



Full wwPDB EM Validation Report ⓘ

Jun 27, 2026 – 02:03 PM EDT

PDB ID : 8UX8 / pdb_00008ux8
EMDB ID : EMD-42714
Title : E. coli 70S ribosome with unmodified Lys-tRNA^{Pro}(GGG) bound to slippery P-site CCC-C codon in the +1 mRNA reading frame
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2023-11-09
Resolution : 3.60 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.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

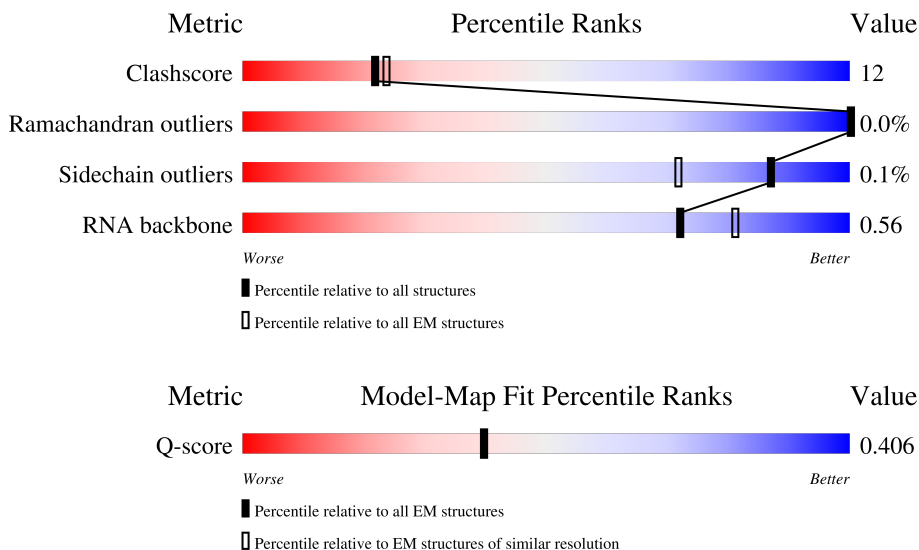
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



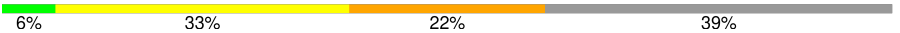
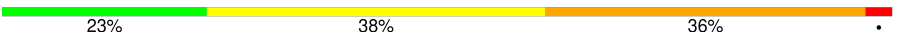
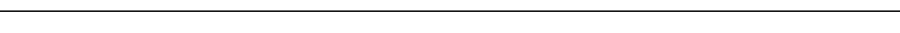
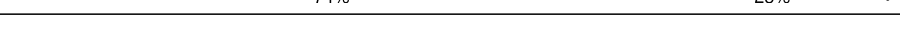
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	1	2904	
2	2	1540	
3	3	120	

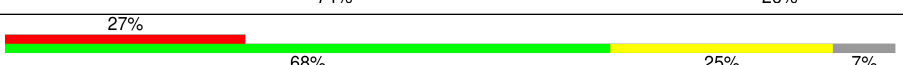
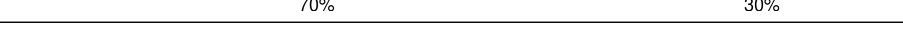
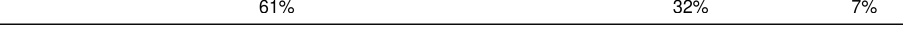
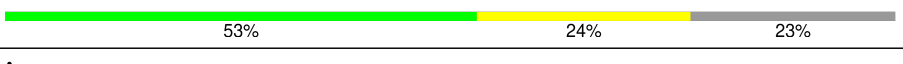
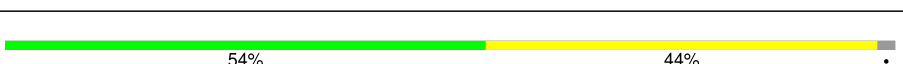
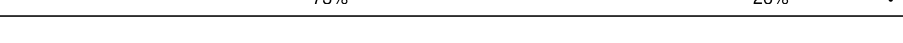
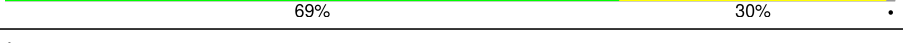
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Mol	Chain	Length	Quality of chain
4	4	18	
5	5	77	
6	A	229	
7	B	273	
8	C	209	
9	D	201	
10	E	179	
11	F	177	
12	G	149	
13	J	142	
14	K	123	
15	L	144	
16	M	136	
17	N	127	
18	O	117	
19	P	115	
20	Q	118	
21	R	103	
22	S	110	
23	T	100	
24	U	104	
25	V	94	
26	W	84	
27	X	78	
28	Y	63	

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Mol	Chain	Length	Quality of chain
29	Z	59	
30	a	70	
31	b	57	
32	c	55	
33	d	46	
34	e	65	
35	f	38	
36	g	241	
37	h	233	
38	i	206	
39	j	167	
40	k	135	
41	l	179	
42	m	130	
43	n	130	
44	o	103	
45	p	129	
46	q	124	
47	r	118	
48	s	101	
49	t	89	
50	u	82	
51	v	84	
52	w	75	
53	x	92	

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Mol	Chain	Length	Quality of chain
54	y	87	75% 24%
55	z	71	20% 87% 11%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 146547 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 RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62334	27814	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	11	Total	C	N	O	P	0	0
			230	103	38	78	11		

- Molecule 5 is a RNA chain called Lys-tRNA^{pro}L.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	77	Total	C	N	O	P	0	0
			1648	733	297	541	77		

- Molecule 6 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	67	Total	C	N	O	S	0	0
			507	321	90	95	1		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 13 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 18 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 19 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 21 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	103	Total	C	N	O		0	0
			788	498	148	142			

- Molecule 25 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 26 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 28 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 30 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 31 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 32 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 33 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 34 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 35 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 38 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 42 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 43 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 44 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 46 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 48 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 49 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 50 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 51 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

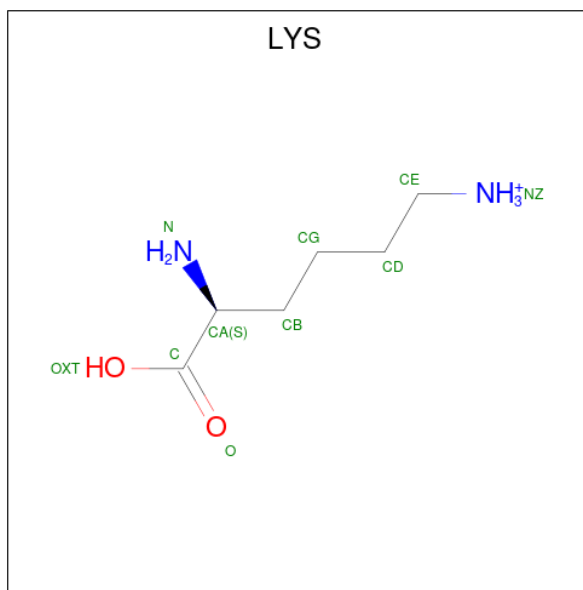
- Molecule 55 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	262	Total 262	Mg 262	0
56	2	111	Total 111	Mg 111	0
56	3	10	Total 10	Mg 10	0
56	5	1	Total 1	Mg 1	0
56	B	3	Total 3	Mg 3	0
56	L	2	Total 2	Mg 2	0
56	M	1	Total 1	Mg 1	0
56	Q	1	Total 1	Mg 1	0
56	X	1	Total 1	Mg 1	0
56	b	1	Total 1	Mg 1	0
56	l	1	Total 1	Mg 1	0
56	z	1	Total 1	Mg 1	0

- Molecule 57 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
57	5	1	Total	C	N	O	0
			9	6	2	1	

- Molecule 58 is water.

Mol	Chain	Residues	Atoms				AltConf
58	1	700	Total	O			0
			700	700			
58	2	341	Total	O			0
			341	341			
58	3	7	Total	O			0
			7	7			
58	4	1	Total	O			0
			1	1			
58	5	10	Total	O			0
			10	10			
58	B	2	Total	O			0
			2	2			
58	C	7	Total	O			0
			7	7			
58	D	10	Total	O			0
			10	10			
58	E	4	Total	O			0
			4	4			
58	F	6	Total	O			0
			6	6			
58	G	12	Total	O			0
			12	12			
58	J	7	Total	O			0
			7	7			
58	K	4	Total	O			0
			4	4			
58	L	3	Total	O			0
			3	3			
58	M	2	Total	O			0
			2	2			
58	N	2	Total	O			0
			2	2			
58	O	6	Total	O			0
			6	6			
58	P	6	Total	O			0
			6	6			
58	Q	7	Total	O			0
			7	7			

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Mol	Chain	Residues	Atoms		AltConf
58	R	7	Total 7	O 7	0
58	S	4	Total 4	O 4	0
58	T	2	Total 2	O 2	0
58	U	6	Total 6	O 6	0
58	V	1	Total 1	O 1	0
58	W	2	Total 2	O 2	0
58	Y	8	Total 8	O 8	0
58	Z	2	Total 2	O 2	0
58	a	2	Total 2	O 2	0
58	b	2	Total 2	O 2	0
58	f	1	Total 1	O 1	0
58	g	20	Total 20	O 20	0
58	h	14	Total 14	O 14	0
58	i	8	Total 8	O 8	0
58	j	3	Total 3	O 3	0
58	k	7	Total 7	O 7	0
58	l	5	Total 5	O 5	0
58	m	3	Total 3	O 3	0
58	n	4	Total 4	O 4	0
58	o	3	Total 3	O 3	0
58	p	5	Total 5	O 5	0

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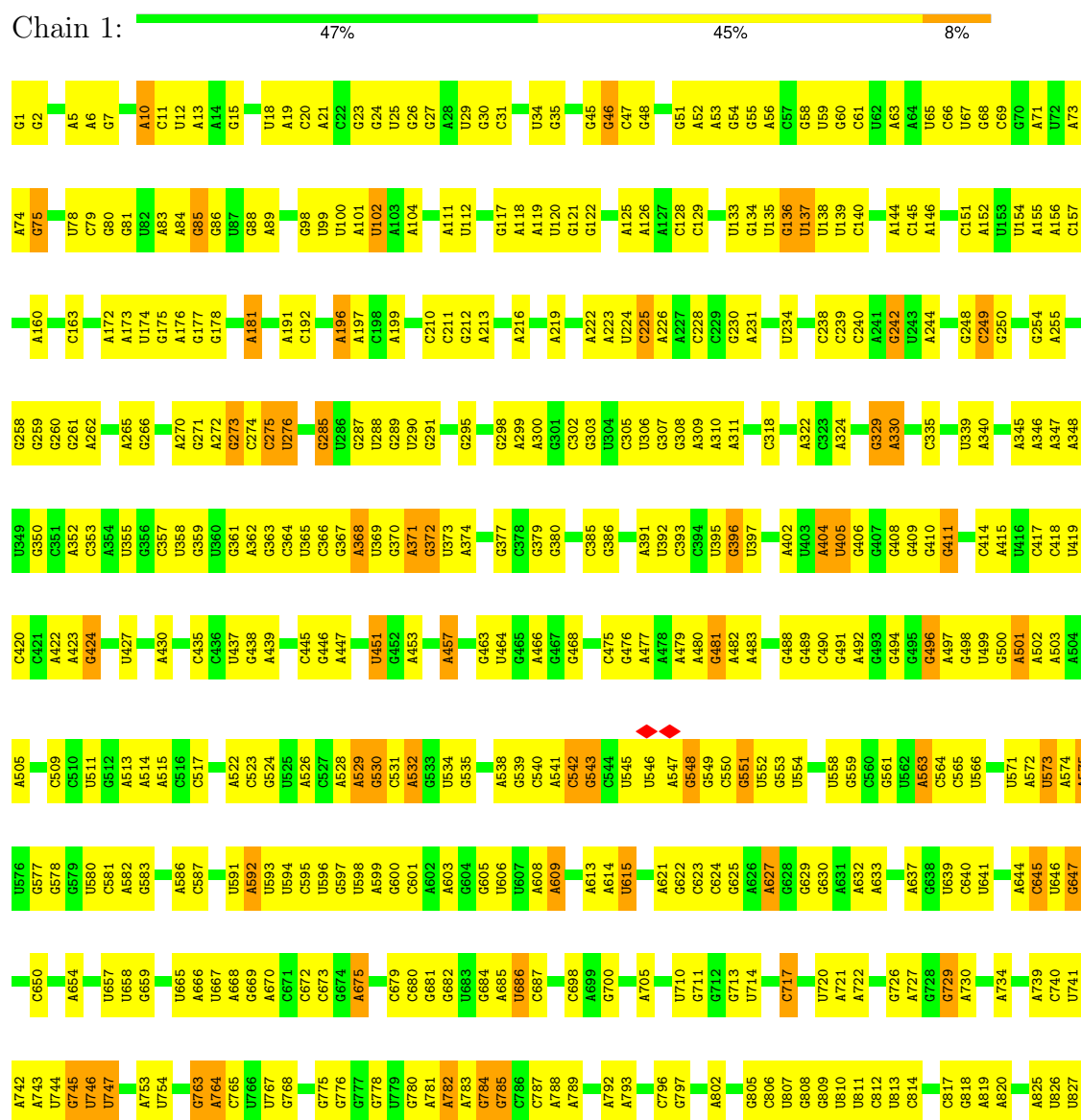
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Mol	Chain	Residues	Atoms		AltConf
58	q	1	Total 1	O 1	0
58	r	4	Total 4	O 4	0
58	t	1	Total 1	O 1	0
58	u	4	Total 4	O 4	0
58	v	3	Total 3	O 3	0
58	w	3	Total 3	O 3	0
58	x	1	Total 1	O 1	0
58	z	4	Total 4	O 4	0

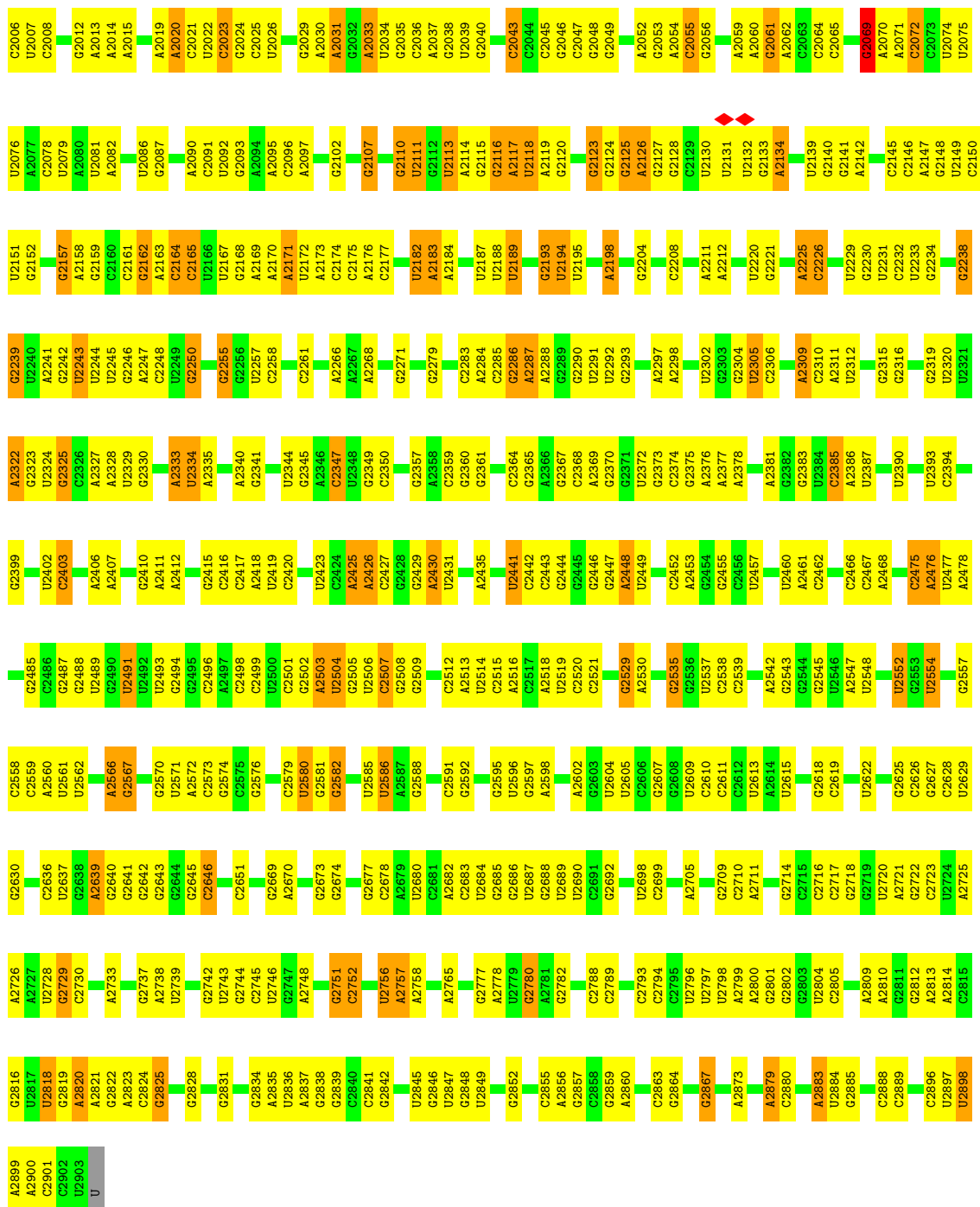
3 Residue-property plots

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

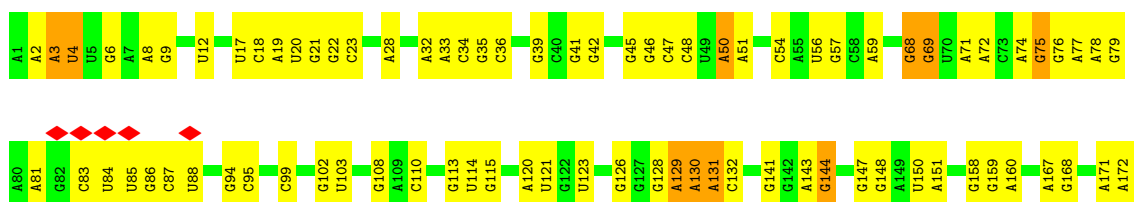
• Molecule 1: 23S rRNA



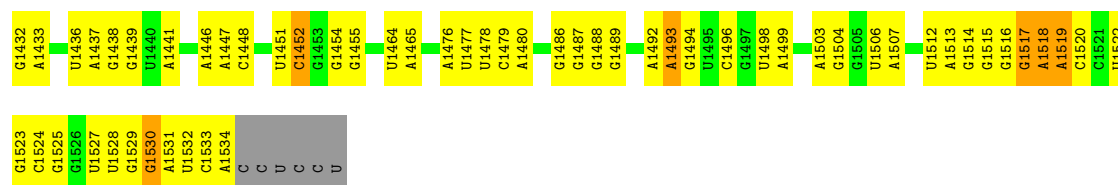
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A1739	A1744	A1745	A1746	U1747	C1748	A1749	G1750	U1751	C1752	G1753	A1754	G1755	G1756	A1757	G1758	G1759	G1760	G1761	A1762	C1764	G1771	A1772	A1773	U1778	U1779	U1780	U1781	A1784	C1788	A1789	C1790	A1791	A1794	C1795	U1798	G1799	C1800	A1801	A1802	A1803	C1804	A1805	C1806	G1807	A1808	A1809	A1810	G1811	U1812	G1813	G1814	A1815
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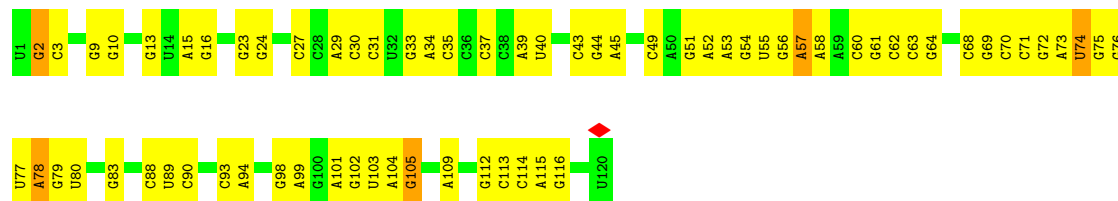
• Molecule 2: 16S ribosomal RNA



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G1343	A1256	A1162	G1084	A1005	G924	U843	A753	G674	A574	C501	A413	A336	G176	G177
G1259	G1258	A1163	U1085	G1006	G925	U844	G755	G675	G575	A502	A414	A337	G258	C178
G1347	C1259	A1167	U1086	U1007	G926	A845	G756	G676	C576	G505	U421	C339	G259	A179
A1350	G1260	U1168	A1092	U1008	G927	G846	A759	U677	C578	G506	C422	U340	G260	U180
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C1352	G1266	A1170	U1095	C1011	G933	U850	G764	U684	C580	U508	G424	A182	C264	A182
G1363	C1267	C1172	C1096	G1013	C934	G851	G765	G688	G581	A509	U425	G351	G265	G183
U1364	U1173	U1173	G1014	G1013	A935	G852	G769	C689	U591	A510	U426	G352	G266	U185
G1355	A1176	A1176	G1015	A1016	A938	G855	G773	G690	G592	C511	U427	A353	C267	C186
G1356	G1177	G1177	G1016	A1017	G939	U855	G773	G691	U593	U512	U428	C354	U268	G187
A1357	A1178	A1178	A1101	A1018	C944	G859	G778	A695	G594	C513	U429	C355	C269	C193
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C1367	G1180	G1180	C109	A1020	G947	A865	A780	U697	C599	C515	U431	G357	G275	A195
G1370	G1181	G1181	U1115	A1021	U952	C866	G786	G700	A600	U516	C436	U358	A196	A196
A1374	G1182	G1182	U1116	A1022	G953	C869	G787	G701	G601	G517	U437	G359	A197	A197
U1375	G1183	G1183	U1117	A1023	A954	U871	A790	A704	U602	C522	U438	G360	A279	C202
U1376	G1184	G1184	C1109	A1024	G955	U876	U783	G705	G603	G521	U439	G361	C280	G203
C1377	G1185	G1185	U1118	U1025	G956	U877	A794	A706	U604	A523	G454	U367	C281	G204
G1379	G1186	G1186	U1119	G1026	U957	U878	U793	A707	U605	C526	G455	U368	C286	A205
C1383	G1187	G1187	U1120	C1027	A958	C876	A794	G708	A609	G527	G456	C372	C289	U209
C1384	G1188	G1188	U1121	U1028	A959	C883	C797	U709	G613	A532	U458	A373	G292	C210
G1305	G1189	G1189	U1122	U1030	U960	C884	C798	U709	C614	C536	A459	A374	G296	G211
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C1394	A1213	A1213	U1127	U1035	G966	U888	G811	G721	A621	G540	U467	A383	G310	U216
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C1397	G1216	G1216	U1130	G1042	A969	U892	G814	U723	C634	U543	C470	A386	A313	U224
A1398	C1217	C1217	U1131	A1043	A970	A893	A815	G727	A635	G544	U471	U387	C314	C225
C1400	G1218	G1218	U1132	G1044	C970	C895	C817	G730	G636	G545	U472	A388	C314	G226
C1401	G1219	G1219	U1133	C1045	G971	C896	C817	G731	A642	G546	U473	A389	U317	U229
C1402	G1220	G1220	U1134	G1046	G972	C897	A816	G732	A643	G547	U474	U390	G318	G230
C1403	A1226	A1226	U1135	A1055	A973	A901	U820	G733	C647	G548	G474	G391	G319	U231
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C1410	A1228	A1228	U1137	C1059	C979	U904	U822	G735	A649	U553	U479	A393	C322	C235
C1411	C1230	C1230	U1138	U1060	G980	U905	C823	C736	A649	A554	U480	A394	U323	A236
C1412	G1231	G1231	U1139	G1061	U981	A908	G824	C737	G650	A554	G481	C395	G324	G237
A1413	A1236	A1236	U1140	G1062	C984	A909	C825	C738	U653	A559	A482	U398	A327	G240
U1414	C1237	C1237	U1141	U1065	C985	C910	U826	C739	C660	A560	G483	G399	A328	A246
G1415	A1238	A1238	U1142	C1066	U989	U911	U828	U740	G661	A563	U484	C401	A329	C330
G1416	A1239	A1239	U1143	U1070	U990	U912	G829	G741	U662	C564	U485	A406	G331	G247
C1419	U1240	U1240	U1144	G1071	U991	A913	G832	G745	A663	G567	C489	U407	C332	A248
C1428	G1241	G1241	U1145	C1072	U992	A914	G833	A746	A664	G568	C490	U408	G332	G251
C1429	G1242	G1242	U1146	U1073	A994	U915	U835	A747	G665	G569	C491	A409	G332	G251
A1428	A1250	A1250	U1147	G1074	A996	U917	U836	G748	A665	G570	C492	U409	G332	G251
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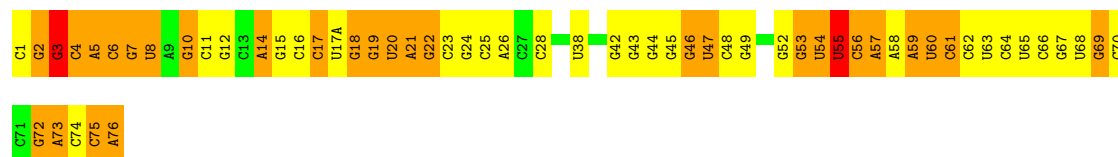
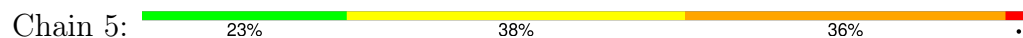
- Molecule 3: 5S ribosomal RNA



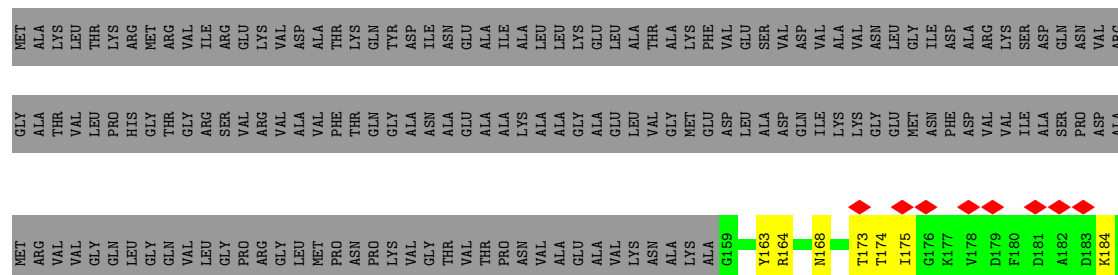
- Molecule 4: mRNA



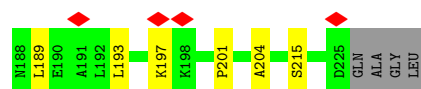
- Molecule 5: Lys-tRNA^{proL}



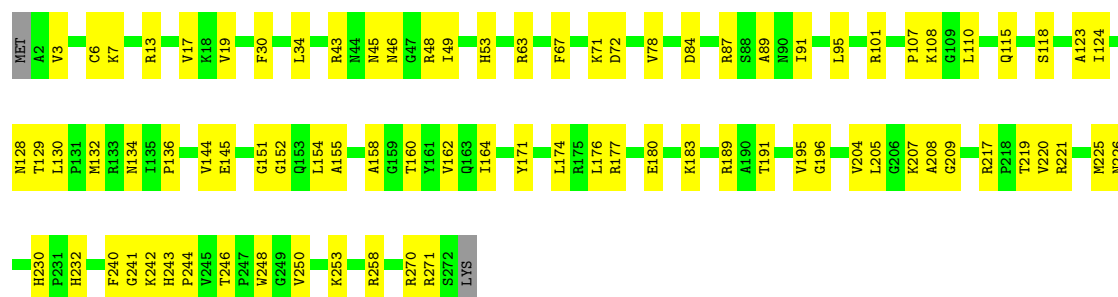
- Molecule 6: Large ribosomal subunit protein uL1



- Molecule 7: 50S ribosomal protein L2

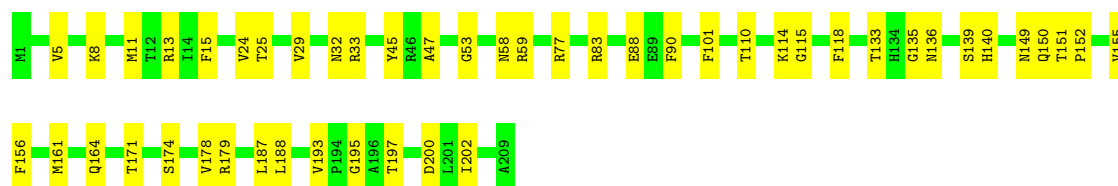


Chain B: 



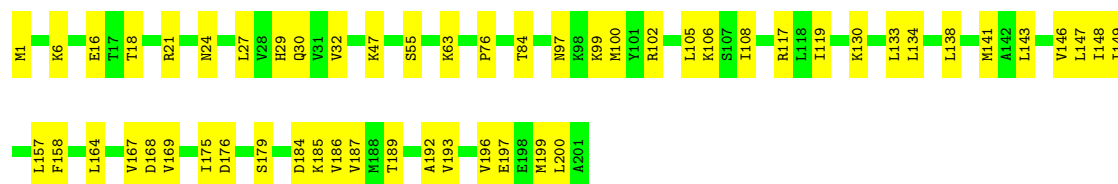
- Molecule 8: 50S ribosomal protein L3

Chain C: 



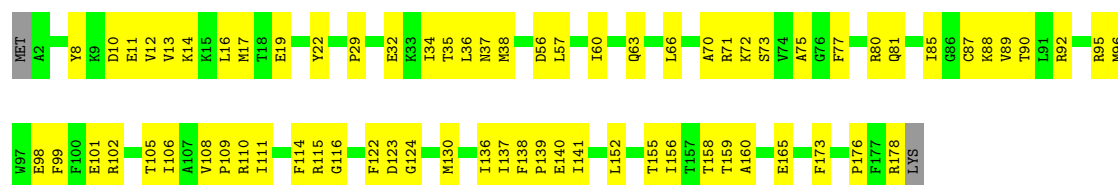
- Molecule 9: 50S ribosomal protein L4

Chain D: 



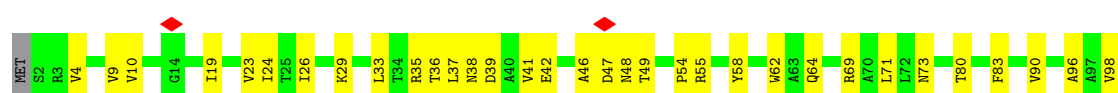
- Molecule 10: 50S ribosomal protein L5

Chain E: 



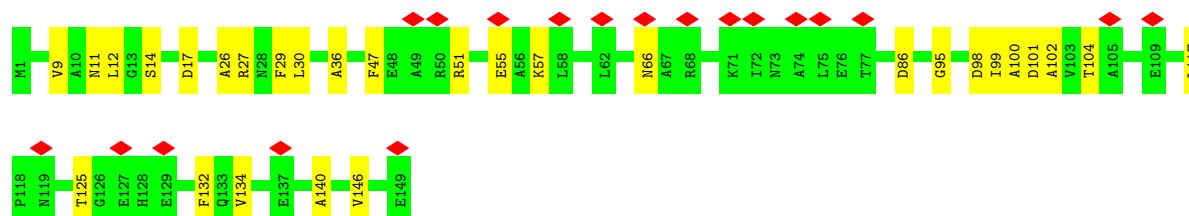
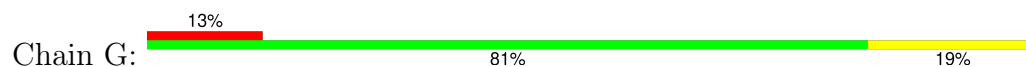
- Molecule 11: 50S ribosomal protein L6

Chain F: 

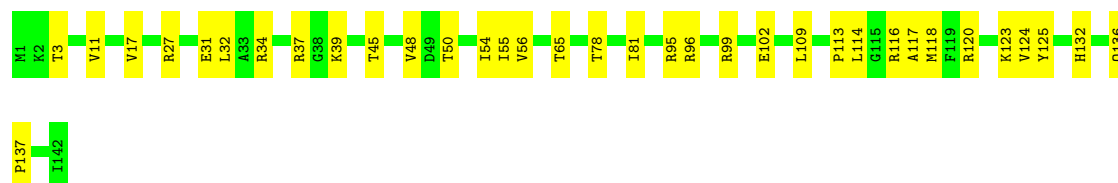




- Molecule 12: 50S ribosomal protein L9



- Molecule 13: Large ribosomal subunit protein uL13



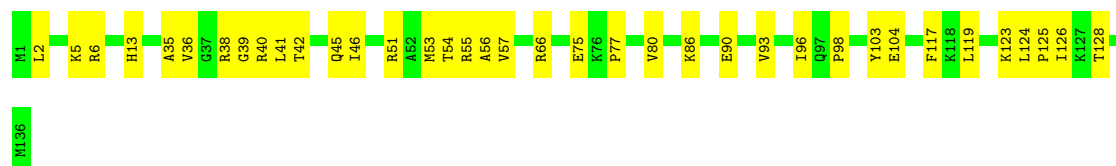
- Molecule 14: 50S ribosomal protein L14



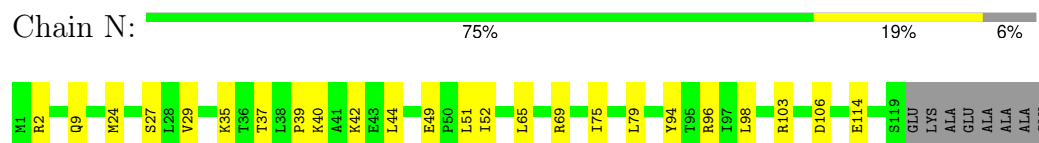
- Molecule 15: 50S ribosomal protein L15



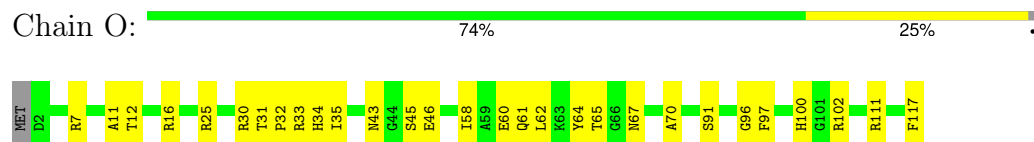
- Molecule 16: 50S ribosomal protein L16



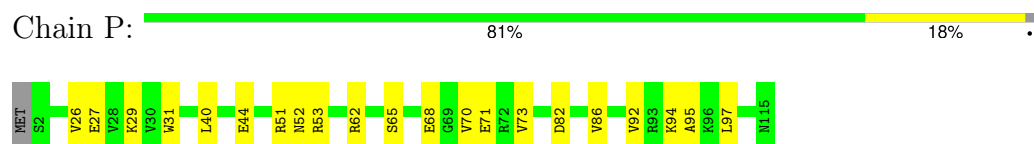
- Molecule 17: 50S ribosomal protein L17



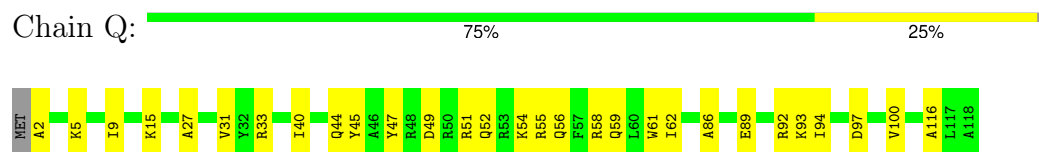
- Molecule 18: Large ribosomal subunit protein uL18



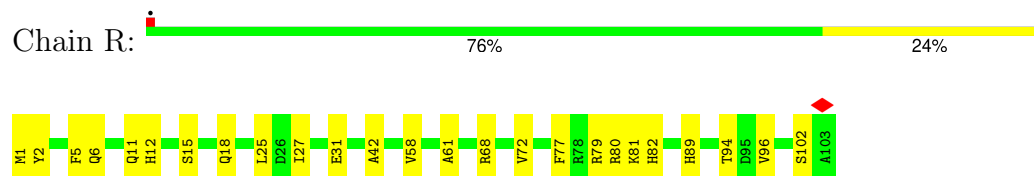
- Molecule 19: Large ribosomal subunit protein bL19



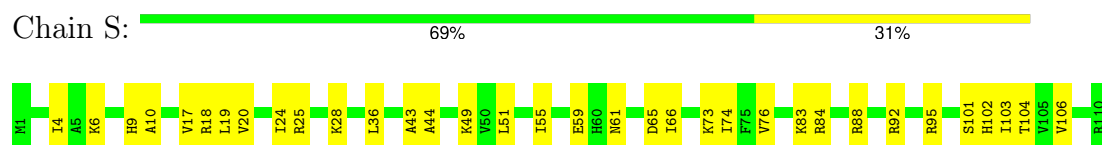
- Molecule 20: 50S ribosomal protein L20



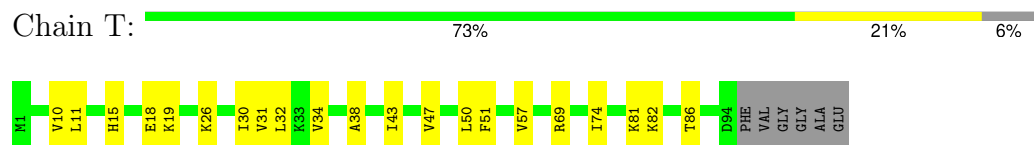
- Molecule 21: Ribosomal protein L21



- Molecule 22: 50S ribosomal protein L22

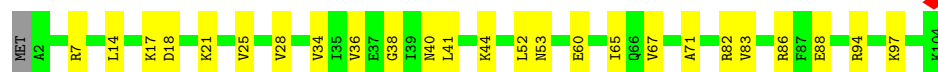


- Molecule 23: 50S ribosomal protein L23



- Molecule 24: 50S ribosomal protein L24

Chain U:  75% 24%



- Molecule 25: Large ribosomal subunit protein bL25

Chain V:  81% 19%



- Molecule 26: Large ribosomal subunit protein bL27

Chain W:  67% 24% 10%



- Molecule 27: 50S ribosomal protein L28

Chain X:  79% 19%



- Molecule 28: Large ribosomal subunit protein uL29

Chain Y:  84% 14%



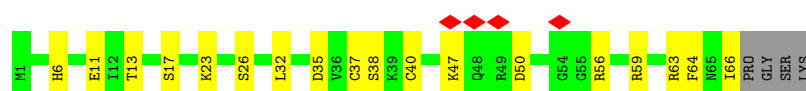
- Molecule 29: 50S ribosomal protein L30

Chain Z:  75% 24%



- Molecule 30: 50S ribosomal protein L31

Chain a:  6% 69% 26% 6%



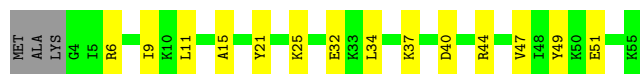
- Molecule 31: 50S ribosomal protein L32

Chain b:  74% 25%



- Molecule 32: 50S ribosomal protein L33

Chain c:  69% 25% 5%



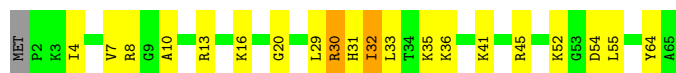
- Molecule 33: 50S ribosomal protein L34

Chain d:  70% 30%



- Molecule 34: 50S ribosomal protein L35

Chain e:  68% 28%



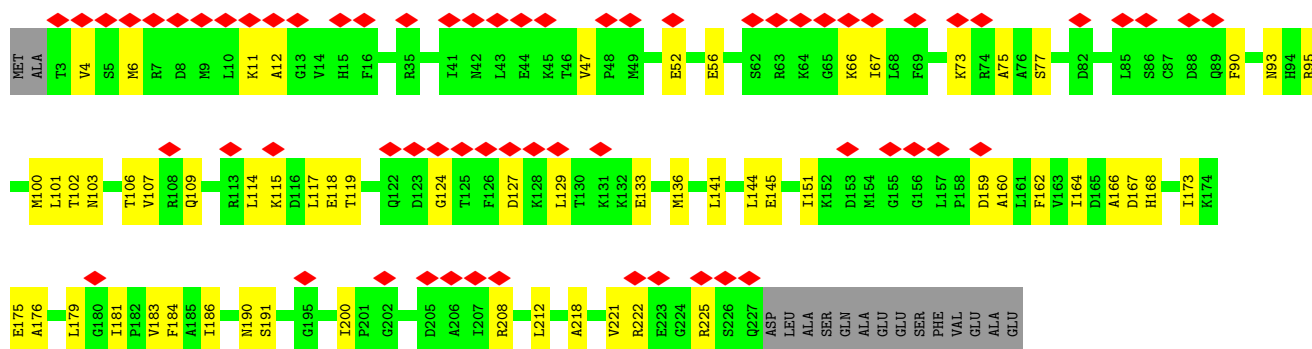
- Molecule 35: 50S ribosomal protein L36

Chain f:  74% 26%



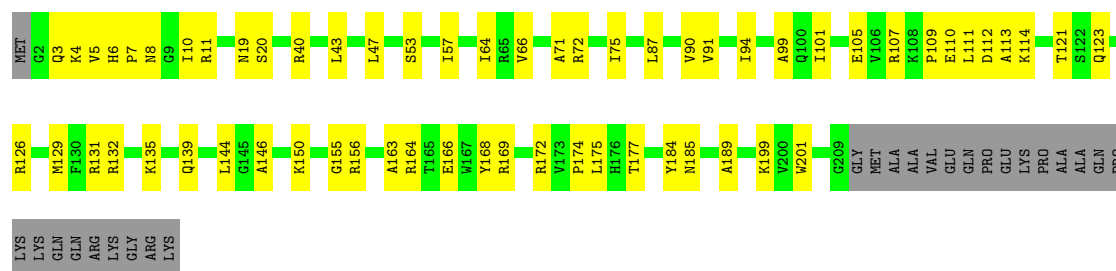
- Molecule 36: 30S ribosomal protein S2

Chain g:  27% 68% 25% 7%



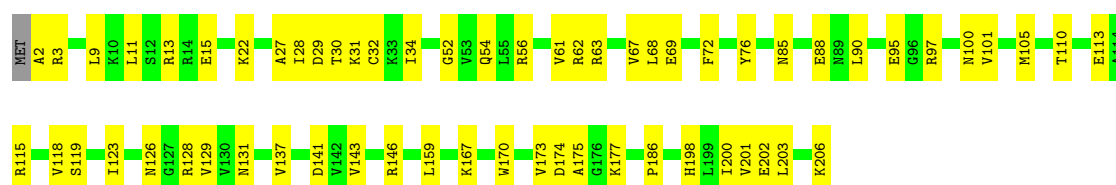
- Molecule 37: 30S ribosomal protein S3

Chain h:  63% 26% 11%



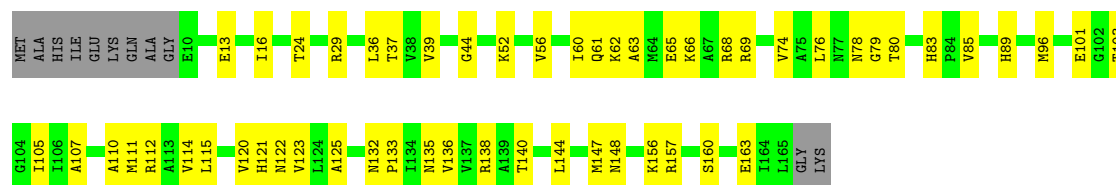
- Molecule 38: 30S ribosomal protein S4

Chain i:  70% 30%



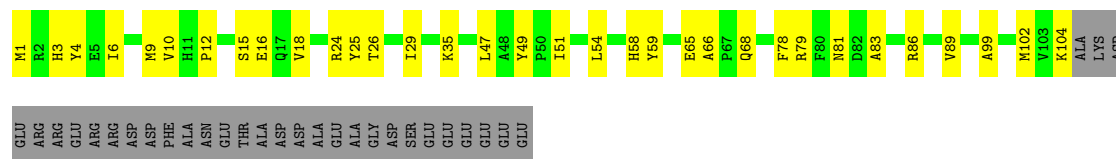
- Molecule 39: 30S ribosomal protein S5

Chain j:  61% 32% 7%



- Molecule 40: 30S ribosomal protein S6

Chain k:  53% 24% 23%



- Molecule 41: 30S ribosomal protein S7

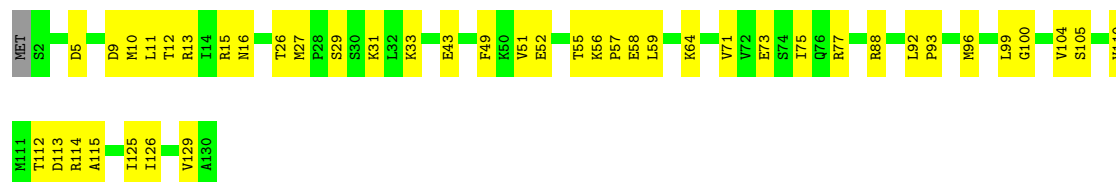
Chain l:  58% 26% 16%





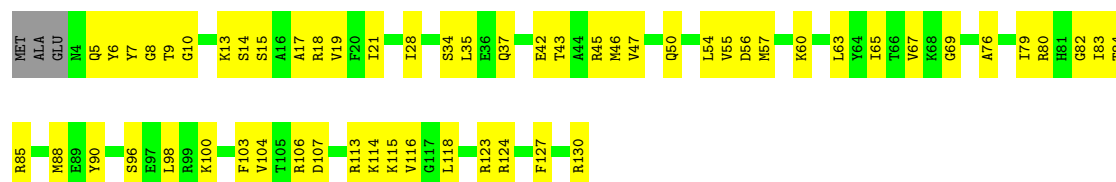
- Molecule 42: Small ribosomal subunit protein uS8

Chain m: 66% 33%



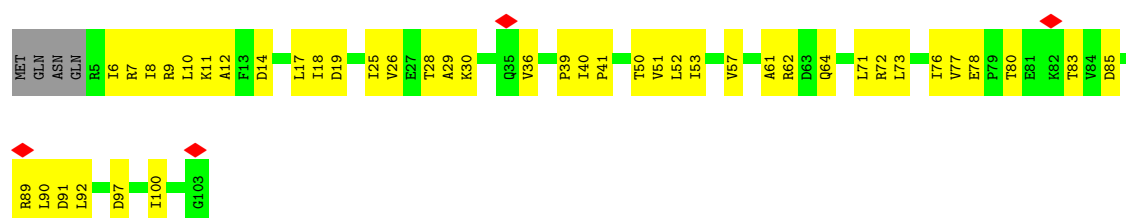
- Molecule 43: Small ribosomal subunit protein uS9

Chain n: 54% 44%



- Molecule 44: Small ribosomal subunit protein uS10

Chain o: 54% 42%



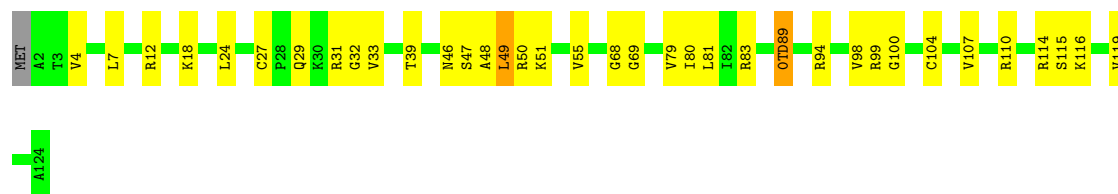
- Molecule 45: 30S ribosomal protein S11

Chain p: 67% 23% 9%

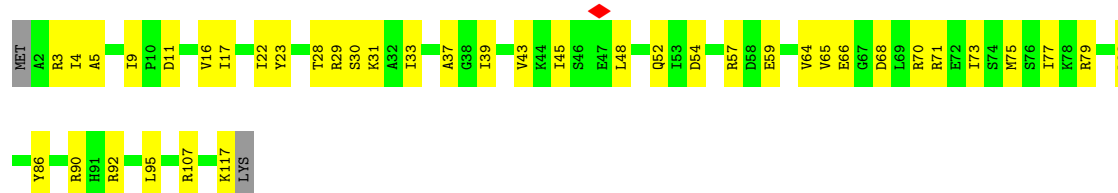


- Molecule 46: Small ribosomal subunit protein uS12

Chain q: 70% 27%



- Molecule 47: 30S ribosomal protein S13



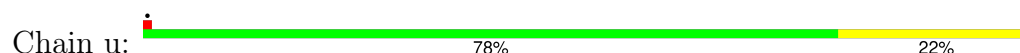
- Molecule 48: Small ribosomal subunit protein uS14



- Molecule 49: Small ribosomal subunit protein uS15



- Molecule 50: 30S ribosomal protein S16

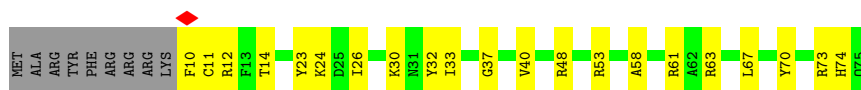


- Molecule 51: Small ribosomal subunit protein uS17



- Molecule 52: 30S ribosomal protein S18





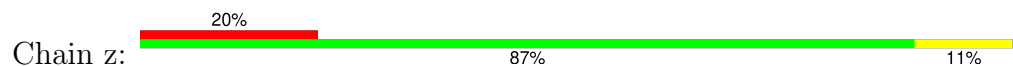
- Molecule 53: Small ribosomal subunit protein uS19



- Molecule 54: 30S ribosomal protein S20



- Molecule 55: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69316	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61.23	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.056	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	547.328, 547.328, 547.328	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.069, 1.069, 1.069	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, UR3, 1MG, MG, 0TD, 6MZ, OMU, OMG, 5MU, 7MG, 4OC, MA6, G7M, 5MC, PSU, OMC, 2MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.14	0/69335	0.25	0/108168
2	2	0.13	0/36590	0.23	0/57074
3	3	0.11	0/2872	0.23	0/4478
4	4	0.34	0/255	0.55	0/394
5	5	0.30	0/1841	0.54	2/2870 (0.1%)
6	A	0.10	0/511	0.28	0/685
7	B	0.14	0/2121	0.29	0/2852
8	C	0.14	0/1586	0.32	0/2134
9	D	0.15	0/1571	0.35	0/2113
10	E	0.14	0/1434	0.38	0/1926
11	F	0.12	0/1333	0.28	0/1805
12	G	0.13	0/1122	0.33	0/1515
13	J	0.16	0/1152	0.34	0/1551
14	K	0.12	0/955	0.25	0/1279
15	L	0.14	0/1062	0.28	0/1413
16	M	0.14	0/1093	0.29	0/1460
17	N	0.15	0/964	0.34	0/1289
18	O	0.13	0/902	0.31	0/1209
19	P	0.14	0/929	0.28	0/1242
20	Q	0.17	0/960	0.33	0/1278
21	R	0.14	0/829	0.34	0/1107
22	S	0.16	0/864	0.35	0/1156
23	T	0.13	0/752	0.29	0/1005
24	U	0.14	0/796	0.32	0/1062
25	V	0.15	0/766	0.36	0/1025
26	W	0.13	0/589	0.25	0/779
27	X	0.15	0/635	0.31	0/848
28	Y	0.13	0/502	0.33	0/667
29	Z	0.13	0/452	0.27	0/605
30	a	0.12	0/531	0.30	0/709
31	b	0.13	0/450	0.29	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	c	0.13	0/433	0.26	0/576
33	d	0.14	0/380	0.26	0/498
34	e	0.39	0/513	0.62	1/676 (0.1%)
35	f	0.13	0/303	0.33	0/397
36	g	0.14	0/1791	0.39	0/2413
37	h	0.14	0/1663	0.36	0/2241
38	i	0.12	0/1665	0.26	0/2227
39	j	0.16	0/1165	0.36	0/1568
40	k	0.15	0/867	0.37	0/1171
41	l	0.14	0/1195	0.37	0/1602
42	m	0.16	0/989	0.39	0/1326
43	n	0.22	0/1034	0.50	0/1375
44	o	0.15	0/800	0.38	0/1082
45	p	0.19	0/893	0.37	0/1205
46	q	0.27	0/960	0.40	0/1286
47	r	0.13	0/909	0.35	0/1215
48	s	0.12	0/817	0.27	0/1088
49	t	0.13	0/722	0.31	0/964
50	u	0.16	0/659	0.33	0/884
51	v	0.12	0/657	0.31	0/881
52	w	0.17	0/553	0.29	0/743
53	x	0.12	0/680	0.28	0/915
54	y	0.16	0/675	0.34	0/895
55	z	0.10	0/597	0.24	0/792
All	All	0.14	0/156674	0.28	3/234317 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	e	30	ARG	N-CA-C	-11.61	92.49	108.86
5	5	55	U	C3'-C2'-O2'	6.24	120.05	110.70
5	5	3	G	C4'-C3'-O3'	5.85	118.18	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	62334	0	31367	1170	0
2	2	32929	0	16587	576	0
3	3	2569	0	1301	46	0
4	4	230	0	119	8	0
5	5	1648	0	833	73	0
6	A	507	0	542	10	0
7	B	2082	0	2154	58	0
8	C	1565	0	1616	40	0
9	D	1552	0	1619	50	0
10	E	1410	0	1444	53	0
11	F	1313	0	1358	32	0
12	G	1111	0	1148	18	0
13	J	1129	0	1162	34	0
14	K	946	0	1023	25	0
15	L	1053	0	1129	30	0
16	M	1074	0	1157	29	0
17	N	951	0	994	17	0
18	O	892	0	923	26	0
19	P	917	0	962	18	0
20	Q	947	0	1019	30	0
21	R	816	0	839	25	0
22	S	857	0	922	26	0
23	T	746	0	811	15	0
24	U	788	0	844	18	0
25	V	753	0	780	17	0
26	W	582	0	599	15	0
27	X	625	0	652	11	0
28	Y	501	0	531	10	0
29	Z	448	0	488	11	0
30	a	522	0	524	19	0
31	b	444	0	458	16	0
32	c	426	0	464	11	0
33	d	377	0	418	16	0
34	e	504	0	572	25	0
35	f	302	0	343	9	0
36	g	1760	0	1787	39	0
37	h	1636	0	1710	42	0
38	i	1643	0	1707	45	0
39	j	1152	0	1196	40	0
40	k	848	0	846	27	0
41	l	1181	0	1238	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	m	979	0	1031	35	0
43	n	1022	0	1070	44	0
44	o	790	0	831	36	0
45	p	877	0	887	28	0
46	q	957	0	1017	34	0
47	r	900	0	965	31	0
48	s	805	0	844	27	0
49	t	714	0	734	23	0
50	u	649	0	666	16	0
51	v	648	0	691	18	0
52	w	544	0	560	15	0
53	x	663	0	688	32	0
54	y	669	0	719	19	0
55	z	589	0	629	6	0
56	1	262	0	0	0	0
56	2	111	0	0	0	0
56	3	10	0	0	0	0
56	5	1	0	0	0	0
56	B	3	0	0	0	0
56	L	2	0	0	0	0
56	M	1	0	0	0	0
56	Q	1	0	0	0	0
56	X	1	0	0	0	0
56	b	1	0	0	0	0
56	l	1	0	0	0	0
56	z	1	0	0	0	0
57	5	9	0	12	0	0
58	1	700	0	0	22	0
58	2	341	0	0	5	0
58	3	7	0	0	0	0
58	4	1	0	0	0	0
58	5	10	0	0	3	0
58	B	2	0	0	0	0
58	C	7	0	0	0	0
58	D	10	0	0	2	0
58	E	4	0	0	1	0
58	F	6	0	0	1	0
58	G	12	0	0	0	0
58	J	7	0	0	3	0
58	K	4	0	0	2	0
58	L	3	0	0	3	0
58	M	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	N	2	0	0	0	0
58	O	6	0	0	1	0
58	P	6	0	0	0	0
58	Q	7	0	0	1	0
58	R	7	0	0	5	0
58	S	4	0	0	1	0
58	T	2	0	0	0	0
58	U	6	0	0	0	0
58	V	1	0	0	0	0
58	W	2	0	0	0	0
58	Y	8	0	0	2	0
58	Z	2	0	0	1	0
58	a	2	0	0	0	0
58	b	2	0	0	0	0
58	f	1	0	0	0	0
58	g	20	0	0	1	0
58	h	14	0	0	2	0
58	i	8	0	0	2	0
58	j	3	0	0	0	0
58	k	7	0	0	1	0
58	l	5	0	0	1	0
58	m	3	0	0	0	0
58	n	4	0	0	0	0
58	o	3	0	0	0	0
58	p	5	0	0	1	0
58	q	1	0	0	0	0
58	r	4	0	0	0	0
58	t	1	0	0	0	0
58	u	4	0	0	0	0
58	v	3	0	0	0	0
58	w	3	0	0	1	0
58	x	1	0	0	0	0
58	z	4	0	0	0	0
All	All	146547	0	97530	2747	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 12.

All (2747) 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)
5:5:67:G:H5'	58:5:206:HOH:O	1.65	0.95
1:1:408:G:H1	1:1:419:U:H3	1.16	0.94
5:5:18:G:H1	5:5:57:A:N6	1.68	0.91
54:y:57:ILE:HG13	54:y:61:GLN:HE22	1.36	0.89
1:1:1270:C:H5''	1:1:1271:G:H5'	1.55	0.88
2:2:246:A:H62	2:2:281:G:N2	1.70	0.88
1:1:377:G:H1	1:1:397:U:H3	1.18	0.87
2:2:458:U:H3	2:2:474:G:H1	0.87	0.86
1:1:572:A:H61	1:1:2029:G:H21	1.21	0.85
1:1:1039:A:C2	1:1:1116:G:N1	2.46	0.84
1:1:586:A:H5'	9:D:84:THR:HG21	1.59	0.83
1:1:2491:U:H5'	1:1:2570:G:H5''	1.62	0.82
44:o:51:VAL:HG23	48:s:81:ARG:HB2	1.63	0.81
1:1:274:C:O2	1:1:363:G:N2	2.14	0.80
8:C:156:PHE:HB3	13:J:81:ILE:HD11	1.64	0.80
5:5:18:G:N1	5:5:57:A:N6	2.28	0.80
36:g:100:MET:HA	36:g:107:VAL:HG21	1.64	0.79
2:2:20:U:O2'	2:2:573:A:N6	2.17	0.78
10:E:38:MET:HG2	10:E:57:LEU:HD22	1.66	0.78
2:2:875:U:O2'	42:m:15:ARG:NH1	2.17	0.77
43:n:96:SER:OG	43:n:100:LYS:NZ	2.17	0.77
1:1:1202:G:N2	15:L:4:ASN:OD1	2.17	0.77
49:t:29:VAL:HG11	49:t:81:LEU:HD21	1.67	0.77
38:i:129:VAL:HG21	38:i:146:ARG:HH21	1.48	0.77
2:2:246:A:N6	2:2:281:G:N2	2.32	0.77
1:1:26:G:H1'	1:1:515:A:H61	1.48	0.77
2:2:335:C:H2'	2:2:336:A:H8	1.50	0.77
3:3:71:C:H42	3:3:105:G:H1	1.33	0.77
2:2:1124:G:O2'	2:2:1145:A:N6	2.17	0.76
17:N:37:THR:HG22	17:N:39:PRO:HD2	1.67	0.76
2:2:673:A:H2'	2:2:674:G:C8	2.21	0.76
1:1:475:C:O2	1:1:479:A:N6	2.19	0.76
13:J:34:ARG:HG3	13:J:39:LYS:HB2	1.68	0.76
2:2:438:U:H3	2:2:496:A:H62	1.34	0.76
7:B:225:MET:HG2	7:B:230:HIS:HB2	1.67	0.76
5:5:54:U:H3	5:5:58:A:H62	1.34	0.75
2:2:826:C:O2	42:m:16:ASN:ND2	2.19	0.75
1:1:1047:G:H21	1:1:1111:A:H62	1.34	0.75
1:1:497:A:H2'	1:1:498:G:H8	1.52	0.74
1:1:1779:U:OP2	1:1:1784:A:N6	2.21	0.74
1:1:698:C:O2'	1:1:734:A:N6	2.19	0.74
53:x:18:LYS:NZ	53:x:32:ARG:O	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:45:G:H5''	1:1:46:G:H5'	1.70	0.74
34:e:32:ILE:HD11	34:e:35:LYS:HG2	1.69	0.74
1:1:447:A:OP1	20:Q:5:LYS:NZ	2.20	0.74
1:1:2117:A:N1	1:1:2171:A:N6	2.35	0.74
47:r:4:ILE:HG23	47:r:57:ARG:HG2	1.70	0.74
5:5:56:C:O2'	10:E:75:ALA:HB2	1.89	0.73
43:n:43:THR:HA	43:n:46:MET:HE3	1.70	0.73
1:1:848:C:H2'	1:1:849:A:H8	1.52	0.73
13:J:114:LEU:O	13:J:118:MET:HB3	1.87	0.73
37:h:11:ARG:NH1	37:h:177:THR:O	2.21	0.73
1:1:2333:A:H4'	1:1:2334:U:H5''	1.70	0.73
2:2:927:G:OP2	4:4:11:A:N6	2.22	0.73
34:e:16:LYS:HE2	34:e:20:GLY:HA2	1.71	0.73
1:1:1215:G:H1	1:1:1234:U:H3	1.34	0.73
1:1:155:A:H2'	1:1:156:A:H8	1.54	0.72
1:1:1868:C:N4	1:1:1869:G:O6	2.22	0.72
36:g:4:VAL:HG11	36:g:212:LEU:HD21	1.69	0.72
43:n:13:LYS:HG3	43:n:14:SER:H	1.55	0.72
12:G:66:ASN:ND2	12:G:134:VAL:O	2.23	0.72
1:1:111:A:O2'	28:Y:58:ASN:ND2	2.23	0.72
1:1:2102:G:N2	1:1:2187:U:O2	2.22	0.72
13:J:27:ARG:NH1	58:J:201:HOH:O	2.23	0.72
1:1:1039:A:N1	1:1:1116:G:O6	2.23	0.71
25:V:48:MET:SD	25:V:51:GLN:NE2	2.62	0.71
27:X:45:ARG:HH21	27:X:47:VAL:HG12	1.55	0.71
54:y:57:ILE:O	54:y:61:GLN:NE2	2.23	0.71
1:1:2188:U:O4	1:1:2189:U:O4	2.07	0.71
2:2:180:U:H3	2:2:195:A:H62	1.36	0.71
1:1:242:G:H5'	34:e:64:TYR:HE2	1.55	0.71
43:n:56:ASP:O	43:n:60:LYS:NZ	2.24	0.71
58:1:3302:HOH:O	17:N:2:ARG:NH1	2.23	0.71
1:1:309:A:N3	1:1:329:G:O2'	2.24	0.70
2:2:981:U:OP1	48:s:9:ARG:NH1	2.25	0.70
1:1:572:A:H61	1:1:2029:G:N2	1.89	0.70
44:o:29:ALA:HB1	44:o:36:VAL:HG21	1.72	0.70
1:1:177:G:N2	1:1:177:G:OP2	2.24	0.70
2:2:297:G:N2	2:2:300:A:OP2	2.25	0.70
2:2:671:G:O2'	40:k:79:ARG:NH2	2.24	0.70
43:n:28:ILE:HG12	43:n:63:LEU:HD21	1.73	0.70
50:u:4:ILE:HG12	50:u:21:VAL:HG22	1.72	0.70
1:1:2758:A:H1'	11:F:38:ASN:HD21	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:429:U:H5'	38:i:9:LEU:HD11	1.74	0.70
10:E:13:VAL:O	10:E:17:MET:HG2	1.92	0.70
38:i:61:VAL:HG21	38:i:200:ILE:HD11	1.73	0.70
9:D:119:ILE:HB	9:D:187:VAL:HG12	1.74	0.70
1:1:274:C:N3	1:1:363:G:N1	2.40	0.70
10:E:105:THR:HG23	10:E:106:ILE:HG13	1.74	0.70
37:h:172:ARG:HG2	37:h:174:PRO:HD3	1.74	0.69
5:5:49:G:H1	5:5:65:U:H3	1.39	0.69
13:J:17:VAL:HG12	13:J:55:ILE:HB	1.74	0.69
1:1:2134:A:N6	1:1:2157:G:O2'	2.26	0.69
14:K:30:ARG:NH2	14:K:37:ASP:OD2	2.25	0.69
1:1:686:U:OP1	33:d:11:LYS:NZ	2.19	0.69
41:l:47:LEU:HD21	41:l:58:GLU:HB3	1.75	0.69
1:1:464:U:H1'	1:1:686:U:H5	1.57	0.69
1:1:497:A:H2'	1:1:498:G:C8	2.28	0.69
2:2:674:G:H2'	2:2:675:A:H8	1.57	0.69
5:5:60:U:OP2	5:5:61:C:N4	2.25	0.69
1:1:196:A:H61	1:1:831:G:N2	1.90	0.69
1:1:463:G:N2	1:1:466:A:OP2	2.24	0.69
2:2:310:G:H5''	50:u:31:ARG:HB2	1.75	0.69
2:2:1261:A:N6	2:2:1274:A:O2'	2.26	0.69
7:B:6:CYS:SG	7:B:13:ARG:NH1	2.66	0.69
9:D:164:LEU:HD22	9:D:167:VAL:HG22	1.75	0.69
1:1:2378:A:HO2'	18:O:91:SER:HG	1.40	0.69
16:M:75:GLU:HB2	16:M:90:GLU:HG3	1.75	0.69
30:a:35:ASP:OD2	47:r:3:ARG:NH1	2.25	0.69
39:j:13:GLU:OE2	39:j:68:ARG:NH1	2.25	0.69
2:2:673:A:H2'	2:2:674:G:H8	1.58	0.69
48:s:54:ASP:HA	48:s:59:ARG:HG3	1.74	0.69
1:1:2515:C:H2'	1:1:2516:A:H8	1.58	0.68
47:r:23:TYR:HB3	47:r:66:GLU:HB3	1.74	0.68
1:1:1047:G:N2	1:1:1111:A:H62	1.90	0.68
37:h:57:ILE:HG23	37:h:64:ILE:HD11	1.74	0.68
2:2:1447:A:OP1	2:2:1448:C:N4	2.25	0.68
11:F:38:ASN:ND2	11:F:64:GLN:OE1	2.27	0.68
1:1:2140:G:N1	1:1:2151:U:N3	2.41	0.68
2:2:946:A:O2'	2:2:1333:A:N3	2.26	0.68
41:l:113:ASP:HB2	41:l:119:ARG:HG3	1.75	0.68
1:1:1429:G:H2'	1:1:1430:G:H8	1.58	0.68
1:1:2530:A:N7	11:F:172:LYS:NZ	2.42	0.68
8:C:5:VAL:H	8:C:32:ASN:HD21	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:581:C:H2'	1:1:582:A:H8	1.58	0.68
1:1:1668:A:N3	1:1:1670:C:N4	2.42	0.68
3:3:104:A:C5	3:3:105:G:H1'	2.28	0.68
1:1:2312:U:O2	10:E:37:ASN:ND2	2.27	0.68
1:1:2031:A:N3	1:1:2455:G:O2'	2.27	0.67
2:2:1266:G:N2	2:2:1269:A:OP2	2.26	0.67
43:n:106:ARG:NH1	43:n:107:ASP:O	2.27	0.67
1:1:2069:G7M:N2	1:1:2442:C:O2	2.21	0.67
2:2:1312:G:OP2	30:a:63:ARG:NH2	2.27	0.67
1:1:535:G:H1	1:1:558:U:H3	1.42	0.67
1:1:1830:C:H2'	1:1:1831:G:H8	1.58	0.67
1:1:2595:G:N2	1:1:2598:A:OP2	2.27	0.67
1:1:2640:G:OP1	13:J:95:ARG:NH1	2.27	0.67
20:Q:49:ASP:HA	20:Q:52:GLN:HB2	1.77	0.67
1:1:1074:G:N2	58:1:3321:HOH:O	2.27	0.67
1:1:2061:G:OP2	9:D:63:LYS:NZ	2.26	0.67
1:1:2188:U:C4	1:1:2189:U:O4	2.47	0.67
10:E:63:GLN:HE21	10:E:89:VAL:HG13	1.58	0.67
1:1:468:G:OP2	33:d:37:LYS:NZ	2.26	0.67
2:2:150:U:H3	2:2:171:A:H62	1.42	0.67
10:E:158:THR:HG22	10:E:160:ALA:H	1.58	0.67
44:o:40:ILE:HD11	44:o:73:LEU:HD23	1.76	0.67
1:1:2220:U:H2'	1:1:2221:G:H8	1.60	0.67
9:D:21:ARG:NH2	58:D:302:HOH:O	2.26	0.67
1:1:219:A:N3	1:1:234:U:O2'	2.26	0.67
21:R:15:SER:H	21:R:18:GLN:HE22	1.42	0.67
1:1:528:A:H5''	13:J:113:PRO:HG3	1.75	0.67
2:2:1054:C:H42	4:4:21:U:H5	1.43	0.67
1:1:270:A:H5'	1:1:271:G:H5''	1.77	0.66
1:1:2376:A:N3	18:O:111:ARG:NH2	2.43	0.66
1:1:2857:G:N2	1:1:2860:A:OP2	2.21	0.66
21:R:72:VAL:O	58:R:201:HOH:O	2.13	0.66
1:1:2076:U:OP2	1:1:2238:G:N2	2.28	0.66
1:1:2796:U:H3	1:1:2799:A:H61	1.43	0.66
43:n:84:THR:HG23	43:n:98:LEU:HD23	1.76	0.66
2:2:1072:G:H21	36:g:106:THR:HG21	1.60	0.66
2:2:246:A:N6	2:2:281:G:H21	1.92	0.66
47:r:86:TYR:OH	47:r:90:ARG:NH1	2.29	0.66
41:l:15:ASP:OD1	41:l:20:SER:N	2.25	0.66
46:q:68:GLY:O	46:q:99:ARG:NH1	2.29	0.66
1:1:572:A:N6	1:1:2029:G:H21	1.92	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1255:G:O2'	2:2:1258:G:N3	2.24	0.66
25:V:69:GLU:OE1	25:V:69:GLU:N	2.28	0.66
2:2:405:U:O4	38:i:2:ALA:N	2.29	0.66
2:2:1027:C:N4	2:2:1034:G:O6	2.29	0.66
45:p:113:VAL:O	52:w:73:ARG:NH1	2.29	0.66
1:1:539:G:H1	1:1:554:U:H3	1.44	0.66
1:1:1287:A:N1	1:1:1649:G:O2'	2.26	0.66
7:B:3:VAL:HG12	7:B:19:VAL:HG22	1.77	0.66
15:L:1:MET:O	58:L:301:HOH:O	2.14	0.66
42:m:43:GLU:OE2	42:m:114:ARG:NH2	2.29	0.66
1:1:302:C:H2'	1:1:303:G:H8	1.62	0.65
1:1:2848:G:O2'	1:1:2867:G:N2	2.29	0.65
8:C:179:ARG:HB3	8:C:188:LEU:HD12	1.79	0.65
1:1:514:A:N3	1:1:581:C:O2'	2.27	0.65
2:2:938:A:N3	2:2:1376:U:O2'	2.25	0.65
26:W:37:ILE:HD11	26:W:82:ILE:HD11	1.77	0.65
7:B:232:HIS:HA	7:B:242:LYS:HD2	1.78	0.65
2:2:1119:C:OP1	43:n:85:ARG:NH2	2.30	0.65
14:K:58:LEU:HD11	14:K:86:LEU:HD23	1.77	0.65
20:Q:33:ARG:NH1	58:Q:301:HOH:O	2.25	0.65
40:k:16:GLU:OE2	40:k:16:GLU:N	2.27	0.65
43:n:42:GLU:HA	43:n:45:ARG:HD2	1.77	0.65
1:1:2460:U:O2	1:1:2493:U:N3	2.30	0.65
2:2:410:G:OP2	38:i:31:LYS:NZ	2.28	0.65
1:1:820:A:H4'	1:1:836:G:H22	1.60	0.65
1:1:1190:G:H5''	15:L:32:GLY:HA2	1.79	0.65
1:1:2258:C:O2'	1:1:2427:C:OP2	2.14	0.65
1:1:747:5MU:O2'	22:S:92:ARG:NH2	2.29	0.65
1:1:1597:A:H5''	1:1:1598:A:H5'	1.77	0.65
17:N:96:ARG:NH1	17:N:114:GLU:OE2	2.30	0.65
41:l:133:THR:HA	41:l:136:LYS:HG2	1.79	0.65
1:1:380:G:N1	1:1:395:U:N3	2.44	0.65
1:1:1016:G:O6	1:1:1147:A:N6	2.29	0.65
2:2:1005:A:H3'	2:2:1006:G:H8	1.61	0.65
7:B:144:VAL:HB	7:B:154:LEU:HB2	1.79	0.65
22:S:25:ARG:NH1	22:S:74:ILE:O	2.27	0.65
25:V:48:MET:HA	25:V:51:GLN:HG3	1.79	0.65
30:a:37:CYS:SG	30:a:38:SER:N	2.66	0.65
2:2:358:U:H2'	2:2:359:G:H8	1.61	0.64
11:F:98:VAL:HG12	11:F:103:ILE:HG12	1.80	0.64
1:1:993:G:OP2	20:Q:51:ARG:NH2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1055:A:O2'	37:h:156:ARG:NH1	2.30	0.64
15:L:2:ARG:NH1	58:L:301:HOH:O	2.25	0.64
30:a:50:ASP:CG	47:r:71:ARG:HH22	2.06	0.64
1:1:1434:A:H2'	1:1:1435:G:H8	1.61	0.64
2:2:501:C:OP1	46:q:114:ARG:NH2	2.23	0.64
2:2:689:C:OP2	45:p:53:ARG:NH2	2.30	0.64
2:2:958:A:OP1	53:x:55:ARG:NH1	2.30	0.64
1:1:411:G:OP2	1:1:2406:A:O2'	2.16	0.64
1:1:2183:A:H2'	1:1:2184:A:C8	2.31	0.64
2:2:246:A:N6	2:2:281:G:C2	2.65	0.64
2:2:393:A:OP2	50:u:12:LYS:NZ	2.20	0.64
1:1:517:C:OP1	31:b:13:ARG:NH2	2.30	0.64
1:1:877:A:O2'	1:1:900:A:N6	2.30	0.64
1:1:918:A:N3	3:3:80:U:O2'	2.28	0.64
42:m:96:MET:HB3	42:m:100:GLY:H	1.61	0.64
1:1:244:A:OP2	34:e:8:ARG:NH2	2.30	0.64
1:1:2250:G:O2'	1:1:2496:C:OP1	2.15	0.64
2:2:335:C:O2'	2:2:1433:A:N3	2.27	0.64
5:5:19:G:OP1	5:5:60:U:N3	2.30	0.64
7:B:225:MET:HG3	7:B:226:ASN:H	1.63	0.64
52:w:37:GLY:O	52:w:63:ARG:NH2	2.31	0.64
1:1:887:A:O2'	1:1:889:C:OP2	2.14	0.64
1:1:2279:G:N7	26:W:14:ARG:NH2	2.46	0.64
1:1:2581:G:N2	1:1:2581:G:OP2	2.30	0.64
38:i:11:LEU:HB3	38:i:63:ARG:HD3	1.78	0.64
38:i:202:GLU:OE1	39:j:112:ARG:NH2	2.30	0.64
1:1:2720:U:OP1	19:P:53:ARG:NH2	2.31	0.64
2:2:222:C:H2'	2:2:223:A:H8	1.63	0.64
11:F:41:VAL:O	11:F:55:ARG:NH2	2.29	0.64
43:n:7:TYR:CG	43:n:8:GLY:N	2.66	0.64
49:t:32:LEU:HD11	49:t:59:MET:HB3	1.80	0.64
1:1:1030:C:N3	58:1:3338:HOH:O	2.30	0.64
1:1:1789:A:OP2	7:B:221:ARG:NH1	2.30	0.64
1:1:2304:G:H22	1:1:2312:U:H3	1.46	0.64
13:J:37:ARG:HA	13:J:118:MET:HE2	1.79	0.64
34:e:32:ILE:HG23	34:e:36:LYS:HZ1	1.62	0.64
2:2:842:U:O3'	2:2:844:G:N2	2.32	0.63
1:1:818:G:N1	1:1:1188:U:OP2	2.27	0.63
1:1:1992:G:N2	1:1:1996:C:O2'	2.31	0.63
37:h:112:ASP:OD1	37:h:113:ALA:N	2.31	0.63
1:1:102:U:O4	28:Y:2:LYS:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:298:G:N1	1:1:339:U:OP2	2.26	0.63
1:1:1807:G:N2	1:1:1810:A:OP2	2.30	0.63
1:1:2116:G:N2	1:1:2161:C:OP1	2.31	0.63
1:1:2618:G:H21	8:C:155:VAL:HG21	1.63	0.63
1:1:1042:G:N2	58:1:3318:HOH:O	2.31	0.63
1:1:1363:C:O2'	1:1:1809:A:N3	2.28	0.63
1:1:2075:U:H1'	1:1:2597:G:H21	1.64	0.63
2:2:103:U:OP2	54:y:9:LYS:NZ	2.28	0.63
5:5:19:G:H3'	5:5:20:U:H5	1.63	0.63
15:L:19:LEU:HD23	15:L:27:LEU:HD13	1.80	0.63
17:N:51:LEU:HB3	17:N:79:LEU:HD21	1.80	0.63
23:T:15:HIS:HB3	23:T:31:VAL:HG23	1.80	0.63
2:2:1356:G:H2'	2:2:1357:A:C8	2.33	0.63
1:1:210:C:OP1	33:d:29:GLN:NE2	2.32	0.63
19:P:26:VAL:HG12	19:P:86:VAL:HG12	1.81	0.63
2:2:1073:U:O2	36:g:103:ASN:ND2	2.31	0.63
41:l:113:ASP:OD2	41:l:122:ASN:ND2	2.32	0.63
2:2:1124:G:O2'	2:2:1127:G:O6	2.17	0.63
8:C:33:ARG:NH2	8:C:53:GLY:O	2.31	0.63
49:t:29:VAL:HG23	49:t:63:ARG:HG3	1.81	0.63
1:1:5:A:H2'	1:1:6:A:H8	1.64	0.62
2:2:844:G:O2'	52:w:12:ARG:NH2	2.32	0.62
8:C:24:VAL:HG12	8:C:178:VAL:HG21	1.79	0.62
9:D:168:ASP:OD1	58:D:301:HOH:O	2.16	0.62
22:S:55:ILE:O	22:S:59:GLU:HG2	1.99	0.62
41:l:138:ARG:NH2	41:l:139:GLU:OE2	2.32	0.62
18:O:43:ASN:ND2	58:O:202:HOH:O	2.33	0.62
36:g:167:ASP:OD1	36:g:168:HIS:N	2.32	0.62
47:r:65:VAL:HG22	47:r:66:GLU:H	1.64	0.62
1:1:1193:G:OP1	15:L:14:LYS:NZ	2.28	0.62
1:1:2107:G:O6	1:1:2182:U:O2	2.17	0.62
2:2:1496:C:H1'	2:2:1517:G:H22	1.65	0.62
9:D:176:ASP:OD1	9:D:179:SER:OG	2.16	0.62
2:2:337:G:H2'	2:2:338:A:H8	1.64	0.62
5:5:3:G:H3'	5:5:3:G:OP2	1.98	0.62
6:A:193:LEU:HG	6:A:197:LYS:HE2	1.79	0.62
53:x:36:ARG:NH2	53:x:75:ALA:O	2.33	0.62
2:2:1396:A:O2'	39:j:29:ARG:NH2	2.32	0.62
10:E:22:TYR:OH	10:E:165:GLU:OE1	2.17	0.62
16:M:103:TYR:HE2	16:M:124:LEU:HD11	1.64	0.62
1:1:2006:C:O2'	1:1:2823:A:N3	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2788:C:O2'	1:1:2809:A:N3	2.29	0.62
1:1:2831:G:OP2	8:C:59:ARG:NH2	2.32	0.62
2:2:12:U:H4'	2:2:526:C:H4'	1.82	0.62
3:3:9:G:O2'	18:O:45:SER:OG	2.18	0.62
10:E:38:MET:HB2	10:E:87:CYS:HB2	1.80	0.62
39:j:107:ALA:HB1	39:j:111:MET:HG2	1.82	0.62
1:1:535:G:N2	58:1:3350:HOH:O	2.33	0.62
2:2:841:C:H2'	2:2:843:U:H5'	1.80	0.62
10:E:72:LYS:NZ	58:E:201:HOH:O	2.30	0.62
29:Z:9:GLN:HB2	29:Z:29:LEU:HD23	1.82	0.62
40:k:29:ILE:HD11	40:k:66:ALA:HB2	1.81	0.62
1:1:529:A:OP2	13:J:116:ARG:NH2	2.30	0.62
1:1:559:G:N3	20:Q:56:GLN:NE2	2.48	0.62
1:1:2548:U:O2	14:K:23:LYS:NZ	2.32	0.62
1:1:2820:A:OP1	58:1:3302:HOH:O	2.16	0.62
2:2:451:A:OP2	50:u:70:ARG:NH2	2.31	0.62
2:2:642:A:N3	42:m:105:SER:OG	2.31	0.62
9:D:147:LEU:HB3	9:D:186:VAL:HG12	1.81	0.62
24:U:41:LEU:HD12	24:U:60:GLU:HG2	1.80	0.62
36:g:167:ASP:OD2	36:g:190:ASN:ND2	2.33	0.62
50:u:6:LEU:HG	50:u:17:TYR:HB3	1.82	0.62
1:1:882:G:O6	1:1:894:U:O4	2.18	0.62
2:2:689:C:OP1	45:p:29:ASN:ND2	2.33	0.62
17:N:49:GLU:HG2	17:N:94:TYR:HB2	1.82	0.62
18:O:30:ARG:HA	18:O:35:ILE:HG22	1.82	0.62
39:j:114:VAL:HG11	39:j:140:THR:HG21	1.80	0.62
53:x:50:ALA:HB1	53:x:57:HIS:HB3	1.80	0.62
1:1:2359:C:O2'	34:e:54:ASP:OD2	2.16	0.62
2:2:458:U:O4	2:2:474:G:O6	2.18	0.62
2:2:516:PSU:O2'	2:2:519:C:N4	2.29	0.62
2:2:1377:A:OP1	41:l:92:ARG:NH2	2.33	0.62
2:2:1522:U:H2'	2:2:1523:G:H8	1.63	0.62
10:E:111:ILE:HD13	10:E:137:ILE:HG21	1.82	0.62
1:1:489:G:N7	22:S:49:LYS:NZ	2.47	0.61
1:1:517:C:OP2	31:b:10:ARG:NH1	2.33	0.61
2:2:1127:G:H22	2:2:1147:C:H42	1.46	0.61
2:2:1317:C:H3'	2:2:1318:A:H8	1.65	0.61
30:a:13:THR:OG1	30:a:23:LYS:NZ	2.25	0.61
6:A:163:TYR:HB2	6:A:173:THR:HG22	1.81	0.61
9:D:106:LYS:HD3	9:D:200:LEU:HD13	1.82	0.61
1:1:250:G:OP2	34:e:13:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:981:A:OP2	1:1:982:C:N4	2.33	0.61
2:2:1005:A:N6	2:2:1024:G:O2'	2.30	0.61
2:2:1241:G:H2'	2:2:1242:G:H8	1.66	0.61
7:B:123:ALA:O	7:B:128:ASN:ND2	2.31	0.61
1:1:2372:U:H2'	1:1:2373:G:H8	1.65	0.61
2:2:1219:A:H2'	2:2:1220:G:H8	1.64	0.61
3:3:75:G:H2'	3:3:76:G:C8	2.35	0.61
7:B:71:LYS:O	7:B:118:SER:OG	2.18	0.61
10:E:29:PRO:HB3	10:E:160:ALA:HB2	1.82	0.61
11:F:90:VAL:O	11:F:160:LYS:HA	1.99	0.61
1:1:242:G:H5'	34:e:64:TYR:CE2	2.36	0.61
1:1:1629:U:O4	1:1:1630:A:N6	2.33	0.61
1:1:2420:C:OP2	34:e:33:LEU:N	2.33	0.61
2:2:385:C:N4	2:2:386:C:N4	2.47	0.61
2:2:714:G:H2'	2:2:715:A:C8	2.36	0.61
24:U:40:ASN:HD21	24:U:65:ILE:HB	1.65	0.61
37:h:72:ARG:HB3	37:h:75:ILE:HG22	1.81	0.61
51:v:76:VAL:HG23	51:v:77:ARG:HG2	1.82	0.61
9:D:149:ILE:HD11	9:D:175:ILE:HG12	1.83	0.61
33:d:34:ARG:NH2	33:d:41:ARG:O	2.25	0.61
47:r:79:ARG:NH2	53:x:65:GLU:OE2	2.33	0.61
52:w:30:LYS:HA	52:w:33:ILE:HG22	1.81	0.61
1:1:2467:C:OP1	35:f:8:LYS:NZ	2.33	0.61
2:2:662:U:O2'	2:2:836:G:OP1	2.18	0.61
2:2:1077:G:N2	2:2:1080:A:OP2	2.29	0.61
38:i:177:LYS:N	58:i:301:HOH:O	2.32	0.61
1:1:196:A:H61	1:1:831:G:H21	1.47	0.61
1:1:806:C:O2	1:1:2444:G:O2'	2.19	0.61
2:2:41:G:H2'	2:2:42:G:H8	1.64	0.61
38:i:27:ALA:HB3	38:i:30:THR:HG23	1.83	0.61
42:m:10:MET:HG3	42:m:27:MET:HE1	1.81	0.61
42:m:104:VAL:HG12	42:m:125:ILE:HA	1.82	0.61
1:1:75:G:H22	1:1:111:A:H2	1.48	0.61
36:g:119:THR:O	36:g:124:GLY:N	2.30	0.61
37:h:8:ASN:ND2	48:s:89:MET:O	2.31	0.61
37:h:20:SER:OG	37:h:40:ARG:NH2	2.34	0.61
19:P:31:TRP:NE1	19:P:82:ASP:OD2	2.34	0.60
1:1:482:A:OP1	58:1:3301:HOH:O	2.16	0.60
58:1:3330:HOH:O	23:T:26:LYS:NZ	2.34	0.60
2:2:352:C:O2	2:2:355:C:N4	2.34	0.60
2:2:490:C:H2'	2:2:491:G:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:946:A:H2'	2:2:947:G:H8	1.66	0.60
11:F:29:LYS:NZ	11:F:80:THR:O	2.34	0.60
1:1:881:G:H22	1:1:895:U:H3	1.49	0.60
1:1:2107:G:O6	1:1:2182:U:C2	2.54	0.60
2:2:380:G:N2	2:2:383:A:OP2	2.30	0.60
2:2:946:A:H2'	2:2:947:G:C8	2.36	0.60
40:k:35:LYS:NZ	58:k:202:HOH:O	2.35	0.60
44:o:8:ILE:HG22	44:o:100:ILE:HG22	1.82	0.60
1:1:686:U:O2	33:d:8:SER:OG	2.16	0.60
1:1:2818:U:OP2	17:N:42:LYS:NZ	2.33	0.60
2:2:401:C:O2'	2:2:621:A:N3	2.32	0.60
2:2:1143:G:H2'	2:2:1144:G:C8	2.37	0.60
2:2:1218:C:H2'	2:2:1219:A:H8	1.65	0.60
7:B:180:GLU:OE2	7:B:270:ARG:NH1	2.35	0.60
41:l:14:PRO:HB2	41:l:19:GLY:HA2	1.84	0.60
44:o:9:ARG:HH12	44:o:71:LEU:HD21	1.67	0.60
1:1:1009:A:O4'	20:Q:59:GLN:NE2	2.34	0.60
2:2:333:U:OP1	54:y:2:ALA:N	2.35	0.60
2:2:1060:U:H2'	2:2:1061:G:H8	1.64	0.60
2:2:1219:A:H2'	2:2:1220:G:C8	2.36	0.60
1:1:212:G:H2'	1:1:213:A:C8	2.37	0.60
1:1:1048:A:H1'	1:1:1112:G:H21	1.65	0.60
1:1:2079:U:O2'	27:X:23:ASN:OD1	2.19	0.60
2:2:28:A:O2'	2:2:296:U:OP1	2.19	0.60
2:2:921:U:O2	39:j:24:THR:OG1	2.19	0.60
2:2:1167:A:O2'	2:2:1169:A:N7	2.35	0.60
1:1:742:A:H2'	1:1:743:A:C8	2.37	0.60
1:1:1443:U:H2'	1:1:1444:G:H8	1.66	0.60
1:1:2111:U:H3	1:1:2145:C:HO2'	1.49	0.60
1:1:2596:U:O2'	7:B:241:GLY:O	2.19	0.60
2:2:375:U:H4'	50:u:6:LEU:HD23	1.83	0.60
1:1:1201:U:H2'	1:1:1202:G:H8	1.67	0.60
1:1:1266:G:OP1	31:b:16:ARG:NE	2.35	0.60
1:1:1447:C:H2'	1:1:1448:G:H8	1.65	0.60
1:1:2304:G:N2	1:1:2312:U:H3	2.00	0.60
43:n:88:MET:HE3	43:n:98:LEU:HD22	1.84	0.60
48:s:41:ARG:NH2	53:x:6:LYS:O	2.27	0.60
1:1:155:A:H2'	1:1:156:A:C8	2.35	0.59
1:1:581:C:H2'	1:1:582:A:C8	2.38	0.59
1:1:1724:G:O6	1:1:1737:G:N2	2.34	0.59
1:1:2684:U:OP2	19:P:51:ARG:NH1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:691:G:O6	45:p:53:ARG:NH1	2.35	0.59
2:2:1162:C:H2'	2:2:1163:A:H8	1.66	0.59
5:5:23:C:H2'	5:5:24:G:C8	2.37	0.59
22:S:73:LYS:HB2	22:S:106:VAL:HB	1.83	0.59
1:1:1039:A:N1	1:1:1116:G:C6	2.70	0.59
1:1:1386:C:H2'	1:1:1387:A:H8	1.67	0.59
2:2:460:A:H2'	2:2:461:A:H8	1.67	0.59
3:3:43:C:O2	10:E:92:ARG:NH1	2.35	0.59
17:N:24:MET:HE1	17:N:40:LYS:HB3	1.84	0.59
30:a:56:ARG:HH21	53:x:68:GLY:HA3	1.68	0.59
44:o:53:ILE:HD11	44:o:61:ALA:HB1	1.84	0.59
1:1:239:C:H2'	1:1:240:C:O4'	2.01	0.59
1:1:1009:A:H5'	20:Q:59:GLN:HG3	1.85	0.59
1:1:1788:C:OP1	7:B:221:ARG:NH2	2.35	0.59
1:1:1798:U:H5''	7:B:258:ARG:HB2	1.84	0.59
2:2:519:C:H5'	46:q:48:ALA:HA	1.84	0.59
2:2:740:U:H4'	49:t:39:LEU:HD21	1.83	0.59
21:R:12:HIS:N	58:R:202:HOH:O	2.36	0.59
1:1:1065:U:O2'	1:1:1066:U:O4'	2.20	0.59
1:1:1857:G:N2	1:1:1884:G:O2'	2.27	0.59
1:1:2126:A:O2'	1:1:2162:G:N2	2.34	0.59
1:1:2419:U:OP1	34:e:41:LYS:NZ	2.33	0.59
2:2:34:C:H2'	2:2:35:G:H8	1.68	0.59
2:2:160:A:H61	2:2:347:G:N2	1.99	0.59
52:w:10:PHE:N	58:w:101:HOH:O	2.35	0.59
1:1:494:G:N3	22:S:61:ASN:ND2	2.46	0.59
1:1:500:G:N1	1:1:503:A:OP2	2.31	0.59
1:1:781:A:OP1	7:B:217:ARG:NH2	2.34	0.59
1:1:1143:A:N7	58:J:201:HOH:O	2.31	0.59
1:1:2049:G:N2	8:C:161:MET:SD	2.75	0.59
2:2:979:C:O2	48:s:59:ARG:NE	2.36	0.59
34:e:31:HIS:O	34:e:32:ILE:C	2.45	0.59
37:h:10:ILE:HG23	37:h:11:ARG:HG3	1.85	0.59
1:1:807:U:OP2	15:L:41:ARG:NH2	2.35	0.59
2:2:1092:A:OP2	41:l:4:ARG:NH2	2.35	0.59
7:B:124:ILE:HD13	7:B:136:PRO:HD3	1.84	0.59
29:Z:16:ARG:O	29:Z:21:LYS:NZ	2.36	0.59
42:m:9:ASP:OD1	42:m:13:ARG:NH1	2.34	0.59
1:1:2092:U:OP2	12:G:27:ARG:NH1	2.34	0.59
1:1:2682:A:C8	8:C:11:MET:HE3	2.38	0.59
2:2:993:G:O2'	2:2:994:A:N7	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:17:C:H3'	5:5:17(A):U:H2'	1.84	0.59
16:M:66:ARG:NH1	16:M:104:GLU:OE2	2.33	0.59
2:2:619:U:H3	38:i:131:ASN:HB3	1.68	0.59
2:2:1157:A:N7	2:2:1180:A:N6	2.50	0.59
2:2:1451:U:OP2	2:2:1452:C:N4	2.36	0.59
10:E:122:PHE:O	10:E:124:GLY:N	2.36	0.59
30:a:17:SER:OG	47:r:54:ASP:OD1	2.19	0.59
33:d:34:ARG:NE	33:d:42:LEU:O	2.36	0.59
1:1:86:G:HO2'	1:1:104:A:HO2'	1.51	0.59
1:1:605:G:OP1	9:D:99:LYS:NZ	2.36	0.59
1:1:630:G:N2	1:1:633:A:OP2	2.31	0.59
1:1:1571:A:H2'	1:1:1572:A:H8	1.68	0.59
3:3:112:G:N2	18:O:45:SER:O	2.29	0.59
30:a:11:GLU:OE1	30:a:23:LYS:HD2	2.03	0.59
37:h:131:ARG:NH2	37:h:168:TYR:OH	2.34	0.59
1:1:917:A:H5''	1:1:2268:A:H61	1.67	0.59
1:1:2812:G:H2'	1:1:2813:A:H8	1.68	0.59
1:1:2845:U:O3'	19:P:53:ARG:NH1	2.36	0.59
2:2:21:G:H2'	2:2:22:G:C8	2.38	0.59
2:2:269:C:H2'	2:2:270:A:C8	2.38	0.59
2:2:677:U:O2	2:2:777:A:O2'	2.21	0.59
8:C:77:ARG:NH2	8:C:200:ASP:OD1	2.35	0.59
1:1:2193:G:O2'	1:1:2194:U:OP1	2.17	0.58
2:2:1253:G:H2'	2:2:1254:A:H8	1.68	0.58
2:2:1384:C:H2'	2:2:1385:G:H8	1.67	0.58
14:K:71:ARG:NH2	14:K:123:LEU:O	2.36	0.58
1:1:563:A:OP2	21:R:79:ARG:NH1	2.36	0.58
1:1:764:A:H5'	7:B:209:GLY:HA2	1.84	0.58
1:1:2475:C:H42	1:1:2529:G:N2	2.01	0.58
14:K:7:MET:HE2	14:K:7:MET:HA	1.85	0.58
45:p:14:LYS:NZ	45:p:15:GLN:O	2.36	0.58
1:1:832:U:H2'	1:1:833:A:H8	1.67	0.58
1:1:870:U:OP1	16:M:6:ARG:NH1	2.36	0.58
1:1:2081:U:H2'	1:1:2082:A:H8	1.69	0.58
1:1:2194:U:H2'	1:1:2195:U:H6	1.67	0.58
2:2:1148:U:H2'	2:2:1149:C:O4'	2.02	0.58
2:2:1513:A:H2'	2:2:1514:G:H8	1.67	0.58
5:5:20:U:H2'	5:5:21:A:H5'	1.83	0.58
9:D:97:ASN:HB2	9:D:100:MET:HG3	1.86	0.58
1:1:358:U:H2'	1:1:359:G:H8	1.68	0.58
1:1:1007:C:H5''	13:J:37:ARG:NH1	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1416:G:O2'	1:1:1417:C:O5'	2.21	0.58
1:1:1434:A:H2'	1:1:1435:G:C8	2.38	0.58
43:n:57:MET:HG2	43:n:60:LYS:HD2	1.85	0.58
46:q:46:ASN:ND2	46:q:89:OTD:SB	2.75	0.58
46:q:114:ARG:HB3	46:q:119:VAL:HB	1.84	0.58
53:x:3:ARG:NH1	53:x:8:GLY:O	2.36	0.58
53:x:31:LEU:HB2	53:x:49:ILE:HG22	1.86	0.58
1:1:1433:A:H2'	1:1:1434:A:H8	1.68	0.58
1:1:2139:U:O2	1:1:2152:G:O6	2.20	0.58
43:n:6:TYR:HB2	43:n:21:ILE:HB	1.84	0.58
1:1:99:U:O2	24:U:7:ARG:NH2	2.35	0.58
9:D:189:THR:H	9:D:192:ALA:HB3	1.69	0.58
45:p:119:ASN:ND2	58:p:201:HOH:O	2.35	0.58
1:1:1048:A:H1'	1:1:1112:G:N2	2.18	0.58
1:1:1386:C:H2'	1:1:1387:A:C8	2.39	0.58
1:1:1432:G:H2'	1:1:1433:A:C8	2.39	0.58
1:1:2045:C:H5''	31:b:15:MET:SD	2.44	0.58
2:2:385:C:C4	2:2:386:C:N4	2.72	0.58
5:5:18:G:N1	5:5:57:A:C6	2.70	0.58
13:J:125:TYR:OH	13:J:132:HIS:NE2	2.34	0.58
1:1:926:G:H2'	1:1:927:A:H8	1.68	0.58
1:1:2816:G:N3	1:1:2883:A:O2'	2.33	0.58
2:2:564:C:OP2	46:q:12:ARG:NH1	2.37	0.58
13:J:31:GLU:OE2	13:J:34:ARG:NH1	2.37	0.58
42:m:5:ASP:OD1	42:m:77:ARG:NH1	2.36	0.58
45:p:87:LYS:HB2	45:p:113:VAL:HG13	1.86	0.58
1:1:632:A:N3	1:1:2403:C:O2'	2.35	0.58
1:1:711:G:H1	1:1:720:U:H3	1.50	0.58
2:2:322:C:H2'	2:2:323:U:C6	2.38	0.58
2:2:438:U:H3	2:2:496:A:N6	2.02	0.58
2:2:727:G:N2	2:2:730:G:OP2	2.33	0.58
39:j:78:ASN:OD1	39:j:79:GLY:N	2.36	0.58
40:k:99:ALA:O	40:k:104:LYS:NZ	2.37	0.58
1:1:2475:C:H42	1:1:2529:G:H22	1.52	0.58
1:1:196:A:N6	1:1:831:G:H21	2.01	0.57
1:1:729:G:O2'	1:1:763:G:H4'	2.04	0.57
1:1:1654:A:N1	1:1:2048:G:O2'	2.36	0.57
2:2:619:U:H4'	38:i:128:ARG:HH22	1.69	0.57
3:3:27:C:OP1	18:O:34:HIS:NE2	2.33	0.57
3:3:37:C:O2	18:O:100:HIS:NE2	2.35	0.57
37:h:155:GLY:HA2	37:h:163:ALA:HB1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:47:VAL:HA	43:n:50:GLN:OE1	2.04	0.57
1:1:5:A:H2'	1:1:6:A:C8	2.39	0.57
1:1:582:A:H2'	1:1:583:G:H8	1.69	0.57
1:1:1858:A:H61	1:1:1884:G:H1'	1.70	0.57
9:D:6:LYS:HG3	9:D:119:ILE:HG23	1.84	0.57
13:J:96:ARG:HH12	13:J:99:ARG:HD3	1.69	0.57
16:M:42:THR:OG1	16:M:45:GLN:HG3	2.04	0.57
47:r:5:ALA:HB1	47:r:65:VAL:HG21	1.87	0.57
47:r:83:LEU:HD11	53:x:65:GLU:HG3	1.86	0.57
1:1:615:U:H3	9:D:176:ASP:HB3	1.70	0.57
37:h:132:ARG:NH2	58:h:303:HOH:O	2.37	0.57
1:1:863:A:H2'	1:1:864:G:H8	1.69	0.57
1:1:948:C:H2'	1:1:949:G:H8	1.69	0.57
1:1:1532:A:N7	58:1:3347:HOH:O	2.32	0.57
2:2:537:G:H5''	46:q:110:ARG:HH12	1.69	0.57
1:1:324:A:OP2	1:1:1205:A:N6	2.37	0.57
1:1:1024:G:HO2'	1:1:1144:A:HO2'	1.44	0.57
1:1:2229:U:H2'	1:1:2230:G:H8	1.70	0.57
2:2:390:U:H2'	2:2:391:G:C8	2.39	0.57
9:D:158:PHE:HA	9:D:169:VAL:HG21	1.85	0.57
10:E:63:GLN:NE2	10:E:90:THR:O	2.36	0.57
37:h:87:LEU:HA	37:h:90:VAL:HG22	1.86	0.57
45:p:20:VAL:HA	45:p:83:GLU:O	2.05	0.57
45:p:29:ASN:HB2	45:p:57:LYS:HE3	1.87	0.57
1:1:2591:C:H2'	1:1:2592:G:H8	1.69	0.57
1:1:2737:G:H2'	1:1:2738:A:C8	2.40	0.57
2:2:292:G:O2'	2:2:609:A:N6	2.37	0.57
3:3:60:C:H2'	3:3:61:G:H8	1.69	0.57
40:k:1:MET:SD	40:k:1:MET:N	2.74	0.57
48:s:90:ARG:NE	48:s:92:GLU:OE2	2.35	0.57
1:1:30:G:O2'	1:1:1214:A:N3	2.27	0.57
1:1:2039:U:H2'	1:1:2040:G:H8	1.69	0.57
1:1:2123:G:H5'	6:A:174:THR:HA	1.87	0.57
2:2:1384:C:H2'	2:2:1385:G:C8	2.39	0.57
5:5:28:C:O2'	47:r:117:LYS:NZ	2.31	0.57
44:o:26:VAL:HG11	44:o:39:PRO:HD3	1.86	0.57
53:x:52:HIS:CD2	53:x:54:GLY:H	2.22	0.57
1:1:793:A:OP2	1:1:2071:A:O2'	2.23	0.57
2:2:320:A:H2'	2:2:321:A:C8	2.40	0.57
2:2:1145:A:O2'	2:2:1146:A:H8	1.88	0.57
49:t:23:GLY:O	49:t:28:GLN:NE2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:498:G:H2'	1:1:499:U:O4'	2.05	0.57
1:1:2576:G:O2'	1:1:2579:C:OP2	2.23	0.57
2:2:206:C:N4	2:2:213:G:H1	2.03	0.57
2:2:713:G:H2'	2:2:714:G:C8	2.39	0.57
2:2:754:C:O5'	49:t:72:ARG:NH2	2.38	0.57
15:L:79:LEU:HD11	15:L:112:LEU:HD12	1.86	0.57
46:q:80:ILE:HG23	46:q:104:CYS:HB2	1.87	0.57
48:s:9:ARG:O	48:s:13:ARG:HG2	2.05	0.57
1:1:83:A:N7	1:1:101:A:N6	2.52	0.57
1:1:639:U:H2'	1:1:640:C:C6	2.40	0.57
1:1:1093:G:H21	1:1:1098:A:H62	1.51	0.57
1:1:1263:U:OP1	31:b:13:ARG:NH1	2.35	0.57
1:1:1288:G:OP1	1:1:1289:C:N4	2.35	0.57
1:1:1433:A:H2'	1:1:1434:A:C8	2.40	0.57
1:1:2328:A:H2'	1:1:2329:U:C6	2.39	0.57
2:2:459:A:H2'	2:2:460:A:H8	1.69	0.57
7:B:246:THR:HG23	7:B:248:TRP:H	1.69	0.57
1:1:1039:A:H2	1:1:1116:G:N1	1.99	0.56
1:1:1539:U:H2'	1:1:1540:G:H8	1.70	0.56
2:2:490:C:H2'	2:2:491:G:C8	2.40	0.56
2:2:1187:G:N3	48:s:100:SER:OG	2.32	0.56
7:B:130:LEU:HD13	7:B:134:ASN:HB2	1.86	0.56
10:E:11:GLU:OE1	10:E:14:LYS:NZ	2.33	0.56
18:O:64:TYR:HB3	18:O:67:ASN:HD22	1.70	0.56
42:m:96:MET:HG3	42:m:99:LEU:HB2	1.86	0.56
51:v:14:SER:HA	51:v:55:ILE:HG22	1.87	0.56
1:1:23:G:H2'	1:1:24:G:H8	1.70	0.56
1:1:464:U:O2	33:d:16:HIS:NE2	2.37	0.56
1:1:1364:G:OP1	27:X:3:ARG:NH1	2.38	0.56
1:1:1962:5MC:H4'	1:1:1963:U:OP1	2.06	0.56
1:1:2591:C:H2'	1:1:2592:G:C8	2.40	0.56
2:2:1412:C:H2'	2:2:1413:A:C8	2.40	0.56
5:5:67:G:C5'	58:5:206:HOH:O	2.38	0.56
1:1:371:A:N6	1:1:402:A:OP2	2.37	0.56
1:1:559:G:N2	20:Q:52:GLN:OE1	2.37	0.56
1:1:1202:G:H2'	1:1:1203:U:C6	2.41	0.56
1:1:1528:A:OP2	1:1:1543:G:N2	2.39	0.56
1:1:1666:G:O2'	14:K:6:THR:OG1	2.21	0.56
1:1:2291:U:O2'	1:1:2374:C:O2	2.22	0.56
1:1:2822:G:OP1	8:C:164:GLN:NE2	2.38	0.56
2:2:738:C:OP1	40:k:4:TYR:OH	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1094:G:N2	58:2:1825:HOH:O	2.36	0.56
2:2:1236:A:H4'	2:2:1304:G:H4'	1.87	0.56
7:B:162:VAL:HG12	7:B:176:LEU:HA	1.87	0.56
9:D:157:LEU:HG	9:D:169:VAL:HG11	1.87	0.56
23:T:38:ALA:O	23:T:81:LYS:NZ	2.31	0.56
32:c:40:ASP:OD1	32:c:49:TYR:OH	2.23	0.56
34:e:31:HIS:CG	34:e:32:ILE:H	2.23	0.56
1:1:160:A:N3	1:1:2208:C:O2'	2.35	0.56
2:2:970:C:N4	43:n:130:ARG:OXT	2.38	0.56
5:5:8:U:O2'	5:5:21:A:N1	2.34	0.56
8:C:25:THR:HG21	8:C:193:VAL:HG22	1.88	0.56
9:D:21:ARG:HE	9:D:106:LYS:HB2	1.70	0.56
12:G:51:ARG:NH2	12:G:55:GLU:OE2	2.39	0.56
22:S:95:ARG:NH2	58:S:201:HOH:O	2.37	0.56
26:W:41:ARG:O	26:W:57:HIS:ND1	2.36	0.56
39:j:115:LEU:HD13	39:j:123:VAL:HG11	1.87	0.56
46:q:80:ILE:HD12	46:q:104:CYS:HB2	1.86	0.56
1:1:1202:G:OP2	1:1:1204:A:O2'	2.23	0.56
1:1:1495:A:N3	1:1:1578:U:O2'	2.36	0.56
1:1:1954:G:O2'	1:1:1956:U:O4	2.21	0.56
2:2:673:A:H4'	40:k:86:ARG:NH1	2.21	0.56
16:M:56:ALA:HB2	16:M:119:LEU:HD12	1.87	0.56
46:q:50:ARG:NE	46:q:89:0TD:OD1	2.35	0.56
51:v:59:VAL:HG12	51:v:78:VAL:HG12	1.86	0.56
1:1:659:G:N2	9:D:30:GLN:OE1	2.39	0.56
1:1:2680:U:O2'	8:C:11:MET:HE1	2.05	0.56
5:5:2:G:H4'	5:5:3:G:OP1	2.05	0.56
5:5:59:A:O2'	5:5:60:U:OP1	2.23	0.56
38:i:11:LEU:HD13	38:i:63:ARG:HG2	1.86	0.56
44:o:80:THR:HG1	44:o:83:THR:HG1	1.52	0.56
45:p:54:GLY:H	45:p:57:LYS:HD3	1.71	0.56
1:1:370:G:O2'	1:1:424:G:OP1	2.23	0.56
1:1:1469:A:H2'	1:1:1470:A:H8	1.70	0.56
1:1:2037:A:H2'	1:1:2038:G:C8	2.40	0.56
1:1:2127:G:H21	1:1:2173:A:H1'	1.70	0.56
2:2:1342:C:H2'	2:2:1343:G:H8	1.71	0.56
5:5:18:G:C6	5:5:57:A:N6	2.74	0.56
1:1:1681:G:H21	1:1:1762:A:H3'	1.69	0.56
1:1:2311:A:N6	58:1:3385:HOH:O	2.39	0.56
1:1:2349:G:OP1	34:e:45:ARG:NH2	2.39	0.56
10:E:32:GLU:OE2	10:E:159:THR:OG1	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:6:LYS:HG2	22:S:104:THR:HG23	1.87	0.56
45:p:64:GLN:HB2	45:p:99:ALA:HB2	1.86	0.56
1:1:552:U:H2'	1:1:553:G:H8	1.71	0.56
1:1:1131:G:HO2'	1:1:2025:C:HO2'	1.43	0.56
1:1:2037:A:H2'	1:1:2038:G:H8	1.71	0.56
37:h:129:MET:HB2	37:h:132:ARG:HD2	1.87	0.56
1:1:2039:U:H2'	1:1:2040:G:C8	2.41	0.56
2:2:910:C:OP2	46:q:18:LYS:NZ	2.31	0.55
19:P:29:LYS:HB3	19:P:40:LEU:HD12	1.87	0.55
37:h:123:GLN:OE1	37:h:126:ARG:NH1	2.39	0.55
1:1:742:A:H2'	1:1:743:A:H8	1.71	0.55
1:1:887:A:OP1	47:r:92:ARG:NH2	2.38	0.55
1:1:2285:C:OP2	32:c:6:ARG:NE	2.27	0.55
2:2:1375:A:H5''	41:l:25:LYS:HD2	1.87	0.55
10:E:111:ILE:HB	10:E:114:PHE:HB2	1.88	0.55
44:o:11:LYS:HG3	44:o:97:ASP:HB3	1.88	0.55
1:1:782:A:N7	7:B:220:VAL:HG21	2.22	0.55
2:2:1041:G:H2'	2:2:1042:A:C8	2.42	0.55
2:2:1250:A:N3	2:2:1370:G:O2'	2.36	0.55
1:1:358:U:H2'	1:1:359:G:C8	2.41	0.55
1:1:851:C:H2'	1:1:852:U:C6	2.41	0.55
3:3:114:C:H2'	3:3:115:A:H8	1.72	0.55
5:5:4:C:O2'	5:5:5:A:OP2	2.24	0.55
13:J:17:VAL:HG13	13:J:137:PRO:HB2	1.88	0.55
15:L:75:ALA:HB2	15:L:105:ILE:HD12	1.88	0.55
1:1:446:G:H5''	20:Q:5:LYS:HE3	1.88	0.55
1:1:629:G:H1'	1:1:639:U:H1'	1.87	0.55
2:2:17:U:H2'	2:2:18:C:C6	2.42	0.55
2:2:660:C:N3	2:2:746:A:N6	2.54	0.55
2:2:1145:A:H2	2:2:1146:A:H62	1.53	0.55
7:B:72:ASP:OD2	7:B:189:ARG:NH2	2.30	0.55
1:1:2286:G:OP2	32:c:6:ARG:NH2	2.39	0.55
2:2:1218:C:H2'	2:2:1219:A:C8	2.42	0.55
22:S:19:LEU:HB3	31:b:22:LEU:HD13	1.89	0.55
41:l:79:ARG:NH1	41:l:81:GLY:O	2.40	0.55
42:m:52:GLU:N	42:m:52:GLU:OE2	2.40	0.55
50:u:21:VAL:HG21	50:u:60:TRP:CD1	2.41	0.55
1:1:1798:U:OP2	7:B:271:ARG:NH1	2.31	0.55
36:g:173:ILE:HG22	36:g:183:VAL:HG11	1.89	0.55
53:x:39:THR:HG22	53:x:70:LYS:HG2	1.89	0.55
1:1:112:U:H5'	28:Y:58:ASN:ND2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:307:G:N1	1:1:310:A:OP2	2.26	0.55
1:1:668:A:H2'	1:1:670:A:H62	1.72	0.55
1:1:721:A:H2'	1:1:722:A:H8	1.72	0.55
1:1:843:G:H2'	1:1:844:A:C8	2.42	0.55
1:1:992:C:OP1	20:Q:47:TYR:OH	2.25	0.55
1:1:1447:C:H2'	1:1:1448:G:C8	2.41	0.55
7:B:67:PHE:HB3	7:B:152:GLY:H	1.71	0.55
10:E:16:LEU:HD23	10:E:29:PRO:HD2	1.89	0.55
39:j:13:GLU:HG2	39:j:39:VAL:HG12	1.89	0.55
45:p:81:ASN:OD1	45:p:106:ARG:NE	2.39	0.55
1:1:372:G:H5''	27:X:61:LYS:HD2	1.89	0.55
1:1:2036:C:H2'	1:1:2037:A:H8	1.71	0.55
1:1:2446:G:N2	1:1:2449:U:O2	2.38	0.55
2:2:459:A:H2'	2:2:460:A:C8	2.42	0.55
2:2:460:A:H2'	2:2:461:A:C8	2.42	0.55
2:2:923:A:O2'	2:2:1399:C:OP2	2.21	0.55
5:5:1:C:O2	5:5:72:G:N1	2.39	0.55
48:s:10:GLU:HG3	48:s:63:ARG:HD2	1.89	0.55
1:1:1065:U:O2'	1:1:1066:U:O5'	2.25	0.55
1:1:2127:G:HO2'	1:1:2128:G:H8	1.54	0.55
1:1:2255:G:O2'	5:5:3:G:OP1	2.25	0.55
2:2:21:G:H2'	2:2:22:G:H8	1.72	0.55
2:2:143:A:H2	2:2:220:G:H1	1.55	0.55
2:2:739:C:O2'	49:t:42:HIS:ND1	2.37	0.55
11:F:96:ALA:HB3	11:F:131:ILE:HD11	1.89	0.55
18:O:61:GLN:OE1	18:O:61:GLN:N	2.40	0.55
35:f:25:VAL:HG12	35:f:35:GLN:HB2	1.89	0.55
41:l:75:VAL:HG11	41:l:148:ASN:HD21	1.72	0.55
2:2:398:U:H2'	2:2:399:G:H8	1.71	0.54
5:5:62:C:H2'	5:5:63:U:C6	2.42	0.54
13:J:32:LEU:HD22	13:J:54:ILE:HG21	1.90	0.54
16:M:53:MET:HE3	16:M:117:PHE:HE1	1.71	0.54
43:n:34:SER:HB3	43:n:37:GLN:OE1	2.06	0.54
51:v:46:VAL:HG21	51:v:61:ILE:HG21	1.89	0.54
1:1:55:G:H2'	1:1:56:A:H8	1.71	0.54
2:2:356:A:N3	2:2:368:U:O2'	2.32	0.54
2:2:859:G:N2	58:2:1835:HOH:O	2.39	0.54
2:2:1513:A:H2'	2:2:1514:G:C8	2.42	0.54
44:o:52:LEU:HD21	44:o:62:ARG:HH21	1.72	0.54
1:1:1752:C:H2'	1:1:1753:G:C8	2.43	0.54
1:1:2562:U:H4'	14:K:25:LEU:HD22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:514:C:H2'	2:2:515:G:C8	2.42	0.54
2:2:1439:G:OP2	54:y:33:LYS:NZ	2.35	0.54
36:g:218:ALA:O	36:g:222:ARG:HG2	2.08	0.54
1:1:99:U:H5''	1:1:100:U:H5'	1.89	0.54
1:1:574:A:N6	1:1:2034:U:OP1	2.41	0.54
2:2:337:G:H2'	2:2:338:A:C8	2.41	0.54
3:3:51:G:H2'	3:3:52:A:C8	2.42	0.54
18:O:60:GLU:HG2	18:O:61:GLN:OE1	2.08	0.54
24:U:25:VAL:HA	24:U:36:VAL:HA	1.88	0.54
24:U:40:ASN:ND2	24:U:65:ILE:HB	2.21	0.54
28:Y:14:LEU:HB3	28:Y:57:LEU:HD21	1.90	0.54
1:1:826:U:O2	1:1:831:G:O6	2.25	0.54
1:1:2241:A:H2'	1:1:2242:G:C8	2.42	0.54
13:J:37:ARG:HA	13:J:118:MET:CE	2.37	0.54
21:R:25:LEU:HG	21:R:94:THR:HG21	1.90	0.54
43:n:10:GLY:HA3	43:n:82:GLY:N	2.23	0.54
1:1:946:C:H2'	1:1:947:A:H8	1.72	0.54
2:2:842:U:H4'	2:2:846:G:C6	2.42	0.54
36:g:102:THR:HA	36:g:179:LEU:HD11	1.90	0.54
41:l:35:LYS:HB3	41:l:38:THR:HG22	1.90	0.54
1:1:258:G:H2'	1:1:259:G:C8	2.43	0.54
1:1:629:G:N3	1:1:639:U:O2'	2.40	0.54
1:1:2096:C:H2'	1:1:2097:A:C8	2.42	0.54
1:1:2140:G:O6	1:1:2151:U:O4	2.26	0.54
2:2:1071:C:H2'	2:2:1072:G:H8	1.72	0.54
41:l:71:PRO:HG3	41:l:99:LEU:HD11	1.90	0.54
1:1:2123:G:N2	6:A:215:SER:OG	2.41	0.54
1:1:2162:G:O2'	1:1:2163:A:N7	2.39	0.54
1:1:2743:U:HO2'	11:F:153:ARG:HH22	1.55	0.54
2:2:1151:A:HO2'	2:2:1152:A:H8	1.55	0.54
2:2:1171:A:H2'	2:2:1172:C:H6	1.73	0.54
5:5:53:G:H2'	5:5:54:U:C5	2.42	0.54
7:B:78:VAL:HG21	7:B:110:LEU:HD11	1.88	0.54
12:G:86:ASP:OD2	40:k:24:ARG:NH1	2.41	0.54
25:V:72:VAL:HG11	25:V:91:PHE:HB3	1.90	0.54
1:1:285:G:O6	1:1:355:U:O2	2.25	0.54
1:1:1063:G:N2	58:1:3369:HOH:O	2.36	0.54
1:1:1141:U:OP1	13:J:27:ARG:NH2	2.40	0.54
1:1:1224:U:OP2	21:R:68:ARG:NH2	2.41	0.54
2:2:895:G:H2'	2:2:896:C:C6	2.43	0.54
7:B:108:LYS:HA	7:B:196:GLY:HA2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:5:PHE:N	58:R:202:HOH:O	2.41	0.54
44:o:10:LEU:HB3	44:o:18:ILE:HD11	1.90	0.54
51:v:17:MET:HE2	51:v:20:SER:HB3	1.89	0.54
53:x:40:ILE:HG12	53:x:71:LEU:HD23	1.90	0.54
1:1:1085:A:N7	1:1:1086:A:N6	2.56	0.54
1:1:2898:U:O3'	13:J:136:GLN:NE2	2.41	0.54
2:2:8:A:N6	38:i:202:GLU:O	2.40	0.54
2:2:1074:G:OP1	39:j:69:ARG:NH2	2.40	0.54
2:2:1209:C:O2'	2:2:1214:C:N4	2.41	0.54
5:5:55:U:O2'	5:5:56:C:H3'	2.08	0.54
8:C:136:ASN:ND2	8:C:139:SER:O	2.41	0.54
9:D:102:ARG:O	9:D:106:LYS:HG2	2.08	0.54
9:D:117:ARG:NH1	9:D:184:ASP:O	2.41	0.54
9:D:146:VAL:H	9:D:167:VAL:HG12	1.72	0.54
12:G:14:SER:N	12:G:17:ASP:OD2	2.41	0.54
13:J:45:THR:HB	13:J:48:VAL:HB	1.89	0.54
21:R:1:MET:HA	21:R:42:ALA:O	2.08	0.54
38:i:13:ARG:HG2	38:i:34:ILE:HA	1.88	0.54
1:1:408:G:H2'	1:1:409:G:H8	1.73	0.53
1:1:565:C:P	21:R:80:ARG:H	2.30	0.53
1:1:797:G:OP1	9:D:55:SER:OG	2.22	0.53
1:1:947:A:H2'	1:1:948:C:C6	2.44	0.53
1:1:1278:C:O2'	17:N:27:SER:OG	2.24	0.53
1:1:1421:G:H2'	1:1:1422:G:H8	1.73	0.53
1:1:2095:A:H5'	12:G:11:ASN:HD22	1.72	0.53
2:2:521:G:O2'	2:2:536:C:O2'	2.25	0.53
2:2:662:U:H2'	2:2:663:A:C8	2.43	0.53
14:K:17:ARG:NH1	58:K:201:HOH:O	2.40	0.53
1:1:863:A:H2'	1:1:864:G:C8	2.42	0.53
1:1:2074:U:H2'	1:1:2075:U:C6	2.43	0.53
1:1:2292:U:H2'	1:1:2293:G:H8	1.74	0.53
2:2:81:A:N6	2:2:88:U:O4	2.41	0.53
2:2:501:C:H2'	2:2:502:A:H8	1.74	0.53
2:2:1515:G:H2'	2:2:1516:2MG:C8	2.43	0.53
12:G:9:VAL:HG11	12:G:12:LEU:HB3	1.90	0.53
24:U:86:ARG:NH2	24:U:88:GLU:OE2	2.36	0.53
37:h:19:ASN:HB3	37:h:40:ARG:HH22	1.73	0.53
44:o:50:THR:HB	44:o:62:ARG:HD3	1.90	0.53
44:o:78:GLU:OE1	44:o:78:GLU:N	2.41	0.53
1:1:145:C:H2'	1:1:146:A:H8	1.73	0.53
1:1:136:G:O6	1:1:144:A:N6	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:414:C:H2'	1:1:415:A:C8	2.43	0.53
1:1:451:U:H4'	9:D:47:LYS:HE3	1.90	0.53
1:1:1197:G:H22	1:1:1249:U:H1'	1.73	0.53
1:1:1576:U:H2'	1:1:1577:C:C6	2.43	0.53
1:1:2487:G:H2'	1:1:2488:G:H8	1.73	0.53
1:1:2626:C:H2'	1:1:2627:G:H8	1.74	0.53
2:2:1342:C:H2'	2:2:1343:G:C8	2.44	0.53
1:1:741:U:H2'	1:1:742:A:C8	2.44	0.53
1:1:1710:G:H2'	1:1:1711:A:C8	2.44	0.53
3:3:83:G:O6	3:3:94:A:N6	2.42	0.53
11:F:23:VAL:HA	11:F:36:THR:HA	1.89	0.53
15:L:28:GLY:HA3	21:R:82:HIS:NE2	2.24	0.53
26:W:47:ALA:HB1	26:W:51:VAL:HG13	1.91	0.53
42:m:75:ILE:CD1	42:m:129:VAL:HG22	2.38	0.53
1:1:858:G:H3'	1:1:859:G:C8	2.44	0.53
1:1:2102:G:H1	1:1:2187:U:H3	1.51	0.53
2:2:1176:A:H2'	2:2:1177:G:H8	1.74	0.53
2:2:1287:A:H2'	2:2:1288:A:C8	2.44	0.53
5:5:53:G:H2'	5:5:54:U:H5	1.74	0.53
14:K:121:GLU:OE1	19:P:65:SER:OG	2.21	0.53
22:S:18:ARG:HG3	22:S:76:VAL:HB	1.91	0.53
37:h:135:LYS:NZ	37:h:139:GLN:HE22	2.07	0.53
1:1:230:G:H2'	1:1:231:A:H8	1.74	0.53
1:1:582:A:H2'	1:1:583:G:C8	2.43	0.53
1:1:1995:U:O2	14:K:3:GLN:NE2	2.37	0.53
1:1:2636:C:O2'	8:C:45:TYR:OH	2.27	0.53
2:2:977:A:OP1	48:s:61:ARG:NH1	2.42	0.53
2:2:1041:G:H2'	2:2:1042:A:H8	1.73	0.53
37:h:135:LYS:NZ	58:h:301:HOH:O	2.24	0.53
1:1:627:A:H5''	15:L:78:ARG:HH21	1.74	0.53
1:1:1746:A:H2'	1:1:1747:U:C6	2.44	0.53
1:1:2113:U:N3	1:1:2114:A:N7	2.56	0.53
2:2:113:G:H2'	2:2:114:U:C6	2.44	0.53
2:2:674:G:H2'	2:2:675:A:C8	2.42	0.53
2:2:1179:A:H2'	2:2:1180:A:C8	2.44	0.53
2:2:1253:G:H2'	2:2:1254:A:C8	2.43	0.53
2:2:1314:C:H2'	2:2:1315:U:H6	1.73	0.53
5:5:62:C:H2'	5:5:63:U:H6	1.74	0.53
24:U:34:VAL:HG13	24:U:67:VAL:HG22	1.91	0.53
43:n:15:SER:OG	43:n:69:GLY:O	2.24	0.53
1:1:1962:5MC:O2'	1:1:1963:U:O5'	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2113:U:O4	1:1:2114:A:N6	2.41	0.53
2:2:1320:C:H1'	53:x:73:GLU:HG2	1.91	0.53
18:O:33:ARG:O	18:O:65:THR:OG1	2.21	0.53
26:W:75:LYS:HE2	26:W:77:ARG:HH22	1.74	0.53
38:i:85:ASN:HB3	38:i:88:GLU:HB2	1.91	0.53
1:1:1548:A:H2'	1:1:1549:A:C8	2.43	0.53
1:1:2261:C:OP1	26:W:19:LYS:NZ	2.35	0.53
1:1:2286:G:H4'	1:1:2287:A:O5'	2.08	0.53
2:2:390:U:H2'	2:2:391:G:H8	1.74	0.53
2:2:1029:U:H2'	2:2:1031:C:H1'	1.91	0.53
2:2:1321:U:H3'	2:2:1322:C:H2'	1.89	0.53
2:2:1518:MA6:O5'	2:2:1518:MA6:H8	2.07	0.53
39:j:148:ASN:ND2	42:m:73:GLU:OE1	2.37	0.53
41:l:97:ASN:O	41:l:101:MET:HE2	2.09	0.53
1:1:135:U:H2'	1:1:136:G:C8	2.44	0.52
1:1:2357:G:N2	1:1:2360:G:OP2	2.33	0.52
1:1:2547:A:H2'	1:1:2548:U:C6	2.43	0.52
2:2:821:G:H2'	2:2:822:U:C6	2.43	0.52
13:J:56:VAL:HB	13:J:124:VAL:HG23	1.90	0.52
44:o:77:VAL:HG23	44:o:78:GLU:OE1	2.10	0.52
49:t:80:GLN:HE22	49:t:84:ARG:HE	1.57	0.52
1:1:483:A:N6	1:1:496:G:H22	2.06	0.52
1:1:545:U:HO2'	1:1:548:G:H1	1.57	0.52
1:1:946:C:H2'	1:1:947:A:C8	2.44	0.52
1:1:1000:A:H2'	1:1:1001:A:C8	2.43	0.52
1:1:1278:C:H2'	1:1:1279:G:H8	1.74	0.52
1:1:1424:G:H2'	1:1:1425:G:C8	2.44	0.52
1:1:1443:U:H2'	1:1:1444:G:C8	2.44	0.52
1:1:2698:U:H2'	1:1:2699:C:C6	2.45	0.52
2:2:1009:U:H2'	2:2:1020:G:H22	1.75	0.52
25:V:6:ALA:HB1	25:V:40:ILE:HB	1.91	0.52
47:r:9:ILE:HD11	47:r:22:ILE:HD11	1.92	0.52
1:1:48:G:N2	1:1:177:G:OP2	2.42	0.52
1:1:151:C:H2'	1:1:152:A:H8	1.74	0.52
1:1:1152:C:H2'	1:1:1153:C:H6	1.74	0.52
2:2:790:A:OP1	5:5:38:U:O2'	2.16	0.52
2:2:1130:A:H62	2:2:1144:G:H21	1.55	0.52
3:3:54:G:H2'	3:3:55:U:C6	2.44	0.52
20:Q:58:ARG:O	20:Q:62:ILE:HG12	2.09	0.52
43:n:28:ILE:HB	43:n:35:LEU:HD22	1.91	0.52
1:1:308:G:H1'	1:1:501:A:OP1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:550:C:N4	1:1:551:G:O6	2.43	0.52
1:1:1068:G:N2	1:1:1095:A:O3'	2.43	0.52
1:1:1306:C:H2'	1:1:1307:A:H8	1.73	0.52
1:1:2047:C:H2'	1:1:2048:G:H8	1.74	0.52
2:2:385:C:N4	2:2:386:C:H41	2.07	0.52
12:G:30:LEU:HB3	12:G:36:ALA:HB3	1.91	0.52
29:Z:16:ARG:HG3	29:Z:54:MET:HE1	1.91	0.52
43:n:19:VAL:HG22	43:n:65:ILE:HG23	1.89	0.52
1:1:408:G:H2'	1:1:409:G:C8	2.45	0.52
1:1:523:C:H2'	1:1:524:G:C8	2.45	0.52
1:1:727:A:OP2	1:1:1431:A:O2'	2.26	0.52
1:1:1702:G:N2	2:2:1428:A:O2'	2.42	0.52
2:2:21:G:H1'	2:2:915:A:H61	1.74	0.52
2:2:545:C:H5'	38:i:69:GLU:HB2	1.91	0.52
2:2:773:G:O6	2:2:807:A:N6	2.43	0.52
8:C:29:VAL:HG21	8:C:187:LEU:HD12	1.92	0.52
31:b:29:SER:HB3	31:b:40:ARG:HD3	1.91	0.52
45:p:34:ILE:HG13	45:p:74:VAL:HG11	1.90	0.52
1:1:228:C:N4	1:1:2407:A:N3	2.57	0.52
2:2:41:G:H2'	2:2:42:G:C8	2.43	0.52
5:5:10:G:C2	5:5:26:A:H1'	2.45	0.52
10:E:73:SER:HB2	10:E:81:GLN:H	1.74	0.52
40:k:47:LEU:HD23	40:k:51:ILE:HD13	1.92	0.52
51:v:80:GLU:OE2	51:v:80:GLU:N	2.42	0.52
54:y:5:LYS:O	54:y:9:LYS:HG2	2.09	0.52
1:1:878:A:N6	58:1:3403:HOH:O	2.43	0.52
1:1:1264:A:OP1	31:b:16:ARG:NH2	2.28	0.52
1:1:1278:C:H2'	1:1:1279:G:C8	2.44	0.52
1:1:2639:A:O3'	13:J:96:ARG:NH2	2.43	0.52
1:1:2720:U:C2	1:1:2721:A:C8	2.98	0.52
2:2:895:G:H2'	2:2:896:C:H6	1.74	0.52
2:2:932:C:H5''	41:l:4:ARG:HD3	1.91	0.52
2:2:1330:U:H4'	47:r:23:TYR:CZ	2.44	0.52
11:F:130:GLU:OE2	58:F:201:HOH:O	2.19	0.52
15:L:85:VAL:HG21	15:L:90:VAL:HG12	1.91	0.52
22:S:51:LEU:O	22:S:55:ILE:HG12	2.10	0.52
23:T:69:ARG:HG2	23:T:74:ILE:HD12	1.91	0.52
1:1:1869:G:N2	1:1:1871:A:O2'	2.43	0.52
1:1:1924:C:H2'	1:1:1925:C:C6	2.45	0.52
1:1:2571:U:O2'	8:C:151:THR:O	2.27	0.52
1:1:2642:G:H2'	1:1:2643:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:229:U:H5''	50:u:33:ILE:HD13	1.92	0.52
2:2:876:C:H1'	42:m:12:THR:HG21	1.92	0.52
10:E:140:GLU:OE1	30:a:26:SER:OG	2.26	0.52
38:i:15:GLU:OE2	38:i:56:ARG:NH2	2.35	0.52
38:i:159:LEU:HD13	38:i:175:ALA:HB1	1.91	0.52
1:1:675:A:N3	1:1:2443:C:O2'	2.40	0.52
1:1:995:C:O2	13:J:3:THR:OG1	2.22	0.52
1:1:2291:U:H2'	1:1:2292:U:C6	2.45	0.52
2:2:160:A:H61	2:2:347:G:H21	1.56	0.52
2:2:363:A:H5'	46:q:81:LEU:HD11	1.92	0.52
3:3:93:C:OP2	25:V:18:ARG:NH1	2.41	0.52
5:5:23:C:H2'	5:5:24:G:H8	1.75	0.52
23:T:47:VAL:HG23	23:T:51:PHE:HD2	1.75	0.52
41:l:26:PHE:HD1	41:l:101:MET:HB3	1.73	0.52
1:1:523:C:H2'	1:1:524:G:H8	1.75	0.52
1:1:1044:C:O2'	1:1:1111:A:N1	2.42	0.52
1:1:2046:G:H5'	31:b:16:ARG:HG3	1.90	0.52
1:1:2074:U:H2'	1:1:2075:U:H6	1.75	0.52
2:2:736:C:H2'	2:2:737:C:H6	1.73	0.52
2:2:1083:U:O2'	2:2:1102:A:OP2	2.27	0.52
2:2:1486:G:H2'	2:2:1487:G:O4'	2.10	0.52
17:N:29:VAL:HG21	17:N:75:ILE:HG23	1.92	0.52
39:j:61:GLN:O	39:j:65:GLU:HG2	2.10	0.52
1:1:1:G:H2'	1:1:2:G:H8	1.75	0.51
1:1:191:A:H2'	1:1:192:C:H6	1.75	0.51
1:1:796:C:H2'	1:1:797:G:C8	2.45	0.51
1:1:1387:A:H2'	1:1:1388:G:H8	1.74	0.51
1:1:1713:A:N6	1:1:1746:A:N1	2.58	0.51
2:2:126:G:OP1	2:2:605:U:O2'	2.24	0.51
38:i:101:VAL:HG21	38:i:137:VAL:HG11	1.91	0.51
41:l:57:SER:HB3	41:l:60:GLU:HG2	1.92	0.51
1:1:468:G:H5''	9:D:55:SER:HB2	1.93	0.51
1:1:641:U:O4	1:1:647:G:O6	2.27	0.51
1:1:713:G:OP2	49:t:89:ARG:NH2	2.42	0.51
1:1:2013:A:N6	1:1:2014:A:N1	2.57	0.51
1:1:2328:A:H2'	1:1:2329:U:H6	1.76	0.51
1:1:2625:G:OP2	58:1:3303:HOH:O	2.19	0.51
2:2:363:A:OP1	46:q:31:ARG:N	2.30	0.51
2:2:1012:A:N6	2:2:1018:G:O6	2.43	0.51
2:2:1151:A:O2'	2:2:1152:A:H8	1.92	0.51
7:B:155:ALA:HB2	7:B:162:VAL:HG13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:104:ASN:ND2	11:F:114:ASP:OD1	2.42	0.51
39:j:16:ILE:HG21	39:j:110:ALA:HB2	1.92	0.51
1:1:30:G:H2'	1:1:31:C:H6	1.74	0.51
1:1:261:G:H2'	1:1:262:A:H8	1.76	0.51
1:1:1478:G:H1	1:1:1513:U:H3	1.59	0.51
1:1:2055:C:H5'	1:1:2056:G:H5''	1.91	0.51
2:2:811:C:O2'	2:2:901:A:N1	2.43	0.51
10:E:8:TYR:HB2	10:E:173:PHE:HZ	1.75	0.51
37:h:53:SER:OG	37:h:112:ASP:OD2	2.17	0.51
38:i:15:GLU:OE2	38:i:63:ARG:NH1	2.44	0.51
39:j:62:LYS:O	39:j:66:LYS:HG2	2.09	0.51
1:1:395:U:O2'	1:1:396:G:N7	2.29	0.51
1:1:2834:G:H2'	1:1:2879:A:H61	1.75	0.51
2:2:269:C:H2'	2:2:270:A:H8	1.74	0.51
47:r:64:VAL:HG13	47:r:68:ASP:HB2	1.92	0.51
1:1:1494:A:H2'	1:1:1495:A:C8	2.46	0.51
1:1:1738:G:HO2'	1:1:1739:A:H8	1.58	0.51
1:1:2743:U:O2'	11:F:153:ARG:NH2	2.31	0.51
2:2:22:G:H2'	2:2:23:C:H6	1.76	0.51
2:2:1317:C:H3'	2:2:1318:A:C8	2.45	0.51
7:B:246:THR:HG22	7:B:250:VAL:H	1.75	0.51
17:N:24:MET:HE2	17:N:44:LEU:HD22	1.93	0.51
20:Q:51:ARG:O	20:Q:55:ARG:HG3	2.11	0.51
36:g:167:ASP:HB3	36:g:191:SER:HA	1.93	0.51
43:n:113:ARG:HE	48:s:101:TRP:CD1	2.29	0.51
1:1:226:A:H1'	1:1:230:G:N2	2.25	0.51
2:2:255:G:H4'	51:v:19:LYS:HD3	1.92	0.51
2:2:1350:A:H2'	2:2:1351:U:O4'	2.10	0.51
12:G:26:ALA:HA	12:G:30:LEU:HD12	1.92	0.51
16:M:40:ARG:HB2	16:M:93:VAL:HG21	1.91	0.51
36:g:6:MET:HE1	36:g:47:VAL:HG21	1.93	0.51
40:k:10:VAL:HB	40:k:58:HIS:HB3	1.92	0.51
42:m:26:THR:HG23	42:m:58:GLU:OE2	2.10	0.51
1:1:2013:A:H2	22:S:88:ARG:HH22	1.57	0.51
1:1:2170:A:H1'	1:1:2171:A:O4'	2.11	0.51
1:1:2692:G:H1'	1:1:2847:U:H1'	1.93	0.51
2:2:514:C:H2'	2:2:515:G:H8	1.76	0.51
2:2:904:U:H2'	2:2:905:U:H6	1.75	0.51
2:2:1130:A:H62	2:2:1144:G:N2	2.08	0.51
5:5:6:C:H2'	5:5:7:G:C8	2.46	0.51
15:L:57:LEU:HD22	34:e:54:ASP:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:746:PSU:O2'	1:1:2611:C:O2'	2.13	0.51
2:2:384:G:H2'	2:2:385:C:C6	2.46	0.51
2:2:471:U:H2'	2:2:472:U:C6	2.46	0.51
2:2:883:C:H2'	2:2:884:U:C6	2.45	0.51
3:3:16:G:N2	3:3:69:G:H1'	2.26	0.51
3:3:104:A:N7	3:3:105:G:H1'	2.25	0.51
36:g:133:GLU:HA	36:g:136:MET:HG3	1.93	0.51
38:i:105:MET:HG3	38:i:173:VAL:HG22	1.91	0.51
48:s:88:ALA:HB2	48:s:96:LEU:HD23	1.92	0.51
1:1:288:U:H2'	1:1:289:G:C8	2.45	0.51
1:1:601:C:O2'	9:D:99:LYS:NZ	2.42	0.51
1:1:1153:C:OP1	20:Q:92:ARG:NH2	2.43	0.51
1:1:2899:A:H2'	1:1:2900:A:C8	2.46	0.51
2:2:275:G:H5'	51:v:16:LYS:HD2	1.91	0.51
5:5:67:G:H2'	5:5:68:U:C6	2.46	0.51
9:D:146:VAL:HA	9:D:185:LYS:O	2.10	0.51
52:w:70:TYR:HB2	52:w:74:HIS:NE2	2.26	0.51
1:1:608:A:H2'	1:1:609:A:H8	1.75	0.51
32:c:11:LEU:HD21	32:c:34:LEU:HD23	1.93	0.51
39:j:89:HIS:NE2	39:j:138:ARG:HD2	2.25	0.51
40:k:49:TYR:HB3	52:w:74:HIS:CE1	2.46	0.51
48:s:49:GLN:OE1	53:x:13:LEU:N	2.44	0.51
1:1:30:G:H2'	1:1:31:C:C6	2.46	0.50
1:1:191:A:H2'	1:1:192:C:C6	2.46	0.50
1:1:591:U:O4	1:1:592:A:N6	2.43	0.50
1:1:843:G:H2'	1:1:844:A:H8	1.74	0.50
1:1:2119:A:N6	1:1:2167:U:O2'	2.44	0.50
2:2:599:C:H2'	2:2:600:A:H8	1.76	0.50
2:2:613:C:H2'	2:2:614:C:C6	2.46	0.50
2:2:1162:C:H2'	2:2:1163:A:C8	2.46	0.50
2:2:1532:U:O4	2:2:1533:C:N4	2.44	0.50
6:A:193:LEU:O	6:A:197:LYS:HG3	2.11	0.50
40:k:49:TYR:OH	40:k:86:ARG:NH2	2.44	0.50
1:1:542:C:N4	1:1:543:G:O6	2.45	0.50
1:1:820:A:C2	1:1:943:A:H4'	2.46	0.50
1:1:851:C:H2'	1:1:852:U:H6	1.76	0.50
1:1:1124:G:O2'	35:f:37:GLN:O	2.28	0.50
1:1:2140:G:N2	1:1:2151:U:O2	2.41	0.50
1:1:2758:A:O2'	11:F:38:ASN:OD1	2.29	0.50
2:2:407:U:H2'	2:2:408:A:C8	2.46	0.50
2:2:501:C:H2'	2:2:502:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:38:MET:HE2	10:E:38:MET:HA	1.93	0.50
34:e:32:ILE:O	34:e:36:LYS:NZ	2.43	0.50
46:q:39:THR:HG22	46:q:49:LEU:HD22	1.93	0.50
1:1:571:U:OP1	21:R:80:ARG:NH2	2.36	0.50
1:1:744:U:H2'	1:1:745:1MG:O4'	2.11	0.50
1:1:2595:G:O2'	1:1:2597:G:O6	2.28	0.50
2:2:912:C:H2'	2:2:913:A:C8	2.46	0.50
2:2:1439:G:OP1	54:y:33:LYS:HD3	2.11	0.50
25:V:1:MET:HE1	25:V:59:GLU:HB3	1.92	0.50
38:i:95:GLU:HA	38:i:100:ASN:ND2	2.26	0.50
38:i:118:VAL:HG22	38:i:123:ILE:HG13	1.94	0.50
42:m:113:ASP:OD1	42:m:114:ARG:N	2.44	0.50
1:1:673:C:H5'	9:D:76:PRO:HD2	1.93	0.50
1:1:767:U:H2'	1:1:768:G:H8	1.77	0.50
1:1:2521:C:C2	1:1:2545:G:N2	2.79	0.50
1:1:2863:C:H2'	1:1:2864:G:C8	2.47	0.50
3:3:39:A:H2'	3:3:40:U:C6	2.47	0.50
12:G:95:GLY:H	12:G:98:ASP:HB2	1.76	0.50
1:1:262:A:N3	1:1:430:A:O2'	2.44	0.50
1:1:832:U:H2'	1:1:833:A:C8	2.45	0.50
1:1:2246:G:H2'	1:1:2247:A:H8	1.77	0.50
1:1:2390:U:OP2	34:e:35:LYS:NZ	2.35	0.50
2:2:33:A:H2'	2:2:34:C:C6	2.46	0.50
38:i:97:ARG:HH21	38:i:115:ARG:HH21	1.59	0.50
47:r:39:ILE:HD11	47:r:52:GLN:HB3	1.93	0.50
49:t:21:ASP:OD1	49:t:21:ASP:N	2.44	0.50
1:1:306:U:H2'	1:1:307:G:O4'	2.11	0.50
1:1:476:G:H2'	58:1:3309:HOH:O	2.11	0.50
1:1:1329:U:OP2	1:1:1330:C:N4	2.39	0.50
1:1:1750:G:H2'	1:1:1751:U:C6	2.46	0.50
1:1:2194:U:H2'	1:1:2195:U:C6	2.46	0.50
1:1:2330:G:H21	26:W:42:GLY:HA2	1.77	0.50
1:1:2579:C:O2'	8:C:136:ASN:OD1	2.29	0.50
2:2:318:G:O6	2:2:336:A:N6	2.45	0.50
2:2:925:G:C2	2:2:927:G:C8	3.00	0.50
12:G:47:PHE:HD1	12:G:51:ARG:HB2	1.77	0.50
1:1:172:A:H2'	1:1:173:A:H8	1.76	0.50
1:1:535:G:N2	58:1:3349:HOH:O	2.33	0.50
1:1:624:C:O2'	1:1:657:U:OP1	2.29	0.50
1:1:2425:A:H5''	1:1:2427:C:O4'	2.12	0.50
2:2:216:U:H4'	2:2:464:U:H4'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:747:A:H2'	2:2:748:G:C8	2.46	0.50
2:2:1003:G:N2	2:2:1005:A:O5'	2.44	0.50
2:2:1124:G:N2	2:2:1125:U:O4	2.44	0.50
10:E:34:ILE:HG13	10:E:96:MET:HE3	1.93	0.50
51:v:8:LEU:HD12	51:v:25:ILE:HG21	1.92	0.50
1:1:20:C:H2'	1:1:21:A:H8	1.77	0.50
1:1:175:G:H2'	1:1:176:A:C8	2.46	0.50
1:1:927:A:H2'	1:1:928:A:H8	1.77	0.50
1:1:1361:G:H2'	1:1:1362:C:H6	1.77	0.50
1:1:2673:G:H2'	1:1:2674:G:H8	1.77	0.50
2:2:1524:C:H2'	2:2:1525:G:H8	1.77	0.50
24:U:28:VAL:HG12	24:U:34:VAL:HG12	1.93	0.50
36:g:162:PHE:HA	36:g:184:PHE:O	2.12	0.50
36:g:221:VAL:O	36:g:225:ARG:HG2	2.12	0.50
39:j:107:ALA:HB2	39:j:125:ALA:HB3	1.94	0.50
45:p:60:PRO:HD3	45:p:91:PRO:HB3	1.93	0.50
49:t:35:GLN:HG3	49:t:59:MET:HE1	1.94	0.50
1:1:288:U:H2'	1:1:289:G:H8	1.76	0.50
1:1:807:U:H2'	1:1:808:G:H8	1.76	0.50
1:1:809:G:H2'	1:1:810:U:C6	2.47	0.50
1:1:833:A:H2'	1:1:834:G:H8	1.77	0.50
1:1:1790:C:O2'	7:B:208:ALA:HB2	2.12	0.50
1:1:1794:A:H2'	1:1:1795:C:C6	2.47	0.50
1:1:1864:U:OP1	1:1:2410:G:O2'	2.28	0.50
1:1:2756:U:H1'	1:1:2757:A:H5''	1.93	0.50
2:2:113:G:H1'	2:2:354:G:H5'	1.94	0.50
2:2:714:G:H1'	2:2:777:A:C8	2.47	0.50
2:2:1414:U:H2'	2:2:1415:G:H8	1.77	0.50
21:R:58:VAL:HG12	21:R:102:SER:HB3	1.94	0.50
24:U:14:LEU:HD21	24:U:71:ALA:HB3	1.94	0.50
39:j:79:GLY:O	39:j:121:HIS:N	2.39	0.50
1:1:154:U:H2'	1:1:155:A:C8	2.47	0.49
2:2:579:A:H2'	2:2:580:C:C6	2.48	0.49
2:2:684:U:O2'	45:p:41:ALA:O	2.30	0.49
2:2:1228:C:OP1	47:r:107:ARG:NH2	2.45	0.49
10:E:35:THR:HB	10:E:155:THR:OG1	2.11	0.49
15:L:79:LEU:HB3	15:L:116:VAL:HG13	1.94	0.49
21:R:89:HIS:O	58:R:201:HOH:O	2.19	0.49
42:m:112:THR:HG23	42:m:115:ALA:H	1.77	0.49
1:1:242:G:H22	1:1:255:A:P	2.34	0.49
1:1:379:G:N1	1:1:396:G:C6	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2233:U:H2'	1:1:2234:G:H8	1.76	0.49
2:2:513:C:H2'	2:2:514:C:C6	2.47	0.49
2:2:1120:C:H2'	2:2:1121:U:C6	2.47	0.49
10:E:115:ARG:O	30:a:47:LYS:NZ	2.45	0.49
50:u:44:SER:N	50:u:47:GLU:OE2	2.45	0.49
54:y:4:ILE:HG23	54:y:7:ALA:H	1.76	0.49
1:1:532:A:N7	1:1:2021:C:O2'	2.45	0.49
1:1:828:U:H2'	1:1:829:A:C8	2.47	0.49
1:1:2048:G:H21	8:C:118:PHE:HZ	1.60	0.49
1:1:2309:A:N6	58:1:3412:HOH:O	2.45	0.49
1:1:2443:C:H2'	1:1:2444:G:H8	1.77	0.49
1:1:2705:A:O2'	1:1:2852:G:OP1	2.22	0.49
2:2:392:C:H2'	2:2:393:A:H8	1.76	0.49
7:B:107:PRO:HA	7:B:195:VAL:HA	1.94	0.49
8:C:11:MET:HB2	8:C:24:VAL:O	2.12	0.49
45:p:34:ILE:N	45:p:43:GLY:O	2.40	0.49
49:t:6:GLU:OE1	49:t:6:GLU:N	2.44	0.49
1:1:587:C:OP2	15:L:21:ARG:NH1	2.45	0.49
1:1:1031:G:H22	1:1:1122:G:H1	1.58	0.49
1:1:1539:U:H2'	1:1:1540:G:C8	2.48	0.49
1:1:1615:C:OP2	1:1:1617:C:N4	2.43	0.49
1:1:2360:G:H1'	15:L:60:ARG:HD2	1.94	0.49
2:2:358:U:H2'	2:2:359:G:C8	2.46	0.49
2:2:676:A:H2'	2:2:677:U:H6	1.77	0.49
2:2:835:U:OP1	52:w:53:ARG:NH2	2.45	0.49
5:5:54:U:H2'	5:5:55:U:H5'	1.92	0.49
20:Q:44:GLN:NE2	21:R:77:PHE:HB3	2.28	0.49
40:k:3:HIS:ND1	40:k:65:GLU:OE1	2.45	0.49
40:k:6:ILE:HG22	40:k:89:VAL:HG13	1.93	0.49
52:w:26:ILE:HG21	52:w:67:LEU:HD12	1.94	0.49
1:1:197:A:H62	1:1:2430:A:H2'	1.76	0.49
1:1:936:A:H2'	1:1:937:C:C6	2.48	0.49
1:1:2888:C:H2'	1:1:2889:C:H6	1.76	0.49
2:2:141:G:OP2	58:2:1801:HOH:O	2.19	0.49
2:2:1128:C:O2'	43:n:18:ARG:NH2	2.44	0.49
2:2:1147:C:O2'	43:n:18:ARG:HD3	2.12	0.49
26:W:59:LEU:HD12	26:W:80:ILE:HD12	1.94	0.49
36:g:117:LEU:HD23	36:g:141:LEU:HD13	1.93	0.49
1:1:299:A:N1	1:1:322:A:O2'	2.34	0.49
1:1:417:C:H2'	1:1:418:C:C6	2.47	0.49
1:1:684:G:N2	1:1:788:A:OP2	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:796:C:H2'	1:1:797:G:H8	1.78	0.49
1:1:1000:A:OP2	1:1:1154:G:N1	2.28	0.49
1:1:1734:G:H2'	1:1:1735:A:H8	1.77	0.49
1:1:1844:C:H2'	1:1:1845:G:H8	1.76	0.49
1:1:2543:G:H21	1:1:2646:C:H5''	1.78	0.49
1:1:2824:C:OP2	1:1:2825:G:N2	2.46	0.49
2:2:552:U:O2'	46:q:83:ARG:O	2.26	0.49
2:2:581:G:N1	2:2:759:A:OP2	2.29	0.49
10:E:66:LEU:HG	10:E:88:LYS:HE3	1.94	0.49
10:E:102:ARG:NH2	30:a:26:SER:HA	2.28	0.49
36:g:52:GLU:O	36:g:56:GLU:HG2	2.13	0.49
47:r:90:ARG:HH21	47:r:95:LEU:HB3	1.76	0.49
1:1:414:C:H1'	1:1:1864:U:H1'	1.95	0.49
1:1:639:U:H2'	1:1:640:C:H6	1.77	0.49
1:1:1475:G:O2'	1:1:1514:G:O6	2.30	0.49
2:2:413:G:H22	2:2:429:U:P	2.36	0.49
2:2:520:A:OP2	46:q:48:ALA:HB1	2.13	0.49
2:2:1005:A:H3'	2:2:1006:G:C8	2.44	0.49
5:5:72:G:P	5:5:72:G:H8	2.35	0.49
10:E:110:ARG:NE	10:E:137:ILE:O	2.46	0.49
38:i:28:ILE:HD12	38:i:34:ILE:HD13	1.94	0.49
1:1:1441:G:H2'	1:1:1442:U:C6	2.47	0.49
1:1:2302:U:O2'	10:E:123:ASP:O	2.17	0.49
1:1:2591:C:N4	1:1:2592:G:O6	2.45	0.49
2:2:859:G:OP2	2:2:869:G:N1	2.43	0.49
2:2:1060:U:OP1	48:s:85:ARG:NH2	2.46	0.49
2:2:1287:A:H2	2:2:1353:G:H1'	1.78	0.49
22:S:17:VAL:HB	22:S:76:VAL:HG11	1.95	0.49
45:p:35:THR:HG23	45:p:41:ALA:HA	1.95	0.49
54:y:36:TYR:CZ	54:y:79:LEU:HD21	2.48	0.49
1:1:580:U:H2'	1:1:581:C:C6	2.48	0.49
1:1:833:A:H2'	1:1:834:G:C8	2.48	0.49
1:1:1133:A:H4'	1:1:1134:A:H5''	1.95	0.49
1:1:1175:A:H4'	1:1:1176:U:H5'	1.94	0.49
1:1:2291:U:H2'	1:1:2292:U:H6	1.76	0.49
2:2:855:U:OP2	2:2:871:U:N3	2.38	0.49
2:2:1100:C:OP2	36:g:95:ARG:HD3	2.12	0.49
2:2:1302:C:C5	47:r:17:ILE:HD11	2.48	0.49
8:C:5:VAL:HG22	8:C:202:ILE:HG12	1.95	0.49
11:F:105:LEU:HB2	11:F:113:VAL:HB	1.93	0.49
26:W:53:CYS:SG	26:W:57:HIS:HA	2.53	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:g:186:ILE:HD13	36:g:200:ILE:HB	1.94	0.49
47:r:11:ASP:HA	47:r:45:ILE:HB	1.94	0.49
49:t:32:LEU:HD23	49:t:63:ARG:HB2	1.95	0.49
1:1:598:U:H2'	1:1:599:A:H8	1.78	0.49
1:1:1281:G:H2'	1:1:1282:U:C6	2.48	0.49
1:1:1392:A:N6	23:T:18:GLU:HG3	2.27	0.49
1:1:1915:U:H2'	1:1:1916:A:C8	2.48	0.49
1:1:2245:U:H5''	1:1:2246:G:H5'	1.95	0.49
1:1:2310:C:H2'	10:E:77:PHE:HE2	1.77	0.49
1:1:2475:C:N4	1:1:2529:G:H22	2.11	0.49
1:1:2812:G:H2'	1:1:2813:A:C8	2.47	0.49
2:2:131:A:H2'	2:2:132:C:C6	2.48	0.49
2:2:602:A:H2'	2:2:603:U:C6	2.48	0.49
2:2:955:U:H2'	2:2:956:U:C6	2.48	0.49
2:2:1304:G:N2	2:2:1334:G:C6	2.81	0.49
5:5:20:U:C2'	5:5:21:A:H5'	2.43	0.49
8:C:101:PHE:CD2	8:C:187:LEU:HD11	2.48	0.49
13:J:81:ILE:HD12	13:J:81:ILE:H	1.78	0.49
27:X:49:LEU:HB3	27:X:51:VAL:HG13	1.93	0.49
38:i:170:TRP:CD2	38:i:186:PRO:HB3	2.47	0.49
51:v:10:GLY:HA3	51:v:25:ILE:HD13	1.94	0.49
54:y:54:MET:O	54:y:57:ILE:HG22	2.13	0.49
1:1:145:C:H2'	1:1:146:A:C8	2.48	0.48
1:1:174:U:H2'	1:1:175:G:H8	1.77	0.48
1:1:511:U:H4'	1:1:1235:G:H4'	1.94	0.48
1:1:1115:G:O2'	1:1:1116:G:H5''	2.13	0.48
1:1:2020:A:H5'	31:b:9:THR:HB	1.94	0.48
1:1:2374:C:N4	1:1:2375:G:O6	2.46	0.48
2:2:780:A:N6	2:2:801:U:OP2	2.38	0.48
19:P:92:VAL:HG11	19:P:97:LEU:HD11	1.94	0.48
43:n:113:ARG:HE	48:s:101:TRP:NE1	2.11	0.48
1:1:871:U:H2'	1:1:872:U:C6	2.48	0.48
1:1:1438:U:H2'	1:1:1439:A:H8	1.77	0.48
1:1:1939:5MU:OP1	1:1:2604:U:O2'	2.31	0.48
1:1:2514:U:H2'	1:1:2515:C:C6	2.48	0.48
2:2:339:C:H2'	2:2:340:U:C6	2.48	0.48
2:2:427:U:O2'	2:2:541:G:OP1	2.29	0.48
2:2:1311:A:OP1	30:a:59:ARG:NH1	2.45	0.48
2:2:1493:A:C1'	4:4:19:G:H1'	2.43	0.48
2:2:1512:U:H2'	2:2:1513:A:C8	2.47	0.48
36:g:118:GLU:OE1	58:g:301:HOH:O	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:665:U:H2'	1:1:666:A:H8	1.78	0.48
1:1:741:U:H2'	1:1:742:A:H8	1.76	0.48
1:1:1042:G:H1'	1:1:1043:C:O4'	2.12	0.48
1:1:1604:C:O2'	1:1:1610:A:N1	2.38	0.48
2:2:1314:C:H2'	2:2:1315:U:C6	2.49	0.48
38:i:62:ARG:HH21	38:i:68:LEU:HA	1.78	0.48
1:1:81:G:O2'	1:1:295:G:O2'	2.30	0.48
1:1:347:A:H2'	1:1:348:A:C8	2.48	0.48
1:1:644:A:H2'	1:1:645:C:O4'	2.12	0.48
1:1:1771:C:H2'	1:1:1772:A:C8	2.49	0.48
1:1:2716:C:H2'	1:1:2717:C:H6	1.78	0.48
2:2:22:G:H2'	2:2:23:C:C6	2.47	0.48
2:2:258:G:H1	2:2:268:U:H3	1.59	0.48
2:2:944:G:N1	2:2:1338:G:OP2	2.39	0.48
2:2:1133:G:H2'	2:2:1134:G:C8	2.48	0.48
2:2:1176:A:H2'	2:2:1177:G:C8	2.47	0.48
2:2:1237:C:H5''	2:2:1238:A:C8	2.47	0.48
21:R:61:ALA:HB1	21:R:96:VAL:HG22	1.94	0.48
39:j:76:LEU:HD11	39:j:120:VAL:HG12	1.95	0.48
1:1:489:G:N3	1:1:1284:A:N6	2.61	0.48
1:1:564:C:OP1	58:1:3304:HOH:O	2.20	0.48
1:1:575:A:OP2	1:1:2499:C:O2'	2.25	0.48
1:1:2372:U:H2'	1:1:2373:G:C8	2.48	0.48
1:1:2509:G:N1	1:1:2580:PSU:O2	2.47	0.48
5:5:15:G:H22	5:5:48:C:N4	2.11	0.48
9:D:184:ASP:OD1	15:L:2:ARG:NH2	2.46	0.48
22:S:20:VAL:HG11	22:S:44:ALA:HA	1.94	0.48
27:X:43:GLU:OE2	27:X:45:ARG:HB3	2.12	0.48
36:g:101:LEU:HD11	36:g:175:GLU:HB3	1.94	0.48
36:g:114:LEU:HD12	36:g:144:LEU:HD23	1.96	0.48
1:1:370:G:P	1:1:423:A:H62	2.37	0.48
1:1:437:U:H2'	1:1:438:G:H8	1.78	0.48
1:1:2176:A:H2'	1:1:2177:C:C6	2.49	0.48
1:1:2677:G:H2'	1:1:2678:C:C6	2.49	0.48
1:1:2799:A:O2'	1:1:2800:A:H5''	2.14	0.48
2:2:18:C:OP1	39:j:132:ASN:ND2	2.45	0.48
2:2:19:A:OP1	39:j:135:ASN:ND2	2.45	0.48
2:2:224:U:OP1	54:y:69:LYS:NZ	2.46	0.48
2:2:1269:A:O2'	2:2:1325:C:O2'	2.22	0.48
3:3:23:G:H2'	3:3:24:G:C5	2.48	0.48
5:5:72:G:C2	5:5:73:A:C5	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:56:ASP:O	10:E:60:ILE:HG12	2.14	0.48
22:S:65:ASP:OD1	22:S:66:ILE:N	2.45	0.48
48:s:46:LEU:HB2	53:x:13:LEU:HD13	1.95	0.48
54:y:39:ILE:HG23	54:y:86:LEU:HD12	1.95	0.48
1:1:445:C:OP1	20:Q:2:ALA:N	2.46	0.48
1:1:587:C:O2	15:L:33:ARG:NH1	2.47	0.48
1:1:641:U:H3	1:1:647:G:H1	1.61	0.48
1:1:948:C:H2'	1:1:949:G:C8	2.48	0.48
1:1:1287:A:C2	1:1:1649:G:H4'	2.49	0.48
1:1:1962:5MC:O2'	1:1:1963:U:H3'	2.13	0.48
1:1:2023:C:H2'	1:1:2024:G:H8	1.78	0.48
1:1:2375:G:N2	1:1:2378:A:OP2	2.42	0.48
2:2:68:G:N2	2:2:151:A:C2	2.79	0.48
2:2:335:C:H2'	2:2:336:A:C8	2.39	0.48
2:2:539:A:H2'	2:2:540:G:H8	1.78	0.48
2:2:1031:C:H4'	2:2:1032:G:C2	2.48	0.48
2:2:1181:G:H1'	2:2:1182:G:C4	2.49	0.48
5:5:56:C:O2'	10:E:75:ALA:CB	2.61	0.48
7:B:225:MET:HG3	7:B:226:ASN:N	2.28	0.48
12:G:132:PHE:HB2	12:G:140:ALA:HB3	1.96	0.48
41:l:53:ARG:NH1	41:l:122:ASN:OD1	2.47	0.48
41:l:79:ARG:HD3	41:l:84:THR:HG22	1.95	0.48
43:n:17:ALA:HB2	43:n:67:VAL:HG23	1.96	0.48
54:y:28:MET:HE1	54:y:67:ILE:HG21	1.95	0.48
1:1:980:A:H8	1:1:980:A:OP1	1.97	0.48
1:1:1987:A:H2'	1:1:1988:G:H8	1.79	0.48
1:1:2061:G:H2'	1:1:2501:C:O2'	2.14	0.48
1:1:2552:OMU:H2'	1:1:2554:U:OP2	2.14	0.48
2:2:78:A:H2'	2:2:79:G:H8	1.78	0.48
2:2:393:A:C2	2:2:394:G:C8	3.02	0.48
2:2:405:U:OP2	38:i:3:ARG:NH1	2.47	0.48
3:3:74:U:H3	25:V:29:ILE:HD11	1.79	0.48
5:5:17:C:OP1	5:5:60:U:O2'	2.27	0.48
5:5:69:G:C2	5:5:70:C:C2	3.02	0.48
7:B:160:THR:HG22	7:B:177:ARG:HG2	1.94	0.48
37:h:3:GLN:HB2	37:h:4:LYS:HD3	1.96	0.48
41:l:26:PHE:HZ	41:l:120:LEU:HD11	1.79	0.48
1:1:600:G:N2	1:1:605:G:O3'	2.47	0.48
1:1:2086:U:H2'	1:1:2087:G:C8	2.49	0.48
1:1:2687:U:H2'	1:1:2688:G:O4'	2.12	0.48
2:2:339:C:H2'	2:2:340:U:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:373:A:N3	2:2:482:A:N6	2.61	0.48
2:2:965:U:H1'	2:2:969:A:C2	2.49	0.48
3:3:2:G:H2'	3:3:3:C:H6	1.79	0.48
5:5:59:A:H2'	5:5:60:U:N1	2.29	0.48
7:B:145:GLU:HG2	7:B:151:GLY:H	1.78	0.48
9:D:105:LEU:HD12	9:D:108:ILE:HD11	1.94	0.48
39:j:157:ARG:HD3	42:m:43:GLU:HG3	1.95	0.48
46:q:100:GLY:N	46:q:104:CYS:O	2.45	0.48
47:r:75:MET:HE3	47:r:79:ARG:HB3	1.95	0.48
52:w:23:TYR:HA	52:w:58:ALA:HB1	1.95	0.48
1:1:685:A:N1	1:1:787:C:H1'	2.29	0.48
1:1:714:U:OP2	49:t:88:ARG:NH1	2.33	0.48
1:1:1105:U:H2'	1:1:1106:G:H8	1.79	0.48
1:1:1858:A:N6	1:1:1884:G:H1'	2.29	0.48
1:1:1953:A:O2'	1:1:2559:C:O2	2.31	0.48
1:1:2007:U:H2'	1:1:2008:C:C6	2.49	0.48
1:1:2271:G:H5'	26:W:20:ARG:HG3	1.95	0.48
1:1:2329:U:H2'	1:1:2330:G:C8	2.48	0.48
1:1:2683:C:OP1	19:P:51:ARG:NH2	2.47	0.48
2:2:68:G:H3'	2:2:69:G:H5''	1.96	0.48
2:2:78:A:H2'	2:2:79:G:C8	2.49	0.48
2:2:496:A:H2'	2:2:496:A:N3	2.27	0.48
2:2:1183:U:O2'	2:2:1185:G:OP2	2.32	0.48
2:2:1216:A:H5''	48:s:5:SER:OG	2.13	0.48
33:d:16:HIS:HB2	33:d:44:VAL:HG11	1.96	0.48
36:g:114:LEU:HG	36:g:145:GLU:OE2	2.14	0.48
1:1:69:C:O2	1:1:73:A:O2'	2.26	0.47
1:1:780:G:C2	1:1:782:A:C2	3.02	0.47
1:1:1427:A:H4'	1:1:1428:C:O4'	2.14	0.47
1:1:2025:C:H2'	1:1:2026:U:C6	2.49	0.47
1:1:2036:C:H2'	1:1:2037:A:C8	2.49	0.47
2:2:634:C:H2'	2:2:635:A:C8	2.49	0.47
2:2:886:G:O6	2:2:912:C:N4	2.47	0.47
7:B:30:PHE:O	7:B:34:LEU:HD23	2.13	0.47
16:M:41:LEU:HD13	16:M:96:ILE:HG13	1.96	0.47
16:M:42:THR:HA	16:M:93:VAL:HA	1.96	0.47
16:M:77:PRO:HD2	16:M:80:VAL:HG11	1.96	0.47
17:N:65:LEU:O	17:N:69:ARG:HG2	2.14	0.47
20:Q:40:ILE:O	20:Q:44:GLN:HG3	2.14	0.47
1:1:1571:A:H2'	1:1:1572:A:C8	2.49	0.47
1:1:1914:C:H2'	1:1:1915:U:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2788:C:H2'	1:1:2789:C:C6	2.49	0.47
1:1:2896:C:H2'	1:1:2897:U:C6	2.50	0.47
2:2:963:G:N2	44:o:57:VAL:HG11	2.30	0.47
2:2:1326:U:H2'	2:2:1327:C:H6	1.78	0.47
2:2:1464:U:H2'	2:2:1465:A:H8	1.79	0.47
5:5:69:G:H2'	5:5:70:C:C6	2.49	0.47
9:D:141:MET:HE1	9:D:143:LEU:HD12	1.95	0.47
10:E:139:PRO:HB2	30:a:32:LEU:HD11	1.96	0.47
23:T:10:VAL:HG13	23:T:11:LEU:HD12	1.95	0.47
24:U:18:ASP:HB2	24:U:21:LYS:HD2	1.97	0.47
38:i:174:ASP:OD2	58:i:301:HOH:O	2.19	0.47
39:j:44:GLY:O	39:j:74:VAL:N	2.48	0.47
1:1:848:C:H2'	1:1:849:A:C8	2.40	0.47
1:1:918:A:H2'	1:1:919:U:O4'	2.15	0.47
1:1:1054:A:H2'	1:1:1055:G:C8	2.49	0.47
1:1:1266:G:OP2	31:b:17:ARG:NH2	2.41	0.47
1:1:1771:C:H2'	1:1:1772:A:H8	1.79	0.47
1:1:1819:A:H5''	7:B:160:THR:HG21	1.96	0.47
2:2:167:A:N6	2:2:168:G:O6	2.47	0.47
2:2:1095:U:P	2:2:1108:G:H1	2.37	0.47
43:n:47:VAL:HG11	43:n:76:ALA:HB1	1.96	0.47
43:n:79:ILE:O	43:n:83:ILE:HG13	2.13	0.47
1:1:418:C:H2'	1:1:419:U:C6	2.50	0.47
1:1:813:U:H2'	1:1:814:C:H6	1.79	0.47
1:1:927:A:O2'	29:Z:39:GLU:OE2	2.32	0.47
1:1:2651:C:N4	58:1:3406:HOH:O	2.43	0.47
2:2:769:G:H4'	2:2:1513:A:H4'	1.95	0.47
2:2:824:G:H2'	2:2:825:A:H8	1.78	0.47
2:2:927:G:P	4:4:11:A:H61	2.37	0.47
2:2:1120:C:H2'	2:2:1121:U:H6	1.80	0.47
5:5:3:G:H1'	5:5:4:C:O5'	2.14	0.47
25:V:32:GLY:O	25:V:93:ARG:NH1	2.46	0.47
31:b:13:ARG:O	31:b:17:ARG:HG2	2.14	0.47
41:l:126:ASP:O	41:l:131:LYS:N	2.41	0.47
1:1:265:A:N1	1:1:427:U:O2'	2.41	0.47
1:1:633:A:H5''	15:L:70:LYS:HD2	1.97	0.47
1:1:729:G:OP2	7:B:207:LYS:NZ	2.42	0.47
1:1:927:A:H2'	1:1:928:A:C8	2.48	0.47
1:1:1361:G:H2'	1:1:1362:C:C6	2.49	0.47
1:1:1431:A:H2'	1:1:1432:G:C8	2.49	0.47
1:1:1509:A:O2'	1:1:1510:G:O5'	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1668:A:O2'	1:1:1674:G:N7	2.36	0.47
1:1:2292:U:H2'	1:1:2293:G:C8	2.49	0.47
1:1:2530:A:OP2	1:1:2535:G:N2	2.47	0.47
3:3:30:C:H1'	3:3:57:A:H61	1.79	0.47
5:5:11:C:H2'	5:5:12:G:C8	2.50	0.47
5:5:22:G:N7	5:5:46:G:N2	2.55	0.47
20:Q:97:ASP:HA	20:Q:100:VAL:HG12	1.97	0.47
1:1:1:G:H2'	1:1:2:G:C8	2.50	0.47
1:1:13:A:O2'	1:1:15:G:N7	2.41	0.47
1:1:417:C:H2'	1:1:418:C:H6	1.80	0.47
1:1:1389:G:N1	1:1:1399:C:N3	2.63	0.47
1:1:1830:C:H2'	1:1:1831:G:C8	2.46	0.47
1:1:2508:G:H1	1:1:2580:PSU:HN3	1.62	0.47
2:2:259:G:H2'	2:2:260:G:H8	1.80	0.47
2:2:715:A:H2'	2:2:716:A:C8	2.49	0.47
37:h:121:THR:HG23	37:h:189:ALA:HB2	1.97	0.47
54:y:57:ILE:HG13	54:y:61:GLN:NE2	2.18	0.47
1:1:365:U:H2'	1:1:366:C:C6	2.49	0.47
1:1:391:A:O2'	1:1:410:G:OP1	2.30	0.47
1:1:1085:A:H2'	1:1:1086:A:C8	2.50	0.47
1:1:1751:U:H2'	1:1:1752:C:C6	2.50	0.47
1:1:2246:G:H2'	1:1:2247:A:C8	2.50	0.47
1:1:2452:C:H2'	1:1:2453:A:O4'	2.15	0.47
1:1:2514:U:H2'	1:1:2515:C:H6	1.80	0.47
2:2:216:U:H2'	2:2:217:C:C6	2.49	0.47
2:2:270:A:H2'	2:2:271:C:C6	2.49	0.47
2:2:454:G:H2'	2:2:455:G:H8	1.79	0.47
2:2:714:G:N2	2:2:777:A:N3	2.52	0.47
2:2:747:A:H2'	2:2:748:G:H8	1.80	0.47
2:2:935:A:O2'	2:2:1383:C:N3	2.47	0.47
2:2:945:G:C2	2:2:946:A:C8	3.03	0.47
2:2:1323:G:H2'	2:2:1324:A:H8	1.80	0.47
2:2:1493:A:H1'	4:4:19:G:H1'	1.96	0.47
10:E:138:PHE:HE2	10:E:152:LEU:HD21	1.79	0.47
15:L:79:LEU:HA	15:L:82:LEU:HD13	1.97	0.47
16:M:36:VAL:HG22	25:V:82:TYR:HB2	1.97	0.47
36:g:106:THR:O	36:g:109:GLN:HG2	2.14	0.47
38:i:54:GLN:HB3	38:i:203:LEU:HB2	1.96	0.47
42:m:55:THR:HG23	42:m:56:LYS:HG2	1.96	0.47
1:1:1234:U:C4	1:1:1235:G:C5	3.03	0.47
1:1:1252:G:N2	20:Q:33:ARG:HB3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2845:U:H2'	1:1:2846:G:C8	2.49	0.47
1:1:2845:U:H5''	19:P:52:ASN:O	2.15	0.47
1:1:2899:A:H2'	1:1:2900:A:H8	1.80	0.47
2:2:695:A:H2'	2:2:696:A:C8	2.50	0.47
2:2:1127:G:H2'	2:2:1128:C:H6	1.79	0.47
14:K:24:VAL:HG13	14:K:33:ALA:HB2	1.96	0.47
16:M:2:LEU:HD22	16:M:46:ILE:HG21	1.97	0.47
37:h:105:GLU:OE1	37:h:107:ARG:NE	2.48	0.47
44:o:36:VAL:HG22	44:o:76:ILE:HG22	1.96	0.47
53:x:36:ARG:HH21	53:x:75:ALA:HB3	1.80	0.47
1:1:1196:C:C2	1:1:1197:G:C8	3.03	0.47
1:1:1817:G:OP1	7:B:87:ARG:NH2	2.39	0.47
1:1:2081:U:H2'	1:1:2082:A:C8	2.49	0.47
1:1:2324:U:H5''	1:1:2325:G:H5''	1.97	0.47
1:1:2340:A:H2'	1:1:2341:G:H8	1.80	0.47
1:1:2347:C:O2'	32:c:21:TYR:OH	2.25	0.47
1:1:2468:A:OP2	1:1:2476:A:N6	2.42	0.47
1:1:2836:U:H2'	1:1:2837:A:H8	1.80	0.47
2:2:382:A:H2'	2:2:383:A:C8	2.49	0.47
2:2:501:C:O2	2:2:549:C:O2'	2.32	0.47
2:2:539:A:H2'	2:2:540:G:C8	2.50	0.47
2:2:575:G:H4'	2:2:576:C:H5''	1.97	0.47
2:2:1171:A:H2'	2:2:1172:C:C6	2.50	0.47
2:2:1414:U:O2	2:2:1487:G:N2	2.47	0.47
5:5:21:A:N7	5:5:47:U:H1'	2.30	0.47
9:D:130:LYS:HB2	9:D:133:LEU:HG	1.97	0.47
13:J:116:ARG:O	13:J:120:ARG:HG3	2.14	0.47
32:c:25:LYS:NZ	32:c:32:GLU:O	2.46	0.47
1:1:1060:U:C2	1:1:1062:G:H5'	2.50	0.47
1:1:1486:U:H2'	1:1:1487:U:H6	1.79	0.47
1:1:1696:G:N2	1:1:1977:A:O2'	2.46	0.47
1:1:1734:G:H2'	1:1:1735:A:C8	2.50	0.47
1:1:2344:U:H3'	32:c:37:LYS:O	2.15	0.47
2:2:777:A:H2'	2:2:778:G:H8	1.79	0.47
2:2:1028:C:N4	58:2:1846:HOH:O	2.44	0.47
2:2:1479:C:H2'	2:2:1480:A:H8	1.80	0.47
5:5:14:A:C2	5:5:15:G:H1'	2.50	0.47
21:R:89:HIS:N	58:R:201:HOH:O	2.39	0.47
36:g:176:ALA:HB1	36:g:181:ILE:HB	1.97	0.47
37:h:110:GLU:HG2	37:h:144:LEU:HD22	1.97	0.47
38:i:110:THR:HG23	38:i:113:GLU:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:y:79:LEU:O	54:y:83:ILE:HG13	2.15	0.47
1:1:175:G:H2'	1:1:176:A:H8	1.80	0.46
1:1:481:G:OP2	24:U:44:LYS:HD2	2.14	0.46
1:1:608:A:H2'	1:1:609:A:C8	2.50	0.46
1:1:1097:U:H3'	1:1:1098:A:H8	1.80	0.46
1:1:1413:A:H2'	1:1:1414:C:C6	2.50	0.46
1:1:1667:G:O2'	1:1:1991:U:O4	2.22	0.46
1:1:2233:U:H2'	1:1:2234:G:C8	2.49	0.46
2:2:436:C:H2'	2:2:437:U:C6	2.50	0.46
2:2:594:U:H2'	2:2:595:A:O4'	2.15	0.46
2:2:1226:C:O2	53:x:83:HIS:NE2	2.47	0.46
36:g:67:ILE:HG22	36:g:160:ALA:HB3	1.97	0.46
37:h:150:LYS:HG3	37:h:201:TRP:CE3	2.50	0.46
1:1:1042:G:O2'	1:1:1043:C:H5''	2.14	0.46
1:1:1056:G:H21	1:1:1104:C:H41	1.61	0.46
1:1:1476:U:H2'	1:1:1477:A:H8	1.79	0.46
1:1:2345:G:N3	1:1:2381:A:H2'	2.30	0.46
2:2:952:U:H4'	2:2:964:A:H61	1.81	0.46
2:2:1391:U:H2'	2:2:1392:G:C8	2.50	0.46
2:2:1454:G:H2'	2:2:1455:G:H8	1.80	0.46
7:B:232:HIS:CG	7:B:240:PHE:HE1	2.33	0.46
22:S:24:ILE:HD13	22:S:36:LEU:HD11	1.96	0.46
23:T:11:LEU:HA	23:T:34:VAL:HG12	1.97	0.46
36:g:115:LYS:HE2	36:g:118:GLU:OE2	2.15	0.46
37:h:11:ARG:NH2	37:h:175:LEU:O	2.40	0.46
39:j:83:HIS:CE1	42:m:96:MET:HE1	2.50	0.46
39:j:133:PRO:HA	39:j:136:VAL:HG22	1.97	0.46
40:k:18:VAL:HG11	40:k:58:HIS:CE1	2.50	0.46
1:1:367:G:H2'	1:1:367:G:N3	2.29	0.46
1:1:494:G:H5''	22:S:4:ILE:HG23	1.98	0.46
1:1:871:U:H2'	1:1:872:U:H6	1.81	0.46
1:1:2477:U:O2	35:f:4:ARG:NH2	2.48	0.46
2:2:264:C:O2'	51:v:66:PRO:O	2.31	0.46
2:2:360:G:H2'	2:2:361:G:C8	2.50	0.46
2:2:510:A:N3	2:2:543:U:H1'	2.31	0.46
2:2:976:G:H5'	48:s:61:ARG:HH22	1.79	0.46
2:2:1343:G:H1'	43:n:123:ARG:NH1	2.31	0.46
2:2:1355:G:H2'	2:2:1356:G:H8	1.80	0.46
58:K:202:HOH:O	19:P:70:VAL:HG13	2.15	0.46
19:P:27:GLU:HB2	19:P:44:GLU:HG2	1.97	0.46
43:n:124:ARG:HH12	43:n:127:PHE:HB2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:o:12:ALA:HB3	44:o:18:ILE:HB	1.96	0.46
47:r:37:ALA:HB2	47:r:59:GLU:OE2	2.15	0.46
49:t:57:LEU:HA	49:t:60:VAL:HG22	1.97	0.46
1:1:586:A:N1	1:1:809:G:O2'	2.39	0.46
1:1:1233:C:C2	1:1:1234:U:C5	3.03	0.46
1:1:1287:A:O5'	17:N:103:ARG:NH2	2.45	0.46
1:1:1917:PSU:O2	1:1:1918:A:N6	2.49	0.46
2:2:59:A:H3'	2:2:331:G:H22	1.81	0.46
2:2:1326:U:C2	2:2:1327:C:C5	3.03	0.46
39:j:144:LEU:O	39:j:147:MET:HG2	2.16	0.46
40:k:26:THR:HA	40:k:29:ILE:HG22	1.97	0.46
1:1:879:G:H2'	1:1:880:G:H8	1.80	0.46
1:1:1501:G:OP1	7:B:101:ARG:NH2	2.33	0.46
1:1:1794:A:H2'	1:1:1795:C:H6	1.80	0.46
1:1:2071:A:H2'	1:1:2072:C:C6	2.49	0.46
1:1:2091:C:H4'	27:X:56:MET:HE1	1.98	0.46
5:5:52:G:H2'	5:5:53:G:C8	2.49	0.46
5:5:52:G:H2'	5:5:53:G:H8	1.79	0.46
12:G:99:ILE:HD11	12:G:117:LEU:HD11	1.97	0.46
43:n:47:VAL:HG22	43:n:80:ARG:HB2	1.97	0.46
1:1:414:C:H2'	1:1:415:A:H8	1.81	0.46
1:1:453:A:N3	1:1:457:A:O2'	2.46	0.46
1:1:935:C:H2'	1:1:936:A:C8	2.50	0.46
1:1:935:C:H2'	1:1:936:A:H8	1.81	0.46
1:1:1117:C:H2'	1:1:1118:C:C6	2.51	0.46
1:1:1359:A:OP2	1:1:1371:G:N1	2.38	0.46
1:1:1569:A:H2'	1:1:1570:A:C8	2.50	0.46
1:1:2610:C:N4	58:1:3396:HOH:O	2.41	0.46
2:2:231:U:H2'	2:2:232:G:H8	1.80	0.46
2:2:674:G:N2	45:p:118:HIS:HB2	2.31	0.46
2:2:745:G:OP1	2:2:851:G:O2'	2.32	0.46
18:O:7:ARG:HD2	18:O:97:PHE:CZ	2.51	0.46
22:S:28:LYS:HE3	22:S:28:LYS:HB3	1.78	0.46
30:a:56:ARG:NH2	53:x:68:GLY:HA3	2.31	0.46
41:l:40:GLU:HA	41:l:43:VAL:HG12	1.96	0.46
49:t:26:GLU:HA	49:t:29:VAL:HG12	1.97	0.46
1:1:272:A:H2'	1:1:273:G:H8	1.81	0.46
1:1:345:A:N3	1:1:347:A:N6	2.63	0.46
1:1:813:U:H2'	1:1:814:C:C6	2.51	0.46
1:1:1141:U:H4'	1:1:1142:A:O4'	2.16	0.46
1:1:1326:U:N3	1:1:1648:U:O2'	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1655:A:N6	1:1:2005:A:O2'	2.48	0.46
1:1:2298:A:OP1	10:E:71:ARG:NH1	2.39	0.46
2:2:71:A:H61	2:2:99:C:H1'	1.81	0.46
2:2:114:U:H2'	2:2:115:G:C8	2.51	0.46
2:2:147:G:H2'	2:2:148:G:C8	2.50	0.46
2:2:751:U:H2'	2:2:752:G:O4'	2.15	0.46
2:2:826:C:H1'	42:m:16:ASN:HD22	1.80	0.46
2:2:1530:G:H2'	2:2:1531:A:C8	2.51	0.46
9:D:29:HIS:HA	9:D:32:VAL:HG22	1.97	0.46
10:E:10:ASP:O	10:E:14:LYS:NZ	2.46	0.46
10:E:136:ILE:HD12	10:E:141:ILE:HG23	1.98	0.46
15:L:41:ARG:NH1	58:L:303:HOH:O	2.47	0.46
20:Q:86:ALA:HB2	20:Q:116:ALA:HB2	1.98	0.46
38:i:85:ASN:HD22	39:j:101:GLU:HG3	1.79	0.46
49:t:12:VAL:HG21	49:t:22:THR:HG22	1.97	0.46
1:1:1812:U:H2'	1:1:1813:G:H8	1.80	0.46
2:2:707:U:H4'	45:p:22:HIS:ND1	2.31	0.46
3:3:77:U:O2	25:V:78:GLN:NE2	2.36	0.46
9:D:1:MET:HE2	9:D:16:GLU:HG2	1.98	0.46
37:h:66:VAL:HB	37:h:101:ILE:HD13	1.98	0.46
44:o:52:LEU:O	48:s:81:ARG:NH1	2.48	0.46
50:u:52:LEU:HD22	50:u:57:ILE:HD11	1.98	0.46
1:1:329:G:O6	24:U:17:LYS:N	2.49	0.46
1:1:959:A:H2'	1:1:960:A:C8	2.51	0.46
1:1:1710:G:H2'	1:1:1711:A:H8	1.81	0.46
1:1:1850:G:H2'	1:1:1851:U:H6	1.81	0.46
1:1:2054:A:H2'	31:b:5:GLN:OE1	2.16	0.46
2:2:1147:C:O2	43:n:18:ARG:NH1	2.49	0.46
2:2:1323:G:H2'	2:2:1324:A:C8	2.51	0.46
3:3:74:U:C4	25:V:37:PRO:HG2	2.50	0.46
5:5:15:G:C2	5:5:59:A:C6	3.03	0.46
10:E:16:LEU:HA	10:E:19:GLU:HG2	1.98	0.46
31:b:53:LYS:HD2	31:b:55:ILE:O	2.16	0.46
53:x:40:ILE:HD11	53:x:74:PHE:HE2	1.81	0.46
1:1:174:U:H2'	1:1:175:G:C8	2.51	0.46
1:1:522:A:H2'	1:1:523:C:C6	2.51	0.46
1:1:1501:G:H4'	7:B:95:LEU:HD11	1.98	0.46
1:1:2029:G:N1	1:1:2033:A:OP2	2.37	0.46
2:2:707:U:H2'	2:2:708:C:C6	2.51	0.46
2:2:865:A:H2'	2:2:866:C:C6	2.51	0.46
11:F:35:ARG:NH2	11:F:71:LEU:HB3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Q:94:ILE:HA	20:Q:97:ASP:OD2	2.16	0.46
38:i:126:ASN:HD21	38:i:141:ASP:CG	2.24	0.46
42:m:93:PRO:HG3	42:m:125:ILE:HD13	1.98	0.46
1:1:88:G:O6	1:1:89:A:N6	2.49	0.45
1:1:121:G:H2'	1:1:122:G:H8	1.80	0.45
1:1:565:C:OP2	21:R:80:ARG:N	2.48	0.45
1:1:807:U:H2'	1:1:808:G:C8	2.51	0.45
1:1:2641:G:H5''	13:J:78:THR:HB	1.98	0.45
2:2:1130:A:N6	2:2:1144:G:H21	2.14	0.45
2:2:1375:A:OP1	41:l:25:LYS:NZ	2.46	0.45
3:3:73:A:N6	3:3:103:U:C2	2.84	0.45
15:L:63:LYS:HA	34:e:13:ARG:HG2	1.97	0.45
44:o:26:VAL:O	44:o:30:LYS:HG2	2.16	0.45
1:1:55:G:H2'	1:1:56:A:C8	2.51	0.45
1:1:291:G:C6	1:1:350:G:C6	3.04	0.45
1:1:357:C:H2'	1:1:358:U:C6	2.51	0.45
1:1:971:G:H2'	1:1:972:A:O4'	2.16	0.45
1:1:1024:G:C6	1:1:1025:G:C6	3.04	0.45
1:1:1030:C:N3	1:1:1124:G:N1	2.64	0.45
2:2:8:A:N7	38:i:206:LYS:HA	2.31	0.45
2:2:748:G:H2'	2:2:749:A:C8	2.52	0.45
18:O:35:ILE:HG21	18:O:102:ARG:HD2	1.98	0.45
35:f:14:CYS:SG	35:f:33:HIS:ND1	2.85	0.45
43:n:47:VAL:CG1	43:n:76:ALA:HB1	2.46	0.45
1:1:305:C:H2'	1:1:306:U:C6	2.51	0.45
1:1:480:A:O2'	1:1:498:G:N2	2.50	0.45
1:1:526:A:O2'	1:1:2043:C:O2	2.26	0.45
1:1:575:A:OP2	1:1:2055:C:N4	2.50	0.45
1:1:1130:U:N3	1:1:2025:C:OP1	2.45	0.45
1:1:1429:G:H2'	1:1:1430:G:C8	2.45	0.45
1:1:1518:C:H2'	1:1:1519:G:H8	1.80	0.45
1:1:1688:U:O2'	1:1:1700:A:N7	2.34	0.45
1:1:2286:G:H5''	1:1:2287:A:OP1	2.17	0.45
1:1:2290:G:H2'	1:1:2291:U:C6	2.52	0.45
1:1:2804:U:H2'	1:1:2805:C:C6	2.51	0.45
2:2:513:C:H2'	2:2:514:C:H6	1.80	0.45
2:2:523:A:H61	46:q:89:0TD:CG	2.28	0.45
2:2:634:C:H2'	2:2:635:A:H8	1.80	0.45
2:2:678:U:H2'	2:2:679:C:H6	1.81	0.45
2:2:704:A:C4	2:2:705:G:C8	3.05	0.45
3:3:101:A:H2'	3:3:102:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:35:ARG:HG2	11:F:35:ARG:HH11	1.81	0.45
37:h:111:LEU:HD22	37:h:146:ALA:HB2	1.99	0.45
44:o:53:ILE:HG22	48:s:85:ARG:HE	1.80	0.45
49:t:88:ARG:HD2	49:t:89:ARG:HH11	1.81	0.45
1:1:19:A:H2'	1:1:20:C:C6	2.51	0.45
1:1:1712:U:OP2	1:1:1713:A:O2'	2.27	0.45
1:1:1791:A:H4'	7:B:205:LEU:HB2	1.98	0.45
1:1:2320:U:H1'	1:1:2322:A:N7	2.32	0.45
2:2:110:C:O2'	50:u:25:ARG:O	2.33	0.45
2:2:113:G:H2'	2:2:114:U:H6	1.78	0.45
2:2:407:U:H2'	2:2:408:A:H8	1.82	0.45
2:2:409:U:OP2	38:i:22:LYS:HD2	2.16	0.45
2:2:1493:A:H1'	4:4:19:G:N3	2.31	0.45
5:5:11:C:H2'	5:5:12:G:H8	1.82	0.45
5:5:18:G:N2	5:5:57:A:C5	2.85	0.45
5:5:63:U:H2'	5:5:64:C:C6	2.51	0.45
11:F:10:VAL:HA	11:F:49:THR:HA	1.98	0.45
14:K:59:LYS:NZ	14:K:89:ASN:O	2.40	0.45
14:K:78:ARG:N	19:P:71:GLU:O	2.48	0.45
37:h:64:ILE:O	37:h:99:ALA:HA	2.17	0.45
45:p:34:ILE:HG12	45:p:70:CYS:SG	2.55	0.45
1:1:65:U:H2'	1:1:66:C:H6	1.81	0.45
1:1:1065:U:O4	1:1:1069:A:O2'	2.33	0.45
1:1:1322:A:O3'	22:S:84:ARG:NH2	2.48	0.45
1:1:1614:A:H61	22:S:88:ARG:H	1.64	0.45
1:1:2315:G:H2'	1:1:2316:G:H8	1.82	0.45
1:1:2385:C:H2'	1:1:2386:A:C8	2.51	0.45
1:1:2519:U:H5'	1:1:2567:G:N2	2.32	0.45
1:1:2836:U:H2'	1:1:2837:A:C8	2.50	0.45
2:2:123:U:H5''	2:2:311:C:O2'	2.17	0.45
2:2:579:A:H2'	2:2:580:C:H6	1.81	0.45
2:2:1437:A:H2'	2:2:1438:G:H8	1.81	0.45
3:3:49:C:OP1	18:O:102:ARG:N	2.49	0.45
3:3:62:C:H2'	3:3:63:C:H6	1.81	0.45
7:B:34:LEU:HD11	7:B:63:ARG:NH1	2.31	0.45
7:B:84:ASP:HB2	7:B:91:ILE:HG23	1.99	0.45
11:F:42:GLU:OE1	11:F:55:ARG:NH1	2.49	0.45
12:G:57:LYS:HD3	12:G:57:LYS:C	2.41	0.45
42:m:11:LEU:HG	42:m:75:ILE:HG13	1.99	0.45
44:o:19:ASP:OD1	44:o:72:ARG:NH2	2.49	0.45
46:q:29:GLN:HB3	46:q:81:LEU:HG	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:r:31:LYS:HB3	47:r:31:LYS:HE2	1.87	0.45
1:1:154:U:H2'	1:1:155:A:H8	1.80	0.45
1:1:287:G:H2'	1:1:288:U:C6	2.51	0.45
1:1:368:A:H2'	1:1:369:U:C6	2.52	0.45
1:1:419:U:H2'	1:1:420:C:C6	2.51	0.45
1:1:1297:C:H2'	1:1:1298:C:C6	2.51	0.45
1:1:2377:A:O2'	18:O:117:PHE:O	2.30	0.45
1:1:2415:G:H2'	1:1:2416:C:C6	2.52	0.45
2:2:175:C:H2'	2:2:176:C:C6	2.52	0.45
2:2:1328:C:H5''	47:r:28:THR:HG21	1.98	0.45
2:2:1351:U:H4'	41:l:33:ASP:OD1	2.16	0.45
3:3:74:U:C4	3:3:75:G:C5	3.05	0.45
10:E:36:LEU:HD21	10:E:99:PHE:CE2	2.52	0.45
14:K:7:MET:HE3	14:K:20:MET:HE3	1.98	0.45
24:U:53:ASN:O	24:U:53:ASN:ND2	2.47	0.45
43:n:116:VAL:HG21	44:o:62:ARG:HB3	1.98	0.45
48:s:24:ARG:HH11	48:s:51:LEU:HD23	1.81	0.45
1:1:627:A:H5''	15:L:78:ARG:NH2	2.32	0.45
1:1:1638:C:O2	1:1:2698:U:O2'	2.35	0.45
1:1:1789:A:H2'	1:1:1790:C:O4'	2.17	0.45
1:1:2467:C:O2	16:M:123:LYS:NZ	2.39	0.45
2:2:1014:A:C2	2:2:1219:A:H1'	2.52	0.45
2:2:1014:A:H2'	2:2:1015:G:C4	2.51	0.45
7:B:53:HIS:CE1	7:B:219:THR:HA	2.52	0.45
10:E:108:VAL:HG21	10:E:176:PRO:HG2	1.98	0.45
11:F:54:PRO:HG3	11:F:62:TRP:CE2	2.52	0.45
18:O:11:ALA:HB2	18:O:96:GLY:N	2.31	0.45
45:p:123:PRO:HD2	55:z:38:TYR:HD1	1.82	0.45
1:1:18:U:O4	1:1:19:A:N6	2.50	0.45
1:1:78:U:H2'	1:1:79:C:C6	2.52	0.45
1:1:79:C:O2'	1:1:346:A:N3	2.45	0.45
1:1:289:G:H2'	1:1:290:U:C6	2.51	0.45
1:1:753:A:H2'	1:1:754:U:C6	2.52	0.45
1:1:1085:A:N1	58:1:3367:HOH:O	2.36	0.45
1:1:1141:U:OP2	13:J:65:THR:OG1	2.29	0.45
1:1:1733:G:H2'	1:1:1734:G:C8	2.52	0.45
1:1:1853:A:N7	1:1:1889:A:N6	2.64	0.45
2:2:472:U:H2'	2:2:473:U:C6	2.52	0.45
2:2:1409:C:H2'	2:2:1410:A:H8	1.82	0.45
3:3:30:C:H2'	3:3:31:C:O4'	2.16	0.45
6:A:184:LYS:O	6:A:187:GLU:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:31:THR:O	18:O:102:ARG:NH1	2.50	0.45
31:b:12:LYS:HA	31:b:12:LYS:HD2	1.83	0.45
1:1:374:A:H4'	1:1:422:A:H2	1.81	0.45
1:1:743:A:OP1	8:C:135:GLY:HA2	2.17	0.45
1:1:1495:A:H2'	1:1:1496:A:C8	2.52	0.45
1:1:1858:A:H2'	1:1:1859:U:O4'	2.17	0.45
1:1:2114:A:H2'	1:1:2167:U:H5'	1.99	0.45
1:1:2387:U:OP1	26:W:55:ARG:NH2	2.50	0.45
1:1:2508:G:H2'	1:1:2509:G:H8	1.81	0.45
1:1:2515:C:H2'	1:1:2516:A:C8	2.47	0.45
1:1:2686:G:H2'	1:1:2687:U:C6	2.51	0.45
1:1:2751:G:OP1	1:1:2751:G:N2	2.50	0.45
2:2:542:G:H2'	2:2:543:U:H6	1.82	0.45
2:2:1287:A:H2'	2:2:1288:A:H8	1.82	0.45
5:5:24:G:H2'	5:5:25:C:C6	2.52	0.45
9:D:148:ILE:HB	9:D:169:VAL:HG12	1.98	0.45
25:V:61:LEU:HB2	25:V:72:VAL:O	2.16	0.45
29:Z:24:LEU:HD11	29:Z:54:MET:SD	2.56	0.45
41:l:30:LEU:HD23	41:l:43:VAL:HB	1.98	0.45
1:1:223:A:N6	1:1:422:A:N1	2.65	0.45
1:1:302:C:H2'	1:1:303:G:C8	2.48	0.45
1:1:499:U:H2'	1:1:500:G:H8	1.82	0.45
1:1:559:G:N2	20:Q:49:ASP:OD2	2.30	0.45
1:1:882:G:O6	1:1:894:U:C4	2.70	0.45
1:1:1298:C:H2'	1:1:1299:G:O4'	2.17	0.45
1:1:1431:A:H2'	1:1:1432:G:H8	1.81	0.45
1:1:1721:G:O2'	1:1:1739:A:N6	2.50	0.45
1:1:2257:U:H2'	1:1:2258:C:C6	2.52	0.45
1:1:2488:G:H2'	1:1:2489:U:C6	2.52	0.45
1:1:2645:G:OP2	1:1:2645:G:N2	2.33	0.45
1:1:2717:C:O2'	19:P:94:LYS:NZ	2.32	0.45
2:2:323:U:H2'	2:2:324:G:O4'	2.16	0.45
2:2:505:G:H2'	2:2:506:G:H8	1.82	0.45
2:2:939:G:O2'	2:2:1375:A:N3	2.47	0.45
5:5:15:G:N2	5:5:59:A:C5	2.85	0.45
1:1:6:A:H2'	1:1:7:G:C8	2.52	0.44
1:1:404:A:H1'	1:1:405:U:OP2	2.17	0.44
1:1:1296:G:OP1	1:1:2709:G:O2'	2.27	0.44
1:1:1315:C:O2'	1:1:1392:A:H1'	2.16	0.44
1:1:1604:C:H2'	1:1:1605:C:C6	2.51	0.44
1:1:1726:C:H2'	1:1:1727:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2090:A:N6	1:1:2230:G:O6	2.50	0.44
1:1:2284:A:HO2'	1:1:2288:A:N6	2.16	0.44
1:1:2466:C:C2	1:1:2485:G:C2	3.05	0.44
2:2:197:A:N1	2:2:220:G:O2'	2.50	0.44
2:2:235:C:H2'	2:2:236:A:H8	1.82	0.44
2:2:509:A:H5'	38:i:52:GLY:HA2	1.99	0.44
2:2:559:A:H4'	2:2:560:A:H3'	1.98	0.44
2:2:570:G:H5'	2:2:820:U:O4'	2.17	0.44
2:2:740:U:H2'	2:2:741:G:H8	1.82	0.44
2:2:1367:C:OP2	43:n:114:LYS:NZ	2.47	0.44
3:3:75:G:N2	25:V:29:ILE:HG21	2.32	0.44
5:5:15:G:H2'	5:5:59:A:N1	2.32	0.44
19:P:68:GLU:OE1	19:P:68:GLU:N	2.50	0.44
41:l:93:PRO:HA	41:l:96:ARG:CD	2.47	0.44
1:1:1071:G:O2'	1:1:1072:C:O4'	2.24	0.44
1:1:1299:G:O6	1:1:1639:C:H5''	2.18	0.44
1:1:1387:A:H2'	1:1:1388:G:C8	2.51	0.44
1:1:2081:U:H3	1:1:2239:G:H1	1.65	0.44
1:1:2728:U:O2'	1:1:2729:G:H8	2.01	0.44
2:2:763:G:H2'	2:2:764:C:C6	2.53	0.44
2:2:1356:G:H2'	2:2:1357:A:H8	1.82	0.44
5:5:59:A:O2'	5:5:60:U:P	2.74	0.44
44:o:6:ILE:HD12	44:o:76:ILE:HD11	1.99	0.44
44:o:85:ASP:O	44:o:89:ARG:HG2	2.18	0.44
47:r:66:GLU:HB2	47:r:70:ARG:HE	1.81	0.44
1:1:58:G:H2'	1:1:59:U:C6	2.52	0.44
1:1:239:C:HO2'	1:1:622:G:HO2'	1.63	0.44
1:1:299:A:OP1	24:U:97:LYS:NZ	2.35	0.44
1:1:632:A:H2'	1:1:633:A:C8	2.52	0.44
1:1:679:C:H2'	1:1:680:C:H6	1.82	0.44
1:1:955:PSU:OP1	16:M:86:LYS:NZ	2.41	0.44
1:1:994:C:OP2	20:Q:54:LYS:NZ	2.36	0.44
1:1:1079:C:H2'	1:1:1080:A:H8	1.81	0.44
1:1:1245:G:O6	1:1:1246:A:N6	2.51	0.44
1:1:1581:G:H2'	1:1:1582:C:C6	2.52	0.44
2:2:318:G:C6	2:2:336:A:C6	3.05	0.44
2:2:750:C:H2'	2:2:751:U:C6	2.52	0.44
21:R:15:SER:H	21:R:18:GLN:NE2	2.11	0.44
42:m:51:VAL:HA	42:m:58:GLU:O	2.17	0.44
43:n:65:ILE:HG21	43:n:79:ILE:HG23	1.99	0.44
49:t:55:GLY:O	49:t:59:MET:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:126:A:H61	33:d:42:LEU:HB3	1.82	0.44
1:1:392:U:H2'	1:1:393:C:C6	2.53	0.44
1:1:593:U:H2'	1:1:594:U:C6	2.52	0.44
1:1:623:C:H2'	1:1:624:C:C6	2.52	0.44
1:1:817:C:O2'	1:1:839:U:H5''	2.17	0.44
1:1:888:C:N4	47:r:92:ARG:HG2	2.32	0.44
1:1:929:U:H1'	29:Z:26:GLY:O	2.16	0.44
1:1:1030:C:O2	35:f:37:GLN:NE2	2.51	0.44
1:1:1310:G:N2	1:1:1313:U:C4	2.85	0.44
1:1:1747:U:H2'	1:1:1748:C:C6	2.52	0.44
1:1:1853:A:N3	1:1:2233:U:O2'	2.43	0.44
2:2:144:G:N1	2:2:179:A:N7	2.66	0.44
2:2:411:A:H1'	2:2:413:G:H5''	2.00	0.44
2:2:458:U:O2	2:2:474:G:N2	2.35	0.44
2:2:777:A:H2'	2:2:778:G:C8	2.53	0.44
2:2:1095:U:H2'	2:2:1096:C:C6	2.52	0.44
3:3:78:A:N6	3:3:98:G:O2'	2.49	0.44
7:B:107:PRO:HD2	7:B:110:LEU:HD22	1.98	0.44
36:g:77:SER:OG	36:g:93:ASN:HB2	2.18	0.44
40:k:81:ASN:HD21	40:k:83:ALA:HB3	1.82	0.44
44:o:14:ASP:HB3	44:o:17:LEU:HB3	2.00	0.44
46:q:81:LEU:HB3	46:q:98:VAL:HG22	2.00	0.44
48:s:49:GLN:NE2	53:x:11:ILE:O	2.46	0.44
1:1:479:A:O2'	1:1:481:G:H5'	2.17	0.44
1:1:623:C:H2'	1:1:624:C:H6	1.82	0.44
1:1:1142:A:C4	1:1:1144:A:N7	2.86	0.44
1:1:1201:U:N3	1:1:1202:G:N7	2.66	0.44
1:1:1837:C:C2	1:1:1904:G:N2	2.85	0.44
1:1:2247:A:H2'	1:1:2248:C:H6	1.82	0.44
1:1:2566:A:N1	14:K:28:SER:OG	2.39	0.44
2:2:1250:A:H2	2:2:1370:G:H1'	1.82	0.44
11:F:175:LYS:HD2	11:F:175:LYS:HA	1.77	0.44
46:q:49:LEU:HD23	46:q:49:LEU:HA	1.50	0.44
1:1:46:G:H2'	1:1:47:C:C6	2.52	0.44
1:1:210:C:H2'	1:1:211:C:C6	2.53	0.44
1:1:418:C:H2'	1:1:419:U:H6	1.83	0.44
1:1:532:A:H2	1:1:2019:A:H2	1.64	0.44
1:1:1039:A:C2	1:1:1116:G:C6	3.04	0.44
1:1:1152:C:H2'	1:1:1153:C:C6	2.52	0.44
1:1:2096:C:H2'	1:1:2097:A:H8	1.83	0.44
1:1:2140:G:H2'	1:1:2141:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:176:C:H2'	2:2:177:G:N3	2.33	0.44
2:2:285:C:H2'	2:2:286:C:H6	1.83	0.44
2:2:613:C:H2'	2:2:614:C:H6	1.83	0.44
9:D:176:ASP:OD1	9:D:176:ASP:N	2.50	0.44
21:R:6:GLN:HG3	21:R:11:GLN:HG2	2.00	0.44
21:R:79:ARG:O	21:R:80:ARG:HG2	2.16	0.44
45:p:34:ILE:HG21	45:p:74:VAL:HG21	2.00	0.44
1:1:479:A:H4'	1:1:480:A:H5'	2.00	0.44
1:1:534:U:O2'	20:Q:49:ASP:OD1	2.35	0.44
1:1:594:U:H2'	1:1:595:C:C6	2.53	0.44
1:1:858:G:H1	1:1:920:A:H61	1.66	0.44
1:1:882:G:H1	1:1:894:U:H3	1.65	0.44
1:1:1117:C:H2'	1:1:1118:C:H6	1.83	0.44
1:1:1353:A:C8	1:1:1354:A:N7	2.85	0.44
1:1:1385:A:H1'	1:1:1386:C:C6	2.53	0.44
1:1:1392:A:H61	23:T:18:GLU:HG3	1.83	0.44
2:2:35:G:N3	46:q:115:SER:HB2	2.32	0.44
2:2:102:G:H2'	2:2:103:U:C6	2.52	0.44
2:2:180:U:C2'	2:2:181:A:H5'	2.47	0.44
2:2:222:C:H2'	2:2:223:A:C8	2.48	0.44
2:2:375:U:O2'	50:u:6:LEU:O	2.35	0.44
2:2:604:G:H2'	2:2:605:U:O4'	2.17	0.44
2:2:1042:A:H2'	2:2:1043:G:O4'	2.18	0.44
8:C:152:PRO:HG3	8:C:156:PHE:CZ	2.53	0.44
9:D:146:VAL:HG21	9:D:187:VAL:HG13	1.99	0.44
9:D:149:ILE:HG22	9:D:187:VAL:O	2.18	0.44
17:N:96:ARG:HD3	17:N:98:LEU:HD21	1.98	0.44
22:S:9:HIS:H	22:S:102:HIS:CE1	2.36	0.44
37:h:184:TYR:HE1	37:h:199:LYS:HB3	1.83	0.44
54:y:76:LYS:O	54:y:80:THR:OG1	2.32	0.44
55:z:11:PRO:HB2	55:z:14:VAL:HG22	1.99	0.44
1:1:6:A:H2'	1:1:7:G:H8	1.83	0.44
1:1:259:G:H2'	1:1:260:G:H8	1.83	0.44
1:1:623:C:C2	1:1:624:C:C5	3.06	0.44
1:1:831:G:O2'	15:L:38:GLN:OE1	2.28	0.44
1:1:1600:C:H2'	1:1:1601:G:H8	1.82	0.44
1:1:1635:A:H2'	1:1:1636:U:O4'	2.18	0.44
1:1:1654:A:O2'	8:C:118:PHE:O	2.28	0.44
1:1:1733:G:H2'	1:1:1734:G:H8	1.83	0.44
1:1:2171:A:O2'	1:1:2173:A:OP1	2.32	0.44
2:2:75:G:H2'	2:2:76:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:424:G:H2'	2:2:425:G:H8	1.82	0.44
2:2:1083:U:H3'	2:2:1084:G:C8	2.52	0.44
2:2:1354:U:H2'	2:2:1355:G:H8	1.81	0.44
15:L:132:ARG:O	15:L:136:GLU:HG2	2.18	0.44
42:m:105:SER:HB2	42:m:126:ILE:HD11	1.99	0.44
43:n:56:ASP:N	43:n:56:ASP:OD1	2.48	0.44
43:n:84:THR:HG21	43:n:104:VAL:HA	2.00	0.44
51:v:8:LEU:O	51:v:60:GLU:HA	2.18	0.44
55:z:32:VAL:O	55:z:36:GLU:HG2	2.18	0.44
1:1:895:U:O4	1:1:897:C:N4	2.51	0.44
1:1:979:A:H2'	1:1:982:C:H42	1.82	0.44
1:1:2243:U:H2'	1:1:2244:U:C6	2.52	0.44
1:1:2539:C:H5'	35:f:3:VAL:HG21	2.00	0.44
2:2:254:G:O2'	51:v:18:GLU:O	2.35	0.44
2:2:355:C:H1'	2:2:388:G:H1'	1.99	0.44
2:2:859:G:H2'	2:2:860:A:C8	2.53	0.44
2:2:1140:C:HO2'	2:2:1141:C:H6	1.64	0.44
2:2:1193:G:O6	37:h:3:GLN:NE2	2.51	0.44
2:2:1321:U:O4	53:x:36:ARG:NH1	2.50	0.44
7:B:17:VAL:HB	7:B:204:VAL:HG22	1.99	0.44
16:M:35:ALA:HA	16:M:128:THR:HG22	1.99	0.44
1:1:363:G:H2'	1:1:364:C:C6	2.52	0.43
1:1:499:U:C2	1:1:500:G:C8	3.06	0.43
1:1:577:G:H2'	1:1:578:G:C8	2.53	0.43
1:1:687:C:H5''	33:d:2:LYS:HE2	2.00	0.43
1:1:1201:U:H2'	1:1:1202:G:C8	2.49	0.43
1:1:1351:C:HO2'	1:1:1571:A:HO2'	1.65	0.43
1:1:1853:A:H2'	1:1:1854:A:C8	2.53	0.43
1:1:2417:C:H2'	1:1:2418:A:H8	1.83	0.43
1:1:2425:A:H4'	1:1:2426:A:O5'	2.18	0.43
1:1:2557:G:H2'	1:1:2558:C:H6	1.83	0.43
1:1:2745:C:H2'	1:1:2746:U:C6	2.53	0.43
2:2:323:U:O4	2:2:327:A:N7	2.51	0.43
2:2:563:A:H2'	2:2:567:G:C8	2.53	0.43
2:2:1347:G:N2	2:2:1374:A:OP2	2.40	0.43
2:2:1401:G:O6	2:2:1504:G:N2	2.51	0.43
5:5:19:G:H3'	5:5:20:U:C5	2.49	0.43
5:5:54:U:C2'	5:5:55:U:H5'	2.47	0.43
10:E:108:VAL:HG12	10:E:109:PRO:HD3	1.98	0.43
14:K:8:LEU:HB2	14:K:19:VAL:HG23	2.00	0.43
16:M:39:GLY:HA3	16:M:126:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:2:TYR:CE1	21:R:42:ALA:HB3	2.52	0.43
36:g:73:LYS:C	36:g:75:ALA:H	2.26	0.43
36:g:166:ALA:HB1	36:g:173:ILE:HD13	2.00	0.43
41:l:78:ARG:NH1	58:l:302:HOH:O	2.51	0.43
44:o:41:PRO:HA	44:o:72:ARG:HD3	2.00	0.43
1:1:10:A:H2'	1:1:11:C:O4'	2.18	0.43
1:1:271:G:N1	1:1:367:G:N7	2.66	0.43
1:1:592:A:C2	34:e:4:ILE:HD11	2.53	0.43
1:1:1600:C:H2'	1:1:1601:G:C8	2.52	0.43
1:1:2636:C:H2'	1:1:2637:U:C6	2.52	0.43
2:2:505:G:H2'	2:2:506:G:C8	2.53	0.43
2:2:591:U:P	42:m:31:LYS:HD3	2.58	0.43
2:2:908:A:H2'	2:2:909:A:H8	1.82	0.43
2:2:1268:G:O2'	2:2:1326:U:O2'	2.26	0.43
2:2:1315:U:H2'	2:2:1316:G:O4'	2.18	0.43
3:3:71:C:H2'	3:3:72:G:O4'	2.18	0.43
38:i:119:SER:HA	38:i:131:ASN:O	2.18	0.43
47:r:16:VAL:HA	47:r:30:SER:OG	2.18	0.43
1:1:644:A:C2	1:1:2369:A:H1'	2.53	0.43
1:1:1219:U:H2'	1:1:1220:G:H8	1.83	0.43
1:1:2821:A:OP2	8:C:115:GLY:N	2.31	0.43
2:2:436:C:H2'	2:2:437:U:H6	1.82	0.43
2:2:887:G:H2'	2:2:888:G:O4'	2.18	0.43
2:2:1319:A:O2'	2:2:1323:G:N7	2.45	0.43
2:2:1355:G:H2'	2:2:1356:G:C8	2.53	0.43
3:3:2:G:H2'	3:3:3:C:C6	2.53	0.43
3:3:70:C:H2'	3:3:71:C:C6	2.53	0.43
7:B:154:LEU:HD12	7:B:176:LEU:HD22	2.00	0.43
13:J:55:ILE:HA	13:J:123:LYS:O	2.19	0.43
21:R:27:ILE:HG22	21:R:31:GLU:HB3	1.99	0.43
30:a:56:ARG:HD2	30:a:56:ARG:HA	1.71	0.43
34:e:29:LEU:HD12	34:e:33:LEU:HD21	2.00	0.43
34:e:32:ILE:O	34:e:33:LEU:HG	2.19	0.43
37:h:150:LYS:HB3	37:h:169:ARG:HG3	2.00	0.43
39:j:52:LYS:HB3	39:j:52:LYS:HE3	1.91	0.43
40:k:15:SER:O	40:k:18:VAL:HG12	2.19	0.43
40:k:29:ILE:HD11	40:k:66:ALA:CB	2.47	0.43
46:q:4:VAL:HG23	51:v:34:TYR:HB3	1.99	0.43
1:1:500:G:H1'	1:1:505:A:H61	1.83	0.43
1:1:561:G:O2'	20:Q:45:TYR:OH	2.20	0.43
1:1:1011:G:C6	1:1:1151:A:C6	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1197:G:C2	1:1:1198:U:C5	3.07	0.43
1:1:1199:U:H2'	1:1:1200:C:C6	2.54	0.43
1:1:1715:G:N2	1:1:1744:A:OP2	2.50	0.43
1:1:2751:G:H5''	1:1:2752:C:H5	1.84	0.43
2:2:647:C:H2'	2:2:648:A:H8	1.82	0.43
2:2:1017:U:O2'	2:2:1018:G:H8	2.01	0.43
3:3:9:G:OP1	18:O:25:ARG:NH2	2.51	0.43
5:5:10:G:H2'	5:5:11:C:C6	2.54	0.43
5:5:61:C:H2'	5:5:62:C:C6	2.54	0.43
8:C:8:LYS:NZ	8:C:195:GLY:O	2.43	0.43
16:M:54:THR:HA	16:M:57:VAL:HG12	2.01	0.43
19:P:62:ARG:HB2	19:P:71:GLU:HG2	2.00	0.43
20:Q:27:ALA:O	20:Q:31:VAL:HG22	2.19	0.43
22:S:83:LYS:HD2	22:S:95:ARG:NH1	2.33	0.43
1:1:138:U:H2'	1:1:140:C:N3	2.34	0.43
1:1:307:G:N2	1:1:309:A:H3'	2.33	0.43
1:1:322:A:H5'	1:1:340:A:H1'	2.00	0.43
1:1:330:A:N7	1:1:1210:G:O2'	2.44	0.43
1:1:681:G:H2'	1:1:682:G:H8	1.83	0.43
1:1:864:G:H2'	1:1:865:C:C6	2.53	0.43
1:1:1501:G:P	7:B:101:ARG:HH22	2.40	0.43
1:1:2033:A:O2'	1:1:2035:G:OP2	2.26	0.43
1:1:2118:U:O4	1:1:2148:G:N2	2.51	0.43
1:1:2134:A:O2'	1:1:2159:G:N3	2.49	0.43
1:1:2461:A:H2'	1:1:2462:C:C6	2.54	0.43
1:1:2557:G:H2'	1:1:2558:C:C6	2.53	0.43
1:1:2837:A:H2'	1:1:2838:G:H8	1.83	0.43
2:2:3:A:H5''	2:2:4:U:O4'	2.19	0.43
2:2:337:G:C2	2:2:338:A:C5	3.06	0.43
2:2:552:U:H2'	2:2:553:A:C8	2.53	0.43
2:2:731:G:H2'	2:2:732:C:C6	2.54	0.43
2:2:1126:U:OP1	44:o:7:ARG:NH2	2.51	0.43
2:2:1313:U:H2'	2:2:1314:C:C6	2.53	0.43
8:C:13:ARG:HD2	8:C:15:PHE:CZ	2.53	0.43
13:J:96:ARG:NH1	13:J:99:ARG:HD3	2.33	0.43
38:i:198:HIS:HA	38:i:201:VAL:HG12	2.00	0.43
47:r:73:ILE:O	47:r:77:ILE:HG13	2.19	0.43
51:v:27:ARG:N	51:v:40:ARG:O	2.41	0.43
52:w:11:CYS:SG	52:w:14:THR:HG23	2.58	0.43
1:1:20:C:H2'	1:1:21:A:C8	2.52	0.43
1:1:438:G:H2'	1:1:439:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:820:A:H2	1:1:943:A:H4'	1.84	0.43
1:1:1030:C:N4	1:1:1124:G:O6	2.52	0.43
1:1:1365:A:P	27:X:28:ARG:HH22	2.41	0.43
1:1:1541:C:H2'	1:1:1542:U:C6	2.53	0.43
1:1:1727:C:N3	1:1:1734:G:N1	2.66	0.43
1:1:1825:U:H2'	1:1:1826:G:C8	2.53	0.43
1:1:1910:G:C2	1:1:1921:G:C2	3.07	0.43
1:1:2284:A:O2'	1:1:2288:A:N6	2.52	0.43
1:1:2537:U:H2'	1:1:2538:C:C6	2.53	0.43
2:2:102:G:H2'	2:2:103:U:H6	1.84	0.43
2:2:953:G:C6	2:2:1229:A:C6	3.07	0.43
2:2:1135:U:O2'	2:2:1136:C:O2	2.22	0.43
10:E:101:GLU:O	10:E:105:THR:HG22	2.18	0.43
11:F:39:ASP:OD1	11:F:58:TYR:OH	2.20	0.43
14:K:75:SER:HB2	19:P:73:VAL:O	2.19	0.43
15:L:79:LEU:HG	15:L:111:ILE:O	2.18	0.43
17:N:35:LYS:HB3	17:N:35:LYS:HE2	1.74	0.43
29:Z:45:ARG:HD3	29:Z:45:ARG:HA	1.85	0.43
34:e:31:HIS:CD2	34:e:32:ILE:HG22	2.53	0.43
35:f:18:LYS:HB2	35:f:18:LYS:HE3	1.83	0.43
37:h:91:VAL:HA	37:h:94:ILE:HG12	1.99	0.43
47:r:43:VAL:HG21	47:r:48:LEU:HD21	2.01	0.43
55:z:10:GLU:OE1	55:z:14:VAL:HG23	2.18	0.43
1:1:275:C:H3'	1:1:276:U:H5''	2.01	0.43
1:1:290:U:H3	1:1:350:G:H1	1.67	0.43
1:1:910:A:H62	16:M:13:HIS:N	2.17	0.43
1:1:1219:U:H2'	1:1:1220:G:C8	2.53	0.43
1:1:2685:G:H2'	1:1:2686:G:H8	1.84	0.43
2:2:158:G:H2'	2:2:159:G:O4'	2.18	0.43
2:2:236:A:H2'	2:2:237:G:C8	2.54	0.43
2:2:376:G:H5''	50:u:5:ARG:HB2	2.00	0.43
6:A:201:PRO:HG2	6:A:204:ALA:HB2	2.01	0.43
24:U:38:GLY:HA2	24:U:41:LEU:HD21	2.00	0.43
1:1:24:G:H2'	1:1:25:U:C6	2.53	0.43
1:1:172:A:H2'	1:1:173:A:C8	2.53	0.43
1:1:192:C:O2'	1:1:802:A:N3	2.45	0.43
1:1:577:G:O2'	1:1:1254:A:OP1	2.37	0.43
1:1:624:C:H2'	1:1:625:G:C8	2.54	0.43
1:1:888:C:H2'	1:1:889:C:C6	2.54	0.43
1:1:976:G:O2'	1:1:1155:A:O2'	2.18	0.43
1:1:1352:U:H1'	1:1:1570:A:H2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1754:A:N1	1:1:2716:C:O2'	2.52	0.43
1:1:1907:G:O6	1:1:1924:C:N4	2.52	0.43
1:1:2588:G:C6	1:1:2607:G:C2	3.07	0.43
2:2:195:A:H1'	2:2:222:C:O2'	2.18	0.43
2:2:470:C:H2'	2:2:471:U:C6	2.54	0.43
2:2:838:G:C6	2:2:849:G:C6	3.07	0.43
2:2:1391:U:H2'	2:2:1392:G:H8	1.82	0.43
2:2:1476:A:H2'	2:2:1477:U:C6	2.53	0.43
2:2:1488:G:H2'	2:2:1489:G:C8	2.54	0.43
20:Q:61:TRP:CH2	20:Q:93:LYS:HB2	2.54	0.43
20:Q:89:GLU:O	21:R:11:GLN:NE2	2.40	0.43
27:X:17:ASN:OD1	27:X:27:ARG:HD2	2.19	0.43
32:c:15:ALA:HB2	32:c:47:VAL:HG21	2.01	0.43
37:h:6:HIS:CD2	48:s:89:MET:HB3	2.54	0.43
40:k:49:TYR:O	40:k:51:ILE:HD12	2.19	0.43
42:m:10:MET:HE1	42:m:33:LYS:HA	2.01	0.43
1:1:156:A:H2'	1:1:157:C:C6	2.54	0.43
1:1:705:A:H4'	7:B:7:LYS:HD2	2.00	0.43
1:1:1353:A:H2'	1:1:1354:A:C8	2.54	0.43
1:1:1645:G:H5''	1:1:1646:C:O4'	2.19	0.43
1:1:1656:C:H2'	1:1:1657:U:H6	1.84	0.43
1:1:1668:A:N1	1:1:1676:A:N6	2.67	0.43
1:1:1882:U:H2'	1:1:1883:U:C6	2.53	0.43
1:1:2002:G:OP2	17:N:9:GLN:NE2	2.52	0.43
1:1:2441:U:OP2	1:1:2586:U:O2'	2.34	0.43
1:1:2780:G:N1	13:J:102:GLU:OE2	2.44	0.43
1:1:2845:U:H2'	1:1:2846:G:H8	1.84	0.43
5:5:10:G:N2	5:5:26:A:H1'	2.34	0.43
16:M:40:ARG:HB2	16:M:93:VAL:CG2	2.49	0.43
22:S:17:VAL:HA	22:S:43:ALA:HB1	2.00	0.43
32:c:15:ALA:HB2	32:c:47:VAL:HG11	2.01	0.43
33:d:46:LYS:HE2	33:d:46:LYS:HB2	1.89	0.43
1:1:177:G:H3'	1:1:178:G:H8	1.84	0.43
1:1:581:C:P	20:Q:33:ARG:HG3	2.59	0.43
1:1:679:C:H2'	1:1:680:C:C6	2.53	0.43
1:1:926:G:H2'	1:1:927:A:C8	2.52	0.43
1:1:1043:C:H2'	1:1:1044:C:O4'	2.19	0.43
1:1:1209:U:H2'	1:1:1210:G:H21	1.83	0.43
1:1:1339:G:OP1	23:T:82:LYS:NZ	2.48	0.43
1:1:2485:G:H5''	16:M:45:GLN:NE2	2.34	0.43
1:1:2723:C:OP1	8:C:114:LYS:NZ	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:45:G:H2'	2:2:46:G:H8	1.84	0.43
11:F:9:VAL:HG11	11:F:73:ASN:HB2	2.00	0.43
16:M:5:LYS:NZ	58:M:301:HOH:O	2.51	0.43
39:j:37:THR:HG22	39:j:63:ALA:HB1	2.01	0.43
1:1:274:C:N4	1:1:363:G:O6	2.52	0.42
1:1:573:U:O2'	1:1:575:A:OP1	2.28	0.42
1:1:666:A:H2'	1:1:667:U:C6	2.54	0.42
1:1:825:A:H2'	1:1:826:U:O4'	2.19	0.42
1:1:872:U:H2'	1:1:873:C:C6	2.54	0.42
1:1:954:G:O3'	16:M:13:HIS:ND1	2.52	0.42
1:1:1707:G:C8	1:1:1756:G:C5	3.07	0.42
1:1:1821:A:H2'	1:1:1822:C:C6	2.54	0.42
1:1:1996:C:P	14:K:31:ARG:HH21	2.41	0.42
1:1:2399:G:C6	1:1:2418:A:C6	3.07	0.42
1:1:2399:G:O6	1:1:2418:A:N6	2.52	0.42
1:1:2552:OMU:O5'	1:1:2552:OMU:H6	2.19	0.42
1:1:2559:C:H2'	1:1:2560:A:H8	1.84	0.42
1:1:2716:C:H2'	1:1:2717:C:C6	2.54	0.42
2:2:34:C:H2'	2:2:35:G:C8	2.51	0.42
2:2:216:U:H2'	2:2:217:C:H6	1.83	0.42
2:2:676:A:H2'	2:2:677:U:C6	2.53	0.42
2:2:736:C:H2'	2:2:737:C:C6	2.53	0.42
2:2:922:G:H2'	2:2:923:A:C8	2.53	0.42
2:2:1250:A:H4'	43:n:69:GLY:HA2	2.01	0.42
2:2:1258:G:H2'	2:2:1259:C:C6	2.54	0.42
2:2:1313:U:H2'	2:2:1314:C:H6	1.83	0.42
36:g:66:LYS:N	36:g:159:ASP:OD2	2.39	0.42
38:i:167:LYS:HE2	38:i:167:LYS:HB2	1.91	0.42
44:o:28:THR:HG21	44:o:90:LEU:HD22	2.02	0.42
1:1:48:G:H22	1:1:177:G:P	2.41	0.42
1:1:102:U:C4	28:Y:4:LYS:HE2	2.54	0.42
1:1:225:C:H2'	1:1:226:A:O4'	2.19	0.42
1:1:592:A:H2	34:e:4:ILE:HD11	1.83	0.42
1:1:1266:G:O2'	1:1:2012:G:O6	2.36	0.42
1:1:1447:C:O2'	1:1:1544:A:N3	2.47	0.42
1:1:1663:G:O6	1:1:1998:A:N6	2.52	0.42
1:1:1914:C:H2'	1:1:1915:U:C6	2.54	0.42
2:2:285:C:H2'	2:2:286:C:C6	2.54	0.42
2:2:313:A:H2'	2:2:314:C:C6	2.54	0.42
2:2:389:A:H3'	2:2:390:U:H6	1.84	0.42
2:2:507:C:OP2	2:2:508:U:O2'	2.24	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1236:A:H2'	2:2:1237:C:C6	2.53	0.42
2:2:1326:U:H2'	2:2:1327:C:C6	2.54	0.42
6:A:175:ILE:HD12	6:A:189:LEU:HG	2.02	0.42
9:D:130:LYS:HA	9:D:130:LYS:HD2	1.89	0.42
9:D:193:VAL:O	9:D:197:GLU:HG3	2.19	0.42
30:a:37:CYS:N	30:a:40:CYS:SG	2.83	0.42
30:a:64:PHE:HE1	30:a:66:ILE:HD13	1.84	0.42
36:g:12:ALA:HA	36:g:208:ARG:HE	1.84	0.42
41:l:131:LYS:HA	41:l:131:LYS:HD2	1.80	0.42
43:n:43:THR:O	43:n:46:MET:HG2	2.18	0.42
46:q:116:LYS:HE3	46:q:116:LYS:HB3	1.87	0.42
48:s:47:LYS:O	48:s:50:THR:OG1	2.35	0.42
1:1:1297:C:OP1	1:1:2710:C:H4'	2.19	0.42
1:1:1469:A:H2'	1:1:1470:A:C8	2.52	0.42
1:1:1518:C:H2'	1:1:1519:G:C8	2.54	0.42
1:1:2230:G:H2'	1:1:2231:U:C6	2.54	0.42
1:1:2820:A:N1	8:C:197:THR:HB	2.35	0.42
2:2:186:C:H2'	2:2:187:G:O4'	2.20	0.42
2:2:438:U:O2'	2:2:439:U:OP2	2.36	0.42
4:4:15:C:H2'	4:4:16:C:C6	2.53	0.42
5:5:3:G:C8	5:5:4:C:C5	3.07	0.42
9:D:196:VAL:HA	9:D:199:MET:HG2	2.00	0.42
12:G:101:ASP:OD1	12:G:102:ALA:N	2.53	0.42
16:M:38:ARG:HB2	16:M:98:PRO:HD3	2.01	0.42
28:Y:56:LEU:HD23	28:Y:56:LEU:HA	1.85	0.42
34:e:52:LYS:HA	34:e:55:LEU:HD12	2.02	0.42
37:h:5:VAL:HG11	37:h:10:ILE:HD12	2.01	0.42
37:h:71:ALA:HB1	37:h:109:PRO:HB3	2.00	0.42
39:j:156:LYS:HD2	42:m:71:VAL:HA	2.01	0.42
43:n:115:LYS:HB2	43:n:118:LEU:HD12	2.00	0.42
49:t:70:LEU:HD12	49:t:70:LEU:HA	1.85	0.42
51:v:22:VAL:HG12	51:v:45:HIS:CD2	2.55	0.42
1:1:84:A:N6	1:1:101:A:H8	2.17	0.42
1:1:438:G:H2'	1:1:439:A:H8	1.84	0.42
1:1:1105:U:H2'	1:1:1106:G:C8	2.54	0.42
1:1:1174:U:H4'	1:1:1177:G:N1	2.34	0.42
1:1:1901:A:OP2	7:B:253:LYS:NZ	2.36	0.42
1:1:2538:C:H2'	1:1:2539:C:H6	1.84	0.42
2:2:21:G:H5'	2:2:573:A:H61	1.83	0.42
2:2:212:G:C4	2:2:213:G:C8	3.07	0.42
2:2:306:A:N6	58:2:1864:HOH:O	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:859:G:H2'	2:2:860:A:H8	1.84	0.42
2:2:958:A:N1	53:x:55:ARG:N	2.68	0.42
2:2:1115:U:H2'	2:2:1116:U:C6	2.54	0.42
2:2:1121:U:H2'	2:2:1122:U:C6	2.55	0.42
22:S:76:VAL:HG22	22:S:103:ILE:HG23	2.01	0.42
38:i:76:TYR:HA	38:i:90:LEU:HD12	2.00	0.42
40:k:25:TYR:CZ	40:k:78:PHE:HE1	2.36	0.42
41:l:40:GLU:O	41:l:44:TYR:HD2	2.02	0.42
1:1:61:C:H5'	58:Y:102:HOH:O	2.20	0.42
1:1:784:G:H5'	1:1:785:G:OP1	2.19	0.42
1:1:1047:G:H21	1:1:1111:A:N6	2.09	0.42
1:1:1204:A:O4'	1:1:1206:G:C8	2.72	0.42
1:1:1658:C:OP1	8:C:140:HIS:NE2	2.42	0.42
1:1:2070:A:H2'	1:1:2071:A:H8	1.84	0.42
1:1:2078:C:H2'	1:1:2079:U:C6	2.54	0.42
1:1:2188:U:C4	1:1:2189:U:C4	3.07	0.42
1:1:2373:G:H2'	1:1:2374:C:C6	2.54	0.42
1:1:2626:C:H2'	1:1:2627:G:C8	2.54	0.42
1:1:2636:C:H2'	1:1:2637:U:H6	1.83	0.42
2:2:851:G:C2	2:2:852:G:C8	3.06	0.42
3:3:63:C:H2'	3:3:64:G:H8	1.84	0.42
3:3:113:C:O2'	18:O:46:GLU:OE2	2.34	0.42
9:D:134:LEU:O	9:D:138:LEU:HD23	2.20	0.42
11:F:24:ILE:HG12	11:F:37:LEU:HD13	2.02	0.42
11:F:46:ALA:O	11:F:48:ASN:N	2.51	0.42
18:O:12:THR:O	18:O:16:ARG:HG2	2.20	0.42
31:b:11:SER:O	31:b:15:MET:HB2	2.19	0.42
46:q:32:GLY:O	46:q:79:VAL:HA	2.19	0.42
47:r:29:ARG:O	47:r:33:ILE:HG12	2.18	0.42
50:u:52:LEU:HD23	50:u:52:LEU:HA	1.94	0.42
54:y:19:LYS:HB2	54:y:19:LYS:HE2	1.86	0.42
1:1:67:U:C2	1:1:68:G:C8	3.08	0.42
1:1:238:C:H1'	1:1:608:A:C2	2.54	0.42
1:1:477:A:H3'	58:1:3309:HOH:O	2.20	0.42
1:1:488:G:N2	1:1:492:A:N7	2.68	0.42
1:1:987:C:O2'	1:1:1000:A:N3	2.41	0.42
1:1:1026:G:OP1	1:1:1134:A:O2'	2.34	0.42
1:1:1060:U:H4'	1:1:1061:U:H2'	2.02	0.42
1:1:1164:C:H2'	1:1:1165:A:H8	1.85	0.42
1:1:1996:C:OP2	14:K:31:ARG:NH2	2.50	0.42
1:1:2411:A:H2'	1:1:2412:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2420:C:OP2	34:e:33:LEU:HB2	2.19	0.42
1:1:2507:C:C2	1:1:2508:G:C8	3.08	0.42
1:1:2628:C:O2'	1:1:2782:G:OP1	2.27	0.42
2:2:837:U:H2'	2:2:838:G:H8	1.85	0.42
2:2:958:A:C2	53:x:55:ARG:HG3	2.55	0.42
2:2:971:G:P	2:2:1231:G:H21	2.41	0.42
2:2:1297:G:O2'	41:l:114:LYS:NZ	2.29	0.42
7:B:43:ARG:NH2	7:B:49:ILE:HD11	2.34	0.42
10:E:115:ARG:HH22	30:a:47:LYS:HA	1.84	0.42
11:F:83:PHE:CE2	11:F:138:LYS:HB2	2.54	0.42
13:J:117:ALA:HA	13:J:120:ARG:HD2	2.01	0.42
37:h:164:ARG:NH2	37:h:166:GLU:OE2	2.50	0.42
39:j:80:THR:OG1	39:j:122:ASN:O	2.24	0.42
1:1:125:A:OP2	33:d:19:ARG:HD3	2.20	0.42
1:1:224:U:O4	1:1:419:U:O2'	2.37	0.42
1:1:930:G:H1'	29:Z:25:LEU:HD21	2.00	0.42
1:1:947:A:H2'	1:1:948:C:H6	1.83	0.42
1:1:1201:U:C2	1:1:1202:G:N7	2.88	0.42
1:1:1286:A:N6	1:1:1329:U:O2	2.52	0.42
1:1:1380:G:H2'	1:1:1381:G:H8	1.85	0.42
1:1:1441:G:H2'	1:1:1442:U:H6	1.84	0.42
1:1:1476:U:H2'	1:1:1477:A:C8	2.54	0.42
1:1:1486:U:H2'	1:1:1487:U:C6	2.54	0.42
1:1:1637:A:H5'	1:1:1760:C:O2'	2.20	0.42
1:1:1867:G:H2'	1:1:1868:C:C6	2.54	0.42
1:1:2618:G:H2'	1:1:2619:C:C6	2.54	0.42
1:1:2899:A:C2	1:1:2900:A:C5	3.07	0.42
2:2:33:A:H2'	2:2:34:C:H6	1.85	0.42
2:2:35:G:H2'	2:2:36:C:H6	1.85	0.42
2:2:317:U:N3	2:2:318:G:N7	2.68	0.42
2:2:514:C:C2	2:2:515:G:N7	2.87	0.42
2:2:553:A:H2'	2:2:554:A:C8	2.55	0.42
2:2:598:U:H2'	2:2:599:C:C6	2.55	0.42
2:2:647:C:H2'	2:2:648:A:C8	2.54	0.42
2:2:739:C:HO2'	49:t:42:HIS:CE1	2.37	0.42
2:2:779:C:H4'	45:p:124:PRO:HA	2.02	0.42
2:2:1402:4OC:H2'	2:2:1403:C:O4'	2.19	0.42
5:5:1:C:H6	5:5:1:C:P	2.43	0.42
5:5:63:U:H2'	5:5:64:C:H6	1.84	0.42
5:5:67:G:C4'	58:5:206:HOH:O	2.68	0.42
6:A:168:ASN:O	6:A:168:ASN:ND2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:45:ASN:OD1	7:B:46:ASN:N	2.53	0.42
8:C:47:ALA:HB2	8:C:83:ARG:HD2	2.00	0.42
11:F:19:ILE:HD12	11:F:24:ILE:HD12	2.01	0.42
13:J:109:LEU:HD23	13:J:109:LEU:HA	1.87	0.42
14:K:103:VAL:O	14:K:122:VAL:HA	2.19	0.42
37:h:43:LEU:O	37:h:47:LEU:HG	2.18	0.42
49:t:32:LEU:O	49:t:36:ILE:HG12	2.20	0.42
1:1:498:G:C6	1:1:499:U:C2	3.08	0.42
1:1:983:A:N6	1:1:984:A:H62	2.18	0.42
1:1:1282:U:H3	1:1:1286:A:H62	1.67	0.42
1:1:1297:C:H2'	1:1:1298:C:H6	1.85	0.42
1:1:1321:A:C4	1:1:1322:A:C8	3.07	0.42
1:1:1387:A:C6	1:1:1401:G:N1	2.88	0.42
1:1:1562:U:H2'	1:1:1563:U:C6	2.55	0.42
1:1:1805:A:H2'	1:1:1806:C:C6	2.55	0.42
1:1:2168:G:H2'	1:1:2169:A:C8	2.54	0.42
1:1:2225:A:H4'	1:1:2226:C:H6	1.83	0.42
1:1:2231:U:H2'	1:1:2232:C:C6	2.55	0.42
1:1:2250:G:H5'	1:1:2250:G:N3	2.33	0.42
2:2:56:U:H2'	2:2:57:G:C8	2.55	0.42
2:2:412:A:H62	2:2:431:A:H61	1.66	0.42
2:2:708:C:H2'	2:2:709:U:C6	2.54	0.42
2:2:891:U:H2'	2:2:892:A:H8	1.85	0.42
2:2:1415:G:H2'	2:2:1416:G:H8	1.85	0.42
3:3:51:G:H3'	18:O:64:TYR:CE1	2.54	0.42
7:B:171:TYR:HD2	7:B:183:LYS:HB3	1.84	0.42
36:g:141:LEU:O	36:g:145:GLU:HG2	2.19	0.42
39:j:160:SER:O	39:j:163:GLU:HG2	2.19	0.42
40:k:12:PRO:HG3	40:k:54:LEU:HD11	2.02	0.42
41:l:102:ARG:HA	41:l:105:VAL:HG12	2.02	0.42
45:p:61:PHE:O	45:p:64:GLN:HG3	2.19	0.42
47:r:45:ILE:O	47:r:45:ILE:HG22	2.19	0.42
52:w:32:TYR:O	52:w:40:VAL:HG12	2.19	0.42
1:1:1095:A:HO2'	1:1:1096:A:H8	1.66	0.42
1:1:1182:G:H2'	1:1:1183:U:O4'	2.20	0.42
1:1:1268:A:H2'	1:1:1269:A:O4'	2.20	0.42
1:1:1548:A:H2'	1:1:1549:A:H8	1.84	0.42
1:1:1672:A:C2	1:1:2582:G:H5'	2.55	0.42
1:1:1904:G:H2'	1:1:1905:C:O4'	2.19	0.42
2:2:673:A:H4'	40:k:86:ARG:HH11	1.85	0.42
2:2:684:U:O2	45:p:41:ALA:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1070:U:H2'	2:2:1071:C:C6	2.55	0.42
2:2:1152:A:H4'	44:o:19:ASP:OD2	2.20	0.42
3:3:33:G:H2'	3:3:34:A:O4'	2.19	0.42
7:B:129:THR:OG1	7:B:191:THR:HG22	2.19	0.42
17:N:103:ARG:HD3	17:N:106:ASP:HB3	2.02	0.42
38:i:67:VAL:HG21	38:i:72:PHE:HD2	1.85	0.42
54:y:33:LYS:HE3	54:y:33:LYS:HB2	1.89	0.42
1:1:409:G:H2'	1:1:410:G:C8	2.55	0.42
1:1:720:U:H2'	1:1:721:A:C8	2.54	0.42
1:1:835:C:H2'	1:1:836:G:H8	1.84	0.42
1:1:885:C:H2'	1:1:886:A:C8	2.55	0.42
1:1:947:A:C6	1:1:971:G:N1	2.88	0.42
1:1:1422:G:C6	1:1:1577:C:N3	2.88	0.42
1:1:1592:C:H2'	1:1:1593:A:C8	2.55	0.42
1:1:1687:G:N2	1:1:1702:G:C6	2.88	0.42
1:1:1996:C:H5	14:K:32:TYR:OH	2.03	0.42
1:1:2014:A:H2'	1:1:2015:A:C8	2.55	0.42
1:1:2742:G:OP1	35:f:24:ARG:NH1	2.52	0.42
1:1:2818:U:H2'	1:1:2819:G:C8	2.55	0.42
2:2:50:A:O2'	2:2:360:G:N2	2.51	0.42
2:2:202:G:O2'	2:2:468:A:H8	2.03	0.42
2:2:598:U:H2'	2:2:599:C:H6	1.84	0.42
2:2:932:C:H5''	41:l:4:ARG:CD	2.49	0.42
6:A:164:ARG:HA	6:A:164:ARG:HD3	1.92	0.42
9:D:24:ASN:HB3	9:D:27:LEU:HG	2.02	0.42
10:E:95:ARG:O	10:E:98:GLU:HG3	2.20	0.42
14:K:18:ARG:HB2	14:K:45:GLU:HG2	2.02	0.42
32:c:9:ILE:HD12	32:c:51:GLU:HB2	2.01	0.42
37:h:129:MET:HA	37:h:129:MET:HE3	2.01	0.42
37:h:135:LYS:HD2	37:h:135:LYS:HA	1.87	0.42
38:i:9:LEU:HD13	38:i:32:CYS:SG	2.59	0.42
39:j:56:VAL:O	39:j:60:ILE:HG12	2.19	0.42
39:j:85:VAL:HG11	39:j:147:MET:HB3	2.02	0.42
46:q:24:LEU:O	46:q:27:CYS:HB3	2.20	0.42
55:z:5:LYS:HE2	55:z:5:LYS:HB2	1.88	0.42
1:1:289:G:H2'	1:1:290:U:H6	1.84	0.41
1:1:596:U:H2'	1:1:597:G:H8	1.84	0.41
1:1:700:G:O2'	1:1:1632:A:N3	2.35	0.41
1:1:764:A:O2'	1:1:765:C:H5'	2.20	0.41
1:1:969:G:H2'	1:1:970:U:C6	2.55	0.41
1:1:1298:C:C2	1:1:1643:G:N2	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1351:C:O2'	1:1:1571:A:O2'	2.31	0.41
1:1:1405:U:H2'	1:1:1406:U:C6	2.54	0.41
1:1:1442:U:H2'	1:1:1443:U:C6	2.55	0.41
1:1:1651:G:H2'	1:1:1652:A:H8	1.85	0.41
1:1:1710:G:C6	1:1:1749:A:C6	3.08	0.41
1:1:2164:C:H3'	1:1:2165:C:H6	1.85	0.41
1:1:2247:A:H2'	1:1:2248:C:C6	2.55	0.41
1:1:2304:G:H4'	10:E:130:MET:HA	2.01	0.41
1:1:2519:U:H5'	1:1:2567:G:H21	1.85	0.41
2:2:193:C:H2'	2:2:194:C:C6	2.55	0.41
2:2:323:U:H3	2:2:327:A:H62	1.68	0.41
2:2:958:A:H1'	2:2:985:C:O2'	2.19	0.41
2:2:1530:G:H2'	2:2:1531:A:H8	1.84	0.41
11:F:109:PHE:CZ	11:F:152:ARG:HD3	2.55	0.41
39:j:16:ILE:HD13	39:j:36:LEU:HG	2.01	0.41
39:j:96:MET:HE1	39:j:144:LEU:HG	2.01	0.41
46:q:89:0TD:H8	46:q:89:0TD:H4	1.75	0.41
1:1:117:G:OP2	1:1:119:A:O2'	2.21	0.41
1:1:682:G:H5'	33:d:26:ASN:CG	2.45	0.41
1:1:792:A:N3	1:1:2072:C:O2'	2.49	0.41
1:1:1276:A:N6	1:1:1645:G:O6	2.53	0.41
1:1:1590:A:H2'	1:1:1591:A:C8	2.54	0.41
1:1:1748:C:H2'	1:1:1749:A:H8	1.86	0.41
1:1:2140:G:O6	1:1:2151:U:C4	2.73	0.41
1:1:2322:A:H2'	1:1:2323:G:C8	2.55	0.41
1:1:2365:G:H4'	26:W:60:PHE:CE1	2.54	0.41
1:1:2547:A:H2'	1:1:2548:U:H6	1.84	0.41
1:1:2669:G:H2'	1:1:2670:A:H8	1.86	0.41
2:2:35:G:H2'	2:2:36:C:C6	2.55	0.41
2:2:214:C:C2	2:2:215:C:C5	3.07	0.41
2:2:765:G:N1	2:2:812:G:O2'	2.41	0.41
2:2:1287:A:N3	2:2:1353:G:O2'	2.39	0.41
2:2:1401:G:H2'	2:2:1402:4OC:O4'	2.18	0.41
2:2:1477:U:H2'	2:2:1478:U:C6	2.55	0.41
2:2:1527:U:H2'	2:2:1528:U:C6	2.55	0.41
16:M:51:ARG:HD2	16:M:55:ARG:HH22	1.85	0.41
23:T:50:LEU:HD11	28:Y:26:PHE:CE2	2.55	0.41
40:k:102:MET:HE3	52:w:24:LYS:HB3	2.00	0.41
42:m:29:SER:OG	42:m:57:PRO:HB2	2.20	0.41
1:1:624:C:H2'	1:1:625:G:H8	1.86	0.41
1:1:2149:U:H2'	1:1:2150:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2813:A:C4	1:1:2814:A:C8	3.08	0.41
1:1:2859:G:H2'	1:1:2860:A:C8	2.55	0.41
2:2:1412:C:H2'	2:2:1413:A:H8	1.83	0.41
7:B:89:ALA:HB2	7:B:158:ALA:HA	2.01	0.41
11:F:26:ILE:HG23	11:F:33:LEU:HB2	2.03	0.41
18:O:7:ARG:HD2	18:O:97:PHE:CE1	2.55	0.41
28:Y:53:VAL:O	28:Y:57:LEU:HD23	2.20	0.41
42:m:64:LYS:HB3	42:m:71:VAL:HG21	2.02	0.41
46:q:7:LEU:HD22	46:q:12:ARG:HD3	2.03	0.41
53:x:29:LYS:HD2	53:x:30:PRO:HD2	2.02	0.41
1:1:85:G:C6	1:1:98:G:N1	2.88	0.41
1:1:686:U:H5''	33:d:11:LYS:NZ	2.34	0.41
1:1:783:A:H8	1:1:1778:U:O2'	2.04	0.41
1:1:826:U:H2'	1:1:828:U:O4'	2.20	0.41
1:1:1464:G:H2'	1:1:1465:G:C8	2.56	0.41
1:1:1537:G:C2	1:1:1538:G:C8	3.09	0.41
1:1:1679:A:H2'	1:1:1680:U:H6	1.86	0.41
1:1:2110:G:OP2	1:1:2110:G:H8	2.02	0.41
1:1:2622:U:O2'	1:1:2825:G:N7	2.52	0.41
58:1:3335:HOH:O	8:C:58:ASN:ND2	2.52	0.41
2:2:959:A:O2'	2:2:984:C:O2'	2.25	0.41
15:L:37:GLY:N	15:L:40:SER:OG	2.52	0.41
26:W:72:LYS:HE2	26:W:79:PHE:CG	2.55	0.41
42:m:92:LEU:HD23	42:m:92:LEU:HA	1.93	0.41
43:n:6:TYR:CD2	43:n:90:TYR:HA	2.55	0.41
51:v:79:VAL:HB	51:v:80:GLU:OE2	2.20	0.41
53:x:4:SER:OG	53:x:6:LYS:HG2	2.21	0.41
53:x:5:LEU:HD23	53:x:5:LEU:H	1.86	0.41
1:1:258:G:H2'	1:1:259:G:H8	1.86	0.41
1:1:605:G:H2'	1:1:606:U:O4'	2.20	0.41
1:1:883:G:N2	1:1:884:U:H5	2.19	0.41
1:1:902:C:H2'	1:1:903:C:C6	2.55	0.41
1:1:1076:C:H2'	1:1:1077:A:C8	2.56	0.41
1:1:1437:C:H2'	1:1:1438:U:C6	2.55	0.41
1:1:1570:A:H2'	1:1:1571:A:C8	2.56	0.41
1:1:1750:G:H2'	1:1:1751:U:H6	1.84	0.41
1:1:2305:U:H2'	1:1:2306:C:C6	2.54	0.41
2:2:20:U:H2'	2:2:21:G:O4'	2.19	0.41
2:2:1308:U:H2'	2:2:1309:G:C8	2.55	0.41
5:5:14:A:C2	5:5:22:G:H1'	2.55	0.41
8:C:88:GLU:HB3	8:C:90:PHE:HE1	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:110:THR:HG22	8:C:171:THR:HG23	2.02	0.41
10:E:34:ILE:HG12	10:E:156:ILE:HG13	2.02	0.41
12:G:125:THR:HA	12:G:146:VAL:HG21	2.03	0.41
14:K:63:VAL:HG12	14:K:107:LEU:HD11	2.02	0.41
16:M:77:PRO:O	16:M:80:VAL:HG12	2.20	0.41
21:R:79:ARG:O	21:R:81:LYS:HG2	2.21	0.41
22:S:17:VAL:HG11	22:S:103:ILE:HG12	2.02	0.41
24:U:83:VAL:CG2	24:U:94:ARG:HB3	2.51	0.41
36:g:93:ASN:OD1	36:g:93:ASN:N	2.51	0.41
41:l:15:ASP:OD1	41:l:15:ASP:N	2.52	0.41
50:u:15:PRO:HG2	50:u:41:PRO:HG2	2.02	0.41
50:u:42:ILE:O	50:u:42:ILE:HG23	2.19	0.41
1:1:29:U:H2'	1:1:30:G:H8	1.85	0.41
1:1:78:U:H2'	1:1:79:C:H6	1.86	0.41
1:1:121:G:H2'	1:1:122:G:C8	2.55	0.41
1:1:249:C:O5'	1:1:2394:C:O2'	2.39	0.41
1:1:272:A:H2'	1:1:273:G:C8	2.55	0.41
1:1:1203:U:O2	1:1:1241:A:N6	2.53	0.41
1:1:1283:G:H22	1:1:1286:A:P	2.43	0.41
1:1:1436:G:H2'	1:1:1437:C:O4'	2.21	0.41
1:1:1649:G:H2'	1:1:1650:A:C8	2.56	0.41
1:1:1744:A:H3'	1:1:1745:A:H8	1.85	0.41
1:1:1874:C:H2'	1:1:1875:G:O4'	2.21	0.41
1:1:2466:C:H2'	1:1:2467:C:H6	1.86	0.41
2:2:592:G:H2'	2:2:593:U:C6	2.56	0.41
2:2:763:G:H2'	2:2:764:C:H6	1.86	0.41
2:2:1160:G:C6	2:2:1161:C:C4	3.08	0.41
2:2:1376:U:H2'	2:2:1377:A:C8	2.56	0.41
5:5:44:G:H2'	5:5:45:G:C8	2.55	0.41
9:D:148:ILE:HD13	9:D:187:VAL:HG21	2.03	0.41
10:E:116:GLY:O	10:E:178:ARG:NH2	2.53	0.41
14:K:23:LYS:HD3	14:K:23:LYS:HA	1.96	0.41
29:Z:58:GLU:O	58:Z:101:HOH:O	2.21	0.41
36:g:114:LEU:HD23	36:g:118:GLU:OE2	2.20	0.41
44:o:9:ARG:NH1	44:o:71:LEU:HD21	2.34	0.41
1:1:18:U:H2'	1:1:19:A:C8	2.55	0.41
1:1:84:A:H4'	1:1:85:G:H5'	2.03	0.41
1:1:500:G:H2'	1:1:502:A:N7	2.35	0.41
1:1:672:C:H2'	1:1:673:C:C6	2.55	0.41
1:1:739:A:H1'	1:1:740:C:H5	1.85	0.41
1:1:983:A:H62	1:1:984:A:H62	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1130:U:C2	8:C:152:PRO:HB3	2.56	0.41
1:1:1183:U:H2'	1:1:1184:U:C6	2.56	0.41
1:1:1993:U:H4'	8:C:133:THR:CG2	2.51	0.41
1:1:2730:C:O3'	8:C:174:SER:OG	2.38	0.41
1:1:2819:G:C6	1:1:2828:G:C6	3.08	0.41
1:1:2838:G:C4	1:1:2839:G:C8	3.08	0.41
2:2:19:A:N1	2:2:917:G:C6	2.89	0.41
2:2:521:G:N7	46:q:50:ARG:NH2	2.65	0.41
2:2:736:C:OP1	52:w:61:ARG:NH1	2.53	0.41
2:2:875:U:HO2'	42:m:15:ARG:NH1	2.18	0.41
2:2:1053:G:N2	2:2:1058:G:O6	2.54	0.41
2:2:1352:C:H2'	2:2:1353:G:C8	2.56	0.41
2:2:1488:G:H2'	2:2:1489:G:H8	1.86	0.41
5:5:6:C:H2'	5:5:7:G:H8	1.85	0.41
29:Z:44:ILE:O	29:Z:48:ILE:HG12	2.19	0.41
34:e:7:VAL:HG23	34:e:10:ALA:HB3	2.03	0.41
36:g:164:ILE:O	36:g:186:ILE:HB	2.20	0.41
37:h:7:PRO:HD2	37:h:184:TYR:CD2	2.55	0.41
39:j:105:ILE:HG22	39:j:123:VAL:HG12	2.03	0.41
42:m:105:SER:HB2	42:m:110:VAL:HG12	2.02	0.41
43:n:54:LEU:HD11	43:n:103:PHE:CD2	2.56	0.41
43:n:55:VAL:O	43:n:57:MET:N	2.52	0.41
44:o:25:ILE:HD11	44:o:92:LEU:HD11	2.02	0.41
46:q:49:LEU:O	46:q:51:LYS:HD3	2.21	0.41
1:1:24:G:H2'	1:1:25:U:H6	1.85	0.41
1:1:54:G:H1'	33:d:35:ARG:HE	1.86	0.41
1:1:126:A:H5'	33:d:19:ARG:HG3	2.02	0.41
1:1:615:U:N3	9:D:176:ASP:HB3	2.34	0.41
1:1:629:G:OP1	1:1:650:C:O2'	2.31	0.41
1:1:641:U:O2'	1:1:2350:C:OP1	2.39	0.41
1:1:778:G:H5''	7:B:48:ARG:HD2	2.03	0.41
1:1:1010:A:N3	1:1:1153:C:H1'	2.35	0.41
1:1:1561:C:H2'	1:1:1562:U:C6	2.56	0.41
1:1:1582:C:H2'	1:1:1583:A:C8	2.56	0.41
1:1:2519:U:O4'	1:1:2542:A:N6	2.54	0.41
1:1:2801:G:H2'	1:1:2802:G:H8	1.86	0.41
2:2:18:C:H5''	39:j:132:ASN:ND2	2.36	0.41
2:2:235:C:H2'	2:2:236:A:C8	2.56	0.41
2:2:1161:C:H2'	2:2:1162:C:H6	1.84	0.41
3:3:70:C:H2'	3:3:71:C:H6	1.86	0.41
5:5:75:C:H2'	5:5:76:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:100:ALA:O	12:G:104:THR:HG23	2.21	0.41
13:J:114:LEU:O	13:J:118:MET:CB	2.64	0.41
16:M:46:ILE:HA	16:M:103:TYR:OH	2.21	0.41
26:W:19:LYS:HA	26:W:19:LYS:HD3	1.84	0.41
39:j:111:MET:HE2	39:j:140:THR:HB	2.02	0.41
48:s:64:CYS:HB2	48:s:80:SER:HB3	2.02	0.41
1:1:112:U:H5'	28:Y:58:ASN:HD21	1.86	0.41
1:1:133:U:H2'	1:1:134:G:H8	1.84	0.41
1:1:181:A:H1'	1:1:435:C:H5'	2.03	0.41
1:1:380:G:OP1	27:X:18:ARG:HB2	2.21	0.41
1:1:464:U:H1'	1:1:686:U:C5	2.47	0.41
1:1:530:G:H4'	1:1:532:A:H62	1.86	0.41
1:1:600:G:H5'	9:D:27:LEU:HD23	2.03	0.41
1:1:645:C:H2'	1:1:647:G:C8	2.56	0.41
1:1:934:U:H2'	1:1:935:C:C6	2.56	0.41
1:1:1069:A:C2	1:1:1096:A:H4'	2.56	0.41
1:1:1071:G:H2'	1:1:1072:C:C6	2.56	0.41
1:1:1287:A:H2'	1:1:1288:G:C4	2.56	0.41
1:1:1295:C:C2	1:1:1296:G:C8	3.08	0.41
1:1:1401:G:H2'	1:1:1402:U:C6	2.56	0.41
1:1:1582:C:O2'	1:1:1583:A:O4'	2.36	0.41
1:1:1594:U:H2'	1:1:1595:C:C6	2.55	0.41
1:1:1637:A:H2'	1:1:1638:C:C6	2.56	0.41
1:1:1678:A:C4	1:1:1679:A:C8	3.09	0.41
1:1:1788:C:H2'	1:1:1789:A:O4'	2.21	0.41
1:1:1802:A:H2'	1:1:1803:A:C8	2.56	0.41
1:1:2291:U:H1'	1:1:2374:C:H1'	2.03	0.41
1:1:2722:G:H2'	1:1:2723:C:C6	2.56	0.41
1:1:2745:C:H2'	1:1:2746:U:H6	1.85	0.41
1:1:2804:U:H2'	1:1:2805:C:H6	1.86	0.41
2:2:171:A:H2'	2:2:172:A:C8	2.56	0.41
2:2:261:U:OP2	54:y:74:ARG:NH1	2.46	0.41
2:2:489:C:H2'	2:2:490:C:H6	1.85	0.41
2:2:542:G:H2'	2:2:543:U:C6	2.55	0.41
2:2:672:U:H2'	2:2:673:A:H8	1.85	0.41
2:2:674:G:H21	45:p:118:HIS:HB2	1.86	0.41
2:2:1318:A:H4'	53:x:10:PHE:CG	2.56	0.41
2:2:1321:U:O2'	53:x:78:ARG:NH2	2.54	0.41
3:3:77:U:H5'	25:V:21:ARG:HH22	1.86	0.41
7:B:132:MET:SD	7:B:164:ILE:HD11	2.61	0.41
7:B:144:VAL:HG11	7:B:174:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:6:LYS:HB3	9:D:6:LYS:HE3	1.85	0.41
10:E:8:TYR:HA	10:E:12:VAL:HB	2.03	0.41
10:E:70:ALA:HB2	10:E:85:ILE:HG13	2.02	0.41
11:F:117:LEU:HD12	11:F:144:VAL:HG21	2.02	0.41
13:J:11:VAL:HG21	13:J:50:THR:HA	2.03	0.41
13:J:118:MET:HG3	58:J:203:HOH:O	2.20	0.41
14:K:116:ILE:HD11	14:K:122:VAL:HG13	2.03	0.41
17:N:52:ILE:HB	17:N:94:TYR:CD2	2.56	0.41
18:O:32:PRO:HA	18:O:102:ARG:HH22	1.86	0.41
18:O:62:LEU:HD21	18:O:70:ALA:CB	2.50	0.41
23:T:18:GLU:HG2	23:T:19:LYS:N	2.36	0.41
23:T:30:ILE:HD12	23:T:32:LEU:HD21	2.03	0.41
24:U:52:LEU:HD23	24:U:52:LEU:O	2.21	0.41
25:V:72:VAL:CG1	25:V:91:PHE:HB3	2.51	0.41
29:Z:56:LYS:HE2	29:Z:58:GLU:HG2	2.03	0.41
36:g:11:LYS:HG3	36:g:208:ARG:NH2	2.36	0.41
38:i:28:ILE:HG13	38:i:29:ASP:N	2.36	0.41
38:i:105:MET:HE1	38:i:143:VAL:HB	2.02	0.41
39:j:24:THR:HG22	39:j:29:ARG:HG3	2.02	0.41
40:k:9:MET:HE2	40:k:59:TYR:CE2	2.55	0.41
44:o:53:ILE:HG22	48:s:85:ARG:NE	2.36	0.41
46:q:39:THR:HG21	46:q:49:LEU:HB3	2.03	0.41
49:t:71:LYS:HG3	49:t:78:TYR:CD2	2.55	0.41
53:x:50:ALA:HA	53:x:59:PRO:HA	2.02	0.41
1:1:12:U:O2	1:1:2626:C:H4'	2.20	0.41
1:1:254:G:O2'	1:1:255:A:O4'	2.35	0.41
1:1:287:G:H2'	1:1:288:U:H6	1.86	0.41
1:1:335:C:H5''	24:U:82:ARG:HD2	2.02	0.41
1:1:659:G:H21	9:D:30:GLN:CD	2.27	0.41
1:1:714:U:H1'	1:1:717:C:H5	1.86	0.41
1:1:1016:G:C6	1:1:1147:A:C6	3.09	0.41
1:1:2125:G:N2	1:1:2171:A:O5'	2.40	0.41
1:1:2364:C:H2'	1:1:2365:G:O4'	2.21	0.41
1:1:2478:A:C8	1:1:2529:G:N7	2.89	0.41
1:1:2834:G:H2'	1:1:2879:A:N6	2.36	0.41
2:2:56:U:H2'	2:2:57:G:H8	1.86	0.41
2:2:129:A:O2'	2:2:130:A:H2'	2.21	0.41
2:2:144:G:N2	2:2:179:A:C8	2.89	0.41
2:2:713:G:H2'	2:2:714:G:H8	1.83	0.41
2:2:1161:C:H2'	2:2:1162:C:C6	2.56	0.41
2:2:1506:U:O2'	2:2:1507:A:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1524:C:H2'	2:2:1525:G:C8	2.54	0.41
2:2:1527:U:P	55:z:45:ARG:HH21	2.44	0.41
3:3:60:C:H2'	3:3:61:G:C8	2.54	0.41
37:h:6:HIS:CE1	37:h:8:ASN:HB3	2.56	0.41
42:m:88:ARG:H	42:m:88:ARG:HG3	1.71	0.41
43:n:84:THR:O	43:n:88:MET:HG2	2.21	0.41
44:o:91:ASP:OD1	44:o:91:ASP:N	2.48	0.41
46:q:33:VAL:C	46:q:55:VAL:HG23	2.46	0.41
52:w:14:THR:HG22	52:w:48:ARG:HE	1.85	0.41
1:1:128:C:H2'	1:1:129:C:H6	1.86	0.40
1:1:223:A:C6	1:1:422:A:C6	3.09	0.40
1:1:477:A:H61	1:1:500:G:H5''	1.85	0.40
1:1:565:C:H2'	1:1:566:U:C6	2.56	0.40
1:1:657:U:H2'	1:1:658:U:C6	2.56	0.40
1:1:1203:U:O5'	1:1:1204:A:H5''	2.20	0.40
1:1:1283:G:N2	1:1:1286:A:OP2	2.54	0.40
1:1:1379:U:O2'	1:1:1380:G:OP1	2.38	0.40
1:1:1413:A:H2'	1:1:1414:C:H6	1.86	0.40
1:1:1735:A:C6	1:1:1736:U:C4	3.09	0.40
1:1:1788:C:H2'	1:1:1789:A:C8	2.56	0.40
1:1:2370:G:H4'	32:c:44:ARG:HH21	1.86	0.40
1:1:2446:G:H4'	1:1:2448:A:N7	2.35	0.40
1:1:2669:G:H2'	1:1:2670:A:C8	2.57	0.40
1:1:2848:G:N7	19:P:95:ALA:HB2	2.36	0.40
2:2:6:G:H22	39:j:103:THR:HG22	1.85	0.40
2:2:745:G:H2'	2:2:746:A:H8	1.86	0.40
2:2:1415:G:C6	2:2:1486:G:C6	3.09	0.40
9:D:18:THR:HA	9:D:106:LYS:HD2	2.02	0.40
16:M:36:VAL:HG13	25:V:82:TYR:CD2	2.56	0.40
36:g:127:ASP:O	36:g:129:LEU:HD22	2.22	0.40
37:h:114:LYS:HB2	37:h:185:ASN:ND2	2.36	0.40
38:i:126:ASN:ND2	38:i:141:ASP:OD1	2.42	0.40
42:m:49:PHE:HB2	42:m:59:LEU:HD11	2.03	0.40
53:x:17:LYS:HD3	53:x:17:LYS:HA	1.89	0.40
1:1:300:A:O2'	1:1:318:C:O2	2.29	0.40
1:1:513:A:H2'	1:1:514:A:C8	2.56	0.40
1:1:1217:U:OP1	20:Q:15:LYS:HD2	2.21	0.40
1:1:1378:A:N3	1:1:1379:U:H2'	2.37	0.40
1:1:1709:U:O2'	1:1:2859:G:N3	2.47	0.40
1:1:1727:C:H2'	1:1:1728:C:O4'	2.20	0.40
1:1:1826:G:H2'	1:1:1827:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2198:A:C4	12:G:29:PHE:HB2	2.56	0.40
1:1:2393:U:H5''	15:L:62:PRO:HB3	2.02	0.40
2:2:1149:C:H2'	2:2:1150:A:C8	2.56	0.40
2:2:1172:C:C2	2:2:1173:U:C5	3.09	0.40
4:4:16:C:H2'	4:4:17:C:C6	2.56	0.40
5:5:72:G:N2	5:5:73:A:C4	2.90	0.40
5:5:72:G:N3	5:5:73:A:C8	2.89	0.40
9:D:105:LEU:HD23	9:D:200:LEU:HD21	2.03	0.40
15:L:29:LYS:HG3	15:L:30:THR:HG23	2.03	0.40
20:Q:9:ILE:H	20:Q:9:ILE:HD12	1.86	0.40
23:T:34:VAL:HG21	23:T:43:ILE:HD11	2.03	0.40
27:X:39:TRP:NE1	27:X:41:GLU:OE2	2.51	0.40
28:Y:32:ALA:O	58:Y:101:HOH:O	2.22	0.40
36:g:90:PHE:HB3	36:g:151:ILE:HD13	2.04	0.40
44:o:50:THR:HG22	44:o:64:GLN:HG3	2.03	0.40
53:x:40:ILE:HD12	53:x:66:MET:O	2.22	0.40
1:1:571:U:H3'	21:R:80:ARG:NH2	2.37	0.40
1:1:1178:C:H2'	1:1:1179:G:H5''	2.02	0.40
1:1:1299:G:O2'	1:1:1301:A:N7	2.52	0.40
1:1:2053:G:H5'	8:C:150:GLN:H	1.85	0.40
1:1:2130:U:O2'	1:1:2134:A:O5'	2.30	0.40
1:1:2290:G:H2'	1:1:2291:U:H6	1.85	0.40
1:1:2560:A:C6	1:1:2561:U:C4	3.10	0.40
1:1:2841:C:H2'	1:1:2842:G:H8	1.86	0.40
1:1:2855:C:H2'	1:1:2856:A:H8	1.85	0.40
2:2:678:U:H2'	2:2:679:C:C6	2.56	0.40
2:2:696:A:H2'	2:2:697:U:C6	2.56	0.40
2:2:836:G:C6	2:2:851:G:C5	3.10	0.40
2:2:911:U:OP2	46:q:94:ARG:NH2	2.54	0.40
2:2:1515:G:H2'	2:2:1516:2MG:H8	1.86	0.40
3:3:29:A:O2'	3:3:58:A:N1	2.48	0.40
8:C:149:ASN:C	8:C:151:THR:H	2.29	0.40
10:E:63:GLN:HA	30:a:6:HIS:HD2	1.86	0.40
11:F:4:VAL:HB	11:F:69:ARG:HD2	2.02	0.40
11:F:26:ILE:CG2	11:F:33:LEU:HB2	2.51	0.40
1:1:52:A:H2'	1:1:53:A:C8	2.57	0.40
1:1:627:A:C6	15:L:111:ILE:HD11	2.57	0.40
1:1:1190:G:H2'	1:1:1191:G:H8	1.87	0.40
1:1:1542:U:H2'	1:1:1543:G:O4'	2.21	0.40
1:1:1684:G:O6	1:1:1705:A:N6	2.55	0.40
1:1:2174:C:H2'	1:1:2175:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:34:C:C2	2:2:35:G:N7	2.89	0.40
2:2:185:U:H2'	2:2:186:C:C6	2.57	0.40
2:2:373:A:C2	2:2:374:A:C8	3.09	0.40
2:2:691:G:OP2	45:p:28:ASN:ND2	2.50	0.40
2:2:799:G:H2'	2:2:800:G:O4'	2.21	0.40
2:2:1152:A:OP1	44:o:72:ARG:NH1	2.39	0.40
3:3:9:G:H2'	3:3:10:G:H8	1.87	0.40
7:B:243:HIS:HA	7:B:244:PRO:HD3	1.97	0.40
23:T:57:VAL:O	23:T:86:THR:HG22	2.21	0.40
41:l:140:ASP:OD1	41:l:143:ARG:NH2	2.36	0.40
1:1:136:G:C5	1:1:137:U:C4	3.10	0.40
1:1:532:A:N3	1:1:532:A:H2'	2.37	0.40
1:1:597:G:H2'	1:1:598:U:C6	2.57	0.40
1:1:886:A:H2'	1:1:887:A:O4'	2.22	0.40
1:1:962:G:H2'	1:1:963:U:H6	1.86	0.40
1:1:980:A:C6	1:1:1136:G:H5'	2.57	0.40
1:1:1409:U:H2'	1:1:1410:G:C8	2.56	0.40
1:1:1445:G:H2'	1:1:1446:C:H6	1.86	0.40
1:1:1473:G:C6	1:1:1519:G:C6	3.10	0.40
1:1:2064:C:H2'	1:1:2065:C:H6	1.86	0.40
1:1:2367:G:C2	1:1:2368:C:C5	3.09	0.40
1:1:2485:G:O3'	16:M:125:PRO:HB3	2.21	0.40
1:1:2710:C:H2'	1:1:2711:A:C8	2.57	0.40
1:1:2809:A:H2'	1:1:2810:A:C8	2.57	0.40
2:2:76:G:H2'	2:2:77:A:H8	1.86	0.40
2:2:629:A:H2'	2:2:630:A:O4'	2.20	0.40
2:2:738:C:H5''	40:k:68:GLN:HG2	2.03	0.40
2:2:786:G:C2	2:2:797:C:C2	3.10	0.40
2:2:1375:A:H2'	2:2:1376:U:O4'	2.21	0.40
2:2:1436:U:O4	2:2:1437:A:N6	2.55	0.40
3:3:62:C:H2'	3:3:63:C:C6	2.56	0.40
10:E:73:SER:OG	10:E:80:ARG:HA	2.21	0.40
10:E:106:ILE:O	10:E:109:PRO:HD2	2.21	0.40
18:O:58:ILE:O	18:O:62:LEU:HB2	2.22	0.40
22:S:10:ALA:N	22:S:101:SER:O	2.50	0.40
26:W:44:LYS:HB3	26:W:44:LYS:HE2	1.94	0.40
44:o:40:ILE:CG1	44:o:73:LEU:HB3	2.51	0.40
45:p:45:ALA:HB3	45:p:70:CYS:HB2	2.03	0.40
46:q:69:GLY:HA3	46:q:107:VAL:HG11	2.03	0.40
51:v:49:GLU:H	51:v:49:GLU:CD	2.30	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	A	65/229 (28%)	63 (97%)	2 (3%)	0	100	100
7	B	269/273 (98%)	257 (96%)	12 (4%)	0	100	100
8	C	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
9	D	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
10	E	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
11	F	173/177 (98%)	168 (97%)	4 (2%)	1 (1%)	21	54
12	G	147/149 (99%)	142 (97%)	5 (3%)	0	100	100
13	J	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
14	K	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
15	L	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
16	M	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
17	N	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
18	O	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
19	P	112/115 (97%)	112 (100%)	0	0	100	100
20	Q	115/118 (98%)	115 (100%)	0	0	100	100
21	R	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
22	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
23	T	92/100 (92%)	89 (97%)	3 (3%)	0	100	100
24	U	101/104 (97%)	98 (97%)	3 (3%)	0	100	100
25	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
26	W	74/84 (88%)	70 (95%)	4 (5%)	0	100	100
27	X	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
28	Y	60/63 (95%)	56 (93%)	4 (7%)	0	100	100
29	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
30	a	64/70 (91%)	59 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	b	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
32	c	50/55 (91%)	50 (100%)	0	0	100	100
33	d	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
34	e	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
35	f	36/38 (95%)	36 (100%)	0	0	100	100
36	g	223/241 (92%)	214 (96%)	9 (4%)	0	100	100
37	h	206/233 (88%)	196 (95%)	10 (5%)	0	100	100
38	i	203/206 (98%)	196 (97%)	7 (3%)	0	100	100
39	j	154/167 (92%)	145 (94%)	9 (6%)	0	100	100
40	k	102/135 (76%)	100 (98%)	2 (2%)	0	100	100
41	l	149/179 (83%)	142 (95%)	7 (5%)	0	100	100
42	m	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
43	n	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
44	o	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
45	p	115/129 (89%)	114 (99%)	1 (1%)	0	100	100
46	q	120/124 (97%)	108 (90%)	12 (10%)	0	100	100
47	r	114/118 (97%)	107 (94%)	7 (6%)	0	100	100
48	s	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
49	t	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
50	u	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
51	v	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
52	w	64/75 (85%)	62 (97%)	2 (3%)	0	100	100
53	x	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
54	y	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
55	z	68/71 (96%)	68 (100%)	0	0	100	100
All	All	5673/6141 (92%)	5465 (96%)	207 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	F	47	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	
6	A	54/177 (30%)	54 (100%)	0	100	100
7	B	216/218 (99%)	215 (100%)	1 (0%)	81	80
8	C	164/164 (100%)	164 (100%)	0	100	100
9	D	165/165 (100%)	165 (100%)	0	100	100
10	E	148/150 (99%)	148 (100%)	0	100	100
11	F	136/138 (99%)	136 (100%)	0	100	100
12	G	114/114 (100%)	114 (100%)	0	100	100
13	J	116/116 (100%)	116 (100%)	0	100	100
14	K	104/104 (100%)	104 (100%)	0	100	100
15	L	103/103 (100%)	103 (100%)	0	100	100
16	M	109/109 (100%)	109 (100%)	0	100	100
17	N	99/103 (96%)	99 (100%)	0	100	100
18	O	86/87 (99%)	86 (100%)	0	100	100
19	P	99/100 (99%)	99 (100%)	0	100	100
20	Q	89/90 (99%)	89 (100%)	0	100	100
21	R	84/84 (100%)	84 (100%)	0	100	100
22	S	93/93 (100%)	93 (100%)	0	100	100
23	T	81/84 (96%)	81 (100%)	0	100	100
24	U	84/85 (99%)	84 (100%)	0	100	100
25	V	78/78 (100%)	78 (100%)	0	100	100
26	W	58/62 (94%)	58 (100%)	0	100	100
27	X	67/68 (98%)	67 (100%)	0	100	100
28	Y	54/55 (98%)	54 (100%)	0	100	100
29	Z	48/49 (98%)	48 (100%)	0	100	100
30	a	59/62 (95%)	59 (100%)	0	100	100
31	b	47/48 (98%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	c	47/49 (96%)	47 (100%)	0	100	100
33	d	38/38 (100%)	38 (100%)	0	100	100
34	e	51/52 (98%)	49 (96%)	2 (4%)	28	54
35	f	34/34 (100%)	34 (100%)	0	100	100
36	g	187/199 (94%)	187 (100%)	0	100	100
37	h	171/190 (90%)	171 (100%)	0	100	100
38	i	172/173 (99%)	172 (100%)	0	100	100
39	j	119/126 (94%)	119 (100%)	0	100	100
40	k	91/116 (78%)	91 (100%)	0	100	100
41	l	124/147 (84%)	124 (100%)	0	100	100
42	m	104/105 (99%)	104 (100%)	0	100	100
43	n	105/107 (98%)	103 (98%)	2 (2%)	50	67
44	o	86/90 (96%)	86 (100%)	0	100	100
45	p	90/99 (91%)	90 (100%)	0	100	100
46	q	102/103 (99%)	100 (98%)	2 (2%)	48	66
47	r	94/96 (98%)	94 (100%)	0	100	100
48	s	83/84 (99%)	83 (100%)	0	100	100
49	t	76/77 (99%)	76 (100%)	0	100	100
50	u	65/65 (100%)	65 (100%)	0	100	100
51	v	74/78 (95%)	74 (100%)	0	100	100
52	w	57/65 (88%)	57 (100%)	0	100	100
53	x	72/79 (91%)	72 (100%)	0	100	100
54	y	65/66 (98%)	65 (100%)	0	100	100
55	z	60/61 (98%)	60 (100%)	0	100	100
All	All	4722/5005 (94%)	4715 (100%)	7 (0%)	87	87

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	B	115	GLN
34	e	30	ARG
34	e	32	ILE
43	n	5	GLN
43	n	9	THR

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Mol	Chain	Res	Type
46	q	47	SER
46	q	49	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
6	A	203	GLN
7	B	53	HIS
7	B	153	GLN
7	B	226	ASN
7	B	260	ASN
11	F	22	GLN
11	F	38	ASN
12	G	11	ASN
13	J	58	ASN
13	J	80	HIS
15	L	104	GLN
16	M	88	ASN
17	N	107	ASN
18	O	29	HIS
19	P	66	ASN
21	R	66	HIS
23	T	48	GLN
24	U	40	ASN
25	V	75	GLN
25	V	87	GLN
28	Y	36	GLN
28	Y	58	ASN
36	g	42	ASN
36	g	122	GLN
36	g	168	HIS
37	h	102	ASN
37	h	139	GLN
38	i	126	ASN
38	i	136	GLN
40	k	14	GLN
40	k	46	GLN
41	l	52	GLN
41	l	148	ASN
44	o	70	HIS
48	s	66	GLN
49	t	80	GLN

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Mol	Chain	Res	Type
50	u	40	ASN
53	x	52	HIS
54	y	48	GLN
54	y	61	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2904 (99%)	456 (15%)	10 (0%)
2	2	1532/1540 (99%)	228 (14%)	3 (0%)
3	3	119/120 (99%)	20 (16%)	0
4	4	10/18 (55%)	8 (80%)	0
5	5	76/77 (98%)	34 (44%)	5 (6%)
All	All	4639/4659 (99%)	746 (16%)	18 (0%)

All (746) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	27	G
1	1	34	U
1	1	35	G
1	1	46	G
1	1	51	G
1	1	60	G
1	1	63	A
1	1	71	A
1	1	74	A
1	1	75	G
1	1	80	G
1	1	85	G
1	1	102	U
1	1	118	A
1	1	120	U
1	1	136	G
1	1	137	U
1	1	139	U
1	1	163	C
1	1	181	A
1	1	196	A
1	1	199	A

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Mol	Chain	Res	Type
1	1	216	A
1	1	222	A
1	1	225	C
1	1	242	G
1	1	248	G
1	1	249	C
1	1	266	G
1	1	273	G
1	1	275	C
1	1	276	U
1	1	285	G
1	1	311	A
1	1	329	G
1	1	330	A
1	1	352	A
1	1	353	C
1	1	361	G
1	1	362	A
1	1	368	A
1	1	371	A
1	1	372	G
1	1	373	U
1	1	385	C
1	1	386	G
1	1	396	G
1	1	405	U
1	1	406	G
1	1	411	G
1	1	424	G
1	1	451	U
1	1	457	A
1	1	481	G
1	1	490	C
1	1	491	G
1	1	496	G
1	1	501	A
1	1	509	C
1	1	529	A
1	1	530	G
1	1	531	C
1	1	532	A
1	1	538	A

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Mol	Chain	Res	Type
1	1	540	C
1	1	541	A
1	1	542	C
1	1	543	G
1	1	546	U
1	1	547	A
1	1	548	G
1	1	549	G
1	1	551	G
1	1	563	A
1	1	573	U
1	1	575	A
1	1	592	A
1	1	603	A
1	1	609	A
1	1	613	A
1	1	614	A
1	1	615	U
1	1	621	A
1	1	627	A
1	1	637	A
1	1	645	C
1	1	646	U
1	1	647	G
1	1	654	A
1	1	669	G
1	1	675	A
1	1	686	U
1	1	710	U
1	1	717	C
1	1	726	G
1	1	729	G
1	1	730	A
1	1	747	5MU
1	1	763	G
1	1	764	A
1	1	775	G
1	1	776	G
1	1	782	A
1	1	784	G
1	1	785	G
1	1	789	A

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Mol	Chain	Res	Type
1	1	805	G
1	1	811	U
1	1	812	C
1	1	819	A
1	1	827	U
1	1	828	U
1	1	845	A
1	1	846	U
1	1	858	G
1	1	859	G
1	1	877	A
1	1	878	A
1	1	884	U
1	1	885	C
1	1	893	C
1	1	895	U
1	1	896	A
1	1	907	G
1	1	910	A
1	1	914	G
1	1	915	C
1	1	919	U
1	1	931	U
1	1	941	A
1	1	946	C
1	1	953	G
1	1	961	C
1	1	973	A
1	1	974	G
1	1	980	A
1	1	983	A
1	1	995	C
1	1	996	A
1	1	1009	A
1	1	1012	U
1	1	1013	C
1	1	1026	G
1	1	1028	A
1	1	1029	A
1	1	1030	C
1	1	1033	U
1	1	1042	G

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Mol	Chain	Res	Type
1	1	1043	C
1	1	1046	A
1	1	1047	G
1	1	1051	G
1	1	1061	U
1	1	1065	U
1	1	1066	U
1	1	1068	G
1	1	1070	A
1	1	1071	G
1	1	1073	A
1	1	1084	A
1	1	1087	G
1	1	1088	A
1	1	1096	A
1	1	1097	U
1	1	1111	A
1	1	1112	G
1	1	1116	G
1	1	1130	U
1	1	1132	U
1	1	1133	A
1	1	1134	A
1	1	1135	C
1	1	1142	A
1	1	1155	A
1	1	1169	A
1	1	1171	G
1	1	1172	C
1	1	1174	U
1	1	1175	A
1	1	1179	G
1	1	1186	G
1	1	1199	U
1	1	1200	C
1	1	1201	U
1	1	1204	A
1	1	1212	G
1	1	1225	G
1	1	1236	G
1	1	1238	G
1	1	1250	G

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Mol	Chain	Res	Type
1	1	1253	A
1	1	1255	U
1	1	1256	G
1	1	1266	G
1	1	1271	G
1	1	1272	A
1	1	1273	U
1	1	1300	G
1	1	1301	A
1	1	1302	A
1	1	1314	C
1	1	1325	U
1	1	1345	C
1	1	1365	A
1	1	1368	G
1	1	1378	A
1	1	1379	U
1	1	1380	G
1	1	1383	A
1	1	1386	C
1	1	1408	G
1	1	1416	G
1	1	1417	C
1	1	1420	A
1	1	1428	C
1	1	1437	C
1	1	1453	A
1	1	1458	U
1	1	1459	G
1	1	1460	U
1	1	1467	U
1	1	1482	G
1	1	1490	A
1	1	1494	A
1	1	1497	U
1	1	1503	A
1	1	1508	A
1	1	1510	G
1	1	1515	A
1	1	1524	G
1	1	1534	U
1	1	1535	A

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Mol	Chain	Res	Type
1	1	1536	C
1	1	1537	G
1	1	1555	G
1	1	1558	C
1	1	1559	U
1	1	1566	A
1	1	1569	A
1	1	1578	U
1	1	1581	G
1	1	1583	A
1	1	1589	U
1	1	1590	A
1	1	1610	A
1	1	1617	C
1	1	1618	6MZ
1	1	1619	G
1	1	1647	U
1	1	1648	U
1	1	1649	G
1	1	1674	G
1	1	1715	G
1	1	1729	U
1	1	1730	C
1	1	1732	C
1	1	1735	A
1	1	1738	G
1	1	1756	G
1	1	1757	A
1	1	1764	C
1	1	1773	A
1	1	1781	U
1	1	1800	C
1	1	1801	A
1	1	1808	A
1	1	1815	A
1	1	1816	C
1	1	1829	A
1	1	1833	C
1	1	1835	2MG
1	1	1848	A
1	1	1858	A
1	1	1864	U

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Mol	Chain	Res	Type
1	1	1865	U
1	1	1866	A
1	1	1869	G
1	1	1872	A
1	1	1906	G
1	1	1913	A
1	1	1916	A
1	1	1924	C
1	1	1927	A
1	1	1929	G
1	1	1930	G
1	1	1931	U
1	1	1937	A
1	1	1955	U
1	1	1963	U
1	1	1964	G
1	1	1967	C
1	1	1970	A
1	1	1971	U
1	1	1972	G
1	1	1991	U
1	1	1992	G
1	1	1993	U
1	1	1997	C
1	1	2020	A
1	1	2022	U
1	1	2023	C
1	1	2030	A
1	1	2031	A
1	1	2033	A
1	1	2043	C
1	1	2052	A
1	1	2055	C
1	1	2059	A
1	1	2060	A
1	1	2061	G
1	1	2062	A
1	1	2069	G7M
1	1	2072	C
1	1	2093	G
1	1	2107	G
1	1	2110	G

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Mol	Chain	Res	Type
1	1	2111	U
1	1	2113	U
1	1	2115	G
1	1	2116	G
1	1	2117	A
1	1	2118	U
1	1	2120	G
1	1	2123	G
1	1	2124	G
1	1	2125	G
1	1	2126	A
1	1	2131	U
1	1	2132	U
1	1	2133	G
1	1	2134	A
1	1	2142	A
1	1	2146	C
1	1	2147	A
1	1	2157	G
1	1	2158	A
1	1	2162	G
1	1	2164	C
1	1	2165	C
1	1	2171	A
1	1	2172	U
1	1	2182	U
1	1	2183	A
1	1	2189	U
1	1	2193	G
1	1	2194	U
1	1	2198	A
1	1	2204	G
1	1	2211	A
1	1	2212	A
1	1	2226	C
1	1	2238	G
1	1	2239	G
1	1	2243	U
1	1	2250	G
1	1	2255	G
1	1	2266	A
1	1	2283	C

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Mol	Chain	Res	Type
1	1	2287	A
1	1	2297	A
1	1	2305	U
1	1	2309	A
1	1	2319	G
1	1	2322	A
1	1	2325	G
1	1	2327	A
1	1	2333	A
1	1	2334	U
1	1	2335	A
1	1	2347	C
1	1	2361	G
1	1	2383	G
1	1	2385	C
1	1	2402	U
1	1	2403	C
1	1	2423	U
1	1	2425	A
1	1	2426	A
1	1	2429	G
1	1	2430	A
1	1	2431	U
1	1	2435	A
1	1	2441	U
1	1	2447	G
1	1	2448	A
1	1	2475	C
1	1	2476	A
1	1	2491	U
1	1	2494	G
1	1	2498	OMC
1	1	2502	G
1	1	2503	2MA
1	1	2504	PSU
1	1	2505	G
1	1	2506	U
1	1	2507	C
1	1	2512	C
1	1	2513	A
1	1	2518	A
1	1	2520	C

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Mol	Chain	Res	Type
1	1	2529	G
1	1	2535	G
1	1	2554	U
1	1	2566	A
1	1	2567	G
1	1	2572	A
1	1	2573	C
1	1	2574	G
1	1	2582	G
1	1	2585	U
1	1	2586	U
1	1	2602	A
1	1	2609	U
1	1	2613	U
1	1	2615	U
1	1	2629	U
1	1	2630	G
1	1	2639	A
1	1	2646	C
1	1	2689	U
1	1	2690	U
1	1	2714	G
1	1	2718	G
1	1	2725	A
1	1	2726	A
1	1	2729	G
1	1	2733	A
1	1	2739	U
1	1	2744	G
1	1	2748	A
1	1	2751	G
1	1	2752	C
1	1	2757	A
1	1	2765	A
1	1	2777	G
1	1	2778	A
1	1	2780	G
1	1	2793	C
1	1	2794	C
1	1	2797	U
1	1	2798	U
1	1	2818	U

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Mol	Chain	Res	Type
1	1	2820	A
1	1	2825	G
1	1	2835	A
1	1	2849	U
1	1	2867	G
1	1	2873	A
1	1	2879	A
1	1	2880	C
1	1	2883	A
1	1	2884	U
1	1	2885	G
1	1	2898	U
1	1	2901	C
2	2	2	A
2	2	3	A
2	2	4	U
2	2	9	G
2	2	32	A
2	2	39	G
2	2	47	C
2	2	48	C
2	2	50	A
2	2	51	A
2	2	54	C
2	2	68	G
2	2	69	G
2	2	72	A
2	2	74	A
2	2	75	G
2	2	83	C
2	2	84	U
2	2	85	U
2	2	86	G
2	2	87	C
2	2	94	G
2	2	95	C
2	2	108	G
2	2	120	A
2	2	121	U
2	2	128	G
2	2	129	A
2	2	130	A

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Mol	Chain	Res	Type
2	2	131	A
2	2	144	G
2	2	173	U
2	2	177	G
2	2	181	A
2	2	183	C
2	2	197	A
2	2	204	G
2	2	209	U
2	2	211	G
2	2	212	G
2	2	226	G
2	2	240	G
2	2	247	G
2	2	251	G
2	2	266	G
2	2	267	C
2	2	279	A
2	2	280	C
2	2	281	G
2	2	289	G
2	2	328	C
2	2	330	C
2	2	332	G
2	2	347	G
2	2	351	G
2	2	352	C
2	2	354	G
2	2	367	U
2	2	372	C
2	2	373	A
2	2	406	G
2	2	412	A
2	2	413	G
2	2	414	A
2	2	421	U
2	2	422	C
2	2	424	G
2	2	429	U
2	2	451	A
2	2	456	A
2	2	457	G

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Mol	Chain	Res	Type
2	2	458	U
2	2	463	U
2	2	464	U
2	2	467	U
2	2	468	A
2	2	478	A
2	2	479	U
2	2	481	G
2	2	484	G
2	2	485	U
2	2	493	A
2	2	496	A
2	2	497	G
2	2	509	A
2	2	511	C
2	2	512	U
2	2	517	G
2	2	518	C
2	2	519	C
2	2	521	G
2	2	527	7MG
2	2	532	A
2	2	547	A
2	2	559	A
2	2	564	C
2	2	572	A
2	2	573	A
2	2	576	C
2	2	577	G
2	2	596	A
2	2	633	G
2	2	650	G
2	2	653	U
2	2	665	A
2	2	687	A
2	2	700	G
2	2	721	G
2	2	723	U
2	2	731	G
2	2	734	G
2	2	747	A
2	2	755	G

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Mol	Chain	Res	Type
2	2	777	A
2	2	793	U
2	2	794	A
2	2	815	A
2	2	817	C
2	2	821	G
2	2	828	U
2	2	829	G
2	2	832	G
2	2	841	C
2	2	844	G
2	2	846	G
2	2	851	G
2	2	889	A
2	2	902	G
2	2	914	A
2	2	926	G
2	2	934	C
2	2	935	A
2	2	960	U
2	2	961	U
2	2	966	2MG
2	2	967	5MC
2	2	968	A
2	2	969	A
2	2	971	G
2	2	975	A
2	2	976	G
2	2	977	A
2	2	989	U
2	2	992	U
2	2	993	G
2	2	996	A
2	2	1004	A
2	2	1008	U
2	2	1009	U
2	2	1010	U
2	2	1018	G
2	2	1021	A
2	2	1023	U
2	2	1026	G
2	2	1030	U

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Mol	Chain	Res	Type
2	2	1032	G
2	2	1044	A
2	2	1045	C
2	2	1064	G
2	2	1065	U
2	2	1066	C
2	2	1085	U
2	2	1094	G
2	2	1095	U
2	2	1101	A
2	2	1108	G
2	2	1124	G
2	2	1132	C
2	2	1133	G
2	2	1135	U
2	2	1136	C
2	2	1137	C
2	2	1139	G
2	2	1140	C
2	2	1141	C
2	2	1142	G
2	2	1147	C
2	2	1149	C
2	2	1151	A
2	2	1152	A
2	2	1158	C
2	2	1159	U
2	2	1167	A
2	2	1176	A
2	2	1184	G
2	2	1196	A
2	2	1197	A
2	2	1213	A
2	2	1214	C
2	2	1227	A
2	2	1228	C
2	2	1239	A
2	2	1257	A
2	2	1261	A
2	2	1269	A
2	2	1275	A
2	2	1279	G

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Mol	Chain	Res	Type
2	2	1280	A
2	2	1286	U
2	2	1287	A
2	2	1299	A
2	2	1300	G
2	2	1302	C
2	2	1305	G
2	2	1317	C
2	2	1320	C
2	2	1322	C
2	2	1363	A
2	2	1379	G
2	2	1384	C
2	2	1398	A
2	2	1419	G
2	2	1429	A
2	2	1432	G
2	2	1441	A
2	2	1446	A
2	2	1452	C
2	2	1492	A
2	2	1493	A
2	2	1494	G
2	2	1499	A
2	2	1503	A
2	2	1517	G
2	2	1519	MA6
2	2	1520	C
2	2	1529	G
2	2	1530	G
2	2	1534	A
3	3	2	G
3	3	13	G
3	3	15	A
3	3	35	C
3	3	44	G
3	3	45	A
3	3	53	A
3	3	56	G
3	3	57	A
3	3	68	C
3	3	74	U

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Mol	Chain	Res	Type
3	3	78	A
3	3	79	G
3	3	88	C
3	3	89	U
3	3	90	C
3	3	99	A
3	3	105	G
3	3	109	A
3	3	116	G
4	4	12	A
4	4	13	U
4	4	15	C
4	4	16	C
4	4	18	C
4	4	19	G
4	4	20	U
4	4	21	U
5	5	2	G
5	5	3	G
5	5	4	C
5	5	5	A
5	5	6	C
5	5	7	G
5	5	8	U
5	5	10	G
5	5	14	A
5	5	16	C
5	5	17	C
5	5	18	G
5	5	19	G
5	5	20	U
5	5	21	A
5	5	22	G
5	5	42	G
5	5	43	G
5	5	46	G
5	5	47	U
5	5	53	G
5	5	54	U
5	5	55	U
5	5	56	C
5	5	57	A

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Mol	Chain	Res	Type
5	5	60	U
5	5	61	C
5	5	66	C
5	5	69	G
5	5	72	G
5	5	73	A
5	5	74	C
5	5	75	C
5	5	76	A

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	404	A
1	1	784	G
1	1	894	U
1	1	1379	U
1	1	1962	5MC
1	1	2193	G
1	1	2225	A
1	1	2286	G
1	1	2425	A
1	1	2756	U
2	2	516	PSU
2	2	1109	C
2	2	1383	C
5	5	2	G
5	5	3	G
5	5	19	G
5	5	59	A
5	5	72	G

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

32 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
1	OMG	1	2251	1,5	23,26,27	0.47	0	32,38,41	0.53	0
2	2MG	2	1207	2	23,26,27	0.46	0	33,38,41	0.48	0
2	PSU	2	516	2	18,21,22	1.08	1 (5%)	21,30,33	1.87	5 (23%)
2	2MG	2	966	2	23,26,27	1.35	4 (17%)	33,38,41	2.28	9 (27%)
2	7MG	2	527	2	23,26,27	1.09	1 (4%)	27,39,42	0.89	2 (7%)
2	5MC	2	967	2	19,22,23	1.53	3 (15%)	26,32,35	1.35	4 (15%)
1	PSU	1	955	1	18,21,22	1.13	1 (5%)	21,30,33	1.85	4 (19%)
2	2MG	2	1516	2	23,26,27	0.48	0	33,38,41	0.57	0
1	5MU	1	1939	56,1	19,22,23	0.42	0	27,32,35	0.49	0
1	2MG	1	2445	1	23,26,27	0.47	0	33,38,41	0.49	0
1	PSU	1	2457	1	18,21,22	1.07	1 (5%)	21,30,33	1.92	6 (28%)
1	G7M	1	2069	1	23,26,27	2.78	9 (39%)	34,39,42	2.22	11 (32%)
1	5MU	1	747	1	19,22,23	0.43	0	27,32,35	0.57	0
1	2MG	1	1835	1	23,26,27	0.45	0	33,38,41	0.48	0
1	PSU	1	2605	1	18,21,22	1.13	1 (5%)	21,30,33	1.96	5 (23%)
1	PSU	1	2504	1	18,21,22	1.57	5 (27%)	21,30,33	2.11	4 (19%)
1	PSU	1	2580	1	18,21,22	1.10	2 (11%)	21,30,33	2.17	6 (28%)
1	1MG	1	745	1	23,26,27	3.10	7 (30%)	33,39,42	1.92	9 (27%)
1	PSU	1	1917	1	18,21,22	1.10	1 (5%)	21,30,33	1.96	5 (23%)
1	6MZ	1	1618	1	22,25,26	3.75	12 (54%)	29,36,39	3.74	12 (41%)
1	PSU	1	746	56,1	18,21,22	1.09	1 (5%)	21,30,33	1.87	5 (23%)
1	OMU	1	2552	1	19,22,23	3.07	8 (42%)	25,31,34	1.82	5 (20%)
2	MA6	2	1519	2	23,26,27	1.53	4 (17%)	33,38,41	3.29	12 (36%)
2	MA6	2	1518	2	23,26,27	1.53	3 (13%)	33,38,41	3.20	11 (33%)
46	0TD	q	89	46	8,9,10	1.78	2 (25%)	6,11,13	1.77	1 (16%)
1	OMC	1	2498	1	19,22,23	0.55	0	25,31,34	0.67	0
2	4OC	2	1402	2	20,23,24	3.20	8 (40%)	25,32,35	0.88	1 (4%)
1	PSU	1	1911	1	18,21,22	1.13	1 (5%)	21,30,33	1.95	5 (23%)
2	5MC	2	1407	2	19,22,23	0.55	0	26,32,35	0.63	0
1	5MC	1	1962	1	19,22,23	0.57	0	26,32,35	0.58	0
2	UR3	2	1498	2	19,22,23	2.80	8 (42%)	26,32,35	1.58	4 (15%)
1	2MA	1	2503	56,1	22,25,26	4.63	14 (63%)	32,37,40	2.98	10 (31%)

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
1	OMG	1	2251	1,5	-	0/9/27/28	0/3/3/3
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
2	7MG	2	527	2	-	3/7/37/38	0/3/3/3
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
1	5MU	1	1939	56,1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	0/9/27/28	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	0/7/25/26	0/3/3/3
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	1/9/27/28	0/3/3/3
1	PSU	1	746	56,1	-	0/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
46	0TD	q	89	46	-	3/7/12/14	-
1	OMC	1	2498	1	-	0/9/27/28	0/2/2/2
2	4OC	2	1402	2	-	1/9/29/30	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
2	UR3	2	1498	2	-	2/7/25/26	0/2/2/2
1	2MA	1	2503	56,1	-	3/7/25/26	0/3/3/3

All (97) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2503	2MA	C4-N3	10.93	1.48	1.34
1	1	1618	6MZ	C3'-C4'	-9.25	1.29	1.53
1	1	1618	6MZ	C6-N6	9.25	1.44	1.34
1	1	2503	2MA	C3'-C4'	-9.14	1.29	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	745	1MG	C2-N3	8.99	1.47	1.33
2	2	1498	UR3	C2-N1	7.45	1.48	1.38
2	2	1402	4OC	C4-N3	7.37	1.45	1.32
1	1	2503	2MA	O4'-C4'	7.30	1.61	1.45
1	1	1618	6MZ	O4'-C4'	7.17	1.60	1.45
1	1	2552	OMU	C2-N1	7.15	1.49	1.38
1	1	2552	OMU	C2-N3	6.97	1.50	1.38
1	1	2503	2MA	C2-N3	6.86	1.45	1.34
1	1	745	1MG	C4-N3	6.75	1.49	1.34
1	1	2069	G7M	C4-N3	6.64	1.49	1.34
1	1	745	1MG	C2-N2	6.35	1.45	1.34
2	2	1402	4OC	C2-N3	6.31	1.48	1.36
2	2	1402	4OC	C6-C5	6.22	1.49	1.35
2	2	1498	UR3	C6-C5	6.14	1.49	1.35
1	1	2069	G7M	C2-N2	5.83	1.47	1.34
1	1	2503	2MA	C6-N1	5.72	1.42	1.35
1	1	2552	OMU	C6-C5	5.71	1.48	1.35
1	1	2503	2MA	C2-N1	5.67	1.43	1.34
1	1	2069	G7M	C2-N3	5.21	1.45	1.33
2	2	1518	MA6	C6-N6	4.98	1.50	1.36
2	2	1519	MA6	C6-N6	4.97	1.50	1.36
2	2	967	5MC	C5-C4	4.96	1.47	1.44
1	1	2503	2MA	O4'-C1'	-4.95	1.30	1.42
2	2	1498	UR3	C2-N3	4.95	1.48	1.39
1	1	1618	6MZ	O4'-C1'	-4.69	1.31	1.42
2	2	1402	4OC	C4-N4	4.66	1.45	1.36
2	2	527	7MG	C5-N7	4.50	1.41	1.35
2	2	1402	4OC	C2-N1	4.33	1.49	1.40
1	1	2552	OMU	C4-N3	4.19	1.45	1.38
1	1	2069	G7M	C5-N7	-4.12	1.34	1.39
1	1	2503	2MA	C5-C6	4.11	1.52	1.41
1	1	2069	G7M	C5-C6	4.08	1.54	1.43
1	1	745	1MG	C5-C6	3.82	1.55	1.45
2	2	516	PSU	C6-C5	3.72	1.39	1.35
1	1	955	PSU	C6-C5	3.72	1.39	1.35
1	1	2605	PSU	C6-C5	3.70	1.39	1.35
2	2	1402	4OC	C5-C4	3.67	1.49	1.41
1	1	1618	6MZ	C5-C4	-3.66	1.32	1.39
1	1	1911	PSU	C6-C5	3.66	1.39	1.35
1	1	2069	G7M	C2-N1	3.65	1.46	1.37
1	1	1917	PSU	C6-C5	3.58	1.39	1.35
1	1	2503	2MA	C6-N6	-3.55	1.25	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2503	2MA	C5-N7	-3.47	1.32	1.39
1	1	745	1MG	C2-N1	3.46	1.43	1.37
1	1	746	PSU	C6-C5	3.41	1.39	1.35
1	1	2457	PSU	C6-C5	3.40	1.39	1.35
1	1	745	1MG	C5-N7	-3.35	1.32	1.39
1	1	2504	PSU	C4-N3	-3.23	1.32	1.38
1	1	2580	PSU	C6-C5	3.20	1.38	1.35
2	2	1402	4OC	C6-N1	3.18	1.45	1.38
1	1	1618	6MZ	C5-N7	-3.11	1.33	1.39
1	1	1618	6MZ	O2'-C2'	-3.09	1.35	1.43
1	1	2503	2MA	O2'-C2'	-3.05	1.35	1.43
2	2	1498	UR3	C6-N1	3.01	1.45	1.38
1	1	2069	G7M	O6-C6	-3.00	1.17	1.23
46	q	89	0TD	CB-CA	-2.91	1.53	1.54
1	1	2552	OMU	O4-C4	-2.90	1.18	1.24
1	1	2552	OMU	C6-N1	2.82	1.44	1.38
2	2	966	2MG	C6-N1	-2.79	1.33	1.38
1	1	2503	2MA	O3'-C3'	2.79	1.49	1.43
2	2	966	2MG	C5-C4	2.78	1.46	1.38
2	2	967	5MC	C6-N1	-2.76	1.33	1.38
1	1	2504	PSU	C6-C5	2.75	1.38	1.35
1	1	2503	2MA	C4-N9	-2.75	1.32	1.37
2	2	1519	MA6	C5-C4	-2.71	1.34	1.39
1	1	1618	6MZ	O3'-C3'	2.68	1.49	1.43
2	2	1518	MA6	C5-C4	-2.68	1.34	1.39
2	2	1402	4OC	O2-C2	-2.64	1.18	1.23
1	1	2069	G7M	C6-N1	2.63	1.43	1.38
1	1	745	1MG	C8-N9	-2.49	1.31	1.37
1	1	2504	PSU	C2-N3	-2.48	1.33	1.37
2	2	1498	UR3	C4-N3	2.44	1.45	1.40
2	2	1518	MA6	C5-N7	-2.42	1.34	1.39
1	1	1618	6MZ	C4-N9	-2.41	1.32	1.37
1	1	2552	OMU	C5-C4	2.39	1.48	1.43
1	1	2552	OMU	O2-C2	-2.36	1.18	1.23
1	1	1618	6MZ	C5-C6	-2.36	1.36	1.41
2	2	966	2MG	C5-N7	-2.35	1.34	1.39
2	2	967	5MC	C6-C5	2.34	1.38	1.34
1	1	1618	6MZ	C8-N9	-2.30	1.33	1.37
2	2	1519	MA6	C5-N7	-2.30	1.34	1.39
1	1	2504	PSU	C2-N1	-2.27	1.33	1.36
2	2	1498	UR3	O4-C4	-2.27	1.18	1.23
2	2	1519	MA6	C8-N9	-2.26	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2504	PSU	C2'-C1'	-2.25	1.50	1.53
2	2	1498	UR3	C5-C4	2.24	1.49	1.43
1	1	2580	PSU	O4'-C1'	-2.19	1.40	1.43
1	1	2069	G7M	C4-N9	-2.17	1.32	1.38
2	2	1498	UR3	O2-C2	-2.14	1.18	1.22
1	1	1618	6MZ	C6-N1	-2.14	1.31	1.35
2	2	966	2MG	C4-N9	-2.06	1.32	1.38
1	1	2503	2MA	C8-N9	-2.04	1.34	1.37
46	q	89	0TD	OD1-CG	2.02	1.28	1.22

All (136) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	N1-C6-N6	-11.98	102.26	116.86
2	2	1518	MA6	N1-C6-N6	-11.59	102.74	116.86
1	1	1618	6MZ	C1'-N9-C8	-11.54	101.47	127.09
1	1	1618	6MZ	C4-N9-C1'	10.19	150.46	126.63
1	1	2503	2MA	C1'-N9-C8	-8.84	107.48	127.09
2	2	1519	MA6	C5-C6-N6	7.94	137.90	125.33
2	2	1518	MA6	C5-C6-N6	7.71	137.54	125.33
2	2	966	2MG	C2-N3-C4	7.14	120.93	112.00
1	1	2504	PSU	N1-C2-N3	6.66	122.19	115.17
1	1	2503	2MA	C4-N9-C1'	6.54	141.94	126.63
2	2	966	2MG	C5-C4-N3	-6.19	118.53	128.39
1	1	2503	2MA	C5-C4-N3	-6.17	120.68	127.18
1	1	2069	G7M	CN7-N7-C5	5.77	134.00	126.80
1	1	1618	6MZ	N1-C2-N3	-5.71	119.93	128.58
1	1	2552	OMU	C4-N3-C2	-5.67	119.57	126.61
2	2	1519	MA6	N1-C2-N3	-5.60	120.10	128.58
2	2	1518	MA6	N1-C2-N3	-5.54	120.20	128.58
1	1	2503	2MA	N9-C8-N7	-5.38	106.30	113.94
2	2	1498	UR3	C4-N3-C2	-5.37	120.25	124.58
1	1	2580	PSU	N1-C2-N3	5.18	120.63	115.17
1	1	2580	PSU	C4-N3-C2	-4.99	119.49	126.37
2	2	1519	MA6	C5-C4-N3	-4.96	119.89	126.72
1	1	1917	PSU	C4-N3-C2	-4.92	119.59	126.37
2	2	1518	MA6	C5-C4-N3	-4.92	119.94	126.72
1	1	1911	PSU	C4-N3-C2	-4.91	119.61	126.37
1	1	746	PSU	C4-N3-C2	-4.90	119.61	126.37
1	1	745	1MG	C5-C4-N3	-4.88	120.62	128.39
1	1	2503	2MA	N3-C4-N9	4.87	133.17	126.99
1	1	1911	PSU	N1-C2-N3	4.85	120.28	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1917	PSU	N1-C2-N3	4.85	120.28	115.17
1	1	2605	PSU	C4-N3-C2	-4.82	119.73	126.37
1	1	1618	6MZ	C9-N6-C6	-4.82	118.38	122.85
1	1	2605	PSU	N1-C2-N3	4.78	120.21	115.17
1	1	2457	PSU	N1-C2-N3	4.77	120.20	115.17
1	1	2457	PSU	C4-N3-C2	-4.71	119.89	126.37
1	1	746	PSU	N1-C2-N3	4.65	120.07	115.17
1	1	955	PSU	C4-N3-C2	-4.61	120.02	126.37
1	1	2503	2MA	C4-N9-C8	4.60	110.57	105.74
2	2	516	PSU	C4-N3-C2	-4.58	120.06	126.37
1	1	955	PSU	N1-C2-N3	4.56	119.97	115.17
2	2	516	PSU	N1-C2-N3	4.54	119.95	115.17
1	1	2069	G7M	CN7-N7-C8	-4.52	117.95	124.79
1	1	1618	6MZ	C5-C4-N3	-4.51	120.50	126.72
2	2	966	2MG	N9-C4-N3	4.50	134.94	125.95
1	1	2504	PSU	C4-N3-C2	-4.33	120.41	126.37
1	1	2069	G7M	C2-N3-C4	4.28	119.67	112.30
2	2	1519	MA6	N9-C8-N7	-4.16	108.03	113.94
2	2	1518	MA6	C4-C5-C6	4.14	120.19	115.91
1	1	1618	6MZ	N9-C8-N7	-4.11	108.10	113.94
2	2	1519	MA6	C4-C5-C6	4.01	120.06	115.91
2	2	1518	MA6	N9-C8-N7	-3.99	108.27	113.94
1	1	745	1MG	C1'-N9-C4	-3.96	114.79	126.49
1	1	2552	OMU	N3-C2-N1	3.95	120.03	114.89
1	1	2069	G7M	C5-C6-N1	3.85	119.81	111.84
1	1	745	1MG	N9-C8-N7	-3.79	106.37	113.40
1	1	2069	G7M	C5-C4-N3	-3.68	121.19	128.15
2	2	967	5MC	C5-C6-N1	-3.64	119.36	123.31
1	1	2552	OMU	C5-C4-N3	3.63	119.88	114.80
1	1	2504	PSU	O2-C2-N1	-3.59	119.09	122.79
2	2	1498	UR3	C5-C4-N3	3.57	119.74	115.04
1	1	2069	G7M	O6-C6-C5	-3.55	120.09	128.01
1	1	2580	PSU	O2-C2-N1	-3.50	119.17	122.79
1	1	745	1MG	N9-C4-N3	3.50	132.94	125.95
1	1	1618	6MZ	C4-C5-C6	3.49	119.68	116.78
1	1	745	1MG	C2-N3-C4	3.44	119.71	111.98
1	1	2069	G7M	C1'-N9-C8	-3.43	115.14	126.74
2	2	1518	MA6	C2-N1-C6	3.38	120.10	111.83
2	2	1519	MA6	C2-N1-C6	3.38	120.09	111.83
2	2	1519	MA6	C2-N3-C4	3.35	120.02	111.83
2	2	966	2MG	C6-C5-N7	3.28	136.27	130.29
2	2	1518	MA6	C2-N3-C4	3.28	119.85	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2069	G7M	C1'-N9-C4	3.27	136.15	126.49
1	1	1618	6MZ	C2-N3-C4	3.22	119.70	111.83
1	1	2457	PSU	O2-C2-N1	-3.15	119.54	122.79
46	q	89	0TD	OD2-CG-CB	3.12	119.89	113.15
1	1	2069	G7M	C2-N1-C6	-3.11	119.47	125.11
2	2	1519	MA6	N3-C4-N9	3.11	132.45	127.17
1	1	1618	6MZ	O4'-C1'-N9	3.09	114.02	108.09
1	1	2503	2MA	C5-N7-C8	3.06	108.27	103.45
2	2	1518	MA6	N3-C4-N9	3.01	132.29	127.17
1	1	955	PSU	O2-C2-N1	-2.99	119.70	122.79
1	1	2552	OMU	O4-C4-C5	-2.93	120.10	125.16
1	1	1917	PSU	O2-C2-N1	-2.89	119.81	122.79
1	1	2580	PSU	C6-C5-C4	2.89	120.12	118.17
1	1	745	1MG	C1'-N9-C8	2.88	134.92	126.73
1	1	2605	PSU	O2-C2-N1	-2.83	119.86	122.79
1	1	2503	2MA	N3-C2-N1	-2.83	120.78	125.77
2	2	1519	MA6	C5-N7-C8	2.82	107.88	103.45
1	1	746	PSU	O2-C2-N1	-2.75	119.95	122.79
1	1	1911	PSU	O2-C2-N1	-2.75	119.95	122.79
1	1	2503	2MA	N6-C6-N1	2.74	120.72	117.03
1	1	2580	PSU	C6-N1-C2	-2.74	120.15	122.69
2	2	1518	MA6	C5-N7-C8	2.71	107.71	103.45
1	1	1618	6MZ	N3-C4-N9	2.66	131.69	127.17
1	1	2580	PSU	O4'-C1'-C2'	2.66	108.83	105.15
1	1	745	1MG	C5-C6-N1	2.63	119.88	115.02
2	2	966	2MG	C4-C5-N7	-2.59	106.57	110.67
2	2	967	5MC	C5-C4-N3	-2.56	119.13	121.75
1	1	955	PSU	C6-N1-C2	-2.54	120.33	122.69
2	2	516	PSU	C6-N1-C2	-2.54	120.34	122.69
2	2	966	2MG	C2-N1-C6	-2.48	121.55	124.55
2	2	516	PSU	O2-C2-N1	-2.48	120.23	122.79
1	1	745	1MG	C8-N7-C5	2.46	108.65	104.26
1	1	2605	PSU	C6-N1-C2	-2.46	120.41	122.69
2	2	1519	MA6	C4-N9-C8	2.45	108.31	105.74
1	1	1911	PSU	C6-N1-C2	-2.45	120.42	122.69
1	1	1618	6MZ	C5-N7-C8	2.44	107.28	103.45
1	1	2457	PSU	C6-N1-C2	-2.43	120.43	122.69
2	2	527	7MG	C4-C5-N7	2.40	108.21	105.38
1	1	1917	PSU	C6-N1-C2	-2.37	120.49	122.69
2	2	967	5MC	C2'-C1'-N1	-2.37	106.67	113.25
2	2	1402	4OC	C6-C5-C4	2.36	119.85	117.00
2	2	1498	UR3	C6-N1-C2	-2.34	119.89	121.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2069	G7M	N9-C4-N3	2.31	130.58	125.95
2	2	967	5MC	O2-C2-N3	-2.28	118.74	122.33
1	1	745	1MG	C8-N9-C4	2.28	110.29	106.03
1	1	2552	OMU	O2-C2-N1	-2.23	119.90	122.80
1	1	2503	2MA	C6-C5-C4	2.22	120.21	117.18
1	1	1618	6MZ	C4-N9-C8	2.22	108.07	105.74
2	2	1498	UR3	C1'-N1-C2	2.21	120.65	117.04
2	2	966	2MG	CM2-N2-C2	-2.19	118.94	123.65
2	2	527	7MG	C5-C4-N9	2.17	109.11	106.33
1	1	746	PSU	C6-N1-C2	-2.17	120.68	122.69
2	2	1519	MA6	C4-C5-N7	-2.16	108.11	110.58
1	1	746	PSU	C6-C5-C4	2.16	119.63	118.17
1	1	2069	G7M	N9-C8-N7	-2.15	107.26	112.48
1	1	2605	PSU	C6-C5-C4	2.15	119.62	118.17
2	2	966	2MG	O6-C6-C5	-2.11	120.95	126.53
1	1	1917	PSU	C6-C5-C4	2.10	119.59	118.17
2	2	1518	MA6	C4-N9-C8	2.08	107.92	105.74
2	2	516	PSU	C3'-C2'-C1'	2.06	104.12	101.69
1	1	2457	PSU	C6-C5-C4	2.05	119.56	118.17
2	2	966	2MG	C5-C6-N1	2.03	118.41	113.25
1	1	1911	PSU	C6-C5-C4	2.02	119.54	118.17
1	1	2504	PSU	C5-C6-N1	-2.02	119.34	122.14
1	1	2457	PSU	O4'-C1'-C2'	2.01	107.94	105.15

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
1	1	2504	PSU	O4'-C4'-C5'-O5'
2	2	967	5MC	O4'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
1	1	2504	PSU	C3'-C4'-C5'-O5'
2	2	527	7MG	C3'-C4'-C5'-O5'
1	1	1835	2MG	O4'-C4'-C5'-O5'
1	1	1835	2MG	C3'-C4'-C5'-O5'
1	1	2503	2MA	O4'-C4'-C5'-O5'
1	1	2503	2MA	C3'-C4'-C5'-O5'
2	2	1519	MA6	C3'-C4'-C5'-O5'
2	2	527	7MG	O4'-C4'-C5'-O5'
2	2	967	5MC	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	2	1498	UR3	O4'-C4'-C5'-O5'
2	2	1498	UR3	C3'-C4'-C5'-O5'
46	q	89	0TD	CG-CB-SB-CSB
46	q	89	0TD	SB-CB-CG-OD1
2	2	527	7MG	C4'-C5'-O5'-P
46	q	89	0TD	CA-CB-SB-CSB
2	2	1402	4OC	O4'-C4'-C5'-O5'
1	1	2503	2MA	C4'-C5'-O5'-P
1	1	1618	6MZ	N1-C6-N6-C9

There are no ring outliers.

15 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	516	PSU	1	0
1	1	955	PSU	1	0
2	2	1516	2MG	2	0
1	1	1939	5MU	1	0
1	1	2069	G7M	1	0
1	1	747	5MU	1	0
1	1	2580	PSU	2	0
1	1	745	1MG	1	0
1	1	1917	PSU	1	0
1	1	746	PSU	1	0
1	1	2552	OMU	2	0
2	2	1518	MA6	1	0
46	q	89	0TD	4	0
2	2	1402	4OC	2	0
1	1	1962	5MC	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 396 ligands modelled in this entry, 395 are monoatomic - leaving 1 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
57	LYS	5	101	5	7,8,9	1.10	1 (14%)	3,8,10	0.54	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
57	LYS	5	101	5	-	3/6/7/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	5	101	LYS	O-C	2.61	1.29	1.20

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	5	101	LYS	CE-CD-CG-CB
57	5	101	LYS	CG-CD-CE-NZ
57	5	101	LYS	CA-CB-CG-CD

There are no ring outliers.

No monomer is involved in short contacts.

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.

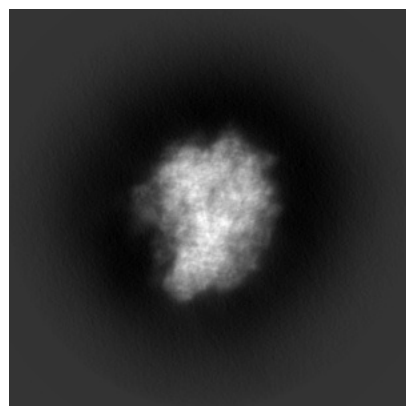
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42714. These allow visual inspection of the internal detail of the map and identification of artifacts.

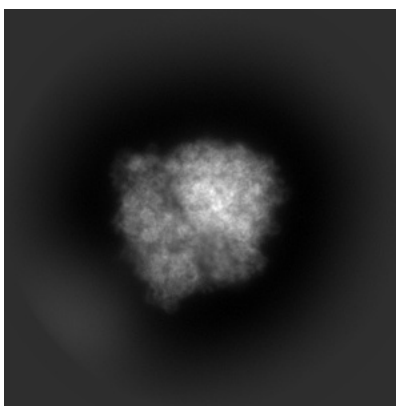
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

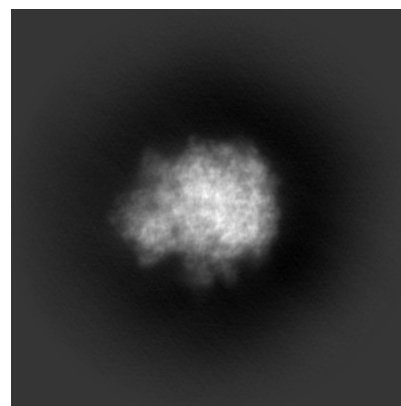
6.1.1 Primary map



X

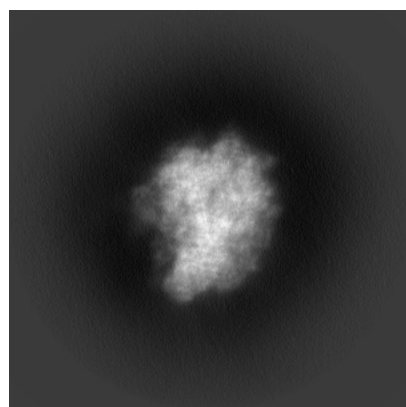


Y

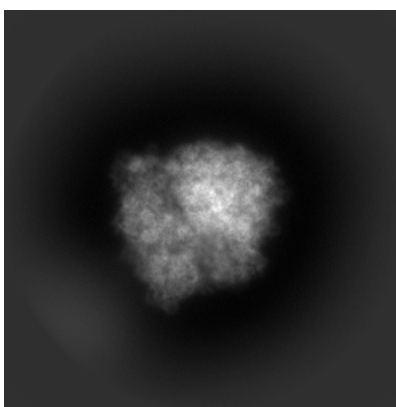


Z

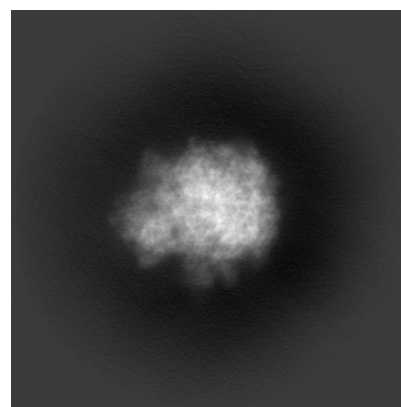
6.1.2 Raw map



X



Y

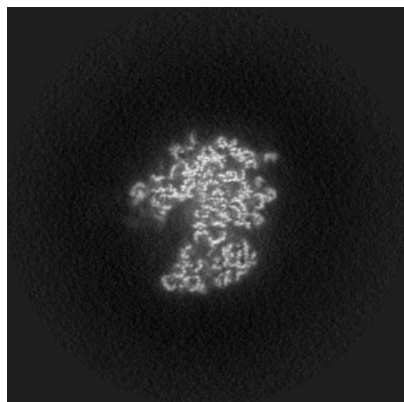


Z

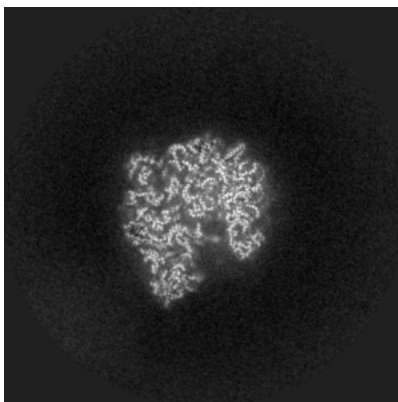
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

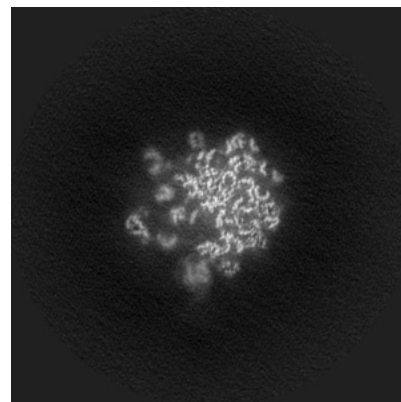
6.2.1 Primary map



X Index: 256

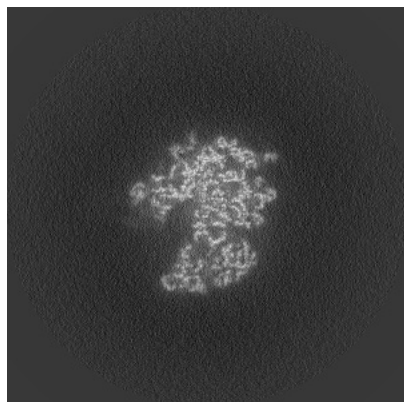


Y Index: 256

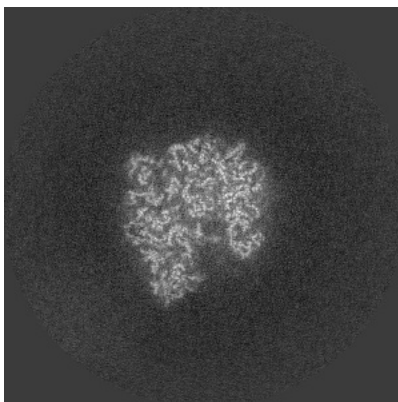


Z Index: 256

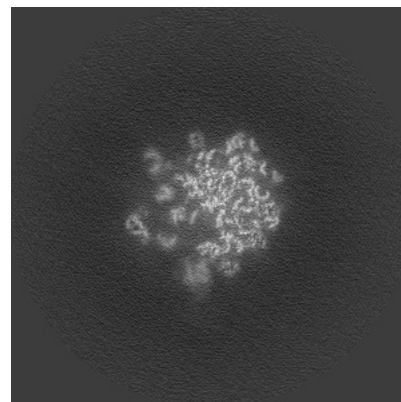
6.2.2 Raw map



X Index: 256



Y Index: 256

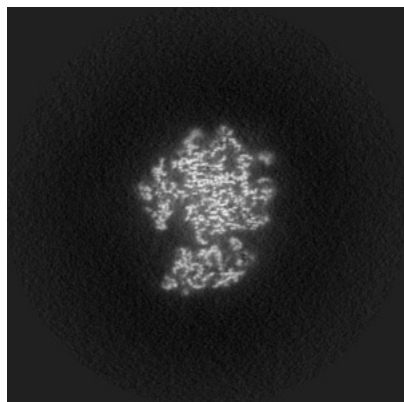


Z Index: 256

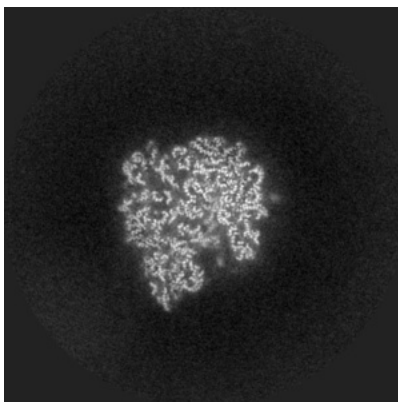
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

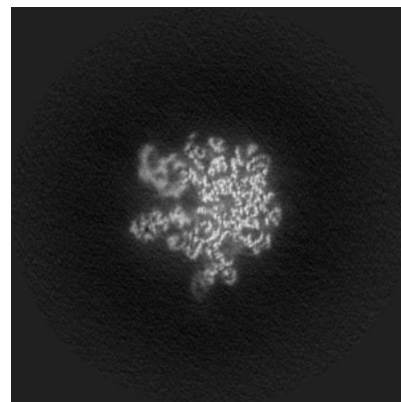
6.3.1 Primary map



X Index: 264

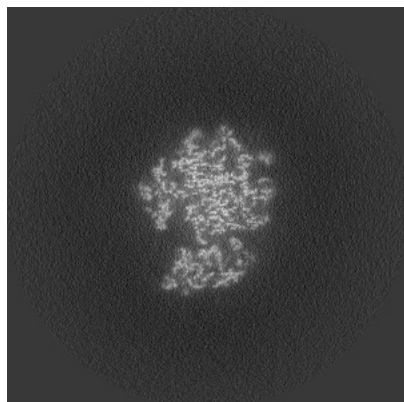


Y Index: 250

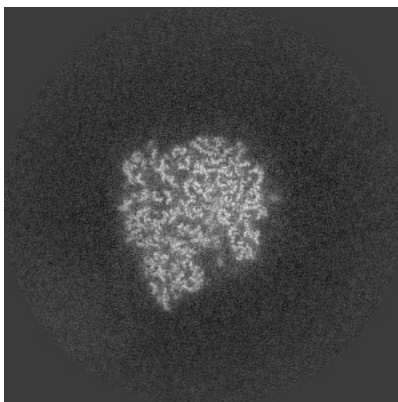


Z Index: 274

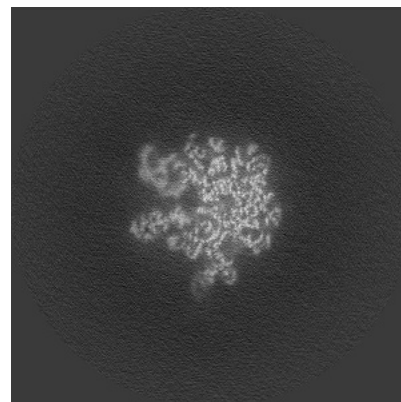
6.3.2 Raw map



X Index: 264



Y Index: 250

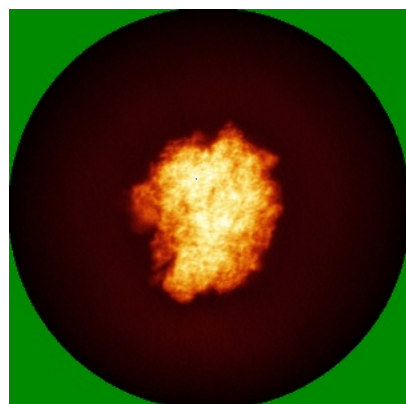


Z Index: 274

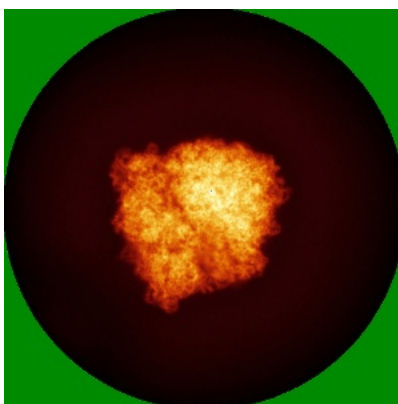
The images above show the largest variance slices of the map in three orthogonal directions.

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

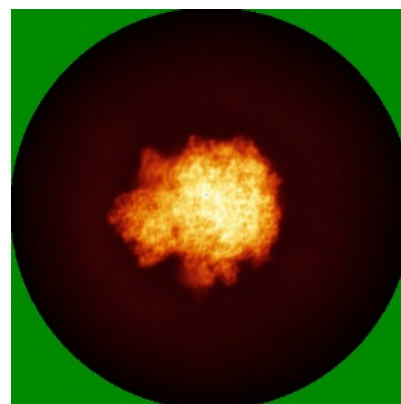
6.4.1 Primary map



X

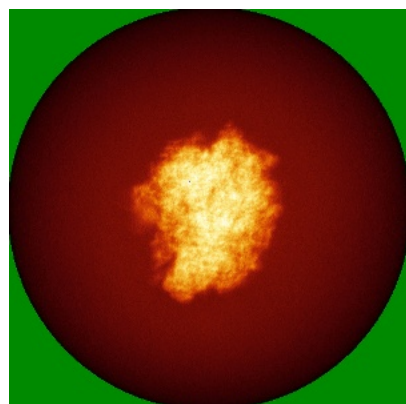


Y

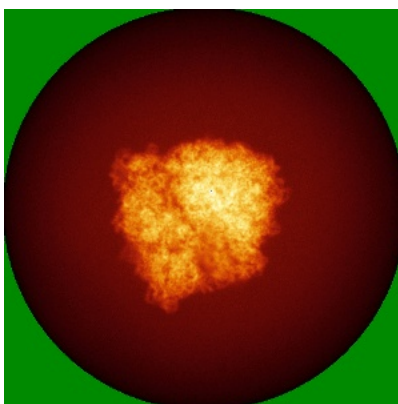


Z

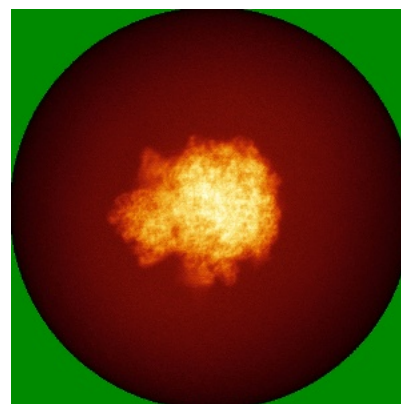
6.4.2 Raw map



X



Y

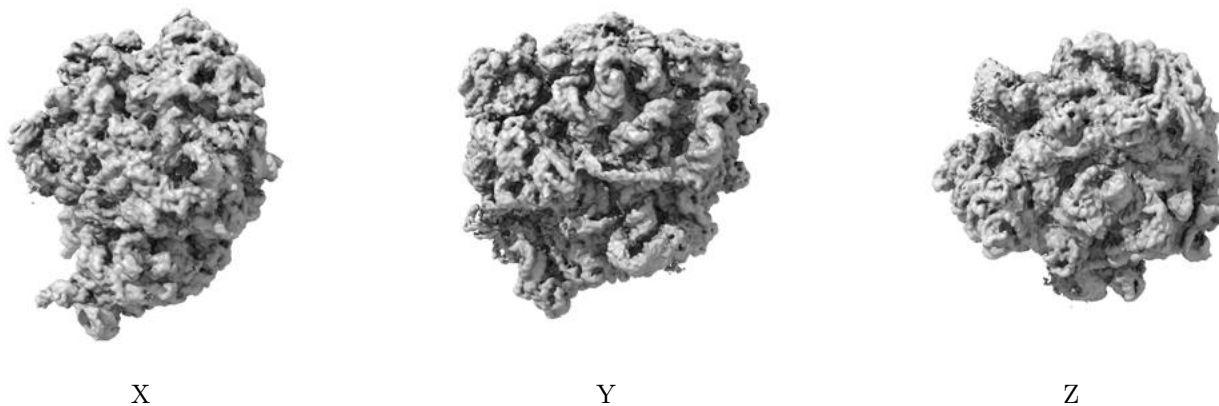


Z

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

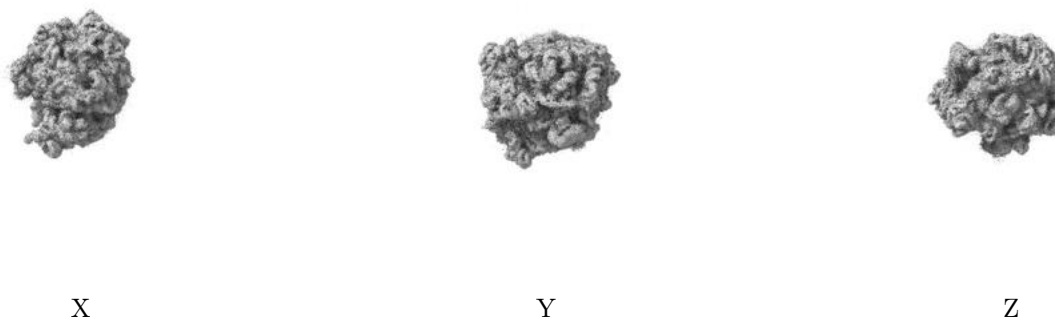
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

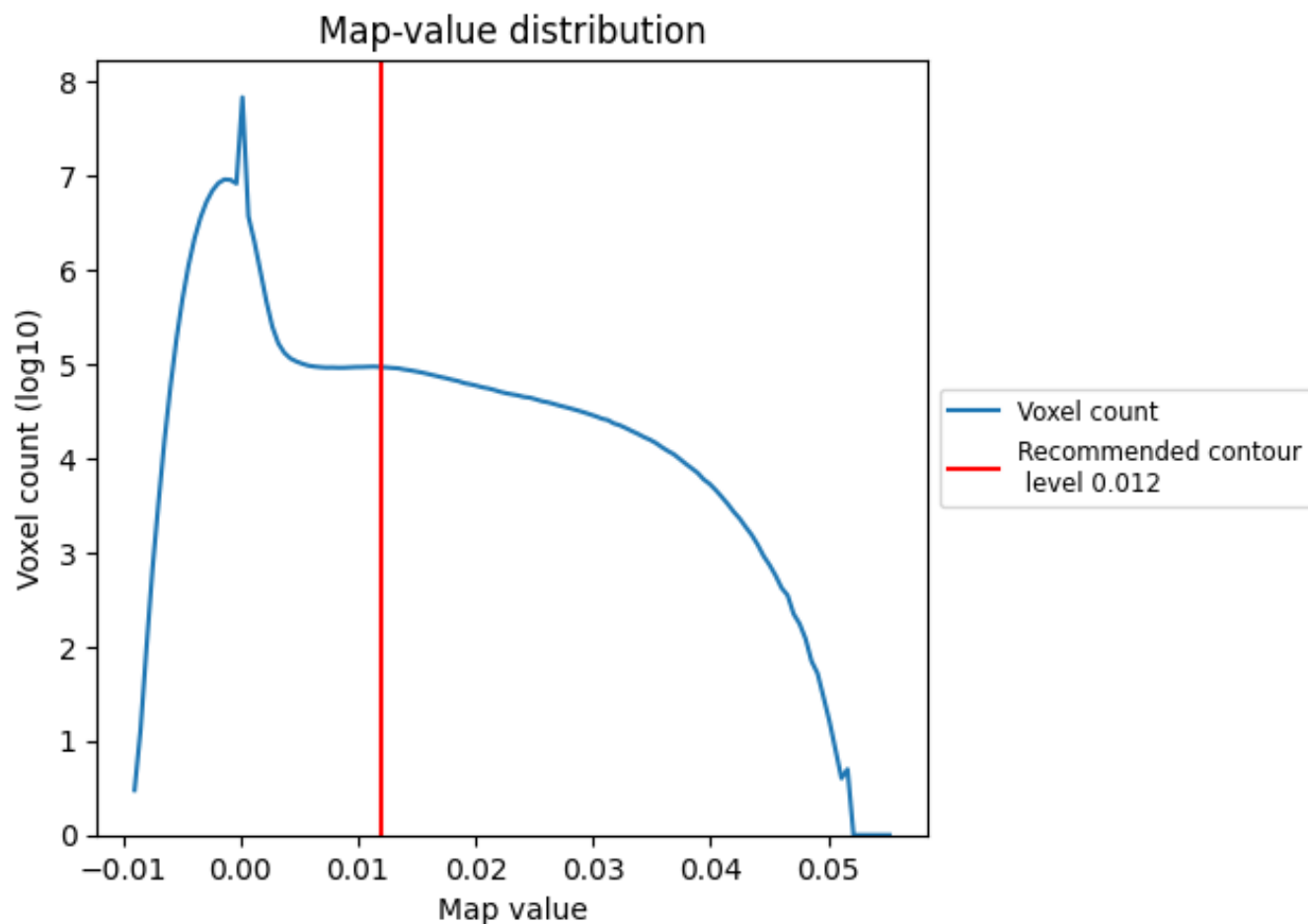
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

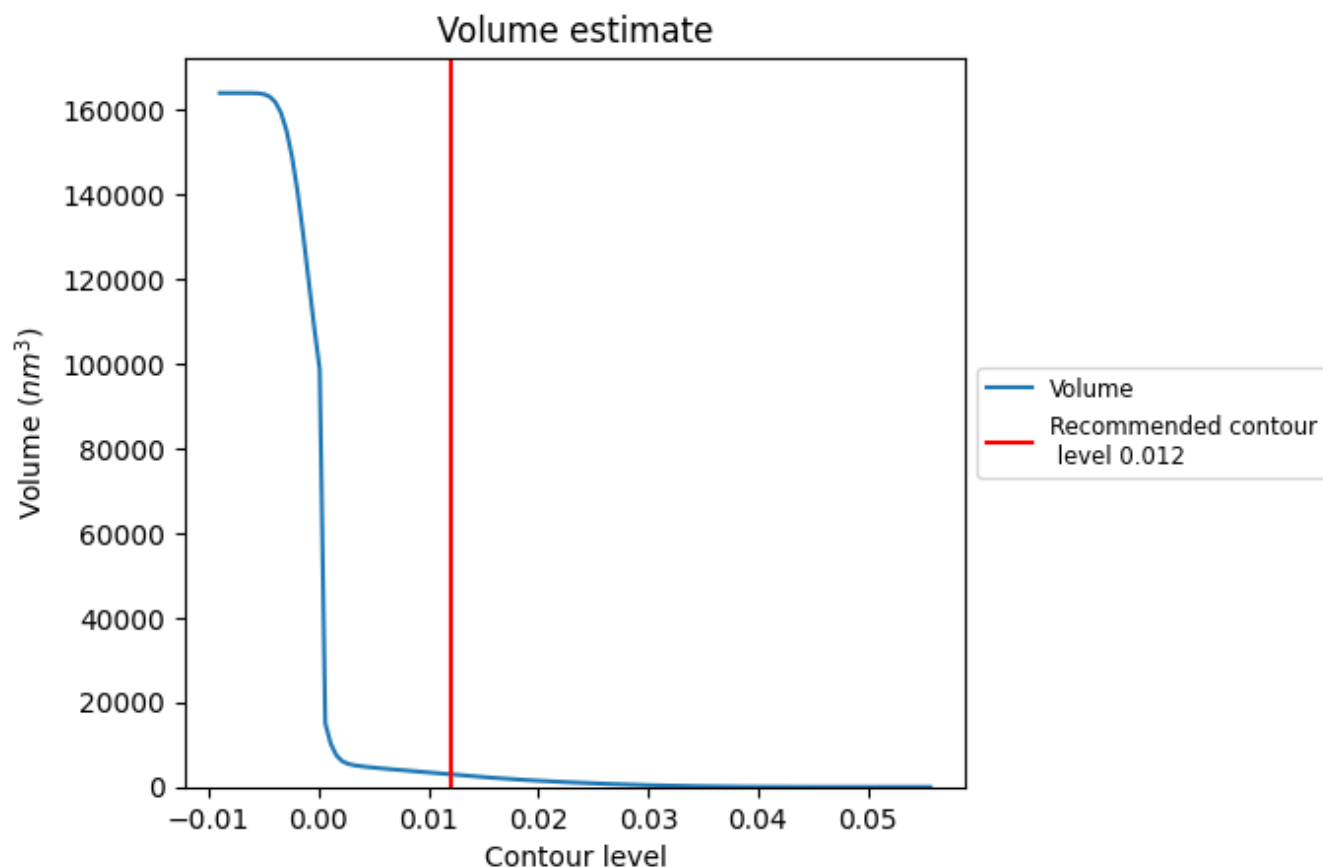
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

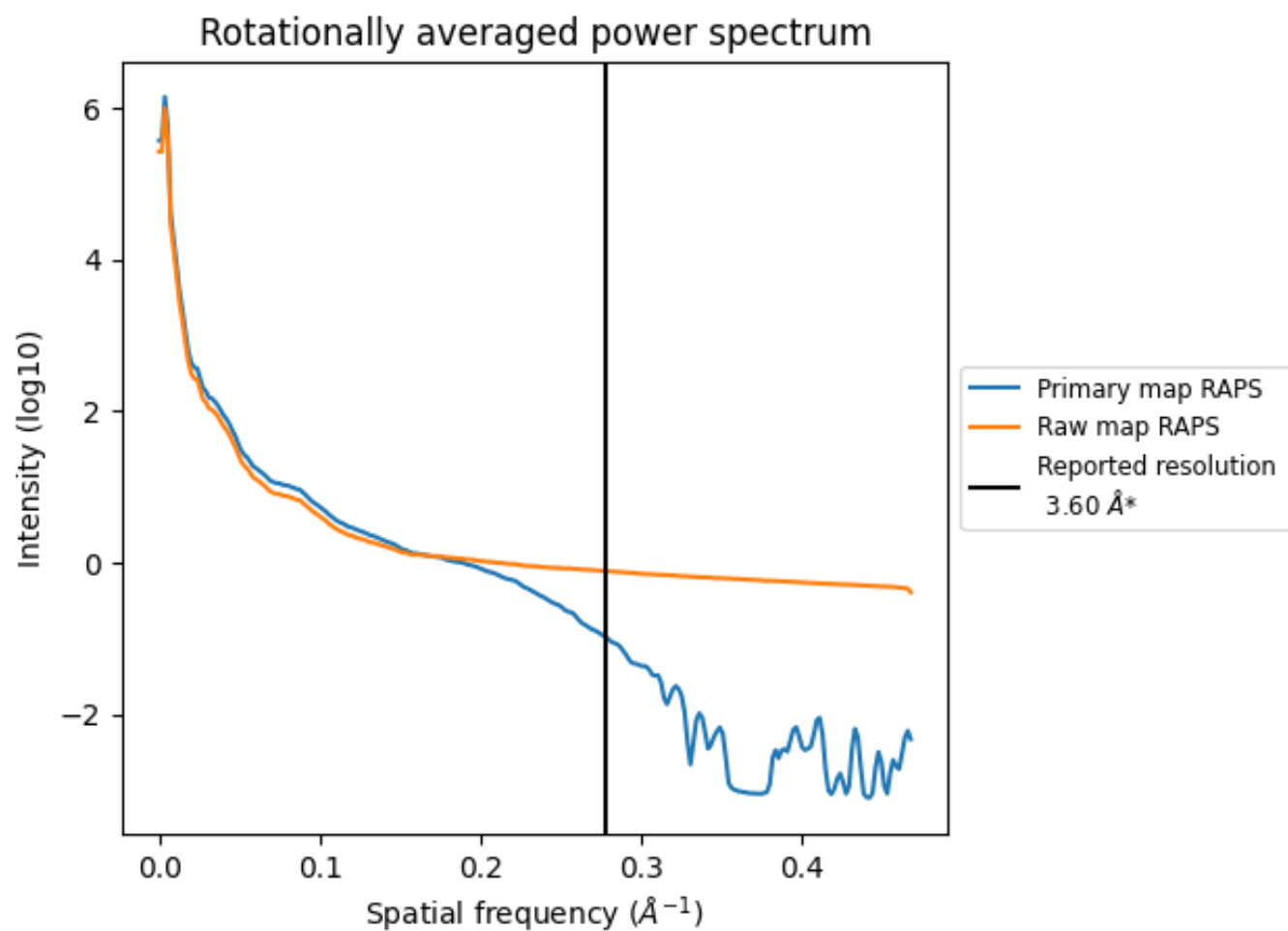
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2984 nm³; this corresponds to an approximate mass of 2696 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 ⓘ

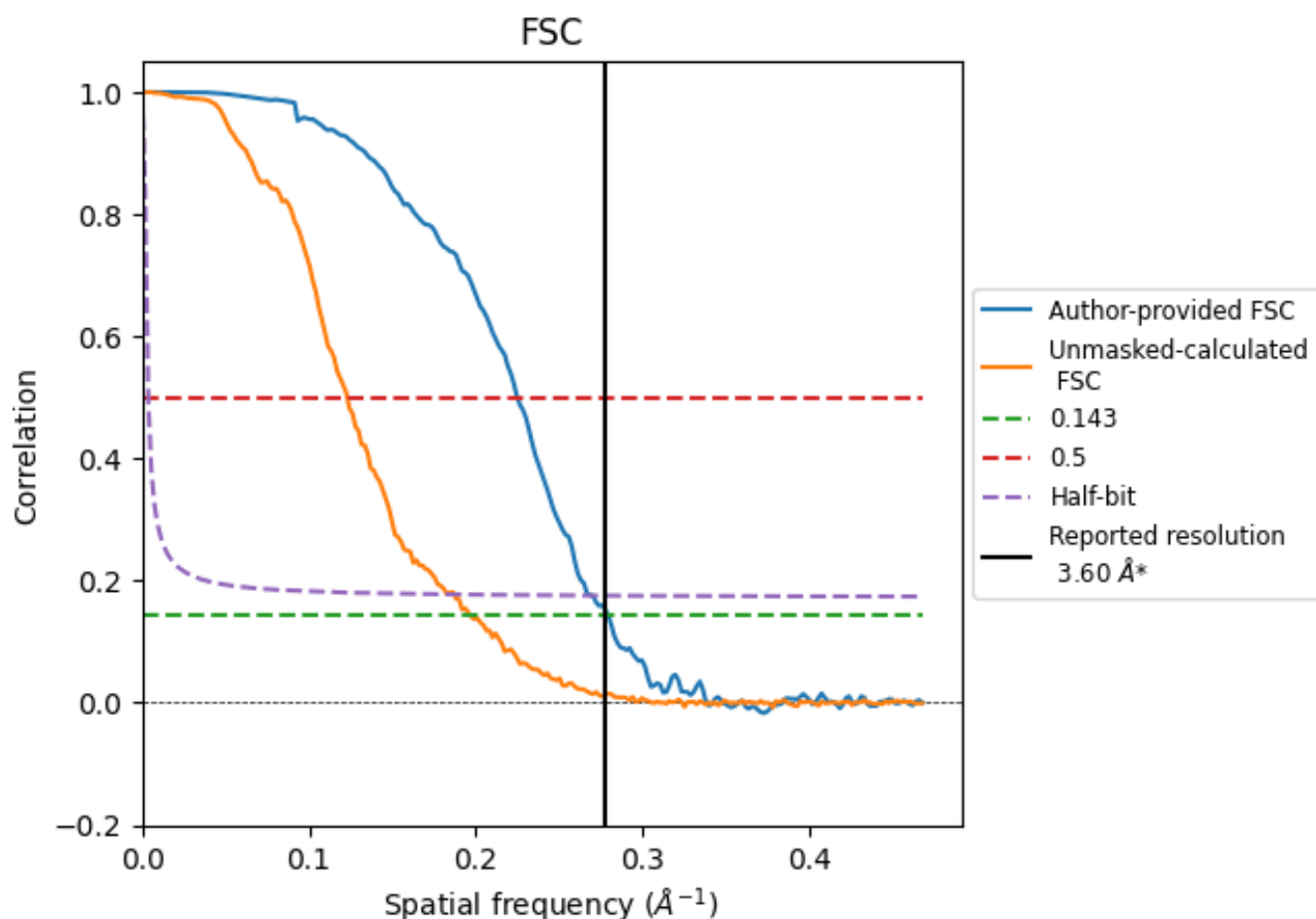


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.278 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

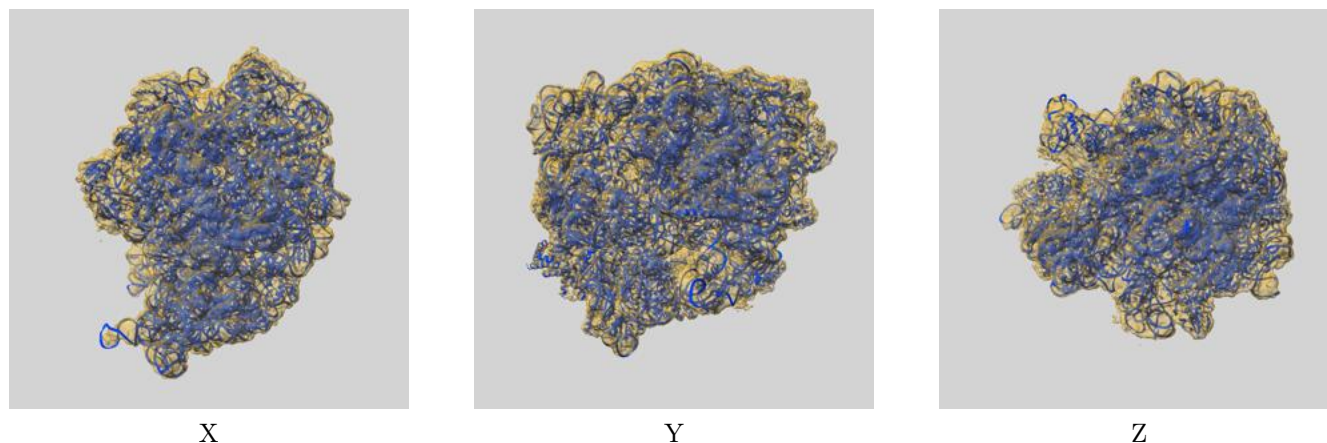
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.58	4.44	3.71
Unmasked-calculated*	5.08	8.13	5.35

*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 5.08 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

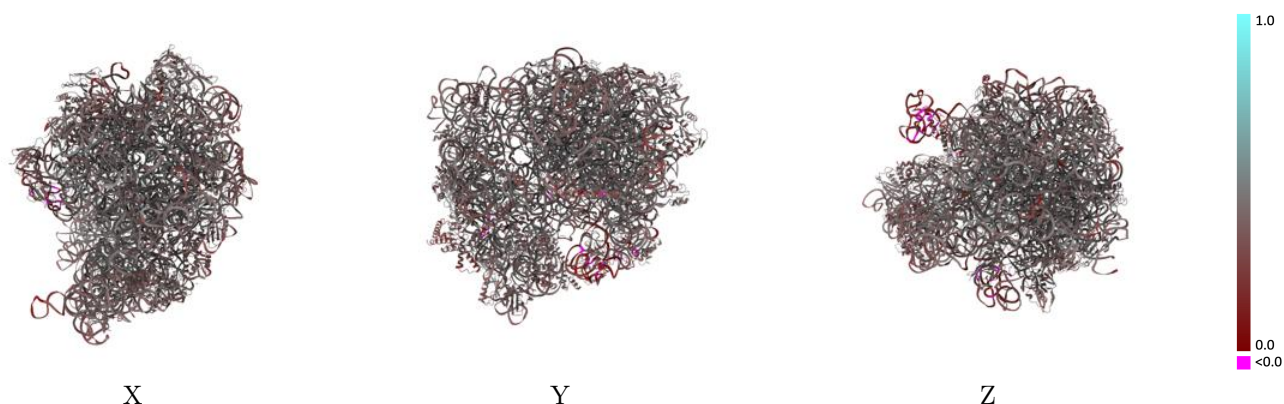
This section contains information regarding the fit between EMDB map EMD-42714 and PDB model 8UX8. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



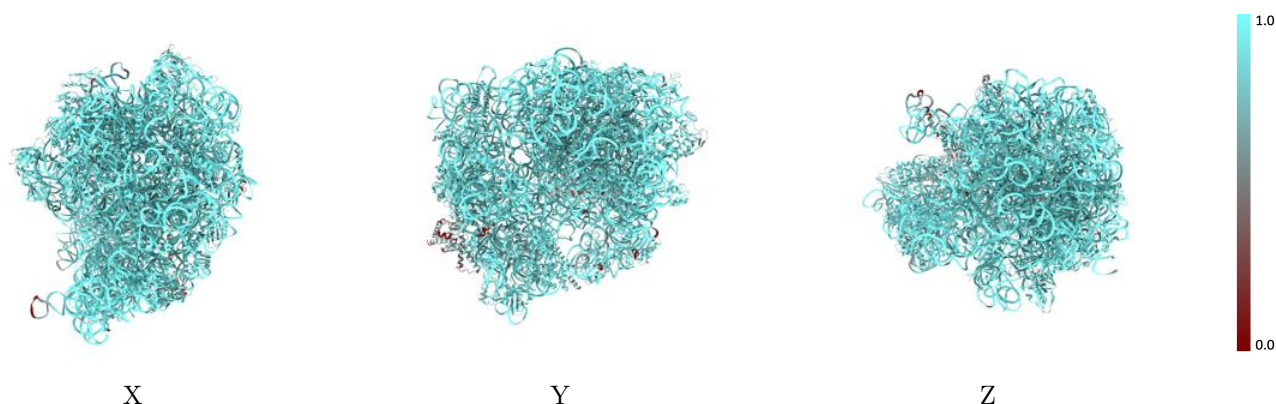
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



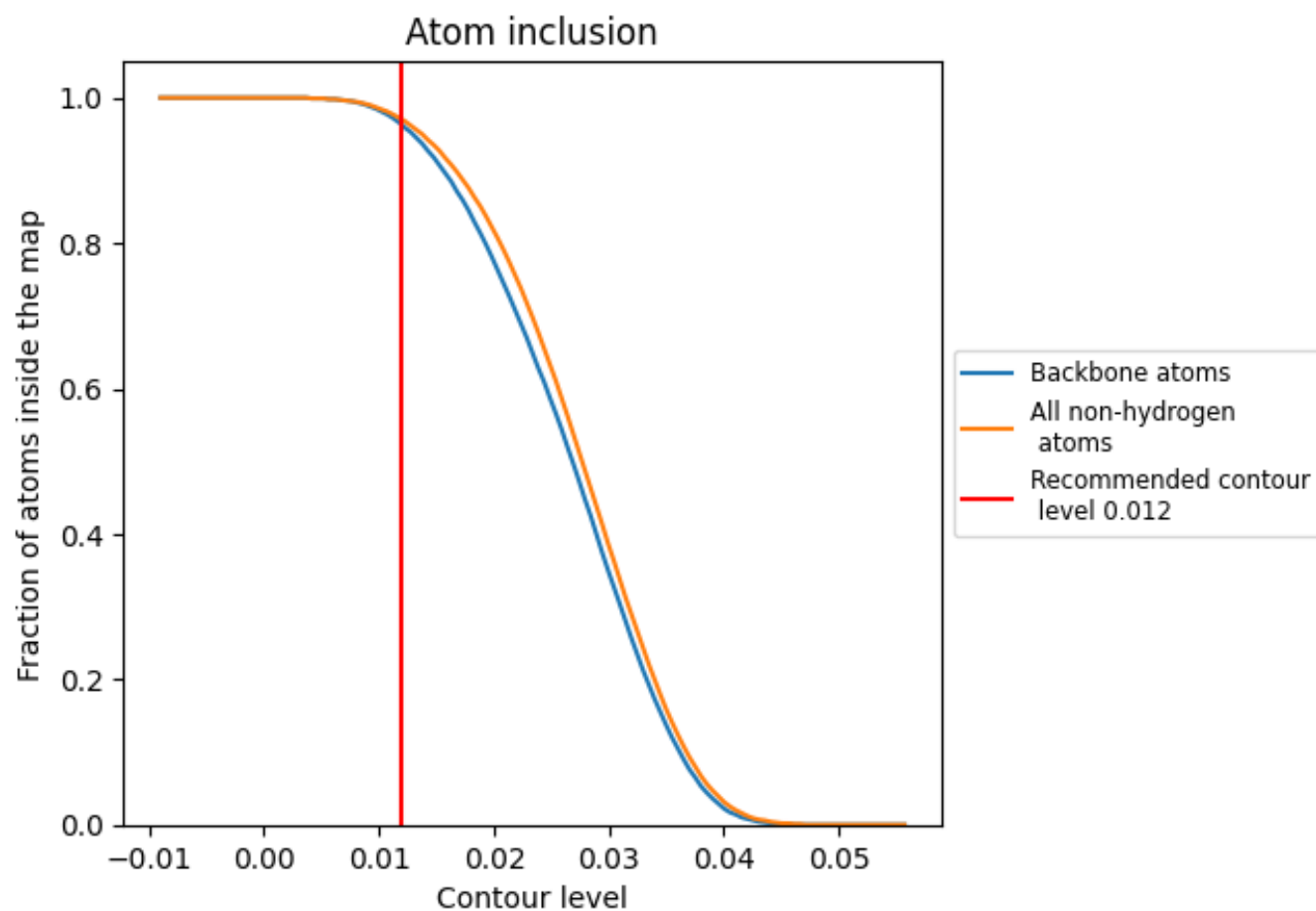
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 97% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.4060
1	 0.9890	 0.4060
2	 0.9870	 0.4080
3	 0.9770	 0.3810
4	 1.0000	 0.3440
5	 1.0000	 0.3840
A	 0.7680	 0.1920
B	 0.9980	 0.4600
C	 0.9680	 0.4520
D	 0.9180	 0.4220
E	 0.9290	 0.3660
F	 0.9180	 0.3970
G	 0.7430	 0.3310
J	 0.9860	 0.4350
K	 0.9970	 0.4530
L	 0.9570	 0.4370
M	 0.9920	 0.4400
N	 0.9950	 0.4330
O	 0.9470	 0.4010
P	 0.9800	 0.4490
Q	 0.9770	 0.4080
R	 0.9320	 0.4390
S	 0.9870	 0.4400
T	 0.9600	 0.4270
U	 0.9250	 0.4120
V	 0.9270	 0.4140
W	 0.9950	 0.4500
X	 0.9870	 0.4330
Y	 0.9280	 0.3600
Z	 0.9470	 0.4310
a	 0.8200	 0.3530
b	 0.9860	 0.4470
c	 0.9950	 0.4220
d	 1.0000	 0.4510
e	 1.0000	 0.4430



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Chain	Atom inclusion	Q-score
f	 1.0000	 0.4460
g	 0.5550	 0.3390
h	 0.9580	 0.4090
i	 0.9280	 0.3870
j	 0.9780	 0.4190
k	 0.9380	 0.4030
l	 0.9550	 0.3640
m	 0.9540	 0.4270
n	 0.9350	 0.4010
o	 0.8710	 0.3690
p	 0.9730	 0.4190
q	 0.9890	 0.4310
r	 0.9230	 0.3740
s	 0.9700	 0.3920
t	 0.9830	 0.3800
u	 0.9390	 0.4220
v	 0.9830	 0.4110
w	 0.9430	 0.3650
x	 0.9400	 0.3940
y	 0.9760	 0.3600
z	 0.7110	 0.3290