	Sidechain
1	c	591	ARG	Sidechain
1	c	592	ARG	Sidechain
1	c	603	ARG	Sidechain
1	c	615	ARG	Sidechain
1	c	618	ARG	Sidechain
1	c	630	ARG	Sidechain
1	c	632	ARG	Sidechain
1	c	674	ARG	Sidechain
1	c	679	ARG	Sidechain
1	d	500	ARG	Sidechain
1	f	511	GLU	Mainchain
1	f	513	ARG	Sidechain
1	f	522	ARG	Sidechain
1	f	533	ARG	Sidechain
1	f	556	ARG	Sidechain
1	f	561	ARG	Sidechain
1	f	566	ARG	Sidechain
1	f	572	ARG	Sidechain
1	f	578	ARG	Sidechain
1	f	591	ARG	Sidechain
1	f	592	ARG	Sidechain
1	f	601	ARG	Sidechain
1	f	603	ARG	Sidechain
1	f	615	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	f	618	ARG	Sidechain
1	f	630	ARG	Sidechain
1	f	632	ARG	Sidechain
1	f	643	ARG	Sidechain
1	f	674	ARG	Sidechain
1	f	679	ARG	Sidechain
1	f	684	ARG	Sidechain
1	g	828	CYS	Peptide
1	h	803	ILE	Peptide
1	h	828	CYS	Peptide
1	i	828	CYS	Peptide
1	i	834	ARG	Sidechain
1	j	828	CYS	Peptide
1	k	828	CYS	Peptide
1	l	757	LEU	Peptide
1	l	771	VAL	Peptide
1	m	815	SER	Peptide
1	m	828	CYS	Peptide
1	p	875	ILE	Peptide
1	u	866	ILE	Peptide
1	v	866	ILE	Peptide
1	v	877	LEU	Peptide
1	w	866	ILE	Peptide
1	w	877	LEU	Peptide
1	x	866	ILE	Peptide
1	y	866	ILE	Peptide
1	z	866	ILE	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	881	0	906	11	0
1	2	881	0	906	23	0
1	A	2425	0	2423	48	0
1	B	1998	0	1977	35	0
1	C	1232	0	1211	30	0
1	D	993	0	1005	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2215	0	2180	34	0
1	F	2469	0	2470	33	0
1	G	1403	0	1365	35	0
1	H	959	0	978	26	0
1	I	3014	0	3010	102	0
1	J	2963	0	2965	124	0
1	K	1637	0	1630	31	0
1	L	1678	0	1669	33	0
1	M	1786	0	1796	78	0
1	N	1723	0	1738	77	0
1	O	465	0	465	25	0
1	P	444	0	446	26	0
1	Q	2876	0	2882	50	0
1	R	2096	0	2111	29	0
1	S	1468	0	1460	22	0
1	T	647	0	652	19	0
1	U	3096	0	3078	50	0
1	V	2121	0	2126	29	0
1	W	1649	0	1638	18	0
1	X	749	0	761	16	0
1	Y	2959	0	2962	104	0
1	Z	2017	0	2003	35	0
1	a	1559	0	1569	109	0
1	b	731	0	710	9	0
1	c	2988	0	2987	133	0
1	d	2057	0	2040	34	0
1	e	725	0	706	10	0
1	f	1586	0	1591	125	0
1	g	729	0	717	11	0
1	h	729	0	717	21	0
1	i	729	0	717	28	0
1	j	729	0	717	18	0
1	k	729	0	717	10	0
1	l	729	0	717	26	0
1	m	729	0	717	24	0
1	n	699	0	733	10	0
1	o	699	0	733	17	0
1	p	699	0	733	16	0
1	q	699	0	733	16	0
1	r	699	0	733	9	0
1	s	699	0	733	11	0
1	t	699	0	733	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	u	881	0	906	17	0
1	v	881	0	906	13	0
1	w	881	0	906	10	0
1	x	881	0	906	18	0
1	y	881	0	906	14	0
1	z	881	0	906	11	0
2	10	1493	0	1518	22	0
2	11	1512	0	1542	18	0
2	12	1493	0	1518	35	0
2	13	1512	0	1542	18	0
2	14	1493	0	1518	20	0
2	15	764	0	797	6	0
2	16	834	0	863	13	0
2	3	1512	0	1542	21	0
2	4	1493	0	1518	21	0
2	5	1512	0	1542	19	0
2	6	1493	0	1518	30	0
2	7	1512	0	1542	18	0
2	8	1493	0	1518	30	0
2	9	1512	0	1542	22	0
3	1A	3325	0	3251	78	0
3	1C	3325	0	3252	62	0
3	1E	3325	0	3249	82	0
3	1G	3325	0	3252	56	0
3	1I	3325	0	3252	44	0
3	1K	3325	0	3252	58	0
3	1M	3325	0	3252	80	0
3	2A	3325	0	3252	73	0
3	2C	3325	0	3250	68	0
3	2E	3325	0	3250	69	0
3	2G	3325	0	3252	52	0
3	2I	3325	0	3251	61	0
3	2K	3325	0	3252	54	0
3	2M	3325	0	3252	63	0
3	3A	3325	0	3251	90	0
3	3C	3325	0	3252	72	0
3	3E	3325	0	3252	48	0
3	3G	3325	0	3252	35	0
3	3I	3325	0	3251	43	0
3	3K	3325	0	3252	54	0
3	3M	3325	0	3252	76	0
3	4A	3325	0	3252	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	4C	3325	0	3252	61	0
3	4E	3325	0	3252	43	0
3	4G	3325	0	3251	46	0
3	4I	3325	0	3252	36	0
3	4K	3325	0	3252	41	0
3	4M	3325	0	3252	81	0
3	5A	3325	0	3252	82	0
3	5C	3325	0	3252	64	0
3	5E	3325	0	3251	43	0
3	5G	3325	0	3252	40	0
3	5I	3325	0	3252	46	0
3	5K	3325	0	3252	34	0
3	5M	3325	0	3252	51	0
3	6A	3325	0	3251	57	0
3	6C	3325	0	3252	48	0
3	6E	3325	0	3251	45	0
3	6G	3325	0	3252	37	0
3	6I	3325	0	3252	50	0
3	6K	3325	0	3252	41	0
3	6M	3325	0	3252	92	0
3	7A	3325	0	3252	42	0
3	7C	3325	0	3252	60	0
3	7E	3325	0	3252	61	0
3	7G	3325	0	3252	46	0
3	7I	3325	0	3252	46	0
3	7K	3325	0	3252	74	0
3	7M	3325	0	3252	76	0
3	8A	3325	0	3251	55	0
3	8C	3325	0	3252	53	0
3	8E	3325	0	3252	65	0
3	8G	3325	0	3252	47	0
3	8I	3325	0	3252	53	0
3	8K	3325	0	3252	72	0
3	8M	3325	0	3252	49	0
3	9A	3325	0	3252	56	0
3	9C	3325	0	3252	51	0
3	9E	3325	0	3251	59	0
3	9G	3325	0	3252	56	0
3	9I	3325	0	3252	65	0
3	9K	3325	0	3252	53	0
3	9M	3325	0	3252	39	0
4	1B	3331	0	3207	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	1D	3331	0	3209	72	0
4	1F	3331	0	3205	68	0
4	1H	3331	0	3209	58	0
4	1J	3331	0	3207	58	0
4	1L	3331	0	3209	62	0
4	1N	3331	0	3207	54	0
4	2B	3331	0	3207	84	0
4	2D	3331	0	3209	71	0
4	2F	3331	0	3207	64	0
4	2H	3331	0	3209	42	0
4	2J	3331	0	3207	57	0
4	2L	3331	0	3209	58	0
4	3B	3331	0	3207	96	0
4	3D	3331	0	3209	66	0
4	3F	3331	0	3207	71	0
4	3H	3331	0	3209	48	0
4	3J	3331	0	3207	54	0
4	3L	3331	0	3209	64	0
4	4B	3331	0	3207	75	0
4	4D	3331	0	3209	52	0
4	4F	3331	0	3207	41	0
4	4H	3331	0	3209	44	0
4	4J	3331	0	3207	44	0
4	4L	3331	0	3209	55	0
4	5B	3331	0	3207	86	0
4	5D	3331	0	3209	45	0
4	5F	3331	0	3207	37	0
4	5H	3331	0	3209	48	0
4	5J	3331	0	3207	50	0
4	5L	3331	0	3209	49	0
4	5N	3331	0	3207	72	0
4	6B	3331	0	3207	69	0
4	6D	3331	0	3209	56	0
4	6F	3331	0	3207	49	0
4	6H	3331	0	3209	65	0
4	6J	3331	0	3207	67	0
4	6L	3331	0	3209	54	0
4	6N	3331	0	3205	88	0
4	7B	3331	0	3207	83	0
4	7D	3331	0	3209	71	0
4	7F	3331	0	3207	63	0
4	7H	3331	0	3209	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	7J	3331	0	3207	76	0
4	7L	3331	0	3209	87	0
4	8B	3331	0	3207	62	0
4	8D	3331	0	3209	55	0
4	8F	3331	0	3207	80	0
4	8H	3331	0	3209	52	0
4	8J	3331	0	3207	79	0
4	8L	3331	0	3209	95	0
4	9B	3331	0	3207	72	0
4	9D	3331	0	3206	56	0
4	9F	3331	0	3207	77	0
4	9H	3331	0	3209	64	0
4	9J	3331	0	3207	60	0
4	9L	3331	0	3207	54	0
5	20	1814	0	1830	30	0
5	21	1815	0	1834	31	0
5	22	1814	0	1830	24	0
5	23	1815	0	1834	23	0
5	24	1814	0	1830	37	0
5	25	1815	0	1834	40	0
5	26	1814	0	1830	32	0
5	27	1815	0	1834	39	0
5	28	1814	0	1830	23	0
5	29	1815	0	1834	36	0
5	30	1814	0	1830	24	0
5	31	1815	0	1834	45	0
5	32	1814	0	1830	30	0
5	33	1321	0	1311	24	0
5	35	1744	0	1764	37	0
5	36	1723	0	1750	17	0
5	37	1744	0	1764	20	0
5	38	1723	0	1750	28	0
5	39	1744	0	1764	34	0
5	40	1723	0	1750	30	0
5	42	1723	0	1750	15	0
5	43	1744	0	1764	30	0
5	44	1723	0	1750	26	0
5	45	1744	0	1764	16	0
5	46	1723	0	1750	20	0
5	47	1744	0	1764	28	0
5	48	1723	0	1750	14	0
5	49	1841	0	1859	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	50	1853	0	1866	38	0
5	51	1841	0	1859	38	0
5	52	1853	0	1866	41	0
5	53	1841	0	1859	37	0
5	54	1853	0	1866	27	0
5	55	1841	0	1859	35	0
5	56	1853	0	1866	28	0
5	57	1841	0	1859	34	0
5	58	1853	0	1866	28	0
5	59	1841	0	1859	26	0
5	60	1853	0	1866	31	0
5	61	1841	0	1859	43	0
5	62	1853	0	1866	45	0
6	63	5055	0	5022	69	0
6	64	5055	0	5022	65	0
6	65	5055	0	5022	69	0
6	66	5055	0	5022	88	0
6	67	5055	0	5022	87	0
6	68	5055	0	5022	87	0
6	69	5055	0	5022	81	0
7	71	1382	0	1347	25	0
7	72	1382	0	1347	23	0
7	73	1382	0	1347	28	0
7	75	1382	0	1347	30	0
7	76	1382	0	1347	19	0
7	77	1382	0	1347	32	0
7	78	1382	0	1347	25	0
7	79	1382	0	1347	16	0
7	80	1382	0	1347	27	0
7	82	1382	0	1347	25	0
7	83	1382	0	1347	38	0
7	84	1382	0	1347	32	0
7	85	1382	0	1347	21	0
7	86	1382	0	1347	23	0
7	87	1382	0	1347	31	0
7	89	1382	0	1347	25	0
7	90	1382	0	1347	27	0
7	91	1382	0	1347	31	0
7	92	1382	0	1347	26	0
7	93	1382	0	1347	23	0
7	94	1382	0	1347	21	0
7	95	1382	0	1347	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	96	1382	0	1347	30	0
7	97	1382	0	1347	20	0
8	A1	2582	0	2580	36	0
8	A2	2582	0	2580	45	0
8	A3	1844	0	1818	38	0
8	A4	1016	0	899	19	0
8	A5	2582	0	2580	39	0
8	A6	2582	0	2580	34	0
8	A7	2582	0	2580	44	0
8	A8	2582	0	2580	28	0
8	A9	1020	0	1043	11	0
9	B1	2055	0	2002	19	0
9	B2	2055	0	2002	30	0
9	B3	2055	0	2002	24	0
9	B4	2055	0	2002	24	0
9	B5	2055	0	2002	41	0
9	B6	2055	0	2002	35	0
9	B7	2055	0	2002	40	0
10	C0	1471	0	1499	13	0
10	C6	1471	0	1499	26	0
10	C7	1471	0	1499	23	0
10	C8	1471	0	1499	31	0
10	C9	1471	0	1499	26	0
10	D0	2197	0	2210	23	0
10	D1	1471	0	1499	23	0
10	D2	1471	0	1499	24	0
10	D3	2197	0	2210	20	0
10	D4	2197	0	2210	16	0
10	D5	2197	0	2210	26	0
10	D6	2197	0	2210	28	0
10	D7	2197	0	2210	23	0
10	D8	2197	0	2210	25	0
10	D9	2197	0	2210	35	0
10	E0	2197	0	2210	21	0
10	E1	2197	0	2210	27	0
10	E2	2197	0	2210	35	0
10	E3	2197	0	2210	30	0
10	E4	2197	0	2210	31	0
10	E5	2197	0	2210	23	0
10	E6	2197	0	2210	39	0
10	E7	2197	0	2210	24	0
10	E8	2197	0	2210	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	E9	2197	0	2210	25	0
10	F1	2197	0	2210	24	0
10	F2	2197	0	2210	42	0
10	F3	2197	0	2210	30	0
11	C1	237	0	242	2	0
11	C2	238	0	239	2	0
11	C3	242	0	244	5	0
11	C4	214	0	212	0	0
11	C5	239	0	243	6	0
12	F0	883	0	883	15	0
12	F5	847	0	844	14	0
12	F6	883	0	883	21	0
12	F7	847	0	844	14	0
12	F8	883	0	883	14	0
12	F9	847	0	844	19	0
12	G0	412	0	416	3	0
12	G1	847	0	844	19	0
12	G2	883	0	883	22	0
12	G3	847	0	844	15	0
12	G4	883	0	883	16	0
12	G5	847	0	844	16	0
12	G6	883	0	883	17	0
12	G7	847	0	844	16	0
12	G8	883	0	883	18	0
12	G9	365	0	364	3	0
12	H0	184	0	174	2	0
12	H1	184	0	174	3	0
12	H2	365	0	364	5	0
12	H3	412	0	416	2	0
12	H4	184	0	174	3	0
12	H5	365	0	364	6	0
12	H6	412	0	416	5	0
12	H7	184	0	174	5	0
12	H8	365	0	364	3	0
12	H9	412	0	416	6	0
12	I1	365	0	364	2	0
12	I2	412	0	416	3	0
12	I3	184	0	174	2	0
12	I4	365	0	364	4	0
12	I5	412	0	416	5	0
12	I6	184	0	174	2	0
12	I7	365	0	364	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	I8	412	0	416	4	0
12	I9	184	0	174	5	0
13	J1	2488	0	2518	42	0
13	J2	2488	0	2518	44	0
13	J3	2488	0	2518	34	0
13	J4	2488	0	2518	29	0
13	J5	2488	0	2518	34	0
13	J6	2488	0	2518	39	0
13	J7	2488	0	2518	22	0
14	K0	1537	0	1507	20	0
14	K1	1537	0	1507	22	0
14	K2	1537	0	1507	16	0
14	K3	1537	0	1507	23	0
14	K4	1537	0	1507	31	0
14	K5	1537	0	1507	18	0
14	K6	1537	0	1507	29	0
14	K7	1537	0	1507	12	0
14	K8	1537	0	1507	17	0
14	K9	1537	0	1507	15	0
14	L0	1537	0	1507	29	0
14	L1	1537	0	1507	29	0
14	L2	1537	0	1507	17	0
14	L3	1537	0	1507	41	0
14	L4	1073	0	1091	20	0
14	L5	1537	0	1507	24	0
14	L6	1537	0	1507	23	0
14	L7	1537	0	1507	30	0
14	L8	1537	0	1507	21	0
14	L9	1537	0	1507	28	0
14	M1	1011	0	1013	18	0
14	M2	1537	0	1507	32	0
14	M3	1537	0	1507	34	0
14	M4	1537	0	1507	27	0
14	M5	1537	0	1507	29	0
14	M6	1537	0	1507	22	0
14	M7	1537	0	1507	37	0
15	1A	32	0	12	1	0
15	1C	32	0	12	0	0
15	1E	32	0	12	0	0
15	1G	32	0	12	0	0
15	1I	32	0	12	0	0
15	1K	32	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	1M	32	0	12	0	0
15	2A	32	0	12	2	0
15	2C	32	0	12	1	0
15	2E	32	0	12	0	0
15	2G	32	0	12	0	0
15	2I	32	0	12	0	0
15	2K	32	0	12	0	0
15	2M	32	0	12	0	0
15	3A	32	0	12	0	0
15	3C	32	0	12	0	0
15	3E	32	0	12	0	0
15	3G	32	0	12	0	0
15	3I	32	0	12	0	0
15	3K	32	0	12	0	0
15	3M	32	0	12	0	0
15	4A	32	0	12	0	0
15	4C	32	0	12	0	0
15	4E	32	0	12	0	0
15	4G	32	0	12	0	0
15	4I	32	0	12	0	0
15	4K	32	0	12	0	0
15	4M	32	0	12	0	0
15	5A	32	0	12	0	0
15	5C	32	0	12	0	0
15	5E	32	0	12	0	0
15	5G	32	0	12	0	0
15	5I	32	0	12	0	0
15	5K	32	0	12	0	0
15	5M	32	0	12	0	0
15	6A	32	0	12	0	0
15	6C	32	0	12	1	0
15	6E	32	0	12	0	0
15	6G	32	0	12	0	0
15	6I	32	0	12	0	0
15	6K	32	0	12	0	0
15	6N	32	0	12	0	0
15	7A	32	0	12	0	0
15	7C	32	0	12	0	0
15	7E	32	0	12	0	0
15	7G	32	0	12	0	0
15	7I	32	0	12	0	0
15	7K	32	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	7M	32	0	12	0	0
15	8A	32	0	12	0	0
15	8C	32	0	12	0	0
15	8E	32	0	12	0	0
15	8G	32	0	12	0	0
15	8I	32	0	12	0	0
15	8K	32	0	12	0	0
15	8M	32	0	12	0	0
15	9A	32	0	12	0	0
15	9C	32	0	12	0	0
15	9E	32	0	12	0	0
15	9G	32	0	12	0	0
15	9I	32	0	12	0	0
15	9K	32	0	12	1	0
15	9M	32	0	12	0	0
16	1A	1	0	0	0	0
16	1C	1	0	0	0	0
16	1E	1	0	0	0	0
16	1G	1	0	0	0	0
16	1I	1	0	0	0	0
16	1K	1	0	0	0	0
16	2A	1	0	0	0	0
16	2C	1	0	0	0	0
16	2E	1	0	0	0	0
16	2G	1	0	0	0	0
16	2I	1	0	0	0	0
16	2K	1	0	0	0	0
16	3A	1	0	0	0	0
16	3C	1	0	0	0	0
16	3E	1	0	0	0	0
16	3G	1	0	0	0	0
16	3I	1	0	0	0	0
16	3K	1	0	0	0	0
16	4A	1	0	0	0	0
16	4C	1	0	0	0	0
16	4E	1	0	0	0	0
16	4G	1	0	0	0	0
16	4I	1	0	0	0	0
16	4K	1	0	0	0	0
16	5A	1	0	0	0	0
16	5C	1	0	0	0	0
16	5E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	5G	1	0	0	0	0
16	5I	1	0	0	0	0
16	5K	1	0	0	0	0
16	6A	1	0	0	0	0
16	6C	1	0	0	0	0
16	6E	1	0	0	0	0
16	6G	1	0	0	0	0
16	6I	1	0	0	0	0
16	6K	1	0	0	0	0
16	7B	1	0	0	0	0
16	7C	1	0	0	0	0
16	7E	1	0	0	0	0
16	7G	1	0	0	0	0
16	7I	1	0	0	0	0
16	7K	1	0	0	0	0
16	8A	1	0	0	0	0
16	8C	1	0	0	0	0
16	8E	1	0	0	1	0
16	8G	1	0	0	0	0
16	8I	1	0	0	0	0
16	8K	1	0	0	0	0
16	9A	1	0	0	0	0
16	9C	1	0	0	0	0
16	9E	1	0	0	0	0
16	9G	1	0	0	0	0
16	9I	1	0	0	0	0
16	9K	1	0	0	0	0
17	1B	28	0	12	1	0
17	1D	28	0	12	2	0
17	1F	28	0	12	1	0
17	1H	28	0	12	0	0
17	1J	28	0	12	0	0
17	1L	28	0	12	0	0
17	1N	28	0	12	0	0
17	2B	28	0	12	2	0
17	2D	28	0	12	0	0
17	2F	28	0	12	1	0
17	2H	28	0	12	2	0
17	2J	28	0	12	0	0
17	2L	28	0	12	1	0
17	3B	28	0	12	2	0
17	3D	28	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	3F	28	0	12	1	0
17	3H	28	0	12	0	0
17	3J	28	0	12	2	0
17	3L	28	0	12	2	0
17	4B	28	0	12	1	0
17	4D	28	0	12	1	0
17	4F	28	0	12	0	0
17	4H	28	0	12	0	0
17	4J	28	0	12	1	0
17	4L	28	0	12	0	0
17	5B	28	0	12	0	0
17	5D	28	0	12	0	0
17	5F	28	0	12	0	0
17	5H	28	0	12	0	0
17	5J	28	0	12	0	0
17	5L	28	0	12	2	0
17	5N	28	0	12	0	0
17	6B	28	0	12	0	0
17	6D	28	0	12	0	0
17	6F	28	0	12	0	0
17	6H	28	0	12	0	0
17	6J	28	0	12	0	0
17	6L	28	0	12	0	0
17	6N	28	0	12	1	0
17	7B	28	0	12	0	0
17	7D	28	0	12	0	0
17	7F	28	0	12	0	0
17	7H	28	0	12	0	0
17	7J	28	0	12	0	0
17	7L	28	0	12	0	0
17	8B	28	0	12	1	0
17	8D	28	0	12	0	0
17	8F	28	0	12	0	0
17	8H	28	0	12	0	0
17	8J	28	0	12	0	0
17	8L	28	0	12	0	0
17	9B	28	0	12	0	0
17	9D	28	0	11	0	0
17	9F	28	0	12	0	0
17	9H	28	0	12	0	0
17	9J	28	0	12	0	0
17	9L	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	806376	0	792189	12039	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (12039) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:682:LYS:HE2	1:l:795:LEU:CD2	1.42	1.49
1:J:577:GLN:NE2	1:J:578:ARG:HD2	1.63	1.14
1:a:607:LEU:HB2	1:f:607:LEU:HB3	1.30	1.14
1:M:682:LYS:CE	1:l:795:LEU:CD2	2.27	1.11
1:a:558:LEU:HD22	1:f:558:LEU:HB3	1.33	1.10
1:M:682:LYS:CE	1:l:795:LEU:HD22	1.81	1.09
1:M:682:LYS:HE2	1:l:795:LEU:HD22	1.30	1.04
1:Y:562:ILE:HD12	1:c:562:ILE:HG12	1.33	1.04
1:a:596:GLU:HB3	1:f:597:ILE:HD11	1.41	1.03
1:Y:607:LEU:HB2	1:c:607:LEU:HB3	1.41	1.02
1:M:682:LYS:HE2	1:l:795:LEU:HD21	1.04	1.00
1:J:577:GLN:HE21	1:J:578:ARG:HD2	1.19	0.98
1:I:656:GLN:HG3	1:J:659:LEU:HD13	1.44	0.97
3:1E:317:LEU:HB2	3:1E:352:LYS:O	1.64	0.97
1:I:610:VAL:HG11	1:J:611:THR:HG22	1.45	0.97
3:4M:430:LYS:O	3:4M:434:GLU:HB2	1.65	0.95
1:Y:607:LEU:HD12	1:c:604:ILE:HD12	1.49	0.94
10:F2:399:SER:O	10:F2:403:GLN:HB2	1.69	0.93
1:J:577:GLN:NE2	1:J:578:ARG:CD	2.31	0.92
1:J:577:GLN:HE21	1:J:578:ARG:CD	1.83	0.92
1:M:682:LYS:CE	1:l:795:LEU:HD21	1.97	0.92
6:68:500:ARG:HH11	6:68:503:LYS:HE2	1.34	0.91
1:J:577:GLN:HG2	1:J:578:ARG:NH1	1.87	0.90
1:I:624:GLN:HB3	1:J:624:GLN:HG3	1.52	0.90
1:Y:607:LEU:CB	1:c:607:LEU:HB3	2.00	0.89
1:a:607:LEU:CB	1:f:607:LEU:HB3	2.01	0.89
1:M:483:ILE:HG22	1:P:657:GLN:HE22	1.38	0.88
1:c:604:ILE:HD13	1:c:607:LEU:HD12	1.55	0.88
6:65:975:LYS:O	6:65:979:ARG:HB2	1.73	0.88
1:J:577:GLN:NE2	1:J:578:ARG:HH11	1.72	0.87
4:2D:11:GLN:HE22	3:2E:249:ASN:H	1.23	0.87
5:58:147:VAL:O	5:58:159:ASP:HB2	1.75	0.86
2:16:196:LYS:O	2:16:200:GLN:HB2	1.74	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1J:200:GLN:HG2	4:1J:266:PHE:HB2	1.56	0.85
6:64:133:ARG:HD2	12:H0:335:ILE:HD12	1.58	0.85
1:G:386:GLU:HB3	1:d:500:ARG:HH12	1.41	0.84
3:6A:255:PHE:O	3:6A:259:LEU:HB2	1.78	0.84
1:G:317:THR:HB	1:c:599:SER:HB2	1.59	0.84
3:2M:141:VAL:HG11	3:2M:172:TRP:HD1	1.43	0.84
3:4G:178:SER:HB3	4:4H:347:ASN:HD22	1.43	0.84
4:6H:274:THR:H	1:g:814:PRO:HG3	1.43	0.84
10:D8:33:ARG:HD3	10:D8:40:ARG:HH22	1.43	0.83
5:50:72:ARG:HB3	5:50:92:THR:O	1.79	0.83
3:6A:214:ARG:HH22	14:K4:252:GLN:HG2	1.42	0.83
1:Y:610:VAL:HG11	1:c:611:THR:HG22	1.59	0.82
2:5:164:GLU:HA	2:5:167:ARG:HD3	1.61	0.82
1:a:604:ILE:HG13	1:f:604:ILE:HG23	1.60	0.82
1:Y:562:ILE:HD11	1:c:562:ILE:HG23	1.62	0.82
4:4B:134:GLN:HA	4:4B:165:GLU:O	1.79	0.82
3:5M:96:LYS:HE3	4:5N:2:ARG:HH12	1.45	0.82
1:a:558:LEU:CD2	1:f:558:LEU:HB3	2.09	0.82
3:1C:11:GLN:HE22	4:1D:247:ASN:H	1.27	0.82
1:I:400:GLU:O	1:I:404:PHE:HB2	1.80	0.81
5:24:100:ASN:O	5:24:179:SER:HB3	1.80	0.81
4:5N:163:ILE:HD11	4:5N:251:ARG:HE	1.43	0.81
3:4I:279:GLU:HB3	3:4I:283:HIS:HB2	1.61	0.81
4:3L:207:LEU:HB3	4:3L:225:LEU:HD22	1.61	0.81
4:8F:318:ARG:HA	4:8F:354:CYS:O	1.81	0.81
1:Y:562:ILE:CD1	1:c:562:ILE:HG12	2.10	0.81
1:o:936:ASP:O	1:o:940:HIS:HB2	1.80	0.81
4:9B:86:ARG:HE	4:9B:87:PRO:HD2	1.46	0.80
1:N:630:ARG:HA	4:9H:276:ARG:HH22	1.47	0.80
9:B5:119:SER:O	9:B5:123:LYS:HB2	1.82	0.80
6:66:844:ALA:O	6:66:848:SER:HB3	1.81	0.79
4:3F:222:TYR:HB2	3:3G:325:PRO:HG3	1.65	0.79
1:I:586:LYS:HB3	1:J:586:LYS:HD3	1.63	0.79
1:M:607:LEU:HB2	1:N:607:LEU:HB3	1.65	0.79
1:M:667:LYS:HB3	3:8G:58:ALA:HB1	1.63	0.78
3:6M:416:GLY:HA3	10:D6:48:ARG:HH22	1.46	0.78
1:H:613:GLN:O	1:H:617:MET:HB2	1.84	0.78
1:K:491:LEU:O	1:K:495:PHE:HB2	1.83	0.78
10:D7:311:LYS:HA	10:D7:403:GLN:HE22	1.49	0.78
4:1J:207:LEU:HB3	4:1J:225:LEU:HD22	1.66	0.78
5:30:119:LEU:HD22	5:31:167:LYS:HZ2	1.46	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:533:ARG:NH2	1:f:534:GLN:HB2	1.98	0.77
1:a:596:GLU:HB3	1:f:597:ILE:CD1	2.14	0.77
3:4M:195:LEU:HD11	3:4M:428:LEU:HD13	1.67	0.77
4:5D:200:GLN:HB3	4:5D:268:ILE:HD11	1.65	0.77
4:5B:54:ALA:HB3	4:5B:58:ARG:HB3	1.64	0.77
7:86:317:GLN:HE22	4:8D:306:ARG:HG3	1.49	0.77
1:a:572:ARG:HB3	1:f:572:ARG:HG3	1.67	0.77
3:2C:392:ASP:HB3	3:2C:422:ARG:HH22	1.48	0.77
5:49:181:GLU:HB3	5:49:185:ARG:HH12	1.48	0.77
4:5H:313:ALA:HB3	4:5H:349:MET:HG2	1.66	0.77
3:2C:178:SER:HB2	3:2C:183:GLU:HG2	1.65	0.77
4:5J:86:ARG:HH12	4:6J:282:ARG:HB3	1.49	0.77
3:6K:269:LEU:HB2	3:6K:379:SER:HB2	1.67	0.76
1:F:469:LEU:HD11	1:f:581:LYS:HD2	1.66	0.76
4:3F:207:LEU:HB3	4:3F:225:LEU:HD22	1.66	0.76
3:4E:51:THR:HG21	3:4E:243:ARG:HG2	1.67	0.76
7:80:284:THR:HG23	7:80:286:TRP:H	1.50	0.76
4:7B:200:GLN:HG2	4:7B:266:PHE:HB2	1.66	0.76
13:J1:353:ARG:HD2	13:J1:354:ALA:H	1.49	0.76
3:4M:298:PRO:HG2	3:4M:308:ARG:HE	1.50	0.76
3:8M:268:MET:HE2	3:8M:378:ILE:HG22	1.67	0.76
1:N:607:LEU:HA	1:N:610:VAL:HB	1.67	0.76
7:92:390:PRO:HD3	14:M3:118:CYS:HB3	1.66	0.76
7:96:350:ARG:HG3	7:96:388:GLU:HB2	1.67	0.76
1:Y:579:LEU:HD13	1:c:579:LEU:HG	1.68	0.76
4:1L:235:GLY:HA2	4:1L:318:ARG:HH12	1.51	0.76
9:B7:514:VAL:O	9:B7:518:CYS:HB2	1.85	0.76
3:3A:240:ALA:HB1	3:3A:356:ASN:HD22	1.50	0.76
1:N:573:GLN:HB3	1:N:576:SER:HB3	1.68	0.76
3:2E:238:LEU:HD21	3:2E:378:ILE:HD13	1.67	0.76
5:32:46:ARG:HH22	5:32:48:VAL:HB	1.50	0.75
1:I:579:LEU:HD21	1:J:579:LEU:HD22	1.66	0.75
3:3I:107:HIS:CE1	3:3I:152:LEU:HD13	2.21	0.75
3:6G:339:ARG:HH22	14:K2:120:GLU:H	1.35	0.75
1:J:577:GLN:CG	1:J:578:ARG:NH1	2.50	0.75
3:7I:392:ASP:O	3:7I:396:ASP:HB2	1.87	0.75
4:8J:253:LEU:O	4:8J:257:LEU:HB3	1.87	0.75
4:6B:253:LEU:O	4:6B:257:LEU:HB2	1.87	0.75
7:93:330:ARG:HH22	7:93:379:LEU:HD12	1.51	0.75
6:69:262:LYS:HE3	6:69:303:LEU:HD12	1.67	0.75
4:8F:329:GLN:HA	4:8F:332:ASN:HB2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8K:202:VAL:HA	3:8K:268:MET:HB2	1.69	0.74
3:9I:178:SER:HB3	3:9I:183:GLU:HG3	1.69	0.74
3:1K:187:SER:HB2	3:1K:391:MET:HE1	1.67	0.74
4:3B:222:TYR:HB2	3:3C:325:PRO:HG2	1.67	0.74
3:3A:106:GLY:HA3	3:3A:148:GLY:HA3	1.69	0.74
1:U:624:GLN:HB2	1:h:807:GLY:HA3	1.69	0.74
1:Y:604:ILE:HA	1:c:604:ILE:HD11	1.67	0.74
1:2:885:GLU:HG2	6:67:916:ARG:HH22	1.52	0.74
8:A5:234:ARG:HG3	8:A6:332:THR:HG21	1.68	0.74
4:5B:201:VAL:HG11	4:5B:377:MET:HE1	1.69	0.74
3:5E:2:ARG:HB2	3:5E:133:GLN:HE21	1.53	0.74
4:8B:207:LEU:HB3	4:8B:225:LEU:HD22	1.69	0.74
8:A1:63:ASN:HD22	1:u:900:GLU:HG3	1.52	0.74
1:K:324:GLU:HA	1:K:327:TRP:HD1	1.52	0.74
1:Y:575:LEU:HB3	1:c:576:SER:HB2	1.70	0.74
8:A5:63:ASN:HD22	1:v:900:GLU:HG3	1.51	0.74
4:8D:86:ARG:HE	4:8D:87:PRO:HD2	1.52	0.74
4:8J:164:MET:HB3	4:8J:197:ASP:H	1.51	0.74
8:A4:59:ALA:H	8:A4:92:TYR:HD1	1.35	0.74
4:4H:317:PHE:HB3	4:4H:321:MET:HE1	1.70	0.74
3:5G:223:THR:HG22	4:5H:322:SER:HA	1.69	0.74
4:6N:360:GLY:H	1:i:824:GLN:HE22	1.36	0.74
7:78:296:ARG:HG3	7:78:321:GLU:HB3	1.69	0.74
4:8L:299:MET:HG3	4:8L:305:PRO:HG3	1.70	0.74
4:9J:318:ARG:HB3	4:9J:354:CYS:HB2	1.69	0.74
1:a:533:ARG:HH12	1:f:533:ARG:HH22	1.36	0.74
3:1A:250:VAL:HG23	3:1A:254:GLU:HG2	1.69	0.74
5:28:35:SER:HB2	5:28:76:LEU:HD21	1.70	0.74
3:8K:269:LEU:HB2	3:8K:379:SER:HB3	1.70	0.74
3:9M:255:PHE:O	3:9M:259:LEU:HB2	1.86	0.73
1:J:577:GLN:CG	1:J:578:ARG:HH11	2.00	0.73
1:L:411:LYS:HA	1:L:414:GLN:HG3	1.70	0.73
1:O:656:GLN:HA	1:P:659:LEU:HD11	1.71	0.73
3:2M:274:PRO:HG2	3:2M:374:ALA:HA	1.69	0.73
3:9G:11:GLN:HE22	4:9H:247:ASN:H	1.36	0.73
4:4L:113:ILE:HG12	4:4L:150:LEU:HD22	1.70	0.73
5:56:45:SER:HA	5:56:72:ARG:HH22	1.53	0.73
3:5C:73:THR:HA	4:5D:46:ARG:HH22	1.53	0.73
1:B:387:ILE:HD13	1:E:388:ARG:HH12	1.53	0.73
4:4B:359:LYS:HA	8:A3:170:ARG:HH12	1.53	0.73
6:67:314:CYS:HB2	6:67:317:GLN:HE21	1.52	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7A:176:GLN:HE22	14:L1:254:PHE:HB2	1.53	0.73
3:8A:301:MET:HE1	3:8A:305:CYS:H	1.53	0.73
3:8E:182:VAL:HA	3:8E:398:MET:HE1	1.70	0.73
4:8B:8:GLN:HE21	4:8B:65:LEU:HG	1.52	0.73
4:8L:317:PHE:HA	4:8L:365:VAL:HG22	1.70	0.73
14:K4:162:LYS:HZ1	14:K4:232:ARG:HA	1.53	0.73
3:5A:91:GLN:HG2	3:5A:121:ARG:HE	1.52	0.73
12:G7:253:THR:HG21	12:G7:262:LEU:HG	1.71	0.73
13:J6:353:ARG:HD2	13:J6:354:ALA:H	1.54	0.73
1:f:564:GLU:O	1:f:565:ASP:C	2.29	0.73
4:1D:258:ILE:HD12	4:1D:264:HIS:HB3	1.70	0.73
4:6B:200:GLN:HG3	4:6B:266:PHE:HB2	1.70	0.73
5:25:158:LEU:O	5:25:173:CYS:HA	1.89	0.73
3:9A:222:PRO:HG2	4:9B:324:LYS:HE2	1.69	0.73
1:Z:326:GLU:HB3	1:Z:330:ARG:HH12	1.53	0.73
4:4B:6:HIS:O	4:4B:63:ALA:HA	1.88	0.73
3:6K:2:ARG:HB3	3:6K:133:GLN:HE21	1.53	0.73
4:6N:248:SER:HA	4:6N:252:LYS:HG3	1.70	0.73
5:61:77:ILE:HD11	5:61:84:PRO:HB3	1.68	0.73
3:6A:105:ARG:HH12	4:6B:251:ARG:HD3	1.51	0.73
4:6L:156:ARG:HH22	4:6L:197:ASP:HB2	1.52	0.73
3:9E:407:TRP:HE1	4:9F:258:ILE:HB	1.54	0.73
1:Y:594:ALA:HB1	1:s:882:GLU:HG2	1.71	0.72
3:2K:71:GLU:HB3	3:2K:98:ASP:HB3	1.70	0.72
5:56:33:ASP:HB3	5:56:36:LEU:H	1.53	0.72
7:83:386:ARG:HG3	14:L2:115:PRO:HB3	1.70	0.72
4:8D:273:LEU:H	4:8D:292:GLN:HE22	1.35	0.72
3:2M:121:ARG:HH12	3:2M:125:LEU:HD22	1.53	0.72
5:20:48:VAL:HG21	5:20:134:LEU:HD12	1.71	0.72
3:2E:53:PHE:HB3	3:2E:61:HIS:HB3	1.72	0.72
4:6B:284:LEU:HD11	4:6B:362:LYS:HB2	1.72	0.72
7:87:378:MET:HE1	14:L7:240:TRP:HB2	1.71	0.72
3:2A:259:LEU:HB3	3:2A:268:MET:HE3	1.72	0.72
5:36:33:ASP:HB3	5:36:36:LEU:HB2	1.72	0.72
4:4J:210:ILE:O	4:4J:214:THR:HB	1.89	0.72
3:5A:68:LEU:HD21	3:5A:149:LEU:HD23	1.70	0.72
4:9L:305:PRO:HB2	4:9L:310:TYR:HE1	1.55	0.72
1:Q:624:GLN:HE22	1:U:624:GLN:HG2	1.55	0.72
4:1F:256:ASN:HD22	4:1F:350:LYS:HG3	1.55	0.72
4:5D:402:GLY:HA3	14:K3:125:VAL:HG21	1.70	0.72
6:67:316:MET:HE1	12:I4:98:LYS:HD3	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:67:490:GLU:HA	6:67:493:ARG:HE	1.53	0.72
3:1M:187:SER:HB2	3:1M:391:MET:HE1	1.72	0.72
4:3D:334:GLN:HE22	4:3D:347:ASN:HA	1.52	0.72
3:3I:89:PRO:HD3	3:4I:282:TYR:HB3	1.72	0.72
3:3M:278:ALA:H	3:3M:369:ALA:HB2	1.55	0.72
5:49:24:VAL:HG13	5:49:201:LEU:HD23	1.72	0.72
13:J6:351:ARG:HD3	13:J6:352:LYS:HG3	1.71	0.72
3:6M:296:PHE:HE1	3:6M:377:MET:HG3	1.55	0.71
3:9K:202:VAL:HA	3:9K:268:MET:HB3	1.70	0.71
5:55:55:GLN:HB2	5:55:151:HIS:HA	1.73	0.71
5:59:33:ASP:HB3	5:59:36:LEU:HB2	1.71	0.71
10:E1:307:MET:HG3	10:E1:396:LEU:HD12	1.71	0.71
13:J7:353:ARG:HD2	13:J7:354:ALA:H	1.54	0.71
1:D:640:ALA:HB2	1:m:826:VAL:HB	1.73	0.71
1:M:682:LYS:HE3	1:l:795:LEU:HD22	1.70	0.71
5:24:67:ARG:HH22	12:F7:263:TYR:HA	1.54	0.71
1:J:577:GLN:HE21	1:J:578:ARG:NH1	1.87	0.71
4:2B:319:GLY:HA3	4:2B:363:MET:HG2	1.72	0.71
3:3A:67:PHE:HB2	3:3A:92:LEU:HG	1.70	0.71
4:2D:65:LEU:HB3	4:2D:73:MET:HE1	1.71	0.71
4:2L:139:LEU:HA	4:2L:145:SER:HB3	1.73	0.71
3:6G:88:HIS:HD2	3:6G:90:GLU:H	1.38	0.71
4:7F:154:LYS:HD2	7:85:286:TRP:HE1	1.55	0.71
3:8E:178:SER:HB3	3:8E:183:GLU:HG3	1.72	0.71
5:49:34:PRO:HB3	5:49:186:ARG:HE	1.54	0.71
4:7H:262:ARG:HH12	14:L5:138:THR:HG22	1.55	0.71
14:L1:200:PHE:HB2	14:L1:220:LEU:HD12	1.72	0.71
4:7D:179:VAL:HG12	4:7D:180:VAL:HG13	1.72	0.71
7:87:371:GLU:HB2	14:L7:240:TRP:HE1	1.54	0.71
3:3A:392:ASP:O	3:3A:396:ASP:HB2	1.90	0.71
14:L7:198:ARG:HH22	14:L7:206:VAL:HA	1.53	0.71
1:a:523:VAL:HG12	1:f:523:VAL:HG12	1.72	0.71
1:Q:542:ALA:HB1	1:Z:431:ALA:HB2	1.71	0.71
5:21:77:ILE:HD13	5:21:127:PRO:HG3	1.72	0.71
4:3B:83:GLN:HB3	6:66:866:ARG:HH22	1.56	0.71
3:4C:132:LEU:HB3	3:4C:164:LYS:HZ1	1.55	0.71
3:5A:53:PHE:HB3	3:5A:61:HIS:HB3	1.73	0.71
4:5B:86:ARG:HH22	4:6B:282:ARG:HB3	1.56	0.71
4:9D:312:THR:HA	4:9D:348:ASN:HB2	1.72	0.71
1:Q:434:ALA:HB3	1:v:859:LEU:HD12	1.73	0.70
3:4E:213:CYS:HA	3:4E:217:LEU:HD13	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5A:178:SER:HB3	4:5B:347:ASN:HD22	1.56	0.70
4:6B:39:ASP:H	1:h:760:ARG:HE	1.38	0.70
4:7B:318:ARG:HA	4:7B:354:CYS:HB3	1.73	0.70
9:B5:160:PRO:HB3	11:C5:220:VAL:HG12	1.71	0.70
4:1L:274:THR:HG21	4:1L:279:GLN:HB3	1.74	0.70
3:1M:153:LEU:O	3:1M:157:LEU:HB2	1.91	0.70
3:5E:102:ASN:HD22	3:5E:105:ARG:HG3	1.56	0.70
3:5I:212:ILE:HD11	3:5I:300:SER:HA	1.73	0.70
4:7B:257:LEU:HD21	4:7B:314:SER:HB2	1.73	0.70
1:M:663:LEU:HD11	1:N:662:ASP:HB3	1.73	0.70
1:Y:513:ARG:HH22	1:c:512:LYS:HD2	1.55	0.70
5:33:140:GLU:HB3	5:33:143:CYS:HB2	1.71	0.70
4:6J:207:LEU:HB3	4:6J:225:LEU:HD11	1.73	0.70
10:F3:305:LEU:HD21	14:M5:142:GLN:HB3	1.72	0.70
2:11:225:ARG:HH12	2:12:226:VAL:HG11	1.55	0.70
5:40:161:ILE:HD11	5:40:168:PHE:HB3	1.73	0.70
4:6L:399:THR:HA	4:6L:403:MET:HB3	1.74	0.70
4:9D:179:VAL:H	3:9E:352:LYS:HE2	1.57	0.70
1:K:358:SER:HA	1:K:361:LEU:HD23	1.72	0.70
5:25:74:LYS:O	5:25:89:VAL:HA	1.91	0.70
3:2E:2:ARG:HH21	3:2E:242:LEU:HA	1.55	0.70
3:5A:88:HIS:HB3	3:5A:91:GLN:HG3	1.73	0.70
3:7M:137:MET:HB2	3:7M:168:ASN:HA	1.73	0.70
3:9A:268:MET:HE2	3:9A:378:ILE:HG22	1.73	0.70
1:J:577:GLN:CD	1:J:578:ARG:HH11	1.99	0.70
3:3I:88:HIS:HB3	3:3I:91:GLN:HG2	1.73	0.70
3:5A:406:HIS:HB2	14:K4:148:ILE:HD13	1.72	0.70
12:F6:200:LEU:HA	12:F6:203:VAL:HG12	1.74	0.70
3:3M:255:PHE:O	3:3M:259:LEU:HB2	1.91	0.70
4:6H:329:GLN:HA	4:6H:332:ASN:HB2	1.74	0.70
6:68:495:LEU:HD23	6:68:498:ARG:HH11	1.56	0.70
4:6L:313:ALA:HB3	4:6L:349:MET:HG2	1.74	0.70
4:8J:203:ASP:HB2	4:8J:377:MET:HE1	1.74	0.70
5:43:203:GLN:HA	5:43:206:LEU:HD13	1.73	0.70
3:7E:178:SER:HB3	4:7F:347:ASN:HD22	1.57	0.70
7:85:317:GLN:HE21	4:8F:307:HIS:HA	1.55	0.70
4:8D:287:PRO:HA	4:8D:329:GLN:HE22	1.57	0.70
8:A2:66:LEU:HA	8:A2:69:MET:HG3	1.72	0.70
1:J:617:MET:HA	1:J:620:ASP:HB2	1.74	0.70
5:59:78:LEU:HD12	5:59:86:HIS:HB3	1.74	0.70
1:f:565:ASP:HB3	1:f:566:ARG:NH2	2.06	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3A:31:GLN:HB3	8:A3:241:LEU:HD21	1.74	0.69
4:5N:7:VAL:O	4:5N:135:ILE:HA	1.92	0.69
6:67:185:ASP:H	6:67:565:ARG:HD3	1.57	0.69
4:8J:24:ILE:HD12	4:8J:241:ARG:HH12	1.56	0.69
4:7B:424:GLN:HE22	10:E6:301:ARG:HH12	1.38	0.69
4:2B:96:GLY:HA3	3:2C:133:GLN:HE22	1.57	0.69
4:3D:42:LEU:HD21	8:A2:229:ARG:HE	1.56	0.69
3:6E:234:VAL:HG21	3:6E:302:MET:HE1	1.74	0.69
3:8A:91:GLN:HE21	3:8A:121:ARG:HH22	1.39	0.69
1:f:677:MET:HE2	1:f:677:MET:HA	1.74	0.69
3:3A:296:PHE:HE1	3:3A:377:MET:HG3	1.57	0.69
4:4B:98:GLY:HA2	3:4C:254:GLU:HG2	1.72	0.69
6:68:589:LEU:HD23	6:68:590:ARG:H	1.57	0.69
8:A6:42:VAL:HG23	8:A6:69:MET:HE1	1.75	0.69
8:A7:386:ARG:HH21	9:B2:161:LEU:HD23	1.57	0.69
3:1K:259:LEU:HD21	3:1K:316:CYS:HB2	1.72	0.69
4:5B:326:VAL:HG12	4:5B:330:MET:HE1	1.73	0.69
4:6N:286:VAL:HA	4:6N:289:LEU:HB3	1.74	0.69
14:L4:185:ILE:O	14:L4:189:ILE:HB	1.92	0.69
1:a:602:ASN:HA	1:a:605:LYS:HD2	1.75	0.69
1:a:611:THR:HA	1:f:610:VAL:HG11	1.72	0.69
4:3B:16:ILE:HA	4:3B:226:ASN:HD21	1.57	0.69
3:5C:51:THR:HG21	3:5C:243:ARG:HG2	1.75	0.69
6:69:181:LEU:HD13	6:69:571:THR:HG22	1.73	0.69
4:6N:313:ALA:O	4:6N:349:MET:HA	1.93	0.69
4:7D:293:MET:HE2	4:7D:367:PHE:HB2	1.74	0.69
7:85:413:ARG:HH22	4:8F:304:ASP:HB3	1.57	0.69
4:1B:178:THR:HG22	4:1B:180:VAL:H	1.57	0.69
5:23:133:MET:HE1	5:23:172:LEU:HD12	1.75	0.69
5:36:161:ILE:HD11	5:36:168:PHE:HB3	1.73	0.69
3:3C:276:ILE:HD12	3:3C:281:ALA:HA	1.75	0.69
5:40:165:GLU:HB3	13:J3:338:LEU:HB2	1.73	0.69
4:6L:7:VAL:HB	4:6L:135:ILE:HG22	1.74	0.69
3:6M:100:ALA:HA	4:6N:252:LYS:HD2	1.75	0.69
8:A8:234:ARG:HG2	8:A9:332:THR:HG21	1.75	0.69
10:D9:67:ALA:O	10:D9:71:GLN:HB2	1.93	0.69
1:V:518:ARG:HG3	1:X:686:PHE:HB3	1.73	0.69
4:1B:7:VAL:HB	4:1B:135:ILE:HG12	1.75	0.69
1:2:879:VAL:HG11	6:67:891:ARG:HH22	1.58	0.69
3:2E:301:MET:HE2	3:2E:377:MET:HE2	1.73	0.69
4:4D:24:ILE:HD12	4:4D:241:ARG:HH12	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:51:218:PRO:HD2	6:63:942:ARG:HG2	1.73	0.69
4:5D:7:VAL:HG12	4:5D:64:ILE:HB	1.75	0.69
5:61:55:GLN:HB2	5:61:151:HIS:HA	1.74	0.69
6:69:589:LEU:HD23	6:69:590:ARG:H	1.56	0.69
4:6D:200:GLN:HG2	4:6D:268:ILE:HD11	1.75	0.69
4:6D:232:ALA:HB2	4:6D:270:PHE:HB2	1.74	0.69
7:77:282:ARG:HH21	7:77:287:LEU:HD12	1.58	0.69
8:A2:328:ARG:HH12	8:A3:227:SER:H	1.41	0.69
13:J3:337:ARG:HH21	13:J3:647:GLU:HA	1.56	0.69
1:Y:607:LEU:HB2	1:c:607:LEU:CB	2.21	0.69
3:3M:75:VAL:HG13	3:3M:92:LEU:HD12	1.75	0.69
5:51:24:VAL:HG13	5:51:201:LEU:HD22	1.75	0.69
4:5N:293:MET:HE2	4:5N:367:PHE:HB2	1.72	0.69
12:G2:227:SER:HB2	12:G2:236:LEU:HD11	1.74	0.69
1:I:429:ARG:HA	1:J:429:ARG:HH12	1.56	0.69
1:J:577:GLN:HE21	1:J:578:ARG:HH11	1.41	0.69
4:1L:256:ASN:HD22	4:1L:350:LYS:HD2	1.58	0.69
3:2I:274:PRO:HG3	3:2I:374:ALA:HA	1.75	0.69
4:3J:224:ASP:HB3	8:A7:257:PRO:HG3	1.75	0.69
4:4D:200:GLN:HB3	4:4D:268:ILE:HD11	1.73	0.69
4:7D:132:GLY:HA3	4:7D:163:ILE:HG22	1.73	0.69
4:7J:397:TRP:HH2	3:7K:260:VAL:HB	1.58	0.69
10:D5:296:MET:HE3	10:D5:389:PHE:HB2	1.74	0.69
3:1A:100:ALA:HA	4:1B:252:LYS:HG2	1.74	0.68
5:44:162:GLN:HB2	5:44:171:LEU:HD11	1.73	0.68
4:5L:313:ALA:HB3	4:5L:349:MET:HG2	1.75	0.68
8:A1:87:VAL:HG12	8:A1:93:VAL:HG12	1.74	0.68
4:1B:207:LEU:HB3	4:1B:225:LEU:HD12	1.76	0.68
3:1I:296:PHE:HE1	3:1I:377:MET:HG3	1.57	0.68
4:2B:134:GLN:HA	4:2B:165:GLU:O	1.93	0.68
4:6F:375:GLN:HG3	4:6F:419:VAL:HG13	1.75	0.68
3:7M:208:ALA:HB2	3:7M:304:LYS:HG2	1.74	0.68
14:L3:152:ARG:HE	14:L3:171:VAL:HG11	1.57	0.68
5:31:55:GLN:HE22	5:31:58:GLY:H	1.42	0.68
3:5M:292:THR:HG21	3:5M:331:ALA:HB1	1.75	0.68
4:8L:323:THR:HG22	4:8L:353:VAL:HG11	1.75	0.68
8:A3:229:ARG:HB3	8:A3:232:ARG:HB2	1.76	0.68
4:1B:201:VAL:HG21	4:1B:374:ILE:HD11	1.76	0.68
4:3H:33:THR:HG22	4:3H:58:ARG:HH12	1.57	0.68
4:3L:12:CYS:HA	17:3L:501:GDP:HN22	1.58	0.68
3:4K:107:HIS:HD2	3:4K:152:LEU:HB2	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J4:353:ARG:HD2	13:J4:354:ALA:H	1.59	0.68
13:J5:353:ARG:HD2	13:J5:354:ALA:H	1.58	0.68
1:S:434:ALA:HB3	1:1:859:LEU:HD12	1.74	0.68
5:29:140:GLU:HG3	5:29:143:CYS:HB2	1.75	0.68
4:3B:44:LEU:HD21	8:A3:209:SER:HA	1.76	0.68
3:7A:175:PRO:HB3	3:7A:390:ARG:HD2	1.75	0.68
4:7D:271:ALA:HB2	4:7D:365:VAL:H	1.58	0.68
4:9F:165:GLU:HB2	4:9F:200:GLN:HE22	1.57	0.68
10:C9:298:GLU:HG3	10:C9:302:ARG:HH22	1.59	0.68
13:J2:351:ARG:HD3	13:J2:352:LYS:HG3	1.75	0.68
1:I:586:LYS:HB3	1:J:586:LYS:CD	2.24	0.68
4:1J:98:GLY:HA2	3:1K:254:GLU:HG2	1.73	0.68
4:2D:317:PHE:HB3	4:2D:321:MET:HE1	1.74	0.68
5:51:56:GLU:HG2	5:51:58:GLY:H	1.59	0.68
5:57:53:ARG:HB2	5:57:149:ILE:HG22	1.75	0.68
3:6A:259:LEU:HB3	3:6A:268:MET:HE1	1.74	0.68
4:7J:121:ARG:O	4:7J:125:GLU:HB2	1.94	0.68
3:8K:88:HIS:HB3	3:8K:91:GLN:HB2	1.73	0.68
10:D9:318:PRO:HA	10:D9:321:ARG:HE	1.57	0.68
4:2H:2:ARG:HB3	4:2H:131:GLN:HB2	1.76	0.68
4:2J:349:MET:HE3	4:2J:350:LYS:H	1.59	0.68
13:J6:405:VAL:O	13:J6:409:LEU:HB2	1.94	0.68
4:1H:7:VAL:HB	4:1H:135:ILE:HG12	1.74	0.68
3:1M:271:SER:HA	3:1M:302:MET:HE1	1.75	0.68
5:20:99:LEU:HD11	5:20:150:MET:HE1	1.76	0.68
3:2M:62:VAL:HG11	3:3M:283:HIS:HD2	1.59	0.68
5:59:56:GLU:HG2	5:59:58:GLY:H	1.59	0.68
4:5N:103:LYS:HA	4:5N:107:THR:HB	1.76	0.68
5:61:206:LEU:HD22	5:62:21:LEU:HG	1.75	0.68
4:7H:383:ASP:HB2	7:82:311:SER:HB3	1.76	0.68
4:8D:44:LEU:HA	4:8D:47:ILE:HD11	1.76	0.68
4:9H:173:PRO:HA	4:9H:380:ARG:HD3	1.76	0.68
4:9H:299:MET:HG2	4:9H:301:CYS:H	1.58	0.68
10:D9:307:MET:HG3	10:D9:396:LEU:HD12	1.75	0.68
14:K5:156:LEU:HD21	14:K5:185:ILE:HD12	1.75	0.68
1:M:665:THR:HG22	3:9G:370:LYS:NZ	2.09	0.68
3:1E:54:SER:HB2	3:1E:64:ARG:HE	1.58	0.68
5:54:148:LEU:HD11	5:54:156:ALA:HB1	1.75	0.68
5:56:50:PHE:HB2	5:56:71:ILE:HD12	1.74	0.68
3:5A:4:VAL:HB	3:5A:133:GLN:HE21	1.59	0.68
4:5N:207:LEU:HB3	4:5N:225:LEU:HD11	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7I:271:SER:HB2	3:7I:377:MET:HB3	1.76	0.68
3:8M:288:VAL:HG21	3:8M:327:ASP:HB3	1.76	0.68
7:92:296:ARG:HG3	7:92:317:GLN:HA	1.75	0.68
3:2G:53:PHE:HB3	3:2G:61:HIS:HB3	1.76	0.68
4:3H:207:LEU:HB3	4:3H:225:LEU:HD22	1.76	0.68
3:5M:265:ILE:HG22	3:5M:380:ASN:HD21	1.59	0.68
6:69:485:LYS:HD2	6:69:486:PRO:HD2	1.75	0.68
3:8K:416:GLY:H	10:F2:48:ARG:HH22	1.40	0.68
1:a:613:GLN:HB3	1:f:614:LEU:HD13	1.74	0.68
1:d:373:LEU:O	1:d:377:HIS:HB2	1.94	0.68
4:1D:210:ILE:HG12	4:1D:213:ARG:HH21	1.58	0.67
3:1G:259:LEU:HD21	3:1G:316:CYS:HB2	1.76	0.67
4:2J:200:GLN:HG2	4:2J:266:PHE:HB2	1.75	0.67
4:4D:375:GLN:HB2	4:4D:419:VAL:HG23	1.74	0.67
4:4J:163:ILE:HG21	4:4J:250:LEU:HB3	1.76	0.67
3:5M:56:THR:HA	3:6M:285:GLN:HB3	1.75	0.67
6:65:561:LEU:HA	6:65:564:MET:HB2	1.76	0.67
3:6I:178:SER:HB3	3:6I:183:GLU:HG3	1.76	0.67
14:K4:171:VAL:HG23	14:K4:181:LEU:HD21	1.76	0.67
1:c:602:ASN:O	1:c:605:LYS:HB3	1.93	0.67
5:39:33:ASP:HB3	5:39:36:LEU:HB2	1.76	0.67
5:42:165:GLU:HB2	13:J4:338:LEU:HB3	1.76	0.67
4:4B:45:GLU:HG2	4:4B:46:ARG:HG2	1.76	0.67
4:7D:37:CYS:HA	1:k:760:ARG:HH12	1.58	0.67
1:f:525:ALA:O	1:f:528:ARG:HB3	1.93	0.67
4:3B:253:LEU:O	4:3B:257:LEU:HB2	1.94	0.67
3:3I:169:PHE:HZ	3:3I:238:LEU:HD22	1.60	0.67
4:4F:30:ILE:HD11	4:4F:47:ILE:HD11	1.77	0.67
6:65:181:LEU:HD23	6:65:571:THR:HG22	1.77	0.67
4:8F:74:ASP:HB3	1:l:791:ARG:HB3	1.75	0.67
13:J3:664:LYS:HD3	13:J3:667:ARG:HH12	1.58	0.67
4:2D:149:THR:HA	4:2D:152:ILE:HD12	1.76	0.67
3:2G:364:PRO:HB2	9:B1:150:MET:HE3	1.76	0.67
4:7B:379:LYS:HG3	7:80:311:SER:HA	1.77	0.67
14:L3:207:ILE:HG23	14:L3:212:ASP:HB2	1.76	0.67
1:h:818:ALA:HB3	1:h:821:ASN:HB2	1.76	0.67
1:M:645:GLN:HB3	1:N:645:GLN:HE21	1.58	0.67
4:1B:200:GLN:HG3	4:1B:266:PHE:HB2	1.76	0.67
3:1M:286:LEU:HB3	3:1M:291:ILE:HD11	1.77	0.67
4:4J:172:SER:HB2	4:4J:205:GLU:HG3	1.77	0.67
1:I:579:LEU:HD12	1:J:576:SER:HA	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:614:LEU:HB3	1:X:614:LEU:HD11	1.77	0.67
5:35:24:VAL:HA	5:35:205:ARG:HH22	1.59	0.67
3:7A:7:ILE:HG22	3:7A:66:VAL:HB	1.76	0.67
4:7B:113:ILE:HA	4:7B:116:VAL:HG12	1.75	0.67
1:c:604:ILE:CD1	1:c:607:LEU:HD12	2.22	0.67
5:28:53:ARG:HH22	6:68:347:PHE:HA	1.59	0.67
4:3H:318:ARG:HE	4:3H:358:PRO:HD3	1.58	0.67
8:A7:33:LEU:HB2	9:B6:494:ARG:HG3	1.77	0.67
12:G1:222:ASP:HB3	12:G1:242:TRP:HE1	1.58	0.67
3:1I:194:LEU:HD12	3:1I:198:THR:HG21	1.77	0.67
3:4I:180:ALA:HB3	3:4I:183:GLU:HG3	1.75	0.67
3:4M:248:LEU:HB2	3:4M:355:ILE:H	1.59	0.67
4:6D:390:ARG:HH11	4:6D:391:ARG:HH21	1.43	0.67
3:8K:195:LEU:HG	14:M6:83:THR:HG21	1.77	0.67
1:A:496:ALA:HA	1:A:499:ARG:HE	1.59	0.67
1:B:343:GLU:HB3	1:Y:455:LYS:HD3	1.75	0.67
1:G:317:THR:CB	1:c:599:SER:HB2	2.24	0.67
1:1:845:MET:HA	9:B5:471:PRO:HG2	1.76	0.67
3:3C:205:ASP:HB2	3:3C:303:ALA:HA	1.75	0.67
3:3C:250:VAL:HG12	3:3C:352:LYS:HE2	1.76	0.67
3:3K:319:TYR:HB3	3:3K:323:VAL:HG11	1.77	0.67
3:3M:89:PRO:HA	3:3M:92:LEU:HB2	1.76	0.67
5:40:34:PRO:HG3	5:40:186:ARG:HB3	1.75	0.67
4:8B:193:VAL:HA	4:8B:265:PHE:HZ	1.60	0.67
14:L1:152:ARG:HE	14:L1:171:VAL:HG11	1.60	0.67
1:a:607:LEU:HB2	1:f:607:LEU:CB	2.16	0.67
1:N:630:ARG:HA	4:9H:276:ARG:NH2	2.09	0.67
4:2L:87:PRO:HB3	9:B6:49:MET:HG2	1.76	0.67
3:8K:332:VAL:HG13	3:8K:351:PHE:HD2	1.59	0.67
4:9J:178:THR:HA	3:9K:258:ASN:HD21	1.60	0.67
14:L8:99:ILE:HG23	14:L8:105:LEU:HD11	1.75	0.67
1:a:526:GLU:OE2	1:f:527:LEU:HB2	1.95	0.67
3:8G:245:ASP:HB2	1:l:788:PRO:HB3	1.77	0.66
12:H6:68:ARG:HH12	12:H7:330:ASP:HB3	1.60	0.66
1:c:684:ARG:O	1:c:685:ASN:C	2.37	0.66
4:3F:248:SER:HA	4:3F:252:LYS:HD2	1.77	0.66
3:4G:51:THR:HG21	3:4G:243:ARG:HG2	1.75	0.66
3:6A:9:VAL:HG22	3:6A:68:LEU:HD23	1.75	0.66
4:6F:253:LEU:O	4:6F:257:LEU:HB2	1.93	0.66
3:8K:170:CYS:HB3	3:8K:203:MET:HA	1.78	0.66
4:9B:318:ARG:HB2	4:9B:364:SER:HB3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4G:433:GLU:HA	6:64:627:PRO:HG2	1.77	0.66
6:69:325:ARG:HG3	6:69:337:LEU:HD11	1.76	0.66
3:7C:101:ASN:HD22	4:7D:256:ASN:HD21	1.43	0.66
3:7G:259:LEU:HD11	3:7G:316:CYS:HB2	1.77	0.66
1:a:523:VAL:CG1	1:f:523:VAL:HG12	2.25	0.66
1:Y:575:LEU:HB3	1:c:576:SER:CB	2.26	0.66
4:2D:71:GLY:HA3	3:2E:2:ARG:HH12	1.59	0.66
3:2M:62:VAL:HG21	3:3M:283:HIS:HA	1.77	0.66
5:52:148:LEU:HD11	5:52:156:ALA:HB1	1.75	0.66
3:7A:70:LEU:HD22	3:7A:99:ALA:HB2	1.78	0.66
3:8G:113:GLU:HG3	3:8G:114:ILE:HD12	1.78	0.66
4:8J:298:ASN:C	4:8J:298:ASN:HD22	2.03	0.66
2:10:222:GLU:HA	2:10:225:ARG:HB3	1.77	0.66
3:1I:56:THR:HA	3:2I:285:GLN:HB2	1.77	0.66
3:6A:56:THR:HA	3:7A:285:GLN:HG2	1.76	0.66
3:7I:3:GLU:HB2	3:7I:132:LEU:HA	1.76	0.66
4:7L:424:GLN:HB2	10:E2:301:ARG:HH12	1.61	0.66
3:7M:107:HIS:HD2	3:7M:152:LEU:HB2	1.60	0.66
3:9E:288:VAL:HG21	3:9E:327:ASP:HB3	1.77	0.66
12:F8:246:PRO:HD2	12:F8:249:LEU:HD12	1.77	0.66
14:K2:156:LEU:HD21	14:K2:185:ILE:HG12	1.78	0.66
4:3F:276:ARG:HH22	8:A5:255:ARG:HD2	1.58	0.66
3:8C:133:GLN:HB3	3:8C:252:VAL:HG11	1.76	0.66
4:9B:114:ASP:HA	4:9B:117:LEU:HG	1.77	0.66
3:1K:55:GLU:HB3	3:2K:285:GLN:HE21	1.61	0.66
5:21:89:VAL:HB	5:21:103:HIS:HB3	1.77	0.66
4:3F:219:THR:HB	3:3G:324:VAL:HG21	1.78	0.66
4:3F:322:SER:HB2	8:A5:359:ASP:HB3	1.78	0.66
3:4I:239:THR:HG23	3:4I:243:ARG:HE	1.61	0.66
4:7L:117:LEU:HA	4:7L:120:VAL:HG12	1.77	0.66
4:8J:97:ALA:HB3	4:8J:143:THR:HG22	1.77	0.66
4:6J:398:TYR:HB3	4:6J:403:MET:HG3	1.77	0.66
3:6M:191:THR:HA	3:6M:194:LEU:HB3	1.78	0.66
3:6M:287:SER:O	3:6M:291:ILE:HB	1.96	0.66
3:7I:311:LYS:H	3:7I:382:THR:HB	1.61	0.66
4:9B:68:LEU:HB3	4:9B:96:GLY:HA2	1.77	0.66
4:9D:51:TYR:HB3	4:9D:59:PHE:HB3	1.77	0.66
1:x:879:VAL:HG13	1:x:880:THR:HG23	1.78	0.66
3:3A:215:ARG:HH12	3:3A:299:ALA:HB1	1.61	0.66
4:3B:200:GLN:HB3	4:3B:268:ILE:HD11	1.76	0.66
4:3B:290:THR:HG21	4:3B:329:GLN:HB3	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4K:216:ASN:HD22	3:4K:275:ILE:HB	1.61	0.66
3:5E:234:VAL:HG21	3:5E:302:MET:HE1	1.78	0.66
6:63:406:ARG:HD2	12:F5:233:ARG:HH22	1.60	0.66
3:7A:68:LEU:HD21	3:7A:149:LEU:HD23	1.78	0.66
10:D6:302:ARG:HA	10:D6:305:LEU:HD12	1.77	0.66
1:c:583:GLN:HA	1:c:586:LYS:HD2	1.78	0.66
1:J:577:GLN:NE2	1:J:578:ARG:NH1	2.43	0.66
1:N:608:ASP:HB3	3:9I:370:LYS:HZ2	1.60	0.66
1:2:911:ILE:HG21	1:2:925:MET:HG2	1.78	0.66
3:3A:70:LEU:HD23	3:3A:145:THR:HG22	1.78	0.66
3:3A:320:ARG:HA	3:3A:356:ASN:HB3	1.78	0.66
7:72:376:GLU:O	7:72:380:TRP:HB3	1.96	0.66
3:7A:222:PRO:HD2	4:7B:324:LYS:HE3	1.78	0.66
4:7F:396:HIS:HA	4:7F:399:THR:HG22	1.77	0.66
4:7J:139:LEU:HB2	4:7J:171:PRO:HD3	1.77	0.66
3:8C:308:ARG:HD2	14:L7:246:GLN:HG3	1.78	0.66
14:L7:100:ALA:HB2	14:L7:105:LEU:HD12	1.78	0.66
3:1A:274:PRO:HG3	3:1A:374:ALA:HA	1.77	0.65
3:2A:221:ARG:HH12	4:2B:325:GLU:H	1.44	0.65
3:2C:329:ASN:HA	3:2C:332:VAL:HG12	1.77	0.65
3:4G:105:ARG:HA	3:4G:109:THR:HB	1.78	0.65
5:62:74:LYS:HB3	5:62:90:GLU:HB3	1.77	0.65
3:6M:73:THR:HA	3:6M:76:ASP:HB2	1.78	0.65
7:80:279:ARG:HH22	10:E6:148:MET:HB3	1.58	0.65
4:8L:179:VAL:HG12	3:8M:258:ASN:HD22	1.60	0.65
10:D2:338:PRO:HB2	10:D2:341:TYR:HB3	1.77	0.65
12:I9:332:THR:HA	12:I9:335:ILE:HD12	1.78	0.65
1:m:757:LEU:HD23	1:m:758:ASN:H	1.61	0.65
3:1C:288:VAL:HA	3:1C:291:ILE:HG12	1.78	0.65
3:1K:398:MET:HE1	4:1L:345:ILE:HG23	1.77	0.65
5:27:91:LEU:HB2	5:27:101:TYR:HB2	1.79	0.65
5:36:122:GLU:HG3	5:36:124:GLY:H	1.60	0.65
6:69:273:LEU:HB2	6:69:433:LEU:HD23	1.79	0.65
4:8B:135:ILE:HB	4:8B:166:THR:HG22	1.79	0.65
12:G3:221:MET:HA	12:G3:224:ARG:HG3	1.78	0.65
1:c:469:LEU:HB3	1:c:473:ARG:HH21	1.59	0.65
3:4C:317:LEU:HD23	3:4C:377:MET:HB2	1.78	0.65
4:7F:319:GLY:HA2	4:7F:357:PRO:HG3	1.78	0.65
3:9A:23:LEU:HD21	3:9A:363:VAL:HG12	1.77	0.65
4:8J:3:GLU:HA	4:8J:49:VAL:HA	1.78	0.65
1:X:630:ARG:HH22	1:i:813:PRO:HA	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1C:200:VAL:HG23	3:1C:268:MET:HE2	1.79	0.65
17:2B:501:GDP:H8	3:2C:248:LEU:HD13	1.62	0.65
4:3J:213:ARG:HH22	9:B4:45:ARG:HD3	1.62	0.65
3:4M:73:THR:HA	3:4M:76:ASP:HB2	1.78	0.65
3:4M:280:LYS:HG2	3:4M:371:VAL:HG23	1.77	0.65
4:5B:7:VAL:HB	4:5B:135:ILE:HG13	1.78	0.65
4:6N:164:MET:HB3	4:6N:197:ASP:H	1.62	0.65
7:78:282:ARG:HH12	7:78:285:ASP:HA	1.58	0.65
3:9I:217:LEU:HD11	3:9I:275:ILE:HG12	1.77	0.65
10:F2:317:LEU:HB3	10:F2:321:ARG:NH1	2.12	0.65
4:2J:64:ILE:HD11	4:2J:123:GLU:HG3	1.78	0.65
3:4I:88:HIS:HB3	3:4I:91:GLN:HG3	1.78	0.65
3:5M:208:ALA:HB2	3:5M:304:LYS:HG2	1.78	0.65
4:6D:8:GLN:HG3	4:6D:65:LEU:HG	1.78	0.65
3:6I:175:PRO:HB3	3:6I:390:ARG:HD2	1.78	0.65
4:9B:318:ARG:HA	4:9B:354:CYS:HB3	1.77	0.65
8:A1:33:LEU:HG	8:A1:77:GLU:HG3	1.78	0.65
12:F6:251:TYR:HD1	12:F6:254:VAL:HG21	1.62	0.65
12:G3:260:ASP:HA	12:G3:263:TYR:HB2	1.78	0.65
13:J6:397:LEU:HA	13:J6:400:LEU:HD12	1.79	0.65
3:4A:23:LEU:HD13	3:4A:364:PRO:HD3	1.76	0.65
4:4F:317:PHE:HB3	4:4F:321:MET:HE1	1.79	0.65
5:56:184:THR:HG22	5:56:188:MET:HE1	1.77	0.65
4:5L:131:GLN:HE21	4:5L:250:LEU:HB2	1.60	0.65
6:69:902:PRO:HD3	1:w:880:THR:HG22	1.77	0.65
3:7I:56:THR:HA	3:8I:285:GLN:HG3	1.79	0.65
3:9E:77:GLU:HA	3:9E:80:THR:HG22	1.78	0.65
8:A7:87:VAL:HG12	8:A7:93:VAL:HG22	1.79	0.65
1:M:610:VAL:HG11	1:N:611:THR:HG22	1.77	0.65
3:2A:112:LYS:HA	3:2A:115:VAL:HG22	1.79	0.65
4:3F:293:MET:HE2	4:3F:365:VAL:HG11	1.79	0.65
5:49:55:GLN:HB2	5:49:151:HIS:HA	1.78	0.65
4:4B:257:LEU:HD21	4:4B:314:SER:HB2	1.79	0.65
3:6M:202:VAL:HA	3:6M:268:MET:HB2	1.78	0.65
4:7L:249:ASP:HB2	4:7L:252:LYS:HG2	1.77	0.65
10:E2:305:LEU:HD21	14:L0:142:GLN:HB3	1.78	0.65
3:3M:370:LYS:HZ3	3:3M:372:MET:HG2	1.62	0.65
4:5D:319:GLY:HA2	4:5D:357:PRO:HG3	1.77	0.65
4:7J:154:LYS:HD2	7:90:286:TRP:HE1	1.60	0.65
1:a:610:VAL:HG11	1:f:611:THR:HA	1.79	0.65
1:Y:523:VAL:HG12	1:c:523:VAL:HG12	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1M:7:ILE:HA	3:1M:66:VAL:HB	1.78	0.65
5:20:147:VAL:HG22	5:20:159:ASP:HB2	1.79	0.65
4:3B:21:TRP:HA	4:3B:24:ILE:HG22	1.78	0.65
4:3F:79:GLY:HA2	6:64:867:TRP:HB3	1.77	0.65
4:4B:207:LEU:HB3	4:4B:225:LEU:HD22	1.77	0.65
5:52:18:VAL:HA	5:52:21:LEU:HD23	1.79	0.65
7:75:278:VAL:HG21	14:K1:126:ILE:HD12	1.79	0.65
7:86:350:ARG:HG2	7:86:379:LEU:HD23	1.78	0.65
4:8B:229:VAL:HA	4:8B:300:MET:HE1	1.78	0.65
4:9H:268:ILE:HG23	4:9H:300:MET:HB2	1.79	0.65
9:B1:17:LEU:HD22	9:B1:491:ARG:HB2	1.79	0.65
1:B:439:LEU:HD21	1:E:437:GLN:HE21	1.62	0.64
1:D:607:LEU:HD23	1:H:603:ARG:HE	1.61	0.64
1:Y:604:ILE:CA	1:c:604:ILE:HD11	2.26	0.64
5:29:164:MET:HB2	5:29:167:LYS:H	1.62	0.64
4:2B:198:GLU:HB2	4:2B:266:PHE:HE1	1.61	0.64
3:3C:269:LEU:HD21	3:3C:305:CYS:HB3	1.78	0.64
3:3K:188:VAL:HG23	3:3K:425:LEU:HD12	1.79	0.64
3:4M:368:LEU:HD12	8:A8:195:ARG:HH21	1.62	0.64
4:6J:380:ARG:HB2	7:76:312:SER:H	1.62	0.64
4:8F:189:VAL:HB	4:8F:415:MET:HE1	1.78	0.64
7:96:280:PRO:HD3	14:M2:129:PRO:HD2	1.79	0.64
3:9C:154:LEU:HD13	3:9C:193:SER:HB3	1.80	0.64
14:M7:179:GLU:HA	14:M7:182:TYR:HD2	1.62	0.64
1:V:626:LEU:HB3	4:6H:276:ARG:HH12	1.61	0.64
3:1K:71:GLU:HG2	4:1L:2:ARG:HH22	1.61	0.64
3:2A:268:MET:HG3	3:2A:380:ASN:HB3	1.80	0.64
3:2I:364:PRO:HB2	9:B2:150:MET:HE3	1.79	0.64
5:54:20:PHE:HB2	6:65:596:PRO:HB3	1.79	0.64
3:7I:195:LEU:HD12	3:7I:428:LEU:HD12	1.80	0.64
3:2A:6:SER:O	3:2A:65:CYS:HA	1.98	0.64
3:2M:160:ASP:HA	6:68:558:LYS:HD3	1.79	0.64
3:3A:53:PHE:HB3	3:3A:61:HIS:HB3	1.80	0.64
3:3A:320:ARG:HB3	3:3A:374:ALA:HB3	1.79	0.64
3:3E:204:LEU:HD13	3:3E:231:ILE:HD12	1.78	0.64
3:3G:215:ARG:HH22	3:3G:299:ALA:HB1	1.63	0.64
4:6H:100:ASN:HB3	4:6H:103:LYS:HB2	1.78	0.64
4:6L:256:ASN:HD22	4:6L:350:LYS:HD2	1.62	0.64
3:8G:154:LEU:HD23	3:8G:193:SER:HB3	1.79	0.64
12:G6:221:MET:HA	12:G6:224:ARG:HD3	1.79	0.64
14:L3:233:LEU:HA	14:L3:236:PHE:HD2	1.60	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L7:185:ILE:HG23	14:L7:189:ILE:HD12	1.77	0.64
1:I:607:LEU:HB2	1:J:607:LEU:HB3	1.80	0.64
5:27:77:ILE:HG21	5:27:127:PRO:HG3	1.78	0.64
3:2G:9:VAL:HG12	3:2G:68:LEU:HB2	1.79	0.64
4:3D:293:MET:HE2	4:3D:365:VAL:HG11	1.79	0.64
4:4H:230:SER:HA	4:4H:233:MET:HB2	1.79	0.64
5:58:49:PRO:HA	5:58:70:PRO:HA	1.79	0.64
3:5C:251:ASP:H	3:5C:254:GLU:HB3	1.63	0.64
6:68:632:PHE:HB3	6:68:835:ILE:HD11	1.79	0.64
4:6B:286:VAL:HA	4:6B:289:LEU:HB3	1.79	0.64
4:7F:187:LEU:HD21	4:7F:403:MET:HE1	1.78	0.64
4:7L:407:GLU:HA	4:7L:410:GLU:HG3	1.78	0.64
4:9F:155:VAL:HG11	4:9F:164:MET:HE2	1.79	0.64
1:Q:579:LEU:HB3	1:U:579:LEU:HD11	1.79	0.64
4:1D:304:ASP:HB3	4:1D:306:ARG:HH11	1.62	0.64
4:2D:112:LEU:HB3	4:2D:147:MET:HE1	1.78	0.64
4:2D:358:PRO:HG2	4:2D:361:LEU:HB2	1.80	0.64
4:2J:100:ASN:HB3	4:2J:103:LYS:HB2	1.78	0.64
4:2L:230:SER:HA	4:2L:233:MET:HE2	1.79	0.64
3:4A:360:PRO:HG2	3:4A:371:VAL:HG23	1.78	0.64
4:4F:256:ASN:HD22	4:4F:350:LYS:HG3	1.61	0.64
4:7J:164:MET:HB3	4:7J:197:ASP:H	1.63	0.64
3:8K:100:ALA:HA	4:8L:252:LYS:HD2	1.79	0.64
3:8K:102:ASN:HB3	3:8K:105:ARG:HB2	1.78	0.64
3:1C:184:PRO:HG3	3:1C:394:LYS:HE3	1.78	0.64
3:1K:273:ALA:HB3	3:1K:375:VAL:H	1.62	0.64
4:3H:321:MET:HE2	4:3H:363:MET:HG2	1.79	0.64
3:3I:274:PRO:HG2	3:3I:374:ALA:HA	1.80	0.64
4:5L:108:GLU:HA	4:5L:111:GLU:HG2	1.79	0.64
5:61:54:LEU:HA	5:61:150:MET:HB2	1.79	0.64
6:68:136:ARG:HA	12:H7:327:GLU:HB2	1.79	0.64
3:6M:192:HIS:HB2	3:6M:421:ALA:HA	1.80	0.64
7:78:412:MET:HE3	4:7F:205:GLU:HA	1.79	0.64
3:8G:176:GLN:HG3	4:8H:331:LEU:HD13	1.80	0.64
1:C:378:GLU:HA	1:C:381:ARG:HG2	1.80	0.64
1:M:491:LEU:O	1:M:495:PHE:HB2	1.97	0.64
5:20:45:SER:HA	5:20:73:VAL:O	1.96	0.64
3:2G:101:ASN:HD22	4:2H:256:ASN:HD21	1.44	0.64
3:3I:271:SER:HB3	3:3I:377:MET:HB3	1.79	0.64
4:5L:135:ILE:HG21	4:5L:152:ILE:HD11	1.79	0.64
6:68:505:GLN:NE2	6:68:509:GLU:OE2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6A:176:GLN:HB3	4:6B:331:LEU:HD11	1.80	0.64
4:6B:379:LYS:HB3	4:6B:419:VAL:HG21	1.80	0.64
4:7D:360:GLY:H	1:k:824:GLN:HE21	1.44	0.64
10:E4:331:ILE:HG23	10:E4:335:LEU:HD13	1.80	0.64
1:1:847:ASP:HB3	1:1:850:ARG:HH22	1.63	0.64
3:1G:191:THR:HG21	3:1G:425:LEU:HD13	1.78	0.64
4:1L:317:PHE:HB3	4:1L:321:MET:HE1	1.79	0.64
5:23:206:LEU:HD23	5:26:22:ALA:HA	1.80	0.64
5:26:111:ARG:HH21	5:26:114:GLN:HE22	1.44	0.64
5:55:56:GLU:HG2	5:55:58:GLY:H	1.63	0.64
4:5B:7:VAL:HG22	4:5B:64:ILE:HB	1.80	0.64
3:9I:7:ILE:HG22	3:9I:66:VAL:HB	1.80	0.64
8:A2:36:PRO:HA	9:B3:8:ILE:HG22	1.80	0.64
10:E6:354:ARG:HE	10:E6:360:ALA:HA	1.62	0.64
12:F7:252:LEU:HA	12:F7:255:VAL:HG12	1.78	0.64
12:G2:264:ILE:HG23	12:G2:268:ARG:HH21	1.63	0.64
3:1C:268:MET:HG3	3:1C:380:ASN:HB3	1.80	0.64
5:37:44:TYR:HB3	5:37:75:ILE:HG22	1.80	0.64
4:3B:320:ARG:HG3	8:A3:230:ARG:HH12	1.61	0.64
5:52:117:GLN:HE22	5:52:173:CYS:H	1.42	0.64
4:5L:201:VAL:HG11	4:5L:377:MET:HE3	1.79	0.64
3:6K:348:PRO:HB2	14:K5:111:LEU:HD22	1.79	0.64
4:6N:135:ILE:HG21	4:6N:152:ILE:HD11	1.80	0.64
4:6N:383:ASP:HA	4:6N:386:THR:HG22	1.80	0.64
7:71:347:ILE:HG21	7:71:350:ARG:HB2	1.80	0.64
7:78:378:MET:HE1	14:K8:235:LYS:HG3	1.80	0.64
3:7K:255:PHE:HZ	3:7K:378:ILE:HD13	1.63	0.64
2:9:205:ILE:HG13	2:9:209:ARG:HH21	1.63	0.64
7:90:330:ARG:HH12	7:90:350:ARG:HH12	1.45	0.64
3:9G:203:MET:HE1	3:9G:267:PHE:HB3	1.79	0.64
3:9M:212:ILE:HD11	3:9M:300:SER:HA	1.79	0.64
12:G7:273:PRO:HD2	12:G7:276:LEU:HD12	1.80	0.64
13:J1:351:ARG:HD3	13:J1:352:LYS:HG3	1.79	0.64
3:3M:53:PHE:HB3	3:3M:61:HIS:HB3	1.80	0.64
4:4J:33:THR:HG22	8:A6:94:ILE:HD13	1.79	0.64
4:4J:73:MET:HE3	4:4J:92:PHE:HB3	1.78	0.64
4:5L:397:TRP:HA	14:K6:89:ARG:HH12	1.63	0.64
3:6M:7:ILE:HG13	3:6M:137:MET:HA	1.80	0.64
3:6M:348:PRO:HB2	14:K6:111:LEU:HD22	1.80	0.64
2:7:262:LEU:HB3	2:8:263:VAL:HG21	1.80	0.64
4:7L:392:LYS:HG3	4:7L:395:LEU:HD13	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9A:166:LYS:HD2	3:9A:198:THR:HA	1.80	0.64
3:9G:1:MET:HA	3:9G:131:GLY:HA3	1.80	0.64
12:G5:253:THR:HG21	12:G5:262:LEU:HG	1.80	0.64
13:J3:392:VAL:HG22	13:J3:444:ALA:HB3	1.79	0.64
14:L4:222:THR:HB	14:L4:225:GLU:HB3	1.79	0.64
4:1D:226:ASN:HD21	17:1D:501:GDP:HN21	1.45	0.63
3:2E:132:LEU:HD22	3:2E:164:LYS:HD3	1.79	0.63
4:3H:215:LEU:HD13	8:A6:257:PRO:HB2	1.80	0.63
5:54:209:ILE:HD12	6:65:600:LEU:HD13	1.78	0.63
3:5I:15:GLN:HG3	3:5I:228:ASN:HD21	1.63	0.63
7:75:376:GLU:O	7:75:380:TRP:HB3	1.98	0.63
3:7A:115:VAL:HG21	3:7A:152:LEU:HD22	1.80	0.63
7:83:279:ARG:HD2	10:E1:146:ALA:HA	1.79	0.63
3:8A:208:ALA:HB2	3:8A:304:LYS:HB2	1.80	0.63
3:8I:123:ARG:HH21	3:8I:124:LYS:HE3	1.63	0.63
8:A2:80:MET:HE3	9:B3:8:ILE:HD11	1.80	0.63
8:A4:47:LYS:HE2	8:A4:99:MET:HE3	1.80	0.63
8:A5:386:ARG:HH21	9:B3:161:LEU:HD23	1.62	0.63
10:D2:44:CYS:HB3	10:D2:48:ARG:HH21	1.62	0.63
1:c:373:LEU:O	1:c:377:HIS:HB2	1.99	0.63
1:C:382:GLN:O	1:C:386:GLU:HB2	1.99	0.63
2:16:223:ARG:HA	2:16:226:VAL:HG12	1.80	0.63
4:1F:140:GLY:HA3	4:1F:181:GLU:HG3	1.80	0.63
3:3M:20:CYS:HB2	3:3M:235:ILE:HD11	1.79	0.63
4:5B:169:VAL:HG12	4:5B:202:ILE:HB	1.79	0.63
4:7L:375:GLN:HB2	4:7L:419:VAL:HG13	1.78	0.63
8:A3:229:ARG:HE	8:A3:232:ARG:HG3	1.63	0.63
14:L3:190:THR:HG21	14:L3:254:PHE:HA	1.80	0.63
1:M:614:LEU:HD13	1:N:614:LEU:HA	1.80	0.63
4:1H:30:ILE:HD12	4:1H:59:PHE:HB2	1.81	0.63
3:2K:274:PRO:HG2	3:2K:371:VAL:HG11	1.81	0.63
4:3D:220:PRO:HG2	3:3E:326:LYS:HD3	1.80	0.63
3:3M:213:CYS:HA	3:3M:217:LEU:HD23	1.81	0.63
5:53:97:LEU:HD23	5:53:188:MET:HG2	1.80	0.63
4:5B:190:HIS:HB2	4:5B:414:ASN:HD22	1.62	0.63
4:5B:253:LEU:O	4:5B:257:LEU:HB2	1.98	0.63
6:63:602:ARG:O	6:63:606:GLN:HB2	1.98	0.63
3:7A:389:SER:HB2	14:L1:232:ARG:HH21	1.63	0.63
3:7G:271:SER:HB2	3:7G:377:MET:HB3	1.80	0.63
3:7K:195:LEU:HD12	3:7K:428:LEU:HD12	1.80	0.63
3:8M:175:PRO:HG3	3:8M:304:LYS:HE3	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9I:338:LYS:HE2	3:9I:341:ILE:HD12	1.79	0.63
1:A:604:ILE:HA	1:F:603:ARG:HH12	1.63	0.63
5:28:162:GLN:HE22	5:28:164:MET:HB3	1.63	0.63
3:3A:385:ALA:HA	3:3A:388:PHE:HB2	1.81	0.63
5:49:78:LEU:HD12	5:49:86:HIS:HB3	1.80	0.63
4:4B:135:ILE:HB	4:4B:166:THR:HG22	1.80	0.63
4:4B:253:LEU:O	4:4B:257:LEU:HB2	1.99	0.63
5:55:77:ILE:HD11	5:55:84:PRO:HB3	1.80	0.63
6:69:952:GLU:HG3	6:69:953:THR:HG23	1.80	0.63
3:6A:202:VAL:HG22	3:6A:268:MET:HB2	1.79	0.63
4:6B:192:LEU:HD21	4:6B:199:VAL:HG21	1.79	0.63
4:6B:388:MET:HE2	3:6C:348:PRO:HD2	1.79	0.63
3:6K:388:PHE:HB3	3:6K:425:LEU:HD21	1.81	0.63
4:7D:173:PRO:HG2	4:7D:302:ALA:HB3	1.79	0.63
4:7J:55:THR:HG21	4:8J:284:LEU:HD23	1.80	0.63
3:9E:314:ALA:HB3	3:9E:380:ASN:HB2	1.80	0.63
3:9K:398:MET:HG3	4:9L:345:ILE:HG22	1.81	0.63
10:E9:62:VAL:HG21	10:E9:305:LEU:HB3	1.80	0.63
4:1H:238:CYS:HA	4:1H:241:ARG:HH21	1.63	0.63
1:2:875:ILE:HG13	1:2:952:ARG:HD3	1.81	0.63
4:3D:308:GLY:HA2	4:3D:426:GLN:HE22	1.64	0.63
4:4F:99:ASN:HD22	3:4G:258:ASN:HD21	1.47	0.63
4:6J:210:ILE:HG13	4:6J:228:LEU:HD21	1.80	0.63
3:6M:73:THR:HB	4:6N:46:ARG:HH12	1.62	0.63
3:7M:9:VAL:HG12	3:7M:146:GLY:HA2	1.81	0.63
3:7M:56:THR:HA	3:8M:285:GLN:HB2	1.80	0.63
4:9D:7:VAL:HB	4:9D:135:ILE:HG22	1.79	0.63
8:A3:125:GLN:HA	8:A3:163:ARG:HH21	1.63	0.63
1:E:320:GLN:OE1	1:f:599:SER:HB2	1.97	0.63
3:1A:408:TYR:HB3	3:1A:413:MET:HB2	1.79	0.63
3:1G:407:TRP:HE1	4:1H:258:ILE:HB	1.63	0.63
4:1J:388:MET:HE1	3:1K:347:CYS:HA	1.79	0.63
4:1L:113:ILE:HA	4:1L:116:VAL:HG12	1.81	0.63
5:25:118:LYS:HE3	6:69:348:THR:HG23	1.79	0.63
5:33:113:MET:HA	5:33:116:ARG:HE	1.62	0.63
3:4A:359:PRO:HD3	8:A4:105:LEU:HD11	1.80	0.63
4:4D:32:PRO:HB2	6:65:913:TYR:HD2	1.63	0.63
3:5A:136:LEU:HD23	3:5A:167:LEU:HG	1.81	0.63
4:5N:216:LYS:H	4:5N:275:SER:HB3	1.63	0.63
3:6G:388:PHE:HB3	3:6G:425:LEU:HD21	1.80	0.63
3:7I:265:ILE:HD11	3:7I:435:VAL:HG21	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:82:376:GLU:O	7:82:380:TRP:HB3	1.99	0.63
4:8D:248:SER:HA	4:8D:252:LYS:HG2	1.78	0.63
3:9K:154:LEU:HD23	3:9K:193:SER:HB3	1.81	0.63
3:9K:180:ALA:HB3	3:9K:183:GLU:HB2	1.81	0.63
10:E6:78:ARG:HD2	10:E6:82:GLY:HA2	1.81	0.63
1:I:671:ALA:HB2	3:8A:58:ALA:HB2	1.81	0.63
1:U:664:ILE:HG22	1:b:381:ARG:HH22	1.62	0.63
5:25:140:GLU:HG3	5:25:143:CYS:HB3	1.79	0.63
4:2D:75:SER:HA	9:B3:76:ARG:HG3	1.79	0.63
5:30:67:ARG:HH22	12:G3:263:TYR:HA	1.63	0.63
3:5M:251:ASP:H	3:5M:254:GLU:HB2	1.62	0.63
3:6E:388:PHE:HB3	3:6E:425:LEU:HD21	1.79	0.63
3:6M:275:ILE:HG13	3:6M:368:LEU:HD21	1.80	0.63
3:8K:74:VAL:HG13	3:8K:75:VAL:HG13	1.81	0.63
10:C6:66:LEU:HB3	10:C6:70:ARG:HH12	1.63	0.63
10:C8:331:ILE:HG23	10:C8:335:LEU:HD12	1.81	0.63
1:f:624:GLN:O	1:f:628:VAL:HG23	1.97	0.63
3:1G:287:SER:HA	3:1G:373:ARG:HH21	1.63	0.63
4:2B:2:ARG:HH12	4:2B:240:LEU:HA	1.64	0.63
3:2G:3:GLU:HA	3:2G:51:THR:HA	1.81	0.63
5:39:74:LYS:HB2	5:39:90:GLU:HB2	1.80	0.63
5:50:209:ILE:HD12	6:64:600:LEU:HD13	1.79	0.63
4:6D:229:VAL:HA	4:6D:300:MET:HE1	1.81	0.63
3:7C:181:VAL:HG13	3:7C:182:VAL:HG13	1.80	0.63
7:84:386:ARG:HG3	14:L3:115:PRO:HB3	1.81	0.63
4:8L:39:ASP:H	1:m:760:ARG:HH21	1.46	0.63
4:9F:21:TRP:HA	4:9F:24:ILE:HG22	1.80	0.63
5:49:113:MET:HE1	5:49:173:CYS:HB3	1.81	0.63
4:4B:32:PRO:HB2	6:66:913:TYR:HD2	1.63	0.63
4:4D:30:ILE:HD11	4:4D:47:ILE:HD11	1.81	0.63
5:53:149:ILE:HB	5:53:157:ARG:HB3	1.81	0.63
3:5I:70:LEU:HD12	3:5I:99:ALA:HB2	1.80	0.63
5:61:78:LEU:HD12	5:61:86:HIS:HB3	1.80	0.63
5:62:48:VAL:HG21	5:62:134:LEU:HD22	1.80	0.63
4:7L:164:MET:HB2	4:7L:197:ASP:H	1.64	0.63
7:84:282:ARG:HH21	7:84:287:LEU:HD12	1.64	0.63
7:84:401:ILE:HD11	14:L3:108:TYR:HB2	1.81	0.63
4:8B:375:GLN:HE21	4:8B:419:VAL:HB	1.64	0.63
4:9J:253:LEU:O	4:9J:257:LEU:HB2	1.98	0.63
12:G6:188:ARG:HE	12:G6:190:ALA:HB3	1.64	0.63
13:J2:353:ARG:HH21	13:J2:357:LEU:HD13	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K1:199:ILE:HG22	14:K1:207:ILE:HD13	1.80	0.63
1:k:746:ASP:HB2	1:k:749:VAL:HG22	1.80	0.63
3:1A:234:VAL:HG22	3:1A:272:TYR:HB3	1.81	0.62
5:25:76:LEU:HD11	5:25:88:ARG:HD2	1.80	0.62
4:2H:92:PHE:HZ	9:B2:49:MET:HG2	1.64	0.62
4:2L:311:LEU:HD23	4:2L:342:VAL:HG21	1.81	0.62
5:31:166:TYR:HD2	5:31:167:LYS:HE3	1.62	0.62
4:3B:219:THR:HB	3:3C:324:VAL:HG21	1.81	0.62
4:3L:91:VAL:HG21	4:3L:116:VAL:HG22	1.79	0.62
3:3M:36:MET:HE2	3:3M:61:HIS:HE1	1.64	0.62
4:4L:73:MET:HE2	4:4L:92:PHE:HB3	1.79	0.62
4:4L:135:ILE:HD13	4:4L:152:ILE:HD11	1.79	0.62
3:5A:175:PRO:HD3	3:5A:304:LYS:HE3	1.79	0.62
4:5J:117:LEU:HD11	4:5J:154:LYS:HD2	1.81	0.62
4:6D:392:LYS:HD3	4:6D:395:LEU:HD13	1.81	0.62
4:6J:232:ALA:HB2	4:6J:270:PHE:HB2	1.80	0.62
3:7I:18:ASN:HD21	1:j:741:MET:HE1	1.64	0.62
7:92:397:SER:HA	7:92:400:CYS:HB2	1.79	0.62
4:9F:265:PHE:HB3	4:9F:374:ILE:HD13	1.81	0.62
4:9L:330:MET:HE1	4:9L:351:SER:HB3	1.81	0.62
12:G1:273:PRO:HD2	12:G1:276:LEU:HD12	1.80	0.62
1:N:640:ALA:HB1	4:8H:56:GLY:O	1.98	0.62
1:Q:451:THR:HG21	1:Z:340:ARG:HD2	1.82	0.62
4:1H:237:THR:HG22	4:1H:250:LEU:HD21	1.81	0.62
5:21:51:GLU:HB3	5:21:147:VAL:HG22	1.80	0.62
4:2F:313:ALA:HB3	4:2F:349:MET:HG2	1.81	0.62
5:37:33:ASP:HB3	5:37:36:LEU:HB2	1.82	0.62
4:3J:100:ASN:HB3	4:3J:103:LYS:HB3	1.82	0.62
3:4E:433:GLU:HA	6:65:627:PRO:HG2	1.81	0.62
4:5D:232:ALA:HB2	4:5D:300:MET:HE1	1.82	0.62
2:8:177:ARG:HA	2:8:180:LYS:HG2	1.80	0.62
3:8I:434:GLU:HB3	14:M2:72:VAL:HG21	1.81	0.62
4:9F:350:LYS:HZ3	4:9F:352:SER:HB2	1.64	0.62
10:E3:338:PRO:HB2	10:E3:341:TYR:HB3	1.81	0.62
10:E6:338:PRO:HB2	10:E6:341:TYR:HB3	1.80	0.62
1:a:603:ARG:HB3	1:f:604:ILE:HG21	1.80	0.62
4:1D:49:VAL:HG11	4:1D:241:ARG:HB3	1.82	0.62
3:1K:188:VAL:HG23	3:1K:391:MET:HE2	1.80	0.62
5:28:24:VAL:HG21	5:28:201:LEU:HB3	1.81	0.62
4:2H:44:LEU:HA	4:2H:47:ILE:HB	1.81	0.62
3:3A:229:ARG:HE	3:3A:363:VAL:HG21	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3D:257:LEU:HD21	4:3D:314:SER:HB2	1.81	0.62
3:3E:222:PRO:HD2	4:3F:324:LYS:HD2	1.82	0.62
3:3M:76:ASP:HA	3:3M:79:ARG:HD3	1.81	0.62
5:43:197:SER:HB3	13:J5:494:GLU:HG2	1.81	0.62
4:4F:67:ASP:HB2	4:4F:73:MET:HE3	1.81	0.62
4:5B:136:THR:HG22	4:5B:167:PHE:HB2	1.80	0.62
3:5C:30:ILE:HG22	3:5C:36:MET:HG3	1.81	0.62
4:6B:30:ILE:HG13	4:6B:51:TYR:HE1	1.63	0.62
4:6J:186:THR:HG23	4:6J:415:MET:HG3	1.80	0.62
3:9A:298:PRO:HB3	3:9A:307:PRO:HD2	1.80	0.62
8:A3:196:LEU:HD11	8:A3:210:GLN:HB3	1.82	0.62
3:1C:274:PRO:HG2	3:1C:374:ALA:HA	1.80	0.62
3:3M:75:VAL:HG12	3:3M:79:ARG:HD2	1.81	0.62
4:5B:198:GLU:HG2	4:5B:200:GLN:HE21	1.64	0.62
6:64:862:VAL:HG22	6:64:925:THR:HG22	1.81	0.62
4:6J:101:TRP:HE3	4:6J:403:MET:HE1	1.64	0.62
3:6M:2:ARG:HG3	3:6M:51:THR:HB	1.82	0.62
3:6M:172:TRP:HE1	3:6M:391:MET:HG3	1.63	0.62
4:7J:41:ASP:HB2	1:n:918:THR:HG22	1.81	0.62
7:94:331:PRO:HB2	7:94:335:ARG:HH21	1.64	0.62
10:F2:110:ILE:HG12	10:F2:283:PHE:HD1	1.65	0.62
1:I:662:ASP:O	1:I:666:VAL:HG23	2.00	0.62
1:Q:331:GLU:HB3	1:Q:335:ARG:HH12	1.64	0.62
4:2D:49:VAL:HG11	4:2D:241:ARG:HG2	1.82	0.62
3:3E:230:LEU:HD11	3:3E:275:ILE:HD12	1.81	0.62
3:4E:250:VAL:HA	3:4E:254:GLU:HG2	1.82	0.62
5:50:167:LYS:HD3	5:53:119:LEU:HD23	1.82	0.62
6:67:151:TYR:HE2	6:67:564:MET:HA	1.65	0.62
3:6G:119:LEU:HD11	3:6G:156:ARG:HB3	1.81	0.62
7:75:279:ARG:HE	10:D3:148:MET:HG3	1.64	0.62
7:79:315:ILE:HG13	7:79:399:THR:HG21	1.81	0.62
3:7E:56:THR:HA	3:8E:285:GLN:HB3	1.81	0.62
3:7G:9:VAL:HG23	3:7G:68:LEU:HD22	1.81	0.62
4:7J:323:THR:HG22	4:7J:353:VAL:HG21	1.80	0.62
7:87:386:ARG:HD2	14:L8:115:PRO:HB3	1.81	0.62
4:8L:174:LYS:HZ1	7:91:412:MET:HG2	1.64	0.62
8:A6:154:THR:HB	8:A7:280:ALA:HB2	1.82	0.62
12:G2:195:PRO:HA	12:G2:198:LYS:HG2	1.81	0.62
14:L3:111:LEU:HB3	14:L3:117:ARG:HD3	1.82	0.62
14:L5:152:ARG:HE	14:L5:171:VAL:HG21	1.64	0.62
1:b:320:GLN:HG2	1:b:323:MET:HG2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1D:113:ILE:HG13	4:1D:150:LEU:HD22	1.81	0.62
4:1D:211:CYS:HA	4:1D:215:LEU:HB2	1.80	0.62
4:1J:362:LYS:HD2	4:1J:363:MET:HG3	1.80	0.62
4:2D:132:GLY:HA3	4:2D:163:ILE:HG22	1.80	0.62
3:3G:109:THR:HG22	3:3G:110:ILE:H	1.65	0.62
5:43:53:ARG:HB2	5:43:149:ILE:HA	1.80	0.62
3:4A:87:PHE:HB3	3:4A:92:LEU:HD21	1.81	0.62
4:4B:20:PHE:HA	4:4B:230:SER:HB2	1.81	0.62
4:4B:318:ARG:HA	4:4B:354:CYS:HB3	1.82	0.62
4:6H:47:ILE:H	1:p:915:ARG:HH21	1.46	0.62
3:7A:332:VAL:HG23	3:7A:351:PHE:HD2	1.64	0.62
3:7C:223:THR:HG22	4:7D:322:SER:HA	1.80	0.62
3:8A:115:VAL:HG21	3:8A:152:LEU:HD22	1.82	0.62
3:8M:90:GLU:HG2	3:8M:121:ARG:HH12	1.64	0.62
3:9C:113:GLU:HG3	3:9C:114:ILE:HG13	1.79	0.62
3:9M:274:PRO:HG2	3:9M:371:VAL:HG11	1.80	0.62
9:B5:36:GLU:HA	9:B5:44:LEU:HD13	1.80	0.62
12:I1:73:ASN:HD22	12:I2:76:ILE:HD11	1.65	0.62
14:L9:89:ARG:HA	14:L9:101:GLY:HA3	1.82	0.62
14:M7:182:TYR:HD1	14:M7:196:VAL:HG13	1.64	0.62
1:Y:534:GLN:HE21	1:c:537:LEU:HD13	1.65	0.62
4:1D:11:GLN:HE22	3:1E:249:ASN:H	1.46	0.62
3:1M:88:HIS:HB3	3:1M:91:GLN:HG2	1.82	0.62
4:2H:64:ILE:HG13	4:2H:89:ASN:HD22	1.63	0.62
3:3A:335:ILE:HA	3:3A:338:LYS:HB2	1.80	0.62
4:3H:87:PRO:HD3	4:4H:281:TYR:HD2	1.65	0.62
4:3L:211:CYS:HA	4:3L:215:LEU:HB2	1.82	0.62
4:7L:210:ILE:HG21	4:7L:273:LEU:HD13	1.80	0.62
2:8:159:LEU:HD11	10:D1:81:ALA:HB2	1.81	0.62
3:8G:200:VAL:HG22	3:8G:268:MET:HE1	1.81	0.62
1:c:512:LYS:HA	1:c:515:VAL:HG12	1.82	0.62
1:j:747:ALA:HB2	1:j:822:PRO:HG3	1.82	0.62
1:A:562:ILE:HA	1:F:566:ARG:HH22	1.65	0.62
1:O:673:LEU:HG	1:P:673:LEU:HB3	1.82	0.62
2:11:162:GLN:HA	2:11:165:ARG:HD2	1.82	0.62
3:1M:209:ILE:HD12	3:1M:227:LEU:HB3	1.82	0.62
4:2B:140:GLY:HA3	17:2B:501:GDP:H4'	1.81	0.62
4:2B:257:LEU:HD12	4:2B:312:THR:HG23	1.81	0.62
5:39:84:PRO:HD2	5:39:124:GLY:HA2	1.82	0.62
3:3K:89:PRO:HG3	3:4K:279:GLU:HG3	1.82	0.62
5:40:203:GLN:HA	5:40:206:LEU:HD12	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4L:44:LEU:HD12	4:4L:47:ILE:HG13	1.81	0.62
5:61:149:ILE:HB	5:61:157:ARG:HB2	1.80	0.62
4:6H:44:LEU:HD11	1:p:922:ARG:HH12	1.65	0.62
4:7H:166:THR:HG21	4:7H:192:LEU:HD11	1.81	0.62
4:9F:149:THR:HG21	4:9F:188:SER:HB2	1.82	0.62
3:9I:2:ARG:HB2	3:9I:133:GLN:HB3	1.81	0.62
1:D:578:ARG:HA	1:D:581:LYS:HG2	1.81	0.62
1:M:673:LEU:HD23	1:N:673:LEU:HB3	1.80	0.62
3:1G:203:MET:HE1	3:1G:267:PHE:HB3	1.82	0.62
5:47:207:HIS:HE1	13:J7:508:CYS:H	1.47	0.62
3:4G:259:LEU:HB3	3:4G:268:MET:HE1	1.82	0.62
6:67:548:LEU:HD23	6:67:551:LYS:HZ1	1.65	0.62
10:C8:100:SER:HB2	10:C8:389:PHE:HZ	1.65	0.62
10:D8:307:MET:HG3	10:D8:396:LEU:HD23	1.82	0.62
5:24:90:GLU:HA	5:24:101:TYR:O	1.99	0.62
5:31:77:ILE:HG21	5:31:127:PRO:HG3	1.82	0.62
3:3K:29:GLY:HA2	8:A7:241:LEU:HD11	1.80	0.62
3:3K:377:MET:HG2	3:3K:379:SER:HB3	1.82	0.62
5:47:211:CYS:HA	5:47:214:LYS:HE3	1.81	0.62
3:4C:322:ASP:HB3	8:A3:105:LEU:HD21	1.80	0.62
7:76:292:CYS:HB2	7:76:318:THR:HG22	1.81	0.62
7:79:287:LEU:HD12	14:K0:179:GLU:HB2	1.82	0.62
3:7A:225:THR:HG22	3:7A:229:ARG:HH21	1.64	0.62
4:8F:80:PRO:HB2	1:l:775:SER:HA	1.81	0.62
7:93:320:TRP:HB2	7:93:396:ASP:HB2	1.82	0.62
10:E6:280:VAL:HG11	10:E6:344:SER:HA	1.82	0.62
10:E9:113:THR:HG23	10:E9:286:ARG:HH22	1.65	0.62
1:G:317:THR:HB	1:c:599:SER:CB	2.27	0.61
4:2D:68:LEU:HD12	4:2D:97:ALA:HB2	1.82	0.61
3:2I:180:ALA:HB3	3:2I:183:GLU:HG3	1.80	0.61
3:3C:223:THR:HA	4:3D:323:THR:HG22	1.81	0.61
6:68:316:MET:HB3	12:H5:98:LYS:HE3	1.80	0.61
7:82:277:TYR:HB3	10:D0:148:MET:HE1	1.81	0.61
10:E5:47:MET:HG2	10:E5:55:TYR:HB2	1.82	0.61
14:L3:154:MET:HE2	14:L3:213:ILE:HG21	1.82	0.61
1:A:394:LYS:HA	1:F:394:LYS:HE2	1.80	0.61
1:V:481:LEU:HA	1:V:484:GLN:HG3	1.82	0.61
3:2E:178:SER:HB2	4:2F:347:ASN:HD22	1.64	0.61
4:2L:268:ILE:HG23	4:2L:300:MET:HE2	1.82	0.61
3:4C:360:PRO:HG2	3:4C:371:VAL:HG23	1.82	0.61
5:52:89:VAL:H	5:52:103:HIS:HB3	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6M:213:CYS:HA	3:6M:217:LEU:HD23	1.81	0.61
10:F1:63:TYR:HD2	14:M4:147:GLN:HG2	1.65	0.61
12:F9:253:THR:HG21	12:F9:262:LEU:HG	1.81	0.61
14:M4:175:ILE:HG21	14:M4:181:LEU:HD21	1.81	0.61
1:I:582:LEU:HB3	1:J:583:GLN:HE21	1.64	0.61
1:M:661:ASN:O	1:M:665:THR:HG23	2.00	0.61
3:2G:180:ALA:HB3	3:2G:183:GLU:HG3	1.81	0.61
4:2J:139:LEU:HD11	4:2J:192:LEU:HD12	1.82	0.61
4:3J:49:VAL:HG11	4:3J:241:ARG:HG2	1.82	0.61
3:4E:233:GLN:HE21	3:4E:368:LEU:HG	1.65	0.61
3:5E:244:PHE:HB2	3:5E:356:ASN:HD21	1.66	0.61
7:85:303:PRO:HB2	10:E0:156:ARG:HH12	1.64	0.61
3:8K:174:SER:HB3	3:8K:207:GLU:HG2	1.82	0.61
4:9B:278:SER:O	4:9B:282:ARG:HB3	2.00	0.61
4:9J:253:LEU:O	4:9J:257:LEU:CB	2.48	0.61
10:E2:347:GLU:HA	10:E2:350:LYS:HD2	1.83	0.61
10:F2:301:ARG:HH22	14:M7:142:GLN:HA	1.66	0.61
1:a:659:LEU:O	1:a:663:LEU:HG	2.00	0.61
1:c:597:ILE:HG13	1:c:598:ALA:N	2.14	0.61
1:C:341:GLU:HG3	1:G:342:MET:HE1	1.82	0.61
1:I:643:ARG:HA	1:I:646:ASN:HD21	1.65	0.61
1:M:656:GLN:CD	1:N:656:GLN:HB3	2.26	0.61
1:Y:617:MET:HG3	1:c:618:ARG:HH12	1.64	0.61
1:Y:621:PHE:CD2	1:c:617:MET:HE1	2.35	0.61
4:1L:152:ILE:HA	4:1L:155:VAL:HG22	1.82	0.61
5:31:46:ARG:HE	5:31:138:ILE:HD12	1.66	0.61
4:6H:98:GLY:H	4:6H:103:LYS:HD2	1.64	0.61
7:72:319:SER:HB3	7:72:398:LYS:HB2	1.81	0.61
3:7M:332:VAL:O	3:7M:336:LYS:HB3	2.01	0.61
7:85:350:ARG:HE	7:85:379:LEU:HD21	1.65	0.61
7:94:413:ARG:HH22	4:9J:380:ARG:HD3	1.65	0.61
4:9B:102:ALA:HB2	4:9B:403:MET:HE3	1.82	0.61
9:B2:150:MET:HE2	11:C3:287:PRO:HD2	1.82	0.61
12:G2:223:LEU:O	12:G2:227:SER:HB3	2.00	0.61
1:a:513:ARG:HG3	1:f:513:ARG:HA	1.81	0.61
3:1A:259:LEU:HD12	3:1A:268:MET:HG2	1.82	0.61
4:1L:213:ARG:HE	4:1L:297:LYS:HG2	1.65	0.61
5:23:206:LEU:HG	5:26:205:ARG:HH12	1.65	0.61
5:33:89:VAL:HB	5:33:103:HIS:HB3	1.81	0.61
3:3A:79:ARG:HH22	3:3A:87:PHE:HB2	1.64	0.61
5:44:36:LEU:HD11	5:44:42:LEU:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5J:8:GLN:HE21	4:5J:65:LEU:HG	1.64	0.61
3:8E:244:PHE:HB2	3:8E:356:ASN:HD21	1.65	0.61
3:9C:273:ALA:HA	3:9C:275:ILE:HG12	1.83	0.61
8:A8:129:VAL:HB	8:A8:163:ARG:HD2	1.82	0.61
10:C6:94:VAL:HG21	10:C6:331:ILE:HG12	1.82	0.61
10:D0:61:ASP:HA	14:L5:142:GLN:HE22	1.65	0.61
10:F3:307:MET:HE3	10:F3:396:LEU:HB3	1.82	0.61
1:d:373:LEU:O	1:d:377:HIS:CB	2.49	0.61
1:o:869:ARG:HG3	1:o:870:GLY:H	1.65	0.61
4:1H:248:SER:HA	4:1H:252:LYS:HD2	1.83	0.61
3:1M:319:TYR:O	3:1M:355:ILE:HA	2.00	0.61
3:4M:279:GLU:HA	3:4M:283:HIS:HD1	1.64	0.61
3:5A:213:CYS:HA	3:5A:217:LEU:HD23	1.82	0.61
3:5C:103:PHE:HD1	3:5C:413:MET:HE1	1.66	0.61
4:5J:54:ALA:HB3	4:5J:58:ARG:HB3	1.82	0.61
4:7D:200:GLN:HG2	4:7D:266:PHE:HB2	1.82	0.61
10:D6:308:VAL:HG11	14:L4:137:GLY:HA3	1.82	0.61
10:E7:145:ASN:HD22	14:L9:129:PRO:HG3	1.66	0.61
1:I:400:GLU:O	1:I:404:PHE:CB	2.49	0.61
2:13:291:GLU:O	2:13:295:PHE:HB2	2.00	0.61
5:25:30:ASP:HA	5:25:190:PHE:HZ	1.66	0.61
5:29:51:GLU:HB3	5:29:147:VAL:HG12	1.81	0.61
5:55:169:ILE:HG23	5:60:169:ILE:HD13	1.82	0.61
4:5B:292:GLN:HG3	4:5B:298:ASN:HD22	1.65	0.61
4:5D:267:LEU:HD21	4:5D:371:SER:HB3	1.82	0.61
3:5M:137:MET:HE3	3:5M:154:LEU:HD21	1.83	0.61
4:8L:101:TRP:HE1	4:8L:188:SER:HB3	1.66	0.61
12:F8:195:PRO:HA	12:F8:198:LYS:HG2	1.81	0.61
1:a:562:ILE:HD13	1:f:562:ILE:HD11	1.81	0.61
1:f:565:ASP:HB3	1:f:566:ARG:HH22	1.65	0.61
1:q:869:ARG:HG3	1:q:870:GLY:H	1.66	0.61
1:C:384:LEU:HD21	1:c:668:GLN:HE22	1.66	0.61
1:M:603:ARG:HB3	1:N:604:ILE:HG12	1.83	0.61
1:1:880:THR:HG22	6:66:902:PRO:HD3	1.83	0.61
4:2L:91:VAL:HG21	4:2L:116:VAL:HG22	1.81	0.61
3:3G:272:TYR:HB3	3:3G:275:ILE:HD11	1.83	0.61
4:3L:99:ASN:HD22	3:3M:258:ASN:HD21	1.48	0.61
3:4C:209:ILE:HG12	3:4C:302:MET:HG2	1.82	0.61
5:57:26:THR:HB	5:57:29:ILE:HB	1.83	0.61
5:57:105:LEU:HD21	5:57:110:PHE:HB2	1.82	0.61
3:5K:203:MET:HG3	3:5K:384:ILE:HD11	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:61:48:VAL:HG21	5:61:134:LEU:HD22	1.82	0.61
6:67:155:ILE:HD11	12:I6:325:PRO:HB3	1.83	0.61
3:6K:292:THR:HG21	3:6K:331:ALA:HB1	1.80	0.61
4:7L:113:ILE:HA	4:7L:116:VAL:HG22	1.83	0.61
7:82:350:ARG:HG2	7:82:379:LEU:HD22	1.81	0.61
7:92:280:PRO:HD3	14:M3:129:PRO:HD2	1.82	0.61
3:9I:100:ALA:HA	4:9J:252:LYS:HG2	1.82	0.61
9:B5:450:GLU:HG3	9:B5:472:VAL:HG22	1.82	0.61
9:B6:523:LYS:HE2	9:B6:525:SER:HB3	1.82	0.61
10:C7:83:ARG:HE	10:C7:88:LEU:HD12	1.64	0.61
13:J7:351:ARG:HD3	13:J7:352:LYS:HG2	1.81	0.61
3:1K:213:CYS:HA	3:1K:217:LEU:HD13	1.82	0.61
3:2E:115:VAL:HG21	3:2E:152:LEU:HD22	1.82	0.61
2:3:179:MET:O	2:3:183:ARG:HB2	1.99	0.61
5:39:26:THR:HG22	5:39:29:ILE:HD12	1.83	0.61
3:3K:104:ALA:HB2	3:3K:413:MET:HG2	1.83	0.61
3:4K:276:ILE:HG13	3:4K:280:LYS:HG3	1.82	0.61
3:4M:113:GLU:HG2	3:4M:114:ILE:HG23	1.82	0.61
3:5A:270:SER:HA	3:5A:377:MET:O	2.00	0.61
4:5B:362:LYS:HD2	4:5B:363:MET:HG3	1.82	0.61
3:6M:101:ASN:HD22	4:6N:256:ASN:HD21	1.45	0.61
4:7J:235:GLY:HA3	4:7J:366:THR:HG21	1.80	0.61
3:7K:245:ASP:HB3	1:j:788:PRO:HB3	1.83	0.61
3:7M:130:THR:HG21	7:91:406:LEU:HD11	1.82	0.61
3:7M:310:GLY:HA3	3:7M:383:ALA:HB2	1.83	0.61
9:B6:514:VAL:O	9:B6:518:CYS:HB2	2.01	0.61
10:E3:301:ARG:HH11	14:M1:141:ILE:HG22	1.65	0.61
1:u:867:PRO:HA	1:u:944:GLN:HE21	1.66	0.61
1:O:642:MET:HA	1:O:645:GLN:HE21	1.66	0.61
1:Q:530:LEU:HD12	1:Q:533:ARG:HE	1.64	0.61
1:Q:530:LEU:HD11	1:Q:533:ARG:HH21	1.66	0.61
1:R:647:LYS:HA	1:g:749:VAL:HG12	1.83	0.61
1:1:880:THR:HA	6:66:902:PRO:HG3	1.82	0.61
3:1M:30:ILE:HG22	3:1M:36:MET:HG2	1.82	0.61
4:3H:77:ARG:HE	6:63:924:THR:HG21	1.66	0.61
3:3M:274:PRO:HG2	3:3M:371:VAL:HG11	1.82	0.61
3:4C:234:VAL:HG21	3:4C:270:SER:HB2	1.83	0.61
3:5E:388:PHE:HB3	3:5E:425:LEU:HD21	1.83	0.61
3:5K:265:ILE:HD12	3:5K:313:MET:HE1	1.82	0.61
4:5L:215:LEU:HD21	4:5L:273:LEU:HD22	1.81	0.61
3:5M:209:ILE:HG12	3:5M:302:MET:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:67:407:LEU:HD22	6:67:411:HIS:CE1	2.35	0.61
3:6A:47:ASP:O	3:6A:50:ASN:HB2	2.01	0.61
3:6I:56:THR:HA	3:7I:285:GLN:HG3	1.82	0.61
4:9F:316:MET:HG2	4:9F:352:SER:HB3	1.81	0.61
10:D4:338:PRO:HB2	10:D4:341:TYR:HB3	1.83	0.61
13:J1:390:GLN:HE22	13:J1:482:LYS:HE2	1.66	0.61
1:A:410:ALA:HA	1:f:522:ARG:HH12	1.66	0.60
1:J:615:ARG:HH12	1:J:619:GLN:HB2	1.66	0.60
1:Q:632:ARG:HH12	1:h:773:ASP:HB2	1.65	0.60
4:1F:49:VAL:HG11	4:1F:241:ARG:HG2	1.80	0.60
3:1G:75:VAL:HG11	3:1G:94:SER:HB3	1.82	0.60
4:1N:284:LEU:HG	4:1N:362:LYS:HB2	1.82	0.60
4:2D:10:GLY:HA2	4:2D:143:THR:HG23	1.81	0.60
4:2H:135:ILE:HB	4:2H:166:THR:HG22	1.81	0.60
5:38:33:ASP:HB3	5:38:36:LEU:HB2	1.82	0.60
4:3H:179:VAL:HG13	3:3I:350:GLY:HA2	1.83	0.60
3:4C:173:PRO:HB2	3:4C:391:MET:HE1	1.82	0.60
3:4I:209:ILE:HG13	3:4I:302:MET:HG2	1.82	0.60
10:D2:62:VAL:HG22	14:K7:142:GLN:HB2	1.81	0.60
1:A:499:ARG:HA	1:F:499:ARG:HH12	1.65	0.60
1:Q:629:LYS:HD3	1:h:771:VAL:HG21	1.83	0.60
1:Z:558:LEU:HD22	1:d:558:LEU:HB3	1.82	0.60
5:22:100:ASN:HB2	5:22:184:THR:HG22	1.82	0.60
5:22:116:ARG:HG3	5:22:117:GLN:HG3	1.82	0.60
5:37:199:LEU:HD12	5:38:199:LEU:HG	1.82	0.60
4:3B:4:ILE:HB	4:3B:50:PHE:HE2	1.66	0.60
3:3G:88:HIS:HB2	3:3G:91:GLN:HG3	1.83	0.60
3:4A:310:GLY:HA3	3:4A:383:ALA:HB2	1.83	0.60
3:4M:276:ILE:HG21	3:4M:280:LYS:HD3	1.81	0.60
4:5F:10:GLY:HA2	4:5F:143:THR:HG23	1.84	0.60
4:5L:2:ARG:HB3	4:5L:131:GLN:HB2	1.83	0.60
5:62:50:PHE:HB2	5:62:71:ILE:HD13	1.83	0.60
4:6D:235:GLY:HA2	4:6D:238:CYS:HB3	1.82	0.60
4:6H:244:GLY:HA2	4:6H:355:ASP:HB2	1.82	0.60
3:6M:60:LYS:HE3	3:6M:62:VAL:HG22	1.82	0.60
4:8F:244:GLY:HA2	4:8F:355:ASP:HB2	1.83	0.60
3:9K:54:SER:HB3	3:9K:64:ARG:HH21	1.66	0.60
10:D9:338:PRO:HB2	10:D9:341:TYR:HB3	1.82	0.60
13:J2:271:LEU:HD13	13:J2:286:LEU:HD13	1.82	0.60
1:A:473:ARG:HH22	1:A:474:LEU:HD13	1.65	0.60
1:Y:603:ARG:HB3	1:c:604:ILE:HG13	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1I:298:PRO:HB3	3:1I:307:PRO:HD2	1.82	0.60
5:24:27:SER:HA	5:24:30:ASP:HB2	1.82	0.60
3:3A:219:ILE:HD11	3:3A:367:ASP:HB2	1.81	0.60
3:4A:223:THR:HG23	3:4A:225:THR:H	1.65	0.60
4:4F:207:LEU:HD13	4:4F:225:LEU:HB3	1.83	0.60
3:5G:238:LEU:HD21	3:5G:378:ILE:HD13	1.83	0.60
6:64:262:LYS:HZ2	6:64:303:LEU:HD13	1.65	0.60
6:67:485:LYS:HB3	6:67:487:TYR:CD1	2.36	0.60
3:6E:178:SER:HB3	3:6E:183:GLU:HG3	1.83	0.60
4:7B:5:VAL:O	4:7B:133:PHE:HA	2.01	0.60
3:7M:119:LEU:HD11	3:7M:156:ARG:HG2	1.83	0.60
4:8D:182:PRO:HG3	4:8D:384:GLN:HE21	1.66	0.60
3:8G:324:VAL:HG12	3:8G:326:LYS:H	1.65	0.60
7:95:350:ARG:HG2	7:95:379:LEU:HD22	1.83	0.60
7:96:412:MET:HG2	4:9H:209:ASP:HB2	1.82	0.60
3:9E:217:LEU:HD12	3:9E:277:SER:HB3	1.83	0.60
12:G8:194:ALA:HB1	12:G8:197:LEU:HD13	1.83	0.60
13:J2:368:GLY:HA2	13:J2:371:ARG:HD3	1.83	0.60
1:a:582:LEU:HB2	1:f:583:GLN:HE22	1.66	0.60
1:J:608:ASP:HA	1:J:611:THR:HG23	1.83	0.60
1:R:673:LEU:HD11	1:V:674:ARG:HH21	1.65	0.60
4:1J:2:ARG:HB3	4:1J:131:GLN:HB2	1.83	0.60
3:2I:195:LEU:HD11	3:2I:428:LEU:HD22	1.82	0.60
3:2M:156:ARG:HA	3:2M:159:VAL:HG12	1.84	0.60
5:31:42:LEU:HD11	5:31:74:LYS:HB3	1.83	0.60
4:4H:257:LEU:HD21	4:4H:314:SER:HB2	1.83	0.60
6:63:602:ARG:O	6:63:606:GLN:CB	2.49	0.60
3:6E:191:THR:HG21	3:6E:425:LEU:HD12	1.83	0.60
7:76:352:VAL:HG11	14:K6:242:ILE:HG23	1.84	0.60
4:7B:324:LYS:O	4:7B:328:GLU:HB3	2.00	0.60
3:7E:211:ASP:HB3	3:7E:215:ARG:HH12	1.66	0.60
4:7J:276:ARG:HG3	1:j:813:PRO:HB3	1.82	0.60
9:B5:150:MET:HE1	11:C5:223:PRO:HD2	1.82	0.60
12:F9:246:PRO:HD3	12:F9:266:PRO:HB3	1.84	0.60
13:J4:318:LEU:HD22	13:J4:475:ALA:HB1	1.82	0.60
1:a:620:ASP:HB3	1:f:621:PHE:HE1	1.66	0.60
2:10:230:ARG:HH21	2:10:234:ARG:HB2	1.65	0.60
3:2C:278:ALA:HB2	9:B5:120:VAL:HG12	1.84	0.60
5:39:184:THR:O	5:39:188:MET:HB2	2.01	0.60
3:4I:363:VAL:HG12	3:4I:368:LEU:HB2	1.83	0.60
5:53:56:GLU:HG2	5:53:58:GLY:H	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:59:75:ILE:HD13	5:59:130:LEU:HD13	1.84	0.60
3:7M:103:PHE:H	3:7M:408:TYR:HE1	1.49	0.60
7:83:270:VAL:HG22	10:E1:155:MET:HE2	1.84	0.60
4:8H:152:ILE:HA	4:8H:164:MET:HE1	1.84	0.60
3:9G:214:ARG:HH12	3:9G:222:PRO:HD3	1.67	0.60
10:C6:293:MET:HG3	10:C6:297:ARG:HE	1.67	0.60
10:C8:86:LEU:HD12	10:C8:319:LEU:HG	1.82	0.60
10:C8:340:LEU:HD21	10:C8:386:LEU:HD11	1.83	0.60
12:G6:273:PRO:HD2	12:G6:276:LEU:HD12	1.83	0.60
12:I8:68:ARG:HE	12:I9:330:ASP:HB3	1.66	0.60
13:J1:417:ILE:HG12	13:J1:600:LEU:HD11	1.83	0.60
1:O:661:ASN:C	1:O:661:ASN:HD22	2.09	0.60
1:Q:469:LEU:HB3	1:Z:362:VAL:HG21	1.84	0.60
4:1F:11:GLN:HA	4:1F:72:THR:HG21	1.83	0.60
3:1G:244:PHE:HB2	3:1G:356:ASN:HD21	1.67	0.60
5:20:214:LYS:HD2	5:25:17:SER:HB2	1.83	0.60
3:3G:71:GLU:HB2	4:3H:2:ARG:HH21	1.66	0.60
3:4I:274:PRO:HB2	3:4I:276:ILE:HG23	1.82	0.60
3:6G:262:TYR:HB2	14:K9:76:LEU:HD12	1.83	0.60
4:6N:330:MET:HE2	4:6N:351:SER:HB3	1.84	0.60
4:7J:405:GLU:HA	4:7J:408:PHE:HD2	1.66	0.60
3:9E:319:TYR:HB3	3:9E:323:VAL:HG11	1.83	0.60
8:A3:182:LEU:HD23	8:A3:189:VAL:HG22	1.83	0.60
10:D5:338:PRO:HB2	10:D5:341:TYR:HB3	1.83	0.60
1:M:673:LEU:O	1:M:677:MET:HG2	2.02	0.60
1:R:434:ALA:HB3	1:y:859:LEU:HD22	1.83	0.60
3:1E:147:SER:HB2	3:1E:190:SER:HB2	1.84	0.60
3:1G:16:ILE:HD11	3:1G:231:ILE:HG21	1.83	0.60
5:25:51:GLU:HB3	5:25:147:VAL:HG22	1.84	0.60
3:2C:159:VAL:HG12	6:66:558:LYS:HE2	1.82	0.60
3:2E:318:MET:HA	3:2E:354:GLY:O	2.01	0.60
4:2F:132:GLY:HA2	4:2F:162:ARG:HB3	1.82	0.60
5:30:47:GLU:HG3	5:30:70:PRO:HB2	1.84	0.60
5:44:158:LEU:HD23	5:44:174:LEU:HD22	1.83	0.60
5:45:207:HIS:HE1	13:J6:508:CYS:H	1.50	0.60
3:4A:251:ASP:H	3:4A:254:GLU:HB2	1.67	0.60
3:4I:195:LEU:HD21	3:4I:428:LEU:HD13	1.84	0.60
3:4I:360:PRO:HG2	3:4I:371:VAL:HG23	1.83	0.60
5:54:119:LEU:HB3	5:54:121:ILE:HG12	1.83	0.60
4:5B:152:ILE:HG23	4:5B:164:MET:HE2	1.83	0.60
6:69:614:PRO:HA	6:69:617:VAL:HG12	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6K:259:LEU:HD11	3:6K:316:CYS:HB2	1.83	0.60
7:73:320:TRP:HD1	7:73:396:ASP:HB2	1.65	0.60
4:7H:65:LEU:HB3	4:7H:73:MET:HE1	1.83	0.60
7:83:350:ARG:HG2	7:83:379:LEU:HD22	1.83	0.60
3:8G:265:ILE:HG23	3:8G:432:TYR:HE1	1.65	0.60
4:8L:119:VAL:HA	4:8L:122:LYS:HD2	1.82	0.60
3:8M:248:LEU:HB2	3:8M:355:ILE:H	1.67	0.60
4:9J:248:SER:HA	4:9J:252:LYS:HD3	1.82	0.60
2:13:201:VAL:HA	2:13:204:LEU:HD12	1.84	0.60
4:2B:273:LEU:H	4:2B:292:GLN:HE22	1.49	0.60
3:2C:180:ALA:HB3	3:2C:183:GLU:HB2	1.82	0.60
3:2E:136:LEU:HD11	3:2E:252:VAL:HG21	1.82	0.60
3:2G:217:LEU:HD21	3:2G:368:LEU:HD23	1.83	0.60
5:39:114:GLN:HG3	5:39:119:LEU:HB2	1.82	0.60
3:3I:250:VAL:HB	3:3I:318:MET:HE1	1.83	0.60
3:3M:332:VAL:HA	3:3M:335:ILE:HG22	1.84	0.60
3:4K:101:ASN:HD22	4:4L:256:ASN:HD21	1.50	0.60
6:67:561:LEU:HA	6:67:564:MET:HB3	1.83	0.60
3:6C:176:GLN:HB3	4:6D:331:LEU:HD21	1.83	0.60
4:6F:164:MET:HB3	4:6F:197:ASP:H	1.67	0.60
4:7L:152:ILE:HG22	4:7L:156:ARG:HH11	1.67	0.60
4:8F:121:ARG:O	4:8F:125:GLU:HB2	2.01	0.60
10:C7:341:TYR:HB2	10:C7:390:MET:HE2	1.83	0.60
10:F2:105:PHE:HE2	10:F2:299:LEU:HD21	1.67	0.60
1:a:558:LEU:HA	1:a:561:ARG:HD2	1.82	0.60
1:C:380:HIS:HA	1:G:381:ARG:HH22	1.66	0.60
1:J:612:PHE:HB2	3:9C:372:MET:HE1	1.83	0.60
1:Q:667:LYS:HE3	3:5A:58:ALA:HB1	1.84	0.60
4:1J:272:PRO:HD2	4:1J:361:LEU:HD13	1.84	0.60
3:1M:30:ILE:HD12	3:1M:34:GLY:HA2	1.84	0.60
5:20:22:ALA:HB1	5:25:203:GLN:HE22	1.65	0.60
3:2C:88:HIS:HD2	3:3C:283:HIS:HB2	1.66	0.60
4:2J:73:MET:HA	4:2J:76:VAL:HG12	1.82	0.60
5:46:131:ILE:HD12	5:46:134:LEU:HD11	1.82	0.60
4:4B:238:CYS:HA	4:4B:241:ARG:HE	1.66	0.60
3:4M:9:VAL:HG12	3:4M:146:GLY:HA2	1.84	0.60
4:5F:16:ILE:HD11	4:5F:229:VAL:HG11	1.83	0.60
4:5N:113:ILE:HD13	4:5N:150:LEU:HB3	1.84	0.60
7:71:376:GLU:O	7:71:380:TRP:HB3	2.02	0.60
3:9C:278:ALA:HA	3:9C:369:ALA:HB2	1.81	0.60
3:9K:311:LYS:H	3:9K:382:THR:HG22	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E3:284:LEU:HB3	10:E3:351:ARG:HH12	1.67	0.60
13:J2:494:GLU:HG3	13:J2:497:TRP:HB3	1.83	0.60
13:J5:339:ARG:HG3	13:J5:341:PRO:HD2	1.83	0.60
1:a:600:LEU:HD22	1:f:604:ILE:HD11	1.84	0.60
1:J:577:GLN:HE21	1:J:578:ARG:CZ	2.15	0.60
3:1A:166:LYS:H	3:1A:199:ASP:HB2	1.65	0.60
3:1G:213:CYS:HA	3:1G:217:LEU:HD23	1.83	0.60
4:1J:17:GLY:HA2	4:1J:20:PHE:HB3	1.84	0.60
3:2C:319:TYR:HB3	3:2C:323:VAL:HG21	1.83	0.60
3:2K:79:ARG:HG3	3:2K:92:LEU:HD22	1.84	0.60
5:30:50:PHE:HB2	5:30:71:ILE:HD12	1.84	0.60
5:32:53:ARG:HG3	5:32:147:VAL:HG13	1.83	0.60
5:35:188:MET:HE1	5:35:191:ARG:HH21	1.67	0.60
3:3A:185:TYR:HE2	3:3A:404:PHE:HB2	1.66	0.60
3:3E:119:LEU:HD12	3:3E:123:ARG:HH12	1.66	0.60
6:65:838:ASN:HB3	6:65:841:ILE:HG22	1.84	0.60
3:6C:71:GLU:HB3	3:6C:98:ASP:HB2	1.84	0.60
3:6G:102:ASN:HD21	3:6G:105:ARG:HG2	1.67	0.60
3:6I:222:PRO:HD2	4:6J:324:LYS:HD2	1.84	0.60
4:7F:16:ILE:HD11	4:7F:136:THR:HB	1.84	0.60
4:7H:325:GLU:HA	4:7H:328:GLU:HG2	1.82	0.60
4:9B:290:THR:HA	4:9B:293:MET:HG2	1.83	0.60
4:9L:317:PHE:HA	4:9L:365:VAL:HG22	1.83	0.60
10:C8:86:LEU:HG	10:C8:313:TYR:HD2	1.67	0.60
10:F2:69:LEU:HD21	10:F2:312:LYS:HD2	1.84	0.60
1:K:376:MET:HG3	1:L:376:MET:SD	2.42	0.59
1:K:513:ARG:HB2	1:L:513:ARG:HE	1.67	0.59
3:1C:2:ARG:HD3	3:1C:242:LEU:HB3	1.84	0.59
4:1N:156:ARG:HH12	4:1N:160:PRO:HA	1.66	0.59
4:1N:358:PRO:HG2	4:1N:361:LEU:HB3	1.83	0.59
4:6D:206:ALA:HB2	4:6D:302:ALA:HB2	1.84	0.59
4:6F:86:ARG:HD3	4:6F:87:PRO:HD2	1.83	0.59
3:6G:234:VAL:HG21	3:6G:302:MET:HE1	1.84	0.59
3:6I:254:GLU:O	3:6I:258:ASN:HB2	2.03	0.59
3:6I:422:ARG:HH12	3:6I:426:ALA:HB2	1.67	0.59
7:76:319:SER:HB3	7:76:398:LYS:HD2	1.84	0.59
3:7A:298:PRO:HA	3:7A:301:MET:HE1	1.84	0.59
3:7K:223:THR:HA	4:7L:323:THR:HG22	1.82	0.59
4:7L:117:LEU:HD21	4:7L:154:LYS:HB3	1.84	0.59
4:8H:54:ALA:HB3	4:8H:58:ARG:HB3	1.83	0.59
7:95:408:ILE:HG22	3:9M:329:ASN:HB3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9D:258:ILE:HG13	4:9D:266:PHE:HZ	1.67	0.59
3:9I:178:SER:HB2	4:9J:347:ASN:HD22	1.66	0.59
3:9M:271:SER:HB3	3:9M:301:MET:HA	1.84	0.59
10:E1:288:PRO:HG3	10:E1:385:GLU:HG3	1.83	0.59
10:E5:338:PRO:HB2	10:E5:341:TYR:HB3	1.84	0.59
4:1B:269:GLY:HA2	4:1B:300:MET:H	1.66	0.59
5:25:136:SER:HA	5:25:139:LYS:HB2	1.82	0.59
4:2F:86:ARG:HB3	4:2F:89:ASN:H	1.66	0.59
5:35:33:ASP:HB3	5:35:36:LEU:HB2	1.84	0.59
5:35:201:LEU:O	5:35:205:ARG:HG3	2.01	0.59
3:3I:119:LEU:HA	3:3I:122:ILE:HB	1.85	0.59
4:3J:276:ARG:HD2	6:69:877:ALA:HB3	1.84	0.59
3:3M:288:VAL:HG11	3:3M:327:ASP:HB2	1.83	0.59
5:49:161:ILE:HG22	5:49:168:PHE:HB3	1.84	0.59
4:4B:2:ARG:HD2	4:4B:131:GLN:HE21	1.67	0.59
3:4E:328:VAL:HG21	3:4E:355:ILE:HD11	1.84	0.59
2:5:195:LYS:HE2	6:63:991:ASP:HB3	1.84	0.59
5:52:50:PHE:HB2	5:52:71:ILE:HG13	1.84	0.59
3:5A:9:VAL:HG23	3:5A:68:LEU:HD22	1.83	0.59
3:5K:272:TYR:HB3	3:5K:275:ILE:HD11	1.84	0.59
6:63:131:ARG:HH21	12:H1:335:ILE:HG23	1.66	0.59
6:66:629:ILE:HG22	6:66:633:VAL:HG23	1.84	0.59
3:6M:276:ILE:HD12	3:6M:281:ALA:HA	1.84	0.59
4:6N:193:VAL:HG12	4:6N:265:PHE:HZ	1.67	0.59
4:8B:358:PRO:HG2	4:8B:361:LEU:HB3	1.84	0.59
4:8H:49:VAL:HG11	4:8H:241:ARG:HG2	1.83	0.59
4:9D:7:VAL:HG22	4:9D:64:ILE:HD13	1.83	0.59
4:9F:51:TYR:HB3	4:9F:59:PHE:HB3	1.84	0.59
9:B6:17:LEU:HD22	9:B6:491:ARG:HB3	1.83	0.59
10:E6:110:ILE:HG23	10:E6:286:ARG:HH12	1.67	0.59
1:Y:604:ILE:N	1:c:604:ILE:HD11	2.17	0.59
5:23:206:LEU:HD21	5:26:205:ARG:HH22	1.67	0.59
4:2F:163:ILE:HD11	4:2F:251:ARG:HG3	1.82	0.59
3:2M:261:PRO:HG2	3:2M:313:MET:HE2	1.85	0.59
5:30:45:SER:HA	5:30:73:VAL:O	2.02	0.59
5:46:167:LYS:HE2	5:47:119:LEU:HA	1.83	0.59
6:65:913:TYR:HE1	8:A2:86:GLN:HG3	1.65	0.59
7:73:386:ARG:HG3	14:K4:115:PRO:HB3	1.83	0.59
4:7B:287:PRO:HA	4:7B:329:GLN:HE22	1.67	0.59
4:7B:316:MET:HE1	4:7B:350:LYS:HZ3	1.67	0.59
3:7C:252:VAL:HA	3:7C:255:PHE:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7H:45:GLU:HG2	4:7H:46:ARG:HG2	1.84	0.59
3:8C:336:LYS:HG2	14:L8:108:TYR:HE1	1.67	0.59
3:8E:269:LEU:HG	3:8E:384:ILE:HD12	1.84	0.59
3:8G:70:LEU:HD12	3:8G:114:ILE:HD13	1.84	0.59
3:9K:348:PRO:HB2	14:M6:111:LEU:HB3	1.84	0.59
8:A1:36:PRO:HG3	9:B1:10:PRO:HG3	1.85	0.59
10:E7:47:MET:HG2	10:E7:55:TYR:HB2	1.83	0.59
13:J1:339:ARG:HH22	13:J1:366:ARG:HG2	1.68	0.59
13:J7:483:LYS:HA	13:J7:509:PHE:HB2	1.84	0.59
14:L6:113:GLU:HG3	14:L6:118:CYS:HA	1.83	0.59
1:G:364:GLU:HA	1:G:367:GLU:HG3	1.83	0.59
4:1B:45:GLU:HG2	4:1B:243:PRO:HD3	1.83	0.59
3:1M:320:ARG:HB2	3:1M:356:ASN:HB3	1.83	0.59
5:21:206:LEU:HD23	5:22:21:LEU:HB3	1.84	0.59
5:29:111:ARG:HH21	6:68:332:LYS:HE3	1.67	0.59
4:2B:293:MET:HE2	4:2B:367:PHE:HB2	1.85	0.59
3:2C:88:HIS:HE2	3:3C:280:LYS:HA	1.66	0.59
5:30:90:GLU:HG3	5:30:102:THR:HG22	1.84	0.59
5:32:214:LYS:HG2	5:32:221:LEU:HD21	1.84	0.59
5:33:175:ASP:HB2	6:67:363:PRO:HD3	1.84	0.59
4:3F:215:LEU:HD13	8:A5:257:PRO:HB2	1.84	0.59
3:3M:319:TYR:HB3	3:3M:323:VAL:HG11	1.84	0.59
3:4A:8:HIS:HE1	3:4A:21:TRP:HE1	1.50	0.59
4:5B:240:LEU:HD11	4:5B:250:LEU:HG	1.84	0.59
3:5C:196:GLU:HA	14:K4:83:THR:HG23	1.84	0.59
4:7H:296:ALA:HA	4:7H:299:MET:HG2	1.83	0.59
7:85:389:GLN:HA	3:8G:339:ARG:HH12	1.67	0.59
4:8B:399:THR:HA	4:8B:403:MET:HB3	1.84	0.59
4:8F:321:MET:HE1	4:8F:363:MET:HE3	1.84	0.59
3:8K:154:LEU:HD23	3:8K:193:SER:HB3	1.84	0.59
3:9I:223:THR:HG23	3:9I:225:THR:H	1.67	0.59
3:9M:171:SER:HA	3:9M:204:LEU:HB2	1.84	0.59
10:D3:338:PRO:HB2	10:D3:341:TYR:HB3	1.84	0.59
10:F3:68:THR:HA	10:F3:71:GLN:HG2	1.84	0.59
14:M4:207:ILE:HG23	14:M4:212:ASP:HB2	1.84	0.59
1:m:738:ALA:HB1	1:m:743:THR:HG21	1.83	0.59
1:A:667:LYS:HG2	1:F:666:VAL:HG21	1.85	0.59
1:Y:677:MET:O	1:Y:681:ILE:HG12	2.01	0.59
4:1F:102:ALA:HA	4:1F:403:MET:HE3	1.84	0.59
3:1M:208:ALA:HB2	3:1M:304:LYS:HG2	1.84	0.59
1:2:917:ARG:H	1:2:922:ARG:HH22	1.49	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2I:245:ASP:HB3	9:B2:76:ARG:HD2	1.82	0.59
5:38:72:ARG:HH12	5:38:74:LYS:HG3	1.67	0.59
3:3I:255:PHE:O	3:3I:259:LEU:HB2	2.02	0.59
4:3J:332:ASN:O	4:3J:336:LYS:HB2	2.02	0.59
5:54:158:LEU:HB2	5:54:174:LEU:HB2	1.85	0.59
3:5G:279:GLU:HG2	8:A1:56:LEU:HD23	1.84	0.59
4:5J:311:LEU:HD23	4:5J:342:VAL:HG21	1.85	0.59
2:6:299:ILE:HG12	13:J1:271:LEU:HD21	1.84	0.59
5:62:26:THR:HG21	5:62:198:LYS:HG2	1.85	0.59
3:6A:209:ILE:HB	3:6A:227:LEU:HD22	1.85	0.59
3:6C:91:GLN:HE21	3:6C:121:ARG:HH22	1.51	0.59
7:72:334:LEU:HD23	7:72:337:LYS:HD2	1.83	0.59
4:7D:99:ASN:HD21	3:7E:258:ASN:HD21	1.51	0.59
7:87:326:PRO:HA	7:87:391:TYR:HB3	1.85	0.59
3:9G:202:VAL:HG22	3:9G:268:MET:HB2	1.84	0.59
13:J6:289:ILE:HG23	13:J6:300:LEU:HD21	1.84	0.59
1:H:589:THR:HA	1:H:592:ARG:HD2	1.85	0.59
1:M:483:ILE:HD12	1:P:654:LEU:HD22	1.84	0.59
1:V:532:GLU:HG3	1:t:927:HIS:HB2	1.85	0.59
3:1A:21:TRP:HA	3:1A:24:PHE:HB2	1.84	0.59
4:2L:342:VAL:HG12	4:2L:345:ILE:H	1.67	0.59
3:3A:286:LEU:HB2	3:3A:373:ARG:HH21	1.66	0.59
4:4D:67:ASP:HB3	4:4D:73:MET:HE1	1.84	0.59
3:5A:269:LEU:HG	3:5A:384:ILE:HD11	1.83	0.59
3:5M:191:THR:HG21	3:5M:425:LEU:HD12	1.83	0.59
4:7F:407:GLU:HA	4:7F:410:GLU:HG2	1.84	0.59
3:7I:16:ILE:HD11	3:7I:138:PHE:HB3	1.85	0.59
7:89:350:ARG:HB3	7:89:352:VAL:HG22	1.83	0.59
4:8J:60:VAL:HG21	4:8J:86:ARG:HH21	1.66	0.59
7:94:405:VAL:HB	3:9K:333:ALA:HB1	1.82	0.59
3:9I:217:LEU:HD23	3:9I:277:SER:HB3	1.84	0.59
9:B3:36:GLU:HA	9:B3:44:LEU:HD13	1.84	0.59
9:B5:118:LEU:HD13	9:B5:148:TYR:HA	1.84	0.59
1:d:512:LYS:HA	1:d:515:VAL:HG12	1.83	0.59
1:r:869:ARG:HG3	1:r:870:GLY:H	1.68	0.59
1:2:894:LEU:HD11	1:2:943:LYS:HG3	1.85	0.59
4:3B:253:LEU:HD22	4:3B:350:LYS:HZ1	1.66	0.59
4:3D:215:LEU:HD13	8:A1:257:PRO:HB2	1.85	0.59
3:4G:195:LEU:HD21	3:4G:428:LEU:HD13	1.84	0.59
5:56:18:VAL:HA	5:56:21:LEU:HD23	1.85	0.59
6:63:598:VAL:HA	6:63:601:GLU:HG2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6D:182:PRO:HG3	4:6D:384:GLN:HG3	1.83	0.59
10:C7:86:LEU:HD21	10:C7:313:TYR:HB2	1.84	0.59
10:D4:301:ARG:HH11	14:L2:143:ARG:HD2	1.67	0.59
10:E8:354:ARG:HD3	10:E8:360:ALA:HA	1.85	0.59
1:p:873:PRO:HG2	1:p:875:ILE:HG12	1.82	0.59
1:B:431:ALA:HB1	1:Y:546:ASN:HD21	1.67	0.59
4:1B:155:VAL:HA	4:1B:158:GLU:HG2	1.83	0.59
3:1C:171:SER:HA	3:1C:204:LEU:HB2	1.85	0.59
4:1F:3:GLU:HA	4:1F:49:VAL:HA	1.84	0.59
5:23:203:GLN:HA	5:23:206:LEU:HD22	1.84	0.59
5:27:71:ILE:HG12	5:27:93:SER:HB2	1.83	0.59
5:31:216:LYS:HD3	5:31:217:SER:H	1.68	0.59
4:3J:172:SER:HB2	4:3J:205:GLU:HG2	1.85	0.59
3:4M:240:ALA:HB1	3:4M:356:ASN:HD22	1.67	0.59
6:63:133:ARG:HD3	12:H1:335:ILE:HG21	1.85	0.59
6:63:503:LYS:O	6:63:507:ARG:HB2	2.02	0.59
4:6H:200:GLN:HG2	4:6H:268:ILE:HD11	1.83	0.59
7:83:357:VAL:HG11	14:L3:218:LYS:HG2	1.85	0.59
7:87:378:MET:HA	7:87:381:PHE:HD2	1.68	0.59
3:8C:117:LEU:HD13	14:M4:250:PRO:HG3	1.83	0.59
7:92:381:PHE:HB3	7:92:384:GLU:HB2	1.85	0.59
10:E5:86:LEU:HD13	10:E5:319:LEU:HB3	1.84	0.59
14:M3:198:ARG:HD3	14:M3:224:GLY:HA2	1.83	0.59
1:u:879:VAL:HG13	1:u:880:THR:HG23	1.84	0.59
5:20:49:PRO:HB2	5:20:68:LEU:HD11	1.85	0.59
5:28:50:PHE:HB2	5:28:71:ILE:HD13	1.85	0.59
3:2E:217:LEU:HD21	3:2E:368:LEU:HD23	1.85	0.59
4:2J:77:ARG:HH21	4:2J:83:GLN:HA	1.68	0.59
3:3A:191:THR:HA	3:3A:194:LEU:HB2	1.84	0.59
5:43:158:LEU:HB3	5:43:174:LEU:HB2	1.84	0.59
5:49:167:LYS:HA	5:52:120:MET:HE2	1.84	0.59
4:4L:178:THR:HG22	3:4M:352:LYS:HZ2	1.68	0.59
4:5F:179:VAL:HG12	3:5G:258:ASN:HD22	1.68	0.59
3:5I:119:LEU:HD22	3:5I:123:ARG:HH22	1.68	0.59
6:63:868:GLU:HG2	6:63:897:LEU:HD21	1.85	0.59
4:6B:7:VAL:HB	4:6B:135:ILE:HG13	1.84	0.59
3:7E:209:ILE:HG21	3:7E:227:LEU:HA	1.84	0.59
3:7I:298:PRO:HG3	3:7I:308:ARG:HE	1.66	0.59
12:I5:103:LYS:HG3	12:I5:104:ILE:HG23	1.85	0.59
4:1D:3:GLU:HA	4:1D:49:VAL:HA	1.84	0.59
3:2A:255:PHE:O	3:2A:259:LEU:HB2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2B:236:VAL:HG13	4:2B:237:THR:HG23	1.85	0.59
3:5A:194:LEU:HA	3:5A:197:HIS:HB2	1.85	0.59
3:5K:320:ARG:HG3	3:5K:360:PRO:HD3	1.85	0.59
4:6N:299:MET:HG3	4:6N:305:PRO:HG2	1.85	0.59
4:8L:211:CYS:HA	4:8L:215:LEU:HB2	1.85	0.59
4:9H:248:SER:HA	4:9H:252:LYS:HD3	1.83	0.59
3:9K:310:GLY:HA3	3:9K:383:ALA:HB2	1.84	0.59
8:A6:103:ARG:HH22	8:A6:109:SER:HB3	1.66	0.59
1:E:424:LEU:HD11	1:p:878:PRO:HA	1.84	0.58
1:R:469:LEU:HD22	1:Y:362:VAL:HG11	1.83	0.58
3:1I:179:THR:HG23	4:1J:351:SER:HB3	1.84	0.58
5:28:113:MET:HA	5:28:116:ARG:HG2	1.83	0.58
5:35:149:ILE:HB	5:35:157:ARG:HG2	1.84	0.58
4:3L:11:GLN:HE22	3:3M:249:ASN:H	1.50	0.58
5:45:21:LEU:HD12	5:45:22:ALA:H	1.67	0.58
5:49:17:SER:HA	5:49:20:PHE:HB3	1.84	0.58
5:52:78:LEU:HD21	5:52:88:ARG:HH12	1.68	0.58
5:53:90:GLU:HA	5:53:101:TYR:O	2.03	0.58
5:58:85:GLN:HA	5:58:107:GLU:HB2	1.83	0.58
3:5A:205:ASP:HB2	3:5A:303:ALA:HA	1.83	0.58
3:5C:165:SER:HB2	3:5C:256:GLN:HE22	1.66	0.58
6:66:181:LEU:HD22	6:66:571:THR:HA	1.85	0.58
7:78:269:LEU:HD21	7:78:328:PRO:HB3	1.85	0.58
3:7A:100:ALA:HA	4:7B:252:LYS:HD3	1.85	0.58
3:7C:66:VAL:HA	3:7C:91:GLN:HB3	1.84	0.58
4:7J:290:THR:HG21	4:7J:329:GLN:HB3	1.84	0.58
3:8K:140:ALA:HA	3:8K:171:SER:HB3	1.85	0.58
3:9C:269:LEU:HD11	3:9C:384:ILE:HB	1.84	0.58
8:A3:179:LYS:HZ1	8:A3:194:GLU:HG2	1.68	0.58
9:B6:511:LEU:HD12	9:B6:519:ALA:HB1	1.84	0.58
1:a:631:LEU:HD23	1:f:635:ASN:HD22	1.68	0.58
1:z:883:THR:HG21	1:z:952:ARG:HH22	1.68	0.58
3:1E:262:TYR:HB2	3:1E:265:ILE:HG22	1.84	0.58
3:1G:247:ALA:HB3	3:1G:355:ILE:HB	1.83	0.58
5:26:105:LEU:HD13	5:26:110:PHE:HB2	1.85	0.58
3:2E:147:SER:HB2	3:2E:190:SER:HB3	1.84	0.58
5:37:206:LEU:HB2	5:38:206:LEU:HD21	1.85	0.58
4:4B:173:PRO:HA	4:4B:380:ARG:HH12	1.68	0.58
4:4D:139:LEU:HA	4:4D:145:SER:HB3	1.85	0.58
5:55:144:PHE:HA	5:55:162:GLN:HB2	1.83	0.58
4:5B:314:SER:HB3	4:5B:368:VAL:HB	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5K:54:SER:HB3	3:5K:64:ARG:HE	1.68	0.58
4:6N:226:ASN:HD21	17:6N:502:GDP:HN1	1.51	0.58
3:7A:140:ALA:HA	3:7A:171:SER:HB2	1.85	0.58
3:7C:229:ARG:HD2	3:7C:363:VAL:HG21	1.85	0.58
4:7D:7:VAL:HB	4:7D:135:ILE:HG22	1.83	0.58
4:8D:113:ILE:HG13	4:8D:150:LEU:HD22	1.85	0.58
10:E6:151:GLN:HA	10:E6:154:ILE:HG12	1.85	0.58
12:G1:195:PRO:HA	12:G1:198:LYS:HE3	1.85	0.58
1:c:617:MET:HA	1:c:617:MET:HE2	1.85	0.58
5:27:21:LEU:HG	5:30:206:LEU:HD12	1.85	0.58
3:2I:250:VAL:HG22	3:2I:352:LYS:HE3	1.86	0.58
4:2J:27:GLU:HA	4:2J:359:LYS:HD2	1.85	0.58
4:2L:89:ASN:HA	4:2L:119:VAL:HG21	1.85	0.58
4:3B:163:ILE:HG21	4:3B:250:LEU:HB3	1.85	0.58
4:3D:311:LEU:HD23	4:3D:342:VAL:HG21	1.84	0.58
5:50:212:LEU:HD21	6:64:601:GLU:HB3	1.83	0.58
4:5L:294:PHE:HB3	6:69:797:MET:HE3	1.85	0.58
6:67:158:ASP:HB2	6:67:161:ALA:HB3	1.85	0.58
6:68:538:ASN:H	6:68:541:ASP:HB2	1.67	0.58
3:6M:219:ILE:HG13	3:6M:222:PRO:HD3	1.85	0.58
4:7B:380:ARG:HG3	4:7B:381:VAL:HG23	1.85	0.58
3:7M:298:PRO:HG3	3:7M:308:ARG:HD3	1.84	0.58
7:92:352:VAL:HG12	14:M2:242:ILE:HG22	1.85	0.58
7:95:412:MET:HG2	4:9L:174:LYS:HG3	1.85	0.58
4:9J:333:VAL:HA	4:9J:336:LYS:HG2	1.85	0.58
8:A3:271:VAL:HG12	8:A3:273:PRO:HD3	1.85	0.58
8:A5:193:PHE:HE1	8:A5:211:VAL:HG13	1.68	0.58
10:E9:66:LEU:HD21	10:E9:312:LYS:HE2	1.85	0.58
13:J6:339:ARG:HG3	13:J6:341:PRO:HD2	1.85	0.58
14:M7:82:TYR:HB2	14:M7:87:ARG:HH12	1.67	0.58
1:w:867:PRO:HB3	1:w:944:GLN:HB3	1.85	0.58
1:I:664:ILE:HG12	3:9A:282:TYR:CD1	2.39	0.58
1:O:666:VAL:HB	1:P:666:VAL:HG11	1.86	0.58
1:S:373:LEU:HD13	1:S:376:MET:HG3	1.85	0.58
4:1N:135:ILE:HG21	4:1N:152:ILE:HD11	1.85	0.58
5:27:80:GLU:HG3	5:27:82:THR:H	1.67	0.58
3:3C:204:LEU:HD23	3:3C:231:ILE:HD12	1.85	0.58
4:5B:54:ALA:HA	4:6B:283:ALA:HB2	1.85	0.58
3:6A:178:SER:HB3	3:6A:183:GLU:HG3	1.85	0.58
4:6B:226:ASN:HA	4:6B:229:VAL:HG22	1.86	0.58
4:6N:47:ILE:H	1:r:915:ARG:HH21	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:72:397:SER:HB2	14:K3:105:LEU:HD11	1.84	0.58
7:79:279:ARG:HE	10:E5:146:ALA:HA	1.67	0.58
3:8K:204:LEU:HD22	3:8K:302:MET:HG3	1.85	0.58
9:B5:74:ALA:HB3	11:C5:231:VAL:HG21	1.86	0.58
13:J1:396:GLN:HA	13:J1:448:ASP:HB2	1.85	0.58
13:J2:466:LEU:HD21	13:J2:496:LEU:HA	1.86	0.58
14:L6:104:TYR:HB3	14:L6:106:TYR:HE1	1.68	0.58
1:M:667:LYS:HB3	3:8G:58:ALA:CB	2.33	0.58
3:1E:30:ILE:HG22	3:1E:36:MET:HG2	1.86	0.58
5:26:148:LEU:HD13	5:26:158:LEU:HD13	1.86	0.58
5:28:109:LEU:HD12	5:28:112:GLN:HE22	1.69	0.58
3:2C:17:GLY:HA2	3:2C:20:CYS:HB3	1.86	0.58
3:3M:311:LYS:HD3	3:3M:344:VAL:HB	1.85	0.58
4:4B:49:VAL:HG11	4:4B:241:ARG:HB3	1.85	0.58
3:5I:3:GLU:HA	3:5I:51:THR:HA	1.84	0.58
5:62:158:LEU:HB2	5:62:174:LEU:HB2	1.86	0.58
3:7I:157:LEU:HB3	3:7I:166:LYS:HE2	1.85	0.58
4:7J:69:GLU:HB3	4:7J:96:GLY:HA2	1.86	0.58
7:89:347:ILE:HG22	7:89:349:SER:H	1.68	0.58
3:8G:274:PRO:HG3	3:8G:374:ALA:HA	1.83	0.58
8:A2:80:MET:HE2	9:B3:465:LEU:HD11	1.85	0.58
8:A2:241:LEU:HD12	8:A2:242:PRO:HD2	1.85	0.58
10:C9:338:PRO:HB2	10:C9:341:TYR:HB3	1.86	0.58
10:D6:86:LEU:HD23	10:D6:319:LEU:HB3	1.86	0.58
1:a:614:LEU:HD23	1:f:614:LEU:HA	1.86	0.58
1:I:631:LEU:CB	1:J:631:LEU:HD13	2.34	0.58
1:L:429:ARG:HH21	1:o:869:ARG:HH21	1.50	0.58
1:Q:580:GLU:HG2	1:U:579:LEU:HD22	1.86	0.58
3:1A:360:PRO:HG2	3:1A:371:VAL:HG23	1.85	0.58
4:1L:7:VAL:HG12	4:1L:64:ILE:HB	1.84	0.58
3:4G:109:THR:HG22	3:4G:110:ILE:H	1.69	0.58
4:5B:203:ASP:HB2	4:5B:301:CYS:HA	1.84	0.58
4:5F:180:VAL:HG22	3:5G:258:ASN:HD21	1.69	0.58
6:64:636:GLU:HA	6:64:639:LEU:HB2	1.84	0.58
6:66:497:ALA:O	6:66:498:ARG:C	2.47	0.58
6:67:822:ARG:HD3	6:67:828:GLU:HB3	1.84	0.58
6:68:500:ARG:HH11	6:68:503:LYS:CE	2.12	0.58
6:68:895:ARG:HH21	9:B6:536:GLU:HG3	1.68	0.58
4:7B:248:SER:HB3	4:7B:252:LYS:HG2	1.85	0.58
3:7G:318:MET:HB2	3:7G:376:CYS:HB3	1.85	0.58
4:7L:193:VAL:HG13	4:7L:418:LEU:HD13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8E:310:GLY:HA3	3:8E:383:ALA:HB2	1.85	0.58
3:8I:392:ASP:O	3:8I:396:ASP:HB2	2.04	0.58
9:B2:48:MET:HE2	9:B2:50:ASP:HB2	1.86	0.58
10:C7:317:LEU:HB3	10:C7:321:ARG:HH12	1.69	0.58
10:D9:354:ARG:HD3	10:D9:360:ALA:HA	1.84	0.58
14:K3:143:ARG:HG2	14:K3:144:PHE:HD2	1.68	0.58
1:a:677:MET:HA	1:f:677:MET:HE3	1.86	0.58
1:I:628:VAL:HG12	1:J:631:LEU:HD12	1.83	0.58
5:31:40:HIS:HB2	5:31:76:LEU:HB3	1.84	0.58
4:4D:163:ILE:HG21	4:4D:250:LEU:HB3	1.84	0.58
3:4I:271:SER:HB2	3:4I:377:MET:HB3	1.84	0.58
5:51:52:ILE:HB	5:51:67:ARG:HB3	1.84	0.58
3:5E:159:VAL:HG13	7:72:351:LYS:HB3	1.86	0.58
3:5M:250:VAL:HG12	3:5M:352:LYS:HE3	1.85	0.58
4:5N:113:ILE:HB	4:5N:150:LEU:HD13	1.84	0.58
4:7B:180:VAL:HG23	4:7B:183:TYR:HD2	1.69	0.58
3:7E:16:ILE:HD11	3:7E:138:PHE:HB3	1.85	0.58
4:7H:20:PHE:HA	4:7H:230:SER:HB2	1.86	0.58
4:8B:47:ILE:HG12	4:8B:51:TYR:HB2	1.86	0.58
7:93:408:ILE:HA	4:9D:174:LYS:HG2	1.85	0.58
7:94:342:SER:HA	14:M7:153:LEU:HD13	1.85	0.58
7:97:331:PRO:HB2	7:97:335:ARG:HH21	1.68	0.58
3:9E:171:SER:HA	3:9E:204:LEU:HB2	1.84	0.58
4:9H:166:THR:HB	4:9H:199:VAL:HA	1.86	0.58
4:9L:135:ILE:HG21	4:9L:152:ILE:HD11	1.86	0.58
10:C9:92:MET:HA	10:C9:95:GLU:HG2	1.86	0.58
14:K1:159:ASN:HD21	14:K1:222:THR:HG22	1.69	0.58
14:L6:148:ILE:HD11	14:L6:173:PRO:HG3	1.86	0.58
1:A:446:LEU:HD21	1:F:450:LEU:HD11	1.85	0.58
1:F:561:ARG:O	1:F:565:ASP:HB2	2.03	0.58
1:I:680:LEU:HD13	1:J:680:LEU:HB3	1.84	0.58
3:1I:217:LEU:HD12	3:1I:367:ASP:HB3	1.85	0.58
5:24:78:LEU:HD13	5:24:86:HIS:HB3	1.85	0.58
5:25:222:LEU:HD12	3:2I:402:ARG:HE	1.69	0.58
5:31:148:LEU:HB3	5:31:158:LEU:HD13	1.85	0.58
5:37:158:LEU:HB3	5:37:174:LEU:HB2	1.85	0.58
3:3C:81:GLY:H	3:3C:84:ARG:HG2	1.69	0.58
3:3E:70:LEU:HD12	3:3E:99:ALA:HB2	1.85	0.58
3:4C:324:VAL:HG12	3:4C:326:LYS:H	1.68	0.58
5:54:148:LEU:HD13	5:54:158:LEU:HD13	1.86	0.58
4:6N:137:HIS:HE1	4:6N:166:THR:HB	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7J:11:GLN:HG3	4:7J:72:THR:HG21	1.84	0.58
4:7J:205:GLU:HA	7:83:412:MET:HE3	1.85	0.58
3:7K:5:ILE:HD12	3:7K:125:LEU:HG	1.84	0.58
7:89:296:ARG:HB2	7:89:317:GLN:HA	1.84	0.58
7:90:301:LEU:HB3	7:90:305:ALA:HB3	1.86	0.58
7:97:340:ASN:HD22	10:F1:49:ARG:HH12	1.51	0.58
4:9B:309:ARG:H	4:9B:372:THR:HG22	1.69	0.58
3:9G:12:ALA:HB3	3:9G:140:ALA:HB2	1.85	0.58
4:9H:114:ASP:HA	4:9H:117:LEU:HD12	1.86	0.58
10:C9:88:LEU:HD11	10:C9:92:MET:HE3	1.84	0.58
13:J5:351:ARG:HD3	13:J5:352:LYS:HG3	1.84	0.58
14:L9:148:ILE:HD11	14:L9:173:PRO:HG2	1.85	0.58
14:M4:178:MET:HE2	14:M4:209:ASP:HA	1.85	0.58
14:M5:152:ARG:HH21	14:M5:216:GLY:H	1.51	0.58
1:a:562:ILE:HD13	1:f:562:ILE:CG1	2.33	0.58
1:Z:429:ARG:HA	1:d:429:ARG:HH12	1.68	0.58
1:Z:468:GLN:HA	1:Z:471:LEU:HD23	1.86	0.58
1:Z:487:HIS:HE1	1:c:665:THR:HG23	1.68	0.58
3:1A:189:LEU:HA	3:1A:192:HIS:CE1	2.39	0.58
4:1F:65:LEU:HB3	4:1F:73:MET:HE3	1.84	0.58
5:27:51:GLU:HB3	5:27:147:VAL:HG12	1.85	0.58
3:2A:241:SER:HA	3:2A:356:ASN:HD22	1.68	0.58
4:2D:200:GLN:HE22	4:2D:266:PHE:HD2	1.52	0.58
3:2E:27:GLU:HB2	3:2E:244:PHE:HZ	1.67	0.58
5:39:197:SER:HA	13:J3:494:GLU:HG3	1.86	0.58
3:3C:272:TYR:HB3	3:3C:275:ILE:HD11	1.86	0.58
4:3D:238:CYS:HB2	4:3D:318:ARG:HH11	1.67	0.58
3:3K:325:PRO:HA	3:3K:328:VAL:HB	1.85	0.58
3:4C:301:MET:HE1	3:4C:307:PRO:HB3	1.86	0.58
5:51:78:LEU:HD23	5:51:85:GLN:HB2	1.86	0.58
4:5B:66:MET:HE3	4:5B:147:MET:HE3	1.86	0.58
4:5J:132:GLY:HA2	4:5J:162:ARG:HB3	1.85	0.58
4:5N:87:PRO:HA	4:5N:90:PHE:HD2	1.68	0.58
6:67:896:LEU:HD22	9:B7:505:PRO:HA	1.86	0.58
4:6N:334:GLN:HE21	4:6N:349:MET:HE3	1.69	0.58
7:77:320:TRP:HE1	14:K6:128:ARG:HH21	1.50	0.58
4:7D:399:THR:HA	4:7D:403:MET:HB3	1.84	0.58
7:82:308:TYR:HA	7:82:324:ILE:HD11	1.86	0.58
7:86:311:SER:HB2	4:8D:380:ARG:HA	1.86	0.58
7:87:401:ILE:HG21	7:87:411:MET:HG2	1.86	0.58
3:8E:236:SER:O	3:8E:240:ALA:HB2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8H:103:LYS:HB3	4:8H:108:GLU:HB2	1.86	0.58
4:8J:65:LEU:HB3	4:8J:73:MET:HE1	1.85	0.58
4:9H:54:ALA:HB3	4:9H:58:ARG:HB3	1.85	0.58
12:I5:68:ARG:HA	12:I6:334:ARG:HG3	1.86	0.58
13:J5:325:LEU:HD13	13:J5:416:VAL:HG22	1.85	0.58
14:M1:200:PHE:HB2	14:M1:220:LEU:HB3	1.86	0.58
14:M3:239:GLU:HG2	14:M3:240:TRP:HD1	1.69	0.58
1:M:650:HIS:O	1:M:654:LEU:HG	2.04	0.58
1:Y:684:ARG:HH22	1:c:683:GLU:HB3	1.69	0.58
2:11:284:LEU:HD11	2:12:284:LEU:HB3	1.85	0.58
4:1B:311:LEU:H	4:1B:371:SER:HA	1.69	0.58
4:1D:202:ILE:HG12	4:1D:229:VAL:HG21	1.85	0.58
3:1E:288:VAL:HG21	3:1E:328:VAL:HG22	1.85	0.58
3:1G:269:LEU:HD11	3:1G:384:ILE:HD11	1.84	0.58
5:24:53:ARG:HB3	5:24:149:ILE:HA	1.84	0.58
5:35:158:LEU:HB3	5:35:174:LEU:HB2	1.86	0.58
3:3K:238:LEU:HD11	3:3K:378:ILE:HD11	1.85	0.58
5:58:218:PRO:HA	5:58:221:LEU:HD13	1.86	0.58
4:5L:213:ARG:HH12	6:69:792:TYR:HA	1.68	0.58
5:61:34:PRO:HG3	5:61:186:ARG:HB3	1.86	0.58
6:63:589:LEU:HD23	6:63:590:ARG:H	1.69	0.58
3:6I:16:ILE:HD11	3:6I:138:PHE:HB3	1.86	0.58
3:6K:119:LEU:HA	3:6K:122:ILE:HG22	1.84	0.58
4:6N:182:PRO:HB2	4:6N:385:PHE:HD1	1.69	0.58
4:7B:11:GLN:HA	4:7B:72:THR:HG21	1.86	0.58
4:7D:113:ILE:HA	4:7D:116:VAL:HG12	1.86	0.58
4:7L:58:ARG:HH22	4:7L:84:LEU:HA	1.69	0.58
3:7M:220:GLU:HG3	1:r:912:PRO:HA	1.86	0.58
7:82:334:LEU:HD11	7:82:347:ILE:HG13	1.86	0.58
7:86:280:PRO:HA	7:86:299:PHE:HA	1.86	0.58
7:87:323:PHE:HB2	7:87:394:TYR:HB2	1.86	0.58
3:8I:223:THR:HG23	3:8I:225:THR:H	1.68	0.58
3:8K:178:SER:HB2	3:8K:183:GLU:HG2	1.86	0.58
3:9I:271:SER:HB3	3:9I:377:MET:HB2	1.86	0.58
3:9K:288:VAL:HG21	3:9K:327:ASP:HB3	1.85	0.58
10:D2:349:PHE:HD1	10:D2:361:TRP:HB3	1.69	0.58
10:D8:338:PRO:HB2	10:D8:341:TYR:HB3	1.84	0.58
1:f:557:ASN:O	1:f:558:LEU:C	2.47	0.58
1:n:890:LEU:HD23	1:n:946:LEU:HG	1.85	0.58
3:1A:189:LEU:HD23	3:1A:192:HIS:HE1	1.68	0.57
4:1N:117:LEU:HA	4:1N:120:VAL:HG22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:26:48:VAL:HG11	5:26:134:LEU:HD12	1.86	0.57
4:2J:359:LYS:HB3	11:C3:271:LEU:HD11	1.86	0.57
4:3L:224:ASP:HB3	8:A8:257:PRO:HG3	1.85	0.57
3:3M:288:VAL:HA	3:3M:291:ILE:HG22	1.85	0.57
3:4C:368:LEU:HD23	3:4C:371:VAL:HG11	1.86	0.57
3:6I:406:HIS:HB2	14:L2:148:ILE:HD12	1.86	0.57
3:7K:180:ALA:HB3	3:7K:183:GLU:HG3	1.84	0.57
4:7L:58:ARG:HD2	4:8L:281:TYR:HB3	1.84	0.57
4:9B:16:ILE:HD11	4:9B:229:VAL:HB	1.85	0.57
3:9K:288:VAL:HG11	3:9K:323:VAL:HG13	1.85	0.57
12:G4:195:PRO:HA	12:G4:198:LYS:HG2	1.86	0.57
14:K8:154:MET:HE1	14:K8:181:LEU:HD21	1.85	0.57
1:p:936:ASP:O	1:p:940:HIS:HB2	2.04	0.57
1:v:875:ILE:HD11	1:v:945:ILE:HG23	1.86	0.57
1:I:624:GLN:HB3	1:J:624:GLN:CG	2.31	0.57
1:J:656:GLN:HA	1:J:659:LEU:HD22	1.86	0.57
1:Q:632:ARG:HB3	1:h:771:VAL:HG23	1.84	0.57
3:1E:5:ILE:HD11	3:1E:132:LEU:HD22	1.86	0.57
4:1F:10:GLY:HA2	4:1F:143:THR:HG23	1.84	0.57
3:3M:9:VAL:HG12	3:3M:146:GLY:HA2	1.86	0.57
5:49:189:THR:HG22	5:50:97:LEU:HD12	1.85	0.57
4:4D:164:MET:H	4:4D:197:ASP:HB2	1.67	0.57
5:51:51:GLU:HB3	5:51:147:VAL:HG13	1.85	0.57
5:52:180:THR:HG23	5:52:183:PHE:H	1.69	0.57
4:5B:135:ILE:O	4:5B:166:THR:HA	2.05	0.57
3:5M:7:ILE:HG22	3:5M:66:VAL:HG22	1.85	0.57
7:73:328:PRO:HB2	7:73:333:LEU:HG	1.86	0.57
4:7D:319:GLY:HA2	4:7D:357:PRO:HG3	1.86	0.57
3:7E:173:PRO:HG2	3:7E:391:MET:HE3	1.86	0.57
4:7L:329:GLN:HA	4:7L:332:ASN:HB3	1.87	0.57
7:89:308:TYR:CZ	7:89:322:PRO:HB2	2.39	0.57
3:8A:178:SER:HB3	3:8A:183:GLU:HG3	1.84	0.57
4:8L:222:TYR:HB3	1:m:803:ILE:HG22	1.86	0.57
4:9D:8:GLN:HE22	4:9D:65:LEU:HB2	1.68	0.57
4:9H:86:ARG:HH12	4:9H:88:ASP:HB3	1.69	0.57
9:B1:81:LEU:HD23	11:C1:267:LEU:HD21	1.86	0.57
9:B7:17:LEU:HD22	9:B7:491:ARG:HB2	1.85	0.57
10:C7:338:PRO:HB2	10:C7:341:TYR:HB3	1.86	0.57
10:E2:301:ARG:HH21	14:L0:142:GLN:HA	1.68	0.57
14:K4:99:ILE:HG13	14:K4:102:ARG:HH21	1.68	0.57
1:K:510:ASP:HA	1:L:513:ARG:HH22	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:586:LYS:HE3	1:c:587:GLU:HB2	1.87	0.57
3:1I:195:LEU:HD21	3:1I:428:LEU:HD22	1.85	0.57
3:1K:161:TYR:HB3	3:1K:164:LYS:HG3	1.86	0.57
4:2B:60:VAL:HG11	4:3B:281:TYR:HB2	1.87	0.57
5:37:185:ARG:HH22	5:38:97:LEU:HB2	1.67	0.57
4:3B:12:CYS:HA	17:3B:501:GDP:HN22	1.69	0.57
3:3C:273:ALA:HB3	3:3C:375:VAL:H	1.69	0.57
4:3H:289:LEU:HD23	4:3H:365:VAL:HG23	1.86	0.57
5:44:188:MET:HG2	5:44:191:ARG:HH21	1.69	0.57
3:5G:183:GLU:HA	3:5G:186:ASN:HD22	1.69	0.57
3:5I:174:SER:HB3	3:5I:207:GLU:HG3	1.86	0.57
4:7J:239:CYS:HB3	4:7J:247:ASN:HB2	1.85	0.57
3:7M:308:ARG:HH22	14:L4:246:GLN:HB3	1.69	0.57
3:8M:292:THR:HG21	3:8M:331:ALA:HB1	1.86	0.57
4:9H:292:GLN:HG2	4:9H:298:ASN:HD22	1.68	0.57
14:M7:79:THR:HG21	14:M7:94:GLY:HA2	1.85	0.57
1:y:904:ILE:HD12	1:y:928:LEU:HD22	1.86	0.57
1:I:643:ARG:HA	1:I:646:ASN:ND2	2.20	0.57
4:1H:91:VAL:HG11	4:1H:116:VAL:HG22	1.86	0.57
4:1N:279:GLN:HG2	4:1N:282:ARG:HH21	1.69	0.57
5:22:161:ILE:HD11	5:22:168:PHE:HB3	1.86	0.57
4:3D:163:ILE:HD11	4:3D:251:ARG:HG3	1.87	0.57
5:40:33:ASP:HB3	5:40:36:LEU:HB2	1.86	0.57
3:5A:121:ARG:HA	3:5A:124:LYS:HE3	1.87	0.57
3:5A:395:PHE:O	3:5A:399:TYR:HB3	2.05	0.57
3:5C:159:VAL:HG13	7:73:351:LYS:HD2	1.86	0.57
3:5M:137:MET:HE1	3:5M:139:ASN:HB3	1.87	0.57
6:63:838:ASN:HB2	6:63:961:LYS:HB3	1.86	0.57
4:6D:299:MET:HE3	4:6D:305:PRO:HG2	1.86	0.57
3:6I:140:ALA:HA	3:6I:171:SER:HB2	1.86	0.57
4:6J:248:SER:HA	4:6J:252:LYS:HD3	1.86	0.57
3:6M:137:MET:HB3	3:6M:168:ASN:HA	1.87	0.57
2:7:205:ILE:HG13	2:7:209:ARG:HH21	1.69	0.57
4:7F:256:ASN:HD22	4:7F:350:LYS:HD3	1.68	0.57
4:7H:152:ILE:HG22	4:7H:195:ASN:HB3	1.87	0.57
10:D6:338:PRO:HB2	10:D6:341:TYR:HB3	1.86	0.57
10:E6:46:ASP:HA	10:E6:49:ARG:HE	1.70	0.57
12:G4:221:MET:HA	12:G4:224:ARG:HE	1.69	0.57
12:G8:192:GLU:HG3	12:G8:194:ALA:H	1.68	0.57
13:J3:351:ARG:HD3	13:J3:352:LYS:HG3	1.85	0.57
13:J5:478:PRO:HG3	13:J5:507:SER:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:917:ARG:HG2	1:q:918:THR:HG23	1.87	0.57
1:C:387:ILE:HD11	1:G:388:ARG:HE	1.70	0.57
1:J:577:GLN:HE21	1:J:578:ARG:NE	2.01	0.57
1:K:506:VAL:O	1:K:510:ASP:HB2	2.03	0.57
1:N:607:LEU:O	1:N:611:THR:HG23	2.04	0.57
1:N:640:ALA:HA	1:N:643:ARG:HD2	1.85	0.57
4:2D:83:GLN:HE22	9:B3:53:SER:HA	1.69	0.57
5:49:144:PHE:HE1	5:49:171:LEU:HD21	1.70	0.57
5:57:33:ASP:HB3	5:57:36:LEU:HB2	1.85	0.57
3:5M:323:VAL:HG13	3:5M:355:ILE:HG23	1.87	0.57
6:63:503:LYS:O	6:63:506:GLU:O	2.22	0.57
3:6I:234:VAL:HG21	3:6I:302:MET:HE1	1.84	0.57
4:8F:2:ARG:HH11	4:8F:240:LEU:HD23	1.68	0.57
3:8I:79:ARG:HG3	3:8I:92:LEU:HD13	1.86	0.57
3:8K:6:SER:HA	3:8K:136:LEU:HB3	1.87	0.57
4:8L:279:GLN:HG2	4:8L:282:ARG:HE	1.68	0.57
7:94:346:TRP:HE1	7:94:351:LYS:HA	1.70	0.57
3:9G:203:MET:HE3	3:9G:387:VAL:HG11	1.86	0.57
4:9L:178:THR:HG22	3:9M:352:LYS:HZ2	1.69	0.57
10:E9:307:MET:HE1	10:E9:400:LEU:HD13	1.87	0.57
12:F0:223:LEU:O	12:F0:227:SER:HB3	2.04	0.57
1:c:561:ARG:O	1:c:562:ILE:C	2.48	0.57
1:C:323:MET:HG3	1:G:319:MET:HE1	1.86	0.57
4:1F:134:GLN:HA	4:1F:165:GLU:O	2.05	0.57
4:1F:179:VAL:HG22	3:1G:258:ASN:HD22	1.69	0.57
3:2K:248:LEU:HB2	3:2K:355:ILE:H	1.70	0.57
5:39:158:LEU:HB3	5:39:174:LEU:HB2	1.86	0.57
5:49:114:GLN:HG3	5:49:119:LEU:HB2	1.84	0.57
4:4B:205:GLU:HG3	3:4C:329:ASN:HD21	1.69	0.57
5:51:220:LEU:HD21	6:63:606:GLN:HG3	1.87	0.57
4:5F:293:MET:HE2	4:5F:365:VAL:HG11	1.85	0.57
4:5J:103:LYS:HA	4:5J:107:THR:HB	1.87	0.57
5:60:205:ARG:HG3	6:68:597:LEU:HD21	1.86	0.57
4:6D:374:ILE:HA	4:6D:377:MET:HG3	1.86	0.57
4:7B:41:ASP:HB3	1:q:944:GLN:HA	1.85	0.57
3:7G:238:LEU:HD12	3:7G:239:THR:HG23	1.87	0.57
7:84:401:ILE:HG12	7:84:411:MET:HE1	1.86	0.57
3:8K:119:LEU:HD13	3:8K:122:ILE:HD11	1.85	0.57
4:9B:207:LEU:HD13	4:9B:225:LEU:HB3	1.87	0.57
3:9I:259:LEU:HD22	3:9I:268:MET:HE2	1.86	0.57
14:L0:198:ARG:HH22	14:L0:206:VAL:HG22	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:879:VAL:HG22	1:v:880:THR:HG23	1.87	0.57
1:D:586:LYS:HD2	1:H:586:LYS:HD2	1.87	0.57
1:Y:588:THR:O	1:Y:592:ARG:HG3	2.05	0.57
4:1J:136:THR:HG22	4:1J:167:PHE:HB2	1.87	0.57
3:1M:265:ILE:HG12	3:1M:380:ASN:HD21	1.70	0.57
4:1N:8:GLN:O	4:1N:66:MET:HB3	2.03	0.57
1:2:879:VAL:HG13	1:2:880:THR:HG23	1.87	0.57
4:2J:293:MET:HE2	4:2J:365:VAL:HG21	1.85	0.57
5:45:197:SER:HB3	13:J6:494:GLU:HG3	1.86	0.57
3:4M:311:LYS:HE2	3:4M:344:VAL:HA	1.85	0.57
5:52:20:PHE:HB2	6:63:596:PRO:HB3	1.86	0.57
3:5I:265:ILE:HG22	3:5I:380:ASN:HD21	1.70	0.57
3:5M:392:ASP:HB3	3:5M:422:ARG:HH22	1.69	0.57
4:5N:7:VAL:HB	4:5N:135:ILE:HG22	1.86	0.57
6:69:498:ARG:HA	6:69:501:ARG:HE	1.70	0.57
3:6G:258:ASN:HD22	3:6G:352:LYS:HD3	1.68	0.57
7:78:279:ARG:HE	10:E4:146:ALA:HA	1.69	0.57
4:7D:407:GLU:HA	4:7D:410:GLU:HB3	1.87	0.57
4:9B:169:VAL:HG12	4:9B:202:ILE:HB	1.87	0.57
4:9H:135:ILE:HD11	4:9H:166:THR:HG23	1.87	0.57
4:9J:207:LEU:HB3	4:9J:225:LEU:HD12	1.86	0.57
3:9M:328:VAL:HG21	3:9M:355:ILE:HG12	1.87	0.57
8:A6:87:VAL:HG12	8:A6:93:VAL:HG22	1.86	0.57
9:B4:512:ARG:HB2	9:B4:520:GLU:HB3	1.87	0.57
11:C3:279:TYR:O	11:C3:283:PHE:HB2	2.04	0.57
1:z:890:LEU:HD22	1:z:942:ILE:HD12	1.87	0.57
1:A:674:ARG:HH21	1:F:673:LEU:HD11	1.69	0.57
2:12:159:LEU:HD22	10:C8:81:ALA:HB2	1.87	0.57
3:1A:11:GLN:HB3	3:1A:74:VAL:HG11	1.87	0.57
4:1F:55:THR:HG23	4:2F:283:ALA:HA	1.87	0.57
3:1M:252:VAL:HA	3:1M:255:PHE:HD2	1.70	0.57
2:3:176:GLU:HA	2:3:179:MET:HG2	1.86	0.57
5:35:119:LEU:HD22	5:38:166:TYR:HE2	1.70	0.57
4:3B:98:GLY:HA3	3:3C:254:GLU:HG2	1.86	0.57
4:3B:215:LEU:HD21	4:3B:228:LEU:HD21	1.87	0.57
3:3G:12:ALA:HB3	3:3G:140:ALA:HB2	1.86	0.57
4:4B:392:LYS:HB2	4:4B:395:LEU:HD22	1.87	0.57
3:4C:180:ALA:HB3	3:4C:183:GLU:HG3	1.87	0.57
3:4C:271:SER:HB3	3:4C:301:MET:HG3	1.85	0.57
3:5A:119:LEU:HD13	3:5A:122:ILE:HD11	1.87	0.57
3:5M:72:PRO:HB3	3:5M:94:SER:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:64:589:LEU:HD23	6:64:590:ARG:H	1.69	0.57
6:66:252:ARG:HE	6:66:445:LEU:HD22	1.70	0.57
7:80:372:TRP:HA	7:80:375:LEU:HD23	1.87	0.57
7:83:326:PRO:HA	7:83:391:TYR:HD2	1.69	0.57
3:8A:53:PHE:HB3	3:8A:61:HIS:HB3	1.87	0.57
4:9H:319:GLY:H	4:9H:355:ASP:HA	1.69	0.57
8:A4:119:SER:HB3	8:A4:122:GLN:HG2	1.87	0.57
12:F8:200:LEU:HA	12:F8:203:VAL:HG12	1.87	0.57
13:J7:392:VAL:HG22	13:J7:444:ALA:HB3	1.87	0.57
14:M7:156:LEU:HD13	14:M7:189:ILE:HD11	1.85	0.57
1:f:533:ARG:HB3	1:f:533:ARG:HH21	1.68	0.57
1:C:424:LEU:HD13	1:q:873:PRO:HB2	1.86	0.57
1:H:644:HIS:HA	1:H:647:LYS:HG3	1.86	0.57
1:J:425:ILE:O	1:J:429:ARG:HB2	2.04	0.57
3:1A:26:LEU:HD22	3:1A:364:PRO:HD2	1.85	0.57
5:20:78:LEU:HD12	5:20:86:HIS:HB3	1.87	0.57
5:39:91:LEU:HD11	5:39:158:LEU:HD22	1.87	0.57
3:3C:398:MET:HE2	4:3D:346:PRO:HD2	1.86	0.57
5:43:44:TYR:HB3	5:43:75:ILE:HG12	1.86	0.57
5:43:132:LYS:HG2	13:J1:337:ARG:HE	1.69	0.57
3:4A:6:SER:O	3:4A:65:CYS:HA	2.04	0.57
3:4A:211:ASP:HA	3:4A:214:ARG:HG3	1.87	0.57
3:4G:108:TYR:HA	3:4G:112:LYS:HE2	1.85	0.57
5:54:212:LEU:HD21	6:65:601:GLU:HB3	1.85	0.57
4:5J:318:ARG:HE	4:5J:358:PRO:HD3	1.70	0.57
4:6H:311:LEU:HD12	4:6H:342:VAL:HG11	1.86	0.57
4:6L:190:HIS:HD2	14:L3:133:VAL:HG11	1.68	0.57
3:7M:66:VAL:HA	3:7M:91:GLN:HB2	1.85	0.57
3:8I:2:ARG:HB3	3:8I:133:GLN:HB3	1.86	0.57
3:8K:192:HIS:HE1	3:8K:421:ALA:HA	1.69	0.57
4:8L:307:HIS:HA	7:91:317:GLN:HE22	1.70	0.57
3:9A:93:ILE:HD11	3:9A:121:ARG:HH12	1.70	0.57
10:D7:75:PRO:HG3	10:E4:135:ASN:HD22	1.70	0.57
10:E9:89:ALA:HA	10:E9:306:MET:HE3	1.85	0.57
12:G3:253:THR:HG21	12:G3:262:LEU:HG	1.87	0.57
13:J1:334:ARG:HG3	13:J1:337:ARG:HH12	1.68	0.57
14:L7:86:HIS:HA	14:L7:89:ARG:HG2	1.87	0.57
1:z:855:LYS:HD2	1:z:930:SER:HB2	1.86	0.57
1:J:589:THR:HB	1:J:592:ARG:HH11	1.70	0.57
1:Q:526:GLU:O	1:Q:530:LEU:HB2	2.04	0.57
2:12:222:GLU:HA	2:12:225:ARG:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1C:104:ALA:HB2	3:1C:413:MET:HE3	1.86	0.57
3:1M:2:ARG:HB2	3:1M:51:THR:HG22	1.87	0.57
4:2B:396:HIS:HB3	6:66:544:ILE:HG23	1.87	0.57
4:2D:131:GLN:HE22	4:2D:249:ASP:HB3	1.68	0.57
4:3B:327:ASP:HA	4:3B:330:MET:HE3	1.87	0.57
3:3C:273:ALA:HB1	3:3C:291:ILE:HB	1.87	0.57
4:3D:10:GLY:HA2	4:3D:143:THR:HG23	1.85	0.57
4:3D:139:LEU:HD13	4:3D:168:SER:HB3	1.87	0.57
4:3H:73:MET:HE3	4:3H:90:PHE:HD1	1.69	0.57
4:3H:237:THR:HG22	4:3H:250:LEU:HD21	1.87	0.57
4:5B:183:TYR:HD2	4:5B:398:TYR:HE2	1.52	0.57
4:5D:171:PRO:HG2	4:5D:185:ALA:HB2	1.87	0.57
3:5I:173:PRO:HG2	3:5I:391:MET:HE1	1.87	0.57
4:5N:238:CYS:O	4:5N:242:PHE:HB2	2.05	0.57
6:65:452:PHE:HE2	6:65:497:ALA:HB2	1.70	0.57
6:66:499:ARG:HG2	6:66:503:LYS:HD3	1.87	0.57
4:6D:149:THR:HA	4:6D:152:ILE:HD12	1.87	0.57
4:6H:238:CYS:HA	4:6H:241:ARG:HH21	1.70	0.57
3:6I:398:MET:HE2	4:6J:345:ILE:HG23	1.87	0.57
4:7D:130:LEU:HB2	4:7D:162:ARG:HE	1.70	0.57
3:7G:176:GLN:HB3	4:7H:331:LEU:HD11	1.86	0.57
3:7G:315:CYS:HB3	3:7G:377:MET:HE1	1.85	0.57
4:7J:318:ARG:HE	4:7J:358:PRO:HD3	1.69	0.57
4:8L:132:GLY:HA2	4:8L:162:ARG:HB3	1.86	0.57
7:94:334:LEU:HD11	7:94:347:ILE:HG23	1.87	0.57
3:9M:217:LEU:HD13	3:9M:275:ILE:HG22	1.87	0.57
1:M:481:LEU:HA	1:M:484:GLN:OE1	2.04	0.56
2:11:324:GLU:HG3	2:12:324:GLU:HA	1.86	0.56
5:21:148:LEU:HA	5:21:158:LEU:HA	1.86	0.56
5:27:162:GLN:HG2	5:27:164:MET:HE3	1.87	0.56
4:2F:47:ILE:HG22	4:2F:51:TYR:HB2	1.87	0.56
4:2F:164:MET:HB3	4:2F:197:ASP:H	1.70	0.56
3:2M:141:VAL:HG11	3:2M:172:TRP:CD1	2.32	0.56
5:39:158:LEU:HD23	5:39:174:LEU:HD22	1.86	0.56
4:3D:100:ASN:HD21	4:3D:397:TRP:HB3	1.69	0.56
3:3M:234:VAL:HG22	3:3M:272:TYR:HB2	1.87	0.56
4:4D:164:MET:HB3	4:4D:197:ASP:H	1.70	0.56
4:4F:201:VAL:HG11	4:4F:374:ILE:HD11	1.87	0.56
4:4J:397:TRP:HE1	3:4K:260:VAL:HG13	1.70	0.56
4:5H:68:LEU:HB3	4:5H:96:GLY:HA2	1.87	0.56
5:60:100:ASN:HD22	5:60:184:THR:HA	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:61:74:LYS:HB2	5:61:90:GLU:HB2	1.87	0.56
4:6N:235:GLY:HA2	4:6N:318:ARG:HD2	1.86	0.56
2:7:287:THR:HB	2:8:288:VAL:HG21	1.87	0.56
7:77:390:PRO:HD2	14:K6:118:CYS:HB3	1.86	0.56
3:7A:137:MET:HB2	3:7A:168:ASN:HA	1.87	0.56
4:7D:2:ARG:HB3	4:7D:131:GLN:HB2	1.85	0.56
3:7G:310:GLY:HA3	3:7G:383:ALA:HB2	1.87	0.56
4:7J:183:TYR:HB3	4:7J:398:TYR:HE2	1.70	0.56
7:86:408:ILE:HG13	7:86:412:MET:HE3	1.87	0.56
7:89:270:VAL:HG22	10:E8:155:MET:HE2	1.86	0.56
3:8K:405:VAL:HG23	3:8K:418:PHE:HE2	1.70	0.56
7:95:408:ILE:HG13	4:9L:174:LYS:HB3	1.87	0.56
4:9F:375:GLN:HE21	4:9F:419:VAL:HB	1.70	0.56
3:9K:5:ILE:HD12	3:9K:122:ILE:HD11	1.86	0.56
3:9M:229:ARG:HH21	3:9M:363:VAL:HB	1.70	0.56
9:B2:133:SER:HB3	9:B2:136:PHE:HB2	1.85	0.56
10:D5:354:ARG:HD3	10:D5:360:ALA:HA	1.87	0.56
10:D6:307:MET:HE1	10:D6:400:LEU:HD13	1.86	0.56
10:D9:62:VAL:HG22	10:D9:309:ILE:HD11	1.87	0.56
10:D9:297:ARG:O	10:D9:301:ARG:HB3	2.05	0.56
12:G4:241:LEU:HD21	12:G4:262:LEU:HB3	1.87	0.56
13:J5:474:ARG:HD3	13:J5:503:GLY:HA2	1.86	0.56
1:c:591:ARG:O	1:c:594:ALA:HB3	2.05	0.56
1:I:631:LEU:HB3	1:J:631:LEU:HD13	1.87	0.56
3:1C:167:LEU:HD13	3:1C:200:VAL:HG11	1.87	0.56
4:1D:396:HIS:HA	4:1D:399:THR:HG22	1.86	0.56
4:1L:101:TRP:HZ2	4:1L:191:GLN:HG3	1.70	0.56
5:21:140:GLU:HG3	5:21:143:CYS:HB3	1.86	0.56
5:21:222:LEU:HD22	3:2G:402:ARG:HG2	1.87	0.56
5:24:222:LEU:HA	5:24:225:GLN:HG2	1.86	0.56
4:2B:220:PRO:HD2	3:2C:326:LYS:HE2	1.87	0.56
4:2L:257:LEU:HD21	4:2L:314:SER:HB3	1.87	0.56
5:31:75:ILE:HG22	5:31:89:VAL:HG22	1.87	0.56
3:3A:138:PHE:HZ	3:3A:235:ILE:HD12	1.71	0.56
4:3F:11:GLN:HG3	4:3F:72:THR:HG21	1.87	0.56
3:3M:9:VAL:HG22	3:3M:68:LEU:HB2	1.86	0.56
5:59:90:GLU:HA	5:59:101:TYR:O	2.05	0.56
3:5G:259:LEU:HD11	3:5G:316:CYS:HB2	1.86	0.56
6:66:820:TRP:HD1	6:66:823:HIS:HE1	1.52	0.56
3:6E:259:LEU:HD21	3:6E:316:CYS:HB2	1.87	0.56
4:7B:190:HIS:HB2	4:7B:414:ASN:HD21	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8A:175:PRO:HB3	3:8A:390:ARG:HD2	1.86	0.56
3:9E:115:VAL:HG21	3:9E:152:LEU:HD22	1.85	0.56
8:A3:47:LYS:HD2	8:A3:53:VAL:HG21	1.86	0.56
12:G2:233:ARG:HH21	12:G2:237:LEU:HD11	1.69	0.56
1:c:589:THR:O	1:c:592:ARG:HB3	2.05	0.56
1:Q:392:GLU:HA	1:Q:395:THR:HG22	1.88	0.56
1:Y:589:THR:HA	1:Y:592:ARG:HD3	1.87	0.56
1:Z:513:ARG:HH21	1:d:512:LYS:HZ2	1.54	0.56
3:1K:324:VAL:HG12	3:1K:326:LYS:H	1.70	0.56
4:1N:215:LEU:HD21	4:1N:228:LEU:HD11	1.87	0.56
5:20:206:LEU:HD12	5:25:21:LEU:HB3	1.86	0.56
5:23:89:VAL:HB	5:23:103:HIS:HB3	1.86	0.56
3:2I:320:ARG:HA	3:2I:356:ASN:O	2.06	0.56
4:2J:112:LEU:HD23	4:2J:147:MET:HE1	1.87	0.56
2:3:324:GLU:HG3	2:4:324:GLU:HA	1.87	0.56
3:3A:96:LYS:HD2	4:3B:129:CYS:HB2	1.86	0.56
4:3B:32:PRO:HA	4:3B:81:PHE:HD1	1.70	0.56
4:3B:390:ARG:HG3	4:3B:391:ARG:HG3	1.86	0.56
3:3E:7:ILE:HD13	3:3E:153:LEU:HD21	1.88	0.56
3:5C:3:GLU:HA	3:5C:51:THR:HA	1.87	0.56
4:5F:319:GLY:HA2	4:5F:357:PRO:HG3	1.87	0.56
6:69:452:PHE:CZ	6:69:493:ARG:HB3	2.40	0.56
3:6C:226:ASN:HA	3:6C:229:ARG:HG3	1.87	0.56
4:6F:329:GLN:HA	4:6F:332:ASN:HB2	1.87	0.56
4:6J:171:PRO:HG2	4:6J:185:ALA:HB2	1.87	0.56
7:75:350:ARG:HG2	7:75:379:LEU:HD21	1.85	0.56
3:7E:259:LEU:HD21	3:7E:316:CYS:HB2	1.86	0.56
3:7I:72:PRO:O	3:7I:76:ASP:HB2	2.04	0.56
4:7L:193:VAL:HG22	4:7L:418:LEU:HD22	1.88	0.56
3:7M:75:VAL:HG21	3:7M:94:SER:HA	1.87	0.56
3:7M:332:VAL:O	3:7M:336:LYS:CB	2.54	0.56
3:8A:73:THR:HG23	3:8A:74:VAL:HG23	1.87	0.56
4:8B:149:THR:HA	4:8B:152:ILE:HG12	1.88	0.56
4:8B:326:VAL:O	4:8B:330:MET:HB2	2.05	0.56
3:8C:194:LEU:HD21	3:8C:203:MET:HE1	1.87	0.56
4:8H:66:MET:HE2	4:8H:116:VAL:HG11	1.86	0.56
3:8I:250:VAL:HG23	3:8I:254:GLU:HG3	1.88	0.56
3:8K:204:LEU:HD21	3:8K:270:SER:HB3	1.87	0.56
4:8L:169:VAL:HA	4:8L:202:ILE:HB	1.86	0.56
7:95:280:PRO:HG3	14:M7:129:PRO:HG3	1.87	0.56
7:96:323:PHE:HB2	7:96:394:TYR:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9E:55:GLU:HG3	3:9E:57:GLY:H	1.71	0.56
4:9F:188:SER:HA	4:9F:191:GLN:HG2	1.87	0.56
8:A3:58:THR:HB	8:A3:61:ARG:HG3	1.87	0.56
9:B5:514:VAL:O	9:B5:518:CYS:HB2	2.05	0.56
10:D0:66:LEU:HD22	10:D0:312:LYS:HE3	1.87	0.56
10:D4:354:ARG:HD3	10:D4:360:ALA:HA	1.87	0.56
10:E0:136:PRO:HB3	10:E4:315:LEU:HD23	1.87	0.56
10:E1:305:LEU:HD21	14:L9:142:GLN:HB3	1.86	0.56
1:c:678:ASN:O	1:c:679:ARG:C	2.48	0.56
1:s:869:ARG:HG3	1:s:870:GLY:H	1.70	0.56
4:1D:246:LEU:HB2	4:1D:353:VAL:H	1.70	0.56
4:1J:257:LEU:HD21	4:1J:314:SER:HB3	1.87	0.56
1:2:899:THR:HG22	1:2:902:ARG:HH22	1.70	0.56
4:2B:362:LYS:HD2	4:2B:363:MET:HG3	1.88	0.56
3:3G:71:GLU:HB3	3:3G:98:ASP:HB3	1.87	0.56
3:3K:195:LEU:HA	3:3K:266:HIS:HE1	1.69	0.56
5:47:156:ALA:HB3	5:47:176:CYS:HB2	1.87	0.56
4:4F:330:MET:HB3	4:4F:349:MET:HG3	1.87	0.56
4:4H:320:ARG:HH21	8:A5:171:SER:HA	1.71	0.56
4:5D:6:HIS:HD2	4:5D:21:TRP:HE1	1.52	0.56
4:5N:156:ARG:HH21	4:5N:164:MET:HG2	1.69	0.56
6:67:486:PRO:HA	6:67:489:LEU:HG	1.88	0.56
6:67:558:LYS:HD3	6:67:561:LEU:HB2	1.87	0.56
3:7E:348:PRO:HB3	14:K0:111:LEU:HD23	1.88	0.56
3:7G:241:SER:HB3	3:7G:249:ASN:HB2	1.87	0.56
7:84:270:VAL:HG13	10:E2:155:MET:HE3	1.87	0.56
10:D0:107:ILE:HD13	10:D0:340:LEU:HD11	1.86	0.56
10:F1:70:ARG:HH12	14:M4:135:THR:HG21	1.70	0.56
14:M1:218:LYS:HE3	14:M1:236:PHE:HB3	1.86	0.56
1:i:801:THR:HG23	1:i:803:ILE:H	1.71	0.56
1:n:869:ARG:HG3	1:n:870:GLY:H	1.71	0.56
1:I:635:ASN:HD22	1:J:638:LEU:HD11	1.70	0.56
2:10:324:GLU:HA	2:9:324:GLU:HG3	1.87	0.56
3:1A:260:VAL:HG23	3:1A:265:ILE:HB	1.87	0.56
4:1D:244:GLY:HA3	4:1D:354:CYS:HA	1.88	0.56
4:1H:164:MET:HB3	4:1H:197:ASP:H	1.69	0.56
4:1H:200:GLN:HB3	4:1H:268:ILE:HD11	1.86	0.56
4:2B:8:GLN:HE21	4:2B:65:LEU:HG	1.70	0.56
4:2J:163:ILE:HD11	4:2J:251:ARG:HD3	1.87	0.56
4:3D:248:SER:HA	4:3D:252:LYS:HD3	1.87	0.56
3:3E:272:TYR:HB3	3:3E:275:ILE:HD11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3J:228:LEU:HG	4:3J:300:MET:HE2	1.87	0.56
4:3L:107:THR:HG22	4:3L:108:GLU:H	1.70	0.56
4:3L:149:THR:HA	4:3L:152:ILE:HD12	1.88	0.56
5:43:19:ASN:HD21	5:44:221:LEU:HD11	1.71	0.56
5:51:114:GLN:HA	5:51:119:LEU:HG	1.86	0.56
4:5H:322:SER:HB3	4:5H:325:GLU:HG2	1.87	0.56
4:5L:12:CYS:HA	17:5L:501:GDP:HN22	1.70	0.56
4:5L:313:ALA:HA	4:5L:369:GLY:HA2	1.88	0.56
6:66:974:GLU:HA	6:66:977:VAL:HG12	1.88	0.56
3:8C:288:VAL:HG13	3:8C:319:TYR:HE2	1.71	0.56
4:8J:318:ARG:HB3	4:8J:354:CYS:HB2	1.86	0.56
3:8K:422:ARG:HH22	10:F2:36:PHE:HB2	1.70	0.56
3:9I:203:MET:HE1	3:9I:267:PHE:HB3	1.88	0.56
4:9J:316:MET:HG2	4:9J:352:SER:HB3	1.87	0.56
8:A2:153:TYR:HB2	8:A2:156:GLU:HG3	1.88	0.56
13:J1:392:VAL:HG22	13:J1:444:ALA:HB3	1.86	0.56
1:y:879:VAL:HG22	1:y:880:THR:HG23	1.86	0.56
1:H:615:ARG:HD2	3:8M:372:MET:HE2	1.86	0.56
1:Y:586:LYS:CE	1:c:587:GLU:HB2	2.36	0.56
3:1A:395:PHE:HZ	3:1A:418:PHE:HB3	1.70	0.56
3:1G:240:ALA:HB1	3:1G:356:ASN:HD22	1.70	0.56
4:2H:12:CYS:HA	17:2H:501:GDP:HN22	1.70	0.56
3:4M:280:LYS:HB2	3:4M:369:ALA:HB1	1.88	0.56
3:4M:377:MET:HE3	3:4M:379:SER:HB3	1.86	0.56
5:50:74:LYS:HB2	5:50:90:GLU:HB3	1.88	0.56
5:53:129:VAL:HA	5:53:132:LYS:HG2	1.88	0.56
3:5C:332:VAL:HG13	3:5C:351:PHE:HD2	1.71	0.56
3:5K:251:ASP:H	3:5K:254:GLU:HB2	1.69	0.56
3:6A:26:LEU:HD22	3:6A:364:PRO:HD3	1.87	0.56
4:6H:117:LEU:HA	4:6H:120:VAL:HG12	1.88	0.56
4:7B:87:PRO:HA	4:7B:90:PHE:HB2	1.88	0.56
3:7K:111:GLY:HA3	3:7K:149:LEU:HD21	1.88	0.56
4:7L:2:ARG:HB2	4:7L:131:GLN:HB2	1.86	0.56
3:8I:7:ILE:HG22	3:8I:66:VAL:HB	1.87	0.56
4:8J:379:LYS:HB3	4:8J:419:VAL:HG11	1.88	0.56
4:9D:257:LEU:HD12	4:9D:312:THR:HG23	1.87	0.56
4:9J:47:ILE:HG12	4:9J:51:TYR:HB2	1.86	0.56
10:D1:331:ILE:HG23	10:D1:335:LEU:HD12	1.86	0.56
12:G3:279:ARG:HH12	12:G3:288:ILE:HB	1.70	0.56
13:J2:341:PRO:HG3	13:J2:362:ALA:HB3	1.86	0.56
1:Y:572:ARG:CB	1:c:572:ARG:HB3	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1K:276:ILE:HA	3:1K:280:LYS:HD2	1.87	0.56
4:1N:271:ALA:HB3	4:1N:365:VAL:H	1.71	0.56
5:21:179:SER:HA	6:63:366:GLN:HG2	1.88	0.56
5:26:149:ILE:HD11	5:26:157:ARG:HD2	1.88	0.56
4:2H:163:ILE:HD11	4:2H:251:ARG:HG3	1.86	0.56
4:3B:21:TRP:CZ3	4:3B:61:PRO:HA	2.41	0.56
4:3B:217:LEU:HD11	8:A2:255:ARG:HH21	1.71	0.56
3:3K:223:THR:HA	4:3L:323:THR:HG22	1.88	0.56
4:4B:286:VAL:HG11	4:4B:326:VAL:HG22	1.87	0.56
4:5D:267:LEU:HD13	4:5D:299:MET:HE1	1.86	0.56
4:5D:282:ARG:HH22	4:5D:292:GLN:HB2	1.70	0.56
2:6:273:GLU:HA	2:6:276:GLU:HG2	1.87	0.56
6:65:589:LEU:HD23	6:65:590:ARG:H	1.71	0.56
3:6C:119:LEU:HD23	3:6C:122:ILE:HD11	1.86	0.56
7:71:376:GLU:O	7:71:380:TRP:CB	2.53	0.56
7:73:350:ARG:HG3	7:73:388:GLU:HB3	1.88	0.56
3:8G:238:LEU:HD13	3:8G:318:MET:HE3	1.86	0.56
4:9B:329:GLN:HA	4:9B:332:ASN:HB2	1.88	0.56
8:A7:100:LEU:HD22	8:A7:103:ARG:HH21	1.69	0.56
8:A9:281:LEU:HB3	8:A9:285:LEU:HD21	1.88	0.56
10:E5:61:ASP:HA	14:L7:142:GLN:HE22	1.69	0.56
1:a:613:GLN:O	1:a:617:MET:HG2	2.05	0.56
1:c:578:ARG:HE	1:c:582:LEU:HD13	1.69	0.56
1:y:858:ALA:HB1	1:y:937:GLY:HA3	1.88	0.56
1:S:446:LEU:HD22	1:W:450:LEU:HD11	1.87	0.56
4:1B:108:GLU:CD	4:1B:109:GLY:H	2.14	0.56
3:2A:167:LEU:HA	3:2A:200:VAL:O	2.06	0.56
3:2M:416:GLY:O	3:2M:420:GLU:HB2	2.06	0.56
4:3F:49:VAL:HG11	4:3F:241:ARG:HG2	1.86	0.56
4:4D:73:MET:HE3	4:4D:92:PHE:HB3	1.88	0.56
4:4D:301:CYS:HB2	4:4D:377:MET:HE1	1.86	0.56
4:4J:65:LEU:HD22	4:4J:90:PHE:HE1	1.71	0.56
5:52:212:LEU:HD11	6:63:601:GLU:HB3	1.88	0.56
4:5B:238:CYS:HA	4:5B:241:ARG:HB2	1.88	0.56
3:5E:262:TYR:HD2	3:5E:265:ILE:HD11	1.69	0.56
4:6B:154:LYS:HD3	7:80:286:TRP:HE1	1.71	0.56
3:6E:212:ILE:HD11	3:6E:300:SER:HA	1.87	0.56
7:71:281:LEU:HD11	7:71:300:GLN:HB3	1.86	0.56
4:7D:38:GLY:HA3	4:7D:43:GLN:HE22	1.70	0.56
4:8H:260:PHE:HB2	4:8H:263:LEU:HD23	1.87	0.56
3:8K:274:PRO:HG3	3:8K:374:ALA:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8L:198:GLU:HG3	4:8L:200:GLN:HE22	1.70	0.56
4:8L:314:SER:HA	4:8L:350:LYS:HB2	1.87	0.56
3:9A:178:SER:HB3	3:9A:183:GLU:HG3	1.88	0.56
4:9F:98:GLY:H	4:9F:103:LYS:HD2	1.71	0.56
10:E0:354:ARG:HE	10:E0:360:ALA:HA	1.70	0.56
10:E4:68:THR:HA	10:E4:71:GLN:HB3	1.88	0.56
14:L8:148:ILE:HD11	14:L8:173:PRO:HG2	1.87	0.56
14:M2:155:TRP:HB2	14:M2:218:LYS:HA	1.86	0.56
1:c:598:ALA:O	1:c:601:ARG:HB3	2.05	0.56
1:c:607:LEU:O	1:c:611:THR:HG23	2.05	0.56
1:f:555:GLY:O	1:f:556:ARG:C	2.49	0.56
1:C:384:LEU:O	1:C:388:ARG:HB2	2.06	0.56
1:M:586:LYS:HE3	1:N:587:GLU:HB3	1.88	0.56
3:1G:3:GLU:HA	3:1G:51:THR:HA	1.86	0.56
3:2I:160:ASP:HA	6:63:558:LYS:HD3	1.87	0.56
4:2J:8:GLN:HB3	4:2J:65:LEU:HA	1.88	0.56
3:3E:264:ARG:HG2	3:3E:428:LEU:HD13	1.88	0.56
3:3K:103:PHE:H	3:3K:408:TYR:HE1	1.53	0.56
5:43:33:ASP:HB3	5:43:36:LEU:HB2	1.86	0.56
3:5I:189:LEU:HD13	3:5I:413:MET:HE1	1.87	0.56
3:5I:335:ILE:HG23	3:5I:341:ILE:HD13	1.88	0.56
4:6F:101:TRP:HE3	4:6F:403:MET:HE1	1.69	0.56
3:6I:58:ALA:CB	1:a:667:LYS:HB3	2.36	0.56
3:6M:324:VAL:HG12	3:6M:326:LYS:H	1.71	0.56
3:7E:212:ILE:O	3:7E:216:ASN:HB2	2.06	0.56
4:7J:358:PRO:HG2	4:7J:361:LEU:HB2	1.88	0.56
3:8I:54:SER:HB3	3:8I:64:ARG:HE	1.71	0.56
3:8K:222:PRO:HD2	4:8L:324:LYS:HZ1	1.70	0.56
8:A2:87:VAL:HG11	1:z:896:LEU:HD11	1.87	0.56
10:D7:338:PRO:HB2	10:D7:341:TYR:HB3	1.86	0.56
10:D7:354:ARG:HD3	10:D7:360:ALA:HA	1.88	0.56
12:F8:230:VAL:HG23	12:F8:232:ASP:H	1.71	0.56
1:D:674:ARG:HE	1:H:673:LEU:HD11	1.71	0.56
1:I:631:LEU:HB3	1:J:631:LEU:HD22	1.88	0.56
1:I:661:ASN:HA	1:I:664:ILE:HG13	1.88	0.56
1:M:534:GLN:HG2	1:N:534:GLN:HB3	1.88	0.56
1:M:638:LEU:HD22	1:N:638:LEU:HB3	1.86	0.56
1:V:517:GLU:HG2	1:V:518:ARG:HE	1.71	0.56
1:X:678:ASN:HD22	1:Y:395:THR:HG21	1.71	0.56
1:Y:607:LEU:HB3	1:c:607:LEU:HB3	1.85	0.56
4:1J:49:VAL:HG21	4:1J:241:ARG:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2B:20:PHE:HA	4:2B:230:SER:HB2	1.88	0.56
4:2L:83:GLN:HE22	6:68:880:PHE:HE2	1.53	0.56
4:3F:187:LEU:HD13	4:3F:403:MET:HE1	1.88	0.56
4:3L:384:GLN:HG2	3:3M:348:PRO:HG2	1.87	0.56
4:4F:268:ILE:HA	4:4F:367:PHE:O	2.05	0.56
3:4M:320:ARG:HG2	3:4M:356:ASN:HB3	1.87	0.56
5:57:55:GLN:HB2	5:57:151:HIS:HA	1.87	0.56
3:5I:286:LEU:HD13	3:5I:371:VAL:HG13	1.88	0.56
4:5J:293:MET:HG3	4:5J:367:PHE:HB2	1.88	0.56
3:5M:319:TYR:HB3	3:5M:323:VAL:HG11	1.88	0.56
6:63:619:ALA:O	6:63:623:CYS:HB2	2.06	0.56
6:64:913:TYR:HE1	8:A1:86:GLN:HB3	1.70	0.56
3:6A:372:MET:HB2	3:6A:373:ARG:HH11	1.70	0.56
4:7F:7:VAL:HB	4:7F:135:ILE:HG13	1.87	0.56
7:84:309:THR:HG22	7:84:311:SER:H	1.69	0.56
3:8I:136:LEU:HA	3:8I:167:LEU:O	2.05	0.56
4:9F:136:THR:HG22	4:9F:167:PHE:HB2	1.88	0.56
10:D2:390:MET:HA	10:D2:393:VAL:HG22	1.87	0.56
14:M3:156:LEU:HD21	14:M3:185:ILE:HG23	1.87	0.56
1:D:682:LYS:HD3	1:j:795:LEU:HD13	1.88	0.55
1:R:571:GLU:HG2	1:R:572:ARG:HD2	1.86	0.55
1:Y:614:LEU:HD23	1:c:614:LEU:HA	1.87	0.55
2:11:317:MET:HG2	2:12:320:GLN:HB2	1.88	0.55
2:14:314:TYR:HA	2:14:317:MET:HE2	1.88	0.55
3:1A:68:LEU:HD22	3:1A:149:LEU:HD21	1.88	0.55
3:2A:75:VAL:HG13	3:2A:92:LEU:HD12	1.88	0.55
4:2F:16:ILE:HD11	4:2F:136:THR:HB	1.87	0.55
4:2J:309:ARG:H	4:2J:372:THR:HG22	1.70	0.55
3:3M:370:LYS:HG2	9:B6:30:ARG:HA	1.87	0.55
3:4A:102:ASN:HB3	3:4A:105:ARG:HB2	1.88	0.55
4:4H:109:GLY:HA2	4:4H:147:MET:HE2	1.88	0.55
3:4M:5:ILE:HD11	3:4M:125:LEU:HD23	1.87	0.55
5:53:77:ILE:HD11	5:53:84:PRO:HB3	1.88	0.55
3:5E:259:LEU:HD21	3:5E:316:CYS:HB2	1.88	0.55
7:76:307:LYS:HE3	7:76:321:GLU:HG3	1.87	0.55
8:A6:216:MET:HG2	8:A6:223:LEU:HB3	1.88	0.55
13:J6:478:PRO:HG3	13:J6:507:SER:HB2	1.88	0.55
1:a:526:GLU:CD	1:f:527:LEU:HB2	2.31	0.55
1:a:572:ARG:HE	1:f:572:ARG:HG3	1.72	0.55
1:p:869:ARG:HB3	1:p:896:LEU:HD11	1.88	0.55
1:U:580:GLU:HB3	1:d:473:ARG:HH12	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:355:ARG:HG2	1:Y:359:ARG:HH21	1.70	0.55
3:1K:298:PRO:HB3	3:1K:307:PRO:HD2	1.89	0.55
5:21:91:LEU:HD21	5:21:148:LEU:HD22	1.87	0.55
5:28:95:ASN:HD22	12:G1:268:ARG:HH21	1.54	0.55
3:4E:9:VAL:HG22	3:4E:68:LEU:HB2	1.88	0.55
4:4L:86:ARG:HH22	4:4L:122:LYS:HZ3	1.54	0.55
5:60:20:PHE:HB2	5:60:205:ARG:HH21	1.71	0.55
6:66:414:VAL:HG13	6:66:435:VAL:HG12	1.87	0.55
3:6C:3:GLU:HG3	3:6C:64:ARG:HH11	1.71	0.55
4:6J:200:GLN:HE22	4:6J:266:PHE:HD2	1.53	0.55
4:6J:245:GLN:HE21	4:6J:353:VAL:HG11	1.71	0.55
4:7H:290:THR:HA	4:7H:293:MET:HE3	1.88	0.55
7:83:282:ARG:HH21	7:83:287:LEU:HB2	1.70	0.55
3:9E:265:ILE:HG22	3:9E:313:MET:HE1	1.89	0.55
10:D9:96:LEU:HD12	10:D9:306:MET:HE1	1.88	0.55
12:F7:273:PRO:HD2	12:F7:276:LEU:HD12	1.89	0.55
13:J6:319:ALA:HA	13:J6:322:LYS:HE3	1.88	0.55
14:K1:97:ARG:HG3	14:K1:123:SER:HB3	1.88	0.55
1:m:790:LEU:HD12	1:m:795:LEU:HB2	1.89	0.55
4:2L:388:MET:HE3	4:2L:394:PHE:HD2	1.71	0.55
5:35:216:LYS:HE3	5:36:220:LEU:HB2	1.88	0.55
4:4H:136:THR:HG22	4:4H:167:PHE:HB2	1.87	0.55
3:4M:70:LEU:HG	3:4M:149:LEU:HD11	1.87	0.55
5:50:158:LEU:HB2	5:50:174:LEU:H	1.72	0.55
5:55:161:ILE:HG22	5:55:168:PHE:HB3	1.89	0.55
5:58:212:LEU:HD21	6:66:601:GLU:HB3	1.88	0.55
4:5J:396:HIS:HA	4:5J:399:THR:HG22	1.89	0.55
5:62:145:LEU:HB2	5:62:161:ILE:HB	1.88	0.55
4:6H:3:GLU:HA	4:6H:49:VAL:HA	1.87	0.55
4:6H:289:LEU:HD13	4:6H:363:MET:HG3	1.87	0.55
3:8E:140:ALA:HA	3:8E:171:SER:HB2	1.88	0.55
3:8I:6:SER:O	3:8I:65:CYS:HA	2.06	0.55
7:94:411:MET:HE2	4:9J:174:LYS:HA	1.87	0.55
7:96:398:LYS:HB3	7:96:415:GLY:HA3	1.86	0.55
3:9E:232:ALA:HA	3:9E:235:ILE:HG12	1.87	0.55
4:9H:149:THR:HB	4:9H:191:GLN:HE21	1.70	0.55
10:C9:305:LEU:HD11	14:K4:142:GLN:HB3	1.86	0.55
12:F9:216:TRP:HZ2	12:F9:228:ILE:HD11	1.71	0.55
12:H8:94:LEU:HD13	12:H9:94:LEU:HD23	1.88	0.55
13:J1:478:PRO:HG3	13:J1:507:SER:HB2	1.87	0.55
1:d:468:GLN:HA	1:d:471:LEU:HD23	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:610:VAL:HG11	1:N:611:THR:HA	1.88	0.55
1:U:336:ALA:HB1	1:U:340:ARG:HH21	1.71	0.55
1:U:426:GLU:HA	1:U:429:ARG:HD2	1.87	0.55
3:1I:261:PRO:HG2	3:1I:313:MET:HE2	1.89	0.55
3:2C:176:GLN:HB3	4:2D:331:LEU:HD11	1.88	0.55
5:37:36:LEU:HD21	5:37:42:LEU:HB2	1.87	0.55
3:3M:169:PHE:HZ	3:3M:238:LEU:HD13	1.70	0.55
3:4A:70:LEU:HD11	3:4A:111:GLY:HA2	1.89	0.55
4:4B:248:SER:HA	4:4B:252:LYS:HD3	1.88	0.55
5:50:55:GLN:HG2	5:50:151:HIS:HA	1.88	0.55
3:5M:105:ARG:HH21	3:5M:110:ILE:HG13	1.71	0.55
3:5M:392:ASP:HA	3:5M:422:ARG:HH12	1.71	0.55
5:60:53:ARG:HG3	5:60:149:ILE:HG23	1.88	0.55
6:63:537:GLU:HG3	12:G0:62:LEU:HD21	1.88	0.55
4:6J:252:LYS:HG2	4:6J:350:LYS:HE3	1.88	0.55
3:7A:274:PRO:HG3	3:7A:286:LEU:HD22	1.88	0.55
3:7E:271:SER:HB2	3:7E:377:MET:HB3	1.87	0.55
7:82:279:ARG:HE	10:D0:146:ALA:HA	1.71	0.55
3:8E:207:GLU:HG2	14:L6:253:PHE:HD1	1.69	0.55
4:8F:37:CYS:HA	1:l:760:ARG:HD2	1.87	0.55
4:8L:130:LEU:HD12	4:8L:162:ARG:HG2	1.88	0.55
3:9M:248:LEU:HB2	3:9M:355:ILE:H	1.71	0.55
3:9M:298:PRO:HB3	3:9M:307:PRO:HD2	1.87	0.55
10:D0:97:ILE:HD13	10:D0:303:LEU:HD11	1.88	0.55
14:K4:100:ALA:HA	14:K4:105:LEU:HD13	1.88	0.55
1:D:614:LEU:HD11	1:H:610:VAL:HG13	1.87	0.55
1:N:584:GLU:O	1:N:587:GLU:HG3	2.06	0.55
4:1B:20:PHE:HA	4:1B:230:SER:HB2	1.87	0.55
3:1E:316:CYS:HB2	3:1E:377:MET:HA	1.88	0.55
5:20:46:ARG:HG2	5:20:47:GLU:H	1.72	0.55
5:23:184:THR:O	5:23:188:MET:HG3	2.07	0.55
4:2B:324:LYS:HA	4:2B:327:ASP:OD2	2.07	0.55
4:2D:69:GLU:HB3	4:2D:96:GLY:HA2	1.87	0.55
3:2E:272:TYR:HB3	3:2E:275:ILE:HD11	1.89	0.55
3:2I:53:PHE:HB3	3:2I:61:HIS:HB3	1.88	0.55
3:2M:385:ALA:HA	3:2M:388:PHE:HD2	1.72	0.55
4:3B:101:TRP:HD1	4:3B:145:SER:HB3	1.72	0.55
5:49:65:VAL:HG22	5:49:67:ARG:HB2	1.88	0.55
5:54:162:GLN:HB2	5:54:171:LEU:HD23	1.89	0.55
5:58:209:ILE:HD11	6:66:600:LEU:HD22	1.88	0.55
5:59:34:PRO:HG3	5:59:186:ARG:HG3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:66:173:ASP:HB3	6:66:176:HIS:HB2	1.89	0.55
3:6A:191:THR:HA	3:6A:194:LEU:HB2	1.88	0.55
4:6F:41:ASP:HB3	1:s:944:GLN:HA	1.88	0.55
7:83:350:ARG:HD3	7:83:388:GLU:HB2	1.89	0.55
4:8D:167:PHE:HZ	4:8D:236:VAL:HG11	1.71	0.55
10:C0:47:MET:HG3	10:C0:55:TYR:HB2	1.88	0.55
10:D9:86:LEU:HB2	10:D9:313:TYR:HD2	1.72	0.55
14:K4:244:LYS:HZ1	14:K4:246:GLN:HB2	1.72	0.55
1:E:384:LEU:HD23	1:E:387:ILE:HD12	1.87	0.55
1:M:675:LYS:HB3	1:M:679:ARG:HH12	1.71	0.55
4:1B:163:ILE:HG13	4:1B:251:ARG:HG2	1.88	0.55
4:1H:175:VAL:HB	3:1I:336:LYS:HD2	1.89	0.55
4:2D:91:VAL:HG21	4:2D:116:VAL:HG22	1.88	0.55
4:3F:99:ASN:HD22	4:3F:141:GLY:HA2	1.71	0.55
5:46:33:ASP:HB3	5:46:36:LEU:HB2	1.89	0.55
3:4A:202:VAL:HG22	3:4A:268:MET:HG3	1.89	0.55
4:4D:316:MET:HE3	4:4D:366:THR:HG23	1.88	0.55
4:4J:66:MET:HE2	4:4J:147:MET:HG2	1.89	0.55
4:5J:424:GLN:HB2	14:K5:143:ARG:NH2	2.20	0.55
4:6L:11:GLN:HG2	4:6L:72:THR:HG21	1.87	0.55
2:7:317:MET:HE3	2:8:316:ARG:HB2	1.88	0.55
3:7A:191:THR:HA	3:7A:194:LEU:HB2	1.89	0.55
4:7F:286:VAL:HG11	4:7F:326:VAL:HA	1.86	0.55
4:7H:289:LEU:HD11	4:7H:363:MET:HG3	1.87	0.55
4:9F:25:SER:HB2	4:9F:30:ILE:HB	1.87	0.55
10:C7:316:CYS:O	10:C7:320:LYS:HB2	2.07	0.55
10:D2:62:VAL:H	14:K7:142:GLN:HG3	1.71	0.55
10:D9:51:TYR:HB3	10:D9:54:HIS:HD2	1.71	0.55
10:F2:354:ARG:HD3	10:F2:360:ALA:HA	1.88	0.55
14:K1:156:LEU:HD13	14:K1:185:ILE:HG23	1.88	0.55
1:s:887:VAL:HA	1:s:890:LEU:HD12	1.88	0.55
1:t:869:ARG:HG3	1:t:870:GLY:H	1.71	0.55
3:1E:15:GLN:HB3	3:1E:228:ASN:HD21	1.72	0.55
4:2H:57:GLY:HA3	9:B2:60:TYR:HE2	1.72	0.55
5:49:44:TYR:HE2	5:49:73:VAL:HG23	1.72	0.55
3:4M:217:LEU:HD11	3:4M:230:LEU:HD21	1.89	0.55
5:52:42:LEU:HD13	5:52:76:LEU:HD11	1.88	0.55
4:5H:289:LEU:HD11	4:5H:363:MET:HG3	1.89	0.55
3:5I:223:THR:HG23	3:5I:225:THR:H	1.71	0.55
4:5L:154:LYS:HD2	7:77:286:TRP:HE1	1.71	0.55
5:60:50:PHE:HB2	5:60:71:ILE:HD13	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:69:133:ARG:HH21	12:H4:335:ILE:HG21	1.71	0.55
4:6D:49:VAL:HG11	4:6D:241:ARG:HG2	1.88	0.55
7:71:357:VAL:HG11	14:K1:218:LYS:HD2	1.88	0.55
7:77:386:ARG:HG3	14:K6:115:PRO:HB3	1.89	0.55
4:7B:198:GLU:HG2	4:7B:266:PHE:HE2	1.71	0.55
4:7J:238:CYS:HB2	4:7J:318:ARG:HH11	1.71	0.55
3:7M:409:VAL:HG13	14:M1:151:PRO:HD3	1.89	0.55
3:8C:298:PRO:HG3	3:8C:308:ARG:HH21	1.71	0.55
4:8L:32:PRO:HD2	1:m:769:ARG:HH12	1.72	0.55
3:9C:73:THR:HG22	4:9D:2:ARG:HH12	1.71	0.55
3:9I:200:VAL:HA	3:9I:266:HIS:HB2	1.89	0.55
3:9I:310:GLY:HA3	3:9I:383:ALA:HB2	1.88	0.55
3:9K:141:VAL:HA	3:9K:147:SER:HB3	1.87	0.55
3:9K:229:ARG:HD2	3:9K:363:VAL:HG21	1.89	0.55
10:E8:86:LEU:HD12	10:E8:319:LEU:HB3	1.89	0.55
10:F1:81:ALA:HB3	10:F1:83:ARG:HD3	1.89	0.55
10:F2:317:LEU:HB3	10:F2:321:ARG:HH12	1.72	0.55
12:F7:220:PRO:HG2	12:F7:223:LEU:HD23	1.88	0.55
13:J7:332:LEU:HD23	13:J7:335:GLN:HE21	1.70	0.55
1:a:582:LEU:HB2	1:f:583:GLN:NE2	2.22	0.55
1:V:467:LEU:O	1:V:470:ARG:HG3	2.07	0.55
2:10:314:TYR:HA	2:10:317:MET:HG3	1.88	0.55
3:1A:213:CYS:HA	3:1A:217:LEU:HB2	1.87	0.55
3:1C:135:PHE:HD1	3:1C:157:LEU:HD21	1.71	0.55
3:1E:288:VAL:HA	3:1E:291:ILE:HG12	1.88	0.55
4:2B:49:VAL:HG13	4:2B:50:PHE:HD1	1.72	0.55
4:2B:392:LYS:HZ1	6:66:541:ASP:HA	1.71	0.55
4:2J:230:SER:HA	4:2J:233:MET:HG2	1.88	0.55
3:3C:262:TYR:HB2	3:3C:265:ILE:HG22	1.87	0.55
4:3D:131:GLN:HE21	4:3D:250:LEU:HB2	1.72	0.55
4:3D:180:VAL:HG23	4:3D:184:ASN:HD21	1.71	0.55
3:4A:53:PHE:HB3	3:4A:61:HIS:HB3	1.88	0.55
3:4A:208:ALA:HB2	3:4A:304:LYS:H	1.72	0.55
4:4B:237:THR:HG22	4:4B:250:LEU:HD21	1.87	0.55
2:5:179:MET:O	2:5:183:ARG:HB2	2.07	0.55
5:53:49:PRO:HA	5:53:70:PRO:HA	1.89	0.55
5:57:42:LEU:HD21	5:57:45:SER:HB2	1.87	0.55
3:5A:16:ILE:HD13	3:5A:231:ILE:HD13	1.88	0.55
4:5H:113:ILE:HG13	4:5H:150:LEU:HD22	1.87	0.55
4:5H:265:PHE:HB3	4:5H:374:ILE:HD13	1.89	0.55
2:6:222:GLU:HA	2:6:225:ARG:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:61:133:MET:HE1	5:61:172:LEU:HD13	1.89	0.55
6:64:822:ARG:HD3	6:64:828:GLU:HB3	1.87	0.55
6:68:133:ARG:HH12	12:H7:332:THR:HA	1.72	0.55
4:6F:49:VAL:HG11	4:6F:241:ARG:HG2	1.86	0.55
4:6F:86:ARG:HH21	4:7F:281:TYR:H	1.55	0.55
4:6F:398:TYR:HB3	4:6F:403:MET:HG3	1.88	0.55
4:6H:257:LEU:HD11	4:6H:314:SER:HB2	1.89	0.55
3:6M:184:PRO:HG3	3:6M:394:LYS:HE2	1.89	0.55
7:77:330:ARG:HH12	7:77:379:LEU:HD21	1.72	0.55
4:7B:397:TRP:CE2	3:7C:257:THR:HA	2.42	0.55
4:7D:377:MET:HA	4:7D:380:ARG:HD3	1.89	0.55
4:7H:167:PHE:HD2	4:7H:202:ILE:HD11	1.72	0.55
3:7K:203:MET:HE1	3:7K:267:PHE:HB3	1.89	0.55
2:8:205:ILE:HB	2:8:209:ARG:HH21	1.72	0.55
7:84:377:ARG:HH12	7:84:382:ASP:H	1.55	0.55
7:85:282:ARG:HH12	7:85:287:LEU:HG	1.72	0.55
4:8J:337:ASN:HA	7:90:289:GLY:HA2	1.89	0.55
7:94:401:ILE:HG21	14:M6:108:TYR:HD2	1.72	0.55
7:95:254:ARG:HB3	7:95:258:GLU:HG3	1.89	0.55
3:9A:415:GLU:HG2	3:9A:418:PHE:HE1	1.71	0.55
4:9D:136:THR:HG22	4:9D:167:PHE:HB2	1.88	0.55
8:A6:336:LYS:HG3	9:B1:22:LEU:HD11	1.88	0.55
9:B7:118:LEU:HD12	9:B7:146:VAL:HG22	1.89	0.55
10:E9:338:PRO:HB2	10:E9:341:TYR:HB3	1.88	0.55
12:G1:245:ALA:HA	12:G1:266:PRO:HG3	1.89	0.55
13:J2:446:VAL:HG22	13:J2:485:ILE:HB	1.87	0.55
13:J2:470:ARG:HA	13:J2:473:VAL:HG22	1.89	0.55
1:a:628:VAL:HG21	1:f:624:GLN:NE2	2.21	0.55
1:c:624:GLN:O	1:c:628:VAL:HG23	2.06	0.55
1:C:436:VAL:HA	1:C:439:LEU:HD12	1.89	0.55
1:Y:512:LYS:HA	1:Y:515:VAL:HG12	1.89	0.55
2:11:275:GLU:HA	2:11:278:HIS:CD2	2.42	0.55
4:2B:318:ARG:HG2	4:2B:354:CYS:HB2	1.88	0.55
4:2F:86:ARG:HG3	4:2F:89:ASN:HD22	1.72	0.55
4:2J:49:VAL:HG11	4:2J:241:ARG:HG2	1.89	0.55
4:3J:86:ARG:HG3	4:3J:89:ASN:HD21	1.71	0.55
4:3L:230:SER:HA	4:3L:233:MET:HE3	1.89	0.55
3:3M:416:GLY:HA3	6:68:590:ARG:HD2	1.87	0.55
5:43:206:LEU:HD12	5:44:206:LEU:HD21	1.87	0.55
2:5:324:GLU:HG3	2:6:324:GLU:HA	1.89	0.55
5:51:195:LEU:HD23	5:52:195:LEU:HD23	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:54:50:PHE:HE1	5:54:160:PHE:HE1	1.54	0.55
6:64:350:ALA:HB1	6:64:359:PRO:HD3	1.89	0.55
6:67:252:ARG:HH11	6:67:445:LEU:HD22	1.71	0.55
4:6B:117:LEU:HA	4:6B:120:VAL:HG12	1.88	0.55
3:6C:310:GLY:HA3	3:6C:383:ALA:HB2	1.89	0.55
3:6M:72:PRO:HG3	4:6N:2:ARG:HH11	1.72	0.55
4:7B:29:GLY:HA3	4:7B:38:GLY:HA3	1.89	0.55
4:7D:317:PHE:HD2	4:7D:321:MET:HE1	1.72	0.55
4:7H:216:LYS:H	4:7H:275:SER:HB3	1.71	0.55
7:83:380:TRP:CD1	7:83:386:ARG:HH21	2.25	0.55
3:9G:180:ALA:HB3	3:9G:183:GLU:HG3	1.89	0.55
10:F1:354:ARG:HD3	10:F1:360:ALA:HA	1.88	0.55
14:K7:156:LEU:HD21	14:K7:185:ILE:HG23	1.88	0.55
14:M4:181:LEU:HA	14:M4:184:GLN:HG2	1.89	0.55
1:F:484:GLN:HA	1:F:487:HIS:CE1	2.42	0.55
1:M:483:ILE:HG22	1:P:657:GLN:NE2	2.15	0.55
1:M:604:ILE:HG12	1:N:603:ARG:HH22	1.72	0.55
1:O:661:ASN:O	1:O:665:THR:HG23	2.07	0.55
1:Y:534:GLN:HE22	1:c:534:GLN:HA	1.71	0.55
2:12:226:VAL:HA	2:12:229:GLU:HG2	1.89	0.55
2:16:155:GLN:HE21	10:D9:122:LYS:HE2	1.71	0.55
3:1E:292:THR:HG21	3:1E:331:ALA:HB1	1.87	0.55
4:1H:397:TRP:HE1	3:1I:260:VAL:HB	1.72	0.55
3:1K:208:ALA:HB2	3:1K:304:LYS:HG2	1.89	0.55
4:1L:323:THR:HG22	4:1L:353:VAL:HG21	1.88	0.55
5:27:50:PHE:HB2	5:27:71:ILE:HD12	1.89	0.55
5:35:22:ALA:HB1	5:35:205:ARG:HD3	1.88	0.55
5:37:211:CYS:HA	5:37:214:LYS:HE3	1.88	0.55
5:38:42:LEU:HD11	5:38:45:SER:HB2	1.89	0.55
4:4B:235:GLY:HA2	4:4B:318:ARG:HD2	1.88	0.55
3:4G:298:PRO:HG3	3:4G:308:ARG:HE	1.72	0.55
5:61:161:ILE:HG22	5:61:168:PHE:HB3	1.88	0.55
6:64:976:GLU:HG3	6:64:979:ARG:HH21	1.70	0.55
6:65:975:LYS:HG2	6:65:979:ARG:HH11	1.72	0.55
6:67:832:GLU:HB2	6:67:967:ARG:HG3	1.89	0.55
6:68:967:ARG:HD3	6:68:970:LEU:HB2	1.89	0.55
3:8A:9:VAL:HG12	3:8A:146:GLY:HA2	1.89	0.55
4:8B:245:GLN:HG3	4:8B:246:LEU:H	1.72	0.55
3:8E:88:HIS:HD2	3:8E:89:PRO:HD2	1.71	0.55
7:91:268:TRP:HE1	7:91:392:ARG:HB2	1.72	0.55
7:92:411:MET:HE3	7:92:412:MET:HG3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9F:222:TYR:HA	4:9F:225:LEU:HD13	1.88	0.55
10:D7:117:THR:HG22	10:D7:132:THR:HG22	1.89	0.55
10:E9:57:ILE:HG12	10:E9:309:ILE:HD13	1.87	0.55
12:G8:200:LEU:HA	12:G8:203:VAL:HG12	1.88	0.55
14:K7:222:THR:HG23	14:K7:224:GLY:H	1.72	0.55
14:L0:233:LEU:HB3	14:L0:236:PHE:HB3	1.89	0.55
14:L1:175:ILE:HG23	14:L1:180:SER:HB3	1.87	0.55
14:L7:155:TRP:CD2	14:L7:241:VAL:HG11	2.41	0.55
1:f:572:ARG:NH1	1:f:576:SER:OG	2.40	0.55
1:D:639:LEU:HD22	1:H:638:LEU:HD11	1.89	0.54
4:1D:396:HIS:CD2	3:1E:263:PRO:HD3	2.42	0.54
4:1H:286:VAL:HA	4:1H:289:LEU:HB2	1.89	0.54
5:32:213:LEU:HD22	5:32:220:LEU:HD21	1.88	0.54
5:49:158:LEU:HD23	5:49:174:LEU:HD23	1.89	0.54
3:4A:221:ARG:HH21	4:4B:325:GLU:HG2	1.72	0.54
4:4F:178:THR:HA	3:4G:352:LYS:HD3	1.89	0.54
3:4M:98:ASP:HB3	3:4M:100:ALA:H	1.72	0.54
3:5C:173:PRO:HB2	3:5C:391:MET:HE1	1.89	0.54
4:5H:66:MET:HE2	4:5H:116:VAL:HG21	1.88	0.54
6:66:485:LYS:HB2	6:66:488:ILE:HG13	1.89	0.54
4:6B:329:GLN:HA	4:6B:332:ASN:HB2	1.89	0.54
4:6H:289:LEU:HD21	4:6H:365:VAL:HG13	1.89	0.54
4:6J:65:LEU:HB3	4:6J:73:MET:HE1	1.89	0.54
3:6M:298:PRO:HG2	3:6M:308:ARG:HH11	1.72	0.54
4:7B:165:GLU:HA	4:7B:198:GLU:O	2.07	0.54
3:7C:271:SER:HB2	3:7C:377:MET:HB3	1.89	0.54
4:7D:130:LEU:H	4:7D:162:ARG:HH21	1.54	0.54
4:7D:167:PHE:CE1	4:7D:233:MET:HG3	2.42	0.54
3:7E:70:LEU:HD12	3:7E:99:ALA:HB2	1.89	0.54
3:7K:310:GLY:H	7:83:385:PRO:HD3	1.72	0.54
3:8M:271:SER:HB3	3:8M:301:MET:HA	1.88	0.54
10:D8:354:ARG:HD3	10:D8:360:ALA:HA	1.89	0.54
10:E6:114:PRO:HB3	10:E6:138:ARG:HD2	1.89	0.54
12:F0:230:VAL:HG11	12:F0:235:LEU:HD23	1.88	0.54
10:F2:68:THR:HA	10:F2:71:GLN:HB3	1.88	0.54
14:L8:91:ASP:HA	14:L8:97:ARG:HH21	1.72	0.54
1:N:578:ARG:HA	1:N:581:LYS:HE2	1.89	0.54
2:13:306:LYS:HB3	2:14:306:LYS:HE2	1.88	0.54
4:1B:268:ILE:HG22	4:1B:300:MET:HB3	1.89	0.54
4:1B:311:LEU:HD23	4:1B:312:THR:HG23	1.89	0.54
4:1D:54:ALA:HA	4:2D:283:ALA:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1D:248:SER:HB2	4:1D:252:LYS:HG3	1.89	0.54
3:1G:387:VAL:HG22	3:1G:390:ARG:HH22	1.71	0.54
4:2D:167:PHE:HA	4:2D:200:GLN:HB2	1.90	0.54
5:36:84:PRO:HD2	5:36:124:GLY:HA2	1.87	0.54
4:3B:229:VAL:HA	4:3B:300:MET:HE1	1.89	0.54
4:3F:217:LEU:HD21	8:A5:260:TRP:HH2	1.70	0.54
2:4:173:GLU:HG3	2:4:177:ARG:HH21	1.72	0.54
5:49:48:VAL:HG21	5:49:134:LEU:HB3	1.89	0.54
2:5:275:GLU:HA	2:5:278:HIS:CE1	2.41	0.54
5:51:98:PHE:H	5:52:185:ARG:HH22	1.55	0.54
5:55:42:LEU:HD21	5:55:45:SER:HB2	1.89	0.54
4:5D:248:SER:HA	4:5D:252:LYS:HD2	1.89	0.54
3:5G:291:ILE:HG22	3:5G:375:VAL:HG12	1.88	0.54
4:6H:74:ASP:HB3	1:g:791:ARG:HB3	1.89	0.54
3:6M:70:LEU:HA	3:6M:95:GLY:HA3	1.90	0.54
4:6N:81:PHE:HD2	4:6N:84:LEU:HD22	1.72	0.54
7:76:326:PRO:HA	7:76:391:TYR:HD2	1.72	0.54
3:7A:384:ILE:HB	3:7A:432:TYR:HE2	1.72	0.54
3:7E:265:ILE:HG22	3:7E:380:ASN:HD21	1.73	0.54
4:7L:424:GLN:HG3	14:L0:143:ARG:HB3	1.89	0.54
7:80:299:PHE:HE2	14:L1:126:ILE:HD12	1.73	0.54
3:8A:75:VAL:HG13	3:8A:92:LEU:HB3	1.89	0.54
3:8A:140:ALA:HA	3:8A:171:SER:HB2	1.89	0.54
4:8F:7:VAL:HG22	4:8F:64:ILE:HD12	1.88	0.54
3:8K:422:ARG:HA	3:8K:425:LEU:HD23	1.89	0.54
7:94:340:ASN:HB3	7:94:361:THR:HG22	1.88	0.54
7:95:397:SER:HB3	14:M7:124:SER:HB2	1.89	0.54
3:9E:318:MET:HB2	3:9E:376:CYS:HB3	1.89	0.54
3:9G:407:TRP:HE1	4:9H:258:ILE:HB	1.72	0.54
8:A7:161:ILE:HD11	8:A7:187:VAL:HG21	1.89	0.54
10:E2:157:TYR:HD1	10:E2:381:MET:HE3	1.71	0.54
10:F2:38:ARG:HH12	10:F2:42:LYS:HE3	1.71	0.54
12:G3:206:ASP:HB3	12:G3:209:TRP:CH2	2.43	0.54
13:J3:338:LEU:HD13	13:J3:359:ARG:HD2	1.89	0.54
14:L1:172:ARG:HH11	14:L1:174:TYR:HB2	1.72	0.54
14:M4:233:LEU:HG	14:M4:236:PHE:HD2	1.72	0.54
1:i:827:HIS:HB2	1:i:834:ARG:NH2	2.23	0.54
1:E:289:VAL:HA	3:1K:283:HIS:HB2	1.89	0.54
2:13:165:ARG:HA	2:13:168:ARG:HE	1.72	0.54
4:1B:32:PRO:HA	4:1B:81:PHE:HE1	1.71	0.54
3:1E:318:MET:HG2	3:1E:354:GLY:HA3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1M:9:VAL:HG22	3:1M:68:LEU:HD23	1.89	0.54
4:1N:14:ASN:HD21	4:1N:67:ASP:HB2	1.73	0.54
5:22:139:LYS:HG3	5:22:140:GLU:H	1.71	0.54
5:27:49:PRO:HA	5:27:70:PRO:HA	1.88	0.54
5:29:84:PRO:HD2	5:29:124:GLY:HA2	1.88	0.54
3:2E:178:SER:HB2	4:2F:347:ASN:ND2	2.22	0.54
3:2I:6:SER:O	3:2I:65:CYS:HA	2.07	0.54
5:39:212:LEU:HB3	5:40:220:LEU:HD21	1.88	0.54
3:3A:161:TYR:HB3	3:3A:164:LYS:HB2	1.90	0.54
4:3H:149:THR:HA	4:3H:152:ILE:HD12	1.88	0.54
5:45:33:ASP:HB3	5:45:36:LEU:HB2	1.89	0.54
3:4A:67:PHE:HB2	3:4A:92:LEU:HD13	1.88	0.54
3:4M:230:LEU:HD11	3:4M:275:ILE:HG23	1.87	0.54
5:52:29:ILE:HD13	5:52:197:SER:HB3	1.88	0.54
5:56:75:ILE:HG13	5:56:89:VAL:HG22	1.88	0.54
3:5A:250:VAL:HG21	3:5A:318:MET:HE1	1.90	0.54
4:5B:358:PRO:HG2	4:5B:361:LEU:HB2	1.88	0.54
3:5C:11:GLN:HE21	3:5C:74:VAL:HG21	1.72	0.54
6:64:416:MET:HE2	6:64:419:VAL:HB	1.88	0.54
6:67:934:LEU:HD12	6:67:938:ARG:HH12	1.72	0.54
6:68:593:PRO:HA	6:68:598:VAL:HG11	1.89	0.54
3:6M:207:GLU:HA	3:6M:210:TYR:HB2	1.89	0.54
3:7E:51:THR:HG21	3:7E:243:ARG:HG2	1.88	0.54
4:7J:107:THR:HG22	4:7J:108:GLU:H	1.73	0.54
3:7M:265:ILE:HG22	3:7M:380:ASN:HD21	1.71	0.54
7:84:313:LEU:HD22	14:L3:109:ASP:HB2	1.90	0.54
4:8D:167:PHE:HE1	4:8D:200:GLN:HE21	1.55	0.54
4:8J:100:ASN:HB3	4:8J:103:LYS:HB2	1.89	0.54
4:8J:117:LEU:HA	4:8J:120:VAL:HG12	1.88	0.54
7:90:357:VAL:HG12	14:L0:240:TRP:HA	1.88	0.54
4:9B:207:LEU:HB3	4:9B:225:LEU:HD22	1.90	0.54
4:9F:178:THR:HA	3:9G:258:ASN:HD21	1.71	0.54
3:9G:288:VAL:HG11	3:9G:327:ASP:HB3	1.89	0.54
3:9K:328:VAL:HG21	3:9K:355:ILE:HD11	1.89	0.54
10:E0:390:MET:HA	10:E0:393:VAL:HG12	1.89	0.54
12:F5:216:TRP:HZ2	12:F5:228:ILE:HD11	1.72	0.54
14:M7:248:LYS:HE3	14:M7:255:VAL:HG11	1.88	0.54
1:a:530:LEU:HD22	1:a:533:ARG:HH21	1.72	0.54
1:c:559:GLU:O	1:c:560:GLN:C	2.51	0.54
1:Y:575:LEU:HD21	1:c:577:GLN:HG3	1.88	0.54
4:1D:152:ILE:HG13	4:1D:164:MET:HE2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1M:101:ASN:HB3	3:1M:182:VAL:HG11	1.89	0.54
5:27:180:THR:HG23	5:27:183:PHE:H	1.73	0.54
3:2A:269:LEU:HD21	3:2A:384:ILE:HD13	1.89	0.54
5:30:160:PHE:O	5:30:171:LEU:HB3	2.07	0.54
4:3B:207:LEU:HA	4:3B:210:ILE:HG12	1.89	0.54
4:3L:136:THR:HG22	4:3L:167:PHE:HB2	1.88	0.54
4:4B:378:PHE:HB3	4:4B:415:MET:HE3	1.88	0.54
3:4G:222:PRO:HD2	4:4H:324:LYS:HD3	1.89	0.54
4:4L:22:GLU:HA	4:4L:81:PHE:HD2	1.71	0.54
3:5A:168:ASN:HB2	3:5A:198:THR:HG21	1.89	0.54
4:5N:189:VAL:HG13	4:5N:415:MET:HE1	1.90	0.54
5:61:158:LEU:HD23	5:61:174:LEU:HD23	1.89	0.54
3:6C:274:PRO:HD3	3:6C:291:ILE:HD11	1.87	0.54
4:6L:101:TRP:HB3	4:6L:398:TYR:HE2	1.72	0.54
4:6N:229:VAL:HA	4:6N:300:MET:HE1	1.89	0.54
4:8B:171:PRO:HG3	4:8B:185:ALA:HB1	1.87	0.54
7:92:379:LEU:HD21	14:M2:242:ILE:HG21	1.89	0.54
7:93:272:ALA:HB1	14:M4:93:PHE:HB2	1.88	0.54
7:95:334:LEU:HD23	7:95:337:LYS:HD2	1.90	0.54
3:9C:2:ARG:HH21	3:9C:133:GLN:HG3	1.72	0.54
4:9H:10:GLY:HA2	4:9H:143:THR:HG23	1.90	0.54
3:9I:327:ASP:HA	3:9I:330:ALA:HB3	1.90	0.54
8:A1:129:VAL:HG23	8:A1:163:ARG:HD2	1.89	0.54
13:J5:405:VAL:HG13	13:J5:409:LEU:HD23	1.88	0.54
14:M7:155:TRP:HB2	14:M7:218:LYS:HA	1.89	0.54
1:t:887:VAL:HA	1:t:890:LEU:HD12	1.87	0.54
1:B:323:MET:HE1	1:E:322:ARG:HE	1.72	0.54
1:I:607:LEU:HD13	1:J:607:LEU:HG	1.90	0.54
1:Q:365:LEU:O	1:Q:369:GLU:HB2	2.07	0.54
1:Y:603:ARG:C	1:c:604:ILE:HD11	2.33	0.54
4:1J:200:GLN:HB3	4:1J:268:ILE:HD11	1.90	0.54
5:23:181:GLU:HG3	5:23:185:ARG:HH12	1.73	0.54
5:28:97:LEU:HD13	5:28:188:MET:HE1	1.89	0.54
4:2L:391:ARG:HH12	12:H6:56:HIS:HE1	1.56	0.54
3:2M:54:SER:HB3	3:2M:64:ARG:HE	1.72	0.54
4:3B:293:MET:HE2	4:3B:367:PHE:HD1	1.72	0.54
3:3M:392:ASP:HA	3:3M:422:ARG:HH22	1.73	0.54
5:44:158:LEU:HB3	5:44:174:LEU:HB2	1.90	0.54
5:49:144:PHE:HA	5:49:162:GLN:HG3	1.89	0.54
3:4C:228:ASN:HA	3:4C:231:ILE:HD12	1.89	0.54
4:4D:178:THR:HG23	4:4D:181:GLU:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4E:100:ALA:HA	4:4F:252:LYS:HG2	1.87	0.54
4:4F:178:THR:O	4:4F:181:GLU:HB2	2.07	0.54
3:4I:222:PRO:HD2	4:4J:324:LYS:HD3	1.89	0.54
3:4K:278:ALA:HB2	3:4K:367:ASP:HA	1.90	0.54
5:50:35:SER:HA	5:50:88:ARG:HH22	1.72	0.54
5:54:167:LYS:HG3	5:57:119:LEU:HD23	1.90	0.54
4:5F:49:VAL:HG11	4:5F:241:ARG:HG2	1.90	0.54
4:5L:274:THR:HG23	4:5L:282:ARG:HH21	1.72	0.54
6:69:177:ALA:HA	6:69:489:LEU:HD21	1.88	0.54
4:6J:64:ILE:HD13	4:6J:120:VAL:HB	1.90	0.54
4:6L:200:GLN:HG3	4:6L:266:PHE:HB2	1.89	0.54
4:7B:34:GLY:HA3	4:7B:58:ARG:HG3	1.88	0.54
3:7E:106:GLY:HA3	3:7E:148:GLY:HA3	1.89	0.54
3:7G:390:ARG:HA	14:K8:192:ILE:HD11	1.89	0.54
2:8:222:GLU:HA	2:8:225:ARG:HB3	1.90	0.54
3:8C:9:VAL:HG22	3:8C:68:LEU:HB2	1.88	0.54
4:8D:396:HIS:HA	4:8D:399:THR:HG22	1.89	0.54
3:8E:3:GLU:HA	3:8E:51:THR:HA	1.89	0.54
7:97:334:LEU:HD23	7:97:337:LYS:HD2	1.90	0.54
4:9B:317:PHE:O	4:9B:354:CYS:HB2	2.08	0.54
3:9C:223:THR:H	3:9C:226:ASN:HD22	1.56	0.54
3:9I:375:VAL:HB	3:9I:377:MET:HE3	1.89	0.54
10:C0:352:TYR:HE2	10:C0:376:ILE:HD11	1.73	0.54
10:D3:284:LEU:HB3	10:D3:351:ARG:HH12	1.71	0.54
10:E4:47:MET:HG2	10:E4:55:TYR:HB2	1.89	0.54
1:U:580:GLU:HB3	1:d:473:ARG:HH22	1.73	0.54
2:10:163:GLU:HG3	10:C7:81:ALA:HB2	1.89	0.54
3:1C:201:ALA:HB3	3:1C:267:PHE:HA	1.89	0.54
5:20:164:MET:HE2	5:21:171:LEU:HD23	1.90	0.54
5:22:54:LEU:HA	5:22:150:MET:HB2	1.89	0.54
5:26:53:ARG:O	5:26:149:ILE:HA	2.08	0.54
3:2C:327:ASP:HA	3:2C:330:ALA:HB3	1.90	0.54
4:2L:152:ILE:HG23	4:2L:164:MET:HE2	1.88	0.54
4:3L:293:MET:HA	4:3L:298:ASN:HD22	1.72	0.54
3:4E:339:ARG:HH11	6:65:844:ALA:HB1	1.71	0.54
5:59:17:SER:HA	5:59:20:PHE:HB3	1.89	0.54
5:59:44:TYR:HB3	5:59:75:ILE:H	1.73	0.54
3:6A:137:MET:HB3	3:6A:168:ASN:HA	1.90	0.54
3:6E:159:VAL:HG13	7:79:351:LYS:HB3	1.90	0.54
3:6I:8:HIS:HD2	3:6I:138:PHE:HB2	1.73	0.54
3:6I:301:MET:HE3	3:6I:307:PRO:HG2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:72:313:LEU:HB2	7:72:315:ILE:HG13	1.88	0.54
3:8A:314:ALA:HB3	3:8A:380:ASN:HB3	1.88	0.54
3:8C:273:ALA:HA	3:8C:275:ILE:HG12	1.88	0.54
4:8F:98:GLY:H	4:8F:103:LYS:HD2	1.73	0.54
3:9E:268:MET:HE2	3:9E:378:ILE:HB	1.90	0.54
4:9F:318:ARG:HG2	4:9F:358:PRO:HD3	1.90	0.54
4:9L:270:PHE:HB2	4:9L:300:MET:HE1	1.90	0.54
3:9M:362:VAL:HG11	3:9M:370:LYS:HA	1.89	0.54
10:E7:368:ASP:HA	10:E7:371:ARG:HB2	1.90	0.54
13:J3:410:THR:HG23	13:J3:413:GLU:H	1.71	0.54
14:L3:107:ALA:H	14:L3:119:HIS:HB3	1.73	0.54
14:L7:175:ILE:HG22	14:L7:210:LEU:HD21	1.90	0.54
1:G:295:TRP:O	1:G:299:ARG:HB2	2.08	0.54
1:J:679:ARG:HH21	1:J:680:LEU:HG	1.72	0.54
4:1J:207:LEU:HD13	4:1J:210:ILE:HD11	1.90	0.54
4:1N:36:TYR:CE1	4:1N:38:GLY:HA3	2.43	0.54
4:1N:133:PHE:HB2	4:1N:164:MET:HB2	1.90	0.54
5:21:74:LYS:HB2	5:21:90:GLU:HB2	1.89	0.54
5:23:51:GLU:HB3	5:23:147:VAL:HG12	1.90	0.54
5:29:53:ARG:HH11	5:29:64:ASP:HB3	1.73	0.54
3:2A:68:LEU:HD11	3:2A:114:ILE:HG12	1.88	0.54
3:2A:130:THR:N	9:B7:41:ARG:HH22	2.05	0.54
5:31:77:ILE:HA	5:31:86:HIS:O	2.07	0.54
5:31:78:LEU:HD23	5:31:85:GLN:HB2	1.90	0.54
5:32:106:ASN:H	5:32:109:LEU:HB2	1.73	0.54
3:3A:215:ARG:NH1	3:3A:299:ALA:HB1	2.23	0.54
4:3D:134:GLN:HE22	4:3D:233:MET:HB3	1.73	0.54
4:3J:267:LEU:HD23	4:3J:299:MET:HG2	1.90	0.54
5:46:121:ILE:HD13	5:46:129:VAL:HG21	1.90	0.54
5:49:33:ASP:HB3	5:49:36:LEU:HB2	1.88	0.54
3:4A:221:ARG:CZ	4:4B:325:GLU:H	2.21	0.54
4:4B:284:LEU:HG	4:4B:362:LYS:HB3	1.90	0.54
2:5:202:GLU:HA	2:5:205:ILE:HG12	1.89	0.54
2:5:317:MET:HE2	2:6:317:MET:HA	1.89	0.54
3:5E:271:SER:HB2	3:5E:377:MET:HB3	1.89	0.54
3:5G:195:LEU:HD12	3:5G:428:LEU:HD22	1.89	0.54
4:5H:191:GLN:HG3	14:K1:133:VAL:HG21	1.90	0.54
5:61:188:MET:HE1	5:62:97:LEU:HB3	1.89	0.54
6:65:141:LEU:HG	6:65:145:MET:HE2	1.88	0.54
3:6C:103:PHE:H	3:6C:408:TYR:HE1	1.55	0.54
4:6H:206:ALA:HB2	4:6H:302:ALA:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6K:26:LEU:HD22	3:6K:364:PRO:HD3	1.90	0.54
4:7J:135:ILE:HB	4:7J:166:THR:HG22	1.88	0.54
3:8I:274:PRO:HG2	3:8I:374:ALA:HA	1.90	0.54
4:8J:290:THR:HG21	4:8J:329:GLN:HB3	1.88	0.54
4:8L:360:GLY:HA3	1:m:816:VAL:HB	1.90	0.54
3:9C:12:ALA:HB3	3:9C:140:ALA:HB2	1.89	0.54
3:9K:336:LYS:HG3	14:M6:112:THR:HG22	1.89	0.54
4:9L:268:ILE:HG23	4:9L:300:MET:HE2	1.90	0.54
12:G4:192:GLU:HG2	12:G4:194:ALA:H	1.73	0.54
12:G4:221:MET:HG2	12:G4:224:ARG:HH21	1.73	0.54
12:G4:223:LEU:O	12:G4:227:SER:HB3	2.07	0.54
13:J7:318:LEU:HD22	13:J7:475:ALA:HB1	1.90	0.54
1:a:617:MET:HB3	1:f:618:ARG:HE	1.73	0.54
1:c:592:ARG:C	1:c:594:ALA:H	2.16	0.54
1:m:768:PRO:HB2	1:m:771:VAL:HG22	1.90	0.54
5:24:54:LEU:HA	5:24:150:MET:HB2	1.90	0.54
5:28:155:LYS:HE2	5:28:177:VAL:HG12	1.90	0.54
4:2D:107:THR:HG22	4:2D:108:GLU:H	1.72	0.54
4:2D:246:LEU:HB3	4:2D:353:VAL:H	1.73	0.54
4:2J:11:GLN:HA	4:2J:72:THR:HG21	1.90	0.54
3:2K:154:LEU:HD21	3:2K:198:THR:HB	1.89	0.54
5:31:91:LEU:HD12	5:31:101:TYR:HB2	1.89	0.54
4:3B:317:PHE:HB3	4:3B:321:MET:HE2	1.89	0.54
3:3C:370:LYS:HB3	9:B5:30:ARG:HE	1.73	0.54
5:40:167:LYS:HD3	5:40:169:ILE:HD11	1.89	0.54
4:6B:396:HIS:HA	4:6B:399:THR:HG22	1.89	0.54
3:6C:189:LEU:HD21	3:6C:418:PHE:HD1	1.73	0.54
4:7H:66:MET:HE1	4:7H:151:LEU:HD22	1.88	0.54
4:7L:396:HIS:HB2	14:L0:90:PHE:HZ	1.72	0.54
4:8L:164:MET:HE2	4:8L:197:ASP:HB2	1.89	0.54
7:95:407:ASP:HA	3:9M:330:ALA:HA	1.89	0.54
3:9A:269:LEU:HD21	3:9A:384:ILE:HD11	1.89	0.54
4:9D:299:MET:HG3	4:9D:301:CYS:H	1.72	0.54
3:9E:122:ILE:HD12	3:9E:135:PHE:HE2	1.73	0.54
4:9F:204:ASN:HA	4:9F:207:LEU:HD12	1.89	0.54
3:9G:100:ALA:HA	4:9H:252:LYS:HG2	1.90	0.54
4:9H:382:SER:HB3	4:9H:415:MET:HE1	1.89	0.54
10:E3:78:ARG:HB3	10:E9:121:ALA:HB2	1.90	0.54
12:F7:199:TRP:HH2	12:F8:224:ARG:HB3	1.73	0.54
12:G8:195:PRO:HA	12:G8:198:LYS:HG2	1.89	0.54
14:L1:114:SER:HB3	14:L1:117:ARG:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:574:LYS:O	1:a:578:ARG:HG2	2.08	0.54
1:A:585:GLU:HA	1:A:588:THR:HG22	1.89	0.54
1:B:351:GLU:HG2	1:Y:458:CYS:HB3	1.89	0.54
1:O:659:LEU:HB3	1:P:659:LEU:HD22	1.90	0.54
2:13:194:LYS:HA	2:13:197:VAL:HG12	1.89	0.54
3:1A:219:ILE:HG22	3:1A:221:ARG:H	1.73	0.54
3:1A:296:PHE:HD2	3:1A:335:ILE:HG12	1.72	0.54
4:1D:189:VAL:HA	4:1D:192:LEU:HB2	1.90	0.54
3:1E:274:PRO:HG2	3:1E:374:ALA:HA	1.90	0.54
4:1J:113:ILE:HG21	4:1J:154:LYS:HD3	1.88	0.54
4:2F:3:GLU:HA	4:2F:49:VAL:HA	1.89	0.54
3:2K:203:MET:HE2	3:2K:267:PHE:HB3	1.90	0.54
4:2L:238:CYS:HB2	4:2L:318:ARG:HH11	1.73	0.54
5:32:24:VAL:HG21	5:32:201:LEU:HB3	1.88	0.54
3:3A:2:ARG:HD3	3:3A:133:GLN:HE21	1.72	0.54
3:3A:195:LEU:HD11	3:3A:428:LEU:HD22	1.90	0.54
4:3D:12:CYS:HB3	4:3D:138:SER:HB2	1.88	0.54
3:3K:12:ALA:HB3	3:3K:140:ALA:HB2	1.90	0.54
3:3M:395:PHE:HD2	3:3M:422:ARG:HH21	1.55	0.54
5:47:114:GLN:HG3	5:47:119:LEU:HB2	1.90	0.54
3:4A:195:LEU:HD11	3:4A:428:LEU:HD22	1.90	0.54
3:4C:23:LEU:HD12	3:4C:363:VAL:HB	1.89	0.54
3:4E:334:THR:HA	3:4E:337:THR:HG22	1.90	0.54
4:4F:320:ARG:HH21	8:A1:171:SER:HA	1.73	0.54
5:61:126:TYR:HE1	5:61:172:LEU:HD11	1.72	0.54
4:6N:421:GLU:HB3	14:L4:140:GLY:HA2	1.90	0.54
7:79:376:GLU:O	7:79:380:TRP:HB3	2.08	0.54
4:7L:136:THR:HG22	4:7L:167:PHE:HB2	1.90	0.54
3:8I:222:PRO:HD2	4:8J:324:LYS:HB3	1.89	0.54
3:9C:180:ALA:HA	4:9D:350:LYS:HD2	1.90	0.54
3:9E:318:MET:HE1	3:9E:378:ILE:HG12	1.88	0.54
3:9I:392:ASP:HA	3:9I:422:ARG:HH12	1.72	0.54
4:9J:358:PRO:HG2	4:9J:361:LEU:HB3	1.90	0.54
3:9K:191:THR:HA	3:9K:194:LEU:HD23	1.89	0.54
8:A6:187:VAL:HG22	8:A6:223:LEU:HD13	1.90	0.54
10:C7:392:THR:HG22	10:C7:395:ARG:HH21	1.72	0.54
10:D0:76:ALA:HB2	10:D0:319:LEU:HD21	1.89	0.54
10:F3:301:ARG:HE	14:M5:143:ARG:HG2	1.72	0.54
10:F3:317:LEU:HB3	10:F3:321:ARG:NH1	2.23	0.54
12:F9:272:THR:HG21	12:F9:289:ILE:HD12	1.90	0.54
13:J4:271:LEU:HD13	13:J4:286:LEU:HD13	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J6:318:LEU:HD22	13:J6:475:ALA:HB1	1.89	0.54
14:K9:154:MET:HE1	14:K9:181:LEU:HD21	1.90	0.54
1:m:777:PRO:HD2	1:m:806:VAL:HA	1.88	0.54
1:A:435:LYS:HB2	1:a:546:ASN:HD21	1.73	0.54
1:N:472:GLU:HA	1:N:475:LYS:HG2	1.90	0.54
1:T:640:ALA:HB2	1:i:826:VAL:HB	1.90	0.54
1:U:341:GLU:HA	1:U:344:ARG:HG2	1.90	0.54
4:1F:207:LEU:HB3	4:1F:225:LEU:HD22	1.89	0.54
3:1I:203:MET:HE1	3:1I:267:PHE:HB3	1.89	0.54
3:1I:269:LEU:HD23	3:1I:303:ALA:HB3	1.90	0.54
4:1J:267:LEU:HD21	4:1J:371:SER:HB3	1.89	0.54
4:1L:180:VAL:HG22	4:1L:183:TYR:HB2	1.90	0.54
5:25:84:PRO:HD2	5:25:124:GLY:HA2	1.89	0.54
5:29:48:VAL:HG22	5:29:138:ILE:HD11	1.90	0.54
5:29:89:VAL:HB	5:29:103:HIS:HB3	1.90	0.54
3:2C:272:TYR:HB3	3:2C:275:ILE:HD11	1.89	0.54
5:32:46:ARG:HG2	5:32:47:GLU:H	1.73	0.54
5:32:161:ILE:HG12	5:32:170:GLU:HA	1.89	0.54
3:3E:208:ALA:HB2	3:3E:304:LYS:HG2	1.89	0.54
4:3L:83:GLN:HE21	8:A7:121:THR:HG21	1.73	0.54
3:4C:229:ARG:HG2	3:4C:363:VAL:HG21	1.89	0.54
4:4J:49:VAL:HG11	4:4J:241:ARG:HB3	1.88	0.54
5:56:162:GLN:HB2	5:56:171:LEU:HD23	1.91	0.54
3:6A:115:VAL:HG21	3:6A:152:LEU:HD22	1.89	0.54
3:7C:6:SER:HA	3:7C:136:LEU:HB2	1.90	0.54
4:7F:163:ILE:HD11	4:7F:251:ARG:HE	1.73	0.54
3:7K:271:SER:HB3	3:7K:301:MET:HA	1.90	0.54
4:8F:130:LEU:HB2	4:8F:162:ARG:HE	1.73	0.54
4:8F:214:THR:HG22	4:8F:297:LYS:HE3	1.89	0.54
4:9D:220:PRO:HG2	3:9E:326:LYS:HE2	1.89	0.54
9:B3:458:HIS:CD2	9:B3:459:ARG:HG2	2.43	0.54
10:C6:83:ARG:HH11	10:C6:88:LEU:HD13	1.73	0.54
13:J5:392:VAL:HG22	13:J5:444:ALA:HB3	1.90	0.54
1:a:611:THR:CA	1:f:610:VAL:HG11	2.38	0.54
1:r:890:LEU:HB3	1:r:942:ILE:HD11	1.90	0.54
1:M:665:THR:HG22	3:9G:370:LYS:HZ1	1.72	0.53
1:N:497:GLN:HA	1:N:500:ARG:HE	1.71	0.53
3:1A:207:GLU:HA	3:1A:210:TYR:HD2	1.73	0.53
4:1B:87:PRO:HA	4:1B:90:PHE:HD2	1.70	0.53
4:1B:412:GLU:HG2	4:1B:415:MET:HE2	1.89	0.53
3:1M:298:PRO:HB3	3:1M:307:PRO:HD2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:24:218:PRO:HA	5:24:221:LEU:HD12	1.88	0.53
5:25:75:ILE:HA	5:25:89:VAL:HG12	1.90	0.53
5:29:24:VAL:HG21	5:29:198:LYS:HG3	1.91	0.53
4:2D:166:THR:HB	4:2D:199:VAL:HA	1.90	0.53
3:3A:227:LEU:HD21	4:3B:324:LYS:HE2	1.90	0.53
3:3C:49:PHE:HD2	3:3C:53:PHE:HB2	1.73	0.53
5:47:214:LYS:HE2	13:J7:306:ARG:HG3	1.89	0.53
4:4D:156:ARG:HG2	4:4D:195:ASN:HD22	1.72	0.53
5:59:87:VAL:HB	5:59:105:LEU:HB2	1.90	0.53
4:5N:182:PRO:HB3	4:5N:384:GLN:HG3	1.90	0.53
3:6A:208:ALA:HB1	3:6A:302:MET:HA	1.91	0.53
3:6K:9:VAL:HG23	3:6K:68:LEU:HD22	1.90	0.53
3:6M:426:ALA:HB3	10:D6:38:ARG:HH12	1.72	0.53
4:7B:207:LEU:HD11	4:7B:229:VAL:HG23	1.91	0.53
7:84:275:HIS:HA	14:L3:95:ASN:HD21	1.71	0.53
3:8C:237:SER:HA	3:8C:240:ALA:HB2	1.89	0.53
4:8D:100:ASN:HD21	4:8D:397:TRP:HB3	1.72	0.53
3:8E:296:PHE:CE2	3:8E:335:ILE:HG21	2.42	0.53
3:8E:398:MET:HE3	3:8E:404:PHE:HD1	1.73	0.53
4:8L:265:PHE:HB3	4:8L:374:ILE:HD13	1.91	0.53
9:B4:44:LEU:HD21	9:B4:515:LEU:HD11	1.90	0.53
10:D2:303:LEU:HD22	10:D2:396:LEU:HD13	1.90	0.53
10:F3:354:ARG:HD2	10:F3:360:ALA:HA	1.90	0.53
12:G1:200:LEU:HD21	12:G1:228:ILE:HD13	1.91	0.53
1:I:617:MET:HE2	1:J:618:ARG:HD3	1.90	0.53
5:24:221:LEU:HD23	5:24:224:LEU:HD12	1.88	0.53
4:2D:318:ARG:HH12	4:2D:358:PRO:HB3	1.73	0.53
4:3F:220:PRO:HB3	8:A5:255:ARG:HH22	1.72	0.53
3:3I:14:ILE:HD11	3:3I:68:LEU:H	1.74	0.53
3:3M:317:LEU:HB3	3:3M:319:TYR:HE1	1.72	0.53
5:50:24:VAL:HG21	5:50:201:LEU:HD13	1.90	0.53
3:5I:88:HIS:CE1	3:5I:90:GLU:HG2	2.43	0.53
4:5N:170:PHE:HB3	4:5N:377:MET:HE2	1.89	0.53
6:64:902:PRO:HG3	1:u:880:THR:HA	1.90	0.53
6:67:534:ARG:HG3	6:67:535:ARG:HG3	1.89	0.53
6:68:847:GLU:CD	6:68:848:SER:H	2.17	0.53
3:7M:171:SER:HA	3:7M:204:LEU:HB2	1.90	0.53
3:7M:237:SER:HB3	3:7M:320:ARG:HH21	1.73	0.53
7:82:386:ARG:HG3	14:K8:115:PRO:HB3	1.90	0.53
3:8M:229:ARG:HD2	3:8M:363:VAL:HG11	1.88	0.53
10:C8:338:PRO:HB2	10:C8:341:TYR:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E5:322:GLU:HG2	10:E5:326:LYS:HZ1	1.73	0.53
12:G4:254:VAL:HG13	12:G4:255:VAL:HG13	1.91	0.53
14:K8:99:ILE:HG13	14:K8:102:ARG:HH21	1.74	0.53
1:a:677:MET:SD	1:f:677:MET:HG2	2.48	0.53
1:w:875:ILE:HD11	1:w:945:ILE:HG23	1.90	0.53
1:J:653:LYS:HZ3	1:J:653:LYS:HA	1.71	0.53
1:X:630:ARG:HH11	4:6N:276:ARG:HH21	1.55	0.53
1:Y:505:GLU:HA	1:Y:508:VAL:HG12	1.88	0.53
4:1B:170:PHE:CE2	4:1B:201:VAL:HA	2.43	0.53
3:1M:6:SER:HB2	3:1M:136:LEU:HD12	1.90	0.53
3:2E:12:ALA:HB3	3:2E:140:ALA:HB2	1.91	0.53
4:3B:54:ALA:HB3	4:3B:58:ARG:HB3	1.90	0.53
4:3D:290:THR:HA	4:3D:293:MET:HE3	1.90	0.53
4:4B:215:LEU:HB3	4:4B:217:LEU:HD13	1.91	0.53
3:4G:296:PHE:HE1	3:4G:317:LEU:HD21	1.73	0.53
4:4H:207:LEU:HB3	4:4H:225:LEU:HG	1.90	0.53
3:5A:88:HIS:CE1	3:6A:284:GLU:OE1	2.61	0.53
4:5H:9:GLY:HA2	4:5H:66:MET:HG2	1.90	0.53
4:5H:11:GLN:HA	4:5H:72:THR:HG21	1.90	0.53
6:68:495:LEU:HD23	6:68:498:ARG:NH1	2.24	0.53
3:6I:167:LEU:HG	3:6I:200:VAL:HB	1.90	0.53
3:7K:312:TYR:HB2	3:7K:343:PHE:HD2	1.74	0.53
3:8A:154:LEU:HG	3:8A:166:LYS:HE2	1.90	0.53
3:8E:139:ASN:O	3:8E:170:CYS:HA	2.08	0.53
4:8H:309:ARG:H	4:8H:372:THR:HG22	1.73	0.53
4:9D:139:LEU:HD21	4:9D:192:LEU:HD22	1.89	0.53
3:9E:271:SER:HB3	3:9E:301:MET:HA	1.91	0.53
4:9H:10:GLY:HA3	4:9H:144:GLY:HA2	1.91	0.53
8:A2:321:VAL:HG13	8:A2:367:PHE:HD2	1.74	0.53
14:K3:143:ARG:HG2	14:K3:144:PHE:CD2	2.43	0.53
14:M1:180:SER:HA	14:M1:183:GLN:HG2	1.90	0.53
1:Y:574:LYS:O	1:Y:578:ARG:HG2	2.08	0.53
3:1E:141:VAL:HG22	3:1E:187:SER:HA	1.91	0.53
5:21:105:LEU:HG	5:21:109:LEU:HD22	1.89	0.53
5:23:164:MET:HB2	5:23:167:LYS:H	1.74	0.53
5:25:120:MET:HA	6:69:339:PRO:HB2	1.89	0.53
5:27:216:LYS:HG3	5:27:217:SER:H	1.73	0.53
3:2A:122:ILE:HG21	3:2A:157:LEU:HD11	1.90	0.53
2:3:261:ARG:HH12	2:3:265:GLU:HB2	1.72	0.53
5:30:49:PRO:HB2	5:30:68:LEU:HG	1.91	0.53
3:3A:339:ARG:HH21	6:67:185:ASP:HB2	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:40:160:PHE:HB2	5:40:172:LEU:HB2	1.90	0.53
5:46:211:CYS:HA	5:46:214:LYS:HE2	1.89	0.53
3:4G:265:ILE:HG21	3:4G:313:MET:HE1	1.88	0.53
4:4H:213:ARG:HH22	4:4H:297:LYS:HB3	1.72	0.53
3:5A:205:ASP:HB3	3:5A:304:LYS:HD3	1.89	0.53
6:63:319:VAL:HG12	6:63:433:LEU:HD21	1.90	0.53
6:63:842:ILE:O	6:63:846:CYS:HB2	2.08	0.53
6:66:975:LYS:HA	6:66:978:LYS:HE3	1.90	0.53
4:6B:174:LYS:HE2	7:73:412:MET:HA	1.90	0.53
4:6H:77:ARG:HH22	4:6H:92:PHE:HZ	1.54	0.53
7:75:299:PHE:HE2	14:K1:128:ARG:HH21	1.56	0.53
3:7A:320:ARG:HG3	3:7A:356:ASN:HB3	1.90	0.53
4:7B:178:THR:HG22	3:7C:352:LYS:HE2	1.91	0.53
4:7J:111:GLU:HA	7:90:398:LYS:HE3	1.90	0.53
7:86:378:MET:HB3	7:86:379:LEU:HD12	1.90	0.53
3:8I:157:LEU:HB3	3:8I:166:LYS:HE2	1.91	0.53
3:8M:88:HIS:HB3	3:8M:91:GLN:HE22	1.74	0.53
4:9L:283:ALA:HB3	4:9L:288:GLU:HG2	1.90	0.53
8:A1:265:PRO:HD2	8:A1:270:PRO:HB3	1.91	0.53
10:C6:341:TYR:HB2	10:C6:390:MET:HG2	1.91	0.53
10:E4:354:ARG:HD3	10:E4:360:ALA:HA	1.91	0.53
13:J1:467:SER:HA	13:J1:470:ARG:HE	1.74	0.53
13:J7:396:GLN:HG2	13:J7:399:ALA:H	1.73	0.53
14:K4:172:ARG:HB2	14:K4:175:ILE:HG12	1.89	0.53
14:K6:191:PRO:HG3	14:K6:196:VAL:HG13	1.91	0.53
14:M4:199:ILE:HD11	14:M4:219:TYR:HB3	1.89	0.53
1:B:372:LEU:O	1:B:376:MET:HG2	2.09	0.53
1:I:375:GLN:HA	1:I:378:GLU:HG3	1.91	0.53
1:M:673:LEU:HD23	1:N:673:LEU:CB	2.39	0.53
1:R:482:GLN:HE22	1:V:481:LEU:HD21	1.72	0.53
4:1D:267:LEU:HD21	4:1D:299:MET:HB3	1.91	0.53
4:1J:11:GLN:HB2	4:1J:72:THR:HG21	1.91	0.53
4:1J:66:MET:HE1	4:1J:151:LEU:HD22	1.90	0.53
5:24:117:GLN:HE22	5:24:119:LEU:HD22	1.74	0.53
3:2A:370:LYS:HE3	9:B7:117:PRO:HG3	1.90	0.53
3:2C:9:VAL:HG12	3:2C:146:GLY:HA2	1.90	0.53
4:2H:68:LEU:HD22	4:2H:97:ALA:HB2	1.90	0.53
5:33:40:HIS:HB2	5:33:76:LEU:HB3	1.90	0.53
5:35:207:HIS:CE1	13:J1:508:CYS:H	2.26	0.53
4:3F:113:ILE:HA	4:3F:116:VAL:HG12	1.90	0.53
4:4L:22:GLU:HA	4:4L:81:PHE:CD2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4M:360:PRO:HG2	3:4M:371:VAL:HG13	1.91	0.53
4:5D:290:THR:HA	4:5D:293:MET:HE2	1.90	0.53
2:6:290:ASN:HA	2:6:293:ARG:HG2	1.89	0.53
5:62:212:LEU:HD22	6:67:601:GLU:HB3	1.90	0.53
6:66:181:LEU:HD13	6:66:571:THR:HG22	1.89	0.53
6:68:902:PRO:HG3	1:x:880:THR:HA	1.90	0.53
3:6A:99:ALA:HB3	3:6A:145:THR:HG22	1.89	0.53
4:6B:19:LYS:HE3	4:6B:22:GLU:HG3	1.91	0.53
3:6G:342:GLN:HG3	14:K2:113:GLU:HG3	1.89	0.53
4:6J:51:TYR:HB3	4:6J:59:PHE:HB3	1.89	0.53
4:8B:7:VAL:HG12	4:8B:64:ILE:HG13	1.91	0.53
3:8C:204:LEU:HD23	3:8C:231:ILE:HD12	1.91	0.53
4:8F:109:GLY:HA2	4:8F:147:MET:HE2	1.91	0.53
4:9B:147:MET:HA	4:9B:150:LEU:HB2	1.90	0.53
3:9C:244:PHE:HB2	3:9C:356:ASN:HD21	1.72	0.53
8:A1:332:THR:HG21	8:A2:234:ARG:HD3	1.90	0.53
10:C8:341:TYR:HA	10:C8:390:MET:HE3	1.90	0.53
10:D5:331:ILE:HG23	10:D5:335:LEU:HG	1.90	0.53
12:G2:188:ARG:HE	12:G2:190:ALA:HB3	1.73	0.53
12:G5:225:TRP:HZ3	12:G6:254:VAL:HB	1.74	0.53
1:I:664:ILE:HG12	3:9A:282:TYR:HB2	1.90	0.53
1:K:436:VAL:HG11	1:L:435:LYS:HZ2	1.74	0.53
4:1J:178:THR:O	4:1J:181:GLU:HG3	2.09	0.53
4:1N:228:LEU:HD12	4:1N:273:LEU:HD13	1.89	0.53
5:25:100:ASN:HD21	5:25:183:PHE:HD2	1.57	0.53
3:2A:180:ALA:HB3	3:2A:183:GLU:HB2	1.91	0.53
3:2C:192:HIS:HE1	6:66:135:LYS:HB3	1.73	0.53
3:2I:70:LEU:HD12	3:2I:99:ALA:HB2	1.90	0.53
3:2K:195:LEU:HD11	3:2K:428:LEU:HD12	1.91	0.53
3:2K:241:SER:HB3	3:2K:249:ASN:HA	1.89	0.53
4:3B:392:LYS:HA	4:3B:395:LEU:HD23	1.91	0.53
4:3F:65:LEU:HB3	4:3F:73:MET:HE1	1.89	0.53
4:3L:287:PRO:HA	4:3L:329:GLN:HE22	1.73	0.53
5:43:103:HIS:HE1	5:43:175:ASP:H	1.56	0.53
5:49:49:PRO:HA	5:49:70:PRO:HA	1.90	0.53
3:4K:313:MET:HE3	3:4K:380:ASN:HB3	1.89	0.53
4:4L:105:HIS:HA	4:4L:150:LEU:HD12	1.91	0.53
3:4M:276:ILE:HD11	3:4M:279:GLU:HG3	1.90	0.53
5:54:167:LYS:HB3	5:54:169:ILE:HG23	1.91	0.53
3:5C:73:THR:HG23	3:5C:74:VAL:HG23	1.89	0.53
4:5N:49:VAL:HG23	4:5N:50:PHE:HD2	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:61:129:VAL:HA	5:61:132:LYS:HB3	1.89	0.53
6:63:891:ARG:HH22	6:63:901:LYS:HB3	1.73	0.53
6:65:273:LEU:HB2	6:65:433:LEU:HD21	1.90	0.53
6:68:621:ARG:HH12	6:68:956:ILE:HD13	1.74	0.53
4:6N:85:PHE:HB3	4:6N:89:ASN:HD21	1.74	0.53
7:76:334:LEU:HA	7:76:337:LYS:HZ3	1.72	0.53
3:7C:12:ALA:HB3	3:7C:140:ALA:HB2	1.90	0.53
3:7I:404:PHE:HZ	4:7J:312:THR:HG21	1.72	0.53
3:7K:75:VAL:HG23	3:7K:79:ARG:HH12	1.74	0.53
4:7L:61:PRO:HG2	4:7L:84:LEU:HB3	1.90	0.53
2:8:300:VAL:HG22	13:J5:283:TRP:CG	2.44	0.53
7:94:307:LYS:HE3	7:94:321:GLU:HB2	1.90	0.53
4:9H:358:PRO:HG2	4:9H:361:LEU:HB2	1.91	0.53
4:9J:64:ILE:HG21	4:9J:120:VAL:HG12	1.91	0.53
8:A1:315:ARG:HH12	9:B3:64:GLU:HG3	1.74	0.53
10:C8:318:PRO:HA	10:C8:321:ARG:HD2	1.89	0.53
10:E1:372:LEU:HD23	10:E1:375:ILE:HD11	1.91	0.53
10:E2:341:TYR:HA	10:E2:390:MET:HE1	1.90	0.53
12:G8:265:GLY:O	12:G8:269:TRP:HB2	2.09	0.53
13:J4:351:ARG:HD3	13:J4:352:LYS:HG3	1.91	0.53
14:L1:200:PHE:HE1	14:L1:206:VAL:HG22	1.74	0.53
1:u:922:ARG:HG2	1:u:926:GLN:HE21	1.73	0.53
1:A:420:HIS:CE1	1:a:534:GLN:HE21	2.26	0.53
1:B:316:LEU:HB2	1:B:320:GLN:HB3	1.91	0.53
4:1B:6:HIS:O	4:1B:63:ALA:HA	2.08	0.53
4:1B:68:LEU:HD12	4:1B:95:THR:HB	1.90	0.53
4:1B:248:SER:HB3	4:1B:350:LYS:HZ1	1.74	0.53
3:1C:317:LEU:HG	3:1C:377:MET:HB2	1.91	0.53
4:1L:215:LEU:HB3	4:1L:217:LEU:HD23	1.91	0.53
4:1N:271:ALA:HB2	4:1N:365:VAL:HG12	1.90	0.53
3:4G:53:PHE:HB3	3:4G:61:HIS:HB3	1.89	0.53
3:4I:26:LEU:HD21	3:4I:364:PRO:HD3	1.91	0.53
5:52:31:GLU:HA	5:52:36:LEU:HD13	1.91	0.53
5:55:120:MET:HE1	5:60:168:PHE:H	1.74	0.53
5:61:42:LEU:HD21	5:61:45:SER:HB2	1.90	0.53
6:66:913:TYR:HE1	8:A3:86:GLN:HG3	1.73	0.53
6:67:617:VAL:HG22	6:67:621:ARG:HH12	1.73	0.53
6:68:913:TYR:HE1	8:A7:86:GLN:HG2	1.73	0.53
3:6E:100:ALA:HA	4:6F:252:LYS:HD3	1.90	0.53
3:6G:130:THR:HG22	7:78:406:LEU:HD22	1.89	0.53
4:7B:156:ARG:HH11	4:7B:160:PRO:HA	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7H:297:LYS:HB3	7:82:416:TRP:HZ3	1.74	0.53
7:82:331:PRO:HB2	7:82:335:ARG:HH21	1.73	0.53
7:83:308:TYR:CZ	7:83:322:PRO:HB2	2.44	0.53
7:89:294:SER:HA	7:89:317:GLN:HB3	1.91	0.53
3:9A:287:SER:HA	3:9A:373:ARG:HH21	1.72	0.53
4:9J:14:ASN:HB3	4:9J:76:VAL:HG11	1.90	0.53
10:E7:62:VAL:HG21	10:E7:305:LEU:HB3	1.90	0.53
12:I9:327:GLU:HG3	12:I9:332:THR:HG21	1.91	0.53
13:J4:269:ARG:HA	13:J4:272:LEU:HD12	1.90	0.53
14:K5:99:ILE:HG23	14:K5:105:LEU:HD11	1.91	0.53
14:K6:97:ARG:HD2	14:K6:123:SER:HB2	1.91	0.53
14:L8:175:ILE:HG23	14:L8:180:SER:HB2	1.90	0.53
14:M3:222:THR:HG23	14:M3:224:GLY:H	1.74	0.53
1:a:585:GLU:O	1:a:589:THR:HG23	2.09	0.53
1:M:656:GLN:NE2	1:N:656:GLN:HB3	2.24	0.53
1:S:392:GLU:HA	1:S:395:THR:HG22	1.91	0.53
1:T:630:ARG:HD3	1:Y:352:LYS:HE3	1.90	0.53
4:1D:379:LYS:HE2	4:1D:419:VAL:HG11	1.91	0.53
3:1K:167:LEU:HA	3:1K:200:VAL:HG23	1.89	0.53
4:1N:311:LEU:HD12	4:1N:342:VAL:HG11	1.90	0.53
1:2:893:GLN:HG3	8:A4:82:MET:HE2	1.90	0.53
5:21:180:THR:HG23	5:21:183:PHE:H	1.73	0.53
5:22:86:HIS:HE2	5:22:104:ALA:HB1	1.74	0.53
4:2B:139:LEU:HA	4:2B:145:SER:HB3	1.91	0.53
4:2B:362:LYS:HZ2	4:2B:363:MET:HE2	1.74	0.53
3:2M:53:PHE:HB3	3:2M:61:HIS:HB3	1.91	0.53
3:3A:102:ASN:HB3	3:3A:105:ARG:HB2	1.90	0.53
4:3B:226:ASN:HA	4:3B:229:VAL:HG12	1.91	0.53
4:3L:132:GLY:HA2	4:3L:162:ARG:HB3	1.89	0.53
3:3M:20:CYS:HG	3:3M:21:TRP:CD1	2.27	0.53
3:4K:9:VAL:HG22	3:4K:68:LEU:HD22	1.90	0.53
3:5C:246:GLY:H	3:5C:249:ASN:HD21	1.57	0.53
4:5N:209:ASP:HA	4:5N:212:PHE:HB2	1.90	0.53
4:6N:42:LEU:HD21	4:6N:356:ILE:HG13	1.91	0.53
4:6N:358:PRO:HG2	4:6N:361:LEU:HB2	1.89	0.53
7:73:376:GLU:O	7:73:380:TRP:HB3	2.08	0.53
3:7C:224:TYR:HD1	3:7C:227:LEU:HD12	1.74	0.53
3:7K:224:TYR:HE2	4:7L:246:LEU:HB2	1.73	0.53
3:8A:195:LEU:HD21	3:8A:428:LEU:HD21	1.91	0.53
4:8B:58:ARG:HH22	4:8B:84:LEU:HA	1.73	0.53
4:9B:260:PHE:HB2	4:9B:263:LEU:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A5:66:LEU:HA	8:A5:69:MET:HE3	1.91	0.53
10:E1:113:THR:HG23	10:E1:286:ARG:HH12	1.72	0.53
10:E5:331:ILE:HG23	10:E5:335:LEU:HG	1.91	0.53
12:F0:188:ARG:HG3	12:F0:190:ALA:H	1.74	0.53
13:J6:392:VAL:HG22	13:J6:444:ALA:HB3	1.90	0.53
1:a:677:MET:HA	1:f:677:MET:CE	2.39	0.53
1:p:911:ILE:HG21	1:p:925:MET:HE1	1.90	0.53
1:I:606:HIS:CE1	1:J:611:THR:HG21	2.44	0.53
1:T:661:ASN:HB3	3:6M:370:LYS:HE3	1.89	0.53
4:1D:215:LEU:HD21	4:1D:273:LEU:HD22	1.89	0.53
3:1E:278:ALA:HA	3:1E:369:ALA:HB2	1.90	0.53
4:1H:73:MET:HE1	4:1H:92:PHE:HB3	1.91	0.53
3:1K:167:LEU:HD21	3:1K:238:LEU:HD23	1.90	0.53
5:20:106:ASN:H	5:20:109:LEU:HB2	1.74	0.53
4:2D:267:LEU:HD13	4:2D:371:SER:HB3	1.89	0.53
4:3B:99:ASN:HD21	3:3C:352:LYS:NZ	2.07	0.53
3:3I:30:ILE:HG22	3:3I:36:MET:HB3	1.90	0.53
4:3J:113:ILE:HA	4:3J:116:VAL:HG12	1.91	0.53
4:3J:211:CYS:HA	4:3J:215:LEU:HB2	1.90	0.53
4:3L:280:GLN:HE22	9:B6:55:LEU:HD22	1.74	0.53
4:4F:198:GLU:HG2	4:4F:266:PHE:HE2	1.72	0.53
5:52:148:LEU:HD13	5:52:158:LEU:HD13	1.91	0.53
5:54:147:VAL:HB	5:54:159:ASP:HB2	1.91	0.53
3:5C:167:LEU:HD22	3:5C:200:VAL:HB	1.91	0.53
5:61:206:LEU:HD21	5:62:20:PHE:HB2	1.89	0.53
4:7F:293:MET:HE3	4:7F:367:PHE:HB2	1.90	0.53
2:8:203:PHE:HA	2:8:206:LYS:HE3	1.90	0.53
3:8E:166:LYS:HB2	3:8E:199:ASP:HB2	1.91	0.53
3:8E:237:SER:HB3	3:8E:376:CYS:HB2	1.91	0.53
8:A8:87:VAL:HG22	8:A8:93:VAL:HG22	1.91	0.53
9:B5:119:SER:HB2	9:B5:150:MET:HG3	1.90	0.53
10:D3:34:VAL:HG21	14:K1:226:PRO:HG3	1.90	0.53
10:E9:354:ARG:HD3	10:E9:360:ALA:HA	1.91	0.53
14:K1:72:VAL:HG23	14:K1:75:ARG:HH21	1.74	0.53
14:L9:204:PHE:HE2	14:L9:237:LEU:HD21	1.74	0.53
1:a:513:ARG:HG3	1:f:513:ARG:CA	2.38	0.53
1:a:574:LYS:HG2	1:a:578:ARG:HH11	1.73	0.53
1:m:812:PRO:HB2	1:m:814:PRO:HG2	1.90	0.53
1:A:601:ARG:HD2	1:p:884:PRO:HD2	1.89	0.53
4:2B:44:LEU:HD21	8:A2:365:THR:HA	1.90	0.53
4:2F:2:ARG:HB3	4:2F:131:GLN:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2I:319:TYR:HB3	3:2I:323:VAL:HG11	1.90	0.53
3:2K:422:ARG:HH12	3:2K:426:ALA:HB2	1.74	0.53
4:3B:135:ILE:HG21	4:3B:152:ILE:HD11	1.89	0.53
4:3J:405:GLU:HA	4:3J:408:PHE:HD1	1.74	0.53
5:45:212:LEU:HD13	5:46:220:LEU:HD11	1.90	0.53
3:4E:360:PRO:HG2	3:4E:371:VAL:HG13	1.91	0.53
4:4J:356:ILE:HD13	8:A6:171:SER:HB3	1.91	0.53
5:51:46:ARG:HH12	5:51:138:ILE:HG21	1.73	0.53
5:53:26:THR:HB	5:53:29:ILE:HB	1.91	0.53
5:54:140:GLU:HG3	5:54:144:PHE:H	1.73	0.53
5:55:77:ILE:HG12	5:55:81:GLU:HA	1.89	0.53
5:56:91:LEU:HB2	5:56:101:TYR:HB2	1.91	0.53
5:57:26:THR:HG22	5:57:29:ILE:HD13	1.91	0.53
4:5B:316:MET:HA	4:5B:352:SER:HB3	1.91	0.53
4:5F:211:CYS:HA	4:5F:215:LEU:HB2	1.91	0.53
3:5G:101:ASN:HD22	4:5H:256:ASN:HD21	1.57	0.53
4:5H:392:LYS:HG2	4:5H:395:LEU:HD13	1.90	0.53
6:68:141:LEU:HD21	6:68:153:VAL:HG21	1.91	0.53
6:69:949:ASN:HA	6:69:952:GLU:HG2	1.90	0.53
7:84:344:ARG:HA	7:84:353:LYS:HE3	1.91	0.53
3:8G:388:PHE:HB3	3:8G:425:LEU:HD22	1.90	0.53
4:8J:104:GLY:HA3	4:8J:146:GLY:HA3	1.91	0.53
3:8K:8:HIS:HD2	3:8K:14:ILE:HD13	1.73	0.53
7:96:272:ALA:HB3	14:M2:93:PHE:HD2	1.74	0.53
10:C0:386:LEU:HG	10:C0:390:MET:HE3	1.91	0.53
10:C6:86:LEU:HB2	10:C6:313:TYR:HD2	1.74	0.53
10:E2:354:ARG:HD3	10:E2:360:ALA:HA	1.90	0.53
10:F1:101:LEU:HD13	10:F1:390:MET:HE3	1.90	0.53
12:G7:251:TYR:HA	12:G8:251:TYR:HE2	1.73	0.53
12:G8:230:VAL:HG11	12:G8:235:LEU:HD13	1.91	0.53
14:M3:195:PRO:HG2	14:M3:197:ARG:HH21	1.73	0.53
1:f:559:GLU:O	1:f:560:GLN:C	2.51	0.53
1:I:618:ARG:CZ	1:J:617:MET:HB3	2.39	0.52
1:K:443:ASN:HD21	1:L:443:ASN:ND2	2.06	0.52
1:X:678:ASN:ND2	1:Y:395:THR:HG21	2.24	0.52
3:1E:285:GLN:HG2	3:1E:372:MET:HE2	1.92	0.52
3:1E:320:ARG:HG3	3:1E:360:PRO:HD3	1.91	0.52
3:1G:223:THR:HG22	3:1G:225:THR:H	1.74	0.52
3:1K:101:ASN:HD22	4:1L:256:ASN:HD21	1.55	0.52
4:2B:286:VAL:HG23	4:2B:321:MET:HE3	1.91	0.52
4:2J:77:ARG:HH12	4:2J:87:PRO:HD3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:37:164:MET:HE2	5:37:167:LYS:HB2	1.91	0.52
3:3E:109:THR:HG21	3:3E:411:GLU:HB2	1.91	0.52
3:4I:174:SER:HB2	3:4I:207:GLU:HG3	1.91	0.52
4:4L:381:VAL:HA	4:4L:384:GLN:HB2	1.90	0.52
3:4M:208:ALA:HB2	3:4M:304:LYS:HG2	1.91	0.52
5:50:182:GLU:HG3	5:50:186:ARG:HE	1.73	0.52
5:53:42:LEU:HA	5:53:76:LEU:HG	1.90	0.52
5:55:49:PRO:HA	5:55:70:PRO:HA	1.91	0.52
3:5M:398:MET:HE1	3:5M:403:ALA:HB3	1.91	0.52
5:61:206:LEU:HA	5:61:209:ILE:HG22	1.91	0.52
3:6E:298:PRO:HB3	3:6E:307:PRO:HD2	1.91	0.52
3:6M:437:ILE:HG22	7:77:382:ASP:HB3	1.91	0.52
7:73:279:ARG:HH12	10:D9:148:MET:H	1.57	0.52
3:7E:217:LEU:HD11	3:7E:275:ILE:HG22	1.91	0.52
4:7J:91:VAL:HG11	4:7J:116:VAL:HG22	1.91	0.52
7:84:352:VAL:HG11	14:L4:242:ILE:HG23	1.92	0.52
4:9L:110:ALA:HA	4:9L:113:ILE:HD12	1.91	0.52
10:C8:66:LEU:HD13	10:C8:69:LEU:HD12	1.91	0.52
10:C9:301:ARG:HH12	14:K4:143:ARG:HD2	1.74	0.52
10:E0:86:LEU:HD12	10:E0:319:LEU:HB3	1.91	0.52
12:G3:216:TRP:HA	12:G3:219:LEU:HD12	1.90	0.52
1:c:592:ARG:C	1:c:594:ALA:N	2.67	0.52
1:c:592:ARG:O	1:c:594:ALA:N	2.42	0.52
1:B:367:GLU:HA	1:B:370:LYS:HE3	1.91	0.52
3:1C:240:ALA:HA	3:1C:243:ARG:HD3	1.91	0.52
3:2A:88:HIS:HB3	3:2A:91:GLN:HG2	1.92	0.52
4:2B:53:GLU:HG2	8:A2:363:GLN:HB3	1.91	0.52
4:2D:229:VAL:HA	4:2D:300:MET:HE1	1.91	0.52
3:2E:9:VAL:HG12	3:2E:68:LEU:HB3	1.90	0.52
4:2J:268:ILE:HA	4:2J:367:PHE:O	2.10	0.52
5:31:88:ARG:HD3	6:66:369:PHE:HE2	1.74	0.52
4:3F:282:ARG:HG3	4:3F:284:LEU:HG	1.90	0.52
4:3J:170:PHE:HD1	4:3J:201:VAL:HG13	1.73	0.52
5:47:199:LEU:HG	5:48:202:LEU:HD21	1.91	0.52
4:4H:221:THR:HG23	4:4H:223:GLY:H	1.74	0.52
2:5:164:GLU:HB2	2:5:168:ARG:HH12	1.75	0.52
4:5N:159:TYR:HB3	4:5N:162:ARG:HG3	1.91	0.52
4:6D:383:ASP:HA	4:6D:386:THR:HG22	1.91	0.52
4:6L:117:LEU:HA	4:6L:120:VAL:HG12	1.92	0.52
7:73:323:PHE:HB2	7:73:394:TYR:HB2	1.90	0.52
4:7H:41:ASP:HB3	1:p:944:GLN:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:84:328:PRO:HG2	7:84:333:LEU:HD21	1.89	0.52
4:8F:133:PHE:HZ	4:8F:159:TYR:HD2	1.56	0.52
4:8H:87:PRO:HA	4:8H:90:PHE:HD2	1.74	0.52
4:8L:113:ILE:HG13	4:8L:150:LEU:HD22	1.91	0.52
4:9D:68:LEU:HD12	4:9D:143:THR:HB	1.92	0.52
4:9F:199:VAL:HG23	4:9F:264:HIS:CE1	2.44	0.52
10:C9:294:SER:O	10:C9:298:GLU:HB2	2.09	0.52
10:D2:316:CYS:O	10:D2:320:LYS:HB2	2.08	0.52
10:D7:331:ILE:HA	10:D7:335:LEU:HD23	1.91	0.52
10:E6:86:LEU:HD12	10:E6:319:LEU:HB3	1.91	0.52
10:E6:284:LEU:HD12	10:E6:382:HIS:HB3	1.90	0.52
10:F3:106:PRO:HB3	10:F3:296:MET:HE1	1.90	0.52
1:a:603:ARG:HB3	1:f:604:ILE:CG2	2.39	0.52
1:a:610:VAL:CG1	1:f:611:THR:HA	2.39	0.52
1:p:869:ARG:HG3	1:p:870:GLY:H	1.73	0.52
3:1A:388:PHE:HZ	3:1A:425:LEU:HD22	1.74	0.52
3:1C:75:VAL:HG13	3:1C:92:LEU:HD12	1.92	0.52
4:1D:274:THR:HG21	4:1D:282:ARG:HD3	1.91	0.52
4:1F:20:PHE:HA	4:1F:230:SER:HB2	1.91	0.52
3:2C:51:THR:HG23	3:2C:52:PHE:HD2	1.74	0.52
3:2E:3:GLU:HA	3:2E:51:THR:HA	1.91	0.52
3:2E:160:ASP:HA	6:65:558:LYS:HE3	1.92	0.52
3:2M:88:HIS:CG	3:3M:283:HIS:HB2	2.43	0.52
4:4B:162:ARG:HH21	6:67:777:ARG:HE	1.57	0.52
3:4E:280:LYS:HD3	3:4E:283:HIS:CG	2.43	0.52
3:4G:102:ASN:HB3	3:4G:105:ARG:HG3	1.91	0.52
3:4K:398:MET:HE2	4:4L:345:ILE:HG23	1.89	0.52
5:56:148:LEU:HD11	5:56:156:ALA:HB1	1.89	0.52
4:5H:248:SER:HA	4:5H:252:LYS:HE3	1.90	0.52
6:64:406:ARG:HH22	12:F9:232:ASP:HA	1.74	0.52
6:66:620:ILE:HG12	6:66:845:VAL:HG21	1.91	0.52
6:67:636:GLU:HA	6:67:639:LEU:HB2	1.90	0.52
3:6M:76:ASP:HA	3:6M:79:ARG:HD3	1.90	0.52
3:6M:137:MET:HE3	3:6M:139:ASN:HB3	1.91	0.52
4:7D:282:ARG:HH12	4:7D:284:LEU:HB3	1.74	0.52
4:7F:34:GLY:HA3	4:7F:58:ARG:HD3	1.90	0.52
3:8A:75:VAL:HG11	3:8A:94:SER:HB3	1.92	0.52
3:8A:88:HIS:CE1	3:8A:90:GLU:HG3	2.44	0.52
3:8K:336:LYS:HD2	14:L9:112:THR:HG22	1.91	0.52
3:9A:310:GLY:HA3	3:9A:383:ALA:HB2	1.91	0.52
4:9D:46:ARG:HH22	4:9D:243:PRO:HB3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9F:130:LEU:H	4:9F:162:ARG:HH21	1.56	0.52
3:9I:5:ILE:HG23	3:9I:125:LEU:HD23	1.91	0.52
3:9I:9:VAL:HG12	3:9I:146:GLY:HA2	1.91	0.52
3:9I:14:ILE:HD13	3:9I:69:ASP:HB2	1.91	0.52
4:9L:117:LEU:HA	4:9L:120:VAL:HG12	1.90	0.52
10:D6:345:MET:HE2	10:D6:369:SER:HB2	1.91	0.52
10:E6:41:ALA:O	10:E6:45:ASN:HB2	2.10	0.52
12:G5:221:MET:HG3	12:G5:224:ARG:HH22	1.75	0.52
12:G7:199:TRP:HH2	12:G8:224:ARG:HB3	1.73	0.52
13:J3:284:ARG:HB3	13:J3:322:LYS:HD3	1.92	0.52
14:L0:228:ALA:HB3	14:L0:233:LEU:HG	1.91	0.52
1:g:787:SER:HB2	1:g:790:LEU:HB2	1.90	0.52
1:K:471:LEU:HG	1:K:475:LYS:HE2	1.91	0.52
1:N:482:GLN:HA	1:N:485:LEU:HD23	1.92	0.52
1:Y:585:GLU:O	1:Y:589:THR:HG23	2.10	0.52
1:Y:614:LEU:HB3	1:Y:615:ARG:HH21	1.74	0.52
2:14:296:ASP:HB2	13:J6:286:LEU:HD22	1.92	0.52
3:1A:274:PRO:HD3	3:1A:375:VAL:H	1.74	0.52
4:1B:215:LEU:HG	4:1B:217:LEU:HD23	1.91	0.52
4:1N:91:VAL:HG11	4:1N:116:VAL:HG22	1.91	0.52
4:2F:179:VAL:HG12	3:2G:258:ASN:HD22	1.74	0.52
3:2I:213:CYS:HA	3:2I:217:LEU:HB2	1.90	0.52
3:2K:101:ASN:HD22	3:2K:143:GLY:HA2	1.74	0.52
3:3C:195:LEU:HA	3:3C:266:HIS:HE1	1.73	0.52
4:3J:173:PRO:HD2	4:3J:205:GLU:HG3	1.92	0.52
3:4I:200:VAL:HG11	3:4I:255:PHE:HE2	1.73	0.52
6:66:131:ARG:HH12	12:I9:335:ILE:HG12	1.74	0.52
3:6I:72:PRO:O	3:6I:76:ASP:HB2	2.08	0.52
3:6M:51:THR:HG21	3:6M:243:ARG:HA	1.90	0.52
4:7B:308:GLY:HA3	4:7B:372:THR:HB	1.91	0.52
4:7H:138:SER:HB2	4:7H:144:GLY:HA3	1.92	0.52
3:7I:88:HIS:HE1	3:8I:284:GLU:HB2	1.75	0.52
3:8A:292:THR:HG21	3:8A:331:ALA:HB1	1.90	0.52
4:8F:274:THR:HB	4:8F:282:ARG:HH11	1.74	0.52
4:8H:61:PRO:HD3	4:8H:84:LEU:HG	1.92	0.52
4:8H:107:THR:HB	14:M2:99:ILE:HG23	1.92	0.52
3:8M:5:ILE:HD12	3:8M:125:LEU:HG	1.90	0.52
2:9:290:ASN:HA	2:9:293:ARG:HG2	1.92	0.52
13:J4:339:ARG:HD2	13:J4:366:ARG:HH12	1.73	0.52
1:c:579:LEU:O	1:c:580:GLU:C	2.52	0.52
1:x:903:ARG:HH22	1:x:931:ARG:HH22	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:334:LEU:HD22	1:U:331:GLU:HG3	1.91	0.52
1:Y:513:ARG:NH2	1:c:512:LYS:HD2	2.24	0.52
4:1B:316:MET:HE2	4:1B:366:THR:HB	1.92	0.52
4:1L:235:GLY:HA3	4:1L:366:THR:HG21	1.90	0.52
3:2E:195:LEU:HD13	3:2E:264:ARG:HH21	1.73	0.52
5:31:182:GLU:O	5:31:186:ARG:HG3	2.10	0.52
5:32:91:LEU:HD12	5:32:101:TYR:HB2	1.91	0.52
5:37:195:LEU:HA	5:37:198:LYS:HG2	1.91	0.52
4:3B:65:LEU:HB3	4:3B:73:MET:HE1	1.90	0.52
4:3F:215:LEU:HD21	4:3F:273:LEU:HD22	1.89	0.52
3:3I:335:ILE:HG23	3:3I:341:ILE:HD13	1.91	0.52
5:44:45:SER:HA	5:44:73:VAL:O	2.09	0.52
3:5C:141:VAL:HA	3:5C:147:SER:HB3	1.92	0.52
3:5C:168:ASN:HD22	3:5C:198:THR:HG21	1.74	0.52
3:5I:180:ALA:HB3	3:5I:183:GLU:HB2	1.92	0.52
4:5J:154:LYS:HD3	7:76:286:TRP:HE1	1.75	0.52
4:5L:65:LEU:HB3	4:5L:73:MET:HE1	1.92	0.52
2:6:175:TYR:HD2	2:6:179:MET:HE1	1.75	0.52
2:6:183:ARG:HA	2:6:186:HIS:CD2	2.45	0.52
5:62:49:PRO:HA	5:62:70:PRO:HA	1.92	0.52
6:67:407:LEU:HD22	6:67:411:HIS:HE1	1.75	0.52
4:7L:235:GLY:HA2	4:7L:238:CYS:HB3	1.92	0.52
7:86:278:VAL:HG11	14:L7:126:ILE:HD12	1.91	0.52
3:8A:91:GLN:NE2	3:8A:121:ARG:HH22	2.08	0.52
3:8C:180:ALA:HB3	3:8C:183:GLU:HB2	1.90	0.52
4:8J:253:LEU:O	4:8J:257:LEU:CB	2.56	0.52
4:8L:68:LEU:HB3	4:8L:112:LEU:HD22	1.91	0.52
3:9A:88:HIS:HB3	3:9A:91:GLN:HB2	1.91	0.52
3:9C:249:ASN:HD21	3:9C:356:ASN:HA	1.75	0.52
3:9I:313:MET:HG3	3:9I:380:ASN:HB3	1.92	0.52
10:D9:331:ILE:HD12	10:D9:335:LEU:HG	1.90	0.52
10:E6:376:ILE:HG13	10:E6:381:MET:HB2	1.91	0.52
10:F2:295:GLN:HA	10:F2:298:GLU:HG3	1.91	0.52
12:F6:222:ASP:HA	12:F6:225:TRP:HD1	1.73	0.52
12:G4:200:LEU:HA	12:G4:203:VAL:HG12	1.91	0.52
13:J2:405:VAL:HG12	13:J2:464:PHE:HE2	1.74	0.52
14:M3:218:LYS:HE2	14:M3:241:VAL:HG22	1.92	0.52
1:t:878:PRO:HB2	1:t:881:ALA:HA	1.91	0.52
1:E:423:ARG:NH2	1:p:877:LEU:H	2.07	0.52
1:Y:601:ARG:CG	1:s:884:PRO:HG3	2.40	0.52
3:1E:215:ARG:HH12	3:1E:299:ALA:HB1	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1F:220:PRO:HD2	3:1G:326:LYS:NZ	2.24	0.52
3:1G:185:TYR:CZ	3:1G:398:MET:HE3	2.45	0.52
3:1G:250:VAL:HA	3:1G:254:GLU:HG3	1.90	0.52
3:1I:259:LEU:HD21	3:1I:316:CYS:HB2	1.92	0.52
3:1M:188:VAL:HG23	3:1M:425:LEU:HD13	1.90	0.52
4:2B:149:THR:HA	4:2B:152:ILE:HG22	1.91	0.52
3:2E:170:CYS:HB2	3:2E:172:TRP:CZ3	2.45	0.52
5:36:52:ILE:HA	5:36:148:LEU:O	2.09	0.52
4:3D:215:LEU:HD11	4:3D:228:LEU:HD21	1.90	0.52
4:3J:215:LEU:HD11	4:3J:273:LEU:HD22	1.90	0.52
2:5:284:LEU:HD11	2:6:284:LEU:HB3	1.90	0.52
3:5G:70:LEU:HD12	3:5G:99:ALA:HB2	1.92	0.52
3:5I:301:MET:HE1	3:5I:377:MET:HE1	1.91	0.52
4:5J:100:ASN:HD22	4:5J:103:LYS:HE2	1.74	0.52
4:6F:113:ILE:HA	4:6F:116:VAL:HG12	1.92	0.52
4:6H:380:ARG:HB3	7:75:312:SER:H	1.75	0.52
7:72:376:GLU:O	7:72:380:TRP:CB	2.57	0.52
4:7H:185:ALA:HB3	4:7H:381:VAL:HG11	1.91	0.52
3:7M:360:PRO:HG2	3:7M:371:VAL:HG23	1.92	0.52
4:8D:171:PRO:HD2	4:8D:380:ARG:HH22	1.75	0.52
4:8F:253:LEU:O	4:8F:257:LEU:HB2	2.09	0.52
4:8J:244:GLY:HA2	4:8J:355:ASP:HB2	1.92	0.52
3:8K:286:LEU:HD21	3:8K:371:VAL:HG13	1.92	0.52
3:8M:77:GLU:HA	3:8M:80:THR:HG22	1.91	0.52
7:94:401:ILE:HD11	14:M6:106:TYR:HB2	1.90	0.52
7:97:280:PRO:HB3	14:M5:129:PRO:HG2	1.92	0.52
7:97:405:VAL:HG11	3:9C:336:LYS:HD2	1.92	0.52
3:9I:68:LEU:HG	3:9I:149:LEU:HD23	1.89	0.52
8:A8:190:THR:HG21	8:A8:217:MET:HB2	1.92	0.52
9:B5:118:LEU:HD12	9:B5:146:VAL:HG22	1.90	0.52
10:C8:401:MET:HG3	10:C8:407:CYS:HB2	1.92	0.52
10:D8:307:MET:HE1	10:D8:400:LEU:HD13	1.91	0.52
10:E0:113:THR:HG23	10:E0:286:ARG:HH22	1.74	0.52
14:M7:148:ILE:HD11	14:M7:173:PRO:HG3	1.92	0.52
1:g:758:ASN:HD22	1:g:829:PRO:HD3	1.74	0.52
1:Y:411:LYS:HB3	1:c:411:LYS:NZ	2.25	0.52
1:Y:572:ARG:HB3	1:c:572:ARG:HB3	1.91	0.52
2:15:225:ARG:HA	2:15:228:GLU:HG2	1.91	0.52
4:1N:309:ARG:HE	4:1N:342:VAL:HA	1.74	0.52
5:24:86:HIS:CE1	5:24:88:ARG:HG3	2.45	0.52
5:26:40:HIS:HD1	5:26:78:LEU:HB2	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:26:51:GLU:HB2	5:26:147:VAL:HG12	1.92	0.52
5:29:222:LEU:HD23	3:2K:401:LYS:HA	1.92	0.52
3:2E:107:HIS:HD1	3:2E:152:LEU:HB2	1.75	0.52
3:2I:179:THR:HG21	4:2J:246:LEU:HD21	1.92	0.52
3:3C:88:HIS:ND1	3:4C:282:TYR:HB3	2.25	0.52
4:3J:97:ALA:HB3	4:3J:143:THR:HG22	1.91	0.52
5:56:119:LEU:HB3	5:56:121:ILE:HG12	1.91	0.52
5:57:91:LEU:HD11	5:57:158:LEU:HD22	1.91	0.52
3:5K:136:LEU:HD23	3:5K:167:LEU:HB2	1.92	0.52
5:61:77:ILE:HD13	5:61:81:GLU:HA	1.90	0.52
6:63:895:ARG:HH12	9:B2:536:GLU:HG2	1.74	0.52
4:6F:117:LEU:HA	4:6F:120:VAL:HG12	1.90	0.52
7:77:347:ILE:HG21	7:77:350:ARG:HB2	1.92	0.52
4:7D:42:LEU:HD11	1:k:753:LEU:HD22	1.92	0.52
3:7M:414:GLU:HA	14:M1:151:PRO:HD2	1.91	0.52
2:8:166:ALA:HA	2:8:169:HIS:CD2	2.44	0.52
7:89:334:LEU:HD21	7:89:347:ILE:HG13	1.90	0.52
3:8I:336:LYS:HG2	14:L5:112:THR:HG22	1.92	0.52
8:A1:54:THR:HG23	8:A1:56:LEU:H	1.75	0.52
8:A6:310:LEU:HD11	8:A6:385:VAL:HA	1.92	0.52
10:C6:101:LEU:HD22	10:C6:338:PRO:HB3	1.92	0.52
10:C6:338:PRO:HB2	10:C6:341:TYR:HB3	1.91	0.52
10:D9:284:LEU:HB3	10:D9:351:ARG:HH12	1.74	0.52
12:G3:220:PRO:HD2	12:G3:223:LEU:HD13	1.92	0.52
12:G7:241:LEU:HD13	12:G7:262:LEU:HB3	1.91	0.52
1:a:614:LEU:HD21	1:a:618:ARG:HH11	1.74	0.52
1:f:579:LEU:O	1:f:582:LEU:N	2.43	0.52
1:s:897:LEU:HD22	1:s:935:VAL:HG23	1.90	0.52
1:G:307:PRO:HB2	1:S:360:ARG:HH22	1.75	0.52
2:10:226:VAL:HG11	2:9:225:ARG:HH22	1.75	0.52
4:1B:73:MET:HB3	4:1B:77:ARG:HH21	1.75	0.52
4:1D:256:ASN:HD22	4:1D:350:LYS:HG3	1.75	0.52
4:1J:167:PHE:HE2	4:1J:233:MET:HG3	1.74	0.52
4:1N:121:ARG:O	4:1N:125:GLU:HB2	2.09	0.52
5:20:50:PHE:HB2	5:20:71:ILE:HD12	1.91	0.52
5:29:120:MET:HA	6:68:339:PRO:HB2	1.91	0.52
3:2A:171:SER:HB2	15:2A:501:GTP:C2	2.44	0.52
4:3B:100:ASN:HD22	4:3B:103:LYS:HD3	1.74	0.52
3:3G:269:LEU:HD23	3:3G:303:ALA:HB3	1.92	0.52
4:3H:102:ALA:HB2	4:3H:403:MET:HE2	1.92	0.52
5:48:114:GLN:HG3	5:48:119:LEU:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4H:317:PHE:HZ	4:4H:330:MET:HE3	1.75	0.52
3:5A:100:ALA:HA	4:5B:252:LYS:HE2	1.92	0.52
3:6A:119:LEU:HA	3:6A:122:ILE:HG12	1.91	0.52
3:6I:223:THR:HG23	3:6I:225:THR:H	1.75	0.52
4:6L:330:MET:HE3	4:6L:351:SER:HB3	1.90	0.52
7:72:327:ASN:H	7:72:391:TYR:HD1	1.58	0.52
7:78:315:ILE:HG13	7:78:399:THR:HG21	1.92	0.52
4:7B:316:MET:O	4:7B:365:VAL:HA	2.09	0.52
7:89:279:ARG:HH11	10:E8:146:ALA:HA	1.73	0.52
4:8J:135:ILE:HD12	4:8J:151:LEU:HD22	1.91	0.52
4:8J:330:MET:HE2	4:8J:351:SER:HB3	1.91	0.52
3:8M:144:GLY:HA2	3:8M:186:ASN:HD21	1.74	0.52
3:9A:227:LEU:HD13	3:9A:230:LEU:HD21	1.91	0.52
4:9B:253:LEU:O	4:9B:257:LEU:HB2	2.09	0.52
4:9F:68:LEU:HB3	4:9F:96:GLY:HA2	1.90	0.52
10:D8:301:ARG:HH12	14:K0:143:ARG:CZ	2.23	0.52
12:F0:233:ARG:HH21	12:F0:236:LEU:HG	1.73	0.52
10:F2:288:PRO:HB2	10:F2:293:MET:HE3	1.90	0.52
10:F3:311:LYS:HD3	10:F3:403:GLN:HE21	1.74	0.52
12:G2:289:ILE:HG23	12:G2:290:LYS:HG3	1.90	0.52
14:M3:178:MET:HA	14:M3:181:LEU:HB2	1.91	0.52
1:P:662:ASP:O	1:P:666:VAL:HG23	2.10	0.52
3:1C:176:GLN:HB3	4:1D:331:LEU:HD21	1.91	0.52
4:1L:32:PRO:HA	4:1L:84:LEU:HD11	1.92	0.52
5:21:77:ILE:HD12	5:21:84:PRO:HB3	1.92	0.52
5:21:217:SER:HB3	4:2H:261:PRO:HG3	1.92	0.52
3:2A:179:THR:HB	4:2B:351:SER:H	1.74	0.52
3:2M:101:ASN:HA	3:2M:144:GLY:H	1.74	0.52
5:32:74:LYS:O	5:32:89:VAL:HA	2.10	0.52
5:33:161:ILE:HG22	5:33:163:SER:H	1.74	0.52
4:3B:211:CYS:HA	4:3B:215:LEU:HD13	1.92	0.52
3:3C:207:GLU:HA	3:3C:210:TYR:HD2	1.75	0.52
3:3G:188:VAL:HG13	3:3G:425:LEU:HD22	1.91	0.52
3:4A:313:MET:H	3:4A:381:SER:HA	1.74	0.52
3:4E:224:TYR:HD1	3:4E:227:LEU:HD12	1.75	0.52
4:4F:51:TYR:HB3	4:4F:59:PHE:HB3	1.92	0.52
5:53:40:HIS:CE1	5:53:88:ARG:HB2	2.45	0.52
5:53:113:MET:HA	5:53:116:ARG:HE	1.75	0.52
5:54:139:LYS:HG3	5:54:140:GLU:H	1.75	0.52
3:5A:103:PHE:H	3:5A:408:TYR:HE1	1.58	0.52
3:5A:419:SER:HB2	10:C9:41:ALA:HB1	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5B:40:SER:HB3	4:5B:43:GLN:HB2	1.92	0.52
5:61:209:ILE:HD13	5:62:224:LEU:HD21	1.90	0.52
6:66:485:LYS:HD3	6:66:487:TYR:CE1	2.45	0.52
4:6D:396:HIS:HA	4:6D:399:THR:HG22	1.91	0.52
3:7G:138:PHE:HE1	3:7G:235:ILE:HG21	1.74	0.52
7:86:350:ARG:HB3	7:86:352:VAL:HG22	1.91	0.52
7:93:353:LYS:HB2	14:M3:243:GLN:HB3	1.92	0.52
3:9C:119:LEU:HD23	3:9C:122:ILE:HD12	1.92	0.52
4:9D:3:GLU:H	4:9D:131:GLN:HB2	1.74	0.52
3:9K:166:LYS:HE3	3:9K:197:HIS:HB3	1.91	0.52
4:9L:286:VAL:HG11	4:9L:326:VAL:HA	1.90	0.52
8:A1:258:VAL:HG23	8:A1:259:THR:HG23	1.92	0.52
8:A7:258:VAL:HG23	8:A7:259:THR:HG23	1.91	0.52
10:D3:354:ARG:HD3	10:D3:360:ALA:HA	1.92	0.52
10:D7:51:TYR:HB3	10:D7:54:HIS:CD2	2.45	0.52
10:F3:107:ILE:HD11	10:F3:280:VAL:HA	1.92	0.52
12:G5:246:PRO:HD2	12:G5:249:LEU:HB2	1.92	0.52
12:I7:73:ASN:HA	12:I7:76:ILE:HG12	1.92	0.52
14:K8:175:ILE:HD11	14:K8:184:GLN:HG3	1.92	0.52
1:L:351:GLU:O	1:L:355:ARG:HG3	2.10	0.52
1:P:676:GLU:O	1:P:680:LEU:HG	2.10	0.52
1:R:585:GLU:HA	1:R:588:THR:HG22	1.91	0.52
4:1B:7:VAL:HG22	4:1B:64:ILE:HB	1.92	0.52
3:1C:205:ASP:HB2	3:1C:304:LYS:H	1.74	0.52
3:1K:325:PRO:HA	3:1K:328:VAL:HG12	1.91	0.52
3:1M:75:VAL:HG22	3:1M:92:LEU:HD23	1.92	0.52
3:1M:288:VAL:HG22	3:1M:373:ARG:HD2	1.92	0.52
4:2D:391:ARG:HD3	3:2E:346:TRP:HB3	1.92	0.52
4:2L:12:CYS:HA	17:2L:501:GDP:HN22	1.74	0.52
3:2M:390:ARG:HH12	3:2M:394:LYS:HB2	1.75	0.52
5:30:214:LYS:HG2	5:30:221:LEU:HD11	1.92	0.52
5:37:212:LEU:HD13	5:38:220:LEU:HD11	1.91	0.52
5:38:72:ARG:NH1	5:38:74:LYS:HG3	2.25	0.52
5:38:184:THR:HG22	5:38:188:MET:HE1	1.92	0.52
4:3D:207:LEU:HB3	4:3D:225:LEU:HG	1.92	0.52
3:3E:26:LEU:HD23	8:A1:241:LEU:HD23	1.92	0.52
3:3E:180:ALA:HB3	3:3E:183:GLU:HG3	1.92	0.52
3:3M:154:LEU:HB3	3:3M:197:HIS:HB3	1.91	0.52
5:43:216:LYS:HZ1	5:44:220:LEU:HD13	1.74	0.52
5:46:169:ILE:HG21	5:47:169:ILE:HG21	1.92	0.52
4:4L:207:LEU:HB3	4:4L:225:LEU:HD22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:68:457:ILE:O	6:68:461:ARG:HG3	2.09	0.52
4:6B:262:ARG:HH12	14:L1:138:THR:HG23	1.75	0.52
4:6D:280:GLN:HG2	4:6D:281:TYR:HD2	1.74	0.52
4:6F:380:ARG:HA	7:71:311:SER:HA	1.91	0.52
4:6H:383:ASP:HA	4:6H:386:THR:HG22	1.92	0.52
7:79:254:ARG:HB3	7:79:258:GLU:HG3	1.91	0.52
4:7F:210:ILE:HD11	4:7F:228:LEU:HD21	1.91	0.52
4:7L:306:ARG:HB3	7:84:317:GLN:HG2	1.91	0.52
7:89:286:TRP:CE3	7:89:293:ILE:HG13	2.45	0.52
3:8C:274:PRO:HG3	3:8C:374:ALA:HA	1.92	0.52
4:8F:55:THR:HG23	4:9F:283:ALA:HA	1.91	0.52
3:8G:319:TYR:HB3	3:8G:323:VAL:HG11	1.92	0.52
4:8L:29:GLY:HA3	4:8L:38:GLY:HA2	1.91	0.52
4:8L:273:LEU:H	4:8L:292:GLN:HE22	1.58	0.52
2:9:268:THR:HA	2:9:271:LYS:HE3	1.91	0.52
7:92:398:LYS:HB3	7:92:415:GLY:HA3	1.92	0.52
7:96:317:GLN:HG3	4:9H:307:HIS:HA	1.91	0.52
4:9F:358:PRO:HG2	4:9F:361:LEU:HB3	1.92	0.52
8:A3:182:LEU:HD21	8:A3:215:LEU:HD11	1.91	0.52
10:C7:347:GLU:HA	10:C7:350:LYS:HE2	1.91	0.52
10:E5:322:GLU:HG2	10:E5:326:LYS:NZ	2.25	0.52
12:G4:246:PRO:HD3	12:G4:266:PRO:HB3	1.91	0.52
14:K0:143:ARG:HB3	14:K0:144:PHE:CD2	2.45	0.52
1:a:628:VAL:HG23	1:f:628:VAL:HG22	1.92	0.52
1:i:797:VAL:HG12	1:i:798:ARG:HD3	1.92	0.52
4:1N:68:LEU:HA	4:1N:93:GLY:HA3	1.92	0.51
5:23:140:GLU:HG3	5:23:143:CYS:HB2	1.92	0.51
5:28:66:GLY:HA3	6:68:346:ARG:HH22	1.74	0.51
3:2E:136:LEU:HD23	3:2E:235:ILE:HD11	1.92	0.51
3:3A:180:ALA:HB3	3:3A:183:GLU:HG2	1.92	0.51
4:3B:113:ILE:HA	4:3B:116:VAL:HG12	1.92	0.51
3:3E:238:LEU:HD23	3:3E:318:MET:HG3	1.92	0.51
4:3F:259:PRO:HG2	4:3F:311:LEU:HD23	1.90	0.51
4:3L:244:GLY:HA3	4:3L:354:CYS:HA	1.92	0.51
3:3M:36:MET:HE2	3:3M:61:HIS:CE1	2.45	0.51
3:4A:325:PRO:HA	3:4A:328:VAL:HG22	1.90	0.51
3:4C:204:LEU:HD22	3:4C:231:ILE:HG12	1.90	0.51
3:4C:408:TYR:HB3	3:4C:413:MET:HG3	1.92	0.51
4:4L:135:ILE:HD11	4:4L:166:THR:HG23	1.91	0.51
5:58:118:LYS:HB2	5:61:167:LYS:HD3	1.90	0.51
5:59:91:LEU:HB2	5:59:101:TYR:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5A:288:VAL:HA	3:5A:291:ILE:HG22	1.92	0.51
3:6C:259:LEU:HD21	3:6C:316:CYS:HB2	1.92	0.51
4:6F:229:VAL:HG12	4:6F:233:MET:HE2	1.91	0.51
3:6K:191:THR:HA	3:6K:194:LEU:HB3	1.91	0.51
4:7B:391:ARG:HG2	3:7C:346:TRP:CG	2.45	0.51
3:7C:388:PHE:HB3	3:7C:425:LEU:HD11	1.92	0.51
4:7D:253:LEU:HD21	4:7D:368:VAL:HG11	1.92	0.51
4:7F:214:THR:HG23	4:7F:297:LYS:HE3	1.92	0.51
7:90:272:ALA:HB1	14:L9:93:PHE:HB2	1.91	0.51
3:9C:311:LYS:HE3	3:9C:344:VAL:HA	1.91	0.51
8:A6:240:PRO:HB3	9:B2:19:ALA:HB1	1.92	0.51
10:C0:316:CYS:O	10:C0:320:LYS:HB3	2.10	0.51
10:C7:365:ASN:HB3	10:C7:368:ASP:HB2	1.92	0.51
12:F0:195:PRO:HA	12:F0:198:LYS:HG2	1.91	0.51
12:G1:225:TRP:HZ2	12:G2:230:VAL:HB	1.75	0.51
14:L5:183:GLN:HA	14:L5:186:THR:HG22	1.92	0.51
1:f:588:THR:HA	1:f:591:ARG:NE	2.26	0.51
1:N:481:LEU:HD12	1:N:484:GLN:HE21	1.75	0.51
1:Y:575:LEU:HD13	1:c:576:SER:HB2	1.92	0.51
3:1G:2:ARG:HG2	3:1G:242:LEU:HD22	1.92	0.51
4:1J:284:LEU:HB2	4:1J:362:LYS:HE3	1.91	0.51
4:1N:240:LEU:HD21	4:1N:250:LEU:HG	1.93	0.51
1:2:897:LEU:HD22	1:2:935:VAL:HG13	1.93	0.51
5:26:46:ARG:O	5:26:72:ARG:HA	2.10	0.51
5:26:112:GLN:HG2	5:26:116:ARG:HH21	1.75	0.51
5:27:91:LEU:HD11	5:27:158:LEU:HD22	1.91	0.51
3:2M:248:LEU:HB2	3:2M:355:ILE:H	1.75	0.51
3:2M:387:VAL:HG22	3:2M:391:MET:HE2	1.92	0.51
5:39:200:ALA:HA	5:39:203:GLN:HG3	1.91	0.51
4:3F:155:VAL:HA	4:3F:158:GLU:HB2	1.92	0.51
4:3F:178:THR:HG23	4:3F:181:GLU:HG3	1.91	0.51
4:3H:391:ARG:HD3	3:3I:346:TRP:HB3	1.92	0.51
3:3K:66:VAL:HG21	3:3K:122:ILE:HG12	1.91	0.51
5:57:171:LEU:HD12	5:57:172:LEU:HB2	1.92	0.51
3:5C:191:THR:HG21	3:5C:425:LEU:HD13	1.92	0.51
4:5D:10:GLY:HA2	4:5D:143:THR:HG23	1.91	0.51
3:5G:3:GLU:HA	3:5G:51:THR:HA	1.92	0.51
5:61:93:SER:HB3	5:61:99:LEU:HB3	1.92	0.51
6:69:306:VAL:HG13	6:69:459:VAL:HG13	1.93	0.51
3:7C:265:ILE:HG22	3:7C:380:ASN:HD21	1.74	0.51
4:7F:112:LEU:HD23	4:7F:147:MET:HE1	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7J:163:ILE:HD11	4:7J:250:LEU:HG	1.91	0.51
4:7L:191:GLN:HB3	4:7L:195:ASN:HD22	1.75	0.51
7:87:268:TRP:CZ2	7:87:392:ARG:HB2	2.45	0.51
4:8B:116:VAL:HG11	4:8B:151:LEU:HD21	1.91	0.51
3:9A:408:TYR:HB3	3:9A:413:MET:HE3	1.91	0.51
3:9I:17:GLY:HA2	3:9I:20:CYS:HB3	1.92	0.51
3:9I:273:ALA:HA	3:9I:275:ILE:HG22	1.92	0.51
10:E2:355:THR:HG23	10:E2:357:ALA:H	1.76	0.51
12:F6:195:PRO:HA	12:F6:198:LYS:HG2	1.91	0.51
12:H5:66:ASN:HA	12:H5:69:LEU:HB2	1.92	0.51
13:J1:366:ARG:HH22	13:J1:369:LEU:HD23	1.75	0.51
1:f:539:ALA:O	1:f:540:SER:C	2.53	0.51
1:h:757:LEU:O	1:h:758:ASN:ND2	2.42	0.51
1:l:747:ALA:HB2	1:l:822:PRO:HB3	1.92	0.51
1:p:872:ALA:H	1:p:893:GLN:HE22	1.58	0.51
1:C:368:GLN:HG2	1:C:372:LEU:HD23	1.91	0.51
1:Z:342:MET:HE2	1:d:342:MET:HE2	1.93	0.51
4:1B:170:PHE:HE2	4:1B:201:VAL:HA	1.75	0.51
3:1K:315:CYS:HB3	3:1K:377:MET:HE1	1.91	0.51
3:1M:209:ILE:HA	3:1M:212:ILE:HG22	1.91	0.51
5:25:155:LYS:HZ1	6:69:363:PRO:HG2	1.75	0.51
5:29:107:GLU:O	5:29:111:ARG:HB2	2.11	0.51
3:2A:409:VAL:HA	3:2A:413:MET:HB2	1.92	0.51
3:2C:3:GLU:HA	3:2C:51:THR:HA	1.92	0.51
3:2C:423:GLU:HG3	6:66:133:ARG:HH12	1.74	0.51
4:2F:86:ARG:HG3	4:2F:89:ASN:ND2	2.25	0.51
5:31:212:LEU:HD23	5:31:215:LEU:HD21	1.91	0.51
5:36:158:LEU:HB3	5:36:174:LEU:HB2	1.92	0.51
3:3C:62:VAL:HG22	3:4C:282:TYR:HA	1.90	0.51
3:3G:320:ARG:HG3	3:3G:360:PRO:HD3	1.91	0.51
4:3J:290:THR:HG21	4:3J:329:GLN:HB3	1.91	0.51
3:3M:195:LEU:HD21	3:3M:428:LEU:HD12	1.93	0.51
5:43:221:LEU:O	5:43:225:GLN:HB2	2.10	0.51
5:49:192:TYR:HD2	5:50:97:LEU:HD13	1.74	0.51
3:4C:222:PRO:HD2	4:4D:324:LYS:HG2	1.92	0.51
3:4G:223:THR:HG23	3:4G:225:THR:H	1.76	0.51
5:59:144:PHE:HE1	5:59:171:LEU:HD12	1.76	0.51
3:5G:56:THR:HA	3:6G:285:GLN:HB2	1.91	0.51
5:62:33:ASP:HB3	5:62:36:LEU:HB2	1.91	0.51
6:68:602:ARG:O	6:68:606:GLN:HB3	2.10	0.51
3:6E:397:LEU:HD13	14:K2:225:GLU:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6J:6:HIS:CE1	4:6J:8:GLN:HE21	2.28	0.51
4:7H:175:VAL:HB	7:82:412:MET:HE1	1.92	0.51
3:7K:16:ILE:HD11	3:7K:231:ILE:HG21	1.92	0.51
3:7M:107:HIS:CD2	3:7M:152:LEU:HB2	2.42	0.51
4:8D:21:TRP:HA	4:8D:24:ILE:HG22	1.92	0.51
3:8E:72:PRO:O	3:8E:76:ASP:HB2	2.10	0.51
3:8E:240:ALA:HB1	3:8E:356:ASN:HD22	1.75	0.51
4:8L:49:VAL:HG11	4:8L:241:ARG:HG2	1.93	0.51
7:93:411:MET:HG2	4:9D:174:LYS:HE3	1.93	0.51
4:9F:101:TRP:HE3	4:9F:403:MET:HE1	1.75	0.51
3:9G:68:LEU:HD21	3:9G:118:SER:HB3	1.93	0.51
3:9I:237:SER:HA	3:9I:320:ARG:HH12	1.75	0.51
4:9J:179:VAL:HG13	4:9J:180:VAL:HG13	1.91	0.51
10:C9:352:TYR:HE2	10:C9:376:ILE:HD11	1.76	0.51
10:E4:58:SER:HA	10:E4:92:MET:HE1	1.91	0.51
13:J3:345:LEU:HD23	13:J3:346:GLN:HG2	1.92	0.51
1:c:638:LEU:HD21	1:k:817:GLY:HA3	1.92	0.51
1:v:892:SER:HA	1:v:895:LEU:HD12	1.93	0.51
1:J:607:LEU:O	1:J:611:THR:HG23	2.10	0.51
1:O:658:ALA:O	1:O:661:ASN:HB3	2.11	0.51
4:1B:121:ARG:O	4:1B:125:GLU:HB2	2.10	0.51
3:1E:100:ALA:O	4:1F:255:VAL:HG11	2.10	0.51
4:1N:66:MET:HE2	4:1N:147:MET:HG2	1.93	0.51
5:24:40:HIS:HE2	5:24:88:ARG:HB2	1.75	0.51
3:2A:223:THR:HG23	3:2A:225:THR:HG22	1.92	0.51
4:2L:174:LYS:HD2	4:2L:175:VAL:H	1.76	0.51
3:2M:272:TYR:HA	3:2M:375:VAL:O	2.09	0.51
5:38:129:VAL:HG12	5:38:133:MET:HE2	1.91	0.51
3:3C:429:GLU:HB3	6:66:576:VAL:HG13	1.93	0.51
4:3D:94:GLN:HE21	6:65:928:VAL:HG11	1.74	0.51
4:3F:42:LEU:HD13	4:3F:356:ILE:HD11	1.91	0.51
4:4B:203:ASP:HB2	4:4B:301:CYS:HA	1.93	0.51
4:4D:68:LEU:HD22	4:4D:97:ALA:HB2	1.91	0.51
4:5J:400:GLY:HA2	14:K5:90:PHE:HE1	1.75	0.51
5:60:213:LEU:HG	5:60:221:LEU:HB2	1.92	0.51
6:68:598:VAL:HA	6:68:601:GLU:HG2	1.92	0.51
6:69:598:VAL:HA	6:69:601:GLU:HG3	1.92	0.51
3:6A:238:LEU:HA	3:6A:318:MET:HE3	1.92	0.51
3:6K:417:GLU:HA	3:6K:420:GLU:HB2	1.91	0.51
3:6M:394:LYS:HA	3:6M:397:LEU:HG	1.92	0.51
7:71:352:VAL:HG12	14:K1:244:LYS:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:75:376:GLU:O	7:75:380:TRP:CB	2.58	0.51
3:7E:223:THR:HG23	3:7E:225:THR:H	1.76	0.51
4:7F:396:HIS:HD2	14:L6:89:ARG:HH22	1.58	0.51
4:7J:5:VAL:HG21	4:7J:124:ALA:HB2	1.93	0.51
3:7K:234:VAL:HG21	3:7K:302:MET:HE1	1.92	0.51
4:7L:119:VAL:HG23	4:7L:122:LYS:HE3	1.90	0.51
7:83:282:ARG:HE	7:83:287:LEU:HD12	1.75	0.51
7:84:401:ILE:HD12	14:L3:106:TYR:HB2	1.91	0.51
3:8A:306:ASP:HB2	14:L8:256:VAL:HG23	1.92	0.51
3:8E:404:PHE:HZ	4:8F:312:THR:HG21	1.75	0.51
4:8F:310:TYR:HA	4:8F:371:SER:HA	1.91	0.51
3:8I:138:PHE:HE2	3:8I:235:ILE:HD13	1.74	0.51
4:9H:135:ILE:HD12	4:9H:137:HIS:CD2	2.45	0.51
8:A3:245:ALA:HB2	9:B7:502:ALA:HB1	1.92	0.51
10:C0:316:CYS:O	10:C0:320:LYS:CB	2.59	0.51
10:E5:57:ILE:HG23	10:E5:306:MET:HE1	1.92	0.51
10:F2:94:VAL:HA	10:F2:97:ILE:HG12	1.92	0.51
13:J4:446:VAL:HG22	13:J4:485:ILE:HB	1.91	0.51
14:K0:183:GLN:HA	14:K0:186:THR:HG22	1.92	0.51
1:M:499:ARG:HG2	1:N:499:ARG:HH12	1.76	0.51
1:Q:684:ARG:HD2	1:U:684:ARG:HE	1.74	0.51
1:R:436:VAL:HG21	1:V:432:LEU:HD11	1.93	0.51
1:U:519:GLU:HA	1:U:522:ARG:HD2	1.93	0.51
1:Y:624:GLN:C	1:c:624:GLN:HE22	2.19	0.51
2:13:280:LYS:HD2	2:14:281:CYS:HB2	1.92	0.51
3:1M:191:THR:HA	3:1M:194:LEU:HB3	1.93	0.51
5:25:169:ILE:HG23	6:69:352:ALA:HB2	1.92	0.51
4:2L:35:THR:HG22	9:B6:59:PRO:HB3	1.92	0.51
3:3E:223:THR:HG23	3:3E:225:THR:H	1.75	0.51
4:3L:391:ARG:HD3	3:3M:346:TRP:HB3	1.93	0.51
3:4A:80:THR:HB	8:A3:174:ARG:HH22	1.75	0.51
3:4C:380:ASN:HD21	3:4C:432:TYR:HE1	1.59	0.51
3:4E:277:SER:H	3:4E:280:LYS:HG3	1.73	0.51
4:4F:205:GLU:HG2	3:4G:329:ASN:HD21	1.76	0.51
3:4I:277:SER:HA	3:4I:367:ASP:HB3	1.93	0.51
3:5C:223:THR:HG23	3:5C:225:THR:H	1.74	0.51
4:5D:272:PRO:HB2	4:5D:361:LEU:HD13	1.92	0.51
5:60:222:LEU:HA	5:60:225:GLN:HG3	1.92	0.51
6:68:330:LEU:HB3	6:68:337:LEU:HD21	1.93	0.51
3:6E:88:HIS:HB3	3:6E:91:GLN:HG3	1.92	0.51
4:6H:246:LEU:HD22	4:6H:352:SER:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:77:258:GLU:HA	7:77:261:ALA:HB3	1.92	0.51
3:7C:119:LEU:HD11	3:7C:156:ARG:HB3	1.91	0.51
3:7C:297:GLU:HG2	3:7C:299:ALA:H	1.75	0.51
3:7E:9:VAL:HG22	3:7E:68:LEU:HD22	1.92	0.51
4:7L:192:LEU:HB3	4:7L:199:VAL:HG21	1.92	0.51
3:8C:348:PRO:HB3	14:L8:111:LEU:HD22	1.93	0.51
3:8E:339:ARG:HA	14:L7:113:GLU:HG2	1.92	0.51
7:93:334:LEU:HD23	7:93:337:LYS:HD2	1.91	0.51
4:9B:189:VAL:HA	4:9B:192:LEU:HB2	1.93	0.51
4:9L:338:SER:HA	4:9L:341:PHE:HD2	1.75	0.51
4:9L:392:LYS:HA	4:9L:395:LEU:HD12	1.92	0.51
8:A3:36:PRO:HA	9:B5:8:ILE:HG22	1.91	0.51
8:A3:168:TRP:HZ3	8:A3:206:VAL:HG11	1.75	0.51
9:B2:453:PHE:HE1	1:v:873:PRO:HB2	1.75	0.51
11:C5:215:TYR:O	11:C5:219:TYR:HB2	2.09	0.51
10:C9:365:ASN:HB3	10:C9:368:ASP:HB2	1.93	0.51
10:D9:93:ALA:HA	10:D9:306:MET:SD	2.50	0.51
10:E4:97:ILE:HD13	10:E4:397:PHE:HD2	1.76	0.51
12:F7:217:ASP:HA	12:F7:224:ARG:HH21	1.75	0.51
1:a:607:LEU:C	1:f:607:LEU:HG	2.36	0.51
1:x:926:GLN:HA	1:x:929:GLU:HG2	1.93	0.51
1:y:945:ILE:HD12	1:y:948:GLN:HE21	1.75	0.51
1:I:544:LEU:HB3	1:J:544:LEU:HB3	1.92	0.51
2:13:162:GLN:HA	2:13:165:ARG:HG2	1.93	0.51
3:1C:181:VAL:HG11	4:1D:312:THR:HG22	1.90	0.51
3:1I:121:ARG:HH21	3:1I:124:LYS:HD2	1.76	0.51
3:1M:377:MET:HE2	3:1M:379:SER:HB2	1.92	0.51
4:1N:230:SER:HA	4:1N:233:MET:SD	2.50	0.51
5:27:52:ILE:HG22	5:27:148:LEU:HG	1.91	0.51
4:2B:100:ASN:H	4:2B:142:GLY:HA3	1.75	0.51
4:2B:321:MET:HB3	9:B7:127:LEU:HD22	1.92	0.51
5:35:139:LYS:HE2	13:J2:648:GLU:HB2	1.92	0.51
4:3D:79:GLY:HA2	6:65:867:TRP:HB3	1.91	0.51
3:3E:261:PRO:HG2	3:3E:313:MET:HE2	1.92	0.51
5:42:214:LYS:HG2	5:42:221:LEU:HD22	1.92	0.51
5:45:110:PHE:HZ	5:45:121:ILE:HG13	1.75	0.51
4:4D:257:LEU:HD21	4:4D:314:SER:HB2	1.92	0.51
4:4H:73:MET:HE3	4:4H:92:PHE:HB3	1.93	0.51
5:52:212:LEU:HD22	6:63:600:LEU:HG	1.93	0.51
3:5I:99:ALA:HA	3:5I:110:ILE:HD11	1.93	0.51
3:5M:184:PRO:HA	3:5M:391:MET:HE1	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:300:VAL:HG22	13:J1:283:TRP:CD2	2.46	0.51
6:69:262:LYS:HE2	6:69:302:VAL:HB	1.93	0.51
4:6B:65:LEU:HD22	4:6B:90:PHE:HE1	1.75	0.51
4:6D:307:HIS:HE1	7:72:296:ARG:HG3	1.75	0.51
4:6H:397:TRP:CG	3:6I:257:THR:HG1	2.29	0.51
4:6J:316:MET:HG2	4:6J:352:SER:HB3	1.92	0.51
7:73:292:CYS:HB2	7:73:318:THR:HG22	1.93	0.51
4:7B:163:ILE:HD13	4:7B:251:ARG:HG3	1.91	0.51
4:7F:323:THR:HA	4:7F:326:VAL:HG12	1.92	0.51
3:7K:51:THR:HG21	3:7K:243:ARG:HG2	1.92	0.51
7:84:299:PHE:HE2	14:L3:126:ILE:HD12	1.76	0.51
3:8E:406:HIS:HA	3:8E:409:VAL:HG12	1.93	0.51
3:8M:244:PHE:HA	1:m:788:PRO:HG3	1.92	0.51
3:9C:115:VAL:HG22	3:9C:153:LEU:HD22	1.92	0.51
3:9G:123:ARG:HH22	3:9G:161:TYR:HB2	1.76	0.51
4:9H:265:PHE:HB3	4:9H:374:ILE:HD13	1.92	0.51
3:9K:119:LEU:HA	3:9K:122:ILE:HG22	1.91	0.51
8:A9:258:VAL:HG23	8:A9:259:THR:HG23	1.91	0.51
10:E4:88:LEU:HG	10:E4:92:MET:HE2	1.92	0.51
10:E6:318:PRO:HA	10:E6:321:ARG:HG2	1.92	0.51
12:H2:65:GLU:HG3	12:H2:68:ARG:HE	1.75	0.51
13:J6:405:VAL:HG12	13:J6:464:PHE:HE2	1.74	0.51
1:a:610:VAL:HG11	1:f:611:THR:HG23	1.93	0.51
1:g:738:ALA:HB1	1:g:743:THR:HG21	1.93	0.51
1:r:879:VAL:HG23	1:r:880:THR:H	1.75	0.51
1:x:867:PRO:HB3	1:x:944:GLN:HB3	1.93	0.51
1:A:681:ILE:HA	1:A:684:ARG:HG2	1.92	0.51
1:S:450:LEU:HD21	1:W:450:LEU:HA	1.92	0.51
3:1C:58:ALA:HB2	9:B5:113:SER:HB2	1.92	0.51
3:1C:184:PRO:HB3	3:1C:394:LYS:HG3	1.93	0.51
3:1E:261:PRO:HD2	3:1E:265:ILE:HG23	1.92	0.51
3:1G:185:TYR:HE2	3:1G:404:PHE:HB2	1.75	0.51
3:1I:152:LEU:HD11	3:1I:156:ARG:HH21	1.76	0.51
4:1J:105:HIS:CE1	4:1J:191:GLN:HE22	2.28	0.51
4:1N:14:ASN:ND2	4:1N:67:ASP:HB2	2.26	0.51
1:2:904:ILE:HD13	1:2:931:ARG:HG3	1.91	0.51
3:2C:167:LEU:HA	3:2C:200:VAL:HB	1.93	0.51
4:2F:83:GLN:HE22	6:64:880:PHE:HE2	1.58	0.51
3:2G:203:MET:HE3	3:2G:267:PHE:HB3	1.92	0.51
4:2L:289:LEU:HD12	4:2L:365:VAL:HG12	1.93	0.51
5:32:29:ILE:HA	5:32:32:MET:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3A:431:ASP:HA	3:3A:434:GLU:HG2	1.91	0.51
5:47:21:LEU:HG	5:47:22:ALA:H	1.75	0.51
4:4B:149:THR:HA	4:4B:152:ILE:HG12	1.93	0.51
4:4B:293:MET:HE1	4:4B:315:ALA:HB2	1.91	0.51
4:4D:86:ARG:HB3	4:4D:89:ASN:HB2	1.92	0.51
4:4J:395:LEU:HD11	4:4J:408:PHE:CE2	2.45	0.51
3:4M:362:VAL:HG21	3:4M:369:ALA:HB3	1.92	0.51
3:5A:88:HIS:HE1	3:6A:284:GLU:CD	2.18	0.51
4:5B:220:PRO:HD2	3:5C:326:LYS:HZ2	1.74	0.51
4:5J:155:VAL:HG12	4:5J:164:MET:HE1	1.92	0.51
6:68:495:LEU:CD2	6:68:498:ARG:HH11	2.21	0.51
3:6E:238:LEU:HD12	3:6E:318:MET:HE3	1.93	0.51
4:6J:271:ALA:HB3	4:6J:365:VAL:HG12	1.93	0.51
7:76:313:LEU:HD22	14:K5:109:ASP:HB2	1.92	0.51
4:7D:317:PHE:CD2	4:7D:321:MET:HE1	2.46	0.51
4:8D:46:ARG:HG2	4:8D:241:ARG:HA	1.93	0.51
4:8H:193:VAL:HG13	4:8H:194:GLU:HG2	1.91	0.51
7:90:386:ARG:HG3	14:L9:115:PRO:HB3	1.93	0.51
7:92:350:ARG:HG3	7:92:388:GLU:HB2	1.91	0.51
3:9A:208:ALA:HB2	3:9A:304:LYS:HB2	1.93	0.51
4:9B:200:GLN:HG2	4:9B:268:ILE:HD11	1.93	0.51
4:9B:382:SER:HA	4:9B:385:PHE:HB3	1.93	0.51
10:E2:120:PRO:HD3	10:E2:130:PRO:HB3	1.93	0.51
10:E5:68:THR:HA	10:E5:71:GLN:HB2	1.93	0.51
14:M1:156:LEU:HD21	14:M1:185:ILE:HD12	1.93	0.51
1:x:940:HIS:CE1	1:x:944:GLN:HE21	2.28	0.51
1:J:363:PHE:HB2	1:U:333:ARG:HH12	1.76	0.51
1:J:531:GLN:HA	1:J:534:GLN:HG2	1.93	0.51
1:N:592:ARG:HE	1:N:593:GLN:HG3	1.76	0.51
1:R:630:ARG:HH21	1:Z:352:LYS:HD3	1.75	0.51
3:1A:98:ASP:H	4:1B:251:ARG:HH22	1.56	0.51
4:1J:218:THR:HG22	4:1J:219:THR:HG23	1.92	0.51
4:1J:309:ARG:H	4:1J:372:THR:HG22	1.76	0.51
4:1L:180:VAL:HG13	4:1L:184:ASN:HD21	1.76	0.51
5:29:179:SER:HA	6:68:366:GLN:HG2	1.91	0.51
4:2D:237:THR:HG22	4:2D:250:LEU:HD21	1.91	0.51
3:3A:248:LEU:H	3:3A:355:ILE:HB	1.75	0.51
4:3F:282:ARG:HH12	4:3F:361:LEU:HD22	1.75	0.51
4:4B:4:ILE:HD11	4:4B:240:LEU:HD22	1.92	0.51
3:4E:268:MET:HE2	3:4E:380:ASN:HB2	1.93	0.51
3:4M:339:ARG:HG3	6:68:841:ILE:HG23	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:57:224:LEU:HD13	6:66:599:ILE:HB	1.92	0.51
4:5L:138:SER:HA	4:5L:169:VAL:HB	1.93	0.51
6:68:902:PRO:HD3	1:x:880:THR:HG22	1.92	0.51
4:6B:182:PRO:HG3	4:6B:384:GLN:HG3	1.92	0.51
4:6F:86:ARG:HH22	4:7F:282:ARG:HG3	1.76	0.51
3:8E:75:VAL:HA	3:8E:78:VAL:HG12	1.93	0.51
4:8F:320:ARG:HE	1:l:744:GLU:HB3	1.76	0.51
4:8J:7:VAL:O	4:8J:135:ILE:HA	2.11	0.51
7:93:350:ARG:HG2	7:93:379:LEU:HD22	1.92	0.51
4:9D:100:ASN:HD21	3:9E:257:THR:HG21	1.76	0.51
3:9E:336:LYS:HE2	14:M4:112:THR:HA	1.93	0.51
4:9F:304:ASP:O	4:9F:307:HIS:CE1	2.64	0.51
10:D0:119:LYS:HA	10:D0:130:PRO:HB3	1.91	0.51
12:F6:274:MET:HA	12:F6:277:ARG:HE	1.76	0.51
14:L1:100:ALA:HA	14:L1:105:LEU:HD13	1.93	0.51
1:f:519:GLU:O	1:f:523:VAL:HG23	2.11	0.51
1:h:779:PRO:HG2	1:h:782:ARG:HD3	1.93	0.51
1:h:803:ILE:HG23	1:h:804:ASN:H	1.76	0.51
1:K:324:GLU:HA	1:K:327:TRP:CD1	2.41	0.51
1:Y:659:LEU:O	1:Y:663:LEU:HG	2.11	0.51
3:1E:269:LEU:HD11	3:1E:384:ILE:HD13	1.92	0.51
4:1H:375:GLN:HE22	4:1H:419:VAL:HA	1.75	0.51
5:26:167:LYS:HA	5:27:120:MET:HE1	1.93	0.51
3:2E:334:THR:HA	3:2E:337:THR:HG22	1.92	0.51
4:2F:293:MET:HG3	4:2F:367:PHE:HB2	1.92	0.51
3:2K:298:PRO:HB3	3:2K:307:PRO:HD2	1.93	0.51
5:36:93:SER:HB2	5:36:99:LEU:HD22	1.91	0.51
4:3B:178:THR:HG22	3:3C:352:LYS:HZ2	1.76	0.51
3:3C:75:VAL:HG12	3:3C:79:ARG:HE	1.76	0.51
3:3I:172:TRP:NE1	3:3I:203:MET:HG2	2.25	0.51
5:43:206:LEU:HD11	5:44:202:LEU:HD12	1.93	0.51
3:4C:200:VAL:HG11	3:4C:255:PHE:HE2	1.75	0.51
3:4G:305:CYS:HB3	3:4G:387:VAL:HB	1.93	0.51
4:4L:205:GLU:HA	4:4L:208:TYR:HD1	1.75	0.51
3:5A:286:LEU:HB3	3:5A:373:ARG:HH21	1.76	0.51
4:5D:238:CYS:HB2	4:5D:318:ARG:HD3	1.92	0.51
4:5L:203:ASP:HB2	4:5L:301:CYS:HA	1.93	0.51
3:5M:11:GLN:HG3	3:5M:74:VAL:HG11	1.92	0.51
6:66:844:ALA:O	6:66:848:SER:CB	2.56	0.51
3:6M:109:THR:HG21	3:6M:411:GLU:HB3	1.93	0.51
7:73:313:LEU:HD23	7:73:315:ILE:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7F:263:LEU:HB3	4:7F:370:ASN:HD21	1.76	0.51
4:7J:136:THR:HG22	4:7J:167:PHE:HB2	1.93	0.51
4:7L:252:LYS:HA	4:7L:255:VAL:HG12	1.92	0.51
7:85:273:LEU:HD12	10:E0:155:MET:HE1	1.92	0.51
7:96:334:LEU:HD21	7:96:347:ILE:HG12	1.93	0.51
7:97:403:GLY:H	14:M5:105:LEU:HB2	1.76	0.51
3:9A:47:ASP:O	3:9A:50:ASN:HB2	2.11	0.51
3:9C:298:PRO:HB3	3:9C:307:PRO:HD2	1.93	0.51
8:A1:161:ILE:HD11	8:A1:187:VAL:HG21	1.92	0.51
12:G2:261:TRP:CE2	12:G2:286:PRO:HG3	2.45	0.51
12:G8:188:ARG:HH11	12:G8:189:PRO:HD2	1.76	0.51
13:J1:470:ARG:O	13:J1:474:ARG:HG2	2.11	0.51
13:J2:345:LEU:HD23	13:J2:346:GLN:HG2	1.93	0.51
14:L7:158:ARG:HH21	14:L7:192:ILE:HG13	1.75	0.51
14:M4:186:THR:HG22	14:M4:196:VAL:H	1.76	0.51
14:M5:148:ILE:HD11	14:M5:173:PRO:HG2	1.93	0.51
1:a:589:THR:HA	1:a:592:ARG:HE	1.75	0.51
1:y:947:PHE:HB3	1:y:951:ARG:HH12	1.76	0.51
1:I:622:GLU:O	1:I:626:LEU:HG	2.11	0.51
1:Y:607:LEU:HD12	1:c:604:ILE:CD1	2.30	0.51
2:12:155:GLN:HA	2:12:158:GLU:HG2	1.93	0.51
3:1A:344:VAL:HG13	3:1A:347:CYS:H	1.74	0.51
4:1B:139:LEU:HA	4:1B:145:SER:HB3	1.91	0.51
4:1D:323:THR:HG21	4:1D:353:VAL:HG11	1.92	0.51
3:2C:88:HIS:ND1	3:2C:90:GLU:HG2	2.26	0.51
3:2C:105:ARG:HA	3:2C:109:THR:HG22	1.92	0.51
4:3F:203:ASP:HB2	4:3F:301:CYS:HA	1.91	0.51
4:3L:299:MET:HG3	4:3L:301:CYS:H	1.76	0.51
5:48:34:PRO:HG3	5:48:186:ARG:HB3	1.91	0.51
3:4K:195:LEU:HD13	3:4K:428:LEU:HD12	1.93	0.51
3:4K:382:THR:HG21	3:4K:436:GLY:HA3	1.92	0.51
4:4L:117:LEU:HA	4:4L:120:VAL:HG12	1.91	0.51
5:55:160:PHE:HE2	5:55:174:LEU:HD23	1.74	0.51
4:5B:327:ASP:HA	4:5B:330:MET:HE2	1.93	0.51
3:5C:11:GLN:HG2	3:5C:74:VAL:HG21	1.93	0.51
4:5N:104:GLY:HA3	4:5N:146:GLY:HA3	1.92	0.51
6:67:974:GLU:HA	6:67:977:VAL:HG22	1.93	0.51
6:69:915:ASN:HB3	6:69:918:ALA:HB2	1.93	0.51
4:6D:100:ASN:HB3	4:6D:103:LYS:HB2	1.92	0.51
3:6E:241:SER:HB2	3:6E:250:VAL:H	1.76	0.51
3:6K:56:THR:HA	3:7K:285:GLN:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6K:189:LEU:HD11	3:6K:418:PHE:HD1	1.76	0.51
3:6K:238:LEU:HD21	3:6K:378:ILE:HD11	1.93	0.51
4:6L:178:THR:HG22	3:6M:352:LYS:HZ3	1.76	0.51
3:6M:319:TYR:HB3	3:6M:323:VAL:HG21	1.93	0.51
7:75:408:ILE:HD12	7:75:412:MET:HE3	1.93	0.51
3:7E:141:VAL:HG13	3:7E:142:GLY:H	1.76	0.51
4:7J:59:PHE:HZ	1:n:922:ARG:HH12	1.59	0.51
4:7J:121:ARG:O	4:7J:125:GLU:CB	2.58	0.51
4:8B:390:ARG:HE	4:8B:391:ARG:HG3	1.76	0.51
3:9A:212:ILE:HG23	3:9A:275:ILE:HD12	1.93	0.51
3:9K:274:PRO:HG3	3:9K:374:ALA:HA	1.92	0.51
4:9L:141:GLY:HA3	17:9L:501:GDP:H5'	1.93	0.51
9:B5:500:HIS:HB2	9:B5:534:THR:HB	1.92	0.51
10:E8:76:ALA:HB2	10:E8:319:LEU:HD11	1.93	0.51
12:F0:275:GLN:HG2	12:F9:274:MET:HE2	1.92	0.51
10:F2:298:GLU:HA	10:F2:301:ARG:HB3	1.92	0.51
12:F9:223:LEU:HG	12:F9:242:TRP:CD1	2.46	0.51
13:J3:439:ARG:HG2	13:J3:680:PHE:HE2	1.76	0.51
13:J3:470:ARG:HB2	13:J3:500:LEU:HA	1.93	0.51
13:J5:418:LEU:HB2	13:J5:472:VAL:HG21	1.93	0.51
1:c:519:GLU:HA	1:c:522:ARG:HD3	1.93	0.51
1:f:578:ARG:O	1:f:581:LYS:HB2	2.11	0.51
1:Y:428:GLU:HB3	1:c:429:ARG:HH22	1.76	0.50
3:1C:256:GLN:O	3:1C:260:VAL:HG12	2.11	0.50
4:1D:257:LEU:HB3	4:1D:266:PHE:CE1	2.46	0.50
5:29:51:GLU:O	5:29:147:VAL:HA	2.10	0.50
3:2A:83:TYR:HB3	3:2A:86:LEU:HD13	1.93	0.50
4:2B:245:GLN:HB2	4:2B:353:VAL:HG23	1.93	0.50
3:2E:177:VAL:HG21	4:2F:327:ASP:HB3	1.93	0.50
3:2G:422:ARG:HH12	3:2G:426:ALA:HB2	1.76	0.50
4:2J:183:TYR:HE1	4:2J:388:MET:HB3	1.76	0.50
4:2L:102:ALA:HB1	4:2L:401:GLU:HB2	1.93	0.50
5:31:41:THR:HG22	5:31:77:ILE:H	1.75	0.50
3:3E:265:ILE:HG12	3:3E:432:TYR:HE1	1.74	0.50
4:3F:224:ASP:HB3	8:A5:257:PRO:HG3	1.92	0.50
3:3I:238:LEU:HD21	3:3I:378:ILE:HG13	1.93	0.50
2:4:311:ARG:HD2	2:4:314:TYR:HE2	1.76	0.50
5:49:42:LEU:HA	5:49:76:LEU:HG	1.93	0.50
4:4B:208:TYR:CE1	4:4B:225:LEU:HD11	2.46	0.50
4:4D:320:ARG:HD2	8:A2:202:PRO:HA	1.92	0.50
3:4G:180:ALA:HB3	3:4G:183:GLU:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4H:86:ARG:HH22	4:4H:122:LYS:HD3	1.75	0.50
3:4I:69:ASP:O	3:4I:94:SER:HA	2.11	0.50
3:4K:253:THR:HA	3:4K:256:GLN:HE21	1.75	0.50
4:4L:289:LEU:HD13	4:4L:365:VAL:HG13	1.93	0.50
4:5B:257:LEU:HD21	4:5B:314:SER:HB2	1.93	0.50
3:5M:6:SER:O	3:5M:65:CYS:HA	2.10	0.50
6:64:906:THR:H	6:64:909:GLN:HE21	1.59	0.50
6:66:881:THR:HG22	9:B5:55:LEU:H	1.76	0.50
4:6J:215:LEU:HD11	4:6J:273:LEU:HD22	1.93	0.50
4:7D:221:THR:HG23	4:7D:223:GLY:H	1.76	0.50
4:8F:190:HIS:CD2	4:8F:414:ASN:HB2	2.46	0.50
4:8J:68:LEU:HD12	4:8J:93:GLY:HA3	1.93	0.50
3:9I:320:ARG:HG3	3:9I:360:PRO:HG3	1.93	0.50
10:D1:390:MET:HA	10:D1:393:VAL:HG22	1.92	0.50
10:E5:89:ALA:HA	10:E5:306:MET:HE2	1.93	0.50
10:E8:27:ARG:HG3	10:E8:30:ARG:HH21	1.76	0.50
10:F2:283:PHE:HE2	10:F2:386:LEU:HD11	1.76	0.50
13:J5:353:ARG:CD	13:J5:354:ALA:H	2.24	0.50
14:K5:181:LEU:O	14:K5:185:ILE:HG12	2.11	0.50
14:L1:179:GLU:HA	14:L1:182:TYR:HD2	1.76	0.50
14:L9:200:PHE:HB2	14:L9:220:LEU:HB3	1.93	0.50
1:a:533:ARG:CZ	1:f:534:GLN:HB2	2.41	0.50
1:q:940:HIS:O	1:q:944:GLN:HG3	2.11	0.50
1:G:381:ARG:NH1	1:G:384:LEU:HD12	2.26	0.50
4:1L:236:VAL:HG13	4:1L:237:THR:HG23	1.92	0.50
4:1N:248:SER:HA	4:1N:252:LYS:HG2	1.93	0.50
5:29:80:GLU:HG3	5:29:83:ASN:H	1.76	0.50
4:2D:80:PRO:HD2	9:B3:77:GLY:HA3	1.91	0.50
3:2G:115:VAL:HG11	3:2G:156:ARG:HE	1.76	0.50
3:5A:88:HIS:HE1	3:6A:284:GLU:OE1	1.93	0.50
6:65:401:ILE:O	6:65:405:LYS:HG2	2.11	0.50
6:68:845:VAL:HA	6:68:848:SER:HB3	1.94	0.50
4:6B:244:GLY:HA2	4:6B:355:ASP:HB2	1.92	0.50
3:6C:298:PRO:HG3	3:6C:307:PRO:HD2	1.92	0.50
3:6I:348:PRO:HB2	14:K1:111:LEU:HD22	1.94	0.50
3:6K:30:ILE:HG22	3:6K:36:MET:HG2	1.92	0.50
4:6L:206:ALA:HB2	4:6L:302:ALA:HB2	1.93	0.50
2:7:160:LEU:HA	2:7:163:GLU:HG3	1.94	0.50
3:7C:64:ARG:HA	3:7C:125:LEU:HD11	1.93	0.50
4:7F:136:THR:HG22	4:7F:167:PHE:HB2	1.93	0.50
3:7K:178:SER:HB3	4:7L:347:ASN:HD22	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8A:274:PRO:HD3	3:8A:374:ALA:HA	1.93	0.50
4:8B:68:LEU:HB3	4:8B:96:GLY:HA2	1.92	0.50
4:8H:117:LEU:HD11	4:8H:154:LYS:HD2	1.93	0.50
4:8J:3:GLU:HG2	4:8J:130:LEU:HD12	1.93	0.50
3:8K:312:TYR:HB2	3:8K:343:PHE:CD1	2.46	0.50
7:90:282:ARG:HH21	7:90:287:LEU:HD12	1.76	0.50
7:94:272:ALA:HB1	14:M6:93:PHE:HB2	1.92	0.50
7:95:272:ALA:HB1	14:M7:93:PHE:HB2	1.93	0.50
4:9H:42:LEU:HD12	4:9H:243:PRO:HG3	1.93	0.50
10:D4:62:VAL:HG21	10:D4:305:LEU:HB3	1.94	0.50
10:D8:94:VAL:HA	10:D8:97:ILE:HG22	1.93	0.50
10:E7:76:ALA:HB2	10:E7:319:LEU:HD11	1.92	0.50
12:G7:276:LEU:HD22	12:G7:279:ARG:HH21	1.76	0.50
14:K0:182:TYR:HE1	14:K0:199:ILE:HG12	1.76	0.50
14:L7:181:LEU:O	14:L7:185:ILE:HG12	2.12	0.50
1:f:564:GLU:HB3	1:f:568:LYS:HD2	1.93	0.50
1:H:629:LYS:HZ1	4:8L:276:ARG:HA	1.77	0.50
1:I:614:LEU:HD13	1:J:614:LEU:HA	1.94	0.50
1:J:359:ARG:HH21	1:U:329:ASP:HA	1.75	0.50
1:L:316:LEU:HA	1:L:319:MET:HE3	1.94	0.50
1:Q:364:GLU:HB3	1:U:365:LEU:HD21	1.92	0.50
1:R:610:VAL:HG13	1:V:614:LEU:HD11	1.93	0.50
2:12:168:ARG:HD3	2:12:171:MET:HE2	1.92	0.50
4:1H:136:THR:HG22	4:1H:167:PHE:HB2	1.92	0.50
4:1N:81:PHE:HA	4:1N:84:LEU:HD13	1.94	0.50
5:21:98:PHE:N	5:22:185:ARG:HH22	2.09	0.50
5:22:54:LEU:H	5:22:64:ASP:HB3	1.74	0.50
5:26:88:ARG:HA	5:26:103:HIS:O	2.11	0.50
3:2A:53:PHE:HB3	3:2A:61:HIS:HB3	1.94	0.50
3:2I:203:MET:HE2	3:2I:267:PHE:HB3	1.93	0.50
3:2K:212:ILE:HD11	3:2K:300:SER:HA	1.93	0.50
3:2K:278:ALA:HB2	9:B4:120:VAL:HG12	1.94	0.50
3:2M:105:ARG:HG2	3:2M:411:GLU:HG3	1.92	0.50
3:2M:121:ARG:HH11	3:2M:121:ARG:HG3	1.77	0.50
4:3F:290:THR:HA	4:3F:293:MET:HE3	1.93	0.50
4:3H:271:ALA:HB1	4:3H:292:GLN:HB3	1.93	0.50
4:3L:322:SER:HB2	8:A8:359:ASP:HB3	1.92	0.50
4:4B:334:GLN:HE22	4:4B:347:ASN:H	1.60	0.50
3:4K:301:MET:HE2	3:4K:307:PRO:HG3	1.93	0.50
3:4M:173:PRO:HG2	3:4M:391:MET:HE3	1.93	0.50
5:50:48:VAL:HG21	5:50:134:LEU:HD22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:51:122:GLU:HG2	5:51:124:GLY:H	1.76	0.50
5:53:78:LEU:HD12	5:53:86:HIS:HB3	1.93	0.50
4:5B:139:LEU:HD21	4:5B:168:SER:HB2	1.92	0.50
3:5C:102:ASN:HB3	3:5C:105:ARG:HB2	1.93	0.50
4:5N:424:GLN:HB3	14:K7:143:ARG:HE	1.77	0.50
6:63:137:THR:HG21	6:63:554:LEU:HD21	1.93	0.50
6:65:845:VAL:HA	6:65:848:SER:HB3	1.93	0.50
4:6B:200:GLN:HG2	4:6B:268:ILE:HD11	1.93	0.50
4:6H:276:ARG:HD2	1:g:813:PRO:HB3	1.93	0.50
3:7I:88:HIS:HD2	3:7I:90:GLU:HG2	1.77	0.50
3:7I:119:LEU:HD11	3:7I:156:ARG:HG2	1.92	0.50
3:7K:339:ARG:HH22	7:83:390:PRO:HG3	1.77	0.50
7:83:368:THR:HG23	7:83:371:GLU:H	1.77	0.50
7:87:296:ARG:HG2	7:87:317:GLN:HE21	1.76	0.50
4:8B:30:ILE:HD11	4:8B:47:ILE:HD11	1.92	0.50
3:8G:154:LEU:HD21	3:8G:198:THR:HG23	1.92	0.50
4:8L:68:LEU:HD22	4:8L:108:GLU:HB3	1.94	0.50
4:8L:116:VAL:HA	4:8L:119:VAL:HG22	1.94	0.50
3:8M:239:THR:HG23	3:8M:242:LEU:HD12	1.93	0.50
7:94:397:SER:HB3	14:M6:124:SER:HB2	1.93	0.50
3:9A:72:PRO:HB3	3:9A:94:SER:HB2	1.92	0.50
4:9D:46:ARG:HH12	4:9D:243:PRO:HD3	1.75	0.50
3:9E:231:ILE:HG12	3:9E:302:MET:HE1	1.91	0.50
3:9G:77:GLU:HA	3:9G:80:THR:HG22	1.93	0.50
8:A3:87:VAL:HG12	8:A3:93:VAL:HB	1.93	0.50
10:E2:284:LEU:C	10:E2:351:ARG:HH12	2.19	0.50
10:E9:110:ILE:HG12	10:E9:283:PHE:HD2	1.76	0.50
12:F5:241:LEU:HD23	12:F5:244:ARG:HD2	1.93	0.50
13:J1:325:LEU:HD21	13:J1:416:VAL:HG22	1.92	0.50
13:J1:345:LEU:HD23	13:J1:346:GLN:HG2	1.94	0.50
13:J3:367:GLU:HG2	13:J3:596:GLN:HG3	1.93	0.50
13:J3:405:VAL:O	13:J3:409:LEU:HB2	2.11	0.50
1:u:872:ALA:HB3	1:u:875:ILE:HG12	1.92	0.50
1:A:558:LEU:HD22	1:F:562:ILE:HD11	1.93	0.50
1:F:603:ARG:HA	1:F:606:HIS:CE1	2.46	0.50
1:Z:507:GLU:HG2	1:e:332:ARG:HE	1.76	0.50
3:1E:60:LYS:HD3	3:2E:283:HIS:HD2	1.75	0.50
4:1F:100:ASN:HD22	4:1F:103:LYS:NZ	2.09	0.50
4:1H:317:PHE:HB3	4:1H:321:MET:HE1	1.93	0.50
4:1L:86:ARG:HG2	4:1L:88:ASP:H	1.77	0.50
4:1L:166:THR:HG21	4:1L:196:ALA:HB1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2B:323:THR:HG22	4:2B:353:VAL:HG21	1.93	0.50
3:2I:298:PRO:HB3	3:2I:307:PRO:HD2	1.93	0.50
3:2I:310:GLY:HA3	3:2I:383:ALA:HB2	1.93	0.50
3:2M:7:ILE:HG23	3:2M:66:VAL:HB	1.94	0.50
3:2M:16:ILE:HG12	3:2M:231:ILE:HG21	1.93	0.50
3:2M:64:ARG:HA	3:2M:125:LEU:HD21	1.93	0.50
3:2M:323:VAL:HG23	3:2M:355:ILE:HG23	1.93	0.50
2:3:220:LYS:HE3	2:3:223:ARG:HH21	1.77	0.50
3:3A:79:ARG:HE	3:3A:92:LEU:HD22	1.75	0.50
3:3A:222:PRO:HD2	4:3B:324:LYS:HE3	1.94	0.50
3:3C:29:GLY:HA2	8:A2:241:LEU:HD11	1.94	0.50
3:3G:238:LEU:HD23	3:3G:318:MET:HG3	1.92	0.50
3:3I:298:PRO:HB3	3:3I:307:PRO:HD2	1.92	0.50
3:3M:241:SER:HA	3:3M:356:ASN:HD22	1.77	0.50
5:47:132:LYS:HE3	13:J6:337:ARG:HE	1.77	0.50
4:4L:55:THR:HG23	3:5M:285:GLN:HA	1.94	0.50
4:4L:384:GLN:NE2	3:4M:348:PRO:HG2	2.27	0.50
5:55:91:LEU:HD11	5:55:158:LEU:HD22	1.93	0.50
3:5C:434:GLU:HA	3:5C:437:ILE:HG12	1.92	0.50
4:5H:424:GLN:HG3	10:C6:301:ARG:HH12	1.76	0.50
3:5K:56:THR:HA	3:6K:285:GLN:HB3	1.94	0.50
6:66:614:PRO:HA	6:66:617:VAL:HG22	1.93	0.50
6:67:873:ARG:HB2	9:B7:37:ARG:HH12	1.75	0.50
6:68:325:ARG:HG3	6:68:337:LEU:HD13	1.93	0.50
6:68:913:TYR:CE1	8:A7:86:GLN:HG2	2.46	0.50
4:6H:7:VAL:HB	4:6H:135:ILE:HG22	1.92	0.50
4:6H:10:GLY:HA2	4:6H:143:THR:HG23	1.92	0.50
4:6H:337:ASN:HD21	7:75:291:ALA:HB2	1.75	0.50
3:6I:269:LEU:HG	3:6I:384:ILE:HD11	1.93	0.50
4:6J:164:MET:HB3	4:6J:197:ASP:H	1.77	0.50
4:6N:207:LEU:HD23	4:6N:225:LEU:HB3	1.93	0.50
4:7D:293:MET:HA	4:7D:298:ASN:HD22	1.76	0.50
3:7G:298:PRO:HB3	3:7G:307:PRO:HD2	1.94	0.50
4:7L:174:LYS:HB2	14:L3:108:TYR:HE1	1.75	0.50
4:7L:189:VAL:HG23	4:7L:415:MET:HE1	1.93	0.50
7:84:381:PHE:HB2	7:84:386:ARG:HH12	1.76	0.50
7:89:376:GLU:O	7:89:380:TRP:HB2	2.11	0.50
4:8D:169:VAL:HG12	4:8D:202:ILE:HB	1.93	0.50
4:8F:232:ALA:HB2	4:8F:270:PHE:HB2	1.93	0.50
7:92:350:ARG:HD3	7:92:379:LEU:HD22	1.94	0.50
3:9C:229:ARG:HD3	3:9C:363:VAL:HG21	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9F:64:ILE:HG13	4:9F:120:VAL:HG12	1.92	0.50
8:A5:179:LYS:HB3	8:A5:189:VAL:HG21	1.93	0.50
9:B1:58:ILE:HD12	9:B1:61:LEU:HD22	1.93	0.50
10:C7:331:ILE:HG23	10:C7:335:LEU:HD12	1.93	0.50
10:D4:284:LEU:HB3	10:D4:351:ARG:HH12	1.76	0.50
10:D8:120:PRO:HD3	10:D8:130:PRO:HB3	1.93	0.50
10:D9:68:THR:HA	10:D9:71:GLN:HB3	1.94	0.50
10:E1:354:ARG:HD3	10:E1:360:ALA:HA	1.92	0.50
10:E3:379:LEU:HB3	10:E3:381:MET:HE3	1.94	0.50
10:E8:63:TYR:CE2	14:M2:142:GLN:HB3	2.46	0.50
12:F6:222:ASP:HA	12:F6:225:TRP:CD1	2.46	0.50
12:G6:268:ARG:HH22	12:G6:290:LYS:HB2	1.76	0.50
14:K3:196:VAL:HA	14:K3:223:SER:HA	1.93	0.50
14:K8:99:ILE:HG23	14:K8:105:LEU:HD11	1.93	0.50
14:L0:200:PHE:HB2	14:L0:220:LEU:HD13	1.93	0.50
14:L9:158:ARG:HH21	14:L9:192:ILE:HG13	1.76	0.50
1:w:862:LEU:HG	1:w:937:GLY:HA2	1.93	0.50
1:C:425:ILE:HG13	1:G:423:ARG:HH21	1.76	0.50
2:13:324:GLU:HG3	2:14:324:GLU:HA	1.94	0.50
4:1B:375:GLN:HE21	4:1B:419:VAL:HG13	1.76	0.50
4:1D:54:ALA:HB3	4:1D:58:ARG:HB2	1.94	0.50
3:1M:262:TYR:HB2	3:1M:265:ILE:HG22	1.93	0.50
1:2:903:ARG:HH12	1:2:931:ARG:HH22	1.60	0.50
1:2:942:ILE:HA	1:2:945:ILE:HG22	1.93	0.50
5:38:162:GLN:HB2	5:38:171:LEU:HD11	1.93	0.50
4:3F:169:VAL:HA	4:3F:202:ILE:HB	1.93	0.50
5:42:34:PRO:HG3	5:42:186:ARG:HB3	1.93	0.50
5:43:71:ILE:HD11	5:43:99:LEU:HD22	1.93	0.50
5:46:148:LEU:HB3	5:46:150:MET:HE3	1.93	0.50
3:4G:217:LEU:HD11	3:4G:230:LEU:HD11	1.93	0.50
4:4L:399:THR:HA	4:4L:403:MET:HB2	1.93	0.50
5:50:26:THR:HG21	5:50:198:LYS:HE3	1.94	0.50
4:5B:42:LEU:HA	4:5B:45:GLU:HG3	1.93	0.50
4:5B:284:LEU:HB2	4:5B:362:LYS:HE3	1.92	0.50
4:5F:77:ARG:HH12	4:5F:92:PHE:HZ	1.59	0.50
6:67:936:ARG:O	6:67:940:GLN:HG2	2.12	0.50
3:6C:154:LEU:HA	3:6C:157:LEU:HB2	1.93	0.50
3:6M:298:PRO:HA	3:6M:301:MET:HG2	1.94	0.50
3:7C:191:THR:HG21	3:7C:425:LEU:HD13	1.92	0.50
4:7L:314:SER:HB3	4:7L:368:VAL:HG23	1.93	0.50
3:7M:143:GLY:O	3:7M:147:SER:CB	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:85:308:TYR:CZ	7:85:322:PRO:HB2	2.47	0.50
4:8F:229:VAL:O	4:8F:233:MET:HB2	2.12	0.50
4:8F:326:VAL:O	4:8F:330:MET:HG2	2.10	0.50
7:91:282:ARG:C	10:F2:142:ARG:HH22	2.19	0.50
3:9C:296:PHE:HD2	3:9C:335:ILE:HG13	1.76	0.50
4:9F:54:ALA:HB3	4:9F:58:ARG:HB3	1.92	0.50
3:9G:157:LEU:HD21	3:9G:166:LYS:HE2	1.94	0.50
4:9H:303:SER:HB3	4:9H:377:MET:HE2	1.94	0.50
3:9I:242:LEU:HD21	3:9I:252:VAL:HG13	1.93	0.50
8:A1:84:TYR:HD1	8:A1:97:GLU:HB3	1.76	0.50
9:B2:36:GLU:HB3	9:B2:44:LEU:HB2	1.94	0.50
10:F2:113:THR:HG23	10:F2:286:ARG:HH22	1.77	0.50
13:J3:271:LEU:HD13	13:J3:286:LEU:HD13	1.94	0.50
13:J3:602:GLY:HA2	13:J3:662:ILE:HG12	1.94	0.50
13:J6:470:ARG:HD2	13:J6:502:PRO:HD2	1.93	0.50
14:L1:220:LEU:HD23	14:L1:236:PHE:CE1	2.47	0.50
14:M1:158:ARG:HH22	14:M1:192:ILE:HG23	1.77	0.50
1:C:403:ARG:O	1:C:407:GLU:HG2	2.11	0.50
1:I:428:GLU:HB3	1:J:429:ARG:NH2	2.27	0.50
1:I:588:THR:HA	1:I:591:ARG:HE	1.75	0.50
1:K:508:VAL:HG13	1:K:509:LEU:HD12	1.91	0.50
1:O:666:VAL:HB	1:P:666:VAL:CG1	2.42	0.50
1:S:359:ARG:HA	1:S:362:VAL:HG12	1.94	0.50
1:Y:594:ALA:HB1	1:s:882:GLU:CG	2.40	0.50
1:Y:604:ILE:HA	1:c:604:ILE:CD1	2.41	0.50
1:Z:429:ARG:N	1:d:429:ARG:HH22	2.09	0.50
2:15:179:MET:O	2:15:183:ARG:HB2	2.11	0.50
4:1D:186:THR:HG21	4:1D:385:PHE:HB2	1.94	0.50
4:1J:135:ILE:HG21	4:1J:152:ILE:HD11	1.94	0.50
5:27:24:VAL:HG22	5:27:201:LEU:HD11	1.94	0.50
4:2D:20:PHE:HA	4:2D:230:SER:HB2	1.93	0.50
3:2G:36:MET:HE2	3:2G:61:HIS:HE1	1.76	0.50
4:2H:25:SER:HB2	4:2H:30:ILE:HB	1.93	0.50
5:35:114:GLN:HG3	5:35:119:LEU:HB2	1.93	0.50
3:3G:88:HIS:CE1	3:4G:283:HIS:HA	2.47	0.50
4:3L:198:GLU:HA	4:3L:264:HIS:HB2	1.93	0.50
2:4:159:LEU:HD22	10:C6:81:ALA:HB2	1.93	0.50
3:4G:277:SER:HA	3:4G:367:ASP:HB3	1.94	0.50
5:55:36:LEU:HD21	5:55:42:LEU:HB2	1.92	0.50
4:5H:171:PRO:HG2	4:5H:185:ALA:HB2	1.93	0.50
3:5M:191:THR:HA	3:5M:194:LEU:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:62:148:LEU:HD13	5:62:158:LEU:HD13	1.94	0.50
6:63:881:THR:HG22	9:B2:54:ILE:HA	1.94	0.50
6:66:636:GLU:HG3	6:66:835:ILE:HG13	1.92	0.50
3:6C:212:ILE:HG23	3:6C:275:ILE:HD12	1.93	0.50
3:6G:191:THR:HA	3:6G:194:LEU:HB3	1.93	0.50
4:6H:338:SER:H	7:75:289:GLY:HA2	1.77	0.50
3:6K:276:ILE:HD12	3:6K:281:ALA:HA	1.94	0.50
4:6L:202:ILE:HG12	4:6L:300:MET:HE2	1.94	0.50
4:6L:307:HIS:CD2	7:77:296:ARG:HD3	2.46	0.50
7:73:376:GLU:O	7:73:380:TRP:CB	2.59	0.50
7:78:376:GLU:O	7:78:380:TRP:CB	2.59	0.50
3:7A:9:VAL:HG12	3:7A:146:GLY:HA2	1.94	0.50
4:7D:170:PHE:HB3	4:7D:380:ARG:HH22	1.75	0.50
3:7M:320:ARG:HH12	3:7M:360:PRO:HG3	1.75	0.50
7:84:350:ARG:HD3	7:84:388:GLU:HG3	1.94	0.50
7:87:408:ILE:O	7:87:412:MET:HG3	2.12	0.50
4:8B:303:SER:HB3	4:8B:377:MET:HB2	1.92	0.50
4:8D:64:ILE:HD11	4:8D:123:GLU:HG3	1.94	0.50
3:8I:316:CYS:HB3	3:8I:378:ILE:HG23	1.94	0.50
4:8J:349:MET:HE1	4:8J:367:PHE:HE1	1.76	0.50
3:8K:306:ASP:HB2	14:L0:256:VAL:HG21	1.94	0.50
3:8K:317:LEU:HD13	3:8K:377:MET:HB3	1.94	0.50
7:91:347:ILE:HD13	7:91:350:ARG:HH21	1.76	0.50
3:9A:147:SER:O	3:9A:151:CYS:CB	2.60	0.50
4:9B:120:VAL:O	4:9B:124:ALA:HB3	2.11	0.50
4:9D:113:ILE:HB	4:9D:117:LEU:HD23	1.93	0.50
4:9F:95:THR:HG23	4:9F:96:GLY:H	1.77	0.50
3:9I:202:VAL:HA	3:9I:268:MET:HB2	1.94	0.50
8:A1:269:LEU:HD12	8:A1:270:PRO:HD2	1.92	0.50
8:A2:240:PRO:HB3	9:B5:19:ALA:HB1	1.94	0.50
9:B6:488:GLU:HG3	9:B6:491:ARG:HH12	1.77	0.50
10:D7:284:LEU:HB3	10:D7:351:ARG:HH12	1.76	0.50
10:E4:307:MET:HG3	10:E4:396:LEU:HD22	1.94	0.50
12:F7:219:LEU:HD23	12:F7:239:ARG:HG3	1.92	0.50
13:J7:405:VAL:HG12	13:J7:464:PHE:HE2	1.76	0.50
14:L1:218:LYS:HE3	14:L1:241:VAL:HG12	1.94	0.50
14:L6:172:ARG:H	14:L6:175:ILE:HD12	1.76	0.50
1:Q:384:LEU:HD23	1:Q:387:ILE:HD11	1.94	0.50
4:1B:134:GLN:HA	4:1B:165:GLU:O	2.12	0.50
3:2I:325:PRO:HA	3:2I:328:VAL:HG12	1.92	0.50
3:2K:268:MET:HG3	3:2K:380:ASN:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3A:323:VAL:HG11	3:3A:355:ILE:HD12	1.94	0.50
4:3D:50:PHE:HD2	4:3D:241:ARG:HD3	1.76	0.50
4:3F:86:ARG:HH12	4:4F:282:ARG:HB3	1.76	0.50
3:3K:220:GLU:HG3	3:3K:221:ARG:HD3	1.93	0.50
5:47:19:ASN:HD21	5:48:221:LEU:HD11	1.77	0.50
4:4J:28:HIS:NE2	4:4J:241:ARG:HD2	2.26	0.50
3:4M:320:ARG:O	3:4M:373:ARG:HA	2.12	0.50
5:61:160:PHE:HB2	5:61:171:LEU:HB2	1.94	0.50
3:6A:119:LEU:HD21	14:L1:247:THR:HG21	1.93	0.50
3:6I:3:GLU:HA	3:6I:51:THR:HG23	1.93	0.50
4:6J:396:HIS:HA	4:6J:399:THR:HG22	1.93	0.50
3:6M:306:ASP:HB3	3:6M:309:HIS:CE1	2.46	0.50
4:7D:424:GLN:HE22	10:E5:301:ARG:HH12	1.59	0.50
3:7I:335:ILE:HA	3:7I:338:LYS:HG2	1.93	0.50
4:7J:10:GLY:HA2	4:7J:143:THR:HG23	1.94	0.50
4:7J:216:LYS:HB2	4:7J:275:SER:HB2	1.93	0.50
7:87:279:ARG:HB2	7:87:300:GLN:HE22	1.76	0.50
3:8E:73:THR:HB	4:8F:46:ARG:HH12	1.76	0.50
3:8I:54:SER:HA	3:8I:64:ARG:HH21	1.77	0.50
3:8K:173:PRO:HG2	3:8K:187:SER:HB2	1.93	0.50
4:8L:15:GLN:HB3	1:m:803:ILE:HD13	1.93	0.50
4:9D:317:PHE:HA	4:9D:365:VAL:HG12	1.93	0.50
4:9J:95:THR:HG23	4:9J:96:GLY:H	1.77	0.50
3:9K:322:ASP:HB3	3:9K:373:ARG:HE	1.77	0.50
9:B2:150:MET:HE1	11:C3:286:LYS:HG2	1.94	0.50
10:C8:95:GLU:HA	10:C8:98:GLU:HG3	1.93	0.50
10:D8:322:GLU:HA	10:D8:325:GLU:HG2	1.93	0.50
14:K4:156:LEU:HB3	14:K4:189:ILE:HD12	1.93	0.50
14:L5:222:THR:HB	14:L5:225:GLU:HB2	1.93	0.50
1:p:884:PRO:HA	1:p:887:VAL:HG12	1.93	0.50
1:A:614:LEU:HB3	1:A:618:ARG:HH22	1.76	0.50
1:B:454:GLU:HG2	1:K:340:ARG:HH22	1.77	0.50
1:N:615:ARG:HH21	3:9I:322:ASP:HB3	1.77	0.50
1:O:659:LEU:HD22	1:P:659:LEU:HB3	1.93	0.50
2:10:320:GLN:HB2	2:9:317:MET:HG2	1.94	0.50
4:1L:16:ILE:HA	4:1L:226:ASN:HD21	1.77	0.50
4:1L:293:MET:HG3	4:1L:294:PHE:HD2	1.76	0.50
5:25:164:MET:HE1	5:25:169:ILE:H	1.76	0.50
3:2G:223:THR:HG23	3:2G:225:THR:H	1.77	0.50
5:30:75:ILE:HG12	5:30:89:VAL:HG12	1.93	0.50
3:3C:239:THR:HA	3:3C:242:LEU:HD23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3D:113:ILE:HD12	4:3D:116:VAL:HB	1.93	0.50
3:3K:268:MET:HE2	3:3K:378:ILE:HG22	1.92	0.50
4:3L:117:LEU:HD11	4:3L:154:LYS:HB3	1.92	0.50
4:3L:398:TYR:HB3	4:3L:403:MET:HG3	1.94	0.50
5:49:235:ARG:NH2	6:64:592:SER:HB2	2.26	0.50
3:4C:259:LEU:HD13	3:4C:268:MET:HE1	1.94	0.50
4:4H:246:LEU:HB3	4:4H:353:VAL:H	1.76	0.50
4:4L:341:PHE:HB3	4:4L:348:ASN:HD21	1.77	0.50
5:50:167:LYS:HE2	5:53:118:LYS:HG3	1.94	0.50
5:52:139:LYS:HG3	5:52:140:GLU:H	1.76	0.50
5:57:133:MET:HE2	5:57:160:PHE:CD2	2.47	0.50
3:5C:68:LEU:HD11	3:5C:118:SER:HB3	1.94	0.50
6:65:495:LEU:HA	6:65:498:ARG:HH11	1.77	0.50
4:6B:215:LEU:HD11	4:6B:273:LEU:HD22	1.92	0.50
4:6J:155:VAL:HG12	4:6J:164:MET:HE1	1.94	0.50
4:6J:326:VAL:O	4:6J:330:MET:HG2	2.12	0.50
4:7H:139:LEU:HD13	4:7H:168:SER:HB2	1.94	0.50
3:8C:196:GLU:HG2	3:8C:197:HIS:H	1.77	0.50
3:8E:306:ASP:HB3	3:8E:309:HIS:HE1	1.77	0.50
3:8K:80:THR:HA	3:8K:84:ARG:HE	1.77	0.50
7:97:405:VAL:HG12	3:9C:333:ALA:HB1	1.94	0.50
3:9C:69:ASP:HB3	3:9C:74:VAL:HG11	1.93	0.50
3:9E:234:VAL:HG22	3:9E:272:TYR:HB2	1.92	0.50
4:9F:68:LEU:HD12	4:9F:97:ALA:HB2	1.94	0.50
3:9G:222:PRO:HD2	4:9H:324:LYS:HB2	1.94	0.50
10:D3:138:ARG:HG3	14:K1:211:ASP:HB2	1.93	0.50
10:E6:51:TYR:HB3	10:E6:54:HIS:CD2	2.47	0.50
10:E6:298:GLU:HG2	14:L8:143:ARG:HH12	1.76	0.50
12:F5:264:ILE:HD13	12:F5:289:ILE:HD13	1.94	0.50
12:F6:219:LEU:HD23	12:F6:239:ARG:HE	1.76	0.50
14:M2:203:ASN:HB2	14:M2:205:ARG:HH22	1.76	0.50
1:c:593:GLN:O	1:c:597:ILE:HG23	2.12	0.50
1:A:604:ILE:HD13	1:F:603:ARG:NH1	2.26	0.50
1:P:678:ASN:O	1:P:681:ILE:HG12	2.12	0.50
1:Y:338:HIS:HB3	1:c:338:HIS:CD2	2.47	0.50
1:Y:439:LEU:HB3	1:c:439:LEU:HD21	1.93	0.50
1:Z:513:ARG:N	1:d:513:ARG:HH22	2.10	0.50
4:1B:99:ASN:HB2	3:1C:254:GLU:HB2	1.94	0.50
4:1B:248:SER:HA	4:1B:252:LYS:HZ3	1.77	0.50
4:1B:392:LYS:HA	4:1B:395:LEU:HD13	1.93	0.50
3:1C:21:TRP:HA	3:1C:24:PHE:HD2	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1D:180:VAL:HG13	4:1D:183:TYR:HB2	1.94	0.50
4:1F:16:ILE:HD11	4:1F:136:THR:HB	1.93	0.50
3:1G:195:LEU:HD13	3:1G:428:LEU:HD21	1.94	0.50
4:1H:296:ALA:HB1	4:1H:304:ASP:HB2	1.92	0.50
3:1I:154:LEU:HD13	3:1I:198:THR:HG22	1.94	0.50
3:1K:102:ASN:ND2	3:1K:105:ARG:HG3	2.27	0.50
3:1M:8:HIS:O	3:1M:68:LEU:HB3	2.12	0.50
5:20:24:VAL:HG21	5:20:201:LEU:HB3	1.93	0.50
3:2A:236:SER:HA	3:2A:243:ARG:HH12	1.77	0.50
3:2E:106:GLY:HA3	3:2E:148:GLY:HA3	1.94	0.50
4:2F:91:VAL:HG11	4:2F:116:VAL:HB	1.94	0.50
3:2I:259:LEU:HB3	3:2I:268:MET:HE3	1.94	0.50
3:2K:179:THR:HG21	4:2L:246:LEU:HD13	1.94	0.50
3:2K:246:GLY:HA3	3:2K:356:ASN:HA	1.93	0.50
5:30:53:ARG:HB3	5:30:149:ILE:HG13	1.92	0.50
5:36:51:GLU:HB3	5:36:147:VAL:HG22	1.94	0.50
5:42:53:ARG:HE	5:42:65:VAL:HA	1.77	0.50
5:42:114:GLN:HA	5:42:119:LEU:HB2	1.92	0.50
5:43:214:LYS:HB3	5:43:221:LEU:HD13	1.94	0.50
5:47:132:LYS:HG2	13:J6:647:GLU:HB2	1.94	0.50
3:4K:176:GLN:HB3	4:4L:331:LEU:HD11	1.94	0.50
3:4K:308:ARG:HH11	6:69:619:ALA:HA	1.76	0.50
2:5:164:GLU:O	2:5:168:ARG:HG2	2.12	0.50
5:55:209:ILE:HG12	5:56:224:LEU:HD11	1.93	0.50
4:5H:193:VAL:HA	4:5H:264:HIS:HE1	1.76	0.50
2:6:268:THR:HA	2:6:271:LYS:HE2	1.93	0.50
5:62:44:TYR:HE2	5:62:73:VAL:HB	1.77	0.50
5:62:212:LEU:HA	5:62:215:LEU:HG	1.93	0.50
6:64:902:PRO:HD3	1:u:880:THR:HG22	1.93	0.50
6:65:620:ILE:HG21	6:65:956:ILE:HG23	1.94	0.50
3:6A:9:VAL:HG12	3:6A:146:GLY:HA2	1.93	0.50
4:6B:86:ARG:HB3	4:6B:89:ASN:HB3	1.92	0.50
3:6C:437:ILE:HG22	7:73:382:ASP:HB3	1.92	0.50
3:6E:220:GLU:HG2	3:6E:221:ARG:HG2	1.92	0.50
4:6L:174:LYS:HA	14:K6:110:GLY:HA3	1.93	0.50
3:6M:9:VAL:HG12	3:6M:146:GLY:HA2	1.94	0.50
4:6N:117:LEU:HA	4:6N:120:VAL:HG12	1.93	0.50
2:7:275:GLU:HA	2:7:278:HIS:CD2	2.47	0.50
4:7D:317:PHE:HA	4:7D:365:VAL:HG12	1.93	0.50
3:7E:12:ALA:HB3	3:7E:140:ALA:HB2	1.92	0.50
4:7J:47:ILE:HG13	4:7J:51:TYR:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7L:397:TRP:HA	14:L0:89:ARG:HH12	1.77	0.50
7:80:397:SER:HA	7:80:400:CYS:HB3	1.93	0.50
4:8B:263:LEU:HD22	4:8B:422:TYR:HE1	1.76	0.50
3:8K:416:GLY:N	10:F2:48:ARG:HH22	2.07	0.50
7:94:334:LEU:HD23	7:94:337:LYS:HD2	1.94	0.50
7:96:384:GLU:HB3	7:96:386:ARG:HH22	1.77	0.50
4:9B:177:ASP:HB2	3:9C:352:LYS:HD2	1.93	0.50
4:9F:207:LEU:HD13	4:9F:225:LEU:HB3	1.93	0.50
8:A7:225:SER:HB2	8:A7:232:ARG:HG3	1.94	0.50
10:D2:66:LEU:HD23	10:D2:69:LEU:HD12	1.93	0.50
10:D2:365:ASN:HB3	10:D2:368:ASP:HB2	1.94	0.50
10:D4:331:ILE:HG23	10:D4:335:LEU:HG	1.94	0.50
10:D6:331:ILE:HA	10:D6:335:LEU:HD23	1.94	0.50
13:J1:328:ALA:HA	13:J1:331:ASN:HB2	1.94	0.50
13:J2:392:VAL:HG22	13:J2:444:ALA:HB3	1.93	0.50
13:J4:345:LEU:HD23	13:J4:346:GLN:HG2	1.93	0.50
14:L4:233:LEU:HD13	14:L4:236:PHE:HD2	1.77	0.50
14:M5:207:ILE:HG23	14:M5:212:ASP:HB2	1.92	0.50
1:a:562:ILE:HD13	1:f:562:ILE:CD1	2.42	0.50
1:a:600:LEU:HD22	1:f:604:ILE:CD1	2.42	0.50
1:k:740:PRO:HB3	1:k:753:LEU:HD23	1.94	0.50
1:B:322:ARG:HD2	1:E:319:MET:HE1	1.94	0.49
1:B:485:LEU:HD22	1:E:486:GLN:HE22	1.76	0.49
4:1L:242:PHE:HB3	4:1L:356:ILE:HD12	1.94	0.49
5:24:29:ILE:HA	5:24:32:MET:HB3	1.94	0.49
4:2B:109:GLY:O	4:2B:113:ILE:HG12	2.12	0.49
3:2C:230:LEU:HD13	3:2C:368:LEU:HD11	1.94	0.49
3:2I:71:GLU:HB3	3:2I:98:ASP:HB2	1.94	0.49
3:2K:420:GLU:HG3	6:69:133:ARG:NH1	2.27	0.49
5:39:202:LEU:HD13	5:40:206:LEU:HD11	1.93	0.49
5:39:212:LEU:HD23	5:39:215:LEU:HD12	1.94	0.49
3:3A:221:ARG:HA	4:3B:324:LYS:HG3	1.94	0.49
5:40:88:ARG:HH12	5:40:90:GLU:HG2	1.77	0.49
4:4D:55:THR:HG23	3:5E:285:GLN:HA	1.94	0.49
4:4D:175:VAL:HG23	3:4E:332:VAL:HG21	1.93	0.49
3:4E:190:SER:O	3:4E:194:LEU:HB2	2.12	0.49
4:4F:207:LEU:HB3	4:4F:225:LEU:HD22	1.93	0.49
3:5E:136:LEU:HD23	3:5E:235:ILE:HD11	1.94	0.49
6:63:503:LYS:O	6:63:506:GLU:C	2.55	0.49
4:7D:397:TRP:HA	14:L7:89:ARG:HH12	1.76	0.49
3:7G:194:LEU:HD23	3:7G:203:MET:HE1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7J:98:GLY:HA2	3:7K:254:GLU:HB3	1.94	0.49
4:7J:293:MET:HE1	4:7J:330:MET:HE1	1.93	0.49
3:7K:154:LEU:HA	3:7K:157:LEU:HD23	1.93	0.49
7:83:352:VAL:HG11	14:L3:242:ILE:HG23	1.94	0.49
4:8B:403:MET:HE2	4:8B:408:PHE:HE1	1.77	0.49
3:8C:66:VAL:HG12	3:8C:91:GLN:HB2	1.94	0.49
3:8E:239:THR:HG23	3:8E:243:ARG:HH21	1.76	0.49
3:8G:298:PRO:HG3	3:8G:308:ARG:HH21	1.77	0.49
3:8I:202:VAL:HG21	3:8I:378:ILE:HD11	1.94	0.49
3:8I:208:ALA:HA	3:8I:304:LYS:HE3	1.94	0.49
7:96:288:PRO:HD2	14:M2:177:SER:HB3	1.94	0.49
7:96:292:CYS:HB2	7:96:318:THR:HG22	1.92	0.49
4:9F:149:THR:HA	4:9F:152:ILE:HG22	1.94	0.49
3:9G:138:PHE:HD1	3:9G:169:PHE:HB2	1.77	0.49
3:9I:70:LEU:HD11	3:9I:110:ILE:HG23	1.94	0.49
4:9J:316:MET:HB2	4:9J:366:THR:HG22	1.93	0.49
8:A6:33:LEU:HG	8:A6:77:GLU:HG3	1.94	0.49
10:E7:305:LEU:HD21	14:M6:142:GLN:HB3	1.94	0.49
12:F6:208:SER:HB2	12:F6:233:ARG:HH21	1.77	0.49
14:L2:99:ILE:HG13	14:L2:105:LEU:HD11	1.94	0.49
14:L5:156:LEU:HD12	14:L5:221:CYS:SG	2.52	0.49
14:M2:99:ILE:HG22	14:M2:102:ARG:HH22	1.75	0.49
1:a:610:VAL:HG11	1:f:611:THR:CA	2.41	0.49
1:Y:575:LEU:HD22	1:c:576:SER:C	2.37	0.49
2:10:306:LYS:HG3	2:9:306:LYS:HG3	1.95	0.49
2:12:186:HIS:HA	2:12:189:GLU:HG3	1.94	0.49
3:1E:180:ALA:HB3	3:1E:183:GLU:HG2	1.93	0.49
4:1L:97:ALA:HA	4:1L:103:LYS:HD2	1.93	0.49
5:23:199:LEU:HD22	5:26:199:LEU:HD13	1.94	0.49
5:24:100:ASN:O	5:24:179:SER:CB	2.57	0.49
5:27:113:MET:HE3	6:65:361:VAL:HA	1.93	0.49
4:3B:57:GLY:HA3	8:A3:162:ARG:HD2	1.93	0.49
3:3K:224:TYR:CD1	4:3L:323:THR:HG21	2.47	0.49
2:4:228:GLU:HB3	2:4:232:ARG:HH21	1.77	0.49
5:52:166:TYR:HD2	5:52:167:LYS:HE2	1.77	0.49
5:54:180:THR:HG23	5:54:183:PHE:H	1.78	0.49
5:59:232:ALA:HA	5:59:235:ARG:HG3	1.93	0.49
3:5E:141:VAL:HG23	3:5E:173:PRO:HD3	1.93	0.49
4:5H:407:GLU:HA	4:5H:410:GLU:HG2	1.93	0.49
4:5L:267:LEU:HD21	4:5L:303:SER:HB2	1.94	0.49
3:5M:119:LEU:HD22	3:5M:156:ARG:HH11	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5N:54:ALA:HB3	4:5N:58:ARG:HB2	1.93	0.49
5:60:162:GLN:HG2	5:60:164:MET:HG2	1.94	0.49
6:64:406:ARG:HH21	6:64:410:GLN:HG3	1.77	0.49
6:66:820:TRP:HD1	6:66:823:HIS:CE1	2.30	0.49
6:67:881:THR:HG22	9:B7:54:ILE:HA	1.93	0.49
6:69:896:LEU:HD23	6:69:897:LEU:HG	1.93	0.49
3:6A:276:ILE:HG23	3:6A:280:LYS:HB2	1.94	0.49
3:6A:320:ARG:HH22	3:6A:360:PRO:HA	1.77	0.49
3:6C:206:ASN:HD21	15:6C:501:GTP:HN22	1.60	0.49
3:6C:298:PRO:HB2	14:K3:249:VAL:HG21	1.94	0.49
4:6D:296:ALA:HB3	7:72:416:TRP:HB3	1.95	0.49
4:6F:388:MET:HG3	3:6G:348:PRO:HD2	1.94	0.49
4:6H:215:LEU:HD21	4:6H:273:LEU:HB3	1.95	0.49
7:76:376:GLU:O	7:76:380:TRP:CB	2.60	0.49
7:77:368:THR:HG23	7:77:371:GLU:H	1.75	0.49
4:7B:73:MET:HE1	4:7B:92:PHE:HA	1.94	0.49
3:7E:410:GLY:C	14:L6:172:ARG:HH21	2.20	0.49
3:7G:134:GLY:HA3	3:7G:165:SER:HB2	1.94	0.49
3:8I:402:ARG:HG3	3:8I:405:VAL:HG11	1.93	0.49
3:9A:306:ASP:HB2	14:M5:256:VAL:HB	1.93	0.49
3:9E:427:ALA:HA	3:9E:430:LYS:HE2	1.93	0.49
3:9G:195:LEU:HD21	3:9G:264:ARG:HH21	1.76	0.49
10:C6:341:TYR:HA	10:C6:390:MET:HE3	1.94	0.49
10:E3:81:ALA:HB3	10:E3:83:ARG:HH21	1.76	0.49
10:E9:92:MET:HE3	10:E9:306:MET:HE1	1.93	0.49
13:J5:271:LEU:HD13	13:J5:286:LEU:HD13	1.93	0.49
13:J6:446:VAL:HG22	13:J6:485:ILE:HB	1.94	0.49
14:L8:111:LEU:HB3	14:L8:117:ARG:HH11	1.76	0.49
14:M3:233:LEU:HA	14:M3:236:PHE:HD2	1.77	0.49
1:a:571:GLU:OE2	1:f:573:GLN:NE2	2.45	0.49
1:s:915:ARG:HH12	1:s:917:ARG:HG3	1.77	0.49
1:A:487:HIS:ND1	1:H:661:ASN:HB3	2.26	0.49
1:O:665:THR:HG22	3:9M:370:LYS:HE2	1.94	0.49
1:V:540:SER:HA	1:V:543:HIS:CD2	2.47	0.49
2:13:205:ILE:HG21	2:14:204:LEU:HD21	1.94	0.49
2:13:275:GLU:HA	2:13:278:HIS:CD2	2.48	0.49
3:1A:19:ALA:HB2	3:1A:228:ASN:HB3	1.93	0.49
4:1B:66:MET:SD	4:1B:147:MET:HB3	2.52	0.49
4:1B:375:GLN:HA	4:1B:378:PHE:HD2	1.77	0.49
3:1E:317:LEU:CB	3:1E:352:LYS:O	2.49	0.49
4:1L:163:ILE:HG12	4:1L:250:LEU:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1L:166:THR:HG23	4:1L:199:VAL:HA	1.94	0.49
5:21:77:ILE:HG22	5:21:87:VAL:HG22	1.95	0.49
3:2I:159:VAL:HG22	6:63:554:LEU:HD22	1.94	0.49
4:2L:267:LEU:HD21	4:2L:371:SER:HB3	1.93	0.49
5:31:53:ARG:HH12	5:31:59:SER:HB2	1.77	0.49
3:3A:373:ARG:HH12	9:B7:33:ASP:HA	1.77	0.49
3:3I:207:GLU:HA	3:3I:210:TYR:HB2	1.95	0.49
3:4I:64:ARG:HG3	3:4I:125:LEU:HD13	1.93	0.49
4:4L:2:ARG:HB3	4:4L:131:GLN:HB2	1.95	0.49
5:55:91:LEU:HB2	5:55:101:TYR:HB2	1.93	0.49
4:5F:136:THR:HG22	4:5F:167:PHE:HB2	1.95	0.49
3:5I:319:TYR:HB3	3:5I:323:VAL:HG21	1.94	0.49
4:5N:314:SER:HA	4:5N:350:LYS:O	2.13	0.49
5:61:40:HIS:CD2	5:61:76:LEU:HB3	2.47	0.49
6:68:915:ASN:HB3	6:68:918:ALA:HB2	1.95	0.49
4:6B:362:LYS:HA	1:h:818:ALA:HB2	1.94	0.49
4:6L:8:GLN:HE22	4:6L:17:GLY:HA3	1.76	0.49
7:75:352:VAL:HG11	14:K5:242:ILE:HG23	1.94	0.49
4:7L:124:ALA:HB2	4:7L:133:PHE:HZ	1.76	0.49
2:8:162:GLN:HA	2:8:165:ARG:HG3	1.94	0.49
7:80:329:PRO:HG2	7:80:332:PHE:HB2	1.93	0.49
7:82:357:VAL:HG11	14:L2:218:LYS:HD2	1.93	0.49
3:8A:332:VAL:HG13	3:8A:351:PHE:HD2	1.77	0.49
3:8I:406:HIS:HA	3:8I:409:VAL:HG12	1.94	0.49
3:8K:70:LEU:HD11	3:8K:110:ILE:HG23	1.94	0.49
4:8L:392:LYS:HG3	4:8L:395:LEU:HD13	1.94	0.49
3:8M:4:VAL:HG21	3:8M:242:LEU:HD13	1.93	0.49
7:90:380:TRP:CD2	7:90:386:ARG:HD2	2.47	0.49
3:9E:139:ASN:O	3:9E:170:CYS:HA	2.12	0.49
3:9E:292:THR:HG21	3:9E:331:ALA:HB1	1.93	0.49
4:9F:272:PRO:HG3	4:9F:364:SER:HA	1.94	0.49
4:9J:149:THR:HG21	4:9J:188:SER:HB2	1.94	0.49
4:9J:384:GLN:HG2	3:9K:348:PRO:HG2	1.95	0.49
10:D8:301:ARG:HH12	14:K0:143:ARG:NH1	2.11	0.49
10:E2:307:MET:HA	10:E2:310:ILE:HG22	1.94	0.49
12:G1:221:MET:HA	12:G1:224:ARG:HE	1.77	0.49
14:M5:178:MET:HA	14:M5:181:LEU:HD12	1.94	0.49
1:C:372:LEU:O	1:C:376:MET:HG2	2.12	0.49
1:J:633:ASP:HB2	4:9B:280:GLN:NE2	2.28	0.49
1:R:481:LEU:HG	1:R:484:GLN:HE21	1.78	0.49
2:12:298:LEU:HA	2:12:301:ARG:HE	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:14:222:GLU:O	2:14:226:VAL:HG23	2.13	0.49
3:1C:132:LEU:HD11	3:1C:135:PHE:HE2	1.77	0.49
4:1D:7:VAL:HB	4:1D:135:ILE:HG22	1.95	0.49
3:1E:271:SER:HB3	3:1E:301:MET:HA	1.94	0.49
4:1H:375:GLN:HE21	4:1H:422:TYR:HB2	1.77	0.49
1:2:941:ARG:HH21	9:B7:468:VAL:HG22	1.77	0.49
3:2A:264:ARG:HH12	6:67:540:PHE:HA	1.77	0.49
4:2B:17:GLY:HA2	4:2B:20:PHE:HB3	1.95	0.49
3:2M:169:PHE:HA	3:2M:202:VAL:HG12	1.94	0.49
4:3J:217:LEU:HD11	8:A7:255:ARG:HH21	1.78	0.49
3:4C:141:VAL:HA	3:4C:147:SER:HB3	1.94	0.49
17:4J:501:GDP:C8	3:4K:248:LEU:HD21	2.47	0.49
4:6N:334:GLN:NE2	4:6N:349:MET:HE3	2.27	0.49
3:7C:327:ASP:HA	3:7C:330:ALA:HB3	1.94	0.49
4:7D:375:GLN:HG2	4:7D:419:VAL:HG13	1.94	0.49
3:7E:318:MET:O	3:7E:375:VAL:HA	2.13	0.49
4:7F:257:LEU:HD21	4:7F:314:SER:HB2	1.93	0.49
3:7G:175:PRO:HG2	3:7G:304:LYS:HG2	1.94	0.49
4:7J:360:GLY:H	1:j:824:GLN:HE21	1.60	0.49
3:7K:312:TYR:HA	3:7K:381:SER:HA	1.93	0.49
4:8B:199:VAL:HB	4:8B:265:PHE:HD1	1.75	0.49
3:8E:217:LEU:HG	3:8E:277:SER:HB3	1.93	0.49
3:8E:332:VAL:HG13	3:8E:351:PHE:HD2	1.76	0.49
4:8F:117:LEU:HA	4:8F:120:VAL:HG22	1.94	0.49
4:8F:208:TYR:CZ	4:8F:220:PRO:HG2	2.48	0.49
4:8L:20:PHE:HA	4:8L:230:SER:HB2	1.93	0.49
7:90:347:ILE:HD11	7:90:350:ARG:HB2	1.94	0.49
4:9B:7:VAL:HB	4:9B:135:ILE:HG13	1.93	0.49
3:9C:9:VAL:HG22	3:9C:68:LEU:HB2	1.94	0.49
10:E6:99:THR:HA	10:E6:103:THR:HG22	1.94	0.49
10:F1:113:THR:HG23	10:F1:286:ARG:HH22	1.77	0.49
12:G6:200:LEU:HA	12:G6:203:VAL:HG12	1.95	0.49
13:J4:485:ILE:HG12	13:J4:511:SER:HB3	1.93	0.49
14:L2:154:MET:HE2	14:L2:156:LEU:HD21	1.94	0.49
1:f:526:GLU:O	1:f:530:LEU:HG	2.12	0.49
1:g:778:SER:HB3	1:g:798:ARG:HH11	1.76	0.49
1:I:465:GLU:HA	1:I:468:GLN:HG3	1.93	0.49
1:J:640:ALA:O	1:J:643:ARG:HG3	2.13	0.49
1:M:607:LEU:HB2	1:N:607:LEU:CB	2.41	0.49
1:M:607:LEU:HD13	1:N:607:LEU:HD13	1.93	0.49
1:Z:485:LEU:O	1:Z:489:GLN:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:10:153:SER:HA	10:D7:123:ASP:HA	1.93	0.49
2:11:205:ILE:HD11	2:12:204:LEU:HD13	1.93	0.49
2:11:260:ARG:HA	2:11:263:VAL:HG12	1.93	0.49
2:16:155:GLN:HA	2:16:158:GLU:HG2	1.93	0.49
3:1C:12:ALA:HB3	3:1C:140:ALA:HB2	1.94	0.49
5:23:155:LYS:HG3	5:23:177:VAL:HG12	1.95	0.49
3:2E:104:ALA:HB2	3:2E:413:MET:HE3	1.93	0.49
3:2E:370:LYS:HG2	9:B3:115:ALA:HB3	1.95	0.49
3:2E:407:TRP:O	3:2E:411:GLU:HB2	2.13	0.49
5:30:166:TYR:HA	5:31:121:ILE:HD11	1.94	0.49
5:37:48:VAL:HG21	5:37:134:LEU:HB3	1.94	0.49
4:3F:135:ILE:O	4:3F:166:THR:HA	2.12	0.49
4:3J:309:ARG:H	4:3J:372:THR:HG22	1.77	0.49
3:3M:228:ASN:HA	3:3M:231:ILE:HG22	1.93	0.49
4:4B:109:GLY:O	4:4B:113:ILE:HB	2.12	0.49
4:4B:287:PRO:HG3	4:4B:329:GLN:NE2	2.27	0.49
3:4E:88:HIS:HB3	3:4E:91:GLN:HB2	1.95	0.49
3:4M:172:TRP:HZ3	3:4M:191:THR:HG21	1.76	0.49
3:4M:204:LEU:HD22	3:4M:231:ILE:HD12	1.94	0.49
5:51:181:GLU:O	5:51:185:ARG:HG2	2.13	0.49
5:53:91:LEU:HB2	5:53:101:TYR:HB2	1.94	0.49
4:5F:290:THR:HA	4:5F:293:MET:HE3	1.94	0.49
4:5J:205:GLU:HB2	6:63:788:LEU:HD22	1.94	0.49
3:5M:198:THR:HG21	3:5M:201:ALA:HB2	1.94	0.49
6:64:330:LEU:HD11	6:64:400:ALA:HA	1.94	0.49
6:69:881:THR:HG22	9:B4:54:ILE:HA	1.95	0.49
4:6H:249:ASP:H	4:6H:252:LYS:HB3	1.78	0.49
3:6K:7:ILE:HG22	3:6K:66:VAL:HB	1.93	0.49
4:6N:253:LEU:O	4:6N:257:LEU:HB2	2.13	0.49
4:7B:190:HIS:HB3	4:7B:415:MET:HE3	1.93	0.49
3:7C:313:MET:HE3	3:7C:382:THR:HG22	1.94	0.49
4:7D:113:ILE:HG13	4:7D:150:LEU:HD11	1.95	0.49
3:7I:225:THR:O	3:7I:229:ARG:HG2	2.11	0.49
4:7J:192:LEU:HG	4:7J:199:VAL:HG21	1.94	0.49
3:7M:53:PHE:HB3	3:7M:61:HIS:HB3	1.94	0.49
3:7M:298:PRO:HB3	3:7M:307:PRO:HD2	1.95	0.49
3:7M:430:LYS:O	3:7M:434:GLU:CB	2.60	0.49
2:8:159:LEU:HA	2:8:162:GLN:HG3	1.93	0.49
7:82:326:PRO:HA	7:82:391:TYR:HD2	1.77	0.49
7:84:247:ILE:HG21	14:L0:73:PHE:HB2	1.94	0.49
3:8E:225:THR:HG21	1:l:742:MET:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8F:179:VAL:HG12	3:8G:258:ASN:HD22	1.78	0.49
7:92:254:ARG:HB3	7:92:258:GLU:HG3	1.93	0.49
4:9D:173:PRO:HG2	4:9D:380:ARG:HB3	1.94	0.49
4:9F:420:SER:HA	4:9F:423:GLN:HG3	1.94	0.49
4:9H:173:PRO:HG2	4:9H:302:ALA:HB3	1.93	0.49
4:9L:6:HIS:HE1	4:9L:8:GLN:HB2	1.77	0.49
8:A5:87:VAL:HG23	1:v:892:SER:HB3	1.95	0.49
8:A8:95:PHE:HB2	8:A8:98:LEU:HD12	1.94	0.49
10:C8:307:MET:HG3	10:C8:396:LEU:HD22	1.93	0.49
12:G3:194:ALA:HB3	12:G3:197:LEU:HD12	1.93	0.49
12:G7:252:LEU:HA	12:G7:255:VAL:HG12	1.95	0.49
13:J4:374:ARG:HH11	13:J4:600:LEU:HD13	1.78	0.49
14:M5:107:ALA:HB3	14:M5:119:HIS:HA	1.94	0.49
1:v:867:PRO:HG3	1:v:944:GLN:HG2	1.94	0.49
1:I:506:VAL:HG11	1:L:332:ARG:HH21	1.76	0.49
1:K:491:LEU:O	1:K:495:PHE:CB	2.57	0.49
1:T:640:ALA:HB3	1:i:828:CYS:HB2	1.94	0.49
1:V:439:LEU:HA	1:V:442:GLU:HG3	1.94	0.49
4:1B:216:LYS:HE2	4:1B:275:SER:HB2	1.95	0.49
4:1D:179:VAL:HG23	3:1E:352:LYS:HD2	1.94	0.49
4:1J:290:THR:HG21	4:1J:329:GLN:HB3	1.95	0.49
4:1N:336:LYS:HD3	4:1N:337:ASN:HB2	1.95	0.49
3:2A:402:ARG:HG2	5:31:222:LEU:HD22	1.94	0.49
4:2B:80:PRO:HG2	9:B5:81:LEU:HD21	1.93	0.49
17:2F:501:GDP:C8	3:2G:248:LEU:HD21	2.47	0.49
4:2H:272:PRO:HG3	4:2H:284:LEU:HD11	1.94	0.49
3:2I:167:LEU:HD23	3:2I:200:VAL:HB	1.94	0.49
3:2I:269:LEU:HD22	3:2I:303:ALA:HB3	1.95	0.49
2:3:314:TYR:HD1	2:3:317:MET:HE1	1.78	0.49
3:3K:203:MET:HE2	3:3K:267:PHE:HB3	1.95	0.49
5:40:164:MET:HE1	5:40:169:ILE:HG12	1.94	0.49
4:4J:20:PHE:HA	4:4J:230:SER:HB2	1.95	0.49
4:4J:169:VAL:HG12	4:4J:202:ILE:HB	1.95	0.49
4:4L:334:GLN:HE22	4:4L:347:ASN:H	1.60	0.49
4:5N:149:THR:HA	4:5N:191:GLN:HE22	1.77	0.49
7:77:320:TRP:HE1	14:K6:128:ARG:NH2	2.10	0.49
3:7A:329:ASN:HA	3:7A:332:VAL:HG12	1.94	0.49
4:7B:262:ARG:HH21	14:L8:139:LEU:HD13	1.76	0.49
3:7C:268:MET:HE3	3:7C:380:ASN:HB2	1.95	0.49
3:7G:133:GLN:HE22	3:7G:242:LEU:HD22	1.78	0.49
4:7H:295:ASP:HB3	4:7H:297:LYS:HG2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7K:274:PRO:HG2	3:7K:371:VAL:HG11	1.94	0.49
7:83:254:ARG:HB3	7:83:258:GLU:HG3	1.94	0.49
4:8B:132:GLY:HA3	4:8B:163:ILE:HG13	1.94	0.49
4:8D:329:GLN:HA	4:8D:332:ASN:HB2	1.94	0.49
4:8H:68:LEU:HD21	4:8H:108:GLU:HB3	1.93	0.49
4:9F:309:ARG:HD3	4:9F:342:VAL:HA	1.95	0.49
4:9L:6:HIS:CE1	4:9L:8:GLN:HB2	2.47	0.49
8:A3:39:LEU:HD11	8:A3:80:MET:HE2	1.94	0.49
9:B4:36:GLU:HG3	9:B4:44:LEU:HD22	1.93	0.49
14:M4:155:TRP:HB3	14:M4:157:TYR:HE1	1.78	0.49
14:M7:223:SER:H	14:M7:225:GLU:HG2	1.77	0.49
1:f:589:THR:O	1:f:592:ARG:HG3	2.13	0.49
1:E:303:GLY:HA2	1:F:498:LYS:HE3	1.93	0.49
2:11:248:LEU:HD23	2:11:251:ARG:HD3	1.95	0.49
2:12:245:GLU:HA	2:12:248:LEU:HB3	1.94	0.49
4:1D:113:ILE:HA	4:1D:116:VAL:HG12	1.93	0.49
3:1E:167:LEU:HG	3:1E:200:VAL:HB	1.94	0.49
3:1G:88:HIS:CD2	3:1G:90:GLU:HG2	2.48	0.49
3:1G:377:MET:HG2	3:1G:379:SER:HB3	1.94	0.49
4:2H:203:ASP:HB2	4:2H:301:CYS:HA	1.94	0.49
5:31:48:VAL:HG21	5:31:134:LEU:HD22	1.95	0.49
5:37:221:LEU:HD21	13:J2:306:ARG:HE	1.77	0.49
5:38:165:GLU:HA	13:J2:337:ARG:HB2	1.95	0.49
4:4D:232:ALA:HB1	4:4D:268:ILE:HG21	1.94	0.49
3:4I:7:ILE:HG21	3:4I:153:LEU:HD21	1.95	0.49
3:4I:265:ILE:HG22	3:4I:380:ASN:HD21	1.77	0.49
5:50:139:LYS:HG3	5:50:140:GLU:H	1.78	0.49
5:56:20:PHE:HB2	6:69:596:PRO:HB3	1.94	0.49
5:59:55:GLN:HB2	5:59:151:HIS:HA	1.94	0.49
3:7C:5:ILE:HG12	3:7C:64:ARG:HG2	1.95	0.49
3:7G:98:ASP:HB3	3:7G:100:ALA:H	1.78	0.49
4:7J:322:SER:HB2	4:7J:325:GLU:OE1	2.13	0.49
7:87:374:ASP:O	7:87:378:MET:HG2	2.12	0.49
4:8F:265:PHE:HB3	4:8F:374:ILE:HD13	1.95	0.49
4:8H:5:VAL:HG11	4:8H:120:VAL:HG23	1.93	0.49
3:8I:217:LEU:HD23	3:8I:275:ILE:HG23	1.95	0.49
7:92:334:LEU:HD23	7:92:337:LYS:HD2	1.94	0.49
7:93:350:ARG:HD3	7:93:379:LEU:HD13	1.94	0.49
7:96:341:SER:HB2	14:M6:216:GLY:HA3	1.95	0.49
3:9E:204:LEU:HG	3:9E:302:MET:HE2	1.95	0.49
3:9G:238:LEU:HD11	3:9G:378:ILE:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A4:66:LEU:HA	8:A4:69:MET:HB3	1.93	0.49
10:E3:354:ARG:HD3	10:E3:360:ALA:HA	1.94	0.49
12:G1:220:PRO:HD2	12:G1:223:LEU:HD12	1.94	0.49
14:K3:148:ILE:HD11	14:K3:173:PRO:HG3	1.93	0.49
14:L0:185:ILE:O	14:L0:189:ILE:HG22	2.13	0.49
1:a:508:VAL:HG22	1:a:512:LYS:HE3	1.95	0.49
1:B:465:GLU:HG2	1:K:355:ARG:HD2	1.94	0.49
1:I:617:MET:HB3	1:I:618:ARG:HH21	1.77	0.49
1:R:495:PHE:HB3	1:V:495:PHE:CE2	2.48	0.49
2:15:194:LYS:HA	2:15:197:VAL:HG12	1.95	0.49
3:1A:75:VAL:HB	3:1A:92:LEU:HD12	1.95	0.49
4:1D:68:LEU:HD12	4:1D:143:THR:HG22	1.94	0.49
3:1E:68:LEU:HD23	3:1E:149:LEU:HD21	1.95	0.49
5:20:195:LEU:HD13	5:25:192:TYR:HE2	1.77	0.49
5:24:52:ILE:HG12	5:24:67:ARG:HB2	1.95	0.49
5:27:97:LEU:HB3	5:27:188:MET:HE2	1.94	0.49
5:30:129:VAL:HG12	5:30:133:MET:HE2	1.95	0.49
4:3B:117:LEU:HA	4:3B:120:VAL:HG12	1.94	0.49
4:3D:135:ILE:HG21	4:3D:152:ILE:HD11	1.94	0.49
4:3F:200:GLN:HG2	4:3F:266:PHE:HB2	1.94	0.49
4:3L:42:LEU:HD23	4:3L:356:ILE:HD11	1.95	0.49
2:4:165:ARG:HA	2:4:168:ARG:HB2	1.93	0.49
5:43:89:VAL:HB	5:43:103:HIS:HB3	1.95	0.49
5:47:135:ASN:HB3	13:J6:648:GLU:HB2	1.95	0.49
3:4A:221:ARG:NH2	4:4B:325:GLU:HG2	2.28	0.49
3:4M:298:PRO:HB3	3:4M:307:PRO:HD2	1.95	0.49
5:52:162:GLN:HB2	5:52:171:LEU:HD23	1.94	0.49
5:52:198:LYS:HA	5:52:201:LEU:HD12	1.95	0.49
4:5H:6:HIS:HD2	4:5H:134:GLN:HB3	1.77	0.49
3:5I:70:LEU:HD23	3:5I:114:ILE:HD13	1.95	0.49
3:5M:389:SER:HA	3:5M:392:ASP:OD2	2.13	0.49
6:69:901:LYS:HG3	1:w:879:VAL:HG11	1.95	0.49
4:6B:174:LYS:HG2	7:73:412:MET:HB3	1.95	0.49
3:6C:209:ILE:HA	3:6C:212:ILE:HB	1.94	0.49
4:6F:16:ILE:HA	4:6F:226:ASN:HB3	1.95	0.49
4:6L:54:ALA:HB3	4:6L:58:ARG:HB3	1.94	0.49
4:7D:170:PHE:HB3	4:7D:380:ARG:HH12	1.78	0.49
4:7F:399:THR:HA	4:7F:403:MET:HB2	1.95	0.49
4:7J:209:ASP:HB2	7:83:412:MET:HB2	1.93	0.49
4:7L:138:SER:HA	4:7L:169:VAL:HB	1.94	0.49
3:7M:5:ILE:HD13	3:7M:64:ARG:HD3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8F:252:LYS:HG3	4:8F:350:LYS:HE3	1.95	0.49
3:8G:12:ALA:HB3	3:8G:140:ALA:HB2	1.94	0.49
4:8H:284:LEU:HD23	4:8H:362:LYS:HE2	1.95	0.49
7:91:254:ARG:HB3	7:91:258:GLU:HG3	1.94	0.49
7:97:282:ARG:HH21	7:97:287:LEU:HB2	1.77	0.49
7:97:347:ILE:HD12	7:97:352:VAL:HB	1.94	0.49
4:9D:192:LEU:HG	4:9D:199:VAL:HG21	1.94	0.49
4:9J:313:ALA:O	4:9J:349:MET:HA	2.12	0.49
10:D6:78:ARG:HB3	10:D6:82:GLY:HA2	1.95	0.49
10:D9:114:PRO:HB3	10:D9:138:ARG:HD2	1.95	0.49
10:F3:331:ILE:HD12	10:F3:335:LEU:HG	1.94	0.49
12:G5:260:ASP:HA	12:G5:263:TYR:HD2	1.78	0.49
13:J1:353:ARG:HH21	13:J1:357:LEU:HD22	1.78	0.49
13:J6:381:ALA:HB1	13:J6:428:LYS:HD2	1.94	0.49
14:M6:82:TYR:HB2	14:M6:87:ARG:HH22	1.77	0.49
1:a:617:MET:HG3	1:f:614:LEU:HD12	1.92	0.49
1:h:740:PRO:HB3	1:h:753:LEU:HD23	1.95	0.49
1:l:771:VAL:HG23	1:l:772:GLU:H	1.77	0.49
1:C:343:GLU:CD	1:Z:455:LYS:HE2	2.38	0.49
1:L:338:HIS:CE1	1:L:342:MET:HE3	2.48	0.49
1:R:593:GLN:O	1:R:597:ILE:HB	2.13	0.49
2:12:199:SER:C	2:12:201:VAL:H	2.21	0.49
2:12:300:VAL:HG22	13:J4:283:TRP:CD2	2.48	0.49
4:1F:135:ILE:HB	4:1F:166:THR:HG22	1.94	0.49
4:1J:398:TYR:HB3	4:1J:408:PHE:HZ	1.78	0.49
3:1K:262:TYR:HB2	3:1K:265:ILE:HG22	1.95	0.49
5:20:106:ASN:HB2	5:20:109:LEU:HD23	1.94	0.49
5:25:158:LEU:HB3	5:25:174:LEU:O	2.13	0.49
3:2E:109:THR:HG21	3:2E:411:GLU:HG3	1.95	0.49
5:31:161:ILE:HG13	5:31:163:SER:H	1.78	0.49
4:3J:228:LEU:HD11	4:3J:273:LEU:HD11	1.94	0.49
4:4L:21:TRP:HA	4:4L:24:ILE:HG22	1.94	0.49
4:5B:313:ALA:HB3	4:5B:349:MET:HB2	1.94	0.49
4:5N:107:THR:HG22	4:5N:108:GLU:H	1.78	0.49
5:62:91:LEU:HB2	5:62:101:TYR:HB3	1.94	0.49
4:6B:47:ILE:H	1:q:915:ARG:HH21	1.60	0.49
4:6D:249:ASP:H	4:6D:252:LYS:HB3	1.77	0.49
4:6L:193:VAL:HG22	4:6L:262:ARG:HH21	1.76	0.49
4:6N:315:ALA:HB1	4:6N:365:VAL:HG21	1.95	0.49
2:7:324:GLU:HG3	2:8:324:GLU:HG2	1.95	0.49
4:7B:334:GLN:HB3	4:7B:349:MET:HE1	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7G:141:VAL:HG22	3:7G:187:SER:HA	1.94	0.49
4:7H:4:ILE:HD11	4:7H:240:LEU:HD13	1.93	0.49
4:7J:245:GLN:HB2	4:7J:353:VAL:HB	1.94	0.49
3:7K:310:GLY:HA3	3:7K:383:ALA:HB2	1.94	0.49
3:7M:287:SER:HA	3:7M:373:ARG:HH22	1.77	0.49
4:8F:418:LEU:HD23	14:M3:139:LEU:HD21	1.94	0.49
3:8I:104:ALA:HA	3:8I:413:MET:HE3	1.95	0.49
3:8M:184:PRO:HG3	3:8M:394:LYS:HD3	1.95	0.49
7:91:279:ARG:HH22	10:F2:148:MET:HE3	1.77	0.49
7:92:411:MET:HE1	4:9F:174:LYS:HG2	1.95	0.49
7:97:381:PHE:HB3	7:97:384:GLU:HB2	1.95	0.49
4:9D:271:ALA:HB2	4:9D:365:VAL:HG22	1.95	0.49
3:9G:119:LEU:HA	3:9G:122:ILE:HG22	1.95	0.49
4:9J:282:ARG:HH21	4:9J:284:LEU:HD13	1.77	0.49
4:9L:271:ALA:HB2	4:9L:298:ASN:HD21	1.77	0.49
3:9M:79:ARG:HH21	3:9M:92:LEU:HB2	1.78	0.49
8:A2:33:LEU:HG	8:A2:77:GLU:HG3	1.95	0.49
8:A7:200:TYR:HB3	8:A7:205:CYS:HB2	1.93	0.49
9:B6:122:TYR:HE2	9:B6:146:VAL:HG11	1.76	0.49
10:C8:100:SER:HB2	10:C8:389:PHE:CZ	2.46	0.49
10:C9:318:PRO:HA	10:C9:321:ARG:HG2	1.95	0.49
10:E2:86:LEU:HD12	10:E2:313:TYR:HB3	1.93	0.49
10:E9:54:HIS:CE1	10:E9:85:PRO:HD3	2.47	0.49
13:J2:418:LEU:HB2	13:J2:472:VAL:HG21	1.94	0.49
13:J3:289:ILE:HG23	13:J3:300:LEU:HD21	1.94	0.49
14:L1:155:TRP:HB2	14:L1:218:LYS:HD3	1.95	0.49
14:L4:220:LEU:HD21	14:L4:236:PHE:HB3	1.95	0.49
14:L5:178:MET:HE1	14:L5:207:ILE:HG22	1.94	0.49
14:M5:218:LYS:HE2	14:M5:241:VAL:HG22	1.94	0.49
1:a:562:ILE:HG21	1:f:562:ILE:HG13	1.93	0.49
1:d:377:HIS:HA	1:d:380:HIS:ND1	2.28	0.49
1:B:469:LEU:HB3	1:K:362:VAL:HG21	1.95	0.49
1:G:302:GLU:HG3	1:G:310:PHE:CD2	2.48	0.49
1:G:399:GLU:HA	1:G:402:GLN:HG2	1.94	0.49
1:I:446:LEU:HB3	1:J:446:LEU:HD22	1.95	0.49
1:I:639:LEU:HD22	1:J:638:LEU:HD21	1.95	0.49
1:L:429:ARG:HH22	1:o:870:GLY:HA2	1.78	0.49
1:M:617:MET:HE2	1:N:618:ARG:HD3	1.94	0.49
2:14:172:PHE:HA	2:14:175:TYR:CE1	2.48	0.49
4:1B:391:ARG:HD2	3:1C:346:TRP:CD2	2.48	0.49
4:1D:70:PRO:HG3	4:1D:92:PHE:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1D:319:GLY:HA2	4:1D:357:PRO:HD3	1.95	0.49
5:25:73:VAL:HG12	5:25:91:LEU:HD22	1.95	0.49
5:28:75:ILE:HG12	5:28:89:VAL:HG12	1.94	0.49
3:2A:17:GLY:HA3	3:2A:67:PHE:HE1	1.78	0.49
4:2F:20:PHE:HA	4:2F:230:SER:HB2	1.95	0.49
4:2F:73:MET:HE2	4:2F:90:PHE:HD1	1.77	0.49
3:2I:274:PRO:HD3	3:2I:375:VAL:HG12	1.95	0.49
3:2K:370:LYS:HE2	9:B4:182:PRO:HG3	1.95	0.49
4:2L:182:PRO:HD3	4:2L:384:GLN:HE22	1.77	0.49
3:2M:324:VAL:HG12	3:2M:326:LYS:H	1.78	0.49
5:46:158:LEU:HB3	5:46:174:LEU:HB2	1.93	0.49
3:4A:395:PHE:HZ	3:4A:418:PHE:HB3	1.77	0.49
3:4I:301:MET:HG3	3:4I:307:PRO:HD3	1.94	0.49
5:50:129:VAL:HG12	5:50:132:LYS:NZ	2.28	0.49
5:52:88:ARG:HA	5:52:104:ALA:H	1.78	0.49
4:5B:14:ASN:HB3	4:5B:76:VAL:HG21	1.94	0.49
3:5M:269:LEU:HD13	3:5M:301:MET:SD	2.53	0.49
6:63:414:VAL:HG22	6:63:435:VAL:HG23	1.95	0.49
6:63:976:GLU:HG2	6:63:979:ARG:HH22	1.77	0.49
6:64:325:ARG:HE	6:64:337:LEU:HD22	1.77	0.49
6:68:861:TRP:HB3	6:68:926:PHE:HB2	1.94	0.49
6:69:326:THR:HG22	6:69:329:GLN:HG3	1.94	0.49
4:6B:398:TYR:HB3	4:6B:403:MET:HG3	1.95	0.49
7:75:356:LEU:HD11	7:75:367:LEU:HD11	1.94	0.49
7:79:376:GLU:O	7:79:380:TRP:CB	2.61	0.49
3:7E:119:LEU:HD13	3:7E:122:ILE:HD11	1.94	0.49
3:7E:191:THR:HG21	3:7E:425:LEU:HD13	1.94	0.49
4:7H:203:ASP:HB2	4:7H:301:CYS:HA	1.93	0.49
3:7M:214:ARG:HH21	3:7M:220:GLU:HA	1.78	0.49
7:84:326:PRO:HA	7:84:391:TYR:HD2	1.78	0.49
4:8F:25:SER:HB2	4:8F:30:ILE:HB	1.95	0.49
4:8L:68:LEU:HA	4:8L:93:GLY:HA3	1.94	0.49
3:8M:212:ILE:HD11	3:8M:300:SER:HA	1.95	0.49
3:9M:137:MET:HG3	3:9M:168:ASN:HA	1.95	0.49
8:A4:84:TYR:HB2	8:A4:98:LEU:HD12	1.95	0.49
9:B1:527:LEU:HD12	9:B1:534:THR:HG22	1.95	0.49
10:D9:317:LEU:HA	10:D9:320:LYS:HG2	1.93	0.49
10:E6:91:GLN:HA	10:E6:94:VAL:HG12	1.95	0.49
10:E7:86:LEU:HD12	10:E7:319:LEU:HB3	1.95	0.49
10:F3:109:ASN:HB2	10:F3:295:GLN:HE22	1.77	0.49
10:F3:113:THR:HG23	10:F3:286:ARG:HH22	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G8:223:LEU:HA	12:G8:226:ILE:HD12	1.95	0.49
12:H7:323:HIS:HB3	12:H7:329:LEU:HD22	1.95	0.49
13:J4:470:ARG:HB2	13:J4:500:LEU:HD23	1.94	0.49
13:J5:289:ILE:HG23	13:J5:300:LEU:HD21	1.94	0.49
1:o:900:GLU:O	1:o:904:ILE:HG13	2.12	0.49
1:I:372:LEU:HB3	1:J:372:LEU:HD11	1.94	0.48
1:J:661:ASN:O	1:J:664:ILE:HG12	2.13	0.48
1:M:662:ASP:O	1:M:666:VAL:HG23	2.13	0.48
1:Y:513:ARG:HH12	1:c:512:LYS:NZ	2.11	0.48
1:1:941:ARG:NH2	9:B5:450:GLU:HA	2.28	0.48
2:12:208:TYR:HB3	2:12:209:ARG:HH21	1.78	0.48
3:1C:332:VAL:HA	3:1C:335:ILE:HD12	1.94	0.48
5:25:144:PHE:CE1	5:25:162:GLN:HG2	2.47	0.48
4:2B:179:VAL:HG23	3:2C:349:THR:HG23	1.95	0.48
4:2H:12:CYS:HB3	4:2H:138:SER:HB2	1.95	0.48
5:32:179:SER:HB3	5:32:183:PHE:HB2	1.94	0.48
3:3A:296:PHE:CD2	3:3A:335:ILE:HG13	2.47	0.48
3:3M:360:PRO:HG3	3:3M:374:ALA:HB2	1.94	0.48
5:44:48:VAL:HG12	5:44:138:ILE:HG13	1.95	0.48
5:45:216:LYS:HZ1	5:46:220:LEU:HD22	1.77	0.48
3:4A:237:SER:HA	3:4A:320:ARG:HE	1.79	0.48
4:4H:198:GLU:HG2	4:4H:266:PHE:HE2	1.78	0.48
4:4J:87:PRO:HA	4:4J:90:PHE:HD2	1.77	0.48
5:53:108:ASP:HA	5:53:111:ARG:HG2	1.94	0.48
3:5A:231:ILE:HA	3:5A:234:VAL:HG12	1.95	0.48
4:5B:134:GLN:HA	4:5B:165:GLU:HG3	1.94	0.48
3:5I:115:VAL:HG21	3:5I:152:LEU:HD22	1.94	0.48
6:64:320:GLN:HB3	6:64:321:ILE:HD12	1.95	0.48
3:7G:5:ILE:HD12	3:7G:132:LEU:HD13	1.95	0.48
3:7K:9:VAL:HG12	3:7K:146:GLY:HA2	1.94	0.48
3:7M:301:MET:HE1	3:7M:305:CYS:H	1.77	0.48
7:85:287:LEU:HD22	14:L6:179:GLU:HB2	1.94	0.48
7:87:382:ASP:HB2	3:8C:437:ILE:HG21	1.94	0.48
4:8B:215:LEU:HD12	4:8B:275:SER:HA	1.93	0.48
3:8E:73:THR:HA	4:8F:46:ARG:HH22	1.77	0.48
4:8J:73:MET:HG3	4:8J:92:PHE:HB3	1.95	0.48
4:8J:268:ILE:HG23	4:8J:300:MET:HE3	1.95	0.48
3:8M:242:LEU:HD21	3:8M:252:VAL:HG23	1.95	0.48
7:96:412:MET:HG3	4:9H:205:GLU:HG3	1.95	0.48
3:9C:259:LEU:HD11	3:9C:316:CYS:HB2	1.95	0.48
4:9D:376:GLU:HA	4:9D:379:LYS:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9G:53:PHE:HB3	3:9G:61:HIS:HB3	1.94	0.48
3:9K:240:ALA:HA	3:9K:243:ARG:HB2	1.93	0.48
8:A9:317:LEU:HD13	8:A9:371:VAL:HG12	1.95	0.48
10:C0:349:PHE:CD1	10:C0:361:TRP:HB3	2.47	0.48
10:C0:365:ASN:HB3	10:C0:368:ASP:HB2	1.95	0.48
10:E4:119:LYS:HA	10:E4:130:PRO:HB3	1.93	0.48
10:E4:361:TRP:HZ3	10:E4:371:ARG:HH21	1.61	0.48
10:F2:317:LEU:HA	10:F2:320:LYS:HG2	1.95	0.48
1:a:530:LEU:O	1:a:534:GLN:HG3	2.12	0.48
1:i:785:CYS:HA	1:i:791:ARG:HG3	1.95	0.48
1:q:887:VAL:HA	1:q:890:LEU:HD12	1.94	0.48
1:E:287:PRO:HB2	1:E:288:LYS:HD2	1.95	0.48
1:N:495:PHE:O	1:N:499:ARG:HG2	2.13	0.48
1:W:412:GLU:HA	1:W:415:LEU:HD12	1.95	0.48
1:1:884:PRO:HA	1:1:887:VAL:HG22	1.94	0.48
3:1I:185:TYR:HE1	3:1I:399:TYR:HD2	1.61	0.48
4:1L:385:PHE:HE2	4:1L:412:GLU:HB2	1.77	0.48
5:21:158:LEU:HG	5:21:174:LEU:HB2	1.96	0.48
5:24:89:VAL:HG22	5:24:103:HIS:HB3	1.95	0.48
3:2A:159:VAL:HG13	6:67:558:LYS:NZ	2.27	0.48
4:2B:54:ALA:HB3	4:2B:58:ARG:HB3	1.94	0.48
4:2B:72:THR:HG22	3:2C:249:ASN:HD22	1.78	0.48
4:2D:83:GLN:NE2	9:B3:54:ILE:H	2.10	0.48
4:2J:314:SER:HA	4:2J:350:LYS:HB3	1.94	0.48
3:2M:193:SER:HB2	3:2M:197:HIS:HD2	1.78	0.48
5:31:109:LEU:HD13	6:66:364:THR:HG22	1.93	0.48
4:3B:9:GLY:HA2	4:3B:66:MET:HG3	1.96	0.48
3:3E:203:MET:HE2	3:3E:267:PHE:HB3	1.94	0.48
4:3J:135:ILE:HB	4:3J:166:THR:HG22	1.95	0.48
5:45:214:LYS:HE3	13:J6:306:ARG:HG3	1.94	0.48
3:4C:194:LEU:HB3	3:4C:267:PHE:HE1	1.78	0.48
4:4H:153:SER:HA	4:4H:195:ASN:HD22	1.78	0.48
4:4L:358:PRO:HG2	4:4L:361:LEU:HB2	1.95	0.48
4:4L:384:GLN:HE22	3:4M:348:PRO:HG2	1.77	0.48
3:5C:306:ASP:HB3	3:5C:309:HIS:CE1	2.48	0.48
4:5D:91:VAL:HB	4:5D:112:LEU:HD21	1.95	0.48
4:5H:399:THR:HA	4:5H:403:MET:HB2	1.95	0.48
4:5L:424:GLN:HB3	14:K6:143:ARG:HG2	1.95	0.48
4:5N:284:LEU:HD23	4:5N:362:LYS:HB2	1.95	0.48
4:5N:289:LEU:HD12	4:5N:365:VAL:HG12	1.94	0.48
6:67:866:ARG:HE	6:67:921:VAL:HG13	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6B:313:ALA:HB1	4:6B:367:PHE:HE1	1.78	0.48
4:6D:230:SER:HA	4:6D:233:MET:HB3	1.94	0.48
3:6M:195:LEU:HD12	3:6M:428:LEU:HD22	1.95	0.48
7:71:320:TRP:HB2	7:71:396:ASP:HB2	1.94	0.48
3:7C:348:PRO:HB2	14:L1:111:LEU:HD22	1.96	0.48
3:7I:222:PRO:HD2	4:7J:324:LYS:HG2	1.96	0.48
3:8I:18:ASN:HD21	3:8I:78:VAL:HG22	1.79	0.48
3:8I:112:LYS:HA	3:8I:115:VAL:HG22	1.95	0.48
7:92:352:VAL:HG13	14:M2:244:LYS:HA	1.94	0.48
7:96:405:VAL:HG11	3:9I:333:ALA:HB3	1.95	0.48
3:9C:397:LEU:HD22	4:9D:346:PRO:HD3	1.93	0.48
4:9H:20:PHE:HB2	4:9H:233:MET:HE3	1.94	0.48
3:9I:115:VAL:HA	3:9I:118:SER:HB2	1.95	0.48
3:9K:93:ILE:HD12	3:9K:117:LEU:HG	1.93	0.48
8:A1:39:LEU:HA	8:A1:42:VAL:HG12	1.95	0.48
10:D0:397:PHE:O	10:D0:401:MET:HG2	2.14	0.48
10:D2:66:LEU:HD21	10:D2:312:LYS:HG3	1.96	0.48
10:D8:325:GLU:HA	10:D8:328:LYS:NZ	2.28	0.48
10:D9:51:TYR:HB3	10:D9:54:HIS:CD2	2.47	0.48
12:G1:264:ILE:HB	12:G1:268:ARG:HD2	1.95	0.48
1:a:600:LEU:HD12	1:f:600:LEU:HB2	1.94	0.48
1:f:574:LYS:O	1:f:577:GLN:HB2	2.13	0.48
3:1A:382:THR:HG21	3:1A:436:GLY:HA3	1.95	0.48
3:1E:237:SER:HA	3:1E:320:ARG:HH11	1.78	0.48
3:1E:390:ARG:HA	3:1E:393:HIS:CE1	2.48	0.48
4:1F:217:LEU:HD23	4:1F:220:PRO:HB3	1.94	0.48
4:1H:112:LEU:HD23	4:1H:147:MET:HE1	1.95	0.48
3:1K:261:PRO:HD2	3:1K:265:ILE:HG23	1.95	0.48
5:23:148:LEU:HD12	5:23:158:LEU:HD13	1.94	0.48
4:2B:135:ILE:HD13	4:2B:152:ILE:HD12	1.94	0.48
4:2B:230:SER:HA	4:2B:233:MET:HB3	1.96	0.48
4:2B:388:MET:HE1	3:2C:347:CYS:HA	1.96	0.48
4:2F:201:VAL:HG21	4:2F:374:ILE:HD11	1.94	0.48
3:2K:232:ALA:HA	3:2K:235:ILE:HD12	1.95	0.48
3:2K:238:LEU:HD11	3:2K:378:ILE:HG13	1.94	0.48
5:33:51:GLU:HB3	5:33:147:VAL:HG22	1.95	0.48
5:38:153:ASN:HD21	5:38:155:LYS:HD3	1.78	0.48
5:46:156:ALA:HB3	5:46:176:CYS:HB2	1.95	0.48
4:4D:207:LEU:HD23	4:4D:225:LEU:HB3	1.94	0.48
3:4K:434:GLU:OE2	6:69:825:ARG:HA	2.13	0.48
5:54:44:TYR:CZ	5:54:46:ARG:HB2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:55:65:VAL:HG22	5:55:67:ARG:HG2	1.95	0.48
5:56:145:LEU:HB2	5:56:161:ILE:HB	1.95	0.48
5:57:98:PHE:H	5:58:185:ARG:HH22	1.60	0.48
5:58:139:LYS:HG3	5:58:140:GLU:H	1.78	0.48
3:5C:313:MET:HE2	3:5C:382:THR:HG22	1.95	0.48
4:5D:20:PHE:HA	4:5D:230:SER:HB2	1.95	0.48
4:5D:207:LEU:HB3	4:5D:225:LEU:HD22	1.95	0.48
5:60:33:ASP:HB3	5:60:36:LEU:HB2	1.95	0.48
5:62:89:VAL:HB	5:62:103:HIS:HB3	1.95	0.48
5:62:139:LYS:HG3	5:62:140:GLU:H	1.77	0.48
3:6C:191:THR:HA	3:6C:194:LEU:HB3	1.95	0.48
3:6I:288:VAL:HA	3:6I:291:ILE:HG22	1.95	0.48
4:6N:138:SER:HA	4:6N:169:VAL:HG22	1.95	0.48
4:6N:330:MET:HE3	4:6N:349:MET:HG3	1.94	0.48
4:7F:113:ILE:HA	4:7F:116:VAL:HG12	1.93	0.48
3:7K:169:PHE:HZ	3:7K:238:LEU:HD13	1.77	0.48
3:7M:305:CYS:SG	3:7M:384:ILE:HA	2.52	0.48
3:8C:319:TYR:HB3	3:8C:323:VAL:HG11	1.94	0.48
3:8E:71:GLU:HG2	3:8E:73:THR:HG22	1.95	0.48
3:8G:67:PHE:HB2	3:8G:92:LEU:HA	1.96	0.48
3:8M:394:LYS:HA	3:8M:397:LEU:HD23	1.94	0.48
3:9G:316:CYS:HA	3:9G:352:LYS:HB3	1.95	0.48
3:9I:204:LEU:HD23	3:9I:209:ILE:HD11	1.96	0.48
3:9K:267:PHE:HE2	3:9K:428:LEU:HD21	1.77	0.48
8:A1:55:GLY:HA3	8:A1:96:LYS:HG3	1.95	0.48
8:A7:80:MET:HE2	9:B6:465:LEU:HD11	1.94	0.48
8:A9:271:VAL:HG12	8:A9:273:PRO:HD3	1.94	0.48
9:B3:163:LEU:HB3	9:B3:167:ARG:NH1	2.29	0.48
10:D2:94:VAL:HG13	10:D2:335:LEU:HD21	1.94	0.48
12:F7:221:MET:HE2	12:F8:230:VAL:HG12	1.95	0.48
14:K6:207:ILE:HG23	14:K6:212:ASP:HB2	1.96	0.48
14:M1:207:ILE:HG23	14:M1:212:ASP:HB2	1.96	0.48
14:M3:99:ILE:HB	14:M3:105:LEU:HD11	1.94	0.48
14:M7:99:ILE:HG13	14:M7:105:LEU:HD11	1.95	0.48
14:M7:185:ILE:HG23	14:M7:189:ILE:HD13	1.95	0.48
1:B:404:PHE:CB	1:E:406:ARG:HH22	2.25	0.48
1:J:601:ARG:HA	1:J:604:ILE:HB	1.96	0.48
1:T:659:LEU:HB3	1:X:663:LEU:HD11	1.94	0.48
4:1D:61:PRO:HD3	4:1D:84:LEU:HG	1.96	0.48
4:1F:120:VAL:HG21	4:1F:151:LEU:HD11	1.95	0.48
3:1G:10:GLY:HA2	3:1G:145:THR:HG23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1M:407:TRP:HZ3	4:1N:255:VAL:HA	1.78	0.48
4:2F:54:ALA:HB3	4:2F:58:ARG:HB2	1.95	0.48
3:2G:259:LEU:HD21	3:2G:316:CYS:HB2	1.95	0.48
3:2G:278:ALA:HB2	9:B1:120:VAL:HG12	1.95	0.48
4:2J:208:TYR:HD2	3:2K:329:ASN:HD22	1.61	0.48
3:3A:240:ALA:HB1	3:3A:356:ASN:ND2	2.24	0.48
4:3B:170:PHE:CE2	4:3B:201:VAL:HG12	2.48	0.48
4:3D:86:ARG:HD2	4:4D:281:TYR:HB3	1.94	0.48
4:3L:11:GLN:HA	4:3L:72:THR:HG21	1.94	0.48
3:3M:392:ASP:HB3	3:3M:422:ARG:HH12	1.78	0.48
2:4:183:ARG:HA	2:4:186:HIS:CD2	2.48	0.48
5:46:165:GLU:HA	13:J6:335:GLN:HA	1.95	0.48
3:4A:3:GLU:HA	3:4A:51:THR:HA	1.96	0.48
3:4A:36:MET:HE3	3:4A:61:HIS:CE1	2.48	0.48
4:4F:217:LEU:HD21	8:A1:112:HIS:HB2	1.95	0.48
4:4J:248:SER:HA	4:4J:252:LYS:HD2	1.94	0.48
2:5:157:PHE:HA	2:5:160:LEU:HD23	1.96	0.48
3:5E:238:LEU:HD12	3:5E:378:ILE:HG13	1.95	0.48
4:5H:272:PRO:HG3	4:5H:284:LEU:HD11	1.95	0.48
3:5K:223:THR:HA	4:5L:323:THR:HG22	1.95	0.48
4:5L:290:THR:HG21	4:5L:329:GLN:HE21	1.78	0.48
4:5L:393:ALA:HA	3:5M:262:TYR:HE2	1.77	0.48
6:68:614:PRO:HA	6:68:617:VAL:HG12	1.94	0.48
7:77:400:CYS:SG	14:K6:105:LEU:HD11	2.53	0.48
7:78:352:VAL:HG23	14:K8:244:LYS:HA	1.96	0.48
4:7B:232:ALA:HB2	4:7B:270:PHE:HB2	1.96	0.48
4:7F:232:ALA:HB2	4:7F:270:PHE:HB2	1.94	0.48
4:7H:104:GLY:HA3	4:7H:146:GLY:HA3	1.95	0.48
4:7L:130:LEU:HG	4:7L:162:ARG:HG2	1.95	0.48
7:86:364:ALA:HA	7:86:367:LEU:HD12	1.95	0.48
7:86:387:LEU:HD23	3:8E:342:GLN:HE22	1.79	0.48
4:8L:11:GLN:HA	4:8L:72:THR:HG21	1.95	0.48
4:8L:135:ILE:HG12	4:8L:166:THR:HA	1.96	0.48
7:93:328:PRO:HG2	7:93:333:LEU:HD21	1.95	0.48
7:96:344:ARG:HA	7:96:353:LYS:HE3	1.95	0.48
4:9B:132:GLY:HA3	4:9B:163:ILE:HG13	1.95	0.48
4:9B:215:LEU:HB3	4:9B:217:LEU:HD23	1.95	0.48
3:9C:252:VAL:HA	3:9C:255:PHE:HD2	1.78	0.48
4:9D:316:MET:HA	4:9D:352:SER:HB3	1.95	0.48
4:9H:69:GLU:HG2	4:9H:71:GLY:H	1.78	0.48
4:9L:42:LEU:HD22	4:9L:356:ILE:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9L:412:GLU:HA	4:9L:415:MET:HE2	1.96	0.48
9:B4:150:MET:HG2	9:B4:151:PRO:O	2.14	0.48
10:D1:340:LEU:HD21	10:D1:386:LEU:HD11	1.95	0.48
10:D2:352:TYR:HE2	10:D2:376:ILE:HD11	1.78	0.48
1:c:590:GLU:HB3	1:c:591:ARG:HE	1.79	0.48
1:m:763:THR:HG21	1:m:769:ARG:HH21	1.78	0.48
1:n:941:ARG:O	1:n:944:GLN:HG2	2.12	0.48
1:E:423:ARG:HD2	1:E:424:LEU:HD22	1.95	0.48
1:Q:548:LEU:HA	1:U:548:LEU:HD13	1.95	0.48
1:S:483:ILE:O	1:S:486:GLN:HB3	2.13	0.48
1:Y:584:GLU:O	1:Y:588:THR:HG23	2.12	0.48
2:13:204:LEU:HD23	2:13:207:LYS:HZ3	1.79	0.48
3:1A:133:GLN:HB3	3:1A:252:VAL:HB	1.95	0.48
3:1C:100:ALA:HA	4:1D:252:LYS:HE2	1.96	0.48
3:1C:139:ASN:HD21	3:1C:168:ASN:HD21	1.62	0.48
3:1E:129:CYS:HB2	3:1E:132:LEU:HD23	1.95	0.48
3:1G:404:PHE:HZ	4:1H:312:THR:HG21	1.78	0.48
3:1M:58:ALA:HB2	9:B6:114:GLY:H	1.78	0.48
5:22:45:SER:HA	5:22:73:VAL:O	2.13	0.48
5:24:166:TYR:HA	5:25:121:ILE:HD11	1.95	0.48
3:2G:311:LYS:NZ	3:2G:342:GLN:HE21	2.11	0.48
5:32:75:ILE:HG12	5:32:89:VAL:HG12	1.95	0.48
3:3G:222:PRO:HD2	4:3H:324:LYS:HD2	1.95	0.48
3:4C:268:MET:HG2	3:4C:380:ASN:HB2	1.94	0.48
3:4I:93:ILE:HD11	3:4I:121:ARG:HG3	1.96	0.48
3:4M:28:HIS:HD1	3:4M:49:PHE:HA	1.78	0.48
5:50:49:PRO:HA	5:50:70:PRO:HA	1.95	0.48
5:50:85:GLN:HA	5:50:107:GLU:HG2	1.95	0.48
5:51:30:ASP:HA	5:51:190:PHE:HZ	1.78	0.48
5:51:87:VAL:HB	5:51:105:LEU:HB2	1.94	0.48
5:57:21:LEU:HD21	5:58:224:LEU:HD21	1.96	0.48
4:5D:308:GLY:HA2	4:5D:426:GLN:HE22	1.77	0.48
2:6:166:ALA:HA	2:6:169:HIS:CD2	2.49	0.48
4:6B:68:LEU:HD12	4:6B:143:THR:HG22	1.94	0.48
3:6G:339:ARG:NH2	14:K2:118:CYS:HB2	2.29	0.48
3:7A:147:SER:O	3:7A:151:CYS:CB	2.61	0.48
3:7I:175:PRO:HB3	3:7I:390:ARG:HD2	1.95	0.48
7:80:331:PRO:HB2	7:80:335:ARG:HH21	1.78	0.48
3:8A:79:ARG:HG3	3:8A:92:LEU:HD22	1.94	0.48
3:8A:288:VAL:HG22	3:8A:373:ARG:HH22	1.79	0.48
4:9B:65:LEU:HD11	4:9B:90:PHE:HD1	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9C:133:GLN:HE22	3:9C:242:LEU:HD22	1.78	0.48
4:9D:271:ALA:HB1	4:9D:289:LEU:HD22	1.94	0.48
4:9F:407:GLU:HA	4:9F:410:GLU:HG3	1.95	0.48
3:9I:208:ALA:HB2	3:9I:304:LYS:HG2	1.95	0.48
4:9J:66:MET:HE1	4:9J:147:MET:HG2	1.96	0.48
8:A4:36:PRO:HA	9:B7:8:ILE:HG22	1.94	0.48
9:B4:34:PRO:HB2	9:B4:36:GLU:OE1	2.14	0.48
9:B4:44:LEU:HD11	9:B4:51:ARG:HH12	1.78	0.48
10:E1:143:ASP:HA	10:E1:146:ALA:HB2	1.95	0.48
10:E4:50:GLU:HG3	10:E4:51:TYR:HD2	1.78	0.48
10:F1:89:ALA:HA	10:F1:306:MET:HE1	1.95	0.48
13:J1:336:GLY:HA2	13:J1:339:ARG:HB3	1.94	0.48
13:J2:309:THR:HA	13:J2:312:ARG:HG2	1.96	0.48
14:L5:236:PHE:HD2	14:L5:237:LEU:HD12	1.78	0.48
1:c:403:ARG:HA	1:c:406:ARG:HD2	1.95	0.48
1:h:805:PRO:HG2	1:h:810:THR:HB	1.95	0.48
1:u:847:ASP:HB3	1:u:850:ARG:HH22	1.78	0.48
1:A:485:LEU:HD13	1:F:485:LEU:HD22	1.94	0.48
1:M:607:LEU:HD13	1:N:607:LEU:HB2	1.95	0.48
1:Q:638:LEU:HB3	1:U:638:LEU:HD23	1.95	0.48
2:12:314:TYR:HA	2:12:317:MET:HG2	1.95	0.48
2:15:222:GLU:O	2:15:226:VAL:HG23	2.12	0.48
4:1F:99:ASN:HB2	3:1G:257:THR:HG21	1.95	0.48
4:1L:201:VAL:HG21	4:1L:374:ILE:HD11	1.95	0.48
3:2I:141:VAL:HG13	3:2I:190:SER:HB3	1.96	0.48
3:2M:277:SER:H	3:2M:280:LYS:HB3	1.79	0.48
5:39:195:LEU:HD23	5:40:195:LEU:HD23	1.95	0.48
4:3H:221:THR:HG23	4:3H:223:GLY:H	1.78	0.48
4:3J:310:TYR:HA	4:3J:371:SER:HA	1.94	0.48
4:3J:396:HIS:HA	4:3J:399:THR:HG22	1.94	0.48
3:3K:76:ASP:HA	3:3K:79:ARG:HB2	1.95	0.48
4:3L:41:ASP:HB3	8:A7:216:MET:HE3	1.95	0.48
4:3L:103:LYS:HD3	4:3L:107:THR:HG21	1.95	0.48
5:43:212:LEU:HD13	5:44:220:LEU:HD11	1.96	0.48
5:46:206:LEU:HA	5:46:209:ILE:HG12	1.94	0.48
5:49:86:HIS:HE1	5:49:88:ARG:HD3	1.79	0.48
3:4E:244:PHE:HB2	3:4E:356:ASN:HD21	1.79	0.48
2:5:164:GLU:HB2	2:5:168:ARG:NH1	2.29	0.48
5:57:148:LEU:HD13	5:57:158:LEU:HB2	1.95	0.48
4:5L:420:SER:O	4:5L:424:GLN:HG3	2.14	0.48
4:6D:313:ALA:HA	4:6D:369:GLY:HA2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6D:407:GLU:HA	4:6D:410:GLU:HG2	1.96	0.48
7:78:273:LEU:HD23	10:E4:155:MET:HE1	1.96	0.48
3:7C:88:HIS:CE1	3:7C:121:ARG:HH12	2.31	0.48
3:7E:169:PHE:CE2	3:7E:235:ILE:HD13	2.49	0.48
4:7L:379:LYS:HD2	4:7L:419:VAL:HG11	1.94	0.48
3:8C:54:SER:HB3	3:8C:64:ARG:HH21	1.78	0.48
3:8K:116:ASP:HB2	14:M7:247:THR:HB	1.96	0.48
3:8K:222:PRO:HB2	3:8K:226:ASN:HB2	1.95	0.48
7:91:278:VAL:HG13	7:91:302:PRO:HG3	1.96	0.48
10:D5:54:HIS:CE1	10:D5:85:PRO:HD3	2.48	0.48
10:E3:301:ARG:NH1	10:E3:305:LEU:HD21	2.28	0.48
10:E5:66:LEU:HD22	10:E5:312:LYS:HE3	1.96	0.48
10:E6:292:ALA:HA	10:E6:295:GLN:HE21	1.78	0.48
10:F1:30:ARG:HH22	14:L7:227:PRO:HD2	1.78	0.48
10:F1:294:SER:HA	10:F1:297:ARG:HG2	1.96	0.48
12:H8:97:LEU:HD13	12:H9:97:LEU:HD22	1.94	0.48
13:J7:345:LEU:HD23	13:J7:346:GLN:HG2	1.94	0.48
14:K4:155:TRP:HH2	14:K4:243:GLN:HE21	1.62	0.48
14:L6:183:GLN:HA	14:L6:186:THR:HG22	1.95	0.48
14:L9:100:ALA:HA	14:L9:105:LEU:HD22	1.96	0.48
1:a:589:THR:HB	1:a:592:ARG:HH21	1.78	0.48
4:1L:171:PRO:HG2	4:1L:185:ALA:HB2	1.94	0.48
5:24:214:LYS:HE2	5:24:221:LEU:HD13	1.96	0.48
3:2A:125:LEU:HD13	3:2A:128:ASN:HD21	1.79	0.48
3:2E:278:ALA:HB2	9:B3:120:VAL:HG12	1.94	0.48
3:2G:172:TRP:HE1	3:2G:391:MET:HE1	1.78	0.48
4:2J:66:MET:HE2	4:2J:147:MET:HE2	1.95	0.48
3:2K:398:MET:HE2	4:2L:346:PRO:HD2	1.95	0.48
5:31:183:PHE:HE2	6:66:366:GLN:HE21	1.62	0.48
5:32:89:VAL:HG22	5:32:103:HIS:ND1	2.29	0.48
3:3C:91:GLN:HB2	3:4C:282:TYR:HE2	1.78	0.48
3:3K:28:HIS:CE1	3:3K:243:ARG:HH11	2.32	0.48
5:45:129:VAL:HA	5:45:132:LYS:NZ	2.29	0.48
5:56:90:GLU:HA	5:56:101:TYR:O	2.14	0.48
5:59:161:ILE:HG22	5:59:168:PHE:HB3	1.95	0.48
4:5J:206:ALA:HB2	4:5J:302:ALA:HB2	1.96	0.48
5:61:221:LEU:HA	5:61:224:LEU:HG	1.94	0.48
5:62:88:ARG:HH12	5:62:90:GLU:HB2	1.79	0.48
6:64:877:ALA:O	6:64:881:THR:HG23	2.14	0.48
6:68:490:GLU:O	6:68:493:ARG:HG2	2.12	0.48
6:68:879:THR:HB	9:B6:519:ALA:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:69:593:PRO:HA	6:69:598:VAL:HG21	1.94	0.48
3:6I:75:VAL:HG12	3:6I:79:ARG:HH21	1.79	0.48
3:6M:103:PHE:H	3:6M:408:TYR:HE1	1.62	0.48
2:7:324:GLU:HG3	2:8:324:GLU:HA	1.96	0.48
7:71:350:ARG:HG2	7:71:379:LEU:HB3	1.94	0.48
4:7B:9:GLY:HA3	4:7B:147:MET:HE1	1.95	0.48
4:7B:51:TYR:HB3	4:7B:59:PHE:HB3	1.96	0.48
3:7C:271:SER:HA	3:7C:302:MET:HG2	1.95	0.48
4:7D:44:LEU:HD21	1:o:922:ARG:HH21	1.78	0.48
4:7F:290:THR:HA	4:7F:293:MET:HG2	1.96	0.48
3:7G:20:CYS:HB2	3:7G:235:ILE:HD11	1.95	0.48
3:7G:184:PRO:HA	3:7G:391:MET:HE1	1.94	0.48
4:7J:37:CYS:HA	1:j:760:ARG:HH22	1.78	0.48
4:7J:80:PRO:HG3	1:j:798:ARG:HB2	1.96	0.48
3:7K:100:ALA:HA	4:7L:252:LYS:HB3	1.94	0.48
3:8A:138:PHE:HZ	3:8A:235:ILE:HG12	1.78	0.48
4:8B:309:ARG:HD3	4:8B:342:VAL:HB	1.96	0.48
3:8C:103:PHE:HD1	3:8C:189:LEU:HD23	1.79	0.48
3:8G:296:PHE:HE2	3:8G:317:LEU:HD21	1.79	0.48
4:8L:7:VAL:HA	4:8L:64:ILE:HB	1.95	0.48
4:8L:304:ASP:HB3	7:91:413:ARG:HH12	1.79	0.48
7:96:357:VAL:HG21	14:M6:218:LYS:HD3	1.96	0.48
10:D2:404:LEU:HD22	10:D2:406:LEU:HG	1.96	0.48
12:G7:246:PRO:HD2	12:G7:249:LEU:HD12	1.95	0.48
13:J6:345:LEU:HD23	13:J6:346:GLN:HG2	1.95	0.48
13:J7:339:ARG:HG3	13:J7:341:PRO:HG2	1.95	0.48
14:K3:200:PHE:HB2	14:K3:220:LEU:HB3	1.95	0.48
1:f:678:ASN:O	1:f:679:ARG:C	2.57	0.48
1:B:422:THR:HA	1:B:425:ILE:HG22	1.96	0.48
1:L:319:MET:SD	1:L:323:MET:HE1	2.54	0.48
1:M:485:LEU:HD21	1:N:484:GLN:HE22	1.79	0.48
1:M:603:ARG:O	1:M:607:LEU:HG	2.14	0.48
1:Y:628:VAL:HG23	1:c:628:VAL:HG22	1.95	0.48
2:12:287:THR:HA	2:12:290:ASN:ND2	2.29	0.48
3:1C:58:ALA:HB3	3:2C:282:TYR:HE1	1.78	0.48
3:1E:298:PRO:HB3	3:1E:307:PRO:HD2	1.95	0.48
4:1H:96:GLY:H	3:1I:2:ARG:HH21	1.60	0.48
4:1H:100:ASN:HB2	4:1H:103:LYS:HG2	1.96	0.48
4:1J:73:MET:HA	4:1J:76:VAL:HG12	1.96	0.48
5:23:127:PRO:O	5:23:131:ILE:HG12	2.12	0.48
5:24:213:LEU:HB3	5:24:221:LEU:HD11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2B:321:MET:HE2	4:2B:362:LYS:HZ1	1.79	0.48
4:2D:345:ILE:HD12	4:2D:346:PRO:HD2	1.96	0.48
4:2D:377:MET:HE2	4:2D:380:ARG:HH22	1.78	0.48
3:2G:217:LEU:HG	3:2G:275:ILE:HG22	1.96	0.48
3:2M:360:PRO:HG3	3:2M:374:ALA:HB2	1.96	0.48
5:37:53:ARG:HD2	5:37:149:ILE:HG12	1.95	0.48
5:37:216:LYS:HZ1	5:38:220:LEU:HD13	1.78	0.48
4:3H:296:ALA:HB1	4:3H:305:PRO:HD2	1.96	0.48
4:3L:179:VAL:HG23	3:3M:352:LYS:HB2	1.96	0.48
5:58:119:LEU:HD11	5:58:172:LEU:HD21	1.95	0.48
4:5D:156:ARG:HH21	4:5D:164:MET:HB2	1.78	0.48
5:61:117:GLN:HE22	5:61:173:CYS:HB3	1.79	0.48
6:63:397:ASN:O	6:63:401:ILE:HG13	2.14	0.48
6:65:133:ARG:HH21	12:I3:335:ILE:HG12	1.78	0.48
4:6D:3:GLU:HA	4:6D:49:VAL:HA	1.95	0.48
7:71:328:PRO:HG2	7:71:392:ARG:HH21	1.79	0.48
7:75:279:ARG:HD2	10:D3:149:TYR:CE1	2.49	0.48
7:78:350:ARG:HG3	7:78:388:GLU:HB2	1.96	0.48
4:7D:68:LEU:HD21	4:7D:108:GLU:HG2	1.95	0.48
3:7G:16:ILE:HD11	3:7G:138:PHE:HB3	1.95	0.48
4:8D:86:ARG:HG3	4:8D:88:ASP:H	1.79	0.48
4:8F:221:THR:HG23	4:8F:223:GLY:H	1.77	0.48
3:8G:310:GLY:HA3	3:8G:383:ALA:HB2	1.96	0.48
3:8M:167:LEU:HD13	3:8M:200:VAL:HG13	1.95	0.48
7:94:347:ILE:HD11	7:94:354:ALA:HB2	1.95	0.48
3:9C:318:MET:HG3	3:9C:376:CYS:HB3	1.94	0.48
4:9D:167:PHE:HA	4:9D:200:GLN:HE22	1.78	0.48
4:9F:132:GLY:HA2	4:9F:162:ARG:HB3	1.95	0.48
8:A4:129:VAL:HG11	8:A4:160:ALA:HB1	1.95	0.48
9:B1:36:GLU:HG3	9:B1:44:LEU:HB2	1.95	0.48
10:E0:297:ARG:HA	10:E0:300:ILE:HG12	1.95	0.48
10:E2:34:VAL:HG11	14:L3:226:PRO:HG2	1.96	0.48
12:F8:245:ALA:HA	12:F8:266:PRO:HG3	1.94	0.48
12:I4:61:THR:HA	12:I4:64:ARG:HG2	1.96	0.48
13:J5:397:LEU:HD23	13:J5:400:LEU:HD12	1.94	0.48
14:K1:207:ILE:HG23	14:K1:212:ASP:HB2	1.96	0.48
14:L8:172:ARG:HB3	14:L8:174:TYR:H	1.79	0.48
1:e:356:GLU:HA	1:e:359:ARG:HG2	1.94	0.48
1:A:640:ALA:HB2	1:l:826:VAL:HB	1.95	0.48
1:G:379:ARG:HB3	1:d:489:GLN:HG2	1.95	0.48
1:K:453:LEU:HD13	1:L:453:LEU:HD22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:387:ILE:HA	1:S:390:ILE:HG22	1.96	0.48
4:1B:342:VAL:HG12	4:1B:345:ILE:H	1.79	0.48
3:1E:12:ALA:O	3:1E:16:ILE:HG12	2.14	0.48
3:1E:223:THR:HG22	4:1F:322:SER:HA	1.94	0.48
4:1J:248:SER:HA	4:1J:252:LYS:HD2	1.95	0.48
3:2C:134:GLY:HA2	3:2C:164:LYS:HB3	1.96	0.48
3:2I:278:ALA:HB2	9:B2:120:VAL:HG12	1.95	0.48
3:3A:152:LEU:O	3:3A:156:ARG:HB2	2.14	0.48
3:3A:215:ARG:HH22	3:3A:299:ALA:C	2.22	0.48
4:3B:124:ALA:HB1	4:3B:130:LEU:HD22	1.96	0.48
3:3C:115:VAL:HA	3:3C:118:SER:HB2	1.96	0.48
3:3C:135:PHE:HD2	3:3C:166:LYS:HG2	1.78	0.48
4:3J:175:VAL:HG13	3:3K:332:VAL:HG11	1.96	0.48
3:3M:172:TRP:HB2	3:3M:203:MET:HB2	1.95	0.48
3:3M:359:PRO:HB2	9:B6:30:ARG:HH21	1.78	0.48
4:4D:318:ARG:HE	4:4D:358:PRO:HD3	1.79	0.48
4:4F:16:ILE:HD11	4:4F:229:VAL:HG11	1.96	0.48
3:4I:3:GLU:HA	3:4I:51:THR:HA	1.95	0.48
4:4L:69:GLU:HB2	4:4L:96:GLY:HA2	1.96	0.48
5:55:48:VAL:HA	5:55:138:ILE:HD11	1.96	0.48
3:5I:100:ALA:HA	4:5J:252:LYS:HG3	1.95	0.48
3:5M:382:THR:HG21	3:5M:436:GLY:HA2	1.96	0.48
6:67:414:VAL:HG22	6:67:436:PRO:HD2	1.95	0.48
6:69:611:ARG:O	6:69:615:ARG:HD3	2.14	0.48
4:6D:164:MET:HB3	4:6D:197:ASP:H	1.78	0.48
4:6D:193:VAL:HG21	4:6D:418:LEU:HD21	1.95	0.48
4:6H:207:LEU:HB3	4:6H:225:LEU:HG	1.95	0.48
7:75:350:ARG:HG3	7:75:388:GLU:HB2	1.96	0.48
7:78:293:ILE:HG22	7:78:295:GLN:HG3	1.96	0.48
3:7C:109:THR:HG21	14:L7:172:ARG:HH12	1.78	0.48
4:7D:11:GLN:HG3	4:7D:72:THR:HG21	1.95	0.48
3:7G:119:LEU:HD11	3:7G:156:ARG:HB3	1.96	0.48
4:7J:20:PHE:CG	4:7J:233:MET:HE2	2.49	0.48
4:7J:271:ALA:HB3	4:7J:365:VAL:HG12	1.96	0.48
4:7L:6:HIS:CD2	4:7L:8:GLN:HG2	2.49	0.48
4:7L:343:GLU:HA	14:L3:197:ARG:HH22	1.79	0.48
3:7M:336:LYS:HZ1	14:L3:111:LEU:C	2.22	0.48
3:8C:141:VAL:HG13	3:8C:190:SER:HB3	1.95	0.48
4:8H:7:VAL:HB	4:8H:135:ILE:HG22	1.96	0.48
4:8J:95:THR:HG23	4:8J:96:GLY:H	1.79	0.48
4:9B:149:THR:HA	4:9B:152:ILE:HG22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9F:226:ASN:HA	4:9F:229:VAL:HG22	1.94	0.48
4:9L:130:LEU:HD12	4:9L:162:ARG:HG2	1.96	0.48
10:C9:86:LEU:HG	10:C9:313:TYR:HD2	1.78	0.48
10:D6:284:LEU:HB3	10:D6:351:ARG:HH12	1.79	0.48
10:D6:354:ARG:HD3	10:D6:360:ALA:HA	1.95	0.48
10:E0:118:LEU:HD13	10:E4:76:ALA:HB1	1.96	0.48
10:E0:148:MET:HE1	14:L6:129:PRO:HG3	1.95	0.48
10:E2:298:GLU:HA	10:E2:301:ARG:HG2	1.96	0.48
10:E6:34:VAL:HG11	14:L1:226:PRO:HG2	1.94	0.48
12:F5:222:ASP:HB2	12:F5:242:TRP:CZ2	2.48	0.48
12:G1:282:ALA:HB2	12:G2:274:MET:HE2	1.94	0.48
13:J5:341:PRO:HG3	13:J5:362:ALA:HB3	1.96	0.48
14:K6:156:LEU:HG	14:K6:185:ILE:HD12	1.96	0.48
14:L2:217:ALA:HB3	14:L2:219:TYR:HE2	1.78	0.48
1:c:572:ARG:O	1:c:573:GLN:C	2.56	0.48
1:A:586:LYS:HG2	1:F:586:LYS:HE2	1.95	0.48
1:C:406:ARG:HH22	1:G:406:ARG:HD3	1.79	0.48
1:I:599:SER:HB2	1:I:603:ARG:HH22	1.78	0.48
1:I:628:VAL:HG13	1:J:628:VAL:HG22	1.96	0.48
1:M:575:LEU:HD12	1:N:573:GLN:HB2	1.94	0.48
1:W:447:HIS:HA	1:W:450:LEU:HD12	1.96	0.48
4:1D:65:LEU:HB3	4:1D:73:MET:HE3	1.95	0.48
3:1I:223:THR:HB	3:1I:225:THR:HG22	1.95	0.48
4:1L:21:TRP:HA	4:1L:24:ILE:HG22	1.96	0.48
5:26:53:ARG:HB2	5:26:149:ILE:HG22	1.95	0.48
4:2B:207:LEU:HD22	4:2B:228:LEU:HD11	1.96	0.48
4:2B:260:PHE:HB2	4:2B:263:LEU:HG	1.96	0.48
3:2C:79:ARG:HG2	3:2C:92:LEU:HD13	1.96	0.48
4:2F:253:LEU:HD13	4:2F:316:MET:HE3	1.96	0.48
3:2G:248:LEU:HB2	3:2G:355:ILE:H	1.79	0.48
2:3:275:GLU:HA	2:3:278:HIS:CD2	2.49	0.48
5:32:108:ASP:HA	5:32:111:ARG:HE	1.78	0.48
5:35:196:LYS:HB3	13:J1:494:GLU:HG2	1.96	0.48
4:3B:64:ILE:HD12	4:3B:119:VAL:HG13	1.96	0.48
4:3D:276:ARG:HE	6:65:878:PRO:HD3	1.78	0.48
4:3D:321:MET:HB3	4:3D:363:MET:HE2	1.96	0.48
4:3F:20:PHE:HA	4:3F:230:SER:HB2	1.96	0.48
4:3F:217:LEU:HD22	8:A5:255:ARG:HH21	1.79	0.48
3:3K:223:THR:HG23	3:3K:225:THR:H	1.78	0.48
3:4C:395:PHE:HD2	3:4C:422:ARG:HH11	1.60	0.48
4:4J:293:MET:HE3	4:4J:367:PHE:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:50:31:GLU:HA	5:50:36:LEU:HD13	1.95	0.48
5:53:42:LEU:HD21	5:53:45:SER:HB2	1.94	0.48
4:5B:311:LEU:HD13	4:5B:342:VAL:HG11	1.95	0.48
3:5C:237:SER:HA	3:5C:320:ARG:HD2	1.94	0.48
4:5D:132:GLY:HA2	4:5D:162:ARG:HB3	1.96	0.48
4:5D:377:MET:HE3	4:5D:377:MET:HB3	1.65	0.48
4:5L:30:ILE:HD11	4:5L:47:ILE:HD11	1.94	0.48
6:68:153:VAL:HG13	6:68:165:VAL:HG13	1.96	0.48
4:6B:64:ILE:HA	4:6B:89:ASN:OD1	2.13	0.48
3:6E:223:THR:HG23	3:6E:225:THR:H	1.79	0.48
4:6H:12:CYS:HB3	4:6H:138:SER:HB2	1.96	0.48
3:6K:91:GLN:HG3	3:6K:121:ARG:HE	1.78	0.48
4:7F:313:ALA:HB1	4:7F:367:PHE:HE1	1.79	0.48
3:8A:232:ALA:HA	3:8A:235:ILE:HG22	1.96	0.48
4:8F:65:LEU:HD12	4:8F:73:MET:HG3	1.95	0.48
4:8J:363:MET:HE2	4:8J:363:MET:HB3	1.78	0.48
3:9E:259:LEU:HD13	3:9E:268:MET:HE1	1.95	0.48
3:9G:119:LEU:HD11	3:9G:156:ARG:HG2	1.95	0.48
4:9L:15:GLN:OE1	4:9L:222:TYR:HB3	2.14	0.48
9:B2:523:LYS:HZ3	9:B2:525:SER:HB3	1.78	0.48
9:B7:48:MET:HE3	9:B7:51:ARG:HE	1.79	0.48
10:E5:63:TYR:CE2	14:L7:142:GLN:HB3	2.49	0.48
10:E7:338:PRO:HB2	10:E7:341:TYR:HB3	1.95	0.48
12:G2:246:PRO:HD2	12:G2:249:LEU:HD12	1.95	0.48
14:M4:196:VAL:HA	14:M4:223:SER:HA	1.95	0.48
1:y:867:PRO:HB3	1:y:944:GLN:HG2	1.96	0.48
1:A:611:THR:HG23	1:A:614:LEU:HD12	1.95	0.47
1:I:429:ARG:CA	1:J:429:ARG:HH12	2.26	0.47
1:I:624:GLN:CB	1:J:624:GLN:HG3	2.35	0.47
1:I:652:MET:HE3	1:J:656:GLN:HG3	1.96	0.47
1:L:404:PHE:HA	1:L:407:GLU:HG2	1.96	0.47
2:13:168:ARG:HA	2:14:168:ARG:HH22	1.78	0.47
4:1D:342:VAL:HG12	4:1D:345:ILE:H	1.79	0.47
3:1I:7:ILE:HD13	3:1I:153:LEU:HD21	1.95	0.47
4:1J:105:HIS:HD2	4:1J:150:LEU:HD22	1.79	0.47
5:20:50:PHE:HD2	5:20:71:ILE:HB	1.79	0.47
5:26:44:TYR:HB3	5:26:75:ILE:HG22	1.95	0.47
5:27:213:LEU:HD11	5:27:220:LEU:HD23	1.96	0.47
3:2C:230:LEU:HD11	3:2C:275:ILE:HD12	1.96	0.47
4:2F:10:GLY:HA2	4:2F:143:THR:HG23	1.96	0.47
4:2J:202:ILE:HD11	4:2J:268:ILE:HD11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2J:285:SER:O	4:2J:289:LEU:HB2	2.14	0.47
3:2M:362:VAL:HG12	3:2M:370:LYS:HB3	1.95	0.47
5:31:144:PHE:HD1	5:31:162:GLN:HA	1.78	0.47
5:39:97:LEU:HD21	5:40:192:TYR:CD2	2.49	0.47
3:3A:28:HIS:HE1	3:3A:48:ALA:O	1.97	0.47
4:3D:321:MET:HE2	4:3D:326:VAL:HG22	1.96	0.47
4:3L:12:CYS:HB3	4:3L:138:SER:HB3	1.96	0.47
2:4:155:GLN:HA	2:4:158:GLU:HG2	1.96	0.47
3:4A:209:ILE:HG23	3:4A:230:LEU:HD13	1.96	0.47
4:4D:358:PRO:HG2	4:4D:361:LEU:HD12	1.95	0.47
4:4J:65:LEU:HD22	4:4J:90:PHE:CE1	2.49	0.47
3:4K:23:LEU:HD13	3:4K:363:VAL:HG22	1.96	0.47
5:53:114:GLN:HB2	5:53:119:LEU:HB2	1.95	0.47
5:53:119:LEU:HD11	5:53:172:LEU:HD13	1.95	0.47
5:53:130:LEU:HA	5:53:133:MET:HE2	1.96	0.47
5:57:90:GLU:HA	5:57:101:TYR:O	2.13	0.47
3:5A:185:TYR:O	3:5A:189:LEU:HB2	2.14	0.47
3:5C:272:TYR:HB3	3:5C:275:ILE:HD11	1.96	0.47
4:5H:313:ALA:HA	4:5H:369:GLY:HA2	1.96	0.47
3:5I:195:LEU:HD12	3:5I:428:LEU:HD22	1.96	0.47
4:5L:159:TYR:HB3	4:5L:162:ARG:HG3	1.96	0.47
4:5N:73:MET:HA	4:5N:76:VAL:HG12	1.95	0.47
5:62:119:LEU:HD13	5:62:121:ILE:HD11	1.96	0.47
4:6B:205:GLU:HB2	7:73:412:MET:HE3	1.96	0.47
4:6F:156:ARG:HH21	4:6F:164:MET:HB2	1.79	0.47
3:6I:407:TRP:CG	4:6J:255:VAL:HG23	2.48	0.47
4:6J:117:LEU:HA	4:6J:120:VAL:HG12	1.94	0.47
7:75:279:ARG:NE	10:D3:148:MET:HG3	2.28	0.47
7:79:341:SER:HB2	14:K9:216:GLY:HA3	1.95	0.47
3:7G:404:PHE:HZ	4:7H:312:THR:HG21	1.79	0.47
3:7I:141:VAL:HG12	3:7I:187:SER:HA	1.95	0.47
3:7M:11:GLN:HG3	3:7M:74:VAL:HG21	1.96	0.47
3:7M:319:TYR:HD2	3:7M:328:VAL:HG22	1.79	0.47
3:8A:32:PRO:HA	3:8A:86:LEU:HD11	1.95	0.47
3:8A:208:ALA:O	3:8A:212:ILE:HG12	2.14	0.47
3:8C:221:ARG:NH1	1:o:913:SER:HB3	2.29	0.47
3:8E:415:GLU:HB3	10:E0:48:ARG:HH22	1.78	0.47
3:8I:348:PRO:HB2	14:L5:111:LEU:HD22	1.96	0.47
4:9F:177:ASP:HB2	3:9G:352:LYS:HD3	1.95	0.47
8:A5:80:MET:HE2	9:B2:465:LEU:HD21	1.95	0.47
10:C7:377:LEU:HD21	10:C7:388:SER:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D1:316:CYS:O	10:D1:320:LYS:CB	2.62	0.47
10:E2:97:ILE:HD13	10:E2:397:PHE:HD2	1.79	0.47
12:F9:223:LEU:HD11	12:F9:239:ARG:HA	1.95	0.47
12:G3:197:LEU:O	12:G3:200:LEU:HB3	2.14	0.47
12:H4:332:THR:HA	12:H4:335:ILE:HD12	1.96	0.47
12:H5:90:ALA:HB1	12:H6:94:LEU:HD11	1.96	0.47
13:J1:355:PRO:HA	13:J1:358:ASP:HB2	1.96	0.47
14:L1:181:LEU:O	14:L1:185:ILE:HG12	2.13	0.47
1:e:338:HIS:O	1:e:342:MET:HB2	2.14	0.47
1:f:534:GLN:HG3	1:f:535:ALA:N	2.29	0.47
1:t:897:LEU:HD22	1:t:935:VAL:HG23	1.96	0.47
1:A:394:LYS:HD2	1:F:394:LYS:HD3	1.95	0.47
1:D:637:THR:HA	1:m:828:CYS:SG	2.54	0.47
1:J:452:PRO:HA	1:J:455:LYS:HG2	1.95	0.47
1:T:611:THR:O	1:T:615:ARG:CB	2.62	0.47
1:Y:601:ARG:HG3	1:Y:604:ILE:HD12	1.96	0.47
2:13:165:ARG:HE	10:D2:336:THR:HG22	1.80	0.47
3:1A:406:HIS:HA	3:1A:409:VAL:HG22	1.96	0.47
4:1D:178:THR:H	3:1E:352:LYS:HD3	1.79	0.47
3:1E:246:GLY:HA3	3:1E:356:ASN:HA	1.94	0.47
3:1E:402:ARG:HE	3:1E:405:VAL:HG11	1.79	0.47
4:1H:174:LYS:HG3	4:1H:175:VAL:H	1.78	0.47
5:24:105:LEU:HD21	5:24:110:PHE:HD1	1.78	0.47
3:2E:151:CYS:O	3:2E:155:GLU:HG3	2.14	0.47
4:2F:205:GLU:HG2	3:2G:329:ASN:HD21	1.79	0.47
4:2H:341:PHE:HD2	4:2H:348:ASN:HD22	1.63	0.47
5:37:135:ASN:HA	5:37:138:ILE:HD12	1.97	0.47
4:3D:215:LEU:HD21	4:3D:273:LEU:HD22	1.96	0.47
3:3G:32:PRO:HG2	8:A5:239:ILE:HD12	1.96	0.47
4:3L:79:GLY:HA2	6:68:867:TRP:HB3	1.95	0.47
3:3M:274:PRO:HD2	3:3M:371:VAL:HG21	1.96	0.47
5:52:209:ILE:HD12	6:63:600:LEU:HD23	1.96	0.47
4:5B:260:PHE:HB2	4:5B:263:LEU:HD13	1.97	0.47
4:5J:87:PRO:HD3	4:6J:281:TYR:HD2	1.78	0.47
6:67:330:LEU:HB3	6:67:337:LEU:HD21	1.96	0.47
6:69:979:ARG:HG2	2:8:211:LEU:HD13	1.96	0.47
3:6M:222:PRO:HD2	4:6N:324:LYS:HE3	1.94	0.47
3:6M:269:LEU:HB2	3:6M:379:SER:HB3	1.96	0.47
4:7D:180:VAL:HG21	4:7D:397:TRP:HH2	1.80	0.47
3:7E:119:LEU:HA	3:7E:122:ILE:HG12	1.96	0.47
4:7F:244:GLY:HA2	4:7F:355:ASP:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7H:73:MET:HG3	4:7H:92:PHE:HB3	1.95	0.47
7:83:308:TYR:CZ	7:83:393:LEU:HG	2.49	0.47
4:8B:95:THR:HG23	4:8B:96:GLY:H	1.78	0.47
4:8B:164:MET:HE3	4:8B:196:ALA:HA	1.96	0.47
3:8G:320:ARG:HD3	3:8G:360:PRO:HG3	1.96	0.47
4:8H:94:GLN:HB3	3:8I:2:ARG:HH12	1.78	0.47
7:91:294:SER:HA	7:91:317:GLN:HB3	1.95	0.47
3:9I:338:LYS:HZ1	3:9I:341:ILE:HB	1.78	0.47
3:9M:77:GLU:HA	3:9M:80:THR:HG22	1.96	0.47
8:A2:125:GLN:HA	8:A2:163:ARG:HH21	1.78	0.47
8:A3:113:VAL:HG22	8:A3:117:LEU:HD13	1.97	0.47
10:C7:386:LEU:O	10:C7:390:MET:HG2	2.14	0.47
10:C8:293:MET:O	10:C8:296:MET:HB3	2.13	0.47
10:D3:51:TYR:HB3	10:D3:54:HIS:CD2	2.49	0.47
10:F2:297:ARG:O	10:F2:301:ARG:HB3	2.14	0.47
12:G7:228:ILE:HG22	12:G8:225:TRP:CD1	2.49	0.47
12:G9:65:GLU:HA	12:G9:68:ARG:HG2	1.96	0.47
14:L6:151:PRO:HG2	14:L6:172:ARG:HH22	1.79	0.47
1:a:562:ILE:CG2	1:f:562:ILE:HG13	2.44	0.47
1:c:397:ALA:HA	1:c:400:GLU:HG2	1.95	0.47
1:f:675:LYS:HA	1:f:675:LYS:HD3	1.67	0.47
1:A:604:ILE:HD11	1:F:600:LEU:HD22	1.96	0.47
1:A:642:MET:HE2	1:l:819:ALA:HB2	1.96	0.47
1:A:663:LEU:HD12	1:A:667:LYS:HE2	1.96	0.47
1:B:339:LYS:HE3	1:B:340:ARG:HH22	1.79	0.47
1:I:603:ARG:HD3	1:I:603:ARG:HA	1.65	0.47
1:J:615:ARG:HG3	1:J:616:THR:N	2.28	0.47
2:10:298:LEU:HD22	2:9:295:PHE:CE1	2.49	0.47
4:1F:326:VAL:O	4:1F:330:MET:HG2	2.14	0.47
3:1M:301:MET:HE1	3:1M:305:CYS:HB3	1.96	0.47
5:26:40:HIS:CD2	5:26:76:LEU:HB3	2.49	0.47
3:2E:263:PRO:HG2	6:65:543:GLN:HG2	1.96	0.47
4:2J:203:ASP:HB2	4:2J:301:CYS:HA	1.95	0.47
3:2M:272:TYR:HE1	3:2M:374:ALA:HB1	1.80	0.47
5:39:203:GLN:HE22	13:J3:497:TRP:NE1	2.12	0.47
4:3F:177:ASP:HB2	3:3G:353:CYS:H	1.79	0.47
4:3H:189:VAL:HA	4:3H:192:LEU:HB2	1.97	0.47
4:3J:20:PHE:HA	4:3J:230:SER:HB2	1.95	0.47
4:3J:207:LEU:HB3	4:3J:225:LEU:HG	1.95	0.47
4:3J:318:ARG:HA	4:3J:354:CYS:HB3	1.96	0.47
4:3L:334:GLN:HE22	4:3L:348:ASN:H	1.60	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3M:325:PRO:HA	3:3M:328:VAL:HG12	1.96	0.47
4:4B:173:PRO:HA	4:4B:380:ARG:HH22	1.79	0.47
3:4C:104:ALA:HB2	3:4C:413:MET:HG2	1.94	0.47
4:4L:49:VAL:HG21	4:4L:241:ARG:HB3	1.96	0.47
5:50:158:LEU:HG	5:50:174:LEU:HD13	1.96	0.47
5:51:129:VAL:HA	5:51:132:LYS:HE2	1.97	0.47
5:55:206:LEU:HD12	5:55:209:ILE:HD12	1.97	0.47
4:5N:263:LEU:HD21	4:5N:425:TYR:HE1	1.79	0.47
5:61:36:LEU:HD21	5:61:42:LEU:HB2	1.96	0.47
6:67:539:ARG:HG3	12:I5:61:THR:HG21	1.96	0.47
6:69:175:MET:HG2	6:69:252:ARG:HD3	1.95	0.47
4:6J:220:PRO:HD2	3:6K:326:LYS:HD2	1.96	0.47
3:6K:177:VAL:HG11	3:6K:210:TYR:HE2	1.78	0.47
7:78:405:VAL:H	3:7G:334:THR:HG22	1.79	0.47
3:7A:223:THR:HG23	3:7A:225:THR:H	1.80	0.47
4:7D:25:SER:HB3	4:7D:30:ILE:HB	1.95	0.47
3:7I:397:LEU:HD13	14:L2:225:GLU:HG2	1.95	0.47
4:7L:116:VAL:HG23	4:7L:117:LEU:HD12	1.95	0.47
3:7M:430:LYS:O	3:7M:434:GLU:HB2	2.14	0.47
3:8E:242:LEU:HD11	3:8E:252:VAL:HG13	1.96	0.47
3:8E:415:GLU:HG2	3:8E:418:PHE:HB2	1.96	0.47
3:8G:77:GLU:HA	3:8G:80:THR:HG22	1.96	0.47
3:8M:217:LEU:HD13	3:8M:275:ILE:HG22	1.94	0.47
4:9F:147:MET:HA	4:9F:150:LEU:HB2	1.95	0.47
4:9H:200:GLN:HG2	4:9H:268:ILE:HD13	1.96	0.47
3:9K:8:HIS:HD2	3:9K:14:ILE:HD13	1.79	0.47
8:A5:63:ASN:HD21	1:v:896:LEU:HB3	1.79	0.47
10:C0:338:PRO:HB2	10:C0:341:TYR:HB3	1.95	0.47
10:D8:151:GLN:O	10:D8:155:MET:HG3	2.13	0.47
10:D8:298:GLU:O	10:D8:302:ARG:HG3	2.14	0.47
10:E4:34:VAL:HG21	14:K9:226:PRO:HG3	1.96	0.47
10:E8:62:VAL:HG22	10:E8:309:ILE:HD11	1.96	0.47
13:J1:485:ILE:HG12	13:J1:511:SER:HB3	1.96	0.47
13:J2:405:VAL:O	13:J2:409:LEU:HB2	2.15	0.47
13:J7:341:PRO:HG3	13:J7:362:ALA:HB3	1.97	0.47
14:K2:97:ARG:HD2	14:K2:123:SER:HB3	1.95	0.47
14:L3:191:PRO:HG3	14:L3:196:VAL:HG23	1.97	0.47
1:j:821:ASN:HD21	1:j:823:LEU:HB2	1.80	0.47
1:x:878:PRO:HB2	1:x:879:VAL:HG12	1.97	0.47
1:D:607:LEU:HB2	1:H:607:LEU:HD12	1.96	0.47
1:F:624:GLN:O	1:F:628:VAL:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:674:ARG:O	1:I:677:MET:HG2	2.14	0.47
1:M:500:ARG:HB3	1:M:504:ARG:HH12	1.79	0.47
3:1A:315:CYS:HA	3:1A:379:SER:HA	1.95	0.47
3:1A:319:TYR:HD2	3:1A:328:VAL:HG22	1.79	0.47
3:1C:394:LYS:HZ2	4:1D:346:PRO:HG2	1.78	0.47
4:1D:135:ILE:HG12	4:1D:166:THR:HG22	1.96	0.47
4:1J:105:HIS:HE1	4:1J:191:GLN:HE22	1.61	0.47
3:1M:394:LYS:HD3	4:1N:346:PRO:HG2	1.96	0.47
4:1N:136:THR:HG22	4:1N:167:PHE:CE1	2.49	0.47
5:25:101:TYR:HB3	5:25:176:CYS:HB3	1.96	0.47
3:2A:10:GLY:O	3:2A:14:ILE:HG12	2.14	0.47
3:2E:260:VAL:HG23	3:2E:265:ILE:O	2.14	0.47
3:2G:271:SER:HB3	3:2G:377:MET:HB3	1.94	0.47
3:2I:408:TYR:HB3	3:2I:413:MET:HE3	1.95	0.47
4:2L:179:VAL:HG23	3:2M:352:LYS:HB2	1.96	0.47
3:2M:112:LYS:HA	3:2M:115:VAL:HG22	1.97	0.47
5:37:158:LEU:HD23	5:37:174:LEU:HD22	1.97	0.47
4:3B:14:ASN:HB3	4:3B:76:VAL:HG21	1.96	0.47
4:3J:163:ILE:HG21	4:3J:250:LEU:HB2	1.95	0.47
5:47:164:MET:HE1	5:47:166:TYR:CZ	2.48	0.47
3:4A:306:ASP:HB2	3:4A:308:ARG:HE	1.79	0.47
4:4H:334:GLN:HE22	4:4H:348:ASN:N	2.12	0.47
5:52:51:GLU:HB3	5:52:147:VAL:HA	1.95	0.47
5:59:42:LEU:HD21	5:59:45:SER:HB2	1.95	0.47
4:5D:403:MET:HE3	4:5D:403:MET:HB2	1.78	0.47
4:5H:417:ASP:HB3	14:K1:139:LEU:HB3	1.96	0.47
5:60:91:LEU:HB3	5:60:101:TYR:HB3	1.96	0.47
6:69:417:LEU:HD12	6:69:417:LEU:HA	1.70	0.47
6:69:976:GLU:HG3	6:69:979:ARG:HH22	1.79	0.47
3:6G:252:VAL:HA	3:6G:255:PHE:HD2	1.79	0.47
7:75:347:ILE:HG21	7:75:350:ARG:HB2	1.96	0.47
4:7B:110:ALA:HA	4:7B:113:ILE:HG22	1.95	0.47
3:7C:137:MET:HE2	3:7C:154:LEU:HD11	1.96	0.47
4:7F:110:ALA:HA	4:7F:113:ILE:HG22	1.95	0.47
3:7K:88:HIS:HB3	3:7K:91:GLN:HG3	1.97	0.47
3:8K:398:MET:HE2	4:8L:345:ILE:HB	1.94	0.47
3:9E:2:ARG:HB3	3:9E:133:GLN:HE22	1.79	0.47
8:A2:323:LEU:HD12	8:A2:328:ARG:HB2	1.95	0.47
10:C9:305:LEU:O	10:C9:309:ILE:HD12	2.14	0.47
10:E1:311:LYS:HG3	10:E1:403:GLN:HE22	1.79	0.47
10:E2:54:HIS:ND1	10:E2:88:LEU:HD21	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:F1:148:MET:HE1	14:L7:129:PRO:HD3	1.95	0.47
12:G6:195:PRO:HA	12:G6:198:LYS:HG2	1.97	0.47
13:J3:453:THR:HG23	13:J3:456:GLU:H	1.79	0.47
13:J3:483:LYS:HD3	13:J3:509:PHE:HB2	1.97	0.47
13:J7:325:LEU:HD13	13:J7:416:VAL:HG22	1.96	0.47
14:K8:97:ARG:HG2	14:K8:123:SER:HB3	1.97	0.47
14:L1:172:ARG:HG2	14:L1:173:PRO:HD2	1.96	0.47
14:M7:86:HIS:HA	14:M7:89:ARG:HB2	1.96	0.47
1:c:423:ARG:NH2	1:t:878:PRO:HD3	2.30	0.47
1:c:649:ASP:HA	1:c:652:MET:HG2	1.96	0.47
1:J:602:ASN:O	1:J:605:LYS:HG3	2.15	0.47
1:K:361:LEU:HD22	1:L:357:TYR:CE2	2.49	0.47
1:M:677:MET:HE3	1:M:677:MET:HB3	1.74	0.47
1:P:654:LEU:O	1:P:657:GLN:HB3	2.13	0.47
3:1A:267:PHE:HE2	3:1A:428:LEU:HD11	1.78	0.47
4:1D:287:PRO:HA	4:1D:329:GLN:HG2	1.95	0.47
3:1E:219:ILE:HD11	3:1E:222:PRO:HB3	1.96	0.47
3:1E:250:VAL:HG21	3:1E:318:MET:SD	2.53	0.47
4:1J:167:PHE:CE2	4:1J:233:MET:HG3	2.50	0.47
3:1M:229:ARG:HD2	3:1M:363:VAL:HG11	1.96	0.47
5:21:184:THR:O	5:21:188:MET:HG2	2.14	0.47
5:29:21:LEU:HA	5:29:205:ARG:HH21	1.79	0.47
4:2H:405:GLU:HA	4:2H:408:PHE:HD1	1.79	0.47
4:2J:186:THR:HG22	4:2J:411:ALA:HB1	1.96	0.47
3:3A:70:LEU:HD22	3:3A:149:LEU:HD22	1.95	0.47
4:3B:219:THR:HA	3:3C:326:LYS:HD2	1.95	0.47
4:3D:66:MET:HG2	4:3D:147:MET:HE3	1.95	0.47
5:49:52:ILE:HG23	5:49:150:MET:HE1	1.95	0.47
3:5C:262:TYR:HB3	14:K4:76:LEU:HD21	1.95	0.47
4:5D:171:PRO:HB3	4:5D:181:GLU:HG2	1.96	0.47
4:5H:100:ASN:HB3	4:5H:103:LYS:HG2	1.96	0.47
3:5I:64:ARG:HA	3:5I:125:LEU:HD11	1.95	0.47
5:61:195:LEU:HD23	5:62:195:LEU:HD23	1.96	0.47
6:66:490:GLU:O	6:66:491:TYR:C	2.57	0.47
6:68:414:VAL:HG23	6:68:439:LYS:HG2	1.97	0.47
3:6C:133:GLN:HG3	3:6C:252:VAL:HB	1.97	0.47
3:6E:70:LEU:HD22	3:6E:145:THR:HG22	1.95	0.47
4:6F:105:HIS:CE1	4:6F:150:LEU:HD12	2.50	0.47
4:6H:287:PRO:HA	4:6H:329:GLN:HE22	1.78	0.47
3:7K:301:MET:HE3	3:7K:307:PRO:HG2	1.96	0.47
4:7L:265:PHE:HB3	4:7L:374:ILE:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7L:390:ARG:HH22	7:84:249:ASN:HA	1.80	0.47
3:7M:191:THR:HA	3:7M:194:LEU:HB3	1.95	0.47
7:89:342:SER:HA	14:L9:155:TRP:HH2	1.80	0.47
4:8D:36:TYR:CZ	4:8D:44:LEU:HD22	2.50	0.47
4:8D:290:THR:HA	4:8D:293:MET:HG2	1.96	0.47
4:8D:424:GLN:HE21	14:M4:143:ARG:HD3	1.78	0.47
4:8F:100:ASN:HB3	4:8F:103:LYS:HB2	1.96	0.47
4:8F:284:LEU:HG	4:8F:362:LYS:HD2	1.94	0.47
3:8G:404:PHE:HZ	4:8H:312:THR:HG21	1.80	0.47
4:8H:102:ALA:HB1	4:8H:401:GLU:HB2	1.97	0.47
7:91:333:LEU:HG	7:91:334:LEU:HD12	1.96	0.47
7:92:380:TRP:HZ3	7:92:388:GLU:HB3	1.79	0.47
7:93:327:ASN:H	7:93:391:TYR:HD2	1.62	0.47
4:9B:206:ALA:HA	4:9B:209:ASP:HB2	1.97	0.47
3:9E:238:LEU:HD12	3:9E:378:ILE:HG21	1.97	0.47
8:A1:174:ARG:HB2	8:A1:177:GLN:HG3	1.95	0.47
8:A8:196:LEU:HA	8:A8:199:THR:HG22	1.97	0.47
9:B1:142:LEU:HD21	9:B1:176:LEU:HD12	1.96	0.47
10:D5:392:THR:HG22	10:D5:395:ARG:HH21	1.80	0.47
10:D7:283:PHE:HD2	10:D7:386:LEU:HD11	1.80	0.47
10:E1:57:ILE:HG23	10:E1:306:MET:HE1	1.97	0.47
10:F2:297:ARG:O	10:F2:301:ARG:CB	2.62	0.47
13:J3:396:GLN:HA	13:J3:448:ASP:HB3	1.95	0.47
13:J5:412:ALA:O	13:J5:416:VAL:HG23	2.14	0.47
14:K4:244:LYS:NZ	14:K4:246:GLN:HB2	2.28	0.47
14:M2:100:ALA:HB2	14:M2:105:LEU:HD12	1.96	0.47
14:M3:181:LEU:O	14:M3:185:ILE:HG12	2.15	0.47
1:a:584:GLU:O	1:a:588:THR:HG23	2.14	0.47
1:f:512:LYS:O	1:f:513:ARG:C	2.58	0.47
1:f:597:ILE:HA	1:f:600:LEU:HD12	1.97	0.47
1:B:485:LEU:HD22	1:E:486:GLN:NE2	2.29	0.47
1:D:579:LEU:HD22	1:H:579:LEU:HD22	1.96	0.47
1:L:378:GLU:O	1:L:381:ARG:HG3	2.14	0.47
1:V:656:GLN:O	1:V:660:GLN:HG3	2.15	0.47
2:11:169:HIS:HA	2:11:172:PHE:CE2	2.49	0.47
2:12:165:ARG:HA	2:12:168:ARG:HB2	1.97	0.47
3:1A:293:ASN:HD21	3:1A:334:THR:HG22	1.79	0.47
3:1E:290:GLU:HA	3:1E:293:ASN:HB2	1.96	0.47
4:1N:166:THR:O	4:1N:199:VAL:HA	2.14	0.47
4:1N:215:LEU:HB3	4:1N:217:LEU:HD23	1.97	0.47
4:2B:119:VAL:HG23	4:2B:122:LYS:HE3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2D:399:THR:HB	6:65:532:GLY:HA2	1.96	0.47
3:2E:395:PHE:HZ	3:2E:418:PHE:HB3	1.80	0.47
4:2F:274:THR:HB	4:2F:279:GLN:HG2	1.97	0.47
4:2H:132:GLY:HA2	4:2H:162:ARG:HB3	1.96	0.47
4:2H:181:GLU:HA	4:2H:184:ASN:HD22	1.79	0.47
3:2I:319:TYR:HE1	3:2I:375:VAL:HG23	1.79	0.47
4:2J:150:LEU:HD11	4:2J:154:LYS:HE3	1.96	0.47
5:36:184:THR:HG22	5:36:188:MET:HE1	1.97	0.47
4:3H:42:LEU:HD23	4:3H:356:ILE:HD11	1.95	0.47
3:3I:248:LEU:HB2	3:3I:355:ILE:H	1.79	0.47
3:3K:88:HIS:CG	3:4K:283:HIS:HB2	2.50	0.47
4:3L:7:VAL:HG13	4:3L:64:ILE:HB	1.96	0.47
3:3M:54:SER:HB2	3:3M:62:VAL:HB	1.96	0.47
3:3M:370:LYS:HE3	9:B6:30:ARG:HB3	1.95	0.47
5:40:53:ARG:HB2	5:40:149:ILE:HG22	1.97	0.47
3:4C:385:ALA:HB2	3:4C:432:TYR:HB2	1.97	0.47
3:4E:265:ILE:HD12	3:4E:313:MET:HE1	1.95	0.47
4:4L:20:PHE:HA	4:4L:230:SER:HB2	1.95	0.47
3:4M:53:PHE:HB3	3:4M:61:HIS:HB3	1.96	0.47
5:55:71:ILE:HG23	5:55:93:SER:HB3	1.96	0.47
5:58:213:LEU:HD11	5:58:220:LEU:HB2	1.96	0.47
3:5A:56:THR:HA	3:6A:285:GLN:HB2	1.97	0.47
3:5A:282:TYR:CE1	8:A4:92:TYR:HB2	2.49	0.47
4:5B:294:PHE:HE2	4:5B:349:MET:HE1	1.80	0.47
4:5B:375:GLN:HG3	4:5B:423:GLN:HB3	1.96	0.47
3:5C:71:GLU:HB3	3:5C:98:ASP:HB2	1.96	0.47
3:5E:234:VAL:HG22	3:5E:272:TYR:HB2	1.97	0.47
3:5G:156:ARG:HH21	14:K1:247:THR:HG22	1.80	0.47
2:6:165:ARG:HA	2:6:168:ARG:HG3	1.96	0.47
3:6A:12:ALA:HB3	3:6A:140:ALA:HB2	1.95	0.47
3:6C:175:PRO:HA	3:6C:394:LYS:HE3	1.95	0.47
4:6F:8:GLN:HE21	4:6F:65:LEU:HG	1.78	0.47
4:6F:105:HIS:CD2	4:6F:150:LEU:HB2	2.49	0.47
3:6G:96:LYS:HA	3:6G:96:LYS:HD3	1.58	0.47
3:6M:264:ARG:HD2	3:6M:264:ARG:HA	1.73	0.47
4:6N:6:HIS:HD1	4:6N:21:TRP:NE1	2.12	0.47
3:7C:5:ILE:HG13	3:7C:132:LEU:HD11	1.97	0.47
3:7C:141:VAL:HG22	3:7C:187:SER:HA	1.96	0.47
3:7C:211:ASP:HB3	3:7C:215:ARG:HH12	1.79	0.47
3:7I:296:PHE:CD2	3:7I:335:ILE:HD13	2.49	0.47
7:82:286:TRP:HZ3	7:82:293:ILE:HG12	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:87:381:PHE:HB3	7:87:384:GLU:HB2	1.97	0.47
3:8A:310:GLY:HA3	3:8A:383:ALA:HB2	1.97	0.47
3:8E:200:VAL:HA	3:8E:266:HIS:HB2	1.95	0.47
4:8L:113:ILE:HA	4:8L:116:VAL:HG22	1.95	0.47
4:9B:206:ALA:HB2	4:9B:302:ALA:HB2	1.97	0.47
3:9C:174:SER:HB3	3:9C:206:ASN:HB2	1.96	0.47
4:9L:135:ILE:HG22	4:9L:166:THR:HA	1.96	0.47
8:A8:258:VAL:HG23	8:A8:259:THR:HG23	1.96	0.47
9:B1:466:MET:HE2	1:u:890:LEU:HD11	1.97	0.47
9:B7:20:ARG:HG2	9:B7:27:PHE:CG	2.50	0.47
10:C6:404:LEU:HD22	10:C6:406:LEU:HB2	1.95	0.47
10:E6:370:ARG:HA	10:E6:370:ARG:HD2	1.77	0.47
10:E9:114:PRO:HG2	10:E9:138:ARG:HB3	1.96	0.47
12:F5:200:LEU:HA	12:F6:225:TRP:HZ3	1.79	0.47
14:L9:181:LEU:O	14:L9:185:ILE:HG12	2.15	0.47
14:L9:244:LYS:HG2	14:L9:246:GLN:HG3	1.97	0.47
1:a:607:LEU:HA	1:a:610:VAL:HG23	1.95	0.47
1:f:647:LYS:HA	1:f:647:LYS:HD2	1.42	0.47
1:A:487:HIS:CE1	1:H:665:THR:HG23	2.50	0.47
1:B:530:LEU:HG	1:E:531:GLN:HE22	1.80	0.47
1:E:373:LEU:HD23	1:E:377:HIS:CD2	2.50	0.47
1:H:613:GLN:O	1:H:617:MET:CB	2.59	0.47
1:I:656:GLN:HA	1:J:659:LEU:CD1	2.44	0.47
1:J:618:ARG:HA	1:J:618:ARG:HD2	1.62	0.47
1:K:411:LYS:HG3	1:L:411:LYS:HZ2	1.79	0.47
1:M:487:HIS:CE1	1:P:661:ASN:HB2	2.50	0.47
1:R:677:MET:HG2	1:V:680:LEU:HD12	1.95	0.47
1:T:673:LEU:HD11	1:X:674:ARG:HH21	1.79	0.47
1:Z:540:SER:O	1:Z:544:LEU:HB3	2.15	0.47
2:10:218:VAL:HA	2:10:221:ARG:HB2	1.97	0.47
2:14:264:GLN:HA	2:14:267:HIS:CE1	2.50	0.47
4:1B:193:VAL:HG11	4:1B:262:ARG:HH11	1.79	0.47
4:1F:47:ILE:HG13	4:1F:51:TYR:HB2	1.97	0.47
4:1F:330:MET:HE3	4:1F:349:MET:HB3	1.96	0.47
3:1K:408:TYR:HD2	3:1K:418:PHE:HZ	1.63	0.47
4:1L:34:GLY:HA3	4:1L:58:ARG:HE	1.78	0.47
4:1L:135:ILE:HD13	4:1L:152:ILE:HD11	1.97	0.47
4:1L:397:TRP:HZ2	3:1M:260:VAL:HB	1.80	0.47
5:20:89:VAL:HG22	5:20:103:HIS:HB3	1.96	0.47
5:26:50:PHE:HD2	5:26:71:ILE:HB	1.79	0.47
5:27:34:PRO:HG3	5:27:186:ARG:HG2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2A:30:ILE:HG13	3:2A:36:MET:HE3	1.96	0.47
3:2A:321:GLY:HA3	3:2A:373:ARG:HA	1.96	0.47
4:2B:167:PHE:CZ	4:2B:233:MET:HG3	2.49	0.47
3:2C:167:LEU:HD13	3:2C:200:VAL:HG11	1.97	0.47
3:2E:316:CYS:HB2	3:2E:377:MET:C	2.40	0.47
3:2G:99:ALA:HA	3:2G:110:ILE:HD11	1.97	0.47
3:2I:177:VAL:HG13	4:2J:327:ASP:HB3	1.97	0.47
4:2J:384:GLN:HG2	3:2K:348:PRO:HB2	1.96	0.47
3:2M:248:LEU:HB2	3:2M:354:GLY:HA2	1.96	0.47
5:31:55:GLN:HG3	5:31:149:ILE:HB	1.96	0.47
5:32:166:TYR:CE1	5:33:129:VAL:HG13	2.50	0.47
3:3A:167:LEU:HG	3:3A:200:VAL:HB	1.97	0.47
3:3C:422:ARG:HG3	6:66:583:LEU:HD11	1.97	0.47
4:3D:65:LEU:HB2	4:3D:90:PHE:HA	1.96	0.47
4:3D:202:ILE:HD13	4:3D:229:VAL:HG21	1.95	0.47
3:3G:105:ARG:HA	3:3G:109:THR:HB	1.96	0.47
3:3K:28:HIS:HE1	3:3K:243:ARG:HH11	1.63	0.47
4:3L:208:TYR:OH	3:3M:325:PRO:HB2	2.15	0.47
3:3M:422:ARG:HG3	6:68:583:LEU:HD11	1.97	0.47
5:44:70:PRO:HG3	13:J5:463:HIS:CE1	2.50	0.47
5:45:116:ARG:HH21	5:45:117:GLN:HE21	1.62	0.47
3:4A:72:PRO:HB3	3:4A:94:SER:HB2	1.97	0.47
3:4A:154:LEU:HD21	3:4A:198:THR:HB	1.96	0.47
4:4B:375:GLN:HE22	4:4B:423:GLN:HB3	1.80	0.47
3:4C:88:HIS:HB3	3:4C:91:GLN:HB2	1.97	0.47
3:4C:280:LYS:HZ3	3:4C:368:LEU:HA	1.80	0.47
4:4D:4:ILE:HD11	4:4D:240:LEU:HD22	1.96	0.47
3:4E:318:MET:O	3:4E:375:VAL:HA	2.14	0.47
4:4F:7:VAL:O	4:4F:135:ILE:HA	2.13	0.47
3:4M:174:SER:HB2	3:4M:207:GLU:HB2	1.96	0.47
5:53:126:TYR:HA	5:53:129:VAL:HG22	1.96	0.47
5:53:159:ASP:HB2	5:53:161:ILE:HD11	1.96	0.47
5:54:44:TYR:HB3	5:54:75:ILE:HB	1.96	0.47
5:57:117:GLN:HG3	5:57:119:LEU:HG	1.97	0.47
5:58:20:PHE:HB3	6:66:596:PRO:HB3	1.97	0.47
5:58:103:HIS:HE2	5:58:174:LEU:HD12	1.78	0.47
3:5A:167:LEU:HD13	3:5A:200:VAL:HG13	1.97	0.47
3:5A:236:SER:O	3:5A:240:ALA:HB2	2.14	0.47
3:5C:298:PRO:HG3	3:5C:307:PRO:HD2	1.97	0.47
4:5D:397:TRP:HA	14:K3:89:ARG:HH22	1.80	0.47
3:5E:270:SER:HA	3:5E:377:MET:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5G:68:LEU:HG	3:5G:93:ILE:HD11	1.97	0.47
3:5G:119:LEU:HD11	3:5G:156:ARG:HB3	1.96	0.47
4:5H:192:LEU:HD23	4:5H:199:VAL:HG21	1.96	0.47
3:5I:163:LYS:HG3	14:K1:104:TYR:HE2	1.79	0.47
4:5J:163:ILE:HG21	4:5J:250:LEU:HB3	1.96	0.47
4:5J:200:GLN:HG2	4:5J:266:PHE:HB2	1.96	0.47
3:5K:14:ILE:HG12	3:5K:67:PHE:HB3	1.97	0.47
4:5L:267:LEU:HD13	4:5L:299:MET:HG3	1.96	0.47
3:5M:170:CYS:O	3:5M:204:LEU:HB2	2.15	0.47
2:6:314:TYR:HA	2:6:317:MET:HG2	1.97	0.47
5:60:45:SER:HA	5:60:72:ARG:HH12	1.80	0.47
5:60:103:HIS:CE1	5:60:174:LEU:HB3	2.49	0.47
5:60:158:LEU:O	5:60:173:CYS:HA	2.15	0.47
6:64:975:LYS:HA	6:64:978:LYS:HG2	1.97	0.47
6:65:151:TYR:HD1	6:65:170:PRO:HD3	1.79	0.47
6:66:145:MET:HE1	6:66:152:GLY:HA2	1.97	0.47
6:67:258:HIS:HD2	6:67:261:LYS:HE3	1.78	0.47
6:69:495:LEU:O	6:69:499:ARG:HG3	2.14	0.47
3:6E:217:LEU:HD21	3:6E:368:LEU:HD23	1.97	0.47
3:6E:417:GLU:HA	3:6E:420:GLU:HG3	1.96	0.47
4:6F:3:GLU:HA	4:6F:49:VAL:HA	1.96	0.47
4:6F:112:LEU:HD23	4:6F:147:MET:HE1	1.97	0.47
3:6G:23:LEU:HD21	3:6G:363:VAL:HG22	1.96	0.47
4:6H:8:GLN:HB2	4:6H:65:LEU:HA	1.96	0.47
4:6J:64:ILE:HD12	4:6J:116:VAL:HG22	1.97	0.47
4:6J:112:LEU:HB3	4:6J:147:MET:HE1	1.96	0.47
4:6J:200:GLN:OE1	4:6J:266:PHE:HB2	2.14	0.47
4:6J:337:ASN:HB3	4:6J:340:TYR:HB2	1.97	0.47
4:6N:416:ASN:HA	4:6N:419:VAL:HG12	1.95	0.47
7:77:376:GLU:O	7:77:380:TRP:HB3	2.14	0.47
3:7A:75:VAL:HG13	3:7A:92:LEU:HD12	1.97	0.47
4:7D:51:TYR:HB3	4:7D:59:PHE:HB3	1.97	0.47
4:7D:381:VAL:HG23	4:7D:384:GLN:HE21	1.79	0.47
3:7E:16:ILE:O	3:7E:20:CYS:HB2	2.14	0.47
3:7E:296:PHE:CD2	3:7E:335:ILE:HD13	2.49	0.47
3:7E:312:TYR:HB2	3:7E:343:PHE:CD1	2.49	0.47
3:7G:196:GLU:HA	14:L6:83:THR:HB	1.97	0.47
4:7H:293:MET:HE2	4:7H:365:VAL:HG21	1.95	0.47
4:7L:305:PRO:HB3	4:7L:310:TYR:HE1	1.80	0.47
7:83:356:LEU:HA	14:L3:240:TRP:CD1	2.50	0.47
7:84:369:GLN:HA	7:84:372:TRP:HD1	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:85:408:ILE:HG22	3:8G:326:LYS:HD2	1.97	0.47
3:8A:105:ARG:HG2	3:8A:411:GLU:HG2	1.96	0.47
3:8A:318:MET:HB2	3:8A:376:CYS:HB3	1.95	0.47
4:8B:140:GLY:HA3	17:8B:501:GDP:H4'	1.95	0.47
4:8D:303:SER:HB3	4:8D:376:GLU:HB2	1.96	0.47
3:8E:200:VAL:HG23	3:8E:266:HIS:HB2	1.97	0.47
4:8F:215:LEU:HD22	1:l:813:PRO:HD2	1.97	0.47
4:8H:372:THR:HA	4:8H:422:TYR:HD1	1.79	0.47
3:8I:339:ARG:HH11	14:L5:113:GLU:HB3	1.80	0.47
4:8L:6:HIS:CD2	4:8L:134:GLN:HG3	2.50	0.47
4:8L:401:GLU:HA	14:M7:98:GLY:HA2	1.96	0.47
7:90:398:LYS:HB3	7:90:415:GLY:HA3	1.97	0.47
7:91:394:TYR:CZ	14:L0:123:SER:HB3	2.49	0.47
7:93:408:ILE:C	4:9D:174:LYS:HZ2	2.22	0.47
7:97:330:ARG:HH22	7:97:372:TRP:HB3	1.78	0.47
3:9A:210:TYR:CE1	4:9B:324:LYS:HE3	2.50	0.47
4:9F:348:ASN:O	4:9F:349:MET:HE2	2.14	0.47
4:9H:117:LEU:HD22	4:9H:121:ARG:HH12	1.80	0.47
3:9I:112:LYS:HA	3:9I:115:VAL:HG12	1.96	0.47
4:9J:113:ILE:HA	4:9J:116:VAL:HG12	1.96	0.47
4:9J:117:LEU:HA	4:9J:120:VAL:HG22	1.96	0.47
3:9K:27:GLU:HB2	3:9K:243:ARG:HH12	1.79	0.47
3:9K:185:TYR:OH	3:9K:398:MET:HG2	2.15	0.47
3:9K:222:PRO:HG2	4:9L:324:LYS:HE2	1.96	0.47
4:9L:201:VAL:HG22	4:9L:267:LEU:HA	1.96	0.47
8:A6:28:PRO:HB2	8:A6:30:GLN:HG2	1.97	0.47
8:A7:352:LEU:HB3	8:A7:367:PHE:CE1	2.49	0.47
8:A8:153:TYR:HB3	8:A8:155:PRO:HD2	1.96	0.47
9:B3:135:SER:HA	9:B3:139:HIS:HE1	1.80	0.47
10:C6:85:PRO:HB2	10:C6:313:TYR:HE2	1.79	0.47
10:C8:399:SER:O	10:C8:403:GLN:HB2	2.15	0.47
10:C9:63:TYR:HB2	14:K4:147:GLN:HG2	1.95	0.47
10:C9:307:MET:HA	10:C9:310:ILE:HG12	1.97	0.47
10:D0:45:ASN:HB3	10:D0:49:ARG:HH21	1.78	0.47
10:D5:76:ALA:HB2	10:D5:319:LEU:HD11	1.97	0.47
10:E1:275:GLU:HA	10:E1:278:VAL:HG12	1.95	0.47
10:E2:392:THR:HA	10:E2:395:ARG:HG2	1.95	0.47
10:E3:35:TRP:CE2	14:L4:228:ALA:HA	2.49	0.47
10:F3:379:LEU:HB3	10:F3:381:MET:HE3	1.97	0.47
12:F6:219:LEU:HA	12:F6:239:ARG:HH21	1.80	0.47
12:H5:91:GLU:HA	12:H5:94:LEU:HD23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I4:85:GLN:O	12:I4:89:ILE:HG12	2.14	0.47
13:J3:353:ARG:HD2	13:J3:353:ARG:HA	1.73	0.47
13:J5:345:LEU:HD23	13:J5:346:GLN:HG2	1.96	0.47
14:K5:199:ILE:HG22	14:K5:207:ILE:HD13	1.96	0.47
14:K8:148:ILE:HD11	14:K8:173:PRO:HG3	1.97	0.47
14:K8:155:TRP:CD2	14:K8:241:VAL:HG21	2.50	0.47
14:L2:204:PHE:HZ	14:L2:237:LEU:HD11	1.79	0.47
14:M7:165:ASP:HB2	14:M7:244:LYS:HE2	1.95	0.47
1:a:598:ALA:CB	1:t:884:PRO:HD2	2.45	0.47
1:c:588:THR:O	1:c:589:THR:C	2.55	0.47
1:h:817:GLY:HA3	1:h:824:GLN:HE21	1.78	0.47
1:p:925:MET:HE2	1:p:925:MET:HB2	1.78	0.47
1:A:428:GLU:HG3	1:F:429:ARG:HH22	1.80	0.47
1:A:638:LEU:HD23	1:K:359:ARG:HH12	1.80	0.47
1:E:310:PHE:CE2	1:F:494:ASN:HB3	2.50	0.47
1:I:582:LEU:HD12	1:I:582:LEU:HA	1.82	0.47
1:Y:625:GLN:HG3	1:c:624:GLN:OE1	2.14	0.47
1:1:861:ALA:HB1	1:1:941:ARG:HB2	1.97	0.47
2:11:299:ILE:HD12	2:12:298:LEU:HD21	1.96	0.47
4:1D:213:ARG:NH2	4:1D:298:ASN:HA	2.30	0.47
4:1D:265:PHE:HB3	4:1D:374:ILE:HD13	1.97	0.47
4:1F:380:ARG:O	4:1F:384:GLN:HG2	2.15	0.47
4:1H:245:GLN:HB2	4:1H:353:VAL:HB	1.97	0.47
3:1M:401:LYS:HE2	3:1M:401:LYS:HB3	1.75	0.47
5:22:51:GLU:HB3	5:22:147:VAL:HG12	1.96	0.47
5:23:225:GLN:HA	5:26:20:PHE:CZ	2.50	0.47
3:2C:223:THR:H	3:2C:226:ASN:HD22	1.62	0.47
3:2K:192:HIS:CD2	6:69:135:LYS:HB2	2.50	0.47
2:3:222:GLU:O	2:3:226:VAL:HG23	2.14	0.47
5:31:158:LEU:HB2	5:31:174:LEU:HB2	1.96	0.47
3:3A:296:PHE:CE1	3:3A:377:MET:HG3	2.44	0.47
3:3E:27:GLU:HG2	3:3E:361:THR:HG21	1.96	0.47
3:3E:250:VAL:HB	3:3E:318:MET:HE1	1.95	0.47
4:3F:205:GLU:HG2	3:3G:329:ASN:HD21	1.80	0.47
3:3K:339:ARG:HH22	6:69:499:ARG:HG2	1.80	0.47
4:3L:15:GLN:HG3	17:3L:501:GDP:HN21	1.80	0.47
4:4B:64:ILE:HD12	4:4B:119:VAL:HG12	1.95	0.47
3:4G:205:ASP:HB2	3:4G:303:ALA:HA	1.96	0.47
3:4K:107:HIS:CD2	3:4K:152:LEU:HB2	2.45	0.47
5:56:127:PRO:O	5:56:131:ILE:HG12	2.14	0.47
3:5A:267:PHE:HE2	3:5A:428:LEU:HD11	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5B:19:LYS:HA	4:5B:22:GLU:HB2	1.97	0.47
4:5D:220:PRO:HD2	3:5E:326:LYS:HE2	1.96	0.47
3:5K:250:VAL:HG23	3:5K:254:GLU:HB3	1.97	0.47
6:66:537:GLU:HG2	12:I8:62:LEU:HD21	1.96	0.47
6:68:621:ARG:HH22	6:68:956:ILE:HG23	1.79	0.47
3:6C:427:ALA:HA	3:6C:430:LYS:HE3	1.97	0.47
3:6M:208:ALA:HB2	3:6M:304:LYS:HB2	1.96	0.47
4:7B:395:LEU:HD11	4:7B:408:PHE:CZ	2.50	0.47
4:7D:309:ARG:HE	4:7D:426:GLN:HA	1.79	0.47
3:8E:306:ASP:HB3	3:8E:309:HIS:CE1	2.50	0.47
4:8F:117:LEU:HD13	7:92:286:TRP:HZ2	1.80	0.47
7:96:267:ASP:HB3	7:96:271:PHE:HE2	1.80	0.47
3:9A:9:VAL:HG22	3:9A:68:LEU:HB3	1.95	0.47
3:9C:306:ASP:HB3	3:9C:309:HIS:HE1	1.80	0.47
3:9E:157:LEU:O	3:9E:161:TYR:HB2	2.14	0.47
4:9L:215:LEU:HD12	4:9L:275:SER:HA	1.97	0.47
8:A8:168:TRP:HE1	8:A8:206:VAL:HG21	1.80	0.47
10:D1:307:MET:HE3	10:D1:396:LEU:HD22	1.96	0.47
10:D3:390:MET:HA	10:D3:393:VAL:HG12	1.96	0.47
10:D5:301:ARG:HH22	14:L3:143:ARG:NH2	2.13	0.47
10:E3:72:GLY:HA3	10:E9:138:ARG:HH11	1.80	0.47
10:F3:67:ALA:HA	10:F3:70:ARG:HE	1.79	0.47
10:F3:93:ALA:HB1	10:F3:306:MET:HE3	1.97	0.47
14:L3:177:SER:HA	14:L3:210:LEU:HD11	1.97	0.47
14:L7:178:MET:HE2	14:L7:182:TYR:CE1	2.50	0.47
14:M4:181:LEU:O	14:M4:185:ILE:HD12	2.14	0.47
1:B:443:ASN:OD1	1:B:447:HIS:CE1	2.68	0.47
1:D:638:LEU:HD13	1:H:638:LEU:HB3	1.97	0.47
1:I:638:LEU:HD22	1:J:638:LEU:HD22	1.97	0.47
1:O:650:HIS:O	1:O:654:LEU:HG	2.15	0.47
1:T:624:GLN:OE1	1:X:624:GLN:HB3	2.15	0.47
3:1A:167:LEU:HD22	3:1A:252:VAL:HG13	1.97	0.47
5:21:48:VAL:HG11	5:21:134:LEU:HD12	1.97	0.47
4:2D:66:MET:HE1	4:2D:151:LEU:HD22	1.96	0.47
3:2I:159:VAL:HG21	6:63:139:THR:HG22	1.95	0.47
4:2J:207:LEU:HA	4:2J:210:ILE:HG22	1.97	0.47
5:35:167:LYS:HE2	5:35:169:ILE:HG12	1.97	0.47
3:3C:323:VAL:HG13	3:3C:355:ILE:HG23	1.96	0.47
4:3D:178:THR:HA	3:3E:352:LYS:HG3	1.97	0.47
4:3H:58:ARG:HH21	4:4H:281:TYR:HE1	1.62	0.47
3:3I:91:GLN:HB3	3:3I:121:ARG:HD2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3K:71:GLU:HB2	4:3L:2:ARG:HH12	1.80	0.47
2:4:295:PHE:O	2:4:299:ILE:HG22	2.15	0.47
3:4I:115:VAL:HG21	3:4I:152:LEU:HD22	1.97	0.47
3:4I:313:MET:HG2	3:4I:346:TRP:CH2	2.50	0.47
3:4M:168:ASN:HD21	3:4M:194:LEU:HD22	1.79	0.47
3:4M:212:ILE:HD12	3:4M:275:ILE:HD13	1.96	0.47
5:55:185:ARG:HA	5:55:188:MET:HE2	1.97	0.47
5:55:220:LEU:HD21	6:69:606:GLN:HB3	1.96	0.47
3:5A:428:LEU:O	3:5A:432:TYR:HB2	2.15	0.47
4:5B:20:PHE:HA	4:5B:230:SER:HB2	1.97	0.47
4:5F:392:LYS:HB3	4:5F:395:LEU:HD22	1.97	0.47
3:5G:77:GLU:HA	3:5G:80:THR:HG22	1.97	0.47
4:5N:135:ILE:HD11	4:5N:166:THR:HG23	1.97	0.47
6:64:157:TRP:NE1	12:H9:72:GLU:HG2	2.30	0.47
6:65:503:LYS:HD3	6:65:503:LYS:HA	1.45	0.47
4:6F:256:ASN:HD22	4:6F:350:LYS:HG3	1.78	0.47
4:6J:9:GLY:HA2	4:6J:66:MET:HG2	1.97	0.47
4:6L:286:VAL:HG22	4:6L:363:MET:HE1	1.97	0.47
3:7C:128:ASN:HD21	3:8C:290:GLU:HB3	1.78	0.47
4:7D:68:LEU:HB3	4:7D:143:THR:HG21	1.96	0.47
4:7H:30:ILE:HG22	4:7H:81:PHE:HE1	1.80	0.47
3:7I:93:ILE:HD12	3:7I:117:LEU:HG	1.96	0.47
3:7K:89:PRO:HD2	3:8K:283:HIS:NE2	2.30	0.47
3:7K:130:THR:HB	7:90:406:LEU:HD13	1.97	0.47
7:87:352:VAL:HG22	14:L7:244:LYS:HA	1.97	0.47
3:8C:202:VAL:HA	3:8C:268:MET:HB2	1.97	0.47
3:8G:215:ARG:HD3	14:L5:250:PRO:HG2	1.97	0.47
4:8J:256:ASN:HD22	4:8J:350:LYS:HD2	1.80	0.47
4:9F:314:SER:HB3	4:9F:350:LYS:HB3	1.97	0.47
3:9I:296:PHE:HB3	3:9I:341:ILE:HD13	1.97	0.47
8:A1:152:VAL:HG13	8:A5:280:ALA:HB3	1.97	0.47
8:A2:332:THR:HG21	8:A2:335:ARG:HH21	1.79	0.47
8:A6:82:MET:HG3	1:w:893:GLN:HG3	1.97	0.47
9:B4:45:ARG:O	9:B4:48:MET:HG2	2.15	0.47
9:B4:475:ASN:HD21	9:B4:539:ARG:HB3	1.79	0.47
11:C5:232:GLU:CD	11:C5:233:VAL:H	2.23	0.47
10:D0:51:TYR:HB3	10:D0:54:HIS:CD2	2.50	0.47
10:D1:86:LEU:HG	10:D1:313:TYR:HD2	1.79	0.47
10:D9:67:ALA:O	10:D9:71:GLN:CB	2.60	0.47
10:E0:301:ARG:HH22	14:M3:143:ARG:NH2	2.13	0.47
10:E1:328:LYS:HD3	10:E1:406:LEU:HD22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E6:51:TYR:CZ	10:E6:79:ASP:HA	2.50	0.47
10:E7:117:THR:HG22	10:E7:132:THR:HG22	1.96	0.47
13:J2:308:ALA:HB1	13:J2:312:ARG:HH21	1.80	0.47
14:L6:117:ARG:HG2	14:L6:119:HIS:CE1	2.49	0.47
1:a:628:VAL:HG21	1:f:624:GLN:HE22	1.78	0.47
1:c:600:LEU:HD23	1:c:600:LEU:HA	1.74	0.47
1:f:594:ALA:O	1:f:597:ILE:HG22	2.14	0.47
1:i:829:PRO:HD2	1:i:834:ARG:HH21	1.80	0.47
1:v:952:ARG:HD3	1:v:952:ARG:HA	1.74	0.47
1:J:359:ARG:HE	1:U:329:ASP:HA	1.80	0.47
1:M:600:LEU:HD13	1:N:600:LEU:HB3	1.97	0.47
1:N:500:ARG:O	1:N:504:ARG:HG2	2.15	0.47
1:X:638:LEU:O	1:X:642:MET:HB2	2.15	0.47
3:1C:167:LEU:HA	3:1C:200:VAL:HG12	1.97	0.47
5:29:50:PHE:HB2	5:29:71:ILE:HD13	1.97	0.47
3:2A:12:ALA:HB3	3:2A:140:ALA:HB2	1.96	0.47
5:31:44:TYR:HB3	5:31:75:ILE:HG12	1.95	0.47
3:3C:208:ALA:HB2	3:3C:304:LYS:HG2	1.97	0.47
3:3K:425:LEU:HD23	3:3K:425:LEU:HA	1.78	0.47
5:44:36:LEU:HD13	5:44:76:LEU:HD11	1.96	0.47
5:47:221:LEU:HD21	13:J7:306:ARG:HG2	1.96	0.47
4:4B:226:ASN:HA	4:4B:229:VAL:HG12	1.97	0.47
4:4D:216:LYS:HE2	6:65:927:VAL:HG21	1.96	0.47
3:4K:259:LEU:HD11	3:4K:316:CYS:HB2	1.97	0.47
4:4L:317:PHE:CD2	4:4L:321:MET:HE1	2.50	0.47
3:4M:385:ALA:HB2	3:4M:432:TYR:HB3	1.97	0.47
5:52:85:GLN:HA	5:52:107:GLU:HB2	1.96	0.47
5:53:48:VAL:HG11	5:53:134:LEU:HD22	1.96	0.47
5:55:33:ASP:HB3	5:55:36:LEU:HB2	1.97	0.47
4:5F:372:THR:HA	4:5F:422:TYR:HD1	1.80	0.47
3:5I:138:PHE:HD1	3:5I:169:PHE:HB2	1.80	0.47
4:5L:155:VAL:HG13	4:5L:164:MET:HE1	1.97	0.47
4:5L:306:ARG:HH22	6:69:793:LEU:HD12	1.80	0.47
5:62:53:ARG:HD2	5:62:149:ILE:HG12	1.97	0.47
6:69:487:TYR:CD2	6:69:488:ILE:HG13	2.50	0.47
3:6A:318:MET:O	3:6A:375:VAL:HA	2.15	0.47
3:6K:397:LEU:HD11	4:6L:346:PRO:HD3	1.97	0.47
4:7B:7:VAL:O	4:7B:135:ILE:HA	2.15	0.47
3:7E:14:ILE:HD11	3:7E:68:LEU:H	1.80	0.47
4:7H:189:VAL:HB	4:7H:415:MET:HE1	1.97	0.47
4:7J:135:ILE:HG21	4:7J:152:ILE:HD11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7L:6:HIS:NE2	4:7L:8:GLN:HG2	2.30	0.47
7:82:278:VAL:HG12	7:82:302:PRO:HG3	1.96	0.47
7:87:396:ASP:HB3	7:87:398:LYS:H	1.80	0.47
3:8E:265:ILE:HG21	3:8E:313:MET:HE1	1.97	0.47
4:8F:211:CYS:HA	4:8F:215:LEU:HB2	1.97	0.47
4:8F:316:MET:HA	4:8F:352:SER:HB3	1.96	0.47
3:8I:265:ILE:HG22	3:8I:380:ASN:HD21	1.80	0.47
2:9:195:LYS:HD3	2:9:198:LEU:HD21	1.97	0.47
3:9C:328:VAL:HG11	3:9C:355:ILE:HD11	1.97	0.47
4:9F:321:MET:HE1	4:9F:326:VAL:HG11	1.97	0.47
4:9L:229:VAL:HG12	4:9L:233:MET:HE1	1.97	0.47
8:A3:79:ASP:HB3	9:B5:465:LEU:HD12	1.96	0.47
9:B6:37:ARG:HH22	9:B6:520:GLU:HG3	1.80	0.47
12:F6:247:VAL:HA	12:F6:250:ARG:HB2	1.97	0.47
12:F7:246:PRO:HD2	12:F7:249:LEU:HD12	1.96	0.47
12:F7:258:ASN:HB2	12:F7:261:TRP:HZ3	1.80	0.47
12:G5:213:ALA:HA	12:G5:216:TRP:HB2	1.96	0.47
13:J4:289:ILE:HG23	13:J4:300:LEU:HD21	1.97	0.47
14:L8:72:VAL:HA	14:L8:75:ARG:HG3	1.97	0.47
14:M5:152:ARG:H	14:M5:171:VAL:HG12	1.80	0.47
14:M5:196:VAL:HA	14:M5:223:SER:HA	1.96	0.47
1:I:599:SER:HA	1:I:602:ASN:HD22	1.80	0.46
1:I:606:HIS:HE1	1:J:611:THR:HG21	1.80	0.46
2:11:291:GLU:O	2:11:295:PHE:HB2	2.14	0.46
2:16:183:ARG:HA	2:16:186:HIS:NE2	2.30	0.46
3:1C:394:LYS:NZ	4:1D:346:PRO:HG2	2.31	0.46
4:1L:44:LEU:HA	4:1L:47:ILE:HB	1.97	0.46
3:1M:60:LYS:HD2	3:1M:60:LYS:HA	1.79	0.46
5:28:117:GLN:HE21	5:28:119:LEU:HD12	1.79	0.46
5:29:34:PRO:HG3	5:29:186:ARG:HG3	1.97	0.46
3:2A:166:LYS:H	3:2A:199:ASP:HB2	1.80	0.46
4:2F:97:ALA:HA	4:2F:103:LYS:HE3	1.97	0.46
4:2F:163:ILE:HG21	4:2F:250:LEU:HB3	1.96	0.46
5:35:93:SER:HB2	5:35:99:LEU:HD23	1.97	0.46
5:37:200:ALA:HB3	13:J2:494:GLU:CD	2.41	0.46
3:3A:75:VAL:HG13	3:3A:92:LEU:HD23	1.97	0.46
3:3A:209:ILE:HG23	3:3A:230:LEU:HD23	1.96	0.46
4:3B:316:MET:HE1	4:3B:368:VAL:HG22	1.96	0.46
4:3D:153:SER:HA	4:3D:195:ASN:HD22	1.80	0.46
3:3M:21:TRP:CZ3	3:3M:63:PRO:HB3	2.50	0.46
3:4A:122:ILE:HD13	3:4A:157:LEU:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4A:141:VAL:HG11	3:4A:172:TRP:CE3	2.50	0.46
3:4A:229:ARG:HD3	3:4A:364:PRO:HB2	1.96	0.46
4:4L:215:LEU:HD11	4:4L:228:LEU:HD21	1.97	0.46
4:4L:272:PRO:HG3	4:4L:364:SER:HA	1.97	0.46
5:51:52:ILE:HG23	5:51:150:MET:HE1	1.97	0.46
5:54:40:HIS:HB3	5:54:76:LEU:HB3	1.96	0.46
5:59:206:LEU:HD22	5:60:21:LEU:HB2	1.96	0.46
3:5G:195:LEU:HD23	14:K2:83:THR:HG21	1.96	0.46
4:5J:7:VAL:HB	4:5J:135:ILE:HG13	1.97	0.46
4:5L:377:MET:HA	4:5L:380:ARG:HD2	1.96	0.46
6:63:882:GLU:HG2	6:63:893:THR:HG21	1.97	0.46
4:6B:138:SER:HA	4:6B:169:VAL:HG22	1.97	0.46
4:6B:200:GLN:HE21	4:6B:266:PHE:HD2	1.63	0.46
4:6H:307:HIS:HA	7:75:317:GLN:HE21	1.80	0.46
4:6J:321:MET:HE2	4:6J:321:MET:HB3	1.80	0.46
3:6M:208:ALA:O	3:6M:212:ILE:HG12	2.15	0.46
7:71:378:MET:HE1	14:K1:235:LYS:HG2	1.97	0.46
4:7B:149:THR:HA	4:7B:152:ILE:HG22	1.96	0.46
4:7D:200:GLN:HB3	4:7D:268:ILE:HD11	1.97	0.46
4:7F:103:LYS:HA	4:7F:107:THR:HG22	1.97	0.46
4:7L:105:HIS:HD2	4:7L:150:LEU:HD22	1.79	0.46
4:7L:200:GLN:HB3	4:7L:266:PHE:HB2	1.97	0.46
4:8D:103:LYS:HA	4:8D:107:THR:HG22	1.97	0.46
3:8K:208:ALA:HB2	3:8K:304:LYS:HB2	1.96	0.46
3:9G:229:ARG:NH1	3:9G:366:GLY:HA2	2.29	0.46
3:9I:180:ALA:HB3	3:9I:183:GLU:HG2	1.97	0.46
4:9J:74:ASP:HA	4:9J:77:ARG:HG2	1.97	0.46
4:9L:204:ASN:HA	4:9L:207:LEU:HD12	1.96	0.46
10:C6:62:VAL:HG22	10:C6:309:ILE:HD11	1.98	0.46
12:F6:238:HIS:CE1	12:F6:241:LEU:HB3	2.50	0.46
12:F8:279:ARG:HE	12:F8:283:LEU:HD11	1.79	0.46
12:G1:225:TRP:HE1	12:G2:229:ALA:HB3	1.81	0.46
13:J6:287:GLU:HG2	13:J6:605:ARG:HH22	1.79	0.46
14:M4:199:ILE:HG23	14:M4:207:ILE:HB	1.96	0.46
1:f:533:ARG:HB3	1:f:533:ARG:NH2	2.30	0.46
1:L:422:THR:HG21	1:o:875:ILE:HG21	1.96	0.46
1:M:684:ARG:HE	1:M:684:ARG:HB2	1.24	0.46
1:N:607:LEU:CA	1:N:610:VAL:HB	2.43	0.46
1:Y:428:GLU:HB3	1:c:429:ARG:NH2	2.30	0.46
2:14:222:GLU:HA	2:14:225:ARG:HB3	1.97	0.46
3:1C:21:TRP:CZ2	3:1C:65:CYS:HB3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1C:143:GLY:H	3:1C:147:SER:HB2	1.80	0.46
3:1M:79:ARG:HB3	3:1M:92:LEU:HD22	1.96	0.46
1:2:938:THR:O	1:2:942:ILE:HG12	2.15	0.46
5:24:52:ILE:H	5:24:67:ARG:HB3	1.80	0.46
3:2A:392:ASP:CG	3:2A:422:ARG:HH22	2.23	0.46
4:2B:393:ALA:HB1	3:2C:261:PRO:HB3	1.96	0.46
3:2E:141:VAL:HG23	3:2E:170:CYS:HB3	1.97	0.46
4:2F:256:ASN:HD22	4:2F:350:LYS:HG3	1.78	0.46
4:2H:284:LEU:HD23	4:2H:362:LYS:HB3	1.97	0.46
3:2I:385:ALA:HB2	3:2I:432:TYR:HB3	1.97	0.46
4:2L:3:GLU:HA	4:2L:49:VAL:HG13	1.97	0.46
5:31:52:ILE:HG22	5:31:148:LEU:HD11	1.97	0.46
5:31:53:ARG:HB3	5:31:149:ILE:HG22	1.97	0.46
5:31:91:LEU:HD11	5:31:158:LEU:HD21	1.97	0.46
5:31:98:PHE:HE1	5:32:185:ARG:HD3	1.79	0.46
5:33:72:ARG:HG2	5:33:74:LYS:HZ2	1.80	0.46
5:33:117:GLN:HE22	6:67:360:VAL:H	1.62	0.46
5:39:89:VAL:O	5:39:102:THR:HA	2.15	0.46
3:3A:205:ASP:H	3:3A:303:ALA:HA	1.79	0.46
3:3C:261:PRO:HD2	3:3C:265:ILE:HG23	1.97	0.46
4:3F:12:CYS:HA	17:3F:501:GDP:C2	2.50	0.46
4:4B:280:GLN:HE21	8:A3:122:GLN:HE22	1.62	0.46
4:4B:314:SER:HA	4:4B:350:LYS:HB3	1.97	0.46
3:4C:17:GLY:HA2	3:4C:20:CYS:HB2	1.97	0.46
4:4F:32:PRO:HB2	6:64:913:TYR:HD2	1.80	0.46
5:51:191:ARG:HH22	5:52:191:ARG:HH22	1.63	0.46
5:59:93:SER:HB2	5:59:99:LEU:HD22	1.96	0.46
3:5A:276:ILE:HD12	3:5A:281:ALA:HB2	1.97	0.46
5:60:50:PHE:HE2	5:60:91:LEU:HD11	1.81	0.46
3:6E:166:LYS:HB3	3:6E:166:LYS:HE3	1.68	0.46
4:6F:309:ARG:H	4:6F:372:THR:HG22	1.79	0.46
4:6J:372:THR:HG21	4:6J:426:GLN:HB3	1.96	0.46
3:6M:185:TYR:HE1	3:6M:399:TYR:HB2	1.80	0.46
4:6N:313:ALA:HB3	4:6N:349:MET:HB3	1.96	0.46
7:72:299:PHE:HE2	14:K3:126:ILE:HD12	1.80	0.46
3:7G:12:ALA:HB3	3:7G:140:ALA:HB2	1.97	0.46
4:7H:117:LEU:HA	4:7H:120:VAL:HG12	1.97	0.46
3:7M:119:LEU:HD23	3:7M:122:ILE:HD11	1.97	0.46
7:83:258:GLU:HA	7:83:261:ALA:HB3	1.96	0.46
3:8C:101:ASN:HD22	3:8C:182:VAL:HG12	1.80	0.46
3:8E:319:TYR:HB3	3:8E:323:VAL:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8E:432:TYR:HA	3:8E:435:VAL:HG12	1.96	0.46
3:8M:301:MET:HE1	3:8M:305:CYS:H	1.80	0.46
7:96:301:LEU:HD11	7:96:307:LYS:HD3	1.97	0.46
3:9A:188:VAL:HG12	3:9A:421:ALA:HB1	1.98	0.46
4:9B:178:THR:HG22	4:9B:180:VAL:H	1.80	0.46
4:9B:293:MET:HE3	4:9B:367:PHE:HB2	1.97	0.46
3:9C:235:ILE:HA	3:9C:238:LEU:HD13	1.98	0.46
4:9D:20:PHE:HA	4:9D:230:SER:HB2	1.97	0.46
3:9M:200:VAL:HG21	3:9M:256:GLN:HE21	1.80	0.46
8:A5:47:LYS:HD3	8:A5:99:MET:HE3	1.96	0.46
8:A7:376:GLU:HG3	8:A7:381:PHE:HE2	1.79	0.46
8:A8:45:GLU:HB3	8:A8:69:MET:HE2	1.97	0.46
10:D1:61:ASP:HA	14:K6:142:GLN:NE2	2.29	0.46
10:D6:355:THR:HG22	10:D6:361:TRP:CD2	2.50	0.46
10:E6:83:ARG:HE	10:E6:88:LEU:HB3	1.80	0.46
10:E8:338:PRO:HB2	10:E8:341:TYR:HB3	1.98	0.46
12:G4:268:ARG:HH12	12:G4:290:LYS:HG3	1.78	0.46
13:J3:418:LEU:HB2	13:J3:472:VAL:HG11	1.97	0.46
1:a:662:ASP:O	1:a:666:VAL:HG23	2.14	0.46
1:B:535:ALA:O	1:B:539:ALA:HB3	2.15	0.46
1:I:327:TRP:HZ2	1:J:330:ARG:HD3	1.81	0.46
1:I:673:LEU:HD11	1:J:674:ARG:HG3	1.97	0.46
1:Q:601:ARG:HH21	1:Q:604:ILE:HD12	1.81	0.46
2:10:274:ARG:HB2	2:9:273:GLU:HG2	1.97	0.46
4:1H:219:THR:HB	3:1I:324:VAL:HG11	1.96	0.46
4:1J:29:GLY:HA3	4:1J:38:GLY:HA3	1.98	0.46
5:23:172:LEU:HD23	6:64:359:PRO:HB2	1.97	0.46
4:2B:99:ASN:HA	4:2B:142:GLY:H	1.81	0.46
4:2B:262:ARG:HE	5:32:217:SER:HB3	1.81	0.46
3:2K:51:THR:HG21	3:2K:243:ARG:HG2	1.98	0.46
5:38:211:CYS:HA	5:38:214:LYS:HE2	1.98	0.46
3:3G:319:TYR:HB3	3:3G:323:VAL:HG11	1.97	0.46
4:3L:101:TRP:H	4:3L:398:TYR:HE1	1.64	0.46
4:4B:382:SER:HB3	4:4B:415:MET:HE1	1.97	0.46
5:51:93:SER:HB2	5:51:99:LEU:HD22	1.98	0.46
5:53:53:ARG:HH12	5:53:63:GLY:H	1.62	0.46
3:5A:202:VAL:HA	3:5A:268:MET:HB3	1.97	0.46
4:5B:86:ARG:NH2	4:6B:282:ARG:HB3	2.27	0.46
3:5G:109:THR:HG22	3:5G:110:ILE:HG23	1.96	0.46
4:5J:326:VAL:O	4:5J:330:MET:HG2	2.15	0.46
3:5M:208:ALA:O	3:5M:212:ILE:HG12	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:61:46:ARG:HH22	5:61:138:ILE:HG21	1.80	0.46
6:64:975:LYS:HG2	6:64:978:LYS:HE3	1.97	0.46
4:6B:47:ILE:H	1:q:915:ARG:NH2	2.14	0.46
4:6D:139:LEU:HA	4:6D:145:SER:HB3	1.97	0.46
4:6N:16:ILE:HD11	4:6N:136:THR:HB	1.97	0.46
7:77:369:GLN:HA	7:77:372:TRP:HD1	1.80	0.46
4:7L:7:VAL:HG22	4:7L:64:ILE:HB	1.98	0.46
3:7M:320:ARG:NH1	3:7M:360:PRO:HG3	2.29	0.46
3:8C:9:VAL:HG12	3:8C:146:GLY:HA2	1.97	0.46
4:8F:23:VAL:O	4:8F:27:GLU:HB2	2.15	0.46
3:8I:119:LEU:HD23	3:8I:122:ILE:HD11	1.96	0.46
4:8L:36:TYR:HE1	4:8L:43:GLN:HB2	1.81	0.46
4:8L:271:ALA:HB2	4:8L:298:ASN:HD21	1.80	0.46
3:8M:244:PHE:HZ	3:8M:320:ARG:HD3	1.80	0.46
7:96:261:ALA:HA	7:96:391:TYR:HD2	1.80	0.46
7:97:350:ARG:HG2	7:97:379:LEU:HD22	1.97	0.46
3:9C:137:MET:HB3	3:9C:168:ASN:HA	1.97	0.46
4:9F:24:ILE:HG13	4:9F:28:HIS:HD2	1.80	0.46
4:9F:27:GLU:HG2	4:9F:359:LYS:HG2	1.96	0.46
4:9H:11:GLN:HG2	4:9H:15:GLN:HE22	1.80	0.46
4:9J:182:PRO:HB3	4:9J:381:VAL:HB	1.97	0.46
4:9J:236:VAL:HA	4:9J:366:THR:HG21	1.98	0.46
8:A7:216:MET:HG2	8:A7:223:LEU:HB3	1.98	0.46
10:D0:305:LEU:HD11	14:L5:142:GLN:HB3	1.98	0.46
10:D2:97:ILE:HD13	10:D2:397:PHE:HD1	1.81	0.46
10:D8:355:THR:HG22	10:D8:361:TRP:CD2	2.50	0.46
10:E2:91:GLN:O	10:E2:95:GLU:HG3	2.15	0.46
10:E2:150:VAL:O	10:E2:154:ILE:HG13	2.16	0.46
10:E3:331:ILE:HA	10:E3:335:LEU:HD23	1.97	0.46
12:F0:219:LEU:HD21	12:F0:223:LEU:HD22	1.97	0.46
12:F5:203:VAL:HG23	12:F5:204:SER:H	1.80	0.46
12:G2:200:LEU:HA	12:G2:203:VAL:HG12	1.96	0.46
12:G8:219:LEU:HD21	12:G8:239:ARG:HB2	1.96	0.46
13:J2:328:ALA:HA	13:J2:331:ASN:HB2	1.97	0.46
14:L3:222:THR:HG23	14:L3:224:GLY:H	1.80	0.46
1:a:562:ILE:HG21	1:f:562:ILE:CD1	2.46	0.46
1:d:375:GLN:O	1:d:378:GLU:HG2	2.16	0.46
1:d:439:LEU:HA	1:d:442:GLU:HG3	1.97	0.46
1:I:586:LYS:CB	1:J:586:LYS:HD3	2.41	0.46
1:K:474:LEU:HD11	1:L:475:LYS:HG3	1.96	0.46
1:L:429:ARG:NH2	1:o:870:GLY:HA2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:530:LEU:O	1:Q:533:ARG:HG3	2.16	0.46
1:V:571:GLU:HA	1:V:574:LYS:HD2	1.96	0.46
1:Z:494:ASN:OD1	1:Z:498:LYS:HE3	2.16	0.46
2:10:237:ALA:HB1	2:9:237:ALA:HB2	1.96	0.46
4:1B:222:TYR:HA	4:1B:225:LEU:HB2	1.97	0.46
4:1D:19:LYS:HE2	4:1D:19:LYS:HB2	1.70	0.46
3:1E:406:HIS:CG	4:1F:261:PRO:HD3	2.50	0.46
4:1N:42:LEU:HA	4:1N:45:GLU:HG2	1.97	0.46
5:21:100:ASN:HD22	5:21:184:THR:HB	1.79	0.46
3:2A:68:LEU:HD12	3:2A:93:ILE:HD13	1.98	0.46
3:2A:319:TYR:CE2	3:2A:328:VAL:HG13	2.50	0.46
3:2C:182:VAL:HG21	4:2D:255:VAL:HG12	1.97	0.46
4:2D:8:GLN:HE21	4:2D:63:ALA:HB1	1.80	0.46
3:2G:276:ILE:HD12	3:2G:281:ALA:HA	1.97	0.46
5:40:52:ILE:HD11	5:40:71:ILE:HD11	1.97	0.46
3:4E:27:GLU:HG2	3:4E:361:THR:HG21	1.97	0.46
4:4H:248:SER:HA	4:4H:252:LYS:HD2	1.98	0.46
3:4M:135:PHE:CZ	3:4M:166:LYS:HG3	2.50	0.46
5:53:52:ILE:HG23	5:53:150:MET:HE1	1.96	0.46
3:5C:72:PRO:HD2	4:5D:2:ARG:HH12	1.80	0.46
3:5G:205:ASP:HB2	3:5G:303:ALA:HA	1.98	0.46
4:5L:375:GLN:HA	4:5L:378:PHE:HD2	1.80	0.46
6:64:967:ARG:HG2	6:64:969:VAL:H	1.79	0.46
6:65:917:PHE:HB3	9:B3:459:ARG:HG3	1.97	0.46
6:67:447:ALA:O	6:67:451:GLU:HG2	2.16	0.46
4:6J:400:GLY:HA3	14:L2:90:PHE:CE1	2.49	0.46
3:6K:415:GLU:HG2	3:6K:418:PHE:HD2	1.80	0.46
3:6M:60:LYS:HE2	3:7M:283:HIS:CD2	2.51	0.46
7:71:375:LEU:HB2	14:K1:240:TRP:CE2	2.50	0.46
4:7B:299:MET:HG3	4:7B:305:PRO:HG3	1.96	0.46
3:7G:348:PRO:HB2	14:K9:111:LEU:HD22	1.98	0.46
4:7J:189:VAL:HB	4:7J:415:MET:HE2	1.96	0.46
4:7J:286:VAL:HG11	4:7J:326:VAL:HA	1.96	0.46
4:7L:12:CYS:HA	4:7L:15:GLN:HE21	1.80	0.46
4:8B:2:ARG:HA	4:8B:131:GLN:HB2	1.97	0.46
4:8J:49:VAL:HG21	4:8J:241:ARG:HB3	1.97	0.46
3:8K:109:THR:HG22	14:M7:172:ARG:HH21	1.80	0.46
3:8M:348:PRO:HB3	14:L0:117:ARG:HH12	1.80	0.46
3:9E:255:PHE:O	3:9E:259:LEU:HB2	2.15	0.46
3:9E:271:SER:O	3:9E:377:MET:HB3	2.16	0.46
4:9J:224:ASP:HA	4:9J:227:HIS:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A2:315:ARG:HH12	9:B5:64:GLU:HG3	1.78	0.46
8:A5:187:VAL:HG13	8:A5:223:LEU:HB2	1.98	0.46
9:B4:134:ILE:HA	9:B4:137:ARG:HE	1.80	0.46
9:B4:527:LEU:HD12	9:B4:534:THR:HG22	1.97	0.46
10:F2:301:ARG:NH2	14:M7:142:GLN:HA	2.29	0.46
12:I8:89:ILE:O	12:I8:93:GLN:HG2	2.16	0.46
13:J2:485:ILE:HG12	13:J2:511:SER:HB3	1.96	0.46
13:J3:658:GLY:O	13:J3:662:ILE:HG13	2.16	0.46
14:K4:200:PHE:HB2	14:K4:220:LEU:HB2	1.98	0.46
14:M1:196:VAL:HA	14:M1:223:SER:HA	1.97	0.46
14:M3:171:VAL:HG12	14:M3:181:LEU:HD21	1.96	0.46
1:c:586:LYS:HE3	1:c:586:LYS:HB3	1.41	0.46
1:d:422:THR:HA	1:d:425:ILE:HG22	1.97	0.46
1:A:600:LEU:HD21	1:F:601:ARG:HG3	1.98	0.46
1:H:678:ASN:HA	1:H:681:ILE:HG22	1.97	0.46
1:K:404:PHE:HA	1:K:407:GLU:HG2	1.98	0.46
3:1C:315:CYS:HB2	3:1C:351:PHE:HA	1.98	0.46
3:1E:319:TYR:HB2	3:1E:355:ILE:HD13	1.97	0.46
17:1F:501:GDP:H8	3:1G:248:LEU:HD11	1.81	0.46
3:1K:194:LEU:HD23	3:1K:267:PHE:HE1	1.80	0.46
3:1M:66:VAL:HA	3:1M:121:ARG:NH2	2.31	0.46
1:2:952:ARG:HB3	1:2:953:LYS:H	1.53	0.46
5:26:45:SER:HA	5:26:73:VAL:O	2.15	0.46
5:27:98:PHE:HE1	5:30:185:ARG:HG2	1.81	0.46
4:2D:263:LEU:HB2	4:2D:422:TYR:CZ	2.50	0.46
4:2H:113:ILE:HA	4:2H:116:VAL:HG12	1.97	0.46
2:3:184:LYS:HA	2:3:187:HIS:CE1	2.50	0.46
5:42:142:HIS:CE1	13:J4:340:ARG:HH12	2.33	0.46
4:4B:3:GLU:H	4:4B:130:LEU:HA	1.81	0.46
3:4E:259:LEU:HD21	3:4E:316:CYS:HB2	1.96	0.46
5:51:42:LEU:HD21	5:51:45:SER:HB2	1.98	0.46
5:51:87:VAL:O	5:51:104:ALA:HA	2.15	0.46
5:56:190:PHE:CE1	5:56:194:ALA:HB2	2.49	0.46
3:5A:276:ILE:HG13	3:5A:369:ALA:HB3	1.97	0.46
3:5A:298:PRO:HB3	3:5A:307:PRO:HD2	1.97	0.46
6:66:900:GLY:HA3	8:A2:268:GLY:HA3	1.97	0.46
6:67:318:PHE:HZ	6:67:440:PHE:HA	1.80	0.46
6:67:499:ARG:O	6:67:502:ALA:HB3	2.16	0.46
6:68:603:PHE:O	6:68:607:TYR:HB2	2.16	0.46
3:6C:405:VAL:HG13	3:6C:418:PHE:HE2	1.79	0.46
4:6D:271:ALA:HB2	4:6D:298:ASN:HD21	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6G:105:ARG:HH12	4:6H:251:ARG:HD3	1.79	0.46
4:6L:404:ASP:HB2	14:L3:130:ARG:HH22	1.81	0.46
4:6N:362:LYS:HE2	1:i:818:ALA:N	2.29	0.46
4:7B:199:VAL:O	4:7B:265:PHE:HA	2.15	0.46
3:7K:339:ARG:HH21	3:7K:342:GLN:HE22	1.64	0.46
4:7L:383:ASP:H	7:84:311:SER:HB3	1.81	0.46
7:83:261:ALA:HA	7:83:391:TYR:CD1	2.51	0.46
4:8D:185:ALA:HB3	4:8D:381:VAL:HG11	1.97	0.46
3:8I:119:LEU:HD11	3:8I:156:ARG:HD2	1.98	0.46
4:8L:222:TYR:HA	4:8L:225:LEU:HD13	1.96	0.46
3:8M:137:MET:HG3	3:8M:154:LEU:HD21	1.97	0.46
4:9F:286:VAL:HG12	4:9F:329:GLN:HG3	1.97	0.46
3:9G:173:PRO:HG2	3:9G:187:SER:HB2	1.97	0.46
3:9G:262:TYR:HB2	3:9G:265:ILE:HG12	1.97	0.46
4:9J:313:ALA:HA	4:9J:369:GLY:HA2	1.97	0.46
9:B2:524:PRO:HA	9:B2:527:LEU:HD12	1.97	0.46
9:B6:456:LYS:HA	9:B6:456:LYS:HD2	1.85	0.46
10:E2:46:ASP:O	10:E2:50:GLU:HG2	2.16	0.46
10:E8:355:THR:HG23	10:E8:357:ALA:H	1.80	0.46
10:F1:92:MET:HG3	10:F1:306:MET:HE2	1.97	0.46
12:G5:199:TRP:HH2	12:G6:224:ARG:HB3	1.81	0.46
14:L4:178:MET:HB3	14:L4:182:TYR:CE2	2.50	0.46
14:L9:183:GLN:HA	14:L9:186:THR:HG22	1.98	0.46
1:f:599:SER:OG	1:f:600:LEU:N	2.49	0.46
1:p:907:GLU:HA	1:p:910:LYS:HD2	1.98	0.46
1:A:610:VAL:HG13	1:F:614:LEU:HD22	1.97	0.46
1:I:471:LEU:HB2	1:J:471:LEU:HD21	1.98	0.46
1:Q:373:LEU:HA	1:Q:376:MET:HB2	1.96	0.46
2:11:237:ALA:HB2	2:12:237:ALA:HB1	1.97	0.46
3:1A:103:PHE:HD2	3:1A:147:SER:HB3	1.79	0.46
4:1F:262:ARG:HH21	4:1F:418:LEU:HB2	1.81	0.46
3:1M:123:ARG:HH22	3:2M:338:LYS:NZ	2.14	0.46
4:1N:135:ILE:HG13	4:1N:166:THR:HG22	1.97	0.46
4:1N:315:ALA:O	4:1N:351:SER:HA	2.16	0.46
5:29:151:HIS:HD2	5:29:153:ASN:HD21	1.64	0.46
4:3B:60:VAL:HB	4:4B:281:TYR:OH	2.16	0.46
3:3C:238:LEU:HD11	3:3C:378:ILE:HD11	1.97	0.46
4:3F:155:VAL:HG23	4:3F:164:MET:HE2	1.97	0.46
5:45:48:VAL:HG21	5:45:134:LEU:HB3	1.98	0.46
5:47:202:LEU:HB3	5:48:206:LEU:HD11	1.97	0.46
5:49:77:ILE:HG22	5:49:87:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4B:73:MET:O	4:4B:77:ARG:HG3	2.16	0.46
4:4D:284:LEU:HD12	4:4D:289:LEU:HD21	1.98	0.46
5:54:145:LEU:HB2	5:54:161:ILE:HB	1.98	0.46
4:5B:111:GLU:HG3	7:73:398:LYS:HG3	1.97	0.46
4:5B:113:ILE:HA	4:5B:116:VAL:HG12	1.96	0.46
3:5C:70:LEU:HD13	3:5C:145:THR:HB	1.98	0.46
3:5I:272:TYR:HB3	3:5I:275:ILE:HD11	1.98	0.46
3:5K:88:HIS:HD2	3:5K:90:GLU:H	1.62	0.46
3:5M:168:ASN:HB3	3:5M:201:ALA:HA	1.96	0.46
4:5N:193:VAL:HG12	4:5N:418:LEU:HD13	1.98	0.46
6:63:141:LEU:O	6:63:145:MET:HG2	2.15	0.46
6:63:632:PHE:HA	6:63:635:LYS:HB3	1.96	0.46
6:66:536:VAL:HG13	12:I8:65:GLU:HG3	1.97	0.46
6:67:485:LYS:HB3	6:67:487:TYR:CE1	2.51	0.46
4:6B:310:TYR:HE2	4:6B:367:PHE:HZ	1.62	0.46
3:6G:88:HIS:CD2	3:6G:90:GLU:H	2.27	0.46
4:6J:219:THR:HG23	3:6K:326:LYS:HD3	1.97	0.46
4:6L:289:LEU:HD13	4:6L:363:MET:HE2	1.96	0.46
4:6N:68:LEU:HA	4:6N:93:GLY:HA3	1.98	0.46
4:6N:341:PHE:HB3	4:6N:348:ASN:ND2	2.31	0.46
7:73:347:ILE:HG21	7:73:350:ARG:HB2	1.97	0.46
7:73:400:CYS:SG	14:K4:105:LEU:HB3	2.56	0.46
7:75:278:VAL:HG12	7:75:302:PRO:HG3	1.96	0.46
7:77:319:SER:HB2	7:77:398:LYS:HD2	1.98	0.46
3:7C:51:THR:HG21	3:7C:243:ARG:HA	1.97	0.46
3:7K:149:LEU:O	3:7K:153:LEU:HD23	2.15	0.46
3:7K:312:TYR:HB2	3:7K:343:PHE:CD2	2.51	0.46
7:84:275:HIS:HA	14:L3:95:ASN:ND2	2.31	0.46
3:8A:168:ASN:HB3	3:8A:201:ALA:HA	1.97	0.46
3:8A:207:GLU:HG3	3:8A:304:LYS:HE3	1.97	0.46
4:8J:15:GLN:HB3	4:8J:226:ASN:ND2	2.30	0.46
4:8J:167:PHE:HZ	4:8J:236:VAL:HG21	1.79	0.46
4:8J:207:LEU:HB3	4:8J:225:LEU:HG	1.96	0.46
4:8J:330:MET:HE3	4:8J:349:MET:HB3	1.97	0.46
3:9A:274:PRO:HG2	3:9A:371:VAL:HG11	1.98	0.46
4:9F:178:THR:O	4:9F:181:GLU:HG2	2.15	0.46
4:9L:299:MET:HE1	4:9L:305:PRO:HG3	1.97	0.46
8:A2:329:LEU:HD23	8:A2:334:PHE:HB2	1.98	0.46
9:B3:17:LEU:HD22	9:B3:491:ARG:HB2	1.97	0.46
10:E4:50:GLU:HG3	10:E4:51:TYR:CD2	2.51	0.46
10:E6:317:LEU:HD12	10:E6:321:ARG:HH12	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E7:87:ASP:HA	10:E7:90:VAL:HG12	1.98	0.46
12:F6:245:ALA:HA	12:F6:266:PRO:HG3	1.98	0.46
13:J6:362:ALA:HA	13:J6:365:ARG:HG2	1.98	0.46
1:c:574:LYS:HE3	1:c:575:LEU:HD22	1.97	0.46
1:C:407:GLU:OE1	1:d:518:ARG:HD3	2.15	0.46
1:O:675:LYS:HA	1:O:675:LYS:HD3	1.62	0.46
1:U:558:LEU:HA	1:U:561:ARG:HD2	1.98	0.46
3:1A:68:LEU:HG	3:1A:93:ILE:HB	1.97	0.46
3:1A:258:ASN:HD22	3:1A:352:LYS:HB2	1.81	0.46
3:1E:151:CYS:HA	3:1E:154:LEU:HD12	1.96	0.46
4:1H:17:GLY:HA2	4:1H:20:PHE:HB3	1.98	0.46
4:1H:391:ARG:HH12	3:1I:346:TRP:CG	2.33	0.46
5:29:78:LEU:HD22	6:68:369:PHE:HE2	1.81	0.46
3:2C:7:ILE:HD12	3:2C:137:MET:HE1	1.97	0.46
3:2C:84:ARG:HG3	3:2C:85:HIS:HD1	1.80	0.46
3:2C:298:PRO:HG3	3:2C:307:PRO:HD2	1.96	0.46
3:2G:12:ALA:HB3	3:2G:140:ALA:HB2	1.96	0.46
4:2J:171:PRO:HG3	4:2J:181:GLU:HG3	1.96	0.46
4:2L:388:MET:HE3	4:2L:394:PHE:CD2	2.51	0.46
5:35:164:MET:HE1	5:38:171:LEU:HB3	1.98	0.46
5:35:214:LYS:HB2	5:35:221:LEU:HD22	1.98	0.46
3:3A:296:PHE:HD2	3:3A:335:ILE:HG13	1.81	0.46
3:3E:203:MET:HE1	3:3E:384:ILE:HG23	1.98	0.46
3:3I:319:TYR:HB3	3:3I:323:VAL:HG21	1.97	0.46
4:4H:377:MET:HE3	4:4H:377:MET:HB2	1.78	0.46
3:4M:281:ALA:HB2	3:4M:370:LYS:H	1.81	0.46
5:50:45:SER:C	5:50:72:ARG:HH12	2.23	0.46
5:51:116:ARG:HE	5:51:117:GLN:HE22	1.63	0.46
5:52:80:GLU:HG3	5:52:83:ASN:H	1.80	0.46
5:55:161:ILE:HA	5:55:170:GLU:HA	1.98	0.46
5:55:167:LYS:HE2	5:55:169:ILE:HD11	1.97	0.46
5:58:148:LEU:HD11	5:58:158:LEU:HD13	1.97	0.46
5:58:180:THR:HG23	5:58:183:PHE:H	1.80	0.46
3:5E:274:PRO:HG2	3:5E:374:ALA:HA	1.97	0.46
3:5G:434:GLU:HA	3:5G:437:ILE:HG12	1.97	0.46
3:5K:401:LYS:HD2	14:K6:144:PHE:CD1	2.51	0.46
4:5N:174:LYS:HB3	6:68:784:TRP:HE1	1.80	0.46
5:61:232:ALA:HA	5:61:235:ARG:HD3	1.97	0.46
6:67:632:PHE:HB3	6:67:835:ILE:HD11	1.97	0.46
6:69:503:LYS:HE2	6:69:503:LYS:HB3	1.43	0.46
4:6D:61:PRO:HD3	4:6D:84:LEU:HG	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6D:286:VAL:HG12	4:6D:329:GLN:NE2	2.30	0.46
4:6F:67:ASP:HB3	4:6F:73:MET:HE1	1.97	0.46
4:6F:73:MET:HA	4:6F:76:VAL:HG12	1.98	0.46
3:6G:326:LYS:HG2	7:71:408:ILE:HD11	1.98	0.46
4:7B:207:LEU:HB3	4:7B:225:LEU:HD22	1.96	0.46
4:7B:380:ARG:HA	7:80:311:SER:HB2	1.97	0.46
3:7C:68:LEU:HG	3:7C:93:ILE:HD11	1.97	0.46
3:7G:121:ARG:CZ	3:7G:124:LYS:HD2	2.45	0.46
3:7I:323:VAL:HG22	3:7I:373:ARG:HG2	1.98	0.46
4:7J:193:VAL:HG23	4:7J:194:GLU:HG2	1.98	0.46
3:7K:339:ARG:HH12	7:83:390:PRO:HD3	1.81	0.46
4:7L:237:THR:HG22	4:7L:250:LEU:HD21	1.98	0.46
7:82:298:SER:HB3	7:82:320:TRP:HZ3	1.81	0.46
7:89:327:ASN:OD1	7:89:391:TYR:HA	2.15	0.46
4:8H:160:PRO:HB2	14:M2:174:TYR:HB3	1.97	0.46
3:8I:217:LEU:HD12	3:8I:219:ILE:HG12	1.98	0.46
4:8J:100:ASN:HD21	4:8J:397:TRP:HB3	1.80	0.46
4:8L:39:ASP:H	1:m:760:ARG:NH2	2.13	0.46
4:9B:173:PRO:HA	4:9B:176:SER:HB3	1.98	0.46
4:9J:156:ARG:HE	4:9J:164:MET:HE3	1.81	0.46
4:9J:308:GLY:HA3	4:9J:373:ALA:HB2	1.97	0.46
9:B2:527:LEU:HD23	9:B2:533:GLN:HG3	1.97	0.46
9:B6:500:HIS:HB2	9:B6:534:THR:HB	1.98	0.46
10:C6:386:LEU:HG	10:C6:390:MET:HE1	1.98	0.46
10:D1:62:VAL:HG22	10:D1:309:ILE:HD11	1.97	0.46
10:E9:92:MET:HG2	10:E9:306:MET:HE2	1.98	0.46
10:F1:62:VAL:HG12	10:F1:309:ILE:HD11	1.98	0.46
12:F9:212:TRP:HB3	12:F9:215:GLN:NE2	2.31	0.46
12:G0:94:LEU:HD23	12:G9:94:LEU:HB3	1.97	0.46
13:J5:453:THR:HG23	13:J5:456:GLU:H	1.81	0.46
14:K1:181:LEU:O	14:K1:185:ILE:HG13	2.15	0.46
14:L3:107:ALA:N	14:L3:119:HIS:HB3	2.31	0.46
14:M5:172:ARG:HB3	14:M5:174:TYR:H	1.81	0.46
1:a:601:ARG:NH2	1:t:884:PRO:O	2.49	0.46
1:f:591:ARG:HG2	1:f:592:ARG:N	2.30	0.46
1:f:602:ASN:O	1:f:605:LYS:HG2	2.15	0.46
1:r:894:LEU:HD11	1:r:946:LEU:HD22	1.98	0.46
1:I:467:LEU:HD21	1:J:467:LEU:HB3	1.98	0.46
1:J:663:LEU:HD23	1:J:663:LEU:HA	1.84	0.46
2:16:226:VAL:HG23	2:16:230:ARG:NH1	2.31	0.46
4:1B:192:LEU:HG	4:1B:196:ALA:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1D:70:PRO:HA	4:1D:73:MET:HB2	1.97	0.46
4:1D:305:PRO:HA	4:1D:373:ALA:HB3	1.98	0.46
4:1F:23:VAL:O	4:1F:27:GLU:HG3	2.15	0.46
5:21:188:MET:HE2	5:22:188:MET:HE1	1.98	0.46
5:21:206:LEU:HA	5:21:209:ILE:HG22	1.98	0.46
5:22:29:ILE:HD12	5:22:194:ALA:HB1	1.98	0.46
5:27:72:ARG:HB2	5:27:92:THR:O	2.16	0.46
5:28:166:TYR:CZ	5:29:129:VAL:HG12	2.51	0.46
3:2A:213:CYS:HA	3:2A:217:LEU:HD23	1.98	0.46
3:2E:96:LYS:HA	3:2E:96:LYS:HD2	1.70	0.46
3:2G:68:LEU:HD23	3:2G:93:ILE:HB	1.97	0.46
4:2H:100:ASN:HD22	4:2H:103:LYS:HE2	1.81	0.46
5:35:182:GLU:HG3	5:35:185:ARG:HH21	1.81	0.46
5:35:214:LYS:HD3	5:35:221:LEU:HD23	1.97	0.46
4:3B:179:VAL:HG13	3:3C:350:GLY:HA2	1.98	0.46
3:3E:195:LEU:HD21	3:3E:428:LEU:HD22	1.98	0.46
4:3H:156:ARG:HH11	4:3H:164:MET:HG2	1.80	0.46
4:3J:64:ILE:HG23	4:3J:89:ASN:HB2	1.98	0.46
4:3J:232:ALA:HB2	4:3J:300:MET:HE1	1.97	0.46
4:3L:16:ILE:HD13	4:3L:226:ASN:HD22	1.80	0.46
3:3M:343:PHE:HE2	3:3M:350:GLY:HA3	1.81	0.46
5:43:202:LEU:HD21	5:44:203:GLN:HG3	1.98	0.46
4:4B:10:GLY:HA2	4:4B:143:THR:HG23	1.98	0.46
3:4M:2:ARG:HD2	3:4M:133:GLN:HG3	1.98	0.46
3:4M:140:ALA:HA	3:4M:171:SER:HB2	1.97	0.46
5:58:91:LEU:HD12	5:58:91:LEU:HA	1.74	0.46
4:5B:324:LYS:H	4:5B:324:LYS:HG2	1.21	0.46
3:5I:2:ARG:HG2	3:5I:51:THR:HG22	1.97	0.46
4:5L:286:VAL:HB	4:5L:325:GLU:HG2	1.98	0.46
3:5M:196:GLU:HA	14:K6:83:THR:HB	1.97	0.46
5:62:42:LEU:HD22	5:62:76:LEU:HD21	1.97	0.46
6:66:494:LYS:HE2	6:66:494:LYS:HB2	1.62	0.46
6:68:915:ASN:HD21	9:B6:459:ARG:HH21	1.64	0.46
6:69:970:LEU:HD22	6:69:974:GLU:HB2	1.98	0.46
3:6A:413:MET:HE2	3:6A:417:GLU:HB3	1.98	0.46
4:6D:272:PRO:HD3	4:6D:289:LEU:HD11	1.97	0.46
3:6E:102:ASN:HB3	3:6E:105:ARG:HB3	1.97	0.46
4:6N:113:ILE:HA	4:6N:116:VAL:HG22	1.97	0.46
7:72:293:ILE:HG22	7:72:295:GLN:HG3	1.97	0.46
7:75:411:MET:HA	7:75:414:ILE:HD11	1.98	0.46
3:7C:344:VAL:HG13	3:7C:346:TRP:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8E:204:LEU:HD13	3:8E:231:ILE:HD13	1.96	0.46
4:8J:191:GLN:HE21	4:8J:191:GLN:HB3	1.66	0.46
4:8L:19:LYS:HD3	1:m:803:ILE:HD12	1.98	0.46
4:8L:91:VAL:HG21	4:8L:116:VAL:HG12	1.97	0.46
7:96:286:TRP:HE1	7:96:293:ILE:HG12	1.80	0.46
8:A3:42:VAL:HG23	8:A3:98:LEU:HD21	1.98	0.46
8:A3:196:LEU:HD21	8:A3:206:VAL:HG23	1.97	0.46
10:C8:305:LEU:O	10:C8:309:ILE:HD12	2.16	0.46
10:D1:93:ALA:O	10:D1:97:ILE:HD12	2.15	0.46
10:D2:315:LEU:HD21	10:D6:137:PHE:HZ	1.81	0.46
10:E8:86:LEU:HG	10:E8:313:TYR:HD2	1.81	0.46
10:F3:53:LEU:HB3	10:F3:65:PHE:HE1	1.81	0.46
13:J1:470:ARG:HA	13:J1:473:VAL:HG12	1.98	0.46
13:J2:284:ARG:HH11	13:J2:322:LYS:HZ3	1.64	0.46
13:J6:368:GLY:HA2	13:J6:371:ARG:HH21	1.81	0.46
13:J6:409:LEU:HD23	13:J6:409:LEU:HA	1.80	0.46
1:c:647:LYS:HA	1:c:647:LYS:HD2	1.48	0.46
1:f:612:PHE:O	1:f:616:THR:HG23	2.16	0.46
1:t:907:GLU:HA	1:t:910:LYS:HD2	1.96	0.46
1:v:855:LYS:HD2	1:v:930:SER:HB2	1.98	0.46
1:x:938:THR:O	1:x:942:ILE:HG12	2.15	0.46
1:A:407:GLU:O	1:A:411:LYS:HG2	2.15	0.46
1:A:527:LEU:HD22	1:F:523:VAL:HG13	1.98	0.46
1:A:679:ARG:HH12	1:A:683:GLU:HB2	1.79	0.46
1:J:630:ARG:HH21	1:J:631:LEU:HG	1.80	0.46
1:N:470:ARG:HH22	1:N:473:ARG:CZ	2.29	0.46
1:S:342:MET:HE2	1:W:342:MET:HE2	1.98	0.46
1:U:584:GLU:HG2	1:d:473:ARG:HD3	1.98	0.46
1:Y:601:ARG:HG2	1:s:884:PRO:HG3	1.98	0.46
1:Y:686:PHE:O	1:Y:687:ALA:C	2.59	0.46
3:1M:104:ALA:HB3	3:1M:411:GLU:OE2	2.16	0.46
5:21:50:PHE:HB2	5:21:71:ILE:HG12	1.98	0.46
3:2A:182:VAL:HA	3:2A:185:TYR:HD2	1.81	0.46
4:2L:169:VAL:HA	4:2L:202:ILE:HB	1.98	0.46
3:3A:324:VAL:HG22	3:3A:326:LYS:HG2	1.97	0.46
4:3B:131:GLN:HA	4:3B:131:GLN:HE21	1.80	0.46
4:3D:237:THR:HG22	4:3D:250:LEU:HD11	1.98	0.46
4:3H:5:VAL:HG23	4:3H:130:LEU:HD11	1.98	0.46
4:3J:25:SER:HB2	4:3J:30:ILE:HB	1.97	0.46
4:3L:152:ILE:HG23	4:3L:164:MET:SD	2.56	0.46
4:4H:265:PHE:HB3	4:4H:374:ILE:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4L:314:SER:HB3	4:4L:368:VAL:HG23	1.97	0.46
3:4M:180:ALA:HB3	3:4M:183:GLU:HG3	1.98	0.46
5:52:205:ARG:O	5:52:209:ILE:HG12	2.16	0.46
5:55:46:ARG:HH12	5:55:138:ILE:HG13	1.81	0.46
3:5E:318:MET:HE3	3:5E:318:MET:HB3	1.86	0.46
4:5N:167:PHE:CE2	4:5N:233:MET:HG3	2.51	0.46
4:5N:420:SER:HA	4:5N:423:GLN:HG2	1.98	0.46
5:62:147:VAL:O	5:62:159:ASP:HB2	2.16	0.46
6:65:141:LEU:O	6:65:145:MET:HG2	2.16	0.46
6:65:163:TYR:HB2	12:I3:329:LEU:HB2	1.98	0.46
6:68:626:GLN:NE2	6:68:627:PRO:HD2	2.31	0.46
6:69:899:ALA:HB1	8:A7:267:LYS:HG3	1.97	0.46
3:6A:96:LYS:HD2	3:6A:96:LYS:HA	1.70	0.46
3:6I:119:LEU:HG	3:6I:156:ARG:HG2	1.98	0.46
3:6K:11:GLN:HB2	3:6K:74:VAL:HG11	1.97	0.46
4:6L:116:VAL:HA	4:6L:119:VAL:HG12	1.98	0.46
3:6M:222:PRO:HG2	4:6N:324:LYS:HD3	1.98	0.46
3:6M:288:VAL:HA	3:6M:291:ILE:HG22	1.96	0.46
4:6N:200:GLN:HG2	4:6N:266:PHE:HB2	1.98	0.46
7:77:301:LEU:HB3	7:77:305:ALA:HB3	1.98	0.46
7:77:308:TYR:CZ	7:77:393:LEU:HD23	2.51	0.46
3:7C:306:ASP:HB3	3:7C:309:HIS:CE1	2.50	0.46
3:7E:236:SER:O	3:7E:240:ALA:HB2	2.16	0.46
3:7G:336:LYS:HG2	14:K9:112:THR:HG22	1.98	0.46
4:7J:154:LYS:HD2	7:90:286:TRP:NE1	2.30	0.46
4:7L:16:ILE:HD11	4:7L:136:THR:HB	1.98	0.46
7:83:364:ALA:HA	7:83:367:LEU:HD12	1.97	0.46
4:8F:156:ARG:HD2	4:8F:156:ARG:HA	1.85	0.46
3:8K:222:PRO:HD2	4:8L:324:LYS:NZ	2.30	0.46
3:8M:390:ARG:NH1	3:8M:391:MET:HE2	2.31	0.46
7:91:334:LEU:HD21	7:91:347:ILE:HG12	1.98	0.46
4:9F:384:GLN:HA	3:9G:348:PRO:HG2	1.98	0.46
3:9G:276:ILE:HD12	3:9G:281:ALA:HA	1.98	0.46
10:C6:340:LEU:HD21	10:C6:386:LEU:HD11	1.98	0.46
10:D7:120:PRO:HD3	10:D7:130:PRO:HB3	1.98	0.46
10:F3:355:THR:HG22	10:F3:361:TRP:CE3	2.51	0.46
12:G6:242:TRP:CZ2	12:G6:250:ARG:HB2	2.51	0.46
13:J1:287:GLU:HG2	13:J1:605:ARG:HH22	1.81	0.46
13:J2:678:ASN:HA	13:J2:681:HIS:CE1	2.51	0.46
13:J3:374:ARG:HD2	13:J3:375:ARG:HH12	1.79	0.46
14:K4:207:ILE:HG23	14:K4:212:ASP:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L4:190:THR:HG21	14:L4:255:VAL:HG23	1.97	0.46
1:c:584:GLU:O	1:c:588:THR:HG23	2.16	0.46
1:c:604:ILE:HG22	1:c:605:LYS:N	2.30	0.46
1:x:890:LEU:HD12	1:x:942:ILE:HG23	1.98	0.46
1:A:397:ALA:O	1:A:401:THR:HG23	2.16	0.46
1:M:474:LEU:HB3	1:N:474:LEU:HD21	1.98	0.46
1:N:677:MET:HE3	1:N:677:MET:HB2	1.66	0.46
1:Y:499:ARG:HD3	1:c:495:PHE:CE1	2.51	0.46
1:Y:673:LEU:HD22	1:c:673:LEU:HB3	1.96	0.46
2:16:172:PHE:HA	2:16:175:TYR:CE1	2.51	0.46
2:16:199:SER:C	2:16:201:VAL:H	2.23	0.46
3:1A:11:GLN:HB2	3:1A:74:VAL:HG21	1.97	0.46
3:1A:77:GLU:HG2	4:1B:243:PRO:HB3	1.98	0.46
4:1D:246:LEU:HB2	4:1D:353:VAL:HG12	1.98	0.46
3:1E:335:ILE:HG23	3:1E:341:ILE:HD11	1.97	0.46
4:1F:113:ILE:HA	4:1F:116:VAL:HG12	1.97	0.46
4:1H:205:GLU:HA	4:1H:208:TYR:HB2	1.97	0.46
3:1K:28:HIS:HD2	3:1K:49:PHE:HA	1.81	0.46
4:1N:42:LEU:HB3	4:1N:242:PHE:HD1	1.80	0.46
5:22:48:VAL:HG11	5:22:134:LEU:HD22	1.97	0.46
5:26:105:LEU:HA	5:26:109:LEU:HD23	1.96	0.46
5:27:44:TYR:HB3	5:27:75:ILE:HB	1.97	0.46
4:2D:290:THR:HG21	4:2D:329:GLN:HB3	1.98	0.46
3:2E:111:GLY:O	3:2E:115:VAL:HG23	2.15	0.46
3:2K:159:VAL:HG21	6:69:139:THR:HG22	1.98	0.46
5:31:76:LEU:HD13	5:31:88:ARG:HE	1.81	0.46
5:33:156:ALA:HB3	5:33:176:CYS:HB2	1.98	0.46
3:3C:107:HIS:HD2	3:3C:152:LEU:HB2	1.81	0.46
3:3C:325:PRO:HA	3:3C:328:VAL:HG12	1.98	0.46
3:3I:88:HIS:ND1	3:3I:89:PRO:HD2	2.30	0.46
3:4A:394:LYS:HB3	3:4A:398:MET:HE1	1.98	0.46
4:4B:239:CYS:HB3	4:4B:247:ASN:OD1	2.16	0.46
4:4D:10:GLY:HA2	4:4D:143:THR:HG23	1.97	0.46
3:5A:103:PHE:HD1	3:5A:147:SER:HB2	1.81	0.46
3:5A:286:LEU:HD12	3:5A:291:ILE:HD12	1.98	0.46
3:5A:406:HIS:HA	3:5A:409:VAL:HG12	1.97	0.46
3:5E:52:PHE:HD2	3:5E:243:ARG:HD3	1.81	0.46
4:5H:166:THR:HG23	4:5H:199:VAL:HG23	1.98	0.46
4:5L:117:LEU:HD13	7:77:286:TRP:HZ2	1.79	0.46
4:6B:51:TYR:HB3	4:6B:59:PHE:HB3	1.97	0.46
4:6J:156:ARG:HG2	4:6J:195:ASN:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6M:305:CYS:HB3	3:6M:387:VAL:HB	1.98	0.46
4:6N:169:VAL:HA	4:6N:202:ILE:HB	1.97	0.46
7:78:308:TYR:CE1	7:78:322:PRO:HB2	2.51	0.46
7:78:350:ARG:HG2	7:78:379:LEU:HB3	1.98	0.46
4:7B:43:GLN:HA	4:7B:242:PHE:HE1	1.80	0.46
3:7C:437:ILE:HD12	7:80:382:ASP:HB3	1.98	0.46
4:7F:252:LYS:HA	4:7F:255:VAL:HG12	1.98	0.46
7:83:344:ARG:HA	7:83:353:LYS:HE3	1.98	0.46
7:89:316:PRO:HA	4:8H:307:HIS:CE1	2.51	0.46
3:8C:250:VAL:HG23	3:8C:254:GLU:HG2	1.98	0.46
3:8K:243:ARG:HG3	3:8K:244:PHE:CD1	2.50	0.46
4:8L:316:MET:HA	4:8L:352:SER:HB3	1.98	0.46
3:8M:312:TYR:HD1	3:8M:381:SER:HB3	1.80	0.46
7:96:350:ARG:HD2	7:96:379:LEU:HD13	1.98	0.46
7:96:399:THR:HA	7:96:414:ILE:HD12	1.98	0.46
4:9B:331:LEU:HA	4:9B:334:GLN:HG3	1.97	0.46
3:9G:204:LEU:HD22	3:9G:302:MET:HE3	1.97	0.46
3:9G:234:VAL:HG22	3:9G:272:TYR:HB2	1.96	0.46
4:9H:20:PHE:HD2	4:9H:233:MET:HE3	1.81	0.46
3:9M:210:TYR:HE1	3:9M:227:LEU:HD21	1.81	0.46
8:A1:155:PRO:HB2	8:A5:269:LEU:HD11	1.97	0.46
8:A3:192:GLU:HG3	8:A3:195:ARG:HH21	1.80	0.46
8:A5:87:VAL:HG22	8:A5:93:VAL:HG12	1.98	0.46
8:A8:28:PRO:HB2	8:A8:30:GLN:HG2	1.97	0.46
10:C8:341:TYR:HB2	10:C8:390:MET:HG2	1.97	0.46
10:D2:305:LEU:O	10:D2:309:ILE:HD12	2.15	0.46
10:D3:57:ILE:HG23	10:D3:306:MET:HE1	1.97	0.46
10:D4:58:SER:HA	10:D4:92:MET:HE1	1.98	0.46
10:D7:355:THR:HG22	10:D7:361:TRP:CD2	2.51	0.46
10:E2:315:LEU:HD22	10:F2:136:PRO:HB3	1.98	0.46
10:E8:67:ALA:O	10:E8:71:GLN:HB2	2.16	0.46
12:F7:221:MET:HG3	12:F7:225:TRP:CD1	2.51	0.46
12:F8:264:ILE:HG23	12:F8:268:ARG:HH11	1.81	0.46
12:G1:246:PRO:HD2	12:G1:249:LEU:HD12	1.98	0.46
12:G8:264:ILE:HG23	12:G8:268:ARG:HH11	1.81	0.46
14:K1:154:MET:HE2	14:K1:156:LEU:HD21	1.97	0.46
1:q:879:VAL:HG13	1:q:880:THR:H	1.80	0.46
1:t:877:LEU:HB3	1:t:878:PRO:HD2	1.97	0.46
1:C:342:MET:HE2	1:C:342:MET:HB2	1.80	0.45
1:I:571:GLU:HG2	1:I:572:ARG:HH21	1.82	0.45
1:I:586:LYS:O	1:I:589:THR:HG22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:623:SER:HA	1:J:626:LEU:HD12	1.99	0.45
1:J:677:MET:HE2	1:J:677:MET:HB3	1.71	0.45
1:Q:639:LEU:HA	1:Q:642:MET:HG2	1.98	0.45
1:Z:451:THR:HG23	1:Z:452:PRO:HD3	1.98	0.45
3:1A:90:GLU:HB3	3:1A:121:ARG:HH11	1.81	0.45
3:1I:133:GLN:HG3	3:1I:252:VAL:HB	1.98	0.45
3:1I:189:LEU:HD21	3:1I:413:MET:HE1	1.97	0.45
3:1K:276:ILE:HG23	3:1K:280:LYS:HB3	1.98	0.45
4:1L:257:LEU:HD11	4:1L:314:SER:HB2	1.98	0.45
3:1M:184:PRO:HA	3:1M:391:MET:HE3	1.98	0.45
1:2:892:SER:HA	8:A4:87:VAL:HG21	1.98	0.45
5:22:121:ILE:HG21	5:22:129:VAL:HG21	1.98	0.45
5:24:47:GLU:HG3	5:24:70:PRO:HB2	1.97	0.45
5:29:35:SER:HB2	5:29:76:LEU:HD13	1.98	0.45
3:2A:149:LEU:HD23	3:2A:153:LEU:HD23	1.98	0.45
3:2A:217:LEU:HA	3:2A:277:SER:HB2	1.98	0.45
3:2A:259:LEU:HD11	3:2A:378:ILE:HD12	1.97	0.45
3:2C:47:ASP:HA	9:B5:516:SER:HA	1.97	0.45
3:2I:320:ARG:HG3	3:2I:360:PRO:HD3	1.98	0.45
4:2J:207:LEU:HD21	4:2J:229:VAL:HG13	1.98	0.45
3:2K:107:HIS:HD2	3:2K:152:LEU:HB2	1.80	0.45
3:2K:398:MET:HE1	4:2L:345:ILE:HG23	1.97	0.45
4:2L:372:THR:HA	4:2L:422:TYR:HD2	1.80	0.45
2:3:194:LYS:HA	2:3:197:VAL:HG12	1.97	0.45
5:31:128:SER:HA	5:31:131:ILE:HB	1.98	0.45
3:3A:323:VAL:HG21	3:3A:355:ILE:HG23	1.98	0.45
4:3B:60:VAL:HB	4:4B:281:TYR:CZ	2.51	0.45
4:3B:198:GLU:HB2	4:3B:266:PHE:CE2	2.51	0.45
4:3D:66:MET:SD	4:3D:116:VAL:HG11	2.56	0.45
3:3I:258:ASN:HD22	3:3I:352:LYS:HD2	1.80	0.45
4:3J:290:THR:HA	4:3J:293:MET:HE2	1.98	0.45
4:4J:149:THR:HA	4:4J:152:ILE:HD12	1.97	0.45
3:4M:52:PHE:CZ	3:4M:239:THR:HG21	2.51	0.45
3:5I:14:ILE:HG12	3:5I:67:PHE:HD1	1.81	0.45
3:5K:83:TYR:HD1	3:5K:86:LEU:HD13	1.80	0.45
3:5M:96:LYS:HE3	4:5N:2:ARG:NH1	2.24	0.45
3:6C:16:ILE:HD11	3:6C:138:PHE:HB3	1.97	0.45
3:6E:174:SER:HB2	3:6E:207:GLU:HG2	1.98	0.45
3:6G:319:TYR:HB3	3:6G:323:VAL:HG11	1.98	0.45
4:6J:244:GLY:HA2	4:6J:355:ASP:HB2	1.97	0.45
3:6M:336:LYS:HG2	14:K6:112:THR:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7C:122:ILE:HG21	3:7C:157:LEU:HD11	1.98	0.45
3:7C:319:TYR:HB3	3:7C:323:VAL:HG21	1.98	0.45
2:8:171:MET:HE3	2:8:174:GLN:HB3	1.98	0.45
7:86:411:MET:HG2	4:8D:174:LYS:HZ1	1.81	0.45
4:8H:156:ARG:HG2	4:8H:195:ASN:HA	1.97	0.45
4:8J:392:LYS:HG3	4:8J:395:LEU:HD11	1.98	0.45
7:97:288:PRO:HB3	14:M5:179:GLU:H	1.81	0.45
3:9A:407:TRP:HZ2	4:9B:258:ILE:HD12	1.81	0.45
3:9E:430:LYS:HA	3:9E:433:GLU:HG3	1.97	0.45
4:9F:240:LEU:HD11	4:9F:250:LEU:H	1.80	0.45
4:9F:268:ILE:HD13	4:9F:368:VAL:HG12	1.98	0.45
3:9I:120:ASP:O	3:9I:123:ARG:HG2	2.16	0.45
3:9I:209:ILE:HD12	3:9I:230:LEU:HD22	1.97	0.45
4:9L:249:ASP:H	4:9L:252:LYS:HD3	1.81	0.45
8:A9:320:LEU:HD13	8:A9:337:GLU:HB3	1.98	0.45
10:C6:377:LEU:HD21	10:C6:388:SER:HB3	1.96	0.45
10:D6:92:MET:HE3	10:D6:92:MET:HB3	1.73	0.45
12:G8:188:ARG:HG3	12:G8:190:ALA:H	1.81	0.45
13:J1:661:GLU:HA	13:J1:664:LYS:HG2	1.97	0.45
14:K9:181:LEU:O	14:K9:185:ILE:HG12	2.15	0.45
1:c:579:LEU:HD12	1:c:579:LEU:HA	1.85	0.45
1:e:375:GLN:HE21	1:e:376:MET:HE3	1.81	0.45
1:D:643:ARG:HE	1:m:826:VAL:HG11	1.81	0.45
1:N:629:LYS:HB2	1:N:629:LYS:HE3	1.51	0.45
1:R:614:LEU:HD22	1:V:610:VAL:HG13	1.98	0.45
1:Z:460:GLN:HE21	1:d:461:ARG:HE	1.64	0.45
2:11:233:ALA:HB2	2:12:234:ARG:NH2	2.32	0.45
4:1H:175:VAL:HG11	3:1I:332:VAL:HG13	1.99	0.45
4:1H:350:LYS:HZ3	4:1H:352:SER:HB3	1.82	0.45
4:1H:407:GLU:HA	4:1H:410:GLU:HB2	1.96	0.45
3:1I:53:PHE:HB3	3:1I:61:HIS:HB3	1.99	0.45
3:1I:70:LEU:HD12	3:1I:145:THR:HG22	1.97	0.45
3:1K:68:LEU:HD12	3:1K:93:ILE:HD12	1.97	0.45
4:1L:253:LEU:HD11	4:1L:368:VAL:HG11	1.97	0.45
3:1M:223:THR:HG23	3:1M:225:THR:H	1.81	0.45
3:1M:250:VAL:HG11	3:1M:318:MET:HE1	1.97	0.45
5:28:103:HIS:HD2	5:28:174:LEU:HB2	1.82	0.45
3:2A:204:LEU:HD12	3:2A:231:ILE:HD12	1.98	0.45
4:2D:253:LEU:HD21	4:2D:316:MET:HE3	1.97	0.45
2:3:260:ARG:HA	2:3:263:VAL:HG12	1.97	0.45
4:3B:417:ASP:O	4:3B:421:GLU:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3C:251:ASP:HB2	3:3C:254:GLU:HG3	1.98	0.45
3:3E:167:LEU:HD22	3:3E:200:VAL:HB	1.98	0.45
3:3K:217:LEU:HD11	3:3K:368:LEU:HD22	1.96	0.45
5:48:203:GLN:HA	5:48:206:LEU:HD12	1.98	0.45
3:4A:24:PHE:HA	3:4A:27:GLU:HG2	1.98	0.45
4:4B:310:TYR:HA	4:4B:371:SER:HA	1.97	0.45
4:4D:379:LYS:HG3	4:4D:419:VAL:HG21	1.97	0.45
3:4E:387:VAL:HG13	3:4E:390:ARG:HH21	1.80	0.45
4:4L:124:ALA:HB1	4:4L:130:LEU:HD13	1.99	0.45
4:4L:219:THR:HB	3:4M:324:VAL:HG21	1.98	0.45
3:4M:319:TYR:HB3	3:4M:323:VAL:HG11	1.97	0.45
5:55:160:PHE:HD2	5:55:172:LEU:HB3	1.81	0.45
4:5H:263:LEU:HD21	4:5H:425:TYR:HE2	1.81	0.45
6:65:174:LEU:HB3	6:65:493:ARG:HH12	1.80	0.45
6:67:842:ILE:HD11	6:67:959:PRO:HD3	1.98	0.45
6:69:545:GLU:O	6:69:549:ARG:HG3	2.15	0.45
3:6A:8:HIS:O	3:6A:68:LEU:HB3	2.16	0.45
3:6A:234:VAL:HG22	3:6A:272:TYR:HB2	1.98	0.45
3:6E:272:TYR:HB3	3:6E:275:ILE:HD11	1.98	0.45
3:6I:136:LEU:HB3	3:6I:138:PHE:HE1	1.81	0.45
4:6J:375:GLN:HG3	4:6J:419:VAL:HG13	1.97	0.45
4:6L:179:VAL:HG12	3:6M:258:ASN:HD21	1.82	0.45
3:6M:88:HIS:HB3	3:6M:91:GLN:HB3	1.98	0.45
7:71:257:ARG:HE	7:71:309:THR:HG23	1.80	0.45
7:79:412:MET:HE2	4:7D:205:GLU:HG3	1.98	0.45
3:7C:210:TYR:CE1	3:7C:227:LEU:HD11	2.50	0.45
3:7K:9:VAL:HB	3:7K:139:ASN:HB3	1.98	0.45
3:7K:292:THR:HG21	3:7K:331:ALA:HB1	1.98	0.45
3:7K:402:ARG:HD2	14:L0:146:VAL:HG22	1.98	0.45
7:85:308:TYR:CE1	7:85:322:PRO:HB2	2.52	0.45
7:89:269:LEU:HD21	7:89:329:PRO:HD2	1.98	0.45
7:89:344:ARG:HA	7:89:353:LYS:HE3	1.98	0.45
3:8C:17:GLY:HA2	3:8C:20:CYS:HB3	1.97	0.45
4:8L:273:LEU:HA	1:m:814:PRO:HG3	1.99	0.45
3:8M:245:ASP:H	1:m:788:PRO:HB3	1.81	0.45
4:9B:42:LEU:HD23	4:9B:46:ARG:HH22	1.81	0.45
4:9L:8:GLN:OE1	4:9L:17:GLY:HA3	2.17	0.45
8:A1:310:LEU:HD11	8:A1:385:VAL:HA	1.98	0.45
8:A2:255:ARG:HA	8:A2:263:PRO:HG3	1.97	0.45
8:A6:200:TYR:HB3	8:A6:205:CYS:HB2	1.98	0.45
8:A8:47:LYS:HG2	8:A8:53:VAL:HG11	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B6:471:PRO:HG2	1:x:845:MET:HA	1.98	0.45
10:D0:390:MET:HA	10:D0:393:VAL:HG12	1.98	0.45
10:D6:331:ILE:HG23	10:D6:335:LEU:HG	1.98	0.45
10:E2:305:LEU:O	10:E2:309:ILE:HD12	2.16	0.45
10:E7:305:LEU:O	10:E7:309:ILE:HG12	2.16	0.45
10:E8:349:PHE:CE1	10:E8:363:ALA:HB1	2.51	0.45
12:F7:216:TRP:HZ2	12:F7:228:ILE:HD11	1.81	0.45
12:G2:253:THR:HG22	12:G2:261:TRP:HB2	1.98	0.45
12:G6:261:TRP:CE2	12:G6:286:PRO:HG3	2.50	0.45
14:K5:114:SER:OG	14:K5:117:ARG:HG2	2.15	0.45
14:L9:202:GLN:HG2	14:L9:218:LYS:HB2	1.98	0.45
1:J:577:GLN:HE22	1:J:578:ARG:CD	2.24	0.45
1:L:384:LEU:HA	1:L:387:ILE:HG22	1.98	0.45
1:R:628:VAL:HB	1:V:628:VAL:HG22	1.97	0.45
1:U:641:GLU:O	1:U:645:GLN:HG2	2.16	0.45
1:Y:383:ALA:O	1:Y:387:ILE:HG12	2.16	0.45
17:1D:501:GDP:C8	3:1E:248:LEU:HD13	2.52	0.45
3:1E:231:ILE:O	3:1E:235:ILE:HG12	2.16	0.45
4:1H:238:CYS:HB2	4:1H:318:ARG:HE	1.80	0.45
4:1L:135:ILE:HG21	4:1L:152:ILE:HD11	1.98	0.45
5:24:53:ARG:HD3	5:24:64:ASP:HB3	1.98	0.45
3:2C:138:PHE:HZ	3:2C:235:ILE:HG12	1.81	0.45
4:2D:387:ALA:HB1	3:2E:346:TRP:HA	1.98	0.45
4:2J:170:PHE:CD2	4:2J:201:VAL:HG13	2.51	0.45
4:2J:320:ARG:HG2	9:B2:127:LEU:HD21	1.98	0.45
3:2M:184:PRO:HG3	3:2M:394:LYS:HG2	1.99	0.45
3:2M:202:VAL:HG22	3:2M:203:MET:H	1.80	0.45
5:30:130:LEU:HA	5:30:133:MET:HE3	1.98	0.45
4:3B:228:LEU:HD11	4:3B:273:LEU:HD11	1.98	0.45
4:3F:113:ILE:HG13	4:3F:117:LEU:HD23	1.98	0.45
4:3F:268:ILE:HG22	4:3F:368:VAL:HG22	1.99	0.45
4:3J:171:PRO:HG3	4:3J:181:GLU:HG2	1.98	0.45
3:4A:334:THR:O	3:4A:338:LYS:HG2	2.16	0.45
4:4B:51:TYR:HB3	4:4B:59:PHE:HB3	1.97	0.45
3:4C:147:SER:HB2	3:4C:190:SER:HB2	1.98	0.45
3:4G:360:PRO:HG3	3:4G:374:ALA:HB2	1.99	0.45
3:4M:224:TYR:HA	3:4M:227:LEU:HD12	1.98	0.45
5:59:188:MET:HA	5:59:191:ARG:HG3	1.97	0.45
4:5B:131:GLN:HG3	4:5B:163:ILE:HD11	1.98	0.45
4:5B:253:LEU:HD21	4:5B:368:VAL:HG11	1.98	0.45
3:5C:185:TYR:HB3	3:5C:408:TYR:HE2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5C:262:TYR:HB2	3:5C:265:ILE:HB	1.99	0.45
4:5D:201:VAL:HG21	4:5D:374:ILE:HD12	1.98	0.45
4:5H:292:GLN:HG2	4:5H:298:ASN:HD22	1.81	0.45
3:5I:159:VAL:HG22	7:75:346:TRP:HH2	1.82	0.45
5:60:89:VAL:HB	5:60:103:HIS:HB3	1.98	0.45
5:62:195:LEU:HD12	5:62:195:LEU:HA	1.81	0.45
6:64:353:GLN:HA	6:64:358:PRO:HG3	1.97	0.45
6:65:490:GLU:O	6:65:493:ARG:HG2	2.15	0.45
6:66:439:LYS:HE2	6:66:439:LYS:HB2	1.80	0.45
6:66:508:GLU:O	6:66:509:GLU:C	2.60	0.45
3:6A:320:ARG:HH12	3:6A:360:PRO:HB3	1.80	0.45
4:6D:207:LEU:HB3	4:6D:225:LEU:HD11	1.97	0.45
3:6I:195:LEU:HD12	3:6I:428:LEU:HD22	1.99	0.45
7:78:261:ALA:HA	7:78:391:TYR:HD2	1.81	0.45
4:7B:28:HIS:HD1	4:7B:47:ILE:HG13	1.82	0.45
3:7E:407:TRP:CG	4:7F:255:VAL:HG23	2.51	0.45
3:7K:407:TRP:CG	4:7L:255:VAL:HG23	2.52	0.45
4:7L:278:SER:HA	4:7L:281:TYR:CE1	2.51	0.45
7:84:308:TYR:CZ	7:84:322:PRO:HB2	2.51	0.45
7:86:386:ARG:HG3	14:L7:115:PRO:HB3	1.97	0.45
7:89:357:VAL:HG11	14:L9:218:LYS:HD3	1.99	0.45
7:89:368:THR:HG23	7:89:371:GLU:H	1.82	0.45
4:8B:205:GLU:HB3	4:8B:302:ALA:HB2	1.99	0.45
4:8J:189:VAL:HA	4:8J:192:LEU:HB2	1.98	0.45
4:8L:279:GLN:HA	4:8L:282:ARG:HG2	1.97	0.45
2:9:165:ARG:HH21	10:C7:333:THR:H	1.63	0.45
7:90:251:VAL:HA	7:90:254:ARG:HE	1.82	0.45
7:95:411:MET:HE1	14:M7:109:ASP:HA	1.99	0.45
3:9E:313:MET:HE3	3:9E:380:ASN:HB3	1.98	0.45
3:9M:9:VAL:HG22	3:9M:68:LEU:HD12	1.98	0.45
8:A2:346:THR:HG23	8:A2:349:LEU:H	1.82	0.45
10:D4:331:ILE:HA	10:D4:335:LEU:HD23	1.97	0.45
10:E1:341:TYR:HA	10:E1:390:MET:HE1	1.99	0.45
10:E3:355:THR:HG22	10:E3:361:TRP:CD2	2.52	0.45
14:K0:154:MET:HE2	14:K0:171:VAL:HB	1.98	0.45
1:c:519:GLU:O	1:c:522:ARG:HB2	2.16	0.45
1:C:323:MET:HA	1:G:323:MET:HE1	1.98	0.45
1:D:681:ILE:HG22	1:D:682:LYS:HG3	1.97	0.45
1:I:660:GLN:O	1:I:664:ILE:HG13	2.16	0.45
1:N:683:GLU:O	1:N:684:ARG:C	2.59	0.45
1:R:523:VAL:HB	1:V:520:TRP:CZ2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:502:LEU:O	1:Y:506:VAL:HG23	2.16	0.45
3:1A:256:GLN:HA	3:1A:260:VAL:HG12	1.97	0.45
4:1B:204:ASN:HA	4:1B:207:LEU:HD12	1.98	0.45
3:1C:27:GLU:HB2	3:1C:361:THR:HG21	1.99	0.45
3:1E:64:ARG:HB3	3:1E:125:LEU:HD21	1.98	0.45
4:1F:105:HIS:CE1	4:1F:191:GLN:HG2	2.52	0.45
4:1H:377:MET:HG2	4:1H:380:ARG:HH21	1.80	0.45
3:1K:107:HIS:HD2	3:1K:152:LEU:HB2	1.81	0.45
5:26:205:ARG:HE	5:26:205:ARG:HB3	1.53	0.45
5:27:117:GLN:HA	5:27:117:GLN:HE21	1.82	0.45
5:29:121:ILE:HG21	5:29:129:VAL:HG11	1.99	0.45
3:2C:51:THR:HG21	3:2C:243:ARG:HG2	1.99	0.45
3:2E:167:LEU:HG	3:2E:200:VAL:HB	1.98	0.45
4:2F:276:ARG:HH22	9:B1:89:ALA:HB2	1.82	0.45
4:2H:236:VAL:HA	4:2H:316:MET:HE3	1.97	0.45
3:2I:261:PRO:HG2	3:2I:313:MET:HE3	1.98	0.45
4:2J:215:LEU:HD11	4:2J:228:LEU:HD21	1.97	0.45
3:2K:70:LEU:HB2	3:2K:145:THR:HG21	1.99	0.45
3:3A:308:ARG:NH2	6:67:568:GLN:HG2	2.32	0.45
3:3E:202:VAL:HA	3:3E:268:MET:HB2	1.98	0.45
5:42:48:VAL:HG21	5:42:134:LEU:HD22	1.98	0.45
5:45:192:TYR:CE1	5:46:191:ARG:HB3	2.52	0.45
4:4L:31:ASP:OD1	4:4L:32:PRO:HD2	2.16	0.45
5:52:145:LEU:HB2	5:52:161:ILE:HB	1.98	0.45
5:56:50:PHE:HE1	5:56:160:PHE:HE1	1.63	0.45
5:57:93:SER:HB2	5:57:99:LEU:HD22	1.98	0.45
5:57:235:ARG:HD3	6:66:593:PRO:HD2	1.99	0.45
3:5G:334:THR:HG21	6:65:780:PRO:HB3	1.98	0.45
4:5H:139:LEU:HD21	4:5H:168:SER:HB2	1.97	0.45
2:6:290:ASN:ND2	2:6:290:ASN:C	2.74	0.45
6:65:418:ASN:HB3	6:65:429:ALA:HB1	1.97	0.45
6:65:491:TYR:HA	6:65:494:LYS:HD3	1.99	0.45
6:67:866:ARG:HH21	6:67:921:VAL:HA	1.80	0.45
3:6A:317:LEU:HD13	3:6A:377:MET:HG2	1.99	0.45
4:6B:375:GLN:HE21	4:6B:379:LYS:HD2	1.82	0.45
3:6G:207:GLU:HG3	3:6G:304:LYS:HE3	1.97	0.45
4:6H:230:SER:HA	4:6H:233:MET:HB3	1.99	0.45
3:6I:91:GLN:HG2	3:6I:121:ARG:HD2	1.98	0.45
3:6M:63:PRO:HG2	3:6M:87:PHE:HD1	1.81	0.45
7:73:412:MET:HB2	7:73:412:MET:HE2	1.80	0.45
7:78:258:GLU:HA	7:78:261:ALA:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7B:252:LYS:NZ	4:7B:256:ASN:HD21	2.15	0.45
4:7D:137:HIS:CE1	4:7D:168:SER:HB3	2.52	0.45
4:7D:286:VAL:HG22	4:7D:321:MET:HE3	1.98	0.45
3:7E:224:TYR:CZ	4:7F:323:THR:HG21	2.51	0.45
3:7I:191:THR:HG21	3:7I:425:LEU:HD22	1.98	0.45
3:7K:319:TYR:HB2	3:7K:355:ILE:HD13	1.99	0.45
4:7L:284:LEU:HD21	4:7L:362:LYS:HB2	1.97	0.45
3:7M:166:LYS:NZ	3:7M:198:THR:HA	2.31	0.45
3:8A:409:VAL:HG13	14:M5:151:PRO:HD3	1.98	0.45
4:8F:186:THR:HA	4:8F:415:MET:HE3	1.98	0.45
3:8I:296:PHE:HA	3:8I:377:MET:HE2	1.99	0.45
4:8J:132:GLY:HA2	4:8J:162:ARG:HB3	1.98	0.45
4:8J:237:THR:HG22	4:8J:250:LEU:HD11	1.97	0.45
4:8L:393:ALA:HA	3:8M:262:TYR:HE1	1.81	0.45
3:9A:191:THR:HA	3:9A:194:LEU:HD23	1.98	0.45
4:9B:229:VAL:HA	4:9B:300:MET:HE1	1.98	0.45
3:9G:204:LEU:HD13	3:9G:231:ILE:HD12	1.99	0.45
4:9H:166:THR:HG21	4:9H:192:LEU:HD11	1.97	0.45
3:9I:19:ALA:HA	3:9I:22:GLU:HG2	1.98	0.45
3:9I:117:LEU:O	3:9I:121:ARG:HG3	2.17	0.45
4:9J:87:PRO:HA	4:9J:90:PHE:HD2	1.79	0.45
4:9L:12:CYS:HB3	4:9L:138:SER:HB2	1.99	0.45
8:A5:382:LEU:O	8:A5:386:ARG:HG2	2.16	0.45
8:A8:72:ARG:HD2	1:y:854:ARG:HD3	1.98	0.45
8:A8:242:PRO:HB2	8:A8:247:ARG:HD3	1.97	0.45
10:C6:305:LEU:O	10:C6:309:ILE:HD12	2.16	0.45
10:C7:305:LEU:O	10:C7:309:ILE:HD12	2.16	0.45
10:D8:68:THR:HA	10:D8:71:GLN:HB3	1.99	0.45
10:E1:92:MET:HA	10:E1:95:GLU:HG2	1.99	0.45
10:E6:87:ASP:O	10:E6:91:GLN:HG3	2.16	0.45
10:E7:47:MET:HE3	10:E7:47:MET:HB2	1.79	0.45
10:E9:56:TYR:HB3	10:E9:65:PHE:HB2	1.97	0.45
10:F3:301:ARG:HD2	14:M5:142:GLN:HA	1.99	0.45
12:G8:197:LEU:HD11	12:G8:216:TRP:CD2	2.52	0.45
13:J5:328:ALA:HA	13:J5:331:ASN:HB2	1.98	0.45
14:K0:155:TRP:CD2	14:K0:241:VAL:HG21	2.52	0.45
14:L9:97:ARG:HG2	14:L9:100:ALA:HB3	1.99	0.45
14:M2:233:LEU:HA	14:M2:236:PHE:HD2	1.80	0.45
14:M6:155:TRP:CE2	14:M6:241:VAL:HG11	2.52	0.45
1:b:381:ARG:HH21	1:b:384:LEU:HD12	1.81	0.45
1:c:664:ILE:O	1:c:668:GLN:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:756:PRO:HB2	1:h:759:ARG:HB2	1.99	0.45
1:B:380:HIS:HA	1:E:381:ARG:HH22	1.82	0.45
1:D:640:ALA:HB3	1:m:828:CYS:SG	2.56	0.45
1:N:608:ASP:HB3	3:9I:370:LYS:NZ	2.31	0.45
1:S:330:ARG:HG3	1:W:327:TRP:CZ2	2.52	0.45
3:1C:60:LYS:HD2	3:2C:282:TYR:CD2	2.51	0.45
4:1F:64:ILE:HG13	4:1F:120:VAL:HG22	1.99	0.45
4:1F:177:ASP:HB3	3:1G:353:CYS:HB2	1.97	0.45
4:1J:44:LEU:HD12	4:1J:47:ILE:HG13	1.98	0.45
3:1M:271:SER:HB3	3:1M:301:MET:HA	1.98	0.45
5:20:97:LEU:HG	5:20:188:MET:HE2	1.99	0.45
5:24:113:MET:O	5:24:117:GLN:HG3	2.16	0.45
5:24:149:ILE:HB	5:24:157:ARG:HB2	1.98	0.45
4:2B:30:ILE:HD11	4:2B:47:ILE:HD11	1.99	0.45
4:2B:395:LEU:HA	4:2B:398:TYR:HD2	1.81	0.45
3:2C:181:VAL:HG23	3:2C:182:VAL:HG23	1.98	0.45
3:2G:100:ALA:HA	4:2H:252:LYS:HG3	1.98	0.45
3:2I:360:PRO:HG3	3:2I:374:ALA:HB2	1.98	0.45
3:2K:204:LEU:HD12	3:2K:209:ILE:HD11	1.97	0.45
4:2L:11:GLN:HA	4:2L:72:THR:HG21	1.98	0.45
4:3B:137:HIS:HE1	4:3B:166:THR:HB	1.80	0.45
3:3C:7:ILE:HB	3:3C:137:MET:HA	1.98	0.45
4:3D:235:GLY:HA3	4:3D:366:THR:HG21	1.99	0.45
4:3H:178:THR:HG22	3:3I:352:LYS:HZ3	1.82	0.45
3:3K:407:TRP:HE1	4:3L:258:ILE:HB	1.81	0.45
3:3M:175:PRO:HG2	3:3M:304:LYS:HD2	1.98	0.45
5:43:73:VAL:HG12	5:43:91:LEU:HD22	1.97	0.45
4:4B:274:THR:HG22	4:4B:275:SER:H	1.82	0.45
4:4F:215:LEU:HB3	4:4F:217:LEU:HD13	1.98	0.45
5:54:75:ILE:HG12	5:54:89:VAL:HG22	1.98	0.45
5:57:91:LEU:HB2	5:57:101:TYR:HB2	1.98	0.45
5:59:215:LEU:HD11	6:68:946:GLN:HA	1.99	0.45
3:5E:264:ARG:HA	3:5E:264:ARG:HD2	1.80	0.45
3:5I:3:GLU:HG2	3:5I:129:CYS:HB3	1.98	0.45
3:5K:242:LEU:HD21	3:5K:252:VAL:HG23	1.98	0.45
3:6A:287:SER:HA	3:6A:373:ARG:NH2	2.32	0.45
3:6E:252:VAL:HA	3:6E:255:PHE:HD2	1.82	0.45
4:6L:132:GLY:HA2	4:6L:162:ARG:HB3	1.98	0.45
3:6M:123:ARG:HH12	3:6M:127:ASP:HB3	1.82	0.45
4:6N:316:MET:HE2	4:6N:366:THR:HG23	1.97	0.45
7:71:350:ARG:HA	7:71:388:GLU:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:73:283:SER:HA	10:D9:142:ARG:HE	1.81	0.45
3:7E:169:PHE:HD1	3:7E:202:VAL:HB	1.82	0.45
4:7J:253:LEU:HD11	4:7J:368:VAL:HG21	1.97	0.45
3:7M:401:LYS:HA	3:7M:401:LYS:HD3	1.89	0.45
7:80:279:ARG:HH21	10:E6:149:TYR:H	1.64	0.45
7:80:378:MET:HB2	7:80:378:MET:HE2	1.61	0.45
7:84:254:ARG:HB3	7:84:258:GLU:HB2	1.97	0.45
7:89:390:PRO:HD2	14:L5:118:CYS:SG	2.56	0.45
3:8C:12:ALA:HB3	3:8C:140:ALA:HB2	1.99	0.45
4:8D:236:VAL:HG13	4:8D:237:THR:HG23	1.97	0.45
3:8I:177:VAL:HB	3:8I:207:GLU:HB2	1.98	0.45
4:8L:64:ILE:HD12	4:8L:119:VAL:HG23	1.97	0.45
7:91:341:SER:H	10:E3:49:ARG:HH22	1.65	0.45
3:9E:107:HIS:HD2	3:9E:152:LEU:HB2	1.82	0.45
4:9F:220:PRO:HD2	3:9G:326:LYS:HD3	1.97	0.45
4:9H:382:SER:HA	4:9H:385:PHE:HD2	1.81	0.45
3:9I:338:LYS:NZ	3:9I:341:ILE:HB	2.32	0.45
3:9M:93:ILE:HD11	3:9M:121:ARG:HE	1.81	0.45
3:9M:326:LYS:HE2	3:9M:326:LYS:HB3	1.77	0.45
8:A7:382:LEU:O	8:A7:386:ARG:HG2	2.15	0.45
8:A9:281:LEU:HD13	8:A9:285:LEU:HD11	1.97	0.45
9:B2:162:LEU:HD12	9:B2:164:LYS:HZ1	1.82	0.45
10:D4:33:ARG:HD3	10:D4:40:ARG:HE	1.82	0.45
10:D6:301:ARG:HD2	14:L4:141:ILE:HA	1.99	0.45
10:D9:120:PRO:HD3	10:D9:130:PRO:HB3	1.98	0.45
10:E0:88:LEU:O	10:E0:92:MET:HG3	2.17	0.45
10:E0:340:LEU:HD21	10:E0:386:LEU:HD11	1.98	0.45
10:E6:46:ASP:O	10:E6:50:GLU:HG2	2.15	0.45
12:F0:246:PRO:HD2	12:F0:249:LEU:HD12	1.99	0.45
10:F2:331:ILE:HA	10:F2:335:LEU:HD23	1.98	0.45
10:F3:396:LEU:HA	10:F3:399:SER:HB3	1.98	0.45
12:G2:223:LEU:HD12	12:G2:242:TRP:CG	2.51	0.45
12:G6:200:LEU:HD21	12:G6:228:ILE:HD13	1.98	0.45
14:K6:217:ALA:HB3	14:K6:219:TYR:HE2	1.81	0.45
14:K8:159:ASN:ND2	14:K8:222:THR:HG22	2.30	0.45
14:L2:207:ILE:HG13	14:L2:219:TYR:HE1	1.81	0.45
14:M3:155:TRP:CD2	14:M3:241:VAL:HG11	2.52	0.45
1:j:805:PRO:HG2	1:j:808:ARG:HB2	1.98	0.45
1:G:423:ARG:HG3	1:q:875:ILE:HD13	1.98	0.45
1:I:520:TRP:HE3	1:J:520:TRP:HB2	1.82	0.45
1:I:647:LYS:HD3	1:I:647:LYS:HA	1.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:520:TRP:HA	1:J:523:VAL:HG12	1.98	0.45
1:Q:533:ARG:CZ	1:U:534:GLN:HB2	2.46	0.45
1:Q:582:LEU:HA	1:Q:586:LYS:HE3	1.98	0.45
1:Y:572:ARG:HB2	1:c:572:ARG:HB3	1.97	0.45
2:12:293:ARG:HH12	13:J4:667:ARG:HB2	1.82	0.45
3:1C:392:ASP:HA	3:1C:422:ARG:HH12	1.81	0.45
3:1G:254:GLU:HB3	3:1G:352:LYS:HZ1	1.81	0.45
4:1L:235:GLY:HA2	4:1L:318:ARG:NH1	2.25	0.45
5:25:162:GLN:HE22	5:25:164:MET:HA	1.81	0.45
3:2A:101:ASN:HA	3:2A:144:GLY:HA3	1.99	0.45
3:2A:156:ARG:O	3:2A:160:ASP:HB2	2.16	0.45
3:2A:271:SER:HB3	3:2A:377:MET:HE2	1.99	0.45
3:2C:211:ASP:HA	3:2C:214:ARG:HG2	1.99	0.45
3:2E:110:ILE:O	3:2E:113:GLU:HG2	2.16	0.45
3:2K:245:ASP:HB2	9:B4:76:ARG:HH11	1.82	0.45
4:3B:217:LEU:HG	4:3B:220:PRO:HG2	1.99	0.45
3:3C:320:ARG:HG2	3:3C:356:ASN:HB3	1.99	0.45
4:3J:346:PRO:C	4:3J:347:ASN:HD22	2.24	0.45
3:3K:398:MET:HG3	4:3L:345:ILE:HD13	1.99	0.45
3:3M:87:PHE:HB3	3:3M:92:LEU:HD21	1.98	0.45
3:4C:425:LEU:HD12	3:4C:428:LEU:HD22	1.98	0.45
3:4K:27:GLU:HB2	3:4K:361:THR:HG21	1.97	0.45
5:51:221:LEU:O	5:51:225:GLN:HG3	2.16	0.45
5:55:206:LEU:HB3	5:56:21:LEU:HD11	1.99	0.45
5:58:119:LEU:HD13	5:58:121:ILE:HD11	1.97	0.45
3:5A:282:TYR:HE1	8:A4:92:TYR:HB2	1.82	0.45
3:5G:177:VAL:HG13	4:5H:327:ASP:HB3	1.99	0.45
4:5H:10:GLY:HA2	4:5H:143:THR:HG23	1.98	0.45
2:6:167:ARG:HG2	2:6:171:MET:HE1	1.99	0.45
6:63:813:GLU:O	6:63:817:MET:HG3	2.17	0.45
6:63:877:ALA:O	6:63:881:THR:HG23	2.16	0.45
6:65:161:ALA:HA	6:65:552:GLN:HB3	1.99	0.45
6:66:270:VAL:HG13	6:66:409:ARG:HE	1.82	0.45
6:68:255:ARG:HA	6:68:255:ARG:HD2	1.80	0.45
6:68:336:THR:H	6:68:407:LEU:HD21	1.82	0.45
4:6H:232:ALA:HB2	4:6H:270:PHE:HB2	1.99	0.45
4:6J:7:VAL:HG11	4:6J:151:LEU:HD22	1.98	0.45
3:6K:221:ARG:NH2	1:t:913:SER:HA	2.31	0.45
3:6M:21:TRP:CZ2	3:6M:65:CYS:HB3	2.52	0.45
3:6M:392:ASP:HB3	3:6M:422:ARG:CZ	2.47	0.45
4:7D:19:LYS:HA	4:7D:22:GLU:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7D:211:CYS:HA	4:7D:215:LEU:HB2	1.99	0.45
3:7I:182:VAL:HG22	4:7J:256:ASN:HD21	1.81	0.45
3:7K:17:GLY:HA3	3:7K:67:PHE:HE1	1.82	0.45
4:7L:273:LEU:HA	4:7L:273:LEU:HD23	1.80	0.45
7:82:288:PRO:HG2	14:K8:180:SER:HA	1.99	0.45
7:86:344:ARG:HA	7:86:353:LYS:HE3	1.99	0.45
3:8A:215:ARG:HH21	14:L8:250:PRO:HD2	1.82	0.45
3:8C:388:PHE:HB3	3:8C:425:LEU:HD12	1.99	0.45
7:90:268:TRP:CD1	7:90:328:PRO:HD3	2.51	0.45
7:90:308:TYR:CE1	7:90:322:PRO:HB2	2.51	0.45
4:9D:147:MET:HE3	4:9D:151:LEU:HD21	1.97	0.45
3:9E:140:ALA:HA	3:9E:171:SER:HB3	1.99	0.45
4:9F:139:LEU:HA	4:9F:145:SER:HB3	1.98	0.45
3:9K:268:MET:HE2	3:9K:268:MET:HB2	1.74	0.45
4:9L:105:HIS:HA	4:9L:150:LEU:HD22	1.99	0.45
8:A2:283:LEU:HG	8:A2:333:GLN:NE2	2.31	0.45
8:A5:152:VAL:HG13	8:A6:280:ALA:HB3	1.99	0.45
8:A5:269:LEU:HG	8:A5:271:VAL:HG23	1.97	0.45
8:A7:33:LEU:HG	8:A7:77:GLU:HB3	1.98	0.45
9:B7:458:HIS:CD2	9:B7:459:ARG:HD3	2.52	0.45
10:C6:341:TYR:O	10:C6:345:MET:HG2	2.17	0.45
10:E4:110:ILE:HD12	10:E4:283:PHE:HA	1.97	0.45
10:E9:97:ILE:HD13	10:E9:397:PHE:HD2	1.81	0.45
13:J1:318:LEU:HD22	13:J1:475:ALA:HB1	1.98	0.45
13:J2:291:ARG:HH21	13:J2:670:GLU:HG3	1.81	0.45
13:J6:397:LEU:HD11	13:J6:447:LEU:HD12	1.99	0.45
14:K7:131:LYS:HD2	14:K7:132:PRO:HD2	1.98	0.45
1:A:435:LYS:HB2	1:a:546:ASN:ND2	2.31	0.45
1:I:499:ARG:HH21	1:J:498:LYS:HZ1	1.65	0.45
1:I:661:ASN:O	1:I:665:THR:HG23	2.17	0.45
1:J:656:GLN:CA	1:J:659:LEU:HD22	2.47	0.45
1:O:679:ARG:HA	1:O:679:ARG:HD3	1.61	0.45
1:Q:526:GLU:O	1:Q:530:LEU:CB	2.65	0.45
1:W:351:GLU:HG3	1:W:355:ARG:HE	1.82	0.45
2:10:268:THR:HA	2:10:271:LYS:HE2	1.99	0.45
2:12:279:ASN:HA	2:12:282:LYS:HE2	1.99	0.45
3:1A:17:GLY:O	3:1A:21:TRP:HD1	2.00	0.45
3:1A:178:SER:HB3	3:1A:183:GLU:HG2	1.99	0.45
4:1B:293:MET:SD	4:1B:367:PHE:HB2	2.56	0.45
3:1E:60:LYS:HE3	3:2E:282:TYR:HB3	1.97	0.45
4:1F:105:HIS:HA	4:1F:150:LEU:HG	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1J:73:MET:HB2	4:1J:73:MET:HE3	1.80	0.45
4:1J:178:THR:HA	3:1K:352:LYS:HD3	1.97	0.45
5:20:67:ARG:NH1	12:F5:263:TYR:HA	2.32	0.45
5:23:228:ALA:HB3	5:26:20:PHE:HZ	1.82	0.45
3:2G:301:MET:HB2	3:2G:301:MET:HE3	1.68	0.45
3:2G:313:MET:HG2	3:2G:344:VAL:HG21	1.99	0.45
4:2H:253:LEU:HD21	4:2H:368:VAL:HG11	1.99	0.45
4:2L:213:ARG:HA	4:2L:216:LYS:HE3	1.99	0.45
3:2M:154:LEU:HD12	3:2M:198:THR:HB	1.99	0.45
3:2M:247:ALA:HB3	3:2M:355:ILE:HB	1.97	0.45
2:3:262:LEU:HB3	2:4:263:VAL:HG11	1.99	0.45
5:32:218:PRO:HA	5:32:221:LEU:HB2	1.98	0.45
3:3E:6:SER:O	3:3E:65:CYS:HA	2.16	0.45
3:3E:205:ASP:HB2	3:3E:303:ALA:HA	1.97	0.45
3:3E:407:TRP:HZ2	4:3F:258:ILE:HB	1.82	0.45
3:3K:88:HIS:HB3	3:3K:91:GLN:HB2	1.98	0.45
4:4D:60:VAL:HG21	3:5E:283:HIS:HA	1.97	0.45
4:4D:100:ASN:HB3	4:4D:103:LYS:HG2	1.99	0.45
4:4J:211:CYS:HA	4:4J:215:LEU:HB2	1.97	0.45
4:4L:309:ARG:H	4:4L:372:THR:HG22	1.82	0.45
3:4M:144:GLY:HA2	3:4M:186:ASN:HD21	1.82	0.45
5:54:108:ASP:HA	5:54:111:ARG:HH21	1.82	0.45
4:5F:417:ASP:HB3	14:K2:139:LEU:HB3	1.98	0.45
3:5K:183:GLU:HA	3:5K:186:ASN:HD22	1.82	0.45
4:5L:293:MET:HG3	4:5L:367:PHE:HB2	1.98	0.45
4:5N:318:ARG:HA	4:5N:354:CYS:HB3	1.97	0.45
6:66:391:ALA:O	6:66:395:ARG:HG2	2.17	0.45
6:66:501:ARG:HE	6:66:501:ARG:HB3	1.57	0.45
6:67:496:ASP:HA	6:67:499:ARG:HE	1.82	0.45
6:68:325:ARG:HD2	6:68:337:LEU:HD22	1.98	0.45
4:6D:135:ILE:HG12	4:6D:166:THR:HG22	1.99	0.45
4:6F:156:ARG:HG2	4:6F:195:ASN:HA	1.97	0.45
4:6F:169:VAL:HA	4:6F:202:ILE:HB	1.98	0.45
3:6M:409:VAL:HG22	3:6M:415:GLU:CD	2.41	0.45
4:6N:326:VAL:O	4:6N:330:MET:HG2	2.17	0.45
2:7:178:HIS:CD2	2:7:182:MET:HE1	2.52	0.45
7:75:364:ALA:HA	7:75:367:LEU:HD23	1.98	0.45
7:77:316:PRO:HB2	7:77:318:THR:HG22	1.99	0.45
3:7A:137:MET:HG3	3:7A:154:LEU:HD12	1.99	0.45
4:7B:274:THR:HG21	4:7B:282:ARG:HG2	1.98	0.45
4:7H:51:TYR:HB3	4:7H:59:PHE:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7J:66:MET:HE2	4:7J:116:VAL:HG21	1.99	0.45
4:7J:182:PRO:HA	4:7J:185:ALA:HB3	1.98	0.45
3:7K:77:GLU:HA	3:7K:80:THR:HG22	1.98	0.45
4:7L:306:ARG:HD2	7:84:291:ALA:HB3	1.98	0.45
3:7M:262:TYR:HD2	3:7M:265:ILE:HD12	1.82	0.45
3:8A:268:MET:HE1	3:8A:380:ASN:HB2	1.99	0.45
3:8E:51:THR:HB	3:8E:243:ARG:HG2	1.98	0.45
4:8F:47:ILE:HG12	4:8F:51:TYR:HB2	1.98	0.45
4:8F:420:SER:HA	4:8F:423:GLN:HG2	1.99	0.45
3:8I:30:ILE:HG22	3:8I:36:MET:HA	1.97	0.45
4:8J:68:LEU:HD23	4:8J:97:ALA:HB2	1.99	0.45
4:8J:269:GLY:O	4:8J:366:THR:HA	2.17	0.45
3:8M:308:ARG:HH11	14:M1:246:GLN:HG3	1.82	0.45
7:90:408:ILE:HG23	7:90:412:MET:HE3	1.97	0.45
4:9B:49:VAL:HG21	4:9B:241:ARG:HB2	1.98	0.45
4:9B:100:ASN:HB3	4:9B:103:LYS:HB2	1.99	0.45
4:9F:318:ARG:O	4:9F:363:MET:HA	2.16	0.45
4:9J:326:VAL:O	4:9J:330:MET:HG2	2.17	0.45
10:D1:338:PRO:HB2	10:D1:341:TYR:HB3	1.99	0.45
10:D1:349:PHE:CD1	10:D1:361:TRP:HB3	2.51	0.45
10:D5:34:VAL:HG11	14:K6:226:PRO:HG2	1.97	0.45
10:D6:293:MET:HE3	10:D6:297:ARG:HG3	1.99	0.45
10:D8:301:ARG:HH22	14:K0:143:ARG:NH1	2.14	0.45
10:E6:319:LEU:HD22	10:F3:118:LEU:HD12	1.99	0.45
10:F1:93:ALA:HB2	10:F1:306:MET:HE3	1.98	0.45
12:G6:237:LEU:HD23	12:G6:239:ARG:HH22	1.81	0.45
12:G9:91:GLU:HA	12:G9:94:LEU:HD23	1.98	0.45
13:J5:374:ARG:HH21	13:J5:600:LEU:HD22	1.81	0.45
1:C:448:ALA:HA	1:G:447:HIS:ND1	2.31	0.45
1:D:642:MET:HE2	1:H:642:MET:HG2	1.99	0.45
1:S:458:CYS:HB3	1:b:351:GLU:OE1	2.17	0.45
1:Y:574:LYS:HB3	1:Y:574:LYS:HE3	1.59	0.45
2:10:296:ASP:O	2:10:299:ILE:HG22	2.16	0.45
3:1C:135:PHE:HE1	3:1C:157:LEU:HD11	1.81	0.45
4:1J:396:HIS:HA	4:1J:399:THR:HG22	1.99	0.45
3:1M:195:LEU:HD12	3:1M:428:LEU:HD22	1.99	0.45
3:1M:227:LEU:O	3:1M:231:ILE:HG12	2.17	0.45
5:24:34:PRO:HG2	5:24:186:ARG:HD3	1.99	0.45
4:2F:183:TYR:HA	4:2F:385:PHE:CE2	2.52	0.45
3:2G:88:HIS:CE1	3:2G:90:GLU:HB2	2.52	0.45
5:31:51:GLU:HB3	5:31:147:VAL:HG22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:35:50:PHE:HB2	5:35:71:ILE:HG13	1.97	0.45
4:3F:159:TYR:HB3	4:3F:162:ARG:HG2	1.99	0.45
3:3G:288:VAL:HA	3:3G:291:ILE:HG22	1.98	0.45
5:43:53:ARG:NH2	5:43:66:GLY:HA2	2.32	0.45
5:43:158:LEU:HD23	5:43:174:LEU:HD22	1.99	0.45
4:4B:167:PHE:CD2	4:4B:233:MET:HG2	2.51	0.45
4:4B:241:ARG:HG3	4:4B:242:PHE:CD2	2.52	0.45
3:4C:311:LYS:HD3	3:4C:344:VAL:HA	1.99	0.45
4:4L:113:ILE:HG13	4:4L:117:LEU:HD23	1.99	0.45
5:57:216:LYS:HD3	5:57:216:LYS:HA	1.78	0.45
4:5B:147:MET:HE2	4:5B:147:MET:HB3	1.71	0.45
4:5B:385:PHE:CE2	4:5B:412:GLU:HB3	2.51	0.45
3:5E:69:ASP:HA	3:5E:145:THR:HG21	1.98	0.45
3:5E:320:ARG:HG2	3:5E:374:ALA:HB3	1.99	0.45
4:5F:207:LEU:HB3	4:5F:225:LEU:HG	1.99	0.45
4:5H:98:GLY:HA2	3:5I:254:GLU:HG3	1.99	0.45
4:5J:113:ILE:HA	4:5J:116:VAL:HG22	1.98	0.45
4:5L:107:THR:HB	14:K6:99:ILE:HG23	1.99	0.45
4:5L:377:MET:HE2	4:5L:377:MET:HB2	1.82	0.45
4:5N:268:ILE:HG22	4:5N:300:MET:HE3	1.99	0.45
5:60:142:HIS:HE1	5:60:165:GLU:HG3	1.82	0.45
5:62:27:SER:HA	5:62:30:ASP:HB2	1.99	0.45
6:63:488:ILE:HG12	6:63:573:HIS:HB2	1.99	0.45
6:65:173:ASP:HB2	6:65:176:HIS:HB2	1.99	0.45
6:66:873:ARG:NH1	9:B5:37:ARG:HH22	2.15	0.45
6:68:323:VAL:HG21	6:68:341:PHE:HZ	1.81	0.45
6:69:326:THR:HG23	6:69:329:GLN:H	1.81	0.45
6:69:873:ARG:HH11	9:B4:523:LYS:HB3	1.82	0.45
6:69:902:PRO:HG3	1:w:880:THR:HA	1.98	0.45
3:6C:12:ALA:HB3	3:6C:140:ALA:HB2	1.99	0.45
4:6H:13:GLY:HA2	4:6H:136:THR:HG22	1.99	0.45
3:6K:138:PHE:HD2	3:6K:169:PHE:HB2	1.82	0.45
4:6N:424:GLN:HE22	14:L4:143:ARG:HB2	1.80	0.45
7:76:281:LEU:HD21	7:76:300:GLN:HB2	1.98	0.45
3:7C:100:ALA:O	4:7D:255:VAL:HG11	2.17	0.45
3:7C:217:LEU:HD21	3:7C:368:LEU:HD23	1.98	0.45
4:7H:302:ALA:HB3	4:7H:380:ARG:NH2	2.31	0.45
7:80:307:LYS:HZ3	7:80:321:GLU:HG3	1.81	0.45
7:86:378:MET:HE3	7:86:378:MET:HB2	1.78	0.45
3:8C:137:MET:HE3	3:8C:139:ASN:HB3	1.98	0.45
4:8D:20:PHE:HA	4:8D:230:SER:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8H:338:SER:HB2	14:L5:195:PRO:HG3	1.98	0.45
3:8K:313:MET:HG2	3:8K:380:ASN:HB3	1.99	0.45
7:93:343:ALA:H	14:M3:155:TRP:HZ2	1.65	0.45
7:93:408:ILE:HG12	4:9D:208:TYR:CD2	2.52	0.45
7:97:268:TRP:O	7:97:272:ALA:HB2	2.17	0.45
3:9A:213:CYS:HA	3:9A:217:LEU:HB3	1.97	0.45
4:9D:171:PRO:HG2	4:9D:380:ARG:HH12	1.82	0.45
3:9G:271:SER:HB3	3:9G:301:MET:HA	1.98	0.45
4:9J:135:ILE:HG21	4:9J:152:ILE:HD11	1.97	0.45
9:B3:79:PRO:HG2	9:B3:80:HIS:HD1	1.81	0.45
9:B4:17:LEU:HD13	9:B4:491:ARG:HG3	1.98	0.45
9:B7:476:ARG:HH22	9:B7:532:GLN:HB2	1.82	0.45
10:C8:70:ARG:HH11	14:K3:135:THR:HG21	1.82	0.45
10:D2:387:PHE:HD1	10:D2:390:MET:HE3	1.82	0.45
13:J2:449:PHE:HZ	13:J2:496:LEU:HD13	1.82	0.45
14:K6:156:LEU:HD23	14:K6:169:PHE:HB3	1.99	0.45
14:M3:235:LYS:HB2	14:M3:235:LYS:HE2	1.75	0.45
1:r:907:GLU:HA	1:r:910:LYS:HD2	1.99	0.45
1:C:448:ALA:HA	1:G:447:HIS:CE1	2.52	0.45
1:D:614:LEU:O	1:D:618:ARG:HG2	2.16	0.45
1:I:617:MET:N	1:I:617:MET:SD	2.90	0.45
1:Q:614:LEU:O	1:Q:618:ARG:HB2	2.17	0.45
2:12:183:ARG:HA	2:12:186:HIS:CE1	2.52	0.45
2:14:183:ARG:HA	2:14:186:HIS:CD2	2.52	0.45
3:1A:194:LEU:O	3:1A:198:THR:HG22	2.17	0.45
3:1A:390:ARG:HA	3:1A:393:HIS:CD2	2.52	0.45
4:1B:395:LEU:HA	4:1B:398:TYR:HD2	1.82	0.45
4:1F:274:THR:HG21	4:1F:279:GLN:HG3	1.99	0.45
4:1H:200:GLN:HE22	4:1H:236:VAL:HG21	1.82	0.45
4:1H:273:LEU:HD12	4:1H:273:LEU:HA	1.86	0.45
3:1I:265:ILE:HG21	3:1I:313:MET:HE1	1.97	0.45
5:27:188:MET:HE3	5:27:191:ARG:HE	1.81	0.45
3:2A:407:TRP:O	3:2A:411:GLU:HB3	2.17	0.45
3:2C:67:PHE:HB2	3:2C:92:LEU:HD23	1.99	0.45
3:2C:105:ARG:NH1	4:2D:251:ARG:HH22	2.15	0.45
3:2E:248:LEU:HB3	3:2E:355:ILE:HG22	1.97	0.45
4:2F:384:GLN:HG2	3:2G:348:PRO:HB2	1.98	0.45
4:2J:135:ILE:HG21	4:2J:152:ILE:HD11	1.99	0.45
4:2L:318:ARG:HE	4:2L:358:PRO:HD3	1.82	0.45
5:32:65:VAL:HG21	12:G5:241:LEU:HG	1.99	0.45
5:35:19:ASN:HD21	5:36:221:LEU:HD11	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:35:110:PHE:HZ	5:35:121:ILE:HG13	1.82	0.45
5:35:205:ARG:HA	5:35:208:ASP:HB2	1.98	0.45
5:38:204:ALA:HA	5:38:207:HIS:CD2	2.52	0.45
3:3A:244:PHE:CD2	3:3A:358:GLN:HG2	2.52	0.45
4:3B:334:GLN:HG2	4:3B:349:MET:HE1	1.99	0.45
4:3F:33:THR:HG21	8:A1:125:GLN:HG3	1.98	0.45
3:3M:62:VAL:HG22	3:3M:88:HIS:HE1	1.82	0.45
3:4C:391:MET:HE3	3:4C:391:MET:HB2	1.76	0.45
3:4E:195:LEU:HD13	3:4E:428:LEU:HD21	1.98	0.45
3:4G:181:VAL:HG21	4:4H:312:THR:HG23	1.99	0.45
4:4L:397:TRP:CD1	3:4M:257:THR:HG1	2.35	0.45
5:51:191:ARG:HH22	5:52:191:ARG:NH2	2.15	0.45
5:59:54:LEU:HD12	5:59:55:GLN:H	1.81	0.45
3:5A:204:LEU:HD23	3:5A:204:LEU:HA	1.83	0.45
4:5B:2:ARG:HB2	4:5B:131:GLN:HB2	1.97	0.45
4:5B:21:TRP:CH2	4:5B:50:PHE:HB3	2.52	0.45
4:5B:36:TYR:CZ	4:5B:44:LEU:HB2	2.52	0.45
3:5C:408:TYR:HD2	3:5C:418:PHE:HZ	1.64	0.45
4:5L:42:LEU:HD22	4:5L:356:ILE:HD11	1.98	0.45
5:61:107:GLU:HG2	5:61:111:ARG:HE	1.82	0.45
6:63:315:VAL:HA	6:63:318:PHE:HB2	1.98	0.45
6:67:486:PRO:O	6:67:489:LEU:HB2	2.16	0.45
3:6A:387:VAL:HG12	3:6A:390:ARG:NH2	2.32	0.45
4:6B:66:MET:SD	4:6B:116:VAL:HG21	2.57	0.45
3:6E:306:ASP:HB3	3:6E:309:HIS:CE1	2.51	0.45
4:6J:380:ARG:HA	7:76:311:SER:HA	1.98	0.45
4:6L:212:PHE:CD1	7:77:409:GLY:HA3	2.51	0.45
3:6M:110:ILE:HG23	3:6M:111:GLY:H	1.82	0.45
3:6M:221:ARG:HA	4:6N:324:LYS:NZ	2.31	0.45
7:71:350:ARG:HG3	7:71:388:GLU:HB3	1.98	0.45
3:7G:306:ASP:HB3	3:7G:309:HIS:CE1	2.51	0.45
4:7H:179:VAL:HG22	4:7H:180:VAL:HG23	1.98	0.45
4:7H:397:TRP:HA	14:L5:89:ARG:HH12	1.81	0.45
3:7K:106:GLY:HA3	3:7K:148:GLY:HA3	1.99	0.45
3:7K:247:ALA:HB3	3:7K:355:ILE:HB	1.98	0.45
3:7K:328:VAL:HG21	3:7K:355:ILE:HD11	1.99	0.45
2:8:297:THR:HA	2:8:300:VAL:HG23	1.99	0.45
7:86:394:TYR:HE1	14:L7:122:TYR:HD2	1.65	0.45
4:8J:39:ASP:O	1:n:944:GLN:HB2	2.17	0.45
4:8L:66:MET:HE3	4:8L:116:VAL:HG11	1.98	0.45
3:8M:11:GLN:HA	3:8M:14:ILE:HB	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:90:397:SER:HA	7:90:400:CYS:HB3	1.98	0.45
4:9F:117:LEU:HA	4:9F:120:VAL:HG22	1.98	0.45
4:9H:91:VAL:HG21	4:9H:116:VAL:HG12	1.99	0.45
3:9I:191:THR:O	3:9I:195:LEU:HB2	2.17	0.45
3:9K:363:VAL:HG13	3:9K:366:GLY:HA3	1.99	0.45
10:C7:94:VAL:HG13	10:C7:335:LEU:HD11	1.99	0.45
10:C8:386:LEU:HG	10:C8:390:MET:HE1	1.99	0.45
10:D6:326:LYS:HD2	10:D6:326:LYS:HA	1.81	0.45
10:D9:143:ASP:HA	10:D9:146:ALA:HB2	1.98	0.45
10:E3:97:ILE:HG13	10:E3:393:VAL:HG13	1.99	0.45
10:E7:68:THR:HA	10:E7:71:GLN:HG3	1.99	0.45
12:F5:240:PHE:HB3	12:F5:244:ARG:NH2	2.31	0.45
13:J2:416:VAL:HG12	13:J2:600:LEU:HG	1.98	0.45
14:K9:99:ILE:HA	14:K9:102:ARG:HG3	1.99	0.45
14:L8:181:LEU:O	14:L8:185:ILE:HG12	2.17	0.45
1:y:942:ILE:HA	1:y:945:ILE:HG22	1.99	0.45
1:C:432:LEU:HA	1:C:435:LYS:HD2	1.98	0.45
1:M:487:HIS:NE2	1:P:661:ASN:HB2	2.32	0.45
1:M:603:ARG:HD3	1:M:603:ARG:HA	1.42	0.45
1:Q:533:ARG:NH1	1:U:534:GLN:HB2	2.32	0.45
1:Q:624:GLN:NE2	1:U:624:GLN:HG2	2.28	0.45
2:13:171:MET:HE1	2:14:171:MET:HE1	1.98	0.45
2:14:220:LYS:HD2	2:14:220:LYS:HA	1.84	0.45
3:1A:223:THR:HG23	3:1A:225:THR:H	1.81	0.45
4:1L:66:MET:HE1	4:1L:116:VAL:HG21	1.98	0.45
3:1M:338:LYS:HE2	3:1M:338:LYS:HB2	1.87	0.45
5:22:122:GLU:HG3	5:22:124:GLY:H	1.81	0.45
4:2B:21:TRP:HZ3	4:2B:50:PHE:HB3	1.81	0.45
4:2D:206:ALA:HB2	4:2D:302:ALA:HB2	1.99	0.45
3:2G:167:LEU:HG	3:2G:200:VAL:HB	1.99	0.45
3:2K:155:GLU:HB3	3:2K:197:HIS:CE1	2.51	0.45
3:2K:207:GLU:HA	3:2K:210:TYR:HD2	1.82	0.45
4:3D:318:ARG:HE	4:3D:358:PRO:HG3	1.82	0.45
4:3J:201:VAL:HG21	4:3J:374:ILE:HD11	1.99	0.45
4:3L:284:LEU:HD22	4:3L:362:LYS:HB3	1.98	0.45
3:3M:205:ASP:O	3:3M:209:ILE:HG12	2.17	0.45
2:4:225:ARG:O	2:4:229:GLU:HB3	2.17	0.45
3:4A:392:ASP:HB3	3:4A:422:ARG:HH22	1.81	0.45
4:4H:20:PHE:CD1	4:4H:233:MET:HE2	2.52	0.45
3:4M:209:ILE:HA	3:4M:212:ILE:HG12	1.98	0.45
2:5:222:GLU:HG2	2:6:223:ARG:HH22	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:50:20:PHE:HB2	6:64:596:PRO:HB3	1.98	0.45
5:50:110:PHE:HA	5:50:113:MET:HG3	1.99	0.45
3:5A:28:HIS:HD2	3:5A:53:PHE:HE2	1.65	0.45
3:5A:395:PHE:O	3:5A:399:TYR:CB	2.65	0.45
4:5B:321:MET:HG2	4:5B:363:MET:HE3	1.99	0.45
3:5E:140:ALA:HA	3:5E:171:SER:HB2	1.98	0.45
3:5G:136:LEU:HD23	3:5G:167:LEU:HB2	1.99	0.45
6:64:536:VAL:HG23	6:64:541:ASP:HB3	1.97	0.45
6:67:879:THR:HB	9:B7:519:ALA:HB3	1.98	0.45
6:68:620:ILE:HD11	6:68:845:VAL:HG21	1.98	0.45
6:69:506:GLU:HG3	6:69:507:ARG:N	2.31	0.45
3:6A:172:TRP:HE1	3:6A:391:MET:HG3	1.81	0.45
4:6L:318:ARG:HA	4:6L:354:CYS:HB3	1.99	0.45
7:71:334:LEU:HD21	7:71:347:ILE:HD13	1.99	0.45
3:7A:352:LYS:HD3	3:7A:352:LYS:HA	1.73	0.45
3:7G:64:ARG:HG3	3:7G:125:LEU:HD22	1.99	0.45
4:7H:286:VAL:HB	4:7H:325:GLU:HG3	1.99	0.45
4:7J:32:PRO:HD3	4:7J:81:PHE:CZ	2.52	0.45
3:7K:203:MET:HE3	3:7K:388:PHE:HZ	1.81	0.45
4:7L:154:LYS:HD3	7:91:286:TRP:HE1	1.82	0.45
3:7M:226:ASN:HA	3:7M:229:ARG:HG2	1.99	0.45
3:7M:288:VAL:N	3:7M:373:ARG:HH12	2.15	0.45
2:8:273:GLU:HA	2:8:276:GLU:HG2	1.99	0.45
4:8B:317:PHE:HB3	4:8B:321:MET:HE2	1.99	0.45
3:8C:34:GLY:HA3	3:8C:60:LYS:HD3	1.98	0.45
3:8C:221:ARG:HH11	1:o:913:SER:HB3	1.82	0.45
3:8E:348:PRO:HB3	14:L7:111:LEU:HD22	1.99	0.45
4:8J:413:SER:O	4:8J:417:ASP:HB2	2.16	0.45
3:8K:77:GLU:HA	3:8K:80:THR:HG22	1.99	0.45
4:8L:86:ARG:NH2	4:8L:87:PRO:HD2	2.32	0.45
4:8L:213:ARG:HG2	7:91:416:TRP:HZ2	1.82	0.45
4:8L:396:HIS:H	4:8L:396:HIS:CD2	2.35	0.45
2:9:258:GLN:HE21	2:9:261:ARG:HH21	1.65	0.45
3:9K:36:MET:HE1	3:9K:61:HIS:CE1	2.52	0.45
3:9K:219:ILE:HD12	3:9K:222:PRO:HB3	1.97	0.45
8:A8:265:PRO:HD2	8:A8:270:PRO:HB3	1.99	0.45
10:C8:345:MET:HE2	10:C8:369:SER:HA	1.99	0.45
10:D3:57:ILE:HG12	10:D3:309:ILE:HD13	1.98	0.45
10:D8:61:ASP:HA	14:K0:142:GLN:NE2	2.32	0.45
10:E1:63:TYR:HE2	14:L9:142:GLN:HG3	1.81	0.45
10:E5:86:LEU:HD12	10:E5:313:TYR:HD2	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E9:311:LYS:HA	10:E9:314:GLU:HG3	1.99	0.45
10:F1:151:GLN:O	10:F1:155:MET:HG2	2.17	0.45
10:F2:67:ALA:O	10:F2:71:GLN:CB	2.65	0.45
12:H5:70:LYS:HE3	12:H5:70:LYS:HB3	1.83	0.45
13:J5:398:ALA:HB2	13:J5:452:LEU:HG	1.99	0.45
14:L1:185:ILE:O	14:L1:189:ILE:HG12	2.16	0.45
14:L8:70:LYS:HG3	14:L8:75:ARG:HG2	1.98	0.45
14:M3:172:ARG:O	14:M3:175:ILE:HG22	2.17	0.45
14:M7:155:TRP:NE1	14:M7:241:VAL:HG21	2.32	0.45
1:a:633:ASP:OD1	1:j:771:VAL:HG22	2.17	0.45
1:f:572:ARG:HD2	1:f:572:ARG:HA	1.76	0.45
1:z:917:ARG:HD3	1:z:917:ARG:HA	1.74	0.45
1:D:618:ARG:HH22	1:H:617:MET:HG2	1.82	0.44
1:D:625:GLN:O	1:D:629:LYS:HG2	2.17	0.44
1:F:418:VAL:O	1:F:422:THR:HG23	2.18	0.44
1:T:642:MET:HA	1:T:645:GLN:HB2	1.98	0.44
3:1A:405:VAL:HA	3:1A:408:TYR:CD2	2.52	0.44
4:1B:35:THR:HG22	4:1B:36:TYR:H	1.82	0.44
3:1C:260:VAL:HG23	3:1C:265:ILE:O	2.16	0.44
3:1E:359:PRO:HB3	3:1E:372:MET:HA	1.98	0.44
5:26:77:ILE:HG23	5:26:84:PRO:HB3	1.99	0.44
5:28:45:SER:HA	5:28:72:ARG:HH12	1.81	0.44
4:2B:133:PHE:HZ	4:2B:159:TYR:HD2	1.63	0.44
3:2C:21:TRP:CZ2	3:2C:65:CYS:HB3	2.52	0.44
4:2F:77:ARG:HH22	4:3F:280:GLN:HE22	1.65	0.44
4:2F:113:ILE:HA	4:2F:116:VAL:HG12	1.99	0.44
3:2I:217:LEU:HD22	3:2I:367:ASP:HB2	1.98	0.44
3:2M:420:GLU:OE1	6:68:133:ARG:HG2	2.17	0.44
2:3:225:ARG:HA	2:3:228:GLU:HB2	2.00	0.44
3:3C:104:ALA:HB2	3:3C:413:MET:HE3	1.99	0.44
3:3E:167:LEU:HD11	3:3E:252:VAL:HG13	1.99	0.44
4:3F:286:VAL:HG22	4:3F:321:MET:HE3	1.99	0.44
3:3M:138:PHE:HE1	3:3M:235:ILE:HG21	1.82	0.44
5:46:36:LEU:HD11	5:46:42:LEU:HD13	2.00	0.44
3:4A:262:TYR:HE1	6:67:823:HIS:HB2	1.80	0.44
4:4B:222:TYR:HB2	3:4C:325:PRO:HG2	1.98	0.44
4:4H:213:ARG:NH2	4:4H:297:LYS:HB3	2.32	0.44
3:4M:96:LYS:HD2	3:4M:96:LYS:HA	1.75	0.44
2:5:221:ARG:O	2:5:224:GLU:HG3	2.17	0.44
5:56:89:VAL:H	5:56:103:HIS:HB3	1.82	0.44
5:59:24:VAL:HG22	5:59:202:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5C:211:ASP:HA	3:5C:214:ARG:HG2	1.99	0.44
4:5D:103:LYS:HA	4:5D:107:THR:HG23	1.99	0.44
4:5F:218:THR:HG23	4:5F:219:THR:H	1.82	0.44
4:5J:203:ASP:HB2	4:5J:377:MET:HE1	1.99	0.44
4:5J:425:TYR:CZ	14:K5:143:ARG:HD2	2.51	0.44
3:5K:401:LYS:HD2	14:K6:144:PHE:CE1	2.52	0.44
3:5M:250:VAL:HG11	3:5M:318:MET:HE1	1.99	0.44
6:64:157:TRP:HE1	12:H9:72:GLU:HG2	1.82	0.44
6:64:406:ARG:HD3	12:F9:233:ARG:HH11	1.82	0.44
3:6K:3:GLU:HA	3:6K:51:THR:HA	1.99	0.44
2:8:204:LEU:HG	2:8:208:TYR:HE2	1.82	0.44
4:8J:248:SER:HA	4:8J:252:LYS:HG3	1.99	0.44
3:8K:312:TYR:HB2	3:8K:343:PHE:CE1	2.52	0.44
4:8L:257:LEU:HD21	4:8L:314:SER:HB2	1.99	0.44
2:9:165:ARG:NH2	10:C7:333:THR:H	2.15	0.44
4:9B:232:ALA:HB2	4:9B:270:PHE:HB2	1.98	0.44
4:9J:253:LEU:O	4:9J:257:LEU:HB3	2.15	0.44
3:9K:242:LEU:HD11	3:9K:252:VAL:HG23	2.00	0.44
9:B6:453:PHE:HA	9:B6:465:LEU:O	2.16	0.44
10:D8:327:ALA:O	10:D8:331:ILE:HG22	2.18	0.44
12:G1:246:PRO:HD3	12:G1:266:PRO:HB3	1.99	0.44
12:G5:252:LEU:HB3	12:G5:261:TRP:CE3	2.52	0.44
12:I2:89:ILE:O	12:I2:93:GLN:HG2	2.17	0.44
13:J2:321:LEU:HD21	13:J2:475:ALA:HB2	1.99	0.44
14:M1:196:VAL:HG21	14:M1:221:CYS:HB3	1.98	0.44
14:M3:180:SER:HA	14:M3:183:GLN:HG2	1.97	0.44
1:c:679:ARG:HD3	1:c:679:ARG:HA	1.65	0.44
1:c:682:LYS:O	1:c:683:GLU:C	2.60	0.44
1:d:502:LEU:O	1:d:506:VAL:HG23	2.17	0.44
1:s:907:GLU:HA	1:s:910:LYS:HD2	2.00	0.44
1:u:867:PRO:HG3	1:u:944:GLN:HG2	1.98	0.44
1:A:506:VAL:O	1:A:510:ASP:HB2	2.18	0.44
1:F:394:LYS:HA	1:F:394:LYS:HD2	1.79	0.44
1:M:617:MET:N	1:M:617:MET:SD	2.89	0.44
1:M:677:MET:HG2	1:M:677:MET:H	1.57	0.44
1:R:510:ASP:O	1:R:513:ARG:HB3	2.16	0.44
1:Y:601:ARG:O	1:Y:604:ILE:HB	2.17	0.44
1:Y:607:LEU:HD22	1:c:611:THR:HG21	2.00	0.44
1:Z:505:GLU:HA	1:Z:508:VAL:HG12	1.98	0.44
1:Z:527:LEU:HD22	1:d:523:VAL:HG13	1.99	0.44
2:10:199:SER:C	2:10:201:VAL:H	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:16:189:GLU:HA	2:16:192:GLU:HG2	1.99	0.44
4:1B:166:THR:HG22	4:1B:168:SER:HB2	1.98	0.44
4:1D:42:LEU:HD13	4:1D:356:ILE:HD11	1.99	0.44
4:1F:173:PRO:HB2	4:1F:174:LYS:HD3	1.99	0.44
4:1F:183:TYR:CZ	4:1F:388:MET:HG2	2.53	0.44
4:1F:289:LEU:HD11	4:1F:363:MET:HG3	1.99	0.44
3:1I:170:CYS:O	3:1I:203:MET:HA	2.17	0.44
4:1J:151:LEU:O	4:1J:155:VAL:HG12	2.17	0.44
3:1K:184:PRO:HA	3:1K:391:MET:HE3	1.98	0.44
5:25:182:GLU:O	5:25:185:ARG:HB2	2.17	0.44
3:2A:23:LEU:HD13	3:2A:363:VAL:HG13	1.98	0.44
3:2C:188:VAL:HG23	3:2C:425:LEU:HG	1.97	0.44
4:2F:290:THR:HA	4:2F:293:MET:HE2	1.99	0.44
4:2L:174:LYS:HD3	3:2M:333:ALA:HB2	2.00	0.44
3:2M:49:PHE:HZ	9:B6:514:VAL:HA	1.82	0.44
3:2M:263:PRO:HG2	6:68:543:GLN:HB3	1.98	0.44
3:3C:320:ARG:HH12	3:3C:360:PRO:HB3	1.81	0.44
4:3F:407:GLU:HA	4:3F:410:GLU:HG2	1.99	0.44
3:3G:251:ASP:H	3:3G:254:GLU:HG3	1.82	0.44
3:3I:301:MET:HE3	3:3I:301:MET:HB3	1.89	0.44
3:3K:244:PHE:HB2	3:3K:356:ASN:HD21	1.82	0.44
3:3K:391:MET:HA	3:3K:394:LYS:HB2	1.99	0.44
4:3L:399:THR:HA	4:3L:403:MET:HB2	1.98	0.44
3:3M:319:TYR:HB2	3:3M:355:ILE:HG12	1.98	0.44
5:42:162:GLN:HB2	5:42:171:LEU:HD11	2.00	0.44
5:49:169:ILE:HD11	5:52:169:ILE:HG21	1.99	0.44
4:4B:170:PHE:CG	4:4B:201:VAL:HG23	2.52	0.44
3:4C:8:HIS:CD2	3:4C:17:GLY:HA3	2.52	0.44
3:4C:181:VAL:HG21	4:4D:312:THR:HG22	1.98	0.44
4:4F:42:LEU:HD22	4:4F:356:ILE:HD11	1.99	0.44
4:4F:45:GLU:O	4:4F:46:ARG:HD3	2.17	0.44
4:4H:201:VAL:HG11	4:4H:374:ILE:HD11	1.99	0.44
3:4I:265:ILE:HG23	3:4I:432:TYR:CZ	2.52	0.44
3:4I:272:TYR:HB3	3:4I:275:ILE:HD11	1.99	0.44
3:4K:358:GLN:HE21	3:4K:359:PRO:HD2	1.82	0.44
5:54:208:ASP:HB3	6:65:597:LEU:HD11	1.99	0.44
5:58:103:HIS:CD2	5:58:105:LEU:HG	2.52	0.44
4:5F:171:PRO:HG2	4:5F:185:ALA:HB2	1.99	0.44
4:5F:330:MET:HE3	4:5F:349:MET:HG2	1.97	0.44
4:5J:102:ALA:HB2	4:5J:403:MET:HE3	1.99	0.44
2:6:264:GLN:HA	2:6:267:HIS:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:63:872:GLU:OE1	8:A6:255:ARG:HD3	2.17	0.44
6:65:510:SER:O	6:65:511:GLY:C	2.60	0.44
6:66:821:SER:HA	6:66:824:ILE:HB	1.99	0.44
6:66:903:ALA:HB2	8:A3:163:ARG:HH12	1.82	0.44
3:6C:271:SER:HB3	3:6C:301:MET:HA	1.99	0.44
3:6I:254:GLU:HA	3:6I:257:THR:HG22	1.98	0.44
4:6L:100:ASN:HD22	4:6L:103:LYS:NZ	2.14	0.44
4:6N:139:LEU:HD13	4:6N:168:SER:HB2	1.99	0.44
4:7J:199:VAL:O	4:7J:265:PHE:HA	2.17	0.44
3:8A:56:THR:HA	3:9A:285:GLN:HG2	1.98	0.44
4:8B:383:ASP:HA	4:8B:386:THR:HG22	1.98	0.44
3:8E:304:LYS:HD3	3:8E:304:LYS:HA	1.76	0.44
3:8E:319:TYR:HA	3:8E:374:ALA:O	2.17	0.44
3:8K:54:SER:HB3	3:8K:64:ARG:HD2	1.99	0.44
4:8L:23:VAL:HG11	4:8L:227:HIS:CD2	2.53	0.44
7:93:411:MET:H	4:9D:174:LYS:HE3	1.81	0.44
3:9A:394:LYS:HA	3:9A:397:LEU:HG	2.00	0.44
4:9B:113:ILE:HA	4:9B:116:VAL:HG12	1.99	0.44
4:9B:285:SER:HB2	4:9B:287:PRO:HD2	1.99	0.44
4:9D:70:PRO:HG3	4:9D:94:GLN:HA	1.98	0.44
4:9D:139:LEU:HD13	4:9D:170:PHE:HE1	1.81	0.44
4:9D:140:GLY:HA3	4:9D:171:PRO:HB3	2.00	0.44
4:9F:30:ILE:HD11	4:9F:47:ILE:HD11	1.99	0.44
4:9H:163:ILE:HD13	4:9H:250:LEU:HB3	1.99	0.44
4:9L:216:LYS:H	4:9L:275:SER:HB2	1.82	0.44
8:A4:58:THR:HA	8:A4:92:TYR:HB3	1.98	0.44
10:C7:304:ASN:O	10:C7:308:VAL:HG23	2.17	0.44
10:D2:320:LYS:HE2	10:D2:404:LEU:HA	1.99	0.44
10:E1:62:VAL:HG22	10:E1:309:ILE:HD11	1.99	0.44
10:E3:109:ASN:HB3	10:E3:292:ALA:HB2	2.00	0.44
10:E8:78:ARG:HB3	10:E8:82:GLY:HA2	1.99	0.44
10:E9:284:LEU:HB3	10:E9:351:ARG:HH22	1.82	0.44
13:J3:397:LEU:HD23	13:J3:400:LEU:HD12	1.98	0.44
13:J4:341:PRO:HG3	13:J4:362:ALA:HB3	1.98	0.44
14:K5:178:MET:HG3	14:K5:182:TYR:CZ	2.53	0.44
1:a:533:ARG:HH12	1:f:533:ARG:NH2	2.08	0.44
1:a:579:LEU:HG	1:a:580:GLU:N	2.32	0.44
1:b:352:LYS:HA	1:b:352:LYS:HD3	1.78	0.44
1:h:758:ASN:HD22	1:h:758:ASN:C	2.23	0.44
1:A:487:HIS:CE1	1:H:661:ASN:HB3	2.53	0.44
1:J:656:GLN:O	1:J:657:GLN:C	2.59	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:639:LEU:HA	1:N:642:MET:HE3	1.99	0.44
1:O:639:LEU:HD22	1:P:638:LEU:HD11	1.98	0.44
1:R:531:GLN:HG2	1:Y:423:ARG:HH22	1.83	0.44
3:1A:301:MET:HE3	3:1A:303:ALA:H	1.82	0.44
4:1B:170:PHE:HD2	4:1B:201:VAL:HG13	1.81	0.44
3:1C:319:TYR:CE2	3:1C:328:VAL:HG13	2.53	0.44
4:1F:34:GLY:HA3	4:1F:58:ARG:HD2	1.99	0.44
4:1F:341:PHE:CZ	4:1F:348:ASN:HB2	2.52	0.44
4:1F:393:ALA:HB1	3:1G:261:PRO:HB3	2.00	0.44
4:1J:55:THR:HG23	4:2J:283:ALA:HA	1.99	0.44
3:1M:11:GLN:HA	3:1M:14:ILE:HG12	1.98	0.44
5:27:111:ARG:HA	5:27:111:ARG:HD2	1.84	0.44
4:2B:58:ARG:HG2	4:3B:281:TYR:HA	1.99	0.44
4:2B:92:PHE:HZ	9:B5:49:MET:HE2	1.82	0.44
3:2G:213:CYS:HA	3:2G:217:LEU:HB2	1.99	0.44
4:2L:286:VAL:HA	4:2L:289:LEU:HB2	1.99	0.44
3:3A:372:MET:HE1	9:B7:31:ALA:C	2.42	0.44
3:3A:382:THR:HA	3:3A:432:TYR:OH	2.17	0.44
4:3D:42:LEU:HD13	4:3D:356:ILE:HD11	1.98	0.44
4:3J:86:ARG:HG3	4:3J:89:ASN:ND2	2.31	0.44
4:3L:326:VAL:O	4:3L:330:MET:HG2	2.18	0.44
5:40:230:GLN:HB3	5:40:234:ARG:HH21	1.82	0.44
4:4F:2:ARG:HB3	4:4F:131:GLN:HG2	2.00	0.44
3:4M:263:PRO:HB2	6:68:815:PHE:HD1	1.82	0.44
5:50:130:LEU:HD23	5:50:172:LEU:HD13	2.00	0.44
5:51:33:ASP:HB3	5:51:190:PHE:CE2	2.52	0.44
5:54:105:LEU:HD22	5:54:109:LEU:HD11	1.99	0.44
5:57:144:PHE:CD1	5:57:162:GLN:HG3	2.52	0.44
5:59:185:ARG:NH1	5:59:186:ARG:HB3	2.32	0.44
3:5C:189:LEU:HD21	3:5C:418:PHE:HA	1.98	0.44
4:5H:45:GLU:HG3	4:5H:46:ARG:HG2	1.99	0.44
3:5I:275:ILE:HG23	3:5I:368:LEU:HD21	1.99	0.44
4:5J:87:PRO:HA	4:5J:90:PHE:HD2	1.82	0.44
6:63:337:LEU:HD21	6:63:415:ILE:HD12	2.00	0.44
3:6C:105:ARG:HG2	3:6C:411:GLU:HG2	1.99	0.44
4:6H:205:GLU:HG2	7:75:412:MET:SD	2.57	0.44
3:6M:54:SER:HB3	3:6M:62:VAL:HB	1.98	0.44
7:76:405:VAL:HG11	7:76:411:MET:HB2	1.98	0.44
7:78:303:PRO:HB2	10:E4:156:ARG:HH21	1.81	0.44
3:7A:212:ILE:HG23	3:7A:275:ILE:HD12	1.98	0.44
4:7B:327:ASP:HA	4:7B:330:MET:HG2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7G:31:GLN:HE22	3:7G:37:PRO:HG2	1.82	0.44
4:7J:8:GLN:HG3	4:7J:14:ASN:HA	1.99	0.44
4:7J:208:TYR:CE1	4:7J:220:PRO:HG2	2.52	0.44
3:7K:107:HIS:HD2	3:7K:152:LEU:HB2	1.83	0.44
3:7K:224:TYR:CD1	4:7L:323:THR:HG21	2.53	0.44
3:7M:195:LEU:HA	3:7M:267:PHE:HZ	1.83	0.44
7:83:331:PRO:HG3	7:83:372:TRP:CE2	2.51	0.44
4:8B:6:HIS:HD1	4:8B:134:GLN:HG3	1.81	0.44
4:8F:311:LEU:HD12	4:8F:370:ASN:ND2	2.32	0.44
3:8K:273:ALA:HA	3:8K:275:ILE:HG22	1.99	0.44
4:8L:87:PRO:HA	4:8L:90:PHE:HD2	1.83	0.44
7:95:268:TRP:HD1	7:95:328:PRO:HD3	1.81	0.44
7:95:324:ILE:HG12	7:95:393:LEU:HG	1.98	0.44
4:9B:324:LYS:O	4:9B:328:GLU:HG2	2.17	0.44
4:9H:318:ARG:HB3	4:9H:364:SER:HB2	2.00	0.44
4:9H:324:LYS:HD2	4:9H:324:LYS:HA	1.70	0.44
9:B7:527:LEU:HD12	9:B7:534:THR:HG22	1.99	0.44
10:D5:84:THR:HG22	10:D5:86:LEU:H	1.82	0.44
10:D7:94:VAL:HA	10:D7:97:ILE:HG22	1.99	0.44
10:E0:61:ASP:HA	14:M3:142:GLN:HE22	1.83	0.44
10:E2:51:TYR:HB3	10:E2:54:HIS:CD2	2.53	0.44
14:K9:99:ILE:HG22	14:K9:102:ARG:HE	1.82	0.44
14:L2:178:MET:HG2	14:L2:210:LEU:HG	2.00	0.44
14:L3:155:TRP:CE3	14:L3:241:VAL:HG21	2.52	0.44
14:M3:186:THR:HG22	14:M3:196:VAL:H	1.81	0.44
1:G:381:ARG:HA	1:G:381:ARG:HD3	1.83	0.44
1:I:364:GLU:HA	1:I:367:GLU:HG3	1.98	0.44
1:I:656:GLN:HA	1:J:659:LEU:HD11	1.99	0.44
1:Q:681:ILE:O	1:Q:685:ASN:HB2	2.18	0.44
4:1B:167:PHE:CD1	4:1B:200:GLN:HB2	2.53	0.44
3:1C:112:LYS:HA	3:1C:115:VAL:HG12	2.00	0.44
3:1C:319:TYR:HE2	3:1C:328:VAL:HG13	1.81	0.44
4:1D:21:TRP:HA	4:1D:24:ILE:HG22	1.99	0.44
3:1E:401:LYS:HE2	4:1F:344:TRP:CD2	2.52	0.44
4:1F:288:GLU:O	4:1F:292:GLN:HG2	2.18	0.44
4:1H:3:GLU:HB3	4:1H:130:LEU:HD23	1.99	0.44
3:1K:122:ILE:HD12	3:1K:157:LEU:HD21	2.00	0.44
4:1N:325:GLU:HA	4:1N:328:GLU:HG2	1.99	0.44
5:20:27:SER:HA	5:20:30:ASP:HB2	1.99	0.44
5:29:53:ARG:HB3	5:29:149:ILE:HA	1.99	0.44
3:2C:15:GLN:HE22	4:2D:245:GLN:HA	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2I:51:THR:HG21	3:2I:243:ARG:HG2	2.00	0.44
3:2K:269:LEU:HD11	3:2K:384:ILE:HD11	1.98	0.44
3:2M:191:THR:HG23	3:2M:425:LEU:HD21	1.99	0.44
5:36:211:CYS:HA	5:36:214:LYS:HE2	2.00	0.44
3:3A:159:VAL:HA	5:61:223:HIS:CE1	2.53	0.44
4:3D:20:PHE:HA	4:3D:230:SER:HB2	1.99	0.44
4:3F:9:GLY:HA2	4:3F:66:MET:HG3	1.99	0.44
4:3J:130:LEU:HB3	4:3J:162:ARG:HH11	1.81	0.44
3:3K:11:GLN:HE22	4:3L:247:ASN:H	1.65	0.44
5:42:143:CYS:HA	5:42:163:SER:HB3	1.99	0.44
3:4A:223:THR:HG23	3:4A:225:THR:N	2.32	0.44
4:4B:19:LYS:HE3	4:4B:227:HIS:HB2	1.99	0.44
4:4B:113:ILE:HG13	4:4B:117:LEU:HD23	1.99	0.44
4:4B:290:THR:HG21	4:4B:329:GLN:HB3	1.97	0.44
3:4C:163:LYS:HE3	6:66:805:GLU:HG2	1.99	0.44
3:4E:26:LEU:HB2	3:4E:364:PRO:HG3	1.99	0.44
3:4E:142:GLY:HA2	3:4E:183:GLU:HG3	1.99	0.44
3:4I:195:LEU:HD11	3:4I:428:LEU:HB2	1.99	0.44
4:4J:187:LEU:HD21	4:4J:408:PHE:HD1	1.82	0.44
3:5G:53:PHE:HB3	3:5G:61:HIS:HB3	1.99	0.44
6:66:558:LYS:HA	6:66:558:LYS:HD3	1.51	0.44
6:66:881:THR:HG21	9:B5:55:LEU:HB2	2.00	0.44
6:67:499:ARG:HE	6:67:499:ARG:HB2	1.75	0.44
6:69:876:ASP:OD1	6:69:878:PRO:HD2	2.17	0.44
3:6A:209:ILE:HG23	3:6A:230:LEU:HD22	1.99	0.44
4:6N:207:LEU:HA	4:6N:210:ILE:HG12	2.00	0.44
2:7:189:GLU:HB3	2:7:190:LYS:H	1.42	0.44
3:7A:195:LEU:HD12	3:7A:428:LEU:HD22	1.98	0.44
3:7E:177:VAL:HG23	4:7F:327:ASP:HB3	2.00	0.44
3:7M:394:LYS:HB3	3:7M:394:LYS:HE2	1.80	0.44
7:80:411:MET:HG3	7:80:412:MET:HE2	1.99	0.44
7:83:327:ASN:OD1	7:83:391:TYR:HA	2.18	0.44
3:8A:269:LEU:HB2	3:8A:379:SER:HB2	2.00	0.44
3:8I:304:LYS:HD3	3:8I:304:LYS:HA	1.62	0.44
4:8J:109:GLY:HA3	4:8J:147:MET:HE1	1.99	0.44
4:8L:117:LEU:HA	4:8L:120:VAL:HG12	1.99	0.44
7:92:308:TYR:HD1	7:92:324:ILE:HG13	1.82	0.44
3:9G:224:TYR:CD2	4:9H:323:THR:HG21	2.52	0.44
4:9H:380:ARG:HE	4:9H:381:VAL:HG13	1.83	0.44
10:C8:343:ALA:O	10:C8:347:GLU:HG2	2.17	0.44
10:C9:331:ILE:HG23	10:C9:335:LEU:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E6:62:VAL:HG21	10:E6:305:LEU:HD22	1.99	0.44
10:E6:86:LEU:HD11	10:E6:313:TYR:HB3	2.00	0.44
12:F7:244:ARG:HG2	12:F7:266:PRO:HG3	1.99	0.44
13:J6:398:ALA:HB2	13:J6:452:LEU:HG	2.00	0.44
14:L0:127:LYS:HE3	14:L0:127:LYS:HB3	1.82	0.44
14:L7:198:ARG:HB3	14:L7:222:THR:HG23	1.99	0.44
14:M7:131:LYS:HD3	14:M7:132:PRO:HD2	2.00	0.44
1:a:594:ALA:HB1	1:t:882:GLU:OE2	2.18	0.44
1:h:757:LEU:HD21	1:h:828:CYS:H	1.82	0.44
1:S:354:SER:HA	1:W:357:TYR:HE2	1.82	0.44
1:Z:365:LEU:HB3	1:d:368:GLN:HE22	1.82	0.44
3:1A:167:LEU:HA	3:1A:200:VAL:O	2.17	0.44
3:1A:272:TYR:HA	3:1A:376:CYS:HA	1.99	0.44
3:1E:75:VAL:HG13	3:1E:92:LEU:HD23	1.99	0.44
3:1G:401:LYS:HD3	4:1H:344:TRP:CD2	2.53	0.44
3:1K:12:ALA:HB3	3:1K:140:ALA:HB2	1.99	0.44
5:22:103:HIS:CE1	5:22:174:LEU:HB2	2.52	0.44
5:24:227:ALA:O	5:24:231:GLN:HB2	2.17	0.44
3:2A:195:LEU:HD11	3:2A:428:LEU:HG	2.00	0.44
4:2D:175:VAL:HG11	3:2E:332:VAL:HG23	1.99	0.44
4:2D:400:GLY:HA2	6:65:548:LEU:HD22	1.99	0.44
4:2F:293:MET:HE3	4:2F:294:PHE:CE2	2.52	0.44
4:2F:391:ARG:HD3	3:2G:346:TRP:CD1	2.52	0.44
3:2G:178:SER:HB3	4:2H:347:ASN:ND2	2.32	0.44
3:2G:414:GLU:HG2	3:2G:416:GLY:H	1.83	0.44
3:2I:122:ILE:HG21	3:2I:157:LEU:HD21	2.00	0.44
3:2I:273:ALA:H	3:2I:375:VAL:HG13	1.83	0.44
3:2M:136:LEU:HD12	3:2M:169:PHE:HE1	1.82	0.44
3:3A:407:TRP:HZ2	4:3B:258:ILE:HB	1.82	0.44
3:3C:12:ALA:HB3	3:3C:140:ALA:HB2	1.99	0.44
4:3D:232:ALA:HB1	4:3D:268:ILE:HG21	1.99	0.44
4:3D:237:THR:HA	4:3D:240:LEU:HD13	1.99	0.44
4:3F:268:ILE:HA	4:3F:367:PHE:O	2.18	0.44
5:43:196:LYS:HD2	13:J5:498:GLU:HG3	1.98	0.44
4:4B:12:CYS:HA	17:4B:501:GDP:C2	2.53	0.44
4:4B:330:MET:SD	4:4B:349:MET:HE3	2.58	0.44
4:4D:138:SER:HA	4:4D:169:VAL:HG22	1.99	0.44
3:4E:22:GLU:HG2	3:4E:364:PRO:HG2	1.98	0.44
3:4E:70:LEU:HD13	3:4E:110:ILE:HG23	1.99	0.44
3:4G:324:VAL:HG12	3:4G:326:LYS:H	1.82	0.44
4:4J:318:ARG:O	4:4J:363:MET:HA	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:52:33:ASP:HB3	5:52:36:LEU:HB2	1.99	0.44
3:5C:26:LEU:HD13	3:5C:364:PRO:HD2	2.00	0.44
4:5F:207:LEU:HA	4:5F:210:ILE:HG12	1.99	0.44
3:5K:82:THR:HG21	1:w:910:LYS:HZ2	1.83	0.44
5:60:69:GLU:HG3	5:60:71:ILE:HD11	2.00	0.44
6:63:593:PRO:HA	6:63:598:VAL:HG21	1.98	0.44
6:63:806:LYS:HD2	6:63:806:LYS:HA	1.84	0.44
6:63:847:GLU:CD	6:63:848:SER:H	2.26	0.44
6:64:593:PRO:HA	6:64:598:VAL:HG11	1.99	0.44
6:65:902:PRO:HG2	1:z:880:THR:OG1	2.16	0.44
6:68:320:GLN:HE22	12:H5:98:LYS:NZ	2.15	0.44
3:6A:105:ARG:NH1	4:6B:251:ARG:HD3	2.27	0.44
3:6C:36:MET:HG2	3:6C:61:HIS:HE1	1.83	0.44
3:6C:339:ARG:HH21	14:K4:120:GLU:HB2	1.83	0.44
3:6C:397:LEU:HD11	4:6D:346:PRO:HD3	1.99	0.44
3:6E:104:ALA:HB2	3:6E:413:MET:HB2	2.00	0.44
4:6F:349:MET:HE1	4:6F:367:PHE:HE1	1.82	0.44
4:6H:323:THR:HG22	4:6H:353:VAL:HG21	1.99	0.44
3:6I:298:PRO:HA	3:6I:301:MET:HE2	1.99	0.44
4:6L:397:TRP:CD2	3:6M:257:THR:HG23	2.53	0.44
3:6M:9:VAL:HG22	3:6M:68:LEU:HD12	2.00	0.44
3:6M:292:THR:HG21	3:6M:331:ALA:HB1	2.00	0.44
4:6N:362:LYS:HZ3	1:i:816:VAL:HG23	1.83	0.44
2:7:295:PHE:CE1	2:8:298:LEU:HD22	2.53	0.44
7:75:251:VAL:HA	7:75:254:ARG:HE	1.81	0.44
4:7D:149:THR:HA	4:7D:152:ILE:HD12	1.99	0.44
3:7I:28:HIS:CE1	3:7I:243:ARG:HD2	2.52	0.44
7:80:400:CYS:SG	14:L1:105:LEU:HB3	2.58	0.44
3:8G:112:LYS:HA	3:8G:115:VAL:HG12	1.99	0.44
4:8H:391:ARG:HA	4:8H:391:ARG:HD3	1.83	0.44
4:8J:141:GLY:C	4:8J:184:ASN:HD21	2.25	0.44
3:8K:298:PRO:HG3	3:8K:308:ARG:NE	2.33	0.44
3:9A:276:ILE:HG23	3:9A:280:LYS:HB2	2.00	0.44
4:9D:66:MET:HB3	4:9D:91:VAL:HG23	2.00	0.44
4:9J:182:PRO:HG2	4:9J:384:GLN:HB3	2.00	0.44
3:9K:206:ASN:HD22	15:9K:501:GTP:HN22	1.66	0.44
8:A2:82:MET:HB2	1:z:889:SER:HB2	1.99	0.44
8:A5:249:PRO:HB2	8:A5:251:TYR:CE1	2.53	0.44
8:A6:39:LEU:HA	8:A6:42:VAL:HG12	2.00	0.44
8:A7:122:GLN:O	8:A7:126:ASP:HB2	2.18	0.44
8:A7:165:TYR:CE2	8:A7:208:PHE:HB2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C8:305:LEU:HD23	14:K3:141:ILE:HG12	1.99	0.44
10:D1:343:ALA:O	10:D1:347:GLU:HG2	2.17	0.44
10:D4:97:ILE:HD13	10:D4:397:PHE:HD1	1.83	0.44
10:D7:74:ASP:HB3	10:D7:77:LYS:HB2	1.99	0.44
10:E2:275:GLU:HA	10:E2:278:VAL:HG22	2.00	0.44
10:E3:31:PRO:HG2	10:E3:33:ARG:HD2	2.00	0.44
10:E4:37:ASP:OD1	10:E4:40:ARG:HB2	2.18	0.44
10:E9:355:THR:HG22	10:E9:361:TRP:CD2	2.53	0.44
12:F9:220:PRO:HD2	12:F9:223:LEU:HD12	2.00	0.44
12:G3:225:TRP:HE3	12:G4:254:VAL:HG23	1.81	0.44
13:J7:273:ARG:HB3	13:J7:312:ARG:HD3	2.00	0.44
14:K0:181:LEU:O	14:K0:185:ILE:HG13	2.17	0.44
14:L4:230:TYR:HA	14:L4:233:LEU:HB2	1.99	0.44
14:L9:178:MET:HE2	14:L9:178:MET:HB2	1.84	0.44
14:M1:181:LEU:O	14:M1:185:ILE:HG12	2.17	0.44
1:c:590:GLU:C	1:c:592:ARG:N	2.74	0.44
1:y:941:ARG:HA	1:y:944:GLN:HE21	1.81	0.44
1:C:347:ALA:HB2	1:Z:455:LYS:HG2	1.98	0.44
1:I:600:LEU:HD11	1:J:597:ILE:HG23	1.98	0.44
1:M:610:VAL:HG13	1:N:614:LEU:CD2	2.47	0.44
1:M:665:THR:OG1	1:M:666:VAL:N	2.51	0.44
1:Q:677:MET:HE1	1:U:677:MET:HA	2.00	0.44
4:1F:311:LEU:HA	4:1F:342:VAL:HG21	2.00	0.44
3:1G:202:VAL:HG21	3:1G:378:ILE:HD12	1.98	0.44
4:1H:284:LEU:HG	4:1H:362:LYS:HB3	2.00	0.44
4:1L:109:GLY:O	4:1L:113:ILE:HG22	2.18	0.44
4:1L:397:TRP:O	4:1L:401:GLU:HG2	2.18	0.44
5:22:34:PRO:HG2	5:22:187:ASP:HA	1.99	0.44
5:28:56:GLU:OE1	5:28:57:THR:HG23	2.17	0.44
3:2A:221:ARG:CZ	4:2B:324:LYS:HG2	2.47	0.44
4:2B:216:LYS:HB2	4:2B:275:SER:HB3	1.98	0.44
4:2D:397:TRP:CH2	3:2E:257:THR:HA	2.53	0.44
4:2F:384:GLN:HA	3:2G:348:PRO:HG2	2.00	0.44
4:2J:311:LEU:HD23	4:2J:342:VAL:HG21	1.99	0.44
3:2M:185:TYR:HE2	3:2M:405:VAL:HG22	1.83	0.44
2:3:247:ASP:HB2	2:3:251:ARG:HH12	1.81	0.44
5:36:61:LEU:HA	5:36:62:PRO:HD3	1.83	0.44
5:39:199:LEU:HD23	5:40:199:LEU:HG	1.99	0.44
4:3B:175:VAL:HG21	3:3C:332:VAL:HG13	1.99	0.44
4:3B:178:THR:H	3:3C:352:LYS:HA	1.83	0.44
4:3D:39:ASP:HA	8:A2:212:MET:HE1	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3F:28:HIS:NE2	4:3F:241:ARG:HD2	2.33	0.44
4:3F:136:THR:HG22	4:3F:167:PHE:HB2	1.99	0.44
3:3I:71:GLU:HB3	3:3I:98:ASP:HB2	1.99	0.44
4:3J:66:MET:HE2	4:3J:66:MET:HB3	1.87	0.44
3:3M:10:GLY:O	3:3M:14:ILE:HG12	2.17	0.44
5:42:52:ILE:HD11	5:42:71:ILE:HD11	2.00	0.44
5:43:217:SER:HB3	5:43:220:LEU:HB2	2.00	0.44
3:4G:408:TYR:HB3	3:4G:413:MET:HG2	1.98	0.44
4:4H:330:MET:O	4:4H:334:GLN:HG3	2.18	0.44
4:4H:349:MET:HE2	4:4H:349:MET:HB2	1.90	0.44
5:52:129:VAL:O	5:52:133:MET:HG3	2.17	0.44
5:53:75:ILE:HG12	5:53:89:VAL:HG22	2.00	0.44
3:5C:265:ILE:HD11	3:5C:431:ASP:HB3	1.99	0.44
3:5G:298:PRO:HB3	3:5G:307:PRO:HD2	1.99	0.44
3:5I:238:LEU:HD12	3:5I:238:LEU:HA	1.86	0.44
3:5K:70:LEU:HD12	3:5K:99:ALA:HB2	2.00	0.44
4:5N:117:LEU:HD11	4:5N:154:LYS:HB3	1.98	0.44
6:64:273:LEU:HD13	6:64:315:VAL:HG22	1.98	0.44
6:68:940:GLN:HA	6:68:940:GLN:HE21	1.83	0.44
6:69:322:ALA:HA	6:69:414:VAL:HG13	1.99	0.44
4:6L:28:HIS:HA	4:6L:43:GLN:HB3	2.00	0.44
3:6M:215:ARG:HH21	14:K7:250:PRO:HG2	1.83	0.44
4:7D:29:GLY:O	4:7D:30:ILE:HD13	2.17	0.44
4:7F:139:LEU:HD22	4:7F:188:SER:HB3	1.98	0.44
4:7F:334:GLN:HE22	4:7F:347:ASN:HA	1.82	0.44
3:7I:110:ILE:HG23	3:7I:111:GLY:H	1.82	0.44
4:7J:16:ILE:HD11	4:7J:136:THR:HB	1.99	0.44
4:8B:359:LYS:HA	4:8B:359:LYS:HD2	1.77	0.44
4:8F:287:PRO:HA	4:8F:329:GLN:HE22	1.83	0.44
4:8H:111:GLU:HA	7:96:398:LYS:HE3	2.00	0.44
3:8M:202:VAL:HA	3:8M:268:MET:HB3	2.00	0.44
4:9B:25:SER:HB2	4:9B:30:ILE:HG12	1.98	0.44
4:9B:64:ILE:HD12	4:9B:119:VAL:HG12	1.98	0.44
4:9B:180:VAL:HG13	4:9B:183:TYR:HD2	1.81	0.44
4:9D:210:ILE:HG12	4:9D:298:ASN:HA	1.99	0.44
3:9E:222:PRO:HD2	4:9F:324:LYS:HG2	2.00	0.44
4:9F:132:GLY:HA3	4:9F:163:ILE:HG13	1.99	0.44
4:9F:414:ASN:HD22	4:9F:417:ASP:HB3	1.83	0.44
3:9I:4:VAL:HG12	3:9I:52:PHE:HA	1.99	0.44
4:9J:361:LEU:HD23	4:9J:364:SER:HB3	1.99	0.44
3:9K:326:LYS:HE2	3:9K:326:LYS:HB3	1.74	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9M:304:LYS:HD2	3:9M:304:LYS:HA	1.66	0.44
8:A1:47:LYS:HG2	8:A1:53:VAL:HG21	1.99	0.44
8:A7:240:PRO:HB3	9:B4:19:ALA:HB1	1.98	0.44
8:A9:342:ASP:HB3	8:A9:380:ILE:HD13	1.99	0.44
11:C2:202:LYS:HD3	11:C2:202:LYS:HA	1.87	0.44
10:C7:86:LEU:HG	10:C7:313:TYR:HD2	1.82	0.44
10:C8:94:VAL:HG21	10:C8:331:ILE:HD11	2.00	0.44
10:D0:110:ILE:HD13	10:D0:282:GLN:HG2	1.99	0.44
10:D9:297:ARG:O	10:D9:301:ARG:CB	2.66	0.44
12:G1:259:MET:HG3	12:G1:263:TYR:HE1	1.82	0.44
12:G2:223:LEU:HD22	12:G2:224:ARG:NH2	2.32	0.44
12:G5:193:VAL:HG22	12:G5:195:PRO:HD3	1.98	0.44
12:H7:333:LEU:HD23	12:H7:334:ARG:HE	1.82	0.44
14:M5:86:HIS:HA	14:M5:89:ARG:HB2	2.00	0.44
1:c:682:LYS:HB3	1:c:682:LYS:HE2	1.47	0.44
1:f:591:ARG:HE	1:f:591:ARG:HB3	1.55	0.44
1:h:761:CYS:HB3	1:h:834:ARG:HH12	1.83	0.44
1:I:631:LEU:HB2	1:J:631:LEU:HD13	1.98	0.44
1:J:578:ARG:CZ	1:J:578:ARG:HA	2.48	0.44
1:K:418:VAL:O	1:K:422:THR:HG23	2.18	0.44
2:12:295:PHE:O	2:12:299:ILE:HG12	2.18	0.44
3:1A:71:GLU:HG3	3:1A:73:THR:HG22	1.99	0.44
4:1B:256:ASN:HD22	4:1B:350:LYS:HE3	1.82	0.44
3:1E:60:LYS:HB2	3:1E:60:LYS:HE2	1.68	0.44
4:1L:220:PRO:HG2	3:1M:326:LYS:HE3	1.99	0.44
3:1M:167:LEU:HD13	3:1M:169:PHE:CZ	2.53	0.44
3:1M:251:ASP:H	3:1M:254:GLU:HB3	1.82	0.44
5:24:193:ASN:HA	5:24:196:LYS:HE3	1.99	0.44
5:27:77:ILE:HD13	5:27:127:PRO:HG2	2.00	0.44
3:2A:56:THR:O	3:2A:60:LYS:HG3	2.17	0.44
3:2A:264:ARG:HH22	6:67:540:PHE:HD1	1.65	0.44
4:2B:101:TRP:CD1	4:2B:146:GLY:HA2	2.52	0.44
3:2I:151:CYS:O	3:2I:155:GLU:HG3	2.18	0.44
4:2J:66:MET:HE1	4:2J:147:MET:HG2	1.99	0.44
3:2K:155:GLU:HB2	6:69:137:THR:HB	2.00	0.44
3:2M:188:VAL:HG13	3:2M:425:LEU:HG	1.99	0.44
5:31:180:THR:HG23	5:31:183:PHE:H	1.83	0.44
2:4:285:GLN:HA	2:4:288:VAL:HG22	2.00	0.44
5:40:53:ARG:HD2	5:40:147:VAL:HG13	1.98	0.44
5:45:114:GLN:HG3	5:45:119:LEU:HB2	1.99	0.44
3:4I:181:VAL:HG23	4:4J:350:LYS:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4J:349:MET:HE3	4:4J:349:MET:HB3	1.94	0.44
3:4M:172:TRP:CZ3	3:4M:191:THR:HG21	2.53	0.44
5:54:53:ARG:HH12	5:54:62:PRO:HA	1.83	0.44
3:5A:209:ILE:HA	3:5A:212:ILE:HG22	1.99	0.44
4:5B:218:THR:HG23	4:5B:219:THR:H	1.81	0.44
4:5F:29:GLY:HA3	4:5F:38:GLY:HA3	1.99	0.44
5:61:17:SER:HA	5:61:20:PHE:HB3	2.00	0.44
6:64:821:SER:HA	6:64:824:ILE:HG12	1.99	0.44
6:64:844:ALA:O	6:64:848:SER:HB3	2.18	0.44
6:66:154:ARG:HH21	12:I9:316:LEU:HB3	1.82	0.44
6:69:268:GLU:HG3	6:69:270:VAL:H	1.81	0.44
6:69:346:ARG:HH21	6:69:347:PHE:HE1	1.63	0.44
4:6B:309:ARG:HE	4:6B:342:VAL:HG23	1.83	0.44
3:6C:324:VAL:HG12	3:6C:326:LYS:H	1.81	0.44
3:6E:274:PRO:HD3	3:6E:291:ILE:HD11	1.99	0.44
3:6G:397:LEU:HD11	4:6H:346:PRO:HD3	2.00	0.44
4:6L:8:GLN:HG3	4:6L:65:LEU:HD13	1.98	0.44
4:7B:166:THR:HG23	4:7B:199:VAL:HG13	2.00	0.44
3:7E:71:GLU:HB2	3:7E:98:ASP:HB2	2.00	0.44
4:7F:169:VAL:HG12	4:7F:202:ILE:HB	1.98	0.44
4:7F:415:MET:HE3	4:7F:415:MET:HB2	1.84	0.44
4:7H:157:GLU:HB3	7:89:286:TRP:CD1	2.53	0.44
3:7K:388:PHE:HB3	3:7K:425:LEU:HD12	2.00	0.44
3:7K:417:GLU:HA	3:7K:420:GLU:HB3	2.00	0.44
3:7M:7:ILE:HD11	3:7M:137:MET:SD	2.58	0.44
2:8:264:GLN:HA	2:8:267:HIS:CE1	2.53	0.44
7:84:377:ARG:HH12	7:84:382:ASP:N	2.14	0.44
7:86:390:PRO:O	7:86:391:TYR:HD1	2.01	0.44
3:8G:101:ASN:HD22	4:8H:256:ASN:ND2	2.16	0.44
4:8H:290:THR:HG21	4:8H:329:GLN:HB3	1.98	0.44
4:8H:402:GLY:H	14:M2:96:GLY:HA3	1.83	0.44
4:8J:305:PRO:HB2	4:8J:310:TYR:CE1	2.53	0.44
3:8K:320:ARG:HH12	3:8K:360:PRO:HA	1.83	0.44
3:8M:187:SER:O	3:8M:191:THR:HG23	2.18	0.44
7:96:392:ARG:HD3	14:M2:122:TYR:CE2	2.52	0.44
3:9C:74:VAL:HG13	3:9C:75:VAL:HG13	2.00	0.44
3:9C:267:PHE:HB3	3:9C:384:ILE:HG12	1.99	0.44
8:A8:379:GLU:HG2	9:B4:164:LYS:HE3	1.99	0.44
9:B2:163:LEU:HB3	9:B2:167:ARG:HH12	1.82	0.44
9:B5:14:ARG:HH21	9:B5:491:ARG:HG2	1.83	0.44
10:E1:96:LEU:HA	10:E1:99:THR:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E4:90:VAL:HG11	10:E4:327:ALA:HB2	1.99	0.44
10:E8:301:ARG:HH22	14:M2:143:ARG:HG2	1.83	0.44
10:E9:51:TYR:HB3	10:E9:54:HIS:CD2	2.52	0.44
10:F1:305:LEU:HD21	14:M4:142:GLN:HB3	1.98	0.44
10:F3:392:THR:O	10:F3:396:LEU:HD12	2.17	0.44
12:G2:223:LEU:HA	12:G2:226:ILE:HG12	1.99	0.44
12:I7:91:GLU:HA	12:I7:94:LEU:HD23	2.00	0.44
14:L3:178:MET:HE3	14:L3:178:MET:HB3	1.67	0.44
1:c:593:GLN:O	1:c:596:GLU:HB3	2.17	0.44
1:f:562:ILE:O	1:f:563:ASP:C	2.60	0.44
1:B:394:LYS:HD2	1:E:394:LYS:HZ2	1.82	0.44
1:F:517:GLU:HA	1:F:520:TRP:NE1	2.33	0.44
1:I:631:LEU:HD11	1:J:632:ARG:HD3	1.98	0.44
1:I:677:MET:HA	1:I:680:LEU:HD12	2.00	0.44
1:P:643:ARG:HD3	1:P:643:ARG:HA	1.35	0.44
1:S:373:LEU:HA	1:S:376:MET:HG2	1.99	0.44
1:S:469:LEU:HB3	1:b:362:VAL:HG21	1.99	0.44
1:W:499:ARG:O	1:W:503:GLU:HG2	2.18	0.44
1:Z:513:ARG:HE	1:d:512:LYS:NZ	2.16	0.44
2:10:179:MET:SD	2:10:180:LYS:HD2	2.57	0.44
4:1B:27:GLU:HG2	4:1B:43:GLN:HE22	1.83	0.44
4:1B:64:ILE:HG21	4:1B:116:VAL:HG13	2.00	0.44
17:1B:501:GDP:H8	17:1B:501:GDP:H2'	1.75	0.44
3:1E:238:LEU:HD21	3:1E:378:ILE:HD13	1.99	0.44
4:1F:112:LEU:HB3	4:1F:147:MET:HE1	2.00	0.44
4:1J:253:LEU:O	4:1J:257:LEU:HB2	2.18	0.44
4:2B:198:GLU:HB2	4:2B:266:PHE:CE1	2.47	0.44
3:2G:195:LEU:HD21	3:2G:428:LEU:HD22	1.99	0.44
4:2L:240:LEU:HD13	4:2L:249:ASP:HB2	2.00	0.44
3:2M:168:ASN:O	3:2M:201:ALA:HA	2.17	0.44
5:31:100:ASN:HD22	5:31:184:THR:HG22	1.83	0.44
5:35:36:LEU:HD21	5:35:42:LEU:HB2	2.00	0.44
3:3A:291:ILE:HD13	3:3A:373:ARG:HB3	1.99	0.44
4:3L:403:MET:HB3	4:3L:408:PHE:HE1	1.82	0.44
5:43:53:ARG:HG3	5:43:149:ILE:HG12	1.98	0.44
5:44:132:LYS:HA	5:44:132:LYS:HD3	1.67	0.44
3:4E:272:TYR:HB3	3:4E:275:ILE:HD11	2.00	0.44
4:4J:66:MET:HE3	4:4J:116:VAL:HG11	2.00	0.44
4:4L:7:VAL:HB	4:4L:135:ILE:HG22	2.00	0.44
4:5F:113:ILE:HA	4:5F:116:VAL:HG12	2.00	0.44
4:5H:304:ASP:HB3	4:5H:307:HIS:HD2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:63:489:LEU:O	6:63:493:ARG:HG3	2.18	0.44
6:67:496:ASP:HB3	6:67:500:ARG:CZ	2.47	0.44
6:67:873:ARG:HB3	9:B7:37:ARG:HH22	1.83	0.44
6:69:845:VAL:HA	6:69:848:SER:HB3	2.00	0.44
4:6B:213:ARG:HE	4:6B:216:LYS:HZ3	1.66	0.44
4:6B:375:GLN:NE2	4:6B:379:LYS:HD2	2.33	0.44
4:6D:380:ARG:HA	7:72:311:SER:HB2	2.00	0.44
3:6G:30:ILE:HD13	3:6G:36:MET:HG3	2.00	0.44
3:6G:262:TYR:HD2	3:6G:265:ILE:HD11	1.83	0.44
4:6H:86:ARG:HB3	4:6H:89:ASN:HB2	2.00	0.44
4:6H:326:VAL:O	4:6H:330:MET:HG2	2.18	0.44
4:6J:290:THR:HA	4:6J:293:MET:HE2	1.99	0.44
3:6K:216:ASN:HB3	3:6K:275:ILE:O	2.18	0.44
3:6M:136:LEU:HB3	3:6M:138:PHE:HE1	1.83	0.44
3:6M:252:VAL:HA	3:6M:255:PHE:HB2	2.00	0.44
4:6N:15:GLN:HB2	1:i:803:ILE:HG13	1.99	0.44
7:73:408:ILE:HA	7:73:411:MET:HE1	1.99	0.44
7:77:313:LEU:H	7:77:315:ILE:HD12	1.83	0.44
4:7B:55:THR:HG23	4:8B:283:ALA:HA	1.99	0.44
3:7E:109:THR:HG22	3:7E:110:ILE:H	1.83	0.44
3:7E:312:TYR:HB2	3:7E:343:PHE:HD1	1.81	0.44
3:7E:404:PHE:HZ	4:7F:312:THR:HG21	1.82	0.44
3:7I:169:PHE:HZ	3:7I:238:LEU:HD22	1.82	0.44
3:7I:420:GLU:HA	3:7I:423:GLU:HG2	1.98	0.44
4:7J:378:PHE:HD2	4:7J:419:VAL:HG12	1.83	0.44
7:87:334:LEU:HD21	7:87:347:ILE:HG12	1.99	0.44
3:8C:195:LEU:HD12	3:8C:266:HIS:HE1	1.82	0.44
4:8D:179:VAL:HB	3:8E:350:GLY:HA2	1.99	0.44
4:8F:98:GLY:HA2	3:8G:254:GLU:HG3	2.00	0.44
3:8G:100:ALA:HA	4:8H:252:LYS:HG2	2.00	0.44
4:8H:313:ALA:HA	4:8H:369:GLY:HA2	2.00	0.44
3:8K:12:ALA:HB3	3:8K:140:ALA:HB2	1.99	0.44
7:90:296:ARG:HH11	7:90:315:ILE:HG23	1.82	0.44
7:94:372:TRP:O	7:94:376:GLU:HG2	2.18	0.44
3:9C:20:CYS:HB2	3:9C:235:ILE:HD11	2.00	0.44
3:9C:209:ILE:HD11	3:9C:230:LEU:HB2	1.98	0.44
4:9J:135:ILE:HB	4:9J:166:THR:HG22	2.00	0.44
3:9K:70:LEU:HD13	3:9K:110:ILE:HG23	2.00	0.44
8:A8:33:LEU:HG	8:A8:77:GLU:HG3	1.99	0.44
10:D5:287:PRO:HA	10:D5:288:PRO:HD3	1.89	0.44
10:D8:76:ALA:HB2	10:D8:319:LEU:HD21	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D9:74:ASP:HB3	10:D9:77:LYS:HB2	1.99	0.44
10:E0:140:LYS:HE2	10:E0:140:LYS:HB2	1.84	0.44
10:E2:107:ILE:HG23	10:E2:283:PHE:CG	2.53	0.44
10:F1:338:PRO:HB2	10:F1:341:TYR:HB3	2.00	0.44
10:F2:86:LEU:HD13	10:F2:319:LEU:HD12	1.98	0.44
10:F3:146:ALA:HB1	10:F3:287:PRO:HD2	1.99	0.44
12:G0:68:ARG:HA	12:H1:334:ARG:HG3	1.98	0.44
13:J6:678:ASN:HA	13:J6:681:HIS:CE1	2.53	0.44
14:L9:170:PHE:HB2	14:L9:172:ARG:HE	1.83	0.44
1:a:586:LYS:HG2	1:f:586:LYS:HG2	1.99	0.44
1:a:610:VAL:O	1:a:613:GLN:HB2	2.18	0.44
1:f:518:ARG:O	1:f:521:LYS:HB2	2.17	0.44
1:f:558:LEU:O	1:f:559:GLU:C	2.61	0.44
1:E:376:MET:HG2	1:E:377:HIS:H	1.83	0.44
1:I:666:VAL:CG1	1:J:666:VAL:HG12	2.48	0.44
1:M:594:ALA:HA	1:M:597:ILE:HD12	2.00	0.44
1:O:646:ASN:O	1:O:649:ASP:HB2	2.18	0.44
1:Y:487:HIS:ND1	1:f:661:ASN:HB3	2.33	0.44
2:10:156:GLU:HB3	10:D7:123:ASP:HB3	1.99	0.44
3:1A:240:ALA:HA	3:1A:243:ARG:HE	1.83	0.44
3:1A:318:MET:HB2	3:1A:376:CYS:O	2.17	0.44
4:1B:139:LEU:HD13	4:1B:170:PHE:CD1	2.53	0.44
4:1F:103:LYS:HB3	4:1F:108:GLU:OE1	2.17	0.44
4:1F:385:PHE:CE2	4:1F:412:GLU:HB2	2.53	0.44
3:1G:397:LEU:HD23	4:1H:346:PRO:HD3	1.99	0.44
4:1L:267:LEU:HD22	4:1L:301:CYS:SG	2.58	0.44
3:2A:67:PHE:HB2	3:2A:92:LEU:HD13	2.00	0.44
4:2F:206:ALA:HB2	4:2F:302:ALA:HB2	2.00	0.44
3:2G:240:ALA:HA	3:2G:243:ARG:HH21	1.83	0.44
3:2G:346:TRP:HE1	3:2G:435:VAL:HG13	1.83	0.44
3:2K:102:ASN:HA	3:2K:408:TYR:HE1	1.82	0.44
4:2L:163:ILE:HG21	4:2L:250:LEU:HB3	2.00	0.44
5:30:67:ARG:HA	5:30:67:ARG:HD3	1.87	0.44
5:35:89:VAL:HB	5:35:103:HIS:HB3	2.00	0.44
5:39:130:LEU:HA	5:39:133:MET:HE2	1.99	0.44
4:3F:41:ASP:HB3	8:A1:229:ARG:HH21	1.82	0.44
3:3M:167:LEU:HD11	3:3M:252:VAL:HG13	2.00	0.44
5:40:48:VAL:HG21	5:40:134:LEU:HD22	2.00	0.44
5:45:19:ASN:HB3	5:45:21:LEU:HD23	2.00	0.44
5:48:211:CYS:HA	5:48:214:LYS:HE2	1.99	0.44
4:4B:117:LEU:HB3	4:4B:121:ARG:HH21	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4D:12:CYS:HB3	4:4D:138:SER:HB3	1.99	0.44
2:5:295:PHE:CE1	2:6:298:LEU:HD22	2.53	0.44
5:57:77:ILE:HG12	5:57:81:GLU:HA	2.00	0.44
4:5B:397:TRP:O	4:5B:401:GLU:HB2	2.18	0.44
3:5C:91:GLN:HE21	3:5C:125:LEU:HD11	1.81	0.44
3:5C:138:PHE:HD1	3:5C:169:PHE:HB2	1.83	0.44
4:5J:154:LYS:HD3	7:76:286:TRP:NE1	2.33	0.44
3:5M:236:SER:O	3:5M:240:ALA:HB2	2.17	0.44
4:5N:253:LEU:HD11	4:5N:257:LEU:HD22	1.99	0.44
6:65:466:CYS:HB3	6:65:470:LYS:NZ	2.33	0.44
6:65:886:HIS:CD2	6:65:888:GLY:H	2.35	0.44
6:67:617:VAL:HG22	6:67:621:ARG:NH1	2.32	0.44
6:68:417:LEU:HG	6:68:418:ASN:H	1.82	0.44
6:68:581:LYS:HD3	6:68:581:LYS:HA	1.81	0.44
3:6A:171:SER:HA	3:6A:204:LEU:HB2	1.99	0.44
3:6A:212:ILE:HG23	3:6A:275:ILE:HD12	1.98	0.44
4:6H:20:PHE:CG	4:6H:233:MET:HE2	2.52	0.44
4:6H:149:THR:HA	4:6H:152:ILE:HD12	1.99	0.44
4:6J:102:ALA:HB2	4:6J:403:MET:HE2	1.98	0.44
4:7D:112:LEU:HB3	4:7D:147:MET:HE1	1.99	0.44
3:7E:70:LEU:HD23	3:7E:70:LEU:HA	1.88	0.44
3:7G:36:MET:HE2	3:7G:49:PHE:HE2	1.83	0.44
4:7L:380:ARG:HD2	4:7L:380:ARG:HA	1.83	0.44
3:7M:183:GLU:HA	3:7M:186:ASN:HB3	1.99	0.44
7:86:376:GLU:O	7:86:380:TRP:HB2	2.18	0.44
4:8B:21:TRP:HZ3	4:8B:50:PHE:HB3	1.82	0.44
4:8D:61:PRO:HG2	4:8D:85:PHE:HA	2.00	0.44
4:8D:152:ILE:HG22	4:8D:195:ASN:HB3	2.00	0.44
4:8D:173:PRO:HG3	4:8D:380:ARG:HD2	1.99	0.44
4:8D:190:HIS:ND1	14:M4:133:VAL:HG11	2.33	0.44
4:8D:238:CYS:HA	4:8D:241:ARG:HH21	1.83	0.44
4:8J:20:PHE:HA	4:8J:230:SER:HB2	1.99	0.44
3:8K:70:LEU:HB3	3:8K:145:THR:HG21	2.00	0.44
7:90:394:TYR:CE1	14:L9:123:SER:HB3	2.53	0.44
3:9A:372:MET:HG2	3:9A:373:ARG:HG2	2.00	0.44
3:9C:227:LEU:HD21	4:9D:324:LYS:HE2	2.00	0.44
8:A1:190:THR:HG22	8:A1:218:SER:HB3	2.00	0.44
10:D0:341:TYR:HA	10:D0:390:MET:HE1	2.00	0.44
10:D1:293:MET:HG3	10:D1:297:ARG:HE	1.82	0.44
10:E1:355:THR:HG22	10:E1:361:TRP:CD2	2.53	0.44
10:E4:83:ARG:NH1	10:E4:88:LEU:HD13	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E5:303:LEU:HG	10:E5:396:LEU:HD13	1.99	0.44
12:F8:238:HIS:CE1	12:F8:259:MET:HG3	2.53	0.44
12:I7:69:LEU:HD23	12:I7:69:LEU:HA	1.87	0.44
13:J1:405:VAL:HG22	13:J1:409:LEU:HD12	2.00	0.44
13:J5:355:PRO:HA	13:J5:358:ASP:HB2	2.00	0.44
13:J7:478:PRO:HG3	13:J7:507:SER:HB2	2.00	0.44
14:K4:153:LEU:HB2	14:K4:216:GLY:H	1.83	0.44
14:M4:91:ASP:HA	14:M4:97:ARG:HH21	1.83	0.44
14:M5:99:ILE:HA	14:M5:102:ARG:HG2	1.99	0.44
1:C:340:ARG:O	1:C:343:GLU:HB3	2.18	0.43
1:O:652:MET:N	1:O:652:MET:SD	2.91	0.43
1:Q:502:LEU:HD13	1:U:502:LEU:HB3	2.00	0.43
1:T:611:THR:O	1:T:615:ARG:HB3	2.17	0.43
1:Y:500:ARG:O	1:Y:503:GLU:HB3	2.18	0.43
3:1I:119:LEU:HD11	3:1I:156:ARG:HG2	2.00	0.43
4:1J:130:LEU:HD11	4:1J:133:PHE:HE2	1.83	0.43
4:1L:134:GLN:HG3	4:1L:165:GLU:HG2	2.00	0.43
4:1N:159:TYR:HB3	4:1N:162:ARG:HG3	2.00	0.43
5:23:222:LEU:HD13	3:2E:402:ARG:HG2	2.00	0.43
5:25:77:ILE:HG21	5:25:127:PRO:HG3	1.99	0.43
3:2C:417:GLU:HA	3:2C:420:GLU:HB3	2.00	0.43
3:2I:260:VAL:HG23	3:2I:265:ILE:O	2.18	0.43
4:2L:101:TRP:HB2	4:2L:184:ASN:HD22	1.82	0.43
3:3A:137:MET:O	3:3A:168:ASN:HA	2.17	0.43
4:3B:121:ARG:O	4:3B:125:GLU:HG2	2.18	0.43
4:3B:199:VAL:HB	4:3B:265:PHE:HD1	1.82	0.43
4:3B:256:ASN:OD1	4:3B:350:LYS:HB3	2.18	0.43
3:3C:154:LEU:HG	3:3C:197:HIS:HB3	2.00	0.43
4:3D:117:LEU:O	4:3D:121:ARG:HG2	2.17	0.43
4:3D:274:THR:HG21	4:3D:282:ARG:HD2	1.98	0.43
3:3E:224:TYR:CZ	4:3F:323:THR:HG21	2.52	0.43
4:3F:21:TRP:HA	4:3F:24:ILE:HG22	1.99	0.43
4:3F:201:VAL:HG11	4:3F:377:MET:HE1	2.00	0.43
4:3F:237:THR:HG22	4:3F:250:LEU:HD21	2.00	0.43
5:43:103:HIS:CE1	5:43:175:ASP:H	2.33	0.43
3:4A:181:VAL:HG13	3:4A:182:VAL:HG13	2.00	0.43
3:4E:64:ARG:HG3	3:4E:125:LEU:HD22	2.00	0.43
3:4K:26:LEU:HD22	3:4K:364:PRO:HG3	1.99	0.43
3:4M:261:PRO:HB2	3:4M:262:TYR:CD2	2.53	0.43
5:51:55:GLN:HB2	5:51:151:HIS:HA	2.00	0.43
4:5B:417:ASP:O	4:5B:421:GLU:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5F:108:GLU:O	4:5F:111:GLU:HG2	2.17	0.43
4:5N:67:ASP:HA	4:5N:143:THR:HG21	1.99	0.43
5:60:223:HIS:HA	5:60:226:LYS:HE3	2.00	0.43
6:64:845:VAL:HA	6:64:848:SER:HB3	2.00	0.43
6:66:311:VAL:O	6:66:315:VAL:HG23	2.18	0.43
3:6A:223:THR:HB	4:6B:322:SER:HB2	2.00	0.43
3:6A:362:VAL:HB	3:6A:370:LYS:HB3	2.00	0.43
4:6B:18:ALA:O	4:6B:22:GLU:HG2	2.18	0.43
3:6C:185:TYR:HE1	3:6C:404:PHE:HB2	1.83	0.43
4:6F:28:HIS:HD1	4:6F:47:ILE:HG13	1.83	0.43
4:6F:86:ARG:NE	4:7F:281:TYR:HB2	2.31	0.43
3:6G:263:PRO:HB3	14:K9:86:HIS:CD2	2.52	0.43
4:6H:132:GLY:HA3	4:6H:163:ILE:HG22	2.00	0.43
4:6H:256:ASN:O	4:6H:312:THR:HG21	2.18	0.43
3:6I:207:GLU:HA	3:6I:210:TYR:HB2	2.00	0.43
7:71:292:CYS:HB2	7:71:318:THR:HB	1.99	0.43
7:72:334:LEU:HD21	7:72:347:ILE:HD13	1.98	0.43
3:7C:4:VAL:HG12	3:7C:134:GLY:H	1.83	0.43
4:7F:86:ARG:HB3	4:7F:89:ASN:HB2	2.00	0.43
3:8A:47:ASP:O	3:8A:50:ASN:HB2	2.17	0.43
3:8C:209:ILE:HD13	3:8C:227:LEU:HD21	2.00	0.43
3:8G:184:PRO:HG3	3:8G:394:LYS:HD2	2.00	0.43
3:8K:326:LYS:HE2	3:8K:326:LYS:HB3	1.74	0.43
7:92:399:THR:HA	7:92:414:ILE:HB	2.00	0.43
7:95:408:ILE:HB	3:9M:333:ALA:HB2	2.00	0.43
3:9A:117:LEU:HD23	3:9A:121:ARG:HH11	1.83	0.43
8:A1:95:PHE:HB2	8:A1:98:LEU:HD12	2.00	0.43
8:A2:286:ALA:HA	8:A2:316:LEU:HD21	2.00	0.43
8:A7:77:GLU:O	8:A7:81:ILE:HD12	2.18	0.43
10:E5:62:VAL:HG12	10:E5:309:ILE:HD11	1.99	0.43
10:E8:141:TYR:O	10:E8:145:ASN:HB2	2.17	0.43
10:E9:331:ILE:HA	10:E9:335:LEU:HD23	1.99	0.43
12:G8:242:TRP:CE3	12:G8:262:LEU:HD21	2.52	0.43
13:J5:295:LEU:HD22	13:J5:426:TRP:HZ3	1.83	0.43
14:M1:200:PHE:O	14:M1:219:TYR:HA	2.18	0.43
1:f:553:ARG:HH11	1:f:554:HIS:HB2	1.82	0.43
1:z:872:ALA:HB3	1:z:875:ILE:HG12	1.98	0.43
1:A:487:HIS:HE1	1:H:665:THR:HG23	1.83	0.43
1:A:507:GLU:OE2	1:E:332:ARG:HG3	2.18	0.43
1:E:379:ARG:HB3	1:c:489:GLN:NE2	2.33	0.43
1:J:659:LEU:HD23	1:J:660:GLN:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:513:ARG:HD2	1:L:513:ARG:HE	1.83	0.43
1:N:579:LEU:O	1:N:583:GLN:HG2	2.17	0.43
1:U:411:LYS:HZ3	1:U:415:LEU:HD11	1.81	0.43
1:W:338:HIS:O	1:W:342:MET:HB2	2.17	0.43
1:X:630:ARG:HH21	1:i:811:ARG:HH12	1.66	0.43
1:Z:412:GLU:HA	1:Z:415:LEU:HD12	2.00	0.43
1:Z:451:THR:O	1:Z:454:GLU:HG3	2.18	0.43
2:13:184:LYS:HA	2:13:187:HIS:CE1	2.53	0.43
3:1E:19:ALA:HA	3:1E:22:GLU:HG2	2.00	0.43
4:1F:163:ILE:HD11	4:1F:251:ARG:HE	1.83	0.43
3:1G:407:TRP:CD1	4:1H:255:VAL:HA	2.53	0.43
5:26:112:GLN:HA	5:26:115:GLU:HG3	2.00	0.43
3:2A:16:ILE:HD11	15:2A:501:GTP:O6	2.18	0.43
3:2A:99:ALA:HA	3:2A:105:ARG:HH11	1.83	0.43
3:2A:154:LEU:HD11	3:2A:166:LYS:HD2	2.00	0.43
3:2E:6:SER:HB3	3:2E:8:HIS:HE2	1.83	0.43
3:2E:66:VAL:HG21	3:2E:122:ILE:HD13	2.00	0.43
17:2H:501:GDP:H8	17:2H:501:GDP:H2'	1.71	0.43
4:2L:158:GLU:HG3	4:2L:159:TYR:CD2	2.53	0.43
3:2M:234:VAL:HG22	3:2M:272:TYR:HB3	1.99	0.43
5:35:97:LEU:HD21	5:36:192:TYR:CG	2.54	0.43
5:35:211:CYS:HB3	13:J1:509:PHE:CE2	2.53	0.43
3:3A:10:GLY:O	3:3A:14:ILE:HG12	2.18	0.43
4:3D:73:MET:HG3	4:3D:92:PHE:CD1	2.53	0.43
3:3E:122:ILE:HG21	3:3E:157:LEU:HD21	1.99	0.43
4:3H:276:ARG:HD2	6:63:877:ALA:HB3	1.99	0.43
4:3J:293:MET:HE1	4:3J:330:MET:HE1	2.00	0.43
4:3L:342:VAL:HG12	4:3L:345:ILE:H	1.83	0.43
5:44:183:PHE:HA	5:44:186:ARG:HG2	1.99	0.43
3:4A:119:LEU:HG	3:4A:123:ARG:HH12	1.83	0.43
3:4A:319:TYR:HD2	3:4A:323:VAL:HG21	1.83	0.43
3:4G:195:LEU:HD23	3:4G:195:LEU:HA	1.88	0.43
5:56:34:PRO:HB3	5:56:186:ARG:HG3	2.00	0.43
4:5D:236:VAL:HG22	4:5D:316:MET:HE1	2.00	0.43
3:5K:222:PRO:HD2	4:5L:324:LYS:HE3	2.00	0.43
2:6:175:TYR:CD2	2:6:179:MET:HE1	2.53	0.43
6:63:614:PRO:HA	6:63:617:VAL:HG12	2.01	0.43
6:63:616:LEU:HD12	6:63:943:LEU:HD11	2.00	0.43
6:66:878:PRO:HB2	9:B5:521:ARG:HH12	1.83	0.43
6:68:485:LYS:HE2	6:68:487:TYR:HE1	1.83	0.43
4:6B:167:PHE:CE2	4:6B:233:MET:HB2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6D:338:SER:H	7:72:289:GLY:HA2	1.83	0.43
3:6E:212:ILE:HD13	3:6E:212:ILE:HA	1.88	0.43
3:6K:159:VAL:HG13	7:83:351:LYS:HB3	2.00	0.43
3:6M:19:ALA:HB2	1:i:742:MET:HE2	1.99	0.43
3:6M:88:HIS:HB3	3:6M:91:GLN:CB	2.48	0.43
3:6M:384:ILE:HA	3:6M:387:VAL:HG12	1.99	0.43
7:73:277:TYR:HB3	10:D9:148:MET:HE2	2.01	0.43
4:7B:42:LEU:HD21	4:7B:243:PRO:HD2	2.00	0.43
3:7E:53:PHE:HB3	3:7E:61:HIS:HB3	2.00	0.43
3:7E:130:THR:HB	7:86:406:LEU:HD21	1.99	0.43
4:7H:399:THR:HA	4:7H:403:MET:HB2	1.98	0.43
3:7I:7:ILE:HG22	3:7I:66:VAL:HB	1.99	0.43
3:7K:398:MET:HE2	4:7L:345:ILE:HG23	2.00	0.43
4:8J:69:GLU:HG2	4:8J:143:THR:HG21	2.00	0.43
4:8L:421:GLU:HB2	14:M7:140:GLY:HA2	2.00	0.43
2:9:217:ALA:HA	2:9:220:LYS:HE2	2.00	0.43
7:93:341:SER:HB2	14:M3:216:GLY:HA3	2.00	0.43
3:9A:292:THR:HG21	3:9A:331:ALA:HB1	1.98	0.43
4:9D:119:VAL:HG23	4:9D:122:LYS:HE2	2.00	0.43
3:9E:70:LEU:HD21	3:9E:149:LEU:HD13	2.00	0.43
8:A1:386:ARG:NH1	9:B5:159:PRO:HG2	2.33	0.43
8:A2:365:THR:O	8:A2:369:VAL:HG23	2.18	0.43
8:A4:124:GLU:HA	8:A4:127:ARG:HG2	1.99	0.43
8:A7:325:LEU:HD21	8:A7:367:PHE:CD2	2.54	0.43
8:A7:379:GLU:HB3	9:B2:164:LYS:HZ2	1.83	0.43
10:C9:301:ARG:NH1	14:K4:143:ARG:HD2	2.33	0.43
10:D3:97:ILE:HD13	10:D3:397:PHE:HD2	1.84	0.43
10:D9:31:PRO:HB2	10:D9:33:ARG:HG2	2.00	0.43
10:E7:37:ASP:OD1	10:E7:40:ARG:HB2	2.18	0.43
10:E9:375:ILE:HG23	10:E9:379:LEU:HD12	2.00	0.43
12:F6:246:PRO:HD3	12:F6:266:PRO:HB3	2.00	0.43
13:J2:281:GLU:HB2	13:J2:323:LYS:HE2	2.00	0.43
14:L0:207:ILE:HG23	14:L0:212:ASP:HB2	1.99	0.43
14:L9:152:ARG:HG2	14:L9:213:ILE:HG22	2.00	0.43
14:M6:239:GLU:HG2	14:M6:240:TRP:CD1	2.53	0.43
1:h:812:PRO:HA	1:h:813:PRO:HD3	1.87	0.43
1:k:758:ASN:HD21	1:k:828:CYS:H	1.66	0.43
1:k:812:PRO:HA	1:k:813:PRO:HD3	1.92	0.43
1:B:473:ARG:HG3	1:B:474:LEU:HD12	1.99	0.43
1:I:673:LEU:HG	1:J:673:LEU:HB3	2.00	0.43
1:J:680:LEU:HD23	1:J:680:LEU:HA	1.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:500:ARG:HA	1:N:503:GLU:HG2	2.00	0.43
1:N:653:LYS:O	1:N:656:GLN:HG3	2.19	0.43
1:O:666:VAL:HA	1:O:669:GLU:HB2	1.99	0.43
1:Q:479:ASP:HB3	1:u:922:ARG:HH21	1.84	0.43
1:Y:574:LYS:HG2	1:Y:578:ARG:HH11	1.83	0.43
2:12:172:PHE:HA	2:12:175:TYR:CE1	2.53	0.43
2:14:268:THR:HA	2:14:271:LYS:HE2	1.99	0.43
3:1A:385:ALA:HB1	3:1A:429:GLU:HG2	1.99	0.43
4:1B:198:GLU:HB3	4:1B:200:GLN:HE22	1.83	0.43
3:1C:180:ALA:HB3	3:1C:183:GLU:HG3	1.99	0.43
4:1D:77:ARG:HD3	4:1D:77:ARG:HA	1.86	0.43
4:1F:220:PRO:HD2	3:1G:326:LYS:HZ3	1.82	0.43
4:1F:392:LYS:HA	4:1F:395:LEU:HD13	2.00	0.43
3:1K:319:TYR:CZ	3:1K:328:VAL:HG23	2.54	0.43
4:1N:9:GLY:HA2	4:1N:66:MET:HB3	2.00	0.43
5:21:80:GLU:HG3	5:21:83:ASN:H	1.82	0.43
5:25:93:SER:HB3	5:25:96:ASP:O	2.18	0.43
4:2B:200:GLN:HE22	4:2B:368:VAL:HG21	1.83	0.43
3:2C:406:HIS:HA	3:2C:409:VAL:HG12	1.98	0.43
3:2I:198:THR:HG21	3:2I:201:ALA:HB2	2.00	0.43
2:3:185:ASN:O	2:3:189:GLU:HG3	2.18	0.43
4:3B:318:ARG:HE	4:3B:358:PRO:HD3	1.82	0.43
4:3B:378:PHE:HA	4:3B:381:VAL:HG12	1.99	0.43
3:3C:224:TYR:HD1	3:3C:227:LEU:HD12	1.83	0.43
4:3H:58:ARG:HG2	4:4H:280:GLN:O	2.18	0.43
4:4J:83:GLN:CD	8:A6:96:LYS:HE2	2.43	0.43
3:4M:5:ILE:HD12	3:4M:64:ARG:HB3	2.00	0.43
3:4M:334:THR:O	3:4M:338:LYS:HB2	2.18	0.43
5:52:185:ARG:HA	5:52:185:ARG:HD2	1.77	0.43
5:54:171:LEU:HB2	5:57:167:LYS:NZ	2.33	0.43
5:56:140:GLU:HB3	5:56:144:PHE:H	1.84	0.43
4:5B:7:VAL:HG11	4:5B:151:LEU:HD23	2.00	0.43
4:5B:187:LEU:HA	4:5B:190:HIS:CE1	2.53	0.43
3:5C:274:PRO:HG2	3:5C:371:VAL:HG11	2.00	0.43
4:5H:86:ARG:HH12	4:6H:282:ARG:HB3	1.83	0.43
4:5H:102:ALA:HB2	4:5H:403:MET:HE3	2.00	0.43
4:5J:355:ASP:HB3	4:5J:356:ILE:HD12	1.99	0.43
3:5M:175:PRO:HG3	3:5M:390:ARG:NH2	2.34	0.43
6:64:881:THR:HG22	9:B1:54:ILE:HA	2.00	0.43
6:65:466:CYS:HA	6:65:469:ARG:HD3	2.00	0.43
6:67:883:ALA:HB2	9:B7:511:LEU:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6B:248:SER:HA	4:6B:252:LYS:HD3	2.00	0.43
3:6M:320:ARG:HE	3:6M:360:PRO:HG3	1.83	0.43
4:6N:19:LYS:HE3	4:6N:19:LYS:HB3	1.85	0.43
4:6N:423:GLN:HA	4:6N:426:GLN:HG2	2.00	0.43
4:7B:73:MET:HA	4:7B:76:VAL:HG12	2.01	0.43
4:7D:283:ALA:O	4:7D:288:GLU:HG2	2.18	0.43
3:7E:254:GLU:HA	3:7E:257:THR:HB	2.00	0.43
3:7I:244:PHE:CE2	3:7I:358:GLN:HG2	2.53	0.43
4:7L:377:MET:HA	4:7L:380:ARG:HG2	2.00	0.43
7:80:330:ARG:HH22	7:80:350:ARG:HH12	1.66	0.43
7:87:352:VAL:HG11	7:87:379:LEU:HD21	1.99	0.43
7:87:356:LEU:HD12	7:87:362:GLU:HB2	2.00	0.43
4:8D:229:VAL:HA	4:8D:300:MET:HE1	1.99	0.43
3:8E:169:PHE:CZ	3:8E:238:LEU:HD22	2.53	0.43
4:8F:267:LEU:O	4:8F:368:VAL:HA	2.18	0.43
4:8F:356:ILE:HG23	1:l:823:LEU:HD22	2.01	0.43
3:8M:88:HIS:HE1	3:9M:280:LYS:HA	1.83	0.43
2:9:275:GLU:HA	2:9:278:HIS:CD2	2.53	0.43
3:9A:320:ARG:NH1	3:9A:358:GLN:HB2	2.34	0.43
4:9B:54:ALA:HB3	4:9B:58:ARG:HB3	2.00	0.43
4:9F:202:ILE:HD12	4:9F:268:ILE:HG21	2.00	0.43
3:9G:406:HIS:HA	3:9G:409:VAL:HG12	1.99	0.43
4:9H:139:LEU:HD23	4:9H:171:PRO:HD2	2.00	0.43
3:9I:228:ASN:HA	3:9I:231:ILE:HG22	2.00	0.43
4:9J:165:GLU:HB2	4:9J:200:GLN:NE2	2.33	0.43
4:9L:391:ARG:HH21	4:9L:393:ALA:HB2	1.83	0.43
9:B4:123:LYS:HE3	9:B4:125:HIS:HE1	1.82	0.43
9:B7:475:ASN:HD21	9:B7:539:ARG:H	1.67	0.43
10:C0:305:LEU:O	10:C0:309:ILE:HD12	2.18	0.43
10:D3:288:PRO:HB2	10:D3:293:MET:HE3	1.99	0.43
10:D3:345:MET:HE2	10:D3:369:SER:HB2	1.99	0.43
10:D4:120:PRO:HD3	10:D4:130:PRO:HB3	2.00	0.43
10:D6:97:ILE:HG21	10:D6:397:PHE:HD2	1.82	0.43
10:D9:66:LEU:HD13	10:D9:312:LYS:HD2	2.00	0.43
10:E2:67:ALA:O	10:E2:71:GLN:HG2	2.18	0.43
12:F5:218:VAL:HG12	12:F5:239:ARG:HH22	1.83	0.43
12:G2:264:ILE:HG23	12:G2:268:ARG:NH2	2.31	0.43
13:J7:401:LYS:HD3	13:J7:404:ILE:HD12	2.00	0.43
14:K4:199:ILE:HG22	14:K4:207:ILE:HD13	2.00	0.43
1:A:451:THR:HA	1:A:454:GLU:HG2	2.00	0.43
1:E:372:LEU:HB3	1:E:377:HIS:HE1	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:643:ARG:HD3	4:8B:57:GLY:HA3	2.00	0.43
1:M:665:THR:HG22	3:9G:370:LYS:HZ2	1.81	0.43
2:11:179:MET:O	2:11:183:ARG:HB2	2.18	0.43
3:1A:120:ASP:HB3	3:1A:124:LYS:NZ	2.34	0.43
3:1A:180:ALA:HB3	3:1A:183:GLU:HB2	2.00	0.43
3:1A:407:TRP:HZ3	4:1B:255:VAL:HA	1.83	0.43
3:1C:90:GLU:HB3	3:1C:121:ARG:HD3	1.99	0.43
3:1C:411:GLU:HG2	3:1C:412:GLY:H	1.83	0.43
4:1D:239:CYS:HB3	4:1D:248:SER:H	1.83	0.43
3:1E:121:ARG:HD2	3:1E:121:ARG:HA	1.72	0.43
3:1E:222:PRO:HD2	4:1F:324:LYS:HD3	2.01	0.43
3:1G:217:LEU:HB3	3:1G:219:ILE:HG12	2.00	0.43
5:21:155:LYS:HG3	5:21:177:VAL:HG12	1.99	0.43
5:29:105:LEU:HD21	5:29:110:PHE:HB2	1.99	0.43
4:2B:132:GLY:HA2	4:2B:162:ARG:HB3	2.00	0.43
3:2E:17:GLY:HA2	3:2E:20:CYS:SG	2.59	0.43
4:2F:213:ARG:HB3	4:2F:297:LYS:HZ1	1.82	0.43
3:2G:217:LEU:HD11	3:2G:230:LEU:HD21	1.99	0.43
4:2H:180:VAL:HG23	4:2H:184:ASN:HD21	1.84	0.43
3:2I:147:SER:HB2	3:2I:190:SER:HB2	2.00	0.43
3:2I:306:ASP:HB3	3:2I:309:HIS:CE1	2.53	0.43
4:2J:148:GLY:O	4:2J:152:ILE:HG12	2.18	0.43
4:2J:361:LEU:H	4:2J:361:LEU:HG	1.66	0.43
5:30:167:LYS:HE3	6:66:359:PRO:HG3	2.00	0.43
5:38:214:LYS:HG3	5:38:221:LEU:HD22	2.01	0.43
4:3D:289:LEU:HD11	4:3D:363:MET:HG2	1.99	0.43
4:3F:208:TYR:CD2	3:3G:326:LYS:HG2	2.54	0.43
4:3H:391:ARG:HH21	3:3I:435:VAL:HA	1.84	0.43
4:3J:46:ARG:HB2	4:3J:241:ARG:HA	2.00	0.43
3:3K:130:THR:HG21	6:69:859:THR:HG21	2.00	0.43
5:47:26:THR:HG22	5:47:29:ILE:HD12	2.00	0.43
3:4A:163:LYS:HE3	6:67:810:LYS:HE3	2.00	0.43
3:4A:168:ASN:O	3:4A:201:ALA:HA	2.18	0.43
4:4H:356:ILE:HD13	8:A5:171:SER:HB3	2.00	0.43
4:4J:187:LEU:HD21	4:4J:408:PHE:CD1	2.53	0.43
3:4M:209:ILE:HG12	3:4M:302:MET:HB2	2.00	0.43
5:51:77:ILE:HG12	5:51:81:GLU:HA	2.00	0.43
5:58:74:LYS:HB2	5:58:90:GLU:HB3	2.00	0.43
3:5G:334:THR:HA	3:5G:337:THR:HG22	1.99	0.43
3:5I:5:ILE:HD12	3:5I:125:LEU:HG	1.98	0.43
3:5M:282:TYR:HD1	3:5M:283:HIS:CD2	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5N:379:LYS:HE3	4:5N:419:VAL:HG21	1.99	0.43
4:5N:385:PHE:O	4:5N:389:PHE:HB2	2.18	0.43
2:6:256:LEU:O	2:6:260:ARG:HG2	2.19	0.43
2:6:296:ASP:O	2:6:300:VAL:HG23	2.17	0.43
5:62:31:GLU:HA	5:62:36:LEU:HD13	2.00	0.43
6:64:619:ALA:O	6:64:623:CYS:HB2	2.19	0.43
6:68:256:VAL:HA	6:68:259:LEU:HD12	1.99	0.43
6:69:598:VAL:O	6:69:602:ARG:HG2	2.18	0.43
4:6B:6:HIS:CG	4:6B:134:GLN:HE21	2.36	0.43
3:6M:79:ARG:NH1	3:6M:92:LEU:HB3	2.34	0.43
7:72:268:TRP:HD1	7:72:325:PHE:HD2	1.67	0.43
7:72:281:LEU:HD21	7:72:300:GLN:HB2	2.00	0.43
7:76:328:PRO:HG2	7:76:333:LEU:HD11	2.01	0.43
3:7C:280:LYS:HA	3:7C:283:HIS:NE2	2.33	0.43
3:7E:319:TYR:HB3	3:7E:323:VAL:HG11	1.98	0.43
4:7F:54:ALA:HB3	4:7F:58:ARG:HB3	2.00	0.43
3:7I:223:THR:HG22	4:7J:322:SER:HA	2.00	0.43
4:7J:302:ALA:HB3	4:7J:380:ARG:HH12	1.84	0.43
4:7L:187:LEU:HA	4:7L:190:HIS:HD2	1.84	0.43
7:80:268:TRP:CD1	7:80:328:PRO:HD3	2.53	0.43
7:87:281:LEU:HD11	7:87:300:GLN:HB3	2.00	0.43
7:89:330:ARG:HD2	7:89:350:ARG:HH22	1.83	0.43
3:8A:388:PHE:HB3	3:8A:425:LEU:HD12	2.01	0.43
3:8G:267:PHE:HB3	3:8G:384:ILE:HD13	2.01	0.43
3:8G:434:GLU:HB3	14:M3:72:VAL:HG21	1.99	0.43
4:8L:87:PRO:HA	4:8L:90:PHE:HB2	2.01	0.43
4:8L:129:CYS:HB2	4:8L:162:ARG:HH21	1.84	0.43
4:8L:404:ASP:O	4:8L:407:GLU:HG2	2.18	0.43
7:91:279:ARG:HE	7:91:279:ARG:HB3	1.57	0.43
7:97:408:ILE:HG23	4:9B:174:LYS:HB3	2.00	0.43
4:9F:205:GLU:HA	4:9F:208:TYR:HB2	1.99	0.43
4:9L:66:MET:HE2	4:9L:147:MET:HE2	2.01	0.43
8:A1:96:LYS:HA	8:A1:99:MET:HG3	1.99	0.43
8:A5:234:ARG:HD2	8:A5:239:ILE:HG12	2.01	0.43
8:A9:382:LEU:HA	8:A9:385:VAL:HG12	2.01	0.43
9:B7:535:ARG:HA	9:B7:535:ARG:HD2	1.83	0.43
10:C0:85:PRO:HB2	10:C0:313:TYR:HE2	1.83	0.43
11:C1:240:PRO:HB2	11:C1:242:ASN:HD21	1.83	0.43
10:C6:349:PHE:CD1	10:C6:361:TRP:HB3	2.54	0.43
10:D2:343:ALA:O	10:D2:347:GLU:HG2	2.17	0.43
10:D3:308:VAL:HA	10:D3:311:LYS:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D9:72:GLY:HA2	14:L1:211:ASP:CG	2.43	0.43
10:E5:293:MET:O	10:E5:297:ARG:HG3	2.18	0.43
13:J2:397:LEU:HG	13:J2:447:LEU:HD11	1.99	0.43
13:J5:396:GLN:HG2	13:J5:399:ALA:H	1.83	0.43
13:J6:405:VAL:HG13	13:J6:409:LEU:HD12	2.00	0.43
13:J6:445:LEU:HB3	13:J6:484:ILE:HD13	1.99	0.43
14:K8:182:TYR:HE1	14:K8:199:ILE:HG13	1.83	0.43
14:L3:233:LEU:HA	14:L3:236:PHE:CD2	2.49	0.43
14:M5:156:LEU:HB3	14:M5:189:ILE:HD12	2.01	0.43
14:M7:97:ARG:HB2	14:M7:123:SER:HA	2.01	0.43
1:b:342:MET:HA	1:e:342:MET:HE1	2.00	0.43
1:G:326:GLU:O	1:G:330:ARG:HG2	2.19	0.43
1:I:680:LEU:HD21	1:J:681:ILE:HD13	1.99	0.43
1:M:617:MET:HG3	1:N:618:ARG:HD3	2.00	0.43
1:P:658:ALA:HA	1:P:661:ASN:HD21	1.83	0.43
1:Q:376:MET:HA	1:Q:376:MET:HE2	2.01	0.43
1:Y:495:PHE:HB3	1:c:495:PHE:CE2	2.53	0.43
1:Y:610:VAL:HG11	1:c:611:THR:CG2	2.41	0.43
3:1A:385:ALA:HA	3:1A:388:PHE:HB3	2.00	0.43
4:1B:73:MET:HA	4:1B:76:VAL:HG22	2.00	0.43
3:1C:212:ILE:HG23	3:1C:216:ASN:HD22	1.83	0.43
3:1E:268:MET:HG3	3:1E:380:ASN:N	2.32	0.43
4:1H:178:THR:HB	4:1H:181:GLU:HB3	2.00	0.43
4:1L:65:LEU:HB3	4:1L:73:MET:HE2	2.00	0.43
3:1M:323:VAL:HB	3:1M:373:ARG:HD3	2.00	0.43
5:27:109:LEU:HD13	6:65:364:THR:HG22	2.00	0.43
4:2B:262:ARG:HD2	5:32:216:LYS:NZ	2.33	0.43
3:2C:264:ARG:H	6:66:543:GLN:NE2	2.17	0.43
3:2E:105:ARG:HG2	3:2E:411:GLU:HG2	2.00	0.43
4:2F:139:LEU:HD12	4:2F:139:LEU:HA	1.69	0.43
4:2F:164:MET:HE2	4:2F:164:MET:HB2	1.88	0.43
4:2F:323:THR:HG22	4:2F:353:VAL:HG21	2.00	0.43
4:2H:117:LEU:HD21	4:2H:154:LYS:HB3	2.00	0.43
3:2I:155:GLU:HG2	3:2I:197:HIS:CE1	2.54	0.43
3:2I:333:ALA:O	3:2I:337:THR:HG23	2.19	0.43
3:2K:107:HIS:HA	3:2K:152:LEU:HD22	2.01	0.43
3:2M:125:LEU:HD12	3:2M:125:LEU:HA	1.83	0.43
5:30:24:VAL:HG21	5:30:201:LEU:HB3	2.00	0.43
5:30:218:PRO:HA	5:30:221:LEU:HB2	2.01	0.43
5:31:221:LEU:O	5:31:225:GLN:HB2	2.18	0.43
5:33:167:LYS:HD3	5:33:169:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3A:390:ARG:O	3:3A:394:LYS:HG2	2.19	0.43
4:3B:229:VAL:O	4:3B:233:MET:HG3	2.18	0.43
3:3C:259:LEU:HD11	3:3C:316:CYS:HB2	2.00	0.43
4:3D:138:SER:HA	4:3D:169:VAL:HG22	2.00	0.43
4:3D:149:THR:HG21	4:3D:188:SER:HB2	2.01	0.43
3:3E:216:ASN:HB3	3:3E:275:ILE:O	2.18	0.43
4:3H:269:GLY:HA2	4:3H:300:MET:HE3	2.01	0.43
3:3I:142:GLY:HA3	3:3I:183:GLU:HG2	2.00	0.43
4:3J:135:ILE:HG13	4:3J:152:ILE:HD11	2.01	0.43
4:3L:248:SER:HA	4:3L:252:LYS:HG2	2.00	0.43
3:4A:169:PHE:HZ	3:4A:238:LEU:HD13	1.84	0.43
4:4B:179:VAL:HG12	3:4C:258:ASN:HB3	2.00	0.43
3:4E:288:VAL:HA	3:4E:291:ILE:HG12	1.99	0.43
3:4E:431:ASP:O	3:4E:435:VAL:HB	2.18	0.43
4:4J:284:LEU:HB3	4:4J:363:MET:HG2	2.00	0.43
3:4K:223:THR:HG22	3:4K:224:TYR:H	1.83	0.43
4:4L:271:ALA:HB2	4:4L:298:ASN:ND2	2.34	0.43
3:4M:317:LEU:HB3	3:4M:319:TYR:CE1	2.52	0.43
5:50:51:GLU:HB3	5:50:147:VAL:HA	2.01	0.43
4:5B:68:LEU:HB3	4:5B:96:GLY:HA2	2.00	0.43
3:5E:248:LEU:HD13	3:5E:355:ILE:HD13	2.00	0.43
3:5M:210:TYR:HB3	4:5N:324:LYS:HD2	2.01	0.43
5:60:162:GLN:HB2	5:60:171:LEU:HD23	2.00	0.43
6:63:403:ALA:HA	6:63:406:ARG:HE	1.82	0.43
6:68:260:TRP:CD1	6:68:437:ARG:HG3	2.52	0.43
3:6E:401:LYS:HE2	3:6E:401:LYS:HB3	1.84	0.43
4:6H:174:LYS:HD2	7:75:412:MET:HA	2.00	0.43
3:6M:109:THR:HB	14:L4:172:ARG:HH12	1.83	0.43
4:6N:191:GLN:HB3	14:L4:133:VAL:HG11	2.00	0.43
7:78:330:ARG:HH12	7:78:376:GLU:HG2	1.84	0.43
3:7A:23:LEU:O	3:7A:27:GLU:HG2	2.18	0.43
4:7B:320:ARG:HH12	1:q:932:LEU:HD21	1.83	0.43
3:7C:83:TYR:HB3	3:7C:87:PHE:HE2	1.82	0.43
3:7C:419:SER:O	3:7C:423:GLU:HG2	2.19	0.43
3:7E:159:VAL:HG13	7:86:351:LYS:HB3	2.00	0.43
3:7E:269:LEU:HD21	3:7E:305:CYS:HB3	2.00	0.43
4:7H:208:TYR:CE2	7:82:408:ILE:HG13	2.53	0.43
3:7M:60:LYS:HZ1	3:7M:86:LEU:HA	1.83	0.43
2:8:161:LEU:HA	2:8:164:GLU:HG3	2.01	0.43
7:85:380:TRP:CD2	7:85:386:ARG:HG2	2.54	0.43
3:8A:240:ALA:HB3	3:8A:320:ARG:NH2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8B:156:ARG:HD3	4:8B:164:MET:HE2	1.99	0.43
3:8C:208:ALA:HB2	3:8C:304:LYS:HG2	1.99	0.43
3:8I:430:LYS:O	3:8I:434:GLU:HB2	2.18	0.43
4:8J:6:HIS:CD2	4:8J:134:GLN:HG3	2.54	0.43
4:8J:299:MET:HE1	4:8J:367:PHE:HD2	1.82	0.43
3:8K:138:PHE:HZ	3:8K:235:ILE:HD13	1.84	0.43
4:8L:113:ILE:HD11	4:8L:147:MET:SD	2.58	0.43
4:8L:262:ARG:HA	4:8L:264:HIS:HD2	1.83	0.43
2:9:307:MET:HA	2:9:310:PHE:CE1	2.53	0.43
7:91:308:TYR:CE1	7:91:322:PRO:HB2	2.53	0.43
4:9B:273:LEU:HA	4:9B:273:LEU:HD23	1.75	0.43
3:9C:76:ASP:HA	3:9C:79:ARG:HB2	2.00	0.43
3:9C:262:TYR:HD2	3:9C:265:ILE:HD13	1.84	0.43
4:9H:321:MET:HE3	4:9H:353:VAL:HG22	1.99	0.43
3:9M:172:TRP:HE1	3:9M:391:MET:HG3	1.83	0.43
8:A6:382:LEU:O	8:A6:386:ARG:HD3	2.18	0.43
9:B6:36:GLU:HB3	9:B6:44:LEU:HD12	1.99	0.43
10:E2:296:MET:SD	10:E2:389:PHE:HB2	2.58	0.43
10:E7:287:PRO:HA	10:E7:288:PRO:HD3	1.90	0.43
10:F3:300:ILE:HD11	10:F3:389:PHE:HD1	1.82	0.43
12:G4:241:LEU:HA	12:G4:244:ARG:HH11	1.84	0.43
12:G7:247:VAL:HA	12:G7:250:ARG:HE	1.83	0.43
12:H0:332:THR:HA	12:H0:335:ILE:HG12	2.01	0.43
13:J1:377:LEU:HB3	13:J1:421:VAL:HG21	2.01	0.43
13:J1:380:ALA:HB1	13:J1:394:TYR:H	1.83	0.43
13:J2:516:GLU:HA	13:J2:519:LEU:HD23	2.00	0.43
14:M1:159:ASN:HB2	14:M1:222:THR:HG22	2.00	0.43
1:f:541:ASN:O	1:f:542:ALA:C	2.61	0.43
1:f:662:ASP:O	1:f:666:VAL:HG23	2.19	0.43
1:I:379:ARG:HH12	1:I:383:ALA:HB2	1.84	0.43
1:P:675:LYS:O	1:P:679:ARG:HD3	2.18	0.43
1:X:673:LEU:HD23	1:X:673:LEU:HA	1.92	0.43
4:1B:66:MET:HE1	4:1B:151:LEU:HD22	2.01	0.43
4:1H:34:GLY:HA3	4:1H:58:ARG:HD2	2.00	0.43
4:1J:288:GLU:HA	4:1J:291:GLN:HG2	1.99	0.43
3:1K:322:ASP:HB3	3:1K:373:ARG:HH21	1.81	0.43
4:1L:58:ARG:HA	4:1L:58:ARG:HD2	1.74	0.43
3:1M:71:GLU:HG3	3:1M:73:THR:H	1.83	0.43
3:1M:240:ALA:HB1	3:1M:356:ASN:HD22	1.82	0.43
4:1N:135:ILE:HB	4:1N:166:THR:HA	2.00	0.43
5:28:77:ILE:HD13	5:28:87:VAL:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2A:192:HIS:CE1	6:67:135:LYS:HB2	2.54	0.43
4:2B:135:ILE:HG22	4:2B:137:HIS:H	1.82	0.43
3:2C:195:LEU:HD13	3:2C:264:ARG:HE	1.82	0.43
4:2D:131:GLN:HE21	4:2D:250:LEU:HB2	1.84	0.43
4:2F:183:TYR:HA	4:2F:385:PHE:HE2	1.84	0.43
3:2G:269:LEU:HD13	3:2G:301:MET:SD	2.58	0.43
4:2H:7:VAL:HG23	4:2H:64:ILE:HB	1.99	0.43
4:2L:164:MET:H	4:2L:197:ASP:HB3	1.84	0.43
4:2L:285:SER:O	4:2L:288:GLU:HG2	2.18	0.43
4:3B:46:ARG:HG2	4:3B:241:ARG:HA	2.01	0.43
4:3B:94:GLN:HG3	6:66:931:PRO:HD3	2.00	0.43
4:3D:219:THR:HG23	3:3E:324:VAL:HG22	2.01	0.43
3:3E:261:PRO:HB2	3:3E:262:TYR:CD1	2.53	0.43
3:3E:338:LYS:HG2	3:3E:339:ARG:H	1.82	0.43
4:3L:372:THR:HG23	4:3L:422:TYR:HD1	1.83	0.43
3:3M:70:LEU:HD12	3:3M:145:THR:HG22	1.99	0.43
3:3M:168:ASN:OD1	3:3M:198:THR:HG21	2.19	0.43
5:49:206:LEU:HB3	5:50:21:LEU:HD21	2.00	0.43
4:4D:2:ARG:HB3	4:4D:131:GLN:HB2	2.00	0.43
5:56:180:THR:HG23	5:56:183:PHE:H	1.84	0.43
5:57:48:VAL:HG22	5:57:138:ILE:HG23	1.99	0.43
5:58:55:GLN:HG3	5:58:151:HIS:ND1	2.33	0.43
4:5B:268:ILE:HD13	4:5B:368:VAL:HG22	2.00	0.43
3:5C:133:GLN:HB3	3:5C:252:VAL:HB	2.00	0.43
3:5E:203:MET:HG3	3:5E:384:ILE:HD11	2.01	0.43
4:5F:119:VAL:HG23	4:5F:122:LYS:HE3	2.01	0.43
3:5G:318:MET:HE3	3:5G:318:MET:HB3	1.90	0.43
3:5K:99:ALA:HA	3:5K:110:ILE:HD11	2.00	0.43
3:5K:132:LEU:HD22	3:5K:164:LYS:HG2	2.01	0.43
4:5N:395:LEU:HA	4:5N:398:TYR:HB3	2.00	0.43
5:61:40:HIS:HD2	5:61:76:LEU:HB3	1.83	0.43
6:65:886:HIS:HD1	9:B3:542:TRP:CG	2.36	0.43
6:66:500:ARG:HA	6:66:503:LYS:HE2	2.00	0.43
6:68:496:ASP:O	6:68:500:ARG:HG2	2.19	0.43
4:6B:252:LYS:HA	4:6B:255:VAL:HG12	2.00	0.43
3:6E:115:VAL:HG21	3:6E:152:LEU:HD23	2.00	0.43
4:6J:164:MET:HE2	4:6J:164:MET:HB2	1.84	0.43
7:71:389:GLN:HE22	14:K2:120:GLU:HB3	1.83	0.43
7:78:261:ALA:HA	7:78:391:TYR:CD2	2.53	0.43
3:7A:101:ASN:HB3	4:7B:252:LYS:HE2	2.01	0.43
3:7E:312:TYR:HA	3:7E:381:SER:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7F:385:PHE:HE2	4:7F:412:GLU:HB2	1.84	0.43
3:7G:125:LEU:HD23	3:7G:125:LEU:HA	1.89	0.43
3:7K:352:LYS:HD2	3:7K:352:LYS:HA	1.69	0.43
4:7L:208:TYR:HB2	7:84:412:MET:HE2	2.01	0.43
3:7M:413:MET:HE3	3:7M:413:MET:HB3	1.81	0.43
2:8:276:GLU:HA	2:8:279:ASN:ND2	2.34	0.43
7:84:299:PHE:CE2	14:L3:126:ILE:HD12	2.52	0.43
7:85:347:ILE:HG21	7:85:350:ARG:HB2	2.01	0.43
4:8B:11:GLN:HB2	4:8B:72:THR:HG21	2.01	0.43
3:8G:60:LYS:HE3	3:8G:60:LYS:HB3	1.87	0.43
3:8I:248:LEU:HB3	3:8I:355:ILE:H	1.82	0.43
4:8J:47:ILE:HG13	4:8J:51:TYR:HB2	2.01	0.43
4:8L:165:GLU:HG3	4:8L:250:LEU:HD13	1.99	0.43
3:8M:250:VAL:HG23	3:8M:254:GLU:HB3	1.99	0.43
7:96:296:ARG:HD2	7:96:317:GLN:HG2	1.99	0.43
3:9A:104:ALA:O	3:9A:108:TYR:HB2	2.17	0.43
3:9A:180:ALA:HB3	3:9A:183:GLU:HG2	2.01	0.43
4:9B:103:LYS:HD3	4:9B:103:LYS:HA	1.86	0.43
4:9B:248:SER:HA	4:9B:252:LYS:HD3	2.00	0.43
3:9C:16:ILE:HA	3:9C:228:ASN:HB3	1.98	0.43
4:9L:156:ARG:HH22	4:9L:164:MET:HB2	1.82	0.43
9:B5:513:LYS:HD3	9:B5:513:LYS:HA	1.79	0.43
10:C7:352:TYR:HE2	10:C7:376:ILE:HD11	1.83	0.43
10:E4:341:TYR:HA	10:E4:390:MET:HE1	2.00	0.43
10:F2:100:SER:HB2	10:F2:389:PHE:HZ	1.83	0.43
13:J2:343:ALA:HA	13:J2:347:GLN:HG2	2.00	0.43
13:J5:446:VAL:HG22	13:J5:485:ILE:HB	2.00	0.43
1:a:617:MET:HB3	1:f:618:ARG:NH1	2.34	0.43
1:D:669:GLU:O	1:D:673:LEU:HB2	2.19	0.43
1:I:537:LEU:HD23	1:J:541:ASN:HD22	1.83	0.43
1:I:589:THR:HG23	1:J:590:GLU:HG3	1.99	0.43
1:J:407:GLU:O	1:J:411:LYS:HG2	2.18	0.43
1:L:379:ARG:NH1	1:L:383:ALA:HB2	2.34	0.43
1:M:499:ARG:CG	1:N:499:ARG:HH22	2.32	0.43
1:M:633:ASP:O	1:M:637:THR:HG23	2.18	0.43
1:N:512:LYS:HA	1:N:515:VAL:HG22	2.00	0.43
1:T:629:LYS:HG2	1:i:771:VAL:HG21	2.00	0.43
1:U:517:GLU:O	1:U:520:TRP:HB3	2.19	0.43
2:12:171:MET:HA	2:12:174:GLN:HB3	2.00	0.43
2:14:245:GLU:O	2:14:249:LYS:HG2	2.19	0.43
4:1B:292:GLN:HG3	4:1B:298:ASN:ND2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1C:11:GLN:NE2	4:1D:247:ASN:H	2.04	0.43
3:1E:429:GLU:HA	3:1E:432:TYR:HD2	1.84	0.43
3:1G:70:LEU:HD12	3:1G:99:ALA:HB2	2.01	0.43
3:1I:168:ASN:O	3:1I:201:ALA:HA	2.19	0.43
3:1M:431:ASP:HA	3:1M:434:GLU:HG3	2.00	0.43
5:20:183:PHE:HA	5:20:186:ARG:HG2	1.99	0.43
5:25:77:ILE:HG22	5:25:87:VAL:HG22	1.99	0.43
5:27:113:MET:HE1	5:27:116:ARG:NH2	2.34	0.43
3:2I:174:SER:HB2	3:2I:207:GLU:HG3	2.00	0.43
4:2L:14:ASN:HD22	4:2L:72:THR:HG23	1.84	0.43
4:2L:221:THR:HG23	4:2L:223:GLY:H	1.83	0.43
3:2M:3:GLU:OE2	3:2M:129:CYS:HB3	2.18	0.43
2:3:177:ARG:HA	2:3:180:LYS:HE2	2.00	0.43
5:35:221:LEU:O	5:35:225:GLN:HB2	2.19	0.43
5:38:61:LEU:HA	5:38:62:PRO:HD3	1.84	0.43
5:38:196:LYS:HA	5:38:199:LEU:HD12	2.01	0.43
5:39:36:LEU:HD21	5:39:42:LEU:HB2	2.01	0.43
5:39:195:LEU:HD11	5:40:199:LEU:HD11	2.00	0.43
4:3B:67:ASP:HA	4:3B:143:THR:HG21	2.01	0.43
3:3E:219:ILE:HD12	3:3E:219:ILE:HA	1.93	0.43
3:3K:27:GLU:HG2	3:3K:361:THR:HG21	2.01	0.43
3:3K:119:LEU:HD11	3:3K:156:ARG:HB3	2.01	0.43
3:3K:191:THR:HG21	3:3K:425:LEU:HD21	2.00	0.43
3:3M:209:ILE:HG23	3:3M:230:LEU:HD23	2.01	0.43
5:40:211:CYS:HA	5:40:214:LYS:HE2	2.01	0.43
5:47:207:HIS:CE1	13:J7:508:CYS:H	2.33	0.43
5:48:33:ASP:HB3	5:48:36:LEU:HB2	2.00	0.43
5:49:129:VAL:O	5:49:133:MET:HG2	2.18	0.43
3:4G:265:ILE:HG23	3:4G:432:TYR:CZ	2.54	0.43
4:4H:372:THR:HG23	4:4H:422:TYR:HB3	2.01	0.43
3:4I:223:THR:HG23	3:4I:225:THR:H	1.84	0.43
3:5A:10:GLY:HA2	3:5A:145:THR:HG23	2.01	0.43
3:5E:250:VAL:HG11	3:5E:352:LYS:HD2	2.01	0.43
3:5E:255:PHE:HZ	3:5E:378:ILE:HG21	1.84	0.43
4:5J:164:MET:HB3	4:5J:197:ASP:H	1.83	0.43
3:5K:109:THR:HG22	14:K6:172:ARG:NH2	2.34	0.43
4:5L:87:PRO:HA	4:5L:90:PHE:HD2	1.82	0.43
6:63:915:ASN:HB3	6:63:918:ALA:HB2	2.01	0.43
6:65:134:PRO:HG3	6:65:546:HIS:NE2	2.33	0.43
6:66:636:GLU:HA	6:66:639:LEU:HB2	2.00	0.43
3:6E:276:ILE:HD11	3:6E:280:LYS:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6M:168:ASN:HB3	3:6M:201:ALA:HA	2.01	0.43
7:73:352:VAL:HG21	14:K3:242:ILE:HG23	2.00	0.43
7:78:278:VAL:HG12	7:78:302:PRO:HG3	1.99	0.43
4:7B:49:VAL:HG11	4:7B:241:ARG:HG2	2.00	0.43
4:7D:77:ARG:HH21	4:7D:90:PHE:HD2	1.67	0.43
4:7D:173:PRO:HA	4:7D:380:ARG:HD2	2.01	0.43
4:7D:201:VAL:HB	4:7D:377:MET:HE1	2.01	0.43
3:7G:11:GLN:HG2	3:7G:74:VAL:HG11	2.00	0.43
4:7H:69:GLU:HB3	4:7H:96:GLY:HA2	1.99	0.43
3:7I:119:LEU:O	3:7I:123:ARG:HG2	2.18	0.43
4:7J:217:LEU:HD23	4:7J:220:PRO:HB3	2.00	0.43
4:7L:397:TRP:CZ2	3:7M:257:THR:HA	2.53	0.43
7:89:258:GLU:HA	7:89:261:ALA:HB3	2.01	0.43
3:8E:71:GLU:HG3	4:8F:2:ARG:HH22	1.83	0.43
4:8F:107:THR:HB	4:8F:108:GLU:H	1.69	0.43
4:8J:167:PHE:CE2	4:8J:233:MET:HG2	2.54	0.43
4:8J:322:SER:O	4:8J:326:VAL:HG23	2.19	0.43
3:8K:386:GLU:HA	3:8K:389:SER:HB3	2.01	0.43
7:94:378:MET:HE2	14:M7:240:TRP:H	1.83	0.43
4:9B:65:LEU:HD11	4:9B:90:PHE:CD1	2.53	0.43
4:9D:179:VAL:HG13	3:9E:350:GLY:HA2	1.99	0.43
4:9H:164:MET:H	4:9H:197:ASP:HB2	1.82	0.43
3:9I:319:TYR:HB3	3:9I:323:VAL:HG11	2.01	0.43
4:9J:8:GLN:HE21	4:9J:14:ASN:HA	1.82	0.43
8:A2:324:TYR:HD1	8:A2:330:SER:HA	1.83	0.43
9:B7:130:LEU:HD21	9:B7:137:ARG:HD3	2.00	0.43
10:E3:94:VAL:HA	10:E3:97:ILE:HG22	2.00	0.43
10:E3:401:MET:HE3	10:E3:401:MET:HB3	1.87	0.43
12:G2:247:VAL:HA	12:G2:250:ARG:HE	1.84	0.43
13:J3:287:GLU:HG3	13:J3:605:ARG:HH22	1.83	0.43
14:L5:72:VAL:HG22	14:L5:75:ARG:HH21	1.83	0.43
1:a:629:LYS:HE2	1:a:629:LYS:HB2	1.58	0.43
1:a:682:LYS:HE2	1:a:682:LYS:HB2	1.57	0.43
1:f:513:ARG:HB3	1:f:514:ALA:H	1.74	0.43
1:i:829:PRO:HD2	1:i:834:ARG:NH2	2.33	0.43
1:m:797:VAL:HG22	1:m:798:ARG:H	1.84	0.43
1:F:523:VAL:HA	1:F:526:GLU:HG2	2.01	0.43
1:I:614:LEU:O	1:I:618:ARG:HG2	2.18	0.43
1:J:500:ARG:HD2	1:J:504:ARG:HH12	1.83	0.43
1:K:433:ALA:HA	1:K:436:VAL:HG12	2.01	0.43
1:M:521:LYS:HD2	1:M:521:LYS:HA	1.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:487:HIS:O	1:N:490:GLN:HG3	2.19	0.43
1:N:647:LYS:HB2	1:N:647:LYS:HE2	1.70	0.43
1:Q:479:ASP:HB3	1:u:922:ARG:NH2	2.33	0.43
1:Q:638:LEU:HD13	1:U:638:LEU:HB3	2.01	0.43
1:V:523:VAL:HG22	1:V:527:LEU:HD23	2.00	0.43
1:Z:365:LEU:HA	1:Z:365:LEU:HD23	1.80	0.43
2:11:298:LEU:HD23	2:11:298:LEU:HA	1.86	0.43
4:1D:201:VAL:HG11	4:1D:374:ILE:HD11	2.00	0.43
4:1F:177:ASP:HB2	3:1G:352:LYS:O	2.18	0.43
3:1G:316:CYS:HA	3:1G:352:LYS:HB3	2.01	0.43
4:1H:183:TYR:HB3	4:1H:398:TYR:HE2	1.83	0.43
4:1J:239:CYS:HB3	4:1J:247:ASN:HA	2.01	0.43
3:1K:297:GLU:HA	3:1K:298:PRO:HD3	1.80	0.43
5:21:40:HIS:CD2	5:21:88:ARG:HH21	2.36	0.43
5:24:179:SER:HB2	5:24:183:PHE:HD2	1.84	0.43
5:27:207:HIS:NE2	5:30:18:VAL:HG22	2.33	0.43
4:2B:212:PHE:HB3	4:2B:213:ARG:CZ	2.48	0.43
4:2D:66:MET:HE3	4:2D:116:VAL:HG21	1.99	0.43
4:2J:19:LYS:HA	4:2J:19:LYS:HD3	1.82	0.43
4:2J:98:GLY:H	4:2J:103:LYS:HD3	1.83	0.43
4:2L:171:PRO:HB3	4:2L:181:GLU:OE1	2.18	0.43
3:2M:212:ILE:O	3:2M:216:ASN:HB2	2.18	0.43
5:35:120:MET:HE3	5:38:167:LYS:HA	2.01	0.43
5:35:136:SER:HB3	5:35:144:PHE:CD2	2.54	0.43
3:3A:224:TYR:HE2	4:3B:246:LEU:HG	1.84	0.43
4:3B:317:PHE:HE2	4:3B:326:VAL:HG13	1.84	0.43
3:3C:136:LEU:HD13	3:3C:235:ILE:HD11	2.01	0.43
3:3I:320:ARG:HD3	3:3I:374:ALA:HB3	2.01	0.43
4:3J:220:PRO:HB3	8:A7:255:ARG:HH22	1.82	0.43
3:3K:214:ARG:HD2	4:3L:324:LYS:HE3	2.00	0.43
5:42:204:ALA:HA	5:42:207:HIS:CD2	2.53	0.43
5:42:206:LEU:HD23	5:42:206:LEU:HA	1.91	0.43
3:4A:178:SER:O	3:4A:183:GLU:HG3	2.19	0.43
3:4A:220:GLU:HG2	3:4A:221:ARG:HB2	2.00	0.43
4:4B:66:MET:HE3	4:4B:147:MET:HG2	2.01	0.43
3:4G:346:TRP:CE3	3:4G:347:CYS:HB2	2.54	0.43
4:4H:149:THR:HA	4:4H:152:ILE:HD12	2.00	0.43
4:4H:236:VAL:HA	4:4H:316:MET:HE3	2.01	0.43
3:4K:291:ILE:HG22	3:4K:375:VAL:HG12	2.01	0.43
5:51:207:HIS:HA	5:52:21:LEU:HD21	2.00	0.43
5:56:139:LYS:HG3	5:56:140:GLU:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5C:96:LYS:HD2	3:5C:96:LYS:HA	1.82	0.43
3:5I:335:ILE:HD13	3:5I:335:ILE:HA	1.90	0.43
4:5J:101:TRP:HE3	4:5J:403:MET:HE1	1.84	0.43
4:5J:313:ALA:HB3	4:5J:349:MET:SD	2.59	0.43
3:5M:398:MET:SD	4:5N:346:PRO:HD3	2.59	0.43
5:62:44:TYR:CZ	5:62:46:ARG:HB2	2.54	0.43
6:63:866:ARG:NH1	6:63:921:VAL:HG13	2.34	0.43
6:63:971:THR:HA	6:63:975:LYS:HE2	2.01	0.43
6:64:915:ASN:HB3	6:64:918:ALA:HB2	2.00	0.43
6:66:939:GLN:HE22	6:66:943:LEU:HD12	1.84	0.43
6:68:500:ARG:NH1	6:68:503:LYS:HE2	2.16	0.43
6:69:861:TRP:CE2	6:69:863:ARG:HD3	2.54	0.43
3:6A:119:LEU:O	3:6A:123:ARG:HG2	2.18	0.43
4:6B:228:LEU:HD11	4:6B:273:LEU:HD11	2.01	0.43
3:6E:342:GLN:HA	14:K3:113:GLU:HB2	2.00	0.43
4:6L:152:ILE:HG22	4:6L:195:ASN:HB3	2.01	0.43
3:6M:265:ILE:HD11	3:6M:435:VAL:HG21	2.01	0.43
3:6M:318:MET:O	3:6M:375:VAL:HA	2.19	0.43
3:6M:407:TRP:HZ2	4:6N:258:ILE:HB	1.84	0.43
4:6N:375:GLN:HE22	4:6N:423:GLN:HB3	1.83	0.43
7:76:251:VAL:HA	7:76:254:ARG:HE	1.84	0.43
3:7C:168:ASN:HB3	3:7C:201:ALA:HA	2.00	0.43
3:7I:231:ILE:O	3:7I:235:ILE:HG12	2.19	0.43
4:7J:90:PHE:HD1	4:7J:92:PHE:HE1	1.67	0.43
4:7L:309:ARG:H	4:7L:372:THR:HG22	1.84	0.43
2:8:172:PHE:HA	2:8:175:TYR:CE1	2.54	0.43
7:85:382:ASP:HB3	3:8G:437:ILE:HD13	1.99	0.43
4:8D:397:TRP:CD2	3:8E:257:THR:HG22	2.54	0.43
4:8F:117:LEU:HD13	7:92:286:TRP:CZ2	2.53	0.43
4:8F:298:ASN:C	4:8F:298:ASN:HD22	2.26	0.43
4:8H:265:PHE:HB3	4:8H:374:ILE:HG12	2.00	0.43
4:8L:143:THR:O	4:8L:147:MET:HB3	2.18	0.43
7:91:268:TRP:NE1	7:91:392:ARG:HB2	2.33	0.43
7:91:395:ALA:HB3	14:L0:121:VAL:HG11	2.00	0.43
4:9D:384:GLN:HE21	3:9E:348:PRO:HB2	1.83	0.43
3:9E:419:SER:HA	3:9E:422:ARG:NE	2.34	0.43
4:9F:210:ILE:HG13	4:9F:300:MET:HE1	1.99	0.43
3:9G:274:PRO:HG3	3:9G:374:ALA:HA	2.00	0.43
3:9I:231:ILE:HA	3:9I:234:VAL:HG12	2.01	0.43
4:9J:21:TRP:HA	4:9J:24:ILE:HG22	2.01	0.43
4:9J:377:MET:HE3	4:9J:377:MET:HB3	1.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9L:391:ARG:HH22	3:9M:262:TYR:HE2	1.66	0.43
9:B3:469:PHE:HB3	1:z:857:THR:HG21	2.00	0.43
9:B7:482:ASP:H	9:B7:532:GLN:NE2	2.17	0.43
10:C9:66:LEU:HD21	10:C9:312:LYS:HG2	2.00	0.43
10:D5:47:MET:HG2	10:D5:55:TYR:HB2	2.00	0.43
10:E1:328:LYS:HD2	10:E1:328:LYS:HA	1.86	0.43
10:E6:62:VAL:HA	10:E6:65:PHE:HB3	2.00	0.43
12:F0:251:TYR:HD1	12:F0:254:VAL:HB	1.82	0.43
13:J5:678:ASN:HA	13:J5:681:HIS:CD2	2.54	0.43
14:K0:157:TYR:HB2	14:K0:220:LEU:HD23	2.00	0.43
14:L3:185:ILE:O	14:L3:189:ILE:HG22	2.18	0.43
14:L8:154:MET:HE2	14:L8:213:ILE:HG21	2.00	0.43
1:a:611:THR:HA	1:f:610:VAL:CG1	2.43	0.43
1:a:666:VAL:HG12	1:f:666:VAL:HG12	2.00	0.43
1:a:677:MET:HE3	1:a:677:MET:HB3	1.65	0.43
1:x:921:GLU:O	1:x:925:MET:HG3	2.18	0.43
1:B:435:LYS:HD2	1:Y:546:ASN:OD1	2.19	0.43
1:I:679:ARG:HA	1:I:679:ARG:HD3	1.73	0.43
1:I:680:LEU:HD21	1:J:681:ILE:HA	2.01	0.43
1:J:636:ALA:O	1:J:639:LEU:HG	2.18	0.43
1:M:604:ILE:HG12	1:N:603:ARG:HH12	1.84	0.43
1:Q:573:GLN:HA	1:U:572:ARG:HH12	1.83	0.43
1:S:341:GLU:HA	1:S:344:ARG:HB2	2.00	0.43
1:T:667:LYS:NZ	1:X:666:VAL:HG21	2.34	0.43
1:Z:463:LYS:HA	1:Z:463:LYS:HD2	1.88	0.43
2:13:184:LYS:HD3	2:13:187:HIS:HE1	1.83	0.43
2:13:204:LEU:HD23	2:13:207:LYS:NZ	2.33	0.43
2:16:217:ALA:HA	2:16:220:LYS:HG2	1.99	0.43
3:1A:211:ASP:O	3:1A:215:ARG:HG2	2.19	0.43
4:1B:175:VAL:HG11	3:1C:329:ASN:HB3	2.00	0.43
4:1B:256:ASN:ND2	4:1B:350:LYS:HE3	2.34	0.43
3:1C:223:THR:HG22	3:1C:225:THR:H	1.83	0.43
3:1C:298:PRO:HG3	3:1C:307:PRO:HD2	2.01	0.43
4:1F:44:LEU:HD12	4:1F:47:ILE:HD13	2.00	0.43
3:1G:242:LEU:HD11	3:1G:252:VAL:HG23	2.01	0.43
4:1H:208:TYR:CE1	3:1I:326:LYS:HB3	2.54	0.43
4:1L:177:ASP:OD1	3:1M:352:LYS:HG3	2.19	0.43
4:1L:179:VAL:HG12	3:1M:351:PHE:HA	2.00	0.43
3:1M:5:ILE:HD13	3:1M:125:LEU:HB3	2.01	0.43
3:1M:325:PRO:HA	3:1M:328:VAL:HB	2.01	0.43
4:1N:285:SER:O	4:1N:289:LEU:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:23:151:HIS:CE1	5:23:155:LYS:HB2	2.54	0.43
5:25:74:LYS:HB2	5:25:90:GLU:HB2	2.01	0.43
5:27:77:ILE:HD12	5:27:84:PRO:HB3	2.01	0.43
3:2A:237:SER:HA	3:2A:320:ARG:HH11	1.84	0.43
3:2C:88:HIS:HE1	3:3C:280:LYS:HG2	1.83	0.43
4:2D:311:LEU:HA	4:2D:342:VAL:HG21	2.01	0.43
5:36:182:GLU:HB3	5:36:186:ARG:HH12	1.84	0.43
3:3C:32:PRO:HG3	8:A2:239:ILE:HG13	2.00	0.43
4:3F:149:THR:HA	4:3F:152:ILE:HD12	1.99	0.43
4:3H:101:TRP:H	4:3H:398:TYR:HE1	1.67	0.43
3:3M:205:ASP:HB2	3:3M:303:ALA:HA	1.99	0.43
5:47:50:PHE:HE2	5:47:91:LEU:HD22	1.84	0.43
5:48:48:VAL:HG21	5:48:134:LEU:HD22	2.00	0.43
4:4B:386:THR:O	4:4B:390:ARG:HB2	2.18	0.43
4:4F:10:GLY:HA2	4:4F:143:THR:HG23	2.01	0.43
4:4F:228:LEU:HD23	4:4F:228:LEU:HA	1.87	0.43
4:4H:12:CYS:SG	4:4H:138:SER:HB3	2.59	0.43
3:4K:205:ASP:HB2	3:4K:303:ALA:HA	2.00	0.43
3:4K:288:VAL:HB	3:4K:327:ASP:HB3	2.00	0.43
3:4M:2:ARG:HB3	3:4M:242:LEU:HD23	2.00	0.43
3:4M:346:TRP:CD1	3:4M:346:TRP:H	2.36	0.43
5:55:52:ILE:HB	5:55:67:ARG:HB2	2.00	0.43
5:57:203:GLN:HG2	5:58:21:LEU:HD11	2.01	0.43
4:5B:135:ILE:HD13	4:5B:164:MET:HE1	2.01	0.43
3:5C:311:LYS:HB3	3:5C:344:VAL:HG22	2.01	0.43
3:5E:163:LYS:HE3	14:K3:104:TYR:CE1	2.52	0.43
4:5F:326:VAL:O	4:5F:330:MET:HG2	2.19	0.43
4:5H:3:GLU:HA	4:5H:49:VAL:HA	1.99	0.43
4:5H:66:MET:HE1	4:5H:151:LEU:HD13	2.00	0.43
4:5J:116:VAL:HG23	4:5J:151:LEU:HD13	2.00	0.43
4:5L:293:MET:HE1	4:5L:330:MET:HE1	2.00	0.43
4:5N:54:ALA:HA	4:6N:283:ALA:HB2	2.01	0.43
4:5N:165:GLU:HA	4:5N:198:GLU:HB2	2.01	0.43
4:5N:246:LEU:HB3	4:5N:353:VAL:H	1.84	0.43
4:5N:256:ASN:HD22	4:5N:350:LYS:HG3	1.83	0.43
2:6:179:MET:HA	2:6:182:MET:HG2	2.01	0.43
5:60:53:ARG:HH12	5:60:62:PRO:HA	1.83	0.43
6:64:417:LEU:HD12	6:64:417:LEU:HA	1.88	0.43
6:66:503:LYS:HE2	6:66:503:LYS:HB2	1.69	0.43
6:69:497:ALA:O	6:69:498:ARG:C	2.62	0.43
6:69:971:THR:HA	6:69:975:LYS:HE2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6F:190:HIS:CD2	14:K9:133:VAL:HG11	2.54	0.43
3:6K:100:ALA:HB1	4:6L:252:LYS:HA	2.01	0.43
3:6K:313:MET:HG3	3:6K:380:ASN:HB3	2.00	0.43
3:7K:174:SER:HB3	3:7K:207:GLU:HB2	2.01	0.43
3:7M:291:ILE:HD12	3:7M:375:VAL:HG23	2.00	0.43
7:84:247:ILE:HD13	14:L0:74:GLU:HB3	2.01	0.43
7:85:390:PRO:HD2	14:L6:118:CYS:SG	2.58	0.43
3:8A:136:LEU:HD23	3:8A:167:LEU:HB3	2.01	0.43
4:8F:150:LEU:O	4:8F:154:LYS:HG3	2.17	0.43
4:8L:86:ARG:HH21	4:8L:87:PRO:HD2	1.84	0.43
4:8L:100:ASN:HD21	4:8L:397:TRP:HB3	1.84	0.43
4:8L:135:ILE:HG21	4:8L:152:ILE:HD12	2.01	0.43
2:9:175:TYR:O	2:9:179:MET:HG2	2.19	0.43
7:96:334:LEU:HG	7:96:337:LYS:HD2	2.00	0.43
3:9A:319:TYR:HB3	3:9A:323:VAL:HG21	2.00	0.43
4:9B:179:VAL:H	3:9C:258:ASN:HD22	1.67	0.43
4:9F:328:GLU:HA	4:9F:331:LEU:HD23	2.00	0.43
4:9J:268:ILE:O	4:9J:300:MET:HB2	2.19	0.43
4:9J:310:TYR:HB2	4:9J:341:PHE:HA	2.00	0.43
3:9K:208:ALA:HA	3:9K:304:LYS:HE2	2.01	0.43
8:A5:382:LEU:HA	8:A5:385:VAL:HG22	2.01	0.43
9:B5:36:GLU:HG3	9:B5:44:LEU:HD22	2.00	0.43
9:B6:16:ALA:O	9:B6:20:ARG:HG2	2.19	0.43
9:B7:482:ASP:HB3	9:B7:484:ASP:OD1	2.18	0.43
10:C8:298:GLU:HG3	10:C8:302:ARG:HE	1.84	0.43
10:C8:349:PHE:CD1	10:C8:361:TRP:HB3	2.54	0.43
10:D1:52:PRO:O	10:D1:56:TYR:HD2	2.02	0.43
10:D1:85:PRO:HB2	10:D1:313:TYR:HE2	1.84	0.43
10:D1:307:MET:HE3	10:D1:396:LEU:HB3	1.99	0.43
10:D4:379:LEU:HB3	10:D4:381:MET:HE3	1.99	0.43
10:D5:46:ASP:O	10:D5:50:GLU:HG2	2.19	0.43
10:E0:312:LYS:HD2	10:E0:312:LYS:HA	1.75	0.43
10:E1:305:LEU:O	10:E1:309:ILE:HG12	2.19	0.43
10:E4:46:ASP:O	10:E4:50:GLU:HG2	2.19	0.43
10:E8:331:ILE:HG23	10:E8:335:LEU:HG	2.00	0.43
12:G3:273:PRO:HD2	12:G3:276:LEU:HD13	1.99	0.43
14:M1:134:VAL:HG11	14:M1:139:LEU:HB2	2.01	0.43
14:M3:227:PRO:HB2	14:M3:233:LEU:HD11	2.01	0.43
1:c:642:MET:HB3	1:c:642:MET:HE2	1.64	0.43
1:c:670:ASN:HD22	1:c:670:ASN:C	2.26	0.43
1:e:378:GLU:HA	1:e:381:ARG:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:565:ASP:CB	1:f:566:ARG:NH2	2.80	0.43
1:f:579:LEU:HA	1:f:582:LEU:HG	2.01	0.43
1:i:746:ASP:HA	1:i:820:SER:HB2	2.01	0.43
1:i:763:THR:HG22	1:i:769:ARG:HD2	2.01	0.43
1:m:825:HIS:HE1	1:m:827:HIS:HB3	1.83	0.43
1:B:327:TRP:HH2	1:E:302:GLU:HG2	1.84	0.43
1:E:378:GLU:HA	1:E:381:ARG:HB2	2.01	0.43
1:F:682:LYS:HA	1:F:682:LYS:HD2	1.84	0.43
1:G:447:HIS:HA	1:G:450:LEU:HB2	2.01	0.43
1:I:327:TRP:CZ2	1:J:330:ARG:HD3	2.54	0.43
1:M:513:ARG:HG3	1:N:509:LEU:HD11	2.00	0.43
1:M:601:ARG:HG2	1:M:602:ASN:N	2.34	0.43
1:T:663:LEU:HG	1:T:667:LYS:HZ3	1.84	0.43
1:Y:359:ARG:HA	1:Y:362:VAL:HG12	2.00	0.43
1:Y:450:LEU:HD22	1:c:446:LEU:HD21	2.00	0.43
1:1:893:GLN:NE2	8:A3:74:GLY:H	2.16	0.43
2:16:159:LEU:HD22	10:C9:81:ALA:HB2	2.01	0.43
3:1A:185:TYR:HE2	3:1A:404:PHE:HB2	1.84	0.43
3:1A:237:SER:HB3	3:1A:320:ARG:HH21	1.84	0.43
3:1E:304:LYS:HA	3:1E:304:LYS:HD2	1.85	0.43
4:1F:293:MET:HG3	4:1F:367:PHE:HB2	2.01	0.43
3:1G:231:ILE:HA	3:1G:234:VAL:HG12	2.00	0.43
3:1M:406:HIS:CG	4:1N:261:PRO:HD3	2.54	0.43
5:20:29:ILE:HA	5:20:32:MET:HB3	2.01	0.43
5:22:216:LYS:HD2	4:2H:262:ARG:HH12	1.83	0.43
3:2A:21:TRP:CZ3	3:2A:52:PHE:HB3	2.54	0.43
4:2D:169:VAL:HG12	4:2D:202:ILE:HB	2.00	0.43
4:2D:229:VAL:HG12	4:2D:233:MET:HE3	2.00	0.43
4:2F:86:ARG:HD3	4:3F:281:TYR:CE1	2.54	0.43
4:2F:260:PHE:HD2	4:2F:263:LEU:HD21	1.84	0.43
4:2J:17:GLY:HA2	4:2J:20:PHE:HB3	2.00	0.43
3:2K:81:GLY:HA3	11:C2:183:TYR:HE2	1.84	0.43
3:2K:88:HIS:ND1	3:3K:282:TYR:HB3	2.34	0.43
5:33:111:ARG:HH22	5:33:122:GLU:HA	1.84	0.43
5:33:162:GLN:OE1	5:33:164:MET:HB2	2.18	0.43
5:36:130:LEU:HA	5:36:133:MET:SD	2.59	0.43
4:3H:215:LEU:HD11	4:3H:228:LEU:HD12	2.01	0.43
4:3H:222:TYR:HD2	3:3I:247:ALA:HB1	1.84	0.43
3:3I:269:LEU:HD21	3:3I:305:CYS:HB3	2.01	0.43
4:3J:322:SER:HB2	8:A7:359:ASP:HB3	2.01	0.43
3:3K:335:ILE:HD13	3:3K:338:LYS:HE2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:4:186:HIS:HA	2:4:189:GLU:HG2	2.01	0.43
3:4A:142:GLY:HA2	3:4A:186:ASN:HB2	2.00	0.43
4:4F:7:VAL:HB	4:4F:135:ILE:HG13	2.00	0.43
4:4L:278:SER:HA	4:4L:281:TYR:CE1	2.54	0.43
3:4M:395:PHE:HD2	3:4M:422:ARG:HH11	1.66	0.43
5:52:49:PRO:HA	5:52:70:PRO:HA	2.01	0.43
5:57:48:VAL:HG21	5:57:134:LEU:HD22	1.99	0.43
3:5A:65:CYS:H	3:5A:91:GLN:HE22	1.67	0.43
3:5A:155:GLU:HG2	3:5A:197:HIS:NE2	2.34	0.43
3:5A:189:LEU:HD21	3:5A:418:PHE:CD1	2.54	0.43
3:5C:109:THR:HG22	3:5C:110:ILE:HG23	2.00	0.43
4:5D:13:GLY:HA2	4:5D:136:THR:HG22	2.01	0.43
3:5G:60:LYS:HD2	3:5G:60:LYS:HA	1.85	0.43
3:5I:215:ARG:HE	3:5I:215:ARG:HB2	1.66	0.43
4:5J:171:PRO:HG2	4:5J:185:ALA:HB2	1.99	0.43
4:5N:86:ARG:NH1	4:6N:282:ARG:HD2	2.34	0.43
4:5N:308:GLY:HA3	4:5N:373:ALA:HB2	2.01	0.43
5:60:139:LYS:HG3	5:60:140:GLU:H	1.83	0.43
4:6D:287:PRO:HA	4:6D:329:GLN:HE22	1.83	0.43
3:6E:319:TYR:HB3	3:6E:323:VAL:HG21	2.00	0.43
3:6G:371:VAL:HG12	3:6G:373:ARG:H	1.84	0.43
4:6H:253:LEU:HD21	4:6H:368:VAL:HG21	2.01	0.43
4:6J:161:ASP:HA	14:L2:174:TYR:HD2	1.82	0.43
4:6J:358:PRO:HG2	4:6J:361:LEU:HD12	2.01	0.43
4:6L:284:LEU:HD12	4:6L:284:LEU:HA	1.85	0.43
3:6M:174:SER:HB3	3:6M:177:VAL:O	2.19	0.43
3:6M:321:GLY:HA2	3:6M:359:PRO:HA	1.99	0.43
3:6M:390:ARG:HD2	14:K7:192:ILE:HD13	2.01	0.43
4:6N:39:ASP:HB3	1:i:759:ARG:HH11	1.83	0.43
4:6N:74:ASP:HB3	1:i:792:ALA:HA	2.01	0.43
7:79:286:TRP:NE1	7:79:293:ILE:HG12	2.34	0.43
3:7M:306:ASP:HB3	3:7M:309:HIS:CE1	2.54	0.43
4:8B:304:ASP:HB3	4:8B:307:HIS:HB3	2.01	0.43
3:8C:423:GLU:HG2	10:F1:38:ARG:HH12	1.83	0.43
4:8F:51:TYR:HB3	4:8F:59:PHE:HB3	1.99	0.43
4:8F:200:GLN:HB3	4:8F:266:PHE:HB2	2.01	0.43
4:8F:222:TYR:HA	4:8F:225:LEU:HD13	2.01	0.43
4:8J:183:TYR:HA	4:8J:385:PHE:HE2	1.83	0.43
4:8L:256:ASN:HB3	4:8L:350:LYS:HD2	2.01	0.43
3:8M:256:GLN:HA	3:8M:259:LEU:HG	1.99	0.43
7:91:258:GLU:HA	7:91:261:ALA:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9G:311:LYS:H	3:9G:382:THR:HB	1.84	0.43
4:9H:187:LEU:HD21	4:9H:408:PHE:CD1	2.54	0.43
4:9J:186:THR:HG22	4:9J:411:ALA:HB1	2.00	0.43
8:A1:345:ILE:HA	8:A1:349:LEU:HD12	2.01	0.43
8:A7:241:LEU:HD12	8:A7:242:PRO:HD2	1.99	0.43
10:C9:86:LEU:HD12	10:C9:319:LEU:HG	2.01	0.43
10:D6:317:LEU:HA	10:D6:320:LYS:HG2	2.00	0.43
10:F2:89:ALA:HB3	10:F2:310:ILE:HD11	2.00	0.43
12:G3:276:LEU:HA	12:G3:279:ARG:HG3	2.01	0.43
12:H8:81:ASP:O	12:H8:85:GLN:HG2	2.19	0.43
12:I1:65:GLU:HA	12:I1:68:ARG:HE	1.84	0.43
12:I2:103:LYS:HG3	12:I2:104:ILE:HG23	2.01	0.43
13:J1:467:SER:O	13:J1:470:ARG:HG2	2.19	0.43
13:J2:470:ARG:HB3	13:J2:500:LEU:HA	2.00	0.43
13:J3:374:ARG:HH12	13:J3:600:LEU:HD13	1.84	0.43
13:J7:289:ILE:HG23	13:J7:300:LEU:HD21	2.01	0.43
14:K0:131:LYS:HE3	14:K0:131:LYS:HB3	1.87	0.43
14:K5:178:MET:HE2	14:K5:210:LEU:HD22	2.01	0.43
14:L6:191:PRO:HG2	14:L6:196:VAL:HG23	2.01	0.43
14:L9:154:MET:HG3	14:L9:219:TYR:CD2	2.53	0.43
14:M6:196:VAL:HG21	14:M6:221:CYS:HB3	1.99	0.43
1:a:530:LEU:HD13	1:f:530:LEU:CB	2.49	0.43
1:c:675:LYS:O	1:c:678:ASN:HB2	2.19	0.43
1:n:873:PRO:HG2	1:n:875:ILE:HG12	2.00	0.43
1:z:952:ARG:HB3	1:z:953:LYS:H	1.53	0.43
1:A:614:LEU:HB3	1:A:618:ARG:HH12	1.83	0.42
1:A:668:GLN:HG3	3:8E:372:MET:HE1	2.00	0.42
1:C:353:LEU:HD12	1:C:353:LEU:HA	1.89	0.42
1:D:682:LYS:HD3	1:j:795:LEU:HD22	2.01	0.42
1:F:603:ARG:NE	1:F:607:LEU:HD23	2.33	0.42
1:I:603:ARG:HB3	1:J:604:ILE:HG12	2.01	0.42
1:J:577:GLN:NE2	1:J:578:ARG:NE	2.64	0.42
1:K:510:ASP:HA	1:L:513:ARG:NH2	2.32	0.42
1:R:664:ILE:HD11	3:6G:282:TYR:CD2	2.54	0.42
1:U:638:LEU:HA	1:U:641:GLU:HG3	2.01	0.42
1:W:443:ASN:HA	1:W:446:LEU:HD12	2.01	0.42
1:Y:364:GLU:OE2	1:c:361:LEU:HD13	2.18	0.42
1:Y:600:LEU:O	1:Y:604:ILE:HG13	2.19	0.42
1:Y:604:ILE:HG12	1:c:603:ARG:HH22	1.84	0.42
1:Y:636:ALA:HB3	1:k:827:HIS:NE2	2.34	0.42
2:11:303:ALA:O	2:11:307:MET:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1A:21:TRP:HE3	3:1A:53:PHE:HE1	1.67	0.42
4:1B:21:TRP:HA	4:1B:24:ILE:HG12	1.99	0.42
3:1E:319:TYR:CE1	3:1E:375:VAL:HG12	2.54	0.42
4:1F:7:VAL:HG13	4:1F:64:ILE:HB	1.99	0.42
3:1G:68:LEU:HD22	3:1G:149:LEU:HD21	2.01	0.42
4:1H:66:MET:HE1	4:1H:116:VAL:HG11	2.01	0.42
4:1J:73:MET:HE1	4:1J:92:PHE:CG	2.53	0.42
3:1M:235:ILE:O	3:1M:238:LEU:HB3	2.19	0.42
3:1M:296:PHE:CZ	3:1M:317:LEU:HD21	2.54	0.42
4:1N:296:ALA:N	4:1N:306:ARG:HH12	2.17	0.42
5:26:67:ARG:HD2	12:G7:263:TYR:HA	2.01	0.42
5:28:73:VAL:HG22	5:28:91:LEU:HD22	2.01	0.42
4:2B:232:ALA:HB2	4:2B:270:PHE:HB2	2.01	0.42
4:2F:105:HIS:CD2	4:2F:150:LEU:HB2	2.54	0.42
3:2M:193:SER:HB2	3:2M:197:HIS:CD2	2.54	0.42
3:3A:104:ALA:HB2	3:3A:413:MET:HB2	2.01	0.42
3:3G:195:LEU:HD11	3:3G:428:LEU:HD13	2.01	0.42
4:3H:293:MET:HE1	4:3H:315:ALA:HB2	2.00	0.42
3:4A:406:HIS:HA	3:4A:409:VAL:HG12	2.00	0.42
3:4C:320:ARG:HD3	3:4C:360:PRO:HB3	2.00	0.42
3:4I:101:ASN:HB2	4:4J:256:ASN:HD21	1.84	0.42
4:4L:200:GLN:NE2	4:4L:268:ILE:HD11	2.34	0.42
5:50:40:HIS:HB3	5:50:76:LEU:HB3	2.00	0.42
5:51:224:LEU:HD21	6:63:603:PHE:HD1	1.83	0.42
5:56:212:LEU:HD11	6:69:601:GLU:HB3	2.01	0.42
3:5A:121:ARG:HD2	3:5A:124:LYS:HE3	2.00	0.42
3:5A:223:THR:H	3:5A:226:ASN:HB3	1.84	0.42
4:5H:220:PRO:HD2	3:5I:326:LYS:HD2	1.99	0.42
4:5L:19:LYS:HE2	4:5L:19:LYS:HB2	1.79	0.42
3:5M:118:SER:O	3:5M:122:ILE:HG12	2.19	0.42
2:6:199:SER:C	2:6:201:VAL:H	2.27	0.42
5:60:48:VAL:HG21	5:60:134:LEU:HG	2.01	0.42
5:61:221:LEU:HD23	5:61:224:LEU:HD21	2.01	0.42
5:62:205:ARG:O	5:62:209:ILE:HD12	2.19	0.42
6:64:337:LEU:H	6:64:407:LEU:HD13	1.83	0.42
6:69:498:ARG:HA	6:69:498:ARG:HD3	1.75	0.42
3:6A:231:ILE:O	3:6A:235:ILE:HG12	2.18	0.42
3:6A:396:ASP:OD1	10:D9:35:TRP:HA	2.18	0.42
4:6B:134:GLN:HB3	4:6B:165:GLU:OE2	2.19	0.42
3:6K:261:PRO:HG2	3:6K:313:MET:HE2	2.00	0.42
7:75:286:TRP:NE1	7:75:293:ILE:HG12	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7A:232:ALA:HA	3:7A:235:ILE:HG22	2.01	0.42
3:7A:250:VAL:HG13	3:7A:255:PHE:HE1	1.83	0.42
4:7B:15:GLN:HG3	4:7B:226:ASN:HD21	1.83	0.42
3:7C:259:LEU:HG	3:7C:268:MET:HE1	2.01	0.42
3:7C:298:PRO:HB3	3:7C:307:PRO:HD2	2.01	0.42
4:7D:68:LEU:HD12	4:7D:93:GLY:HA3	1.99	0.42
4:7D:124:ALA:HB1	4:7D:130:LEU:HD21	2.01	0.42
3:7E:70:LEU:HD21	3:7E:114:ILE:HG21	2.00	0.42
3:7E:195:LEU:HG	3:7E:428:LEU:HD13	2.00	0.42
4:7H:376:GLU:O	4:7H:380:ARG:HB2	2.19	0.42
4:7J:100:ASN:ND2	4:7J:103:LYS:HB2	2.34	0.42
3:7K:255:PHE:CZ	3:7K:378:ILE:HD13	2.48	0.42
4:7L:20:PHE:CG	4:7L:233:MET:HE3	2.54	0.42
3:7M:28:HIS:HA	3:7M:49:PHE:HE1	1.84	0.42
7:84:378:MET:HB3	14:L4:242:ILE:HG13	2.00	0.42
4:8D:358:PRO:HG2	4:8D:361:LEU:HB3	2.01	0.42
3:8E:212:ILE:HD11	3:8E:300:SER:HA	2.00	0.42
3:8G:215:ARG:HH12	3:8G:299:ALA:HB1	1.83	0.42
4:8J:189:VAL:O	4:8J:193:VAL:HG13	2.19	0.42
4:8L:244:GLY:HA3	4:8L:354:CYS:HA	2.02	0.42
4:8L:274:THR:H	1:m:814:PRO:HD3	1.84	0.42
7:91:279:ARG:NH1	10:F2:148:MET:H	2.16	0.42
7:94:295:GLN:HB3	7:94:320:TRP:CD2	2.54	0.42
3:9E:336:LYS:HD2	14:M4:108:TYR:CE2	2.54	0.42
3:9G:154:LEU:HD21	3:9G:198:THR:HB	2.01	0.42
3:9I:240:ALA:HB3	3:9I:320:ARG:NH2	2.34	0.42
3:9K:391:MET:HA	3:9K:394:LYS:HD2	2.01	0.42
3:9K:406:HIS:CG	4:9L:261:PRO:HG3	2.54	0.42
9:B5:527:LEU:HD12	9:B5:534:THR:HG22	2.01	0.42
10:D2:335:LEU:HD23	10:D2:335:LEU:HA	1.92	0.42
10:D4:307:MET:HE1	10:D4:400:LEU:HD13	2.01	0.42
10:E8:62:VAL:HG21	10:E8:305:LEU:HB3	2.01	0.42
12:F0:254:VAL:HG23	12:F9:225:TRP:CE3	2.53	0.42
10:F2:67:ALA:O	10:F2:71:GLN:HB2	2.19	0.42
12:F9:242:TRP:HE3	12:F9:262:LEU:HD11	1.84	0.42
12:G5:226:ILE:HD12	12:G5:235:LEU:HD21	2.01	0.42
12:G7:252:LEU:HA	12:G7:252:LEU:HD23	1.88	0.42
13:J1:271:LEU:HD13	13:J1:286:LEU:HD13	2.01	0.42
13:J4:678:ASN:HA	13:J4:681:HIS:CE1	2.53	0.42
13:J5:428:LYS:HE2	13:J5:428:LYS:HB2	1.85	0.42
14:K9:159:ASN:HD21	14:K9:220:LEU:HB3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L2:134:VAL:HG21	14:L2:139:LEU:HD23	2.01	0.42
14:M7:111:LEU:HB3	14:M7:117:ARG:NH1	2.34	0.42
1:c:604:ILE:HD13	1:c:604:ILE:HA	1.40	0.42
1:f:556:ARG:O	1:f:559:GLU:HB2	2.19	0.42
1:j:793:GLN:HB2	1:j:795:LEU:HD11	2.00	0.42
1:y:875:ILE:HD13	1:y:948:GLN:HG3	2.01	0.42
1:N:603:ARG:O	1:N:606:HIS:HB3	2.19	0.42
1:Q:361:LEU:O	1:Q:365:LEU:HD23	2.20	0.42
1:R:625:GLN:HA	1:R:628:VAL:HG12	2.00	0.42
1:S:369:GLU:HG3	1:W:368:GLN:HE22	1.84	0.42
2:16:221:ARG:HH22	6:67:971:THR:HG21	1.83	0.42
3:1A:10:GLY:O	3:1A:14:ILE:HG12	2.19	0.42
4:1D:289:LEU:HD23	4:1D:317:PHE:HE1	1.82	0.42
4:1F:17:GLY:HA2	4:1F:20:PHE:HB3	2.01	0.42
4:1L:68:LEU:HA	4:1L:93:GLY:HA3	2.01	0.42
3:1M:104:ALA:HA	3:1M:107:HIS:HB3	2.01	0.42
3:1M:202:VAL:HG12	3:1M:268:MET:HB2	2.01	0.42
4:1N:385:PHE:HZ	4:1N:408:PHE:HB3	1.83	0.42
5:20:199:LEU:HB2	5:25:199:LEU:HD21	2.00	0.42
3:2C:36:MET:HE2	3:2C:61:HIS:NE2	2.34	0.42
4:2D:344:TRP:CD1	4:2D:344:TRP:H	2.37	0.42
4:2F:8:GLN:HG3	4:2F:14:ASN:HD22	1.84	0.42
4:2F:179:VAL:HG23	3:2G:350:GLY:HA2	2.01	0.42
4:2H:334:GLN:HE22	4:2H:347:ASN:HA	1.84	0.42
4:2L:391:ARG:HH12	12:H6:56:HIS:CE1	2.36	0.42
5:31:225:GLN:HA	5:32:20:PHE:CZ	2.54	0.42
5:35:224:LEU:HD11	5:36:216:LYS:HD2	2.01	0.42
5:38:99:LEU:HG	5:38:101:TYR:HE2	1.84	0.42
5:39:89:VAL:HB	5:39:103:HIS:HB3	2.02	0.42
5:39:188:MET:HE1	5:40:188:MET:SD	2.59	0.42
3:3A:64:ARG:HG2	3:3A:125:LEU:HD11	2.01	0.42
4:3D:39:ASP:HB2	8:A2:154:THR:HG23	2.01	0.42
3:3E:102:ASN:H	3:3E:144:GLY:HA3	1.84	0.42
4:3F:135:ILE:HG21	4:3F:152:ILE:HD11	2.01	0.42
4:3F:252:LYS:HG2	4:3F:350:LYS:HE3	2.01	0.42
5:40:201:LEU:HD23	5:40:201:LEU:HA	1.92	0.42
5:44:214:LYS:HG2	5:44:221:LEU:HD22	2.00	0.42
3:4A:12:ALA:HB3	3:4A:140:ALA:HB2	2.01	0.42
3:4E:6:SER:O	3:4E:65:CYS:HA	2.19	0.42
4:4F:406:MET:HE3	4:4F:406:MET:HB3	1.92	0.42
3:4K:247:ALA:HB3	3:4K:355:ILE:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:59:129:VAL:HA	5:59:132:LYS:HB2	2.02	0.42
3:5A:172:TRP:CH2	3:5A:391:MET:HE3	2.54	0.42
4:5B:49:VAL:HG23	4:5B:50:PHE:CD2	2.54	0.42
3:5C:17:GLY:HA2	3:5C:20:CYS:HB3	2.01	0.42
3:5C:195:LEU:HD12	3:5C:266:HIS:CE1	2.54	0.42
3:5E:208:ALA:O	3:5E:212:ILE:HG12	2.19	0.42
3:5E:407:TRP:CG	4:5F:255:VAL:HG23	2.54	0.42
4:5N:173:PRO:HA	4:5N:176:SER:HB3	2.00	0.42
4:5N:212:PHE:HE1	4:5N:220:PRO:HG3	1.84	0.42
2:6:313:SER:O	2:6:316:ARG:HD3	2.19	0.42
5:62:20:PHE:HD1	6:67:596:PRO:HB3	1.83	0.42
5:62:100:ASN:HD22	5:62:184:THR:HA	1.84	0.42
6:66:560:ALA:O	6:66:564:MET:HG2	2.19	0.42
6:68:892:GLN:NE2	1:x:878:PRO:HB3	2.35	0.42
6:69:256:VAL:HG12	6:69:441:GLU:HG3	2.01	0.42
3:6A:77:GLU:HA	3:6A:80:THR:HG22	2.00	0.42
3:6C:36:MET:HG2	3:6C:61:HIS:CE1	2.53	0.42
4:6D:174:LYS:HA	14:K3:110:GLY:HA3	2.00	0.42
4:6D:403:MET:HE3	4:6D:407:GLU:OE2	2.18	0.42
3:6E:140:ALA:HA	3:6E:171:SER:HB2	2.00	0.42
4:6H:67:ASP:HB2	4:6H:73:MET:HE3	2.01	0.42
4:6N:162:ARG:HD3	4:6N:162:ARG:HA	1.77	0.42
4:6N:170:PHE:HB3	4:6N:203:ASP:OD1	2.19	0.42
2:7:291:GLU:O	2:7:295:PHE:HB2	2.19	0.42
3:7A:138:PHE:HZ	3:7A:235:ILE:HG12	1.84	0.42
3:7E:169:PHE:CD1	3:7E:202:VAL:HB	2.55	0.42
4:7H:307:HIS:CD2	7:82:296:ARG:HH21	2.36	0.42
3:7K:68:LEU:HD11	3:7K:153:LEU:HD21	2.01	0.42
2:8:268:THR:HA	2:8:271:LYS:HE2	2.00	0.42
7:82:390:PRO:HD2	14:K8:118:CYS:SG	2.58	0.42
7:85:316:PRO:HB2	7:85:318:THR:HG22	2.02	0.42
7:87:350:ARG:HD2	7:87:379:LEU:HD13	2.02	0.42
4:8F:397:TRP:O	4:8F:401:GLU:HG2	2.18	0.42
4:8H:207:LEU:HD21	4:8H:229:VAL:HG23	2.01	0.42
4:8H:239:CYS:HB3	4:8H:247:ASN:HB2	2.01	0.42
3:8K:197:HIS:HA	14:M6:84:GLY:HA2	1.99	0.42
4:8L:190:HIS:HB2	4:8L:414:ASN:HD22	1.83	0.42
4:8L:284:LEU:HD13	4:8L:362:LYS:HG2	2.00	0.42
3:9A:12:ALA:O	3:9A:16:ILE:HG12	2.19	0.42
3:9A:240:ALA:HA	3:9A:243:ARG:HE	1.84	0.42
4:9B:268:ILE:HD13	4:9B:368:VAL:HG12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9C:119:LEU:HA	3:9C:122:ILE:HD12	2.01	0.42
3:9E:409:VAL:HA	3:9E:413:MET:HG3	2.01	0.42
3:9G:324:VAL:HG12	3:9G:326:LYS:H	1.84	0.42
3:9I:271:SER:HA	3:9I:302:MET:HE3	2.01	0.42
3:9K:209:ILE:HG22	3:9K:227:LEU:HD22	2.01	0.42
8:A2:245:ALA:HB1	9:B5:524:PRO:HB2	2.01	0.42
8:A5:386:ARG:HH12	9:B3:159:PRO:HG2	1.83	0.42
8:A6:161:ILE:HD11	8:A6:187:VAL:HG21	2.00	0.42
8:A9:317:LEU:HD23	8:A9:317:LEU:HA	1.90	0.42
9:B1:490:HIS:CD2	9:B1:531:PRO:HG3	2.54	0.42
9:B7:485:GLU:OE1	9:B7:532:GLN:HB3	2.19	0.42
10:C6:47:MET:HG3	10:C6:55:TYR:HB2	2.02	0.42
10:C6:343:ALA:O	10:C6:347:GLU:HG2	2.19	0.42
10:D1:61:ASP:HA	14:K6:142:GLN:HE22	1.84	0.42
10:D5:328:LYS:HD2	10:D5:328:LYS:HA	1.78	0.42
10:D8:83:ARG:HG2	10:D8:326:LYS:HZ1	1.84	0.42
10:E8:372:LEU:HA	10:E8:375:ILE:HG22	2.00	0.42
10:F3:63:TYR:CD2	14:M5:147:GLN:HG2	2.54	0.42
12:G1:283:LEU:HD23	12:G1:283:LEU:HA	1.88	0.42
12:G2:274:MET:HA	12:G2:277:ARG:HE	1.84	0.42
13:J1:412:ALA:O	13:J1:416:VAL:HG23	2.19	0.42
13:J2:501:ARG:O	13:J2:505:GLU:HG3	2.19	0.42
13:J4:284:ARG:HD3	13:J4:322:LYS:HB3	2.01	0.42
14:L4:186:THR:HG23	14:L4:191:PRO:HG3	2.01	0.42
14:L8:100:ALA:HB3	14:L8:123:SER:HA	2.01	0.42
14:M2:203:ASN:HB2	14:M2:205:ARG:HH12	1.84	0.42
1:l:757:LEU:HD23	1:l:757:LEU:HA	1.95	0.42
1:z:880:THR:HB	1:z:881:ALA:H	1.66	0.42
1:B:404:PHE:HB3	1:E:406:ARG:HH22	1.84	0.42
1:J:643:ARG:HE	1:J:643:ARG:HB2	1.38	0.42
1:N:470:ARG:HH12	1:N:473:ARG:NH1	2.17	0.42
1:N:636:ALA:O	1:N:639:LEU:HB2	2.19	0.42
1:P:656:GLN:HA	1:P:659:LEU:HD12	2.01	0.42
1:V:620:ASP:O	1:V:624:GLN:HG3	2.20	0.42
1:Y:632:ARG:HE	1:Y:632:ARG:HB2	1.71	0.42
3:1A:208:ALA:O	3:1A:212:ILE:HG12	2.18	0.42
4:1B:117:LEU:HD11	4:1B:154:LYS:HB3	2.01	0.42
3:1E:394:LYS:O	3:1E:398:MET:HG2	2.19	0.42
4:1H:208:TYR:CE1	4:1H:225:LEU:HD11	2.54	0.42
3:1I:248:LEU:HD22	3:1I:354:GLY:HA2	2.01	0.42
4:1L:10:GLY:HA2	4:1L:143:THR:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1L:215:LEU:HD11	4:1L:228:LEU:HD21	2.00	0.42
5:22:51:GLU:HG3	5:22:66:GLY:HA3	2.01	0.42
5:25:116:ARG:HG3	5:25:117:GLN:HG3	2.01	0.42
5:27:48:VAL:HG22	5:27:138:ILE:HD11	2.01	0.42
4:2D:290:THR:HA	4:2D:293:MET:HE3	2.01	0.42
3:2E:378:ILE:H	3:2E:378:ILE:HD12	1.85	0.42
3:2G:147:SER:HB2	3:2G:190:SER:HB3	2.01	0.42
3:2K:212:ILE:HD13	3:2K:212:ILE:HA	1.90	0.42
4:2L:274:THR:HB	4:2L:279:GLN:HG2	2.00	0.42
5:32:167:LYS:HD2	5:32:167:LYS:HA	1.86	0.42
3:3A:272:TYR:HE1	3:3A:374:ALA:HB1	1.84	0.42
3:3C:246:GLY:HA2	3:3C:357:TYR:CD2	2.54	0.42
4:3D:208:TYR:HB3	3:3E:326:LYS:HG3	2.00	0.42
3:3M:119:LEU:HD11	3:3M:156:ARG:HH11	1.84	0.42
5:44:77:ILE:HG22	5:44:87:VAL:HG22	2.01	0.42
5:44:230:GLN:HB3	5:44:234:ARG:HH21	1.84	0.42
5:47:42:LEU:HD13	5:47:74:LYS:HG3	2.01	0.42
3:4A:22:GLU:HG2	3:4A:83:TYR:OH	2.20	0.42
4:4B:173:PRO:HA	4:4B:380:ARG:NH1	2.33	0.42
3:4C:251:ASP:HB2	3:4C:254:GLU:HG3	2.01	0.42
4:4D:7:VAL:HB	4:4D:135:ILE:HG13	2.01	0.42
3:4E:203:MET:HE3	3:4E:267:PHE:CD2	2.54	0.42
3:4G:23:LEU:HD13	3:4G:363:VAL:HG22	2.00	0.42
3:4G:284:GLU:HB2	3:4G:286:LEU:HG	2.01	0.42
4:4J:82:GLY:H	8:A6:96:LYS:NZ	2.16	0.42
4:4J:138:SER:HA	4:4J:169:VAL:HG23	2.00	0.42
3:4M:51:THR:HG21	3:4M:243:ARG:HG2	2.00	0.42
5:56:158:LEU:HB2	5:56:174:LEU:HB2	2.01	0.42
5:57:167:LYS:HE2	5:57:169:ILE:HD11	2.00	0.42
4:5B:171:PRO:HB3	4:5B:181:GLU:OE2	2.20	0.42
3:5C:402:ARG:HA	3:5C:402:ARG:HD3	1.81	0.42
4:5D:6:HIS:HD2	4:5D:21:TRP:NE1	2.15	0.42
4:5F:64:ILE:HD12	4:5F:119:VAL:HG13	2.01	0.42
4:5F:306:ARG:HH21	6:65:793:LEU:HD23	1.85	0.42
3:5M:318:MET:O	3:5M:375:VAL:HA	2.20	0.42
4:5N:406:MET:HE3	4:5N:406:MET:O	2.20	0.42
6:64:507:ARG:HD3	6:64:507:ARG:HA	1.81	0.42
6:67:157:TRP:HA	6:67:162:GLY:O	2.19	0.42
6:67:912:GLU:HG2	6:67:914:LYS:HG3	2.01	0.42
6:69:154:ARG:HD2	6:69:156:HIS:HE2	1.84	0.42
6:69:416:MET:HE1	6:69:433:LEU:HD13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6A:396:ASP:HA	3:6A:399:TYR:HB3	2.01	0.42
4:6B:134:GLN:HA	4:6B:165:GLU:O	2.19	0.42
4:6D:407:GLU:HB3	14:K0:130:ARG:NH1	2.34	0.42
3:6E:342:GLN:HG2	14:K3:113:GLU:HB3	2.01	0.42
4:6F:68:LEU:HB3	4:6F:96:GLY:HA2	2.01	0.42
4:6H:179:VAL:HG12	3:6I:258:ASN:OD1	2.19	0.42
3:6I:319:TYR:HB2	3:6I:355:ILE:HD13	2.00	0.42
4:6L:237:THR:HA	4:6L:240:LEU:HD23	2.01	0.42
4:6L:326:VAL:O	4:6L:330:MET:HG2	2.20	0.42
3:6M:269:LEU:HG	3:6M:384:ILE:HD11	2.01	0.42
2:7:182:MET:HE3	2:8:179:MET:HE1	2.01	0.42
7:75:313:LEU:HB2	7:75:315:ILE:HG13	2.00	0.42
4:7B:390:ARG:HH12	4:7B:391:ARG:NH2	2.17	0.42
4:7D:109:GLY:O	4:7D:113:ILE:HG12	2.19	0.42
4:7D:131:GLN:HG2	4:7D:240:LEU:HD21	2.00	0.42
4:7D:424:GLN:NE2	10:E5:301:ARG:HH12	2.15	0.42
3:7E:224:TYR:HD2	4:7F:245:GLN:HB3	1.84	0.42
3:7E:301:MET:HG3	3:7E:307:PRO:HD3	2.02	0.42
4:7F:73:MET:HE2	4:7F:73:MET:HB3	1.82	0.42
3:7M:189:LEU:HD11	3:7M:418:PHE:CD1	2.55	0.42
7:83:340:ASN:HB3	7:83:361:THR:HG22	2.01	0.42
3:8C:253:THR:HA	3:8C:256:GLN:HE21	1.84	0.42
3:8C:259:LEU:HA	3:8C:314:ALA:HB1	2.00	0.42
4:8F:289:LEU:HD22	4:8F:363:MET:HG2	2.01	0.42
4:8H:6:HIS:HA	4:8H:134:GLN:O	2.19	0.42
3:8I:215:ARG:HD3	14:L9:250:PRO:HG2	2.01	0.42
4:8L:385:PHE:HE2	4:8L:412:GLU:HB3	1.83	0.42
3:9A:147:SER:O	3:9A:151:CYS:HB3	2.19	0.42
4:9F:274:THR:HG21	4:9F:282:ARG:HG3	2.00	0.42
3:9G:73:THR:HB	4:9H:46:ARG:HH21	1.85	0.42
4:9J:272:PRO:HG3	4:9J:289:LEU:HD11	2.01	0.42
3:9K:258:ASN:ND2	3:9K:352:LYS:HD3	2.33	0.42
8:A4:79:ASP:HA	8:A4:82:MET:HE3	2.01	0.42
8:A4:81:ILE:HD12	8:A4:81:ILE:HA	1.89	0.42
8:A6:157:LEU:HD11	8:A6:222:PHE:HD2	1.84	0.42
9:B6:447:PRO:HG2	1:x:857:THR:HG22	2.02	0.42
10:D1:39:ASP:HA	10:D1:42:LYS:HG2	2.00	0.42
10:D3:375:ILE:HG23	10:D3:379:LEU:HD12	2.01	0.42
10:D5:62:VAL:HG21	10:D5:305:LEU:HB3	2.02	0.42
10:D7:92:MET:HB2	10:D7:306:MET:HE2	2.02	0.42
10:D8:47:MET:HE3	10:D8:55:TYR:HD1	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D9:86:LEU:HB2	10:D9:313:TYR:CD2	2.54	0.42
10:E2:53:LEU:O	10:E2:57:ILE:HG12	2.19	0.42
10:E5:37:ASP:OD1	10:E5:40:ARG:HB3	2.20	0.42
12:F9:222:ASP:HB3	12:F9:242:TRP:HE1	1.85	0.42
12:G7:280:ALA:HB2	12:G7:289:ILE:HD11	2.01	0.42
13:J2:396:GLN:HG2	13:J2:399:ALA:H	1.84	0.42
13:J6:271:LEU:HD21	13:J6:286:LEU:HD13	2.01	0.42
14:K3:233:LEU:HB3	14:K3:237:LEU:HD23	2.00	0.42
14:M2:186:THR:HG23	14:M2:196:VAL:HG12	2.01	0.42
1:f:601:ARG:HA	1:f:604:ILE:HD11	2.01	0.42
1:f:677:MET:HA	1:f:677:MET:CE	2.47	0.42
1:i:763:THR:HG22	1:i:769:ARG:HH11	1.83	0.42
1:D:589:THR:HA	1:D:592:ARG:HE	1.85	0.42
1:Y:376:MET:SD	1:c:376:MET:HE2	2.60	0.42
2:11:295:PHE:CZ	2:12:298:LEU:HD22	2.54	0.42
2:12:239:ARG:HD2	2:12:239:ARG:HA	1.78	0.42
3:1A:268:MET:HG3	3:1A:380:ASN:HA	2.01	0.42
3:1C:68:LEU:HD22	3:1C:118:SER:HB2	2.01	0.42
4:1F:100:ASN:ND2	4:1F:103:LYS:HG3	2.33	0.42
4:1J:6:HIS:HA	4:1J:134:GLN:O	2.19	0.42
3:1K:318:MET:HE3	3:1K:318:MET:HB3	1.91	0.42
3:1M:427:ALA:HA	3:1M:430:LYS:HG2	2.02	0.42
5:20:188:MET:SD	5:25:188:MET:HE2	2.59	0.42
5:21:149:ILE:HD12	5:21:149:ILE:HA	1.85	0.42
5:21:181:GLU:O	5:21:185:ARG:HB2	2.20	0.42
5:24:138:ILE:HD13	5:24:138:ILE:HA	1.91	0.42
5:27:188:MET:HE3	5:27:191:ARG:HG2	2.01	0.42
3:2A:37:PRO:HB3	9:B7:480:TYR:HD2	1.84	0.42
3:2A:159:VAL:HG13	6:67:558:LYS:HZ1	1.83	0.42
3:2A:269:LEU:HD21	3:2A:384:ILE:HG21	2.01	0.42
4:2B:290:THR:HA	4:2B:293:MET:HG3	2.01	0.42
3:2E:158:SER:HA	3:2E:166:LYS:HE3	2.01	0.42
3:2E:280:LYS:HB2	3:2E:280:LYS:HE3	1.77	0.42
3:2G:102:ASN:HB3	3:2G:105:ARG:HG3	2.01	0.42
3:2I:404:PHE:HZ	4:2J:312:THR:HG21	1.84	0.42
3:2K:103:PHE:HB2	3:2K:186:ASN:HD22	1.83	0.42
5:32:172:LEU:HD12	5:32:172:LEU:HA	1.92	0.42
5:33:77:ILE:HG21	5:33:127:PRO:HG3	2.00	0.42
5:39:24:VAL:HG23	5:39:26:THR:HG23	2.01	0.42
3:3A:188:VAL:HG13	3:3A:425:LEU:HG	2.01	0.42
4:3B:312:THR:HG22	4:3B:370:ASN:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3G:84:ARG:HH12	8:A5:232:ARG:HD3	1.83	0.42
3:3I:112:LYS:HE3	3:3I:112:LYS:HB3	1.91	0.42
4:3J:89:ASN:HB3	4:3J:119:VAL:HG21	2.01	0.42
4:3L:385:PHE:HE2	4:3L:412:GLU:HB2	1.84	0.42
2:4:196:LYS:HG3	2:4:200:GLN:OE1	2.19	0.42
5:46:162:GLN:HB2	5:46:171:LEU:HD11	2.01	0.42
5:49:155:LYS:HG3	5:49:177:VAL:HA	2.01	0.42
3:4A:377:MET:SD	3:4A:379:SER:HB3	2.59	0.42
4:4B:27:GLU:HG2	4:4B:241:ARG:NH2	2.34	0.42
4:4B:280:GLN:HE21	8:A3:122:GLN:NE2	2.17	0.42
3:4C:8:HIS:CE1	3:4C:21:TRP:HE1	2.37	0.42
3:4C:124:LYS:HB2	3:4C:124:LYS:HE2	1.87	0.42
4:4D:173:PRO:HD2	4:4D:205:GLU:HG2	2.01	0.42
3:4K:229:ARG:HB3	3:4K:363:VAL:HG11	2.01	0.42
3:4K:254:GLU:HA	3:4K:257:THR:HG22	2.01	0.42
4:4L:163:ILE:HD12	4:4L:254:ALA:HB2	2.01	0.42
2:5:259:TYR:HE2	2:6:260:ARG:HD2	1.84	0.42
5:50:103:HIS:CD2	5:50:174:LEU:HD23	2.55	0.42
5:57:17:SER:HA	5:57:20:PHE:HB3	2.01	0.42
5:57:77:ILE:HD11	5:57:84:PRO:HB3	2.01	0.42
4:5B:100:ASN:HB3	4:5B:103:LYS:HG3	2.02	0.42
4:5B:285:SER:O	4:5B:288:GLU:HG3	2.19	0.42
3:5C:73:THR:HA	4:5D:46:ARG:NH2	2.28	0.42
4:5D:260:PHE:HB2	4:5D:263:LEU:HD12	2.01	0.42
3:5E:169:PHE:HZ	3:5E:238:LEU:HD13	1.84	0.42
4:5F:54:ALA:HB3	4:5F:58:ARG:HB3	2.01	0.42
3:5G:96:LYS:HD2	4:5H:129:CYS:HB3	2.02	0.42
3:5K:5:ILE:HD12	3:5K:125:LEU:HB3	2.01	0.42
2:6:218:VAL:HA	2:6:221:ARG:HB2	2.01	0.42
6:65:975:LYS:HB2	6:65:975:LYS:HE3	1.78	0.42
6:66:459:VAL:O	6:66:463:ARG:HG2	2.18	0.42
3:6A:15:GLN:HE22	4:6B:245:GLN:HA	1.84	0.42
3:6C:403:ALA:HB1	4:6D:259:PRO:HB3	2.02	0.42
4:6D:132:GLY:HA2	4:6D:162:ARG:HB3	2.00	0.42
4:6F:23:VAL:O	4:6F:27:GLU:HB2	2.19	0.42
4:6H:235:GLY:HA2	4:6H:238:CYS:HB3	2.01	0.42
4:6H:398:TYR:HD2	4:6H:408:PHE:HZ	1.66	0.42
4:6N:8:GLN:HG3	4:6N:65:LEU:HA	2.01	0.42
4:7B:54:ALA:HB3	4:7B:58:ARG:HB3	2.00	0.42
3:7G:100:ALA:O	4:7H:255:VAL:HG11	2.19	0.42
3:7I:409:VAL:HG22	3:7I:415:GLU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7L:139:LEU:HA	4:7L:145:SER:HB3	2.01	0.42
7:87:369:GLN:HA	7:87:372:TRP:HD1	1.84	0.42
7:89:293:ILE:HG22	7:89:295:GLN:HG3	2.00	0.42
3:8A:108:TYR:HE2	3:8A:413:MET:HA	1.83	0.42
4:8B:299:MET:HE2	4:8B:299:MET:HB3	1.84	0.42
3:8C:100:ALA:HA	4:8D:252:LYS:HD2	2.01	0.42
3:8E:339:ARG:HG2	3:8E:342:GLN:NE2	2.34	0.42
4:8H:7:VAL:HA	4:8H:64:ILE:HB	2.01	0.42
4:8H:135:ILE:HD12	4:8H:137:HIS:HD2	1.84	0.42
4:9B:359:LYS:HD2	4:9B:359:LYS:HA	1.86	0.42
4:9D:60:VAL:HG11	4:9D:86:ARG:HD3	2.02	0.42
3:9E:265:ILE:HA	3:9E:432:TYR:HE1	1.83	0.42
4:9H:313:ALA:HB3	4:9H:349:MET:HG3	2.02	0.42
3:9K:83:TYR:HD2	3:9K:86:LEU:HD22	1.84	0.42
8:A2:39:LEU:HD22	9:B3:458:HIS:HE1	1.83	0.42
8:A8:335:ARG:HB3	9:B4:22:LEU:HD22	2.00	0.42
8:A8:366:PRO:HA	8:A8:369:VAL:HG22	2.00	0.42
9:B1:118:LEU:HA	9:B1:121:VAL:HG12	2.00	0.42
10:C0:74:ASP:HA	10:C0:75:PRO:HD3	1.87	0.42
10:D0:157:TYR:CZ	10:D0:356:PRO:HD3	2.55	0.42
10:D1:316:CYS:O	10:D1:320:LYS:HB2	2.20	0.42
10:E1:110:ILE:HD12	10:E1:283:PHE:HA	2.01	0.42
10:E1:301:ARG:HD3	14:L9:142:GLN:HA	2.02	0.42
10:E3:375:ILE:HG23	10:E3:379:LEU:HD12	2.01	0.42
10:E6:97:ILE:HD13	10:E6:397:PHE:HD1	1.84	0.42
12:F6:286:PRO:HA	12:F6:289:ILE:HG22	1.99	0.42
12:G7:242:TRP:CE2	12:G7:250:ARG:HD2	2.54	0.42
13:J3:412:ALA:O	13:J3:416:VAL:HG23	2.19	0.42
13:J6:295:LEU:HB3	13:J6:441:SER:HB3	2.01	0.42
14:K0:200:PHE:CE2	14:K0:227:PRO:HD3	2.55	0.42
14:L6:104:TYR:HB3	14:L6:106:TYR:CE1	2.53	0.42
1:d:426:GLU:O	1:d:429:ARG:HB2	2.19	0.42
1:e:388:ARG:O	1:e:392:GLU:HG3	2.19	0.42
1:C:414:GLN:C	1:d:522:ARG:HH22	2.28	0.42
1:L:355:ARG:HH22	1:W:322:ARG:NE	2.17	0.42
1:Q:446:LEU:HD13	1:U:446:LEU:HB2	2.00	0.42
1:S:370:LYS:HD2	1:S:370:LYS:HA	1.82	0.42
1:S:477:SER:O	1:S:480:ARG:HG2	2.19	0.42
1:Z:460:GLN:HG2	1:d:461:ARG:HH21	1.85	0.42
2:14:196:LYS:O	2:14:200:GLN:HG2	2.19	0.42
3:1C:269:LEU:HD12	3:1C:384:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1E:212:ILE:HD12	3:1E:302:MET:HB3	2.00	0.42
3:1K:79:ARG:HB3	3:1K:92:LEU:HD12	2.02	0.42
3:1M:398:MET:HE3	3:1M:403:ALA:HB3	2.01	0.42
5:25:155:LYS:HD2	5:25:176:CYS:O	2.19	0.42
4:2B:3:GLU:HA	4:2B:49:VAL:HA	2.02	0.42
4:2B:298:ASN:O	4:2B:298:ASN:ND2	2.52	0.42
3:2C:12:ALA:HA	15:2C:501:GTP:C5	2.55	0.42
3:2G:158:SER:HA	3:2G:166:LYS:HE3	2.02	0.42
4:2J:313:ALA:HB1	4:2J:367:PHE:CE1	2.55	0.42
4:2L:265:PHE:HD2	4:2L:378:PHE:HZ	1.66	0.42
5:37:129:VAL:HA	5:37:132:LYS:HD2	2.01	0.42
5:39:120:MET:HE3	5:39:120:MET:HB2	1.95	0.42
3:3A:9:VAL:HG23	3:3A:149:LEU:HD23	2.01	0.42
4:3F:79:GLY:HA3	6:64:867:TRP:HE3	1.84	0.42
4:3F:80:PRO:HG2	8:A5:254:ARG:HD2	2.01	0.42
4:3L:64:ILE:HD12	4:3L:119:VAL:HG12	2.01	0.42
4:3L:167:PHE:CE2	4:3L:233:MET:HG2	2.54	0.42
5:40:48:VAL:HG13	5:40:138:ILE:HG13	2.01	0.42
5:48:121:ILE:HG21	5:48:129:VAL:HG21	2.02	0.42
3:4A:335:ILE:HG23	3:4A:341:ILE:HD13	2.00	0.42
3:4C:268:MET:HE2	3:4C:378:ILE:HG22	2.00	0.42
3:4G:434:GLU:OE2	6:64:825:ARG:HD3	2.19	0.42
4:4H:66:MET:HE2	4:4H:66:MET:HB3	1.95	0.42
4:4H:221:THR:HG23	4:4H:223:GLY:N	2.34	0.42
3:4M:280:LYS:NZ	3:4M:286:LEU:HD13	2.34	0.42
3:4M:304:LYS:HD3	3:4M:304:LYS:HA	1.88	0.42
2:5:216:VAL:HG11	6:63:979:ARG:CZ	2.50	0.42
5:51:49:PRO:HA	5:51:70:PRO:HA	2.01	0.42
5:52:226:LYS:HD2	5:52:226:LYS:HA	1.92	0.42
5:53:52:ILE:HB	5:53:67:ARG:HB3	2.01	0.42
5:56:74:LYS:HE3	5:56:90:GLU:OE2	2.19	0.42
3:5A:14:ILE:HD12	3:5A:67:PHE:HB3	2.02	0.42
4:5F:86:ARG:HA	4:6F:281:TYR:HD2	1.84	0.42
4:5J:391:ARG:HD2	14:K5:73:PHE:CE2	2.54	0.42
4:5J:399:THR:HA	4:5J:403:MET:HB2	2.01	0.42
2:6:317:MET:HE2	2:6:317:MET:HB3	2.00	0.42
5:61:20:PHE:HE2	5:62:225:GLN:HA	1.84	0.42
6:63:845:VAL:HA	6:63:848:SER:HB3	2.01	0.42
6:65:596:PRO:HA	6:65:599:ILE:HG22	2.01	0.42
6:65:934:LEU:HD23	6:65:937:LEU:HD21	2.01	0.42
6:65:970:LEU:HD22	6:65:974:GLU:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6B:6:HIS:CD2	4:6B:134:GLN:HE21	2.37	0.42
4:6B:273:LEU:N	4:6B:292:GLN:HE22	2.17	0.42
4:6F:311:LEU:HD12	4:6F:342:VAL:HG21	2.01	0.42
4:6H:357:PRO:HG2	1:g:821:ASN:ND2	2.35	0.42
4:6J:101:TRP:CE3	4:6J:403:MET:HE1	2.49	0.42
4:6J:376:GLU:HA	4:6J:379:LYS:HG2	2.00	0.42
4:6N:361:LEU:HD12	4:6N:364:SER:HB3	2.00	0.42
2:7:161:LEU:O	2:7:165:ARG:HD2	2.19	0.42
7:77:330:ARG:HA	7:77:330:ARG:HD3	1.94	0.42
4:7F:203:ASP:O	4:7F:207:LEU:HG	2.19	0.42
4:7H:49:VAL:HG11	4:7H:241:ARG:HG2	2.02	0.42
2:8:304:GLU:HA	2:8:307:MET:HE2	2.02	0.42
7:80:279:ARG:HD3	7:80:279:ARG:HA	1.78	0.42
3:8A:265:ILE:HG22	3:8A:380:ASN:HD21	1.83	0.42
4:8B:134:GLN:HA	4:8B:165:GLU:O	2.18	0.42
4:8D:150:LEU:O	4:8D:154:LYS:HG2	2.19	0.42
4:8D:303:SER:N	4:8D:377:MET:HE3	2.35	0.42
3:8E:106:GLY:HA3	3:8E:148:GLY:HA3	2.00	0.42
3:8E:274:PRO:HD3	3:8E:291:ILE:HD11	2.02	0.42
3:8G:328:VAL:HG21	3:8G:355:ILE:HD11	2.01	0.42
3:8I:308:ARG:HE	3:8I:308:ARG:HB2	1.68	0.42
2:9:194:LYS:HA	2:9:197:VAL:HG12	2.02	0.42
7:96:351:LYS:HE2	7:96:351:LYS:HB2	1.87	0.42
3:9C:304:LYS:HD2	3:9C:304:LYS:HA	1.74	0.42
3:9C:319:TYR:HD2	3:9C:328:VAL:HG22	1.83	0.42
4:9D:306:ARG:HB2	4:9D:340:TYR:CZ	2.55	0.42
3:9G:343:PHE:CD2	14:M3:112:THR:HB	2.54	0.42
10:C0:348:ALA:HA	10:C0:351:ARG:HG2	2.01	0.42
10:D1:84:THR:HG23	10:D1:87:ASP:H	1.84	0.42
10:D2:392:THR:O	10:D2:395:ARG:HG2	2.19	0.42
10:D6:306:MET:O	10:D6:310:ILE:HG12	2.18	0.42
10:E0:93:ALA:O	10:E0:97:ILE:HG12	2.20	0.42
10:E3:281:GLU:O	10:E3:285:GLU:HG2	2.19	0.42
10:E5:61:ASP:HA	14:L7:142:GLN:NE2	2.35	0.42
10:E7:100:SER:HB3	10:E7:299:LEU:HD21	2.01	0.42
12:F8:230:VAL:HG21	12:F8:235:LEU:HD13	2.02	0.42
12:G2:222:ASP:HA	12:G2:225:TRP:CD1	2.55	0.42
12:G5:210:LEU:HB3	12:G5:211:LYS:H	1.59	0.42
13:J2:287:GLU:HG2	13:J2:670:GLU:OE2	2.20	0.42
14:K8:159:ASN:HD21	14:K8:222:THR:HG22	1.83	0.42
14:L0:169:PHE:HE1	14:L0:171:VAL:HG22	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L3:244:LYS:HB3	14:L3:246:GLN:H	1.84	0.42
1:f:638:LEU:HD21	1:j:817:GLY:HA3	2.00	0.42
1:B:394:LYS:HZ3	1:E:395:THR:HG23	1.84	0.42
1:S:425:ILE:O	1:S:429:ARG:HB2	2.19	0.42
1:T:635:ASN:ND2	1:X:631:LEU:HD12	2.35	0.42
1:T:647:LYS:HA	1:i:749:VAL:HG12	2.00	0.42
1:Y:647:LYS:HE2	1:Y:647:LYS:HB2	1.44	0.42
2:12:264:GLN:HA	2:12:267:HIS:CE1	2.54	0.42
2:12:294:GLU:HA	2:12:297:THR:HG22	2.02	0.42
4:1L:270:PHE:HE1	4:1L:318:ARG:HH21	1.68	0.42
3:1M:296:PHE:CE1	3:1M:317:LEU:HD21	2.54	0.42
3:1M:385:ALA:HB2	3:1M:432:TYR:HB3	2.00	0.42
5:20:89:VAL:O	5:20:102:THR:HA	2.20	0.42
5:20:97:LEU:HD21	5:25:188:MET:HE1	2.01	0.42
5:21:17:SER:HB2	5:22:214:LYS:HE2	2.01	0.42
4:2B:332:ASN:OD1	4:2B:336:LYS:HE2	2.19	0.42
3:2C:28:HIS:CE1	3:2C:243:ARG:HD2	2.55	0.42
3:2E:157:LEU:HB3	3:2E:166:LYS:NZ	2.35	0.42
3:2I:204:LEU:HD13	3:2I:231:ILE:HG12	2.02	0.42
3:2K:318:MET:HE2	3:2K:318:MET:HB3	1.66	0.42
5:32:166:TYR:HE1	5:33:129:VAL:HG13	1.83	0.42
5:33:120:MET:HA	6:67:339:PRO:HB2	2.02	0.42
5:39:36:LEU:HD23	5:39:76:LEU:HD23	2.00	0.42
3:3A:209:ILE:HG22	3:3A:227:LEU:HD12	2.00	0.42
3:3A:276:ILE:HG22	3:3A:280:LYS:HB3	2.01	0.42
4:3B:105:HIS:ND1	4:3B:150:LEU:HD12	2.35	0.42
3:3E:102:ASN:ND2	3:3E:105:ARG:HG3	2.35	0.42
3:3I:138:PHE:HZ	3:3I:235:ILE:HG12	1.85	0.42
4:3J:346:PRO:O	4:3J:347:ASN:ND2	2.50	0.42
3:3M:119:LEU:HA	3:3M:119:LEU:HD23	1.88	0.42
5:40:114:GLN:HG3	5:40:119:LEU:HB2	2.00	0.42
4:4B:284:LEU:HB3	4:4B:363:MET:SD	2.60	0.42
3:4G:165:SER:HB2	3:4G:199:ASP:OD2	2.19	0.42
4:4H:42:LEU:HD23	4:4H:42:LEU:HA	1.85	0.42
4:4J:294:PHE:CZ	4:4J:333:VAL:HG11	2.55	0.42
3:4K:310:GLY:HA3	3:4K:383:ALA:HB2	2.01	0.42
5:52:103:HIS:CD2	5:52:174:LEU:HD23	2.54	0.42
3:5A:119:LEU:HA	3:5A:122:ILE:HG12	2.00	0.42
3:5A:319:TYR:HB3	3:5A:323:VAL:HG21	2.01	0.42
4:5B:165:GLU:HB3	4:5B:198:GLU:HB3	2.02	0.42
4:5B:291:GLN:HA	6:67:799:PHE:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5D:313:ALA:HA	4:5D:369:GLY:HA2	2.01	0.42
4:5J:10:GLY:HA2	4:5J:143:THR:HG23	2.01	0.42
3:5K:17:GLY:HA2	3:5K:20:CYS:HB2	2.01	0.42
4:5N:212:PHE:CD2	6:68:785:VAL:HG13	2.54	0.42
6:63:858:PRO:HA	6:63:930:THR:HG23	2.01	0.42
6:65:260:TRP:CD1	6:65:437:ARG:HG2	2.55	0.42
6:68:322:ALA:HB1	6:68:416:MET:HB2	2.00	0.42
3:6C:391:MET:HE2	3:6C:391:MET:HB2	1.77	0.42
3:6E:169:PHE:HD2	3:6E:204:LEU:HD11	1.84	0.42
4:6H:388:MET:HG3	3:6I:348:PRO:HD2	2.00	0.42
3:6I:180:ALA:HB3	3:6I:183:GLU:HG2	2.01	0.42
4:6J:111:GLU:HA	7:83:398:LYS:HG2	2.01	0.42
3:6K:315:CYS:HB2	3:6K:377:MET:HE3	2.01	0.42
4:6N:189:VAL:HA	4:6N:192:LEU:HB2	2.00	0.42
7:72:352:VAL:HG23	14:K2:244:LYS:HA	2.00	0.42
7:79:296:ARG:HG3	7:79:317:GLN:HA	2.01	0.42
3:7A:224:TYR:HE2	4:7B:246:LEU:HD23	1.84	0.42
4:7B:263:LEU:HD11	4:7B:425:TYR:HE2	1.84	0.42
3:7E:116:ASP:HB3	14:L6:247:THR:HG23	2.02	0.42
4:7H:87:PRO:HA	4:7H:90:PHE:HD1	1.84	0.42
3:7I:106:GLY:HA3	3:7I:148:GLY:HA3	2.02	0.42
3:7K:100:ALA:O	4:7L:255:VAL:HG11	2.20	0.42
4:7L:101:TRP:HB2	4:7L:184:ASN:HD22	1.85	0.42
4:7L:310:TYR:HE2	4:7L:367:PHE:HZ	1.67	0.42
7:80:347:ILE:HG22	7:80:349:SER:H	1.84	0.42
7:87:334:LEU:HD11	7:87:347:ILE:HG23	2.01	0.42
3:8A:215:ARG:HH22	14:L8:249:VAL:HB	1.84	0.42
3:8A:352:LYS:HD3	3:8A:352:LYS:HA	1.81	0.42
4:8H:396:HIS:HA	4:8H:399:THR:HG22	2.01	0.42
3:8I:145:THR:HG23	3:8I:149:LEU:HD12	2.01	0.42
7:90:279:ARG:HG3	7:90:300:GLN:HE22	1.84	0.42
7:90:330:ARG:HH12	7:90:350:ARG:NH1	2.14	0.42
7:91:402:LYS:HD3	7:91:402:LYS:HA	1.88	0.42
4:9B:130:LEU:HB3	4:9B:162:ARG:NE	2.34	0.42
3:9C:53:PHE:HD2	3:9C:61:HIS:HB3	1.85	0.42
4:9D:170:PHE:CE2	4:9D:201:VAL:HG12	2.55	0.42
3:9E:75:VAL:O	3:9E:79:ARG:HG2	2.18	0.42
3:9I:7:ILE:HD11	3:9I:137:MET:HG2	2.01	0.42
4:9J:7:VAL:HG13	4:9J:64:ILE:HB	2.02	0.42
8:A2:37:HIS:HB3	8:A2:40:THR:HG22	2.00	0.42
8:A2:265:PRO:HD2	8:A2:270:PRO:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B5:142:LEU:HD23	9:B5:142:LEU:HA	1.88	0.42
10:D0:86:LEU:HD13	10:D0:319:LEU:HB3	2.01	0.42
10:D5:301:ARG:HH22	14:L3:143:ARG:CZ	2.33	0.42
10:D7:148:MET:HE1	14:K2:129:PRO:HG3	2.01	0.42
10:D7:293:MET:HB3	10:D7:297:ARG:NH1	2.35	0.42
10:D9:86:LEU:HD12	10:D9:313:TYR:HB2	2.00	0.42
10:E7:372:LEU:HA	10:E7:375:ILE:HG22	2.01	0.42
10:E9:294:SER:HA	10:E9:297:ARG:HG2	2.01	0.42
12:F9:196:ASP:O	12:F9:200:LEU:HB2	2.20	0.42
12:F9:212:TRP:HB3	12:F9:215:GLN:HE21	1.85	0.42
13:J1:296:ARG:HD3	13:J1:302:LEU:HD23	2.01	0.42
13:J3:466:LEU:HD13	13:J3:496:LEU:HA	2.01	0.42
13:J4:647:GLU:HA	13:J4:651:GLU:HB2	2.01	0.42
13:J7:328:ALA:HA	13:J7:331:ASN:HB2	2.02	0.42
1:a:624:GLN:OE1	1:f:625:GLN:NE2	2.52	0.42
1:a:633:ASP:OD2	1:j:831:ALA:HB3	2.20	0.42
1:c:574:LYS:HB3	1:c:574:LYS:HE2	1.47	0.42
1:j:740:PRO:HG3	1:j:753:LEU:HD23	2.02	0.42
1:F:452:PRO:HA	1:F:455:LYS:HG2	2.01	0.42
1:I:618:ARG:NH2	1:J:617:MET:HB3	2.35	0.42
1:J:584:GLU:O	1:J:588:THR:HG23	2.19	0.42
1:M:463:LYS:HD3	1:M:463:LYS:HA	1.82	0.42
1:P:664:ILE:HA	1:P:667:LYS:HD2	2.01	0.42
1:U:656:GLN:O	1:U:660:GLN:HG2	2.19	0.42
3:1I:136:LEU:HA	3:1I:167:LEU:O	2.19	0.42
3:1M:67:PHE:HD2	3:1M:92:LEU:HG	1.85	0.42
5:22:34:PRO:HB3	5:22:186:ARG:HH11	1.84	0.42
5:22:164:MET:HE2	5:22:169:ILE:HD13	2.02	0.42
3:2A:21:TRP:HA	3:2A:24:PHE:HB2	2.00	0.42
4:2B:164:MET:HB3	4:2B:197:ASP:HB2	2.02	0.42
4:2H:19:LYS:HA	4:2H:19:LYS:HD3	1.80	0.42
4:2H:260:PHE:HD2	4:2H:263:LEU:HD12	1.85	0.42
5:31:143:CYS:HA	5:31:163:SER:HB3	2.02	0.42
5:31:166:TYR:O	5:31:167:LYS:HE2	2.20	0.42
5:32:50:PHE:HD2	5:32:148:LEU:HD22	1.84	0.42
5:32:148:LEU:HD13	5:32:158:LEU:HD13	2.01	0.42
5:35:195:LEU:HA	5:35:198:LYS:HD2	2.01	0.42
5:37:214:LYS:HB3	5:37:221:LEU:HD22	2.02	0.42
4:3B:139:LEU:HG	4:3B:168:SER:HB2	2.02	0.42
4:3B:293:MET:HE2	4:3B:367:PHE:CD1	2.54	0.42
4:3B:378:PHE:HD2	4:3B:422:TYR:HE2	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3C:88:HIS:HE1	3:4C:283:HIS:H	1.67	0.42
3:3C:182:VAL:HG21	4:3D:255:VAL:HG12	2.01	0.42
4:3F:290:THR:HA	4:3F:293:MET:HG2	2.02	0.42
4:3J:140:GLY:HA3	4:3J:181:GLU:HG3	2.02	0.42
4:3J:361:LEU:HD21	8:A7:259:THR:HA	2.02	0.42
4:3L:254:ALA:O	4:3L:258:ILE:HG12	2.20	0.42
5:42:166:TYR:HB2	13:J4:338:LEU:HG	2.01	0.42
5:47:110:PHE:HZ	5:47:121:ILE:HG13	1.85	0.42
5:48:61:LEU:HA	5:48:62:PRO:HD3	1.82	0.42
3:4C:21:TRP:CZ2	3:4C:65:CYS:HB3	2.55	0.42
3:4C:71:GLU:HG2	3:4C:73:THR:H	1.84	0.42
3:4E:210:TYR:CD1	3:4E:227:LEU:HD21	2.54	0.42
4:4F:215:LEU:HD21	4:4F:273:LEU:HD22	2.01	0.42
4:4H:256:ASN:O	4:4H:312:THR:HG21	2.20	0.42
4:4L:113:ILE:HA	4:4L:116:VAL:HG12	2.01	0.42
5:55:51:GLU:HB3	5:55:147:VAL:HA	2.02	0.42
4:5D:310:TYR:CD1	4:5D:371:SER:HB2	2.55	0.42
5:60:188:MET:HB3	5:60:191:ARG:HH21	1.85	0.42
6:63:602:ARG:O	6:63:606:GLN:HB3	2.18	0.42
6:64:419:VAL:HG12	12:H9:100:ALA:HA	2.01	0.42
6:64:873:ARG:HA	9:B1:521:ARG:HB2	2.02	0.42
6:65:471:LEU:HD23	6:65:471:LEU:HA	1.89	0.42
6:66:145:MET:HE2	6:66:153:VAL:HG13	2.01	0.42
6:67:454:ASN:ND2	6:67:457:ILE:HD13	2.35	0.42
6:69:877:ALA:O	6:69:881:THR:HG23	2.19	0.42
3:6C:268:MET:HG2	3:6C:380:ASN:HA	2.02	0.42
4:6J:225:LEU:HD12	4:6J:225:LEU:HA	1.74	0.42
4:6L:282:ARG:HH22	4:6L:292:GLN:HG3	1.83	0.42
4:6N:377:MET:HE2	4:6N:377:MET:HA	2.02	0.42
7:71:308:TYR:CE1	7:71:322:PRO:HB2	2.55	0.42
3:7G:250:VAL:HG12	3:7G:352:LYS:HE3	2.01	0.42
4:7H:326:VAL:O	4:7H:330:MET:HB2	2.19	0.42
4:7J:100:ASN:HD21	4:7J:103:LYS:HB2	1.85	0.42
4:7J:113:ILE:HD11	4:7J:151:LEU:HD13	2.02	0.42
4:7J:186:THR:HA	4:7J:415:MET:HE1	2.01	0.42
3:7M:11:GLN:HA	3:7M:14:ILE:HG22	2.02	0.42
3:8A:166:LYS:HZ3	3:8A:198:THR:HA	1.84	0.42
3:8C:262:TYR:CG	14:M5:76:LEU:HD13	2.54	0.42
4:8F:362:LYS:HA	1:l:818:ALA:HB2	2.01	0.42
4:8H:375:GLN:HG3	4:8H:419:VAL:HG13	2.02	0.42
3:8I:390:ARG:O	3:8I:394:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8K:286:LEU:HB3	3:8K:373:ARG:HH21	1.84	0.42
7:93:351:LYS:HE2	7:93:351:LYS:HB2	1.87	0.42
3:9A:394:LYS:HE3	14:M5:193:ALA:HB2	2.01	0.42
3:9E:209:ILE:HD13	3:9E:231:ILE:HD11	2.02	0.42
3:9G:97:GLU:HA	4:9H:2:ARG:HH22	1.85	0.42
3:9I:317:LEU:HD23	3:9I:377:MET:SD	2.60	0.42
3:9I:391:MET:HE2	3:9I:391:MET:HB3	1.76	0.42
4:9J:240:LEU:HD11	4:9J:250:LEU:HG	2.01	0.42
4:9J:286:VAL:HG22	4:9J:363:MET:HE1	2.00	0.42
3:9K:208:ALA:HB2	3:9K:304:LYS:HG2	2.02	0.42
3:9K:319:TYR:HD1	3:9K:328:VAL:HG22	1.84	0.42
4:9L:344:TRP:CD1	4:9L:344:TRP:H	2.36	0.42
3:9M:391:MET:HA	3:9M:394:LYS:HG2	2.01	0.42
9:B1:30:ARG:HB2	9:B1:523:LYS:HE3	2.02	0.42
9:B5:154:PRO:HB2	9:B5:158:ALA:HB3	2.00	0.42
10:E3:86:LEU:HD13	10:E3:319:LEU:HD12	2.02	0.42
12:F0:226:ILE:HG12	12:F9:225:TRP:CD1	2.54	0.42
10:F2:351:ARG:HH22	10:F2:382:HIS:HB2	1.85	0.42
12:F5:196:ASP:HA	12:F5:199:TRP:CE2	2.55	0.42
12:G5:225:TRP:CZ2	12:G6:226:ILE:HD11	2.54	0.42
13:J4:325:LEU:HD13	13:J4:416:VAL:HG22	2.02	0.42
14:K4:175:ILE:HD12	14:K4:180:SER:HB3	2.02	0.42
14:K5:100:ALA:HB2	14:K5:105:LEU:HD12	2.01	0.42
1:a:598:ALA:HA	1:t:884:PRO:HD2	2.02	0.42
1:d:388:ARG:O	1:d:392:GLU:HG3	2.19	0.42
1:l:790:LEU:HD22	1:l:795:LEU:HB2	2.02	0.42
1:o:949:ALA:O	1:o:953:LYS:HG2	2.19	0.42
1:y:947:PHE:HB3	1:y:951:ARG:NH1	2.35	0.42
1:E:495:PHE:HB3	1:G:310:PHE:CE1	2.54	0.42
1:H:614:LEU:O	1:H:617:MET:HB3	2.20	0.42
1:H:626:LEU:HD11	4:8L:276:ARG:CZ	2.50	0.42
1:M:618:ARG:HD3	1:N:617:MET:HG3	2.02	0.42
1:R:446:LEU:HD13	1:V:446:LEU:HG	2.01	0.42
1:Y:436:VAL:HG13	1:c:435:LYS:HZ1	1.84	0.42
4:1D:134:GLN:HA	4:1D:165:GLU:O	2.20	0.42
3:1E:260:VAL:HA	3:1E:261:PRO:HD3	1.81	0.42
3:1M:323:VAL:HG13	3:1M:355:ILE:HG23	2.02	0.42
4:1N:68:LEU:H	4:1N:143:THR:HG21	1.85	0.42
1:2:897:LEU:HD21	8:A4:73:TYR:HB2	2.00	0.42
5:28:44:TYR:CZ	5:28:46:ARG:HD3	2.55	0.42
3:2A:431:ASP:HA	3:2A:434:GLU:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2B:113:ILE:HG21	4:2B:154:LYS:HG3	2.00	0.42
4:2B:178:THR:O	4:2B:181:GLU:HG2	2.20	0.42
3:2E:154:LEU:HD11	3:2E:168:ASN:ND2	2.35	0.42
3:2E:208:ALA:HB2	3:2E:304:LYS:HG2	2.02	0.42
4:2H:20:PHE:HA	4:2H:230:SER:OG	2.20	0.42
3:2I:16:ILE:HG13	3:2I:228:ASN:ND2	2.35	0.42
4:2J:54:ALA:HB3	4:2J:58:ARG:HB3	2.01	0.42
3:2M:180:ALA:HB3	3:2M:183:GLU:HG3	2.01	0.42
5:31:33:ASP:HB3	5:31:36:LEU:HD23	2.00	0.42
5:32:203:GLN:HA	5:32:206:LEU:HG	2.01	0.42
5:35:23:GLN:C	5:35:205:ARG:HH12	2.28	0.42
5:39:127:PRO:HA	5:39:130:LEU:HD12	2.01	0.42
4:3B:104:GLY:O	4:3B:147:MET:HB3	2.19	0.42
4:3B:396:HIS:HA	4:3B:399:THR:HG22	2.00	0.42
4:3D:161:ASP:HB3	4:3D:162:ARG:HD3	2.02	0.42
3:3E:71:GLU:HG2	3:3E:73:THR:HG22	2.02	0.42
3:3G:4:VAL:HG21	3:3G:136:LEU:HD13	2.00	0.42
3:3K:298:PRO:HB3	3:3K:307:PRO:HD2	2.02	0.42
5:47:114:GLN:HA	5:47:119:LEU:HG	2.01	0.42
5:47:116:ARG:HH21	5:47:117:GLN:HE21	1.67	0.42
3:5A:6:SER:HA	3:5A:136:LEU:O	2.20	0.42
4:5B:322:SER:HB3	4:5B:324:LYS:HE2	2.01	0.42
3:5C:132:LEU:HB3	3:5C:164:LYS:HE3	2.01	0.42
3:5E:287:SER:O	3:5E:291:ILE:HG12	2.19	0.42
4:5H:54:ALA:HB3	4:5H:58:ARG:HB3	2.00	0.42
3:5K:318:MET:HB2	3:5K:376:CYS:HB3	2.01	0.42
4:5N:242:PHE:CD1	4:5N:356:ILE:HB	2.54	0.42
4:5N:385:PHE:CE2	4:5N:412:GLU:HB3	2.55	0.42
5:61:84:PRO:HG2	5:61:123:PHE:CD2	2.55	0.42
6:63:165:VAL:HG11	6:63:557:LEU:HD23	2.01	0.42
6:69:581:LYS:HD3	6:69:581:LYS:HA	1.81	0.42
3:6I:274:PRO:HD3	3:6I:291:ILE:HD11	2.00	0.42
4:6J:156:ARG:HD2	4:6J:156:ARG:HA	1.76	0.42
3:6K:264:ARG:HA	3:6K:264:ARG:HD2	1.78	0.42
4:6L:391:ARG:HG3	3:6M:346:TRP:HB3	2.00	0.42
4:6N:8:GLN:HG2	4:6N:65:LEU:HG	2.01	0.42
4:6N:271:ALA:HB3	4:6N:365:VAL:HG12	2.02	0.42
7:78:308:TYR:CZ	7:78:322:PRO:HB2	2.54	0.42
3:7A:149:LEU:HA	3:7A:149:LEU:HD12	1.67	0.42
4:7D:227:HIS:CD2	1:k:812:PRO:HD3	2.55	0.42
4:7F:424:GLN:NE2	14:L6:143:ARG:HB3	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7I:115:VAL:HB	3:7I:149:LEU:HD22	2.01	0.42
3:7K:115:VAL:HG22	3:7K:153:LEU:HD22	2.02	0.42
4:7L:49:VAL:HG11	4:7L:241:ARG:HG2	2.02	0.42
3:7M:3:GLU:HA	3:7M:51:THR:HA	2.01	0.42
3:7M:260:VAL:HG23	3:7M:265:ILE:O	2.20	0.42
7:87:312:SER:O	4:8B:380:ARG:HG2	2.19	0.42
3:8A:237:SER:HA	3:8A:320:ARG:NH1	2.34	0.42
3:8E:60:LYS:HD2	3:8E:60:LYS:HA	1.84	0.42
3:8E:169:PHE:HZ	3:8E:238:LEU:HD22	1.84	0.42
3:8E:335:ILE:HD13	3:8E:338:LYS:HE2	2.02	0.42
4:8H:19:LYS:HA	4:8H:19:LYS:HD3	1.82	0.42
4:8H:47:ILE:HG13	4:8H:51:TYR:HB2	2.01	0.42
4:8H:191:GLN:HA	14:M2:133:VAL:HG21	2.01	0.42
4:8J:20:PHE:O	4:8J:24:ILE:HG12	2.19	0.42
3:8K:14:ILE:HG23	3:8K:67:PHE:HD2	1.84	0.42
7:93:268:TRP:HE1	7:93:392:ARG:HB2	1.85	0.42
3:9E:286:LEU:HD21	3:9E:373:ARG:H	1.85	0.42
4:9F:248:SER:HA	4:9F:252:LYS:HD3	2.01	0.42
3:9G:286:LEU:HD12	3:9G:286:LEU:HA	1.81	0.42
4:9L:233:MET:HA	4:9L:236:VAL:HG12	2.02	0.42
8:A7:154:THR:HB	8:A8:280:ALA:HB2	2.01	0.42
9:B6:119:SER:HB2	9:B6:150:MET:HB3	2.01	0.42
9:B7:486:ALA:HA	9:B7:489:ILE:HG22	2.01	0.42
10:E0:137:PHE:HE2	10:E4:312:LYS:HG3	1.85	0.42
10:E1:399:SER:O	10:E1:403:GLN:HG3	2.19	0.42
10:E6:317:LEU:HD12	10:E6:321:ARG:HH22	1.85	0.42
10:F2:70:ARG:HH12	14:M7:135:THR:HG21	1.85	0.42
10:F2:307:MET:HE1	10:F2:400:LEU:HD13	2.00	0.42
12:G7:261:TRP:CD1	12:G7:286:PRO:HG3	2.55	0.42
12:H2:94:LEU:HB2	12:H3:97:LEU:HD12	2.01	0.42
12:H4:327:GLU:HG3	12:H4:332:THR:HG21	2.02	0.42
13:J1:486:PHE:HB3	13:J1:489:SER:HB3	2.01	0.42
13:J1:659:ASP:HA	13:J1:662:ILE:HD12	2.02	0.42
14:K5:104:TYR:HB3	14:K5:106:TYR:CZ	2.55	0.42
14:K6:190:THR:HG21	14:K6:254:PHE:HA	2.02	0.42
14:M2:148:ILE:HD11	14:M2:173:PRO:HG2	2.02	0.42
14:M2:233:LEU:HA	14:M2:236:PHE:CD2	2.55	0.42
14:M7:158:ARG:HD3	14:M7:191:PRO:HA	2.02	0.42
1:h:811:ARG:HG3	1:h:812:PRO:HD2	2.02	0.42
1:h:817:GLY:HA3	1:h:824:GLN:NE2	2.35	0.42
1:i:830:SER:O	1:i:834:ARG:HG3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:939:THR:HG22	1:q:943:LYS:HZ3	1.85	0.42
1:G:408:ALA:O	1:G:412:GLU:HG3	2.20	0.42
1:I:574:LYS:HA	1:I:574:LYS:HD2	1.46	0.42
1:N:480:ARG:HA	1:N:483:ILE:HG22	2.02	0.42
1:N:603:ARG:NH1	1:N:604:ILE:HG13	2.34	0.42
1:N:605:LYS:HA	1:N:605:LYS:HD2	1.38	0.42
1:W:357:TYR:HA	1:W:360:ARG:HG2	2.02	0.42
1:Y:446:LEU:HD23	1:c:446:LEU:HD22	2.02	0.42
2:13:160:LEU:O	2:13:163:GLU:HG3	2.20	0.42
4:1B:310:TYR:HA	4:1B:371:SER:HB2	2.01	0.42
4:1F:21:TRP:HZ3	4:1F:50:PHE:HB3	1.84	0.42
4:1H:375:GLN:NE2	4:1H:419:VAL:HA	2.35	0.42
4:1H:387:ALA:HA	4:1H:390:ARG:HE	1.83	0.42
3:1I:138:PHE:CE1	3:1I:235:ILE:HD13	2.55	0.42
3:1I:417:GLU:HA	3:1I:420:GLU:HB3	2.01	0.42
3:1K:141:VAL:HA	3:1K:147:SER:HB3	2.02	0.42
3:1M:158:SER:HB3	3:1M:166:LYS:NZ	2.35	0.42
5:24:101:TYR:CD1	5:24:178:GLN:HA	2.54	0.42
5:26:65:VAL:HG21	12:G7:241:LEU:HG	2.01	0.42
5:27:205:ARG:O	5:27:209:ILE:HG12	2.20	0.42
5:28:49:PRO:HB2	5:28:68:LEU:HD11	2.01	0.42
4:2B:73:MET:HE3	4:2B:90:PHE:HB3	2.00	0.42
4:2B:156:ARG:HD3	4:2B:164:MET:HE2	2.01	0.42
4:2B:244:GLY:HA2	4:2B:355:ASP:HB2	2.02	0.42
4:2B:250:LEU:HA	4:2B:253:LEU:HB2	2.00	0.42
4:2D:199:VAL:HG23	4:2D:265:PHE:HA	2.01	0.42
4:2F:39:ASP:HB2	8:A5:314:PHE:CD1	2.55	0.42
3:2G:108:TYR:HA	3:2G:112:LYS:HE2	2.02	0.42
3:2K:2:ARG:HB3	3:2K:242:LEU:HD12	2.01	0.42
3:2K:298:PRO:HG2	3:2K:308:ARG:NH1	2.34	0.42
5:30:29:ILE:HD12	5:30:194:ALA:HB1	2.02	0.42
5:30:103:HIS:CE1	5:30:174:LEU:HB2	2.55	0.42
5:39:88:ARG:NH1	5:39:104:ALA:HB2	2.34	0.42
3:3A:239:THR:HB	3:3A:242:LEU:HD12	2.02	0.42
3:3C:80:THR:HA	3:3C:84:ARG:HD2	2.02	0.42
4:3D:68:LEU:HA	4:3D:68:LEU:HD23	1.85	0.42
4:3H:175:VAL:HG12	3:3I:336:LYS:HE3	2.01	0.42
4:3L:45:GLU:HB3	8:A7:213:GLN:HE21	1.84	0.42
3:3M:137:MET:HE1	3:3M:153:LEU:HD23	2.01	0.42
3:3M:295:ALA:HB1	3:3M:377:MET:SD	2.60	0.42
2:5:262:LEU:O	2:5:265:GLU:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:50:89:VAL:HB	5:50:103:HIS:HB3	2.02	0.42
5:53:73:VAL:HG21	5:53:134:LEU:HD13	2.02	0.42
5:55:30:ASP:HA	5:55:190:PHE:HE1	1.84	0.42
5:55:46:ARG:HH22	5:55:138:ILE:HG21	1.84	0.42
5:57:155:LYS:HG2	5:57:177:VAL:HG22	2.02	0.42
3:5A:169:PHE:HA	3:5A:202:VAL:O	2.20	0.42
3:5C:72:PRO:HD2	4:5D:2:ARG:NH1	2.34	0.42
3:5G:282:TYR:HB3	3:5G:283:HIS:CE1	2.55	0.42
4:5J:167:PHE:CE2	4:5J:233:MET:HG3	2.55	0.42
6:65:896:LEU:HD23	6:65:897:LEU:HG	2.01	0.42
6:67:249:ASP:HA	6:67:252:ARG:HG2	2.01	0.42
6:69:619:ALA:O	6:69:623:CYS:HB2	2.20	0.42
4:6B:162:ARG:HA	4:6B:162:ARG:HD3	1.90	0.42
3:6C:196:GLU:HA	14:L1:83:THR:HB	2.01	0.42
3:6E:306:ASP:HB2	14:K2:256:VAL:HG23	2.01	0.42
4:6F:12:CYS:HB3	4:6F:138:SER:HB2	2.02	0.42
3:6G:166:LYS:HE3	3:6G:166:LYS:HB3	1.85	0.42
4:6L:100:ASN:ND2	4:6L:103:LYS:HG3	2.34	0.42
3:6M:105:ARG:HG2	3:6M:411:GLU:HG3	2.01	0.42
4:6N:286:VAL:HG12	4:6N:289:LEU:HD22	2.01	0.42
7:73:395:ALA:HB3	14:K4:121:VAL:HG11	2.01	0.42
3:7A:18:ASN:HD21	3:7A:78:VAL:HG22	1.85	0.42
4:7B:5:VAL:HB	4:7B:133:PHE:CD1	2.55	0.42
4:7B:221:THR:HG22	4:7B:223:GLY:H	1.84	0.42
4:7B:326:VAL:O	4:7B:330:MET:HG2	2.20	0.42
3:7G:274:PRO:HG2	3:7G:371:VAL:HG11	2.02	0.42
4:7H:64:ILE:HD12	4:7H:119:VAL:HG12	2.02	0.42
4:7H:313:ALA:HA	4:7H:369:GLY:HA2	2.01	0.42
3:7K:21:TRP:HA	3:7K:24:PHE:HB2	2.01	0.42
3:7K:174:SER:HB2	3:7K:177:VAL:O	2.20	0.42
3:7K:305:CYS:SG	3:7K:384:ILE:HA	2.60	0.42
4:7L:150:LEU:HD12	4:7L:153:SER:HB2	2.02	0.42
7:82:264:GLN:HG2	7:82:327:ASN:HB2	2.01	0.42
7:86:314:ALA:HB2	4:8D:302:ALA:HB1	2.01	0.42
4:8B:396:HIS:HB2	14:M5:90:PHE:HZ	1.84	0.42
4:8F:130:LEU:H	4:8F:162:ARG:HH21	1.68	0.42
4:8F:285:SER:HB2	4:8F:287:PRO:HD2	2.00	0.42
3:8G:53:PHE:HB3	3:8G:61:HIS:HB3	2.02	0.42
3:8I:397:LEU:HD23	3:8I:397:LEU:HA	1.79	0.42
4:8J:113:ILE:O	4:8J:117:LEU:HD23	2.19	0.42
4:8J:303:SER:HB2	4:8J:376:GLU:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8K:189:LEU:HD22	3:8K:418:PHE:HE1	1.84	0.42
4:8L:171:PRO:HG3	4:8L:185:ALA:HB1	2.02	0.42
3:8M:62:VAL:HG11	3:9M:283:HIS:HB3	2.02	0.42
7:97:268:TRP:CD1	7:97:328:PRO:HD3	2.55	0.42
3:9E:174:SER:HB3	3:9E:207:GLU:H	1.85	0.42
3:9E:212:ILE:HD11	3:9E:300:SER:HA	2.02	0.42
3:9G:286:LEU:HB3	3:9G:373:ARG:HH21	1.84	0.42
4:9J:273:LEU:HA	4:9J:273:LEU:HD23	1.82	0.42
4:9J:289:LEU:HD22	4:9J:363:MET:HE2	2.02	0.42
4:9L:216:LYS:HD3	4:9L:216:LYS:HA	1.78	0.42
4:9L:286:VAL:HG21	4:9L:326:VAL:HG22	2.01	0.42
8:A8:241:LEU:HD12	8:A8:242:PRO:HD2	2.02	0.42
9:B6:145:PRO:HA	9:B6:178:ASN:HB2	2.02	0.42
9:B6:488:GLU:HA	9:B6:491:ARG:NH1	2.35	0.42
10:E4:306:MET:O	10:E4:310:ILE:HG12	2.20	0.42
10:E6:298:GLU:HG2	14:L8:143:ARG:NH1	2.35	0.42
10:E6:399:SER:O	10:E6:403:GLN:HB3	2.19	0.42
10:E8:345:MET:HE2	10:E8:369:SER:HB2	2.02	0.42
12:F0:264:ILE:HG12	12:F0:290:LYS:HG3	2.02	0.42
12:F5:220:PRO:HD2	12:F5:223:LEU:HD12	2.02	0.42
13:J4:501:ARG:O	13:J4:505:GLU:HG3	2.19	0.42
14:K2:97:ARG:HA	14:K2:123:SER:HB2	2.02	0.42
14:L3:155:TRP:HZ3	14:L3:168:PRO:HG3	1.84	0.42
14:M1:199:ILE:HA	14:M1:220:LEU:O	2.20	0.42
14:M5:76:LEU:HD12	14:M5:77:THR:HG23	2.02	0.42
1:d:352:LYS:HD2	1:d:352:LYS:HA	1.74	0.42
1:o:897:LEU:HA	1:o:900:GLU:HB3	2.01	0.42
1:J:572:ARG:HH11	1:J:575:LEU:HD11	1.85	0.42
1:L:323:MET:HB2	1:L:323:MET:HE2	1.74	0.42
1:L:331:GLU:O	1:L:335:ARG:HG2	2.20	0.42
1:M:638:LEU:O	1:M:639:LEU:C	2.62	0.42
1:M:643:ARG:NH1	1:M:647:LYS:HG2	2.35	0.42
1:O:660:GLN:HE21	1:O:660:GLN:HB2	1.66	0.42
1:R:664:ILE:HD11	3:6G:282:TYR:CE2	2.55	0.42
1:V:551:ALA:HA	1:V:554:HIS:HD1	1.84	0.42
4:1B:246:LEU:HB2	4:1B:353:VAL:H	1.84	0.42
3:1G:265:ILE:HD13	3:1G:432:TYR:CE1	2.55	0.42
4:1J:222:TYR:HB2	3:1K:325:PRO:HG3	2.02	0.42
3:1K:248:LEU:HB3	3:1K:354:GLY:HA2	2.00	0.42
3:1K:394:LYS:O	3:1K:398:MET:HG2	2.20	0.42
5:20:166:TYR:CE2	5:21:172:LEU:HD22	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:27:19:ASN:HA	5:27:23:GLN:HE21	1.84	0.42
5:28:103:HIS:CD2	5:28:174:LEU:HB2	2.55	0.42
3:2A:364:PRO:HB3	9:B7:149:ASP:HB3	2.01	0.42
4:2B:330:MET:HA	4:2B:333:VAL:HG12	2.02	0.42
4:2B:375:GLN:HE22	4:2B:419:VAL:HA	1.85	0.42
4:2D:248:SER:HA	4:2D:252:LYS:HG2	2.02	0.42
3:2G:308:ARG:HE	3:2G:308:ARG:HB2	1.72	0.42
3:2I:204:LEU:HD22	3:2I:302:MET:HE2	2.02	0.42
4:2L:4:ILE:HB	4:2L:50:PHE:HE1	1.85	0.42
3:2M:188:VAL:HG12	3:2M:421:ALA:HB1	2.02	0.42
5:33:113:MET:HE3	5:33:113:MET:HB3	1.92	0.42
3:3A:32:PRO:HG3	8:A3:239:ILE:HD12	2.02	0.42
3:3A:103:PHE:CE1	3:3A:189:LEU:HG	2.55	0.42
3:3C:9:VAL:HA	3:3C:68:LEU:HB2	2.00	0.42
3:3E:205:ASP:O	3:3E:209:ILE:HG12	2.20	0.42
4:3H:65:LEU:HB3	4:3H:73:MET:HE1	2.02	0.42
4:3H:285:SER:O	4:3H:288:GLU:HG3	2.19	0.42
3:3K:265:ILE:HG21	3:3K:313:MET:HE1	2.01	0.42
3:4A:209:ILE:HG12	3:4A:231:ILE:HD11	2.01	0.42
4:4F:294:PHE:CZ	4:4F:349:MET:HE1	2.55	0.42
3:4I:105:ARG:HG2	3:4I:411:GLU:HG3	2.02	0.42
4:4J:360:GLY:HA3	8:A6:118:SER:HB3	2.01	0.42
4:4L:42:LEU:HD12	8:A7:174:ARG:HE	1.85	0.42
3:4M:107:HIS:HD2	3:4M:152:LEU:HB2	1.85	0.42
5:53:117:GLN:HG3	5:53:119:LEU:HG	2.02	0.42
5:53:195:LEU:HA	5:53:198:LYS:HD2	2.02	0.42
3:5A:149:LEU:HD12	3:5A:149:LEU:HA	1.79	0.42
3:5I:358:GLN:HA	3:5I:359:PRO:HD3	1.90	0.42
4:5J:20:PHE:CG	4:5J:233:MET:HE2	2.55	0.42
3:5K:231:ILE:HD13	3:5K:231:ILE:HA	1.90	0.42
4:5L:32:PRO:HG3	4:5L:81:PHE:HE1	1.84	0.42
3:5M:83:TYR:HD1	3:5M:86:LEU:HD13	1.84	0.42
4:5N:272:PRO:HG3	4:5N:284:LEU:HD11	2.01	0.42
5:62:52:ILE:HD13	5:62:148:LEU:HB3	2.01	0.42
6:63:249:ASP:O	6:63:253:LYS:HG2	2.20	0.42
6:66:249:ASP:O	6:66:253:LYS:HG2	2.20	0.42
6:68:501:ARG:O	6:68:502:ALA:C	2.63	0.42
4:6D:259:PRO:HD2	4:6D:263:LEU:HD11	2.02	0.42
3:6E:124:LYS:HB2	3:6E:124:LYS:HE2	1.81	0.42
3:6E:239:THR:HG22	3:6E:242:LEU:HD12	2.01	0.42
3:6K:318:MET:HE3	3:6K:318:MET:HB3	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6N:313:ALA:HB1	4:6N:367:PHE:HE1	1.84	0.42
4:7B:287:PRO:HA	4:7B:329:GLN:NE2	2.34	0.42
3:7C:298:PRO:HG3	3:7C:308:ARG:HD2	2.02	0.42
4:7D:174:LYS:O	14:K0:110:GLY:HA3	2.19	0.42
3:7E:422:ARG:NH1	3:7E:426:ALA:HB2	2.34	0.42
3:7G:88:HIS:HB3	3:7G:91:GLN:HG3	2.02	0.42
3:7G:401:LYS:HD2	14:L5:144:PHE:CE2	2.55	0.42
3:7M:195:LEU:HD12	3:7M:428:LEU:HD22	2.01	0.42
7:82:376:GLU:O	7:82:380:TRP:CB	2.65	0.42
7:83:334:LEU:HD13	7:83:339:PHE:HZ	1.85	0.42
7:85:282:ARG:HH22	7:85:287:LEU:HB2	1.85	0.42
4:8B:318:ARG:HG2	4:8B:354:CYS:HB2	2.02	0.42
4:8D:91:VAL:HG21	4:8D:116:VAL:HG12	2.02	0.42
4:8H:237:THR:HG22	4:8H:250:LEU:HD11	2.00	0.42
4:8L:343:GLU:HB3	14:L0:197:ARG:NH2	2.34	0.42
3:8M:417:GLU:HA	3:8M:420:GLU:HG3	2.01	0.42
7:91:293:ILE:HG13	7:91:295:GLN:HG3	2.02	0.42
7:93:401:ILE:HD11	14:M4:108:TYR:N	2.35	0.42
4:9D:12:CYS:HB3	4:9D:138:SER:HB2	2.02	0.42
3:9E:13:GLY:HA2	3:9E:16:ILE:HG22	2.01	0.42
3:9G:280:LYS:HA	3:9G:283:HIS:CE1	2.55	0.42
4:9H:236:VAL:HG13	4:9H:237:THR:HG23	2.02	0.42
3:9I:54:SER:HB2	3:9I:64:ARG:HH11	1.85	0.42
3:9K:387:VAL:HG22	3:9K:390:ARG:HH22	1.85	0.42
3:9K:407:TRP:HE1	4:9L:258:ILE:HG23	1.84	0.42
4:9L:179:VAL:HG12	3:9M:258:ASN:HA	2.02	0.42
8:A9:350:ASP:O	8:A9:354:ARG:HG3	2.20	0.42
9:B7:41:ARG:HG2	9:B7:44:LEU:HD23	2.01	0.42
9:B7:482:ASP:H	9:B7:532:GLN:HE22	1.68	0.42
10:C8:402:GLU:HA	10:C8:407:CYS:HB3	2.02	0.42
10:C9:83:ARG:NH1	10:C9:88:LEU:HD13	2.35	0.42
10:C9:349:PHE:CD1	10:C9:361:TRP:HB3	2.55	0.42
10:D6:280:VAL:HG12	10:D6:347:GLU:HG3	2.02	0.42
10:E3:140:LYS:HG3	10:E3:142:ARG:H	1.84	0.42
10:E7:93:ALA:O	10:E7:97:ILE:HG12	2.20	0.42
10:E7:322:GLU:HA	10:E7:325:GLU:HG2	2.01	0.42
12:F0:261:TRP:CD2	12:F0:286:PRO:HG3	2.55	0.42
10:F2:100:SER:HB2	10:F2:389:PHE:CZ	2.54	0.42
12:F5:251:TYR:HD2	12:F5:252:LEU:HD22	1.85	0.42
12:F6:249:LEU:HD23	12:F6:252:LEU:HD12	2.02	0.42
12:G6:280:ALA:HA	12:G6:288:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J2:300:LEU:HD12	13:J2:312:ARG:HH11	1.84	0.42
13:J3:474:ARG:HB2	13:J3:503:GLY:HA2	2.01	0.42
13:J4:478:PRO:HG3	13:J4:507:SER:HB2	2.01	0.42
13:J7:677:MET:HE3	13:J7:677:MET:HB3	1.98	0.42
14:K0:251:SER:HB3	14:K0:255:VAL:HG12	2.00	0.42
14:L6:97:ARG:HG2	14:L6:123:SER:HB3	2.02	0.42
14:L8:204:PHE:CE1	14:L8:237:LEU:HD21	2.54	0.42
14:M7:152:ARG:O	14:M7:170:PHE:HA	2.20	0.42
1:a:596:GLU:O	1:a:600:LEU:HG	2.20	0.42
1:c:578:ARG:HD2	1:c:578:ARG:HA	1.94	0.42
1:e:375:GLN:HA	1:e:378:GLU:HG2	2.00	0.42
1:f:512:LYS:HE3	1:f:512:LYS:HB2	1.49	0.42
1:x:896:LEU:HD23	1:x:896:LEU:HA	1.86	0.42
1:x:897:LEU:HD21	1:x:938:THR:HB	2.02	0.42
1:B:520:TRP:HA	1:B:523:VAL:HG12	2.02	0.41
1:E:320:GLN:CD	1:f:599:SER:HB2	2.45	0.41
1:L:334:LEU:HB3	1:L:335:ARG:HH22	1.85	0.41
1:N:466:ASP:O	1:N:470:ARG:HG2	2.20	0.41
1:S:429:ARG:HH11	1:S:429:ARG:HD3	1.74	0.41
1:Y:363:PHE:O	1:Y:366:GLN:HG3	2.19	0.41
3:1A:9:VAL:HG13	3:1A:149:LEU:HD23	2.02	0.41
3:1C:66:VAL:HG11	3:1C:122:ILE:HD11	2.02	0.41
3:1C:156:ARG:HH21	3:1C:159:VAL:HG21	1.84	0.41
3:1G:347:CYS:HA	3:1G:348:PRO:HD3	1.92	0.41
3:1I:32:PRO:HG3	3:1I:83:TYR:HE1	1.85	0.41
3:1K:288:VAL:HG11	3:1K:327:ASP:HB3	2.02	0.41
3:1M:319:TYR:HB3	3:1M:323:VAL:HG21	2.00	0.41
4:1N:42:LEU:HB3	4:1N:242:PHE:CD1	2.55	0.41
4:1N:166:THR:OG1	4:1N:199:VAL:HG22	2.20	0.41
3:2C:403:ALA:HA	4:2D:260:PHE:CE2	2.55	0.41
4:2D:64:ILE:HD12	4:2D:119:VAL:HG12	2.02	0.41
3:2E:107:HIS:HD2	3:2E:108:TYR:CE2	2.38	0.41
3:2E:335:ILE:HD13	3:2E:335:ILE:HA	1.89	0.41
3:2M:209:ILE:HA	3:2M:212:ILE:HG12	2.02	0.41
5:33:48:VAL:HG22	5:33:138:ILE:HD11	2.02	0.41
5:33:77:ILE:HD11	5:33:81:GLU:HA	2.02	0.41
3:3C:217:LEU:HG	3:3C:275:ILE:HG22	2.01	0.41
3:3E:36:MET:HE2	3:3E:36:MET:HB3	1.87	0.41
3:3E:209:ILE:HA	3:3E:212:ILE:HG22	2.02	0.41
3:3I:70:LEU:HD22	3:3I:110:ILE:HG22	2.02	0.41
4:3J:14:ASN:HB3	4:3J:76:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4B:107:THR:HG21	4:4B:401:GLU:HG2	2.01	0.41
3:4G:191:THR:HG21	3:4G:425:LEU:HD13	2.02	0.41
3:4G:229:ARG:HH11	3:4G:363:VAL:HG12	1.85	0.41
3:4K:233:GLN:HE21	3:4K:368:LEU:HD13	1.84	0.41
5:54:134:LEU:HA	5:54:137:CYS:SG	2.60	0.41
3:5A:102:ASN:H	3:5A:144:GLY:HA2	1.84	0.41
4:5B:334:GLN:HE21	4:5B:334:GLN:HB2	1.72	0.41
3:5C:259:LEU:HB3	3:5C:268:MET:HE1	2.02	0.41
3:5E:304:LYS:HA	3:5E:304:LYS:HD3	1.90	0.41
3:5I:178:SER:HB2	4:5J:347:ASN:ND2	2.35	0.41
3:5K:306:ASP:HB3	3:5K:309:HIS:CE1	2.55	0.41
4:5N:183:TYR:HA	4:5N:385:PHE:HE1	1.85	0.41
4:5N:250:LEU:HD23	4:5N:250:LEU:HA	1.86	0.41
5:60:19:ASN:O	5:60:23:GLN:HB2	2.20	0.41
5:61:18:VAL:HG22	5:62:214:LYS:HZ2	1.84	0.41
5:61:26:THR:HB	5:61:29:ILE:HB	2.02	0.41
6:65:327:SER:HA	6:65:330:LEU:HG	2.02	0.41
6:66:510:SER:O	6:66:511:GLY:C	2.63	0.41
6:68:842:ILE:HD11	6:68:959:PRO:HD3	2.01	0.41
4:6D:65:LEU:HD13	4:6D:90:PHE:HE1	1.85	0.41
4:6F:280:GLN:HG2	4:6F:281:TYR:HD1	1.85	0.41
3:6G:103:PHE:H	3:6G:408:TYR:HE1	1.68	0.41
4:6H:28:HIS:HE2	4:6H:241:ARG:HD2	1.85	0.41
4:6J:28:HIS:HE2	4:6J:241:ARG:HH11	1.66	0.41
4:6J:398:TYR:HD2	4:6J:403:MET:HE3	1.84	0.41
3:6K:222:PRO:HD2	4:6L:324:LYS:HD3	2.00	0.41
4:6L:47:ILE:HG13	4:6L:51:TYR:HB2	2.02	0.41
4:6L:87:PRO:HA	4:6L:90:PHE:CD2	2.55	0.41
4:6L:235:GLY:HA2	4:6L:238:CYS:HB3	2.01	0.41
4:6L:312:THR:HA	4:6L:348:ASN:HB3	2.02	0.41
4:6N:19:LYS:HA	4:6N:22:GLU:HB2	2.02	0.41
4:6N:267:LEU:HD22	4:6N:301:CYS:SG	2.60	0.41
7:71:299:PHE:HZ	14:K2:128:ARG:HD3	1.84	0.41
7:71:316:PRO:HB2	7:71:318:THR:HG22	2.00	0.41
7:72:299:PHE:CE2	14:K3:126:ILE:HD12	2.55	0.41
7:72:347:ILE:HG21	7:72:350:ARG:HB2	2.02	0.41
7:77:279:ARG:HH21	10:D5:149:TYR:HB2	1.85	0.41
7:79:382:ASP:HB3	3:7E:437:ILE:HG12	2.02	0.41
3:7A:207:GLU:HB2	14:L1:253:PHE:CD2	2.55	0.41
4:7B:316:MET:HE1	4:7B:350:LYS:NZ	2.33	0.41
4:7D:262:ARG:HA	4:7D:262:ARG:HD3	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:7H:420:SER:O	4:7H:424:GLN:HG3	2.20	0.41
3:7K:70:LEU:HD12	3:7K:99:ALA:HB2	2.01	0.41
3:7M:312:TYR:HB2	3:7M:343:PHE:CD1	2.54	0.41
3:7M:430:LYS:HE2	3:7M:434:GLU:HG3	2.02	0.41
7:80:307:LYS:NZ	7:80:321:GLU:HG3	2.35	0.41
4:8B:409:THR:HA	4:8B:412:GLU:HG3	2.01	0.41
3:8C:306:ASP:HB3	3:8C:309:HIS:CE1	2.55	0.41
4:8F:8:GLN:OE1	4:8F:17:GLY:HA3	2.20	0.41
4:8F:276:ARG:HG2	1:l:813:PRO:HG3	2.02	0.41
3:8G:320:ARG:HG2	3:8G:358:GLN:O	2.19	0.41
3:8M:18:ASN:O	3:8M:22:GLU:HG2	2.19	0.41
3:9A:28:HIS:CD2	3:9A:49:PHE:HB3	2.55	0.41
3:9A:209:ILE:HG21	3:9A:230:LEU:HD11	2.02	0.41
4:9B:416:ASN:HA	4:9B:419:VAL:HG22	2.01	0.41
4:9F:46:ARG:NH1	4:9F:46:ARG:HB2	2.34	0.41
4:9F:290:THR:HA	4:9F:293:MET:HG2	2.02	0.41
4:9H:268:ILE:HD12	4:9H:367:PHE:O	2.19	0.41
4:9J:172:SER:HB3	4:9J:205:GLU:OE2	2.20	0.41
3:9K:285:GLN:HG3	3:9K:287:SER:H	1.85	0.41
3:9K:359:PRO:HA	3:9K:360:PRO:HD3	1.97	0.41
3:9M:117:LEU:HD12	3:9M:117:LEU:HA	1.91	0.41
3:9M:296:PHE:CE1	3:9M:377:MET:HG2	2.55	0.41
8:A2:318:LYS:HD2	9:B5:60:TYR:CE1	2.55	0.41
8:A5:387:ARG:HA	8:A5:387:ARG:HD3	1.96	0.41
8:A6:382:LEU:HD23	8:A6:382:LEU:HA	1.94	0.41
8:A8:323:LEU:HD12	8:A8:328:ARG:HG2	2.02	0.41
10:C0:293:MET:HE3	10:C0:297:ARG:HG3	2.01	0.41
10:C8:66:LEU:HD11	10:C8:312:LYS:HE3	2.01	0.41
10:C8:88:LEU:HG	10:C8:92:MET:HE1	2.01	0.41
10:D0:37:ASP:OD1	10:D0:40:ARG:HB2	2.20	0.41
10:D3:397:PHE:O	10:D3:401:MET:HG2	2.20	0.41
10:D5:63:TYR:CZ	14:L3:142:GLN:HB3	2.55	0.41
10:D6:318:PRO:HD2	10:E3:133:PHE:HB3	2.00	0.41
10:E0:361:TRP:CE2	10:E0:372:LEU:HD12	2.55	0.41
10:F2:61:ASP:HA	14:M7:142:GLN:NE2	2.35	0.41
12:G3:223:LEU:HD21	12:G3:239:ARG:HA	2.02	0.41
13:J6:418:LEU:HB2	13:J6:472:VAL:HG21	2.01	0.41
14:L4:248:LYS:HD3	14:L4:255:VAL:HG11	2.02	0.41
14:M4:148:ILE:HD13	14:M4:148:ILE:HA	1.95	0.41
1:f:581:LYS:HB3	1:f:581:LYS:HE2	1.36	0.41
1:u:904:ILE:HG21	1:u:932:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:917:ARG:HA	1:u:917:ARG:HD2	1.85	0.41
1:v:862:LEU:HG	1:v:937:GLY:HA2	2.01	0.41
1:D:600:LEU:O	1:D:604:ILE:HG12	2.20	0.41
1:E:387:ILE:HG12	1:c:500:ARG:HD3	2.02	0.41
1:I:534:GLN:HG2	1:J:534:GLN:HE22	1.85	0.41
1:I:628:VAL:O	1:I:629:LYS:C	2.63	0.41
1:I:631:LEU:HD21	1:J:632:ARG:HG3	2.01	0.41
1:J:625:GLN:NE2	1:J:629:LYS:HB3	2.35	0.41
1:J:626:LEU:O	1:J:629:LYS:HE2	2.21	0.41
1:M:599:SER:HB2	1:M:603:ARG:HH22	1.84	0.41
1:U:373:LEU:HA	1:U:376:MET:HG2	2.00	0.41
4:1B:192:LEU:HD21	4:1B:199:VAL:HG11	2.02	0.41
4:1D:178:THR:N	3:1E:352:LYS:HD3	2.35	0.41
3:1I:297:GLU:HA	3:1I:298:PRO:HD3	1.90	0.41
5:24:20:PHE:HZ	5:29:224:LEU:HB3	1.84	0.41
5:25:127:PRO:O	5:25:131:ILE:HD12	2.20	0.41
5:29:144:PHE:HE1	5:29:162:GLN:HG2	1.85	0.41
4:2B:190:HIS:CD2	4:2B:414:ASN:HD22	2.38	0.41
4:2F:186:THR:HG22	4:2F:411:ALA:HB1	2.02	0.41
4:2F:272:PRO:HG3	4:2F:364:SER:HA	2.02	0.41
4:2H:66:MET:SD	4:2H:151:LEU:HD22	2.59	0.41
3:2I:195:LEU:HD12	3:2I:195:LEU:HA	1.82	0.41
3:2M:70:LEU:HD23	3:2M:145:THR:HG23	2.02	0.41
3:3A:26:LEU:HB3	3:3A:361:THR:HG21	2.02	0.41
3:3C:228:ASN:HA	3:3C:231:ILE:HG12	2.01	0.41
4:3D:304:ASP:HA	4:3D:305:PRO:HD3	1.84	0.41
4:3H:205:GLU:HA	4:3H:208:TYR:HD1	1.85	0.41
4:3H:248:SER:HA	4:3H:252:LYS:HD2	2.01	0.41
3:3I:102:ASN:HD21	3:3I:407:TRP:HB3	1.86	0.41
4:3J:313:ALA:HB1	4:3J:367:PHE:HE1	1.85	0.41
3:4A:402:ARG:HB3	3:4A:405:VAL:HG11	2.01	0.41
4:4D:282:ARG:HE	4:4D:282:ARG:HB3	1.66	0.41
3:4K:417:GLU:HA	3:4K:420:GLU:HG3	2.02	0.41
4:4L:336:LYS:HD3	4:4L:336:LYS:HA	1.86	0.41
3:4M:271:SER:HB3	3:4M:301:MET:HA	2.01	0.41
5:56:90:GLU:OE1	5:56:92:THR:HG23	2.20	0.41
3:5A:3:GLU:O	3:5A:133:GLN:HG2	2.20	0.41
3:5A:219:ILE:HG13	3:5A:367:ASP:HB2	2.02	0.41
3:5A:224:TYR:HA	3:5A:227:LEU:HG	2.02	0.41
4:5B:397:TRP:CE2	3:5C:257:THR:HA	2.55	0.41
4:5F:201:VAL:HG21	4:5F:374:ILE:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5G:172:TRP:HE1	3:5G:391:MET:HG3	1.85	0.41
4:5H:293:MET:HG3	4:5H:367:PHE:HB2	2.02	0.41
4:5L:309:ARG:H	4:5L:372:THR:HG22	1.85	0.41
6:64:542:GLU:OE2	12:H9:61:THR:HG23	2.20	0.41
6:66:456:ASP:HA	6:66:459:VAL:HG12	2.02	0.41
6:66:581:LYS:HA	6:66:581:LYS:HD3	1.74	0.41
6:67:500:ARG:HB3	6:67:501:ARG:HH21	1.85	0.41
6:68:542:GLU:HA	6:68:545:GLU:HG3	2.01	0.41
3:6A:195:LEU:HD21	3:6A:264:ARG:HE	1.85	0.41
4:6B:117:LEU:HA	4:6B:117:LEU:HD23	1.92	0.41
4:6D:390:ARG:NH1	4:6D:391:ARG:HH21	2.15	0.41
4:6F:383:ASP:HB3	7:71:311:SER:HB2	2.01	0.41
4:6H:297:LYS:HG3	7:75:416:TRP:CE2	2.55	0.41
3:6I:66:VAL:HG22	3:6I:121:ARG:HG3	2.02	0.41
3:6K:7:ILE:HG21	3:6K:122:ILE:HD12	2.03	0.41
3:6M:175:PRO:HB3	3:6M:390:ARG:NH1	2.35	0.41
7:77:295:GLN:HB3	7:77:320:TRP:CD1	2.55	0.41
7:77:376:GLU:O	7:77:380:TRP:CB	2.68	0.41
3:7C:336:LYS:HD2	14:L1:112:THR:HG22	2.01	0.41
3:7E:21:TRP:CZ2	3:7E:65:CYS:HB3	2.55	0.41
4:7F:272:PRO:HB2	4:7F:282:ARG:HH22	1.85	0.41
4:7H:29:GLY:HA3	4:7H:36:TYR:HE2	1.85	0.41
3:7I:219:ILE:HD11	3:7I:222:PRO:HB3	2.02	0.41
3:7K:161:TYR:HA	14:L9:104:TYR:OH	2.20	0.41
7:87:290:GLU:HG2	4:8B:340:TYR:CE1	2.55	0.41
4:8B:215:LEU:HG	4:8B:217:LEU:HD23	2.01	0.41
4:8F:377:MET:HE3	4:8F:377:MET:HB3	1.94	0.41
4:8F:411:ALA:O	4:8F:415:MET:HG2	2.21	0.41
3:8K:200:VAL:HA	3:8K:266:HIS:HB2	2.02	0.41
7:97:408:ILE:HD11	4:9B:172:SER:HB2	2.01	0.41
3:9A:202:VAL:HG22	3:9A:268:MET:HG3	2.02	0.41
3:9C:241:SER:HB3	3:9C:249:ASN:HB3	2.02	0.41
3:9C:321:GLY:HA2	3:9C:359:PRO:HA	2.02	0.41
3:9E:166:LYS:H	3:9E:199:ASP:HB2	1.84	0.41
3:9G:397:LEU:HD21	14:M2:225:GLU:HB3	2.02	0.41
3:9I:88:HIS:HB3	3:9I:90:GLU:HG3	2.02	0.41
3:9I:182:VAL:HG22	3:9I:185:TYR:HB2	2.01	0.41
4:9J:167:PHE:HD1	4:9J:202:ILE:HD11	1.85	0.41
3:9M:274:PRO:HD3	3:9M:291:ILE:HD11	2.02	0.41
9:B4:512:ARG:NH2	9:B4:522:GLY:HA2	2.35	0.41
10:C9:343:ALA:O	10:C9:347:GLU:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D2:303:LEU:HD22	10:D2:396:LEU:HB3	2.02	0.41
10:D4:322:GLU:HA	10:D4:325:GLU:HG2	2.03	0.41
10:D6:78:ARG:HH22	10:E3:118:LEU:HG	1.85	0.41
10:E3:51:TYR:CZ	10:E3:79:ASP:HA	2.55	0.41
10:E3:287:PRO:HA	10:E3:288:PRO:HD3	1.91	0.41
10:E8:68:THR:HA	10:E8:71:GLN:HB3	2.01	0.41
10:F3:401:MET:HG2	10:F3:406:LEU:HB2	2.01	0.41
13:J5:672:LYS:HE3	13:J5:672:LYS:HB3	1.87	0.41
14:K1:159:ASN:ND2	14:K1:222:THR:HG22	2.34	0.41
14:L0:170:PHE:HB2	14:L0:172:ARG:NH1	2.34	0.41
14:L3:180:SER:HA	14:L3:183:GLN:HG2	2.02	0.41
14:L5:89:ARG:HD2	14:L5:102:ARG:HH11	1.85	0.41
14:L7:156:LEU:HD13	14:L7:189:ILE:HD11	2.02	0.41
14:M3:220:LEU:HD21	14:M3:236:PHE:CG	2.55	0.41
14:M5:195:PRO:HG2	14:M5:197:ARG:NH2	2.36	0.41
14:M7:100:ALA:HB2	14:M7:105:LEU:HD12	2.01	0.41
1:c:604:ILE:O	1:c:607:LEU:HB2	2.20	0.41
1:f:578:ARG:HD3	1:f:578:ARG:HA	1.26	0.41
1:E:423:ARG:HH21	1:p:875:ILE:HG13	1.85	0.41
1:G:399:GLU:HG3	1:G:403:ARG:HH21	1.85	0.41
1:M:485:LEU:HD11	1:N:484:GLN:HE22	1.85	0.41
1:T:639:LEU:HB3	1:i:826:VAL:HG12	2.01	0.41
1:V:474:LEU:HD23	1:V:474:LEU:HA	1.92	0.41
1:Y:586:LYS:O	1:Y:589:THR:OG1	2.35	0.41
1:1:882:GLU:HA	1:1:885:GLU:HB2	2.03	0.41
3:1A:105:ARG:HD2	3:1A:109:THR:HG21	2.03	0.41
3:1E:243:ARG:HG3	3:1E:244:PHE:CD1	2.56	0.41
3:1E:406:HIS:HA	3:1E:409:VAL:HG12	2.02	0.41
3:1K:204:LEU:HD12	3:1K:209:ILE:HD11	2.01	0.41
3:1M:317:LEU:HD13	3:1M:351:PHE:CE2	2.56	0.41
5:29:164:MET:HB3	5:29:166:TYR:CD1	2.56	0.41
3:2C:153:LEU:HA	3:2C:156:ARG:HB2	2.02	0.41
4:2D:403:MET:HE2	4:2D:403:MET:HB2	1.92	0.41
3:2E:100:ALA:O	4:2F:255:VAL:HG11	2.20	0.41
4:2F:187:LEU:HD13	4:2F:403:MET:HE1	2.02	0.41
4:2F:358:PRO:HB2	4:2F:361:LEU:HD12	2.03	0.41
4:2H:172:SER:HB3	4:2H:205:GLU:HB2	2.02	0.41
3:2I:319:TYR:CE2	3:2I:328:VAL:HG23	2.55	0.41
4:2L:178:THR:O	4:2L:181:GLU:HG3	2.20	0.41
2:3:205:ILE:HD12	2:4:208:TYR:HE2	1.85	0.41
3:3A:66:VAL:HB	3:3A:121:ARG:CZ	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3A:102:ASN:H	3:3A:144:GLY:HA3	1.85	0.41
4:3B:11:GLN:HA	4:3B:72:THR:HG21	2.03	0.41
4:3B:220:PRO:HG2	8:A2:255:ARG:HH22	1.85	0.41
4:3B:237:THR:HG23	4:3B:240:LEU:HD22	2.02	0.41
4:3B:257:LEU:HD21	4:3B:314:SER:OG	2.19	0.41
3:3C:167:LEU:HD12	3:3C:168:ASN:H	1.85	0.41
3:3E:406:HIS:CD2	4:3F:261:PRO:HD3	2.55	0.41
4:3F:163:ILE:HD11	4:3F:250:LEU:HB2	2.02	0.41
4:3L:35:THR:HB	8:A7:162:ARG:HD2	2.01	0.41
4:3L:221:THR:HG21	8:A8:253:PRO:HD2	2.01	0.41
3:3M:132:LEU:HD22	3:3M:164:LYS:HD2	2.03	0.41
3:3M:422:ARG:HD2	6:68:580:PRO:HG3	2.02	0.41
2:4:300:VAL:HG22	13:J2:283:TRP:CE2	2.55	0.41
5:45:193:ASN:O	5:45:196:LYS:HG2	2.20	0.41
4:4J:70:PRO:HG3	4:4J:94:GLN:HE22	1.84	0.41
4:4J:216:LYS:HD3	4:4J:216:LYS:HA	1.83	0.41
4:4J:334:GLN:NE2	4:4J:349:MET:H	2.18	0.41
3:4K:217:LEU:HD23	3:4K:219:ILE:HD11	2.01	0.41
4:4L:256:ASN:O	4:4L:312:THR:HG21	2.19	0.41
3:4M:319:TYR:CD1	3:4M:375:VAL:HG22	2.54	0.41
5:50:172:LEU:HD23	5:50:172:LEU:HA	1.95	0.41
4:5B:331:LEU:O	4:5B:335:ASN:HB2	2.20	0.41
3:5G:103:PHE:H	3:5G:408:TYR:HE1	1.69	0.41
3:5I:156:ARG:HH21	14:K5:247:THR:HG22	1.85	0.41
3:5I:159:VAL:HG13	7:75:351:LYS:HB3	2.02	0.41
3:5I:242:LEU:HD21	3:5I:251:ASP:HA	2.01	0.41
6:64:311:VAL:O	6:64:315:VAL:HG23	2.20	0.41
6:64:324:SER:HA	6:64:416:MET:HG2	2.02	0.41
6:66:494:LYS:HB3	6:66:498:ARG:HH21	1.85	0.41
6:67:258:HIS:CD2	6:67:261:LYS:HE3	2.54	0.41
6:67:806:LYS:HB3	6:67:806:LYS:HE2	1.93	0.41
3:6A:121:ARG:NH1	3:6A:124:LYS:HD2	2.35	0.41
3:6C:79:ARG:HH22	3:6C:94:SER:HB3	1.85	0.41
4:6D:42:LEU:HD11	4:6D:243:PRO:HG3	2.02	0.41
3:6E:274:PRO:HG2	3:6E:371:VAL:HG11	2.03	0.41
4:6F:268:ILE:HA	4:6F:367:PHE:O	2.21	0.41
3:6I:401:LYS:HD2	4:6J:344:TRP:CG	2.55	0.41
7:72:278:VAL:HG13	7:72:302:PRO:HG3	2.02	0.41
7:76:286:TRP:CZ2	7:76:293:ILE:HG12	2.55	0.41
4:7B:69:GLU:HG3	4:7B:96:GLY:HA2	2.02	0.41
3:7C:88:HIS:HB3	3:7C:91:GLN:OE1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7C:262:TYR:HD2	3:7C:265:ILE:HD13	1.85	0.41
4:7F:105:HIS:ND1	4:7F:106:TYR:HD1	2.19	0.41
4:7F:391:ARG:HG2	3:7G:346:TRP:CD1	2.54	0.41
3:7G:141:VAL:HG13	3:7G:173:PRO:HD3	2.02	0.41
3:7G:288:VAL:HG13	3:7G:319:TYR:HE2	1.86	0.41
4:7H:316:MET:HE3	4:7H:316:MET:HB3	1.83	0.41
4:7J:109:GLY:O	4:7J:113:ILE:HB	2.20	0.41
3:7K:237:SER:HA	3:7K:320:ARG:HD2	2.02	0.41
4:7L:207:LEU:HB3	4:7L:225:LEU:HD22	2.02	0.41
3:7M:164:LYS:HA	3:7M:164:LYS:HD3	1.70	0.41
7:80:378:MET:HE3	14:K0:240:TRP:HB2	2.02	0.41
7:87:385:PRO:HB3	3:8C:342:GLN:HE22	1.85	0.41
7:87:385:PRO:HB3	3:8C:342:GLN:NE2	2.35	0.41
4:8B:6:HIS:NE2	4:8B:8:GLN:HB3	2.36	0.41
3:8C:319:TYR:HB3	3:8C:323:VAL:HG21	2.01	0.41
4:8H:391:ARG:HG3	3:8I:346:TRP:CD1	2.56	0.41
4:8J:39:ASP:HB3	1:n:944:GLN:CD	2.45	0.41
4:8J:257:LEU:HD12	4:8J:312:THR:OG1	2.20	0.41
3:8K:134:GLY:HA3	3:8K:165:SER:HB2	2.01	0.41
3:8K:141:VAL:HG12	3:8K:187:SER:HA	2.02	0.41
3:8K:192:HIS:O	3:8K:196:GLU:HG2	2.21	0.41
3:8K:278:ALA:HA	3:8K:369:ALA:HB2	2.01	0.41
4:8L:105:HIS:HA	4:8L:150:LEU:HD12	2.00	0.41
7:92:317:GLN:HG3	4:9F:307:HIS:HB3	2.01	0.41
7:95:334:LEU:HA	7:95:337:LYS:HZ3	1.85	0.41
7:96:278:VAL:HG13	7:96:302:PRO:HG3	2.03	0.41
3:9A:244:PHE:HB2	3:9A:320:ARG:HH22	1.84	0.41
4:9D:4:ILE:HD13	4:9D:4:ILE:HA	1.97	0.41
4:9H:19:LYS:HA	4:9H:19:LYS:HD2	1.88	0.41
3:9I:301:MET:HG3	3:9I:307:PRO:HD3	2.02	0.41
8:A1:36:PRO:HA	9:B1:8:ILE:HG22	2.01	0.41
8:A2:57:THR:HG23	8:A2:95:PHE:HE1	1.85	0.41
8:A3:39:LEU:HA	8:A3:42:VAL:HG22	2.02	0.41
8:A6:79:ASP:O	8:A6:83:ARG:HG2	2.20	0.41
8:A6:242:PRO:HG3	9:B2:26:PHE:HZ	1.86	0.41
8:A7:383:LYS:HB3	8:A7:383:LYS:HE2	1.69	0.41
9:B7:34:PRO:HG2	9:B7:37:ARG:H	1.85	0.41
10:D7:86:LEU:HB3	10:D7:319:LEU:HD21	2.02	0.41
10:D7:367:ALA:O	10:D7:371:ARG:HD3	2.20	0.41
10:E2:287:PRO:HA	10:E2:288:PRO:HD3	1.78	0.41
10:E3:151:GLN:O	10:E3:155:MET:HG3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E8:325:GLU:HA	10:E8:328:LYS:NZ	2.34	0.41
12:F0:241:LEU:HD23	12:F0:262:LEU:HD22	2.01	0.41
12:G1:197:LEU:HD12	12:G1:216:TRP:CG	2.56	0.41
12:G5:261:TRP:CD1	12:G5:286:PRO:HB3	2.55	0.41
12:H2:65:GLU:HA	12:H2:68:ARG:HG2	2.02	0.41
12:I5:96:ASN:C	12:I5:96:ASN:HD22	2.28	0.41
13:J2:393:VAL:HG11	13:J2:422:PHE:HE1	1.84	0.41
13:J3:660:GLU:O	13:J3:664:LYS:HG2	2.20	0.41
14:K4:162:LYS:HB2	14:K4:163:HIS:CD2	2.55	0.41
14:K6:99:ILE:HG13	14:K6:105:LEU:HD22	2.02	0.41
14:K7:207:ILE:HG12	14:K7:213:ILE:HD11	2.02	0.41
14:M2:178:MET:HE1	14:M2:207:ILE:HG22	2.02	0.41
14:M4:182:TYR:O	14:M4:186:THR:HG23	2.19	0.41
1:a:680:LEU:HD22	1:f:680:LEU:HB3	2.03	0.41
1:b:368:GLN:OE1	1:e:365:LEU:HD12	2.21	0.41
1:c:599:SER:O	1:c:600:LEU:C	2.64	0.41
1:A:607:LEU:HD11	1:F:603:ARG:NH2	2.35	0.41
1:I:618:ARG:NH1	1:J:617:MET:SD	2.93	0.41
1:M:639:LEU:HA	1:M:639:LEU:HD13	1.83	0.41
1:N:600:LEU:HD13	1:N:600:LEU:HA	1.81	0.41
1:P:682:LYS:HD3	1:P:682:LYS:HA	1.78	0.41
1:R:495:PHE:HB3	1:V:495:PHE:CZ	2.55	0.41
1:R:681:ILE:O	1:R:685:ASN:HB2	2.21	0.41
1:U:360:ARG:HD2	1:U:360:ARG:HA	1.94	0.41
1:W:406:ARG:HA	1:W:406:ARG:HD3	1.87	0.41
2:10:218:VAL:HG21	6:65:975:LYS:HD3	2.01	0.41
3:1A:431:ASP:HA	3:1A:434:GLU:HG2	2.01	0.41
4:1D:318:ARG:HG2	4:1D:354:CYS:HB3	2.03	0.41
4:1H:199:VAL:HG23	4:1H:264:HIS:HD2	1.84	0.41
4:1J:165:GLU:HG3	4:1J:250:LEU:HD22	2.02	0.41
3:1K:101:ASN:HD22	4:1L:256:ASN:ND2	2.18	0.41
3:1K:113:GLU:HG3	3:1K:114:ILE:HG13	2.02	0.41
3:1K:132:LEU:HB3	3:1K:164:LYS:HZ2	1.85	0.41
3:1K:189:LEU:HD23	3:1K:189:LEU:HA	1.93	0.41
4:1N:314:SER:HB2	4:1N:368:VAL:O	2.20	0.41
4:1N:372:THR:HG21	4:1N:426:GLN:HB3	2.02	0.41
1:2:845:MET:HA	9:B7:471:PRO:HG2	2.02	0.41
1:2:857:THR:HG22	9:B7:447:PRO:HG2	2.03	0.41
5:27:55:GLN:HE21	5:27:149:ILE:HD12	1.84	0.41
3:2A:140:ALA:HB3	3:2A:146:GLY:HA3	2.01	0.41
4:2D:104:GLY:HA2	4:2D:109:GLY:HA3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2D:356:ILE:HA	4:2D:357:PRO:HD3	1.89	0.41
4:2H:273:LEU:HD12	4:2H:298:ASN:HD21	1.84	0.41
3:2I:319:TYR:CE1	3:2I:375:VAL:HG23	2.55	0.41
4:2L:7:VAL:HG22	4:2L:64:ILE:HB	2.02	0.41
2:3:171:MET:HE1	2:4:171:MET:HE1	2.03	0.41
5:35:101:TYR:HD1	5:35:178:GLN:HA	1.86	0.41
3:3A:311:LYS:HE3	3:3A:311:LYS:HB2	1.94	0.41
3:3E:191:THR:HG21	3:3E:425:LEU:HD13	2.02	0.41
4:3F:3:GLU:HA	4:3F:49:VAL:HA	2.03	0.41
4:3H:26:ASP:HB3	8:A6:264:GLN:NE2	2.36	0.41
3:3M:298:PRO:HB3	3:3M:307:PRO:HD2	2.02	0.41
5:44:52:ILE:HG23	5:44:150:MET:HE1	2.02	0.41
5:47:212:LEU:HD23	5:47:215:LEU:HD12	2.03	0.41
5:49:148:LEU:HD13	5:49:158:LEU:HB2	2.01	0.41
3:4A:8:HIS:CE1	3:4A:21:TRP:HE1	2.35	0.41
3:4C:203:MET:HE3	3:4C:267:PHE:CD1	2.55	0.41
3:4E:205:ASP:H	3:4E:303:ALA:HA	1.85	0.41
4:4F:169:VAL:HG12	4:4F:202:ILE:HB	2.02	0.41
4:4J:19:LYS:HD2	4:4J:19:LYS:HA	1.88	0.41
5:50:136:SER:O	5:50:140:GLU:HG3	2.21	0.41
5:53:19:ASN:O	5:53:23:GLN:HG3	2.21	0.41
5:55:182:GLU:O	5:55:186:ARG:HG2	2.21	0.41
5:58:198:LYS:HD2	5:58:198:LYS:HA	1.73	0.41
4:5B:11:GLN:HA	4:5B:72:THR:HG21	2.02	0.41
4:5B:135:ILE:HB	4:5B:166:THR:HG22	2.01	0.41
3:5C:248:LEU:H	3:5C:355:ILE:HB	1.85	0.41
3:5G:185:TYR:HE2	3:5G:398:MET:HE2	1.85	0.41
4:5H:153:SER:HA	4:5H:195:ASN:HD22	1.85	0.41
17:5L:501:GDP:H8	17:5L:501:GDP:H2'	1.70	0.41
6:65:861:TRP:CE2	6:65:863:ARG:HD3	2.56	0.41
6:68:152:GLY:HA3	6:68:154:ARG:HH12	1.85	0.41
6:68:967:ARG:HG2	6:68:969:VAL:H	1.84	0.41
6:69:944:TYR:O	6:69:948:ARG:HG2	2.20	0.41
3:6A:240:ALA:HA	3:6A:243:ARG:HE	1.85	0.41
4:6D:12:CYS:HB3	4:6D:138:SER:HB2	2.03	0.41
4:6D:306:ARG:HG2	4:6D:340:TYR:CZ	2.55	0.41
4:6F:86:ARG:HE	4:7F:281:TYR:HD2	1.69	0.41
3:6G:112:LYS:HE3	3:6G:156:ARG:HH12	1.85	0.41
3:6I:68:LEU:HD12	3:6I:68:LEU:HA	1.76	0.41
4:6J:105:HIS:CE1	4:6J:150:LEU:HD12	2.54	0.41
4:6L:329:GLN:HA	4:6L:332:ASN:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6M:336:LYS:HE2	14:K6:112:THR:HA	2.02	0.41
7:73:329:PRO:HG2	7:73:332:PHE:HB2	2.03	0.41
3:7A:209:ILE:HG21	3:7A:227:LEU:HG	2.02	0.41
4:7B:95:THR:HG23	4:7B:96:GLY:H	1.85	0.41
3:7C:316:CYS:SG	3:7C:352:LYS:HB3	2.60	0.41
3:7E:272:TYR:HD2	3:7E:275:ILE:HG12	1.85	0.41
3:7I:165:SER:HB2	3:7I:256:GLN:HE22	1.85	0.41
4:7J:110:ALA:HA	4:7J:113:ILE:HG22	2.02	0.41
7:80:320:TRP:CD1	14:L1:126:ILE:HD11	2.56	0.41
3:8A:10:GLY:O	3:8A:14:ILE:HG12	2.19	0.41
4:8B:375:GLN:NE2	4:8B:419:VAL:HB	2.34	0.41
3:8C:147:SER:HB2	3:8C:190:SER:HB2	2.02	0.41
4:8J:238:CYS:HB2	4:8J:354:CYS:HB3	1.91	0.41
3:8K:409:VAL:HG22	3:8K:415:GLU:HB3	2.03	0.41
2:9:163:GLU:HG2	2:9:167:ARG:HH11	1.86	0.41
2:9:248:LEU:O	2:9:252:THR:HG23	2.20	0.41
7:91:280:PRO:HA	7:91:299:PHE:HA	2.02	0.41
4:9B:318:ARG:HG3	4:9B:354:CYS:SG	2.60	0.41
3:9C:434:GLU:HA	3:9C:437:ILE:HG22	2.02	0.41
4:9F:6:HIS:CD2	4:9F:134:GLN:HG3	2.55	0.41
4:9H:269:GLY:N	4:9H:367:PHE:HB2	2.34	0.41
3:9I:209:ILE:HG21	3:9I:227:LEU:HD13	2.02	0.41
8:A2:315:ARG:HH22	9:B5:64:GLU:HG3	1.84	0.41
8:A2:345:ILE:HB	9:B7:24:PRO:HG3	2.02	0.41
8:A5:276:VAL:HG21	8:A5:326:SER:HB2	2.02	0.41
9:B2:135:SER:HA	9:B2:139:HIS:HE1	1.86	0.41
9:B5:514:VAL:HG11	9:B5:520:GLU:HB2	2.02	0.41
10:C8:97:ILE:HD13	10:C8:397:PHE:HD1	1.85	0.41
10:D5:35:TRP:CE2	14:K6:228:ALA:HA	2.56	0.41
10:D5:284:LEU:HB3	10:D5:351:ARG:HH22	1.84	0.41
10:D7:404:LEU:HD23	10:D7:404:LEU:HA	1.93	0.41
10:E5:36:PHE:CZ	10:E5:38:ARG:HD2	2.56	0.41
10:E8:61:ASP:HA	14:M2:142:GLN:NE2	2.36	0.41
10:F2:47:MET:O	10:F2:51:TYR:HB2	2.20	0.41
12:G4:242:TRP:CZ2	12:G4:250:ARG:HB3	2.56	0.41
13:J4:353:ARG:NH2	13:J4:357:LEU:HD13	2.36	0.41
14:K2:190:THR:HG21	14:K2:254:PHE:HA	2.02	0.41
14:K7:155:TRP:CD2	14:K7:241:VAL:HG11	2.55	0.41
14:M3:204:PHE:HE2	14:M3:237:LEU:HD21	1.86	0.41
14:M7:146:VAL:HG12	14:M7:148:ILE:HG22	2.03	0.41
1:a:574:LYS:HE3	1:a:574:LYS:HB3	1.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:591:ARG:O	1:a:592:ARG:C	2.63	0.41
1:a:661:ASN:O	1:a:665:THR:HG23	2.21	0.41
1:B:410:ALA:HA	1:B:413:HIS:CE1	2.56	0.41
1:G:302:GLU:HG3	1:G:310:PHE:HD2	1.85	0.41
1:I:586:LYS:HD3	1:I:586:LYS:HA	1.79	0.41
1:I:669:GLU:HB3	1:J:670:ASN:HD21	1.85	0.41
1:M:499:ARG:HG3	1:N:499:ARG:HH22	1.85	0.41
1:O:659:LEU:HB2	1:P:659:LEU:HD13	2.01	0.41
1:P:661:ASN:OD1	1:P:662:ASP:N	2.53	0.41
1:Q:397:ALA:HB1	1:U:401:THR:HG21	2.02	0.41
1:T:630:ARG:HH11	1:Y:352:LYS:HE3	1.84	0.41
1:T:673:LEU:HD21	1:X:674:ARG:HH21	1.85	0.41
1:U:334:LEU:HA	1:U:334:LEU:HD23	1.83	0.41
1:U:418:VAL:O	1:U:422:THR:HG23	2.21	0.41
1:Y:366:GLN:HA	1:Y:369:GLU:HG3	2.01	0.41
1:Z:491:LEU:HD23	1:Z:491:LEU:HA	1.89	0.41
2:12:238:GLU:O	2:12:242:LYS:HG3	2.21	0.41
3:1A:301:MET:HE1	3:1A:305:CYS:H	1.85	0.41
4:1B:100:ASN:HB3	4:1B:103:LYS:HB2	2.01	0.41
4:1F:66:MET:HG2	4:1F:116:VAL:HG21	2.02	0.41
4:1F:156:ARG:HD3	4:1F:164:MET:HE2	2.03	0.41
3:1I:207:GLU:HA	3:1I:210:TYR:HD2	1.86	0.41
4:1J:99:ASN:HB3	4:1J:178:THR:HG21	2.02	0.41
4:1J:268:ILE:HA	4:1J:367:PHE:O	2.21	0.41
3:1K:75:VAL:HG13	3:1K:79:ARG:HH12	1.85	0.41
4:2B:262:ARG:HD2	5:32:216:LYS:HZ2	1.83	0.41
4:2D:201:VAL:HG21	4:2D:374:ILE:HD11	2.02	0.41
4:2D:356:ILE:HG23	11:C5:209:PHE:HZ	1.85	0.41
3:2E:376:CYS:HB2	3:2E:378:ILE:HD12	2.02	0.41
4:2F:19:LYS:HE3	9:B1:82:SER:HB2	2.03	0.41
4:2F:60:VAL:HA	4:2F:61:PRO:HD3	1.89	0.41
4:2L:334:GLN:HE22	4:2L:348:ASN:N	2.18	0.41
4:2L:376:GLU:HA	4:2L:379:LYS:HG2	2.01	0.41
5:33:127:PRO:O	5:33:131:ILE:HG12	2.20	0.41
5:38:53:ARG:HD3	5:38:61:LEU:HD22	2.01	0.41
5:38:74:LYS:HB3	5:38:76:LEU:HD13	2.03	0.41
3:3A:397:LEU:HD11	4:3B:346:PRO:HD3	2.01	0.41
3:3C:72:PRO:HA	3:3C:94:SER:HB2	2.01	0.41
4:3D:100:ASN:ND2	4:3D:397:TRP:HB3	2.33	0.41
4:3F:54:ALA:HB3	4:3F:58:ARG:HB2	2.02	0.41
3:3G:172:TRP:CZ2	3:3G:391:MET:HE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3I:79:ARG:HG2	3:3I:92:LEU:HD13	2.02	0.41
3:3I:147:SER:HB2	3:3I:190:SER:HB3	2.03	0.41
5:43:28:ALA:HB1	5:43:32:MET:HE1	2.02	0.41
5:43:181:GLU:O	5:43:185:ARG:HG2	2.20	0.41
3:4A:262:TYR:HD1	6:67:820:TRP:HB3	1.84	0.41
4:4B:260:PHE:HB2	4:4B:263:LEU:HG	2.01	0.41
4:4D:19:LYS:HB2	4:4D:19:LYS:HE2	1.94	0.41
3:4G:250:VAL:HG22	3:4G:352:LYS:NZ	2.36	0.41
4:4L:392:LYS:HD2	6:68:823:HIS:CE1	2.55	0.41
3:4M:217:LEU:HA	3:4M:277:SER:HB2	2.03	0.41
5:50:103:HIS:CD2	5:50:105:LEU:HB2	2.56	0.41
3:5A:65:CYS:H	3:5A:91:GLN:NE2	2.18	0.41
4:5H:260:PHE:O	4:5H:263:LEU:HB2	2.20	0.41
4:5J:14:ASN:HD21	4:5J:67:ASP:HB2	1.85	0.41
4:5L:149:THR:HG21	4:5L:188:SER:HB2	2.03	0.41
6:64:485:LYS:HD2	6:64:487:TYR:CE1	2.55	0.41
6:66:134:PRO:HG3	6:66:546:HIS:CE1	2.55	0.41
6:68:336:THR:N	6:68:407:LEU:HD21	2.35	0.41
3:6A:10:GLY:O	3:6A:14:ILE:HG12	2.20	0.41
3:6K:134:GLY:HA3	3:6K:165:SER:HB3	2.02	0.41
4:6L:169:VAL:HG12	4:6L:202:ILE:HB	2.03	0.41
4:6N:6:HIS:CD2	4:6N:134:GLN:HG3	2.56	0.41
4:6N:173:PRO:HG3	4:6N:377:MET:HE1	2.02	0.41
7:71:269:LEU:HD21	7:71:328:PRO:HB3	2.02	0.41
7:79:249:ASN:HB3	4:7D:390:ARG:HD2	2.03	0.41
4:7H:200:GLN:HG2	4:7H:266:PHE:HB2	2.03	0.41
3:7K:342:GLN:HE21	14:L2:114:SER:C	2.28	0.41
4:8B:4:ILE:HA	4:8B:132:GLY:O	2.19	0.41
4:8B:5:VAL:HB	4:8B:133:PHE:CD1	2.56	0.41
4:8D:163:ILE:HD13	4:8D:250:LEU:HB3	2.03	0.41
4:8F:108:GLU:HG3	14:M3:99:ILE:HD12	2.02	0.41
4:8F:206:ALA:O	4:8F:210:ILE:HG12	2.21	0.41
3:8G:208:ALA:O	3:8G:212:ILE:HG12	2.21	0.41
4:8J:259:PRO:HG2	4:8J:311:LEU:HD13	2.02	0.41
3:8K:301:MET:HG3	3:8K:307:PRO:HD3	2.02	0.41
4:8L:135:ILE:HD12	4:8L:137:HIS:CD2	2.55	0.41
4:8L:308:GLY:HA3	4:8L:372:THR:HB	2.03	0.41
3:8M:419:SER:HB2	3:8M:422:ARG:NH2	2.35	0.41
7:91:279:ARG:HH12	10:F2:148:MET:H	1.69	0.41
7:95:268:TRP:CD1	7:95:328:PRO:HD3	2.54	0.41
3:9A:14:ILE:HD13	3:9A:14:ILE:HA	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:9B:32:PRO:HG3	4:9B:81:PHE:CZ	2.55	0.41
3:9I:52:PHE:HZ	3:9I:239:THR:HB	1.84	0.41
3:9M:9:VAL:HG12	3:9M:146:GLY:HA2	2.01	0.41
9:B3:45:ARG:HE	9:B3:45:ARG:HB2	1.70	0.41
9:B5:111:GLN:HA	9:B5:112:PRO:HD3	1.93	0.41
10:D0:340:LEU:HD12	10:D0:340:LEU:HA	1.86	0.41
10:D5:110:ILE:HD13	10:D5:282:GLN:HG2	2.02	0.41
10:D8:143:ASP:HA	10:D8:146:ALA:HB2	2.01	0.41
10:D9:105:PHE:HD2	10:D9:299:LEU:HD11	1.86	0.41
12:G5:274:MET:HE3	12:G5:278:LEU:HG	2.02	0.41
12:H6:71:ALA:HA	12:H6:74:LYS:HE2	2.01	0.41
13:J3:446:VAL:HG21	13:J3:523:ILE:HD12	2.03	0.41
13:J5:367:GLU:O	13:J5:371:ARG:HG2	2.21	0.41
14:K3:79:THR:HG21	14:K3:94:GLY:HA2	2.00	0.41
14:L0:97:ARG:HG2	14:L0:100:ALA:HB3	2.01	0.41
14:M6:82:TYR:C	14:M6:87:ARG:HH12	2.28	0.41
1:c:572:ARG:HA	1:c:572:ARG:HD3	1.55	0.41
1:c:588:THR:OG1	1:c:589:THR:N	2.52	0.41
1:q:918:THR:O	1:q:922:ARG:HG2	2.20	0.41
1:x:904:ILE:HG23	1:x:928:LEU:HB3	2.03	0.41
1:y:886:GLN:O	1:y:890:LEU:HG	2.21	0.41
1:M:610:VAL:CG1	1:N:611:THR:HA	2.49	0.41
1:U:518:ARG:NH1	1:V:686:PHE:HB3	2.35	0.41
2:15:222:GLU:O	2:15:225:ARG:HD3	2.20	0.41
4:1F:290:THR:HG21	4:1F:329:GLN:HB3	2.03	0.41
4:1H:177:ASP:O	3:1I:352:LYS:HA	2.21	0.41
3:1K:119:LEU:HD13	3:1K:122:ILE:HD11	2.02	0.41
4:1N:148:GLY:O	4:1N:152:ILE:HD12	2.20	0.41
4:1N:204:ASN:HA	4:1N:207:LEU:HG	2.02	0.41
1:2:921:GLU:O	1:2:925:MET:HG3	2.20	0.41
5:26:35:SER:HB3	5:26:76:LEU:HD11	2.03	0.41
3:2E:394:LYS:O	3:2E:398:MET:HG2	2.21	0.41
5:38:45:SER:HA	5:38:73:VAL:O	2.21	0.41
3:3A:30:ILE:HG22	3:3A:31:GLN:O	2.20	0.41
3:3A:118:SER:O	3:3A:122:ILE:HG12	2.20	0.41
3:3A:321:GLY:HA3	3:3A:372:MET:O	2.20	0.41
3:3C:221:ARG:HA	4:3D:324:LYS:HE2	2.03	0.41
3:3C:319:TYR:HB3	3:3C:323:VAL:HG11	2.02	0.41
4:3J:112:LEU:HD21	6:69:929:PRO:HG2	2.02	0.41
3:3K:327:ASP:OD1	9:B4:39:ALA:HB2	2.20	0.41
5:42:117:GLN:HE22	5:42:173:CYS:H	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:44:114:GLN:HA	5:44:119:LEU:HB2	2.01	0.41
5:45:182:GLU:HB3	5:45:186:ARG:HH21	1.85	0.41
5:49:56:GLU:CD	5:49:58:GLY:H	2.29	0.41
3:4A:227:LEU:O	3:4A:231:ILE:HG12	2.20	0.41
3:4G:67:PHE:HB2	3:4G:92:LEU:HA	2.02	0.41
3:4G:311:LYS:HE2	3:4G:344:VAL:HA	2.03	0.41
3:4I:194:LEU:HD13	3:4I:267:PHE:HE2	1.86	0.41
3:4I:262:TYR:HB2	3:4I:265:ILE:HD12	2.02	0.41
2:5:258:GLN:HA	2:5:261:ARG:HG3	2.03	0.41
5:51:127:PRO:O	5:51:131:ILE:HD12	2.21	0.41
5:55:84:PRO:HG2	5:55:123:PHE:CE2	2.56	0.41
5:58:87:VAL:O	5:58:104:ALA:HA	2.21	0.41
5:58:103:HIS:NE2	5:58:174:LEU:HD12	2.35	0.41
3:5A:135:PHE:O	3:5A:167:LEU:HB2	2.21	0.41
3:5C:332:VAL:HG13	3:5C:351:PHE:CD2	2.54	0.41
4:5F:256:ASN:O	4:5F:312:THR:HG21	2.21	0.41
3:5G:21:TRP:CZ2	3:5G:65:CYS:HB3	2.56	0.41
3:5G:238:LEU:HA	3:5G:238:LEU:HD23	1.84	0.41
3:5K:204:LEU:HD13	3:5K:231:ILE:HD12	2.02	0.41
3:5K:209:ILE:HG22	3:5K:227:LEU:HD22	2.02	0.41
4:5N:101:TRP:HZ2	4:5N:149:THR:HG21	1.86	0.41
5:62:91:LEU:HD12	5:62:101:TYR:CE1	2.55	0.41
6:64:861:TRP:CE2	6:64:863:ARG:HD3	2.55	0.41
6:65:501:ARG:HE	6:65:501:ARG:HB3	1.79	0.41
6:67:488:ILE:O	6:67:492:SER:OG	2.38	0.41
6:67:891:ARG:HB2	6:67:893:THR:HG23	2.03	0.41
4:6B:273:LEU:H	4:6B:292:GLN:HE22	1.68	0.41
3:6C:67:PHE:HB2	3:6C:92:LEU:HD13	2.03	0.41
3:6C:136:LEU:HA	3:6C:167:LEU:HB2	2.03	0.41
3:6E:216:ASN:HB3	3:6E:275:ILE:O	2.21	0.41
3:6I:313:MET:HG2	3:6I:380:ASN:O	2.21	0.41
4:6J:61:PRO:HD3	4:6J:84:LEU:HG	2.03	0.41
4:6N:7:VAL:HB	4:6N:135:ILE:HD13	2.02	0.41
7:75:295:GLN:HB3	7:75:320:TRP:CE3	2.55	0.41
4:7F:316:MET:HB2	4:7F:366:THR:OG1	2.20	0.41
4:7H:140:GLY:HA3	4:7H:171:PRO:HG3	2.02	0.41
4:7J:207:LEU:HD13	4:7J:225:LEU:HB3	2.02	0.41
3:7K:304:LYS:HA	3:7K:304:LYS:HD3	1.79	0.41
4:7L:113:ILE:HB	4:7L:147:MET:HE1	2.02	0.41
4:7L:153:SER:HA	4:7L:156:ARG:NH1	2.36	0.41
3:7M:163:LYS:HD2	14:L0:104:TYR:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:80:394:TYR:HE1	14:L1:122:TYR:HD2	1.67	0.41
7:82:251:VAL:HA	7:82:254:ARG:HD2	2.03	0.41
3:8A:88:HIS:HB3	3:8A:91:GLN:HE22	1.86	0.41
4:8B:51:TYR:HA	4:8B:60:VAL:O	2.20	0.41
4:8F:43:GLN:HE21	1:l:823:LEU:HB2	1.85	0.41
4:8H:399:THR:HG23	14:M2:90:PHE:HE2	1.86	0.41
4:8L:12:CYS:O	4:8L:16:ILE:HG12	2.21	0.41
7:94:330:ARG:HH11	7:94:375:LEU:HG	1.84	0.41
7:97:268:TRP:O	7:97:272:ALA:CB	2.67	0.41
3:9A:352:LYS:HA	3:9A:352:LYS:HD3	1.72	0.41
4:9F:384:GLN:HE21	14:M3:111:LEU:HD21	1.86	0.41
4:9H:396:HIS:CE1	3:9I:263:PRO:HD3	2.56	0.41
4:9J:12:CYS:HB2	4:9J:138:SER:HB2	2.01	0.41
10:C8:66:LEU:HD11	10:C8:312:LYS:HG2	2.02	0.41
10:D4:355:THR:HG22	10:D4:361:TRP:CD2	2.55	0.41
10:D5:31:PRO:HB2	10:D5:33:ARG:HG2	2.03	0.41
10:D6:107:ILE:HG23	10:D6:283:PHE:CG	2.55	0.41
10:E1:105:PHE:HD2	10:E1:299:LEU:HD11	1.85	0.41
10:E2:56:TYR:HE2	10:E2:68:THR:HG21	1.85	0.41
10:E7:106:PRO:HB3	10:E7:296:MET:HG2	2.02	0.41
12:F0:238:HIS:HE1	12:F0:259:MET:HG3	1.85	0.41
12:F6:264:ILE:HG13	12:F6:290:LYS:HG3	2.03	0.41
12:G4:208:SER:HB2	12:G4:233:ARG:NH2	2.36	0.41
12:G4:261:TRP:CE2	12:G4:286:PRO:HG3	2.55	0.41
13:J4:658:GLY:O	13:J4:662:ILE:HG13	2.21	0.41
14:L5:153:LEU:HD12	14:L5:154:MET:H	1.85	0.41
1:c:522:ARG:O	1:c:526:GLU:HG2	2.20	0.41
1:c:603:ARG:HH21	1:c:603:ARG:HB3	1.84	0.41
1:f:562:ILE:HD12	1:f:562:ILE:HA	1.89	0.41
1:o:877:LEU:HD22	1:o:945:ILE:HD12	2.01	0.41
1:x:940:HIS:O	1:x:944:GLN:HG3	2.20	0.41
1:C:330:ARG:HH11	1:G:327:TRP:CG	2.39	0.41
1:K:323:MET:HA	1:K:326:GLU:HB2	2.02	0.41
1:R:467:LEU:HD22	1:V:467:LEU:HD13	2.02	0.41
1:U:370:LYS:HE3	1:U:370:LYS:HB3	1.67	0.41
1:Y:562:ILE:HD12	1:c:562:ILE:CG1	2.25	0.41
3:1A:227:LEU:HD22	15:1A:501:GTP:HN1	1.85	0.41
4:1B:21:TRP:O	4:1B:25:SER:HB3	2.21	0.41
4:1D:43:GLN:HE21	4:1D:359:LYS:NZ	2.19	0.41
4:1F:54:ALA:HA	4:2F:283:ALA:HB2	2.02	0.41
3:1G:164:LYS:HE2	3:1G:164:LYS:HB2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1G:406:HIS:CD2	4:1H:261:PRO:HD3	2.55	0.41
4:1H:379:LYS:HA	4:1H:379:LYS:HD2	1.87	0.41
5:24:33:ASP:HA	5:24:34:PRO:HD3	1.95	0.41
5:25:162:GLN:NE2	5:25:164:MET:SD	2.87	0.41
5:29:144:PHE:CE1	5:29:162:GLN:HG2	2.55	0.41
5:29:218:PRO:HG2	3:2K:405:VAL:HG12	2.03	0.41
4:2B:20:PHE:HZ	4:2B:50:PHE:HE2	1.68	0.41
3:2C:10:GLY:O	3:2C:14:ILE:HG12	2.20	0.41
4:2F:385:PHE:HZ	4:2F:408:PHE:HD2	1.68	0.41
4:2H:13:GLY:HA2	4:2H:136:THR:HG22	2.02	0.41
3:2K:276:ILE:HD12	3:2K:281:ALA:HA	2.02	0.41
4:2L:378:PHE:HB3	4:2L:419:VAL:HG22	2.03	0.41
5:31:77:ILE:HG22	5:31:87:VAL:HG22	2.03	0.41
5:38:164:MET:HG2	5:38:165:GLU:HG3	2.02	0.41
3:3G:406:HIS:CD2	4:3H:261:PRO:HD3	2.56	0.41
4:3J:391:ARG:HD3	3:3K:346:TRP:HD1	1.86	0.41
3:3M:167:LEU:HD23	3:3M:200:VAL:HB	2.03	0.41
5:46:72:ARG:HD2	5:46:74:LYS:HE3	2.02	0.41
3:4E:227:LEU:O	3:4E:231:ILE:HG13	2.21	0.41
3:4E:317:LEU:HD23	3:4E:377:MET:HB2	2.02	0.41
4:4F:13:GLY:HA2	4:4F:16:ILE:HG22	2.03	0.41
3:4G:208:ALA:HB2	3:4G:304:LYS:HG2	2.01	0.41
3:4G:276:ILE:HD12	3:4G:281:ALA:HA	2.03	0.41
4:4H:278:SER:HB3	4:4H:282:ARG:HH21	1.86	0.41
3:4I:338:LYS:HB2	3:4I:338:LYS:HE2	1.85	0.41
5:53:130:LEU:HD21	5:53:174:LEU:HD11	2.02	0.41
5:59:73:VAL:HG13	5:59:91:LEU:HD23	2.03	0.41
4:5B:199:VAL:HG13	4:5B:265:PHE:HA	2.03	0.41
4:5B:318:ARG:HE	4:5B:358:PRO:HD3	1.85	0.41
3:5C:12:ALA:HB3	3:5C:140:ALA:HB2	2.02	0.41
4:5D:306:ARG:H	4:5D:306:ARG:HG2	1.68	0.41
3:5E:163:LYS:HB2	14:K3:104:TYR:HE1	1.86	0.41
4:5H:163:ILE:HG21	4:5H:250:LEU:HB3	2.03	0.41
3:5K:262:TYR:HD2	3:5K:265:ILE:HD11	1.86	0.41
4:5L:167:PHE:CZ	4:5L:233:MET:HG3	2.55	0.41
4:5N:173:PRO:HB3	4:5N:380:ARG:NH1	2.36	0.41
2:6:239:ARG:HD2	2:6:239:ARG:HA	1.77	0.41
6:64:151:TYR:HD2	6:64:564:MET:HG2	1.86	0.41
6:65:485:LYS:HB2	6:65:488:ILE:HG13	2.02	0.41
6:66:263:VAL:HA	6:66:303:LEU:HD21	2.02	0.41
6:67:845:VAL:HA	6:67:848:SER:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:67:915:ASN:HD21	9:B7:459:ARG:HH22	1.67	0.41
4:6F:186:THR:HA	4:6F:415:MET:HE1	2.03	0.41
4:6J:284:LEU:HD23	4:6J:362:LYS:HB2	2.03	0.41
3:6M:118:SER:O	3:6M:122:ILE:HG12	2.21	0.41
3:6M:421:ALA:O	3:6M:425:LEU:HG	2.20	0.41
7:77:400:CYS:N	7:77:414:ILE:HD12	2.36	0.41
3:7A:219:ILE:HD13	1:q:909:SER:O	2.21	0.41
4:7F:420:SER:HA	4:7F:423:GLN:HG2	2.02	0.41
3:7I:176:GLN:HB3	4:7J:331:LEU:HD21	2.03	0.41
3:7K:156:ARG:HD2	3:7K:156:ARG:HA	1.89	0.41
3:7K:198:THR:HG22	3:7K:199:ASP:O	2.20	0.41
4:7L:50:PHE:CE2	4:7L:241:ARG:HD3	2.56	0.41
2:8:296:ASP:O	2:8:300:VAL:HG23	2.20	0.41
7:80:279:ARG:O	7:80:299:PHE:HA	2.21	0.41
7:83:257:ARG:HD3	14:L2:117:ARG:HB3	2.01	0.41
7:85:412:MET:HE2	4:8F:205:GLU:HB2	2.03	0.41
7:86:313:LEU:HB2	7:86:315:ILE:HG13	2.03	0.41
7:87:268:TRP:CE2	7:87:325:PHE:HB2	2.55	0.41
7:89:416:TRP:CD1	4:8H:297:LYS:HG2	2.55	0.41
4:8B:139:LEU:HD11	4:8B:192:LEU:HD11	2.03	0.41
3:8G:240:ALA:HB1	3:8G:356:ASN:ND2	2.36	0.41
3:8G:311:LYS:H	3:8G:382:THR:HB	1.85	0.41
4:8H:299:MET:SD	4:8H:305:PRO:HG3	2.61	0.41
4:8J:249:ASP:O	4:8J:252:LYS:HB2	2.20	0.41
3:8M:141:VAL:HG11	3:8M:172:TRP:CE3	2.56	0.41
7:94:296:ARG:HG3	7:94:317:GLN:HA	2.02	0.41
3:9G:323:VAL:HB	3:9G:355:ILE:HD12	2.02	0.41
9:B2:130:LEU:HB2	9:B2:137:ARG:HD3	2.03	0.41
10:D0:324:ALA:O	10:D0:328:LYS:HG3	2.20	0.41
10:E3:50:GLU:HG3	10:E3:51:TYR:CD2	2.56	0.41
10:E5:86:LEU:O	10:E5:90:VAL:HG23	2.21	0.41
12:F8:280:ALA:HA	12:F8:288:ILE:HD11	2.02	0.41
12:G6:247:VAL:O	12:G6:250:ARG:HG3	2.21	0.41
12:I4:79:ASP:HA	12:I4:82:ARG:HG2	2.02	0.41
13:J1:652:THR:O	13:J1:656:ARG:HG2	2.21	0.41
13:J2:483:LYS:HB2	13:J2:483:LYS:HE2	1.81	0.41
14:K4:133:VAL:HG12	14:K4:134:VAL:HG23	2.03	0.41
14:K9:154:MET:HE2	14:K9:156:LEU:HD21	2.03	0.41
14:L4:139:LEU:HD23	14:L4:139:LEU:HA	1.81	0.41
14:M4:200:PHE:HE2	14:M4:227:PRO:HD3	1.86	0.41
1:c:576:SER:O	1:c:579:LEU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:599:SER:C	1:c:601:ARG:N	2.78	0.41
1:f:528:ARG:O	1:f:529:GLU:C	2.62	0.41
1:o:937:GLY:O	1:o:940:HIS:HB3	2.19	0.41
1:A:674:ARG:O	1:A:677:MET:HB2	2.21	0.41
1:L:370:LYS:HD3	1:L:370:LYS:HA	1.92	0.41
1:N:674:ARG:HA	1:N:674:ARG:HD2	1.33	0.41
1:O:653:LYS:HZ2	1:P:652:MET:HE2	1.86	0.41
1:Q:498:LYS:HD2	1:U:499:ARG:NE	2.36	0.41
1:Q:618:ARG:NH2	1:U:617:MET:HG3	2.34	0.41
1:S:384:LEU:HA	1:S:387:ILE:HG12	2.02	0.41
1:U:637:THR:HG21	1:h:816:VAL:HG21	2.03	0.41
1:Y:562:ILE:HG12	1:c:566:ARG:CZ	2.50	0.41
2:10:295:PHE:HZ	2:9:298:LEU:HD13	1.86	0.41
3:1A:11:GLN:HA	3:1A:14:ILE:HG12	2.03	0.41
4:1B:28:HIS:HA	4:1B:43:GLN:HE21	1.86	0.41
4:1B:285:SER:O	4:1B:288:GLU:HG3	2.21	0.41
3:1C:8:HIS:CD2	3:1C:17:GLY:HA3	2.56	0.41
4:1D:220:PRO:HD2	3:1E:326:LYS:HZ3	1.85	0.41
4:1D:330:MET:HA	4:1D:333:VAL:HG12	2.02	0.41
3:1E:36:MET:HE2	3:1E:36:MET:HB3	1.88	0.41
3:1E:133:GLN:HB3	3:1E:252:VAL:HB	2.03	0.41
3:1E:240:ALA:O	3:1E:244:PHE:HB2	2.20	0.41
3:1E:324:VAL:O	3:1E:328:VAL:HG23	2.21	0.41
3:1K:398:MET:SD	4:1L:345:ILE:HG12	2.61	0.41
4:1L:266:PHE:HD1	4:1L:368:VAL:HG12	1.85	0.41
4:1L:377:MET:HE2	4:1L:377:MET:HB2	1.88	0.41
1:2:890:LEU:HD12	1:2:942:ILE:HB	2.03	0.41
5:20:50:PHE:CD2	5:20:71:ILE:HB	2.56	0.41
5:27:117:GLN:HE21	5:27:117:GLN:CA	2.34	0.41
5:29:148:LEU:HD12	5:29:158:LEU:HD13	2.02	0.41
5:29:217:SER:HB3	4:2L:261:PRO:HG3	2.01	0.41
3:2A:280:LYS:HA	3:2A:280:LYS:HD2	1.87	0.41
4:2D:390:ARG:HG3	4:2D:391:ARG:HG3	2.03	0.41
4:2H:73:MET:HE3	4:2H:73:MET:HB2	1.94	0.41
3:2I:155:GLU:HA	3:2I:197:HIS:CD2	2.56	0.41
4:2J:2:ARG:HB3	4:2J:131:GLN:HB2	2.02	0.41
5:39:213:LEU:HD13	5:39:224:LEU:HD13	2.03	0.41
3:3A:51:THR:HB	3:3A:243:ARG:HG2	2.02	0.41
3:3A:406:HIS:CD2	4:3B:261:PRO:HG3	2.55	0.41
4:3B:64:ILE:HD13	4:3B:89:ASN:OD1	2.21	0.41
4:3B:276:ARG:HH22	6:66:878:PRO:HG3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3C:230:LEU:HD11	3:3C:275:ILE:HG23	2.03	0.41
3:3C:242:LEU:HD11	3:3C:252:VAL:H	1.86	0.41
3:3G:28:HIS:CE1	3:3G:243:ARG:HD2	2.56	0.41
3:3G:360:PRO:HG3	3:3G:374:ALA:HB2	2.02	0.41
4:3H:228:LEU:HD23	4:3H:300:MET:HE2	2.02	0.41
4:3H:389:PHE:HZ	4:3H:405:GLU:HB2	1.85	0.41
17:3J:501:GDP:C8	3:3K:248:LEU:HD13	2.56	0.41
3:3K:107:HIS:CD2	3:3K:152:LEU:HD13	2.55	0.41
5:40:40:HIS:HB3	5:40:76:LEU:HB3	2.02	0.41
5:42:201:LEU:HD23	5:42:201:LEU:HA	1.90	0.41
5:44:52:ILE:O	5:44:66:GLY:HA3	2.20	0.41
5:49:52:ILE:HD12	5:49:150:MET:HE1	2.03	0.41
4:4F:8:GLN:HE21	4:4F:65:LEU:HG	1.86	0.41
4:4F:326:VAL:O	4:4F:330:MET:HG2	2.21	0.41
4:4J:389:PHE:HZ	4:4J:405:GLU:HG2	1.84	0.41
3:4K:242:LEU:HA	3:4K:242:LEU:HD23	1.89	0.41
3:4M:280:LYS:HZ1	3:4M:286:LEU:HD13	1.85	0.41
5:50:126:TYR:HA	5:50:129:VAL:HG22	2.02	0.41
5:51:215:LEU:HG	6:63:949:ASN:HD21	1.86	0.41
5:53:126:TYR:HE1	5:53:172:LEU:HD21	1.86	0.41
5:55:32:MET:HE1	5:55:190:PHE:HA	2.03	0.41
3:5A:411:GLU:HA	14:K4:172:ARG:NH1	2.35	0.41
3:5A:415:GLU:HG3	10:C9:48:ARG:HH12	1.85	0.41
3:5A:434:GLU:HA	3:5A:437:ILE:HG12	2.03	0.41
4:5B:292:GLN:HG3	4:5B:298:ASN:ND2	2.33	0.41
3:5C:210:TYR:CE1	3:5C:227:LEU:HD11	2.56	0.41
4:5D:122:LYS:HG3	4:6D:291:GLN:OE1	2.21	0.41
4:5D:134:GLN:HA	4:5D:165:GLU:O	2.21	0.41
3:5E:10:GLY:O	3:5E:14:ILE:HG12	2.21	0.41
4:5F:73:MET:HA	4:5F:76:VAL:HG12	2.01	0.41
4:5F:316:MET:O	4:5F:365:VAL:HA	2.21	0.41
3:5G:21:TRP:CZ3	3:5G:52:PHE:HB3	2.56	0.41
4:5H:202:ILE:HD13	4:5H:229:VAL:HG13	2.02	0.41
3:5I:138:PHE:HZ	3:5I:235:ILE:HG12	1.85	0.41
5:60:144:PHE:CE1	5:60:162:GLN:HG3	2.56	0.41
5:60:195:LEU:HD13	5:60:198:LYS:HG3	2.03	0.41
6:63:454:ASN:HD21	6:63:457:ILE:HD12	1.86	0.41
6:63:845:VAL:HG12	6:63:947:LEU:HD21	2.03	0.41
6:64:151:TYR:HD1	6:64:170:PRO:HD3	1.86	0.41
6:64:332:LYS:HB2	6:64:332:LYS:HE3	1.87	0.41
6:65:617:VAL:HG21	6:65:955:GLU:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:66:540:PHE:O	6:66:544:ILE:HG12	2.20	0.41
6:68:337:LEU:HD23	6:68:337:LEU:HA	1.90	0.41
4:6H:167:PHE:CZ	4:6H:233:MET:HG3	2.56	0.41
3:6I:58:ALA:HB2	1:a:667:LYS:HB3	2.01	0.41
3:6I:313:MET:HE1	3:6I:435:VAL:HG11	2.03	0.41
3:6K:168:ASN:HB3	3:6K:201:ALA:HA	2.02	0.41
3:6M:422:ARG:NH1	3:6M:426:ALA:HB2	2.36	0.41
4:6N:211:CYS:HA	4:6N:215:LEU:HB2	2.02	0.41
7:76:325:PHE:HD2	7:76:326:PRO:HD2	1.85	0.41
3:7A:147:SER:O	3:7A:151:CYS:HB2	2.21	0.41
3:7C:144:GLY:HA2	3:7C:186:ASN:HD21	1.83	0.41
3:7C:250:VAL:HG11	3:7C:352:LYS:NZ	2.35	0.41
4:7D:257:LEU:HD13	4:7D:312:THR:HG23	2.02	0.41
3:7E:316:CYS:SG	3:7E:318:MET:HE3	2.61	0.41
3:7G:263:PRO:HG2	14:L6:82:TYR:CE1	2.55	0.41
3:7K:189:LEU:HD13	3:7K:418:PHE:HA	2.01	0.41
3:7K:317:LEU:HB3	3:7K:319:TYR:CE2	2.56	0.41
7:83:266:ASN:O	7:83:270:VAL:HG23	2.21	0.41
7:87:279:ARG:NH2	10:F3:149:TYR:HB2	2.35	0.41
4:8B:416:ASN:HA	4:8B:419:VAL:HG22	2.03	0.41
4:8D:86:ARG:NH2	4:9D:278:SER:HA	2.36	0.41
4:8D:206:ALA:O	4:8D:210:ILE:HG12	2.21	0.41
4:8D:295:ASP:HB2	4:8D:297:LYS:HE2	2.02	0.41
3:8E:145:THR:HB	16:8E:502:MG:MG	1.44	0.41
3:8E:301:MET:SD	3:8E:307:PRO:HG3	2.60	0.41
4:8F:125:GLU:HB3	4:8F:126:GLY:H	1.66	0.41
4:8H:181:GLU:HA	4:8H:184:ASN:HD22	1.85	0.41
3:8I:71:GLU:HB2	4:8J:2:ARG:HH21	1.85	0.41
4:8J:64:ILE:HD12	4:8J:64:ILE:HG23	1.89	0.41
4:8L:217:LEU:HD13	4:8L:276:ARG:HH21	1.85	0.41
3:8M:422:ARG:HA	3:8M:425:LEU:HG	2.01	0.41
7:90:375:LEU:HD22	14:L0:240:TRP:CZ2	2.56	0.41
7:90:378:MET:HE1	14:L0:234:GLU:HG3	2.03	0.41
7:97:308:TYR:CZ	7:97:322:PRO:HB2	2.56	0.41
3:9A:169:PHE:CE2	3:9A:235:ILE:HD13	2.56	0.41
3:9A:306:ASP:HB3	3:9A:309:HIS:CE1	2.56	0.41
4:9B:86:ARG:NE	4:9B:87:PRO:HD2	2.24	0.41
4:9B:174:LYS:HD3	4:9B:205:GLU:HA	2.02	0.41
4:9D:210:ILE:HG21	4:9D:228:LEU:HD11	2.03	0.41
4:9D:268:ILE:HG23	4:9D:300:MET:HE2	2.03	0.41
3:9E:270:SER:HA	3:9E:377:MET:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9G:311:LYS:HE2	3:9G:344:VAL:HG23	2.02	0.41
8:A5:161:ILE:HD11	8:A5:187:VAL:HG21	2.03	0.41
9:B5:49:MET:SD	9:B5:52:LYS:HD2	2.61	0.41
9:B7:511:LEU:HB3	9:B7:519:ALA:HB1	2.03	0.41
10:C9:386:LEU:HD12	10:C9:386:LEU:HA	1.93	0.41
10:D1:43:ALA:O	10:D1:47:MET:HG3	2.20	0.41
10:D5:298:GLU:HA	10:D5:301:ARG:HG2	2.02	0.41
10:E1:34:VAL:HG21	14:L2:226:PRO:HG3	2.02	0.41
10:E8:47:MET:HE3	10:E8:55:TYR:HD1	1.86	0.41
10:F1:104:SER:HA	10:F1:340:LEU:HD21	2.01	0.41
10:F1:110:ILE:HG12	10:F1:283:PHE:HD1	1.86	0.41
10:F2:71:GLN:CD	14:M7:152:ARG:HE	2.28	0.41
10:F3:84:THR:H	10:F3:87:ASP:HB2	1.86	0.41
12:F6:265:GLY:HA2	12:F6:266:PRO:HD3	1.93	0.41
12:F7:226:ILE:HD11	12:F8:251:TYR:CD1	2.56	0.41
13:J1:654:THR:HG22	13:J1:657:ARG:HH21	1.86	0.41
13:J2:380:ALA:HB1	13:J2:393:VAL:HG13	2.02	0.41
13:J4:377:LEU:HG	13:J4:400:LEU:HD21	2.02	0.41
13:J5:485:ILE:HG12	13:J5:511:SER:HB3	2.03	0.41
1:r:873:PRO:HG2	1:r:875:ILE:HG12	2.02	0.41
1:s:877:LEU:HB3	1:s:878:PRO:HD2	2.02	0.41
1:y:917:ARG:HD2	1:y:917:ARG:HA	1.95	0.41
1:B:394:LYS:HB2	1:B:394:LYS:HE2	1.84	0.41
1:C:424:LEU:HB3	1:G:423:ARG:HH12	1.86	0.41
1:D:684:ARG:CZ	1:H:684:ARG:HG2	2.51	0.41
1:I:499:ARG:HH22	1:L:329:ASP:HB2	1.86	0.41
1:I:628:VAL:HB	1:I:632:ARG:HH21	1.86	0.41
1:I:632:ARG:O	1:I:633:ASP:C	2.64	0.41
1:J:601:ARG:HE	1:J:601:ARG:HB3	1.56	0.41
1:K:327:TRP:CZ3	1:L:327:TRP:HE3	2.38	0.41
1:M:496:ALA:O	1:M:499:ARG:HB2	2.21	0.41
1:M:610:VAL:HG11	1:N:611:THR:CG2	2.49	0.41
1:M:614:LEU:HD13	1:N:614:LEU:CA	2.48	0.41
1:N:494:ASN:O	1:N:497:GLN:HG3	2.21	0.41
1:Y:592:ARG:HG3	1:Y:592:ARG:H	1.76	0.41
2:10:179:MET:HA	2:10:182:MET:HG3	2.02	0.41
2:12:159:LEU:HA	2:12:162:GLN:HG2	2.03	0.41
2:14:320:GLN:HA	2:14:323:GLU:HG2	2.03	0.41
3:1A:25:CYS:HB3	3:1A:30:ILE:HB	2.03	0.41
4:1B:3:GLU:HB2	4:1B:130:LEU:HD13	2.03	0.41
4:1B:191:GLN:HE22	4:1B:195:ASN:HD21	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1B:326:VAL:O	4:1B:330:MET:HG3	2.21	0.41
3:1C:185:TYR:HE2	3:1C:404:PHE:HD2	1.67	0.41
4:1D:338:SER:HA	4:1D:341:PHE:HD2	1.85	0.41
3:1E:166:LYS:H	3:1E:199:ASP:HB2	1.85	0.41
3:1G:222:PRO:HD2	4:1H:324:LYS:HB2	2.03	0.41
3:1G:262:TYR:HB2	3:1G:265:ILE:HG22	2.02	0.41
3:1G:406:HIS:HA	3:1G:409:VAL:HG12	2.03	0.41
4:1H:113:ILE:HG13	4:1H:117:LEU:HD23	2.03	0.41
4:1H:235:GLY:HA2	4:1H:238:CYS:HB3	2.02	0.41
3:1I:265:ILE:HG22	3:1I:380:ASN:HD21	1.85	0.41
4:1J:105:HIS:CD2	4:1J:150:LEU:HD13	2.56	0.41
4:1J:230:SER:HA	4:1J:233:MET:HB3	2.03	0.41
4:1J:376:GLU:HA	4:1J:379:LYS:HG2	2.03	0.41
3:1K:395:PHE:HE2	3:1K:422:ARG:HB2	1.86	0.41
4:1L:7:VAL:HG22	4:1L:135:ILE:HG22	2.03	0.41
4:1L:212:PHE:CE2	3:1M:326:LYS:HD2	2.55	0.41
3:1M:107:HIS:HD2	3:1M:152:LEU:HB2	1.85	0.41
3:1M:167:LEU:HA	3:1M:200:VAL:O	2.21	0.41
3:1M:274:PRO:HG3	3:1M:286:LEU:HG	2.03	0.41
4:1N:133:PHE:HB3	4:1N:135:ILE:HD11	2.03	0.41
5:22:232:ALA:HA	5:22:235:ARG:HG2	2.03	0.41
5:23:77:ILE:HD13	5:23:127:PRO:HG3	2.03	0.41
5:26:98:PHE:CD1	5:26:188:MET:HE1	2.56	0.41
5:26:145:LEU:HD11	5:26:168:PHE:CZ	2.56	0.41
5:27:17:SER:HA	5:27:20:PHE:HB3	2.03	0.41
5:27:89:VAL:HB	5:27:103:HIS:HB3	2.03	0.41
5:29:44:TYR:HB3	5:29:75:ILE:H	1.85	0.41
5:29:101:TYR:HB3	5:29:176:CYS:SG	2.61	0.41
3:2A:52:PHE:O	3:2A:64:ARG:HG3	2.21	0.41
3:2A:247:ALA:HB3	3:2A:355:ILE:HG23	2.03	0.41
4:2B:294:PHE:CE1	4:2B:333:VAL:HG11	2.56	0.41
3:2C:121:ARG:HA	3:2C:121:ARG:HD2	1.86	0.41
4:2D:260:PHE:HA	4:2D:261:PRO:HD3	1.92	0.41
3:2E:88:HIS:HB3	3:2E:91:GLN:HG2	2.03	0.41
3:2E:275:ILE:HG23	3:2E:368:LEU:HD21	2.03	0.41
4:2F:7:VAL:HG22	4:2F:64:ILE:HD12	2.03	0.41
4:2H:205:GLU:HG2	3:2I:329:ASN:HD21	1.85	0.41
3:2I:28:HIS:CE1	3:2I:243:ARG:HD2	2.56	0.41
4:2J:33:THR:HG21	9:B4:70:TRP:HZ3	1.85	0.41
4:2J:253:LEU:O	4:2J:257:LEU:HB2	2.20	0.41
3:2K:70:LEU:HD12	3:2K:145:THR:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2K:289:ALA:HA	3:2K:331:ALA:HB2	2.03	0.41
4:2L:36:TYR:CZ	4:2L:38:GLY:HA3	2.56	0.41
3:2M:138:PHE:CD1	3:2M:169:PHE:HB2	2.56	0.41
3:2M:278:ALA:HB1	9:B6:121:VAL:HG22	2.02	0.41
2:3:222:GLU:HG2	2:4:222:GLU:OE1	2.20	0.41
2:3:314:TYR:HA	2:3:317:MET:SD	2.61	0.41
5:30:139:LYS:HG3	5:30:140:GLU:H	1.85	0.41
5:32:89:VAL:HG13	5:32:103:HIS:HE1	1.86	0.41
5:35:44:TYR:CE2	5:35:46:ARG:HB2	2.56	0.41
3:3A:167:LEU:HD13	3:3A:252:VAL:HG22	2.03	0.41
3:3A:177:VAL:HG22	3:3A:207:GLU:HG3	2.02	0.41
3:3A:219:ILE:HD13	3:3A:219:ILE:HG21	1.89	0.41
4:3B:97:ALA:HA	4:3B:103:LYS:HE3	2.02	0.41
4:3D:130:LEU:HD11	4:3D:133:PHE:CE1	2.56	0.41
3:3E:112:LYS:HA	3:3E:115:VAL:HG12	2.02	0.41
4:3F:230:SER:HA	4:3F:233:MET:HE3	2.03	0.41
3:3G:104:ALA:HB2	3:3G:413:MET:HE3	2.01	0.41
3:3G:358:GLN:HA	3:3G:359:PRO:HD3	1.95	0.41
4:3H:377:MET:HE2	4:3H:377:MET:HB3	1.79	0.41
3:3K:88:HIS:CD2	3:4K:283:HIS:H	2.39	0.41
3:3K:320:ARG:HG2	3:3K:374:ALA:HB3	2.02	0.41
3:3K:406:HIS:HA	3:3K:409:VAL:HG12	2.03	0.41
4:3L:320:ARG:HG3	8:A7:230:ARG:HH22	1.86	0.41
3:3M:67:PHE:HB2	3:3M:92:LEU:HD13	2.02	0.41
3:3M:296:PHE:CE1	3:3M:335:ILE:HG21	2.56	0.41
5:43:206:LEU:HG	5:44:206:LEU:HD11	2.02	0.41
5:49:235:ARG:HH22	6:64:592:SER:HB2	1.85	0.41
3:4A:124:LYS:HE2	4:5B:291:GLN:HG2	2.03	0.41
3:4A:265:ILE:HG23	3:4A:432:TYR:CZ	2.55	0.41
3:4C:28:HIS:HE1	3:4C:243:ARG:HH11	1.67	0.41
4:4D:86:ARG:HH21	3:5E:284:GLU:HG3	1.85	0.41
4:4D:260:PHE:HD2	4:4D:263:LEU:HD21	1.86	0.41
4:4D:293:MET:HE1	4:4D:315:ALA:HB2	2.03	0.41
3:4E:26:LEU:HD22	3:4E:364:PRO:HB3	2.03	0.41
4:4F:68:LEU:HD23	4:4F:68:LEU:HA	1.87	0.41
4:4F:316:MET:HA	4:4F:352:SER:HB3	2.03	0.41
3:4G:204:LEU:HD13	3:4G:231:ILE:HG12	2.01	0.41
4:4H:20:PHE:CE2	4:4H:24:ILE:HG13	2.55	0.41
4:4J:64:ILE:HD12	4:4J:119:VAL:HG13	2.02	0.41
3:4K:394:LYS:HD3	4:4L:346:PRO:HB2	2.02	0.41
4:4L:91:VAL:HG12	4:4L:112:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4L:396:HIS:HD2	6:68:814:ARG:HH11	1.68	0.41
3:4M:6:SER:O	3:4M:65:CYS:HA	2.21	0.41
3:4M:137:MET:HB3	3:4M:168:ASN:HB3	2.02	0.41
3:4M:315:CYS:HB3	3:4M:377:MET:HE1	2.01	0.41
3:4M:318:MET:HE2	3:4M:318:MET:HB2	1.94	0.41
5:50:130:LEU:HD21	5:50:174:LEU:HD11	2.03	0.41
5:50:134:LEU:O	5:50:138:ILE:HG13	2.20	0.41
5:50:162:GLN:HG2	5:50:164:MET:HB2	2.02	0.41
5:51:98:PHE:H	5:52:185:ARG:NH2	2.19	0.41
5:51:202:LEU:HD12	5:51:202:LEU:HA	1.82	0.41
5:52:110:PHE:HA	5:52:113:MET:HG3	2.03	0.41
5:57:191:ARG:HH11	5:57:195:LEU:HD23	1.86	0.41
5:59:174:LEU:HD12	5:59:174:LEU:HA	1.96	0.41
3:5A:136:LEU:HA	3:5A:167:LEU:HB2	2.03	0.41
3:5A:411:GLU:HG2	14:K4:172:ARG:HH12	1.86	0.41
4:5B:222:TYR:HD2	4:5B:225:LEU:HD22	1.86	0.41
4:5B:239:CYS:HB2	4:5B:248:SER:H	1.86	0.41
3:5C:238:LEU:HD21	3:5C:378:ILE:HD11	2.03	0.41
4:5D:345:ILE:HB	4:5D:348:ASN:ND2	2.36	0.41
3:5E:88:HIS:CE1	3:5E:90:GLU:HG2	2.55	0.41
3:5E:363:VAL:HG23	3:5E:366:GLY:HA3	2.02	0.41
3:5G:10:GLY:O	3:5G:14:ILE:HG12	2.21	0.41
4:5H:217:LEU:HD23	4:5H:217:LEU:HA	1.96	0.41
4:5H:396:HIS:HA	4:5H:399:THR:HG22	2.01	0.41
3:5I:56:THR:HA	3:6I:285:GLN:HB2	2.03	0.41
4:5J:65:LEU:HB3	4:5J:73:MET:HE1	2.02	0.41
4:5J:86:ARG:HB3	4:5J:89:ASN:HB2	2.03	0.41
3:5K:12:ALA:HB3	3:5K:140:ALA:HB2	2.01	0.41
3:5K:103:PHE:HD1	3:5K:413:MET:HE1	1.85	0.41
4:5L:91:VAL:HG11	4:5L:116:VAL:HG12	2.02	0.41
4:5N:205:GLU:HB2	6:68:788:LEU:HD22	2.02	0.41
5:60:61:LEU:HD23	5:60:61:LEU:HA	1.91	0.41
5:61:56:GLU:CD	5:61:58:GLY:H	2.29	0.41
5:61:202:LEU:HD22	5:62:202:LEU:HD13	2.03	0.41
5:62:74:LYS:HD3	5:62:74:LYS:HA	1.92	0.41
5:62:91:LEU:O	5:62:101:TYR:HB3	2.20	0.41
5:62:129:VAL:HA	5:62:132:LYS:HG2	2.03	0.41
5:62:134:LEU:HD23	5:62:134:LEU:HA	1.96	0.41
6:64:139:THR:HB	6:64:561:LEU:HD11	2.03	0.41
6:64:151:TYR:CE2	6:64:564:MET:HA	2.56	0.41
6:65:461:ARG:HA	6:65:464:VAL:HG12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:66:970:LEU:HD22	6:66:974:GLU:HB2	2.02	0.41
6:67:417:LEU:HD12	6:67:417:LEU:HA	1.93	0.41
6:67:599:ILE:HD13	6:67:599:ILE:HA	1.92	0.41
6:67:877:ALA:O	6:67:881:THR:HG23	2.20	0.41
6:68:595:ASP:O	6:68:598:VAL:HG12	2.21	0.41
4:6B:48:ASN:HB3	1:q:915:ARG:NE	2.35	0.41
4:6B:392:LYS:NZ	4:6B:405:GLU:HG2	2.36	0.41
3:6C:22:GLU:HB3	3:6C:83:TYR:HE1	1.85	0.41
3:6C:231:ILE:HD13	3:6C:231:ILE:HA	1.80	0.41
4:6D:7:VAL:HB	4:6D:135:ILE:HG22	2.02	0.41
3:6G:208:ALA:O	3:6G:212:ILE:HG12	2.21	0.41
3:6G:209:ILE:HB	3:6G:227:LEU:HD22	2.02	0.41
4:6H:208:TYR:HA	4:6H:225:LEU:HD11	2.03	0.41
4:6H:297:LYS:HG3	7:75:416:TRP:CZ2	2.56	0.41
3:6I:21:TRP:CZ3	3:6I:52:PHE:HB3	2.55	0.41
4:6J:7:VAL:HB	4:6J:135:ILE:HG13	2.03	0.41
4:6J:65:LEU:HD22	4:6J:90:PHE:CE1	2.55	0.41
4:6L:125:GLU:HG2	4:7L:336:LYS:HZ3	1.86	0.41
4:6L:271:ALA:HB3	4:6L:365:VAL:HG22	2.03	0.41
3:6M:230:LEU:HA	3:6M:230:LEU:HD23	1.77	0.41
4:6N:156:ARG:HE	4:6N:195:ASN:HA	1.86	0.41
4:6N:361:LEU:HD11	1:i:814:PRO:HG2	2.02	0.41
4:6N:411:ALA:O	4:6N:415:MET:HG2	2.20	0.41
2:7:175:TYR:HA	2:7:178:HIS:HB3	2.02	0.41
7:73:397:SER:HA	7:73:400:CYS:HB3	2.02	0.41
4:7B:7:VAL:HG23	4:7B:64:ILE:HB	2.02	0.41
4:7B:8:GLN:HE21	4:7B:65:LEU:HG	1.86	0.41
4:7B:256:ASN:CG	4:7B:350:LYS:HG3	2.46	0.41
4:7B:256:ASN:ND2	4:7B:350:LYS:HG3	2.36	0.41
4:7B:309:ARG:HH21	4:7B:342:VAL:HA	1.86	0.41
4:7B:330:MET:HA	4:7B:333:VAL:HG12	2.02	0.41
3:7E:10:GLY:O	3:7E:14:ILE:HG12	2.20	0.41
4:7J:148:GLY:O	4:7J:152:ILE:HG12	2.21	0.41
3:7K:288:VAL:HA	3:7K:291:ILE:HG22	2.02	0.41
4:7L:28:HIS:NE2	4:7L:241:ARG:HD2	2.36	0.41
3:7M:96:LYS:HA	3:7M:96:LYS:HD2	1.88	0.41
3:7M:209:ILE:HG21	3:7M:227:LEU:HG	2.03	0.41
3:7M:410:GLY:C	14:M1:172:ARG:HH21	2.28	0.41
7:80:271:PHE:CZ	7:80:302:PRO:HB3	2.55	0.41
7:82:399:THR:HA	7:82:414:ILE:HD12	2.03	0.41
7:85:273:LEU:HD23	7:85:273:LEU:HA	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:86:296:ARG:NH2	4:8D:307:HIS:HB3	2.35	0.41
3:8A:158:SER:HB2	3:8A:197:HIS:HB3	2.03	0.41
3:8A:377:MET:HE2	3:8A:377:MET:HB2	1.94	0.41
3:8C:70:LEU:HB3	3:8C:97:GLU:O	2.21	0.41
3:8C:88:HIS:HB3	3:8C:91:GLN:CD	2.45	0.41
4:8D:47:ILE:HD13	4:8D:47:ILE:HA	1.90	0.41
4:8D:154:LYS:HE3	7:93:286:TRP:CZ2	2.55	0.41
4:8D:207:LEU:HB3	4:8D:225:LEU:HD11	2.03	0.41
3:8E:194:LEU:O	3:8E:198:THR:HG21	2.21	0.41
3:8E:230:LEU:HD12	3:8E:230:LEU:HA	1.88	0.41
3:8E:250:VAL:HG23	3:8E:254:GLU:HB2	2.03	0.41
4:8H:65:LEU:HB3	4:8H:73:MET:HE1	2.02	0.41
4:8H:271:ALA:HB3	4:8H:365:VAL:HG12	2.02	0.41
3:8I:102:ASN:HB2	4:8J:255:VAL:HG11	2.02	0.41
4:8J:6:HIS:HB2	4:8J:134:GLN:HE21	1.86	0.41
4:8J:118:ASP:O	4:8J:122:LYS:HG2	2.21	0.41
4:8J:135:ILE:HG21	4:8J:152:ILE:HD11	2.03	0.41
4:8J:156:ARG:HH22	4:8J:197:ASP:HB2	1.86	0.41
4:8J:307:HIS:NE2	7:90:296:ARG:HB3	2.36	0.41
3:8K:407:TRP:HE1	4:8L:258:ILE:HB	1.86	0.41
4:8L:208:TYR:HB3	7:91:412:MET:SD	2.61	0.41
7:91:340:ASN:HB3	7:91:361:THR:HG22	2.02	0.41
7:92:251:VAL:HA	7:92:254:ARG:HD2	2.03	0.41
7:94:268:TRP:CE2	7:94:325:PHE:HB2	2.56	0.41
4:9B:326:VAL:O	4:9B:330:MET:HG2	2.21	0.41
3:9E:315:CYS:HB3	3:9E:350:GLY:O	2.20	0.41
4:9F:24:ILE:HD12	4:9F:24:ILE:HA	1.87	0.41
4:9H:77:ARG:HA	4:9H:77:ARG:HD2	1.73	0.41
4:9H:110:ALA:HA	4:9H:113:ILE:HG12	2.03	0.41
4:9H:226:ASN:HA	4:9H:229:VAL:HG12	2.03	0.41
4:9H:344:TRP:CD1	4:9H:344:TRP:H	2.39	0.41
3:9I:215:ARG:HH12	14:M6:249:VAL:HB	1.86	0.41
3:9I:244:PHE:HD2	3:9I:358:GLN:HG2	1.85	0.41
4:9J:49:VAL:HG11	4:9J:241:ARG:HB3	2.03	0.41
4:9J:68:LEU:HD21	4:9J:109:GLY:HA2	2.03	0.41
3:9K:264:ARG:CZ	3:9K:431:ASP:HB3	2.51	0.41
4:9L:124:ALA:HB1	4:9L:130:LEU:HD21	2.02	0.41
3:9M:144:GLY:HA2	3:9M:186:ASN:HD21	1.86	0.41
8:A1:313:LYS:HD2	8:A1:313:LYS:HA	1.89	0.41
8:A4:78:ALA:O	8:A4:82:MET:HB3	2.21	0.41
8:A6:319:LYS:HE3	9:B2:61:LEU:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B5:152:PRO:HD2	9:B5:173:TRP:CE2	2.56	0.41
11:C3:293:LYS:HA	11:C3:293:LYS:HD3	1.82	0.41
10:D0:370:ARG:HD3	10:D0:370:ARG:HA	1.82	0.41
10:D6:315:LEU:HB2	10:E3:136:PRO:HG3	2.03	0.41
10:E3:85:PRO:HA	10:E3:88:LEU:HG	2.02	0.41
10:E6:101:LEU:HG	10:E6:393:VAL:HG11	2.03	0.41
10:F3:290:LYS:HA	10:F3:293:MET:HG2	2.02	0.41
12:F6:220:PRO:HG3	12:F6:243:THR:HB	2.02	0.41
12:F6:230:VAL:HG21	12:F6:235:LEU:HD13	2.03	0.41
12:F8:249:LEU:HD23	12:F8:252:LEU:HD12	2.03	0.41
12:H2:91:GLU:HA	12:H2:94:LEU:HD23	2.02	0.41
12:I5:59:SER:HB2	12:I5:63:ARG:HH12	1.86	0.41
13:J2:317:PHE:CE2	13:J2:474:ARG:HB3	2.56	0.41
14:K2:155:TRP:CE2	14:K2:241:VAL:HG11	2.55	0.41
14:K5:79:THR:HG21	14:K5:94:GLY:HA2	2.02	0.41
14:K7:155:TRP:HZ3	14:K7:168:PRO:HG3	1.86	0.41
14:L6:156:LEU:HD23	14:L6:169:PHE:HB3	2.03	0.41
14:M4:74:GLU:O	14:M4:78:ASP:HB2	2.21	0.41
14:M5:126:ILE:HB	14:M5:128:ARG:HH22	1.85	0.41
14:M6:82:TYR:HB2	14:M6:87:ARG:NH2	2.36	0.41
14:M6:229:ALA:HB3	14:M6:232:ARG:HG2	2.03	0.41
1:a:537:LEU:CD2	1:f:537:LEU:HB3	2.51	0.41
1:a:618:ARG:O	1:a:619:GLN:C	2.63	0.41
1:a:675:LYS:HB2	1:a:675:LYS:HE2	1.76	0.41
1:c:674:ARG:HD3	1:c:674:ARG:HA	1.56	0.41
1:n:890:LEU:HD21	1:n:945:ILE:HG22	2.03	0.41
1:n:932:LEU:HA	1:n:935:VAL:HG12	2.02	0.41
1:o:887:VAL:HA	1:o:890:LEU:HD12	2.03	0.41
1:t:868:ALA:H	1:t:871:LEU:HD11	1.85	0.41
1:t:882:GLU:HG3	1:t:883:THR:HG23	2.02	0.41
1:A:420:HIS:NE2	1:a:534:GLN:NE2	2.68	0.41
1:B:535:ALA:O	1:B:539:ALA:CB	2.69	0.41
1:E:475:LYS:HE3	1:E:475:LYS:HB2	1.86	0.41
1:G:301:GLY:HA3	1:G:307:PRO:HA	2.03	0.41
1:I:607:LEU:CB	1:J:607:LEU:HB3	2.47	0.41
1:O:678:ASN:HB2	1:O:679:ARG:HH21	1.86	0.41
1:W:318:GLU:O	1:W:322:ARG:HD3	2.21	0.41
3:1A:25:CYS:SG	3:1A:86:LEU:HD11	2.61	0.41
3:1C:70:LEU:HD23	3:1C:145:THR:HG22	2.03	0.41
4:1D:164:MET:O	4:1D:166:THR:HG23	2.21	0.41
3:1E:181:VAL:HG22	4:1F:348:ASN:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1E:205:ASP:HB2	3:1E:303:ALA:HA	2.03	0.41
3:1E:311:LYS:HE3	3:1E:344:VAL:HG23	2.03	0.41
3:1G:175:PRO:HB3	3:1G:390:ARG:HD2	2.03	0.41
4:1H:13:GLY:HA2	4:1H:16:ILE:HG22	2.02	0.41
4:1J:199:VAL:O	4:1J:265:PHE:HA	2.20	0.41
3:1K:260:VAL:HG23	3:1K:265:ILE:O	2.21	0.41
3:1K:276:ILE:HG22	3:1K:369:ALA:HB3	2.03	0.41
4:1N:418:LEU:HA	4:1N:421:GLU:HB2	2.03	0.41
5:23:134:LEU:HD23	5:23:134:LEU:HA	1.87	0.41
5:24:161:ILE:HG12	5:24:170:GLU:HG3	2.03	0.41
5:25:40:HIS:CD2	5:25:76:LEU:HD13	2.56	0.41
3:2A:130:THR:H	9:B7:41:ARG:HH22	1.68	0.41
4:2B:152:ILE:HD13	4:2B:152:ILE:HG21	1.93	0.41
4:2B:321:MET:HE2	4:2B:362:LYS:NZ	2.35	0.41
3:2C:195:LEU:HA	3:2C:266:HIS:HE1	1.85	0.41
4:2J:207:LEU:HD23	4:2J:225:LEU:HB3	2.03	0.41
4:2L:87:PRO:HB2	9:B6:50:ASP:OD1	2.20	0.41
5:33:160:PHE:HE2	5:33:174:LEU:HD13	1.85	0.41
3:3A:208:ALA:HB1	3:3A:301:MET:O	2.21	0.41
3:3E:301:MET:HG3	3:3E:307:PRO:HD3	2.01	0.41
3:3K:259:LEU:HD13	3:3K:268:MET:HE2	2.02	0.41
4:3L:193:VAL:HA	4:3L:264:HIS:CE1	2.56	0.41
2:4:268:THR:HA	2:4:271:LYS:HG2	2.03	0.41
3:4C:3:GLU:HA	3:4C:51:THR:HA	2.03	0.41
3:4C:100:ALA:HA	4:4D:252:LYS:HE3	2.02	0.41
3:4E:407:TRP:HZ2	4:4F:258:ILE:HB	1.86	0.41
3:4G:70:LEU:HD12	3:4G:99:ALA:HB2	2.03	0.41
4:4J:83:GLN:H	4:4J:83:GLN:HG2	1.71	0.41
3:4K:22:GLU:HG2	3:4K:364:PRO:HD2	2.03	0.41
3:4M:36:MET:HE3	3:4M:61:HIS:NE2	2.36	0.41
3:4M:88:HIS:ND1	4:5N:281:TYR:HB3	2.36	0.41
3:4M:88:HIS:O	3:4M:91:GLN:HG2	2.21	0.41
3:4M:261:PRO:HB2	3:4M:262:TYR:HD2	1.86	0.41
5:50:119:LEU:HD13	5:50:121:ILE:HD11	2.02	0.41
4:5B:153:SER:HA	4:5B:195:ASN:HD22	1.86	0.41
4:5B:321:MET:HE1	4:5B:326:VAL:HG22	2.03	0.41
3:5C:68:LEU:HD12	3:5C:149:LEU:HD21	2.02	0.41
3:5G:28:HIS:CE1	3:5G:243:ARG:HD2	2.56	0.41
3:5I:121:ARG:HD2	3:5I:121:ARG:HA	1.84	0.41
4:5J:272:PRO:HG3	4:5J:364:SER:HA	2.03	0.41
4:5J:385:PHE:CE1	4:5J:412:GLU:HB2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:5M:75:VAL:HA	3:5M:78:VAL:HG12	2.02	0.41
6:66:877:ALA:O	6:66:881:THR:HG23	2.21	0.41
6:69:505:GLN:O	6:69:506:GLU:C	2.64	0.41
4:6D:326:VAL:O	4:6D:330:MET:HG2	2.21	0.41
4:6D:334:GLN:HE22	4:6D:347:ASN:HA	1.86	0.41
3:6E:180:ALA:HB3	3:6E:183:GLU:HG2	2.03	0.41
3:6I:262:TYR:HB2	3:6I:265:ILE:HG12	2.02	0.41
4:6J:3:GLU:HG3	4:6J:48:ASN:O	2.21	0.41
4:6J:4:ILE:HB	4:6J:50:PHE:HE1	1.86	0.41
4:6N:7:VAL:HG22	4:6N:64:ILE:HG22	2.02	0.41
2:7:213:SER:HA	2:7:216:VAL:HG12	2.02	0.41
7:73:381:PHE:HB3	7:73:384:GLU:HB2	2.02	0.41
7:77:261:ALA:HA	7:77:391:TYR:CG	2.55	0.41
4:7B:268:ILE:O	4:7B:300:MET:HG2	2.20	0.41
3:7E:222:PRO:HD2	4:7F:324:LYS:HD3	2.01	0.41
4:7H:12:CYS:HB3	4:7H:138:SER:OG	2.21	0.41
3:7K:103:PHE:CD1	3:7K:148:GLY:HA2	2.56	0.41
3:7M:9:VAL:HG22	3:7M:68:LEU:HD22	2.03	0.41
3:7M:139:ASN:O	3:7M:170:CYS:HA	2.20	0.41
2:8:300:VAL:HG22	13:J5:283:TRP:CD2	2.56	0.41
7:83:334:LEU:HD11	7:83:347:ILE:HD13	2.03	0.41
7:85:325:PHE:O	7:85:391:TYR:HB3	2.21	0.41
7:89:347:ILE:HG12	7:89:350:ARG:NH2	2.36	0.41
4:8B:388:MET:HE2	3:8C:348:PRO:HD2	2.03	0.41
3:8C:180:ALA:HA	4:8D:350:LYS:HD3	2.03	0.41
3:8C:298:PRO:HB3	3:8C:307:PRO:HD2	2.03	0.41
4:8D:7:VAL:HG12	4:8D:64:ILE:HD13	2.03	0.41
4:8D:321:MET:HE2	4:8D:321:MET:HB2	1.88	0.41
3:8E:264:ARG:HD3	14:M4:81:TYR:O	2.21	0.41
4:8F:80:PRO:HD2	1:l:804:ASN:HD22	1.86	0.41
3:8I:302:MET:H	3:8I:302:MET:HG2	1.66	0.41
4:8J:344:TRP:CD1	4:8J:344:TRP:H	2.38	0.41
4:8J:390:ARG:NH1	4:8J:391:ARG:HH12	2.18	0.41
3:8K:105:ARG:HH22	4:8L:251:ARG:NH1	2.19	0.41
3:8K:139:ASN:HD21	3:8K:168:ASN:HD21	1.68	0.41
4:8L:101:TRP:HB3	4:8L:398:TYR:HE1	1.86	0.41
7:92:330:ARG:NE	7:92:350:ARG:HH12	2.19	0.41
7:93:317:GLN:HG3	4:9D:307:HIS:HD2	1.86	0.41
7:95:412:MET:HB3	4:9L:174:LYS:HE2	2.02	0.41
7:96:293:ILE:HG22	7:96:295:GLN:HG3	2.01	0.41
4:9L:8:GLN:NE2	4:9L:14:ASN:HA	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9M:163:LYS:HE2	3:9M:163:LYS:HB2	1.94	0.41
3:9M:262:TYR:HA	3:9M:263:PRO:HD3	1.94	0.41
8:A7:179:LYS:O	8:A7:183:GLN:HG3	2.20	0.41
9:B2:527:LEU:HD22	9:B2:534:THR:HG22	2.03	0.41
9:B6:116:GLN:O	9:B6:146:VAL:HG23	2.21	0.41
10:C6:57:ILE:HG23	10:C6:306:MET:HE1	2.02	0.41
10:D7:42:LYS:HE2	10:D7:42:LYS:HB2	1.73	0.41
10:D8:110:ILE:HG12	10:D8:283:PHE:HD1	1.86	0.41
10:D8:397:PHE:O	10:D8:401:MET:HG2	2.21	0.41
10:D9:46:ASP:O	10:D9:50:GLU:HG2	2.20	0.41
10:E2:37:ASP:HB3	10:E2:39:ASP:OD1	2.21	0.41
10:E4:45:ASN:O	10:E4:49:ARG:HG2	2.21	0.41
10:E4:316:CYS:SG	10:E4:319:LEU:HD23	2.61	0.41
10:E6:384:HIS:CE1	10:E6:385:GLU:HG3	2.56	0.41
10:E8:61:ASP:HA	14:M2:142:GLN:HE22	1.86	0.41
10:F1:284:LEU:HD11	10:F1:382:HIS:HB3	2.03	0.41
10:F1:296:MET:HE1	10:F1:386:LEU:HD23	2.03	0.41
10:F3:62:VAL:HG22	14:M5:142:GLN:NE2	2.36	0.41
12:G3:261:TRP:HZ2	12:G3:284:GLU:HA	1.86	0.41
13:J2:322:LYS:HE2	13:J2:322:LYS:HB2	1.85	0.41
13:J3:317:PHE:HE1	13:J3:474:ARG:HB3	1.84	0.41
14:K9:70:LYS:HA	14:K9:70:LYS:HD2	1.83	0.41
14:L7:198:ARG:HA	14:L7:198:ARG:HD2	1.92	0.41
1:a:617:MET:CG	1:f:618:ARG:HE	2.33	0.41
1:g:768:PRO:O	1:g:771:VAL:HG12	2.21	0.41
1:j:821:ASN:ND2	1:j:823:LEU:HB2	2.36	0.41
1:B:340:ARG:HD2	1:Y:447:HIS:CE1	2.57	0.40
1:B:527:LEU:O	1:B:531:GLN:HB2	2.20	0.40
1:G:384:LEU:HD23	1:G:384:LEU:HA	1.85	0.40
1:I:649:ASP:OD2	1:J:645:GLN:NE2	2.54	0.40
1:O:659:LEU:HD13	1:P:659:LEU:HD13	2.03	0.40
1:R:647:LYS:HB3	1:R:647:LYS:HE3	1.94	0.40
1:V:477:SER:O	1:V:481:LEU:HG	2.21	0.40
1:W:330:ARG:HG3	1:W:334:LEU:HD23	2.02	0.40
1:Z:450:LEU:HA	1:d:450:LEU:HD21	2.02	0.40
1:1:896:LEU:HD11	8:A3:87:VAL:HG11	2.03	0.40
2:16:220:LYS:O	2:16:223:ARG:HD3	2.21	0.40
3:1A:154:LEU:HD23	3:1A:154:LEU:HA	1.83	0.40
3:1A:195:LEU:HD11	3:1A:428:LEU:HD12	2.02	0.40
4:1B:276:ARG:HD2	4:1B:276:ARG:HA	1.93	0.40
3:1G:429:GLU:HA	3:1G:432:TYR:HB2	2.01	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1J:68:LEU:HD12	4:1J:143:THR:HG22	2.02	0.40
3:1K:101:ASN:N	4:1L:252:LYS:HZ1	2.18	0.40
3:1K:395:PHE:HD2	3:1K:422:ARG:HD3	1.85	0.40
5:27:51:GLU:O	5:27:147:VAL:HA	2.22	0.40
3:2A:122:ILE:HG12	3:2A:157:LEU:HD11	2.02	0.40
3:2A:166:LYS:HB2	3:2A:199:ASP:H	1.86	0.40
3:2C:274:PRO:HG3	3:2C:286:LEU:HD12	2.01	0.40
3:2C:288:VAL:HA	3:2C:291:ILE:HG12	2.02	0.40
3:2C:405:VAL:HG22	3:2C:418:PHE:HE1	1.86	0.40
4:2D:103:LYS:HD3	4:2D:107:THR:HG21	2.03	0.40
3:2I:251:ASP:HB2	3:2I:254:GLU:HG3	2.03	0.40
3:2K:221:ARG:HB3	4:2L:322:SER:OG	2.22	0.40
5:33:88:ARG:HE	5:33:88:ARG:HB3	1.69	0.40
5:39:195:LEU:HA	5:39:195:LEU:HD12	1.90	0.40
3:3C:189:LEU:HD21	3:3C:413:MET:HE1	2.02	0.40
4:3D:239:CYS:HB3	4:3D:247:ASN:HB2	2.03	0.40
4:3F:321:MET:HE2	4:3F:326:VAL:HG22	2.03	0.40
4:3H:213:ARG:HH21	4:3H:297:LYS:HB3	1.86	0.40
3:3K:284:GLU:HB2	3:3K:286:LEU:HG	2.02	0.40
5:40:199:LEU:O	5:40:203:GLN:HB2	2.21	0.40
5:48:52:ILE:HD11	5:48:71:ILE:HD11	2.03	0.40
4:4B:25:SER:HA	4:4B:30:ILE:HG22	2.03	0.40
3:4C:225:THR:HG21	8:A2:202:PRO:HG2	2.03	0.40
4:4D:207:LEU:HB3	4:4D:225:LEU:HD22	2.03	0.40
4:4D:318:ARG:NE	4:4D:358:PRO:HD3	2.36	0.40
4:4D:398:TYR:HD2	4:4D:403:MET:HE3	1.86	0.40
4:4J:83:GLN:NE2	8:A6:94:ILE:HD11	2.36	0.40
4:4J:215:LEU:HD11	4:4J:273:LEU:HD22	2.03	0.40
3:4M:265:ILE:HG23	3:4M:432:TYR:HE1	1.86	0.40
5:54:116:ARG:HH21	5:54:157:ARG:NH2	2.18	0.40
5:58:181:GLU:O	5:58:185:ARG:HB2	2.22	0.40
3:5A:52:PHE:HE2	3:5A:243:ARG:HD3	1.86	0.40
3:5A:70:LEU:HD22	3:5A:99:ALA:HB2	2.02	0.40
3:5A:272:TYR:HE1	3:5A:374:ALA:HB1	1.85	0.40
3:5C:177:VAL:HG13	4:5D:327:ASP:HB3	2.02	0.40
4:5D:410:GLU:O	4:5D:414:ASN:HB2	2.21	0.40
4:5F:32:PRO:HD3	4:5F:81:PHE:CZ	2.56	0.40
4:5J:273:LEU:HD23	4:5J:273:LEU:HA	1.87	0.40
3:5M:10:GLY:HA2	3:5M:145:THR:HG23	2.03	0.40
5:62:157:ARG:HA	5:62:174:LEU:O	2.20	0.40
6:63:452:PHE:CZ	6:63:493:ARG:HB3	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:63:875:PRO:O	9:B2:51:ARG:HD3	2.22	0.40
6:64:260:TRP:HA	6:64:263:VAL:HG12	2.03	0.40
6:64:397:ASN:O	6:64:401:ILE:HG12	2.21	0.40
6:65:397:ASN:HA	6:65:400:ALA:HB3	2.03	0.40
6:66:325:ARG:HG3	6:66:337:LEU:HD22	2.04	0.40
6:66:632:PHE:O	6:66:636:GLU:HG2	2.21	0.40
6:67:498:ARG:HA	6:67:498:ARG:HD3	1.83	0.40
6:67:554:LEU:HA	6:67:557:LEU:HD12	2.02	0.40
6:69:151:TYR:CD2	6:69:564:MET:HG2	2.57	0.40
6:69:329:GLN:HA	6:69:332:LYS:HD3	2.03	0.40
3:6C:259:LEU:HD11	3:6C:316:CYS:HB2	2.02	0.40
4:6D:154:LYS:HD3	7:79:286:TRP:HE1	1.86	0.40
3:6E:68:LEU:HD12	3:6E:93:ILE:HB	2.03	0.40
4:6F:210:ILE:HG13	4:6F:228:LEU:HD21	2.03	0.40
4:6H:8:GLN:OE1	4:6H:17:GLY:HA3	2.20	0.40
3:6I:122:ILE:HD13	3:6I:122:ILE:HA	1.89	0.40
4:6J:298:ASN:O	4:6J:298:ASN:ND2	2.54	0.40
7:76:334:LEU:HD23	7:76:339:PHE:CZ	2.56	0.40
3:7C:316:CYS:SG	3:7C:318:MET:HE2	2.60	0.40
4:7D:207:LEU:HB3	4:7D:225:LEU:HG	2.03	0.40
4:7F:171:PRO:HG3	4:7F:185:ALA:HB1	2.03	0.40
4:7F:221:THR:HG23	4:7F:223:GLY:H	1.86	0.40
4:7F:391:ARG:HD2	14:L6:73:PHE:CE2	2.55	0.40
4:7H:19:LYS:HD2	4:7H:22:GLU:HG3	2.03	0.40
4:7H:73:MET:HA	4:7H:73:MET:HE2	2.03	0.40
4:7H:174:LYS:HA	4:7H:174:LYS:HD2	1.80	0.40
4:7J:8:GLN:O	4:7J:66:MET:HG3	2.21	0.40
3:7K:339:ARG:HD2	3:7K:339:ARG:HA	1.83	0.40
4:7L:85:PHE:HB2	4:7L:90:PHE:CE2	2.56	0.40
4:7L:361:LEU:HD23	4:7L:364:SER:HB3	2.03	0.40
3:7M:143:GLY:O	3:7M:147:SER:HB3	2.20	0.40
7:80:394:TYR:CZ	14:L1:123:SER:HB3	2.56	0.40
7:83:376:GLU:O	7:83:380:TRP:HB3	2.21	0.40
7:83:398:LYS:HE2	7:83:398:LYS:HB2	1.94	0.40
3:8A:297:GLU:HG2	3:8A:299:ALA:H	1.86	0.40
4:8B:221:THR:HG23	4:8B:224:ASP:H	1.85	0.40
4:8B:270:PHE:HD1	4:8B:366:THR:HG22	1.85	0.40
3:8G:306:ASP:HB2	14:L5:256:VAL:HG23	2.02	0.40
3:8I:417:GLU:HA	3:8I:420:GLU:HG3	2.02	0.40
4:8J:317:PHE:HB3	4:8J:321:MET:HE2	2.02	0.40
3:8M:192:HIS:HB2	3:8M:421:ALA:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:92:287:LEU:HB3	14:M3:179:GLU:HB2	2.03	0.40
3:9A:140:ALA:HA	3:9A:171:SER:HB2	2.03	0.40
3:9A:274:PRO:HD3	3:9A:374:ALA:HA	2.03	0.40
3:9A:335:ILE:HD12	3:9A:335:ILE:HA	1.97	0.40
4:9B:16:ILE:HD12	4:9B:16:ILE:HA	1.80	0.40
4:9B:262:ARG:HD3	4:9B:262:ARG:HA	1.89	0.40
4:9D:316:MET:HE2	4:9D:366:THR:HG23	2.03	0.40
3:9E:9:VAL:HG12	3:9E:146:GLY:HA2	2.02	0.40
3:9E:166:LYS:HB2	3:9E:199:ASP:HB2	2.03	0.40
3:9E:259:LEU:HB3	3:9E:380:ASN:ND2	2.35	0.40
4:9F:7:VAL:HG23	4:9F:64:ILE:HB	2.01	0.40
3:9G:320:ARG:HH12	3:9G:358:GLN:HB2	1.86	0.40
4:9H:60:VAL:HG21	4:9H:86:ARG:HB3	2.04	0.40
4:9H:314:SER:HB3	4:9H:350:LYS:HB3	2.02	0.40
3:9I:188:VAL:HG11	3:9I:395:PHE:CD1	2.57	0.40
4:9J:138:SER:HA	4:9J:169:VAL:HG23	2.03	0.40
4:9L:21:TRP:HA	4:9L:24:ILE:HB	2.03	0.40
4:9L:207:LEU:HD22	4:9L:228:LEU:HD21	2.02	0.40
4:9L:403:MET:HE1	4:9L:408:PHE:CE2	2.56	0.40
3:9M:316:CYS:O	3:9M:377:MET:HA	2.20	0.40
8:A4:75:THR:HG23	8:A4:78:ALA:H	1.86	0.40
8:A6:234:ARG:HD2	8:A6:239:ILE:HG12	2.03	0.40
8:A8:75:THR:HG23	8:A8:78:ALA:H	1.85	0.40
8:A8:180:GLU:O	8:A8:184:ARG:HG3	2.21	0.40
10:C6:390:MET:HA	10:C6:393:VAL:HG12	2.03	0.40
10:C7:67:ALA:HA	10:C7:70:ARG:HG2	2.03	0.40
10:C7:349:PHE:HD1	10:C7:361:TRP:HB3	1.86	0.40
10:D0:63:TYR:CD2	14:L5:147:GLN:HG2	2.56	0.40
10:D5:392:THR:O	10:D5:396:LEU:HG	2.20	0.40
10:D7:66:LEU:HD22	10:D7:312:LYS:NZ	2.36	0.40
10:D9:110:ILE:HG12	10:D9:283:PHE:HA	2.02	0.40
12:F9:260:ASP:HA	12:F9:263:TYR:CD2	2.56	0.40
12:I7:65:GLU:HA	12:I7:68:ARG:HE	1.86	0.40
13:J1:362:ALA:HA	13:J1:365:ARG:HH11	1.86	0.40
13:J2:470:ARG:HB3	13:J2:500:LEU:HD23	2.03	0.40
13:J4:353:ARG:HD2	13:J4:354:ALA:N	2.32	0.40
1:a:619:GLN:HG3	1:a:620:ASP:N	2.36	0.40
1:c:560:GLN:O	1:c:561:ARG:C	2.64	0.40
1:d:328:ILE:HA	1:d:331:GLU:HG3	2.03	0.40
1:u:862:LEU:HG	1:u:937:GLY:HA2	2.03	0.40
1:u:908:LEU:HD23	1:u:908:LEU:HA	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:911:ILE:HG23	1:u:921:GLU:HG3	2.02	0.40
1:C:342:MET:HA	1:G:342:MET:HE2	2.03	0.40
1:D:579:LEU:HD22	1:H:579:LEU:HD13	2.02	0.40
1:I:643:ARG:CZ	1:I:646:ASN:HD22	2.33	0.40
1:J:643:ARG:HA	1:J:646:ASN:ND2	2.35	0.40
1:M:499:ARG:O	1:M:503:GLU:HG2	2.21	0.40
1:U:676:GLU:HA	1:U:679:ARG:HB3	2.03	0.40
1:X:638:LEU:HD21	1:i:817:GLY:HA3	2.01	0.40
1:Y:684:ARG:O	1:Y:685:ASN:C	2.64	0.40
1:Z:467:LEU:HD22	1:Z:470:ARG:HH21	1.86	0.40
1:Z:488:GLU:HB3	1:d:488:GLU:CD	2.46	0.40
3:1E:184:PRO:O	3:1E:188:VAL:HG22	2.21	0.40
4:1F:28:HIS:CE1	4:1F:241:ARG:HD2	2.57	0.40
3:1G:174:SER:HA	3:1G:175:PRO:HD3	1.96	0.40
4:1H:192:LEU:HD12	4:1H:199:VAL:HG22	2.03	0.40
3:1I:154:LEU:HD23	3:1I:154:LEU:HA	1.90	0.40
3:1I:217:LEU:HD11	3:1I:368:LEU:HD22	2.02	0.40
4:1J:172:SER:HA	4:1J:173:PRO:HD3	1.97	0.40
4:1L:270:PHE:HD1	4:1L:366:THR:HG22	1.86	0.40
5:20:139:LYS:HE2	5:20:139:LYS:HB2	1.91	0.40
3:2A:259:LEU:HD22	3:2A:268:MET:HG2	2.03	0.40
3:2C:210:TYR:HB3	4:2D:324:LYS:NZ	2.36	0.40
4:2F:8:GLN:HE21	4:2F:65:LEU:HG	1.85	0.40
4:2F:77:ARG:HH22	4:3F:280:GLN:NE2	2.19	0.40
3:2G:10:GLY:O	3:2G:14:ILE:HG12	2.22	0.40
3:2G:11:GLN:HE22	4:2H:247:ASN:HB2	1.86	0.40
4:2H:112:LEU:HD23	4:2H:112:LEU:HA	1.93	0.40
3:2I:200:VAL:HG22	3:2I:268:MET:HE1	2.02	0.40
4:2J:13:GLY:HA2	4:2J:16:ILE:HG22	2.03	0.40
4:2J:289:LEU:HD23	4:2J:317:PHE:HE1	1.86	0.40
3:2M:296:PHE:CE1	3:2M:335:ILE:HG21	2.55	0.40
5:39:220:LEU:HD21	5:40:216:LYS:HB3	2.03	0.40
3:3A:211:ASP:O	3:3A:215:ARG:HG2	2.21	0.40
4:3B:12:CYS:HA	17:3B:501:GDP:N2	2.34	0.40
4:3B:69:GLU:HA	4:3B:70:PRO:HD3	1.92	0.40
3:3C:397:LEU:HD23	4:3D:346:PRO:HD3	2.03	0.40
3:3E:339:ARG:HH11	3:3E:339:ARG:HG2	1.86	0.40
3:3I:10:GLY:O	3:3I:14:ILE:HG12	2.20	0.40
3:3I:28:HIS:CE1	3:3I:243:ARG:HD2	2.56	0.40
4:3L:187:LEU:HA	4:3L:190:HIS:HD2	1.86	0.40
3:3M:296:PHE:CD1	3:3M:335:ILE:HG12	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:40:88:ARG:NH1	5:40:102:THR:HG23	2.36	0.40
5:44:188:MET:HE2	5:44:188:MET:HB3	1.91	0.40
5:44:212:LEU:HD23	5:44:212:LEU:HA	1.89	0.40
3:4A:5:ILE:HD13	3:4A:135:PHE:HE1	1.86	0.40
3:4A:437:ILE:HB	6:67:964:THR:HG21	2.03	0.40
3:4E:210:TYR:CE1	3:4E:227:LEU:HD11	2.56	0.40
4:4H:51:TYR:HB3	4:4H:59:PHE:HB3	2.03	0.40
4:4L:103:LYS:HA	4:4L:107:THR:HG23	2.03	0.40
5:51:126:TYR:CZ	5:51:130:LEU:HD21	2.56	0.40
5:55:157:ARG:HD2	5:55:175:ASP:HB3	2.03	0.40
5:57:40:HIS:HD1	5:57:78:LEU:HD13	1.86	0.40
3:5A:138:PHE:HZ	3:5A:235:ILE:HG12	1.85	0.40
3:5A:172:TRP:CZ2	3:5A:391:MET:HE3	2.56	0.40
3:5A:398:MET:SD	4:5B:346:PRO:HD2	2.61	0.40
4:5B:21:TRP:CZ2	4:5B:63:ALA:HB2	2.56	0.40
4:5F:273:LEU:HD23	4:5F:273:LEU:HA	1.88	0.40
3:5K:102:ASN:HB3	3:5K:105:ARG:HB3	2.04	0.40
4:5L:396:HIS:CD2	3:5M:263:PRO:HD3	2.56	0.40
3:5M:165:SER:HB3	3:5M:256:GLN:HE22	1.86	0.40
3:5M:387:VAL:HG23	3:5M:390:ARG:NH2	2.36	0.40
4:5N:313:ALA:HB1	4:5N:367:PHE:HE1	1.86	0.40
4:5N:385:PHE:HE2	4:5N:412:GLU:HB3	1.86	0.40
5:62:73:VAL:HA	5:62:91:LEU:HD23	2.02	0.40
6:64:495:LEU:HD12	6:64:498:ARG:HH22	1.86	0.40
6:66:251:TYR:HE2	6:66:467:GLU:HG3	1.87	0.40
6:67:503:LYS:O	6:67:504:ALA:C	2.64	0.40
3:6C:311:LYS:NZ	3:6C:344:VAL:HA	2.36	0.40
4:6D:219:THR:HA	3:6E:326:LYS:HE3	2.02	0.40
3:6E:134:GLY:HA2	3:6E:165:SER:O	2.22	0.40
4:6F:198:GLU:HG2	4:6F:266:PHE:HE2	1.85	0.40
3:6G:403:ALA:HA	4:6H:260:PHE:HE1	1.87	0.40
4:6L:20:PHE:HA	4:6L:230:SER:HB2	2.02	0.40
4:6L:304:ASP:HA	4:6L:305:PRO:HD3	1.90	0.40
4:6N:100:ASN:HB3	4:6N:103:LYS:HB2	2.02	0.40
4:6N:284:LEU:HD12	4:6N:284:LEU:HA	1.89	0.40
7:77:279:ARG:NH2	10:D5:149:TYR:HB2	2.37	0.40
7:79:284:THR:HB	7:79:287:LEU:HD22	2.02	0.40
4:7F:49:VAL:HG11	4:7F:241:ARG:HG2	2.03	0.40
4:7H:28:HIS:HD2	4:7H:43:GLN:HB3	1.86	0.40
2:8:294:GLU:HA	2:8:297:THR:HG22	2.03	0.40
7:83:352:VAL:HG13	14:L3:243:GLN:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:87:281:LEU:HB2	7:87:298:SER:HA	2.03	0.40
7:87:350:ARG:HH21	7:87:380:TRP:HE3	1.69	0.40
7:89:247:ILE:HD12	14:M2:74:GLU:HB3	2.03	0.40
4:8F:68:LEU:HB3	4:8F:96:GLY:HA2	2.03	0.40
4:8F:132:GLY:HA2	4:8F:162:ARG:HB3	2.04	0.40
3:8G:117:LEU:HD11	14:M2:250:PRO:HG3	2.02	0.40
3:8K:223:THR:HG22	4:8L:322:SER:HA	2.02	0.40
3:8M:173:PRO:HG2	3:8M:391:MET:HE1	2.03	0.40
7:92:351:LYS:HE2	7:92:351:LYS:HB2	1.84	0.40
4:9B:153:SER:HA	4:9B:195:ASN:HB3	2.02	0.40
8:A1:317:LEU:HD21	8:A1:343:VAL:HG21	2.02	0.40
8:A5:87:VAL:HG21	1:v:896:LEU:HG	2.03	0.40
10:C6:392:THR:HA	10:C6:395:ARG:HG2	2.02	0.40
10:D0:284:LEU:HD21	10:D0:347:GLU:OE1	2.22	0.40
10:D1:100:SER:HB2	10:D1:389:PHE:HZ	1.87	0.40
10:D8:150:VAL:O	10:D8:154:ILE:HD12	2.21	0.40
10:E4:98:GLU:O	10:E4:102:CYS:HB2	2.21	0.40
10:E7:84:THR:HG23	10:E7:87:ASP:H	1.87	0.40
10:E9:316:CYS:O	10:E9:320:LYS:HG3	2.22	0.40
10:F1:35:TRP:CE2	14:L7:228:ALA:HA	2.56	0.40
12:G1:216:TRP:CZ2	12:G1:228:ILE:HD11	2.56	0.40
12:G2:246:PRO:HD3	12:G2:266:PRO:HB3	2.03	0.40
12:G4:227:SER:HB2	12:G4:236:LEU:HG	2.03	0.40
12:G6:248:ASP:O	12:G6:252:LEU:HG	2.21	0.40
13:J1:474:ARG:NE	13:J1:503:GLY:HA3	2.36	0.40
13:J6:659:ASP:HA	13:J6:662:ILE:HD12	2.01	0.40
14:K7:155:TRP:CD1	14:K7:241:VAL:HG21	2.56	0.40
14:L0:113:GLU:HG3	14:L0:118:CYS:HA	2.03	0.40
14:L9:134:VAL:HG11	14:L9:139:LEU:HD22	2.03	0.40
1:a:533:ARG:NH1	1:f:533:ARG:HH22	2.11	0.40
1:a:617:MET:HG3	1:f:618:ARG:HE	1.86	0.40
1:a:636:ALA:HB3	1:j:827:HIS:NE2	2.36	0.40
1:b:372:LEU:HD23	1:b:372:LEU:HA	1.95	0.40
1:l:823:LEU:HD23	1:l:823:LEU:H	1.85	0.40
1:o:897:LEU:HA	1:o:897:LEU:HD23	1.87	0.40
1:A:481:LEU:HD12	1:A:481:LEU:HA	1.96	0.40
1:B:323:MET:HA	1:E:323:MET:HE1	2.03	0.40
1:F:473:ARG:NH2	1:f:581:LYS:HG2	2.36	0.40
1:G:329:ASP:O	1:G:333:ARG:HG2	2.22	0.40
1:H:578:ARG:HD3	1:H:581:LYS:HD3	2.03	0.40
1:J:640:ALA:C	4:8B:56:GLY:HA3	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:593:GLN:HA	1:Q:596:GLU:HB2	2.03	0.40
1:Q:635:ASN:HD21	1:U:631:LEU:HD12	1.86	0.40
2:10:294:GLU:HA	2:10:297:THR:HG22	2.04	0.40
2:12:231:LYS:HB2	2:12:231:LYS:HE3	1.90	0.40
2:14:167:ARG:HA	2:14:170:THR:HG22	2.02	0.40
2:15:184:LYS:HA	2:15:187:HIS:CE1	2.56	0.40
4:1B:388:MET:HE1	3:1C:347:CYS:HB2	2.03	0.40
4:1D:237:THR:HG23	4:1D:240:LEU:HD13	2.02	0.40
3:1E:164:LYS:H	3:1E:164:LYS:HG2	1.66	0.40
4:1F:246:LEU:HB2	4:1F:353:VAL:H	1.86	0.40
4:1F:271:ALA:HB1	4:1F:292:GLN:HG3	2.03	0.40
4:1F:308:GLY:HA3	4:1F:373:ALA:HB2	2.04	0.40
3:1G:17:GLY:HA2	3:1G:20:CYS:HB3	2.03	0.40
3:1G:316:CYS:SG	3:1G:352:LYS:HD3	2.62	0.40
4:1H:138:SER:HA	4:1H:169:VAL:HB	2.03	0.40
3:1I:174:SER:HB2	3:1I:177:VAL:O	2.20	0.40
4:1J:154:LYS:O	4:1J:157:GLU:HG2	2.20	0.40
3:1M:180:ALA:HA	4:1N:350:LYS:HB3	2.04	0.40
5:23:26:THR:HA	5:23:29:ILE:HD12	2.03	0.40
3:2C:7:ILE:HB	3:2C:137:MET:SD	2.61	0.40
4:2D:107:THR:HG22	4:2D:108:GLU:OE1	2.22	0.40
4:2D:174:LYS:HE2	4:2D:174:LYS:HB3	1.89	0.40
4:2D:199:VAL:HG22	4:2D:264:HIS:CD2	2.57	0.40
4:2D:377:MET:HA	4:2D:380:ARG:NH2	2.37	0.40
3:2E:329:ASN:HA	3:2E:332:VAL:HG22	2.03	0.40
4:2F:384:GLN:O	4:2F:388:MET:HG3	2.22	0.40
3:2G:241:SER:HB2	3:2G:249:ASN:HA	2.04	0.40
3:2K:30:ILE:HD13	3:2K:36:MET:HB2	2.03	0.40
3:2K:407:TRP:CD2	4:2L:255:VAL:HG12	2.56	0.40
2:3:251:ARG:HA	2:3:254:THR:HG22	2.02	0.40
5:31:42:LEU:HD13	5:31:76:LEU:HG	2.04	0.40
3:3A:79:ARG:NE	3:3A:92:LEU:HD22	2.36	0.40
3:3A:308:ARG:HH21	6:67:568:GLN:HG2	1.87	0.40
3:3A:362:VAL:HG22	3:3A:363:VAL:O	2.21	0.40
4:3B:167:PHE:CE2	4:3B:233:MET:HB2	2.55	0.40
4:3D:395:LEU:HD12	4:3D:395:LEU:HA	1.84	0.40
4:3H:290:THR:HG21	4:3H:329:GLN:HB3	2.02	0.40
4:3H:297:LYS:HE2	4:3H:297:LYS:HB2	1.86	0.40
3:3K:77:GLU:OE1	8:A7:231:SER:HB3	2.22	0.40
3:3K:259:LEU:HD21	3:3K:316:CYS:HB2	2.03	0.40
4:3L:6:HIS:CE1	4:3L:8:GLN:HB3	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:40:114:GLN:HA	5:40:119:LEU:HD12	2.03	0.40
5:43:48:VAL:O	5:43:71:ILE:HG22	2.21	0.40
5:46:128:SER:HA	5:46:131:ILE:HG22	2.04	0.40
5:46:203:GLN:HA	5:46:206:LEU:HG	2.03	0.40
5:47:54:LEU:HD12	5:47:150:MET:HB2	2.02	0.40
5:47:75:ILE:HG22	5:47:89:VAL:HG22	2.02	0.40
5:47:84:PRO:HD2	5:47:124:GLY:HA2	2.03	0.40
5:48:51:GLU:HB3	5:48:147:VAL:HG22	2.02	0.40
5:49:149:ILE:HB	5:49:157:ARG:HB2	2.04	0.40
3:4A:9:VAL:HG22	3:4A:68:LEU:HB3	2.03	0.40
3:4A:221:ARG:HA	3:4A:221:ARG:HD2	1.92	0.40
3:4C:422:ARG:HA	3:4C:422:ARG:HD2	1.82	0.40
4:4D:178:THR:HG21	17:4D:501:GDP:H5'	2.03	0.40
3:4G:138:PHE:HZ	3:4G:235:ILE:HG12	1.86	0.40
4:4L:297:LYS:HA	4:4L:297:LYS:HD2	1.94	0.40
5:51:77:ILE:HD12	5:51:77:ILE:HA	1.96	0.40
5:53:69:GLU:HA	5:53:70:PRO:HD3	1.98	0.40
5:53:162:GLN:HG2	5:53:171:LEU:HD11	2.04	0.40
5:59:220:LEU:HD21	6:68:606:GLN:HG3	2.04	0.40
3:5A:428:LEU:O	3:5A:432:TYR:CB	2.70	0.40
4:5B:65:LEU:HB3	4:5B:73:MET:HE3	2.04	0.40
4:5B:178:THR:HA	3:5C:258:ASN:HD21	1.85	0.40
4:5D:68:LEU:HD12	4:5D:97:ALA:HB2	2.04	0.40
3:5E:167:LEU:HA	3:5E:200:VAL:O	2.22	0.40
4:5F:378:PHE:HB2	4:5F:419:VAL:HG22	2.03	0.40
3:5G:320:ARG:HG3	3:5G:360:PRO:HD3	2.04	0.40
3:5I:28:HIS:CE1	3:5I:243:ARG:HD2	2.56	0.40
3:5I:383:ALA:O	3:5I:386:GLU:HG3	2.22	0.40
3:5M:10:GLY:O	3:5M:14:ILE:HG12	2.22	0.40
3:5M:205:ASP:O	3:5M:209:ILE:HG13	2.22	0.40
4:5N:86:ARG:HH12	4:6N:281:TYR:C	2.29	0.40
4:5N:117:LEU:HD23	4:5N:117:LEU:HA	1.95	0.40
4:5N:266:PHE:CD1	4:5N:370:ASN:HB3	2.56	0.40
4:5N:291:GLN:HE21	4:5N:291:GLN:HB3	1.68	0.40
4:5N:407:GLU:HA	4:5N:410:GLU:HG3	2.04	0.40
5:61:199:LEU:HD22	5:62:195:LEU:HD11	2.03	0.40
5:62:26:THR:HG22	5:62:201:LEU:HD23	2.03	0.40
4:6B:2:ARG:HD3	4:6B:240:LEU:HD12	2.03	0.40
4:6F:154:LYS:O	4:6F:158:GLU:HB2	2.22	0.40
4:6F:380:ARG:HB2	7:71:312:SER:H	1.86	0.40
3:6G:306:ASP:HB3	3:6G:309:HIS:HE1	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6J:286:VAL:HG12	4:6J:329:GLN:HG3	2.04	0.40
4:6L:379:LYS:HE2	4:6L:419:VAL:HG11	2.03	0.40
3:6M:140:ALA:HA	3:6M:171:SER:HB2	2.02	0.40
4:6N:66:MET:HE3	4:6N:151:LEU:HD22	2.04	0.40
2:7:296:ASP:HA	2:7:299:ILE:HG22	2.03	0.40
2:7:318:LYS:HD2	2:7:318:LYS:HA	1.94	0.40
7:72:313:LEU:HD22	14:K3:109:ASP:HB2	2.02	0.40
7:77:264:GLN:HG2	7:77:327:ASN:HB2	2.04	0.40
3:7A:88:HIS:HA	3:7A:89:PRO:HD3	1.95	0.40
4:7B:3:GLU:HG2	4:7B:127:CYS:SG	2.62	0.40
4:7B:98:GLY:HA2	3:7C:254:GLU:HB3	2.01	0.40
4:7B:105:HIS:CD2	4:7B:150:LEU:HB2	2.56	0.40
4:7B:252:LYS:HZ2	4:7B:256:ASN:HD21	1.69	0.40
3:7G:154:LEU:HD23	3:7G:154:LEU:HA	1.97	0.40
4:7J:103:LYS:HA	4:7J:107:THR:HB	2.02	0.40
4:7L:208:TYR:CE1	4:7L:225:LEU:HD11	2.57	0.40
3:7M:134:GLY:HA2	3:7M:165:SER:O	2.20	0.40
7:84:272:ALA:HB1	14:L3:93:PHE:HB2	2.03	0.40
3:8A:23:LEU:HA	3:8A:23:LEU:HD23	1.87	0.40
4:8B:167:PHE:HD2	4:8B:233:MET:HE3	1.86	0.40
3:8C:5:ILE:HG12	3:8C:132:LEU:HD11	2.02	0.40
3:8E:15:GLN:HA	3:8E:18:ASN:HB2	2.04	0.40
3:8I:252:VAL:O	3:8I:256:GLN:HG2	2.21	0.40
3:8K:319:TYR:HB2	3:8K:355:ILE:HG22	2.03	0.40
3:8K:417:GLU:HA	3:8K:420:GLU:HB3	2.03	0.40
3:8M:115:VAL:HG21	3:8M:152:LEU:HG	2.04	0.40
7:91:257:ARG:HD3	14:L0:117:ARG:HG2	2.03	0.40
7:92:342:SER:HA	14:M2:155:TRP:HZ2	1.85	0.40
4:9B:397:TRP:O	4:9B:401:GLU:HB2	2.20	0.40
3:9C:3:GLU:HA	3:9C:51:THR:HA	2.03	0.40
3:9E:11:GLN:HE21	3:9E:71:GLU:HG2	1.85	0.40
4:9F:16:ILE:HD11	4:9F:229:VAL:HG21	2.02	0.40
4:9F:101:TRP:CE3	4:9F:403:MET:HE1	2.56	0.40
4:9F:203:ASP:OD2	4:9F:205:GLU:HG3	2.22	0.40
4:9H:289:LEU:HD21	4:9H:365:VAL:HG13	2.02	0.40
8:A7:43:CYS:O	8:A7:47:LYS:HG2	2.20	0.40
8:A7:381:PHE:O	8:A7:385:VAL:HG23	2.22	0.40
10:C6:302:ARG:O	10:C6:306:MET:HG2	2.21	0.40
10:C7:48:ARG:HG3	10:C7:55:TYR:CD2	2.57	0.40
10:D5:120:PRO:HD3	10:D5:130:PRO:HB3	2.02	0.40
10:E6:305:LEU:O	10:E6:309:ILE:HD12	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E8:113:THR:HG23	10:E8:286:ARG:HH22	1.86	0.40
10:F3:60:TYR:HE2	10:F3:302:ARG:HH11	1.68	0.40
12:G5:198:LYS:HD3	12:G6:199:TRP:HH2	1.86	0.40
12:G8:249:LEU:HD23	12:G8:252:LEU:HD12	2.02	0.40
13:J6:411:PRO:HG3	13:J6:464:PHE:HE1	1.86	0.40
14:K0:225:GLU:HG2	14:K0:226:PRO:O	2.22	0.40
14:K3:156:LEU:HD11	14:K3:169:PHE:HB2	2.03	0.40
14:L6:227:PRO:HB2	14:L6:233:LEU:HD11	2.02	0.40
14:M3:97:ARG:HA	14:M3:123:SER:HB2	2.04	0.40
1:a:607:LEU:HA	1:a:610:VAL:CG2	2.51	0.40
1:c:682:LYS:C	1:c:684:ARG:N	2.79	0.40
1:f:561:ARG:HD3	1:f:562:ILE:HD13	2.01	0.40
1:i:740:PRO:HB2	1:i:745:HIS:CD2	2.55	0.40
1:q:897:LEU:HD12	1:q:942:ILE:HD12	2.04	0.40
1:t:936:ASP:O	1:t:940:HIS:HB2	2.21	0.40
1:w:872:ALA:HB3	1:w:875:ILE:HG12	2.04	0.40
1:C:415:LEU:N	1:d:522:ARG:HH22	2.19	0.40
1:G:418:VAL:O	1:G:421:GLU:HG3	2.22	0.40
1:I:585:GLU:HB3	1:I:586:LYS:HZ2	1.86	0.40
1:J:572:ARG:HD3	1:J:572:ARG:HA	1.28	0.40
1:K:384:LEU:HA	1:K:387:ILE:HG22	2.02	0.40
1:K:416:GLN:HA	1:K:419:LEU:HD12	2.03	0.40
1:O:667:LYS:HZ3	1:O:667:LYS:HG3	1.78	0.40
1:Q:639:LEU:O	1:Q:642:MET:HB2	2.20	0.40
1:R:577:GLN:HE22	1:R:581:LYS:HD2	1.86	0.40
1:U:654:LEU:HD12	1:2:917:ARG:NE	2.37	0.40
1:W:418:VAL:O	1:W:422:THR:HG23	2.21	0.40
3:1A:19:ALA:HB1	3:1A:232:ALA:HB2	2.03	0.40
4:1B:179:VAL:HG22	3:1C:350:GLY:HA3	2.04	0.40
4:1D:293:MET:HE3	4:1D:367:PHE:CD1	2.57	0.40
3:1E:387:VAL:HA	3:1E:390:ARG:HG2	2.03	0.40
4:1F:390:ARG:HD2	4:1F:391:ARG:HG2	2.03	0.40
3:1G:297:GLU:HG3	3:1G:299:ALA:H	1.87	0.40
4:1J:98:GLY:O	3:1K:257:THR:HG21	2.21	0.40
3:1M:251:ASP:HB2	3:1M:254:GLU:HB2	2.02	0.40
5:24:72:ARG:HB2	5:24:92:THR:HG23	2.03	0.40
5:24:117:GLN:O	5:25:167:LYS:HE3	2.21	0.40
4:2J:39:ASP:HB2	8:A7:314:PHE:CE2	2.56	0.40
4:2J:139:LEU:HD12	4:2J:170:PHE:CE1	2.57	0.40
3:2M:119:LEU:HA	3:2M:122:ILE:HG22	2.02	0.40
3:2M:272:TYR:HB2	3:2M:376:CYS:SG	2.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:31:235:ARG:HD3	5:31:238:GLN:HE21	1.87	0.40
5:33:33:ASP:HB3	5:33:36:LEU:HD23	2.04	0.40
5:38:206:LEU:HD23	5:38:206:LEU:HA	1.91	0.40
5:39:129:VAL:HA	13:J4:337:ARG:HH21	1.87	0.40
3:3A:351:PHE:O	3:3A:352:LYS:HD3	2.22	0.40
4:3B:135:ILE:HG22	4:3B:137:HIS:ND1	2.36	0.40
3:3C:11:GLN:HB2	3:3C:74:VAL:HG21	2.03	0.40
3:3C:217:LEU:HD22	3:3C:367:ASP:HB3	2.03	0.40
4:3F:178:THR:H	3:3G:352:LYS:HA	1.87	0.40
3:3G:172:TRP:HZ2	3:3G:391:MET:HE1	1.87	0.40
3:3G:346:TRP:CE3	3:3G:347:CYS:HB2	2.57	0.40
4:3H:320:ARG:HG3	8:A5:230:ARG:NH2	2.36	0.40
3:3I:338:LYS:HD2	3:3I:341:ILE:HD12	2.03	0.40
4:3J:180:VAL:HG23	4:3J:184:ASN:ND2	2.37	0.40
4:3J:191:GLN:O	4:3J:195:ASN:HB2	2.21	0.40
4:3L:318:ARG:HG2	4:3L:354:CYS:SG	2.61	0.40
3:3M:107:HIS:ND1	3:3M:152:LEU:HG	2.37	0.40
2:4:268:THR:HA	2:4:271:LYS:HE2	2.03	0.40
5:47:228:ALA:HB2	5:48:209:ILE:HD11	2.03	0.40
5:49:114:GLN:HA	5:49:119:LEU:HD12	2.04	0.40
4:4F:20:PHE:HA	4:4F:230:SER:OG	2.21	0.40
3:4G:397:LEU:HD12	4:4H:344:TRP:HA	2.03	0.40
3:4K:102:ASN:HB3	3:4K:105:ARG:HB2	2.04	0.40
5:51:149:ILE:HB	5:51:157:ARG:HB3	2.04	0.40
5:56:111:ARG:HH12	5:56:123:PHE:HB2	1.86	0.40
5:58:167:LYS:NZ	5:61:171:LEU:HA	2.36	0.40
3:5E:223:THR:HG23	3:5E:225:THR:H	1.86	0.40
3:5E:320:ARG:HG3	3:5E:360:PRO:HG3	2.04	0.40
3:5E:343:PHE:HE2	3:5E:350:GLY:HA3	1.87	0.40
4:5J:107:THR:HG22	4:5J:108:GLU:H	1.86	0.40
4:5L:54:ALA:HA	4:6L:283:ALA:HB2	2.04	0.40
5:60:108:ASP:HA	5:60:111:ARG:HE	1.87	0.40
6:65:915:ASN:HD21	9:B3:459:ARG:NH2	2.19	0.40
6:66:262:LYS:HB3	6:66:303:LEU:HG	2.02	0.40
6:67:975:LYS:HA	6:67:978:LYS:HE3	2.03	0.40
4:6B:290:THR:HG21	4:6B:329:GLN:HB3	2.02	0.40
4:6B:379:LYS:HE2	7:73:310:SER:HB2	2.03	0.40
3:6C:169:PHE:HZ	3:6C:238:LEU:HD13	1.87	0.40
4:6D:207:LEU:HD23	4:6D:225:LEU:HG	2.04	0.40
3:6E:244:PHE:CE2	3:6E:358:GLN:HG2	2.57	0.40
4:6F:2:ARG:HE	4:6F:2:ARG:HB2	1.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6G:272:TYR:HB3	3:6G:275:ILE:HD11	2.03	0.40
4:6H:190:HIS:CD2	14:K8:133:VAL:HG11	2.56	0.40
3:6I:245:ASP:HB2	1:g:788:PRO:HB3	2.03	0.40
4:6J:14:ASN:HD22	4:6J:72:THR:HG23	1.86	0.40
3:6K:71:GLU:HG3	3:6K:73:THR:H	1.86	0.40
4:6N:42:LEU:HD12	1:i:753:LEU:HD22	2.03	0.40
7:72:257:ARG:HE	7:72:309:THR:HG23	1.86	0.40
7:77:330:ARG:HD2	7:77:350:ARG:HH22	1.86	0.40
7:78:334:LEU:HD13	7:78:339:PHE:HZ	1.87	0.40
7:79:351:LYS:HB2	7:79:351:LYS:HE2	1.82	0.40
4:7B:190:HIS:ND1	4:7B:191:GLN:HG3	2.36	0.40
3:7C:167:LEU:HD23	3:7C:167:LEU:HA	1.94	0.40
3:7C:434:GLU:HA	3:7C:437:ILE:HD11	2.03	0.40
4:7D:180:VAL:HG12	4:7D:388:MET:HE1	2.03	0.40
4:7F:253:LEU:HD21	4:7F:368:VAL:HG21	2.02	0.40
3:7I:102:ASN:HB2	3:7I:105:ARG:HB2	2.04	0.40
3:7I:324:VAL:HG12	3:7I:326:LYS:H	1.86	0.40
4:7J:60:VAL:HA	4:7J:61:PRO:HD3	1.97	0.40
3:7K:306:ASP:HA	3:7K:307:PRO:HD3	1.89	0.40
3:7M:5:ILE:O	3:7M:135:PHE:HA	2.21	0.40
3:7M:324:VAL:O	3:7M:328:VAL:HG23	2.22	0.40
7:86:317:GLN:NE2	4:8D:306:ARG:HG3	2.25	0.40
3:8A:119:LEU:HD23	3:8A:122:ILE:HD11	2.03	0.40
3:8G:142:GLY:HA2	3:8G:173:PRO:HG3	2.02	0.40
4:8J:397:TRP:CD1	14:M6:89:ARG:HH22	2.39	0.40
7:91:351:LYS:HE2	7:91:351:LYS:HB2	1.81	0.40
7:93:293:ILE:HG22	7:93:295:GLN:HG3	2.04	0.40
7:95:327:ASN:HB2	7:95:391:TYR:CD1	2.57	0.40
7:97:405:VAL:HG13	14:M5:108:TYR:CE2	2.57	0.40
3:9A:232:ALA:HA	3:9A:235:ILE:HG22	2.03	0.40
3:9E:406:HIS:HA	3:9E:409:VAL:HG12	2.03	0.40
4:9F:241:ARG:HH21	4:9F:242:PHE:HE2	1.68	0.40
4:9F:321:MET:HG2	4:9F:353:VAL:HG13	2.04	0.40
3:9G:234:VAL:HG21	3:9G:302:MET:HE1	2.02	0.40
3:9G:244:PHE:HB2	3:9G:358:GLN:NE2	2.36	0.40
3:9K:202:VAL:HG22	3:9K:268:MET:HG2	2.04	0.40
4:9L:244:GLY:HA3	4:9L:354:CYS:HA	2.02	0.40
8:A6:106:SER:O	8:A6:110:GLU:HB2	2.22	0.40
9:B6:513:LYS:HB2	9:B6:513:LYS:HE2	1.93	0.40
10:D3:110:ILE:HD13	10:D3:282:GLN:HG2	2.03	0.40
10:D3:355:THR:HG22	10:D3:361:TRP:CD2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D4:375:ILE:HG23	10:D4:379:LEU:HD12	2.03	0.40
10:D6:51:TYR:HE1	10:D6:77:LYS:HG3	1.86	0.40
10:E0:62:VAL:HG11	10:E0:305:LEU:HD22	2.03	0.40
10:E1:372:LEU:O	10:E1:376:ILE:HG12	2.22	0.40
10:E2:307:MET:HE1	10:E2:400:LEU:HD13	2.03	0.40
10:E2:338:PRO:HB2	10:E2:341:TYR:HB3	2.02	0.40
10:E4:76:ALA:HB2	10:E4:319:LEU:HD21	2.03	0.40
10:E7:50:GLU:HG3	10:E7:51:TYR:CD2	2.56	0.40
10:F1:67:ALA:HA	10:F1:70:ARG:HE	1.86	0.40
10:F2:70:ARG:NH1	14:M7:135:THR:HG21	2.37	0.40
12:F9:212:TRP:CD1	12:F9:212:TRP:H	2.38	0.40
12:G1:206:ASP:HB3	12:G1:209:TRP:CH2	2.56	0.40
14:K9:100:ALA:HB2	14:K9:105:LEU:HD12	2.02	0.40
14:L5:192:ILE:HG22	14:L5:254:PHE:CZ	2.56	0.40
14:M3:89:ARG:HH21	14:M3:90:PHE:HE1	1.70	0.40
14:M6:100:ALA:HA	14:M6:105:LEU:HB2	2.03	0.40
1:a:617:MET:HB3	1:f:618:ARG:NE	2.36	0.40
1:a:684:ARG:O	1:a:685:ASN:C	2.62	0.40
1:c:373:LEU:O	1:c:377:HIS:CB	2.68	0.40
1:o:879:VAL:HG13	1:o:880:THR:H	1.87	0.40
1:r:919:ALA:HA	1:r:922:ARG:HG2	2.03	0.40
1:I:372:LEU:O	1:I:376:MET:HG2	2.21	0.40
1:I:537:LEU:HB3	1:J:537:LEU:HB3	2.03	0.40
1:I:641:GLU:O	1:I:644:HIS:ND1	2.54	0.40
1:J:359:ARG:HH12	1:U:332:ARG:NH1	2.19	0.40
1:J:619:GLN:O	1:J:622:GLU:HB3	2.22	0.40
1:K:335:ARG:HH21	1:L:334:LEU:HD21	1.85	0.40
1:N:579:LEU:HD22	1:N:579:LEU:HA	1.83	0.40
1:O:686:PHE:O	1:O:687:ALA:C	2.65	0.40
1:Q:342:MET:HA	1:U:342:MET:HE1	2.04	0.40
1:R:592:ARG:NH2	1:V:593:GLN:HG3	2.37	0.40
1:U:639:LEU:O	1:U:642:MET:HB2	2.21	0.40
1:Y:604:ILE:O	1:Y:605:LYS:C	2.63	0.40
1:Z:502:LEU:O	1:Z:505:GLU:HG2	2.22	0.40
2:14:199:SER:C	2:14:201:VAL:H	2.28	0.40
3:1A:103:PHE:CD2	3:1A:147:SER:HB3	2.57	0.40
3:1A:208:ALA:HB2	3:1A:304:LYS:HG2	2.03	0.40
4:1B:66:MET:HE2	4:1B:116:VAL:HG21	2.03	0.40
3:1C:259:LEU:HD22	3:1C:268:MET:HG2	2.03	0.40
4:1D:11:GLN:NE2	3:1E:248:LEU:HA	2.36	0.40
4:1D:16:ILE:HD13	4:1D:226:ASN:HD22	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1D:161:ASP:HB2	4:1D:162:ARG:HH11	1.87	0.40
3:1E:268:MET:SD	3:1E:380:ASN:HB3	2.62	0.40
4:1J:152:ILE:HG22	4:1J:195:ASN:HB3	2.04	0.40
4:1L:85:PHE:HB2	4:1L:90:PHE:HE1	1.87	0.40
3:1M:213:CYS:HA	3:1M:217:LEU:HB3	2.03	0.40
3:1M:419:SER:HA	3:1M:422:ARG:HB2	2.02	0.40
4:1N:361:LEU:HD12	4:1N:361:LEU:HA	1.94	0.40
5:28:166:TYR:CZ	5:29:172:LEU:HD11	2.56	0.40
5:29:167:LYS:HE2	5:29:169:ILE:HD11	2.04	0.40
3:2A:241:SER:HB3	3:2A:249:ASN:HB3	2.04	0.40
3:2E:254:GLU:HA	3:2E:257:THR:HG22	2.03	0.40
3:2I:406:HIS:HA	3:2I:409:VAL:HG22	2.03	0.40
3:2K:134:GLY:HA3	3:2K:165:SER:HB2	2.03	0.40
4:2L:258:ILE:HG12	4:2L:266:PHE:HZ	1.86	0.40
5:35:184:THR:O	5:35:188:MET:HG2	2.21	0.40
5:35:213:LEU:HB2	5:35:221:LEU:HD13	2.04	0.40
5:39:203:GLN:O	5:39:206:LEU:HG	2.21	0.40
4:3B:149:THR:HA	4:3B:152:ILE:HD12	2.03	0.40
4:3H:178:THR:H	3:3I:352:LYS:HA	1.87	0.40
3:3I:58:ALA:HB2	3:4I:372:MET:HE3	2.02	0.40
17:3J:501:GDP:H8	3:3K:248:LEU:HD13	1.87	0.40
2:4:197:VAL:HA	2:4:200:GLN:HG2	2.02	0.40
5:43:167:LYS:HE3	5:43:169:ILE:HG12	2.02	0.40
5:46:166:TYR:HA	13:J6:338:LEU:HB2	2.04	0.40
3:4A:207:GLU:HA	3:4A:210:TYR:HB2	2.03	0.40
4:4B:101:TRP:HB3	4:4B:398:TYR:HE2	1.87	0.40
4:4B:391:ARG:HG3	3:4C:346:TRP:CD1	2.57	0.40
3:4C:248:LEU:HB2	3:4C:355:ILE:H	1.86	0.40
3:4C:280:LYS:HE2	3:4C:371:VAL:CG1	2.52	0.40
4:4D:54:ALA:HB3	4:4D:58:ARG:HB3	2.02	0.40
4:4D:176:SER:HB2	3:4E:349:THR:OG1	2.22	0.40
4:4F:230:SER:HA	4:4F:233:MET:HB3	2.04	0.40
4:4H:310:TYR:HA	4:4H:371:SER:HA	2.04	0.40
4:4J:201:VAL:HG22	4:4J:266:PHE:O	2.21	0.40
3:4M:10:GLY:O	3:4M:14:ILE:HG12	2.22	0.40
5:51:20:PHE:CZ	5:52:229:GLN:HG3	2.57	0.40
5:53:55:GLN:HB2	5:53:151:HIS:HA	2.04	0.40
5:53:205:ARG:O	5:53:209:ILE:HG12	2.21	0.40
5:57:134:LEU:O	5:57:138:ILE:HG12	2.22	0.40
5:58:157:ARG:HA	5:58:174:LEU:O	2.21	0.40
3:5C:274:PRO:HB2	3:5C:276:ILE:HG12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5F:100:ASN:HD22	4:5F:103:LYS:HE2	1.87	0.40
4:5J:239:CYS:SG	4:5J:247:ASN:HB3	2.62	0.40
4:5J:289:LEU:HD22	4:5J:363:MET:HG2	2.02	0.40
4:5L:86:ARG:HD3	4:5L:88:ASP:HB2	2.04	0.40
4:5L:250:LEU:HD23	4:5L:250:LEU:HA	1.88	0.40
4:5N:266:PHE:CE1	4:5N:370:ASN:HB3	2.56	0.40
2:6:155:GLN:HA	2:6:158:GLU:HG2	2.02	0.40
6:63:891:ARG:NH2	6:63:901:LYS:HB3	2.34	0.40
6:65:611:ARG:HA	6:65:611:ARG:HD3	1.92	0.40
6:66:903:ALA:HB3	8:A3:127:ARG:HH21	1.86	0.40
6:66:913:TYR:CE1	8:A3:86:GLN:HG3	2.54	0.40
6:67:144:ARG:HB3	6:67:564:MET:SD	2.61	0.40
6:69:397:ASN:ND2	6:69:430:THR:HG21	2.37	0.40
6:69:595:ASP:O	6:69:599:ILE:HG12	2.21	0.40
6:69:612:GLU:HG3	6:69:943:LEU:HD12	2.03	0.40
3:6A:319:TYR:HB3	3:6A:323:VAL:HG11	2.04	0.40
3:6A:331:ALA:O	3:6A:335:ILE:HG12	2.22	0.40
4:6B:73:MET:HA	4:6B:76:VAL:HG22	2.04	0.40
3:6C:244:PHE:HB3	3:6C:358:GLN:NE2	2.36	0.40
3:6C:345:ASP:HA	14:K4:114:SER:HB2	2.04	0.40
3:6I:58:ALA:HB1	1:a:667:LYS:HB3	2.04	0.40
3:6I:246:GLY:HA3	3:6I:356:ASN:HA	2.03	0.40
3:6I:311:LYS:HE3	3:6I:311:LYS:HB2	1.80	0.40
4:6L:380:ARG:HB2	7:77:311:SER:HB2	2.04	0.40
7:78:290:GLU:HG2	4:7F:340:TYR:HE2	1.87	0.40
3:7A:292:THR:HG21	3:7A:331:ALA:HB1	2.04	0.40
4:7B:23:VAL:O	4:7B:27:GLU:HG2	2.21	0.40
3:7E:7:ILE:HG21	3:7E:153:LEU:HD21	2.03	0.40
4:7F:100:ASN:HB2	4:7F:103:LYS:HD2	2.03	0.40
4:7H:256:ASN:HB2	4:7H:350:LYS:HD2	2.03	0.40
3:7I:88:HIS:CD2	3:7I:90:GLU:HG2	2.54	0.40
4:7L:6:HIS:HE2	4:7L:8:GLN:HG2	1.87	0.40
4:7L:174:LYS:HB2	14:L3:108:TYR:CE1	2.54	0.40
4:7L:398:TYR:HB3	4:7L:403:MET:HE3	2.02	0.40
4:7L:411:ALA:O	4:7L:415:MET:HG2	2.21	0.40
3:7M:143:GLY:O	3:7M:147:SER:HB2	2.21	0.40
3:7M:230:LEU:HD23	3:7M:230:LEU:HA	1.95	0.40
7:82:261:ALA:HA	7:82:391:TYR:CD1	2.57	0.40
7:83:350:ARG:CZ	7:83:387:LEU:HB3	2.51	0.40
4:8B:60:VAL:HG11	4:9B:281:TYR:HB3	2.04	0.40
3:8C:51:THR:HG21	3:8C:243:ARG:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8E:208:ALA:O	3:8E:212:ILE:HG12	2.22	0.40
3:8G:308:ARG:HD3	3:8G:340:THR:HG23	2.03	0.40
3:8I:339:ARG:NH1	14:L5:113:GLU:HB3	2.36	0.40
3:8K:387:VAL:HG13	3:8K:390:ARG:HH22	1.87	0.40
4:8L:38:GLY:HA3	4:8L:43:GLN:HG3	2.02	0.40
3:8M:265:ILE:HG23	3:8M:432:TYR:OH	2.22	0.40
7:90:269:LEU:O	7:90:273:LEU:HB2	2.22	0.40
7:93:413:ARG:HB3	7:93:416:TRP:HA	2.04	0.40
7:96:401:ILE:HD13	7:96:411:MET:HB3	2.03	0.40
3:9A:71:GLU:HG3	3:9A:73:THR:HG22	2.03	0.40
4:9B:133:PHE:HB2	4:9B:164:MET:HA	2.02	0.40
3:9E:340:THR:HG23	3:9E:341:ILE:HG23	2.03	0.40
4:9F:130:LEU:HD23	4:9F:162:ARG:HG3	2.04	0.40
4:9H:262:ARG:CZ	4:9H:421:GLU:HB2	2.52	0.40
4:9J:244:GLY:HA2	4:9J:355:ASP:HB2	2.03	0.40
3:9K:3:GLU:HG2	3:9K:64:ARG:NH1	2.37	0.40
9:B2:511:LEU:HD12	9:B2:519:ALA:HB1	2.04	0.40
9:B6:527:LEU:HD12	9:B6:534:THR:HG22	2.04	0.40
10:C9:322:GLU:O	10:C9:325:GLU:HG2	2.22	0.40
10:E2:66:LEU:HD11	10:E2:312:LYS:NZ	2.36	0.40
10:E7:71:GLN:HB2	14:M6:152:ARG:NH2	2.36	0.40
10:E7:372:LEU:O	10:E7:376:ILE:HG12	2.21	0.40
12:F5:226:ILE:HG13	12:F6:251:TYR:CZ	2.57	0.40
12:G8:246:PRO:HD2	12:G8:249:LEU:HD12	2.03	0.40
12:H2:76:ILE:HD11	12:H3:80:PHE:CG	2.56	0.40
13:J6:486:PHE:HB3	13:J6:489:SER:HB3	2.04	0.40
14:L7:155:TRP:CD1	14:L7:241:VAL:HG21	2.57	0.40
14:M2:157:TYR:HB3	14:M2:236:PHE:CE1	2.57	0.40
1:c:375:GLN:NE2	1:c:376:MET:HG2	2.36	0.40
1:c:599:SER:OG	1:c:600:LEU:N	2.53	0.40
1:c:662:ASP:O	1:c:666:VAL:HG23	2.21	0.40
1:e:377:HIS:HA	1:e:380:HIS:HB2	2.02	0.40
1:f:638:LEU:HD23	1:f:638:LEU:HA	1.82	0.40
1:w:952:ARG:HA	1:w:952:ARG:HD2	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	1	110/954 (12%)	96 (87%)	12 (11%)	2 (2%)	7 26
1	2	110/954 (12%)	95 (86%)	14 (13%)	1 (1%)	14 43
1	A	290/954 (30%)	286 (99%)	4 (1%)	0	100 100
1	B	239/954 (25%)	232 (97%)	7 (3%)	0	100 100
1	C	146/954 (15%)	137 (94%)	9 (6%)	0	100 100
1	D	116/954 (12%)	116 (100%)	0	0	100 100
1	E	267/954 (28%)	255 (96%)	11 (4%)	1 (0%)	30 60
1	F	297/954 (31%)	293 (99%)	4 (1%)	0	100 100
1	G	168/954 (18%)	154 (92%)	11 (6%)	3 (2%)	7 26
1	H	112/954 (12%)	112 (100%)	0	0	100 100
1	I	358/954 (38%)	354 (99%)	4 (1%)	0	100 100
1	J	352/954 (37%)	346 (98%)	6 (2%)	0	100 100
1	K	195/954 (20%)	194 (100%)	1 (0%)	0	100 100
1	L	200/954 (21%)	198 (99%)	2 (1%)	0	100 100
1	M	211/954 (22%)	207 (98%)	4 (2%)	0	100 100
1	N	204/954 (21%)	197 (97%)	7 (3%)	0	100 100
1	O	55/954 (6%)	50 (91%)	5 (9%)	0	100 100
1	P	52/954 (6%)	46 (88%)	6 (12%)	0	100 100
1	Q	340/954 (36%)	336 (99%)	2 (1%)	2 (1%)	22 51
1	R	250/954 (26%)	242 (97%)	8 (3%)	0	100 100
1	S	173/954 (18%)	167 (96%)	6 (4%)	0	100 100
1	T	75/954 (8%)	75 (100%)	0	0	100 100
1	U	370/954 (39%)	367 (99%)	3 (1%)	0	100 100
1	V	256/954 (27%)	255 (100%)	1 (0%)	0	100 100
1	W	196/954 (20%)	196 (100%)	0	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	X	88/954 (9%)	86 (98%)	2 (2%)	0	100	100
1	Y	352/954 (37%)	345 (98%)	7 (2%)	0	100	100
1	Z	241/954 (25%)	241 (100%)	0	0	100	100
1	a	183/954 (19%)	176 (96%)	7 (4%)	0	100	100
1	b	83/954 (9%)	83 (100%)	0	0	100	100
1	c	357/954 (37%)	334 (94%)	18 (5%)	5 (1%)	9	32
1	d	246/954 (26%)	245 (100%)	1 (0%)	0	100	100
1	e	83/954 (9%)	82 (99%)	1 (1%)	0	100	100
1	f	188/954 (20%)	162 (86%)	21 (11%)	5 (3%)	4	18
1	g	98/954 (10%)	85 (87%)	12 (12%)	1 (1%)	13	40
1	h	98/954 (10%)	69 (70%)	29 (30%)	0	100	100
1	i	98/954 (10%)	89 (91%)	8 (8%)	1 (1%)	13	40
1	j	98/954 (10%)	82 (84%)	14 (14%)	2 (2%)	6	24
1	k	98/954 (10%)	82 (84%)	16 (16%)	0	100	100
1	l	98/954 (10%)	72 (74%)	26 (26%)	0	100	100
1	m	98/954 (10%)	71 (72%)	26 (26%)	1 (1%)	13	40
1	n	86/954 (9%)	75 (87%)	10 (12%)	1 (1%)	11	35
1	o	86/954 (9%)	74 (86%)	11 (13%)	1 (1%)	11	35
1	p	86/954 (9%)	75 (87%)	8 (9%)	3 (4%)	3	14
1	q	86/954 (9%)	73 (85%)	11 (13%)	2 (2%)	5	21
1	r	86/954 (9%)	76 (88%)	6 (7%)	4 (5%)	2	10
1	s	86/954 (9%)	76 (88%)	8 (9%)	2 (2%)	5	21
1	t	86/954 (9%)	73 (85%)	9 (10%)	4 (5%)	2	10
1	u	110/954 (12%)	95 (86%)	13 (12%)	2 (2%)	7	26
1	v	110/954 (12%)	96 (87%)	13 (12%)	1 (1%)	14	43
1	w	110/954 (12%)	95 (86%)	13 (12%)	2 (2%)	7	26
1	x	110/954 (12%)	95 (86%)	12 (11%)	3 (3%)	4	18
1	y	110/954 (12%)	94 (86%)	16 (14%)	0	100	100
1	z	110/954 (12%)	94 (86%)	15 (14%)	1 (1%)	14	43
2	10	173/410 (42%)	168 (97%)	4 (2%)	1 (1%)	22	51
2	11	175/410 (43%)	171 (98%)	2 (1%)	2 (1%)	12	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	12	173/410 (42%)	169 (98%)	3 (2%)	1 (1%)	22	51
2	13	175/410 (43%)	172 (98%)	3 (2%)	0	100	100
2	14	173/410 (42%)	170 (98%)	2 (1%)	1 (1%)	22	51
2	15	86/410 (21%)	85 (99%)	1 (1%)	0	100	100
2	16	95/410 (23%)	91 (96%)	3 (3%)	1 (1%)	12	37
2	3	175/410 (43%)	173 (99%)	2 (1%)	0	100	100
2	4	173/410 (42%)	169 (98%)	3 (2%)	1 (1%)	22	51
2	5	175/410 (43%)	172 (98%)	1 (1%)	2 (1%)	12	37
2	6	173/410 (42%)	168 (97%)	4 (2%)	1 (1%)	22	51
2	7	175/410 (43%)	172 (98%)	2 (1%)	1 (1%)	22	51
2	8	173/410 (42%)	167 (96%)	5 (3%)	1 (1%)	22	51
2	9	175/410 (43%)	171 (98%)	2 (1%)	2 (1%)	12	37
3	1A	424/453 (94%)	383 (90%)	40 (9%)	1 (0%)	44	72
3	1C	424/453 (94%)	388 (92%)	34 (8%)	2 (0%)	25	55
3	1E	424/453 (94%)	386 (91%)	37 (9%)	1 (0%)	44	72
3	1G	424/453 (94%)	388 (92%)	35 (8%)	1 (0%)	44	72
3	1I	424/453 (94%)	393 (93%)	29 (7%)	2 (0%)	25	55
3	1K	424/453 (94%)	391 (92%)	33 (8%)	0	100	100
3	1M	424/453 (94%)	378 (89%)	45 (11%)	1 (0%)	44	72
3	2A	424/453 (94%)	371 (88%)	51 (12%)	2 (0%)	25	55
3	2C	424/453 (94%)	395 (93%)	29 (7%)	0	100	100
3	2E	424/453 (94%)	393 (93%)	29 (7%)	2 (0%)	25	55
3	2G	424/453 (94%)	395 (93%)	29 (7%)	0	100	100
3	2I	424/453 (94%)	405 (96%)	19 (4%)	0	100	100
3	2K	424/453 (94%)	392 (92%)	32 (8%)	0	100	100
3	2M	424/453 (94%)	385 (91%)	39 (9%)	0	100	100
3	3A	424/453 (94%)	397 (94%)	25 (6%)	2 (0%)	25	55
3	3C	424/453 (94%)	397 (94%)	27 (6%)	0	100	100
3	3E	424/453 (94%)	405 (96%)	18 (4%)	1 (0%)	44	72
3	3G	424/453 (94%)	402 (95%)	22 (5%)	0	100	100
3	3I	424/453 (94%)	400 (94%)	24 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3K	424/453 (94%)	397 (94%)	25 (6%)	2 (0%)	25	55
3	3M	424/453 (94%)	394 (93%)	28 (7%)	2 (0%)	25	55
3	4A	424/453 (94%)	379 (89%)	45 (11%)	0	100	100
3	4C	424/453 (94%)	393 (93%)	31 (7%)	0	100	100
3	4E	424/453 (94%)	385 (91%)	38 (9%)	1 (0%)	44	72
3	4G	424/453 (94%)	393 (93%)	31 (7%)	0	100	100
3	4I	424/453 (94%)	389 (92%)	34 (8%)	1 (0%)	44	72
3	4K	424/453 (94%)	394 (93%)	29 (7%)	1 (0%)	44	72
3	4M	424/453 (94%)	386 (91%)	36 (8%)	2 (0%)	25	55
3	5A	424/453 (94%)	393 (93%)	28 (7%)	3 (1%)	19	48
3	5C	424/453 (94%)	400 (94%)	24 (6%)	0	100	100
3	5E	424/453 (94%)	392 (92%)	31 (7%)	1 (0%)	44	72
3	5G	424/453 (94%)	400 (94%)	23 (5%)	1 (0%)	44	72
3	5I	424/453 (94%)	400 (94%)	23 (5%)	1 (0%)	44	72
3	5K	424/453 (94%)	396 (93%)	27 (6%)	1 (0%)	44	72
3	5M	424/453 (94%)	382 (90%)	40 (9%)	2 (0%)	25	55
3	6A	424/453 (94%)	408 (96%)	16 (4%)	0	100	100
3	6C	424/453 (94%)	403 (95%)	21 (5%)	0	100	100
3	6E	424/453 (94%)	407 (96%)	17 (4%)	0	100	100
3	6G	424/453 (94%)	394 (93%)	30 (7%)	0	100	100
3	6I	424/453 (94%)	402 (95%)	22 (5%)	0	100	100
3	6K	424/453 (94%)	403 (95%)	21 (5%)	0	100	100
3	6M	424/453 (94%)	399 (94%)	24 (6%)	1 (0%)	44	72
3	7A	424/453 (94%)	402 (95%)	22 (5%)	0	100	100
3	7C	424/453 (94%)	383 (90%)	40 (9%)	1 (0%)	44	72
3	7E	424/453 (94%)	395 (93%)	27 (6%)	2 (0%)	25	55
3	7G	424/453 (94%)	376 (89%)	46 (11%)	2 (0%)	25	55
3	7I	424/453 (94%)	391 (92%)	32 (8%)	1 (0%)	44	72
3	7K	424/453 (94%)	393 (93%)	31 (7%)	0	100	100
3	7M	424/453 (94%)	392 (92%)	32 (8%)	0	100	100
3	8A	424/453 (94%)	404 (95%)	20 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	8C	424/453 (94%)	380 (90%)	43 (10%)	1 (0%)	44 72
3	8E	424/453 (94%)	385 (91%)	37 (9%)	2 (0%)	25 55
3	8G	424/453 (94%)	383 (90%)	41 (10%)	0	100 100
3	8I	424/453 (94%)	377 (89%)	45 (11%)	2 (0%)	25 55
3	8K	424/453 (94%)	380 (90%)	42 (10%)	2 (0%)	25 55
3	8M	424/453 (94%)	397 (94%)	26 (6%)	1 (0%)	44 72
3	9A	424/453 (94%)	409 (96%)	15 (4%)	0	100 100
3	9C	424/453 (94%)	383 (90%)	41 (10%)	0	100 100
3	9E	424/453 (94%)	387 (91%)	35 (8%)	2 (0%)	25 55
3	9G	424/453 (94%)	382 (90%)	41 (10%)	1 (0%)	44 72
3	9I	424/453 (94%)	374 (88%)	48 (11%)	2 (0%)	25 55
3	9K	424/453 (94%)	388 (92%)	36 (8%)	0	100 100
3	9M	424/453 (94%)	398 (94%)	26 (6%)	0	100 100
4	1B	424/449 (94%)	395 (93%)	29 (7%)	0	100 100
4	1D	424/449 (94%)	379 (89%)	44 (10%)	1 (0%)	44 72
4	1F	424/449 (94%)	382 (90%)	42 (10%)	0	100 100
4	1H	424/449 (94%)	382 (90%)	41 (10%)	1 (0%)	44 72
4	1J	424/449 (94%)	391 (92%)	31 (7%)	2 (0%)	25 55
4	1L	424/449 (94%)	386 (91%)	36 (8%)	2 (0%)	25 55
4	1N	424/449 (94%)	385 (91%)	39 (9%)	0	100 100
4	2B	424/449 (94%)	389 (92%)	35 (8%)	0	100 100
4	2D	424/449 (94%)	389 (92%)	35 (8%)	0	100 100
4	2F	424/449 (94%)	389 (92%)	35 (8%)	0	100 100
4	2H	424/449 (94%)	392 (92%)	32 (8%)	0	100 100
4	2J	424/449 (94%)	392 (92%)	31 (7%)	1 (0%)	44 72
4	2L	424/449 (94%)	394 (93%)	29 (7%)	1 (0%)	44 72
4	3B	424/449 (94%)	383 (90%)	39 (9%)	2 (0%)	25 55
4	3D	424/449 (94%)	387 (91%)	37 (9%)	0	100 100
4	3F	424/449 (94%)	395 (93%)	28 (7%)	1 (0%)	44 72
4	3H	424/449 (94%)	392 (92%)	31 (7%)	1 (0%)	44 72
4	3J	424/449 (94%)	394 (93%)	29 (7%)	1 (0%)	44 72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	3L	424/449 (94%)	396 (93%)	28 (7%)	0	100	100
4	4B	424/449 (94%)	395 (93%)	29 (7%)	0	100	100
4	4D	424/449 (94%)	393 (93%)	31 (7%)	0	100	100
4	4F	424/449 (94%)	398 (94%)	26 (6%)	0	100	100
4	4H	424/449 (94%)	410 (97%)	14 (3%)	0	100	100
4	4J	424/449 (94%)	401 (95%)	23 (5%)	0	100	100
4	4L	424/449 (94%)	391 (92%)	32 (8%)	1 (0%)	44	72
4	5B	424/449 (94%)	380 (90%)	39 (9%)	5 (1%)	11	35
4	5D	424/449 (94%)	397 (94%)	26 (6%)	1 (0%)	44	72
4	5F	424/449 (94%)	402 (95%)	20 (5%)	2 (0%)	25	55
4	5H	424/449 (94%)	401 (95%)	22 (5%)	1 (0%)	44	72
4	5J	424/449 (94%)	393 (93%)	29 (7%)	2 (0%)	25	55
4	5L	424/449 (94%)	391 (92%)	33 (8%)	0	100	100
4	5N	424/449 (94%)	381 (90%)	42 (10%)	1 (0%)	44	72
4	6B	424/449 (94%)	399 (94%)	25 (6%)	0	100	100
4	6D	424/449 (94%)	406 (96%)	18 (4%)	0	100	100
4	6F	424/449 (94%)	407 (96%)	17 (4%)	0	100	100
4	6H	424/449 (94%)	408 (96%)	16 (4%)	0	100	100
4	6J	424/449 (94%)	405 (96%)	19 (4%)	0	100	100
4	6L	424/449 (94%)	402 (95%)	22 (5%)	0	100	100
4	6N	424/449 (94%)	399 (94%)	25 (6%)	0	100	100
4	7B	424/449 (94%)	386 (91%)	36 (8%)	2 (0%)	25	55
4	7D	424/449 (94%)	377 (89%)	45 (11%)	2 (0%)	25	55
4	7F	424/449 (94%)	382 (90%)	41 (10%)	1 (0%)	44	72
4	7H	424/449 (94%)	387 (91%)	35 (8%)	2 (0%)	25	55
4	7J	424/449 (94%)	379 (89%)	44 (10%)	1 (0%)	44	72
4	7L	424/449 (94%)	388 (92%)	34 (8%)	2 (0%)	25	55
4	8B	424/449 (94%)	375 (88%)	46 (11%)	3 (1%)	19	48
4	8D	424/449 (94%)	375 (88%)	46 (11%)	3 (1%)	19	48
4	8F	424/449 (94%)	377 (89%)	45 (11%)	2 (0%)	25	55
4	8H	424/449 (94%)	387 (91%)	35 (8%)	2 (0%)	25	55

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Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	8J	424/449 (94%)	387 (91%)	33 (8%)	4 (1%)	14	43
4	8L	424/449 (94%)	371 (88%)	52 (12%)	1 (0%)	44	72
4	9B	424/449 (94%)	373 (88%)	48 (11%)	3 (1%)	19	48
4	9D	424/449 (94%)	379 (89%)	42 (10%)	3 (1%)	19	48
4	9F	424/449 (94%)	383 (90%)	39 (9%)	2 (0%)	25	55
4	9H	424/449 (94%)	385 (91%)	37 (9%)	2 (0%)	25	55
4	9J	424/449 (94%)	388 (92%)	31 (7%)	5 (1%)	11	35
4	9L	424/449 (94%)	383 (90%)	41 (10%)	0	100	100
5	20	223/263 (85%)	194 (87%)	28 (13%)	1 (0%)	30	60
5	21	223/263 (85%)	197 (88%)	26 (12%)	0	100	100
5	22	223/263 (85%)	199 (89%)	22 (10%)	2 (1%)	14	43
5	23	223/263 (85%)	201 (90%)	22 (10%)	0	100	100
5	24	223/263 (85%)	194 (87%)	27 (12%)	2 (1%)	14	43
5	25	223/263 (85%)	198 (89%)	24 (11%)	1 (0%)	30	60
5	26	223/263 (85%)	197 (88%)	25 (11%)	1 (0%)	30	60
5	27	223/263 (85%)	195 (87%)	28 (13%)	0	100	100
5	28	223/263 (85%)	199 (89%)	23 (10%)	1 (0%)	30	60
5	29	223/263 (85%)	196 (88%)	26 (12%)	1 (0%)	30	60
5	30	223/263 (85%)	197 (88%)	24 (11%)	2 (1%)	14	43
5	31	223/263 (85%)	199 (89%)	24 (11%)	0	100	100
5	32	223/263 (85%)	200 (90%)	22 (10%)	1 (0%)	30	60
5	33	163/263 (62%)	143 (88%)	20 (12%)	0	100	100
5	35	215/263 (82%)	205 (95%)	9 (4%)	1 (0%)	25	55
5	36	211/263 (80%)	205 (97%)	6 (3%)	0	100	100
5	37	215/263 (82%)	202 (94%)	12 (6%)	1 (0%)	25	55
5	38	211/263 (80%)	201 (95%)	10 (5%)	0	100	100
5	39	215/263 (82%)	205 (95%)	8 (4%)	2 (1%)	14	43
5	40	211/263 (80%)	203 (96%)	8 (4%)	0	100	100
5	42	211/263 (80%)	205 (97%)	6 (3%)	0	100	100
5	43	215/263 (82%)	203 (94%)	11 (5%)	1 (0%)	25	55
5	44	211/263 (80%)	206 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	45	215/263 (82%)	207 (96%)	7 (3%)	1 (0%)	25	55
5	46	211/263 (80%)	204 (97%)	7 (3%)	0	100	100
5	47	215/263 (82%)	204 (95%)	10 (5%)	1 (0%)	25	55
5	48	211/263 (80%)	206 (98%)	5 (2%)	0	100	100
5	49	228/263 (87%)	207 (91%)	21 (9%)	0	100	100
5	50	231/263 (88%)	208 (90%)	21 (9%)	2 (1%)	14	43
5	51	228/263 (87%)	203 (89%)	24 (10%)	1 (0%)	30	60
5	52	231/263 (88%)	201 (87%)	29 (13%)	1 (0%)	30	60
5	53	228/263 (87%)	206 (90%)	20 (9%)	2 (1%)	14	43
5	54	231/263 (88%)	209 (90%)	21 (9%)	1 (0%)	30	60
5	55	228/263 (87%)	208 (91%)	19 (8%)	1 (0%)	30	60
5	56	231/263 (88%)	211 (91%)	19 (8%)	1 (0%)	30	60
5	57	228/263 (87%)	205 (90%)	21 (9%)	2 (1%)	14	43
5	58	231/263 (88%)	208 (90%)	21 (9%)	2 (1%)	14	43
5	59	228/263 (87%)	209 (92%)	17 (8%)	2 (1%)	14	43
5	60	231/263 (88%)	210 (91%)	18 (8%)	3 (1%)	10	33
5	61	228/263 (87%)	207 (91%)	19 (8%)	2 (1%)	14	43
5	62	231/263 (88%)	210 (91%)	20 (9%)	1 (0%)	30	60
6	63	611/1010 (60%)	553 (90%)	56 (9%)	2 (0%)	37	65
6	64	611/1010 (60%)	556 (91%)	53 (9%)	2 (0%)	37	65
6	65	611/1010 (60%)	550 (90%)	59 (10%)	2 (0%)	37	65
6	66	611/1010 (60%)	545 (89%)	64 (10%)	2 (0%)	37	65
6	67	611/1010 (60%)	552 (90%)	57 (9%)	2 (0%)	37	65
6	68	611/1010 (60%)	534 (87%)	76 (12%)	1 (0%)	44	72
6	69	611/1010 (60%)	546 (89%)	61 (10%)	4 (1%)	19	48
7	71	168/416 (40%)	155 (92%)	13 (8%)	0	100	100
7	72	168/416 (40%)	152 (90%)	16 (10%)	0	100	100
7	73	168/416 (40%)	158 (94%)	10 (6%)	0	100	100
7	75	168/416 (40%)	152 (90%)	15 (9%)	1 (1%)	22	51
7	76	168/416 (40%)	150 (89%)	17 (10%)	1 (1%)	22	51
7	77	168/416 (40%)	153 (91%)	15 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	78	168/416 (40%)	154 (92%)	14 (8%)	0	100	100
7	79	168/416 (40%)	153 (91%)	14 (8%)	1 (1%)	22	51
7	80	168/416 (40%)	149 (89%)	19 (11%)	0	100	100
7	82	168/416 (40%)	152 (90%)	16 (10%)	0	100	100
7	83	168/416 (40%)	152 (90%)	16 (10%)	0	100	100
7	84	168/416 (40%)	153 (91%)	15 (9%)	0	100	100
7	85	168/416 (40%)	150 (89%)	18 (11%)	0	100	100
7	86	168/416 (40%)	151 (90%)	16 (10%)	1 (1%)	22	51
7	87	168/416 (40%)	150 (89%)	17 (10%)	1 (1%)	22	51
7	89	168/416 (40%)	153 (91%)	14 (8%)	1 (1%)	22	51
7	90	168/416 (40%)	154 (92%)	13 (8%)	1 (1%)	22	51
7	91	168/416 (40%)	151 (90%)	16 (10%)	1 (1%)	22	51
7	92	168/416 (40%)	146 (87%)	22 (13%)	0	100	100
7	93	168/416 (40%)	149 (89%)	19 (11%)	0	100	100
7	94	168/416 (40%)	147 (88%)	21 (12%)	0	100	100
7	95	168/416 (40%)	147 (88%)	21 (12%)	0	100	100
7	96	168/416 (40%)	151 (90%)	17 (10%)	0	100	100
7	97	168/416 (40%)	148 (88%)	20 (12%)	0	100	100
8	A1	319/502 (64%)	300 (94%)	18 (6%)	1 (0%)	37	65
8	A2	319/502 (64%)	299 (94%)	16 (5%)	4 (1%)	10	33
8	A3	228/502 (45%)	204 (90%)	23 (10%)	1 (0%)	30	60
8	A4	138/502 (28%)	120 (87%)	18 (13%)	0	100	100
8	A5	319/502 (64%)	293 (92%)	26 (8%)	0	100	100
8	A6	319/502 (64%)	295 (92%)	24 (8%)	0	100	100
8	A7	319/502 (64%)	298 (93%)	20 (6%)	1 (0%)	37	65
8	A8	319/502 (64%)	299 (94%)	19 (6%)	1 (0%)	37	65
8	A9	124/502 (25%)	119 (96%)	5 (4%)	0	100	100
9	B1	251/556 (45%)	227 (90%)	24 (10%)	0	100	100
9	B2	251/556 (45%)	234 (93%)	16 (6%)	1 (0%)	30	60
9	B3	251/556 (45%)	231 (92%)	20 (8%)	0	100	100
9	B4	251/556 (45%)	230 (92%)	21 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
9	B5	251/556 (45%)	224 (89%)	26 (10%)	1 (0%)	30 60
9	B6	251/556 (45%)	221 (88%)	29 (12%)	1 (0%)	30 60
9	B7	251/556 (45%)	222 (88%)	29 (12%)	0	100 100
10	C0	180/582 (31%)	170 (94%)	10 (6%)	0	100 100
10	C6	180/582 (31%)	171 (95%)	9 (5%)	0	100 100
10	C7	180/582 (31%)	171 (95%)	9 (5%)	0	100 100
10	C8	180/582 (31%)	165 (92%)	15 (8%)	0	100 100
10	C9	180/582 (31%)	171 (95%)	9 (5%)	0	100 100
10	D0	268/582 (46%)	243 (91%)	25 (9%)	0	100 100
10	D1	180/582 (31%)	168 (93%)	12 (7%)	0	100 100
10	D2	180/582 (31%)	174 (97%)	5 (3%)	1 (1%)	22 51
10	D3	268/582 (46%)	240 (90%)	28 (10%)	0	100 100
10	D4	268/582 (46%)	244 (91%)	24 (9%)	0	100 100
10	D5	268/582 (46%)	244 (91%)	24 (9%)	0	100 100
10	D6	268/582 (46%)	243 (91%)	25 (9%)	0	100 100
10	D7	268/582 (46%)	246 (92%)	22 (8%)	0	100 100
10	D8	268/582 (46%)	246 (92%)	22 (8%)	0	100 100
10	D9	268/582 (46%)	245 (91%)	23 (9%)	0	100 100
10	E0	268/582 (46%)	248 (92%)	20 (8%)	0	100 100
10	E1	268/582 (46%)	244 (91%)	24 (9%)	0	100 100
10	E2	268/582 (46%)	242 (90%)	26 (10%)	0	100 100
10	E3	268/582 (46%)	244 (91%)	24 (9%)	0	100 100
10	E4	268/582 (46%)	243 (91%)	25 (9%)	0	100 100
10	E5	268/582 (46%)	243 (91%)	25 (9%)	0	100 100
10	E6	268/582 (46%)	241 (90%)	27 (10%)	0	100 100
10	E7	268/582 (46%)	250 (93%)	18 (7%)	0	100 100
10	E8	268/582 (46%)	244 (91%)	24 (9%)	0	100 100
10	E9	268/582 (46%)	250 (93%)	18 (7%)	0	100 100
10	F1	268/582 (46%)	244 (91%)	24 (9%)	0	100 100
10	F2	268/582 (46%)	248 (92%)	20 (8%)	0	100 100
10	F3	268/582 (46%)	246 (92%)	22 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	C1	28/351 (8%)	26 (93%)	2 (7%)	0	100	100
11	C2	28/351 (8%)	26 (93%)	2 (7%)	0	100	100
11	C3	28/351 (8%)	27 (96%)	1 (4%)	0	100	100
11	C4	25/351 (7%)	24 (96%)	1 (4%)	0	100	100
11	C5	28/351 (8%)	25 (89%)	3 (11%)	0	100	100
12	F0	105/783 (13%)	90 (86%)	13 (12%)	2 (2%)	6	25
12	F5	100/783 (13%)	90 (90%)	8 (8%)	2 (2%)	6	24
12	F6	105/783 (13%)	89 (85%)	15 (14%)	1 (1%)	13	40
12	F7	100/783 (13%)	91 (91%)	6 (6%)	3 (3%)	3	17
12	F8	105/783 (13%)	89 (85%)	14 (13%)	2 (2%)	6	25
12	F9	100/783 (13%)	90 (90%)	8 (8%)	2 (2%)	6	24
12	G0	48/783 (6%)	48 (100%)	0	0	100	100
12	G1	100/783 (13%)	90 (90%)	7 (7%)	3 (3%)	3	17
12	G2	105/783 (13%)	89 (85%)	14 (13%)	2 (2%)	6	25
12	G3	100/783 (13%)	89 (89%)	8 (8%)	3 (3%)	3	17
12	G4	105/783 (13%)	90 (86%)	13 (12%)	2 (2%)	6	25
12	G5	100/783 (13%)	89 (89%)	9 (9%)	2 (2%)	6	24
12	G6	105/783 (13%)	91 (87%)	13 (12%)	1 (1%)	13	40
12	G7	100/783 (13%)	92 (92%)	6 (6%)	2 (2%)	6	24
12	G8	105/783 (13%)	91 (87%)	12 (11%)	2 (2%)	6	25
12	G9	42/783 (5%)	42 (100%)	0	0	100	100
12	H0	22/783 (3%)	21 (96%)	1 (4%)	0	100	100
12	H1	22/783 (3%)	21 (96%)	1 (4%)	0	100	100
12	H2	42/783 (5%)	42 (100%)	0	0	100	100
12	H3	48/783 (6%)	48 (100%)	0	0	100	100
12	H4	22/783 (3%)	19 (86%)	3 (14%)	0	100	100
12	H5	42/783 (5%)	42 (100%)	0	0	100	100
12	H6	48/783 (6%)	48 (100%)	0	0	100	100
12	H7	22/783 (3%)	22 (100%)	0	0	100	100
12	H8	42/783 (5%)	42 (100%)	0	0	100	100
12	H9	48/783 (6%)	48 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	I1	42/783 (5%)	42 (100%)	0	0	100	100
12	I2	48/783 (6%)	48 (100%)	0	0	100	100
12	I3	22/783 (3%)	20 (91%)	2 (9%)	0	100	100
12	I4	42/783 (5%)	42 (100%)	0	0	100	100
12	I5	48/783 (6%)	47 (98%)	1 (2%)	0	100	100
12	I6	22/783 (3%)	20 (91%)	2 (9%)	0	100	100
12	I7	42/783 (5%)	42 (100%)	0	0	100	100
12	I8	48/783 (6%)	48 (100%)	0	0	100	100
12	I9	22/783 (3%)	21 (96%)	1 (4%)	0	100	100
13	J1	302/871 (35%)	288 (95%)	13 (4%)	1 (0%)	37	65
13	J2	302/871 (35%)	288 (95%)	13 (4%)	1 (0%)	37	65
13	J3	302/871 (35%)	289 (96%)	13 (4%)	0	100	100
13	J4	302/871 (35%)	294 (97%)	7 (2%)	1 (0%)	37	65
13	J5	302/871 (35%)	290 (96%)	11 (4%)	1 (0%)	37	65
13	J6	302/871 (35%)	291 (96%)	11 (4%)	0	100	100
13	J7	302/871 (35%)	290 (96%)	12 (4%)	0	100	100
14	K0	187/256 (73%)	177 (95%)	10 (5%)	0	100	100
14	K1	187/256 (73%)	175 (94%)	12 (6%)	0	100	100
14	K2	187/256 (73%)	172 (92%)	14 (8%)	1 (0%)	25	55
14	K3	187/256 (73%)	176 (94%)	11 (6%)	0	100	100
14	K4	187/256 (73%)	174 (93%)	12 (6%)	1 (0%)	25	55
14	K5	187/256 (73%)	175 (94%)	11 (6%)	1 (0%)	25	55
14	K6	187/256 (73%)	175 (94%)	12 (6%)	0	100	100
14	K7	187/256 (73%)	175 (94%)	12 (6%)	0	100	100
14	K8	187/256 (73%)	175 (94%)	12 (6%)	0	100	100
14	K9	187/256 (73%)	177 (95%)	10 (5%)	0	100	100
14	L0	187/256 (73%)	178 (95%)	9 (5%)	0	100	100
14	L1	187/256 (73%)	174 (93%)	13 (7%)	0	100	100
14	L2	187/256 (73%)	174 (93%)	13 (7%)	0	100	100
14	L3	187/256 (73%)	172 (92%)	15 (8%)	0	100	100
14	L4	130/256 (51%)	122 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	L5	187/256 (73%)	179 (96%)	8 (4%)	0	100	100
14	L6	187/256 (73%)	179 (96%)	8 (4%)	0	100	100
14	L7	187/256 (73%)	176 (94%)	11 (6%)	0	100	100
14	L8	187/256 (73%)	173 (92%)	14 (8%)	0	100	100
14	L9	187/256 (73%)	178 (95%)	9 (5%)	0	100	100
14	M1	123/256 (48%)	114 (93%)	8 (6%)	1 (1%)	16	45
14	M2	187/256 (73%)	174 (93%)	13 (7%)	0	100	100
14	M3	187/256 (73%)	172 (92%)	15 (8%)	0	100	100
14	M4	187/256 (73%)	172 (92%)	15 (8%)	0	100	100
14	M5	187/256 (73%)	169 (90%)	18 (10%)	0	100	100
14	M6	187/256 (73%)	172 (92%)	14 (8%)	1 (0%)	25	55
14	M7	187/256 (73%)	171 (91%)	15 (8%)	1 (0%)	25	55
All	All	99858/206100 (48%)	92192 (92%)	7369 (7%)	297 (0%)	38	65

All (297) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	10	200	GLN
2	11	189	GLU
4	1L	278	SER
4	1L	280	GLN
5	39	21	LEU
3	3E	282	TYR
3	3K	112	LYS
3	3M	110	ILE
5	45	21	LEU
2	5	189	GLU
5	58	165	GLU
3	5A	220	GLU
4	5J	39	ASP
4	5N	163	ILE
2	6	200	GLN
6	69	991	ASP
2	7	189	GLU
3	7E	141	VAL
3	7I	112	LYS
4	7L	296	ALA
4	8B	355	ASP

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Mol	Chain	Res	Type
4	8D	43	GLN
4	8F	125	GLU
4	8J	127	CYS
3	8K	112	LYS
4	8L	55	THR
2	9	189	GLU
2	9	190	LYS
4	9B	355	ASP
4	9D	42	LEU
4	9H	355	ASP
4	9J	127	CYS
4	9J	355	ASP
10	D2	331	ILE
12	F0	214	ASP
12	F5	209	TRP
12	F5	211	LYS
12	F7	211	LYS
12	F9	209	TRP
12	F9	211	LYS
12	G1	209	TRP
12	G1	211	LYS
12	G3	209	TRP
12	G3	211	LYS
12	G4	214	ASP
12	G5	209	TRP
12	G5	211	LYS
12	G7	209	TRP
12	G7	211	LYS
1	c	561	ARG
1	n	879	VAL
1	p	882	GLU
1	r	879	VAL
2	12	200	GLN
2	14	200	GLN
3	1C	273	ALA
3	1G	346	TRP
4	1J	108	GLU
5	24	61	LEU
5	29	27	SER
3	2E	179	THR
5	35	64	ASP
5	37	64	ASP

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Mol	Chain	Res	Type
4	3B	181	GLU
4	3H	178	THR
4	3J	220	PRO
3	3K	110	ILE
2	4	200	GLN
3	4M	368	LEU
2	5	190	LYS
3	5A	141	VAL
4	5B	128	ASP
4	5F	178	THR
3	5I	112	LYS
4	5J	178	THR
5	60	85	GLN
3	6M	112	LYS
3	7E	177	VAL
4	7L	338	SER
4	8B	95	THR
3	8E	82	THR
3	8E	278	ALA
4	8J	30	ILE
4	8J	95	THR
4	8J	355	ASP
4	9F	95	THR
4	9F	127	CYS
4	9J	95	THR
12	F0	193	VAL
12	F8	193	VAL
12	G2	193	VAL
12	G4	193	VAL
1	c	559	GLU
1	c	562	ILE
1	c	593	GLN
1	f	559	GLU
1	g	829	PRO
1	j	819	ALA
1	j	829	PRO
1	o	879	VAL
1	q	879	VAL
1	s	879	VAL
1	t	877	LEU
1	t	879	VAL
1	E	377	HIS

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Mol	Chain	Res	Type
1	G	288	LYS
1	G	293	SER
3	1A	82	THR
4	1D	219	THR
3	1E	346	TRP
4	1H	220	PRO
5	20	61	LEU
5	22	61	LEU
5	24	16	ASP
5	26	61	LEU
5	28	61	LEU
3	2A	261	PRO
4	2J	355	ASP
5	30	61	LEU
5	32	61	LEU
5	39	64	ASP
5	47	64	ASP
3	4E	274	PRO
4	4L	108	GLU
3	5A	278	ALA
4	5B	355	ASP
3	5G	179	THR
3	5K	112	LYS
5	60	165	GLU
5	61	165	GLU
6	64	850	LEU
4	7B	95	THR
3	7C	82	THR
4	7F	393	ALA
3	7G	82	THR
4	8D	55	THR
3	8I	278	ALA
4	9D	43	GLN
3	9E	278	ALA
4	9J	125	GLU
8	A2	287	ALA
8	A2	379	GLU
8	A2	387	ARG
12	F8	214	ASP
12	G8	214	ASP
13	J2	648	GLU
14	K2	144	PHE

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Mol	Chain	Res	Type
1	f	566	ARG
1	i	829	PRO
1	p	877	LEU
1	q	877	LEU
1	x	881	ALA
1	z	880	THR
1	Q	581	LYS
3	1I	109	THR
4	1J	39	ASP
3	1M	86	LEU
1	2	881	ALA
5	22	16	ASP
4	2L	108	GLU
5	30	16	ASP
4	3F	220	PRO
3	4I	280	LYS
5	50	165	GLU
5	53	165	GLU
5	56	165	GLU
4	5B	178	THR
4	5D	108	GLU
3	5E	179	THR
4	5F	220	PRO
3	5M	247	ALA
6	64	848	SER
6	65	848	SER
6	65	850	LEU
6	66	850	LEU
6	67	850	LEU
3	7G	112	LYS
4	7H	178	THR
2	8	200	GLN
7	86	390	PRO
7	87	390	PRO
4	8B	125	GLU
4	9B	95	THR
4	9D	178	THR
3	9E	82	THR
3	9G	274	PRO
3	9I	278	ALA
4	9J	30	ILE
8	A1	226	SER

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Mol	Chain	Res	Type
8	A2	226	SER
8	A8	226	SER
9	B2	179	ALA
9	B6	48	MET
12	F6	193	VAL
12	G1	206	ASP
12	G3	206	ASP
12	G8	193	VAL
13	J1	648	GLU
13	J5	648	GLU
14	M1	144	PHE
1	f	565	ASP
1	m	829	PRO
1	p	879	VAL
1	r	882	GLU
1	t	883	THR
1	u	881	ALA
1	w	878	PRO
1	G	377	HIS
1	Q	390	ILE
1	1	880	THR
2	16	200	GLN
3	3A	220	GLU
4	3B	220	PRO
3	3M	283	HIS
5	43	64	ASP
3	4K	220	GLU
5	50	57	THR
5	52	57	THR
5	54	165	GLU
5	55	61	LEU
5	57	61	LEU
5	57	165	GLU
5	58	57	THR
5	59	61	LEU
5	59	165	GLU
4	5H	178	THR
3	5M	141	VAL
5	61	61	LEU
6	63	848	SER
6	66	499	ARG
6	68	848	SER

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Mol	Chain	Res	Type
6	69	850	LEU
7	79	390	PRO
4	7D	108	GLU
4	8D	95	THR
4	8H	95	THR
7	90	390	PRO
4	9B	218	THR
4	9H	336	LYS
8	A7	226	SER
9	B5	48	MET
12	F7	206	ASP
12	F7	208	SER
12	G2	214	ASP
14	K4	144	PHE
14	M7	71	ASN
1	c	680	LEU
1	f	513	ARG
1	r	877	LEU
1	x	878	PRO
1	1	878	PRO
2	11	190	LYS
3	1I	179	THR
5	25	27	SER
3	4M	179	THR
4	5B	108	GLU
5	60	57	THR
5	62	57	THR
6	63	507	ARG
6	69	848	SER
4	7J	174	LYS
3	8C	197	HIS
4	8H	178	THR
3	8K	197	HIS
3	8M	261	PRO
7	91	390	PRO
8	A3	229	ARG
12	G6	213	ALA
13	J4	648	GLU
14	K5	144	PHE
14	M6	144	PHE
1	f	679	ARG
1	s	877	LEU

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Mol	Chain	Res	Type
1	t	882	GLU
1	v	881	ALA
1	w	880	THR
1	x	880	THR
6	67	627	PRO
3	2A	110	ILE
3	2E	110	ILE
3	3A	261	PRO
5	53	61	LEU
6	69	627	PRO
4	8F	272	PRO
3	9I	74	VAL
3	1C	110	ILE
5	51	61	LEU
4	5B	220	PRO
7	76	390	PRO
4	7B	272	PRO
4	7H	180	VAL
7	75	390	PRO
4	7D	180	VAL
7	89	390	PRO
3	8I	74	VAL
1	r	883	THR
1	u	878	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	93/790 (12%)	93 (100%)	0	100	100
1	2	93/790 (12%)	93 (100%)	0	100	100
1	A	259/790 (33%)	259 (100%)	0	100	100
1	B	208/790 (26%)	208 (100%)	0	100	100
1	C	129/790 (16%)	129 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	109/790 (14%)	109 (100%)	0	100 100
1	E	229/790 (29%)	229 (100%)	0	100 100
1	F	264/790 (33%)	264 (100%)	0	100 100
1	G	146/790 (18%)	146 (100%)	0	100 100
1	H	105/790 (13%)	105 (100%)	0	100 100
1	I	317/790 (40%)	271 (86%)	46 (14%)	2 10
1	J	313/790 (40%)	262 (84%)	51 (16%)	2 7
1	K	171/790 (22%)	171 (100%)	0	100 100
1	L	176/790 (22%)	174 (99%)	2 (1%)	70 83
1	M	189/790 (24%)	153 (81%)	36 (19%)	1 5
1	N	183/790 (23%)	141 (77%)	42 (23%)	0 2
1	O	49/790 (6%)	26 (53%)	23 (47%)	0 0
1	P	48/790 (6%)	33 (69%)	15 (31%)	0 0
1	Q	304/790 (38%)	304 (100%)	0	100 100
1	R	222/790 (28%)	222 (100%)	0	100 100
1	S	154/790 (20%)	154 (100%)	0	100 100
1	T	71/790 (9%)	71 (100%)	0	100 100
1	U	327/790 (41%)	327 (100%)	0	100 100
1	V	224/790 (28%)	223 (100%)	1 (0%)	89 94
1	W	173/790 (22%)	173 (100%)	0	100 100
1	X	81/790 (10%)	81 (100%)	0	100 100
1	Y	311/790 (39%)	282 (91%)	29 (9%)	7 25
1	Z	209/790 (26%)	209 (100%)	0	100 100
1	a	164/790 (21%)	126 (77%)	38 (23%)	0 2
1	b	76/790 (10%)	76 (100%)	0	100 100
1	c	316/790 (40%)	265 (84%)	51 (16%)	2 8
1	d	214/790 (27%)	214 (100%)	0	100 100
1	e	76/790 (10%)	76 (100%)	0	100 100
1	f	169/790 (21%)	110 (65%)	59 (35%)	0 0
1	g	84/790 (11%)	84 (100%)	0	100 100
1	h	84/790 (11%)	83 (99%)	1 (1%)	67 81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	i	84/790 (11%)	84 (100%)	0	100	100
1	j	84/790 (11%)	84 (100%)	0	100	100
1	k	84/790 (11%)	84 (100%)	0	100	100
1	l	84/790 (11%)	84 (100%)	0	100	100
1	m	84/790 (11%)	84 (100%)	0	100	100
1	n	76/790 (10%)	76 (100%)	0	100	100
1	o	76/790 (10%)	76 (100%)	0	100	100
1	p	76/790 (10%)	76 (100%)	0	100	100
1	q	76/790 (10%)	76 (100%)	0	100	100
1	r	76/790 (10%)	76 (100%)	0	100	100
1	s	76/790 (10%)	76 (100%)	0	100	100
1	t	76/790 (10%)	76 (100%)	0	100	100
1	u	93/790 (12%)	93 (100%)	0	100	100
1	v	93/790 (12%)	93 (100%)	0	100	100
1	w	93/790 (12%)	93 (100%)	0	100	100
1	x	93/790 (12%)	93 (100%)	0	100	100
1	y	93/790 (12%)	93 (100%)	0	100	100
1	z	93/790 (12%)	93 (100%)	0	100	100
2	10	155/355 (44%)	155 (100%)	0	100	100
2	11	157/355 (44%)	157 (100%)	0	100	100
2	12	155/355 (44%)	155 (100%)	0	100	100
2	13	157/355 (44%)	157 (100%)	0	100	100
2	14	155/355 (44%)	155 (100%)	0	100	100
2	15	80/355 (22%)	80 (100%)	0	100	100
2	16	87/355 (24%)	87 (100%)	0	100	100
2	3	157/355 (44%)	157 (100%)	0	100	100
2	4	155/355 (44%)	155 (100%)	0	100	100
2	5	157/355 (44%)	157 (100%)	0	100	100
2	6	155/355 (44%)	154 (99%)	1 (1%)	84	91
2	7	157/355 (44%)	157 (100%)	0	100	100
2	8	155/355 (44%)	155 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	9	157/355 (44%)	157 (100%)	0	100	100
3	1A	359/379 (95%)	359 (100%)	0	100	100
3	1C	359/379 (95%)	359 (100%)	0	100	100
3	1E	359/379 (95%)	359 (100%)	0	100	100
3	1G	359/379 (95%)	359 (100%)	0	100	100
3	1I	359/379 (95%)	359 (100%)	0	100	100
3	1K	359/379 (95%)	359 (100%)	0	100	100
3	1M	359/379 (95%)	359 (100%)	0	100	100
3	2A	359/379 (95%)	359 (100%)	0	100	100
3	2C	359/379 (95%)	359 (100%)	0	100	100
3	2E	359/379 (95%)	358 (100%)	1 (0%)	91	95
3	2G	359/379 (95%)	359 (100%)	0	100	100
3	2I	359/379 (95%)	359 (100%)	0	100	100
3	2K	359/379 (95%)	359 (100%)	0	100	100
3	2M	359/379 (95%)	359 (100%)	0	100	100
3	3A	359/379 (95%)	359 (100%)	0	100	100
3	3C	359/379 (95%)	359 (100%)	0	100	100
3	3E	359/379 (95%)	359 (100%)	0	100	100
3	3G	359/379 (95%)	359 (100%)	0	100	100
3	3I	359/379 (95%)	359 (100%)	0	100	100
3	3K	359/379 (95%)	359 (100%)	0	100	100
3	3M	359/379 (95%)	359 (100%)	0	100	100
3	4A	359/379 (95%)	359 (100%)	0	100	100
3	4C	359/379 (95%)	359 (100%)	0	100	100
3	4E	359/379 (95%)	359 (100%)	0	100	100
3	4G	359/379 (95%)	359 (100%)	0	100	100
3	4I	359/379 (95%)	359 (100%)	0	100	100
3	4K	359/379 (95%)	359 (100%)	0	100	100
3	4M	359/379 (95%)	359 (100%)	0	100	100
3	5A	359/379 (95%)	358 (100%)	1 (0%)	91	95
3	5C	359/379 (95%)	359 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	5E	359/379 (95%)	359 (100%)	0	100	100
3	5G	359/379 (95%)	359 (100%)	0	100	100
3	5I	359/379 (95%)	358 (100%)	1 (0%)	91	95
3	5K	359/379 (95%)	359 (100%)	0	100	100
3	5M	359/379 (95%)	359 (100%)	0	100	100
3	6A	359/379 (95%)	359 (100%)	0	100	100
3	6C	359/379 (95%)	359 (100%)	0	100	100
3	6E	359/379 (95%)	359 (100%)	0	100	100
3	6G	359/379 (95%)	359 (100%)	0	100	100
3	6I	359/379 (95%)	359 (100%)	0	100	100
3	6K	359/379 (95%)	359 (100%)	0	100	100
3	6M	359/379 (95%)	359 (100%)	0	100	100
3	7A	359/379 (95%)	359 (100%)	0	100	100
3	7C	359/379 (95%)	359 (100%)	0	100	100
3	7E	359/379 (95%)	359 (100%)	0	100	100
3	7G	359/379 (95%)	359 (100%)	0	100	100
3	7I	359/379 (95%)	359 (100%)	0	100	100
3	7K	359/379 (95%)	359 (100%)	0	100	100
3	7M	359/379 (95%)	359 (100%)	0	100	100
3	8A	359/379 (95%)	358 (100%)	1 (0%)	91	95
3	8C	359/379 (95%)	359 (100%)	0	100	100
3	8E	359/379 (95%)	359 (100%)	0	100	100
3	8G	359/379 (95%)	359 (100%)	0	100	100
3	8I	359/379 (95%)	359 (100%)	0	100	100
3	8K	359/379 (95%)	359 (100%)	0	100	100
3	8M	359/379 (95%)	359 (100%)	0	100	100
3	9A	359/379 (95%)	359 (100%)	0	100	100
3	9C	359/379 (95%)	359 (100%)	0	100	100
3	9E	359/379 (95%)	359 (100%)	0	100	100
3	9G	359/379 (95%)	359 (100%)	0	100	100
3	9I	359/379 (95%)	359 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	9K	359/379 (95%)	359 (100%)	0	100	100
3	9M	359/379 (95%)	359 (100%)	0	100	100
4	1B	364/381 (96%)	364 (100%)	0	100	100
4	1D	364/381 (96%)	364 (100%)	0	100	100
4	1F	364/381 (96%)	364 (100%)	0	100	100
4	1H	364/381 (96%)	364 (100%)	0	100	100
4	1J	364/381 (96%)	364 (100%)	0	100	100
4	1L	364/381 (96%)	364 (100%)	0	100	100
4	1N	364/381 (96%)	364 (100%)	0	100	100
4	2B	364/381 (96%)	364 (100%)	0	100	100
4	2D	364/381 (96%)	364 (100%)	0	100	100
4	2F	364/381 (96%)	364 (100%)	0	100	100
4	2H	364/381 (96%)	364 (100%)	0	100	100
4	2J	364/381 (96%)	364 (100%)	0	100	100
4	2L	364/381 (96%)	364 (100%)	0	100	100
4	3B	364/381 (96%)	363 (100%)	1 (0%)	91	95
4	3D	364/381 (96%)	364 (100%)	0	100	100
4	3F	364/381 (96%)	363 (100%)	1 (0%)	91	95
4	3H	364/381 (96%)	364 (100%)	0	100	100
4	3J	364/381 (96%)	363 (100%)	1 (0%)	91	95
4	3L	364/381 (96%)	364 (100%)	0	100	100
4	4B	364/381 (96%)	364 (100%)	0	100	100
4	4D	364/381 (96%)	364 (100%)	0	100	100
4	4F	364/381 (96%)	364 (100%)	0	100	100
4	4H	364/381 (96%)	364 (100%)	0	100	100
4	4J	364/381 (96%)	364 (100%)	0	100	100
4	4L	364/381 (96%)	364 (100%)	0	100	100
4	5B	364/381 (96%)	364 (100%)	0	100	100
4	5D	364/381 (96%)	364 (100%)	0	100	100
4	5F	364/381 (96%)	364 (100%)	0	100	100
4	5H	364/381 (96%)	364 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	5J	364/381 (96%)	364 (100%)	0	100	100
4	5L	364/381 (96%)	364 (100%)	0	100	100
4	5N	364/381 (96%)	363 (100%)	1 (0%)	91	95
4	6B	364/381 (96%)	364 (100%)	0	100	100
4	6D	364/381 (96%)	364 (100%)	0	100	100
4	6F	364/381 (96%)	364 (100%)	0	100	100
4	6H	364/381 (96%)	364 (100%)	0	100	100
4	6J	364/381 (96%)	364 (100%)	0	100	100
4	6L	364/381 (96%)	364 (100%)	0	100	100
4	6N	364/381 (96%)	364 (100%)	0	100	100
4	7B	364/381 (96%)	364 (100%)	0	100	100
4	7D	364/381 (96%)	364 (100%)	0	100	100
4	7F	364/381 (96%)	364 (100%)	0	100	100
4	7H	364/381 (96%)	364 (100%)	0	100	100
4	7J	364/381 (96%)	364 (100%)	0	100	100
4	7L	364/381 (96%)	364 (100%)	0	100	100
4	8B	364/381 (96%)	364 (100%)	0	100	100
4	8D	364/381 (96%)	364 (100%)	0	100	100
4	8F	364/381 (96%)	363 (100%)	1 (0%)	91	95
4	8H	364/381 (96%)	364 (100%)	0	100	100
4	8J	364/381 (96%)	362 (100%)	2 (0%)	86	92
4	8L	364/381 (96%)	364 (100%)	0	100	100
4	9B	364/381 (96%)	364 (100%)	0	100	100
4	9D	364/381 (96%)	364 (100%)	0	100	100
4	9F	364/381 (96%)	364 (100%)	0	100	100
4	9H	364/381 (96%)	364 (100%)	0	100	100
4	9J	364/381 (96%)	364 (100%)	0	100	100
4	9L	364/381 (96%)	364 (100%)	0	100	100
5	20	205/227 (90%)	205 (100%)	0	100	100
5	21	205/227 (90%)	205 (100%)	0	100	100
5	22	205/227 (90%)	205 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	23	205/227 (90%)	205 (100%)	0	100	100
5	24	205/227 (90%)	205 (100%)	0	100	100
5	25	205/227 (90%)	205 (100%)	0	100	100
5	26	205/227 (90%)	205 (100%)	0	100	100
5	27	205/227 (90%)	204 (100%)	1 (0%)	86	92
5	28	205/227 (90%)	205 (100%)	0	100	100
5	29	205/227 (90%)	204 (100%)	1 (0%)	86	92
5	30	205/227 (90%)	205 (100%)	0	100	100
5	31	205/227 (90%)	205 (100%)	0	100	100
5	32	205/227 (90%)	205 (100%)	0	100	100
5	33	152/227 (67%)	152 (100%)	0	100	100
5	35	197/227 (87%)	197 (100%)	0	100	100
5	36	193/227 (85%)	193 (100%)	0	100	100
5	37	197/227 (87%)	197 (100%)	0	100	100
5	38	193/227 (85%)	193 (100%)	0	100	100
5	39	197/227 (87%)	197 (100%)	0	100	100
5	40	193/227 (85%)	193 (100%)	0	100	100
5	42	193/227 (85%)	193 (100%)	0	100	100
5	43	197/227 (87%)	197 (100%)	0	100	100
5	44	193/227 (85%)	193 (100%)	0	100	100
5	45	197/227 (87%)	197 (100%)	0	100	100
5	46	193/227 (85%)	193 (100%)	0	100	100
5	47	197/227 (87%)	197 (100%)	0	100	100
5	48	193/227 (85%)	193 (100%)	0	100	100
5	49	206/227 (91%)	206 (100%)	0	100	100
5	50	207/227 (91%)	207 (100%)	0	100	100
5	51	206/227 (91%)	206 (100%)	0	100	100
5	52	207/227 (91%)	207 (100%)	0	100	100
5	53	206/227 (91%)	206 (100%)	0	100	100
5	54	207/227 (91%)	207 (100%)	0	100	100
5	55	206/227 (91%)	206 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	56	207/227 (91%)	207 (100%)	0	100	100
5	57	206/227 (91%)	206 (100%)	0	100	100
5	58	207/227 (91%)	207 (100%)	0	100	100
5	59	206/227 (91%)	206 (100%)	0	100	100
5	60	207/227 (91%)	207 (100%)	0	100	100
5	61	206/227 (91%)	206 (100%)	0	100	100
5	62	207/227 (91%)	206 (100%)	1 (0%)	86	92
6	63	541/863 (63%)	541 (100%)	0	100	100
6	64	541/863 (63%)	531 (98%)	10 (2%)	54	74
6	65	541/863 (63%)	529 (98%)	12 (2%)	47	69
6	66	541/863 (63%)	530 (98%)	11 (2%)	50	71
6	67	541/863 (63%)	528 (98%)	13 (2%)	44	67
6	68	541/863 (63%)	528 (98%)	13 (2%)	44	67
6	69	541/863 (63%)	528 (98%)	13 (2%)	44	67
7	71	151/364 (42%)	151 (100%)	0	100	100
7	72	151/364 (42%)	151 (100%)	0	100	100
7	73	151/364 (42%)	151 (100%)	0	100	100
7	75	151/364 (42%)	151 (100%)	0	100	100
7	76	151/364 (42%)	151 (100%)	0	100	100
7	77	151/364 (42%)	151 (100%)	0	100	100
7	78	151/364 (42%)	151 (100%)	0	100	100
7	79	151/364 (42%)	151 (100%)	0	100	100
7	80	151/364 (42%)	151 (100%)	0	100	100
7	82	151/364 (42%)	151 (100%)	0	100	100
7	83	151/364 (42%)	151 (100%)	0	100	100
7	84	151/364 (42%)	151 (100%)	0	100	100
7	85	151/364 (42%)	151 (100%)	0	100	100
7	86	151/364 (42%)	151 (100%)	0	100	100
7	87	151/364 (42%)	151 (100%)	0	100	100
7	89	151/364 (42%)	151 (100%)	0	100	100
7	90	151/364 (42%)	151 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	91	151/364 (42%)	151 (100%)	0	100	100
7	92	151/364 (42%)	151 (100%)	0	100	100
7	93	151/364 (42%)	151 (100%)	0	100	100
7	94	151/364 (42%)	151 (100%)	0	100	100
7	95	151/364 (42%)	151 (100%)	0	100	100
7	96	151/364 (42%)	151 (100%)	0	100	100
7	97	151/364 (42%)	151 (100%)	0	100	100
8	A1	287/428 (67%)	287 (100%)	0	100	100
8	A2	287/428 (67%)	287 (100%)	0	100	100
8	A3	209/428 (49%)	209 (100%)	0	100	100
8	A4	94/428 (22%)	94 (100%)	0	100	100
8	A5	287/428 (67%)	287 (100%)	0	100	100
8	A6	287/428 (67%)	287 (100%)	0	100	100
8	A7	287/428 (67%)	287 (100%)	0	100	100
8	A8	287/428 (67%)	287 (100%)	0	100	100
8	A9	111/428 (26%)	111 (100%)	0	100	100
9	B1	225/479 (47%)	225 (100%)	0	100	100
9	B2	225/479 (47%)	225 (100%)	0	100	100
9	B3	225/479 (47%)	225 (100%)	0	100	100
9	B4	225/479 (47%)	225 (100%)	0	100	100
9	B5	225/479 (47%)	225 (100%)	0	100	100
9	B6	225/479 (47%)	225 (100%)	0	100	100
9	B7	225/479 (47%)	225 (100%)	0	100	100
10	C0	154/501 (31%)	154 (100%)	0	100	100
10	C6	154/501 (31%)	154 (100%)	0	100	100
10	C7	154/501 (31%)	154 (100%)	0	100	100
10	C8	154/501 (31%)	154 (100%)	0	100	100
10	C9	154/501 (31%)	154 (100%)	0	100	100
10	D0	234/501 (47%)	234 (100%)	0	100	100
10	D1	154/501 (31%)	154 (100%)	0	100	100
10	D2	154/501 (31%)	154 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	D3	234/501 (47%)	234 (100%)	0	100	100
10	D4	234/501 (47%)	234 (100%)	0	100	100
10	D5	234/501 (47%)	234 (100%)	0	100	100
10	D6	234/501 (47%)	234 (100%)	0	100	100
10	D7	234/501 (47%)	234 (100%)	0	100	100
10	D8	234/501 (47%)	234 (100%)	0	100	100
10	D9	234/501 (47%)	234 (100%)	0	100	100
10	E0	234/501 (47%)	234 (100%)	0	100	100
10	E1	234/501 (47%)	234 (100%)	0	100	100
10	E2	234/501 (47%)	234 (100%)	0	100	100
10	E3	234/501 (47%)	234 (100%)	0	100	100
10	E4	234/501 (47%)	234 (100%)	0	100	100
10	E5	234/501 (47%)	234 (100%)	0	100	100
10	E6	234/501 (47%)	234 (100%)	0	100	100
10	E7	234/501 (47%)	234 (100%)	0	100	100
10	E8	234/501 (47%)	234 (100%)	0	100	100
10	E9	234/501 (47%)	234 (100%)	0	100	100
10	F1	234/501 (47%)	234 (100%)	0	100	100
10	F2	234/501 (47%)	234 (100%)	0	100	100
10	F3	234/501 (47%)	234 (100%)	0	100	100
11	C1	28/305 (9%)	28 (100%)	0	100	100
11	C2	27/305 (9%)	27 (100%)	0	100	100
11	C3	28/305 (9%)	28 (100%)	0	100	100
11	C4	26/305 (8%)	26 (100%)	0	100	100
11	C5	27/305 (9%)	27 (100%)	0	100	100
12	F0	95/596 (16%)	95 (100%)	0	100	100
12	F5	92/596 (15%)	92 (100%)	0	100	100
12	F6	95/596 (16%)	95 (100%)	0	100	100
12	F7	92/596 (15%)	92 (100%)	0	100	100
12	F8	95/596 (16%)	95 (100%)	0	100	100
12	F9	92/596 (15%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	G0	43/596 (7%)	43 (100%)	0	100	100
12	G1	92/596 (15%)	92 (100%)	0	100	100
12	G2	95/596 (16%)	95 (100%)	0	100	100
12	G3	92/596 (15%)	92 (100%)	0	100	100
12	G4	95/596 (16%)	95 (100%)	0	100	100
12	G5	92/596 (15%)	92 (100%)	0	100	100
12	G6	95/596 (16%)	95 (100%)	0	100	100
12	G7	92/596 (15%)	92 (100%)	0	100	100
12	G8	95/596 (16%)	95 (100%)	0	100	100
12	G9	37/596 (6%)	37 (100%)	0	100	100
12	H0	22/596 (4%)	22 (100%)	0	100	100
12	H1	22/596 (4%)	22 (100%)	0	100	100
12	H2	37/596 (6%)	37 (100%)	0	100	100
12	H3	43/596 (7%)	43 (100%)	0	100	100
12	H4	22/596 (4%)	22 (100%)	0	100	100
12	H5	37/596 (6%)	37 (100%)	0	100	100
12	H6	43/596 (7%)	43 (100%)	0	100	100
12	H7	22/596 (4%)	22 (100%)	0	100	100
12	H8	37/596 (6%)	37 (100%)	0	100	100
12	H9	43/596 (7%)	43 (100%)	0	100	100
12	I1	37/596 (6%)	37 (100%)	0	100	100
12	I2	43/596 (7%)	43 (100%)	0	100	100
12	I3	22/596 (4%)	22 (100%)	0	100	100
12	I4	37/596 (6%)	37 (100%)	0	100	100
12	I5	43/596 (7%)	34 (79%)	9 (21%)	1	4
12	I6	22/596 (4%)	22 (100%)	0	100	100
12	I7	37/596 (6%)	37 (100%)	0	100	100
12	I8	43/596 (7%)	43 (100%)	0	100	100
12	I9	22/596 (4%)	22 (100%)	0	100	100
13	J1	262/721 (36%)	262 (100%)	0	100	100
13	J2	262/721 (36%)	262 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	J3	262/721 (36%)	262 (100%)	0	100	100
13	J4	262/721 (36%)	262 (100%)	0	100	100
13	J5	262/721 (36%)	262 (100%)	0	100	100
13	J6	262/721 (36%)	262 (100%)	0	100	100
13	J7	262/721 (36%)	262 (100%)	0	100	100
14	K0	166/223 (74%)	166 (100%)	0	100	100
14	K1	166/223 (74%)	166 (100%)	0	100	100
14	K2	166/223 (74%)	166 (100%)	0	100	100
14	K3	166/223 (74%)	166 (100%)	0	100	100
14	K4	166/223 (74%)	166 (100%)	0	100	100
14	K5	166/223 (74%)	165 (99%)	1 (1%)	84	91
14	K6	166/223 (74%)	166 (100%)	0	100	100
14	K7	166/223 (74%)	166 (100%)	0	100	100
14	K8	166/223 (74%)	166 (100%)	0	100	100
14	K9	166/223 (74%)	166 (100%)	0	100	100
14	L0	166/223 (74%)	166 (100%)	0	100	100
14	L1	166/223 (74%)	166 (100%)	0	100	100
14	L2	166/223 (74%)	166 (100%)	0	100	100
14	L3	166/223 (74%)	165 (99%)	1 (1%)	84	91
14	L4	119/223 (53%)	119 (100%)	0	100	100
14	L5	166/223 (74%)	166 (100%)	0	100	100
14	L6	166/223 (74%)	166 (100%)	0	100	100
14	L7	166/223 (74%)	166 (100%)	0	100	100
14	L8	166/223 (74%)	166 (100%)	0	100	100
14	L9	166/223 (74%)	166 (100%)	0	100	100
14	M1	112/223 (50%)	112 (100%)	0	100	100
14	M2	166/223 (74%)	166 (100%)	0	100	100
14	M3	166/223 (74%)	166 (100%)	0	100	100
14	M4	166/223 (74%)	166 (100%)	0	100	100
14	M5	166/223 (74%)	166 (100%)	0	100	100
14	M6	166/223 (74%)	160 (96%)	6 (4%)	30	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
14	M7	166/223 (74%)	166 (100%)	0	100 100
All	All	86983/171994 (51%)	86485 (99%)	498 (1%)	82 91

All (498) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	572	ARG
1	I	574	LYS
1	I	575	LEU
1	I	578	ARG
1	I	581	LYS
1	I	584	GLU
1	I	586	LYS
1	I	587	GLU
1	I	592	ARG
1	I	593	GLN
1	I	601	ARG
1	I	603	ARG
1	I	605	LYS
1	I	606	HIS
1	I	610	VAL
1	I	611	THR
1	I	612	PHE
1	I	613	GLN
1	I	615	ARG
1	I	617	MET
1	I	624	GLN
1	I	625	GLN
1	I	628	VAL
1	I	629	LYS
1	I	630	ARG
1	I	631	LEU
1	I	632	ARG
1	I	635	ASN
1	I	639	LEU
1	I	642	MET
1	I	643	ARG
1	I	644	HIS
1	I	646	ASN
1	I	647	LYS
1	I	652	MET
1	I	656	GLN

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Mol	Chain	Res	Type
1	I	659	LEU
1	I	664	ILE
1	I	673	LEU
1	I	674	ARG
1	I	675	LYS
1	I	677	MET
1	I	679	ARG
1	I	682	LYS
1	I	683	GLU
1	I	684	ARG
1	J	572	ARG
1	J	574	LYS
1	J	575	LEU
1	J	577	GLN
1	J	578	ARG
1	J	579	LEU
1	J	580	GLU
1	J	581	LYS
1	J	583	GLN
1	J	586	LYS
1	J	587	GLU
1	J	590	GLU
1	J	592	ARG
1	J	601	ARG
1	J	603	ARG
1	J	604	ILE
1	J	605	LYS
1	J	606	HIS
1	J	607	LEU
1	J	610	VAL
1	J	613	GLN
1	J	614	LEU
1	J	615	ARG
1	J	616	THR
1	J	618	ARG
1	J	620	ASP
1	J	621	PHE
1	J	624	GLN
1	J	629	LYS
1	J	630	ARG
1	J	631	LEU
1	J	632	ARG

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Mol	Chain	Res	Type
1	J	633	ASP
1	J	643	ARG
1	J	644	HIS
1	J	652	MET
1	J	653	LYS
1	J	657	GLN
1	J	659	LEU
1	J	663	LEU
1	J	664	ILE
1	J	667	LYS
1	J	668	GLN
1	J	673	LEU
1	J	674	ARG
1	J	675	LYS
1	J	677	MET
1	J	679	ARG
1	J	680	LEU
1	J	682	LYS
1	J	684	ARG
1	L	382	GLN
1	L	414	GLN
1	M	596	GLU
1	M	600	LEU
1	M	601	ARG
1	M	603	ARG
1	M	605	LYS
1	M	606	HIS
1	M	611	THR
1	M	612	PHE
1	M	613	GLN
1	M	615	ARG
1	M	617	MET
1	M	618	ARG
1	M	621	PHE
1	M	624	GLN
1	M	628	VAL
1	M	629	LYS
1	M	630	ARG
1	M	632	ARG
1	M	634	GLU
1	M	635	ASN
1	M	638	LEU

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Mol	Chain	Res	Type
1	M	639	LEU
1	M	643	ARG
1	M	645	GLN
1	M	647	LYS
1	M	653	LYS
1	M	654	LEU
1	M	656	GLN
1	M	660	GLN
1	M	675	LYS
1	M	677	MET
1	M	679	ARG
1	M	681	ILE
1	M	682	LYS
1	M	683	GLU
1	M	684	ARG
1	N	574	LYS
1	N	575	LEU
1	N	576	SER
1	N	579	LEU
1	N	582	LEU
1	N	584	GLU
1	N	586	LYS
1	N	589	THR
1	N	590	GLU
1	N	591	ARG
1	N	592	ARG
1	N	596	GLU
1	N	597	ILE
1	N	599	SER
1	N	600	LEU
1	N	603	ARG
1	N	605	LYS
1	N	607	LEU
1	N	610	VAL
1	N	613	GLN
1	N	615	ARG
1	N	617	MET
1	N	618	ARG
1	N	621	PHE
1	N	622	GLU
1	N	623	SER
1	N	624	GLN

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Mol	Chain	Res	Type
1	N	626	LEU
1	N	629	LYS
1	N	631	LEU
1	N	633	ASP
1	N	643	ARG
1	N	652	MET
1	N	653	LYS
1	N	655	ASP
1	N	659	LEU
1	N	667	LYS
1	N	668	GLN
1	N	674	ARG
1	N	675	LYS
1	N	677	MET
1	N	684	ARG
1	O	632	ARG
1	O	633	ASP
1	O	635	ASN
1	O	638	LEU
1	O	639	LEU
1	O	642	MET
1	O	643	ARG
1	O	644	HIS
1	O	645	GLN
1	O	647	LYS
1	O	652	MET
1	O	653	LYS
1	O	656	GLN
1	O	659	LEU
1	O	660	GLN
1	O	661	ASN
1	O	669	GLU
1	O	673	LEU
1	O	675	LYS
1	O	677	MET
1	O	679	ARG
1	O	680	LEU
1	O	683	GLU
1	P	632	ARG
1	P	633	ASP
1	P	634	GLU
1	P	638	LEU

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Mol	Chain	Res	Type
1	P	643	ARG
1	P	647	LYS
1	P	652	MET
1	P	653	LYS
1	P	656	GLN
1	P	660	GLN
1	P	663	LEU
1	P	668	GLN
1	P	669	GLU
1	P	679	ARG
1	P	682	LYS
1	V	484	GLN
1	Y	572	ARG
1	Y	574	LYS
1	Y	580	GLU
1	Y	581	LYS
1	Y	585	GLU
1	Y	586	LYS
1	Y	587	GLU
1	Y	592	ARG
1	Y	597	ILE
1	Y	601	ARG
1	Y	603	ARG
1	Y	607	LEU
1	Y	614	LEU
1	Y	615	ARG
1	Y	617	MET
1	Y	624	GLN
1	Y	631	LEU
1	Y	632	ARG
1	Y	639	LEU
1	Y	643	ARG
1	Y	647	LYS
1	Y	654	LEU
1	Y	659	LEU
1	Y	668	GLN
1	Y	673	LEU
1	Y	675	LYS
1	Y	677	MET
1	Y	679	ARG
1	Y	680	LEU
5	27	117	GLN

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Mol	Chain	Res	Type
5	29	112	GLN
3	2E	329	ASN
4	3B	131	GLN
4	3F	334	GLN
4	3J	347	ASN
3	5A	342	GLN
3	5I	31	GLN
4	5N	291	GLN
2	6	290	ASN
5	62	90	GLU
6	64	488	ILE
6	64	489	LEU
6	64	494	LYS
6	64	495	LEU
6	64	501	ARG
6	64	503	LYS
6	64	505	GLN
6	64	507	ARG
6	64	508	GLU
6	64	510	SER
6	65	488	ILE
6	65	494	LYS
6	65	495	LEU
6	65	500	ARG
6	65	501	ARG
6	65	503	LYS
6	65	505	GLN
6	65	506	GLU
6	65	507	ARG
6	65	508	GLU
6	65	509	GLU
6	65	510	SER
6	66	488	ILE
6	66	490	GLU
6	66	494	LYS
6	66	495	LEU
6	66	496	ASP
6	66	498	ARG
6	66	500	ARG
6	66	501	ARG
6	66	503	LYS
6	66	506	GLU

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Mol	Chain	Res	Type
6	66	510	SER
6	67	487	TYR
6	67	488	ILE
6	67	490	GLU
6	67	492	SER
6	67	493	ARG
6	67	495	LEU
6	67	498	ARG
6	67	499	ARG
6	67	503	LYS
6	67	505	GLN
6	67	506	GLU
6	67	507	ARG
6	67	510	SER
6	68	488	ILE
6	68	489	LEU
6	68	494	LYS
6	68	496	ASP
6	68	498	ARG
6	68	500	ARG
6	68	501	ARG
6	68	503	LYS
6	68	505	GLN
6	68	506	GLU
6	68	507	ARG
6	68	509	GLU
6	68	510	SER
6	69	489	LEU
6	69	490	GLU
6	69	494	LYS
6	69	496	ASP
6	69	498	ARG
6	69	500	ARG
6	69	501	ARG
6	69	503	LYS
6	69	505	GLN
6	69	506	GLU
6	69	507	ARG
6	69	509	GLU
6	69	510	SER
3	8A	283	HIS
4	8F	370	ASN

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Mol	Chain	Res	Type
4	8J	191	GLN
4	8J	298	ASN
12	I5	72	GLU
12	I5	74	LYS
12	I5	75	ASN
12	I5	78	ARG
12	I5	81	ASP
12	I5	84	TYR
12	I5	86	ARG
12	I5	92	VAL
12	I5	93	GLN
14	K5	142	GLN
14	L3	82	TYR
14	M6	75	ARG
14	M6	77	THR
14	M6	79	THR
14	M6	81	TYR
14	M6	82	TYR
14	M6	83	THR
1	a	571	GLU
1	a	574	LYS
1	a	576	SER
1	a	579	LEU
1	a	580	GLU
1	a	581	LYS
1	a	585	GLU
1	a	586	LYS
1	a	587	GLU
1	a	590	GLU
1	a	591	ARG
1	a	601	ARG
1	a	605	LYS
1	a	607	LEU
1	a	611	THR
1	a	615	ARG
1	a	616	THR
1	a	619	GLN
1	a	623	SER
1	a	624	GLN
1	a	629	LYS
1	a	630	ARG
1	a	631	LEU

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Mol	Chain	Res	Type
1	a	639	LEU
1	a	643	ARG
1	a	653	LYS
1	a	656	GLN
1	a	660	GLN
1	a	664	ILE
1	a	668	GLN
1	a	673	LEU
1	a	675	LYS
1	a	676	GLU
1	a	677	MET
1	a	679	ARG
1	a	680	LEU
1	a	681	ILE
1	a	682	LYS
1	c	567	SER
1	c	569	ASP
1	c	571	GLU
1	c	572	ARG
1	c	574	LYS
1	c	575	LEU
1	c	578	ARG
1	c	579	LEU
1	c	581	LYS
1	c	583	GLN
1	c	584	GLU
1	c	586	LYS
1	c	587	GLU
1	c	589	THR
1	c	591	ARG
1	c	595	ASP
1	c	597	ILE
1	c	599	SER
1	c	601	ARG
1	c	603	ARG
1	c	604	ILE
1	c	610	VAL
1	c	613	GLN
1	c	614	LEU
1	c	615	ARG
1	c	617	MET
1	c	618	ARG

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Mol	Chain	Res	Type
1	c	624	GLN
1	c	625	GLN
1	c	626	LEU
1	c	629	LYS
1	c	641	GLU
1	c	642	MET
1	c	643	ARG
1	c	644	HIS
1	c	647	LYS
1	c	654	LEU
1	c	657	GLN
1	c	659	LEU
1	c	663	LEU
1	c	665	THR
1	c	667	LYS
1	c	670	ASN
1	c	673	LEU
1	c	674	ARG
1	c	675	LYS
1	c	677	MET
1	c	679	ARG
1	c	680	LEU
1	c	681	ILE
1	c	682	LYS
1	f	512	LYS
1	f	518	ARG
1	f	520	TRP
1	f	522	ARG
1	f	527	LEU
1	f	533	ARG
1	f	534	GLN
1	f	537	LEU
1	f	552	ILE
1	f	562	ILE
1	f	563	ASP
1	f	571	GLU
1	f	572	ARG
1	f	574	LYS
1	f	575	LEU
1	f	576	SER
1	f	578	ARG
1	f	579	LEU

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Mol	Chain	Res	Type
1	f	581	LYS
1	f	584	GLU
1	f	587	GLU
1	f	588	THR
1	f	590	GLU
1	f	591	ARG
1	f	592	ARG
1	f	595	ASP
1	f	596	GLU
1	f	597	ILE
1	f	599	SER
1	f	601	ARG
1	f	602	ASN
1	f	604	ILE
1	f	605	LYS
1	f	606	HIS
1	f	607	LEU
1	f	613	GLN
1	f	614	LEU
1	f	617	MET
1	f	627	GLU
1	f	630	ARG
1	f	631	LEU
1	f	634	GLU
1	f	638	LEU
1	f	639	LEU
1	f	641	GLU
1	f	642	MET
1	f	645	GLN
1	f	647	LYS
1	f	652	MET
1	f	653	LYS
1	f	656	GLN
1	f	664	ILE
1	f	673	LEU
1	f	674	ARG
1	f	675	LYS
1	f	677	MET
1	f	679	ARG
1	f	680	LEU
1	f	682	LYS
1	h	758	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1216) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	402	GLN
1	A	405	GLN
1	A	456	GLN
1	A	482	GLN
1	A	487	HIS
1	B	416	GLN
1	B	447	HIS
1	B	482	GLN
1	B	489	GLN
1	D	583	GLN
1	D	661	ASN
1	E	338	HIS
1	E	437	GLN
1	E	447	HIS
1	E	489	GLN
1	E	494	ASN
1	F	487	HIS
1	F	557	ASN
1	F	593	GLN
1	F	661	ASN
1	F	678	ASN
1	G	416	GLN
1	G	443	ASN
1	G	447	HIS
1	I	348	HIS
1	I	494	ASN
1	I	583	GLN
1	I	602	ASN
1	I	613	GLN
1	I	624	GLN
1	I	625	GLN
1	I	635	ASN
1	I	650	HIS
1	I	661	ASN
1	I	685	ASN
1	J	460	GLN
1	J	468	GLN
1	J	478	ASN
1	J	490	GLN
1	J	534	GLN
1	J	541	ASN

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Mol	Chain	Res	Type
1	J	554	HIS
1	J	577	GLN
1	J	583	GLN
1	J	613	GLN
1	J	619	GLN
1	J	624	GLN
1	J	625	GLN
1	J	646	ASN
1	K	377	HIS
1	K	405	GLN
1	K	443	ASN
1	L	338	HIS
1	L	414	GLN
1	M	486	GLN
1	M	487	HIS
1	M	613	GLN
1	M	644	HIS
1	M	646	ASN
1	N	484	GLN
1	N	487	HIS
1	N	573	GLN
1	N	577	GLN
1	N	583	GLN
1	N	602	ASN
1	N	645	GLN
1	N	646	ASN
1	N	660	GLN
1	N	661	ASN
1	O	645	GLN
1	O	656	GLN
1	O	660	GLN
1	O	670	ASN
1	P	656	GLN
1	Q	380	HIS
1	Q	382	GLN
1	Q	468	GLN
1	Q	487	HIS
1	Q	489	GLN
1	Q	546	ASN
1	Q	573	GLN
1	Q	624	GLN
1	Q	625	GLN

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Mol	Chain	Res	Type
1	Q	646	ASN
1	Q	668	GLN
1	R	482	GLN
1	R	484	GLN
1	R	545	GLN
1	R	550	ASN
1	R	624	GLN
1	R	625	GLN
1	R	656	GLN
1	S	338	HIS
1	S	414	GLN
1	T	656	GLN
1	U	494	ASN
1	U	624	GLN
1	U	660	GLN
1	U	678	ASN
1	V	468	GLN
1	V	482	GLN
1	V	484	GLN
1	V	545	GLN
1	V	583	GLN
1	V	624	GLN
1	V	661	ASN
1	V	670	ASN
1	W	348	HIS
1	W	368	GLN
1	W	443	ASN
1	W	482	GLN
1	X	624	GLN
1	X	625	GLN
1	X	670	ASN
1	X	678	ASN
1	Y	447	HIS
1	Y	534	GLN
1	Y	546	ASN
1	Y	613	GLN
1	Y	656	GLN
1	Z	482	GLN
1	Z	486	GLN
1	Z	487	HIS
1	1	950	GLN
2	10	264	GLN

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Mol	Chain	Res	Type
2	10	279	ASN
2	11	278	HIS
2	12	267	HIS
2	13	200	GLN
2	13	264	GLN
2	13	279	ASN
2	14	162	GLN
2	14	186	HIS
2	16	187	HIS
3	1A	176	GLN
3	1A	192	HIS
3	1A	226	ASN
3	1A	258	ASN
3	1A	285	GLN
3	1A	358	GLN
4	1B	14	ASN
4	1B	94	GLN
4	1B	191	GLN
4	1B	424	GLN
3	1C	8	HIS
3	1C	11	GLN
3	1C	85	HIS
3	1C	91	GLN
3	1C	139	ASN
3	1C	216	ASN
3	1C	233	GLN
3	1C	258	ASN
4	1D	11	GLN
4	1D	43	GLN
4	1D	89	ASN
4	1D	99	ASN
4	1D	131	GLN
4	1D	226	ASN
4	1D	227	HIS
4	1D	245	GLN
4	1D	256	ASN
4	1D	307	HIS
4	1D	332	ASN
4	1D	414	ASN
3	1E	168	ASN
3	1E	206	ASN
3	1E	285	GLN

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Mol	Chain	Res	Type
3	1E	342	GLN
4	1F	99	ASN
4	1F	100	ASN
4	1F	256	ASN
4	1F	332	ASN
4	1F	348	ASN
3	1G	85	HIS
3	1G	197	HIS
3	1G	233	GLN
3	1G	256	GLN
3	1G	258	ASN
3	1G	266	HIS
3	1G	283	HIS
3	1G	285	GLN
3	1G	356	ASN
3	1G	393	HIS
4	1H	83	GLN
4	1H	137	HIS
4	1H	184	ASN
4	1H	204	ASN
4	1H	264	HIS
4	1H	280	GLN
4	1H	298	ASN
4	1H	307	HIS
4	1H	329	GLN
4	1H	334	GLN
3	1I	15	GLN
3	1I	206	ASN
3	1I	309	HIS
3	1I	342	GLN
3	1I	380	ASN
4	1J	191	GLN
4	1J	347	ASN
3	1K	11	GLN
3	1K	28	HIS
3	1K	35	GLN
3	1K	88	HIS
3	1K	107	HIS
3	1K	192	HIS
3	1K	216	ASN
3	1K	233	GLN
4	1L	184	ASN

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Mol	Chain	Res	Type
4	1L	256	ASN
4	1L	298	ASN
3	1M	50	ASN
3	1M	107	HIS
3	1M	133	GLN
3	1M	192	HIS
3	1M	249	ASN
3	1M	256	GLN
3	1M	380	ASN
3	1M	393	HIS
4	1N	48	ASN
4	1N	134	GLN
4	1N	292	GLN
4	1N	298	ASN
5	20	193	ASN
5	22	162	GLN
5	23	193	ASN
5	23	233	HIS
5	24	19	ASN
5	24	207	HIS
5	24	236	GLN
5	25	117	GLN
5	25	162	GLN
5	25	203	GLN
5	25	230	GLN
5	26	151	HIS
5	27	178	GLN
5	27	229	GLN
5	28	86	HIS
5	29	23	GLN
5	29	86	HIS
5	29	100	ASN
5	29	112	GLN
5	29	151	HIS
5	29	153	ASN
3	2A	139	ASN
3	2A	197	HIS
3	2A	206	ASN
3	2A	258	ASN
3	2A	293	ASN
3	2A	329	ASN
4	2B	137	HIS

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Mol	Chain	Res	Type
4	2B	292	GLN
4	2B	334	GLN
4	2B	414	ASN
3	2C	15	GLN
3	2C	101	ASN
3	2C	102	ASN
3	2C	107	HIS
3	2C	133	GLN
3	2C	226	ASN
4	2D	11	GLN
4	2D	43	GLN
4	2D	83	GLN
4	2D	131	GLN
4	2D	195	ASN
4	2D	200	GLN
4	2D	347	ASN
4	2D	426	GLN
3	2E	91	GLN
3	2E	133	GLN
3	2E	168	ASN
3	2E	176	GLN
3	2E	206	ASN
3	2E	256	GLN
3	2E	283	HIS
4	2F	14	ASN
4	2F	83	GLN
4	2F	100	ASN
4	2F	191	GLN
4	2F	195	ASN
4	2F	245	GLN
4	2F	256	ASN
4	2F	329	GLN
3	2G	18	ASN
3	2G	61	HIS
3	2G	85	HIS
3	2G	88	HIS
3	2G	101	ASN
3	2G	107	HIS
3	2G	233	GLN
3	2G	258	ASN
3	2G	329	ASN
3	2G	342	GLN

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Mol	Chain	Res	Type
3	2G	356	ASN
4	2H	52	ASN
4	2H	89	ASN
4	2H	94	GLN
4	2H	100	ASN
4	2H	247	ASN
4	2H	291	GLN
4	2H	329	GLN
4	2H	334	GLN
4	2H	348	ASN
4	2H	375	GLN
4	2H	423	GLN
4	2H	426	GLN
3	2I	28	HIS
3	2I	139	ASN
3	2I	168	ASN
3	2I	197	HIS
3	2I	228	ASN
4	2J	99	ASN
4	2J	204	ASN
4	2J	307	HIS
4	2J	332	ASN
4	2J	334	GLN
3	2K	15	GLN
3	2K	35	GLN
3	2K	101	ASN
3	2K	107	HIS
3	2K	133	GLN
3	2K	192	HIS
3	2K	258	ASN
3	2K	285	GLN
3	2K	329	ASN
3	2K	342	GLN
4	2L	11	GLN
4	2L	14	ASN
4	2L	105	HIS
4	2L	134	GLN
4	2L	264	HIS
4	2L	280	GLN
4	2L	334	GLN
4	2L	414	ASN
3	2M	85	HIS

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Mol	Chain	Res	Type
3	2M	101	ASN
3	2M	168	ASN
3	2M	197	HIS
3	2M	216	ASN
2	3	264	GLN
2	3	279	ASN
5	30	103	HIS
5	30	135	ASN
5	31	100	ASN
5	32	86	HIS
5	32	106	ASN
5	33	40	HIS
5	33	142	HIS
5	35	55	GLN
5	35	100	ASN
5	36	207	HIS
5	36	223	HIS
5	37	40	HIS
5	37	86	HIS
5	37	103	HIS
5	37	135	ASN
5	39	229	GLN
3	3A	139	ASN
3	3A	192	HIS
3	3A	358	GLN
4	3B	99	ASN
4	3B	131	GLN
4	3B	191	GLN
4	3B	226	ASN
4	3B	245	GLN
4	3B	280	GLN
4	3B	334	GLN
3	3C	176	GLN
3	3C	226	ASN
3	3C	233	GLN
3	3C	266	HIS
3	3C	283	HIS
3	3C	356	ASN
4	3D	11	GLN
4	3D	83	GLN
4	3D	100	ASN
4	3D	131	GLN

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Mol	Chain	Res	Type
4	3D	134	GLN
4	3D	195	ASN
4	3D	204	ASN
4	3D	245	GLN
4	3D	329	GLN
4	3D	334	GLN
4	3D	348	ASN
4	3D	414	ASN
3	3E	102	ASN
3	3E	216	ASN
3	3E	329	ASN
3	3E	380	ASN
4	3F	11	GLN
4	3F	43	GLN
4	3F	280	GLN
4	3F	347	ASN
4	3F	348	ASN
4	3F	375	GLN
4	3F	423	GLN
4	3F	426	GLN
3	3G	88	HIS
3	3G	101	ASN
3	3G	258	ASN
3	3G	342	GLN
3	3G	358	GLN
4	3H	52	ASN
4	3H	131	GLN
4	3H	227	HIS
4	3H	332	ASN
4	3H	334	GLN
4	3H	375	GLN
4	3H	426	GLN
3	3I	102	ASN
3	3I	168	ASN
3	3I	176	GLN
3	3I	197	HIS
3	3I	226	ASN
3	3I	233	GLN
3	3I	258	ASN
3	3I	285	GLN
4	3J	14	ASN
4	3J	43	GLN

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Mol	Chain	Res	Type
4	3J	131	GLN
3	3K	61	HIS
3	3K	88	HIS
3	3K	197	HIS
3	3K	226	ASN
3	3K	233	GLN
3	3K	266	HIS
3	3K	293	ASN
3	3K	393	HIS
4	3L	6	HIS
4	3L	11	GLN
4	3L	52	ASN
4	3L	94	GLN
4	3L	99	ASN
4	3L	105	HIS
4	3L	190	HIS
4	3L	280	GLN
4	3L	329	GLN
4	3L	384	GLN
4	3L	414	ASN
3	3M	8	HIS
3	3M	35	GLN
3	3M	50	ASN
3	3M	88	HIS
3	3M	102	ASN
3	3M	233	GLN
3	3M	258	ASN
3	3M	342	GLN
2	4	162	GLN
2	4	187	HIS
5	40	40	HIS
5	40	85	GLN
5	40	117	GLN
5	40	135	ASN
5	40	178	GLN
5	40	223	HIS
5	42	162	GLN
5	43	19	ASN
5	43	103	HIS
5	44	103	HIS
5	45	100	ASN
5	45	223	HIS

Continued on next page...

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Mol	Chain	Res	Type
5	45	229	GLN
5	46	142	HIS
5	47	207	HIS
5	47	229	GLN
5	48	207	HIS
5	49	151	HIS
5	49	223	HIS
3	4A	342	GLN
4	4B	89	ASN
4	4B	94	GLN
4	4B	131	GLN
4	4B	280	GLN
4	4B	334	GLN
4	4B	375	GLN
4	4B	416	ASN
3	4C	11	GLN
3	4C	28	HIS
3	4C	31	GLN
3	4C	35	GLN
3	4C	50	ASN
3	4C	91	GLN
3	4C	128	ASN
3	4C	168	ASN
3	4C	249	ASN
3	4C	329	ASN
3	4C	380	ASN
4	4D	14	ASN
4	4D	15	GLN
4	4D	89	ASN
4	4D	195	ASN
4	4D	329	GLN
3	4E	216	ASN
3	4E	309	HIS
3	4E	406	HIS
4	4F	8	GLN
4	4F	11	GLN
4	4F	94	GLN
4	4F	131	GLN
4	4F	247	ASN
4	4F	256	ASN
4	4F	280	GLN
4	4F	292	GLN

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Mol	Chain	Res	Type
4	4F	329	GLN
4	4F	335	ASN
4	4F	348	ASN
3	4G	8	HIS
3	4G	61	HIS
3	4G	128	ASN
3	4G	216	ASN
3	4G	249	ASN
3	4G	258	ASN
3	4G	406	HIS
4	4H	15	GLN
4	4H	52	ASN
4	4H	131	GLN
4	4H	137	HIS
4	4H	264	HIS
4	4H	347	ASN
4	4H	348	ASN
3	4I	35	GLN
3	4I	393	HIS
4	4J	8	GLN
4	4J	11	GLN
4	4J	43	GLN
4	4J	94	GLN
4	4J	100	ASN
3	4K	15	GLN
3	4K	88	HIS
3	4K	101	ASN
3	4K	107	HIS
3	4K	216	ASN
3	4K	226	ASN
3	4K	258	ASN
3	4K	293	ASN
3	4K	358	GLN
3	4K	380	ASN
4	4L	6	HIS
4	4L	11	GLN
4	4L	99	ASN
4	4L	195	ASN
4	4L	200	GLN
4	4L	279	GLN
4	4L	280	GLN
4	4L	292	GLN

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Mol	Chain	Res	Type
4	4L	329	GLN
4	4L	375	GLN
4	4L	384	GLN
4	4L	426	GLN
3	4M	35	GLN
3	4M	168	ASN
3	4M	258	ASN
5	50	40	HIS
5	50	153	ASN
5	52	112	GLN
5	52	135	ASN
5	52	193	ASN
5	53	40	HIS
5	53	203	GLN
5	55	19	ASN
5	55	223	HIS
5	56	142	HIS
5	56	193	ASN
5	56	223	HIS
5	56	230	GLN
5	57	23	GLN
5	57	55	GLN
5	57	85	GLN
5	57	117	GLN
5	58	95	ASN
5	58	203	GLN
5	59	95	ASN
3	5A	88	HIS
3	5A	91	GLN
3	5A	133	GLN
3	5A	309	HIS
4	5B	15	GLN
4	5B	99	ASN
4	5B	256	ASN
4	5B	329	GLN
4	5B	370	ASN
4	5B	414	ASN
3	5C	11	GLN
3	5C	15	GLN
3	5C	91	GLN
3	5C	139	ASN
3	5C	226	ASN

Continued on next page...

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Mol	Chain	Res	Type
3	5C	249	ASN
3	5C	256	GLN
3	5C	266	HIS
3	5C	329	ASN
3	5C	356	ASN
4	5D	14	ASN
4	5D	43	GLN
4	5D	105	HIS
4	5D	200	GLN
4	5D	291	GLN
4	5D	292	GLN
4	5D	426	GLN
3	5E	91	GLN
3	5E	102	ASN
3	5E	107	HIS
3	5E	356	ASN
4	5F	100	ASN
4	5F	134	GLN
4	5F	332	ASN
4	5F	347	ASN
3	5G	31	GLN
3	5G	35	GLN
3	5G	101	ASN
3	5G	197	HIS
3	5G	216	ASN
3	5G	258	ASN
3	5G	309	HIS
4	5H	83	GLN
4	5H	99	ASN
4	5H	100	ASN
4	5H	134	GLN
4	5H	190	HIS
4	5H	195	ASN
4	5H	245	GLN
4	5H	307	HIS
4	5H	329	GLN
4	5H	337	ASN
4	5H	424	GLN
3	5I	28	HIS
3	5I	102	ASN
3	5I	380	ASN
3	5I	393	HIS

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Mol	Chain	Res	Type
4	5J	8	GLN
4	5J	43	GLN
4	5J	105	HIS
4	5J	134	GLN
4	5J	137	HIS
4	5J	190	HIS
4	5J	291	GLN
4	5J	298	ASN
4	5J	426	GLN
3	5K	88	HIS
3	5K	91	GLN
3	5K	216	ASN
3	5K	226	ASN
3	5K	233	GLN
3	5K	283	HIS
3	5K	356	ASN
3	5K	393	HIS
4	5L	8	GLN
4	5L	14	ASN
4	5L	89	ASN
4	5L	131	GLN
4	5L	195	ASN
4	5L	292	GLN
4	5L	329	GLN
3	5M	107	HIS
3	5M	206	ASN
3	5M	256	GLN
3	5M	380	ASN
4	5N	94	GLN
4	5N	190	HIS
4	5N	256	ASN
4	5N	335	ASN
4	5N	348	ASN
4	5N	414	ASN
4	5N	424	GLN
2	6	174	GLN
2	6	187	HIS
5	60	106	ASN
5	60	178	GLN
5	60	231	GLN
5	61	40	HIS
5	61	103	HIS

Continued on next page...

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Mol	Chain	Res	Type
5	61	106	ASN
5	62	207	HIS
6	63	340	HIS
6	63	626	GLN
6	64	450	HIS
6	64	628	ASN
6	64	886	HIS
6	65	179	GLN
6	65	412	ASN
6	65	915	ASN
6	66	340	HIS
6	66	366	GLN
6	66	543	GLN
6	66	553	GLN
6	66	573	HIS
6	67	317	GLN
6	67	402	GLN
6	67	411	HIS
6	67	481	GLN
6	67	886	HIS
6	67	909	GLN
6	67	940	GLN
6	68	179	GLN
6	68	320	GLN
6	68	329	GLN
6	68	366	GLN
6	68	450	HIS
6	68	782	ASN
6	68	909	GLN
6	69	275	GLN
6	69	505	GLN
6	69	568	GLN
6	69	816	ASN
3	6A	15	GLN
3	6A	258	ASN
4	6B	43	GLN
4	6B	134	GLN
4	6B	245	GLN
4	6B	375	GLN
3	6C	18	ASN
3	6C	31	GLN
3	6C	35	GLN

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Mol	Chain	Res	Type
3	6C	61	HIS
3	6C	107	HIS
3	6C	133	GLN
3	6C	206	ASN
3	6C	216	ASN
3	6C	233	GLN
3	6C	406	HIS
4	6D	15	GLN
4	6D	89	ASN
4	6D	99	ASN
4	6D	298	ASN
4	6D	307	HIS
4	6D	334	GLN
4	6D	335	ASN
4	6D	414	ASN
4	6D	423	GLN
4	6D	426	GLN
3	6E	35	GLN
3	6E	102	ASN
3	6E	133	GLN
3	6E	176	GLN
3	6E	258	ASN
4	6F	8	GLN
4	6F	99	ASN
4	6F	227	HIS
4	6F	414	ASN
3	6G	28	HIS
3	6G	61	HIS
3	6G	88	HIS
3	6G	101	ASN
3	6G	192	HIS
3	6G	197	HIS
3	6G	283	HIS
3	6G	329	ASN
3	6G	342	GLN
4	6H	131	GLN
4	6H	264	HIS
4	6H	292	GLN
4	6H	329	GLN
4	6H	337	ASN
4	6H	348	ASN
3	6I	88	HIS

Continued on next page...

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Mol	Chain	Res	Type
3	6I	283	HIS
3	6I	285	GLN
4	6J	8	GLN
4	6J	134	GLN
4	6J	191	GLN
4	6J	414	ASN
3	6K	15	GLN
3	6K	133	GLN
3	6K	216	ASN
3	6K	249	ASN
3	6K	258	ASN
4	6L	94	GLN
4	6L	99	ASN
4	6L	100	ASN
4	6L	105	HIS
4	6L	190	HIS
4	6L	245	GLN
4	6L	256	ASN
4	6L	279	GLN
4	6L	291	GLN
4	6L	337	ASN
3	6M	101	ASN
3	6M	176	GLN
4	6N	89	ASN
4	6N	204	ASN
4	6N	247	ASN
4	6N	291	GLN
4	6N	298	ASN
4	6N	337	ASN
4	6N	348	ASN
4	6N	375	GLN
2	7	264	GLN
7	71	370	HIS
7	72	300	GLN
7	73	248	HIS
7	73	370	HIS
7	75	295	GLN
7	75	317	GLN
7	76	275	HIS
7	77	366	ASN
3	7A	107	HIS
4	7B	43	GLN

Continued on next page...

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Mol	Chain	Res	Type
4	7B	191	GLN
4	7B	256	ASN
4	7B	292	GLN
4	7B	329	GLN
4	7B	332	ASN
3	7C	15	GLN
3	7C	61	HIS
3	7C	101	ASN
3	7C	128	ASN
3	7C	133	GLN
3	7C	233	GLN
3	7C	309	HIS
4	7D	99	ASN
4	7D	191	GLN
4	7D	279	GLN
4	7D	329	GLN
4	7D	334	GLN
4	7D	384	GLN
4	7D	426	GLN
3	7E	18	ASN
3	7E	28	HIS
3	7E	216	ASN
3	7E	233	GLN
3	7E	329	ASN
3	7E	356	ASN
4	7F	99	ASN
4	7F	195	ASN
4	7F	329	GLN
4	7F	370	ASN
3	7G	88	HIS
3	7G	176	GLN
3	7G	186	ASN
3	7G	309	HIS
3	7G	380	ASN
4	7H	28	HIS
4	7H	94	GLN
4	7H	134	GLN
4	7H	200	GLN
4	7H	291	GLN
4	7H	416	ASN
3	7I	28	HIS
3	7I	61	HIS

Continued on next page...

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Mol	Chain	Res	Type
3	7I	88	HIS
3	7I	358	GLN
4	7J	14	ASN
4	7J	83	GLN
4	7J	131	GLN
4	7J	256	ASN
4	7J	279	GLN
4	7J	307	HIS
4	7J	334	GLN
3	7K	28	HIS
3	7K	31	GLN
3	7K	101	ASN
3	7K	107	HIS
3	7K	329	ASN
3	7K	342	GLN
4	7L	329	GLN
4	7L	332	ASN
4	7L	334	GLN
4	7L	348	ASN
3	7M	176	GLN
3	7M	393	HIS
7	83	248	HIS
7	83	317	GLN
7	84	248	HIS
7	84	274	HIS
7	85	295	GLN
7	87	275	HIS
7	87	370	HIS
7	89	276	GLN
3	8A	293	ASN
3	8A	380	ASN
4	8B	8	GLN
4	8B	280	GLN
4	8B	329	GLN
4	8B	335	ASN
4	8B	375	GLN
3	8C	133	GLN
3	8C	168	ASN
3	8C	228	ASN
3	8C	249	ASN
3	8C	256	GLN
3	8C	309	HIS

Continued on next page...

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Mol	Chain	Res	Type
4	8D	15	GLN
4	8D	100	ASN
4	8D	279	GLN
4	8D	280	GLN
4	8D	292	GLN
4	8D	329	GLN
4	8D	384	GLN
4	8D	416	ASN
3	8E	61	HIS
3	8E	91	GLN
3	8E	101	ASN
3	8E	128	ASN
3	8E	139	ASN
3	8E	342	GLN
3	8E	380	ASN
4	8F	190	HIS
4	8F	226	ASN
4	8F	348	ASN
4	8F	370	ASN
3	8G	18	ASN
3	8G	88	HIS
3	8G	101	ASN
3	8G	107	HIS
3	8G	128	ASN
3	8G	258	ASN
3	8G	283	HIS
3	8G	356	ASN
4	8H	375	GLN
4	8H	424	GLN
3	8I	18	ASN
3	8I	91	GLN
3	8I	380	ASN
4	8J	11	GLN
4	8J	99	ASN
4	8J	100	ASN
4	8J	134	GLN
4	8J	204	ASN
4	8J	226	ASN
4	8J	256	ASN
4	8J	334	GLN
4	8J	384	GLN
4	8J	424	GLN

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Mol	Chain	Res	Type
3	8K	28	HIS
3	8K	35	GLN
3	8K	50	ASN
3	8K	85	HIS
3	8K	168	ASN
3	8K	192	HIS
3	8K	283	HIS
3	8K	285	GLN
4	8L	6	HIS
4	8L	8	GLN
4	8L	15	GLN
4	8L	48	ASN
4	8L	52	ASN
4	8L	131	GLN
4	8L	200	GLN
4	8L	256	ASN
4	8L	264	HIS
4	8L	414	ASN
3	8M	249	ASN
3	8M	285	GLN
3	8M	393	HIS
2	9	258	GLN
7	90	275	HIS
7	90	300	GLN
7	91	264	GLN
7	91	275	HIS
7	91	317	GLN
7	92	266	ASN
7	92	276	GLN
7	93	248	HIS
7	95	248	HIS
7	96	370	HIS
7	97	340	ASN
3	9A	28	HIS
3	9A	88	HIS
4	9B	52	ASN
4	9B	292	GLN
4	9B	298	ASN
3	9C	50	ASN
3	9C	128	ASN
3	9C	168	ASN
3	9C	206	ASN

Continued on next page...

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Mol	Chain	Res	Type
3	9C	226	ASN
3	9C	249	ASN
3	9C	258	ASN
3	9C	309	HIS
4	9D	8	GLN
4	9D	43	GLN
4	9D	48	ASN
4	9D	89	ASN
4	9D	100	ASN
4	9D	200	GLN
4	9D	292	GLN
4	9D	329	GLN
3	9E	133	GLN
3	9E	139	ASN
3	9E	256	GLN
3	9E	258	ASN
3	9E	309	HIS
4	9F	8	GLN
4	9F	43	GLN
4	9F	134	GLN
4	9F	245	GLN
4	9F	247	ASN
4	9F	329	GLN
4	9F	414	ASN
3	9G	11	GLN
3	9G	88	HIS
3	9G	101	ASN
3	9G	139	ASN
3	9G	283	HIS
3	9G	285	GLN
3	9G	358	GLN
4	9H	94	GLN
4	9H	99	ASN
4	9H	100	ASN
4	9H	105	HIS
4	9H	134	GLN
4	9H	247	ASN
4	9H	280	GLN
4	9H	298	ASN
3	9I	233	GLN
3	9I	258	ASN
4	9J	94	GLN

Continued on next page...

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Mol	Chain	Res	Type
4	9J	191	GLN
4	9J	195	ASN
4	9J	204	ASN
4	9J	329	GLN
4	9J	334	GLN
4	9J	347	ASN
3	9K	8	HIS
3	9K	11	GLN
3	9K	216	ASN
3	9K	258	ASN
3	9K	266	HIS
3	9K	285	GLN
3	9K	293	ASN
3	9K	329	ASN
4	9L	6	HIS
4	9L	43	GLN
4	9L	332	ASN
4	9L	335	ASN
4	9L	424	GLN
4	9L	426	GLN
3	9M	15	GLN
3	9M	101	ASN
3	9M	107	HIS
3	9M	228	ASN
3	9M	256	GLN
3	9M	283	HIS
3	9M	329	ASN
8	A1	35	ASN
8	A1	122	GLN
8	A1	213	GLN
8	A1	278	GLN
8	A2	112	HIS
8	A2	167	GLN
8	A2	278	GLN
8	A3	122	GLN
8	A4	112	HIS
8	A5	63	ASN
8	A5	213	GLN
8	A5	279	HIS
8	A5	333	GLN
8	A6	63	ASN
8	A6	213	GLN

Continued on next page...

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Mol	Chain	Res	Type
8	A6	264	GLN
8	A7	167	GLN
8	A8	30	GLN
8	A8	256	ASN
8	A8	264	GLN
8	A8	363	GLN
9	B1	88	HIS
9	B1	475	ASN
9	B1	533	GLN
9	B2	169	GLN
9	B3	458	HIS
9	B3	483	GLN
9	B3	500	HIS
9	B3	506	GLN
9	B4	125	HIS
9	B4	169	GLN
9	B4	509	ASN
9	B4	540	HIS
9	B5	532	GLN
9	B6	169	GLN
9	B6	506	GLN
9	B7	462	HIS
9	B7	483	GLN
11	C4	150	GLN
10	C8	403	GLN
10	D0	384	HIS
10	D0	403	GLN
10	D1	54	HIS
10	D3	32	ASN
10	D3	384	HIS
10	D3	403	GLN
10	D4	384	HIS
10	D7	403	GLN
10	D8	54	HIS
10	D9	91	GLN
10	E0	273	GLN
10	E1	54	HIS
10	E1	145	ASN
10	E1	295	GLN
10	E1	403	GLN
10	E2	32	ASN
10	E2	109	ASN

Continued on next page...

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Mol	Chain	Res	Type
10	E2	295	GLN
10	E2	382	HIS
10	E3	295	GLN
10	E4	145	ASN
10	E4	295	GLN
10	E4	382	HIS
10	E5	295	GLN
10	E6	54	HIS
10	E6	151	GLN
10	E6	152	HIS
10	E6	295	GLN
10	E6	365	ASN
10	E6	403	GLN
10	E7	145	ASN
10	E7	273	GLN
10	E8	152	HIS
10	E8	403	GLN
10	E9	109	ASN
10	F1	145	ASN
10	F3	382	HIS
12	G6	258	ASN
12	H3	56	HIS
12	H3	58	ASN
12	H3	95	ASN
12	H6	56	HIS
12	H6	58	ASN
12	H6	85	GLN
12	H9	85	GLN
12	I1	73	ASN
12	I4	95	ASN
12	I5	73	ASN
12	I5	75	ASN
12	I5	85	GLN
12	I7	95	ASN
13	J1	331	ASN
13	J1	390	GLN
13	J1	488	ASN
13	J2	423	GLN
13	J2	681	HIS
13	J3	463	HIS
13	J5	506	HIS
13	J5	681	HIS

Continued on next page...

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Mol	Chain	Res	Type
13	J6	423	GLN
13	J7	335	GLN
13	J7	390	GLN
13	J7	506	HIS
14	K0	202	GLN
14	K0	246	GLN
14	K1	163	HIS
14	K3	142	GLN
14	K4	243	GLN
14	K5	95	ASN
14	K5	147	GLN
14	K5	163	HIS
14	K6	202	GLN
14	K6	252	GLN
14	K7	147	GLN
14	K9	95	ASN
14	K9	142	GLN
14	K9	202	GLN
14	K9	243	GLN
14	L0	71	ASN
14	L1	147	GLN
14	L1	163	HIS
14	L2	142	GLN
14	L2	159	ASN
14	L2	243	GLN
14	L2	252	GLN
14	L3	163	HIS
14	L4	243	GLN
14	L5	142	GLN
14	L6	95	ASN
14	L6	184	GLN
14	L6	243	GLN
14	L8	163	HIS
14	L9	95	ASN
14	L9	163	HIS
14	M3	202	GLN
14	M3	246	GLN
14	M4	163	HIS
14	M6	202	GLN
1	a	624	GLN
1	a	645	GLN
1	a	660	GLN

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Mol	Chain	Res	Type
1	c	368	GLN
1	c	414	GLN
1	c	420	HIS
1	c	573	GLN
1	c	577	GLN
1	c	583	GLN
1	c	613	GLN
1	c	619	GLN
1	c	685	ASN
1	d	338	HIS
1	d	368	GLN
1	d	420	HIS
1	d	482	GLN
1	e	348	HIS
1	e	375	GLN
1	f	573	GLN
1	f	619	GLN
1	f	624	GLN
1	f	625	GLN
1	f	635	ASN
1	f	650	HIS
1	f	656	GLN
1	f	670	ASN
1	g	821	ASN
1	h	758	ASN
1	h	794	GLN
1	i	824	GLN
1	j	821	ASN
1	k	758	ASN
1	l	745	HIS
1	o	893	GLN
1	o	944	GLN
1	p	927	HIS
1	q	927	HIS
1	q	944	GLN
1	q	950	GLN
1	q	954	ASN
1	v	893	GLN
1	v	944	GLN
1	x	944	GLN
1	y	948	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 174 ligands modelled in this entry, 54 are monoatomic - leaving 120 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
15	GTP	4I	501	16	29,34,34	1.27	1 (3%)	35,54,54	1.31	5 (14%)
15	GTP	3E	501	16	29,34,34	1.26	2 (6%)	35,54,54	1.29	4 (11%)
17	GDP	4H	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.46	6 (20%)
17	GDP	4B	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.24	2 (6%)
17	GDP	9D	501	-	25,30,30	1.03	2 (8%)	30,47,47	1.19	3 (10%)
17	GDP	7B	502	-	25,30,30	0.99	1 (4%)	30,47,47	1.27	4 (13%)
15	GTP	1I	501	16	29,34,34	1.24	2 (6%)	35,54,54	1.28	4 (11%)
15	GTP	6I	501	16	29,34,34	1.24	2 (6%)	35,54,54	1.26	4 (11%)
17	GDP	5J	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.13	2 (6%)
15	GTP	9G	501	-	29,34,34	1.31	3 (10%)	35,54,54	1.27	4 (11%)
17	GDP	6N	502	-	25,30,30	0.99	1 (4%)	30,47,47	1.21	3 (10%)
17	GDP	6H	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.19	3 (10%)
17	GDP	3J	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.13	2 (6%)
17	GDP	7J	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.19	2 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
17	GDP	8H	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.15	1 (3%)
15	GTP	1M	501	-	29,34,34	1.22	2 (6%)	35,54,54	1.29	4 (11%)
15	GTP	7E	501	16	29,34,34	1.26	2 (6%)	35,54,54	1.27	4 (11%)
17	GDP	4D	501	-	25,30,30	0.96	1 (4%)	30,47,47	1.17	2 (6%)
15	GTP	5G	501	16	29,34,34	1.18	2 (6%)	35,54,54	1.30	4 (11%)
17	GDP	9F	501	-	25,30,30	1.01	1 (4%)	30,47,47	1.19	4 (13%)
17	GDP	6B	501	-	25,30,30	1.05	1 (4%)	30,47,47	1.24	5 (16%)
17	GDP	2D	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.32	3 (10%)
17	GDP	5N	501	-	25,30,30	1.02	1 (4%)	30,47,47	1.43	4 (13%)
15	GTP	8A	501	16	29,34,34	1.22	2 (6%)	35,54,54	1.26	4 (11%)
17	GDP	8L	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.20	4 (13%)
15	GTP	3K	501	16	29,34,34	1.20	2 (6%)	35,54,54	1.30	4 (11%)
15	GTP	5K	501	16	29,34,34	1.24	2 (6%)	35,54,54	1.26	4 (11%)
17	GDP	1H	501	-	25,30,30	0.96	1 (4%)	30,47,47	1.08	1 (3%)
15	GTP	8K	501	-	29,34,34	1.25	3 (10%)	35,54,54	1.33	5 (14%)
15	GTP	9M	501	-	29,34,34	1.22	2 (6%)	35,54,54	1.29	4 (11%)
15	GTP	2K	501	16	29,34,34	1.22	2 (6%)	35,54,54	1.28	4 (11%)
15	GTP	2E	501	16	29,34,34	1.28	4 (13%)	35,54,54	1.37	4 (11%)
17	GDP	6J	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.25	4 (13%)
15	GTP	9K	501	16	29,34,34	1.29	4 (13%)	35,54,54	1.41	7 (20%)
15	GTP	9C	501	-	29,34,34	1.22	2 (6%)	35,54,54	1.26	4 (11%)
17	GDP	8B	501	-	25,30,30	1.00	2 (8%)	30,47,47	1.32	6 (20%)
17	GDP	8D	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.15	2 (6%)
15	GTP	4A	501	16	29,34,34	1.28	2 (6%)	35,54,54	1.46	7 (20%)
15	GTP	3A	501	16	29,34,34	1.21	2 (6%)	35,54,54	1.30	3 (8%)
17	GDP	5B	501	-	25,30,30	1.02	1 (4%)	30,47,47	1.17	3 (10%)
17	GDP	4F	501	-	25,30,30	0.96	1 (4%)	30,47,47	1.16	2 (6%)
17	GDP	2F	501	-	25,30,30	1.01	2 (8%)	30,47,47	1.16	3 (10%)
15	GTP	4G	501	16	29,34,34	1.19	2 (6%)	35,54,54	1.27	3 (8%)
15	GTP	5E	501	16	29,34,34	1.22	2 (6%)	35,54,54	1.29	4 (11%)
17	GDP	7L	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.23	4 (13%)
15	GTP	6E	501	16	29,34,34	1.20	2 (6%)	35,54,54	1.27	3 (8%)
15	GTP	6G	501	16	29,34,34	1.21	2 (6%)	35,54,54	1.35	5 (14%)
15	GTP	3G	501	16	29,34,34	1.24	2 (6%)	35,54,54	1.25	4 (11%)
17	GDP	3B	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.16	3 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
15	GTP	9E	501	16	29,34,34	1.31	5 (17%)	35,54,54	1.26	3 (8%)
17	GDP	4L	501	-	25,30,30	0.95	1 (4%)	30,47,47	1.03	2 (6%)
17	GDP	9H	501	-	25,30,30	1.01	2 (8%)	30,47,47	1.25	4 (13%)
15	GTP	2A	501	16	29,34,34	1.30	4 (13%)	35,54,54	1.48	4 (11%)
17	GDP	9J	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.19	3 (10%)
17	GDP	1B	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.15	1 (3%)
15	GTP	5I	501	16	29,34,34	1.20	2 (6%)	35,54,54	1.32	3 (8%)
17	GDP	1F	501	-	25,30,30	1.01	2 (8%)	30,47,47	1.14	2 (6%)
15	GTP	7I	501	16	29,34,34	1.23	2 (6%)	35,54,54	1.33	5 (14%)
15	GTP	5M	501	-	29,34,34	1.22	1 (3%)	35,54,54	1.46	6 (17%)
15	GTP	9I	501	16	29,34,34	1.28	4 (13%)	35,54,54	1.35	4 (11%)
15	GTP	7M	501	-	29,34,34	1.25	2 (6%)	35,54,54	1.36	4 (11%)
17	GDP	4J	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.24	2 (6%)
15	GTP	7C	501	16	29,34,34	1.18	2 (6%)	35,54,54	1.34	4 (11%)
17	GDP	5D	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.22	3 (10%)
17	GDP	6L	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.11	1 (3%)
17	GDP	9L	501	-	25,30,30	1.03	2 (8%)	30,47,47	1.13	2 (6%)
15	GTP	5A	501	16	29,34,34	1.24	2 (6%)	35,54,54	1.32	4 (11%)
15	GTP	1A	501	16	29,34,34	1.41	5 (17%)	35,54,54	1.29	5 (14%)
17	GDP	6D	501	-	25,30,30	0.99	1 (4%)	30,47,47	1.17	2 (6%)
17	GDP	5F	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.24	3 (10%)
17	GDP	9B	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.21	3 (10%)
15	GTP	8C	501	-	29,34,34	1.17	1 (3%)	35,54,54	1.34	4 (11%)
17	GDP	2B	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.14	2 (6%)
17	GDP	7F	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.22	5 (16%)
17	GDP	5H	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.14	3 (10%)
17	GDP	7D	501	-	25,30,30	0.95	1 (4%)	30,47,47	1.19	4 (13%)
15	GTP	7G	501	16	29,34,34	1.27	2 (6%)	35,54,54	1.34	4 (11%)
17	GDP	8J	501	-	25,30,30	1.01	1 (4%)	30,47,47	1.21	3 (10%)
15	GTP	6A	501	16	29,34,34	1.18	2 (6%)	35,54,54	1.29	5 (14%)
15	GTP	7K	501	16	29,34,34	1.30	3 (10%)	35,54,54	1.37	5 (14%)
17	GDP	1D	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.18	2 (6%)
15	GTP	4K	501	16	29,34,34	1.20	2 (6%)	35,54,54	1.33	3 (8%)
17	GDP	3L	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.10	2 (6%)
17	GDP	1J	501	-	25,30,30	0.95	1 (4%)	30,47,47	1.17	3 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
17	GDP	3H	501	-	25,30,30	0.96	1 (4%)	30,47,47	1.16	3 (10%)
15	GTP	2G	501	16	29,34,34	1.24	2 (6%)	35,54,54	1.33	4 (11%)
15	GTP	9A	501	16	29,34,34	1.25	3 (10%)	35,54,54	1.27	4 (11%)
15	GTP	2M	501	-	29,34,34	1.22	2 (6%)	35,54,54	1.33	5 (14%)
17	GDP	2J	501	-	25,30,30	1.01	1 (4%)	30,47,47	1.20	3 (10%)
15	GTP	1E	501	16	29,34,34	1.18	2 (6%)	35,54,54	1.31	4 (11%)
17	GDP	1N	501	-	25,30,30	1.02	2 (8%)	30,47,47	1.23	5 (16%)
17	GDP	5L	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.06	1 (3%)
15	GTP	3I	501	16	29,34,34	1.23	2 (6%)	35,54,54	1.35	5 (14%)
15	GTP	6C	501	16	29,34,34	1.24	2 (6%)	35,54,54	1.26	4 (11%)
15	GTP	3C	501	16	29,34,34	1.21	2 (6%)	35,54,54	1.30	4 (11%)
15	GTP	6N	501	-	29,34,34	1.38	3 (10%)	35,54,54	1.42	6 (17%)
17	GDP	3F	501	-	25,30,30	1.01	1 (4%)	30,47,47	1.20	4 (13%)
17	GDP	8F	501	-	25,30,30	1.02	2 (8%)	30,47,47	1.26	5 (16%)
15	GTP	4C	501	16	29,34,34	1.18	2 (6%)	35,54,54	1.32	4 (11%)
15	GTP	2C	501	16	29,34,34	1.21	2 (6%)	35,54,54	1.34	4 (11%)
15	GTP	5C	501	16	29,34,34	1.20	2 (6%)	35,54,54	1.32	3 (8%)
17	GDP	7H	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.19	3 (10%)
15	GTP	1C	501	16	29,34,34	1.24	2 (6%)	35,54,54	1.40	5 (14%)
17	GDP	2L	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.08	1 (3%)
17	GDP	2H	501	-	25,30,30	1.00	1 (4%)	30,47,47	1.15	3 (10%)
15	GTP	3M	501	-	29,34,34	1.25	3 (10%)	35,54,54	1.31	4 (11%)
15	GTP	4M	501	-	29,34,34	1.23	2 (6%)	35,54,54	1.23	4 (11%)
17	GDP	1L	501	-	25,30,30	1.01	1 (4%)	30,47,47	1.14	2 (6%)
15	GTP	8M	501	-	29,34,34	1.27	3 (10%)	35,54,54	1.32	5 (14%)
17	GDP	3D	501	-	25,30,30	0.97	1 (4%)	30,47,47	1.18	1 (3%)
17	GDP	6F	501	-	25,30,30	0.98	1 (4%)	30,47,47	1.21	3 (10%)
15	GTP	1G	501	16	29,34,34	1.16	2 (6%)	35,54,54	1.37	6 (17%)
15	GTP	7A	501	16	29,34,34	1.24	3 (10%)	35,54,54	1.29	4 (11%)
15	GTP	8G	501	-	29,34,34	1.21	2 (6%)	35,54,54	1.30	5 (14%)
15	GTP	6K	501	16	29,34,34	1.17	2 (6%)	35,54,54	1.33	5 (14%)
15	GTP	8E	501	16	29,34,34	1.30	2 (6%)	35,54,54	1.27	4 (11%)
15	GTP	1K	501	16	29,34,34	1.23	2 (6%)	35,54,54	1.36	5 (14%)
15	GTP	2I	501	16	29,34,34	1.21	2 (6%)	35,54,54	1.32	4 (11%)
15	GTP	8I	501	16	29,34,34	1.18	2 (6%)	35,54,54	1.33	3 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
15	GTP	4E	501	16	29,34,34	1.26	2 (6%)	35,54,54	1.28	5 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	GTP	4I	501	16	-	8/18/38/38	0/3/3/3
15	GTP	3E	501	16	-	10/18/38/38	0/3/3/3
17	GDP	4H	501	-	-	4/12/32/32	0/3/3/3
17	GDP	4B	501	-	-	4/12/32/32	0/3/3/3
17	GDP	9D	501	-	-	1/12/32/32	0/3/3/3
17	GDP	7B	502	-	-	6/12/32/32	0/3/3/3
15	GTP	1I	501	16	-	8/18/38/38	0/3/3/3
15	GTP	6I	501	16	-	7/18/38/38	0/3/3/3
17	GDP	5J	501	-	-	4/12/32/32	0/3/3/3
15	GTP	9G	501	-	-	9/18/38/38	0/3/3/3
17	GDP	6N	502	-	-	5/12/32/32	0/3/3/3
17	GDP	6H	501	-	-	4/12/32/32	0/3/3/3
17	GDP	3J	501	-	-	5/12/32/32	0/3/3/3
17	GDP	7J	501	-	-	6/12/32/32	0/3/3/3
17	GDP	8H	501	-	-	4/12/32/32	0/3/3/3
15	GTP	1M	501	-	-	7/18/38/38	0/3/3/3
15	GTP	7E	501	16	-	4/18/38/38	0/3/3/3
17	GDP	4D	501	-	-	4/12/32/32	0/3/3/3
15	GTP	5G	501	16	-	5/18/38/38	0/3/3/3
17	GDP	9F	501	-	-	2/12/32/32	0/3/3/3
17	GDP	6B	501	-	-	5/12/32/32	0/3/3/3
17	GDP	2D	501	-	-	4/12/32/32	0/3/3/3
17	GDP	5N	501	-	-	3/12/32/32	0/3/3/3
15	GTP	8A	501	16	-	5/18/38/38	0/3/3/3
17	GDP	8L	501	-	-	8/12/32/32	0/3/3/3
15	GTP	3K	501	16	-	6/18/38/38	0/3/3/3
15	GTP	5K	501	16	-	5/18/38/38	0/3/3/3
17	GDP	1H	501	-	-	6/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	GTP	8K	501	-	-	6/18/38/38	0/3/3/3
15	GTP	9M	501	-	-	8/18/38/38	0/3/3/3
15	GTP	2K	501	16	-	7/18/38/38	0/3/3/3
15	GTP	2E	501	16	-	5/18/38/38	0/3/3/3
17	GDP	6J	501	-	-	4/12/32/32	0/3/3/3
15	GTP	9K	501	16	-	7/18/38/38	0/3/3/3
15	GTP	9C	501	-	-	7/18/38/38	0/3/3/3
17	GDP	8B	501	-	-	7/12/32/32	0/3/3/3
17	GDP	8D	501	-	-	3/12/32/32	0/3/3/3
15	GTP	4A	501	16	-	4/18/38/38	0/3/3/3
15	GTP	3A	501	16	-	7/18/38/38	0/3/3/3
17	GDP	5B	501	-	-	4/12/32/32	0/3/3/3
17	GDP	4F	501	-	-	4/12/32/32	0/3/3/3
17	GDP	2F	501	-	-	5/12/32/32	0/3/3/3
15	GTP	4G	501	16	-	7/18/38/38	0/3/3/3
15	GTP	5E	501	16	-	6/18/38/38	0/3/3/3
17	GDP	7L	501	-	-	3/12/32/32	0/3/3/3
15	GTP	6E	501	16	-	7/18/38/38	0/3/3/3
15	GTP	6G	501	16	-	9/18/38/38	0/3/3/3
15	GTP	3G	501	16	-	4/18/38/38	0/3/3/3
17	GDP	3B	501	-	-	3/12/32/32	0/3/3/3
15	GTP	9E	501	16	-	7/18/38/38	0/3/3/3
17	GDP	4L	501	-	-	4/12/32/32	0/3/3/3
17	GDP	9H	501	-	-	5/12/32/32	0/3/3/3
15	GTP	2A	501	16	-	6/18/38/38	0/3/3/3
17	GDP	9J	501	-	-	3/12/32/32	0/3/3/3
17	GDP	1B	501	-	-	4/12/32/32	0/3/3/3
15	GTP	5I	501	16	-	8/18/38/38	0/3/3/3
17	GDP	1F	501	-	-	5/12/32/32	0/3/3/3
15	GTP	7I	501	16	-	5/18/38/38	0/3/3/3
15	GTP	5M	501	-	-	9/18/38/38	0/3/3/3
15	GTP	9I	501	16	-	7/18/38/38	0/3/3/3
15	GTP	7M	501	-	-	8/18/38/38	0/3/3/3
17	GDP	4J	501	-	-	5/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	GTP	7C	501	16	-	6/18/38/38	0/3/3/3
17	GDP	5D	501	-	-	3/12/32/32	0/3/3/3
17	GDP	6L	501	-	-	2/12/32/32	0/3/3/3
17	GDP	9L	501	-	-	0/12/32/32	0/3/3/3
15	GTP	5A	501	16	-	7/18/38/38	0/3/3/3
15	GTP	1A	501	16	-	6/18/38/38	0/3/3/3
17	GDP	6D	501	-	-	6/12/32/32	0/3/3/3
17	GDP	5F	501	-	-	3/12/32/32	0/3/3/3
17	GDP	9B	501	-	-	3/12/32/32	0/3/3/3
15	GTP	8C	501	-	-	6/18/38/38	0/3/3/3
17	GDP	2B	501	-	-	6/12/32/32	0/3/3/3
17	GDP	7F	501	-	-	5/12/32/32	0/3/3/3
17	GDP	5H	501	-	-	7/12/32/32	0/3/3/3
17	GDP	7D	501	-	-	3/12/32/32	0/3/3/3
15	GTP	7G	501	16	-	4/18/38/38	0/3/3/3
17	GDP	8J	501	-	-	3/12/32/32	0/3/3/3
15	GTP	6A	501	16	-	6/18/38/38	0/3/3/3
15	GTP	7K	501	16	-	7/18/38/38	0/3/3/3
17	GDP	1D	501	-	-	5/12/32/32	0/3/3/3
15	GTP	4K	501	16	-	8/18/38/38	0/3/3/3
17	GDP	3L	501	-	-	5/12/32/32	0/3/3/3
17	GDP	1J	501	-	-	7/12/32/32	0/3/3/3
17	GDP	3H	501	-	-	3/12/32/32	0/3/3/3
15	GTP	2G	501	16	-	8/18/38/38	0/3/3/3
15	GTP	9A	501	16	-	6/18/38/38	0/3/3/3
15	GTP	2M	501	-	-	8/18/38/38	0/3/3/3
17	GDP	2J	501	-	-	3/12/32/32	0/3/3/3
15	GTP	1E	501	16	-	7/18/38/38	0/3/3/3
17	GDP	1N	501	-	-	6/12/32/32	0/3/3/3
17	GDP	5L	501	-	-	7/12/32/32	0/3/3/3
15	GTP	3I	501	16	-	6/18/38/38	0/3/3/3
15	GTP	6C	501	16	-	6/18/38/38	0/3/3/3
15	GTP	3C	501	16	-	6/18/38/38	0/3/3/3
15	GTP	6N	501	-	-	5/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	GDP	3F	501	-	-	5/12/32/32	0/3/3/3
17	GDP	8F	501	-	-	5/12/32/32	0/3/3/3
15	GTP	4C	501	16	-	5/18/38/38	0/3/3/3
15	GTP	2C	501	16	-	6/18/38/38	0/3/3/3
15	GTP	5C	501	16	-	5/18/38/38	0/3/3/3
17	GDP	7H	501	-	-	3/12/32/32	0/3/3/3
15	GTP	1C	501	16	-	4/18/38/38	0/3/3/3
17	GDP	2L	501	-	-	5/12/32/32	0/3/3/3
17	GDP	2H	501	-	-	9/12/32/32	0/3/3/3
15	GTP	3M	501	-	-	6/18/38/38	0/3/3/3
15	GTP	4M	501	-	-	7/18/38/38	0/3/3/3
17	GDP	1L	501	-	-	5/12/32/32	0/3/3/3
15	GTP	8M	501	-	-	5/18/38/38	0/3/3/3
17	GDP	3D	501	-	-	3/12/32/32	0/3/3/3
17	GDP	6F	501	-	-	7/12/32/32	0/3/3/3
15	GTP	1G	501	16	-	4/18/38/38	0/3/3/3
15	GTP	7A	501	16	-	6/18/38/38	0/3/3/3
15	GTP	8G	501	-	-	9/18/38/38	0/3/3/3
15	GTP	6K	501	16	-	7/18/38/38	0/3/3/3
15	GTP	8E	501	16	-	6/18/38/38	0/3/3/3
15	GTP	1K	501	16	-	9/18/38/38	0/3/3/3
15	GTP	2I	501	16	-	7/18/38/38	0/3/3/3
15	GTP	8I	501	16	-	7/18/38/38	0/3/3/3
15	GTP	4E	501	16	-	8/18/38/38	0/3/3/3

All (210) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	6N	501	GTP	C5-C6	-4.58	1.38	1.47
15	6C	501	GTP	C5-C6	-4.55	1.38	1.47
15	4I	501	GTP	C5-C6	-4.50	1.38	1.47
15	9G	501	GTP	C5-C6	-4.43	1.38	1.47
15	7G	501	GTP	C5-C6	-4.42	1.38	1.47
15	2C	501	GTP	C5-C6	-4.38	1.38	1.47
15	6K	501	GTP	C5-C6	-4.38	1.38	1.47
15	6I	501	GTP	C5-C6	-4.36	1.38	1.47
15	1I	501	GTP	C5-C6	-4.36	1.38	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	2E	501	GTP	C5-C6	-4.35	1.38	1.47
15	3E	501	GTP	C5-C6	-4.35	1.38	1.47
15	4E	501	GTP	C5-C6	-4.35	1.38	1.47
15	2G	501	GTP	C5-C6	-4.33	1.38	1.47
15	7I	501	GTP	C5-C6	-4.33	1.38	1.47
15	4M	501	GTP	C5-C6	-4.32	1.38	1.47
15	7A	501	GTP	C5-C6	-4.32	1.38	1.47
15	5K	501	GTP	C5-C6	-4.32	1.38	1.47
15	3G	501	GTP	C5-C6	-4.31	1.38	1.47
15	7K	501	GTP	C5-C6	-4.31	1.38	1.47
15	8G	501	GTP	C5-C6	-4.29	1.39	1.47
15	3I	501	GTP	C5-C6	-4.29	1.39	1.47
15	6G	501	GTP	C5-C6	-4.29	1.39	1.47
15	8E	501	GTP	C5-C6	-4.28	1.39	1.47
15	7E	501	GTP	C5-C6	-4.26	1.39	1.47
15	4C	501	GTP	C5-C6	-4.26	1.39	1.47
15	2I	501	GTP	C5-C6	-4.26	1.39	1.47
15	5E	501	GTP	C5-C6	-4.25	1.39	1.47
15	2K	501	GTP	C5-C6	-4.25	1.39	1.47
15	3K	501	GTP	C5-C6	-4.25	1.39	1.47
15	7C	501	GTP	C5-C6	-4.23	1.39	1.47
15	1A	501	GTP	C5-C6	-4.23	1.39	1.47
15	6E	501	GTP	C5-C6	-4.22	1.39	1.47
15	4K	501	GTP	C5-C6	-4.22	1.39	1.47
15	6A	501	GTP	C5-C6	-4.22	1.39	1.47
15	8C	501	GTP	C5-C6	-4.21	1.39	1.47
15	1K	501	GTP	C5-C6	-4.21	1.39	1.47
15	5A	501	GTP	C5-C6	-4.21	1.39	1.47
15	8A	501	GTP	C5-C6	-4.21	1.39	1.47
15	3M	501	GTP	C5-C6	-4.20	1.39	1.47
15	5C	501	GTP	C5-C6	-4.20	1.39	1.47
15	1G	501	GTP	C5-C6	-4.20	1.39	1.47
15	8K	501	GTP	C5-C6	-4.20	1.39	1.47
15	5G	501	GTP	C5-C6	-4.20	1.39	1.47
15	9C	501	GTP	C5-C6	-4.20	1.39	1.47
15	3C	501	GTP	C5-C6	-4.20	1.39	1.47
15	8I	501	GTP	C5-C6	-4.19	1.39	1.47
15	1M	501	GTP	C5-C6	-4.19	1.39	1.47
15	4G	501	GTP	C5-C6	-4.18	1.39	1.47
15	9K	501	GTP	C5-C6	-4.17	1.39	1.47
15	5I	501	GTP	C5-C6	-4.17	1.39	1.47
15	5M	501	GTP	C5-C6	-4.16	1.39	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	9M	501	GTP	C5-C6	-4.14	1.39	1.47
15	1E	501	GTP	C5-C6	-4.14	1.39	1.47
15	9A	501	GTP	C5-C6	-4.14	1.39	1.47
15	1C	501	GTP	C5-C6	-4.13	1.39	1.47
15	4A	501	GTP	C5-C6	-4.13	1.39	1.47
15	9E	501	GTP	C5-C6	-4.11	1.39	1.47
15	2M	501	GTP	C5-C6	-4.10	1.39	1.47
15	9I	501	GTP	C5-C6	-4.09	1.39	1.47
15	8M	501	GTP	C5-C6	-4.09	1.39	1.47
15	7M	501	GTP	C5-C6	-4.07	1.39	1.47
15	3A	501	GTP	C5-C6	-4.05	1.39	1.47
15	2A	501	GTP	C5-C6	-3.78	1.40	1.47
15	6N	501	GTP	PB-O3B	3.43	1.63	1.59
15	1A	501	GTP	PB-O3B	2.91	1.62	1.59
17	2D	501	GDP	C6-N1	-2.82	1.33	1.37
17	4B	501	GDP	C6-N1	-2.75	1.33	1.37
17	2J	501	GDP	C6-N1	-2.72	1.33	1.37
17	1L	501	GDP	C6-N1	-2.69	1.33	1.37
17	3F	501	GDP	C6-N1	-2.67	1.33	1.37
17	6F	501	GDP	C6-N1	-2.66	1.33	1.37
15	1A	501	GTP	PA-O3A	2.65	1.62	1.59
15	1A	501	GTP	PB-O3A	2.64	1.62	1.59
17	6B	501	GDP	C6-N1	-2.60	1.33	1.37
17	5B	501	GDP	C6-N1	-2.58	1.33	1.37
17	6J	501	GDP	C6-N1	-2.57	1.33	1.37
17	9F	501	GDP	C6-N1	-2.56	1.33	1.37
17	1B	501	GDP	C6-N1	-2.56	1.33	1.37
17	5L	501	GDP	C6-N1	-2.54	1.33	1.37
17	5N	501	GDP	C6-N1	-2.52	1.33	1.37
17	2L	501	GDP	C6-N1	-2.49	1.34	1.37
17	1F	501	GDP	C6-N1	-2.47	1.34	1.37
15	9K	501	GTP	PA-O3A	2.47	1.62	1.59
17	2F	501	GDP	C6-N1	-2.46	1.34	1.37
17	3B	501	GDP	C6-N1	-2.45	1.34	1.37
17	7B	502	GDP	C6-N1	-2.44	1.34	1.37
17	7J	501	GDP	C6-N1	-2.44	1.34	1.37
17	8D	501	GDP	C6-N1	-2.44	1.34	1.37
17	8H	501	GDP	C6-N1	-2.43	1.34	1.37
17	2H	501	GDP	C6-N1	-2.42	1.34	1.37
17	7F	501	GDP	C6-N1	-2.41	1.34	1.37
17	3J	501	GDP	C6-N1	-2.41	1.34	1.37
15	7K	501	GTP	PB-O3A	2.40	1.62	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	6L	501	GDP	C6-N1	-2.40	1.34	1.37
17	7L	501	GDP	C6-N1	-2.39	1.34	1.37
15	9E	501	GTP	PB-O3A	2.39	1.62	1.59
17	9D	501	GDP	C6-N1	-2.37	1.34	1.37
17	4J	501	GDP	C6-N1	-2.37	1.34	1.37
17	5H	501	GDP	C6-N1	-2.37	1.34	1.37
15	8K	501	GTP	PB-O3B	2.36	1.62	1.59
17	8J	501	GDP	C6-N1	-2.36	1.34	1.37
17	1J	501	GDP	C6-N1	-2.36	1.34	1.37
17	3H	501	GDP	C6-N1	-2.36	1.34	1.37
15	9K	501	GTP	PB-O3A	2.36	1.62	1.59
17	4D	501	GDP	C6-N1	-2.34	1.34	1.37
17	4L	501	GDP	C6-N1	-2.34	1.34	1.37
17	3D	501	GDP	C6-N1	-2.34	1.34	1.37
17	6D	501	GDP	C6-N1	-2.34	1.34	1.37
17	9D	501	GDP	PA-O3A	2.32	1.62	1.59
17	4H	501	GDP	C6-N1	-2.32	1.34	1.37
17	1N	501	GDP	C6-N1	-2.32	1.34	1.37
17	4F	501	GDP	C6-N1	-2.32	1.34	1.37
17	3L	501	GDP	C6-N1	-2.32	1.34	1.37
15	8M	501	GTP	PB-O3B	2.31	1.62	1.59
17	9B	501	GDP	C6-N1	-2.31	1.34	1.37
17	6H	501	GDP	C6-N1	-2.29	1.34	1.37
17	5D	501	GDP	C6-N1	-2.29	1.34	1.37
17	6N	502	GDP	C6-N1	-2.29	1.34	1.37
17	7H	501	GDP	C6-N1	-2.29	1.34	1.37
17	2B	501	GDP	C6-N1	-2.28	1.34	1.37
17	5F	501	GDP	C6-N1	-2.28	1.34	1.37
17	5J	501	GDP	C6-N1	-2.27	1.34	1.37
15	9E	501	GTP	PA-O3A	2.27	1.61	1.59
15	2A	501	GTP	PB-O3B	2.26	1.61	1.59
15	8I	501	GTP	C2-N3	2.24	1.38	1.33
17	7D	501	GDP	C6-N1	-2.24	1.34	1.37
17	8L	501	GDP	C6-N1	-2.24	1.34	1.37
17	1H	501	GDP	C6-N1	-2.24	1.34	1.37
15	4A	501	GTP	PB-O3B	2.23	1.61	1.59
15	8M	501	GTP	C2-N3	2.23	1.38	1.33
17	9H	501	GDP	C6-N1	-2.23	1.34	1.37
15	9G	501	GTP	C2-N3	2.23	1.38	1.33
17	8B	501	GDP	C6-N1	-2.22	1.34	1.37
15	9I	501	GTP	C2-N3	2.22	1.38	1.33
15	9M	501	GTP	C2-N3	2.22	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	2K	501	GTP	C2-N3	2.22	1.38	1.33
17	9J	501	GDP	C6-N1	-2.21	1.34	1.37
15	1G	501	GTP	C2-N3	2.20	1.38	1.33
15	9K	501	GTP	C2-N3	2.20	1.38	1.33
15	3E	501	GTP	C2-N3	2.20	1.38	1.33
17	8F	501	GDP	C6-N1	-2.20	1.34	1.37
15	1M	501	GTP	C2-N3	2.19	1.38	1.33
17	9L	501	GDP	C6-N1	-2.19	1.34	1.37
15	2E	501	GTP	C2-N3	2.19	1.38	1.33
15	8K	501	GTP	C2-N3	2.19	1.38	1.33
15	2I	501	GTP	C2-N3	2.18	1.38	1.33
15	9E	501	GTP	PB-O3B	2.18	1.61	1.59
15	4K	501	GTP	C2-N3	2.18	1.38	1.33
15	9I	501	GTP	PB-O3A	2.17	1.61	1.59
15	8E	501	GTP	C2-N3	2.17	1.38	1.33
15	2M	501	GTP	C2-N3	2.17	1.38	1.33
15	2C	501	GTP	C2-N3	2.17	1.38	1.33
15	1E	501	GTP	C2-N3	2.17	1.38	1.33
15	1K	501	GTP	C2-N3	2.16	1.38	1.33
15	9A	501	GTP	C2-N3	2.16	1.38	1.33
15	6G	501	GTP	C2-N3	2.16	1.38	1.33
15	5G	501	GTP	C2-N3	2.16	1.38	1.33
15	9I	501	GTP	PB-O3B	2.15	1.61	1.59
15	1A	501	GTP	C2-N3	2.15	1.38	1.33
17	9L	501	GDP	PA-O3A	2.15	1.61	1.59
15	9A	501	GTP	PB-O3B	2.14	1.61	1.59
15	5C	501	GTP	C2-N3	2.14	1.38	1.33
15	9C	501	GTP	C2-N3	2.14	1.38	1.33
15	3C	501	GTP	C2-N3	2.14	1.38	1.33
15	5I	501	GTP	C2-N3	2.13	1.38	1.33
15	3A	501	GTP	C2-N3	2.13	1.38	1.33
15	3M	501	GTP	C2-N3	2.13	1.38	1.33
15	6I	501	GTP	C2-N3	2.13	1.38	1.33
15	1C	501	GTP	C2-N3	2.13	1.38	1.33
15	7C	501	GTP	C2-N3	2.12	1.38	1.33
15	7M	501	GTP	C2-N3	2.12	1.38	1.33
17	9H	501	GDP	PA-O3A	2.12	1.61	1.59
17	1D	501	GDP	C6-N1	-2.12	1.34	1.37
15	6N	501	GTP	C2-N3	2.12	1.38	1.33
15	6C	501	GTP	C2-N3	2.12	1.38	1.33
15	3K	501	GTP	C2-N3	2.12	1.38	1.33
15	6E	501	GTP	C2-N3	2.12	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	5A	501	GTP	C2-N3	2.11	1.38	1.33
15	7G	501	GTP	C2-N3	2.11	1.38	1.33
17	1F	501	GDP	O4'-C1'	2.11	1.43	1.40
15	1I	501	GTP	C2-N3	2.11	1.38	1.33
17	1N	501	GDP	PA-O3A	2.11	1.61	1.59
15	6A	501	GTP	C2-N3	2.10	1.38	1.33
15	9E	501	GTP	C2-N3	2.10	1.38	1.33
15	4G	501	GTP	C2-N3	2.10	1.38	1.33
15	7I	501	GTP	C2-N3	2.10	1.38	1.33
15	5K	501	GTP	C2-N3	2.10	1.38	1.33
15	4M	501	GTP	C2-N3	2.09	1.38	1.33
15	5E	501	GTP	C2-N3	2.09	1.38	1.33
15	7A	501	GTP	C2-N3	2.09	1.38	1.33
15	6K	501	GTP	C2-N3	2.09	1.38	1.33
17	8F	501	GDP	PA-O3A	2.08	1.61	1.59
15	3G	501	GTP	C2-N3	2.08	1.38	1.33
15	7E	501	GTP	C2-N3	2.08	1.38	1.33
15	7K	501	GTP	C2-N3	2.07	1.38	1.33
15	7A	501	GTP	PB-O3B	2.07	1.61	1.59
15	4E	501	GTP	C2-N3	2.07	1.38	1.33
15	8A	501	GTP	C2-N3	2.07	1.38	1.33
17	8B	501	GDP	PA-O3A	2.06	1.61	1.59
15	8G	501	GTP	C2-N3	2.06	1.38	1.33
15	3I	501	GTP	C2-N3	2.06	1.38	1.33
15	2A	501	GTP	PB-O3A	2.05	1.61	1.59
15	4C	501	GTP	C2-N3	2.05	1.38	1.33
15	2G	501	GTP	C2-N3	2.04	1.38	1.33
15	9G	501	GTP	PA-O3A	2.04	1.61	1.59
15	2A	501	GTP	C2-N3	2.03	1.38	1.33
17	2F	501	GDP	O4'-C1'	2.03	1.43	1.40
15	2E	501	GTP	PA-O3A	2.03	1.61	1.59
15	2E	501	GTP	PB-O3A	2.02	1.61	1.59
15	3M	501	GTP	PB-O3B	2.01	1.61	1.59

All (435) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	2A	501	GTP	C8-N7-C5	5.07	111.18	102.55
17	5N	501	GDP	O4'-C1'-N9	-4.57	102.69	108.75
15	9I	501	GTP	C8-N7-C5	3.94	109.26	102.55
17	4H	501	GDP	O4'-C1'-N9	-3.86	103.62	108.75
15	8E	501	GTP	C8-N7-C5	3.73	108.89	102.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	1C	501	GTP	C8-N7-C5	3.71	108.87	102.55
15	6E	501	GTP	C8-N7-C5	3.71	108.87	102.55
17	2D	501	GDP	O4'-C1'-N9	-3.71	103.82	108.75
15	5I	501	GTP	C8-N7-C5	3.71	108.86	102.55
15	8M	501	GTP	C8-N7-C5	3.71	108.86	102.55
15	3M	501	GTP	C8-N7-C5	3.70	108.84	102.55
15	5A	501	GTP	C8-N7-C5	3.69	108.84	102.55
15	4A	501	GTP	C8-N7-C5	3.68	108.81	102.55
15	2E	501	GTP	C8-N7-C5	3.67	108.80	102.55
15	7E	501	GTP	C8-N7-C5	3.67	108.80	102.55
15	8K	501	GTP	C8-N7-C5	3.67	108.80	102.55
15	5M	501	GTP	C8-N7-C5	3.67	108.79	102.55
15	7M	501	GTP	C8-N7-C5	3.67	108.79	102.55
15	3C	501	GTP	C8-N7-C5	3.66	108.78	102.55
15	5C	501	GTP	C8-N7-C5	3.66	108.78	102.55
15	3A	501	GTP	C8-N7-C5	3.66	108.77	102.55
15	2M	501	GTP	C8-N7-C5	3.65	108.76	102.55
15	8I	501	GTP	C8-N7-C5	3.65	108.76	102.55
15	1K	501	GTP	C8-N7-C5	3.65	108.76	102.55
15	3I	501	GTP	C8-N7-C5	3.64	108.74	102.55
15	9E	501	GTP	C8-N7-C5	3.63	108.73	102.55
15	2K	501	GTP	C8-N7-C5	3.63	108.73	102.55
15	1E	501	GTP	C8-N7-C5	3.63	108.73	102.55
15	2G	501	GTP	C8-N7-C5	3.63	108.73	102.55
15	3G	501	GTP	C8-N7-C5	3.63	108.73	102.55
15	5E	501	GTP	C8-N7-C5	3.63	108.72	102.55
15	4C	501	GTP	C8-N7-C5	3.62	108.71	102.55
15	9K	501	GTP	C8-N7-C5	3.62	108.71	102.55
15	4G	501	GTP	C8-N7-C5	3.61	108.69	102.55
15	2I	501	GTP	C8-N7-C5	3.61	108.69	102.55
15	7G	501	GTP	C8-N7-C5	3.60	108.69	102.55
15	9A	501	GTP	C8-N7-C5	3.60	108.68	102.55
15	2C	501	GTP	C8-N7-C5	3.60	108.68	102.55
15	5G	501	GTP	C8-N7-C5	3.60	108.67	102.55
15	7C	501	GTP	C8-N7-C5	3.59	108.67	102.55
15	3K	501	GTP	C8-N7-C5	3.59	108.67	102.55
15	7K	501	GTP	C8-N7-C5	3.59	108.66	102.55
15	6I	501	GTP	C8-N7-C5	3.59	108.66	102.55
15	6N	501	GTP	C8-N7-C5	3.58	108.65	102.55
15	9C	501	GTP	C8-N7-C5	3.58	108.64	102.55
15	4K	501	GTP	C8-N7-C5	3.58	108.64	102.55
15	1A	501	GTP	C8-N7-C5	3.57	108.63	102.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	6A	501	GTP	C8-N7-C5	3.57	108.63	102.55
15	1G	501	GTP	C8-N7-C5	3.55	108.60	102.55
15	4E	501	GTP	C8-N7-C5	3.55	108.59	102.55
15	8C	501	GTP	C8-N7-C5	3.55	108.59	102.55
15	6G	501	GTP	C8-N7-C5	3.55	108.58	102.55
17	4H	501	GDP	C4'-O4'-C1'	3.53	113.16	109.92
15	3E	501	GTP	C8-N7-C5	3.53	108.56	102.55
15	7A	501	GTP	C8-N7-C5	3.52	108.55	102.55
15	9G	501	GTP	C8-N7-C5	3.52	108.53	102.55
15	4M	501	GTP	C8-N7-C5	3.51	108.53	102.55
15	6K	501	GTP	C8-N7-C5	3.51	108.53	102.55
15	9M	501	GTP	C8-N7-C5	3.51	108.52	102.55
15	8G	501	GTP	C8-N7-C5	3.51	108.52	102.55
15	1I	501	GTP	C8-N7-C5	3.50	108.50	102.55
15	2A	501	GTP	C2-N1-C6	-3.49	118.72	125.11
15	8A	501	GTP	C8-N7-C5	3.49	108.50	102.55
15	1M	501	GTP	C8-N7-C5	3.49	108.49	102.55
15	6C	501	GTP	C8-N7-C5	3.49	108.48	102.55
15	5K	501	GTP	C8-N7-C5	3.44	108.40	102.55
17	4B	501	GDP	C8-N7-C5	3.43	108.39	102.55
15	7I	501	GTP	C8-N7-C5	3.43	108.38	102.55
15	6N	501	GTP	C5-C6-N1	3.29	120.35	114.07
15	4I	501	GTP	C8-N7-C5	3.25	108.09	102.55
15	3A	501	GTP	C5-C6-N1	3.13	120.04	114.07
15	8K	501	GTP	C5-C6-N1	3.11	120.01	114.07
15	2A	501	GTP	C5-C6-N1	3.09	119.97	114.07
15	6N	501	GTP	C2-N1-C6	-3.08	119.47	125.11
15	7C	501	GTP	C5-C6-N1	3.06	119.90	114.07
15	3M	501	GTP	C5-C6-N1	3.05	119.89	114.07
15	4A	501	GTP	C2-N1-C6	-3.03	119.56	125.11
17	3D	501	GDP	C8-N7-C5	3.02	107.70	102.55
15	9G	501	GTP	C5-C6-N1	3.02	119.84	114.07
15	5I	501	GTP	C5-C6-N1	3.02	119.83	114.07
15	8E	501	GTP	C2-N1-C6	-3.01	119.61	125.11
15	8E	501	GTP	C5-C6-N1	3.01	119.81	114.07
15	1C	501	GTP	C5-C6-N1	3.00	119.80	114.07
15	9K	501	GTP	C5-C6-N1	3.00	119.80	114.07
15	2E	501	GTP	C2-N1-C6	-3.00	119.62	125.11
15	8K	501	GTP	C2-N1-C6	-2.99	119.64	125.11
15	9A	501	GTP	C5-C6-N1	2.98	119.75	114.07
15	8M	501	GTP	C5-C6-N1	2.98	119.75	114.07
15	2E	501	GTP	C5-C6-N1	2.97	119.74	114.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	3A	501	GTP	C2-N1-C6	-2.97	119.67	125.11
15	3K	501	GTP	C5-C6-N1	2.96	119.72	114.07
15	9I	501	GTP	C2-N1-C6	-2.96	119.69	125.11
15	1E	501	GTP	C5-C6-N1	2.96	119.72	114.07
15	5G	501	GTP	C5-C6-N1	2.95	119.71	114.07
15	7E	501	GTP	C5-C6-N1	2.95	119.70	114.07
15	5M	501	GTP	C4'-O4'-C1'	-2.95	107.22	109.92
15	7A	501	GTP	C5-C6-N1	2.95	119.69	114.07
15	4K	501	GTP	C5-C6-N1	2.95	119.69	114.07
15	3M	501	GTP	C2-N1-C6	-2.94	119.73	125.11
15	4A	501	GTP	C5-C6-N1	2.94	119.68	114.07
15	9K	501	GTP	C2-N1-C6	-2.94	119.73	125.11
15	1K	501	GTP	C5-C6-N1	2.94	119.67	114.07
15	6A	501	GTP	C5-C6-N1	2.94	119.67	114.07
17	2D	501	GDP	C8-N7-C5	2.93	107.54	102.55
15	9G	501	GTP	C2-N1-C6	-2.93	119.74	125.11
15	3C	501	GTP	C5-C6-N1	2.93	119.66	114.07
15	1G	501	GTP	C2-N1-C6	-2.93	119.75	125.11
15	2I	501	GTP	C5-C6-N1	2.93	119.66	114.07
15	9I	501	GTP	C5-C6-N1	2.93	119.66	114.07
15	6E	501	GTP	C5-C6-N1	2.93	119.66	114.07
15	1G	501	GTP	C5-C6-N1	2.93	119.65	114.07
15	2G	501	GTP	C5-C6-N1	2.92	119.64	114.07
15	3E	501	GTP	C5-C6-N1	2.92	119.64	114.07
15	7C	501	GTP	C2-N1-C6	-2.92	119.77	125.11
15	8C	501	GTP	C2-N1-C6	-2.92	119.77	125.11
15	2C	501	GTP	C5-C6-N1	2.92	119.64	114.07
17	1J	501	GDP	C8-N7-C5	2.92	107.52	102.55
17	1J	501	GDP	C4'-O4'-C1'	2.92	112.60	109.92
15	1I	501	GTP	C5-C6-N1	2.92	119.64	114.07
15	6C	501	GTP	C5-C6-N1	2.92	119.63	114.07
15	1C	501	GTP	C2-N1-C6	-2.91	119.78	125.11
15	2I	501	GTP	C2-N1-C6	-2.91	119.78	125.11
15	7M	501	GTP	C5-C6-N1	2.91	119.63	114.07
15	6A	501	GTP	C2-N1-C6	-2.91	119.78	125.11
17	9L	501	GDP	C8-N7-C5	2.91	107.50	102.55
15	8I	501	GTP	C5-C6-N1	2.91	119.61	114.07
15	5C	501	GTP	C5-C6-N1	2.90	119.61	114.07
15	9A	501	GTP	C2-N1-C6	-2.90	119.80	125.11
15	1K	501	GTP	C2-N1-C6	-2.90	119.80	125.11
15	7I	501	GTP	C5-C6-N1	2.90	119.60	114.07
15	2C	501	GTP	C2-N1-C6	-2.90	119.81	125.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	8M	501	GTP	C2-N1-C6	-2.90	119.81	125.11
15	9M	501	GTP	C2-N1-C6	-2.90	119.81	125.11
17	1L	501	GDP	C8-N7-C5	2.89	107.47	102.55
17	9B	501	GDP	C8-N7-C5	2.89	107.47	102.55
15	9M	501	GTP	C5-C6-N1	2.89	119.59	114.07
15	6I	501	GTP	C5-C6-N1	2.89	119.58	114.07
15	2M	501	GTP	C5-C6-N1	2.89	119.58	114.07
15	2K	501	GTP	C5-C6-N1	2.89	119.58	114.07
15	2K	501	GTP	C2-N1-C6	-2.89	119.83	125.11
17	9H	501	GDP	C8-N7-C5	2.89	107.46	102.55
15	4C	501	GTP	C5-C6-N1	2.88	119.57	114.07
17	1N	501	GDP	C8-N7-C5	2.88	107.46	102.55
15	6G	501	GTP	C5-C6-N1	2.88	119.57	114.07
17	5B	501	GDP	C8-N7-C5	2.88	107.45	102.55
17	7H	501	GDP	C8-N7-C5	2.88	107.45	102.55
15	3E	501	GTP	C2-N1-C6	-2.88	119.84	125.11
15	1E	501	GTP	C2-N1-C6	-2.88	119.84	125.11
15	3C	501	GTP	C2-N1-C6	-2.88	119.85	125.11
15	6K	501	GTP	C5-C6-N1	2.87	119.56	114.07
15	6C	501	GTP	C2-N1-C6	-2.87	119.85	125.11
15	8C	501	GTP	C5-C6-N1	2.87	119.54	114.07
15	5M	501	GTP	C5-C6-N1	2.86	119.53	114.07
15	5E	501	GTP	C5-C6-N1	2.86	119.53	114.07
17	8L	501	GDP	C8-N7-C5	2.86	107.42	102.55
15	9C	501	GTP	C5-C6-N1	2.86	119.53	114.07
15	4E	501	GTP	C5-C6-N1	2.86	119.53	114.07
15	3K	501	GTP	C2-N1-C6	-2.86	119.88	125.11
15	3G	501	GTP	C5-C6-N1	2.86	119.53	114.07
17	8F	501	GDP	C8-N7-C5	2.86	107.41	102.55
15	4G	501	GTP	C5-C6-N1	2.86	119.52	114.07
17	4D	501	GDP	C8-N7-C5	2.86	107.41	102.55
15	9E	501	GTP	C5-C6-N1	2.85	119.52	114.07
17	6N	502	GDP	C8-N7-C5	2.85	107.41	102.55
15	5I	501	GTP	C2-N1-C6	-2.85	119.89	125.11
17	2B	501	GDP	C8-N7-C5	2.85	107.40	102.55
15	4K	501	GTP	C2-N1-C6	-2.85	119.89	125.11
15	7I	501	GTP	C2-N1-C6	-2.85	119.90	125.11
15	5G	501	GTP	C2-N1-C6	-2.85	119.90	125.11
15	5C	501	GTP	C2-N1-C6	-2.85	119.90	125.11
17	5J	501	GDP	C8-N7-C5	2.85	107.39	102.55
17	4L	501	GDP	C8-N7-C5	2.85	107.39	102.55
17	4J	501	GDP	C8-N7-C5	2.84	107.39	102.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	6D	501	GDP	C8-N7-C5	2.84	107.39	102.55
15	7K	501	GTP	C5-C6-N1	2.84	119.49	114.07
15	6K	501	GTP	C2-N1-C6	-2.84	119.91	125.11
15	1M	501	GTP	C2-N1-C6	-2.84	119.91	125.11
17	5N	501	GDP	C8-N7-C5	2.84	107.38	102.55
15	7G	501	GTP	C5-C6-N1	2.84	119.48	114.07
17	5L	501	GDP	C8-N7-C5	2.83	107.37	102.55
15	2M	501	GTP	C2-N1-C6	-2.83	119.93	125.11
15	7E	501	GTP	C2-N1-C6	-2.83	119.94	125.11
17	2J	501	GDP	C8-N7-C5	2.83	107.36	102.55
17	5D	501	GDP	C8-N7-C5	2.82	107.36	102.55
17	5H	501	GDP	C8-N7-C5	2.82	107.36	102.55
17	1B	501	GDP	C8-N7-C5	2.82	107.35	102.55
15	1M	501	GTP	C5-C6-N1	2.82	119.44	114.07
17	3J	501	GDP	C8-N7-C5	2.82	107.34	102.55
15	5A	501	GTP	C5-C6-N1	2.81	119.43	114.07
15	1A	501	GTP	C5-C6-N1	2.81	119.43	114.07
17	1H	501	GDP	C8-N7-C5	2.81	107.33	102.55
15	2G	501	GTP	C2-N1-C6	-2.81	119.97	125.11
17	8D	501	GDP	C8-N7-C5	2.80	107.32	102.55
15	6E	501	GTP	C2-N1-C6	-2.80	119.98	125.11
17	7J	501	GDP	C8-N7-C5	2.80	107.32	102.55
15	5K	501	GTP	C5-C6-N1	2.80	119.41	114.07
15	8G	501	GTP	C5-C6-N1	2.80	119.41	114.07
15	6G	501	GTP	C2-N1-C6	-2.80	119.99	125.11
17	7F	501	GDP	C8-N7-C5	2.80	107.31	102.55
15	5M	501	GTP	C2-N1-C6	-2.80	119.99	125.11
15	4A	501	GTP	O4'-C1'-N9	2.80	112.45	108.75
15	9C	501	GTP	C2-N1-C6	-2.80	119.99	125.11
15	3I	501	GTP	C5-C6-N1	2.79	119.40	114.07
17	6H	501	GDP	C8-N7-C5	2.79	107.30	102.55
15	5E	501	GTP	C2-N1-C6	-2.79	120.00	125.11
17	4F	501	GDP	C8-N7-C5	2.79	107.29	102.55
17	9D	501	GDP	C8-N7-C5	2.78	107.29	102.55
17	8J	501	GDP	C8-N7-C5	2.78	107.29	102.55
17	3L	501	GDP	C8-N7-C5	2.78	107.29	102.55
17	9J	501	GDP	C8-N7-C5	2.78	107.28	102.55
17	5F	501	GDP	C8-N7-C5	2.78	107.28	102.55
17	7B	502	GDP	C8-N7-C5	2.78	107.27	102.55
15	1A	501	GTP	C2-N1-C6	-2.77	120.04	125.11
17	3B	501	GDP	C8-N7-C5	2.77	107.27	102.55
17	8J	501	GDP	C4'-O4'-C1'	2.77	112.46	109.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	2H	501	GDP	C8-N7-C5	2.76	107.26	102.55
15	8I	501	GTP	C2-N1-C6	-2.76	120.05	125.11
15	7M	501	GTP	C2-N1-C6	-2.76	120.05	125.11
17	2F	501	GDP	C8-N7-C5	2.75	107.23	102.55
15	5K	501	GTP	C2-N1-C6	-2.75	120.08	125.11
15	3G	501	GTP	C2-N1-C6	-2.75	120.08	125.11
15	5A	501	GTP	C2-N1-C6	-2.74	120.10	125.11
15	6N	501	GTP	O6-C6-C5	-2.74	118.89	124.32
17	6L	501	GDP	C8-N7-C5	2.74	107.21	102.55
15	9E	501	GTP	C2-N1-C6	-2.73	120.11	125.11
17	2L	501	GDP	C8-N7-C5	2.73	107.20	102.55
17	8H	501	GDP	C8-N7-C5	2.73	107.20	102.55
15	6I	501	GTP	C2-N1-C6	-2.73	120.11	125.11
15	7K	501	GTP	C2-N1-C6	-2.73	120.12	125.11
15	1I	501	GTP	C2-N1-C6	-2.73	120.12	125.11
17	9F	501	GDP	C8-N7-C5	2.72	107.19	102.55
15	4C	501	GTP	C2-N1-C6	-2.72	120.12	125.11
15	4M	501	GTP	C5-C6-N1	2.72	119.26	114.07
15	8A	501	GTP	C5-C6-N1	2.72	119.25	114.07
15	8G	501	GTP	C2-N1-C6	-2.71	120.15	125.11
15	2A	501	GTP	O6-C6-N1	-2.69	117.42	120.62
15	5M	501	GTP	O4'-C1'-N9	2.69	112.31	108.75
17	7D	501	GDP	C8-N7-C5	2.69	107.13	102.55
15	4G	501	GTP	C2-N1-C6	-2.68	120.20	125.11
17	3H	501	GDP	C8-N7-C5	2.67	107.09	102.55
17	1D	501	GDP	C8-N7-C5	2.64	107.05	102.55
15	7G	501	GTP	C2-N1-C6	-2.63	120.29	125.11
15	1C	501	GTP	O4'-C1'-N9	2.63	112.23	108.75
17	1F	501	GDP	C8-N7-C5	2.62	107.00	102.55
15	7A	501	GTP	C2-N1-C6	-2.61	120.33	125.11
17	6B	501	GDP	C8-N7-C5	2.59	106.97	102.55
15	8A	501	GTP	C2-N1-C6	-2.58	120.38	125.11
15	3I	501	GTP	C2-N1-C6	-2.58	120.38	125.11
15	1G	501	GTP	C4'-O4'-C1'	2.57	112.28	109.92
17	3F	501	GDP	C8-N7-C5	2.56	106.91	102.55
15	4I	501	GTP	C5-C6-N1	2.56	118.95	114.07
15	4E	501	GTP	C2-N1-C6	-2.55	120.43	125.11
17	4H	501	GDP	C8-N7-C5	2.55	106.90	102.55
17	6F	501	GDP	C8-N7-C5	2.55	106.89	102.55
17	2J	501	GDP	C4'-O4'-C1'	2.55	112.26	109.92
17	7L	501	GDP	C8-N7-C5	2.54	106.87	102.55
17	2F	501	GDP	C4'-O4'-C1'	2.54	112.25	109.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	9G	501	GTP	O6-C6-C5	-2.53	119.30	124.32
17	7B	502	GDP	C5-C6-N1	2.53	118.89	114.07
17	9B	501	GDP	C4'-O4'-C1'	2.51	112.22	109.92
17	3J	501	GDP	C4'-O4'-C1'	2.50	112.22	109.92
17	6J	501	GDP	O6-C6-C5	-2.48	119.40	124.32
15	4M	501	GTP	C2-N1-C6	-2.48	120.57	125.11
17	8B	501	GDP	C8-N7-C5	2.48	106.76	102.55
17	7D	501	GDP	C4'-O4'-C1'	2.46	112.17	109.92
17	6J	501	GDP	C8-N7-C5	2.45	106.73	102.55
17	2H	501	GDP	O3B-PB-O3A	2.43	112.78	104.64
15	2E	501	GTP	O6-C6-C5	-2.43	119.51	124.32
15	9K	501	GTP	C4'-O4'-C1'	2.43	112.15	109.92
15	1K	501	GTP	O2B-PB-O3A	2.42	113.83	107.27
17	8F	501	GDP	O4'-C1'-N9	-2.42	105.53	108.75
17	6F	501	GDP	C5-C6-N1	2.40	118.66	114.07
17	8B	501	GDP	C4'-O4'-C1'	2.40	112.12	109.92
15	4A	501	GTP	N2-C2-N1	2.38	121.79	116.76
17	1F	501	GDP	C4'-O4'-C1'	2.37	112.10	109.92
17	6B	501	GDP	O3B-PB-O3A	2.37	112.58	104.64
17	7B	502	GDP	O3B-PB-O3A	2.36	112.56	104.64
15	4E	501	GTP	O2A-PA-O3A	2.36	113.66	107.27
17	3F	501	GDP	C4'-O4'-C1'	2.36	112.08	109.92
15	8E	501	GTP	O6-C6-C5	-2.35	119.65	124.32
15	6N	501	GTP	O3G-PG-O3B	2.35	112.53	104.64
17	8B	501	GDP	O6-C6-C5	-2.33	119.69	124.32
15	9K	501	GTP	O2B-PB-O3A	2.32	113.54	107.27
17	7B	502	GDP	O2A-PA-O3A	2.31	113.52	107.27
17	7J	501	GDP	C5-C6-N1	2.31	118.47	114.07
17	6B	501	GDP	C5-C6-N1	2.30	118.46	114.07
17	2H	501	GDP	O2A-PA-O3A	2.30	113.50	107.27
15	4A	501	GTP	O6-C6-C5	-2.30	119.76	124.32
17	5H	501	GDP	O3B-PB-O3A	2.30	112.34	104.64
17	8F	501	GDP	O3B-PB-O3A	2.29	112.33	104.64
17	1N	501	GDP	O3B-PB-O3A	2.29	112.32	104.64
15	6K	501	GTP	O2B-PB-O3B	2.28	113.43	107.27
15	6G	501	GTP	O2B-PB-O3A	2.28	113.42	107.27
17	9D	501	GDP	O3B-PB-O3A	2.27	112.25	104.64
17	4J	501	GDP	C4'-O4'-C1'	2.26	111.99	109.92
15	4I	501	GTP	C2-N1-C6	-2.25	120.98	125.11
17	8L	501	GDP	O3B-PB-O3A	2.25	112.19	104.64
17	9F	501	GDP	C4'-O4'-C1'	2.25	111.98	109.92
17	4H	501	GDP	C2'-C3'-C4'	2.24	106.94	102.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	6N	501	GTP	O2B-PB-O3B	2.24	113.31	107.27
17	8B	501	GDP	O4'-C1'-N9	-2.23	105.78	108.75
17	3B	501	GDP	O2A-PA-O3A	2.23	113.31	107.27
17	5F	501	GDP	C5-C6-N1	2.23	118.33	114.07
17	1N	501	GDP	O2A-PA-O3A	2.22	113.29	107.27
17	8L	501	GDP	C4'-O4'-C1'	2.22	111.96	109.92
17	9F	501	GDP	C5-C6-N1	2.22	118.31	114.07
17	5D	501	GDP	C4'-O4'-C1'	2.22	111.95	109.92
17	8F	501	GDP	N2-C2-N1	2.21	121.42	116.76
17	9L	501	GDP	O2A-PA-O3A	2.20	113.22	107.27
15	3E	501	GTP	O6-C6-C5	-2.20	119.97	124.32
15	7G	501	GTP	O6-C6-C5	-2.19	119.97	124.32
17	5N	501	GDP	C5-C6-N1	2.19	118.25	114.07
15	6C	501	GTP	O6-C6-C5	-2.19	119.99	124.32
17	8D	501	GDP	C5-C6-N1	2.18	118.24	114.07
17	3B	501	GDP	C4'-O4'-C1'	2.18	111.92	109.92
17	7H	501	GDP	C4'-O4'-C1'	2.18	111.92	109.92
15	1G	501	GTP	O2B-PB-O3A	2.18	113.17	107.27
15	7I	501	GTP	O6-C6-C5	-2.18	120.00	124.32
17	6J	501	GDP	C4'-O4'-C1'	2.18	111.92	109.92
17	8F	501	GDP	O2A-PA-O3A	2.18	113.16	107.27
15	4I	501	GTP	O2B-PB-O3A	2.17	113.14	107.27
15	2M	501	GTP	O2B-PB-O3A	2.17	113.13	107.27
17	3F	501	GDP	C5-C6-N1	2.17	118.20	114.07
17	3F	501	GDP	O4'-C1'-N9	-2.17	105.87	108.75
15	2G	501	GTP	O6-C6-C5	-2.16	120.03	124.32
17	9H	501	GDP	C4'-O4'-C1'	2.16	111.90	109.92
17	7F	501	GDP	O3B-PB-O3A	2.16	111.88	104.64
17	6J	501	GDP	C5-C6-N1	2.16	118.19	114.07
15	2C	501	GTP	O6-C6-C5	-2.16	120.04	124.32
17	5H	501	GDP	O2A-PA-O3A	2.16	113.10	107.27
17	9D	501	GDP	C5-C6-N1	2.16	118.18	114.07
15	6K	501	GTP	O6-C6-C5	-2.15	120.06	124.32
17	7F	501	GDP	O2A-PA-O3A	2.15	113.07	107.27
15	1I	501	GTP	O6-C6-C5	-2.14	120.07	124.32
17	7L	501	GDP	C5-C6-N1	2.14	118.15	114.07
17	6B	501	GDP	C4'-O4'-C1'	2.13	111.88	109.92
17	7D	501	GDP	O6-C6-C5	-2.13	120.09	124.32
15	9A	501	GTP	O6-C6-C5	-2.13	120.09	124.32
15	6A	501	GTP	O6-C6-C5	-2.13	120.09	124.32
17	3H	501	GDP	C4'-O4'-C1'	2.13	111.88	109.92
17	9J	501	GDP	C5-C6-N1	2.13	118.13	114.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	6N	502	GDP	C4'-O4'-C1'	2.13	111.87	109.92
17	7L	501	GDP	O6-C6-C5	-2.13	120.11	124.32
15	2I	501	GTP	O6-C6-C5	-2.13	120.11	124.32
17	9J	501	GDP	C4'-O4'-C1'	2.12	111.87	109.92
17	7D	501	GDP	C5-C6-N1	2.12	118.12	114.07
15	8M	501	GTP	O4'-C1'-N9	2.12	111.56	108.75
17	6F	501	GDP	C4'-O4'-C1'	2.12	111.87	109.92
15	9M	501	GTP	O6-C6-C5	-2.12	120.12	124.32
17	3L	501	GDP	C5-C6-N1	2.12	118.11	114.07
15	8C	501	GTP	O6-C6-C5	-2.11	120.13	124.32
17	8B	501	GDP	O3B-PB-O3A	2.11	111.71	104.64
15	2K	501	GTP	O6-C6-C5	-2.11	120.14	124.32
15	2M	501	GTP	O6-C6-C5	-2.11	120.14	124.32
15	7K	501	GTP	O6-C6-C5	-2.11	120.14	124.32
15	8G	501	GTP	O6-C6-C5	-2.11	120.14	124.32
15	5E	501	GTP	O6-C6-C5	-2.10	120.15	124.32
17	9B	501	GDP	C5-C6-N1	2.10	118.08	114.07
17	4F	501	GDP	C5-C6-N1	2.10	118.08	114.07
17	4H	501	GDP	C5-C6-N1	2.10	118.08	114.07
15	1E	501	GTP	O6-C6-C5	-2.10	120.16	124.32
15	3K	501	GTP	O6-C6-C5	-2.10	120.16	124.32
15	1A	501	GTP	O6-C6-C5	-2.10	120.16	124.32
17	5D	501	GDP	C5-C6-N1	2.10	118.07	114.07
17	1D	501	GDP	C5-C6-N1	2.10	118.07	114.07
15	8M	501	GTP	O6-C6-C5	-2.09	120.17	124.32
15	7I	501	GTP	O2B-PB-O3B	2.09	112.92	107.27
15	1A	501	GTP	O2B-PB-O3A	2.09	112.92	107.27
15	9K	501	GTP	O6-C6-C5	-2.09	120.18	124.32
15	1G	501	GTP	O6-C6-C5	-2.09	120.18	124.32
17	5F	501	GDP	O3B-PB-O3A	2.09	111.64	104.64
15	7A	501	GTP	O6-C6-C5	-2.09	120.19	124.32
17	3H	501	GDP	C5-C6-N1	2.08	118.04	114.07
15	9K	501	GTP	O2A-PA-O3A	2.08	112.90	107.27
15	7C	501	GTP	O6-C6-C5	-2.08	120.19	124.32
15	9C	501	GTP	O6-C6-C5	-2.08	120.20	124.32
15	7E	501	GTP	O6-C6-C5	-2.08	120.20	124.32
15	6G	501	GTP	O6-C6-C5	-2.08	120.20	124.32
17	5J	501	GDP	C5-C6-N1	2.08	118.03	114.07
15	1K	501	GTP	O6-C6-C5	-2.08	120.20	124.32
15	8K	501	GTP	O3G-PG-O3B	2.08	111.60	104.64
17	1J	501	GDP	C5-C6-N1	2.07	118.02	114.07
17	9H	501	GDP	C5-C6-N1	2.07	118.02	114.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
17	7F	501	GDP	C4'-O4'-C1'	2.07	111.82	109.92
17	5B	501	GDP	O3B-PB-O3A	2.07	111.58	104.64
15	7K	501	GTP	O2B-PB-O3B	2.07	112.87	107.27
15	5K	501	GTP	O6-C6-C5	-2.07	120.22	124.32
15	7M	501	GTP	O6-C6-C5	-2.07	120.22	124.32
15	3I	501	GTP	O4'-C1'-N9	2.07	111.48	108.75
15	3C	501	GTP	O6-C6-C5	-2.06	120.23	124.32
17	4D	501	GDP	C5-C6-N1	2.06	118.00	114.07
17	6N	502	GDP	C5-C6-N1	2.06	118.00	114.07
17	5N	501	GDP	C4'-O4'-C1'	2.06	111.81	109.92
15	6I	501	GTP	O6-C6-C5	-2.06	120.24	124.32
17	2B	501	GDP	O2A-PA-O3A	2.06	112.83	107.27
15	4A	501	GTP	O3G-PG-O3B	2.05	111.53	104.64
15	4I	501	GTP	O6-C6-C5	-2.05	120.25	124.32
15	3M	501	GTP	O6-C6-C5	-2.05	120.25	124.32
15	5M	501	GTP	O6-C6-C5	-2.05	120.25	124.32
17	6H	501	GDP	C4'-O4'-C1'	2.05	111.80	109.92
17	1L	501	GDP	C5-C6-N1	2.05	117.98	114.07
17	4B	501	GDP	C2-N1-C6	-2.05	121.36	125.11
17	6B	501	GDP	O2A-PA-O3A	2.05	112.81	107.27
15	8K	501	GTP	O6-C6-C5	-2.05	120.26	124.32
17	8L	501	GDP	C5-C6-N1	2.05	117.98	114.07
17	4H	501	GDP	O6-C6-C5	-2.05	120.26	124.32
17	1N	501	GDP	C5-C6-N1	2.05	117.97	114.07
17	2J	501	GDP	C5-C6-N1	2.04	117.97	114.07
17	6H	501	GDP	C5-C6-N1	2.04	117.97	114.07
15	4C	501	GTP	O6-C6-C5	-2.04	120.27	124.32
15	1M	501	GTP	O6-C6-C5	-2.04	120.27	124.32
15	1C	501	GTP	O6-C6-C5	-2.04	120.27	124.32
17	7F	501	GDP	C5-C6-N1	2.04	117.97	114.07
15	4M	501	GTP	O6-C6-C5	-2.04	120.27	124.32
17	8J	501	GDP	C5-C6-N1	2.04	117.96	114.07
15	3G	501	GTP	O6-C6-C5	-2.04	120.28	124.32
17	9H	501	GDP	O3B-PB-O3A	2.04	111.47	104.64
17	2F	501	GDP	C5-C6-N1	2.04	117.96	114.07
15	9I	501	GTP	O6-C6-C5	-2.04	120.28	124.32
17	5B	501	GDP	C4'-O4'-C1'	2.04	111.79	109.92
17	1N	501	GDP	C4'-O4'-C1'	2.04	111.79	109.92
17	8B	501	GDP	C2'-C3'-C4'	2.03	106.53	102.61
17	4L	501	GDP	C5-C6-N1	2.03	117.94	114.07
17	7H	501	GDP	C5-C6-N1	2.03	117.94	114.07
17	7L	501	GDP	C4'-O4'-C1'	2.03	111.78	109.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	5G	501	GTP	C4'-O4'-C1'	2.02	111.78	109.92
15	6A	501	GTP	O2B-PB-O3B	2.02	112.73	107.27
17	9F	501	GDP	O3B-PB-O3A	2.02	111.40	104.64
15	8A	501	GTP	O6-C6-C5	-2.01	120.33	124.32
17	2D	501	GDP	C4'-O4'-C1'	2.01	111.77	109.92
15	5A	501	GTP	O6-C6-C5	-2.01	120.34	124.32
15	8G	501	GTP	O2B-PB-O3A	2.01	112.70	107.27
17	6D	501	GDP	C5-C6-N1	2.00	117.89	114.07
15	4E	501	GTP	O2B-PB-O3A	2.00	112.69	107.27
15	3I	501	GTP	O6-C6-C5	-2.00	120.35	124.32

There are no chirality outliers.

All (664) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	1A	501	GTP	C5'-O5'-PA-O3A
15	1A	501	GTP	C5'-O5'-PA-O1A
15	1A	501	GTP	C5'-O5'-PA-O2A
15	1C	501	GTP	O4'-C4'-C5'-O5'
15	1E	501	GTP	C5'-O5'-PA-O3A
15	1E	501	GTP	C5'-O5'-PA-O1A
15	1E	501	GTP	C5'-O5'-PA-O2A
15	1I	501	GTP	C5'-O5'-PA-O3A
15	1I	501	GTP	C5'-O5'-PA-O2A
15	1K	501	GTP	C5'-O5'-PA-O3A
15	1K	501	GTP	C5'-O5'-PA-O2A
15	1M	501	GTP	C5'-O5'-PA-O3A
15	1M	501	GTP	C5'-O5'-PA-O2A
15	1M	501	GTP	O4'-C4'-C5'-O5'
15	2A	501	GTP	PB-O3B-PG-O2G
15	2A	501	GTP	C5'-O5'-PA-O3A
15	2A	501	GTP	C5'-O5'-PA-O2A
15	2C	501	GTP	C5'-O5'-PA-O3A
15	2C	501	GTP	C5'-O5'-PA-O1A
15	2C	501	GTP	O4'-C4'-C5'-O5'
15	2G	501	GTP	C5'-O5'-PA-O3A
15	2G	501	GTP	C5'-O5'-PA-O1A
15	2G	501	GTP	C5'-O5'-PA-O2A
15	2I	501	GTP	C5'-O5'-PA-O3A
15	2I	501	GTP	C5'-O5'-PA-O1A
15	2I	501	GTP	C5'-O5'-PA-O2A
15	2K	501	GTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
15	2K	501	GTP	C5'-O5'-PA-O1A
15	2K	501	GTP	C5'-O5'-PA-O2A
15	2K	501	GTP	O4'-C4'-C5'-O5'
15	2M	501	GTP	C5'-O5'-PA-O3A
15	2M	501	GTP	C5'-O5'-PA-O1A
15	2M	501	GTP	C5'-O5'-PA-O2A
15	2M	501	GTP	O4'-C4'-C5'-O5'
15	3A	501	GTP	C5'-O5'-PA-O3A
15	3A	501	GTP	C5'-O5'-PA-O2A
15	3A	501	GTP	O4'-C4'-C5'-O5'
15	3C	501	GTP	C5'-O5'-PA-O3A
15	3C	501	GTP	C5'-O5'-PA-O1A
15	3C	501	GTP	C5'-O5'-PA-O2A
15	3E	501	GTP	PB-O3B-PG-O2G
15	3E	501	GTP	C5'-O5'-PA-O3A
15	3E	501	GTP	C5'-O5'-PA-O1A
15	3E	501	GTP	C5'-O5'-PA-O2A
15	3G	501	GTP	PB-O3A-PA-O5'
15	3G	501	GTP	O4'-C4'-C5'-O5'
15	3I	501	GTP	C5'-O5'-PA-O3A
15	3I	501	GTP	C5'-O5'-PA-O1A
15	3I	501	GTP	O4'-C4'-C5'-O5'
15	3K	501	GTP	C5'-O5'-PA-O3A
15	3K	501	GTP	C5'-O5'-PA-O1A
15	3K	501	GTP	C5'-O5'-PA-O2A
15	3M	501	GTP	C5'-O5'-PA-O3A
15	3M	501	GTP	C5'-O5'-PA-O1A
15	3M	501	GTP	O4'-C4'-C5'-O5'
15	3M	501	GTP	C3'-C4'-C5'-O5'
15	4A	501	GTP	C5'-O5'-PA-O3A
15	4C	501	GTP	C5'-O5'-PA-O3A
15	4C	501	GTP	C5'-O5'-PA-O2A
15	4E	501	GTP	C5'-O5'-PA-O3A
15	4E	501	GTP	C5'-O5'-PA-O1A
15	4E	501	GTP	C5'-O5'-PA-O2A
15	4G	501	GTP	C5'-O5'-PA-O3A
15	4G	501	GTP	C5'-O5'-PA-O1A
15	4G	501	GTP	C5'-O5'-PA-O2A
15	4I	501	GTP	C5'-O5'-PA-O3A
15	4I	501	GTP	C5'-O5'-PA-O2A
15	4I	501	GTP	O4'-C4'-C5'-O5'
15	4K	501	GTP	C5'-O5'-PA-O3A

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Mol	Chain	Res	Type	Atoms
15	4K	501	GTP	C5'-O5'-PA-O1A
15	4K	501	GTP	C5'-O5'-PA-O2A
15	4M	501	GTP	C5'-O5'-PA-O3A
15	4M	501	GTP	C5'-O5'-PA-O1A
15	4M	501	GTP	C5'-O5'-PA-O2A
15	5A	501	GTP	C5'-O5'-PA-O3A
15	5A	501	GTP	C5'-O5'-PA-O1A
15	5A	501	GTP	C5'-O5'-PA-O2A
15	5C	501	GTP	C5'-O5'-PA-O3A
15	5C	501	GTP	C5'-O5'-PA-O1A
15	5C	501	GTP	C5'-O5'-PA-O2A
15	5E	501	GTP	C5'-O5'-PA-O3A
15	5E	501	GTP	C5'-O5'-PA-O1A
15	5E	501	GTP	C5'-O5'-PA-O2A
15	5G	501	GTP	C5'-O5'-PA-O3A
15	5G	501	GTP	C5'-O5'-PA-O2A
15	5I	501	GTP	C5'-O5'-PA-O3A
15	5I	501	GTP	C5'-O5'-PA-O2A
15	5M	501	GTP	PB-O3A-PA-O5'
15	5M	501	GTP	O4'-C4'-C5'-O5'
15	6A	501	GTP	C5'-O5'-PA-O3A
15	6A	501	GTP	C5'-O5'-PA-O2A
15	6C	501	GTP	C5'-O5'-PA-O3A
15	6C	501	GTP	C5'-O5'-PA-O1A
15	6C	501	GTP	O4'-C4'-C5'-O5'
15	6E	501	GTP	C5'-O5'-PA-O3A
15	6E	501	GTP	C5'-O5'-PA-O1A
15	6E	501	GTP	C5'-O5'-PA-O2A
15	6G	501	GTP	C5'-O5'-PA-O3A
15	6G	501	GTP	C5'-O5'-PA-O2A
15	6K	501	GTP	PB-O3A-PA-O5'
15	6K	501	GTP	C5'-O5'-PA-O3A
15	6K	501	GTP	C5'-O5'-PA-O2A
15	7A	501	GTP	C5'-O5'-PA-O3A
15	7A	501	GTP	C5'-O5'-PA-O2A
15	7C	501	GTP	C5'-O5'-PA-O3A
15	7C	501	GTP	C5'-O5'-PA-O1A
15	7G	501	GTP	PB-O3A-PA-O5'
15	7K	501	GTP	PB-O3A-PA-O5'
15	7K	501	GTP	C5'-O5'-PA-O3A
15	7K	501	GTP	C5'-O5'-PA-O1A
15	7K	501	GTP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
15	7K	501	GTP	O4'-C4'-C5'-O5'
15	7M	501	GTP	C5'-O5'-PA-O3A
15	7M	501	GTP	C5'-O5'-PA-O2A
15	8A	501	GTP	PB-O3A-PA-O5'
15	8C	501	GTP	C5'-O5'-PA-O3A
15	8C	501	GTP	C5'-O5'-PA-O1A
15	8C	501	GTP	C5'-O5'-PA-O2A
15	8E	501	GTP	PB-O3B-PG-O2G
15	8G	501	GTP	C5'-O5'-PA-O3A
15	8G	501	GTP	C5'-O5'-PA-O2A
15	8I	501	GTP	C5'-O5'-PA-O3A
15	8I	501	GTP	C5'-O5'-PA-O2A
15	8K	501	GTP	C5'-O5'-PA-O3A
15	8K	501	GTP	C5'-O5'-PA-O1A
15	8K	501	GTP	C5'-O5'-PA-O2A
15	8K	501	GTP	O4'-C4'-C5'-O5'
15	8M	501	GTP	PB-O3B-PG-O2G
15	9C	501	GTP	C5'-O5'-PA-O3A
15	9C	501	GTP	C5'-O5'-PA-O1A
15	9C	501	GTP	C5'-O5'-PA-O2A
15	9C	501	GTP	O4'-C4'-C5'-O5'
15	9E	501	GTP	PB-O3A-PA-O5'
15	9E	501	GTP	C5'-O5'-PA-O1A
15	9G	501	GTP	C5'-O5'-PA-O3A
15	9G	501	GTP	C5'-O5'-PA-O1A
15	9I	501	GTP	PB-O3B-PG-O2G
15	9I	501	GTP	C5'-O5'-PA-O3A
15	9I	501	GTP	C5'-O5'-PA-O1A
15	9K	501	GTP	C5'-O5'-PA-O3A
15	9K	501	GTP	C5'-O5'-PA-O2A
15	9M	501	GTP	C5'-O5'-PA-O3A
15	9M	501	GTP	C5'-O5'-PA-O1A
15	9M	501	GTP	C5'-O5'-PA-O2A
17	1B	501	GDP	C5'-O5'-PA-O3A
17	1D	501	GDP	C5'-O5'-PA-O3A
17	1D	501	GDP	C5'-O5'-PA-O1A
17	1D	501	GDP	C5'-O5'-PA-O2A
17	1F	501	GDP	C5'-O5'-PA-O3A
17	1F	501	GDP	C5'-O5'-PA-O1A
17	1F	501	GDP	C5'-O5'-PA-O2A
17	1H	501	GDP	C5'-O5'-PA-O3A
17	1H	501	GDP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
17	1H	501	GDP	C5'-O5'-PA-O2A
17	1J	501	GDP	C5'-O5'-PA-O3A
17	1J	501	GDP	C5'-O5'-PA-O1A
17	1J	501	GDP	C5'-O5'-PA-O2A
17	1L	501	GDP	C5'-O5'-PA-O3A
17	1L	501	GDP	C5'-O5'-PA-O1A
17	1L	501	GDP	C5'-O5'-PA-O2A
17	1N	501	GDP	C5'-O5'-PA-O3A
17	1N	501	GDP	C5'-O5'-PA-O2A
17	2B	501	GDP	PA-O3A-PB-O3B
17	2B	501	GDP	C5'-O5'-PA-O3A
17	2B	501	GDP	C5'-O5'-PA-O1A
17	2B	501	GDP	C5'-O5'-PA-O2A
17	2D	501	GDP	C5'-O5'-PA-O3A
17	2D	501	GDP	C5'-O5'-PA-O2A
17	2D	501	GDP	C3'-C4'-C5'-O5'
17	2F	501	GDP	C5'-O5'-PA-O3A
17	2F	501	GDP	C5'-O5'-PA-O2A
17	2H	501	GDP	PA-O3A-PB-O3B
17	2H	501	GDP	C5'-O5'-PA-O3A
17	2H	501	GDP	C5'-O5'-PA-O2A
17	2J	501	GDP	C5'-O5'-PA-O3A
17	2J	501	GDP	C5'-O5'-PA-O1A
17	2J	501	GDP	C5'-O5'-PA-O2A
17	2L	501	GDP	C5'-O5'-PA-O3A
17	2L	501	GDP	C5'-O5'-PA-O1A
17	2L	501	GDP	C5'-O5'-PA-O2A
17	3D	501	GDP	C5'-O5'-PA-O3A
17	3D	501	GDP	C5'-O5'-PA-O1A
17	3D	501	GDP	C5'-O5'-PA-O2A
17	3F	501	GDP	C5'-O5'-PA-O3A
17	3F	501	GDP	C5'-O5'-PA-O2A
17	3H	501	GDP	C5'-O5'-PA-O3A
17	3H	501	GDP	C5'-O5'-PA-O1A
17	3H	501	GDP	C5'-O5'-PA-O2A
17	3J	501	GDP	C5'-O5'-PA-O3A
17	3J	501	GDP	C5'-O5'-PA-O1A
17	3J	501	GDP	C5'-O5'-PA-O2A
17	3L	501	GDP	C5'-O5'-PA-O3A
17	3L	501	GDP	C5'-O5'-PA-O1A
17	3L	501	GDP	C5'-O5'-PA-O2A
17	3L	501	GDP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
17	4B	501	GDP	C5'-O5'-PA-O3A
17	4B	501	GDP	C5'-O5'-PA-O1A
17	4B	501	GDP	C5'-O5'-PA-O2A
17	4D	501	GDP	C5'-O5'-PA-O3A
17	4D	501	GDP	C5'-O5'-PA-O1A
17	4F	501	GDP	C5'-O5'-PA-O3A
17	4F	501	GDP	C5'-O5'-PA-O1A
17	4F	501	GDP	C5'-O5'-PA-O2A
17	4H	501	GDP	C5'-O5'-PA-O3A
17	4H	501	GDP	C5'-O5'-PA-O1A
17	4H	501	GDP	C5'-O5'-PA-O2A
17	4J	501	GDP	C5'-O5'-PA-O3A
17	4J	501	GDP	C5'-O5'-PA-O1A
17	4J	501	GDP	C5'-O5'-PA-O2A
17	4L	501	GDP	C5'-O5'-PA-O3A
17	4L	501	GDP	C5'-O5'-PA-O2A
17	5B	501	GDP	C5'-O5'-PA-O3A
17	5B	501	GDP	C5'-O5'-PA-O1A
17	5B	501	GDP	C5'-O5'-PA-O2A
17	5D	501	GDP	C5'-O5'-PA-O3A
17	5D	501	GDP	C5'-O5'-PA-O1A
17	5F	501	GDP	C5'-O5'-PA-O3A
17	5F	501	GDP	C5'-O5'-PA-O2A
17	5H	501	GDP	C5'-O5'-PA-O3A
17	5H	501	GDP	C5'-O5'-PA-O1A
17	5J	501	GDP	C5'-O5'-PA-O3A
17	5J	501	GDP	C5'-O5'-PA-O1A
17	5J	501	GDP	C5'-O5'-PA-O2A
17	5L	501	GDP	C5'-O5'-PA-O3A
17	5L	501	GDP	C5'-O5'-PA-O1A
17	5L	501	GDP	C5'-O5'-PA-O2A
17	5N	501	GDP	C5'-O5'-PA-O3A
17	5N	501	GDP	C5'-O5'-PA-O1A
17	6B	501	GDP	C5'-O5'-PA-O3A
17	6B	501	GDP	C5'-O5'-PA-O1A
17	6B	501	GDP	C5'-O5'-PA-O2A
17	6D	501	GDP	C5'-O5'-PA-O3A
17	6D	501	GDP	C5'-O5'-PA-O1A
17	6F	501	GDP	C5'-O5'-PA-O3A
17	6F	501	GDP	C5'-O5'-PA-O1A
17	6H	501	GDP	C5'-O5'-PA-O3A
17	6H	501	GDP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
17	6J	501	GDP	C5'-O5'-PA-O3A
17	6J	501	GDP	C5'-O5'-PA-O1A
17	6J	501	GDP	C5'-O5'-PA-O2A
17	6N	502	GDP	C5'-O5'-PA-O3A
17	6N	502	GDP	C5'-O5'-PA-O1A
17	6N	502	GDP	C5'-O5'-PA-O2A
17	7B	502	GDP	C5'-O5'-PA-O3A
17	7B	502	GDP	C5'-O5'-PA-O2A
17	7D	501	GDP	C5'-O5'-PA-O3A
17	7D	501	GDP	C5'-O5'-PA-O1A
17	7F	501	GDP	C5'-O5'-PA-O3A
17	7F	501	GDP	C5'-O5'-PA-O1A
17	7F	501	GDP	C5'-O5'-PA-O2A
17	7H	501	GDP	C5'-O5'-PA-O3A
17	7H	501	GDP	C5'-O5'-PA-O1A
17	7H	501	GDP	C5'-O5'-PA-O2A
17	7J	501	GDP	PA-O3A-PB-O2B
17	7J	501	GDP	PA-O3A-PB-O3B
17	7J	501	GDP	C5'-O5'-PA-O3A
17	7J	501	GDP	C5'-O5'-PA-O2A
17	7L	501	GDP	C5'-O5'-PA-O3A
17	7L	501	GDP	C5'-O5'-PA-O1A
17	8B	501	GDP	C5'-O5'-PA-O3A
17	8B	501	GDP	C5'-O5'-PA-O1A
17	8B	501	GDP	C5'-O5'-PA-O2A
17	8D	501	GDP	C5'-O5'-PA-O3A
17	8D	501	GDP	C5'-O5'-PA-O1A
17	8F	501	GDP	PA-O3A-PB-O3B
17	8F	501	GDP	C5'-O5'-PA-O3A
17	8F	501	GDP	C5'-O5'-PA-O1A
17	8F	501	GDP	C5'-O5'-PA-O2A
17	8H	501	GDP	C5'-O5'-PA-O3A
17	8H	501	GDP	C5'-O5'-PA-O1A
17	8J	501	GDP	C5'-O5'-PA-O3A
17	8J	501	GDP	C5'-O5'-PA-O1A
17	8L	501	GDP	C5'-O5'-PA-O3A
17	8L	501	GDP	C5'-O5'-PA-O1A
17	8L	501	GDP	C5'-O5'-PA-O2A
17	9B	501	GDP	C5'-O5'-PA-O3A
17	9B	501	GDP	C5'-O5'-PA-O2A
17	9F	501	GDP	C5'-O5'-PA-O3A
17	9F	501	GDP	C5'-O5'-PA-O2A

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Mol	Chain	Res	Type	Atoms
17	9H	501	GDP	C5'-O5'-PA-O3A
17	9H	501	GDP	C5'-O5'-PA-O1A
17	9H	501	GDP	C5'-O5'-PA-O2A
17	9J	501	GDP	C5'-O5'-PA-O3A
17	9J	501	GDP	C5'-O5'-PA-O1A
17	9J	501	GDP	C5'-O5'-PA-O2A
15	1C	501	GTP	C3'-C4'-C5'-O5'
15	1K	501	GTP	O4'-C4'-C5'-O5'
15	1K	501	GTP	C3'-C4'-C5'-O5'
15	1M	501	GTP	C3'-C4'-C5'-O5'
15	2C	501	GTP	C3'-C4'-C5'-O5'
15	2K	501	GTP	C3'-C4'-C5'-O5'
15	2M	501	GTP	C3'-C4'-C5'-O5'
15	3A	501	GTP	C3'-C4'-C5'-O5'
15	3G	501	GTP	C3'-C4'-C5'-O5'
15	3I	501	GTP	C3'-C4'-C5'-O5'
15	3K	501	GTP	O4'-C4'-C5'-O5'
15	3K	501	GTP	C3'-C4'-C5'-O5'
15	4I	501	GTP	C3'-C4'-C5'-O5'
15	5M	501	GTP	C3'-C4'-C5'-O5'
15	6C	501	GTP	C3'-C4'-C5'-O5'
15	6E	501	GTP	O4'-C4'-C5'-O5'
15	6E	501	GTP	C3'-C4'-C5'-O5'
15	6I	501	GTP	C3'-C4'-C5'-O5'
15	7C	501	GTP	O4'-C4'-C5'-O5'
15	7C	501	GTP	C3'-C4'-C5'-O5'
15	7I	501	GTP	C3'-C4'-C5'-O5'
15	7K	501	GTP	C3'-C4'-C5'-O5'
15	8I	501	GTP	O4'-C4'-C5'-O5'
15	8I	501	GTP	C3'-C4'-C5'-O5'
15	8K	501	GTP	C3'-C4'-C5'-O5'
15	8M	501	GTP	O4'-C4'-C5'-O5'
15	8M	501	GTP	C3'-C4'-C5'-O5'
15	9C	501	GTP	C3'-C4'-C5'-O5'
15	9M	501	GTP	O4'-C4'-C5'-O5'
15	9M	501	GTP	C3'-C4'-C5'-O5'
17	1B	501	GDP	C3'-C4'-C5'-O5'
17	2H	501	GDP	C3'-C4'-C5'-O5'
17	4L	501	GDP	C3'-C4'-C5'-O5'
17	6F	501	GDP	O4'-C4'-C5'-O5'
17	6F	501	GDP	C3'-C4'-C5'-O5'
17	8L	501	GDP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
15	2E	501	GTP	O4'-C4'-C5'-O5'
15	2E	501	GTP	C3'-C4'-C5'-O5'
15	3E	501	GTP	O4'-C4'-C5'-O5'
15	3E	501	GTP	C3'-C4'-C5'-O5'
15	4G	501	GTP	O4'-C4'-C5'-O5'
15	4M	501	GTP	C3'-C4'-C5'-O5'
15	6I	501	GTP	O4'-C4'-C5'-O5'
15	7G	501	GTP	O4'-C4'-C5'-O5'
15	7G	501	GTP	C3'-C4'-C5'-O5'
15	7I	501	GTP	O4'-C4'-C5'-O5'
17	1B	501	GDP	O4'-C4'-C5'-O5'
17	1J	501	GDP	C3'-C4'-C5'-O5'
17	2D	501	GDP	O4'-C4'-C5'-O5'
17	2L	501	GDP	C3'-C4'-C5'-O5'
17	3B	501	GDP	C3'-C4'-C5'-O5'
17	3J	501	GDP	C3'-C4'-C5'-O5'
17	3L	501	GDP	O4'-C4'-C5'-O5'
17	4L	501	GDP	O4'-C4'-C5'-O5'
15	4G	501	GTP	C3'-C4'-C5'-O5'
15	4M	501	GTP	O4'-C4'-C5'-O5'
15	6G	501	GTP	O4'-C4'-C5'-O5'
15	6G	501	GTP	C3'-C4'-C5'-O5'
15	7A	501	GTP	O4'-C4'-C5'-O5'
17	2B	501	GDP	C4'-C5'-O5'-PA
15	2I	501	GTP	C3'-C4'-C5'-O5'
15	7A	501	GTP	C3'-C4'-C5'-O5'
15	8A	501	GTP	C3'-C4'-C5'-O5'
17	2F	501	GDP	C3'-C4'-C5'-O5'
15	1I	501	GTP	C3'-C4'-C5'-O5'
15	6N	501	GTP	C3'-C4'-C5'-O5'
15	8C	501	GTP	C3'-C4'-C5'-O5'
17	1D	501	GDP	C3'-C4'-C5'-O5'
17	1F	501	GDP	C3'-C4'-C5'-O5'
17	1J	501	GDP	O4'-C4'-C5'-O5'
17	3J	501	GDP	O4'-C4'-C5'-O5'
17	6D	501	GDP	C3'-C4'-C5'-O5'
17	8L	501	GDP	O4'-C4'-C5'-O5'
15	1E	501	GTP	C3'-C4'-C5'-O5'
15	2G	501	GTP	C3'-C4'-C5'-O5'
15	4K	501	GTP	C3'-C4'-C5'-O5'
15	8A	501	GTP	O4'-C4'-C5'-O5'
15	9I	501	GTP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
17	2F	501	GDP	O4'-C4'-C5'-O5'
17	2L	501	GDP	O4'-C4'-C5'-O5'
17	2H	501	GDP	PA-O3A-PB-O1B
17	5H	501	GDP	PA-O3A-PB-O1B
17	6B	501	GDP	PA-O3A-PB-O1B
17	7B	502	GDP	PA-O3A-PB-O1B
17	7F	501	GDP	PA-O3A-PB-O1B
15	7M	501	GTP	C3'-C4'-C5'-O5'
15	9A	501	GTP	C3'-C4'-C5'-O5'
15	9G	501	GTP	C3'-C4'-C5'-O5'
17	2H	501	GDP	O4'-C4'-C5'-O5'
17	4H	501	GDP	C3'-C4'-C5'-O5'
17	8B	501	GDP	C3'-C4'-C5'-O5'
15	1G	501	GTP	PA-O3A-PB-O1B
15	3A	501	GTP	PB-O3A-PA-O1A
15	4E	501	GTP	PB-O3A-PA-O1A
15	8I	501	GTP	PB-O3A-PA-O1A
17	2H	501	GDP	C4'-C5'-O5'-PA
15	2I	501	GTP	O4'-C4'-C5'-O5'
15	9E	501	GTP	PG-O3B-PB-O3A
15	1A	501	GTP	C4'-C5'-O5'-PA
15	9K	501	GTP	C4'-C5'-O5'-PA
15	8C	501	GTP	O4'-C4'-C5'-O5'
15	1A	501	GTP	PB-O3A-PA-O5'
15	1G	501	GTP	PB-O3A-PA-O5'
15	1I	501	GTP	PB-O3A-PA-O5'
15	1K	501	GTP	PB-O3A-PA-O5'
15	1M	501	GTP	PB-O3A-PA-O5'
15	2A	501	GTP	PB-O3A-PA-O5'
15	2K	501	GTP	PB-O3A-PA-O5'
15	2M	501	GTP	PB-O3A-PA-O5'
15	3E	501	GTP	PB-O3A-PA-O5'
15	4A	501	GTP	PB-O3A-PA-O5'
15	4I	501	GTP	PB-O3A-PA-O5'
15	5K	501	GTP	PB-O3A-PA-O5'
15	6G	501	GTP	PB-O3A-PA-O5'
15	6I	501	GTP	PB-O3A-PA-O5'
15	6N	501	GTP	PB-O3A-PA-O5'
15	7E	501	GTP	PB-O3A-PA-O5'
15	7I	501	GTP	PB-O3A-PA-O5'
15	7M	501	GTP	PB-O3A-PA-O5'
15	8E	501	GTP	PB-O3A-PA-O5'

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Mol	Chain	Res	Type	Atoms
15	8G	501	GTP	PB-O3A-PA-O5'
15	8I	501	GTP	PB-O3A-PA-O5'
15	8M	501	GTP	PB-O3A-PA-O5'
15	9A	501	GTP	PB-O3A-PA-O5'
15	9G	501	GTP	PB-O3A-PA-O5'
15	9I	501	GTP	PB-O3A-PA-O5'
15	1I	501	GTP	O4'-C4'-C5'-O5'
15	6I	501	GTP	PB-O3B-PG-O1G
15	9G	501	GTP	PB-O3B-PG-O1G
15	3G	501	GTP	PB-O3B-PG-O2G
15	6G	501	GTP	PB-O3B-PG-O2G
15	9A	501	GTP	PB-O3B-PG-O2G
17	7F	501	GDP	PA-O3A-PB-O3B
15	4K	501	GTP	O4'-C4'-C5'-O5'
15	5K	501	GTP	C3'-C4'-C5'-O5'
15	6N	501	GTP	O4'-C4'-C5'-O5'
15	9I	501	GTP	O4'-C4'-C5'-O5'
15	3E	501	GTP	C4'-C5'-O5'-PA
15	4E	501	GTP	C4'-C5'-O5'-PA
15	5C	501	GTP	C4'-C5'-O5'-PA
15	1I	501	GTP	PA-O3A-PB-O2B
15	1M	501	GTP	PA-O3A-PB-O2B
15	2I	501	GTP	PA-O3A-PB-O2B
15	2M	501	GTP	PA-O3A-PB-O2B
15	3E	501	GTP	PA-O3A-PB-O2B
15	4K	501	GTP	PA-O3A-PB-O2B
15	6A	501	GTP	PA-O3A-PB-O2B
15	6K	501	GTP	PA-O3A-PB-O2B
17	6H	501	GDP	PB-O3A-PA-O2A
17	6J	501	GDP	PB-O3A-PA-O2A
17	8H	501	GDP	PB-O3A-PA-O1A
15	1E	501	GTP	O4'-C4'-C5'-O5'
15	2G	501	GTP	O4'-C4'-C5'-O5'
15	3C	501	GTP	C3'-C4'-C5'-O5'
15	4E	501	GTP	C3'-C4'-C5'-O5'
15	5I	501	GTP	C3'-C4'-C5'-O5'
15	6K	501	GTP	C3'-C4'-C5'-O5'
15	1I	501	GTP	C4'-C5'-O5'-PA
15	2C	501	GTP	C4'-C5'-O5'-PA
15	2I	501	GTP	C4'-C5'-O5'-PA
15	2K	501	GTP	C4'-C5'-O5'-PA
15	3I	501	GTP	C4'-C5'-O5'-PA

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Mol	Chain	Res	Type	Atoms
15	3M	501	GTP	C4'-C5'-O5'-PA
15	4C	501	GTP	C4'-C5'-O5'-PA
15	4K	501	GTP	C4'-C5'-O5'-PA
15	4M	501	GTP	C4'-C5'-O5'-PA
15	5I	501	GTP	C4'-C5'-O5'-PA
15	6A	501	GTP	C4'-C5'-O5'-PA
15	6K	501	GTP	C4'-C5'-O5'-PA
15	7A	501	GTP	C4'-C5'-O5'-PA
15	8C	501	GTP	C4'-C5'-O5'-PA
15	8I	501	GTP	C4'-C5'-O5'-PA
15	8K	501	GTP	C4'-C5'-O5'-PA
15	9C	501	GTP	C4'-C5'-O5'-PA
15	7M	501	GTP	O4'-C4'-C5'-O5'
15	9A	501	GTP	O4'-C4'-C5'-O5'
17	1H	501	GDP	C3'-C4'-C5'-O5'
17	3B	501	GDP	O4'-C4'-C5'-O5'
17	8B	501	GDP	O4'-C4'-C5'-O5'
15	1C	501	GTP	C5'-O5'-PA-O1A
15	2A	501	GTP	C5'-O5'-PA-O1A
15	2C	501	GTP	C5'-O5'-PA-O2A
15	2E	501	GTP	C5'-O5'-PA-O1A
15	3I	501	GTP	C5'-O5'-PA-O2A
15	3M	501	GTP	C5'-O5'-PA-O2A
15	4A	501	GTP	C5'-O5'-PA-O1A
15	6C	501	GTP	C5'-O5'-PA-O2A
15	7C	501	GTP	C5'-O5'-PA-O2A
15	7E	501	GTP	C5'-O5'-PA-O1A
15	8E	501	GTP	C5'-O5'-PA-O1A
17	1B	501	GDP	C5'-O5'-PA-O2A
17	4D	501	GDP	C5'-O5'-PA-O2A
17	5D	501	GDP	C5'-O5'-PA-O2A
17	5H	501	GDP	C5'-O5'-PA-O2A
17	5N	501	GDP	C5'-O5'-PA-O2A
17	6D	501	GDP	C5'-O5'-PA-O2A
17	6F	501	GDP	C5'-O5'-PA-O2A
17	6H	501	GDP	C5'-O5'-PA-O2A
17	7D	501	GDP	C5'-O5'-PA-O2A
17	7L	501	GDP	C5'-O5'-PA-O2A
17	8D	501	GDP	C5'-O5'-PA-O2A
17	8H	501	GDP	C5'-O5'-PA-O2A
17	8J	501	GDP	C5'-O5'-PA-O2A
15	1E	501	GTP	C4'-C5'-O5'-PA

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Mol	Chain	Res	Type	Atoms
15	1G	501	GTP	C4'-C5'-O5'-PA
15	1K	501	GTP	C4'-C5'-O5'-PA
15	1M	501	GTP	C4'-C5'-O5'-PA
15	2G	501	GTP	C4'-C5'-O5'-PA
15	2M	501	GTP	C4'-C5'-O5'-PA
15	3A	501	GTP	C4'-C5'-O5'-PA
15	3C	501	GTP	C4'-C5'-O5'-PA
15	3K	501	GTP	C4'-C5'-O5'-PA
15	4A	501	GTP	C4'-C5'-O5'-PA
15	4G	501	GTP	C4'-C5'-O5'-PA
15	5A	501	GTP	C4'-C5'-O5'-PA
15	5E	501	GTP	C4'-C5'-O5'-PA
15	5G	501	GTP	C4'-C5'-O5'-PA
15	5M	501	GTP	C4'-C5'-O5'-PA
15	6C	501	GTP	C4'-C5'-O5'-PA
15	6E	501	GTP	C4'-C5'-O5'-PA
15	6G	501	GTP	C4'-C5'-O5'-PA
15	7C	501	GTP	C4'-C5'-O5'-PA
15	7I	501	GTP	C4'-C5'-O5'-PA
15	7K	501	GTP	C4'-C5'-O5'-PA
15	7M	501	GTP	C4'-C5'-O5'-PA
15	8G	501	GTP	C4'-C5'-O5'-PA
15	9I	501	GTP	C4'-C5'-O5'-PA
15	9M	501	GTP	C4'-C5'-O5'-PA
17	3B	501	GDP	C4'-C5'-O5'-PA
17	5L	501	GDP	C4'-C5'-O5'-PA
17	7J	501	GDP	C4'-C5'-O5'-PA
17	8L	501	GDP	C4'-C5'-O5'-PA
17	9B	501	GDP	C4'-C5'-O5'-PA
15	5M	501	GTP	PB-O3B-PG-O1G
17	1F	501	GDP	O4'-C4'-C5'-O5'
15	2E	501	GTP	PA-O3A-PB-O1B
15	4C	501	GTP	PB-O3A-PA-O1A
15	5A	501	GTP	PA-O3A-PB-O2B
15	5E	501	GTP	PA-O3A-PB-O2B
15	6G	501	GTP	PA-O3A-PB-O1B
15	7M	501	GTP	PA-O3A-PB-O1B
15	9K	501	GTP	PB-O3A-PA-O2A
15	9M	501	GTP	PA-O3A-PB-O2B
17	1J	501	GDP	PB-O3A-PA-O2A
17	2H	501	GDP	PB-O3A-PA-O1A
17	5H	501	GDP	PB-O3A-PA-O1A

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Mol	Chain	Res	Type	Atoms
17	5L	501	GDP	PB-O3A-PA-O2A
17	6D	501	GDP	PB-O3A-PA-O2A
17	6L	501	GDP	PB-O3A-PA-O2A
17	7B	502	GDP	PB-O3A-PA-O2A
17	8B	501	GDP	PB-O3A-PA-O2A
15	5K	501	GTP	C4'-C5'-O5'-PA
15	9E	501	GTP	C4'-C5'-O5'-PA
15	8G	501	GTP	C3'-C4'-C5'-O5'
15	9G	501	GTP	O4'-C4'-C5'-O5'
17	1D	501	GDP	O4'-C4'-C5'-O5'
15	6N	501	GTP	C4'-C5'-O5'-PA
15	7E	501	GTP	C4'-C5'-O5'-PA
15	8M	501	GTP	C4'-C5'-O5'-PA
15	9A	501	GTP	C4'-C5'-O5'-PA
17	5B	501	GDP	C4'-C5'-O5'-PA
17	7B	502	GDP	C4'-C5'-O5'-PA
17	8F	501	GDP	PA-O3A-PB-O1B
17	5H	501	GDP	C4'-C5'-O5'-PA
17	6B	501	GDP	C4'-C5'-O5'-PA
15	5A	501	GTP	C3'-C4'-C5'-O5'
15	2G	501	GTP	PB-O3A-PA-O1A
15	4C	501	GTP	PB-O3A-PA-O2A
17	1H	501	GDP	PB-O3A-PA-O2A
17	1N	501	GDP	PB-O3A-PA-O2A
17	3F	501	GDP	PB-O3A-PA-O2A
17	4B	501	GDP	PB-O3A-PA-O2A
17	4J	501	GDP	PB-O3A-PA-O2A
17	5H	501	GDP	PB-O3A-PA-O2A
17	5L	501	GDP	PB-O3A-PA-O1A
17	6L	501	GDP	PB-O3A-PA-O1A
17	6N	502	GDP	PB-O3A-PA-O1A
17	6N	502	GDP	PB-O3A-PA-O2A
17	7B	502	GDP	PB-O3A-PA-O1A
15	3A	501	GTP	PB-O3A-PA-O5'
15	5I	501	GTP	PB-O3A-PA-O5'
15	1C	501	GTP	C4'-C5'-O5'-PA
15	7G	501	GTP	C4'-C5'-O5'-PA
15	8A	501	GTP	C4'-C5'-O5'-PA
15	8E	501	GTP	C4'-C5'-O5'-PA
17	5F	501	GDP	C4'-C5'-O5'-PA
15	8G	501	GTP	PG-O3B-PB-O3A
15	4E	501	GTP	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
15	5K	501	GTP	O4'-C4'-C5'-O5'
15	4I	501	GTP	C4'-C5'-O5'-PA
15	6I	501	GTP	C4'-C5'-O5'-PA
17	9D	501	GDP	C4'-C5'-O5'-PA
15	3C	501	GTP	O4'-C4'-C5'-O5'
17	5L	501	GDP	C3'-C4'-C5'-O5'
15	1K	501	GTP	PB-O3B-PG-O1G
17	1N	501	GDP	PA-O3A-PB-O1B
17	7J	501	GDP	PA-O3A-PB-O1B
15	1K	501	GTP	PB-O3B-PG-O2G
15	2G	501	GTP	PB-O3B-PG-O2G
15	4K	501	GTP	PB-O3B-PG-O2G
15	5M	501	GTP	PB-O3B-PG-O2G
15	5M	501	GTP	PB-O3B-PG-O3G
15	6I	501	GTP	PB-O3B-PG-O2G
15	6I	501	GTP	PB-O3B-PG-O3G
15	9G	501	GTP	PB-O3B-PG-O2G
15	9G	501	GTP	PB-O3B-PG-O3G
17	2B	501	GDP	PA-O3A-PB-O2B
15	2E	501	GTP	C4'-C5'-O5'-PA
15	9G	501	GTP	C4'-C5'-O5'-PA
15	5I	501	GTP	O4'-C4'-C5'-O5'
15	6K	501	GTP	O4'-C4'-C5'-O5'
15	7E	501	GTP	C3'-C4'-C5'-O5'
17	3F	501	GDP	C3'-C4'-C5'-O5'
15	1G	501	GTP	PA-O3A-PB-O2B
15	1I	501	GTP	PA-O3A-PB-O1B
15	1K	501	GTP	PB-O3A-PA-O1A
15	2A	501	GTP	PB-O3A-PA-O2A
15	3E	501	GTP	PA-O3A-PB-O1B
15	4E	501	GTP	PB-O3A-PA-O2A
15	4M	501	GTP	PA-O3A-PB-O2B
15	5C	501	GTP	PA-O3A-PB-O2B
15	5E	501	GTP	PA-O3A-PB-O1B
15	5G	501	GTP	PA-O3A-PB-O1B
15	5G	501	GTP	PA-O3A-PB-O2B
15	5I	501	GTP	PA-O3A-PB-O2B
15	5K	501	GTP	PB-O3A-PA-O2A
15	6A	501	GTP	PA-O3A-PB-O1B
15	6G	501	GTP	PA-O3A-PB-O2B
15	7A	501	GTP	PA-O3A-PB-O2B
15	7M	501	GTP	PA-O3A-PB-O2B

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Mol	Chain	Res	Type	Atoms
15	8A	501	GTP	PB-O3A-PA-O1A
15	8G	501	GTP	PG-O3B-PB-O2B
15	9E	501	GTP	PB-O3A-PA-O1A
15	9K	501	GTP	PA-O3A-PB-O1B
15	9K	501	GTP	PA-O3A-PB-O2B
15	9K	501	GTP	PB-O3A-PA-O1A
17	1H	501	GDP	PB-O3A-PA-O1A
17	1J	501	GDP	PB-O3A-PA-O1A
17	1L	501	GDP	PB-O3A-PA-O2A
17	1N	501	GDP	PB-O3A-PA-O1A
17	2H	501	GDP	PB-O3A-PA-O2A
17	3F	501	GDP	PB-O3A-PA-O1A
17	4D	501	GDP	PB-O3A-PA-O2A
17	4F	501	GDP	PB-O3A-PA-O2A
17	6D	501	GDP	PB-O3A-PA-O1A
17	6F	501	GDP	PB-O3A-PA-O1A
17	6F	501	GDP	PB-O3A-PA-O2A
17	8B	501	GDP	PB-O3A-PA-O1A
17	8L	501	GDP	PB-O3A-PA-O2A
17	9H	501	GDP	PB-O3A-PA-O2A
15	8E	501	GTP	C3'-C4'-C5'-O5'
17	5J	501	GDP	C4'-C5'-O5'-PA
15	8G	501	GTP	O4'-C4'-C5'-O5'
17	9H	501	GDP	C3'-C4'-C5'-O5'
17	1N	501	GDP	C4'-C5'-O5'-PA
15	1A	501	GTP	PB-O3A-PA-O2A
15	1E	501	GTP	PA-O3A-PB-O2B
15	4G	501	GTP	PA-O3A-PB-O2B
15	4I	501	GTP	PB-O3A-PA-O1A
15	4I	501	GTP	PB-O3A-PA-O2A
15	5A	501	GTP	PA-O3A-PB-O1B
15	5I	501	GTP	PA-O3A-PB-O1B
15	5M	501	GTP	PB-O3A-PA-O1A
15	5M	501	GTP	PB-O3A-PA-O2A
15	6E	501	GTP	PA-O3A-PB-O2B
15	6N	501	GTP	PG-O3B-PB-O2B
15	7I	501	GTP	PB-O3A-PA-O2A
15	8E	501	GTP	PB-O3A-PA-O2A
15	8G	501	GTP	PG-O3B-PB-O1B
15	9A	501	GTP	PB-O3A-PA-O2A
15	9C	501	GTP	PG-O3B-PB-O2B
15	9E	501	GTP	PG-O3B-PB-O2B

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Mol	Chain	Res	Type	Atoms
15	9E	501	GTP	PB-O3A-PA-O2A
15	9M	501	GTP	PA-O3A-PB-O1B
17	1L	501	GDP	PB-O3A-PA-O1A
17	2F	501	GDP	PB-O3A-PA-O2A
17	4J	501	GDP	PB-O3A-PA-O1A
17	8L	501	GDP	PB-O3A-PA-O1A
15	6A	501	GTP	C3'-C4'-C5'-O5'

There are no ring outliers.

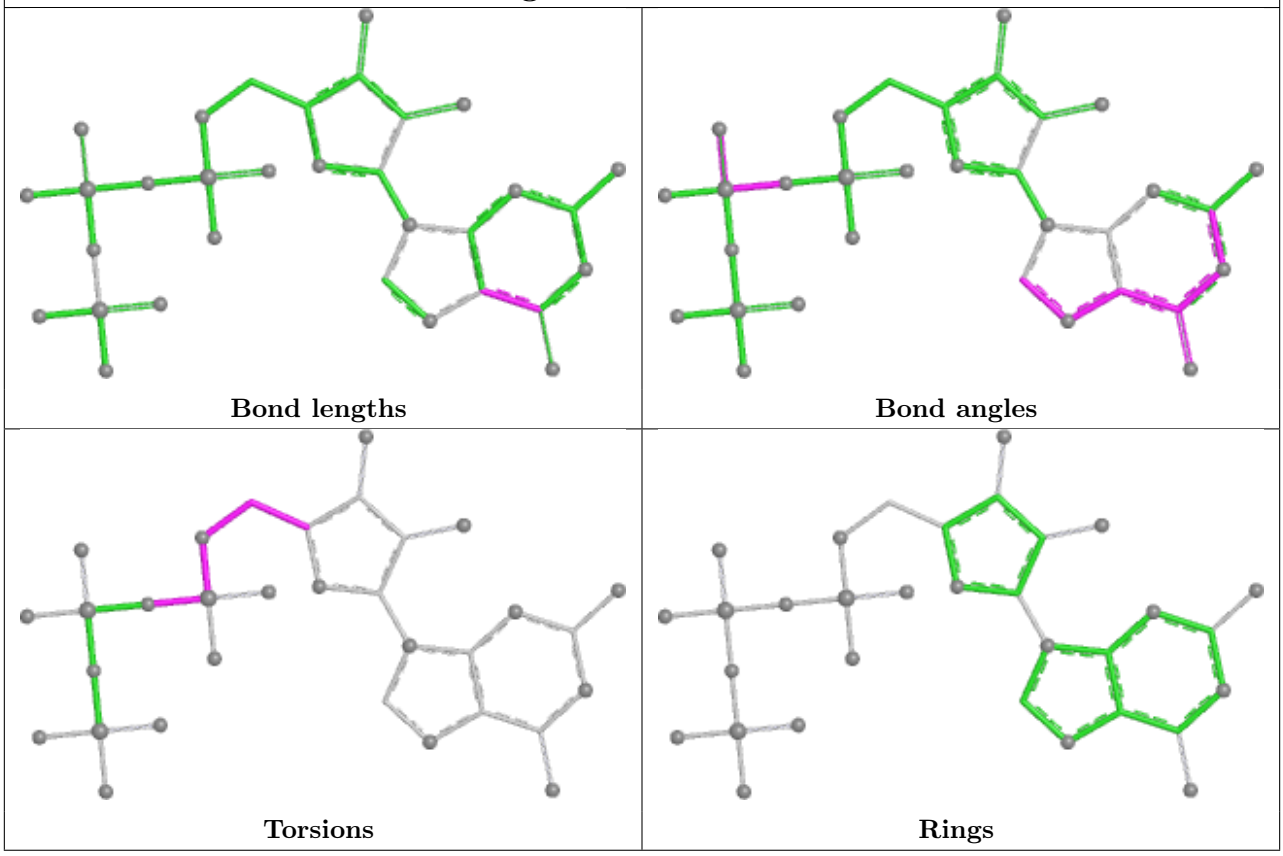
23 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	4B	501	GDP	1	0
17	6N	502	GDP	1	0
17	3J	501	GDP	2	0
17	4D	501	GDP	1	0
15	9K	501	GTP	1	0
17	8B	501	GDP	1	0
17	2F	501	GDP	1	0
17	3B	501	GDP	2	0
15	2A	501	GTP	2	0
17	1B	501	GDP	1	0
17	1F	501	GDP	1	0
17	4J	501	GDP	1	0
17	9L	501	GDP	1	0
15	1A	501	GTP	1	0
17	2B	501	GDP	2	0
17	1D	501	GDP	2	0
17	3L	501	GDP	2	0
17	5L	501	GDP	2	0
15	6C	501	GTP	1	0
17	3F	501	GDP	1	0
15	2C	501	GTP	1	0
17	2L	501	GDP	1	0
17	2H	501	GDP	2	0

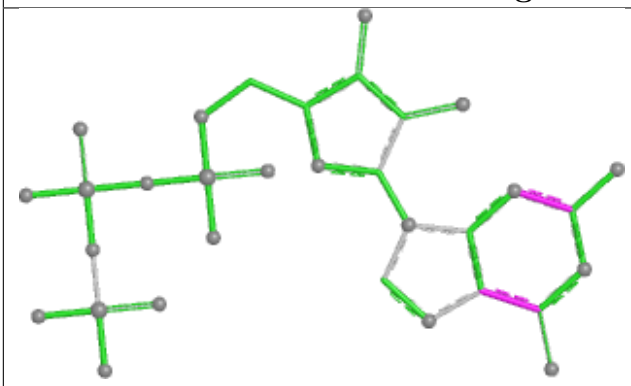
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

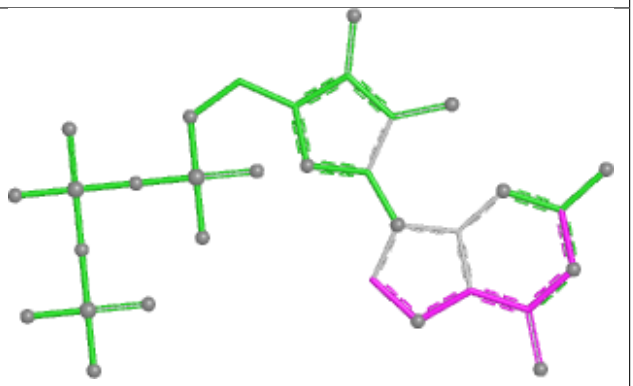
Ligand GTP 4I 501



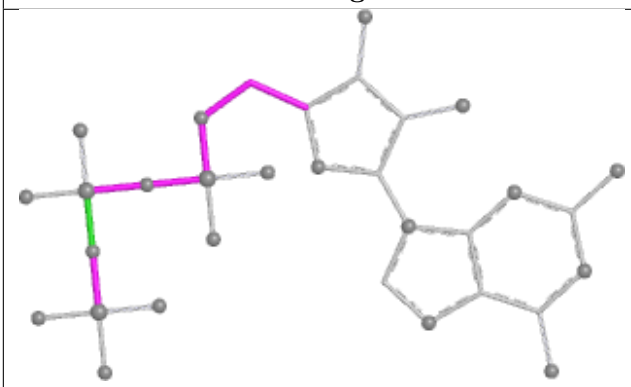
Ligand GTP 3E 501



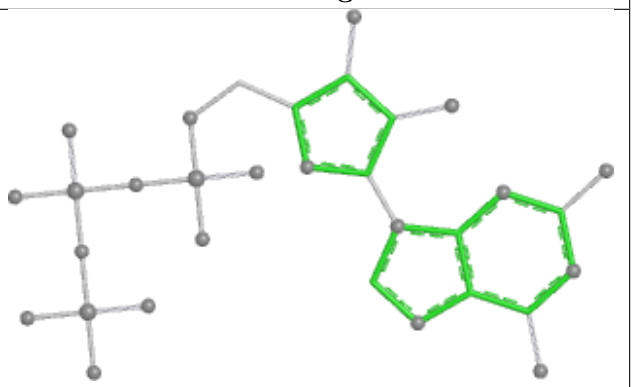
Bond lengths



Bond angles

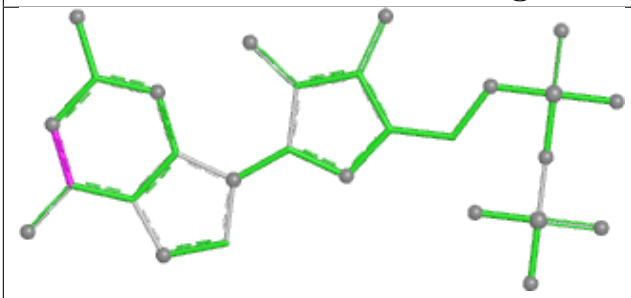


Torsions

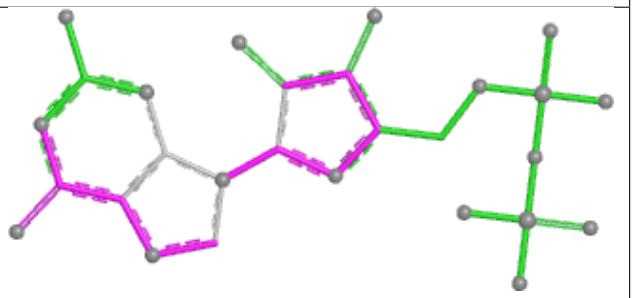


Rings

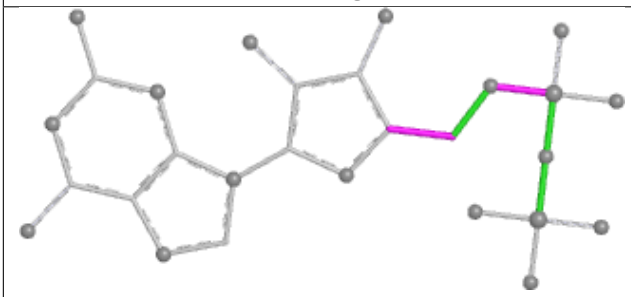
Ligand GDP 4H 501



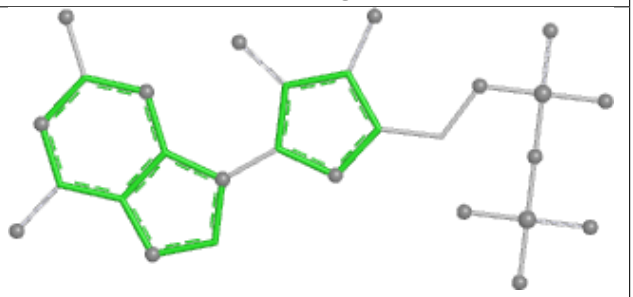
Bond lengths



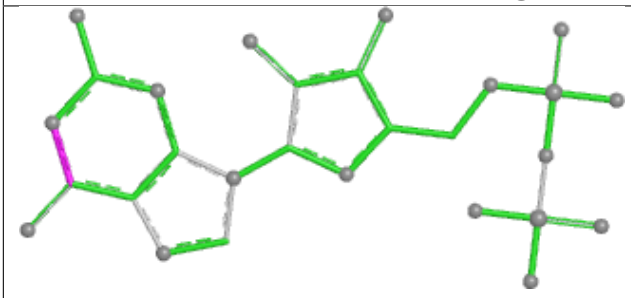
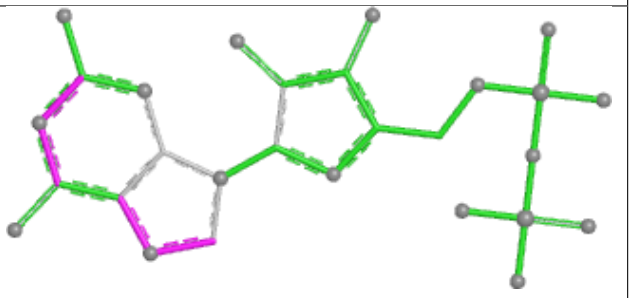
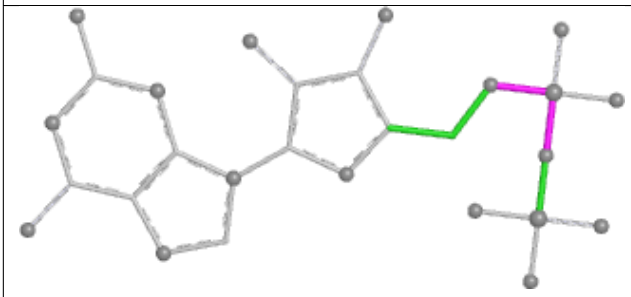
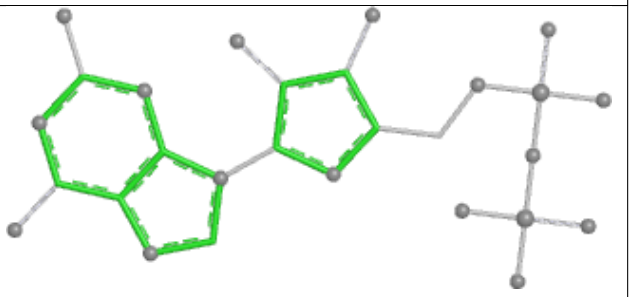
Bond angles



Torsions



Rings

Ligand GDP 4B 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

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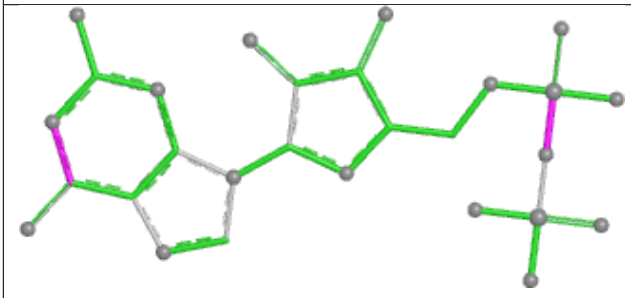
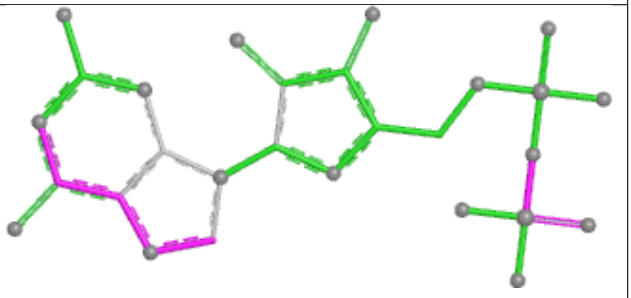
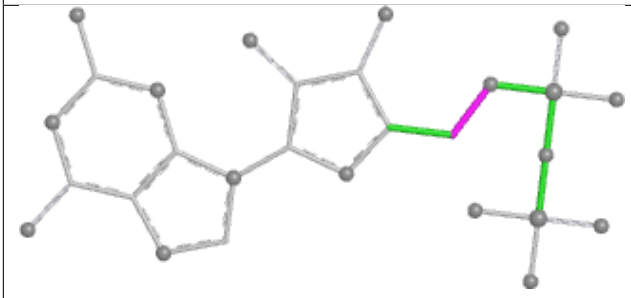
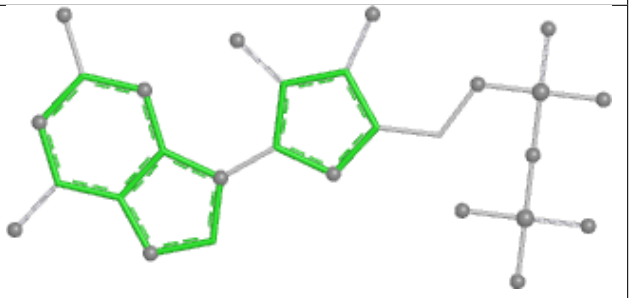
 Bond lengths	 Bond angles
 Torsions	 Rings

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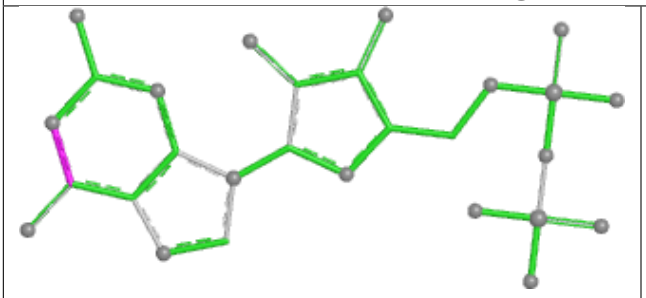

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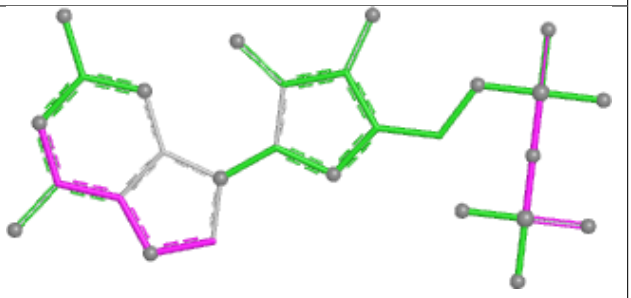

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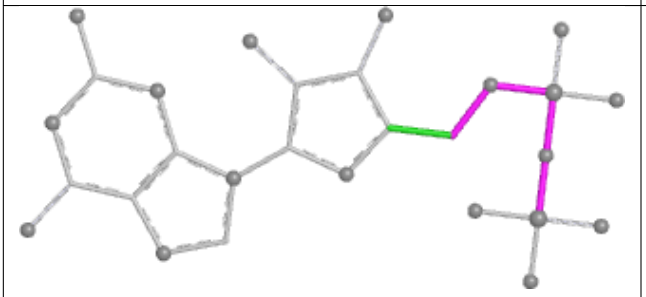

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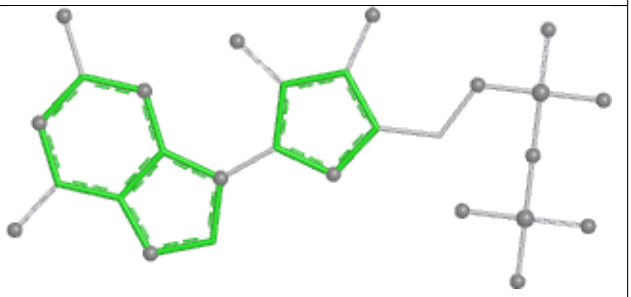
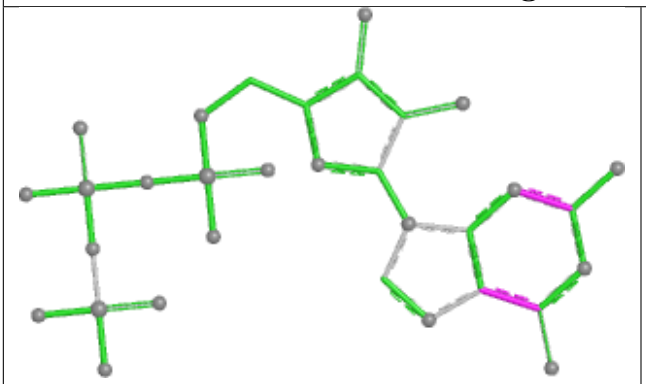


Rings

Ligand GTP 1I 501



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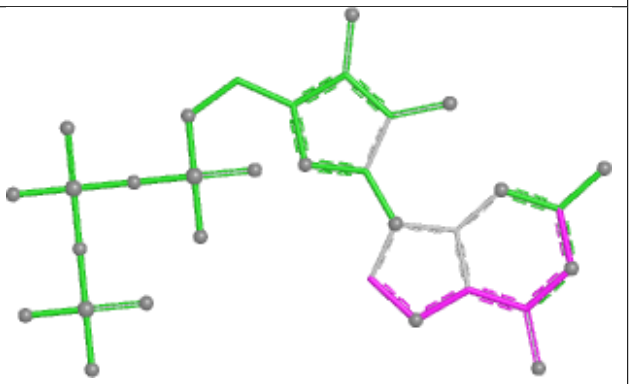

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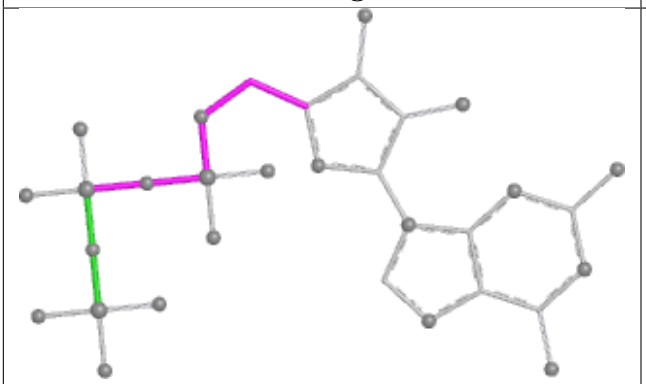

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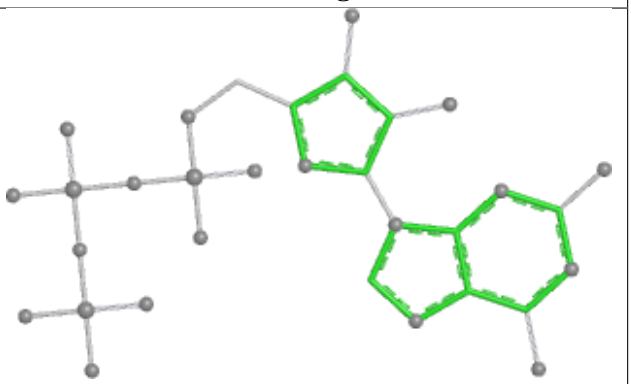
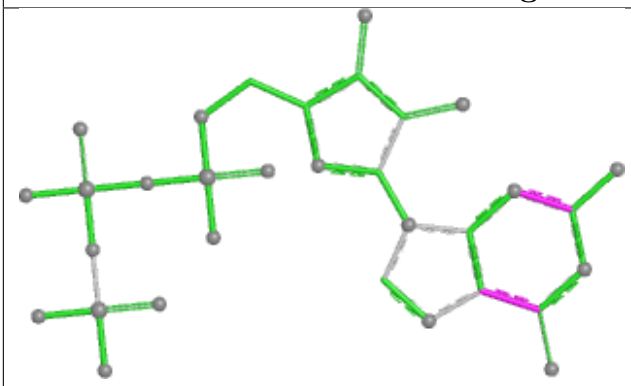


Rings

Ligand GTP 6I 501



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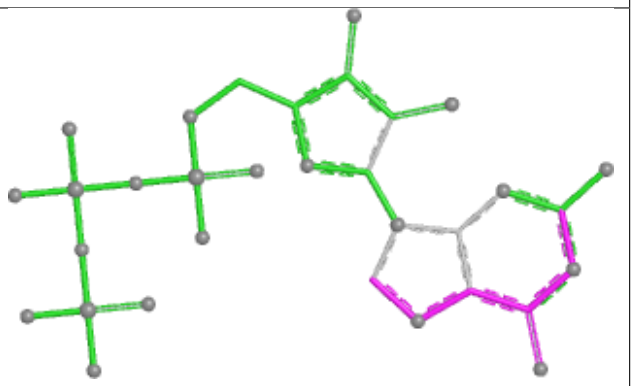

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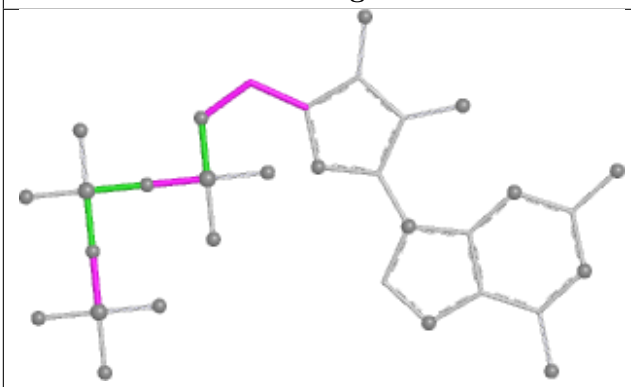

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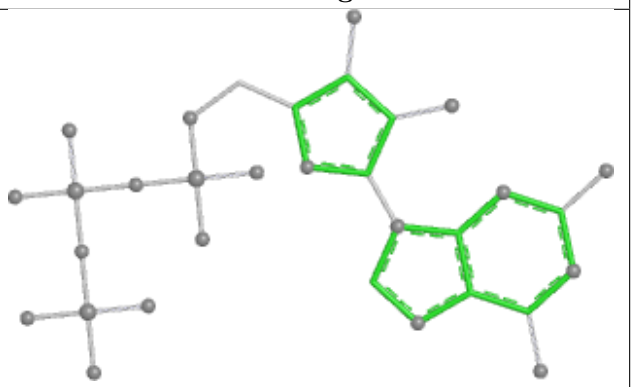
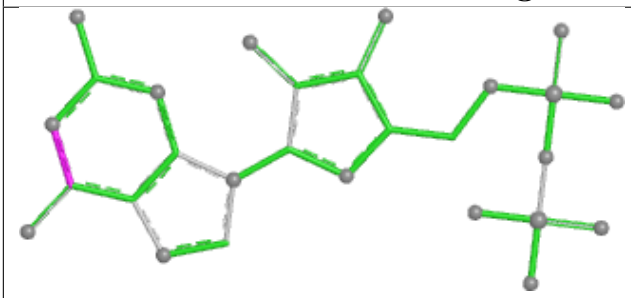


Rings

Ligand GDP 5J 501



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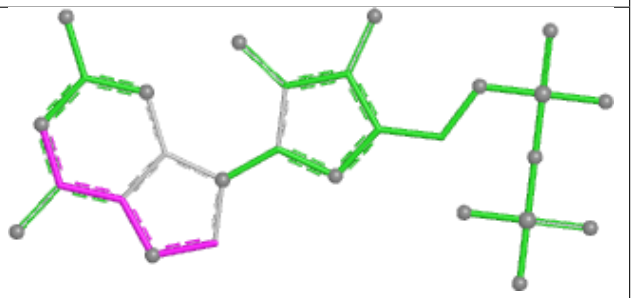

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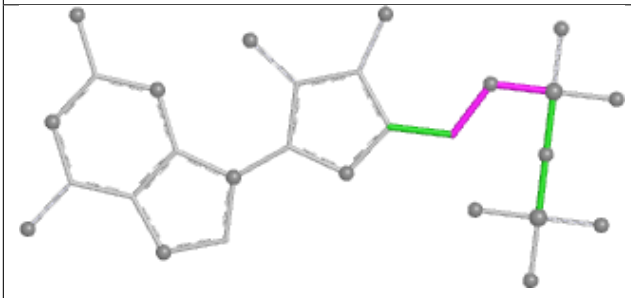

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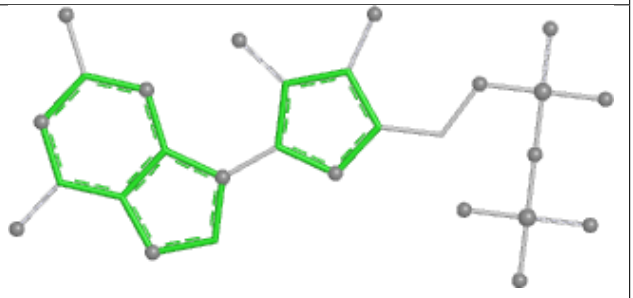

Rings

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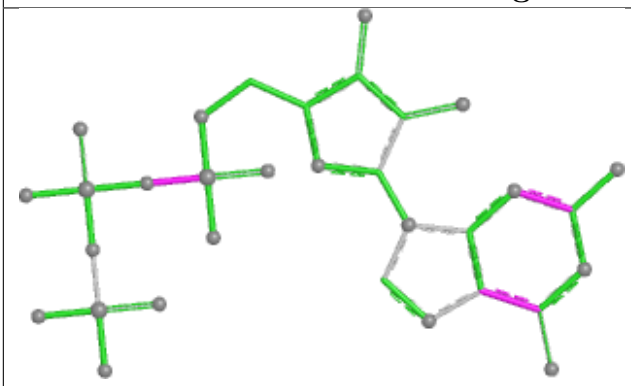

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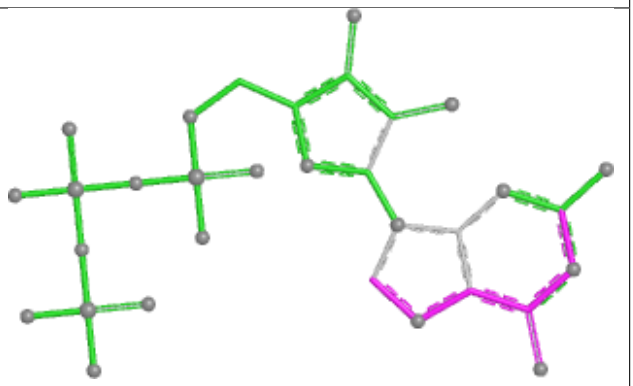

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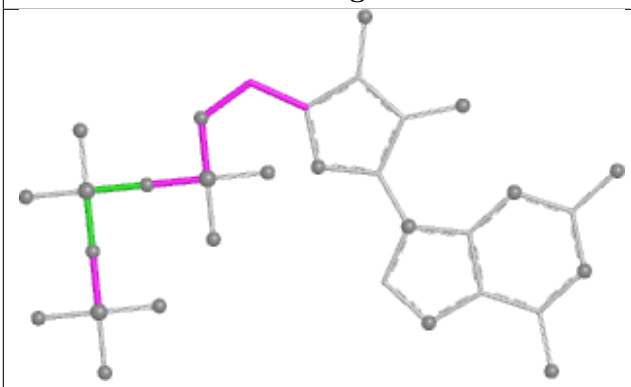

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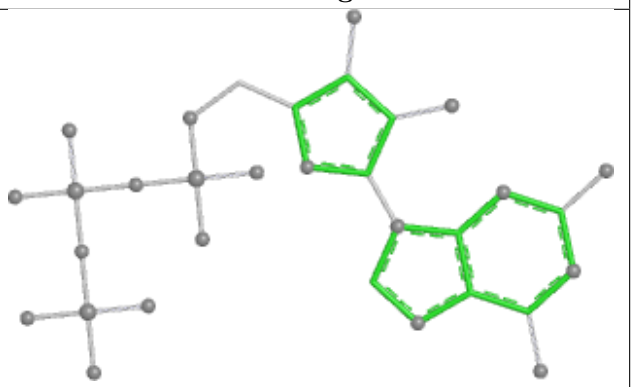

Rings

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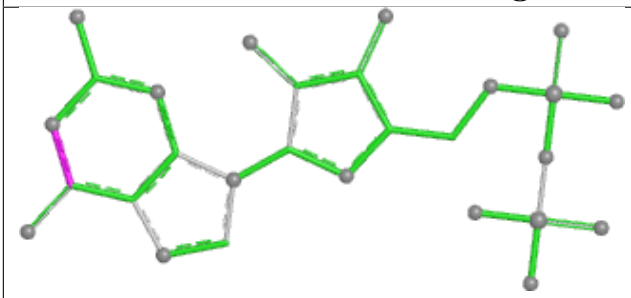

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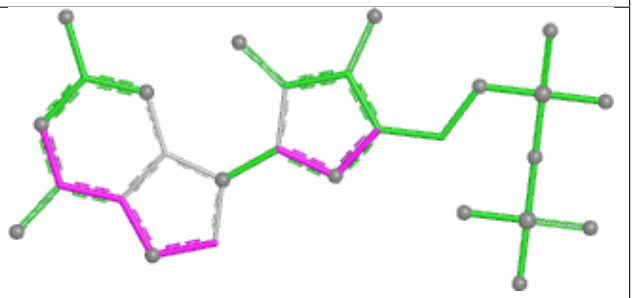

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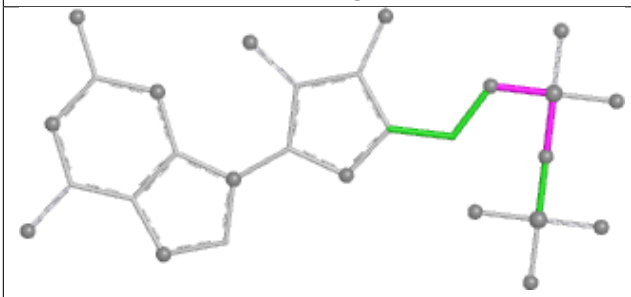

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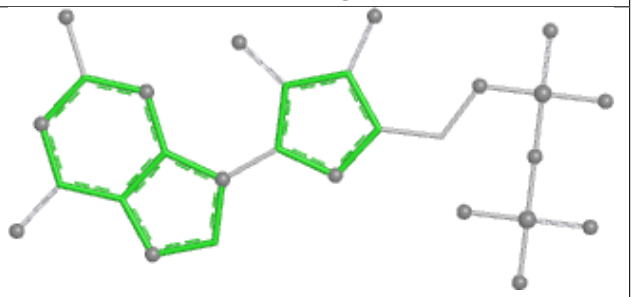

Rings

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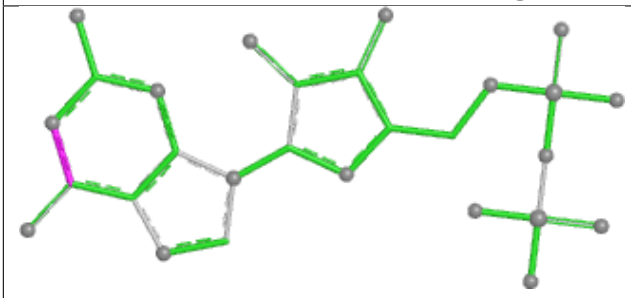
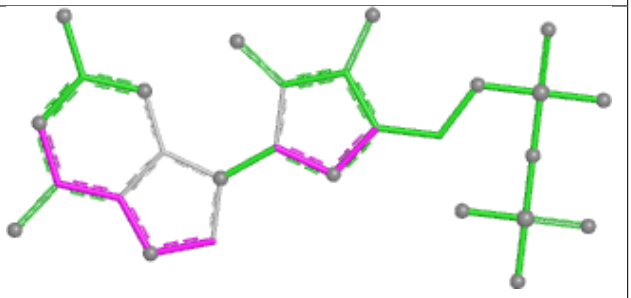
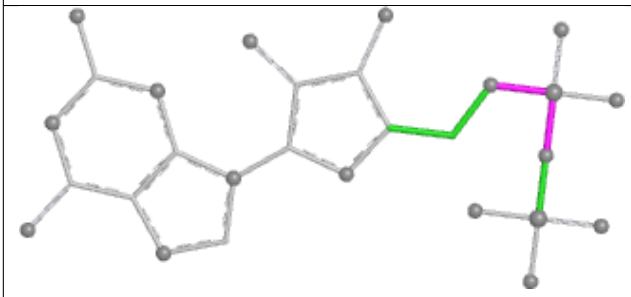
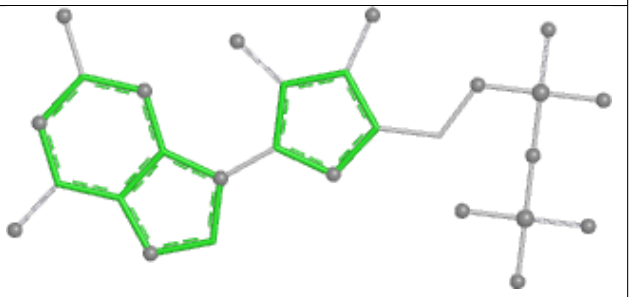
 Bond lengths	 Bond angles
 Torsions	 Rings

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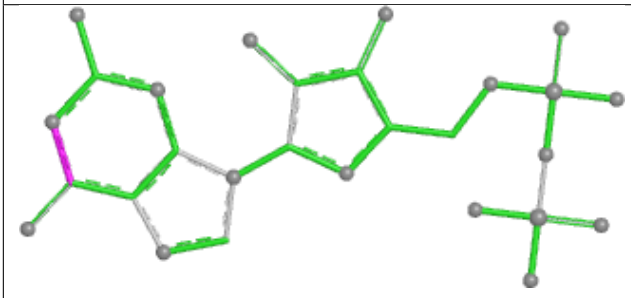
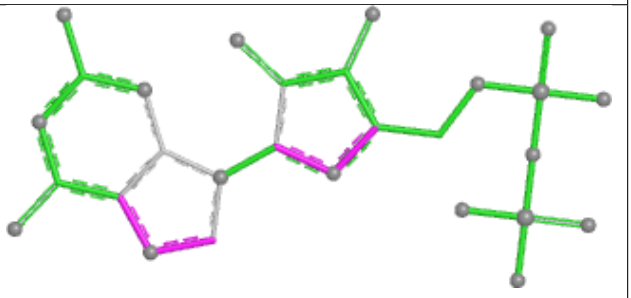
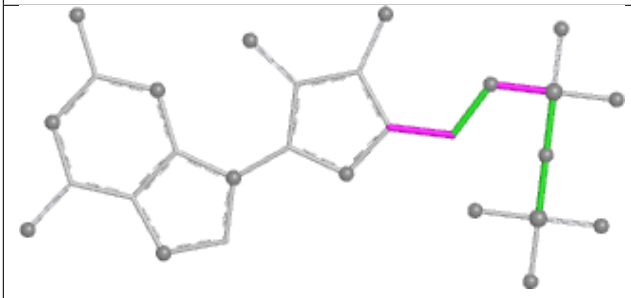
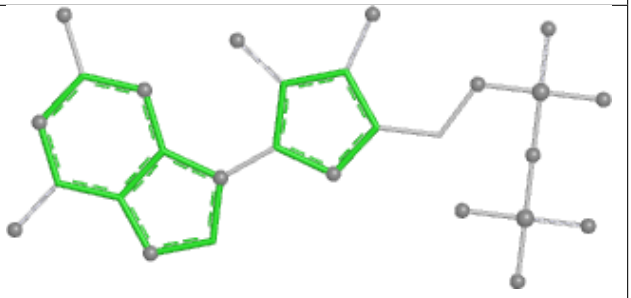
 Bond lengths	 Bond angles
 Torsions	 Rings

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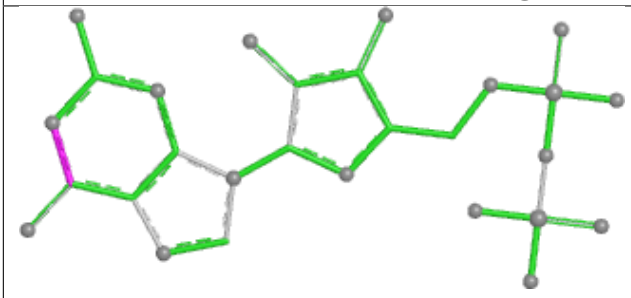
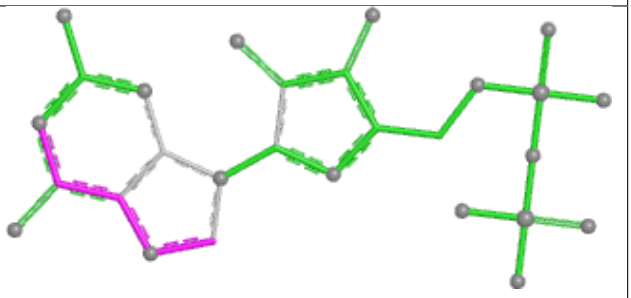
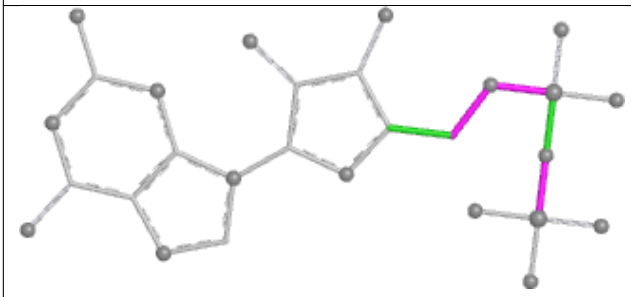
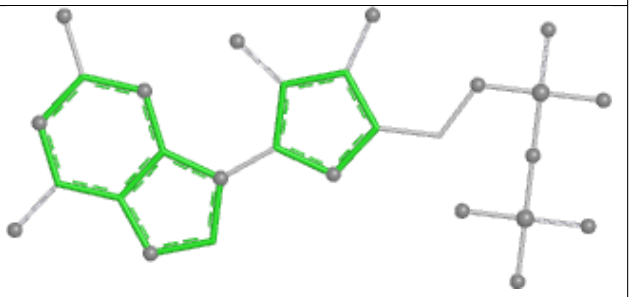
 Bond lengths	 Bond angles
 Torsions	 Rings

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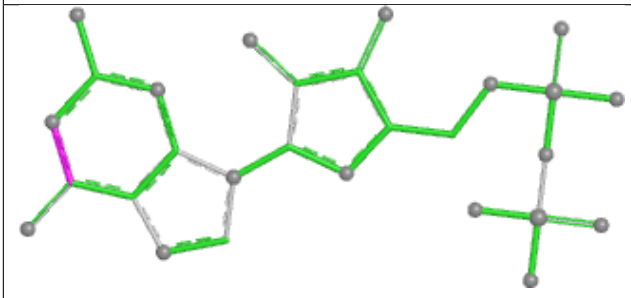
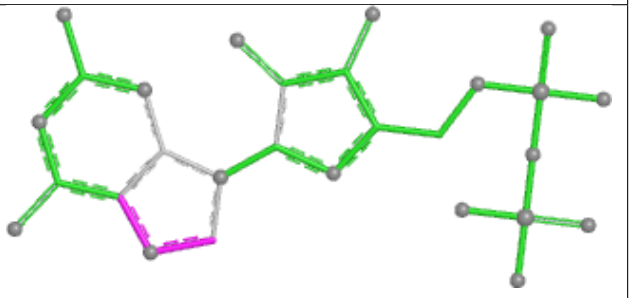
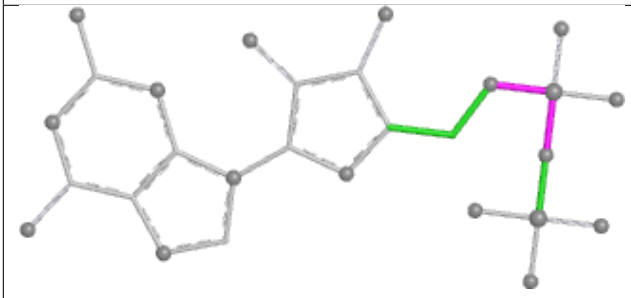
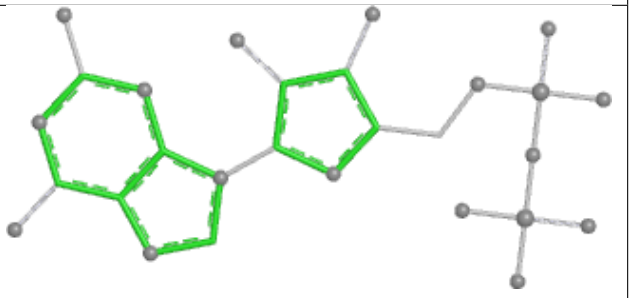
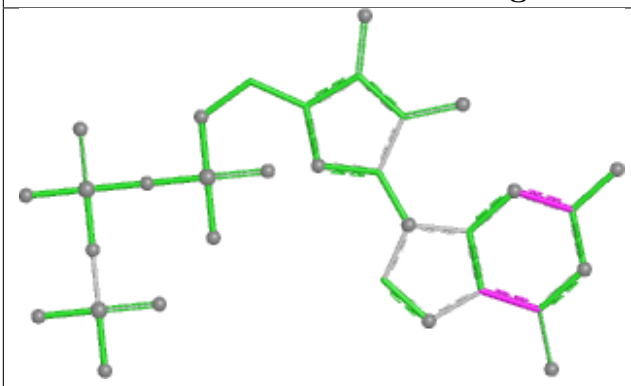
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 1M 501



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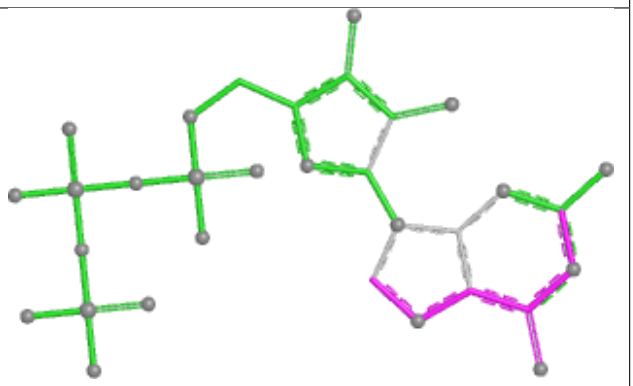

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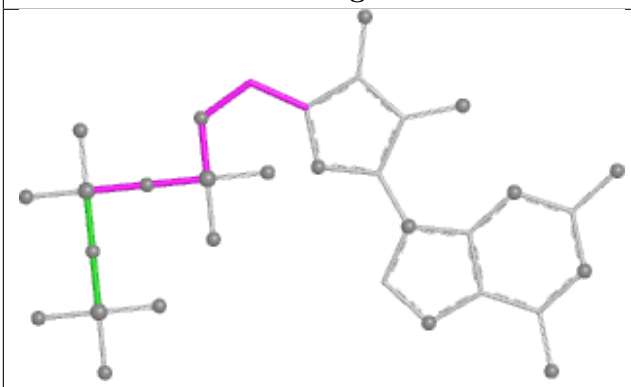

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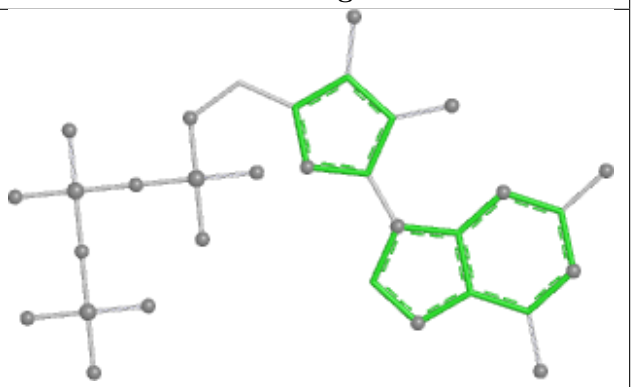
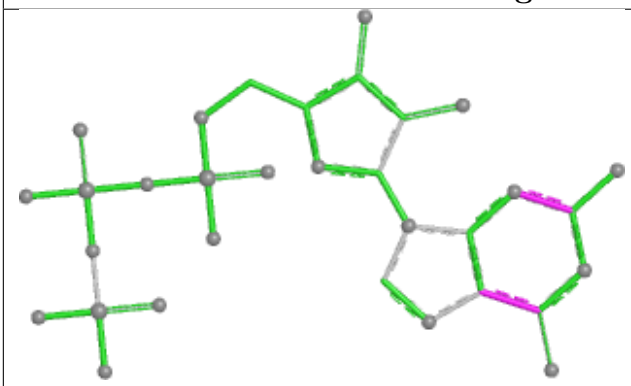


Rings

Ligand GTP 7E 501



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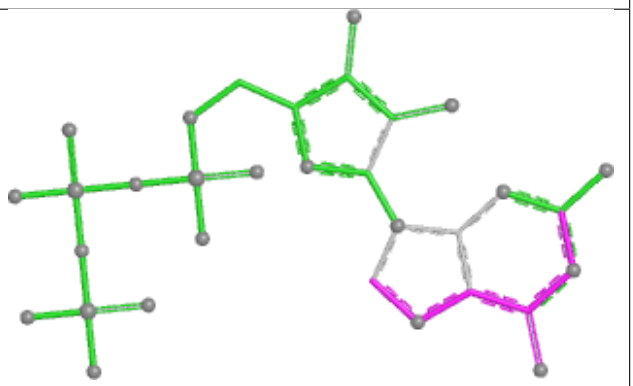
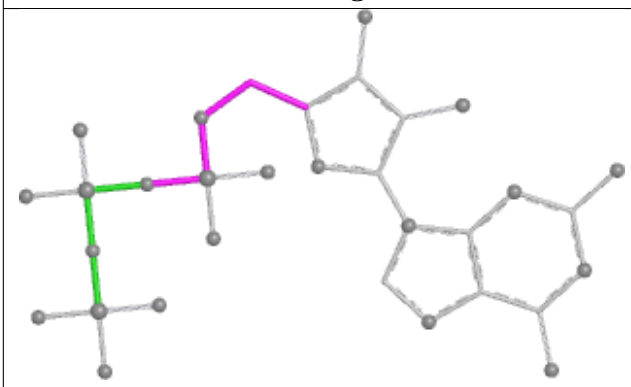
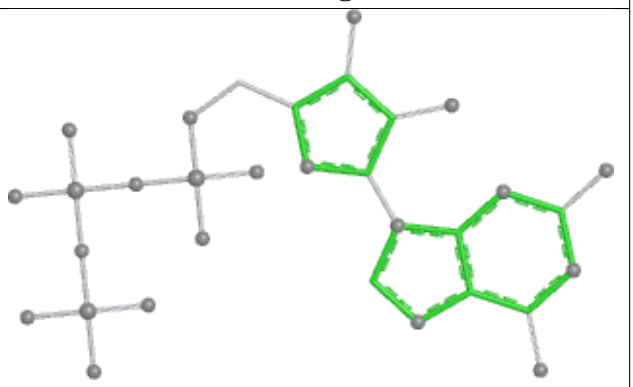


Bond angles

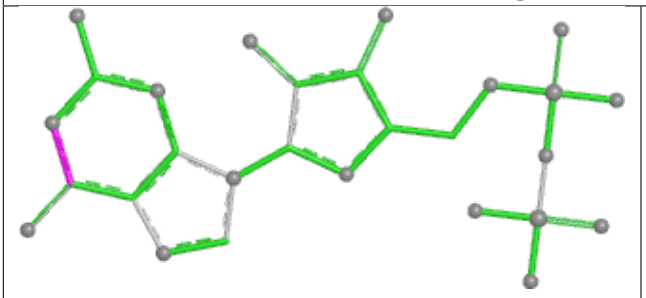


Torsions



Rings

Ligand GDP 4D 501



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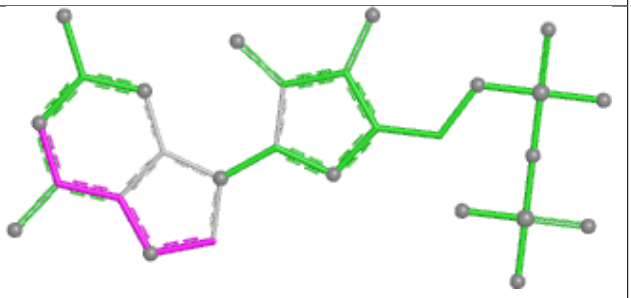

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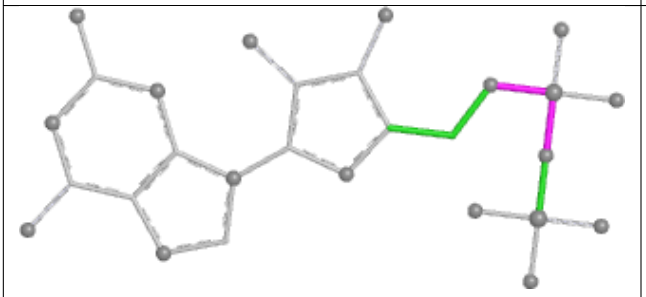

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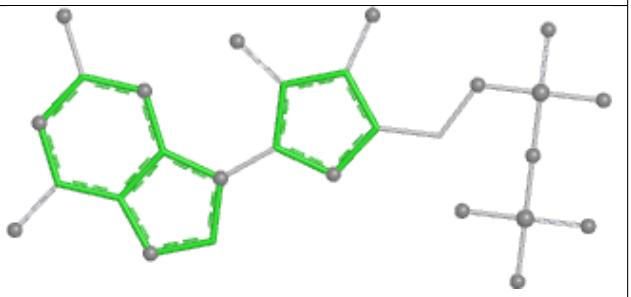
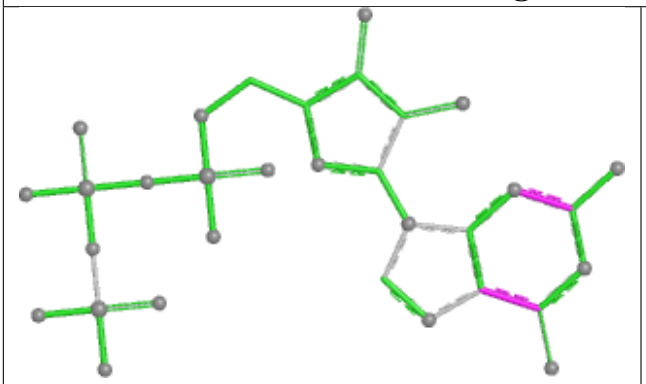


Rings

Ligand GTP 5G 501



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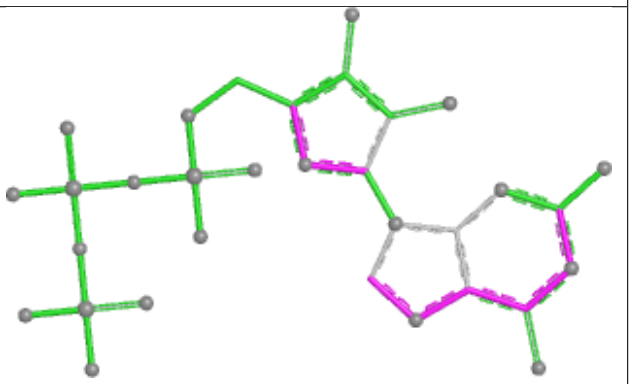

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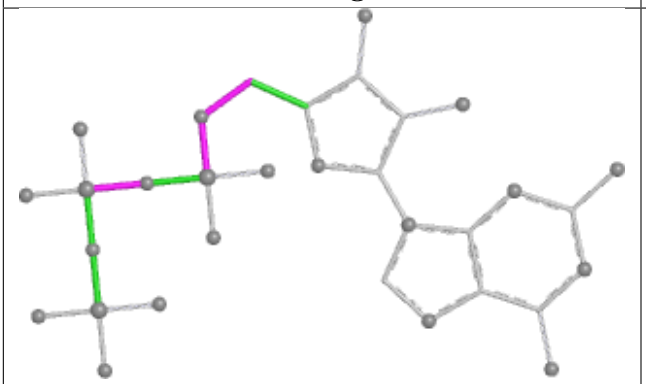

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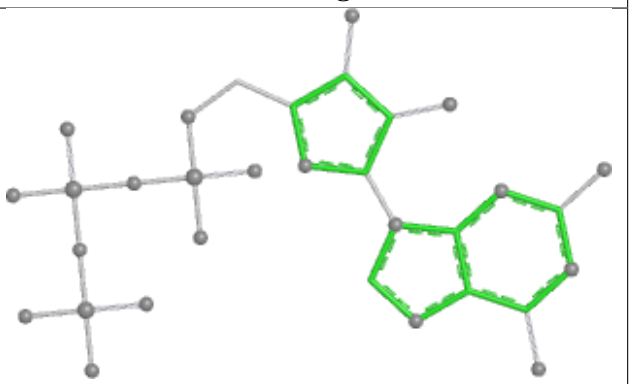
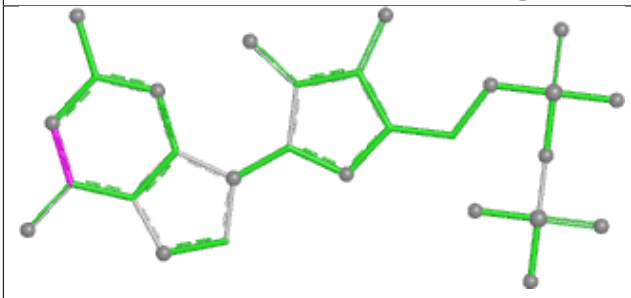
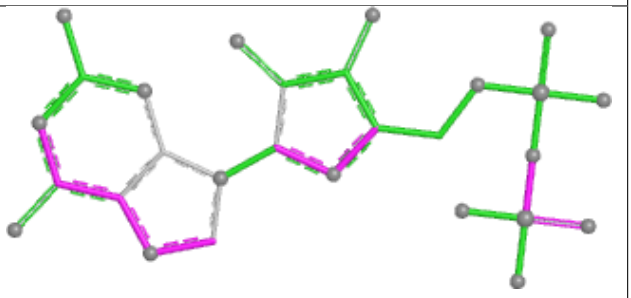
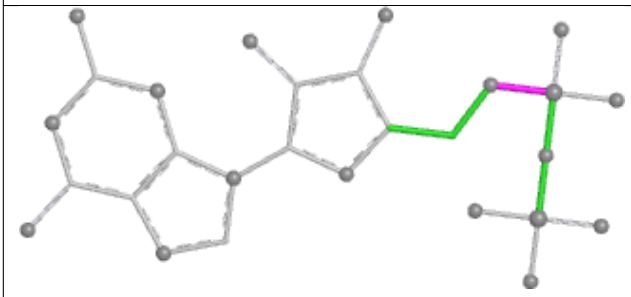
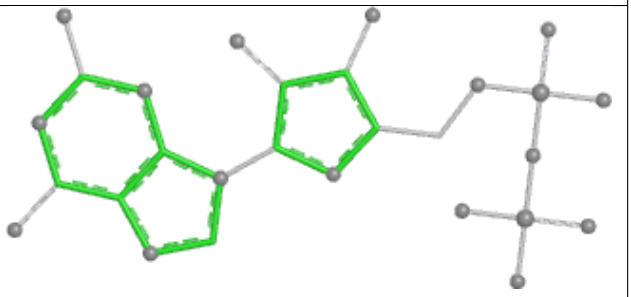
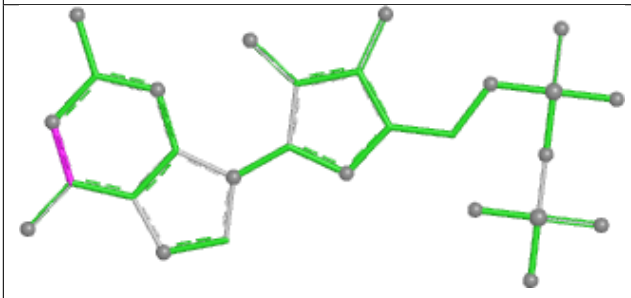
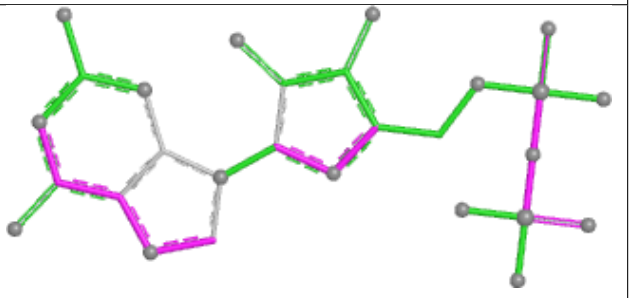
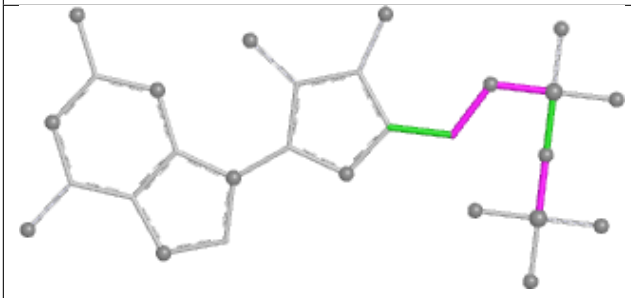
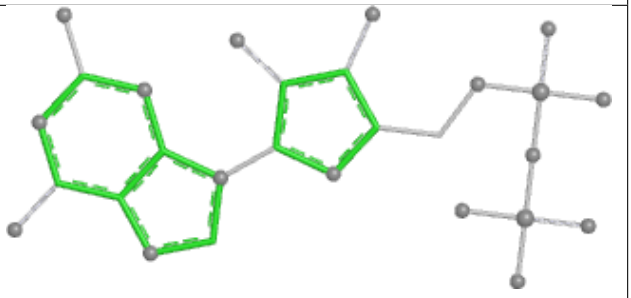
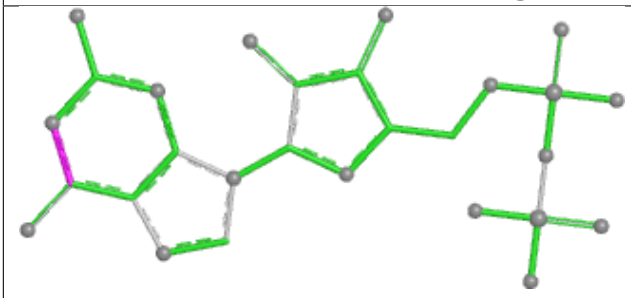


Rings

Ligand GDP 9F 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 6B 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 2D 501



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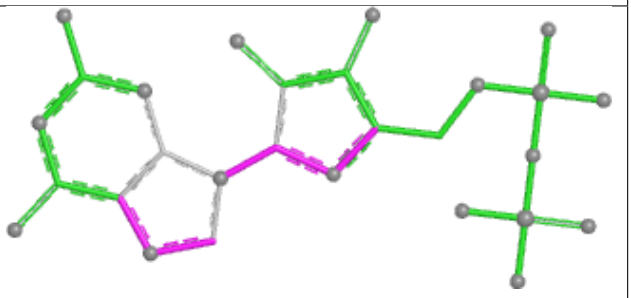

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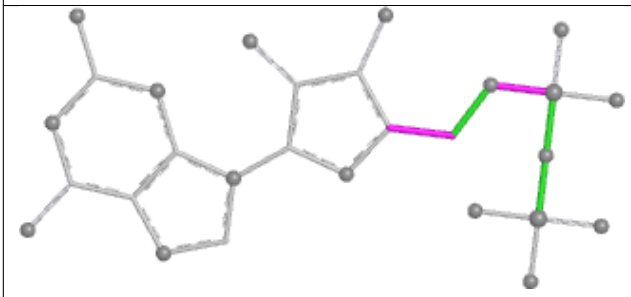

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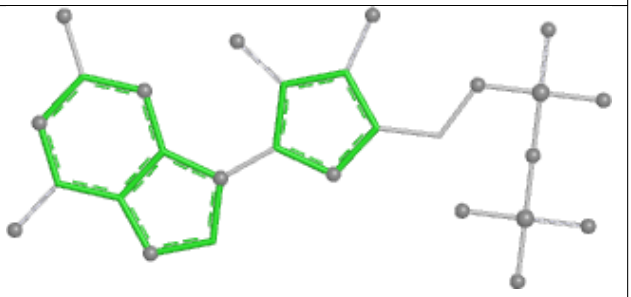
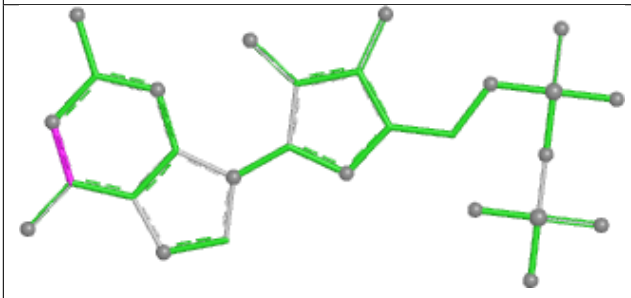


Rings

Ligand GDP 5N 501



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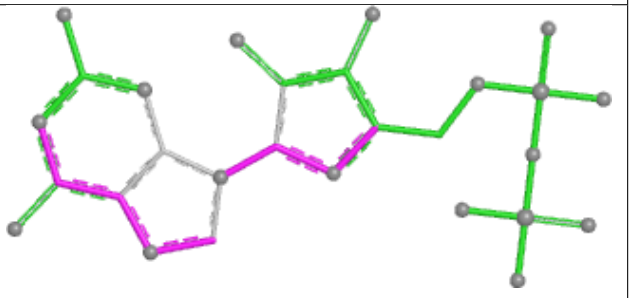

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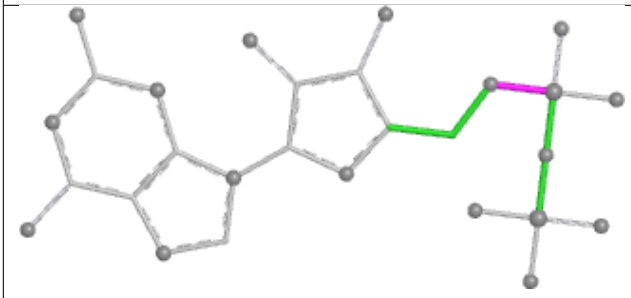

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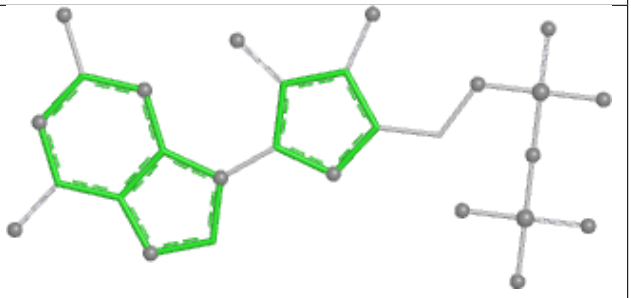
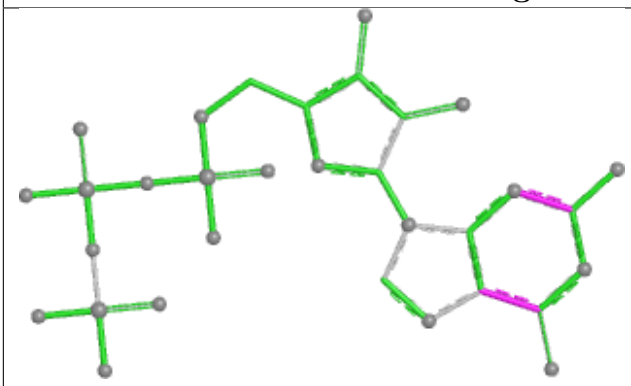


Rings

Ligand GTP 8A 501



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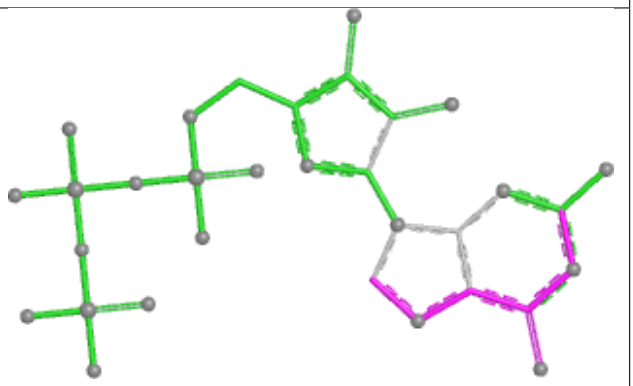

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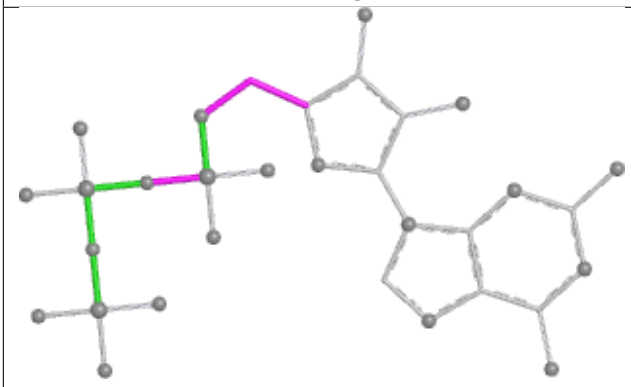

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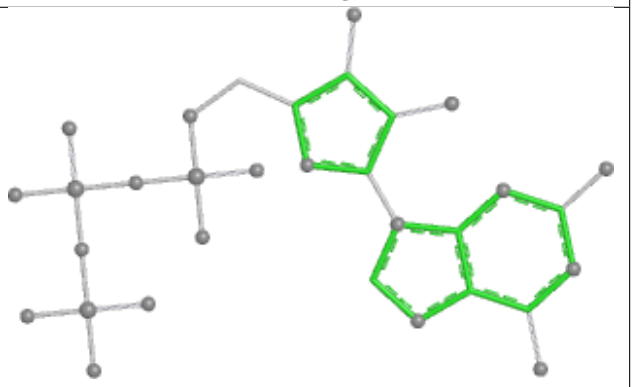
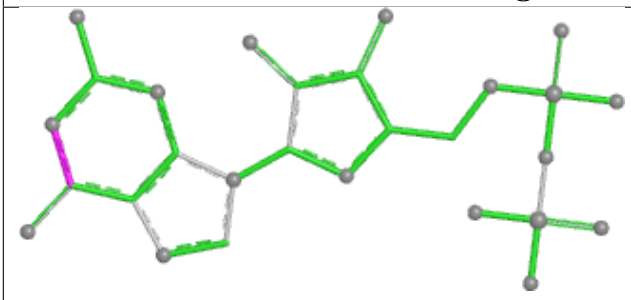


Rings

Ligand GDP 8L 501



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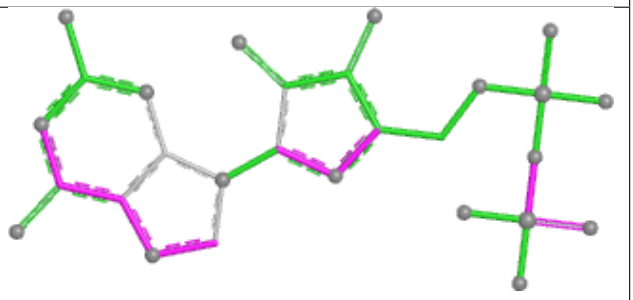

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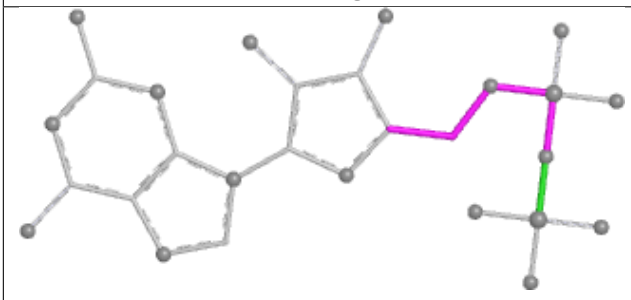

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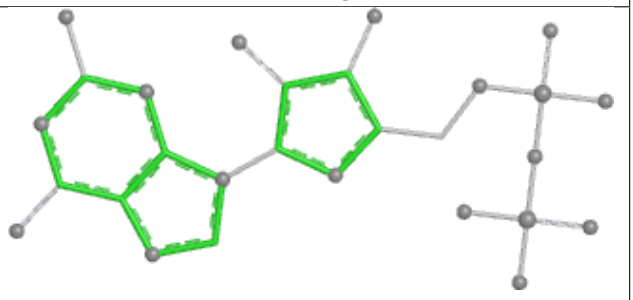
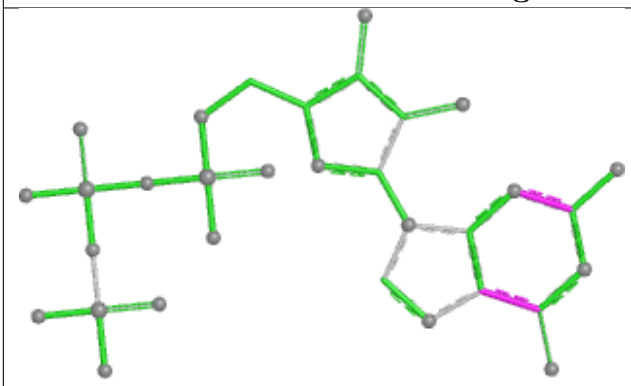


Rings

Ligand GTP 3K 501



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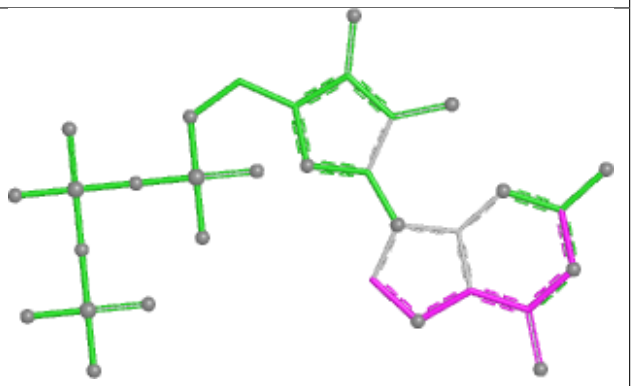

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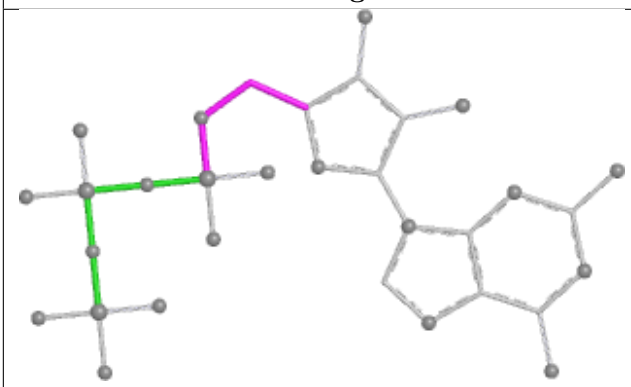

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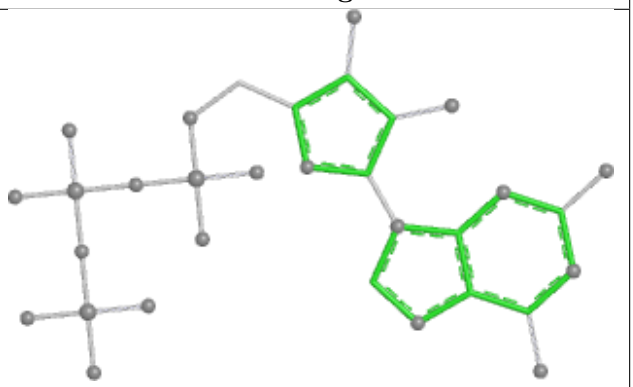
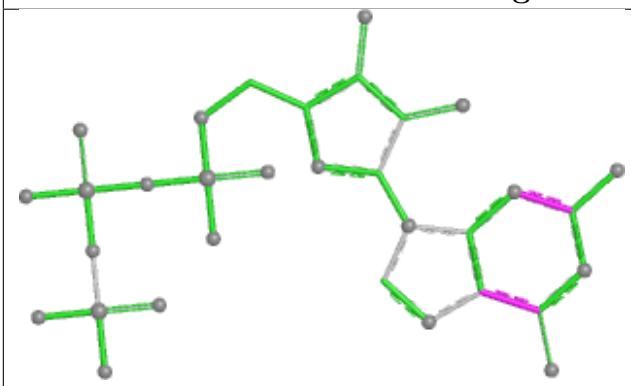


Rings

Ligand GTP 5K 501



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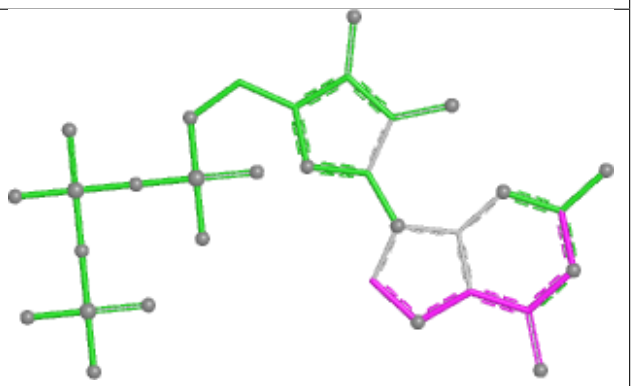

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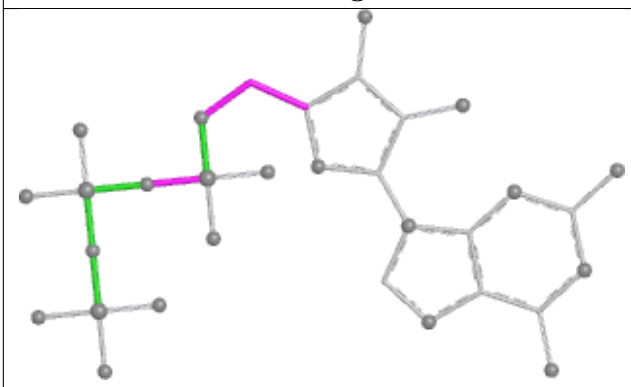

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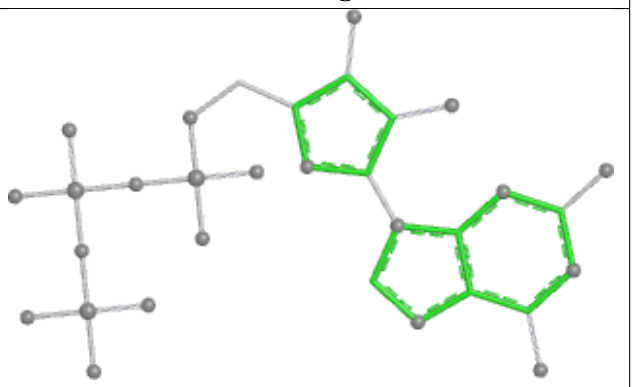
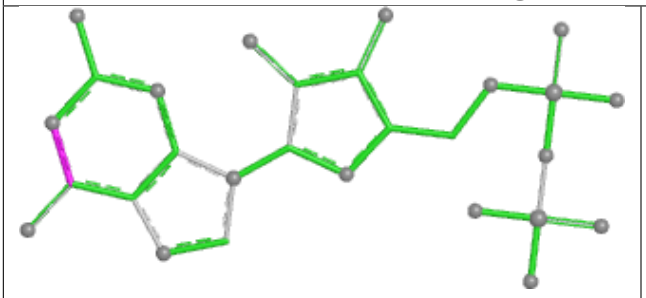


Rings

Ligand GDP 1H 501



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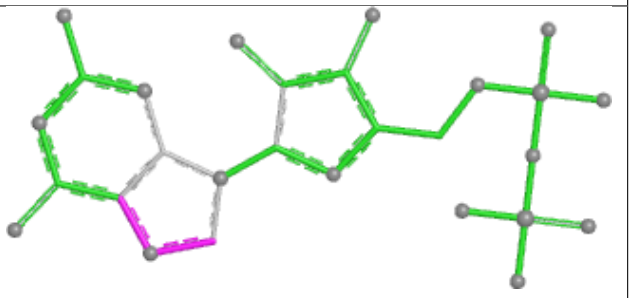

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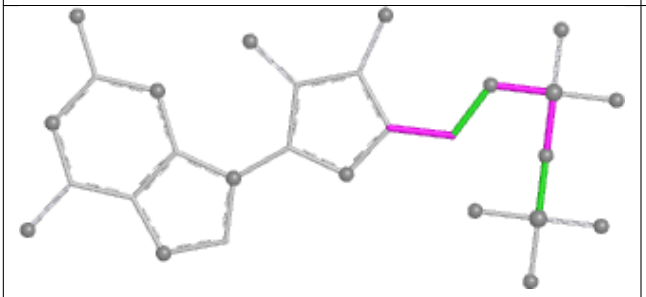

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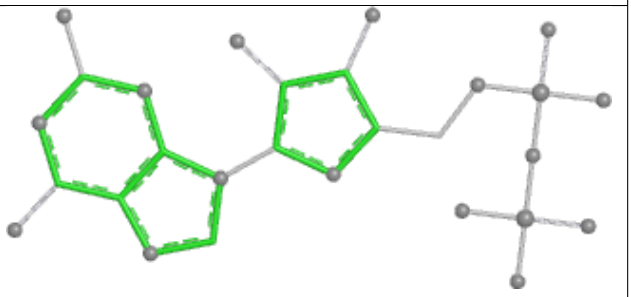
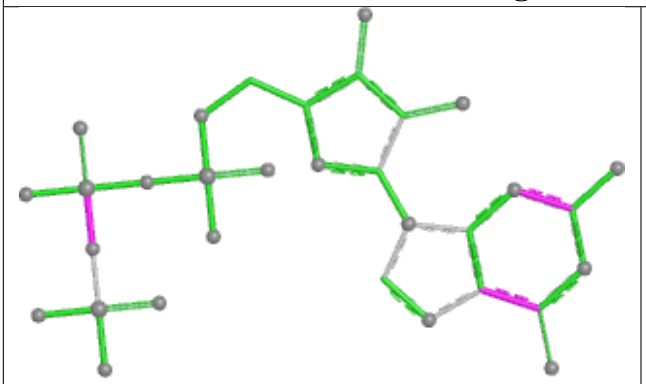


Rings

Ligand GTP 8K 501



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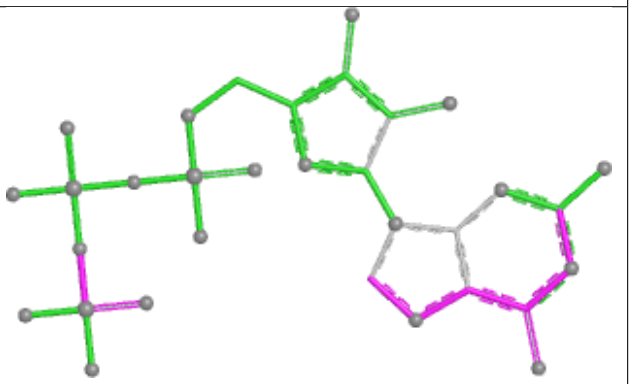

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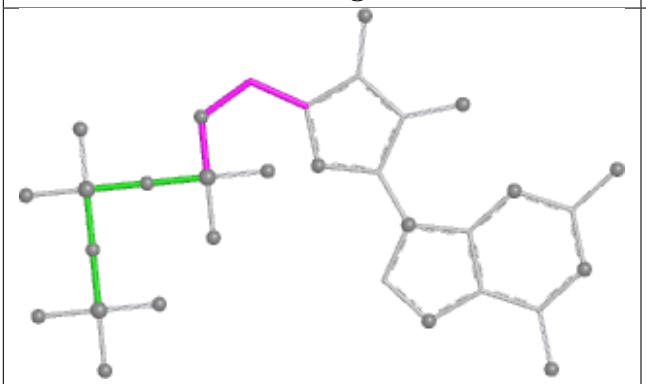

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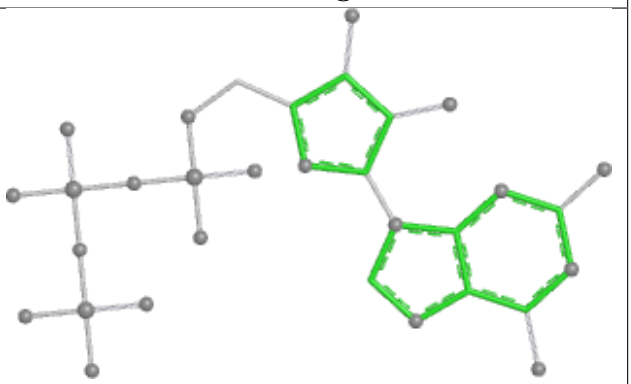
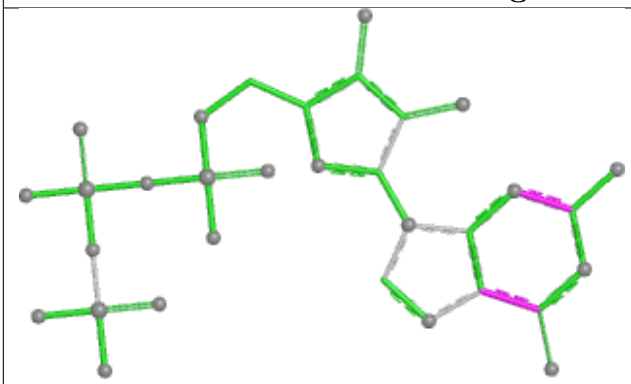


Rings

Ligand GTP 9M 501



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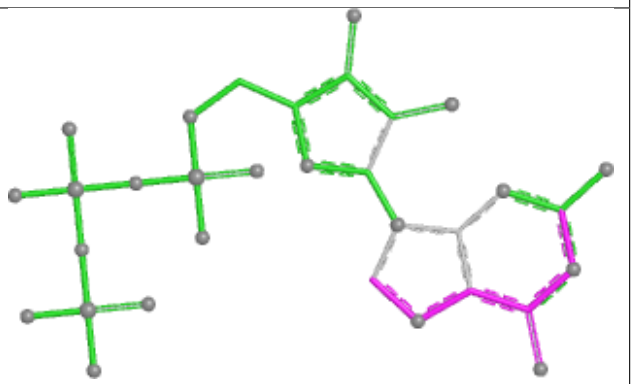
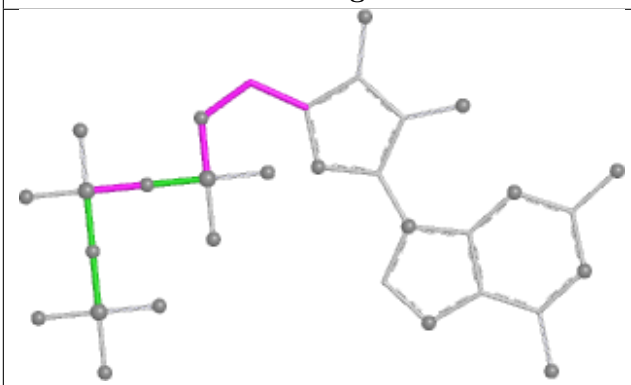


Bond angles



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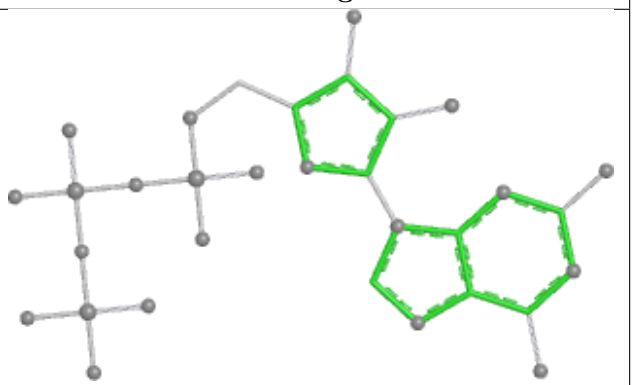
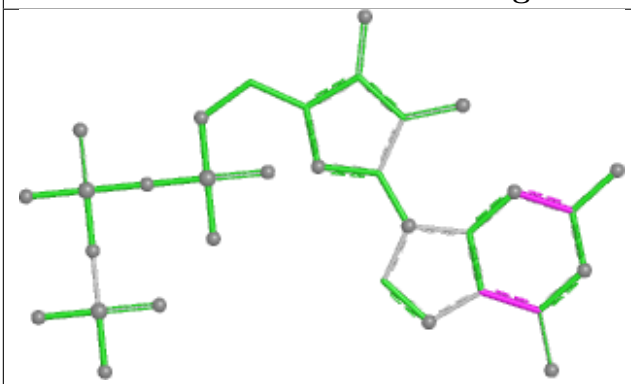
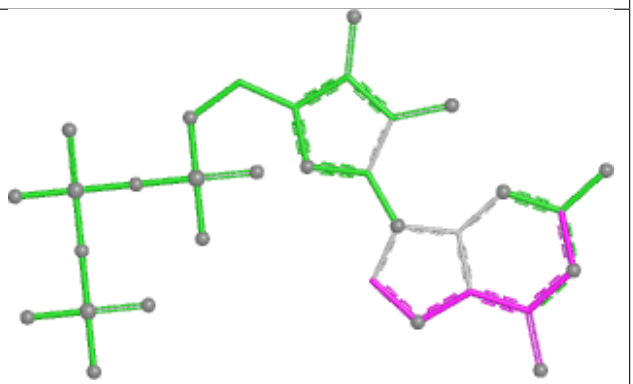


Rings

Ligand GTP 2K 501



Bond lengths



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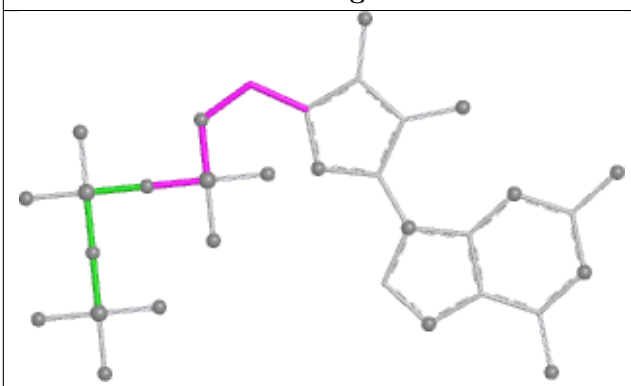
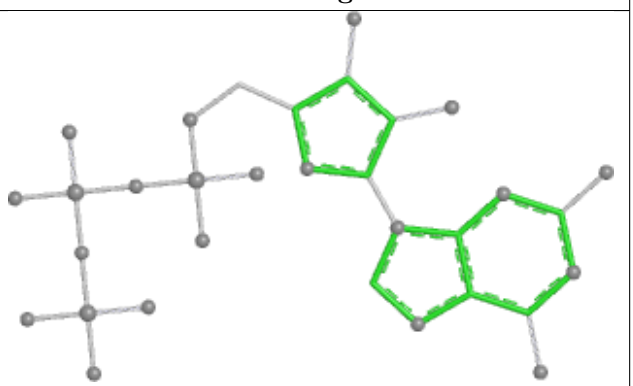
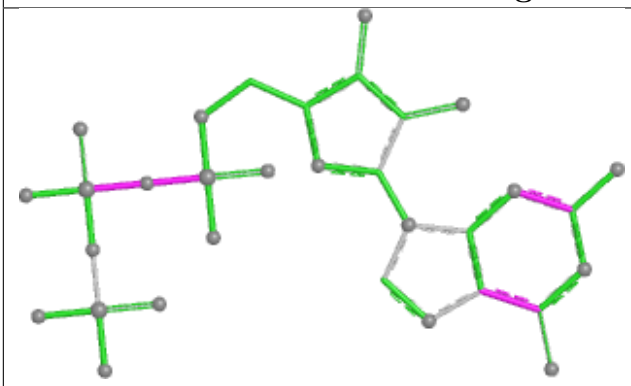


Torsions



Rings

Ligand GTP 2E 501



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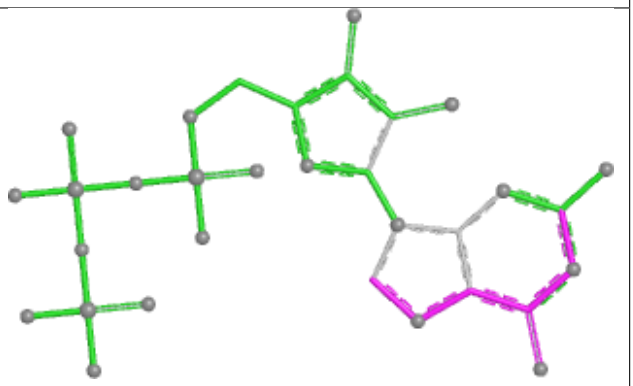

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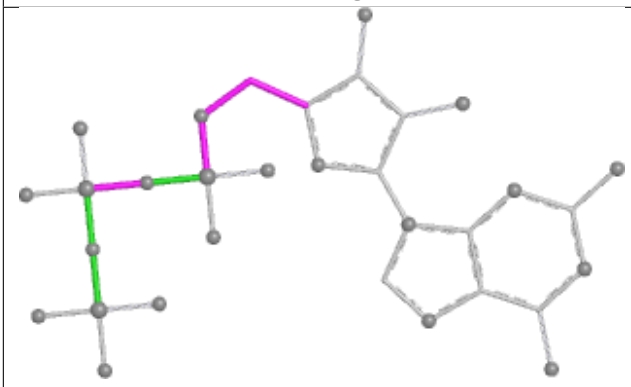

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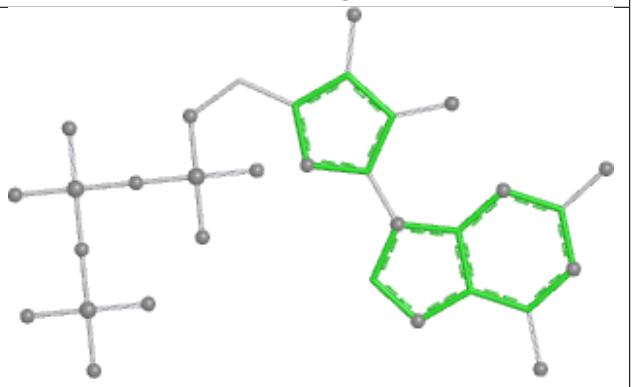
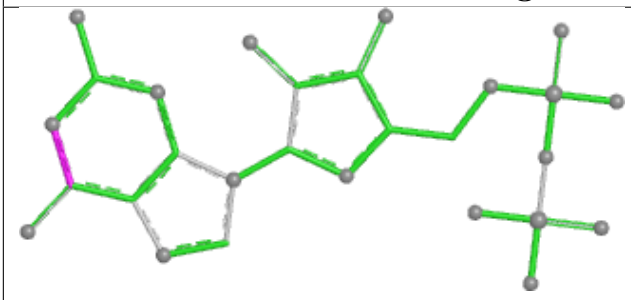


Rings

Ligand GDP 6J 501



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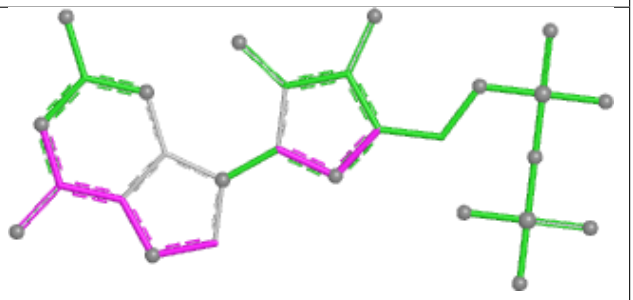

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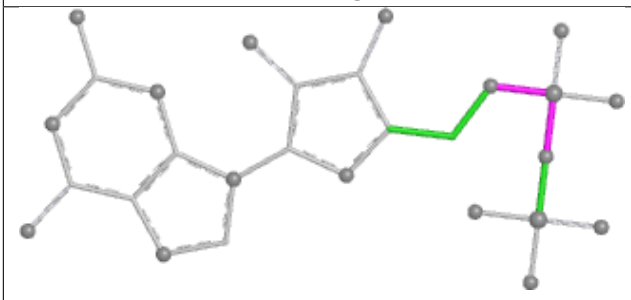

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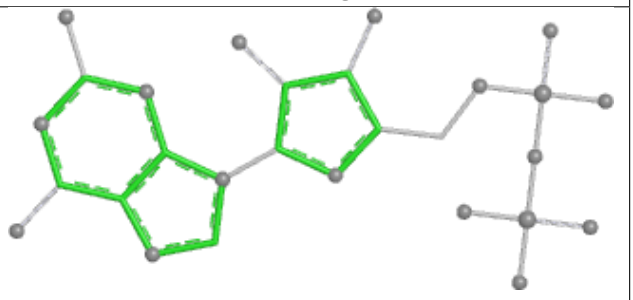
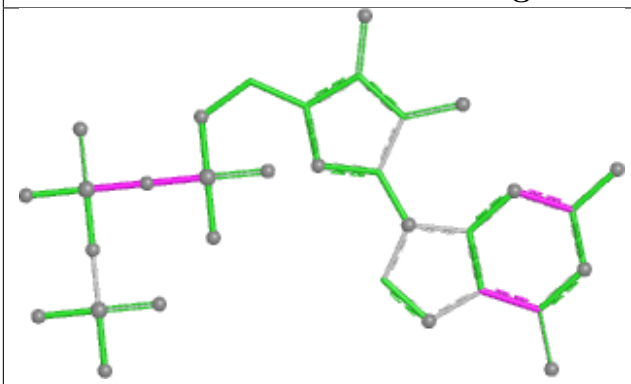


Rings

Ligand GTP 9K 501



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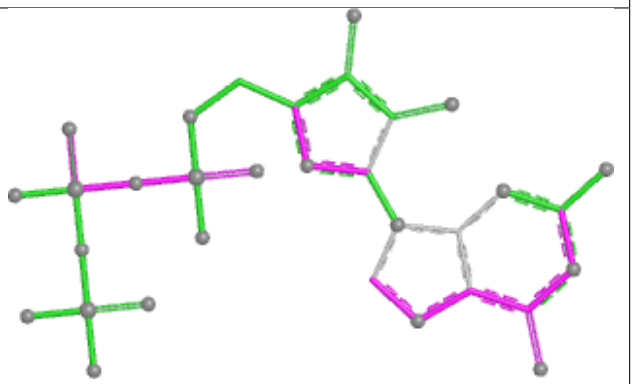

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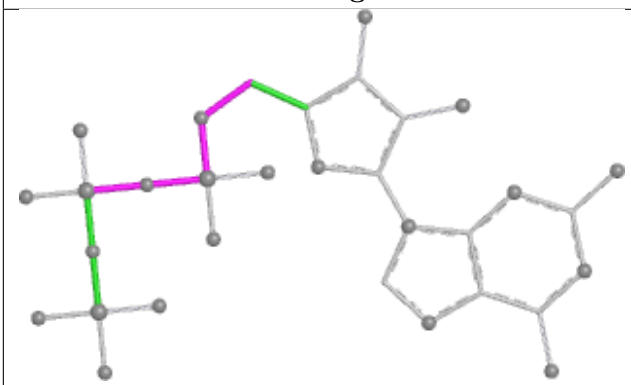

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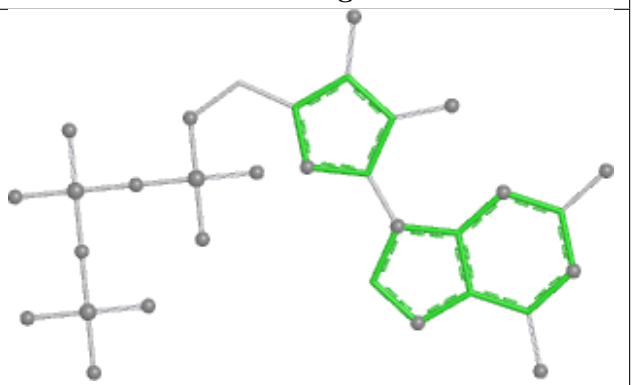
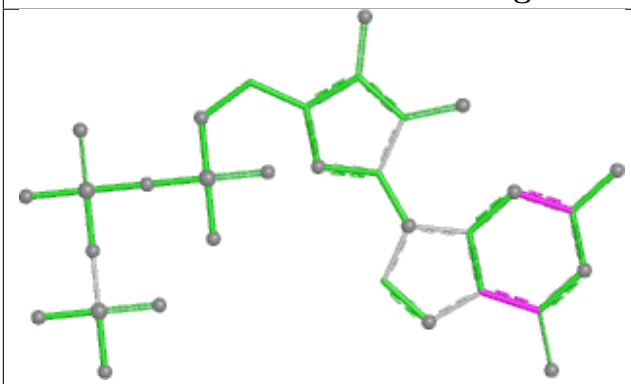


Rings

Ligand GTP 9C 501



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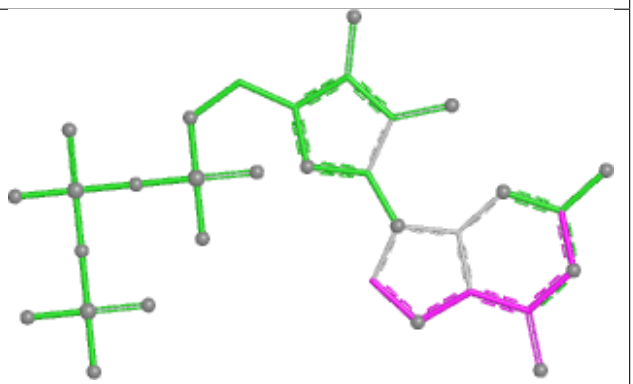

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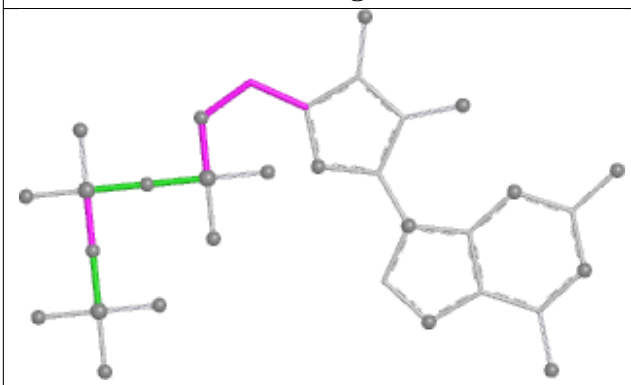

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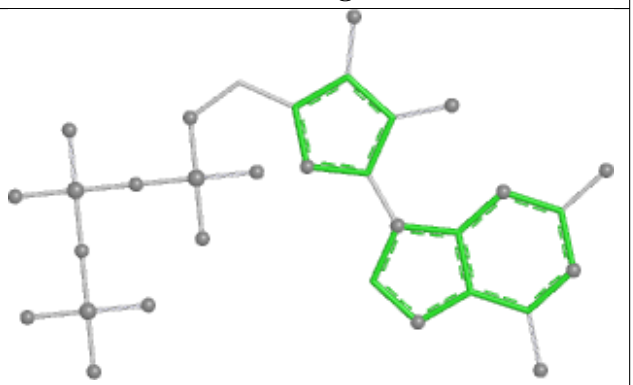
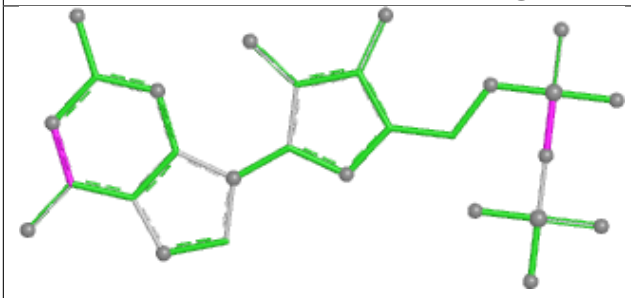
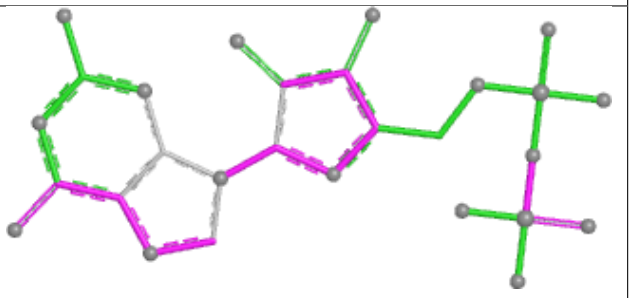
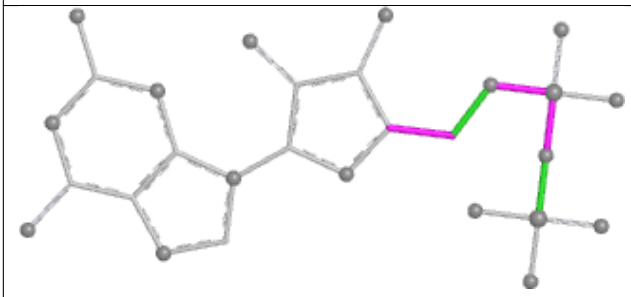
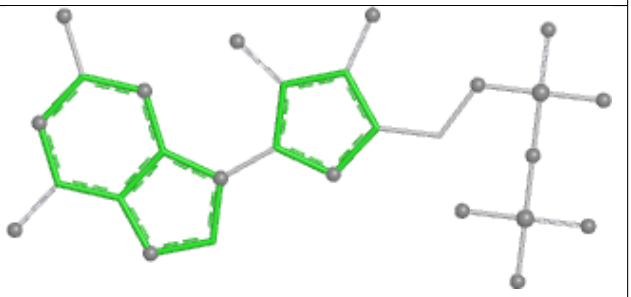


Rings

Ligand GDP 8B 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

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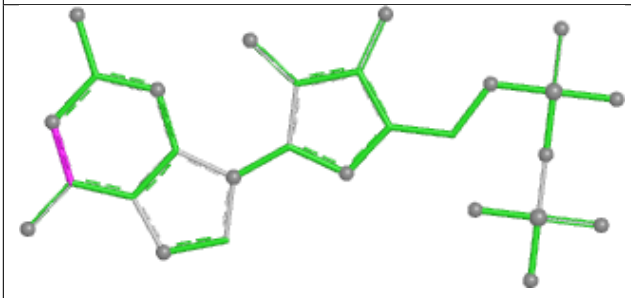
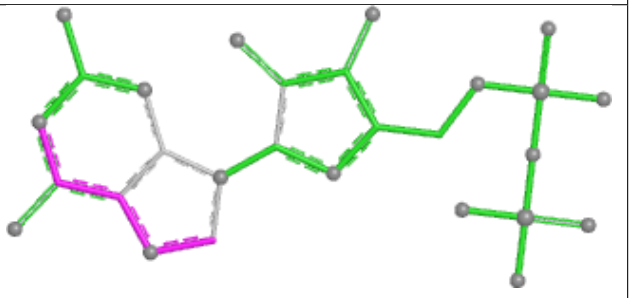
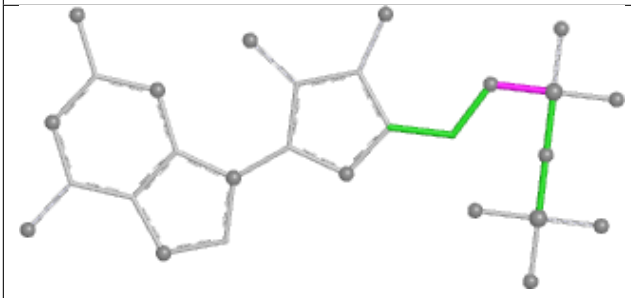
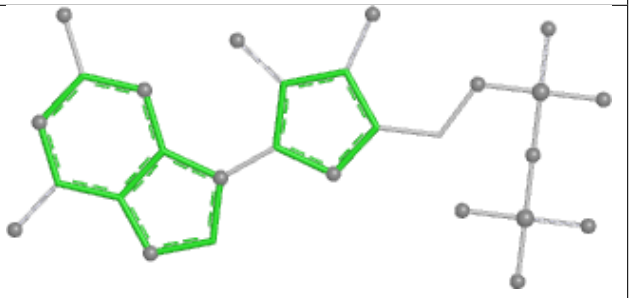
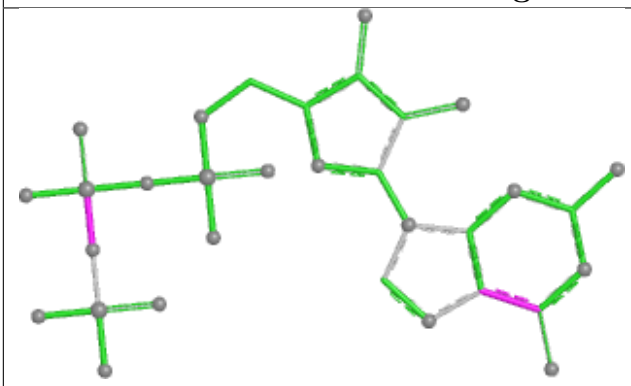
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 4A 501



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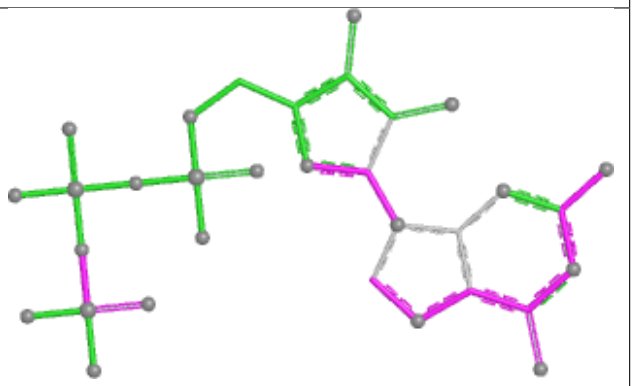

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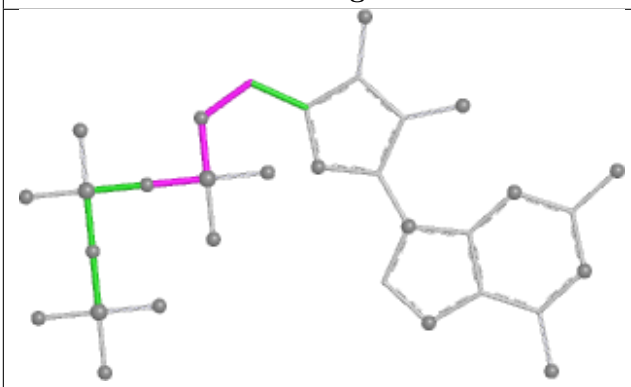

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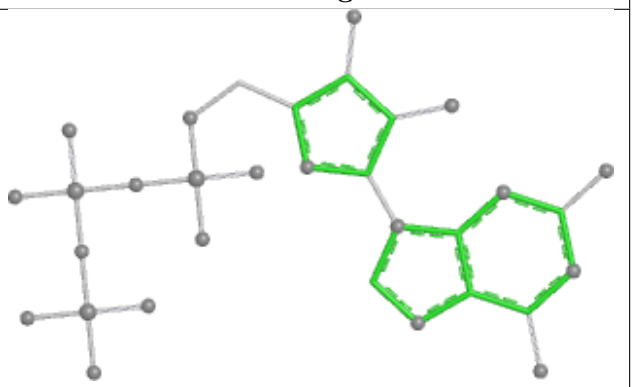
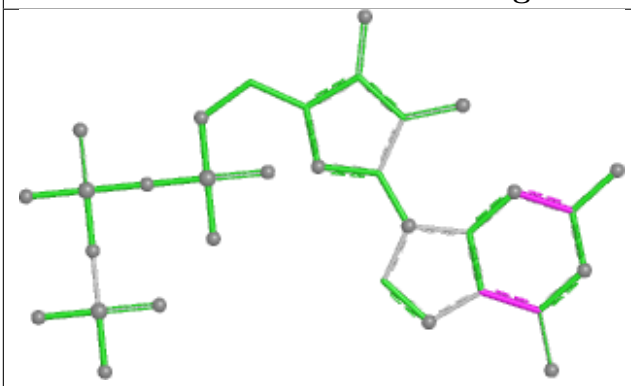


Rings

Ligand GTP 3A 501



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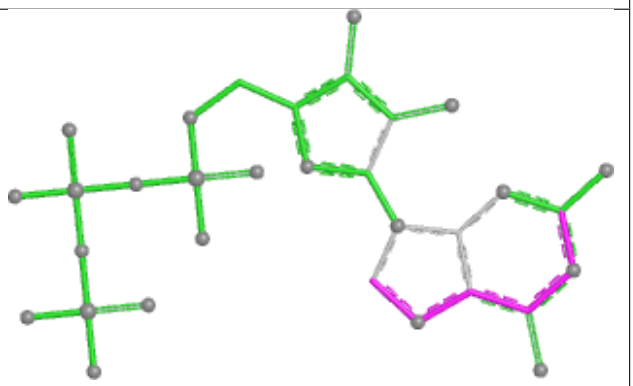

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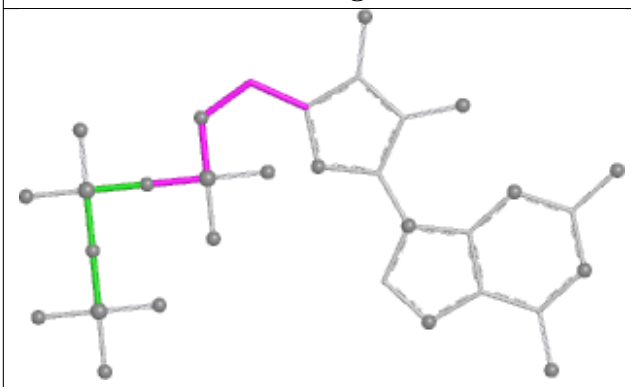

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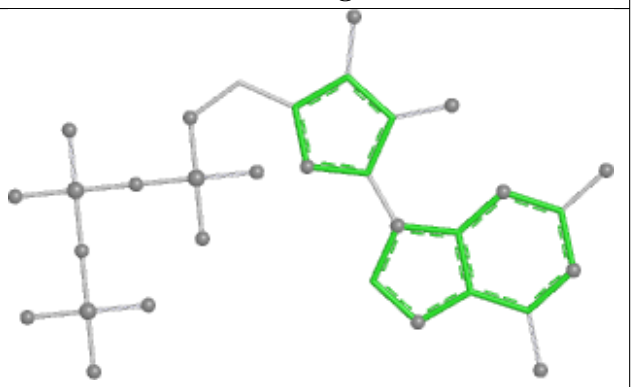
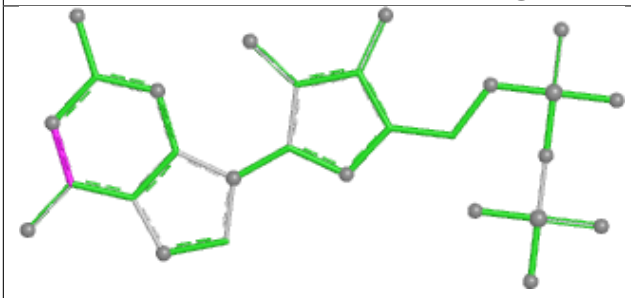
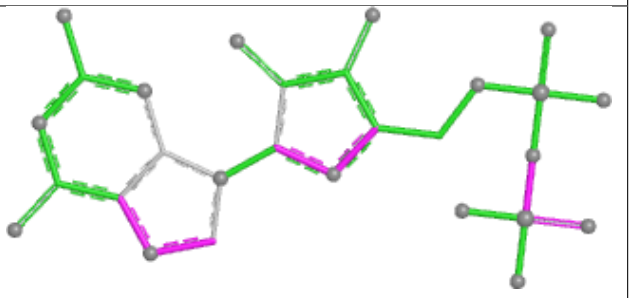
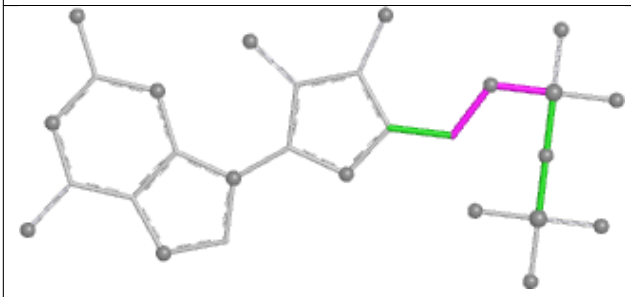
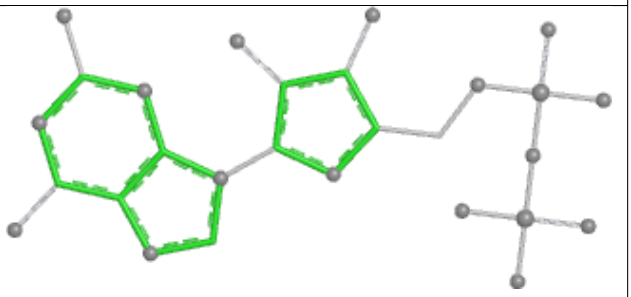
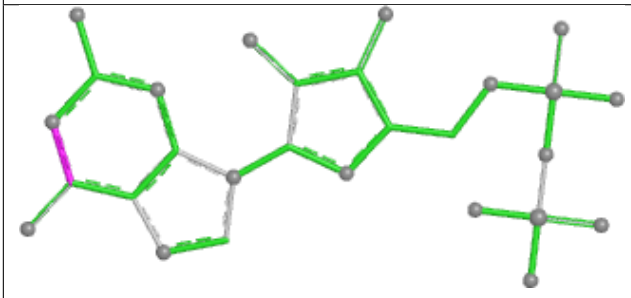
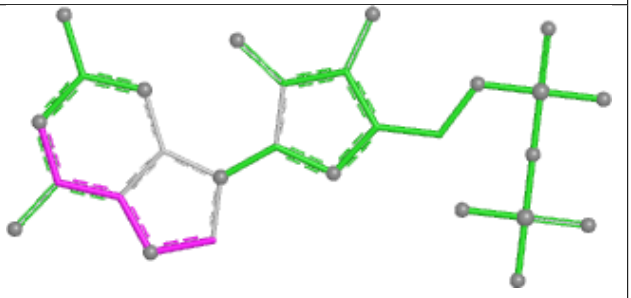
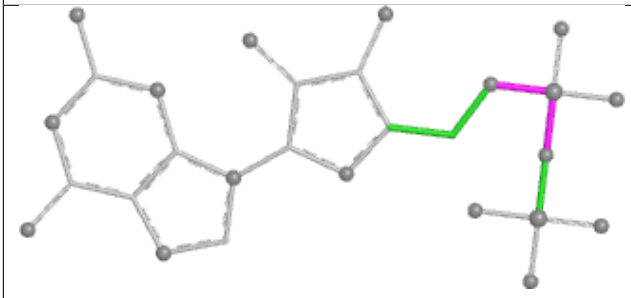
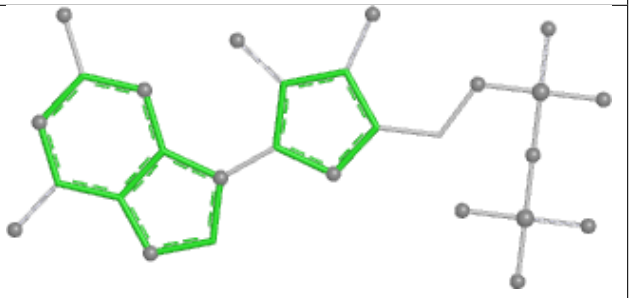
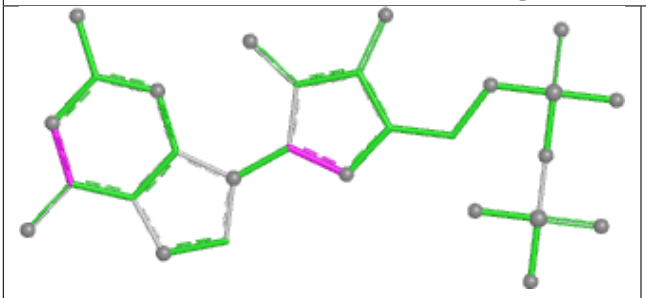


Rings

Ligand GDP 5B 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 4F 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 2F 501



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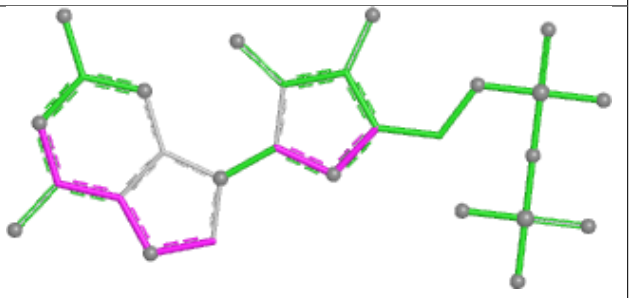

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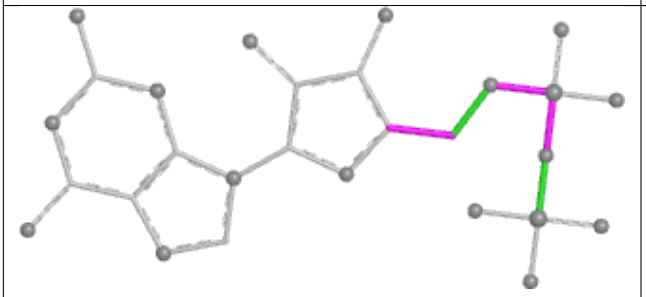

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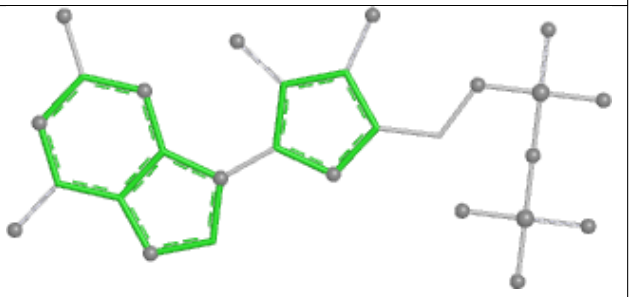
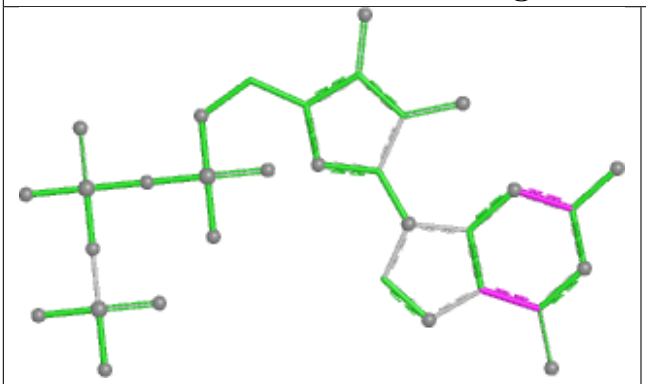


Rings

Ligand GTP 4G 501



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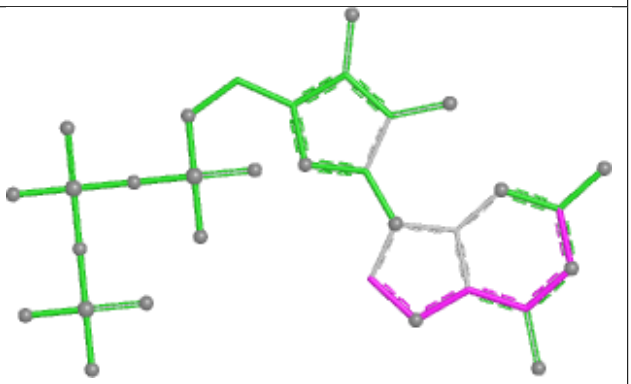

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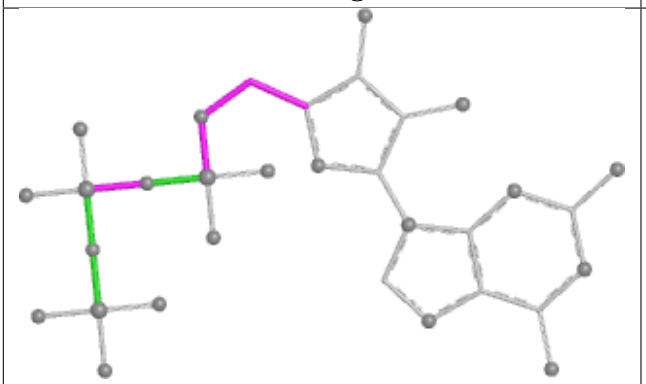

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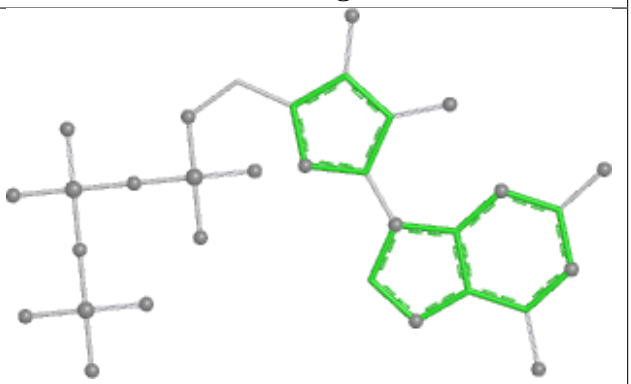
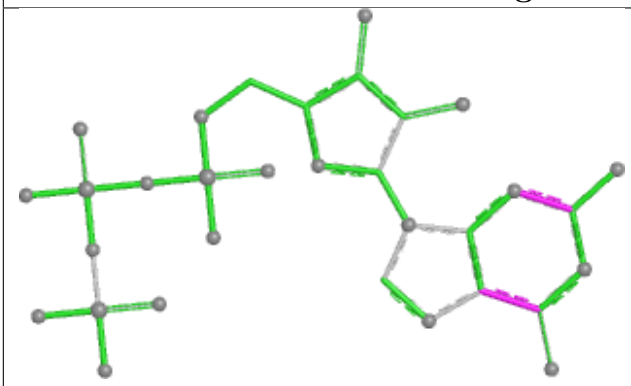


Rings

Ligand GTP 5E 501



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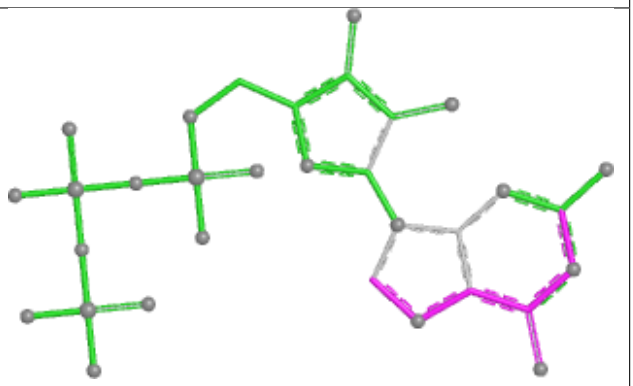
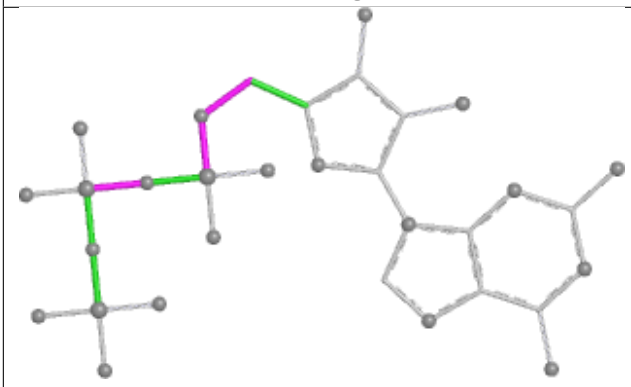


Bond angles



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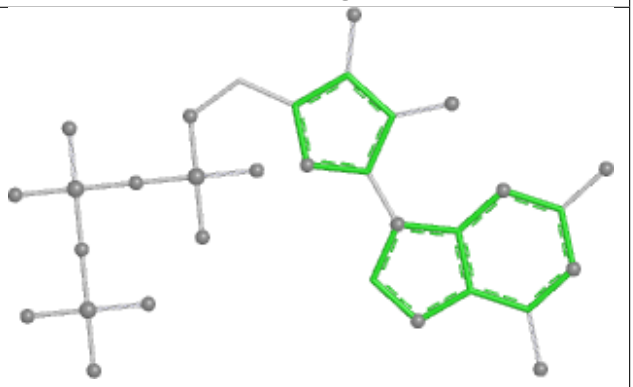
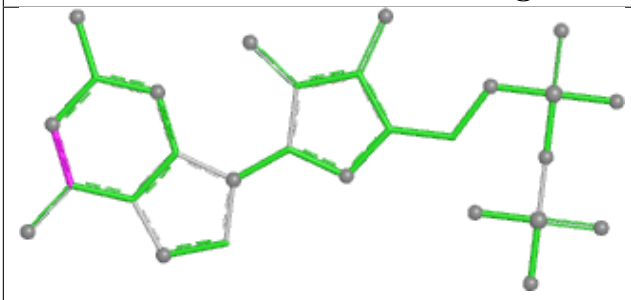


Rings

Ligand GDP 7L 501



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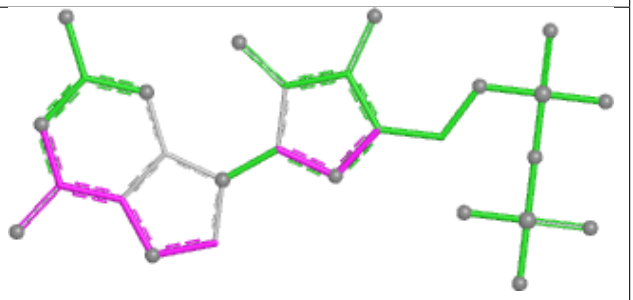

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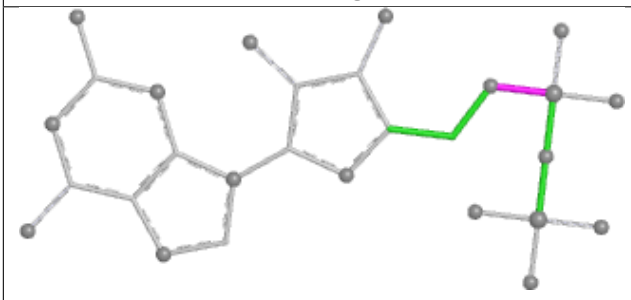

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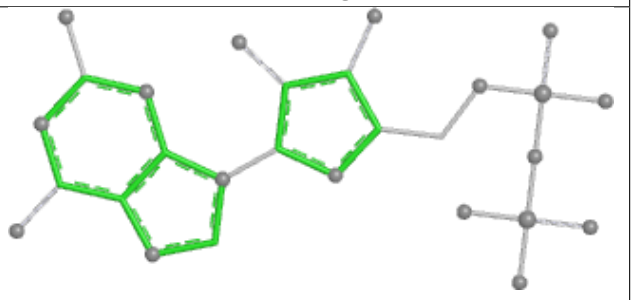
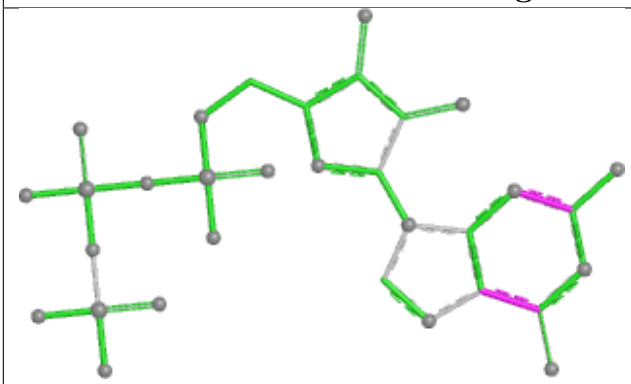


Rings

Ligand GTP 6E 501



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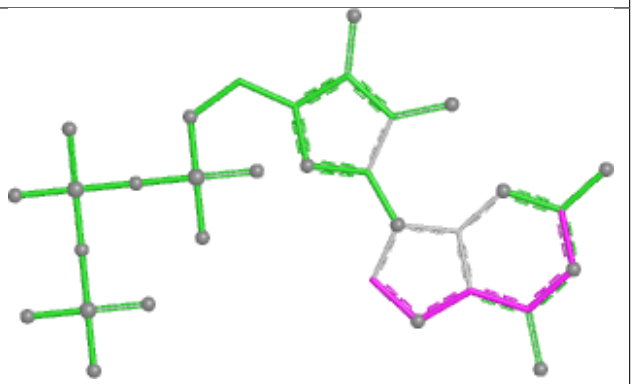

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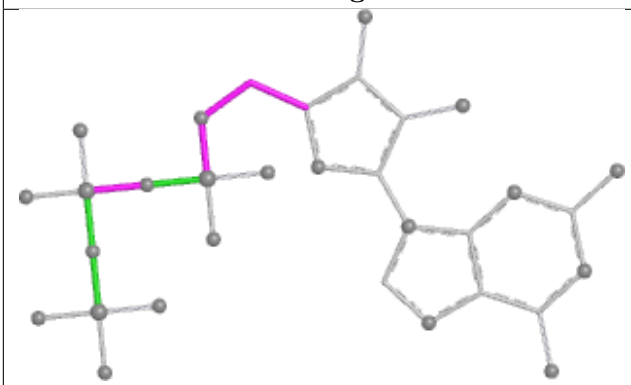

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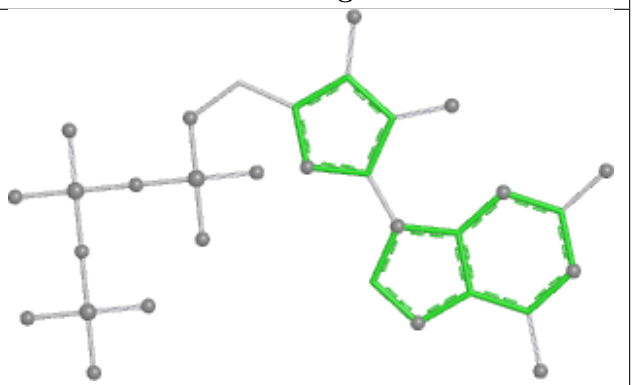
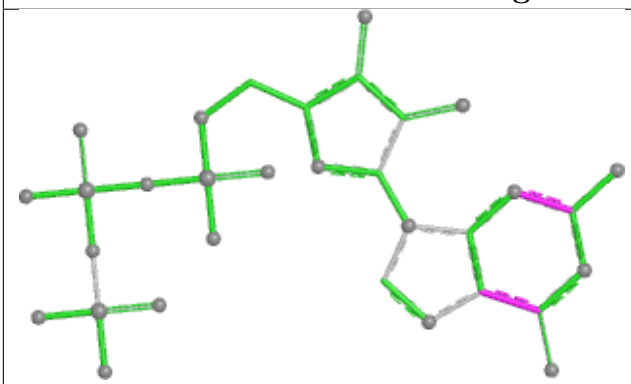


Rings

Ligand GTP 6G 501



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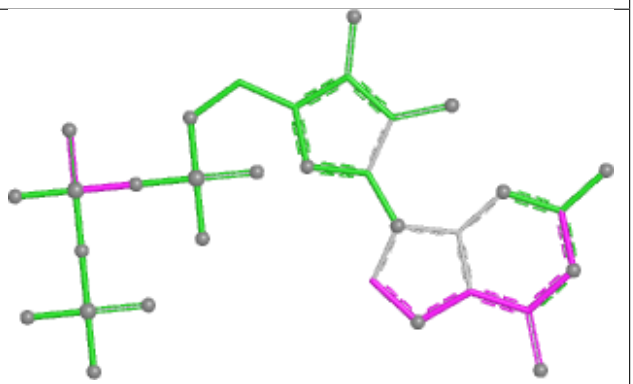

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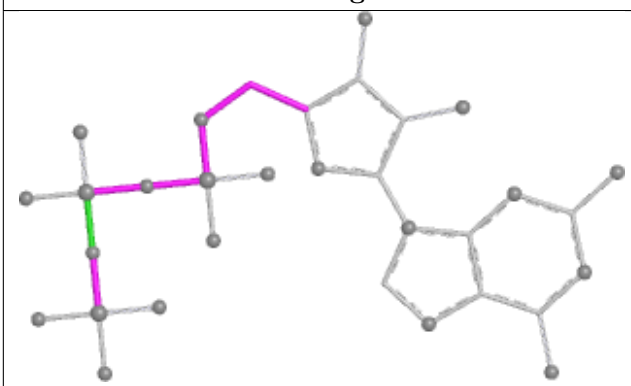

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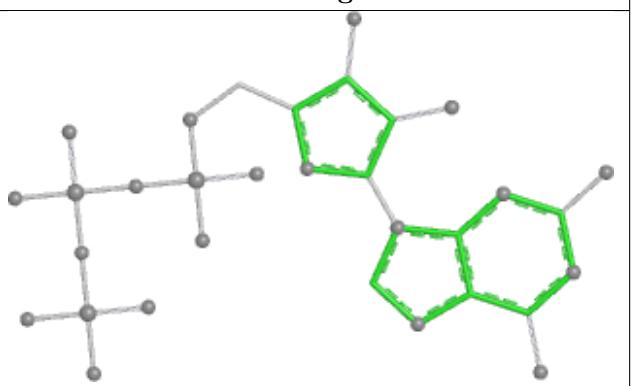
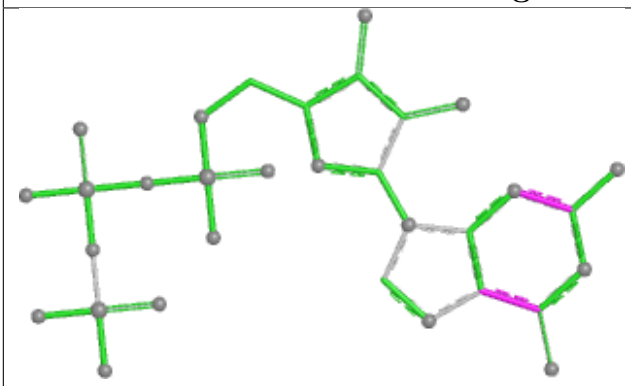


Rings

Ligand GTP 3G 501



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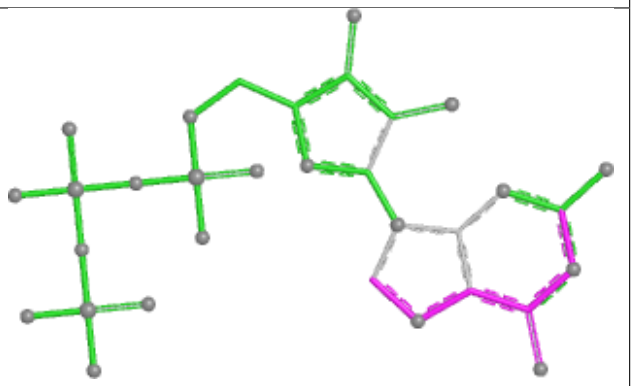

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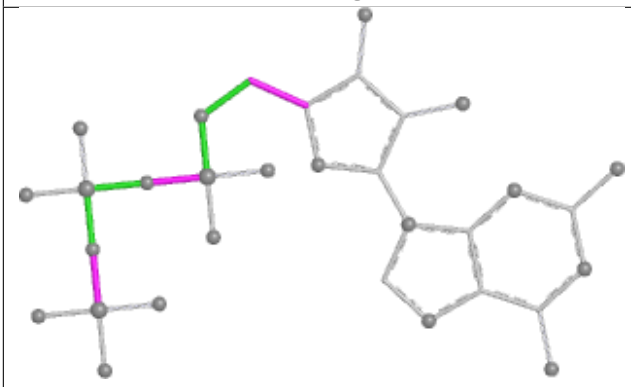

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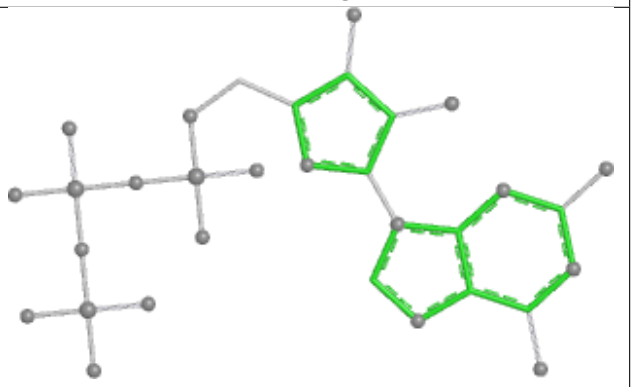

Rings

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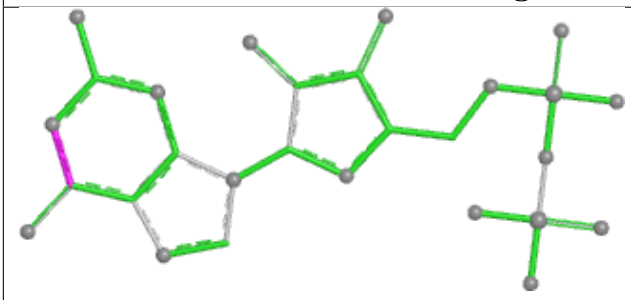

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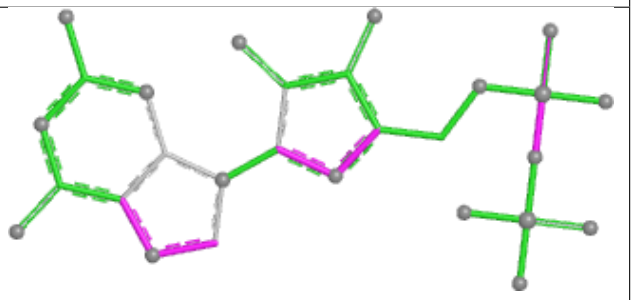

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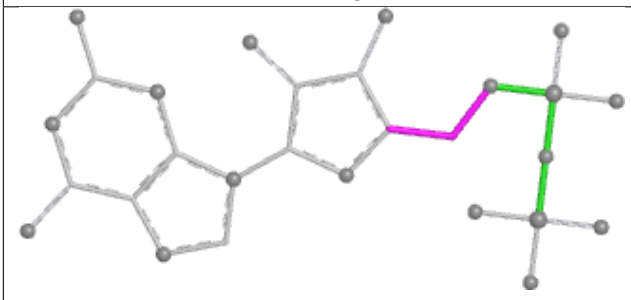

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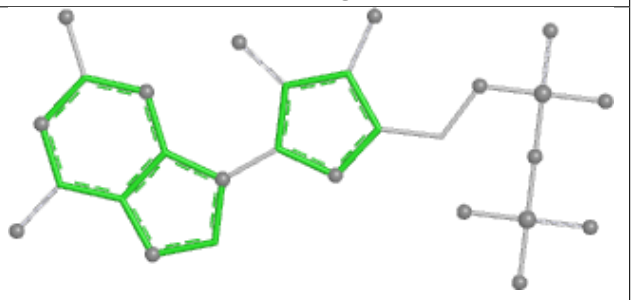

Rings

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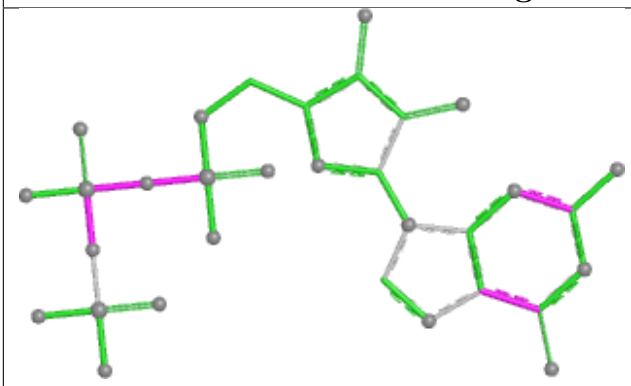

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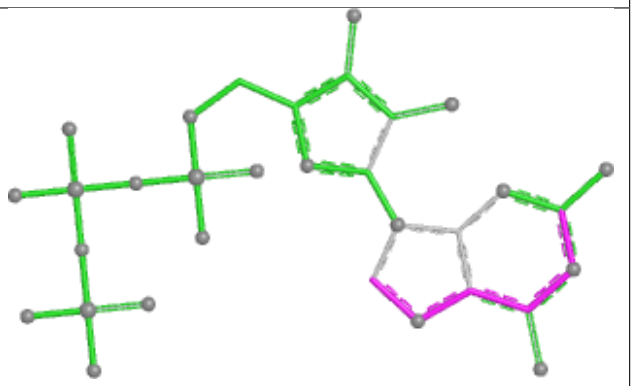

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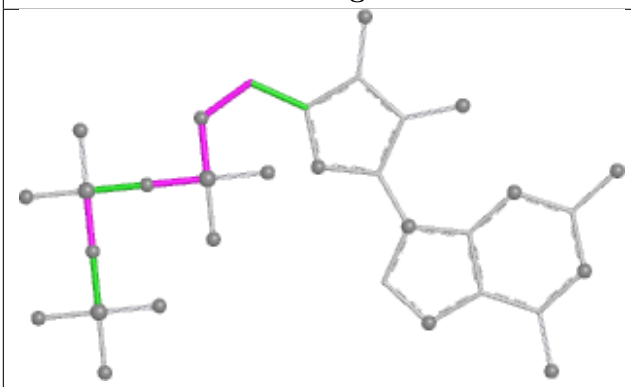

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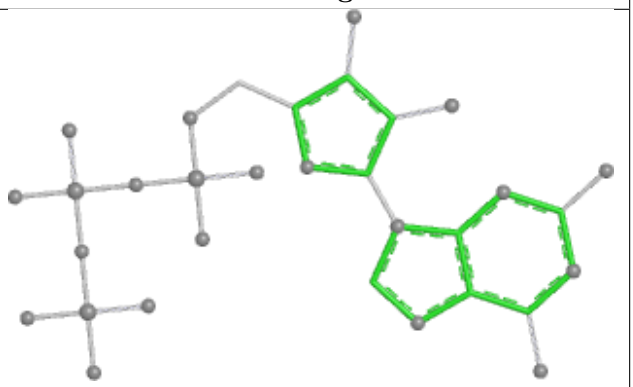

Rings

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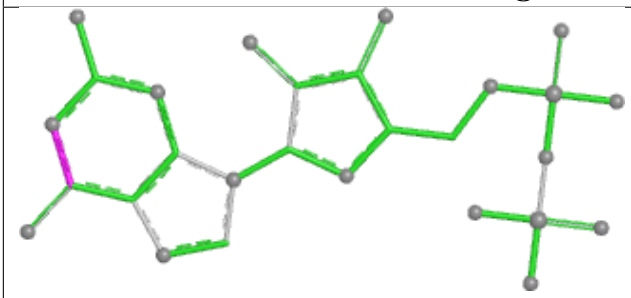

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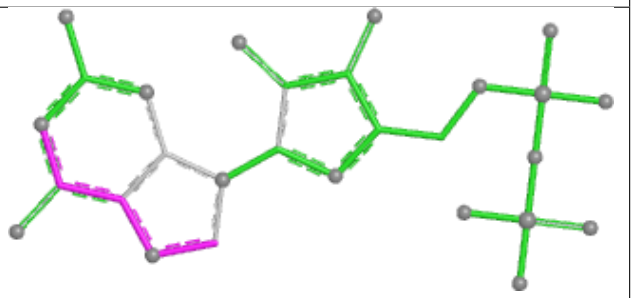

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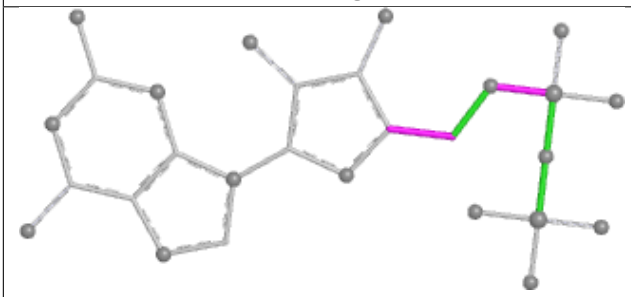

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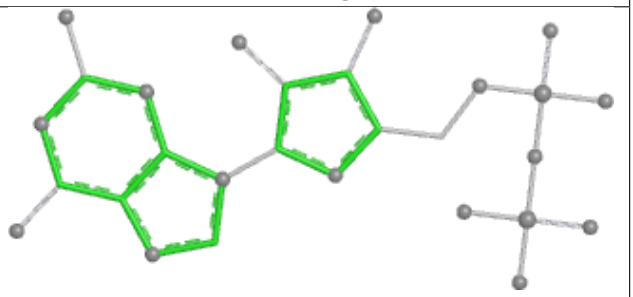

Rings

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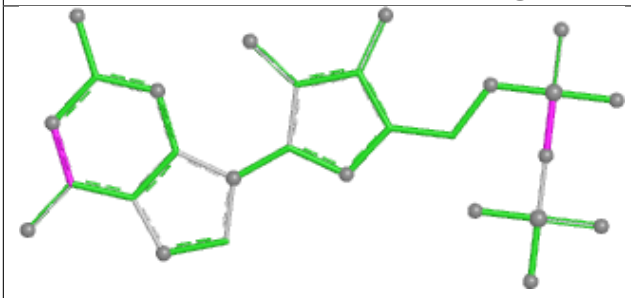
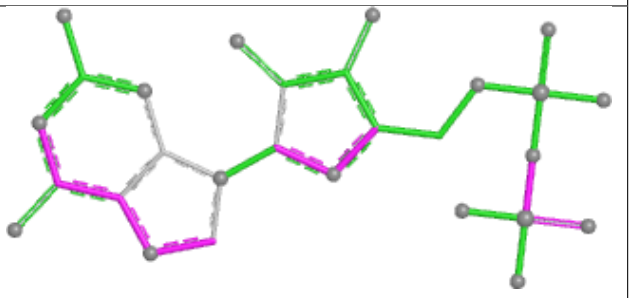
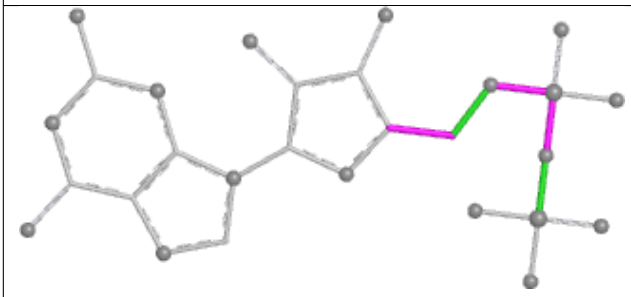
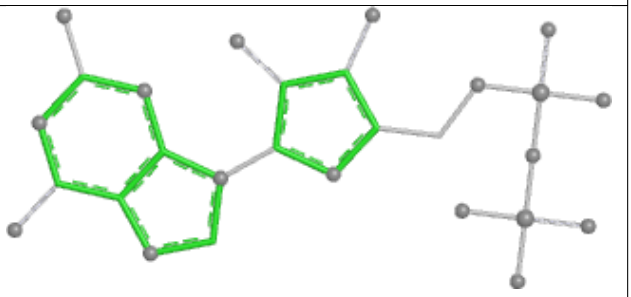
 Bond lengths	 Bond angles
 Torsions	 Rings

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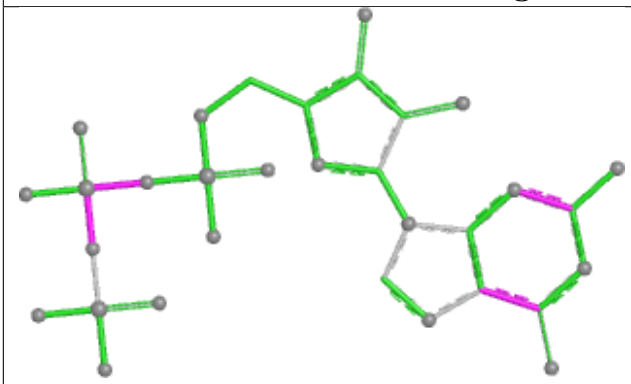
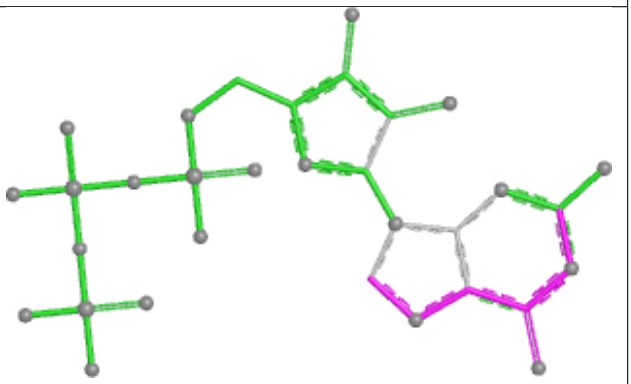
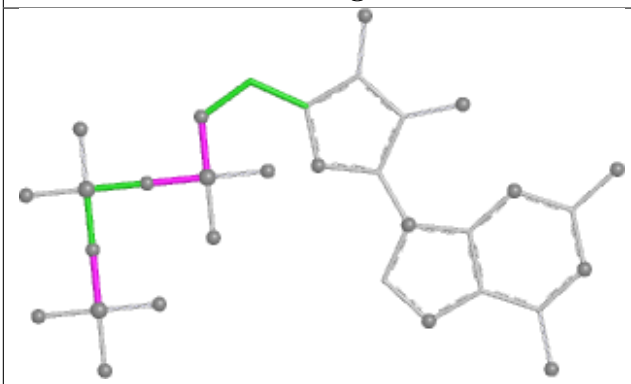
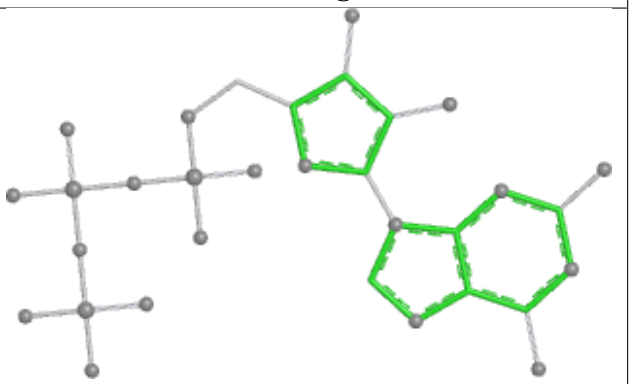
 Bond lengths	 Bond angles
 Torsions	 Rings

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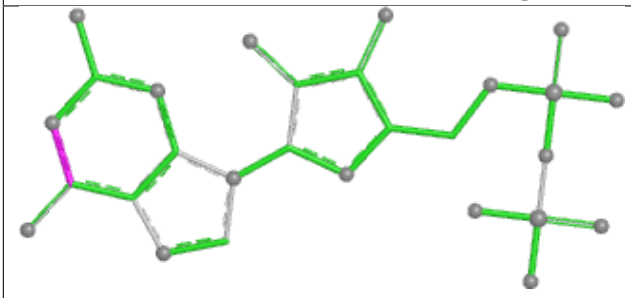
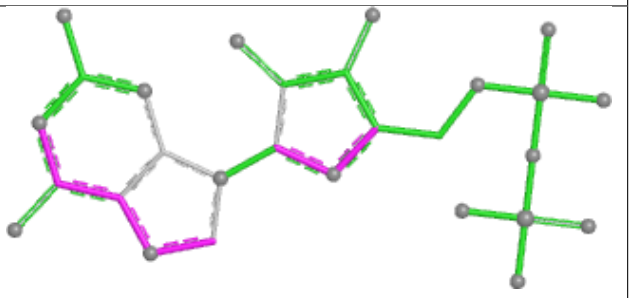
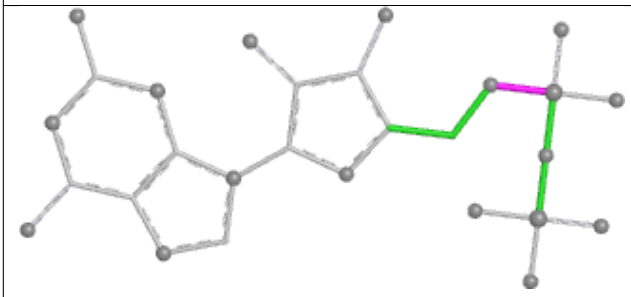
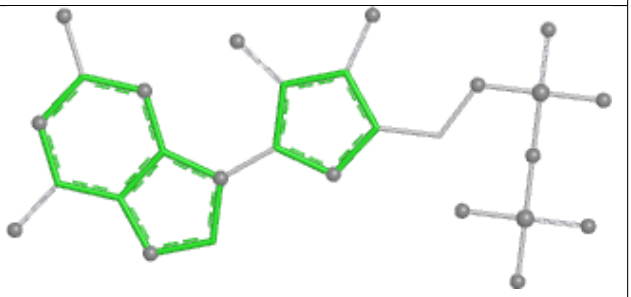
	
Bond lengths	Bond angles
	
Torsions	Rings

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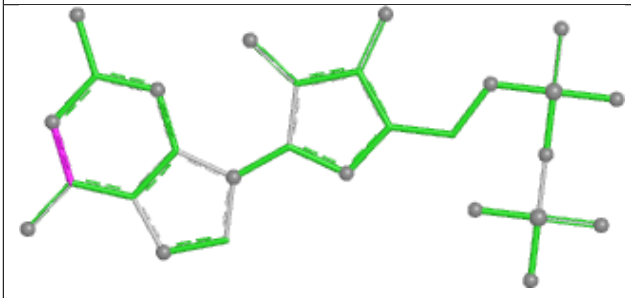	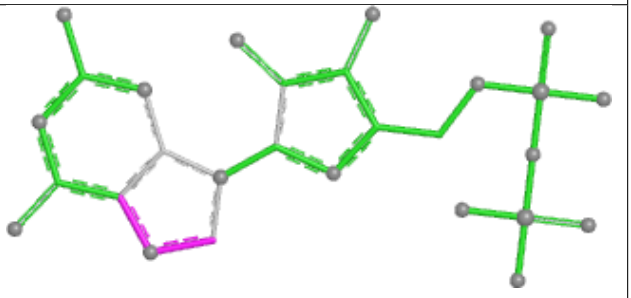
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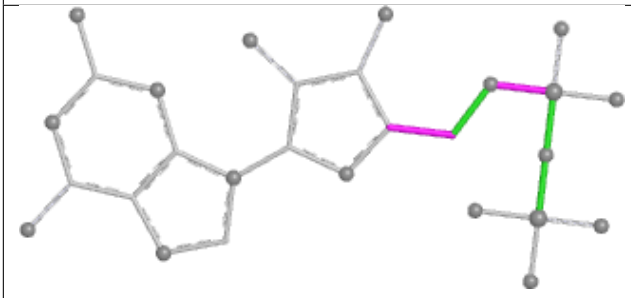
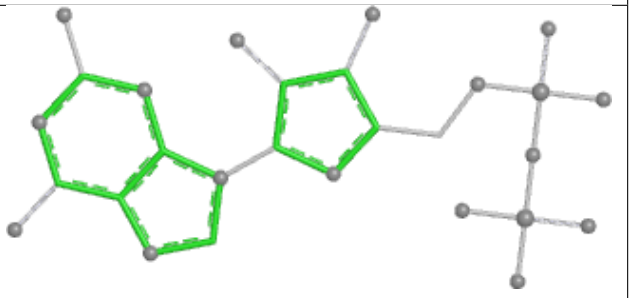
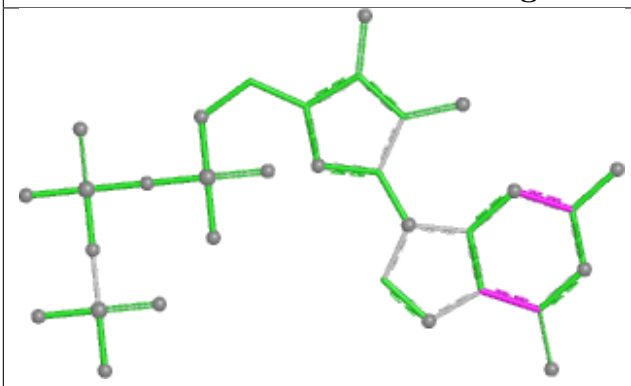
	
Torsions	Rings

Ligand GTP 5I 501



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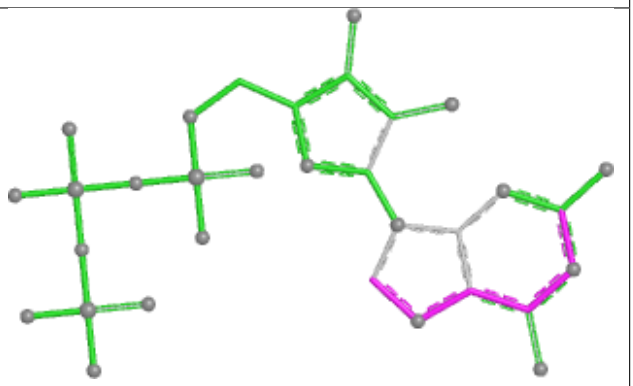

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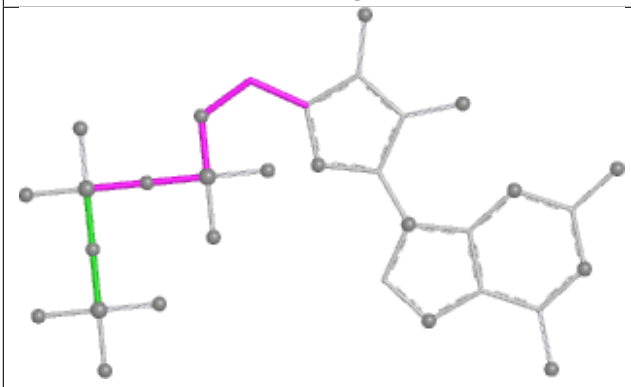

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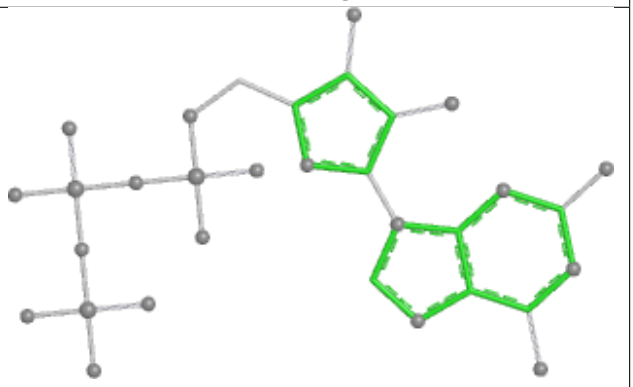
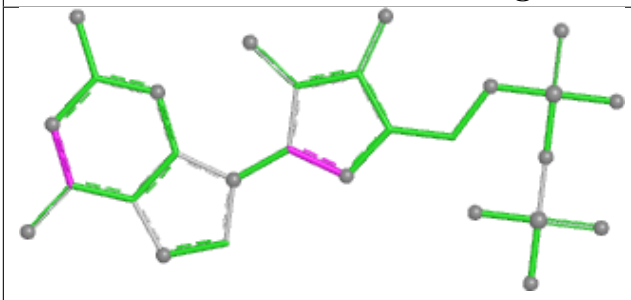


Rings

Ligand GDP 1F 501



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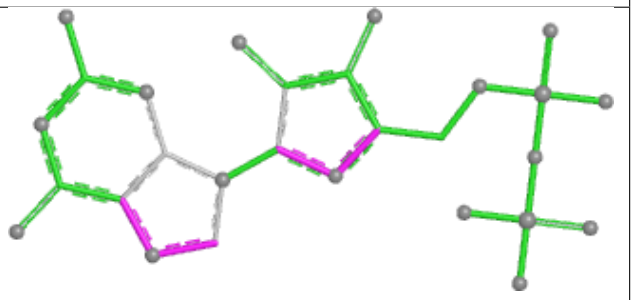

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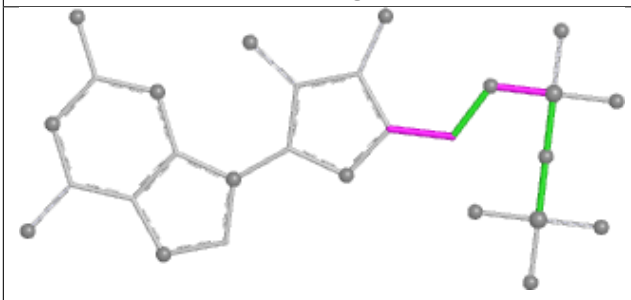

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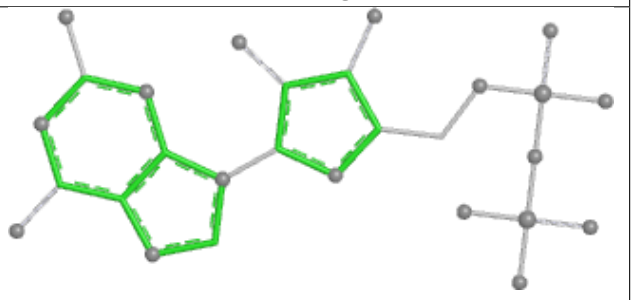
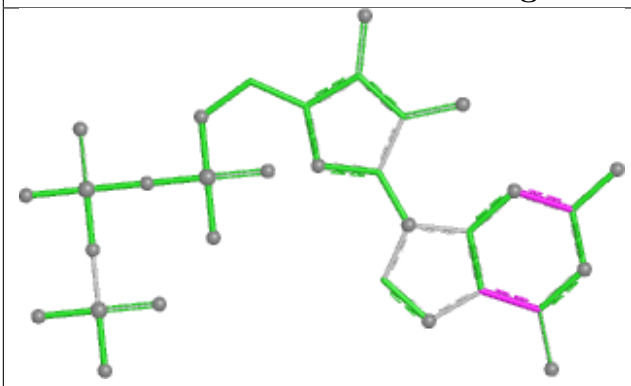


Rings

Ligand GTP 7I 501



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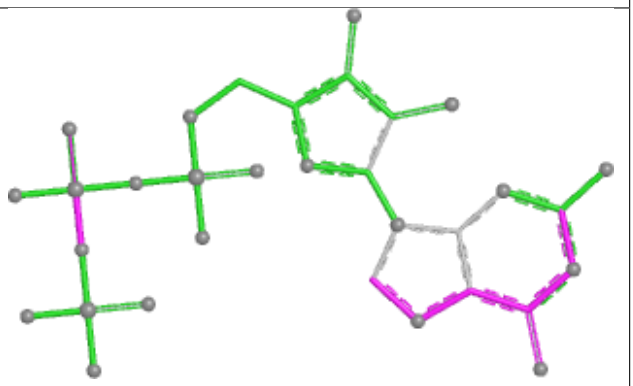

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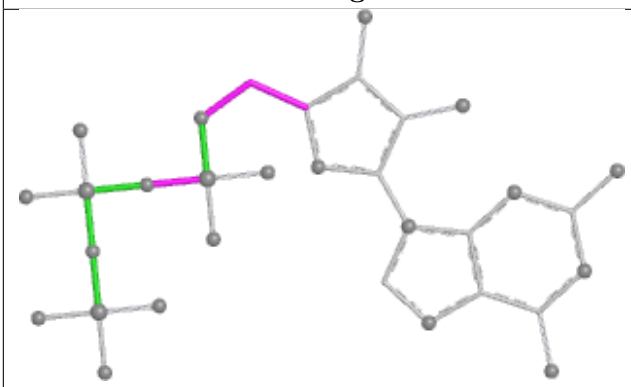

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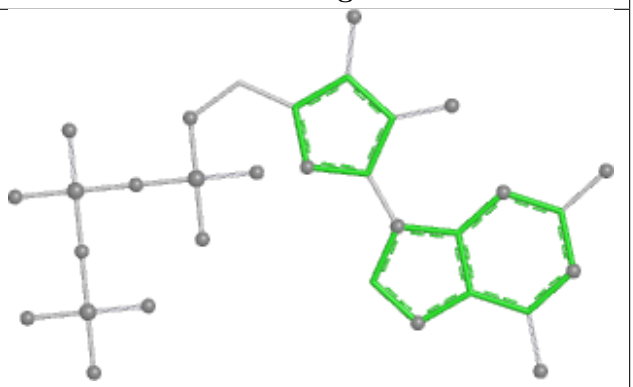
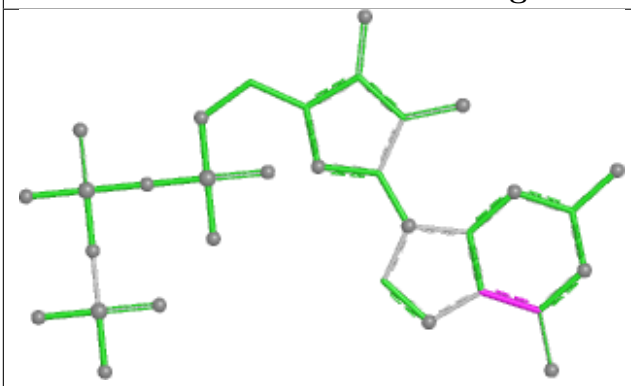


Rings

Ligand GTP 5M 501



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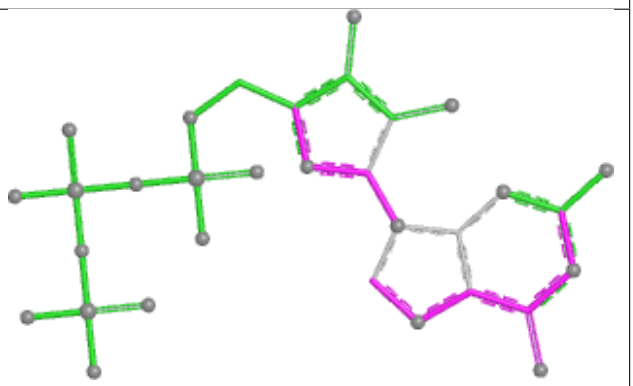

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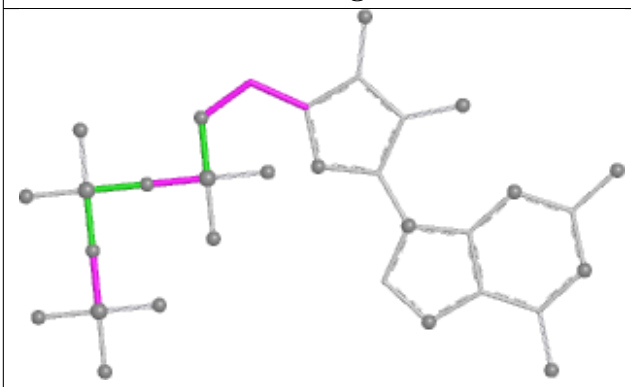
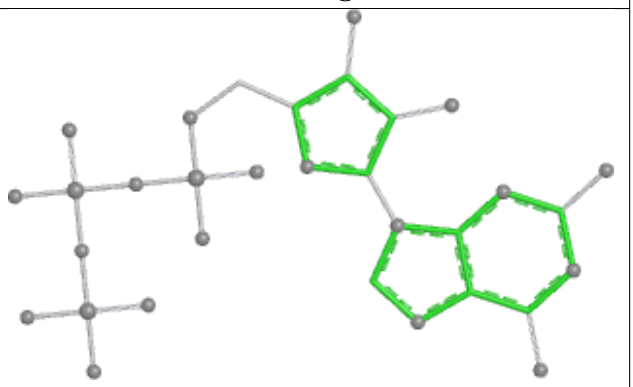
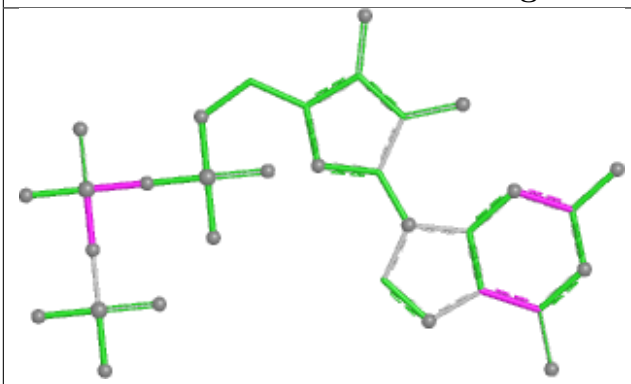


Torsions



Rings

Ligand GTP 9I 501



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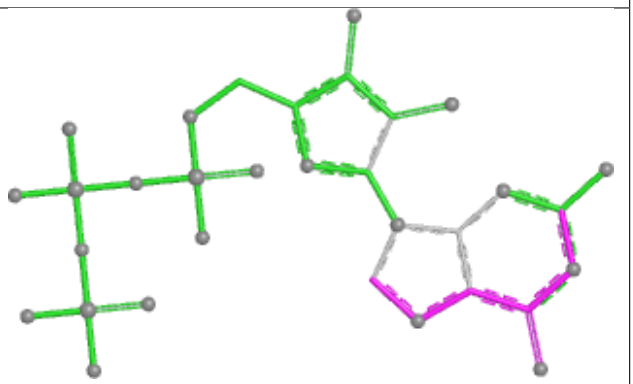

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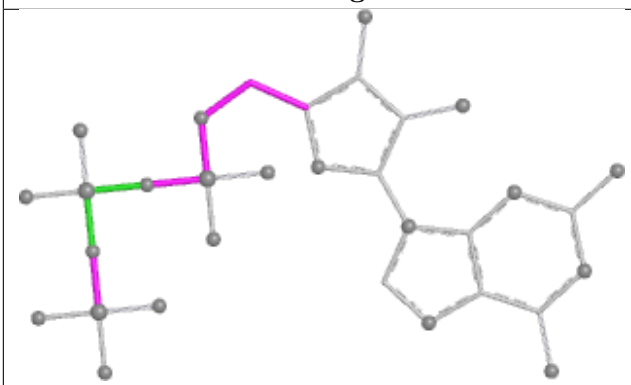

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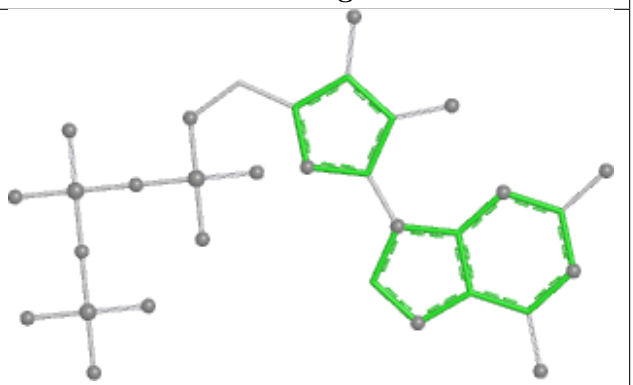
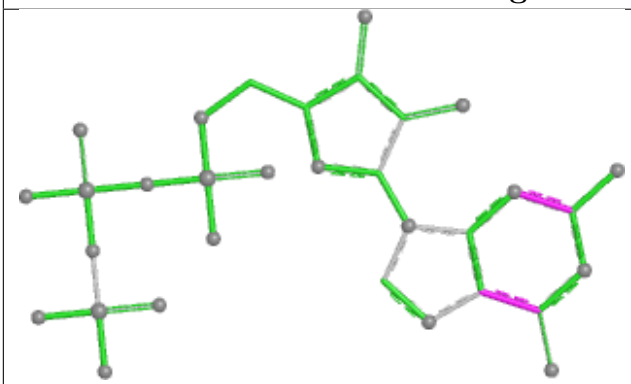


Rings

Ligand GTP 7M 501



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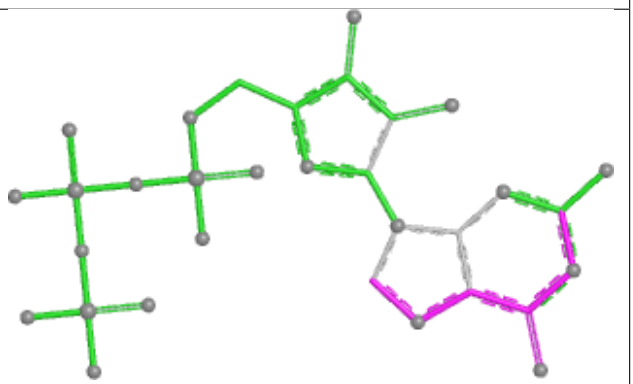

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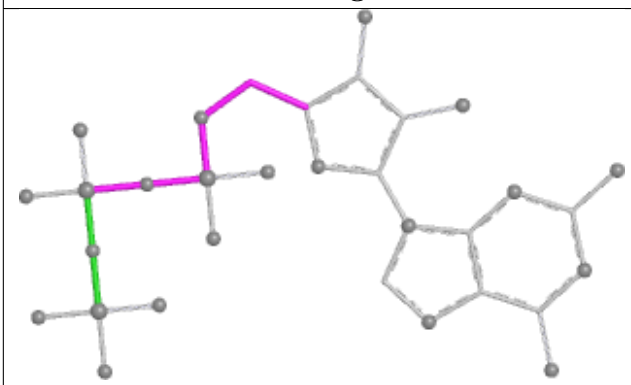

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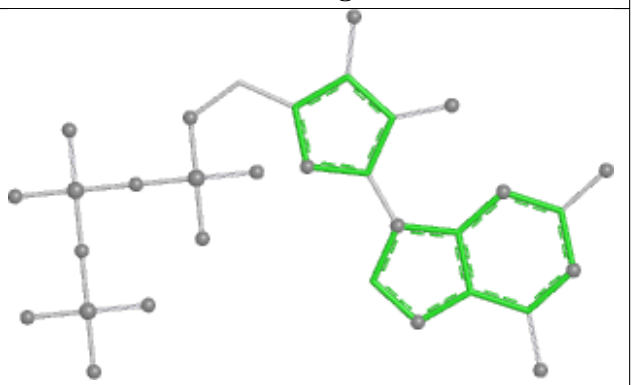
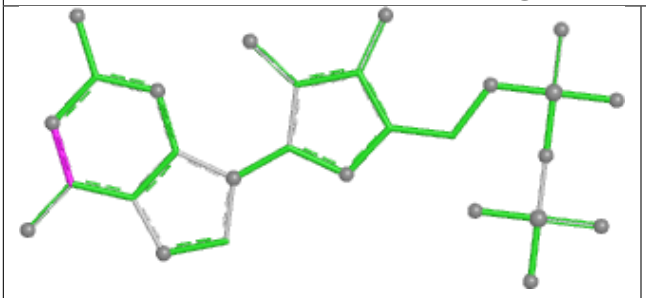


Rings

Ligand GDP 4J 501



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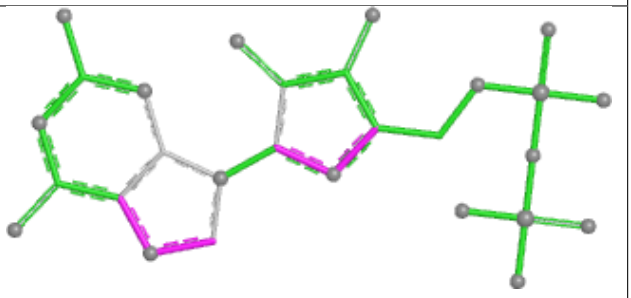

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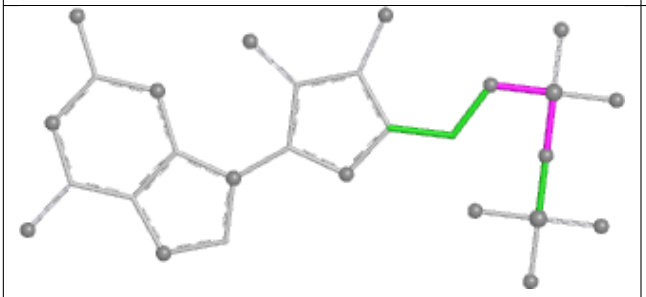

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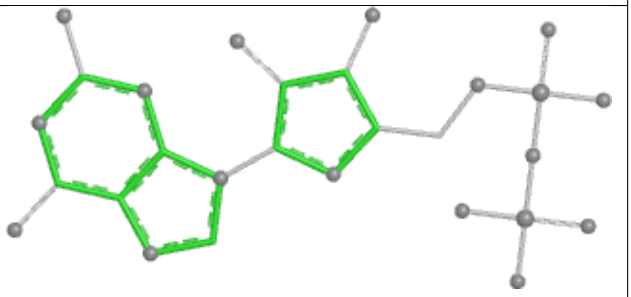
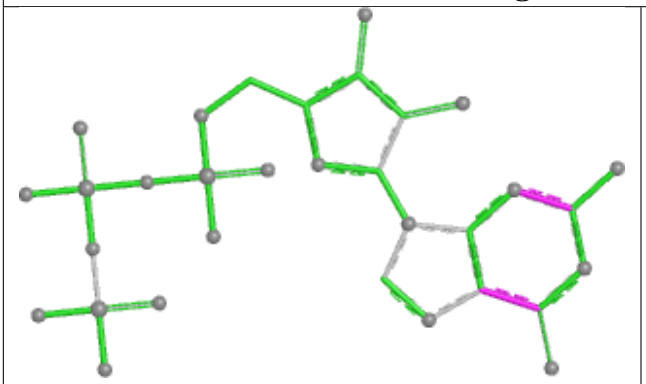


Rings

Ligand GTP 7C 501



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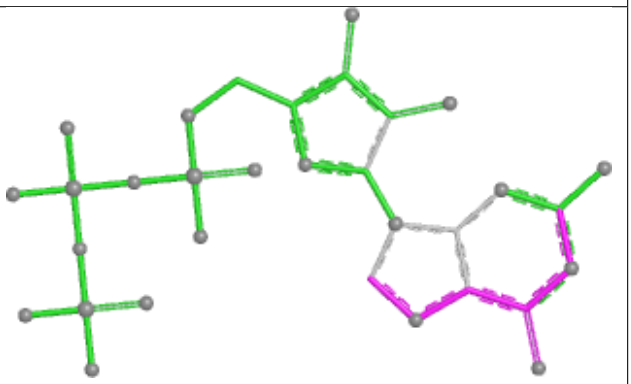

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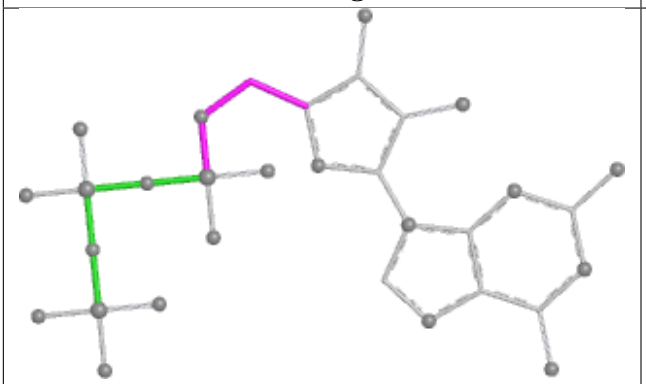

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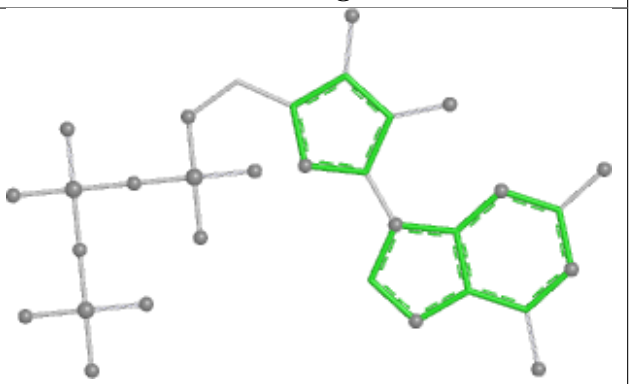
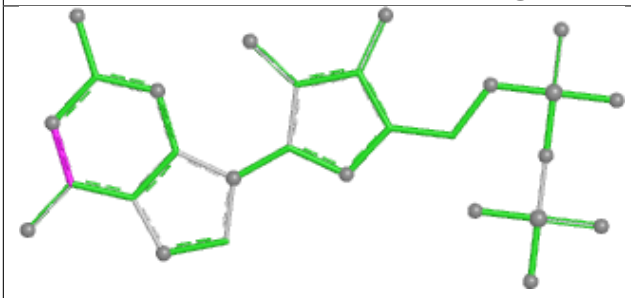
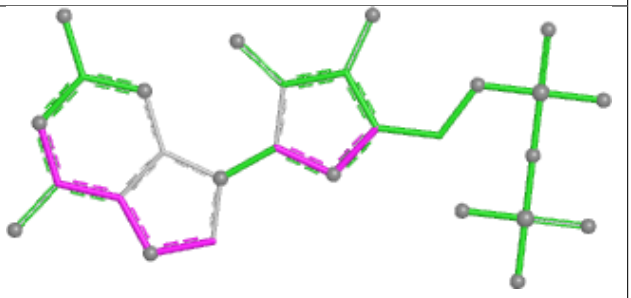
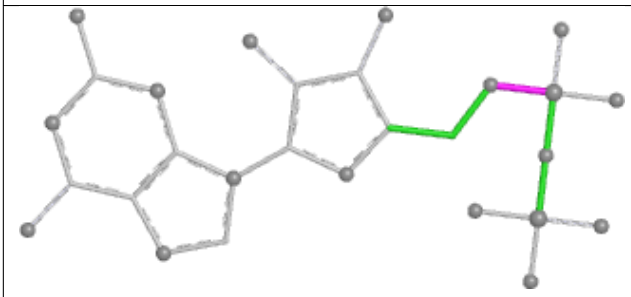
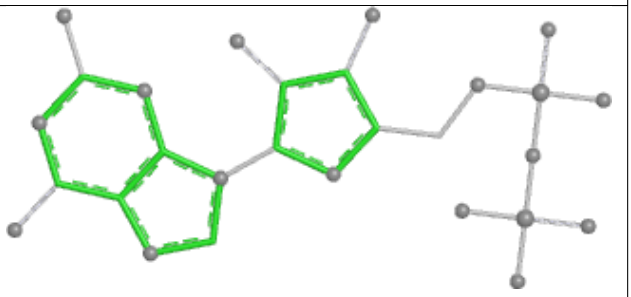
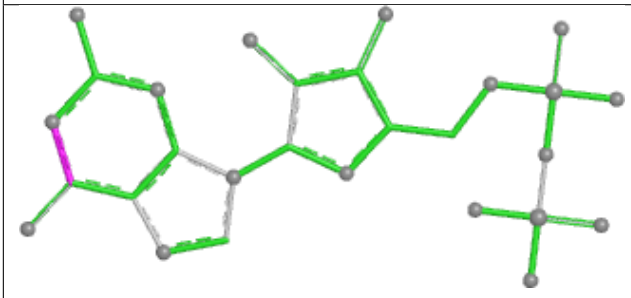
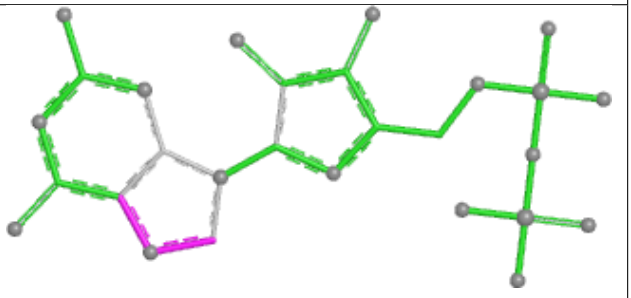
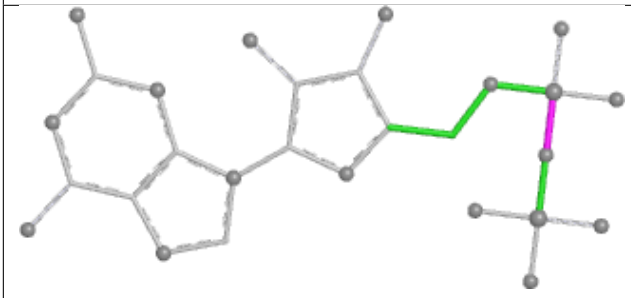
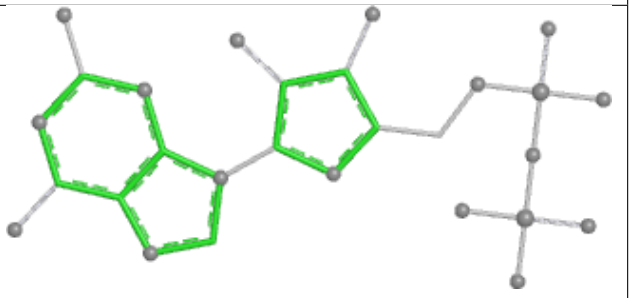
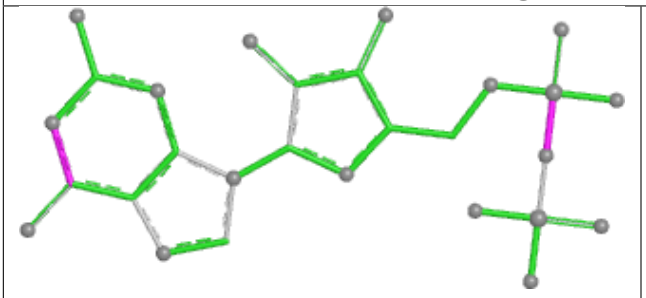


Rings

Ligand GDP 5D 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 6L 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 9L 501



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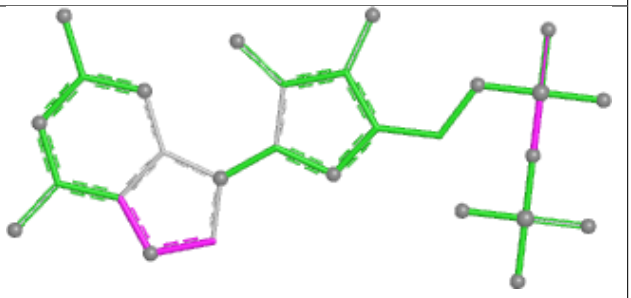

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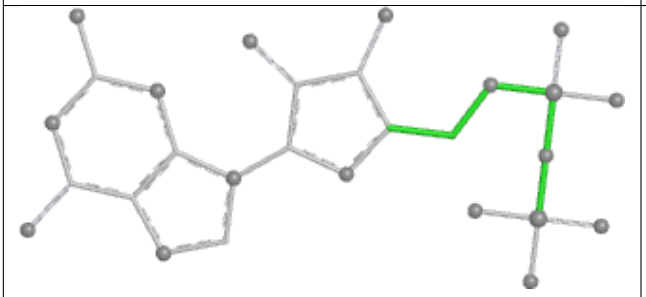

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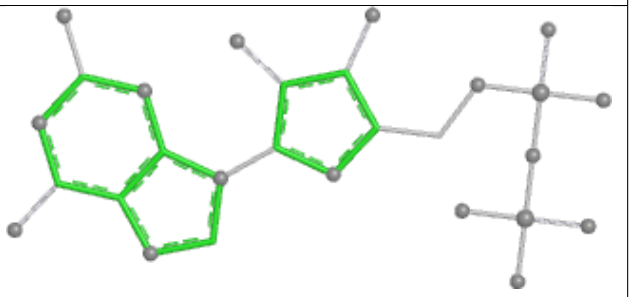
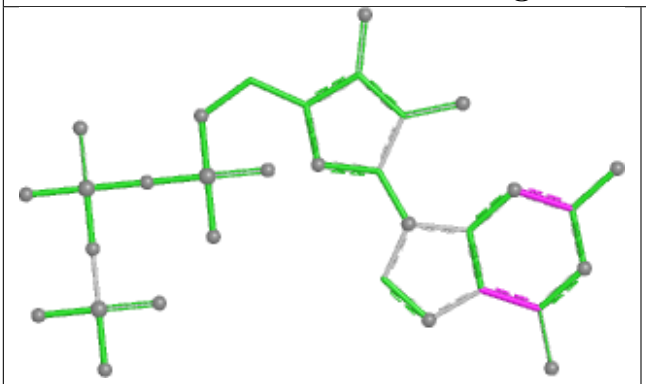


Rings

Ligand GTP 5A 501



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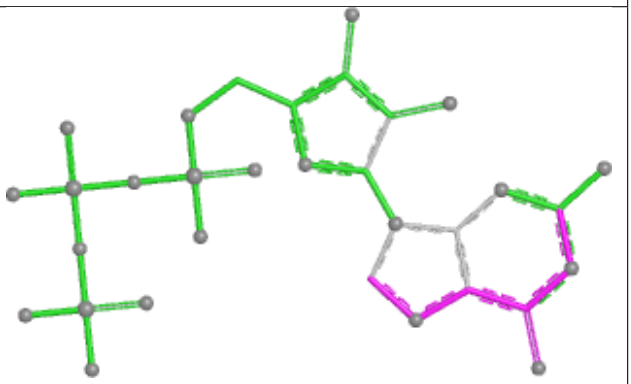

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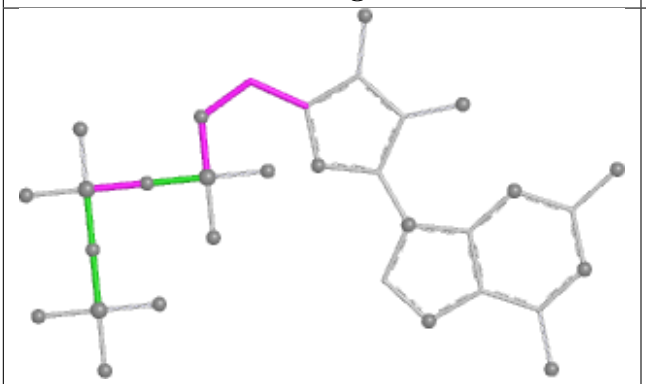

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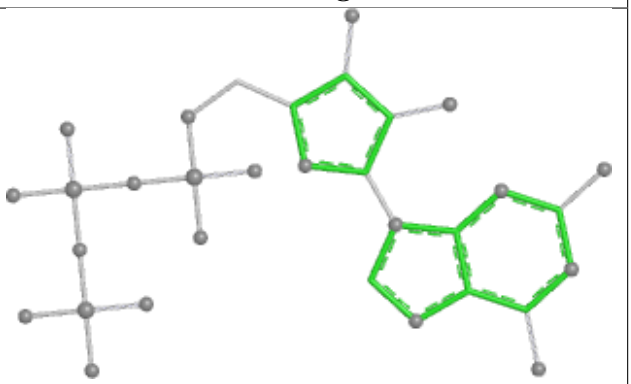

Rings

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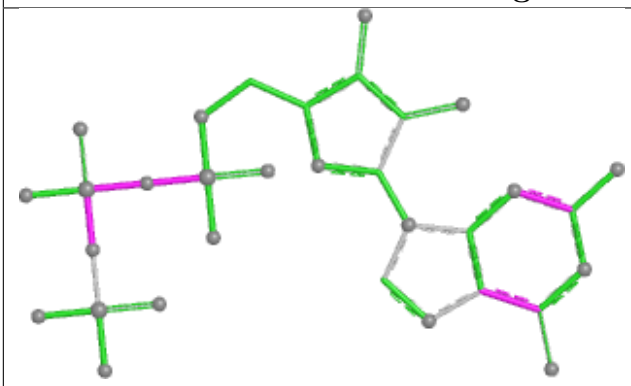

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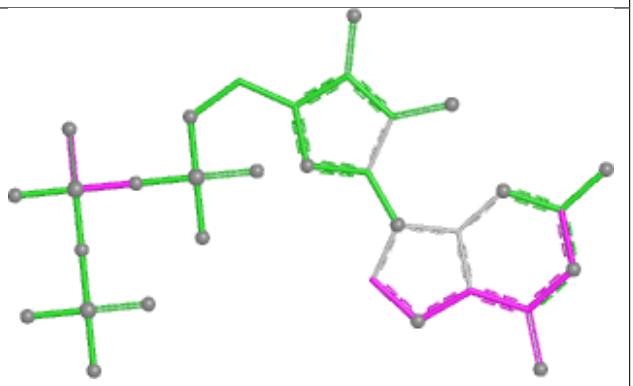

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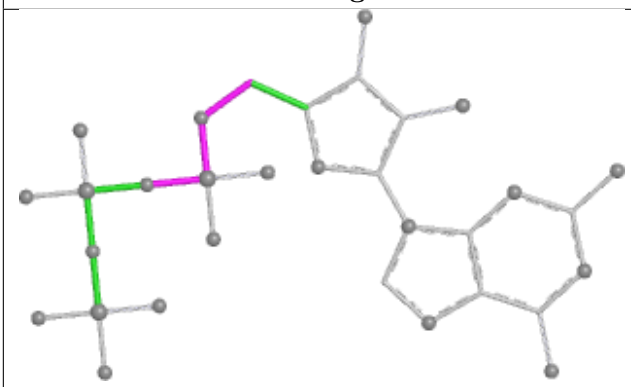

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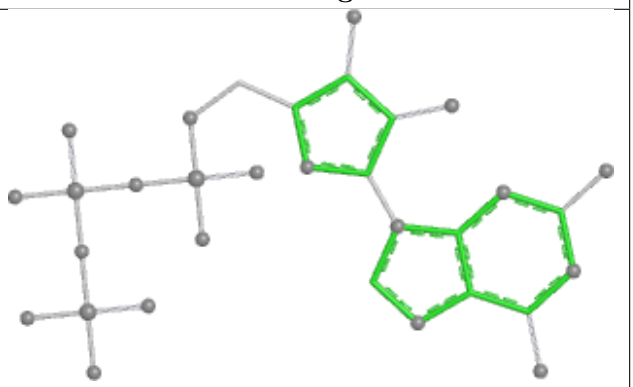
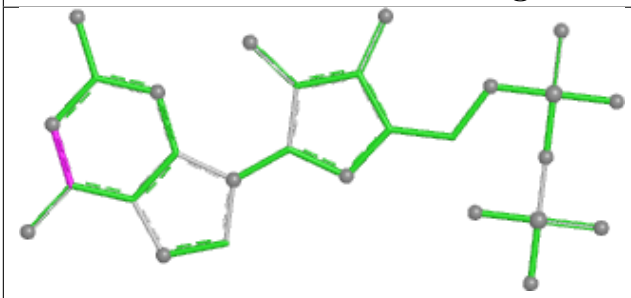


Rings

Ligand GDP 6D 501



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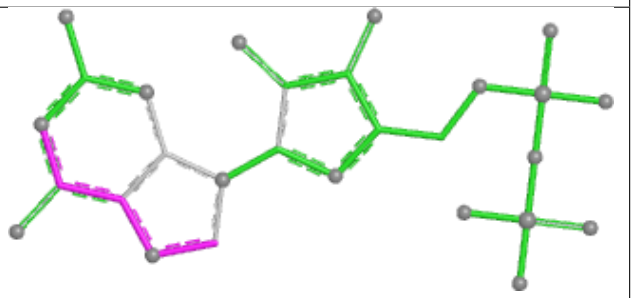

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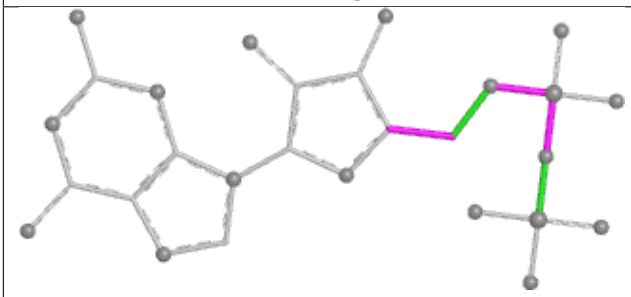

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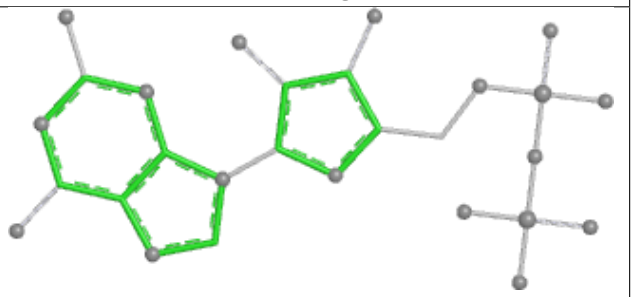
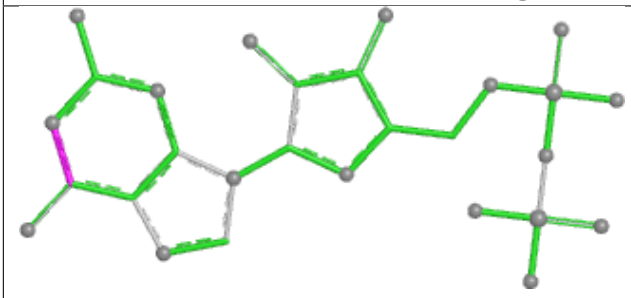
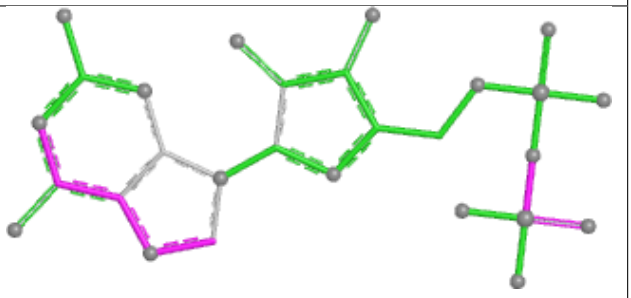
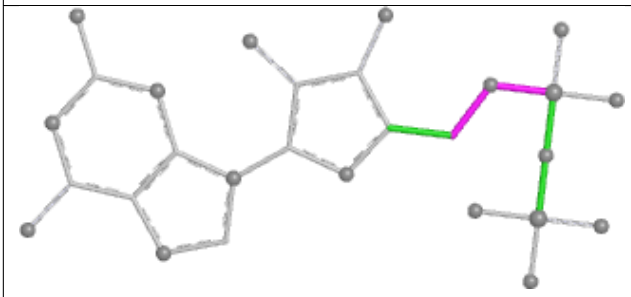
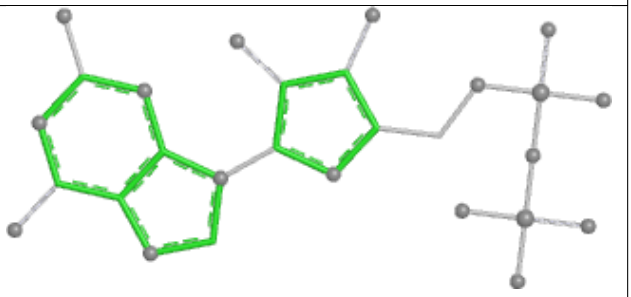
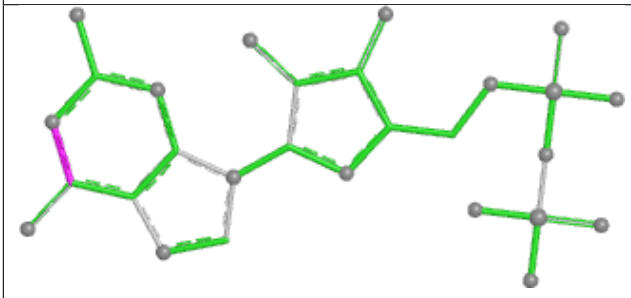
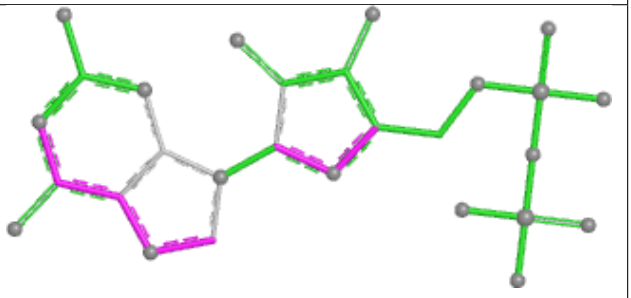
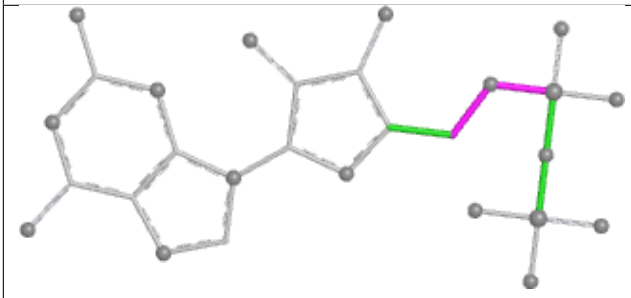
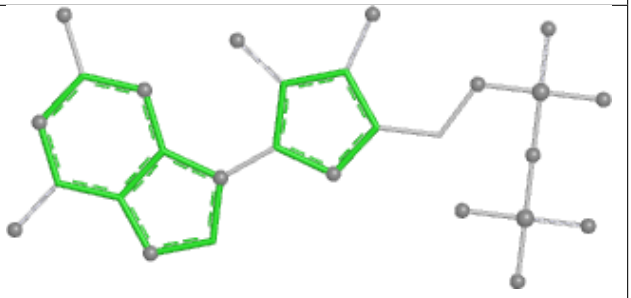
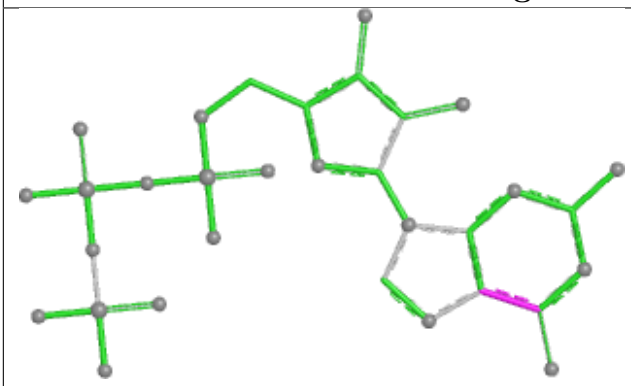


Rings

Ligand GDP 5F 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 9B 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 8C 501



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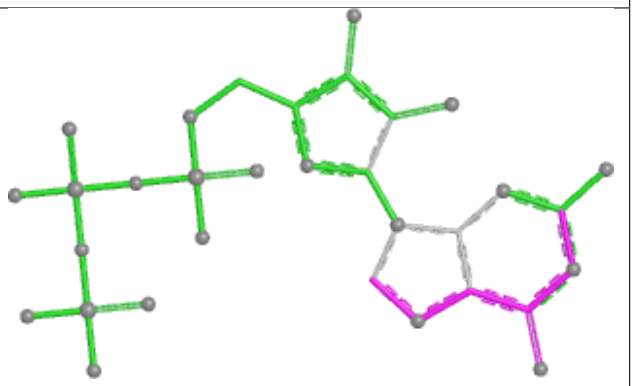

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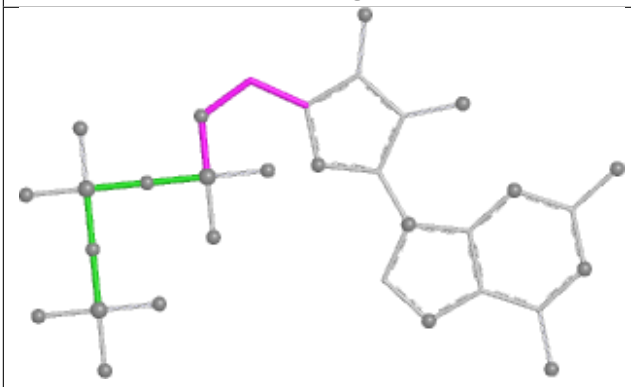
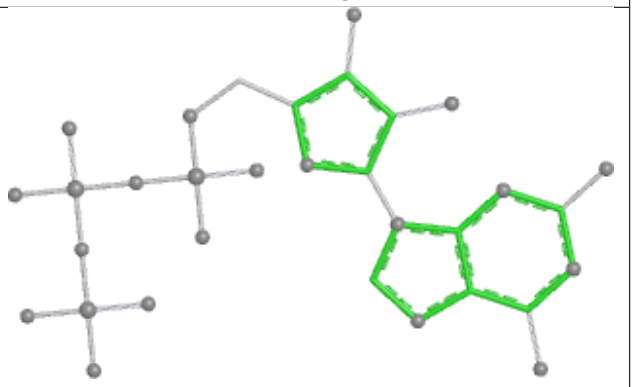
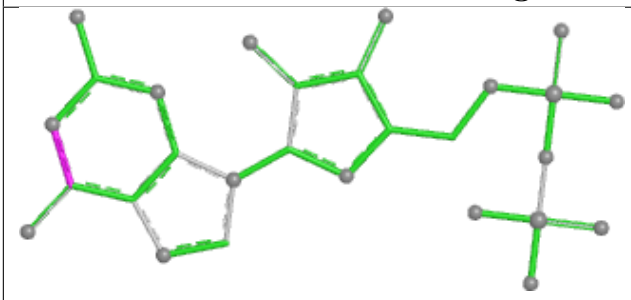


Torsions

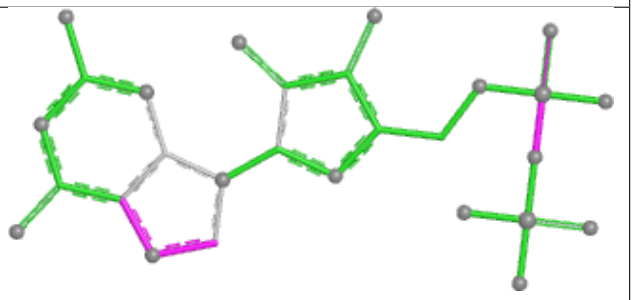


Rings

Ligand GDP 2B 501



Bond lengths



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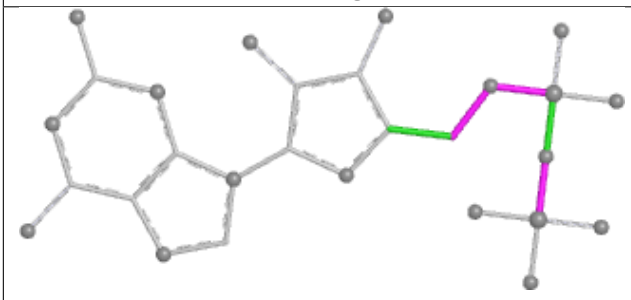
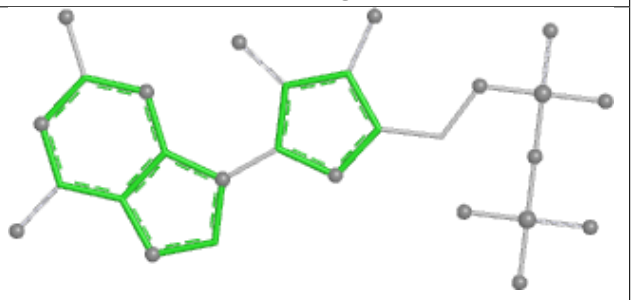
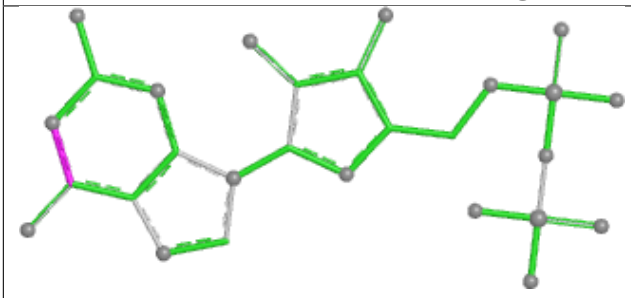
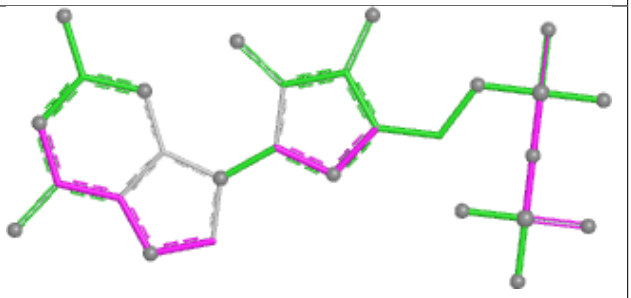
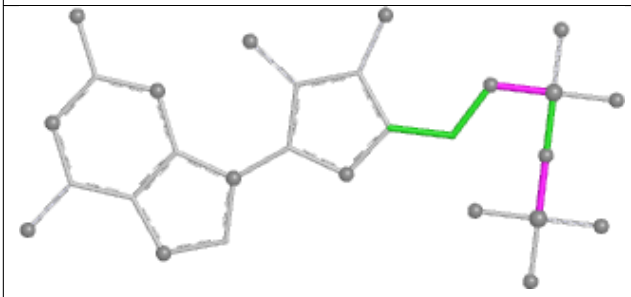
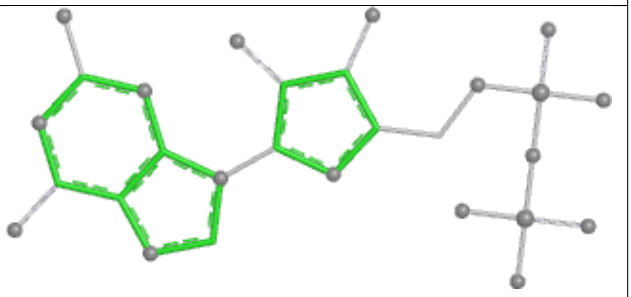
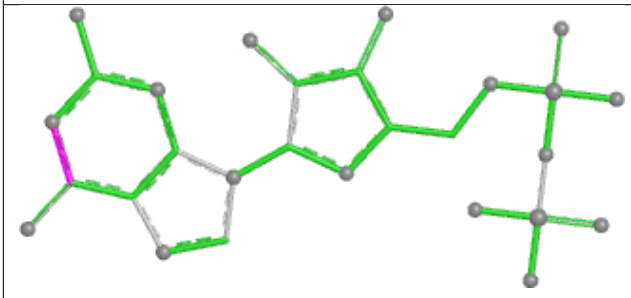
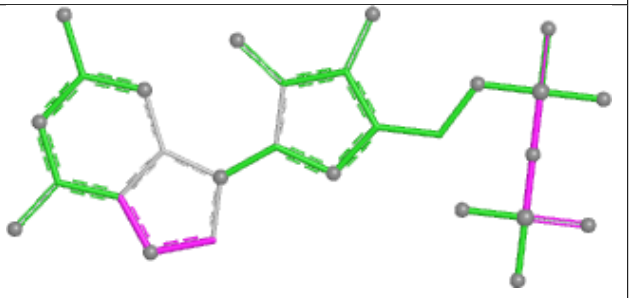
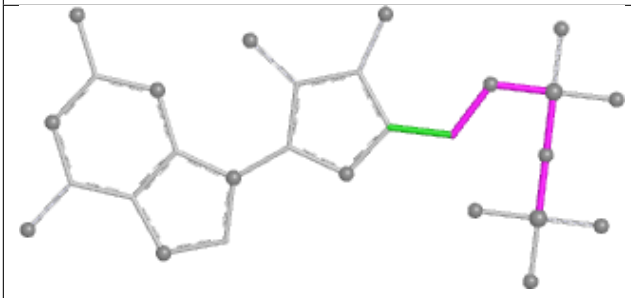
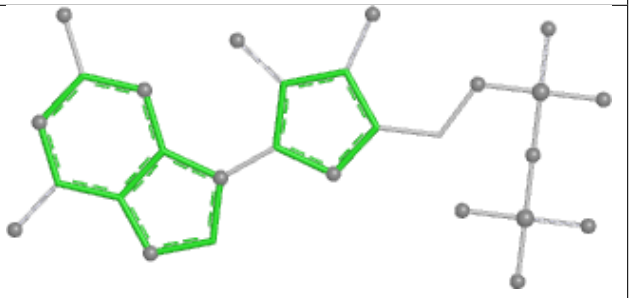


Torsions



Rings

Ligand GDP 7F 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 5H 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

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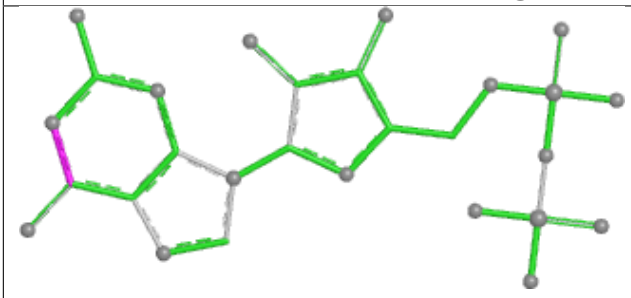
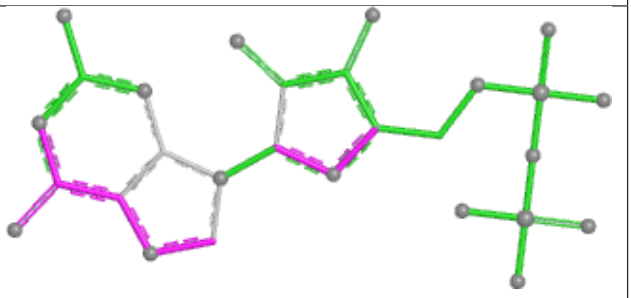
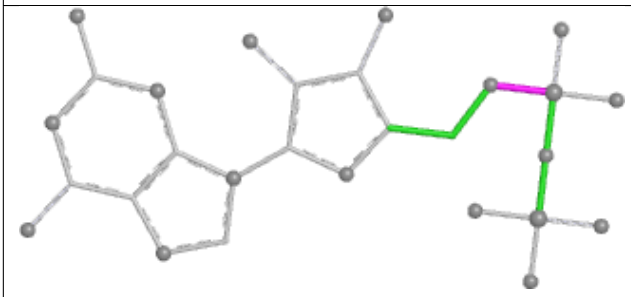
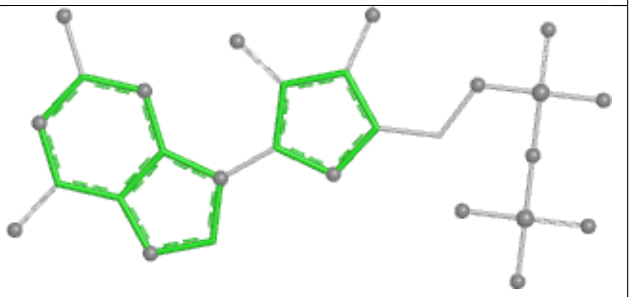
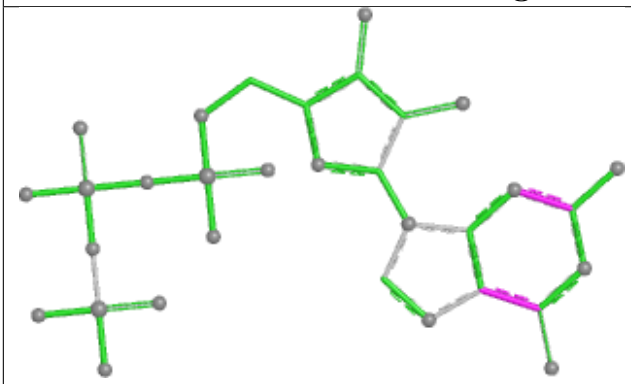
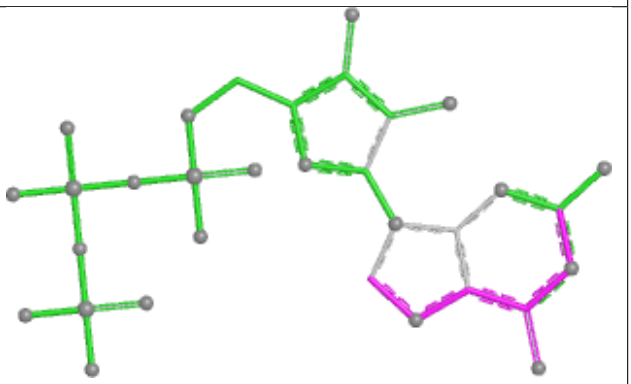
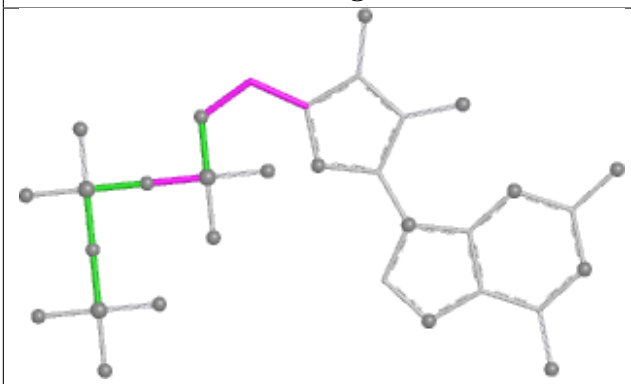
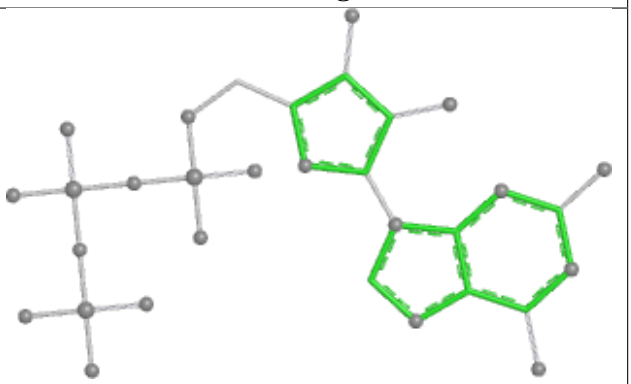
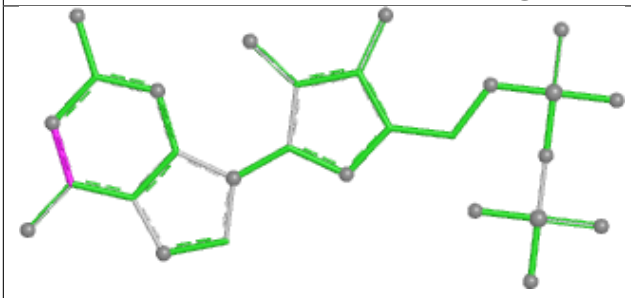
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 7G 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 8J 501



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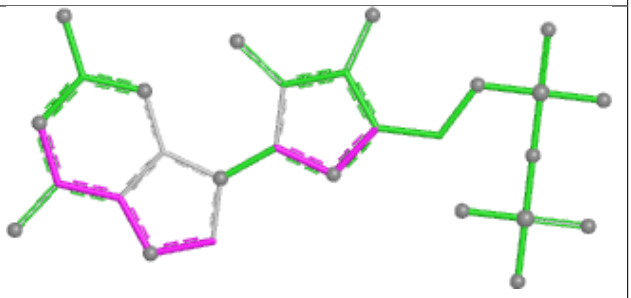

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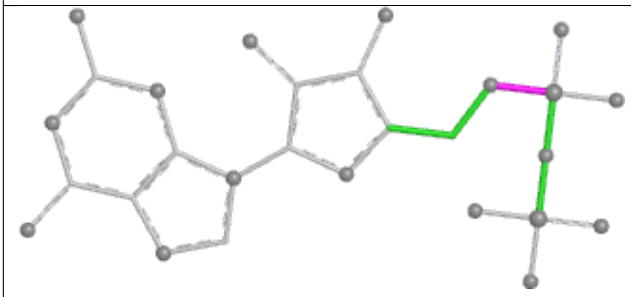

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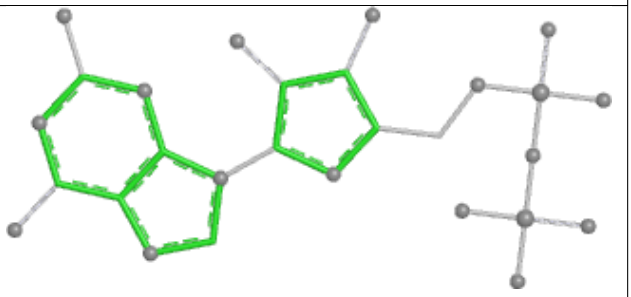
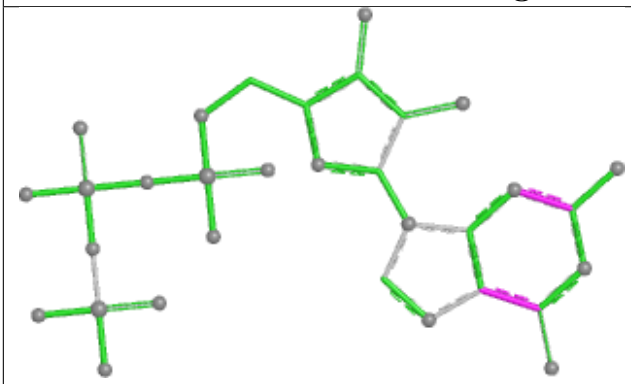


Rings

Ligand GTP 6A 501



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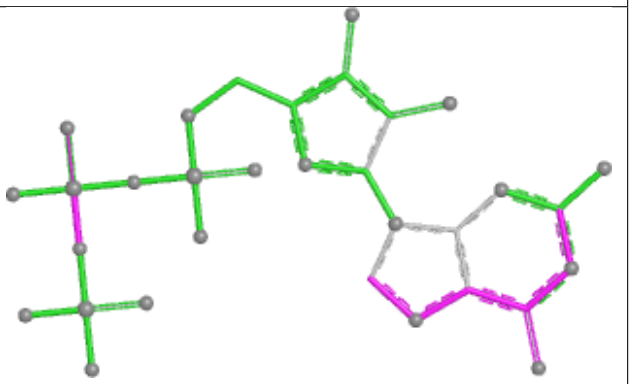

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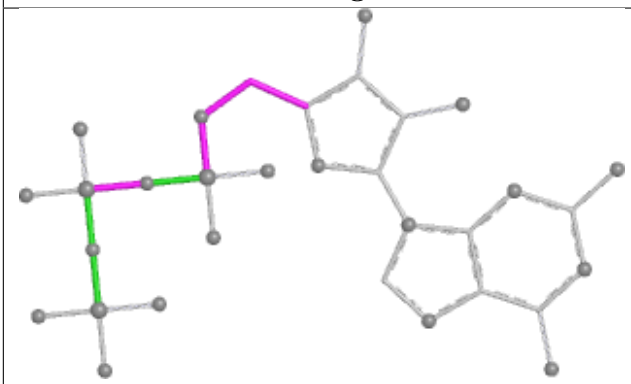

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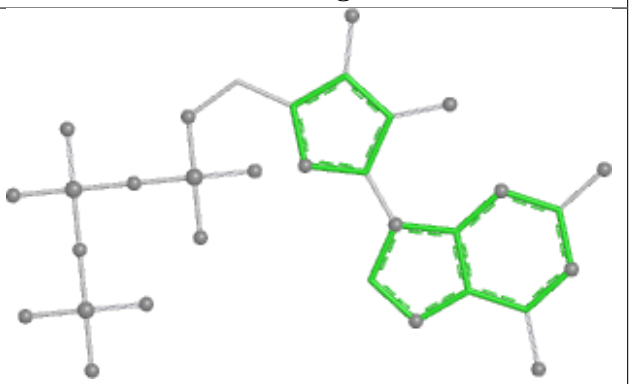
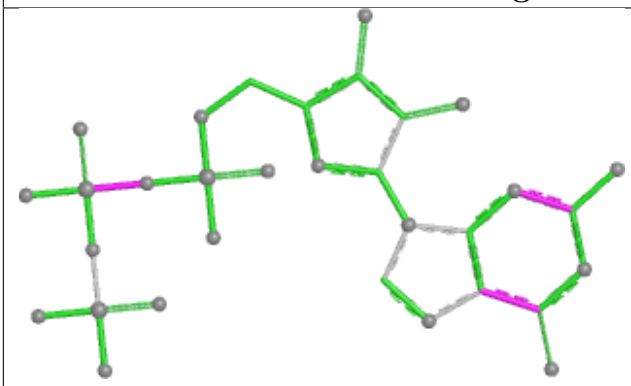


Rings

Ligand GTP 7K 501



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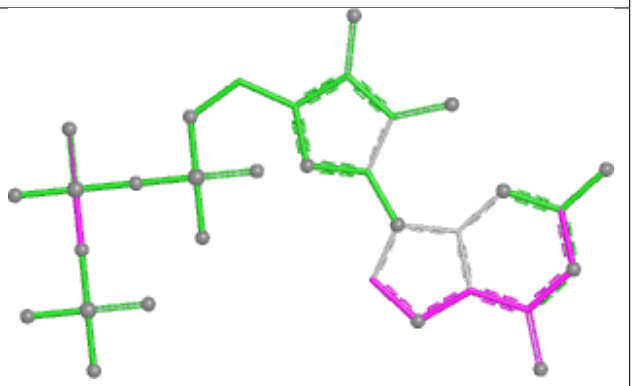

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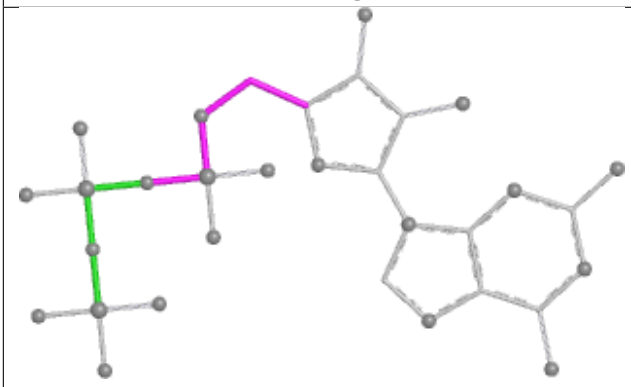

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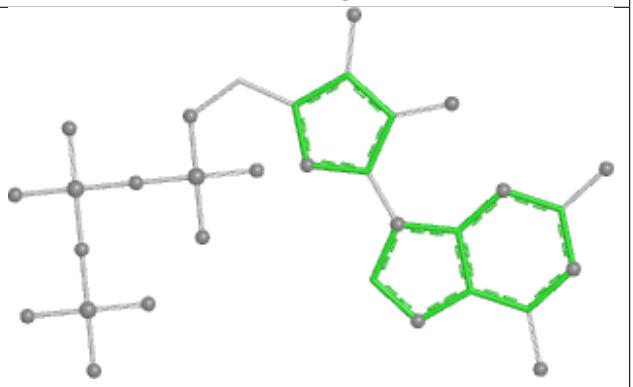
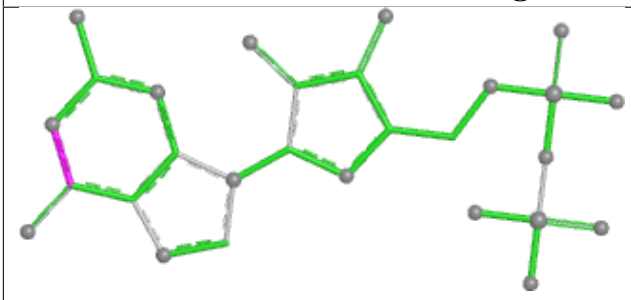


Rings

Ligand GDP 1D 501



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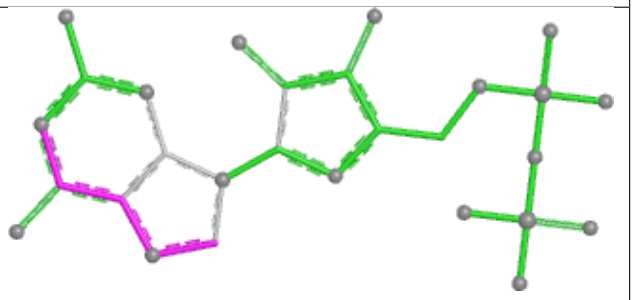

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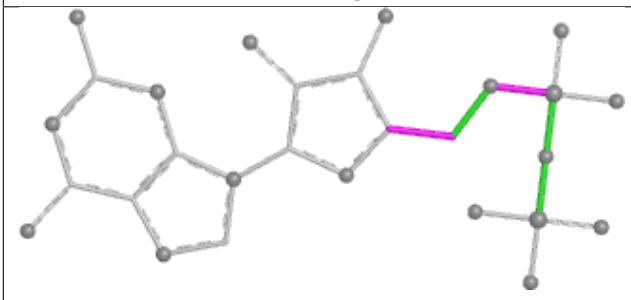

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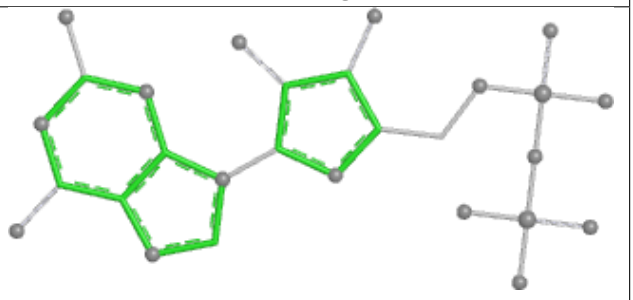

Rings

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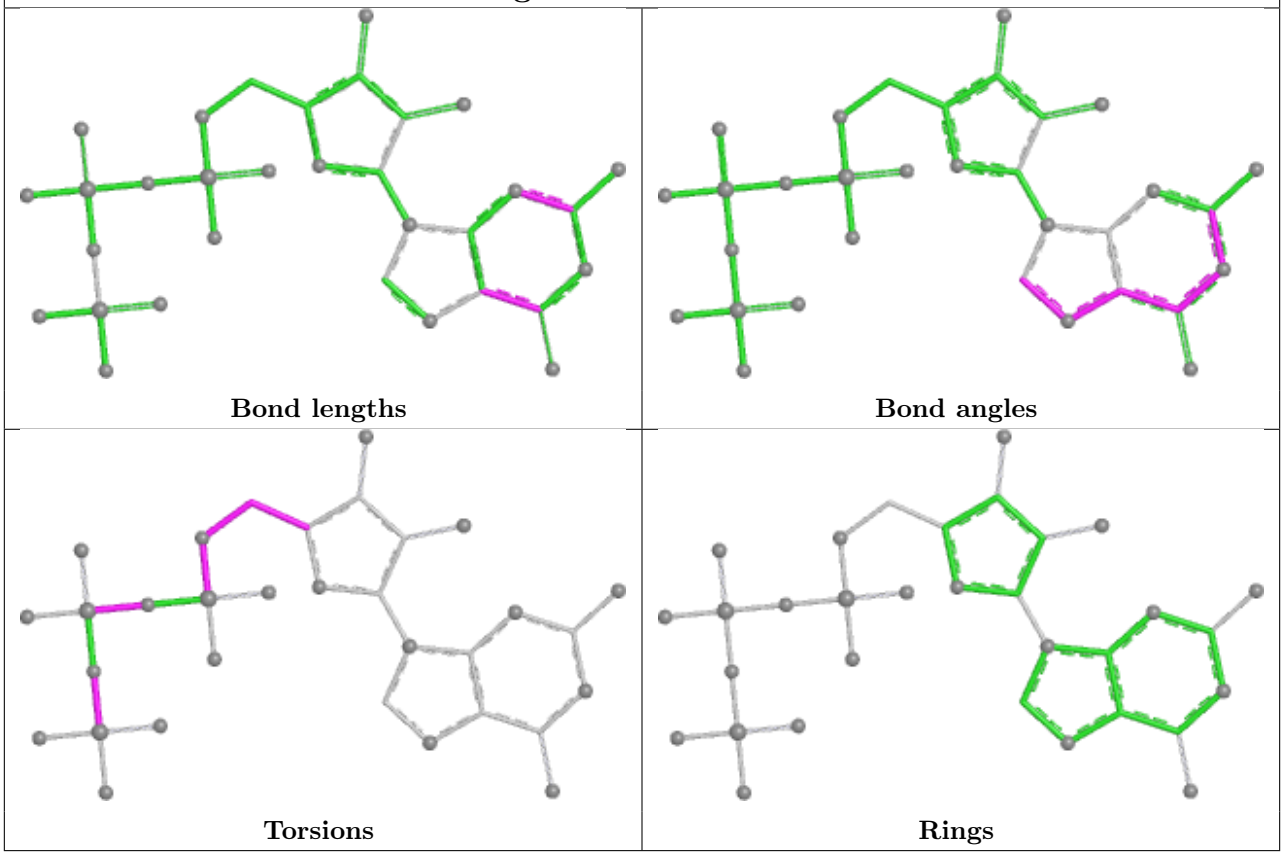

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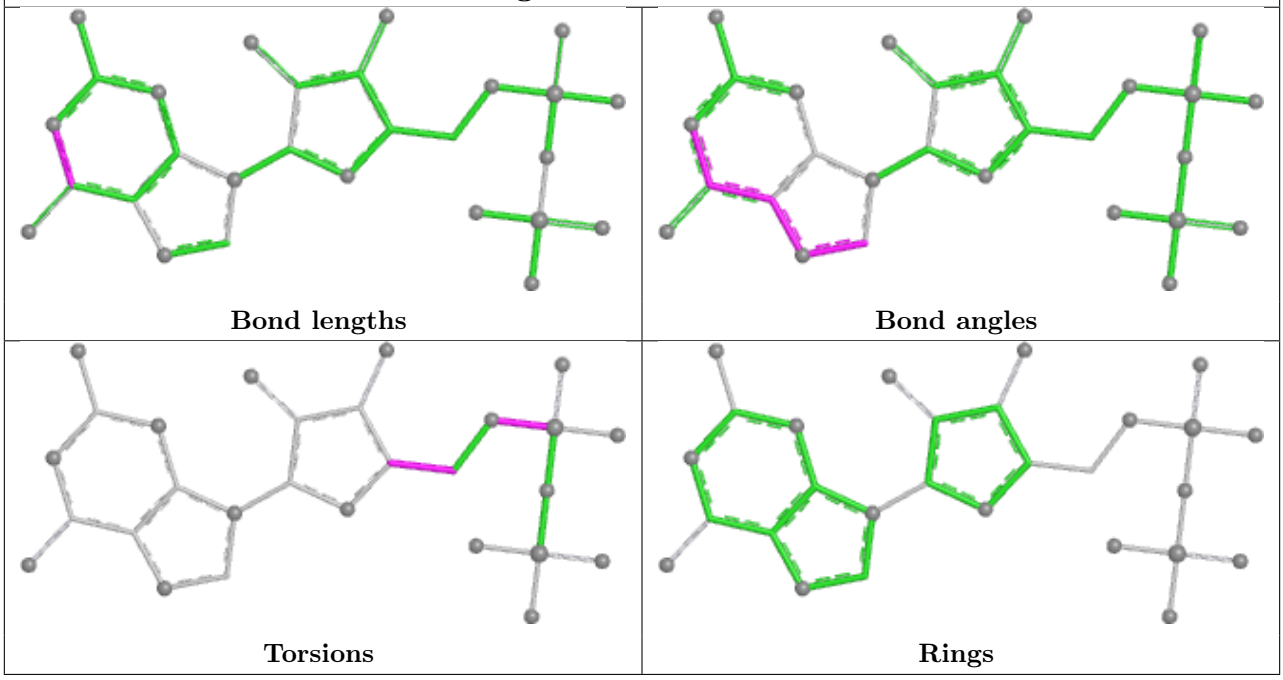

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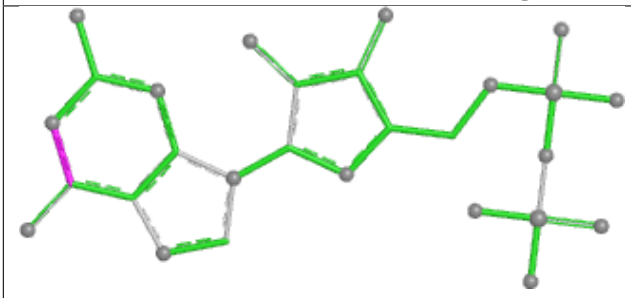
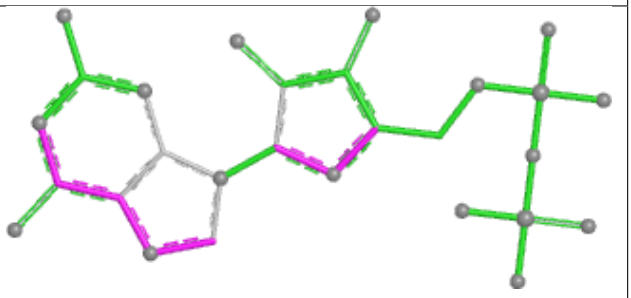
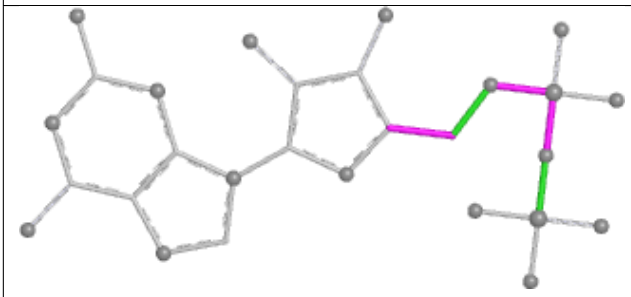
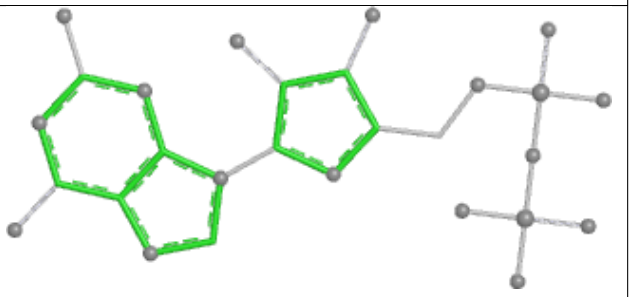
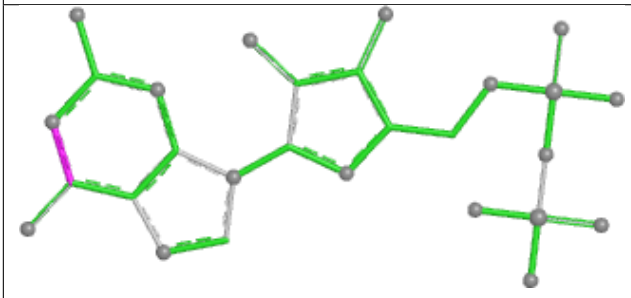
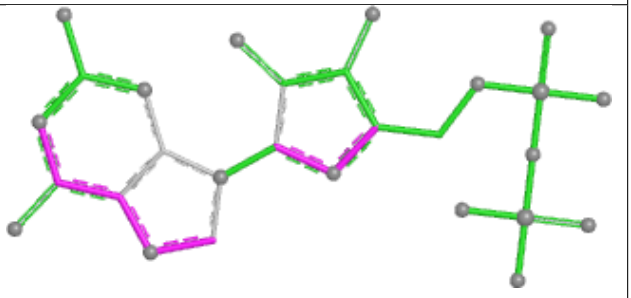
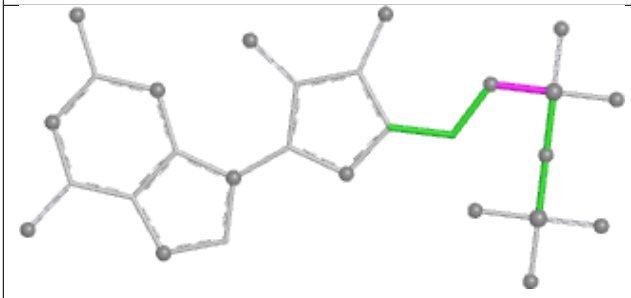
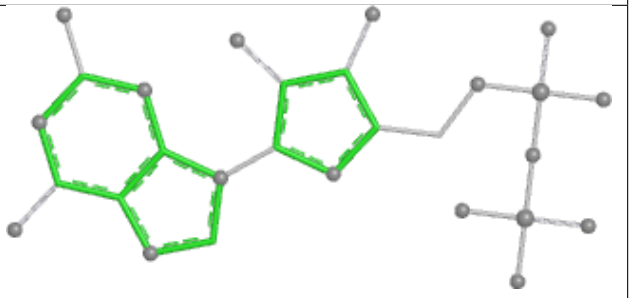
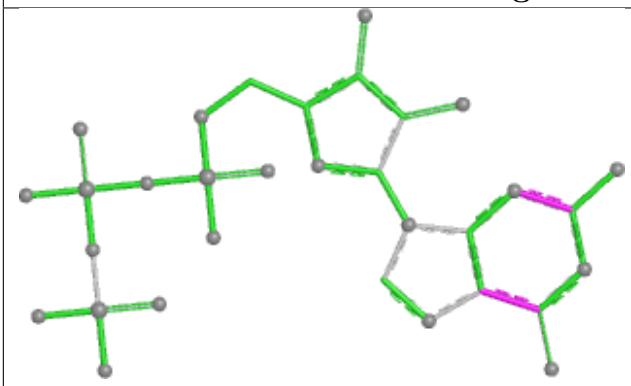
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 3H 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 2G 501



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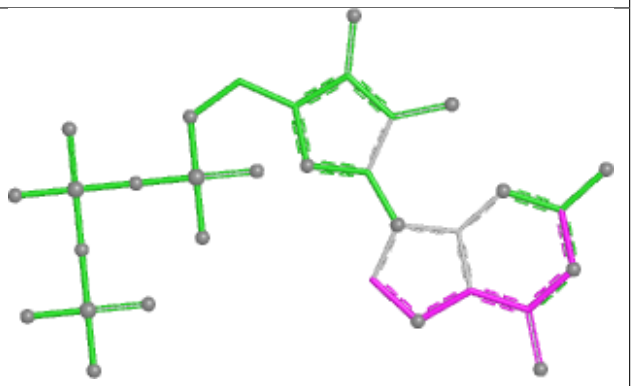

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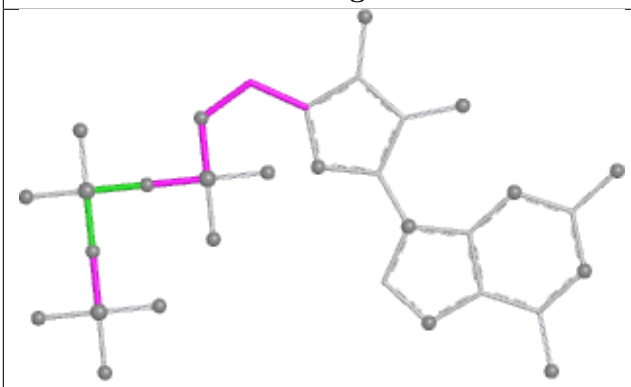
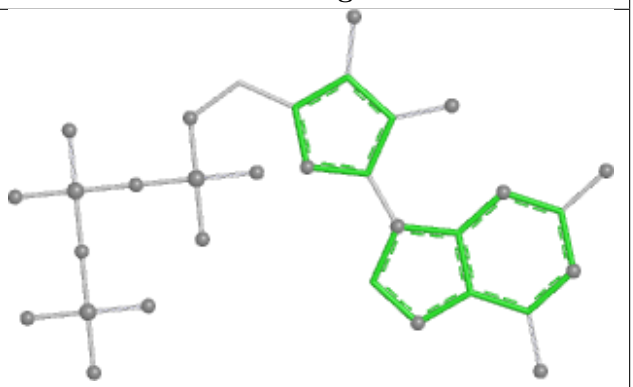
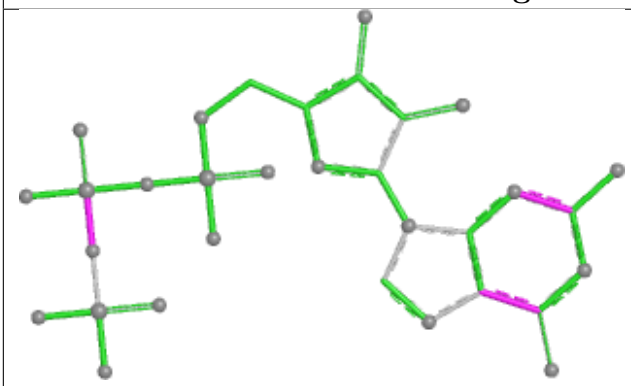


Torsions



Rings

Ligand GTP 9A 501



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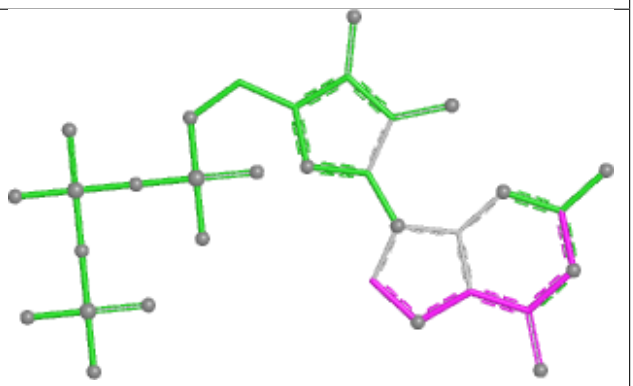

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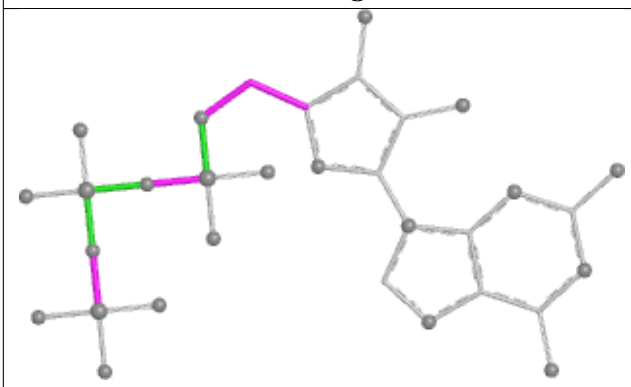

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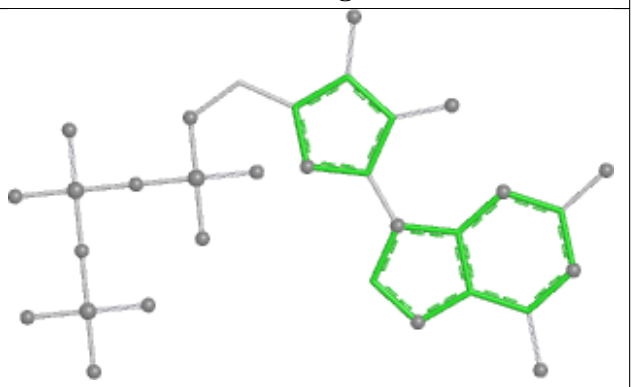
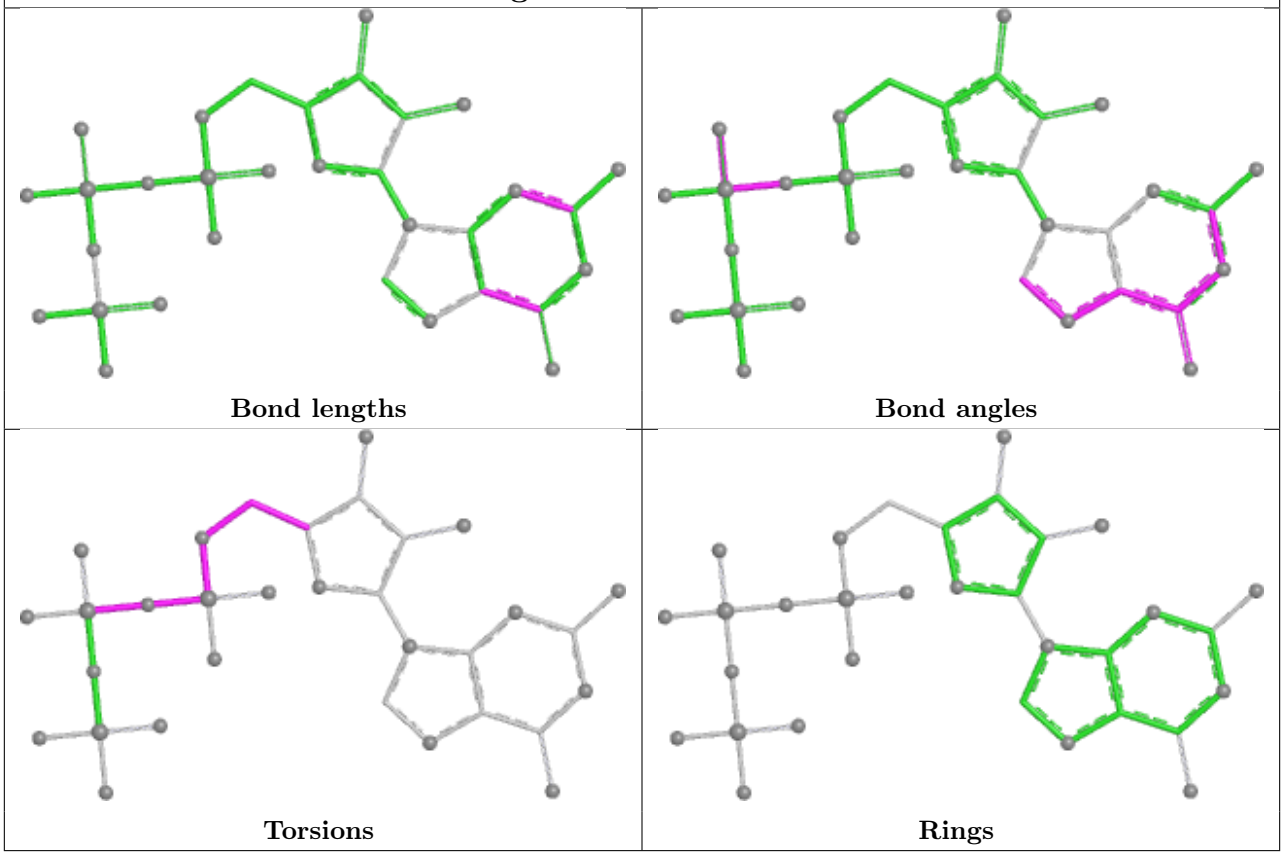
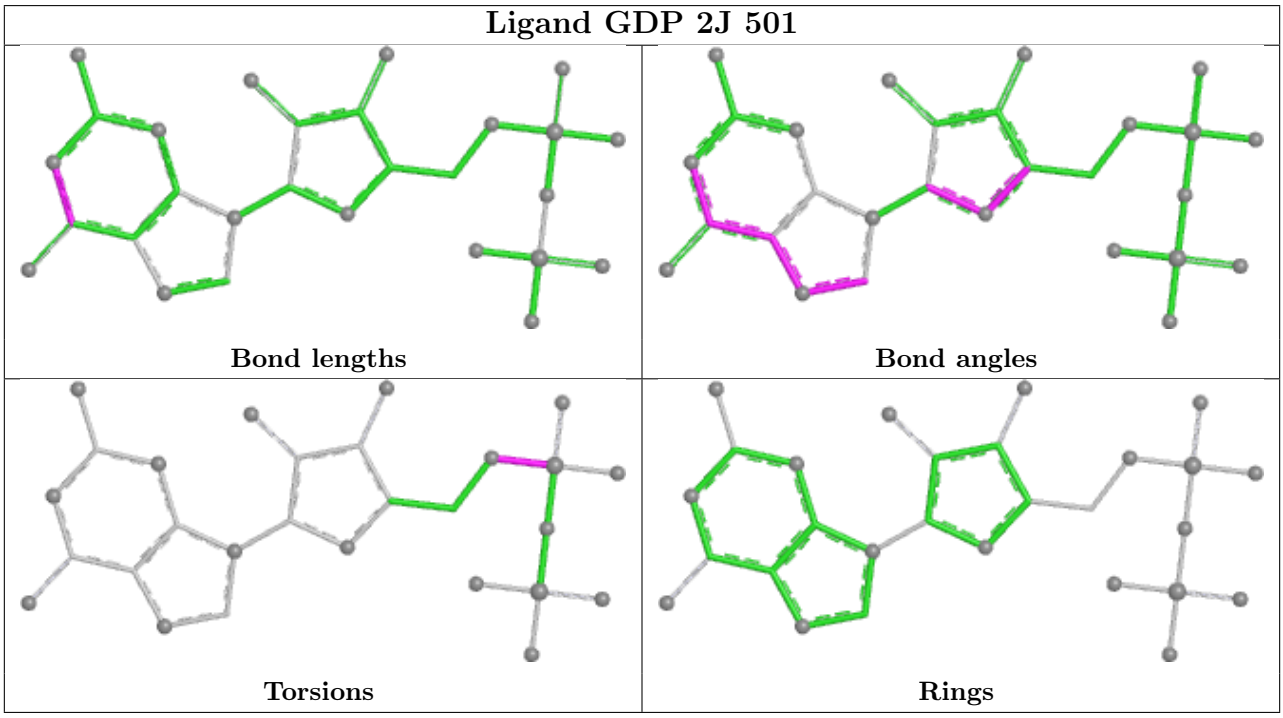


Rings

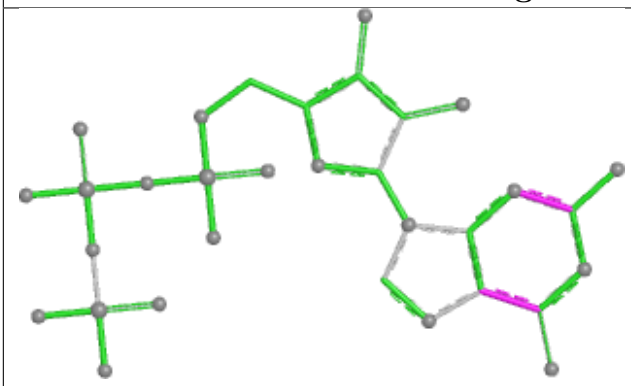
Ligand GTP 2M 501



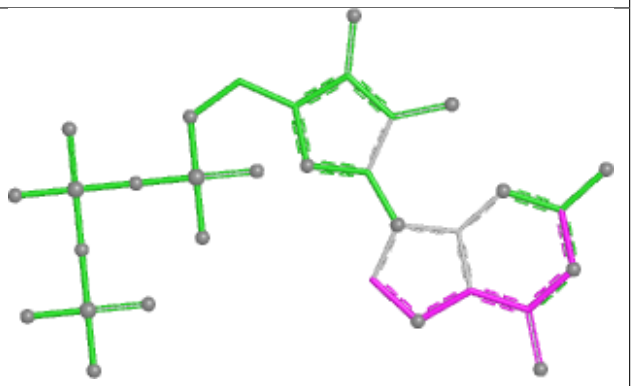
Ligand GDP 2J 501



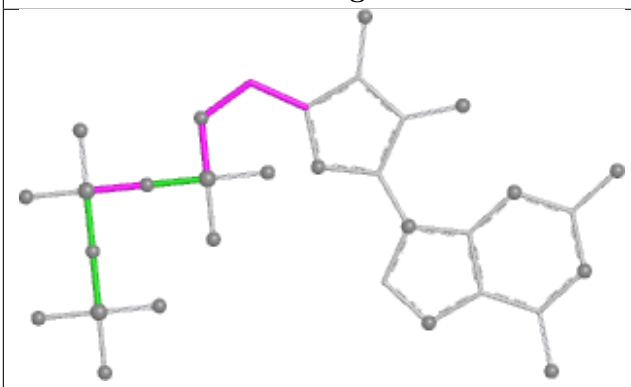
Ligand GTP 1E 501



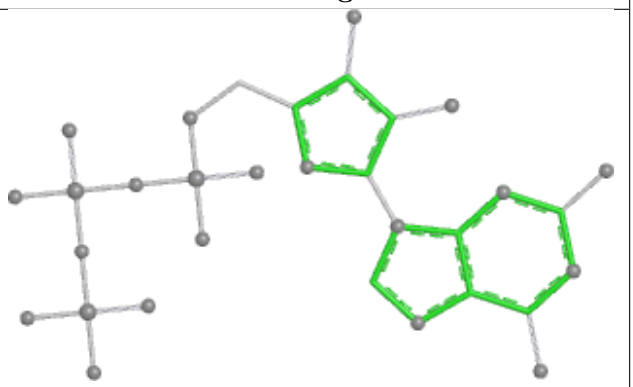
Bond lengths



Bond angles

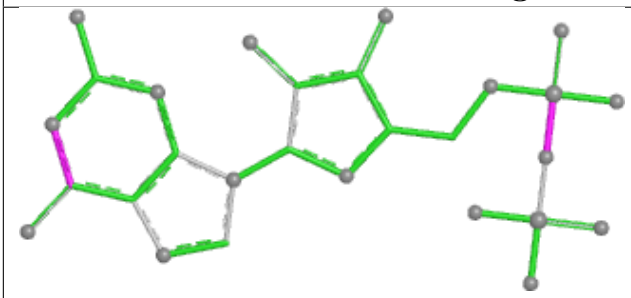


Torsions



Rings

Ligand GDP 1N 501



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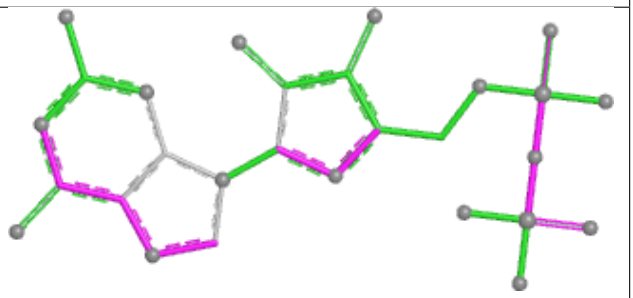

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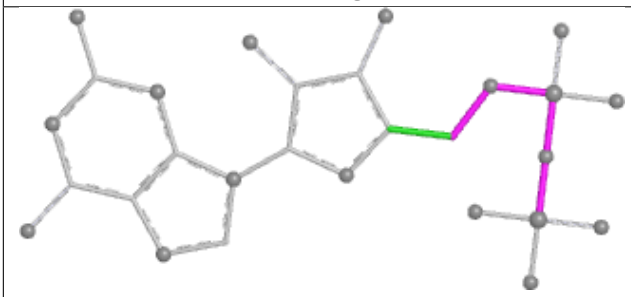

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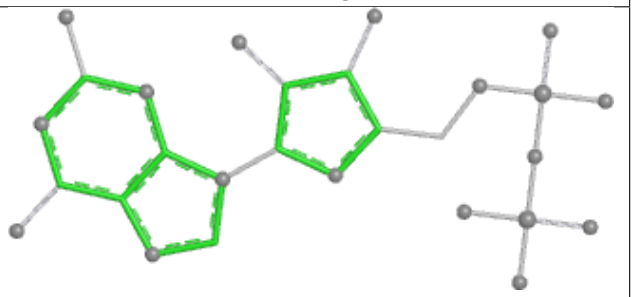
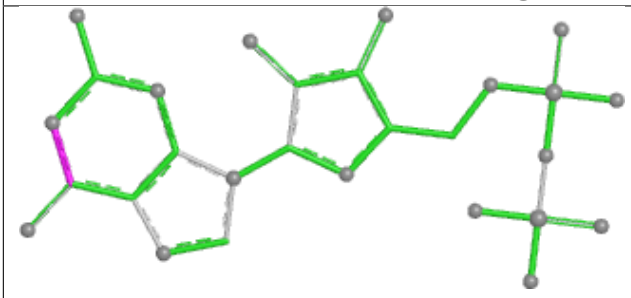
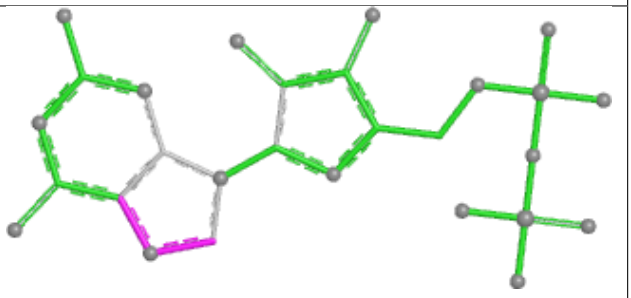
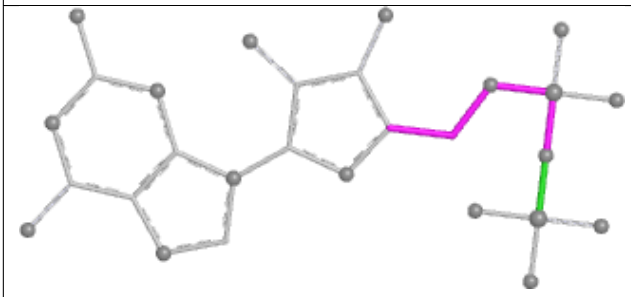
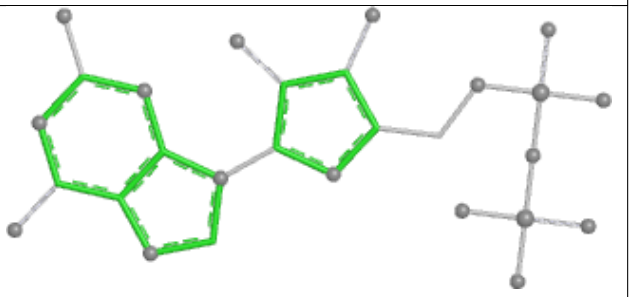
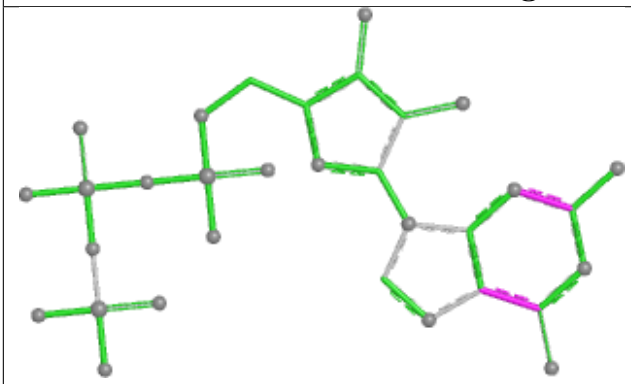
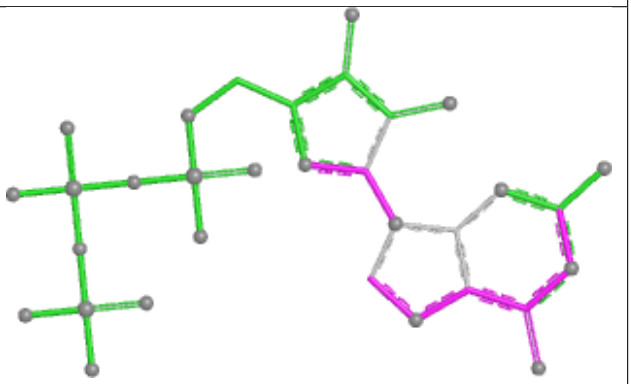
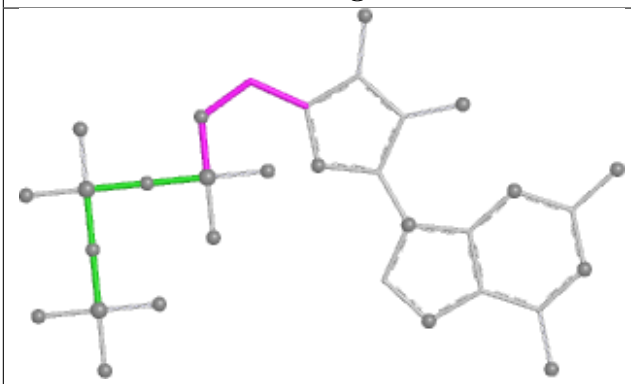
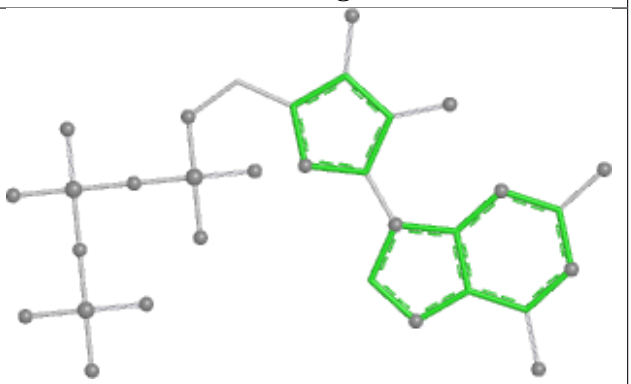
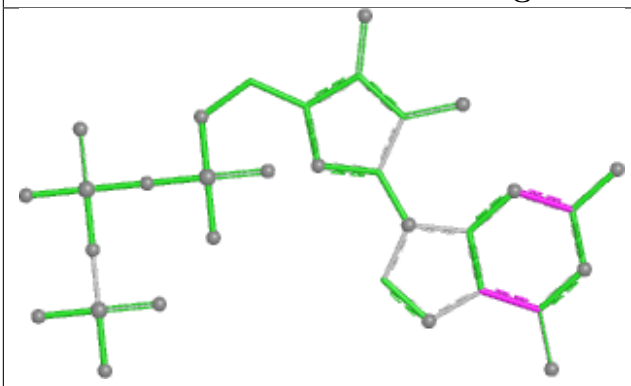


Rings

Ligand GDP 5L 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 3I 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 6C 501



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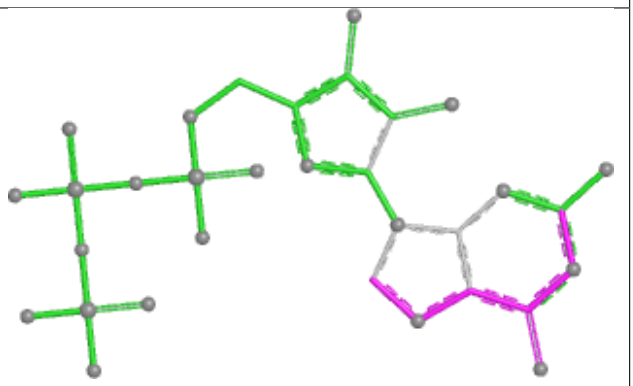

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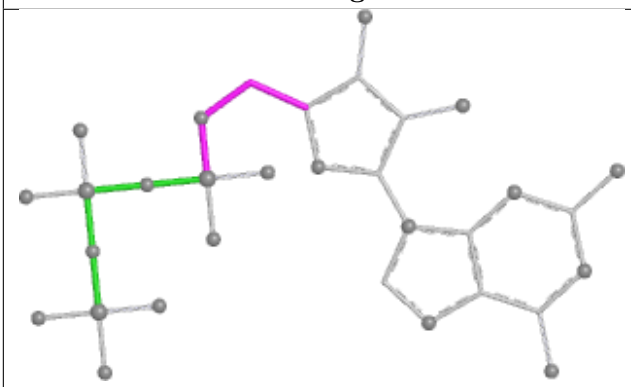

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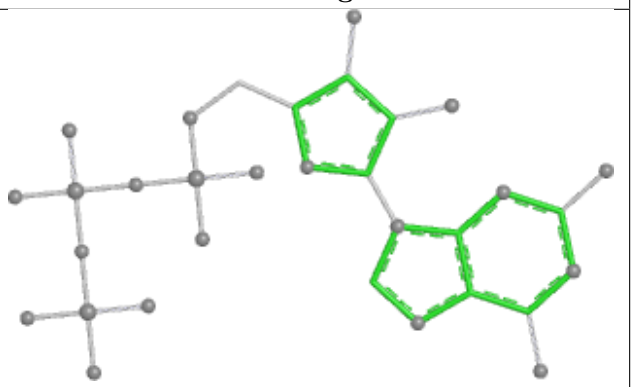

Rings

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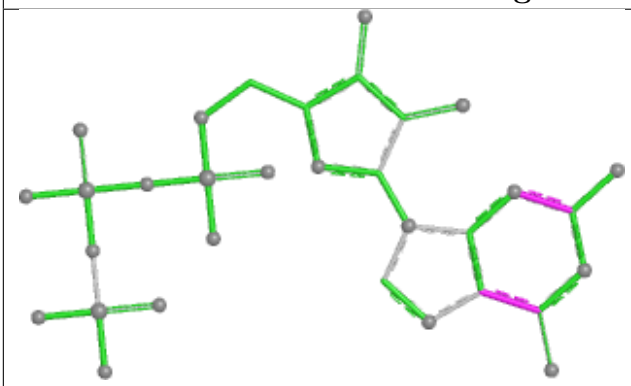

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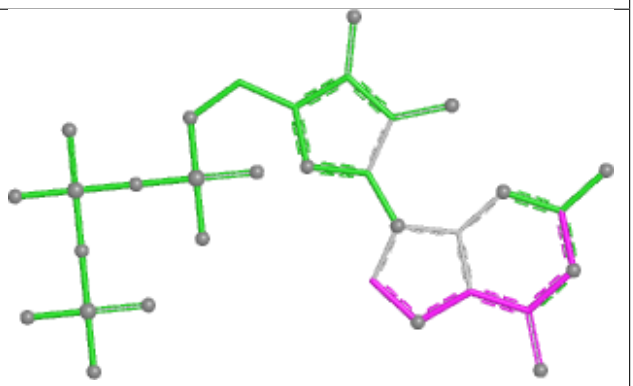

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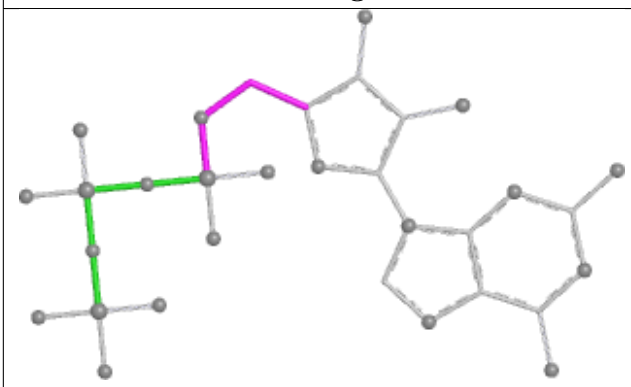

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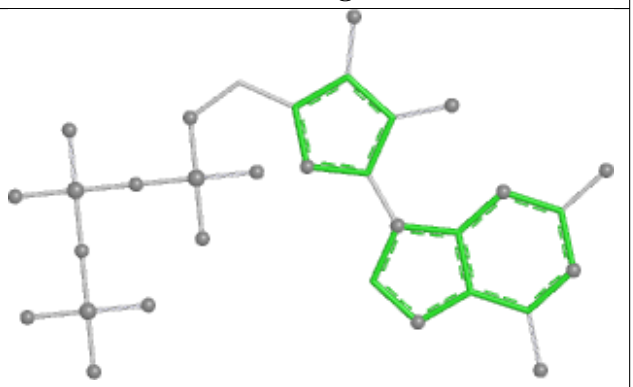
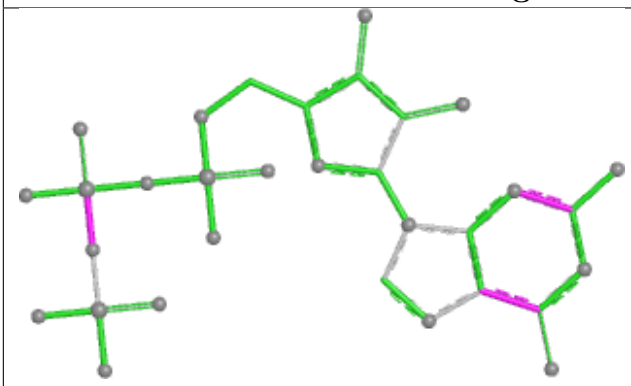


Rings

Ligand GTP 6N 501



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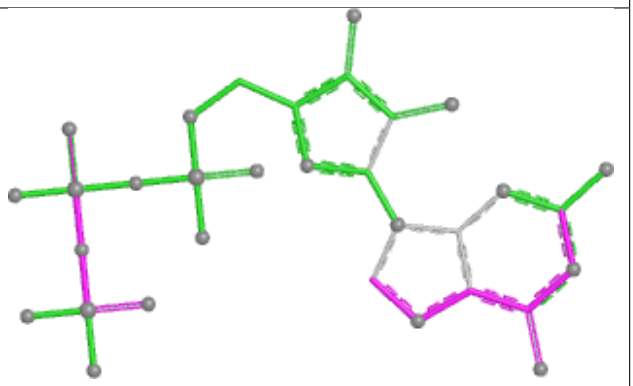

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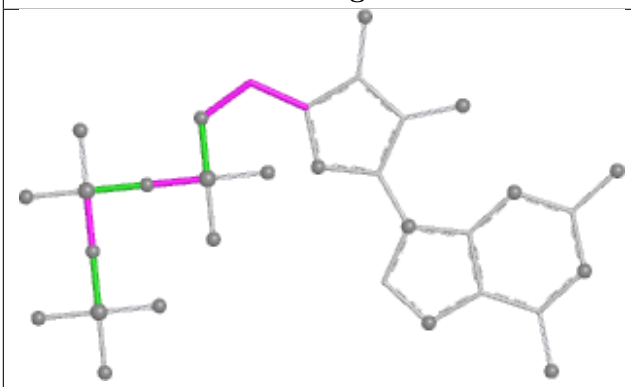

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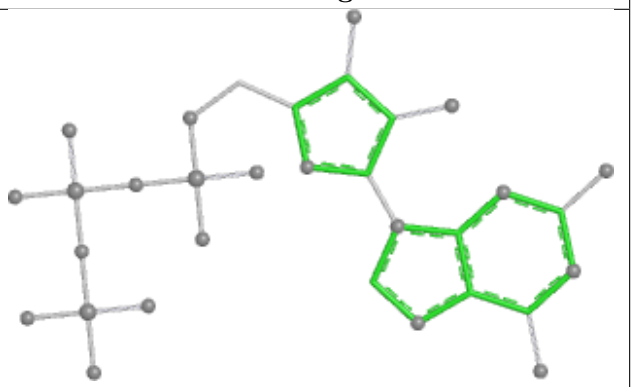

Rings

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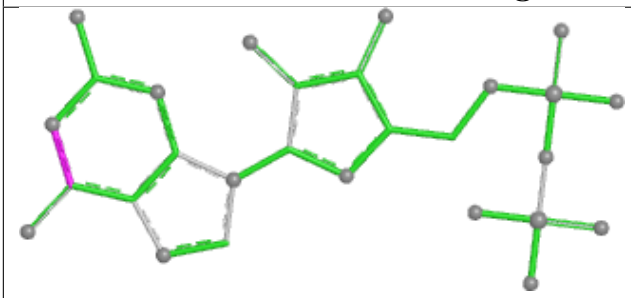

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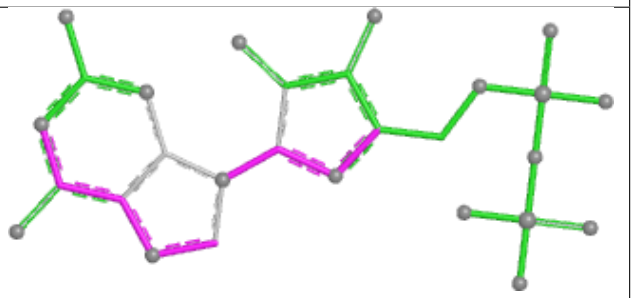

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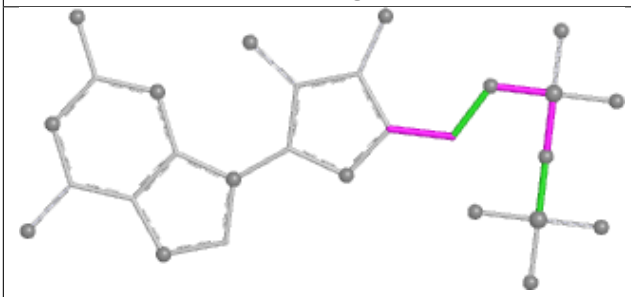

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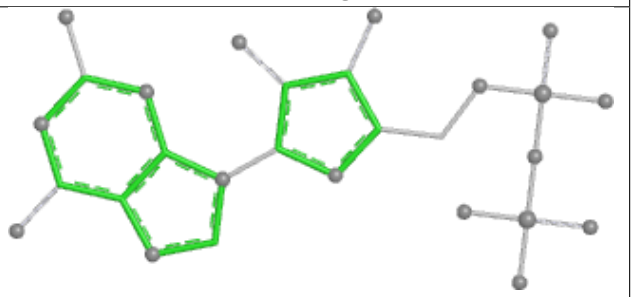

Rings

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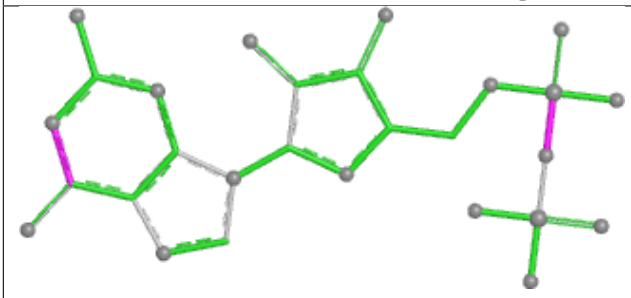
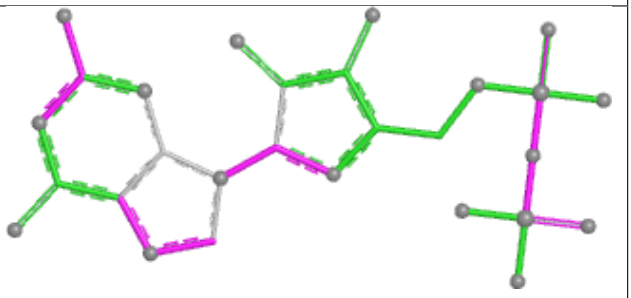
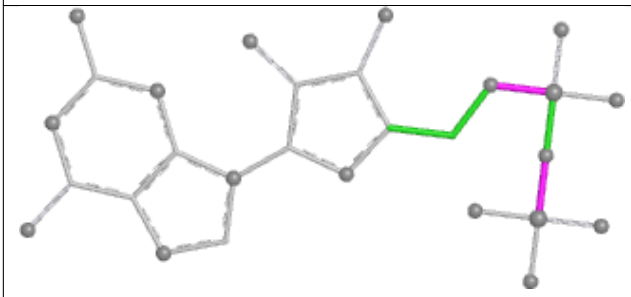
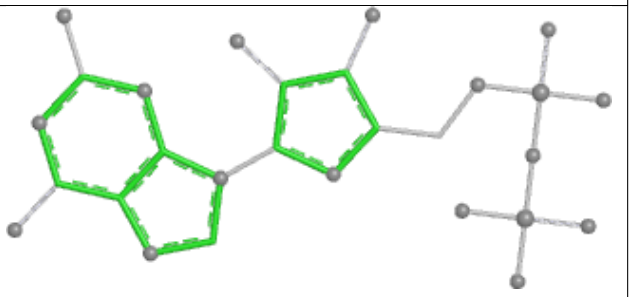
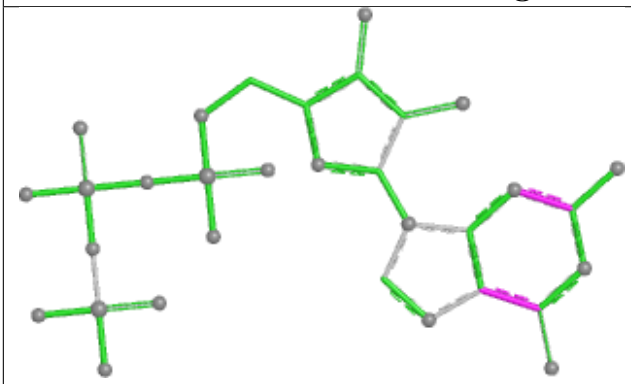
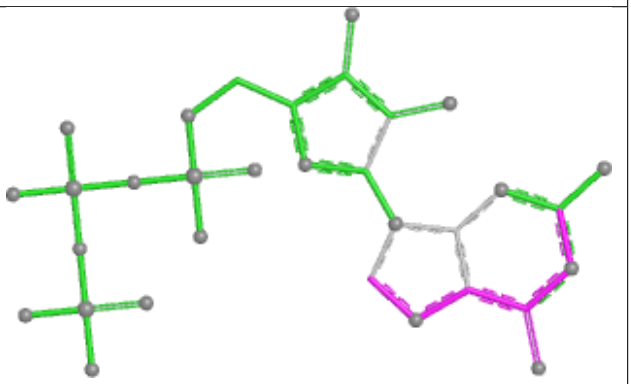
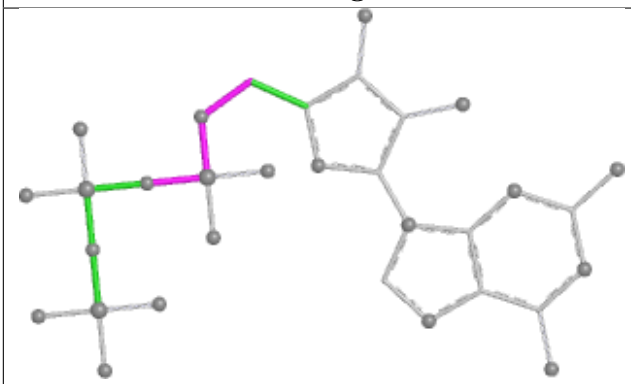
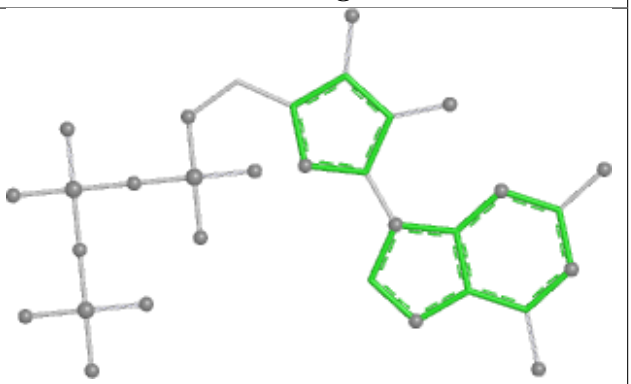
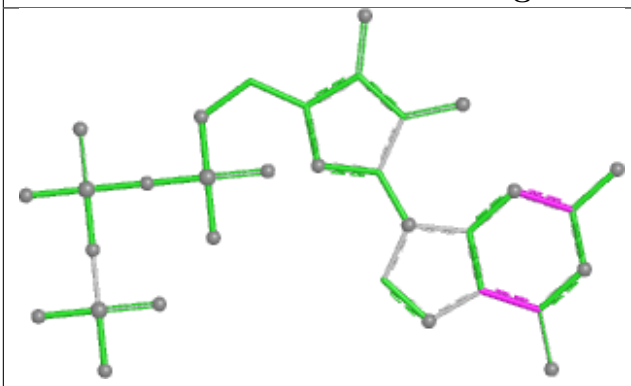
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 4C 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 2C 501



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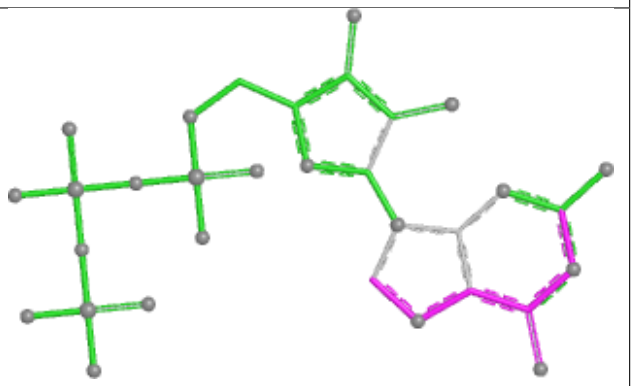

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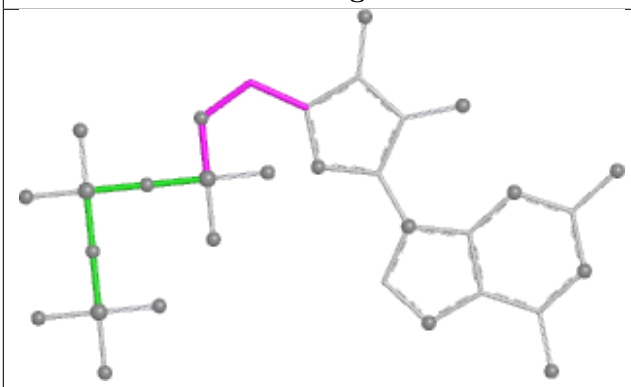

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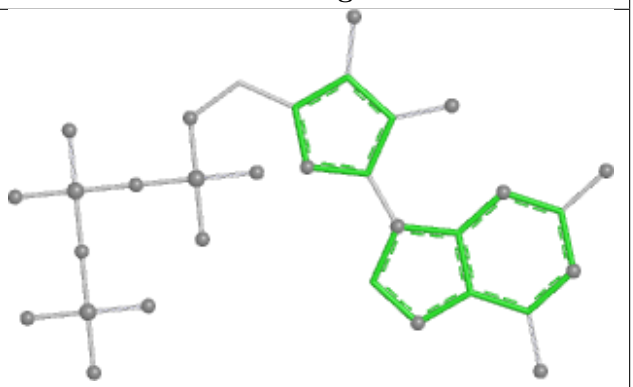
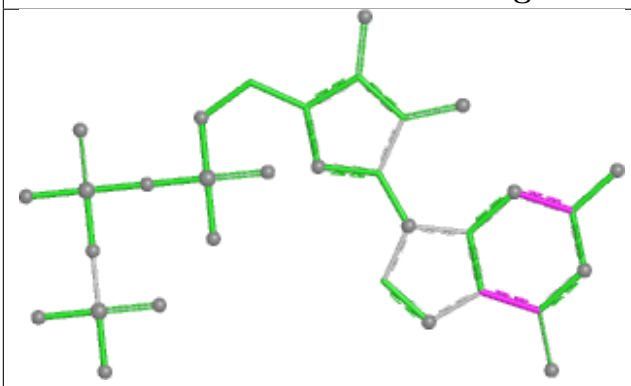


Rings

Ligand GTP 5C 501



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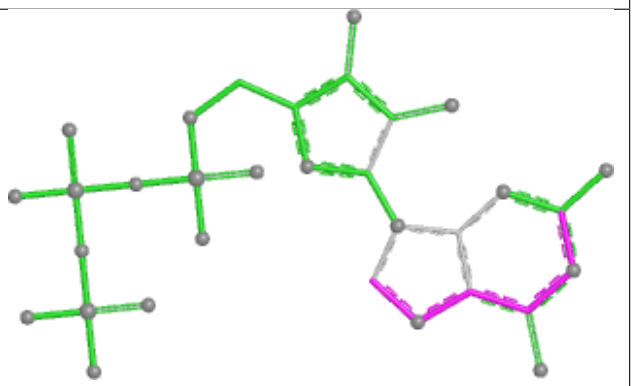
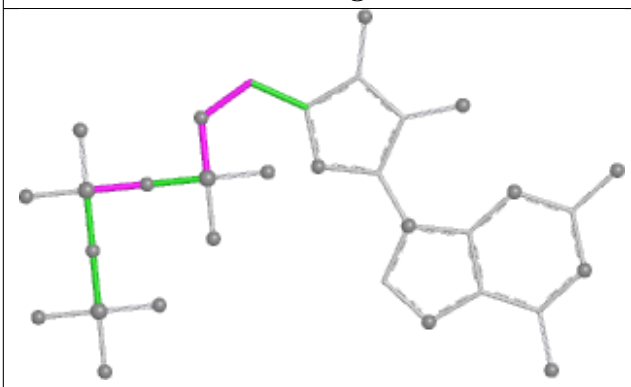


Bond angles



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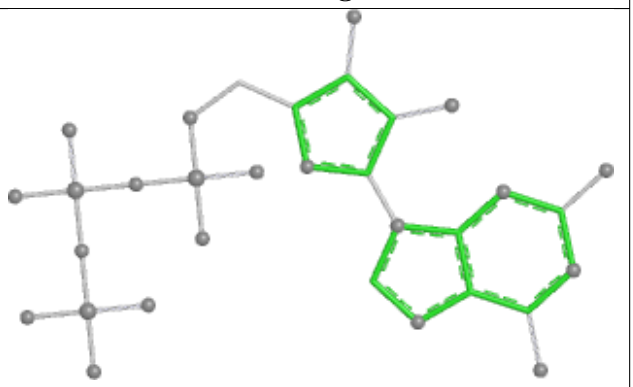
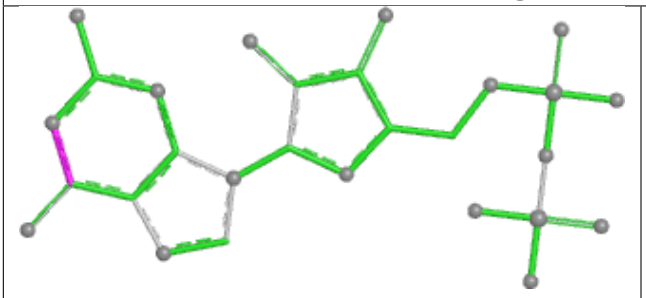


Rings

Ligand GDP 7H 501



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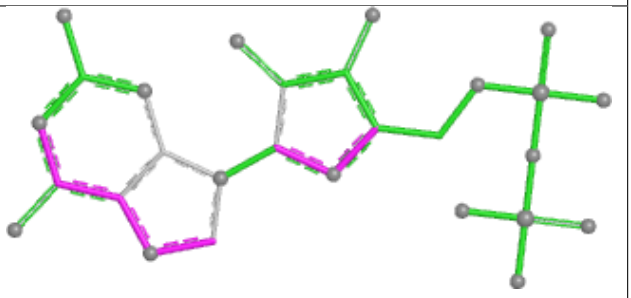

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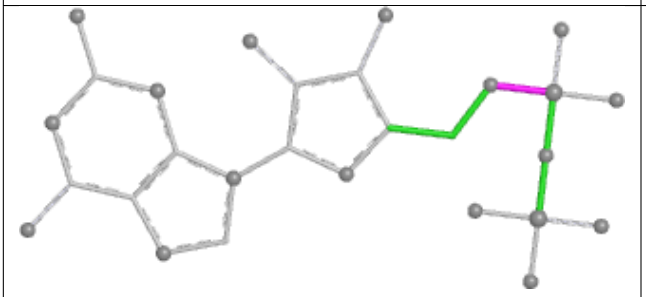

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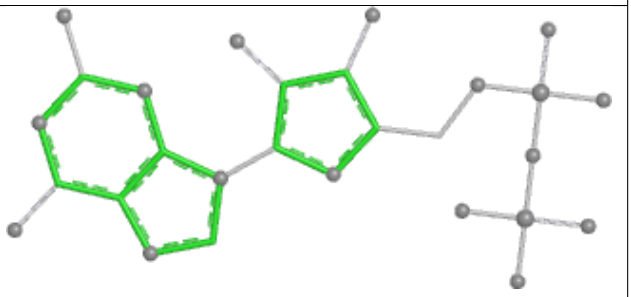
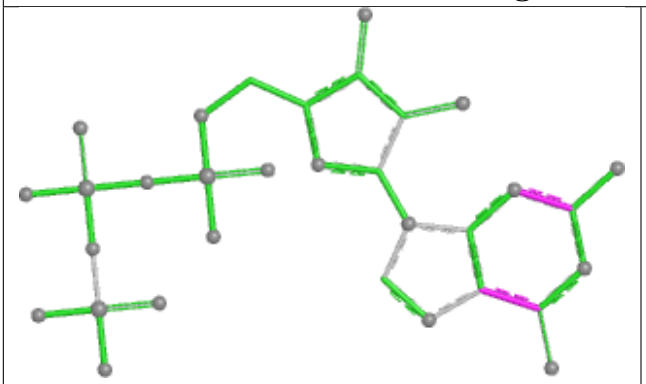


Rings

Ligand GTP 1C 501



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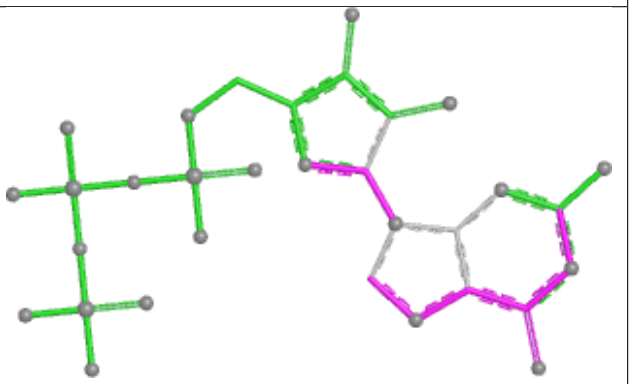
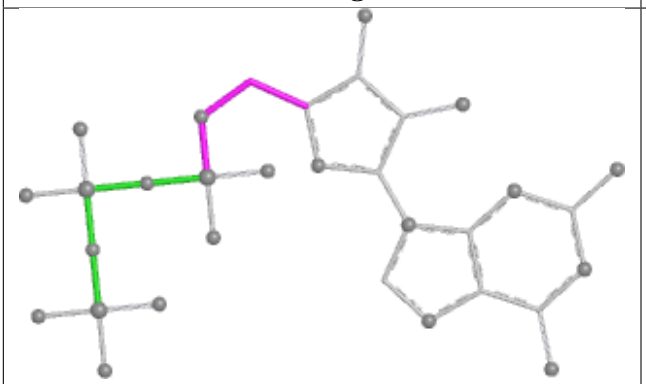
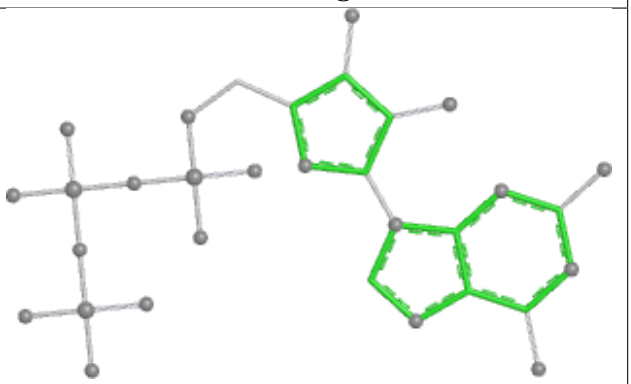


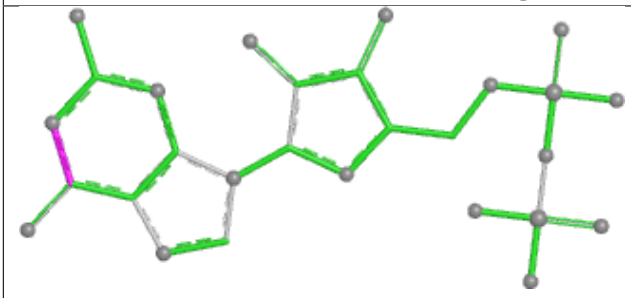
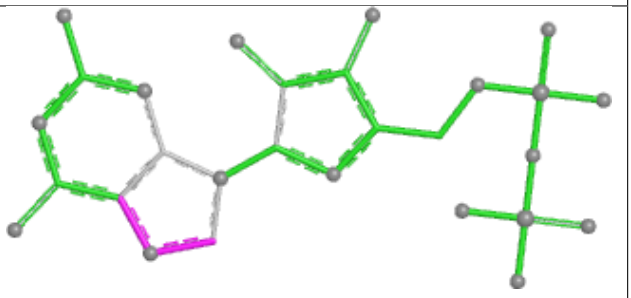
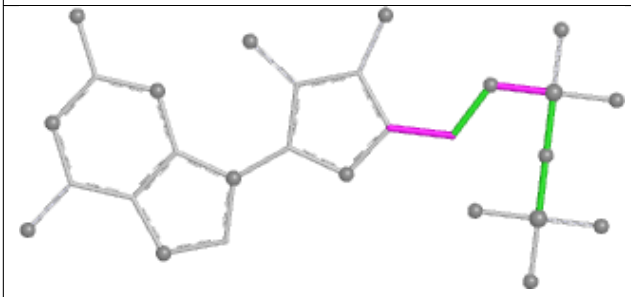
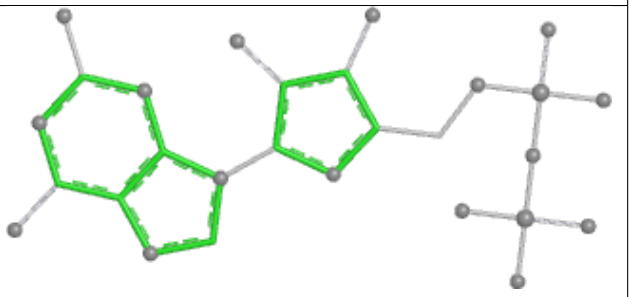
Bond angles



Torsions



Rings

Ligand GDP 2L 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

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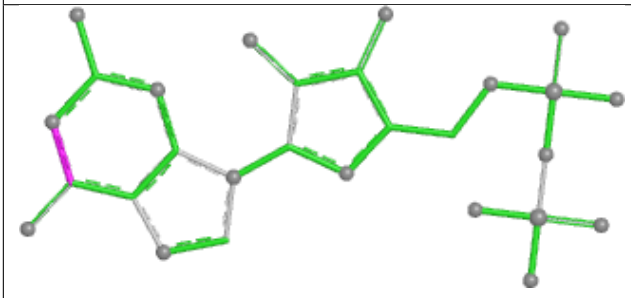
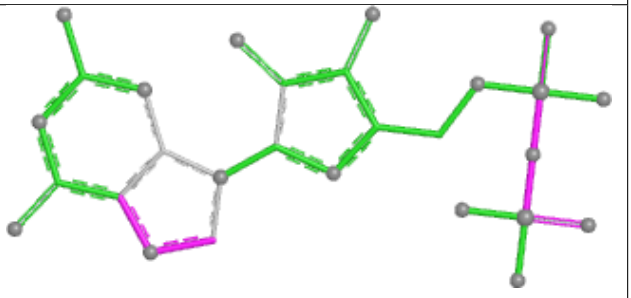
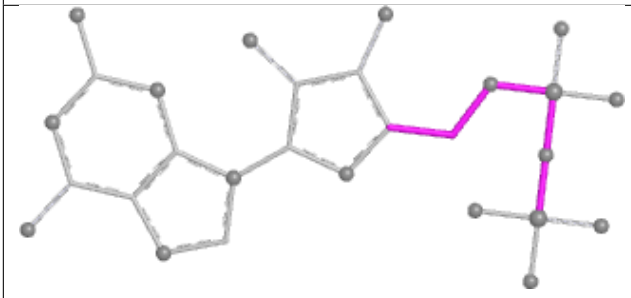
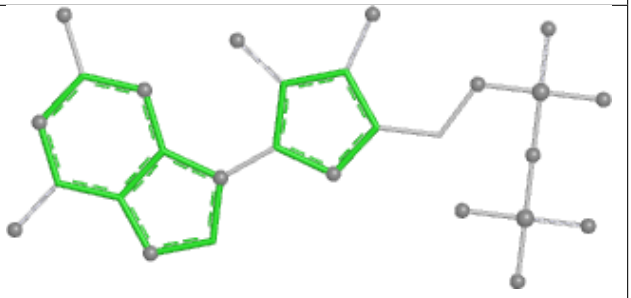
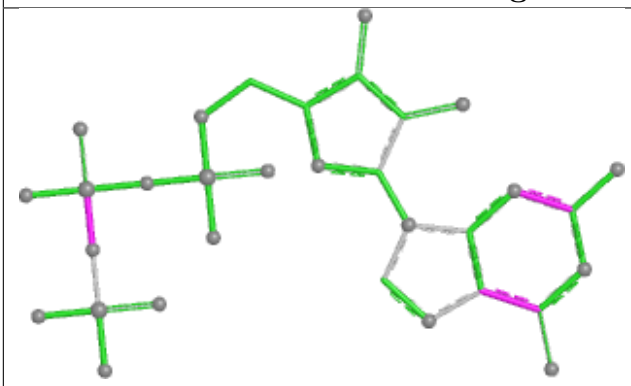
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GTP 3M 501



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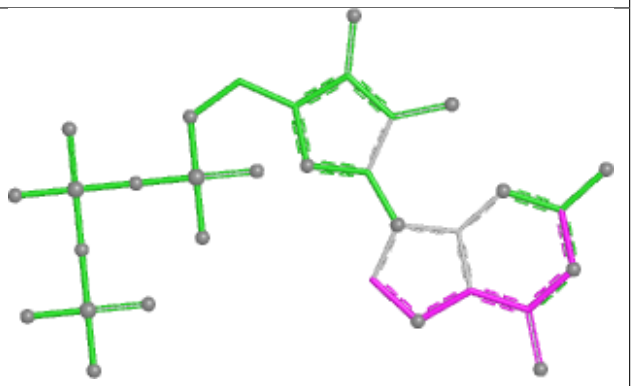

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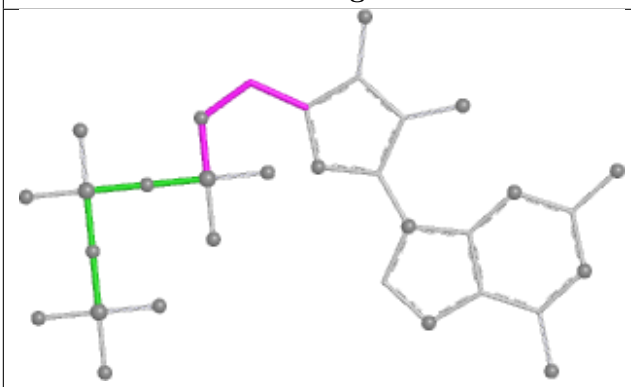

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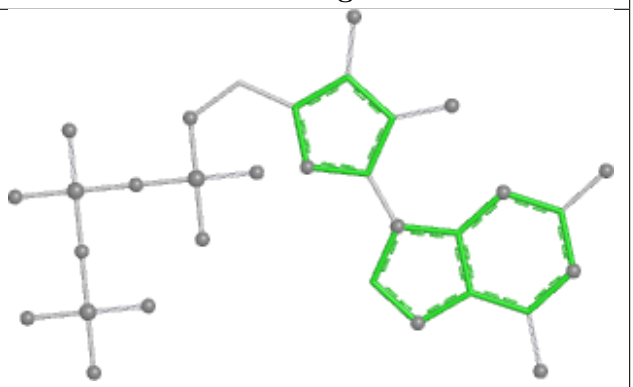
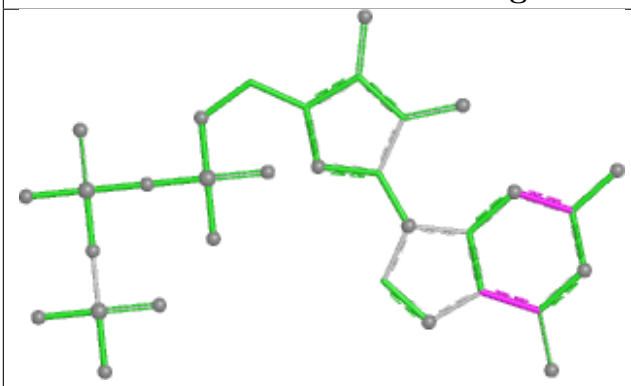


Rings

Ligand GTP 4M 501



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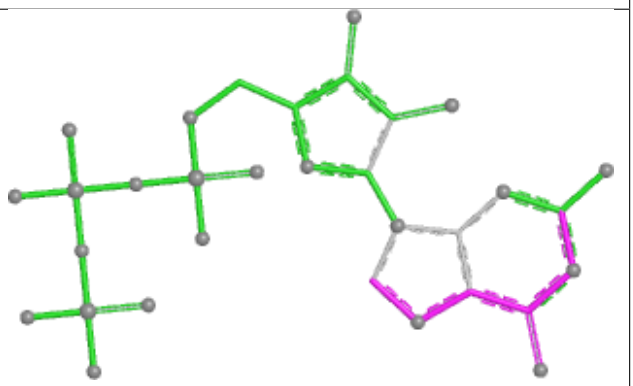
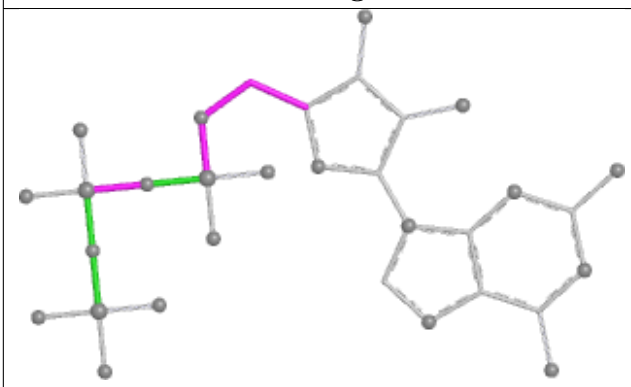


Bond angles



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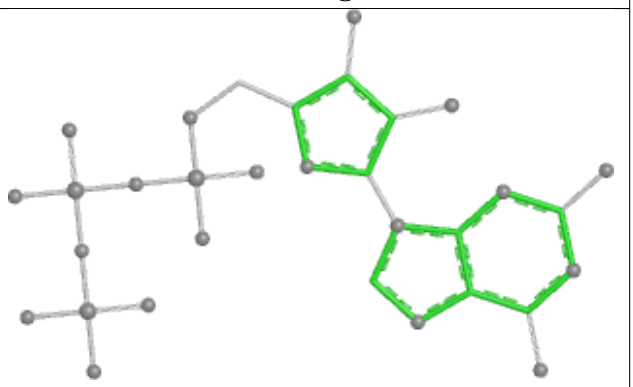

Rings

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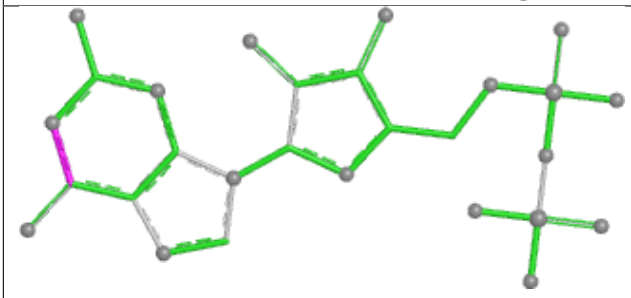
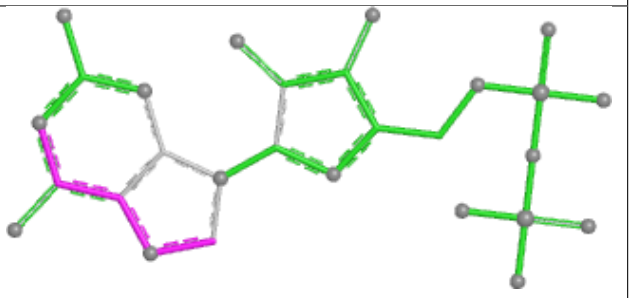
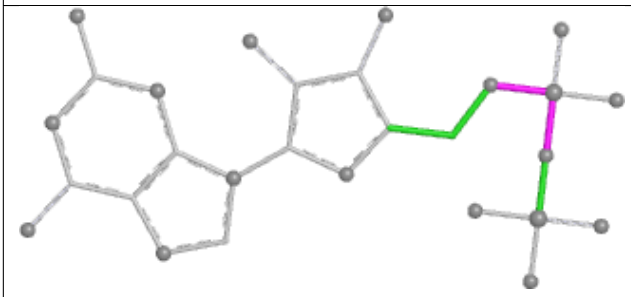
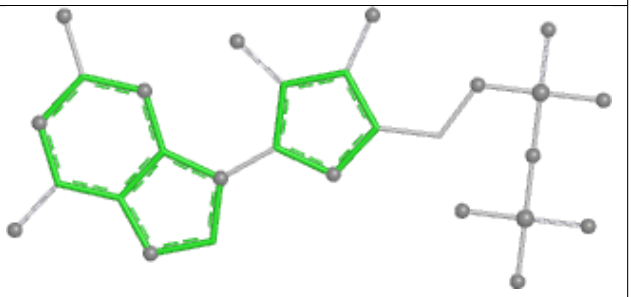
 Bond lengths	 Bond angles
 Torsions	 Rings

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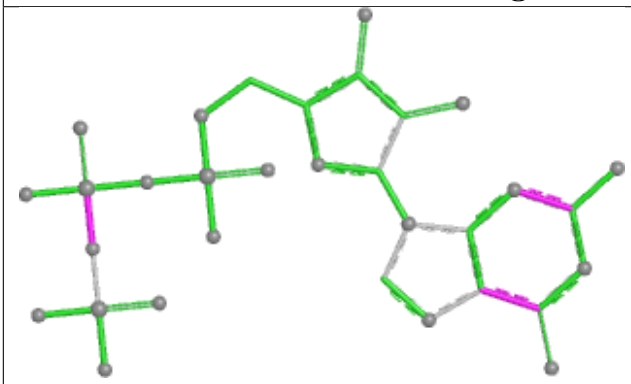
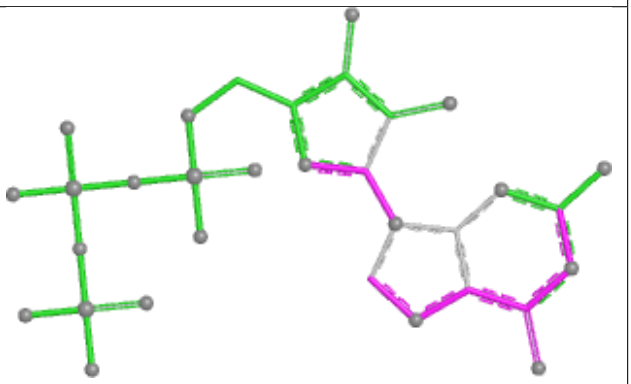
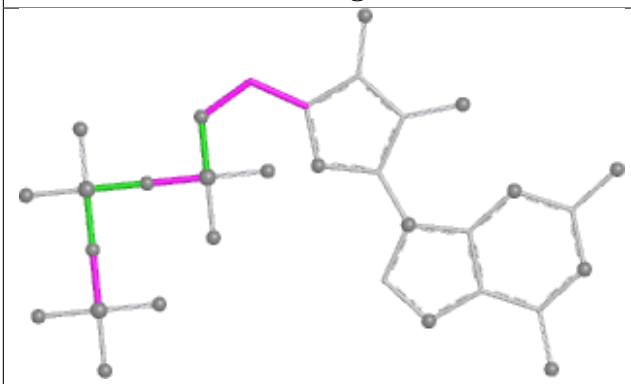
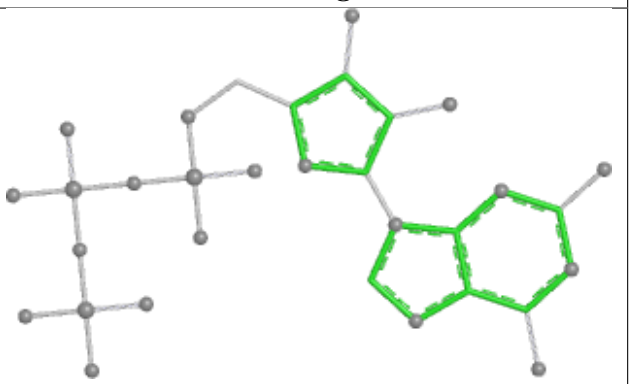
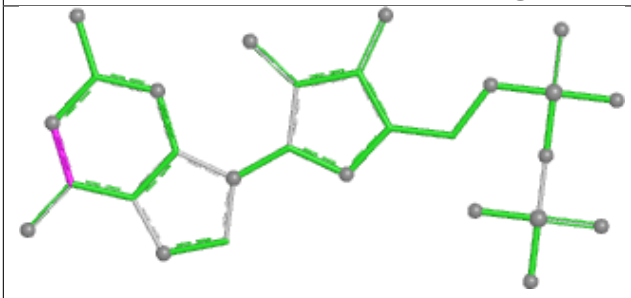
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GDP 3D 501



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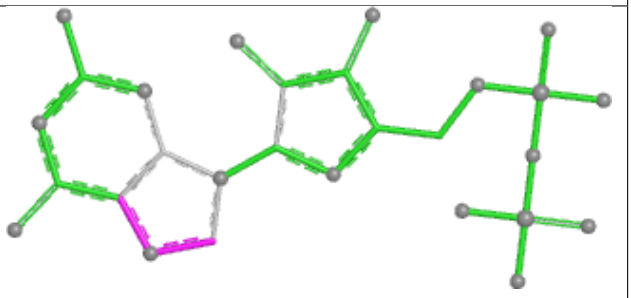

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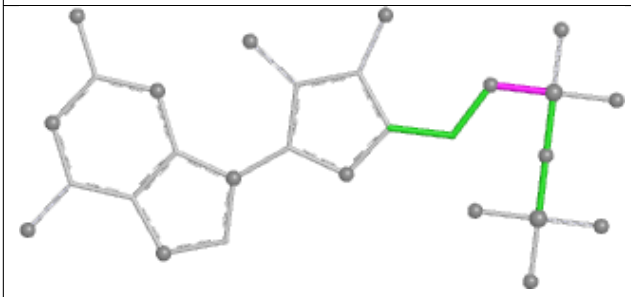

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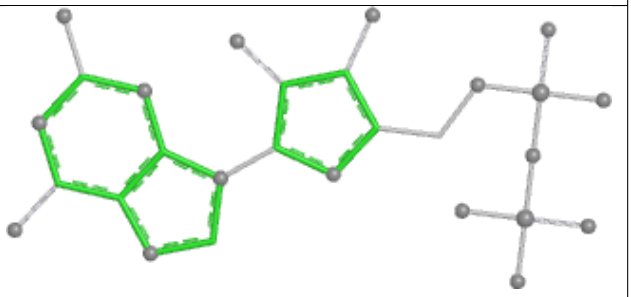
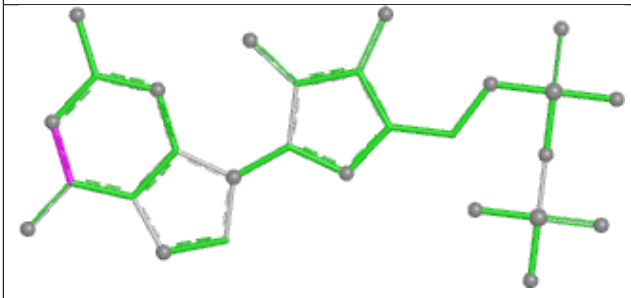


Rings

Ligand GDP 6F 501



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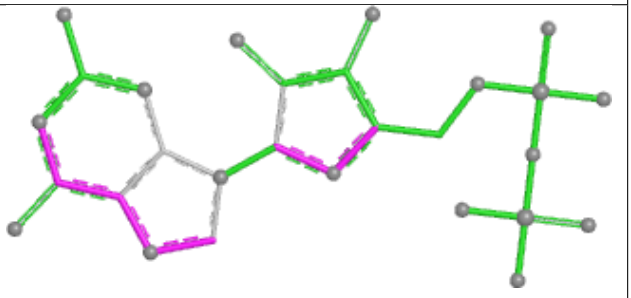

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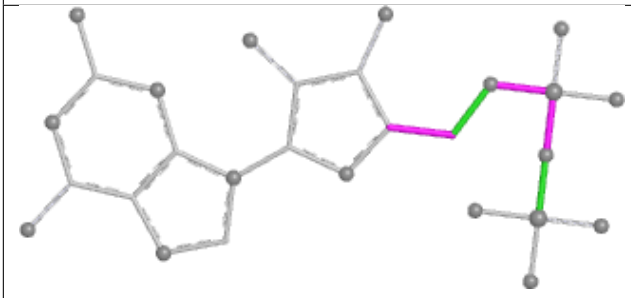

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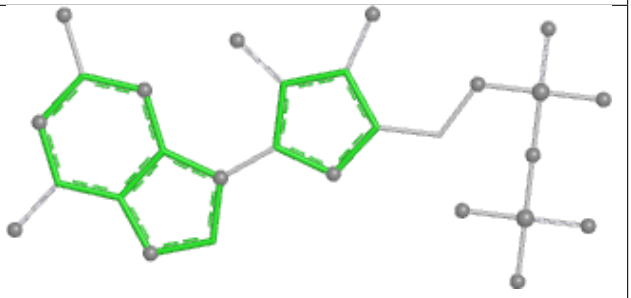

Rings

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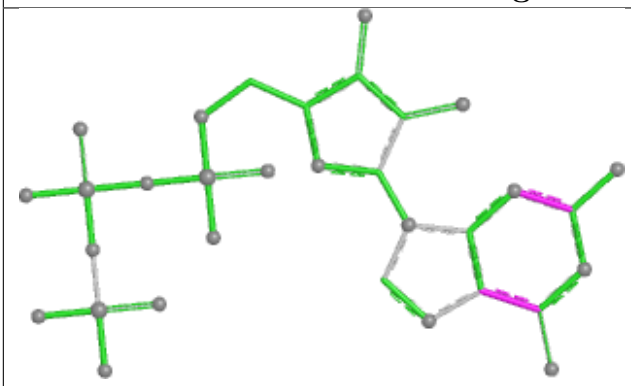

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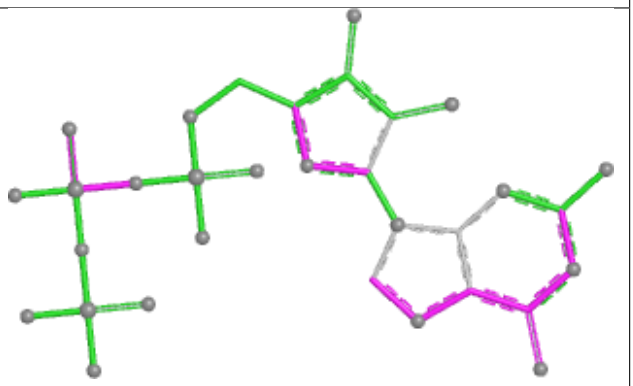

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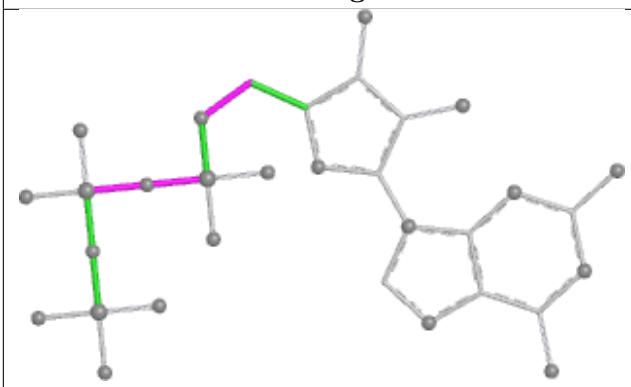

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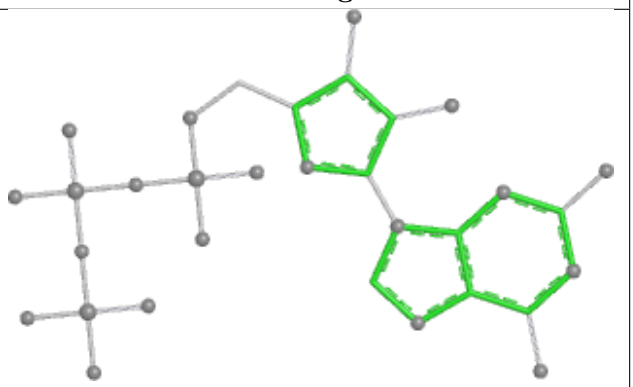
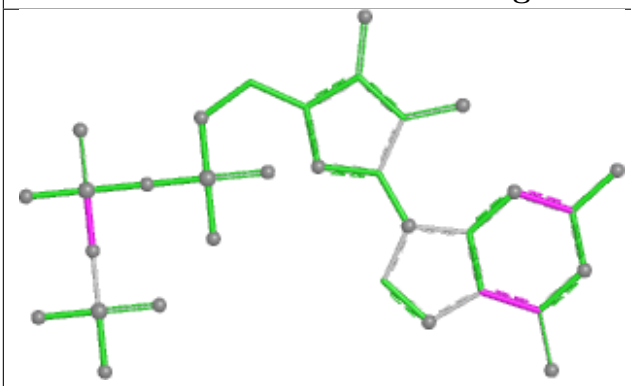


Rings

Ligand GTP 7A 501



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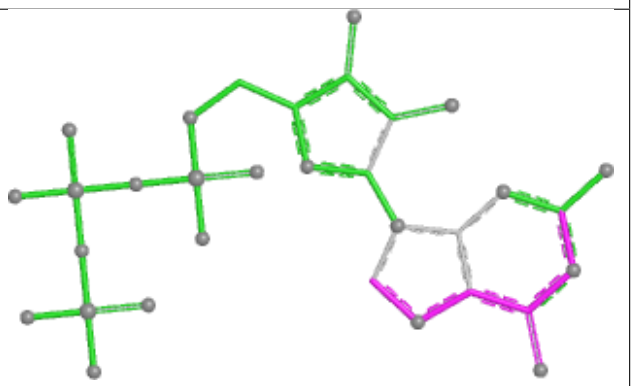

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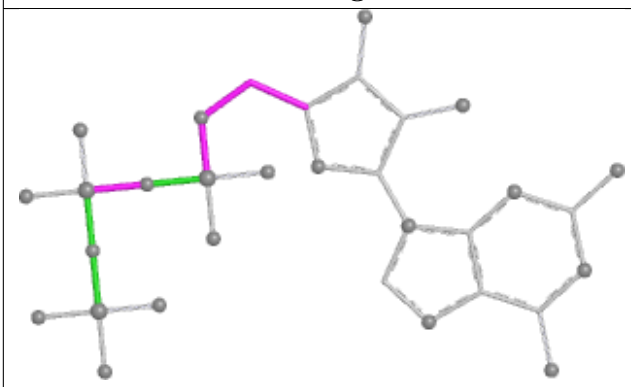

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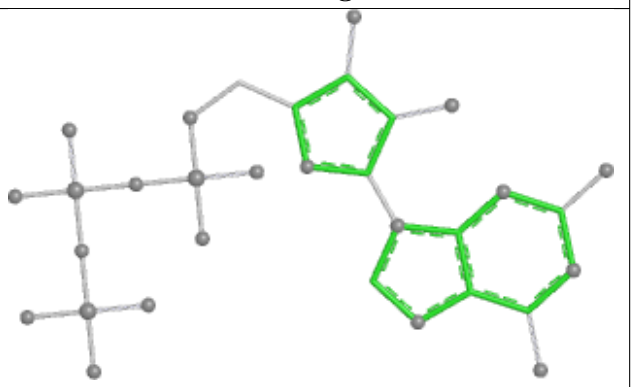
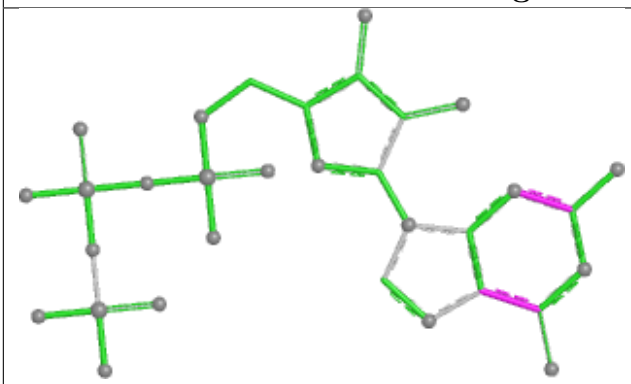


Rings

Ligand GTP 8G 501



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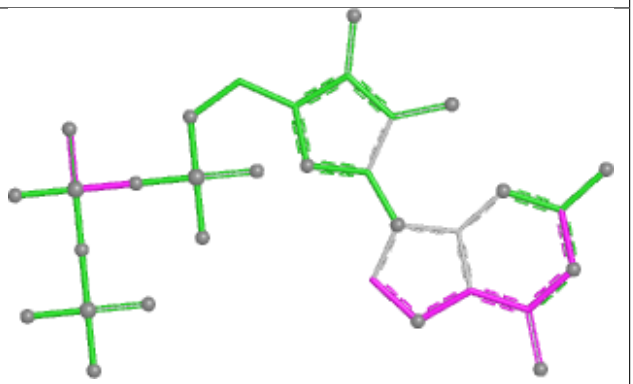

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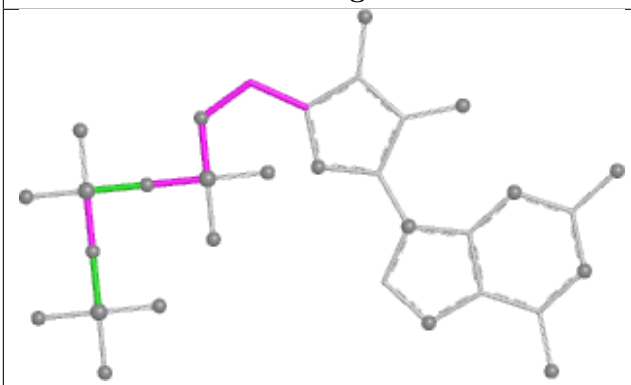

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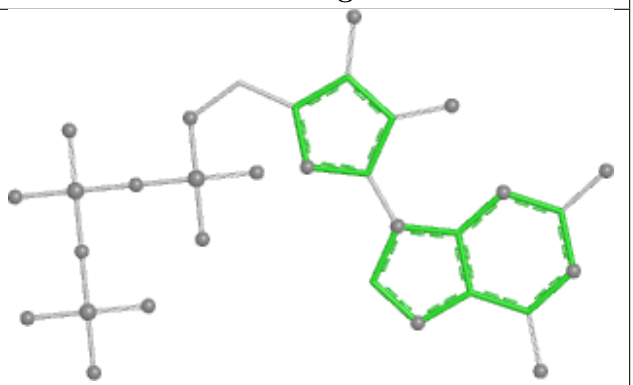
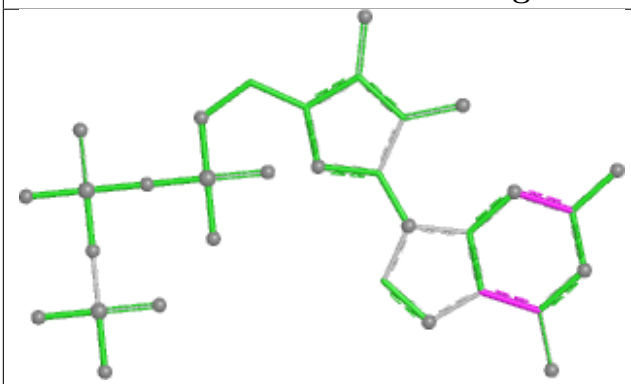


Rings

Ligand GTP 6K 501



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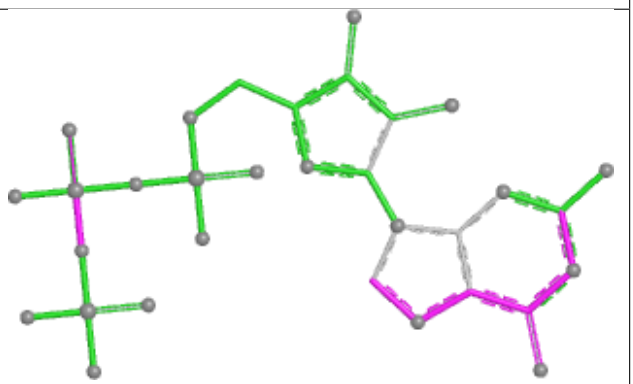

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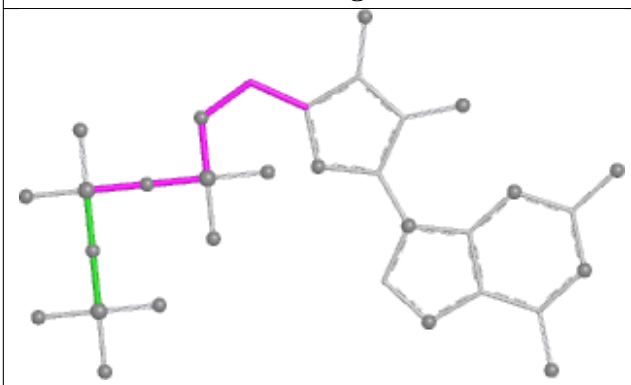

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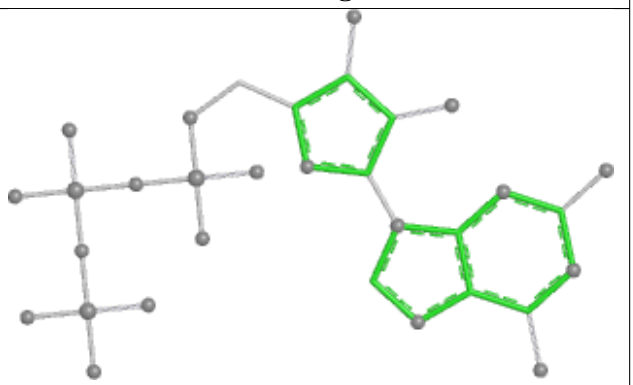
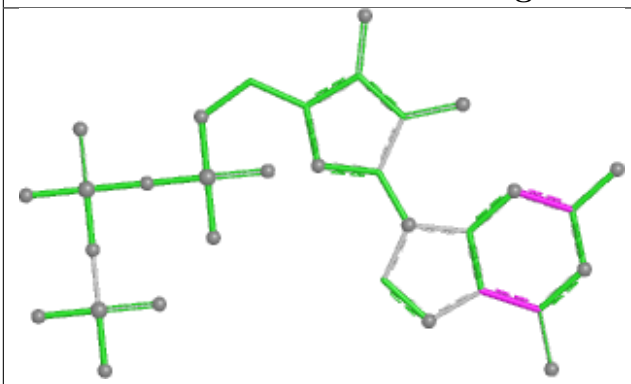


Rings

Ligand GTP 8E 501



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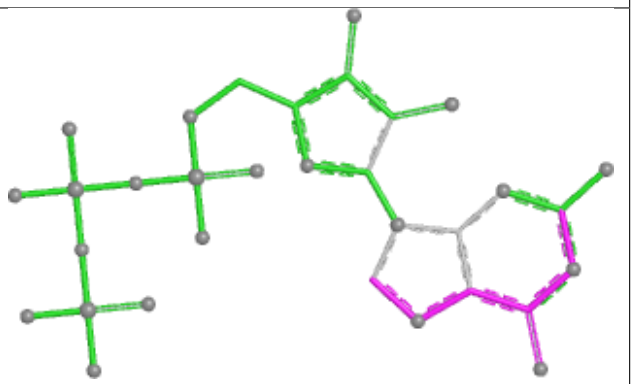
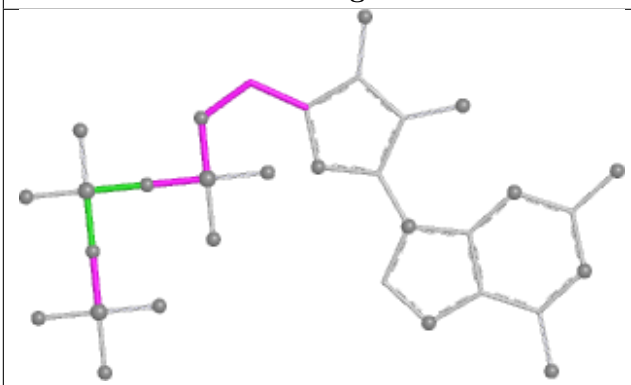


Bond angles



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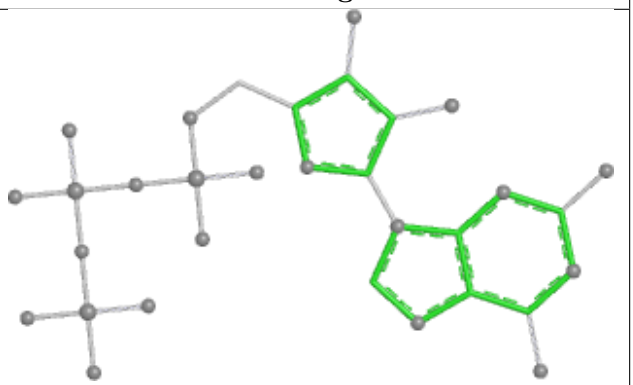
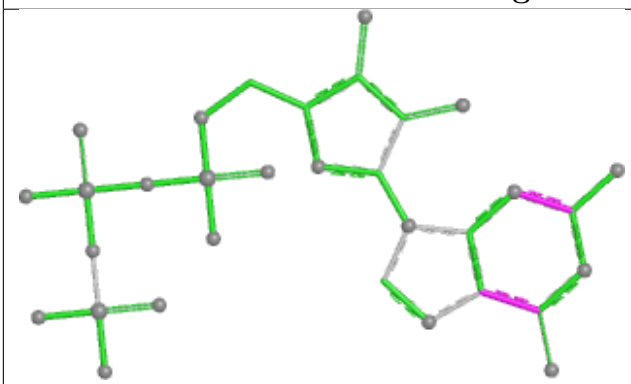


Rings

Ligand GTP 1K 501



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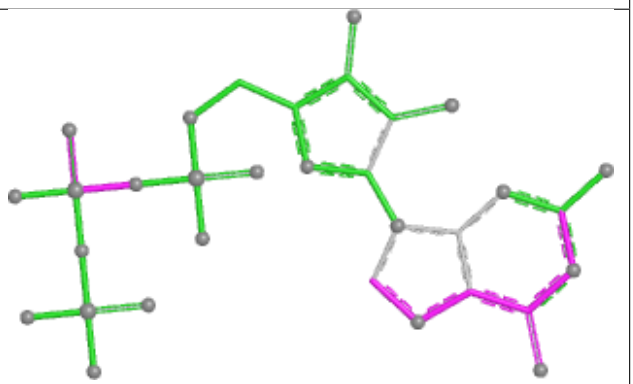
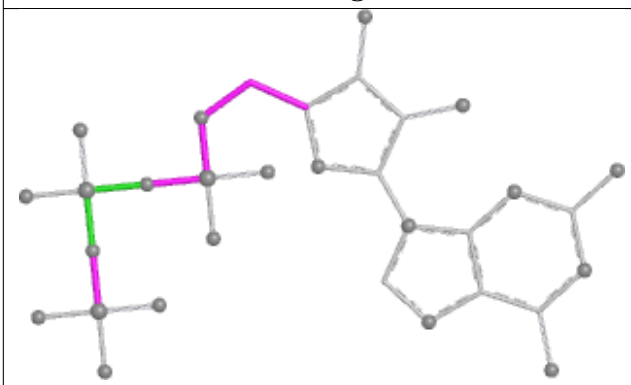
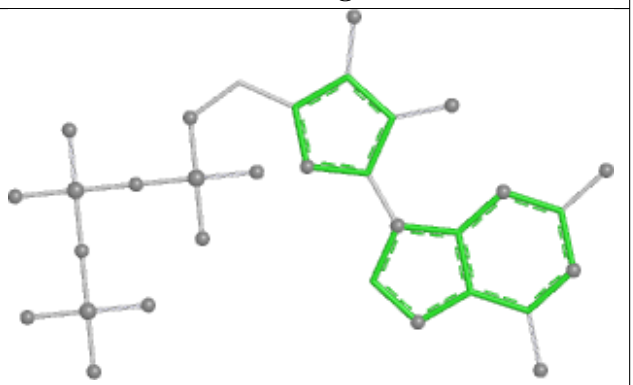


Bond angles

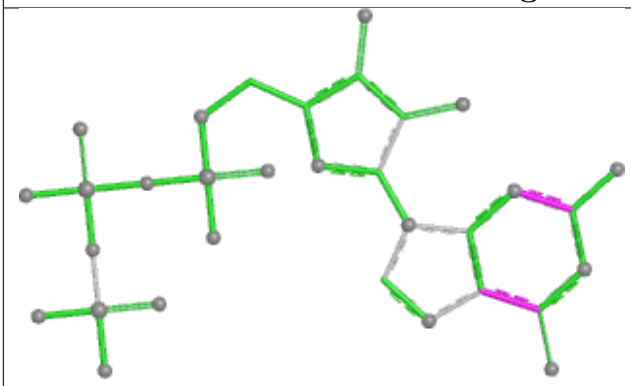


Torsions

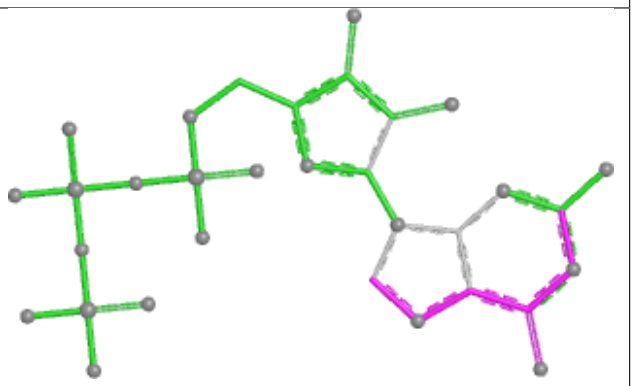


Rings

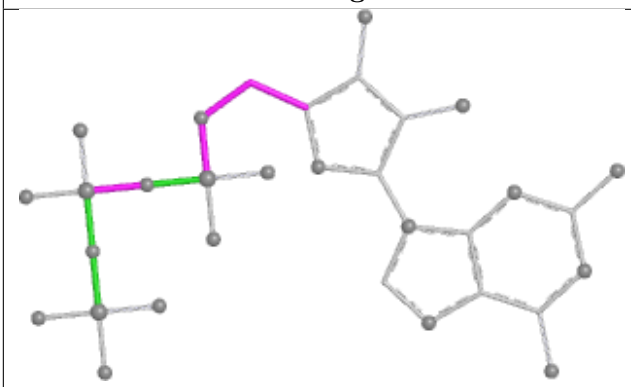
Ligand GTP 2I 501



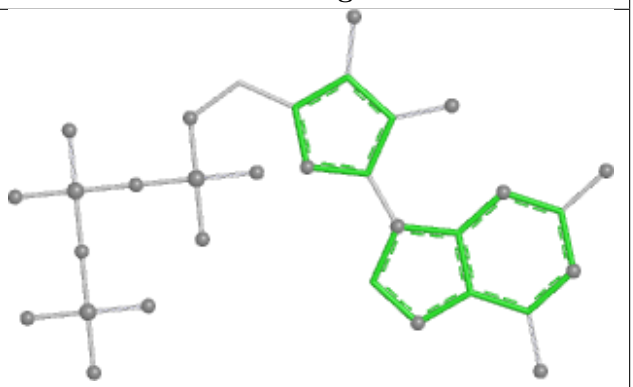
Bond lengths



Bond angles

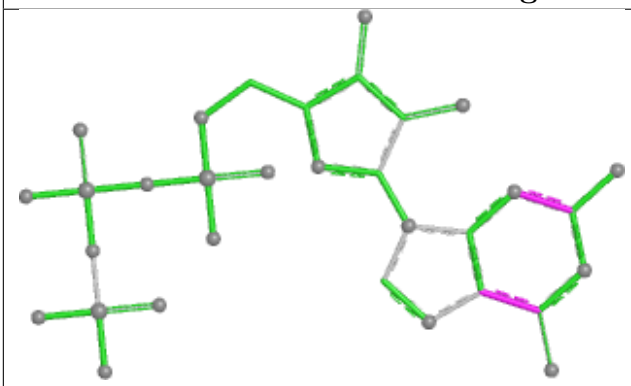


Torsions

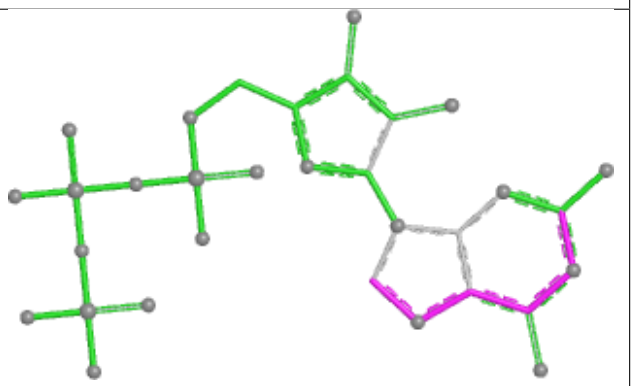


Rings

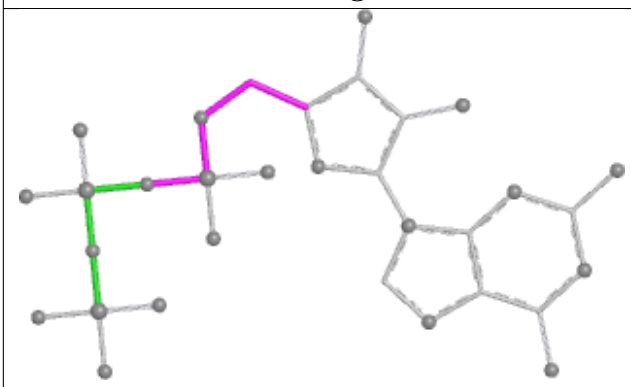
Ligand GTP 8I 501



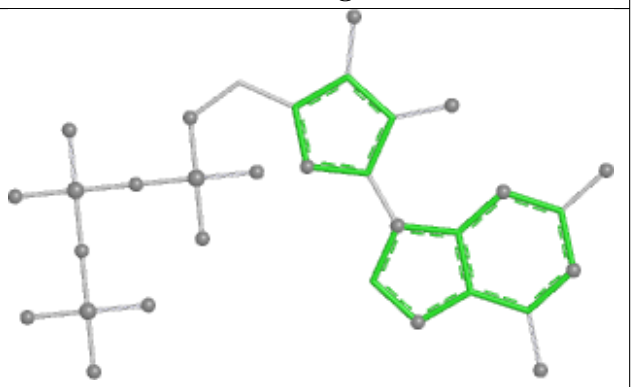
Bond lengths



Bond angles

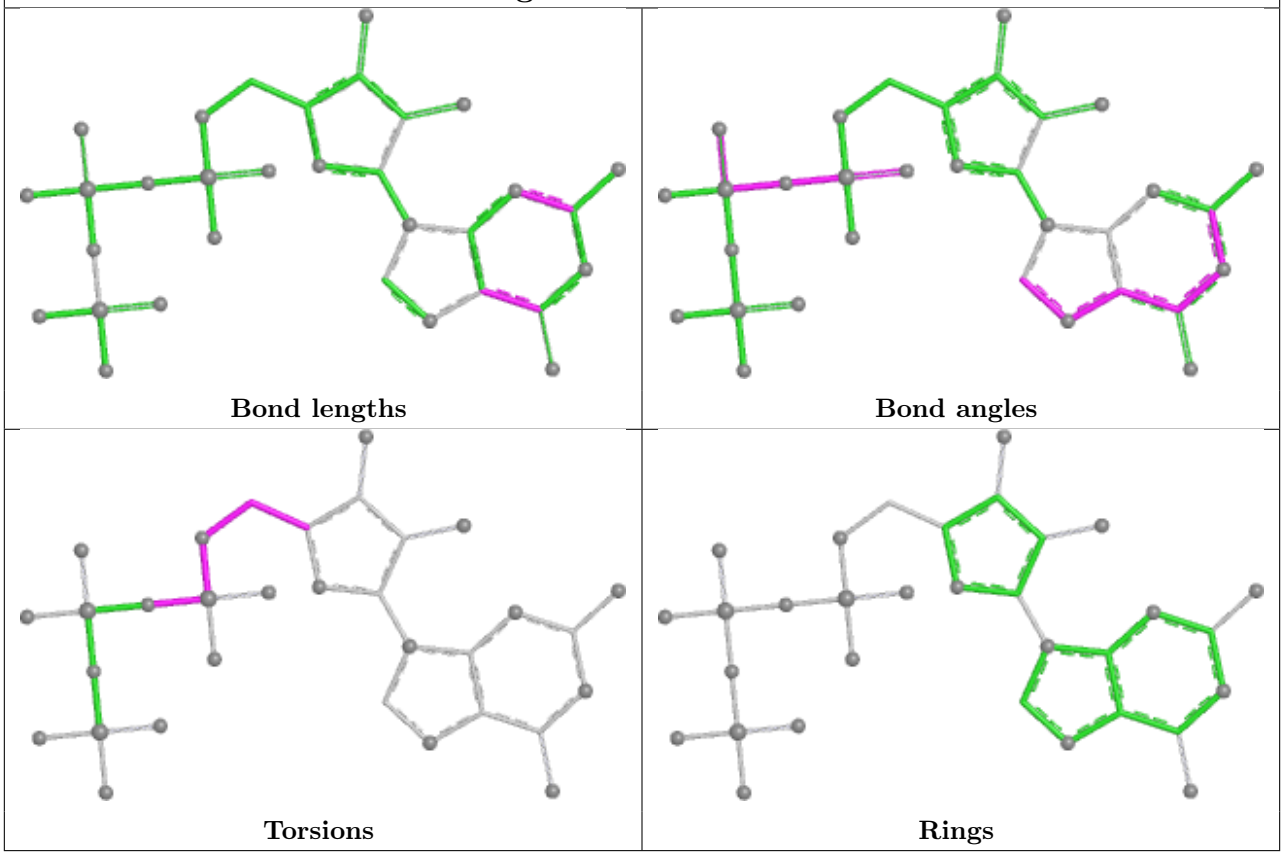


Torsions



Rings

Ligand GTP 4E 501



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

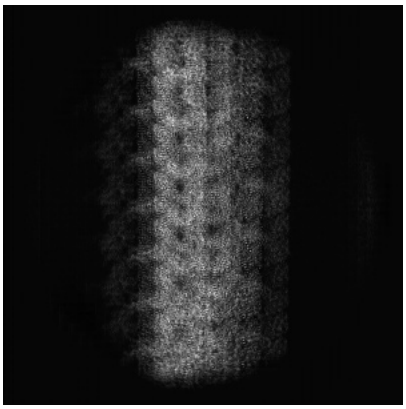
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-72715. These allow visual inspection of the internal detail of the map and identification of artifacts.

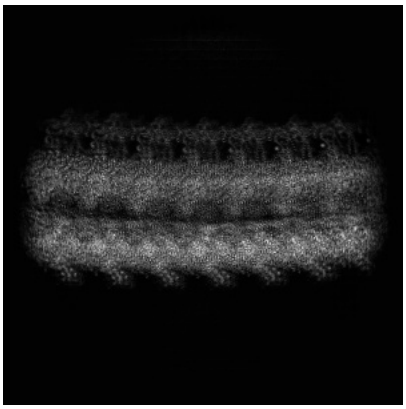
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

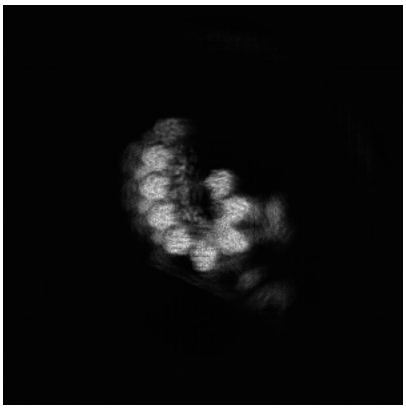
6.1.1 Primary map



X

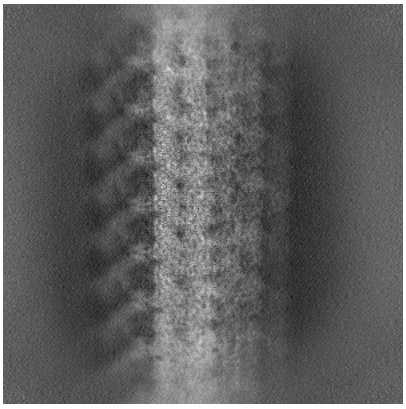


Y

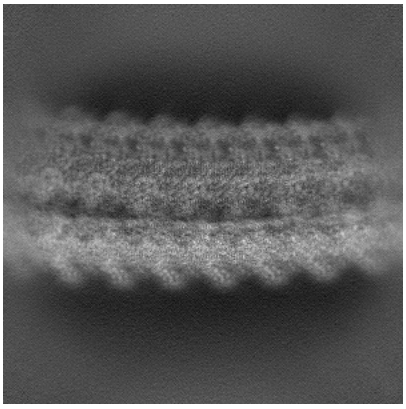


Z

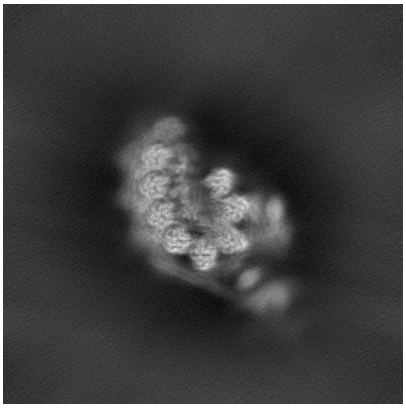
6.1.2 Raw map



X



Y

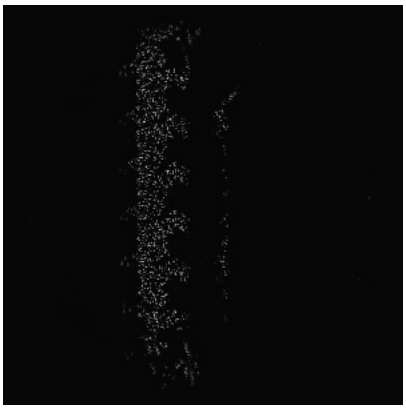


Z

The images above show the map projected in three orthogonal directions.

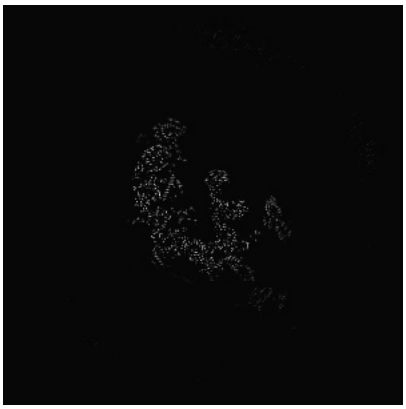
6.2 Central slices (i)

6.2.1 Primary map



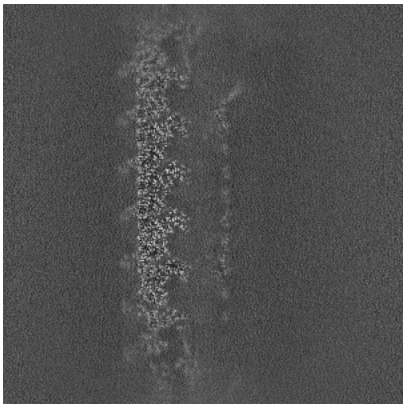
X Index: 256

Y Index: 256

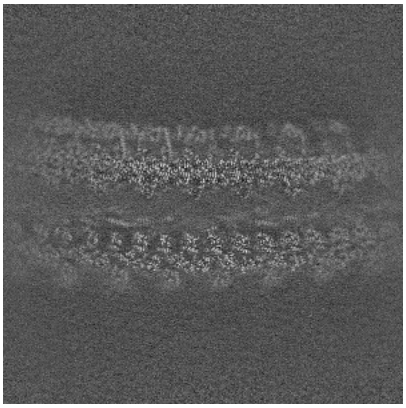


Z Index: 256

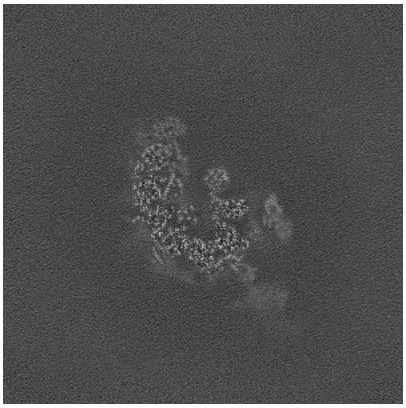
6.2.2 Raw map



X Index: 256



Y Index: 256



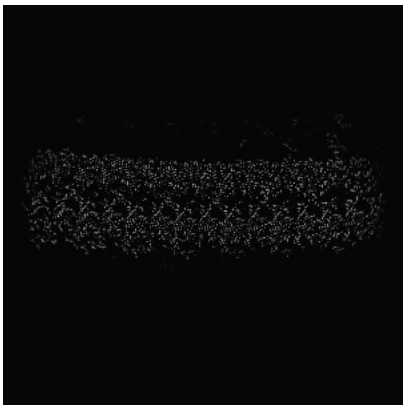
Z Index: 256

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

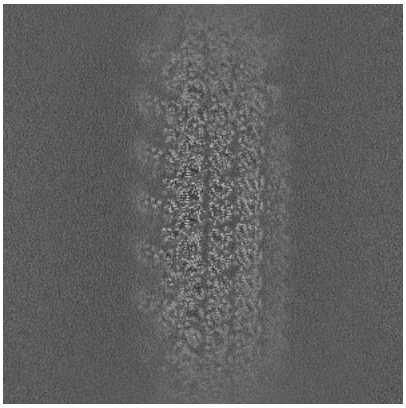
X Index: 201



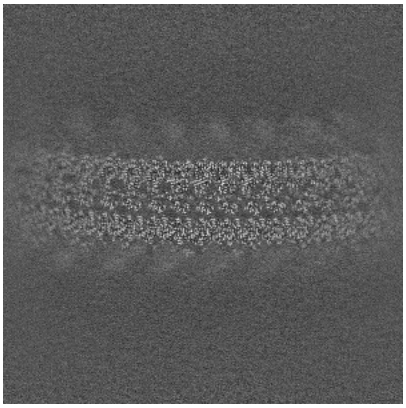
Y Index: 206

Z Index: 188

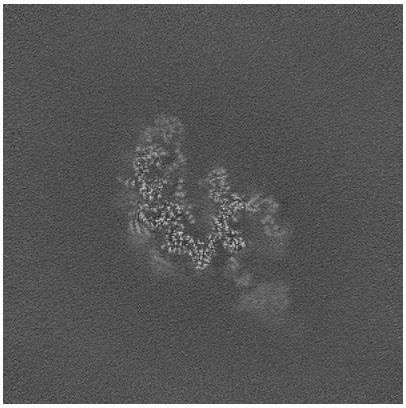
6.3.2 Raw map



X Index: 201



Y Index: 203

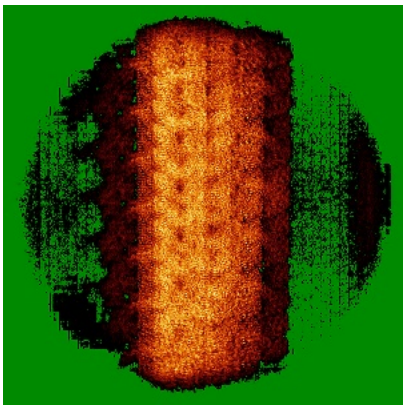


Z Index: 265

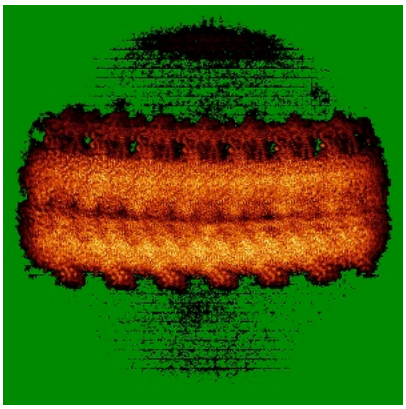
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

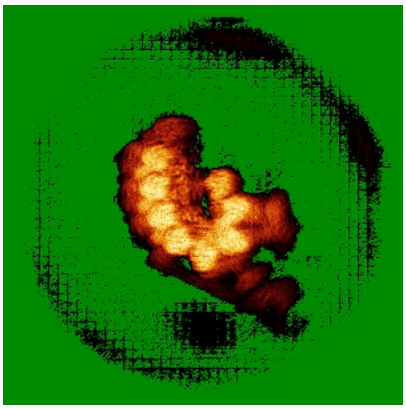
6.4.1 Primary map



X

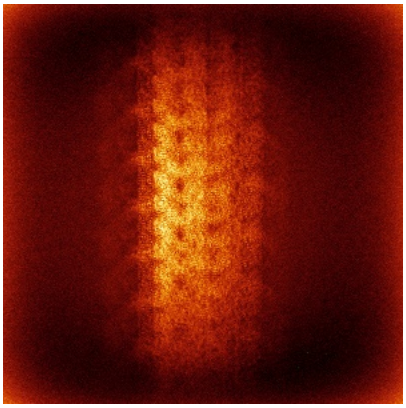


Y

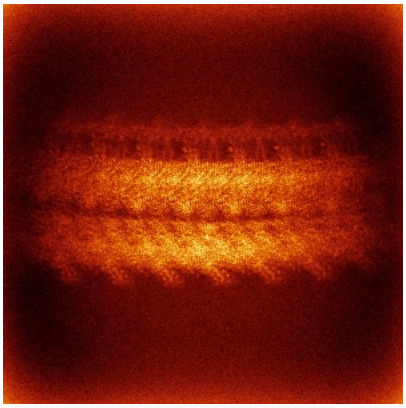


Z

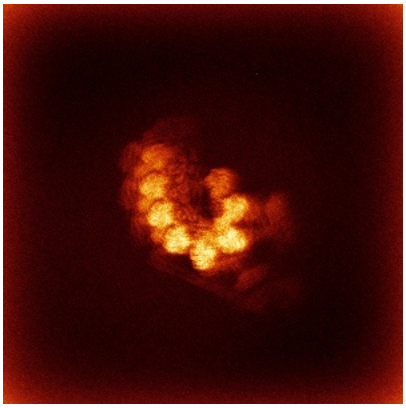
6.4.2 Raw map



X



Y

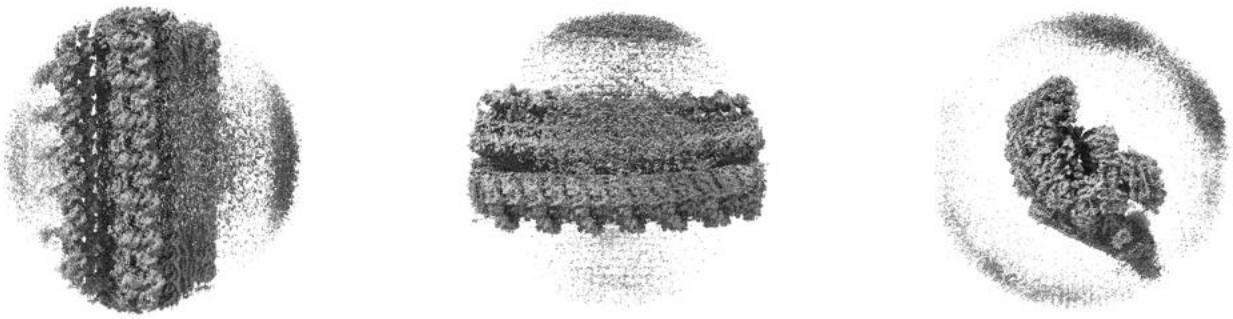


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

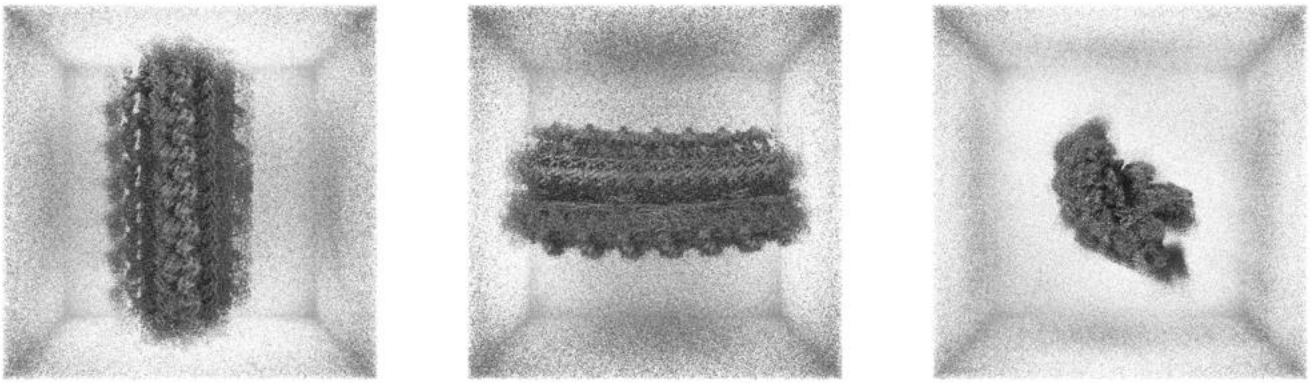
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

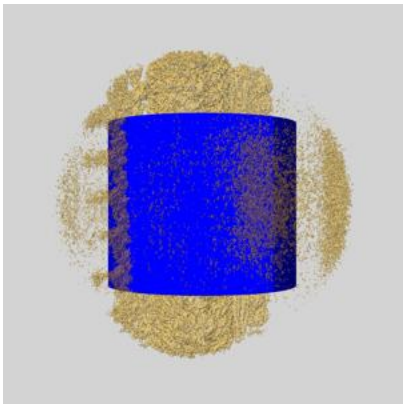
6.6 Mask visualisation

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

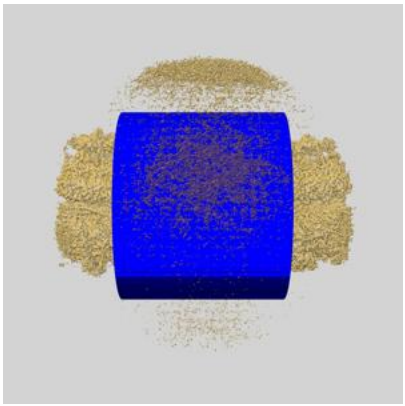
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

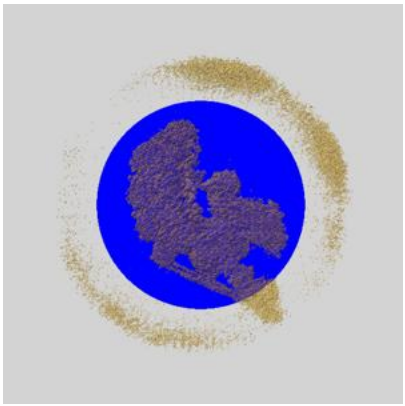
6.6.1 emd_72715_msk_1.map



X



Y

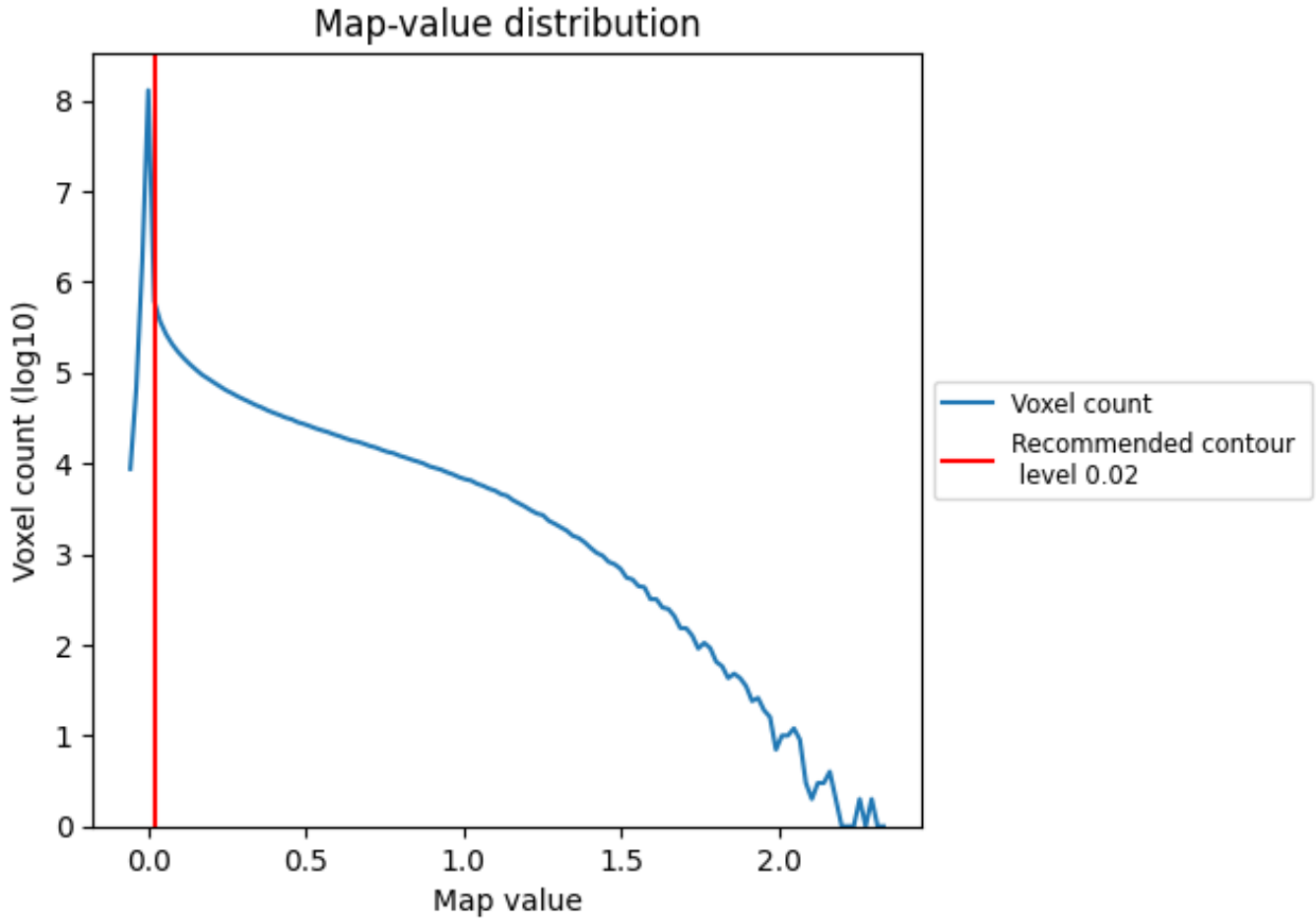


Z

7 Map analysis

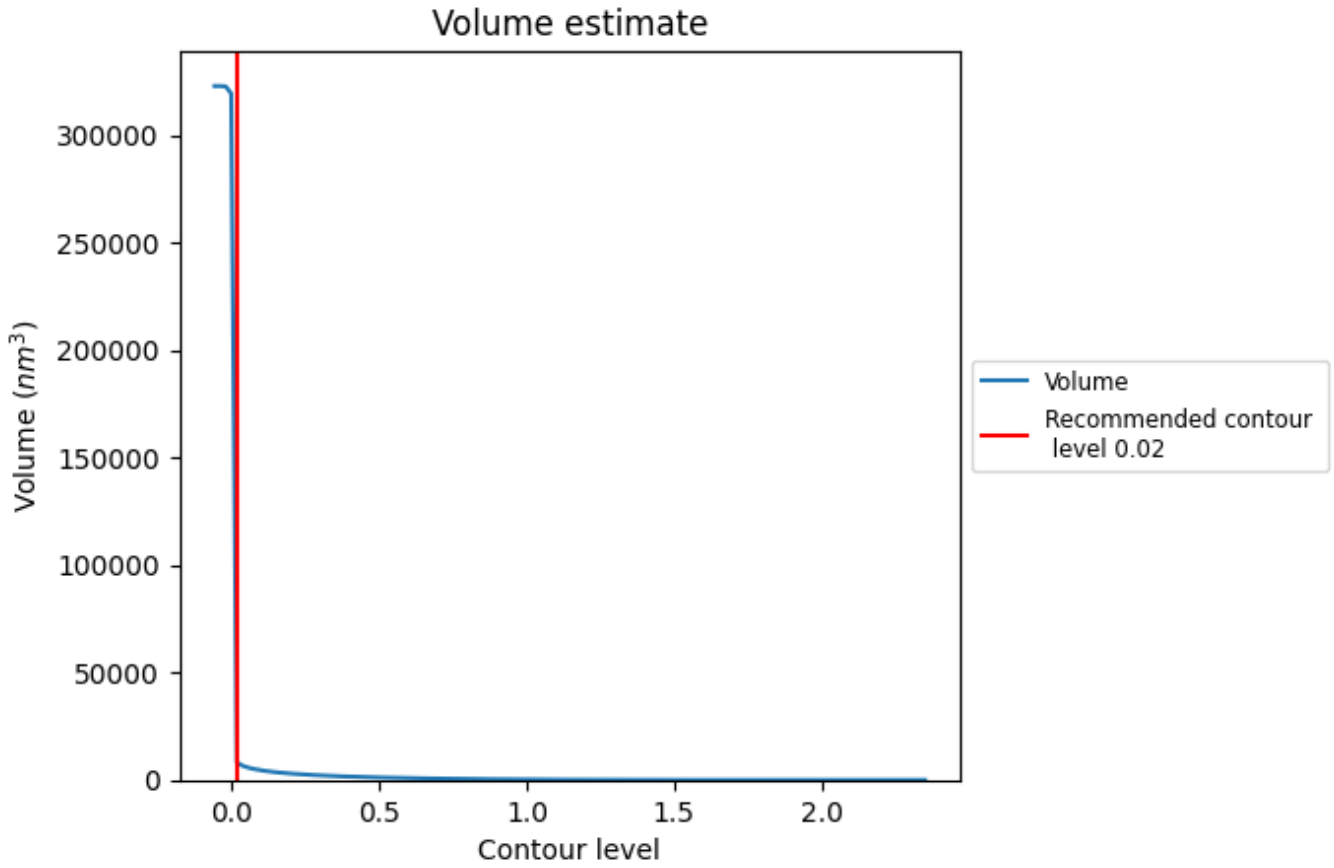
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

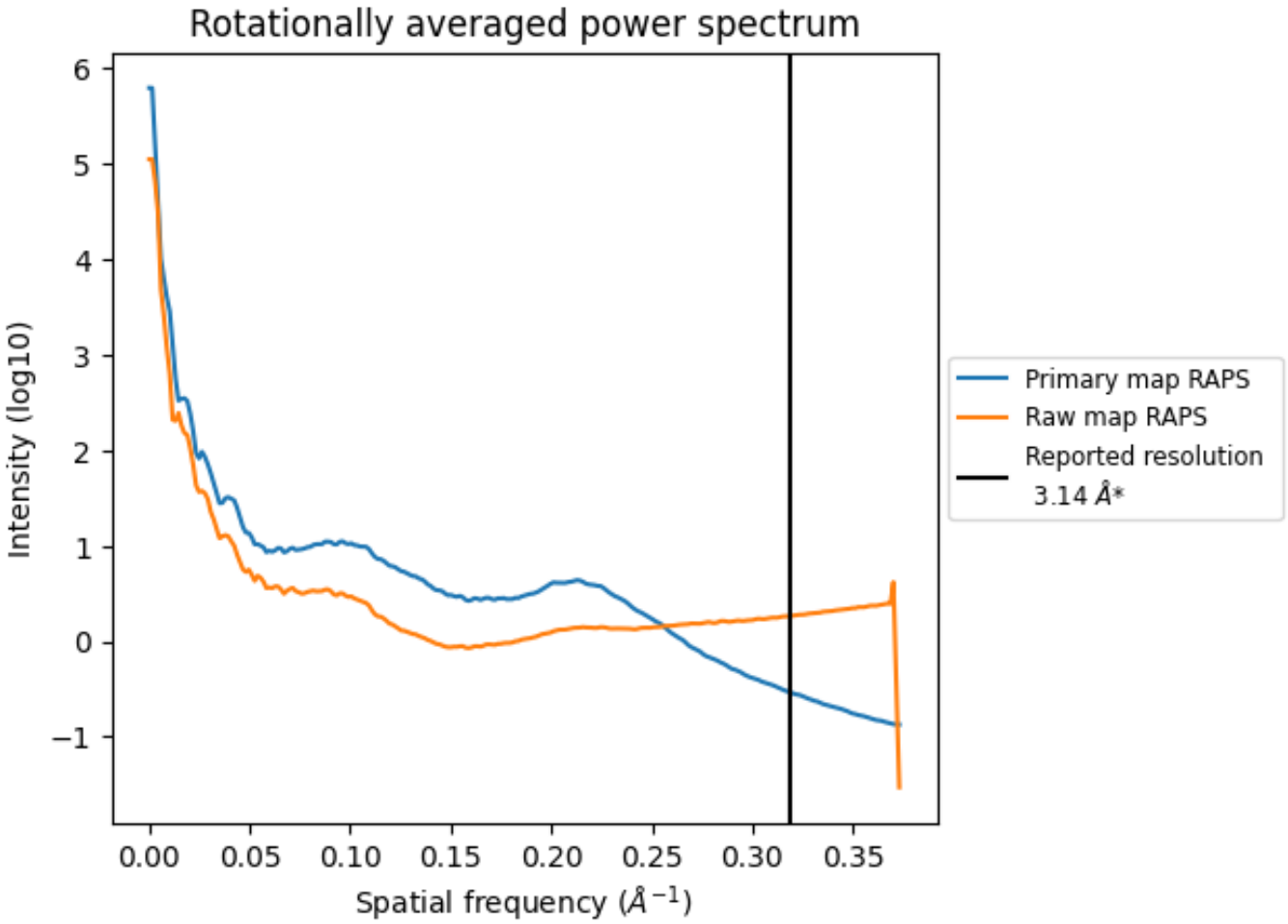
7.2 Volume estimate



The volume at the recommended contour level is 7892 nm^3; this corresponds to an approximate mass of 7129 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

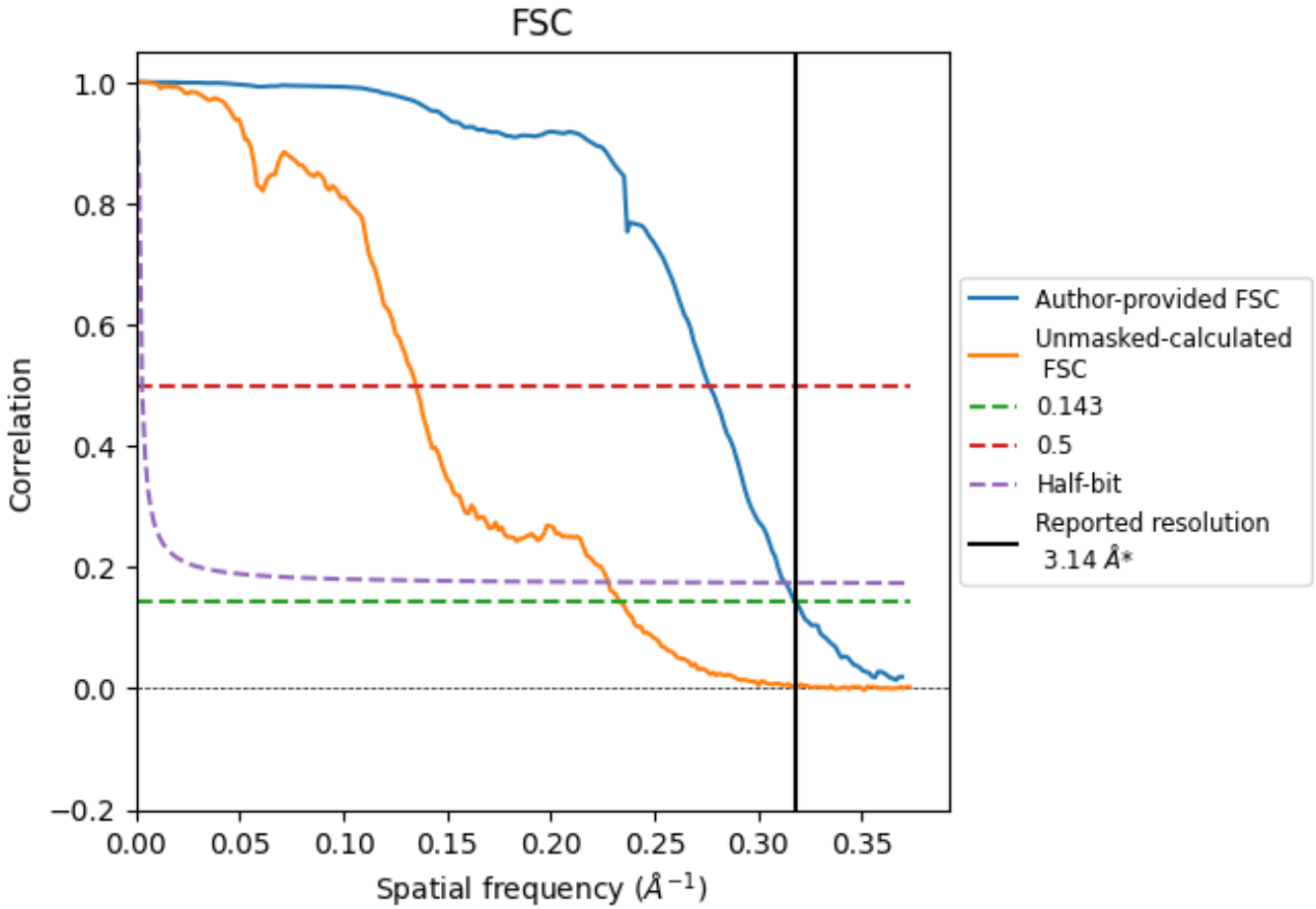


*Reported resolution corresponds to spatial frequency of 0.318 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.318 Å^{-1}

8.2 Resolution estimates (i)

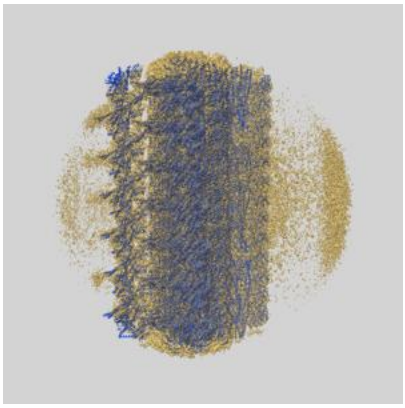
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.14	-	-
Author-provided FSC curve	3.14	3.62	3.19
Unmasked-calculated*	4.29	7.41	4.39

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.29 differs from the reported value 3.14 by more than 10 %

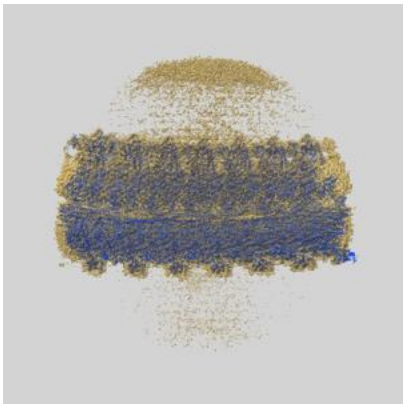
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-72715 and PDB model 9Y9Z. Per-residue inclusion information can be found in section 3 on page 47.

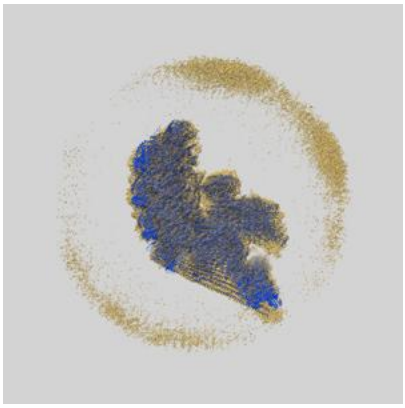
9.1 Map-model overlay



X



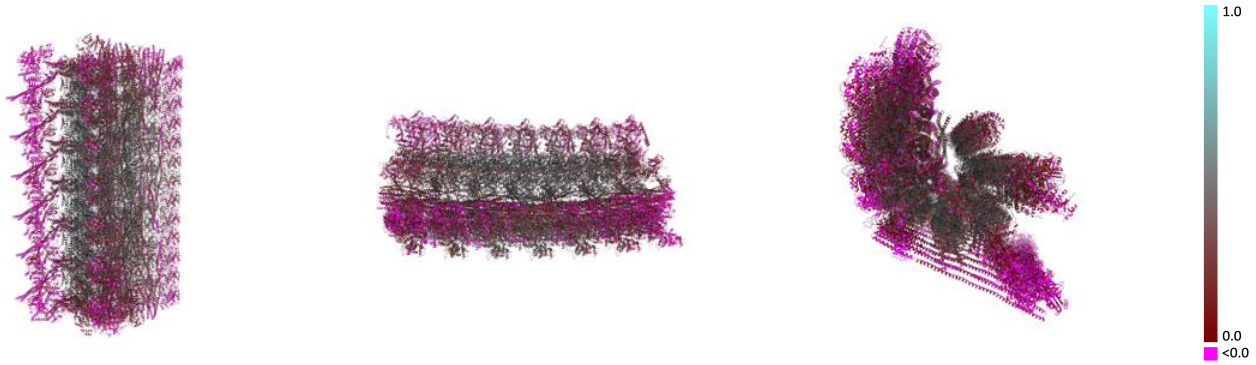
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

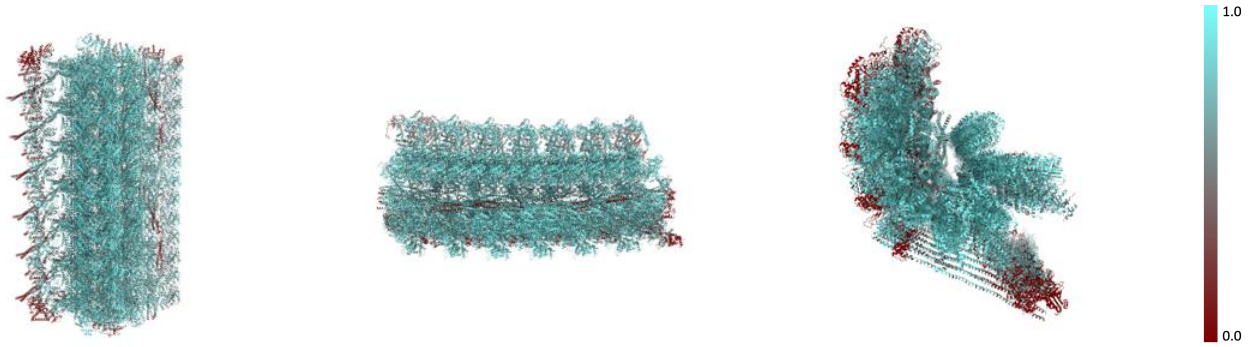
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

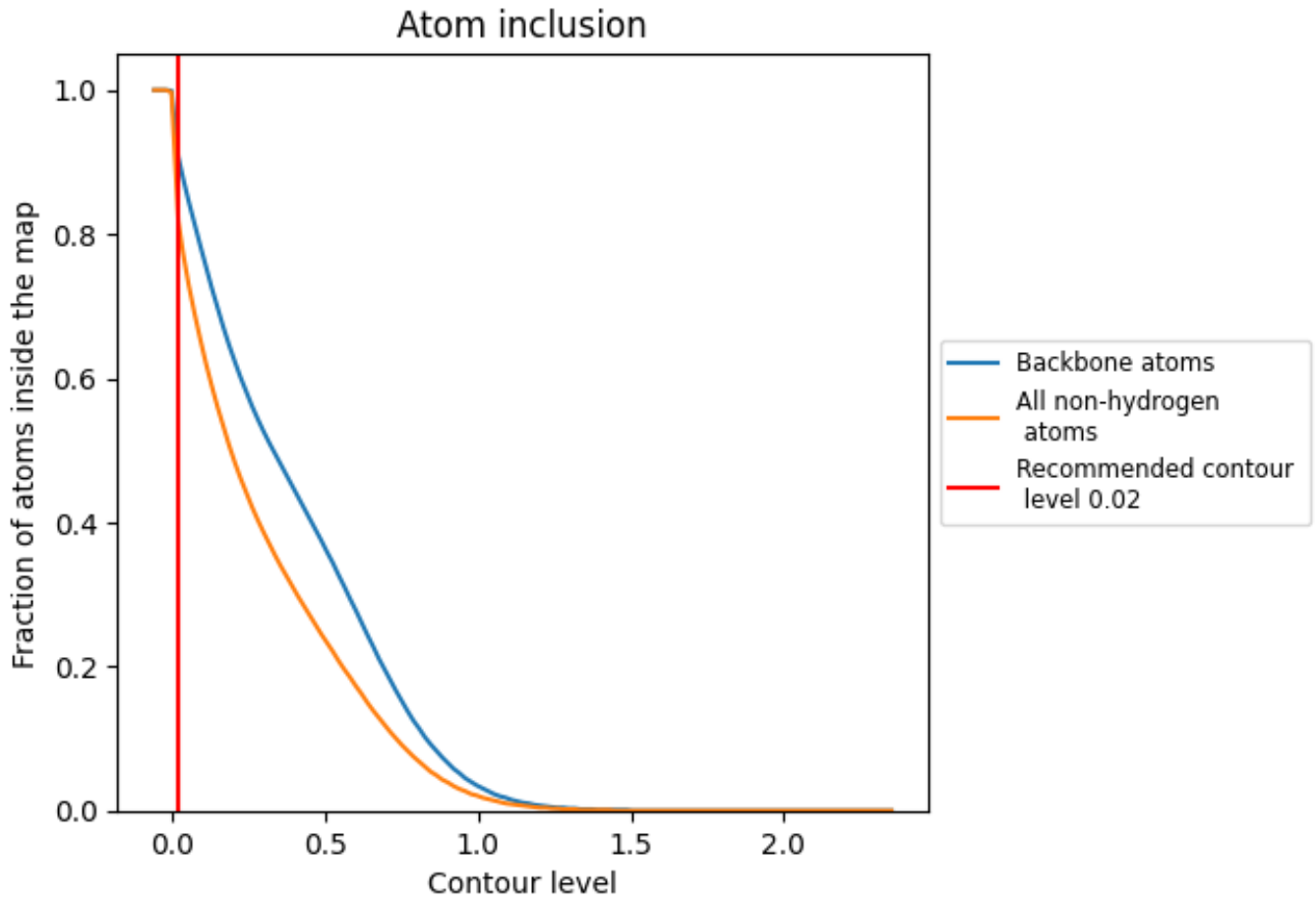
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8180	0.2870
1	0.8720	0.3290
10	0.4430	0.0160
11	0.5150	0.0350
12	0.4880	0.0270
13	0.5500	0.0410
14	0.4560	-0.0070
15	0.5160	0.0440
16	0.4690	0.0150
1A	0.7850	0.1560
1B	0.8330	0.1940
1C	0.8930	0.3150
1D	0.9090	0.3450
1E	0.9340	0.3860
1F	0.9380	0.3940
1G	0.9340	0.4010
1H	0.9200	0.3940
1I	0.9410	0.4180
1J	0.9340	0.3980
1K	0.9430	0.3970
1L	0.9380	0.3620
1M	0.8900	0.2710
1N	0.8280	0.1970
2	0.8460	0.2230
20	0.8620	0.2940
21	0.8360	0.3120
22	0.8670	0.3070
23	0.8430	0.3060
24	0.8190	0.1780
25	0.8140	0.2360
26	0.8410	0.2490
27	0.8250	0.2400
28	0.7750	0.1090
29	0.7810	0.1700
2A	0.8650	0.2330

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Chain	Atom inclusion	Q-score
2B	0.9080	0.3010
2C	0.9330	0.3710
2D	0.9570	0.4300
2E	0.9600	0.4620
2F	0.9580	0.4700
2G	0.9690	0.4950
2H	0.9660	0.4890
2I	0.9640	0.4790
2J	0.9650	0.4630
2K	0.9590	0.4440
2L	0.9540	0.4050
2M	0.9130	0.3230
3	0.5800	0.0980
30	0.8210	0.1740
31	0.7610	0.1260
32	0.7620	0.1160
33	0.3890	0.0110
35	0.5420	0.0020
36	0.5410	0.0060
37	0.5540	0.0160
38	0.5380	-0.0060
39	0.4790	-0.0030
3A	0.8720	0.2660
3B	0.9110	0.3380
3C	0.9480	0.4170
3D	0.9620	0.4610
3E	0.9680	0.4800
3F	0.9670	0.4840
3G	0.9690	0.5040
3H	0.9660	0.5010
3I	0.9640	0.4880
3J	0.9630	0.4750
3K	0.9610	0.4520
3L	0.9430	0.4200
3M	0.9190	0.3510
4	0.4900	0.0750
40	0.4900	0.0070
42	0.1760	-0.0320
43	0.5250	0.0020
44	0.5210	-0.0070
45	0.4940	-0.0050
46	0.4110	-0.0130

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Chain	Atom inclusion	Q-score
47	0.3890	-0.0290
48	0.0650	-0.0470
49	0.7740	0.2020
4A	0.8970	0.3030
4B	0.9390	0.3790
4C	0.9330	0.4220
4D	0.9610	0.4770
4E	0.9420	0.4530
4F	0.9650	0.4910
4G	0.9500	0.4820
4H	0.9670	0.4960
4I	0.9500	0.4720
4J	0.9630	0.4730
4K	0.9490	0.4430
4L	0.9490	0.4180
4M	0.9090	0.3290
5	0.5690	0.0520
50	0.7630	0.1910
51	0.7510	0.1470
52	0.7430	0.1530
53	0.7530	0.1690
54	0.7320	0.1280
55	0.7450	0.1250
56	0.7280	0.1140
57	0.7360	0.1180
58	0.7000	0.0940
59	0.4710	0.0500
5A	0.8560	0.2540
5B	0.9270	0.3550
5C	0.9560	0.4300
5D	0.9570	0.4620
5E	0.9660	0.4840
5F	0.9620	0.4870
5G	0.9630	0.4990
5H	0.9740	0.4970
5I	0.9610	0.4840
5J	0.9630	0.4770
5K	0.9640	0.4790
5L	0.9590	0.4510
5M	0.9410	0.4000
5N	0.9070	0.3150
6	0.4730	0.0310

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Chain	Atom inclusion	Q-score
60	0.6670	0.0600
61	0.6900	0.0700
62	0.5130	0.0290
63	0.8780	0.3680
64	0.8750	0.3680
65	0.8560	0.3340
66	0.8170	0.2500
67	0.6970	0.1190
68	0.8090	0.2120
69	0.8590	0.3140
6A	0.8670	0.2540
6B	0.9250	0.3390
6C	0.9570	0.4230
6D	0.9520	0.4420
6E	0.9570	0.4650
6F	0.9490	0.4530
6G	0.9670	0.4830
6H	0.9550	0.4650
6I	0.9610	0.4780
6J	0.9550	0.4390
6K	0.9570	0.4390
6L	0.9420	0.3770
6M	0.9130	0.2980
6N	0.8310	0.1840
7	0.5780	0.0460
71	0.7830	0.3430
72	0.7040	0.2800
73	0.7000	0.2110
75	0.7800	0.3190
76	0.7140	0.2890
77	0.6850	0.2000
78	0.9060	0.4040
79	0.8820	0.3640
7A	0.8720	0.2280
7B	0.9150	0.3050
7C	0.9440	0.3950
7D	0.9480	0.4220
7E	0.9580	0.4530
7F	0.9590	0.4620
7G	0.9580	0.4760
7H	0.9590	0.4650
7I	0.9580	0.4610

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Chain	Atom inclusion	Q-score
7J	0.9640	0.4380
7K	0.9530	0.3960
7L	0.9210	0.3240
7M	0.8860	0.2420
8	0.5140	0.0490
80	0.8270	0.2680
82	0.9110	0.4050
83	0.8910	0.3370
84	0.8180	0.2140
85	0.8330	0.3480
86	0.7950	0.3020
87	0.7670	0.2220
89	0.8370	0.3400
8A	0.8010	0.1570
8B	0.8540	0.2150
8C	0.9060	0.3060
8D	0.9190	0.3400
8E	0.9450	0.3940
8F	0.9500	0.4250
8G	0.9580	0.4370
8H	0.9480	0.4200
8I	0.9490	0.4070
8J	0.9420	0.3680
8K	0.9100	0.2910
8L	0.8660	0.2120
8M	0.8000	0.1350
9	0.4880	0.0150
90	0.7920	0.2480
91	0.7230	0.1270
92	0.1710	-0.0220
93	0.1090	-0.0430
94	0.1200	-0.0540
95	0.1140	-0.0670
96	0.2990	0.0360
97	0.0950	-0.0620
9A	0.5830	0.0100
9B	0.7110	0.0660
9C	0.6480	0.0520
9D	0.6460	0.0790
9E	0.7460	0.1370
9F	0.7910	0.1870
9G	0.8550	0.2470

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Chain	Atom inclusion	Q-score
9H	0.8410	0.2120
9I	0.7280	0.1290
9J	0.6380	0.0920
9K	0.6480	0.0800
9L	0.6430	0.0380
9M	0.5290	0.0140
A	0.8370	0.2940
A1	0.9560	0.4760
A2	0.9390	0.4220
A3	0.9210	0.3660
A4	0.9020	0.2850
A5	0.9520	0.4790
A6	0.9560	0.4780
A7	0.9480	0.4490
A8	0.8720	0.3350
A9	0.8870	0.3080
B	0.8900	0.3430
B1	0.9640	0.4850
B2	0.9570	0.4850
B3	0.9540	0.4670
B4	0.9460	0.4480
B5	0.9350	0.3930
B6	0.9220	0.3770
B7	0.8390	0.2290
C	0.8260	0.2690
C0	0.5670	0.1580
C1	0.8880	0.4320
C2	0.8810	0.4010
C3	0.8490	0.3620
C4	0.8530	0.3910
C5	0.8340	0.3160
C6	0.6020	0.1900
C7	0.6280	0.1910
C8	0.5530	0.1180
C9	0.5220	0.0490
D	0.8000	0.2060
D0	0.9040	0.4060
D1	0.5650	0.1010
D2	0.5330	0.0510
D3	0.5600	0.2240
D4	0.5330	0.2000
D5	0.5520	0.1470

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Chain	Atom inclusion	Q-score
D6	0.4160	0.0020
D7	0.5930	0.2430
D8	0.5430	0.1740
D9	0.4990	0.0940
E	0.8200	0.2770
E0	0.8910	0.3420
E1	0.8690	0.3200
E2	0.8060	0.2010
E3	0.5130	0.0690
E4	0.8920	0.3760
E5	0.8680	0.3160
E6	0.8200	0.2020
E7	0.8570	0.2700
E8	0.8930	0.3720
E9	0.1590	-0.0250
F	0.8450	0.2850
F0	0.7550	0.1350
F1	0.8710	0.2800
F2	0.7510	0.1320
F3	0.7660	0.1470
F5	0.7740	0.1530
F6	0.7590	0.1540
F7	0.7890	0.1280
F8	0.7350	0.0780
F9	0.7910	0.1830
G	0.8120	0.2450
G0	0.8790	0.3430
G1	0.7100	0.0340
G2	0.6360	0.0250
G3	0.7800	0.0990
G4	0.7160	0.0860
G5	0.6830	0.0350
G6	0.6440	0.0560
G7	0.7780	0.1230
G8	0.7280	0.1030
G9	0.8550	0.3090
H	0.8070	0.2100
H0	0.9180	0.4250
H1	0.8900	0.4110
H2	0.8550	0.2350
H3	0.8090	0.2250
H4	0.8520	0.3390

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Chain	Atom inclusion	Q-score
H5	0.7780	0.1580
H6	0.7860	0.1490
H7	0.8410	0.2150
H8	0.9120	0.3630
H9	0.8570	0.3440
I	0.6290	0.1280
I1	0.8180	0.2370
I2	0.8220	0.2690
I3	0.8790	0.3430
I4	0.7090	0.0610
I5	0.6730	0.0850
I6	0.7420	0.1420
I7	0.7810	0.1420
I8	0.7710	0.1170
I9	0.8190	0.2740
J	0.6270	0.1200
J1	0.6210	0.0200
J2	0.5850	0.0070
J3	0.5640	0.0160
J4	0.3470	-0.0280
J5	0.5730	0.0130
J6	0.5170	0.0080
J7	0.1640	-0.0340
K	0.7370	0.1660
K0	0.9500	0.4320
K1	0.9460	0.4710
K2	0.9510	0.4620
K3	0.9420	0.4270
K4	0.8920	0.3100
K5	0.9430	0.4550
K6	0.9290	0.4030
K7	0.8170	0.2320
K8	0.9540	0.4850
K9	0.9500	0.4710
L	0.7420	0.1600
L0	0.8850	0.2760
L1	0.8830	0.3060
L2	0.9470	0.4550
L3	0.8990	0.3380
L4	0.8790	0.2500
L5	0.9550	0.4660
L6	0.9460	0.4430

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Chain	Atom inclusion	Q-score
L7	0.9310	0.3820
L8	0.8590	0.2590
L9	0.9450	0.4090
M	0.5380	0.1150
M1	0.7630	0.1140
M2	0.8220	0.3040
M3	0.8200	0.2830
M4	0.7430	0.1880
M5	0.6760	0.1050
M6	0.7930	0.2210
M7	0.7120	0.1010
N	0.5870	0.1330
O	0.6130	0.0700
P	0.5950	0.1140
Q	0.8230	0.2860
R	0.8310	0.2940
S	0.8040	0.2630
T	0.8540	0.2880
U	0.8140	0.2840
V	0.8320	0.2860
W	0.7870	0.2480
X	0.7960	0.2570
Y	0.8310	0.2760
Z	0.8280	0.2860
a	0.8000	0.2370
b	0.6930	0.1290
c	0.8250	0.2730
d	0.7900	0.2290
e	0.7030	0.1590
f	0.8230	0.2610
g	0.9150	0.4330
h	0.8290	0.2840
i	0.7590	0.2010
j	0.7870	0.3120
k	0.7660	0.3040
l	0.8310	0.3250
m	0.7380	0.1950
n	0.8030	0.2780
o	0.7440	0.1950
p	0.8130	0.3110
q	0.7510	0.1500
r	0.7510	0.1240

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Chain	Atom inclusion	Q-score
s	0.3560	0.1210
t	0.2560	0.0590
u	0.9140	0.4200
v	0.8990	0.4130
w	0.9060	0.3970
x	0.8980	0.3460
y	0.6970	0.1400
z	0.8940	0.3800