



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 12:27 AM UTC

PDB ID : 7BL3 / pdb_00007bl3
EMDB ID : EMD-12216
Title : pre-50S-ObgE particle state 2
Authors : Hilal, T.; Nikolay, R.; Spahn, C.M.T.
Deposited on : 2021-01-18
Resolution : 3.50 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
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

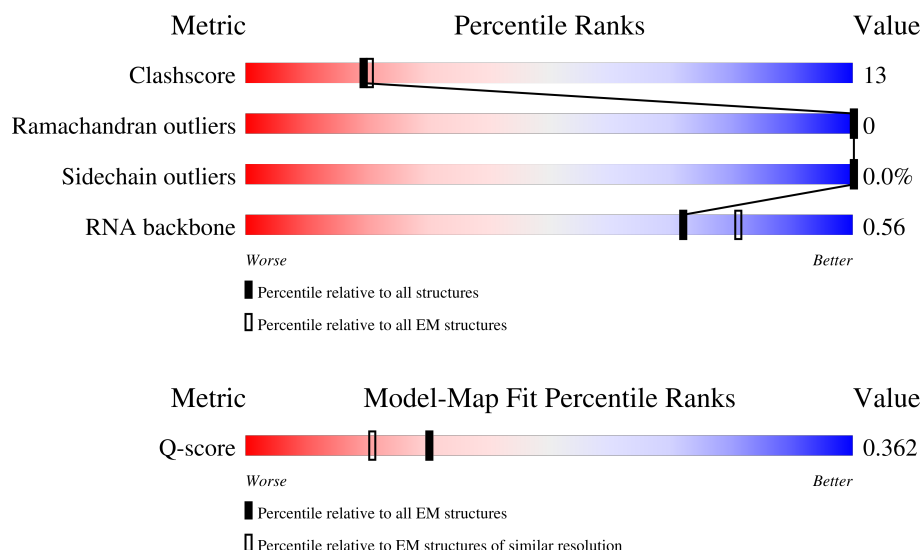
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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

Mol	Chain	Length	Quality of chain
1	A	2919	
2	B	119	
3	9P	390	

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Mol	Chain	Length	Quality of chain
4	b	70	
5	C	273	
6	D	209	
7	E	201	
8	G	177	
9	J	142	
10	L	144	
11	N	127	
12	O	117	
13	Q	118	
14	R	103	
15	S	110	
16	T	100	
17	U	104	
18	V	94	
19	W	85	
20	X	78	
21	Y	63	
22	Z	59	
23	0	57	
24	1	55	
25	2	46	
26	I	142	
27	K	123	
28	P	115	

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Mol	Chain	Length	Quality of chain
29	6	105	63% 74% 23% •
30	H	149	87% 71% 29%
31	F	179	92% 69% 30% ••

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 92831 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2902	Total	C	N	O	P	0	0
			62301	27793	11465	20141	2902		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 3 is a protein called GTPase ObgE/CgtA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	9P	338	Total	C	N	O	S	0	0
			2582	1626	453	490	13		

- Molecule 4 is a protein called 50S ribosomal protein L31.

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

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L6.

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

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 11 is a protein called 50S ribosomal protein L17.

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

- Molecule 12 is a protein called 50S ribosomal protein L18.

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

- Molecule 13 is a protein called 50S ribosomal protein L20.

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

- Molecule 14 is a protein called 50S ribosomal protein L21.

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

- Molecule 15 is a protein called 50S ribosomal protein L22.

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

- Molecule 16 is a protein called 50S ribosomal protein L23.

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

- Molecule 17 is a protein called 50S ribosomal protein L24.

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

- Molecule 18 is a protein called 50S ribosomal protein L25.

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

- Molecule 19 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	76	Total	C	N	O	S	0	0
			575	356	117	101	1		

- Molecule 20 is a protein called 50S ribosomal protein L28.

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

- Molecule 21 is a protein called 50S ribosomal protein L29.

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

- Molecule 22 is a protein called 50S ribosomal protein L30.

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

- Molecule 23 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 24 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 25 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 26 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 27 is a protein called 50S ribosomal protein L14.

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

- Molecule 28 is a protein called 50S ribosomal protein L19.

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

- Molecule 29 is a protein called Ribosomal silencing factor RsfS.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	6	102	Total	C	N	O	S	0	0
			780	485	133	157	5		

- Molecule 30 is a protein called 50S ribosomal protein L9.

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

- Molecule 31 is a protein called 50S ribosomal protein L5.

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

- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	b	1	Total	Zn	0
			1	1	

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	Q	1	Total	Mg	0
			1	1	

- Molecule 34 is water.

Mol	Chain	Residues	Atoms		AltConf
34	A	21	Total	O	0
			21	21	
34	B	1	Total	O	0
			1	1	
34	C	2	Total	O	0
			2	2	

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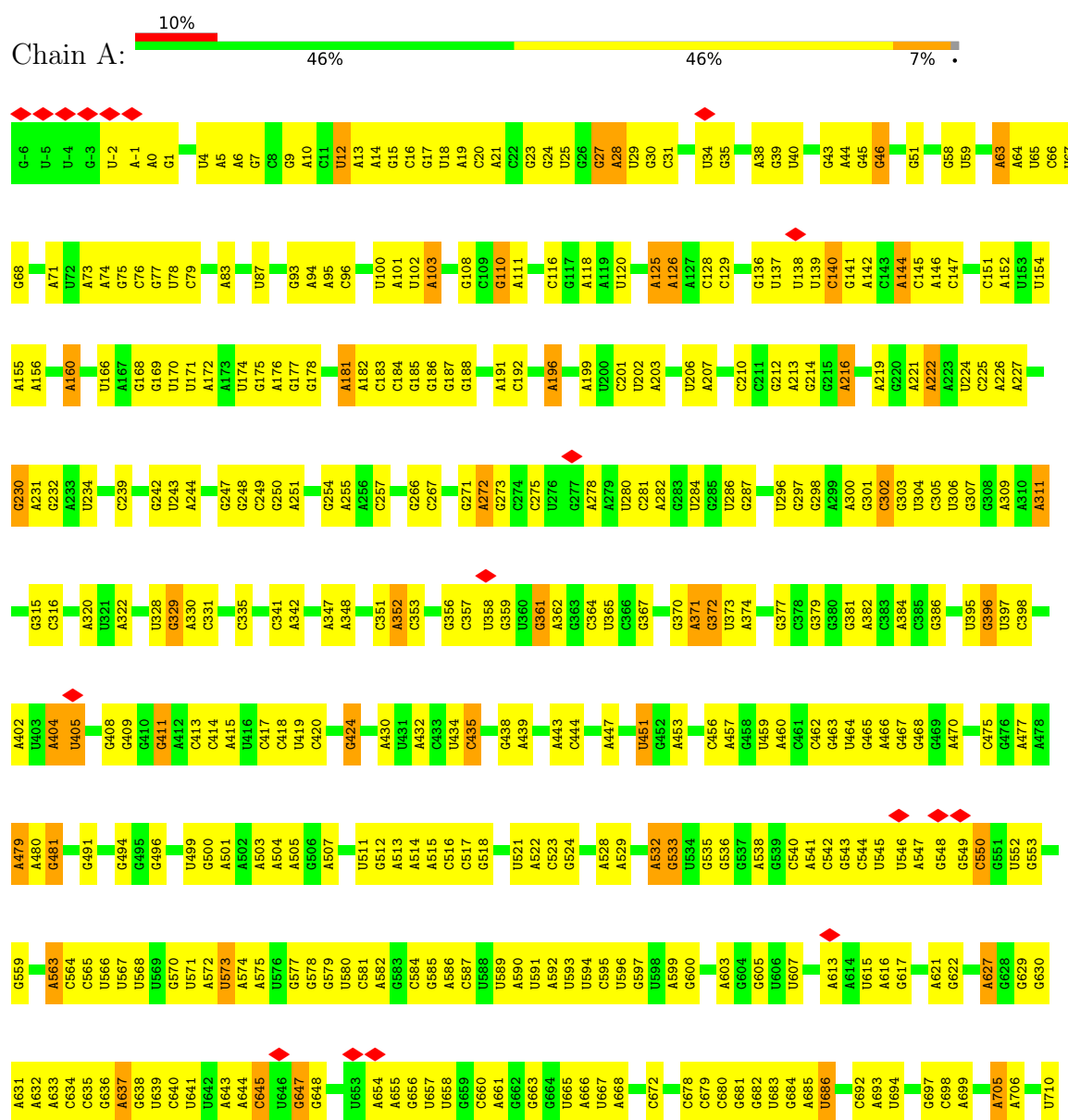
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Mol	Chain	Residues	Atoms		AltConf
34	L	1	Total 1	O 1	0
34	N	1	Total 1	O 1	0
34	S	1	Total 1	O 1	0

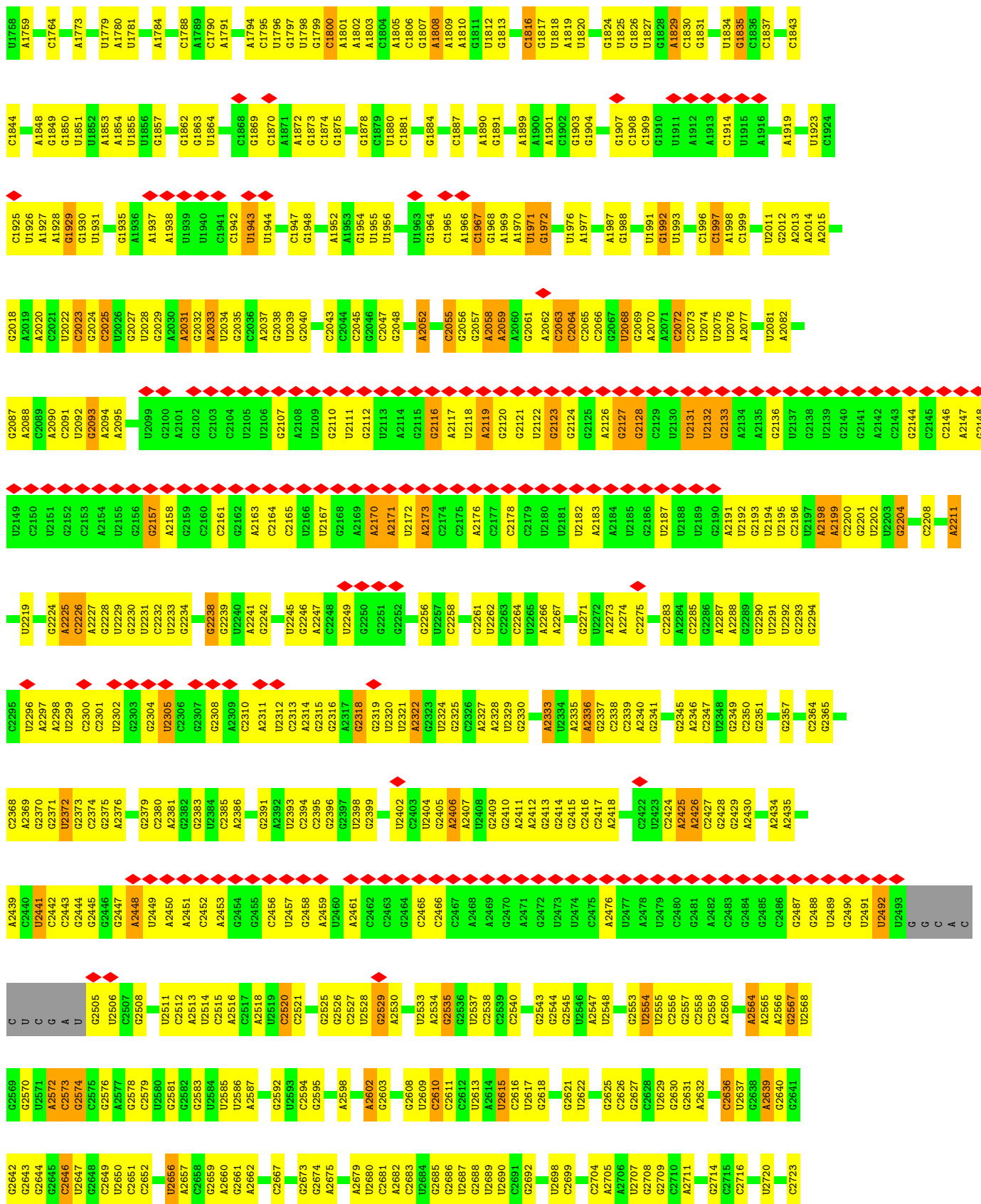
3 Residue-property plots

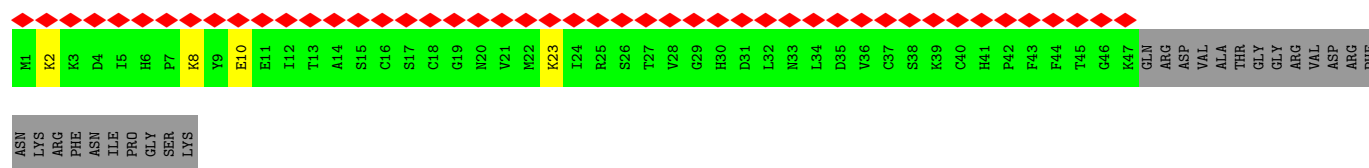
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 23S ribosomal RNA

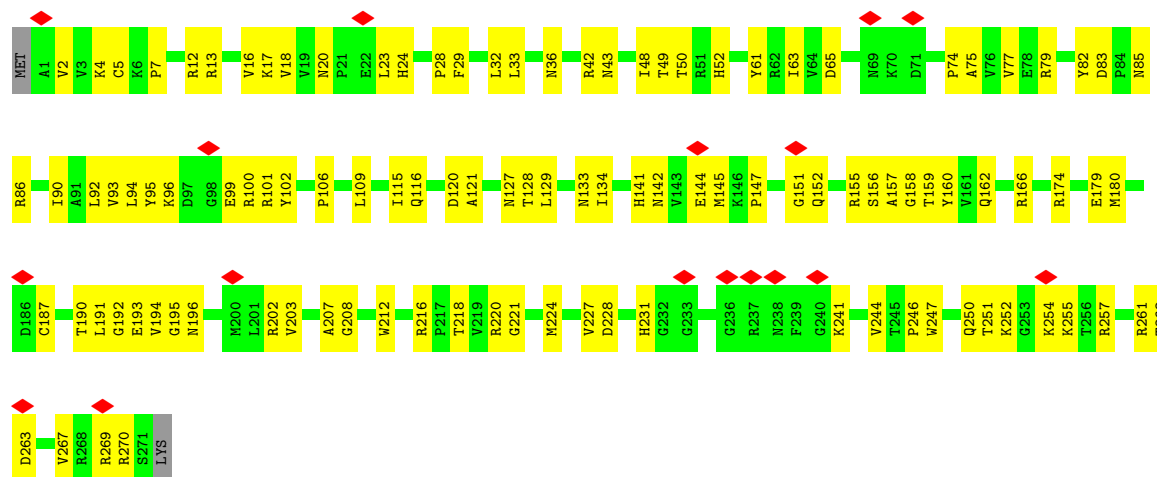




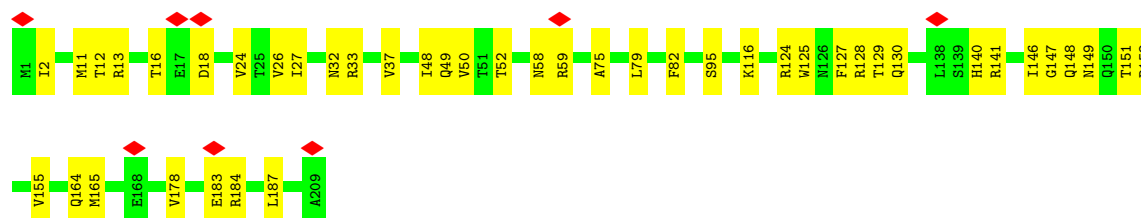
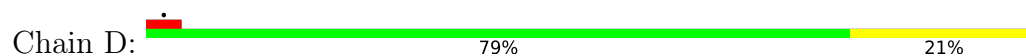




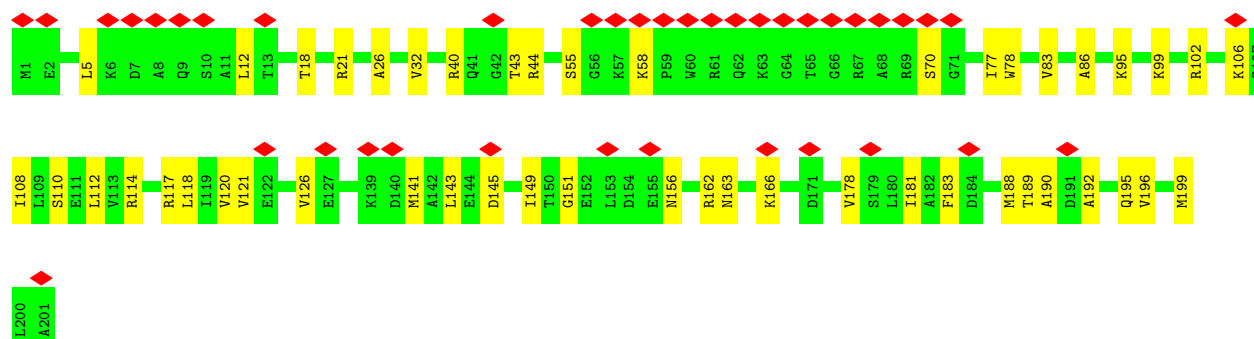
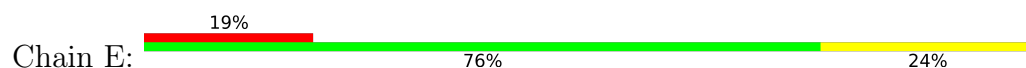
• Molecule 5: 50S ribosomal protein L2



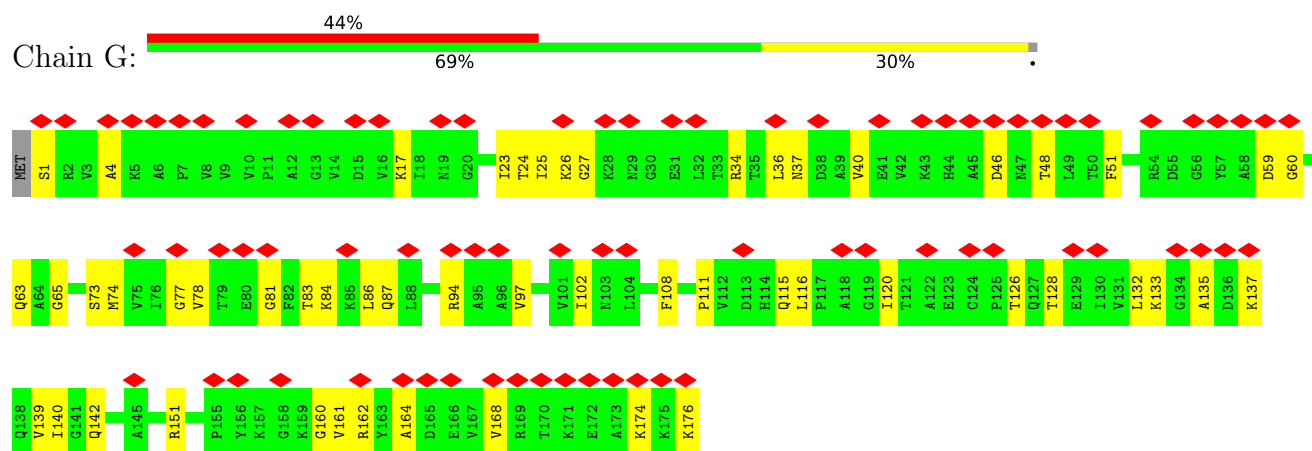
• Molecule 6: 50S ribosomal protein L3



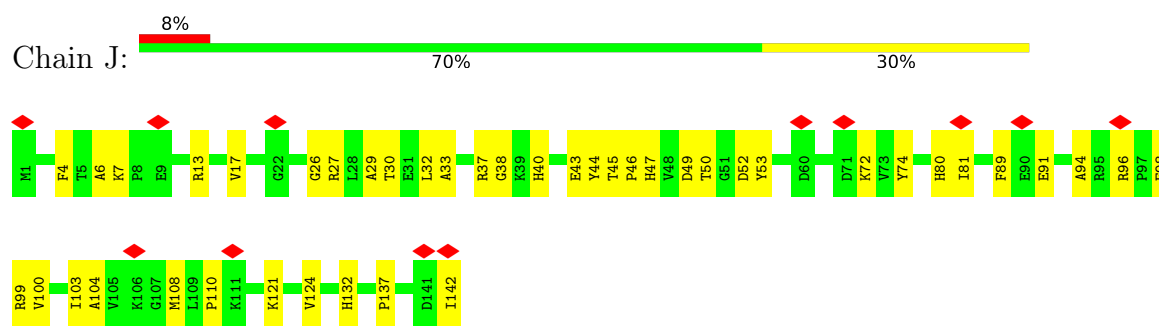
• Molecule 7: 50S ribosomal protein L4



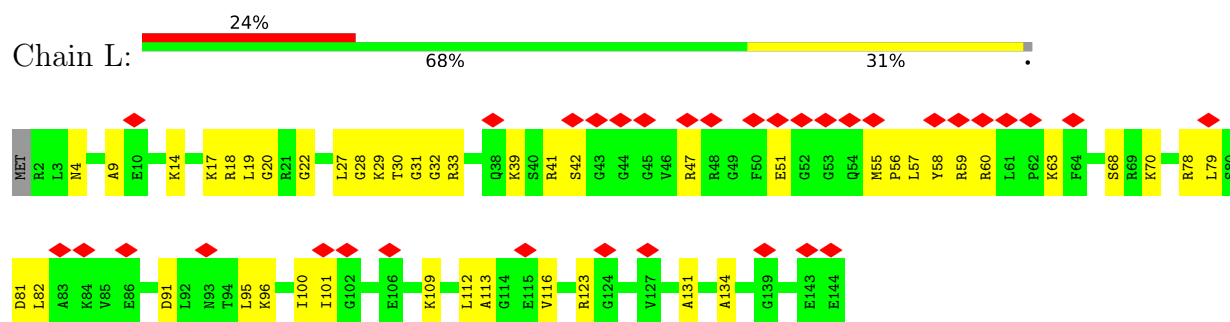
- Molecule 8: 50S ribosomal protein L6



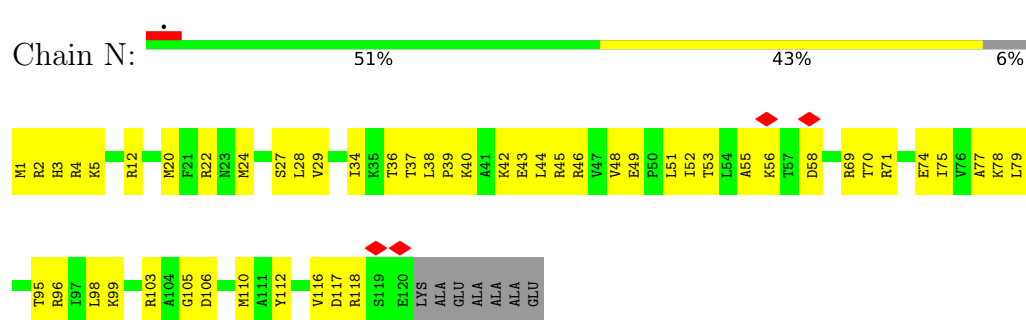
- Molecule 9: 50S ribosomal protein L13



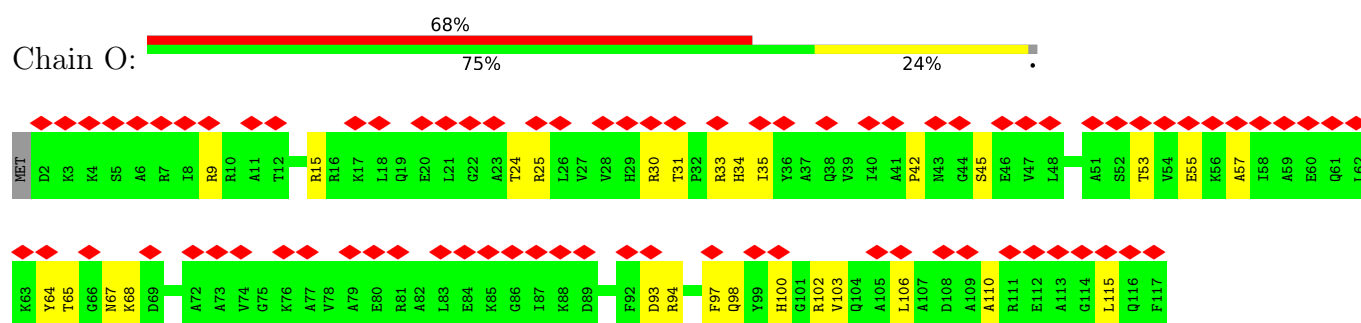
- Molecule 10: 50S ribosomal protein L15



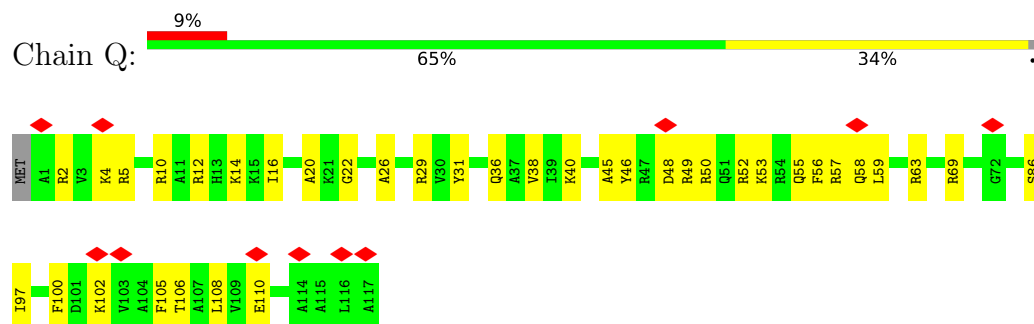
- Molecule 11: 50S ribosomal protein L17



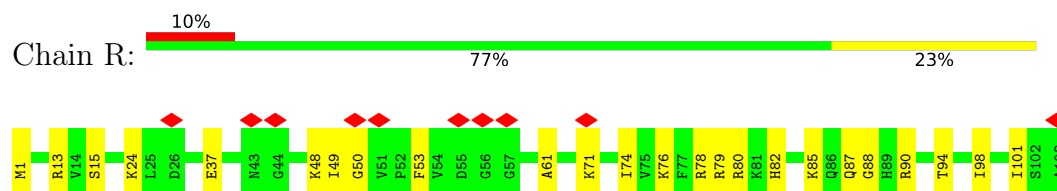
- Molecule 12: 50S ribosomal protein L18



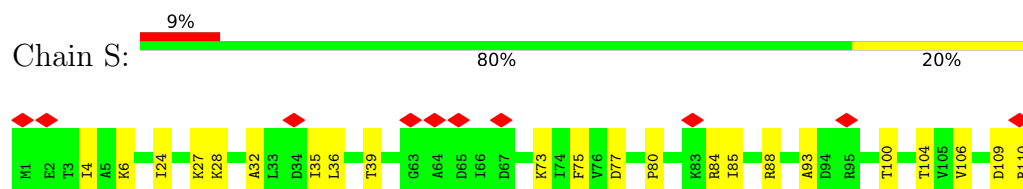
- Molecule 13: 50S ribosomal protein L20



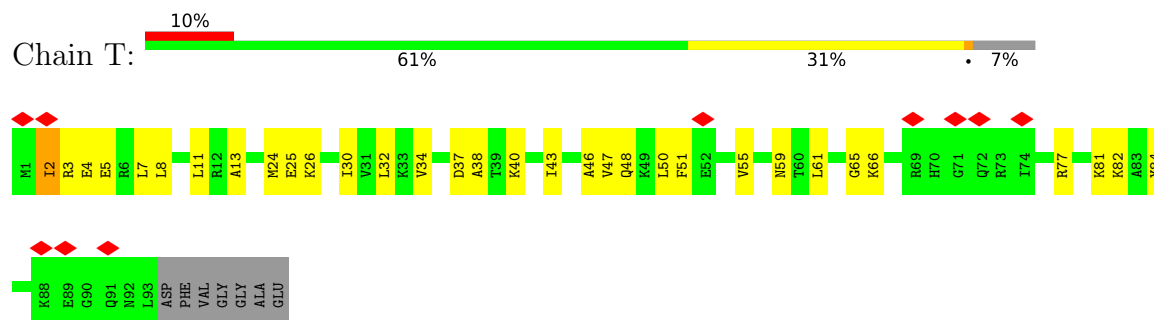
- Molecule 14: 50S ribosomal protein L21



- Molecule 15: 50S ribosomal protein L22

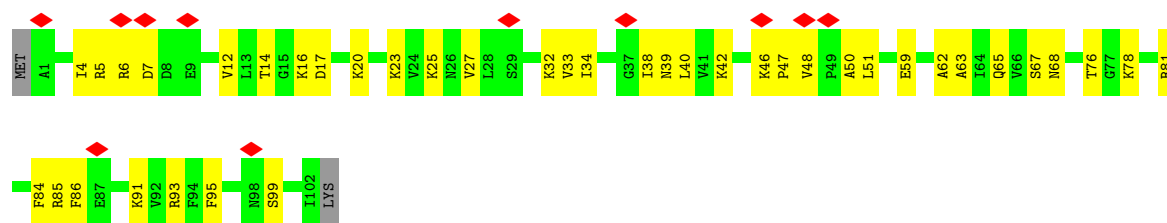


- Molecule 16: 50S ribosomal protein L23

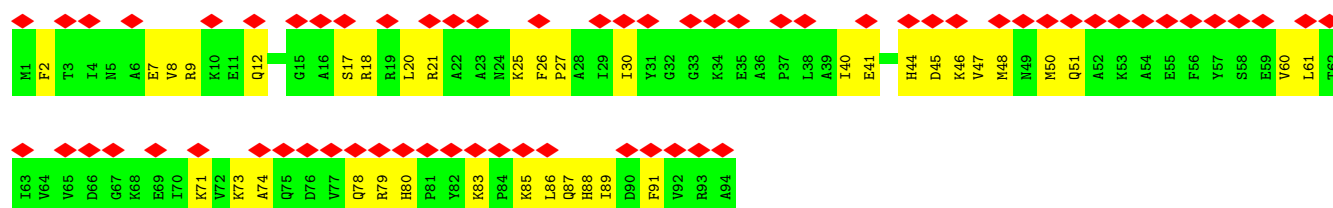


- Molecule 17: 50S ribosomal protein L24

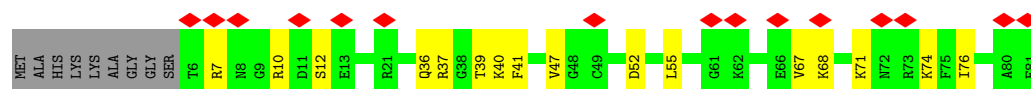




- Molecule 18: 50S ribosomal protein L25



- Molecule 19: 50S ribosomal protein L27



- Molecule 20: 50S ribosomal protein L28



- Molecule 21: 50S ribosomal protein L29



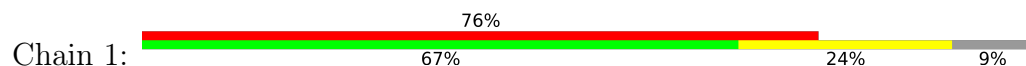
- Molecule 22: 50S ribosomal protein L30



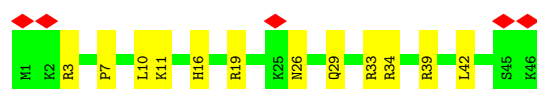
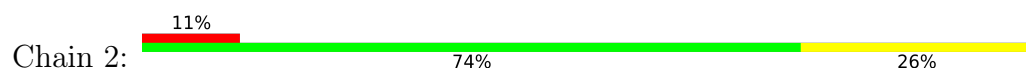
- Molecule 23: 50S ribosomal protein L32



• Molecule 24: 50S ribosomal protein L33



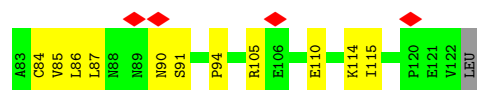
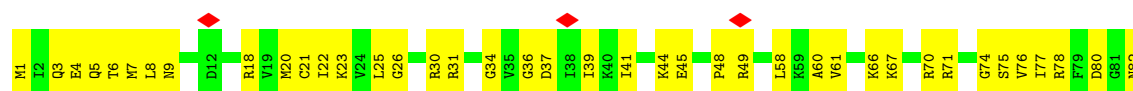
• Molecule 25: 50S ribosomal protein L34



• Molecule 26: 50S ribosomal protein L11

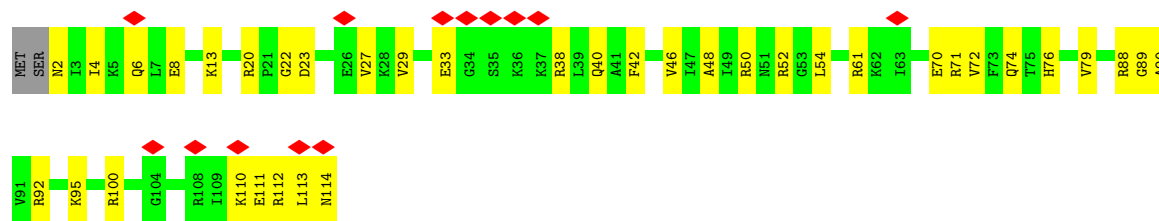


• Molecule 27: 50S ribosomal protein L14

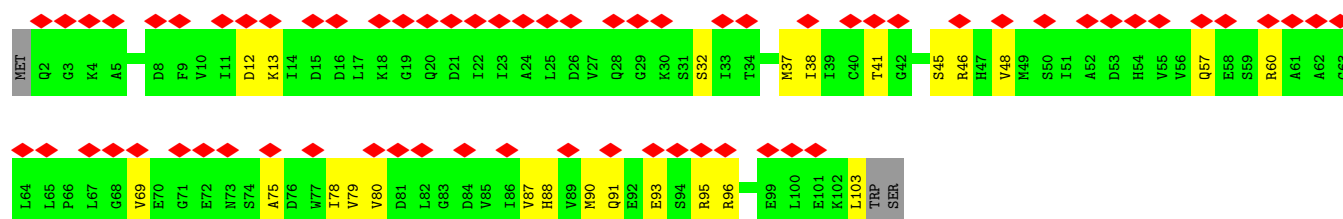
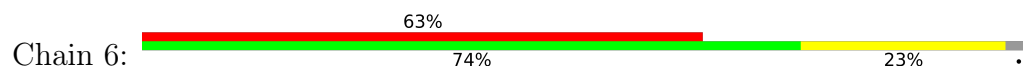


• Molecule 28: 50S ribosomal protein L19

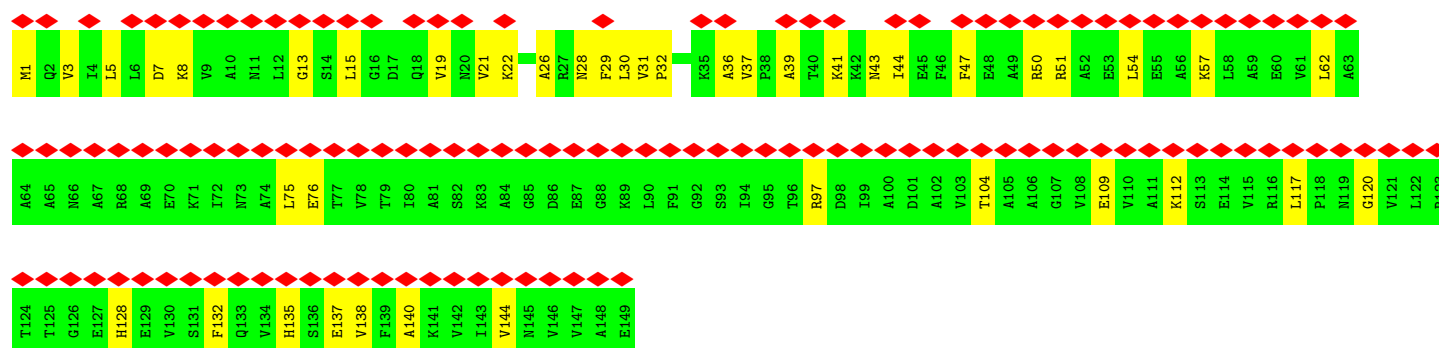
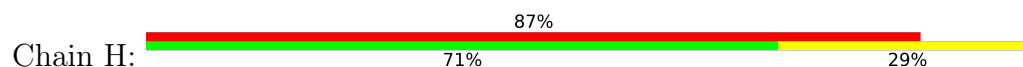




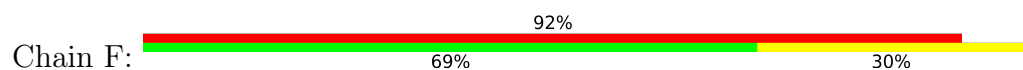
• Molecule 29: Ribosomal silencing factor RsfS



• Molecule 30: 50S ribosomal protein L9



• Molecule 31: 50S ribosomal protein L5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23445	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	Not provided	
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	12.748	Depositor
Minimum map value	-6.150	Depositor
Average map value	0.034	Depositor
Map value standard deviation	0.805	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	334.8, 334.8, 334.8	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.24, 1.24, 1.24	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.08	0/69777	0.20	0/108853
2	B	0.08	0/2847	0.20	0/4440
3	9P	0.14	0/2626	0.41	0/3542
4	b	0.11	0/371	0.30	0/496
5	C	0.13	0/2121	0.40	1/2852 (0.0%)
6	D	0.14	0/1586	0.39	1/2134 (0.0%)
7	E	0.11	0/1571	0.32	0/2113
8	G	0.32	1/1343 (0.1%)	0.55	3/1816 (0.2%)
9	J	0.13	0/1152	0.32	0/1551
10	L	0.14	0/1054	0.44	0/1403
11	N	0.14	0/973	0.43	0/1301
12	O	0.12	0/902	0.34	0/1209
13	Q	0.11	0/960	0.32	0/1278
14	R	0.13	0/829	0.40	0/1107
15	S	0.12	0/864	0.34	0/1156
16	T	0.16	0/744	0.51	2/994 (0.2%)
17	U	0.16	0/787	0.45	0/1051
18	V	0.16	0/766	0.40	0/1025
19	W	0.13	0/582	0.35	0/769
20	X	0.14	0/635	0.40	0/848
21	Y	0.13	0/510	0.41	0/677
22	Z	0.14	0/453	0.41	0/605
23	0	0.16	0/450	0.41	0/599
24	1	0.11	0/416	0.30	0/554
25	2	0.14	0/380	0.40	0/498
26	I	0.13	0/1046	0.47	0/1410
27	K	0.14	0/947	0.39	0/1268
28	P	0.14	0/923	0.41	0/1234
29	6	0.12	0/787	0.35	0/1062
30	H	0.13	0/1121	0.42	0/1515
31	F	0.14	0/1434	0.43	2/1926 (0.1%)
All	All	0.11	1/100957 (0.0%)	0.27	9/151286 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	9P	0	1
26	I	0	1
31	F	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	G	111	PRO	CG-CD	-10.05	1.16	1.50

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	G	111	PRO	N-CD-CG	-13.03	83.65	103.20
8	G	111	PRO	CA-N-CD	-9.74	98.36	112.00
8	G	111	PRO	CA-CB-CG	-7.57	90.12	104.50
16	T	2	ILE	CA-C-N	5.99	132.48	121.70
16	T	2	ILE	C-N-CA	5.99	132.48	121.70
6	D	147	GLY	N-CA-C	5.50	117.33	110.29
5	C	203	VAL	N-CA-C	-5.36	108.28	113.53
31	F	175	PRO	CA-C-N	5.00	131.09	121.54
31	F	175	PRO	C-N-CA	5.00	131.09	121.54

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	9P	190	PRO	Peptide
31	F	175	PRO	Peptide
26	I	5	GLN	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	62301	0	31334	1176	0
2	B	2548	0	1292	62	0
3	9P	2582	0	2607	88	0
4	b	364	0	364	4	0
5	C	2082	0	2157	93	0
6	D	1565	0	1616	44	0
7	E	1552	0	1619	42	0
8	G	1323	0	1374	43	0
9	J	1129	0	1162	42	0
10	L	1045	0	1117	44	0
11	N	960	0	1000	40	0
12	O	892	0	923	25	0
13	Q	947	0	1022	44	0
14	R	816	0	839	24	0
15	S	857	0	922	18	0
16	T	738	0	807	31	0
17	U	779	0	834	31	0
18	V	753	0	780	27	0
19	W	575	0	589	20	0
20	X	625	0	655	21	0
21	Y	509	0	543	18	0
22	Z	449	0	491	22	0
23	0	444	0	461	22	0
24	1	409	0	440	11	0
25	2	377	0	418	13	0
26	I	1032	0	1088	24	0
27	K	938	0	1012	40	0
28	P	911	0	957	33	0
29	6	780	0	783	14	0
30	H	1110	0	1148	32	0
31	F	1410	0	1447	51	0
32	b	1	0	0	0	0
33	Q	1	0	0	0	0
34	A	21	0	0	0	0
34	B	1	0	0	0	0
34	C	2	0	0	0	0
34	L	1	0	0	0	0
34	N	1	0	0	0	0
34	S	1	0	0	0	0
All	All	92831	0	61801	1901	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 13.

All (1901) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1800:C:N4	1:A:1817:G:H22	1.58	1.01
1:A:1800:C:H42	1:A:1817:G:N2	1.57	1.01
2:B:78:A:H62	2:B:98:G:N2	1.58	1.00
1:A:950:G:H1	1:A:967:U:H3	1.09	0.98
1:A:377:G:H1	1:A:397:U:H3	1.01	0.98
1:A:954:G:H1	1:A:963:U:H3	1.10	0.95
2:B:78:A:N6	2:B:98:G:H21	1.64	0.94
1:A:1800:C:H42	1:A:1817:G:H22	1.01	0.94
1:A:408:G:H1	1:A:419:U:H3	1.09	0.93
19:W:36:GLN:HE22	19:W:41:PHE:H	1.17	0.91
27:K:78:ARG:HB3	28:P:70:GLU:HB3	1.52	0.91
1:A:2530:A:OP2	8:G:174:LYS:NZ	2.11	0.84
2:B:78:A:H62	2:B:98:G:H21	0.84	0.83
1:A:1287:A:N6	1:A:1649:G:O2'	2.10	0.83
1:A:1800:C:N3	1:A:1817:G:N1	2.27	0.82
1:A:1834:U:H5''	1:A:1835:G:H5'	1.60	0.82
3:9P:304:LEU:HD11	3:9P:306:TRP:HB2	1.61	0.82
16:T:61:LEU:HB2	16:T:82:LYS:HB2	1.61	0.81
1:A:284:U:H3	1:A:356:G:H1	1.27	0.81
1:A:78:U:H3	1:A:108:G:H1	1.29	0.80
1:A:1278:C:H4'	11:N:34:ILE:HD11	1.63	0.80
1:A:2020:A:H5'	23:O:8:THR:HB	1.61	0.80
27:K:61:VAL:HG23	27:K:87:LEU:HD11	1.62	0.80
22:Z:23:LEU:HD12	22:Z:28:LEU:HD11	1.64	0.80
26:I:46:ASP:HA	26:I:50:LYS:HD2	1.65	0.79
1:A:1242:U:H3	10:L:4:ASN:HD21	1.31	0.78
9:J:96:ARG:NH2	9:J:98:GLU:OE2	2.16	0.78
6:D:151:THR:HG23	6:D:152:PRO:HD3	1.67	0.77
28:P:112:ARG:NH1	28:P:114:ASN:OD1	2.18	0.76
1:A:1079:C:O2'	26:I:133:ARG:NH2	2.19	0.76
5:C:36:ASN:HB2	5:C:61:TYR:HB2	1.65	0.76
1:A:465:G:H21	1:A:684:G:H1'	1.50	0.76
5:C:250:GLN:NE2	5:C:251:THR:O	2.18	0.76
8:G:87:GLN:HE22	8:G:164:ALA:HA	1.51	0.76
1:A:1138:G:H21	9:J:108:MET:HE1	1.50	0.75
11:N:2:ARG:HA	11:N:5:LYS:HE2	1.67	0.75
17:U:6:ARG:NH1	17:U:25:LYS:O	2.19	0.75
11:N:24:MET:HG3	11:N:44:LEU:HD13	1.70	0.73
1:A:629:G:N3	1:A:639:U:O2'	2.20	0.73
2:B:93:C:H5''	18:V:18:ARG:HH12	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1855:U:H3	1:A:1887:C:H42	1.37	0.73
17:U:17:ASP:HB2	17:U:20:LYS:HD3	1.69	0.73
1:A:475:C:O2	1:A:479:A:N6	2.21	0.73
1:A:807:U:OP2	10:L:41:ARG:NH1	2.21	0.73
1:A:1270:C:H5''	1:A:1271:G:H5'	1.71	0.73
12:O:25:ARG:HB2	12:O:93:ASP:HB2	1.70	0.73
1:A:177:G:OP2	1:A:177:G:N2	2.18	0.73
8:G:132:LEU:HB3	8:G:140:ILE:HD11	1.69	0.73
1:A:210:C:OP1	25:2:29:GLN:NE2	2.22	0.72
1:A:1791:A:N1	1:A:1829:A:H4'	2.05	0.72
1:A:1190:G:H5''	10:L:32:GLY:HA2	1.70	0.72
18:V:17:SER:HA	18:V:20:LEU:HD23	1.71	0.72
2:B:39:A:H62	4:b:2:LYS:HE3	1.55	0.72
18:V:18:ARG:O	18:V:21:ARG:NH1	2.23	0.72
6:D:12:THR:HG22	6:D:13:ARG:H	1.55	0.71
1:A:513:A:O2'	13:Q:10:ARG:NH2	2.22	0.71
1:A:1779:U:OP2	1:A:1784:A:N6	2.22	0.71
1:A:1805:A:N3	5:C:49:THR:OG1	2.23	0.71
5:C:145:MET:SD	5:C:152:GLN:NE2	2.63	0.71
1:A:2371:G:H1'	24:1:38:PHE:HE1	1.54	0.71
11:N:37:THR:HA	11:N:110:MET:HA	1.73	0.71
1:A:2296:U:OP2	12:O:9:ARG:NH2	2.24	0.70
1:A:1992:G:N2	1:A:1996:C:O2'	2.24	0.70
2:B:9:G:OP2	12:O:15:ARG:NH1	2.24	0.70
12:O:31:THR:OG1	12:O:34:HIS:O	2.09	0.70
1:A:1966:A:N1	3:9P:133:SER:OG	2.23	0.70
30:H:5:LEU:HD22	30:H:13:GLY:HA3	1.73	0.70
1:A:820:A:H4'	1:A:836:G:H22	1.57	0.70
1:A:1066:U:N3	1:A:1069:A:OP2	2.24	0.70
23:O:12:ARG:HH11	23:O:16:ARG:HH12	1.40	0.70
8:G:23:ILE:HG23	8:G:25:ILE:HD11	1.74	0.69
29:6:41:THR:OG1	29:6:95:ARG:NH1	2.25	0.69
1:A:1668:A:N3	1:A:1670:C:N4	2.41	0.69
1:A:994:C:OP1	13:Q:52:ARG:NH2	2.24	0.69
26:I:4:VAL:HG12	26:I:5:GLN:H	1.56	0.69
1:A:1966:A:N3	1:A:2592:G:O2'	2.24	0.69
2:B:94:A:OP2	18:V:18:ARG:NH1	2.26	0.69
13:Q:45:ALA:HB1	13:Q:49:ARG:HH12	1.58	0.69
5:C:74:PRO:HG2	5:C:96:LYS:HG2	1.75	0.69
31:F:34:THR:HG22	31:F:36:ASN:HB2	1.74	0.69
1:A:1386:C:H2'	1:A:1387:A:H8	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1453:A:N6	11:N:74:GLU:OE1	2.26	0.68
3:9P:25:ARG:HD3	3:9P:30:PRO:HA	1.74	0.68
1:A:987:C:O2'	1:A:1000:A:N3	2.27	0.68
1:A:2683:C:OP1	28:P:50:ARG:NH2	2.25	0.68
1:A:1943:U:H5''	3:9P:129:ARG:HE	1.58	0.68
1:A:2848:G:O2'	1:A:2867:G:N2	2.27	0.68
1:A:1363:C:O2'	1:A:1809:A:N3	2.22	0.68
28:P:22:GLY:H	28:P:46:VAL:HG13	1.59	0.68
1:A:1287:A:N6	11:N:106:ASP:OD2	2.26	0.68
1:A:2884:U:O2'	23:O:49:ARG:NH1	2.27	0.68
3:9P:2:LYS:HB2	8:G:176:LYS:H	1.59	0.68
1:A:1490:A:N1	5:C:96:LYS:NZ	2.42	0.67
6:D:32:ASN:ND2	6:D:52:THR:OG1	2.27	0.67
31:F:38:GLY:O	31:F:149:ARG:NH2	2.27	0.67
1:A:16:C:H2'	1:A:17:G:H8	1.59	0.67
1:A:467:G:OP1	25:2:33:ARG:NH2	2.27	0.67
1:A:974:G:O2'	1:A:989:G:N2	2.27	0.67
1:A:1443:U:H2'	1:A:1444:G:H8	1.60	0.67
1:A:698:C:O2'	1:A:734:A:N6	2.21	0.67
1:A:1800:C:O2	1:A:1817:G:O6	2.13	0.67
1:A:2405:G:O2'	1:A:2411:A:N6	2.28	0.67
1:A:993:G:OP2	13:Q:50:ARG:NH2	2.28	0.67
1:A:1943:U:H4'	1:A:1944:U:H3'	1.77	0.67
1:A:83:A:O2'	1:A:103:A:N6	2.27	0.67
1:A:212:G:H2'	1:A:213:A:C8	2.30	0.67
1:A:1830:C:H2'	1:A:1831:G:H8	1.60	0.67
1:A:1039:A:H61	1:A:1116:G:H1	1.43	0.66
22:Z:16:LEU:HB2	22:Z:19:HIS:HD2	1.60	0.66
21:Y:21:LEU:HD23	21:Y:25:GLN:HG3	1.76	0.66
1:A:2262:U:OP1	19:W:37:ARG:NH2	2.28	0.66
1:A:1999:C:O2	1:A:2687:U:O2'	2.14	0.66
3:9P:160:ALA:H	3:9P:237:ARG:HH22	1.40	0.66
3:9P:189:TYR:HB2	3:9P:190:PRO:HD2	1.77	0.66
1:A:1754:A:N1	1:A:2716:C:O2'	2.29	0.65
1:A:2258:C:O2'	1:A:2427:C:OP2	2.14	0.65
2:B:48:U:P	12:O:30:ARG:HH22	2.19	0.65
1:A:516:C:H5''	23:O:9:ARG:HH12	1.61	0.65
1:A:2788:C:O2'	1:A:2809:A:N3	2.27	0.65
17:U:85:ARG:HH12	17:U:99:SER:HB3	1.60	0.65
1:A:1013:C:H2'	1:A:1014:A:H8	1.62	0.65
1:A:1863:G:H4'	1:A:2411:A:H4'	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:998:C:OP2	13:Q:57:ARG:NH2	2.29	0.65
1:A:2581:G:N2	1:A:2581:G:OP2	2.29	0.65
3:9P:287:LEU:HD12	3:9P:288:LEU:HG	1.78	0.65
5:C:93:VAL:HG21	5:C:115:ILE:HD11	1.79	0.65
27:K:26:GLY:HA3	27:K:30:ARG:HH11	1.61	0.65
30:H:47:PHE:O	30:H:51:ARG:N	2.28	0.65
11:N:77:ALA:O	11:N:81:ASN:ND2	2.30	0.65
1:A:1665:A:OP1	27:K:66:LYS:NZ	2.30	0.65
1:A:1153:C:OP1	13:Q:91:ARG:NH2	2.30	0.64
1:A:1341:G:OP1	1:A:1397:U:N3	2.30	0.64
10:L:51:GLU:OE2	10:L:60:ARG:NH1	2.30	0.64
15:S:85:ILE:HD11	15:S:93:ALA:HB1	1.79	0.64
11:N:43:GLU:HA	11:N:46:ARG:HG3	1.79	0.64
1:A:1607:C:N4	1:A:1622:G:OP2	2.29	0.64
2:B:30:C:H1'	2:B:57:A:H61	1.62	0.64
6:D:129:THR:OG1	6:D:140:HIS:O	2.15	0.64
30:H:8:LYS:HD3	30:H:15:LEU:HD11	1.78	0.64
27:K:58:LEU:HD11	27:K:86:LEU:HD12	1.78	0.64
1:A:815:C:OP2	14:R:85:LYS:NZ	2.23	0.64
1:A:2320:U:O2'	1:A:2322:A:N6	2.31	0.64
18:V:18:ARG:HG2	18:V:21:ARG:HH12	1.63	0.64
29:6:37:MET:HE1	29:6:103:LEU:HB3	1.79	0.64
1:A:647:G:N2	1:A:2350:C:O2'	2.31	0.64
1:A:1779:U:H5''	1:A:1780:A:H5''	1.80	0.64
1:A:2336:A:H61	19:W:39:THR:HG21	1.63	0.64
1:A:942:G:OP1	10:L:39:LYS:NZ	2.31	0.63
1:A:1582:C:O2'	1:A:1585:C:N3	2.25	0.63
1:A:2081:U:H2'	1:A:2082:A:H8	1.63	0.63
1:A:2840:C:H5''	11:N:53:THR:HG21	1.80	0.63
1:A:1223:G:N2	1:A:1226:A:OP2	2.29	0.63
10:L:57:LEU:HD12	10:L:60:ARG:HD2	1.79	0.63
3:9P:38:ASP:OD1	3:9P:129:ARG:NH2	2.31	0.63
7:E:145:ASP:HA	7:E:166:LYS:HB3	1.81	0.63
9:J:80:HIS:CD2	9:J:81:ILE:HG22	2.33	0.63
1:A:1788:C:OP1	5:C:220:ARG:NH2	2.30	0.63
6:D:33:ARG:NH1	6:D:75:ALA:O	2.32	0.63
1:A:968:C:H2'	1:A:969:G:H8	1.63	0.63
1:A:1323:C:OP1	15:S:84:ARG:NH1	2.27	0.63
5:C:28:PRO:HG2	5:C:33:LEU:HD11	1.81	0.63
11:N:103:ARG:HG2	11:N:105:GLY:H	1.64	0.63
27:K:80:ASP:OD2	28:P:61:ARG:NH1	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2229:U:H2'	1:A:2230:G:H8	1.62	0.63
8:G:46:ASP:O	8:G:48:THR:N	2.27	0.63
1:A:1753:G:H5''	28:P:92:ARG:HD3	1.81	0.63
3:9P:266:LEU:HD22	3:9P:278:ARG:HH12	1.64	0.63
5:C:5:CYS:SG	5:C:12:ARG:NH2	2.72	0.63
1:A:571:U:O2'	1:A:573:U:OP2	2.17	0.62
1:A:372:G:OP2	20:X:61:LYS:NZ	2.31	0.62
1:A:2405:G:N1	1:A:2411:A:OP2	2.32	0.62
30:H:97:ARG:HG2	30:H:112:LYS:HD3	1.81	0.62
9:J:29:ALA:HA	9:J:32:LEU:HD12	1.81	0.62
9:J:40:HIS:NE2	9:J:52:ASP:OD2	2.32	0.62
24:1:10:LEU:HD21	24:1:33:LEU:HD13	1.81	0.62
1:A:566:U:OP1	10:L:29:LYS:NZ	2.33	0.62
1:A:865:C:O2	1:A:867:C:N4	2.32	0.62
17:U:14:THR:OG1	17:U:68:ASN:ND2	2.32	0.62
1:A:1798:U:O2'	1:A:1802:A:N3	2.28	0.62
26:I:32:VAL:HG21	26:I:58:ILE:HD13	1.82	0.62
1:A:607:U:OP1	7:E:95:LYS:NZ	2.32	0.62
17:U:46:LYS:HD2	17:U:47:PRO:HD2	1.82	0.62
5:C:144:GLU:HB2	5:C:187:CYS:HB3	1.81	0.62
11:N:1:MET:HE3	11:N:3:HIS:HD2	1.65	0.62
1:A:213:A:H2'	1:A:214:G:C8	2.35	0.61
1:A:1258:U:H2'	1:A:1259:G:H8	1.65	0.61
1:A:1799:G:OP2	5:C:269:ARG:NH2	2.32	0.61
11:N:1:MET:HE3	11:N:3:HIS:CD2	2.35	0.61
24:1:24:LYS:NZ	24:1:29:LYS:O	2.33	0.61
1:A:166:U:O2'	20:X:44:ARG:NH2	2.33	0.61
1:A:395:U:O2'	1:A:396:G:N7	2.33	0.61
1:A:1278:C:O2'	11:N:27:SER:OG	2.16	0.61
1:A:516:C:OP1	23:O:9:ARG:NH1	2.34	0.61
1:A:1248:G:OP1	7:E:44:ARG:NH2	2.33	0.61
5:C:244:VAL:HG12	5:C:250:GLN:HA	1.82	0.61
1:A:1353:A:OP2	1:A:1377:G:N1	2.27	0.61
1:A:2595:G:N2	1:A:2598:A:OP2	2.22	0.61
3:9P:2:LYS:HE2	8:G:176:LYS:H	1.65	0.61
3:9P:11:VAL:HG21	3:9P:45:VAL:HG11	1.81	0.61
1:A:645:C:N4	1:A:2349:G:N3	2.46	0.61
1:A:1420:A:O2'	1:A:2211:A:N7	2.33	0.61
1:A:2256:G:O2'	19:W:7:ARG:NH2	2.34	0.61
5:C:83:ASP:HB2	5:C:90:ILE:HG12	1.83	0.61
1:A:462:C:N4	1:A:463:G:O6	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:U:H4'	1:A:1235:G:H4'	1.82	0.61
1:A:1323:C:H5''	15:S:84:ARG:HH22	1.66	0.61
5:C:52:HIS:HA	5:C:216:ARG:HB2	1.82	0.61
3:9P:47:MET:HB3	3:9P:115:LEU:HB3	1.82	0.61
3:9P:190:PRO:O	3:9P:192:THR:OG1	2.10	0.61
1:A:2705:A:O2'	1:A:2852:G:OP1	2.18	0.61
2:B:43:C:O2'	31:F:91:ARG:O	2.18	0.61
18:V:2:PHE:HB2	18:V:61:LEU:HG	1.82	0.61
9:J:89:PHE:HE1	9:J:100:VAL:HG11	1.66	0.60
30:H:30:LEU:HB3	30:H:36:ALA:HB3	1.81	0.60
1:A:464:U:O2	25:2:16:HIS:NE2	2.33	0.60
3:9P:13:ALA:HB2	3:9P:118:ALA:HB1	1.83	0.60
1:A:743:A:O2'	1:A:1659:G:OP1	2.17	0.60
1:A:2091:C:H4'	20:X:55:MET:HE1	1.83	0.60
1:A:444:C:OP1	7:E:40:ARG:NH2	2.34	0.60
1:A:2443:C:H2'	1:A:2444:G:H8	1.67	0.60
1:A:2526:G:H1	1:A:2537:U:H3	1.48	0.60
1:A:1323:C:H5''	15:S:84:ARG:NH2	2.17	0.60
1:A:2816:G:N3	1:A:2883:A:O2'	2.32	0.60
1:A:2451:A:H1'	3:9P:25:ARG:HH12	1.65	0.60
3:9P:158:LEU:O	3:9P:237:ARG:NH2	2.34	0.60
10:L:30:THR:HB	10:L:33:ARG:HB2	1.83	0.60
1:A:177:G:H3'	1:A:178:G:H8	1.66	0.60
1:A:629:G:H1'	1:A:639:U:H1'	1.84	0.60
1:A:1386:C:H2'	1:A:1387:A:C8	2.37	0.60
1:A:2453:A:O2'	1:A:2572:A:N3	2.26	0.60
2:B:9:G:H1'	12:O:45:SER:HA	1.84	0.60
22:Z:36:GLU:O	22:Z:37:ARG:NH1	2.33	0.60
30:H:104:THR:HG22	30:H:109:GLU:HA	1.83	0.60
1:A:966:G:H4'	1:A:2271:G:H22	1.67	0.60
3:9P:164:MET:HB3	3:9P:213:ASP:HA	1.84	0.60
27:K:34:GLY:N	27:K:37:ASP:OD2	2.31	0.60
1:A:1649:G:H2'	1:A:1650:A:H8	1.66	0.60
1:A:1123:C:H2'	1:A:1124:G:H8	1.66	0.59
1:A:2298:A:N6	1:A:2318:G:H21	2.00	0.59
1:A:2368:C:H2'	1:A:2369:A:H8	1.67	0.59
5:C:151:GLY:O	5:C:155:ARG:NH1	2.33	0.59
31:F:101:ARG:NH2	31:F:139:GLU:OE2	2.34	0.59
1:A:27:G:H22	1:A:512:G:H1'	1.67	0.59
1:A:918:A:N3	2:B:80:U:O2'	2.32	0.59
30:H:1:MET:N	30:H:21:VAL:O	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2047:C:O2'	1:A:2823:A:N1	2.35	0.59
3:9P:97:ILE:HB	3:9P:153:LEU:HB3	1.84	0.59
5:C:17:LYS:HA	5:C:202:ARG:HH22	1.68	0.59
12:O:33:ARG:O	12:O:65:THR:OG1	2.20	0.59
22:Z:26:LEU:HD21	22:Z:46:MET:HB3	1.85	0.59
1:A:584:C:N4	1:A:585:G:O6	2.35	0.59
1:A:2093:G:O3'	30:H:22:LYS:HE3	2.02	0.59
1:A:311:A:N6	1:A:329:G:OP1	2.35	0.59
1:A:1295:C:H2'	1:A:1296:G:H8	1.67	0.59
1:A:2123:G:H2'	1:A:2124:G:H8	1.68	0.59
3:9P:161:ASP:H	3:9P:210:VAL:HG23	1.67	0.59
1:A:1952:A:H62	27:K:22:ILE:HD11	1.68	0.59
6:D:151:THR:CG2	6:D:152:PRO:HD3	2.32	0.59
9:J:80:HIS:CG	9:J:81:ILE:H	2.21	0.59
24:1:28:THR:HG23	24:1:29:LYS:HG2	1.85	0.59
1:A:617:G:OP1	7:E:102:ARG:NH2	2.36	0.59
1:A:1826:G:O2'	1:A:1971:U:OP2	2.21	0.59
1:A:2761:A:N3	8:G:142:GLN:NE2	2.51	0.59
2:B:55:U:H1'	31:F:25:MET:HE1	1.84	0.59
6:D:149:ASN:O	6:D:152:PRO:HD2	2.02	0.59
17:U:6:ARG:HE	17:U:7:ASP:H	1.51	0.59
30:H:26:ALA:HA	30:H:30:LEU:HD12	1.84	0.59
1:A:764:A:H5'	5:C:208:GLY:HA2	1.85	0.59
1:A:780:G:N1	5:C:228:ASP:OD2	2.36	0.59
1:A:1258:U:H2'	1:A:1259:G:C8	2.37	0.59
1:A:1857:G:O2'	1:A:1884:G:N2	2.35	0.59
1:A:1997:C:H2'	1:A:1998:A:H8	1.66	0.59
5:C:257:ARG:NH2	5:C:262:THR:OG1	2.36	0.59
17:U:5:ARG:HE	17:U:93:ARG:HD3	1.68	0.59
1:A:2621:G:O3'	6:D:164:GLN:NE2	2.36	0.59
1:A:2857:G:N2	1:A:2860:A:OP2	2.26	0.58
1:A:160:A:N3	1:A:2208:C:O2'	2.34	0.58
9:J:53:TYR:HA	9:J:121:LYS:HB3	1.84	0.58
1:A:2673:G:H2'	1:A:2674:G:H8	1.67	0.58
2:B:57:A:O2'	31:F:26:GLN:OE1	2.21	0.58
18:V:73:LYS:NZ	18:V:74:ALA:H	2.01	0.58
26:I:115:ASP:O	26:I:116:MET:HE2	2.03	0.58
31:F:103:ILE:HD11	31:F:174:PHE:HA	1.84	0.58
1:A:1278:C:H2'	1:A:1279:G:C8	2.39	0.58
1:A:2131:U:H5'	1:A:2132:U:H5''	1.84	0.58
5:C:94:LEU:HD13	5:C:100:ARG:HE	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:P:27:VAL:HG23	28:P:42:PHE:HB3	1.83	0.58
10:L:19:LEU:HB2	10:L:31:GLY:HA3	1.84	0.58
29:6:57:GLN:OE1	29:6:60:ARG:NH2	2.35	0.58
1:A:5:A:H2'	1:A:6:A:H8	1.69	0.58
1:A:31:C:O2'	1:A:1238:G:OP1	2.21	0.58
1:A:832:U:H2'	1:A:833:A:H8	1.67	0.58
1:A:581:C:H2'	1:A:582:A:H8	1.69	0.58
1:A:1666:G:N3	27:K:3:GLN:NE2	2.52	0.58
1:A:1853:A:N3	1:A:2233:U:O2'	2.33	0.58
5:C:134:ILE:O	5:C:166:ARG:NH1	2.33	0.58
1:A:1016:G:O6	1:A:1147:A:N6	2.37	0.58
1:A:1071:G:N2	1:A:1089:A:H2'	2.19	0.58
8:G:27:GLY:HA3	8:G:78:VAL:HB	1.86	0.58
11:N:28:LEU:HD12	11:N:44:LEU:HD21	1.85	0.58
1:A:1154:G:OP2	13:Q:57:ARG:NH1	2.36	0.58
1:A:1818:U:H2'	5:C:155:ARG:HD3	1.85	0.58
1:A:2293:G:H5''	12:O:94:ARG:HH22	1.68	0.58
1:A:2824:C:OP2	1:A:2825:G:N2	2.37	0.58
19:W:74:LYS:HA	19:W:74:LYS:HE3	1.86	0.58
1:A:1996:C:OP2	27:K:31:ARG:NH2	2.37	0.58
1:A:2443:C:H2'	1:A:2444:G:C8	2.39	0.58
2:B:28:C:H2'	2:B:29:A:H8	1.68	0.58
1:A:2743:U:OP2	1:A:2755:C:N4	2.34	0.57
3:9P:71:GLN:HB2	3:9P:81:LYS:H	1.66	0.57
14:R:1:MET:HE2	14:R:101:ILE:HB	1.85	0.57
26:I:48:ILE:HG13	26:I:49:GLU:H	1.69	0.57
4:b:23:LYS:O	31:F:2:LYS:NZ	2.34	0.57
13:Q:86:SER:OG	14:R:50:GLY:O	2.22	0.57
14:R:61:ALA:HA	14:R:98:ILE:HA	1.86	0.57
1:A:272:A:H2'	1:A:273:G:H8	1.67	0.57
1:A:322:A:OP1	7:E:162:ARG:NE	2.33	0.57
1:A:881:G:H1	1:A:895:U:H3	1.52	0.57
1:A:910:A:N3	1:A:2264:C:O2'	2.35	0.57
1:A:2032:G:H21	6:D:151:THR:HB	1.69	0.57
1:A:2692:G:N3	1:A:2847:U:O2'	2.37	0.57
27:K:39:ILE:O	27:K:60:ALA:N	2.35	0.57
31:F:35:LEU:HG	31:F:151:LEU:HD11	1.84	0.57
1:A:770:G:H5'	25:2:10:LEU:HD23	1.87	0.57
1:A:903:C:N4	1:A:904:G:O6	2.37	0.57
1:A:2163:A:OP1	1:A:2170:A:O2'	2.20	0.57
1:A:2461:A:H1'	1:A:2492:U:N3	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:144:GLU:HG2	5:C:151:GLY:H	1.70	0.57
1:A:2512:C:H5''	6:D:127:PHE:HE1	1.69	0.57
10:L:112:LEU:HB3	10:L:131:ALA:HA	1.87	0.57
27:K:7:MET:HG2	27:K:20:MET:HB2	1.86	0.57
1:A:2874:C:H5''	11:N:4:ARG:HH21	1.69	0.57
5:C:179:GLU:OE1	5:C:269:ARG:NH1	2.38	0.57
1:A:1009:A:H5'	13:Q:58:GLN:HG3	1.86	0.57
1:A:2077:A:N3	1:A:2434:A:O2'	2.34	0.57
1:A:648:G:O2'	1:A:2351:G:OP1	2.21	0.57
26:I:52:LEU:HD11	26:I:81:LYS:HE2	1.85	0.57
1:A:301:G:OP2	17:U:81:ARG:NH1	2.38	0.57
1:A:329:G:O6	17:U:16:LYS:N	2.38	0.57
11:N:86:ARG:NH2	11:N:117:ASP:OD1	2.38	0.57
1:A:1429:G:H2'	1:A:1430:G:H8	1.69	0.57
1:A:2602:A:C8	3:9P:31:LYS:HD2	2.40	0.57
2:B:11:C:OP1	19:W:68:LYS:NZ	2.25	0.57
19:W:7:ARG:O	19:W:10:ARG:NH1	2.37	0.57
31:F:32:LYS:NZ	31:F:34:THR:OG1	2.27	0.57
31:F:103:ILE:HD11	31:F:175:PRO:HD3	1.85	0.57
1:A:782:A:C6	5:C:224:MET:HE1	2.39	0.56
1:A:1264:A:OP1	23:O:15:ARG:NH1	2.37	0.56
1:A:2642:G:H5''	9:J:80:HIS:CD2	2.40	0.56
5:C:95:TYR:HB2	5:C:99:GLU:HB2	1.87	0.56
1:A:18:U:H2'	1:A:19:A:C8	2.39	0.56
1:A:414:C:H2'	1:A:415:A:H8	1.68	0.56
1:A:935:C:H2'	1:A:936:A:H8	1.70	0.56
1:A:2245:U:H5''	1:A:2246:G:H5'	1.85	0.56
1:A:2315:G:H2'	1:A:2316:G:C8	2.40	0.56
1:A:2728:U:HO2'	1:A:2729:G:H8	1.53	0.56
9:J:108:MET:HA	9:J:108:MET:HE3	1.87	0.56
1:A:1183:U:O2'	22:Z:29:ARG:NH1	2.39	0.56
1:A:1213:A:H2'	1:A:1214:A:H8	1.70	0.56
1:A:2120:G:H2'	1:A:2121:G:H8	1.70	0.56
1:A:2298:A:OP1	31:F:71:LYS:NZ	2.38	0.56
1:A:2646:C:OP2	1:A:2732:G:O2'	2.23	0.56
3:9P:99:GLN:HG3	3:9P:151:GLU:HB2	1.88	0.56
22:Z:48:ASN:HA	22:Z:51:SER:HB3	1.86	0.56
1:A:247:G:OP2	1:A:249:C:N4	2.38	0.56
2:B:93:C:H5''	18:V:18:ARG:NH1	2.21	0.56
8:G:84:LYS:HB3	8:G:132:LEU:HB2	1.86	0.56
27:K:48:PRO:HB2	27:K:49:ARG:HH11	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:877:A:O2'	1:A:900:A:N6	2.37	0.56
23:O:38:LEU:HB2	23:O:41:HIS:HB2	1.88	0.56
1:A:1012:U:OP2	13:Q:69:ARG:NH1	2.38	0.56
1:A:2324:U:O2'	1:A:2337:G:OP1	2.24	0.56
1:A:2374:C:N4	1:A:2375:G:O6	2.39	0.56
1:A:2756:U:H1'	1:A:2757:A:H5''	1.86	0.56
9:J:4:PHE:O	13:Q:63:ARG:NH2	2.37	0.56
1:A:591:U:O4	1:A:592:A:N6	2.38	0.56
1:A:1825:U:H2'	1:A:1826:G:H8	1.71	0.56
1:A:2039:U:H2'	1:A:2040:G:C8	2.41	0.56
1:A:2092:U:O4	1:A:2227:A:N6	2.32	0.56
2:B:60:C:H2'	2:B:61:G:H8	1.69	0.56
5:C:20:ASN:HB3	5:C:23:LEU:HB2	1.88	0.56
1:A:351:C:H2'	1:A:352:A:C8	2.40	0.56
1:A:728:G:O2'	1:A:730:A:O4'	2.22	0.56
1:A:1649:G:H2'	1:A:1650:A:C8	2.41	0.56
1:A:961:C:O2	1:A:2031:A:N6	2.39	0.56
1:A:2052:A:H4'	6:D:148:GLN:O	2.06	0.56
1:A:2312:U:O2'	31:F:36:ASN:ND2	2.39	0.56
18:V:60:VAL:HB	18:V:71:LYS:HD2	1.88	0.56
30:H:135:HIS:HB3	30:H:138:VAL:HB	1.87	0.56
1:A:630:G:N2	1:A:633:A:OP2	2.35	0.56
1:A:1987:A:H2'	1:A:1988:G:H8	1.71	0.56
1:A:2760:C:H2'	1:A:2761:A:H8	1.70	0.56
7:E:151:GLY:HA2	7:E:195:GLN:HE22	1.70	0.56
25:2:34:ARG:HH11	25:2:39:ARG:HD2	1.71	0.56
28:P:90:ALA:HB2	28:P:112:ARG:HA	1.88	0.56
1:A:1837:C:O2'	1:A:1927:A:N3	2.31	0.55
3:9P:204:ASP:HB3	3:9P:207:LYS:HD2	1.87	0.55
27:K:25:LEU:O	27:K:30:ARG:NH1	2.39	0.55
1:A:351:C:H2'	1:A:352:A:H8	1.71	0.55
1:A:371:A:N6	1:A:402:A:OP2	2.38	0.55
1:A:468:G:N7	25:2:39:ARG:NH2	2.54	0.55
1:A:1463:C:H2'	1:A:1464:G:H8	1.71	0.55
1:A:2285:C:H5	24:1:5:ARG:HH12	1.53	0.55
3:9P:94:THR:H	3:9P:108:MET:HB3	1.71	0.55
17:U:84:PHE:HE2	17:U:93:ARG:HG2	1.71	0.55
1:A:1123:C:H2'	1:A:1124:G:C8	2.41	0.55
1:A:2023:C:H2'	1:A:2024:G:H8	1.72	0.55
1:A:2329:U:H2'	1:A:2330:G:C8	2.41	0.55
20:X:18:SER:OG	20:X:22:ASN:OD1	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Z:17:PRO:HD2	22:Z:18:LYS:H	1.71	0.55
1:A:1164:C:H2'	1:A:1165:A:H8	1.71	0.55
7:E:77:ILE:HG13	7:E:78:TRP:HD1	1.72	0.55
31:F:109:ARG:HE	31:F:136:ILE:HG22	1.72	0.55
1:A:251:A:H4'	10:L:47:ARG:HH21	1.72	0.55
1:A:796:C:H2'	1:A:797:G:C8	2.41	0.55
1:A:2329:U:H2'	1:A:2330:G:H8	1.70	0.55
3:9P:17:GLY:N	3:9P:40:GLY:O	2.37	0.55
21:Y:45:GLN:O	21:Y:49:ASP:N	2.39	0.55
1:A:18:U:O3'	13:Q:22:GLY:HA2	2.05	0.55
1:A:1407:G:H2'	1:A:1408:G:H8	1.70	0.55
1:A:1855:U:H3	1:A:1887:C:N4	2.02	0.55
1:A:2313:C:H5'	31:F:87:LYS:HD2	1.89	0.55
1:A:1067:A:N3	3:9P:223:GLU:HB2	2.21	0.55
1:A:1712:U:OP2	1:A:1713:A:O2'	2.23	0.55
1:A:2202:U:O2'	1:A:2204:G:OP1	2.20	0.55
1:A:2292:U:H2'	1:A:2293:G:H8	1.72	0.55
6:D:2:ILE:HG13	6:D:82:PHE:HB2	1.88	0.55
9:J:6:ALA:H	9:J:45:THR:HG21	1.72	0.55
9:J:17:VAL:HG23	9:J:137:PRO:HB2	1.89	0.55
7:E:83:VAL:HB	7:E:86:ALA:HB2	1.89	0.55
10:L:20:GLY:H	10:L:28:GLY:HA2	1.72	0.55
18:V:8:VAL:HA	18:V:40:ILE:HG22	1.89	0.55
27:K:8:LEU:HD22	27:K:84:CYS:SG	2.47	0.55
1:A:59:U:H1'	1:A:73:A:H2'	1.89	0.55
1:A:63:A:O3'	16:T:77:ARG:NH1	2.41	0.55
1:A:665:U:H2'	1:A:666:A:H8	1.72	0.55
1:A:414:C:H2'	1:A:415:A:C8	2.42	0.54
1:A:272:A:H2'	1:A:273:G:C8	2.42	0.54
1:A:1353:A:H2'	1:A:1354:A:H8	1.72	0.54
1:A:1441:G:H2'	1:A:1442:U:C6	2.42	0.54
1:A:1447:C:O2'	1:A:1544:A:N3	2.38	0.54
1:A:1599:U:OP2	16:T:40:LYS:NZ	2.33	0.54
1:A:2730:C:H2'	1:A:2731:G:C8	2.42	0.54
5:C:77:VAL:HG11	5:C:109:LEU:HD21	1.89	0.54
31:F:110:ILE:HD13	31:F:136:ILE:HG21	1.89	0.54
1:A:175:G:H2'	1:A:176:A:C8	2.43	0.54
1:A:532:A:N1	1:A:2035:G:N2	2.55	0.54
1:A:660:C:H2'	1:A:661:A:H8	1.73	0.54
1:A:1539:U:H2'	1:A:1540:G:H8	1.72	0.54
1:A:1736:U:O4	1:A:1737:G:N2	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1947:C:H2'	1:A:1948:G:H8	1.70	0.54
9:J:72:LYS:HE3	9:J:74:TYR:HE1	1.71	0.54
1:A:219:A:N3	1:A:234:U:O2'	2.40	0.54
1:A:239:C:O2'	1:A:622:G:O2'	2.20	0.54
1:A:463:G:N2	1:A:466:A:OP2	2.32	0.54
1:A:1901:A:OP2	5:C:252:LYS:NZ	2.38	0.54
1:A:2451:A:H1'	3:9P:25:ARG:NH1	2.23	0.54
1:A:2528:U:O2'	1:A:2530:A:OP1	2.24	0.54
5:C:106:PRO:HG2	5:C:109:LEU:HB2	1.89	0.54
5:C:128:THR:HA	5:C:190:THR:HA	1.89	0.54
5:C:160:TYR:HB3	5:C:193:GLU:HG3	1.89	0.54
16:T:2:ILE:HA	16:T:3:ARG:C	2.32	0.54
18:V:45:ASP:HA	18:V:48:MET:HE2	1.89	0.54
1:A:1229:C:H2'	1:A:1230:A:C8	2.43	0.54
8:G:94:ARG:HH11	8:G:94:ARG:HG3	1.72	0.54
22:Z:8:GLN:HB2	22:Z:28:LEU:HD13	1.88	0.54
1:A:572:A:N6	1:A:2029:G:H21	2.05	0.54
1:A:663:G:H5''	10:L:17:LYS:HZ2	1.73	0.54
1:A:1869:G:O2'	1:A:1872:A:N6	2.41	0.54
2:B:85:G:H2'	2:B:86:G:H8	1.73	0.54
5:C:142:ASN:HB3	5:C:190:THR:HG22	1.88	0.54
1:A:373:U:H2'	1:A:374:A:H8	1.73	0.54
1:A:639:U:H2'	1:A:640:C:C6	2.42	0.54
1:A:796:C:H2'	1:A:797:G:H8	1.72	0.54
1:A:1225:G:OP1	14:R:88:GLY:N	2.31	0.54
1:A:2037:A:H2'	1:A:2038:G:C8	2.42	0.54
1:A:2347:C:H5'	24:1:37:LYS:HZ3	1.73	0.54
1:A:2368:C:H2'	1:A:2369:A:C8	2.43	0.54
11:N:49:GLU:HA	11:N:52:ILE:HD12	1.90	0.54
27:K:105:ARG:NH2	28:P:40:GLN:OE1	2.41	0.54
1:A:64:A:H5'	16:T:77:ARG:HH12	1.73	0.54
1:A:328:U:O2'	17:U:65:GLN:NE2	2.41	0.54
1:A:663:G:O3'	10:L:17:LYS:NZ	2.39	0.54
1:A:934:U:H2'	1:A:935:C:H6	1.73	0.54
1:A:1288:G:OP2	1:A:1288:G:N2	2.41	0.54
2:B:114:C:H2'	2:B:115:A:C8	2.43	0.54
3:9P:41:ASP:HB2	3:9P:82:ARG:HG3	1.90	0.54
5:C:152:GLN:HA	5:C:155:ARG:HD2	1.90	0.54
9:J:38:GLY:HA3	9:J:50:THR:HG23	1.89	0.54
1:A:633:A:O2'	1:A:2404:U:OP1	2.26	0.54
1:A:645:C:H5'	1:A:647:G:N7	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:851:C:O2'	22:Z:42:ALA:O	2.25	0.54
1:A:2345:G:H4'	1:A:2346:A:H3'	1.90	0.54
9:J:13:ARG:NH1	9:J:49:ASP:OD2	2.41	0.54
9:J:44:TYR:HA	9:J:50:THR:HG21	1.89	0.54
1:A:965:C:N4	1:A:966:G:O6	2.42	0.53
1:A:1666:G:O2'	27:K:6:THR:OG1	2.25	0.53
3:9P:93:GLY:H	3:9P:108:MET:HB3	1.73	0.53
7:E:141:MET:HE1	7:E:143:LEU:HD12	1.90	0.53
16:T:2:ILE:HG23	16:T:4:GLU:N	2.23	0.53
30:H:7:ASP:CG	30:H:8:LYS:H	2.16	0.53
1:A:980:A:H2'	1:A:981:A:C4	2.43	0.53
1:A:2262:U:H5''	19:W:37:ARG:HH12	1.72	0.53
1:A:2310:C:H2'	1:A:2311:A:H4'	1.90	0.53
1:A:2340:A:H2'	1:A:2341:G:H8	1.73	0.53
1:A:2349:G:O6	1:A:2369:A:N6	2.42	0.53
3:9P:235:LEU:O	3:9P:236:GLU:HG2	2.09	0.53
3:9P:329:MET:HE2	3:9P:333:ILE:HD13	1.89	0.53
10:L:79:LEU:HG	10:L:112:LEU:HA	1.90	0.53
1:A:447:A:OP1	13:Q:4:LYS:NZ	2.36	0.53
1:A:559:G:N2	13:Q:48:ASP:OD1	2.41	0.53
1:A:692:C:H2'	1:A:693:A:H8	1.74	0.53
1:A:1500:G:O3'	5:C:100:ARG:NH2	2.41	0.53
1:A:1538:G:H2'	1:A:1539:U:C6	2.44	0.53
1:A:1597:A:H5''	1:A:1598:A:H5'	1.89	0.53
6:D:148:GLN:HB2	6:D:152:PRO:HG2	1.89	0.53
7:E:189:THR:HG23	7:E:192:ALA:H	1.73	0.53
8:G:17:LYS:HB3	8:G:24:THR:HB	1.90	0.53
17:U:25:LYS:N	17:U:34:ILE:O	2.37	0.53
19:W:47:VAL:HG11	19:W:55:LEU:HD23	1.90	0.53
1:A:581:C:H2'	1:A:582:A:C8	2.43	0.53
1:A:833:A:H2'	1:A:834:G:H8	1.73	0.53
1:A:1437:C:HO2'	1:A:1516:G:HO2'	1.56	0.53
22:Z:40:THR:HB	22:Z:43:ILE:HD12	1.89	0.53
29:6:48:VAL:HG12	29:6:78:ILE:HD12	1.91	0.53
1:A:741:U:H2'	1:A:742:A:H8	1.72	0.53
1:A:1528:A:OP2	1:A:1543:G:N2	2.41	0.53
1:A:1710:G:H2'	1:A:1711:A:C8	2.42	0.53
1:A:1715:G:O2'	1:A:1743:G:O6	2.22	0.53
1:A:2320:U:HO2'	1:A:2322:A:H62	1.55	0.53
1:A:2487:G:H2'	1:A:2488:G:H8	1.72	0.53
2:B:28:C:H2'	2:B:29:A:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:65:ASP:OD1	5:C:101:ARG:NH1	2.41	0.53
7:E:196:VAL:HA	7:E:199:MET:HG2	1.91	0.53
17:U:6:ARG:HG3	17:U:7:ASP:H	1.72	0.53
1:A:1140:C:H5'	9:J:26:GLY:HA3	1.89	0.53
1:A:1844:C:H4'	5:C:255:LYS:HE3	1.90	0.53
1:A:1969:A:H2'	1:A:1972:G:H21	1.72	0.53
1:A:2525:G:H2'	1:A:2526:G:H8	1.74	0.53
1:A:2643:G:H2'	1:A:2644:G:H8	1.73	0.53
10:L:96:LYS:HG2	10:L:101:ILE:HD11	1.89	0.53
27:K:77:ILE:HG13	28:P:71:ARG:NH1	2.24	0.53
1:A:16:C:H2'	1:A:17:G:C8	2.43	0.53
1:A:632:A:H4'	10:L:68:SER:HB2	1.90	0.53
1:A:1102:C:H2'	1:A:1103:A:H8	1.74	0.53
1:A:1229:C:H2'	1:A:1230:A:H8	1.74	0.53
1:A:1428:C:N4	1:A:1570:A:OP2	2.38	0.53
1:A:1638:C:O2	1:A:2698:U:O2'	2.26	0.53
1:A:1825:U:H4'	5:C:231:HIS:HE1	1.73	0.53
3:9P:200:VAL:HG12	3:9P:210:VAL:HG12	1.90	0.53
9:J:80:HIS:CD2	9:J:81:ILE:H	2.27	0.53
23:0:42:ILE:HG22	23:0:48:TYR:HB2	1.88	0.53
1:A:171:U:H2'	1:A:172:A:C8	2.44	0.53
1:A:249:C:OP1	10:L:59:ARG:NH2	2.42	0.53
1:A:937:C:H2'	1:A:938:G:C8	2.44	0.53
1:A:2204:G:O2'	5:C:147:PRO:O	2.24	0.53
1:A:2820:A:N3	11:N:4:ARG:HD2	2.24	0.53
1:A:2861:U:H2'	1:A:2862:G:H8	1.73	0.53
3:9P:256:VAL:HG13	3:9P:259:ALA:HB3	1.91	0.53
6:D:37:VAL:HG13	6:D:48:ILE:HG22	1.91	0.53
7:E:58:LYS:NZ	7:E:70:SER:O	2.29	0.53
20:X:31:ASN:OD1	20:X:33:HIS:NE2	2.42	0.53
29:6:45:SER:HB3	29:6:75:ALA:HB3	1.89	0.53
1:A:580:U:H2'	1:A:581:C:H6	1.74	0.53
1:A:1205:A:O2'	7:E:166:LYS:NZ	2.41	0.53
1:A:2529:G:O2'	3:9P:58:ASP:OD1	2.27	0.53
27:K:90:ASN:OD1	27:K:91:SER:N	2.42	0.53
1:A:926:G:H2'	1:A:927:A:H8	1.74	0.52
1:A:2013:A:N6	1:A:2014:A:N1	2.57	0.52
1:A:78:U:O4	1:A:108:G:O6	2.27	0.52
1:A:242:G:O2'	1:A:254:G:O6	2.26	0.52
1:A:1682:G:OP2	1:A:1699:G:N2	2.33	0.52
3:9P:8:SER:HB3	3:9P:153:LEU:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:29:VAL:O	11:N:78:LYS:NZ	2.25	0.52
19:W:36:GLN:NE2	19:W:41:PHE:H	1.98	0.52
30:H:39:ALA:HB1	30:H:44:ILE:HG23	1.91	0.52
1:A:1816:C:H5''	5:C:61:TYR:HE2	1.74	0.52
1:A:2241:A:H2'	1:A:2242:G:C8	2.44	0.52
26:I:15:GLY:HA2	26:I:50:LYS:HB3	1.91	0.52
1:A:1864:U:OP1	1:A:2410:G:O2'	2.28	0.52
1:A:2845:U:H4'	28:P:52:ARG:HE	1.75	0.52
5:C:106:PRO:HD2	5:C:109:LEU:HD13	1.91	0.52
10:L:100:ILE:HG23	10:L:101:ILE:HG23	1.90	0.52
1:A:306:U:H2'	1:A:307:G:O4'	2.09	0.52
1:A:443:A:N7	7:E:40:ARG:HD3	2.24	0.52
1:A:552:U:H2'	1:A:553:G:H8	1.74	0.52
1:A:1026:G:H2'	1:A:1027:A:H8	1.73	0.52
1:A:1812:U:H2'	1:A:1813:G:H8	1.74	0.52
1:A:1903:G:H2'	1:A:1904:G:H8	1.75	0.52
1:A:2885:G:N1	23:O:29:VAL:O	2.39	0.52
11:N:12:ARG:CZ	11:N:20:MET:HE1	2.40	0.52
13:Q:87:VAL:HG13	14:R:49:ILE:HD11	1.90	0.52
28:P:38:ARG:NH2	29:6:32:SER:O	2.43	0.52
31:F:56:LEU:HB2	31:F:64:PRO:HG3	1.91	0.52
1:A:989:G:OP2	22:Z:11:SER:OG	2.22	0.52
7:E:126:VAL:O	7:E:156:ASN:ND2	2.43	0.52
31:F:128:SER:O	31:F:129:MET:HE2	2.09	0.52
1:A:2441:U:H2'	1:A:2442:C:H6	1.75	0.52
16:T:66:LYS:H	16:T:77:ARG:HB2	1.74	0.52
1:A:1364:G:H3'	20:X:1:SER:HA	1.90	0.52
1:A:2133:G:H22	1:A:2157:G:H1'	1.74	0.52
1:A:2292:U:H2'	1:A:2293:G:C8	2.44	0.52
1:A:13:A:O2'	1:A:15:G:N7	2.43	0.52
1:A:541:A:N6	1:A:553:G:O6	2.43	0.52
1:A:577:G:O2'	1:A:1254:A:OP1	2.28	0.52
1:A:698:C:H5''	1:A:699:A:H5'	1.90	0.52
1:A:1734:G:H2'	1:A:1735:A:C8	2.45	0.52
1:A:2395:C:H2'	1:A:2396:G:H8	1.75	0.52
3:9P:90:VAL:HG11	3:9P:94:THR:HG21	1.92	0.52
10:L:58:TYR:O	10:L:63:LYS:NZ	2.43	0.52
1:A:171:U:H2'	1:A:172:A:H8	1.74	0.52
1:A:1043:C:O2	1:A:1048:A:O2'	2.26	0.52
1:A:2057:G:H2'	1:A:2058:A:C8	2.45	0.52
1:A:2553:G:C2	1:A:2583:G:H1'	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2687:U:H2'	1:A:2688:G:O4'	2.10	0.52
11:N:51:LEU:HD21	11:N:69:ARG:HD2	1.92	0.52
1:A:188:G:H5'	20:X:13:THR:HG21	1.92	0.51
7:E:32:VAL:HG13	7:E:178:VAL:HG12	1.91	0.51
10:L:79:LEU:HD11	10:L:112:LEU:HB2	1.92	0.51
16:T:59:ASN:HB2	16:T:84:TYR:HB2	1.91	0.51
1:A:580:U:H2'	1:A:581:C:C6	2.46	0.51
1:A:660:C:H2'	1:A:661:A:C8	2.44	0.51
1:A:710:U:H2'	1:A:711:G:H8	1.74	0.51
2:B:49:C:OP2	12:O:30:ARG:NH1	2.43	0.51
11:N:96:ARG:HH11	11:N:116:VAL:HG13	1.74	0.51
1:A:201:C:OP1	20:X:17:ARG:NH1	2.32	0.51
1:A:1400:U:H2'	1:A:1401:G:C8	2.46	0.51
5:C:116:GLN:O	5:C:127:ASN:ND2	2.37	0.51
5:C:162:GLN:HB2	5:C:174:ARG:HB3	1.91	0.51
1:A:1567:G:OP2	5:C:82:TYR:OH	2.27	0.51
1:A:1997:C:H2'	1:A:1998:A:C8	2.44	0.51
1:A:2123:G:H2'	1:A:2124:G:C8	2.44	0.51
1:A:2898:U:H2'	1:A:2899:A:H8	1.75	0.51
22:Z:10:ARG:HH21	22:Z:10:ARG:HG2	1.76	0.51
29:6:69:VAL:HG23	29:6:80:VAL:HG12	1.93	0.51
1:A:2090:A:N6	1:A:2230:G:O6	2.43	0.51
2:B:14:U:OP2	2:B:70:C:O2'	2.28	0.51
10:L:55:MET:HE2	10:L:59:ARG:HD3	1.91	0.51
10:L:78:ARG:HB3	10:L:113:ALA:HB3	1.91	0.51
1:A:5:A:H2'	1:A:6:A:C8	2.45	0.51
1:A:1223:G:N7	14:R:71:LYS:NZ	2.58	0.51
1:A:1309:G:H4'	25:2:7:PRO:HB2	1.93	0.51
1:A:2072:C:H2'	1:A:2073:C:H6	1.76	0.51
1:A:2076:U:OP2	1:A:2238:G:N2	2.44	0.51
1:A:2391:G:O2'	1:A:2424:C:N4	2.44	0.51
8:G:59:ASP:OD1	8:G:60:GLY:N	2.42	0.51
1:A:636:G:N7	10:L:109:LYS:NZ	2.46	0.51
1:A:2298:A:N6	1:A:2318:G:N2	2.59	0.51
1:A:2512:C:H5''	6:D:127:PHE:CE1	2.46	0.51
1:A:2515:C:H2'	1:A:2516:A:H8	1.76	0.51
1:A:2685:G:H2'	1:A:2686:G:H8	1.75	0.51
6:D:128:ARG:H	6:D:128:ARG:HD3	1.76	0.51
8:G:4:ALA:HB1	8:G:51:PHE:HB2	1.92	0.51
9:J:98:GLU:CD	9:J:98:GLU:H	2.18	0.51
1:A:564:C:O4'	13:Q:36:GLN:NE2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1013:C:H2'	1:A:1014:A:C8	2.45	0.51
1:A:1045:C:O2	1:A:1047:G:N1	2.43	0.51
1:A:1907:G:O6	1:A:1923:U:O2	2.29	0.51
1:A:2528:U:O2	1:A:2535:G:O6	2.29	0.51
2:B:40:U:H3'	2:B:41:G:H4'	1.93	0.51
3:9P:230:ARG:HA	3:9P:233:LYS:NZ	2.26	0.51
6:D:116:LYS:HZ3	6:D:165:MET:HE3	1.76	0.51
8:G:116:LEU:HD23	8:G:120:ILE:HG22	1.93	0.51
17:U:7:ASP:HB3	17:U:23:LYS:HD3	1.92	0.51
1:A:184:C:H2'	1:A:185:G:C8	2.45	0.51
1:A:968:C:H2'	1:A:969:G:C8	2.43	0.51
1:A:970:U:H2'	1:A:971:G:H8	1.76	0.51
1:A:1952:A:N6	27:K:22:ILE:HD11	2.25	0.51
1:A:2642:G:H2'	1:A:2643:G:H8	1.74	0.51
1:A:2780:G:O6	9:J:99:ARG:NH1	2.44	0.51
1:A:2822:G:O2'	1:A:2825:G:N1	2.43	0.51
3:9P:261:ILE:O	3:9P:265:GLU:HG3	2.11	0.51
1:A:304:U:H2'	1:A:305:C:C6	2.46	0.50
1:A:377:G:N2	1:A:397:U:O2	2.35	0.50
1:A:685:A:C2	1:A:787:C:H1'	2.46	0.50
1:A:750:A:OP1	1:A:1615:C:N4	2.41	0.50
1:A:827:U:O2'	1:A:2068:U:N3	2.44	0.50
1:A:1081:U:H4'	26:I:123:ALA:HB1	1.92	0.50
1:A:2849:U:O4	28:P:20:ARG:NH2	2.44	0.50
1:A:25:U:H3	1:A:515:A:H61	1.59	0.50
1:A:813:U:H2'	1:A:814:C:H6	1.77	0.50
1:A:832:U:H2'	1:A:833:A:C8	2.44	0.50
1:A:1035:U:H2'	1:A:1036:G:H8	1.76	0.50
5:C:75:ALA:HB3	5:C:115:ILE:HG13	1.94	0.50
9:J:46:PRO:HD3	13:Q:59:LEU:HD13	1.93	0.50
10:L:17:LYS:HB2	10:L:27:LEU:HD21	1.92	0.50
16:T:8:LEU:HD21	21:Y:22:LEU:HA	1.93	0.50
31:F:65:LEU:O	31:F:86:CYS:HA	2.10	0.50
1:A:24:G:H2'	1:A:25:U:C6	2.46	0.50
1:A:1746:A:H2'	1:A:1747:U:C6	2.47	0.50
1:A:2294:G:OP1	12:O:98:GLN:NE2	2.39	0.50
1:A:2543:G:H2'	1:A:2544:G:C8	2.46	0.50
5:C:250:GLN:OE1	5:C:254:LYS:HG2	2.11	0.50
12:O:55:GLU:HG3	12:O:57:ALA:H	1.77	0.50
1:A:305:C:H2'	1:A:306:U:C6	2.46	0.50
1:A:2075:U:OP1	5:C:241:LYS:NZ	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2548:U:O2	27:K:23:LYS:NZ	2.37	0.50
3:9P:23:PHE:HA	3:9P:34:PRO:HA	1.92	0.50
5:C:32:LEU:HD12	5:C:63:ILE:HB	1.93	0.50
25:2:3:ARG:NE	25:2:3:ARG:HA	2.27	0.50
28:P:88:ARG:HE	28:P:112:ARG:NH2	2.08	0.50
29:6:12:ASP:OD1	29:6:13:LYS:N	2.44	0.50
1:A:280:U:O4	1:A:361:G:N2	2.44	0.50
1:A:1358:G:O2'	1:A:1373:A:N6	2.44	0.50
1:A:2063:C:OP1	1:A:2439:A:N6	2.45	0.50
8:G:86:LEU:HD23	8:G:132:LEU:HD23	1.93	0.50
28:P:23:ASP:OD1	28:P:89:GLY:N	2.39	0.50
1:A:224:U:O4	1:A:419:U:O2'	2.29	0.50
1:A:1148:U:H2'	1:A:1149:G:C8	2.46	0.50
1:A:1204:A:N6	1:A:1242:U:O4	2.45	0.50
1:A:1563:U:H2'	1:A:1564:C:C6	2.47	0.50
1:A:2065:C:H2'	1:A:2066:C:H6	1.76	0.50
1:A:2723:C:H4'	11:N:1:MET:HE2	1.94	0.50
8:G:77:GLY:HA2	8:G:81:GLY:HA2	1.93	0.50
17:U:40:LEU:HG	17:U:59:GLU:OE2	2.11	0.50
28:P:8:GLU:OE2	28:P:54:LEU:N	2.45	0.50
1:A:19:A:H2'	1:A:20:C:C6	2.47	0.50
1:A:741:U:H2'	1:A:742:A:C8	2.46	0.50
1:A:1820:U:N3	5:C:158:GLY:HA3	2.27	0.50
1:A:2199:A:N1	1:A:2226:C:N4	2.60	0.50
2:B:49:C:H2'	2:B:50:A:C8	2.47	0.50
16:T:8:LEU:HD23	21:Y:21:LEU:HB3	1.94	0.50
1:A:65:U:H2'	1:A:66:C:H6	1.75	0.50
1:A:937:C:H2'	1:A:938:G:H8	1.76	0.50
1:A:1709:U:H2'	1:A:1710:G:H8	1.77	0.50
1:A:2452:C:H3'	1:A:2453:A:H8	1.77	0.50
2:B:86:G:OP2	2:B:88:C:N4	2.45	0.50
1:A:64:A:H2'	1:A:65:U:C6	2.47	0.50
1:A:76:C:H1'	21:Y:55:THR:HG21	1.93	0.50
1:A:542:C:H2'	1:A:543:G:H8	1.77	0.50
1:A:848:C:H2'	1:A:849:A:C8	2.46	0.50
1:A:928:A:H2'	1:A:929:U:C6	2.47	0.50
1:A:1807:G:O2'	1:A:1809:A:N6	2.39	0.50
1:A:2063:C:O2'	1:A:2064:C:H5'	2.12	0.50
18:V:17:SER:HB3	18:V:27:PRO:HG3	1.94	0.50
1:A:225:C:N3	1:A:231:A:N6	2.60	0.49
1:A:605:G:OP1	7:E:99:LYS:NZ	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1276:A:N6	1:A:1645:G:O6	2.45	0.49
1:A:1418:G:H1'	1:A:1581:G:N2	2.27	0.49
1:A:1564:C:H2'	1:A:1565:C:C6	2.47	0.49
1:A:1801:A:N6	5:C:261:ARG:HH12	2.09	0.49
1:A:1817:G:H5''	5:C:86:ARG:HH12	1.76	0.49
2:B:49:C:H2'	2:B:50:A:H8	1.77	0.49
9:J:98:GLU:HB2	9:J:124:VAL:HG23	1.94	0.49
13:Q:108:LEU:HD22	14:R:48:LYS:HZ1	1.76	0.49
15:S:28:LYS:O	15:S:32:ALA:N	2.42	0.49
31:F:56:LEU:HD12	31:F:64:PRO:HB3	1.94	0.49
1:A:755:U:H2'	1:A:756:A:C8	2.46	0.49
1:A:1357:C:H2'	1:A:1358:G:O4'	2.13	0.49
3:9P:60:ARG:HG3	3:9P:61:PHE:HD1	1.76	0.49
6:D:24:VAL:HG12	6:D:178:VAL:HG21	1.93	0.49
1:A:749:A:H5'	1:A:1271:G:H1'	1.95	0.49
1:A:770:G:OP2	25:2:11:LYS:NZ	2.44	0.49
1:A:1651:G:H4'	11:N:39:PRO:HG2	1.93	0.49
1:A:184:C:H2'	1:A:185:G:H8	1.77	0.49
1:A:1830:C:H2'	1:A:1831:G:C8	2.44	0.49
1:A:2305:U:C2	31:F:132:ARG:HA	2.47	0.49
1:A:2688:G:N1	1:A:2720:U:OP2	2.31	0.49
14:R:37:GLU:HB2	14:R:53:PHE:CD1	2.47	0.49
17:U:95:PHE:O	17:U:99:SER:HA	2.12	0.49
1:A:222:A:H61	1:A:232:G:H1'	1.77	0.49
1:A:781:A:OP1	5:C:216:ARG:NH2	2.45	0.49
1:A:873:C:H2'	1:A:874:G:C8	2.48	0.49
1:A:1509:A:HO2'	1:A:1510:G:H8	1.59	0.49
1:A:2364:C:H2'	1:A:2365:G:O4'	2.13	0.49
1:A:2898:U:H2'	1:A:2899:A:C8	2.47	0.49
16:T:37:ASP:OD1	16:T:38:ALA:N	2.45	0.49
1:A:302:C:H2'	1:A:303:G:C8	2.47	0.49
1:A:438:G:H2'	1:A:439:A:C8	2.47	0.49
1:A:693:A:O2'	1:A:1353:A:N3	2.39	0.49
1:A:746:U:HO2'	1:A:2611:C:HO2'	1.55	0.49
1:A:1012:U:O4	9:J:30:THR:HG21	2.12	0.49
1:A:1364:G:N2	1:A:1367:A:OP2	2.29	0.49
1:A:1380:G:H1'	1:A:1569:A:H61	1.77	0.49
1:A:2553:G:N2	1:A:2583:G:H1'	2.28	0.49
2:B:70:C:H2'	2:B:71:C:H6	1.78	0.49
3:9P:215:PRO:HD2	3:9P:231:PHE:HB3	1.94	0.49
7:E:18:THR:HA	7:E:106:LYS:HE3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:R:71:LYS:HE3	14:R:90:ARG:HD2	1.94	0.49
26:I:20:SER:HA	26:I:24:GLY:HA2	1.94	0.49
31:F:70:ARG:C	31:F:71:LYS:HD3	2.38	0.49
1:A:18:U:H2'	1:A:19:A:H8	1.78	0.49
1:A:1709:U:H2'	1:A:1710:G:C8	2.47	0.49
1:A:1819:A:H5''	5:C:159:THR:HG21	1.95	0.49
1:A:2514:U:H2'	1:A:2515:C:C6	2.47	0.49
1:A:2883:A:OP2	23:O:49:ARG:NH2	2.35	0.49
13:Q:49:ARG:O	13:Q:53:LYS:NZ	2.42	0.49
1:A:605:G:O2'	1:A:657:U:O2	2.31	0.49
1:A:833:A:H2'	1:A:834:G:C8	2.47	0.49
1:A:1352:U:H1'	1:A:1570:A:H2	1.78	0.49
1:A:1570:A:H2'	1:A:1571:A:C8	2.48	0.49
5:C:92:LEU:HD11	5:C:100:ARG:HB3	1.95	0.49
29:6:79:VAL:HG12	29:6:88:HIS:HA	1.95	0.49
1:A:275:C:N3	1:A:362:A:N6	2.61	0.49
1:A:995:C:OP1	13:Q:52:ARG:NH1	2.46	0.49
1:A:1022:G:N7	1:A:1140:C:N4	2.61	0.49
1:A:1501:G:H2'	1:A:1502:A:H8	1.78	0.49
1:A:1710:G:H2'	1:A:1711:A:H8	1.78	0.49
2:B:113:C:H2'	2:B:114:C:C6	2.48	0.49
14:R:98:ILE:HD12	14:R:101:ILE:HD11	1.93	0.49
23:O:27:LEU:HD12	23:O:36:LYS:HB3	1.94	0.49
1:A:1024:G:O2'	1:A:1144:A:O2'	2.22	0.49
1:A:1590:A:H2'	1:A:1591:A:H8	1.78	0.49
1:A:2037:A:H2'	1:A:2038:G:H8	1.76	0.49
7:E:108:ILE:HD11	7:E:181:ILE:HG21	1.94	0.49
8:G:25:ILE:HD13	8:G:74:MET:HE3	1.94	0.49
1:A:24:G:H1'	15:S:77:ASP:HB3	1.95	0.48
1:A:247:G:O2'	1:A:250:G:O6	2.31	0.48
1:A:347:A:H2'	1:A:348:A:C8	2.48	0.48
1:A:1400:U:H2'	1:A:1401:G:H8	1.77	0.48
1:A:2014:A:O2'	1:A:2015:A:O4'	2.21	0.48
3:9P:74:ALA:HB3	3:9P:78:CYS:HB2	1.95	0.48
11:N:55:ALA:HB2	11:N:79:LEU:HD23	1.95	0.48
18:V:51:GLN:HG2	18:V:86:LEU:HD11	1.95	0.48
1:A:226:A:H5'	1:A:257:C:H4'	1.94	0.48
1:A:404:A:H4'	1:A:405:U:O5'	2.12	0.48
1:A:1463:C:H2'	1:A:1464:G:C8	2.46	0.48
1:A:2815:C:H2'	1:A:2816:G:H8	1.78	0.48
1:A:2883:A:OP1	23:O:48:TYR:OH	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:I:79:LEU:HA	26:I:83:ALA:HB3	1.96	0.48
1:A:829:A:N6	1:A:2247:A:O2'	2.40	0.48
1:A:929:U:H2'	1:A:930:G:C8	2.48	0.48
1:A:1005:C:H2'	1:A:1006:C:C6	2.48	0.48
1:A:1272:A:O2'	1:A:1274:A:OP1	2.26	0.48
1:A:1361:G:H2'	1:A:1362:C:C6	2.48	0.48
1:A:1447:C:H2'	1:A:1448:G:H8	1.77	0.48
1:A:1716:U:H2'	1:A:1717:A:H8	1.78	0.48
1:A:2417:C:H2'	1:A:2418:A:H8	1.77	0.48
1:A:2544:G:H2'	1:A:2545:G:C8	2.48	0.48
2:B:1:U:OP2	18:V:89:ILE:N	2.37	0.48
26:I:133:ARG:H	26:I:137:LEU:HD12	1.78	0.48
27:K:18:ARG:HB3	27:K:45:GLU:HB2	1.94	0.48
1:A:29:U:H2'	1:A:30:G:H8	1.78	0.48
1:A:341:C:H2'	1:A:342:A:C8	2.49	0.48
1:A:577:G:H2'	1:A:578:G:C8	2.48	0.48
1:A:1424:G:H2'	1:A:1425:G:C8	2.49	0.48
1:A:1431:A:H2'	1:A:1432:G:H8	1.78	0.48
1:A:2047:C:H2'	1:A:2048:G:H8	1.78	0.48
1:A:2398:U:H2'	1:A:2399:G:H8	1.77	0.48
1:A:2425:A:H4'	1:A:2426:A:O5'	2.14	0.48
1:A:2543:G:H21	1:A:2646:C:H5''	1.77	0.48
18:V:78:GLN:NE2	18:V:88:HIS:HB3	2.28	0.48
28:P:33:GLU:OE2	28:P:38:ARG:NE	2.42	0.48
1:A:1518:C:H2'	1:A:1519:G:C8	2.49	0.48
1:A:2241:A:H2'	1:A:2242:G:H8	1.78	0.48
9:J:49:ASP:OD1	9:J:121:LYS:NZ	2.46	0.48
18:V:73:LYS:HZ3	18:V:74:ALA:H	1.60	0.48
1:A:2195:U:H2'	1:A:2196:C:H6	1.78	0.48
1:A:2548:U:O2'	27:K:4:GLU:OE2	2.31	0.48
1:A:2863:C:H2'	1:A:2864:G:H8	1.78	0.48
13:Q:55:GLN:HA	13:Q:58:GLN:HB3	1.95	0.48
14:R:49:ILE:O	14:R:49:ILE:HG13	2.13	0.48
22:Z:19:HIS:HD1	22:Z:50:VAL:HG12	1.77	0.48
1:A:151:C:H2'	1:A:152:A:H8	1.77	0.48
1:A:315:G:H2'	1:A:316:C:C6	2.49	0.48
1:A:370:G:O2'	1:A:424:G:OP1	2.27	0.48
1:A:904:G:H2'	1:A:905:A:C8	2.48	0.48
3:9P:323:ASP:OD1	3:9P:324:LEU:N	2.47	0.48
5:C:194:VAL:HG22	5:C:195:GLY:H	1.77	0.48
12:O:67:ASN:OD1	12:O:68:LYS:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:2:ILE:HG23	16:T:4:GLU:HB2	1.94	0.48
30:H:28:ASN:HA	30:H:32:PRO:HG2	1.96	0.48
30:H:132:PHE:HB2	30:H:140:ALA:HB3	1.94	0.48
31:F:128:SER:HA	31:F:154:THR:HA	1.96	0.48
1:A:477:A:N6	1:A:501:A:OP1	2.46	0.48
1:A:665:U:H2'	1:A:666:A:C8	2.48	0.48
1:A:1039:A:N6	1:A:1116:G:H1	2.12	0.48
1:A:1164:C:H2'	1:A:1165:A:C8	2.49	0.48
1:A:1365:A:OP1	20:X:2:ARG:HD3	2.13	0.48
1:A:1431:A:H2'	1:A:1432:G:C8	2.49	0.48
1:A:1628:G:H2'	1:A:1629:U:C6	2.49	0.48
1:A:2776:A:O2'	1:A:2782:G:N7	2.40	0.48
3:9P:44:ASP:OD1	3:9P:120:GLY:N	2.47	0.48
13:Q:105:PHE:HA	13:Q:108:LEU:HD23	1.96	0.48
20:X:30:PRO:HB2	20:X:32:LEU:HG	1.94	0.48
20:X:38:TRP:NE1	20:X:40:GLU:OE1	2.46	0.48
27:K:94:PRO:HD2	27:K:114:LYS:HG3	1.96	0.48
29:6:91:GLN:HG3	29:6:93:GLU:H	1.79	0.48
1:A:411:G:OP2	1:A:2406:A:O2'	2.23	0.48
1:A:1015:U:H2'	1:A:1016:G:H8	1.79	0.48
1:A:1542:U:H2'	1:A:1543:G:O4'	2.13	0.48
1:A:1747:U:H2'	1:A:1748:C:C6	2.49	0.48
1:A:1801:A:N6	1:A:2201:G:O2'	2.34	0.48
1:A:2564:A:C6	1:A:2647:U:H4'	2.49	0.48
1:A:2626:C:H2'	1:A:2627:G:H8	1.79	0.48
1:A:2847:U:H2'	1:A:2848:G:O4'	2.14	0.48
1:A:2876:G:H5''	28:P:2:ASN:HB2	1.95	0.48
3:9P:167:MET:HE1	3:9P:258:ASN:ND2	2.28	0.48
29:6:38:ILE:HB	29:6:87:VAL:HG12	1.95	0.48
31:F:56:LEU:HD13	31:F:88:VAL:HG23	1.95	0.48
1:A:667:U:H2'	1:A:668:A:O4'	2.14	0.48
1:A:2116:G:O6	1:A:2171:A:N6	2.46	0.48
1:A:2386:A:O2'	19:W:52:ASP:OD1	2.32	0.48
1:A:2543:G:H2'	1:A:2544:G:H8	1.78	0.48
1:A:2626:C:H2'	1:A:2627:G:C8	2.49	0.48
1:A:2707:U:H2'	1:A:2708:G:C8	2.49	0.48
17:U:17:ASP:OD1	17:U:17:ASP:N	2.43	0.48
26:I:48:ILE:HG13	26:I:49:GLU:N	2.29	0.48
27:K:5:GLN:HA	27:K:20:MET:SD	2.54	0.48
1:A:2182:U:H2'	1:A:2183:A:H8	1.78	0.47
5:C:141:HIS:ND1	5:C:192:GLY:O	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:S:24:ILE:HD13	15:S:36:LEU:HD11	1.96	0.47
1:A:300:A:OP2	17:U:81:ARG:NH2	2.46	0.47
1:A:417:C:H2'	1:A:418:C:C6	2.50	0.47
1:A:813:U:H2'	1:A:814:C:C6	2.49	0.47
1:A:981:A:OP2	1:A:982:C:N4	2.46	0.47
1:A:1496:A:H2'	1:A:1498:C:C5	2.49	0.47
1:A:1813:G:H21	5:C:50:THR:HB	1.79	0.47
1:A:2836:U:H2'	1:A:2837:A:C8	2.49	0.47
16:T:11:LEU:HD11	16:T:32:LEU:HD22	1.96	0.47
20:X:9:LYS:HZ1	20:X:53:LYS:HD3	1.80	0.47
26:I:80:LYS:HB3	26:I:86:LYS:HD3	1.95	0.47
28:P:29:VAL:HG13	28:P:79:VAL:HG12	1.95	0.47
1:A:25:U:H3	1:A:515:A:N6	2.11	0.47
1:A:286:U:H2'	1:A:287:G:H8	1.79	0.47
1:A:335:C:O2	17:U:67:SER:OG	2.20	0.47
1:A:347:A:H2'	1:A:348:A:H8	1.78	0.47
1:A:542:C:H2'	1:A:543:G:C8	2.49	0.47
1:A:1541:C:H2'	1:A:1542:U:H6	1.78	0.47
1:A:1734:G:H2'	1:A:1735:A:H8	1.79	0.47
1:A:2027:G:H2'	1:A:2028:U:C6	2.50	0.47
1:A:2618:G:H21	6:D:155:VAL:HG21	1.79	0.47
1:A:2863:C:H2'	1:A:2864:G:C8	2.48	0.47
3:9P:115:LEU:HD12	3:9P:116:LEU:H	1.80	0.47
26:I:16:MET:SD	26:I:17:ALA:N	2.87	0.47
26:I:55:PRO:HD3	26:I:74:PRO:HD3	1.95	0.47
1:A:514:A:N3	1:A:581:C:O2'	2.39	0.47
1:A:639:U:H2'	1:A:640:C:H6	1.79	0.47
1:A:692:C:H2'	1:A:693:A:C8	2.49	0.47
1:A:2848:G:H1'	1:A:2868:A:H61	1.78	0.47
5:C:257:ARG:NH1	5:C:263:ASP:OD1	2.28	0.47
1:A:1438:U:H2'	1:A:1439:A:H8	1.80	0.47
1:A:1592:C:H2'	1:A:1593:A:C8	2.50	0.47
1:A:2333:A:H3'	19:W:71:LYS:HZ3	1.80	0.47
1:A:2707:U:H2'	1:A:2708:G:H8	1.79	0.47
1:A:2838:G:C4	1:A:2839:G:C8	3.03	0.47
2:B:85:G:H2'	2:B:86:G:C8	2.49	0.47
6:D:12:THR:HG22	6:D:13:ARG:N	2.27	0.47
18:V:7:GLU:OE1	18:V:7:GLU:N	2.47	0.47
27:K:21:CYS:HA	27:K:41:ILE:HA	1.96	0.47
31:F:37:MET:HG3	31:F:149:ARG:HH21	1.80	0.47
1:A:302:C:H2'	1:A:303:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:566:U:H2'	1:A:567:U:C6	2.49	0.47
1:A:1790:C:O2'	5:C:207:ALA:HB2	2.14	0.47
1:A:2261:C:C5	19:W:12:SER:HB3	2.50	0.47
1:A:2372:U:H2'	1:A:2373:G:H8	1.79	0.47
3:9P:254:ASP:O	3:9P:258:ASN:ND2	2.47	0.47
6:D:27:ILE:HB	6:D:187:LEU:HB3	1.96	0.47
18:V:9:ARG:HH21	18:V:12:GLN:HA	1.79	0.47
28:P:48:ALA:HB1	28:P:95:LYS:HZ3	1.80	0.47
1:A:358:U:H2'	1:A:359:G:H8	1.78	0.47
1:A:970:U:H2'	1:A:971:G:C8	2.49	0.47
1:A:1435:G:H2'	1:A:1436:G:C8	2.49	0.47
1:A:1907:G:O6	1:A:1923:U:C2	2.67	0.47
1:A:2074:U:H2'	1:A:2075:U:C6	2.50	0.47
1:A:2333:A:H3'	19:W:71:LYS:NZ	2.30	0.47
1:A:2395:C:H2'	1:A:2396:G:C8	2.50	0.47
1:A:2578:G:N2	6:D:130:GLN:OE1	2.48	0.47
1:A:2692:G:H1'	1:A:2847:U:H1'	1.97	0.47
6:D:32:ASN:HB3	6:D:50:VAL:HG21	1.97	0.47
3:9P:190:PRO:O	3:9P:192:THR:N	2.48	0.47
3:9P:214:ILE:HD11	3:9P:235:LEU:HD22	1.96	0.47
7:E:21:ARG:HH12	7:E:106:LYS:HB2	1.79	0.47
19:W:7:ARG:HA	19:W:7:ARG:HD2	1.65	0.47
1:A:500:G:N1	1:A:503:A:OP2	2.35	0.47
1:A:1130:U:C2	1:A:2025:C:H5'	2.50	0.47
1:A:1251:C:H5	13:Q:5:ARG:HH22	1.63	0.47
1:A:1299:G:H5''	1:A:1300:G:H5''	1.96	0.47
1:A:1442:U:H2'	1:A:1443:U:C6	2.50	0.47
9:J:30:THR:HA	9:J:108:MET:HE2	1.97	0.47
12:O:110:ALA:HB1	12:O:115:LEU:HD22	1.96	0.47
1:A:413:C:H2'	1:A:414:C:C6	2.50	0.47
1:A:459:U:H2'	1:A:460:A:H8	1.79	0.47
1:A:523:C:H5''	1:A:540:C:O2'	2.14	0.47
1:A:1038:G:H2'	1:A:1039:A:C8	2.50	0.47
1:A:1167:C:H2'	1:A:1168:G:C8	2.50	0.47
1:A:1441:G:H2'	1:A:1442:U:H6	1.78	0.47
1:A:1802:A:H2'	1:A:1803:A:C8	2.50	0.47
17:U:48:VAL:HG13	17:U:50:ALA:O	2.15	0.47
1:A:373:U:H2'	1:A:374:A:C8	2.51	0.46
1:A:640:C:H2'	1:A:641:U:C6	2.50	0.46
1:A:1190:G:H2'	1:A:1191:G:H8	1.79	0.46
1:A:1571:A:H2'	1:A:1572:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2320:U:HO2'	1:A:2322:A:N6	2.13	0.46
1:A:2398:U:H2'	1:A:2399:G:C8	2.49	0.46
1:A:2511:U:H5''	6:D:128:ARG:HH12	1.79	0.46
10:L:55:MET:HE3	10:L:56:PRO:HD2	1.98	0.46
20:X:4:CYS:HB3	20:X:9:LYS:H	1.79	0.46
27:K:76:VAL:O	28:P:71:ARG:NH2	2.47	0.46
1:A:373:U:OP2	20:X:53:LYS:NZ	2.48	0.46
1:A:565:C:H2'	1:A:566:U:C6	2.50	0.46
1:A:1249:U:H2'	10:L:18:ARG:HH22	1.80	0.46
1:A:1282:U:H3	1:A:1286:A:H62	1.64	0.46
2:B:42:C:C6	31:F:65:LEU:HD11	2.50	0.46
2:B:114:C:H2'	2:B:115:A:H8	1.78	0.46
16:T:26:LYS:HE3	16:T:26:LYS:HB3	1.77	0.46
31:F:35:LEU:N	31:F:88:VAL:O	2.49	0.46
1:A:76:C:H2'	1:A:77:G:H8	1.81	0.46
1:A:196:A:H61	1:A:831:G:N2	2.14	0.46
1:A:951:C:N4	1:A:952:G:O6	2.49	0.46
1:A:2291:U:H2'	1:A:2292:U:C6	2.50	0.46
1:A:2505:G:N2	1:A:2610:C:O2	2.48	0.46
1:A:2639:A:H2'	1:A:2640:G:O4'	2.15	0.46
1:A:-2:U:H2'	1:A:-1:A:C8	2.50	0.46
1:A:848:C:H2'	1:A:849:A:H8	1.80	0.46
1:A:934:U:H2'	1:A:935:C:C6	2.50	0.46
1:A:1048:A:H1'	1:A:1112:G:N2	2.31	0.46
1:A:1443:U:H2'	1:A:1444:G:C8	2.45	0.46
1:A:1693:U:O4	1:A:1976:U:O2'	2.26	0.46
7:E:12:LEU:HD23	7:E:12:LEU:H	1.80	0.46
1:A:753:A:H2'	1:A:754:U:H6	1.80	0.46
1:A:756:A:H2'	1:A:757:G:O4'	2.16	0.46
1:A:930:G:H1'	22:Z:24:LEU:HD21	1.96	0.46
1:A:1057:A:N6	1:A:1087:G:OP2	2.49	0.46
1:A:1826:G:H2'	1:A:1827:U:C6	2.50	0.46
1:A:1952:A:C2	1:A:2560:A:H1'	2.50	0.46
3:9P:191:PHE:CE2	3:9P:193:THR:HB	2.51	0.46
3:9P:281:VAL:HG23	3:9P:311:TYR:HB2	1.97	0.46
5:C:61:TYR:HA	5:C:85:ASN:HD21	1.80	0.46
7:E:21:ARG:HH22	7:E:106:LYS:HD3	1.80	0.46
8:G:120:ILE:HD12	8:G:140:ILE:HD13	1.96	0.46
14:R:24:LYS:HA	14:R:94:THR:OG1	2.16	0.46
18:V:44:HIS:NE2	18:V:86:LEU:O	2.45	0.46
22:Z:10:ARG:HG2	22:Z:10:ARG:NH2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:0:53:VAL:HG22	23:0:54:ILE:H	1.80	0.46
27:K:41:ILE:HD11	27:K:86:LEU:HD13	1.98	0.46
1:A:-2:U:H2'	1:A:-1:A:H8	1.81	0.46
1:A:414:C:O3'	1:A:1878:G:N2	2.49	0.46
1:A:574:A:N6	1:A:2034:U:OP1	2.47	0.46
1:A:967:U:H2'	1:A:968:C:H6	1.79	0.46
1:A:1035:U:H2'	1:A:1036:G:C8	2.50	0.46
1:A:2441:U:OP2	1:A:2586:U:O2'	2.34	0.46
1:A:2540:C:O2'	1:A:2740:A:N3	2.40	0.46
6:D:58:ASN:OD1	6:D:59:ARG:N	2.48	0.46
10:L:14:LYS:HE3	10:L:14:LYS:HB3	1.79	0.46
10:L:95:LEU:HD12	10:L:100:ILE:HG21	1.98	0.46
1:A:125:A:H5''	25:2:19:ARG:HB2	1.98	0.46
1:A:341:C:H2'	1:A:342:A:H8	1.81	0.46
1:A:579:G:H2'	1:A:580:U:H6	1.80	0.46
1:A:638:G:H2'	1:A:639:U:H6	1.80	0.46
1:A:666:A:H2'	1:A:667:U:C6	2.51	0.46
1:A:806:C:H3'	10:L:41:ARG:HH12	1.81	0.46
1:A:1361:G:H2'	1:A:1362:C:H6	1.80	0.46
1:A:2537:U:H2'	1:A:2538:C:C6	2.51	0.46
2:B:42:C:H1'	31:F:62:GLN:HB3	1.97	0.46
1:A:1000:A:H2'	1:A:1001:A:C8	2.50	0.46
1:A:1165:A:H2'	1:A:1166:G:H8	1.79	0.46
1:A:1181:U:H2'	1:A:1182:G:C8	2.51	0.46
1:A:1186:G:H2'	1:A:1187:G:O4'	2.15	0.46
1:A:1190:G:H2'	1:A:1191:G:C8	2.51	0.46
1:A:1418:G:H1'	1:A:1581:G:H22	1.80	0.46
1:A:2074:U:H2'	1:A:2075:U:H6	1.80	0.46
1:A:2195:U:H2'	1:A:2196:C:C6	2.51	0.46
2:B:60:C:H2'	2:B:61:G:C8	2.50	0.46
11:N:117:ASP:OD1	11:N:118:ARG:N	2.49	0.46
18:V:25:LYS:HE3	18:V:41:GLU:HB3	1.97	0.46
31:F:157:THR:HG22	31:F:159:ALA:H	1.80	0.46
1:A:183:C:H1'	1:A:432:A:C2	2.51	0.46
1:A:202:U:H2'	1:A:203:A:O4'	2.16	0.46
1:A:599:A:H2'	1:A:600:G:H8	1.80	0.46
1:A:863:A:H2'	1:A:864:G:C8	2.51	0.46
1:A:1790:C:O3'	1:A:1791:A:H8	1.99	0.46
1:A:2393:U:H2'	1:A:2394:C:H6	1.81	0.46
1:A:2680:U:H2'	1:A:2681:C:C6	2.51	0.46
1:A:2698:U:H2'	1:A:2699:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:121:ALA:HB3	5:C:129:LEU:HD13	1.98	0.46
13:Q:26:ALA:HA	13:Q:29:ARG:HG2	1.97	0.46
15:S:109:ASP:OD1	15:S:110:ARG:N	2.48	0.46
1:A:168:G:H2'	1:A:169:G:H8	1.81	0.46
1:A:596:U:H2'	1:A:597:G:H8	1.81	0.46
1:A:744:U:H2'	1:A:745:G:O4'	2.15	0.46
1:A:1160:G:H2'	1:A:1161:C:C6	2.51	0.46
1:A:1566:A:O4'	5:C:212:TRP:NE1	2.49	0.46
1:A:2011:U:H2'	1:A:2012:G:O4'	2.16	0.46
1:A:2557:G:H2'	1:A:2558:C:H6	1.81	0.46
2:B:41:G:H5''	31:F:65:LEU:HG	1.98	0.46
2:B:83:G:O6	2:B:94:A:N6	2.48	0.46
2:B:113:C:H2'	2:B:114:C:H6	1.81	0.46
5:C:7:PRO:HB3	5:C:13:ARG:HG3	1.98	0.46
27:K:75:SER:HB3	28:P:71:ARG:NH2	2.31	0.46
28:P:90:ALA:HB3	28:P:110:LYS:HG3	1.96	0.46
29:6:90:MET:HE1	29:6:95:ARG:HA	1.98	0.46
30:H:50:ARG:O	30:H:54:LEU:N	2.37	0.46
1:A:12:U:O2	1:A:2626:C:H4'	2.16	0.45
1:A:23:G:H2'	1:A:24:G:H8	1.81	0.45
1:A:2660:A:H8	1:A:2660:A:OP1	1.99	0.45
6:D:11:MET:HE2	6:D:11:MET:HB3	1.88	0.45
7:E:26:ALA:HB2	10:L:9:ALA:HB2	1.98	0.45
31:F:105:ILE:O	31:F:109:ARG:HG2	2.16	0.45
1:A:58:G:O2'	1:A:73:A:N1	2.40	0.45
1:A:819:A:H5'	1:A:973:A:N1	2.32	0.45
1:A:1569:A:H2'	1:A:1570:A:C8	2.51	0.45
1:A:2301:C:H2'	1:A:2302:U:C6	2.51	0.45
1:A:2304:G:N2	1:A:2312:U:H3	2.14	0.45
1:A:2404:U:H3	1:A:2413:G:H1	1.64	0.45
1:A:2416:C:C2	1:A:2417:C:C5	3.04	0.45
1:A:2564:A:H2'	1:A:2565:A:C8	2.51	0.45
1:A:2642:G:H5''	9:J:80:HIS:CG	2.51	0.45
1:A:2788:C:H2'	1:A:2789:C:C6	2.51	0.45
2:B:48:U:H4'	12:O:100:HIS:NE2	2.31	0.45
7:E:121:VAL:O	7:E:190:ALA:N	2.48	0.45
16:T:34:VAL:HG11	16:T:43:ILE:HD12	1.98	0.45
16:T:47:VAL:HG21	16:T:55:VAL:HG21	1.98	0.45
20:X:2:ARG:O	20:X:2:ARG:HG2	2.16	0.45
28:P:13:LYS:HD3	28:P:76:HIS:HA	1.99	0.45
31:F:104:THR:HB	31:F:105:ILE:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:A:H2'	1:A:7:G:H8	1.81	0.45
1:A:145:C:H2'	1:A:146:A:C8	2.51	0.45
1:A:494:G:H4'	15:S:6:LYS:HG3	1.98	0.45
1:A:579:G:H2'	1:A:580:U:C6	2.52	0.45
1:A:967:U:H2'	1:A:968:C:C6	2.51	0.45
1:A:1406:U:H2'	1:A:1407:G:C8	2.52	0.45
1:A:1444:G:H2'	1:A:1445:G:H8	1.82	0.45
1:A:1592:C:H2'	1:A:1593:A:H8	1.81	0.45
1:A:2191:A:H2'	1:A:2192:U:H6	1.81	0.45
2:B:9:G:OP1	12:O:25:ARG:NH1	2.50	0.45
2:B:49:C:O3'	12:O:68:LYS:NZ	2.47	0.45
8:G:137:LYS:HA	8:G:140:ILE:HG22	1.99	0.45
21:Y:6:LEU:HD23	21:Y:56:LEU:HD11	1.98	0.45
31:F:99:PHE:HE1	31:F:174:PHE:HE2	1.64	0.45
1:A:286:U:H2'	1:A:287:G:C8	2.52	0.45
1:A:364:C:H2'	1:A:365:U:C6	2.50	0.45
1:A:417:C:H2'	1:A:418:C:H6	1.81	0.45
1:A:451:U:O2	1:A:453:A:N6	2.50	0.45
1:A:840:C:H2'	1:A:841:G:H8	1.82	0.45
1:A:1683:U:H2'	1:A:1684:G:C8	2.52	0.45
1:A:1730:C:O2	1:A:1731:G:N1	2.49	0.45
1:A:1926:U:H3	1:A:1929:G:H1	1.63	0.45
1:A:2345:G:O2'	1:A:2381:A:N3	2.46	0.45
1:A:2679:A:H2'	1:A:2680:U:C6	2.51	0.45
2:B:70:C:H2'	2:B:71:C:C6	2.52	0.45
2:B:78:A:N6	2:B:98:G:N2	2.41	0.45
3:9P:12:VAL:HG21	3:9P:66:ARG:HH11	1.80	0.45
6:D:13:ARG:NH1	28:P:74:GLN:HG2	2.32	0.45
8:G:151:ARG:HA	8:G:151:ARG:HD3	1.81	0.45
14:R:78:ARG:HG2	14:R:78:ARG:HH21	1.82	0.45
16:T:50:LEU:HD21	21:Y:26:PHE:CZ	2.52	0.45
26:I:27:LEU:HD23	26:I:27:LEU:H	1.81	0.45
30:H:19:VAL:HG13	30:H:21:VAL:HG23	1.98	0.45
1:A:320:A:N3	7:E:163:ASN:ND2	2.64	0.45
1:A:381:G:H2'	1:A:382:A:C8	2.51	0.45
1:A:2081:U:H2'	1:A:2082:A:C8	2.47	0.45
1:A:2514:U:H5''	9:J:81:ILE:HD11	1.98	0.45
1:A:2773:C:H2'	1:A:2774:C:H6	1.82	0.45
2:B:39:A:N7	4:b:2:LYS:NZ	2.61	0.45
7:E:5:LEU:HD13	7:E:120:VAL:HG12	1.98	0.45
17:U:6:ARG:HG3	17:U:7:ASP:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:U:76:THR:HG23	17:U:78:LYS:H	1.80	0.45
27:K:58:LEU:HD12	27:K:87:LEU:O	2.16	0.45
1:A:154:U:H2'	1:A:155:A:H8	1.82	0.45
1:A:379:G:N1	1:A:396:G:O6	2.50	0.45
1:A:627:A:H2'	10:L:78:ARG:HH11	1.82	0.45
1:A:1816:C:H5''	5:C:61:TYR:CE2	2.52	0.45
10:L:116:VAL:HG11	10:L:134:ALA:HB1	1.98	0.45
1:A:698:C:HO2'	1:A:734:A:H61	1.54	0.45
1:A:909:A:H2'	1:A:912:C:H5	1.82	0.45
1:A:1843:C:H5''	5:C:254:LYS:HE3	1.99	0.45
1:A:1903:G:H2'	1:A:1904:G:C8	2.52	0.45
1:A:1954:G:O2'	1:A:1956:U:O4	2.30	0.45
1:A:2315:G:H2'	1:A:2316:G:H8	1.81	0.45
1:A:2557:G:H2'	1:A:2558:C:C6	2.51	0.45
3:9P:218:ILE:HG23	3:9P:219:GLU:CD	2.41	0.45
5:C:92:LEU:HB2	5:C:102:TYR:CE1	2.52	0.45
26:I:132:ALA:O	26:I:133:ARG:HG3	2.16	0.45
27:K:71:ARG:HB2	27:K:75:SER:HB2	1.98	0.45
30:H:7:ASP:CG	30:H:8:LYS:N	2.74	0.45
1:A:465:G:N2	1:A:684:G:O2'	2.50	0.45
1:A:724:U:H2'	1:A:725:G:O4'	2.17	0.45
1:A:740:C:H5'	1:A:1784:A:H2'	1.99	0.45
1:A:856:G:H2'	1:A:857:G:C8	2.52	0.45
1:A:931:U:O2	1:A:1167:C:O2'	2.30	0.45
1:A:1807:G:N2	1:A:1810:A:OP2	2.32	0.45
1:A:1874:C:H2'	1:A:1875:G:O4'	2.17	0.45
1:A:1890:A:H3'	1:A:1891:G:H8	1.82	0.45
1:A:2192:U:H2'	1:A:2193:G:H8	1.81	0.45
1:A:2511:U:H5''	6:D:128:ARG:NH1	2.32	0.45
1:A:2631:G:H2'	1:A:2632:A:H8	1.82	0.45
8:G:162:ARG:HH11	8:G:168:VAL:HB	1.82	0.45
12:O:103:VAL:HA	12:O:106:LEU:HD12	1.99	0.45
27:K:85:VAL:HG11	27:K:115:ILE:HD11	1.99	0.45
1:A:281:C:H2'	1:A:282:A:C8	2.52	0.45
1:A:596:U:H2'	1:A:597:G:C8	2.52	0.45
1:A:656:G:H2'	1:A:657:U:C6	2.52	0.45
1:A:974:G:O4'	1:A:990:A:N6	2.49	0.45
1:A:1183:U:H4'	22:Z:29:ARG:NH2	2.32	0.45
1:A:1248:G:C6	13:Q:2:ARG:HD2	2.51	0.45
1:A:2299:U:O4	1:A:2300:C:N4	2.49	0.45
1:A:2305:U:O4	31:F:151:LEU:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2409:G:H2'	1:A:2410:G:O4'	2.17	0.45
1:A:2508:G:O2'	1:A:2554:U:O2'	2.33	0.45
1:A:2514:U:H3	1:A:2570:G:H1	1.65	0.45
1:A:2801:G:H2'	1:A:2802:G:C8	2.52	0.45
11:N:24:MET:HE1	11:N:36:THR:HG21	1.99	0.45
11:N:42:LYS:HA	11:N:45:ARG:NH1	2.31	0.45
14:R:74:ILE:O	14:R:87:GLN:N	2.50	0.45
14:R:79:ARG:HG2	14:R:80:ARG:NH2	2.32	0.45
21:Y:32:ALA:HB2	21:Y:37:LEU:HD22	1.98	0.45
30:H:117:LEU:HG	30:H:120:GLY:O	2.17	0.45
1:A:1408:G:H1	1:A:1594:U:H3	1.65	0.45
1:A:1434:A:HO2'	1:A:1435:G:H8	1.63	0.45
1:A:2291:U:H1'	1:A:2374:C:H1'	2.00	0.45
1:A:2636:C:H2'	1:A:2637:U:C6	2.52	0.45
3:9P:159:LEU:HA	3:9P:237:ARG:HH22	1.81	0.45
3:9P:159:LEU:HA	3:9P:237:ARG:NH2	2.32	0.45
5:C:42:ARG:NH2	5:C:48:ILE:HD11	2.32	0.45
18:V:83:LYS:HB3	18:V:85:LYS:HE2	1.97	0.45
1:A:301:G:O2'	1:A:302:C:O5'	2.35	0.44
1:A:570:G:O2'	1:A:983:A:N1	2.35	0.44
1:A:686:U:H2'	1:A:788:A:N1	2.31	0.44
1:A:844:A:N1	1:A:845:A:N6	2.65	0.44
1:A:868:U:H2'	1:A:869:G:H8	1.82	0.44
1:A:1636:U:H2'	1:A:1637:A:C8	2.53	0.44
1:A:1720:U:H2'	1:A:1721:G:O4'	2.17	0.44
1:A:2063:C:H2'	1:A:2064:C:H6	1.82	0.44
1:A:2311:A:C5	31:F:40:GLY:HA2	2.51	0.44
1:A:2372:U:H2'	1:A:2373:G:C8	2.53	0.44
1:A:2559:C:H2'	1:A:2560:A:H8	1.83	0.44
14:R:76:LYS:HB2	14:R:85:LYS:HB3	1.99	0.44
17:U:42:LYS:HB3	17:U:59:GLU:OE1	2.18	0.44
1:A:78:U:H2'	1:A:79:C:C6	2.52	0.44
1:A:152:A:N6	1:A:175:G:O6	2.51	0.44
1:A:532:A:H4'	1:A:533:G:C8	2.51	0.44
1:A:812:C:OP1	13:Q:12:ARG:NH2	2.50	0.44
1:A:1614:A:H61	15:S:88:ARG:H	1.65	0.44
1:A:1752:C:H2'	1:A:1753:G:C8	2.52	0.44
1:A:2660:A:C2	3:9P:198:LEU:HG	2.53	0.44
1:A:2737:G:H2'	1:A:2738:A:C8	2.52	0.44
2:B:39:A:O2'	2:B:40:U:O4'	2.33	0.44
6:D:183:GLU:CD	6:D:184:ARG:HG3	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:97:VAL:HG22	8:G:102:ILE:HG12	1.99	0.44
11:N:22:ARG:HD3	11:N:71:ARG:HB2	1.99	0.44
12:O:24:THR:HG22	12:O:42:PRO:HD3	1.99	0.44
13:Q:108:LEU:HD22	14:R:48:LYS:NZ	2.32	0.44
1:A:227:A:C2	1:A:2407:A:H1'	2.52	0.44
1:A:307:G:N2	1:A:309:A:H3'	2.32	0.44
1:A:693:A:H2'	1:A:694:U:C6	2.52	0.44
1:A:1329:U:OP2	1:A:1330:C:N4	2.37	0.44
1:A:2299:U:N3	1:A:2318:G:N2	2.64	0.44
1:A:2704:C:H2'	1:A:2705:A:O4'	2.18	0.44
3:9P:243:HIS:NE2	3:9P:245:ILE:HD11	2.33	0.44
9:J:33:ALA:HB2	9:J:108:MET:HB3	1.99	0.44
9:J:45:THR:HG22	13:Q:63:ARG:HH21	1.81	0.44
13:Q:20:ALA:HB2	13:Q:38:VAL:HG23	1.99	0.44
13:Q:106:THR:O	13:Q:110:GLU:HG2	2.18	0.44
16:T:25:GLU:OE2	16:T:25:GLU:N	2.51	0.44
17:U:4:ILE:HG21	17:U:33:VAL:HG11	1.99	0.44
17:U:32:LYS:HA	17:U:65:GLN:HA	1.99	0.44
1:A:96:C:H4'	21:Y:41:HIS:CD2	2.53	0.44
1:A:742:A:H2'	1:A:743:A:C8	2.52	0.44
1:A:1445:G:O6	1:A:1466:U:O2	2.36	0.44
1:A:2045:C:H5''	23:O:14:MET:HE3	2.00	0.44
1:A:2229:U:H2'	1:A:2230:G:C8	2.49	0.44
1:A:2298:A:H62	1:A:2318:G:N2	2.16	0.44
1:A:2414:G:C2	1:A:2415:G:C8	3.06	0.44
1:A:2573:C:O2'	1:A:2574:G:OP2	2.33	0.44
1:A:2685:G:H2'	1:A:2686:G:C8	2.52	0.44
1:A:2906:C:H2'	1:A:2907:A:C8	2.53	0.44
24:1:39:ASP:OD1	24:1:48:TYR:OH	2.27	0.44
27:K:9:ASN:OD1	27:K:18:ARG:NH1	2.48	0.44
31:F:110:ILE:HD11	31:F:136:ILE:HD13	1.99	0.44
1:A:9:G:H21	1:A:2800:A:H61	1.65	0.44
1:A:397:U:OP2	20:X:9:LYS:NZ	2.37	0.44
1:A:1026:G:H2'	1:A:1027:A:C8	2.51	0.44
1:A:1266:G:N2	1:A:2013:A:OP2	2.42	0.44
1:A:1534:U:O2'	1:A:1537:G:O6	2.24	0.44
1:A:1857:G:N2	1:A:1884:G:N3	2.65	0.44
1:A:2191:A:H2'	1:A:2192:U:C6	2.53	0.44
1:A:2224:G:H4'	1:A:2226:C:C2	2.53	0.44
9:J:104:ALA:O	9:J:108:MET:HG2	2.17	0.44
18:V:80:HIS:HB2	18:V:83:LYS:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:C:H2'	1:A:524:G:H8	1.83	0.44
1:A:638:G:H2'	1:A:639:U:C6	2.52	0.44
1:A:1264:A:O5'	1:A:1265:A:H2'	2.18	0.44
1:A:1417:C:H2'	1:A:1418:G:O4'	2.17	0.44
1:A:1654:A:H2'	1:A:1655:A:H8	1.82	0.44
1:A:2315:G:H21	31:F:124:ARG:CZ	2.30	0.44
1:A:2594:C:H2'	1:A:2595:G:C8	2.53	0.44
1:A:2745:C:H2'	1:A:2746:U:C6	2.53	0.44
8:G:86:LEU:HD12	8:G:161:VAL:HG22	1.99	0.44
16:T:37:ASP:O	16:T:81:LYS:NZ	2.45	0.44
27:K:36:GLY:HA3	27:K:110:GLU:HG3	2.00	0.44
28:P:42:PHE:CE2	28:P:71:ARG:HG2	2.53	0.44
1:A:230:G:H2'	1:A:231:A:C8	2.53	0.44
1:A:540:C:N4	1:A:541:A:H62	2.16	0.44
1:A:875:G:H2'	1:A:876:C:C6	2.52	0.44
1:A:1147:A:H2'	1:A:1148:U:H6	1.83	0.44
1:A:1529:G:H1	1:A:1542:U:H3	1.66	0.44
1:A:1825:U:H2'	1:A:1826:G:C8	2.50	0.44
1:A:2376:A:H62	12:O:94:ARG:HH11	1.64	0.44
1:A:2506:U:O2	1:A:2583:G:O6	2.35	0.44
1:A:2760:C:H2'	1:A:2761:A:C8	2.52	0.44
1:A:2834:G:H2'	1:A:2879:A:H61	1.83	0.44
6:D:33:ARG:HA	6:D:95:SER:HA	1.99	0.44
8:G:151:ARG:HG3	8:G:160:GLY:HA2	1.99	0.44
16:T:48:GLN:HE22	16:T:55:VAL:HB	1.82	0.44
27:K:70:ARG:HD2	27:K:74:GLY:HA2	1.99	0.44
30:H:39:ALA:HA	30:H:43:ASN:HB2	2.00	0.44
1:A:6:A:H2'	1:A:7:G:C8	2.53	0.44
1:A:174:U:H2'	1:A:175:G:C8	2.53	0.44
1:A:1218:G:OP2	13:Q:14:LYS:NZ	2.31	0.44
1:A:1405:U:H2'	1:A:1406:U:C6	2.53	0.44
1:A:1697:G:OP2	1:A:1698:A:O2'	2.28	0.44
1:A:2616:C:H2'	1:A:2617:U:C6	2.53	0.44
1:A:2756:U:H4'	1:A:2757:A:OP1	2.16	0.44
13:Q:49:ARG:HG3	13:Q:49:ARG:NH1	2.33	0.44
16:T:50:LEU:HD23	16:T:51:PHE:CD1	2.53	0.44
1:A:0:A:H2'	1:A:1:G:C8	2.53	0.44
1:A:175:G:H2'	1:A:176:A:H8	1.82	0.44
1:A:457:A:N1	1:A:470:A:H5''	2.33	0.44
1:A:499:U:H2'	1:A:500:G:O4'	2.18	0.44
1:A:536:G:H21	9:J:47:HIS:CG	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:549:G:H5''	1:A:550:C:C6	2.53	0.44
1:A:974:G:H1'	1:A:975:A:C8	2.52	0.44
1:A:1491:G:H1'	5:C:99:GLU:OE1	2.17	0.44
1:A:1576:U:H2'	1:A:1577:C:C6	2.53	0.44
1:A:1738:G:O2'	1:A:1739:A:H8	2.00	0.44
1:A:2457:U:H2'	1:A:2458:G:C8	2.53	0.44
1:A:2530:A:H5'	8:G:174:LYS:NZ	2.33	0.44
1:A:2587:A:H61	1:A:2608:G:H1'	1.83	0.44
8:G:24:THR:HG22	8:G:26:LYS:HG2	2.00	0.44
10:L:91:ASP:OD1	10:L:123:ARG:NH2	2.50	0.44
1:A:682:G:H5'	25:2:26:ASN:CG	2.42	0.43
1:A:705:A:H2'	1:A:706:A:H8	1.81	0.43
1:A:969:G:H2'	1:A:970:U:C6	2.53	0.43
1:A:1411:U:H2'	1:A:1412:U:C6	2.53	0.43
1:A:1817:G:C5'	5:C:86:ARG:HH12	2.31	0.43
1:A:2028:U:O4	1:A:2033:A:N7	2.51	0.43
1:A:2728:U:O2'	1:A:2729:G:H8	2.01	0.43
6:D:59:ARG:HA	6:D:59:ARG:HD3	1.86	0.43
7:E:21:ARG:NH1	7:E:106:LYS:HB2	2.32	0.43
11:N:29:VAL:HB	11:N:75:ILE:HD12	1.99	0.43
11:N:49:GLU:OE2	11:N:95:THR:HG22	2.18	0.43
12:O:30:ARG:HG2	12:O:97:PHE:CE1	2.53	0.43
13:Q:49:ARG:HG3	13:Q:49:ARG:HH11	1.83	0.43
21:Y:22:LEU:HD23	21:Y:23:ARG:HE	1.83	0.43
25:2:34:ARG:HD2	25:2:42:LEU:HD13	1.98	0.43
28:P:113:LEU:O	28:P:113:LEU:HD23	2.17	0.43
1:A:1419:A:H61	1:A:1495:A:H2	1.66	0.43
1:A:2528:U:H4'	1:A:2529:G:N7	2.33	0.43
3:9P:59:TYR:OH	3:9P:89:LYS:O	2.35	0.43
7:E:192:ALA:HA	7:E:195:GLN:NE2	2.33	0.43
30:H:41:LYS:HA	30:H:41:LYS:HD2	1.84	0.43
1:A:38:A:N3	7:E:43:THR:HB	2.33	0.43
1:A:77:G:H2'	1:A:78:U:H6	1.83	0.43
1:A:535:G:H4'	13:Q:52:ARG:HD3	1.99	0.43
1:A:643:A:H2'	1:A:644:A:C4	2.54	0.43
1:A:758:C:H2'	1:A:759:G:C8	2.53	0.43
1:A:940:G:H2'	1:A:941:A:O4'	2.18	0.43
1:A:1306:C:H2'	1:A:1307:A:H8	1.82	0.43
1:A:1943:U:H5''	3:9P:129:ARG:NE	2.32	0.43
1:A:2039:U:H2'	1:A:2040:G:H8	1.82	0.43
1:A:2290:G:H2'	1:A:2291:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2651:C:H2'	1:A:2652:C:C6	2.54	0.43
1:A:2659:G:N2	1:A:2661:G:H3'	2.33	0.43
5:C:23:LEU:HD21	5:C:82:TYR:HB2	1.99	0.43
7:E:110:SER:HB3	7:E:114:ARG:HH12	1.83	0.43
16:T:7:LEU:HD23	16:T:46:ALA:HA	2.00	0.43
29:6:96:ARG:HD2	29:6:96:ARG:HA	1.72	0.43
1:A:4:U:H2'	1:A:5:A:H8	1.82	0.43
1:A:413:C:H2'	1:A:414:C:H6	1.84	0.43
1:A:418:C:H2'	1:A:419:U:H6	1.82	0.43
1:A:1257:C:C2	1:A:1258:U:C5	3.06	0.43
1:A:1880:U:H2'	1:A:1881:C:C6	2.54	0.43
1:A:2889:C:H2'	1:A:2890:G:O4'	2.18	0.43
3:9P:329:MET:O	3:9P:333:ILE:HG12	2.18	0.43
6:D:49:GLN:OE1	6:D:79:LEU:HD13	2.18	0.43
18:V:79:ARG:C	18:V:87:GLN:HE22	2.26	0.43
1:A:516:C:C5'	23:0:9:ARG:HH12	2.28	0.43
1:A:1199:U:H2'	1:A:1200:C:H6	1.84	0.43
1:A:1383:A:O2'	1:A:1384:A:O4'	2.31	0.43
1:A:1682:G:H2'	1:A:1683:U:C6	2.53	0.43
1:A:2032:G:N2	6:D:151:THR:HB	2.33	0.43
1:A:2192:U:C2	1:A:2193:G:C8	3.07	0.43
1:A:2233:U:H2'	1:A:2234:G:C8	2.54	0.43
1:A:2547:A:H2'	1:A:2548:U:C6	2.53	0.43
2:B:48:U:H2'	2:B:49:C:C6	2.53	0.43
5:C:129:LEU:HD12	5:C:133:ASN:HB2	2.00	0.43
16:T:61:LEU:O	16:T:81:LYS:HG3	2.19	0.43
17:U:27:VAL:HA	17:U:33:VAL:HA	2.00	0.43
22:Z:16:LEU:HB2	22:Z:19:HIS:CD2	2.47	0.43
1:A:541:A:H2'	1:A:542:C:C6	2.53	0.43
1:A:754:U:H2'	1:A:755:U:C6	2.54	0.43
1:A:820:A:H2'	1:A:821:A:C8	2.54	0.43
1:A:850:U:O2'	22:Z:22:THR:HA	2.19	0.43
1:A:905:A:H2'	1:A:906:U:C6	2.54	0.43
1:A:935:C:H2'	1:A:936:A:C8	2.51	0.43
1:A:1511:G:H2'	1:A:1512:C:H6	1.84	0.43
1:A:1539:U:H2'	1:A:1540:G:C8	2.51	0.43
1:A:1998:A:OP2	6:D:141:ARG:NH1	2.35	0.43
1:A:2058:A:H61	1:A:2611:C:N4	2.17	0.43
1:A:2194:U:H2'	1:A:2195:U:H6	1.82	0.43
1:A:2370:G:H2'	1:A:2371:G:C8	2.53	0.43
1:A:2621:G:H2'	1:A:2622:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2625:G:H2'	1:A:2626:C:C6	2.54	0.43
1:A:2649:C:H2'	1:A:2650:U:C6	2.53	0.43
1:A:2801:G:H2'	1:A:2802:G:H8	1.83	0.43
1:A:2861:U:H2'	1:A:2862:G:C8	2.52	0.43
3:9P:52:ASN:O	3:9P:52:ASN:ND2	2.51	0.43
3:9P:92:VAL:HA	3:9P:108:MET:HG3	2.00	0.43
3:9P:125:LEU:HD22	3:9P:129:ARG:HG2	2.00	0.43
5:C:221:GLY:O	5:C:224:MET:HB2	2.18	0.43
8:G:37:ASN:HD21	8:G:63:GLN:HB3	1.84	0.43
8:G:73:SER:HB2	8:G:137:LYS:HD3	1.99	0.43
8:G:87:GLN:OE1	8:G:87:GLN:N	2.51	0.43
9:J:43:GLU:OE1	9:J:43:GLU:N	2.51	0.43
24:1:36:LYS:HD2	24:1:45:HIS:HB3	2.01	0.43
1:A:191:A:H2'	1:A:192:C:C6	2.53	0.43
1:A:528:A:H2'	1:A:529:A:H5''	2.01	0.43
1:A:1071:G:H21	1:A:1089:A:H2'	1.82	0.43
1:A:1147:A:H2'	1:A:1148:U:C6	2.54	0.43
1:A:1148:U:H2'	1:A:1149:G:H8	1.83	0.43
1:A:1378:A:O2'	1:A:1380:G:OP2	2.37	0.43
1:A:1440:U:H2'	1:A:1441:G:C8	2.54	0.43
1:A:1528:A:N6	1:A:1543:G:O2'	2.52	0.43
1:A:2198:A:C2	30:H:29:PHE:HB2	2.53	0.43
1:A:2345:G:H5'	1:A:2347:C:H5'	2.00	0.43
3:9P:255:PRO:O	3:9P:257:GLU:N	2.52	0.43
16:T:65:GLY:HA2	16:T:77:ARG:HB2	1.99	0.43
20:X:67:LEU:HB3	20:X:71:ARG:HH12	1.83	0.43
23:O:10:SER:O	23:O:14:MET:HG3	2.18	0.43
25:2:3:ARG:HA	25:2:3:ARG:HE	1.84	0.43
27:K:20:MET:HE3	27:K:44:LYS:HE3	2.00	0.43
1:A:151:C:H2'	1:A:152:A:C8	2.53	0.43
1:A:499:U:H3	1:A:503:A:H62	1.66	0.43
1:A:513:A:H2'	1:A:514:A:H8	1.84	0.43
1:A:563:A:C6	1:A:2018:G:C5	3.06	0.43
1:A:1149:G:H2'	1:A:1150:C:C6	2.54	0.43
1:A:1535:A:H5'	1:A:1536:C:C5	2.53	0.43
1:A:1837:C:H2'	1:A:1899:A:H61	1.83	0.43
1:A:1967:C:H2'	1:A:1968:G:O4'	2.19	0.43
1:A:2293:G:H2'	1:A:2294:G:C8	2.54	0.43
1:A:2328:A:H2'	1:A:2329:U:C6	2.53	0.43
1:A:2489:U:H2'	1:A:2490:G:O4'	2.19	0.43
12:O:33:ARG:HA	12:O:64:TYR:OH	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:W:41:PHE:HD2	19:W:76:ILE:HD11	1.83	0.43
1:A:170:U:H2'	1:A:171:U:C6	2.54	0.43
1:A:572:A:H61	1:A:2029:G:H21	1.67	0.43
1:A:814:C:OP1	14:R:85:LYS:HD2	2.18	0.43
1:A:1141:U:H4'	1:A:1142:A:O4'	2.19	0.43
1:A:1433:A:H2'	1:A:1434:A:C8	2.54	0.43
1:A:1733:G:H2'	1:A:1734:G:H8	1.83	0.43
1:A:1796:U:H2'	1:A:1797:G:C8	2.54	0.43
1:A:2789:C:H5'	1:A:2809:A:H1'	2.00	0.43
5:C:52:HIS:CD2	5:C:218:THR:HA	2.54	0.43
11:N:44:LEU:O	11:N:48:VAL:HG12	2.19	0.43
28:P:71:ARG:HE	28:P:72:VAL:H	1.65	0.43
31:F:103:ILE:HD12	31:F:103:ILE:HA	1.91	0.43
1:A:593:U:H2'	1:A:594:U:C6	2.53	0.43
1:A:1091:G:N1	1:A:1101:U:C2	2.87	0.43
1:A:1234:U:H2'	1:A:1235:G:O4'	2.18	0.43
1:A:2905:A:H2'	1:A:2906:C:C6	2.54	0.43
7:E:112:LEU:HB3	7:E:118:LEU:HB2	2.00	0.43
11:N:69:ARG:O	11:N:70:THR:OG1	2.24	0.43
18:V:30:ILE:HG22	18:V:91:PHE:HB2	2.01	0.43
30:H:62:LEU:HD11	30:H:135:HIS:CE1	2.54	0.43
1:A:434:U:O2	1:A:435:C:N4	2.45	0.42
1:A:536:G:H4'	13:Q:56:PHE:CZ	2.54	0.42
1:A:693:A:N6	1:A:770:G:O6	2.52	0.42
1:A:760:G:H2'	1:A:761:A:O4'	2.19	0.42
1:A:835:C:C2	1:A:836:G:C8	3.06	0.42
1:A:1142:A:H4'	9:J:27:ARG:HH22	1.84	0.42
1:A:1201:U:H2'	1:A:1202:G:C8	2.54	0.42
1:A:1279:G:H2'	1:A:1280:G:C8	2.54	0.42
1:A:1389:G:H2'	1:A:1390:U:C6	2.54	0.42
1:A:2055:C:H5'	1:A:2056:G:H5''	2.01	0.42
1:A:2119:A:H61	1:A:2167:U:H1'	1.83	0.42
3:9P:1:MET:N	3:9P:195:VAL:HG11	2.34	0.42
5:C:180:MET:HB2	5:C:267:VAL:HB	2.01	0.42
9:J:37:ARG:HH22	9:J:110:PRO:HG2	1.84	0.42
9:J:99:ARG:O	9:J:103:ILE:HD12	2.18	0.42
11:N:38:LEU:HB3	11:N:39:PRO:HD3	2.00	0.42
1:A:77:G:H2'	1:A:78:U:C6	2.55	0.42
1:A:137:U:H5''	1:A:140:C:C5	2.55	0.42
1:A:521:U:H2'	1:A:522:A:C8	2.54	0.42
1:A:1353:A:H2'	1:A:1354:A:C8	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1403:A:H2'	1:A:1404:C:C6	2.54	0.42
1:A:1447:C:H2'	1:A:1448:G:C8	2.53	0.42
1:A:1688:U:O2'	1:A:1700:A:N7	2.49	0.42
1:A:1947:C:H2'	1:A:1948:G:C8	2.51	0.42
1:A:2193:G:H2'	1:A:2194:U:H6	1.84	0.42
1:A:2219:U:O2'	30:H:97:ARG:NH2	2.52	0.42
1:A:2228:G:H2'	1:A:2229:U:C6	2.54	0.42
1:A:2572:A:P	6:D:149:ASN:HD21	2.42	0.42
1:A:2660:A:H2'	1:A:2661:G:C5	2.54	0.42
1:A:2816:G:H2'	1:A:2817:U:H6	1.84	0.42
3:9P:240:VAL:HA	3:9P:276:LYS:NZ	2.34	0.42
5:C:191:LEU:HD23	5:C:191:LEU:HA	1.90	0.42
30:H:31:VAL:HB	30:H:32:PRO:HD3	2.00	0.42
1:A:128:C:H2'	1:A:129:C:H6	1.84	0.42
1:A:281:C:H2'	1:A:282:A:H8	1.84	0.42
1:A:438:G:H2'	1:A:439:A:H8	1.84	0.42
1:A:980:A:H8	1:A:980:A:OP1	2.03	0.42
1:A:1288:G:H5''	1:A:1289:C:C5	2.55	0.42
1:A:1316:U:H2'	1:A:1317:G:C8	2.55	0.42
1:A:1328:A:O2'	1:A:1329:U:O5'	2.36	0.42
2:B:29:A:O2'	2:B:58:A:N1	2.42	0.42
3:9P:95:ARG:HG3	3:9P:157:MET:HE2	2.02	0.42
13:Q:46:TYR:HE2	13:Q:50:ARG:NH2	2.18	0.42
13:Q:108:LEU:HD13	14:R:48:LYS:HZ1	1.84	0.42
14:R:15:SER:O	14:R:98:ILE:HD11	2.19	0.42
26:I:11:GLN:NE2	26:I:55:PRO:HG3	2.34	0.42
1:A:45:G:H5'	1:A:46:G:H5'	2.02	0.42
1:A:729:G:O2'	1:A:763:G:H4'	2.19	0.42
1:A:745:G:O2'	1:A:748:G:H1'	2.20	0.42
1:A:969:G:H2'	1:A:970:U:H6	1.83	0.42
1:A:1032:A:H2	1:A:1122:G:H22	1.67	0.42
1:A:1561:C:H2'	1:A:1562:U:H6	1.85	0.42
1:A:2514:U:H2'	1:A:2515:C:H6	1.84	0.42
1:A:2527:C:H2'	1:A:2528:U:O4'	2.19	0.42
1:A:2602:A:H8	3:9P:32:GLY:H	1.67	0.42
1:A:2875:C:H2'	1:A:2876:G:C8	2.54	0.42
1:A:2885:G:H22	23:O:29:VAL:HG23	1.84	0.42
2:B:84:G:H2'	2:B:85:G:H8	1.85	0.42
3:9P:205:ASN:HB3	29:6:46:ARG:HB2	2.01	0.42
3:9P:293:ALA:HA	3:9P:296:LYS:HB2	2.01	0.42
6:D:79:LEU:HD23	6:D:79:LEU:HA	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:W:40:LYS:HG3	19:W:41:PHE:HD1	1.85	0.42
27:K:8:LEU:HG	27:K:82:ASN:HB2	2.00	0.42
30:H:128:HIS:N	30:H:144:VAL:O	2.51	0.42
31:F:72:SER:HB2	31:F:80:GLN:H	1.83	0.42
1:A:28:A:H2'	1:A:29:U:C6	2.55	0.42
1:A:356:G:H2'	1:A:357:C:C6	2.54	0.42
1:A:464:U:O4	1:A:788:A:C5	2.72	0.42
1:A:538:A:H4'	9:J:7:LYS:HG2	2.00	0.42
1:A:811:U:H3'	10:L:22:GLY:HA2	2.01	0.42
1:A:2231:U:H2'	1:A:2232:C:C6	2.53	0.42
1:A:2813:A:H2'	1:A:2814:A:H8	1.84	0.42
1:A:2818:U:H2'	1:A:2819:G:C8	2.54	0.42
2:B:116:G:H2'	2:B:117:G:C8	2.55	0.42
5:C:42:ARG:HG2	5:C:48:ILE:HG13	2.01	0.42
6:D:124:ARG:HD3	6:D:125:TRP:NE1	2.34	0.42
13:Q:93:ILE:O	13:Q:97:ILE:HG12	2.19	0.42
13:Q:102:LYS:HB2	13:Q:102:LYS:HE2	1.71	0.42
31:F:122:ASP:O	31:F:124:ARG:NH1	2.52	0.42
1:A:30:G:O2'	1:A:1214:A:N3	2.50	0.42
1:A:39:G:H1'	7:E:43:THR:HG21	2.00	0.42
1:A:206:U:C2	1:A:207:A:C8	3.08	0.42
1:A:755:U:H2'	1:A:756:A:H8	1.83	0.42
1:A:1015:U:H2'	1:A:1016:G:C8	2.54	0.42
1:A:2576:G:O2'	1:A:2579:C:OP2	2.29	0.42
1:A:2749:A:H5'	8:G:1:SER:N	2.35	0.42
9:J:142:ILE:HD13	9:J:142:ILE:HA	1.96	0.42
15:S:4:ILE:HG23	15:S:106:VAL:HG22	2.01	0.42
27:K:77:ILE:HG13	28:P:71:ARG:HH12	1.85	0.42
1:A:110:G:H2'	1:A:111:A:H8	1.85	0.42
1:A:146:A:H2'	1:A:147:C:C6	2.55	0.42
1:A:418:C:H2'	1:A:419:U:C6	2.55	0.42
1:A:817:C:H2'	1:A:818:G:O4'	2.19	0.42
1:A:1494:A:H2'	1:A:1495:A:C8	2.55	0.42
1:A:2144:G:O2'	1:A:2147:A:N6	2.53	0.42
1:A:2412:A:H2'	1:A:2413:G:O4'	2.20	0.42
7:E:151:GLY:HA2	7:E:195:GLN:NE2	2.34	0.42
8:G:4:ALA:HB2	8:G:65:GLY:HA2	2.00	0.42
8:G:120:ILE:HD11	8:G:139:VAL:HG13	2.02	0.42
11:N:24:MET:HE2	11:N:40:LYS:HB3	2.02	0.42
13:Q:102:LYS:O	13:Q:106:THR:HG23	2.20	0.42
23:O:54:ILE:HG13	23:O:55:ALA:N	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:G:N2	1:A:512:G:H1'	2.31	0.42
1:A:128:C:H2'	1:A:129:C:C6	2.54	0.42
1:A:397:U:H2'	1:A:398:C:C6	2.55	0.42
1:A:634:C:H2'	1:A:635:C:C6	2.55	0.42
1:A:754:U:C2	1:A:755:U:C5	3.08	0.42
1:A:860:U:H2'	1:A:861:A:H8	1.85	0.42
1:A:928:A:H2'	1:A:929:U:H6	1.85	0.42
1:A:969:G:N2	1:A:984:A:O2'	2.52	0.42
1:A:1818:U:H2'	5:C:155:ARG:HB2	2.02	0.42
1:A:1935:G:N2	1:A:1964:G:O4'	2.52	0.42
2:B:19:C:H2'	2:B:20:G:C8	2.55	0.42
2:B:51:G:H5''	12:O:64:TYR:CD2	2.55	0.42
6:D:12:THR:O	6:D:24:VAL:N	2.46	0.42
8:G:115:GLN:OE1	8:G:115:GLN:HA	2.20	0.42
13:Q:100:PHE:HD2	14:R:13:ARG:HH12	1.66	0.42
14:R:82:HIS:O	14:R:82:HIS:ND1	2.52	0.42
22:Z:19:HIS:O	22:Z:22:THR:OG1	2.31	0.42
23:O:33:SER:HB3	23:O:47:TYR:HD2	1.85	0.42
1:A:93:G:H2'	1:A:94:A:H8	1.85	0.42
1:A:116:C:O2'	1:A:126:A:H1'	2.20	0.42
1:A:686:U:H6	1:A:788:A:H61	1.68	0.42
1:A:1188:U:C2	1:A:1189:A:C8	3.07	0.42
1:A:1873:G:H2'	1:A:1874:C:H6	1.85	0.42
1:A:2093:G:C8	1:A:2225:A:H2'	2.55	0.42
1:A:2094:A:H5'	30:H:22:LYS:HZ1	1.83	0.42
1:A:2229:U:O2	20:X:33:HIS:HE1	2.03	0.42
1:A:2465:C:H2'	1:A:2466:C:C6	2.55	0.42
2:B:42:C:C5	31:F:65:LEU:HD11	2.55	0.42
2:B:74:U:H2'	2:B:75:G:O4'	2.20	0.42
2:B:106:G:H2'	2:B:107:G:O4'	2.19	0.42
3:9P:5:ASP:OD2	3:9P:6:GLU:N	2.53	0.42
6:D:16:THR:OG1	6:D:18:ASP:OD1	2.33	0.42
7:E:77:ILE:HG13	7:E:78:TRP:CD1	2.54	0.42
7:E:117:ARG:NH2	7:E:183:PHE:O	2.43	0.42
10:L:81:ASP:O	10:L:82:LEU:HG	2.20	0.42
12:O:35:ILE:O	12:O:53:THR:OG1	2.25	0.42
16:T:2:ILE:HG23	16:T:4:GLU:H	1.83	0.42
16:T:38:ALA:HB3	16:T:81:LYS:HD2	2.01	0.42
24:1:39:ASP:HB2	24:1:42:VAL:HG12	2.01	0.42
30:H:41:LYS:HD2	30:H:44:ILE:HD11	2.01	0.42
1:A:309:A:H1'	1:A:329:G:C4	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:G:H2'	1:A:409:G:C8	2.55	0.42
1:A:475:C:N3	1:A:479:A:N7	2.68	0.42
1:A:627:A:O4'	1:A:637:A:N6	2.53	0.42
1:A:710:U:H2'	1:A:711:G:C8	2.53	0.42
1:A:1435:G:H2'	1:A:1436:G:H8	1.85	0.42
1:A:1824:G:H2'	1:A:1825:U:C6	2.55	0.42
3:9P:2:LYS:HE2	8:G:176:LYS:N	2.31	0.42
3:9P:45:VAL:HB	3:9P:118:ALA:HB3	2.01	0.42
5:C:246:PRO:HG2	5:C:247:TRP:CZ3	2.55	0.42
8:G:84:LYS:O	8:G:132:LEU:N	2.45	0.42
11:N:56:LYS:HE3	11:N:87:PHE:O	2.20	0.42
20:X:52:ALA:O	20:X:56:ARG:HG3	2.20	0.42
20:X:67:LEU:HA	20:X:70:LEU:HD23	2.01	0.42
21:Y:2:LYS:HG2	21:Y:52:ARG:HD3	2.01	0.42
30:H:135:HIS:CD2	30:H:137:GLU:HG2	2.55	0.42
1:A:155:A:H2'	1:A:156:A:C8	2.55	0.41
1:A:419:U:H2'	1:A:420:C:C6	2.55	0.41
1:A:587:C:C2	10:L:19:LEU:HD11	2.55	0.41
1:A:657:U:H2'	1:A:658:U:C6	2.55	0.41
1:A:807:U:H5	10:L:41:ARG:NH2	2.18	0.41
1:A:874:G:H2'	1:A:875:G:H8	1.85	0.41
1:A:1341:G:O4'	16:T:61:LEU:HD21	2.20	0.41
1:A:1352:U:H1'	1:A:1570:A:C2	2.54	0.41
1:A:1406:U:H2'	1:A:1407:G:H8	1.85	0.41
1:A:1520:U:H2'	1:A:1521:G:O4'	2.20	0.41
1:A:1873:G:H2'	1:A:1874:C:C6	2.55	0.41
1:A:2058:A:H2'	1:A:2059:A:C8	2.55	0.41
1:A:2065:C:H2'	1:A:2066:C:C6	2.55	0.41
2:B:95:U:H2'	2:B:96:G:C8	2.55	0.41
3:9P:235:LEU:HG	3:9P:236:GLU:H	1.85	0.41
8:G:77:GLY:HA3	8:G:135:ALA:O	2.20	0.41
26:I:129:GLU:HA	26:I:132:ALA:HB3	2.01	0.41
31:F:69:ALA:N	31:F:82:TYR:O	2.52	0.41
31:F:134:GLN:HE22	31:F:148:VAL:HA	1.85	0.41
1:A:514:A:C4	1:A:515:A:C8	3.08	0.41
1:A:1095:A:N1	3:9P:189:TYR:HE2	2.19	0.41
1:A:1279:G:H2'	1:A:1280:G:H8	1.84	0.41
1:A:1532:A:N6	1:A:1540:G:O6	2.53	0.41
1:A:1541:C:H2'	1:A:1542:U:C6	2.54	0.41
1:A:2052:A:C8	6:D:146:ILE:HD11	2.55	0.41
1:A:2063:C:H2'	1:A:2064:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2072:C:H2'	1:A:2073:C:C6	2.54	0.41
1:A:2093:G:H2'	1:A:2094:A:C8	2.55	0.41
1:A:2679:A:H2'	1:A:2680:U:H6	1.85	0.41
1:A:2850:A:N7	1:A:2868:A:O2'	2.43	0.41
1:A:2909:C:H2'	1:A:2910:G:H8	1.84	0.41
3:9P:258:ASN:OD1	3:9P:259:ALA:N	2.52	0.41
6:D:26:VAL:HG21	28:P:4:ILE:HD13	2.01	0.41
7:E:120:VAL:HA	7:E:188:MET:O	2.20	0.41
11:N:58:ASP:HA	11:N:80:PHE:HD1	1.84	0.41
15:S:35:ILE:O	15:S:39:THR:OG1	2.27	0.41
19:W:67:VAL:O	19:W:68:LYS:HE2	2.20	0.41
24:1:37:LYS:HD3	24:1:37:LYS:HA	1.76	0.41
26:I:3:LYS:HG3	26:I:4:VAL:H	1.85	0.41
26:I:9:LYS:HD3	26:I:55:PRO:HB3	2.01	0.41
31:F:120:SER:HB2	31:F:129:MET:HE1	2.01	0.41
1:A:100:U:H4'	1:A:101:A:H5'	2.02	0.41
1:A:297:G:H2'	1:A:298:G:O4'	2.20	0.41
1:A:358:U:H2'	1:A:359:G:C8	2.54	0.41
1:A:599:A:H2'	1:A:600:G:C8	2.56	0.41
1:A:697:G:H2'	1:A:698:C:C6	2.54	0.41
1:A:1372:U:H2'	1:A:1373:A:C8	2.55	0.41
1:A:1818:U:H3'	5:C:156:SER:H	1.84	0.41
1:A:1850:G:H2'	1:A:1851:U:C6	2.56	0.41
1:A:1862:G:O6	1:A:1881:C:N4	2.53	0.41
1:A:2087:G:H2'	1:A:2088:A:H8	1.84	0.41
1:A:2643:G:H2'	1:A:2644:G:C8	2.54	0.41
1:A:2774:C:H2'	1:A:2775:G:O4'	2.19	0.41
11:N:110:MET:SD	11:N:110:MET:N	2.92	0.41
18:V:46:LYS:NZ	18:V:50:MET:SD	2.92	0.41
21:Y:38:GLN:OE1	21:Y:38:GLN:N	2.53	0.41
26:I:20:SER:HB3	26:I:21:PRO:HD3	2.02	0.41
28:P:88:ARG:NH2	28:P:111:GLU:OE2	2.53	0.41
1:A:31:C:H4'	1:A:1238:G:H4'	2.03	0.41
1:A:102:U:H5	21:Y:1:MET:H2	1.69	0.41
1:A:136:G:O6	1:A:144:A:N6	2.53	0.41
1:A:170:U:H2'	1:A:171:U:H6	1.85	0.41
1:A:419:U:H2'	1:A:420:C:H6	1.85	0.41
1:A:523:C:H2'	1:A:524:G:C8	2.55	0.41
1:A:728:G:H4'	5:C:12:ARG:HD2	2.03	0.41
1:A:924:G:H2'	1:A:925:A:H8	1.86	0.41
1:A:1092:C:H2'	1:A:1093:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1308:A:H2'	1:A:1309:G:O4'	2.20	0.41
1:A:1378:A:H4'	1:A:1379:U:OP1	2.20	0.41
1:A:1496:A:H2'	1:A:1498:C:H5	1.85	0.41
1:A:1658:C:H2'	1:A:1659:G:H8	1.85	0.41
1:A:1798:U:OP2	5:C:270:ARG:NH1	2.39	0.41
1:A:1805:A:H2'	1:A:1806:C:C6	2.55	0.41
1:A:2417:C:H2'	1:A:2418:A:C8	2.55	0.41
1:A:2622:U:O2'	1:A:2825:G:N7	2.54	0.41
3:9P:71:GLN:HB2	3:9P:81:LYS:N	2.34	0.41
5:C:2:VAL:HG12	5:C:18:VAL:HG22	2.02	0.41
5:C:269:ARG:HA	5:C:269:ARG:HD2	1.95	0.41
17:U:51:LEU:O	17:U:51:LEU:HD12	2.20	0.41
30:H:75:LEU:O	30:H:76:GLU:HG3	2.21	0.41
1:A:24:G:H2'	1:A:25:U:H6	1.85	0.41
1:A:181:A:H1'	1:A:435:C:H5'	2.02	0.41
1:A:459:U:H2'	1:A:460:A:C8	2.55	0.41
1:A:594:U:H2'	1:A:595:C:C6	2.56	0.41
1:A:775:G:C5	1:A:794:A:C8	3.09	0.41
1:A:1201:U:H2'	1:A:1202:G:H8	1.86	0.41
1:A:1630:A:N6	1:A:1637:A:H61	2.17	0.41
1:A:1635:A:H2'	1:A:1636:U:O4'	2.19	0.41
1:A:1678:A:C4	1:A:1679:A:C8	3.08	0.41
1:A:2087:G:H2'	1:A:2088:A:C8	2.55	0.41
1:A:2379:G:H2'	1:A:2380:C:C6	2.56	0.41
1:A:2556:C:H1'	3:9P:78:CYS:HA	2.01	0.41
2:B:42:C:O2'	2:B:43:C:OP1	2.37	0.41
2:B:116:G:H2'	2:B:117:G:H8	1.84	0.41
3:9P:173:SER:HB3	3:9P:186:VAL:HG22	2.02	0.41
4:b:8:LYS:HB3	4:b:10:GLU:OE1	2.20	0.41
5:C:157:ALA:HB1	5:C:196:ASN:O	2.20	0.41
9:J:72:LYS:HE3	9:J:74:TYR:CE1	2.55	0.41
31:F:159:ALA:HB1	31:F:164:GLU:HB2	2.03	0.41
1:A:521:U:H2'	1:A:522:A:H8	1.86	0.41
1:A:797:G:OP1	7:E:55:SER:HB2	2.20	0.41
1:A:1270:C:N4	1:A:1648:U:O4	2.53	0.41
1:A:1440:U:H2'	1:A:1441:G:H8	1.84	0.41
1:A:1571:A:H2'	1:A:1572:A:H8	1.86	0.41
1:A:1589:U:H2'	1:A:1590:A:C8	2.56	0.41
3:9P:25:ARG:HB2	3:9P:29:ILE:O	2.21	0.41
9:J:91:GLU:HA	9:J:94:ALA:HB3	2.01	0.41
13:Q:87:VAL:HG22	14:R:49:ILE:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:V:83:LYS:HB3	18:V:85:LYS:HZ3	1.86	0.41
22:Z:18:LYS:HE3	22:Z:18:LYS:HB2	1.81	0.41
31:F:28:PRO:HB3	31:F:159:ALA:HB2	2.02	0.41
1:A:9:G:N2	1:A:2800:A:H61	2.18	0.41
1:A:216:A:C8	1:A:432:A:N6	2.88	0.41
1:A:541:A:H2'	1:A:542:C:H6	1.85	0.41
1:A:1429:G:H2'	1:A:1430:G:C8	2.51	0.41
1:A:1826:G:H2'	1:A:1827:U:H6	1.85	0.41
1:A:2544:G:H1'	1:A:2646:C:H5'	2.02	0.41
1:A:2749:A:H5'	8:G:1:SER:H1	1.86	0.41
1:A:2875:C:H2'	1:A:2876:G:H8	1.86	0.41
2:B:112:G:N2	12:O:45:SER:O	2.48	0.41
3:9P:249:PRO:HB2	3:9P:252:GLY:H	1.85	0.41
6:D:184:ARG:HD3	28:P:6:GLN:HE22	1.86	0.41
7:E:192:ALA:HA	7:E:195:GLN:HE22	1.85	0.41
17:U:34:ILE:HD13	17:U:63:ALA:HA	2.02	0.41
30:H:135:HIS:HD2	30:H:138:VAL:HG23	1.86	0.41
1:A:155:A:H2'	1:A:156:A:H8	1.86	0.41
1:A:408:G:O6	1:A:419:U:O4	2.39	0.41
1:A:517:C:OP1	23:O:12:ARG:NH2	2.54	0.41
1:A:589:U:H2'	1:A:590:A:H8	1.85	0.41
1:A:748:G:OP1	15:S:88:ARG:NH1	2.53	0.41
1:A:1203:U:O2'	10:L:4:ASN:HB2	2.19	0.41
1:A:2554:U:H2'	1:A:2555:U:C6	2.56	0.41
1:A:2567:G:H2'	1:A:2568:U:C6	2.55	0.41
1:A:2843:G:H2'	1:A:2844:G:C8	2.56	0.41
2:B:43:C:H2'	31:F:91:ARG:HB3	2.01	0.41
6:D:33:ARG:H	6:D:33:ARG:HG2	1.68	0.41
7:E:102:ARG:O	7:E:106:LYS:HG3	2.21	0.41
10:L:112:LEU:HD22	10:L:131:ALA:N	2.36	0.41
21:Y:21:LEU:HA	21:Y:25:GLN:HB2	2.03	0.41
30:H:3:VAL:HG23	30:H:37:VAL:C	2.46	0.41
1:A:67:U:C2	1:A:68:G:C8	3.08	0.41
1:A:183:C:H1'	1:A:432:A:H2	1.86	0.41
1:A:634:C:H2'	1:A:635:C:H6	1.86	0.41
1:A:732:C:H2'	1:A:733:G:O4'	2.20	0.41
1:A:1233:C:H2'	1:A:1234:U:C6	2.55	0.41
1:A:1407:G:H2'	1:A:1408:G:C8	2.53	0.41
1:A:1656:C:H2'	1:A:1657:U:H6	1.86	0.41
1:A:1664:A:H61	1:A:1996:C:H42	1.69	0.41
1:A:1746:A:H2'	1:A:1747:U:H6	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1798:U:H5''	5:C:257:ARG:HB2	2.03	0.41
1:A:1806:C:H1'	5:C:43:ASN:HD21	1.86	0.41
1:A:1808:A:H3'	1:A:1809:A:C8	2.56	0.41
1:A:1848:A:H2'	1:A:1849:G:O4'	2.21	0.41
1:A:1853:A:H2'	1:A:1854:A:C8	2.55	0.41
1:A:2120:G:H2'	1:A:2121:G:C8	2.53	0.41
1:A:2266:A:H4'	1:A:2267:A:N3	2.36	0.41
1:A:2615:U:H2'	1:A:2616:C:C6	2.56	0.41
1:A:2899:A:H2'	1:A:2900:A:C8	2.56	0.41
2:B:115:A:H2'	2:B:116:G:H8	1.85	0.41
5:C:120:ASP:OD1	5:C:121:ALA:N	2.49	0.41
7:E:149:ILE:HG23	7:E:188:MET:HA	2.03	0.41
11:N:99:LYS:HB3	23:O:41:HIS:CE1	2.55	0.41
15:S:27:LYS:HE3	15:S:27:LYS:HB3	1.65	0.41
15:S:73:LYS:HE2	15:S:75:PHE:CD1	2.55	0.41
15:S:80:PRO:O	15:S:100:THR:OG1	2.33	0.41
17:U:12:VAL:HG21	17:U:38:ILE:HG21	2.02	0.41
22:Z:40:THR:HG22	22:Z:42:ALA:H	1.86	0.41
23:O:11:LYS:HA	23:O:11:LYS:HD3	1.83	0.41
31:F:175:PRO:O	31:F:176:PHE:CG	2.73	0.41
1:A:465:G:HO2'	1:A:683:U:HO2'	1.55	0.41
1:A:585:G:H21	1:A:1254:A:N6	2.19	0.41
1:A:742:A:H2'	1:A:743:A:H8	1.85	0.41
1:A:784:G:C4	5:C:227:VAL:HG21	2.56	0.41
1:A:1759:A:H1'	1:A:2711:A:C2	2.56	0.41
1:A:1927:A:H2'	1:A:1928:A:C8	2.55	0.41
1:A:1942:C:P	1:A:1943:U:H2'	2.61	0.41
1:A:2313:C:H2'	1:A:2314:A:H8	1.84	0.41
1:A:2627:G:N2	1:A:2777:G:OP2	2.51	0.41
1:A:2834:G:H1'	1:A:2883:A:N6	2.36	0.41
1:A:2908:A:H2'	1:A:2909:C:C6	2.56	0.41
7:E:40:ARG:HD2	7:E:40:ARG:HA	1.77	0.41
8:G:36:LEU:HD22	8:G:40:VAL:HG21	2.02	0.41
10:L:55:MET:CE	10:L:59:ARG:HD3	2.51	0.41
16:T:37:ASP:CG	16:T:38:ALA:H	2.29	0.41
19:W:41:PHE:HA	19:W:74:LYS:HB2	2.04	0.41
30:H:54:LEU:HA	30:H:57:LYS:HG2	2.03	0.41
31:F:24:VAL:HG23	31:F:25:MET:SD	2.61	0.41
1:A:43:G:H2'	1:A:44:A:C8	2.57	0.40
1:A:181:A:H2'	1:A:182:A:C8	2.56	0.40
1:A:296:U:H2'	1:A:297:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:987:C:H2'	1:A:988:A:O4'	2.21	0.40
1:A:1323:C:P	15:S:84:ARG:HH12	2.40	0.40
1:A:2520:C:H2'	1:A:2521:C:C6	2.56	0.40
1:A:2906:C:H2'	1:A:2907:A:H8	1.86	0.40
3:9P:241:LEU:HD23	3:9P:241:LEU:HA	1.95	0.40
8:G:83:THR:HG22	8:G:133:LYS:HD3	2.02	0.40
19:W:41:PHE:CD2	19:W:76:ILE:HD11	2.56	0.40
28:P:70:GLU:OE1	28:P:100:ARG:NH1	2.54	0.40
1:A:563:A:H4'	13:Q:40:LYS:NZ	2.36	0.40
1:A:565:C:H2'	1:A:566:U:H6	1.85	0.40
1:A:1283:G:H1'	1:A:1329:U:O2	2.20	0.40
1:A:1296:G:OP1	1:A:2709:G:O2'	2.26	0.40
1:A:1462:C:C2	1:A:1463:C:C5	3.09	0.40
1:A:1499:C:C2	1:A:1500:G:C8	3.10	0.40
1:A:1505:A:H2'	1:A:1506:U:C6	2.57	0.40
1:A:1696:G:N2	1:A:1977:A:O2'	2.52	0.40
1:A:1850:G:H2'	1:A:1851:U:H6	1.87	0.40
1:A:2346:A:O2'	24:1:37:LYS:NZ	2.48	0.40
2:B:37:C:H42	2:B:49:C:H1'	1.86	0.40
3:9P:108:MET:HE2	3:9P:108:MET:HA	2.03	0.40
3:9P:217:LEU:HD22	3:9P:229:ILE:HG22	2.03	0.40
8:G:126:THR:HG23	8:G:128:THR:H	1.86	0.40
12:O:68:LYS:HG2	12:O:102:ARG:HA	2.03	0.40
16:T:5:GLU:H	16:T:5:GLU:CD	2.28	0.40
16:T:13:ALA:HA	21:Y:30:MET:HE1	2.03	0.40
17:U:86:PHE:CE1	17:U:91:LYS:HG2	2.56	0.40
21:Y:51:ALA:O	21:Y:55:THR:HG23	2.21	0.40
31:F:110:ILE:HB	31:F:113:PHE:HB2	2.04	0.40
1:A:7:G:H5'	9:J:132:HIS:HE1	1.85	0.40
1:A:39:G:H2'	1:A:40:U:C6	2.55	0.40
1:A:305:C:H2'	1:A:306:U:H6	1.84	0.40
1:A:481:G:N1	1:A:507:A:H1'	2.36	0.40
1:A:592:A:H2'	1:A:593:U:C6	2.57	0.40
1:A:672:C:H5	10:L:42:SER:HB2	1.86	0.40
1:A:753:A:H2'	1:A:754:U:C6	2.56	0.40
1:A:1301:A:C4	1:A:1303:G:C8	3.09	0.40
1:A:1550:C:H2'	1:A:1551:A:H8	1.86	0.40
1:A:1794:A:H2'	1:A:1795:C:C6	2.56	0.40
1:A:2338:C:H2'	1:A:2339:C:C6	2.56	0.40
1:A:2656:U:H2'	1:A:2657:A:C8	2.56	0.40
1:A:2895:G:H2'	1:A:2896:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:9P:322:LYS:HB3	3:9P:326:TRP:CZ3	2.57	0.40
5:C:24:HIS:CG	5:C:79:ARG:HD2	2.56	0.40
5:C:29:PHE:HD2	5:C:32:LEU:HD23	1.85	0.40
6:D:125:TRP:HB2	6:D:127:PHE:CE2	2.56	0.40
8:G:34:ARG:NH1	8:G:36:LEU:HA	2.36	0.40
9:J:99:ARG:HE	9:J:99:ARG:HB3	1.66	0.40
10:L:70:LYS:HE2	10:L:70:LYS:HB3	1.82	0.40
16:T:24:MET:HE1	16:T:30:ILE:HB	2.03	0.40
20:X:41:SER:OG	20:X:64:ASP:OD1	2.37	0.40
21:Y:37:LEU:O	21:Y:37:LEU:HD23	2.21	0.40
21:Y:49:ASP:OD1	21:Y:52:ARG:NH2	2.51	0.40
22:Z:18:LYS:O	22:Z:22:THR:HG23	2.21	0.40
27:K:1:MET:HB2	27:K:67:LYS:HE3	2.03	0.40
1:A:87:U:H3	1:A:95:A:H61	1.68	0.40
1:A:186:G:H2'	1:A:187:G:H8	1.87	0.40
1:A:243:U:H2'	1:A:244:A:C8	2.56	0.40
1:A:357:C:H2'	1:A:358:U:C6	2.57	0.40
1:A:727:A:H2'	1:A:728:G:O4'	2.21	0.40
1:A:1510:G:H2'	1:A:1511:G:H8	1.86	0.40
1:A:1511:G:H2'	1:A:1512:C:C6	2.57	0.40
1:A:1684:G:O6	1:A:1705:A:N6	2.54	0.40
1:A:1851:U:H3	1:A:1891:G:H1	1.69	0.40
1:A:2127:G:H4'	1:A:2128:G:OP1	2.21	0.40
1:A:2161:C:O2'	1:A:2173:A:O5'	2.37	0.40
1:A:2448:A:H1'	1:A:2451:A:N6	2.37	0.40
1:A:2667:C:H1'	8:G:108:PHE:CD2	2.56	0.40
1:A:2840:C:C2	1:A:2841:C:C5	3.10	0.40
1:A:2841:C:H2'	1:A:2842:G:C8	2.56	0.40
2:B:90:C:H2'	2:B:91:C:O4'	2.21	0.40
3:9P:209:PHE:CE1	3:9P:328:VAL:HG21	2.56	0.40
3:9P:267:GLU:HG3	3:9P:272:ASP:OD1	2.22	0.40
5:C:24:HIS:ND1	5:C:79:ARG:HD2	2.36	0.40
15:S:6:LYS:HB3	15:S:104:THR:HG23	2.03	0.40
17:U:39:ASN:HB3	17:U:62:ALA:HB3	2.02	0.40
26:I:4:VAL:HG12	26:I:5:GLN:N	2.30	0.40
1:A:20:C:H2'	1:A:21:A:C8	2.57	0.40
1:A:479:A:H1'	1:A:481:G:H5'	2.04	0.40
1:A:549:G:H5''	1:A:550:C:H6	1.87	0.40
1:A:678:C:H2'	1:A:679:C:H6	1.86	0.40
1:A:680:C:H2'	1:A:681:G:H8	1.86	0.40
1:A:851:C:H2'	1:A:852:U:H6	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:932:U:O2'	1:A:934:U:O4	2.30	0.40
1:A:959:A:H2'	1:A:960:A:C8	2.56	0.40
1:A:963:U:H2'	1:A:964:C:C6	2.57	0.40
1:A:2123:G:O6	1:A:2176:A:N6	2.55	0.40
1:A:2200:C:H2'	1:A:2201:G:H8	1.86	0.40
1:A:2350:C:H2'	1:A:2351:G:O4'	2.21	0.40
1:A:2533:U:H2'	1:A:2534:A:O4'	2.22	0.40
1:A:2673:G:H2'	1:A:2674:G:C8	2.53	0.40
1:A:2675:A:H5''	27:K:31:ARG:HG2	2.03	0.40
1:A:2834:G:H1'	1:A:2883:A:H61	1.86	0.40
5:C:4:LYS:HG2	5:C:16:VAL:HG22	2.03	0.40
10:L:112:LEU:HD23	10:L:112:LEU:H	1.87	0.40
11:N:98:LEU:O	11:N:112:TYR:N	2.52	0.40
13:Q:16:ILE:HG13	13:Q:31:TYR:HE1	1.87	0.40
18:V:26:PHE:CE1	18:V:47:VAL:HG11	2.56	0.40
31:F:91:ARG:HD2	31:F:92:GLY:H	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	9P	336/390 (86%)	313 (93%)	23 (7%)	0	100	100
4	b	45/70 (64%)	43 (96%)	2 (4%)	0	100	100
5	C	269/273 (98%)	250 (93%)	19 (7%)	0	100	100
6	D	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
7	E	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
8	G	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
9	J	140/142 (99%)	135 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	L	141/144 (98%)	121 (86%)	20 (14%)	0	100	100
11	N	118/127 (93%)	113 (96%)	5 (4%)	0	100	100
12	O	114/117 (97%)	105 (92%)	9 (8%)	0	100	100
13	Q	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
14	R	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
15	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
16	T	91/100 (91%)	80 (88%)	11 (12%)	0	100	100
17	U	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
18	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
19	W	74/85 (87%)	72 (97%)	2 (3%)	0	100	100
20	X	75/78 (96%)	75 (100%)	0	0	100	100
21	Y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
22	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
23	0	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
24	1	48/55 (87%)	47 (98%)	1 (2%)	0	100	100
25	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
26	I	139/142 (98%)	113 (81%)	26 (19%)	0	100	100
27	K	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
28	P	111/115 (96%)	106 (96%)	5 (4%)	0	100	100
29	6	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
30	H	147/149 (99%)	133 (90%)	14 (10%)	0	100	100
31	F	175/179 (98%)	162 (93%)	13 (7%)	0	100	100
All	All	3554/3735 (95%)	3325 (94%)	229 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	
3	9P	273/321 (85%)	272 (100%)	1 (0%)	84	81
4	b	43/62 (69%)	43 (100%)	0	100	100
5	C	216/218 (99%)	216 (100%)	0	100	100
6	D	164/164 (100%)	164 (100%)	0	100	100
7	E	165/165 (100%)	165 (100%)	0	100	100
8	G	137/138 (99%)	137 (100%)	0	100	100
9	J	116/116 (100%)	116 (100%)	0	100	100
10	L	102/103 (99%)	102 (100%)	0	100	100
11	N	100/103 (97%)	100 (100%)	0	100	100
12	O	86/87 (99%)	86 (100%)	0	100	100
13	Q	89/90 (99%)	89 (100%)	0	100	100
14	R	84/84 (100%)	84 (100%)	0	100	100
15	S	93/93 (100%)	93 (100%)	0	100	100
16	T	80/84 (95%)	80 (100%)	0	100	100
17	U	83/85 (98%)	83 (100%)	0	100	100
18	V	78/78 (100%)	78 (100%)	0	100	100
19	W	56/63 (89%)	56 (100%)	0	100	100
20	X	67/68 (98%)	67 (100%)	0	100	100
21	Y	55/55 (100%)	55 (100%)	0	100	100
22	Z	48/49 (98%)	48 (100%)	0	100	100
23	0	47/48 (98%)	47 (100%)	0	100	100
24	1	45/49 (92%)	45 (100%)	0	100	100
25	2	38/38 (100%)	38 (100%)	0	100	100
26	I	109/110 (99%)	109 (100%)	0	100	100
27	K	103/104 (99%)	103 (100%)	0	100	100
28	P	98/100 (98%)	98 (100%)	0	100	100
29	6	88/91 (97%)	88 (100%)	0	100	100
30	H	114/114 (100%)	114 (100%)	0	100	100
31	F	148/150 (99%)	148 (100%)	0	100	100
All	All	2925/3030 (96%)	2924 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
3	9P	52	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
3	9P	143	ASN
5	C	14	HIS
5	C	52	HIS
6	D	32	ASN
6	D	49	GLN
6	D	185	ASN
7	E	94	GLN
8	G	21	GLN
8	G	44	HIS
9	J	80	HIS
10	L	4	ASN
14	R	12	HIS
14	R	89	HIS
17	U	65	GLN
17	U	68	ASN
18	V	80	HIS
19	W	36	GLN
21	Y	58	ASN
26	I	42	ASN
26	I	104	GLN
27	K	3	GLN
29	6	47	HIS
30	H	28	ASN
30	H	73	ASN
30	H	135	HIS
31	F	22	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2899/2919 (99%)	436 (15%)	14 (0%)
2	B	118/119 (99%)	18 (15%)	0
All	All	3017/3038 (99%)	454 (15%)	14 (0%)

All (454) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	12	U
1	A	14	A
1	A	27	G
1	A	28	A
1	A	34	U
1	A	35	G
1	A	46	G
1	A	51	G
1	A	63	A
1	A	71	A
1	A	74	A
1	A	75	G
1	A	103	A
1	A	110	G
1	A	118	A
1	A	120	U
1	A	125	A
1	A	126	A
1	A	138	U
1	A	139	U
1	A	140	C
1	A	141	G
1	A	142	A
1	A	144	A
1	A	160	A
1	A	181	A
1	A	196	A
1	A	199	A
1	A	216	A
1	A	221	A
1	A	222	A
1	A	230	G
1	A	248	G
1	A	255	A
1	A	266	G
1	A	267	C
1	A	272	A
1	A	278	A
1	A	302	C
1	A	311	A
1	A	329	G
1	A	330	A

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Mol	Chain	Res	Type
1	A	331	C
1	A	352	A
1	A	353	C
1	A	361	G
1	A	367	G
1	A	371	A
1	A	372	G
1	A	384	A
1	A	386	G
1	A	396	G
1	A	405	U
1	A	411	G
1	A	424	G
1	A	430	A
1	A	435	C
1	A	451	U
1	A	456	C
1	A	480	A
1	A	481	G
1	A	491	G
1	A	496	G
1	A	504	A
1	A	505	A
1	A	518	G
1	A	532	A
1	A	533	G
1	A	544	C
1	A	545	U
1	A	546	U
1	A	547	A
1	A	548	G
1	A	550	C
1	A	563	A
1	A	568	U
1	A	573	U
1	A	575	A
1	A	586	A
1	A	603	A
1	A	613	A
1	A	615	U
1	A	616	A
1	A	621	A

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Mol	Chain	Res	Type
1	A	627	A
1	A	631	A
1	A	637	A
1	A	645	C
1	A	647	G
1	A	654	A
1	A	655	A
1	A	686	U
1	A	705	A
1	A	726	G
1	A	729	G
1	A	730	A
1	A	747	U
1	A	764	A
1	A	770	G
1	A	775	G
1	A	776	G
1	A	782	A
1	A	784	G
1	A	785	G
1	A	789	A
1	A	791	C
1	A	792	A
1	A	805	G
1	A	812	C
1	A	819	A
1	A	827	U
1	A	829	A
1	A	830	G
1	A	845	A
1	A	846	U
1	A	847	U
1	A	857	G
1	A	858	G
1	A	860	U
1	A	866	A
1	A	878	A
1	A	879	G
1	A	885	C
1	A	896	A
1	A	910	A
1	A	915	C

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Mol	Chain	Res	Type
1	A	931	U
1	A	941	A
1	A	946	C
1	A	953	G
1	A	961	C
1	A	965	C
1	A	973	A
1	A	974	G
1	A	980	A
1	A	983	A
1	A	985	C
1	A	995	C
1	A	996	A
1	A	1009	A
1	A	1010	A
1	A	1012	U
1	A	1013	C
1	A	1017	G
1	A	1022	G
1	A	1026	G
1	A	1027	A
1	A	1033	U
1	A	1040	A
1	A	1046	A
1	A	1047	G
1	A	1057	A
1	A	1059	G
1	A	1060	U
1	A	1061	U
1	A	1063	G
1	A	1065	U
1	A	1066	U
1	A	1067	A
1	A	1070	A
1	A	1071	G
1	A	1072	C
1	A	1073	A
1	A	1074	G
1	A	1075	C
1	A	1081	U
1	A	1082	U
1	A	1083	U

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Mol	Chain	Res	Type
1	A	1087	G
1	A	1089	A
1	A	1092	C
1	A	1093	G
1	A	1098	A
1	A	1099	G
1	A	1104	C
1	A	1111	A
1	A	1112	G
1	A	1130	U
1	A	1132	U
1	A	1133	A
1	A	1135	C
1	A	1136	G
1	A	1142	A
1	A	1168	G
1	A	1171	G
1	A	1173	U
1	A	1174	U
1	A	1175	A
1	A	1176	U
1	A	1180	U
1	A	1181	U
1	A	1212	G
1	A	1224	U
1	A	1225	G
1	A	1236	G
1	A	1238	G
1	A	1253	A
1	A	1256	G
1	A	1266	G
1	A	1272	A
1	A	1300	G
1	A	1301	A
1	A	1314	C
1	A	1325	U
1	A	1329	U
1	A	1341	G
1	A	1345	C
1	A	1360	G
1	A	1365	A
1	A	1378	A

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Mol	Chain	Res	Type
1	A	1379	U
1	A	1416	G
1	A	1419	A
1	A	1435	G
1	A	1452	G
1	A	1458	U
1	A	1461	C
1	A	1482	G
1	A	1493	C
1	A	1496	A
1	A	1497	U
1	A	1504	A
1	A	1509	A
1	A	1510	G
1	A	1515	A
1	A	1523	U
1	A	1532	A
1	A	1533	C
1	A	1534	U
1	A	1535	A
1	A	1555	G
1	A	1566	A
1	A	1569	A
1	A	1578	U
1	A	1583	A
1	A	1585	C
1	A	1599	U
1	A	1603	A
1	A	1607	C
1	A	1608	A
1	A	1619	G
1	A	1634	A
1	A	1646	C
1	A	1647	U
1	A	1648	U
1	A	1652	A
1	A	1674	G
1	A	1715	G
1	A	1729	U
1	A	1730	C
1	A	1732	C
1	A	1736	U

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Mol	Chain	Res	Type
1	A	1738	G
1	A	1754	A
1	A	1757	A
1	A	1764	C
1	A	1773	A
1	A	1781	U
1	A	1800	C
1	A	1808	A
1	A	1816	C
1	A	1829	A
1	A	1835	G
1	A	1870	C
1	A	1908	C
1	A	1909	C
1	A	1914	C
1	A	1919	A
1	A	1925	C
1	A	1929	G
1	A	1930	G
1	A	1931	U
1	A	1937	A
1	A	1938	A
1	A	1943	U
1	A	1955	U
1	A	1965	C
1	A	1967	C
1	A	1970	A
1	A	1971	U
1	A	1972	G
1	A	1991	U
1	A	1992	G
1	A	1993	U
1	A	1997	C
1	A	2022	U
1	A	2023	C
1	A	2025	C
1	A	2031	A
1	A	2033	A
1	A	2043	C
1	A	2052	A
1	A	2055	C
1	A	2059	A

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Mol	Chain	Res	Type
1	A	2061	G
1	A	2062	A
1	A	2063	C
1	A	2064	C
1	A	2068	U
1	A	2069	G
1	A	2070	A
1	A	2072	C
1	A	2093	G
1	A	2095	A
1	A	2107	G
1	A	2110	G
1	A	2111	U
1	A	2112	G
1	A	2116	G
1	A	2117	A
1	A	2118	U
1	A	2119	A
1	A	2122	U
1	A	2123	G
1	A	2126	A
1	A	2128	G
1	A	2131	U
1	A	2132	U
1	A	2133	G
1	A	2136	G
1	A	2146	C
1	A	2148	G
1	A	2157	G
1	A	2158	A
1	A	2164	C
1	A	2165	C
1	A	2170	A
1	A	2171	A
1	A	2172	U
1	A	2173	A
1	A	2178	C
1	A	2187	U
1	A	2198	A
1	A	2199	A
1	A	2204	G
1	A	2211	A

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Mol	Chain	Res	Type
1	A	2225	A
1	A	2226	C
1	A	2238	G
1	A	2239	G
1	A	2249	U
1	A	2274	A
1	A	2275	C
1	A	2283	C
1	A	2287	A
1	A	2288	A
1	A	2297	A
1	A	2305	U
1	A	2308	G
1	A	2318	G
1	A	2319	G
1	A	2321	U
1	A	2322	A
1	A	2325	G
1	A	2327	A
1	A	2333	A
1	A	2335	A
1	A	2336	A
1	A	2357	G
1	A	2372	U
1	A	2383	G
1	A	2385	C
1	A	2402	U
1	A	2406	A
1	A	2425	A
1	A	2426	A
1	A	2428	G
1	A	2429	G
1	A	2430	A
1	A	2435	A
1	A	2441	U
1	A	2445	G
1	A	2447	G
1	A	2448	A
1	A	2449	U
1	A	2450	A
1	A	2456	C
1	A	2459	A

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Mol	Chain	Res	Type
1	A	2476	A
1	A	2491	U
1	A	2492	U
1	A	2513	A
1	A	2518	A
1	A	2520	C
1	A	2529	G
1	A	2535	G
1	A	2554	U
1	A	2564	A
1	A	2566	A
1	A	2567	G
1	A	2572	A
1	A	2573	C
1	A	2574	G
1	A	2585	U
1	A	2602	A
1	A	2603	G
1	A	2609	U
1	A	2610	C
1	A	2613	U
1	A	2615	U
1	A	2629	U
1	A	2630	G
1	A	2636	C
1	A	2639	A
1	A	2646	C
1	A	2656	U
1	A	2662	A
1	A	2682	A
1	A	2689	U
1	A	2690	U
1	A	2714	G
1	A	2726	A
1	A	2729	G
1	A	2733	A
1	A	2744	G
1	A	2748	A
1	A	2757	A
1	A	2765	A
1	A	2778	A
1	A	2780	G

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Mol	Chain	Res	Type
1	A	2791	G
1	A	2798	U
1	A	2818	U
1	A	2820	A
1	A	2825	G
1	A	2835	A
1	A	2849	U
1	A	2850	A
1	A	2867	G
1	A	2872	A
1	A	2873	A
1	A	2880	C
1	A	2884	U
1	A	2885	G
1	A	2886	A
2	B	2	G
2	B	15	A
2	B	23	G
2	B	24	G
2	B	35	C
2	B	36	C
2	B	37	C
2	B	39	A
2	B	41	G
2	B	42	C
2	B	43	C
2	B	44	G
2	B	52	A
2	B	87	U
2	B	89	U
2	B	90	C
2	B	99	A
2	B	109	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	271	G
1	A	404	A
1	A	479	A
1	A	995	C
1	A	1224	U

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Mol	Chain	Res	Type
1	A	1328	A
1	A	1378	A
1	A	1606	C
1	A	2058	A
1	A	2127	G
1	A	2273	A
1	A	2425	A
1	A	2573	C
1	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 [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

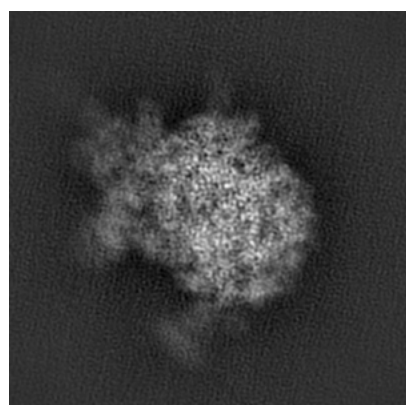
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12216. These allow visual inspection of the internal detail of the map and identification of artifacts.

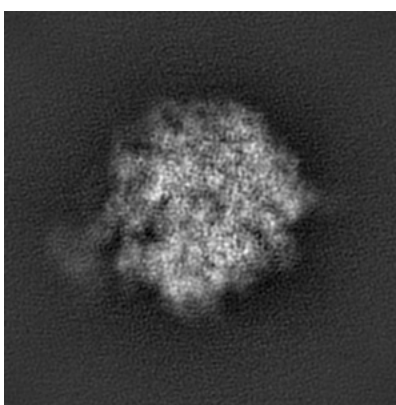
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

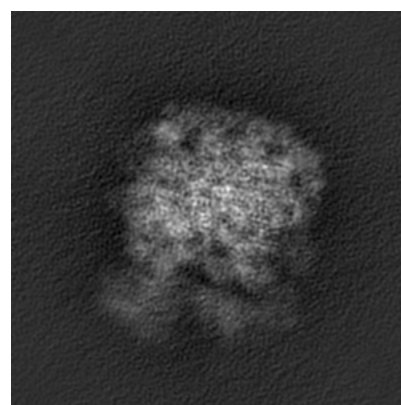
6.1.1 Primary map



X



Y

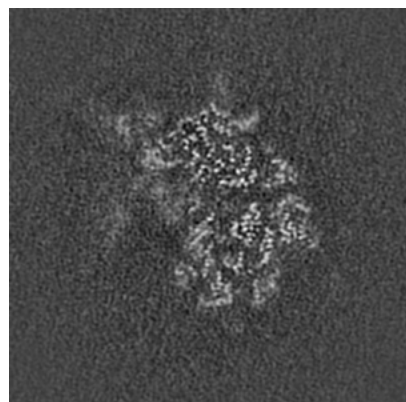


Z

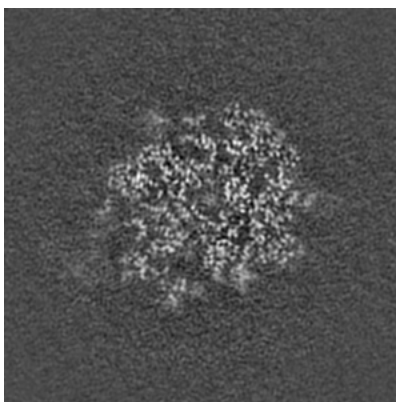
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

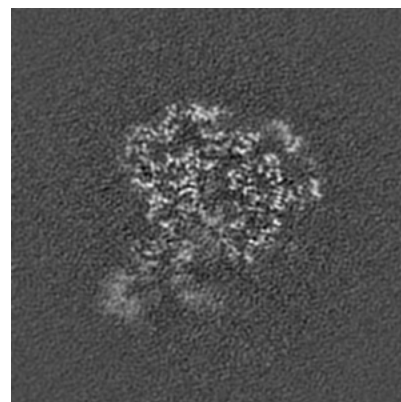
6.2.1 Primary map



X Index: 135



Y Index: 135

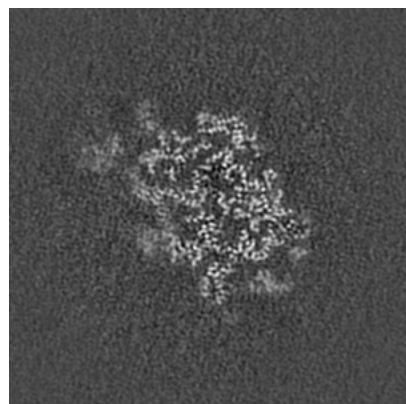


Z Index: 135

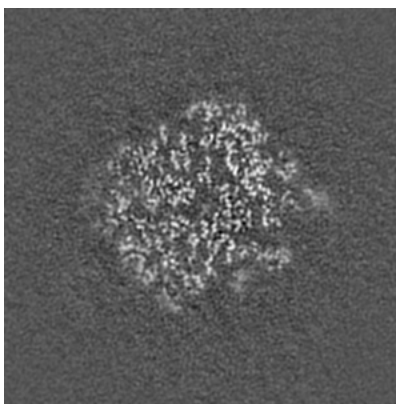
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

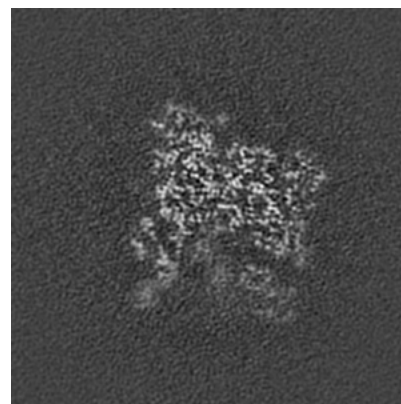
6.3.1 Primary map



X Index: 157



Y Index: 146

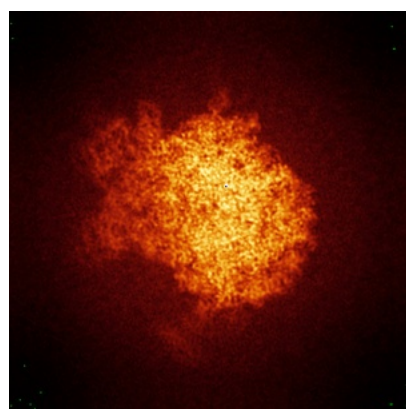


Z Index: 151

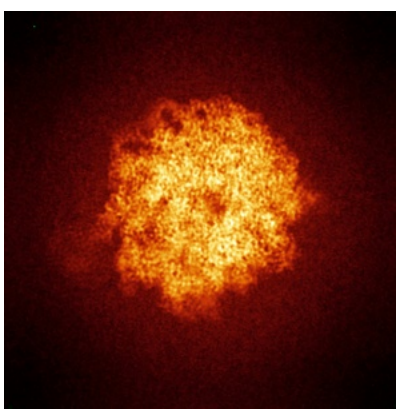
The images above show the largest variance slices of the map in three orthogonal directions.

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

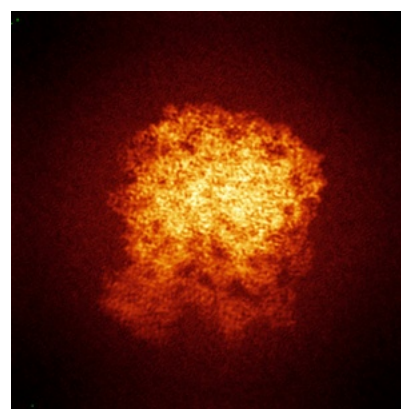
6.4.1 Primary map



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



X



Y



Z

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.

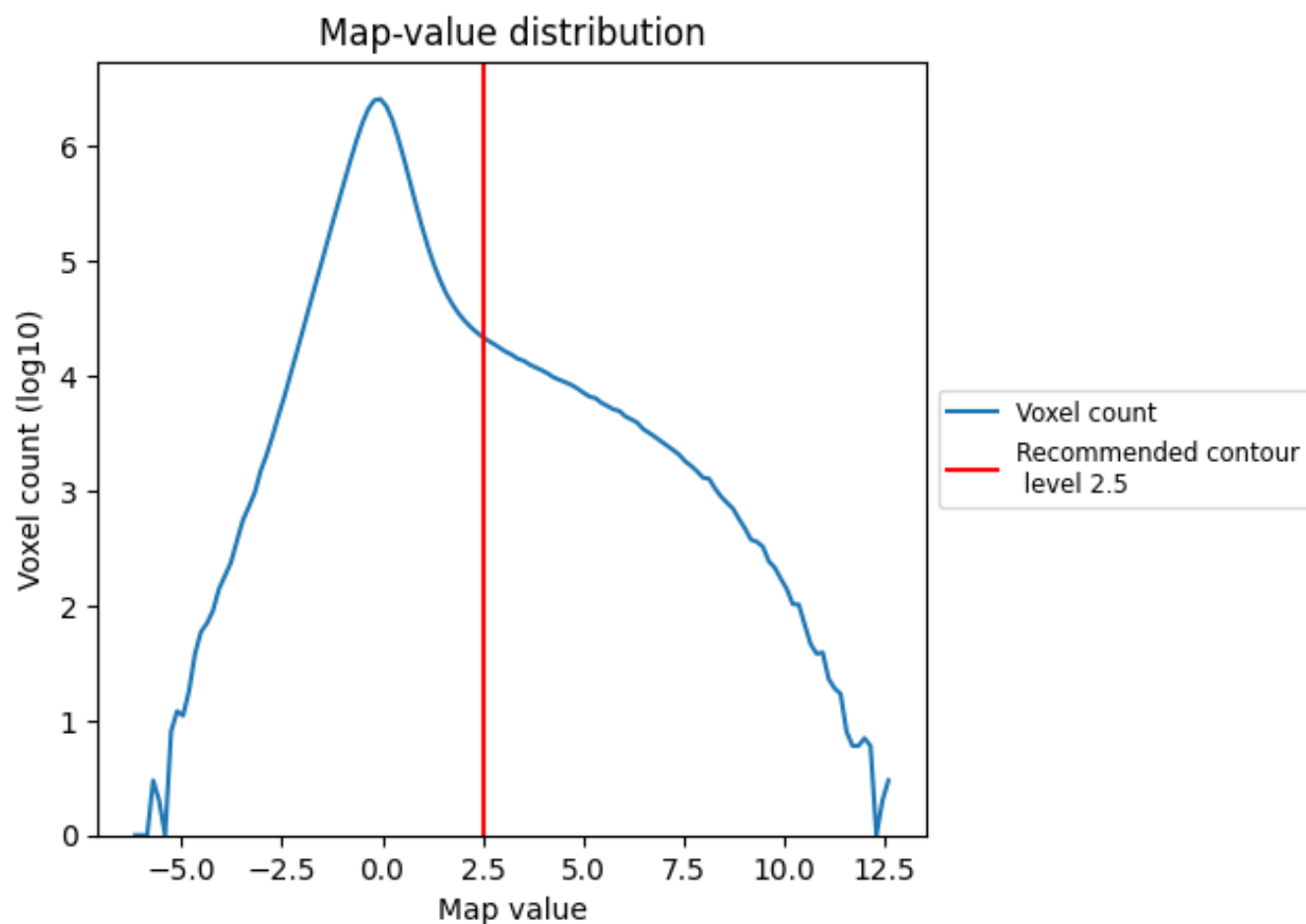
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

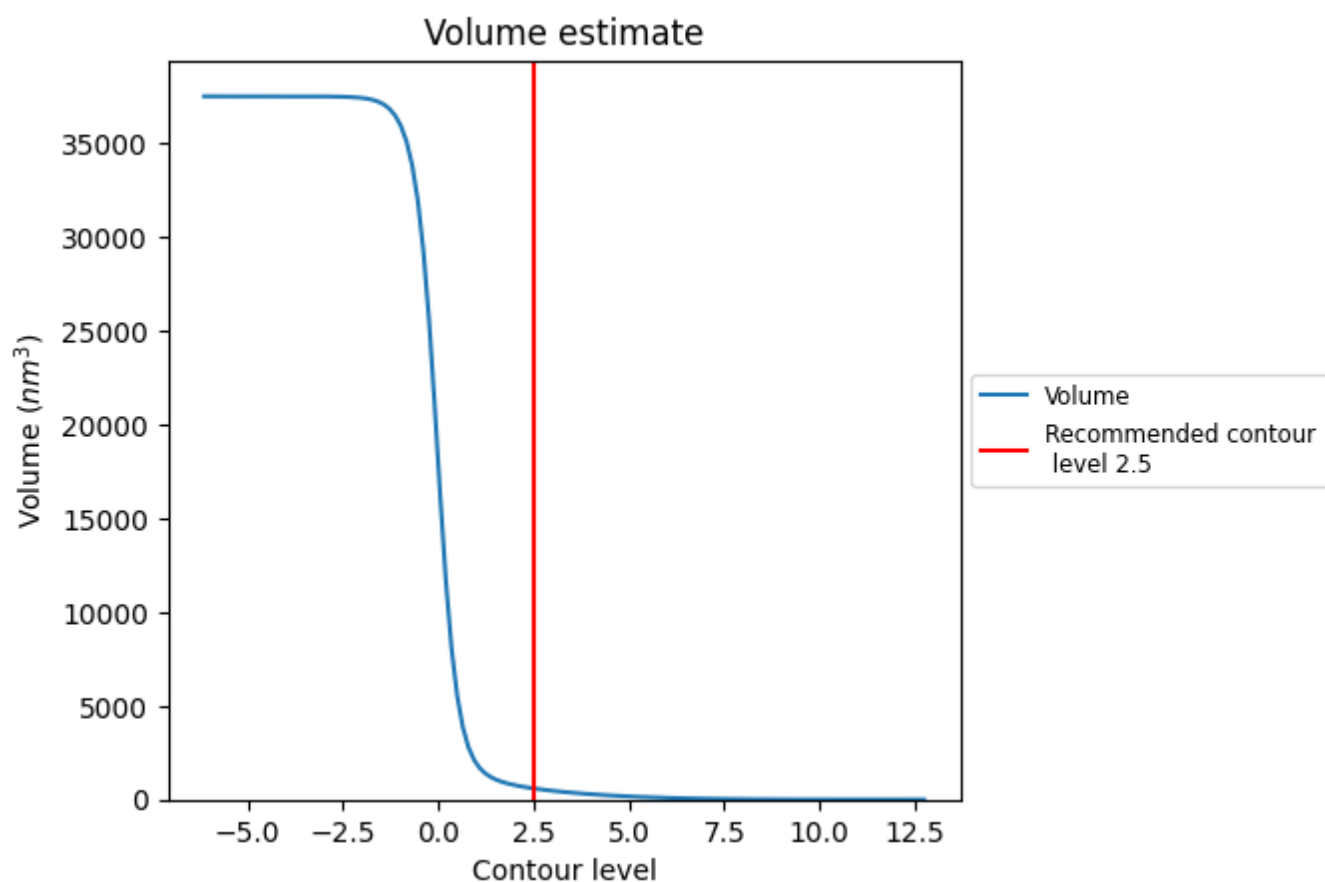
This section contains the results of statistical analysis of the map.

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.

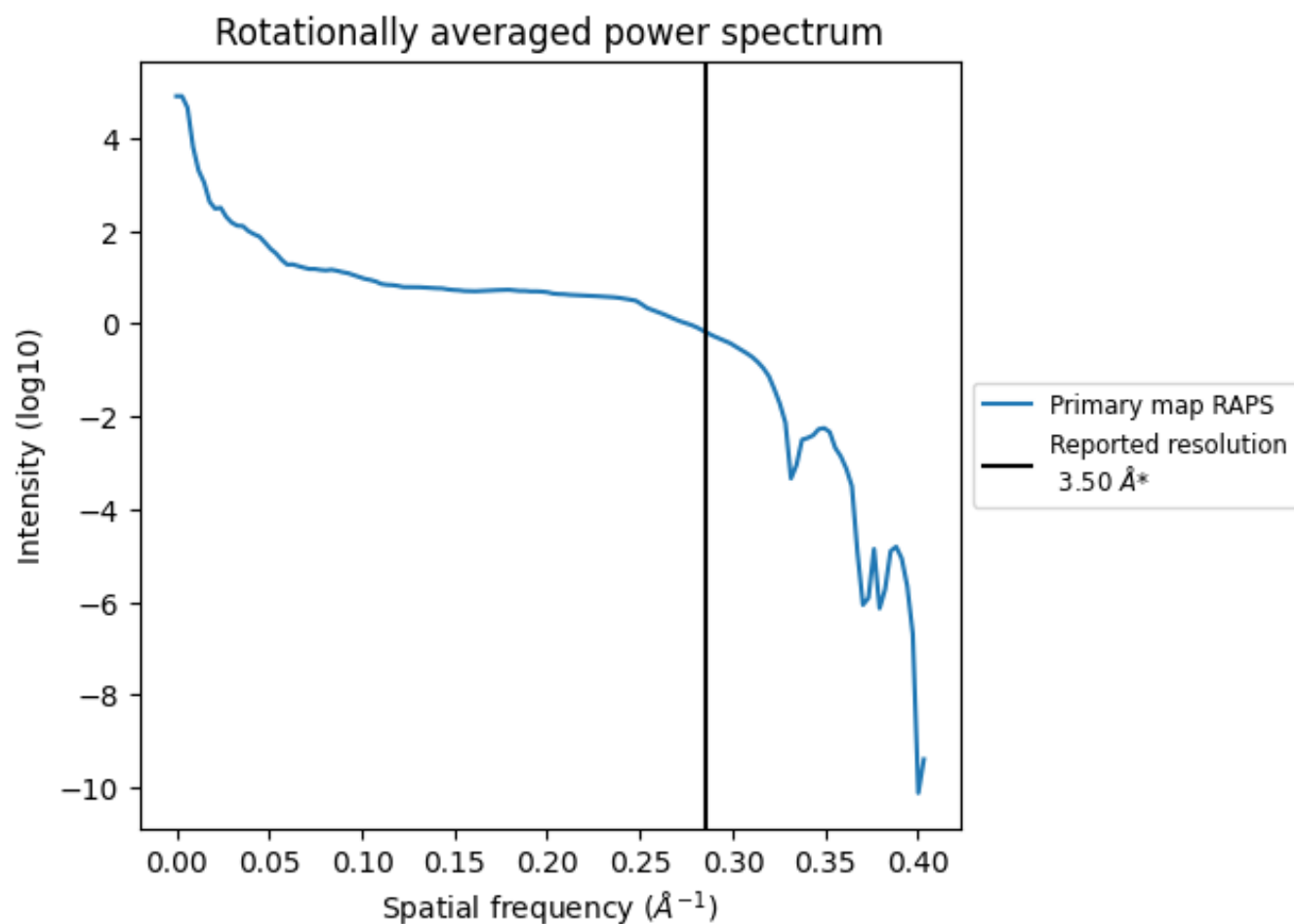
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 594 nm³; this corresponds to an approximate mass of 537 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 ⓘ

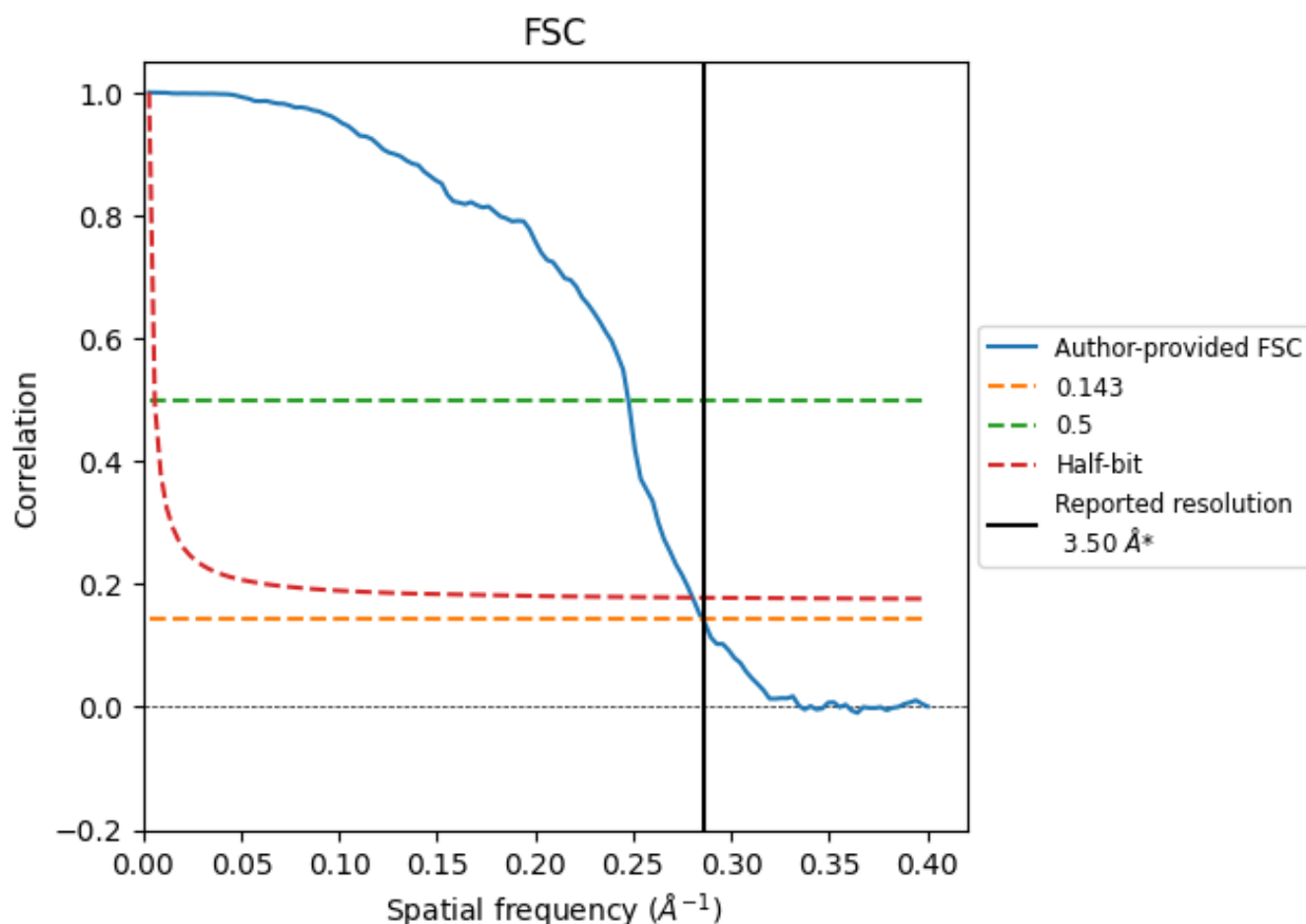


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

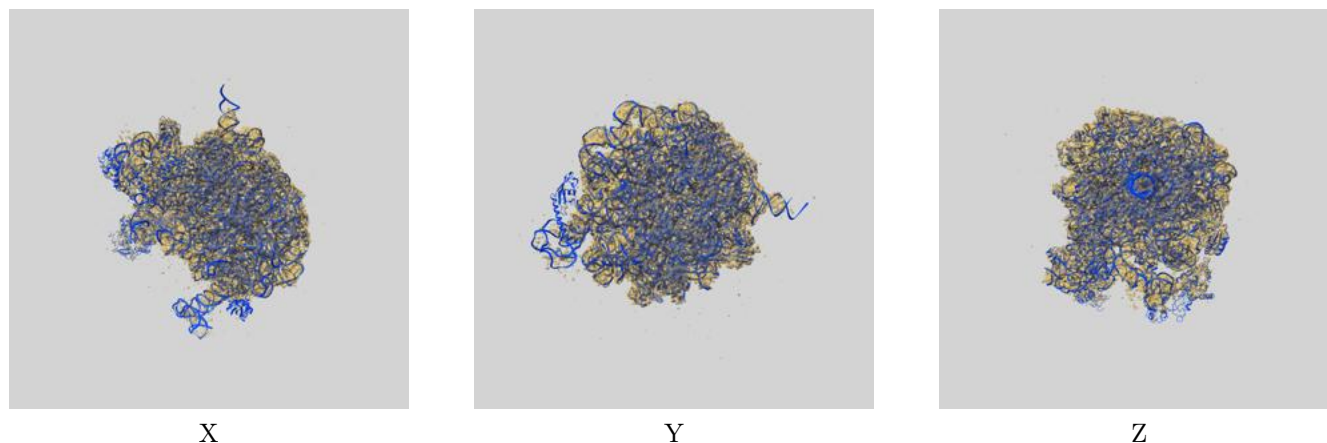
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.51	4.04	3.57
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

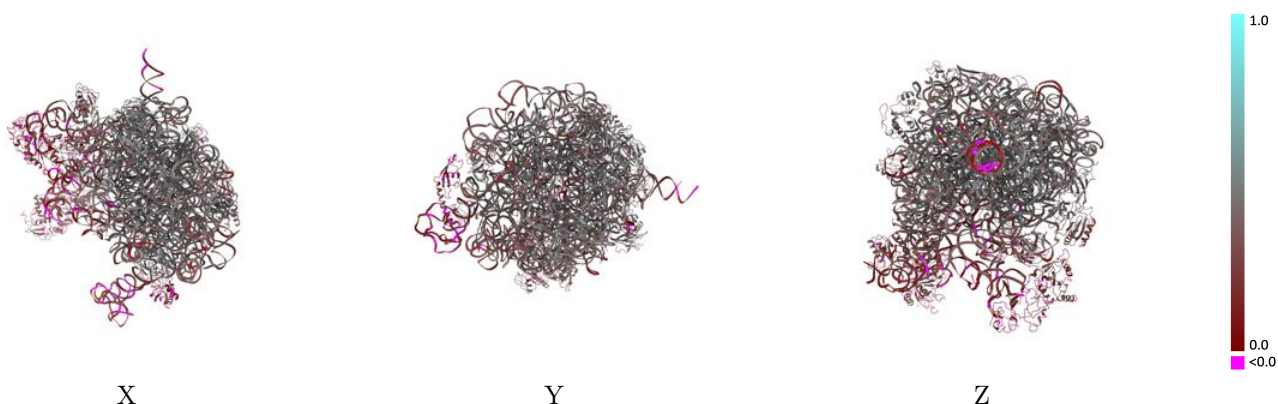
This section contains information regarding the fit between EMDB map EMD-12216 and PDB model 7BL3. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



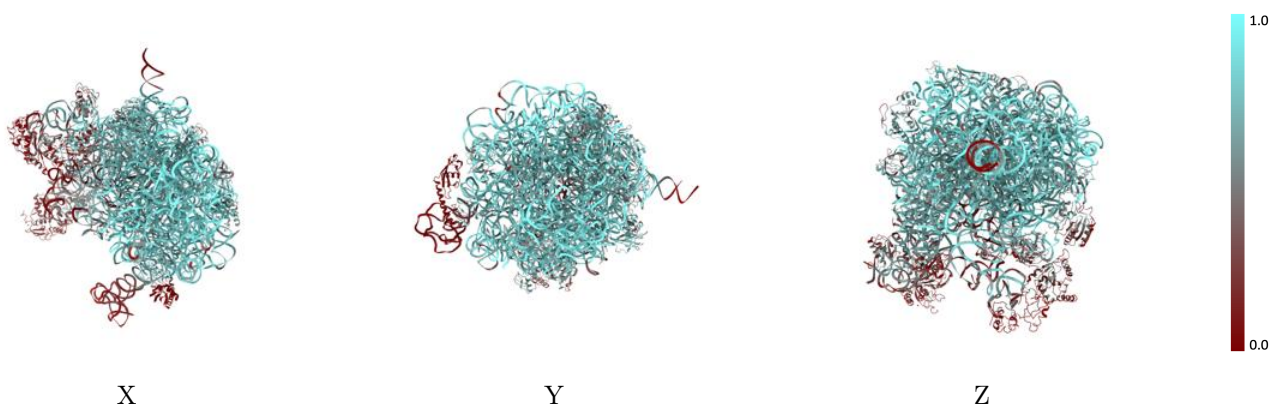
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



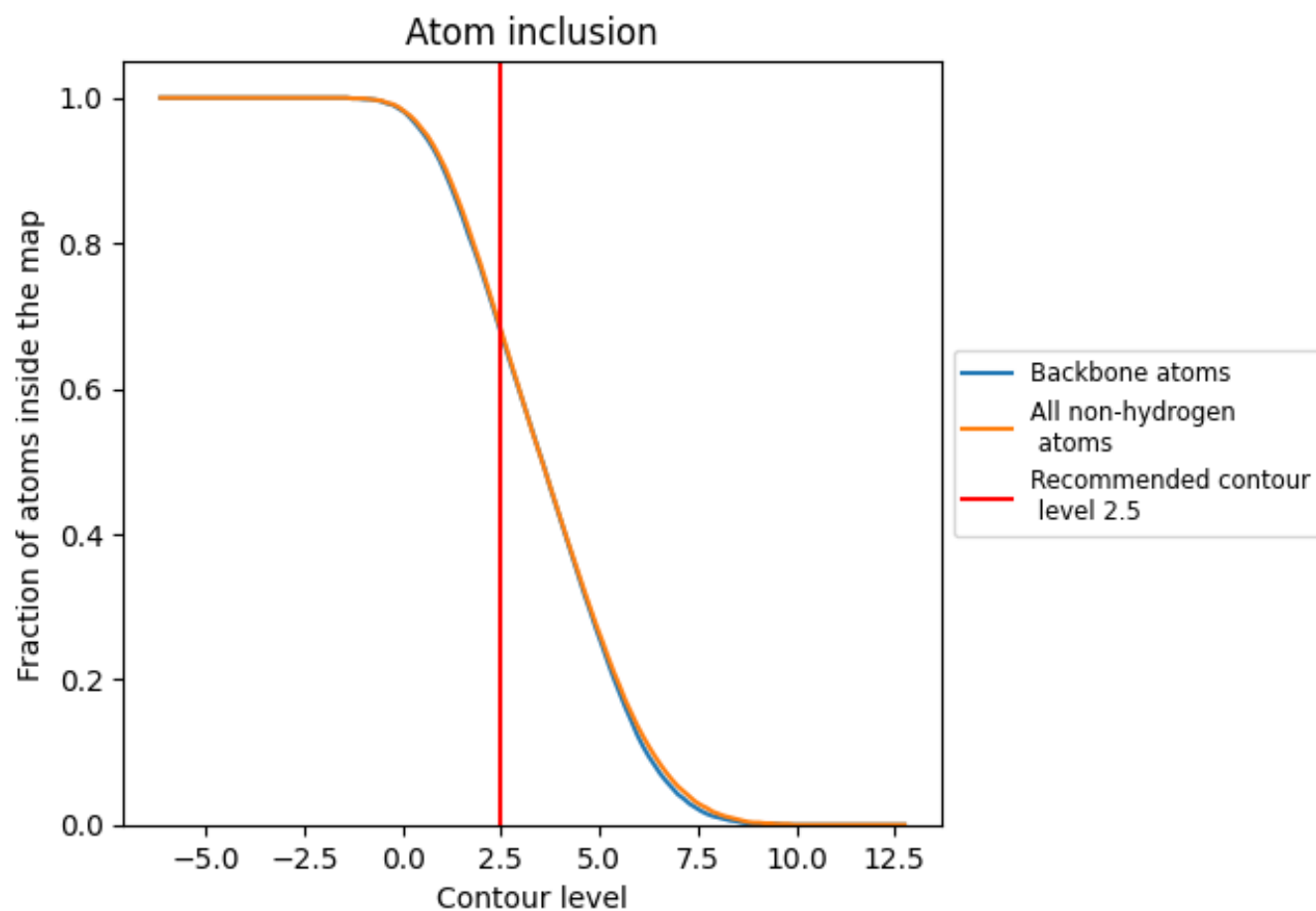
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 68% of all backbone atoms, 68% 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	 0.6800	 0.3620
0	 0.6260	 0.4120
1	 0.2620	 0.2880
2	 0.6960	 0.4590
6	 0.3220	 0.3050
9P	 0.3630	 0.2690
A	 0.7660	 0.3710
B	 0.5230	 0.2230
C	 0.7100	 0.4430
D	 0.7020	 0.4530
E	 0.5930	 0.3910
F	 0.1240	 0.1670
G	 0.4420	 0.3140
H	 0.1320	 0.2030
I	 0.0320	 0.1490
J	 0.6840	 0.4460
K	 0.6540	 0.4260
L	 0.5380	 0.3650
N	 0.7260	 0.4500
O	 0.3050	 0.2340
P	 0.6540	 0.4220
Q	 0.7260	 0.4500
R	 0.6660	 0.4280
S	 0.6990	 0.4600
T	 0.6550	 0.4130
U	 0.6520	 0.4100
V	 0.3120	 0.2630
W	 0.5420	 0.3800
X	 0.6510	 0.4340
Y	 0.6300	 0.3870
Z	 0.6360	 0.4270
b	 0.0110	 0.1090

