



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 10:35 AM UTC

PDB ID : 7BL4 / pdb_00007bl4
EMDB ID : EMD-12217
Title : in vitro reconstituted 50S-ObgE-GMPPNP-RsfS particle
Authors : Hilal, T.; Nikolay, R.; Spahn, C.M.T.
Deposited on : 2021-01-18
Resolution : 2.40 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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) : 2.49

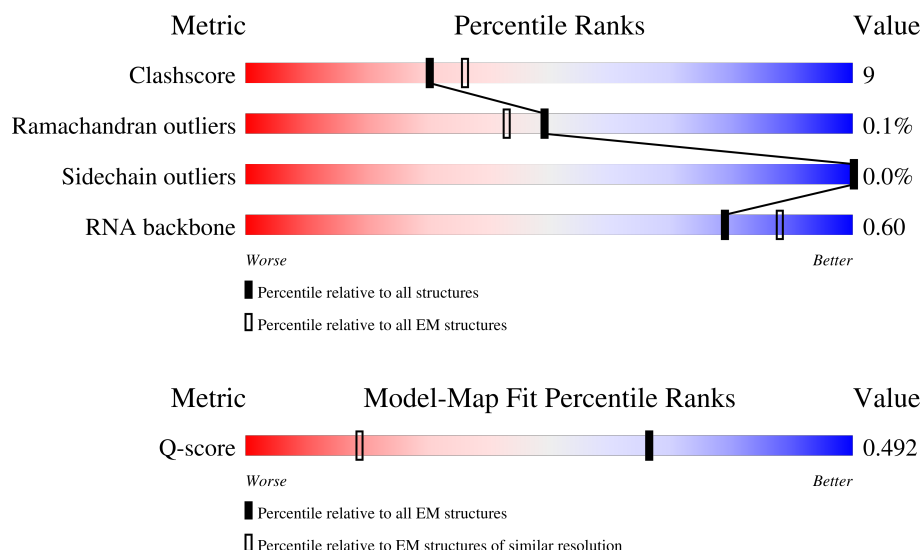
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 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	5628 (1.90 - 2.90)

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	g	38	8% 71% 29%
2	C	273	73% 26%
3	D	209	6% 78% 22%

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Mol	Chain	Length	Quality of chain
4	E	201	
5	F	179	
6	G	177	
7	J	142	
8	L	144	
9	N	127	
10	O	117	
11	Q	118	
12	R	103	
13	S	110	
14	T	100	
15	U	104	
16	V	94	
17	W	85	
18	X	78	
19	Y	63	
20	Z	59	
21	0	57	
22	1	55	
23	2	46	
24	K	123	
25	P	115	
26	M	136	
27	H	149	
28	d	70	

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Mol	Chain	Length	Quality of chain
29	A	2904	5% 56% 40%
30	B	119	58% 40%
31	6	105	9% 70% 27%
32	9	390	12% 65% 22% 13%
33	3	65	71% 25%

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 93560 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L36.

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

- Molecule 2 is a protein called 50S ribosomal protein L2.

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

- Molecule 3 is a protein called 50S ribosomal protein L3.

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

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	193	Total	C	N	O	S	0	0
			1483	932	266	280	5		

- Molecule 5 is a protein called 50S ribosomal protein L5.

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

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 7 is a protein called 50S ribosomal protein L13.

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

- Molecule 8 is a protein called 50S ribosomal protein L15.

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

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 10 is a protein called 50S ribosomal protein L18.

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

- Molecule 11 is a protein called 50S ribosomal protein L20.

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

- Molecule 12 is a protein called 50S ribosomal protein L21.

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

- Molecule 13 is a protein called 50S ribosomal protein L22.

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

- Molecule 14 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 15 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 16 is a protein called 50S ribosomal protein L25.

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

- Molecule 17 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	W	76	Total	C	N	O	S	0	0
			577	357	117	102	1		

- Molecule 18 is a protein called 50S ribosomal protein L28.

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

- Molecule 19 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 22 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 24 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 25 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	113	Total	C	N	O	S	0	0
			911	571	178	161	1		

- Molecule 26 is a protein called 50S ribosomal protein L16.

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

- Molecule 27 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	47	Total	C	N	O	S	0	0
			364	227	64	67	6		

- Molecule 29 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A	2897	Total	C	N	O	P	0	0
			62195	27745	11446	20107	2897		

- Molecule 30 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B	119	Total	C	N	O	P	0	0
			2548	1135	466	829	118		

- Molecule 31 is a protein called Ribosomal silencing factor RsfS.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	6	102	Total	C	N	O	S	0	0
			780	485	133	157	5		

- Molecule 32 is a protein called GTPase ObgE/CgtA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	9	338	Total	C	N	O	S	0	0
			2582	1626	453	490	13		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

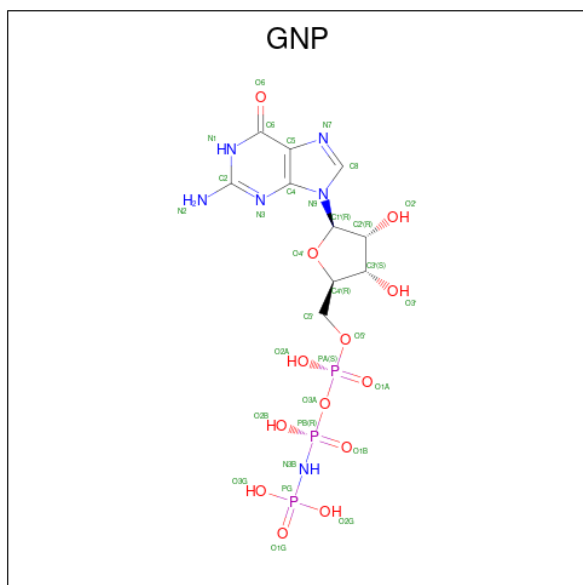
- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
34	g	1	Total	Zn	0
			1	1	
34	d	1	Total	Zn	0
			1	1	

- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
35	A	3	Total	Mg	0
			3	3	
35	6	2	Total	Mg	0
			2	2	
35	9	1	Total	Mg	0
			1	1	

- Molecule 36 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
36	9	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 37 is water.

Mol	Chain	Residues	Atoms		AltConf
37	C	2	Total	O	0
			2	2	
37	F	1	Total	O	0
			1	1	
37	L	1	Total	O	0
			1	1	
37	N	3	Total	O	0
			3	3	
37	S	1	Total	O	0
			1	1	

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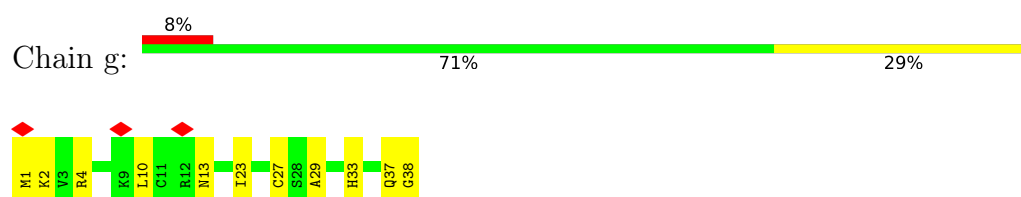
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Mol	Chain	Residues	Atoms		AltConf
37	A	18	Total 18	O 18	0
37	B	1	Total 1	O 1	0
37	6	3	Total 3	O 3	0
37	9	5	Total 5	O 5	0

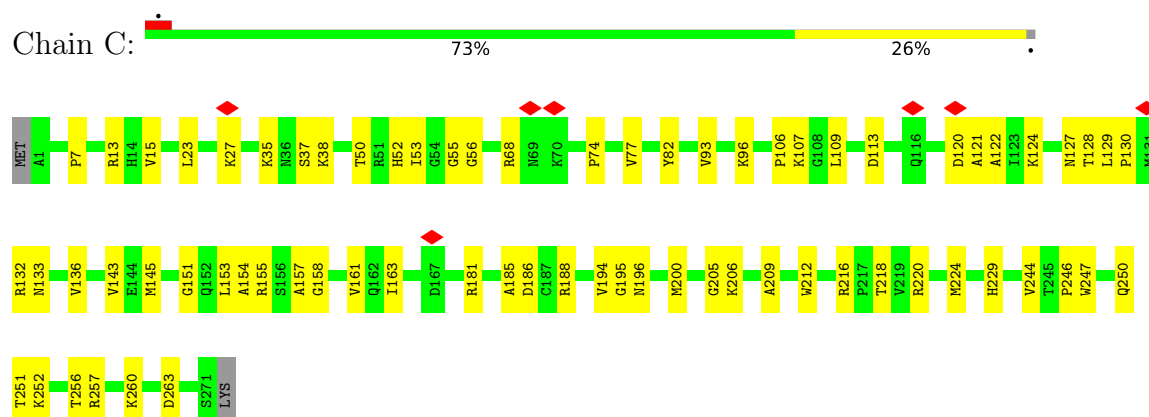
3 Residue-property plots

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.

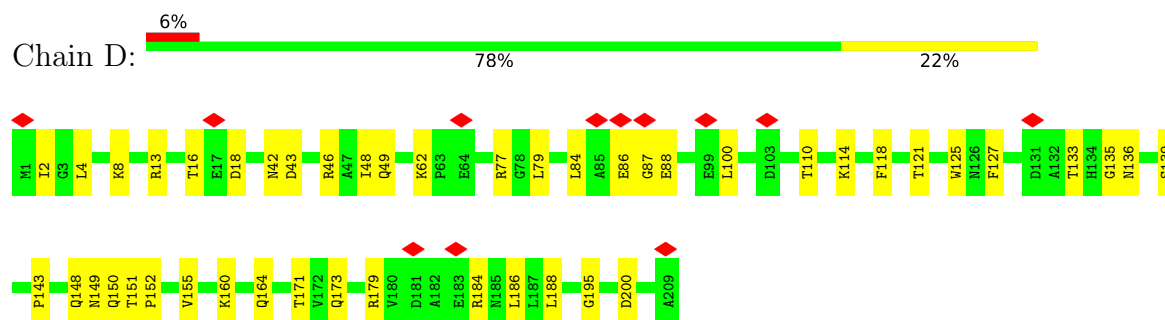
• Molecule 1: 50S ribosomal protein L36



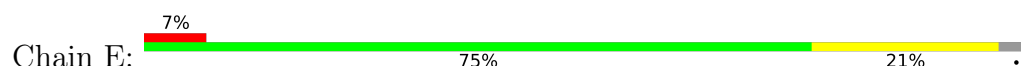
• Molecule 2: 50S ribosomal protein L2

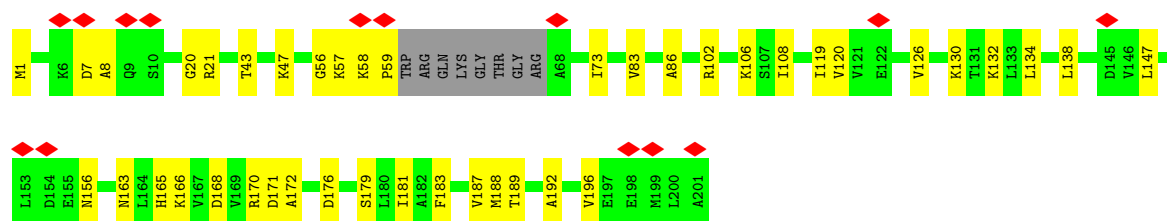


• Molecule 3: 50S ribosomal protein L3

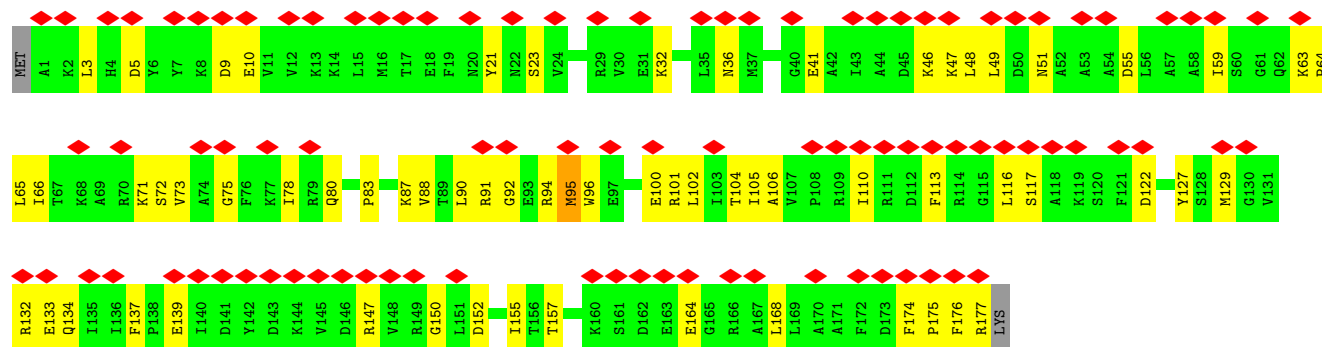


• Molecule 4: 50S ribosomal protein L4

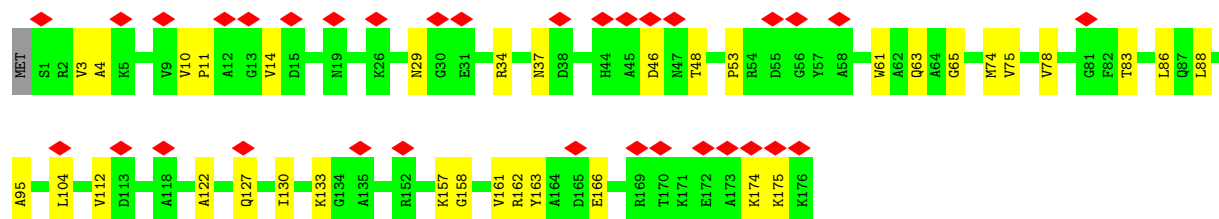
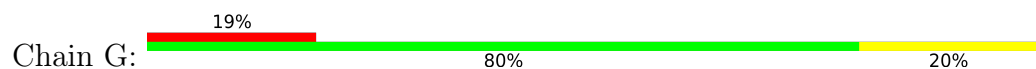




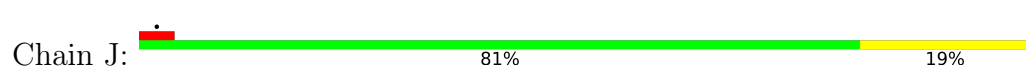
• Molecule 5: 50S ribosomal protein L5



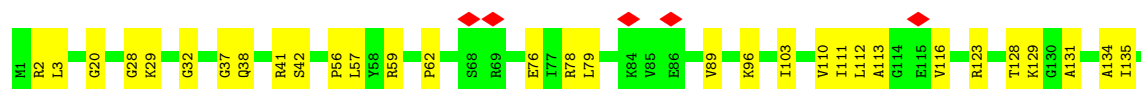
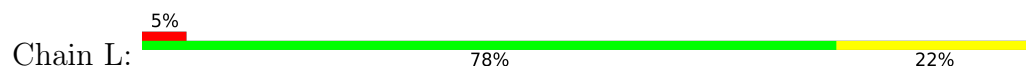
• Molecule 6: 50S ribosomal protein L6



• Molecule 7: 50S ribosomal protein L13

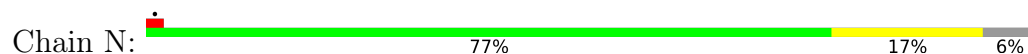


• Molecule 8: 50S ribosomal protein L15

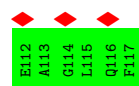
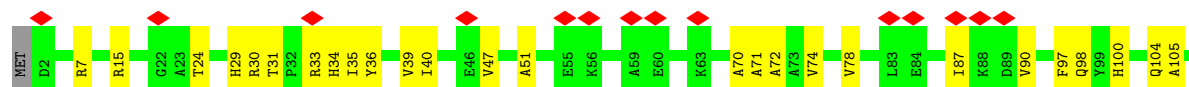
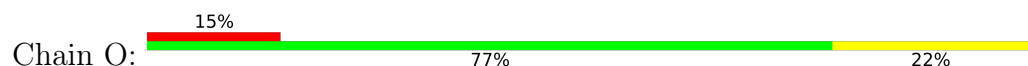




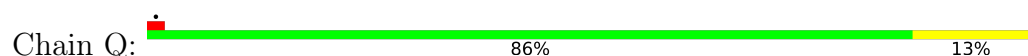
- Molecule 9: 50S ribosomal protein L17



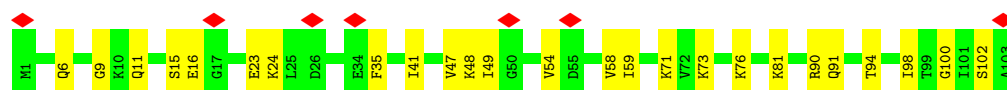
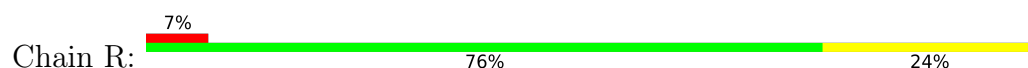
- Molecule 10: 50S ribosomal protein L18



- Molecule 11: 50S ribosomal protein L20



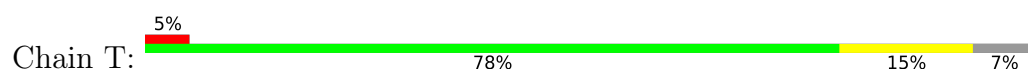
- Molecule 12: 50S ribosomal protein L21



- Molecule 13: 50S ribosomal protein L22



- Molecule 14: 50S ribosomal protein L23

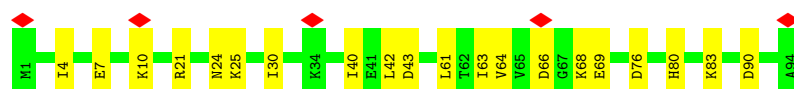
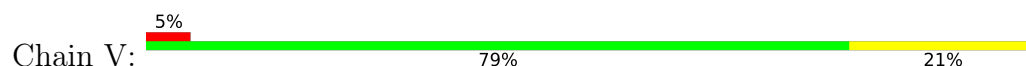




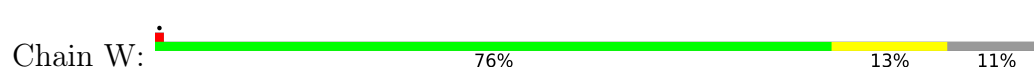
- Molecule 15: 50S ribosomal protein L24



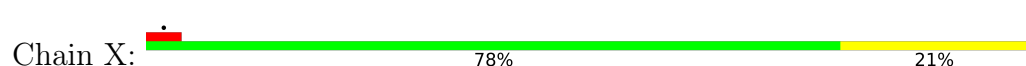
- Molecule 16: 50S ribosomal protein L25



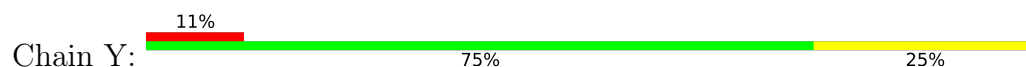
- Molecule 17: 50S ribosomal protein L27



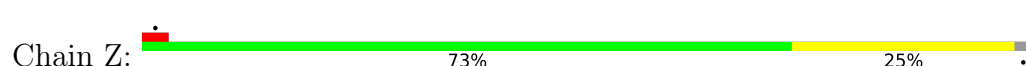
- Molecule 18: 50S ribosomal protein L28



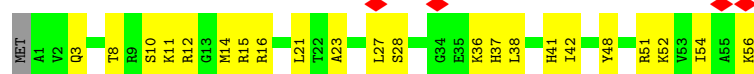
- Molecule 19: 50S ribosomal protein L29



- Molecule 20: 50S ribosomal protein L30



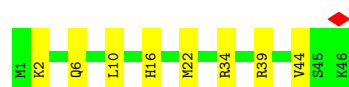
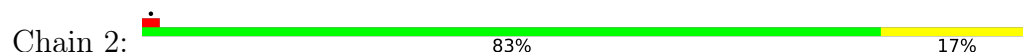
- Molecule 21: 50S ribosomal protein L32



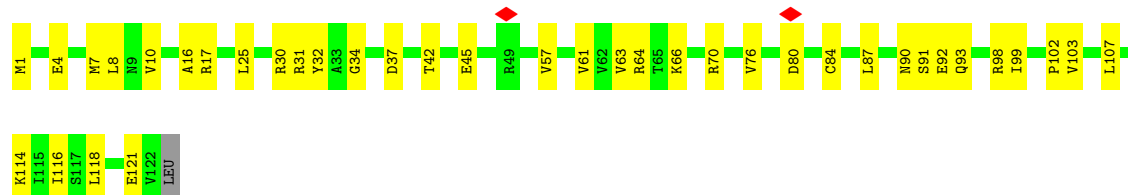
- Molecule 22: 50S ribosomal protein L33



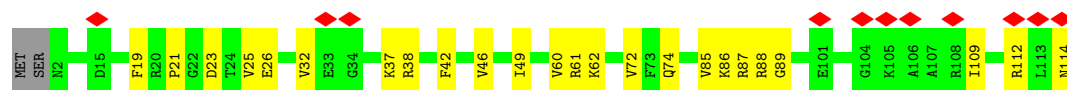
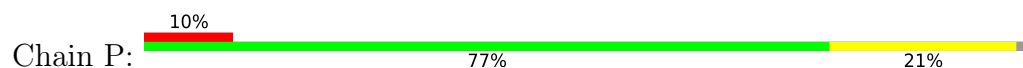
- Molecule 23: 50S ribosomal protein L34



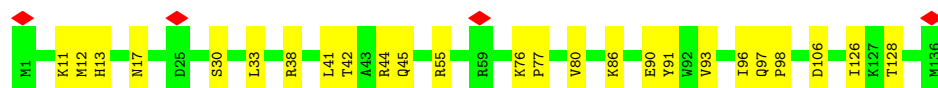
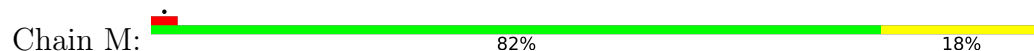
- Molecule 24: 50S ribosomal protein L14



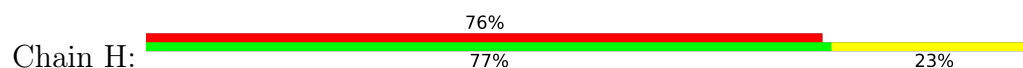
- Molecule 25: 50S ribosomal protein L19



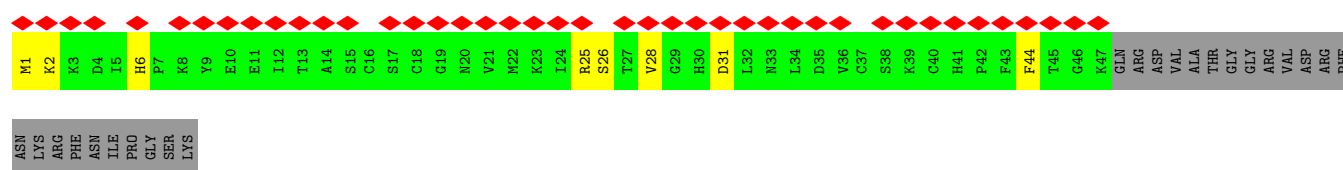
- Molecule 26: 50S ribosomal protein L16



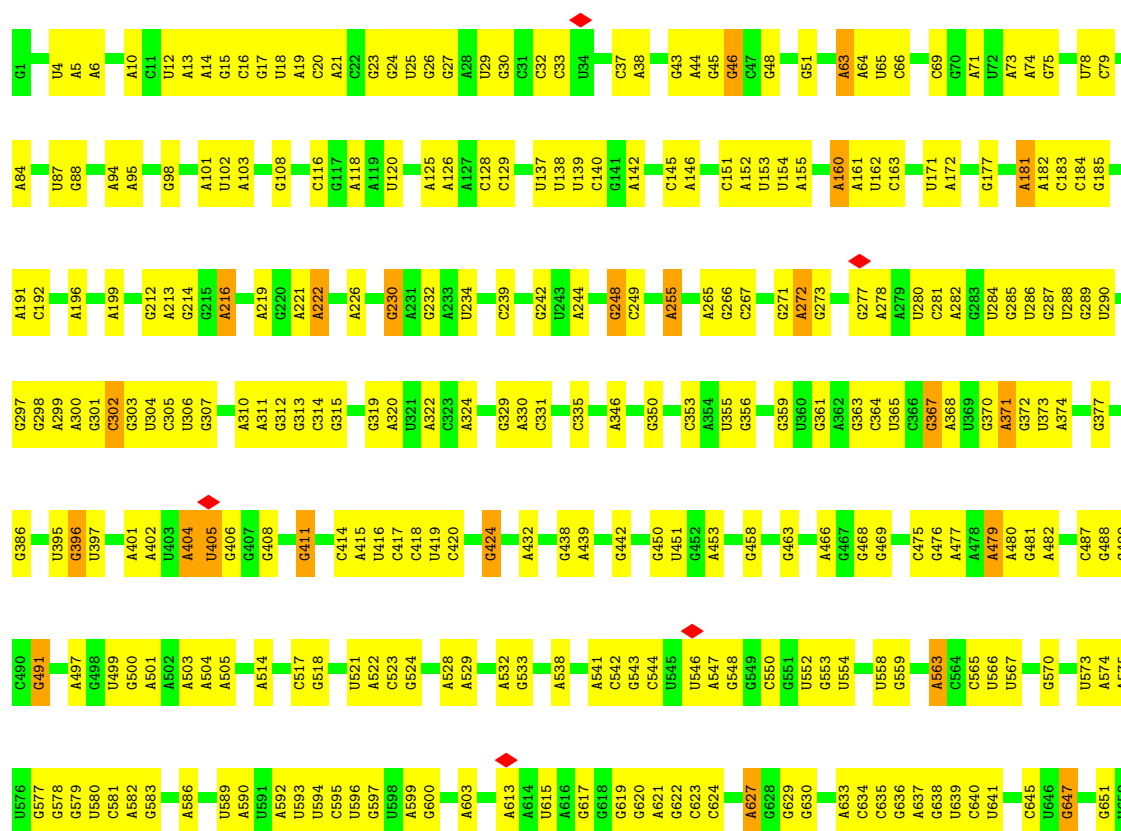
- Molecule 27: 50S ribosomal protein L9

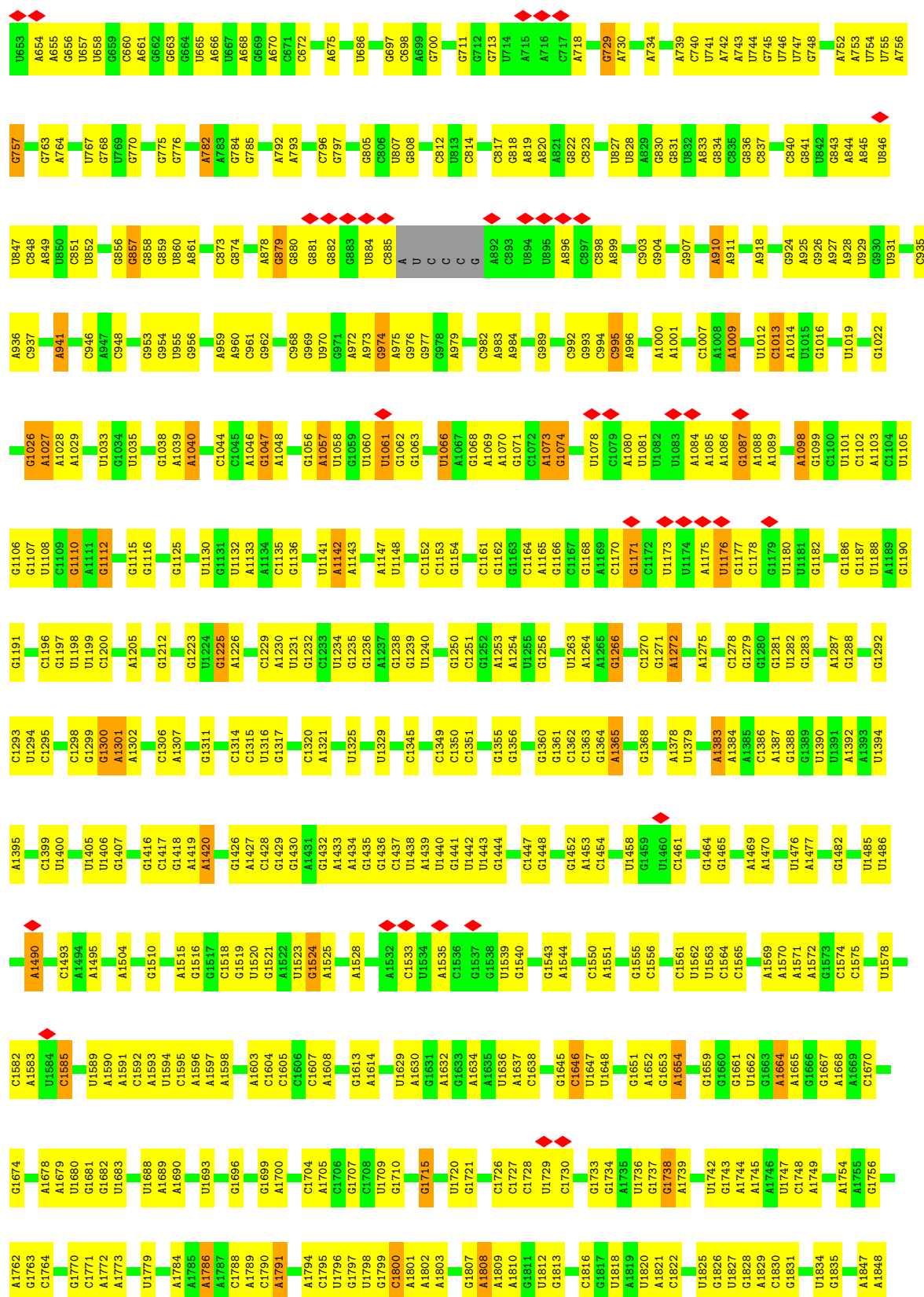


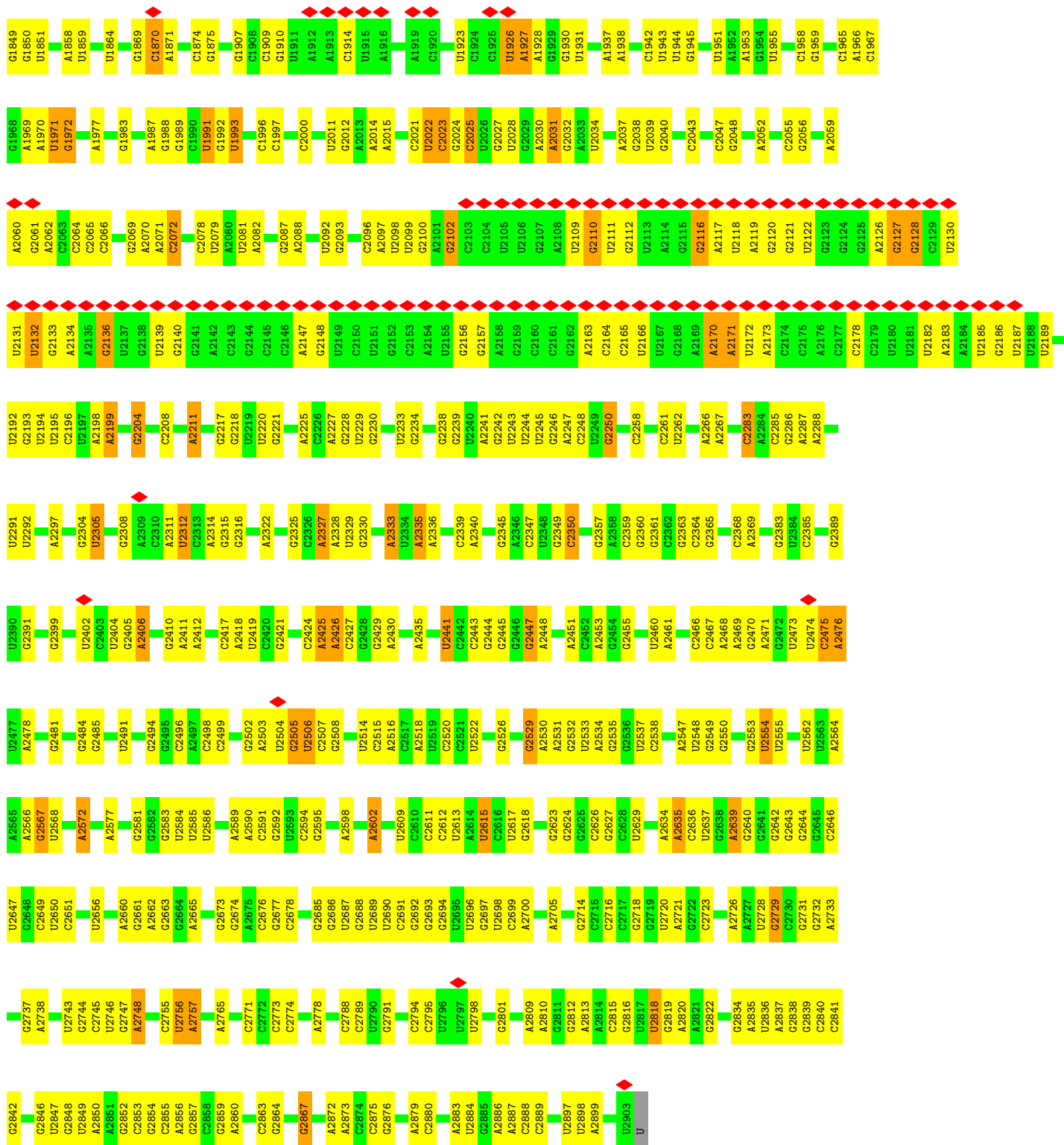
- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 23S ribosomal RNA

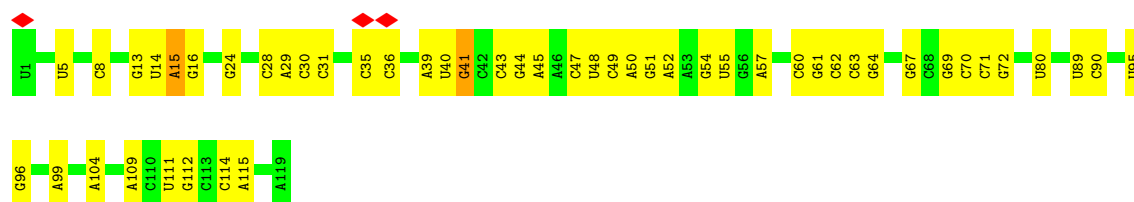




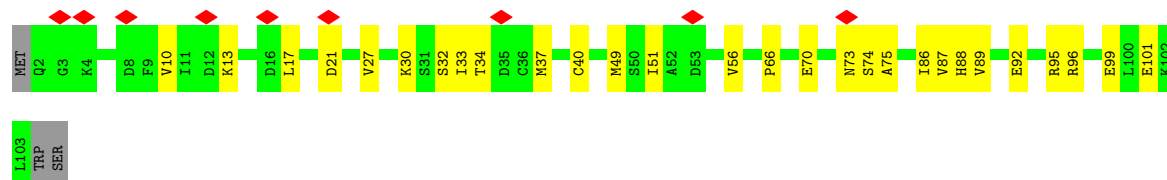


• Molecule 30: 5S ribosomal RNA

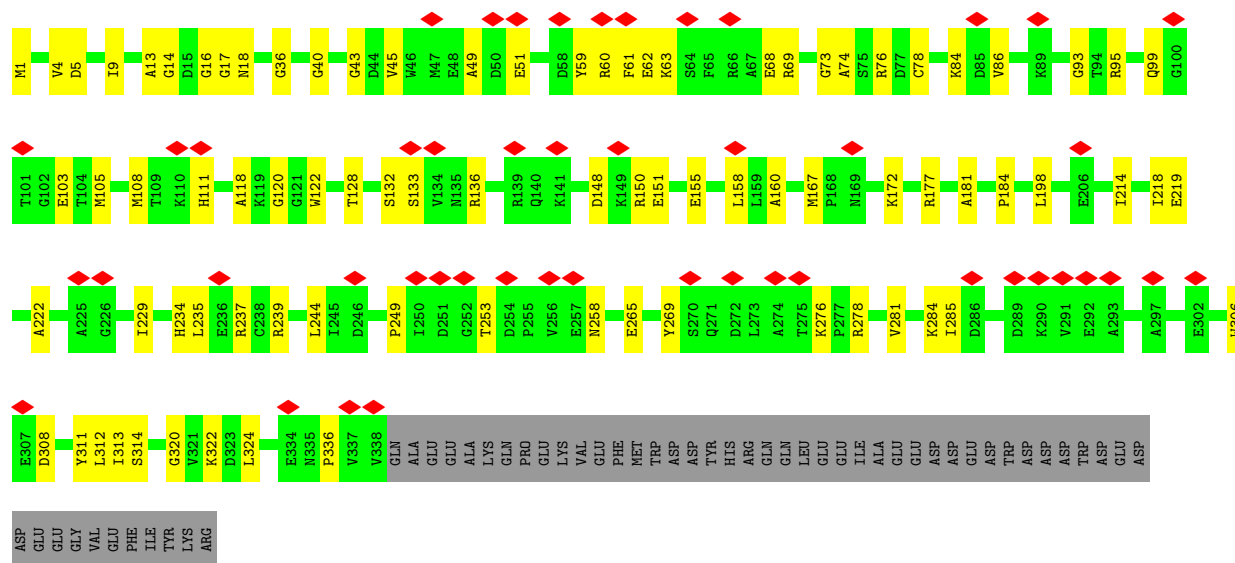
Chain B: 58% 40%



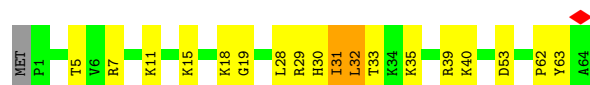
- Molecule 31: Ribosomal silencing factor RsfS



- Molecule 32: GTPase ObgE/CgtA



- Molecule 33: 50S ribosomal protein L35



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	190393	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	2200	Depositor
Maximum defocus (nm)	Not provided	
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	22.582	Depositor
Minimum map value	-9.349	Depositor
Average map value	-0.044	Depositor
Map value standard deviation	0.814	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	363.6, 363.6, 363.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.01, 1.01, 1.01	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	g	0.14	0/303	0.34	0/397
2	C	0.12	0/2121	0.34	0/2852
3	D	0.12	0/1586	0.32	0/2134
4	E	0.11	0/1499	0.34	0/2016
5	F	0.14	0/1434	0.46	3/1926 (0.2%)
6	G	0.11	0/1343	0.32	0/1816
7	J	0.12	0/1152	0.32	0/1551
8	L	0.12	0/1062	0.37	0/1413
9	N	0.12	0/973	0.38	0/1301
10	O	0.12	0/902	0.35	0/1209
11	Q	0.12	0/960	0.36	0/1278
12	R	0.12	0/829	0.37	0/1107
13	S	0.12	0/864	0.33	0/1156
14	T	0.13	0/744	0.37	0/994
15	U	0.15	0/787	0.40	0/1051
16	V	0.11	0/766	0.32	0/1025
17	W	0.11	0/584	0.29	0/772
18	X	0.13	0/635	0.32	0/848
19	Y	0.12	0/510	0.36	0/677
20	Z	0.12	0/453	0.35	0/605
21	0	0.13	0/450	0.36	0/599
22	1	0.12	0/416	0.32	0/554
23	2	0.12	0/380	0.36	0/498
24	K	0.14	0/947	0.34	0/1268
25	P	0.11	0/923	0.32	0/1234
26	M	0.13	0/1093	0.33	0/1460
27	H	0.13	0/1121	0.34	0/1515
28	d	0.08	0/371	0.25	0/496
29	A	0.09	0/69659	0.20	0/108672
30	B	0.07	0/2847	0.15	0/4440
31	6	0.11	0/787	0.29	0/1062
32	9	0.13	0/2626	0.36	0/3542

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	3	0.13	0/513	0.46	0/676
All	All	0.10	0/101640	0.25	3/152144 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	175	PRO	CA-C-N	5.85	132.71	121.54
5	F	175	PRO	C-N-CA	5.85	132.71	121.54
5	F	95	MET	CA-CB-CG	5.28	124.65	114.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	g	302	0	340	7	0
2	C	2082	0	2157	56	0
3	D	1565	0	1616	35	0
4	E	1483	0	1548	28	0
5	F	1410	0	1447	53	0
6	G	1323	0	1374	22	0
7	J	1129	0	1162	24	0
8	L	1053	0	1129	27	0
9	N	960	0	1000	19	0
10	O	892	0	923	16	0
11	Q	947	0	1022	18	0
12	R	816	0	839	18	0
13	S	857	0	922	23	0
14	T	738	0	807	10	0
15	U	779	0	834	26	0
16	V	753	0	780	12	0
17	W	577	0	594	9	0
18	X	625	0	655	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	Y	509	0	543	12	0
20	Z	449	0	491	11	0
21	0	444	0	461	17	0
22	1	409	0	440	9	0
23	2	377	0	418	6	0
24	K	938	0	1012	30	0
25	P	911	0	957	18	0
26	M	1074	0	1157	18	0
27	H	1110	0	1148	22	0
28	d	364	0	364	7	0
29	A	62195	0	31280	850	0
30	B	2548	0	1292	35	0
31	6	780	0	783	20	0
32	9	2582	0	2606	65	0
33	3	504	0	574	17	0
34	d	1	0	0	0	0
34	g	1	0	0	0	0
35	6	2	0	0	0	0
35	9	1	0	0	0	0
35	A	3	0	0	0	0
36	9	32	0	13	1	0
37	6	3	0	0	0	0
37	9	5	0	0	0	0
37	A	18	0	0	2	0
37	B	1	0	0	0	0
37	C	2	0	0	0	0
37	F	1	0	0	0	0
37	L	1	0	0	0	0
37	N	3	0	0	0	0
37	S	1	0	0	0	0
All	All	93560	0	62688	1371	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 9.

All (1371) 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)
29:A:1040:A:N6	29:A:1115:G:H1	1.68	0.89
29:A:285:G:H1	29:A:355:U:H3	1.19	0.89
29:A:1040:A:H61	29:A:1115:G:H1	0.93	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1171:G:N1	29:A:1178:C:N3	2.27	0.81
4:E:56:GLY:HA2	4:E:73:ILE:HG12	1.65	0.77
21:O:27:LEU:HB2	21:O:36:LYS:HE2	1.66	0.77
4:E:163:ASN:ND2	29:A:320:A:N3	2.33	0.77
29:A:1779:U:OP2	29:A:1784:A:N6	2.17	0.75
29:A:475:C:O2	29:A:479:A:N6	2.20	0.74
32:9:158:LEU:HB2	32:9:234:HIS:HB3	1.69	0.74
31:6:34:THR:HG21	31:6:86:ILE:HG12	1.68	0.74
29:A:1270:C:H5''	29:A:1271:G:H5'	1.70	0.74
32:9:5:ASP:O	32:9:60:ARG:NH1	2.21	0.73
32:9:51:GLU:HG3	32:9:111:HIS:HB2	1.72	0.72
10:O:30:ARG:NH2	30:B:48:U:OP1	2.23	0.72
29:A:698:C:O2'	29:A:734:A:N6	2.23	0.72
31:6:56:VAL:HG13	31:6:66:PRO:HG2	1.71	0.71
29:A:1060:U:H4'	29:A:1061:U:H5'	1.71	0.71
29:A:2059:A:H61	29:A:2503:A:H3'	1.57	0.70
3:D:13:ARG:HH12	25:P:74:GLN:HE21	1.40	0.70
29:A:2204:G:H1	29:A:2220:U:H3	1.41	0.69
33:3:30:HIS:O	33:3:32:LEU:N	2.22	0.69
2:C:220:ARG:NH1	29:A:1789:A:OP2	2.26	0.69
29:A:2848:G:O2'	29:A:2867:G:N2	2.25	0.69
2:C:23:LEU:HD21	2:C:82:TYR:HB2	1.76	0.68
10:O:24:THR:HG22	10:O:90:VAL:HG23	1.76	0.68
5:F:129:MET:HA	29:A:2304:G:H4'	1.75	0.68
27:H:129:GLU:HG2	27:H:143:ILE:HG12	1.75	0.68
29:A:2120:G:H2'	29:A:2121:G:H8	1.59	0.68
8:L:62:PRO:HB2	33:3:29:ARG:HH11	1.59	0.67
29:A:2102:G:H1	29:A:2187:U:H3	1.43	0.67
9:N:22:ARG:HG3	9:N:70:THR:HA	1.76	0.67
32:9:177:ARG:HD3	32:9:184:PRO:HD2	1.77	0.67
20:Z:36:GLU:O	20:Z:37:ARG:NH1	2.27	0.67
2:C:35:LYS:NZ	2:C:37:SER:OG	2.28	0.67
29:A:1386:C:H2'	29:A:1387:A:H8	1.60	0.66
29:A:1966:A:N6	32:9:133:SER:OG	2.28	0.66
10:O:40:ILE:HG12	10:O:47:VAL:HG12	1.76	0.66
26:M:77:PRO:HG2	26:M:80:VAL:HG21	1.76	0.66
2:C:122:ALA:O	2:C:127:ASN:ND2	2.27	0.66
22:1:21:THR:HG21	29:A:2419:U:H4'	1.77	0.66
5:F:132:ARG:HA	5:F:150:GLY:HA2	1.78	0.66
18:X:42:GLU:OE1	18:X:44:ARG:NH2	2.28	0.66
24:K:61:VAL:HG23	24:K:87:LEU:HD11	1.75	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2656:U:O2	29:A:2665:A:N7	2.29	0.65
7:J:102:GLU:HB2	7:J:119:PHE:HE1	1.60	0.65
11:Q:5:ARG:HH11	29:A:1251:C:P	2.19	0.65
11:Q:5:ARG:HH12	29:A:1251:C:H2'	1.59	0.65
29:A:1056:G:H5''	29:A:1057:A:H5'	1.79	0.65
4:E:168:ASP:OD2	4:E:170:ARG:NH1	2.30	0.65
15:U:87:GLU:CD	15:U:88:ASP:H	2.04	0.65
29:A:1796:U:H2'	29:A:1797:G:H8	1.62	0.65
15:U:88:ASP:OD1	15:U:89:GLY:N	2.29	0.65
29:A:377:G:H1	29:A:397:U:H3	1.44	0.65
29:A:820:A:H4'	29:A:836:G:H22	1.61	0.65
32:9:93:GLY:H	32:9:108:MET:HB2	1.63	0.64
1:g:37:GLN:HE21	29:A:1125:G:H4'	1.62	0.64
4:E:147:LEU:HB2	4:E:183:PHE:HD2	1.62	0.64
7:J:3:THR:OG1	29:A:995:C:O2	2.14	0.64
16:V:80:HIS:HD2	16:V:83:LYS:HB2	1.60	0.64
29:A:2182:U:H2'	29:A:2183:A:H8	1.61	0.64
13:S:23:LEU:HD22	21:0:23:ALA:HB2	1.79	0.64
29:A:1826:G:O2'	29:A:1971:U:OP2	2.15	0.64
29:A:2229:U:H2'	29:A:2230:G:H8	1.63	0.64
29:A:2473:U:OP1	29:A:2529:G:N2	2.30	0.64
6:G:122:ALA:HB1	6:G:130:ILE:HD11	1.79	0.64
14:T:1:MET:SD	14:T:2:ILE:N	2.69	0.64
33:3:5:THR:HG22	33:3:62:PRO:HD2	1.80	0.64
4:E:171:ASP:OD2	4:E:172:ALA:N	2.30	0.64
11:Q:52:ARG:NH2	29:A:994:C:OP1	2.31	0.64
29:A:324:A:OP2	29:A:1205:A:N6	2.31	0.64
29:A:463:G:N2	29:A:466:A:OP2	2.26	0.64
29:A:668:A:H2'	29:A:670:A:H62	1.62	0.64
29:A:2339:C:H2'	29:A:2340:A:H8	1.62	0.64
29:A:2857:G:N2	29:A:2860:A:OP2	2.22	0.64
2:C:143:VAL:HB	2:C:153:LEU:HB2	1.79	0.63
29:A:2258:C:O2'	29:A:2427:C:OP2	2.16	0.63
29:A:2468:A:OP2	29:A:2476:A:N6	2.31	0.63
7:J:17:VAL:HG22	7:J:55:ILE:HB	1.81	0.63
29:A:395:U:O2'	29:A:396:G:N7	2.27	0.63
25:P:88:ARG:NH1	25:P:114:ASN:OD1	2.31	0.63
30:B:5:U:OP1	30:B:61:G:O2'	2.13	0.63
2:C:132:ARG:NH2	2:C:186:ASP:OD1	2.31	0.63
29:A:1597:A:H5''	29:A:1598:A:H5'	1.78	0.63
14:T:18:GLU:OE2	29:A:1392:A:N6	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:U:81:ARG:HG3	15:U:96:LYS:HD3	1.79	0.63
29:A:78:U:H3	29:A:108:G:H1	1.45	0.63
29:A:249:C:O2	33:3:11:LYS:NZ	2.31	0.63
29:A:818:G:N1	29:A:1188:U:OP2	2.27	0.63
5:F:63:LYS:HD2	5:F:64:PRO:HD2	1.81	0.62
29:A:1721:G:O2'	29:A:1739:A:N6	2.32	0.62
29:A:2507:C:O3'	32:9:76:ARG:NH2	2.32	0.62
29:A:1086:A:O2'	29:A:1087:G:N7	2.32	0.62
32:9:5:ASP:OD2	32:9:234:HIS:NE2	2.27	0.62
20:Z:2:LYS:HD2	20:Z:3:THR:H	1.65	0.62
11:Q:50:ARG:NH2	29:A:993:G:OP2	2.33	0.62
29:A:284:U:H3	29:A:356:G:H1	1.47	0.62
10:O:39:VAL:HG11	10:O:87:ILE:HD13	1.80	0.62
20:Z:11:SER:HB2	20:Z:31:ILE:HD11	1.81	0.62
24:K:93:GLN:OE1	24:K:114:LYS:NZ	2.33	0.62
29:A:1664:A:H61	29:A:1996:C:H42	1.47	0.61
12:R:98:ILE:HG22	12:R:100:GLY:H	1.65	0.61
17:W:37:ARG:NH2	29:A:2262:U:OP1	2.33	0.61
29:A:1016:G:O6	29:A:1147:A:N6	2.34	0.61
29:A:1437:C:HO2'	29:A:1516:G:HO2'	1.47	0.61
29:A:370:G:O2'	29:A:424:G:OP1	2.16	0.61
29:A:2246:G:H2'	29:A:2247:A:H8	1.65	0.61
29:A:272:A:H2'	29:A:273:G:H8	1.65	0.61
14:T:8:LEU:HD12	14:T:50:LEU:HD21	1.83	0.61
29:A:488:G:H22	29:A:491:G:H5''	1.66	0.61
29:A:500:G:N1	29:A:503:A:OP2	2.30	0.61
31:6:37:MET:HE3	31:6:88:HIS:HE2	1.66	0.61
12:R:49:ILE:HG22	12:R:54:VAL:HG23	1.83	0.61
25:P:87:ARG:HH21	25:P:109:ILE:HG13	1.64	0.61
10:O:72:ALA:HB2	10:O:105:ALA:HB1	1.83	0.61
15:U:67:SER:OG	29:A:335:C:O2	2.16	0.61
29:A:1394:U:H4'	29:A:1603:A:H4'	1.84	0.60
31:6:40:CYS:HB2	31:6:89:VAL:HG12	1.82	0.60
29:A:1429:G:H2'	29:A:1430:G:H8	1.66	0.60
29:A:918:A:N3	30:B:80:U:O2'	2.32	0.60
29:A:1171:G:N2	29:A:1178:C:O2	2.16	0.60
24:K:107:LEU:HB2	24:K:116:ILE:HD11	1.84	0.60
29:A:2855:C:H2'	29:A:2856:A:H8	1.66	0.60
31:6:33:ILE:HG13	31:6:34:THR:HG23	1.84	0.60
29:A:1363:C:O2'	29:A:1809:A:N3	2.31	0.60
29:A:1315:C:O2'	29:A:1392:A:N3	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Q:90:ASP:H	12:R:11:GLN:NE2	2.00	0.60
14:T:11:LEU:O	19:Y:29:ARG:NH1	2.34	0.60
29:A:1306:C:H2'	29:A:1307:A:H8	1.67	0.60
29:A:1704:C:H2'	29:A:1705:A:C8	2.37	0.60
30:B:60:C:H2'	30:B:61:G:H8	1.66	0.60
25:P:25:VAL:HG22	25:P:85:VAL:HG22	1.82	0.59
29:A:16:C:H2'	29:A:17:G:H8	1.68	0.59
2:C:181:ARG:NH1	29:A:1800:C:OP2	2.36	0.59
6:G:104:LEU:HB2	6:G:112:VAL:HB	1.84	0.59
7:J:80:HIS:CD2	7:J:81:ILE:HG22	2.37	0.59
29:A:1528:A:OP2	29:A:1543:G:N2	2.34	0.59
7:J:80:HIS:CG	7:J:81:ILE:H	2.20	0.59
29:A:371:A:N6	29:A:402:A:OP2	2.36	0.59
32:9:13:ALA:HB1	32:9:120:GLY:HA2	1.85	0.59
10:O:100:HIS:HA	10:O:104:GLN:HE22	1.66	0.59
29:A:2581:G:N2	29:A:2581:G:OP2	2.36	0.59
3:D:164:GLN:NE2	29:A:2822:G:OP1	2.35	0.59
29:A:1026:G:H2'	29:A:1027:A:H8	1.68	0.59
29:A:2447:G:H1	29:A:2451:A:H62	1.50	0.59
2:C:96:LYS:NZ	29:A:1490:A:N7	2.51	0.59
32:9:285:ILE:HD11	32:9:312:LEU:HD12	1.83	0.59
33:3:30:HIS:C	33:3:32:LEU:H	2.11	0.59
13:S:55:ILE:HG23	13:S:66:ILE:HD11	1.85	0.59
29:A:1073:A:H3'	29:A:1074:G:H5''	1.83	0.59
19:Y:31:GLN:HB2	19:Y:36:GLN:HB2	1.85	0.58
27:H:26:ALA:HA	27:H:30:LEU:HD12	1.85	0.58
29:A:272:A:H2'	29:A:273:G:C8	2.38	0.58
29:A:1926:U:O2'	29:A:1927:A:N7	2.34	0.58
29:A:514:A:N3	29:A:581:C:O2'	2.36	0.58
3:D:48:ILE:HG23	3:D:84:LEU:HD11	1.84	0.58
21:0:54:ILE:HG23	21:0:56:LYS:H	1.68	0.58
29:A:639:U:H2'	29:A:640:C:H6	1.67	0.58
29:A:2673:G:H2'	29:A:2674:G:H8	1.68	0.58
27:H:117:LEU:HG	27:H:120:GLY:HA2	1.85	0.58
29:A:411:G:OP2	29:A:2406:A:O2'	2.20	0.58
29:A:645:C:H2'	29:A:647:G:C8	2.38	0.58
29:A:1629:U:O4	29:A:1630:A:N6	2.36	0.58
2:C:244:VAL:HG12	2:C:250:GLN:HA	1.84	0.58
4:E:83:VAL:HB	4:E:86:ALA:HB2	1.86	0.58
20:Z:8:GLN:HB3	20:Z:28:LEU:HD13	1.85	0.58
27:H:127:GLU:OE1	27:H:145:ASN:ND2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:521:U:H2'	29:A:522:A:H8	1.69	0.58
29:A:84:A:H62	29:A:101:A:H2	1.52	0.58
29:A:1171:G:O6	29:A:1178:C:N4	2.36	0.58
25:P:26:GLU:HB2	25:P:86:LYS:NZ	2.19	0.58
26:M:45:GLN:NE2	29:A:2485:G:OP1	2.35	0.58
29:A:1830:C:H2'	29:A:1831:G:H8	1.68	0.58
29:A:1907:G:O6	29:A:1923:U:O2	2.22	0.58
29:A:2368:C:H2'	29:A:2369:A:H8	1.68	0.58
12:R:91:GLN:NE2	29:A:993:G:N3	2.51	0.58
16:V:64:VAL:HG12	16:V:69:GLU:HG2	1.85	0.58
15:U:5:ARG:HH22	15:U:93:ARG:HD3	1.68	0.57
29:A:581:C:H2'	29:A:582:A:H8	1.68	0.57
2:C:15:VAL:HG22	2:C:205:GLY:HA3	1.84	0.57
12:R:35:PHE:HB2	12:R:59:ILE:HB	1.87	0.57
29:A:160:A:N3	29:A:2208:C:O2'	2.35	0.57
29:A:1704:C:H2'	29:A:1705:A:H8	1.67	0.57
29:A:1420:A:O2'	29:A:2211:A:N7	2.36	0.57
29:A:1709:U:O2'	29:A:2859:G:N3	2.37	0.57
18:X:58:ILE:HG22	18:X:66:VAL:HG11	1.87	0.57
3:D:42:ASN:ND2	3:D:43:ASP:OD1	2.36	0.57
8:L:29:LYS:NZ	29:A:567:U:OP2	2.37	0.57
29:A:1288:G:OP2	29:A:1288:G:N2	2.38	0.57
2:C:220:ARG:NH2	29:A:1788:C:OP1	2.38	0.57
3:D:8:LYS:NZ	3:D:195:GLY:O	2.34	0.57
22:1:32:LYS:HE2	22:1:50:GLU:HB3	1.86	0.57
27:H:77:THR:OG1	27:H:145:ASN:OD1	2.21	0.57
29:A:848:C:H2'	29:A:849:A:H8	1.69	0.57
29:A:1386:C:H2'	29:A:1387:A:C8	2.38	0.57
29:A:2469:A:N6	29:A:2481:G:O2'	2.34	0.57
29:A:2591:C:H2'	29:A:2592:G:H8	1.69	0.57
32:9:313:ILE:HD13	32:9:324:LEU:HD13	1.85	0.57
29:A:2246:G:H2'	29:A:2247:A:C8	2.39	0.57
1:g:23:ILE:HB	1:g:38:GLY:HA3	1.87	0.57
3:D:173:GLN:NE2	29:A:2771:C:O2'	2.35	0.57
5:F:66:ILE:HD12	5:F:83:PRO:HB3	1.85	0.57
7:J:118:MET:HA	7:J:121:LYS:HE2	1.86	0.57
8:L:116:VAL:HG11	8:L:134:ALA:HB1	1.86	0.57
15:U:81:ARG:NH1	29:A:300:A:O5'	2.36	0.57
29:A:2163:A:OP1	29:A:2170:A:O2'	2.23	0.57
6:G:46:ASP:O	6:G:48:THR:N	2.38	0.57
11:Q:48:ASP:HA	11:Q:51:GLN:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:W:63:VAL:HG12	17:W:78:ILE:HG12	1.87	0.57
18:X:22:ASN:OD1	29:A:2079:U:O2'	2.22	0.57
11:Q:85:ALA:HB1	11:Q:111:LYS:HE3	1.86	0.56
14:T:24:MET:HE2	14:T:30:ILE:HG22	1.87	0.56
20:Z:15:ARG:O	20:Z:20:LYS:NZ	2.38	0.56
29:A:219:A:N3	29:A:234:U:O2'	2.34	0.56
29:A:482:A:O2'	29:A:497:A:N1	2.38	0.56
6:G:4:ALA:HB2	6:G:65:GLY:HA2	1.86	0.56
11:Q:91:ARG:NH2	29:A:1153:C:OP1	2.38	0.56
29:A:935:C:H2'	29:A:936:A:H8	1.69	0.56
29:A:2530:A:OP2	29:A:2535:G:N2	2.39	0.56
30:B:28:C:H2'	30:B:29:A:C8	2.40	0.56
33:3:32:LEU:HA	33:3:35:LYS:HE3	1.86	0.56
3:D:4:LEU:HD21	3:D:100:LEU:HD21	1.87	0.56
29:A:1434:A:H2'	29:A:1435:G:H8	1.69	0.56
29:A:2515:C:H2'	29:A:2516:A:H8	1.70	0.56
32:9:9:ILE:HD11	32:9:59:TYR:HB3	1.86	0.56
5:F:117:SER:O	5:F:127:TYR:OH	2.16	0.56
29:A:581:C:H2'	29:A:582:A:C8	2.41	0.56
29:A:1791:A:N6	29:A:1828:G:O2'	2.38	0.56
23:2:34:ARG:NH1	29:A:466:A:OP1	2.38	0.56
8:L:76:GLU:OE2	29:A:636:G:N1	2.31	0.56
15:U:32:LYS:HB3	15:U:63:ALA:HB1	1.86	0.56
29:A:639:U:H2'	29:A:640:C:C6	2.40	0.56
29:A:629:G:N3	29:A:639:U:O2'	2.39	0.56
5:F:127:TYR:CZ	5:F:129:MET:HE1	2.41	0.56
6:G:175:LYS:HE2	29:A:2530:A:H5'	1.88	0.56
9:N:5:LYS:NZ	29:A:2000:C:OP1	2.39	0.56
14:T:38:ALA:HB3	14:T:81:LYS:HD2	1.87	0.56
24:K:99:ILE:HG12	24:K:118:LEU:HD12	1.86	0.56
29:A:1038:G:H2'	29:A:1039:A:C8	2.41	0.56
29:A:2532:G:N2	29:A:2663:G:O2'	2.38	0.56
2:C:38:LYS:NZ	2:C:55:GLY:O	2.35	0.56
18:X:32:LEU:HD12	18:X:49:ARG:HG2	1.88	0.56
24:K:80:ASP:OD2	25:P:61:ARG:NH1	2.38	0.56
29:A:962:G:H21	29:A:2250:G:H1	1.52	0.56
30:B:14:U:OP2	30:B:70:C:O2'	2.24	0.56
9:N:45:ARG:NH1	29:A:2838:G:O2'	2.39	0.56
19:Y:30:MET:HE3	19:Y:30:MET:HA	1.88	0.56
8:L:128:THR:HG23	8:L:131:ALA:H	1.71	0.55
25:P:21:PRO:HG3	25:P:49:ILE:HD13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2474:U:H5''	29:A:2475:C:H5	1.70	0.55
3:D:151:THR:OG1	29:A:2032:G:N2	2.39	0.55
19:Y:23:ARG:O	19:Y:27:ASN:ND2	2.39	0.55
29:A:239:C:HO2'	29:A:622:G:HO2'	1.54	0.55
29:A:2047:C:H2'	29:A:2048:G:H8	1.71	0.55
4:E:58:LYS:HD2	4:E:59:PRO:HD2	1.88	0.55
29:A:1518:C:H2'	29:A:1519:G:H8	1.71	0.55
29:A:2473:U:OP1	29:A:2475:C:N4	2.38	0.55
29:A:1589:U:H2'	29:A:1590:A:H8	1.70	0.55
29:A:476:G:N1	29:A:479:A:OP2	2.37	0.55
29:A:371:A:H61	29:A:401:A:H3'	1.72	0.55
29:A:1664:A:H61	29:A:1996:C:N4	2.03	0.55
18:X:9:LYS:NZ	29:A:397:U:OP2	2.23	0.55
29:A:177:G:OP2	29:A:177:G:N2	2.21	0.55
29:A:1056:G:H21	29:A:1103:A:H62	1.53	0.55
29:A:1958:C:H2'	29:A:1959:G:H8	1.72	0.55
29:A:2898:U:H2'	29:A:2899:A:C8	2.41	0.55
27:H:7:ASP:HB2	27:H:35:LYS:HA	1.89	0.55
29:A:1057:A:N6	29:A:1087:G:OP2	2.40	0.55
32:9:285:ILE:HB	32:9:314:SER:HB2	1.88	0.55
33:3:32:LEU:HD23	33:3:40:LYS:HG2	1.88	0.55
12:R:24:LYS:HA	12:R:94:THR:HG23	1.88	0.55
29:A:2327:A:H2'	29:A:2328:A:C8	2.42	0.55
6:G:88:LEU:HG	6:G:161:VAL:HG12	1.89	0.54
29:A:184:C:H2'	29:A:185:G:H8	1.72	0.54
29:A:1102:C:H2'	29:A:1103:A:H8	1.72	0.54
29:A:1796:U:H2'	29:A:1797:G:C8	2.41	0.54
26:M:12:MET:HA	29:A:910:A:H62	1.71	0.54
29:A:1019:U:OP1	29:A:1035:U:O2'	2.21	0.54
29:A:1316:U:H2'	29:A:1317:G:H8	1.72	0.54
29:A:2339:C:H2'	29:A:2340:A:C8	2.42	0.54
18:X:5:GLN:O	18:X:73:ARG:NH1	2.40	0.54
29:A:580:U:H2'	29:A:581:C:C6	2.43	0.54
29:A:1802:A:H2'	29:A:1803:A:C8	2.42	0.54
20:Z:42:ALA:O	29:A:851:C:O2'	2.25	0.54
24:K:7:MET:HA	24:K:7:MET:HE3	1.90	0.54
24:K:30:ARG:NH1	24:K:32:TYR:O	2.41	0.54
29:A:2836:U:H2'	29:A:2837:A:H8	1.73	0.54
24:K:92:GLU:O	24:K:93:GLN:NE2	2.41	0.54
24:K:114:LYS:HG2	31:6:70:GLU:HG2	1.88	0.54
29:A:1190:G:H2'	29:A:1191:G:H8	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:13:ARG:NH1	29:A:1693:U:O2'	2.40	0.54
15:U:14:THR:OG1	29:A:310:A:OP1	2.25	0.54
29:A:1141:U:H4'	29:A:1142:A:O4'	2.08	0.54
29:A:2109:U:N3	29:A:2110:G:O6	2.41	0.54
5:F:127:TYR:CE2	5:F:129:MET:HE1	2.42	0.54
8:L:42:SER:OG	29:A:672:C:OP2	2.25	0.54
10:O:98:GLN:OE1	30:B:47:C:O2'	2.26	0.54
24:K:63:VAL:HG12	24:K:64:ARG:HG3	1.89	0.54
29:A:1592:C:H2'	29:A:1593:A:H8	1.72	0.54
29:A:2743:U:OP2	29:A:2755:C:N4	2.40	0.54
30:B:28:C:H2'	30:B:29:A:H8	1.72	0.54
15:U:81:ARG:HH12	29:A:300:A:H3'	1.72	0.54
16:V:66:ASP:HB2	16:V:68:LYS:HZ1	1.72	0.54
32:9:4:VAL:HG22	32:9:60:ARG:HH11	1.72	0.54
8:L:78:ARG:HB3	8:L:113:ALA:HB3	1.90	0.54
10:O:51:ALA:HB3	10:O:78:VAL:HG22	1.90	0.54
17:W:26:SER:HB3	17:W:62:LYS:HE3	1.90	0.54
29:A:20:C:H2'	29:A:21:A:H8	1.73	0.54
29:A:2898:U:H2'	29:A:2899:A:H8	1.73	0.54
16:V:25:LYS:HG2	16:V:43:ASP:HA	1.90	0.53
26:M:38:ARG:HG2	26:M:98:PRO:HD3	1.90	0.53
29:A:2233:U:H2'	29:A:2234:G:C8	2.43	0.53
29:A:2328:A:H2'	29:A:2329:U:C6	2.42	0.53
31:6:21:ASP:HB3	31:6:95:ARG:HH12	1.74	0.53
29:A:1668:A:N3	29:A:1670:C:N4	2.56	0.53
2:C:145:MET:HE1	29:A:1800:C:H2'	1.88	0.53
18:X:49:ARG:NH2	29:A:1364:G:OP2	2.37	0.53
29:A:924:G:H2'	29:A:925:A:H8	1.73	0.53
31:6:99:GLU:HG2	31:6:101:GLU:HG3	1.90	0.53
4:E:102:ARG:NH2	29:A:617:G:OP1	2.41	0.53
29:A:574:A:N6	29:A:2034:U:OP1	2.42	0.53
29:A:651:G:H5'	33:3:18:LYS:HG3	1.90	0.53
1:g:27:CYS:HB2	1:g:33:HIS:HB2	1.89	0.53
7:J:99:ARG:HA	7:J:102:GLU:OE2	2.08	0.53
29:A:843:G:H2'	29:A:844:A:C8	2.44	0.53
22:1:33:LEU:HD11	29:A:2286:G:C8	2.43	0.53
29:A:2099:U:H2'	29:A:2100:G:H8	1.72	0.53
2:C:209:ALA:HA	2:C:212:TRP:CE2	2.44	0.53
5:F:48:LEU:HA	5:F:51:ASN:HB2	1.91	0.53
6:G:158:GLY:O	6:G:162:ARG:NH1	2.40	0.53
24:K:76:VAL:H	25:P:72:VAL:HG22	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:151:C:H2'	29:A:152:A:H8	1.73	0.53
29:A:1176:U:H2'	29:A:1177:G:C8	2.44	0.53
29:A:1355:G:H2'	29:A:1356:G:H8	1.74	0.53
7:J:93:ILE:HD13	7:J:100:VAL:HG21	1.90	0.53
13:S:49:LYS:NZ	29:A:491:G:O6	2.42	0.53
16:V:40:ILE:HD12	16:V:42:LEU:HD21	1.91	0.53
29:A:1476:U:H2'	29:A:1477:A:H8	1.74	0.53
32:9:281:VAL:HG11	32:9:324:LEU:HD11	1.91	0.53
1:g:10:LEU:HD12	1:g:33:HIS:HD2	1.74	0.52
26:M:41:LEU:HD11	26:M:96:ILE:HD13	1.91	0.52
29:A:13:A:O2'	29:A:15:G:N7	2.41	0.52
2:C:257:ARG:NH1	2:C:263:ASP:OD2	2.43	0.52
3:D:148:GLN:O	29:A:2052:A:H4'	2.09	0.52
10:O:29:HIS:HB3	10:O:36:TYR:HB2	1.90	0.52
29:A:1278:C:H2'	29:A:1279:G:H8	1.73	0.52
29:A:2460:U:H2'	29:A:2461:A:H8	1.74	0.52
8:L:29:LYS:HE3	29:A:566:U:OP1	2.09	0.52
12:R:71:LYS:HA	12:R:90:ARG:HG2	1.90	0.52
19:Y:39:GLN:O	19:Y:39:GLN:HG2	2.10	0.52
27:H:30:LEU:HB3	27:H:36:ALA:HB3	1.90	0.52
29:A:1754:A:N1	29:A:2716:C:O2'	2.38	0.52
29:A:1987:A:H2'	29:A:1988:G:H8	1.74	0.52
29:A:2233:U:H2'	29:A:2234:G:H8	1.74	0.52
32:9:105:MET:HE1	32:9:150:ARG:HD3	1.91	0.52
7:J:49:ASP:CG	7:J:121:LYS:HZ3	2.17	0.52
29:A:18:U:H2'	29:A:19:A:H8	1.74	0.52
29:A:1834:U:H5''	29:A:1835:G:H5'	1.91	0.52
14:T:2:ILE:HA	14:T:3:ARG:C	2.35	0.52
29:A:729:G:O2'	29:A:763:G:H4'	2.10	0.52
29:A:860:U:H2'	29:A:861:A:H8	1.74	0.52
29:A:926:G:H2'	29:A:927:A:C8	2.45	0.52
29:A:2217:G:H2'	29:A:2218:G:H8	1.75	0.52
29:A:2453:A:H61	29:A:2499:C:H42	1.57	0.52
33:3:28:LEU:HA	33:3:32:LEU:HD21	1.92	0.52
24:K:25:LEU:HD22	29:A:2562:U:H4'	1.92	0.52
29:A:2473:U:H5'	32:9:62:GLU:OE1	2.08	0.52
32:9:95:ARG:HB2	32:9:155:GLU:HB2	1.90	0.52
2:C:74:PRO:HD2	2:C:96:LYS:HG2	1.91	0.52
31:6:92:GLU:OE2	31:6:96:ARG:NH2	2.43	0.52
3:D:46:ARG:HH12	3:D:86:GLU:HA	1.75	0.52
5:F:101:ARG:NH1	28:d:25:ARG:O	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2250:G:O2'	29:A:2496:C:OP1	2.26	0.52
32:9:61:PHE:HB2	32:9:63:LYS:NZ	2.24	0.52
32:9:158:LEU:HD11	32:9:198:LEU:HD21	1.91	0.52
9:N:73:ASN:OD1	29:A:1454:C:N4	2.42	0.52
22:1:5:ARG:NH2	29:A:2285:C:OP2	2.40	0.52
3:D:62:LYS:HD3	29:A:2810:A:H4'	1.91	0.52
4:E:119:ILE:HB	4:E:187:VAL:HG22	1.90	0.52
29:A:1080:A:N6	29:A:1088:A:OP1	2.43	0.52
29:A:2441:U:OP2	29:A:2586:U:O2'	2.27	0.52
29:A:2847:U:H2'	29:A:2848:G:O4'	2.10	0.52
4:E:189:THR:HG23	4:E:192:ALA:H	1.74	0.51
5:F:72:SER:N	5:F:80:GLN:OE1	2.43	0.51
7:J:27:ARG:NH2	29:A:1143:A:OP1	2.43	0.51
26:M:11:LYS:O	29:A:911:A:N6	2.41	0.51
29:A:373:U:H2'	29:A:374:A:H8	1.75	0.51
29:A:755:U:H2'	29:A:756:A:H8	1.75	0.51
18:X:6:VAL:HG13	18:X:7:THR:HG23	1.92	0.51
23:2:39:ARG:NH2	29:A:468:G:O6	2.42	0.51
29:A:20:C:H2'	29:A:21:A:C8	2.45	0.51
29:A:145:C:H2'	29:A:146:A:H8	1.75	0.51
27:H:16:GLY:HA3	27:H:51:ARG:HH22	1.75	0.51
29:A:45:G:H5'	29:A:46:G:H5'	1.92	0.51
29:A:582:A:H2'	29:A:583:G:H8	1.74	0.51
5:F:91:ARG:NE	30:B:45:A:O4'	2.44	0.51
17:W:35:ARG:HG2	17:W:35:ARG:HH11	1.75	0.51
29:A:171:U:H2'	29:A:172:A:C8	2.45	0.51
29:A:1105:U:H2'	29:A:1106:G:H8	1.74	0.51
29:A:2636:C:H2'	29:A:2637:U:H6	1.76	0.51
21:0:15:ARG:NH1	29:A:1264:A:OP1	2.40	0.51
25:P:23:ASP:OD1	25:P:89:GLY:N	2.42	0.51
27:H:94:ILE:HG23	27:H:98:ASP:HB2	1.92	0.51
29:A:290:U:H3	29:A:350:G:H1	1.58	0.51
29:A:355:U:H2'	29:A:356:G:C8	2.45	0.51
29:A:1469:A:H2'	29:A:1470:A:H8	1.75	0.51
29:A:2131:U:H5'	29:A:2132:U:H5''	1.93	0.51
32:9:281:VAL:HG12	32:9:311:TYR:HB2	1.92	0.51
29:A:18:U:H2'	29:A:19:A:C8	2.46	0.51
29:A:2698:U:H2'	29:A:2699:C:C6	2.44	0.51
2:C:194:VAL:HG22	2:C:195:GLY:H	1.76	0.51
20:Z:2:LYS:HD2	20:Z:3:THR:N	2.25	0.51
29:A:1231:U:H2'	29:A:1232:G:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:68:ARG:NH1	2:C:128:THR:OG1	2.44	0.51
5:F:132:ARG:HG3	5:F:133:GLU:HG3	1.92	0.51
24:K:64:ARG:NH1	24:K:102:PRO:O	2.40	0.51
26:M:17:ASN:O	26:M:38:ARG:NH2	2.43	0.51
2:C:256:THR:OG1	29:A:1797:G:O2'	2.28	0.51
9:N:35:LYS:HG2	9:N:110:MET:HE2	1.91	0.51
10:O:31:THR:OG1	10:O:34:HIS:O	2.19	0.51
29:A:477:A:OP1	29:A:501:A:N6	2.44	0.51
29:A:1681:G:N2	29:A:1763:G:OP2	2.40	0.51
29:A:2705:A:O2'	29:A:2852:G:OP1	2.28	0.51
3:D:46:ARG:HH22	3:D:87:GLY:H	1.58	0.51
8:L:89:VAL:HG11	8:L:123:ARG:HH22	1.76	0.51
13:S:37:THR:HG23	13:S:38:TYR:CD1	2.46	0.51
24:K:98:ARG:NH2	31:6:99:GLU:O	2.44	0.51
29:A:713:G:H21	29:A:718:A:H62	1.59	0.51
29:A:741:U:H2'	29:A:742:A:H8	1.76	0.51
29:A:1361:G:H2'	29:A:1362:C:C6	2.46	0.51
30:B:13:G:O2'	30:B:15:A:OP2	2.25	0.51
2:C:77:VAL:HG22	2:C:113:ASP:H	1.75	0.50
29:A:355:U:H2'	29:A:356:G:H8	1.75	0.50
29:A:753:A:H2'	29:A:754:U:H6	1.76	0.50
29:A:843:G:H2'	29:A:844:A:H8	1.77	0.50
29:A:910:A:H2'	29:A:911:A:C8	2.45	0.50
21:0:42:ILE:HG22	21:0:48:TYR:HB2	1.94	0.50
29:A:1864:U:OP1	29:A:2410:G:O2'	2.29	0.50
29:A:2443:C:H2'	29:A:2444:G:H8	1.76	0.50
29:A:2788:C:H2'	29:A:2789:C:C6	2.46	0.50
16:V:80:HIS:CD2	16:V:83:LYS:HB2	2.42	0.50
29:A:796:C:H2'	29:A:797:G:C8	2.47	0.50
4:E:43:THR:HB	29:A:38:A:N3	2.26	0.50
9:N:103:ARG:NH1	29:A:1287:A:O4'	2.44	0.50
29:A:281:C:H2'	29:A:282:A:H8	1.76	0.50
29:A:630:G:N2	29:A:633:A:OP2	2.33	0.50
29:A:1682:G:OP2	29:A:1699:G:N2	2.45	0.50
29:A:2594:C:N4	29:A:2595:G:O6	2.44	0.50
29:A:2836:U:H2'	29:A:2837:A:C8	2.46	0.50
3:D:77:ARG:NH2	3:D:200:ASP:OD1	2.45	0.50
18:X:2:ARG:NH2	29:A:1365:A:OP1	2.43	0.50
21:0:16:ARG:NE	29:A:1266:G:OP2	2.44	0.50
29:A:302:C:H2'	29:A:303:G:H8	1.76	0.50
29:A:1351:C:O2'	29:A:1571:A:O2'	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1443:U:H2'	29:A:1444:G:H8	1.76	0.50
29:A:1528:A:N6	29:A:1543:G:O2'	2.45	0.50
29:A:2537:U:H2'	29:A:2538:C:H6	1.76	0.50
13:S:109:ASP:OD1	13:S:109:ASP:N	2.45	0.50
26:M:90:GLU:HG3	26:M:91:TYR:HD1	1.76	0.50
29:A:171:U:H2'	29:A:172:A:H8	1.77	0.50
29:A:1098:A:H3'	29:A:1099:G:H8	1.77	0.50
29:A:1417:C:H2'	29:A:1418:G:O4'	2.11	0.50
29:A:1748:C:H2'	29:A:1749:A:H8	1.76	0.50
5:F:90:LEU:HD12	5:F:94:ARG:HB3	1.93	0.50
29:A:1688:U:O2'	29:A:1700:A:N7	2.36	0.50
29:A:1748:C:H2'	29:A:1749:A:C8	2.46	0.50
5:F:150:GLY:HA3	29:A:2305:U:N3	2.26	0.50
13:S:22:ASP:OD1	13:S:25:ARG:NH1	2.40	0.50
29:A:969:G:H2'	29:A:970:U:C6	2.47	0.50
3:D:16:THR:OG1	3:D:18:ASP:OD1	2.24	0.50
6:G:83:THR:HG22	6:G:133:LYS:HE3	1.94	0.50
13:S:31:GLN:O	13:S:35:ILE:HG12	2.12	0.50
15:U:88:ASP:O	15:U:90:LYS:N	2.45	0.50
29:A:408:G:H1	29:A:419:U:H3	1.59	0.50
29:A:1720:U:H2'	29:A:1721:G:O4'	2.11	0.50
29:A:2470:G:H2'	29:A:2471:A:H8	1.77	0.50
32:9:36:GLY:H	32:9:128:THR:HG23	1.76	0.50
2:C:121:ALA:HB3	2:C:129:LEU:HD13	1.92	0.49
15:U:81:ARG:NH1	29:A:301:G:OP2	2.43	0.49
29:A:1434:A:H2'	29:A:1435:G:C8	2.46	0.49
29:A:2027:G:H2'	29:A:2028:U:C6	2.47	0.49
29:A:2329:U:H2'	29:A:2330:G:C8	2.47	0.49
29:A:2589:A:H2'	29:A:2590:A:H8	1.77	0.49
29:A:2591:C:H2'	29:A:2592:G:C8	2.47	0.49
30:B:95:U:H2'	30:B:96:G:H8	1.77	0.49
32:9:229:ILE:HD12	32:9:269:TYR:HD1	1.77	0.49
7:J:32:LEU:HD22	7:J:54:ILE:HG21	1.93	0.49
29:A:647:G:N2	29:A:2350:C:O2'	2.45	0.49
29:A:755:U:H2'	29:A:756:A:C8	2.47	0.49
29:A:1266:G:O2'	29:A:2012:G:O6	2.25	0.49
29:A:1361:G:H2'	29:A:1362:C:H6	1.76	0.49
4:E:126:VAL:O	4:E:156:ASN:ND2	2.45	0.49
4:E:165:HIS:HB3	4:E:166:LYS:NZ	2.27	0.49
5:F:101:ARG:NH2	5:F:139:GLU:OE2	2.45	0.49
7:J:7:LYS:HG3	29:A:538:A:H4'	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:N:38:LEU:HD21	9:N:99:LYS:HE3	1.94	0.49
24:K:42:THR:HG22	24:K:57:VAL:HG22	1.94	0.49
29:A:968:C:H2'	29:A:969:G:H8	1.77	0.49
29:A:1432:G:H2'	29:A:1433:A:C8	2.46	0.49
32:9:61:PHE:HB2	32:9:63:LYS:HZ2	1.77	0.49
2:C:206:LYS:NZ	29:A:729:G:OP2	2.42	0.49
29:A:65:U:H2'	29:A:66:C:H6	1.77	0.49
29:A:2099:U:H2'	29:A:2100:G:C8	2.47	0.49
29:A:2166:U:O4	29:A:2170:A:N6	2.43	0.49
15:U:93:ARG:HB2	15:U:102:ILE:HG13	1.94	0.49
22:1:22:THR:HG21	29:A:2286:G:H1	1.77	0.49
29:A:948:C:O2	29:A:984:A:O2'	2.21	0.49
29:A:2081:U:H2'	29:A:2082:A:H8	1.77	0.49
29:A:2443:C:H2'	29:A:2444:G:C8	2.47	0.49
31:6:17:LEU:HD23	31:6:51:ILE:HA	1.93	0.49
2:C:52:HIS:HA	2:C:216:ARG:HB2	1.95	0.49
5:F:36:ASN:HB3	5:F:152:ASP:HB2	1.95	0.49
19:Y:6:LEU:HD23	19:Y:56:LEU:HD11	1.95	0.49
29:A:244:A:OP2	33:3:7:ARG:NH2	2.44	0.49
29:A:796:C:H2'	29:A:797:G:H8	1.76	0.49
29:A:1794:A:H2'	29:A:1795:C:C6	2.47	0.49
3:D:84:LEU:HD23	3:D:88:GLU:O	2.13	0.49
29:A:145:C:H2'	29:A:146:A:C8	2.48	0.49
29:A:418:C:H2'	29:A:419:U:C6	2.48	0.49
29:A:1161:C:H2'	29:A:1162:G:H8	1.76	0.49
29:A:2014:A:H2'	29:A:2015:A:C8	2.47	0.49
5:F:91:ARG:HB2	30:B:43:C:O2'	2.12	0.49
9:N:45:ARG:HH12	29:A:2838:G:H1'	1.78	0.49
24:K:66:LYS:HB3	29:A:1665:A:H5''	1.93	0.49
29:A:29:U:H2'	29:A:30:G:H8	1.78	0.49
29:A:1447:C:O2'	29:A:1544:A:N3	2.40	0.49
32:9:68:GLU:OE2	32:9:84:LYS:HG2	2.12	0.49
4:E:132:LYS:HE3	29:A:320:A:OP2	2.11	0.49
8:L:110:VAL:HG12	8:L:110:VAL:O	2.13	0.49
12:R:23:GLU:O	12:R:94:THR:OG1	2.29	0.49
25:P:19:PHE:HE2	25:P:46:VAL:HG21	1.76	0.49
29:A:1028:A:H2'	29:A:1029:A:C8	2.48	0.49
29:A:1790:C:H2'	29:A:1791:A:C5	2.48	0.49
29:A:2728:U:O2'	29:A:2729:G:H8	1.95	0.49
30:B:30:C:H1'	30:B:57:A:H61	1.76	0.49
5:F:71:LYS:NZ	5:F:72:SER:O	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:H:54:LEU:HA	27:H:57:LYS:HG2	1.94	0.49
29:A:807:U:H2'	29:A:808:G:H8	1.78	0.49
29:A:1165:A:H2'	29:A:1166:G:H8	1.77	0.49
29:A:1726:C:H2'	29:A:1727:C:C6	2.48	0.49
29:A:2315:G:H2'	29:A:2316:G:H8	1.78	0.49
2:C:260:LYS:HE2	29:A:2227:A:H5''	1.94	0.48
5:F:41:GLU:OE2	5:F:147:ARG:NH2	2.46	0.48
29:A:1009:A:N3	29:A:1153:C:O2'	2.43	0.48
29:A:1130:U:C2	29:A:2025:C:H5'	2.48	0.48
29:A:2023:C:H2'	29:A:2024:G:H8	1.78	0.48
29:A:2508:G:H5'	32:9:76:ARG:NH2	2.28	0.48
2:C:151:GLY:O	2:C:155:ARG:HD2	2.13	0.48
3:D:149:ASN:O	3:D:152:PRO:HD2	2.13	0.48
9:N:107:ASN:O	9:N:107:ASN:ND2	2.46	0.48
24:K:34:GLY:N	24:K:37:ASP:OD2	2.35	0.48
29:A:161:A:OP2	29:A:162:U:O2'	2.27	0.48
29:A:1563:U:H2'	29:A:1564:C:C6	2.48	0.48
5:F:104:THR:HG23	5:F:105:ILE:HG12	1.95	0.48
5:F:137:PHE:CE2	5:F:139:GLU:HB2	2.48	0.48
29:A:599:A:H2'	29:A:600:G:H8	1.79	0.48
29:A:1564:C:H2'	29:A:1565:C:C6	2.48	0.48
29:A:2693:G:H2'	29:A:2694:G:H8	1.76	0.48
15:U:24:VAL:HA	15:U:35:VAL:HG22	1.94	0.48
29:A:979:A:H2'	29:A:982:C:H42	1.77	0.48
29:A:1084:A:N3	29:A:1105:U:O2'	2.44	0.48
29:A:1518:C:H2'	29:A:1519:G:C8	2.48	0.48
29:A:1808:A:H3'	29:A:1809:A:C8	2.49	0.48
29:A:2549:G:H2'	29:A:2550:G:H8	1.77	0.48
30:B:63:C:H2'	30:B:64:G:H8	1.78	0.48
5:F:139:GLU:HA	28:d:28:VAL:HG22	1.95	0.48
26:M:42:THR:HG22	26:M:93:VAL:HG12	1.96	0.48
29:A:741:U:H2'	29:A:742:A:C8	2.48	0.48
29:A:1198:U:H2'	29:A:1199:U:C6	2.49	0.48
29:A:1278:C:H2'	29:A:1279:G:C8	2.48	0.48
29:A:2636:C:H2'	29:A:2637:U:C6	2.48	0.48
31:6:37:MET:HE3	31:6:88:HIS:NE2	2.26	0.48
8:L:79:LEU:HB3	8:L:116:VAL:HB	1.95	0.48
18:X:38:TRP:CD1	27:H:32:PRO:HA	2.48	0.48
25:P:42:PHE:HE2	25:P:60:VAL:HG13	1.79	0.48
29:A:64:A:H2'	29:A:65:U:C6	2.48	0.48
29:A:1794:A:H2'	29:A:1795:C:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:B:16:G:N2	30:B:69:G:H1'	2.29	0.48
32:9:16:GLY:O	32:9:69:ARG:NH1	2.47	0.48
11:Q:93:ILE:HG13	12:R:11:GLN:HG3	1.95	0.48
13:S:73:LYS:HB2	13:S:106:VAL:HB	1.94	0.48
29:A:419:U:H2'	29:A:420:C:C6	2.48	0.48
29:A:1733:G:H2'	29:A:1734:G:C8	2.48	0.48
29:A:1744:A:H3'	29:A:1745:A:H8	1.77	0.48
23:2:16:HIS:HB2	23:2:44:VAL:HG11	1.96	0.48
29:A:1850:G:H2'	29:A:1851:U:C6	2.49	0.48
29:A:2737:G:H2'	29:A:2738:A:C8	2.48	0.48
29:A:2854:G:H2'	29:A:2855:C:C6	2.49	0.48
30:B:51:G:O6	30:B:52:A:N6	2.46	0.48
31:6:10:VAL:HG11	31:6:87:VAL:HG21	1.96	0.48
33:3:30:HIS:ND1	33:3:31:ILE:HG12	2.29	0.48
4:E:181:ILE:HG22	8:L:3:LEU:HD12	1.95	0.48
29:A:675:A:N3	29:A:2443:C:O2'	2.41	0.48
29:A:903:C:H2'	29:A:904:G:H8	1.78	0.48
29:A:2417:C:H2'	29:A:2418:A:H8	1.79	0.48
2:C:106:PRO:HG2	2:C:109:LEU:HB2	1.94	0.48
7:J:57:LEU:HD21	7:J:130:HIS:HB3	1.96	0.48
7:J:80:HIS:CD2	7:J:81:ILE:H	2.31	0.48
9:N:110:MET:HE3	9:N:110:MET:HA	1.95	0.48
25:P:112:ARG:HH11	25:P:114:ASN:HD21	1.60	0.48
29:A:286:U:H2'	29:A:287:G:H8	1.79	0.48
29:A:558:U:H2'	29:A:559:G:C8	2.49	0.48
29:A:881:G:H2'	29:A:882:G:H8	1.78	0.48
29:A:2243:U:H2'	29:A:2244:U:C6	2.49	0.48
29:A:2875:C:H2'	29:A:2876:G:C8	2.49	0.48
4:E:21:ARG:HH22	4:E:106:LYS:HE3	1.78	0.47
21:0:3:GLN:OE1	29:A:1263:U:O2'	2.22	0.47
23:2:10:LEU:HD22	29:A:770:G:H5''	1.96	0.47
29:A:582:A:H2'	29:A:583:G:C8	2.49	0.47
32:9:249:PRO:HG2	32:9:253:THR:H	1.79	0.47
2:C:224:MET:HE2	29:A:782:A:N1	2.28	0.47
5:F:21:TYR:OH	5:F:164:GLU:OE1	2.32	0.47
29:A:4:U:H2'	29:A:5:A:H8	1.79	0.47
29:A:69:C:O2	29:A:73:A:O2'	2.29	0.47
29:A:414:C:H2'	29:A:415:A:C8	2.49	0.47
29:A:2602:A:H2	32:9:136:ARG:HH21	1.60	0.47
29:A:299:A:N1	29:A:322:A:O2'	2.37	0.47
29:A:1106:G:H2'	29:A:1107:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2065:C:H2'	29:A:2066:C:H6	1.80	0.47
29:A:2854:G:H2'	29:A:2855:C:H6	1.80	0.47
10:O:104:GLN:OE1	10:O:104:GLN:N	2.47	0.47
19:Y:2:LYS:HE2	29:A:102:U:C2	2.49	0.47
29:A:191:A:H2'	29:A:192:C:C6	2.49	0.47
29:A:660:C:H2'	29:A:661:A:H8	1.79	0.47
29:A:1281:G:H2'	29:A:1282:U:C6	2.49	0.47
15:U:38:ILE:HG21	15:U:64:ILE:HG13	1.96	0.47
27:H:14:SER:OG	27:H:17:ASP:OD2	2.26	0.47
29:A:43:G:H2'	29:A:44:A:C8	2.50	0.47
29:A:1828:G:OP2	37:A:3101:HOH:O	2.20	0.47
29:A:2071:A:H2'	29:A:2072:C:C6	2.50	0.47
29:A:2731:G:H2'	29:A:2732:G:C8	2.49	0.47
29:A:2816:G:N3	29:A:2883:A:O2'	2.42	0.47
29:A:2837:A:H2'	29:A:2838:G:H8	1.79	0.47
32:9:313:ILE:HG22	32:9:320:GLY:HA3	1.97	0.47
27:H:116:ARG:HB2	27:H:133:GLN:HG3	1.97	0.47
29:A:822:G:H2'	29:A:823:C:C6	2.50	0.47
29:A:1469:A:H2'	29:A:1470:A:C8	2.49	0.47
29:A:2127:G:H2'	29:A:2128:G:C8	2.49	0.47
2:C:246:PRO:HG2	2:C:247:TRP:CZ3	2.50	0.47
5:F:3:LEU:HD12	5:F:100:GLU:HG2	1.96	0.47
5:F:150:GLY:HA3	29:A:2305:U:H3	1.80	0.47
6:G:10:VAL:HG12	6:G:75:VAL:HG11	1.97	0.47
8:L:112:LEU:O	29:A:627:A:N6	2.42	0.47
15:U:84:PHE:CE2	15:U:93:ARG:HG2	2.50	0.47
29:A:184:C:H2'	29:A:185:G:C8	2.48	0.47
29:A:305:C:H2'	29:A:306:U:C6	2.50	0.47
29:A:1429:G:H2'	29:A:1430:G:C8	2.48	0.47
29:A:2037:A:H2'	29:A:2038:G:C8	2.49	0.47
29:A:2554:U:H2'	29:A:2555:U:C6	2.50	0.47
32:9:13:ALA:HB3	32:9:148:ASP:H	1.80	0.47
11:Q:53:LYS:NZ	29:A:994:C:OP2	2.43	0.47
29:A:314:C:H2'	29:A:315:G:C8	2.50	0.47
29:A:475:C:N3	29:A:479:A:N7	2.63	0.47
29:A:577:G:O2'	29:A:1254:A:OP1	2.32	0.47
32:9:76:ARG:O	32:9:76:ARG:HG2	2.15	0.47
8:L:38:GLN:OE1	29:A:831:G:O2'	2.33	0.47
24:K:63:VAL:HG13	24:K:103:VAL:HG13	1.96	0.47
29:A:151:C:H2'	29:A:152:A:C8	2.49	0.47
29:A:417:C:H2'	29:A:418:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:589:U:H2'	29:A:590:A:C8	2.50	0.47
29:A:594:U:H3	29:A:663:G:H1	1.62	0.47
29:A:2855:C:H2'	29:A:2856:A:C8	2.49	0.47
32:9:74:ALA:HB3	32:9:78:CYS:HB2	1.96	0.47
33:3:15:LYS:HE2	33:3:19:GLY:HA2	1.95	0.47
2:C:155:ARG:HD3	29:A:1818:U:H2'	1.97	0.47
5:F:23:SER:OG	30:B:55:U:O2'	2.33	0.47
29:A:1485:U:H2'	29:A:1486:U:C6	2.50	0.47
29:A:2192:U:H2'	29:A:2193:G:H8	1.80	0.47
32:9:17:GLY:HA2	32:9:69:ARG:HH12	1.80	0.47
3:D:114:LYS:NZ	29:A:2723:C:OP1	2.44	0.46
4:E:188:MET:HE1	4:E:196:VAL:HG11	1.96	0.46
5:F:176:PHE:HE2	28:d:44:PHE:HB3	1.81	0.46
29:A:972:A:OP2	29:A:973:A:O2'	2.30	0.46
29:A:1013:C:H2'	29:A:1014:A:H8	1.79	0.46
29:A:1085:A:O2'	29:A:1086:A:O4'	2.27	0.46
29:A:1550:C:H2'	29:A:1551:A:H8	1.80	0.46
29:A:2022:U:O2'	29:A:2617:U:H5'	2.16	0.46
29:A:2359:C:O2'	33:3:53:ASP:OD2	2.28	0.46
29:A:2595:G:N2	29:A:2598:A:OP2	2.28	0.46
8:L:32:GLY:HA2	29:A:1190:G:H5''	1.96	0.46
29:A:438:G:H2'	29:A:439:A:C8	2.49	0.46
29:A:746:U:O2'	29:A:2611:C:O2'	2.26	0.46
29:A:2649:C:H2'	29:A:2650:U:H6	1.80	0.46
32:9:172:LYS:NZ	32:9:214:ILE:O	2.49	0.46
3:D:151:THR:HB	3:D:152:PRO:HD3	1.97	0.46
13:S:37:THR:HB	13:S:48:LYS:HE3	1.96	0.46
13:S:93:ALA:HB2	29:A:1614:A:C2	2.51	0.46
16:V:7:GLU:OE2	16:V:7:GLU:N	2.49	0.46
16:V:30:ILE:HD11	16:V:63:ILE:HG13	1.97	0.46
29:A:927:A:H2'	29:A:928:A:C8	2.50	0.46
29:A:1198:U:H2'	29:A:1199:U:H6	1.80	0.46
29:A:1696:G:N2	29:A:1977:A:O2'	2.46	0.46
29:A:2193:G:H2'	29:A:2194:U:C6	2.50	0.46
29:A:2425:A:H4'	29:A:2426:A:O5'	2.14	0.46
29:A:2590:A:H2'	29:A:2591:C:H6	1.79	0.46
3:D:135:GLY:HA2	29:A:743:A:OP1	2.15	0.46
3:D:150:GLN:HG2	29:A:2572:A:N7	2.30	0.46
5:F:87:LYS:NZ	29:A:2314:A:OP1	2.49	0.46
6:G:29:ASN:HB3	6:G:78:VAL:HA	1.97	0.46
29:A:1300:G:H4'	29:A:1301:A:H5''	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2031:A:N3	29:A:2455:G:O2'	2.39	0.46
29:A:2788:C:O2'	29:A:2809:A:N3	2.41	0.46
5:F:55:ASP:O	5:F:59:ILE:HG12	2.15	0.46
12:R:6:GLN:NE2	12:R:9:GLY:H	2.14	0.46
20:Z:4:ILE:HB	20:Z:39:ASP:OD1	2.15	0.46
29:A:577:G:H2'	29:A:578:G:C8	2.51	0.46
29:A:833:A:H2'	29:A:834:G:C8	2.50	0.46
29:A:1738:G:O2'	29:A:1739:A:H8	1.98	0.46
29:A:1942:C:OP2	29:A:1943:U:O2'	2.19	0.46
29:A:2078:C:H2'	29:A:2079:U:C6	2.50	0.46
29:A:2508:G:P	32:9:76:ARG:HH22	2.38	0.46
30:B:114:C:H2'	30:B:115:A:C8	2.51	0.46
3:D:2:ILE:HD13	3:D:48:ILE:HD11	1.98	0.46
6:G:174:LYS:HD2	6:G:174:LYS:O	2.16	0.46
25:P:32:VAL:HG12	25:P:37:LYS:HG2	1.97	0.46
29:A:2537:U:H2'	29:A:2538:C:C6	2.50	0.46
29:A:2660:A:H4'	32:9:181:ALA:O	2.14	0.46
32:9:306:TRP:CE3	32:9:308:ASP:HB2	2.50	0.46
2:C:56:GLY:HA2	2:C:212:TRP:HA	1.97	0.46
2:C:251:THR:HG22	2:C:252:LYS:H	1.80	0.46
19:Y:32:ALA:HB2	19:Y:37:LEU:HD13	1.97	0.46
29:A:499:U:H2'	29:A:500:G:O4'	2.15	0.46
29:A:754:U:O2'	29:A:1272:A:N1	2.45	0.46
29:A:1771:C:H2'	29:A:1772:A:C8	2.51	0.46
29:A:1869:G:N2	29:A:1871:A:O2'	2.49	0.46
29:A:2241:A:H2'	29:A:2242:G:C8	2.50	0.46
29:A:2266:A:H4'	29:A:2267:A:N3	2.31	0.46
29:A:2643:G:H2'	29:A:2644:G:H8	1.79	0.46
5:F:72:SER:OG	5:F:78:ILE:O	2.29	0.46
6:G:37:ASN:HD22	6:G:63:GLN:CD	2.24	0.46
14:T:50:LEU:HD23	19:Y:26:PHE:CZ	2.51	0.46
15:U:5:ARG:NH2	15:U:5:ARG:HB2	2.30	0.46
29:A:5:A:H2'	29:A:6:A:H8	1.80	0.46
29:A:742:A:H2'	29:A:743:A:C8	2.51	0.46
29:A:753:A:H2'	29:A:754:U:C6	2.51	0.46
29:A:1298:C:H2'	29:A:1299:G:O4'	2.16	0.46
29:A:2522:U:O2'	29:A:2647:U:OP1	2.28	0.46
1:g:1:MET:N	29:A:2526:G:N3	2.64	0.46
2:C:50:THR:HG23	2:C:53:ILE:HD12	1.98	0.46
10:O:15:ARG:HH21	30:B:8:C:H5''	1.80	0.46
16:V:21:ARG:HA	16:V:25:LYS:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1592:C:H2'	29:A:1593:A:C8	2.50	0.46
29:A:1682:G:H2'	29:A:1683:U:C6	2.51	0.46
29:A:2567:G:H2'	29:A:2568:U:C6	2.50	0.46
29:A:2815:C:H2'	29:A:2816:G:H8	1.81	0.46
29:A:2863:C:H2'	29:A:2864:G:C8	2.51	0.46
30:B:111:U:H2'	30:B:112:G:H8	1.81	0.46
32:9:244:LEU:HD23	32:9:281:VAL:HG23	1.98	0.46
2:C:68:ARG:HG3	2:C:128:THR:HG21	1.98	0.46
3:D:149:ASN:OD1	3:D:150:GLN:N	2.49	0.46
4:E:108:ILE:HD12	4:E:181:ILE:HD11	1.98	0.46
7:J:125:TYR:OH	7:J:132:HIS:NE2	2.47	0.46
13:S:28:LYS:HZ3	13:S:70:LYS:HG3	1.81	0.46
29:A:404:A:H4'	29:A:405:U:O5'	2.14	0.46
29:A:1387:A:H2'	29:A:1388:G:C8	2.51	0.46
29:A:2691:C:H2'	29:A:2692:G:H8	1.81	0.46
30:B:63:C:H2'	30:B:64:G:C8	2.51	0.46
2:C:7:PRO:HB3	2:C:13:ARG:HG3	1.98	0.45
3:D:179:ARG:HB2	3:D:188:LEU:HD12	1.97	0.45
17:W:29:ALA:N	17:W:60:ASP:OD1	2.50	0.45
20:Z:37:ARG:NH2	29:A:929:U:H4'	2.30	0.45
29:A:25:U:H2'	29:A:26:G:O4'	2.17	0.45
29:A:181:A:H2'	29:A:182:A:H8	1.81	0.45
29:A:191:A:H2'	29:A:192:C:H6	1.81	0.45
29:A:558:U:H2'	29:A:559:G:H8	1.80	0.45
29:A:1965:C:H5''	29:A:1966:A:H2'	1.98	0.45
15:U:6:ARG:HG3	15:U:7:ASP:H	1.81	0.45
16:V:10:LYS:HD3	16:V:10:LYS:HA	1.72	0.45
29:A:856:G:H2'	29:A:857:G:C8	2.52	0.45
29:A:935:C:H2'	29:A:936:A:C8	2.50	0.45
29:A:1062:G:H2'	29:A:1063:G:C8	2.51	0.45
29:A:1571:A:H2'	29:A:1572:A:H8	1.81	0.45
29:A:1682:G:H2'	29:A:1683:U:H6	1.82	0.45
29:A:2875:C:H2'	29:A:2876:G:H8	1.81	0.45
32:9:118:ALA:HB1	32:9:148:ASP:HB2	1.98	0.45
2:C:77:VAL:HG12	2:C:93:VAL:HG12	1.98	0.45
4:E:43:THR:O	29:A:442:G:N2	2.43	0.45
10:O:33:ARG:HG3	10:O:34:HIS:CD2	2.51	0.45
11:Q:5:ARG:HH12	29:A:1251:C:H6	1.62	0.45
13:S:17:VAL:HG12	13:S:76:VAL:HG21	1.98	0.45
24:K:116:ILE:HG22	31:6:33:ILE:HD13	1.97	0.45
29:A:154:U:H2'	29:A:155:A:H8	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:304:U:H2'	29:A:305:C:C6	2.52	0.45
29:A:873:C:H2'	29:A:874:G:C8	2.51	0.45
29:A:1664:A:N6	29:A:1996:C:H42	2.13	0.45
29:A:2687:U:H2'	29:A:2688:G:O4'	2.17	0.45
4:E:176:ASP:OD1	4:E:179:SER:OG	2.33	0.45
14:T:44:LYS:O	14:T:48:GLN:HG2	2.16	0.45
29:A:5:A:H2'	29:A:6:A:C8	2.52	0.45
29:A:24:G:H2'	29:A:25:U:C6	2.51	0.45
29:A:154:U:H2'	29:A:155:A:C8	2.52	0.45
29:A:306:U:H2'	29:A:307:G:O4'	2.17	0.45
29:A:489:G:N2	29:A:1320:C:H5''	2.31	0.45
29:A:2345:G:H5'	29:A:2347:C:H5'	1.98	0.45
2:C:224:MET:HE2	29:A:782:A:C6	2.52	0.45
5:F:73:VAL:HG22	5:F:75:GLY:H	1.82	0.45
29:A:415:A:H2'	29:A:416:U:C6	2.51	0.45
29:A:458:G:O2'	29:A:469:G:O6	2.33	0.45
29:A:1874:C:H2'	29:A:1875:G:O4'	2.16	0.45
29:A:2087:G:H2'	29:A:2088:A:H8	1.82	0.45
29:A:2192:U:H2'	29:A:2193:G:C8	2.51	0.45
32:9:103:GLU:N	32:9:103:GLU:OE2	2.50	0.45
1:g:13:ASN:HD22	1:g:29:ALA:HB2	1.80	0.45
7:J:37:ARG:NH2	29:A:1007:C:OP1	2.50	0.45
20:Z:15:ARG:HG3	20:Z:53:MET:HE1	1.97	0.45
29:A:242:G:N2	29:A:255:A:OP2	2.37	0.45
29:A:754:U:H2'	29:A:755:U:C6	2.52	0.45
7:J:80:HIS:CG	7:J:81:ILE:N	2.84	0.45
11:Q:5:ARG:NH1	29:A:1251:C:O5'	2.50	0.45
13:S:29:VAL:HG11	13:S:55:ILE:HD11	1.98	0.45
24:K:31:ARG:HH22	29:A:2676:C:P	2.39	0.45
29:A:657:U:H2'	29:A:658:U:C6	2.52	0.45
29:A:837:C:N3	29:A:941:A:N6	2.65	0.45
29:A:1651:G:H2'	29:A:1652:A:C8	2.51	0.45
29:A:2139:U:H2'	29:A:2140:G:H8	1.81	0.45
3:D:136:ASN:ND2	3:D:139:SER:O	2.39	0.45
5:F:32:LYS:HD3	5:F:91:ARG:HH22	1.81	0.45
27:H:94:ILE:HB	27:H:122:LEU:HD12	1.99	0.45
29:A:23:G:H2'	29:A:24:G:H8	1.82	0.45
29:A:289:G:H2'	29:A:290:U:C6	2.52	0.45
29:A:744:U:H2'	29:A:745:G:O4'	2.16	0.45
29:A:1066:U:N3	29:A:1069:A:OP2	2.50	0.45
29:A:2291:U:H2'	29:A:2292:U:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2405:G:O2'	29:A:2411:A:N6	2.48	0.45
29:A:2553:G:N2	29:A:2583:G:H1'	2.32	0.45
29:A:2692:G:H1'	29:A:2847:U:H1'	1.98	0.45
29:A:2699:C:H2'	29:A:2700:A:H8	1.82	0.45
6:G:53:PRO:HG3	6:G:61:TRP:CD1	2.52	0.45
21:O:37:HIS:ND1	21:O:38:LEU:O	2.50	0.45
29:A:959:A:H2'	29:A:960:A:C8	2.51	0.45
29:A:1320:C:H2'	29:A:1329:U:OP1	2.17	0.45
29:A:1802:A:H2'	29:A:1803:A:H8	1.82	0.45
29:A:2696:U:H2'	29:A:2697:G:H8	1.82	0.45
29:A:2720:U:C2	29:A:2721:A:C8	3.04	0.45
30:B:70:C:H2'	30:B:71:C:H6	1.82	0.45
30:B:114:C:H2'	30:B:115:A:H8	1.82	0.45
2:C:129:LEU:HD12	2:C:133:ASN:HB2	1.98	0.45
29:A:807:U:H2'	29:A:808:G:C8	2.52	0.45
29:A:840:C:H2'	29:A:841:G:H8	1.82	0.45
29:A:1152:C:H2'	29:A:1153:C:H6	1.82	0.45
29:A:1229:C:H2'	29:A:1230:A:H8	1.81	0.45
29:A:2333:A:H5'	29:A:2335:A:H1'	1.98	0.45
29:A:2391:G:O2'	29:A:2424:C:N4	2.37	0.45
4:E:130:LYS:NZ	29:A:320:A:OP1	2.39	0.44
6:G:174:LYS:HA	32:9:1:MET:HE1	2.00	0.44
9:N:27:SER:OG	29:A:1278:C:O2'	2.32	0.44
20:Z:40:THR:HG22	20:Z:42:ALA:H	1.82	0.44
24:K:4:GLU:OE2	29:A:2548:U:O2'	2.34	0.44
29:A:212:G:H2'	29:A:213:A:C8	2.52	0.44
29:A:1062:G:H2'	29:A:1063:G:H8	1.82	0.44
29:A:1447:C:H2'	29:A:1448:G:H8	1.81	0.44
29:A:2100:G:H1	29:A:2189:U:H3	1.65	0.44
29:A:2130:U:O2'	29:A:2134:A:O4'	2.29	0.44
29:A:2136:G:H22	29:A:2156:G:H1'	1.82	0.44
29:A:2304:G:H22	29:A:2312:U:H3	1.65	0.44
29:A:2466:C:H2'	29:A:2467:C:C6	2.52	0.44
29:A:2818:U:H2'	29:A:2819:G:C8	2.52	0.44
24:K:1:MET:SD	24:K:1:MET:N	2.90	0.44
27:H:117:LEU:HD13	27:H:130:VAL:HG23	1.99	0.44
29:A:29:U:H2'	29:A:30:G:C8	2.52	0.44
29:A:314:C:H2'	29:A:315:G:H8	1.81	0.44
29:A:364:C:H2'	29:A:365:U:C6	2.52	0.44
29:A:638:G:H2'	29:A:639:U:C6	2.52	0.44
29:A:743:A:O2'	29:A:1659:G:OP1	2.34	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:814:C:H1'	29:A:1225:G:H21	1.82	0.44
29:A:1107:G:H2'	29:A:1108:U:C6	2.52	0.44
29:A:1292:G:H2'	29:A:1293:C:C6	2.53	0.44
29:A:1550:C:H2'	29:A:1551:A:C8	2.53	0.44
29:A:1771:C:H2'	29:A:1772:A:H8	1.83	0.44
29:A:1847:A:O2'	29:A:1848:A:H8	2.00	0.44
29:A:2247:A:H2'	29:A:2248:C:H6	1.80	0.44
29:A:2417:C:H2'	29:A:2418:A:C8	2.52	0.44
7:J:7:LYS:HE3	29:A:538:A:H5''	1.99	0.44
7:J:99:ARG:HE	7:J:103:ILE:HD11	1.82	0.44
29:A:528:A:H2'	29:A:529:A:H5''	1.98	0.44
29:A:640:C:H2'	29:A:641:U:C6	2.53	0.44
29:A:754:U:H2'	29:A:755:U:H6	1.82	0.44
29:A:1387:A:H2'	29:A:1388:G:H8	1.83	0.44
29:A:1830:C:H2'	29:A:1831:G:C8	2.49	0.44
29:A:1965:C:OP1	29:A:1966:A:O2'	2.32	0.44
29:A:2812:G:H2'	29:A:2813:A:H8	1.82	0.44
4:E:1:MET:HE1	4:E:20:GLY:HA3	1.99	0.44
9:N:28:LEU:HD23	9:N:48:VAL:HG11	1.98	0.44
21:0:11:LYS:HD3	21:0:14:MET:HE3	1.98	0.44
22:1:6:GLU:OE2	22:1:26:LYS:HB2	2.17	0.44
23:2:22:MET:HE3	23:2:22:MET:HB3	1.85	0.44
26:M:76:LYS:HD2	29:A:956:G:H5''	1.99	0.44
29:A:116:C:O2'	29:A:126:A:N3	2.47	0.44
29:A:968:C:H2'	29:A:969:G:C8	2.52	0.44
29:A:1733:G:H2'	29:A:1734:G:H8	1.81	0.44
29:A:2577:A:O4'	29:A:2612:C:N4	2.51	0.44
32:9:222:ALA:HB2	32:9:265:GLU:HB3	2.00	0.44
5:F:65:LEU:HD22	30:B:41:G:H5''	1.99	0.44
15:U:53:GLN:HG3	15:U:54:PRO:HD3	1.98	0.44
15:U:98:ASN:OD1	15:U:100:GLU:HG2	2.17	0.44
24:K:70:ARG:HD2	24:K:76:VAL:HG12	1.98	0.44
29:A:183:C:O2'	29:A:432:A:N3	2.37	0.44
29:A:570:G:H2'	29:A:2030:A:N7	2.33	0.44
29:A:903:C:H2'	29:A:904:G:C8	2.52	0.44
29:A:1229:C:H2'	29:A:1230:A:C8	2.53	0.44
29:A:1275:A:OP2	29:A:1646:C:N4	2.50	0.44
29:A:1594:U:H2'	29:A:1595:C:C6	2.53	0.44
3:D:49:GLN:NE2	3:D:79:LEU:HD23	2.32	0.44
8:L:79:LEU:HD11	8:L:112:LEU:HG	1.99	0.44
29:A:565:C:H2'	29:A:566:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1186:G:H2'	29:A:1187:G:O4'	2.18	0.44
29:A:1190:G:H2'	29:A:1191:G:C8	2.52	0.44
29:A:2626:C:H2'	29:A:2627:G:H8	1.82	0.44
29:A:2747:G:O6	29:A:2755:C:H5''	2.18	0.44
30:B:72:G:H21	30:B:104:A:H62	1.65	0.44
2:C:136:VAL:HG13	2:C:163:ILE:HG22	1.99	0.44
3:D:155:VAL:HG21	29:A:2618:G:H21	1.83	0.44
5:F:9:ASP:OD2	5:F:10:GLU:N	2.51	0.44
27:H:104:THR:HG22	27:H:109:GLU:HA	2.00	0.44
29:A:301:G:O2'	29:A:302:C:O5'	2.32	0.44
29:A:1825:U:H2'	29:A:1826:G:C8	2.52	0.44
29:A:1826:G:H2'	29:A:1827:U:C6	2.52	0.44
29:A:2047:C:H2'	29:A:2048:G:C8	2.52	0.44
29:A:2064:C:H2'	29:A:2065:C:C6	2.52	0.44
29:A:2685:G:H2'	29:A:2686:G:H8	1.82	0.44
29:A:2699:C:H2'	29:A:2700:A:C8	2.53	0.44
29:A:2897:U:H2'	29:A:2898:U:C6	2.53	0.44
33:3:31:ILE:O	33:3:33:THR:N	2.51	0.44
7:J:80:HIS:CD2	29:A:2642:G:H5''	2.53	0.44
13:S:24:ILE:HD13	13:S:36:LEU:HD11	1.99	0.44
15:U:3:LYS:HD2	15:U:82:VAL:HB	2.00	0.44
25:P:38:ARG:NH2	31:6:32:SER:O	2.51	0.44
26:M:13:HIS:CG	29:A:954:G:H5''	2.52	0.44
29:A:579:G:H2'	29:A:580:U:C6	2.52	0.44
29:A:633:A:O2'	29:A:2404:U:OP1	2.36	0.44
29:A:1562:U:H2'	29:A:1563:U:C6	2.53	0.44
29:A:1595:C:H2'	29:A:1596:A:C8	2.53	0.44
29:A:2065:C:H2'	29:A:2066:C:C6	2.53	0.44
29:A:2220:U:C2	29:A:2221:G:C8	3.06	0.44
29:A:2229:U:H2'	29:A:2230:G:C8	2.48	0.44
29:A:2514:U:H2'	29:A:2515:C:C6	2.53	0.44
29:A:2838:G:C4	29:A:2839:G:C8	3.05	0.44
32:9:14:GLY:HA3	32:9:43:GLY:H	1.83	0.44
7:J:21:THR:HG23	7:J:61:LYS:HB3	1.99	0.44
14:T:61:LEU:HD11	14:T:82:LYS:HD3	1.99	0.44
17:W:38:GLY:HA2	29:A:2330:G:H21	1.83	0.44
21:0:8:THR:HG23	21:0:10:SER:H	1.82	0.44
21:0:28:SER:O	21:0:36:LYS:HD2	2.18	0.44
29:A:974:G:O2'	29:A:989:G:N2	2.50	0.44
29:A:1078:U:H1'	29:A:1088:A:H2	1.83	0.44
8:L:20:GLY:HA2	8:L:28:GLY:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:32:C:H2'	29:A:33:C:C6	2.53	0.43
29:A:84:A:N1	29:A:98:G:O2'	2.40	0.43
29:A:593:U:H2'	29:A:594:U:H6	1.83	0.43
29:A:1582:C:O2'	29:A:1585:C:N3	2.47	0.43
29:A:1747:U:H2'	29:A:1748:C:H6	1.83	0.43
29:A:2547:A:H2'	29:A:2548:U:C6	2.53	0.43
32:9:16:GLY:HA3	32:9:122:TRP:O	2.18	0.43
5:F:47:LYS:O	5:F:51:ASN:ND2	2.51	0.43
5:F:48:LEU:H	5:F:48:LEU:HD23	1.82	0.43
8:L:41:ARG:NH1	29:A:807:U:OP2	2.51	0.43
12:R:76:LYS:NZ	29:A:992:C:OP1	2.44	0.43
21:0:12:ARG:NH2	29:A:517:C:OP1	2.40	0.43
26:M:97:GLN:N	26:M:97:GLN:OE1	2.51	0.43
29:A:297:G:H2'	29:A:298:G:O4'	2.18	0.43
29:A:879:G:H2'	29:A:880:G:H8	1.82	0.43
29:A:1570:A:H2'	29:A:1571:A:C8	2.53	0.43
29:A:1727:C:H2'	29:A:1728:C:O4'	2.18	0.43
29:A:1858:A:H2'	29:A:1859:U:O4'	2.18	0.43
29:A:1988:G:H2'	29:A:1989:G:C8	2.53	0.43
29:A:2120:G:H2'	29:A:2121:G:C8	2.47	0.43
32:9:167:MET:SD	32:9:258:ASN:HB2	2.58	0.43
32:9:235:LEU:C	32:9:237:ARG:H	2.24	0.43
2:C:157:ALA:HB1	2:C:196:ASN:O	2.19	0.43
2:C:218:THR:O	29:A:1789:A:H5''	2.17	0.43
4:E:134:LEU:O	4:E:138:LEU:HG	2.19	0.43
5:F:174:PHE:CZ	5:F:177:ARG:HB3	2.53	0.43
15:U:39:ASN:ND2	15:U:64:ILE:HD11	2.33	0.43
29:A:488:G:N1	29:A:491:G:OP2	2.51	0.43
29:A:767:U:H2'	29:A:768:G:H8	1.83	0.43
29:A:1969:A:H2'	29:A:1972:G:H21	1.82	0.43
29:A:2070:A:H2'	29:A:2071:A:C8	2.54	0.43
30:B:49:C:H2'	30:B:50:A:C8	2.53	0.43
2:C:130:PRO:HA	2:C:188:ARG:HA	2.00	0.43
27:H:10:ALA:O	27:H:12:LEU:HD23	2.19	0.43
29:A:280:U:O4	29:A:361:G:N2	2.51	0.43
29:A:282:A:N6	29:A:359:G:O6	2.52	0.43
29:A:451:U:O2	29:A:453:A:N6	2.51	0.43
29:A:552:U:H2'	29:A:553:G:H8	1.83	0.43
29:A:1040:A:N1	29:A:1115:G:N2	2.49	0.43
29:A:1130:U:N3	29:A:2025:C:OP1	2.45	0.43
29:A:1164:C:H2'	29:A:1165:A:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1390:U:H3	29:A:1395:A:H62	1.67	0.43
29:A:1561:C:H2'	29:A:1562:U:C6	2.54	0.43
29:A:1590:A:H2'	29:A:1591:A:H8	1.83	0.43
29:A:1737:G:N7	29:A:1738:G:C6	2.87	0.43
32:9:306:TRP:CD1	32:9:306:TRP:H	2.37	0.43
2:C:209:ALA:HA	2:C:212:TRP:CZ2	2.54	0.43
4:E:57:LYS:HA	4:E:57:LYS:HD3	1.88	0.43
9:N:71:ARG:HD2	9:N:71:ARG:HA	1.80	0.43
13:S:58:ALA:O	13:S:62:ASP:HB2	2.18	0.43
15:U:81:ARG:NH1	29:A:300:A:H3'	2.33	0.43
28:d:31:ASP:OD1	28:d:31:ASP:N	2.50	0.43
29:A:319:G:H2'	29:A:320:A:C8	2.53	0.43
29:A:623:C:H2'	29:A:624:C:C6	2.54	0.43
29:A:2039:U:H2'	29:A:2040:G:C8	2.53	0.43
32:9:63:LYS:H	32:9:63:LYS:HD2	1.82	0.43
26:M:55:ARG:HE	29:A:2469:A:H4'	1.84	0.43
29:A:858:G:H3'	29:A:859:G:C8	2.53	0.43
29:A:1433:A:H2'	29:A:1434:A:C8	2.53	0.43
29:A:1438:U:H2'	29:A:1439:A:C8	2.53	0.43
29:A:1709:U:H2'	29:A:1710:G:C8	2.53	0.43
29:A:2092:U:OP1	29:A:2199:A:O2'	2.28	0.43
29:A:2247:A:H2'	29:A:2248:C:C6	2.54	0.43
32:9:17:GLY:N	32:9:40:GLY:O	2.52	0.43
7:J:15:TRP:CE3	7:J:55:ILE:HD11	2.54	0.43
29:A:152:A:H2'	29:A:153:U:C6	2.53	0.43
29:A:248:G:O5'	29:A:249:C:H5''	2.19	0.43
29:A:660:C:H2'	29:A:661:A:C8	2.53	0.43
29:A:1028:A:H2'	29:A:1029:A:H8	1.84	0.43
29:A:1747:U:H2'	29:A:1748:C:C6	2.53	0.43
29:A:2841:C:H2'	29:A:2842:G:H8	1.83	0.43
32:9:322:LYS:HA	32:9:322:LYS:HD3	1.79	0.43
2:C:257:ARG:NE	29:A:1799:G:OP1	2.52	0.43
24:K:98:ARG:HH22	31:6:99:GLU:HB3	1.83	0.43
27:H:15:LEU:O	27:H:51:ARG:NH1	2.36	0.43
29:A:629:G:H1'	29:A:639:U:H1'	2.00	0.43
29:A:1645:G:H5''	29:A:1646:C:H5'	2.00	0.43
29:A:2193:G:H2'	29:A:2194:U:H6	1.82	0.43
29:A:2643:G:H2'	29:A:2644:G:C8	2.54	0.43
2:C:200:MET:SD	2:C:200:MET:N	2.92	0.43
5:F:92:GLY:H	5:F:95:MET:HE2	1.84	0.43
29:A:4:U:H2'	29:A:5:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:450:G:OP2	37:A:3102:HOH:O	2.21	0.43
29:A:656:G:H2'	29:A:657:U:C6	2.54	0.43
29:A:1807:G:N2	29:A:1810:A:OP2	2.34	0.43
29:A:2677:G:H2'	29:A:2678:C:C6	2.54	0.43
6:G:86:LEU:HB2	6:G:130:ILE:HG23	2.00	0.43
8:L:57:LEU:HD22	33:3:53:ASP:HB3	2.01	0.43
15:U:46:LYS:H	15:U:46:LYS:HD2	1.84	0.43
24:K:102:PRO:HA	24:K:121:GLU:HB2	2.01	0.43
28:d:1:MET:HE3	28:d:2:LYS:H	1.83	0.43
29:A:94:A:H2'	29:A:95:A:C8	2.54	0.43
29:A:634:C:H2'	29:A:635:C:C6	2.53	0.43
29:A:1223:G:N2	29:A:1226:A:OP2	2.41	0.43
29:A:1539:U:H2'	29:A:1540:G:C8	2.54	0.43
29:A:1638:C:O2	29:A:2698:U:O2'	2.35	0.43
29:A:1927:A:H2'	29:A:1928:A:C8	2.54	0.43
29:A:2064:C:H2'	29:A:2065:C:H6	1.84	0.43
31:6:73:ASN:OD1	31:6:74:SER:N	2.52	0.43
2:C:27:LYS:HD2	2:C:27:LYS:N	2.33	0.42
5:F:110:ILE:HG23	5:F:113:PHE:HB2	2.00	0.42
13:S:59:GLU:OE2	13:S:59:GLU:HA	2.18	0.42
21:0:38:LEU:HB2	21:0:41:HIS:HB2	2.01	0.42
29:A:216:A:C8	29:A:432:A:N6	2.87	0.42
29:A:1000:A:H2'	29:A:1001:A:C8	2.54	0.42
29:A:1013:C:H2'	29:A:1014:A:C8	2.53	0.42
32:9:218:ILE:HG12	32:9:219:GLU:H	1.84	0.42
32:9:239:ARG:NH1	32:9:336:PRO:HA	2.34	0.42
32:9:276:LYS:O	32:9:278:ARG:N	2.52	0.42
3:D:110:THR:HG22	3:D:171:THR:HG23	2.01	0.42
3:D:125:TRP:CD2	3:D:160:LYS:HD2	2.54	0.42
5:F:134:GLN:H	5:F:134:GLN:CD	2.27	0.42
24:K:92:GLU:N	24:K:92:GLU:OE1	2.52	0.42
29:A:521:U:H2'	29:A:522:A:C8	2.51	0.42
29:A:580:U:H2'	29:A:581:C:H6	1.83	0.42
29:A:1147:A:H2'	29:A:1148:U:C6	2.54	0.42
29:A:2283:C:OP2	29:A:2389:G:O2'	2.31	0.42
3:D:13:ARG:NH1	25:P:74:GLN:HE21	2.13	0.42
6:G:163:TYR:HD2	6:G:166:GLU:HB2	1.83	0.42
13:S:2:GLU:HA	13:S:108:SER:HB3	1.99	0.42
13:S:78:GLU:OE2	29:A:24:G:N2	2.52	0.42
21:0:51:ARG:NH2	21:0:52:LYS:O	2.52	0.42
29:A:589:U:H2'	29:A:590:A:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:592:A:O2'	33:3:63:TYR:OH	2.31	0.42
29:A:623:C:H2'	29:A:624:C:H6	1.83	0.42
29:A:1435:G:H2'	29:A:1436:G:H8	1.83	0.42
29:A:1443:U:H2'	29:A:1444:G:C8	2.53	0.42
29:A:2626:C:H2'	29:A:2627:G:C8	2.54	0.42
29:A:2756:U:H1'	29:A:2757:A:H5''	2.00	0.42
29:A:2841:C:H2'	29:A:2842:G:C8	2.54	0.42
32:9:45:VAL:HG12	32:9:86:VAL:HB	2.00	0.42
32:9:158:LEU:HG	32:9:160:ALA:H	1.84	0.42
1:g:2:LYS:HD3	1:g:4:ARG:CZ	2.49	0.42
26:M:30:SER:N	26:M:106:ASP:OD2	2.51	0.42
26:M:44:ARG:HD3	29:A:2484:G:OP1	2.18	0.42
27:H:9:VAL:HG22	27:H:10:ALA:H	1.84	0.42
29:A:594:U:H2'	29:A:595:C:C6	2.55	0.42
29:A:1048:A:H1'	29:A:1112:G:N2	2.34	0.42
29:A:2411:A:H2'	29:A:2412:A:H8	1.84	0.42
29:A:2639:A:H2'	29:A:2640:G:O4'	2.19	0.42
29:A:2818:U:H2'	29:A:2819:G:H8	1.85	0.42
29:A:2853:C:H2'	29:A:2854:G:C8	2.54	0.42
2:C:124:LYS:HB2	2:C:127:ASN:ND2	2.34	0.42
3:D:133:THR:OG1	29:A:1993:U:H4'	2.18	0.42
13:S:41:LYS:HE3	21:0:21:LEU:HD11	2.01	0.42
16:V:4:ILE:HG12	16:V:61:LEU:HD21	2.01	0.42
25:P:88:ARG:HE	25:P:112:ARG:HH12	1.67	0.42
27:H:86:ASP:OD1	27:H:86:ASP:N	2.52	0.42
29:A:302:C:H2'	29:A:303:G:C8	2.54	0.42
29:A:541:A:H2'	29:A:542:C:C6	2.54	0.42
29:A:793:A:OP2	29:A:2071:A:O2'	2.38	0.42
29:A:1196:C:C2	29:A:1197:G:C8	3.07	0.42
29:A:1387:A:H5'	29:A:1469:A:H1'	2.01	0.42
29:A:1464:G:H2'	29:A:1465:G:C8	2.54	0.42
29:A:1689:A:H2'	29:A:1690:A:C8	2.55	0.42
29:A:2505:G:H1'	29:A:2506:U:OP2	2.19	0.42
30:B:30:C:H2'	30:B:31:C:O4'	2.20	0.42
4:E:47:LYS:HE2	29:A:451:U:H4'	2.00	0.42
6:G:11:PRO:HD2	6:G:14:VAL:HG21	2.02	0.42
6:G:157:LYS:HE3	6:G:157:LYS:HB3	1.71	0.42
13:S:18:ARG:HG3	13:S:76:VAL:HB	2.00	0.42
22:1:9:LYS:O	22:1:51:ALA:N	2.52	0.42
27:H:125:THR:HA	27:H:146:VAL:HG13	2.02	0.42
29:A:417:C:H2'	29:A:418:C:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1405:U:H2'	29:A:1406:U:C6	2.53	0.42
29:A:1438:U:H2'	29:A:1439:A:H8	1.85	0.42
29:A:2533:U:H2'	29:A:2534:A:O4'	2.20	0.42
29:A:2642:G:H2'	29:A:2643:G:H8	1.85	0.42
29:A:2846:G:H2'	29:A:2847:U:C6	2.54	0.42
2:C:132:ARG:HG2	2:C:185:ALA:HB1	2.02	0.42
4:E:181:ILE:HG23	8:L:2:ARG:HB3	2.02	0.42
29:A:226:A:H1'	29:A:230:G:N2	2.35	0.42
29:A:873:C:H2'	29:A:874:G:H8	1.85	0.42
29:A:1667:G:O2'	29:A:1991:U:O4	2.30	0.42
29:A:2195:U:H2'	29:A:2196:C:H6	1.84	0.42
29:A:2349:G:O6	29:A:2369:A:N6	2.53	0.42
29:A:2364:C:H2'	29:A:2365:G:O4'	2.19	0.42
29:A:2589:A:H2'	29:A:2590:A:C8	2.54	0.42
29:A:2688:G:N1	29:A:2720:U:OP2	2.28	0.42
30:B:29:A:H2'	30:B:30:C:C6	2.55	0.42
32:9:172:LYS:HG2	32:9:244:LEU:HD12	2.02	0.42
10:O:7:ARG:HD2	10:O:97:PHE:CE1	2.54	0.42
29:A:78:U:H2'	29:A:79:C:C6	2.55	0.42
29:A:128:C:H2'	29:A:129:C:C6	2.55	0.42
29:A:367:G:C6	29:A:368:A:C6	3.08	0.42
29:A:697:G:H2'	29:A:698:C:C6	2.55	0.42
29:A:700:G:O2'	29:A:1632:A:N3	2.46	0.42
29:A:1153:C:H2'	29:A:1154:G:O4'	2.20	0.42
29:A:1170:C:N4	29:A:1171:G:O6	2.53	0.42
29:A:1399:C:H2'	29:A:1400:U:C6	2.55	0.42
19:Y:37:LEU:HD23	19:Y:37:LEU:O	2.19	0.42
23:2:2:LYS:HE2	23:2:6:GLN:HG3	2.01	0.42
29:A:976:G:H2'	29:A:977:G:H8	1.85	0.42
29:A:1589:U:H2'	29:A:1590:A:C8	2.54	0.42
29:A:1637:A:H2'	29:A:1638:C:C6	2.55	0.42
29:A:1652:A:H2'	29:A:1653:G:O4'	2.20	0.42
29:A:2656:U:C2	29:A:2665:A:N7	2.87	0.42
30:B:39:A:H2'	30:B:40:U:C6	2.54	0.42
3:D:118:PHE:O	29:A:1654:A:O2'	2.32	0.42
5:F:63:LYS:H	28:d:6:HIS:CE1	2.37	0.42
5:F:127:TYR:HD2	5:F:155:ILE:HD12	1.85	0.42
9:N:55:ALA:HB2	9:N:79:LEU:HD23	2.02	0.42
27:H:53:GLU:HG2	27:H:54:LEU:N	2.35	0.42
29:A:181:A:H2'	29:A:182:A:C8	2.55	0.42
29:A:1441:G:H2'	29:A:1442:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1850:G:H2'	29:A:1851:U:H6	1.84	0.42
29:A:2508:G:H5'	32:9:76:ARG:HH22	1.85	0.42
29:A:2696:U:H2'	29:A:2697:G:C8	2.55	0.42
29:A:2888:C:H2'	29:A:2889:C:C6	2.54	0.42
30:B:95:U:H2'	30:B:96:G:C8	2.55	0.42
2:C:224:MET:SD	2:C:229:HIS:HB2	2.60	0.41
8:L:78:ARG:NH2	29:A:627:A:OP1	2.44	0.41
13:S:38:TYR:OH	21:0:36:LYS:O	2.35	0.41
29:A:281:C:H2'	29:A:282:A:C8	2.55	0.41
29:A:1821:A:H2'	29:A:1822:C:H6	1.85	0.41
31:6:13:LYS:HD3	31:6:13:LYS:HA	1.76	0.41
32:9:265:GLU:H	32:9:265:GLU:CD	2.28	0.41
2:C:120:ASP:OD1	2:C:121:ALA:N	2.46	0.41
2:C:196:ASN:OD1	2:C:196:ASN:N	2.51	0.41
19:Y:3:ALA:HA	19:Y:6:LEU:HD12	2.01	0.41
24:K:8:LEU:HD13	24:K:84:CYS:SG	2.60	0.41
24:K:17:ARG:HB2	24:K:45:GLU:HG3	2.02	0.41
29:A:1680:U:H2'	29:A:1681:G:O4'	2.20	0.41
29:A:2470:G:H2'	29:A:2471:A:C8	2.55	0.41
29:A:2773:C:H2'	29:A:2774:C:H6	1.85	0.41
32:9:284:LYS:HG2	36:9:402:GNP:C5	2.50	0.41
2:C:158:GLY:HA3	29:A:1820:U:N3	2.35	0.41
5:F:101:ARG:HH22	28:d:26:SER:HB2	1.85	0.41
7:J:102:GLU:HB2	7:J:119:PHE:CE1	2.48	0.41
8:L:56:PRO:HD2	8:L:59:ARG:HG3	2.01	0.41
11:Q:108:LEU:HD22	12:R:48:LYS:HD3	2.03	0.41
15:U:46:LYS:HD2	15:U:46:LYS:N	2.35	0.41
29:A:1047:G:N2	29:A:1110:G:O2'	2.49	0.41
29:A:1406:U:H2'	29:A:1407:G:H8	1.84	0.41
29:A:1681:G:H21	29:A:1762:A:H3'	1.85	0.41
29:A:1943:U:O4'	29:A:1945:G:H5'	2.21	0.41
29:A:2097:A:H2'	29:A:2098:U:C6	2.54	0.41
29:A:2692:G:N3	29:A:2847:U:O2'	2.53	0.41
3:D:121:THR:HG21	3:D:143:PRO:HB3	2.02	0.41
6:G:3:VAL:HG11	29:A:2748:A:H4'	2.02	0.41
6:G:34:ARG:HB3	6:G:74:MET:HE1	2.02	0.41
9:N:20:MET:HE2	9:N:20:MET:HB3	1.98	0.41
18:X:16:ASN:HB2	18:X:24:THR:HB	2.02	0.41
29:A:523:C:H2'	29:A:524:G:H8	1.84	0.41
29:A:739:A:N3	29:A:740:C:N4	2.61	0.41
29:A:739:A:H1'	29:A:740:C:H5	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1105:U:H2'	29:A:1106:G:C8	2.54	0.41
29:A:1435:G:H2'	29:A:1436:G:C8	2.56	0.41
29:A:1604:C:H2'	29:A:1605:C:H6	1.86	0.41
29:A:2590:A:H2'	29:A:2591:C:C6	2.55	0.41
29:A:2649:C:H2'	29:A:2650:U:C6	2.56	0.41
32:9:63:LYS:H	32:9:63:LYS:CD	2.34	0.41
2:C:257:ARG:HB2	29:A:1798:U:H5''	2.03	0.41
5:F:64:PRO:HA	5:F:88:VAL:HG22	2.03	0.41
5:F:116:LEU:O	5:F:177:ARG:HA	2.21	0.41
9:N:90:ARG:NH2	9:N:116:VAL:HG11	2.35	0.41
17:W:15:LYS:NZ	29:A:2261:C:OP1	2.45	0.41
24:K:10:VAL:HG21	24:K:16:ALA:O	2.20	0.41
25:P:42:PHE:CE1	25:P:62:LYS:HE2	2.56	0.41
26:M:96:ILE:HD11	26:M:126:ILE:HD11	2.02	0.41
29:A:593:U:H2'	29:A:594:U:C6	2.54	0.41
29:A:596:U:H2'	29:A:597:G:H8	1.86	0.41
29:A:974:G:H1'	29:A:975:A:C8	2.54	0.41
29:A:1311:G:H21	29:A:1603:A:H62	1.67	0.41
29:A:1604:C:H2'	29:A:1605:C:C6	2.56	0.41
29:A:1636:U:H2'	29:A:1637:A:C8	2.55	0.41
29:A:1779:U:H5	29:A:1784:A:N7	2.19	0.41
29:A:1786:A:H1'	29:A:1938:A:N6	2.35	0.41
5:F:96:TRP:O	5:F:100:GLU:HG3	2.20	0.41
11:Q:40:LYS:HE3	29:A:563:A:H4'	2.02	0.41
29:A:822:G:H2'	29:A:823:C:H6	1.85	0.41
29:A:1282:U:H2'	29:A:1283:G:O4'	2.20	0.41
29:A:1539:U:H2'	29:A:1540:G:H8	1.84	0.41
29:A:2650:U:H2'	29:A:2651:C:H6	1.85	0.41
2:C:154:ALA:HB2	2:C:161:VAL:HG23	2.03	0.41
8:L:37:GLY:O	8:L:41:ARG:HG3	2.21	0.41
8:L:96:LYS:NZ	8:L:103:ILE:O	2.53	0.41
10:O:35:ILE:HD11	10:O:71:ALA:HA	2.02	0.41
21:O:3:GLN:HG2	29:A:2615:U:H1'	2.02	0.41
29:A:1161:C:H2'	29:A:1162:G:C8	2.54	0.41
29:A:1199:U:H2'	29:A:1200:C:H6	1.85	0.41
29:A:1239:G:H2'	29:A:1240:U:O4'	2.21	0.41
29:A:1591:A:H2'	29:A:1592:C:H6	1.85	0.41
29:A:1848:A:H2'	29:A:1849:G:O4'	2.21	0.41
29:A:2228:G:H2'	29:A:2229:U:C6	2.56	0.41
29:A:2411:A:H2'	29:A:2412:A:C8	2.55	0.41
29:A:2425:A:H5''	29:A:2427:C:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:2794:C:H2'	29:A:2795:C:H6	1.86	0.41
29:A:2834:G:H2'	29:A:2879:A:H61	1.85	0.41
32:9:49:ALA:HB2	32:9:108:MET:SD	2.61	0.41
5:F:5:ASP:OD2	5:F:5:ASP:N	2.54	0.41
5:F:59:ILE:HA	5:F:137:PHE:HE2	1.86	0.41
5:F:122:ASP:OD2	5:F:122:ASP:N	2.52	0.41
12:R:15:SER:OG	12:R:16:GLU:N	2.54	0.41
24:K:90:ASN:OD1	24:K:91:SER:N	2.52	0.41
26:M:86:LYS:NZ	29:A:955:U:OP1	2.41	0.41
29:A:222:A:N6	29:A:232:G:H1'	2.36	0.41
29:A:312:G:C2	29:A:313:G:N7	2.89	0.41
29:A:745:G:O2'	29:A:748:G:H1'	2.21	0.41
29:A:898:C:H2'	29:A:899:A:H8	1.85	0.41
29:A:936:A:H2'	29:A:937:C:C6	2.56	0.41
29:A:1440:U:H2'	29:A:1441:G:C8	2.56	0.41
29:A:1812:U:H2'	29:A:1813:G:H8	1.85	0.41
29:A:2363:G:OP2	33:3:39:ARG:HD3	2.20	0.41
29:A:2691:C:H2'	29:A:2692:G:C8	2.56	0.41
29:A:2794:C:H2'	29:A:2795:C:C6	2.56	0.41
32:9:18:ASN:O	32:9:73:GLY:N	2.47	0.41
32:9:99:GLN:HB2	32:9:151:GLU:HB2	2.02	0.41
3:D:121:THR:HB	3:D:127:PHE:CD2	2.56	0.41
6:G:10:VAL:HA	6:G:11:PRO:HD3	1.95	0.41
7:J:43:GLU:HG3	11:Q:99:VAL:HG13	2.03	0.41
10:O:70:ALA:O	10:O:74:VAL:HG12	2.21	0.41
11:Q:5:ARG:NH1	29:A:1251:C:H6	2.18	0.41
12:R:41:ILE:HB	12:R:47:VAL:HB	2.03	0.41
12:R:73:LYS:HE2	12:R:73:LYS:HB2	1.87	0.41
12:R:81:LYS:HD2	29:A:973:A:H5''	2.03	0.41
13:S:53:SER:O	13:S:57:ASN:HB2	2.21	0.41
15:U:5:ARG:CG	15:U:6:ARG:H	2.34	0.41
16:V:76:ASP:HB3	16:V:90:ASP:OD2	2.21	0.41
29:A:63:A:H2'	29:A:64:A:C8	2.56	0.41
29:A:152:A:H2'	29:A:153:U:H6	1.86	0.41
29:A:288:U:H2'	29:A:289:G:C8	2.56	0.41
29:A:363:G:H2'	29:A:364:C:C6	2.56	0.41
29:A:414:C:H2'	29:A:415:A:H8	1.85	0.41
29:A:969:G:H2'	29:A:970:U:H6	1.86	0.41
29:A:1383:A:H2'	29:A:1384:A:C8	2.56	0.41
29:A:1495:A:H2	29:A:1578:U:H1'	1.85	0.41
29:A:1520:U:H2'	29:A:1521:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1591:A:H2'	29:A:1592:C:C6	2.56	0.41
29:A:1594:U:H2'	29:A:1595:C:H6	1.85	0.41
29:A:1742:U:H2'	29:A:1743:G:O4'	2.21	0.41
29:A:1770:G:C6	29:A:1983:G:C6	3.09	0.41
29:A:2070:A:H2'	29:A:2071:A:H8	1.85	0.41
29:A:2116:G:O6	29:A:2171:A:N6	2.54	0.41
29:A:2623:G:H2'	29:A:2624:G:C8	2.56	0.41
29:A:2840:C:H2'	29:A:2841:C:C6	2.56	0.41
30:B:54:G:H2'	30:B:55:U:C6	2.55	0.41
30:B:70:C:H2'	30:B:71:C:C6	2.56	0.41
32:9:132:SER:OG	32:9:133:SER:N	2.54	0.41
5:F:59:ILE:HA	5:F:137:PHE:CE2	2.56	0.41
5:F:102:LEU:HD12	5:F:106:ALA:HB3	2.03	0.41
5:F:157:THR:HG21	5:F:168:LEU:HD13	2.03	0.41
9:N:103:ARG:HG3	9:N:110:MET:SD	2.61	0.41
17:W:35:ARG:HG2	17:W:35:ARG:NH1	2.35	0.41
19:Y:13:GLU:HB3	19:Y:57:LEU:HD11	2.02	0.41
25:P:37:LYS:HB2	25:P:37:LYS:HE2	1.93	0.41
29:A:817:C:H2'	29:A:818:G:O4'	2.21	0.41
29:A:851:C:H2'	29:A:852:U:C6	2.56	0.41
29:A:1316:U:H2'	29:A:1317:G:C8	2.53	0.41
29:A:1442:U:H2'	29:A:1443:U:C6	2.56	0.41
29:A:1574:C:C2	29:A:1575:C:C5	3.09	0.41
29:A:1707:G:C8	29:A:1756:G:C5	3.09	0.41
29:A:1870:C:H5''	29:A:1871:A:N7	2.35	0.41
29:A:2011:U:H2'	29:A:2012:G:O4'	2.21	0.41
29:A:2136:G:N2	29:A:2156:G:O2'	2.54	0.41
29:A:2250:G:H21	29:A:2496:C:H4'	1.86	0.41
29:A:2399:G:O6	29:A:2418:A:N6	2.53	0.41
29:A:2897:U:H2'	29:A:2898:U:H6	1.86	0.41
30:B:40:U:H3'	30:B:41:G:H4'	2.02	0.41
31:6:49:MET:HE3	31:6:75:ALA:HB2	2.02	0.41
8:L:111:ILE:HG21	29:A:636:G:C6	2.56	0.40
22:1:7:LYS:NZ	29:A:2421:G:OP1	2.55	0.40
29:A:213:A:H2'	29:A:214:G:C8	2.56	0.40
29:A:286:U:H2'	29:A:287:G:C8	2.54	0.40
29:A:665:U:H2'	29:A:666:A:H8	1.86	0.40
29:A:1275:A:N1	29:A:1295:C:O2'	2.48	0.40
29:A:1315:C:H2'	29:A:1316:U:C6	2.56	0.40
29:A:1360:G:C8	29:A:1361:G:C8	3.08	0.40
29:A:1426:G:OP2	29:A:1427:A:O2'	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:A:1821:A:H2'	29:A:1822:C:C6	2.56	0.40
29:A:2245:U:H5''	29:A:2246:G:H5'	2.02	0.40
3:D:149:ASN:HB3	29:A:2572:A:OP2	2.20	0.40
4:E:7:ASP:OD2	4:E:8:ALA:N	2.54	0.40
6:G:95:ALA:N	6:G:127:GLN:O	2.54	0.40
8:L:129:LYS:HG2	29:A:636:G:OP1	2.21	0.40
12:R:58:VAL:HG12	12:R:102:SER:HB2	2.03	0.40
15:U:81:ARG:HH11	29:A:300:A:P	2.43	0.40
29:A:619:G:H3'	29:A:620:G:H21	1.86	0.40
29:A:1349:C:C2	29:A:1350:C:C5	3.10	0.40
29:A:1485:U:H2'	29:A:1486:U:H6	1.86	0.40
29:A:1951:U:O2'	29:A:1953:A:N7	2.48	0.40
30:B:62:C:H2'	30:B:63:C:C6	2.57	0.40
2:C:224:MET:HG2	29:A:782:A:C2	2.57	0.40
9:N:2:ARG:HD3	29:A:2822:G:O6	2.22	0.40
13:S:2:GLU:OE1	13:S:2:GLU:N	2.55	0.40
22:1:8:ILE:HD13	22:1:24:LYS:HG2	2.04	0.40
29:A:418:C:H2'	29:A:419:U:H6	1.85	0.40
29:A:475:C:H2'	29:A:476:G:O4'	2.22	0.40
29:A:566:U:H2'	29:A:567:U:C6	2.57	0.40
29:A:1715:G:O2'	29:A:1743:G:O6	2.28	0.40
29:A:1826:G:H2'	29:A:1827:U:H6	1.86	0.40
29:A:1909:C:H2'	29:A:1910:G:C8	2.56	0.40
29:A:2097:A:H2'	29:A:2098:U:H6	1.87	0.40
29:A:2634:A:H2'	29:A:2635:A:C8	2.56	0.40
29:A:2745:C:H2'	29:A:2746:U:C6	2.57	0.40
30:B:62:C:H2'	30:B:63:C:H6	1.86	0.40
2:C:107:LYS:HA	2:C:195:GLY:HA2	2.03	0.40
3:D:184:ARG:HB3	3:D:186:LEU:HD13	2.04	0.40
4:E:120:VAL:HA	4:E:188:MET:O	2.21	0.40
9:N:45:ARG:HD3	9:N:97:ILE:HD11	2.03	0.40
11:Q:87:VAL:HG13	12:R:49:ILE:HD11	2.03	0.40
17:W:12:SER:OG	29:A:2262:U:OP2	2.34	0.40
29:A:48:G:N2	29:A:177:G:OP2	2.54	0.40
29:A:87:U:H5''	29:A:88:G:H5'	2.03	0.40
29:A:487:C:H2'	29:A:488:G:O4'	2.20	0.40
29:A:756:A:H2'	29:A:757:G:O4'	2.21	0.40
29:A:1524:G:H2'	29:A:1525:A:H8	1.86	0.40
29:A:1678:A:C4	29:A:1679:A:C8	3.10	0.40
29:A:2127:G:H4'	29:A:2128:G:OP1	2.21	0.40
29:A:2357:G:N2	29:A:2360:G:OP2	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:6:27:VAL:HG13	31:6:30:LYS:HB3	2.04	0.40
5:F:46:LYS:HA	5:F:49:LEU:HD23	2.03	0.40
8:L:131:ALA:O	8:L:135:ILE:HG13	2.22	0.40
11:Q:90:ASP:OD1	11:Q:90:ASP:C	2.65	0.40
26:M:33:LEU:HD11	26:M:128:THR:HB	2.03	0.40
29:A:37:C:H2'	29:A:38:A:H8	1.86	0.40
29:A:404:A:H5'	29:A:406:G:C8	2.56	0.40
29:A:553:G:H2'	29:A:554:U:H6	1.86	0.40
29:A:594:U:H2'	29:A:595:C:H6	1.87	0.40
29:A:858:G:OP2	29:A:858:G:H8	2.04	0.40
29:A:1234:U:H2'	29:A:1235:G:O4'	2.21	0.40
29:A:1661:G:H2'	29:A:1662:U:C6	2.56	0.40
29:A:1825:U:H2'	29:A:1826:G:H8	1.86	0.40
29:A:2185:U:C2	29:A:2186:G:C8	3.10	0.40
29:A:2584:U:H2'	29:A:2585:U:O4'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	g	36/38 (95%)	36 (100%)	0	0	100	100
2	C	269/273 (98%)	252 (94%)	17 (6%)	0	100	100
3	D	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
4	E	189/201 (94%)	185 (98%)	4 (2%)	0	100	100
5	F	175/179 (98%)	159 (91%)	16 (9%)	0	100	100
6	G	174/177 (98%)	168 (97%)	6 (3%)	0	100	100
7	J	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
8	L	142/144 (99%)	129 (91%)	13 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	N	118/127 (93%)	108 (92%)	10 (8%)	0	100	100
10	O	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
11	Q	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
12	R	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
13	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
14	T	91/100 (91%)	83 (91%)	8 (9%)	0	100	100
15	U	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
16	V	92/94 (98%)	92 (100%)	0	0	100	100
17	W	74/85 (87%)	72 (97%)	2 (3%)	0	100	100
18	X	75/78 (96%)	75 (100%)	0	0	100	100
19	Y	61/63 (97%)	51 (84%)	10 (16%)	0	100	100
20	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
21	0	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
22	1	48/55 (87%)	48 (100%)	0	0	100	100
23	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
24	K	120/123 (98%)	111 (92%)	9 (8%)	0	100	100
25	P	111/115 (96%)	107 (96%)	4 (4%)	0	100	100
26	M	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
27	H	147/149 (99%)	133 (90%)	14 (10%)	0	100	100
28	d	45/70 (64%)	44 (98%)	1 (2%)	0	100	100
31	6	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
32	9	336/390 (86%)	319 (95%)	17 (5%)	0	100	100
33	3	62/65 (95%)	56 (90%)	4 (6%)	2 (3%)	3	3
All	All	3638/3832 (95%)	3452 (95%)	184 (5%)	2 (0%)	49	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	3	31	ILE
33	3	32	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	g	34/34 (100%)	34 (100%)	0	100	100
2	C	216/218 (99%)	216 (100%)	0	100	100
3	D	164/164 (100%)	164 (100%)	0	100	100
4	E	159/165 (96%)	159 (100%)	0	100	100
5	F	148/150 (99%)	148 (100%)	0	100	100
6	G	137/138 (99%)	137 (100%)	0	100	100
7	J	116/116 (100%)	116 (100%)	0	100	100
8	L	103/103 (100%)	103 (100%)	0	100	100
9	N	100/103 (97%)	100 (100%)	0	100	100
10	O	86/87 (99%)	86 (100%)	0	100	100
11	Q	89/90 (99%)	89 (100%)	0	100	100
12	R	84/84 (100%)	84 (100%)	0	100	100
13	S	93/93 (100%)	93 (100%)	0	100	100
14	T	80/84 (95%)	80 (100%)	0	100	100
15	U	83/85 (98%)	83 (100%)	0	100	100
16	V	78/78 (100%)	77 (99%)	1 (1%)	61	80
17	W	57/63 (90%)	57 (100%)	0	100	100
18	X	67/68 (98%)	67 (100%)	0	100	100
19	Y	55/55 (100%)	55 (100%)	0	100	100
20	Z	48/49 (98%)	48 (100%)	0	100	100
21	0	47/48 (98%)	47 (100%)	0	100	100
22	1	45/49 (92%)	45 (100%)	0	100	100
23	2	38/38 (100%)	38 (100%)	0	100	100
24	K	103/104 (99%)	103 (100%)	0	100	100
25	P	98/100 (98%)	98 (100%)	0	100	100
26	M	109/109 (100%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	H	114/114 (100%)	114 (100%)	0	100	100
28	d	43/62 (69%)	43 (100%)	0	100	100
31	6	88/91 (97%)	88 (100%)	0	100	100
32	9	273/321 (85%)	273 (100%)	0	100	100
33	3	51/52 (98%)	51 (100%)	0	100	100
All	All	3006/3115 (96%)	3005 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	V	24	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	g	13	ASN
1	g	37	GLN
2	C	133	ASN
2	C	142	ASN
3	D	67	HIS
5	F	26	GLN
5	F	126	ASN
6	G	115	GLN
7	J	80	HIS
7	J	136	GLN
8	L	35	HIS
9	N	9	GLN
11	Q	55	GLN
11	Q	80	ASN
12	R	11	GLN
12	R	87	GLN
19	Y	20	ASN
19	Y	25	GLN
19	Y	27	ASN
24	K	5	GLN
25	P	65	ASN
25	P	74	GLN
27	H	73	ASN
32	9	71	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	A	2895/2904 (99%)	377 (13%)	9 (0%)
30	B	118/119 (99%)	11 (9%)	0
All	All	3013/3023 (99%)	388 (12%)	9 (0%)

All (388) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	A	10	A
29	A	12	U
29	A	14	A
29	A	27	G
29	A	46	G
29	A	51	G
29	A	63	A
29	A	71	A
29	A	74	A
29	A	75	G
29	A	103	A
29	A	118	A
29	A	120	U
29	A	125	A
29	A	137	U
29	A	138	U
29	A	139	U
29	A	140	C
29	A	142	A
29	A	160	A
29	A	163	C
29	A	181	A
29	A	196	A
29	A	199	A
29	A	216	A
29	A	221	A
29	A	222	A
29	A	230	G
29	A	248	G
29	A	255	A
29	A	265	A
29	A	266	G
29	A	267	C
29	A	271	G

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Mol	Chain	Res	Type
29	A	272	A
29	A	277	G
29	A	278	A
29	A	302	C
29	A	311	A
29	A	329	G
29	A	330	A
29	A	331	C
29	A	346	A
29	A	353	C
29	A	367	G
29	A	371	A
29	A	372	G
29	A	386	G
29	A	396	G
29	A	404	A
29	A	405	U
29	A	411	G
29	A	424	G
29	A	480	A
29	A	481	G
29	A	491	G
29	A	504	A
29	A	505	A
29	A	518	G
29	A	532	A
29	A	533	G
29	A	543	G
29	A	544	C
29	A	546	U
29	A	547	A
29	A	548	G
29	A	550	C
29	A	563	A
29	A	573	U
29	A	575	A
29	A	586	A
29	A	603	A
29	A	613	A
29	A	615	U
29	A	621	A
29	A	627	A

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Mol	Chain	Res	Type
29	A	637	A
29	A	647	G
29	A	654	A
29	A	655	A
29	A	686	U
29	A	711	G
29	A	729	G
29	A	730	A
29	A	747	U
29	A	752	A
29	A	757	G
29	A	764	A
29	A	775	G
29	A	776	G
29	A	782	A
29	A	784	G
29	A	785	G
29	A	792	A
29	A	805	G
29	A	812	C
29	A	819	A
29	A	827	U
29	A	828	U
29	A	830	G
29	A	845	A
29	A	846	U
29	A	847	U
29	A	857	G
29	A	878	A
29	A	879	G
29	A	884	U
29	A	885	C
29	A	896	A
29	A	907	G
29	A	910	A
29	A	931	U
29	A	941	A
29	A	946	C
29	A	953	G
29	A	961	C
29	A	974	G
29	A	983	A

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Mol	Chain	Res	Type
29	A	995	C
29	A	996	A
29	A	1009	A
29	A	1012	U
29	A	1013	C
29	A	1022	G
29	A	1026	G
29	A	1027	A
29	A	1033	U
29	A	1040	A
29	A	1044	C
29	A	1046	A
29	A	1047	G
29	A	1058	U
29	A	1061	U
29	A	1066	U
29	A	1068	G
29	A	1070	A
29	A	1071	G
29	A	1073	A
29	A	1074	G
29	A	1081	U
29	A	1087	G
29	A	1089	A
29	A	1098	A
29	A	1101	U
29	A	1110	G
29	A	1112	G
29	A	1116	G
29	A	1132	U
29	A	1133	A
29	A	1135	C
29	A	1136	G
29	A	1142	A
29	A	1168	G
29	A	1171	G
29	A	1173	U
29	A	1175	A
29	A	1176	U
29	A	1180	U
29	A	1182	G
29	A	1212	G

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Mol	Chain	Res	Type
29	A	1225	G
29	A	1236	G
29	A	1238	G
29	A	1250	G
29	A	1253	A
29	A	1256	G
29	A	1266	G
29	A	1272	A
29	A	1294	U
29	A	1300	G
29	A	1301	A
29	A	1302	A
29	A	1314	C
29	A	1321	A
29	A	1325	U
29	A	1345	C
29	A	1365	A
29	A	1368	G
29	A	1378	A
29	A	1379	U
29	A	1383	A
29	A	1416	G
29	A	1419	A
29	A	1420	A
29	A	1428	C
29	A	1452	G
29	A	1453	A
29	A	1458	U
29	A	1461	C
29	A	1482	G
29	A	1490	A
29	A	1493	C
29	A	1504	A
29	A	1510	G
29	A	1515	A
29	A	1523	U
29	A	1524	G
29	A	1533	C
29	A	1535	A
29	A	1555	G
29	A	1556	C
29	A	1569	A

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Mol	Chain	Res	Type
29	A	1583	A
29	A	1585	C
29	A	1607	C
29	A	1608	A
29	A	1613	G
29	A	1634	A
29	A	1646	C
29	A	1647	U
29	A	1648	U
29	A	1654	A
29	A	1664	A
29	A	1674	G
29	A	1715	G
29	A	1729	U
29	A	1730	C
29	A	1736	U
29	A	1738	G
29	A	1764	C
29	A	1773	A
29	A	1786	A
29	A	1791	A
29	A	1800	C
29	A	1801	A
29	A	1808	A
29	A	1816	C
29	A	1829	A
29	A	1870	C
29	A	1914	C
29	A	1926	U
29	A	1927	A
29	A	1930	G
29	A	1931	U
29	A	1937	A
29	A	1944	U
29	A	1955	U
29	A	1967	C
29	A	1970	A
29	A	1971	U
29	A	1972	G
29	A	1991	U
29	A	1992	G
29	A	1993	U

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Mol	Chain	Res	Type
29	A	1997	C
29	A	2021	C
29	A	2022	U
29	A	2023	C
29	A	2025	C
29	A	2031	A
29	A	2043	C
29	A	2055	C
29	A	2056	G
29	A	2060	A
29	A	2061	G
29	A	2062	A
29	A	2069	G
29	A	2072	C
29	A	2093	G
29	A	2096	C
29	A	2102	G
29	A	2110	G
29	A	2111	U
29	A	2112	G
29	A	2116	G
29	A	2117	A
29	A	2118	U
29	A	2119	A
29	A	2122	U
29	A	2126	A
29	A	2128	G
29	A	2132	U
29	A	2133	G
29	A	2136	G
29	A	2147	A
29	A	2148	G
29	A	2157	G
29	A	2164	C
29	A	2165	C
29	A	2170	A
29	A	2171	A
29	A	2172	U
29	A	2173	A
29	A	2178	C
29	A	2198	A
29	A	2199	A

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Mol	Chain	Res	Type
29	A	2204	G
29	A	2211	A
29	A	2225	A
29	A	2238	G
29	A	2239	G
29	A	2250	G
29	A	2283	C
29	A	2287	A
29	A	2288	A
29	A	2297	A
29	A	2305	U
29	A	2308	G
29	A	2311	A
29	A	2312	U
29	A	2322	A
29	A	2325	G
29	A	2327	A
29	A	2333	A
29	A	2335	A
29	A	2336	A
29	A	2350	C
29	A	2361	G
29	A	2383	G
29	A	2385	C
29	A	2402	U
29	A	2406	A
29	A	2425	A
29	A	2426	A
29	A	2429	G
29	A	2430	A
29	A	2435	A
29	A	2441	U
29	A	2445	G
29	A	2447	G
29	A	2448	A
29	A	2475	C
29	A	2476	A
29	A	2478	A
29	A	2491	U
29	A	2494	G
29	A	2498	C
29	A	2502	G

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Mol	Chain	Res	Type
29	A	2504	U
29	A	2505	G
29	A	2506	U
29	A	2518	A
29	A	2520	C
29	A	2529	G
29	A	2531	A
29	A	2554	U
29	A	2564	A
29	A	2566	A
29	A	2567	G
29	A	2572	A
29	A	2602	A
29	A	2609	U
29	A	2613	U
29	A	2615	U
29	A	2629	U
29	A	2635	A
29	A	2639	A
29	A	2646	C
29	A	2661	G
29	A	2662	A
29	A	2689	U
29	A	2690	U
29	A	2714	G
29	A	2718	G
29	A	2726	A
29	A	2729	G
29	A	2733	A
29	A	2744	G
29	A	2748	A
29	A	2757	A
29	A	2765	A
29	A	2778	A
29	A	2791	G
29	A	2798	U
29	A	2801	G
29	A	2818	U
29	A	2820	A
29	A	2835	A
29	A	2849	U
29	A	2850	A

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Mol	Chain	Res	Type
29	A	2867	G
29	A	2872	A
29	A	2873	A
29	A	2880	C
29	A	2884	U
29	A	2886	A
29	A	2887	A
30	B	15	A
30	B	24	G
30	B	35	C
30	B	36	C
30	B	41	G
30	B	44	G
30	B	67	G
30	B	89	U
30	B	90	C
30	B	99	A
30	B	109	A

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	A	271	G
29	A	404	A
29	A	479	A
29	A	1057	A
29	A	1378	A
29	A	2127	G
29	A	2425	A
29	A	2505	G
29	A	2756	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 8 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
36	GNP	9	402	35	34,34,34	1.28	5 (14%)	47,54,54	0.66	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
36	GNP	9	402	35	-	2/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	9	402	GNP	PB-O3A	4.39	1.64	1.59
36	9	402	GNP	PB-O1B	3.12	1.50	1.46
36	9	402	GNP	PG-N3B	2.90	1.70	1.63
36	9	402	GNP	PG-O1G	2.72	1.50	1.46
36	9	402	GNP	PB-O2B	-2.30	1.50	1.56

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

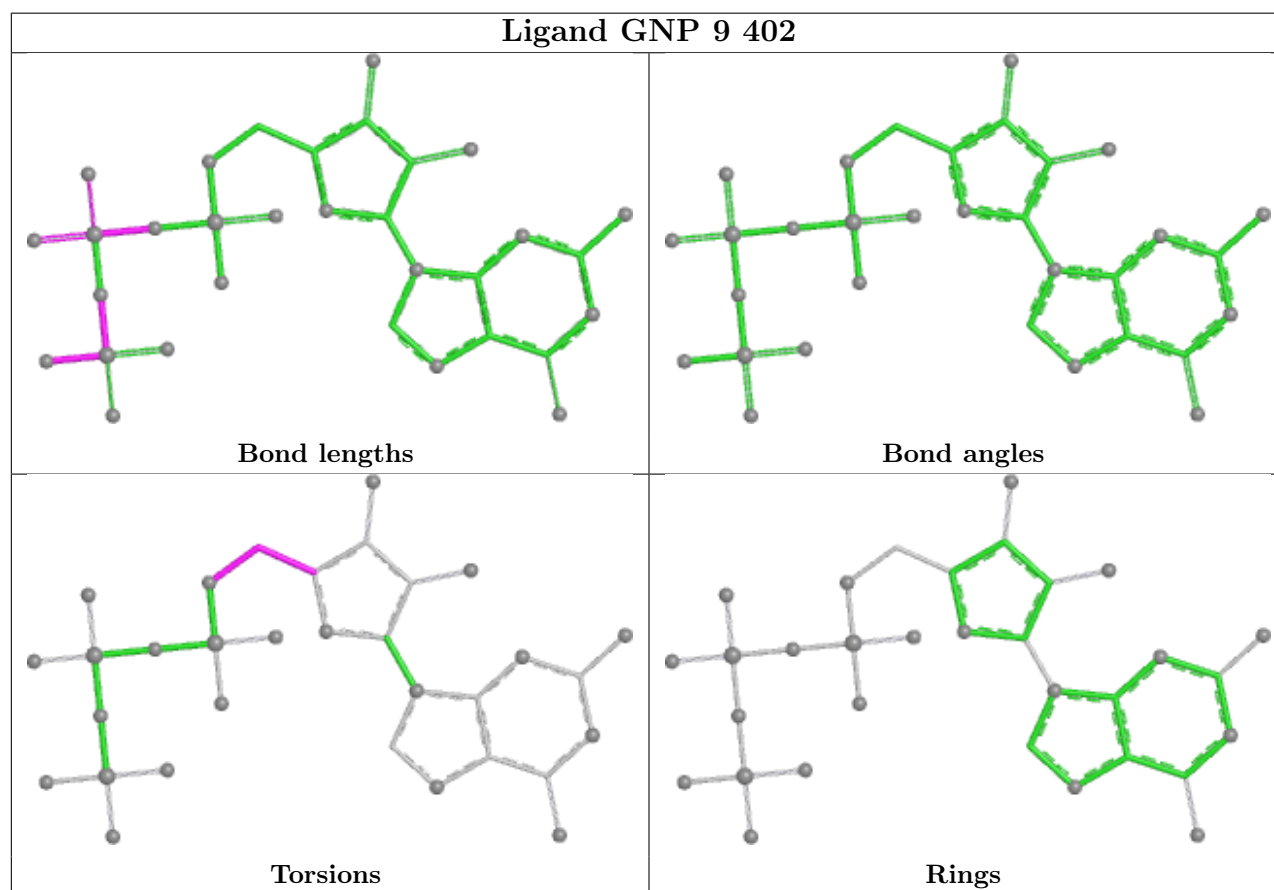
Mol	Chain	Res	Type	Atoms
36	9	402	GNP	O4'-C4'-C5'-O5'
36	9	402	GNP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	9	402	GNP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

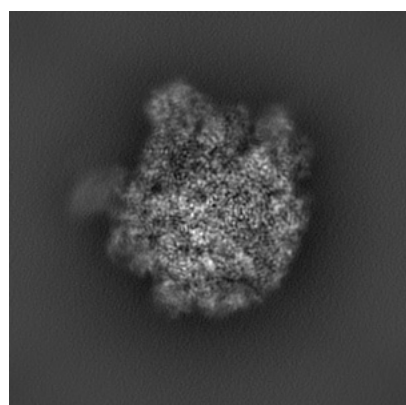
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12217. These allow visual inspection of the internal detail of the map and identification of artifacts.

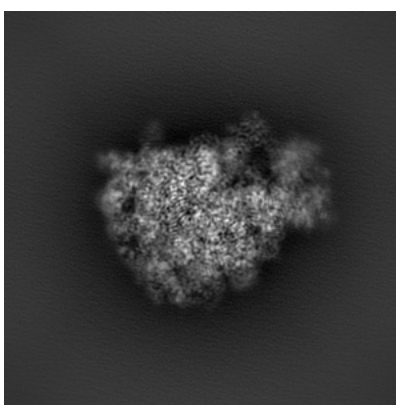
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

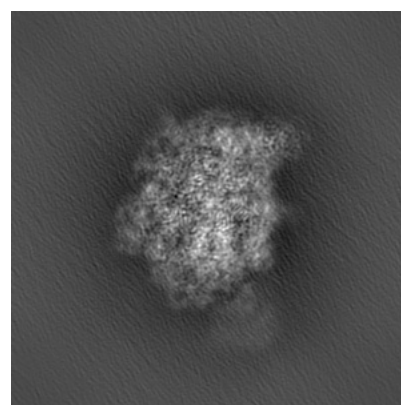
6.1.1 Primary map



X



Y

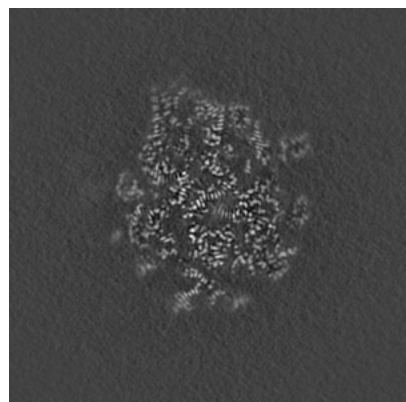


Z

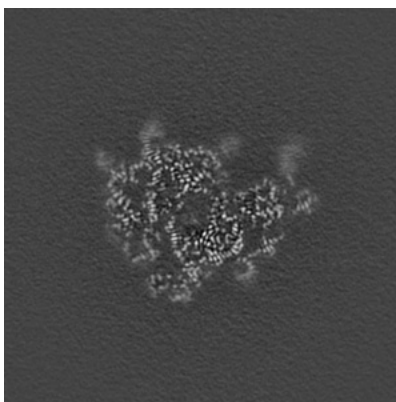
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

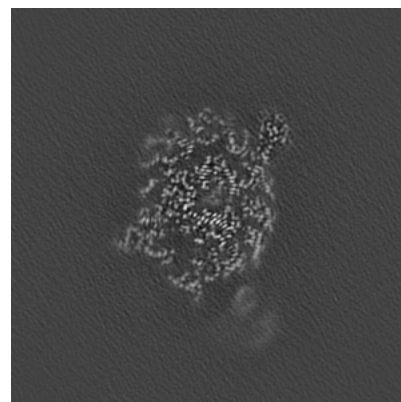
6.2.1 Primary map



X Index: 180



Y Index: 180

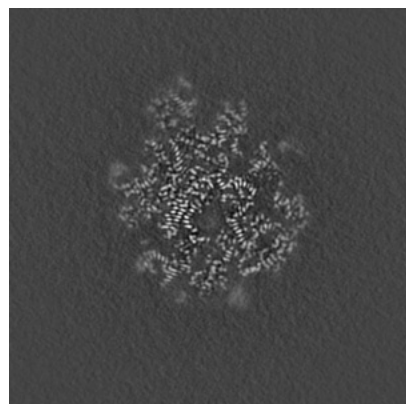


Z Index: 180

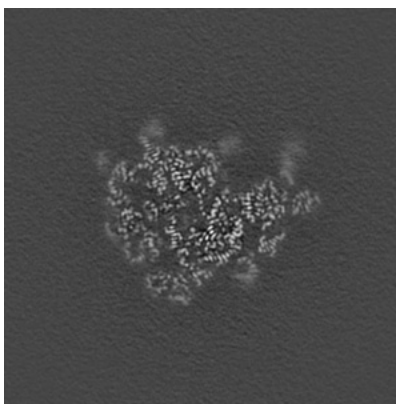
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

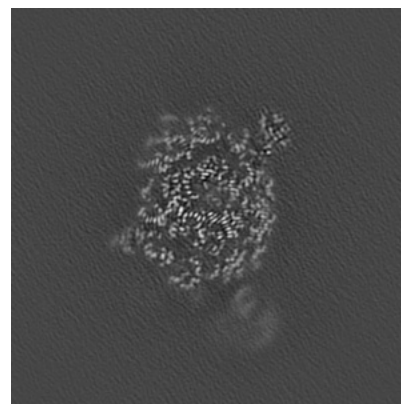
6.3.1 Primary map



X Index: 170



Y Index: 178

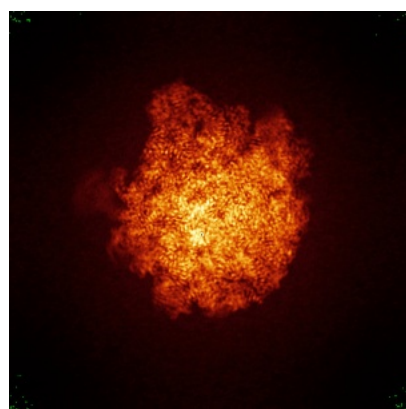


Z Index: 182

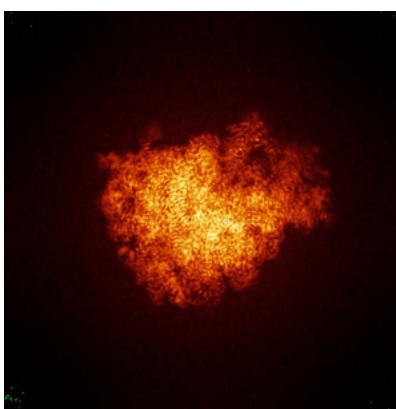
The images above show the largest variance slices of the map in three orthogonal directions.

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

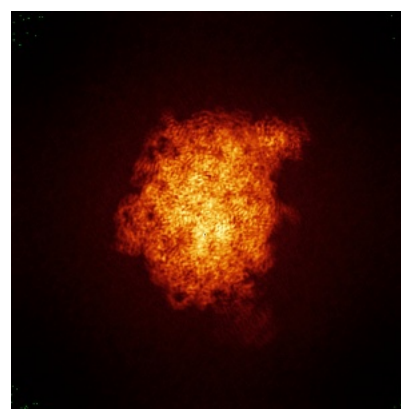
6.4.1 Primary map



X



Y



Z

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 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

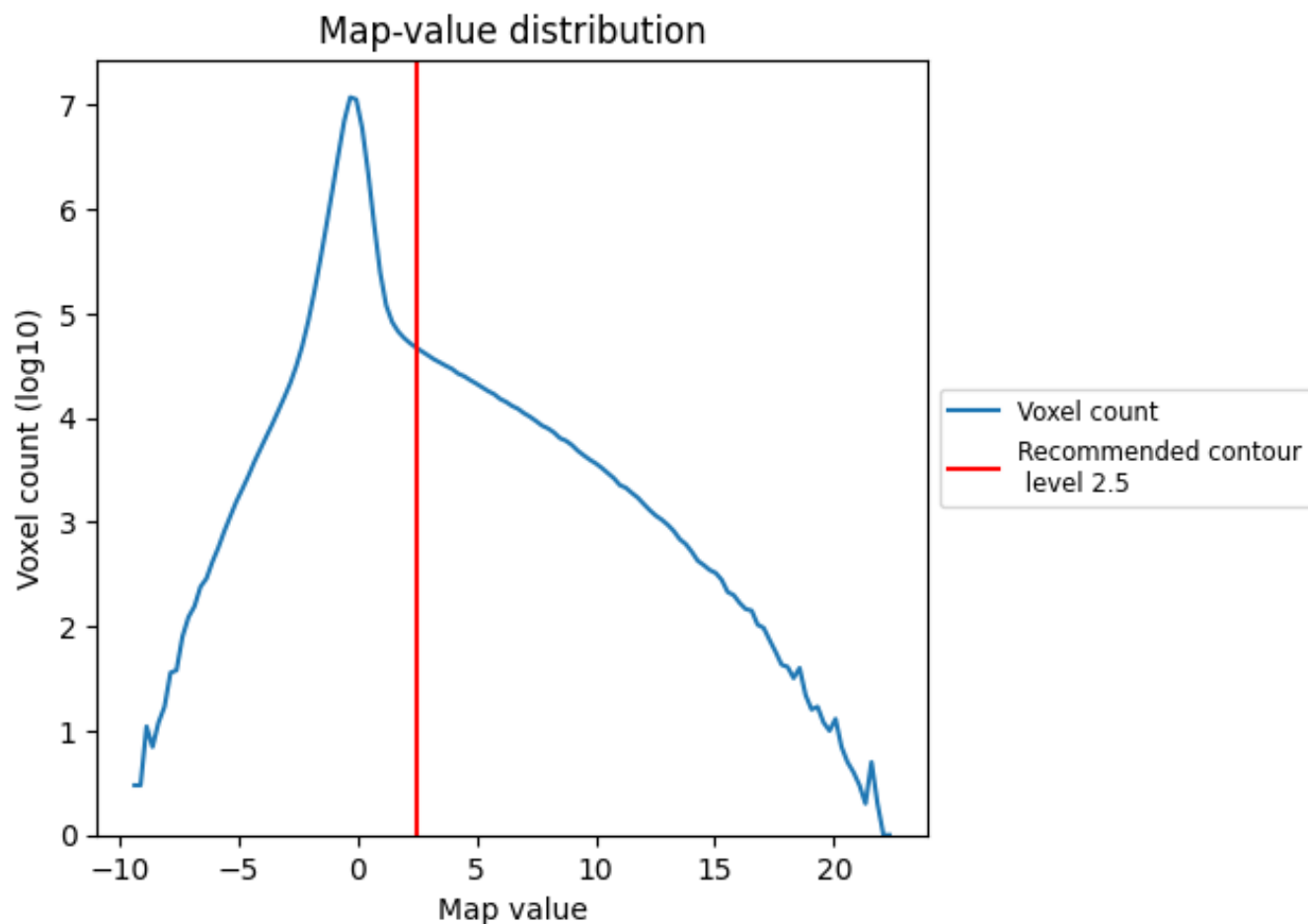
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

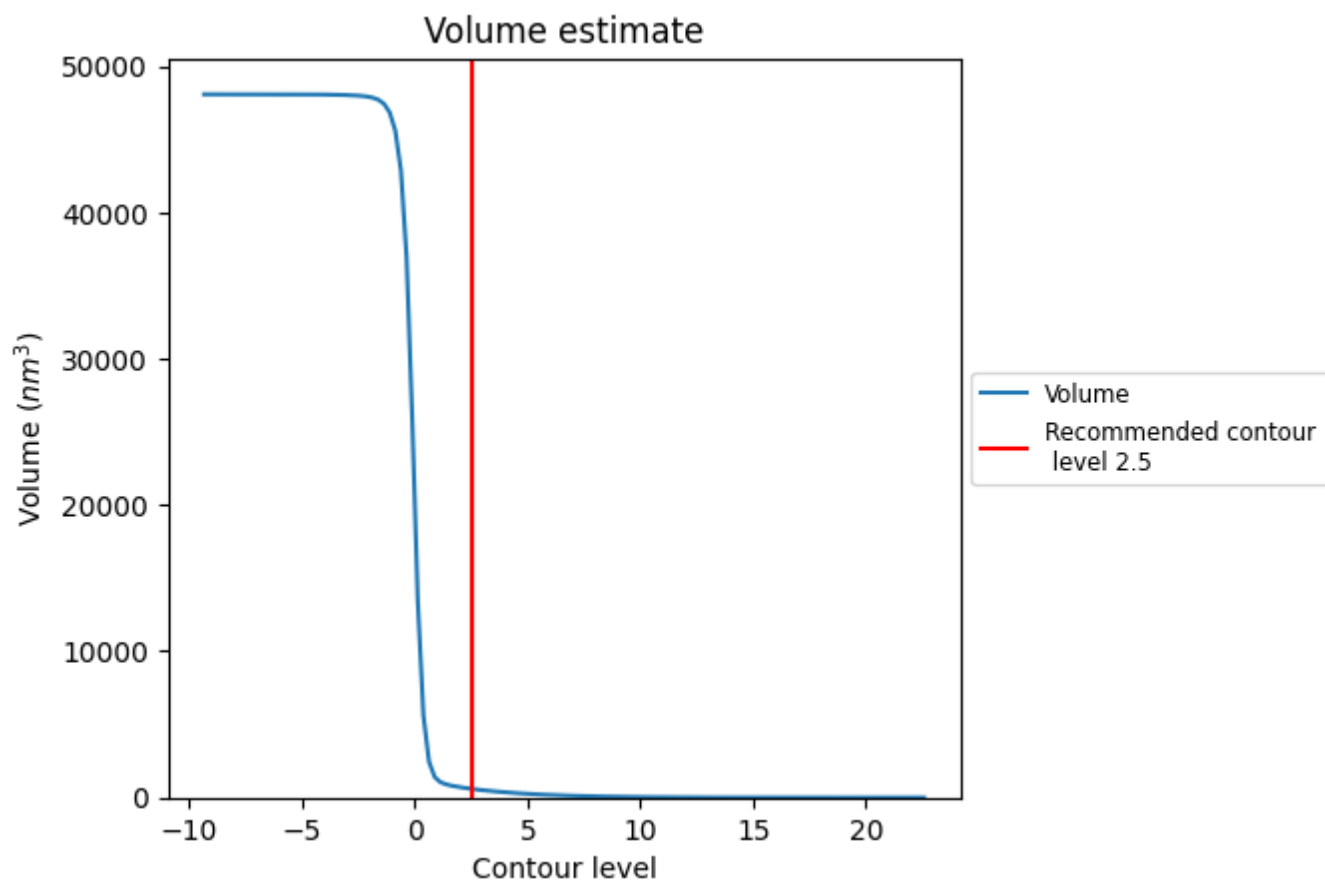
This section contains the results of statistical analysis of the map.

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.

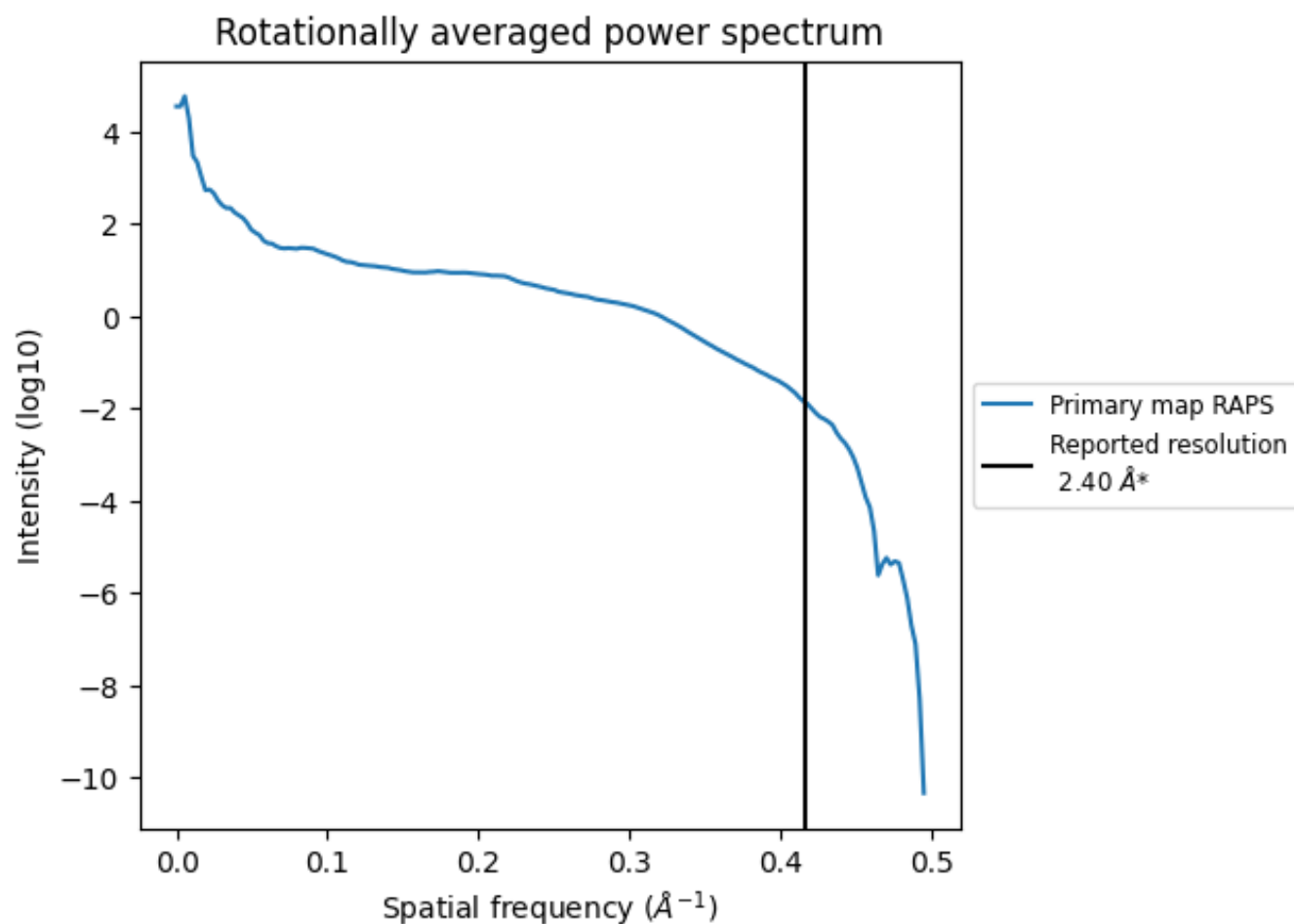
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 597 nm³; this corresponds to an approximate mass of 540 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 ⓘ

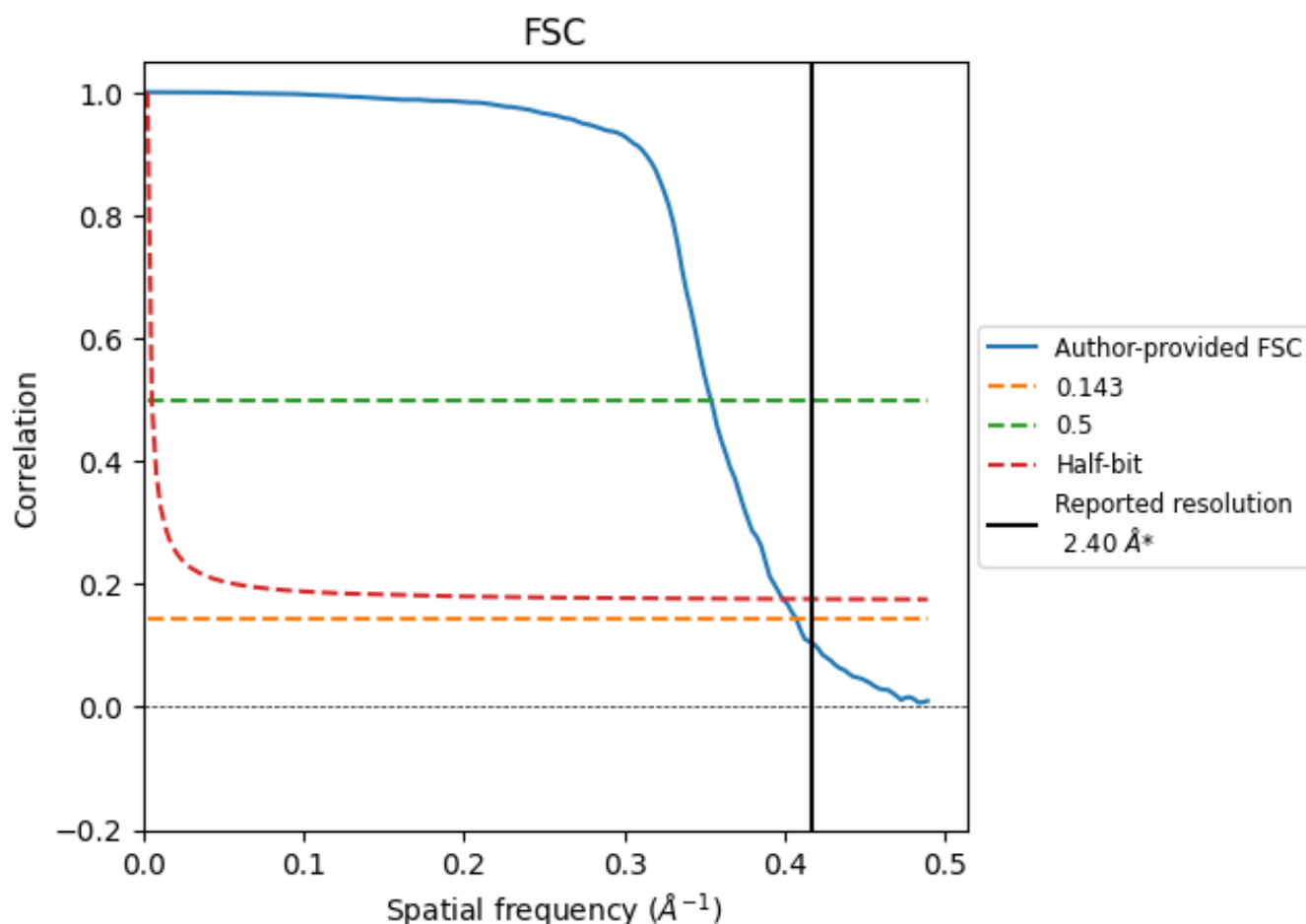


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

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 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

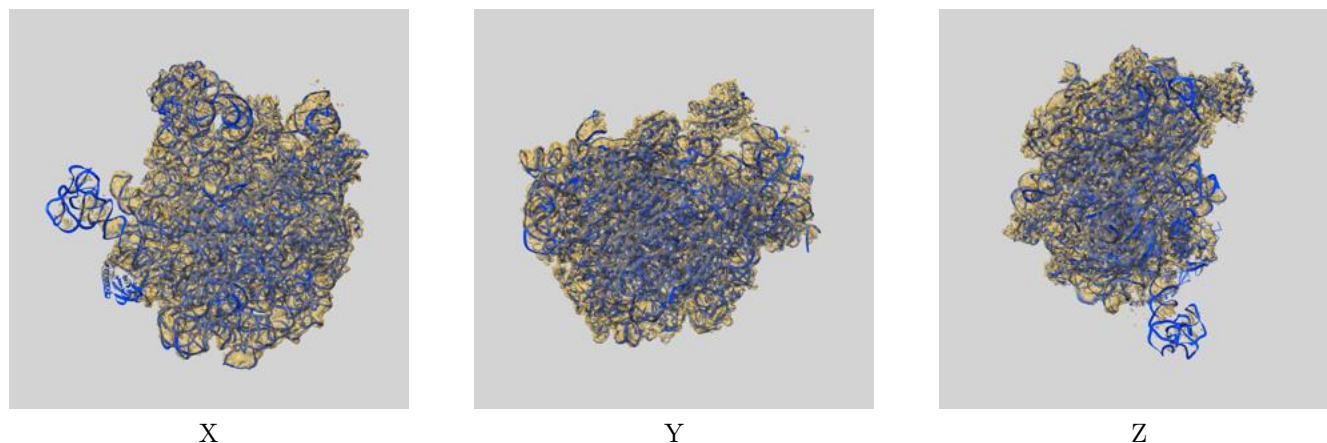
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.46	2.83	2.51
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

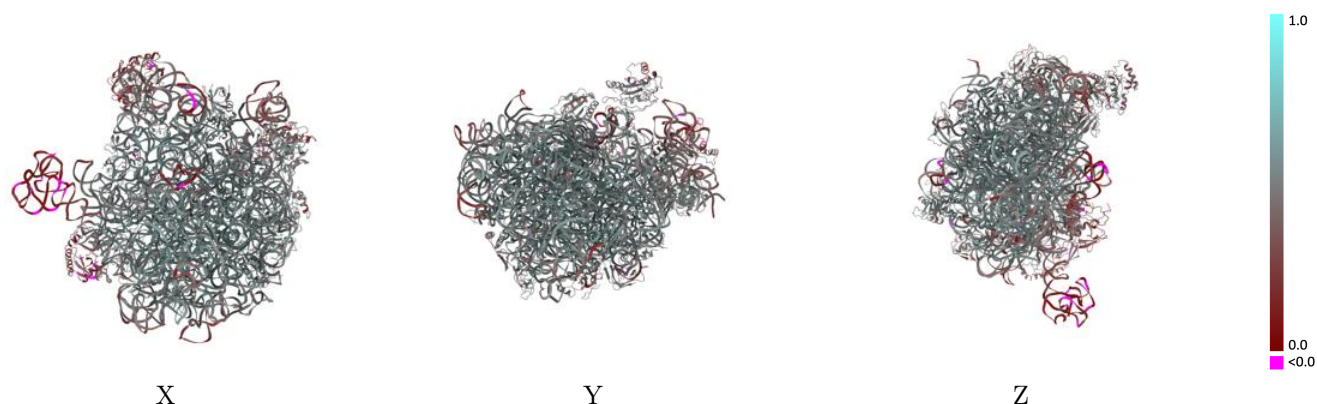
This section contains information regarding the fit between EMDB map EMD-12217 and PDB model 7BL4. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



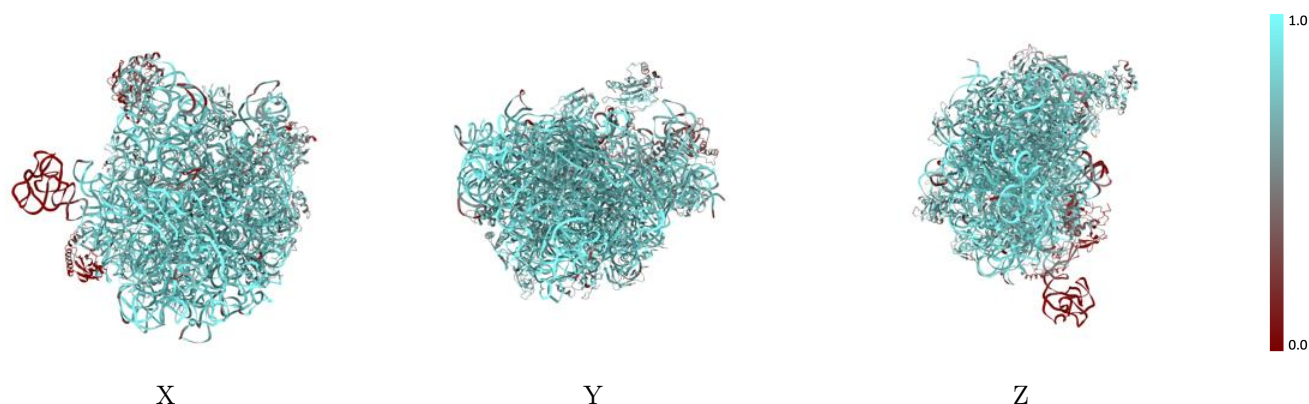
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



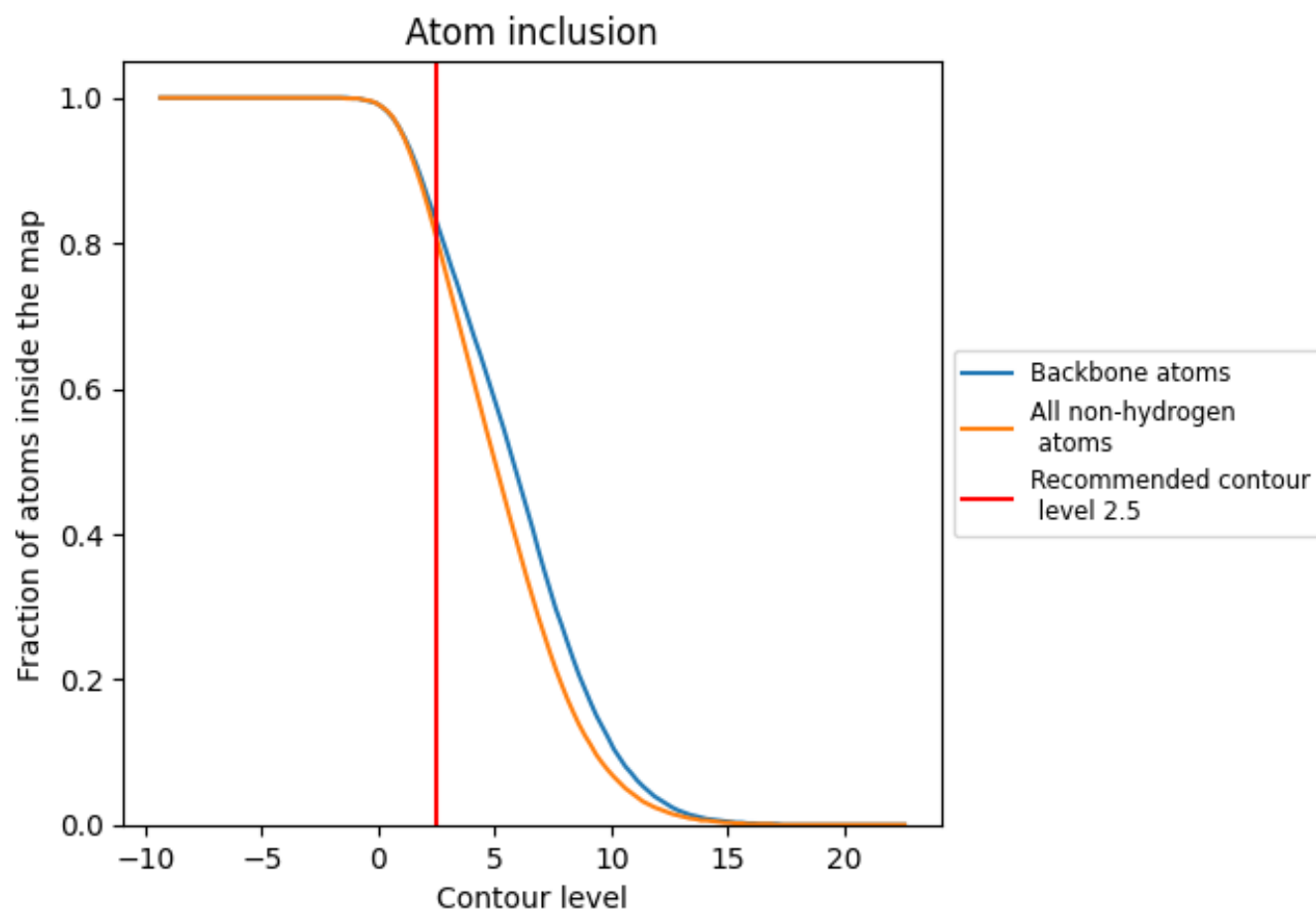
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 81% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8070	 0.4920
0	 0.7340	 0.4890
1	 0.7060	 0.5000
2	 0.8340	 0.5840
3	 0.8110	 0.5410
6	 0.7070	 0.4610
9	 0.6450	 0.4460
A	 0.8680	 0.5010
B	 0.8530	 0.4730
C	 0.7890	 0.5260
D	 0.7160	 0.5110
E	 0.6990	 0.4970
F	 0.3930	 0.3250
G	 0.5710	 0.4280
H	 0.2090	 0.2510
J	 0.7420	 0.5190
K	 0.7770	 0.5130
L	 0.7470	 0.5010
M	 0.7590	 0.5180
N	 0.7650	 0.5210
O	 0.6490	 0.4340
P	 0.7060	 0.4870
Q	 0.8060	 0.5420
R	 0.7370	 0.4910
S	 0.7610	 0.5280
T	 0.7160	 0.5000
U	 0.6320	 0.4350
V	 0.7140	 0.4850
W	 0.7860	 0.5350
X	 0.7740	 0.5210
Y	 0.6780	 0.4250
Z	 0.7390	 0.4940
d	 0.1960	 0.2170
g	 0.6450	 0.5040

