



Full wwPDB EM Validation Report ⓘ

Jul 21, 2025 – 09:42 PM EDT

PDB ID : 8VUU / pdb_00008vuu
EMDB ID : EMD-43569
Title : Anisomycin-bound mammalian ribosome with partially accommodated A-site tRNA
Authors : Loerch, S.; Petrossian, E.; Smith, P.R.; Campbell, Z.T.
Deposited on : 2024-01-31
Resolution : 3.80 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:

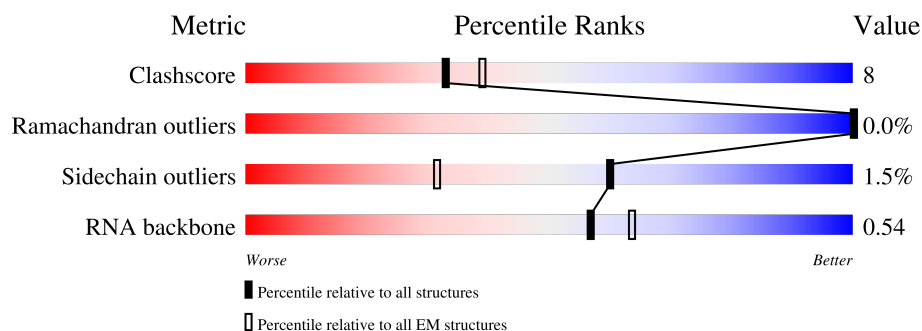
EMDB validation analysis : 0.0.1.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

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 3.80 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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 $\leq 5\%$. 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	A	257	<div> <div>63%</div> <div>75%</div> <div>22%</div> <div>.</div> </div>
2	B	403	<div> <div>59%</div> <div>75%</div> <div>23%</div> <div>.</div> </div>
3	C	413	<div> <div>49%</div> <div>70%</div> <div>17%</div> <div>12%</div> </div>
4	D	297	<div> <div>64%</div> <div>85%</div> <div>14%</div> <div>.</div> </div>
5	E	291	<div> <div>57%</div> <div>62%</div> <div>16%</div> <div>22%</div> </div>
6	F	249	<div> <div>55%</div> <div>72%</div> <div>19%</div> <div>9%</div> </div>
7	G	319	<div> <div>41%</div> <div>61%</div> <div>11%</div> <div>28%</div> </div>

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Mol	Chain	Length	Quality of chain
8	H	192	
9	I	214	
10	J	178	
11	K	211	
12	L	218	
13	M	204	
14	N	203	
15	O	213	
16	P	188	
17	Q	212	
18	R	224	
19	S	160	
20	T	128	
21	U	140	
22	V	157	
23	W	156	
24	X	145	
25	Y	136	
26	Z	148	
27	AA	245	
28	BA	115	
29	CA	125	
30	DA	135	
31	EA	110	
32	FA	129	

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Mol	Chain	Length	Quality of chain
33	GA	123	
34	HA	105	
35	IA	97	
36	JA	70	
37	KA	51	
38	LA	128	
39	MA	25	
40	NA	106	
41	OA	92	
42	PA	137	
43	RA	165	
44	SA	76	
45	TA	76	
46	VA	12	
47	WA	3584	
48	XA	120	
49	YA	156	
50	ZA	1869	
51	AB	295	
52	BB	264	
53	CB	293	
54	DB	281	
55	EB	263	
56	FB	204	
57	GB	249	

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Mol	Chain	Length	Quality of chain
58	HB	432	
59	IB	208	
60	JB	194	
61	KB	165	
62	LB	158	
63	MB	132	
64	NB	151	
65	OB	151	
66	PB	145	
67	QB	172	
68	RB	135	
69	SB	152	
70	TB	145	
71	UB	119	
72	VB	83	
73	WB	130	
74	XB	143	
75	YB	131	
76	ZB	124	
77	AC	115	
78	BC	84	
79	CC	69	
80	DC	56	
81	EC	133	
82	FC	188	

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Mol	Chain	Length	Quality of chain
83	GC	317	<div><div></div><div>95%</div><div>69%</div><div>29%</div><div>••</div></div>
84	IC	4	<div><div></div><div>100%</div><div>75%</div><div>25%</div></div>
85	b	318	<div><div></div><div>52%</div><div>39%</div><div>12%</div><div>•</div><div>47%</div></div>
86	At	74	<div><div></div><div>81%</div><div>51%</div><div>41%</div><div>5%</div><div>•</div></div>

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 218724 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	250	Total	C	N	O	S	0	0
			1914	1199	392	317	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	397	Total	C	N	O	S	0	0
			3196	2035	603	545	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2395	1514	439	428	14		

- Molecule 5 is a protein called L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	228	Total	C	N	O	S	0	0
			1823	1173	349	298	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	227	Total	C	N	O	S	0	0
			1897	1217	366	305	9		

- Molecule 7 is a protein called L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	229	Total	C	N	O	S	0	0
			1850	1181	356	309	4		

- Molecule 8 is a protein called L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	171	Total	C	N	O	S	0	0
			1372	867	256	243	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	46	ILE	-	insertion	UNP G1TPV0
K	47	ALA	-	insertion	UNP G1TPV0
K	48	PRO	-	insertion	UNP G1TPV0
K	49	ARG	-	insertion	UNP G1TPV0
K	50	PRO	-	insertion	UNP G1TPV0
K	51	ALA	-	insertion	UNP G1TPV0
K	52	ALA	-	insertion	UNP G1TPV0
K	53	GLY	-	insertion	UNP G1TPV0
K	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	156	Total	C	N	O	S	0	0
			1266	793	245	219	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	43	SER	ALA	conflict	UNP G1TVT6

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	4	ASP	ASN	conflict	UNP G1TFE0
P	14	ARG	TRP	conflict	UNP G1TFE0
P	53	MET	LEU	conflict	UNP G1TFE0
P	58	ARG	TRP	conflict	UNP G1TFE0
P	75	ARG	GLN	conflict	UNP G1TFE0
P	80	ALA	PRO	conflict	UNP G1TFE0
P	86	VAL	ILE	conflict	UNP G1TFE0

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Chain	Residue	Modelled	Actual	Comment	Reference
P	104	ARG	HIS	conflict	UNP G1TFE0
P	110	ARG	CYS	conflict	UNP G1TFE0
P	137	VAL	GLY	conflict	UNP G1TFE0
P	157	GLY	ARG	conflict	UNP G1TFE0
P	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	101	Total	C	N	O	S	0	0
			826	530	144	150	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	18	LEU	VAL	conflict	UNP G1TSG1
T	32	GLY	ARG	conflict	UNP G1TSG1
T	36	ALA	GLU	conflict	UNP G1TSG1
T	39	PHE	SER	conflict	UNP G1TSG1
T	54	GLY	ARG	conflict	UNP G1TSG1
T	60	VAL	ALA	conflict	UNP G1TSG1
T	62	SER	THR	conflict	UNP G1TSG1
T	63	LEU	ILE	conflict	UNP G1TSG1

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Chain	Residue	Modelled	Actual	Comment	Reference
T	97	ARG	HIS	conflict	UNP G1TSG1
T	106	THR	SER	conflict	UNP G1TSG1
T	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	135	Total	C	N	O	S	0	0
			1004	631	191	177	5		

- Molecule 22 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	110	Total	C	N	O	S	0	0
			887	555	179	149	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	78	SER	PHE	conflict	UNP G1SE28

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 27 is a protein called L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AA	107	Total	C	N	O	S	0	0
			873	542	195	133	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	99	Total	C	N	O	S	0	0
			769	486	135	141	7		

- Molecule 29 is a protein called L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CA	108	Total	C	N	O	S	0	0
			893	563	172	156	2		

- Molecule 30 is a protein called L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DA	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	EA	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	FA	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	GA	121	Total	C	N	O	S	0	0
			1008	637	203	167	1		

- Molecule 34 is a protein called L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	HA	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	IA	87	Total	C	N	O	S	0	0
			716	440	159	112	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	JA	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JA	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	KA	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LA	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	MA	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NA	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	OA	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	PA	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	RA	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 44 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SA	76	Total	C	N	O	P	0	0
			1622	726	300	521	75		

- Molecule 45 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	TA	76	Total	C	N	O	P	0	0
			1615	722	286	532	75		

- Molecule 46 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	VA	12	Total	C	N	O	P	0	0
			249	112	39	86	12		

- Molecule 47 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	WA	3578	Total	C	N	O	P	0	0
			76735	34173	14061	24923	3578		

- Molecule 48 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	XA	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
XA	2	U	N	conflict	GB X06789.1
XA	36	C	N	conflict	GB X06789.1
XA	102	U	N	conflict	GB X06789.1
XA	112	U	N	conflict	GB X06789.1
XA	114	U	N	conflict	GB X06789.1
XA	119	U	C	conflict	GB X06789.1
XA	120	U	N	conflict	GB X06789.1

- Molecule 49 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	YA	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 50 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	ZA	1716	Total	C	N	O	P	0	0
			36623	16347	6572	11989	1715		

- Molecule 51 is a protein called RPSA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 52 is a protein called S3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 53 is a protein called S2-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CB	220	Total	C	N	O	S	0	0
			1707	1105	293	300	9		

- Molecule 54 is a protein called S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	DB	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 55 is a protein called S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	EB	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EB	25	GLY	SER	conflict	UNP G1TK17
EB	51	ARG	LYS	conflict	UNP G1TK17
EB	78	THR	ALA	conflict	UNP G1TK17
EB	156	VAL	MET	conflict	UNP G1TK17

- Molecule 56 is a protein called S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	FB	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 57 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	GB	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 58 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	HB	185	Total	C	N	O	S	0	0
			1489	952	271	265	1		

- Molecule 59 is a protein called S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	IB	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
IB	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 60 is a protein called S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	JB	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 61 is a protein called S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	KB	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 62 is a protein called S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LB	144	Total	C	N	O	S	0	0
			1180	752	223	199	6		

- Molecule 63 is a protein called S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	MB	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 64 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	NB	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 65 is a protein called S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	OB	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 66 is a protein called S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	PB	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 67 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	QB	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 68 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	RB	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 69 is a protein called S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SB	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 70 is a protein called S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	TB	142	Total	C	N	O	S	0	0
			1104	693	212	196	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TB	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 71 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	UB	102	Total	C	N	O	S	0	0
			808	507	154	143	4		

- Molecule 72 is a protein called S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	VB	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VB	3	ASN	SER	conflict	UNP G1TM82
VB	4	ASP	ASN	conflict	UNP G1TM82
VB	33	GLN	PRO	conflict	UNP G1TM82
VB	50	PHE	SER	conflict	UNP G1TM82
VB	75	ALA	SER	conflict	UNP G1TM82
VB	76	ASP	HIS	conflict	UNP G1TM82
VB	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 73 is a protein called S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	WB	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	XB	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 75 is a protein called S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	YB	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 76 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	ZB	85	Total	C	N	O	S	0	0
			683	439	128	115	1		

- Molecule 77 is a protein called S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AC	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	28	ARG	CYS	conflict	UNP G1TFE8
AC	56	ALA	VAL	conflict	UNP G1TFE8
AC	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 78 is a protein called S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BC	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 79 is a protein called S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CC	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 80 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	DC	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 81 is a protein called S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	EC	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 82 is a protein called S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	FC	69	Total	C	N	O	S	0	0
			564	357	105	95	7		

- Molecule 83 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	GC	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 84 is a protein called nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
84	IC	4	Total	C	N	O	0	0
			20	12	4	4		

- Molecule 85 is a protein called RPLP0.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	b	167	Total	C	N	O	S	0	0
			1279	813	228	229	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	82	LEU	ILE	conflict	UNP G1SPK4

- Molecule 86 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
86	At	74	Total	C	N	O	P	S	0	0
			1582	705	282	520	74	1		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	I	1	Total	Mg	0
			1	1	
87	FA	1	Total	Mg	0
			1	1	
87	WA	80	Total	Mg	0
			80	80	

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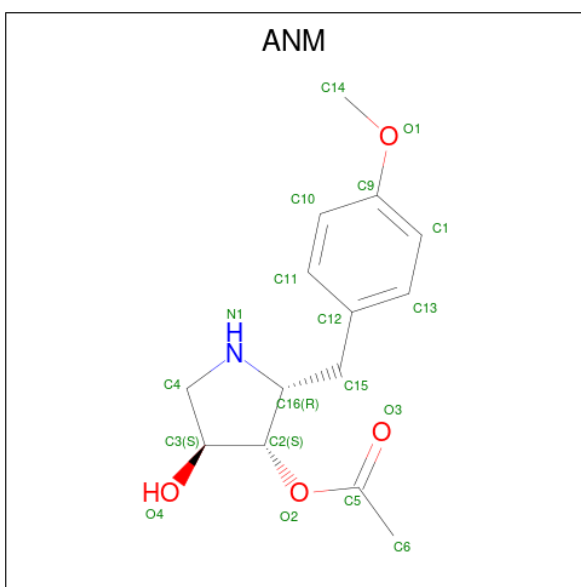
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
87	XA	1	Total 1	Mg 1	0
87	ZA	18	Total 18	Mg 18	0
87	AC	1	Total 1	Mg 1	0

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

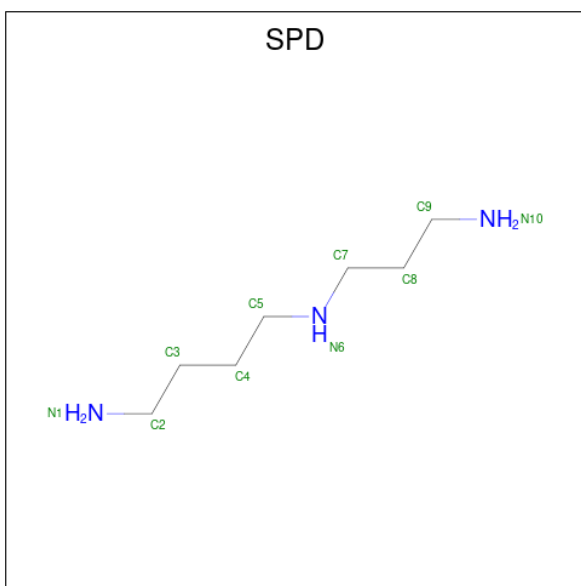
Mol	Chain	Residues	Atoms		AltConf
88	FA	1	Total 1	Zn 1	0
88	IA	1	Total 1	Zn 1	0
88	LA	1	Total 1	Zn 1	0
88	NA	1	Total 1	Zn 1	0
88	OA	1	Total 1	Zn 1	0
88	AC	1	Total 1	Zn 1	0
88	DC	1	Total 1	Zn 1	0
88	FC	1	Total 1	Zn 1	0

- Molecule 89 is ANISOMYCIN (CCD ID: ANM) (formula: C₁₄H₁₉NO₄).



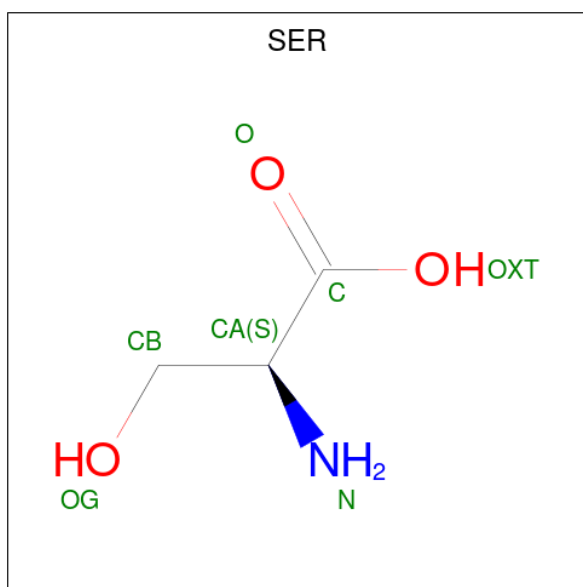
Mol	Chain	Residues	Atoms				AltConf
89	WA	1	Total	C	N	O	0
			19	14	1	4	

- Molecule 90 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			AltConf
90	WA	1	Total	C	N	0
			10	7	3	

- Molecule 91 is SERINE (CCD ID: SER) (formula: $C_3H_7NO_3$).

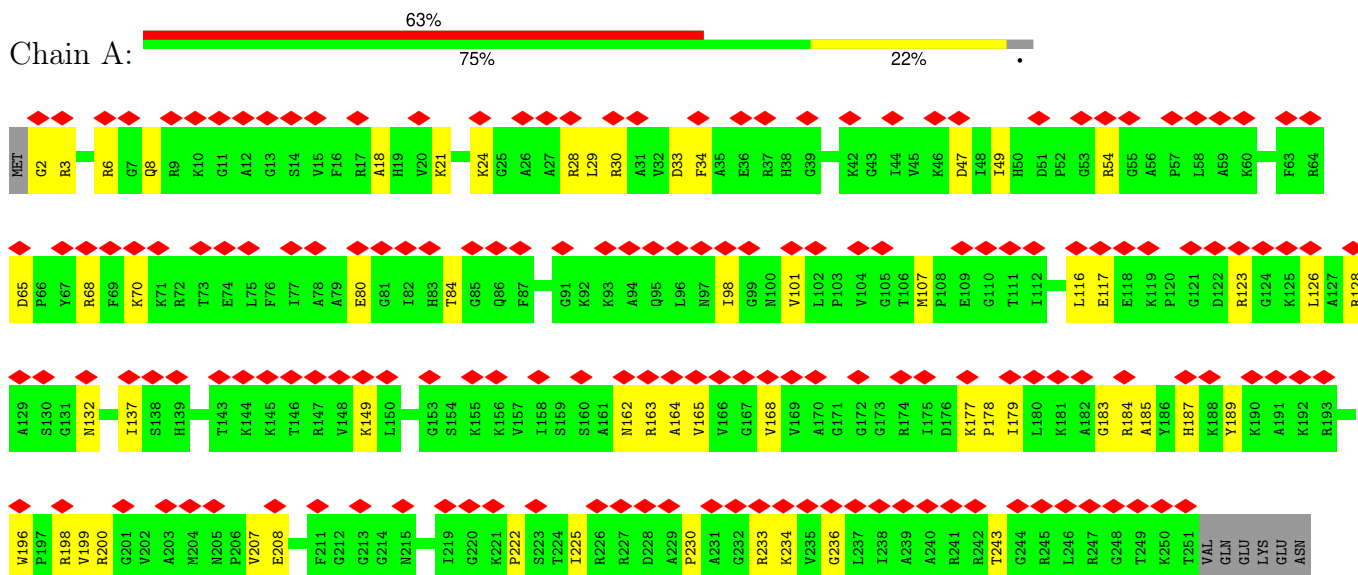


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
91	ZA	1	6	3	1	2	0

3 Residue-property plots [i](#)

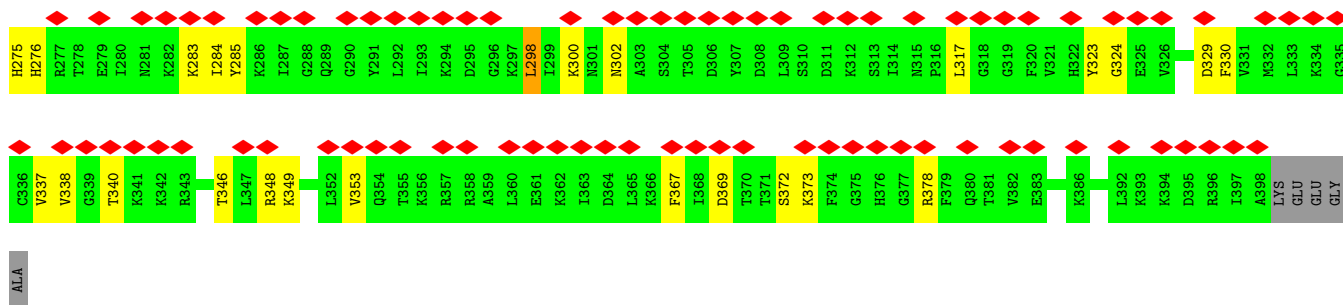
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: uL2

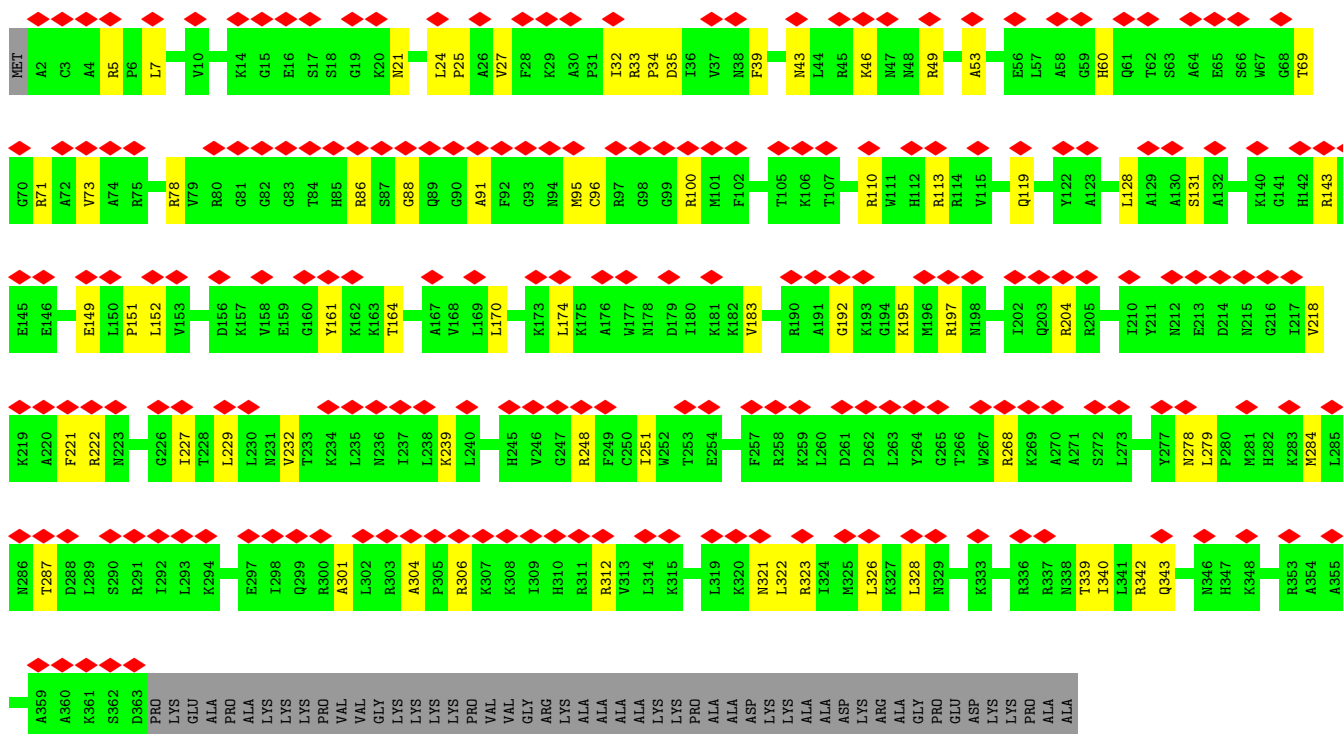


• Molecule 2: uL3

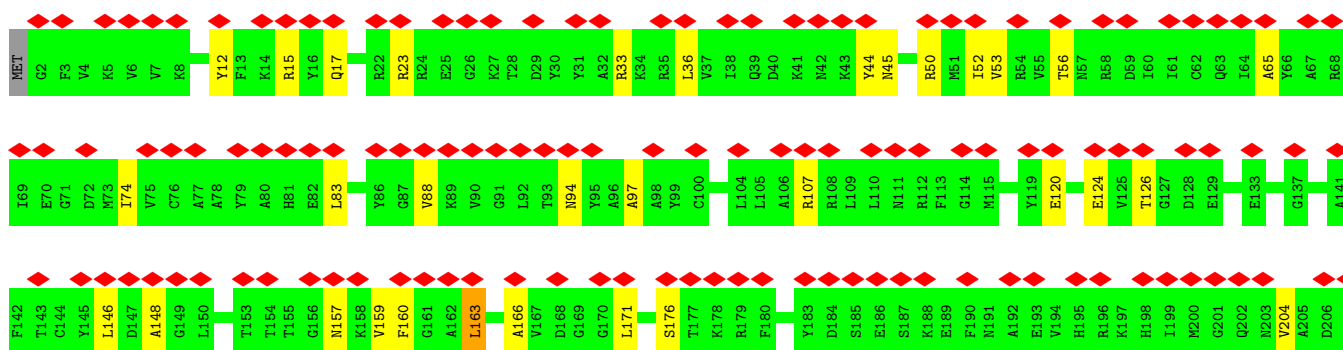
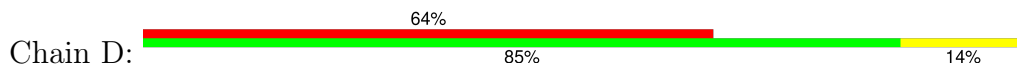


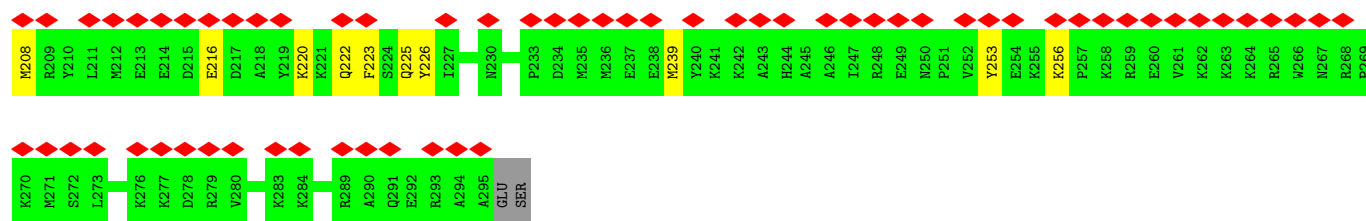


• Molecule 3: uL4

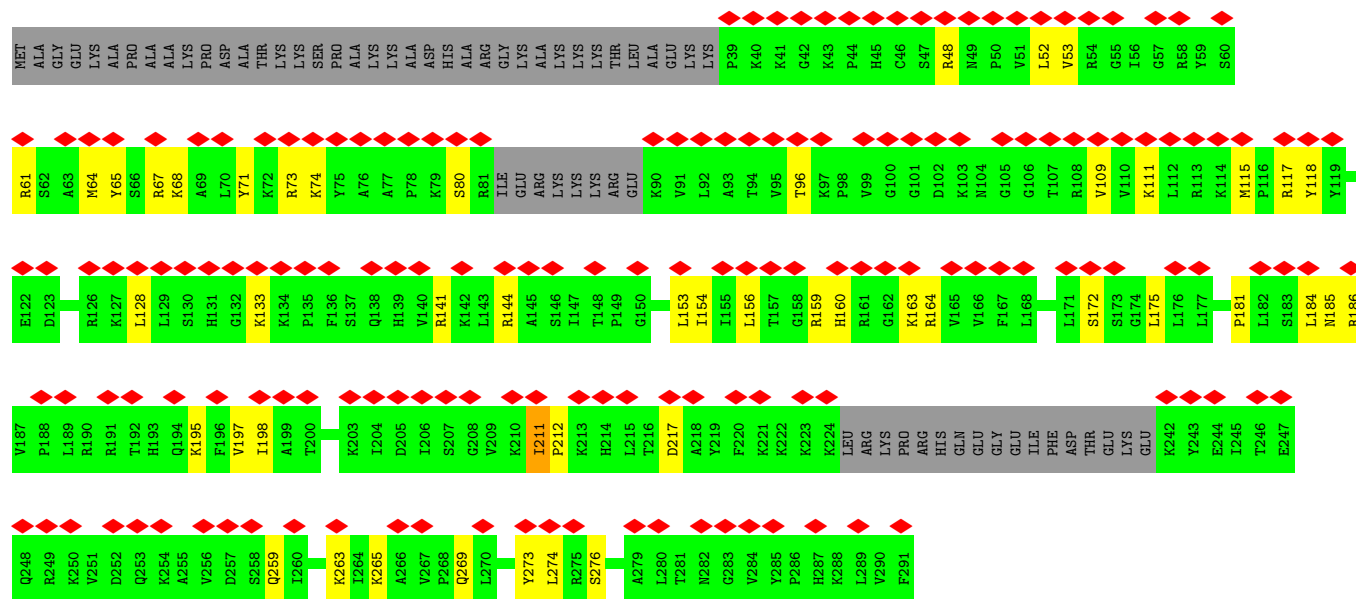


• Molecule 4: uL18

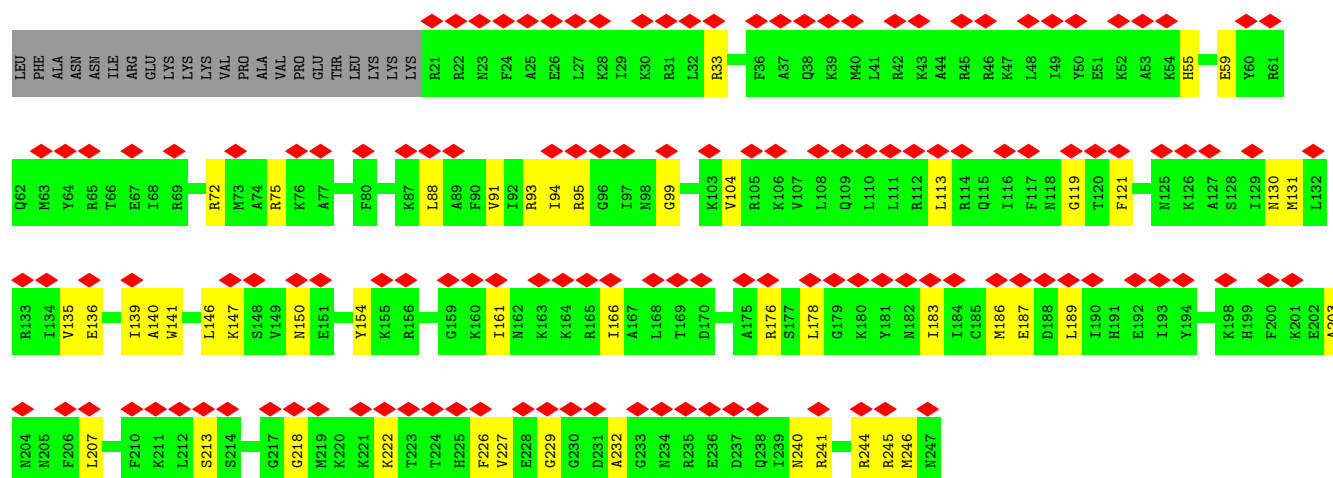




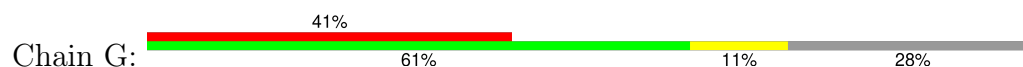
• Molecule 5: L6

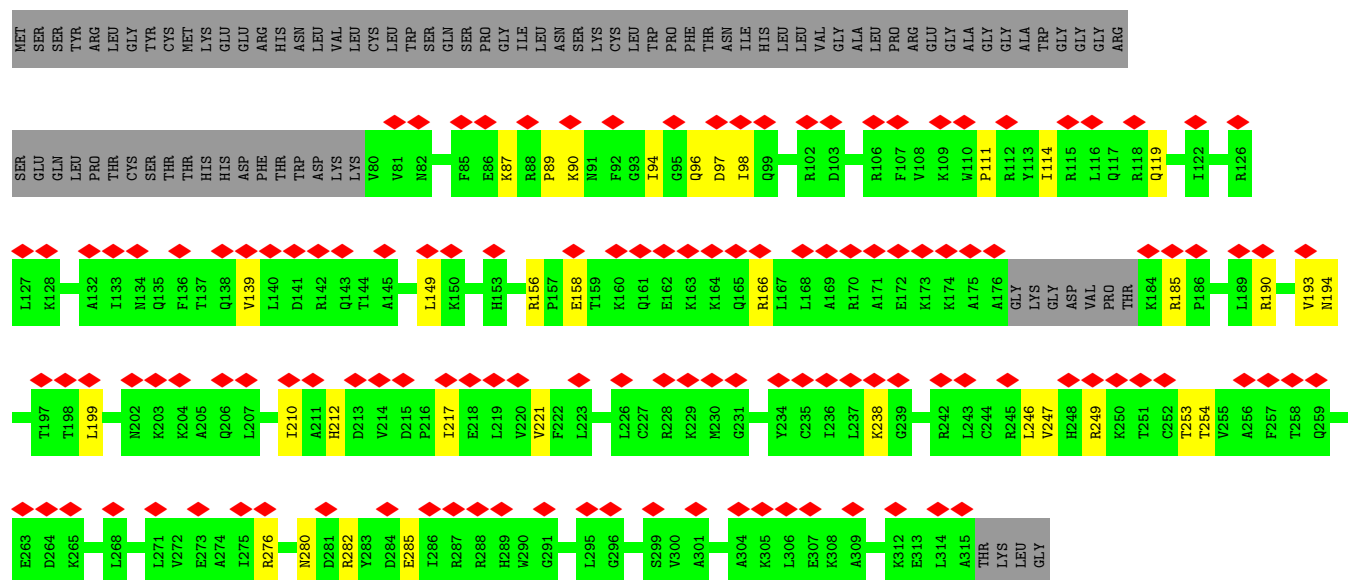


• Molecule 6: uL30

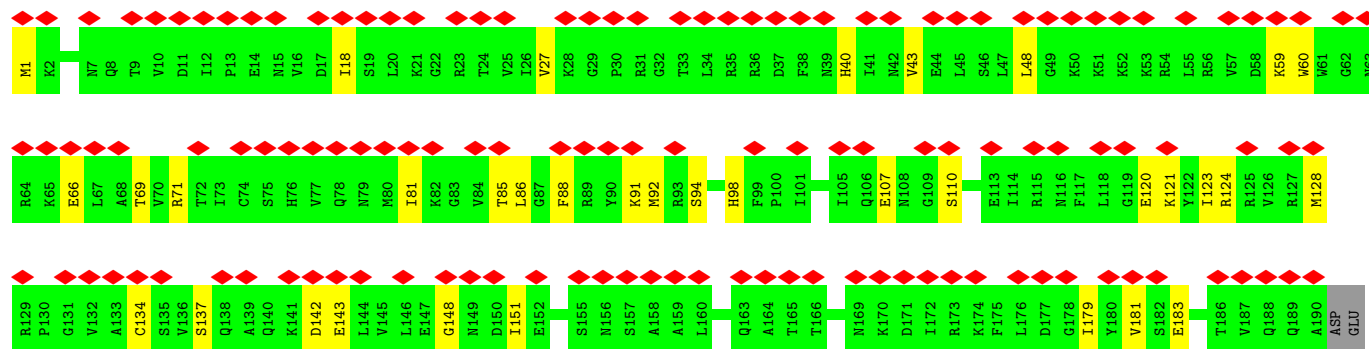
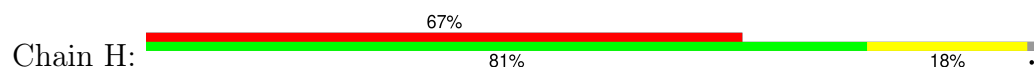


• Molecule 7: L7A

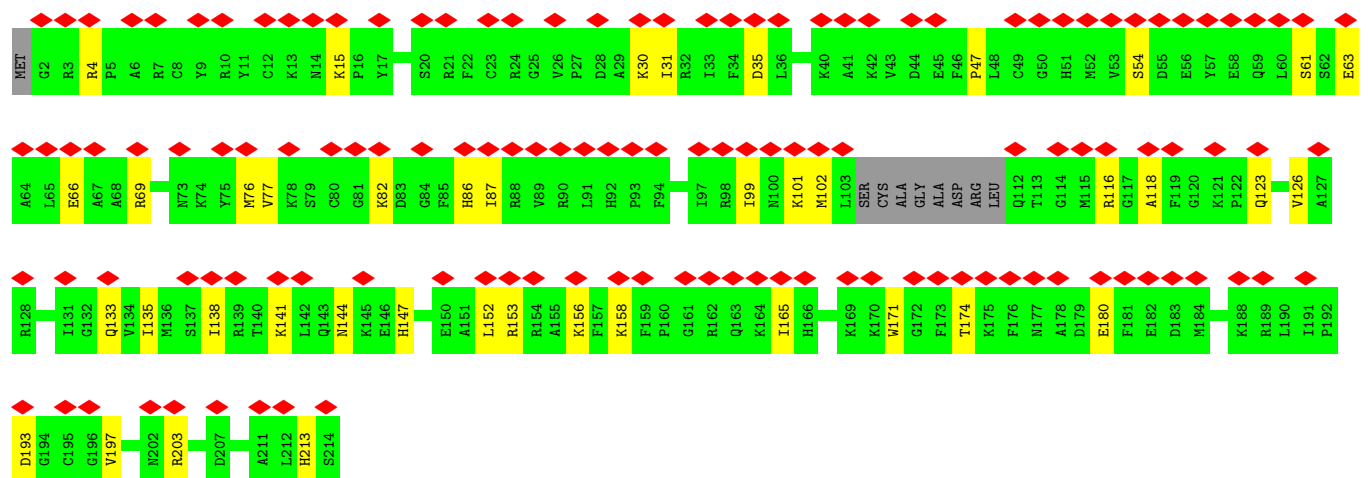
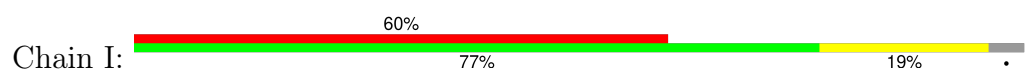




• Molecule 8: L9

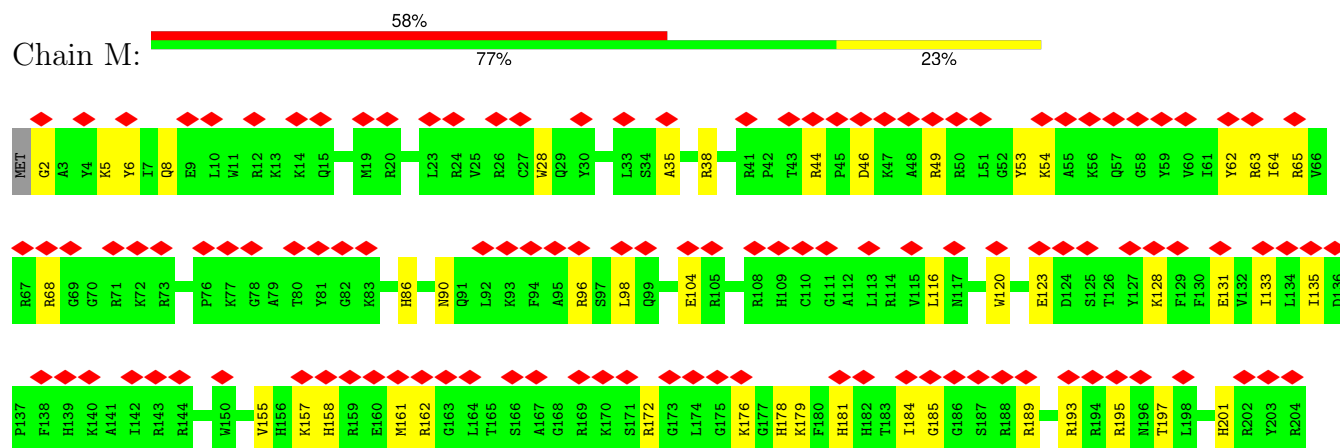


• Molecule 9: L10



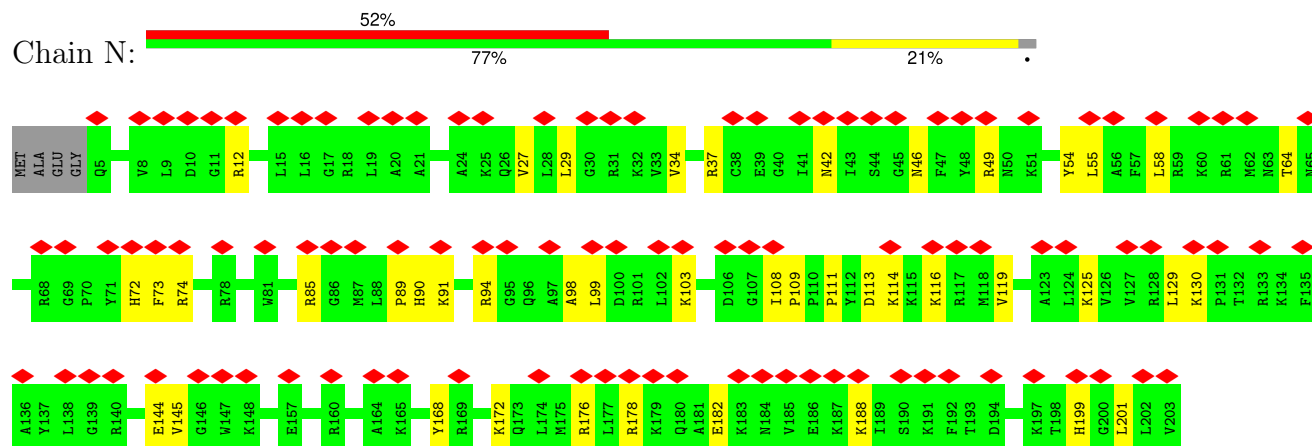
- Molecule 13: L15

Chain M:



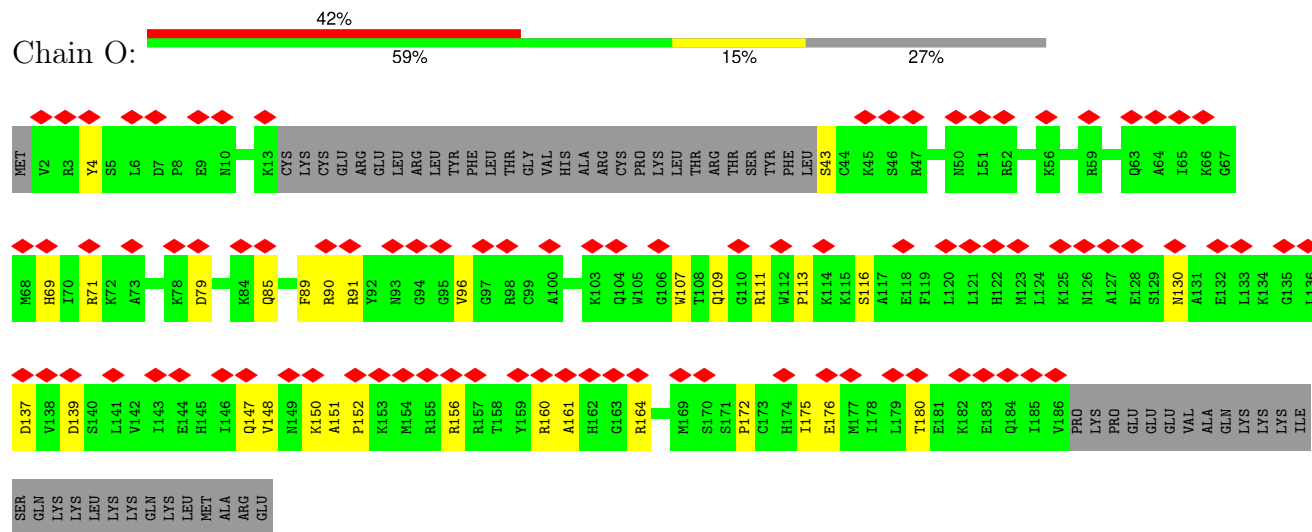
- Molecule 14: uL13

Chain N:



- Molecule 15: uL22

Chain O:

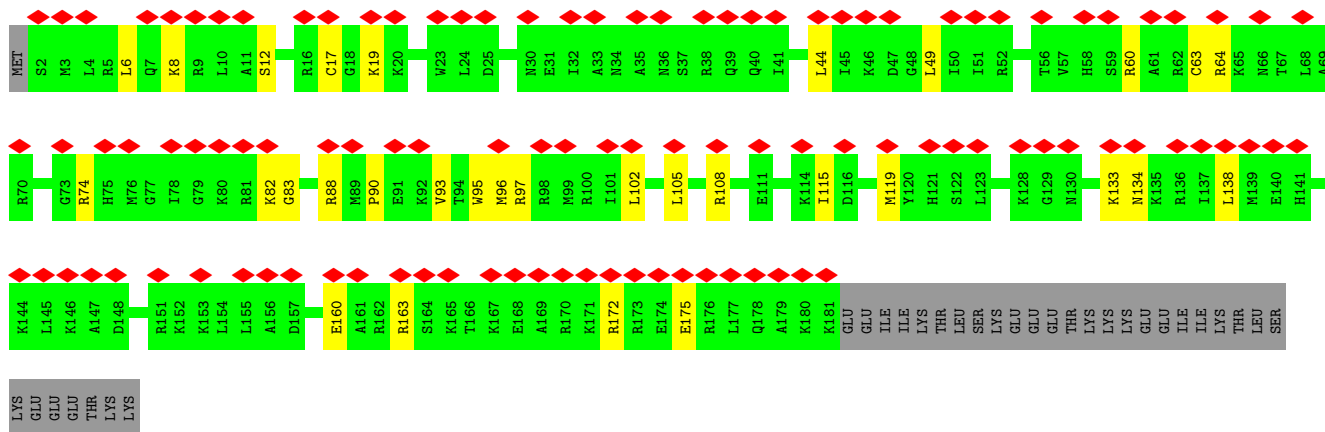


- Molecule 16: eL18

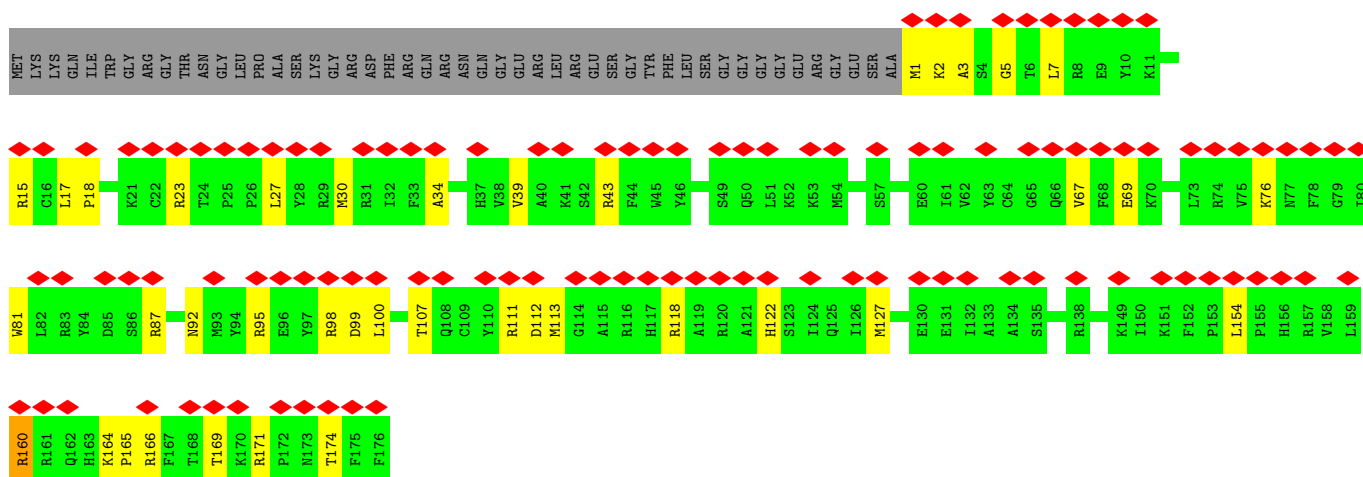
Chain P:



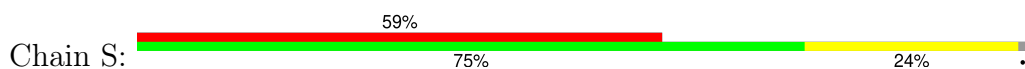
- Molecule 17: eL19

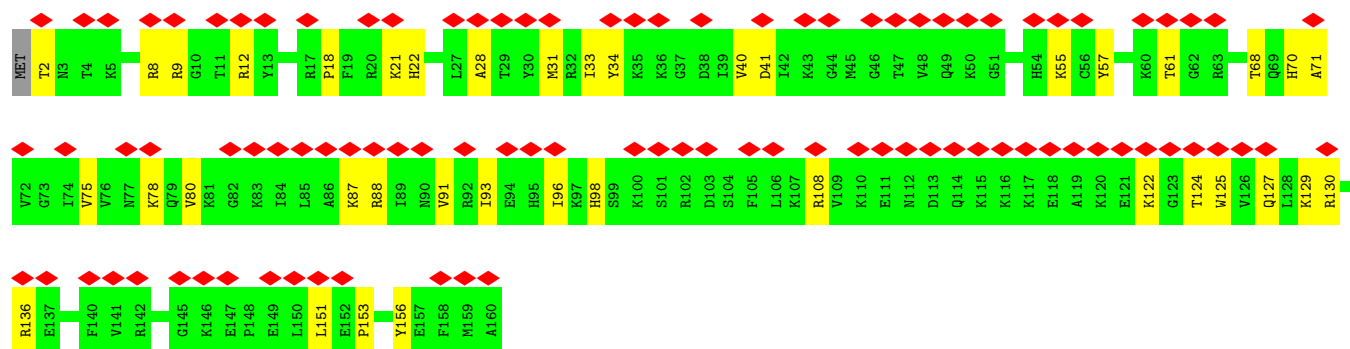


- Molecule 18: L18A

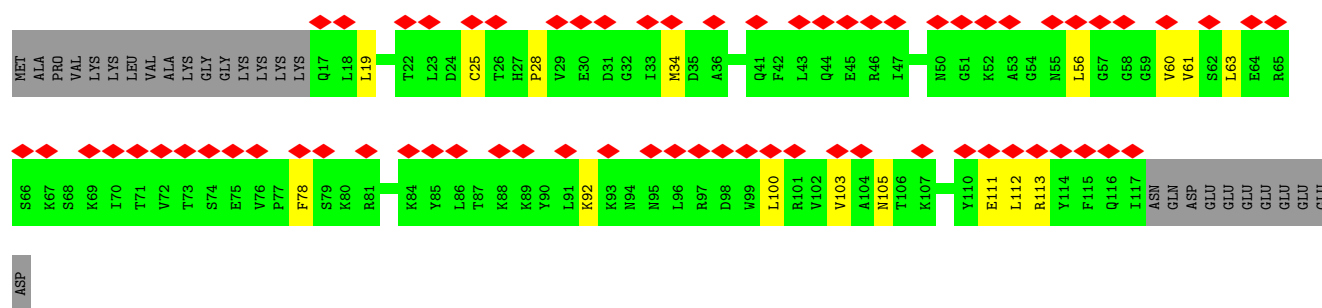


- Molecule 19: eL21

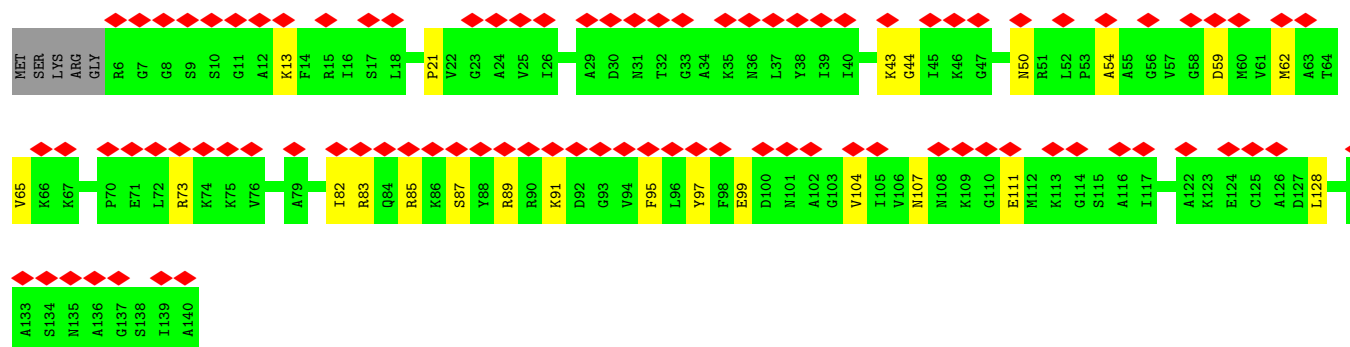
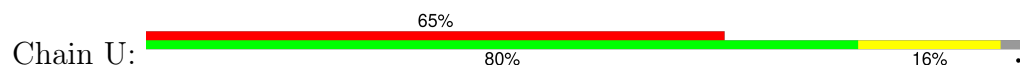




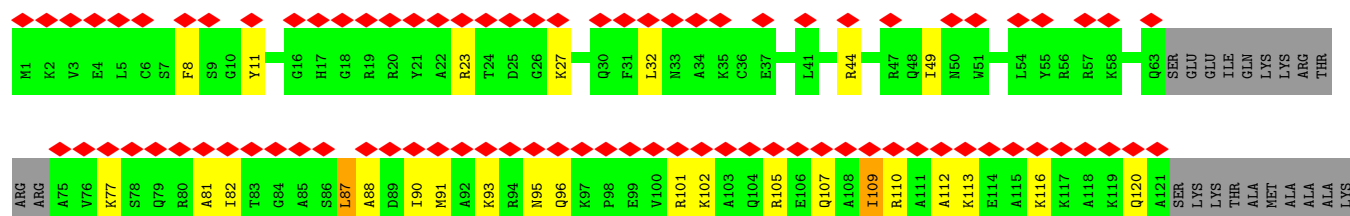
• Molecule 20: eL22



• Molecule 21: L23



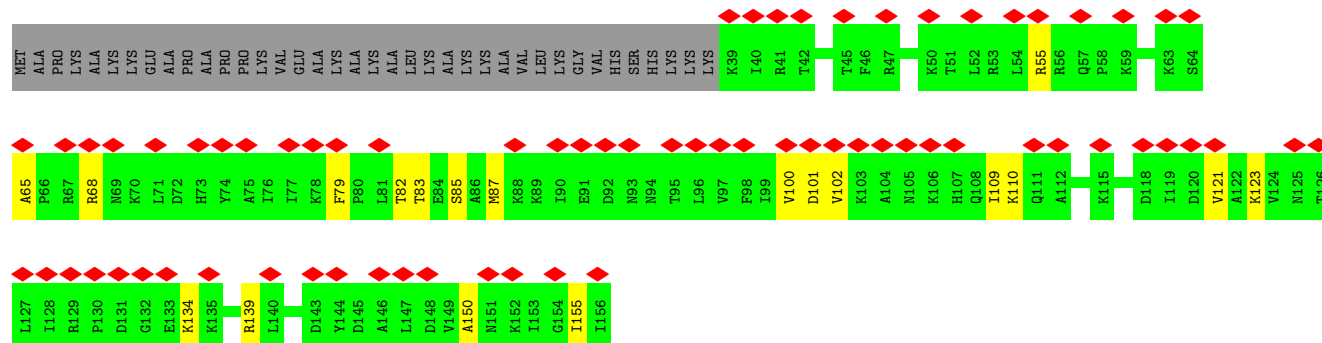
• Molecule 22: uL24



PRO THR
LYS LYS
ALA ALA
PRO PRO
LYS LYS
GLN LYS
ILE LYS
VAL LYS
PRO LYS
VAL LYS
GLU LYS
SER LYS
ALA LYS
PRO LYS
ARG LYS
GLY LYS
GLY LYS
ARG LYS

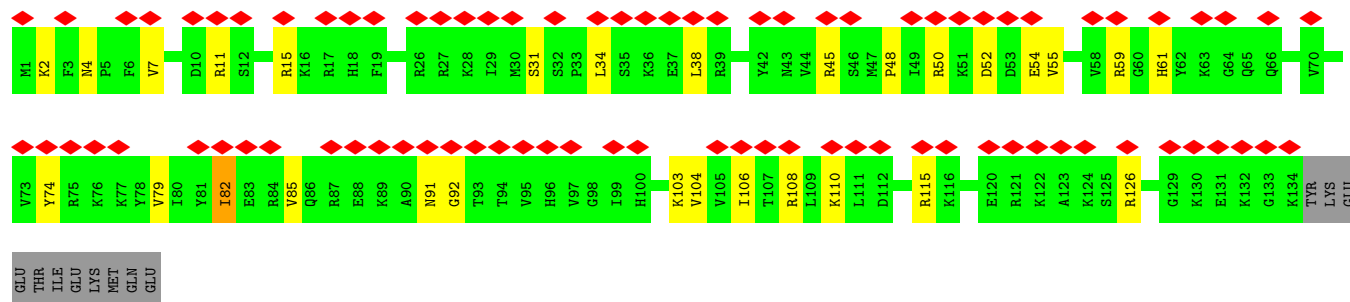
• Molecule 23: uL23

Chain W: 45% 63% 12% 24%



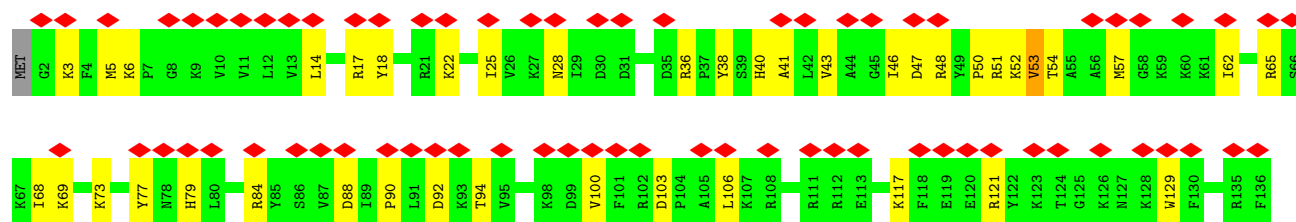
• Molecule 24: L26

Chain X: 57% 72% 19% 8%



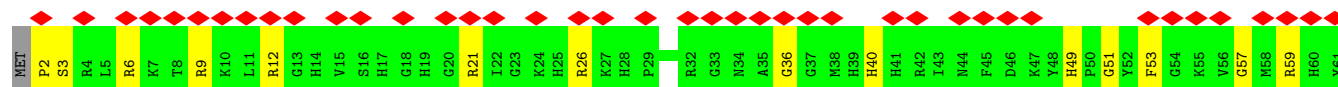
• Molecule 25: L27

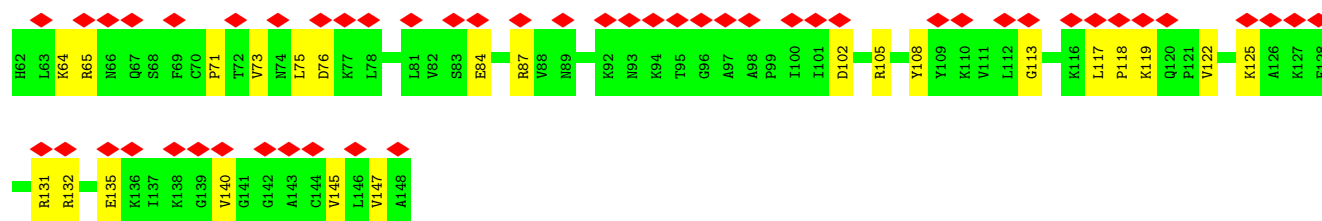
Chain Y: 51% 69% 29% ..



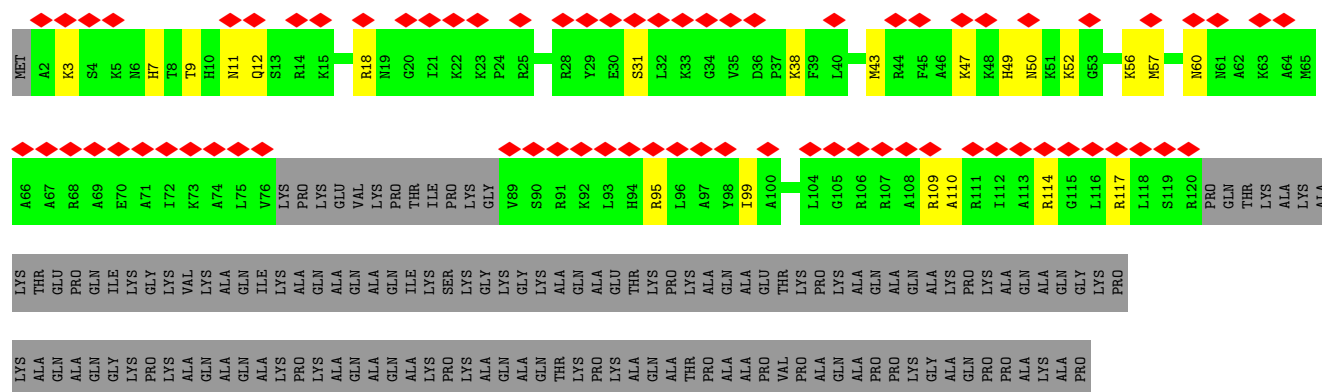
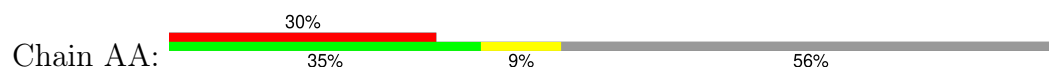
• Molecule 26: L27A

Chain Z: 61% 74% 25%

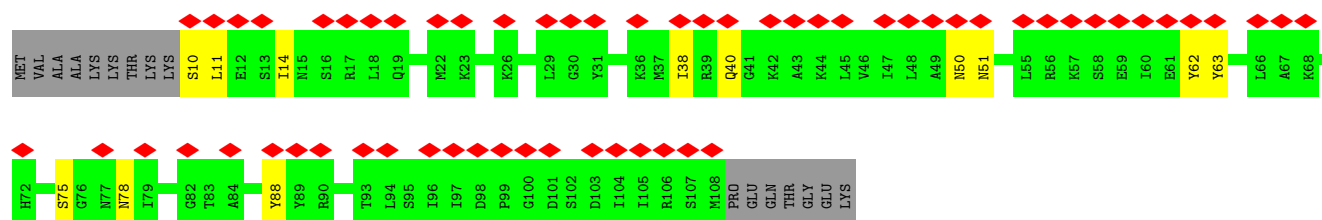
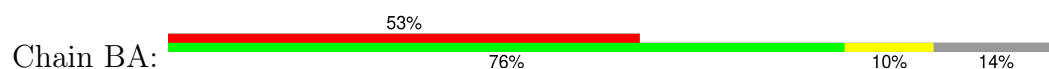




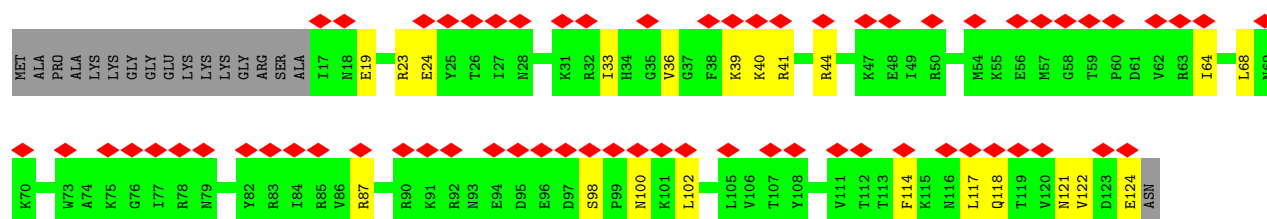
• Molecule 27: L29



• Molecule 28: eL30

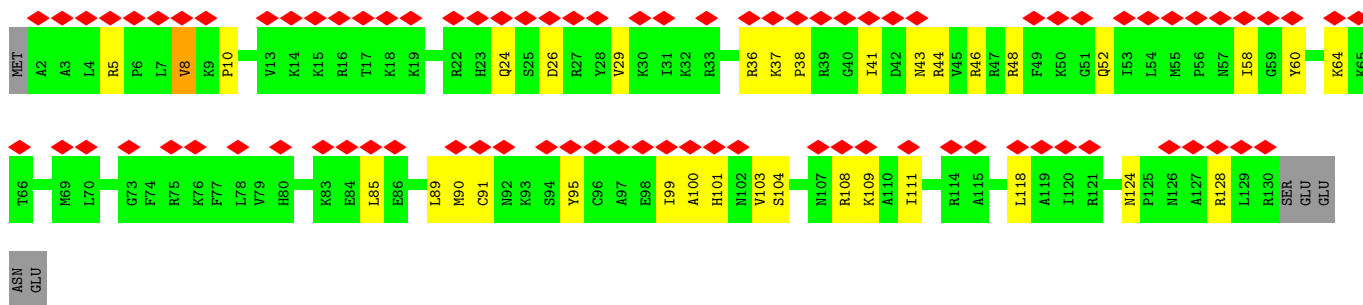


• Molecule 29: L31

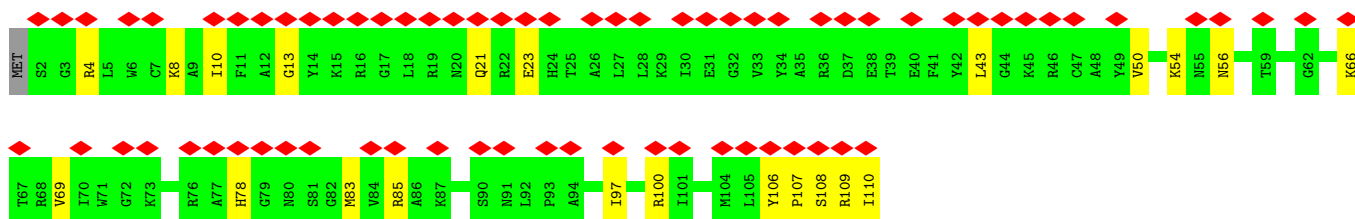
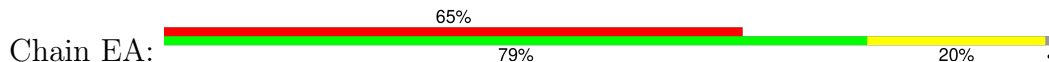


• Molecule 30: L32

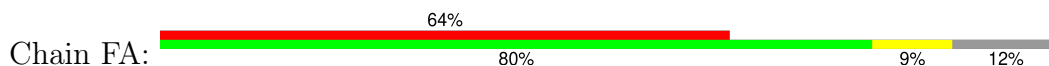




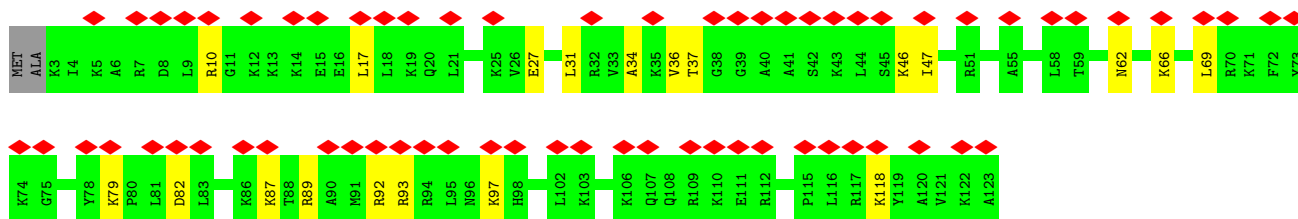
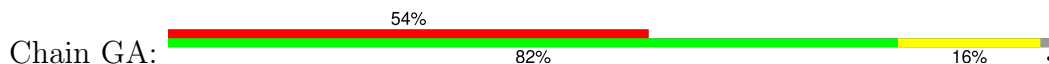
• Molecule 31: eL33



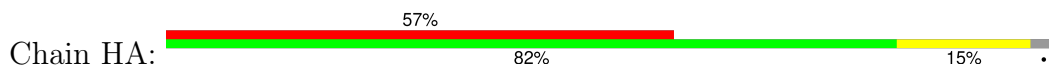
• Molecule 32: L34

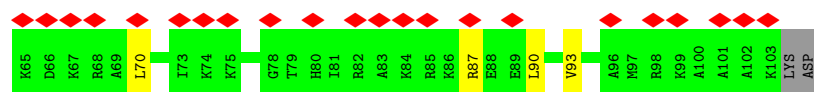


• Molecule 33: L35

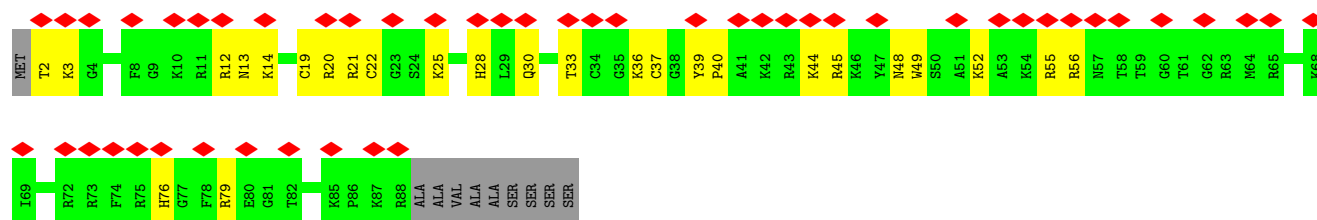


• Molecule 34: L36

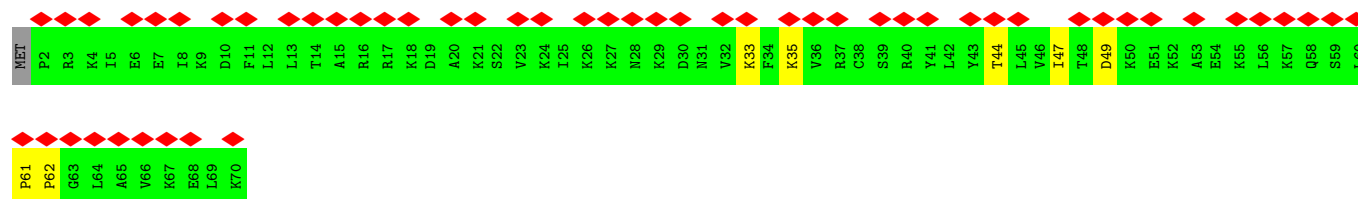
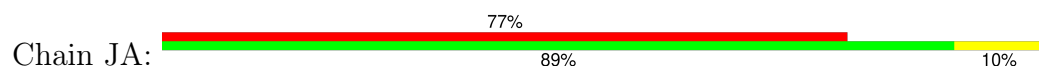




• Molecule 35: L37



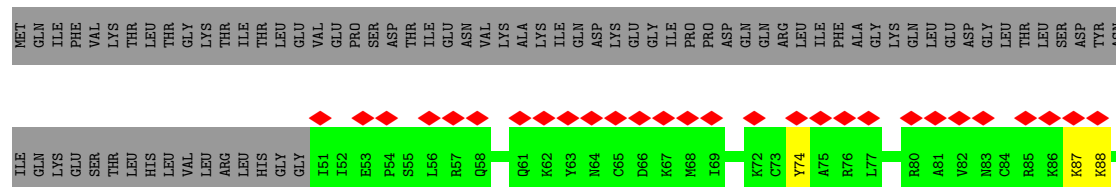
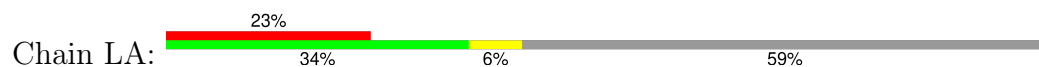
• Molecule 36: eL38



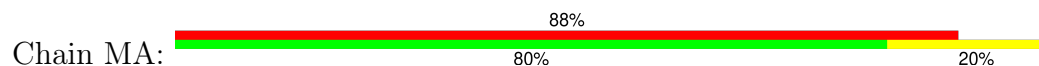
• Molecule 37: eL39



• Molecule 38: eL40

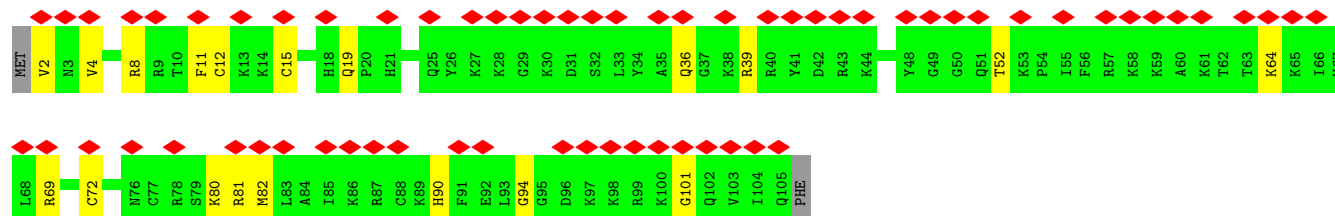
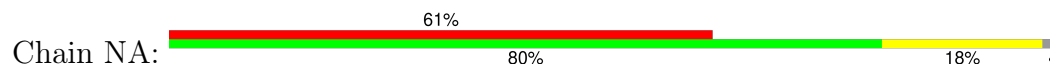


• Molecule 39: eL41

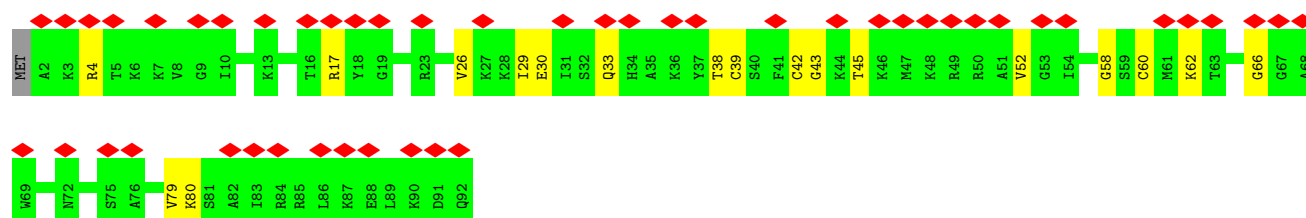
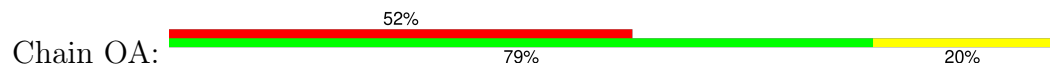




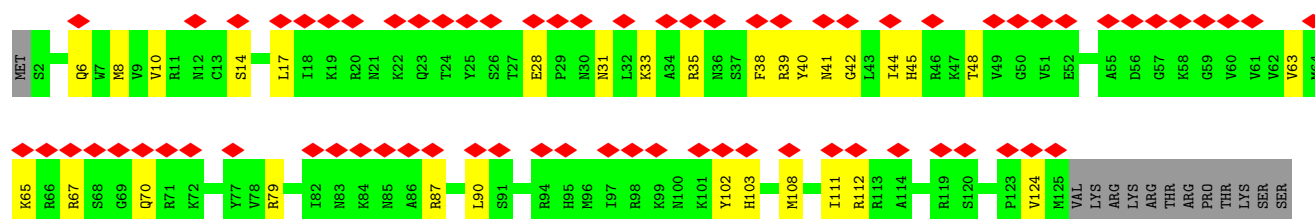
• Molecule 40: eL42



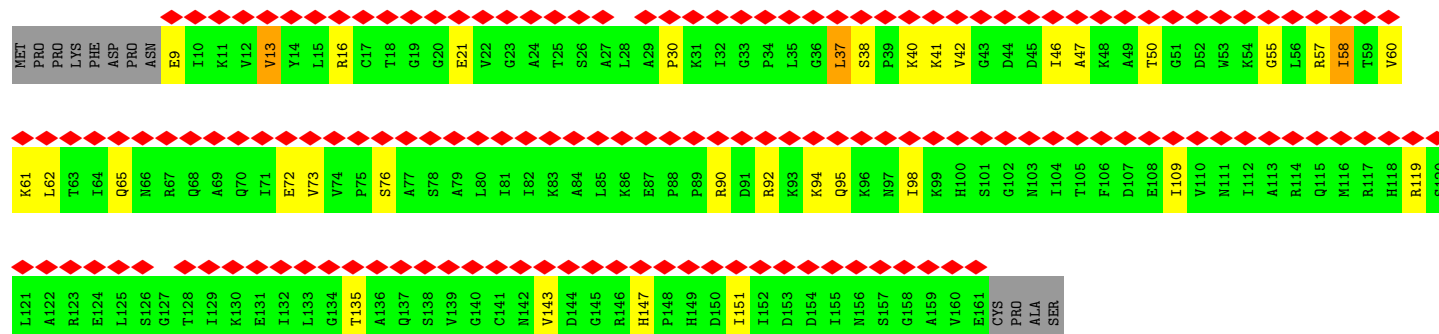
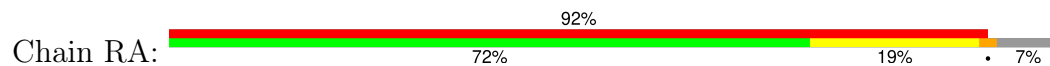
• Molecule 41: eL43



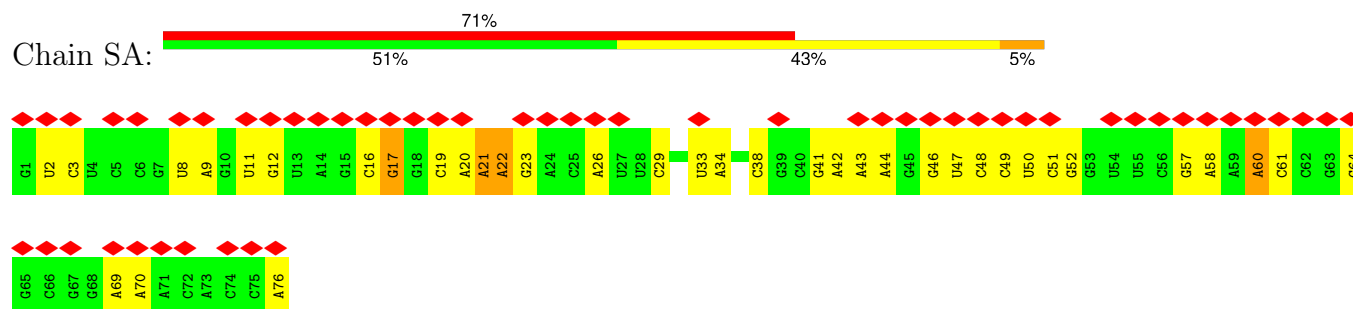
• Molecule 42: L28



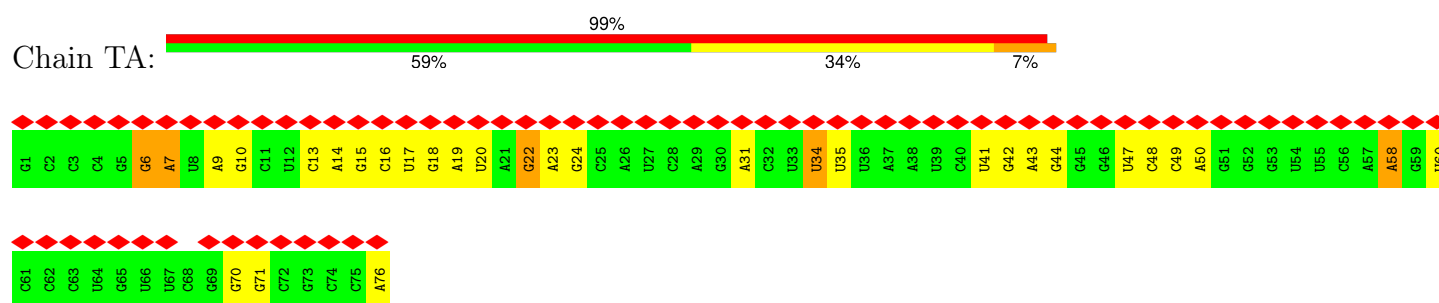
• Molecule 43: L12



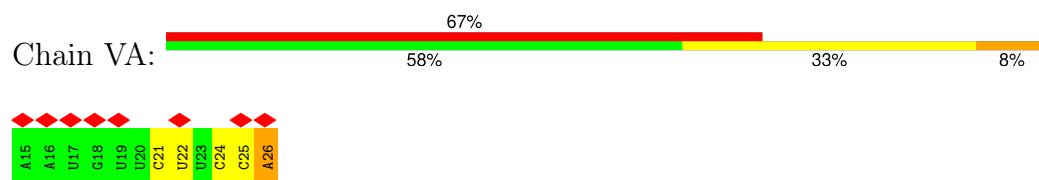
- Molecule 44: P-site tRNA



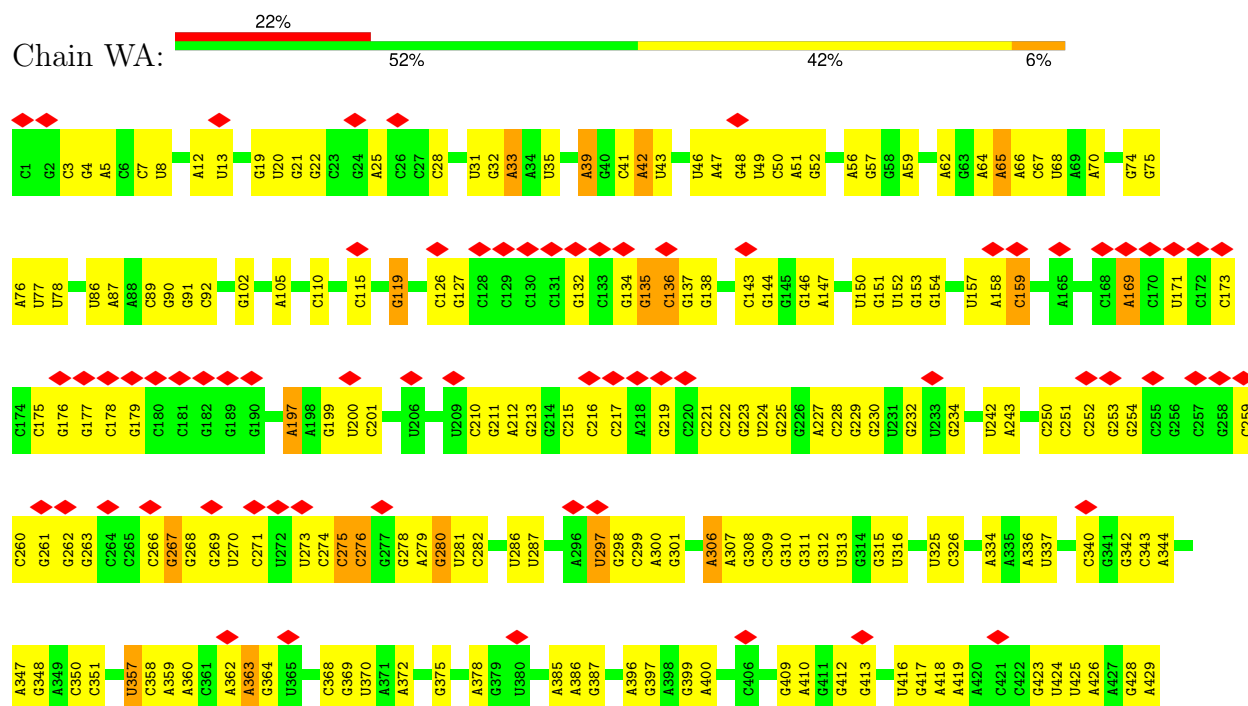
- Molecule 45: E-site tRNA



- Molecule 46: mRNA

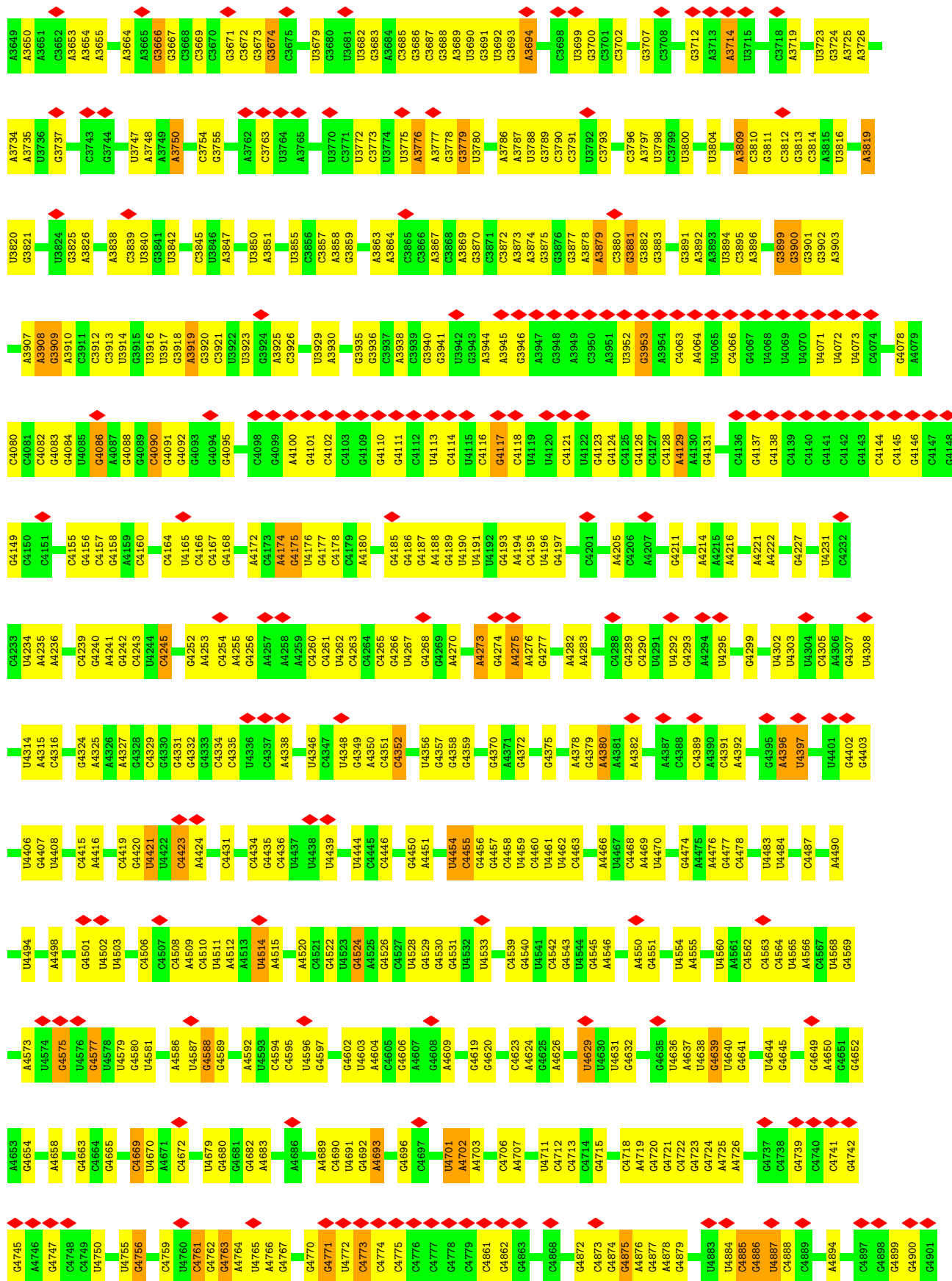


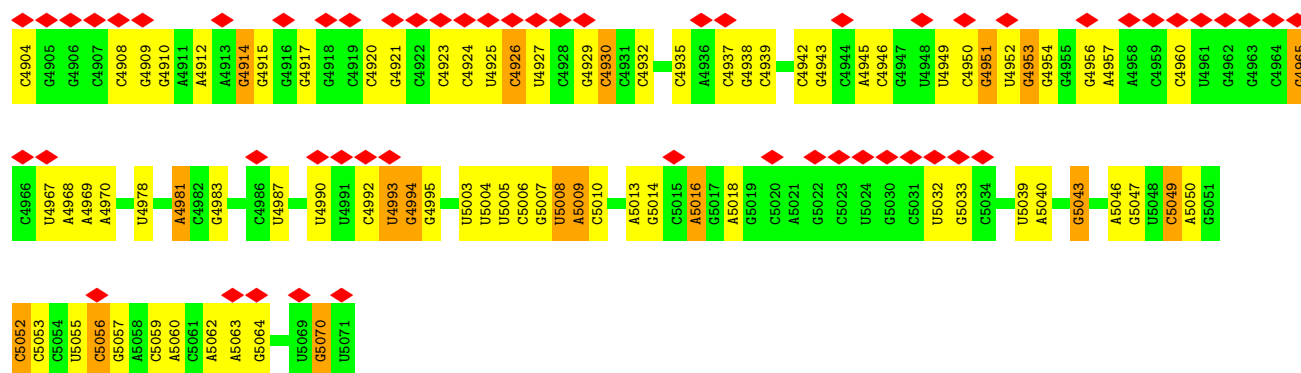
- Molecule 47: 28S rRNA



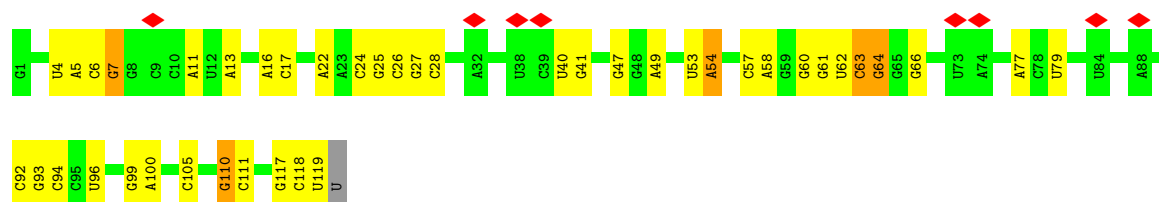


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G2778	G2779	G2780	C2786	C2787	C2788	A2789	U2790	G2791	U2792	C2793	C2796	A2797	G2798	G2799	A2800	C2807	A2808	G2813	G2814	A2815	G2816	C2819	A2827	U2828	G2829	U2830	G2832	G2833	A2834	A2835	U2836	A2837	U2838	G2839	G2840	G2844	U2845	A2846	A2847	G2850	A2851	G2857	G2858	A2859	A2860	G2861	G2862	G2863	G2864								
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A2109	G2110	A2111	G2112	U2113	G2114	G2115	A2116	G2117	G2118	C2260	G2261	C2262	A2265	G2266	C2267	C2268	U2269	A2270	G2277	A2278	C2279	G2280	A2281	G2285	G2286	A2287	G2288	C2291	C2297	G2298	A2302	G2303	C2304	C2305	G2308	A2309	A2310	G2311	G2312	G2313	U2314	A2315	G2316	G2317	G2318	G2319	G2320	G2321	G2322	G2323	G2324						
U2040	G2041	A2042	A2043	G2048	A2049	U2050	G2053	G2054	C2055	U2056	G2057	G2058	A2059	G2060	C2061	G2062	U2063	C2064	G2067	G2068	C2069	G2070	A2071	U2072	A2073	G2077	G2078	C2079	C2080	G2081	U2082	C2083	G2084	C2085	U2086	C2089	U2092	G2093	G2094	G2095	C2096	A2097	G2098	A2099	G2100	C2101	G2102	A2103	G2104	A2105	A2106	A2107	G2108				
G1978	C1979	C1980	A1981	U1982	G1983	G1984	A1985	A1986	G1987	U1988	C1989	G1990	G1991	A1992	A1993	U1994	C1995	C1996	G1997	C1998	U1999	A2000	A2001	G2002	G2003	A2004	G2005	U2006	G2007	U2008	G2009	U2010	A2011	A2012	C2013	A2014	A2015	C2016	U2017	C2018	A2019	C2020	U2021	U2022	G2023	G2026	A2027	A2028	U2029	A2030	A2031	A2032	C2033	U2034	A2035	G2036	C2039
C1915	G1916	C1917	G1918	U1919	A1920	G1921	C1922	G1923	G1924	A1925	C1926	G1927	C1928	U1929	C1930	A1931	U1932	C1933	A1934	G1935	A1936	C1937	C1938	C1939	A1941	G1942	A1943	A1944	A1945	U1949	G1950	U1951	U1952	G1953	U1956	G1957	A1958	U1959	A1960	U1961	A1962	G1963	A1964	C1965	A1966	G1967	C1968	A1969	G1970	A1971	A1972	U1973	G1974	C1975	G1976	G1977	
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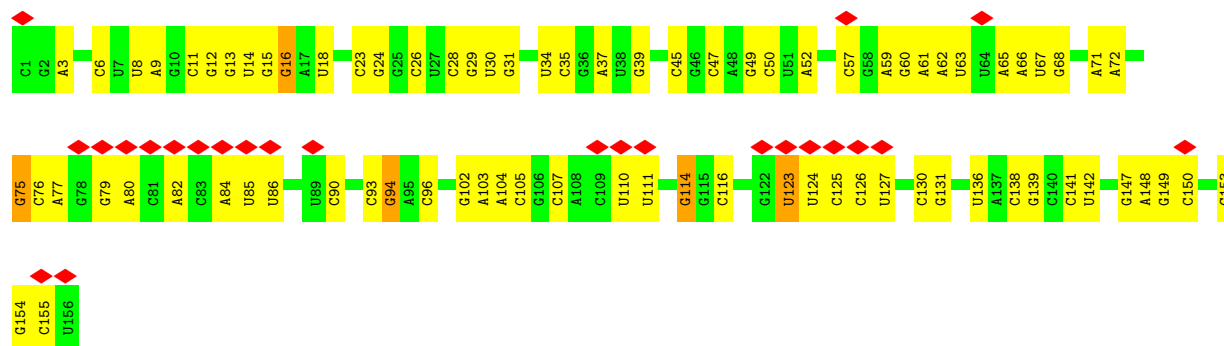




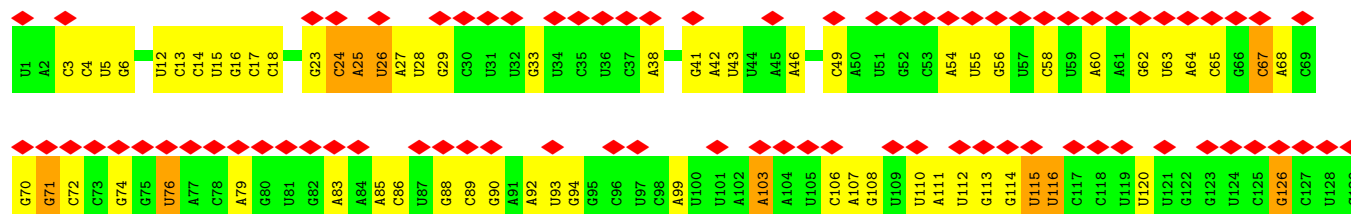
• Molecule 48: 5S rRNA

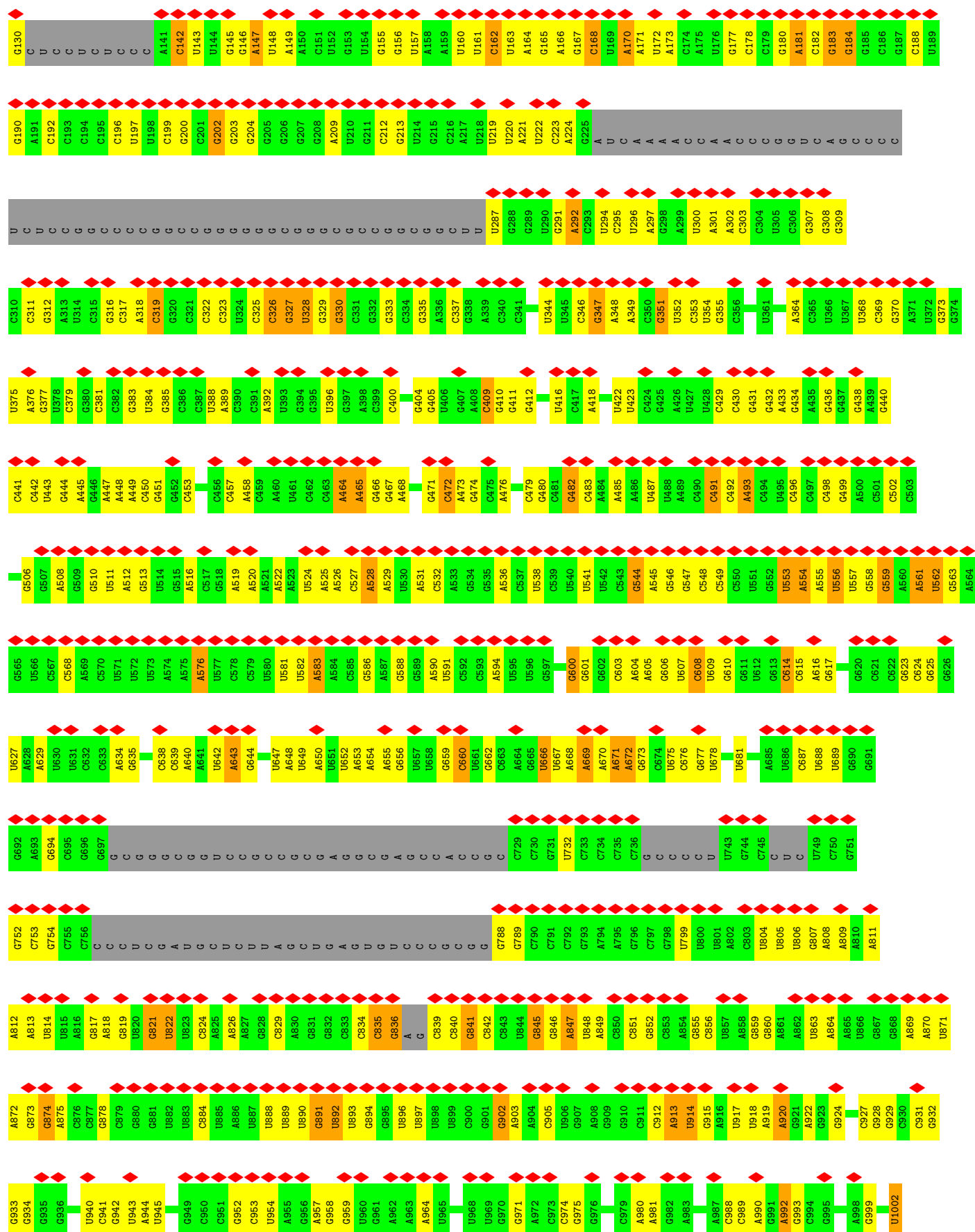


• Molecule 49: 5.8S rRNA



• Molecule 50: 18S rRNA



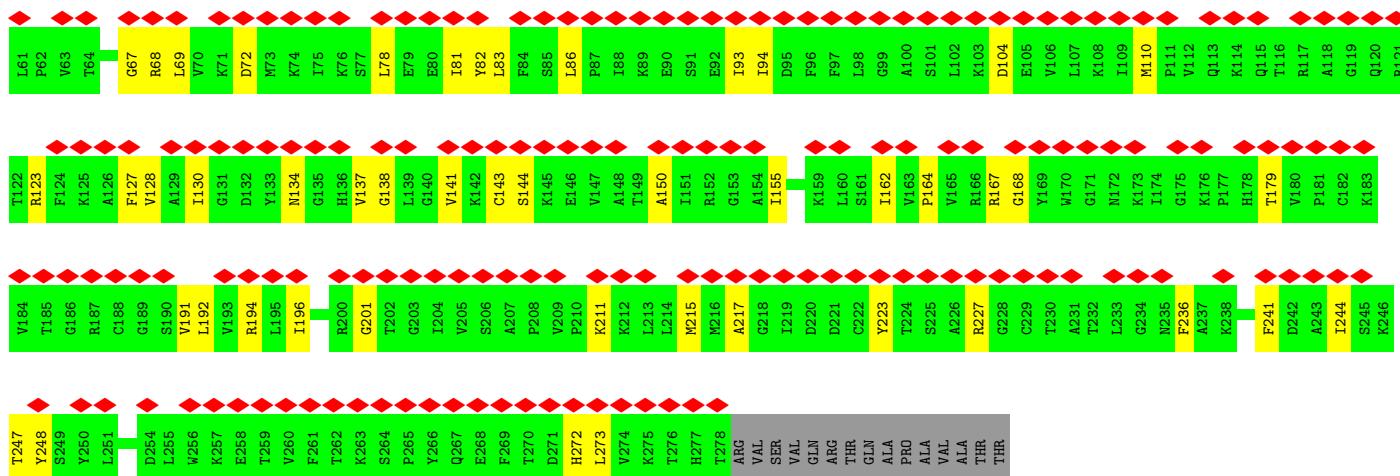


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G1760	U1761	C	G	C	C	C	C	A	C	G	G1771	C1772	C1773	C1774	U1775	G1776	G1777	C1778	G1779	G1780	A1781	G1782	C1783	G1784	G1785	U1786	G1787	A1788	A1791	U1797	C1798	C1799	A1800	A1801	C1802	U1803	U1804	G1805	A1806	C1807	U1808	U1809	U1810	C1811	U1812	A1813										
U1691	U1692	U1693	C1698	A1699	C1700	G1704	G1705	G1706	U1707	C1708	U1711	A1712	C1713	U1714	A1715	C1716	C1717	U1720	U1721	G1722	G1723	U1724	A1725	G1726	G1727	U1728	U1729	U1730	A1731	G1732	U1733	G1734	A1735	G1736	G1737	U1741	C1742	G1743	G1744	A1745	U1746	G1747	G1748	G1749	C1750	C1751	C1752	C1753	G1754	C1755	C1756	G1757	G1758	G1759		
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U1003	U1004	G1005	C1006	C1007	A1008	A1011	A1012	U1013	G1014	U1015	U1016	U1017	U1018	C1019	A1020	U1021	U1022	A1023	C1026	A1027	A1028	G1029	A1030	C1031	G1032	A1033	A1034	A1035	A1036	G1037	G1043	G1044	U1045	U1046	C1047	G1048	G1054	A1055	U1056	C1057	A1058	G1059	A1060	U1061	C1062	A1063	C1064	G1065	A1070	G1071	U1072	C1075	G1076			
C1079	U1080	U1081	A1082	A1083	A1084	G1085	G1086	A1087	U1088	G1089	C1090	C1091	G1092	A1093	C1094	C1095	C1098	G1099	A1100	U1101	C1102	C1103	G1104	G1105	C1106	G1110	U1111	U1112	A1113	U1114	U1115	C1116	C1117	C1118	A1119	U1120	G1121	G1126	C1127	C1128	G1129	G1130	G1131	C1132	A1133	G1134	C1135	U1136	U1137	C1138	C1139	A1143	A1144	A1145		

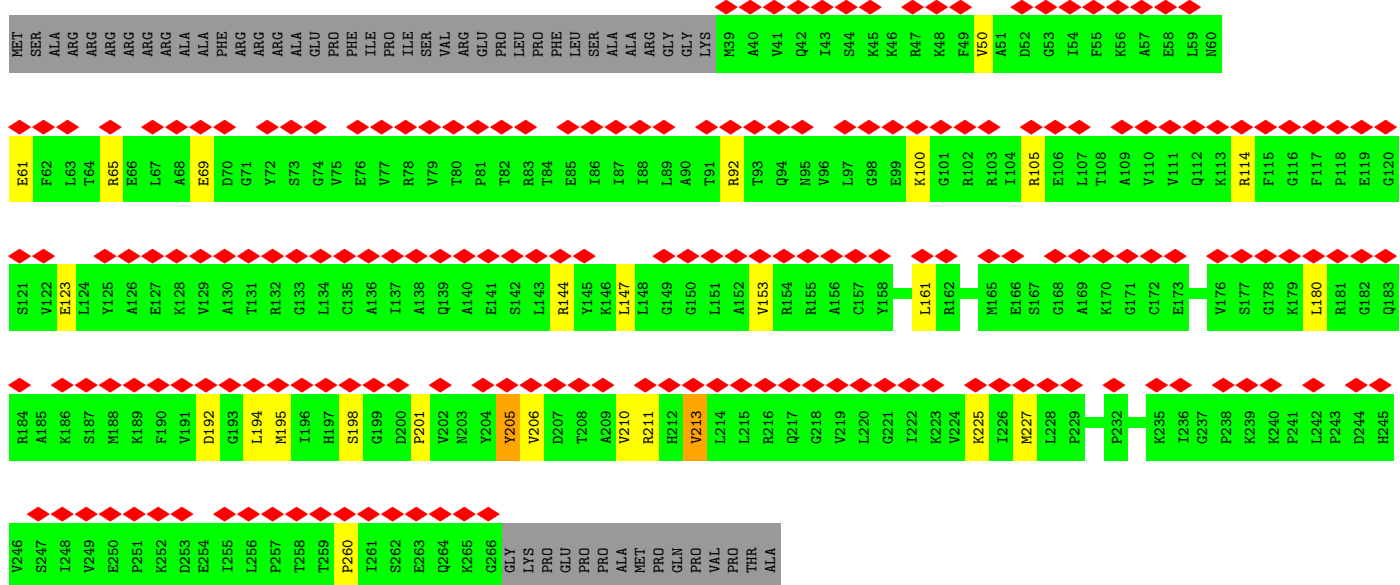
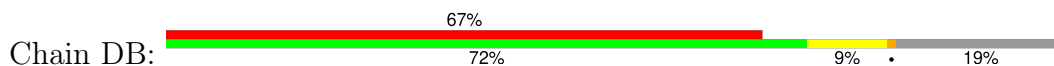
Chain AB:

- Molecule 52: S3A

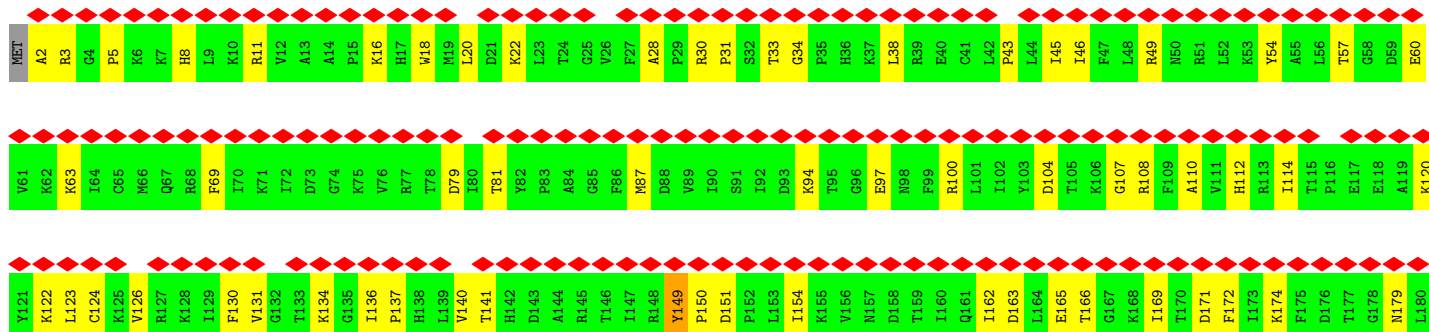
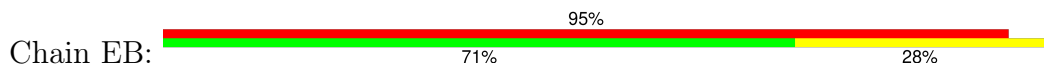
- Molecule 53: S2-like



• Molecule 54: S3

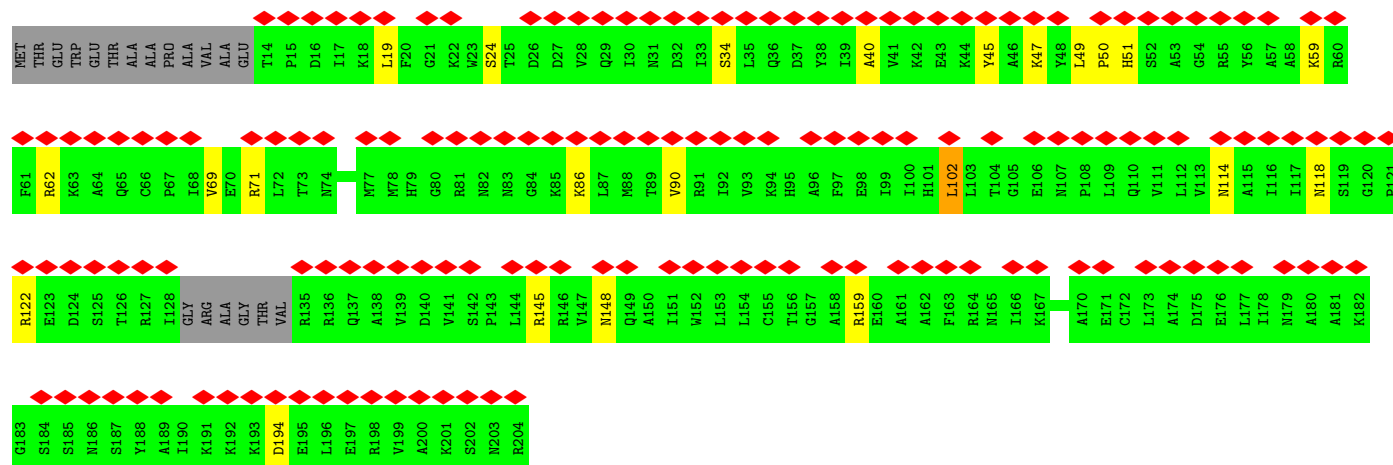
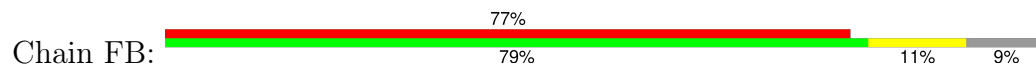


• Molecule 55: S4

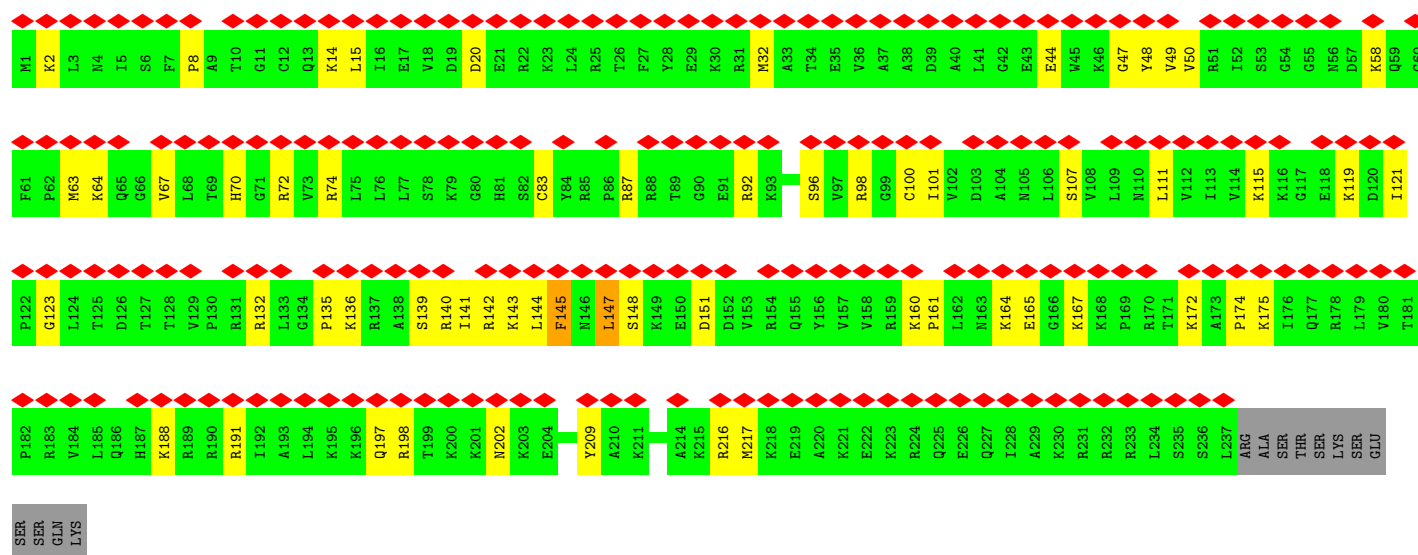
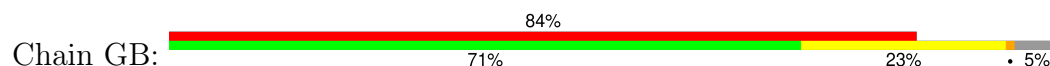




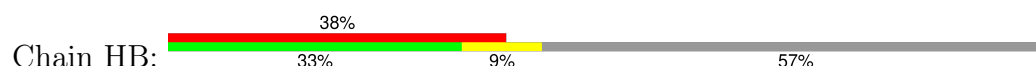
• Molecule 56: S5



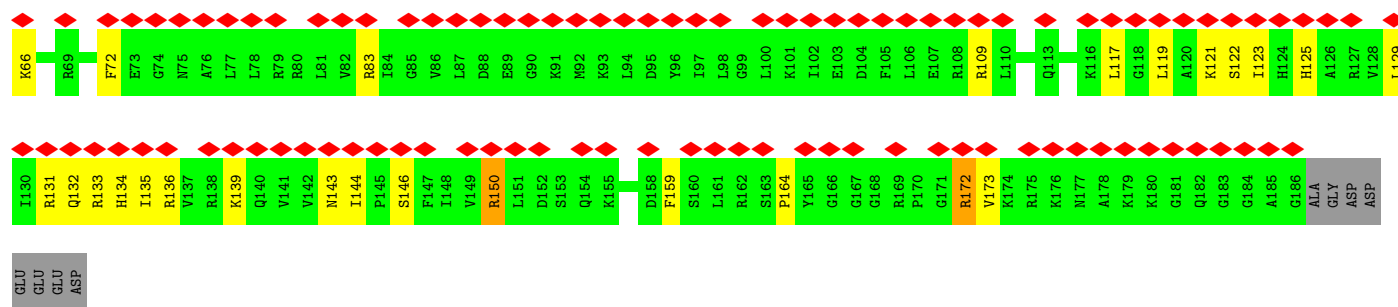
• Molecule 57: eS6



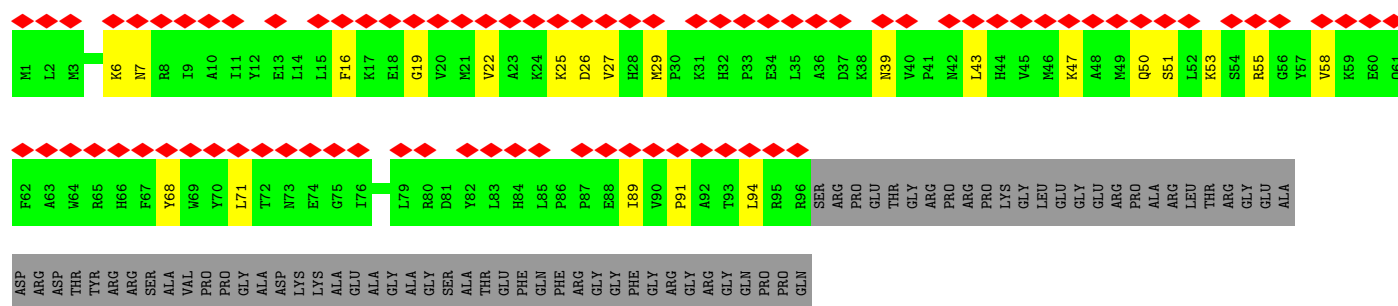
• Molecule 58: eS7



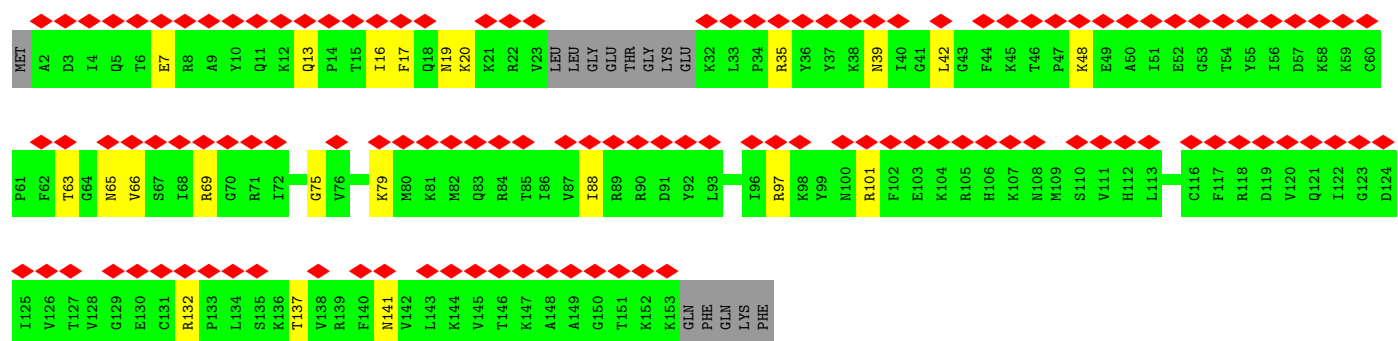
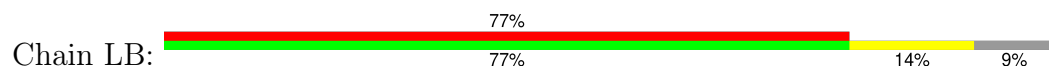




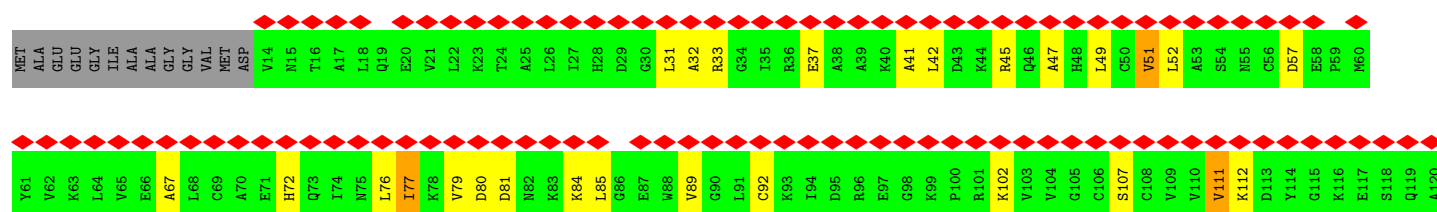
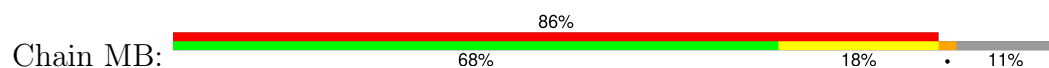
• Molecule 61: S10



• Molecule 62: S11

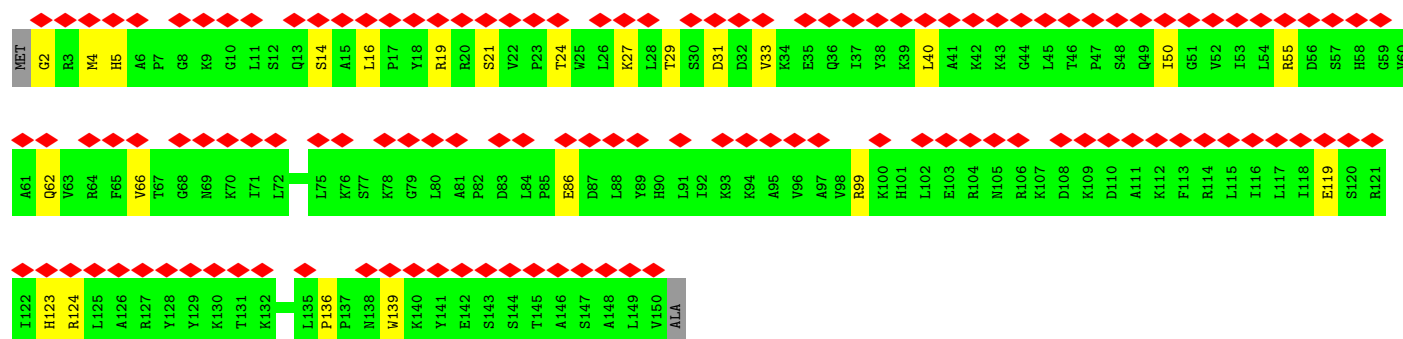
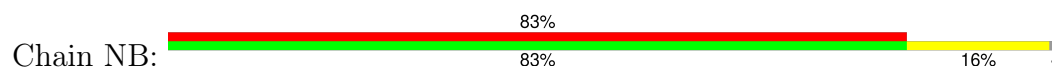


• Molecule 63: S12

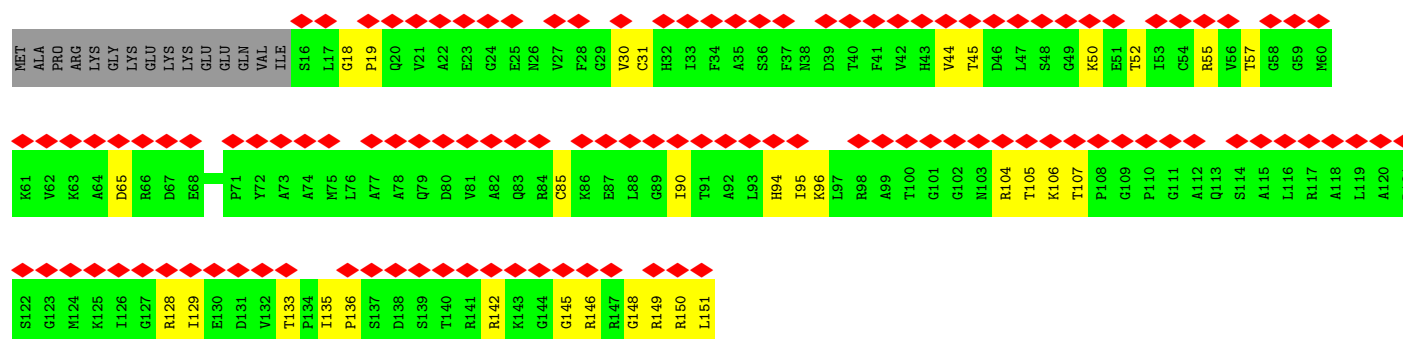
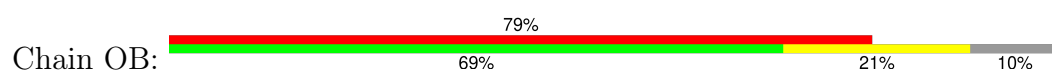




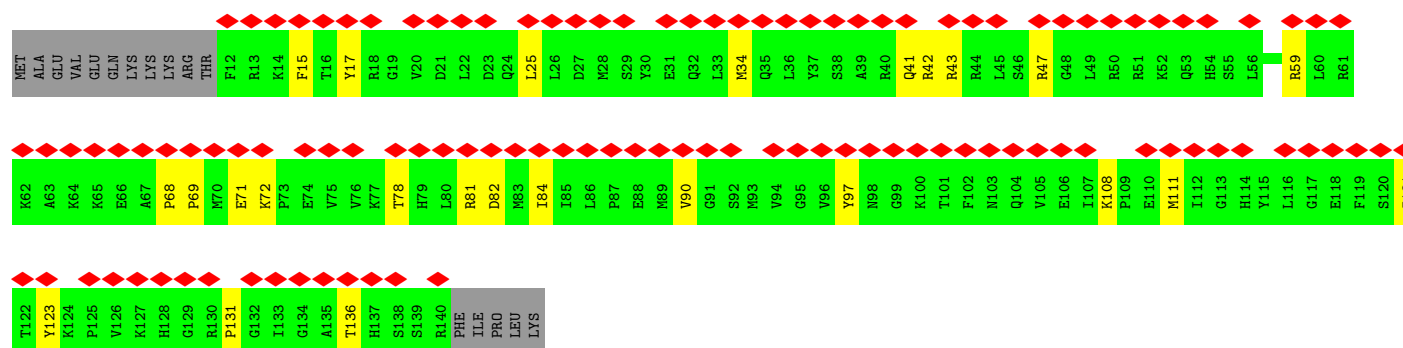
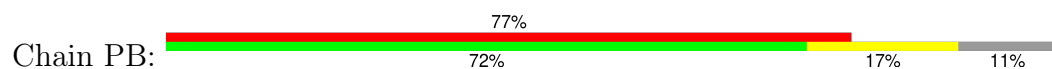
• Molecule 64: uS15



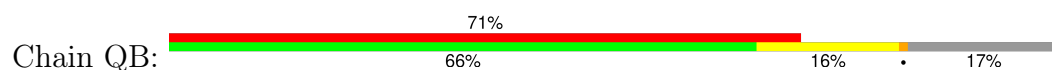
• Molecule 65: S14

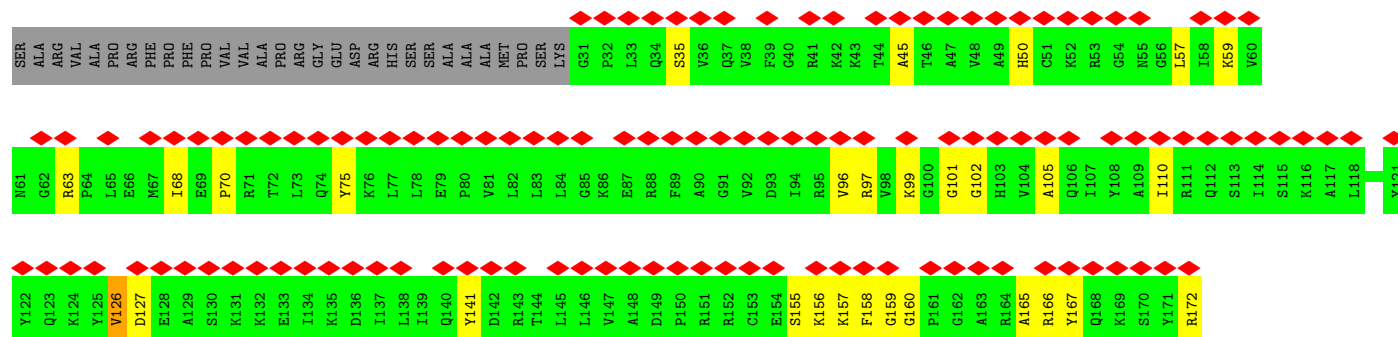


• Molecule 66: S15

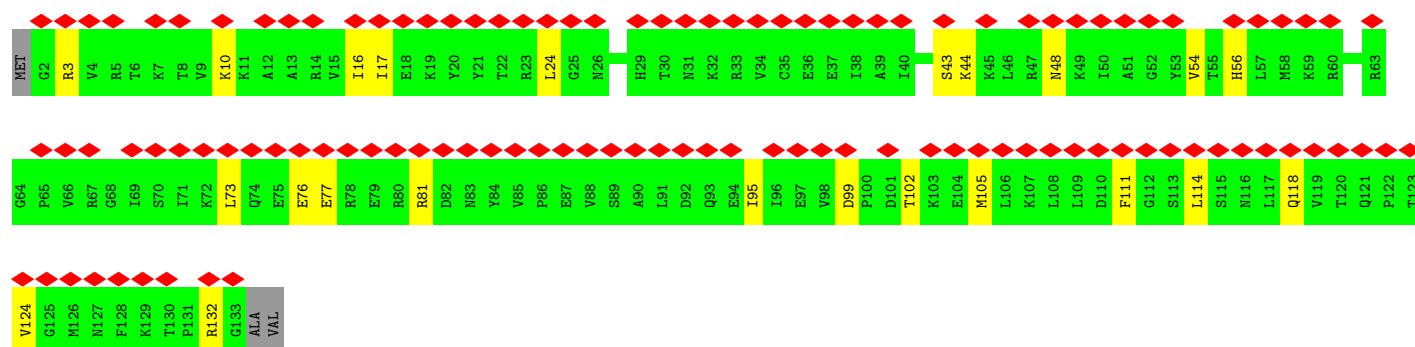
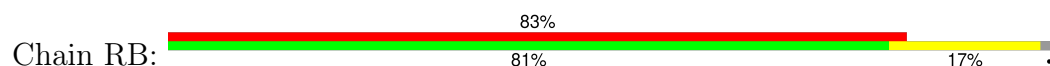


• Molecule 67: uS9

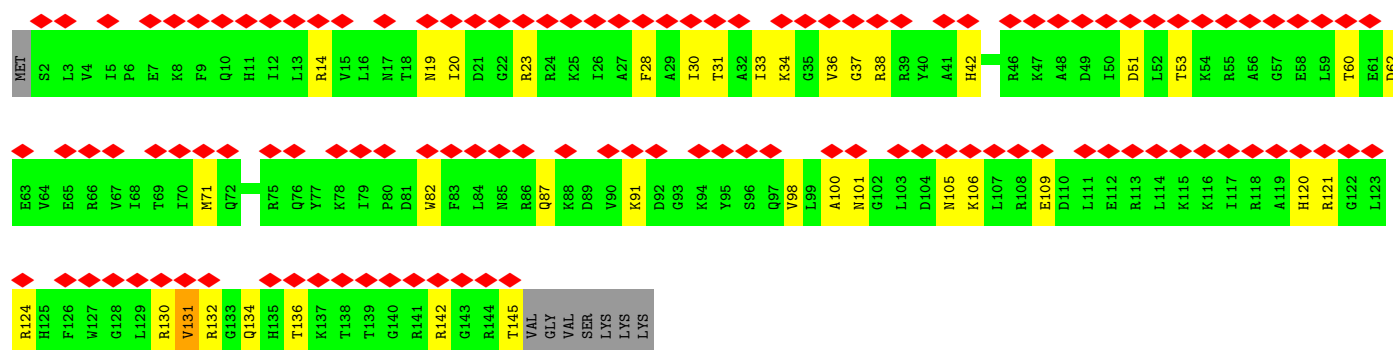
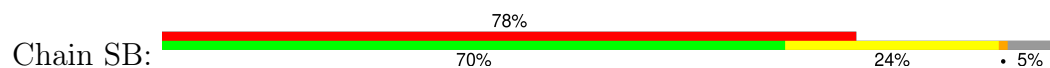




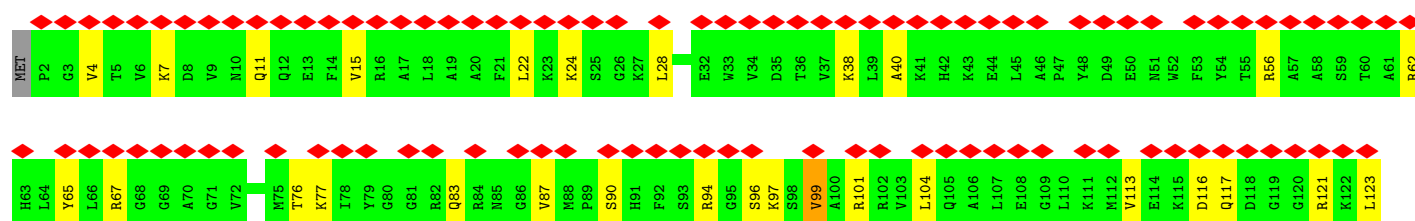
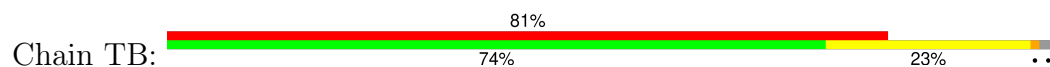
• Molecule 68: eS17

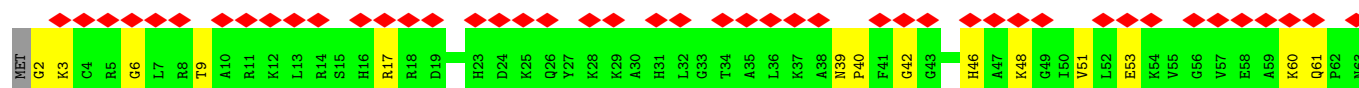


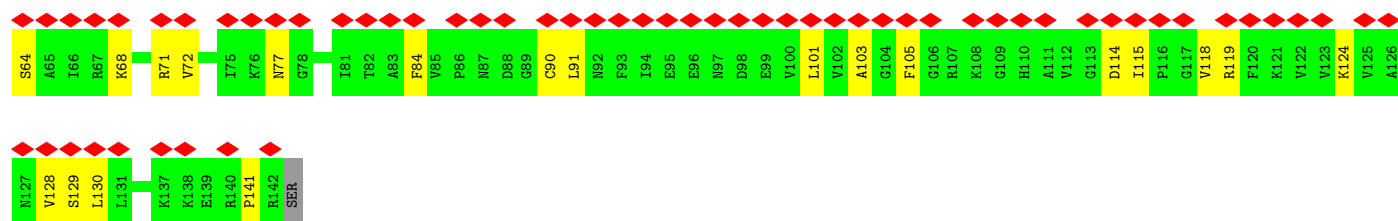
• Molecule 69: S18



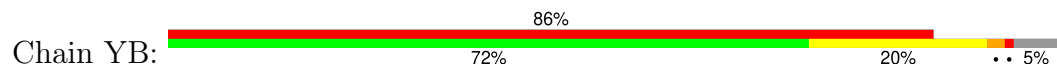
• Molecule 70: S19



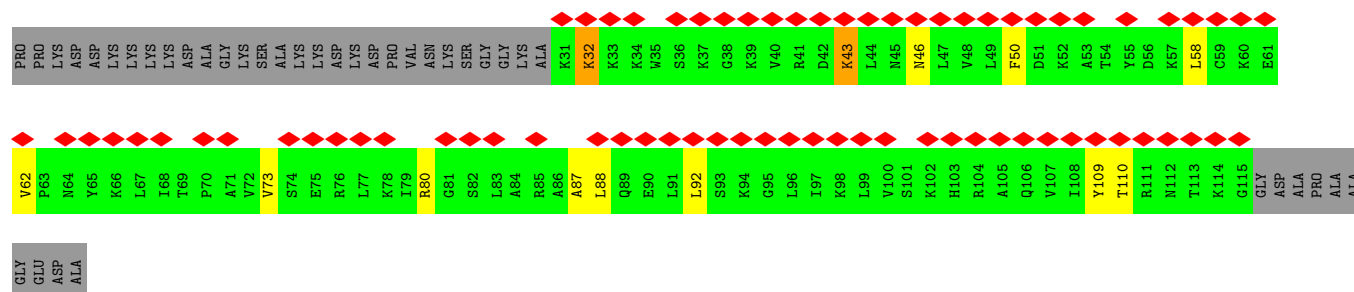




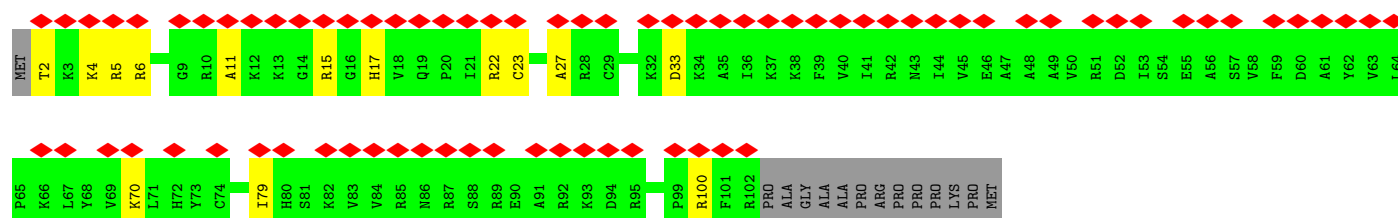
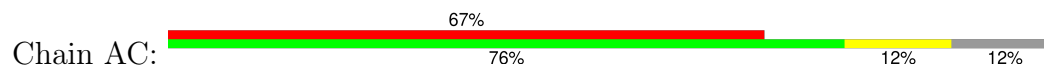
• Molecule 75: S24



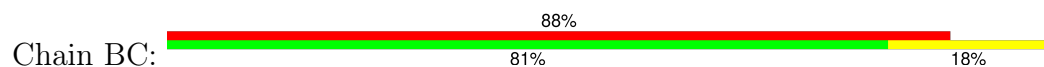
• Molecule 76: eS25

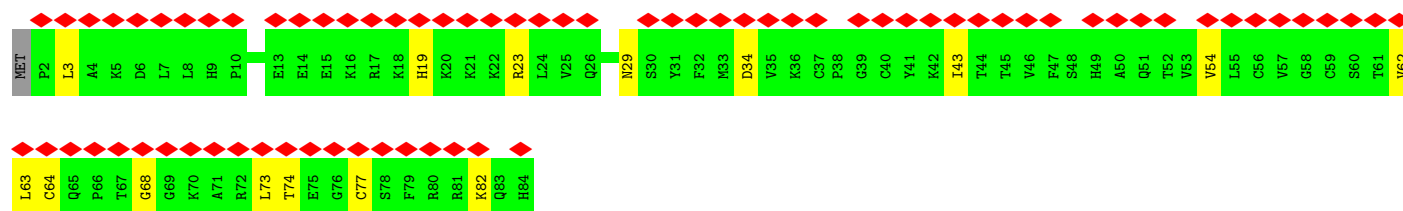


• Molecule 77: S26

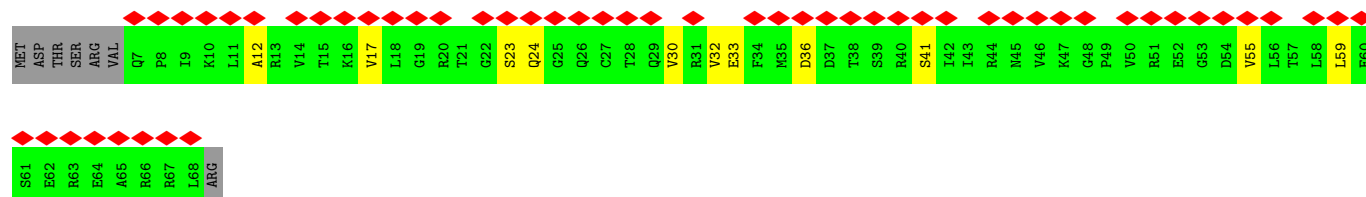
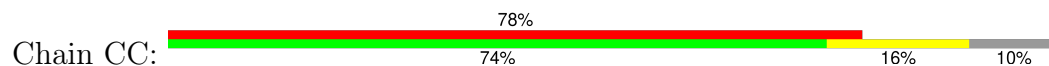


• Molecule 78: S27

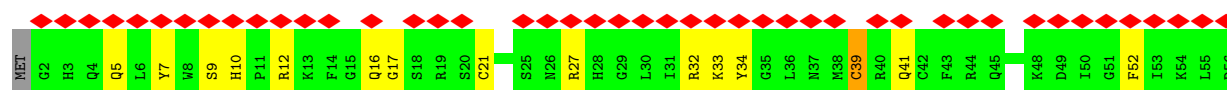
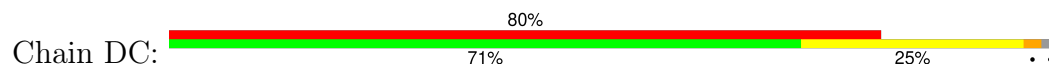




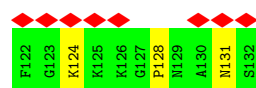
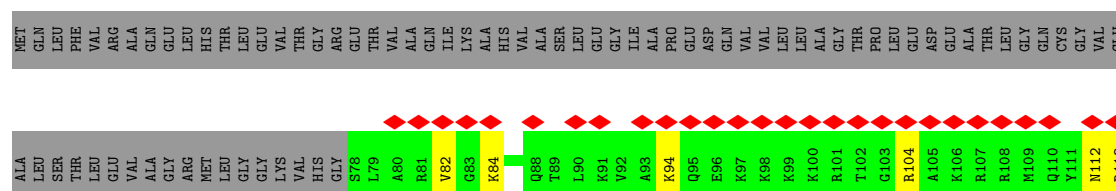
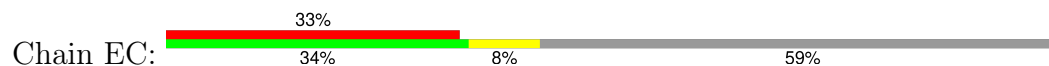
• Molecule 79: S28



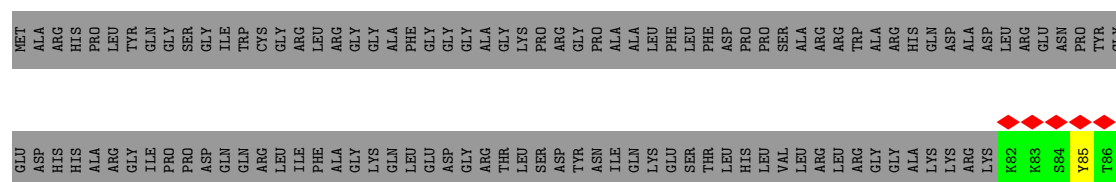
• Molecule 80: uS14

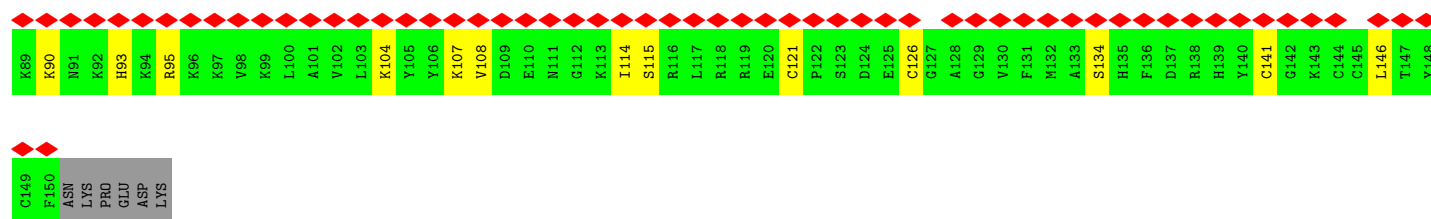


• Molecule 81: S30

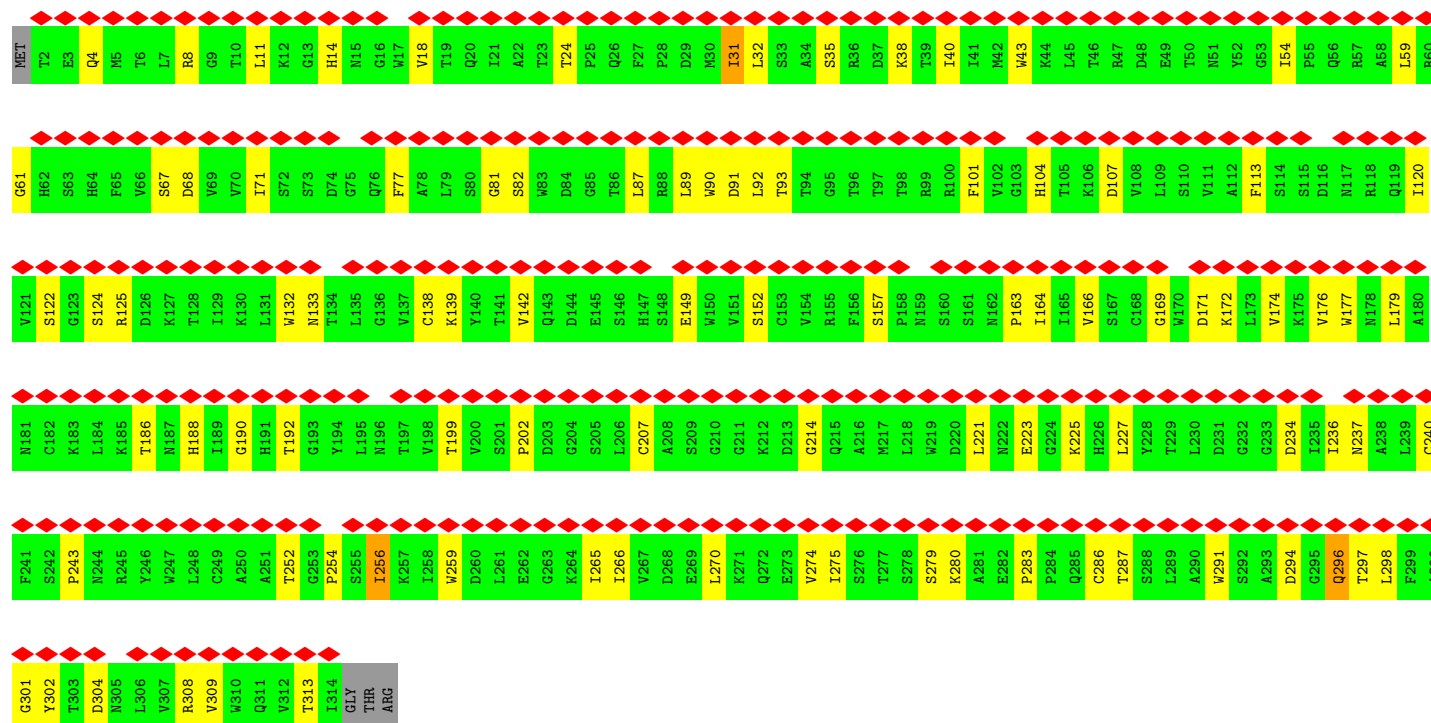


• Molecule 82: S27A

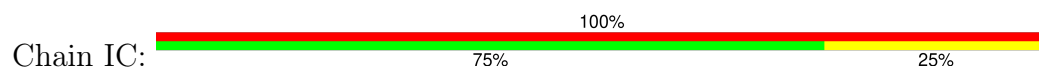




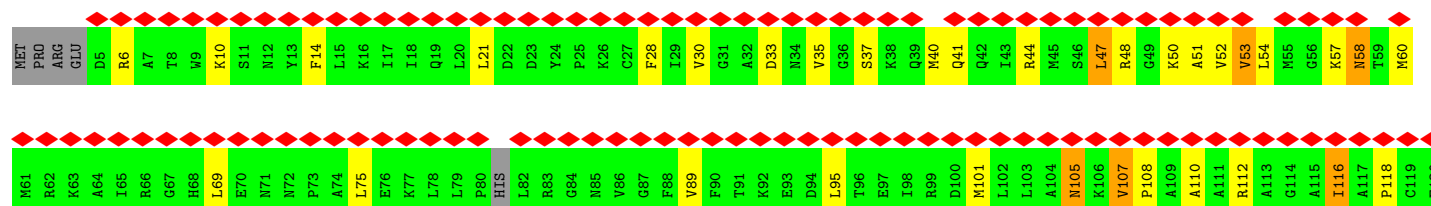
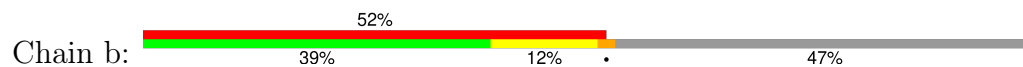
• Molecule 83: RACK1



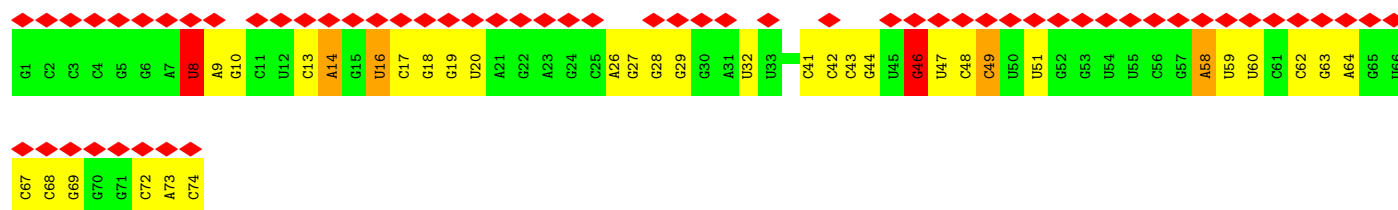
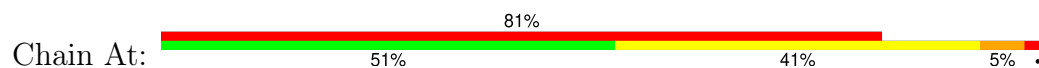
• Molecule 84: nascent chain



• Molecule 85: RPLP0



- Molecule 86: A-site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1508	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	24.363	Depositor
Minimum map value	-18.068	Depositor
Average map value	0.008	Depositor
Map value standard deviation	1.504	Depositor
Recommended contour level	7	Depositor
Map size (Å)	686.87994, 686.87994, 686.87994	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 4SU, SPD, ANM, PSU, H2U, MG, 7MG, ZN

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	A	0.07	0/1952	0.21	0/2617
2	B	0.08	0/3264	0.22	0/4371
3	C	0.07	0/2937	0.20	0/3946
4	D	0.08	0/2441	0.21	0/3269
5	E	0.08	0/1859	0.22	0/2491
6	F	0.08	0/1933	0.22	0/2577
7	G	0.08	0/1881	0.20	0/2532
8	H	0.07	0/1535	0.24	0/2063
9	I	0.07	0/1702	0.19	0/2272
10	J	0.07	0/1395	0.23	0/1863
11	K	0.08	0/1733	0.21	0/2316
12	L	0.08	0/1158	0.20	0/1547
13	M	0.08	0/1746	0.22	0/2338
14	N	0.09	0/1662	0.22	0/2222
15	O	0.07	0/1292	0.22	0/1733
16	P	0.07	0/1539	0.23	0/2054
17	Q	0.08	0/1524	0.19	0/2013
18	R	0.08	0/1501	0.23	0/2012
19	S	0.07	0/1326	0.20	0/1770
20	T	0.08	0/840	0.25	0/1127
21	U	0.08	0/1018	0.23	0/1364
22	V	0.11	0/900	0.29	0/1194
23	W	0.07	0/984	0.20	0/1323
24	X	0.06	0/1132	0.19	0/1504
25	Y	0.07	0/1130	0.20	0/1507
26	Z	0.08	0/1191	0.21	0/1590
27	AA	0.06	0/886	0.16	0/1171
28	BA	0.07	0/779	0.18	0/1044
29	CA	0.08	0/908	0.20	0/1223
30	DA	0.07	0/1082	0.20	0/1443
31	EA	0.08	0/895	0.21	0/1198
32	FA	0.07	0/916	0.22	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	GA	0.07	0/1016	0.19	0/1341
34	HA	0.07	0/841	0.20	0/1112
35	IA	0.08	0/731	0.21	0/966
36	JA	0.07	0/575	0.20	0/761
37	KA	0.07	0/459	0.19	0/608
38	LA	0.08	0/435	0.24	0/575
39	MA	0.07	0/240	0.16	0/305
40	NA	0.07	0/864	0.20	0/1140
41	OA	0.08	0/718	0.20	0/953
42	PA	0.07	0/1010	0.22	0/1354
43	RA	0.10	0/1174	0.27	0/1582
44	SA	0.08	0/1815	0.21	0/2828
45	TA	0.09	0/1804	0.21	0/2810
46	VA	0.06	0/276	0.18	0/426
47	WA	0.09	0/85840	0.21	0/133885
48	XA	0.08	0/2836	0.18	0/4421
49	YA	0.09	0/3701	0.22	0/5766
50	ZA	0.40	6/40949 (0.0%)	0.22	0/63819
51	AB	0.09	0/1747	0.21	0/2374
52	BB	0.07	0/1756	0.22	0/2350
53	CB	0.07	0/1744	0.23	0/2358
54	DB	0.08	0/1796	0.21	0/2417
55	EB	0.09	0/2118	0.26	0/2849
56	FB	0.08	0/1492	0.23	0/2005
57	GB	0.10	0/1946	0.26	0/2590
58	HB	0.09	0/1511	0.24	0/2022
59	IB	0.08	0/1715	0.21	0/2287
60	JB	0.09	0/1550	0.23	0/2069
61	KB	0.08	0/834	0.23	0/1125
62	LB	0.07	0/1200	0.24	0/1604
63	MB	0.08	0/918	0.23	0/1233
64	NB	0.07	0/1226	0.20	0/1649
65	OB	0.07	0/1029	0.23	0/1380
66	PB	0.08	0/1079	0.21	0/1441
67	QB	0.09	0/1146	0.25	0/1534
68	RB	0.09	0/1082	0.24	0/1452
69	SB	0.08	0/1208	0.23	0/1618
70	TB	0.07	0/1123	0.20	0/1504
71	UB	0.08	0/818	0.23	0/1099
72	VB	0.06	0/643	0.20	0/860
73	WB	0.08	0/1051	0.25	0/1406
74	XB	0.07	0/1116	0.21	0/1490
75	YB	1.33	3/1028 (0.3%)	0.96	6/1366 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	ZB	0.07	0/691	0.21	0/922
77	AC	0.08	0/828	0.23	0/1109
78	BC	0.06	0/665	0.19	0/891
79	CC	0.09	0/490	0.25	0/656
80	DC	0.06	0/470	0.19	0/623
81	EC	0.07	0/447	0.20	0/587
82	FC	0.06	0/576	0.20	0/764
83	GC	0.09	0/2493	0.28	0/3394
84	IC	0.05	0/19	0.14	0/25
85	b	0.12	0/1298	0.28	0/1752
86	At	0.14	0/1652	0.19	0/2573
All	All	0.21	9/234830 (0.0%)	0.22	6/344944 (0.0%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
75	YB	7	ILE	CA-CB	38.96	1.99	1.54
50	ZA	836	G	N1-C2	34.92	2.07	1.37
50	ZA	836	G	C6-N1	34.13	2.07	1.39
50	ZA	836	G	C2-N3	33.58	2.00	1.32
50	ZA	836	G	C5-C6	32.20	2.06	1.42
50	ZA	836	G	N3-C4	31.59	1.98	1.35
50	ZA	836	G	C5-C4	28.89	1.96	1.38
75	YB	7	ILE	CB-CG2	12.83	1.94	1.52
75	YB	7	ILE	CB-CG1	9.56	1.72	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
75	YB	7	ILE	CA-CB-CG1	19.95	144.31	110.40
75	YB	7	ILE	CA-CB-CG2	14.62	135.35	110.50
75	YB	7	ILE	CG1-CB-CG2	-12.87	72.10	110.70
75	YB	7	ILE	N-CA-C	-11.20	91.64	107.99
75	YB	7	ILE	CB-CA-C	10.78	125.75	110.98
75	YB	7	ILE	N-CA-CB	10.78	123.83	111.21

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	A	1914	0	2013	48	0
2	B	3196	0	3339	70	0
3	C	2883	0	3053	50	0
4	D	2395	0	2427	32	0
5	E	1823	0	1995	38	0
6	F	1897	0	2021	37	0
7	G	1850	0	1991	22	0
8	H	1516	0	1597	20	0
9	I	1664	0	1712	26	0
10	J	1372	0	1412	20	0
11	K	1702	0	1820	25	0
12	L	1137	0	1211	21	0
13	M	1701	0	1749	35	0
14	N	1630	0	1778	35	0
15	O	1266	0	1302	23	0
16	P	1515	0	1634	32	0
17	Q	1508	0	1664	22	0
18	R	1462	0	1508	31	0
19	S	1298	0	1366	31	0
20	T	826	0	852	12	0
21	U	1004	0	1063	16	0
22	V	887	0	935	27	0
23	W	967	0	1040	13	0
24	X	1115	0	1205	19	0
25	Y	1107	0	1182	27	0
26	Z	1162	0	1209	30	0
27	AA	873	0	949	18	0
28	BA	769	0	803	8	0
29	CA	893	0	932	12	0
30	DA	1064	0	1160	27	0
31	EA	876	0	912	18	0
32	FA	906	0	998	9	0
33	GA	1008	0	1142	17	0
34	HA	830	0	916	11	0
35	IA	716	0	750	24	0
36	JA	569	0	637	5	0
37	KA	447	0	480	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	LA	429	0	465	5	0
39	MA	239	0	289	5	0
40	NA	851	0	920	13	0
41	OA	708	0	757	16	0
42	PA	994	0	1051	21	0
43	RA	1160	0	1218	23	0
44	SA	1622	0	825	21	0
45	TA	1615	0	820	15	0
46	VA	249	0	128	3	0
47	WA	76735	0	38764	1133	0
48	XA	2538	0	1286	31	0
49	YA	3314	0	1683	48	0
50	ZA	36623	0	18504	679	0
51	AB	1710	0	1711	26	0
52	BB	1729	0	1803	24	0
53	CB	1707	0	1793	26	0
54	DB	1768	0	1863	18	0
55	EB	2076	0	2177	55	0
56	FB	1471	0	1522	18	0
57	GB	1923	0	2089	48	0
58	HB	1489	0	1582	25	0
59	IB	1686	0	1772	27	0
60	JB	1525	0	1640	37	0
61	KB	810	0	836	15	0
62	LB	1180	0	1254	18	0
63	MB	908	0	939	17	0
64	NB	1202	0	1289	16	0
65	OB	1016	0	1039	22	0
66	PB	1058	0	1104	17	0
67	QB	1128	0	1195	24	0
68	RB	1068	0	1121	16	0
69	SB	1190	0	1249	25	0
70	TB	1104	0	1140	24	0
71	UB	808	0	878	17	0
72	VB	636	0	637	12	0
73	WB	1034	0	1080	21	0
74	XB	1098	0	1167	22	0
75	YB	1011	0	1083	72	0
76	ZB	683	0	761	10	0
77	AC	814	0	864	13	0
78	BC	651	0	672	9	0
79	CC	488	0	514	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	DC	459	0	449	13	0
81	EC	443	0	492	11	0
82	FC	564	0	577	11	0
83	GC	2436	0	2393	51	0
84	IC	20	0	10	1	0
85	b	1279	0	1344	27	0
86	At	1582	0	807	18	0
87	AC	1	0	0	0	0
87	FA	1	0	0	0	0
87	I	1	0	0	0	0
87	WA	80	0	0	0	0
87	XA	1	0	0	0	0
87	ZA	18	0	0	0	0
88	AC	1	0	0	0	0
88	DC	1	0	0	0	0
88	FA	1	0	0	0	0
88	FC	1	0	0	0	0
88	IA	1	0	0	0	0
88	LA	1	0	0	0	0
88	NA	1	0	0	0	0
88	OA	1	0	0	0	0
89	WA	19	0	19	1	0
90	WA	10	0	19	1	0
91	ZA	6	0	4	0	0
All	All	218724	0	162355	3038	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 (3038) 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)
75:YB:7:ILE:CB	75:YB:7:ILE:CG2	1.94	1.45
50:ZA:836:G:C4	50:ZA:836:G:C5	1.96	1.44
50:ZA:836:G:N1	75:YB:7:ILE:HA	1.22	1.43
50:ZA:836:G:C5	50:ZA:836:G:C6	2.06	1.42
75:YB:7:ILE:CA	75:YB:7:ILE:HB	1.49	1.40
50:ZA:836:G:N3	75:YB:7:ILE:HB	1.29	1.40
75:YB:7:ILE:CB	75:YB:7:ILE:CA	1.99	1.39
50:ZA:836:G:C4	50:ZA:836:G:N3	1.98	1.31
50:ZA:836:G:C2	75:YB:7:ILE:CB	2.14	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:836:G:N3	50:ZA:836:G:C2	1.99	1.29
50:ZA:836:G:C4	75:YB:7:ILE:HB	1.73	1.23
50:ZA:836:G:N1	50:ZA:836:G:C2	2.07	1.22
75:YB:7:ILE:CG2	75:YB:7:ILE:CG1	2.16	1.22
50:ZA:836:G:N1	50:ZA:836:G:C6	2.07	1.22
50:ZA:836:G:C4	75:YB:7:ILE:CB	2.23	1.21
50:ZA:836:G:C6	75:YB:7:ILE:CA	2.26	1.18
50:ZA:836:G:N3	75:YB:7:ILE:CB	2.08	1.15
50:ZA:836:G:C6	75:YB:7:ILE:CB	2.29	1.15
50:ZA:836:G:N1	75:YB:7:ILE:CA	2.09	1.14
50:ZA:836:G:C2	75:YB:7:ILE:CA	2.31	1.14
50:ZA:836:G:C5	75:YB:7:ILE:N	2.17	1.13
50:ZA:836:G:C6	75:YB:7:ILE:HA	1.84	1.12
50:ZA:836:G:C5	75:YB:7:ILE:CB	2.33	1.11
50:ZA:836:G:N1	75:YB:7:ILE:CB	2.14	1.10
50:ZA:836:G:C2	75:YB:7:ILE:HB	1.85	1.09
50:ZA:836:G:C4	75:YB:7:ILE:CA	2.43	1.01
50:ZA:836:G:C5	75:YB:7:ILE:CA	2.43	1.01
35:IA:2:THR:N	47:WA:3644:A:HO2'	1.63	0.96
47:WA:2847:A:H61	47:WA:3845:C:N4	1.64	0.94
50:ZA:1652:G:H1	50:ZA:1672:U:H3	0.96	0.94
44:SA:50:U:H3	44:SA:64:G:H1	1.02	0.94
75:YB:7:ILE:CG1	75:YB:7:ILE:HG21	1.97	0.94
47:WA:4456:G:H1	47:WA:4528:U:H3	1.11	0.92
47:WA:2847:A:H61	47:WA:3845:C:H42	0.98	0.92
50:ZA:677:G:H21	50:ZA:1028:A:H62	1.10	0.92
50:ZA:1288:U:H3	50:ZA:1311:C:H42	1.11	0.91
47:WA:2847:A:N6	47:WA:3845:C:H42	1.69	0.90
50:ZA:442:C:N4	50:ZA:449:A:H62	1.68	0.89
50:ZA:836:G:C2	75:YB:7:ILE:C	2.50	0.89
50:ZA:442:C:H42	50:ZA:449:A:H62	0.91	0.88
50:ZA:1351:G:H1	50:ZA:1360:U:H3	0.89	0.88
50:ZA:836:G:C5	75:YB:7:ILE:CG1	2.55	0.88
50:ZA:836:G:N3	75:YB:7:ILE:CA	2.39	0.86
50:ZA:442:C:H42	50:ZA:449:A:N6	1.72	0.85
50:ZA:1743:G:H21	50:ZA:1791:A:H62	1.23	0.84
75:YB:7:ILE:CG2	75:YB:7:ILE:CD1	2.56	0.84
47:WA:2485:G:H1	47:WA:2497:U:H3	1.25	0.83
85:b:47:LEU:O	85:b:51:ALA:N	2.08	0.83
47:WA:1249:U:H3	47:WA:1268:G:H1	1.26	0.82
50:ZA:562:U:H2'	50:ZA:563:G:H8	1.43	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:YB:7:ILE:CB	75:YB:7:ILE:HA	2.06	0.81
75:YB:7:ILE:HG21	75:YB:7:ILE:HG13	1.64	0.80
50:ZA:836:G:N3	75:YB:7:ILE:C	2.41	0.78
50:ZA:677:G:N2	50:ZA:1028:A:H62	1.81	0.77
47:WA:2575:A:H62	47:WA:2763:U:H3	1.33	0.77
50:ZA:836:G:C5	75:YB:7:ILE:HG12	2.18	0.77
50:ZA:1288:U:H3	50:ZA:1311:C:N4	1.83	0.77
75:YB:7:ILE:CG2	75:YB:7:ILE:HD12	2.14	0.77
47:WA:2659:G:N2	47:WA:2679:G:O6	2.19	0.76
85:b:47:LEU:HD12	85:b:53:VAL:HG22	1.68	0.76
50:ZA:836:G:N1	75:YB:7:ILE:CG2	2.49	0.76
50:ZA:491:C:H3'	75:YB:104:ARG:HB2	1.67	0.76
3:C:78:ARG:HB3	3:C:88:GLY:HA2	1.69	0.75
50:ZA:851:C:H5''	50:ZA:852:G:H5'	1.68	0.75
50:ZA:1737:G:H1	50:ZA:1797:U:H3	1.35	0.74
50:ZA:836:G:C2	75:YB:7:ILE:HA	2.22	0.74
50:ZA:957:A:H3'	50:ZA:958:G:H21	1.51	0.73
47:WA:3699:U:H5''	47:WA:3700:G:H5'	1.70	0.73
55:EB:137:PRO:HB2	55:EB:150:PRO:HD2	1.69	0.73
86:At:51:U:H3	86:At:63:G:H1	1.35	0.73
85:b:57:LYS:HB3	85:b:60:MET:HG2	1.70	0.73
50:ZA:839:C:H5''	75:YB:47:MET:HE2	1.70	0.73
50:ZA:836:G:C4	75:YB:7:ILE:N	2.56	0.73
22:V:82:ILE:HG13	57:GB:135:PRO:HD2	1.69	0.73
48:XA:28:C:H1'	48:XA:54:A:H61	1.55	0.72
55:EB:94:LYS:HB3	75:YB:16:ARG:HB2	1.70	0.72
50:ZA:1472:C:H42	50:ZA:1476:A:H62	1.35	0.72
50:ZA:197:U:H3	50:ZA:202:G:H1	0.82	0.71
50:ZA:817:G:H21	50:ZA:847:A:H62	1.37	0.71
50:ZA:526:A:N1	50:ZA:559:G:O6	2.24	0.71
44:SA:29:C:H5''	66:PB:136:THR:HG21	1.73	0.71
50:ZA:836:G:C4	75:YB:7:ILE:CG1	2.74	0.71
47:WA:3643:U:OP2	47:WA:3648:A:N6	2.25	0.70
11:K:56:ARG:O	11:K:116:ARG:NH1	2.25	0.70
47:WA:4476:A:OP2	47:WA:4478:C:N4	2.25	0.70
55:EB:185:GLY:H	55:EB:189:LEU:HD13	1.57	0.70
73:WB:11:LEU:HD12	73:WB:74:VAL:HG23	1.74	0.69
25:Y:50:PRO:HD3	25:Y:68:ILE:HG13	1.73	0.69
47:WA:995:U:H3	47:WA:1071:G:H1	1.39	0.69
2:B:249:ARG:NH1	47:WA:2839:U:OP1	2.25	0.69
4:D:52:ILE:HD13	48:XA:6:C:H4'	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:265:LYS:NZ	47:WA:4935:C:OP2	2.26	0.69
50:ZA:677:G:H21	50:ZA:1028:A:N6	1.89	0.69
50:ZA:1711:U:H3	50:ZA:1822:A:H61	1.41	0.69
2:B:324:GLY:HA2	47:WA:5053:C:H4'	1.74	0.69
67:QB:96:VAL:HG11	67:QB:110:ILE:HG13	1.73	0.69
7:G:111:PRO:HD2	7:G:114:ILE:HD12	1.74	0.69
47:WA:308:G:OP2	47:WA:308:G:N2	2.23	0.69
47:WA:2022:U:H2'	47:WA:2023:G:H8	1.56	0.69
2:B:276:HIS:ND1	47:WA:4718:C:OP1	2.25	0.68
55:EB:191:ARG:HH11	55:EB:245:ARG:HH21	1.41	0.68
57:GB:140:ARG:O	57:GB:144:LEU:HB3	1.94	0.68
50:ZA:694:G:H22	50:ZA:732:U:H3	1.42	0.68
50:ZA:1091:C:HO2'	73:WB:2:VAL:N	1.90	0.68
50:ZA:522:A:OP1	60:JB:146:SER:OG	2.11	0.68
13:M:120:TRP:HE1	13:M:123:GLU:HB3	1.59	0.68
50:ZA:836:G:C2	75:YB:7:ILE:CG2	2.77	0.68
83:GC:31:ILE:HG23	83:GC:43:TRP:HB2	1.76	0.68
22:V:90:ILE:HB	57:GB:147:LEU:HB3	1.75	0.67
50:ZA:1286:G:N2	50:ZA:1312:G:O2'	2.28	0.67
47:WA:2320:G:N2	47:WA:2323:G:OP2	2.26	0.67
50:ZA:562:U:H2'	50:ZA:563:G:C8	2.29	0.67
50:ZA:1497:G:N7	61:KB:25:LYS:NZ	2.43	0.67
14:N:116:LYS:HE3	18:R:169:THR:HG21	1.77	0.67
50:ZA:836:G:C4	75:YB:7:ILE:HG12	2.30	0.67
47:WA:3850:U:H2'	47:WA:3851:A:H8	1.60	0.67
47:WA:1543:C:H1'	47:WA:2450:G:H21	1.60	0.66
50:ZA:1743:G:N2	50:ZA:1791:A:H62	1.93	0.66
57:GB:63:MET:HG2	57:GB:98:ARG:HB3	1.77	0.66
43:RA:46:ILE:HD11	43:RA:62:LEU:HD21	1.76	0.66
45:TA:15:G:N2	45:TA:48:C:O2	2.28	0.66
2:B:11:HIS:NE2	47:WA:4460:C:OP1	2.24	0.66
50:ZA:126:G:H1'	50:ZA:181:A:H1'	1.77	0.66
50:ZA:1670:C:H2'	50:ZA:1671:G:H8	1.61	0.66
85:b:57:LYS:HD2	85:b:60:MET:HE2	1.76	0.66
9:I:54:SER:HB2	9:I:135:ILE:HD11	1.77	0.66
47:WA:416:U:H4'	47:WA:2332:G:H4'	1.78	0.66
50:ZA:43:U:OP2	50:ZA:485:A:N6	2.29	0.66
50:ZA:326:C:OP2	50:ZA:327:G:N2	2.28	0.66
1:A:207:VAL:HG13	1:A:208:GLU:HG3	1.77	0.66
47:WA:470:A:H62	47:WA:685:G:H21	1.44	0.66
47:WA:1998:C:H5''	85:b:48:ARG:HG3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:2409:G:OP2	47:WA:2409:G:N2	2.26	0.66
47:WA:2603:A:N6	47:WA:2746:A:OP2	2.28	0.66
50:ZA:1139:C:H42	50:ZA:1149:A:H62	1.43	0.66
67:QB:156:LYS:NZ	67:QB:160:GLY:O	2.29	0.66
35:IA:20:ARG:HG2	37:KA:8:ARG:HH12	1.60	0.65
47:WA:762:G:H22	47:WA:905:U:H3	1.42	0.65
31:EA:100:ARG:NH1	47:WA:4755:U:OP1	2.30	0.65
47:WA:1205:G:H2'	47:WA:1206:G:H8	1.60	0.65
47:WA:1726:G:N2	47:WA:1878:U:OP1	2.30	0.65
50:ZA:1112:U:O2	50:ZA:1121:G:O6	2.15	0.65
50:ZA:1396:A:O2'	50:ZA:1398:G:N7	2.28	0.65
50:ZA:377:G:H5'	59:IB:98:LYS:HB3	1.79	0.65
75:YB:7:ILE:CG2	75:YB:7:ILE:HG13	2.18	0.65
2:B:249:ARG:NH2	47:WA:3847:A:OP2	2.29	0.65
8:H:40:HIS:HD1	47:WA:4703:A:HO2'	1.40	0.65
47:WA:1959:U:O2'	85:b:6:ARG:NH1	2.30	0.65
47:WA:2467:C:H1'	47:WA:3674:G:H1	1.62	0.65
15:O:161:ALA:HB2	47:WA:1599:G:H5'	1.78	0.65
47:WA:4501:G:N2	47:WA:4531:G:N3	2.34	0.65
50:ZA:396:U:OP2	62:LB:79:LYS:NZ	2.29	0.65
52:BB:122:GLU:O	52:BB:165:ARG:NH1	2.30	0.65
5:E:159:ARG:NH1	47:WA:4942:C:OP1	2.29	0.65
5:E:186:ARG:HH21	47:WA:4938:G:H2'	1.61	0.65
14:N:89:PRO:HD3	47:WA:1916:C:H4'	1.78	0.65
50:ZA:482:G:N1	50:ZA:485:A:OP2	2.29	0.65
70:TB:76:THR:HB	70:TB:94:ARG:HB3	1.77	0.65
47:WA:2494:C:H2'	47:WA:2495:G:H8	1.62	0.65
50:ZA:1165:G:OP2	50:ZA:1165:G:N2	2.26	0.65
69:SB:101:ASN:O	69:SB:105:ASN:ND2	2.30	0.65
21:U:50:ASN:ND2	47:WA:4459:U:OP1	2.30	0.64
47:WA:1334:C:H2'	47:WA:1335:A:H8	1.61	0.64
50:ZA:1560:U:HO2'	50:ZA:1583:C:HO2'	1.44	0.64
83:GC:4:GLN:HB3	83:GC:313:THR:HB	1.79	0.64
1:A:128:ARG:NH1	47:WA:3683:G:OP2	2.30	0.64
47:WA:1996:C:H2'	47:WA:1997:G:C8	2.33	0.64
50:ZA:1854:U:H2'	50:ZA:1855:G:H8	1.62	0.64
71:UB:46:LYS:NZ	71:UB:97:ILE:O	2.30	0.64
5:E:115:MET:O	42:PA:87:ARG:NH1	2.31	0.64
6:F:218:GLY:O	6:F:245:ARG:NH2	2.30	0.64
46:VA:26:A:N6	50:ZA:1698:C:OP1	2.30	0.64
50:ZA:836:G:C6	75:YB:7:ILE:N	2.64	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:1075:C:H2'	50:ZA:1076:G:H8	1.62	0.64
8:H:85:THR:HG23	8:H:86:LEU:HG	1.80	0.64
10:J:75:ARG:NH1	48:XA:40:U:O2	2.30	0.64
47:WA:4090:C:H2'	47:WA:4091:G:H8	1.62	0.64
50:ZA:1576:G:H2'	50:ZA:1577:G:C8	2.33	0.64
19:S:70:HIS:NE2	47:WA:4329:C:OP1	2.30	0.64
50:ZA:1227:G:N2	50:ZA:1635:C:O2'	2.30	0.64
11:K:59:VAL:HB	47:WA:74:G:H5'	1.78	0.64
43:RA:90:ARG:HD3	43:RA:98:ILE:HD12	1.79	0.64
48:XA:53:U:H4'	48:XA:54:A:H5'	1.80	0.64
50:ZA:166:A:H4'	57:GB:8:PRO:HB3	1.78	0.64
55:EB:134:LYS:H	55:EB:136:ILE:HG12	1.62	0.64
4:D:176:SER:HB3	47:WA:4325:A:H4'	1.80	0.64
47:WA:4543:G:N2	47:WA:4546:A:OP2	2.26	0.64
50:ZA:1477:U:OP2	68:RB:3:ARG:NH2	2.31	0.64
65:OB:105:THR:HG22	65:OB:107:THR:H	1.62	0.64
5:E:96:THR:HG22	5:E:109:VAL:HG22	1.80	0.64
50:ZA:110:U:H3	50:ZA:351:G:H1	1.46	0.64
70:TB:126:GLN:OE1	70:TB:129:ARG:NH2	2.31	0.64
9:I:203:ARG:NH1	48:XA:105:C:OP2	2.31	0.63
47:WA:2461:G:N2	47:WA:2464:C:OP2	2.31	0.63
47:WA:20:U:H3'	47:WA:21:G:H8	1.64	0.63
83:GC:256:ILE:HG23	83:GC:270:LEU:HB2	1.81	0.63
25:Y:48:ARG:HB3	25:Y:69:LYS:HB3	1.79	0.63
37:KA:5:LYS:NZ	47:WA:2409:G:N7	2.46	0.63
2:B:20:LYS:HD3	47:WA:4719:A:H4'	1.79	0.63
6:F:189:LEU:HD21	6:F:207:LEU:HD21	1.81	0.63
16:P:54:SER:OG	16:P:57:ASN:ND2	2.31	0.63
47:WA:33:A:H3'	47:WA:47:A:H61	1.64	0.63
50:ZA:65:C:OP1	57:GB:136:LYS:NZ	2.31	0.63
50:ZA:1528:G:O2'	50:ZA:1666:C:OP1	2.15	0.63
50:ZA:1606:G:O2'	50:ZA:1632:G:N2	2.32	0.63
22:V:105:ARG:HE	50:ZA:328:U:H5''	1.63	0.63
44:SA:33:U:OP2	67:QB:172:ARG:NH2	2.31	0.63
47:WA:2413:C:H2'	47:WA:2414:A:H8	1.63	0.63
50:ZA:1192:U:OP1	74:XB:119:ARG:NH1	2.31	0.63
69:SB:38:ARG:O	69:SB:42:HIS:ND1	2.31	0.63
73:WB:105:THR:HG23	73:WB:126:LEU:HD11	1.81	0.63
25:Y:88:ASP:O	25:Y:121:ARG:NH1	2.31	0.63
47:WA:4995:G:O6	47:WA:5060:A:N1	2.32	0.63
50:ZA:1130:G:N2	50:ZA:1130:G:OP2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:GC:67:SER:H	83:GC:82:SER:HA	1.62	0.63
4:D:45:ASN:HB2	19:S:33:ILE:HD13	1.80	0.63
11:K:48:PRO:HG3	33:GA:118:LYS:HE3	1.80	0.63
14:N:125:LYS:HG3	14:N:129:LEU:HD12	1.79	0.63
77:AC:23:CYS:O	77:AC:27:ALA:HA	1.98	0.63
20:T:28:PRO:HB2	20:T:34:MET:HG2	1.81	0.63
47:WA:4920:C:H2'	47:WA:4921:G:H8	1.63	0.63
18:R:34:ALA:HB1	18:R:39:VAL:HG23	1.80	0.63
32:FA:66:ARG:HH22	47:WA:2520:G:H5'	1.64	0.63
50:ZA:1156:U:O4	53:CB:194:ARG:NH1	2.32	0.63
54:DB:144:ARG:HG3	54:DB:213:VAL:HG22	1.81	0.63
74:XB:68:LYS:HE2	81:EC:82:VAL:HG22	1.80	0.63
9:I:158:LYS:NZ	47:WA:4431:C:N3	2.47	0.62
50:ZA:103:A:H5'	59:IB:12:ARG:HH12	1.63	0.62
50:ZA:333:G:OP1	57:GB:197:GLN:NE2	2.32	0.62
50:ZA:913:A:N6	58:HB:357:SER:O	2.32	0.62
51:AB:36:GLN:O	51:AB:53:ARG:NH1	2.32	0.62
3:C:152:LEU:HD21	3:C:174:LEU:HD13	1.81	0.62
12:L:74:ARG:NH1	47:WA:737:C:OP1	2.30	0.62
44:SA:38:C:O2'	50:ZA:1058:A:OP1	2.16	0.62
30:DA:36:ARG:NH1	47:WA:1663:C:OP1	2.32	0.62
47:WA:1929:U:OP1	47:WA:1951:U:O2'	2.16	0.62
50:ZA:975:G:H21	65:OB:50:LYS:HA	1.62	0.62
57:GB:44:GLU:HG2	57:GB:119:LYS:HE3	1.81	0.62
50:ZA:93:U:O2'	55:EB:8:HIS:NE2	2.32	0.62
50:ZA:112:U:H3	50:ZA:349:A:H61	1.47	0.62
50:ZA:296:U:O2'	55:EB:131:VAL:O	2.12	0.62
1:A:80:GLU:HG3	41:OA:66:GLY:HA2	1.81	0.62
9:I:77:VAL:HG23	9:I:82:LYS:HA	1.81	0.62
18:R:87:ARG:HH21	47:WA:2036:G:H5'	1.64	0.62
50:ZA:162:C:H5''	57:GB:87:ARG:HH22	1.63	0.62
50:ZA:1608:U:O4	50:ZA:1632:G:N2	2.33	0.62
65:OB:148:GLY:O	65:OB:150:ARG:NH1	2.32	0.62
47:WA:3946:G:H1	47:WA:4071:U:H3	1.48	0.62
50:ZA:1147:C:OP1	77:AC:6:ARG:NH1	2.32	0.62
50:ZA:1587:G:H21	70:TB:77:LYS:HD3	1.63	0.62
56:FB:71:ARG:NH2	56:FB:148:ASN:OD1	2.31	0.62
57:GB:2:LYS:HB3	57:GB:15:LEU:HD11	1.82	0.62
38:LA:92:THR:HG22	38:LA:94:ASN:H	1.64	0.62
47:WA:369:G:N2	47:WA:372:A:OP2	2.26	0.62
50:ZA:929:G:N2	50:ZA:1013:U:O2	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:1277:C:H2'	50:ZA:1278:A:H8	1.65	0.62
73:WB:52:ILE:HG22	73:WB:61:ILE:HG12	1.81	0.62
6:F:227:VAL:HA	18:R:39:VAL:HG12	1.82	0.62
21:U:13:LYS:NZ	21:U:59:ASP:OD1	2.32	0.62
30:DA:8:VAL:HG22	30:DA:10:PRO:HD3	1.82	0.62
47:WA:1908:U:H2'	47:WA:1909:A:H8	1.65	0.62
50:ZA:116:U:H3	50:ZA:347:G:H1	1.48	0.62
50:ZA:1160:U:O4	74:XB:3:LYS:NZ	2.32	0.62
50:ZA:1654:G:OP1	70:TB:90:SER:OG	2.17	0.62
75:YB:7:ILE:HD12	75:YB:7:ILE:HG23	1.80	0.62
3:C:86:ARG:HH22	3:C:91:ALA:HA	1.65	0.62
33:GA:79:LYS:HE3	47:WA:136:C:H41	1.63	0.62
47:WA:1852:A:N3	47:WA:2285:G:O2'	2.31	0.62
47:WA:4080:C:O2'	47:WA:4174:A:N6	2.33	0.62
47:WA:4128:C:H5''	47:WA:4129:A:H5''	1.81	0.62
50:ZA:1566:G:N7	70:TB:101:ARG:NH2	2.48	0.62
1:A:3:ARG:HD2	1:A:208:GLU:HG2	1.82	0.61
55:EB:87:MET:HE2	55:EB:123:LEU:HB2	1.82	0.61
47:WA:1996:C:H2'	47:WA:1997:G:H8	1.65	0.61
42:PA:6:GLN:HG3	42:PA:44:ILE:HD12	1.82	0.61
47:WA:1094:C:H2'	47:WA:1095:G:C8	2.35	0.61
50:ZA:346:C:O3'	55:EB:30:ARG:NH1	2.33	0.61
50:ZA:525:A:H4'	81:EC:104:ARG:HH22	1.65	0.61
60:JB:136:ARG:NH1	60:JB:159:PHE:O	2.32	0.61
75:YB:6:THR:HB	75:YB:28:LEU:HB2	1.82	0.61
3:C:268:ARG:HH11	47:WA:493:U:H5''	1.64	0.61
17:Q:44:LEU:HD22	17:Q:49:LEU:HD12	1.81	0.61
19:S:40:VAL:HG12	19:S:98:HIS:HA	1.82	0.61
26:Z:21:ARG:NH2	47:WA:1319:U:OP1	2.30	0.61
47:WA:1727:U:H2'	47:WA:1728:U:H6	1.65	0.61
50:ZA:1447:G:OP1	71:UB:87:ARG:NH2	2.33	0.61
2:B:242:ARG:NH2	47:WA:2858:C:O2	2.33	0.61
47:WA:4455:C:O2	47:WA:4531:G:N2	2.34	0.61
50:ZA:38:A:H5''	60:JB:5:ARG:HB3	1.83	0.61
50:ZA:190:G:OP1	59:IB:141:ARG:NH1	2.34	0.61
50:ZA:1674:G:OP1	56:FB:51:HIS:NE2	2.34	0.61
33:GA:31:LEU:HB3	33:GA:47:ILE:HG22	1.81	0.61
50:ZA:1473:G:N2	50:ZA:1476:A:OP2	2.32	0.61
15:O:160:ARG:NH2	47:WA:1599:G:OP1	2.34	0.61
47:WA:2779:G:H5''	47:WA:2780:G:H5'	1.83	0.61
47:WA:4606:G:N2	47:WA:4609:A:OP2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:99:A:H61	50:ZA:433:A:H1'	1.66	0.61
73:WB:42:MET:HE2	73:WB:49:GLU:HA	1.82	0.61
47:WA:756:U:H3	47:WA:911:G:H1	1.48	0.61
47:WA:2505:G:N2	47:WA:4086:G:O5'	2.34	0.61
50:ZA:161:U:O2'	57:GB:87:ARG:NH1	2.33	0.61
83:GC:199:THR:HG21	83:GC:240:CYS:HA	1.82	0.61
83:GC:259:TRP:HD1	83:GC:266:ILE:HA	1.65	0.61
31:EA:21:GLN:NE2	47:WA:1311:C:O2	2.34	0.61
50:ZA:1064:C:H2'	50:ZA:1065:G:H8	1.66	0.61
65:OB:142:ARG:HB3	77:AC:22:ARG:HD3	1.83	0.61
75:YB:7:ILE:HG21	75:YB:7:ILE:CD1	2.28	0.61
18:R:69:GLU:OE2	18:R:76:LYS:NZ	2.34	0.60
20:T:113:ARG:NH2	47:WA:2704:C:O3'	2.33	0.60
47:WA:2737:G:H2'	47:WA:2738:G:H8	1.66	0.60
47:WA:4575:G:N2	47:WA:4724:G:OP2	2.33	0.60
49:YA:11:C:H2'	49:YA:12:G:H8	1.66	0.60
50:ZA:1634:A:O2'	69:SB:142:ARG:NH1	2.34	0.60
55:EB:126:VAL:HA	55:EB:141:THR:HA	1.83	0.60
6:F:146:LEU:O	6:F:150:ASN:ND2	2.33	0.60
30:DA:44:ARG:NH2	47:WA:1314:A:O2'	2.34	0.60
45:TA:15:G:N2	45:TA:48:C:C2	2.68	0.60
47:WA:1978:G:O6	47:WA:1993:A:N6	2.34	0.60
50:ZA:443:U:H3	50:ZA:447:A:H62	1.47	0.60
50:ZA:1521:C:OP2	69:SB:136:THR:OG1	2.17	0.60
62:LB:66:VAL:HG11	62:LB:141:ASN:HD22	1.65	0.60
64:NB:136:PRO:HG2	64:NB:139:TRP:HB2	1.83	0.60
16:P:82:VAL:HG12	16:P:84:GLY:H	1.66	0.60
17:Q:64:ARG:NE	47:WA:2618:C:OP1	2.33	0.60
26:Z:125:LYS:HG2	26:Z:145:VAL:HB	1.83	0.60
35:IA:49:TRP:O	47:WA:1648:A:O2'	2.20	0.60
47:WA:1571:U:H2'	47:WA:1572:G:H8	1.67	0.60
47:WA:2337:C:H2'	47:WA:2338:G:H8	1.64	0.60
47:WA:3863:A:H2'	47:WA:3864:A:H8	1.66	0.60
47:WA:4240:G:H2'	47:WA:4241:A:H8	1.66	0.60
49:YA:47:C:H1'	49:YA:61:A:H2'	1.84	0.60
50:ZA:1498:A:OP2	54:DB:65:ARG:NH2	2.31	0.60
53:CB:123:ARG:NH1	53:CB:143:CYS:SG	2.74	0.60
57:GB:142:ARG:HA	57:GB:147:LEU:HG	1.81	0.60
59:IB:131:PRO:HD2	59:IB:134:GLU:HB2	1.83	0.60
5:E:61:ARG:HB2	47:WA:1243:C:H5''	1.83	0.60
47:WA:86:U:H2'	47:WA:87:A:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:95:ARG:NH2	47:WA:1897:G:OP1	2.34	0.60
15:O:130:ASN:OD1	47:WA:399:G:N2	2.34	0.60
47:WA:955:G:H2'	47:WA:956:G:H8	1.66	0.60
47:WA:1975:G:H2'	47:WA:1976:U:H2'	1.82	0.60
47:WA:3811:G:N2	47:WA:3811:G:OP2	2.35	0.60
47:WA:4874:G:H4'	47:WA:4875:G:H5'	1.82	0.60
51:AB:127:PRO:HG3	51:AB:146:ALA:HB1	1.83	0.60
68:RB:17:ILE:HD11	68:RB:54:VAL:HA	1.83	0.60
80:DC:17:GLY:O	80:DC:27:ARG:NH1	2.34	0.60
2:B:15:GLY:O	47:WA:4589:G:N2	2.29	0.60
29:CA:23:ARG:HG2	29:CA:121:ASN:HA	1.84	0.60
47:WA:2546:G:N1	49:YA:123:U:O2	2.29	0.60
47:WA:4899:G:H2'	47:WA:4900:G:H8	1.65	0.60
50:ZA:527:C:H2'	50:ZA:528:A:C8	2.36	0.60
3:C:46:LYS:HB3	3:C:49:ARG:HH21	1.66	0.60
6:F:241:ARG:NH2	47:WA:945:C:OP1	2.35	0.60
30:DA:99:ILE:HG21	30:DA:108:ARG:HG2	1.83	0.60
50:ZA:16:G:H5'	50:ZA:669:A:H61	1.67	0.60
50:ZA:1692:U:H2'	50:ZA:1693:G:C8	2.37	0.60
68:RB:111:PHE:HB3	68:RB:114:LEU:HD11	1.82	0.60
34:HA:41:ARG:HH12	47:WA:308:G:H2'	1.66	0.60
47:WA:3671:G:N2	47:WA:3674:G:OP2	2.35	0.60
47:WA:3809:A:HO2'	50:ZA:1816:G:HO2'	1.48	0.60
50:ZA:491:C:P	75:YB:105:LYS:H	2.23	0.60
78:BC:34:ASP:HB2	78:BC:82:LYS:HD2	1.84	0.60
1:A:101:VAL:HG22	1:A:165:VAL:HG22	1.83	0.60
1:A:179:ILE:O	47:WA:3655:A:O2'	2.14	0.60
14:N:49:ARG:NH1	47:WA:1932:U:OP2	2.31	0.60
47:WA:3879:A:N3	47:WA:4403:G:O2'	2.34	0.60
47:WA:4588:G:O6	47:WA:4719:A:N6	2.35	0.60
65:OB:45:THR:HG22	65:OB:52:THR:HA	1.83	0.60
83:GC:77:PHE:HB3	83:GC:89:LEU:HD11	1.83	0.60
5:E:48:ARG:HB2	5:E:64:MET:HE1	1.83	0.60
33:GA:47:ILE:HD11	49:YA:49:G:H5'	1.84	0.60
38:LA:88:LYS:NZ	47:WA:4487:C:O2'	2.35	0.60
47:WA:1565:A:H2'	47:WA:1566:A:C8	2.37	0.60
47:WA:2522:C:H2'	47:WA:2523:G:H8	1.66	0.60
47:WA:3687:C:H2'	47:WA:3688:G:H8	1.66	0.60
47:WA:3899:G:N2	47:WA:3900:G:O6	2.33	0.60
47:WA:4260:C:H2'	47:WA:4261:C:H6	1.67	0.60
47:WA:4696:G:OP1	47:WA:4696:G:N2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:PB:108:LYS:HB3	66:PB:111:MET:HG3	1.84	0.60
86:At:13:C:H42	86:At:46:7MG:HN22	1.49	0.60
30:DA:48:ARG:NH2	47:WA:2281:A:O2'	2.34	0.59
32:FA:29:ARG:NH1	47:WA:2524:G:OP1	2.35	0.59
47:WA:3719:A:OP2	47:WA:3737:G:N2	2.34	0.59
2:B:252:ALA:HB1	47:WA:4526:G:C2	2.37	0.59
40:NA:69:ARG:HG3	40:NA:82:MET:HE1	1.84	0.59
47:WA:1745:A:N1	47:WA:1791:C:O2'	2.33	0.59
47:WA:2742:U:O2'	47:WA:2744:G:N2	2.34	0.59
47:WA:3879:A:O2'	47:WA:4402:G:N2	2.34	0.59
53:CB:68:ARG:NH1	53:CB:72:ASP:OD1	2.35	0.59
83:GC:214:GLY:HA2	83:GC:236:ILE:HG13	1.83	0.59
9:I:116:ARG:NH2	47:WA:4196:U:O2'	2.35	0.59
50:ZA:635:G:H5''	81:EC:94:LYS:HD3	1.84	0.59
50:ZA:1048:G:H21	50:ZA:1070:A:H62	1.48	0.59
66:PB:123:TYR:OH	69:SB:124:ARG:NH1	2.35	0.59
71:UB:80:PHE:HB3	80:DC:52:PHE:HB3	1.82	0.59
16:P:150:ARG:NH2	47:WA:1501:C:OP1	2.35	0.59
49:YA:15:G:H2'	49:YA:16:G:C4	2.37	0.59
50:ZA:836:G:C2	75:YB:8:ARG:N	2.70	0.59
28:BA:50:ASN:ND2	28:BA:75:SER:O	2.35	0.59
34:HA:48:CYS:SG	34:HA:49:GLY:N	2.75	0.59
48:XA:57:C:H2'	48:XA:58:A:H8	1.67	0.59
50:ZA:1550:G:H3'	50:ZA:1579:A:H61	1.65	0.59
83:GC:107:ASP:OD2	83:GC:125:ARG:NH1	2.35	0.59
2:B:117:ARG:NH2	47:WA:4987:U:OP1	2.35	0.59
47:WA:2589:A:OP2	47:WA:2590:C:N4	2.35	0.59
48:XA:92:C:H2'	48:XA:93:G:H8	1.67	0.59
50:ZA:1403:C:OP2	50:ZA:1405:A:N6	2.34	0.59
83:GC:174:VAL:HB	83:GC:188:HIS:HB2	1.85	0.59
4:D:166:ALA:HB1	4:D:171:LEU:HD12	1.85	0.59
50:ZA:1864:U:OP2	77:AC:5:ARG:NH2	2.34	0.59
66:PB:121:ILE:HG22	69:SB:120:HIS:HD2	1.66	0.59
19:S:75:VAL:HG22	19:S:88:ARG:HG2	1.83	0.59
50:ZA:1276:A:H1'	61:KB:50:GLN:HE22	1.66	0.59
50:ZA:1558:C:H2'	50:ZA:1559:C:C6	2.37	0.59
1:A:225:ILE:HD11	1:A:233:ARG:HG3	1.84	0.59
3:C:33:ARG:NH1	47:WA:1353:G:OP1	2.33	0.59
44:SA:21:A:O2'	44:SA:22:A:O5'	2.20	0.59
50:ZA:1139:C:N4	50:ZA:1149:A:H62	2.00	0.59
50:ZA:1228:A:H2'	50:ZA:1229:G:C8	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:HB:258:GLU:HG3	58:HB:286:ALA:HB3	1.85	0.59
47:WA:1671:A:N3	47:WA:1854:U:O2'	2.32	0.58
50:ZA:1259:A:N6	50:ZA:1519:U:OP1	2.36	0.58
50:ZA:1565:C:OP2	70:TB:101:ARG:NH1	2.36	0.58
57:GB:148:SER:N	57:GB:151:ASP:OD2	2.36	0.58
62:LB:65:ASN:O	62:LB:132:ARG:NH1	2.31	0.58
82:FC:121:CYS:CB	82:FC:126:CYS:SG	2.89	0.58
11:K:116:ARG:NH2	11:K:155:MET:O	2.36	0.58
47:WA:215:C:H5''	47:WA:216:C:H5'	1.85	0.58
50:ZA:1110:G:H4'	68:RB:124:VAL:HB	1.84	0.58
52:BB:146:ARG:HB2	52:BB:149:GLN:HB2	1.85	0.58
1:A:179:ILE:HG23	1:A:184:ARG:HB2	1.85	0.58
2:B:95:THR:HG22	47:WA:4912:A:H4'	1.85	0.58
26:Z:26:ARG:NH2	47:WA:1658:U:OP2	2.30	0.58
47:WA:2577:U:O2	47:WA:2760:G:N2	2.32	0.58
47:WA:4095:G:H22	47:WA:4117:G:H1	1.52	0.58
3:C:149:GLU:HG2	3:C:151:PRO:HD2	1.86	0.58
9:I:101:LYS:NZ	9:I:102:MET:O	2.35	0.58
47:WA:2445:G:OP2	47:WA:2518:G:N2	2.34	0.58
47:WA:4770:G:H2'	47:WA:4771:G:C8	2.38	0.58
50:ZA:106:C:OP1	50:ZA:431:G:O2'	2.16	0.58
1:A:70:LYS:NZ	47:WA:2505:G:N7	2.51	0.58
2:B:224:LYS:NZ	47:WA:4669:C:OP1	2.36	0.58
3:C:110:ARG:NH1	47:WA:1510:A:OP1	2.31	0.58
5:E:71:TYR:HA	5:E:74:LYS:HE2	1.85	0.58
8:H:1:MET:N	47:WA:1953:G:OP2	2.36	0.58
25:Y:103:ASP:HB3	25:Y:106:LEU:HB2	1.84	0.58
39:MA:11:ARG:NH2	50:ZA:1844:U:OP1	2.36	0.58
47:WA:2413:C:H2'	47:WA:2414:A:C8	2.38	0.58
50:ZA:496:C:OP1	55:EB:49:ARG:NH1	2.36	0.58
60:JB:42:GLU:OE1	60:JB:45:ARG:NH2	2.37	0.58
12:L:30:VAL:O	18:R:98:ARG:NH1	2.37	0.58
17:Q:83:GLY:N	47:WA:2814:A:OP1	2.33	0.58
41:OA:39:CYS:HB3	41:OA:42:CYS:SG	2.43	0.58
47:WA:260:C:H2'	47:WA:261:G:C8	2.39	0.58
47:WA:299:C:H2'	47:WA:300:A:H8	1.68	0.58
50:ZA:311:C:H5''	50:ZA:312:G:H5''	1.85	0.58
4:D:83:LEU:HB3	4:D:88:VAL:HB	1.86	0.58
19:S:87:LYS:NZ	47:WA:4302:U:OP1	2.36	0.58
23:W:83:THR:HG22	23:W:85:SER:H	1.68	0.58
47:WA:1777:A:H3'	47:WA:1778:A:H8	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:655:A:H4'	50:ZA:656:G:H3'	1.85	0.58
50:ZA:1535:U:H3	56:FB:159:ARG:HE	1.51	0.58
50:ZA:1658:G:OP2	50:ZA:1660:C:N4	2.37	0.58
51:AB:8:LEU:HD11	72:VB:39:VAL:HG11	1.85	0.58
53:CB:201:GLY:O	60:JB:54:ARG:NH2	2.36	0.58
67:QB:102:GLY:H	67:QB:105:ALA:HB3	1.69	0.58
2:B:373:LYS:HD2	47:WA:4629:U:H4'	1.85	0.58
3:C:96:CYS:HA	47:WA:2354:U:H1'	1.84	0.58
11:K:140:SER:OG	11:K:143:GLU:OE1	2.22	0.58
14:N:178:ARG:NH1	14:N:182:GLU:OE2	2.36	0.58
25:Y:73:LYS:HE2	47:WA:2582:U:H5''	1.85	0.58
33:GA:89:ARG:NH1	49:YA:37:A:OP2	2.35	0.58
50:ZA:526:A:H2'	50:ZA:527:C:C6	2.38	0.58
51:AB:57:LYS:NZ	51:AB:160:ALA:O	2.34	0.58
51:AB:77:ILE:HG12	51:AB:99:ILE:HB	1.86	0.58
55:EB:112:HIS:NE2	55:EB:237:SER:O	2.36	0.58
10:J:99:PHE:O	10:J:159:LYS:NZ	2.37	0.58
47:WA:3909:G:N2	84:IC:197:PHE:O	2.35	0.58
50:ZA:1362:U:H5''	50:ZA:1363:C:H5	1.69	0.58
3:C:39:PHE:O	3:C:43:ASN:ND2	2.30	0.58
4:D:223:PHE:HB3	4:D:226:TYR:HB2	1.85	0.58
5:E:181:PRO:HB2	5:E:184:LEU:HB2	1.86	0.58
26:Z:84:GLU:OE2	26:Z:87:ARG:NH2	2.36	0.58
26:Z:132:ARG:NH1	47:WA:1470:C:OP1	2.37	0.58
37:KA:23:ILE:HG23	37:KA:38:ASN:HB2	1.84	0.58
50:ZA:874:G:N3	58:HB:352:GLN:NE2	2.41	0.58
5:E:141:ARG:NH1	5:E:172:SER:O	2.37	0.57
11:K:54:PRO:O	11:K:56:ARG:NH1	2.37	0.57
56:FB:51:HIS:HA	56:FB:86:LYS:HE2	1.86	0.57
67:QB:45:ALA:HB2	67:QB:101:GLY:HA3	1.85	0.57
86:At:68:C:H2'	86:At:69:G:H8	1.67	0.57
3:C:312:ARG:NH2	47:WA:2077:G:OP1	2.37	0.57
6:F:136:GLU:OE1	48:XA:96:U:O2'	2.21	0.57
16:P:22:ASP:OD1	16:P:22:ASP:N	2.37	0.57
50:ZA:915:G:OP2	50:ZA:915:G:N2	2.35	0.57
50:ZA:1401:A:H4'	71:UB:52:GLY:HA3	1.86	0.57
55:EB:18:TRP:HB3	55:EB:20:LEU:HD13	1.86	0.57
6:F:93:ARG:NH1	6:F:113:LEU:O	2.35	0.57
14:N:119:VAL:HG11	18:R:171:ARG:HG2	1.86	0.57
17:Q:105:LEU:HD23	17:Q:138:LEU:HD23	1.86	0.57
18:R:174:THR:HG1	47:WA:4765:U:HO2'	1.48	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:CA:24:GLU:OE2	29:CA:87:ARG:NH1	2.38	0.57
47:WA:115:C:O2'	47:WA:276:C:OP1	2.22	0.57
50:ZA:614:C:O2'	74:XB:64:SER:OG	2.19	0.57
65:OB:106:LYS:HE3	65:OB:136:PRO:HD2	1.86	0.57
6:F:135:VAL:HG23	6:F:139:ILE:HD13	1.85	0.57
6:F:176:ARG:NH1	47:WA:2103:A:N7	2.52	0.57
15:O:147:GLN:NE2	15:O:176:GLU:OE2	2.38	0.57
36:JA:35:LYS:NZ	47:WA:2695:G:OP1	2.34	0.57
2:B:223:THR:HB	2:B:275:HIS:H	1.69	0.57
4:D:17:GLN:O	47:WA:4267:U:N3	2.37	0.57
11:K:18:TRP:NE1	47:WA:1518:G:O2'	2.38	0.57
25:Y:22:LYS:NZ	25:Y:129:TRP:O	2.37	0.57
42:PA:63:VAL:HG22	42:PA:79:ARG:HG2	1.87	0.57
47:WA:2560:C:H2'	47:WA:2561:G:C8	2.39	0.57
48:XA:63:C:H5'	48:XA:64:G:H5''	1.86	0.57
50:ZA:638:C:OP1	81:EC:113:ARG:NH1	2.32	0.57
50:ZA:1015:U:O2'	64:NB:55:ARG:NH1	2.36	0.57
8:H:91:LYS:HD3	8:H:183:GLU:HB3	1.86	0.57
19:S:108:ARG:NH1	47:WA:1839:A:OP1	2.37	0.57
25:Y:25:ILE:HA	25:Y:43:VAL:HG12	1.86	0.57
25:Y:100:VAL:HG13	25:Y:106:LEU:HB3	1.87	0.57
26:Z:64:LYS:NZ	47:WA:70:A:OP2	2.36	0.57
29:CA:64:ILE:HG23	29:CA:68:LEU:HD23	1.87	0.57
47:WA:35:U:O2'	47:WA:1527:A:N1	2.36	0.57
50:ZA:71:G:O2'	50:ZA:72:C:O4'	2.18	0.57
50:ZA:1228:A:H2'	50:ZA:1229:G:H8	1.69	0.57
50:ZA:1263:U:O2	80:DC:16:GLN:NE2	2.32	0.57
1:A:21:LYS:HG2	47:WA:1543:C:H5''	1.87	0.57
3:C:340:ILE:HD13	5:E:53:VAL:HG21	1.85	0.57
13:M:68:ARG:HA	13:M:98:LEU:HD21	1.87	0.57
25:Y:5:MET:O	25:Y:28:ASN:ND2	2.38	0.57
33:GA:89:ARG:NH2	47:WA:19:G:OP2	2.37	0.57
38:LA:87:LYS:NZ	47:WA:1931:A:O5'	2.38	0.57
42:PA:28:GLU:HB2	42:PA:31:ASN:HB2	1.86	0.57
43:RA:16:ARG:CZ	43:RA:57:ARG:HB2	2.34	0.57
58:HB:311:GLN:HA	58:HB:314:GLN:HB2	1.87	0.57
59:IB:135:GLU:O	59:IB:139:LYS:HB2	2.05	0.57
32:FA:41:ALA:O	32:FA:52:ARG:NH1	2.37	0.57
58:HB:268:LEU:HD13	58:HB:320:GLU:HG2	1.86	0.57
72:VB:15:ARG:NH1	72:VB:33:GLN:OE1	2.37	0.57
1:A:107:MET:HE1	1:A:164:ALA:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:2599:G:H2'	47:WA:2600:A:C8	2.40	0.57
56:FB:114:ASN:OD1	56:FB:118:ASN:ND2	2.38	0.57
78:BC:54:VAL:HG13	78:BC:63:LEU:HB2	1.87	0.57
2:B:163:LEU:HD23	2:B:180:LEU:HD21	1.87	0.57
16:P:175:GLU:OE2	26:Z:49:HIS:ND1	2.38	0.57
32:FA:6:THR:HG22	47:WA:2402:G:H21	1.70	0.57
35:IA:19:CYS:HB3	35:IA:22:CYS:SG	2.45	0.57
41:OA:4:ARG:NH2	47:WA:1557:G:O6	2.37	0.57
50:ZA:88:G:N2	50:ZA:499:G:O3'	2.37	0.57
50:ZA:142:C:N4	50:ZA:329:G:OP2	2.38	0.56
50:ZA:1220:A:N3	50:ZA:1677:U:O2'	2.33	0.56
80:DC:5:GLN:O	80:DC:9:SER:OG	2.22	0.56
34:HA:29:ARG:HH22	47:WA:276:C:H2'	1.70	0.56
47:WA:3612:A:H2'	47:WA:3613:A:H8	1.70	0.56
50:ZA:510:G:OP1	60:JB:4:ALA:N	2.37	0.56
50:ZA:616:A:OP1	74:XB:68:LYS:NZ	2.39	0.56
50:ZA:642:U:H4'	50:ZA:644:G:H4'	1.85	0.56
50:ZA:1804:U:H2'	50:ZA:1805:G:H8	1.69	0.56
55:EB:30:ARG:O	55:EB:81:THR:OG1	2.19	0.56
57:GB:58:LYS:HA	57:GB:107:SER:HB2	1.87	0.56
58:HB:384:VAL:HG22	58:HB:390:ARG:HG2	1.87	0.56
60:JB:37:LEU:HD13	60:JB:42:GLU:HB2	1.87	0.56
25:Y:52:LYS:O	25:Y:65:ARG:NH2	2.38	0.56
30:DA:36:ARG:NH2	47:WA:2324:G:OP1	2.38	0.56
38:LA:74:TYR:O	47:WA:4474:G:O2'	2.23	0.56
47:WA:1804:A:H5''	47:WA:1805:G:H5'	1.86	0.56
47:WA:3691:G:O2'	47:WA:3820:U:OP2	2.23	0.56
47:WA:4950:C:OP2	47:WA:4951:G:O2'	2.20	0.56
50:ZA:1298:G:H4'	66:PB:78:THR:HA	1.87	0.56
50:ZA:1781:A:H2'	50:ZA:1782:G:C8	2.40	0.56
51:AB:85:ARG:HH21	51:AB:201:LEU:HD12	1.71	0.56
53:CB:94:ILE:HD12	53:CB:162:ILE:HD11	1.86	0.56
54:DB:69:GLU:O	54:DB:92:ARG:NH2	2.38	0.56
62:LB:13:GLN:HB2	62:LB:16:ILE:HG12	1.87	0.56
69:SB:23:ARG:NH2	76:ZB:46:ASN:O	2.37	0.56
73:WB:86:LEU:HD21	73:WB:113:HIS:HB2	1.86	0.56
75:YB:10:ARG:HB3	75:YB:24:VAL:HB	1.86	0.56
2:B:113:GLU:HB3	2:B:178:ALA:HB2	1.87	0.56
4:D:33:ARG:NE	48:XA:7:G:OP1	2.35	0.56
17:Q:97:ARG:NH2	47:WA:2727:A:OP2	2.38	0.56
47:WA:916:U:H4'	47:WA:917:A:H5'	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:2018:C:H2'	47:WA:2019:A:H8	1.71	0.56
50:ZA:846:G:OP2	55:EB:108:ARG:NH1	2.37	0.56
56:FB:59:LYS:HB2	56:FB:62:ARG:HB2	1.88	0.56
64:NB:19:ARG:HH21	64:NB:21:SER:HB2	1.70	0.56
1:A:6:ARG:HH12	1:A:199:VAL:H	1.52	0.56
35:IA:13:ASN:ND2	47:WA:1620:G:OP1	2.37	0.56
47:WA:711:G:H2'	47:WA:712:A:H8	1.70	0.56
47:WA:1826:G:H2'	47:WA:1827:A:H8	1.70	0.56
50:ZA:681:U:H4'	74:XB:9:THR:HG22	1.86	0.56
67:QB:57:LEU:HD11	67:QB:59:LYS:HE3	1.88	0.56
67:QB:68:ILE:HG22	67:QB:70:PRO:HD2	1.86	0.56
86:At:62:C:H2'	86:At:63:G:H8	1.70	0.56
2:B:108:GLU:OE2	2:B:138:GLN:NE2	2.38	0.56
50:ZA:429:C:H2'	50:ZA:430:C:H6	1.71	0.56
50:ZA:1324:G:H1	50:ZA:1504:U:H3	1.52	0.56
52:BB:40:ASN:OD1	52:BB:75:GLN:NE2	2.38	0.56
70:TB:113:VAL:HG12	70:TB:123:LEU:HD23	1.87	0.56
16:P:172:ARG:HD2	26:Z:57:GLY:HA3	1.86	0.56
19:S:127:GLN:NE2	19:S:129:LYS:O	2.38	0.56
30:DA:100:ALA:O	30:DA:108:ARG:NH2	2.39	0.56
47:WA:436:C:H2'	47:WA:437:G:H8	1.70	0.56
47:WA:2871:U:O2'	47:WA:2883:A:N7	2.38	0.56
47:WA:3882:G:H2'	47:WA:3883:G:C8	2.41	0.56
50:ZA:453:C:O2'	57:GB:92:ARG:O	2.23	0.56
50:ZA:654:A:OP2	50:ZA:655:A:O2'	2.23	0.56
50:ZA:788:G:H2'	50:ZA:789:G:H8	1.71	0.56
50:ZA:1017:U:OP1	64:NB:62:GLN:NE2	2.34	0.56
50:ZA:1230:C:OP1	69:SB:130:ARG:NH2	2.37	0.56
50:ZA:1293:A:N6	50:ZA:1294:G:O6	2.39	0.56
50:ZA:1617:G:N1	50:ZA:1620:A:OP2	2.37	0.56
14:N:72:HIS:N	47:WA:4588:G:OP1	2.39	0.56
16:P:108:ARG:NH2	47:WA:1356:A:OP1	2.39	0.56
18:R:67:VAL:HA	47:WA:730:G:H1	1.71	0.56
19:S:78:LYS:NZ	47:WA:4303:U:OP1	2.39	0.56
46:VA:25:C:N4	50:ZA:1698:C:O2	2.39	0.56
49:YA:28:C:H2'	49:YA:29:G:H8	1.69	0.56
53:CB:134:ASN:OD1	53:CB:167:ARG:NH2	2.39	0.56
53:CB:168:GLY:N	53:CB:179:THR:O	2.38	0.56
4:D:88:VAL:HA	4:D:239:MET:HE3	1.86	0.56
4:D:256:LYS:HD2	48:XA:117:G:H5'	1.88	0.56
22:V:77:LYS:NZ	50:ZA:146:G:OP1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:15:ARG:NH1	47:WA:230:G:OP1	2.38	0.56
47:WA:2043:A:N7	47:WA:4436:C:O2'	2.38	0.56
47:WA:3690:U:H2'	47:WA:3691:G:H8	1.70	0.56
47:WA:3872:C:H2'	47:WA:3873:A:H8	1.71	0.56
50:ZA:491:C:O2'	50:ZA:493:A:N7	2.33	0.56
75:YB:7:ILE:HG21	75:YB:7:ILE:HD12	1.87	0.56
1:A:117:GLU:OE2	1:A:163:ARG:NH1	2.37	0.56
2:B:228:TYR:O	47:WA:2837:A:O2'	2.23	0.56
15:O:150:LYS:O	49:YA:13:G:O2'	2.23	0.56
22:V:93:LYS:HA	22:V:96:GLN:HG3	1.88	0.56
43:RA:90:ARG:HH21	43:RA:95:GLN:HB3	1.70	0.56
47:WA:1335:A:H2'	47:WA:1336:A:H8	1.70	0.56
50:ZA:516:A:N1	50:ZA:643:A:O2'	2.34	0.56
50:ZA:1758:G:H2'	50:ZA:1759:G:C8	2.40	0.56
60:JB:59:GLU:O	60:JB:62:THR:OG1	2.24	0.56
6:F:93:ARG:HB2	6:F:113:LEU:HB3	1.87	0.55
6:F:104:VAL:HG13	6:F:135:VAL:HG12	1.88	0.55
11:K:35:ARG:NH2	47:WA:337:U:OP1	2.39	0.55
47:WA:4956:G:H2'	47:WA:4957:A:H8	1.70	0.55
75:YB:102:THR:OG1	75:YB:107:ARG:NH2	2.39	0.55
82:FC:141:CYS:HB3	82:FC:146:LEU:H	1.70	0.55
10:J:13:ARG:O	10:J:136:ARG:NH1	2.39	0.55
41:OA:4:ARG:NH1	47:WA:1556:A:OP2	2.38	0.55
47:WA:4994:G:H2'	47:WA:4995:G:H8	1.72	0.55
50:ZA:432:G:OP1	55:EB:2:ALA:N	2.39	0.55
50:ZA:1474:A:H3'	50:ZA:1475:G:H21	1.71	0.55
82:FC:107:LYS:HD2	82:FC:115:SER:HB3	1.88	0.55
85:b:107:VAL:HG12	85:b:110:ALA:H	1.71	0.55
2:B:13:SER:HB2	47:WA:4624:A:H4'	1.87	0.55
16:P:151:HIS:ND1	16:P:164:LYS:O	2.39	0.55
32:FA:61:PRO:HA	32:FA:64:LEU:HD13	1.88	0.55
50:ZA:538:U:O4	50:ZA:546:G:N1	2.39	0.55
75:YB:10:ARG:NH1	75:YB:26:ASP:OD2	2.39	0.55
6:F:33:ARG:NH1	47:WA:1274:C:OP2	2.37	0.55
39:MA:15:ARG:NH2	50:ZA:1183:A:OP1	2.39	0.55
47:WA:520:C:H2'	47:WA:521:U:H5	1.71	0.55
47:WA:1657:C:O2	47:WA:4392:A:O2'	2.24	0.55
50:ZA:94:G:HO2'	50:ZA:508:A:HO2'	1.51	0.55
50:ZA:318:A:H3'	50:ZA:319:C:H5''	1.86	0.55
50:ZA:1668:U:OP1	67:QB:159:GLY:N	2.37	0.55
61:KB:27:VAL:HG13	61:KB:43:LEU:HD13	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:369:ASP:OD2	2:B:373:LYS:NZ	2.39	0.55
8:H:60:TRP:O	47:WA:4766:A:N6	2.32	0.55
47:WA:4741:C:N4	47:WA:4742:G:O6	2.40	0.55
50:ZA:375:U:H4'	62:LB:7:GLU:HG2	1.87	0.55
50:ZA:1309:C:OP1	82:FC:104:LYS:NZ	2.39	0.55
51:AB:214:GLU:OE2	68:RB:81:ARG:NH1	2.39	0.55
6:F:55:HIS:NE2	6:F:59:GLU:OE2	2.40	0.55
12:L:91:TRP:HA	12:L:94:LYS:HE2	1.89	0.55
16:P:121:LEU:HD22	16:P:125:GLN:HG2	1.89	0.55
47:WA:417:G:OP1	47:WA:2331:U:O2'	2.25	0.55
50:ZA:600:G:H2'	50:ZA:601:G:H8	1.72	0.55
50:ZA:1018:U:O2'	64:NB:86:GLU:OE2	2.24	0.55
68:RB:95:ILE:HD11	68:RB:118:GLN:HB2	1.89	0.55
74:XB:124:LYS:HG2	74:XB:129:SER:HA	1.88	0.55
13:M:49:ARG:HH12	47:WA:152:U:P	2.29	0.55
24:X:34:LEU:HD23	24:X:38:LEU:HB3	1.89	0.55
47:WA:692:C:H2'	47:WA:693:A:H8	1.72	0.55
47:WA:4861:C:H2'	47:WA:4862:G:H8	1.72	0.55
50:ZA:1103:C:H2'	50:ZA:1104:G:C8	2.41	0.55
50:ZA:1139:C:H42	50:ZA:1149:A:N6	2.03	0.55
50:ZA:1261:C:O2	80:DC:10:HIS:NE2	2.33	0.55
50:ZA:1869:A:N6	52:BB:114:VAL:O	2.40	0.55
31:EA:23:GLU:OE2	47:WA:438:G:N2	2.39	0.55
47:WA:1826:G:H2'	47:WA:1827:A:C8	2.42	0.55
47:WA:2611:G:H1	47:WA:2732:U:H3	1.53	0.55
47:WA:4995:G:H1	47:WA:5060:A:H2	1.53	0.55
50:ZA:917:U:C4	50:ZA:918:U:O4	2.60	0.55
50:ZA:992:A:N7	77:AC:15:ARG:NH2	2.51	0.55
50:ZA:1126:G:OP1	51:AB:41:ARG:NH1	2.40	0.55
51:AB:184:ARG:HD3	51:AB:191:ARG:HG2	1.89	0.55
63:MB:79:VAL:HG21	63:MB:85:LEU:HD13	1.89	0.55
69:SB:28:PHE:O	69:SB:31:THR:OG1	2.20	0.55
72:VB:73:ALA:HB1	72:VB:78:ILE:HB	1.88	0.55
73:WB:55:ASP:OD1	73:WB:56:HIS:N	2.40	0.55
1:A:132:ASN:ND2	47:WA:3685:C:OP1	2.40	0.55
6:F:178:LEU:HD21	6:F:203:ALA:HA	1.88	0.55
7:G:194:ASN:ND2	47:WA:151:G:N7	2.55	0.55
13:M:63:ARG:NH1	13:M:131:GLU:OE2	2.40	0.55
13:M:157:LYS:O	13:M:162:ARG:NH1	2.40	0.55
16:P:65:ARG:NH1	47:WA:1504:G:OP1	2.40	0.55
17:Q:90:PRO:HG2	17:Q:93:VAL:HB	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RA:21:GLU:OE1	43:RA:92:ARG:NH2	2.39	0.55
47:WA:1392:G:N2	47:WA:1395:G:OP2	2.35	0.55
50:ZA:1221:G:O2'	50:ZA:1676:U:O2	2.21	0.55
52:BB:63:LYS:NZ	52:BB:89:GLU:O	2.39	0.55
2:B:57:VAL:HG22	2:B:73:VAL:HG22	1.88	0.55
29:CA:36:VAL:HG11	29:CA:44:ARG:HG2	1.88	0.55
31:EA:43:LEU:O	31:EA:109:ARG:NH1	2.39	0.55
37:KA:45:ARG:HH21	47:WA:2798:G:H5'	1.72	0.55
43:RA:16:ARG:HB3	47:WA:1977:G:C8	2.41	0.55
50:ZA:1652:G:O6	50:ZA:1672:U:O4	2.25	0.55
55:EB:212:ASP:OD1	55:EB:213:ALA:N	2.40	0.55
58:HB:408:VAL:HG13	58:HB:425:PHE:HB2	1.88	0.55
73:WB:80:ASP:OD1	73:WB:124:LYS:NZ	2.37	0.55
86:At:26:A:H61	86:At:44:G:H1	1.54	0.55
1:A:2:GLY:N	47:WA:3921:C:OP1	2.40	0.54
5:E:52:LEU:HG	5:E:53:VAL:HG23	1.87	0.54
47:WA:964:G:O2'	47:WA:2265:A:N6	2.36	0.54
47:WA:1665:C:O2'	47:WA:2322:G:N2	2.40	0.54
47:WA:3635:C:H2'	47:WA:3636:G:C8	2.42	0.54
47:WA:3809:A:O2'	50:ZA:1816:G:O2'	2.17	0.54
57:GB:198:ARG:O	57:GB:202:ASN:ND2	2.32	0.54
1:A:187:HIS:NE2	47:WA:1615:A:OP2	2.39	0.54
1:A:196:TRP:NE1	47:WA:3655:A:OP1	2.40	0.54
18:R:23:ARG:HH12	47:WA:1206:G:H5'	1.72	0.54
25:Y:90:PRO:O	25:Y:117:LYS:NZ	2.41	0.54
35:IA:21:ARG:NH2	35:IA:37:CYS:O	2.40	0.54
40:NA:36:GLN:OE1	40:NA:39:ARG:NH2	2.39	0.54
47:WA:56:A:H2'	47:WA:57:G:C8	2.42	0.54
47:WA:126:C:H2'	47:WA:127:G:H8	1.72	0.54
47:WA:3855:U:O2'	47:WA:4981:A:N3	2.39	0.54
52:BB:86:LEU:HB3	52:BB:98:THR:HB	1.88	0.54
52:BB:98:THR:O	52:BB:232:HIS:NE2	2.39	0.54
59:IB:27:TYR:HB3	59:IB:49:ARG:HH12	1.71	0.54
3:C:192:GLY:O	3:C:195:LYS:NZ	2.40	0.54
13:M:96:ARG:NH2	13:M:104:GLU:OE1	2.40	0.54
14:N:130:LYS:NZ	47:WA:2057:G:O5'	2.39	0.54
33:GA:87:LYS:O	33:GA:92:ARG:NH1	2.40	0.54
42:PA:38:PHE:O	42:PA:45:HIS:NE2	2.35	0.54
44:SA:41:G:O2'	50:ZA:1639:G:N2	2.41	0.54
47:WA:983:G:OP1	47:WA:1243:C:N4	2.40	0.54
47:WA:1200:G:N2	47:WA:1201:G:O6	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:5014:G:O2'	47:WA:5016:A:OP1	2.18	0.54
50:ZA:822:U:H3	50:ZA:826:A:H62	1.55	0.54
67:QB:35:SER:OG	67:QB:50:HIS:NE2	2.38	0.54
47:WA:39:A:H61	47:WA:1682:G:H21	1.56	0.54
47:WA:2485:G:H2'	47:WA:2486:A:H8	1.72	0.54
50:ZA:326:C:H4'	50:ZA:327:G:H21	1.72	0.54
50:ZA:373:G:OP1	62:LB:137:THR:OG1	2.21	0.54
50:ZA:1617:G:O6	66:PB:43:ARG:NH1	2.41	0.54
63:MB:52:LEU:HD23	63:MB:76:LEU:HD11	1.89	0.54
67:QB:158:PHE:O	67:QB:166:ARG:NH1	2.40	0.54
69:SB:51:ASP:OD2	69:SB:53:THR:OG1	2.25	0.54
70:TB:38:LYS:NZ	70:TB:40:ALA:O	2.38	0.54
77:AC:11:ALA:HB3	77:AC:33:ASP:HB2	1.89	0.54
1:A:29:LEU:O	1:A:123:ARG:NH1	2.40	0.54
6:F:213:SER:OG	6:F:246:MET:O	2.25	0.54
9:I:152:LEU:HB3	9:I:165:ILE:HD12	1.90	0.54
16:P:30:LYS:NZ	42:PA:8:MET:SD	2.75	0.54
18:R:95:ARG:NH1	18:R:112:ASP:OD2	2.41	0.54
24:X:11:ARG:HG3	47:WA:229:G:H5''	1.88	0.54
47:WA:428:G:H2'	47:WA:429:A:C8	2.42	0.54
47:WA:491:C:H2'	47:WA:492:G:H8	1.73	0.54
47:WA:735:G:H1	47:WA:934:G:N2	2.05	0.54
48:XA:28:C:O2'	48:XA:54:A:N1	2.41	0.54
50:ZA:15:U:O2'	50:ZA:669:A:N6	2.40	0.54
50:ZA:62:G:O2'	50:ZA:172:U:OP1	2.25	0.54
5:E:144:ARG:NH1	31:EA:110:ILE:OXT	2.36	0.54
11:K:109:SER:O	11:K:113:ASN:ND2	2.35	0.54
13:M:2:GLY:N	47:WA:115:C:OP1	2.41	0.54
13:M:5:LYS:HE2	34:HA:37:THR:HG22	1.90	0.54
15:O:96:VAL:HB	15:O:109:GLN:HE21	1.73	0.54
16:P:179:GLY:H	26:Z:51:GLY:HA2	1.72	0.54
17:Q:74:ARG:NE	47:WA:2893:U:OP2	2.40	0.54
26:Z:117:LEU:HD12	26:Z:118:PRO:HD2	1.90	0.54
40:NA:8:ARG:NH2	47:WA:4234:U:O4	2.35	0.54
42:PA:14:SER:HB3	42:PA:17:LEU:HG	1.88	0.54
42:PA:67:ARG:NH1	47:WA:667:G:OP2	2.40	0.54
43:RA:94:LYS:N	47:WA:1981:A:OP1	2.39	0.54
47:WA:67:C:OP2	47:WA:312:G:N2	2.37	0.54
50:ZA:16:G:H21	50:ZA:1195:A:H62	1.56	0.54
50:ZA:197:U:O4	50:ZA:202:G:O6	2.26	0.54
50:ZA:1688:C:H2'	50:ZA:1689:C:H6	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:GB:164:LYS:HG2	57:GB:165:GLU:HG3	1.89	0.54
71:UB:56:MET:HG3	71:UB:86:LYS:HD3	1.90	0.54
14:N:74:ARG:N	47:WA:4587:U:OP1	2.41	0.54
35:IA:44:LYS:N	47:WA:22:G:OP1	2.37	0.54
47:WA:262:G:H2'	47:WA:263:G:H8	1.73	0.54
47:WA:911:G:H2'	47:WA:912:G:H8	1.73	0.54
47:WA:1890:A:N6	47:WA:3875:G:O2'	2.40	0.54
47:WA:2311:G:O2'	49:YA:18:U:O2	2.26	0.54
49:YA:30:U:H2'	49:YA:31:G:C8	2.43	0.54
50:ZA:167:G:H21	57:GB:132:ARG:HB2	1.73	0.54
50:ZA:432:G:H2'	50:ZA:433:A:H8	1.72	0.54
55:EB:11:ARG:HA	55:EB:28:ALA:HB2	1.88	0.54
57:GB:136:LYS:NZ	57:GB:175:LYS:O	2.32	0.54
58:HB:355:PRO:HG2	58:HB:358:ARG:HG2	1.89	0.54
3:C:143:ARG:NH1	47:WA:2302:A:N7	2.56	0.54
22:V:102:LYS:HA	22:V:105:ARG:HD3	1.90	0.54
41:OA:30:GLU:HA	41:OA:33:GLN:HG2	1.89	0.54
47:WA:137:G:H2'	47:WA:138:G:C8	2.42	0.54
47:WA:1249:U:O4	47:WA:1268:G:O6	2.26	0.54
47:WA:4596:U:H2'	47:WA:4597:G:H8	1.72	0.54
50:ZA:557:U:H2'	50:ZA:558:G:C8	2.43	0.54
50:ZA:1092:G:OP1	64:NB:2:GLY:N	2.41	0.54
50:ZA:1285:G:OP2	63:MB:107:SER:OG	2.26	0.54
55:EB:162:ILE:HG22	55:EB:169:ILE:HA	1.90	0.54
83:GC:304:ASP:OD2	83:GC:308:ARG:NH2	2.41	0.54
1:A:30:ARG:NH1	1:A:33:ASP:OD2	2.40	0.54
7:G:282:ARG:NH2	7:G:285:GLU:OE1	2.41	0.54
33:GA:27:GLU:OE2	33:GA:46:LYS:NZ	2.37	0.54
47:WA:1972:A:H5'	85:b:37:SER:HB2	1.89	0.54
50:ZA:409:C:H2'	50:ZA:410:G:C8	2.43	0.54
50:ZA:1004:U:H2'	50:ZA:1005:G:H8	1.72	0.54
50:ZA:1079:C:H4'	50:ZA:1182:A:H61	1.73	0.54
50:ZA:1367:U:O2'	50:ZA:1466:G:O2'	2.25	0.54
50:ZA:1373:C:O2'	68:RB:10:LYS:NZ	2.28	0.54
83:GC:202:PRO:HG2	83:GC:243:PRO:HA	1.90	0.54
2:B:175:GLN:HG3	47:WA:4987:U:H4'	1.90	0.54
12:L:34:ASN:ND2	47:WA:1926:C:OP1	2.41	0.54
18:R:81:TRP:HB3	18:R:127:MET:HE3	1.90	0.54
19:S:68:THR:OG1	19:S:71:ALA:O	2.24	0.54
25:Y:3:LYS:O	25:Y:6:LYS:NZ	2.39	0.54
35:IA:12:ARG:NH2	47:WA:1619:G:O3'	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RA:61:LYS:HB2	43:RA:72:GLU:HG2	1.89	0.54
44:SA:26:A:H61	44:SA:44:A:H61	1.54	0.54
47:WA:1398:G:HO2'	47:WA:1470:C:HO2'	1.49	0.54
47:WA:1513:U:H2'	47:WA:1514:G:H8	1.72	0.54
47:WA:1972:A:N6	47:WA:2018:C:OP2	2.33	0.54
55:EB:163:ASP:HB3	55:EB:166:THR:HB	1.88	0.54
7:G:96:GLN:O	47:WA:4126:G:N2	2.40	0.53
13:M:181:HIS:O	13:M:195:ARG:NH2	2.41	0.53
24:X:11:ARG:NH1	47:WA:229:G:OP1	2.39	0.53
47:WA:1482:C:O2'	47:WA:1484:G:OP2	2.25	0.53
47:WA:1857:G:O6	47:WA:1882:G:N2	2.41	0.53
47:WA:3655:A:C2	47:WA:3694:A:H4'	2.43	0.53
47:WA:3699:U:O2'	47:WA:3819:A:OP2	2.24	0.53
50:ZA:920:A:O2'	50:ZA:922:A:O5'	2.26	0.53
50:ZA:1389:C:OP1	68:RB:43:SER:OG	2.21	0.53
59:IB:178:ARG:HE	59:IB:181:GLN:HG3	1.73	0.53
61:KB:51:SER:OG	61:KB:55:ARG:NH1	2.41	0.53
64:NB:99:ARG:NH2	64:NB:119:GLU:OE2	2.41	0.53
85:b:47:LEU:O	85:b:50:LYS:N	2.40	0.53
9:I:15:LYS:NZ	47:WA:1864:U:O3'	2.41	0.53
26:Z:65:ARG:NH2	47:WA:86:U:O2'	2.41	0.53
47:WA:1734:C:H2'	47:WA:1735:G:C8	2.43	0.53
47:WA:4276:A:H2'	47:WA:4277:G:H8	1.73	0.53
58:HB:245:LYS:NZ	58:HB:269:GLU:OE2	2.42	0.53
7:G:87:LYS:HG2	7:G:89:PRO:HD3	1.89	0.53
19:S:91:VAL:HB	19:S:96:ILE:HD11	1.91	0.53
30:DA:89:LEU:HD13	30:DA:118:LEU:HD22	1.89	0.53
47:WA:4241:A:H2'	47:WA:4242:G:H8	1.73	0.53
50:ZA:1342:U:N3	50:ZA:1483:A:N1	2.48	0.53
50:ZA:1472:C:N4	50:ZA:1476:A:H62	2.04	0.53
21:U:21:PRO:HA	21:U:54:ALA:HA	1.89	0.53
21:U:65:VAL:HB	21:U:73:ARG:HA	1.89	0.53
23:W:110:LYS:HG3	23:W:121:VAL:HB	1.90	0.53
47:WA:2424:C:HO2'	47:WA:3859:G:HO2'	1.53	0.53
47:WA:5055:U:OP1	47:WA:5056:C:N4	2.41	0.53
50:ZA:974:C:H2'	50:ZA:975:G:H8	1.72	0.53
53:CB:72:ASP:OD2	53:CB:272:HIS:NE2	2.40	0.53
35:IA:20:ARG:NH1	35:IA:39:TYR:OH	2.42	0.53
42:PA:39:ARG:NH1	47:WA:2268:C:O2'	2.41	0.53
47:WA:759:G:H2'	47:WA:760:G:H8	1.73	0.53
47:WA:2554:G:H21	47:WA:2768:A:H62	1.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:3952:U:H2'	47:WA:3953:G:C8	2.44	0.53
50:ZA:527:C:H2'	50:ZA:528:A:H8	1.74	0.53
50:ZA:959:G:OP1	65:OB:104:ARG:NH2	2.41	0.53
14:N:12:ARG:HB2	14:N:37:ARG:HD2	1.91	0.53
15:O:71:ARG:NH2	15:O:139:ASP:OD1	2.41	0.53
26:Z:71:PRO:HG2	26:Z:108:TYR:HA	1.91	0.53
40:NA:15:CYS:SG	40:NA:19:GLN:NE2	2.82	0.53
47:WA:4421:U:OP1	47:WA:4423:C:N4	2.38	0.53
51:AB:157:VAL:O	72:VB:65:SER:OG	2.26	0.53
63:MB:92:CYS:SG	63:MB:102:LYS:NZ	2.79	0.53
22:V:23:ARG:HH21	22:V:27:LYS:HG3	1.74	0.53
42:PA:35:ARG:NH2	47:WA:2267:G:OP1	2.42	0.53
47:WA:3920:G:OP2	90:WA:5179:SPD:N10	2.41	0.53
50:ZA:616:A:H62	50:ZA:625:G:N2	2.07	0.53
55:EB:122:LYS:NZ	55:EB:124:CYS:SG	2.69	0.53
12:L:96:GLU:OE2	12:L:100:ARG:NH2	2.41	0.53
14:N:94:ARG:HD2	47:WA:1311:C:H5''	1.91	0.53
21:U:43:LYS:HD3	21:U:62:MET:HE2	1.90	0.53
47:WA:1797:A:N3	48:XA:79:U:O2'	2.40	0.53
50:ZA:1465:A:OP1	68:RB:56:HIS:NE2	2.38	0.53
5:E:160:HIS:HB3	5:E:163:LYS:HD2	1.89	0.53
10:J:136:ARG:HG3	10:J:157:ILE:HD11	1.89	0.53
10:J:146:ARG:HG2	10:J:147:ARG:HG3	1.89	0.53
16:P:37:ARG:NH1	47:WA:2089:C:OP2	2.39	0.53
30:DA:37:LYS:HD2	30:DA:38:PRO:HD2	1.91	0.53
47:WA:1974:G:N1	47:WA:1997:G:O6	2.42	0.53
47:WA:4346:U:H3	47:WA:4370:G:H1	1.57	0.53
47:WA:4637:A:H2	47:WA:4665:G:H21	1.56	0.53
47:WA:4706:C:H2'	47:WA:4707:A:H8	1.74	0.53
50:ZA:1644:C:H4'	67:QB:166:ARG:HB2	1.90	0.53
19:S:8:ARG:NH1	47:WA:4335:C:O2	2.42	0.53
23:W:65:ALA:HB2	33:GA:69:LEU:HD11	1.91	0.53
37:KA:2:SER:O	37:KA:5:LYS:NZ	2.35	0.53
44:SA:17:G:OP2	44:SA:60:A:O2'	2.26	0.53
47:WA:1771:G:H2'	47:WA:1772:A:O4'	2.09	0.53
47:WA:4239:C:N4	47:WA:4240:G:O6	2.41	0.53
50:ZA:106:C:H2'	50:ZA:107:A:H8	1.75	0.53
50:ZA:924:G:O6	50:ZA:1019:C:N4	2.42	0.53
52:BB:144:LYS:HD3	52:BB:208:HIS:HB3	1.90	0.53
53:CB:192:LEU:HB3	53:CB:227:ARG:HB3	1.91	0.53
56:FB:50:PRO:HG2	56:FB:90:VAL:HG22	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:WB:66:THR:HG21	73:WB:68:ARG:HH11	1.73	0.53
83:GC:237:ASN:ND2	83:GC:286:CYS:O	2.37	0.53
85:b:35:VAL:HG23	85:b:40:MET:HG2	1.91	0.53
16:P:178:ARG:HD3	26:Z:53:PHE:HB2	1.91	0.52
25:Y:79:HIS:ND1	47:WA:2582:U:O2'	2.41	0.52
43:RA:9:GLU:O	43:RA:65:GLN:NE2	2.42	0.52
47:WA:359:A:N3	47:WA:363:A:O2'	2.41	0.52
47:WA:2411:U:H4'	47:WA:2430:A:H4'	1.91	0.52
47:WA:2642:G:H2'	47:WA:2643:A:C8	2.43	0.52
47:WA:4512:A:N1	47:WA:4594:C:H4'	2.24	0.52
55:EB:104:ASP:HB2	55:EB:110:ALA:HB2	1.90	0.52
59:IB:80:ASP:OD1	59:IB:81:VAL:N	2.42	0.52
2:B:224:LYS:HG2	2:B:340:THR:HB	1.91	0.52
2:B:231:VAL:HG11	2:B:251:VAL:HG23	1.91	0.52
6:F:226:PHE:N	6:F:232:ALA:O	2.42	0.52
11:K:35:ARG:NH1	47:WA:105:A:O2'	2.42	0.52
16:P:69:LYS:NZ	47:WA:1460:C:OP1	2.35	0.52
16:P:168:ARG:NH1	47:WA:86:U:OP2	2.41	0.52
18:R:5:GLY:O	18:R:111:ARG:NH2	2.42	0.52
44:SA:8:U:O2'	44:SA:21:A:N1	2.37	0.52
50:ZA:5:U:H2'	50:ZA:6:G:H8	1.73	0.52
64:NB:40:LEU:HD12	64:NB:50:ILE:HG23	1.91	0.52
2:B:213:GLN:NE2	2:B:285:TYR:O	2.39	0.52
6:F:75:ARG:NE	47:WA:731:G:OP2	2.37	0.52
14:N:54:TYR:OH	14:N:73:PHE:O	2.28	0.52
35:IA:76:HIS:NE2	49:YA:93:C:OP1	2.34	0.52
42:PA:67:ARG:HA	42:PA:70:GLN:HE21	1.74	0.52
47:WA:3923:U:H1'	47:WA:4545:G:H21	1.74	0.52
50:ZA:12:U:H5''	53:CB:110:MET:HE2	1.91	0.52
50:ZA:183:G:O2'	50:ZA:184:G:O5'	2.27	0.52
52:BB:106:THR:HG22	52:BB:108:ASP:H	1.74	0.52
69:SB:23:ARG:HH21	76:ZB:80:ARG:HH21	1.56	0.52
27:AA:47:LYS:NZ	47:WA:1466:C:O3'	2.42	0.52
39:MA:1:MET:HB2	50:ZA:1706:G:H5'	1.91	0.52
47:WA:4:G:H2'	47:WA:5:A:H8	1.73	0.52
47:WA:424:U:H2'	47:WA:425:U:C6	2.44	0.52
47:WA:1317:C:N4	47:WA:1318:G:O6	2.42	0.52
47:WA:1334:C:H2'	47:WA:1335:A:C8	2.43	0.52
47:WA:2498:G:H2'	47:WA:2499:C:C6	2.45	0.52
50:ZA:1337:C:H4'	71:UB:67:LYS:HB3	1.91	0.52
50:ZA:1743:G:H21	50:ZA:1791:A:N6	2.01	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:OB:142:ARG:O	77:AC:22:ARG:NH1	2.42	0.52
11:K:7:GLY:O	26:Z:49:HIS:NE2	2.37	0.52
13:M:8:GLN:NE2	47:WA:279:A:OP2	2.43	0.52
13:M:90:ASN:ND2	47:WA:3930:A:OP1	2.43	0.52
20:T:60:VAL:HG13	20:T:61:VAL:HG23	1.91	0.52
20:T:111:GLU:OE1	20:T:113:ARG:NH1	2.43	0.52
27:AA:56:LYS:O	27:AA:60:ASN:ND2	2.35	0.52
47:WA:1647:C:H2'	47:WA:1648:A:C8	2.44	0.52
47:WA:2555:A:H2	47:WA:2767:A:H62	1.57	0.52
47:WA:3850:U:O2'	47:WA:4636:U:O4	2.26	0.52
47:WA:4260:C:H2'	47:WA:4261:C:C6	2.43	0.52
47:WA:5046:A:H2'	47:WA:5047:G:H8	1.74	0.52
50:ZA:409:C:H2'	50:ZA:410:G:H8	1.74	0.52
50:ZA:652:U:H2'	50:ZA:653:A:C8	2.44	0.52
50:ZA:1425:G:H5''	67:QB:57:LEU:HD22	1.90	0.52
60:JB:131:ARG:NH1	60:JB:131:ARG:O	2.43	0.52
64:NB:24:THR:O	64:NB:27:LYS:NZ	2.43	0.52
83:GC:91:ASP:OD2	83:GC:93:THR:OG1	2.23	0.52
5:E:133:LYS:HG3	47:WA:1286:G:H21	1.75	0.52
47:WA:478:G:H2'	47:WA:479:G:H8	1.75	0.52
50:ZA:224:A:OP1	62:LB:20:LYS:NZ	2.40	0.52
50:ZA:643:A:OP1	60:JB:38:ARG:NH2	2.43	0.52
50:ZA:836:G:C2	75:YB:7:ILE:HG22	2.43	0.52
55:EB:203:GLY:HA2	62:LB:42:LEU:HD22	1.92	0.52
63:MB:42:LEU:O	63:MB:72:HIS:ND1	2.43	0.52
2:B:189:THR:HG23	2:B:192:GLU:H	1.75	0.52
3:C:78:ARG:NH1	3:C:88:GLY:O	2.43	0.52
10:J:146:ARG:NH1	48:XA:27:G:OP1	2.43	0.52
13:M:116:LEU:HD22	13:M:135:ILE:HD11	1.90	0.52
13:M:172:ARG:NH1	47:WA:62:A:OP1	2.43	0.52
33:GA:10:ARG:NH2	49:YA:65:A:O2'	2.42	0.52
47:WA:1766:G:C8	47:WA:1768:A:H5''	2.45	0.52
50:ZA:432:G:H2'	50:ZA:433:A:C8	2.43	0.52
50:ZA:1308:U:O2'	82:FC:134:SER:N	2.41	0.52
51:AB:145:ILE:HG12	51:AB:159:ILE:HB	1.90	0.52
52:BB:107:ARG:NH1	65:OB:133:THR:O	2.41	0.52
3:C:339:THR:HG22	3:C:342:ARG:HH22	1.74	0.52
5:E:80:SER:OG	47:WA:1272:A:N1	2.42	0.52
5:E:118:TYR:HB3	47:WA:457:G:H5''	1.92	0.52
14:N:113:ASP:OD1	14:N:114:LYS:N	2.42	0.52
47:WA:153:G:H2'	47:WA:154:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:1202:U:H2'	50:ZA:1203:G:H8	1.75	0.52
69:SB:14:ARG:NH1	69:SB:19:ASN:OD1	2.36	0.52
2:B:261:ARG:HB2	14:N:64:THR:HG21	1.92	0.52
6:F:229:GLY:HA3	18:R:2:LYS:HD3	1.92	0.52
47:WA:1496:U:H2'	47:WA:1497:G:C8	2.44	0.52
47:WA:1558:C:O2'	47:WA:2671:C:OP1	2.24	0.52
47:WA:4276:A:H2'	47:WA:4277:G:C8	2.45	0.52
47:WA:4929:G:H5''	47:WA:4930:C:C5	2.45	0.52
47:WA:5046:A:H2'	47:WA:5047:G:C8	2.45	0.52
50:ZA:92:A:H61	50:ZA:444:G:H1'	1.75	0.52
50:ZA:659:G:O2'	50:ZA:662:G:O3'	2.28	0.52
50:ZA:928:G:H2'	50:ZA:929:G:C8	2.45	0.52
50:ZA:980:A:H2'	50:ZA:981:A:C8	2.45	0.52
60:JB:133:ARG:HB3	60:JB:143:ASN:HD22	1.75	0.52
4:D:65:ALA:HB2	4:D:74:ILE:HD13	1.92	0.52
4:D:204:VAL:HG12	4:D:208:MET:HE2	1.91	0.52
13:M:158:HIS:HB3	13:M:161:MET:HB2	1.92	0.52
14:N:34:VAL:HG22	14:N:103:LYS:HB3	1.92	0.52
27:AA:95:ARG:NH1	47:WA:1267:G:OP2	2.43	0.52
42:PA:28:GLU:OE2	42:PA:41:ASN:ND2	2.43	0.52
47:WA:169:A:N1	47:WA:267:G:C2	2.78	0.52
47:WA:470:A:H62	47:WA:685:G:N2	2.08	0.52
47:WA:1788:A:O2'	47:WA:1790:A:OP2	2.25	0.52
47:WA:2285:G:H2'	47:WA:2286:G:H8	1.75	0.52
47:WA:2542:C:H2'	47:WA:2543:G:H8	1.75	0.52
47:WA:3692:U:H2'	47:WA:3693:G:O4'	2.10	0.52
47:WA:3734:A:H2'	47:WA:3735:A:C8	2.45	0.52
47:WA:4771:G:H2'	47:WA:4772:U:C6	2.45	0.52
50:ZA:562:U:H1'	60:JB:132:GLN:HB3	1.92	0.52
50:ZA:1452:A:H61	50:ZA:1473:G:H21	1.58	0.52
53:CB:191:VAL:HG11	53:CB:236:PHE:HA	1.92	0.52
3:C:195:LYS:HE3	47:WA:2335:G:H5''	1.92	0.51
28:BA:78:ASN:HD21	41:OA:43:GLY:HA3	1.74	0.51
47:WA:86:U:H2'	47:WA:87:A:C8	2.43	0.51
47:WA:759:G:H2'	47:WA:760:G:C8	2.45	0.51
47:WA:1079:G:H22	47:WA:1244:A:H2	1.58	0.51
47:WA:1986:A:C8	47:WA:2013:C:H4'	2.44	0.51
47:WA:3918:G:H2'	47:WA:3919:A:H8	1.75	0.51
50:ZA:223:C:H5''	62:LB:20:LYS:HE2	1.93	0.51
50:ZA:808:A:H2'	50:ZA:809:A:C8	2.45	0.51
58:HB:377:ILE:HG21	58:HB:380:LYS:HE3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SB:36:VAL:HG21	69:SB:71:MET:HE3	1.92	0.51
83:GC:172:LYS:HE3	83:GC:192:THR:HA	1.90	0.51
5:E:164:ARG:NH1	12:L:106:ASP:OD2	2.43	0.51
13:M:53:TYR:HB2	13:M:133:ILE:HD13	1.92	0.51
30:DA:104:SER:HB2	47:WA:2305:C:H5''	1.92	0.51
47:WA:1528:G:H2'	47:WA:1529:A:H8	1.75	0.51
47:WA:2031:A:H2'	47:WA:2032:A:C8	2.45	0.51
50:ZA:1812:U:H2'	50:ZA:1813:A:H8	1.74	0.51
55:EB:206:ASP:HB2	55:EB:222:LEU:HD12	1.92	0.51
14:N:29:LEU:HB3	31:EA:10:ILE:HG21	1.93	0.51
16:P:67:ILE:HD12	16:P:96:PRO:HD2	1.92	0.51
31:EA:78:HIS:HB2	31:EA:85:ARG:HG3	1.92	0.51
40:NA:11:PHE:O	40:NA:81:ARG:NH1	2.42	0.51
47:WA:1808:G:H2'	47:WA:1809:C:H6	1.75	0.51
50:ZA:5:U:H2'	50:ZA:6:G:C8	2.45	0.51
50:ZA:807:G:H2'	50:ZA:808:A:C8	2.46	0.51
50:ZA:1662:U:O4	50:ZA:1663:A:N6	2.40	0.51
58:HB:356:ARG:HD3	58:HB:359:THR:HG21	1.91	0.51
79:CC:17:VAL:HA	79:CC:30:VAL:HG23	1.92	0.51
83:GC:87:LEU:HB2	83:GC:101:PHE:HB2	1.91	0.51
20:T:25:CYS:HB3	20:T:112:LEU:HD13	1.93	0.51
26:Z:36:GLY:HA3	26:Z:40:HIS:CD2	2.46	0.51
37:KA:16:LYS:HG3	37:KA:49:LEU:HD21	1.92	0.51
47:WA:49:U:H2'	47:WA:50:C:H6	1.76	0.51
47:WA:714:C:H2'	47:WA:715:G:H8	1.74	0.51
47:WA:990:C:H2'	47:WA:991:C:H6	1.74	0.51
47:WA:1963:G:N2	47:WA:2026:G:O2'	2.43	0.51
47:WA:4187:G:H2'	47:WA:4188:A:H8	1.75	0.51
47:WA:4565:U:C2	47:WA:4566:A:C8	2.98	0.51
47:WA:4652:G:H4'	47:WA:5010:C:H4'	1.91	0.51
50:ZA:14:C:H2'	50:ZA:15:U:C6	2.45	0.51
50:ZA:67:C:O4'	57:GB:172:LYS:NZ	2.43	0.51
50:ZA:561:A:H5'	60:JB:164:PRO:HG2	1.93	0.51
50:ZA:941:C:H2'	50:ZA:942:G:C8	2.45	0.51
50:ZA:1103:C:H2'	50:ZA:1104:G:H8	1.76	0.51
50:ZA:1778:C:H2'	50:ZA:1779:G:C8	2.45	0.51
66:PB:68:PRO:HG2	66:PB:71:GLU:HB3	1.91	0.51
75:YB:29:HIS:O	75:YB:29:HIS:ND1	2.43	0.51
2:B:163:LEU:HB3	2:B:180:LEU:HD11	1.91	0.51
5:E:184:LEU:O	47:WA:4885:C:N4	2.43	0.51
11:K:101:ARG:NE	47:WA:75:G:O2'	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:120:GLN:HG2	50:ZA:322:C:H5''	1.92	0.51
45:TA:49:C:H2'	45:TA:50:A:H8	1.76	0.51
47:WA:1727:U:H2'	47:WA:1728:U:C6	2.45	0.51
47:WA:2479:A:H2	47:WA:2480:C:H41	1.57	0.51
50:ZA:92:A:H1'	55:EB:3:ARG:HH12	1.74	0.51
7:G:139:VAL:HG11	7:G:238:LYS:HG3	1.92	0.51
11:K:25:TRP:HB2	13:M:201:HIS:HA	1.93	0.51
18:R:164:LYS:HB2	18:R:165:PRO:HD3	1.93	0.51
47:WA:62:A:N3	47:WA:77:U:O2'	2.38	0.51
47:WA:2558:G:H2'	47:WA:2559:G:C8	2.45	0.51
47:WA:3612:A:H2'	47:WA:3613:A:C8	2.46	0.51
47:WA:5049:C:O2'	47:WA:5052:C:OP2	2.26	0.51
50:ZA:12:U:H2'	50:ZA:13:C:H6	1.76	0.51
50:ZA:524:U:P	81:EC:104:ARG:HH21	2.33	0.51
50:ZA:649:U:H2'	50:ZA:650:A:H8	1.75	0.51
50:ZA:964:A:O2'	50:ZA:1054:G:O2'	2.27	0.51
50:ZA:1030:A:H2'	50:ZA:1031:A:H8	1.76	0.51
58:HB:258:GLU:OE1	58:HB:258:GLU:N	2.44	0.51
73:WB:18:GLU:HG2	73:WB:65:LEU:HD13	1.92	0.51
78:BC:74:THR:OG1	78:BC:77:CYS:SG	2.68	0.51
2:B:223:THR:HG23	47:WA:4626:A:H5'	1.93	0.51
7:G:90:LYS:NZ	47:WA:4128:C:OP1	2.44	0.51
10:J:27:GLY:HA2	10:J:68:ILE:HG23	1.92	0.51
27:AA:49:HIS:HB3	27:AA:52:LYS:HE2	1.92	0.51
35:IA:3:LYS:HB3	47:WA:3644:A:C4	2.45	0.51
37:KA:21:ARG:NH1	49:YA:52:A:OP1	2.44	0.51
45:TA:23:A:H2'	45:TA:24:G:C8	2.46	0.51
47:WA:274:C:H2'	47:WA:275:C:C6	2.46	0.51
47:WA:1513:U:H2'	47:WA:1514:G:C8	2.46	0.51
47:WA:2388:U:H2'	47:WA:2389:G:H8	1.76	0.51
47:WA:2733:C:H2'	47:WA:2734:G:H8	1.76	0.51
47:WA:3654:A:N6	47:WA:3693:G:O2'	2.43	0.51
47:WA:3877:G:N1	47:WA:3881:G:OP1	2.35	0.51
50:ZA:817:G:N2	50:ZA:847:A:H62	2.06	0.51
50:ZA:848:U:H2'	50:ZA:849:A:H8	1.76	0.51
50:ZA:1294:G:H2'	50:ZA:1295:A:H8	1.75	0.51
50:ZA:1627:C:OP1	70:TB:83:GLN:NE2	2.44	0.51
50:ZA:1656:G:H1	50:ZA:1668:U:H3	1.58	0.51
57:GB:140:ARG:O	57:GB:144:LEU:CB	2.57	0.51
83:GC:225:LYS:HZ3	83:GC:227:LEU:HD11	1.76	0.51
2:B:298:LEU:HD13	2:B:300:LYS:HE3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:31:ILE:HB	9:I:66:GLU:HB2	1.93	0.51
37:KA:24:PRO:HG2	37:KA:27:ILE:HB	1.92	0.51
42:PA:112:ARG:NH1	47:WA:2266:C:OP1	2.44	0.51
47:WA:1335:A:H2'	47:WA:1336:A:C8	2.46	0.51
50:ZA:931:C:H2'	50:ZA:932:G:C8	2.46	0.51
50:ZA:1513:C:H2'	50:ZA:1514:G:H8	1.75	0.51
50:ZA:1625:U:H2'	50:ZA:1626:C:H6	1.75	0.51
69:SB:124:ARG:HB2	69:SB:131:VAL:HG13	1.93	0.51
47:WA:494:G:H2'	47:WA:495:C:C6	2.45	0.51
47:WA:1935:G:H2'	47:WA:1936:A:C8	2.45	0.51
50:ZA:443:U:O4	50:ZA:447:A:N7	2.43	0.51
1:A:198:ARG:NH2	47:WA:3690:U:OP2	2.44	0.51
2:B:234:ARG:NH2	47:WA:4568:U:O2'	2.44	0.51
15:O:151:ALA:HB3	15:O:172:PRO:HG2	1.93	0.51
21:U:13:LYS:O	47:WA:4619:G:O2'	2.28	0.51
47:WA:2869:C:N4	47:WA:2886:G:O6	2.44	0.51
47:WA:4350:A:O2'	47:WA:4352:C:OP2	2.25	0.51
47:WA:4994:G:H2'	47:WA:4995:G:C8	2.46	0.51
83:GC:132:TRP:CD1	83:GC:138:CYS:HA	2.46	0.51
2:B:113:GLU:OE2	2:B:169:ARG:N	2.43	0.50
8:H:43:VAL:HG12	8:H:59:LYS:HD3	1.92	0.50
35:IA:52:LYS:HG2	35:IA:55:ARG:HH22	1.76	0.50
47:WA:308:G:H8	47:WA:310:G:H1'	1.75	0.50
47:WA:1502:A:H5''	47:WA:1503:C:H5'	1.93	0.50
47:WA:2092:U:OP1	47:WA:2268:C:N4	2.44	0.50
47:WA:3647:U:O2'	47:WA:4555:A:N3	2.40	0.50
49:YA:8:U:H2'	49:YA:9:A:C8	2.46	0.50
49:YA:67:U:H2'	49:YA:68:G:H8	1.74	0.50
50:ZA:917:U:H1'	58:HB:356:ARG:HG2	1.93	0.50
50:ZA:940:U:H3	50:ZA:1002:U:H3	1.59	0.50
50:ZA:1447:G:OP1	71:UB:85:HIS:ND1	2.39	0.50
74:XB:90:CYS:HB3	74:XB:130:LEU:HD11	1.93	0.50
3:C:306:ARG:HG2	47:WA:2101:C:H3'	1.93	0.50
4:D:146:LEU:HD22	4:D:163:LEU:HD13	1.93	0.50
35:IA:33:THR:HG22	35:IA:40:PRO:HG2	1.92	0.50
44:SA:34:A:H61	46:VA:21:C:H42	1.58	0.50
47:WA:1363:G:H2'	47:WA:1364:G:H8	1.76	0.50
47:WA:4742:G:N2	47:WA:4745:G:OP2	2.44	0.50
47:WA:4763:G:H2'	47:WA:4764:A:H8	1.76	0.50
50:ZA:24:C:H2'	50:ZA:25:A:C8	2.47	0.50
50:ZA:60:A:N3	50:ZA:316:G:O2'	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:941:C:H2'	50:ZA:942:G:H8	1.77	0.50
50:ZA:1781:A:H2'	50:ZA:1782:G:H8	1.73	0.50
50:ZA:1856:C:H2'	50:ZA:1857:G:C8	2.46	0.50
54:DB:260:PRO:HA	83:GC:190:GLY:HA3	1.93	0.50
7:G:276:ARG:HG3	7:G:280:ASN:HB2	1.92	0.50
12:L:70:GLN:NE2	47:WA:939:A:N1	2.51	0.50
24:X:74:TYR:OH	49:YA:75:G:OP2	2.25	0.50
44:SA:51:C:H2'	44:SA:52:G:H8	1.76	0.50
47:WA:1677:C:O2'	47:WA:1678:C:OP1	2.25	0.50
50:ZA:107:A:H2'	50:ZA:108:G:C8	2.46	0.50
50:ZA:1238:U:H3	50:ZA:1242:U:H5	1.58	0.50
63:MB:41:ALA:HA	63:MB:45:ARG:HB2	1.93	0.50
69:SB:30:ILE:HG22	69:SB:36:VAL:HG11	1.93	0.50
69:SB:98:VAL:HG11	69:SB:106:LYS:HG3	1.93	0.50
2:B:240:LEU:HD21	2:B:252:ALA:HB2	1.92	0.50
7:G:97:ASP:OD1	7:G:98:ILE:N	2.44	0.50
19:S:2:THR:N	47:WA:4222:A:OP2	2.44	0.50
37:KA:37:TYR:O	47:WA:362:A:N6	2.43	0.50
43:RA:37:LEU:HD12	43:RA:42:VAL:HB	1.94	0.50
47:WA:1886:C:H2'	47:WA:1887:G:H8	1.76	0.50
47:WA:4908:C:H2'	47:WA:4909:G:H8	1.77	0.50
50:ZA:788:G:H2'	50:ZA:789:G:C8	2.46	0.50
50:ZA:1271:C:OP1	82:FC:90:LYS:NZ	2.41	0.50
50:ZA:1492:U:O2'	50:ZA:1495:G:OP1	2.24	0.50
61:KB:7:ASN:ND2	61:KB:39:ASN:O	2.44	0.50
13:M:44:ARG:NH1	47:WA:280:G:OP2	2.34	0.50
13:M:155:VAL:O	13:M:162:ARG:NH2	2.45	0.50
22:V:116:LYS:NZ	50:ZA:330:G:O6	2.39	0.50
34:HA:29:ARG:HE	34:HA:32:ARG:HB3	1.76	0.50
43:RA:16:ARG:CZ	47:WA:1976:U:H4'	2.42	0.50
47:WA:212:A:H2'	47:WA:213:G:H8	1.75	0.50
47:WA:3600:C:H2'	47:WA:3601:A:H8	1.76	0.50
47:WA:3686:G:H2'	47:WA:3687:C:C6	2.47	0.50
47:WA:4241:A:H2'	47:WA:4242:G:C8	2.46	0.50
50:ZA:202:G:H2'	50:ZA:203:G:C8	2.47	0.50
50:ZA:1036:A:N3	50:ZA:1844:U:O2'	2.45	0.50
86:At:58:A:O2'	86:At:60:U:OP2	2.30	0.50
4:D:23:ARG:NH2	47:WA:4282:A:OP2	2.43	0.50
5:E:172:SER:OG	5:E:217:ASP:OD2	2.30	0.50
8:H:92:MET:HG2	8:H:181:VAL:HG22	1.93	0.50
8:H:94:SER:HB3	8:H:142:ASP:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:187:LYS:NZ	16:P:188:ASN:O	2.42	0.50
37:KA:48:LYS:NZ	47:WA:2793:C:OP1	2.43	0.50
47:WA:299:C:H2'	47:WA:300:A:C8	2.44	0.50
47:WA:1606:G:H2'	47:WA:1607:G:C8	2.47	0.50
47:WA:3847:A:H4'	47:WA:4670:U:H4'	1.93	0.50
50:ZA:319:C:OP1	50:ZA:319:C:H4'	2.12	0.50
50:ZA:522:A:OP2	60:JB:45:ARG:NH1	2.45	0.50
50:ZA:841:G:O4'	75:YB:8:ARG:NH1	2.44	0.50
50:ZA:1798:C:H2'	50:ZA:1799:G:O4'	2.12	0.50
53:CB:244:ILE:O	53:CB:247:THR:OG1	2.27	0.50
55:EB:100:ARG:HB2	55:EB:114:ILE:HD13	1.92	0.50
83:GC:223:GLU:HB2	83:GC:225:LYS:HE3	1.93	0.50
1:A:178:PRO:HD2	41:OA:26:VAL:HG22	1.94	0.50
2:B:261:ARG:HD3	47:WA:3872:C:H4'	1.93	0.50
47:WA:1384:G:H2'	47:WA:1385:G:H8	1.77	0.50
47:WA:1678:C:H41	47:WA:4380:A:H2'	1.76	0.50
50:ZA:65:C:O2'	50:ZA:67:C:OP2	2.21	0.50
50:ZA:107:A:H2'	50:ZA:108:G:H8	1.77	0.50
50:ZA:388:U:H2'	50:ZA:389:A:C8	2.47	0.50
50:ZA:1536:G:H2'	50:ZA:1537:A:C8	2.47	0.50
11:K:16:LYS:HG2	47:WA:46:U:H5''	1.94	0.50
47:WA:260:C:H2'	47:WA:261:G:H8	1.77	0.50
47:WA:1332:A:H5''	47:WA:3867:A:H5''	1.93	0.50
47:WA:2813:G:H22	47:WA:2815:A:H3'	1.76	0.50
47:WA:4701:U:H1'	47:WA:4702:A:H5''	1.93	0.50
50:ZA:183:G:O2'	50:ZA:184:G:O4'	2.29	0.50
50:ZA:600:G:H2'	50:ZA:601:G:C8	2.46	0.50
51:AB:156:TYR:OH	72:VB:61:ARG:NH1	2.45	0.50
83:GC:294:ASP:OD2	83:GC:296:GLN:NE2	2.40	0.50
16:P:14:ARG:NH2	47:WA:2085:C:OP2	2.44	0.50
22:V:105:ARG:HG2	50:ZA:328:U:C6	2.46	0.50
43:RA:135:THR:HG22	47:WA:1975:G:H21	1.77	0.50
47:WA:1300:C:H2'	47:WA:1301:G:H8	1.76	0.50
47:WA:2031:A:H2'	47:WA:2032:A:H8	1.77	0.50
47:WA:2419:A:H61	47:WA:2432:C:H1'	1.77	0.50
47:WA:2753:G:H2'	47:WA:2754:G:H8	1.77	0.50
47:WA:3935:G:H2'	47:WA:3936:G:H8	1.77	0.50
49:YA:28:C:H2'	49:YA:29:G:C8	2.46	0.50
50:ZA:522:A:OP1	60:JB:45:ARG:NH2	2.45	0.50
50:ZA:553:U:OP1	81:EC:112:ASN:ND2	2.45	0.50
50:ZA:1232:U:H2'	50:ZA:1233:G:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:1541:G:H4'	70:TB:15:VAL:HG11	1.94	0.50
70:TB:22:LEU:HG	70:TB:28:LEU:HD21	1.94	0.50
1:A:225:ILE:HD13	1:A:234:LYS:HA	1.93	0.49
1:A:243:THR:N	47:WA:3747:U:O2'	2.43	0.49
5:E:117:ARG:HH11	42:PA:87:ARG:HH22	1.59	0.49
5:E:273:TYR:O	5:E:276:SER:OG	2.27	0.49
22:V:91:MET:O	22:V:95:ASN:ND2	2.42	0.49
41:OA:38:THR:HA	41:OA:45:THR:HA	1.94	0.49
42:PA:90:LEU:HG	42:PA:111:ILE:HG23	1.94	0.49
47:WA:975:G:OP1	47:WA:2261:G:N2	2.45	0.49
47:WA:1571:U:H2'	47:WA:1572:G:C8	2.45	0.49
47:WA:1872:C:H2'	47:WA:1873:A:H8	1.77	0.49
47:WA:3687:C:H2'	47:WA:3688:G:C8	2.44	0.49
47:WA:4644:U:H2'	47:WA:4645:G:H8	1.77	0.49
50:ZA:126:G:H21	50:ZA:180:G:H21	1.59	0.49
50:ZA:440:G:H2'	50:ZA:441:C:C6	2.47	0.49
50:ZA:928:G:H21	78:BC:68:GLY:HA2	1.77	0.49
1:A:18:ALA:HB2	47:WA:3679:U:H5''	1.94	0.49
8:H:128:MET:HE2	8:H:134:CYS:HB2	1.94	0.49
13:M:35:ALA:HA	13:M:65:ARG:HG2	1.95	0.49
14:N:168:TYR:OH	47:WA:4770:G:OP1	2.30	0.49
21:U:107:ASN:HD21	21:U:111:GLU:HB2	1.77	0.49
24:X:31:SER:HA	24:X:48:PRO:HA	1.93	0.49
47:WA:1736:G:N2	47:WA:1737:U:O4	2.38	0.49
47:WA:3850:U:H2'	47:WA:3851:A:C8	2.43	0.49
47:WA:4273:A:H2'	47:WA:4274:G:C4	2.47	0.49
47:WA:4690:C:H2'	47:WA:4691:U:C6	2.46	0.49
50:ZA:822:U:O4	50:ZA:826:A:N7	2.45	0.49
50:ZA:1330:G:N2	50:ZA:1335:G:O6	2.45	0.49
50:ZA:1808:U:H2'	50:ZA:1809:A:C8	2.46	0.49
2:B:263:ALA:HB3	2:B:266:VAL:HG23	1.94	0.49
4:D:44:TYR:O	47:WA:1825:G:O2'	2.30	0.49
11:K:31:ARG:HD2	11:K:35:ARG:HH21	1.76	0.49
12:L:111:LYS:HE3	14:N:199:HIS:HE1	1.78	0.49
17:Q:108:ARG:HH22	47:WA:2901:C:P	2.34	0.49
29:CA:118:GLN:OE1	47:WA:5057:G:N2	2.45	0.49
47:WA:428:G:H2'	47:WA:429:A:H8	1.77	0.49
47:WA:1247:C:H2'	47:WA:1248:G:H8	1.78	0.49
47:WA:1998:C:H41	47:WA:2002:G:H22	1.58	0.49
47:WA:2751:C:H2'	47:WA:2752:G:H8	1.76	0.49
47:WA:3796:C:H2'	47:WA:3797:A:H8	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:YA:102:G:OP2	49:YA:104:A:O2'	2.27	0.49
55:EB:151:ASP:OD2	57:GB:216:ARG:NH1	2.40	0.49
83:GC:166:VAL:HG22	83:GC:176:VAL:HG22	1.95	0.49
29:CA:114:PHE:HA	29:CA:117:LEU:HD22	1.95	0.49
47:WA:281:U:H2'	47:WA:282:C:H6	1.77	0.49
47:WA:423:G:H2'	47:WA:424:U:C6	2.47	0.49
47:WA:1205:G:H2'	47:WA:1206:G:C8	2.44	0.49
47:WA:3702:C:O2'	47:WA:3776:A:H1'	2.12	0.49
47:WA:4603:U:H2'	47:WA:4604:A:H8	1.78	0.49
50:ZA:1036:A:H4'	50:ZA:1855:G:H21	1.76	0.49
50:ZA:1352:G:H1	50:ZA:1359:U:H3	1.60	0.49
50:ZA:1808:U:H2'	50:ZA:1809:A:H8	1.77	0.49
9:I:133:GLN:NE2	47:WA:1787:C:OP1	2.45	0.49
14:N:90:HIS:HE1	14:N:91:LYS:HE3	1.77	0.49
22:V:109:ILE:HG22	50:ZA:327:G:H5''	1.93	0.49
47:WA:986:U:H2'	47:WA:987:C:C6	2.48	0.49
47:WA:3913:C:H2'	47:WA:3914:U:H6	1.77	0.49
50:ZA:993:G:OP1	50:ZA:1131:G:N2	2.27	0.49
57:GB:48:TYR:OH	57:GB:119:LYS:O	2.26	0.49
65:OB:95:ILE:HB	65:OB:129:ILE:HG23	1.94	0.49
70:TB:104:LEU:HB3	70:TB:121:ARG:HE	1.77	0.49
73:WB:27:ILE:HG13	73:WB:61:ILE:HB	1.94	0.49
18:R:1:MET:HE2	18:R:43:ARG:HG3	1.95	0.49
24:X:82:ILE:HD12	24:X:85:VAL:HG21	1.95	0.49
35:IA:56:ARG:NE	47:WA:375:G:O6	2.38	0.49
47:WA:1505:A:H4'	47:WA:1506:G:H5'	1.95	0.49
47:WA:2021:C:H2'	47:WA:2022:U:C6	2.46	0.49
47:WA:2054:G:O2'	47:WA:2059:A:N1	2.44	0.49
47:WA:4663:G:N2	47:WA:5006:C:O3'	2.46	0.49
47:WA:4926:C:O2'	47:WA:4927:U:O4'	2.25	0.49
50:ZA:429:C:H2'	50:ZA:430:C:C6	2.48	0.49
50:ZA:860:G:H21	73:WB:107:SER:HB2	1.77	0.49
1:A:8:GLN:HA	47:WA:3669:C:H4'	1.95	0.49
1:A:189:TYR:CG	1:A:196:TRP:HB2	2.48	0.49
2:B:246:ARG:NH2	47:WA:4560:U:OP2	2.36	0.49
8:H:137:SER:HB3	8:H:143:GLU:HB3	1.94	0.49
17:Q:160:GLU:OE1	17:Q:163:ARG:NH2	2.45	0.49
40:NA:64:LYS:HD2	47:WA:4372:G:H5''	1.95	0.49
47:WA:308:G:C8	47:WA:310:G:H1'	2.47	0.49
47:WA:652:C:H2'	47:WA:653:G:H8	1.77	0.49
47:WA:2000:A:N7	85:b:44:ARG:NH2	2.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:2788:C:H5''	47:WA:2789:A:H5'	1.95	0.49
47:WA:3672:C:N4	47:WA:3673:G:O6	2.46	0.49
47:WA:3810:C:H2'	47:WA:3811:G:C4	2.48	0.49
47:WA:4460:C:H2'	47:WA:4461:U:C6	2.48	0.49
50:ZA:148:U:H2'	50:ZA:149:A:H8	1.78	0.49
50:ZA:1599:U:OP2	76:ZB:46:ASN:ND2	2.44	0.49
52:BB:62:LEU:HD23	52:BB:65:ARG:HE	1.77	0.49
57:GB:165:GLU:OE1	57:GB:167:LYS:NZ	2.43	0.49
69:SB:82:TRP:O	69:SB:87:GLN:NE2	2.46	0.49
85:b:143:ILE:HD11	85:b:219:VAL:HB	1.95	0.49
8:H:120:GLU:OE1	8:H:124:ARG:NH2	2.44	0.49
15:O:4:TYR:OH	47:WA:400:A:OP1	2.30	0.49
25:Y:92:ASP:OD2	25:Y:94:THR:OG1	2.22	0.49
43:RA:47:ALA:O	43:RA:50:THR:OG1	2.30	0.49
47:WA:158:A:H4'	47:WA:159:C:H5''	1.95	0.49
50:ZA:145:G:OP2	57:GB:139:SER:OG	2.23	0.49
50:ZA:608:C:O4'	81:EC:131:ASN:ND2	2.46	0.49
50:ZA:1803:U:H2'	50:ZA:1804:U:C6	2.48	0.49
67:QB:155:SER:O	67:QB:157:LYS:NZ	2.31	0.49
1:A:98:ILE:HD11	41:OA:80:LYS:HA	1.95	0.49
2:B:5:LYS:NZ	47:WA:4503:U:OP1	2.45	0.49
10:J:40:LEU:HD12	10:J:70:VAL:HG22	1.95	0.49
47:WA:2083:C:H2'	47:WA:2084:G:C8	2.48	0.49
50:ZA:1529:C:O2'	70:TB:87:VAL:O	2.24	0.49
54:DB:153:VAL:HG21	54:DB:180:LEU:HD22	1.95	0.49
56:FB:47:LYS:NZ	67:QB:141:TYR:O	2.46	0.49
57:GB:160:LYS:HD2	57:GB:161:PRO:HD2	1.95	0.49
64:NB:33:VAL:HG21	64:NB:66:VAL:HG11	1.94	0.49
65:OB:31:CYS:HB3	65:OB:44:VAL:HG22	1.94	0.49
66:PB:81:ARG:NH1	66:PB:97:TYR:O	2.40	0.49
67:QB:126:VAL:HG12	67:QB:127:ASP:H	1.78	0.49
83:GC:234:ASP:HB2	83:GC:252:THR:HB	1.93	0.49
1:A:117:GLU:O	1:A:162:ASN:ND2	2.46	0.49
4:D:222:GLN:NE2	48:XA:47:G:N3	2.55	0.49
13:M:185:GLY:HA2	47:WA:78:U:H5''	1.95	0.49
13:M:189:ARG:HH21	47:WA:28:C:H3'	1.77	0.49
21:U:13:LYS:HD2	21:U:128:LEU:HD11	1.95	0.49
26:Z:131:ARG:NH1	26:Z:135:GLU:OE2	2.46	0.49
30:DA:44:ARG:NH2	30:DA:52:GLN:OE1	2.46	0.49
47:WA:2416:G:H2'	47:WA:2417:U:H6	1.78	0.49
47:WA:2618:C:H2'	47:WA:2619:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:1083:A:N7	50:ZA:1841:C:O2'	2.42	0.49
57:GB:14:LYS:HD2	57:GB:123:GLY:HA3	1.95	0.49
63:MB:81:ASP:HB3	63:MB:84:LYS:HB2	1.94	0.49
10:J:112:HIS:CE1	10:J:126:TYR:H	2.31	0.48
15:O:79:ASP:OD2	15:O:85:GLN:NE2	2.46	0.48
47:WA:429:A:H2'	47:WA:430:G:H8	1.78	0.48
47:WA:1074:G:N2	47:WA:1075:G:O6	2.32	0.48
47:WA:2575:A:N7	47:WA:2763:U:O4	2.46	0.48
47:WA:2851:A:N1	47:WA:2859:A:N6	2.60	0.48
47:WA:5039:U:H2'	47:WA:5040:A:C8	2.48	0.48
50:ZA:891:G:H5''	50:ZA:892:U:H4'	1.93	0.48
50:ZA:1670:C:H2'	50:ZA:1671:G:C8	2.46	0.48
54:DB:147:LEU:HD11	54:DB:153:VAL:HG22	1.95	0.48
6:F:72:ARG:NH2	47:WA:728:C:OP1	2.40	0.48
6:F:94:ILE:HD13	6:F:140:ALA:HB2	1.95	0.48
17:Q:82:LYS:O	47:WA:2865:G:O2'	2.22	0.48
23:W:110:LYS:NZ	23:W:121:VAL:O	2.45	0.48
25:Y:84:ARG:N	28:BA:62:TYR:OH	2.45	0.48
45:TA:23:A:H2'	45:TA:24:G:H8	1.78	0.48
47:WA:1323:G:N2	47:WA:3878:A:O4'	2.45	0.48
50:ZA:15:U:H2'	50:ZA:16:G:O4'	2.14	0.48
50:ZA:145:G:H2'	50:ZA:146:G:C8	2.48	0.48
50:ZA:1098:C:H2'	50:ZA:1099:G:C8	2.48	0.48
50:ZA:1237:C:H2'	50:ZA:1238:U:C6	2.48	0.48
55:EB:43:PRO:HD2	55:EB:46:ILE:HD11	1.95	0.48
58:HB:268:LEU:O	58:HB:272:SER:OG	2.28	0.48
58:HB:289:ILE:HD12	58:HB:417:LYS:HG2	1.95	0.48
73:WB:50:PHE:HB3	73:WB:63:VAL:HG13	1.95	0.48
11:K:46:ILE:HB	11:K:49:ARG:HB2	1.94	0.48
44:SA:22:A:H2'	44:SA:23:G:C8	2.49	0.48
47:WA:1103:C:H2'	47:WA:1104:G:C8	2.48	0.48
47:WA:2751:C:H2'	47:WA:2752:G:C8	2.49	0.48
47:WA:3600:C:H2'	47:WA:3601:A:C8	2.48	0.48
47:WA:3929:U:H2'	47:WA:3930:A:H8	1.77	0.48
47:WA:5007:G:N2	47:WA:5043:G:O2'	2.47	0.48
49:YA:11:C:H2'	49:YA:12:G:C8	2.48	0.48
50:ZA:804:U:H5''	73:WB:82:GLN:HG2	1.95	0.48
50:ZA:1776:G:H2'	50:ZA:1777:G:H8	1.78	0.48
57:GB:64:LYS:HB3	57:GB:67:VAL:HG23	1.95	0.48
66:PB:43:ARG:HH12	66:PB:47:ARG:HH11	1.62	0.48
73:WB:11:LEU:HA	73:WB:14:ILE:HG12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
83:GC:40:ILE:HB	83:GC:59:LEU:HB2	1.95	0.48
3:C:239:LYS:O	3:C:248:ARG:NH1	2.43	0.48
10:J:29:SER:OG	10:J:67:LYS:O	2.27	0.48
33:GA:62:ASN:ND2	49:YA:60:G:O6	2.36	0.48
47:WA:1098:G:H1	47:WA:1210:C:H42	1.61	0.48
47:WA:1463:C:H2'	47:WA:1464:A:H8	1.78	0.48
47:WA:2380:G:N2	47:WA:2383:A:OP2	2.38	0.48
50:ZA:190:G:O2'	50:ZA:209:A:N6	2.46	0.48
50:ZA:526:A:H2'	50:ZA:527:C:H6	1.77	0.48
50:ZA:952:G:H2'	50:ZA:953:C:C6	2.48	0.48
50:ZA:1079:C:O2'	50:ZA:1182:A:N1	2.46	0.48
50:ZA:1845:A:H2'	50:ZA:1846:G:C8	2.48	0.48
55:EB:174:LYS:O	55:EB:179:ASN:ND2	2.47	0.48
68:RB:77:GLU:HG2	68:RB:81:ARG:HE	1.79	0.48
83:GC:32:LEU:HD11	83:GC:92:LEU:HD21	1.95	0.48
9:I:66:GLU:OE1	9:I:69:ARG:NH1	2.46	0.48
34:HA:33:LEU:HB2	47:WA:308:G:H3'	1.94	0.48
47:WA:325:U:H2'	47:WA:326:C:C6	2.49	0.48
47:WA:357:U:O2	47:WA:359:A:N6	2.47	0.48
47:WA:1210:C:H2'	47:WA:1211:G:H8	1.77	0.48
47:WA:4090:C:H2'	47:WA:4091:G:C8	2.46	0.48
47:WA:4577:G:N3	47:WA:5070:G:O2'	2.45	0.48
50:ZA:1004:U:H2'	50:ZA:1005:G:C8	2.49	0.48
85:b:107:VAL:HG22	85:b:108:PRO:HD2	1.95	0.48
2:B:302:ASN:HD22	2:B:330:PHE:HE2	1.61	0.48
6:F:178:LEU:HB3	6:F:183:ILE:HB	1.95	0.48
19:S:9:ARG:O	19:S:55:LYS:NZ	2.40	0.48
22:V:116:LYS:HD2	50:ZA:322:C:N4	2.29	0.48
30:DA:26:ASP:OD2	47:WA:435:A:O2'	2.31	0.48
47:WA:301:G:N2	47:WA:4178:C:O2'	2.47	0.48
47:WA:483:G:O2'	47:WA:486:C:OP2	2.31	0.48
47:WA:1928:C:H2'	47:WA:1929:U:C6	2.47	0.48
47:WA:2591:C:H2'	47:WA:2592:G:O4'	2.14	0.48
47:WA:3666:G:H2'	47:WA:3667:G:H8	1.77	0.48
47:WA:4358:G:H2'	47:WA:4359:G:H8	1.78	0.48
50:ZA:563:G:O6	60:JB:172:ARG:NH2	2.38	0.48
50:ZA:582:U:H2'	50:ZA:583:A:H5''	1.95	0.48
50:ZA:839:C:H42	75:YB:48:TYR:HB2	1.77	0.48
50:ZA:1499:U:H2'	50:ZA:1500:G:H8	1.78	0.48
54:DB:114:ARG:HB2	61:KB:22:VAL:HG11	1.96	0.48
66:PB:34:MET:HG2	66:PB:42:ARG:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:SB:91:LYS:NZ	69:SB:109:GLU:OE1	2.41	0.48
83:GC:207:CYS:HB2	83:GC:221:LEU:HD21	1.94	0.48
2:B:82:PRO:HG3	2:B:171:LEU:HD21	1.96	0.48
4:D:124:GLU:OE1	4:D:126:THR:OG1	2.30	0.48
5:E:65:TYR:HA	5:E:68:LYS:HZ2	1.79	0.48
5:E:269:GLN:HG2	47:WA:4932:C:H5''	1.94	0.48
22:V:116:LYS:HD2	50:ZA:322:C:H41	1.78	0.48
25:Y:41:ALA:HB2	25:Y:77:TYR:HE1	1.78	0.48
26:Z:12:ARG:NH1	47:WA:2347:G:OP2	2.46	0.48
41:OA:39:CYS:CB	41:OA:42:CYS:SG	3.01	0.48
47:WA:1525:A:N3	47:WA:4391:C:O2'	2.42	0.48
47:WA:3719:A:N3	47:WA:4180:A:O2'	2.43	0.48
47:WA:3895:C:H2'	47:WA:3896:A:H8	1.78	0.48
47:WA:3918:G:H2'	47:WA:3919:A:C8	2.49	0.48
50:ZA:821:G:C6	60:JB:150:ARG:HD2	2.49	0.48
63:MB:49:LEU:HB3	63:MB:111:VAL:HG13	1.95	0.48
4:D:253:TYR:OH	48:XA:117:G:OP1	2.31	0.48
9:I:153:ARG:HA	9:I:156:LYS:HE2	1.94	0.48
15:O:137:ASP:OD1	15:O:137:ASP:N	2.47	0.48
25:Y:17:ARG:NH2	25:Y:18:TYR:OH	2.47	0.48
47:WA:275:C:O2'	47:WA:276:C:OP1	2.30	0.48
47:WA:1330:G:O2'	47:WA:2351:A:OP1	2.31	0.48
47:WA:2542:C:H2'	47:WA:2543:G:C8	2.49	0.48
47:WA:4165:U:H5'	47:WA:4166:C:H5''	1.95	0.48
50:ZA:436:G:OP2	50:ZA:471:G:O2'	2.32	0.48
50:ZA:666:U:H2'	50:ZA:667:U:C6	2.49	0.48
50:ZA:1536:G:H2'	50:ZA:1537:A:H8	1.78	0.48
50:ZA:1683:C:O2	79:CC:24:GLN:NE2	2.46	0.48
69:SB:60:THR:OG1	69:SB:62:ASP:OD1	2.30	0.48
70:TB:116:ASP:OD1	70:TB:117:GLN:N	2.45	0.48
75:YB:68:LYS:HB2	75:YB:68:LYS:HE3	1.61	0.48
2:B:317:LEU:HB2	2:B:372:SER:HB2	1.95	0.48
3:C:197:ARG:NH1	47:WA:351:C:OP2	2.37	0.48
3:C:321:ASN:ND2	47:WA:1283:G:OP1	2.42	0.48
15:O:90:ARG:HE	49:YA:3:A:HO2'	1.62	0.48
15:O:148:VAL:HG22	15:O:175:ILE:HG23	1.96	0.48
18:R:30:MET:HG2	19:S:151:LEU:HB2	1.95	0.48
47:WA:1215:U:O2'	47:WA:1217:G:O4'	2.28	0.48
47:WA:1471:C:H2'	47:WA:1472:G:H8	1.79	0.48
47:WA:2560:C:H2'	47:WA:2561:G:H8	1.79	0.48
47:WA:2850:G:O2'	47:WA:3840:U:O4	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:4197:G:O2'	47:WA:4444:U:OP1	2.21	0.48
49:YA:30:U:H2'	49:YA:31:G:H8	1.79	0.48
50:ZA:1776:G:H2'	50:ZA:1777:G:C8	2.48	0.48
61:KB:91:PRO:HD2	61:KB:94:LEU:HD12	1.95	0.48
83:GC:286:CYS:HA	83:GC:302:TYR:HA	1.94	0.48
2:B:254:ILE:HG23	2:B:266:VAL:HG11	1.96	0.48
12:L:106:ASP:OD1	12:L:109:ARG:NH1	2.46	0.48
18:R:127:MET:HA	19:S:153:PRO:HD2	1.96	0.48
45:TA:6:G:O2'	45:TA:7:A:O5'	2.32	0.48
47:WA:3:C:N4	47:WA:4:G:O6	2.47	0.48
47:WA:306:A:H2'	47:WA:307:A:C8	2.48	0.48
47:WA:1944:A:H2'	47:WA:1945:A:C8	2.49	0.48
47:WA:2521:U:O2'	47:WA:2532:U:O2	2.26	0.48
47:WA:2899:G:H2'	47:WA:2900:G:H8	1.79	0.48
47:WA:4131:G:O6	47:WA:4158:G:N2	2.46	0.48
47:WA:4194:A:H2'	47:WA:4195:C:H6	1.78	0.48
47:WA:4240:G:H2'	47:WA:4241:A:C8	2.46	0.48
47:WA:4942:C:H5'	47:WA:4943:G:H5''	1.95	0.48
48:XA:4:U:H2'	48:XA:5:A:H8	1.79	0.48
50:ZA:348:A:H2'	50:ZA:349:A:C8	2.49	0.48
50:ZA:1856:C:H2'	50:ZA:1857:G:H8	1.79	0.48
4:D:94:ASN:OD1	4:D:97:ALA:N	2.36	0.47
6:F:99:GLY:HA2	47:WA:1879:G:H4'	1.95	0.47
14:N:27:VAL:HG13	14:N:98:ALA:HB1	1.96	0.47
21:U:85:ARG:NH1	21:U:99:GLU:O	2.39	0.47
27:AA:99:ILE:O	27:AA:109:ARG:NH1	2.47	0.47
31:EA:13:GLY:HA2	31:EA:97:ILE:HD12	1.95	0.47
40:NA:80:LYS:O	47:WA:4348:U:O2'	2.27	0.47
43:RA:109:ILE:HD11	43:RA:143:VAL:HG21	1.96	0.47
47:WA:2761:G:H2'	47:WA:2762:G:C4	2.49	0.47
47:WA:2876:U:O4	47:WA:3825:G:O2'	2.29	0.47
47:WA:4554:U:H2'	47:WA:4555:A:C8	2.49	0.47
47:WA:4920:C:H2'	47:WA:4921:G:C8	2.46	0.47
48:XA:110:G:H2'	48:XA:111:C:C6	2.49	0.47
54:DB:210:VAL:O	54:DB:211:ARG:NH1	2.44	0.47
59:IB:67:TRP:NE1	59:IB:191:GLU:OE2	2.42	0.47
60:JB:131:ARG:NH1	60:JB:143:ASN:OD1	2.47	0.47
83:GC:132:TRP:HD1	83:GC:138:CYS:HA	1.78	0.47
83:GC:149:GLU:H	83:GC:171:ASP:HB3	1.79	0.47
85:b:33:ASP:OD1	85:b:33:ASP:N	2.47	0.47
86:At:67:C:H2'	86:At:68:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:12:TYR:OH	47:WA:4267:U:OP1	2.32	0.47
31:EA:54:LYS:HB3	47:WA:443:G:H5''	1.95	0.47
37:KA:2:SER:N	47:WA:2408:G:N7	2.61	0.47
47:WA:711:G:H2'	47:WA:712:A:C8	2.48	0.47
47:WA:4508:C:H2'	47:WA:4509:A:C8	2.49	0.47
50:ZA:411:G:H2'	50:ZA:412:G:H8	1.78	0.47
50:ZA:506:G:OP1	75:YB:108:LYS:NZ	2.38	0.47
50:ZA:902:G:H2'	50:ZA:903:A:H8	1.79	0.47
52:BB:179:ASN:HB3	52:BB:183:GLU:HB2	1.95	0.47
57:GB:2:LYS:HD3	57:GB:15:LEU:HD21	1.96	0.47
5:E:111:LYS:NZ	47:WA:2261:G:O2'	2.38	0.47
47:WA:652:C:H2'	47:WA:653:G:C8	2.49	0.47
47:WA:1292:G:H2'	47:WA:1293:G:C8	2.49	0.47
47:WA:1746:U:H2'	47:WA:1747:G:H8	1.79	0.47
47:WA:1760:G:H2'	47:WA:1761:G:H8	1.78	0.47
47:WA:2081:G:H2'	47:WA:2082:U:C6	2.49	0.47
47:WA:4763:G:H2'	47:WA:4764:A:C8	2.49	0.47
50:ZA:836:G:C5	75:YB:7:ILE:HB	2.44	0.47
50:ZA:1447:G:H2'	50:ZA:1448:A:C8	2.49	0.47
73:WB:87:GLU:OE1	73:WB:90:GLN:NE2	2.47	0.47
78:BC:62:VAL:HG23	78:BC:74:THR:HG21	1.96	0.47
85:b:128:THR:OG1	85:b:129:GLY:N	2.45	0.47
6:F:154:TYR:OH	6:F:187:GLU:OE2	2.32	0.47
9:I:35:ASP:HB2	9:I:86:HIS:HE2	1.78	0.47
29:CA:122:VAL:HG12	29:CA:124:GLU:H	1.80	0.47
42:PA:108:MET:HE2	47:WA:2265:A:H5''	1.97	0.47
47:WA:1827:A:H2'	47:WA:1828:G:C8	2.48	0.47
47:WA:4712:C:H2'	47:WA:4713:C:C6	2.49	0.47
50:ZA:528:A:H2'	50:ZA:529:A:H8	1.78	0.47
50:ZA:1337:C:H2'	50:ZA:1338:G:C8	2.50	0.47
61:KB:26:ASP:HB3	61:KB:29:MET:HE3	1.97	0.47
65:OB:85:CYS:HB3	65:OB:90:ILE:HB	1.95	0.47
1:A:230:PRO:HG2	1:A:233:ARG:HB3	1.95	0.47
9:I:61:SER:HA	9:I:126:VAL:HG23	1.97	0.47
10:J:16:ARG:HD2	10:J:137:PRO:HG3	1.96	0.47
31:EA:56:ASN:OD1	31:EA:66:LYS:NZ	2.37	0.47
47:WA:66:A:H61	47:WA:282:C:HO2'	1.61	0.47
47:WA:462:G:H2'	47:WA:463:A:C8	2.49	0.47
47:WA:932:C:H2'	47:WA:933:A:C8	2.49	0.47
47:WA:1656:G:N2	47:WA:1680:C:OP1	2.47	0.47
47:WA:2329:G:H2'	47:WA:2330:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:2396:G:O4'	47:WA:2399:G:N2	2.44	0.47
47:WA:2469:U:H4'	47:WA:2470:U:H5'	1.96	0.47
47:WA:2733:C:H2'	47:WA:2734:G:C8	2.50	0.47
47:WA:3776:A:H2'	47:WA:3777:A:C8	2.49	0.47
47:WA:3938:A:N6	47:WA:4177:G:O6	2.47	0.47
47:WA:4619:G:H2'	47:WA:4620:G:C8	2.50	0.47
50:ZA:54:A:OP1	75:YB:112:ASN:ND2	2.48	0.47
50:ZA:202:G:H2'	50:ZA:203:G:H8	1.79	0.47
50:ZA:852:G:H1'	62:LB:97:ARG:HH21	1.80	0.47
50:ZA:1480:A:O2'	71:UB:79:ARG:NH2	2.48	0.47
50:ZA:1491:G:H2'	50:ZA:1492:U:C6	2.49	0.47
51:AB:164:ASN:O	51:AB:170:SER:OG	2.25	0.47
61:KB:51:SER:O	61:KB:55:ARG:HG2	2.15	0.47
63:MB:49:LEU:HD11	63:MB:77:ILE:HG12	1.97	0.47
67:QB:63:ARG:HG2	70:TB:7:LYS:HB3	1.96	0.47
68:RB:73:LEU:O	68:RB:76:GLU:HG3	2.14	0.47
80:DC:33:LYS:HE2	80:DC:34:TYR:CZ	2.49	0.47
83:GC:107:ASP:O	83:GC:124:SER:OG	2.26	0.47
83:GC:152:SER:H	83:GC:169:GLY:HA2	1.79	0.47
2:B:378:ARG:HE	22:V:32:LEU:HD21	1.79	0.47
27:AA:50:ASN:OD1	47:WA:1828:G:N2	2.45	0.47
30:DA:91:CYS:HB3	30:DA:95:TYR:HD2	1.78	0.47
47:WA:20:U:H3'	47:WA:21:G:C8	2.48	0.47
47:WA:1975:G:C2'	47:WA:1976:U:H2'	2.44	0.47
47:WA:2491:C:O2'	47:WA:2493:C:N4	2.48	0.47
47:WA:3913:C:H2'	47:WA:3914:U:C6	2.49	0.47
47:WA:4498:A:H61	47:WA:4506:C:H42	1.63	0.47
47:WA:4761:C:H2'	47:WA:4762:G:C8	2.50	0.47
50:ZA:527:C:H4'	60:JB:121:LYS:HB2	1.95	0.47
50:ZA:1036:A:H4'	50:ZA:1855:G:N2	2.30	0.47
51:AB:70:ASN:HD21	51:AB:72:ALA:HB3	1.79	0.47
57:GB:70:HIS:HA	57:GB:101:ILE:HB	1.96	0.47
59:IB:114:GLU:OE2	59:IB:123:ARG:NH1	2.47	0.47
64:NB:29:THR:OG1	64:NB:31:ASP:OD1	2.29	0.47
66:PB:17:TYR:HB3	66:PB:25:LEU:HD11	1.97	0.47
71:UB:64:THR:HG22	71:UB:79:ARG:HG2	1.95	0.47
3:C:278:ASN:OD1	3:C:279:LEU:N	2.47	0.47
5:E:128:LEU:HB3	47:WA:965:A:N6	2.29	0.47
6:F:161:ILE:HB	6:F:166:ILE:HD12	1.96	0.47
16:P:18:PRO:HG3	16:P:29:VAL:HG21	1.96	0.47
16:P:91:ARG:HB3	26:Z:76:ASP:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:36:ARG:NH1	47:WA:2582:U:OP1	2.38	0.47
27:AA:7:HIS:ND1	47:WA:1674:U:OP1	2.41	0.47
35:IA:55:ARG:NH2	47:WA:364:G:O6	2.46	0.47
47:WA:66:A:O2'	47:WA:326:C:O2	2.33	0.47
47:WA:268:G:H2'	47:WA:269:G:H8	1.80	0.47
47:WA:1575:G:H2'	47:WA:1576:G:C4	2.50	0.47
47:WA:1735:G:N3	47:WA:4216:A:H2'	2.30	0.47
47:WA:1903:C:H2'	47:WA:1904:G:H8	1.78	0.47
47:WA:3863:A:H2'	47:WA:3864:A:C8	2.46	0.47
47:WA:4929:G:H5''	47:WA:4930:C:H5	1.80	0.47
47:WA:4969:A:H2'	47:WA:4970:A:H8	1.79	0.47
49:YA:148:A:H2'	49:YA:149:G:C8	2.49	0.47
50:ZA:74:G:N2	50:ZA:76:U:O4	2.38	0.47
50:ZA:126:G:N2	50:ZA:180:G:H21	2.13	0.47
50:ZA:287:U:H3	55:EB:131:VAL:HG11	1.80	0.47
50:ZA:671:A:H4'	50:ZA:672:A:H5''	1.96	0.47
50:ZA:1144:A:H2'	50:ZA:1145:A:C8	2.50	0.47
50:ZA:1630:A:H5''	69:SB:37:GLY:N	2.30	0.47
50:ZA:1797:U:H2'	50:ZA:1798:C:C6	2.49	0.47
50:ZA:1854:U:H5''	65:OB:150:ARG:HH21	1.80	0.47
53:CB:69:LEU:HG	53:CB:273:LEU:HD21	1.97	0.47
60:JB:109:ARG:HH21	60:JB:146:SER:HB3	1.78	0.47
68:RB:132:ARG:H	68:RB:132:ARG:HD2	1.79	0.47
71:UB:56:MET:HB2	71:UB:86:LYS:HB3	1.96	0.47
10:J:18:ARG:N	10:J:133:VAL:O	2.48	0.47
19:S:57:TYR:OH	47:WA:4302:U:O3'	2.30	0.47
47:WA:7:C:H2'	47:WA:8:U:C6	2.50	0.47
47:WA:429:A:H2'	47:WA:430:G:C8	2.50	0.47
47:WA:2039:C:H2'	47:WA:2040:U:C6	2.50	0.47
47:WA:2083:C:H2'	47:WA:2084:G:H8	1.80	0.47
47:WA:2760:G:H2'	47:WA:2761:G:N7	2.29	0.47
47:WA:4886:G:H2'	47:WA:4887:U:C6	2.49	0.47
48:XA:62:U:O2'	48:XA:64:G:O4'	2.33	0.47
50:ZA:212:C:H2'	50:ZA:213:G:C8	2.50	0.47
50:ZA:1422:G:H2'	50:ZA:1423:C:H4'	1.97	0.47
50:ZA:1733:U:H2'	50:ZA:1734:G:O4'	2.15	0.47
51:AB:76:VAL:HG12	51:AB:123:VAL:HB	1.95	0.47
54:DB:206:VAL:HG12	54:DB:227:MET:HA	1.96	0.47
82:FC:121:CYS:HB3	82:FC:126:CYS:SG	2.54	0.47
85:b:116:ILE:HG22	85:b:118:PRO:HD2	1.97	0.47
3:C:328:LEU:HB3	6:F:186:MET:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:86:TRP:O	12:L:89:THR:OG1	2.31	0.47
37:KA:47:THR:HG22	37:KA:49:LEU:H	1.79	0.47
47:WA:470:A:N6	47:WA:685:G:H21	2.10	0.47
47:WA:674:C:H2'	47:WA:675:G:H8	1.80	0.47
47:WA:2581:G:N2	47:WA:2584:A:OP2	2.32	0.47
47:WA:2880:G:OP2	47:WA:2881:A:O2'	2.31	0.47
50:ZA:594:A:O4'	50:ZA:643:A:N6	2.48	0.47
57:GB:74:ARG:HG2	57:GB:96:SER:HB3	1.97	0.47
57:GB:141:ILE:HG22	57:GB:147:LEU:HD11	1.96	0.47
60:JB:135:ILE:HA	60:JB:159:PHE:HA	1.96	0.47
71:UB:54:VAL:HB	71:UB:88:LEU:HG	1.97	0.47
72:VB:59:ILE:HD12	78:BC:3:LEU:HD11	1.96	0.47
1:A:179:ILE:HG21	1:A:185:ALA:HB2	1.97	0.47
2:B:215:GLU:OE2	2:B:349:LYS:NZ	2.47	0.47
5:E:67:ARG:NE	47:WA:1076:G:OP1	2.48	0.47
5:E:156:LEU:HD11	5:E:198:ILE:HG13	1.96	0.47
36:JA:47:ILE:HG22	36:JA:49:ASP:H	1.79	0.47
45:TA:42:G:H2'	45:TA:43:A:H8	1.78	0.47
47:WA:158:A:N1	47:WA:276:C:O2'	2.44	0.47
47:WA:747:G:H2'	47:WA:748:A:C8	2.50	0.47
47:WA:1941:A:H5'	47:WA:1942:G:H4'	1.97	0.47
47:WA:3772:U:H2'	47:WA:3773:C:C6	2.50	0.47
50:ZA:522:A:H5'	60:JB:144:ILE:HG23	1.97	0.47
50:ZA:1236:G:O2'	66:PB:131:PRO:O	2.24	0.47
50:ZA:1542:C:H4'	70:TB:11:GLN:HB2	1.97	0.47
58:HB:284:THR:HG23	58:HB:303:PRO:HG3	1.96	0.47
60:JB:129:LEU:HD22	60:JB:134:HIS:ND1	2.29	0.47
69:SB:132:ARG:HB2	69:SB:134:GLN:HE22	1.80	0.47
83:GC:24:THR:HB	83:GC:71:ILE:HG12	1.97	0.47
1:A:236:GLY:N	47:WA:3689:A:O2'	2.40	0.46
8:H:92:MET:HE2	8:H:179:ILE:HG22	1.97	0.46
14:N:12:ARG:HD3	14:N:37:ARG:HH11	1.80	0.46
27:AA:18:ARG:NH2	47:WA:1671:A:OP1	2.43	0.46
42:PA:31:ASN:ND2	42:PA:40:TYR:O	2.48	0.46
43:RA:30:PRO:HG3	47:WA:2011:A:N6	2.30	0.46
47:WA:146:G:H2'	47:WA:147:A:H8	1.80	0.46
47:WA:1292:G:H2'	47:WA:1293:G:H8	1.81	0.46
47:WA:1565:A:O2'	64:NB:123:HIS:NE2	2.38	0.46
47:WA:1635:G:O6	47:WA:3920:G:O2'	2.33	0.46
47:WA:1751:A:H2'	47:WA:1752:G:C8	2.50	0.46
47:WA:2413:C:O2'	47:WA:2528:C:O2	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:2523:G:H2'	47:WA:2524:G:H8	1.80	0.46
47:WA:3725:A:H2'	47:WA:3726:A:H8	1.80	0.46
47:WA:3935:G:H2'	47:WA:3936:G:C8	2.49	0.46
47:WA:4706:C:H2'	47:WA:4707:A:C8	2.50	0.46
50:ZA:64:A:H2	50:ZA:83:A:H62	1.63	0.46
50:ZA:164:A:OP1	57:GB:83:CYS:N	2.46	0.46
50:ZA:317:C:H2'	50:ZA:318:A:C8	2.51	0.46
50:ZA:422:U:H2'	50:ZA:423:U:H6	1.80	0.46
50:ZA:433:A:H2'	50:ZA:434:G:C8	2.50	0.46
59:IB:48:VAL:HG11	59:IB:54:LYS:HD2	1.97	0.46
86:At:68:C:H2'	86:At:69:G:C8	2.48	0.46
8:H:88:PHE:HB2	8:H:148:GLY:O	2.15	0.46
15:O:90:ARG:NE	49:YA:3:A:O2'	2.43	0.46
27:AA:11:ASN:ND2	47:WA:1671:A:OP1	2.42	0.46
35:IA:36:LYS:HA	35:IA:45:ARG:HH21	1.81	0.46
47:WA:2376:A:H2'	47:WA:2377:A:H8	1.81	0.46
47:WA:3734:A:H2'	47:WA:3735:A:H8	1.78	0.46
50:ZA:805:U:H2'	50:ZA:806:U:C6	2.51	0.46
50:ZA:1201:U:H2'	50:ZA:1202:U:C6	2.50	0.46
50:ZA:1203:G:H2'	50:ZA:1204:A:C8	2.50	0.46
50:ZA:1587:G:N7	70:TB:67:ARG:HD3	2.31	0.46
50:ZA:1614:A:H2'	50:ZA:1615:U:C6	2.50	0.46
70:TB:65:TYR:HE1	70:TB:128:GLN:HG3	1.79	0.46
2:B:329:ASP:OD1	2:B:329:ASP:N	2.48	0.46
17:Q:96:MET:HG3	47:WA:2669:C:H5'	1.96	0.46
27:AA:31:SER:HB2	47:WA:1465:C:H5''	1.97	0.46
28:BA:88:TYR:HB2	47:WA:2662:A:H62	1.80	0.46
42:PA:42:GLY:O	42:PA:48:THR:OG1	2.31	0.46
44:SA:50:U:O4	44:SA:64:G:O6	2.33	0.46
47:WA:175:C:H2'	47:WA:176:G:H8	1.81	0.46
47:WA:2364:U:H2'	47:WA:2365:A:H8	1.80	0.46
47:WA:2376:A:H2'	47:WA:2377:A:C8	2.51	0.46
47:WA:3601:A:H2'	47:WA:3602:G:C8	2.50	0.46
47:WA:4682:G:H2'	47:WA:4683:A:C8	2.50	0.46
50:ZA:222:U:H5''	62:LB:17:PHE:CG	2.50	0.46
50:ZA:479:C:H2'	50:ZA:480:G:C8	2.49	0.46
50:ZA:502:C:H1'	55:EB:63:LYS:HE2	1.97	0.46
50:ZA:512:A:C2	50:ZA:513:G:C8	3.03	0.46
50:ZA:1568:C:O2	50:ZA:1627:C:O2'	2.30	0.46
2:B:92:TYR:HB2	2:B:159:VAL:HB	1.96	0.46
17:Q:102:LEU:HD22	17:Q:138:LEU:HD22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:273:U:H2'	47:WA:274:C:C6	2.50	0.46
47:WA:1176:G:H2'	47:WA:1177:G:C8	2.51	0.46
47:WA:1448:C:H2'	47:WA:1449:C:H6	1.80	0.46
48:XA:4:U:H2'	48:XA:5:A:C8	2.51	0.46
50:ZA:24:C:O2'	50:ZA:25:A:OP1	2.31	0.46
50:ZA:120:U:O2'	55:EB:79:ASP:OD2	2.24	0.46
50:ZA:440:G:H2'	50:ZA:441:C:H6	1.79	0.46
50:ZA:1277:C:H2'	50:ZA:1278:A:C8	2.49	0.46
50:ZA:1324:G:O2'	50:ZA:1510:G:O2'	2.29	0.46
50:ZA:1488:C:H3'	50:ZA:1489:A:H4'	1.97	0.46
50:ZA:1494:U:H4'	50:ZA:1495:G:H5''	1.98	0.46
50:ZA:1758:G:H2'	50:ZA:1759:G:H8	1.79	0.46
51:AB:102:ARG:HA	51:AB:102:ARG:HD2	1.67	0.46
74:XB:46:HIS:HB3	74:XB:101:LEU:HD11	1.98	0.46
8:H:71:ARG:HD3	47:WA:4693:A:H4'	1.97	0.46
10:J:19:LYS:HD3	10:J:75:ARG:NH2	2.30	0.46
12:L:29:ASP:OD1	12:L:30:VAL:N	2.48	0.46
16:P:178:ARG:N	26:Z:51:GLY:HA2	2.31	0.46
22:V:82:ILE:HG22	57:GB:145:PHE:CD2	2.50	0.46
25:Y:3:LYS:NZ	28:BA:40:GLN:O	2.45	0.46
47:WA:735:G:H1	47:WA:934:G:H21	1.63	0.46
47:WA:1300:C:H2'	47:WA:1301:G:C8	2.51	0.46
47:WA:2760:G:H2'	47:WA:2761:G:C8	2.50	0.46
47:WA:3628:G:O6	47:WA:3838:A:N6	2.48	0.46
47:WA:3650:A:H1'	47:WA:3787:A:H61	1.81	0.46
47:WA:3872:C:H2'	47:WA:3873:A:C8	2.49	0.46
47:WA:3912:C:H2'	47:WA:3913:C:C6	2.51	0.46
50:ZA:404:G:H2'	50:ZA:405:G:H8	1.80	0.46
50:ZA:918:U:H2'	50:ZA:919:A:O4'	2.16	0.46
50:ZA:1220:A:H4'	56:FB:145:ARG:HH22	1.80	0.46
50:ZA:1513:C:OP1	80:DC:12:ARG:NH1	2.48	0.46
63:MB:33:ARG:NH2	63:MB:89:VAL:O	2.48	0.46
72:VB:11:LEU:HD23	72:VB:11:LEU:H	1.81	0.46
83:GC:59:LEU:HD23	83:GC:90:TRP:CD2	2.51	0.46
1:A:183:GLY:HA2	47:WA:1615:A:H5'	1.97	0.46
2:B:83:PRO:O	2:B:167:GLN:NE2	2.49	0.46
2:B:283:LYS:HD3	2:B:285:TYR:HE1	1.80	0.46
13:M:123:GLU:OE1	13:M:128:LYS:NZ	2.48	0.46
14:N:46:ASN:OD1	14:N:49:ARG:N	2.38	0.46
21:U:43:LYS:HD2	47:WA:4510:C:H5''	1.96	0.46
30:DA:124:ASN:N	30:DA:124:ASN:OD1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:PA:65:LYS:O	42:PA:102:TYR:OH	2.24	0.46
47:WA:520:C:H2'	47:WA:521:U:C5	2.50	0.46
47:WA:1437:G:O2'	47:WA:2107:A:N6	2.48	0.46
47:WA:2522:C:H2'	47:WA:2523:G:C8	2.47	0.46
47:WA:3796:C:H2'	47:WA:3797:A:C8	2.50	0.46
47:WA:4156:G:H2'	47:WA:4157:C:C6	2.51	0.46
47:WA:4483:U:H2'	47:WA:4484:U:H6	1.81	0.46
47:WA:4619:G:H2'	47:WA:4620:G:H8	1.79	0.46
49:YA:114:G:H1	49:YA:136:U:H3	1.63	0.46
50:ZA:1528:G:H2'	50:ZA:1529:C:C6	2.50	0.46
55:EB:149:TYR:HB3	57:GB:209:TYR:CE1	2.51	0.46
62:LB:101:ARG:NH1	74:XB:6:GLY:O	2.47	0.46
1:A:65:ASP:OD2	1:A:68:ARG:N	2.48	0.46
35:IA:48:ASN:N	47:WA:52:G:OP1	2.38	0.46
47:WA:1103:C:H2'	47:WA:1104:G:H8	1.81	0.46
47:WA:1623:A:H5''	47:WA:2453:A:H5'	1.98	0.46
47:WA:4190:U:H2'	47:WA:4191:U:C6	2.51	0.46
47:WA:4262:U:H2'	47:WA:4263:C:H6	1.80	0.46
47:WA:5007:G:H22	47:WA:5043:G:H1'	1.81	0.46
49:YA:12:G:C2	49:YA:13:G:C8	3.04	0.46
50:ZA:164:A:O2'	50:ZA:165:G:O4'	2.23	0.46
50:ZA:656:G:OP2	50:ZA:662:G:N2	2.48	0.46
50:ZA:942:G:H2'	50:ZA:943:U:C6	2.51	0.46
50:ZA:1086:G:O2'	50:ZA:1088:U:OP2	2.30	0.46
58:HB:274:LEU:HD21	58:HB:316:ARG:HD2	1.97	0.46
60:JB:136:ARG:HD2	60:JB:139:LYS:HA	1.97	0.46
70:TB:96:SER:HB3	70:TB:99:VAL:HG22	1.97	0.46
83:GC:133:ASN:HB3	83:GC:139:LYS:HD2	1.97	0.46
3:C:7:LEU:HB3	3:C:21:ASN:HB3	1.98	0.46
3:C:32:ILE:HG22	3:C:34:PRO:HD3	1.97	0.46
22:V:112:ALA:O	22:V:116:LYS:HG2	2.16	0.46
24:X:52:ASP:OD2	24:X:110:LYS:NZ	2.46	0.46
47:WA:1208:C:H2'	47:WA:1209:G:H8	1.80	0.46
47:WA:1658:U:H2'	47:WA:1659:G:H8	1.80	0.46
47:WA:1778:A:H2'	47:WA:1779:C:H6	1.81	0.46
47:WA:2650:G:H2'	47:WA:2651:G:H8	1.81	0.46
47:WA:3913:C:H1'	47:WA:4397:U:H3	1.80	0.46
47:WA:4580:G:H2'	47:WA:4581:U:H6	1.80	0.46
48:XA:13:A:OP2	48:XA:66:G:N2	2.44	0.46
50:ZA:300:U:O4	50:ZA:301:A:N6	2.49	0.46
50:ZA:511:U:O2'	50:ZA:576:A:N6	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:1279:C:H2'	50:ZA:1280:G:C8	2.50	0.46
50:ZA:1375:G:H2'	50:ZA:1376:A:C8	2.51	0.46
50:ZA:1617:G:N2	50:ZA:1619:A:H3'	2.31	0.46
50:ZA:1692:U:H2'	50:ZA:1693:G:H8	1.80	0.46
50:ZA:1828:C:H2'	50:ZA:1829:G:C8	2.51	0.46
52:BB:122:GLU:HG2	52:BB:140:VAL:HG12	1.97	0.46
54:DB:100:LYS:O	54:DB:105:ARG:NH1	2.46	0.46
57:GB:47:GLY:O	57:GB:115:LYS:NZ	2.38	0.46
59:IB:64:ASN:O	59:IB:186:ASP:HA	2.15	0.46
1:A:34:PHE:HE2	7:G:94:ILE:HD11	1.80	0.46
2:B:80:GLU:OE1	2:B:323:TYR:OH	2.31	0.46
5:E:185:ASN:ND2	5:E:274:LEU:O	2.42	0.46
5:E:259:GLN:O	5:E:263:LYS:NZ	2.45	0.46
41:OA:17:ARG:NH2	47:WA:1579:G:OP1	2.46	0.46
47:WA:3929:U:H2'	47:WA:3930:A:C8	2.51	0.46
49:YA:67:U:H2'	49:YA:68:G:C8	2.50	0.46
50:ZA:55:U:OP1	50:ZA:451:G:N1	2.40	0.46
50:ZA:1204:A:O2'	50:ZA:1700:C:OP2	2.31	0.46
55:EB:130:PHE:HE1	55:EB:140:VAL:HG23	1.80	0.46
59:IB:142:SER:OG	59:IB:143:LYS:N	2.48	0.46
83:GC:8:ARG:HB3	83:GC:309:VAL:HG23	1.97	0.46
1:A:200:ARG:NH2	47:WA:3653:A:OP2	2.44	0.46
3:C:110:ARG:O	3:C:113:ARG:NH1	2.33	0.46
4:D:148:ALA:HB2	4:D:159:VAL:HG21	1.97	0.46
6:F:222:LYS:HE3	47:WA:1909:A:H4'	1.98	0.46
47:WA:1647:C:H2'	47:WA:1648:A:H8	1.81	0.46
47:WA:2297:C:H2'	47:WA:2298:G:H8	1.79	0.46
47:WA:2499:C:H2'	47:WA:2500:C:C6	2.50	0.46
47:WA:4770:G:O2'	47:WA:4875:G:O6	2.33	0.46
49:YA:130:C:H2'	49:YA:131:G:H8	1.81	0.46
50:ZA:170:A:H2'	50:ZA:171:A:C8	2.50	0.46
50:ZA:404:G:H2'	50:ZA:405:G:C8	2.51	0.46
50:ZA:929:G:H21	50:ZA:1104:G:H4'	1.81	0.46
50:ZA:944:A:H2'	50:ZA:945:U:H6	1.81	0.46
53:CB:83:LEU:HG	72:VB:15:ARG:HG3	1.98	0.46
57:GB:50:VAL:HG13	57:GB:111:LEU:HB3	1.98	0.46
3:C:323:ARG:HB2	47:WA:1283:G:H5'	1.97	0.45
47:WA:680:C:H2'	47:WA:681:G:H8	1.81	0.45
47:WA:1326:A:H2	47:WA:3877:G:H21	1.64	0.45
47:WA:1678:C:N4	47:WA:4380:A:H2'	2.29	0.45
47:WA:1881:C:H2'	47:WA:1882:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:4091:G:H2'	47:WA:4092:G:H8	1.81	0.45
48:XA:118:C:H2'	48:XA:119:U:C6	2.51	0.45
50:ZA:1232:U:H2'	50:ZA:1233:G:C8	2.51	0.45
50:ZA:1386:A:OP2	54:DB:198:SER:OG	2.29	0.45
50:ZA:1731:A:H2'	50:ZA:1732:G:C8	2.51	0.45
53:CB:81:ILE:HG23	53:CB:86:LEU:HB2	1.98	0.45
55:EB:94:LYS:HB2	75:YB:17:LEU:HD23	1.98	0.45
62:LB:17:PHE:CZ	62:LB:19:ASN:HB2	2.51	0.45
12:L:24:LEU:HD11	12:L:86:TRP:CG	2.51	0.45
47:WA:1808:G:H2'	47:WA:1809:C:C6	2.51	0.45
47:WA:1813:G:H2'	47:WA:1814:C:H6	1.81	0.45
47:WA:2832:G:H2'	47:WA:2833:G:H8	1.80	0.45
47:WA:4314:U:H2'	47:WA:4315:A:C8	2.50	0.45
47:WA:4509:A:H2'	47:WA:4510:C:C6	2.51	0.45
47:WA:5059:C:H2'	47:WA:5060:A:C8	2.50	0.45
50:ZA:89:C:H2'	50:ZA:90:G:C8	2.51	0.45
50:ZA:116:U:O4	50:ZA:347:G:O6	2.33	0.45
50:ZA:687:C:O2'	58:HB:341:LYS:NZ	2.49	0.45
50:ZA:1245:G:N2	71:UB:72:GLU:OE2	2.49	0.45
50:ZA:1780:G:H2'	50:ZA:1781:A:C8	2.52	0.45
50:ZA:1845:A:H2'	50:ZA:1846:G:H8	1.82	0.45
58:HB:246:ILE:HG21	58:HB:254:PRO:HB3	1.99	0.45
58:HB:307:LEU:HD22	58:HB:334:ALA:HB2	1.97	0.45
65:OB:149:ARG:HH12	65:OB:151:LEU:HD13	1.81	0.45
71:UB:67:LYS:NZ	71:UB:78:ASP:OD1	2.34	0.45
75:YB:7:ILE:HB	75:YB:7:ILE:C	2.35	0.45
21:U:44:GLY:HA2	47:WA:4511:U:H5'	1.97	0.45
28:BA:50:ASN:OD1	28:BA:51:ASN:N	2.49	0.45
47:WA:1388:C:O2'	47:WA:1504:G:N2	2.48	0.45
47:WA:1404:C:H2'	47:WA:1405:G:C8	2.52	0.45
47:WA:1448:C:H2'	47:WA:1449:C:C6	2.52	0.45
47:WA:2861:G:O2'	47:WA:3839:C:O2'	2.24	0.45
49:YA:153:C:H2'	49:YA:154:G:C8	2.52	0.45
50:ZA:287:U:H3	55:EB:131:VAL:HG21	1.81	0.45
50:ZA:379:C:O2	59:IB:5:ARG:NH1	2.50	0.45
50:ZA:411:G:H2'	50:ZA:412:G:C8	2.52	0.45
50:ZA:430:C:H2'	50:ZA:431:G:H8	1.81	0.45
50:ZA:639:C:H2'	50:ZA:640:A:H8	1.82	0.45
50:ZA:1016:U:H5''	64:NB:14:SER:HB2	1.97	0.45
50:ZA:1351:G:N2	50:ZA:1360:U:O2	2.32	0.45
50:ZA:1512:C:H2'	50:ZA:1513:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:1579:A:O2'	50:ZA:1581:C:OP2	2.32	0.45
50:ZA:1693:G:N2	50:ZA:1834:A:H8	2.14	0.45
65:OB:30:VAL:HG21	65:OB:96:LYS:HE3	1.98	0.45
2:B:317:LEU:HB3	47:WA:5003:U:H4'	1.98	0.45
3:C:25:PRO:HB2	3:C:27:VAL:HG12	1.99	0.45
3:C:152:LEU:HD23	3:C:251:ILE:HG12	1.99	0.45
3:C:284:MET:HE2	3:C:287:THR:HA	1.98	0.45
7:G:156:ARG:NE	7:G:246:LEU:O	2.39	0.45
11:K:66:TYR:OH	47:WA:1384:G:OP1	2.28	0.45
13:M:54:LYS:NZ	47:WA:153:G:OP2	2.45	0.45
26:Z:75:LEU:HG	26:Z:113:GLY:HA2	1.98	0.45
27:AA:38:LYS:HD3	47:WA:1818:C:H4'	1.97	0.45
31:EA:54:LYS:HE3	47:WA:4750:U:H5''	1.98	0.45
44:SA:50:U:O2	44:SA:64:G:N2	2.38	0.45
47:WA:229:G:H2'	47:WA:230:G:H8	1.82	0.45
47:WA:4969:A:H2'	47:WA:4970:A:C8	2.51	0.45
50:ZA:12:U:H2'	50:ZA:13:C:C6	2.51	0.45
50:ZA:614:C:O2	74:XB:64:SER:OG	2.31	0.45
50:ZA:678:U:OP2	50:ZA:1026:C:N4	2.37	0.45
50:ZA:1199:A:OP1	77:AC:2:THR:OG1	2.32	0.45
50:ZA:1777:G:H2'	50:ZA:1778:C:C6	2.51	0.45
78:BC:64:CYS:HB3	78:BC:73:LEU:HD23	1.98	0.45
85:b:58:ASN:OD1	85:b:58:ASN:N	2.50	0.45
15:O:156:ARG:NH1	47:WA:2422:A:OP2	2.50	0.45
16:P:88:ASP:OD2	16:P:108:ARG:NH1	2.50	0.45
24:X:54:GLU:HB2	24:X:108:ARG:HB3	1.98	0.45
31:EA:50:VAL:HG22	31:EA:69:VAL:HG22	1.99	0.45
45:TA:14:A:H3'	45:TA:15:G:H8	1.82	0.45
47:WA:268:G:H2'	47:WA:269:G:C8	2.52	0.45
47:WA:311:G:H2'	47:WA:312:G:H8	1.82	0.45
47:WA:1432:C:H2'	47:WA:1433:C:H6	1.82	0.45
47:WA:2082:U:H2'	47:WA:2083:C:C6	2.52	0.45
47:WA:2378:A:H2'	47:WA:2379:C:C6	2.51	0.45
47:WA:4113:U:H2'	47:WA:4114:C:H6	1.82	0.45
47:WA:4176:U:H2'	47:WA:4177:G:H8	1.82	0.45
50:ZA:1203:G:H2'	50:ZA:1204:A:H8	1.82	0.45
50:ZA:1654:G:H2'	50:ZA:1655:C:C6	2.51	0.45
54:DB:61:GLU:OE2	54:DB:65:ARG:NE	2.50	0.45
55:EB:69:PHE:HB3	75:YB:17:LEU:HD22	1.99	0.45
3:C:119:GLN:NE2	47:WA:1352:C:O2	2.50	0.45
3:C:321:ASN:OD1	47:WA:1282:C:O2'	2.26	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:118:ALA:O	47:WA:1866:G:O2'	2.28	0.45
22:V:101:ARG:O	22:V:105:ARG:HG3	2.17	0.45
33:GA:66:LYS:HG2	49:YA:96:C:H5''	1.97	0.45
47:WA:275:C:H2'	47:WA:276:C:C6	2.51	0.45
47:WA:469:C:H2'	47:WA:470:A:H8	1.81	0.45
47:WA:1956:U:H2'	47:WA:1957:G:C8	2.52	0.45
47:WA:2694:U:H2'	47:WA:2695:G:O4'	2.16	0.45
47:WA:4072:U:H2'	47:WA:4073:U:C6	2.51	0.45
47:WA:4718:C:H2'	47:WA:4719:A:C8	2.52	0.45
48:XA:77:A:H62	48:XA:99:G:H21	1.63	0.45
50:ZA:17:C:H2'	50:ZA:18:C:C6	2.52	0.45
50:ZA:292:A:O2'	62:LB:39:ASN:O	2.22	0.45
50:ZA:609:U:N3	50:ZA:610:G:N7	2.64	0.45
50:ZA:974:C:H2'	50:ZA:975:G:C8	2.52	0.45
52:BB:138:PHE:O	52:BB:213:ARG:N	2.49	0.45
56:FB:19:LEU:HG	56:FB:24:SER:HA	1.98	0.45
62:LB:35:ARG:HH21	62:LB:63:THR:HG21	1.82	0.45
69:SB:124:ARG:NE	69:SB:130:ARG:O	2.38	0.45
74:XB:51:VAL:HG22	74:XB:72:VAL:HG22	1.98	0.45
1:A:8:GLN:O	47:WA:3669:C:O2'	2.35	0.45
9:I:87:ILE:HG12	9:I:138:ILE:HG12	1.98	0.45
11:K:130:LYS:HE3	11:K:132:SER:HB2	1.98	0.45
12:L:41:PRO:HG3	12:L:73:VAL:HG12	1.99	0.45
18:R:99:ASP:OD1	18:R:100:LEU:N	2.46	0.45
25:Y:54:THR:H	25:Y:57:MET:HE2	1.81	0.45
29:CA:33:ILE:HD11	29:CA:41:ARG:HB3	1.99	0.45
47:WA:1622:U:H2'	47:WA:1623:A:H8	1.80	0.45
47:WA:2541:C:H2'	47:WA:2542:C:C6	2.52	0.45
47:WA:4091:G:H2'	47:WA:4092:G:C8	2.52	0.45
47:WA:4137:G:H2'	47:WA:4138:G:H8	1.82	0.45
47:WA:4289:G:H2'	47:WA:4290:C:C6	2.52	0.45
50:ZA:223:C:H2'	50:ZA:224:A:C8	2.52	0.45
50:ZA:430:C:H2'	50:ZA:431:G:C8	2.52	0.45
50:ZA:639:C:H2'	50:ZA:640:A:C8	2.51	0.45
50:ZA:919:A:H5''	64:NB:16:LEU:HD12	1.99	0.45
50:ZA:1354:G:N2	50:ZA:1357:A:OP2	2.36	0.45
50:ZA:1458:G:OP1	83:GC:279:SER:OG	2.27	0.45
50:ZA:1811:C:H2'	50:ZA:1812:U:C6	2.52	0.45
50:ZA:1864:U:H5'	77:AC:79:ILE:HD11	1.99	0.45
53:CB:137:VAL:HB	53:CB:217:ALA:HA	1.99	0.45
54:DB:50:VAL:HG21	80:DC:34:TYR:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:KB:19:GLY:HA2	61:KB:71:LEU:HD12	1.98	0.45
75:YB:10:ARG:HH21	75:YB:24:VAL:HG11	1.81	0.45
6:F:131:MET:O	6:F:135:VAL:HG22	2.17	0.45
9:I:30:LYS:HD3	9:I:63:GLU:HG3	1.99	0.45
14:N:37:ARG:HH21	14:N:108:ILE:HD11	1.81	0.45
47:WA:1492:G:H2'	47:WA:1493:A:H8	1.81	0.45
47:WA:2807:C:H2'	47:WA:2808:A:C8	2.52	0.45
47:WA:4953:G:H2'	47:WA:4954:G:H8	1.80	0.45
50:ZA:219:U:H2'	50:ZA:220:U:C6	2.52	0.45
50:ZA:447:A:H4'	55:EB:3:ARG:HD2	1.99	0.45
50:ZA:562:U:P	60:JB:164:PRO:HD2	2.57	0.45
50:ZA:954:U:O2	65:OB:55:ARG:NH2	2.45	0.45
53:CB:128:VAL:HG11	53:CB:155:ILE:HG12	1.99	0.45
55:EB:107:GLY:HA2	55:EB:189:LEU:HB3	1.98	0.45
60:JB:122:SER:HB3	60:JB:125:HIS:HB2	1.99	0.45
63:MB:51:VAL:HG13	63:MB:77:ILE:HG13	1.98	0.45
70:TB:130:ASP:OD1	70:TB:133:ARG:NH2	2.50	0.45
83:GC:18:VAL:HA	83:GC:35:SER:HA	1.98	0.45
1:A:116:LEU:HB3	1:A:126:LEU:HB2	1.99	0.45
2:B:77:THR:HG21	2:B:337:VAL:HG22	1.99	0.45
2:B:220:ILE:HB	2:B:346:THR:HB	1.98	0.45
14:N:85:ARG:HG3	14:N:99:LEU:HD11	1.99	0.45
24:X:4:ASN:N	47:WA:243:A:OP1	2.50	0.45
40:NA:4:VAL:O	40:NA:94:GLY:N	2.50	0.45
47:WA:1293:G:H2'	47:WA:1294:C:C6	2.51	0.45
47:WA:1505:A:H1'	47:WA:1506:G:C8	2.52	0.45
47:WA:2080:C:H2'	47:WA:2081:G:C8	2.52	0.45
47:WA:2599:G:H2'	47:WA:2600:A:H8	1.81	0.45
47:WA:2729:C:H2'	47:WA:2730:U:C6	2.52	0.45
47:WA:4461:U:H2'	47:WA:4462:U:C6	2.52	0.45
47:WA:4529:G:OP2	47:WA:4529:G:N2	2.50	0.45
47:WA:4956:G:H2'	47:WA:4957:A:C8	2.52	0.45
49:YA:75:G:H2'	49:YA:76:C:C6	2.52	0.45
50:ZA:1619:A:O2'	66:PB:82:ASP:OD2	2.33	0.45
56:FB:40:ALA:HB1	56:FB:45:TYR:CD1	2.52	0.45
63:MB:47:ALA:HA	63:MB:112:LYS:HB3	1.99	0.45
74:XB:46:HIS:CD2	74:XB:103:ALA:HB2	2.52	0.45
1:A:24:LYS:HG3	1:A:49:ILE:HD12	1.98	0.45
2:B:43:LEU:HB3	2:B:183:ILE:HG21	1.99	0.45
8:H:66:GLU:OE1	8:H:66:GLU:N	2.50	0.45
10:J:56:THR:HG22	10:J:64:ARG:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:9:ILE:HG13	26:Z:49:HIS:CE1	2.52	0.45
19:S:41:ASP:HA	19:S:61:THR:HA	1.99	0.45
20:T:92:LYS:HZ3	47:WA:2628:U:H3'	1.82	0.45
47:WA:300:A:H2'	47:WA:301:G:H8	1.80	0.45
47:WA:1820:G:OP2	47:WA:1820:G:N2	2.33	0.45
47:WA:2108:G:O2'	47:WA:2110:G:OP2	2.32	0.45
47:WA:4899:G:H2'	47:WA:4900:G:C8	2.51	0.45
50:ZA:959:G:H1	65:OB:65:ASP:HB3	1.82	0.45
50:ZA:1093:A:H2'	50:ZA:1094:C:C6	2.52	0.45
50:ZA:1113:A:H2'	50:ZA:1114:U:C6	2.52	0.45
50:ZA:1198:G:H2'	50:ZA:1199:A:C8	2.51	0.45
50:ZA:1199:A:H2'	50:ZA:1200:A:C8	2.52	0.45
50:ZA:1605:G:O2'	50:ZA:1606:G:O4'	2.31	0.45
50:ZA:1705:C:H2'	50:ZA:1706:G:C8	2.51	0.45
74:XB:128:VAL:HG21	74:XB:141:PRO:HD3	1.97	0.45
1:A:28:ARG:HB3	1:A:123:ARG:HB3	1.99	0.44
11:K:62:PRO:HG3	47:WA:74:G:H1'	1.99	0.44
11:K:63:THR:O	11:K:67:HIS:N	2.50	0.44
50:ZA:694:G:N1	50:ZA:732:U:O4	2.50	0.44
55:EB:246:LEU:HD23	55:EB:250:GLU:HB3	1.99	0.44
56:FB:40:ALA:HB1	56:FB:45:TYR:CG	2.52	0.44
69:SB:121:ARG:HG3	69:SB:131:VAL:HG11	1.98	0.44
83:GC:67:SER:N	83:GC:81:GLY:O	2.50	0.44
4:D:36:LEU:HG	4:D:50:ARG:HD2	1.98	0.44
14:N:172:LYS:HG3	47:WA:4875:G:H22	1.83	0.44
18:R:17:LEU:HD11	19:S:136:ARG:HH21	1.82	0.44
24:X:2:LYS:HD2	24:X:7:VAL:HB	1.99	0.44
24:X:50:ARG:HB2	24:X:115:ARG:NH2	2.32	0.44
40:NA:2:VAL:N	40:NA:90:HIS:O	2.51	0.44
45:TA:22:G:H2'	45:TA:23:A:H8	1.82	0.44
47:WA:212:A:H2'	47:WA:213:G:C8	2.53	0.44
47:WA:478:G:H2'	47:WA:479:G:C8	2.51	0.44
47:WA:1806:A:H4'	47:WA:1807:A:O5'	2.17	0.44
47:WA:4265:C:H2'	47:WA:4266:G:O4'	2.17	0.44
47:WA:4454:U:O4'	89:WA:5178:ANM:H1	2.18	0.44
50:ZA:457:C:H2'	50:ZA:458:A:H8	1.82	0.44
50:ZA:652:U:H2'	50:ZA:653:A:H8	1.81	0.44
50:ZA:964:A:HO2'	50:ZA:1054:G:HO2'	1.60	0.44
50:ZA:1146:C:H2'	50:ZA:1147:C:C6	2.52	0.44
50:ZA:1146:C:O2'	50:ZA:1150:A:N1	2.45	0.44
50:ZA:1689:C:C2	50:ZA:1690:U:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:MB:57:ASP:OD1	63:MB:57:ASP:N	2.51	0.44
73:WB:101:PHE:HA	73:WB:113:HIS:CE1	2.52	0.44
85:b:47:LEU:HD22	85:b:51:ALA:HB3	1.97	0.44
2:B:257:TRP:CD1	47:WA:3901:G:H5''	2.53	0.44
8:H:18:ILE:HG12	8:H:27:VAL:HG22	1.99	0.44
10:J:52:LYS:NZ	40:NA:101:GLY:O	2.45	0.44
13:M:193:ARG:O	13:M:197:THR:OG1	2.21	0.44
17:Q:12:SER:OG	17:Q:17:CYS:O	2.24	0.44
26:Z:59:ARG:NH2	47:WA:89:C:OP1	2.47	0.44
33:GA:34:ALA:HA	33:GA:37:THR:HG22	1.99	0.44
39:MA:2:ARG:HB3	39:MA:5:TRP:CD1	2.52	0.44
47:WA:1346:C:H2'	47:WA:1347:A:H8	1.81	0.44
47:WA:1622:U:H2'	47:WA:1623:A:C8	2.52	0.44
47:WA:1881:C:O2'	47:WA:1893:A:N3	2.42	0.44
47:WA:2069:C:H2'	47:WA:2070:C:C6	2.52	0.44
50:ZA:70:G:N2	50:ZA:71:G:O6	2.50	0.44
50:ZA:89:C:H2'	50:ZA:90:G:H8	1.81	0.44
50:ZA:156:G:H2'	50:ZA:157:U:C6	2.53	0.44
50:ZA:615:C:O2	81:EC:84:LYS:NZ	2.42	0.44
50:ZA:836:G:C6	75:YB:7:ILE:CG1	3.01	0.44
50:ZA:1337:C:H2'	50:ZA:1338:G:H8	1.82	0.44
50:ZA:1450:G:N7	68:RB:44:LYS:NZ	2.66	0.44
50:ZA:1690:U:H2'	50:ZA:1691:U:H6	1.82	0.44
51:AB:58:LEU:HD11	51:AB:178:LEU:HB2	1.99	0.44
60:JB:32:ILE:HG12	60:JB:37:LEU:HB2	1.98	0.44
74:XB:39:ASN:OD1	74:XB:42:GLY:N	2.50	0.44
80:DC:21:CYS:HB2	80:DC:39:CYS:SG	2.57	0.44
83:GC:236:ILE:HG12	83:GC:252:THR:HG22	1.99	0.44
86:At:43:C:H2'	86:At:44:G:C8	2.52	0.44
3:C:222:ARG:NE	47:WA:225:G:OP1	2.50	0.44
16:P:33:ARG:HG2	16:P:48:LEU:HD21	2.00	0.44
16:P:62:SER:OG	47:WA:1504:G:OP2	2.27	0.44
25:Y:46:ILE:HG23	25:Y:68:ILE:HG23	1.99	0.44
29:CA:98:SER:OG	29:CA:100:ASN:OD1	2.33	0.44
30:DA:58:ILE:HD12	47:WA:2321:C:N4	2.33	0.44
43:RA:119:ARG:NH1	47:WA:1974:G:O2'	2.50	0.44
47:WA:227:A:N6	47:WA:242:U:O4'	2.51	0.44
47:WA:2081:G:H2'	47:WA:2082:U:H6	1.82	0.44
47:WA:2364:U:H2'	47:WA:2365:A:C8	2.52	0.44
47:WA:2859:A:H2'	47:WA:2860:A:O4'	2.18	0.44
47:WA:4063:C:H2'	47:WA:4064:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:603:C:H1'	50:ZA:604:A:N7	2.32	0.44
50:ZA:829:C:O2'	50:ZA:845:G:N2	2.50	0.44
50:ZA:1047:C:H2'	50:ZA:1048:G:O4'	2.18	0.44
50:ZA:1588:A:H2'	50:ZA:1589:A:H8	1.83	0.44
50:ZA:1731:A:H2'	50:ZA:1732:G:H8	1.83	0.44
68:RB:16:ILE:HG22	68:RB:24:LEU:HD11	2.00	0.44
70:TB:11:GLN:OE1	70:TB:62:ARG:NE	2.50	0.44
75:YB:29:HIS:HB2	75:YB:32:LYS:HG3	1.99	0.44
6:F:88:LEU:HD11	6:F:121:PHE:HB3	1.99	0.44
19:S:87:LYS:HE3	47:WA:4302:U:H5''	2.00	0.44
30:DA:24:GLN:NE2	47:WA:1317:C:O5'	2.50	0.44
41:OA:58:GLY:O	47:WA:2654:G:N1	2.47	0.44
42:PA:10:VAL:HG21	42:PA:44:ILE:HD11	2.00	0.44
47:WA:712:A:H2'	47:WA:713:C:C6	2.52	0.44
47:WA:1579:G:O2'	47:WA:1614:G:O5'	2.32	0.44
47:WA:1618:U:H2'	47:WA:1619:G:H8	1.82	0.44
47:WA:1623:A:H2'	47:WA:1624:U:C6	2.52	0.44
47:WA:1665:C:H2'	47:WA:1666:U:H6	1.83	0.44
47:WA:2319:C:H2'	47:WA:2320:G:C8	2.53	0.44
47:WA:2374:U:H2'	47:WA:2375:C:C6	2.52	0.44
47:WA:2786:C:H2'	47:WA:2787:C:H6	1.82	0.44
47:WA:3654:A:H2'	47:WA:3655:A:C8	2.52	0.44
50:ZA:912:C:H3'	50:ZA:913:A:H3'	2.00	0.44
50:ZA:1839:U:H2'	50:ZA:1840:U:C6	2.53	0.44
52:BB:82:ARG:NH1	52:BB:191:ASP:OD1	2.50	0.44
59:IB:12:ARG:HH21	59:IB:18:ARG:HG3	1.83	0.44
86:At:27:G:H2'	86:At:28:G:H8	1.83	0.44
2:B:229:LYS:HG3	2:B:272:LYS:HD3	1.99	0.44
7:G:158:GLU:OE2	7:G:166:ARG:NH2	2.38	0.44
11:K:91:ALA:HB1	11:K:96:ILE:HB	1.98	0.44
12:L:46:ARG:HH11	47:WA:942:U:H5	1.65	0.44
47:WA:228:C:H2'	47:WA:229:G:H8	1.83	0.44
47:WA:2378:A:H2'	47:WA:2379:C:H6	1.82	0.44
47:WA:4174:A:H3'	47:WA:4175:G:H8	1.82	0.44
50:ZA:676:C:H2'	50:ZA:677:G:O4'	2.18	0.44
50:ZA:688:U:OP1	58:HB:354:ARG:NH2	2.50	0.44
50:ZA:1304:U:OP1	82:FC:93:HIS:HB2	2.18	0.44
50:ZA:1677:U:OP1	56:FB:71:ARG:NH2	2.50	0.44
58:HB:285:ALA:HB3	58:HB:301:PHE:HB2	1.99	0.44
69:SB:34:LYS:HB3	69:SB:100:ALA:HA	1.99	0.44
79:CC:33:GLU:HG2	79:CC:41:SER:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:82:ILE:HG22	21:U:83:ARG:HG3	1.98	0.44
45:TA:41:U:H2'	45:TA:42:G:C8	2.53	0.44
45:TA:43:A:H2'	45:TA:44:G:C8	2.53	0.44
47:WA:419:A:N3	47:WA:1334:C:O2'	2.49	0.44
47:WA:423:G:H2'	47:WA:424:U:H6	1.83	0.44
47:WA:1394:A:H2'	47:WA:1395:G:C8	2.52	0.44
47:WA:1619:G:H1'	47:WA:2515:A:N6	2.32	0.44
47:WA:1802:U:H2'	47:WA:1803:A:C8	2.53	0.44
47:WA:1944:A:N6	47:WA:2041:G:H2'	2.32	0.44
47:WA:2061:C:H2'	47:WA:2062:G:C8	2.52	0.44
47:WA:2260:C:H5''	47:WA:2261:G:C8	2.53	0.44
47:WA:2450:G:H2'	47:WA:2451:A:C8	2.52	0.44
47:WA:2523:G:H2'	47:WA:2524:G:C8	2.52	0.44
47:WA:4596:U:H2'	47:WA:4597:G:C8	2.53	0.44
50:ZA:17:C:H4'	50:ZA:1166:G:C8	2.52	0.44
50:ZA:1202:U:H2'	50:ZA:1203:G:C8	2.52	0.44
50:ZA:1217:A:H2'	50:ZA:1218:C:C6	2.53	0.44
50:ZA:1804:U:H2'	50:ZA:1805:G:C8	2.50	0.44
54:DB:201:PRO:O	54:DB:205:TYR:HB2	2.17	0.44
65:OB:106:LYS:HD2	65:OB:135:ILE:HG22	1.99	0.44
86:At:8:4SU:H5''	86:At:49:C:H5'	2.00	0.44
86:At:9:A:O2'	86:At:10:G:N7	2.51	0.44
3:C:60:HIS:NE2	3:C:100:ARG:HD3	2.33	0.44
3:C:183:VAL:HG22	3:C:204:ARG:HB3	1.98	0.44
15:O:69:HIS:NE2	15:O:139:ASP:O	2.45	0.44
16:P:35:LEU:O	16:P:39:THR:OG1	2.22	0.44
18:R:95:ARG:NE	18:R:113:MET:SD	2.91	0.44
20:T:19:LEU:HD22	20:T:78:PHE:H	1.83	0.44
23:W:68:ARG:NH2	49:YA:60:G:OP1	2.51	0.44
26:Z:119:LYS:HA	26:Z:140:VAL:HG13	1.99	0.44
47:WA:1346:C:H2'	47:WA:1347:A:C8	2.53	0.44
47:WA:1507:C:H2'	47:WA:1508:G:H8	1.83	0.44
47:WA:4594:C:H2'	47:WA:4595:C:C6	2.52	0.44
47:WA:4649:G:H2'	47:WA:4650:A:H8	1.83	0.44
49:YA:141:C:H2'	49:YA:142:U:C6	2.52	0.44
50:ZA:544:G:H2'	50:ZA:545:A:H8	1.83	0.44
59:IB:81:VAL:HG22	59:IB:102:VAL:HG12	1.99	0.44
3:C:218:VAL:HA	3:C:229:LEU:HG	2.00	0.44
4:D:17:GLN:NE2	19:S:22:HIS:O	2.46	0.44
9:I:144:ASN:HB3	9:I:147:HIS:HB2	1.99	0.44
13:M:98:LEU:HD22	13:M:128:LYS:HD2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:42:ASN:HD22	14:N:125:LYS:HD3	1.83	0.44
15:O:164:ARG:NH2	47:WA:1598:U:O2'	2.51	0.44
16:P:158:THR:O	16:P:161:SER:OG	2.32	0.44
19:S:12:ARG:HD2	47:WA:4211:G:H4'	1.99	0.44
19:S:71:ALA:HB3	47:WA:4315:A:H4'	2.00	0.44
29:CA:39:LYS:HG3	29:CA:40:LYS:HG2	1.99	0.44
34:HA:60:LEU:HA	34:HA:63:VAL:HG22	1.98	0.44
37:KA:26:TRP:HE1	49:YA:50:C:H2'	1.83	0.44
47:WA:692:C:H2'	47:WA:693:A:C8	2.52	0.44
47:WA:2449:U:H2'	47:WA:2450:G:H8	1.83	0.44
47:WA:2467:C:H2'	47:WA:2468:G:O4'	2.18	0.44
47:WA:2554:G:N2	47:WA:2768:A:H62	2.15	0.44
47:WA:2777:C:H2'	47:WA:2778:G:C8	2.53	0.44
47:WA:3869:A:H2'	47:WA:3870:G:C8	2.52	0.44
47:WA:3895:C:H2'	47:WA:3896:A:C8	2.52	0.44
50:ZA:1248:U:H2'	50:ZA:1249:C:C6	2.53	0.44
50:ZA:1430:C:H2'	50:ZA:1431:G:C8	2.52	0.44
50:ZA:1555:U:H2'	50:ZA:1556:A:C8	2.53	0.44
50:ZA:1590:C:H2'	50:ZA:1591:C:O4'	2.18	0.44
56:FB:49:LEU:HD11	67:QB:75:TYR:HB3	1.99	0.44
75:YB:39:GLU:HA	75:YB:42:GLU:HG2	2.00	0.44
1:A:208:GLU:CD	47:WA:1631:G:H22	2.26	0.43
2:B:56:ILE:HD11	2:B:74:GLU:HB2	2.00	0.43
5:E:144:ARG:NH2	31:EA:108:SER:O	2.52	0.43
7:G:217:ILE:O	7:G:221:VAL:HG23	2.18	0.43
10:J:44:THR:O	10:J:78:LYS:NZ	2.37	0.43
14:N:176:ARG:NH2	47:WA:4771:G:OP1	2.51	0.43
21:U:89:ARG:HB2	21:U:95:PHE:CE2	2.53	0.43
25:Y:53:VAL:HG21	25:Y:62:ILE:HG23	2.00	0.43
27:AA:57:MET:HE2	47:WA:1813:G:H21	1.83	0.43
27:AA:110:ALA:HB1	47:WA:1273:G:H5'	2.00	0.43
31:EA:4:ARG:NH1	47:WA:4756:G:OP1	2.50	0.43
35:IA:28:HIS:CE1	35:IA:30:GLN:HB2	2.53	0.43
47:WA:269:G:H2'	47:WA:270:U:C6	2.53	0.43
47:WA:961:A:H1'	47:WA:2078:G:H5''	2.00	0.43
47:WA:991:C:H2'	47:WA:992:C:H6	1.84	0.43
47:WA:1094:C:H2'	47:WA:1095:G:H8	1.79	0.43
47:WA:1729:U:H2'	47:WA:1730:U:H6	1.83	0.43
47:WA:1867:G:N2	47:WA:1870:A:OP2	2.29	0.43
47:WA:1969:A:H2'	47:WA:1970:G:H8	1.83	0.43
47:WA:3650:A:H1'	47:WA:3787:A:N6	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:3754:C:H2'	47:WA:3779:G:H5''	2.00	0.43
50:ZA:375:U:H2'	50:ZA:376:A:C8	2.53	0.43
50:ZA:1101:U:H2'	50:ZA:1102:G:H8	1.82	0.43
50:ZA:1713:C:H2'	50:ZA:1714:U:C6	2.53	0.43
76:ZB:32:LYS:HE2	76:ZB:32:LYS:H	1.82	0.43
76:ZB:73:VAL:HG21	76:ZB:88:LEU:HD11	2.01	0.43
83:GC:124:SER:OG	83:GC:125:ARG:N	2.51	0.43
45:TA:70:G:H2'	45:TA:71:G:C8	2.52	0.43
47:WA:229:G:H2'	47:WA:230:G:C8	2.52	0.43
47:WA:1528:G:H2'	47:WA:1529:A:C8	2.53	0.43
47:WA:1561:G:H2'	47:WA:1562:A:H8	1.82	0.43
47:WA:2492:U:H3'	47:WA:2493:C:C6	2.54	0.43
47:WA:2580:G:H2'	47:WA:2581:G:H8	1.83	0.43
47:WA:4580:G:H2'	47:WA:4581:U:C6	2.53	0.43
50:ZA:115:U:H2'	50:ZA:116:U:C6	2.54	0.43
50:ZA:344:U:O2'	55:EB:34:GLY:O	2.30	0.43
50:ZA:498:C:H2'	50:ZA:499:G:C8	2.53	0.43
51:AB:176:TRP:NE1	51:AB:197:VAL:O	2.49	0.43
64:NB:4:MET:HG2	64:NB:5:HIS:CD2	2.53	0.43
71:UB:69:PRO:HB3	80:DC:41:GLN:HG2	2.00	0.43
3:C:343:GLN:HG2	47:WA:725:C:H1'	1.99	0.43
4:D:15:ARG:HH11	47:WA:1745:A:H1'	1.84	0.43
16:P:122:THR:OG1	16:P:124:ASP:OD1	2.27	0.43
17:Q:60:ARG:NH2	17:Q:63:CYS:SG	2.88	0.43
18:R:118:ARG:NH2	47:WA:2061:C:O2'	2.51	0.43
26:Z:2:PRO:HD3	47:WA:1511:C:H5''	2.00	0.43
30:DA:5:ARG:NH1	47:WA:454:U:O2	2.51	0.43
47:WA:39:A:H61	47:WA:1682:G:N2	2.14	0.43
47:WA:1683:G:OP2	47:WA:1855:G:N1	2.50	0.43
47:WA:4462:U:H2'	47:WA:4463:C:C6	2.54	0.43
47:WA:4483:U:H2'	47:WA:4484:U:C6	2.53	0.43
50:ZA:295:C:H2'	50:ZA:296:U:C6	2.53	0.43
50:ZA:1201:U:H2'	50:ZA:1202:U:H6	1.83	0.43
50:ZA:1801:A:H2'	50:ZA:1802:C:C6	2.52	0.43
55:EB:54:TYR:OH	55:EB:97:GLU:OE1	2.33	0.43
2:B:57:VAL:HB	2:B:367:PHE:HB3	1.99	0.43
17:Q:6:LEU:HD22	47:WA:2414:A:H5''	2.00	0.43
22:V:44:ARG:NH1	47:WA:3617:G:O2'	2.50	0.43
23:W:101:ASP:OD1	23:W:102:VAL:N	2.51	0.43
30:DA:109:LYS:NZ	30:DA:128:ARG:O	2.49	0.43
40:NA:12:CYS:HB3	40:NA:15:CYS:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:228:C:H2'	47:WA:229:G:C8	2.53	0.43
47:WA:347:A:H2'	47:WA:348:G:C8	2.53	0.43
47:WA:2649:A:H62	47:WA:2688:G:H8	1.65	0.43
47:WA:3724:G:H2'	47:WA:3725:A:H8	1.81	0.43
47:WA:4718:C:H2'	47:WA:4719:A:H8	1.82	0.43
47:WA:4990:U:H5	47:WA:5062:A:H2'	1.83	0.43
47:WA:5013:A:H2'	47:WA:5014:G:H8	1.84	0.43
50:ZA:1797:U:H2'	50:ZA:1798:C:H6	1.83	0.43
50:ZA:1809:A:H2'	50:ZA:1810:U:C6	2.53	0.43
50:ZA:1810:U:H2'	50:ZA:1811:C:C6	2.53	0.43
55:EB:171:ASP:OD1	55:EB:172:PHE:N	2.44	0.43
68:RB:102:THR:O	68:RB:105:MET:HG3	2.17	0.43
76:ZB:58:LEU:HD12	76:ZB:62:VAL:HG21	1.99	0.43
3:C:161:TYR:HE2	3:C:170:LEU:HD22	1.84	0.43
22:V:110:ARG:HG2	50:ZA:326:C:O2'	2.18	0.43
30:DA:103:VAL:O	30:DA:128:ARG:NH1	2.52	0.43
35:IA:79:ARG:NH1	49:YA:94:G:O4'	2.52	0.43
47:WA:1944:A:N3	47:WA:4434:C:O2'	2.42	0.43
47:WA:2644:A:N6	47:WA:2645:G:O6	2.51	0.43
47:WA:4391:C:H2'	47:WA:4392:A:C8	2.53	0.43
50:ZA:220:U:H2'	50:ZA:221:A:H8	1.84	0.43
51:AB:125:THR:O	51:AB:147:LEU:HB2	2.18	0.43
56:FB:50:PRO:HB3	56:FB:69:VAL:HG12	2.00	0.43
59:IB:119:LEU:HD11	59:IB:153:LYS:HG3	2.01	0.43
63:MB:79:VAL:HG11	63:MB:85:LEU:HB2	1.99	0.43
69:SB:20:ILE:HD11	69:SB:33:ILE:HG13	2.00	0.43
78:BC:19:HIS:O	78:BC:23:ARG:HG3	2.18	0.43
5:E:195:LYS:NZ	47:WA:712:A:OP1	2.34	0.43
7:G:253:THR:OG1	47:WA:150:U:OP2	2.25	0.43
15:O:113:PRO:HB2	15:O:116:SER:HB2	2.01	0.43
18:R:166:ARG:HD2	47:WA:1921:G:C2	2.54	0.43
20:T:105:ASN:HD21	20:T:111:GLU:HB2	1.83	0.43
23:W:102:VAL:HA	23:W:134:LYS:HE3	2.00	0.43
44:SA:42:A:H2'	44:SA:43:A:C8	2.54	0.43
47:WA:1179:G:H2'	47:WA:1180:G:C8	2.54	0.43
47:WA:2607:G:H2'	47:WA:2608:G:C8	2.54	0.43
47:WA:3798:U:O2'	50:ZA:1720:U:O2'	2.22	0.43
47:WA:3912:C:H2'	47:WA:3913:C:H6	1.84	0.43
47:WA:4739:G:N1	47:WA:4965:G:O6	2.51	0.43
47:WA:5032:U:H2'	47:WA:5033:G:H8	1.83	0.43
50:ZA:824:C:H5'	60:JB:150:ARG:HH22	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:ZA:1406:G:H2'	50:ZA:1407:U:C6	2.53	0.43
50:ZA:1452:A:H61	50:ZA:1473:G:N2	2.17	0.43
50:ZA:1616:U:H2'	50:ZA:1617:G:C8	2.54	0.43
50:ZA:1668:U:OP2	67:QB:167:TYR:OH	2.29	0.43
50:ZA:1864:U:OP2	77:AC:4:LYS:NZ	2.43	0.43
54:DB:195:MET:HE2	54:DB:225:LYS:HB3	2.01	0.43
55:EB:136:ILE:HG23	55:EB:149:TYR:CE1	2.53	0.43
55:EB:151:ASP:HB3	55:EB:154:ILE:HG12	1.99	0.43
57:GB:32:MET:HB2	57:GB:100:CYS:HB2	2.00	0.43
60:JB:29:LEU:HB3	81:EC:115:PHE:HE2	1.84	0.43
60:JB:150:ARG:H	60:JB:150:ARG:HG2	1.51	0.43
79:CC:36:ASP:OD1	79:CC:36:ASP:N	2.52	0.43
1:A:47:ASP:HA	1:A:84:THR:HG22	2.00	0.43
2:B:248:LEU:N	47:WA:2840:G:OP1	2.52	0.43
5:E:153:LEU:HD13	5:E:197:VAL:HG21	2.00	0.43
13:M:65:ARG:NH2	47:WA:2459:G:OP1	2.52	0.43
19:S:34:TYR:HE2	19:S:93:ILE:HG23	1.83	0.43
25:Y:38:TYR:CE2	25:Y:40:HIS:HB3	2.54	0.43
30:DA:85:LEU:HD22	30:DA:111:ILE:HG23	2.00	0.43
45:TA:58:A:O2'	45:TA:60:U:OP2	2.33	0.43
47:WA:252:C:H2'	47:WA:253:G:C8	2.53	0.43
47:WA:1689:U:H2'	47:WA:1690:G:C8	2.53	0.43
47:WA:1963:G:C8	85:b:60:MET:HE1	2.54	0.43
47:WA:2287:A:H2'	47:WA:2288:G:H8	1.82	0.43
47:WA:3712:G:H1'	47:WA:3714:A:N6	2.34	0.43
47:WA:4773:C:H2'	47:WA:4774:C:C6	2.54	0.43
50:ZA:172:U:N3	50:ZA:337:C:O2'	2.51	0.43
50:ZA:610:G:O6	50:ZA:634:A:N6	2.51	0.43
52:BB:71:LEU:HD23	52:BB:79:VAL:HG22	2.01	0.43
56:FB:122:ARG:HE	79:CC:59:LEU:HD21	1.83	0.43
63:MB:80:ASP:OD1	63:MB:80:ASP:N	2.52	0.43
71:UB:21:ARG:HB3	71:UB:115:THR:HB	2.01	0.43
75:YB:27:VAL:HB	75:YB:69:THR:OG1	2.18	0.43
6:F:147:LYS:HD2	47:WA:947:G:H3'	2.01	0.43
18:R:15:ARG:HB3	18:R:27:LEU:HG	2.01	0.43
22:V:11:TYR:HB2	22:V:32:LEU:HD22	2.01	0.43
24:X:59:ARG:HB2	24:X:103:LYS:HD2	2.01	0.43
32:FA:73:HIS:ND1	47:WA:2753:G:OP1	2.41	0.43
47:WA:913:U:H2'	47:WA:914:G:O4'	2.18	0.43
47:WA:1463:C:H2'	47:WA:1464:A:C8	2.53	0.43
47:WA:1878:U:H2'	47:WA:1879:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:1963:G:H8	85:b:60:MET:HE1	1.83	0.43
47:WA:2580:G:H2'	47:WA:2581:G:C8	2.53	0.43
47:WA:2766:A:H2'	47:WA:2767:A:H8	1.83	0.43
47:WA:3870:G:N2	47:WA:3902:G:O2'	2.35	0.43
47:WA:4083:G:H2'	47:WA:4084:G:C8	2.54	0.43
50:ZA:354:U:H2'	50:ZA:355:G:C8	2.54	0.43
50:ZA:623:G:C2	50:ZA:624:C:C5	3.06	0.43
1:A:222:PRO:HG2	47:WA:3707:G:H1'	2.01	0.43
15:O:43:SER:HB3	15:O:180:THR:HG22	2.00	0.43
20:T:105:ASN:ND2	20:T:111:GLU:HB2	2.34	0.43
33:GA:89:ARG:O	33:GA:93:ARG:HG2	2.18	0.43
47:WA:672:G:H2'	47:WA:673:C:C6	2.54	0.43
47:WA:2454:G:H21	47:WA:2509:A:H62	1.65	0.43
47:WA:4861:C:H2'	47:WA:4862:G:C8	2.53	0.43
47:WA:4951:G:H5'	47:WA:4953:G:H5'	2.00	0.43
50:ZA:519:A:H2'	50:ZA:520:A:H8	1.83	0.43
50:ZA:1143:A:O3'	50:ZA:1355:C:N4	2.52	0.43
50:ZA:1249:C:OP2	50:ZA:1250:A:O2'	2.27	0.43
2:B:20:LYS:HB3	47:WA:4569:G:H5'	2.01	0.43
18:R:107:THR:O	18:R:111:ARG:HG2	2.19	0.43
23:W:100:VAL:HG21	23:W:109:ILE:HD11	2.01	0.43
45:TA:34:U:C4	50:ZA:1218:C:H5'	2.53	0.43
47:WA:1507:C:H2'	47:WA:1508:G:C8	2.54	0.43
47:WA:1878:U:H2'	47:WA:1879:G:H8	1.83	0.43
47:WA:4262:U:H2'	47:WA:4263:C:C6	2.54	0.43
50:ZA:12:U:O2'	50:ZA:1356:G:O2'	2.32	0.43
50:ZA:167:G:H2'	50:ZA:168:C:C6	2.54	0.43
50:ZA:556:U:H2'	50:ZA:557:U:C6	2.53	0.43
50:ZA:835:C:H42	75:YB:8:ARG:HE	1.66	0.43
50:ZA:846:G:P	55:EB:108:ARG:HH12	2.41	0.43
50:ZA:1453:C:OP1	68:RB:48:ASN:ND2	2.52	0.43
50:ZA:1689:C:H2'	50:ZA:1690:U:H6	1.84	0.43
50:ZA:1858:G:OP2	65:OB:146:ARG:NH2	2.42	0.43
57:GB:20:ASP:OD1	57:GB:20:ASP:N	2.52	0.43
57:GB:121:ILE:HG22	57:GB:123:GLY:H	1.83	0.43
73:WB:113:HIS:NE2	73:WB:114:GLU:OE2	2.52	0.43
3:C:128:LEU:O	3:C:131:SER:OG	2.32	0.42
20:T:103:VAL:HG21	20:T:113:ARG:CZ	2.49	0.42
27:AA:114:ARG:HG3	27:AA:117:ARG:HH22	1.84	0.42
29:CA:39:LYS:HE3	47:WA:2372:A:H5'	2.00	0.42
33:GA:66:LYS:NZ	33:GA:82:ASP:OD2	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:1779:C:H2'	47:WA:1780:C:H6	1.84	0.42
47:WA:1960:A:OP1	85:b:10:LYS:NZ	2.46	0.42
47:WA:2449:U:H1'	47:WA:2746:A:H2	1.83	0.42
47:WA:2516:G:O2'	47:WA:2745:A:N6	2.52	0.42
47:WA:3635:C:H2'	47:WA:3636:G:H8	1.81	0.42
47:WA:3892:A:N6	47:WA:4573:A:O4'	2.52	0.42
47:WA:4254:C:OP2	47:WA:4255:A:O2'	2.34	0.42
50:ZA:616:A:H62	50:ZA:625:G:H21	1.66	0.42
50:ZA:1134:G:H2'	50:ZA:1135:C:C6	2.53	0.42
50:ZA:1294:G:H2'	50:ZA:1295:A:C8	2.53	0.42
50:ZA:1650:A:H5''	67:QB:165:ALA:HB2	1.99	0.42
50:ZA:1673:U:H2'	50:ZA:1674:G:O4'	2.19	0.42
53:CB:67:GLY:HA2	53:CB:93:ILE:HD11	2.00	0.42
56:FB:34:SER:HA	79:CC:55:VAL:HB	2.00	0.42
60:JB:129:LEU:HD22	60:JB:134:HIS:HD1	1.83	0.42
3:C:95:MET:O	47:WA:1337:G:N2	2.50	0.42
9:I:171:TRP:O	9:I:174:THR:OG1	2.32	0.42
21:U:91:LYS:HA	21:U:91:LYS:HD3	1.88	0.42
24:X:61:HIS:N	47:WA:232:G:O6	2.47	0.42
39:MA:2:ARG:NE	50:ZA:1842:C:OP2	2.41	0.42
40:NA:52:THR:HG22	47:WA:43:U:H4'	2.01	0.42
47:WA:4110:G:H2'	47:WA:4111:G:H8	1.84	0.42
47:WA:5013:A:H2'	47:WA:5014:G:C8	2.54	0.42
50:ZA:220:U:H4'	59:IB:176:ALA:HB3	2.01	0.42
50:ZA:352:U:H2'	50:ZA:353:C:C6	2.54	0.42
50:ZA:642:U:OP1	60:JB:41:ARG:N	2.51	0.42
50:ZA:1298:G:O2'	50:ZA:1299:A:H8	2.03	0.42
50:ZA:1858:G:OP1	77:AC:17:HIS:NE2	2.51	0.42
52:BB:136:ARG:HB2	52:BB:218:LEU:HD11	2.01	0.42
83:GC:157:SER:HB2	83:GC:164:ILE:HB	2.00	0.42
85:b:28:PHE:HB2	85:b:89:VAL:HG22	2.01	0.42
2:B:242:ARG:HA	2:B:248:LEU:HD22	2.01	0.42
7:G:212:HIS:ND1	7:G:238:LYS:HA	2.34	0.42
9:I:4:ARG:HD3	47:WA:4407:G:H4'	2.01	0.42
15:O:107:TRP:CD1	15:O:109:GLN:H	2.37	0.42
47:WA:31:U:H3	47:WA:51:A:H61	1.66	0.42
47:WA:65:A:H61	47:WA:75:G:H1'	1.84	0.42
47:WA:477:C:H2'	47:WA:478:G:H8	1.84	0.42
47:WA:1526:A:H62	47:WA:1653:G:H1	1.65	0.42
47:WA:1886:C:H2'	47:WA:1887:G:C8	2.55	0.42
47:WA:1944:A:H61	47:WA:2041:G:H2'	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:2000:A:H1'	47:WA:2021:C:O2'	2.20	0.42
47:WA:2626:G:H2'	47:WA:2627:U:C6	2.54	0.42
47:WA:4245:C:OP2	47:WA:4266:G:N2	2.48	0.42
50:ZA:675:U:H2'	50:ZA:676:C:C6	2.55	0.42
50:ZA:953:C:H5''	52:BB:24:PRO:HB2	2.01	0.42
50:ZA:1032:C:H2'	50:ZA:1033:G:O4'	2.19	0.42
50:ZA:1531:A:H4'	50:ZA:1605:G:H5'	2.01	0.42
53:CB:104:ASP:HB3	53:CB:130:ILE:HG13	2.01	0.42
57:GB:188:LYS:HA	57:GB:191:ARG:HH11	1.83	0.42
83:GC:254:PRO:HB3	83:GC:283:PRO:HB2	2.00	0.42
2:B:35:ASP:HB3	2:B:186:ASN:ND2	2.34	0.42
12:L:6:PHE:O	12:L:11:ARG:NE	2.51	0.42
23:W:79:PHE:HB2	33:GA:36:VAL:HG21	2.01	0.42
24:X:55:VAL:HG12	24:X:106:ILE:HG12	2.01	0.42
29:CA:19:GLU:HB3	29:CA:102:LEU:HD21	2.02	0.42
38:LA:99:LYS:HD2	47:WA:4476:A:H5''	2.01	0.42
44:SA:11:U:H2'	44:SA:12:G:C8	2.54	0.42
47:WA:368:C:N4	47:WA:369:G:O6	2.52	0.42
47:WA:1435:A:H62	47:WA:1453:G:H21	1.67	0.42
47:WA:1850:C:H2'	47:WA:1851:U:O4'	2.19	0.42
47:WA:1956:U:H2'	47:WA:1957:G:H8	1.84	0.42
47:WA:2285:G:H2'	47:WA:2286:G:C8	2.53	0.42
47:WA:3857:C:H2'	47:WA:3858:A:H8	1.85	0.42
47:WA:4194:A:H2'	47:WA:4195:C:C6	2.54	0.42
47:WA:4508:C:H2'	47:WA:4509:A:H8	1.84	0.42
47:WA:4539:C:H2'	47:WA:4540:G:C8	2.55	0.42
50:ZA:808:A:H2	50:ZA:855:G:H22	1.67	0.42
50:ZA:902:G:H2'	50:ZA:903:A:C8	2.54	0.42
51:AB:122:LEU:HB2	51:AB:142:LEU:HD21	2.02	0.42
58:HB:382:ILE:HG12	58:HB:392:ILE:HG12	2.01	0.42
70:TB:7:LYS:HA	70:TB:11:GLN:HE22	1.85	0.42
85:b:112:ARG:HE	85:b:121:VAL:HG11	1.84	0.42
12:L:11:ARG:HD3	12:L:57:LEU:HB3	2.00	0.42
17:Q:88:ARG:O	47:WA:2727:A:N6	2.52	0.42
30:DA:101:HIS:HD1	47:WA:2327:C:P	2.41	0.42
47:WA:90:G:OP2	47:WA:92:C:N4	2.51	0.42
47:WA:416:U:H2'	47:WA:417:G:O4'	2.19	0.42
47:WA:1428:G:N1	47:WA:1460:C:OP2	2.38	0.42
47:WA:1547:G:H2'	47:WA:1548:C:C6	2.55	0.42
47:WA:2061:C:H2'	47:WA:2062:G:H8	1.82	0.42
47:WA:2077:G:H2'	47:WA:2078:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:4116:C:H2'	47:WA:4117:G:C8	2.55	0.42
47:WA:4564:C:H2'	47:WA:4565:U:H6	1.84	0.42
50:ZA:422:U:H2'	50:ZA:423:U:C6	2.55	0.42
50:ZA:1847:G:H2'	50:ZA:1848:U:C6	2.55	0.42
55:EB:197:ASN:HB3	55:EB:209:HIS:HB2	2.00	0.42
7:G:149:LEU:HD22	7:G:246:LEU:HD21	2.00	0.42
7:G:185:ARG:NH2	47:WA:119:G:O4'	2.51	0.42
14:N:201:LEU:O	47:WA:4874:G:N2	2.53	0.42
19:S:129:LYS:HE2	47:WA:1838:G:H4'	2.01	0.42
37:KA:15:LYS:HD3	49:YA:45:C:P	2.59	0.42
47:WA:286:U:H2'	47:WA:287:U:C6	2.55	0.42
47:WA:2416:G:H2'	47:WA:2417:U:C6	2.54	0.42
47:WA:2701:C:H2'	47:WA:2702:G:H8	1.84	0.42
47:WA:4494:U:O2'	47:WA:4514:U:O2	2.23	0.42
47:WA:4993:U:H2'	47:WA:4994:G:C8	2.53	0.42
50:ZA:23:G:O2'	50:ZA:416:U:OP1	2.38	0.42
50:ZA:220:U:H2'	50:ZA:221:A:C8	2.55	0.42
50:ZA:912:C:O2'	50:ZA:914:U:O2'	2.28	0.42
50:ZA:1128:C:H2'	50:ZA:1129:G:C8	2.54	0.42
50:ZA:1474:A:O5'	50:ZA:1475:G:N2	2.51	0.42
50:ZA:1541:G:OP1	70:TB:56:ARG:NE	2.50	0.42
50:ZA:1572:C:H2'	50:ZA:1573:G:C8	2.54	0.42
50:ZA:1673:U:OP1	67:QB:105:ALA:N	2.53	0.42
51:AB:158:ASP:OD1	72:VB:60:ARG:NH1	2.49	0.42
52:BB:28:LYS:NZ	52:BB:50:THR:OG1	2.36	0.42
53:CB:127:PHE:HD1	53:CB:141:VAL:HG22	1.84	0.42
79:CC:23:SER:OG	79:CC:24:GLN:OE1	2.31	0.42
18:R:92:ASN:HD21	19:S:156:TYR:HB3	1.84	0.42
23:W:123:LYS:HG2	23:W:139:ARG:HB3	2.00	0.42
24:X:126:ARG:NH1	47:WA:197:A:O5'	2.53	0.42
28:BA:10:SER:OG	28:BA:11:LEU:N	2.52	0.42
47:WA:250:C:H2'	47:WA:251:C:C6	2.54	0.42
47:WA:1741:G:H2'	47:WA:1742:C:C6	2.55	0.42
47:WA:1969:A:H2'	47:WA:1970:G:C8	2.54	0.42
47:WA:1998:C:H41	47:WA:2002:G:N2	2.17	0.42
47:WA:2013:C:H3'	47:WA:2014:A:H8	1.84	0.42
47:WA:2310:A:H4'	47:WA:2336:C:H4'	2.02	0.42
47:WA:3874:A:H2'	47:WA:3875:G:H8	1.85	0.42
47:WA:3925:A:H2'	47:WA:3926:C:C6	2.54	0.42
47:WA:4349:G:H2'	47:WA:4350:A:C8	2.54	0.42
47:WA:4435:G:H2'	47:WA:4436:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:4993:U:O2'	47:WA:4994:G:H5'	2.20	0.42
50:ZA:85:A:H2'	50:ZA:86:C:H6	1.85	0.42
50:ZA:483:C:H5''	74:XB:48:LYS:HE3	2.02	0.42
50:ZA:1501:C:H2'	50:ZA:1502:C:H6	1.85	0.42
51:AB:24:HIS:HD2	51:AB:48:ILE:HD12	1.84	0.42
59:IB:36:THR:O	59:IB:96:LEU:N	2.52	0.42
59:IB:157:LYS:NZ	59:IB:158:ILE:O	2.51	0.42
72:VB:10:ASP:N	72:VB:10:ASP:OD1	2.51	0.42
76:ZB:92:LEU:HD22	76:ZB:109:TYR:HE1	1.85	0.42
85:b:105:ASN:O	85:b:105:ASN:ND2	2.51	0.42
2:B:117:ARG:HA	2:B:177:LYS:HD3	2.01	0.42
6:F:240:ASN:O	6:F:244:ARG:HG2	2.19	0.42
7:G:210:ILE:HA	7:G:254:THR:HG22	2.01	0.42
15:O:152:PRO:HG3	49:YA:14:U:H5''	2.02	0.42
18:R:15:ARG:HH12	18:R:18:PRO:HG3	1.84	0.42
20:T:56:LEU:HD13	20:T:63:LEU:HD13	2.01	0.42
23:W:55:ARG:NH2	49:YA:116:C:O2'	2.52	0.42
30:DA:64:LYS:NZ	47:WA:2081:G:OP2	2.47	0.42
35:IA:14:LYS:HE3	47:WA:2407:G:H5''	2.02	0.42
43:RA:30:PRO:HG3	47:WA:2011:A:H61	1.84	0.42
43:RA:60:VAL:HG22	43:RA:73:VAL:HA	2.01	0.42
47:WA:1560:A:H2'	47:WA:1561:G:H8	1.85	0.42
47:WA:2391:A:H2'	47:WA:2392:G:C8	2.55	0.42
47:WA:3690:U:H2'	47:WA:3691:G:C8	2.51	0.42
47:WA:3702:C:H2'	47:WA:3748:A:H61	1.85	0.42
47:WA:3724:G:H2'	47:WA:3725:A:C8	2.55	0.42
47:WA:4295:U:OP2	47:WA:4331:G:O2'	2.30	0.42
48:XA:92:C:H2'	48:XA:93:G:C8	2.50	0.42
49:YA:57:C:O2	49:YA:61:A:O2'	2.30	0.42
50:ZA:28:U:H2'	50:ZA:29:G:H8	1.84	0.42
50:ZA:301:A:O2'	59:IB:73:THR:O	2.34	0.42
50:ZA:1588:A:H2'	50:ZA:1589:A:C8	2.54	0.42
53:CB:196:ILE:HB	53:CB:223:TYR:HB2	2.01	0.42
54:DB:161:LEU:HD21	54:DB:192:ASP:HB2	2.01	0.42
55:EB:31:PRO:HG3	55:EB:43:PRO:HG3	2.01	0.42
1:A:168:VAL:HG13	41:OA:79:VAL:HG11	2.02	0.42
4:D:146:LEU:HD21	4:D:159:VAL:HG22	2.01	0.42
13:M:46:ASP:OD1	13:M:46:ASP:N	2.53	0.42
20:T:28:PRO:HB3	20:T:100:LEU:HD11	2.01	0.42
24:X:45:ARG:NH2	47:WA:199:G:OP2	2.53	0.42
34:HA:90:LEU:HA	34:HA:93:VAL:HG12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RA:38:SER:HB3	43:RA:41:LYS:HB3	2.01	0.42
47:WA:7:C:H2'	47:WA:8:U:H6	1.85	0.42
47:WA:1092:C:H2'	47:WA:1093:A:H8	1.85	0.42
47:WA:1677:C:HO2'	47:WA:1678:C:P	2.40	0.42
47:WA:2607:G:H2'	47:WA:2608:G:H8	1.85	0.42
47:WA:2635:U:H2'	47:WA:2636:C:C6	2.55	0.42
47:WA:2656:C:H2'	47:WA:2657:C:C6	2.55	0.42
47:WA:2660:G:O2'	47:WA:2677:G:N2	2.53	0.42
47:WA:4303:U:OP2	47:WA:4305:C:N4	2.53	0.42
47:WA:4983:G:OP2	47:WA:4983:G:N2	2.47	0.42
49:YA:130:C:H2'	49:YA:131:G:C8	2.54	0.42
50:ZA:54:A:H3'	50:ZA:451:G:H22	1.85	0.42
50:ZA:303:C:H5''	59:IB:75:LYS:HE3	2.01	0.42
50:ZA:812:A:H5'	55:EB:16:LYS:HD3	2.01	0.42
50:ZA:1661:A:OP2	80:DC:32:ARG:NH1	2.43	0.42
51:AB:70:ASN:ND2	51:AB:73:ASP:OD1	2.45	0.42
53:CB:138:GLY:HA2	53:CB:241:PHE:HE1	1.84	0.42
60:JB:123:ILE:H	60:JB:123:ILE:HG13	1.63	0.42
65:OB:145:GLY:O	77:AC:22:ARG:NH2	2.53	0.42
72:VB:32:ILE:HG12	72:VB:60:ARG:HD2	2.00	0.42
83:GC:287:THR:N	83:GC:301:GLY:O	2.30	0.42
3:C:164:THR:HG21	47:WA:223:G:H2'	2.02	0.42
4:D:107:ARG:HH12	4:D:120:GLU:HA	1.85	0.42
6:F:91:VAL:HG13	6:F:141:TRP:HB3	2.02	0.42
7:G:119:GLN:HG3	13:M:28:TRP:HH2	1.85	0.42
7:G:247:VAL:HG21	7:G:249:ARG:NH1	2.35	0.42
9:I:76:MET:HG3	9:I:87:ILE:HD11	2.01	0.42
12:L:44:ARG:HD3	47:WA:939:A:H4'	2.01	0.42
12:L:47:ARG:HH22	12:L:69:ARG:HA	1.84	0.42
13:M:176:LYS:NZ	47:WA:65:A:N3	2.58	0.42
14:N:29:LEU:HB3	31:EA:10:ILE:HD13	2.02	0.42
17:Q:60:ARG:HH12	47:WA:2617:C:H5''	1.85	0.42
18:R:122:HIS:HB2	48:XA:94:C:H4'	2.01	0.42
26:Z:9:ARG:HH22	47:WA:2346:U:H2'	1.85	0.42
26:Z:26:ARG:HA	26:Z:26:ARG:HD3	1.84	0.42
30:DA:90:MET:HG3	42:PA:33:LYS:HA	2.01	0.42
47:WA:342:G:H2'	47:WA:343:C:H6	1.84	0.42
47:WA:1203:C:H2'	47:WA:1204:G:C8	2.55	0.42
47:WA:1384:G:C2	47:WA:1385:G:N7	2.88	0.42
47:WA:1540:U:H2'	47:WA:1541:G:H8	1.85	0.42
47:WA:2421:C:H2'	47:WA:2422:A:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:3790:C:N4	47:WA:3814:C:O4'	2.52	0.42
47:WA:4155:C:H2'	47:WA:4156:G:C8	2.55	0.42
47:WA:4469:A:H2'	47:WA:4470:U:C6	2.55	0.42
50:ZA:146:G:O2'	50:ZA:147:A:H8	2.03	0.42
50:ZA:660:C:O5'	74:XB:2:GLY:N	2.53	0.42
50:ZA:675:U:H2'	50:ZA:676:C:H6	1.83	0.42
50:ZA:1238:U:H2'	50:ZA:1239:U:O4'	2.20	0.42
50:ZA:1279:C:H2'	50:ZA:1280:G:H8	1.84	0.42
50:ZA:1309:C:H41	82:FC:95:ARG:HH22	1.67	0.42
50:ZA:1716:C:H2'	50:ZA:1717:C:H6	1.84	0.42
52:BB:62:LEU:O	52:BB:88:THR:OG1	2.34	0.42
53:CB:82:TYR:CZ	53:CB:164:PRO:HD3	2.55	0.42
55:EB:136:ILE:HG23	55:EB:149:TYR:CZ	2.55	0.42
73:WB:18:GLU:HG3	73:WB:69:LEU:HD23	2.01	0.42
74:XB:84:PHE:HB2	74:XB:118:VAL:HG11	2.01	0.42
75:YB:103:SER:H	75:YB:106:GLN:HE21	1.67	0.42
2:B:213:GLN:OE1	2:B:214:ASP:N	2.53	0.41
13:M:38:ARG:HB2	13:M:62:TYR:CZ	2.55	0.41
18:R:154:LEU:HD12	18:R:154:LEU:HA	1.85	0.41
22:V:93:LYS:HE2	57:GB:151:ASP:HA	2.02	0.41
23:W:150:ALA:HB1	23:W:155:ILE:HG13	2.01	0.41
28:BA:38:ILE:HG21	28:BA:63:TYR:HB3	2.02	0.41
31:EA:106:TYR:HB2	31:EA:107:PRO:HD3	2.02	0.41
44:SA:2:U:H2'	44:SA:3:C:H6	1.84	0.41
47:WA:270:U:H2'	47:WA:271:C:H6	1.85	0.41
47:WA:484:G:H5'	47:WA:485:U:H5''	2.00	0.41
47:WA:1944:A:H2'	47:WA:1945:A:H8	1.85	0.41
47:WA:2424:C:H2'	47:WA:2425:A:C8	2.55	0.41
50:ZA:563:G:N7	50:ZA:586:G:N2	2.68	0.41
50:ZA:581:U:OP1	60:JB:133:ARG:NH2	2.53	0.41
50:ZA:1297:U:O4	66:PB:59:ARG:NH2	2.53	0.41
50:ZA:1752:C:H2'	50:ZA:1753:C:C6	2.55	0.41
55:EB:81:THR:OG1	55:EB:81:THR:O	2.38	0.41
57:GB:72:ARG:HA	57:GB:98:ARG:HA	2.02	0.41
66:PB:41:GLN:HG3	66:PB:84:ILE:HD13	2.01	0.41
73:WB:93:LEU:HB2	73:WB:102:ILE:HD11	2.01	0.41
74:XB:60:LYS:HG2	74:XB:114:ASP:HA	2.02	0.41
83:GC:256:ILE:HD11	83:GC:298:LEU:HD21	2.02	0.41
83:GC:291:TRP:CE2	83:GC:298:LEU:HD13	2.55	0.41
1:A:54:ARG:NH2	47:WA:3682:U:OP1	2.47	0.41
3:C:71:ARG:HB2	3:C:73:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:91:VAL:O	6:F:119:GLY:HA2	2.20	0.41
12:L:31:ILE:H	12:L:36:ALA:HA	1.85	0.41
13:M:86:HIS:CG	47:WA:33:A:H5'	2.55	0.41
14:N:188:LYS:HD2	47:WA:4894:A:H5''	2.02	0.41
18:R:3:ALA:HA	18:R:7:LEU:HD21	2.03	0.41
19:S:18:PRO:HB2	19:S:21:LYS:HD2	2.02	0.41
36:JA:35:LYS:HG2	36:JA:44:THR:HG22	2.02	0.41
43:RA:16:ARG:NH2	43:RA:57:ARG:O	2.53	0.41
47:WA:177:G:H2'	47:WA:178:C:C6	2.55	0.41
47:WA:368:C:H2'	47:WA:369:G:C8	2.56	0.41
47:WA:396:A:H2'	47:WA:397:G:C8	2.55	0.41
47:WA:1778:A:H2'	47:WA:1779:C:C6	2.55	0.41
47:WA:1960:A:O2'	47:WA:2027:A:N6	2.52	0.41
47:WA:2342:C:H2'	47:WA:2343:A:H8	1.84	0.41
47:WA:2832:G:H2'	47:WA:2833:G:C8	2.55	0.41
47:WA:2864:G:N3	47:WA:3626:A:H2'	2.34	0.41
47:WA:4082:C:H2'	47:WA:4083:G:H8	1.84	0.41
47:WA:5004:U:H2'	47:WA:5005:U:C6	2.56	0.41
50:ZA:553:U:O2'	50:ZA:554:A:H8	2.03	0.41
50:ZA:821:G:N1	60:JB:83:ARG:HD3	2.35	0.41
50:ZA:863:U:H2'	50:ZA:864:A:C8	2.55	0.41
50:ZA:917:U:H2'	50:ZA:918:U:C6	2.56	0.41
50:ZA:1367:U:H2'	50:ZA:1368:U:C6	2.55	0.41
50:ZA:1722:G:H1	50:ZA:1812:U:H3	1.67	0.41
52:BB:34:LYS:HB2	52:BB:97:LEU:HD23	2.01	0.41
52:BB:126:ASP:OD1	52:BB:126:ASP:N	2.53	0.41
76:ZB:43:LYS:H	76:ZB:43:LYS:HD2	1.85	0.41
82:FC:121:CYS:SG	82:FC:126:CYS:HB3	2.57	0.41
1:A:177:LYS:HB2	41:OA:29:ILE:HG21	2.01	0.41
2:B:217:ILE:HD13	2:B:284:ILE:HD11	2.03	0.41
3:C:322:LEU:O	3:C:326:LEU:HG	2.20	0.41
5:E:73:ARG:HD3	47:WA:989:C:H41	1.85	0.41
8:H:18:ILE:HD11	8:H:81:ILE:HD11	2.02	0.41
9:I:180:GLU:H	9:I:180:GLU:HG3	1.69	0.41
9:I:193:ASP:OD2	47:WA:1752:G:N2	2.54	0.41
13:M:179:LYS:HE3	47:WA:313:U:H5''	2.02	0.41
26:Z:3:SER:HA	26:Z:6:ARG:HH11	1.85	0.41
30:DA:29:VAL:HB	47:WA:1334:C:H5''	2.02	0.41
31:EA:83:MET:HE3	31:EA:83:MET:HB3	1.94	0.41
43:RA:13:VAL:HG13	43:RA:62:LEU:HB2	2.02	0.41
44:SA:43:A:H2'	44:SA:44:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:1914:G:H2'	47:WA:1915:C:C6	2.55	0.41
47:WA:2600:A:H2'	47:WA:2601:G:O4'	2.20	0.41
47:WA:4176:U:H2'	47:WA:4177:G:C8	2.55	0.41
47:WA:4406:U:O2'	47:WA:4408:U:O4	2.32	0.41
47:WA:4631:U:H2'	47:WA:4632:G:H8	1.85	0.41
47:WA:4725:A:H2'	47:WA:4726:A:C8	2.55	0.41
48:XA:24:C:H2'	48:XA:25:G:O4'	2.20	0.41
50:ZA:49:C:H2'	50:ZA:472:C:H41	1.84	0.41
50:ZA:464:A:H5'	50:ZA:465:A:C8	2.56	0.41
50:ZA:928:G:H2'	50:ZA:929:G:H8	1.85	0.41
50:ZA:1361:G:H1'	50:ZA:1379:A:N7	2.35	0.41
50:ZA:1550:G:O2'	50:ZA:1558:C:O2	2.23	0.41
50:ZA:1562:C:H2'	50:ZA:1563:G:H8	1.83	0.41
53:CB:211:LYS:HE2	53:CB:215:MET:HE3	2.02	0.41
58:HB:304:VAL:HG22	58:HB:334:ALA:HB1	2.02	0.41
59:IB:106:SER:HB3	59:IB:171:LEU:HG	2.02	0.41
61:KB:6:LYS:HB3	61:KB:6:LYS:HE3	1.84	0.41
83:GC:104:HIS:NE2	83:GC:122:SER:OG	2.52	0.41
4:D:33:ARG:HH21	48:XA:7:G:H4'	1.85	0.41
4:D:157:ASN:HB3	4:D:160:PHE:HD2	1.85	0.41
6:F:176:ARG:HH12	47:WA:2102:G:N2	2.18	0.41
7:G:190:ARG:HG3	7:G:199:LEU:HD11	2.02	0.41
22:V:81:ALA:HA	57:GB:145:PHE:CE1	2.55	0.41
25:Y:47:ASP:N	25:Y:69:LYS:O	2.53	0.41
47:WA:490:C:H2'	47:WA:491:C:C6	2.55	0.41
47:WA:707:C:HO2'	47:WA:1300:C:HO2'	1.54	0.41
47:WA:1781:U:H2'	47:WA:1782:A:C8	2.55	0.41
47:WA:2002:G:O6	85:b:41:GLN:NE2	2.53	0.41
47:WA:2388:U:H2'	47:WA:2389:G:C8	2.53	0.41
47:WA:4719:A:H2'	47:WA:4720:G:O4'	2.21	0.41
50:ZA:988:C:OP2	77:AC:70:LYS:NZ	2.54	0.41
65:OB:94:HIS:CE1	65:OB:128:ARG:HG3	2.54	0.41
74:XB:91:LEU:HD23	81:EC:82:VAL:HG21	2.02	0.41
86:At:27:G:H2'	86:At:28:G:C8	2.55	0.41
3:C:221:PHE:HB3	3:C:227:ILE:HG21	2.02	0.41
3:C:301:ALA:HB1	16:P:132:LYS:HE3	2.01	0.41
5:E:154:ILE:HB	5:E:198:ILE:HB	2.02	0.41
17:Q:133:LYS:HG3	17:Q:134:ASN:HD22	1.86	0.41
22:V:113:LYS:HD3	50:ZA:326:C:H1'	2.02	0.41
30:DA:43:ASN:OD1	30:DA:46:ARG:N	2.44	0.41
31:EA:8:LYS:HB3	31:EA:100:ARG:HD2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:HA:70:LEU:HD13	34:HA:87:ARG:HE	1.85	0.41
35:IA:3:LYS:HB3	47:WA:3644:A:C5	2.56	0.41
36:JA:33:LYS:NZ	47:WA:2695:G:OP2	2.47	0.41
47:WA:1775:U:H2'	47:WA:1776:C:C6	2.56	0.41
47:WA:1920:U:O4'	47:WA:2067:G:N2	2.53	0.41
47:WA:2030:C:H2'	47:WA:2031:A:H8	1.86	0.41
47:WA:2626:G:H2'	47:WA:2627:U:H6	1.85	0.41
47:WA:2737:G:H2'	47:WA:2738:G:C8	2.48	0.41
47:WA:4563:C:H2'	47:WA:4564:C:C6	2.56	0.41
50:ZA:944:A:H2'	50:ZA:945:U:C6	2.55	0.41
50:ZA:1088:U:H4'	50:ZA:1089:G:OP2	2.21	0.41
50:ZA:1654:G:H2'	50:ZA:1655:C:H6	1.85	0.41
57:GB:49:VAL:HG23	57:GB:115:LYS:HE3	2.02	0.41
78:BC:23:ARG:NH2	78:BC:29:ASN:OD1	2.53	0.41
3:C:53:ALA:O	49:YA:26:C:O2'	2.34	0.41
5:E:211:ILE:HD12	5:E:212:PRO:HD2	2.02	0.41
13:M:6:TYR:CZ	34:HA:40:VAL:HG22	2.55	0.41
14:N:55:LEU:HD23	14:N:58:LEU:HD12	2.03	0.41
25:Y:51:ARG:HB2	25:Y:65:ARG:HE	1.86	0.41
26:Z:73:VAL:HB	26:Z:108:TYR:CG	2.55	0.41
32:FA:9:ARG:HG2	32:FA:34:TYR:CZ	2.55	0.41
43:RA:55:GLY:O	43:RA:92:ARG:NH1	2.52	0.41
44:SA:50:U:H2'	44:SA:51:C:C6	2.55	0.41
47:WA:197:A:N6	47:WA:242:U:H3	2.17	0.41
47:WA:424:U:H2'	47:WA:425:U:H6	1.85	0.41
47:WA:1208:C:H2'	47:WA:1209:G:C8	2.56	0.41
47:WA:1343:U:H2'	47:WA:1344:A:C8	2.55	0.41
47:WA:1363:G:H2'	47:WA:1364:G:C8	2.55	0.41
47:WA:1671:A:C2	47:WA:1854:U:H4'	2.55	0.41
47:WA:1974:G:C6	47:WA:1997:G:O6	2.74	0.41
47:WA:2685:C:H2'	47:WA:2686:C:C6	2.56	0.41
47:WA:2813:G:N2	47:WA:2815:A:H3'	2.34	0.41
47:WA:4157:C:H2'	47:WA:4158:G:O4'	2.20	0.41
47:WA:4937:C:H2'	47:WA:4938:G:C8	2.56	0.41
49:YA:66:A:H2'	49:YA:67:U:C6	2.55	0.41
50:ZA:1403:C:O2	50:ZA:1433:C:N4	2.54	0.41
50:ZA:1406:G:H2'	50:ZA:1407:U:H6	1.85	0.41
50:ZA:1407:U:H4'	67:QB:97:ARG:NH2	2.35	0.41
50:ZA:1446:A:H1'	71:UB:55:ARG:HD2	2.01	0.41
50:ZA:1669:G:C8	67:QB:156:LYS:HD3	2.56	0.41
50:ZA:1809:A:H2'	50:ZA:1810:U:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:AB:19:LEU:HD13	51:AB:19:LEU:HA	1.88	0.41
51:AB:33:GLN:HB3	51:AB:154:LEU:HD12	2.03	0.41
51:AB:149:ASN:OD1	51:AB:150:THR:N	2.44	0.41
6:F:130:ASN:ND2	47:WA:1729:U:OP1	2.54	0.41
9:I:4:ARG:NH1	9:I:99:ILE:HG13	2.36	0.41
9:I:99:ILE:HG22	9:I:123:GLN:HB2	2.03	0.41
14:N:172:LYS:HG3	47:WA:4875:G:N2	2.35	0.41
19:S:122:LYS:HB3	19:S:124:THR:HG22	2.02	0.41
22:V:107:GLN:HA	22:V:110:ARG:HD3	2.02	0.41
30:DA:60:TYR:HB2	47:WA:2321:C:H1'	2.02	0.41
43:RA:16:ARG:HG3	43:RA:58:ILE:C	2.45	0.41
45:TA:9:A:O2'	45:TA:10:G:N7	2.49	0.41
47:WA:41:C:O2'	47:WA:42:A:H5'	2.20	0.41
47:WA:175:C:H2'	47:WA:176:G:C8	2.56	0.41
47:WA:176:G:H2'	47:WA:177:G:H8	1.85	0.41
47:WA:221:C:H2'	47:WA:222:C:C6	2.56	0.41
47:WA:378:A:O2'	47:WA:413:G:N2	2.39	0.41
47:WA:436:C:H2'	47:WA:437:G:C8	2.54	0.41
47:WA:992:C:O2	47:WA:1076:G:N2	2.53	0.41
47:WA:1390:A:H2'	47:WA:1391:U:C6	2.56	0.41
47:WA:1740:A:H2'	47:WA:1741:G:H8	1.85	0.41
47:WA:1897:G:H2'	47:WA:1898:A:O4'	2.21	0.41
47:WA:2650:G:H2'	47:WA:2651:G:C8	2.55	0.41
47:WA:2705:G:C6	47:WA:2716:G:C6	3.08	0.41
47:WA:3609:U:H2'	47:WA:3610:A:C8	2.56	0.41
47:WA:4275:A:H2'	47:WA:4276:A:C8	2.55	0.41
50:ZA:26:U:H2'	50:ZA:27:A:H8	1.86	0.41
50:ZA:65:C:C6	57:GB:174:PRO:HB3	2.56	0.41
50:ZA:989:C:OP2	52:BB:155:TYR:OH	2.32	0.41
50:ZA:1221:G:H2'	50:ZA:1222:G:H8	1.86	0.41
50:ZA:1386:A:H2'	50:ZA:1387:G:O4'	2.20	0.41
57:GB:98:ARG:NH1	57:GB:101:ILE:O	2.41	0.41
60:JB:129:LEU:HD22	60:JB:134:HIS:CE1	2.56	0.41
2:B:54:THR:OG1	2:B:55:HIS:N	2.54	0.41
2:B:161:ARG:HG2	2:B:184:GLN:HA	2.02	0.41
7:G:139:VAL:HG21	7:G:238:LYS:HG3	2.02	0.41
8:H:98:HIS:ND1	47:WA:4604:A:H5''	2.36	0.41
10:J:129:ASP:OD1	47:WA:4252:G:O2'	2.27	0.41
16:P:49:LYS:O	16:P:53:MET:HG3	2.21	0.41
44:SA:2:U:H2'	44:SA:3:C:C6	2.56	0.41
47:WA:102:G:HO2'	47:WA:1383:U:HO2'	1.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:176:G:N1	47:WA:261:G:O6	2.54	0.41
47:WA:1729:U:H2'	47:WA:1730:U:C6	2.55	0.41
47:WA:2063:U:H2'	47:WA:2064:C:O4'	2.20	0.41
47:WA:2080:C:H2'	47:WA:2081:G:H8	1.85	0.41
47:WA:2485:G:H2'	47:WA:2486:A:C8	2.54	0.41
47:WA:3610:A:H2'	47:WA:3611:G:C8	2.56	0.41
47:WA:4457:G:H2'	47:WA:4458:C:H6	1.84	0.41
47:WA:4462:U:H2'	47:WA:4463:C:H6	1.85	0.41
47:WA:4691:U:H2'	47:WA:4692:G:O4'	2.21	0.41
48:XA:16:A:H2'	48:XA:17:C:C6	2.56	0.41
50:ZA:63:U:H2'	50:ZA:64:A:H5''	2.02	0.41
50:ZA:647:U:H2'	50:ZA:648:A:C8	2.55	0.41
50:ZA:1383:A:H4'	54:DB:194:LEU:HG	2.03	0.41
50:ZA:1427:C:H2'	50:ZA:1429:G:C8	2.55	0.41
55:EB:120:LYS:NZ	55:EB:165:GLU:OE2	2.39	0.41
74:XB:40:PRO:O	74:XB:77:ASN:ND2	2.54	0.41
86:At:13:C:H2'	86:At:14:A:C8	2.56	0.41
1:A:243:THR:HB	47:WA:3750:A:H5''	2.02	0.41
3:C:5:ARG:NE	3:C:24:LEU:O	2.45	0.41
10:J:15:LEU:HB2	10:J:165:TRP:CD1	2.56	0.41
10:J:19:LYS:HE3	10:J:133:VAL:HG21	2.03	0.41
11:K:27:ASN:HB3	49:YA:29:G:H5''	2.03	0.41
12:L:25:VAL:HG22	12:L:38:VAL:HB	2.03	0.41
15:O:91:ARG:NH1	47:WA:423:G:OP1	2.51	0.41
19:S:130:ARG:HH21	47:WA:1730:U:H1'	1.86	0.41
24:X:2:LYS:HE3	24:X:2:LYS:HB3	1.94	0.41
25:Y:28:ASN:OD1	25:Y:28:ASN:N	2.54	0.41
26:Z:147:VAL:HA	34:HA:6:PRO:HG2	2.02	0.41
30:DA:41:ILE:HG12	47:WA:1319:U:OP2	2.20	0.41
35:IA:13:ASN:HD21	47:WA:1620:G:P	2.44	0.41
35:IA:25:LYS:NZ	47:WA:370:U:O3'	2.40	0.41
47:WA:31:U:H2'	47:WA:32:G:O4'	2.21	0.41
47:WA:32:G:H21	47:WA:50:C:H5	1.69	0.41
47:WA:269:G:H2'	47:WA:270:U:H6	1.85	0.41
47:WA:297:U:C2	47:WA:298:G:C8	3.09	0.41
47:WA:952:C:H2'	47:WA:953:C:C6	2.55	0.41
47:WA:1217:G:H2'	47:WA:1218:G:H8	1.86	0.41
47:WA:1835:G:N2	47:WA:1837:G:O4'	2.54	0.41
47:WA:1974:G:H2'	47:WA:1975:G:O4'	2.21	0.41
47:WA:2039:C:H2'	47:WA:2040:U:H6	1.85	0.41
47:WA:2342:C:H2'	47:WA:2343:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:2417:U:H2'	47:WA:2418:G:O4'	2.20	0.41
47:WA:4910:G:H2'	47:WA:4914:G:H21	1.85	0.41
47:WA:5006:C:H2'	47:WA:5007:G:O4'	2.20	0.41
48:XA:60:G:H2'	48:XA:61:G:H8	1.86	0.41
50:ZA:183:G:N3	50:ZA:183:G:H2'	2.36	0.41
50:ZA:445:A:H2	55:EB:5:PRO:HG3	1.86	0.41
50:ZA:605:A:H4'	81:EC:128:PRO:HD2	2.02	0.41
50:ZA:808:A:H61	50:ZA:856:C:H42	1.69	0.41
50:ZA:852:G:H1'	62:LB:97:ARG:NH2	2.35	0.41
50:ZA:927:C:H2'	50:ZA:928:G:C8	2.56	0.41
50:ZA:1023:A:OP2	64:NB:124:ARG:NH1	2.48	0.41
50:ZA:1198:G:H2'	50:ZA:1199:A:H8	1.86	0.41
50:ZA:1393:G:H2'	50:ZA:1394:G:C8	2.56	0.41
50:ZA:1625:U:H2'	50:ZA:1626:C:C6	2.55	0.41
50:ZA:1627:C:C2	50:ZA:1628:C:C5	3.09	0.41
50:ZA:1631:U:O4	50:ZA:1632:G:N1	2.54	0.41
50:ZA:1688:C:H2'	50:ZA:1689:C:C6	2.54	0.41
53:CB:144:SER:HB3	53:CB:150:ALA:HB2	2.02	0.41
56:FB:102:LEU:HG	76:ZB:110:THR:HG21	2.02	0.41
59:IB:4:SER:OG	59:IB:6:ASP:OD2	2.35	0.41
60:JB:119:LEU:H	60:JB:119:LEU:HD23	1.86	0.41
61:KB:53:LYS:HE2	61:KB:53:LYS:HB3	1.94	0.41
61:KB:58:VAL:HG12	61:KB:71:LEU:HD23	2.02	0.41
63:MB:32:ALA:HB1	63:MB:37:GLU:HB3	2.02	0.41
63:MB:67:ALA:HB3	82:FC:114:ILE:HD11	2.02	0.41
72:VB:16:LYS:HG2	72:VB:23:ILE:HG22	2.02	0.41
76:ZB:50:PHE:HE2	76:ZB:87:ALA:HB2	1.85	0.41
83:GC:61:GLY:HA3	83:GC:90:TRP:HZ2	1.85	0.41
83:GC:265:ILE:HD12	83:GC:265:ILE:HA	1.98	0.41
1:A:137:ILE:HD11	1:A:149:LYS:HB2	2.03	0.41
2:B:226:LYS:O	2:B:229:LYS:NZ	2.53	0.41
6:F:244:ARG:HA	6:F:244:ARG:HD3	1.97	0.41
8:H:66:GLU:O	8:H:69:THR:OG1	2.36	0.41
14:N:109:PRO:HB2	14:N:111:PRO:HD2	2.04	0.41
17:Q:95:TRP:CD1	47:WA:1574:U:H4'	2.57	0.41
18:R:160:ARG:HA	18:R:160:ARG:CZ	2.51	0.41
21:U:87:SER:HA	21:U:97:TYR:HB3	2.02	0.41
24:X:91:ASN:OD1	24:X:92:GLY:N	2.54	0.41
25:Y:14:LEU:HB3	32:FA:88:ARG:HB2	2.03	0.41
40:NA:19:GLN:NE2	40:NA:72:CYS:SG	2.94	0.41
47:WA:437:G:H2'	47:WA:438:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:1343:U:H2'	47:WA:1344:A:H8	1.86	0.41
47:WA:1856:G:N2	47:WA:4396:A:O4'	2.53	0.41
47:WA:2385:C:H5'	47:WA:2386:U:H5	1.86	0.41
47:WA:2691:C:H2'	47:WA:2692:C:C6	2.56	0.41
47:WA:4639:G:H2'	47:WA:4640:U:C6	2.55	0.41
50:ZA:479:C:H2'	50:ZA:480:G:H8	1.85	0.41
50:ZA:647:U:H2'	50:ZA:648:A:H8	1.86	0.41
50:ZA:1297:U:N3	50:ZA:1300:U:OP2	2.52	0.41
54:DB:161:LEU:HD11	54:DB:192:ASP:HB3	2.01	0.41
59:IB:125:LYS:H	59:IB:125:LYS:HD2	1.86	0.41
61:KB:22:VAL:HG22	61:KB:68:TYR:HD1	1.86	0.41
75:YB:56:PHE:HA	75:YB:94:HIS:CE1	2.55	0.41
83:GC:107:ASP:N	83:GC:107:ASP:OD1	2.54	0.41
83:GC:163:PRO:HB2	83:GC:179:LEU:HB3	2.03	0.41
3:C:304:ALA:HB1	47:WA:2101:C:C6	2.55	0.40
4:D:225:GLN:HG2	48:XA:49:A:H5''	2.02	0.40
8:H:107:GLU:HB2	8:H:110:SER:HB2	2.03	0.40
14:N:144:GLU:OE1	47:WA:4683:A:O2'	2.33	0.40
15:O:89:PHE:CE1	15:O:111:ARG:HB2	2.56	0.40
19:S:28:ALA:HA	19:S:31:MET:HG2	2.02	0.40
27:AA:117:ARG:NH1	47:WA:1274:C:OP1	2.54	0.40
36:JA:61:PRO:HA	36:JA:62:PRO:HD3	1.98	0.40
47:WA:343:C:H2'	47:WA:344:A:C8	2.56	0.40
47:WA:1481:G:H2'	47:WA:1482:C:C6	2.57	0.40
47:WA:1848:G:H2'	47:WA:1849:C:C6	2.57	0.40
47:WA:1874:G:O2'	47:WA:4221:A:N3	2.47	0.40
47:WA:1999:U:H4'	85:b:44:ARG:NH1	2.36	0.40
47:WA:2640:G:H1	47:WA:2699:A:H61	1.69	0.40
47:WA:4415:C:H2'	47:WA:4416:A:O4'	2.21	0.40
50:ZA:181:A:H8	50:ZA:181:A:OP2	2.04	0.40
50:ZA:624:C:H2'	50:ZA:625:G:C8	2.56	0.40
50:ZA:1566:G:H1	70:TB:97:LYS:NZ	2.19	0.40
50:ZA:1628:C:H2'	50:ZA:1629:C:C6	2.55	0.40
79:CC:12:ALA:HB1	79:CC:32:VAL:HB	2.03	0.40
1:A:28:ARG:HE	1:A:123:ARG:HD3	1.86	0.40
3:C:35:ASP:N	3:C:35:ASP:OD1	2.54	0.40
4:D:216:GLU:HG3	4:D:220:LYS:HE2	2.03	0.40
5:E:68:LYS:HB3	5:E:73:ARG:HH21	1.86	0.40
9:I:47:PRO:HD2	9:I:141:LYS:HA	2.02	0.40
10:J:56:THR:HG22	10:J:63:ARG:HA	2.03	0.40
12:L:106:ASP:HA	12:L:109:ARG:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:145:VAL:O	47:WA:4713:C:O2'	2.35	0.40
17:Q:8:LYS:HE3	17:Q:19:LYS:HB2	2.03	0.40
17:Q:172:ARG:HA	17:Q:175:GLU:HG2	2.03	0.40
19:S:124:THR:OG1	19:S:125:TRP:N	2.54	0.40
21:U:82:ILE:HG13	21:U:104:VAL:HG13	2.03	0.40
22:V:8:PHE:HZ	22:V:49:ILE:HD12	1.86	0.40
32:FA:66:ARG:NH2	47:WA:2519:A:O3'	2.55	0.40
44:SA:51:C:H2'	44:SA:52:G:C8	2.55	0.40
47:WA:423:G:C6	49:YA:12:G:C6	3.10	0.40
47:WA:469:C:H2'	47:WA:470:A:C8	2.56	0.40
47:WA:912:G:H2'	47:WA:913:U:C6	2.56	0.40
47:WA:1405:G:H2'	47:WA:1406:G:C8	2.56	0.40
47:WA:2762:G:H4'	47:WA:2763:U:H5'	2.03	0.40
47:WA:4623:C:H2'	47:WA:4624:A:H8	1.87	0.40
47:WA:4637:A:O2'	47:WA:4639:G:OP1	2.34	0.40
47:WA:4680:G:N2	47:WA:4715:G:H1'	2.36	0.40
47:WA:4772:U:H2'	47:WA:4773:C:C5	2.57	0.40
49:YA:138:C:H2'	49:YA:139:G:C8	2.56	0.40
50:ZA:111:A:O2'	62:LB:69:ARG:NH1	2.55	0.40
50:ZA:467:G:H2'	50:ZA:468:A:C8	2.56	0.40
50:ZA:1428:G:O6	67:QB:99:LYS:NZ	2.52	0.40
50:ZA:1653:U:H2'	50:ZA:1654:G:C8	2.56	0.40
52:BB:117:TRP:HB3	52:BB:152:LYS:O	2.22	0.40
53:CB:78:LEU:HD23	53:CB:81:ILE:HD12	2.03	0.40
59:IB:103:LEU:HD13	59:IB:170:LYS:HD2	2.04	0.40
62:LB:75:GLY:HA3	62:LB:88:ILE:HD12	2.02	0.40
66:PB:68:PRO:HA	66:PB:69:PRO:HD3	1.98	0.40
73:WB:11:LEU:HD13	73:WB:72:CYS:SG	2.62	0.40
86:At:63:G:H2'	86:At:64:A:H8	1.87	0.40
2:B:29:VAL:HG13	2:B:348:ARG:HD3	2.02	0.40
2:B:60:VAL:HG12	2:B:62:ARG:HG2	2.03	0.40
4:D:53:VAL:HG11	4:D:159:VAL:HA	2.04	0.40
4:D:56:THR:HG21	48:XA:26:C:H5''	2.02	0.40
5:E:175:LEU:HD21	47:WA:4943:G:C5	2.57	0.40
13:M:38:ARG:NH2	49:YA:142:U:OP1	2.54	0.40
13:M:178:HIS:ND1	47:WA:68:U:OP1	2.35	0.40
16:P:85:THR:HG22	16:P:104:ARG:HB2	2.03	0.40
23:W:82:THR:HA	23:W:87:MET:HE3	2.03	0.40
27:AA:9:THR:HA	27:AA:12:GLN:HG2	2.03	0.40
27:AA:43:MET:HG2	27:AA:47:LYS:HE2	2.03	0.40
41:OA:42:CYS:HB3	41:OA:60:CYS:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:OA:62:LYS:NZ	47:WA:4123:G:N7	2.68	0.40
47:WA:211:G:C2	47:WA:212:A:C8	3.09	0.40
47:WA:425:U:H2'	47:WA:426:A:H8	1.85	0.40
47:WA:1555:A:C2	47:WA:1577:A:H1'	2.56	0.40
47:WA:2002:G:N3	47:WA:2002:G:H3'	2.37	0.40
47:WA:3723:U:H2'	47:WA:3724:G:H8	1.87	0.40
47:WA:4188:A:H2'	47:WA:4189:G:H8	1.86	0.40
47:WA:4324:G:N2	47:WA:4327:A:OP2	2.50	0.40
47:WA:4568:U:H2'	47:WA:4569:G:O4'	2.21	0.40
47:WA:4701:U:H4'	47:WA:4702:A:OP1	2.22	0.40
47:WA:4990:U:C5	47:WA:5062:A:H2'	2.56	0.40
50:ZA:196:C:H2'	50:ZA:197:U:C6	2.56	0.40
50:ZA:373:G:O6	50:ZA:392:A:N6	2.54	0.40
50:ZA:528:A:H2'	50:ZA:529:A:C8	2.56	0.40
50:ZA:813:A:H2'	50:ZA:814:U:O4'	2.20	0.40
50:ZA:1034:A:H3'	50:ZA:1035:A:H8	1.86	0.40
50:ZA:1410:C:H2'	50:ZA:1411:G:C8	2.56	0.40
50:ZA:1410:C:H2'	50:ZA:1411:G:H8	1.85	0.40
50:ZA:1753:C:H2'	50:ZA:1754:G:C8	2.56	0.40
55:EB:31:PRO:HG2	55:EB:38:LEU:HG	2.03	0.40
58:HB:343:THR:H	58:HB:346:SER:HG	1.68	0.40
65:OB:18:GLY:HA2	65:OB:19:PRO:HD3	1.97	0.40
66:PB:15:PHE:CE2	66:PB:17:TYR:HB2	2.56	0.40
71:UB:61:LEU:HD22	80:DC:34:TYR:CZ	2.57	0.40
75:YB:10:ARG:NH2	75:YB:24:VAL:HG11	2.36	0.40
85:b:50:LYS:HD2	85:b:101:MET:SD	2.62	0.40
2:B:234:ARG:NH2	2:B:268:ARG:O	2.39	0.40
3:C:69:THR:HG21	47:WA:3908:A:H2'	2.03	0.40
11:K:48:PRO:HG2	11:K:49:ARG:HD2	2.04	0.40
16:P:3:VAL:HG21	47:WA:2279:C:H5''	2.03	0.40
19:S:130:ARG:N	47:WA:1839:A:OP2	2.48	0.40
22:V:87:LEU:HD12	22:V:88:ALA:H	1.86	0.40
33:GA:97:LYS:HD3	47:WA:135:G:C6	2.57	0.40
35:IA:20:ARG:HH12	49:YA:102:G:P	2.44	0.40
47:WA:360:A:C4	49:YA:24:G:H1'	2.56	0.40
47:WA:418:A:H4'	47:WA:2313:C:H5'	2.03	0.40
47:WA:1475:U:H2'	47:WA:1476:C:C6	2.57	0.40
47:WA:1779:C:H2'	47:WA:1780:C:C6	2.56	0.40
47:WA:1819:U:H2'	47:WA:1820:G:O4'	2.20	0.40
47:WA:1848:G:H2'	47:WA:1849:C:H6	1.86	0.40
47:WA:3789:G:H1'	47:WA:3791:C:H41	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:WA:4419:C:H2'	47:WA:4420:G:O4'	2.22	0.40
47:WA:4539:C:H2'	47:WA:4540:G:H8	1.85	0.40
50:ZA:26:U:H2'	50:ZA:27:A:C8	2.56	0.40
50:ZA:467:G:H2'	50:ZA:468:A:H8	1.86	0.40
50:ZA:818:A:H2'	50:ZA:819:G:C8	2.57	0.40
50:ZA:1512:C:O2'	80:DC:7:TYR:O	2.27	0.40
50:ZA:1572:C:H2'	50:ZA:1573:G:H8	1.86	0.40
55:EB:57:THR:OG1	55:EB:60:GLU:HG2	2.21	0.40
59:IB:107:THR:OG1	59:IB:108:PRO:HD3	2.21	0.40
61:KB:16:PHE:HE2	61:KB:89:ILE:HG22	1.86	0.40
74:XB:53:GLU:HG2	74:XB:71:ARG:HB3	2.03	0.40
83:GC:87:LEU:HD22	83:GC:132:TRP:HZ3	1.86	0.40
86:At:26:A:N6	86:At:44:G:H1	2.18	0.40
86:At:28:G:H2'	86:At:29:G:H8	1.87	0.40
2:B:243:LYS:HE2	47:WA:4528:U:H4'	2.03	0.40
6:F:75:ARG:NH2	47:WA:729:U:OP1	2.55	0.40
11:K:102:ARG:HA	47:WA:75:G:C5	2.57	0.40
17:Q:115:ILE:HG22	17:Q:119:MET:HE3	2.03	0.40
26:Z:102:ASP:HB3	26:Z:105:ARG:HB3	2.03	0.40
27:AA:3:LYS:HG2	47:WA:4196:U:H5''	2.04	0.40
47:WA:223:G:H4'	47:WA:225:G:C8	2.56	0.40
47:WA:253:G:H2'	47:WA:254:G:C8	2.55	0.40
47:WA:358:C:H2'	47:WA:359:A:C8	2.57	0.40
47:WA:446:C:H1'	47:WA:2316:G:H4'	2.04	0.40
47:WA:1496:U:H2'	47:WA:1497:G:H8	1.85	0.40
47:WA:2761:G:O2'	47:WA:2762:G:O4'	2.34	0.40
47:WA:2879:G:N2	47:WA:3826:A:O2'	2.54	0.40
47:WA:4274:G:N2	47:WA:4274:G:OP2	2.55	0.40
47:WA:4524:G:H5''	47:WA:4526:G:C8	2.57	0.40
47:WA:4542:C:H2'	47:WA:4543:G:C8	2.56	0.40
47:WA:5008:U:H4'	47:WA:5009:A:H5'	2.04	0.40
50:ZA:431:G:C2	50:ZA:432:G:C8	3.09	0.40
57:GB:217:MET:HE2	57:GB:217:MET:HA	2.04	0.40
67:QB:157:LYS:HB2	67:QB:166:ARG:NH2	2.37	0.40
75:YB:29:HIS:CD2	75:YB:35:VAL:HG23	2.57	0.40
86:At:41:C:H2'	86:At:42:C:C6	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	A	248/257 (96%)	243 (98%)	5 (2%)	0	100	100
2	B	395/403 (98%)	386 (98%)	9 (2%)	0	100	100
3	C	360/413 (87%)	353 (98%)	7 (2%)	0	100	100
4	D	292/297 (98%)	286 (98%)	6 (2%)	0	100	100
5	E	222/291 (76%)	220 (99%)	2 (1%)	0	100	100
6	F	225/249 (90%)	219 (97%)	6 (3%)	0	100	100
7	G	225/319 (70%)	222 (99%)	3 (1%)	0	100	100
8	H	188/192 (98%)	183 (97%)	5 (3%)	0	100	100
9	I	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
10	J	169/178 (95%)	168 (99%)	1 (1%)	0	100	100
11	K	208/211 (99%)	201 (97%)	7 (3%)	0	100	100
12	L	136/218 (62%)	131 (96%)	5 (4%)	0	100	100
13	M	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
14	N	197/203 (97%)	195 (99%)	2 (1%)	0	100	100
15	O	154/213 (72%)	151 (98%)	3 (2%)	0	100	100
16	P	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
17	Q	178/212 (84%)	174 (98%)	4 (2%)	0	100	100
18	R	174/224 (78%)	171 (98%)	3 (2%)	0	100	100
19	S	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
20	T	99/128 (77%)	95 (96%)	4 (4%)	0	100	100
21	U	133/140 (95%)	130 (98%)	3 (2%)	0	100	100
22	V	106/157 (68%)	106 (100%)	0	0	100	100
23	W	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
24	X	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
25	Y	133/136 (98%)	133 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	Z	145/148 (98%)	142 (98%)	3 (2%)	0	100	100
27	AA	103/245 (42%)	100 (97%)	3 (3%)	0	100	100
28	BA	97/115 (84%)	96 (99%)	1 (1%)	0	100	100
29	CA	106/125 (85%)	105 (99%)	1 (1%)	0	100	100
30	DA	127/135 (94%)	125 (98%)	2 (2%)	0	100	100
31	EA	107/110 (97%)	107 (100%)	0	0	100	100
32	FA	112/129 (87%)	110 (98%)	2 (2%)	0	100	100
33	GA	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
34	HA	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
35	IA	85/97 (88%)	83 (98%)	2 (2%)	0	100	100
36	JA	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
37	KA	48/51 (94%)	48 (100%)	0	0	100	100
38	LA	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
39	MA	23/25 (92%)	23 (100%)	0	0	100	100
40	NA	102/106 (96%)	100 (98%)	2 (2%)	0	100	100
41	OA	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
42	PA	122/137 (89%)	118 (97%)	4 (3%)	0	100	100
43	RA	151/165 (92%)	140 (93%)	11 (7%)	0	100	100
51	AB	215/295 (73%)	211 (98%)	4 (2%)	0	100	100
52	BB	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
53	CB	218/293 (74%)	215 (99%)	3 (1%)	0	100	100
54	DB	226/281 (80%)	225 (100%)	1 (0%)	0	100	100
55	EB	260/263 (99%)	252 (97%)	8 (3%)	0	100	100
56	FB	181/204 (89%)	176 (97%)	5 (3%)	0	100	100
57	GB	235/249 (94%)	231 (98%)	4 (2%)	0	100	100
58	HB	181/432 (42%)	177 (98%)	4 (2%)	0	100	100
59	IB	204/208 (98%)	199 (98%)	5 (2%)	0	100	100
60	JB	183/194 (94%)	182 (100%)	1 (0%)	0	100	100
61	KB	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
62	LB	140/158 (89%)	139 (99%)	1 (1%)	0	100	100
63	MB	115/132 (87%)	109 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	NB	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
65	OB	134/151 (89%)	130 (97%)	4 (3%)	0	100	100
66	PB	127/145 (88%)	125 (98%)	2 (2%)	0	100	100
67	QB	140/172 (81%)	136 (97%)	4 (3%)	0	100	100
68	RB	130/135 (96%)	129 (99%)	1 (1%)	0	100	100
69	SB	142/152 (93%)	140 (99%)	2 (1%)	0	100	100
70	TB	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
71	UB	100/119 (84%)	97 (97%)	3 (3%)	0	100	100
72	VB	81/83 (98%)	81 (100%)	0	0	100	100
73	WB	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
74	XB	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
75	YB	122/131 (93%)	118 (97%)	4 (3%)	0	100	100
76	ZB	83/124 (67%)	82 (99%)	1 (1%)	0	100	100
77	AC	99/115 (86%)	97 (98%)	2 (2%)	0	100	100
78	BC	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
79	CC	60/69 (87%)	60 (100%)	0	0	100	100
80	DC	53/56 (95%)	53 (100%)	0	0	100	100
81	EC	53/133 (40%)	50 (94%)	3 (6%)	0	100	100
82	FC	67/188 (36%)	66 (98%)	1 (2%)	0	100	100
83	GC	311/317 (98%)	299 (96%)	12 (4%)	0	100	100
84	IC	2/4 (50%)	2 (100%)	0	0	100	100
85	b	165/318 (52%)	154 (93%)	10 (6%)	1 (1%)	22	55
All	All	11553/13817 (84%)	11306 (98%)	246 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
85	b	225	VAL

5.3.2 Protein sidechains ⓘ

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	A	192/199 (96%)	192 (100%)	0	100	100
2	B	344/348 (99%)	340 (99%)	4 (1%)	67	77
3	C	302/337 (90%)	301 (100%)	1 (0%)	91	92
4	D	247/250 (99%)	246 (100%)	1 (0%)	89	91
5	E	201/251 (80%)	200 (100%)	1 (0%)	86	90
6	F	198/218 (91%)	198 (100%)	0	100	100
7	G	197/273 (72%)	196 (100%)	1 (0%)	86	90
8	H	169/171 (99%)	165 (98%)	4 (2%)	44	62
9	I	175/181 (97%)	173 (99%)	2 (1%)	70	79
10	J	144/149 (97%)	140 (97%)	4 (3%)	38	59
11	K	175/176 (99%)	174 (99%)	1 (1%)	84	88
12	L	117/161 (73%)	117 (100%)	0	100	100
13	M	171/172 (99%)	169 (99%)	2 (1%)	67	77
14	N	171/173 (99%)	171 (100%)	0	100	100
15	O	137/190 (72%)	137 (100%)	0	100	100
16	P	164/165 (99%)	162 (99%)	2 (1%)	67	77
17	Q	159/191 (83%)	159 (100%)	0	100	100
18	R	157/192 (82%)	156 (99%)	1 (1%)	84	88
19	S	139/140 (99%)	138 (99%)	1 (1%)	81	86
20	T	91/114 (80%)	91 (100%)	0	100	100
21	U	103/107 (96%)	103 (100%)	0	100	100
22	V	89/126 (71%)	87 (98%)	2 (2%)	47	64
23	W	106/134 (79%)	106 (100%)	0	100	100
24	X	124/135 (92%)	121 (98%)	3 (2%)	44	62
25	Y	117/118 (99%)	116 (99%)	1 (1%)	75	82
26	Z	119/120 (99%)	118 (99%)	1 (1%)	79	84
27	AA	87/184 (47%)	87 (100%)	0	100	100
28	BA	85/98 (87%)	84 (99%)	1 (1%)	67	77
29	CA	98/110 (89%)	98 (100%)	0	100	100
30	DA	115/121 (95%)	114 (99%)	1 (1%)	75	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	EA	88/89 (99%)	88 (100%)	0	100	100
32	FA	98/109 (90%)	98 (100%)	0	100	100
33	GA	109/110 (99%)	108 (99%)	1 (1%)	75	82
34	HA	86/89 (97%)	85 (99%)	1 (1%)	67	77
35	IA	74/80 (92%)	74 (100%)	0	100	100
36	JA	64/65 (98%)	64 (100%)	0	100	100
37	KA	47/48 (98%)	47 (100%)	0	100	100
38	LA	48/116 (41%)	46 (96%)	2 (4%)	25	49
39	MA	24/24 (100%)	24 (100%)	0	100	100
40	NA	92/94 (98%)	92 (100%)	0	100	100
41	OA	74/75 (99%)	73 (99%)	1 (1%)	62	75
42	PA	108/121 (89%)	106 (98%)	2 (2%)	52	69
43	RA	126/137 (92%)	119 (94%)	7 (6%)	17	43
51	AB	180/244 (74%)	177 (98%)	3 (2%)	56	72
52	BB	194/231 (84%)	192 (99%)	2 (1%)	73	80
53	CB	186/225 (83%)	185 (100%)	1 (0%)	86	90
54	DB	190/232 (82%)	187 (98%)	3 (2%)	58	73
55	EB	224/225 (100%)	219 (98%)	5 (2%)	47	64
56	FB	158/170 (93%)	156 (99%)	2 (1%)	65	76
57	GB	207/218 (95%)	204 (99%)	3 (1%)	62	75
58	HB	165/360 (46%)	162 (98%)	3 (2%)	54	71
59	IB	178/180 (99%)	177 (99%)	1 (1%)	84	88
60	JB	161/168 (96%)	154 (96%)	7 (4%)	25	49
61	KB	87/136 (64%)	86 (99%)	1 (1%)	70	79
62	LB	130/142 (92%)	129 (99%)	1 (1%)	79	84
63	MB	99/108 (92%)	95 (96%)	4 (4%)	27	50
64	NB	130/131 (99%)	130 (100%)	0	100	100
65	OB	106/119 (89%)	105 (99%)	1 (1%)	75	82
66	PB	115/130 (88%)	113 (98%)	2 (2%)	56	72
67	QB	117/140 (84%)	116 (99%)	1 (1%)	75	82
68	RB	119/121 (98%)	118 (99%)	1 (1%)	79	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	SB	125/132 (95%)	123 (98%)	2 (2%)	58	73
70	TB	112/115 (97%)	109 (97%)	3 (3%)	40	60
71	UB	93/107 (87%)	90 (97%)	3 (3%)	34	56
72	VB	67/67 (100%)	66 (98%)	1 (2%)	60	74
73	WB	112/113 (99%)	109 (97%)	3 (3%)	40	60
74	XB	113/115 (98%)	109 (96%)	4 (4%)	31	54
75	YB	107/113 (95%)	102 (95%)	5 (5%)	22	46
76	ZB	75/102 (74%)	73 (97%)	2 (3%)	40	60
77	AC	88/98 (90%)	87 (99%)	1 (1%)	70	79
78	BC	75/76 (99%)	74 (99%)	1 (1%)	65	76
79	CC	55/62 (89%)	55 (100%)	0	100	100
80	DC	48/49 (98%)	47 (98%)	1 (2%)	48	66
81	EC	46/106 (43%)	45 (98%)	1 (2%)	47	64
82	FC	62/154 (40%)	60 (97%)	2 (3%)	34	56
83	GC	272/275 (99%)	255 (94%)	17 (6%)	15	40
85	b	138/258 (54%)	119 (86%)	19 (14%)	3	17
All	All	10065/11683 (86%)	9911 (98%)	154 (2%)	60	74

All (154) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	162	VAL
2	B	298	LEU
2	B	338	VAL
2	B	353	VAL
3	C	232	VAL
4	D	163	LEU
5	E	211	ILE
7	G	193	VAL
8	H	48	LEU
8	H	121	LYS
8	H	123	ILE
8	H	151	ILE
9	I	197	VAL
9	I	213	HIS
10	J	20	LEU

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Mol	Chain	Res	Type
10	J	22	LEU
10	J	117	ILE
10	J	129	ASP
11	K	63	THR
13	M	64	ILE
13	M	184	ILE
16	P	22	ASP
16	P	83	VAL
18	R	160	ARG
19	S	80	VAL
22	V	87	LEU
22	V	109	ILE
24	X	79	VAL
24	X	82	ILE
24	X	104	VAL
25	Y	53	VAL
26	Z	122	VAL
28	BA	14	ILE
30	DA	8	VAL
33	GA	17	LEU
34	HA	43	MET
38	LA	100	LYS
38	LA	101	VAL
41	OA	52	VAL
42	PA	103	HIS
42	PA	124	VAL
43	RA	13	VAL
43	RA	37	LEU
43	RA	40	LYS
43	RA	58	ILE
43	RA	76	SER
43	RA	147	HIS
43	RA	151	ILE
51	AB	19	LEU
51	AB	87	VAL
51	AB	124	VAL
52	BB	126	ASP
52	BB	127	VAL
53	CB	248	TYR
54	DB	123	GLU
54	DB	205	TYR
54	DB	213	VAL

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Mol	Chain	Res	Type
55	EB	22	LYS
55	EB	33	THR
55	EB	45	ILE
55	EB	149	TYR
55	EB	222	LEU
56	FB	102	LEU
56	FB	194	ASP
57	GB	143	LYS
57	GB	145	PHE
57	GB	147	LEU
58	HB	284	THR
58	HB	330	VAL
58	HB	372	VAL
59	IB	125	LYS
60	JB	42	GLU
60	JB	66	LYS
60	JB	72	PHE
60	JB	117	LEU
60	JB	150	ARG
60	JB	172	ARG
60	JB	173	VAL
61	KB	47	LYS
62	LB	48	LYS
63	MB	31	LEU
63	MB	51	VAL
63	MB	77	ILE
63	MB	111	VAL
65	OB	57	THR
66	PB	72	LYS
66	PB	90	VAL
67	QB	126	VAL
68	RB	99	ASP
69	SB	131	VAL
69	SB	145	THR
70	TB	4	VAL
70	TB	24	LYS
70	TB	99	VAL
71	UB	17	ILE
71	UB	18	HIS
71	UB	68	THR
72	VB	11	LEU
73	WB	24	GLN

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Mol	Chain	Res	Type
73	WB	74	VAL
73	WB	105	THR
74	XB	17	ARG
74	XB	61	GLN
74	XB	105	PHE
74	XB	115	ILE
75	YB	5	VAL
75	YB	7	ILE
75	YB	8	ARG
75	YB	47	MET
75	YB	48	TYR
76	ZB	32	LYS
76	ZB	43	LYS
77	AC	100	ARG
78	BC	43	ILE
80	DC	39	CYS
81	EC	124	LYS
82	FC	85	TYR
82	FC	108	VAL
83	GC	11	LEU
83	GC	14	HIS
83	GC	31	ILE
83	GC	38	LYS
83	GC	54	ILE
83	GC	68	ASP
83	GC	113	PHE
83	GC	120	ILE
83	GC	142	VAL
83	GC	177	TRP
83	GC	186	THR
83	GC	256	ILE
83	GC	274	VAL
83	GC	275	ILE
83	GC	280	LYS
83	GC	296	GLN
83	GC	297	THR
85	b	14	PHE
85	b	21	LEU
85	b	30	VAL
85	b	47	LEU
85	b	52	VAL
85	b	53	VAL

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Mol	Chain	Res	Type
85	b	54	LEU
85	b	58	ASN
85	b	69	LEU
85	b	75	LEU
85	b	95	LEU
85	b	105	ASN
85	b	107	VAL
85	b	116	ILE
85	b	135	THR
85	b	149	ARG
85	b	155	LEU
85	b	219	VAL
85	b	222	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (72) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	ASN
3	C	21	ASN
3	C	50	GLN
3	C	203	GLN
3	C	212	ASN
3	C	245	HIS
3	C	329	ASN
4	D	275	GLN
6	F	23	ASN
6	F	98	ASN
7	G	99	GLN
7	G	248	HIS
11	K	149	GLN
12	L	125	ASN
13	M	57	GLN
13	M	90	ASN
13	M	182	HIS
18	R	156	HIS
20	T	38	ASN
21	U	27	ASN
22	V	45	ASN
22	V	48	GLN
22	V	104	GLN
23	W	107	HIS
28	BA	15	ASN

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Mol	Chain	Res	Type
28	BA	51	ASN
29	CA	18	ASN
29	CA	116	ASN
30	DA	24	GLN
31	EA	55	ASN
40	NA	19	GLN
42	PA	21	ASN
42	PA	30	ASN
42	PA	31	ASN
42	PA	100	ASN
43	RA	137	GLN
43	RA	142	ASN
43	RA	156	ASN
52	BB	158	HIS
52	BB	160	GLN
52	BB	186	ASN
54	DB	95	ASN
54	DB	245	HIS
55	EB	50	ASN
55	EB	224	ASN
56	FB	79	HIS
59	IB	99	ASN
59	IB	155	ASN
59	IB	168	GLN
60	JB	113	GLN
61	KB	61	GLN
62	LB	141	ASN
63	MB	55	ASN
64	NB	58	HIS
64	NB	90	HIS
66	PB	53	GLN
67	QB	37	GLN
68	RB	29	HIS
69	SB	72	GLN
70	TB	51	ASN
74	XB	20	GLN
74	XB	92	ASN
75	YB	106	GLN
76	ZB	45	ASN
76	ZB	46	ASN
77	AC	43	ASN
77	AC	80	HIS

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Mol	Chain	Res	Type
78	BC	84	HIS
80	DC	3	HIS
83	GC	222	ASN
85	b	68	HIS
85	b	71	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	SA	75/76 (98%)	17 (22%)	3 (4%)
45	TA	75/76 (98%)	15 (20%)	0
46	VA	11/12 (91%)	3 (27%)	0
47	WA	3558/3584 (99%)	607 (17%)	22 (0%)
48	XA	118/120 (98%)	9 (7%)	0
49	YA	155/156 (99%)	35 (22%)	0
50	ZA	1707/1869 (91%)	311 (18%)	10 (0%)
86	At	73/74 (98%)	15 (20%)	0
All	All	5772/5967 (96%)	1012 (17%)	35 (0%)

All (1012) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	SA	9	A
44	SA	16	C
44	SA	17	G
44	SA	19	C
44	SA	20	A
44	SA	21	A
44	SA	22	A
44	SA	46	G
44	SA	47	U
44	SA	48	C
44	SA	49	C
44	SA	58	A
44	SA	60	A
44	SA	61	C
44	SA	69	A
44	SA	70	A
44	SA	76	A
45	TA	6	G
45	TA	7	A

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Mol	Chain	Res	Type
45	TA	13	C
45	TA	16	C
45	TA	17	U
45	TA	18	G
45	TA	19	A
45	TA	20	U
45	TA	22	G
45	TA	31	A
45	TA	34	U
45	TA	35	U
45	TA	47	U
45	TA	58	A
45	TA	76	A
46	VA	22	U
46	VA	24	C
46	VA	26	A
47	WA	12	A
47	WA	13	U
47	WA	25	A
47	WA	33	A
47	WA	39	A
47	WA	42	A
47	WA	48	G
47	WA	59	A
47	WA	64	A
47	WA	65	A
47	WA	76	A
47	WA	91	G
47	WA	110	C
47	WA	119	G
47	WA	132	G
47	WA	134	G
47	WA	135	G
47	WA	136	C
47	WA	143	C
47	WA	144	G
47	WA	157	U
47	WA	159	C
47	WA	169	A
47	WA	171	U
47	WA	173	C
47	WA	179	G

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Mol	Chain	Res	Type
47	WA	197	A
47	WA	200	U
47	WA	201	C
47	WA	210	C
47	WA	217	C
47	WA	219	G
47	WA	224	U
47	WA	234	G
47	WA	259	C
47	WA	266	C
47	WA	267	G
47	WA	276	C
47	WA	278	G
47	WA	280	G
47	WA	297	U
47	WA	306	A
47	WA	309	C
47	WA	315	G
47	WA	316	U
47	WA	334	A
47	WA	336	A
47	WA	340	C
47	WA	350	C
47	WA	357	U
47	WA	363	A
47	WA	386	A
47	WA	387	G
47	WA	409	G
47	WA	410	A
47	WA	412	G
47	WA	449	C
47	WA	450	G
47	WA	452	A
47	WA	454	U
47	WA	455	C
47	WA	467	U
47	WA	468	U
47	WA	482	C
47	WA	483	G
47	WA	484	G
47	WA	485	U
47	WA	487	C

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Mol	Chain	Res	Type
47	WA	488	G
47	WA	493	U
47	WA	494	G
47	WA	499	C
47	WA	500	G
47	WA	506	G
47	WA	511	U
47	WA	521	U
47	WA	643	G
47	WA	662	C
47	WA	667	G
47	WA	668	A
47	WA	697	C
47	WA	698	G
47	WA	705	C
47	WA	720	C
47	WA	732	G
47	WA	739	C
47	WA	741	G
47	WA	751	G
47	WA	758	G
47	WA	763	G
47	WA	905	U
47	WA	907	C
47	WA	910	G
47	WA	915	U
47	WA	917	A
47	WA	919	A
47	WA	920	G
47	WA	929	C
47	WA	930	G
47	WA	933	A
47	WA	936	A
47	WA	937	G
47	WA	938	C
47	WA	939	A
47	WA	940	G
47	WA	941	C
47	WA	943	C
47	WA	944	G
47	WA	946	C
47	WA	949	A

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Mol	Chain	Res	Type
47	WA	950	U
47	WA	964	G
47	WA	965	A
47	WA	966	G
47	WA	971	A
47	WA	972	C
47	WA	974	C
47	WA	984	C
47	WA	989	C
47	WA	1078	C
47	WA	1085	C
47	WA	1104	G
47	WA	1186	C
47	WA	1193	G
47	WA	1201	G
47	WA	1202	G
47	WA	1216	C
47	WA	1217	G
47	WA	1220	C
47	WA	1221	C
47	WA	1222	C
47	WA	1240	G
47	WA	1243	C
47	WA	1244	A
47	WA	1246	G
47	WA	1253	C
47	WA	1255	G
47	WA	1258	A
47	WA	1259	A
47	WA	1268	G
47	WA	1271	G
47	WA	1272	A
47	WA	1274	C
47	WA	1275	G
47	WA	1282	C
47	WA	1286	G
47	WA	1287	U
47	WA	1289	G
47	WA	1290	G
47	WA	1294	C
47	WA	1295	G
47	WA	1298	G

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Mol	Chain	Res	Type
47	WA	1303	C
47	WA	1305	A
47	WA	1328	A
47	WA	1341	U
47	WA	1356	A
47	WA	1360	G
47	WA	1361	G
47	WA	1366	U
47	WA	1372	G
47	WA	1379	G
47	WA	1381	C
47	WA	1383	U
47	WA	1389	A
47	WA	1396	G
47	WA	1399	A
47	WA	1400	A
47	WA	1414	G
47	WA	1421	G
47	WA	1435	A
47	WA	1448	C
47	WA	1459	G
47	WA	1485	C
47	WA	1499	A
47	WA	1500	G
47	WA	1504	G
47	WA	1516	U
47	WA	1518	G
47	WA	1520	A
47	WA	1525	A
47	WA	1527	A
47	WA	1536	A
47	WA	1549	A
47	WA	1555	A
47	WA	1566	A
47	WA	1568	C
47	WA	1576	G
47	WA	1580	U
47	WA	1593	U
47	WA	1598	U
47	WA	1604	U
47	WA	1614	G
47	WA	1616	C

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Mol	Chain	Res	Type
47	WA	1626	G
47	WA	1627	G
47	WA	1633	A
47	WA	1635	G
47	WA	1636	A
47	WA	1640	A
47	WA	1643	G
47	WA	1652	A
47	WA	1656	G
47	WA	1663	C
47	WA	1678	C
47	WA	1679	U
47	WA	1693	G
47	WA	1726	G
47	WA	1743	G
47	WA	1744	A
47	WA	1757	C
47	WA	1762	G
47	WA	1765	C
47	WA	1766	G
47	WA	1767	A
47	WA	1770	C
47	WA	1771	G
47	WA	1772	A
47	WA	1773	U
47	WA	1777	A
47	WA	1783	U
47	WA	1787	C
47	WA	1789	A
47	WA	1805	G
47	WA	1806	A
47	WA	1807	A
47	WA	1817	G
47	WA	1821	G
47	WA	1823	G
47	WA	1824	U
47	WA	1829	C
47	WA	1830	C
47	WA	1836	U
47	WA	1838	G
47	WA	1839	A
47	WA	1844	G

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Mol	Chain	Res	Type
47	WA	1857	G
47	WA	1871	G
47	WA	1883	C
47	WA	1899	A
47	WA	1912	G
47	WA	1918	G
47	WA	1920	U
47	WA	1922	C
47	WA	1923	C
47	WA	1924	G
47	WA	1931	A
47	WA	1933	C
47	WA	1943	A
47	WA	1950	G
47	WA	1971	G
47	WA	1974	G
47	WA	1975	G
47	WA	1976	U
47	WA	1977	G
47	WA	1978	G
47	WA	1984	G
47	WA	1986	A
47	WA	1987	G
47	WA	1988	U
47	WA	1989	C
47	WA	1992	A
47	WA	1993	A
47	WA	1999	U
47	WA	2000	A
47	WA	2003	G
47	WA	2004	A
47	WA	2005	G
47	WA	2013	C
47	WA	2014	A
47	WA	2023	G
47	WA	2026	G
47	WA	2027	A
47	WA	2028	A
47	WA	2033	C
47	WA	2034	U
47	WA	2048	G
47	WA	2049	A

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Mol	Chain	Res	Type
47	WA	2050	U
47	WA	2057	G
47	WA	2058	G
47	WA	2064	C
47	WA	2071	A
47	WA	2073	A
47	WA	2086	U
47	WA	2095	G
47	WA	2096	C
47	WA	2097	A
47	WA	2099	A
47	WA	2100	G
47	WA	2102	G
47	WA	2104	G
47	WA	2106	A
47	WA	2107	A
47	WA	2109	A
47	WA	2114	G
47	WA	2118	C
47	WA	2261	G
47	WA	2262	C
47	WA	2269	U
47	WA	2270	A
47	WA	2277	G
47	WA	2291	C
47	WA	2302	A
47	WA	2303	G
47	WA	2308	G
47	WA	2315	A
47	WA	2318	G
47	WA	2333	G
47	WA	2335	G
47	WA	2350	G
47	WA	2353	C
47	WA	2362	A
47	WA	2384	A
47	WA	2385	C
47	WA	2386	U
47	WA	2397	A
47	WA	2411	U
47	WA	2412	C
47	WA	2424	C

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Mol	Chain	Res	Type
47	WA	2427	U
47	WA	2435	G
47	WA	2436	G
47	WA	2443	C
47	WA	2477	G
47	WA	2485	G
47	WA	2490	C
47	WA	2491	C
47	WA	2492	U
47	WA	2493	C
47	WA	2505	G
47	WA	2506	C
47	WA	2507	C
47	WA	2509	A
47	WA	2514	A
47	WA	2515	A
47	WA	2519	A
47	WA	2531	A
47	WA	2539	A
47	WA	2546	G
47	WA	2547	U
47	WA	2548	G
47	WA	2549	G
47	WA	2555	A
47	WA	2584	A
47	WA	2585	C
47	WA	2588	G
47	WA	2591	C
47	WA	2622	G
47	WA	2625	A
47	WA	2629	C
47	WA	2660	G
47	WA	2664	G
47	WA	2682	G
47	WA	2683	G
47	WA	2688	G
47	WA	2689	U
47	WA	2697	A
47	WA	2698	A
47	WA	2709	U
47	WA	2710	U
47	WA	2711	C

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Mol	Chain	Res	Type
47	WA	2712	C
47	WA	2713	G
47	WA	2716	G
47	WA	2721	C
47	WA	2723	G
47	WA	2727	A
47	WA	2728	G
47	WA	2742	U
47	WA	2756	G
47	WA	2759	A
47	WA	2760	G
47	WA	2762	G
47	WA	2766	A
47	WA	2771	U
47	WA	2789	A
47	WA	2790	U
47	WA	2792	U
47	WA	2796	C
47	WA	2800	A
47	WA	2808	A
47	WA	2816	C
47	WA	2828	U
47	WA	2829	G
47	WA	2830	U
47	WA	2835	A
47	WA	2844	G
47	WA	2857	G
47	WA	3599	G
47	WA	3600	C
47	WA	3617	G
47	WA	3618	U
47	WA	3627	G
47	WA	3628	G
47	WA	3637	A
47	WA	3664	A
47	WA	3666	G
47	WA	3674	G
47	WA	3694	A
47	WA	3714	A
47	WA	3750	A
47	WA	3755	G
47	WA	3763	C

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Mol	Chain	Res	Type
47	WA	3775	U
47	WA	3776	A
47	WA	3778	G
47	WA	3779	G
47	WA	3780	U
47	WA	3786	A
47	WA	3788	U
47	WA	3793	C
47	WA	3800	U
47	WA	3804	U
47	WA	3809	A
47	WA	3812	C
47	WA	3813	G
47	WA	3816	U
47	WA	3819	A
47	WA	3821	G
47	WA	3842	U
47	WA	3879	A
47	WA	3880	C
47	WA	3881	G
47	WA	3891	G
47	WA	3894	U
47	WA	3899	G
47	WA	3900	G
47	WA	3903	A
47	WA	3907	A
47	WA	3908	A
47	WA	3909	G
47	WA	3910	A
47	WA	3916	U
47	WA	3917	U
47	WA	3919	A
47	WA	3940	G
47	WA	3941	G
47	WA	3944	A
47	WA	3945	A
47	WA	3953	G
47	WA	4066	C
47	WA	4078	G
47	WA	4086	G
47	WA	4088	G
47	WA	4090	C

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Mol	Chain	Res	Type
47	WA	4100	A
47	WA	4101	G
47	WA	4102	C
47	WA	4118	C
47	WA	4121	C
47	WA	4124	G
47	WA	4129	A
47	WA	4144	C
47	WA	4145	C
47	WA	4146	G
47	WA	4149	G
47	WA	4160	C
47	WA	4164	C
47	WA	4167	C
47	WA	4168	G
47	WA	4172	A
47	WA	4174	A
47	WA	4175	G
47	WA	4185	G
47	WA	4186	G
47	WA	4193	G
47	WA	4205	A
47	WA	4214	A
47	WA	4227	G
47	WA	4231	U
47	WA	4235	A
47	WA	4236	A
47	WA	4243	C
47	WA	4245	C
47	WA	4253	A
47	WA	4256	G
47	WA	4268	G
47	WA	4270	A
47	WA	4273	A
47	WA	4275	A
47	WA	4283	A
47	WA	4292	U
47	WA	4293	G
47	WA	4299	G
47	WA	4307	G
47	WA	4308	U
47	WA	4316	C

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Mol	Chain	Res	Type
47	WA	4332	G
47	WA	4334	C
47	WA	4338	A
47	WA	4351	C
47	WA	4352	C
47	WA	4356	U
47	WA	4357	G
47	WA	4375	G
47	WA	4378	A
47	WA	4379	G
47	WA	4380	A
47	WA	4382	A
47	WA	4389	C
47	WA	4396	A
47	WA	4397	U
47	WA	4421	U
47	WA	4423	C
47	WA	4424	A
47	WA	4439	U
47	WA	4446	C
47	WA	4450	G
47	WA	4451	A
47	WA	4454	U
47	WA	4455	C
47	WA	4466	A
47	WA	4468	C
47	WA	4477	G
47	WA	4490	A
47	WA	4502	U
47	WA	4514	U
47	WA	4515	A
47	WA	4520	A
47	WA	4522	G
47	WA	4524	G
47	WA	4530	G
47	WA	4533	U
47	WA	4550	A
47	WA	4551	G
47	WA	4562	C
47	WA	4575	G
47	WA	4577	G
47	WA	4579	U

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Mol	Chain	Res	Type
47	WA	4586	A
47	WA	4588	G
47	WA	4592	A
47	WA	4602	G
47	WA	4629	U
47	WA	4638	U
47	WA	4639	G
47	WA	4641	G
47	WA	4654	G
47	WA	4658	A
47	WA	4669	C
47	WA	4672	C
47	WA	4679	U
47	WA	4689	A
47	WA	4693	A
47	WA	4702	A
47	WA	4711	U
47	WA	4721	G
47	WA	4722	C
47	WA	4723	G
47	WA	4747	G
47	WA	4756	G
47	WA	4759	C
47	WA	4761	C
47	WA	4763	G
47	WA	4767	G
47	WA	4771	G
47	WA	4773	C
47	WA	4775	C
47	WA	4872	G
47	WA	4873	C
47	WA	4875	G
47	WA	4876	A
47	WA	4877	G
47	WA	4878	A
47	WA	4879	G
47	WA	4884	U
47	WA	4885	C
47	WA	4887	U
47	WA	4888	C
47	WA	4904	C
47	WA	4914	G

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Mol	Chain	Res	Type
47	WA	4915	G
47	WA	4917	G
47	WA	4923	C
47	WA	4924	C
47	WA	4925	U
47	WA	4926	C
47	WA	4930	C
47	WA	4939	C
47	WA	4945	A
47	WA	4946	C
47	WA	4949	U
47	WA	4951	G
47	WA	4952	U
47	WA	4953	G
47	WA	4960	C
47	WA	4965	G
47	WA	4967	U
47	WA	4968	A
47	WA	4978	U
47	WA	4981	A
47	WA	4992	C
47	WA	4993	U
47	WA	4994	G
47	WA	5008	U
47	WA	5009	A
47	WA	5016	A
47	WA	5018	A
47	WA	5043	G
47	WA	5049	C
47	WA	5050	A
47	WA	5052	C
47	WA	5056	C
47	WA	5063	A
47	WA	5064	G
47	WA	5070	G
48	XA	7	G
48	XA	11	A
48	XA	22	A
48	XA	41	G
48	XA	54	A
48	XA	63	C
48	XA	64	G

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Mol	Chain	Res	Type
48	XA	100	A
48	XA	110	G
49	YA	6	C
49	YA	16	G
49	YA	23	C
49	YA	34	U
49	YA	35	C
49	YA	39	G
49	YA	59	A
49	YA	62	A
49	YA	63	U
49	YA	71	A
49	YA	72	A
49	YA	75	G
49	YA	77	A
49	YA	79	G
49	YA	80	A
49	YA	82	A
49	YA	84	A
49	YA	85	U
49	YA	86	U
49	YA	90	C
49	YA	94	G
49	YA	103	A
49	YA	105	C
49	YA	107	C
49	YA	110	U
49	YA	111	U
49	YA	114	G
49	YA	123	U
49	YA	124	U
49	YA	125	C
49	YA	126	C
49	YA	127	U
49	YA	147	G
49	YA	150	C
49	YA	155	C
50	ZA	3	C
50	ZA	4	C
50	ZA	25	A
50	ZA	26	U
50	ZA	33	G

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Mol	Chain	Res	Type
50	ZA	41	G
50	ZA	42	A
50	ZA	46	A
50	ZA	56	G
50	ZA	58	C
50	ZA	67	C
50	ZA	68	A
50	ZA	71	G
50	ZA	76	U
50	ZA	79	A
50	ZA	103	A
50	ZA	113	G
50	ZA	114	G
50	ZA	115	U
50	ZA	116	U
50	ZA	126	G
50	ZA	130	G
50	ZA	142	C
50	ZA	143	U
50	ZA	147	A
50	ZA	155	G
50	ZA	160	U
50	ZA	162	C
50	ZA	163	U
50	ZA	168	C
50	ZA	170	A
50	ZA	173	A
50	ZA	177	G
50	ZA	178	C
50	ZA	181	A
50	ZA	182	C
50	ZA	183	G
50	ZA	184	G
50	ZA	188	C
50	ZA	192	C
50	ZA	199	C
50	ZA	200	G
50	ZA	202	G
50	ZA	204	G
50	ZA	291	G
50	ZA	292	A
50	ZA	294	U

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Mol	Chain	Res	Type
50	ZA	297	A
50	ZA	302	A
50	ZA	307	G
50	ZA	308	G
50	ZA	309	G
50	ZA	319	C
50	ZA	323	C
50	ZA	325	C
50	ZA	326	C
50	ZA	327	G
50	ZA	328	U
50	ZA	330	G
50	ZA	335	G
50	ZA	347	G
50	ZA	351	G
50	ZA	364	A
50	ZA	368	U
50	ZA	369	C
50	ZA	370	G
50	ZA	381	C
50	ZA	383	G
50	ZA	384	U
50	ZA	385	G
50	ZA	400	C
50	ZA	409	C
50	ZA	418	A
50	ZA	438	G
50	ZA	448	A
50	ZA	450	C
50	ZA	464	A
50	ZA	465	A
50	ZA	466	G
50	ZA	472	C
50	ZA	473	A
50	ZA	474	G
50	ZA	476	A
50	ZA	482	G
50	ZA	487	U
50	ZA	491	C
50	ZA	492	C
50	ZA	493	A
50	ZA	528	A

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Mol	Chain	Res	Type
50	ZA	531	A
50	ZA	532	C
50	ZA	536	A
50	ZA	541	U
50	ZA	544	G
50	ZA	547	G
50	ZA	548	C
50	ZA	549	C
50	ZA	554	A
50	ZA	555	A
50	ZA	556	U
50	ZA	559	G
50	ZA	561	A
50	ZA	562	U
50	ZA	568	C
50	ZA	576	A
50	ZA	583	A
50	ZA	588	G
50	ZA	590	A
50	ZA	591	U
50	ZA	600	G
50	ZA	606	G
50	ZA	607	U
50	ZA	608	C
50	ZA	614	C
50	ZA	617	G
50	ZA	627	U
50	ZA	629	A
50	ZA	643	A
50	ZA	660	C
50	ZA	666	U
50	ZA	668	A
50	ZA	669	A
50	ZA	670	A
50	ZA	671	A
50	ZA	672	A
50	ZA	673	G
50	ZA	689	U
50	ZA	752	G
50	ZA	753	C
50	ZA	754	G
50	ZA	799	U

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Mol	Chain	Res	Type
50	ZA	811	A
50	ZA	821	G
50	ZA	822	U
50	ZA	834	C
50	ZA	835	C
50	ZA	840	C
50	ZA	841	G
50	ZA	842	C
50	ZA	845	G
50	ZA	847	A
50	ZA	859	G
50	ZA	869	A
50	ZA	870	A
50	ZA	871	U
50	ZA	872	A
50	ZA	873	G
50	ZA	874	G
50	ZA	875	A
50	ZA	878	G
50	ZA	884	C
50	ZA	888	U
50	ZA	889	U
50	ZA	890	U
50	ZA	891	G
50	ZA	892	U
50	ZA	893	U
50	ZA	894	G
50	ZA	896	U
50	ZA	897	U
50	ZA	902	G
50	ZA	905	C
50	ZA	913	A
50	ZA	914	U
50	ZA	920	A
50	ZA	933	G
50	ZA	934	G
50	ZA	971	G
50	ZA	990	A
50	ZA	992	A
50	ZA	999	G
50	ZA	1002	U
50	ZA	1008	A

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Mol	Chain	Res	Type
50	ZA	1023	A
50	ZA	1027	A
50	ZA	1045	U
50	ZA	1061	U
50	ZA	1062	A
50	ZA	1083	A
50	ZA	1085	C
50	ZA	1115	U
50	ZA	1116	C
50	ZA	1117	C
50	ZA	1118	C
50	ZA	1121	G
50	ZA	1133	A
50	ZA	1138	C
50	ZA	1148	A
50	ZA	1149	A
50	ZA	1153	C
50	ZA	1154	U
50	ZA	1170	A
50	ZA	1195	A
50	ZA	1207	G
50	ZA	1208	A
50	ZA	1215	C
50	ZA	1216	C
50	ZA	1220	A
50	ZA	1224	G
50	ZA	1241	A
50	ZA	1242	U
50	ZA	1251	A
50	ZA	1253	A
50	ZA	1256	G
50	ZA	1257	G
50	ZA	1259	A
50	ZA	1264	C
50	ZA	1274	G
50	ZA	1275	G
50	ZA	1285	G
50	ZA	1286	G
50	ZA	1297	U
50	ZA	1298	G
50	ZA	1299	A
50	ZA	1301	A

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Mol	Chain	Res	Type
50	ZA	1302	G
50	ZA	1303	C
50	ZA	1305	C
50	ZA	1312	G
50	ZA	1313	A
50	ZA	1333	U
50	ZA	1342	U
50	ZA	1354	G
50	ZA	1371	U
50	ZA	1372	U
50	ZA	1378	A
50	ZA	1382	A
50	ZA	1395	C
50	ZA	1396	A
50	ZA	1397	U
50	ZA	1418	C
50	ZA	1419	C
50	ZA	1422	G
50	ZA	1423	C
50	ZA	1424	G
50	ZA	1428	G
50	ZA	1434	C
50	ZA	1435	C
50	ZA	1436	C
50	ZA	1437	C
50	ZA	1438	A
50	ZA	1439	A
50	ZA	1442	U
50	ZA	1452	A
50	ZA	1454	A
50	ZA	1464	C
50	ZA	1466	G
50	ZA	1474	A
50	ZA	1475	G
50	ZA	1476	A
50	ZA	1477	U
50	ZA	1489	A
50	ZA	1490	G
50	ZA	1494	U
50	ZA	1498	A
50	ZA	1521	C
50	ZA	1522	A

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Mol	Chain	Res	Type
50	ZA	1531	A
50	ZA	1533	A
50	ZA	1535	U
50	ZA	1536	G
50	ZA	1548	G
50	ZA	1551	U
50	ZA	1552	G
50	ZA	1553	C
50	ZA	1555	U
50	ZA	1560	U
50	ZA	1567	G
50	ZA	1570	G
50	ZA	1580	A
50	ZA	1585	U
50	ZA	1587	G
50	ZA	1588	A
50	ZA	1601	A
50	ZA	1604	G
50	ZA	1605	G
50	ZA	1606	G
50	ZA	1621	U
50	ZA	1623	A
50	ZA	1638	G
50	ZA	1646	C
50	ZA	1648	G
50	ZA	1665	G
50	ZA	1680	G
50	ZA	1698	C
50	ZA	1699	A
50	ZA	1721	U
50	ZA	1722	G
50	ZA	1725	U
50	ZA	1726	G
50	ZA	1744	G
50	ZA	1745	A
50	ZA	1748	G
50	ZA	1753	C
50	ZA	1757	G
50	ZA	1773	C
50	ZA	1774	C
50	ZA	1780	G
50	ZA	1783	C

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Mol	Chain	Res	Type
50	ZA	1824	A
50	ZA	1826	G
50	ZA	1831	A
50	ZA	1836	G
50	ZA	1838	U
50	ZA	1849	G
50	ZA	1851	A
50	ZA	1861	G
50	ZA	1862	G
50	ZA	1863	A
50	ZA	1865	C
50	ZA	1869	A
86	At	8	4SU
86	At	14	A
86	At	16	H2U
86	At	17	C
86	At	18	G
86	At	19	G
86	At	46	7MG
86	At	47	U
86	At	48	C
86	At	49	C
86	At	58	A
86	At	59	U
86	At	72	C
86	At	73	A
86	At	74	C

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	SA	20	A
44	SA	21	A
44	SA	57	G
47	WA	12	A
47	WA	275	C
47	WA	385	A
47	WA	505	G
47	WA	971	A
47	WA	1293	G
47	WA	1635	G
47	WA	1677	C

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Mol	Chain	Res	Type
47	WA	1806	A
47	WA	1820	G
47	WA	2048	G
47	WA	2095	G
47	WA	2268	C
47	WA	2384	A
47	WA	2508	G
47	WA	2697	A
47	WA	3627	G
47	WA	4117	G
47	WA	4450	G
47	WA	4701	U
47	WA	4886	G
47	WA	4951	G
50	ZA	24	C
50	ZA	383	G
50	ZA	553	U
50	ZA	561	A
50	ZA	752	G
50	ZA	841	G
50	ZA	870	A
50	ZA	890	U
50	ZA	1137	U
50	ZA	1433	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z > 2$
86	H2U	At	20	86	18,21,22	0.44	0	19,30,33	1.05	1 (5%)
86	H2U	At	16	86	18,21,22	0.47	0	19,30,33	1.02	1 (5%)
86	7MG	At	46	86	23,26,27	3.44	10 (43%)	27,39,42	2.22	9 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
86	PSU	At	32	86	18,21,22	4.57	6 (33%)	21,30,33	2.95	5 (23%)
86	4SU	At	8	86	18,21,22	3.87	8 (44%)	25,30,33	2.32	4 (16%)

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
86	H2U	At	20	86	-	1/7/38/39	0/2/2/2
86	H2U	At	16	86	-	1/7/38/39	0/2/2/2
86	7MG	At	46	86	-	3/7/37/38	0/3/3/3
86	PSU	At	32	86	-	0/7/25/26	0/2/2/2
86	4SU	At	8	86	-	0/7/25/26	0/2/2/2

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	At	32	PSU	C6-C5	12.62	1.49	1.35
86	At	32	PSU	C2-N1	10.00	1.49	1.36
86	At	46	7MG	C8-N9	8.71	1.51	1.45
86	At	8	4SU	C4-N3	8.22	1.46	1.37
86	At	32	PSU	C2-N3	7.55	1.49	1.37
86	At	46	7MG	C5-N7	7.29	1.44	1.35
86	At	8	4SU	C2-N1	7.20	1.49	1.38
86	At	8	4SU	C2-N3	7.01	1.50	1.38
86	At	46	7MG	C2-N3	5.94	1.47	1.33
86	At	8	4SU	C6-C5	5.77	1.48	1.35
86	At	46	7MG	C4-N9	5.36	1.44	1.37
86	At	8	4SU	C5-C4	5.34	1.48	1.42
86	At	32	PSU	C6-N1	5.19	1.44	1.36
86	At	8	4SU	C4-S4	-4.92	1.60	1.68
86	At	46	7MG	C2-N2	4.82	1.45	1.34
86	At	32	PSU	C4-N3	4.10	1.46	1.38
86	At	46	7MG	C2-N1	3.87	1.47	1.37
86	At	46	7MG	C5-C6	3.58	1.52	1.43
86	At	46	7MG	C6-N1	3.25	1.44	1.38
86	At	8	4SU	C6-N1	2.93	1.45	1.38
86	At	46	7MG	O6-C6	-2.72	1.18	1.23
86	At	8	4SU	O2-C2	-2.38	1.18	1.23
86	At	32	PSU	C1'-C5	2.27	1.55	1.50
86	At	46	7MG	C5-C4	2.13	1.44	1.37

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	At	8	4SU	C4-N3-C2	-7.97	119.68	127.31
86	At	32	PSU	N1-C2-N3	7.70	123.29	115.17
86	At	32	PSU	C4-N3-C2	-6.30	117.69	126.37
86	At	46	7MG	C2-N3-C4	5.68	122.08	112.30
86	At	8	4SU	C5-C4-N3	5.59	119.95	114.75
86	At	32	PSU	C6-N1-C2	-5.58	117.51	122.69
86	At	46	7MG	C5-C6-N1	4.50	118.87	110.94
86	At	32	PSU	C6-C5-C4	4.32	121.09	118.17
86	At	32	PSU	O2-C2-N1	-4.32	118.33	122.79
86	At	46	7MG	C4-C5-N7	4.02	110.12	105.38
86	At	8	4SU	C5-C4-S4	-3.92	119.83	124.31
86	At	46	7MG	C2-N1-C6	-3.81	118.21	125.11
86	At	8	4SU	N3-C2-N1	3.76	119.78	114.89
86	At	46	7MG	C5-C4-N3	-3.63	121.32	128.13
86	At	16	H2U	C5-C4-N3	-3.40	113.07	116.69
86	At	20	H2U	C5-C4-N3	-3.31	113.16	116.69
86	At	46	7MG	C5-C4-N9	2.84	109.97	106.33
86	At	46	7MG	O6-C6-C5	-2.62	121.20	127.62
86	At	46	7MG	N9-C8-N7	2.37	106.73	103.37
86	At	46	7MG	N9-C4-N3	2.22	128.72	125.46

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	At	46	7MG	O4'-C4'-C5'-O5'
86	At	46	7MG	C3'-C4'-C5'-O5'
86	At	16	H2U	C4'-C5'-O5'-P
86	At	46	7MG	C4'-C5'-O5'-P
86	At	20	H2U	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	At	46	7MG	1	0
86	At	8	4SU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 113 ligands modelled in this entry, 110 are monoatomic - leaving 3 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	$\# Z > 2$
89	ANM	WA	5178	-	20,20,20	4.07	7 (35%)	24,27,27	1.47	2 (8%)
90	SPD	WA	5179	-	9,9,9	0.27	0	8,8,8	0.26	0
91	SER	ZA	1919	-	4,5,6	0.58	0	1,5,7	0.56	0

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
89	ANM	WA	5178	-	-	4/10/23/23	0/2/2/2
90	SPD	WA	5179	-	-	0/7/7/7	-
91	SER	ZA	1919	-	-	0/2/4/6	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	WA	5178	ANM	C3-C2	-11.63	1.32	1.53
89	WA	5178	ANM	C16-N1	-8.79	1.30	1.47
89	WA	5178	ANM	C2-C16	7.55	1.68	1.53
89	WA	5178	ANM	C4-C3	4.06	1.58	1.53
89	WA	5178	ANM	C4-N1	3.88	1.60	1.47
89	WA	5178	ANM	O2-C5	3.67	1.43	1.35
89	WA	5178	ANM	C6-C5	2.50	1.57	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	WA	5178	ANM	O2-C5-C6	5.41	120.73	111.09
89	WA	5178	ANM	C12-C15-C16	-2.05	109.93	113.40

There are no chirality outliers.

All (4) torsion outliers are listed below:

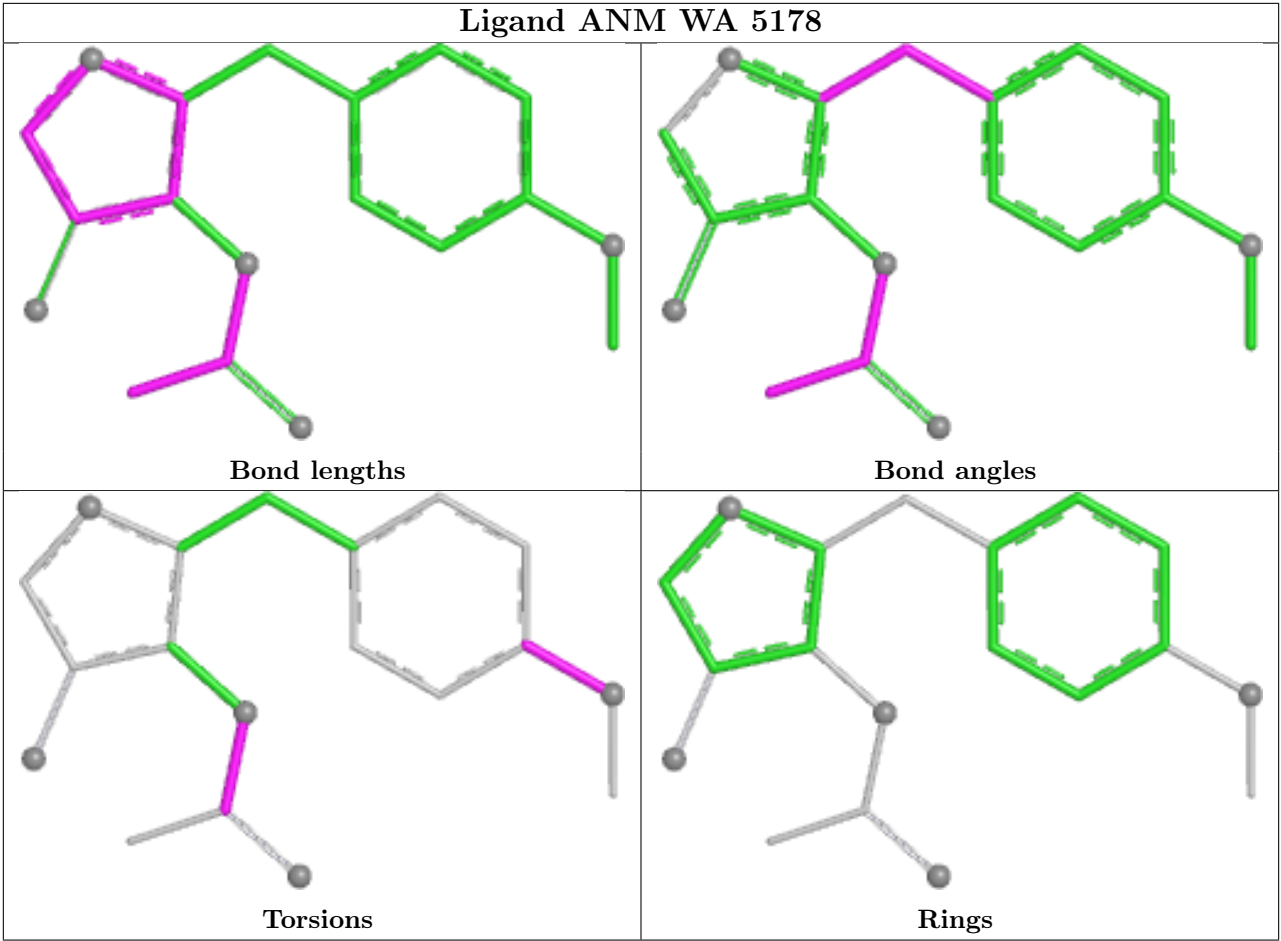
Mol	Chain	Res	Type	Atoms
89	WA	5178	ANM	C6-C5-O2-C2
89	WA	5178	ANM	O3-C5-O2-C2
89	WA	5178	ANM	C1-C9-O1-C14
89	WA	5178	ANM	C10-C9-O1-C14

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
89	WA	5178	ANM	1	0
90	WA	5179	SPD	1	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 than 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.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
47	WA	20

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	WA	2118:C	O3'	2260:C	P	37.44
1	WA	1225:G	O3'	1239:G	P	19.90
1	WA	763:G	O3'	904:C	P	18.09
1	WA	996:C	O3'	1070:G	P	17.05
1	WA	524:C	O3'	639:G	P	16.87

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	WA	4103:C	O3'	4109:G	P	16.48
1	WA	4779:C	O3'	4861:C	P	15.12
1	WA	1698:C	O3'	1722:C	P	14.84
1	WA	1366:U	O3'	1370:A	P	14.17
1	WA	5024:U	O3'	5030:G	P	13.83
1	WA	2904:G	O3'	3598:A	P	12.90
1	WA	3954:A	O3'	4063:C	P	11.16
1	WA	182:G	O3'	189:G	P	10.47
1	WA	1186:C	O3'	1189:C	P	9.69
1	WA	4731:A	O3'	4737:G	P	9.21
1	WA	4742:G	O3'	4745:G	P	7.29
1	WA	501:G	O3'	505:G	P	5.98
1	WA	513:U	O3'	516:C	P	5.54
1	WA	1106:U	O3'	1174:G	P	5.01
1	WA	4901:G	O3'	4904:C	P	3.32

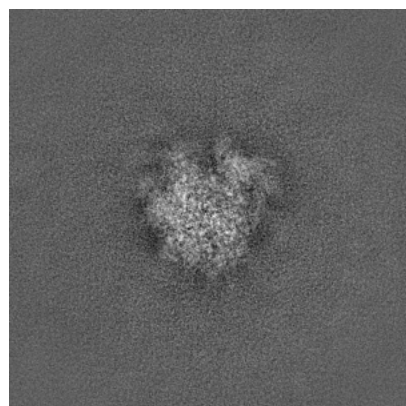
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43569. These allow visual inspection of the internal detail of the map and identification of artifacts.

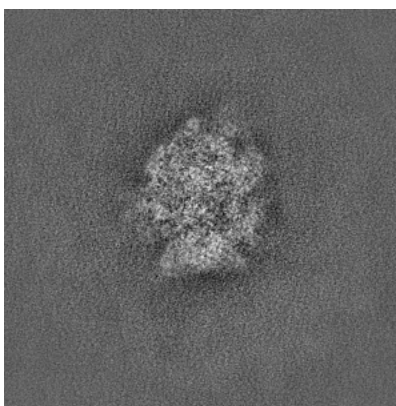
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

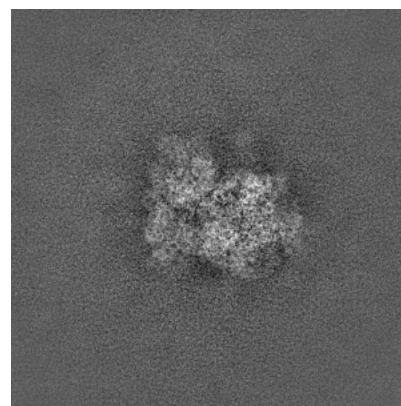
6.1.1 Primary map



X

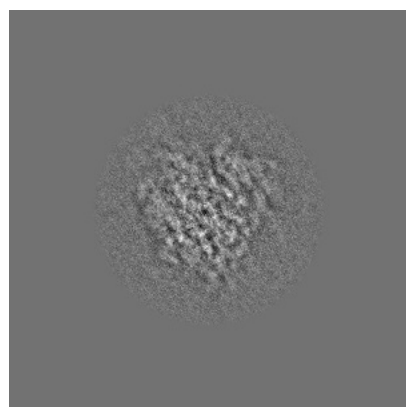


Y

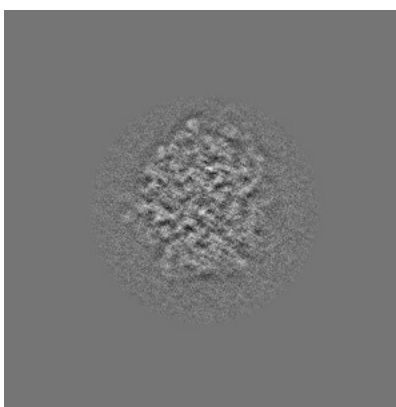


Z

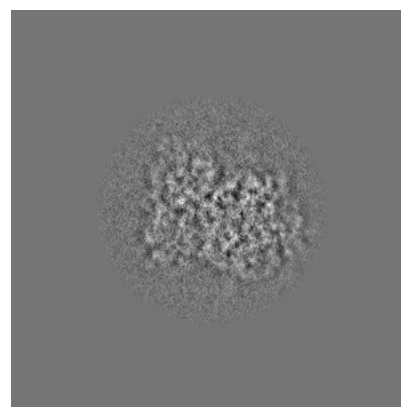
6.1.2 Raw map



X



Y

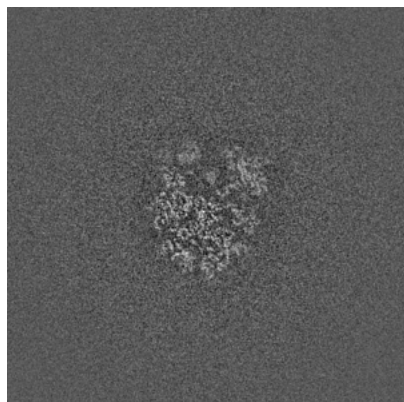


Z

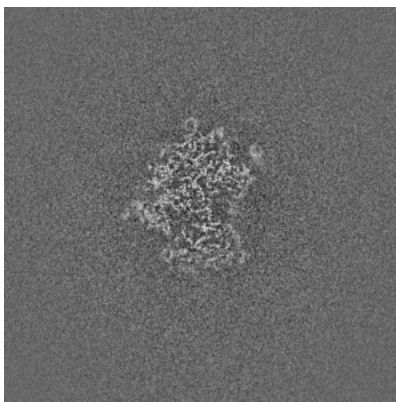
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

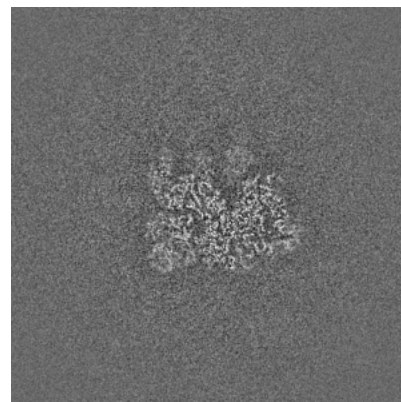
6.2.1 Primary map



X Index: 324

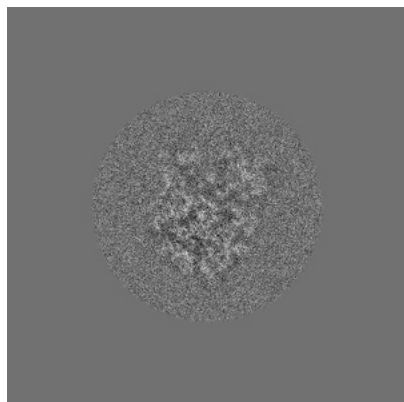


Y Index: 324

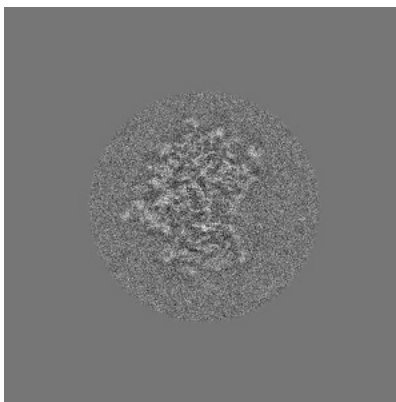


Z Index: 324

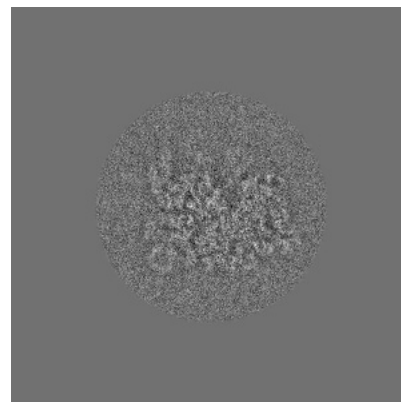
6.2.2 Raw map



X Index: 324



Y Index: 324

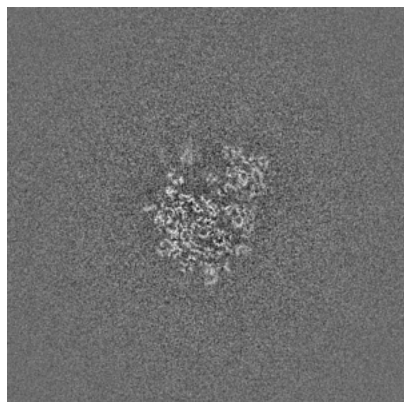


Z Index: 324

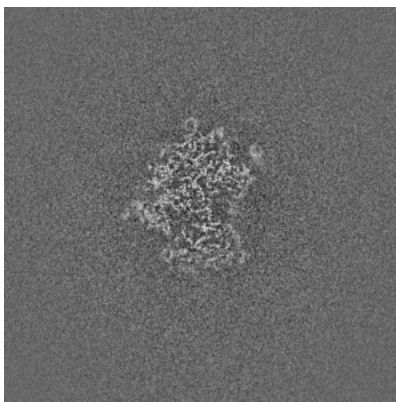
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

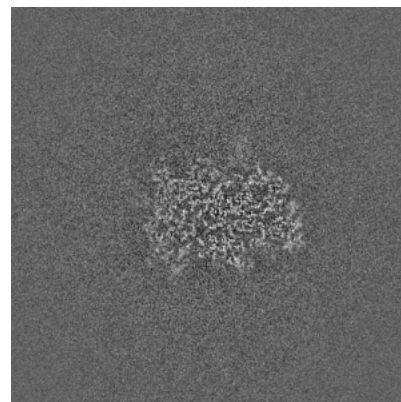
6.3.1 Primary map



X Index: 320

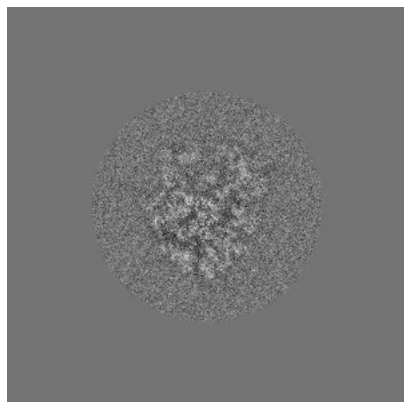


Y Index: 324

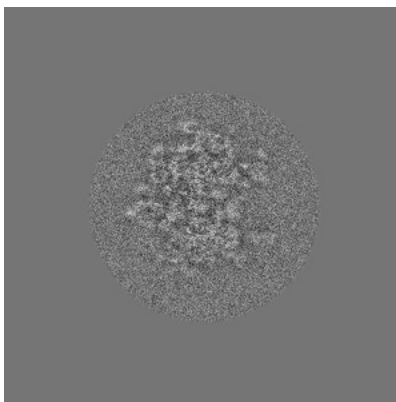


Z Index: 311

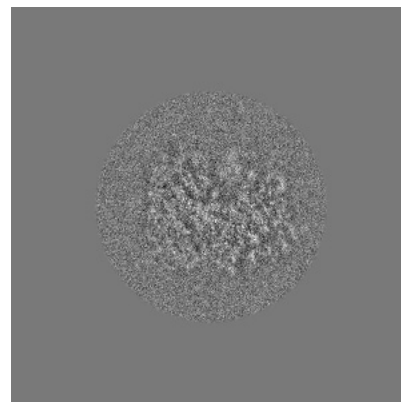
6.3.2 Raw map



X Index: 325



Y Index: 333

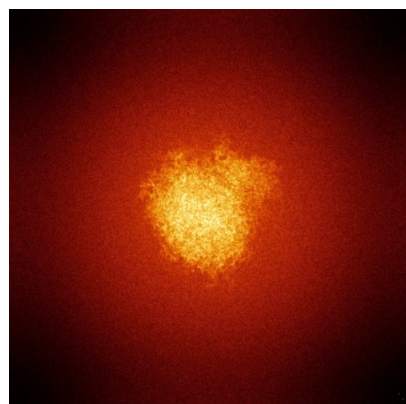


Z Index: 331

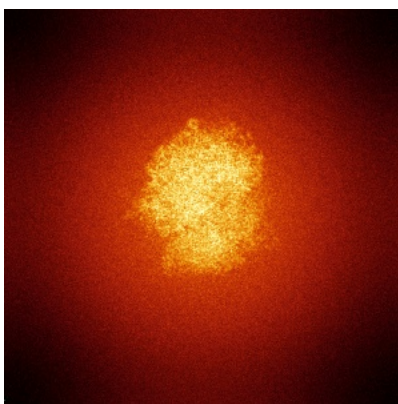
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

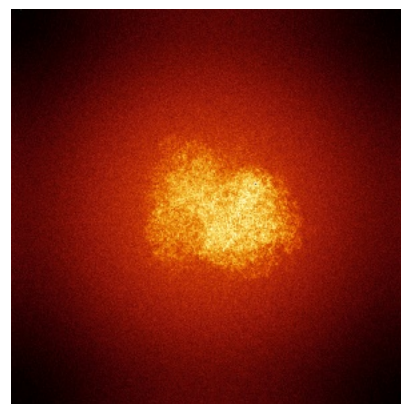
6.4.1 Primary map



X

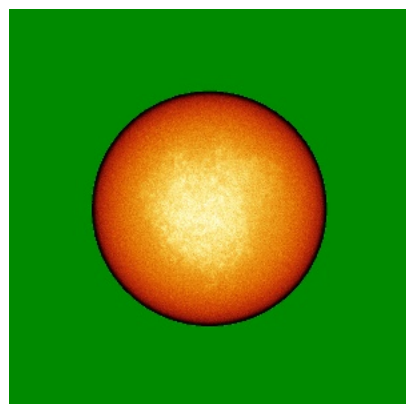


Y

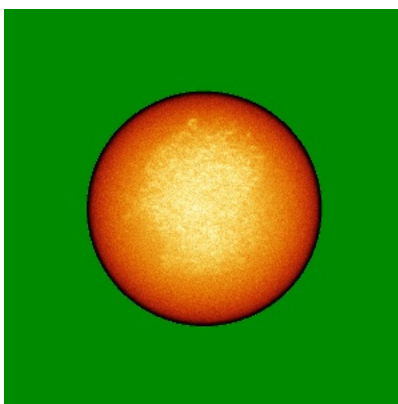


Z

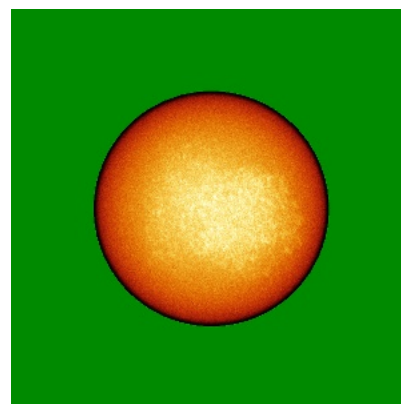
6.4.2 Raw map



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.

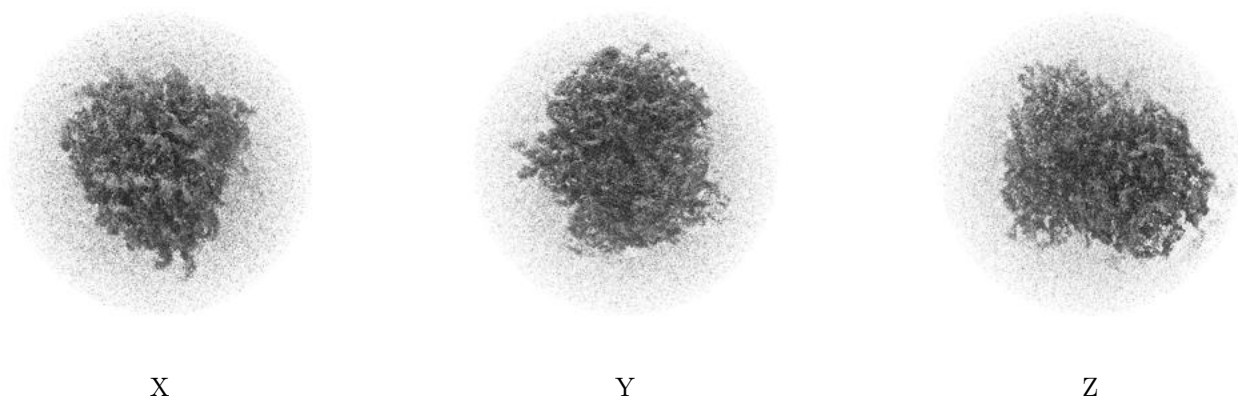
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 7.0. 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



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.

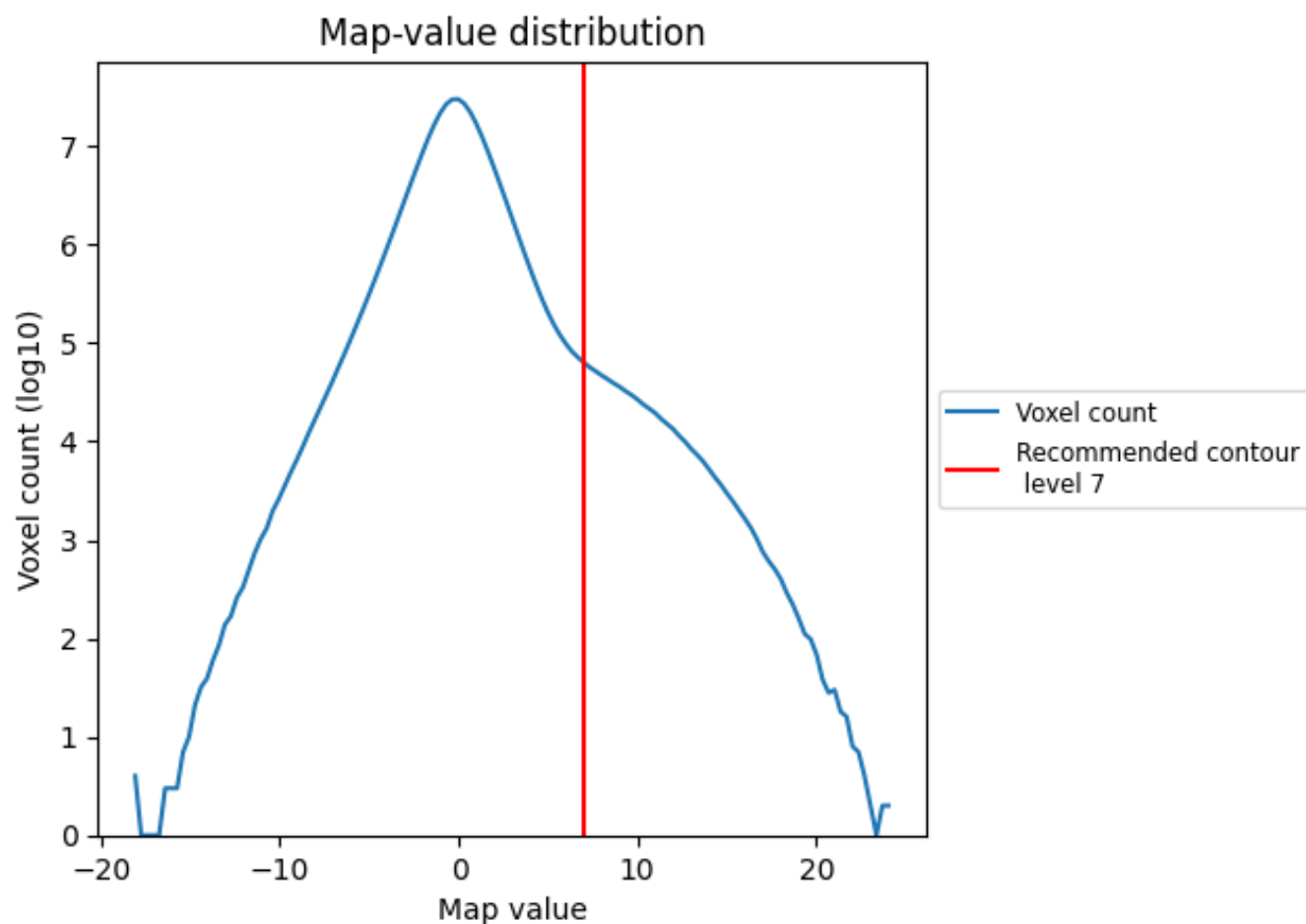
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

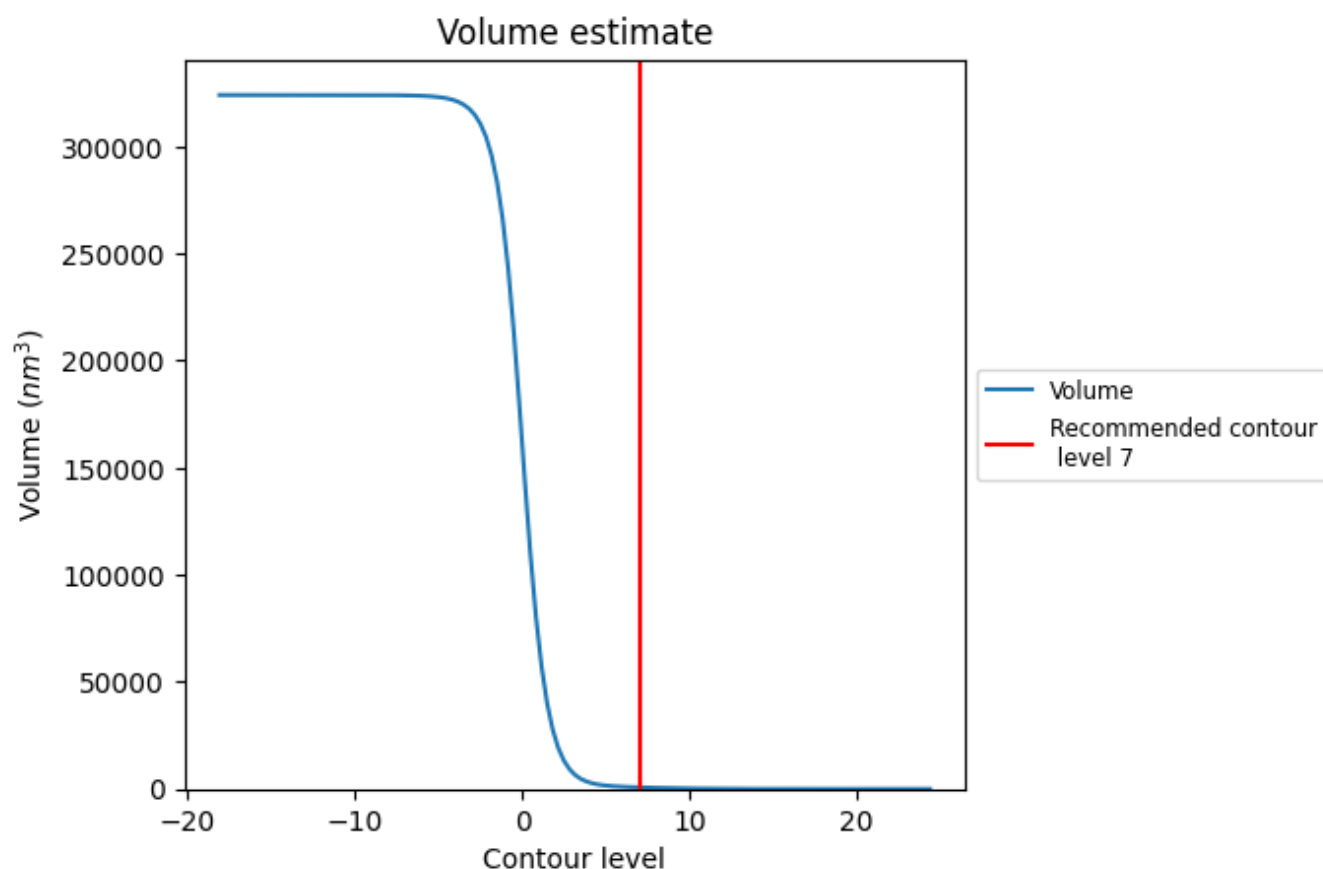
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

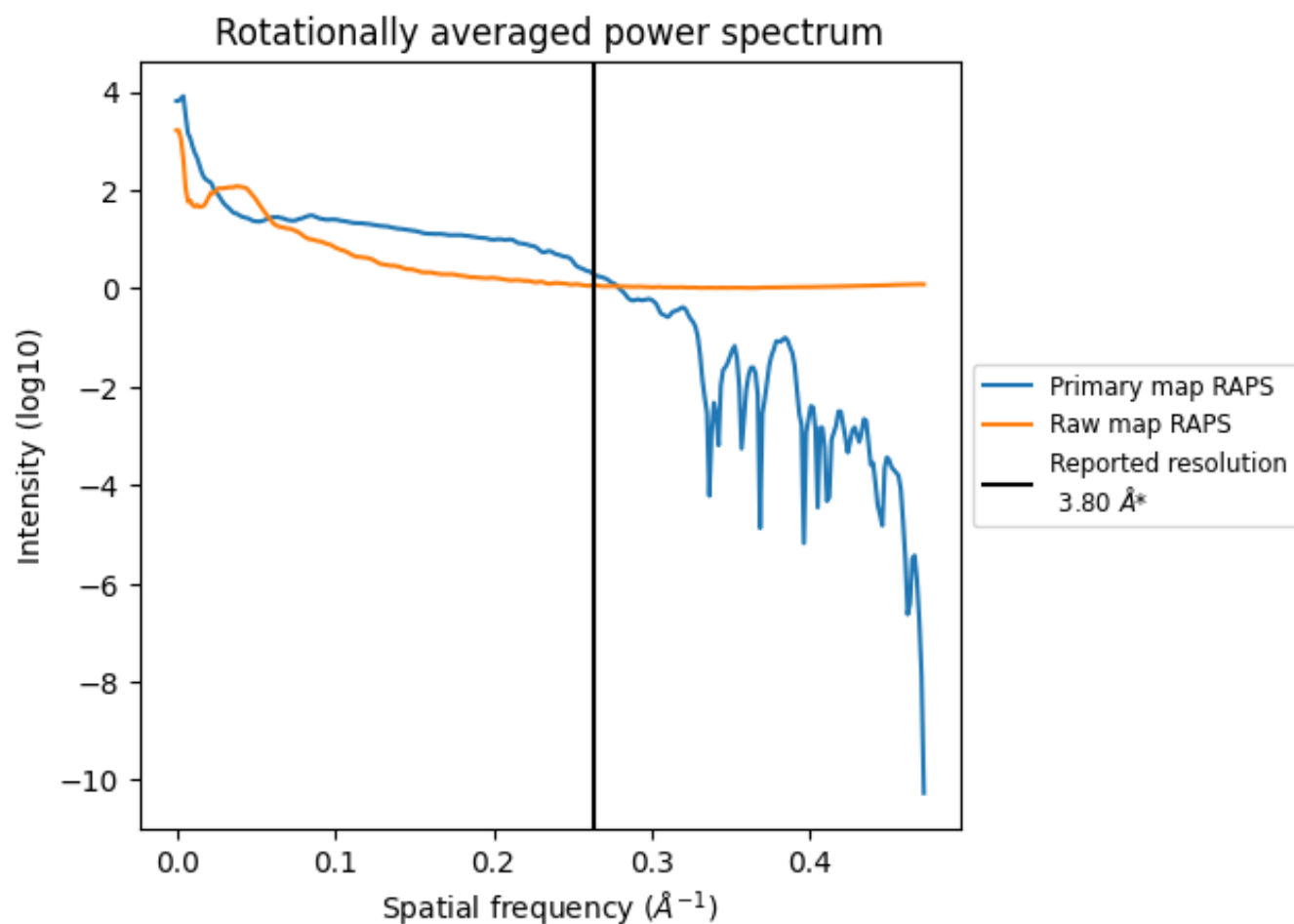
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 724 nm^3 ; this corresponds to an approximate mass of 654 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 ⓘ

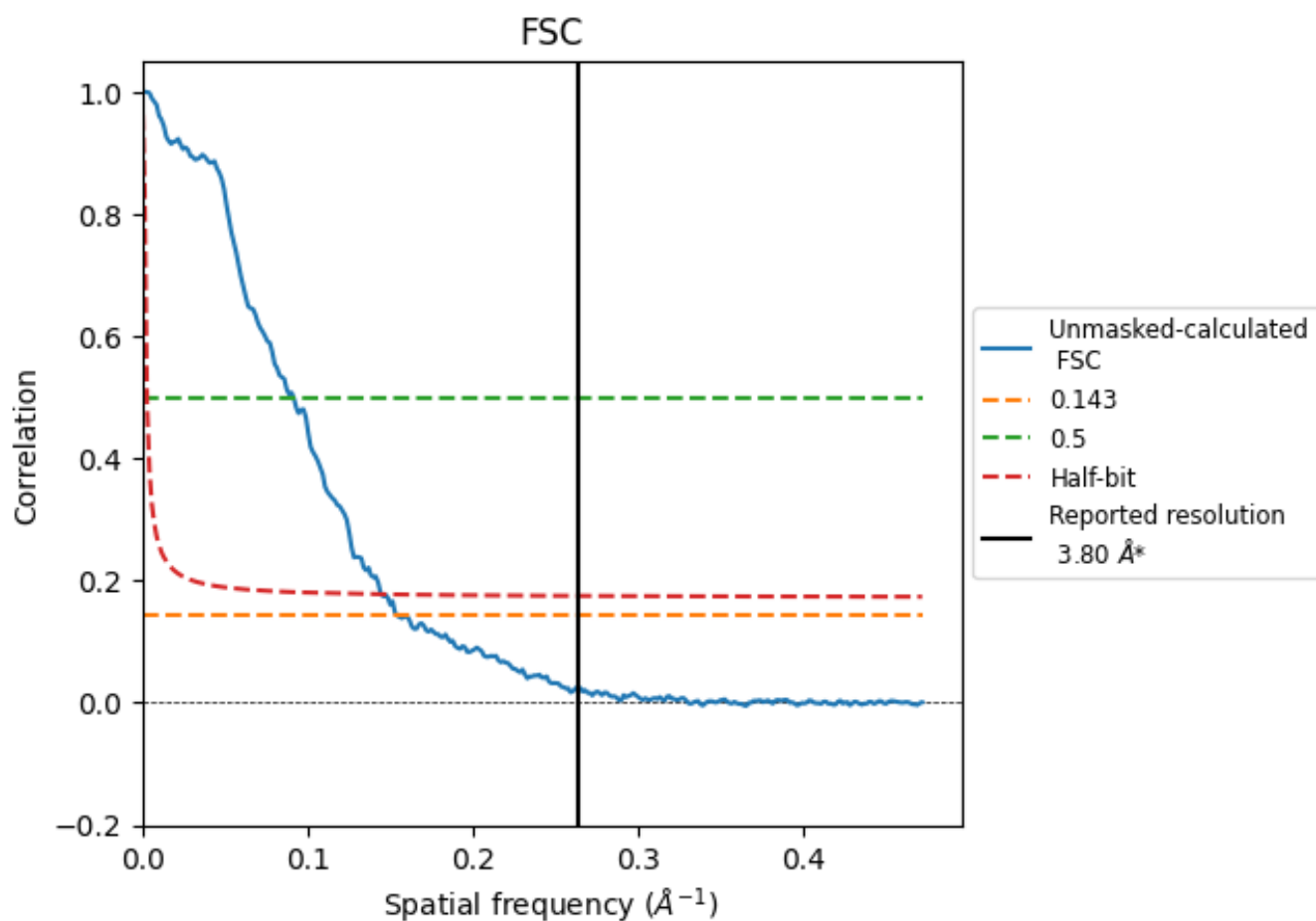


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

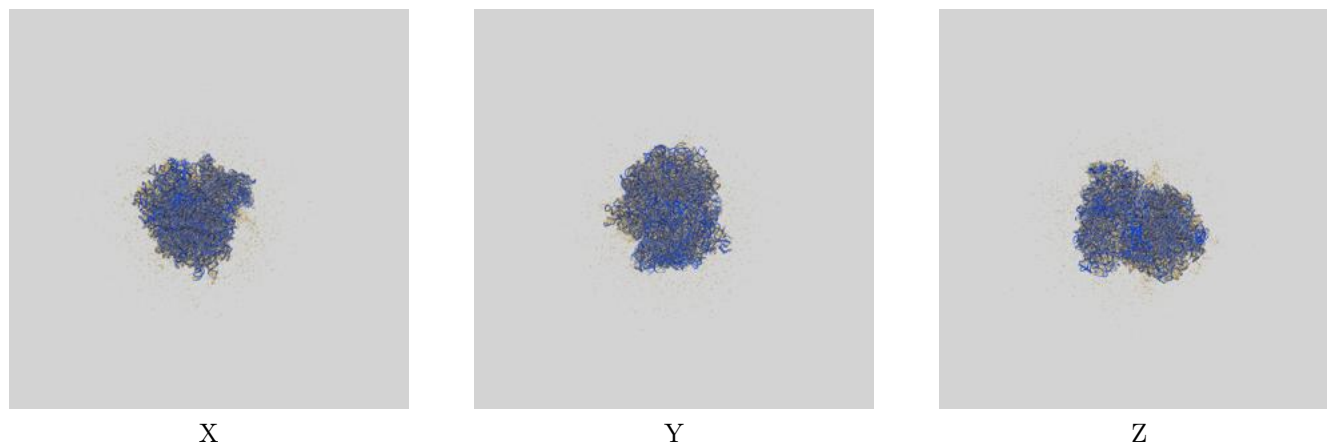
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.49	10.93	6.91

*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 6.49 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

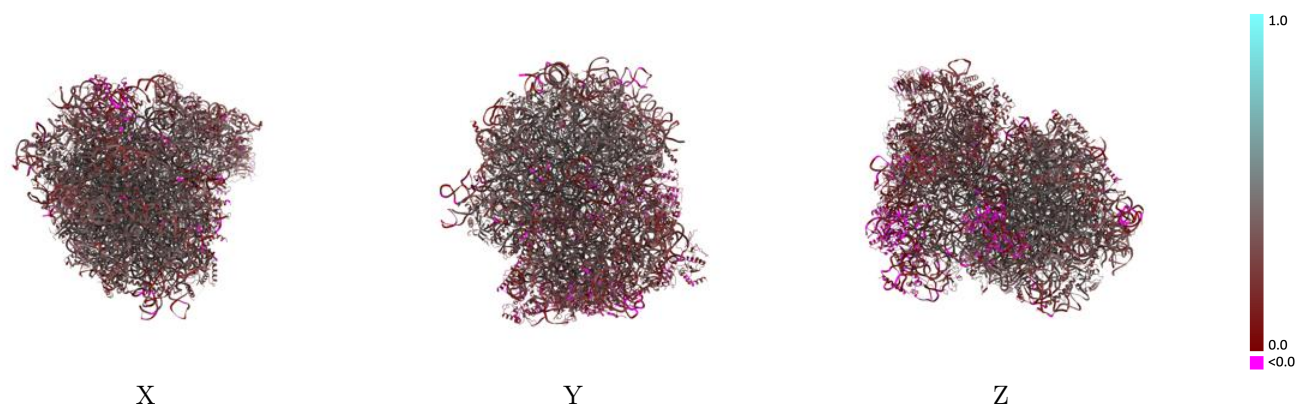
This section contains information regarding the fit between EMDB map EMD-43569 and PDB model 8VVU. Per-residue inclusion information can be found in [section 3](#) on [page 25](#).

9.1 Map-model overlay [i](#)



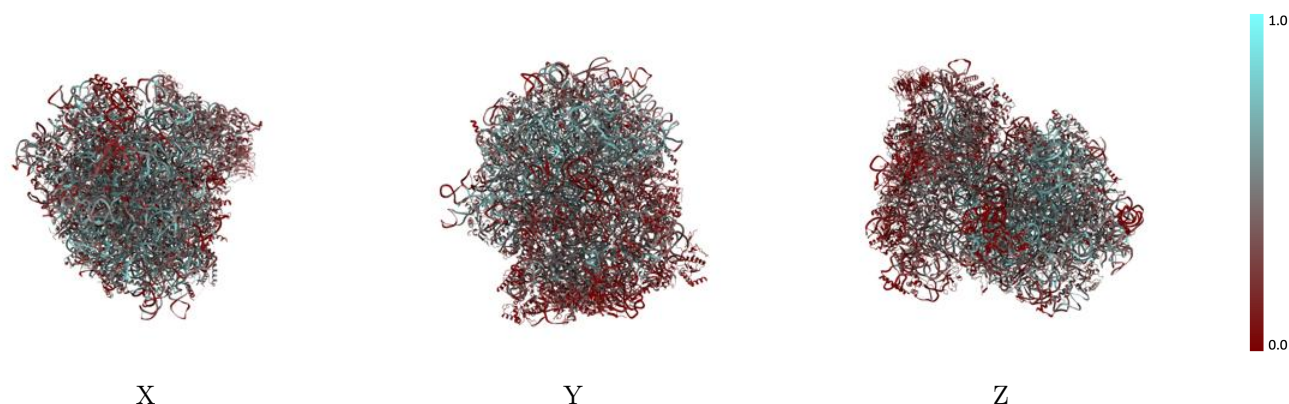
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



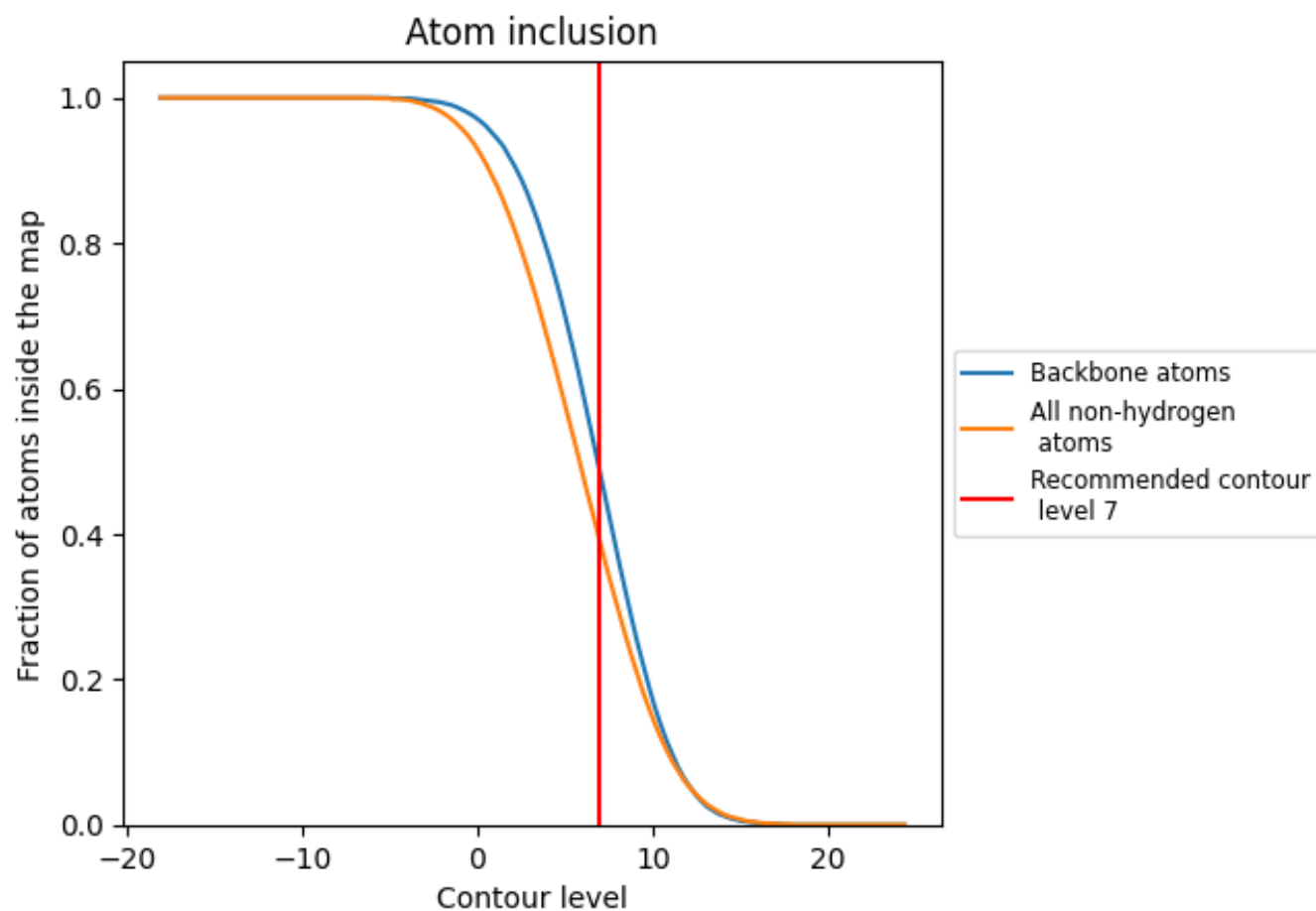
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (7).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 39% 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 (7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3890	 0.3110
A	 0.3430	 0.3890
AA	 0.3150	 0.2980
AB	 0.2230	 0.2650
AC	 0.2340	 0.3270
At	 0.2220	 0.2100
B	 0.3600	 0.3730
BA	 0.3320	 0.3210
BB	 0.1800	 0.2300
BC	 0.1630	 0.2540
C	 0.3800	 0.3740
CA	 0.3550	 0.3570
CB	 0.2250	 0.3050
CC	 0.1790	 0.2500
D	 0.3380	 0.3140
DA	 0.3380	 0.3840
DB	 0.2270	 0.2860
DC	 0.2530	 0.3310
E	 0.2860	 0.3230
EA	 0.3490	 0.3990
EB	 0.0810	 0.0240
EC	 0.2230	 0.2220
F	 0.3760	 0.3640
FA	 0.3160	 0.3660
FB	 0.2190	 0.2640
FC	 0.0960	 0.2040
G	 0.3590	 0.3140
GA	 0.3970	 0.3440
GB	 0.1510	 0.1960
GC	 0.1170	 0.2140
H	 0.3320	 0.3310
HA	 0.3730	 0.3390
HB	 0.1480	 0.2150
I	 0.3490	 0.3780
IA	 0.3900	 0.3970























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Chain	Atom inclusion	Q-score
IB	 0.2110	 0.2780
IC	 0.1000	 0.3680
J	 0.2820	 0.2820
JA	 0.2710	 0.3010
JB	 0.2530	 0.2520
K	 0.3810	 0.3560
KA	 0.3610	 0.3550
KB	 0.2220	 0.2430
L	 0.3720	 0.3480
LA	 0.3800	 0.3530
LB	 0.2170	 0.3180
M	 0.3680	 0.3950
MA	 0.2940	 0.3540
MB	 0.0780	 0.1740
N	 0.3890	 0.3610
NA	 0.3320	 0.3760
NB	 0.2250	 0.2840
O	 0.3880	 0.3750
OA	 0.3880	 0.3580
OB	 0.1800	 0.2650
P	 0.3920	 0.3870
PA	 0.3750	 0.3780
PB	 0.2040	 0.2490
Q	 0.3680	 0.3140
QB	 0.2110	 0.2720
R	 0.3500	 0.3790
RA	 0.0250	 0.0600
RB	 0.2000	 0.2580
S	 0.3380	 0.3630
SA	 0.3190	 0.2880
SB	 0.2400	 0.2660
T	 0.3070	 0.2930
TA	 0.0660	 0.1450
TB	 0.2060	 0.2670
U	 0.3190	 0.3800
UB	 0.2150	 0.2810
V	 0.2310	 0.2420
VA	 0.3330	 0.3430
VB	 0.2150	 0.2990
W	 0.3630	 0.3520
WA	 0.5260	 0.3490
WB	 0.1980	 0.3130

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Chain	Atom inclusion	Q-score
X	 0.3530	 0.3570
XA	 0.6260	 0.3690
XB	 0.2690	 0.3310
Y	 0.3700	 0.3410
YA	 0.5590	 0.3550
YB	 0.0960	 0.0590
Z	 0.3600	 0.3980
ZA	 0.3750	 0.2630
ZB	 0.1990	 0.2260
b	 0.0220	 0.0650