



Full wwPDB EM Validation Report ⓘ

May 1, 2025 – 01:22 pm BST

PDB ID : 9G6J / pdb_00009g6j
EMDB ID : EMD-51103
Title : The structure of the *Candida albicans* ribosome with tRNA-fMet, mRNA, and compounds (GEN and MFQ) with strong density for the P-site tRNA
Authors : Kolosova, O.; Zgadzay, Y.; Jenner, L.B.; Guskov, A.; Yusupov, M.
Deposited on : 2024-07-18
Resolution : 2.15 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:

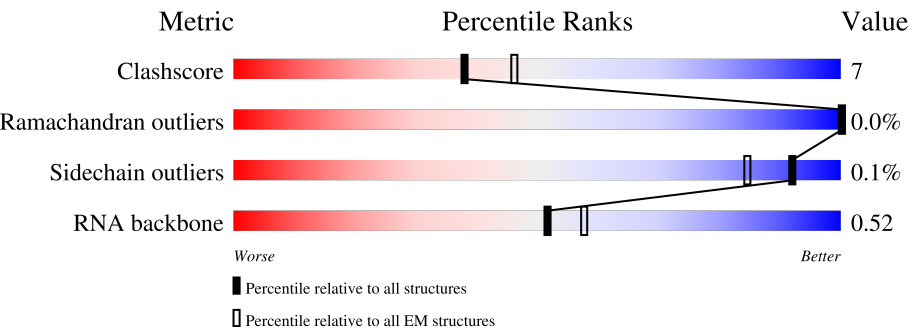
EMDB validation analysis : 0.0.1.dev118
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.15 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.





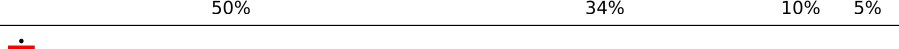
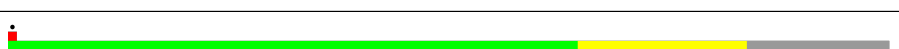



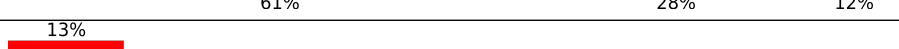



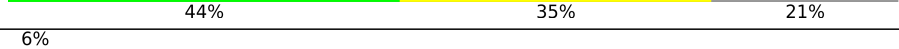

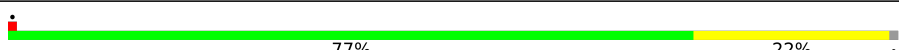


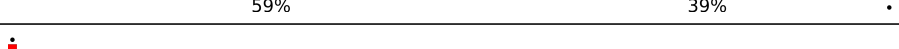







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	0	172	<div><div>85%15%.</div></div>
2	1	3359	<div><div>61%25%5%9%.</div></div>
3	2	160	<div><div>91%9%.</div></div>
4	3	121	<div><div>79%20%.</div></div>
5	4	158	<div><div>66%31%..</div></div>
6	6	137	<div><div>85%10%..</div></div>
7	7	155	<div><div>32%8%60%</div></div>













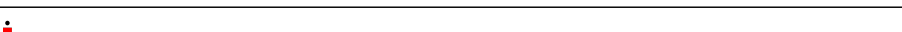

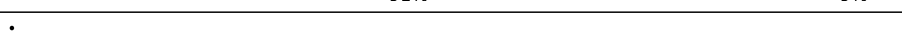

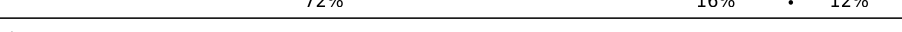








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Mol	Chain	Length	Quality of chain
8	8	142	
9	9	127	
10	A	1787	
11	B	261	
12	C	256	
13	D	249	
14	E	251	
15	F	262	
16	G	225	
17	H	236	
18	I	186	
19	J	206	
20	K	189	
21	L	118	
22	M	155	
23	N	143	
24	O	151	
25	P	132	
26	Q	142	
27	T	145	
28	R	142	
29	S	137	
30	U	145	
31	V	119	
32	W	87	


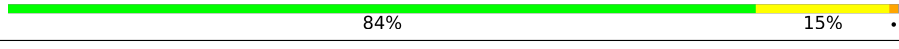
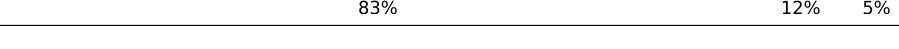
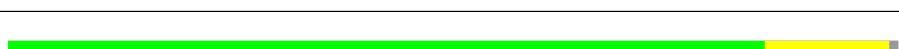



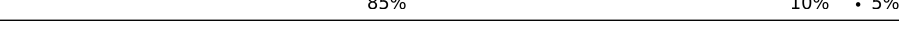



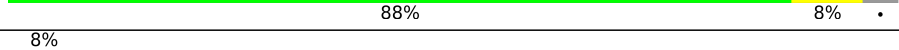











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Mol	Chain	Length	Quality of chain
33	X	130	
34	Y	145	
35	Z	135	
36	a	105	
37	b	119	
38	c	82	
39	d	67	
40	e	56	
41	f	63	
42	g	193	
43	h	317	
44	j	254	
45	k	389	
46	l	363	
47	m	298	
48	n	176	
49	o	241	
50	p	262	
51	q	191	
52	r	220	
53	s	174	
54	t	202	
55	u	131	
56	v	204	
57	w	200	

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Mol	Chain	Length	Quality of chain
58	x	185	
59	y	186	
60	z	190	
61	AA	136	
62	AB	149	
63	AC	63	
64	AD	106	
65	AE	112	
66	AF	131	
67	AG	107	
68	AH	122	
69	AI	120	
70	AJ	99	
71	AK	90	
72	AL	78	
73	AM	51	
74	AN	52	
75	AO	25	
76	AP	106	
77	AQ	92	
78	AT	77	
78	PT	77	
79	MR	39	

2 Entry composition [i](#)

There are 83 unique types of molecules in this entry. The entry contains 197424 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 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	171	Total	C	N	O	S	2	0
			1442	933	262	244	3		

- Molecule 2 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	3066	Total	C	N	O	P	0	0
			65536	29280	11774	21416	3066		

- Molecule 3 is a protein called Ribosomal 60S subunit protein L21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	159	Total	C	N	O	S	2	0
			1276	807	244	223	2		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	121	Total	C	N	O	P	0	0
			2579	1153	463	842	121		

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	156	Total	C	N	O	P	0	0
			3313	1482	581	1094	156		

- Molecule 6 is a protein called Ribosomal 60S subunit protein L23B.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	131	Total	C	N	O	S	1	0
			986	621	186	171	8		

- Molecule 7 is a protein called Ribosomal 60S subunit protein L24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	62	Total	C	N	O	S	0	0
			516	328	102	85	1		

- Molecule 8 is a protein called Ribosomal 60S subunit protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	121	Total	C	N	O	S	0	0
			974	622	175	176	1		

- Molecule 9 is a protein called Ribosomal 60S subunit protein L26B.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	9	125	Total	C	N	O	0	0
			980	613	189	178		

- Molecule 10 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	1692	Total	C	N	O	P	0	0
			36083	16130	6412	11849	1692		

- Molecule 11 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	208	Total	C	N	O	S	0	0
			1627	1041	284	297	5		

- Molecule 12 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	214	Total	C	N	O	S	0	0
			1724	1094	313	313	4		

- Molecule 13 is a protein called Ribosomal 40S subunit protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	216	Total	C	N	O	S	0	0
			1620	1033	287	295	5		

- Molecule 14 is a protein called Ribosomal 40S subunit protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	222	Total	C	N	O	S	0	0
			1701	1084	310	303	4		

- Molecule 15 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	260	Total	C	N	O	S	0	0
			2055	1306	386	358	5		

- Molecule 16 is a protein called Ribosomal 40S subunit protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	199	Total	C	N	O	S	0	0
			1572	983	294	291	4		

- Molecule 17 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	226	Total	C	N	O	S	0	0
			1820	1133	351	330	6		

- Molecule 18 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I	182	Total	C	N	O		0	0
			1466	939	264	263			

- Molecule 19 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J	203	Total	C	N	O	S	0	0
			1579	973	322	283	1		

- Molecule 20 is a protein called Ribosomal 40S subunit protein S9B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	K	178	Total	C	N	O	S	0	0
			1453	918	286	248	1		

- Molecule 21 is a protein called Ribosomal 40S subunit protein S10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L	93	Total	C	N	O	S	0	0
			783	511	129	142	1		

- Molecule 22 is a protein called Ribosomal 40S subunit protein S11A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	M	141	Total	C	N	O	S	0	0
			1129	722	212	192	3		

- Molecule 23 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	N	71	Total	C	N	O	S	0	0
			539	341	95	99	4		

- Molecule 24 is a protein called Ribosomal 40S subunit protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	O	150	Total	C	N	O	S	0	0
			1187	757	219	210	1		

- Molecule 25 is a protein called Ribosomal 40S subunit protein S14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	127	Total	C	N	O	S	0	0
			942	579	186	174	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	119	IAS	ASP	conflict	UNP A0A1D8PDT3

- Molecule 26 is a protein called Ribosomal 40S subunit protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Q	115	Total	C	N	O	S	0	0
			906	578	164	158	6		

- Molecule 27 is a protein called Ribosomal 40S subunit protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	142	Total	C	N	O	S	0	0
			1169	733	228	205	3		

- Molecule 28 is a protein called Ribosomal 40S subunit protein S16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	141	Total	C	N	O	S	0	0
			1102	706	202	193	1		

- Molecule 29 is a protein called Ribosomal 40S subunit protein S17B.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	118	Total	C	N	O	S	0	0
			954	602	176	175	1		

- Molecule 30 is a protein called Ribosomal 40S subunit protein S19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	141	Total	C	N	O	S	0	0
			1100	689	210	200	1		

- Molecule 31 is a protein called Ribosomal 40S subunit protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	V	100	Total	C	N	O	S	0	0
			790	499	146	143	2		

- Molecule 32 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	W	87	Total	C	N	O	S	0	0
			676	415	126	133	2		

- Molecule 33 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	X	129	Total	C	N	O	S	0	0
			1032	655	191	183	3		

- Molecule 34 is a protein called Ribosomal 40S subunit protein S23B.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Y	143	Total	C	N	O	S	0	0
			1110	701	219	188	2		

- Molecule 35 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Z	132	Total	C	N	O		0	0
			1072	670	216	186			

- Molecule 36 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	a	72	Total	C	N	O		0	0
			578	369	103	106			

- Molecule 37 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	b	98	Total	C	N	O	S	0	0
			779	482	163	128	6		

- Molecule 38 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	c	81	Total	C	N	O	S	0	0
			614	383	110	114	7		

- Molecule 39 is a protein called Ribosomal 40S subunit protein S28B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	d	62	Total	C	N	O	S	0	0
			487	299	98	88	2		

- Molecule 40 is a protein called Ribosomal 40S subunit protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	e	55	Total	C	N	O	S	0	0
			454	281	94	75	4		

- Molecule 41 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	f	58	Total	C	N	O	S	0	0
			461	289	93	77	2		

- Molecule 42 is a protein called Ubiquitin-ribosomal 40S subunit protein S31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	g	70	Total	C	N	O	S	0	0
			565	358	111	90	6		

- Molecule 43 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	h	241	Total	C	N	O	S	0	0
			1854	1176	319	355	4		

- Molecule 44 is a protein called Ribosomal 60S subunit protein L2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	249	Total	C	N	O	S	1	0
			1894	1185	377	330	2		

- Molecule 45 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	386	Total	C	N	O	S	1	0
			3084	1955	584	538	7		

- Molecule 46 is a protein called Ribosomal 60S subunit protein L4B.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	l	361	Total	C	N	O	S	0	0
			2751	1729	529	490	3		

- Molecule 47 is a protein called Ribosomal 60S subunit protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	292	Total	C	N	O	S	0	0
			2394	1526	416	450	2		

- Molecule 48 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	n	155	Total	C	N	O	1	0
			1237	794	226	217		

- Molecule 49 is a protein called Ribosomal 60S subunit protein L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	o	230	Total	C	N	O	S	1	0
			1860	1193	343	323	1		

- Molecule 50 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	231	Total	C	N	O	S	0	0
			1795	1150	319	323	3		

- Molecule 51 is a protein called Ribosomal 60S subunit protein L9B.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	189	Total	C	N	O	S	0	0
			1510	953	275	278	4		

- Molecule 52 is a protein called Ribosomal 60S subunit protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	218	Total	C	N	O	S	0	0
			1759	1110	336	305	8		

- Molecule 53 is a protein called Ribosomal 60S subunit protein L11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	172	Total	C	N	O	S	1	0
			1385	864	262	255	4		

- Molecule 54 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	t	195	Total	C	N	O	0	0
			1573	986	311	276		

- Molecule 55 is a protein called Ribosomal 60S subunit protein L14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	u	130	Total	C	N	O	S	0	0
			1029	660	193	175	1		

- Molecule 56 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	v	203	Total	C	N	O	S	0	0
			1713	1075	356	280	2		

- Molecule 57 is a protein called Ribosomal 60S subunit protein L16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	w	199	Total	C	N	O	S	0	0
			1590	1025	294	269	2		

- Molecule 58 is a protein called Ribosomal 60S subunit protein L17B.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	x	172	Total	C	N	O		0	0
			1375	850	279	246			

- Molecule 59 is a protein called Ribosomal 60S subunit protein L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	y	185	Total	C	N	O		3	0
			1478	930	302	246			

- Molecule 60 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	z	180	Total	C	N	O	S	1	0
			1471	910	313	245	3		

- Molecule 61 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AA	135	Total	C	N	O	S	0	0
			1087	705	197	183	2		

- Molecule 62 is a protein called Ribosomal 60S subunit protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AB	148	Total	C	N	O	S	0	0
			1170	741	231	197	1		

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AC	60	Total	C	N	O	S	1	0
			489	305	105	78	1		

- Molecule 64 is a protein called Ribosomal 60S subunit protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AD	96	Total	C	N	O	S	0	0
			729	469	121	137	2		

- Molecule 65 is a protein called Ribosomal 60S subunit protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AE	108	Total	C	N	O	S	0	0
			881	558	166	155	2		

- Molecule 66 is a protein called Ribosomal 60S subunit protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AF	125	Total	C	N	O	S	1	0
			1015	649	197	168	1		

- Molecule 67 is a protein called Ribosomal 60S subunit protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AG	106	Total	C	N	O	S	3	0
			867	558	166	142	1		

- Molecule 68 is a protein called Ribosomal 60S subunit protein L34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	AH	112	Total	C	N	O	S	4	0
			913	567	188	154	4		

- Molecule 69 is a protein called Ribosomal 60S subunit protein L35A.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	AI	119	Total	C	N	O	1	0
			990	629	195	166		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AJ	97	Total	C	N	O	S	1	0
			764	476	157	130	1		

- Molecule 71 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AK	86	Total	C	N	O	S	0	0
			677	413	148	110	6		

- Molecule 72 is a protein called Ribosomal 60S subunit protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	AL	77	Total	C	N	O	1	0
			623	398	116	109		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	AM	50	Total	C	N	O	1	0
			446	280	100	66		

- Molecule 74 is a protein called Rpl40bp.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AN	52	Total	C	N	O	S	1	0
			427	265	89	67	6		

- Molecule 75 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AO	25	Total	C	N	O	S	0	0
			236	144	63	28	1		

- Molecule 76 is a protein called Ribosomal 60S subunit protein L42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AP	105	Total	C	N	O	S	2	0
			863	547	171	140	5		

- Molecule 77 is a protein called Ribosomal 60S subunit protein L43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AQ	91	Total	C	N	O	S	0	0
			698	430	140	124	4		

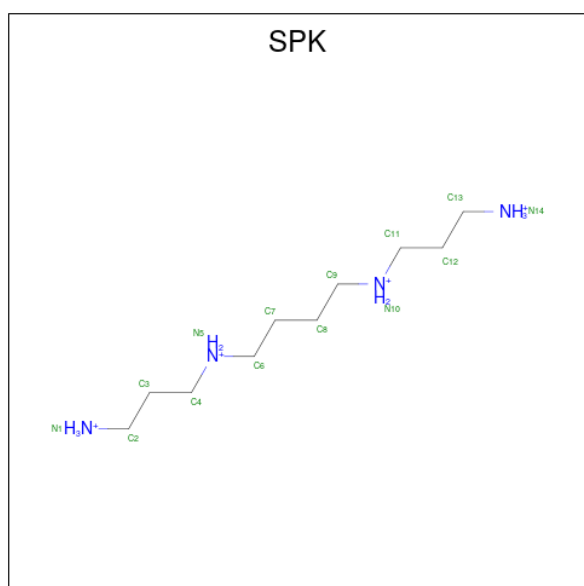
- Molecule 78 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	PT	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		
78	AT	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		

- Molecule 79 is a RNA chain called mRNA.

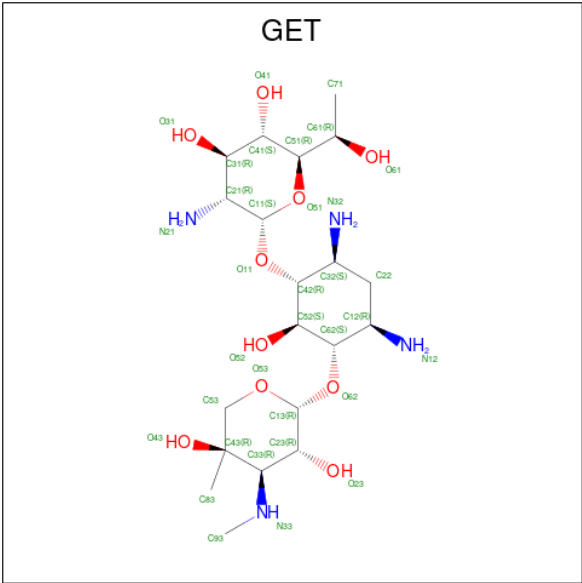
Mol	Chain	Residues	Atoms					AltConf	Trace
79	MR	11	Total	C	N	O	P	0	0
			229	103	36	79	11		

- Molecule 80 is SPERMINE (FULLY PROTONATED FORM) (CCD ID: SPK) (formula: $C_{10}H_{30}N_4$).



Mol	Chain	Residues	Atoms			AltConf
80	1	1	Total	C	N	0
			14	10	4	

- Molecule 81 is GENETICIN (CCD ID: GET) (formula: C₂₀H₄₀N₄O₁₀) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	

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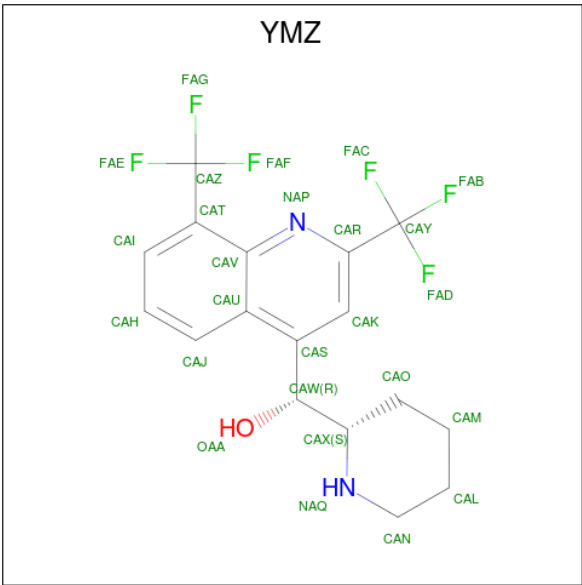
Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	1	1	Total	C	N	O	0
			34	20	4	10	
81	A	1	Total	C	N	O	0
			34	20	4	10	
81	A	1	Total	C	N	O	0
			34	20	4	10	
81	A	1	Total	C	N	O	0
			34	20	4	10	
81	AT	1	Total	C	N	O	0
			34	20	4	10	

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

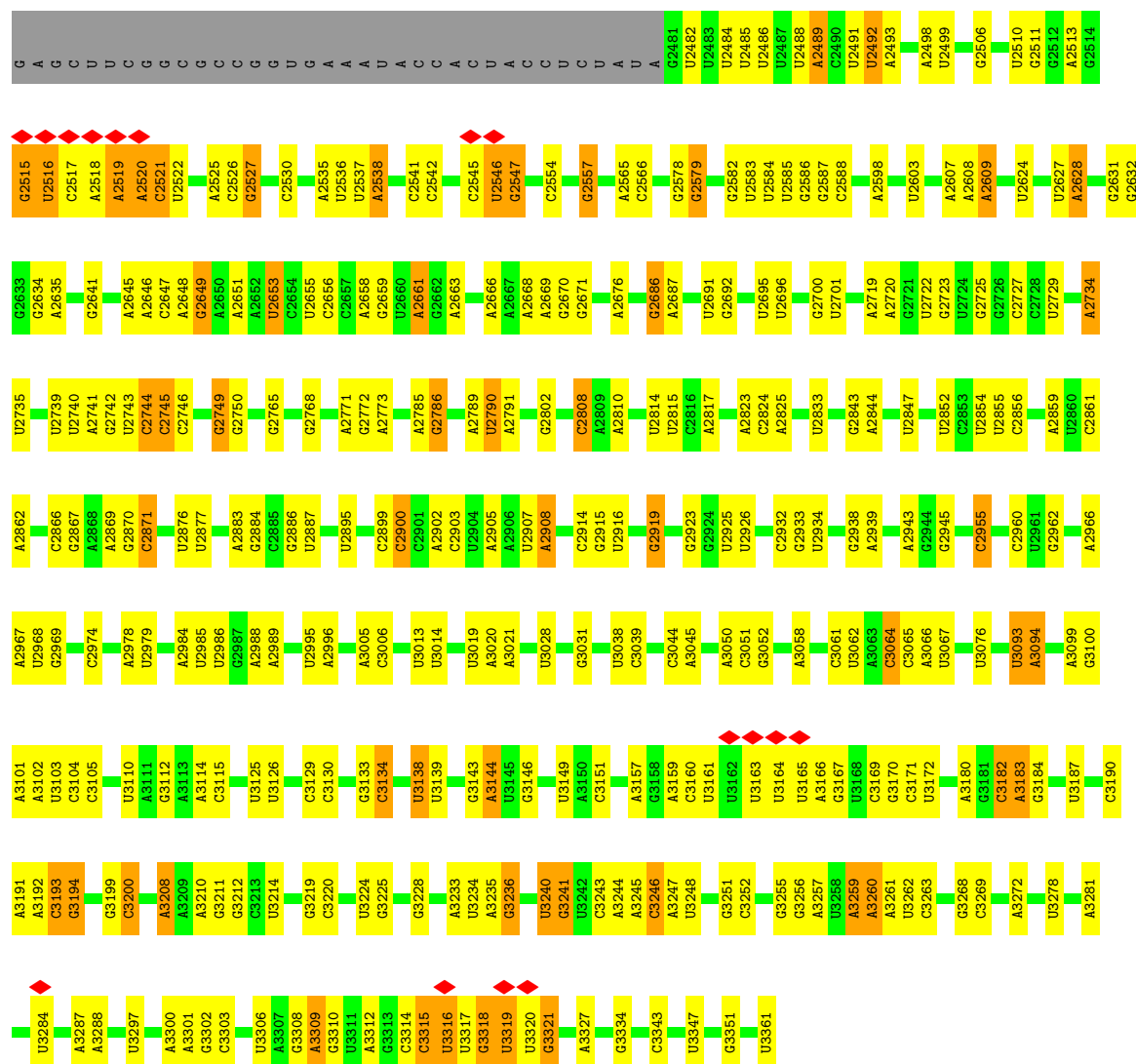
Mol	Chain	Residues	Atoms		AltConf
82	b	1	Total	Zn	0
			1	1	
82	e	1	Total	Zn	0
			1	1	
82	AH	1	Total	Zn	0
			1	1	
82	AK	1	Total	Zn	0
			1	1	
82	AN	1	Total	Zn	0
			1	1	
82	AP	1	Total	Zn	0
			1	1	
82	AQ	1	Total	Zn	0
			1	1	

- Molecule 83 is (11R,12S)- Mefloquine (CCD ID: YMZ) (formula: C₁₇H₁₆F₆N₂O) (labeled as "Ligand of Interest" by depositor).

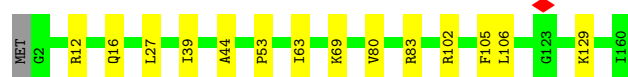
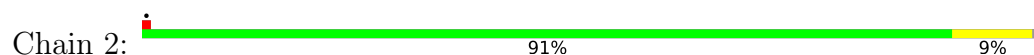


Mol	Chain	Residues	Atoms					AltConf
			Total	C	F	N	O	
83	AQ	1	26	17	6	2	1	0

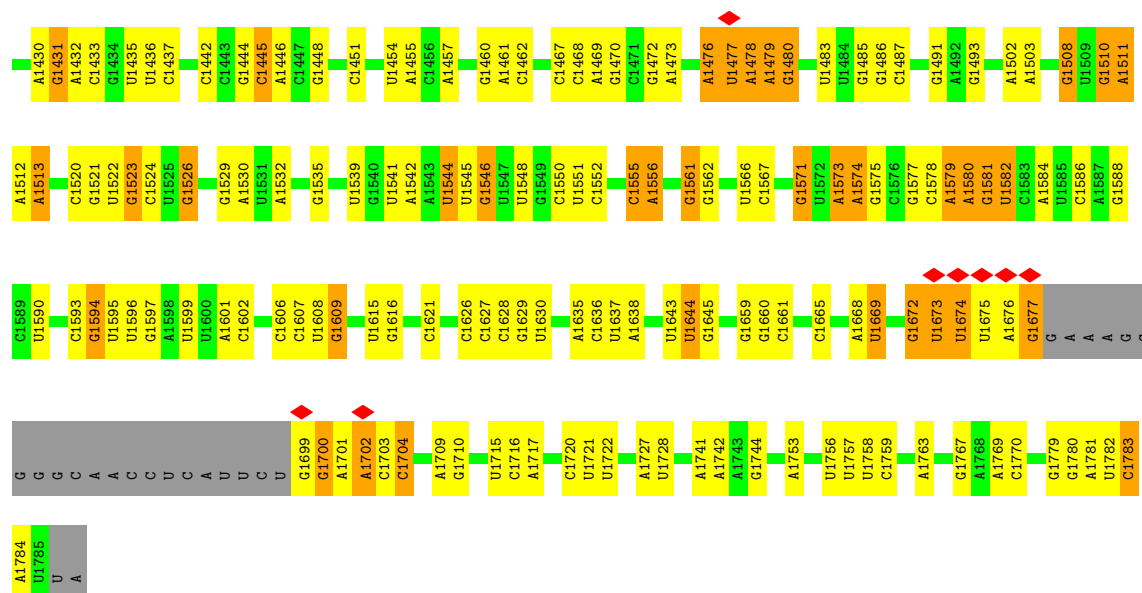




• Molecule 3: Ribosomal 60S subunit protein L21A

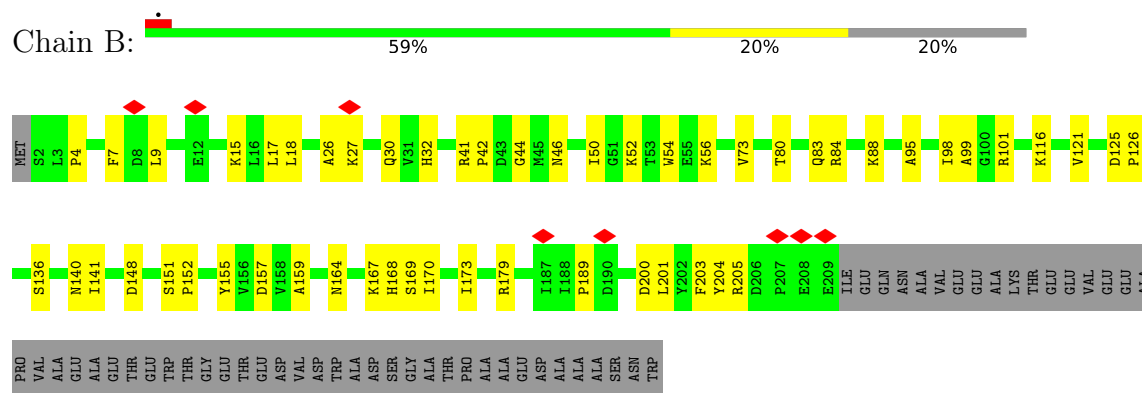






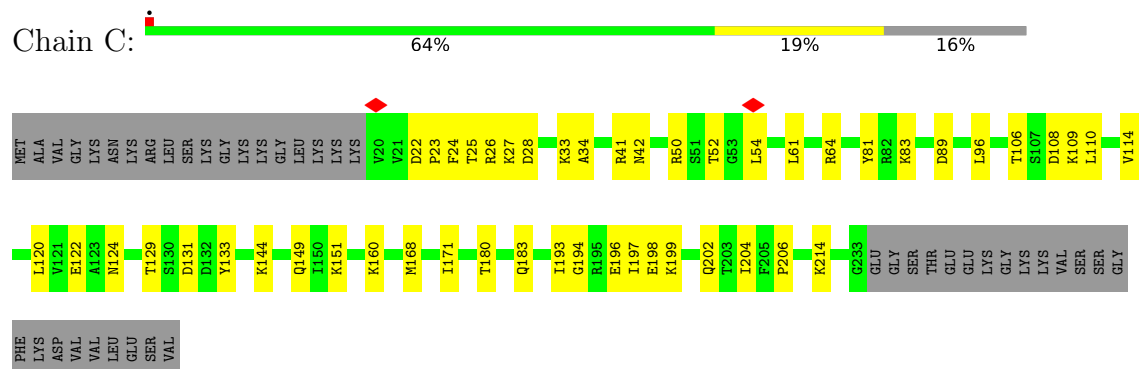
• Molecule 11: 40S ribosomal protein S0

Chain B:



• Molecule 12: 40S ribosomal protein S1

Chain C:



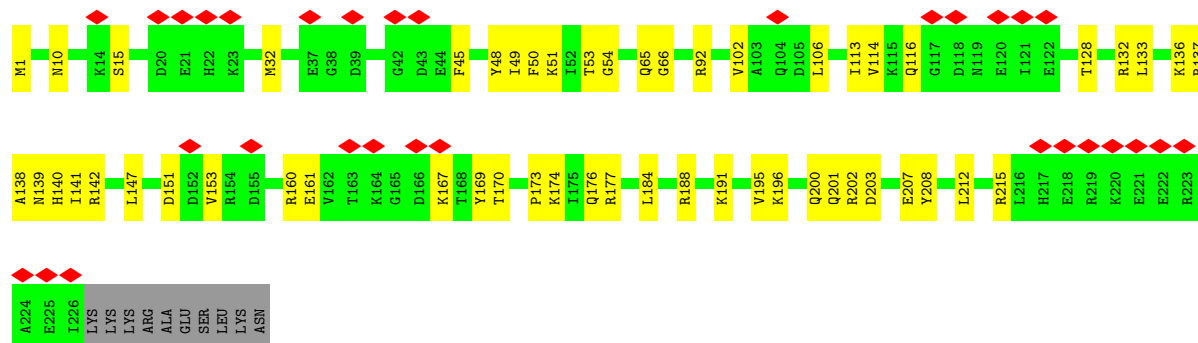
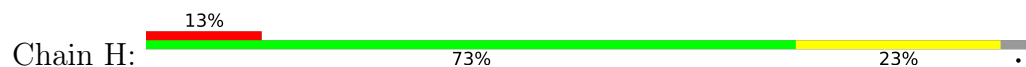
• Molecule 13: Ribosomal 40S subunit protein S2

Chain D:

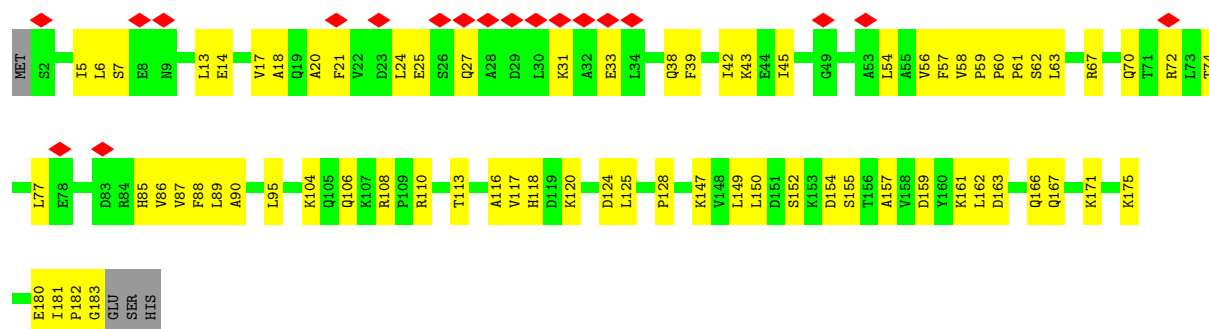




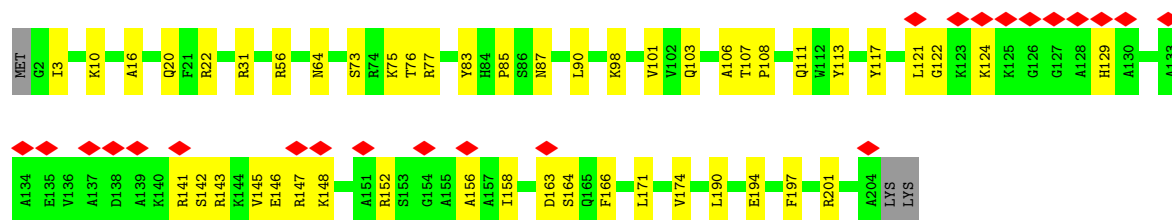
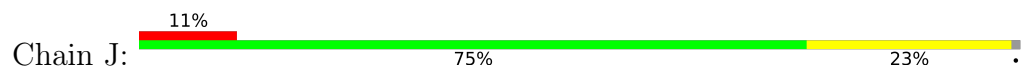
• Molecule 17: 40S ribosomal protein S6



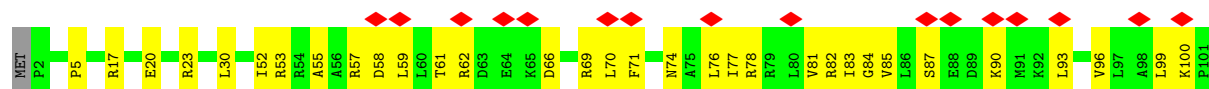
• Molecule 18: 40S ribosomal protein S7



• Molecule 19: 40S ribosomal protein S8

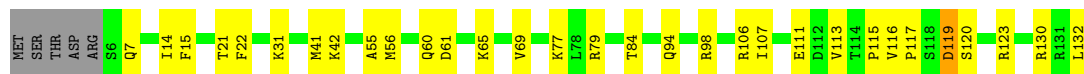


• Molecule 20: Ribosomal 40S subunit protein S9B



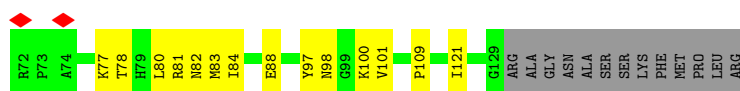
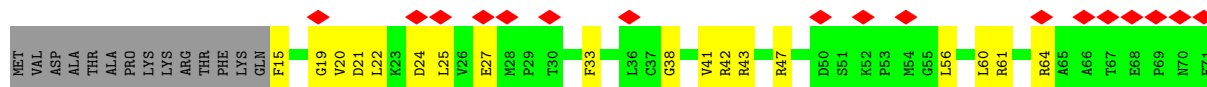
- Molecule 25: Ribosomal 40S subunit protein S14B

Chain P:  73% 23% . .



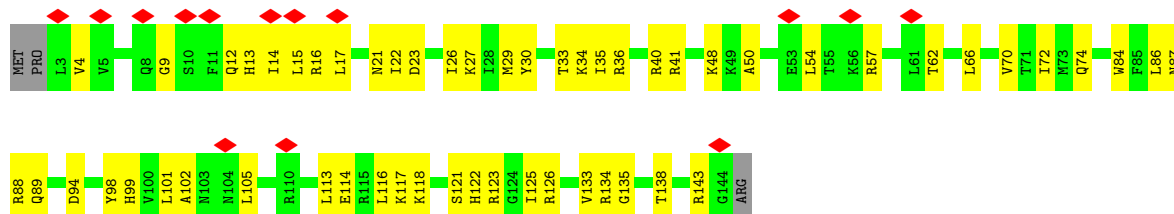
- Molecule 26: Ribosomal 40S subunit protein S15

Chain Q:  13% 58% 23% 19%



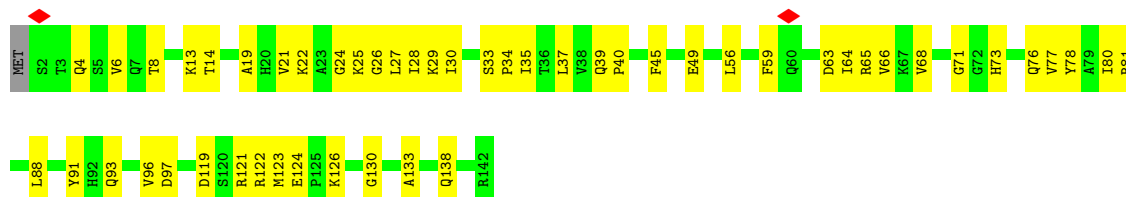
- Molecule 27: Ribosomal 40S subunit protein S18B

Chain T:  10% 59% 39%



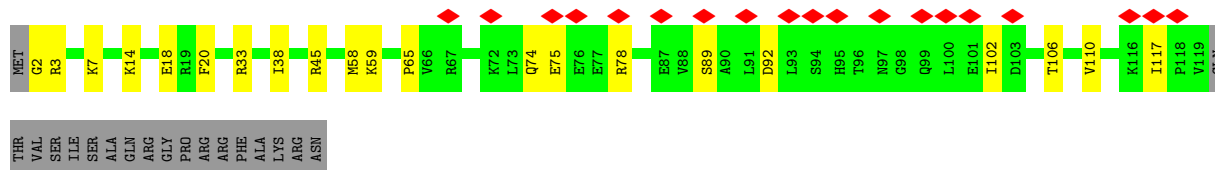
- Molecule 28: Ribosomal 40S subunit protein S16A

Chain R:  63% 36%

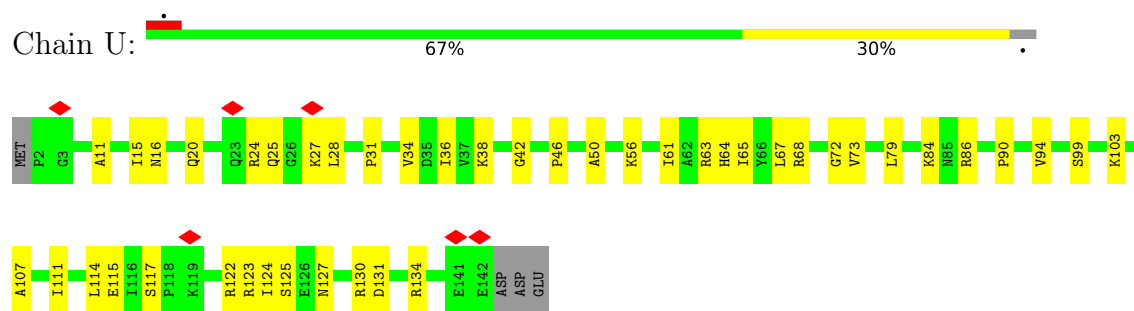


- Molecule 29: Ribosomal 40S subunit protein S17B

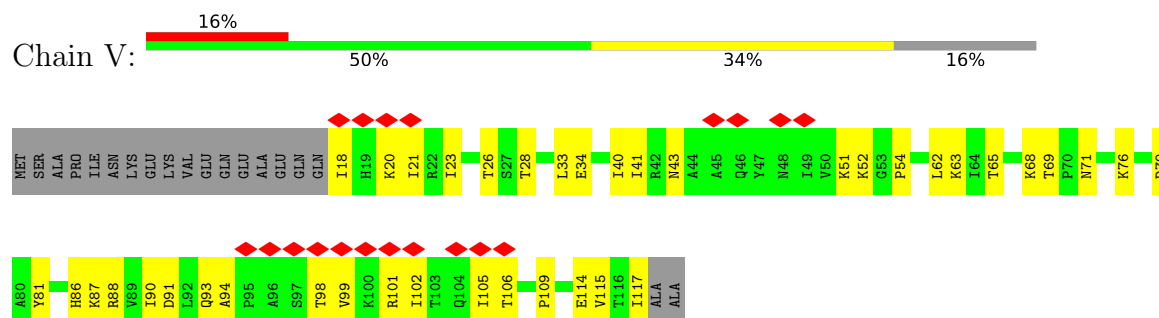
Chain S:  14% 71% 15% 14%



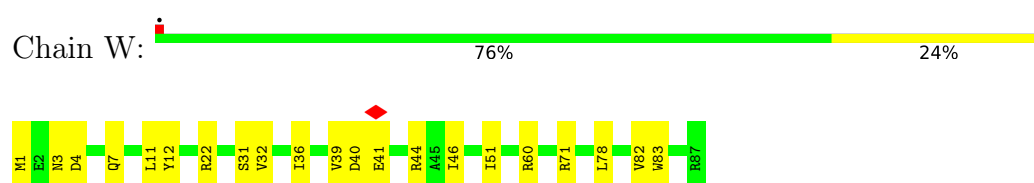
- Molecule 30: Ribosomal 40S subunit protein S19A



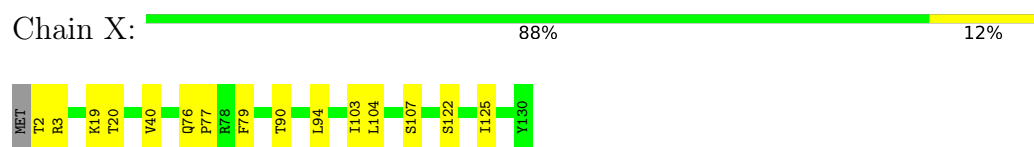
- Molecule 31: Ribosomal 40S subunit protein S20



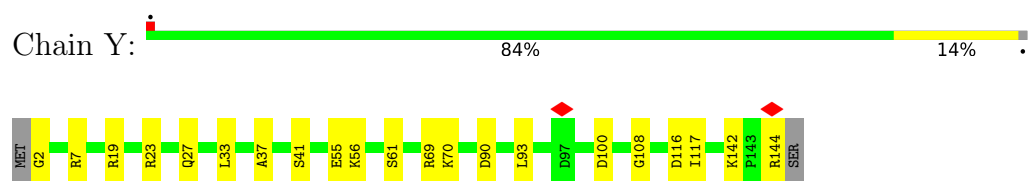
- Molecule 32: 40S ribosomal protein S21



- Molecule 33: 40S ribosomal protein S22-A

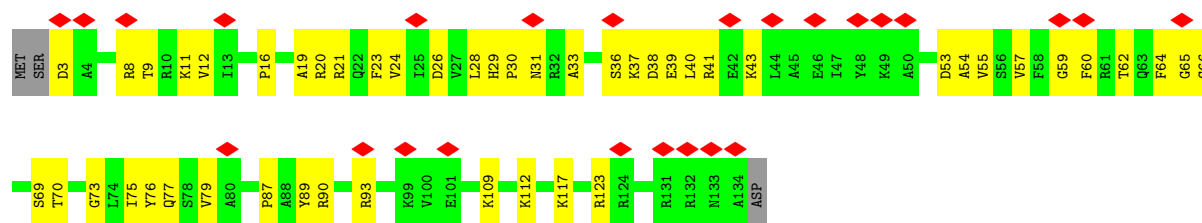


- Molecule 34: Ribosomal 40S subunit protein S23B

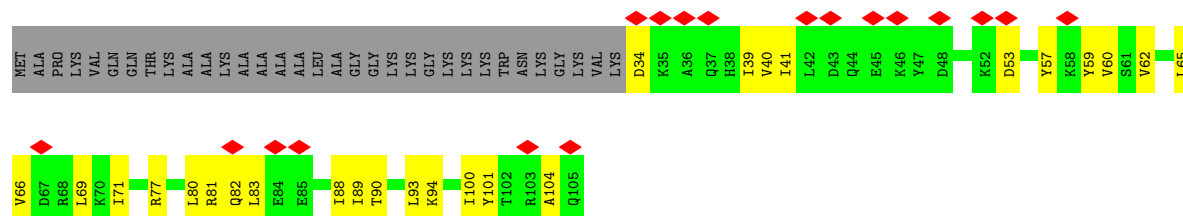
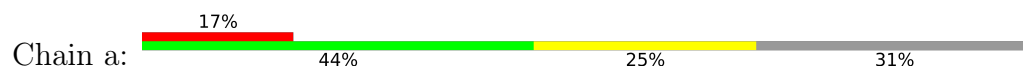


- Molecule 35: 40S ribosomal protein S24

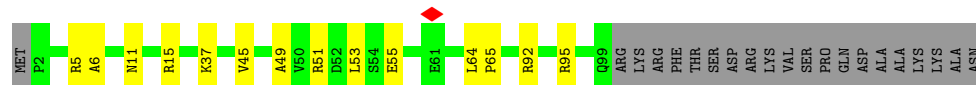




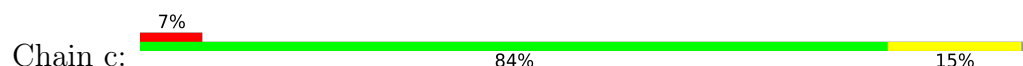
• Molecule 36: 40S ribosomal protein S25



• Molecule 37: 40S ribosomal protein S26



• Molecule 38: 40S ribosomal protein S27



• Molecule 39: Ribosomal 40S subunit protein S28B



• Molecule 40: Ribosomal 40S subunit protein S29A



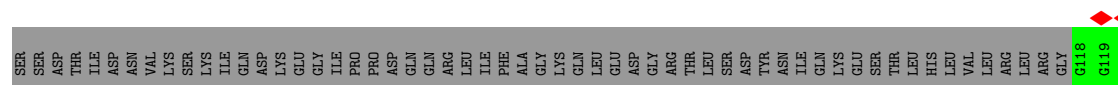
• Molecule 41: 40S ribosomal protein S30

Chain f: 



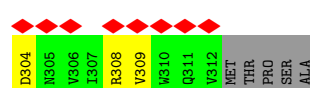
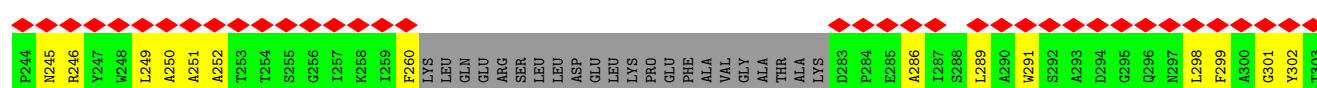
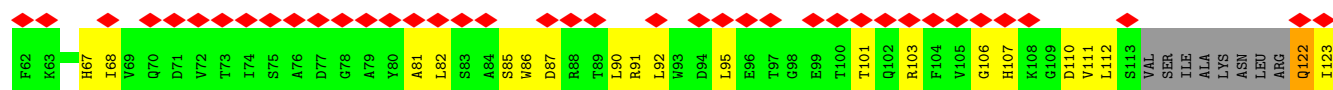
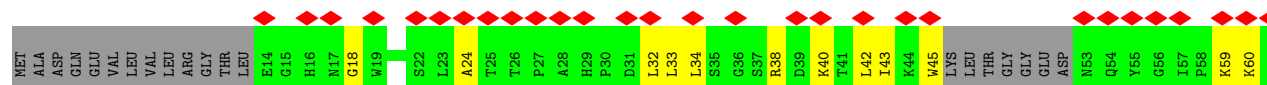
- Molecule 42: Ubiquitin-ribosomal 40S subunit protein S31 fusion protein

Chain g: 




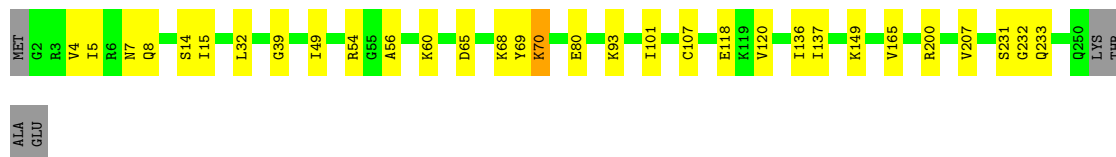
- Molecule 43: Guanine nucleotide-binding protein subunit beta-like protein

Chain h: 




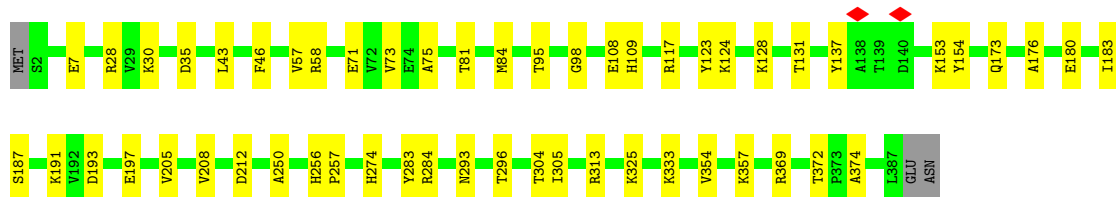
- Molecule 44: Ribosomal 60S subunit protein L2A

Chain j:  86% 12%




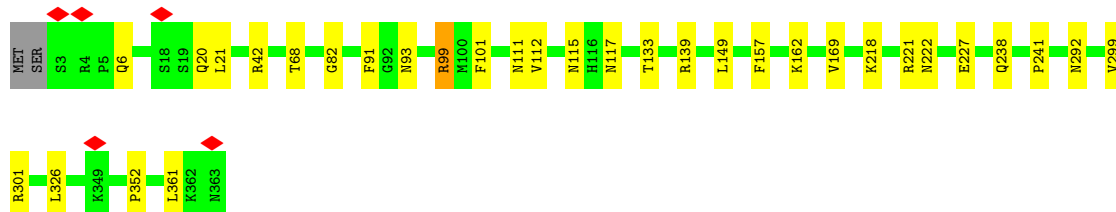
- Molecule 45: 60S ribosomal protein L3

Chain k:  85% 14%




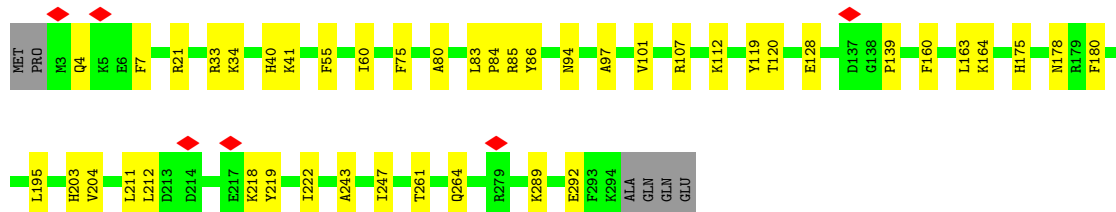
- Molecule 46: Ribosomal 60S subunit protein L4B

Chain l:  91% 9%



- Molecule 47: Ribosomal 60S subunit protein L5

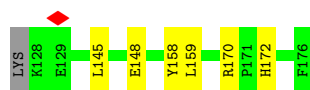
Chain m:  83% 15%



- Molecule 48: 60S ribosomal protein L6

Chain n:  72% 16% 12%





- Molecule 49: Ribosomal 60S subunit protein L7A

Chain o: 86% 10% 5%



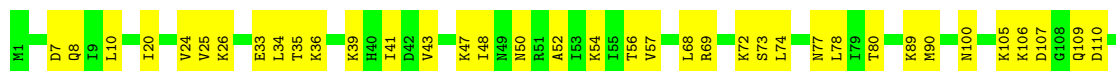
- Molecule 50: 60S ribosomal protein L8

Chain p: 77% 11% 12%



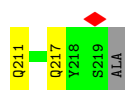
- Molecule 51: Ribosomal 60S subunit protein L9B

Chain q: 75% 24%



- Molecule 52: Ribosomal 60S subunit protein L10

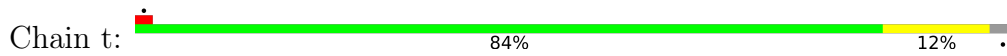
Chain r: 84% 15%



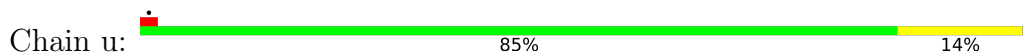
- Molecule 53: Ribosomal 60S subunit protein L11B

Chain s: 68% 31%

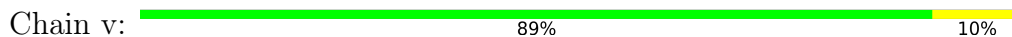
- Molecule 54: 60S ribosomal protein L13



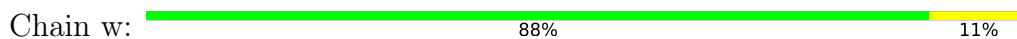
- Molecule 55: Ribosomal 60S subunit protein L14B



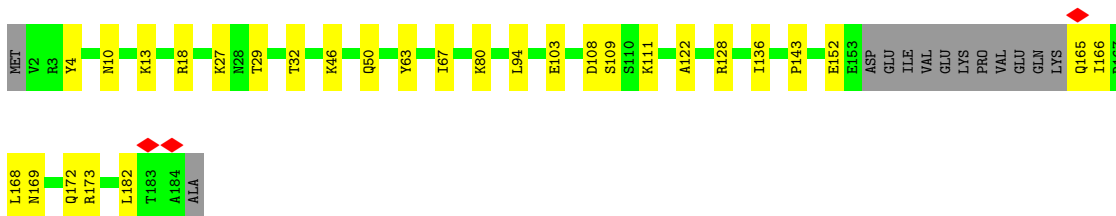
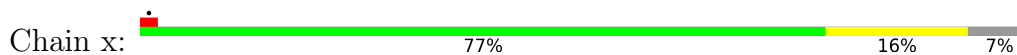
- Molecule 56: Ribosomal protein L15




- Molecule 57: Ribosomal 60S subunit protein L16A



- Molecule 58: Ribosomal 60S subunit protein L17B




- Molecule 59: Ribosomal 60S subunit protein L18A

Chain y:  84% 15% ..




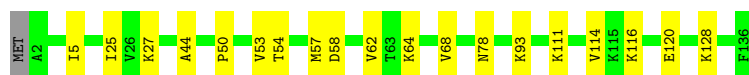
- Molecule 60: Ribosomal protein L19

Chain z:  83% 12% 5%




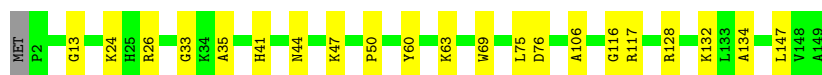
- Molecule 61: 60S ribosomal protein L27

Chain AA:  85% 14% .




- Molecule 62: Ribosomal 60S subunit protein L28

Chain AB:  85% 14% .




- Molecule 63: 60S ribosomal protein L29

Chain AC:  87% 8% 5%




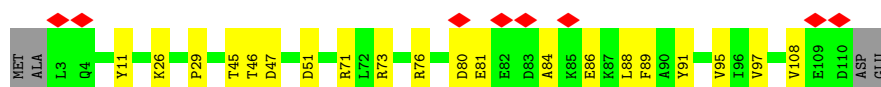
- Molecule 64: Ribosomal 60S subunit protein L30

Chain AD:  75% 15% 9%




- Molecule 65: Ribosomal 60S subunit protein L31B

Chain AE:  7% 79% 18% .




- Molecule 66: Ribosomal 60S subunit protein L32

Chain AF:  85% 10% 5%



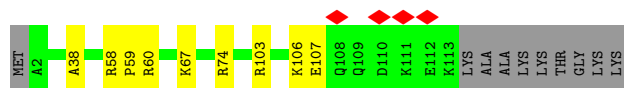
- Molecule 67: Ribosomal 60S subunit protein L33A

Chain AG:  89% 10% .




- Molecule 68: Ribosomal 60S subunit protein L34B

Chain AH:  84% 7% 8%




- Molecule 69: Ribosomal 60S subunit protein L35A

Chain AI:  83% 16% .




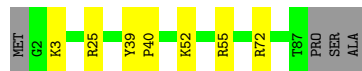
- Molecule 70: 60S ribosomal protein L36

Chain AJ:  75% 23% .




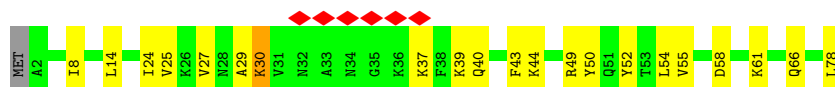
- Molecule 71: Ribosomal protein L37

Chain AK:  88% 8% .



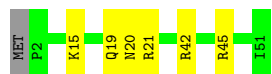
- Molecule 72: Ribosomal 60S subunit protein L38

Chain AL:  8% 72% 26% ..



- Molecule 73: 60S ribosomal protein L39

Chain AM:  86% 12% .




- Molecule 74: Rpl40bp

Chain AN:  90% 10% .




- Molecule 75: Small ribosomal subunit protein eS32

Chain AO:  72% 28% .

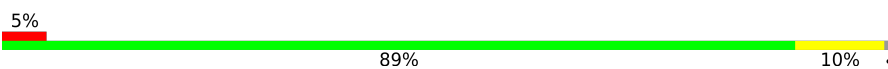


- Molecule 76: Ribosomal 60S subunit protein L42A

Chain AP:  83% 16% .



- Molecule 77: Ribosomal 60S subunit protein L43A

Chain AQ:  5% 89% 10% .



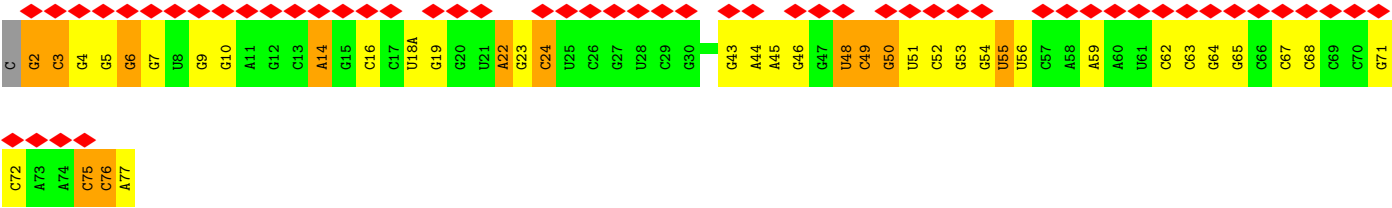
- Molecule 78: tRNA-fMet

Chain PT:  64% 32% . .



- Molecule 78: tRNA-fMet

Chain AT:  47% 71% 36% 16% .



● Molecule 79: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63238	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 ($e^-/\text{\AA}^2$)	29.7	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.999	Depositor
Minimum map value	-0.786	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.057	Depositor
Recommended contour level	0.174	Depositor
Map size (Å)	510.3, 510.3, 510.3	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.729, 0.729, 0.729	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GET, SPK, MLZ, OMG, IAS, OMC, YMZ, 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	0	0.29	0/1483	0.46	0/1997
2	1	0.40	0/73296	0.41	0/114257
3	2	0.30	0/1305	0.40	0/1749
4	3	0.33	0/2884	0.33	0/4492
5	4	0.40	0/3702	0.40	0/5764
6	6	0.30	0/994	0.48	2/1339 (0.1%)
7	7	0.31	0/528	0.45	0/701
8	8	0.31	0/990	0.44	0/1337
9	9	0.31	0/990	0.46	0/1322
10	A	0.32	0/40362	0.40	0/62888
11	B	0.26	0/1666	0.46	0/2273
12	C	0.27	0/1750	0.42	0/2354
13	D	0.28	0/1648	0.43	0/2237
14	E	0.24	0/1725	0.45	0/2316
15	F	0.24	0/2096	0.43	0/2822
16	G	0.24	0/1588	0.46	0/2139
17	H	0.22	0/1845	0.41	0/2464
18	I	0.25	0/1490	0.44	0/2004
19	J	0.26	0/1606	0.45	0/2150
20	K	0.23	0/1478	0.44	0/1978
21	L	0.21	0/801	0.52	0/1081
22	M	0.28	0/1154	0.44	0/1553
23	N	0.19	0/541	0.49	0/726
24	O	0.27	0/1210	0.43	0/1631
25	P	0.29	0/944	0.43	0/1265
26	Q	0.23	0/924	0.46	0/1243
27	T	0.24	0/1186	0.47	0/1590
28	R	0.25	0/1120	0.52	0/1500
29	S	0.24	0/966	0.46	0/1295
30	U	0.24	0/1120	0.46	0/1508
31	V	0.24	0/800	0.45	0/1082
32	W	0.28	0/683	0.49	0/918

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	X	0.32	0/1049	0.44	0/1412
34	Y	0.25	0/1128	0.43	0/1505
35	Z	0.22	0/1086	0.46	0/1447
36	a	0.23	0/585	0.52	0/789
37	b	0.29	0/791	0.42	0/1060
38	c	0.25	0/624	0.40	0/843
39	d	0.25	0/489	0.45	0/654
40	e	0.23	0/466	0.44	0/620
41	f	0.24	0/469	0.52	0/626
42	g	0.23	0/575	0.58	0/760
43	h	0.19	0/1898	0.46	0/2584
44	j	0.35	0/1931	0.50	0/2592
45	k	0.33	0/3156	0.45	0/4246
46	l	0.30	0/2799	0.46	0/3777
47	m	0.26	0/2447	0.44	0/3294
48	n	0.28	0/1258	0.41	0/1696
49	o	0.30	0/1896	0.48	0/2544
50	p	0.30	0/1825	0.46	0/2458
51	q	0.27	0/1528	0.41	0/2055
52	r	0.26	0/1795	0.40	0/2411
53	s	0.25	0/1404	0.46	0/1880
54	t	0.31	0/1600	0.49	0/2147
55	u	0.30	0/1044	0.47	0/1407
56	v	0.34	0/1753	0.47	0/2347
57	w	0.31	0/1620	0.44	0/2167
58	x	0.32	0/1398	0.45	0/1879
59	y	0.30	0/1511	0.49	0/2022
60	z	0.29	0/1492	0.45	0/1983
61	AA	0.27	0/1112	0.38	0/1488
62	AB	0.32	0/1199	0.48	0/1607
63	AC	0.27	0/502	0.38	0/666
64	AD	0.27	0/738	0.36	0/994
65	AE	0.29	0/894	0.45	0/1201
66	AF	0.32	0/1039	0.46	0/1390
67	AG	0.32	0/895	0.40	0/1201
68	AH	0.30	0/934	0.48	0/1242
69	AI	0.30	0/1004	0.51	0/1337
70	AJ	0.27	0/772	0.42	0/1023
71	AK	0.36	0/690	0.51	0/916
72	AL	0.29	0/632	0.43	0/842
73	AM	0.32	0/458	0.43	0/609
74	AN	0.25	0/436	0.40	0/577
75	AO	0.27	0/237	0.65	0/304

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AP	0.29	0/861	0.40	0/1136
77	AQ	0.30	0/705	0.44	0/940
78	AT	0.17	0/1813	0.35	0/2825
78	PT	0.24	0/1813	0.32	0/2825
79	MR	0.23	0/254	0.29	0/392
All	All	0.33	0/211480	0.42	2/310695 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
25	P	0	1
28	R	0	1
46	l	0	1
48	n	0	1
All	All	0	4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	6	103	VAL	CA-C-N	5.17	135.64	120.97
6	6	103	VAL	C-N-CA	5.17	135.64	120.97

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
25	P	119	IAS	Peptide
28	R	39	GLN	Peptide
46	l	99	ARG	Sidechain
48	n	25	ARG	Sidechain

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	0	1442	0	1500	17	0
2	1	65536	0	32944	560	0
3	2	1276	0	1333	13	0
4	3	2579	0	1304	15	0
5	4	3313	0	1674	23	0
6	6	986	0	1040	10	0
7	7	516	0	534	13	0
8	8	974	0	1032	9	0
9	9	980	0	1058	12	0
10	A	36083	0	18151	561	0
11	B	1627	0	1644	44	0
12	C	1724	0	1805	36	0
13	D	1620	0	1715	33	0
14	E	1701	0	1802	61	0
15	F	2055	0	2137	70	0
16	G	1572	0	1644	48	0
17	H	1820	0	1896	46	0
18	I	1466	0	1561	49	0
19	J	1579	0	1602	39	0
20	K	1453	0	1532	61	0
21	L	783	0	799	41	0
22	M	1129	0	1183	17	0
23	N	539	0	573	21	0
24	O	1187	0	1249	22	0
25	P	942	0	980	21	0
26	Q	906	0	940	23	0
27	T	1169	0	1216	48	0
28	R	1102	0	1168	36	0
29	S	954	0	1008	21	0
30	U	1100	0	1114	35	0
31	V	790	0	855	33	0
32	W	676	0	677	21	0
33	X	1032	0	1066	13	0
34	Y	1110	0	1182	16	0
35	Z	1072	0	1123	38	0
36	a	578	0	613	21	0
37	b	779	0	832	15	0
38	c	614	0	630	8	0
39	d	487	0	523	20	0
40	e	454	0	430	12	0
41	f	461	0	499	15	0
42	g	565	0	605	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	h	1854	0	1793	71	0
44	j	1894	0	1975	23	0
45	k	3084	0	3173	42	0
46	l	2751	0	2879	31	0
47	m	2394	0	2362	31	0
48	n	1237	0	1316	22	0
49	o	1860	0	1958	15	0
50	p	1795	0	1915	21	0
51	q	1510	0	1582	27	0
52	r	1759	0	1802	20	0
53	s	1385	0	1418	39	0
54	t	1573	0	1644	23	0
55	u	1029	0	1116	16	0
56	v	1713	0	1764	19	0
57	w	1590	0	1705	17	0
58	x	1375	0	1403	17	0
59	y	1478	0	1590	23	0
60	z	1471	0	1583	15	0
61	AA	1087	0	1154	14	0
62	AB	1170	0	1203	21	0
63	AC	489	0	522	4	0
64	AD	729	0	775	9	0
65	AE	881	0	932	13	0
66	AF	1015	0	1095	13	0
67	AG	867	0	932	8	0
68	AH	913	0	998	7	0
69	AI	990	0	1094	14	0
70	AJ	764	0	851	16	0
71	AK	677	0	697	5	0
72	AL	623	0	688	15	0
73	AM	446	0	488	4	0
74	AN	427	0	473	4	0
75	AO	236	0	285	6	0
76	AP	863	0	931	13	0
77	AQ	698	0	734	9	0
78	AT	1623	0	825	26	0
78	PT	1623	0	825	11	0
79	MR	229	0	117	0	0
80	1	14	0	30	3	0
81	1	408	0	480	20	0
81	A	102	0	120	5	0
81	AT	34	0	40	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
82	AH	1	0	0	0	0
82	AK	1	0	0	0	0
82	AN	1	0	0	0	0
82	AP	1	0	0	0	0
82	AQ	1	0	0	0	0
82	b	1	0	0	0	0
82	e	1	0	0	0	0
83	AQ	26	0	0	1	0
All	All	197424	0	146440	2458	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 7.

All (2458) 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)
78:AT:51:U:H3	78:AT:65:G:H1	1.05	1.01
2:1:437:G:H22	2:1:620:A:H61	1.13	0.96
46:l:139:ARG:HH21	46:l:241:PRO:HG2	1.33	0.94
10:A:1575:G:H1	10:A:1595:U:H3	0.94	0.91
10:A:1040:U:H3	10:A:1049:G:H1	1.16	0.91
2:1:1560:U:H3	2:1:1571:G:H1	0.97	0.91
2:1:2380:A:H2'	46:l:68:THR:HG21	1.53	0.88
46:l:111:ASN:HD22	56:v:201:ARG:HB3	1.39	0.87
27:T:17:LEU:HB2	27:T:22:ILE:HB	1.58	0.86
19:J:107:THR:HG22	19:J:111:GLN:HE22	1.41	0.86
2:1:1014:G:H1	2:1:1030:U:H3	1.24	0.84
10:A:1529:G:N2	10:A:1556:A:OP2	2.10	0.84
10:A:188:U:O2	10:A:193:G:O6	1.96	0.83
27:T:41:ARG:NH2	30:U:36:ILE:O	2.11	0.83
14:E:47:LEU:HB3	14:E:85:ILE:HG22	1.57	0.83
2:1:71:C:O2'	54:t:66:ASN:ND2	2.11	0.83
2:1:280:U:OP2	80:1:3401:SPK:N5	2.13	0.82
2:1:1635:C:OP2	68:AH:74:ARG:NH1	2.10	0.82
2:1:2488:U:HO2'	2:1:2489:A:H8	1.26	0.82
2:1:1682:U:O2	2:1:1684:U:O2'	1.96	0.81
2:1:2334:A:H61	2:1:2955:C:H5	1.28	0.81
10:A:57:G:OP1	35:Z:112:LYS:NZ	2.14	0.80
45:k:313:ARG:O	45:k:333:LYS:NZ	2.15	0.80
61:AA:54:THR:H	61:AA:57:MET:HE2	1.46	0.80
2:1:3013:U:OP1	6:6:12:ARG:NH1	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:h:122:GLN:N	43:h:122:GLN:HE21	1.77	0.80
25:P:56:MET:SD	25:P:60:GLN:NE2	2.55	0.80
14:E:41:ARG:HH12	14:E:50:ILE:HD12	1.47	0.80
31:V:34:GLU:OE2	31:V:88:ARG:NH1	2.12	0.80
14:E:9:LYS:HG2	31:V:62:LEU:HD11	1.63	0.80
47:m:261:THR:OG1	47:m:264:GLN:OE1	1.99	0.79
65:AE:80:ASP:OD1	65:AE:81:GLU:N	2.15	0.79
2:1:2086:C:H1'	2:1:3309:A:H8	1.45	0.79
15:F:105:VAL:HG23	15:F:191:ARG:HG2	1.64	0.79
42:g:182:TYR:HE1	42:g:187:HIS:HA	1.47	0.79
10:A:1369:G:O2'	10:A:1370:A:O5'	2.01	0.79
2:1:538:G:H1	2:1:547:U:H3	1.25	0.79
27:T:70:VAL:O	27:T:74:GLN:NE2	2.15	0.79
15:F:35:PRO:HD2	15:F:83:PRO:HG2	1.64	0.78
2:1:1808:G:N7	61:AA:64:LYS:NZ	2.32	0.78
10:A:509:A:N6	10:A:537:G:O6	2.17	0.78
24:O:99:ARG:NH2	24:O:119:GLU:OE2	2.15	0.78
27:T:16:ARG:NH1	27:T:17:LEU:O	2.16	0.78
2:1:437:G:N2	2:1:620:A:H61	1.82	0.78
17:H:142:ARG:HE	17:H:153:VAL:HG21	1.48	0.77
43:h:176:LYS:HA	43:h:188:ASP:HA	1.66	0.77
43:h:175:VAL:HB	43:h:189:PHE:HB2	1.66	0.77
2:1:3308:G:H21	2:1:3327:A:H2	1.29	0.77
56:v:33:LYS:O	56:v:65:ARG:NH2	2.18	0.77
10:A:512:G:H1	10:A:541:C:H5	1.31	0.77
10:A:750:G:H21	10:A:753:C:H4'	1.48	0.77
21:L:18:GLU:H	21:L:89:LEU:HB3	1.50	0.77
11:B:189:PRO:O	32:W:44:ARG:NH2	2.17	0.77
17:H:161:GLU:HB2	17:H:170:THR:HG22	1.67	0.77
49:o:218:GLN:NE2	49:o:222:GLN:OE1	2.18	0.76
10:A:1630:U:OP1	81:A:1802:GET:N21	2.19	0.76
51:q:110:ASP:O	51:q:127:LYS:NZ	2.19	0.76
53:s:59:ILE:HD11	53:s:65:ILE:HD13	1.66	0.76
11:B:52:LYS:HD3	32:W:82:VAL:HG23	1.66	0.76
19:J:76:THR:HG22	19:J:108:PRO:HG2	1.66	0.76
54:t:63:VAL:HA	54:t:66:ASN:OD1	1.85	0.76
75:AO:1:MET:HE3	75:AO:6:ARG:HG2	1.68	0.76
10:A:853:G:H1	10:A:945:U:H3	1.33	0.75
15:F:19:MET:SD	15:F:108:LYS:NZ	2.56	0.75
15:F:198:ARG:HG3	15:F:208:VAL:HG22	1.67	0.75
43:h:299:PHE:HB3	43:h:309:VAL:HG12	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:J:85:PRO:O	22:M:11:ARG:NH1	2.18	0.75
35:Z:38:ASP:HA	35:Z:41:ARG:HG3	1.69	0.75
10:A:4:C:H5	10:A:20:G:H1	1.32	0.75
10:A:586:U:O2	41:f:57:ASN:ND2	2.19	0.75
30:U:27:LYS:HD2	30:U:111:ILE:HG23	1.68	0.75
10:A:1278:U:H3	10:A:1307:A:H62	1.34	0.75
10:A:869:A:O2'	12:C:124:ASN:ND2	2.20	0.75
70:AJ:56:LEU:HD22	70:AJ:89:MET:HG3	1.68	0.75
10:A:510:A:O2'	20:K:133:HIS:NE2	2.18	0.74
42:g:180:ARG:HH21	42:g:191:LYS:HG3	1.52	0.74
68:AH:58:ARG:HD3	68:AH:59:PRO:HD2	1.69	0.74
13:D:111:LYS:HD3	13:D:122:ALA:HB1	1.69	0.74
69:AI:38:ARG:NH1	69:AI:40:SER:O	2.21	0.74
23:N:97:LEU:HD23	23:N:100:TRP:HE1	1.52	0.74
10:A:189:G:N7	19:J:143:ARG:NH2	2.35	0.73
26:Q:100:LYS:HG3	26:Q:101:VAL:HG13	1.71	0.73
10:A:763:C:OP2	10:A:764:U:N3	2.20	0.73
2:1:538:G:N2	2:1:547:U:O2	2.19	0.73
2:1:2086:C:H1'	2:1:3309:A:C8	2.23	0.73
10:A:880:G:H1	10:A:902:U:H3	1.33	0.73
18:I:155:SER:HB2	18:I:181:ILE:HD13	1.71	0.73
2:1:1345:G:N2	46:l:292:ASN:O	2.22	0.73
13:D:134:ILE:HD12	13:D:213:ILE:HG13	1.71	0.73
27:T:14:ILE:HG22	27:T:16:ARG:H	1.54	0.73
42:g:147:TYR:O	42:g:159:LEU:N	2.21	0.73
10:A:1156:A:H2'	10:A:1157:G:C8	2.25	0.72
2:1:3139:U:OP2	67:AG:63:LYS:NZ	2.22	0.72
28:R:28:ILE:HD12	28:R:35:ILE:HD12	1.71	0.72
31:V:33:LEU:HD21	31:V:88:ARG:HD3	1.71	0.72
2:1:2790:U:H5''	63:AC:1:MET:HA	1.72	0.72
11:B:155:TYR:HA	32:W:60:ARG:HG2	1.72	0.72
78:AT:6:G:H2'	78:AT:7:G:C8	2.25	0.72
2:1:3245:A:O2'	2:1:3246:C:O4'	2.08	0.71
2:1:3278:U:H4'	45:k:173:GLN:HG3	1.70	0.71
35:Z:41:ARG:NH1	35:Z:55:VAL:O	2.22	0.71
10:A:1276:G:H1	10:A:1309:G:H22	1.38	0.71
50:p:83:LEU:HD12	50:p:181:VAL:HG12	1.72	0.71
2:1:3166:A:H2'	2:1:3167:G:H8	1.54	0.71
10:A:1551:U:OP1	30:U:38:LYS:NZ	2.24	0.71
10:A:445:U:OP1	15:F:49:ARG:NH1	2.23	0.71
10:A:1306:A:OP2	11:B:101:ARG:NH2	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:59:LEU:HA	20:K:62:ARG:HD2	1.73	0.71
43:h:153:SER:H	43:h:170:SER:HA	1.55	0.71
10:A:813:U:O2'	10:A:814:A:O4'	2.07	0.71
53:s:108:GLU:HG3	53:s:111:ASP:HB2	1.73	0.71
10:A:1511:A:H2'	10:A:1512:A:C8	2.26	0.71
16:G:157:ARG:HG3	16:G:224:ASN:HD21	1.55	0.71
78:PT:22:A:H61	78:PT:47:G:H2'	1.53	0.70
2:1:2653:U:H5'	53:s:65:ILE:HD11	1.73	0.70
10:A:1460:G:H2'	10:A:1461:A:C8	2.26	0.70
43:h:124:VAL:HG12	43:h:134:VAL:HG22	1.73	0.70
53:s:18:VAL:HG22	53:s:70:THR:HG22	1.72	0.70
10:A:854:A:H61	10:A:943:U:H5	1.36	0.70
10:A:1219:A:OP2	10:A:1230:G:O2'	2.08	0.70
2:1:963:A:OP1	62:AB:47:LYS:NZ	2.24	0.70
5:4:66:A:OP1	69:AI:10:ARG:NH2	2.24	0.70
10:A:123:G:OP1	15:F:77:ARG:NH2	2.21	0.70
30:U:28:LEU:HA	30:U:111:ILE:HD11	1.74	0.70
1:0:168:PRO:HG3	57:w:125:LEU:HD13	1.74	0.70
2:1:2651:A:O2'	53:s:52:TYR:OH	2.08	0.70
51:q:57:VAL:HG23	51:q:68:LEU:HD13	1.72	0.70
17:H:137:ARG:HD2	17:H:177:ARG:HD2	1.74	0.70
2:1:3318:G:H5''	2:1:3319:U:H4'	1.74	0.70
10:A:217:A:N1	10:A:828:U:O2'	2.23	0.70
2:1:1029:U:O2'	2:1:1030:U:O5'	2.09	0.70
50:p:28:PHE:HE1	61:AA:53:VAL:HG12	1.57	0.69
10:A:478:G:H1	10:A:506:U:H3	1.40	0.69
10:A:583:A:OP1	41:f:15:LYS:NZ	2.26	0.69
6:6:10:LYS:NZ	6:6:54:ALA:O	2.25	0.69
16:G:21:GLN:HG3	16:G:37:GLN:HE21	1.58	0.69
2:1:405:U:O4	81:1:3403:GET:O61	2.07	0.69
10:A:405:A:H2'	10:A:406:C:C6	2.27	0.69
20:K:66:ASP:HB3	20:K:69:ARG:HB3	1.74	0.69
41:f:50:THR:OG1	41:f:53:LYS:O	2.10	0.69
61:AA:53:VAL:HG11	61:AA:62:VAL:HG13	1.73	0.69
16:G:157:ARG:HG3	16:G:224:ASN:ND2	2.08	0.69
10:A:512:G:HO2'	10:A:513:A:H8	1.39	0.69
10:A:1275:U:H2'	10:A:1276:G:C8	2.28	0.69
10:A:1324:C:O2'	10:A:1326:A:N7	2.25	0.69
2:1:2421:A:O2'	2:1:2422:C:O5'	2.10	0.69
10:A:568:A:N6	34:Y:116:ASP:OD1	2.26	0.69
2:1:547:U:H2'	2:1:548:G:C8	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1949:G:H1	2:1:2070:A:H2'	1.58	0.69
2:1:3166:A:H2'	2:1:3167:G:C8	2.26	0.69
10:A:677:G:H2'	10:A:678:A:H8	1.57	0.69
2:1:545:G:N2	2:1:546:C:O2'	2.26	0.68
10:A:520:U:H5''	35:Z:37:LYS:HG3	1.75	0.68
78:AT:14:A:N1	78:AT:22:A:O2'	2.25	0.68
47:m:85:ARG:NH2	47:m:86:TYR:OH	2.26	0.68
2:1:972:U:OP1	59:y:144:ARG:NH2	2.25	0.68
10:A:1024:A:O2'	10:A:1025:G:O5'	2.12	0.68
19:J:20:GLN:NE2	19:J:22:ARG:O	2.27	0.68
43:h:112:LEU:HD21	43:h:128:ARG:HE	1.59	0.68
2:1:1814:U:O2'	2:1:1815:U:O5'	2.12	0.68
10:A:760:G:N2	10:A:770:C:N3	2.42	0.68
10:A:1399:U:OP2	29:S:3:ARG:NH2	2.26	0.68
26:Q:21:ASP:OD1	26:Q:22:LEU:N	2.26	0.68
10:A:137:A:H4'	10:A:138:C:H5'	1.74	0.68
18:I:152:SER:HB3	18:I:183:GLY:HA2	1.76	0.68
43:h:243:SER:OG	43:h:246:ARG:O	2.10	0.68
32:W:22:ARG:NH2	33:X:19:LYS:O	2.27	0.68
53:s:4:LYS:HG3	53:s:6:GLN:H	1.59	0.68
76:AP:7:THR:HB	76:AP:22:GLN:HE21	1.57	0.68
10:A:317:U:H4'	10:A:321:A:C8	2.28	0.68
2:1:3314:C:H2'	2:1:3315:C:C6	2.30	0.67
10:A:1042:U:H3'	10:A:1043:U:H2'	1.76	0.67
17:H:137:ARG:HB3	17:H:140:HIS:HD2	1.58	0.67
10:A:1629:G:H5'	75:AO:1:MET:HG3	1.77	0.67
53:s:26:SER:OG	53:s:64:LYS:O	2.11	0.67
10:A:1420:U:H4'	40:e:24:CYS:HB2	1.75	0.67
11:B:88:LYS:HE2	11:B:201:LEU:HD21	1.76	0.67
20:K:83:ILE:HA	20:K:149:ARG:HG3	1.75	0.67
65:AE:73:ARG:NH1	65:AE:108:VAL:HG11	2.09	0.67
2:1:2790:U:H5'	2:1:2790:U:H6	1.60	0.67
2:1:3192:A:O2'	55:u:126:LYS:NZ	2.26	0.67
18:I:45:ILE:HG21	18:I:171:LYS:HD3	1.75	0.67
58:x:108:ASP:OD2	58:x:111:LYS:NZ	2.27	0.67
19:J:158:ILE:HD11	19:J:163:ASP:HB3	1.75	0.67
10:A:945:U:H5'	24:O:55:ARG:HD3	1.77	0.67
34:Y:142:LYS:HE2	34:Y:144:ARG:HD3	1.77	0.67
10:A:1276:G:H22	10:A:1309:G:N2	1.93	0.67
43:h:127:SER:H	43:h:152:VAL:HG13	1.60	0.67
52:r:53:VAL:HG21	52:r:166:ILE:HD12	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:400:G:H4'	2:1:401:U:H5''	1.77	0.67
2:1:2520:A:H1'	2:1:2521:C:H5	1.60	0.67
14:E:41:ARG:HG2	31:V:109:PRO:HB3	1.76	0.67
10:A:66:U:O2	17:H:160:ARG:NE	2.25	0.66
2:1:538:G:O2'	2:1:539:G:OP1	2.13	0.66
2:1:545:G:N2	2:1:546:C:HO2'	1.92	0.66
2:1:617:A:H5'	2:1:619:A:H1'	1.76	0.66
81:1:3409:GET:N33	4:3:90:A:OP1	2.28	0.66
14:E:76:LYS:NZ	21:L:20:VAL:O	2.28	0.66
10:A:1699:G:H22	10:A:1700:G:H21	1.41	0.66
52:r:207:GLU:OE2	52:r:211:GLN:NE2	2.28	0.66
2:1:62:A:OP1	56:v:172:ARG:NH2	2.28	0.66
66:AF:77:VAL:HG13	66:AF:82:ASP:HB2	1.76	0.66
51:q:105:LYS:NZ	51:q:110:ASP:OD1	2.28	0.66
2:1:1189:A:OP1	57:w:50:ARG:NH2	2.26	0.66
12:C:171:ILE:HD13	12:C:196:GLU:HG3	1.78	0.66
30:U:127:ASN:OD1	30:U:130:ARG:NH1	2.29	0.66
2:1:2810:A:OP1	52:r:154:ARG:NH1	2.29	0.66
10:A:529:C:O2'	10:A:530:U:OP1	2.12	0.66
21:L:18:GLU:HB3	21:L:89:LEU:HD23	1.78	0.66
61:AA:78:ASN:HA	64:AD:37:ARG:HH22	1.59	0.66
7:7:1:MET:N	45:k:71:GLU:OE2	2.29	0.66
10:A:58:U:OP1	10:A:454:G:O2'	2.13	0.66
16:G:61:TYR:OH	39:d:52:ASP:OD1	2.13	0.66
2:1:1809:A:H2'	2:1:1810:A:C8	2.31	0.66
10:A:1445:C:OP2	27:T:138:THR:OG1	2.13	0.66
11:B:126:PRO:HG2	11:B:151:SER:HB3	1.77	0.66
31:V:40:ILE:HD11	31:V:90:ILE:HD13	1.78	0.66
45:k:35:ASP:OD2	45:k:191:LYS:NZ	2.25	0.66
10:A:654:G:O3'	10:A:676:G:N1	2.26	0.66
12:C:33:LYS:NZ	12:C:42:ASN:OD1	2.25	0.66
24:O:63:ALA:O	24:O:67:THR:OG1	2.14	0.66
10:A:675:U:H2'	10:A:676:G:C8	2.31	0.65
10:A:1242:U:O2'	21:L:8:ARG:NH2	2.29	0.65
10:A:1763:A:OP2	75:AO:11:ARG:NH2	2.29	0.65
43:h:304:ASP:OD2	43:h:308:ARG:NH2	2.28	0.65
10:A:1236:U:O2'	10:A:1237:C:O2	2.09	0.65
10:A:1043:U:O2'	10:A:1045:U:OP2	2.13	0.65
10:A:1156:A:H2'	10:A:1157:G:H8	1.60	0.65
2:1:2191:A:H2'	2:1:2192:A:C8	2.31	0.65
4:3:8:G:O6	47:m:21:ARG:NH2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:D:137:GLY:HA2	32:W:1:MET:HE1	1.77	0.65
18:I:163:ASP:OD2	18:I:167:GLN:NE2	2.29	0.65
2:1:547:U:H2'	2:1:548:G:H8	1.62	0.65
20:K:96:VAL:HG23	20:K:99:LEU:HD12	1.79	0.65
27:T:27:LYS:HD2	27:T:57:ARG:HG2	1.77	0.65
10:A:1270:U:H1'	10:A:1271:U:H5	1.60	0.65
33:X:90:THR:HG23	33:X:94:LEU:HD12	1.76	0.65
2:1:1936:G:H21	2:1:3327:A:H8	1.42	0.65
10:A:1451:C:OP1	28:R:138:GLN:NE2	2.28	0.65
15:F:205:PHE:HD2	15:F:221:ARG:HE	1.43	0.65
2:1:2808:OMC:H5	2:1:2824:C:H42	1.45	0.65
48:n:71:ASN:ND2	48:n:159:LEU:O	2.19	0.65
2:1:730:A:H2'	2:1:731:U:H2'	1.78	0.65
21:L:77:ARG:NH2	21:L:86:ILE:O	2.30	0.65
30:U:42:GLY:HA3	30:U:94:VAL:HG21	1.78	0.65
2:1:1303:G:OP2	57:w:60:ARG:NH1	2.30	0.64
10:A:871:U:OP1	12:C:214:LYS:NZ	2.30	0.64
10:A:1529:G:N2	10:A:1555:C:H1'	2.12	0.64
36:a:83:LEU:HB3	36:a:89:ILE:HG12	1.78	0.64
43:h:90:LEU:HD11	43:h:111:VAL:HG11	1.79	0.64
15:F:54:TYR:OH	15:F:97:GLU:OE1	2.14	0.64
46:l:301:ARG:HH21	59:y:41:ASP:HB3	1.63	0.64
65:AE:73:ARG:HH12	65:AE:108:VAL:HG11	1.62	0.64
10:A:903:U:H2'	10:A:904:A:C8	2.31	0.64
19:J:124:LYS:HD2	19:J:129:HIS:CE1	2.31	0.64
27:T:29:MET:HB2	27:T:54:LEU:HD12	1.80	0.64
32:W:3:ASN:HD21	32:W:7:GLN:HB2	1.63	0.64
31:V:20:LYS:HG2	31:V:93:GLN:HE22	1.61	0.64
16:G:57:SER:OG	16:G:167:ARG:NH2	2.31	0.64
21:L:80:LEU:HB3	21:L:82:ILE:HG23	1.78	0.64
43:h:176:LYS:HG2	43:h:178:TRP:HE1	1.63	0.64
70:AJ:93:ILE:HG22	70:AJ:97:ARG:HH12	1.61	0.64
2:1:2090:U:H4'	2:1:2091:A:O5'	1.97	0.64
10:A:1339:G:O6	10:A:1354:U:O2	2.15	0.64
54:t:126:PHE:HD2	69:AI:115:LYS:HG3	1.62	0.64
10:A:1270:U:H1'	10:A:1271:U:C5	2.33	0.64
31:V:105:ILE:HG13	31:V:106:THR:HG23	1.80	0.64
11:B:26:ALA:O	11:B:46:ASN:ND2	2.31	0.64
46:l:299:VAL:HG21	59:y:132:PRO:HB2	1.79	0.64
10:A:1305:U:H3'	11:B:101:ARG:HH21	1.61	0.64
14:E:40:VAL:HG12	14:E:49:VAL:HG22	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:h:166:VAL:O	43:h:178:TRP:N	2.29	0.63
62:AB:24:LYS:O	62:AB:26:ARG:HG2	1.98	0.63
10:A:656:C:H1'	10:A:674:C:H42	1.62	0.63
31:V:21:ILE:HD13	31:V:117:ILE:HD13	1.80	0.63
76:AP:7:THR:HB	76:AP:22:GLN:NE2	2.13	0.63
76:AP:38:GLN:OE1	76:AP:41:ARG:NH2	2.31	0.63
2:1:162:U:H2'	2:1:163:A:C8	2.33	0.63
2:1:2579:G:OP1	44:j:233:GLN:NE2	2.29	0.63
10:A:1378:U:OP1	29:S:59:LYS:NZ	2.32	0.63
21:L:88:PRO:HD2	21:L:91:ARG:HD2	1.79	0.63
17:H:203:ASP:O	17:H:207:GLU:HG3	1.98	0.63
32:W:51:ILE:HG21	32:W:78:LEU:HD21	1.79	0.63
10:A:504:A:O2'	10:A:505:U:OP1	2.14	0.63
26:Q:56:LEU:HD22	26:Q:80:LEU:HD11	1.79	0.63
43:h:112:LEU:H	43:h:127:SER:HA	1.62	0.63
10:A:988:A:H2'	10:A:990:A:N7	2.13	0.63
10:A:1221:A:H2'	10:A:1222:G:H8	1.63	0.63
2:1:1560:U:O4	2:1:1571:G:O6	2.16	0.63
2:1:2163:G:O2'	2:1:2292:U:OP2	2.16	0.63
14:E:173:ILE:HG12	14:E:186:LYS:HG2	1.81	0.63
10:A:456:G:OP1	35:Z:109:LYS:NZ	2.20	0.63
45:k:58:ARG:HD2	45:k:354:VAL:HB	1.80	0.63
51:q:109:GLN:HB3	51:q:127:LYS:HE2	1.80	0.63
10:A:1703:C:O2'	10:A:1704:C:O5'	2.12	0.63
29:S:89:SER:HB3	29:S:92:ASP:HB2	1.81	0.63
51:q:100:ASN:HB3	51:q:115:ARG:HB2	1.80	0.63
10:A:1460:G:H2'	10:A:1461:A:H8	1.62	0.62
14:E:17:VAL:HG11	40:e:22:ARG:HH11	1.63	0.62
72:AL:24:ILE:HG23	72:AL:78:LEU:HD13	1.81	0.62
59:y:178:ARG:HH21	62:AB:50:PRO:HG2	1.63	0.62
10:A:1431:G:N2	42:g:129:THR:OG1	2.28	0.62
11:B:167:LYS:NZ	11:B:204:TYR:O	2.21	0.62
2:1:252:U:H5'	2:1:253:A:H8	1.64	0.62
10:A:1526:G:H4'	27:T:40:ARG:HH12	1.65	0.62
11:B:84:ARG:O	11:B:88:LYS:HG2	2.00	0.62
10:A:822:G:O2'	10:A:823:G:N3	2.32	0.62
16:G:34:GLN:O	16:G:37:GLN:NE2	2.32	0.62
52:r:36:LEU:HD21	52:r:69:ARG:HH11	1.64	0.62
2:1:1611:U:H2'	2:1:1612:U:C6	2.33	0.62
38:c:72:LYS:NZ	38:c:73:LEU:O	2.32	0.62
50:p:119:GLU:CD	50:p:120:GLY:H	2.08	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1007:A:H2'	2:1:1008:A:C8	2.35	0.62
10:A:477:C:OP1	20:K:121:SER:OG	2.16	0.62
18:I:42:ILE:HD12	18:I:56:VAL:HG22	1.82	0.62
40:e:33:LYS:HE2	40:e:34:TYR:CZ	2.35	0.62
2:1:1173:G:C6	67:AG:20:LYS:HE2	2.35	0.62
2:1:1834:C:H5''	2:1:1835:A:H5'	1.82	0.62
11:B:98:ILE:HD11	11:B:116:LYS:HD2	1.81	0.62
1:0:82:GLU:HG2	1:0:87:ILE:HG12	1.80	0.61
2:1:163:A:H2'	2:1:164:U:N1	2.15	0.61
2:1:583:A:H5''	67:AG:70:LYS:HE2	1.80	0.61
2:1:1657:G:H2'	2:1:1658:G:C8	2.35	0.61
10:A:472:A:H5''	20:K:144:PRO:HD2	1.81	0.61
42:g:181:GLN:HE21	42:g:190:LEU:N	1.98	0.61
53:s:109:HIS:HD2	53:s:123:TYR:H	1.48	0.61
78:PT:24:C:H2'	78:PT:25:U:C6	2.34	0.61
30:U:16:ASN:OD1	30:U:56:LYS:NZ	2.31	0.61
42:g:182:TYR:OH	42:g:187:HIS:ND1	2.30	0.61
15:F:199:GLU:OE2	15:F:201:HIS:NE2	2.33	0.61
26:Q:41:VAL:HG13	26:Q:84:ILE:HD13	1.83	0.61
43:h:122:GLN:N	43:h:122:GLN:NE2	2.49	0.61
27:T:22:ILE:HD11	27:T:35:ILE:HG13	1.82	0.61
45:k:81:THR:HB	45:k:205:VAL:HG11	1.82	0.61
2:1:1204:U:H2'	74:AN:33:ASN:ND2	2.16	0.61
10:A:1420:U:H2'	10:A:1422:A:H5'	1.81	0.61
51:q:69:ARG:NH1	51:q:73:SER:OG	2.33	0.61
10:A:12:U:H2'	10:A:13:C:C6	2.36	0.61
10:A:521:G:N1	10:A:526:U:OP2	2.30	0.61
10:A:1355:A:O2'	10:A:1358:G:OP1	2.16	0.61
28:R:30:ILE:HD12	28:R:80:ILE:HD13	1.82	0.61
36:a:59:TYR:HE1	36:a:100:ILE:HG23	1.65	0.61
39:d:8:THR:HG21	39:d:59:SER:HB3	1.82	0.61
45:k:372:THR:HG22	45:k:374:ALA:H	1.65	0.61
65:AE:76:ARG:HD3	65:AE:88:LEU:HD13	1.83	0.61
78:AT:51:U:H2'	78:AT:52:C:C6	2.36	0.61
6:6:75:PRO:HG2	6:6:105:PRO:HD3	1.82	0.61
10:A:1597:G:H4'	16:G:98:MET:HE1	1.82	0.61
12:C:120:LEU:HD21	12:C:122:GLU:HG3	1.82	0.61
78:AT:44:A:H2'	78:AT:45:A:C8	2.35	0.61
33:X:77:PRO:HG3	34:Y:7:ARG:O	2.00	0.61
14:E:29:GLU:HG3	14:E:66:ARG:HH21	1.65	0.61
49:o:185:GLU:HG2	49:o:196:VAL:HG21	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:z:172:ARG:HB3	60:z:176:ARG:HH12	1.66	0.61
2:1:2488:U:O2'	2:1:2489:A:H5''	2.00	0.61
10:A:308:C:H4'	34:Y:33:LEU:HD23	1.83	0.61
20:K:78:ARG:HH12	20:K:82:ARG:NH2	1.98	0.61
76:AP:61:LYS:NZ	76:AP:63:LYS:O	2.33	0.61
10:A:1675:U:H2'	10:A:1676:A:C4	2.36	0.60
2:1:3241:G:N2	58:x:172:GLN:HE21	1.99	0.60
10:A:327:G:H5''	19:J:98:LYS:HB3	1.83	0.60
10:A:511:U:H2'	10:A:512:G:C8	2.36	0.60
10:A:1423:U:H4'	14:E:177:LEU:HD11	1.82	0.60
18:I:5:ILE:HD11	18:I:18:ALA:HB2	1.83	0.60
20:K:70:LEU:O	20:K:74:ASN:ND2	2.34	0.60
2:1:803:A:H61	2:1:930:G:H22	1.50	0.60
2:1:2413:G:H4'	56:v:24:ARG:HH22	1.66	0.60
2:1:2488:U:O2'	2:1:2489:A:H8	1.85	0.60
10:A:444:A:H5''	15:F:57:ASN:HD22	1.65	0.60
10:A:652:C:H5''	10:A:653:G:H8	1.67	0.60
13:D:163:ARG:HD3	13:D:165:ILE:HD11	1.83	0.60
27:T:66:LEU:O	27:T:70:VAL:HG23	2.00	0.60
31:V:43:ASN:HB3	31:V:102:ILE:HD12	1.81	0.60
34:Y:56:LYS:HG2	34:Y:93:LEU:HD11	1.83	0.60
45:k:95:THR:OG1	45:k:98:GLY:O	2.19	0.60
48:n:3:GLN:HG2	66:AF:75:TYR:HA	1.83	0.60
10:A:479:A:H2'	10:A:480:U:C5	2.36	0.60
28:R:24:GLY:HA3	28:R:63:ASP:HB2	1.83	0.60
28:R:45:PHE:O	28:R:49:GLU:HG3	2.00	0.60
77:AQ:82:THR:HG21	83:AQ:301:YMZ:CAV	2.31	0.60
2:1:2260:U:OP1	2:1:2945:G:O2'	2.20	0.60
25:P:42:LYS:NZ	25:P:61:ASP:OD2	2.23	0.60
1:0:42:TRP:CD1	1:0:53:LYS:HE2	2.37	0.60
28:R:68:VAL:HG11	28:R:80:ILE:HD11	1.84	0.60
31:V:87:LYS:C	31:V:88:ARG:HD2	2.27	0.60
44:j:101:ILE:HG13	44:j:165:VAL:HG22	1.82	0.60
10:A:758:C:OP1	15:F:22:LYS:N	2.30	0.60
18:I:87:VAL:HG11	18:I:125:LEU:HD23	1.82	0.60
50:p:92:PHE:O	50:p:96:ASN:ND2	2.34	0.60
10:A:698:C:H2'	10:A:699:U:C6	2.36	0.60
18:I:21:PHE:HE1	18:I:77:LEU:HD11	1.65	0.60
78:AT:6:G:H2'	78:AT:7:G:H8	1.63	0.60
2:1:1623:U:O2'	2:1:1626:U:O2	2.17	0.60
10:A:188:U:O2	10:A:193:G:C6	2.55	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:T:30:TYR:O	27:T:33:THR:OG1	2.17	0.60
46:l:301:ARG:NH2	59:y:41:ASP:HB3	2.15	0.60
10:A:1526:G:H4'	27:T:40:ARG:NH1	2.17	0.60
2:1:564:G:H2'	2:1:565:A:C8	2.36	0.59
2:1:1713:U:H2'	2:1:1714:G:C8	2.37	0.59
2:1:2985:U:H2'	2:1:2986:U:C6	2.37	0.59
10:A:1395:G:N2	10:A:1398:G:OP2	2.33	0.59
31:V:81:TYR:HB3	40:e:52:PHE:HB3	1.83	0.59
2:1:3144:A:O2'	57:w:6:LYS:NZ	2.35	0.59
2:1:3180:A:OP2	55:u:118:LYS:NZ	2.31	0.59
2:1:3244:A:H2'	2:1:3245:A:N3	2.17	0.59
10:A:544:U:H2'	10:A:545:U:C6	2.37	0.59
2:1:1116:A:H2'	2:1:1117:U:C6	2.37	0.59
2:1:1774:G:O2'	2:1:1776:G:OP2	2.18	0.59
2:1:2932:C:H2'	2:1:2933:G:C8	2.36	0.59
2:1:3260:A:H2'	2:1:3261:A:C8	2.37	0.59
11:B:141:ILE:O	32:W:60:ARG:NH2	2.35	0.59
15:F:184:THR:N	15:F:224:ASN:O	2.26	0.59
10:A:511:U:H4'	20:K:131:GLN:HB3	1.83	0.59
13:D:117:ALA:O	13:D:121:LYS:HG3	2.02	0.59
37:b:51:ARG:NH1	39:d:37:SER:O	2.35	0.59
43:h:107:HIS:CE1	43:h:133:LYS:HD3	2.37	0.59
55:u:120:ARG:NH1	57:w:186:THR:O	2.35	0.59
45:k:108:GLU:OE1	45:k:109:HIS:NE2	2.35	0.59
2:1:896:G:H1'	2:1:1585:A:N6	2.17	0.59
2:1:3093:U:H1'	2:1:3094:A:H5''	1.84	0.59
10:A:500:U:H1'	10:A:501:G:C8	2.38	0.59
66:AF:112:LYS:HE2	66:AF:116:LEU:HD11	1.84	0.59
10:A:210:U:H2'	10:A:211:A:H5''	1.85	0.59
10:A:1596:U:O2'	16:G:105:GLY:O	2.15	0.59
10:A:215:A:N7	10:A:830:G:O2'	2.35	0.59
12:C:131:ASP:OD2	12:C:180:THR:OG1	2.20	0.59
42:g:162:GLU:OE1	42:g:171:GLY:N	2.36	0.59
2:1:619:A:O2'	67:AG:60:ARG:NH2	2.36	0.58
10:A:1676:A:H8	10:A:1701:A:C6	2.21	0.58
18:I:17:VAL:HG21	18:I:42:ILE:HG21	1.83	0.58
20:K:57:ARG:O	20:K:61:THR:HG23	2.02	0.58
26:Q:56:LEU:HD13	26:Q:78:THR:HG21	1.84	0.58
72:AL:40:GLN:HE21	72:AL:55:VAL:HG13	1.68	0.58
76:AP:8:ARG:NH1	76:AP:10:THR:HG21	2.18	0.58
2:1:660:U:H2'	2:1:661:C:C6	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1214:G:H1	23:N:47:GLU:CD	2.11	0.58
30:U:61:ILE:O	30:U:65:ILE:HG12	2.02	0.58
16:G:40:VAL:HB	16:G:67:PRO:HB2	1.85	0.58
25:P:21:THR:HG21	25:P:55:ALA:HB2	1.84	0.58
10:A:1286:U:H5'	13:D:83:LYS:HD3	1.85	0.58
15:F:45:VAL:HB	15:F:80:THR:HG22	1.84	0.58
11:B:15:LYS:HZ3	29:S:117:ILE:HB	1.67	0.58
20:K:77:ILE:HD11	20:K:93:LEU:HB2	1.86	0.58
2:1:1491:U:H5	2:1:1831:A:N1	2.02	0.58
16:G:81:ARG:HD3	16:G:82:PHE:CE2	2.39	0.58
18:I:14:GLU:HG3	18:I:42:ILE:HG12	1.84	0.58
10:A:405:A:H2'	10:A:406:C:H6	1.66	0.58
10:A:481:A:H2'	10:A:482:C:O4'	2.04	0.58
10:A:1145:A:H2'	10:A:1146:C:C6	2.39	0.58
58:x:103:GLU:OE2	58:x:109:SER:OG	2.14	0.58
5:4:26:U:H2'	5:4:27:U:C6	2.39	0.58
10:A:1198:G:O2'	10:A:1229:A:N7	2.36	0.58
10:A:1297:A:OP1	29:S:2:GLY:N	2.37	0.58
10:A:1317:C:OP2	29:S:45:ARG:NH1	2.37	0.58
10:A:1551:U:H2'	10:A:1552:C:C6	2.38	0.58
10:A:1659:G:H2'	10:A:1660:G:C8	2.38	0.58
14:E:133:LYS:HE2	14:E:192:ASP:OD1	2.04	0.58
20:K:62:ARG:O	20:K:69:ARG:NH1	2.37	0.58
30:U:20:GLN:HG2	30:U:24:ARG:HH12	1.67	0.58
10:A:1094:G:OP2	34:Y:27:GLN:NE2	2.36	0.58
10:A:1215:A:N6	10:A:1240:G:H1'	2.19	0.58
10:A:1546:G:H5''	27:T:135:GLY:HA3	1.85	0.58
14:E:115:PRO:HG2	14:E:118:ARG:HD3	1.84	0.58
16:G:143:ARG:HB2	39:d:57:MET:HE2	1.85	0.58
21:L:35:ILE:HG22	21:L:37:THR:HG22	1.86	0.58
47:m:60:ILE:HB	47:m:80:ALA:HB2	1.85	0.58
10:A:746:G:N2	10:A:747:A:H62	2.02	0.58
34:Y:100:ASP:OD1	34:Y:144:ARG:NH1	2.37	0.58
58:x:4:TYR:OH	58:x:18:ARG:HG3	2.04	0.58
58:x:29:THR:HA	58:x:32:THR:HG22	1.86	0.58
2:1:3160:C:H2'	2:1:3161:U:C6	2.38	0.57
10:A:1602:C:OP1	39:d:18:ARG:NH2	2.36	0.57
2:1:1653:C:O2'	2:1:1793:A:OP2	2.19	0.57
10:A:535:G:C6	20:K:171:ARG:HD3	2.39	0.57
18:I:85:HIS:ND1	18:I:161:LYS:HG2	2.19	0.57
44:j:65:ASP:OD2	44:j:68:LYS:HG2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:t:168:ALA:HB1	62:AB:147:LEU:HD21	1.85	0.57
2:1:1091:U:O4'	3:2:129:LYS:NZ	2.36	0.57
60:z:138:LEU:O	60:z:142:ILE:HG13	2.05	0.57
2:1:495:C:H4'	48:n:79:ASN:HD21	1.68	0.57
2:1:2384:C:H2'	2:1:2385:C:C6	2.39	0.57
28:R:27:LEU:HD11	28:R:29:LYS:HD3	1.87	0.57
30:U:65:ILE:HG21	30:U:114:LEU:HD22	1.86	0.57
59:y:126:GLN:O	59:y:130:ARG:HG2	2.05	0.57
2:1:437:G:H22	2:1:620:A:N6	1.93	0.57
2:1:1617:A:H2'	2:1:1618:U:C6	2.39	0.57
2:1:2933:G:H2'	2:1:2934:U:C6	2.40	0.57
2:1:266:C:OP1	56:v:5:LYS:NZ	2.37	0.57
10:A:65:A:OP1	17:H:176:GLN:NE2	2.30	0.57
10:A:1019:C:HO2'	33:X:2:THR:N	2.03	0.57
28:R:93:GLN:O	43:h:60:LYS:NZ	2.23	0.57
36:a:65:LEU:O	36:a:69:LEU:HB2	2.05	0.57
4:3:55:A:OP1	53:s:2:SER:N	2.38	0.57
10:A:65:A:H2	10:A:84:A:H62	1.50	0.57
10:A:1369:G:O2'	10:A:1370:A:H8	1.87	0.57
30:U:64:HIS:CD2	30:U:68:ARG:HD2	2.40	0.57
36:a:39:ILE:HB	36:a:71:ILE:HA	1.86	0.57
2:1:2669:A:H2'	2:1:2670:G:C8	2.39	0.57
10:A:1215:A:H61	10:A:1240:G:H1'	1.68	0.57
14:E:42:LYS:HG2	14:E:47:LEU:HD13	1.85	0.57
23:N:70:SER:O	23:N:74:LEU:N	2.38	0.57
2:1:2899:C:H2'	2:1:2900:C:C6	2.40	0.57
10:A:765:U:OP2	35:Z:9:THR:OG1	2.22	0.57
10:A:856:G:H2'	10:A:857:G:C8	2.39	0.57
10:A:1289:G:H1'	10:A:1307:A:C2	2.40	0.57
18:I:5:ILE:HG22	18:I:7:SER:H	1.70	0.57
37:b:64:LEU:HD12	37:b:65:PRO:HD2	1.87	0.57
44:j:8:GLN:HE21	44:j:231:SER:C	2.12	0.57
2:1:2919:G:N3	45:k:250:ALA:HB1	2.20	0.56
10:A:108:A:H2'	10:A:109:G:C8	2.40	0.56
15:F:191:ARG:HD2	15:F:246:LYS:HB2	1.85	0.56
21:L:16:PHE:O	21:L:88:PRO:HB3	2.05	0.56
43:h:208:CYS:SG	43:h:209:ALA:N	2.78	0.56
53:s:109:HIS:CD2	53:s:123:TYR:H	2.23	0.56
78:AT:19:G:N2	78:AT:59:A:O5'	2.38	0.56
2:1:2527:G:C5	50:p:34:ASN:ND2	2.73	0.56
13:D:173:ILE:O	13:D:180:LYS:NZ	2.30	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:159:ALA:HB3	20:K:162:SER:HB2	1.88	0.56
38:c:40:CYS:SG	38:c:41:LEU:N	2.77	0.56
39:d:32:PHE:HD2	39:d:38:ARG:HB2	1.71	0.56
44:j:4:VAL:HG13	44:j:8:GLN:OE1	2.05	0.56
44:j:137:ILE:HD11	44:j:149:LYS:HB2	1.88	0.56
78:AT:44:A:H2'	78:AT:45:A:H8	1.70	0.56
2:1:2686:G:H4'	2:1:2687:A:H5''	1.88	0.56
10:A:583:A:H2'	10:A:584:G:H8	1.70	0.56
10:A:1342:A:H5'	10:A:1343:G:OP2	2.06	0.56
10:A:1347:U:O2'	10:A:1348:U:H5''	2.05	0.56
20:K:112:GLN:HG3	20:K:148:VAL:HG21	1.86	0.56
23:N:31:VAL:HA	23:N:34:THR:HG22	1.86	0.56
28:R:6:VAL:HG22	28:R:21:VAL:HB	1.87	0.56
28:R:34:PRO:HD2	28:R:37:LEU:HD21	1.87	0.56
31:V:54:PRO:HB3	31:V:90:ILE:HD11	1.87	0.56
2:1:732:U:C4	2:1:733:A:H1'	2.41	0.56
10:A:52:U:H2'	10:A:53:G:C8	2.40	0.56
10:A:1368:A:O2'	10:A:1369:G:N2	2.33	0.56
10:A:1669:U:H5'	17:H:65:GLN:HE21	1.70	0.56
27:T:114:GLU:HG2	27:T:118:LYS:HE2	1.88	0.56
72:AL:49:ARG:HD3	72:AL:50:TYR:CE2	2.41	0.56
2:1:239:A:H3'	2:1:240:C:H5''	1.86	0.56
2:1:2740:U:H2'	2:1:2741:A:H8	1.70	0.56
10:A:805:U:H5''	10:A:806:A:OP2	2.05	0.56
18:I:58:VAL:N	18:I:89:LEU:O	2.38	0.56
20:K:78:ARG:HA	20:K:81:VAL:HG22	1.87	0.56
2:1:2808:OMC:H5	2:1:2824:C:N4	2.04	0.56
10:A:653:G:H4'	10:A:654:G:H5'	1.87	0.56
10:A:1535:G:O2'	27:T:89:GLN:NE2	2.39	0.56
10:A:1579:A:H2'	10:A:1580:A:H8	1.69	0.56
10:A:815:U:O2'	10:A:816:U:O5'	2.24	0.56
10:A:825:U:H1'	10:A:826:U:H5	1.70	0.56
20:K:78:ARG:HH12	20:K:82:ARG:HH21	1.53	0.56
34:Y:69:ARG:HG3	34:Y:117:ILE:HG12	1.88	0.56
61:AA:111:LYS:HA	61:AA:114:VAL:HG12	1.87	0.56
2:1:2535:A:OP1	44:j:69:TYR:OH	2.18	0.56
2:1:2583:U:H2'	2:1:2584:U:C6	2.39	0.56
10:A:1026:G:H2'	10:A:1027:G:C8	2.41	0.56
13:D:47:SER:OG	13:D:49:GLU:OE1	2.24	0.56
15:F:127:LYS:HE3	15:F:142:HIS:HA	1.88	0.56
44:j:80:GLU:HG3	77:AQ:66:GLY:HA2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:k:117:ARG:HD3	45:k:176:ALA:O	2.05	0.56
53:s:28:ASP:OD1	53:s:29:ARG:N	2.39	0.56
2:1:72:A:N7	54:t:66:ASN:HB3	2.21	0.56
2:1:772:U:H5	2:1:2691:U:O2	1.89	0.56
2:1:2519:A:H4'	2:1:2520:A:O5'	2.05	0.56
10:A:256:C:H5''	19:J:75:LYS:HB2	1.88	0.56
10:A:508:G:H2'	10:A:509:A:O4'	2.05	0.56
14:E:41:ARG:NH1	14:E:50:ILE:HD12	2.18	0.56
18:I:110:ARG:HD3	18:I:113:THR:HG21	1.88	0.56
66:AF:80:VAL:HG13	66:AF:112:LYS:HD2	1.88	0.56
2:1:1807:G:H2'	2:1:1808:G:O4'	2.06	0.56
2:1:2960:C:OP1	57:w:69:LYS:HE2	2.06	0.56
10:A:1248:G:H2'	10:A:1249:G:O4'	2.06	0.56
10:A:1384:U:H2'	10:A:1386:A:C5	2.41	0.56
15:F:179:ARG:NH1	15:F:230:THR:O	2.39	0.56
16:G:76:LYS:HD3	28:R:121:ARG:HD2	1.88	0.56
30:U:25:GLN:NE2	30:U:27:LYS:HE3	2.21	0.56
49:o:174:PHE:CZ	49:o:195:GLN:HG2	2.41	0.56
2:1:1592:C:H2'	2:1:1593:C:C6	2.41	0.55
10:A:78:A:O2'	17:H:173:PRO:O	2.24	0.55
10:A:1472:G:N2	10:A:1580:A:OP1	2.32	0.55
21:L:3:ILE:HB	21:L:8:ARG:NH2	2.21	0.55
28:R:63:ASP:OD1	28:R:65:ARG:NH1	2.38	0.55
41:f:29:LYS:HD3	41:f:35:TYR:CE1	2.40	0.55
2:1:158:A:H2'	2:1:159:A:C8	2.42	0.55
2:1:2527:G:N7	50:p:34:ASN:ND2	2.54	0.55
2:1:2655:U:H2'	2:1:2656:C:C6	2.41	0.55
10:A:261:C:O2'	10:A:262:G:H5'	2.06	0.55
14:E:171:ILE:HG12	14:E:188:LYS:HG2	1.88	0.55
19:J:143:ARG:HE	19:J:147:ARG:HH21	1.53	0.55
54:t:64:LYS:HE3	62:AB:69:TRP:CD1	2.41	0.55
5:4:52:A:OP1	73:AM:21[B]:ARG:NH1	2.36	0.55
10:A:501:G:O2'	10:A:502:U:O4'	2.17	0.55
16:G:63:GLN:HE22	16:G:66:ASN:HB2	1.71	0.55
27:T:123:ARG:HG3	27:T:133:VAL:HB	1.89	0.55
51:q:20:ILE:HG12	51:q:25:VAL:HG22	1.87	0.55
51:q:110:ASP:HB3	51:q:128:ILE:HD12	1.89	0.55
10:A:255:A:N3	19:J:64:ASN:ND2	2.54	0.55
10:A:536:A:O2'	10:A:537:G:N2	2.39	0.55
10:A:1579:A:H2'	10:A:1580:A:C8	2.41	0.55
20:K:58:ASP:O	20:K:62:ARG:HG3	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:l:218:LYS:HA	46:l:221:ARG:HG3	1.88	0.55
2:1:653:C:H2'	2:1:654:A:C8	2.41	0.55
2:1:782:A:H4'	2:1:783:G:H5'	1.89	0.55
10:A:824:U:H2'	10:A:825:U:C2	2.42	0.55
10:A:1016:U:H4'	10:A:1017:G:OP2	2.06	0.55
21:L:19:GLY:HA3	21:L:68:LEU:HD22	1.89	0.55
32:W:11:LEU:HD12	32:W:12:TYR:HB3	1.87	0.55
36:a:40:VAL:HG13	36:a:41:ILE:HG23	1.88	0.55
42:g:177:MET:O	42:g:179:ASP:N	2.40	0.55
2:1:113:A:OP1	56:v:54:LYS:NZ	2.40	0.55
4:3:112:G:H2'	4:3:113:C:C6	2.42	0.55
19:J:174:VAL:HG23	19:J:190:LEU:HD21	1.88	0.55
46:l:42:ARG:HG2	46:l:112:VAL:HG11	1.89	0.55
10:A:127:G:C2	17:H:195:VAL:HG22	2.42	0.55
10:A:250:U:OP1	15:F:133:LYS:NZ	2.39	0.55
17:H:50:PHE:CE1	17:H:113:ILE:HG12	2.41	0.55
23:N:66:VAL:HG21	23:N:71:ILE:HB	1.87	0.55
46:l:93:ASN:HD22	46:l:101:PHE:HB2	1.71	0.55
53:s:26:SER:OG	53:s:63:GLU:OE2	2.25	0.55
65:AE:46:THR:OG1	65:AE:86:GLU:OE2	2.20	0.55
2:1:3019:U:O2'	2:1:3020:A:H5'	2.06	0.55
10:A:443:A:H5''	15:F:59:ARG:HH12	1.72	0.55
10:A:1615:U:H2'	10:A:1616:G:C8	2.42	0.55
13:D:96:VAL:HG21	13:D:203:GLU:HG3	1.88	0.55
20:K:133:HIS:CE1	20:K:163:PRO:HG2	2.41	0.55
2:1:904:G:O6	81:l:3412:GET:H12	2.07	0.55
54:t:77:LEU:HD22	54:t:87:PRO:HG3	1.88	0.55
65:AE:45:THR:HG21	65:AE:89:PHE:HA	1.89	0.55
2:1:120:A:O2'	50:p:106:LYS:NZ	2.37	0.55
2:1:662:U:H2'	2:1:663:A:C8	2.42	0.55
14:E:17:VAL:HG11	40:e:22:ARG:NH1	2.21	0.55
47:m:107:ARG:HH12	47:m:120:THR:HA	1.72	0.55
53:s:83:GLY:HA3	53:s:127:PHE:HE2	1.72	0.55
2:1:1432:U:O4	46:l:68:THR:HG23	2.07	0.54
2:1:1563:A:H2'	2:1:1564:U:C6	2.42	0.54
2:1:2988:A:H2'	2:1:2989:A:C8	2.42	0.54
14:E:59:VAL:HB	14:E:67:ILE:HD11	1.90	0.54
19:J:163:ASP:HA	19:J:166:PHE:HD2	1.72	0.54
32:W:3:ASN:ND2	32:W:7:GLN:HB2	2.21	0.54
52:r:38:ARG:NH2	52:r:45:GLU:OE1	2.27	0.54
2:1:1800:A:H2'	2:1:1801:C:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:82:ARG:HD3	20:K:149:ARG:HG2	1.90	0.54
58:x:10:ASN:ND2	58:x:13:LYS:HG3	2.21	0.54
76:AP:8:ARG:HG2	76:AP:10:THR:HG23	1.89	0.54
7:7:9:SER:HA	7:7:52:THR:HG22	1.89	0.54
10:A:446:C:OP1	15:F:29:PRO:HD3	2.08	0.54
10:A:533:A:OP1	20:K:168:ARG:NH2	2.36	0.54
12:C:168:MET:HA	12:C:197:ILE:HD12	1.89	0.54
12:C:180:THR:HG23	12:C:183:GLN:H	1.72	0.54
24:O:54:LEU:HB3	24:O:60:VAL:HB	1.87	0.54
51:q:47:LYS:HB2	55:u:5:VAL:HG22	1.89	0.54
2:1:654:A:H2'	2:1:655:A:C8	2.43	0.54
2:1:2116:A:C4	71:AK:3:LYS:HB3	2.41	0.54
10:A:772:A:C4	15:F:19:MET:HG2	2.42	0.54
10:A:1479:A:H4'	10:A:1480:G:O5'	2.07	0.54
10:A:1699:G:C6	10:A:1700:G:H1'	2.42	0.54
16:G:34:GLN:HA	16:G:37:GLN:HE22	1.72	0.54
2:1:428:U:H2'	2:1:429:U:C6	2.42	0.54
12:C:160:LYS:HD2	12:C:204:ILE:HG23	1.89	0.54
43:h:32:LEU:HD21	43:h:95:LEU:HD22	1.89	0.54
75:AO:2:ARG:O	75:AO:4:LYS:N	2.40	0.54
2:1:368:G:H3'	81:1:3403:GET:H212	1.72	0.54
2:1:417:A:H2'	2:1:418:A:C8	2.42	0.54
10:A:188:U:H2'	10:A:189:G:C8	2.43	0.54
14:E:24:GLU:OE1	21:L:61:TRP:NE1	2.33	0.54
20:K:87:SER:OG	20:K:90:LYS:NZ	2.21	0.54
43:h:245:ASN:OD1	43:h:246:ARG:N	2.40	0.54
72:AL:29:ALA:HB1	72:AL:37:LYS:HD2	1.89	0.54
8:8:108:LEU:HD23	8:8:125:ARG:HD3	1.89	0.54
10:A:52:U:H2'	10:A:53:G:H8	1.72	0.54
10:A:822:G:O2'	10:A:823:G:H5''	2.07	0.54
10:A:871:U:O2'	25:P:116:VAL:O	2.26	0.54
12:C:108:ASP:OD1	12:C:109:LYS:N	2.40	0.54
15:F:31:PRO:HB3	15:F:43:PRO:HG3	1.89	0.54
2:1:2077:A:O2'	2:1:2078:A:H5'	2.08	0.54
2:1:2749:G:C2	62:AB:60:TYR:CE1	2.96	0.54
10:A:271:G:O6	10:A:281:U:O2	2.26	0.54
24:O:65:VAL:HG23	24:O:66:VAL:HG13	1.89	0.54
46:l:6:GLN:HB3	46:l:20:GLN:HB3	1.90	0.54
2:1:1106:U:H2'	2:1:1107:U:C6	2.43	0.54
10:A:1512:A:H2'	10:A:1513:A:C8	2.43	0.54
10:A:1677:G:N2	10:A:1699:G:H5''	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:h:166:VAL:H	43:h:178:TRP:C	2.16	0.54
69:AI:38:ARG:NH1	69:AI:40:SER:OG	2.41	0.54
2:1:211:G:H2'	46:l:222:ASN:OD1	2.08	0.54
2:1:694:C:H2'	2:1:695:G:C8	2.43	0.54
10:A:1551:U:H2'	10:A:1552:C:H6	1.73	0.54
27:T:101:LEU:O	27:T:105:LEU:N	2.39	0.54
78:AT:51:U:O2	78:AT:65:G:N2	2.30	0.54
10:A:512:G:N7	20:K:171:ARG:NH2	2.56	0.53
10:A:921:G:N7	37:b:15:ARG:NH1	2.46	0.53
10:A:1669:U:H5'	17:H:65:GLN:NE2	2.22	0.53
15:F:22:LYS:HB3	15:F:23:LEU:HD12	1.90	0.53
27:T:86:LEU:HB2	27:T:99:HIS:HB2	1.89	0.53
56:v:105:ARG:HG2	56:v:108:ARG:HH21	1.73	0.53
2:1:535:C:H2'	2:1:536:A:H8	1.73	0.53
2:1:653:C:H2'	2:1:654:A:H8	1.72	0.53
2:1:1911:A:H2'	2:1:1912:U:C6	2.44	0.53
10:A:218:A:H2'	10:A:219:A:O4'	2.07	0.53
10:A:1301:G:P	29:S:7:LYS:HG3	2.49	0.53
31:V:23:ILE:HD13	31:V:115:VAL:HG22	1.90	0.53
70:AJ:60:ILE:HG21	70:AJ:90:THR:HG22	1.88	0.53
2:1:912:G:N1	44:j:207:VAL:HG11	2.24	0.53
2:1:2867:G:O2'	74:AN:24:TYR:O	2.25	0.53
10:A:402:G:H2'	10:A:403:C:H6	1.73	0.53
10:A:1487:C:P	30:U:122:ARG:HH22	2.31	0.53
18:I:70:GLN:HG3	18:I:88:PHE:HD2	1.73	0.53
27:T:9:GLY:O	27:T:12:GLN:NE2	2.29	0.53
38:c:56:CYS:SG	38:c:57:ASP:N	2.80	0.53
50:p:147:LYS:HG3	50:p:174:MET:HE3	1.90	0.53
2:1:763:U:O2'	2:1:764:C:OP2	2.20	0.53
2:1:1091:U:H4'	2:1:1092:U:H5'	1.91	0.53
2:1:1663:A:H2'	2:1:1664:G:C8	2.44	0.53
2:1:2491:U:OP2	81:1:3413:GET:N32	2.41	0.53
14:E:33:GLN:HG2	14:E:58:GLY:HA3	1.89	0.53
25:P:15:PHE:HD1	25:P:79:ARG:HG3	1.73	0.53
78:PT:51:U:H2'	78:PT:52:C:C6	2.43	0.53
2:1:1035:U:H2'	2:1:1036:A:C8	2.43	0.53
2:1:1867:U:O2'	60:z:58:HIS:ND1	2.38	0.53
2:1:3138:U:H2'	2:1:3139:U:C6	2.43	0.53
4:3:39:U:H4'	53:s:44:THR:HG23	1.89	0.53
10:A:738:A:H2'	10:A:739:A:O4'	2.08	0.53
10:A:747:A:H2'	10:A:748:G:H8	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1323:C:H1'	10:A:1396:A:C4	2.43	0.53
10:A:1699:G:H22	10:A:1700:G:N2	2.07	0.53
25:P:56:MET:O	25:P:60:GLN:HG3	2.08	0.53
36:a:90:THR:HG23	36:a:104:ALA:HA	1.90	0.53
42:g:142:LEU:HB3	42:g:145:LEU:HD23	1.91	0.53
2:1:1570:A:H2'	2:1:1571:G:O4'	2.08	0.53
2:1:2740:U:H2'	2:1:2741:A:C8	2.43	0.53
7:7:35:LYS:HE3	7:7:51:TRP:CZ2	2.43	0.53
13:D:143:LEU:O	13:D:169:ARG:NH2	2.41	0.53
2:1:539:G:H8	2:1:539:G:O5'	1.92	0.53
5:4:2:A:C4	5:4:3:A:C8	2.97	0.53
31:V:18:ILE:HD13	31:V:94:ALA:HA	1.90	0.53
39:d:44:VAL:HG11	39:d:48:VAL:HG21	1.91	0.53
43:h:123:ILE:N	43:h:135:TRP:O	2.33	0.53
78:AT:2:G:H2'	78:AT:3:C:O4'	2.09	0.53
1:0:66:GLU:HG2	1:0:98:THR:HG22	1.91	0.53
2:1:972:U:P	59:y:144:ARG:HH22	2.32	0.53
2:1:1303:G:H4'	2:1:1304:A:O5'	2.08	0.53
10:A:415:A:H4'	10:A:416:G:O5'	2.09	0.53
10:A:484:G:H22	10:A:500:U:H3	1.57	0.53
10:A:516:A:H1'	10:A:532:A:H61	1.73	0.53
10:A:924:A:H2'	10:A:925:A:C8	2.43	0.53
10:A:985:C:H5	10:A:988:A:OP2	1.91	0.53
10:A:1676:A:H8	10:A:1701:A:N1	2.07	0.53
43:h:43:ILE:H	43:h:43:ILE:HD12	1.74	0.53
44:j:107:CYS:HB2	44:j:136:ILE:HD12	1.91	0.53
47:m:119:TYR:OH	47:m:139:PRO:O	2.25	0.53
47:m:128:GLU:O	47:m:164:LYS:NZ	2.40	0.53
10:A:207:U:H2'	10:A:208:A:C8	2.44	0.53
11:B:83:GLN:HB3	11:B:99:ALA:HB1	1.91	0.53
14:E:116:ILE:HD13	14:E:143:LEU:HD22	1.90	0.53
22:M:132:SER:HB3	22:M:135:VAL:HB	1.91	0.53
27:T:41:ARG:HH11	30:U:46:PRO:HD3	1.72	0.53
43:h:85:SER:HB3	43:h:87:ASP:OD1	2.08	0.53
48:n:57:LEU:HD11	48:n:63:LEU:HB2	1.90	0.53
78:AT:48:U:H4'	78:AT:49:C:C5	2.44	0.53
2:1:939:U:H3'	62:AB:13:GLY:HA2	1.90	0.53
2:1:1344:U:OP1	59:y:39:ARG:NH1	2.42	0.53
2:1:1761:U:H2'	2:1:1762:G:O4'	2.08	0.53
10:A:298:A:H2'	10:A:299:A:C8	2.44	0.53
10:A:677:G:H2'	10:A:678:A:C8	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:18:LEU:HD21	29:S:102:ILE:HD13	1.91	0.53
24:O:40:TYR:CZ	24:O:53:ILE:HG21	2.44	0.53
44:j:8:GLN:HE21	44:j:232:GLY:N	2.07	0.53
2:1:1116:A:H2'	2:1:1117:U:H6	1.74	0.52
10:A:1659:G:H2'	10:A:1660:G:H8	1.74	0.52
10:A:1660:G:H2'	10:A:1661:C:H6	1.74	0.52
16:G:143:ARG:HH21	39:d:57:MET:HE1	1.74	0.52
25:P:7:GLN:NE2	25:P:106:ARG:HG3	2.24	0.52
53:s:65:ILE:HG13	53:s:66:ALA:N	2.24	0.52
2:1:795:G:O2'	54:t:18:TRP:NE1	2.39	0.52
2:1:1344:U:H5'	2:1:1347:U:OP1	2.09	0.52
2:1:2988:A:H2'	2:1:2989:A:H8	1.74	0.52
10:A:479:A:H2'	10:A:480:U:C6	2.44	0.52
10:A:592:A:H4'	10:A:593:G:H5'	1.91	0.52
10:A:721:C:O2'	10:A:722:A:H8	1.92	0.52
17:H:49:ILE:HG13	17:H:114:VAL:HB	1.91	0.52
18:I:118:HIS:CE1	18:I:175:LYS:HZ1	2.28	0.52
27:T:122:HIS:CE1	27:T:126:ARG:HD2	2.45	0.52
30:U:64:HIS:CE1	30:U:79:LEU:HD22	2.44	0.52
42:g:182:TYR:CE1	42:g:187:HIS:HA	2.36	0.52
51:q:48:ILE:HD11	51:q:54:LYS:HE3	1.91	0.52
52:r:187:ASN:OD1	52:r:217:GLN:HB2	2.09	0.52
2:1:229:C:H2'	2:1:230:G:O4'	2.09	0.52
10:A:737:A:H2'	10:A:738:A:O4'	2.09	0.52
10:A:1129:U:H2'	10:A:1130:U:C6	2.43	0.52
11:B:148:ASP:HB2	11:B:164:ASN:OD1	2.10	0.52
43:h:123:ILE:O	43:h:135:TRP:N	2.26	0.52
46:l:157:PHE:CD1	46:l:169:VAL:HG11	2.44	0.52
54:t:2:ALA:HB3	62:AB:41:HIS:CE1	2.45	0.52
65:AE:45:THR:HG22	65:AE:47:ASP:H	1.73	0.52
2:1:545:G:H22	2:1:546:C:HO2'	1.55	0.52
2:1:2404:U:H2'	2:1:2405:U:C6	2.44	0.52
2:1:2498:A:H2'	2:1:2499:U:C6	2.44	0.52
2:1:3199:G:H2'	2:1:3200:C:C6	2.44	0.52
10:A:184:C:P	19:J:152:ARG:HH22	2.33	0.52
10:A:1595:U:C5	28:R:123:MET:HE1	2.44	0.52
18:I:59:PRO:HG2	18:I:62:SER:OG	2.09	0.52
20:K:126:ARG:HG2	41:f:33:ARG:HH21	1.75	0.52
43:h:249:LEU:N	43:h:260:PHE:O	2.43	0.52
55:u:120:ARG:HH12	57:w:187:ALA:HA	1.75	0.52
7:7:11:SER:HB2	45:k:369:ARG:HD2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:247:U:OP1	22:M:34:TRP:NE1	2.30	0.52
10:A:740:A:O2'	10:A:741:A:OP1	2.26	0.52
10:A:1221:A:H2'	10:A:1222:G:C8	2.42	0.52
10:A:1606:C:H2'	10:A:1607:C:H6	1.75	0.52
17:H:1:MET:HE3	17:H:106:LEU:HB2	1.90	0.52
18:I:43:LYS:HD3	18:I:171:LYS:HZ1	1.75	0.52
18:I:162:LEU:O	18:I:166:GLN:HG3	2.10	0.52
20:K:139:GLN:NE2	35:Z:64:PHE:O	2.35	0.52
52:r:30:LYS:HG3	52:r:63:GLU:HG3	1.92	0.52
64:AD:55:LYS:O	64:AD:59:GLU:HG2	2.09	0.52
2:1:164:U:C2	2:1:165:C:C6	2.98	0.52
9:9:52:GLN:O	9:9:70:VAL:HB	2.09	0.52
10:A:189:G:O6	19:J:147:ARG:NH2	2.43	0.52
10:A:965:G:H4'	10:A:1763:A:H4'	1.92	0.52
10:A:1478:A:H1'	10:A:1480:G:C4	2.45	0.52
15:F:57:ASN:O	15:F:61:VAL:HG23	2.10	0.52
20:K:83:ILE:O	20:K:107:ARG:NE	2.40	0.52
27:T:23:ASP:HB3	27:T:26:ILE:HD13	1.90	0.52
58:x:67:ILE:HD11	58:x:80:LYS:HB3	1.92	0.52
2:1:2557:G:C6	8:8:24:LEU:HD21	2.45	0.52
2:1:2744:C:H1'	2:1:2745:C:H5	1.75	0.52
2:1:3044:C:H2'	2:1:3045:A:O4'	2.10	0.52
2:1:3159:A:H2'	2:1:3160:C:C6	2.44	0.52
10:A:652:C:H5''	10:A:653:G:C8	2.45	0.52
10:A:1629:G:N7	81:A:1801:GET:N33	2.58	0.52
10:A:1660:G:H2'	10:A:1661:C:C6	2.44	0.52
30:U:86:ARG:NH1	30:U:90:PRO:O	2.42	0.52
60:z:60:ARG:O	60:z:64:ARG:HG3	2.10	0.52
76:AP:104:LEU:HD23	76:AP:106:PHE:H	1.74	0.52
2:1:307:A:H2'	2:1:308:A:C8	2.45	0.52
3:2:12:ARG:O	3:2:16:GLN:HG3	2.10	0.52
7:7:23:ARG:HG2	7:7:24:GLY:N	2.25	0.52
11:B:52:LYS:HE2	32:W:82:VAL:HA	1.91	0.52
17:H:191:LYS:O	17:H:195:VAL:HG23	2.10	0.52
18:I:60:PRO:HG2	18:I:61:PRO:HD3	1.91	0.52
24:O:128:TYR:O	24:O:131:THR:HG22	2.10	0.52
43:h:218:ILE:HD12	43:h:220:TRP:CZ2	2.44	0.52
53:s:19:LEU:O	53:s:68:HIS:HA	2.10	0.52
2:1:437:G:H1	2:1:620:A:N6	2.08	0.52
2:1:730:A:H4'	2:1:730:A:OP1	2.10	0.52
2:1:2485:U:H2'	2:1:2486:U:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:C:25:THR:O	12:C:50:ARG:NH1	2.42	0.52
19:J:190:LEU:HD22	19:J:194:GLU:HG2	1.91	0.52
68:AH:38:ALA:O	68:AH:58:ARG:NH2	2.42	0.52
10:A:1561:G:H5'	10:A:1562:G:OP1	2.10	0.52
10:A:1571:G:N7	28:R:13:LYS:HD3	2.25	0.52
10:A:1578:C:H2'	10:A:1579:A:C8	2.45	0.52
26:Q:60:LEU:O	26:Q:64:ARG:HG2	2.10	0.52
30:U:25:GLN:OE1	30:U:27:LYS:HG2	2.09	0.52
51:q:7:ASP:OD1	51:q:56:THR:OG1	2.13	0.52
58:x:13:LYS:HE2	58:x:152:GLU:HB2	1.93	0.52
58:x:165:GLN:OE1	58:x:166:ILE:N	2.43	0.52
72:AL:40:GLN:HE21	72:AL:55:VAL:CG1	2.23	0.52
2:1:941:C:H2'	2:1:942:U:C6	2.44	0.51
10:A:1168:A:O2'	10:A:1169:A:OP1	2.23	0.51
12:C:106:THR:OG1	12:C:108:ASP:OD1	2.24	0.51
15:F:118:GLU:HG3	15:F:121:TYR:OH	2.11	0.51
16:G:93:LEU:HD12	16:G:172:ILE:HG23	1.92	0.51
29:S:14:LYS:O	29:S:18:GLU:HG3	2.10	0.51
41:f:37:ARG:O	41:f:41:THR:HG23	2.10	0.51
52:r:43:VAL:HG21	52:r:197:VAL:HG13	1.90	0.51
2:1:436:A:H2'	2:1:437:G:C8	2.44	0.51
2:1:539:G:H2'	2:1:540:C:O4'	2.10	0.51
2:1:1287:A:H2'	2:1:1288:C:O4'	2.10	0.51
2:1:1662:G:H2'	2:1:1663:A:C8	2.45	0.51
14:E:176:VAL:HB	14:E:183:LEU:HB2	1.92	0.51
16:G:27:THR:HG21	28:R:28:ILE:HG12	1.90	0.51
24:O:74:ILE:O	24:O:78:ASN:ND2	2.38	0.51
57:w:77:PRO:HB3	57:w:139:VAL:HG12	1.91	0.51
2:1:1692:A:H2'	2:1:1693:A:C8	2.46	0.51
2:1:2641:G:H4'	47:m:4:GLN:OE1	2.09	0.51
10:A:530:U:OP2	35:Z:65:GLY:N	2.38	0.51
10:A:1236:U:H5	42:g:138:ARG:HD2	1.75	0.51
17:H:45:PHE:HA	17:H:48:TYR:HD2	1.75	0.51
32:W:40:ASP:HB3	32:W:46:ILE:HD11	1.92	0.51
43:h:68:ILE:O	43:h:85:SER:OG	2.16	0.51
2:1:1113:G:OP1	63:AC:4:SER:HB2	2.11	0.51
2:1:1493:C:H2'	2:1:1494:A:C8	2.46	0.51
2:1:2825:A:H1'	52:r:158:LYS:HD2	1.91	0.51
2:1:3287:A:H2'	2:1:3288:A:C8	2.46	0.51
10:A:584:G:H2'	10:A:585:C:H6	1.75	0.51
10:A:953:U:H2'	10:A:954:C:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1104:U:H2'	2:1:1105:U:C6	2.45	0.51
5:4:73:U:OP1	9:9:24:SER:OG	2.23	0.51
10:A:393:U:H2'	10:A:394:G:O4'	2.11	0.51
10:A:870:G:H2'	10:A:871:U:C6	2.45	0.51
10:A:1180:C:OP1	31:V:76:LYS:NZ	2.37	0.51
10:A:1523:G:H4'	36:a:34:ASP:HA	1.91	0.51
15:F:15:PRO:HG3	15:F:39:ARG:HD3	1.92	0.51
47:m:160:PHE:HA	47:m:163:LEU:HB3	1.92	0.51
1:0:155:ARG:HD3	1:0:172:TYR:CD1	2.46	0.51
2:1:3064:C:O2'	2:1:3066:A:OP2	2.24	0.51
22:M:77:SER:HB3	22:M:85:ILE:HG12	1.93	0.51
24:O:15:ALA:O	38:c:28:PRO:HG3	2.10	0.51
26:Q:43:ARG:O	26:Q:47:ARG:HG3	2.11	0.51
32:W:36:ILE:HB	32:W:51:ILE:HG23	1.92	0.51
64:AD:11:ASN:OD1	64:AD:12:ILE:N	2.44	0.51
2:1:1530:A:H2'	2:1:1531:A:C8	2.46	0.51
10:A:482:C:N3	10:A:503:A:N6	2.59	0.51
10:A:561:U:H4'	41:f:17:GLN:NE2	2.24	0.51
10:A:1276:G:H22	10:A:1309:G:H22	1.55	0.51
10:A:1335:U:H2'	10:A:1336:G:C8	2.46	0.51
10:A:1593:C:H2'	10:A:1594:G:C8	2.46	0.51
57:w:62:ALA:HA	57:w:71:PRO:HD2	1.93	0.51
76:AP:8:ARG:HD3	76:AP:72:LEU:HD21	1.93	0.51
76:AP:28:TYR:HB3	76:AP:69:VAL:HB	1.93	0.51
2:1:282:G:OP1	80:1:3401:SPK:N14	2.30	0.51
2:1:3297:U:OP1	7:7:35:LYS:HD3	2.10	0.51
10:A:279:G:OP2	10:A:279:G:H8	1.94	0.51
10:A:944:U:H5'	24:O:15:ALA:O	2.11	0.51
21:L:15:LEU:HD12	21:L:19:GLY:O	2.10	0.51
24:O:132:VAL:HG23	24:O:134:VAL:HG23	1.91	0.51
51:q:36:LYS:HZ3	51:q:74:LEU:HD13	1.75	0.51
54:t:2:ALA:HB1	62:AB:33:GLY:O	2.11	0.51
2:1:907:C:H5''	44:j:15:ILE:HD13	1.93	0.51
2:1:2634:G:H2'	2:1:2635:A:C8	2.46	0.51
10:A:17:C:H2'	10:A:18:C:C6	2.46	0.51
10:A:1399:U:O2'	10:A:1400:U:OP1	2.29	0.51
10:A:1523:G:H5'	36:a:34:ASP:HA	1.93	0.51
13:D:120:ILE:O	13:D:124:ILE:HG13	2.11	0.51
15:F:141:THR:OG1	15:F:143:ASP:OD1	2.27	0.51
20:K:84:GLY:HA3	20:K:107:ARG:CZ	2.41	0.51
20:K:170:GLY:O	20:K:174:ARG:HG3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:L:88:PRO:O	21:L:90:THR:N	2.44	0.51
31:V:63:LYS:HD3	31:V:65:THR:OG1	2.11	0.51
43:h:176:LYS:HG3	43:h:188:ASP:HB3	1.92	0.51
2:1:1093:G:H4'	3:2:129:LYS:HG2	1.91	0.51
2:1:1720:U:H1'	2:1:1721:C:C6	2.46	0.51
10:A:16:G:H2'	10:A:17:C:C6	2.46	0.51
10:A:310:A:OP2	81:A:1803:GET:N21	2.44	0.51
10:A:1342:A:H3'	10:A:1343:G:H8	1.76	0.51
10:A:1721:U:H2'	10:A:1722:U:C6	2.45	0.51
11:B:136:SER:HB2	11:B:141:ILE:HB	1.93	0.51
15:F:148:ARG:NH2	17:H:201:GLN:OE1	2.44	0.51
18:I:20:ALA:O	18:I:24:LEU:HB2	2.11	0.51
20:K:55:ALA:O	20:K:59:LEU:HG	2.11	0.51
33:X:104:LEU:HD23	33:X:125:ILE:HA	1.91	0.51
34:Y:70:LYS:HE3	41:f:8:LEU:HA	1.92	0.51
46:l:227:GLU:OE1	46:l:238:GLN:HG2	2.10	0.51
56:v:115:VAL:HA	56:v:134:LEU:HD23	1.93	0.51
57:w:179:LEU:HD23	57:w:183:LYS:HE2	1.92	0.51
78:PT:69:C:H2'	78:PT:70:C:C6	2.46	0.51
2:1:1593:C:H2'	2:1:1594:G:C8	2.46	0.50
2:1:1757:A:O2'	2:1:1758:U:O5'	2.28	0.50
10:A:521:G:OP1	35:Z:59:GLY:N	2.44	0.50
10:A:1469:A:H2'	10:A:1470:G:C8	2.46	0.50
10:A:1602:C:N4	16:G:80:LYS:O	2.44	0.50
26:Q:19:GLY:HA2	27:T:94:ASP:HA	1.92	0.50
43:h:291:TRP:CZ3	43:h:298:LEU:HB2	2.45	0.50
67:AG:8:TYR:CE1	67:AG:99:ARG:HG2	2.45	0.50
2:1:170:G:H2'	2:1:171:G:H8	1.76	0.50
2:1:762:U:H4'	2:1:763:U:O4'	2.11	0.50
2:1:849:G:OP2	77:AQ:2:THR:HG21	2.10	0.50
10:A:1329:A:H2'	10:A:1330:A:C8	2.47	0.50
23:N:36:LEU:HB2	23:N:41:LEU:HD12	1.93	0.50
43:h:112:LEU:HD13	43:h:153:SER:HA	1.93	0.50
43:h:240:LEU:HA	43:h:251:ALA:HA	1.93	0.50
2:1:25:A:H2'	2:1:26:C:H6	1.76	0.50
10:A:82:U:H2'	10:A:83:G:O4'	2.10	0.50
10:A:1048:U:H2'	10:A:1049:G:O4'	2.11	0.50
10:A:1550:C:OP1	30:U:84:LYS:HE2	2.11	0.50
13:D:71:LEU:HB3	13:D:99:ILE:HD11	1.92	0.50
17:H:208:TYR:CE2	17:H:212:LEU:HD11	2.47	0.50
22:M:55:ASP:HB3	22:M:58:CYS:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:T:16:ARG:O	27:T:17:LEU:HD22	2.11	0.50
2:l:498:C:O2	48:n:22:LYS:HE3	2.11	0.50
2:l:1172:C:H2'	2:l:1173:G:N2	2.27	0.50
10:A:821:U:H2'	10:A:822:G:C8	2.47	0.50
10:A:1338:U:H2'	10:A:1339:G:H5''	1.94	0.50
10:A:1486:G:OP1	30:U:122:ARG:NH1	2.45	0.50
13:D:40:VAL:HG21	13:D:63:ILE:HG23	1.93	0.50
13:D:96:VAL:HG22	13:D:110:ILE:HG12	1.93	0.50
14:E:134:GLY:HA3	14:E:157:PHE:O	2.11	0.50
23:N:46:ARG:NH2	23:N:50:LYS:HE2	2.27	0.50
35:Z:54:ALA:O	35:Z:76:TYR:N	2.40	0.50
42:g:178:LYS:O	42:g:180:ARG:HG2	2.11	0.50
44:j:49:ILE:HD11	44:j:60:LYS:HE2	1.93	0.50
51:q:77:ASN:HA	51:q:80:THR:HG22	1.92	0.50
62:AB:60:TYR:CE2	62:AB:63:LYS:HA	2.46	0.50
2:l:485:A:H2'	2:l:486:C:H6	1.76	0.50
16:G:135:ASP:HA	16:G:138:VAL:HG22	1.93	0.50
27:T:94:ASP:OD2	27:T:98:TYR:OH	2.17	0.50
45:k:193:ASP:O	45:k:197:GLU:HG2	2.11	0.50
56:v:114:ARG:HG2	56:v:137:PRO:HG3	1.93	0.50
1:0:10:ILE:HG12	1:0:26:ARG:HG3	1.92	0.50
10:A:824:U:H2'	10:A:825:U:N3	2.26	0.50
12:C:28:ASP:OD2	12:C:50:ARG:HG2	2.12	0.50
18:I:149:LEU:HD12	18:I:182:PRO:HG3	1.94	0.50
31:V:54:PRO:HA	31:V:90:ILE:HG13	1.92	0.50
35:Z:3:ASP:CG	35:Z:31:ASN:HD21	2.18	0.50
42:g:149:LYS:HB2	42:g:159:LEU:HD13	1.92	0.50
2:l:1345:G:H5''	2:l:1346:U:H5''	1.94	0.50
2:l:2627:U:H4'	2:l:2628:A:O4'	2.11	0.50
2:l:2734:A:H2'	2:l:2735:U:H6	1.76	0.50
70:AJ:2:ALA:O	70:AJ:11:ASN:ND2	2.32	0.50
78:AT:67:C:H2'	78:AT:68:C:C6	2.47	0.50
2:l:498:C:H5''	48:n:25:ARG:NH1	2.27	0.50
2:l:1031:A:H2'	2:l:1032:A:O4'	2.12	0.50
4:3:113:C:H2'	4:3:114:U:O4'	2.11	0.50
5:4:23:U:OP1	9:9:16:ARG:NH1	2.45	0.50
7:7:20:LEU:CD1	7:7:30:ARG:HG2	2.42	0.50
10:A:402:G:H2'	10:A:403:C:C6	2.46	0.50
19:J:113:TYR:OH	19:J:156:ALA:O	2.29	0.50
31:V:98:THR:O	31:V:102:ILE:HG12	2.12	0.50
67:AG:49:ILE:HD11	67:AG:71:VAL:HG22	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:AI:47:VAL:O	69:AI:51:ILE:HG13	2.11	0.50
10:A:1:U:H5''	13:D:171:LYS:HE3	1.92	0.50
10:A:150:U:O2'	17:H:15:SER:HB2	2.11	0.50
10:A:1486:G:OP2	30:U:73:VAL:HG12	2.12	0.50
12:C:89:ASP:N	12:C:89:ASP:OD1	2.44	0.50
16:G:177:ILE:HD13	16:G:180:ARG:HH21	1.77	0.50
60:z:25:ASP:HB3	60:z:28:GLU:HB2	1.93	0.50
60:z:163:ARG:O	60:z:167:ARG:HG3	2.12	0.50
78:PT:32:G:H2'	78:PT:33:C:H6	1.76	0.50
2:1:208:A:H4'	2:1:210:A:N7	2.26	0.49
2:1:1007:A:H2'	2:1:1008:A:H8	1.75	0.49
2:1:2525:A:H2'	2:1:2526:C:O4'	2.11	0.49
2:1:3182:C:C6	58:x:182:LEU:HD22	2.46	0.49
9:9:51:ARG:HG2	9:9:52:GLN:H	1.76	0.49
10:A:121:U:H2'	10:A:122:U:C6	2.47	0.49
10:A:1149:G:O2'	10:A:1599:U:O2	2.29	0.49
10:A:1539:U:O2'	10:A:1584:A:N3	2.37	0.49
10:A:1628:C:H2'	10:A:1629:G:C8	2.46	0.49
14:E:41:ARG:HA	31:V:109:PRO:HB3	1.93	0.49
18:I:157:ALA:O	18:I:161:LYS:NZ	2.42	0.49
20:K:17:ARG:O	20:K:23:ARG:NH1	2.45	0.49
35:Z:87:PRO:HG2	35:Z:89:TYR:CE1	2.47	0.49
49:o:158:ARG:HG3	49:o:201:TRP:CD2	2.47	0.49
51:q:26:LYS:HG3	51:q:33:GLU:OE2	2.12	0.49
56:v:98:LEU:HD12	56:v:128:LYS:HD2	1.94	0.49
2:1:93:G:H2'	2:1:94:A:C8	2.46	0.49
2:1:175:G:C4	2:1:176:G:C8	3.00	0.49
2:1:2719:A:H2'	2:1:2720:A:C8	2.47	0.49
9:9:116:LYS:HG2	9:9:126:ALA:HB1	1.93	0.49
10:A:480:U:H2'	10:A:481:A:C4	2.48	0.49
10:A:590:A:O2'	10:A:594:C:OP1	2.28	0.49
10:A:891:A:H2'	10:A:892:A:C8	2.47	0.49
10:A:1086:G:O3'	33:X:76:GLN:HG2	2.12	0.49
10:A:1508:G:O2'	10:A:1510:G:OP2	2.24	0.49
35:Z:16:PRO:C	35:Z:19:ALA:H	2.21	0.49
48:n:170:ARG:HB3	48:n:172:HIS:CE1	2.47	0.49
49:o:83:PHE:HB2	49:o:137:PRO:HG3	1.93	0.49
2:1:535:C:H2'	2:1:536:A:C8	2.47	0.49
2:1:2824:C:N3	52:r:158:LYS:HE3	2.27	0.49
10:A:788:A:C8	33:X:107:SER:HA	2.48	0.49
10:A:1369:G:H1'	10:A:1370:A:OP1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1635:A:H2'	10:A:1636:C:C6	2.47	0.49
11:B:56:LYS:NZ	11:B:159:ALA:O	2.44	0.49
18:I:147:LYS:NZ	18:I:180:GLU:OE2	2.45	0.49
31:V:69:THR:OG1	31:V:71:ASN:OD1	2.29	0.49
37:b:45:VAL:HB	37:b:64:LEU:HD21	1.94	0.49
38:c:33:MET:HE1	38:c:73:LEU:HD11	1.94	0.49
43:h:286:ALA:HB2	43:h:302:TYR:CZ	2.47	0.49
53:s:78:GLU:O	53:s:81:GLU:HG2	2.12	0.49
58:x:46:LYS:O	58:x:50:GLN:HG3	2.11	0.49
74:AN:18:SER:OG	74:AN:28:PRO:O	2.30	0.49
2:1:496:A:H2'	2:1:497:U:C6	2.48	0.49
2:1:2659:G:H4'	47:m:7:PHE:CZ	2.48	0.49
2:1:2876:U:H2'	2:1:2877:U:C6	2.48	0.49
4:3:27:A:H2'	4:3:28:C:C6	2.48	0.49
10:A:207:U:H2'	10:A:208:A:H8	1.77	0.49
10:A:378:U:C4	20:K:5:PRO:HB3	2.47	0.49
10:A:478:G:O6	10:A:506:U:O4	2.31	0.49
10:A:483:A:H1'	10:A:503:A:H2	1.78	0.49
10:A:535:G:C5	20:K:171:ARG:HD3	2.47	0.49
23:N:62:LEU:HG	23:N:120:CYS:HB3	1.94	0.49
28:R:19:ALA:HA	28:R:66:VAL:HA	1.94	0.49
31:V:98:THR:O	31:V:101:ARG:HG2	2.12	0.49
36:a:53:ASP:OD2	36:a:57:TYR:OH	2.25	0.49
58:x:128:ARG:HD2	58:x:136:ILE:HG21	1.95	0.49
7:7:20:LEU:HD13	7:7:30:ARG:HG2	1.94	0.49
10:A:820:U:O2'	10:A:821:U:OP1	2.24	0.49
14:E:73:LEU:HD22	21:L:65:TYR:HD2	1.77	0.49
14:E:219:ILE:HD12	14:E:220:PRO:HD2	1.95	0.49
18:I:113:THR:O	18:I:117:VAL:HG23	2.12	0.49
21:L:55:VAL:HG12	21:L:68:LEU:HD12	1.93	0.49
28:R:126:LYS:HE2	28:R:130:GLY:O	2.12	0.49
35:Z:36:SER:O	35:Z:40:LEU:HD12	2.13	0.49
43:h:169:ALA:HB2	43:h:199:ILE:HD13	1.93	0.49
61:AA:5:ILE:HG23	61:AA:25:ILE:HD13	1.94	0.49
62:AB:75:LEU:HD11	62:AB:134:ALA:HA	1.95	0.49
2:1:2181:U:H2'	2:1:2182:C:C6	2.48	0.49
3:2:69:LYS:HG3	47:m:40:HIS:CD2	2.47	0.49
10:A:470:U:O2'	10:A:754:A:N3	2.43	0.49
10:A:773:A:H2	15:F:249:ILE:HD13	1.76	0.49
11:B:41:ARG:HG2	11:B:42:PRO:HD2	1.93	0.49
20:K:58:ASP:O	20:K:61:THR:OG1	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:m:180:PHE:HB3	47:m:195:LEU:HD13	1.94	0.49
57:w:9:VAL:HG12	57:w:118:ARG:HG3	1.95	0.49
60:z:105:LEU:HD23	60:z:138:LEU:HD23	1.95	0.49
76:AP:8:ARG:CZ	76:AP:10:THR:HG21	2.43	0.49
2:1:1011:C:H1'	2:1:1013:U:H5	1.76	0.49
2:1:1012:U:O2'	2:1:1013:U:O5'	2.28	0.49
2:1:3208:A:H4'	45:k:95:THR:HG22	1.95	0.49
8:8:73:MET:HE1	8:8:142:ILE:HB	1.94	0.49
10:A:483:A:H2'	10:A:484:G:O4'	2.13	0.49
10:A:921:G:O6	37:b:15:ARG:NH1	2.43	0.49
18:I:159:ASP:HA	18:I:162:LEU:HD13	1.94	0.49
29:S:65:PRO:HB3	29:S:74:GLN:OE1	2.13	0.49
43:h:132:VAL:HB	43:h:178:TRP:HZ3	1.77	0.49
46:l:111:ASN:ND2	56:v:201:ARG:HB3	2.17	0.49
50:p:160:PRO:HB2	50:p:162:GLU:OE1	2.12	0.49
2:1:258:U:H2'	2:1:259:C:C6	2.48	0.49
2:1:1077:U:H5'	2:1:1078:U:C5	2.48	0.49
2:1:1496:G:H2'	2:1:1497:U:O4'	2.13	0.49
2:1:1589:A:OP1	68:AH:60:ARG:NH1	2.46	0.49
2:1:2185:A:H5''	2:1:2186:A:C2	2.46	0.49
2:1:2196:G:OP1	70:AJ:67:ARG:NH2	2.36	0.49
10:A:286:A:H2'	10:A:287:U:O4'	2.12	0.49
10:A:444:A:C6	10:A:445:U:C4	3.01	0.49
10:A:473:A:P	20:K:126:ARG:HH21	2.35	0.49
10:A:530:U:H4'	35:Z:66:GLY:HA2	1.94	0.49
20:K:100:LYS:HB3	20:K:102:GLU:OE1	2.13	0.49
20:K:136:VAL:HG21	20:K:146:PHE:CE1	2.47	0.49
23:N:52:LEU:HD11	23:N:60:CYS:SG	2.53	0.49
50:p:29:GLU:OE2	61:AA:128:LYS:NZ	2.35	0.49
55:u:19:VAL:HG11	55:u:55:ILE:HD12	1.94	0.49
64:AD:22:SER:OG	64:AD:99:ASP:OD1	2.22	0.49
78:AT:71:G:H2'	78:AT:72:C:C6	2.48	0.49
2:1:543:C:H1'	2:1:546:C:H5	1.77	0.49
10:A:148:C:O4'	17:H:132:ARG:NH1	2.46	0.49
16:G:65:ARG:NE	16:G:65:ARG:HA	2.27	0.49
19:J:106:ALA:HB2	19:J:171:LEU:HG	1.94	0.49
31:V:20:LYS:HG2	31:V:93:GLN:NE2	2.26	0.49
42:g:161:ARG:HG2	42:g:162:GLU:H	1.78	0.49
78:AT:75:C:H2'	78:AT:76:C:H5'	1.95	0.49
1:0:28:ARG:NH1	46:l:361:LEU:O	2.42	0.49
1:0:164:GLN:HG2	1:0:166:THR:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2932:C:H2'	2:1:2933:G:H8	1.78	0.49
10:A:15:U:H2'	10:A:16:G:O4'	2.13	0.49
10:A:142:G:O2'	10:A:143:A:O5'	2.22	0.49
10:A:1214:G:N1	23:N:47:GLU:OE2	2.43	0.49
10:A:1783:C:O2	37:b:92:ARG:HB3	2.13	0.49
24:O:66:VAL:HG23	24:O:67:THR:HG23	1.94	0.49
2:1:370:U:H4'	2:1:404:G:H5'	1.95	0.48
2:1:487:C:H2'	2:1:488:G:O4'	2.13	0.48
2:1:1794:A:H2'	2:1:1795:A:C8	2.48	0.48
10:A:1051:C:H5''	12:C:151:LYS:HE2	1.95	0.48
13:D:92:ARG:HE	13:D:114:LYS:HA	1.77	0.48
15:F:45:VAL:HG23	15:F:61:VAL:HG11	1.95	0.48
15:F:180:LEU:HD12	15:F:193:GLY:O	2.13	0.48
16:G:45:LYS:HD3	16:G:119:GLU:OE2	2.13	0.48
21:L:18:GLU:N	21:L:89:LEU:HB3	2.25	0.48
26:Q:25:LEU:HD11	26:Q:33:PHE:CE1	2.48	0.48
43:h:18:GLY:HA3	43:h:38:ARG:HB2	1.94	0.48
45:k:284:ARG:NH1	45:k:293:ASN:O	2.43	0.48
48:n:42:LEU:HD11	48:n:84:ILE:HG13	1.95	0.48
65:AE:26:LYS:HA	65:AE:29:PRO:HG2	1.94	0.48
2:1:109:G:OP2	54:t:73:ARG:NH2	2.42	0.48
2:1:2285:G:O2'	2:1:2288:U:OP2	2.18	0.48
10:A:103:A:H4'	10:A:105:A:C8	2.48	0.48
10:A:142:G:H1	10:A:169:A:H61	1.61	0.48
13:D:44:LYS:HE2	13:D:241:GLU:HG2	1.96	0.48
18:I:70:GLN:HG3	18:I:88:PHE:CD2	2.48	0.48
46:l:301:ARG:NH1	59:y:38:ARG:O	2.44	0.48
2:1:184:C:OP1	81:1:3410:GET:O41	2.27	0.48
10:A:4:C:H5	10:A:20:G:N1	2.07	0.48
10:A:584:G:H2'	10:A:585:C:C6	2.48	0.48
10:A:750:G:C4	20:K:149:ARG:NH1	2.81	0.48
10:A:763:C:O2'	10:A:764:U:OP2	2.22	0.48
10:A:1227:A:O2'	10:A:1229:A:OP1	2.23	0.48
10:A:1541:U:H2'	10:A:1542:A:O4'	2.14	0.48
10:A:1542:A:P	26:Q:47:ARG:HE	2.36	0.48
29:S:33:ARG:HG3	43:h:128:ARG:HH11	1.78	0.48
52:r:185:LYS:HA	52:r:190:VAL:HG22	1.95	0.48
2:1:719:G:N7	81:1:3405:GET:H831	2.28	0.48
2:1:2158:A:H2'	2:1:2159:C:C6	2.48	0.48
2:1:2742:G:H2'	2:1:2743:U:C6	2.47	0.48
6:6:77:ILE:HD12	6:6:103:VAL:HG11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1132:A:H2'	10:A:1133:C:C6	2.48	0.48
10:A:1720:C:H2'	10:A:1721:U:C6	2.48	0.48
30:U:11:ALA:O	30:U:15:ILE:HD12	2.12	0.48
51:q:161:ILE:O	51:q:164:ILE:HG22	2.13	0.48
2:1:437:G:O2'	2:1:438:A:OP1	2.29	0.48
2:1:1593:C:H2'	2:1:1594:G:H8	1.79	0.48
2:1:2582:G:OP1	81:1:3412:GET:H531	2.13	0.48
2:1:3259:A:H2'	2:1:3260:A:O4'	2.13	0.48
10:A:189:G:H1'	10:A:193:G:C2	2.48	0.48
10:A:1341:U:H2'	10:A:1342:A:H8	1.78	0.48
10:A:1676:A:H2'	10:A:1699:G:O6	2.14	0.48
64:AD:29:TYR:OH	64:AD:57:GLU:OE2	2.31	0.48
2:1:357:A:O4'	46:l:82:GLY:HA3	2.13	0.48
2:1:2345:A:H2'	2:1:2346:A:C8	2.49	0.48
2:1:2384:C:H2'	2:1:2385:C:H6	1.78	0.48
2:1:2520:A:H1'	2:1:2521:C:C5	2.45	0.48
3:2:102:ARG:O	3:2:106:LEU:HG	2.14	0.48
15:F:31:PRO:HG2	15:F:38:LEU:HG	1.95	0.48
21:L:50:THR:HG22	21:L:55:VAL:HG23	1.96	0.48
27:T:48:LYS:NZ	30:U:50:ALA:HB2	2.29	0.48
60:z:134:HIS:CD2	60:z:136:ARG:HB3	2.49	0.48
66:AF:17[A]:LYS:HB3	66:AF:17[A]:LYS:HE3	1.54	0.48
2:1:546:C:H2'	2:1:547:U:O4'	2.13	0.48
2:1:1347:U:O4	59:y:31[B]:LYS:NZ	2.47	0.48
2:1:2855:U:H2'	2:1:2856:C:C6	2.49	0.48
2:1:2974:C:O2'	45:k:180:GLU:OE2	2.22	0.48
10:A:880:G:H2'	10:A:881:U:C6	2.49	0.48
10:A:1002:U:H2'	10:A:1003:U:C6	2.48	0.48
10:A:1072:A:H2'	10:A:1073:A:C8	2.48	0.48
11:B:27:LYS:NZ	11:B:44:GLY:HA3	2.28	0.48
16:G:30:PRO:HB2	16:G:33:VAL:HG23	1.94	0.48
20:K:82:ARG:CD	20:K:149:ARG:HG2	2.44	0.48
20:K:83:ILE:HD11	20:K:147:THR:HB	1.96	0.48
22:M:28:ASN:HA	22:M:30:LYS:NZ	2.28	0.48
26:Q:80:LEU:HD13	26:Q:83:MET:HB2	1.95	0.48
27:T:4:VAL:HG12	36:a:82:GLN:HG2	1.95	0.48
39:d:35:ASP:HB3	39:d:38:ARG:HH21	1.78	0.48
53:s:33:ALA:HA	53:s:36:VAL:HG12	1.96	0.48
78:AT:51:U:H2'	78:AT:52:C:H6	1.77	0.48
2:1:516:U:OP1	46:l:352:PRO:HD2	2.14	0.48
2:1:1909:A:N3	2:1:2098:A:H2'	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:80:ARG:NH2	6:6:115:THR:O	2.45	0.48
10:A:820:U:H2'	10:A:821:U:C2	2.49	0.48
10:A:1131:G:H2'	10:A:1132:A:C8	2.49	0.48
12:C:28:ASP:CG	12:C:50:ARG:HG2	2.39	0.48
12:C:64:ARG:HE	25:P:31:LYS:HD2	1.78	0.48
14:E:60:LEU:H	14:E:67:ILE:HG12	1.79	0.48
28:R:14:THR:OG1	28:R:71:GLY:HA2	2.14	0.48
2:1:912:G:H5'	2:1:913:A:OP1	2.14	0.48
2:1:1617:A:H2'	2:1:1618:U:H6	1.78	0.48
3:2:27:LEU:HD11	47:m:34:LYS:HA	1.96	0.48
10:A:69:G:P	35:Z:123:ARG:HH12	2.37	0.48
10:A:1285:A:H5''	13:D:81:VAL:HG11	1.96	0.48
10:A:1448:G:OP2	27:T:143:ARG:NH1	2.47	0.48
43:h:59:LYS:O	43:h:60:LYS:HD2	2.14	0.48
44:j:68:LYS:HG3	44:j:70[A]:LYS:HB3	1.95	0.48
44:j:68:LYS:HG3	44:j:70[B]:LYS:HB3	1.95	0.48
49:o:32:LYS:HB2	49:o:32:LYS:HE2	1.72	0.48
2:1:529:A:O2'	2:1:531:G:OP2	2.31	0.48
2:1:1569:C:H2'	2:1:1570:A:C8	2.49	0.48
2:1:2669:A:H2'	2:1:2670:G:H8	1.79	0.48
10:A:1473:A:OP1	40:e:34:TYR:OH	2.26	0.48
10:A:1485:G:H5''	30:U:72:GLY:HA3	1.96	0.48
14:E:133:LYS:HG3	14:E:157:PHE:HB3	1.96	0.48
20:K:17:ARG:HD2	20:K:20:GLU:OE2	2.14	0.48
21:L:46:LEU:O	21:L:50:THR:HG23	2.14	0.48
30:U:99:SER:O	30:U:103:LYS:HG2	2.14	0.48
43:h:191:GLY:O	43:h:192:HIS:ND1	2.47	0.48
76:AP:71:ARG:NH2	76:AP:80:LYS:HE2	2.28	0.48
2:1:163:A:H2'	2:1:164:U:C6	2.49	0.47
2:1:210:A:OP2	46:l:222:ASN:HB2	2.13	0.47
10:A:123:G:P	15:F:77:ARG:HH22	2.35	0.47
10:A:278:U:H4'	10:A:279:G:OP2	2.13	0.47
10:A:1578:C:H2'	10:A:1579:A:H8	1.78	0.47
14:E:124:LEU:HD11	14:E:153:TYR:HB3	1.96	0.47
17:H:196:LYS:O	17:H:200:GLN:HG3	2.14	0.47
22:M:29:LYS:C	22:M:30:LYS:HD3	2.39	0.47
43:h:170:SER:O	43:h:196:ILE:HB	2.13	0.47
78:PT:69:C:H2'	78:PT:70:C:H6	1.78	0.47
1:0:171:PHE:O	1:0:172:TYR:HB2	2.13	0.47
2:1:422:A:C2	2:1:2341:A:H4'	2.49	0.47
2:1:1093:G:H2'	2:1:1093:G:N3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1800:A:H2'	2:1:1801:C:H6	1.79	0.47
2:1:2603:U:OP1	2:1:2729:U:O2'	2.31	0.47
2:1:2607:A:H4'	2:1:2608:A:O5'	2.14	0.47
3:2:39:ILE:HG12	3:2:63:ILE:HD13	1.95	0.47
10:A:188:U:H2'	10:A:189:G:H8	1.77	0.47
10:A:242:A:OP1	15:F:155:ARG:NE	2.45	0.47
10:A:933:A:H2'	10:A:934:C:H6	1.78	0.47
15:F:181:VAL:HG11	15:F:195:ILE:HD11	1.95	0.47
21:L:71:GLU:HA	21:L:74:GLU:HG3	1.96	0.47
29:S:33:ARG:HG3	43:h:128:ARG:NH1	2.29	0.47
43:h:301:GLY:C	43:h:302:TYR:HD1	2.22	0.47
61:AA:27:LYS:NZ	61:AA:93:LYS:O	2.47	0.47
2:1:299:G:H5''	70:AJ:84:ARG:NH2	2.28	0.47
2:1:1028:C:H2'	2:1:1029:U:C6	2.49	0.47
2:1:2208:C:H2'	2:1:2209:C:O4'	2.14	0.47
10:A:623:C:H2'	10:A:624:U:C6	2.50	0.47
10:A:679:C:H2'	10:A:680:C:H6	1.79	0.47
10:A:1202:A:H4'	21:L:44:LYS:HE3	1.97	0.47
13:D:73:ASP:HB3	13:D:99:ILE:HD13	1.95	0.47
35:Z:11:LYS:O	35:Z:23:PHE:HA	2.14	0.47
39:d:32:PHE:HZ	39:d:59:SER:HB2	1.80	0.47
53:s:28:ASP:HB2	53:s:32:ARG:HH21	1.79	0.47
2:1:716:G:O2'	2:1:717:A:OP1	2.23	0.47
2:1:2385:C:H2'	2:1:2386:U:H6	1.78	0.47
2:1:2506:G:H5''	50:p:249:LYS:HE3	1.94	0.47
2:1:3261:A:H2'	2:1:3262:U:C6	2.50	0.47
10:A:177:A:N6	17:H:202:ARG:HH21	2.12	0.47
10:A:216:A:C6	10:A:829:A:H1'	2.49	0.47
10:A:444:A:N6	10:A:459:G:H21	2.12	0.47
10:A:988:A:H2'	10:A:990:A:C8	2.49	0.47
14:E:178:MET:HB2	14:E:181:GLY:O	2.14	0.47
15:F:11:ARG:HA	15:F:28:ALA:HB2	1.96	0.47
43:h:34:LEU:HD12	43:h:42:LEU:HD12	1.96	0.47
2:1:2210:A:H2'	2:1:2211:A:C8	2.49	0.47
2:1:2485:U:H2'	2:1:2486:U:H6	1.79	0.47
10:A:733:U:O2'	33:X:122:SER:O	2.31	0.47
10:A:1566:U:H2'	10:A:1567:C:C6	2.48	0.47
15:F:100:ARG:HH21	15:F:118:GLU:HG2	1.79	0.47
24:O:102:LEU:HD23	24:O:102:LEU:HA	1.71	0.47
30:U:63:ARG:O	30:U:67:LEU:HD23	2.14	0.47
42:g:181:GLN:HE21	42:g:190:LEU:H	1.60	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:j:39:GLY:HA2	44:j:93:LYS:HG2	1.96	0.47
55:u:105:LEU:HD22	55:u:109:GLU:HB3	1.97	0.47
55:u:120:ARG:NH1	57:w:186:THR:HG23	2.28	0.47
72:AL:43:PHE:HE1	72:AL:66:GLN:HG2	1.79	0.47
2:1:429:U:H2'	2:1:430:G:H8	1.79	0.47
2:1:771:A:N6	81:1:3407:GET:H531	2.29	0.47
2:1:777:G:N7	81:1:3404:GET:H712	2.30	0.47
2:1:1552:C:C5	81:1:3406:GET:H131	2.49	0.47
2:1:2385:C:H2'	2:1:2386:U:C6	2.50	0.47
2:1:2870:G:N7	74:AN:49:LYS:HE3	2.29	0.47
10:A:474:U:H5''	10:A:475:A:O4'	2.14	0.47
10:A:583:A:H2'	10:A:584:G:C8	2.49	0.47
10:A:613:A:O2'	10:A:619:A:N1	2.44	0.47
10:A:933:A:H2'	10:A:934:C:C6	2.50	0.47
16:G:25:LEU:HD11	28:R:56:LEU:HD23	1.96	0.47
16:G:73:THR:HG22	16:G:91:GLU:OE2	2.15	0.47
18:I:6:LEU:HD23	18:I:38:GLN:HB3	1.95	0.47
20:K:151:ASP:O	20:K:155:HIS:ND1	2.46	0.47
22:M:22:ASN:HB3	22:M:25:ALA:HB2	1.96	0.47
23:N:57:ALA:HB2	23:N:124:LYS:HA	1.97	0.47
26:Q:61:ARG:NE	26:Q:88:GLU:OE2	2.46	0.47
43:h:110:ASP:HB2	43:h:128:ARG:HD2	1.96	0.47
53:s:137:ARG:O	53:s:141:ARG:HG2	2.14	0.47
54:t:169:TYR:CD2	62:AB:132:LYS:HG3	2.49	0.47
1:0:8:GLN:HG2	1:0:62:ASN:HB2	1.97	0.47
2:1:258:U:H2'	2:1:259:C:H6	1.79	0.47
2:1:374:A:N3	2:1:376:G:H5''	2.29	0.47
2:1:2656:C:O2'	53:s:99:THR:HG21	2.14	0.47
80:1:3401:SPK:H9B	80:1:3401:SPK:H6B	1.66	0.47
10:A:265:U:H2'	10:A:266:C:H6	1.79	0.47
10:A:512:G:O2'	10:A:513:A:H8	1.95	0.47
10:A:530:U:OP1	35:Z:64:PHE:HA	2.15	0.47
10:A:1783:C:H5	37:b:6:ALA:H	1.60	0.47
13:D:107:GLY:HA3	13:D:131:ILE:HD13	1.97	0.47
14:E:12:LEU:HD23	31:V:28:THR:HG23	1.96	0.47
15:F:103:TYR:HB2	15:F:182:MET:HE2	1.97	0.47
15:F:181:VAL:HG12	15:F:227:VAL:HA	1.97	0.47
15:F:183:VAL:HG13	15:F:220:THR:HG21	1.96	0.47
16:G:183:SER:OG	16:G:190:ILE:HA	2.14	0.47
19:J:103:GLN:HA	19:J:171:LEU:O	2.15	0.47
20:K:137:GLY:HA2	20:K:155:HIS:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:L:11:ILE:O	21:L:15:LEU:HB2	2.14	0.47
28:R:124:GLU:HG2	28:R:133:ALA:HB1	1.97	0.47
35:Z:39:GLU:HB3	35:Z:43:LYS:NZ	2.29	0.47
35:Z:62:THR:HA	35:Z:69:SER:HA	1.95	0.47
36:a:60:VAL:HG23	36:a:101:TYR:HB2	1.97	0.47
43:h:291:TRP:CD2	43:h:298:LEU:HD13	2.50	0.47
48:n:65:SER:HB2	48:n:75:LEU:HD23	1.96	0.47
52:r:54:SER:HB2	52:r:135:ILE:HD11	1.97	0.47
52:r:179:ASP:OD1	52:r:180:GLU:N	2.47	0.47
54:t:28:GLN:HG3	56:v:200:TRP:HZ3	1.80	0.47
64:AD:19:THR:HG21	64:AD:94:ILE:HD12	1.95	0.47
64:AD:28:GLY:O	64:AD:32:VAL:HG23	2.15	0.47
69:AI:92:LEU:HD22	69:AI:96:GLU:HB3	1.97	0.47
1:0:84:ARG:HD3	4:3:89:G:H4'	1.97	0.47
2:1:72:A:C4	70:AJ:14:ARG:HD2	2.50	0.47
2:1:407:A:C2	5:4:17:A:H1'	2.50	0.47
2:1:2260:U:O2	2:1:2288:U:H4'	2.14	0.47
10:A:918:A:OP2	37:b:37:LYS:HE3	2.14	0.47
16:G:133:VAL:HG22	16:G:198:LEU:HD23	1.96	0.47
30:U:20:GLN:HG2	30:U:24:ARG:NH1	2.29	0.47
46:l:139:ARG:NH2	46:l:241:PRO:HG2	2.14	0.47
50:p:172:LYS:HG2	50:p:227:TYR:CD2	2.49	0.47
56:v:114:ARG:CG	56:v:137:PRO:HG3	2.45	0.47
2:1:1556:G:N7	8:8:36:LYS:NZ	2.42	0.47
2:1:3039:C:H3'	60:z:62:ARG:HH22	1.79	0.47
5:4:149:A:H2'	5:4:150:G:C8	2.50	0.47
11:B:84:ARG:HD3	11:B:203:PHE:O	2.15	0.47
11:B:126:PRO:HB2	11:B:152:PRO:HD2	1.97	0.47
13:D:44:LYS:HD2	13:D:238:TYR:CE1	2.50	0.47
13:D:111:LYS:HD3	13:D:122:ALA:CB	2.43	0.47
14:E:214:ASP:CG	14:E:215:GLU:H	2.23	0.47
24:O:100:LYS:O	24:O:103:GLU:HG2	2.15	0.47
27:T:36:ARG:HG2	27:T:105:LEU:HD23	1.97	0.47
30:U:117:SER:HB3	30:U:123:ARG:HG2	1.96	0.47
53:s:40:LEU:HD13	53:s:114:ILE:HD11	1.97	0.47
60:z:38:ARG:O	60:z:42:ARG:HG3	2.14	0.47
2:1:2887:U:C5	45:k:7:GLU:HG3	2.50	0.47
10:A:529:C:HO2'	10:A:530:U:P	2.37	0.47
10:A:656:C:H1'	10:A:674:C:N4	2.27	0.47
13:D:54:HIS:CE1	13:D:234:PRO:HD3	2.50	0.47
17:H:10:ASN:HB3	17:H:128:THR:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:a:88:ILE:O	36:a:104:ALA:HB2	2.15	0.47
45:k:256:HIS:HA	45:k:257:PRO:C	2.39	0.47
54:t:124:VAL:HG21	69:AI:120:ALA:HB3	1.97	0.47
2:1:2854:U:H2'	2:1:2855:U:C6	2.51	0.46
10:A:29:U:H2'	10:A:30:G:H8	1.80	0.46
10:A:116:U:H2'	10:A:117:U:C6	2.50	0.46
10:A:1369:G:OP1	31:V:88:ARG:NH2	2.48	0.46
12:C:81:TYR:CD2	12:C:109:LYS:HE2	2.50	0.46
17:H:32:MET:HE3	17:H:54:GLY:HA2	1.97	0.46
45:k:46:PHE:CE2	45:k:205:VAL:HG12	2.50	0.46
62:AB:76:ASP:HB3	62:AB:116:GLY:HA3	1.97	0.46
2:1:1814:U:H2'	2:1:1815:U:C6	2.49	0.46
2:1:2322:U:H2'	2:1:2323:A:C8	2.51	0.46
2:1:2966:A:H2'	2:1:2967:A:O4'	2.15	0.46
15:F:103:TYR:HB3	15:F:190:GLY:HA2	1.97	0.46
18:I:67:ARG:NH2	18:I:124:ASP:OD1	2.47	0.46
19:J:145:VAL:HA	19:J:148:LYS:HG2	1.96	0.46
27:T:121:SER:O	27:T:125:ILE:HG12	2.15	0.46
34:Y:19:ARG:O	34:Y:23:ARG:HG3	2.14	0.46
40:e:30:LEU:HA	40:e:39:CYS:HA	1.96	0.46
43:h:24:ALA:O	43:h:33:LEU:HD12	2.15	0.46
1:0:95:ARG:HG2	1:0:95:ARG:HH11	1.78	0.46
2:1:788:G:H2'	2:1:789:C:C6	2.50	0.46
2:1:1684:U:H2'	2:1:1685:U:C5	2.51	0.46
2:1:2925:U:H2'	2:1:2926:U:H2'	1.97	0.46
2:1:3261:A:H2'	2:1:3262:U:H6	1.80	0.46
10:A:66:U:C6	17:H:133:LEU:HD22	2.50	0.46
10:A:1092:G:O2'	10:A:1093:G:H5'	2.14	0.46
13:D:123:ALA:HA	13:D:126:ILE:HG22	1.96	0.46
16:G:212:LYS:NZ	16:G:216:GLU:OE2	2.47	0.46
51:q:90:MET:HE2	51:q:179:ILE:HG22	1.96	0.46
52:r:135:ILE:HG22	52:r:136:MET:HG3	1.97	0.46
58:x:94:LEU:HA	58:x:94:LEU:HD23	1.83	0.46
61:AA:116:LYS:O	61:AA:120:GLU:HG3	2.14	0.46
2:1:58:G:H2'	5:4:33:A:O2'	2.16	0.46
2:1:2107:U:H2'	2:1:2108:G:C8	2.50	0.46
2:1:2397:A:H2'	2:1:2398:C:C6	2.51	0.46
2:1:3236:G:N2	48:n:108:GLU:OE1	2.46	0.46
10:A:584:G:OP1	41:f:23:LYS:HE2	2.15	0.46
10:A:650:G:H8	10:A:650:G:OP2	1.98	0.46
15:F:151:ASP:OD2	17:H:215:ARG:NH2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:110:GLN:NE2	20:K:126:ARG:HB2	2.31	0.46
27:T:116:LEU:HD21	27:T:123:ARG:HH21	1.80	0.46
29:S:106:THR:O	29:S:110:VAL:HG23	2.15	0.46
43:h:110:ASP:O	43:h:128:ARG:N	2.37	0.46
43:h:250:ALA:HB1	43:h:289:LEU:HD23	1.97	0.46
47:m:55:PHE:CE2	47:m:60:ILE:HG12	2.49	0.46
49:o:188:THR:O	49:o:190:GLY:N	2.48	0.46
53:s:7:ASN:OD1	53:s:8:VAL:N	2.49	0.46
78:AT:54:G:H2'	78:AT:55:U:C6	2.50	0.46
2:1:1466:U:H2'	2:1:1467:U:C6	2.51	0.46
2:1:1543:G:H5''	56:v:108:ARG:NH1	2.31	0.46
2:1:1817:U:O4	68:AH:67:LYS:NZ	2.46	0.46
10:A:637:U:P	18:I:113:THR:HB	2.56	0.46
10:A:1226:G:H4'	26:Q:77:LYS:O	2.16	0.46
12:C:26:ARG:HA	12:C:50:ARG:NH1	2.30	0.46
12:C:131:ASP:OD1	12:C:131:ASP:N	2.48	0.46
14:E:222:PRO:HG2	43:h:190:ILE:HD11	1.96	0.46
20:K:123:HIS:CE1	41:f:37:ARG:HB2	2.51	0.46
28:R:78:TYR:O	28:R:81:ARG:HG2	2.16	0.46
51:q:33:GLU:OE2	51:q:35:THR:OG1	2.30	0.46
59:y:83:VAL:O	59:y:103:ALA:HA	2.16	0.46
2:1:726:G:H5''	59:y:43:PRO:HB2	1.97	0.46
2:1:976:A:N6	2:1:1100:G:O2'	2.49	0.46
2:1:2386:U:H5'	63:AC:1:MET:SD	2.56	0.46
24:O:110:ASP:O	24:O:114:ARG:HG2	2.16	0.46
31:V:41:ILE:HD13	31:V:51:LYS:HD2	1.97	0.46
34:Y:55:GLU:HG2	34:Y:56:LYS:H	1.80	0.46
35:Z:29:HIS:NE2	35:Z:33:ALA:O	2.35	0.46
36:a:77:ARG:HB3	36:a:81:ARG:HH12	1.81	0.46
47:m:218:LYS:HZ2	47:m:222:ILE:HD11	1.80	0.46
70:AJ:36:THR:O	70:AJ:40:ARG:HG3	2.16	0.46
2:1:1059:G:O2'	2:1:1093:G:N2	2.49	0.46
6:6:135:VAL:HG11	7:7:26:SER:OG	2.15	0.46
10:A:255:A:H1'	19:J:73:SER:OG	2.16	0.46
10:A:302:U:H2'	10:A:303:C:C6	2.51	0.46
10:A:510:A:OP2	20:K:172:VAL:HB	2.16	0.46
10:A:1276:G:N2	10:A:1309:G:H22	2.11	0.46
16:G:109:LYS:O	16:G:113:ILE:HG13	2.15	0.46
30:U:64:HIS:ND1	30:U:79:LEU:HD22	2.31	0.46
45:k:57:VAL:HG22	45:k:73:VAL:HG22	1.97	0.46
47:m:97:ALA:O	47:m:101:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:r:38:ARG:NH1	52:r:83:ASP:O	2.47	0.46
62:AB:60:TYR:CG	62:AB:63:LYS:HD3	2.50	0.46
2:1:3129:C:H2'	2:1:3130:C:H6	1.81	0.46
10:A:29:U:H2'	10:A:30:G:C8	2.51	0.46
10:A:478:G:C6	10:A:479:A:C6	3.03	0.46
10:A:1369:G:HO2'	10:A:1370:A:P	2.35	0.46
11:B:15:LYS:NZ	29:S:117:ILE:HB	2.30	0.46
14:E:148:ALA:O	14:E:149:LYS:HE2	2.15	0.46
15:F:176:ASP:OD1	15:F:177:THR:N	2.43	0.46
16:G:187:ILE:HD13	36:a:66:VAL:HG11	1.98	0.46
20:K:141:VAL:HG11	20:K:146:PHE:CG	2.50	0.46
47:m:75:PHE:CE1	47:m:112:LYS:HE2	2.50	0.46
48:n:39:LEU:HD13	48:n:83:VAL:HG11	1.96	0.46
2:1:30:C:H4'	56:v:96:LYS:HE2	1.98	0.46
2:1:2649:G:O2'	2:1:2651:A:N1	2.44	0.46
11:B:17:LEU:HD13	11:B:50:ILE:HG23	1.96	0.46
13:D:142:ASN:HB2	32:W:3:ASN:HA	1.97	0.46
14:E:174:ARG:HB2	14:E:185:ILE:HD11	1.97	0.46
15:F:151:ASP:HB3	15:F:154:ILE:HG13	1.98	0.46
23:N:96:LEU:HB3	23:N:100:TRP:CZ2	2.50	0.46
26:Q:56:LEU:HD23	26:Q:83:MET:SD	2.56	0.46
73:AM:20:ASN:ND2	73:AM:42:ARG:O	2.36	0.46
2:1:1543:G:OP1	56:v:108:ARG:NH2	2.49	0.46
2:1:2405:U:H2'	2:1:2406:U:C6	2.51	0.46
2:1:2978:A:H2'	2:1:2979:U:O4'	2.15	0.46
10:A:93:A:C6	10:A:396:G:C6	3.04	0.46
10:A:295:U:OP1	15:F:37:LYS:HE3	2.16	0.46
10:A:872:A:H5''	25:P:115:PRO:HB3	1.97	0.46
10:A:1226:G:H5'	26:Q:77:LYS:HB2	1.98	0.46
12:C:194:GLY:O	12:C:198:GLU:HG3	2.15	0.46
14:E:72:SER:OG	21:L:20:VAL:HG11	2.16	0.46
18:I:171:LYS:HE2	18:I:171:LYS:HB3	1.68	0.46
19:J:141:ARG:HB3	19:J:146:GLU:HG2	1.98	0.46
72:AL:25:VAL:HG11	72:AL:66:GLN:NE2	2.30	0.46
2:1:28:C:H4'	2:1:61:A:H4'	1.98	0.45
2:1:169:G:N7	2:1:249:G:N2	2.63	0.45
2:1:1782:G:H2'	2:1:1783:A:C8	2.51	0.45
2:1:3309:A:N3	2:1:3309:A:H2'	2.30	0.45
9:9:86:GLN:HB3	9:9:94:SER:OG	2.16	0.45
10:A:211:A:H2'	10:A:212:G:O4'	2.15	0.45
10:A:245:A:O2'	22:M:37:ASP:O	2.28	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1393:U:H2'	10:A:1394:G:C8	2.51	0.45
21:L:13:GLN:O	21:L:17:GLN:HG3	2.16	0.45
21:L:88:PRO:C	21:L:90:THR:H	2.25	0.45
27:T:4:VAL:N	36:a:82:GLN:OE1	2.32	0.45
31:V:41:ILE:HG23	31:V:51:LYS:HE3	1.98	0.45
45:k:46:PHE:CZ	45:k:84:MET:HG3	2.51	0.45
55:u:121:ARG:O	55:u:125:LYS:HG2	2.16	0.45
60:z:162:ARG:O	60:z:165:ARG:HG2	2.16	0.45
65:AE:51:ASP:OD1	65:AE:91:TYR:OH	2.33	0.45
2:1:602:A:H2'	2:1:603:C:C6	2.51	0.45
10:A:93:A:O2'	15:F:4:GLY:HA3	2.16	0.45
10:A:137:A:O4'	10:A:139:U:H5'	2.16	0.45
10:A:141:G:P	17:H:139:ASN:HD22	2.39	0.45
10:A:676:G:N2	10:A:677:G:H22	2.14	0.45
10:A:767:G:H2'	10:A:768:C:C6	2.51	0.45
10:A:827:C:H3'	10:A:828:U:O4'	2.16	0.45
11:B:140:ASN:ND2	32:W:31:SER:O	2.37	0.45
13:D:237:VAL:HG23	13:D:238:TYR:CD2	2.50	0.45
27:T:16:ARG:HB2	53:s:110:ILE:HD12	1.97	0.45
28:R:73:HIS:O	28:R:77:VAL:HG23	2.16	0.45
31:V:21:ILE:HG13	31:V:99:VAL:HG21	1.98	0.45
47:m:289:LYS:HA	47:m:292:GLU:HG2	1.98	0.45
78:PT:22:A:N6	78:PT:47:G:H2'	2.26	0.45
2:1:38:A:H5''	62:AB:35:ALA:HB2	1.97	0.45
2:1:1172:C:H2'	2:1:1173:G:H21	1.82	0.45
2:1:1655:U:H2'	2:1:1656:C:C6	2.50	0.45
2:1:2823:A:O2'	78:AT:64:G:O2'	2.28	0.45
10:A:25:C:H4'	10:A:26:A:O5'	2.14	0.45
10:A:479:A:O2'	10:A:480:U:O5'	2.34	0.45
10:A:598:U:OP2	34:Y:108:GLY:HA2	2.17	0.45
10:A:815:U:O2'	10:A:816:U:H6	1.99	0.45
10:A:907:G:O2'	10:A:908:A:H5'	2.16	0.45
14:E:23:ASN:O	14:E:27:THR:HG23	2.17	0.45
19:J:83:TYR:HB3	19:J:101:VAL:HB	1.98	0.45
28:R:49:GLU:OE1	28:R:81:ARG:NH2	2.45	0.45
30:U:31:PRO:HG2	30:U:34:VAL:HG13	1.97	0.45
31:V:41:ILE:HD11	31:V:54:PRO:HD3	1.97	0.45
78:AT:55:U:H2'	78:AT:56:U:O4'	2.16	0.45
2:1:805:G:OP1	81:1:3412:GET:N12	2.50	0.45
2:1:1552:C:H5'	2:1:1552:C:O2	2.16	0.45
2:1:2557:G:H2'	2:1:2557:G:N3	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2647:C:OP2	2:1:2648:A:O2'	2.18	0.45
10:A:157:U:C6	35:Z:117:LYS:HG2	2.51	0.45
14:E:46:LYS:HE2	14:E:86:ALA:HB2	1.98	0.45
18:I:85:HIS:CE1	18:I:161:LYS:HG2	2.50	0.45
22:M:17:PRO:O	22:M:19:ILE:HD12	2.16	0.45
25:P:117:PRO:HB3	25:P:120:SER:HB3	1.99	0.45
35:Z:53:ASP:HB2	35:Z:79:VAL:HG22	1.98	0.45
57:w:122:PRO:HA	57:w:125:LEU:HD12	1.99	0.45
66:AF:87:LEU:HD13	66:AF:116:LEU:HD22	1.97	0.45
2:1:253:A:H2'	2:1:254:A:C8	2.51	0.45
2:1:716:G:OP1	62:AB:117:ARG:NH2	2.49	0.45
2:1:1199:A:H2'	2:1:1200:A:C8	2.51	0.45
2:1:1562:G:H2'	2:1:1563:A:O4'	2.17	0.45
5:4:146:U:H2'	5:4:147:U:C6	2.52	0.45
10:A:522:U:O2	10:A:525:A:H8	2.00	0.45
10:A:560:G:H2'	10:A:561:U:O2	2.16	0.45
10:A:650:G:H2'	10:A:651:C:H5'	1.99	0.45
10:A:1575:G:O6	10:A:1595:U:O4	2.35	0.45
11:B:200:ASP:O	11:B:203:PHE:HB2	2.17	0.45
12:C:23:PRO:HB3	12:C:26:ARG:NH2	2.32	0.45
16:G:63:GLN:NE2	16:G:66:ASN:HD22	2.15	0.45
19:J:121:LEU:HD22	19:J:163:ASP:HB2	1.98	0.45
19:J:197:PHE:O	19:J:201:ARG:HG2	2.16	0.45
20:K:127:VAL:HG13	41:f:33:ARG:HH22	1.81	0.45
21:L:12:HIS:HA	21:L:15:LEU:HB3	1.98	0.45
40:e:46:LYS:O	40:e:50:ILE:HG13	2.16	0.45
43:h:33:LEU:HD11	43:h:299:PHE:CE1	2.51	0.45
45:k:81:THR:CB	45:k:205:VAL:HG11	2.46	0.45
45:k:304:THR:HG22	45:k:305:ILE:N	2.30	0.45
54:t:131:LYS:HB2	54:t:134:GLU:OE1	2.15	0.45
67:AG:38:PRO:O	67:AG:42:LYS:HG3	2.16	0.45
72:AL:30[A]:LYS:HE3	72:AL:30[A]:LYS:HB3	1.73	0.45
2:1:619:A:H2'	2:1:620:A:C8	2.51	0.45
2:1:1561:U:HO2'	2:1:1562:G:P	2.39	0.45
2:1:1923:G:C8	77:AQ:16:VAL:HG12	2.52	0.45
10:A:60:U:H2'	10:A:62:A:H2	1.81	0.45
10:A:366:U:H2'	10:A:367:A:O4'	2.17	0.45
10:A:1065:U:O2'	10:A:1066:A:H5'	2.17	0.45
11:B:73:VAL:O	11:B:95:ALA:HB1	2.17	0.45
12:C:26:ARG:HA	12:C:50:ARG:CZ	2.47	0.45
14:E:76:LYS:HZ1	21:L:20:VAL:C	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:138:ALA:HA	17:H:141:ILE:HD12	1.98	0.45
19:J:3:ILE:H	19:J:3:ILE:HD12	1.82	0.45
36:a:93:LEU:HD23	36:a:94:LYS:N	2.32	0.45
39:d:10:ALA:HB1	39:d:30:VAL:HB	1.98	0.45
51:q:50:ASN:OD1	55:u:2:SER:HB2	2.16	0.45
66:AF:80:VAL:HG13	66:AF:112:LYS:CD	2.46	0.45
72:AL:27:VAL:HG11	72:AL:39:LYS:HE3	1.99	0.45
2:1:1028:C:H2'	2:1:1029:U:O4'	2.17	0.45
2:1:1060:A:H4'	2:1:1061:A:O5'	2.16	0.45
2:1:2527:G:C8	50:p:34:ASN:ND2	2.84	0.45
2:1:3193:C:H4'	2:1:3194:G:O5'	2.16	0.45
10:A:149:G:C2	10:A:150:U:C4	3.05	0.45
10:A:330:U:OP1	19:J:56:ARG:NH2	2.50	0.45
10:A:507:G:H2'	10:A:508:G:C8	2.51	0.45
10:A:773:A:OP1	15:F:108:LYS:NZ	2.49	0.45
10:A:904:A:H2'	10:A:905:C:C6	2.52	0.45
16:G:39:GLU:OE2	16:G:41:LYS:HD3	2.17	0.45
21:L:32:HIS:HD2	21:L:35:ILE:HB	1.81	0.45
22:M:16:GLN:HB3	22:M:19:ILE:HD13	1.99	0.45
43:h:33:LEU:HB3	43:h:45:TRP:HB2	1.99	0.45
47:m:243:ALA:O	47:m:247:ILE:HG13	2.17	0.45
53:s:17:LEU:HD11	53:s:127:PHE:HB3	1.98	0.45
68:AH:106[B]:LYS:HB3	68:AH:106[B]:LYS:HE3	1.74	0.45
1:0:113:ARG:NH1	2:1:1207:U:O2'	2.49	0.45
2:1:1284:U:H2'	2:1:1285:G:H8	1.82	0.45
2:1:2347:G:H2'	2:1:2348:G:C8	2.51	0.45
2:1:2967:A:H4'	5:4:1:A:C2	2.52	0.45
10:A:151:G:H2'	10:A:152:G:H8	1.81	0.45
10:A:188:U:H1'	10:A:194:G:N2	2.31	0.45
10:A:1193:A:H5''	10:A:1194:C:OP2	2.17	0.45
10:A:1335:U:H2'	10:A:1336:G:H8	1.82	0.45
10:A:1716:C:H2'	10:A:1717:A:O4'	2.17	0.45
12:C:61:LEU:HD23	12:C:96:LEU:HD21	1.97	0.45
15:F:233:GLY:C	15:F:234:LYS:HD2	2.41	0.45
43:h:38:ARG:HD3	43:h:68:ILE:HG23	1.98	0.45
51:q:41:ILE:HG22	51:q:43:VAL:HG13	1.99	0.45
2:1:277:G:H2'	2:1:278:U:C6	2.52	0.45
2:1:2407:G:H2'	2:1:2408:A:C8	2.52	0.45
10:A:122:U:H2'	10:A:123:G:H5''	1.99	0.45
10:A:500:U:H1'	10:A:501:G:N7	2.31	0.45
10:A:1145:A:H2'	10:A:1146:C:H6	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1205:C:H5''	21:L:52:LYS:HZ2	1.81	0.45
10:A:1477:U:H4'	10:A:1478:A:H5'	1.99	0.45
15:F:125:LYS:O	15:F:141:THR:HA	2.16	0.45
20:K:123:HIS:HB3	41:f:33:ARG:NH1	2.32	0.45
21:L:38:ARG:HD3	21:L:41:PHE:CZ	2.52	0.45
25:P:79:ARG:HB3	25:P:113:VAL:HG23	1.99	0.45
25:P:84:THR:O	25:P:123:ARG:HD2	2.17	0.45
25:P:98:ARG:HD2	37:b:49:ALA:HB2	1.97	0.45
27:T:113:LEU:O	27:T:117:LYS:HG3	2.16	0.45
30:U:25:GLN:HE22	30:U:27:LYS:HE3	1.81	0.45
42:g:161:ARG:HD2	42:g:174:MET:SD	2.57	0.45
46:l:91:PHE:O	46:l:99:ARG:HD3	2.17	0.45
2:1:671:U:OP1	59:y:21:SER:OG	2.27	0.45
2:1:1918:A:H2'	2:1:1919:C:O4'	2.17	0.45
2:1:3247:A:H2'	2:1:3248:U:C6	2.52	0.45
5:4:81:A:H2'	5:4:82:U:C6	2.52	0.45
10:A:480:U:H2'	10:A:481:A:N3	2.32	0.45
10:A:1072:A:H5'	10:A:1283:U:C5	2.52	0.45
10:A:1213:G:C8	23:N:119:SER:HB3	2.51	0.45
12:C:24:PHE:HA	12:C:27:LYS:HG2	1.99	0.45
14:E:43:THR:OG1	14:E:46:LYS:O	2.21	0.45
14:E:110:LEU:HD23	14:E:176:VAL:HG21	1.99	0.45
35:Z:21:ARG:HH21	35:Z:75:ILE:HG13	1.81	0.45
45:k:108:GLU:HG3	45:k:137:TYR:CG	2.52	0.45
49:o:158:ARG:HG3	49:o:201:TRP:CG	2.52	0.45
2:1:592:U:H2'	2:1:607:G:O6	2.17	0.44
2:1:740:A:H4'	59:y:142:GLY:O	2.18	0.44
2:1:3169:C:H2'	2:1:3170:G:C8	2.52	0.44
2:1:3318:G:OP1	19:J:77:ARG:NH2	2.50	0.44
5:4:38:U:O2'	69:AI:83:LYS:HE2	2.16	0.44
10:A:476:A:N1	10:A:508:G:O6	2.49	0.44
10:A:1155:G:C2	10:A:1156:A:C8	3.04	0.44
10:A:1214:G:O6	23:N:46:ARG:HB3	2.17	0.44
10:A:1626:C:H2'	10:A:1627:C:O4'	2.17	0.44
10:A:1759:C:P	75:AO:2:ARG:HD2	2.57	0.44
18:I:21:PHE:CE1	18:I:77:LEU:HD11	2.49	0.44
53:s:32:ARG:HG2	53:s:120:ILE:HA	2.00	0.44
2:1:271:C:H2'	2:1:272:G:O4'	2.16	0.44
2:1:696:U:H2'	2:1:697:A:O4'	2.17	0.44
2:1:1816:U:OP2	2:1:1817:U:H5''	2.17	0.44
2:1:2995:U:H2'	2:1:2996:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:3302:G:H2'	2:1:3303:C:C6	2.53	0.44
10:A:775:A:H2'	10:A:776:U:O4'	2.18	0.44
10:A:1192:C:H42	10:A:1442:C:H5	1.65	0.44
10:A:1668:A:H1'	17:H:66:GLY:HA2	1.98	0.44
10:A:1672:G:H2'	10:A:1674:U:N3	2.32	0.44
15:F:86:PHE:HE2	15:F:226:PHE:CG	2.35	0.44
15:F:105:VAL:CG2	15:F:191:ARG:HG2	2.41	0.44
51:q:8:GLN:HB3	51:q:72:LYS:HD3	1.99	0.44
51:q:106:LYS:NZ	51:q:125:GLU:OE1	2.30	0.44
58:x:168:LEU:O	58:x:173:ARG:NH1	2.49	0.44
59:y:178:ARG:NH2	62:AB:50:PRO:HG2	2.31	0.44
78:AT:67:C:H2'	78:AT:68:C:H6	1.80	0.44
2:1:172:C:O2'	2:1:173:C:OP1	2.31	0.44
2:1:189:U:OP1	9:9:37:LYS:NZ	2.37	0.44
2:1:1080:A:H2'	2:1:1081:A:C8	2.52	0.44
2:1:2668:A:H2'	2:1:2669:A:C8	2.52	0.44
10:A:578:A:O2'	10:A:580:U:OP1	2.35	0.44
10:A:1263:G:O6	10:A:1416:U:H5	2.01	0.44
10:A:1435:U:H2'	10:A:1436:U:C6	2.52	0.44
22:M:23:PRO:O	22:M:29:LYS:NZ	2.51	0.44
24:O:25:TRP:O	24:O:27:LYS:NZ	2.40	0.44
25:P:65:LYS:O	25:P:69:VAL:HG23	2.18	0.44
27:T:62:THR:O	27:T:66:LEU:HD13	2.17	0.44
36:a:69:LEU:HB3	36:a:71:ILE:HG23	1.99	0.44
43:h:160:SER:HB3	43:h:204:ASP:O	2.17	0.44
48:n:81:ARG:HD3	48:n:81:ARG:HA	1.76	0.44
49:o:108:GLN:NE2	49:o:204:LYS:HG2	2.32	0.44
59:y:19:PRO:HG3	59:y:30:VAL:HG21	2.00	0.44
69:AI:118:ILE:HG22	69:AI:119:LYS:N	2.33	0.44
78:AT:3:C:H2'	78:AT:4:G:H8	1.82	0.44
2:1:1093:G:H5''	3:2:129:LYS:HE3	1.99	0.44
2:1:1104:U:H2'	2:1:1105:U:H6	1.83	0.44
4:3:3:U:H2'	4:3:4:U:C6	2.51	0.44
10:A:78:A:H2'	10:A:79:C:C6	2.53	0.44
10:A:85:A:N3	10:A:146:A:O2'	2.50	0.44
10:A:151:G:H2'	10:A:152:G:C8	2.51	0.44
10:A:738:A:OP1	15:F:187:ARG:N	2.45	0.44
10:A:903:U:H2'	10:A:904:A:H8	1.76	0.44
10:A:1317:C:O2'	14:E:163:GLN:HB3	2.17	0.44
10:A:1635:A:H2'	10:A:1636:C:H6	1.83	0.44
14:E:142:LYS:HA	14:E:148:ALA:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:137:ARG:HE	17:H:140:HIS:CD2	2.36	0.44
18:I:74:THR:HG23	18:I:86:VAL:HG23	1.99	0.44
20:K:163:PRO:HB3	20:K:169:ALA:O	2.17	0.44
24:O:25:TRP:CD2	38:c:82:LYS:HD3	2.53	0.44
43:h:40:LYS:HG2	43:h:67:HIS:O	2.18	0.44
45:k:187:SER:O	45:k:191:LYS:HG3	2.18	0.44
48:n:46:PHE:HB3	48:n:49:LYS:HG3	2.00	0.44
72:AL:58:ASP:HB2	72:AL:61:LYS:HB3	2.00	0.44
2:1:685:U:OP2	54:t:36:ARG:NH2	2.45	0.44
2:1:1387:C:C2	66:AF:104:ARG:HD3	2.53	0.44
3:2:44:ALA:HB2	3:2:53:PRO:HG2	1.99	0.44
10:A:1420:U:H2'	10:A:1422:A:C5'	2.45	0.44
16:G:140:SER:HB3	16:G:210:ALA:HB1	1.98	0.44
19:J:142:SER:O	19:J:145:VAL:HG12	2.18	0.44
32:W:71:ARG:HG3	32:W:83:TRP:CE2	2.52	0.44
54:t:4:SER:O	62:AB:44:ASN:ND2	2.49	0.44
55:u:118:LYS:HG2	55:u:121:ARG:HH21	1.83	0.44
2:1:1045:C:H2'	2:1:1046:U:C6	2.53	0.44
2:1:2201:A:H2'	2:1:2202:A:C8	2.52	0.44
2:1:2876:U:H2'	2:1:2877:U:H6	1.83	0.44
2:1:3005:A:H2'	2:1:3006:C:H6	1.82	0.44
10:A:141:G:H2'	10:A:142:G:C8	2.52	0.44
10:A:249:A:H2	15:F:131:LEU:HD12	1.82	0.44
10:A:737:A:H5'	15:F:219:VAL:HG13	2.00	0.44
10:A:1436:U:H2'	10:A:1437:C:C6	2.53	0.44
13:D:165:ILE:HB	13:D:192:TYR:HB2	2.00	0.44
15:F:205:PHE:HD2	15:F:221:ARG:NE	2.13	0.44
35:Z:60:PHE:HA	35:Z:70:THR:O	2.18	0.44
43:h:81:ALA:C	43:h:82:LEU:HD12	2.42	0.44
2:1:25:A:H2'	2:1:26:C:C6	2.52	0.44
2:1:560:C:OP2	55:u:70:ARG:HD2	2.18	0.44
2:1:623:A:H2'	2:1:624:U:C6	2.53	0.44
2:1:849:G:N7	77:AQ:2:THR:HG23	2.33	0.44
2:1:922:A:H2'	2:1:923:C:C6	2.53	0.44
2:1:1683:U:H5''	2:1:1684:U:O4'	2.18	0.44
2:1:3260:A:H2'	2:1:3261:A:H8	1.83	0.44
10:A:72:A:OP2	17:H:167:LYS:HE3	2.18	0.44
10:A:1057:C:H3'	10:A:1058:G:H5''	1.99	0.44
10:A:1205:C:H2'	10:A:1206:A:C8	2.53	0.44
11:B:204:TYR:CG	11:B:205:ARG:N	2.85	0.44
16:G:100:ASN:O	16:G:102:ARG:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:K:83:ILE:HG23	20:K:85:VAL:HG23	2.00	0.44
20:K:123:HIS:CE1	41:f:37:ARG:HD3	2.52	0.44
26:Q:24:ASP:HA	26:Q:27:GLU:HG2	2.00	0.44
47:m:41:LYS:HE2	47:m:41:LYS:HA	2.00	0.44
47:m:218:LYS:NZ	47:m:222:ILE:HD11	2.33	0.44
54:t:62:THR:O	54:t:65:TYR:N	2.41	0.44
61:AA:50:PRO:HD3	61:AA:68:VAL:HG12	1.98	0.44
2:1:1593:C:H5'	2:1:1692:A:H1'	2.00	0.44
2:1:2648:A:H4'	2:1:2649:G:O4'	2.17	0.44
10:A:524:A:P	35:Z:93:ARG:HH21	2.37	0.44
10:A:835:A:H2'	10:A:836:U:C6	2.53	0.44
10:A:1305:U:H3'	11:B:101:ARG:NH2	2.31	0.44
14:E:143:LEU:C	14:E:145:ALA:H	2.25	0.44
15:F:99:PHE:HE1	15:F:113:ARG:HE	1.66	0.44
27:T:13:HIS:O	27:T:15:LEU:HD12	2.18	0.44
30:U:64:HIS:CD2	30:U:68:ARG:NH1	2.86	0.44
33:X:40:VAL:HG11	33:X:103:ILE:HD12	2.00	0.44
52:r:103:LEU:HB2	52:r:108:ALA:HB1	1.99	0.44
1:0:95:ARG:HG2	1:0:95:ARG:NH1	2.32	0.44
2:1:214:G:H5''	9:9:12:ARG:HG3	2.00	0.44
2:1:733:A:H8	2:1:733:A:OP2	2.01	0.44
2:1:977:U:O2'	2:1:978:C:OP2	2.27	0.44
2:1:2126:U:H2'	2:1:2127:A:C5	2.52	0.44
2:1:2492:U:H5'	50:p:69:ARG:HG3	1.98	0.44
4:3:48:C:OP1	47:m:94:ASN:ND2	2.50	0.44
5:4:56:G:H2'	5:4:57:C:O4'	2.18	0.44
5:4:65:A:OP1	69:AI:53:ARG:HD3	2.18	0.44
6:6:23:MET:HE3	6:6:100:GLY:HA3	2.00	0.44
10:A:1218:G:H1	10:A:1237:C:H5	1.66	0.44
10:A:1433:C:O4'	42:g:122:ARG:NH2	2.51	0.44
10:A:1703:C:HO2'	10:A:1704:C:P	2.39	0.44
17:H:142:ARG:HE	17:H:153:VAL:CG2	2.25	0.44
19:J:117:TYR:CE2	19:J:156:ALA:HA	2.53	0.44
25:P:107:ILE:HG13	37:b:53:LEU:HD23	2.00	0.44
29:S:20:PHE:CE2	29:S:38:ILE:HD12	2.53	0.44
31:V:68:LYS:NZ	31:V:79:ASP:OD1	2.33	0.44
45:k:43:LEU:HB2	45:k:208:VAL:HG22	2.00	0.44
51:q:34:LEU:HB3	51:q:78:LEU:HD22	2.00	0.44
56:v:159:ARG:HB2	56:v:164:LEU:HB2	2.00	0.44
60:z:86:ASP:OD1	60:z:90:PRO:HA	2.17	0.44
70:AJ:3:LYS:HD2	70:AJ:12:LYS:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:398:A:H1'	2:1:1412:C:OP1	2.18	0.43
2:1:904:G:C4	81:1:3412:GET:H832	2.53	0.43
2:1:2538:A:C2	50:p:33:LYS:HG3	2.53	0.43
10:A:78:A:H2	17:H:174:LYS:HG3	1.82	0.43
10:A:151:G:O2'	10:A:152:G:OP1	2.31	0.43
10:A:1238:U:H5''	42:g:172:ILE:HG23	1.99	0.43
10:A:1584:A:C8	40:e:14:PHE:CD1	3.06	0.43
11:B:7:PHE:CE2	32:W:39:VAL:HG11	2.53	0.43
18:I:27:GLN:OE1	18:I:72:ARG:NH2	2.50	0.43
18:I:63:LEU:O	18:I:67:ARG:HG2	2.17	0.43
43:h:197:SER:OG	43:h:237:VAL:O	2.34	0.43
47:m:178:ASN:HA	47:m:183:TRP:CD2	2.53	0.43
49:o:182:LEU:HD21	49:o:200:LEU:HD11	2.00	0.43
68:AH:103:ARG:O	68:AH:107:GLU:HG3	2.17	0.43
70:AJ:61:ARG:NH2	70:AJ:93:ILE:HG23	2.33	0.43
1:0:130:GLU:OE1	1:0:130:GLU:N	2.50	0.43
2:1:74:G:H5'	54:t:58:VAL:HB	2.00	0.43
2:1:397:A:H5'	2:1:399:A:OP1	2.17	0.43
2:1:1911:A:H2'	2:1:1912:U:H6	1.83	0.43
2:1:3256:G:H2'	2:1:3257:A:H8	1.83	0.43
10:A:280:C:H2'	10:A:281:U:O4'	2.18	0.43
10:A:451:C:O2	10:A:451:C:H2'	2.18	0.43
11:B:9:LEU:HD13	11:B:54:TRP:HB2	2.01	0.43
13:D:51:ILE:HG23	13:D:56:LEU:HB2	1.99	0.43
14:E:104:GLU:OE2	14:E:174:ARG:NE	2.32	0.43
26:Q:20:VAL:HG12	26:Q:25:LEU:HB2	2.01	0.43
43:h:92:LEU:HD22	43:h:101:THR:HB	2.00	0.43
44:j:54:ARG:HG2	44:j:56:ALA:H	1.82	0.43
57:w:107:GLU:HG2	57:w:148:TRP:CZ2	2.53	0.43
2:1:755:U:H2'	2:1:756:G:O4'	2.19	0.43
2:1:2515:G:H1'	2:1:2516:U:O5'	2.18	0.43
10:A:532:A:H3'	10:A:533:A:H8	1.84	0.43
10:A:751:U:H5''	10:A:753:C:OP2	2.18	0.43
10:A:1325:U:O4	28:R:8:THR:HA	2.19	0.43
12:C:52:THR:HG23	12:C:54:LEU:H	1.84	0.43
12:C:129:THR:OG1	12:C:133:TYR:HB2	2.17	0.43
13:D:139:TRP:CZ3	20:K:61:THR:HG22	2.53	0.43
14:E:53:ALA:O	14:E:92:VAL:HG23	2.19	0.43
21:L:16:PHE:HE1	21:L:73:VAL:HG13	1.83	0.43
22:M:77:SER:HB3	22:M:85:ILE:CG1	2.47	0.43
35:Z:90:ARG:HA	35:Z:93:ARG:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:d:16:LEU:HB2	39:d:27:GLN:HB2	1.98	0.43
59:y:153:PHE:O	59:y:161:LYS:HE2	2.18	0.43
66:AF:33:TRP:CH2	66:AF:53:GLN:HG2	2.53	0.43
70:AJ:42:ILE:O	70:AJ:46:VAL:HG23	2.18	0.43
1:0:138[A]:GLN:HA	1:0:141:LYS:HB3	2.00	0.43
2:1:1029:U:O2'	2:1:1030:U:P	2.75	0.43
2:1:1099:A:N3	2:1:1099:A:H2'	2.32	0.43
2:1:1396:U:H2'	2:1:1397:G:O4'	2.19	0.43
5:4:21:C:O2'	5:4:22:U:H5'	2.19	0.43
10:A:184:C:OP1	19:J:152:ARG:NH2	2.51	0.43
10:A:283:G:H2'	10:A:284:C:C6	2.52	0.43
10:A:974:U:H2'	10:A:975:C:C6	2.54	0.43
10:A:1298:A:N3	10:A:1300:U:H5'	2.33	0.43
11:B:200:ASP:OD2	29:S:89:SER:HA	2.17	0.43
12:C:180:THR:HG22	12:C:183:GLN:CD	2.43	0.43
14:E:76:LYS:NZ	21:L:20:VAL:HG13	2.34	0.43
16:G:27:THR:HB	28:R:27:LEU:HD12	2.00	0.43
17:H:132:ARG:O	17:H:133:LEU:HD23	2.18	0.43
18:I:39:PHE:HB2	18:I:57:PHE:O	2.18	0.43
21:L:75:PHE:CZ	21:L:79:GLU:HG3	2.53	0.43
25:P:77:LYS:HD2	25:P:113:VAL:HG11	1.99	0.43
26:Q:15:PHE:HD2	26:Q:109:PRO:HB2	1.83	0.43
28:R:119:ASP:OD2	28:R:121:ARG:HD3	2.19	0.43
39:d:44:VAL:HG11	39:d:48:VAL:CG2	2.48	0.43
43:h:112:LEU:N	43:h:126:ALA:O	2.52	0.43
43:h:252:ALA:HB2	43:h:289:LEU:CD1	2.48	0.43
48:n:50:ARG:HD3	48:n:158:TYR:CZ	2.53	0.43
59:y:44:PHE:CD2	59:y:134:GLY:HA3	2.53	0.43
2:1:1505:A:H2'	2:1:1506:G:C8	2.53	0.43
2:1:2138:G:H2'	2:1:2139:G:C8	2.52	0.43
2:1:2164:U:OP2	44:j:200:ARG:HD2	2.18	0.43
2:1:3138:U:H2'	2:1:3139:U:H6	1.84	0.43
2:1:3300:A:H2'	2:1:3301:A:C8	2.53	0.43
6:6:135:VAL:HG11	7:7:26:SER:CB	2.49	0.43
10:A:654:G:O2'	10:A:676:G:N1	2.51	0.43
10:A:892:A:H2'	10:A:893:U:H6	1.82	0.43
10:A:1007:C:O2'	10:A:1110:A:N1	2.50	0.43
10:A:1242:U:H2'	21:L:2:LEU:HA	2.01	0.43
17:H:51:LYS:NZ	17:H:53:THR:HG22	2.33	0.43
17:H:102:VAL:HG13	17:H:106:LEU:HD12	2.00	0.43
21:L:7:ASP:HB2	21:L:37:THR:OG1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:l:133:THR:HG22	46:l:149:LEU:HD12	2.01	0.43
47:m:211:LEU:HD21	47:m:222:ILE:HD12	2.01	0.43
50:p:57:VAL:O	50:p:61:ARG:HG3	2.19	0.43
51:q:24:VAL:HG23	51:q:39:LYS:HE2	1.99	0.43
2:1:252:U:H5'	2:1:253:A:C8	2.51	0.43
2:1:2335:A:H2'	2:1:2336:A:C8	2.53	0.43
2:1:2919:G:C2	45:k:250:ALA:HB1	2.53	0.43
2:1:3038:U:H2'	2:1:3039:C:H6	1.84	0.43
2:1:3190:C:H2'	2:1:3191:A:H8	1.82	0.43
10:A:310:A:C2	10:A:312:C:H2'	2.54	0.43
10:A:1476:A:O2'	10:A:1477:U:OP2	2.35	0.43
10:A:1727:A:H2'	10:A:1728:U:C6	2.54	0.43
12:C:193:ILE:O	12:C:197:ILE:HG12	2.19	0.43
20:K:107:ARG:O	20:K:148:VAL:HG22	2.18	0.43
46:l:352:PRO:HB2	49:o:68:LYS:HB2	2.01	0.43
64:AD:38:THR:OG1	64:AD:40:LYS:HG2	2.19	0.43
2:1:11:A:H2'	2:1:12:A:C8	2.54	0.43
2:1:3110:U:OP1	45:k:274:HIS:ND1	2.50	0.43
2:1:3315:C:H4'	2:1:3316:U:OP1	2.19	0.43
4:3:90:A:H2'	4:3:91:G:O4'	2.19	0.43
10:A:590:A:H2'	10:A:591:A:O4'	2.18	0.43
10:A:814:A:N3	10:A:815:U:H5	2.16	0.43
10:A:1544:U:O2'	10:A:1545:U:H2'	2.19	0.43
81:A:1803:GET:H111	81:A:1803:GET:O52	2.19	0.43
16:G:143:ARG:NH2	39:d:57:MET:HE1	2.33	0.43
20:K:52:ILE:HG23	20:K:76:LEU:HD11	2.01	0.43
27:T:87:ASN:OD1	27:T:88:ARG:N	2.43	0.43
28:R:4:GLN:OE1	28:R:91:TYR:OH	2.22	0.43
28:R:13:LYS:HA	28:R:122:ARG:NH1	2.33	0.43
48:n:39:LEU:HB3	48:n:83:VAL:HG13	2.00	0.43
51:q:107:ASP:O	51:q:109:GLN:HG2	2.19	0.43
65:AE:95:VAL:HG12	65:AE:97:VAL:HG13	2.00	0.43
2:1:162:U:O2'	2:1:163:A:H5'	2.19	0.43
2:1:264:G:OP1	70:AJ:34:GLN:HG2	2.18	0.43
2:1:1328:A:H2'	2:1:1329:C:C6	2.53	0.43
2:1:3233:A:H5''	48:n:45:ARG:NH1	2.34	0.43
2:1:3240:U:H5'	67:AG:66:VAL:HG21	2.00	0.43
5:4:37:A:H5''	5:4:39:G:O4'	2.18	0.43
8:8:50:SER:HB2	69:AI:66:VAL:HG11	1.99	0.43
10:A:177:A:N1	17:H:202:ARG:NH2	2.67	0.43
10:A:687:A:C2'	10:A:688:G:H5'	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:746:G:H22	10:A:747:A:H62	1.65	0.43
10:A:1157:G:H2'	10:A:1158:C:O4'	2.18	0.43
10:A:1336:G:H2'	10:A:1337:C:O4'	2.19	0.43
11:B:164:ASN:O	11:B:170:ILE:HD11	2.19	0.43
16:G:26:ALA:HB2	28:R:25:LYS:HG3	2.00	0.43
17:H:48:TYR:HB3	17:H:50:PHE:CE1	2.54	0.43
18:I:54:LEU:O	18:I:86:VAL:HA	2.18	0.43
19:J:85:PRO:HB3	22:M:12:ALA:HB2	2.00	0.43
23:N:24:ILE:HG22	23:N:26:ASP:OD1	2.18	0.43
27:T:22:ILE:HA	27:T:34:LYS:HD3	1.99	0.43
34:Y:37:ALA:HA	34:Y:41:SER:OG	2.19	0.43
36:a:83:LEU:HD23	36:a:89:ILE:HG23	2.01	0.43
42:g:162:GLU:HA	42:g:172:ILE:O	2.19	0.43
43:h:123:ILE:HB	43:h:135:TRP:HB2	2.01	0.43
48:n:91:ASN:O	48:n:148:GLU:HG2	2.18	0.43
53:s:52:TYR:HA	53:s:61:ARG:HG3	2.00	0.43
55:u:109:GLU:O	55:u:113:VAL:HG23	2.18	0.43
56:v:180:PHE:O	56:v:184:LYS:HB2	2.19	0.43
78:PT:59:A:O2'	78:PT:61:U:OP2	2.27	0.43
2:1:2692:G:OP1	59:y:180:ARG:NH1	2.52	0.43
2:1:3038:U:H2'	2:1:3039:C:C6	2.54	0.43
6:6:117:PRO:HG3	7:7:26:SER:HA	2.01	0.43
10:A:168:U:O2	10:A:265:U:H1'	2.18	0.43
10:A:512:G:N1	10:A:541:C:H5	2.06	0.43
10:A:646:G:H2'	10:A:647:C:C6	2.53	0.43
10:A:1203:G:N2	10:A:1430:A:OP2	2.45	0.43
11:B:121:VAL:HG23	11:B:141:ILE:HG21	2.01	0.43
14:E:110:LEU:HG	14:E:178:MET:CE	2.49	0.43
16:G:42:LEU:HG	16:G:43:PHE:CD2	2.54	0.43
35:Z:12:VAL:HG22	35:Z:23:PHE:HB3	2.00	0.43
39:d:12:VAL:HG13	39:d:28:VAL:HB	2.01	0.43
39:d:16:LEU:HB2	39:d:27:GLN:CB	2.49	0.43
73:AM:15:LYS:O	73:AM:19:GLN:HG3	2.19	0.43
2:1:1814:U:H2'	2:1:1815:U:C5	2.54	0.43
2:1:2413:G:H4'	56:v:24:ARG:NH2	2.32	0.43
2:1:2734:A:H2'	2:1:2735:U:C6	2.52	0.43
5:4:117:C:H2'	5:4:118:C:H6	1.83	0.43
5:4:154:C:H5''	50:p:182:LYS:HD3	2.01	0.43
10:A:585:C:H2'	10:A:586:U:C6	2.54	0.43
10:A:1296:U:O3'	29:S:2:GLY:HA3	2.19	0.43
17:H:147:LEU:HD22	17:H:151:ASP:OD2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:I:13:LEU:HD21	18:I:54:LEU:HD11	2.01	0.43
41:f:41:THR:HA	41:f:45:VAL:HB	2.01	0.43
72:AL:24:ILE:HB	72:AL:44:LYS:HB2	2.01	0.43
77:AQ:74:ALA:O	77:AQ:78:THR:HG23	2.19	0.43
2:1:161:G:H2'	2:1:162:U:H5'	2.01	0.42
2:1:792:U:H2'	2:1:793:U:C6	2.54	0.42
2:1:1058:A:H4'	3:2:105:PHE:CE1	2.53	0.42
2:1:2251:G:N2	2:1:2289:G:H2'	2.34	0.42
2:1:2785:A:H2'	2:1:2786:G:O4'	2.19	0.42
2:1:3112:G:N7	45:k:28:ARG:NH2	2.66	0.42
10:A:260:U:O2'	10:A:261:C:H5'	2.18	0.42
10:A:1209:A:H2'	10:A:1210:U:H6	1.84	0.42
14:E:214:ASP:OD1	14:E:215:GLU:N	2.51	0.42
27:T:16:ARG:HD3	53:s:110:ILE:HD12	2.01	0.42
54:t:180:LYS:HD3	54:t:181:TYR:CE2	2.54	0.42
59:y:165:ILE:HD11	59:y:172:PHE:HB3	2.00	0.42
72:AL:8:ILE:HD12	72:AL:54:LEU:HD21	2.00	0.42
72:AL:14:LEU:HD21	72:AL:52:TYR:CD2	2.54	0.42
2:1:178:U:H2'	2:1:179:C:C6	2.54	0.42
2:1:848:U:C6	77:AQ:2:THR:HG22	2.54	0.42
2:1:1124:U:H2'	2:1:1125:A:O4'	2.19	0.42
2:1:1493:C:H2'	2:1:1494:A:H8	1.83	0.42
2:1:2745:C:H2'	2:1:2746:C:H6	1.84	0.42
2:1:2823:A:HO2'	78:AT:64:G:HO2'	1.57	0.42
2:1:3262:U:H2'	2:1:3263:C:H6	1.85	0.42
9:9:27:ARG:HG2	9:9:78:PHE:CE1	2.54	0.42
9:9:106:ILE:HG21	9:9:109:LEU:HD23	2.00	0.42
10:A:256:C:C5'	19:J:75:LYS:HB2	2.49	0.42
10:A:504:A:HO2'	10:A:505:U:P	2.40	0.42
10:A:883:A:H5''	25:P:41:MET:HE3	2.01	0.42
10:A:1205:C:H2'	10:A:1206:A:H8	1.83	0.42
10:A:1546:G:N7	27:T:134:ARG:HD3	2.34	0.42
10:A:1715:U:H2'	10:A:1716:C:C6	2.53	0.42
11:B:169:SER:O	11:B:173:ILE:HG12	2.19	0.42
12:C:22:ASP:HB3	12:C:25:THR:HG23	2.01	0.42
12:C:83:LYS:NZ	25:P:111:GLU:OE2	2.45	0.42
14:E:81:SER:O	14:E:84:GLY:N	2.38	0.42
14:E:128:MET:HG3	14:E:155:ASP:OD2	2.19	0.42
18:I:150:LEU:HB2	18:I:181:ILE:HG12	2.01	0.42
23:N:71:ILE:HD11	42:g:145:LEU:HD21	1.99	0.42
26:Q:38:GLY:O	26:Q:42:ARG:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:c:15:GLU:OE2	38:c:23:THR:HB	2.20	0.42
40:e:10:HIS:CD2	40:e:11:PRO:HD2	2.54	0.42
62:AB:128:ARG:HG2	70:AJ:7:ALA:HB2	2.01	0.42
2:1:1832:C:O2'	2:1:1838:A:N1	2.49	0.42
2:1:1844:G:OP2	73:AM:45:ARG:HD3	2.19	0.42
2:1:2182:C:H2'	2:1:2183:U:C6	2.53	0.42
2:1:2491:U:OP1	81:1:3413:GET:O61	2.33	0.42
2:1:2546:U:H5'	2:1:2547:G:C8	2.54	0.42
2:1:2938:G:H2'	2:1:2939:A:C8	2.53	0.42
6:6:38:ALA:HB3	6:6:59:MET:HB2	2.01	0.42
10:A:66:U:OP2	17:H:136:LYS:NZ	2.51	0.42
10:A:1222:G:C4	10:A:1223:A:C8	3.07	0.42
10:A:1784:A:H4'	37:b:95:ARG:HG3	2.00	0.42
13:D:137:GLY:N	13:D:148:SER:O	2.39	0.42
16:G:129:PRO:O	16:G:133:VAL:HG23	2.19	0.42
47:m:178:ASN:HA	47:m:183:TRP:CG	2.54	0.42
58:x:27:LYS:HE2	58:x:63:TYR:CD1	2.53	0.42
1:0:43:TYR:OH	1:0:47:LYS:HE2	2.20	0.42
2:1:561:U:H2'	2:1:562:C:C6	2.54	0.42
2:1:623:A:H2'	2:1:624:U:H6	1.84	0.42
2:1:1186:A:N3	2:1:1186:A:H2'	2.35	0.42
2:1:2266:G:H2'	2:1:2267:U:C6	2.55	0.42
2:1:2852:U:H1'	45:k:250:ALA:HB3	2.02	0.42
2:1:2855:U:H2'	2:1:2856:C:H6	1.84	0.42
10:A:154:A:H2'	10:A:155:A:O4'	2.19	0.42
10:A:675:U:H2'	10:A:676:G:H8	1.83	0.42
10:A:1399:U:O2'	10:A:1402:G:OP1	2.27	0.42
10:A:1521:G:HO2'	10:A:1522:U:P	2.42	0.42
13:D:171:LYS:NZ	13:D:192:TYR:OH	2.50	0.42
15:F:136:VAL:HG11	15:F:148:ARG:HD2	2.01	0.42
16:G:147:THR:HG21	39:d:25:VAL:HG21	2.02	0.42
22:M:56:LYS:HG3	22:M:57:LYS:HG3	2.01	0.42
29:S:58:MET:HE3	29:S:58:MET:HB3	1.86	0.42
48:n:158:TYR:CG	55:u:108:PHE:HD1	2.37	0.42
72:AL:25:VAL:HG11	72:AL:66:GLN:HE21	1.84	0.42
2:1:1180:A:H2'	2:1:1181:C:C6	2.54	0.42
2:1:1338:G:H2'	2:1:1339:A:O4'	2.19	0.42
2:1:1387:C:N3	66:AF:104:ARG:HD3	2.35	0.42
2:1:1474:C:H2'	2:1:1475:U:C6	2.54	0.42
2:1:3219:G:H2'	2:1:3220:C:C6	2.54	0.42
8:8:71:THR:O	8:8:75:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:9:51:ARG:HG2	9:9:52:GLN:N	2.35	0.42
10:A:142:G:N7	17:H:137:ARG:NH2	2.68	0.42
10:A:215:A:N3	10:A:215:A:H2'	2.34	0.42
10:A:946:U:O2'	24:O:86:GLU:OE2	2.38	0.42
10:A:1226:G:H4'	26:Q:78:THR:HA	2.00	0.42
10:A:1548:U:H4'	10:A:1586:C:H4'	2.02	0.42
10:A:1675:U:O2'	10:A:1676:A:O4'	2.23	0.42
15:F:98:HIS:HB2	15:F:114:ILE:HG13	2.01	0.42
18:I:25:GLU:O	18:I:31:LYS:HD3	2.19	0.42
18:I:128:PRO:HB2	18:I:154:ASP:HB3	2.00	0.42
25:P:94:GLN:OE1	37:b:45:VAL:HA	2.20	0.42
35:Z:3:ASP:OD2	35:Z:31:ASN:ND2	2.49	0.42
43:h:126:ALA:HB2	43:h:155:VAL:HG22	2.00	0.42
50:p:108:GLU:O	50:p:111:THR:HG22	2.20	0.42
55:u:27:ALA:HB2	55:u:45:ILE:HD13	2.01	0.42
2:1:87:A:H2'	2:1:88:G:O4'	2.19	0.42
2:1:678:G:H5''	46:l:115:ASN:OD1	2.20	0.42
2:1:1079:G:H2'	2:1:1080:A:C8	2.54	0.42
2:1:1302:G:C6	57:w:63:THR:HA	2.54	0.42
2:1:1706:C:H2'	2:1:1707:U:C6	2.54	0.42
2:1:2579:G:H5'	44:j:233:GLN:HG2	2.01	0.42
2:1:2587:G:H2'	2:1:2588:C:H6	1.84	0.42
2:1:2655:U:H2'	2:1:2656:C:H6	1.85	0.42
2:1:2658:A:H2'	2:1:2659:G:O4'	2.20	0.42
2:1:2790:U:H5'	2:1:2790:U:C6	2.47	0.42
3:2:69:LYS:HA	47:m:40:HIS:CE1	2.54	0.42
4:3:7:G:OP1	47:m:33:ARG:NH1	2.53	0.42
10:A:119:A:H1'	10:A:395:A:C5	2.55	0.42
10:A:1042:U:C5	10:A:1048:U:C4	3.07	0.42
10:A:1423:U:O2'	14:E:182:VAL:HG23	2.20	0.42
10:A:1444:G:H2'	10:A:1444:G:N3	2.34	0.42
11:B:52:LYS:O	11:B:56:LYS:HG2	2.19	0.42
11:B:125:ASP:OD1	11:B:164:ASN:ND2	2.53	0.42
17:H:184:LEU:HB3	17:H:188:ARG:HH12	1.85	0.42
20:K:30:LEU:HD21	20:K:102:GLU:HG3	2.01	0.42
31:V:62:LEU:HG	40:e:34:TYR:CZ	2.55	0.42
43:h:40:LYS:HG2	43:h:67:HIS:C	2.44	0.42
43:h:195:TYR:O	43:h:212:GLY:HA3	2.19	0.42
55:u:17:ARG:HG2	55:u:57:LEU:HD22	2.02	0.42
63:AC:20:GLY:HA3	63:AC:21:ILE:HA	1.84	0.42
76:AP:105:GLN:OE1	76:AP:105:GLN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:158:A:H2'	2:1:159:A:H8	1.84	0.42
2:1:1015:G:O6	2:1:1029:U:C4	2.72	0.42
2:1:1835:A:O2'	2:1:1836:U:H5''	2.19	0.42
5:4:85:G:C8	5:4:85:G:H3'	2.55	0.42
10:A:524:A:OP2	35:Z:93:ARG:NH2	2.32	0.42
10:A:728:U:OP1	18:I:104:LYS:N	2.53	0.42
10:A:799:G:N3	60:z:162:ARG:NH1	2.68	0.42
10:A:1020:G:O2'	33:X:3:ARG:HD2	2.20	0.42
10:A:1049:G:H2'	10:A:1050:A:C8	2.54	0.42
14:E:157:PHE:HE2	14:E:190:MET:HE1	1.84	0.42
31:V:52:LYS:HE2	31:V:91:ASP:HB2	2.01	0.42
37:b:51:ARG:O	37:b:55:GLU:HG2	2.20	0.42
43:h:216:VAL:HG22	43:h:218:ILE:HG23	2.02	0.42
50:p:117:ILE:HG22	50:p:122:THR:HA	2.02	0.42
53:s:75:LYS:O	53:s:79:ILE:HG13	2.19	0.42
69:AI:17:LEU:HD13	69:AI:58:ILE:HG13	2.02	0.42
2:1:381:U:H2'	2:1:382:U:C6	2.55	0.42
2:1:771:A:H62	81:1:3407:GET:H531	1.83	0.42
2:1:2908:A:OP2	81:1:3408:GET:N32	2.53	0.42
2:1:3061:C:H2'	2:1:3062:U:O4'	2.19	0.42
8:8:99:VAL:HG11	8:8:124:ILE:HD13	2.02	0.42
10:A:267:G:H2'	10:A:268:C:C6	2.55	0.42
10:A:327:G:H2'	10:A:328:G:C8	2.54	0.42
10:A:352:C:H5''	19:J:16:ALA:HB2	2.02	0.42
10:A:679:C:H2'	10:A:680:C:C6	2.55	0.42
10:A:1389:U:OP1	29:S:2:GLY:HA2	2.20	0.42
10:A:1741:A:C5	81:A:1801:GET:H21	2.54	0.42
14:E:52:LYS:HA	14:E:90:GLU:O	2.19	0.42
14:E:56:THR:O	14:E:56:THR:HG22	2.20	0.42
14:E:121:TYR:HB3	14:E:125:ARG:NH1	2.34	0.42
16:G:25:LEU:HB3	28:R:26:GLY:O	2.20	0.42
17:H:142:ARG:NE	17:H:153:VAL:HG21	2.25	0.42
39:d:58:GLU:HG3	39:d:60:GLU:HG2	2.02	0.42
49:o:39:ARG:HG2	49:o:39:ARG:HH11	1.85	0.42
10:A:840:A:H3'	10:A:841:A:H5''	2.01	0.42
16:G:197:GLU:OE2	16:G:208:SER:HB2	2.20	0.42
18:I:33:GLU:OE1	18:I:33:GLU:N	2.50	0.42
21:L:3:ILE:HB	21:L:8:ARG:HH21	1.83	0.42
31:V:23:ILE:HD12	31:V:114:GLU:O	2.20	0.42
32:W:51:ILE:CG2	32:W:78:LEU:HD21	2.48	0.42
45:k:28:ARG:CZ	45:k:30:LYS:HE2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:n:73:VAL:HA	48:n:74:PRO:HD3	1.93	0.42
58:x:122:ALA:HB3	58:x:143:PRO:HB2	2.00	0.42
71:AK:25:ARG:O	71:AK:25:ARG:HG2	2.19	0.42
2:1:88:G:N7	59:y:171:LYS:NZ	2.67	0.42
2:1:423:A:H2'	2:1:424:G:O4'	2.20	0.42
2:1:2587:G:H2'	2:1:2588:C:C6	2.55	0.42
2:1:3318:G:H3'	2:1:3319:U:O3'	2.20	0.42
10:A:327:G:H2'	10:A:328:G:H8	1.83	0.42
10:A:757:G:N2	10:A:759:A:H1'	2.35	0.42
10:A:1520:C:OP2	36:a:77:ARG:NH2	2.50	0.42
10:A:1643:U:H5''	10:A:1644:U:OP2	2.20	0.42
10:A:1675:U:O2	10:A:1702:A:N6	2.52	0.42
10:A:1757:U:H2'	10:A:1758:U:C6	2.54	0.42
15:F:123:LEU:HA	15:F:160:VAL:O	2.20	0.42
15:F:159:THR:OG1	15:F:227:VAL:HB	2.20	0.42
19:J:87:ASN:HB3	19:J:90:LEU:HD13	2.02	0.42
29:S:75:GLU:HA	29:S:78:ARG:HG2	2.02	0.42
52:r:68:ALA:HB1	52:r:155:ALA:HB1	2.02	0.42
53:s:93:SER:HB2	53:s:173:ASP:HA	2.02	0.42
53:s:109:HIS:CD2	53:s:109:HIS:H	2.37	0.42
64:AD:88:ARG:CZ	77:AQ:44:LYS:HG2	2.49	0.42
78:AT:48:U:H4'	78:AT:49:C:C6	2.54	0.42
2:1:1690:U:O2'	2:1:1691:U:H5'	2.19	0.41
2:1:1795:A:H2'	2:1:1796:A:C8	2.55	0.41
2:1:2155:G:N2	44:j:118:GLU:OE2	2.52	0.41
2:1:2354:G:H2'	2:1:2355:G:C8	2.55	0.41
2:1:2883:A:H4'	2:1:2884:G:C8	2.54	0.41
4:3:3:U:H2'	4:3:4:U:H6	1.85	0.41
10:A:184:C:H2'	10:A:185:G:O4'	2.20	0.41
10:A:772:A:OP2	15:F:106:LYS:HG2	2.19	0.41
14:E:76:LYS:HZ1	21:L:20:VAL:HG13	1.85	0.41
16:G:140:SER:HB2	16:G:171:ALA:HB1	2.00	0.41
20:K:137:GLY:N	20:K:155:HIS:O	2.24	0.41
45:k:212:ASP:OD1	45:k:354:VAL:HG22	2.20	0.41
45:k:283:TYR:OH	45:k:325:LYS:HD2	2.19	0.41
53:s:25:GLU:OE2	53:s:29:ARG:HD3	2.20	0.41
54:t:154:PRO:HB3	62:AB:106:ALA:CB	2.50	0.41
59:y:177:GLY:HA2	59:y:184:PHE:CE2	2.55	0.41
2:1:1358:C:H2'	2:1:1359:A:C8	2.55	0.41
2:1:2541:C:H2'	2:1:2542:C:H6	1.85	0.41
2:1:2869:A:H2'	2:1:2871:C:H5''	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:156:U:C4	10:A:418:A:H4'	2.55	0.41
10:A:753:C:H2'	10:A:754:A:O4'	2.20	0.41
10:A:784:U:H2'	10:A:785:G:C8	2.55	0.41
10:A:1661:C:OP1	17:H:92:ARG:NH1	2.44	0.41
10:A:1700:G:H2'	10:A:1701:A:N7	2.35	0.41
10:A:1783:C:C6	37:b:5:ARG:HB3	2.55	0.41
13:D:170:GLY:O	20:K:53:ARG:NH2	2.53	0.41
19:J:122:GLY:C	19:J:124:LYS:H	2.29	0.41
24:O:89:TYR:HE1	24:O:150:VAL:HA	1.84	0.41
24:O:102:LEU:HD12	24:O:115:LEU:HD22	2.01	0.41
31:V:26:THR:HA	31:V:86:HIS:O	2.20	0.41
43:h:200:THR:HG22	43:h:209:ALA:HB3	2.02	0.41
53:s:8:VAL:O	53:s:11:GLU:HG2	2.21	0.41
53:s:80:LEU:HD22	53:s:129:VAL:HG11	2.03	0.41
60:z:172:ARG:HB3	60:z:176:ARG:NH1	2.32	0.41
61:AA:44:ALA:HB1	61:AA:114:VAL:HG21	2.02	0.41
2:1:108:A:H4'	2:1:109:G:OP1	2.20	0.41
2:1:117:U:O2	2:1:120:A:H5''	2.21	0.41
2:1:437:G:HO2'	2:1:438:A:P	2.43	0.41
2:1:2661:A:H2'	2:1:2661:A:N3	2.35	0.41
2:1:2739:U:H2'	2:1:2740:U:C6	2.55	0.41
2:1:3190:C:H2'	2:1:3191:A:C8	2.55	0.41
10:A:1065:U:H2'	10:A:1066:A:O4'	2.20	0.41
10:A:1399:U:P	29:S:3:ARG:HH22	2.43	0.41
10:A:1419:G:N1	40:e:45:GLU:OE2	2.47	0.41
10:A:1476:A:H5''	10:A:1480:G:H21	1.86	0.41
10:A:1552:C:OP1	27:T:41:ARG:HD3	2.20	0.41
15:F:103:TYR:HA	15:F:108:LYS:O	2.20	0.41
16:G:43:PHE:CZ	16:G:115:LYS:HB2	2.56	0.41
23:N:52:LEU:HD21	23:N:60:CYS:SG	2.61	0.41
32:W:4:ASP:OD1	32:W:4:ASP:N	2.53	0.41
35:Z:19:ALA:HB1	35:Z:77:GLN:HE21	1.85	0.41
69:AI:15:GLU:O	69:AI:18:GLU:HG3	2.21	0.41
71:AK:52:LYS:HE2	71:AK:55:ARG:NH2	2.36	0.41
76:AP:37:ALA:O	76:AP:41:ARG:HG3	2.20	0.41
78:PT:7:G:O2'	78:PT:50:G:O5'	2.38	0.41
78:AT:49:C:H4'	78:AT:50:G:H5''	2.01	0.41
2:1:406:G:O6	81:1:3403:GET:N32	2.48	0.41
2:1:1066:U:H2'	2:1:1067:U:O4'	2.20	0.41
2:1:2608:A:H5''	2:1:2609:A:H5'	2.02	0.41
2:1:3013:U:H2'	2:1:3014:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:95:G:OP2	71:AK:72:ARG:NH1	2.42	0.41
10:A:397:A:H4'	15:F:3:ARG:HG2	2.02	0.41
10:A:519:A:O3'	35:Z:36:SER:HA	2.20	0.41
10:A:1520:C:H4'	10:A:1526:G:O6	2.20	0.41
10:A:1532:A:P	27:T:134:ARG:HG3	2.59	0.41
11:B:179:ARG:HG2	11:B:179:ARG:HH11	1.84	0.41
15:F:12:LEU:HD23	15:F:12:LEU:HA	1.79	0.41
16:G:148:ARG:HH21	39:d:22:ARG:NH2	2.18	0.41
18:I:5:ILE:HG22	18:I:7:SER:N	2.34	0.41
18:I:95:LEU:O	18:I:108:ARG:NH1	2.53	0.41
18:I:116:ALA:O	18:I:120:LYS:HG2	2.20	0.41
20:K:83:ILE:HA	20:K:149:ARG:HA	2.02	0.41
23:N:64:ASP:OD1	23:N:72:ILE:HG12	2.21	0.41
26:Q:81:ARG:HD2	26:Q:97:TYR:O	2.20	0.41
26:Q:98:ASN:ND2	26:Q:121:ILE:O	2.49	0.41
30:U:114:LEU:HD23	30:U:124:ILE:HD12	2.02	0.41
35:Z:9:THR:HA	35:Z:24:VAL:O	2.21	0.41
41:f:54:ARG:HD2	41:f:54:ARG:C	2.45	0.41
43:h:106:GLY:HA3	43:h:133:LYS:HE2	2.01	0.41
44:j:14:SER:OG	44:j:15:ILE:N	2.52	0.41
46:l:326:LEU:HD23	46:l:326:LEU:HA	1.86	0.41
54:t:61:PRO:O	54:t:62:THR:HB	2.20	0.41
65:AE:76:ARG:CD	65:AE:88:LEU:HD13	2.49	0.41
77:AQ:36:LYS:HE2	77:AQ:48:GLN:OE1	2.20	0.41
2:1:6:C:H2'	2:1:7:C:C6	2.55	0.41
2:1:2584:U:H2'	2:1:2585:U:O4'	2.21	0.41
4:3:19:C:H2'	4:3:20:A:C8	2.55	0.41
7:7:23:ARG:HG2	7:7:24:GLY:H	1.84	0.41
10:A:1224:U:H2'	10:A:1225:U:C6	2.55	0.41
10:A:1573:A:H2'	10:A:1574:A:O4'	2.21	0.41
11:B:168:HIS:HD1	11:B:203:PHE:HE2	1.66	0.41
21:L:2:LEU:HD23	21:L:2:LEU:H	1.85	0.41
23:N:96:LEU:HD12	23:N:100:TRP:CH2	2.56	0.41
28:R:59:PHE:CE1	28:R:88:LEU:HD22	2.56	0.41
36:a:80:LEU:HD22	36:a:101:TYR:CD2	2.56	0.41
42:g:183:CYS:HB2	42:g:186:CYS:SG	2.60	0.41
52:r:10:ARG:HD3	52:r:11:TYR:CE2	2.54	0.41
53:s:33:ALA:O	53:s:36:VAL:HG12	2.20	0.41
2:1:1296:G:O6	81:1:3409:GET:N21	2.52	0.41
2:1:1357:U:H2'	2:1:1358:C:C6	2.56	0.41
2:1:1841:G:H5''	2:1:1842:C:H5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2079:C:HO2'	2:1:2080:U:H6	1.65	0.41
2:1:2203:U:H2'	2:1:2204:U:C6	2.55	0.41
2:1:2902:A:H2'	2:1:2903:C:C6	2.55	0.41
8:8:49:LYS:NZ	8:8:51:VAL:O	2.51	0.41
10:A:202:G:H2'	10:A:203:U:O4'	2.20	0.41
10:A:757:G:OP1	15:F:22:LYS:NZ	2.40	0.41
10:A:919:C:H1'	37:b:11:ASN:OD1	2.21	0.41
17:H:48:TYR:CE1	17:H:116:GLN:HA	2.55	0.41
21:L:38:ARG:HB2	21:L:41:PHE:CG	2.56	0.41
22:M:118:GLU:HG2	22:M:121:ASP:OD2	2.20	0.41
27:T:101:LEU:HB3	27:T:102:ALA:H	1.67	0.41
38:c:45:THR:HG23	38:c:82:LYS:HE3	2.01	0.41
42:g:163:CYS:HA	42:g:164:PRO:HD3	1.94	0.41
48:n:57:LEU:CD1	48:n:63:LEU:HB2	2.51	0.41
59:y:176:ARG:HA	59:y:182:ARG:O	2.20	0.41
2:1:18:U:H2'	2:1:19:A:C8	2.55	0.41
2:1:783:G:H2'	2:1:784:C:C6	2.55	0.41
2:1:1029:U:HO2'	2:1:1030:U:P	2.42	0.41
2:1:1556:G:C8	8:8:36:LYS:NZ	2.87	0.41
2:1:1611:U:H2'	2:1:1612:U:H6	1.81	0.41
2:1:1663:A:H2'	2:1:1664:G:H8	1.86	0.41
2:1:3021:A:C5	45:k:75:ALA:HB2	2.55	0.41
2:1:3099:A:H2'	2:1:3100:G:O4'	2.21	0.41
3:2:80:VAL:HB	3:2:83:ARG:NH1	2.36	0.41
10:A:206:U:H2'	10:A:207:U:C6	2.56	0.41
10:A:443:A:H2'	10:A:444:A:H8	1.85	0.41
10:A:1637:U:H2'	10:A:1638:A:C8	2.56	0.41
10:A:1701:A:C6	10:A:1702:A:N7	2.89	0.41
11:B:4:PRO:HG3	32:W:41:GLU:HA	2.01	0.41
11:B:30:GLN:HG2	11:B:32:HIS:H	1.86	0.41
12:C:110:LEU:O	12:C:114:VAL:HG23	2.21	0.41
13:D:176:SER:HB2	13:D:177:PRO:HD2	2.03	0.41
15:F:60:GLU:CD	35:Z:20:ARG:HH22	2.28	0.41
15:F:159:THR:HB	15:F:173:ILE:HD13	2.02	0.41
21:L:44:LYS:HD3	21:L:44:LYS:HA	1.85	0.41
23:N:28:LEU:HD23	23:N:28:LEU:H	1.85	0.41
28:R:30:ILE:N	28:R:33:SER:O	2.43	0.41
30:U:131:ASP:OD1	30:U:134:ARG:NH2	2.50	0.41
35:Z:8:ARG:HB3	35:Z:26:ASP:HB2	2.02	0.41
43:h:90:LEU:CD1	43:h:111:VAL:HG11	2.48	0.41
65:AE:81:GLU:O	65:AE:84:ALA:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:AF:33:TRP:HH2	66:AF:53:GLN:HG2	1.85	0.41
71:AK:39:TYR:CD1	71:AK:40:PRO:HA	2.56	0.41
2:1:648:C:H2'	2:1:649:G:C8	2.56	0.41
2:1:1115:C:H2'	2:1:1116:A:C8	2.56	0.41
2:1:1715:G:N7	60:z:121:HIS:HE1	2.18	0.41
2:1:1724:G:N3	2:1:1724:G:H5'	2.36	0.41
2:1:2281:A:OP1	75:AO:23:ARG:HG2	2.21	0.41
5:4:19:C:H2'	5:4:20:U:C6	2.56	0.41
10:A:137:A:H4'	10:A:138:C:C5'	2.48	0.41
10:A:271:G:O6	10:A:281:U:C2	2.74	0.41
10:A:1087:G:N7	34:Y:2:GLY:N	2.69	0.41
10:A:1581:G:H2'	10:A:1582:U:O4'	2.21	0.41
15:F:194:VAL:HG12	15:F:211:LYS:O	2.20	0.41
16:G:50:ASP:OD1	16:G:128:ASN:ND2	2.54	0.41
25:P:130:ARG:HH21	25:P:132:LEU:HD11	1.85	0.41
28:R:22:LYS:O	28:R:63:ASP:N	2.44	0.41
36:a:62:VAL:O	36:a:66:VAL:HG23	2.21	0.41
52:r:48:LEU:O	52:r:139:ARG:HA	2.21	0.41
53:s:21:ILE:HD12	53:s:37:LEU:HG	2.02	0.41
70:AJ:93:ILE:HG22	70:AJ:97:ARG:NH1	2.30	0.41
78:AT:75:C:C4	78:AT:76:C:H1'	2.56	0.41
2:1:39:A:H5''	62:AB:35:ALA:HB1	2.02	0.41
2:1:673:C:H5'	46:l:117:ASN:HD21	1.85	0.41
2:1:737:U:H2'	2:1:738:G:O4'	2.20	0.41
2:1:1291:G:H2'	2:1:1292:C:C6	2.56	0.41
2:1:2632:G:OP1	2:1:2722:U:O2'	2.39	0.41
2:1:2645:A:OP1	53:s:95:ASN:HA	2.21	0.41
2:1:2695:U:H2'	2:1:2696:U:C6	2.56	0.41
2:1:2802:G:H1'	2:1:2833:U:C2	2.56	0.41
2:1:2915:G:H2'	2:1:2916:U:O4'	2.20	0.41
2:1:3104:C:H2'	2:1:3105:C:C6	2.55	0.41
2:1:3125:U:H4'	2:1:3126:U:O5'	2.21	0.41
2:1:3240:U:O2'	2:1:3241:G:OP1	2.25	0.41
7:7:18:GLY:HA3	7:7:31:PHE:O	2.20	0.41
9:9:63:LYS:HD3	9:9:63:LYS:HA	1.86	0.41
10:A:168:U:OP1	10:A:265:U:O2'	2.33	0.41
10:A:835:A:H2'	10:A:836:U:H6	1.85	0.41
10:A:1239:U:OP1	42:g:185:LYS:HD2	2.20	0.41
10:A:1608:U:H2'	10:A:1609:G:O4'	2.21	0.41
10:A:1673:U:H1'	10:A:1704:C:O2'	2.21	0.41
12:C:34:ALA:HB3	12:C:41:ARG:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:E:41:ARG:O	14:E:47:LEU:HD12	2.21	0.41
15:F:118:GLU:HA	15:F:121:TYR:HE1	1.86	0.41
16:G:34:GLN:CA	16:G:37:GLN:HE22	2.34	0.41
24:O:38:ILE:HG22	24:O:42:ARG:HE	1.85	0.41
27:T:84:TRP:HA	27:T:89:GLN:OE1	2.20	0.41
35:Z:19:ALA:HB1	35:Z:77:GLN:NE2	2.36	0.41
43:h:112:LEU:HD21	43:h:128:ARG:NE	2.32	0.41
44:j:5:ILE:HG13	44:j:7:ASN:HB2	2.03	0.41
45:k:153:LYS:HD3	45:k:154:TYR:CZ	2.56	0.41
45:k:283:TYR:CE1	45:k:354:VAL:HG11	2.56	0.41
47:m:83:LEU:N	47:m:84:PRO:HD2	2.36	0.41
47:m:203:HIS:CD2	47:m:204:VAL:HG23	2.56	0.41
48:n:33:LEU:HD23	48:n:33:LEU:HA	1.92	0.41
49:o:108:GLN:HE22	49:o:204:LYS:HG2	1.85	0.41
49:o:136:TYR:CD2	49:o:230:GLU:O	2.74	0.41
50:p:117:ILE:HA	50:p:121:LYS:O	2.21	0.41
50:p:221:ALA:O	50:p:226:LYS:HE3	2.21	0.41
51:q:157:ASN:C	51:q:157:ASN:HD22	2.28	0.41
52:r:150:GLU:O	52:r:154:ARG:HG3	2.21	0.41
78:PT:25:U:H2'	78:PT:26:C:O4'	2.21	0.41
2:1:597:U:H2'	2:1:598:U:O4'	2.21	0.41
2:1:827:G:O2'	2:1:1860:A:N3	2.51	0.41
2:1:1303:G:C4	57:w:61:LYS:HD3	2.56	0.41
2:1:1591:U:C2	2:1:1592:C:C5	3.09	0.41
2:1:2631:G:H4'	2:1:2723:G:O2'	2.21	0.41
4:3:59:U:H2'	4:3:60:G:C8	2.56	0.41
11:B:80:THR:HA	11:B:83:GLN:OE1	2.21	0.41
19:J:31:ARG:HB2	19:J:56:ARG:HH22	1.86	0.41
35:Z:28:LEU:O	35:Z:30:PRO:HD3	2.21	0.41
44:j:32:LEU:HD11	44:j:120:VAL:HG22	2.02	0.41
46:l:162:LYS:HB3	46:l:162:LYS:HE3	1.93	0.41
51:q:10:LEU:O	51:q:52:ALA:HA	2.20	0.41
2:1:156:A:N7	70:AJ:25:ILE:HG12	2.36	0.40
2:1:314:U:H2'	2:1:315:C:C6	2.55	0.40
2:1:929:A:N3	46:l:99:ARG:NH2	2.69	0.40
2:1:1115:C:H2'	2:1:1116:A:H8	1.86	0.40
2:1:1470:A:H2'	2:1:1471:A:O4'	2.21	0.40
2:1:1550:U:H3'	2:1:1551:U:H5''	2.04	0.40
2:1:2516:U:O2'	2:1:2519:A:N6	2.54	0.40
2:1:3321:G:H8	2:1:3321:G:OP2	2.04	0.40
5:4:10:A:H2'	5:4:11:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:167:A:O2'	10:A:168:U:H3'	2.21	0.40
10:A:244:G:N2	22:M:38:VAL:O	2.42	0.40
10:A:772:A:OP1	15:F:106:LYS:NZ	2.40	0.40
10:A:801:A:O4'	18:I:106:GLN:NE2	2.54	0.40
10:A:1214:G:C2	10:A:1240:G:C2	3.08	0.40
10:A:1709:A:H2'	10:A:1710:G:O4'	2.22	0.40
12:C:144:LYS:HB3	12:C:206:PRO:HB2	2.02	0.40
12:C:199:LYS:O	12:C:202:GLN:HG3	2.21	0.40
15:F:249:ILE:HD12	20:K:71:PHE:CE2	2.56	0.40
28:R:96:VAL:HG12	28:R:97:ASP:N	2.36	0.40
34:Y:61:SER:HB2	34:Y:116:ASP:OD2	2.21	0.40
47:m:212:LEU:HD13	47:m:219:TYR:CE2	2.56	0.40
49:o:134:TYR:CZ	49:o:228:ASN:HB2	2.57	0.40
51:q:89:LYS:HB2	51:q:183:GLU:HB3	2.02	0.40
53:s:14:ILE:HD13	53:s:131:MET:SD	2.61	0.40
57:w:35:VAL:HG22	57:w:104:LYS:HB2	2.03	0.40
78:AT:23:G:H2'	78:AT:24:C:C6	2.56	0.40
78:AT:46:G:O6	81:AT:101:GET:N21	2.54	0.40
2:1:163:A:H2'	2:1:164:U:C1'	2.51	0.40
2:1:921:A:O2'	81:1:3412:GET:H32	2.22	0.40
2:1:1042:A:H2'	2:1:1045:C:C5	2.56	0.40
2:1:1142:C:H4'	2:1:1327:U:C4	2.56	0.40
2:1:1569:C:H2'	2:1:1570:A:H8	1.86	0.40
2:1:3241:G:O6	58:x:169:ASN:ND2	2.55	0.40
2:1:3256:G:H2'	2:1:3257:A:C8	2.56	0.40
10:A:687:A:O2'	10:A:688:G:H5'	2.22	0.40
10:A:786:G:H21	33:X:107:SER:HB3	1.86	0.40
10:A:1160:U:H2'	10:A:1161:G:C8	2.56	0.40
11:B:157:ASP:OD2	32:W:32:VAL:HG21	2.21	0.40
12:C:149:GLN:HE21	12:C:151:LYS:HG3	1.86	0.40
14:E:72:SER:HA	14:E:75:VAL:HG22	2.03	0.40
17:H:161:GLU:HG3	17:H:169:TYR:O	2.21	0.40
20:K:53:ARG:O	20:K:57:ARG:HB2	2.21	0.40
28:R:21:VAL:HG22	28:R:64:ILE:HG22	2.04	0.40
30:U:115:GLU:OE2	30:U:125:SER:HA	2.21	0.40
43:h:68:ILE:HD12	43:h:86:TRP:CD2	2.56	0.40
48:n:145:LEU:HD23	48:n:145:LEU:HA	1.86	0.40
66:AF:83:LEU:HD12	66:AF:112:LYS:HD3	2.03	0.40
72:AL:30[B]:LYS:HB3	72:AL:30[B]:LYS:HE3	1.75	0.40
2:1:904:G:N2	81:1:3412:GET:H933	2.37	0.40
2:1:3133:G:H2'	2:1:3134:C:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:425:C:C4	10:A:426:A:N7	2.89	0.40
10:A:566:G:OP1	34:Y:90:ASP:HA	2.21	0.40
25:P:14:ILE:HA	25:P:22:PHE:O	2.21	0.40
27:T:50:ALA:HB2	27:T:72:ILE:HD12	2.02	0.40
28:R:76:GLN:O	28:R:80:ILE:HG13	2.21	0.40
43:h:32:LEU:CD2	43:h:95:LEU:HD13	2.52	0.40
45:k:58:ARG:O	45:k:71:GLU:HA	2.21	0.40
46:l:20:GLN:C	46:l:21:LEU:HD12	2.46	0.40
53:s:30:LEU:HD21	53:s:47:GLN:HG2	2.02	0.40
61:AA:58:ASP:O	61:AA:62:VAL:HG23	2.21	0.40
70:AJ:88:GLU:O	70:AJ:92:VAL:HG23	2.21	0.40
78:PT:51:U:H2'	78:PT:52:C:H6	1.85	0.40
2:1:949:G:O2'	2:1:1112:G:H5'	2.21	0.40
2:1:2181:U:H2'	2:1:2182:C:H6	1.85	0.40
2:1:2671:G:H5''	3:2:16:GLN:HE21	1.86	0.40
2:1:2719:A:H5'	47:m:175:HIS:HA	2.02	0.40
2:1:2862:A:O2'	2:1:2905:A:N3	2.50	0.40
2:1:3005:A:H2'	2:1:3006:C:C6	2.55	0.40
2:1:3066:A:H2'	2:1:3067:U:C6	2.56	0.40
2:1:3183:A:O2'	2:1:3243:C:H5	2.05	0.40
10:A:336:C:OP2	19:J:10:LYS:HD3	2.20	0.40
10:A:761:G:C2	10:A:769:U:O2	2.75	0.40
10:A:871:U:C2	10:A:872:A:C8	3.09	0.40
10:A:1228:G:H2'	10:A:1228:G:N3	2.35	0.40
10:A:1542:A:O2'	26:Q:82:ASN:ND2	2.34	0.40
14:E:52:LYS:NZ	14:E:91:ARG:O	2.35	0.40
14:E:75:VAL:HA	14:E:80:LEU:HD12	2.02	0.40
18:I:60:PRO:HB3	18:I:90:ALA:HB1	2.03	0.40
21:L:23:ALA:O	21:L:64:TYR:N	2.53	0.40
24:O:45:LEU:HD13	24:O:49:GLN:HG2	2.03	0.40
30:U:107:ALA:O	30:U:111:ILE:HG13	2.22	0.40
33:X:77:PRO:HD2	33:X:79:PHE:CE2	2.56	0.40
43:h:91:ARG:HH11	43:h:103:ARG:HH11	1.70	0.40
45:k:296:THR:OG1	45:k:357:LYS:O	2.31	0.40
54:t:49:ARG:HD2	69:AI:116:PHE:CE2	2.56	0.40
2:1:377:A:H1'	2:1:392:G:N2	2.37	0.40
2:1:438:A:N1	2:1:489:G:O2'	2.52	0.40
2:1:1612:U:H2'	2:1:1613:G:C8	2.57	0.40
2:1:1764:C:H2'	2:1:1765:G:C8	2.56	0.40
10:A:1521:G:O2'	10:A:1522:U:OP2	2.32	0.40
10:A:1546:G:C8	27:T:134:ARG:HD3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:E:70:LEU:O	14:E:74:ILE:HG12	2.22	0.40
16:G:225:ARG:HG2	39:d:61:ARG:HH12	1.87	0.40
19:J:163:ASP:OD1	19:J:164:SER:N	2.54	0.40
23:N:97:LEU:HA	23:N:100:TRP:NE1	2.36	0.40
27:T:21:ASN:O	27:T:34:LYS:HE2	2.20	0.40
33:X:20:THR:O	33:X:20:THR:HG22	2.21	0.40
35:Z:57:VAL:HA	35:Z:73:GLY:HA2	2.04	0.40
45:k:81:THR:HB	45:k:205:VAL:CG1	2.51	0.40
45:k:123:TYR:CZ	45:k:124:LYS:HG3	2.57	0.40
45:k:128:LYS:O	45:k:131:THR:OG1	2.34	0.40
45:k:183:ILE:HD13	45:k:183:ILE:HG21	1.91	0.40
61:AA:53:VAL:HA	61:AA:57:MET:HE1	2.01	0.40
65:AE:11:TYR:O	65:AE:71:ARG:HD2	2.21	0.40
66:AF:90:THR:HG22	66:AF:118:VAL:HG22	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	171/172 (99%)	169 (99%)	2 (1%)	0	100	100
3	2	159/160 (99%)	156 (98%)	3 (2%)	0	100	100
6	6	129/137 (94%)	127 (98%)	2 (2%)	0	100	100
7	7	60/155 (39%)	59 (98%)	1 (2%)	0	100	100
8	8	119/142 (84%)	117 (98%)	2 (2%)	0	100	100
9	9	123/127 (97%)	120 (98%)	3 (2%)	0	100	100
11	B	206/261 (79%)	192 (93%)	14 (7%)	0	100	100
12	C	212/256 (83%)	203 (96%)	9 (4%)	0	100	100
13	D	214/249 (86%)	209 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	E	220/251 (88%)	211 (96%)	9 (4%)	0	100	100
15	F	258/262 (98%)	240 (93%)	18 (7%)	0	100	100
16	G	195/225 (87%)	187 (96%)	8 (4%)	0	100	100
17	H	224/236 (95%)	212 (95%)	12 (5%)	0	100	100
18	I	180/186 (97%)	170 (94%)	10 (6%)	0	100	100
19	J	201/206 (98%)	193 (96%)	8 (4%)	0	100	100
20	K	176/189 (93%)	163 (93%)	13 (7%)	0	100	100
21	L	91/118 (77%)	84 (92%)	7 (8%)	0	100	100
22	M	139/155 (90%)	132 (95%)	7 (5%)	0	100	100
23	N	65/143 (46%)	53 (82%)	12 (18%)	0	100	100
24	O	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
25	P	124/132 (94%)	122 (98%)	2 (2%)	0	100	100
26	Q	113/142 (80%)	103 (91%)	10 (9%)	0	100	100
27	T	140/145 (97%)	125 (89%)	15 (11%)	0	100	100
28	R	139/142 (98%)	132 (95%)	6 (4%)	1 (1%)	19	13
29	S	116/137 (85%)	111 (96%)	5 (4%)	0	100	100
30	U	139/145 (96%)	135 (97%)	4 (3%)	0	100	100
31	V	98/119 (82%)	93 (95%)	5 (5%)	0	100	100
32	W	85/87 (98%)	78 (92%)	7 (8%)	0	100	100
33	X	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
34	Y	141/145 (97%)	134 (95%)	7 (5%)	0	100	100
35	Z	130/135 (96%)	118 (91%)	12 (9%)	0	100	100
36	a	70/105 (67%)	62 (89%)	8 (11%)	0	100	100
37	b	96/119 (81%)	92 (96%)	4 (4%)	0	100	100
38	c	79/82 (96%)	70 (89%)	9 (11%)	0	100	100
39	d	60/67 (90%)	57 (95%)	3 (5%)	0	100	100
40	e	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
41	f	56/63 (89%)	53 (95%)	3 (5%)	0	100	100
42	g	66/193 (34%)	51 (77%)	15 (23%)	0	100	100
43	h	229/317 (72%)	198 (86%)	31 (14%)	0	100	100
44	j	248/254 (98%)	239 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	k	385/389 (99%)	376 (98%)	9 (2%)	0	100	100
46	l	359/363 (99%)	349 (97%)	10 (3%)	0	100	100
47	m	290/298 (97%)	278 (96%)	12 (4%)	0	100	100
48	n	152/176 (86%)	147 (97%)	5 (3%)	0	100	100
49	o	229/241 (95%)	224 (98%)	5 (2%)	0	100	100
50	p	229/262 (87%)	222 (97%)	7 (3%)	0	100	100
51	q	187/191 (98%)	181 (97%)	6 (3%)	0	100	100
52	r	216/220 (98%)	212 (98%)	4 (2%)	0	100	100
53	s	171/174 (98%)	170 (99%)	1 (1%)	0	100	100
54	t	193/202 (96%)	183 (95%)	8 (4%)	2 (1%)	13	8
55	u	128/131 (98%)	124 (97%)	4 (3%)	0	100	100
56	v	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
57	w	197/200 (98%)	194 (98%)	3 (2%)	0	100	100
58	x	168/185 (91%)	162 (96%)	6 (4%)	0	100	100
59	y	186/186 (100%)	180 (97%)	6 (3%)	0	100	100
60	z	179/190 (94%)	177 (99%)	2 (1%)	0	100	100
61	AA	133/136 (98%)	133 (100%)	0	0	100	100
62	AB	146/149 (98%)	142 (97%)	4 (3%)	0	100	100
63	AC	59/63 (94%)	59 (100%)	0	0	100	100
64	AD	94/106 (89%)	93 (99%)	1 (1%)	0	100	100
65	AE	106/112 (95%)	102 (96%)	4 (4%)	0	100	100
66	AF	124/131 (95%)	124 (100%)	0	0	100	100
67	AG	107/107 (100%)	105 (98%)	2 (2%)	0	100	100
68	AH	114/122 (93%)	112 (98%)	2 (2%)	0	100	100
69	AI	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
70	AJ	96/99 (97%)	95 (99%)	1 (1%)	0	100	100
71	AK	84/90 (93%)	81 (96%)	3 (4%)	0	100	100
72	AL	76/78 (97%)	74 (97%)	2 (3%)	0	100	100
73	AM	49/51 (96%)	47 (96%)	2 (4%)	0	100	100
74	AN	51/52 (98%)	51 (100%)	0	0	100	100
75	AO	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	AP	103/106 (97%)	100 (97%)	3 (3%)	0	100	100
77	AQ	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
All	All	10641/11747 (91%)	10202 (96%)	435 (4%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	R	40	PRO
54	t	5	LYS
54	t	63	VAL
75	AO	3	ASP

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	0	158/157 (101%)	158 (100%)	0	100	100
3	2	135/134 (101%)	135 (100%)	0	100	100
6	6	101/103 (98%)	101 (100%)	0	100	100
7	7	56/127 (44%)	56 (100%)	0	100	100
8	8	108/121 (89%)	108 (100%)	0	100	100
9	9	110/112 (98%)	110 (100%)	0	100	100
11	B	176/215 (82%)	176 (100%)	0	100	100
12	C	194/229 (85%)	194 (100%)	0	100	100
13	D	174/198 (88%)	174 (100%)	0	100	100
14	E	173/196 (88%)	173 (100%)	0	100	100
15	F	218/220 (99%)	218 (100%)	0	100	100
16	G	173/197 (88%)	173 (100%)	0	100	100
17	H	195/204 (96%)	195 (100%)	0	100	100
18	I	163/167 (98%)	163 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	J	157/160 (98%)	157 (100%)	0	100	100
20	K	153/160 (96%)	153 (100%)	0	100	100
21	L	87/104 (84%)	87 (100%)	0	100	100
22	M	122/134 (91%)	122 (100%)	0	100	100
23	N	60/123 (49%)	60 (100%)	0	100	100
24	O	129/130 (99%)	129 (100%)	0	100	100
25	P	96/101 (95%)	96 (100%)	0	100	100
26	Q	99/121 (82%)	99 (100%)	0	100	100
27	T	126/129 (98%)	126 (100%)	0	100	100
28	R	115/116 (99%)	115 (100%)	0	100	100
29	S	106/122 (87%)	106 (100%)	0	100	100
30	U	113/117 (97%)	113 (100%)	0	100	100
31	V	90/105 (86%)	90 (100%)	0	100	100
32	W	71/71 (100%)	71 (100%)	0	100	100
33	X	112/113 (99%)	112 (100%)	0	100	100
34	Y	116/118 (98%)	116 (100%)	0	100	100
35	Z	109/112 (97%)	109 (100%)	0	100	100
36	a	64/85 (75%)	64 (100%)	0	100	100
37	b	84/102 (82%)	84 (100%)	0	100	100
38	c	72/73 (99%)	72 (100%)	0	100	100
39	d	54/58 (93%)	54 (100%)	0	100	100
40	e	47/48 (98%)	47 (100%)	0	100	100
41	f	50/54 (93%)	50 (100%)	0	100	100
42	g	60/175 (34%)	60 (100%)	0	100	100
43	h	199/263 (76%)	198 (100%)	1 (0%)	86	91
44	j	191/194 (98%)	189 (99%)	2 (1%)	73	78
45	k	326/328 (99%)	326 (100%)	0	100	100
46	l	290/292 (99%)	290 (100%)	0	100	100
47	m	247/252 (98%)	247 (100%)	0	100	100
48	n	135/154 (88%)	135 (100%)	0	100	100
49	o	195/204 (96%)	195 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	p	193/216 (89%)	193 (100%)	0	100	100
51	q	168/170 (99%)	168 (100%)	0	100	100
52	r	185/186 (100%)	185 (100%)	0	100	100
53	s	148/149 (99%)	148 (100%)	0	100	100
54	t	163/168 (97%)	163 (100%)	0	100	100
55	u	108/109 (99%)	108 (100%)	0	100	100
56	v	177/178 (99%)	177 (100%)	0	100	100
57	w	166/167 (99%)	166 (100%)	0	100	100
58	x	142/154 (92%)	142 (100%)	0	100	100
59	y	156/154 (101%)	154 (99%)	2 (1%)	65	71
60	z	148/153 (97%)	148 (100%)	0	100	100
61	AA	117/118 (99%)	117 (100%)	0	100	100
62	AB	120/121 (99%)	120 (100%)	0	100	100
63	AC	48/49 (98%)	46 (96%)	2 (4%)	25	24
64	AD	81/90 (90%)	81 (100%)	0	100	100
65	AE	97/100 (97%)	97 (100%)	0	100	100
66	AF	111/115 (96%)	109 (98%)	2 (2%)	54	59
67	AG	94/92 (102%)	94 (100%)	0	100	100
68	AH	99/102 (97%)	99 (100%)	0	100	100
69	AI	106/106 (100%)	106 (100%)	0	100	100
70	AJ	78/79 (99%)	78 (100%)	0	100	100
71	AK	70/73 (96%)	70 (100%)	0	100	100
72	AL	69/69 (100%)	67 (97%)	2 (3%)	37	38
73	AM	47/47 (100%)	47 (100%)	0	100	100
74	AN	48/47 (102%)	48 (100%)	0	100	100
75	AO	24/24 (100%)	24 (100%)	0	100	100
76	AP	90/89 (101%)	90 (100%)	0	100	100
77	AQ	72/73 (99%)	72 (100%)	0	100	100
All	All	9134/9896 (92%)	9123 (100%)	11 (0%)	92	95

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	h	122	GLN
44	j	70[A]	LYS
44	j	70[B]	LYS
59	y	31[A]	LYS
59	y	31[B]	LYS
63	AC	14[A]	ARG
63	AC	14[B]	ARG
66	AF	17[A]	LYS
66	AF	17[B]	LYS
72	AL	30[A]	LYS
72	AL	30[B]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (99) such sidechains are listed below:

Mol	Chain	Res	Type
3	2	16	GLN
8	8	60	HIS
9	9	44	ASN
12	C	124	ASN
13	D	84	GLN
14	E	102	GLN
15	F	188	ASN
16	G	37	GLN
16	G	63	GLN
16	G	103	ASN
16	G	104	ASN
16	G	131	GLN
16	G	139	ASN
17	H	69	HIS
17	H	139	ASN
17	H	217	HIS
18	I	48	ASN
18	I	146	GLN
19	J	111	GLN
19	J	129	HIS
19	J	132	HIS
19	J	165	GLN
20	K	131	GLN
20	K	176	ASN
21	L	13	GLN
22	M	14	GLN
25	P	7	GLN
27	T	74	GLN

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Mol	Chain	Res	Type
27	T	89	GLN
27	T	137	HIS
29	S	42	GLN
29	S	48	ASN
29	S	99	GLN
30	U	64	HIS
30	U	138	GLN
31	V	19	HIS
31	V	93	GLN
32	W	29	HIS
33	X	12	ASN
34	Y	18	HIS
35	Z	77	GLN
36	a	98	GLN
38	c	26	GLN
40	e	3	HIS
40	e	53	ASN
41	f	5	HIS
41	f	17	GLN
42	g	181	GLN
43	h	65	HIS
44	j	8	GLN
44	j	97	ASN
44	j	205	ASN
45	k	182	GLN
45	k	224	HIS
45	k	316	ASN
46	l	111	ASN
46	l	141	HIS
46	l	176	HIS
46	l	297	GLN
46	l	321	ASN
48	n	71	ASN
48	n	91	ASN
49	o	91	ASN
50	p	205	ASN
51	q	46	ASN
51	q	77	ASN
54	t	66	ASN
54	t	106	GLN
56	v	32	GLN
56	v	91	GLN

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Mol	Chain	Res	Type
56	v	95	GLN
57	w	51	ASN
57	w	123	GLN
58	x	34	GLN
58	x	99	GLN
58	x	137	ASN
60	z	7	GLN
60	z	130	ASN
62	AB	14	ASN
62	AB	38	GLN
62	AB	49	HIS
63	AC	17	HIS
65	AE	16	HIS
65	AE	20	HIS
65	AE	68	ASN
66	AF	21	HIS
66	AF	53	GLN
67	AG	31	GLN
67	AG	106	ASN
69	AI	34	GLN
69	AI	59	ASN
69	AI	99	GLN
71	AK	20	ASN
72	AL	40	GLN
72	AL	66	GLN
73	AM	17	GLN
76	AP	22	GLN
77	AQ	48	GLN
77	AQ	56	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	1685/1787 (94%)	385 (22%)	26 (1%)
2	1	3060/3359 (91%)	467 (15%)	34 (1%)
4	3	120/121 (99%)	9 (7%)	0
5	4	155/158 (98%)	20 (12%)	1 (0%)
78	AT	76/77 (98%)	21 (27%)	1 (1%)
78	PT	75/77 (97%)	14 (18%)	0
79	MR	10/39 (25%)	0	0
All	All	5181/5618 (92%)	916 (17%)	62 (1%)

All (916) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	5	A
2	1	25	A
2	1	39	A
2	1	42	A
2	1	48	A
2	1	58	G
2	1	59	A
2	1	64	A
2	1	65	A
2	1	71	C
2	1	91	G
2	1	98	A
2	1	108	A
2	1	109	G
2	1	110	C
2	1	121	A
2	1	134	U
2	1	135	G
2	1	145	U
2	1	155	A
2	1	156	A
2	1	161	G
2	1	163	A
2	1	164	U
2	1	166	U
2	1	173	C
2	1	175	G
2	1	189	U
2	1	190	U
2	1	199	C
2	1	205	G
2	1	209	C
2	1	212	A
2	1	217	G
2	1	218	A
2	1	230	G
2	1	239	A
2	1	240	C
2	1	243	G
2	1	249	G
2	1	250	U
2	1	251	G

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Mol	Chain	Res	Type
2	1	252	U
2	1	253	A
2	1	257	U
2	1	269	G
2	1	286	U
2	1	295	A
2	1	305	U
2	1	323	A
2	1	329	U
2	1	339	C
2	1	349	A
2	1	350	C
2	1	376	G
2	1	377	A
2	1	398	A
2	1	401	U
2	1	402	A
2	1	403	C
2	1	420	G
2	1	421	G
2	1	422	A
2	1	438	A
2	1	439	C
2	1	506	A
2	1	517	A
2	1	531	G
2	1	537	C
2	1	538	G
2	1	539	G
2	1	541	U
2	1	542	U
2	1	543	C
2	1	544	U
2	1	545	G
2	1	546	C
2	1	549	U
2	1	555	A
2	1	556	U
2	1	557	A
2	1	564	G
2	1	566	C
2	1	568	A

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Mol	Chain	Res	Type
2	1	576	A
2	1	577	G
2	1	590	A
2	1	599	U
2	1	600	U
2	1	602	A
2	1	609	A
2	1	618	U
2	1	619	A
2	1	620	A
2	1	634	C
2	1	647	A
2	1	658	A
2	1	675	A
2	1	679	U
2	1	703	A
2	1	710	G
2	1	713	A
2	1	717	A
2	1	730	A
2	1	732	U
2	1	759	G
2	1	763	U
2	1	772	U
2	1	773	U
2	1	777	G
2	1	781	G
2	1	802	A
2	1	813	A
2	1	826	A
2	1	845	C
2	1	857	C
2	1	870	U
2	1	875	U
2	1	892	A
2	1	893	U
2	1	903	G
2	1	904	G
2	1	910	A
2	1	912	G
2	1	913	A
2	1	919	C

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Mol	Chain	Res	Type
2	1	921	A
2	1	933	G
2	1	940	C
2	1	955	C
2	1	956	U
2	1	975	U
2	1	976	A
2	1	978	C
2	1	990	G
2	1	996	C
2	1	997	G
2	1	998	A
2	1	1006	G
2	1	1011	C
2	1	1012	U
2	1	1013	U
2	1	1014	G
2	1	1016	G
2	1	1029	U
2	1	1030	U
2	1	1033	C
2	1	1037	U
2	1	1043	A
2	1	1045	C
2	1	1060	A
2	1	1061	A
2	1	1077	U
2	1	1078	U
2	1	1090	A
2	1	1091	U
2	1	1092	U
2	1	1094	A
2	1	1099	A
2	1	1100	G
2	1	1113	G
2	1	1127	G
2	1	1149	A
2	1	1155	A
2	1	1170	G
2	1	1174	G
2	1	1176	A
2	1	1177	U

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Mol	Chain	Res	Type
2	1	1178	G
2	1	1188	C
2	1	1189	A
2	1	1192	C
2	1	1197	C
2	1	1205	G
2	1	1216	U
2	1	1283	A
2	1	1304	A
2	1	1305	U
2	1	1322	A
2	1	1326	A
2	1	1345	G
2	1	1346	U
2	1	1347	U
2	1	1348	U
2	1	1352	C
2	1	1353	G
2	1	1382	A
2	1	1395	U
2	1	1415	A
2	1	1421	U
2	1	1430	G
2	1	1433	C
2	1	1442	A
2	1	1446	G
2	1	1477	A
2	1	1483	G
2	1	1498	C
2	1	1504	C
2	1	1523	C
2	1	1524	G
2	1	1529	U
2	1	1532	G
2	1	1535	A
2	1	1551	U
2	1	1552	C
2	1	1556	G
2	1	1558	G
2	1	1560	U
2	1	1561	U
2	1	1562	G

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Mol	Chain	Res	Type
2	1	1563	A
2	1	1565	U
2	1	1566	U
2	1	1567	U
2	1	1568	U
2	1	1569	C
2	1	1571	G
2	1	1574	C
2	1	1585	A
2	1	1589	A
2	1	1601	A
2	1	1603	U
2	1	1625	U
2	1	1635	C
2	1	1638	A
2	1	1639	A
2	1	1641	U
2	1	1653	C
2	1	1654	G
2	1	1679	A
2	1	1683	U
2	1	1720	U
2	1	1721	C
2	1	1732	G
2	1	1746	A
2	1	1747	G
2	1	1758	U
2	1	1760	U
2	1	1761	U
2	1	1762	G
2	1	1763	C
2	1	1774	G
2	1	1776	G
2	1	1792	G
2	1	1793	A
2	1	1808	G
2	1	1811	U
2	1	1812	A
2	1	1814	U
2	1	1815	U
2	1	1816	U
2	1	1817	U

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Mol	Chain	Res	Type
2	1	1835	A
2	1	1838	A
2	1	1842	C
2	1	1845	C
2	1	1862	C
2	1	1872	U
2	1	1874	G
2	1	1876	U
2	1	1902	G
2	1	1944	G
2	1	2070	A
2	1	2072	C
2	1	2078	A
2	1	2089	G
2	1	2090	U
2	1	2091	A
2	1	2092	C
2	1	2099	G
2	1	2100	G
2	1	2109	A
2	1	2118	U
2	1	2122	A
2	1	2136	A
2	1	2147	G
2	1	2166	A
2	1	2185	A
2	1	2186	A
2	1	2187	U
2	1	2188	G
2	1	2222	A
2	1	2227	G
2	1	2233	A
2	1	2235	C
2	1	2250	G
2	1	2251	G
2	1	2259	A
2	1	2260	U
2	1	2276	U
2	1	2285	G
2	1	2288	U
2	1	2291	A
2	1	2292	U

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Mol	Chain	Res	Type
2	1	2293	G
2	1	2312	U
2	1	2313	G
2	1	2314	U
2	1	2341	A
2	1	2351	A
2	1	2352	C
2	1	2353	G
2	1	2363	G
2	1	2366	U
2	1	2371	G
2	1	2372	G
2	1	2375	A
2	1	2380	A
2	1	2381	G
2	1	2382	A
2	1	2389	U
2	1	2397	A
2	1	2420	G
2	1	2422	C
2	1	2482	U
2	1	2484	U
2	1	2489	A
2	1	2492	U
2	1	2493	A
2	1	2510	U
2	1	2511	G
2	1	2513	A
2	1	2515	G
2	1	2516	U
2	1	2517	C
2	1	2518	A
2	1	2519	A
2	1	2520	A
2	1	2521	C
2	1	2522	U
2	1	2527	G
2	1	2530	C
2	1	2536	U
2	1	2537	U
2	1	2538	A
2	1	2545	C

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Mol	Chain	Res	Type
2	1	2546	U
2	1	2547	G
2	1	2554	C
2	1	2557	G
2	1	2565	A
2	1	2566	C
2	1	2578	G
2	1	2579	G
2	1	2586	G
2	1	2598	A
2	1	2609	A
2	1	2624	U
2	1	2628	A
2	1	2646	A
2	1	2649	G
2	1	2653	U
2	1	2661	A
2	1	2663	A
2	1	2666	A
2	1	2676	A
2	1	2686	G
2	1	2700	G
2	1	2701	U
2	1	2725	G
2	1	2727	C
2	1	2734	A
2	1	2744	C
2	1	2745	C
2	1	2749	G
2	1	2750	G
2	1	2768	G
2	1	2771	A
2	1	2772	G
2	1	2773	A
2	1	2786	G
2	1	2789	A
2	1	2790	U
2	1	2791	A
2	1	2814	U
2	1	2815	U
2	1	2817	A
2	1	2843	G

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Mol	Chain	Res	Type
2	1	2844	A
2	1	2847	U
2	1	2859	A
2	1	2861	C
2	1	2866	C
2	1	2871	C
2	1	2886	G
2	1	2895	U
2	1	2900	C
2	1	2907	U
2	1	2908	A
2	1	2914	C
2	1	2919	G
2	1	2923	G
2	1	2943	A
2	1	2955	C
2	1	2962	G
2	1	2968	U
2	1	2969	G
2	1	2984	A
2	1	3028	U
2	1	3031	G
2	1	3050	A
2	1	3051	C
2	1	3052	G
2	1	3058	A
2	1	3064	C
2	1	3065	C
2	1	3076	U
2	1	3094	A
2	1	3101	A
2	1	3102	A
2	1	3103	U
2	1	3114	A
2	1	3115	C
2	1	3134	C
2	1	3138	U
2	1	3143	G
2	1	3144	A
2	1	3146	G
2	1	3149	U
2	1	3151	C

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Mol	Chain	Res	Type
2	1	3157	A
2	1	3163	U
2	1	3164	U
2	1	3165	U
2	1	3171	C
2	1	3172	U
2	1	3182	C
2	1	3183	A
2	1	3184	G
2	1	3187	U
2	1	3194	G
2	1	3200	C
2	1	3208	A
2	1	3210	A
2	1	3211	G
2	1	3212	G
2	1	3214	U
2	1	3224	U
2	1	3225	G
2	1	3228	G
2	1	3235	A
2	1	3236	G
2	1	3241	G
2	1	3246	C
2	1	3251	G
2	1	3252	C
2	1	3255	G
2	1	3259	A
2	1	3260	A
2	1	3269	C
2	1	3272	A
2	1	3281	A
2	1	3284	U
2	1	3306	U
2	1	3309	A
2	1	3310	G
2	1	3312	A
2	1	3316	U
2	1	3318	G
2	1	3319	U
2	1	3320	U
2	1	3321	G

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Mol	Chain	Res	Type
2	1	3334	G
2	1	3343	C
2	1	3347	U
2	1	3351	G
2	1	3361	U
4	3	22	A
4	3	42	A
4	3	54	U
4	3	55	A
4	3	65	G
4	3	73	C
4	3	76	A
4	3	102	A
4	3	112	G
5	4	34	U
5	4	35	C
5	4	53	A
5	4	59	A
5	4	62	C
5	4	63	G
5	4	81	A
5	4	84	C
5	4	86	U
5	4	87	G
5	4	95	G
5	4	102	U
5	4	104	A
5	4	105	A
5	4	106	C
5	4	111	A
5	4	113	U
5	4	125	U
5	4	126	A
5	4	152	G
10	A	25	C
10	A	26	A
10	A	27	U
10	A	34	G
10	A	42	G
10	A	45	U
10	A	47	A
10	A	57	G

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Mol	Chain	Res	Type
10	A	59	C
10	A	63	G
10	A	66	U
10	A	74	U
10	A	75	U
10	A	76	A
10	A	77	U
10	A	78	A
10	A	81	G
10	A	84	A
10	A	100	A
10	A	104	A
10	A	111	U
10	A	114	C
10	A	115	G
10	A	123	G
10	A	124	A
10	A	127	G
10	A	129	A
10	A	138	C
10	A	139	U
10	A	142	G
10	A	143	A
10	A	151	G
10	A	152	G
10	A	154	A
10	A	159	U
10	A	166	A
10	A	167	A
10	A	174	C
10	A	176	U
10	A	177	A
10	A	190	U
10	A	192	U
10	A	193	G
10	A	199	G
10	A	200	A
10	A	201	U
10	A	202	G
10	A	211	A
10	A	213	A
10	A	215	A

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Mol	Chain	Res	Type
10	A	216	A
10	A	217	A
10	A	218	A
10	A	219	A
10	A	255	A
10	A	259	U
10	A	260	U
10	A	261	C
10	A	262	G
10	A	268	C
10	A	269	A
10	A	270	U
10	A	274	C
10	A	276	U
10	A	277	G
10	A	278	U
10	A	279	G
10	A	283	G
10	A	285	G
10	A	299	A
10	A	312	C
10	A	314	A
10	A	319	C
10	A	320	G
10	A	327	G
10	A	331	A
10	A	335	G
10	A	336	C
10	A	350	A
10	A	357	A
10	A	358	A
10	A	359	C
10	A	388	G
10	A	398	A
10	A	399	A
10	A	400	C
10	A	402	G
10	A	414	A
10	A	416	G
10	A	421	G
10	A	422	C
10	A	423	A

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Mol	Chain	Res	Type
10	A	424	G
10	A	432	G
10	A	437	U
10	A	442	C
10	A	446	C
10	A	457	G
10	A	458	A
10	A	466	A
10	A	475	A
10	A	479	A
10	A	480	U
10	A	482	C
10	A	483	A
10	A	485	G
10	A	500	U
10	A	501	G
10	A	503	A
10	A	505	U
10	A	506	U
10	A	509	A
10	A	512	G
10	A	515	U
10	A	525	A
10	A	530	U
10	A	533	A
10	A	537	G
10	A	539	A
10	A	540	A
10	A	547	G
10	A	553	A
10	A	554	A
10	A	555	G
10	A	556	U
10	A	557	C
10	A	563	C
10	A	566	G
10	A	577	A
10	A	580	U
10	A	592	A
10	A	593	G
10	A	604	A
10	A	617	A

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Mol	Chain	Res	Type
10	A	618	A
10	A	620	A
10	A	621	A
10	A	622	G
10	A	648	U
10	A	650	G
10	A	651	C
10	A	652	C
10	A	653	G
10	A	654	G
10	A	655	U
10	A	678	A
10	A	682	A
10	A	686	G
10	A	688	G
10	A	689	C
10	A	690	C
10	A	693	U
10	A	694	C
10	A	696	U
10	A	701	G
10	A	722	A
10	A	723	G
10	A	725	A
10	A	728	U
10	A	730	U
10	A	740	A
10	A	741	A
10	A	750	G
10	A	751	U
10	A	752	U
10	A	756	A
10	A	759	A
10	A	760	G
10	A	763	C
10	A	764	U
10	A	765	U
10	A	766	U
10	A	767	G
10	A	771	G
10	A	773	A
10	A	778	U

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Mol	Chain	Res	Type
10	A	779	U
10	A	787	A
10	A	796	A
10	A	798	A
10	A	799	G
10	A	803	G
10	A	804	U
10	A	805	U
10	A	806	A
10	A	807	U
10	A	813	U
10	A	814	A
10	A	816	U
10	A	818	U
10	A	819	G
10	A	820	U
10	A	821	U
10	A	823	G
10	A	824	U
10	A	826	U
10	A	828	U
10	A	829	A
10	A	831	G
10	A	839	U
10	A	842	U
10	A	848	A
10	A	858	U
10	A	869	A
10	A	877	G
10	A	879	U
10	A	881	U
10	A	891	A
10	A	898	G
10	A	910	G
10	A	911	A
10	A	918	A
10	A	920	U
10	A	945	U
10	A	951	A
10	A	971	G
10	A	973	A
10	A	977	A

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Mol	Chain	Res	Type
10	A	988	A
10	A	989	U
10	A	1005	A
10	A	1011	A
10	A	1013	C
10	A	1024	A
10	A	1025	G
10	A	1035	G
10	A	1036	U
10	A	1038	G
10	A	1042	U
10	A	1043	U
10	A	1044	U
10	A	1046	A
10	A	1047	U
10	A	1055	A
10	A	1056	U
10	A	1057	C
10	A	1058	G
10	A	1059	G
10	A	1061	A
10	A	1066	A
10	A	1067	C
10	A	1077	A
10	A	1079	G
10	A	1081	C
10	A	1085	G
10	A	1123	A
10	A	1128	A
10	A	1131	G
10	A	1135	G
10	A	1143	C
10	A	1145	A
10	A	1152	G
10	A	1168	A
10	A	1169	A
10	A	1170	U
10	A	1171	U
10	A	1179	A
10	A	1181	A
10	A	1184	G
10	A	1185	G

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Mol	Chain	Res	Type
10	A	1186	G
10	A	1187	A
10	A	1193	A
10	A	1197	G
10	A	1202	A
10	A	1203	G
10	A	1213	G
10	A	1214	G
10	A	1215	A
10	A	1217	U
10	A	1218	G
10	A	1219	A
10	A	1221	A
10	A	1229	A
10	A	1230	G
10	A	1231	C
10	A	1236	U
10	A	1237	C
10	A	1241	A
10	A	1242	U
10	A	1258	G
10	A	1270	U
10	A	1276	G
10	A	1284	G
10	A	1299	U
10	A	1300	U
10	A	1301	G
10	A	1306	A
10	A	1325	U
10	A	1329	A
10	A	1330	A
10	A	1336	G
10	A	1339	G
10	A	1342	A
10	A	1343	G
10	A	1346	U
10	A	1348	U
10	A	1349	G
10	A	1352	G
10	A	1355	A
10	A	1356	U
10	A	1357	A

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Mol	Chain	Res	Type
10	A	1359	U
10	A	1360	C
10	A	1369	G
10	A	1370	A
10	A	1376	U
10	A	1377	A
10	A	1381	A
10	A	1382	U
10	A	1384	U
10	A	1385	C
10	A	1392	A
10	A	1398	G
10	A	1399	U
10	A	1400	U
10	A	1401	U
10	A	1413	A
10	A	1414	G
10	A	1422	A
10	A	1431	G
10	A	1432	A
10	A	1445	C
10	A	1446	A
10	A	1454	U
10	A	1455	A
10	A	1457	A
10	A	1462	C
10	A	1468	C
10	A	1476	A
10	A	1477	U
10	A	1478	A
10	A	1479	A
10	A	1480	G
10	A	1483	U
10	A	1491	G
10	A	1493	G
10	A	1502	A
10	A	1503	A
10	A	1508	G
10	A	1510	G
10	A	1511	A
10	A	1513	A
10	A	1523	G

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Mol	Chain	Res	Type
10	A	1524	C
10	A	1526	G
10	A	1530	A
10	A	1544	U
10	A	1546	G
10	A	1556	A
10	A	1561	G
10	A	1571	G
10	A	1574	A
10	A	1577	G
10	A	1580	A
10	A	1582	U
10	A	1588	G
10	A	1590	U
10	A	1594	G
10	A	1601	A
10	A	1609	G
10	A	1621	C
10	A	1644	U
10	A	1645	G
10	A	1665	C
10	A	1669	U
10	A	1672	G
10	A	1673	U
10	A	1674	U
10	A	1677	G
10	A	1700	G
10	A	1702	A
10	A	1704	C
10	A	1742	A
10	A	1744	G
10	A	1753	A
10	A	1756	U
10	A	1767	G
10	A	1769	A
10	A	1770	C
10	A	1779	G
10	A	1780	G
10	A	1781	A
10	A	1782	U
10	A	1783	C
78	PT	3	C

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Mol	Chain	Res	Type
78	PT	4	G
78	PT	5	G
78	PT	9	G
78	PT	17	C
78	PT	20	G
78	PT	21	U
78	PT	22	A
78	PT	48	U
78	PT	49	C
78	PT	50	G
78	PT	53	G
78	PT	75	C
78	PT	77	A
78	AT	3	C
78	AT	5	G
78	AT	6	G
78	AT	9	G
78	AT	10	G
78	AT	14	A
78	AT	16	C
78	AT	18(A)	U
78	AT	22	A
78	AT	24	C
78	AT	43	G
78	AT	48	U
78	AT	49	C
78	AT	50	G
78	AT	53	G
78	AT	55	U
78	AT	62	C
78	AT	63	C
78	AT	75	C
78	AT	76	C
78	AT	77	A

All (62) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	172	C
2	1	538	G
2	1	563	U
2	1	586	G

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Mol	Chain	Res	Type
2	1	601	U
2	1	892	A
2	1	912	G
2	1	1012	U
2	1	1029	U
2	1	1060	A
2	1	1099	A
2	1	1346	U
2	1	1347	U
2	1	1430	G
2	1	1559	C
2	1	1567	U
2	1	1762	G
2	1	1815	U
2	1	2090	U
2	1	2515	G
2	1	2519	A
2	1	2557	G
2	1	2789	A
2	1	2790	U
2	1	3028	U
2	1	3093	U
2	1	3163	U
2	1	3193	C
2	1	3234	U
2	1	3240	U
2	1	3268	G
2	1	3309	A
2	1	3315	C
2	1	3317	U
5	4	85	G
10	A	25	C
10	A	137	A
10	A	151	G
10	A	176	U
10	A	214	U
10	A	259	U
10	A	415	A
10	A	504	A
10	A	505	U
10	A	514	G
10	A	529	C

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Mol	Chain	Res	Type
10	A	553	A
10	A	740	A
10	A	763	C
10	A	820	U
10	A	876	A
10	A	1168	A
10	A	1335	U
10	A	1369	G
10	A	1398	G
10	A	1467	C
10	A	1479	A
10	A	1555	C
10	A	1573	A
10	A	1579	A
10	A	1581	G
78	AT	2	G

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

6 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	$\# Z > 2$
25	IAS	P	119	25	6,7,8	1.19	0	5,8,10	1.44	1 (20%)
2	OMC	1	2808	2	19,22,23	2.84	8 (42%)	26,31,34	1.13	2 (7%)
76	MLZ	AP	40	76	8,9,10	0.80	0	4,9,11	0.62	0
2	OMG	1	2765	2	18,26,27	2.34	8 (44%)	19,38,41	1.53	4 (21%)
6	MLZ	6	110	6	8,9,10	0.77	0	4,9,11	0.56	0
76	MLZ	AP	55	76	8,9,10	0.71	0	4,9,11	0.64	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
25	IAS	P	119	25	-	2/5/6/8	-
2	OMC	1	2808	2	-	2/9/27/28	0/2/2/2
76	MLZ	AP	40	76	-	3/7/8/10	-
2	OMG	1	2765	2	-	0/5/27/28	0/3/3/3
6	MLZ	6	110	6	-	2/7/8/10	-
76	MLZ	AP	55	76	-	1/7/8/10	-

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	2808	OMC	C2-N3	5.76	1.48	1.36
2	1	2808	OMC	C6-C5	5.61	1.48	1.35
2	1	2765	OMG	C2-N3	4.96	1.45	1.33
2	1	2808	OMC	C2-N1	4.57	1.49	1.40
2	1	2808	OMC	C4-N4	4.56	1.44	1.33
2	1	2765	OMG	C4-N3	4.40	1.48	1.37
2	1	2808	OMC	C4-N3	4.34	1.43	1.34
2	1	2765	OMG	C2-N2	3.77	1.43	1.34
2	1	2808	OMC	O2-C2	-3.37	1.17	1.23
2	1	2765	OMG	C6-N1	3.17	1.42	1.37
2	1	2765	OMG	C5-C4	-3.04	1.35	1.43
2	1	2765	OMG	O6-C6	-2.97	1.17	1.23
2	1	2808	OMC	C6-N1	2.93	1.45	1.38
2	1	2765	OMG	C5-C6	2.57	1.52	1.47
2	1	2808	OMC	C5-C4	2.33	1.48	1.42
2	1	2765	OMG	C2-N1	2.07	1.42	1.37

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	2765	OMG	C5-C6-N1	3.68	120.45	113.95
2	1	2808	OMC	O2-C2-N3	-3.18	117.15	122.33
2	1	2765	OMG	C2-N1-C6	-2.85	119.84	125.10
2	1	2765	OMG	C8-N7-C5	2.51	107.78	102.99
25	P	119	IAS	CA-CB-CG	-2.43	98.55	113.74
2	1	2808	OMC	C6-C5-C4	2.36	121.31	117.50
2	1	2765	OMG	O6-C6-C5	-2.32	119.83	124.37

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	1	2808	OMC	O4'-C1'-N1-C2
2	1	2808	OMC	O4'-C1'-N1-C6
25	P	119	IAS	C-CA-CB-CG
76	AP	40	MLZ	CG-CD-CE-NZ
6	6	110	MLZ	CE-CD-CG-CB
25	P	119	IAS	N-CA-CB-CG
76	AP	55	MLZ	CA-CB-CG-CD
76	AP	40	MLZ	CE-CD-CG-CB
6	6	110	MLZ	CD-CE-NZ-CM
76	AP	40	MLZ	CD-CE-NZ-CM

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	1	2808	OMC	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 25 ligands modelled in this entry, 7 are monoatomic - leaving 18 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	$\# Z > 2$
81	GET	A	1801	-	33,36,36	0.46	0	43,55,55	0.84	3 (6%)
81	GET	1	3412	-	33,36,36	0.53	0	43,55,55	0.63	0
81	GET	1	3403	-	33,36,36	0.56	0	43,55,55	0.92	2 (4%)
80	SPK	1	3401	-	13,13,13	0.39	0	12,12,12	0.90	0
81	GET	1	3402	-	33,36,36	0.44	0	43,55,55	0.63	1 (2%)
81	GET	A	1803	-	33,36,36	0.47	0	43,55,55	0.81	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
83	YMZ	AQ	301	-	28,28,28	1.20	1 (3%)	41,43,43	1.47	5 (12%)
81	GET	1	3413	-	33,36,36	0.44	0	43,55,55	0.98	2 (4%)
81	GET	1	3409	-	33,36,36	0.50	0	43,55,55	0.78	1 (2%)
81	GET	AT	101	-	33,36,36	0.49	0	43,55,55	0.64	1 (2%)
81	GET	1	3404	-	33,36,36	0.55	0	43,55,55	0.88	2 (4%)
81	GET	A	1802	-	33,36,36	0.44	0	43,55,55	0.87	2 (4%)
81	GET	1	3407	-	33,36,36	0.45	0	43,55,55	0.77	2 (4%)
81	GET	1	3410	-	33,36,36	0.42	0	43,55,55	0.71	1 (2%)
81	GET	1	3411	-	33,36,36	0.46	0	43,55,55	0.77	2 (4%)
81	GET	1	3405	-	33,36,36	0.43	0	43,55,55	0.80	1 (2%)
81	GET	1	3406	-	33,36,36	0.49	0	43,55,55	0.92	1 (2%)
81	GET	1	3408	-	33,36,36	0.42	0	43,55,55	0.69	1 (2%)

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
81	GET	A	1801	-	-	1/13/74/74	1/3/3/3
81	GET	1	3412	-	-	1/13/74/74	0/3/3/3
81	GET	1	3403	-	-	7/13/74/74	1/3/3/3
80	SPK	1	3401	-	-	6/11/11/11	-
81	GET	1	3402	-	-	1/13/74/74	0/3/3/3
81	GET	A	1803	-	-	7/13/74/74	0/3/3/3
83	YMZ	AQ	301	-	-	7/20/28/28	0/3/3/3
81	GET	1	3413	-	-	3/13/74/74	0/3/3/3
81	GET	1	3409	-	-	3/13/74/74	1/3/3/3
81	GET	AT	101	-	-	2/13/74/74	1/3/3/3
81	GET	1	3404	-	-	3/13/74/74	1/3/3/3
81	GET	A	1802	-	-	1/13/74/74	0/3/3/3
81	GET	1	3407	-	-	1/13/74/74	0/3/3/3
81	GET	1	3410	-	-	1/13/74/74	0/3/3/3
81	GET	1	3411	-	-	1/13/74/74	0/3/3/3
81	GET	1	3405	-	-	1/13/74/74	0/3/3/3
81	GET	1	3406	-	-	1/13/74/74	0/3/3/3
81	GET	1	3408	-	-	1/13/74/74	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	AQ	301	YMZ	CAW-CAX	5.17	1.60	1.53

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	AQ	301	YMZ	CAK-CAR-NAP	4.54	128.32	125.50
81	1	3405	GET	O11-C11-C21	4.33	115.67	108.22
81	1	3406	GET	O11-C11-C21	4.02	115.14	108.22
81	A	1802	GET	O11-C11-C21	3.63	114.47	108.22
81	1	3413	GET	O11-C11-C21	3.60	114.41	108.22
81	1	3404	GET	O62-C62-C12	-3.28	101.36	109.18
83	AQ	301	YMZ	CAK-CAS-CAW	-3.25	117.66	120.30
81	1	3413	GET	O11-C42-C32	-3.19	101.56	109.18
83	AQ	301	YMZ	CAS-CAK-CAR	-3.19	117.11	118.87
81	1	3410	GET	O11-C11-C21	3.19	113.70	108.22
81	A	1803	GET	O11-C42-C32	-3.05	101.89	109.18
81	1	3408	GET	O11-C11-C21	2.97	113.33	108.22
81	1	3403	GET	O62-C62-C52	-2.96	99.41	107.28
81	1	3402	GET	O11-C11-C21	2.95	113.30	108.22
83	AQ	301	YMZ	CAK-CAR-CAY	-2.88	116.46	120.10
81	AT	101	GET	O62-C62-C12	-2.79	102.52	109.18
81	1	3404	GET	O11-C11-C21	2.70	112.86	108.22
81	1	3407	GET	O62-C62-C12	-2.68	102.78	109.18
81	A	1802	GET	O62-C62-C12	-2.66	102.83	109.18
81	1	3409	GET	O11-C11-C21	2.65	112.78	108.22
83	AQ	301	YMZ	CAR-NAP-CAV	-2.58	114.47	116.89
81	1	3407	GET	O11-C11-C21	2.53	112.58	108.22
81	A	1803	GET	O11-C11-C21	2.35	112.26	108.22
81	1	3411	GET	O62-C62-C12	-2.34	103.59	109.18
81	A	1801	GET	O11-C42-C32	-2.20	103.93	109.18
81	A	1801	GET	O11-C11-C21	2.19	111.99	108.22
81	1	3403	GET	O11-C11-C21	2.18	111.97	108.22
81	A	1801	GET	O62-C62-C12	-2.08	104.22	109.18
81	1	3411	GET	O11-C11-C21	2.03	111.72	108.22

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	1	3402	GET	C23-C33-N33-C93
81	1	3403	GET	C21-C11-O11-C42

Continued on next page...

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Mol	Chain	Res	Type	Atoms
81	1	3403	GET	C41-C51-C61-O61
81	1	3403	GET	C41-C51-C61-C71
81	1	3403	GET	O51-C51-C61-C71
81	1	3404	GET	C23-C33-N33-C93
81	1	3405	GET	C23-C33-N33-C93
81	1	3406	GET	C23-C33-N33-C93
81	1	3407	GET	C23-C33-N33-C93
81	1	3408	GET	C23-C33-N33-C93
81	1	3410	GET	C23-C33-N33-C93
81	1	3411	GET	C23-C33-N33-C93
81	1	3412	GET	C23-C33-N33-C93
81	1	3413	GET	C23-C33-N33-C93
81	A	1801	GET	C23-C33-N33-C93
81	A	1802	GET	C23-C33-N33-C93
81	A	1803	GET	C41-C51-C61-O61
81	A	1803	GET	C41-C51-C61-C71
81	A	1803	GET	O51-C51-C61-O61
81	A	1803	GET	O51-C51-C61-C71
81	A	1803	GET	C23-C33-N33-C93
81	AT	101	GET	C23-C33-N33-C93
80	1	3401	SPK	N5-C6-C7-C8
80	1	3401	SPK	C3-C4-N5-C6
80	1	3401	SPK	C7-C6-N5-C4
81	1	3409	GET	O51-C11-O11-C42
81	1	3413	GET	C52-C42-O11-C11
81	AT	101	GET	O51-C11-O11-C42
81	A	1803	GET	C52-C42-O11-C11
83	AQ	301	YMZ	CAK-CAS-CAW-OAA
83	AQ	301	YMZ	CAU-CAS-CAW-OAA
83	AQ	301	YMZ	CAS-CAW-CAX-NAQ
81	1	3403	GET	O51-C11-O11-C42
81	1	3404	GET	O53-C13-O62-C62
81	1	3413	GET	C32-C42-O11-C11
81	A	1803	GET	C32-C42-O11-C11
80	1	3401	SPK	C6-C7-C8-C9
83	AQ	301	YMZ	CAV-CAT-CAZ-FAE
81	1	3409	GET	C52-C42-O11-C11
81	1	3404	GET	C23-C13-O62-C62
83	AQ	301	YMZ	CAS-CAW-CAX-CAO
83	AQ	301	YMZ	OAA-CAW-CAX-CAO
80	1	3401	SPK	C12-C11-N10-C9
81	1	3403	GET	O51-C51-C61-O61

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Mol	Chain	Res	Type	Atoms
81	1	3403	GET	C52-C62-O62-C13
81	1	3409	GET	C23-C33-N33-C93
80	1	3401	SPK	C8-C9-N10-C11
83	AQ	301	YMZ	CAI-CAT-CAZ-FAE

All (5) ring outliers are listed below:

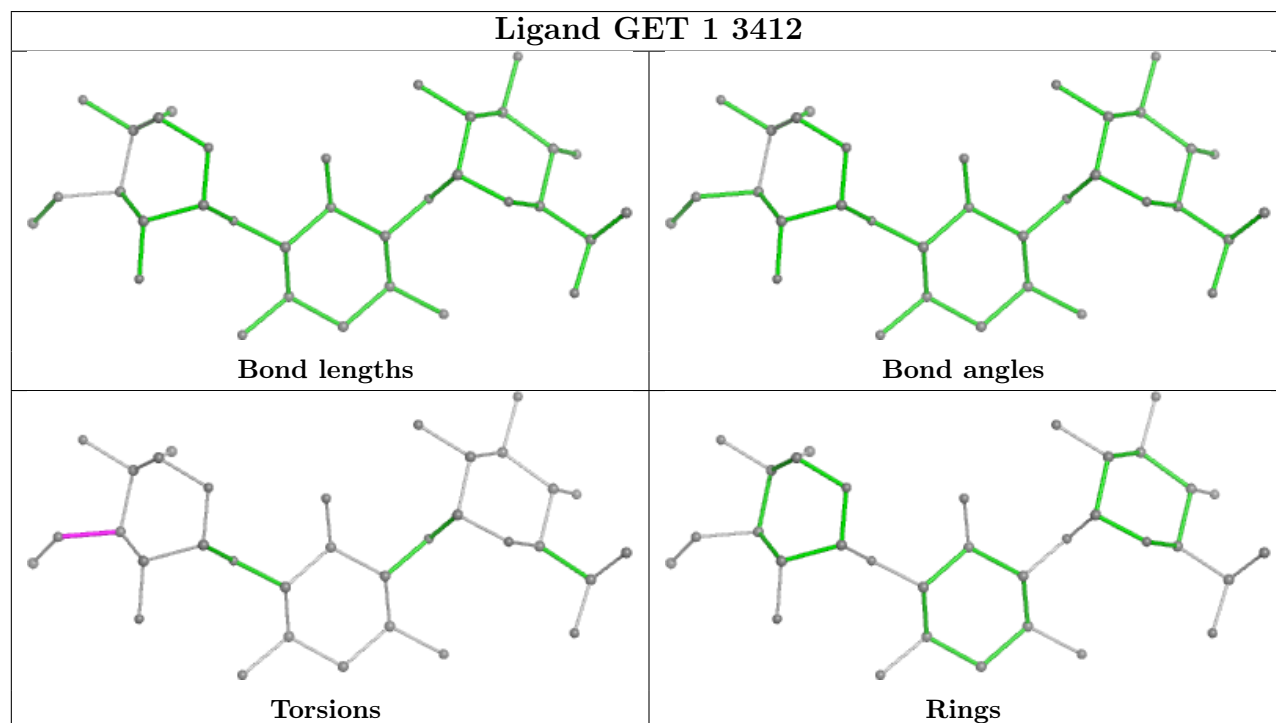
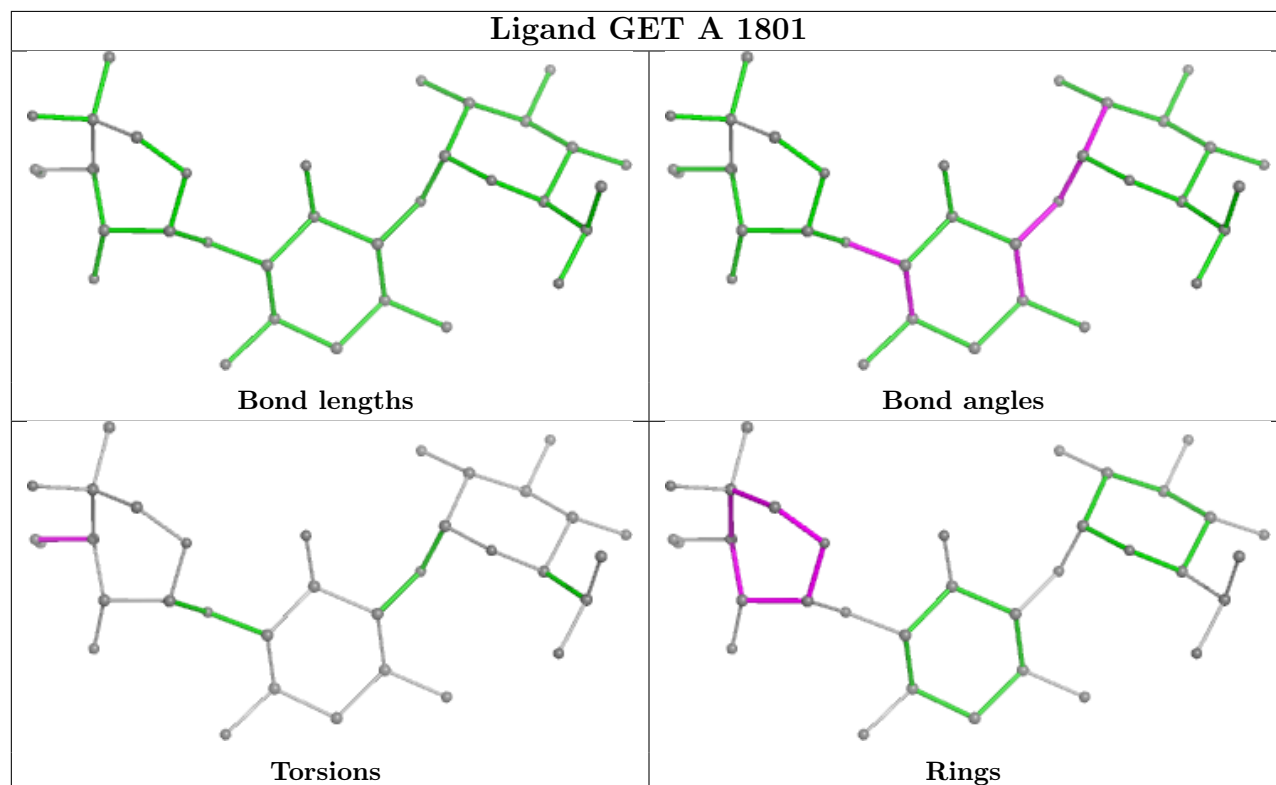
Mol	Chain	Res	Type	Atoms
81	1	3403	GET	C11-C21-C31-C41-C51-O51
81	1	3409	GET	C13-C23-C33-C43-C53-O53
81	1	3404	GET	C13-C23-C33-C43-C53-O53
81	A	1801	GET	C13-C23-C33-C43-C53-O53
81	AT	101	GET	C11-C21-C31-C41-C51-O51

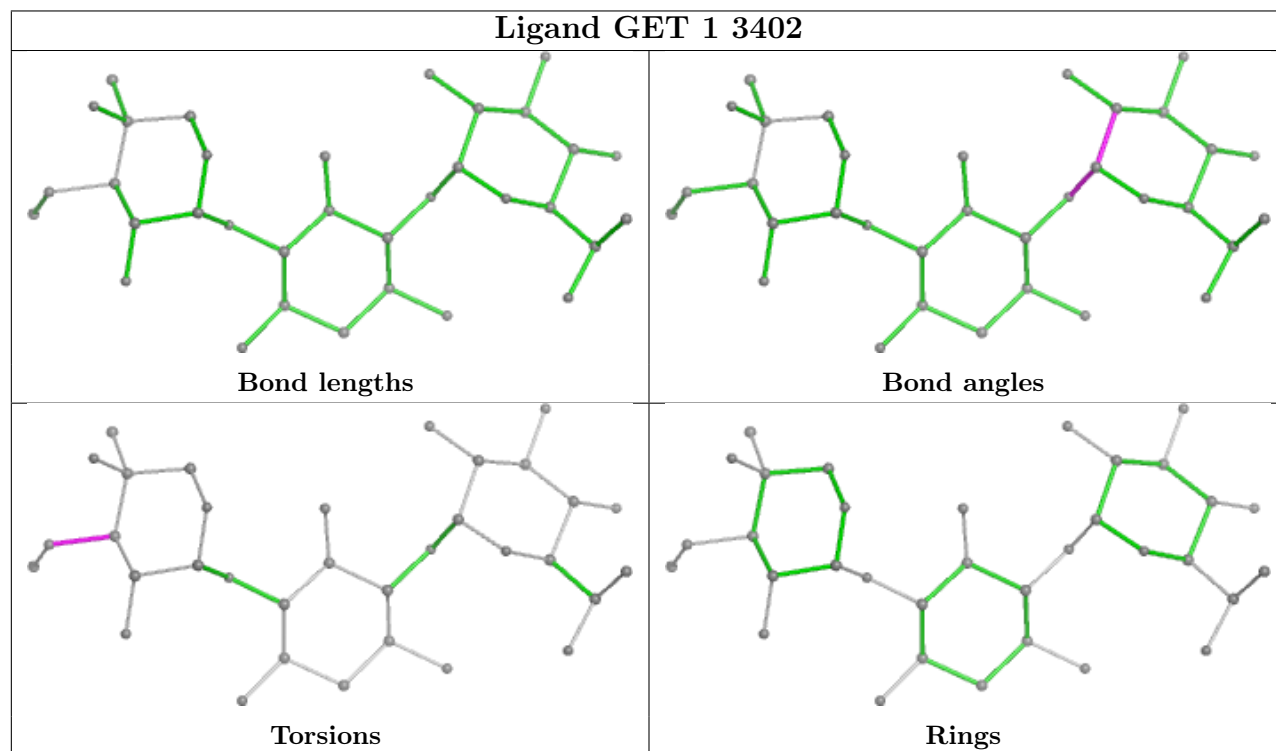
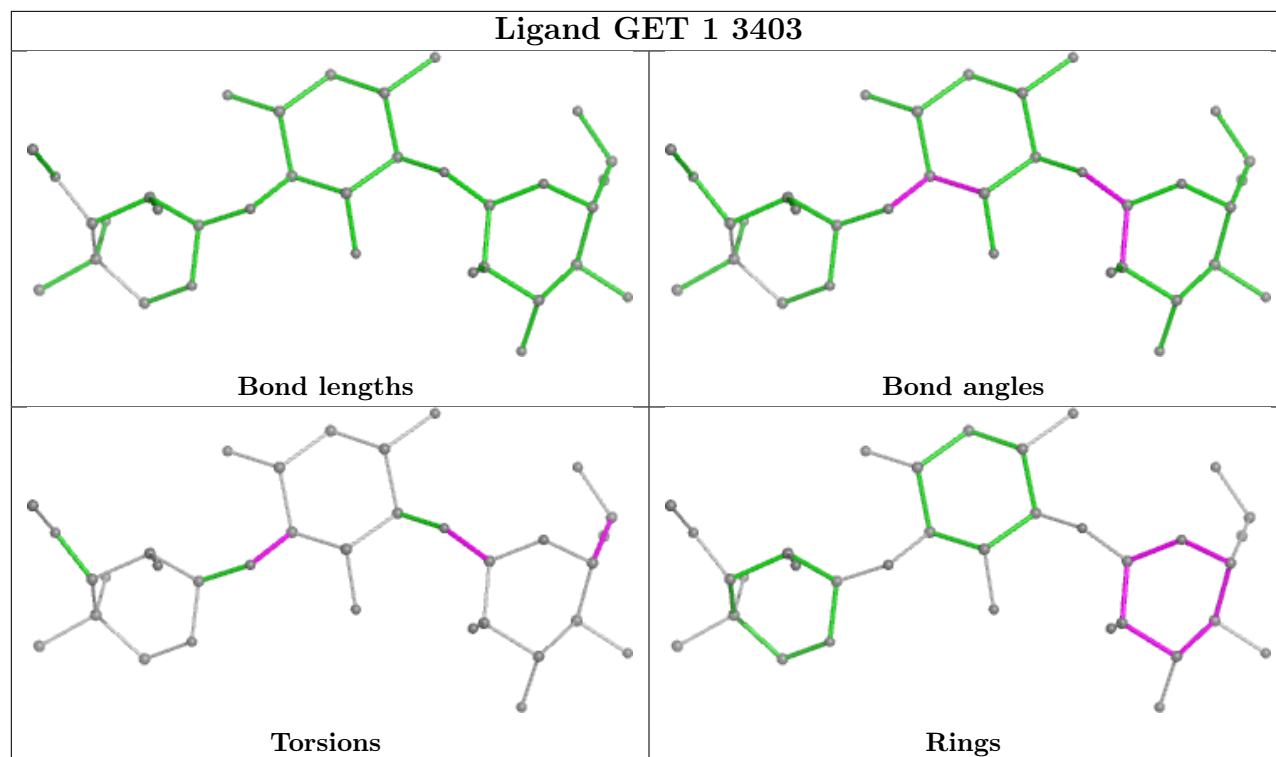
16 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	A	1801	GET	2	0
81	1	3412	GET	6	0
81	1	3403	GET	3	0
80	1	3401	SPK	3	0
81	A	1803	GET	2	0
83	AQ	301	YMZ	1	0
81	1	3413	GET	2	0
81	1	3409	GET	2	0
81	AT	101	GET	1	0
81	1	3404	GET	1	0
81	A	1802	GET	1	0
81	1	3407	GET	2	0
81	1	3410	GET	1	0
81	1	3405	GET	1	0
81	1	3406	GET	1	0
81	1	3408	GET	1	0

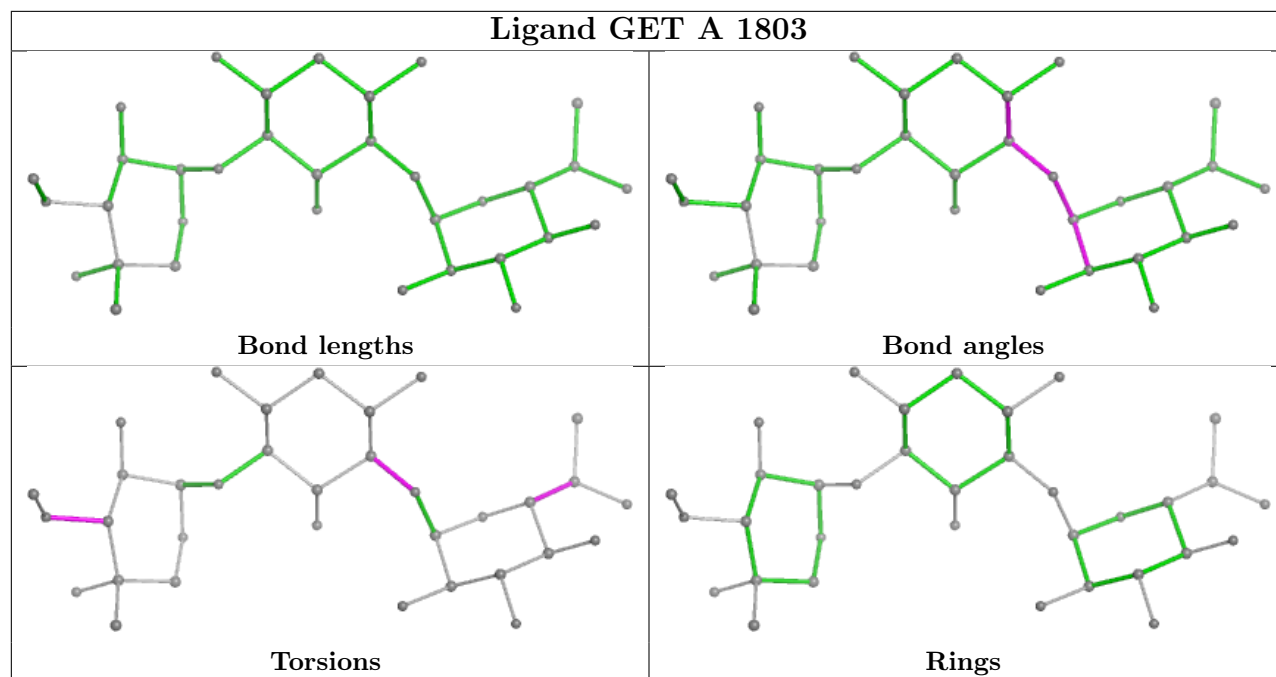
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

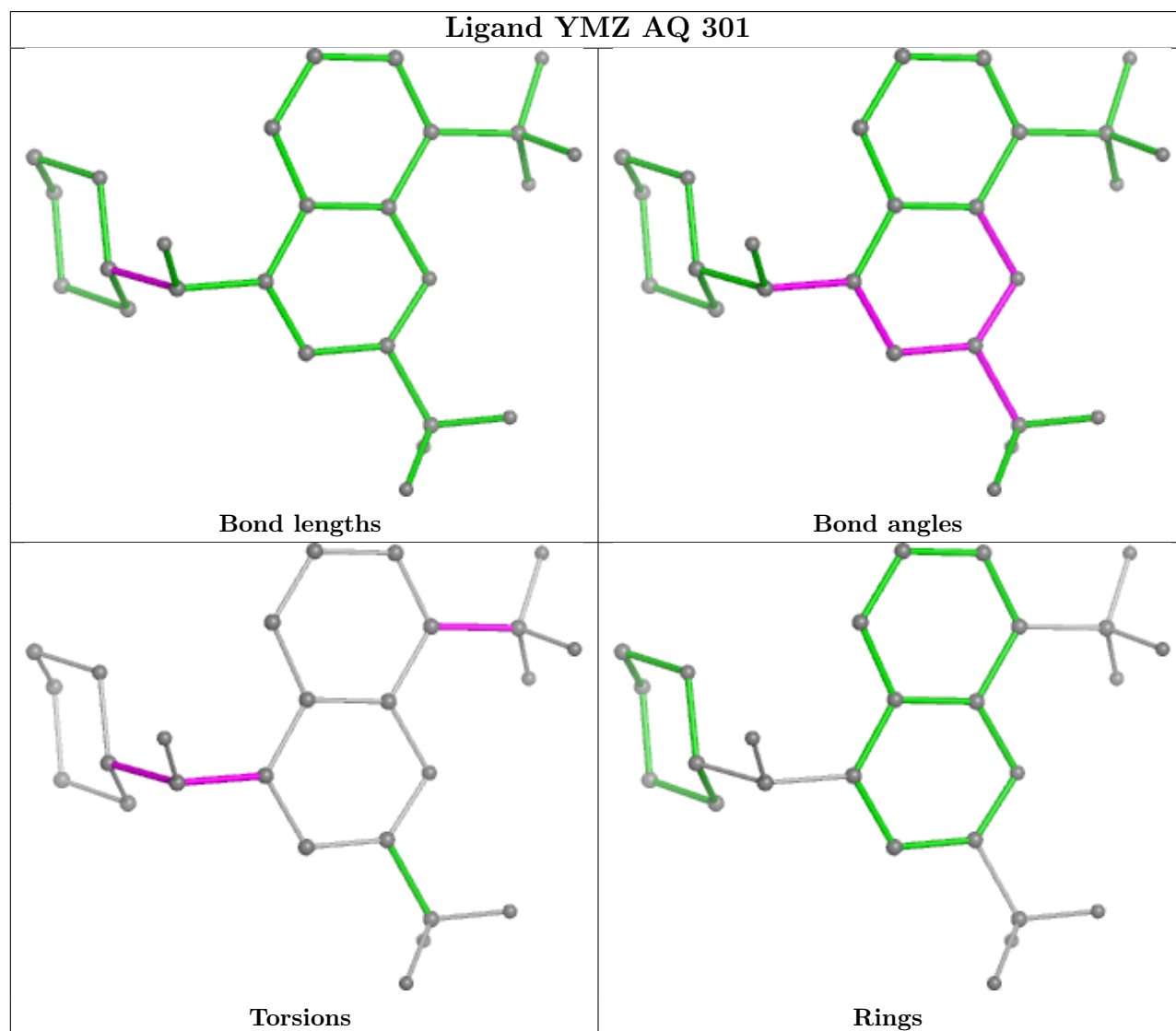


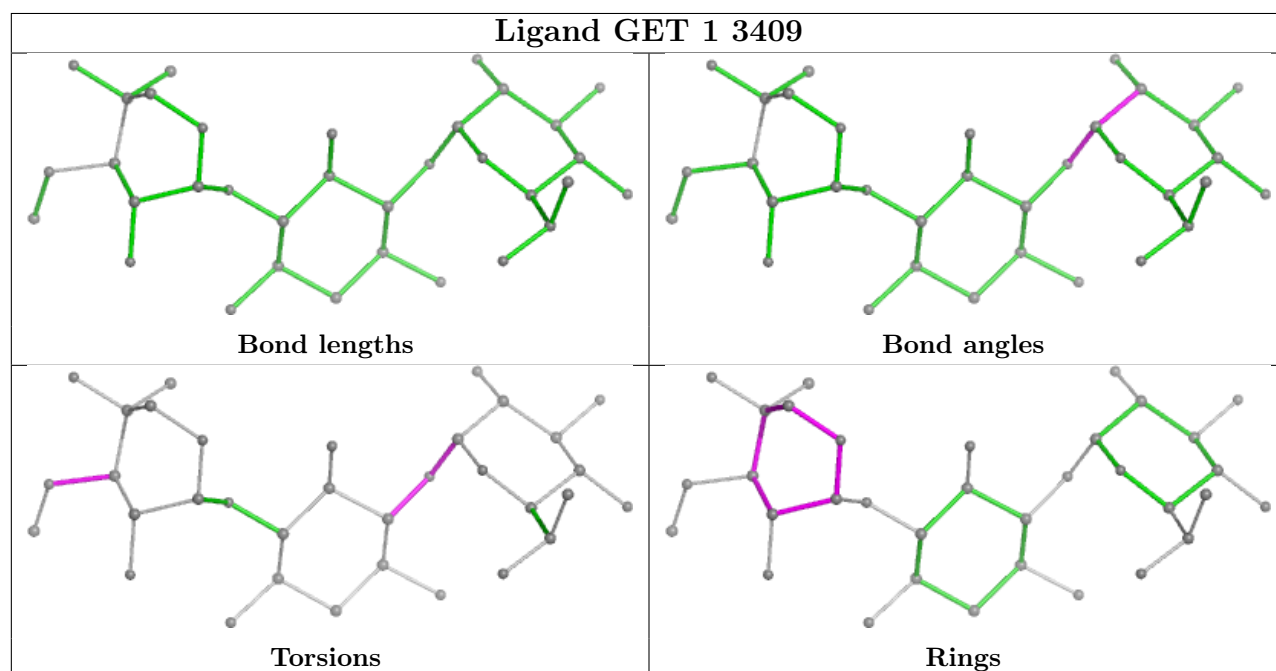
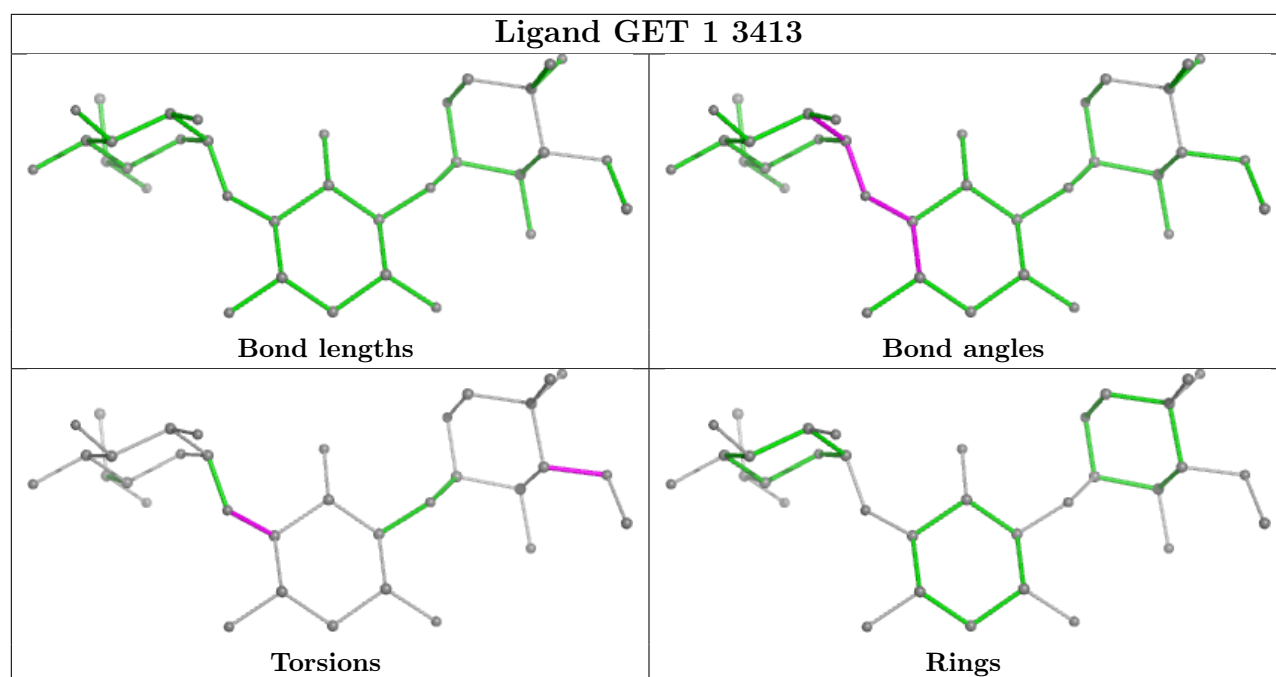


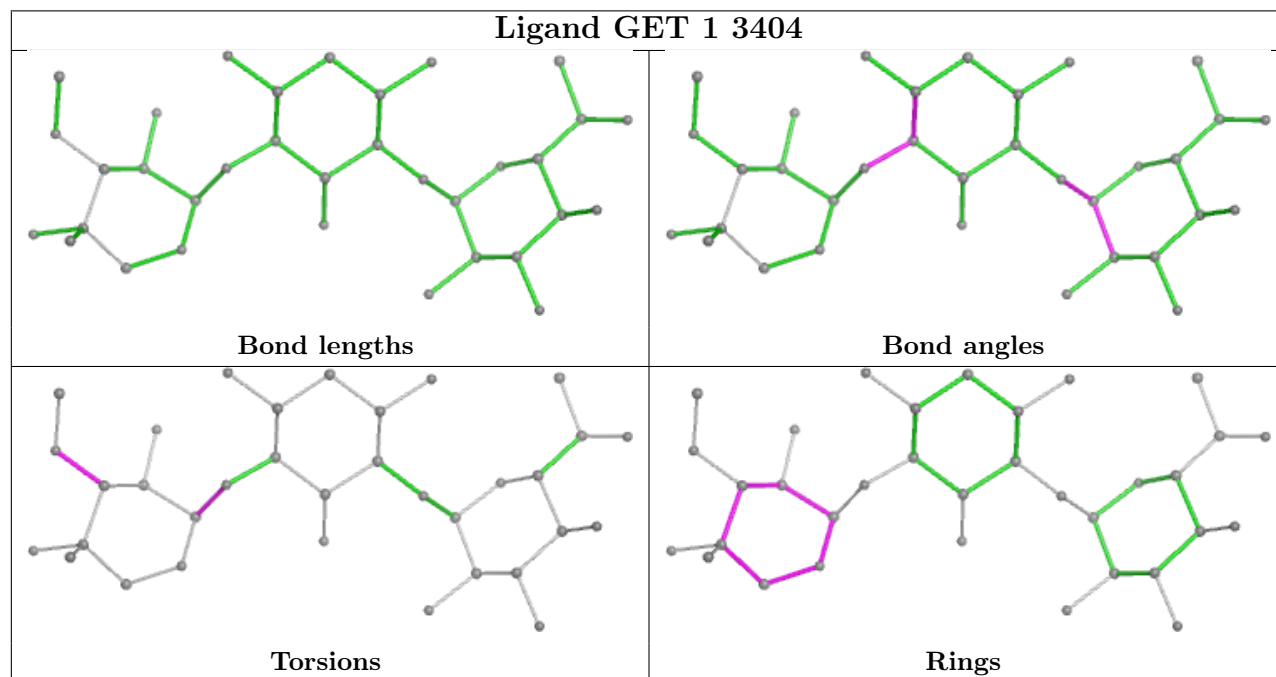
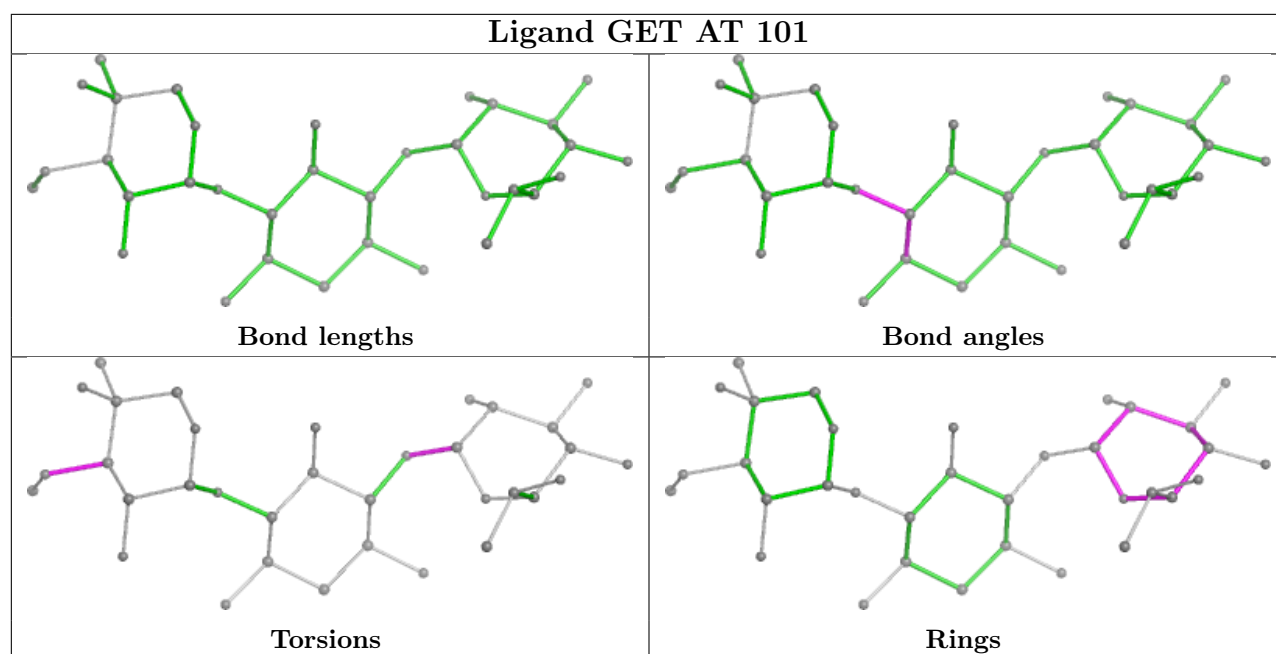
Ligand GET A 1803

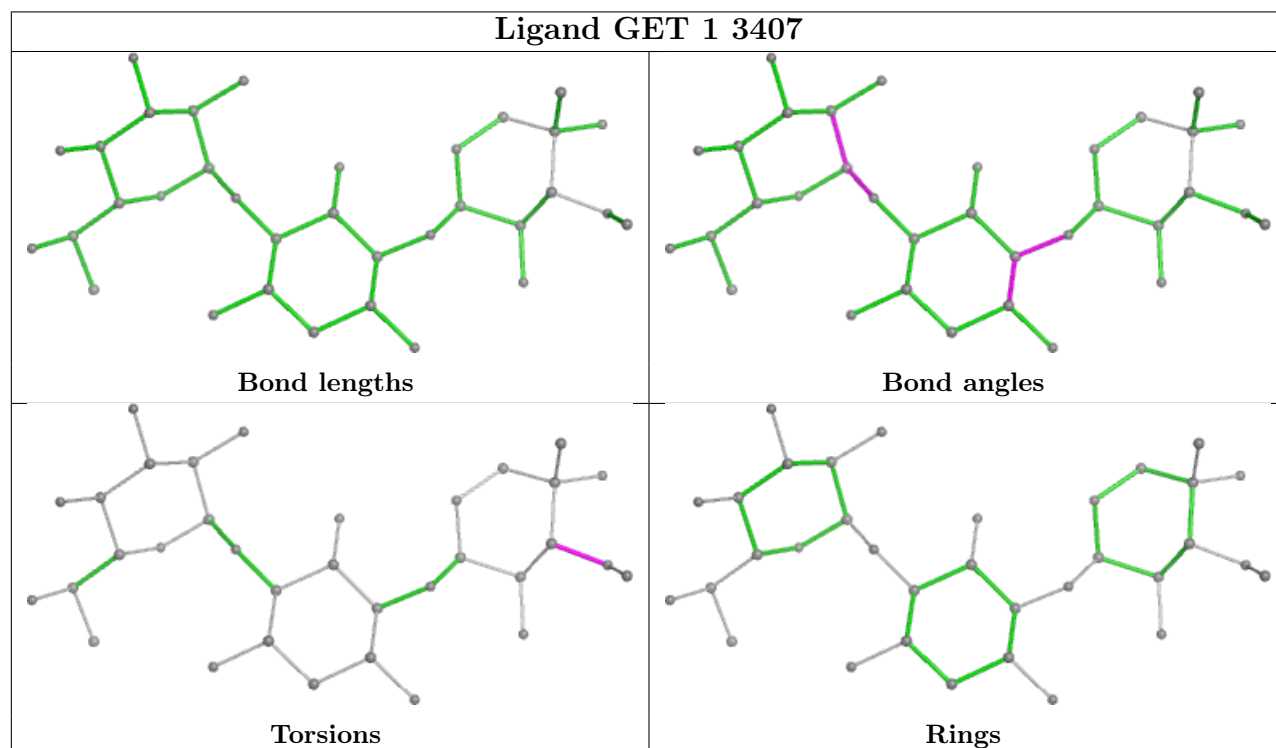
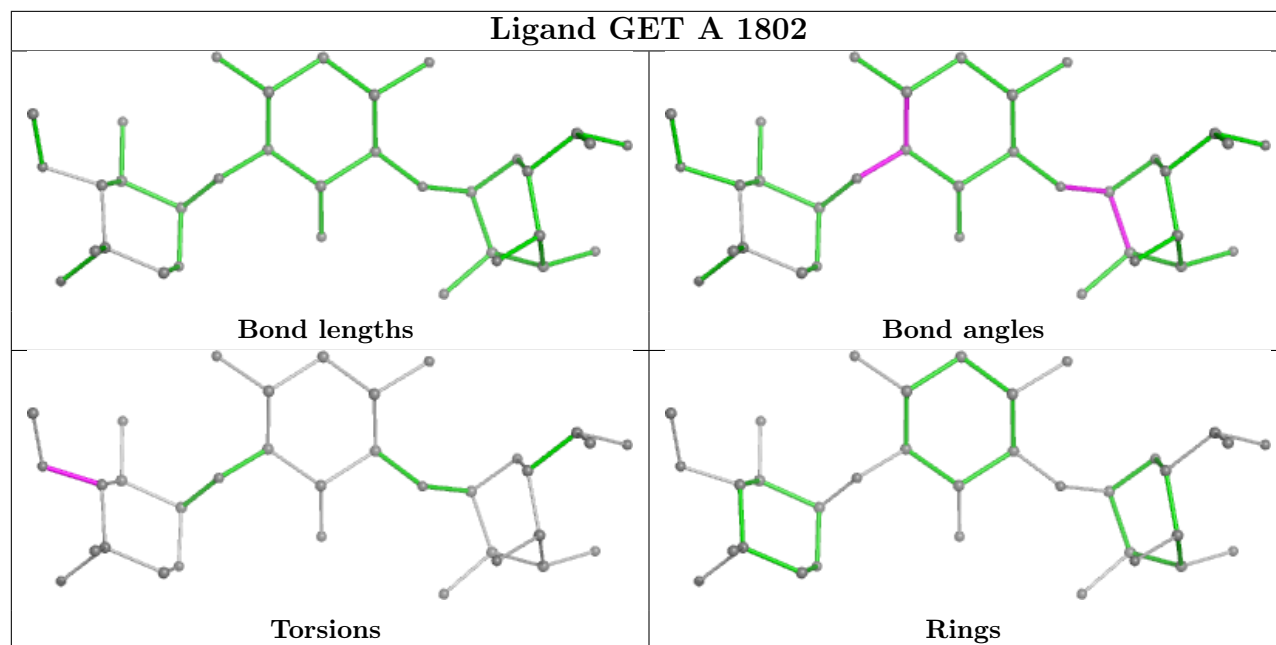


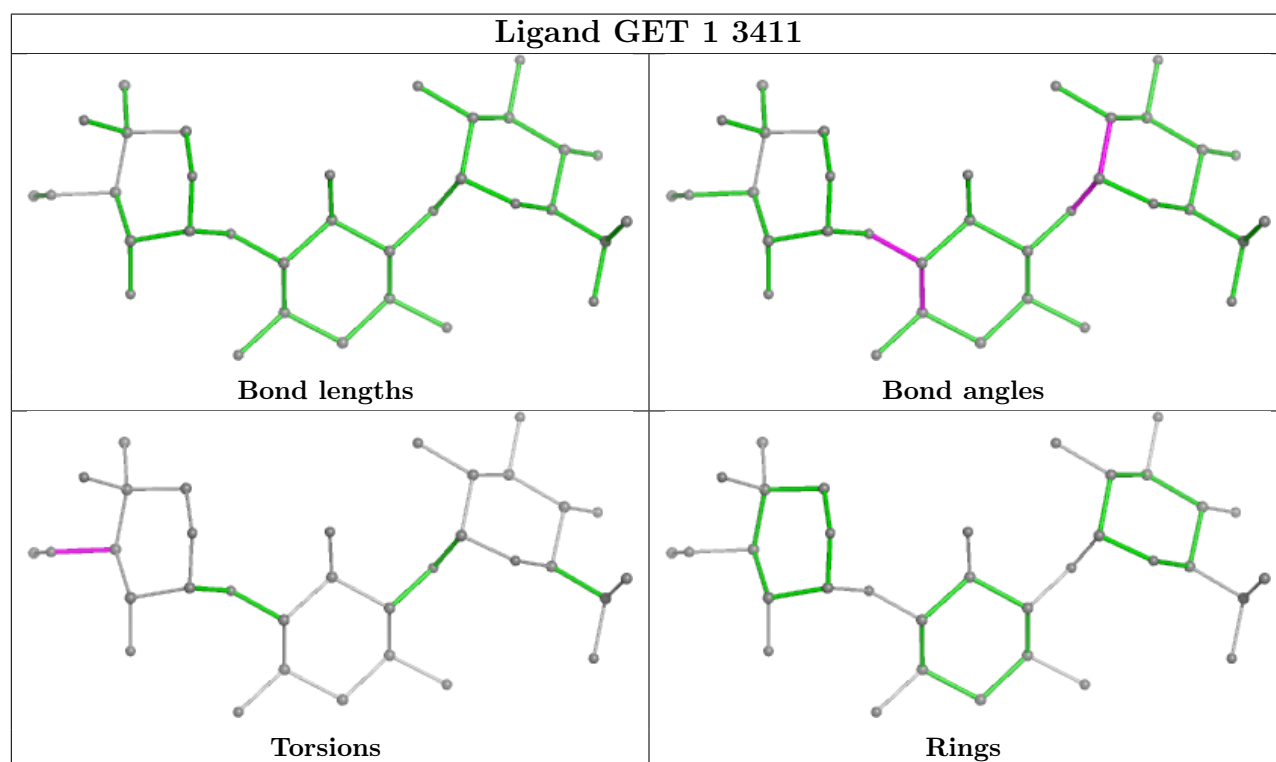
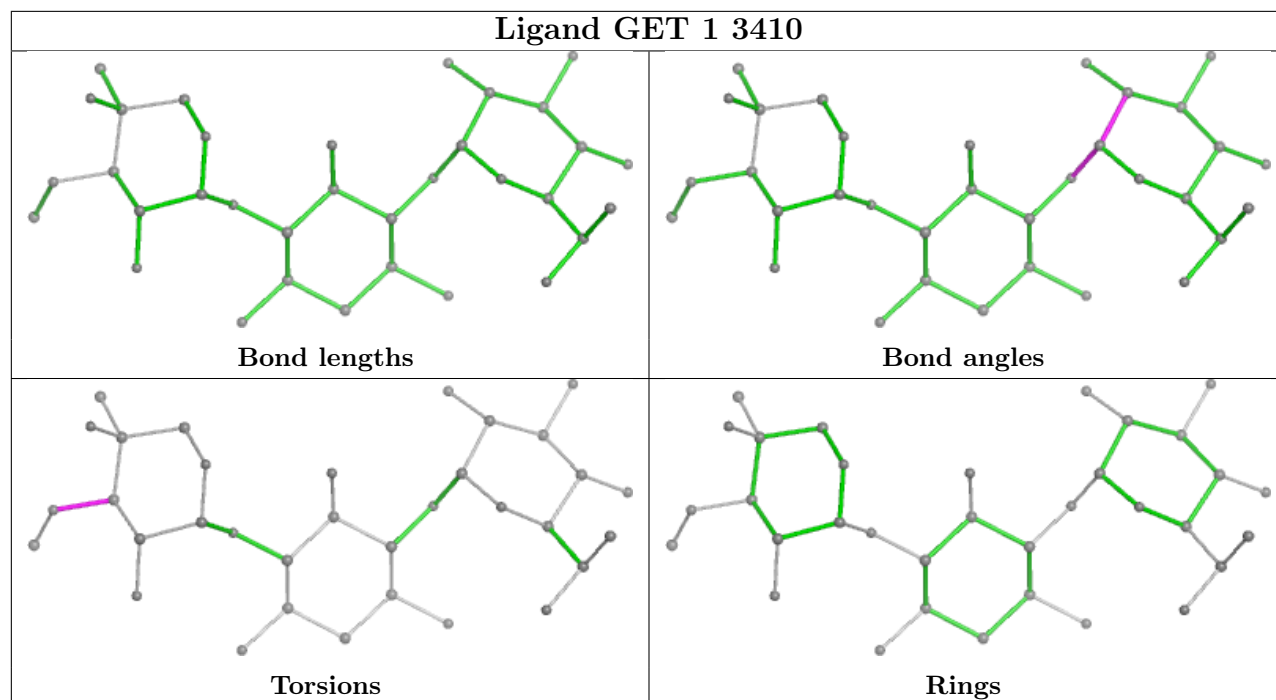
Ligand YMZ AQ 301

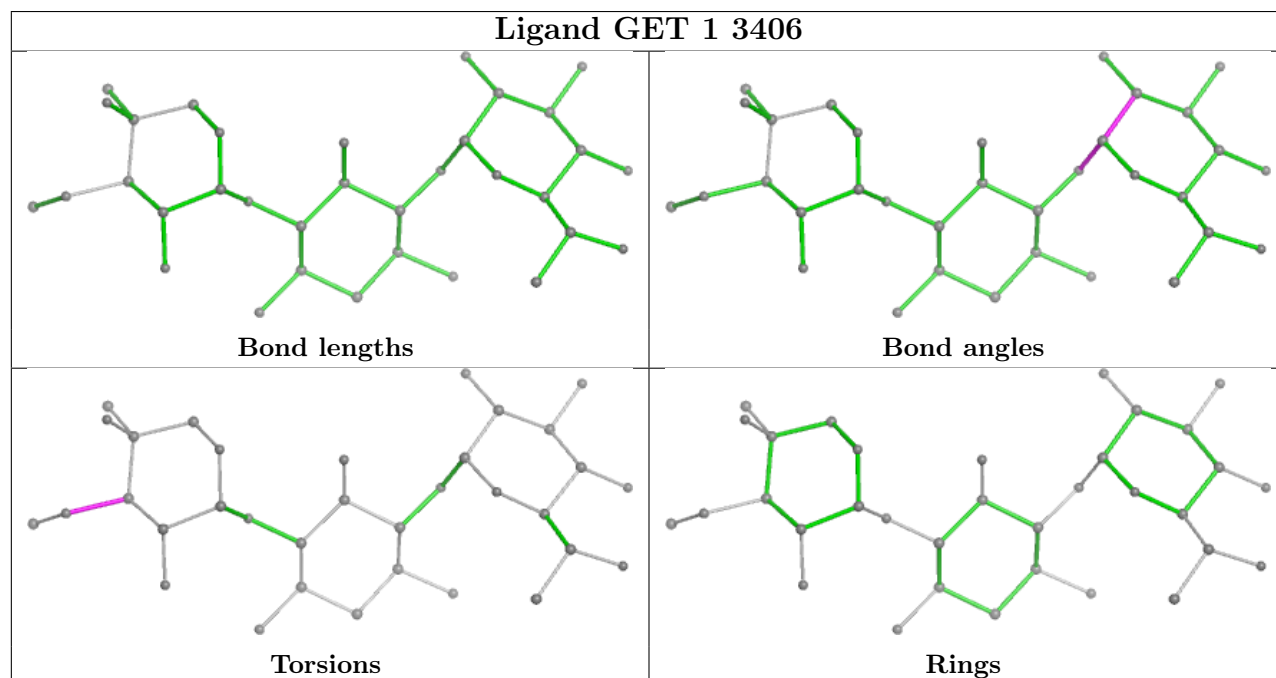
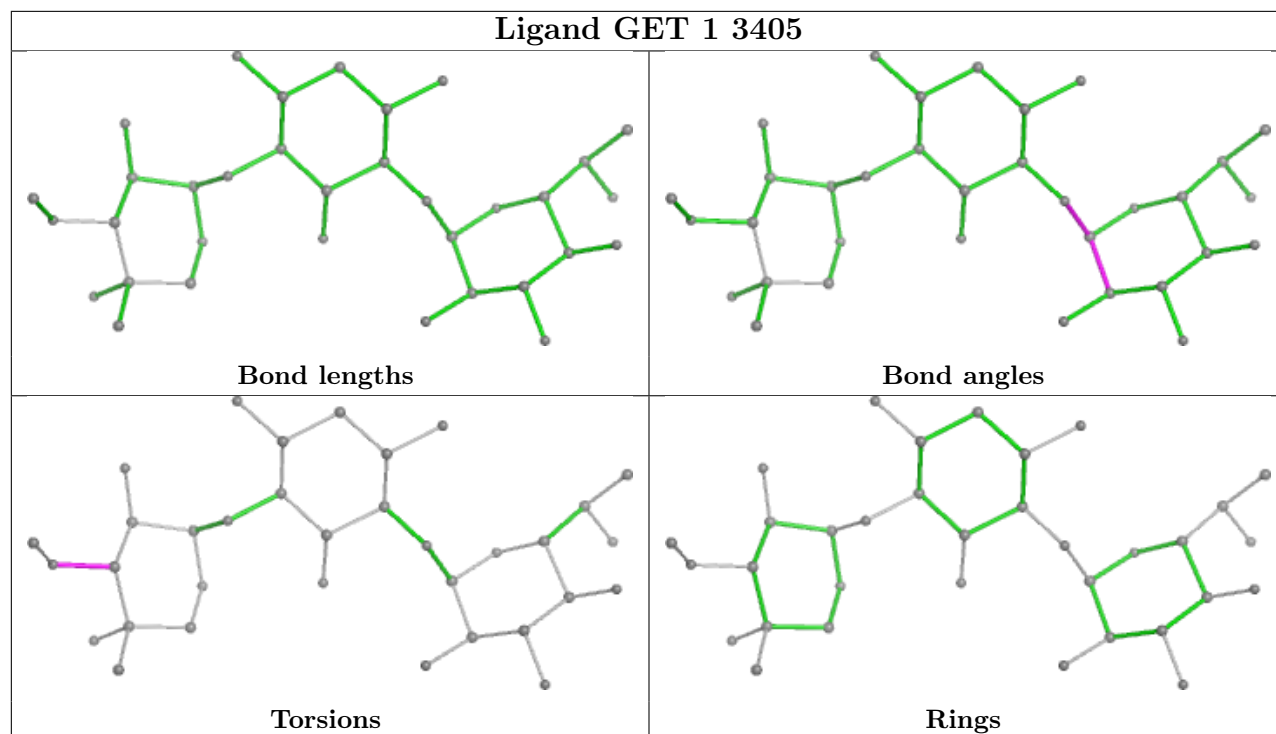


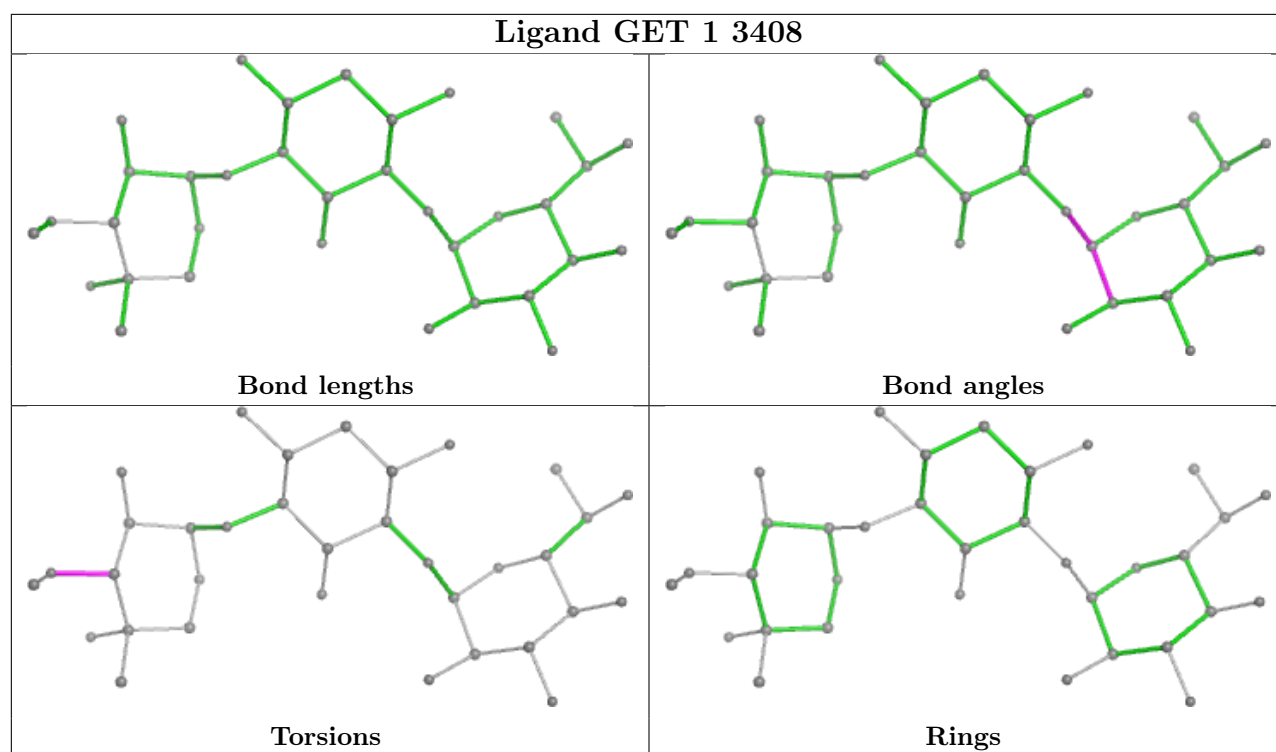












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

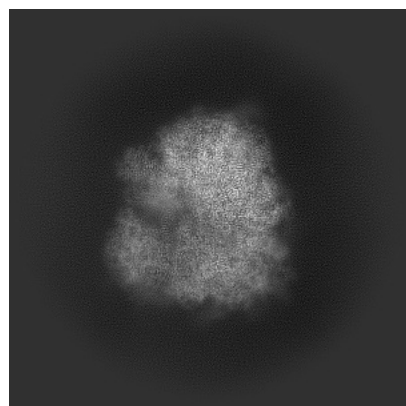
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51103. These allow visual inspection of the internal detail of the map and identification of artifacts.

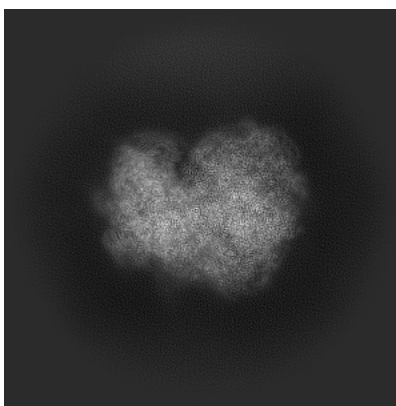
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

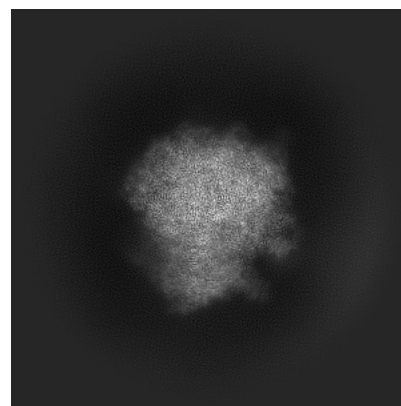
6.1.1 Primary map



X

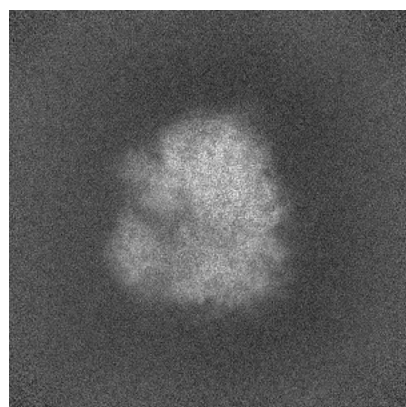


Y

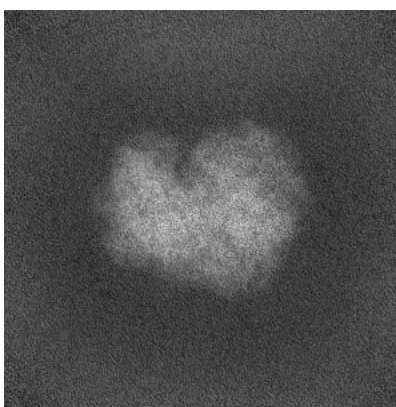


Z

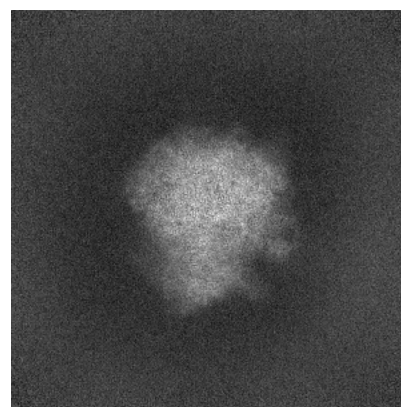
6.1.2 Raw map



X



Y

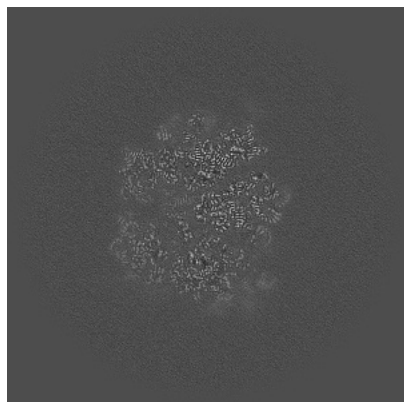


Z

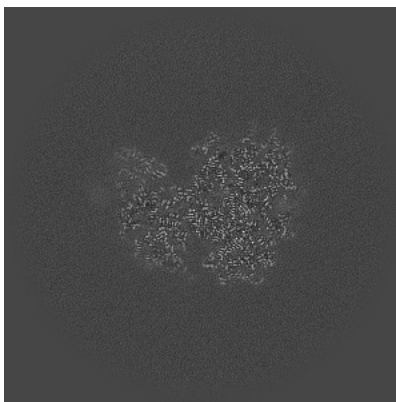
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

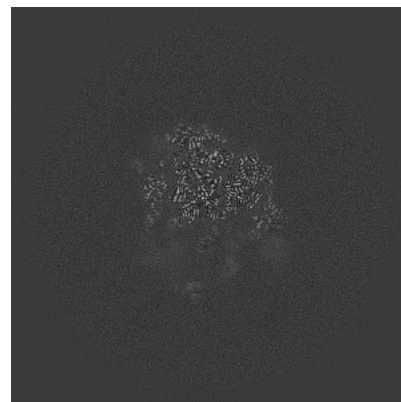
6.2.1 Primary map



X Index: 350

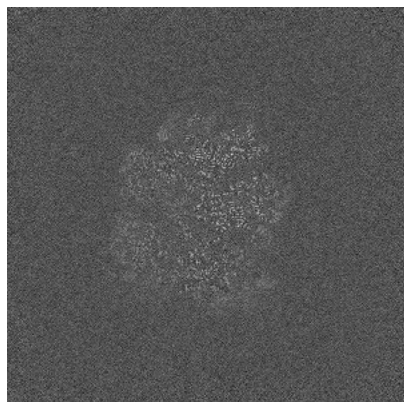


Y Index: 350

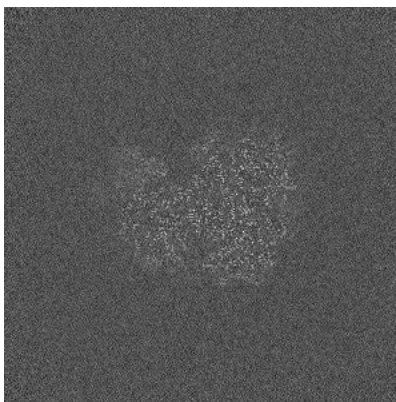


Z Index: 350

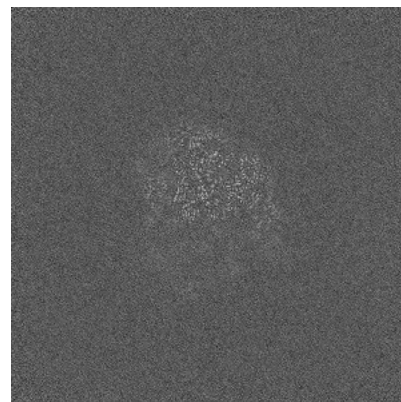
6.2.2 Raw map



X Index: 350



Y Index: 350

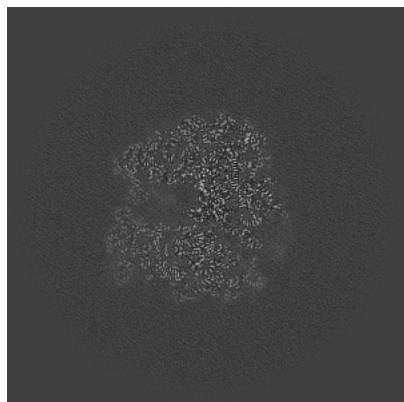


Z Index: 350

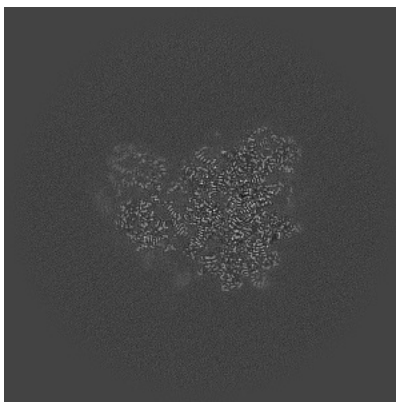
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

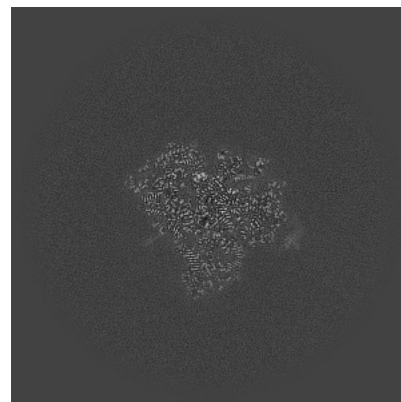
6.3.1 Primary map



X Index: 324

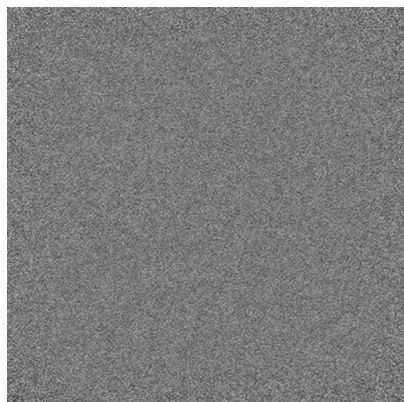


Y Index: 363

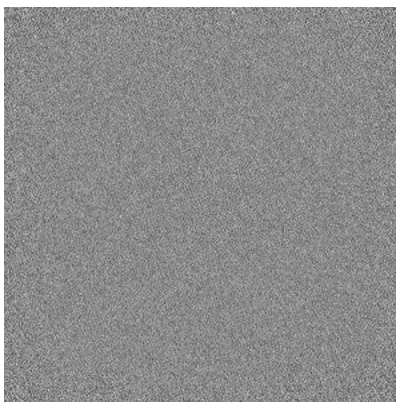


Z Index: 423

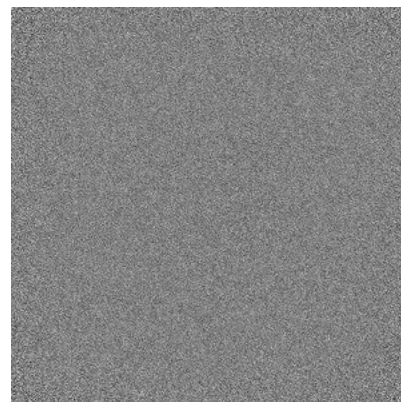
6.3.2 Raw map



X Index: 0



Y Index: 0

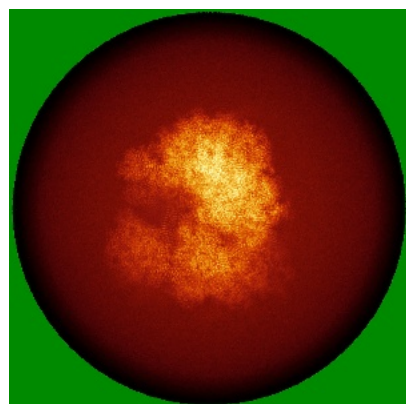


Z Index: 0

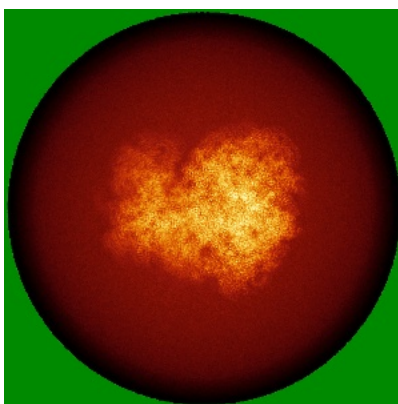
The images above show the largest variance slices of the map in three orthogonal directions.

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

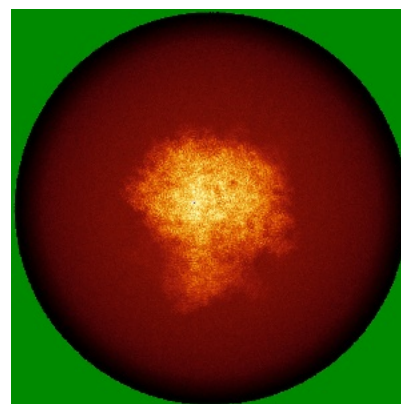
6.4.1 Primary map



X

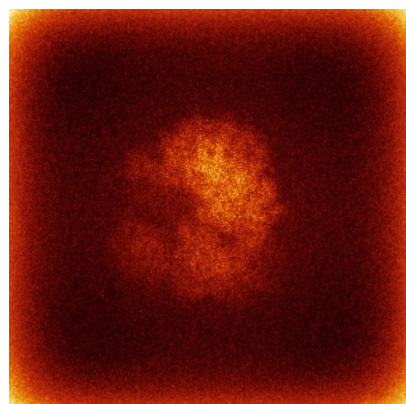


Y

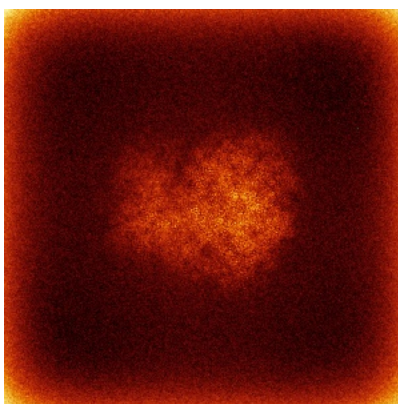


Z

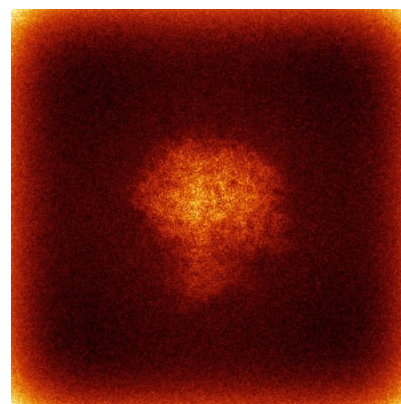
6.4.2 Raw map



X



Y

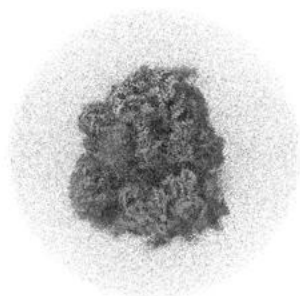


Z

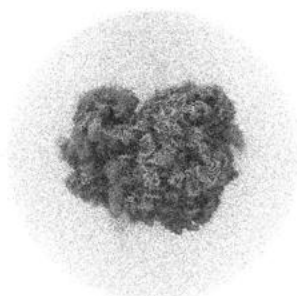
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

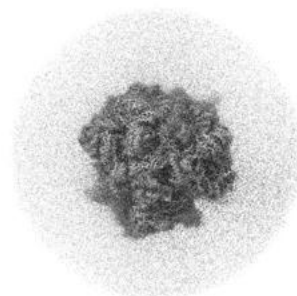
6.5.1 Primary map



X



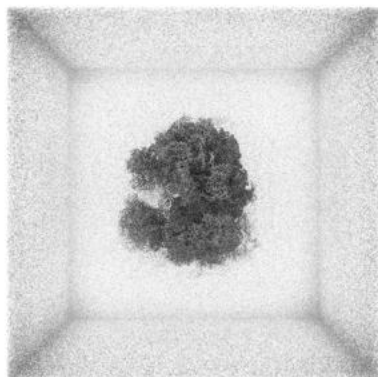
Y



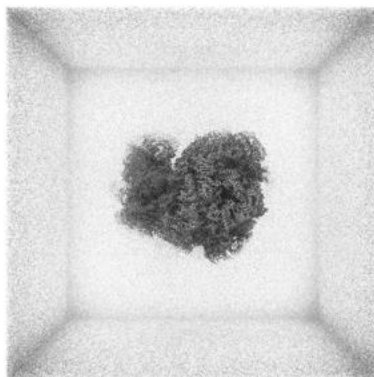
Z

The images above show the 3D surface view of the map at the recommended contour level 0.174. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

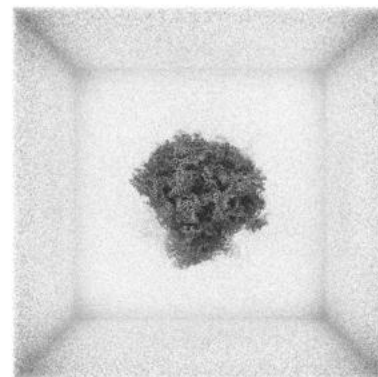
6.5.2 Raw map



X



Y



Z

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

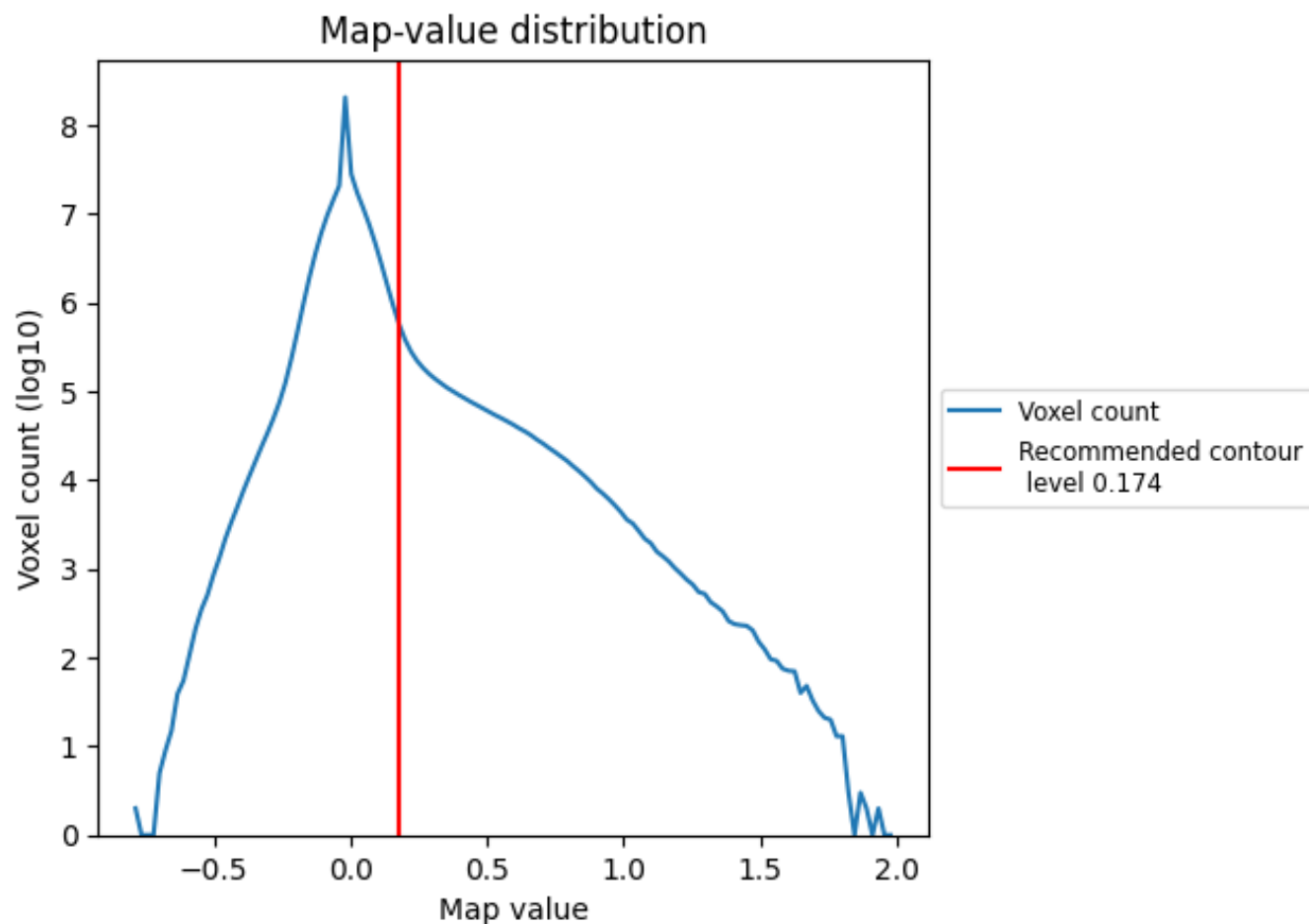
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

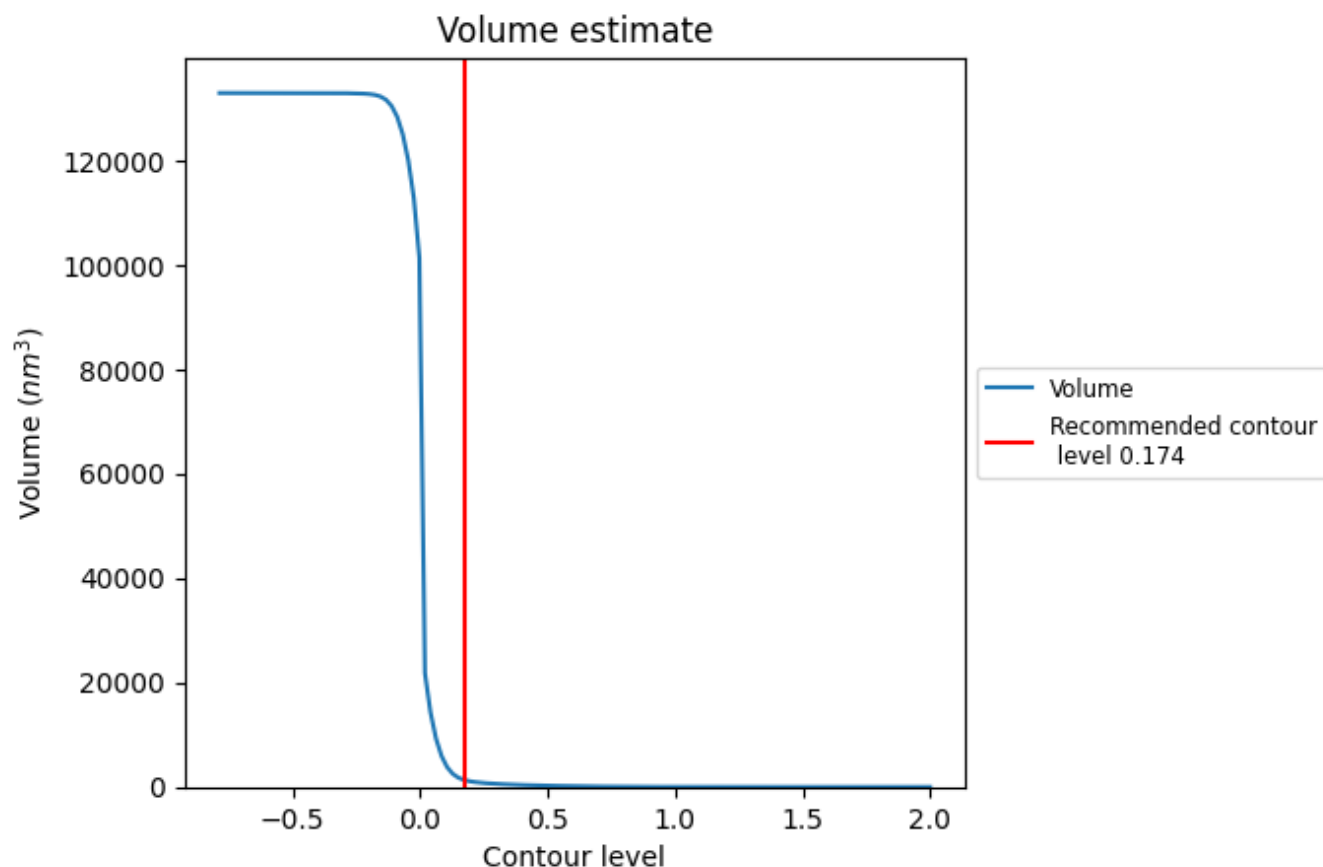
This section contains the results of statistical analysis of the map.

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.

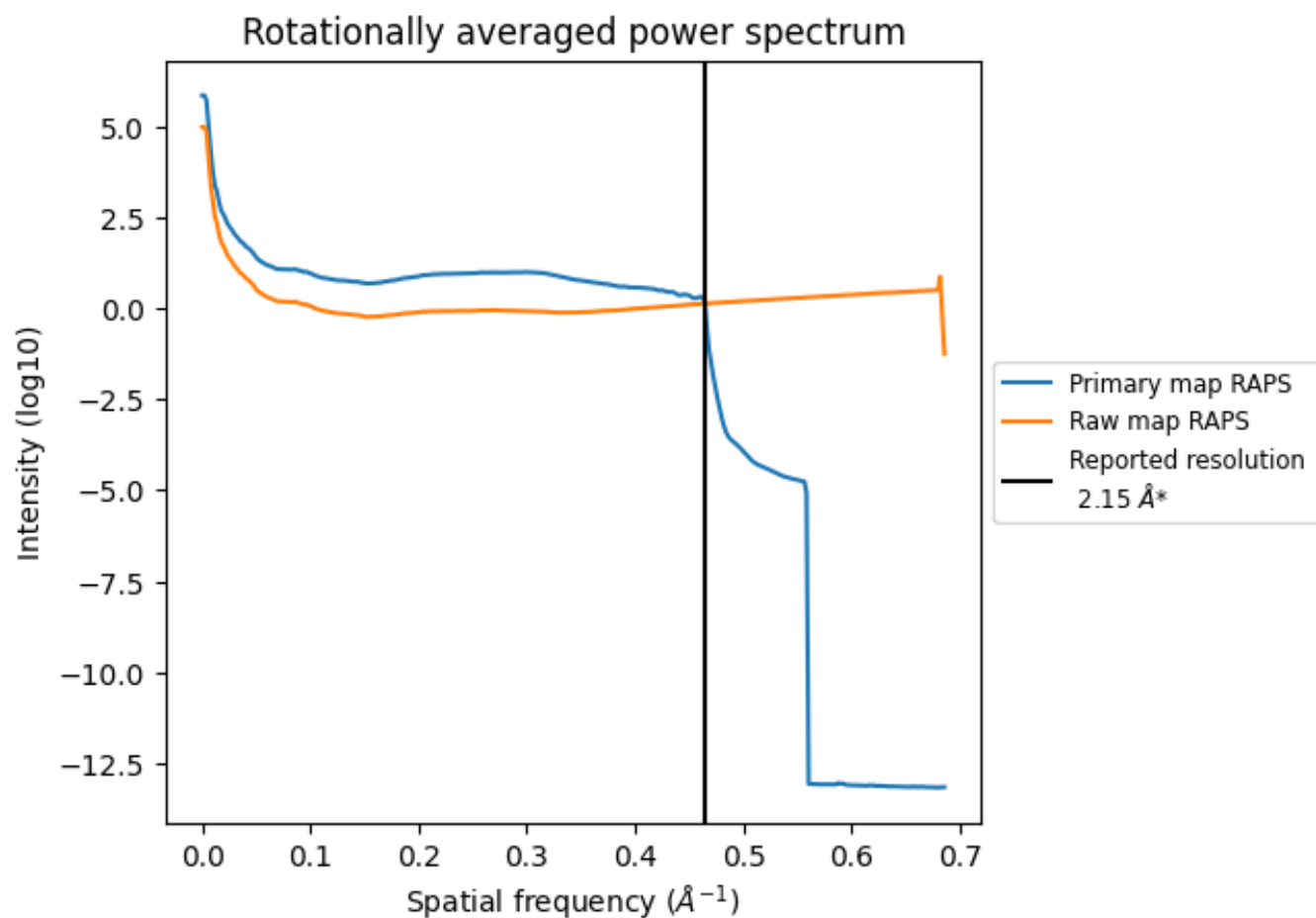
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1328 nm³; this corresponds to an approximate mass of 1200 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 ⓘ

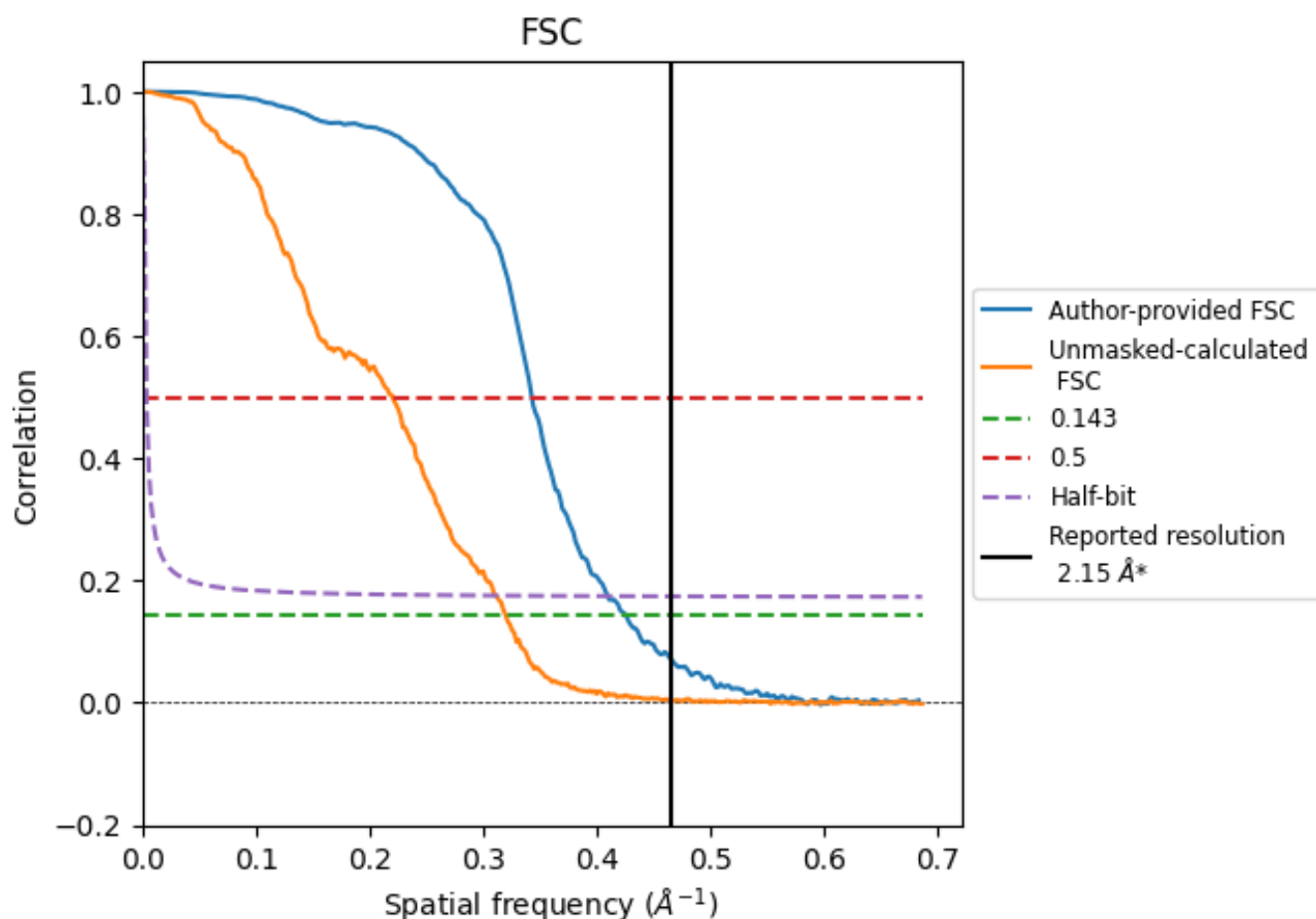


*Reported resolution corresponds to spatial frequency of 0.465 \AA^{-1}

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 0.465 \AA^{-1}

8.2 Resolution estimates [i](#)

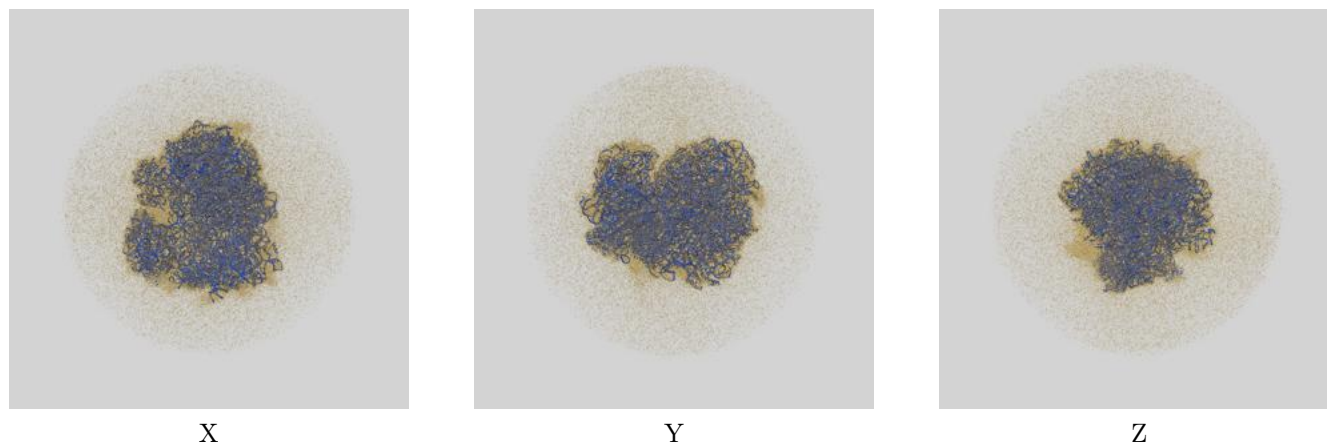
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.15	-	-
Author-provided FSC curve	2.35	2.92	2.44
Unmasked-calculated*	3.13	4.54	3.21

*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 3.13 differs from the reported value 2.15 by more than 10 %

9 Map-model fit [i](#)

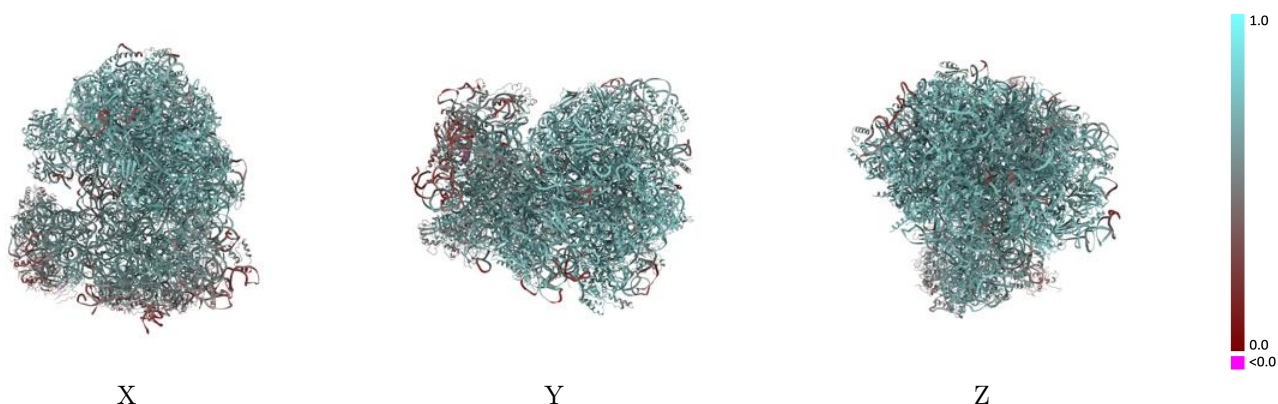
This section contains information regarding the fit between EMDB map EMD-51103 and PDB model 9G6J. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



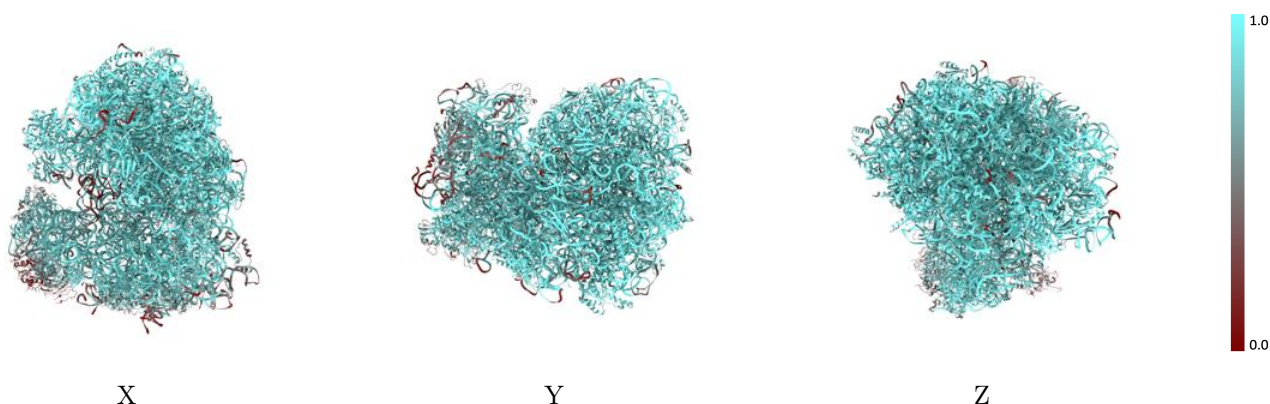
The images above show the 3D surface view of the map at the recommended contour level 0.174 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



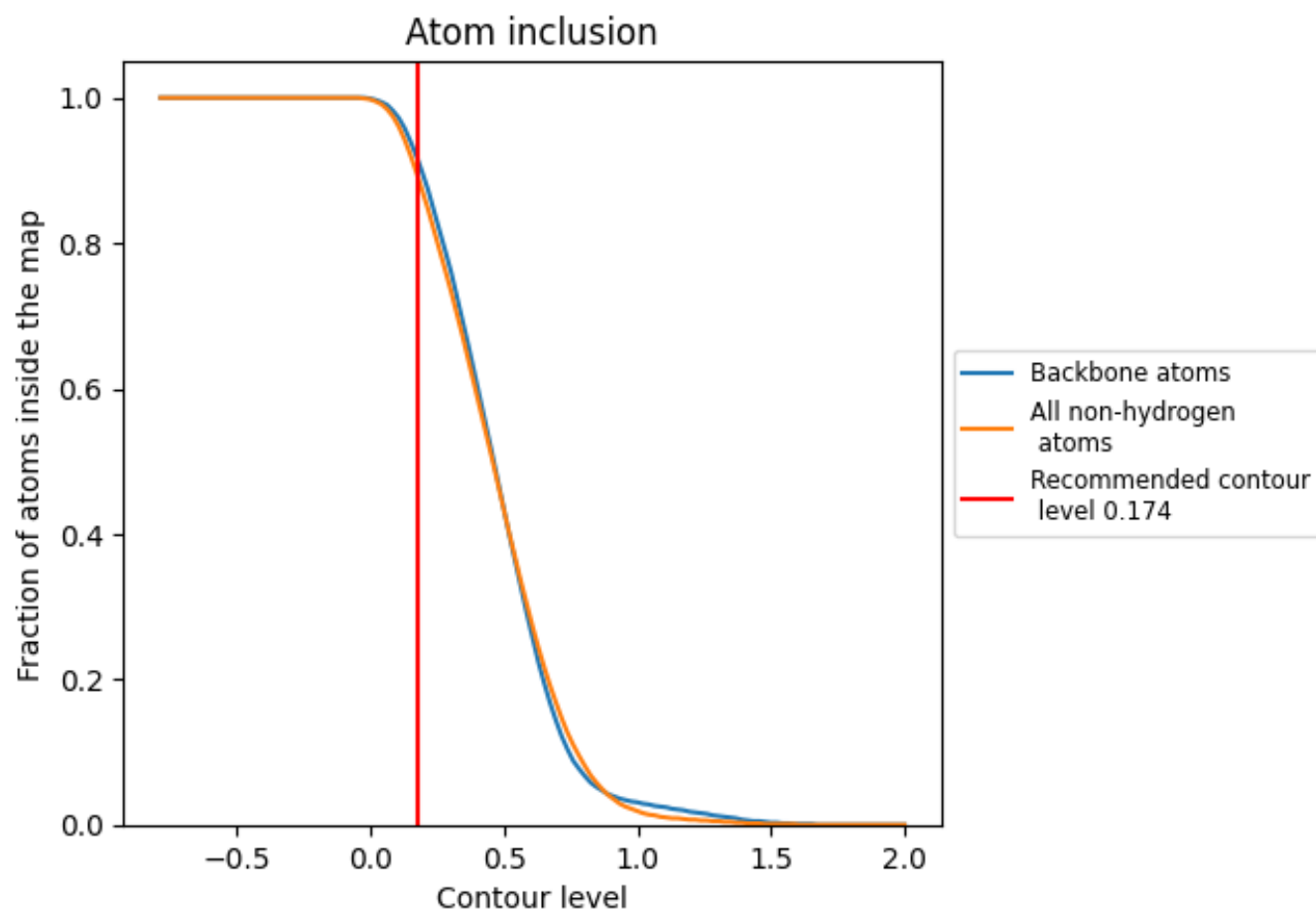
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.174).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.174) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8950	 0.6390
0	 0.9620	 0.6990
1	 0.9580	 0.6800
2	 0.9310	 0.6870
3	 0.9860	 0.6790
4	 0.9750	 0.6880
6	 0.9680	 0.7110
7	 0.9560	 0.7010
8	 0.9570	 0.6950
9	 0.9450	 0.6940
A	 0.8870	 0.5980
AA	 0.9270	 0.6730
AB	 0.9780	 0.7240
AC	 0.9190	 0.6710
AD	 0.9360	 0.6800
AE	 0.9040	 0.6790
AF	 0.9610	 0.7080
AG	 0.9770	 0.7170
AH	 0.9280	 0.6880
AI	 0.9400	 0.6750
AJ	 0.9140	 0.6570
AK	 0.9860	 0.7250
AL	 0.8020	 0.6000
AM	 0.9620	 0.6940
AN	 0.9210	 0.6730
AO	 0.7440	 0.6170
AP	 0.9150	 0.6830
AQ	 0.8930	 0.6780
AT	 0.2820	 0.4020
B	 0.8530	 0.6000
C	 0.9060	 0.6490
D	 0.9310	 0.6590
E	 0.7600	 0.5540
F	 0.7410	 0.4980
G	 0.8000	 0.5790









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Chain	Atom inclusion	Q-score
H	 0.7030	 0.5070
I	 0.7310	 0.5470
J	 0.8130	 0.5820
K	 0.6390	 0.4360
L	 0.6160	 0.4630
M	 0.8750	 0.6210
MR	 0.8080	 0.5800
N	 0.2060	 0.3150
O	 0.9300	 0.6550
P	 0.9510	 0.6710
PT	 0.8480	 0.5940
Q	 0.6670	 0.5060
R	 0.8150	 0.5850
S	 0.7050	 0.5240
T	 0.7210	 0.5210
U	 0.7790	 0.5500
V	 0.6990	 0.5040
W	 0.8740	 0.6260
X	 0.9630	 0.6990
Y	 0.8980	 0.6320
Z	 0.6050	 0.4280
a	 0.5830	 0.4750
b	 0.9330	 0.6720
c	 0.8620	 0.6260
d	 0.7520	 0.5520
e	 0.9250	 0.6320
f	 0.5950	 0.4550
g	 0.3290	 0.3560
h	 0.2570	 0.3990
j	 0.9780	 0.7280
k	 0.9680	 0.7140
l	 0.9450	 0.6960
m	 0.8840	 0.6410
n	 0.9080	 0.6450
o	 0.9450	 0.6970
p	 0.9320	 0.6730
q	 0.9170	 0.6610
r	 0.9270	 0.6700
s	 0.8280	 0.5810
t	 0.9280	 0.6860
u	 0.9490	 0.6810
v	 0.9930	 0.7330

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Chain	Atom inclusion	Q-score
w	 0.9600	 0.7090
x	 0.9560	 0.7060
y	 0.9770	 0.7140
z	 0.9130	 0.6680