



Full wwPDB EM Validation Report ⓘ

Aug 24, 2026 – 11:13 AM EDT

PDB ID : 9E1S / pdb_00009e1s
EMDB ID : EMD-47419
Title : Cryo-EM structure of the ribosome-tunnel occluding hibernation factor bound to the Mycobacterium tuberculosis C- 50S ribosomal subunit
Authors : Majumdar, S.; Ojha, A.K.; Agrawal, R.K.
Deposited on : 2024-10-21
Resolution : 2.39 Å(reported)
Based on initial model : 7MT7

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

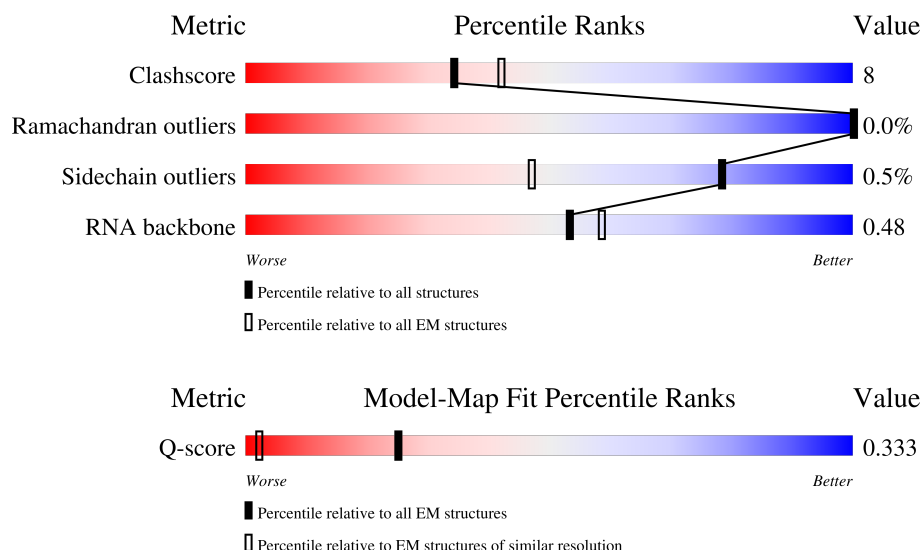
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 2.39 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	4884 (1.90 - 2.89)

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	7	24	
2	I	3138	
3	1	62	

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Mol	Chain	Length	Quality of chain
4	0	57	
5	2	47	
6	3	64	
7	4	37	
8	B	115	
9	C	280	
10	D	217	
11	E	223	
12	F	187	
13	G	179	
14	H	152	
15	J	195	
16	K	122	
17	L	146	
18	M	138	
19	N	180	
20	O	122	
21	P	113	
22	Q	129	
23	R	104	
24	S	197	
25	T	100	
26	V	215	
27	W	86	
28	Y	77	

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Mol	Chain	Length	Quality of chain
29	Z	65	9% 72% 18% 9%
30	b	54	17% 69% 22% 9%
31	y	78	13% 81% 18% •
32	U	105	13% 64% 19% • • 14%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 94689 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	7	22	Total	C	N	O	0	0
			186	111	47	28		

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	3118	Total	C	N	O	P	0	0
			66956	29845	12340	21653	3118		

- Molecule 3 is a protein called Ribosomal tunnel occlusion factor-RTOF.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1	51	Total	C	N	O	S	0	0
			395	231	87	76	1		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	0	53	Total	C	N	O	0	0
			421	262	93	66		

- Molecule 5 is a protein called 50S ribosomal protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	2	42	Total	C	N	O	S	0	0
			358	212	94	51	1		

- Molecule 6 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	3	62	Total	C	N	O	0	0
			494	298	112	84		

- Molecule 7 is a protein called 50S ribosomal protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	4	37	Total	C	N	O	S	0	0
			299	182	66	47	4		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	115	Total	C	N	O	P	0	0
			2458	1097	456	790	115		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	272	Total	C	N	O	S	0	0
			2088	1277	437	369	5		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	213	Total	C	N	O	S	0	0
			1590	985	307	292	6		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	207	Total	C	N	O	S	0	0
			1552	958	303	289	2		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	170	Total	C	N	O	S	0	0
			1335	834	254	242	5		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	174	Total	C	N	O	S	0	0
			1330	836	249	244	1		

- Molecule 14 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	47	Total	C	N	O	S	0	0
			350	220	64	65	1		

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	146	Total	C	N	O	S	0	0
			1143	724	217	199	3		

- Molecule 16 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	121	Total	C	N	O	S	0	0
			934	585	179	168	2		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	142	Total	C	N	O	S	0	0
			1060	656	215	187	2		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	134	Total	C	N	O	S	0	0
			1072	679	215	177	1		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	116	Total	C	N	O	S	0	0
			908	574	175	158	1		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	116	Total	C	N	O	S	0	0
			886	541	188	157			

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	112	Total	C	N	O	S	0	0
			907	573	174	159	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	122	Total	C	N	O		0	0
			980	608	205	167			

- Molecule 23 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	98	Total	C	N	O		0	0
			742	472	136	134			

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	113	Total	C	N	O		0	0
			860	533	178	149			

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	95	Total	C	N	O		0	0
			741	469	138	134			

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	177	Total	C	N	O		0	0
			1319	822	243	254			

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	74	Total	C	N	O		0	0
			546	336	111	99			

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	65	Total	C	N	O	S	0	0
			541	331	106	103	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	59	Total	C	N	O		0	0
			476	293	101	82			

- Molecule 30 is a protein called 50S ribosomal protein bL33-c minus.

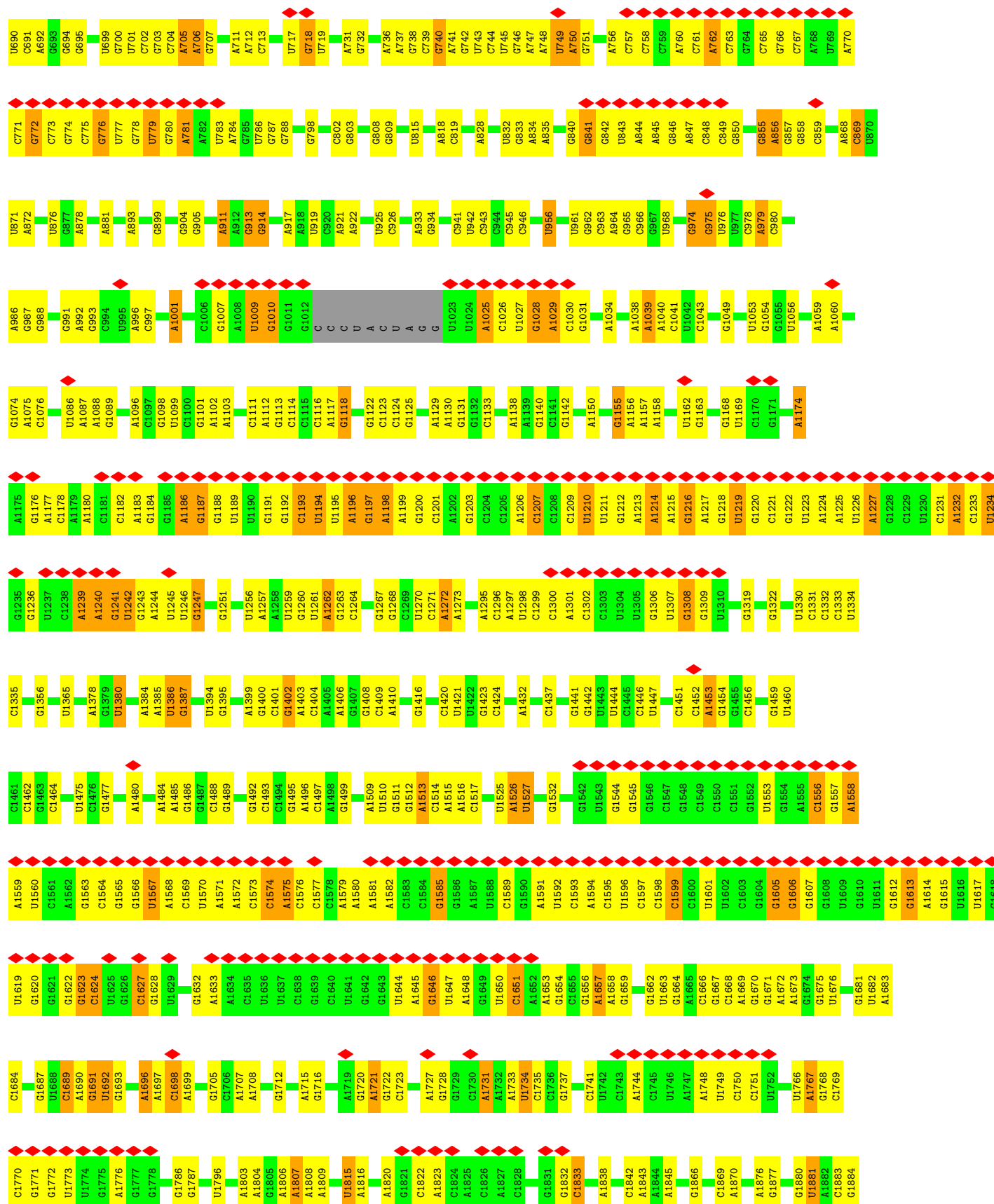
Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	49	Total	C	N	O		0	0
			424	263	89	72			

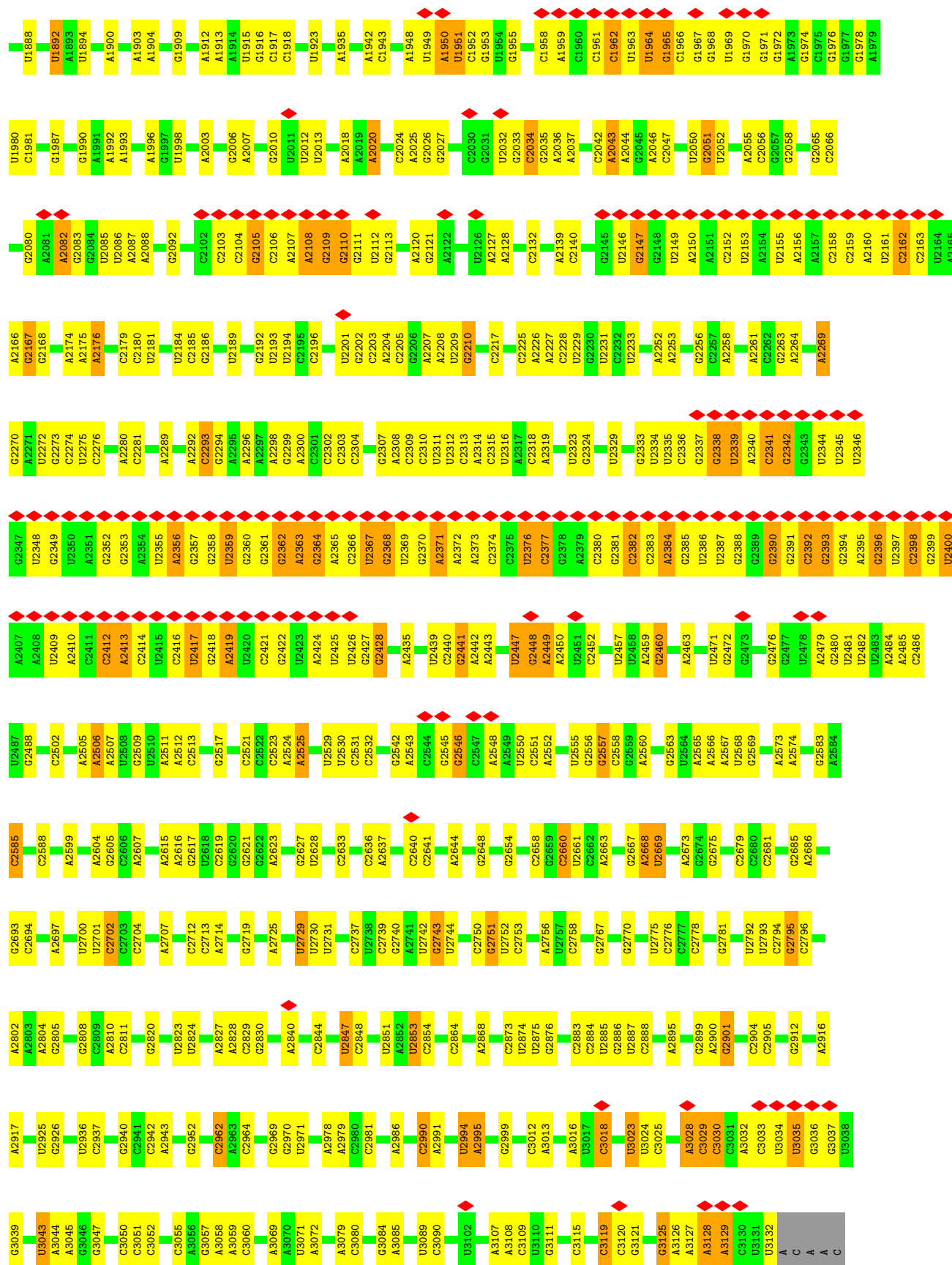
- Molecule 31 is a protein called 50S ribosomal protein bL28-c minus.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	y	78	Total	C	N	O	S	0	0
			639	389	143	106	1		

- Molecule 32 is a protein called 50S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	U	90	Total	C	N	O	S	0	0
			699	430	138	129	2		

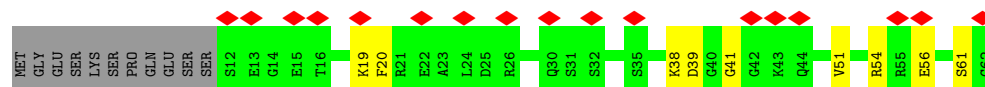




A

- Molecule 3: Ribosomal tunnel occlusion factor-RTOF

Chain 1: 



- Molecule 4: 50S ribosomal protein L32

Chain 0: 



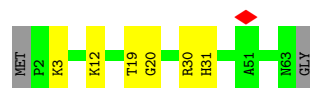
- Molecule 5: 50S ribosomal protein bL34

Chain 2: 



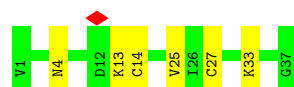
- Molecule 6: 50S ribosomal protein L35

Chain 3: 



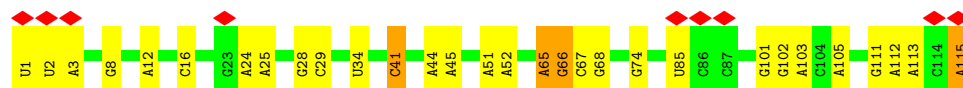
- Molecule 7: 50S ribosomal protein bL36

Chain 4: 



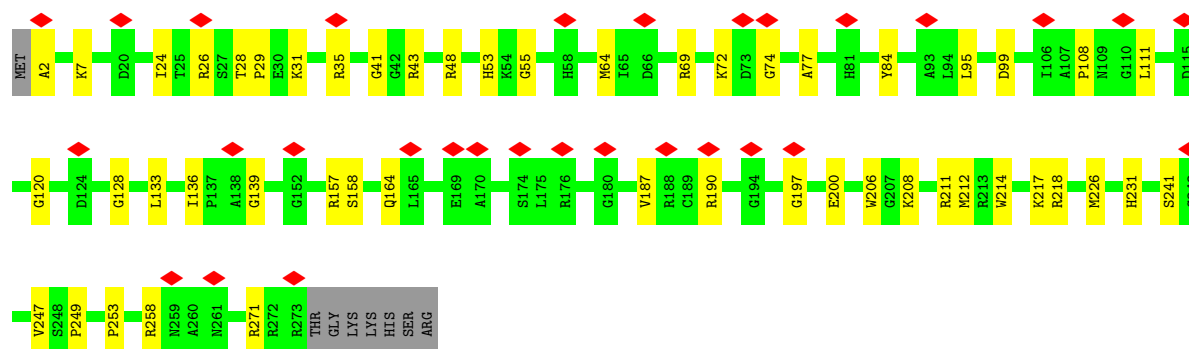
- Molecule 8: 5S ribosomal RNA

Chain B: 

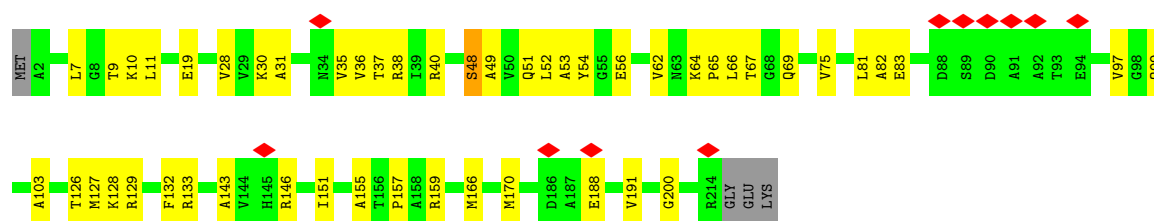
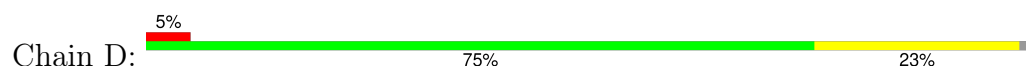


- Molecule 9: 50S ribosomal protein L2

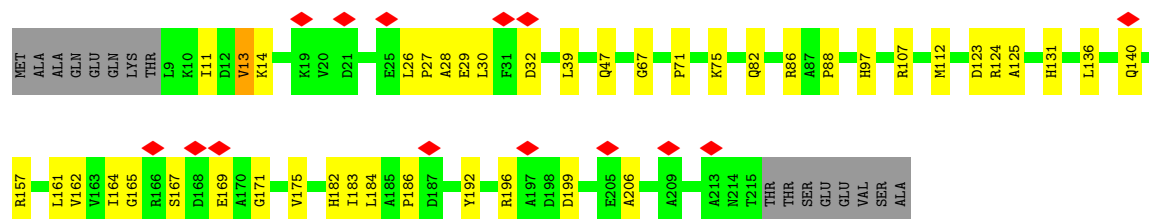
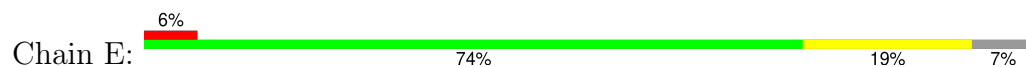
Chain C: 



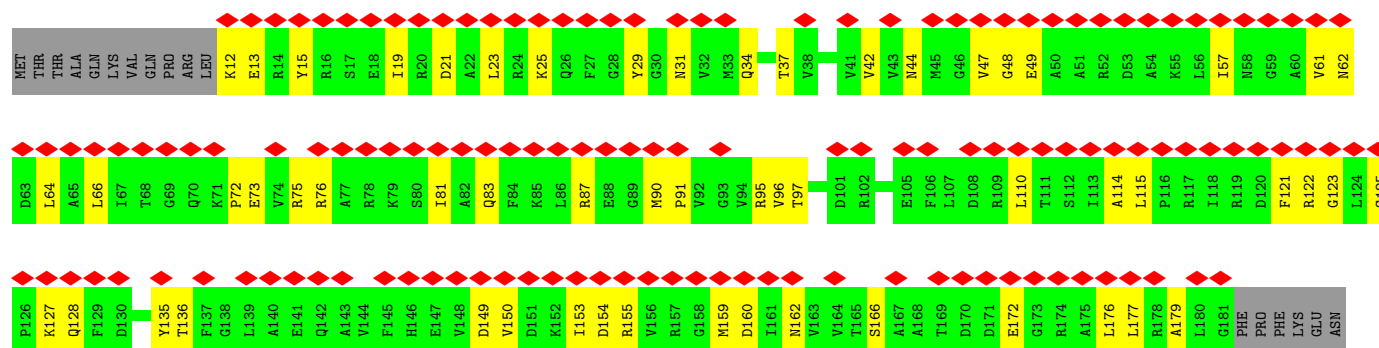
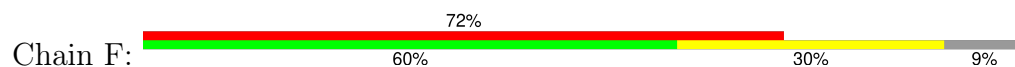
• Molecule 10: 50S ribosomal protein L3



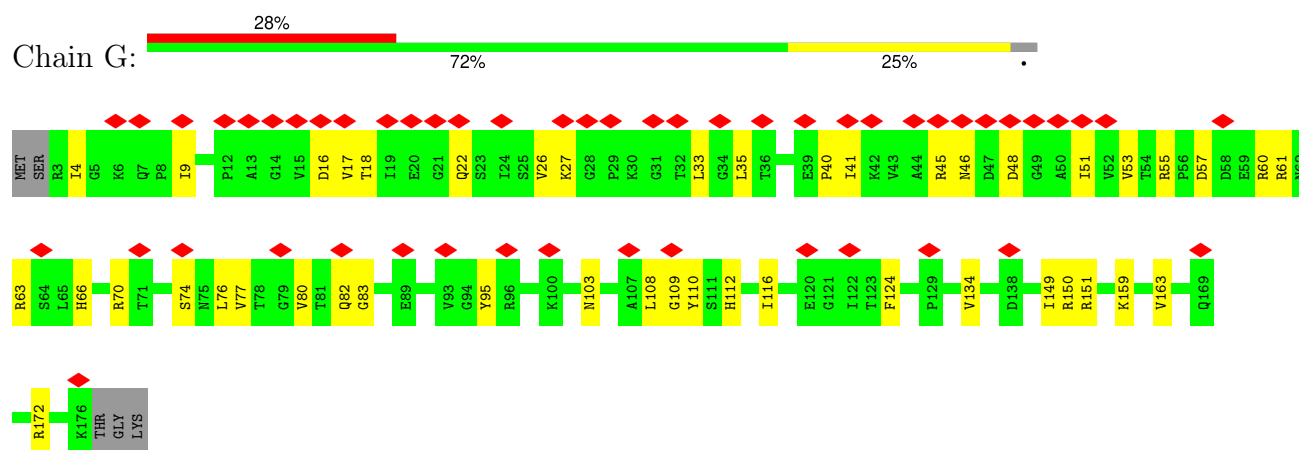
• Molecule 11: 50S ribosomal protein L4



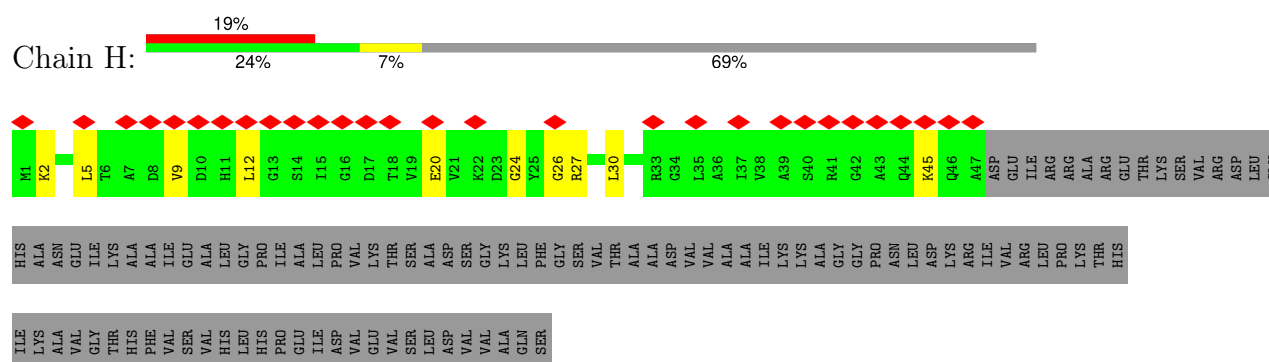
• Molecule 12: 50S ribosomal protein L5



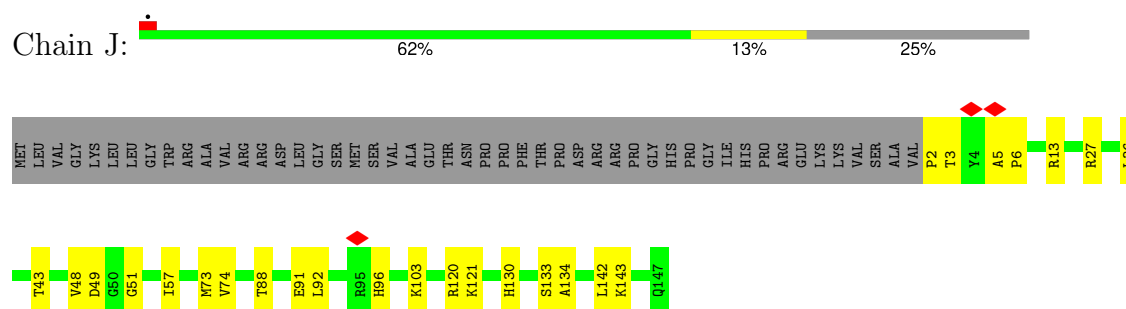
• Molecule 13: 50S ribosomal protein L6



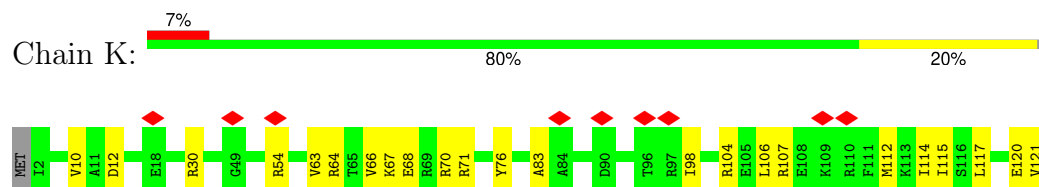
- Molecule 14: 50S ribosomal protein L9



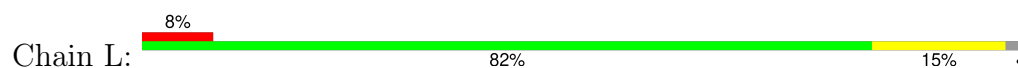
- Molecule 15: 50S ribosomal protein L13

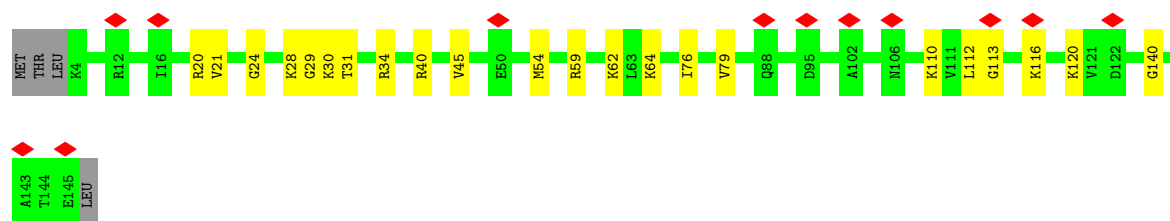


- Molecule 16: Large ribosomal subunit protein uL14

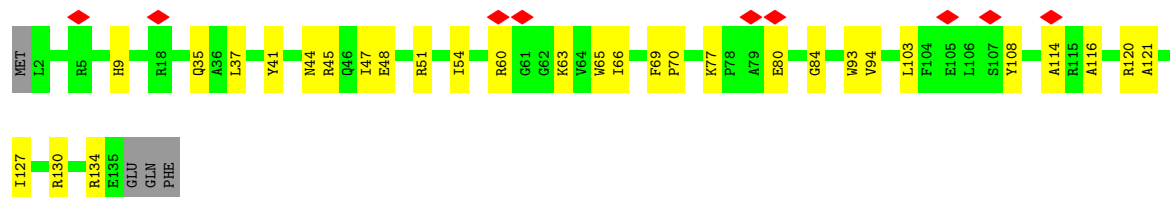
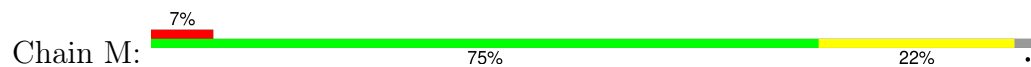


- Molecule 17: 50S ribosomal protein L15

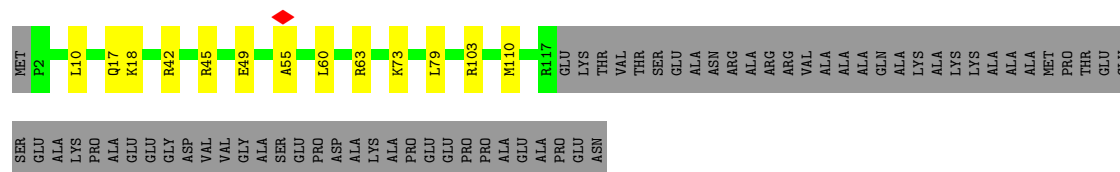




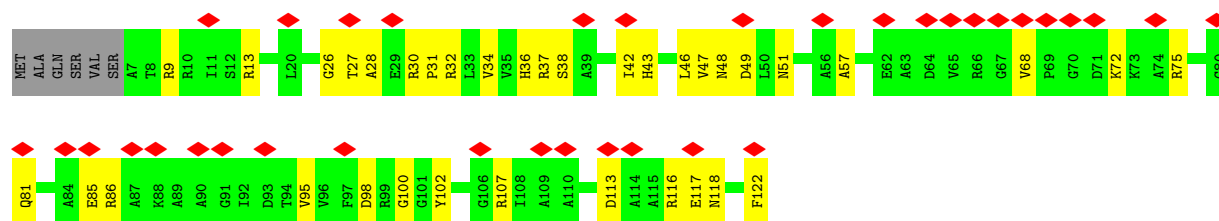
- Molecule 18: 50S ribosomal protein L16



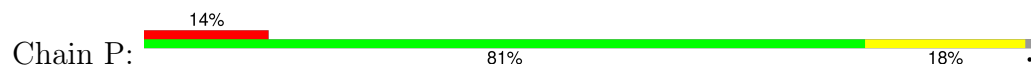
- Molecule 19: 50S ribosomal protein L17



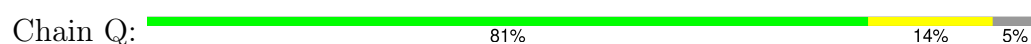
- Molecule 20: 50S ribosomal protein L18

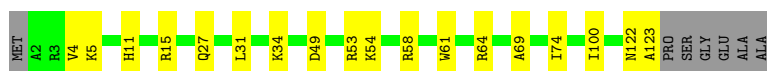


- Molecule 21: 50S ribosomal protein L19

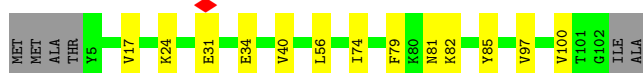
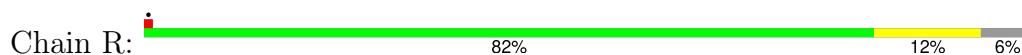


- Molecule 22: 50S ribosomal protein L20

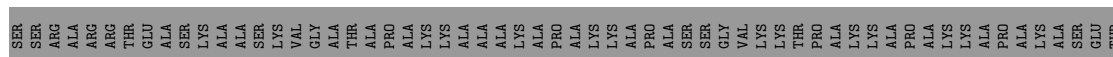




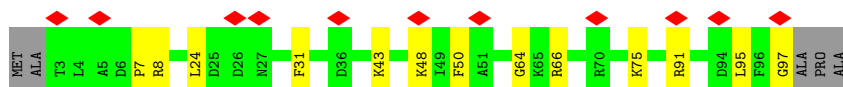
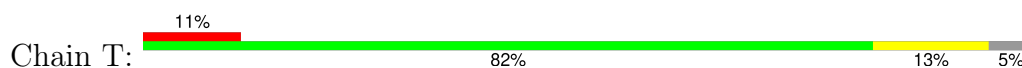
- Molecule 23: Large ribosomal subunit protein bL21



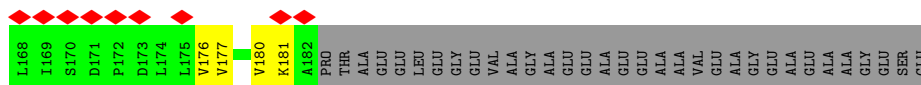
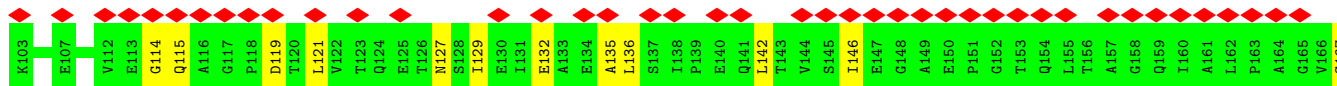
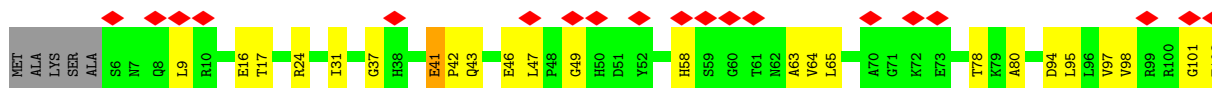
- Molecule 24: 50S ribosomal protein L22



- Molecule 25: 50S ribosomal protein L23



- Molecule 26: 50S ribosomal protein L25



- Molecule 27: 50S ribosomal protein L27

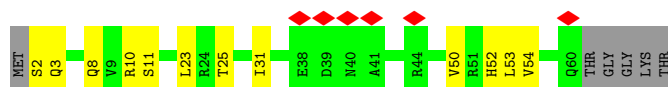




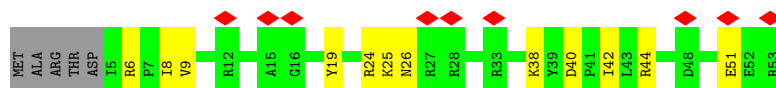
- Molecule 28: 50S ribosomal protein L29



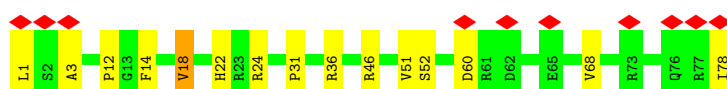
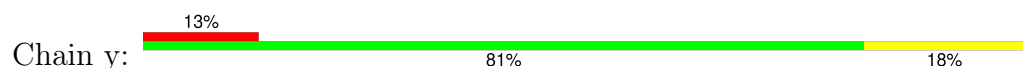
- Molecule 29: 50S ribosomal protein L30



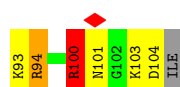
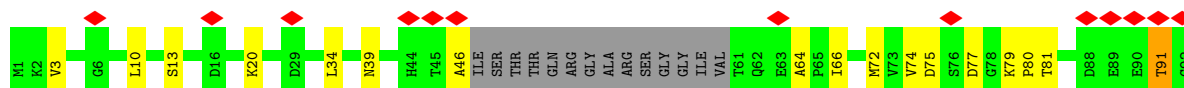
- Molecule 30: 50S ribosomal protein bL33-c minus



- Molecule 31: 50S ribosomal protein bL28-c minus



- Molecule 32: 50S ribosomal protein uL24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	257214	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.75	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.369	Depositor
Minimum map value	-2.646	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.137	Depositor
Recommended contour level	0.377	Depositor
Map size ($\text{\AA}$)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	7	0.21	0/188	0.33	0/243
2	I	0.21	0/74973	0.36	3/116979 (0.0%)
3	1	0.16	0/399	0.32	0/522
4	0	0.25	0/427	0.46	0/570
5	2	0.20	0/361	0.39	0/473
6	3	0.20	0/499	0.40	0/664
7	4	0.19	0/303	0.33	0/402
8	B	0.15	0/2749	0.28	0/4284
9	C	0.20	0/2129	0.42	1/2861 (0.0%)
10	D	0.21	0/1613	0.48	1/2174 (0.0%)
11	E	0.19	0/1575	0.43	0/2129
12	F	0.16	0/1352	0.42	0/1817
13	G	0.17	0/1351	0.40	0/1824
14	H	0.16	0/353	0.41	0/474
15	J	0.19	0/1170	0.37	0/1584
16	K	0.18	0/944	0.37	0/1268
17	L	0.18	0/1073	0.38	0/1432
18	M	0.21	0/1098	0.39	0/1481
19	N	0.20	0/925	0.37	0/1242
20	O	0.16	0/895	0.36	0/1202
21	P	0.17	0/922	0.36	0/1236
22	Q	0.20	0/992	0.43	0/1329
23	R	0.17	0/751	0.33	0/1009
24	S	0.18	0/874	0.34	0/1186
25	T	0.17	0/751	0.32	0/1012
26	V	0.50	3/1336 (0.2%)	0.90	6/1820 (0.3%)
27	W	0.25	0/551	0.53	0/735
28	Y	0.16	0/544	0.36	0/727
29	Z	0.21	0/480	0.49	0/645
30	b	0.18	0/431	0.38	0/578
31	y	0.17	0/649	0.37	0/868
32	U	0.60	0/705	0.86	0/941
All	All	0.21	3/103363 (0.0%)	0.38	11/155711 (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
6	3	0	1
11	E	0	1
17	L	0	1
32	U	0	2
All	All	0	5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	V	42	PRO	CB-CG	-11.04	0.94	1.49
26	V	42	PRO	CG-CD	-10.73	1.14	1.50
26	V	42	PRO	N-CD	-5.34	1.40	1.47

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	V	42	PRO	CB-CG-CD	23.09	179.99	106.10
26	V	42	PRO	CA-CB-CG	-15.69	74.69	104.50
26	V	42	PRO	N-CD-CG	-14.56	81.36	103.20
26	V	42	PRO	CA-N-CD	-7.03	102.16	112.00
9	C	197	GLY	N-CA-C	6.13	120.61	112.77
2	I	740	G	C4-N9-C1'	5.88	144.16	126.50
2	I	91	A	C2'-C3'-O3'	5.58	117.87	109.50
2	I	600	G	O4'-C1'-N9	5.22	116.03	108.20
26	V	41	GLU	CA-C-N	5.18	126.31	119.84
26	V	41	GLU	C-N-CA	5.18	126.31	119.84
10	D	48	SER	N-CA-C	5.13	116.91	110.91

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	3	30	ARG	Peptide
11	E	13	VAL	Peptide
17	L	20	ARG	Peptide
32	U	100	ARG	Sidechain
32	U	94	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	7	186	0	202	3	0
2	I	66956	0	33720	831	0
3	1	395	0	389	8	0
4	0	421	0	461	9	0
5	2	358	0	390	5	0
6	3	494	0	533	4	0
7	4	299	0	326	5	0
8	B	2458	0	1253	17	0
9	C	2088	0	2123	41	0
10	D	1590	0	1633	36	0
11	E	1552	0	1593	30	0
12	F	1335	0	1372	46	0
13	G	1330	0	1390	38	0
14	H	350	0	367	7	0
15	J	1143	0	1173	20	0
16	K	934	0	993	26	0
17	L	1060	0	1119	26	0
18	M	1072	0	1115	23	0
19	N	908	0	956	10	0
20	O	886	0	924	28	0
21	P	907	0	947	14	0
22	Q	980	0	1028	14	0
23	R	742	0	799	8	0
24	S	860	0	903	15	0
25	T	741	0	792	10	0
26	V	1319	0	1365	25	0
27	W	546	0	567	25	0
28	Y	541	0	551	13	0
29	Z	476	0	509	9	0
30	b	424	0	442	10	0
31	y	639	0	668	12	0
32	U	699	0	738	14	0
All	All	94689	0	61341	1245	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (1245) 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)
2:I:842:G:H21	2:I:847:A:N6	1.35	1.25
2:I:1557:G:H21	2:I:1648:A:N6	1.52	1.07
2:I:1585:G:H1	2:I:1619:U:H3	1.02	1.02
2:I:842:G:N2	2:I:847:A:N6	2.10	0.99
2:I:91:A:H4'	2:I:92:A:H5'	1.42	0.97
2:I:1557:G:N2	2:I:1648:A:H62	1.61	0.96
2:I:2006:G:H1	2:I:2217:C:H5	1.10	0.96
2:I:1955:G:H22	2:I:1974:G:H1	1.00	0.96
2:I:1689:C:N3	2:I:1697:A:N6	2.14	0.94
2:I:1517:C:H5	2:I:1532:G:H1	1.15	0.94
2:I:1222:G:H21	2:I:1227:A:N6	1.66	0.93
2:I:1955:G:N2	2:I:1974:G:H1	1.65	0.93
2:I:842:G:N2	2:I:847:A:H62	1.65	0.92
2:I:2309:C:H5	2:I:2675:G:H1	1.15	0.92
2:I:946:C:H5	2:I:1322:G:H1	1.15	0.90
9:C:72:LYS:HD3	9:C:120:GLY:HA2	1.55	0.89
18:M:41:TYR:HB3	18:M:94:VAL:HG21	1.55	0.88
2:I:1557:G:H21	2:I:1648:A:H62	0.90	0.88
2:I:1183:A:H61	2:I:1234:U:H3	1.17	0.88
2:I:842:G:N2	2:I:847:A:C5	2.43	0.87
2:I:79:C:HO2'	2:I:429:A:H8	1.23	0.86
2:I:2174:A:H2	2:I:2181:U:H3	1.22	0.86
2:I:842:G:N2	2:I:847:A:C6	2.42	0.85
2:I:2574:A:H61	27:W:43:THR:HG21	1.38	0.85
2:I:689:G:H1	17:L:34:ARG:HE	1.26	0.83
2:I:289:A:H1'	2:I:304:G:H1'	1.62	0.82
2:I:841:G:H2'	2:I:842:G:H8	1.43	0.81
2:I:1959:A:H61	2:I:1969:U:H3	1.28	0.81
11:E:26:LEU:HD13	11:E:30:LEU:HD22	1.63	0.81
17:L:30:LYS:HD2	17:L:31:THR:HG23	1.64	0.80
2:I:1951:U:O4	2:I:1978:G:N1	2.11	0.80
2:I:1684:C:OP2	2:I:1698:C:N4	2.15	0.79
2:I:2658:C:H5''	30:b:8:ILE:HD13	1.64	0.79
27:W:39:ARG:HH21	27:W:58:THR:HG21	1.45	0.79
16:K:120:GLU:OE1	21:P:64:SER:OG	1.99	0.79
2:I:1187:G:O6	2:I:1210:U:O2	2.01	0.78
16:K:71:ARG:HH12	16:K:122:LEU:HD11	1.49	0.78
9:C:72:LYS:NZ	9:C:190:ARG:HE	1.82	0.77
2:I:91:A:C4'	2:I:92:A:H5'	2.13	0.77
2:I:2962:C:OP1	10:D:128:LYS:NZ	2.18	0.77
2:I:740:G:N3	17:L:112:LEU:HD21	2.00	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1222:G:N2	2:I:1227:A:H62	1.82	0.76
27:W:56:ASP:HB3	27:W:58:THR:HG23	1.66	0.76
2:I:2367:U:H4'	2:I:2396:G:H1	1.49	0.76
2:I:1567:U:O2	2:I:1569:C:N4	2.19	0.75
2:I:856:A:OP1	2:I:1669:A:O2'	2.04	0.75
2:I:428:A:H1'	2:I:429:A:H2	1.51	0.75
2:I:1243:G:H2'	2:I:1244:A:C8	2.22	0.74
2:I:1654:G:HO2'	2:I:1822:C:HO2'	1.35	0.74
2:I:2729:U:H5'	2:I:2808:G:H5''	1.69	0.74
2:I:1222:G:N2	2:I:1227:A:N6	2.34	0.74
2:I:2051:G:OP2	9:C:157:ARG:NH2	2.21	0.74
14:H:24:GLY:HA2	14:H:27:ARG:HB3	1.70	0.74
2:I:1174:A:OP2	2:I:1240:A:N6	2.21	0.73
30:b:9:VAL:HG13	30:b:51:GLU:HG3	1.71	0.73
2:I:942:U:H2'	2:I:943:C:C6	2.24	0.73
2:I:281:G:H1	2:I:307:U:H3	1.37	0.73
2:I:2362:G:O6	2:I:2406:A:N1	2.21	0.73
2:I:979:A:H62	2:I:1056:U:H3	1.36	0.72
2:I:2447:U:H3	2:I:2452:C:H41	1.35	0.72
2:I:2447:U:H4'	2:I:2447:U:OP1	1.89	0.72
9:C:35:ARG:NH1	9:C:64:MET:SD	2.63	0.72
2:I:841:G:H2'	2:I:842:G:C8	2.23	0.72
2:I:161:G:O2'	2:I:169:A:N6	2.23	0.72
12:F:87:ARG:HA	12:F:90:MET:HE2	1.71	0.72
2:I:2542:G:H22	2:I:2550:U:H3	1.36	0.72
2:I:1971:G:H2'	2:I:1972:G:C8	2.25	0.71
2:I:2373:A:N6	2:I:2393:G:OP1	2.23	0.71
10:D:128:LYS:HG2	10:D:170:MET:HE1	1.72	0.71
8:B:24:A:H2	8:B:113:A:H1'	1.55	0.71
14:H:27:ARG:NH1	31:y:60:ASP:OD2	2.22	0.71
26:V:37:GLY:HA2	26:V:97:VAL:HG22	1.72	0.71
2:I:2013:U:H5	2:I:2018:A:N7	1.89	0.71
2:I:2080:G:N2	2:I:2132:C:O2	2.20	0.71
2:I:974:G:O2'	2:I:975:G:O5'	2.07	0.70
12:F:136:THR:OG1	12:F:162:ASN:OD1	2.08	0.70
12:F:29:TYR:OH	12:F:172:GLU:OE1	2.05	0.70
9:C:217:LYS:NZ	9:C:218:ARG:O	2.25	0.70
19:N:10:LEU:HB2	19:N:17:GLN:HG3	1.74	0.70
2:I:978:C:H2'	2:I:979:A:H5''	1.74	0.70
2:I:835:A:OP1	9:C:7:LYS:NZ	2.24	0.69
2:I:1967:G:H2'	2:I:1968:G:C8	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Y:14:THR:O	28:Y:64:ARG:NH1	2.24	0.69
2:I:3035:U:H3'	2:I:3036:G:H8	1.57	0.69
2:I:871:U:H2'	2:I:872:A:C8	2.28	0.69
2:I:2146:U:H2'	2:I:2147:G:O4'	1.93	0.68
2:I:2566:A:H2'	2:I:2567:A:C8	2.28	0.68
29:Z:50:VAL:HG13	29:Z:53:LEU:HD12	1.73	0.68
2:I:1953:G:H1	2:I:1976:G:H1	1.41	0.68
2:I:1962:C:O2'	2:I:1964:U:OP2	2.11	0.68
15:J:74:VAL:HG21	15:J:92:LEU:HD12	1.76	0.68
16:K:104:ARG:NH2	21:P:40:GLN:OE1	2.26	0.68
2:I:740:G:H21	17:L:112:LEU:HG	1.58	0.68
2:I:1495:G:N7	31:y:1:LEU:HB2	2.08	0.68
2:I:1187:G:C6	2:I:1210:U:O2	2.46	0.68
13:G:112:HIS:O	13:G:112:HIS:ND1	2.27	0.68
2:I:193:A:H2'	2:I:194:G:C8	2.28	0.68
9:C:72:LYS:HZ3	9:C:190:ARG:HE	1.39	0.68
27:W:50:ASN:HB2	27:W:83:SER:HB3	1.75	0.68
18:M:37:LEU:HD11	18:M:130:ARG:HG3	1.76	0.68
2:I:1184:G:H1	2:I:1233:C:H42	1.42	0.67
28:Y:5:VAL:HG21	28:Y:21:ARG:HH12	1.60	0.67
2:I:2513:C:O2'	18:M:84:GLY:O	2.13	0.67
2:I:2338:G:H2'	2:I:2339:U:C2	2.29	0.67
2:I:3127:A:H4'	2:I:3128:A:N3	2.10	0.67
2:I:2036:A:H2'	2:I:2037:A:C8	2.30	0.66
2:I:1244:A:H2'	2:I:1245:U:C6	2.30	0.66
2:I:1721:A:H2'	2:I:1722:G:C8	2.30	0.66
2:I:3071:U:H2'	2:I:3072:A:C8	2.30	0.66
12:F:73:GLU:OE1	12:F:95:ARG:NH2	2.24	0.66
13:G:40:PRO:HG3	13:G:61:ARG:HH12	1.59	0.66
2:I:1614:A:H2'	2:I:1615:G:H8	1.60	0.66
16:K:98:ILE:HD12	16:K:117:LEU:HB2	1.76	0.66
20:O:13:ARG:NH1	20:O:100:GLY:O	2.28	0.66
2:I:1176:G:N3	2:I:1239:A:N6	2.44	0.66
9:C:24:ILE:HG22	9:C:26:ARG:H	1.61	0.66
2:I:1953:G:N2	2:I:1976:G:H22	1.93	0.66
2:I:79:C:O2'	2:I:429:A:H8	1.79	0.65
2:I:675:G:N1	2:I:2269:A:OP1	2.27	0.65
2:I:1246:U:H2'	2:I:1247:G:C8	2.32	0.65
12:F:64:LEU:HB3	12:F:72:PRO:HG3	1.76	0.65
28:Y:23:ARG:HG2	28:Y:23:ARG:HH11	1.61	0.65
2:I:1245:U:H2'	2:I:1246:U:H6	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1880:G:H5''	2:I:1881:U:H5''	1.77	0.65
2:I:740:G:C2	17:L:110:LYS:HD2	2.31	0.65
2:I:1452:C:O2'	24:S:21:ARG:NH2	2.26	0.65
28:Y:20:GLU:O	28:Y:24:GLU:HG3	1.95	0.65
2:I:1707:A:H2'	2:I:1708:A:C8	2.32	0.65
8:B:74:G:H5''	26:V:17:THR:HG21	1.79	0.65
1:7:21:ARG:NH2	2:I:1111:C:O2	2.29	0.65
2:I:448:U:H2'	2:I:449:A:H8	1.61	0.65
2:I:1822:C:H2'	2:I:1823:A:C8	2.32	0.65
21:P:33:GLU:OE2	21:P:38:ARG:NH2	2.30	0.65
2:I:679:G:O2'	2:I:1385:A:OP1	2.14	0.65
2:I:1218:G:H1'	2:I:1219:U:H5	1.61	0.65
12:F:150:VAL:HA	12:F:153:ILE:HD12	1.80	0.64
27:W:71:ILE:HD11	27:W:76:LYS:HA	1.78	0.64
2:I:2034:C:OP1	9:C:258:ARG:NH2	2.31	0.64
18:M:44:ASN:ND2	18:M:93:TRP:HB2	2.12	0.64
2:I:2412:C:OP2	2:I:2413:A:N6	2.24	0.64
26:V:31:ILE:HD11	26:V:47:LEU:HD12	1.79	0.64
2:I:2033:G:N2	2:I:2052:U:O2'	2.31	0.64
2:I:2707:A:OP1	18:M:120:ARG:NH1	2.31	0.64
27:W:49:VAL:HG22	27:W:82:GLY:HA2	1.77	0.64
2:I:3033:C:N4	2:I:3036:G:OP2	2.31	0.64
2:I:2346:U:OP1	2:I:2387:U:O2'	2.16	0.64
10:D:127:MET:SD	10:D:146:ARG:HA	2.38	0.64
2:I:83:G:P	32:U:94:ARG:HH12	2.20	0.64
2:I:471:G:H22	2:I:481:U:H3	1.46	0.64
24:S:56:PRO:O	24:S:60:VAL:HG23	1.98	0.63
25:T:8:ARG:O	28:Y:33:ARG:NH2	2.31	0.63
2:I:961:U:H2'	2:I:962:G:C8	2.32	0.63
2:I:127:A:H5''	2:I:128:C:C6	2.33	0.63
2:I:1454:G:H5'	3:I:41:GLY:HA2	1.79	0.63
2:I:2392:C:O2'	2:I:2393:G:N2	2.31	0.63
2:I:3028:A:N6	2:I:3030:C:OP2	2.31	0.63
11:E:157:ARG:NH1	11:E:199:ASP:OD2	2.31	0.63
20:O:27:THR:HG23	20:O:30:ARG:H	1.64	0.63
2:I:732:G:N1	2:I:740:G:N7	2.46	0.63
26:V:129:ILE:HD11	26:V:142:LEU:HD12	1.81	0.63
2:I:1512:G:H2'	2:I:1513:A:H5''	1.79	0.63
2:I:2087:A:H2'	2:I:2088:A:C8	2.34	0.63
12:F:76:ARG:HH11	12:F:91:PRO:HD3	1.63	0.63
2:I:428:A:H1'	2:I:429:A:C2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:765:C:N4	2:I:766:G:O6	2.31	0.63
2:I:1658:A:H61	2:I:1815:U:H3	1.47	0.63
2:I:1949:U:C5	2:I:1951:U:H5''	2.34	0.63
12:F:19:ILE:HD12	12:F:179:ALA:HB1	1.81	0.63
20:O:72:LYS:HB3	20:O:107:ARG:HD3	1.80	0.63
2:I:307:U:H2'	2:I:308:G:H8	1.64	0.62
28:Y:13:LEU:HB3	28:Y:17:GLU:HB2	1.80	0.62
12:F:44:ASN:HB2	12:F:160:ASP:HB2	1.80	0.62
2:I:1027:U:O2'	2:I:1028:G:O4'	2.16	0.62
2:I:2275:U:H2'	2:I:2276:C:C6	2.33	0.62
2:I:738:G:H2'	2:I:739:C:H6	1.63	0.62
2:I:899:G:OP2	5:2:14:ARG:NH2	2.33	0.62
2:I:1129:A:H2'	2:I:1130:A:C8	2.33	0.62
2:I:2447:U:H3	2:I:2452:C:N4	1.97	0.62
2:I:1544:G:H2'	2:I:1545:G:C8	2.35	0.62
2:I:2481:U:H2'	2:I:2482:U:C6	2.34	0.62
2:I:572:A:H4'	32:U:46:ALA:HB3	1.82	0.62
2:I:2936:U:H2'	2:I:2937:C:C6	2.35	0.62
2:I:307:U:H2'	2:I:308:G:C8	2.35	0.61
2:I:683:C:H2'	2:I:684:U:C6	2.36	0.61
2:I:2981:C:O2'	13:G:151:ARG:NH2	2.33	0.61
2:I:1176:G:C4	2:I:1239:A:C6	2.88	0.61
2:I:2302:C:H2'	2:I:2303:C:C6	2.35	0.61
2:I:1442:G:H21	2:I:1838:A:H62	1.47	0.61
25:T:7:PRO:HG3	25:T:48:LYS:HD3	1.82	0.61
25:T:66:ARG:HG2	25:T:75:LYS:HG3	1.81	0.61
2:I:609:U:H2'	2:I:610:G:C8	2.36	0.61
11:E:47:GLN:HE22	11:E:192:TYR:H	1.46	0.61
2:I:616:A:C2	2:I:2280:A:H2'	2.36	0.61
2:I:1573:C:H2'	2:I:1574:C:C6	2.35	0.61
2:I:2847:U:O2'	3:1:56:GLU:OE2	2.17	0.61
15:J:5:ALA:HB3	15:J:6:PRO:HD3	1.81	0.61
8:B:1:U:OP2	8:B:115:A:N6	2.34	0.61
2:I:2311:U:H2'	2:I:2312:U:C6	2.36	0.61
13:G:26:VAL:HG11	13:G:77:VAL:HG22	1.83	0.61
2:I:1672:A:H2'	2:I:1673:A:C8	2.36	0.61
2:I:2042:C:O2'	2:I:2043:A:O4'	2.17	0.61
2:I:2367:U:H5''	2:I:2368:G:H2'	1.83	0.61
28:Y:22:LEU:O	28:Y:26:LYS:HG2	2.01	0.61
2:I:676:A:C4	2:I:2293:C:H5'	2.36	0.60
2:I:1656:G:O2'	2:I:1816:A:N6	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2339:U:O4	2:I:2424:A:N6	2.33	0.60
2:I:711:A:H2'	2:I:712:A:C8	2.36	0.60
2:I:2263:G:H2'	2:I:2264:A:C8	2.36	0.60
2:I:743:U:H2'	2:I:744:C:C6	2.37	0.60
2:I:2109:G:H2'	2:I:2110:G:C8	2.36	0.60
2:I:738:G:H2'	2:I:739:C:C6	2.36	0.60
2:I:746:G:N2	2:I:749:U:OP2	2.34	0.60
2:I:8:U:H3	2:I:3129:A:N6	2.00	0.60
2:I:682:C:H2'	2:I:683:C:C6	2.37	0.60
2:I:961:U:H2'	2:I:962:G:H8	1.66	0.60
2:I:1488:C:H2'	2:I:1489:G:O4'	2.01	0.60
2:I:2127:A:H2'	2:I:2128:A:C8	2.35	0.60
2:I:353:G:H2'	2:I:354:G:H8	1.67	0.60
24:S:11:PRO:HG2	24:S:119:SER:HB3	1.84	0.60
11:E:13:VAL:HG22	11:E:14:LYS:H	1.67	0.60
2:I:1025:A:H5'	2:I:1026:C:H5	1.67	0.60
2:I:1563:G:H2'	2:I:1564:C:C6	2.37	0.59
2:I:1453:A:H1'	3:I:39:ASP:HA	1.84	0.59
15:J:13:ARG:NH2	15:J:49:ASP:O	2.35	0.59
2:I:220:G:H22	2:I:237:U:H4'	1.67	0.59
13:G:70:ARG:NH1	13:G:74:SER:OG	2.35	0.59
2:I:617:A:H4'	2:I:618:U:OP2	2.02	0.59
2:I:2338:G:N1	2:I:2427:G:N7	2.50	0.59
2:I:2374:C:OP1	2:I:2376:U:N3	2.34	0.59
20:O:36:HIS:HB3	20:O:43:HIS:HB2	1.84	0.59
2:I:285:G:N2	2:I:303:U:O2'	2.36	0.59
11:E:13:VAL:HG11	11:E:131:HIS:HB3	1.84	0.59
2:I:718:G:N1	11:E:183:ILE:O	2.36	0.59
2:I:834:A:N6	2:I:855:G:H1'	2.18	0.59
2:I:1182:C:H2'	2:I:1183:A:H8	1.66	0.59
2:I:1492:G:H2'	2:I:1493:C:C6	2.37	0.59
20:O:34:VAL:HA	20:O:98:ASP:HB3	1.85	0.59
2:I:2654:G:H5''	17:L:64:LYS:HD2	1.84	0.59
2:I:3044:A:H2'	2:I:3045:A:C8	2.38	0.59
2:I:293:G:H2'	2:I:294:G:C8	2.38	0.59
23:R:79:PHE:CZ	23:R:81:ASN:HA	2.37	0.59
2:I:325:G:N2	2:I:452:A:N1	2.51	0.58
2:I:1959:A:N6	2:I:1969:U:H3	1.99	0.58
26:V:80:ALA:N	26:V:94:ASP:OD1	2.33	0.58
2:I:2552:A:H5'	12:F:42:VAL:HG21	1.86	0.58
11:E:162:VAL:HG12	11:E:164:ILE:HG12	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:847:A:OP2	2:I:848:C:N4	2.26	0.58
2:I:1572:A:H61	2:I:1632:G:H1'	1.69	0.58
7:4:14:CYS:HB3	7:4:27:CYS:HB2	1.85	0.58
12:F:48:GLY:O	12:F:87:ARG:NH2	2.30	0.58
18:M:60:ARG:H	18:M:60:ARG:HD3	1.67	0.58
8:B:1:U:H2'	8:B:2:U:H6	1.68	0.58
2:I:622:U:H2'	2:I:623:C:C6	2.38	0.58
6:3:19:THR:HG22	6:3:20:GLY:H	1.69	0.58
10:D:10:LYS:NZ	10:D:200:GLY:O	2.34	0.58
16:K:107:ARG:HA	16:K:112:MET:HE1	1.85	0.58
25:T:50:PHE:O	25:T:91:ARG:NH2	2.36	0.58
2:I:1416:G:N2	2:I:1459:G:H5''	2.18	0.58
2:I:490:A:H2'	2:I:491:A:C8	2.38	0.58
2:I:2565:A:H2'	2:I:2566:A:C8	2.39	0.58
28:Y:36:MET:HG2	28:Y:41:LEU:HD23	1.84	0.58
2:I:1243:G:H2'	2:I:1244:A:H8	1.68	0.58
2:I:2092:G:H2'	2:I:2121:G:H22	1.68	0.58
2:I:656:U:H2'	2:I:657:G:O4'	2.03	0.57
2:I:974:G:H1'	2:I:976:U:O4	2.04	0.57
2:I:2042:C:H2'	2:I:2043:A:C8	2.39	0.57
2:I:1206:A:OP2	2:I:1207:C:N4	2.38	0.57
2:I:925:U:H2'	2:I:926:C:C6	2.39	0.57
12:F:128:GLN:HG2	12:F:135:TYR:HB3	1.86	0.57
2:I:843:U:O2'	2:I:846:G:O6	2.22	0.57
27:W:49:VAL:HG22	27:W:82:GLY:CA	2.34	0.57
2:I:300:G:H2'	2:I:301:G:H4'	1.87	0.57
2:I:2292:A:H5''	2:I:2293:C:H5''	1.86	0.57
12:F:115:LEU:HB3	12:F:121:PHE:CZ	2.39	0.57
32:U:10:LEU:HD22	32:U:80:PRO:HG3	1.86	0.57
2:I:1692:U:H1'	19:N:63:ARG:HD2	1.86	0.57
26:V:115:GLN:H	26:V:146:ILE:HG21	1.69	0.57
15:J:6:PRO:HB2	15:J:48:VAL:HG21	1.85	0.57
2:I:1967:G:H2'	2:I:1968:G:H8	1.70	0.57
2:I:1605:G:O2'	2:I:1606:G:OP1	2.22	0.57
12:F:57:ILE:HG12	12:F:91:PRO:HB3	1.87	0.57
13:G:159:LYS:O	13:G:172:ARG:NH2	2.37	0.57
16:K:71:ARG:HH22	16:K:122:LEU:HD21	1.69	0.57
2:I:1087:A:H2'	2:I:1088:A:C8	2.40	0.56
2:I:1444:U:H5	2:I:1838:A:N1	2.02	0.56
2:I:1564:C:H2'	2:I:1565:G:C8	2.40	0.56
2:I:2425:U:H2'	2:I:2426:U:O4'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:348:U:H2'	2:I:349:G:H8	1.70	0.56
12:F:110:LEU:HA	12:F:114:ALA:HB3	1.87	0.56
27:W:68:GLU:HG2	27:W:81:VAL:HG23	1.86	0.56
29:Z:2:SER:OG	29:Z:3:GLN:N	2.38	0.56
2:I:689:G:N2	17:L:34:ARG:HH21	2.03	0.56
2:I:749:U:O2'	2:I:750:A:OP2	2.21	0.56
2:I:1186:A:O2'	2:I:1187:G:O5'	2.22	0.56
2:I:1689:C:H2'	2:I:1696:A:H61	1.70	0.56
2:I:1721:A:H2'	2:I:1722:G:H8	1.69	0.56
2:I:2204:A:N3	2:I:2830:G:O2'	2.37	0.56
2:I:2457:U:OP2	31:y:46:ARG:NH2	2.38	0.56
2:I:2567:A:H2'	2:I:2568:U:C6	2.40	0.56
2:I:2916:A:H2'	2:I:2917:A:C8	2.40	0.56
2:I:1206:A:N6	2:I:1218:G:OP1	2.28	0.56
8:B:1:U:H2'	8:B:2:U:C6	2.40	0.56
14:H:9:VAL:HB	14:H:12:LEU:HB2	1.88	0.56
2:I:1380:U:H4'	22:Q:4:VAL:HG21	1.87	0.56
2:I:2003:A:O2'	2:I:2196:C:OP1	2.21	0.56
2:I:1203:G:H5'	2:I:2712:C:H4'	1.86	0.56
2:I:2303:C:H2'	2:I:2304:C:C6	2.40	0.56
12:F:49:GLU:HG3	12:F:155:ARG:HH21	1.71	0.56
2:I:1157:A:H2'	2:I:1158:A:C8	2.41	0.56
2:I:2293:C:O2'	2:I:2742:U:H5'	2.06	0.56
2:I:2775:U:H2'	2:I:2776:C:C6	2.41	0.56
20:O:37:ARG:HG3	20:O:42:ILE:CD1	2.35	0.56
2:I:2256:G:O2'	22:Q:34:LYS:HE3	2.06	0.56
2:I:2367:U:H5'	2:I:2396:G:H22	1.70	0.56
20:O:46:LEU:HD11	20:O:95:VAL:HG11	1.87	0.56
2:I:158:U:H2'	2:I:159:C:C6	2.41	0.55
2:I:2442:A:H2'	2:I:2443:A:H8	1.72	0.55
2:I:2524:A:H4'	2:I:2525:A:O4'	2.05	0.55
2:I:1650:U:H2'	2:I:1651:C:O4'	2.06	0.55
9:C:72:LYS:HD3	9:C:120:GLY:CA	2.34	0.55
11:E:11:ILE:HD13	11:E:26:LEU:HD11	1.87	0.55
2:I:1614:A:H2'	2:I:1615:G:C8	2.41	0.55
2:I:1123:C:OP1	22:Q:53:ARG:NH2	2.38	0.55
2:I:2335:U:H3	2:I:2428:G:H1	1.55	0.55
13:G:53:VAL:HG21	13:G:70:ARG:HB2	1.88	0.55
2:I:220:G:N2	2:I:237:U:H4'	2.20	0.55
2:I:353:G:H2'	2:I:354:G:C8	2.42	0.55
2:I:636:U:O4	2:I:648:G:N1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:732:G:N1	2:I:740:G:C8	2.75	0.55
2:I:1244:A:H2'	2:I:1245:U:H6	1.72	0.55
2:I:1923:U:O2'	2:I:1935:A:N7	2.31	0.55
2:I:2545:G:H5'	2:I:2546:G:N2	2.22	0.55
10:D:35:VAL:HA	10:D:53:ALA:O	2.06	0.55
27:W:12:ASN:HB3	27:W:14:ARG:HH12	1.72	0.55
2:I:298:G:O6	2:I:340:U:C4	2.60	0.55
32:U:75:ASP:HB3	32:U:81:THR:HG21	1.88	0.55
2:I:600:G:OP1	2:I:1365:U:O2'	2.21	0.55
2:I:704:C:HO2'	2:I:705:A:H8	1.55	0.55
2:I:2707:A:N6	2:I:2719:G:O2'	2.39	0.55
11:E:167:SER:O	11:E:167:SER:OG	2.24	0.55
2:I:1722:G:H2'	2:I:1723:C:C6	2.42	0.54
9:C:108:PRO:HD2	9:C:111:LEU:HD12	1.88	0.54
26:V:98:VAL:HA	26:V:102:GLU:OE1	2.06	0.54
26:V:114:GLY:HA2	26:V:146:ILE:HG13	1.90	0.54
2:I:488:U:H2'	2:I:489:G:O4'	2.07	0.54
22:Q:122:ASN:OD1	22:Q:123:ALA:N	2.40	0.54
2:I:677:A:OP2	2:I:2737:C:O2'	2.25	0.54
2:I:1295:A:H2'	2:I:1296:C:C6	2.43	0.54
2:I:348:U:H2'	2:I:349:G:C8	2.42	0.54
2:I:503:C:H2'	2:I:504:A:C8	2.42	0.54
2:I:2660:C:C5	6:3:31:HIS:HE1	2.24	0.54
2:I:1619:U:H2'	2:I:1620:G:H8	1.73	0.54
2:I:2442:A:H2'	2:I:2443:A:C8	2.42	0.54
10:D:38:ARG:HB3	10:D:51:GLN:HB3	1.89	0.54
2:I:2109:G:H2'	2:I:2110:G:H8	1.72	0.54
2:I:1124:C:OP2	22:Q:54:LYS:NZ	2.41	0.54
2:I:1298:U:H2'	2:I:1299:C:C6	2.42	0.54
16:K:115:ILE:HG23	16:K:121:VAL:HG21	1.89	0.54
2:I:1198:A:C2	2:I:1226:U:H5'	2.43	0.54
2:I:1950:A:O2'	2:I:1951:U:H5	1.91	0.54
2:I:2335:U:H2'	2:I:2336:C:C6	2.43	0.54
2:I:340:U:H2'	2:I:341:A:C4	2.43	0.54
2:I:372:G:HO2'	2:I:373:G:H8	1.56	0.54
2:I:654:G:H2'	2:I:655:G:H5''	1.90	0.54
26:V:64:VAL:HG11	26:V:136:LEU:HD22	1.90	0.54
2:I:774:G:H2'	2:I:775:C:C6	2.42	0.53
2:I:1672:A:H2'	2:I:1673:A:H8	1.72	0.53
2:I:2082:A:H2'	2:I:2083:G:O4'	2.07	0.53
11:E:71:PRO:HG2	11:E:82:GLN:HG3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:61:VAL:HG13	12:F:72:PRO:HD2	1.90	0.53
20:O:81:GLN:O	20:O:85:GLU:HG2	2.08	0.53
2:I:1216:G:N2	2:I:1219:U:O4	2.41	0.53
2:I:1222:G:H2'	2:I:1223:U:C5	2.43	0.53
2:I:3025:C:H1'	10:D:65:PRO:HG3	1.90	0.53
2:I:917:A:H1'	5:2:7:THR:HG21	1.90	0.53
2:I:992:A:H2'	2:I:993:G:C8	2.43	0.53
2:I:1197:G:N3	2:I:1198:A:N6	2.52	0.53
2:I:2024:C:H2'	2:I:2025:A:C5	2.42	0.53
11:E:182:HIS:CE1	11:E:196:ARG:HH22	2.26	0.53
31:y:18:VAL:HG22	31:y:24:ARG:HG2	1.90	0.53
2:I:1980:U:H2'	2:I:1981:C:C6	2.43	0.53
2:I:2055:A:H2'	2:I:2056:C:C6	2.42	0.53
2:I:2112:U:H2'	2:I:2113:G:O4'	2.08	0.53
2:I:2529:U:H2'	2:I:2530:U:C6	2.44	0.53
11:E:165:GLY:O	11:E:167:SER:N	2.36	0.53
4:O:27:LEU:HD11	4:O:44:LEU:HD13	1.91	0.53
11:E:186:PRO:HG3	11:E:206:ALA:HB1	1.91	0.53
2:I:5:A:H2'	2:I:6:A:C8	2.44	0.53
2:I:738:G:C5	2:I:739:C:H5	2.27	0.53
2:I:1544:G:H2'	2:I:1545:G:H8	1.72	0.53
12:F:37:THR:H	12:F:166:SER:HB3	1.73	0.53
18:M:116:ALA:O	18:M:120:ARG:HG2	2.09	0.53
2:I:91:A:H4'	2:I:92:A:C5'	2.29	0.53
2:I:2770:G:O2'	2:I:2895:A:N1	2.42	0.53
2:I:1667:G:H2'	2:I:1668:C:C6	2.44	0.53
2:I:1953:G:H22	2:I:1976:G:N2	2.06	0.53
2:I:2402:G:N2	2:I:2405:G:OP2	2.41	0.53
2:I:2792:U:H2'	2:I:2793:U:C6	2.44	0.53
2:I:745:U:N3	2:I:749:U:O4	2.42	0.53
2:I:2530:U:H2'	2:I:2531:C:C6	2.44	0.53
5:2:44:THR:OG1	5:2:45:LEU:N	2.42	0.53
11:E:140:GLN:OE1	11:E:169:GLU:HB3	2.08	0.53
29:Z:10:ARG:NH1	29:Z:52:HIS:O	2.42	0.53
2:I:630:U:H2'	2:I:631:C:C6	2.44	0.52
24:S:83:THR:HB	24:S:116:VAL:HB	1.90	0.52
2:I:503:C:H2'	2:I:504:A:H8	1.75	0.52
2:I:1039:A:H2'	2:I:1040:A:C8	2.44	0.52
12:F:49:GLU:N	12:F:49:GLU:OE1	2.42	0.52
2:I:705:A:O2'	2:I:706:A:OP2	2.25	0.52
2:I:1242:U:H2'	2:I:1243:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:202:U:H4'	31:y:22:HIS:HB3	1.90	0.52
2:I:647:G:C2	2:I:648:G:H1'	2.44	0.52
27:W:43:THR:HG23	27:W:43:THR:O	2.10	0.52
2:I:274:A:H8	2:I:275:C:C6	2.27	0.52
2:I:855:G:HO2'	2:I:856:A:P	2.33	0.52
2:I:1186:A:O2'	2:I:1187:G:H8	1.93	0.52
15:J:3:THR:OG1	22:Q:64:ARG:NH1	2.43	0.52
17:L:120:LYS:HE2	17:L:140:GLY:HA3	1.90	0.52
18:M:35:GLN:OE1	18:M:130:ARG:NH2	2.41	0.52
2:I:52:A:H2'	2:I:53:A:C8	2.44	0.52
18:M:54:ILE:HG13	18:M:121:ALA:HB2	1.90	0.52
20:O:113:ASP:O	20:O:117:GLU:HG2	2.09	0.52
2:I:302:U:O2'	2:I:303:U:H4'	2.09	0.52
2:I:738:G:C4	2:I:739:C:C5	2.98	0.52
2:I:913:G:H5'	2:I:914:G:OP1	2.09	0.52
2:I:1408:G:H2'	2:I:1409:C:C6	2.45	0.52
2:I:2448:G:H5''	2:I:2449:A:H2'	1.90	0.52
10:D:56:GLU:CD	10:D:56:GLU:H	2.17	0.52
10:D:64:LYS:HA	10:D:67:THR:HG22	1.92	0.52
17:L:54:MET:O	17:L:59:ARG:NH1	2.43	0.52
2:I:731:A:C6	17:L:112:LEU:HD13	2.45	0.52
2:I:740:G:N2	17:L:110:LYS:HD2	2.25	0.52
2:I:704:C:O2'	2:I:705:A:H8	1.92	0.52
20:O:31:PRO:HB2	20:O:46:LEU:HG	1.92	0.52
2:I:1423:G:H2'	2:I:1424:C:C6	2.45	0.51
9:C:69:ARG:O	9:C:72:LYS:HE3	2.10	0.51
27:W:81:VAL:HG22	27:W:83:SER:HA	1.93	0.51
2:I:2511:A:H2'	2:I:2512:A:C8	2.45	0.51
2:I:2795:G:H2'	2:I:2796:C:C6	2.45	0.51
2:I:152:C:H2'	2:I:153:C:C6	2.45	0.51
2:I:706:A:H5''	2:I:784:A:H61	1.75	0.51
2:I:1692:U:O2'	19:N:60:LEU:HD13	2.10	0.51
2:I:2307:G:H2'	2:I:2308:A:C8	2.44	0.51
2:I:2338:G:O2'	2:I:2339:U:OP1	2.24	0.51
2:I:2418:G:OP2	2:I:2419:A:N6	2.43	0.51
2:I:2545:G:H5'	2:I:2546:G:H21	1.76	0.51
2:I:3071:U:H2'	2:I:3072:A:H8	1.75	0.51
16:K:71:ARG:NH1	16:K:122:LEU:HD11	2.21	0.51
2:I:746:G:O2'	2:I:748:A:N7	2.36	0.51
2:I:1194:U:H2'	2:I:1195:U:C6	2.46	0.51
12:F:122:ARG:C	12:F:122:ARG:HH11	2.17	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:88:THR:OG1	15:J:91:GLU:HG3	2.11	0.51
2:I:1580:A:N6	2:I:1623:G:N7	2.58	0.51
2:I:2184:U:H2'	2:I:2185:C:C6	2.45	0.51
27:W:39:ARG:O	27:W:40:GLN:HG2	2.11	0.51
2:I:736:A:H2'	2:I:737:A:C8	2.45	0.51
9:C:72:LYS:O	9:C:74:GLY:N	2.41	0.51
2:I:917:A:H1'	5:2:7:THR:CG2	2.41	0.51
2:I:1558:A:OP2	2:I:1645:A:N6	2.35	0.51
2:I:2339:U:H2'	2:I:2340:A:H8	1.75	0.51
23:R:24:LYS:HG2	23:R:97:VAL:HG22	1.93	0.51
2:I:403:G:H4'	2:I:405:A:N7	2.26	0.51
2:I:345:G:N2	2:I:346:G:O6	2.43	0.51
2:I:749:U:N3	2:I:751:G:O6	2.40	0.51
2:I:855:G:O2'	2:I:856:A:O5'	2.24	0.51
2:I:1737:G:N2	9:C:99:ASP:O	2.40	0.51
2:I:2303:C:H2'	2:I:2304:C:H6	1.76	0.51
2:I:2636:C:H2'	2:I:2637:A:C8	2.45	0.51
13:G:95:TYR:CD1	13:G:108:LEU:HB2	2.46	0.51
2:I:705:A:HO2'	2:I:706:A:P	2.33	0.51
2:I:841:G:N3	2:I:842:G:C8	2.79	0.51
2:I:1168:G:H22	2:I:1245:U:H3	1.58	0.51
2:I:581:G:H2'	2:I:582:G:O4'	2.11	0.50
2:I:1199:A:N6	2:I:1226:U:O2'	2.43	0.50
2:I:1644:U:H5''	2:I:1645:A:H2'	1.92	0.50
2:I:2583:G:N3	2:I:2619:C:H2'	2.25	0.50
2:I:2904:C:N4	13:G:109:GLY:O	2.43	0.50
9:C:2:ALA:HB3	9:C:200:GLU:HG3	1.92	0.50
18:M:134:ARG:HD3	26:V:127:ASN:ND2	2.26	0.50
2:I:209:A:H2'	2:I:210:C:O4'	2.11	0.50
2:I:689:G:H22	17:L:34:ARG:NH2	2.09	0.50
2:I:1564:C:H2'	2:I:1565:G:H8	1.75	0.50
2:I:1605:G:H2'	2:I:1606:G:C8	2.46	0.50
2:I:2032:U:OP2	9:C:271:ARG:NH2	2.44	0.50
2:I:2484:A:H2'	2:I:2485:A:C8	2.46	0.50
10:D:62:VAL:HG13	10:D:66:LEU:HD23	1.93	0.50
2:I:1124:C:N3	15:J:2:PRO:HA	2.26	0.50
2:I:1409:C:H2'	2:I:1410:A:C8	2.47	0.50
2:I:1612:G:C6	2:I:1613:G:O6	2.64	0.50
2:I:1658:A:H2'	2:I:1659:G:O4'	2.10	0.50
2:I:2399:G:C8	2:I:2400:U:H2'	2.46	0.50
8:B:29:C:OP1	20:O:9:ARG:NH1	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2289:A:H4'	10:D:151:ILE:HG13	1.92	0.50
2:I:2627:G:H5''	2:I:2628:U:O4'	2.11	0.50
16:K:121:VAL:O	16:K:122:LEU:HB2	2.11	0.50
27:W:42:GLY:O	27:W:43:THR:HG22	2.12	0.50
2:I:358:U:H3'	2:I:359:C:O4'	2.12	0.50
2:I:788:G:H4'	11:E:107:ARG:O	2.12	0.50
2:I:855:G:O2'	2:I:856:A:H8	1.94	0.50
2:I:979:A:C8	29:Z:25:THR:HG21	2.47	0.50
2:I:244:G:O5'	6:3:3:LYS:HD3	2.11	0.50
2:I:746:G:O5'	2:I:746:G:H8	1.95	0.50
2:I:858:G:C5	9:C:208:LYS:HB2	2.46	0.50
9:C:53:HIS:HB3	9:C:218:ARG:O	2.12	0.50
13:G:41:ILE:HD13	13:G:55:ARG:HB3	1.93	0.50
13:G:46:ASN:ND2	13:G:48:ASP:OD1	2.44	0.50
16:K:76:TYR:HB2	21:P:72:THR:HB	1.93	0.50
2:I:1570:U:N3	2:I:1633:A:OP2	2.42	0.50
2:I:1917:C:H2'	2:I:1918:C:C6	2.46	0.50
2:I:2551:C:OP1	12:F:75:ARG:NE	2.44	0.50
13:G:9:ILE:HB	13:G:51:ILE:HB	1.93	0.50
15:J:74:VAL:HG13	15:J:103:LYS:HE2	1.94	0.50
27:W:19:GLN:HG3	27:W:41:ARG:HH12	1.77	0.50
2:I:2557:G:N3	2:I:2558:C:N4	2.60	0.50
2:I:1182:C:H2'	2:I:1183:A:C8	2.47	0.50
13:G:150:ARG:NH1	13:G:163:VAL:O	2.45	0.50
2:I:683:C:H2'	2:I:684:U:H6	1.77	0.49
2:I:690:U:H1'	11:E:97:HIS:HB3	1.94	0.49
2:I:911:A:N1	9:C:226:MET:HE2	2.27	0.49
20:O:38:SER:O	20:O:107:ARG:NH2	2.32	0.49
31:y:3:ALA:HB1	31:y:12:PRO:HG3	1.93	0.49
2:I:328:A:N6	2:I:447:G:C4	2.80	0.49
2:I:332:C:H2'	2:I:333:U:C6	2.47	0.49
2:I:712:A:H2'	2:I:713:C:O4'	2.12	0.49
2:I:1334:U:H2'	2:I:1335:C:C6	2.47	0.49
2:I:1462:C:H2'	2:I:1464:C:C5	2.47	0.49
2:I:1808:A:H2'	2:I:1809:A:C8	2.47	0.49
13:G:82:GLN:NE2	13:G:83:GLY:O	2.45	0.49
20:O:81:GLN:HG2	20:O:118:ASN:HD21	1.76	0.49
2:I:2887:U:H2'	2:I:2888:C:H6	1.78	0.49
14:H:5:LEU:HD21	14:H:12:LEU:HB3	1.94	0.49
2:I:1116:C:H2'	2:I:1117:A:O4'	2.12	0.49
2:I:740:G:H22	17:L:110:LYS:HB3	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:975:G:H2'	2:I:975:G:N3	2.27	0.49
2:I:1409:C:H2'	2:I:1410:A:H8	1.77	0.49
2:I:2052:U:H5''	9:C:158:SER:OG	2.12	0.49
4:O:28:VAL:HG22	4:O:38:LYS:HE3	1.94	0.49
2:I:942:U:H2'	2:I:943:C:H6	1.76	0.49
2:I:2345:U:O2	2:I:2417:U:O2'	2.27	0.49
2:I:2427:G:H2'	2:I:2428:G:O4'	2.13	0.49
9:C:226:MET:SD	9:C:231:HIS:HB2	2.52	0.49
2:I:832:U:H2'	2:I:833:G:O4'	2.13	0.49
2:I:871:U:H2'	2:I:872:A:H8	1.73	0.49
2:I:1953:G:N2	2:I:1976:G:N2	2.58	0.49
2:I:2778:C:O2'	2:I:2978:A:N3	2.43	0.49
2:I:3089:U:H2'	2:I:3090:C:C6	2.48	0.49
13:G:55:ARG:HG2	13:G:66:HIS:HB2	1.95	0.49
13:G:95:TYR:HB2	13:G:108:LEU:HD13	1.95	0.49
2:I:230:U:H5''	2:I:231:U:H5	1.78	0.49
2:I:484:G:H2'	2:I:485:C:C6	2.48	0.49
2:I:740:G:N2	17:L:112:LEU:HG	2.27	0.49
2:I:1575:A:H2'	2:I:1576:C:C6	2.48	0.49
2:I:1771:G:C6	2:I:1772:G:C4	3.01	0.49
2:I:2189:U:OP1	16:K:54:ARG:NH2	2.46	0.49
2:I:2356:A:H2	2:I:2359:U:H3	1.60	0.49
11:E:30:LEU:HD23	11:E:30:LEU:O	2.13	0.49
18:M:63:LYS:HD3	18:M:65:TRP:CZ2	2.48	0.49
26:V:78:THR:HA	26:V:95:LEU:HD23	1.95	0.49
2:I:2371:A:N6	2:I:2392:C:OP2	2.45	0.49
15:J:49:ASP:OD1	15:J:121:LYS:NZ	2.44	0.49
26:V:132:GLU:HB3	26:V:167:SER:HB3	1.94	0.49
27:W:47:PRO:O	27:W:73:ARG:NH2	2.44	0.49
2:I:731:A:N6	17:L:112:LEU:HD13	2.28	0.49
2:I:1222:G:H2'	2:I:1223:U:C6	2.48	0.49
2:I:2402:G:N2	2:I:2406:A:H4'	2.27	0.49
2:I:2566:A:H2'	2:I:2567:A:H8	1.77	0.49
26:V:37:GLY:HA2	26:V:97:VAL:CG2	2.41	0.49
32:U:81:THR:HB	32:U:100:ARG:HG2	1.94	0.49
2:I:1451:C:C5	2:I:1460:U:H5''	2.48	0.48
2:I:2439:U:O2'	2:I:2441:G:OP1	2.29	0.48
11:E:39:LEU:HD11	11:E:112:MET:HB3	1.95	0.48
22:Q:58:ARG:HA	22:Q:61:TRP:CE3	2.48	0.48
2:I:1593:C:H2'	2:I:1594:A:H8	1.78	0.48
2:I:1915:U:H2'	2:I:1916:G:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:9:THR:OG1	10:D:54:TYR:OH	2.26	0.48
2:I:699:U:H2'	2:I:700:G:C8	2.49	0.48
2:I:1675:G:H2'	2:I:1676:U:C6	2.48	0.48
2:I:1832:G:H5''	2:I:1833:C:H5'	1.93	0.48
11:E:136:LEU:HD11	11:E:162:VAL:HG11	1.94	0.48
18:M:103:LEU:HD11	18:M:127:ILE:HD11	1.96	0.48
2:I:430:A:H2'	2:I:431:A:C8	2.47	0.48
2:I:743:U:H2'	2:I:744:C:H6	1.76	0.48
2:I:956:U:HO2'	2:I:2668:A:H2	1.60	0.48
2:I:1038:A:H2'	2:I:1041:C:C5	2.47	0.48
2:I:2020:A:H1'	2:I:2176:A:N6	2.29	0.48
2:I:2829:C:H2'	2:I:2830:G:C8	2.48	0.48
13:G:124:PHE:HE1	13:G:134:VAL:HG13	1.78	0.48
29:Z:8:GLN:HB3	29:Z:31:ILE:O	2.14	0.48
2:I:502:C:H2'	2:I:503:C:C6	2.48	0.48
2:I:699:U:H2'	2:I:700:G:H8	1.78	0.48
2:I:761:C:H2'	2:I:762:A:H8	1.78	0.48
2:I:868:A:H1'	2:I:869:C:H5	1.78	0.48
2:I:1733:A:H2'	2:I:1735:C:C5	2.49	0.48
2:I:2981:C:OP1	7:4:33:LYS:NZ	2.39	0.48
3:1:61:SER:OG	3:1:61:SER:O	2.31	0.48
9:C:77:ALA:HB1	9:C:95:LEU:HB3	1.96	0.48
26:V:58:HIS:O	26:V:63:ALA:HB2	2.13	0.48
2:I:738:G:C4	2:I:739:C:H5	2.32	0.48
2:I:841:G:C4	2:I:842:G:N7	2.81	0.48
2:I:1122:G:H5''	23:R:74:ILE:HD13	1.95	0.48
2:I:1331:C:H2'	2:I:1332:C:C6	2.48	0.48
13:G:57:ASP:OD1	13:G:57:ASP:N	2.39	0.48
2:I:197:A:H61	2:I:200:C:H3'	1.79	0.48
2:I:1187:G:H2'	2:I:1188:G:C8	2.48	0.48
2:I:2409:U:O2'	2:I:2413:A:N6	2.45	0.48
2:I:2940:G:OP1	19:N:73:LYS:NZ	2.47	0.48
13:G:95:TYR:CG	13:G:108:LEU:HB2	2.49	0.48
16:K:98:ILE:HD13	16:K:114:ILE:HG23	1.96	0.48
20:O:26:GLY:HA3	20:O:32:ARG:HB2	1.96	0.48
20:O:57:ALA:O	20:O:86:ARG:NH1	2.45	0.48
30:b:6:ARG:HA	30:b:25:LYS:O	2.14	0.48
2:I:107:G:H21	2:I:429:A:H62	1.62	0.48
2:I:162:A:H2'	2:I:163:A:C8	2.49	0.48
2:I:617:A:H3'	2:I:618:U:N1	2.28	0.48
2:I:1420:C:H2'	2:I:1421:U:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1594:A:N6	2:I:1612:G:O6	2.47	0.48
9:C:133:LEU:HD23	9:C:136:ILE:HD12	1.95	0.48
2:I:855:G:HO2'	2:I:856:A:H8	1.61	0.48
2:I:1308:G:H2'	2:I:1309:G:H8	1.79	0.48
9:C:247:VAL:HG12	9:C:253:PRO:HA	1.96	0.48
18:M:41:TYR:HB3	18:M:94:VAL:CG2	2.37	0.48
31:y:3:ALA:O	31:y:12:PRO:HD3	2.13	0.48
2:I:1223:U:H3	2:I:1227:A:N6	2.12	0.47
2:I:1771:G:N2	2:I:1776:A:H61	2.11	0.47
2:I:2994:U:H1'	2:I:2995:A:H5''	1.96	0.47
12:F:135:TYR:CZ	12:F:177:LEU:HB2	2.49	0.47
24:S:30:VAL:HG11	24:S:54:SER:HA	1.95	0.47
2:I:678:U:H2'	2:I:679:G:C8	2.48	0.47
4:O:24:LYS:NZ	24:S:33:LEU:O	2.46	0.47
17:L:112:LEU:HA	17:L:112:LEU:HD23	1.49	0.47
27:W:75:ARG:O	27:W:77:THR:N	2.46	0.47
2:I:1053:U:H2'	2:I:1054:G:C8	2.49	0.47
2:I:1218:G:H1'	2:I:1219:U:C5	2.47	0.47
2:I:1297:A:H2'	2:I:1298:U:C6	2.49	0.47
13:G:16:ASP:HB2	13:G:27:LYS:HD3	1.96	0.47
20:O:68:VAL:HG11	20:O:75:ARG:HE	1.78	0.47
2:I:502:C:H2'	2:I:503:C:H6	1.79	0.47
5:2:18:VAL:O	5:2:23:LEU:HD22	2.14	0.47
2:I:332:C:H2'	2:I:333:U:H6	1.79	0.47
2:I:2384:A:H2'	2:I:2385:G:O4'	2.14	0.47
2:I:3059:A:H3'	2:I:3060:C:O2	2.14	0.47
9:C:241:SER:O	9:C:241:SER:OG	2.32	0.47
12:F:12:LYS:HD3	12:F:13:GLU:H	1.79	0.47
20:O:37:ARG:HG3	20:O:42:ILE:HD12	1.95	0.47
21:P:103:ARG:HD2	21:P:106:LYS:HB2	1.97	0.47
24:S:51:GLN:O	24:S:53:ALA:N	2.45	0.47
32:U:91:THR:C	32:U:93:LYS:H	2.23	0.47
2:I:140:G:H2'	2:I:141:A:C8	2.49	0.47
2:I:152:C:H2'	2:I:153:C:H6	1.79	0.47
2:I:298:G:O6	2:I:340:U:O4	2.32	0.47
2:I:872:A:O2'	2:I:1894:U:OP1	2.30	0.47
2:I:2523:C:OP2	30:b:26:ASN:ND2	2.47	0.47
4:O:27:LEU:HD23	4:O:41:ARG:HD2	1.97	0.47
9:C:43:ARG:HA	9:C:48:ARG:O	2.15	0.47
9:C:139:GLY:HA2	9:C:164:GLN:NE2	2.30	0.47
25:T:8:ARG:HG2	28:Y:30:PHE:CG	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:131:A:H2'	2:I:132:G:H8	1.80	0.47
2:I:384:U:C2	32:U:80:PRO:HG2	2.49	0.47
2:I:1130:A:H2'	2:I:1131:G:O4'	2.15	0.47
2:I:1645:A:H2	2:I:1646:G:H21	1.63	0.47
2:I:1707:A:H2'	2:I:1708:A:H8	1.76	0.47
2:I:1786:G:H2'	2:I:1787:G:H8	1.78	0.47
2:I:2471:U:H2'	2:I:2472:G:C8	2.50	0.47
24:S:98:ARG:HG3	24:S:104:PHE:CD2	2.50	0.47
26:V:121:LEU:N	26:V:180:VAL:O	2.37	0.47
31:y:68:VAL:HG13	31:y:78:ILE:HG21	1.97	0.47
32:U:10:LEU:HD22	32:U:80:PRO:CG	2.43	0.47
2:I:12:U:O2	2:I:2864:C:H4'	2.14	0.47
2:I:2109:G:C6	2:I:2110:G:C6	3.03	0.47
13:G:9:ILE:N	13:G:51:ILE:O	2.48	0.47
13:G:149:ILE:HG22	13:G:163:VAL:HG11	1.97	0.47
20:O:27:THR:OG1	20:O:28:ALA:N	2.48	0.47
2:I:775:C:H2'	2:I:776:G:C8	2.50	0.47
2:I:1987:G:OP1	21:P:92:ARG:HD3	2.15	0.47
2:I:2006:G:N1	2:I:2217:C:H5	1.94	0.47
2:I:2087:A:N1	2:I:2324:G:H1'	2.30	0.47
8:B:44:A:C4	8:B:45:A:C8	3.03	0.47
8:B:111:G:H2'	8:B:112:A:C8	2.49	0.47
2:I:44:A:H2'	2:I:45:G:O4'	2.14	0.47
2:I:1581:A:N6	2:I:1623:G:H1'	2.29	0.47
2:I:1786:G:H2'	2:I:1787:G:C8	2.49	0.47
2:I:2110:G:C6	2:I:2111:G:N7	2.83	0.47
2:I:2364:G:H21	2:I:2367:U:P	2.38	0.47
2:I:3111:G:H5''	21:P:3:ARG:HH22	1.79	0.47
24:S:69:GLN:HG3	24:S:76:PRO:HG3	1.96	0.47
2:I:1177:A:H1'	2:I:1241:G:N2	2.31	0.46
2:I:2701:U:H2'	2:I:2702:C:O4'	2.16	0.46
12:F:154:ASP:OD1	12:F:154:ASP:N	2.48	0.46
13:G:112:HIS:O	13:G:112:HIS:CG	2.65	0.46
22:Q:11:HIS:O	22:Q:15:ARG:HG3	2.15	0.46
2:I:668:U:OP1	17:L:30:LYS:HE2	2.16	0.46
2:I:744:C:H2'	2:I:745:U:C6	2.50	0.46
2:I:2752:U:H2'	2:I:2753:C:C6	2.49	0.46
11:E:27:PRO:C	11:E:29:GLU:H	2.23	0.46
12:F:21:ASP:O	12:F:25:LYS:HG2	2.14	0.46
15:J:5:ALA:HB2	22:Q:100:ILE:HD13	1.95	0.46
16:K:70:ARG:HG3	16:K:76:TYR:CZ	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:252:G:H2'	2:I:253:A:C8	2.50	0.46
2:I:344:C:H2'	2:I:345:G:O4'	2.16	0.46
2:I:2065:G:H2'	2:I:2066:C:C6	2.51	0.46
2:I:2323:U:H2'	2:I:2324:G:C8	2.50	0.46
8:B:12:A:N1	8:B:68:G:O2'	2.39	0.46
10:D:7:LEU:HD11	10:D:82:ALA:HB3	1.96	0.46
28:Y:14:THR:OG1	28:Y:15:ASP:N	2.48	0.46
2:I:773:C:H2'	2:I:774:G:H8	1.80	0.46
2:I:1038:A:H2'	2:I:1041:C:H5	1.79	0.46
2:I:1525:U:H4'	2:I:1838:A:H4'	1.97	0.46
2:I:1627:C:C4	9:C:187:VAL:HG21	2.50	0.46
2:I:2530:U:H2'	2:I:2531:C:H6	1.80	0.46
2:I:2704:C:OP1	7:4:4:ASN:HB3	2.14	0.46
2:I:1769:C:H2'	2:I:1770:C:C6	2.51	0.46
2:I:2042:C:O2'	2:I:2043:A:O5'	2.32	0.46
11:E:27:PRO:O	11:E:29:GLU:N	2.44	0.46
26:V:101:GLY:HA2	26:V:135:ALA:HA	1.98	0.46
2:I:306:G:N3	14:H:45:LYS:HE3	2.30	0.46
2:I:408:C:H2'	2:I:409:G:O4'	2.16	0.46
2:I:2480:G:H2'	2:I:2481:U:O4'	2.15	0.46
2:I:2569:G:O2'	27:W:42:GLY:O	2.13	0.46
2:I:3079:A:H2'	2:I:3080:C:O4'	2.15	0.46
10:D:40:ARG:HB2	10:D:49:ALA:H	1.81	0.46
13:G:60:ARG:HA	13:G:63:ARG:HE	1.79	0.46
14:H:26:GLY:HA2	14:H:30:LEU:HB2	1.98	0.46
2:I:691:C:H2'	2:I:692:A:C8	2.51	0.46
2:I:1298:U:H2'	2:I:1299:C:H6	1.80	0.46
2:I:2700:U:H2'	2:I:2701:U:C6	2.51	0.46
2:I:2750:C:H2'	2:I:2751:G:O4'	2.15	0.46
17:L:24:GLY:O	17:L:29:GLY:HA2	2.15	0.46
2:I:828:A:H4'	2:I:1869:C:C4	2.51	0.46
2:I:2292:A:C5'	2:I:2293:C:H5''	2.44	0.46
16:K:63:VAL:HG12	16:K:106:LEU:HD11	1.98	0.46
16:K:71:ARG:HD2	21:P:71:ARG:NH2	2.30	0.46
17:L:79:VAL:HG22	17:L:113:GLY:HA2	1.97	0.46
2:I:289:A:C6	2:I:290:A:H2	2.34	0.46
2:I:878:A:H4'	2:I:1402:G:N3	2.31	0.46
2:I:3050:C:C4	2:I:3051:C:C5	3.04	0.46
12:F:42:VAL:HG22	12:F:162:ASN:HB3	1.97	0.46
13:G:95:TYR:CD2	13:G:108:LEU:HD22	2.51	0.46
26:V:114:GLY:HA2	26:V:146:ILE:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:620:C:H4'	2:I:621:G:C8	2.51	0.46
2:I:840:G:C6	2:I:850:G:N1	2.84	0.46
2:I:1987:G:N2	2:I:1990:G:OP2	2.43	0.46
2:I:2978:A:H2'	2:I:2979:A:C8	2.51	0.46
4:0:24:LYS:HD3	24:S:33:LEU:HD22	1.97	0.46
4:0:30:VAL:O	4:0:32:VAL:HG13	2.16	0.46
13:G:18:THR:O	13:G:18:THR:OG1	2.33	0.46
27:W:68:GLU:H	27:W:81:VAL:CG2	2.28	0.46
2:I:621:G:H2'	2:I:622:U:C6	2.52	0.45
2:I:1102:A:H8	2:I:1102:A:OP1	1.99	0.45
2:I:1196:A:H3'	2:I:1197:G:H8	1.81	0.45
2:I:1219:U:C2	2:I:1231:C:H1'	2.50	0.45
8:B:24:A:C2	8:B:113:A:H1'	2.44	0.45
2:I:158:U:H2'	2:I:159:C:H6	1.81	0.45
2:I:738:G:C5	2:I:739:C:C5	3.03	0.45
2:I:747:A:N1	2:I:2607:A:O2'	2.47	0.45
2:I:760:A:H2'	2:I:760:A:N3	2.31	0.45
2:I:776:G:H8	2:I:776:G:OP2	1.99	0.45
2:I:979:A:H8	29:Z:25:THR:HG21	1.81	0.45
2:I:1183:A:N6	2:I:1234:U:H3	1.98	0.45
2:I:1260:G:HO2'	2:I:1262:A:H2	1.62	0.45
2:I:1484:A:H2'	2:I:1485:A:C8	2.51	0.45
2:I:1962:C:O2'	2:I:1965:G:N2	2.49	0.45
2:I:2887:U:H2'	2:I:2888:C:C6	2.51	0.45
12:F:149:ASP:O	12:F:153:ILE:HG13	2.16	0.45
27:W:53:ARG:O	27:W:59:LEU:N	2.32	0.45
32:U:75:ASP:HB3	32:U:81:THR:CG2	2.46	0.45
2:I:732:G:C6	2:I:740:G:N7	2.84	0.45
2:I:818:A:H2'	2:I:819:C:C6	2.51	0.45
2:I:840:G:C4	2:I:841:G:H1'	2.52	0.45
2:I:1307:U:H5''	2:I:1308:G:C8	2.52	0.45
2:I:1446:C:H2'	2:I:1447:U:C6	2.51	0.45
2:I:2743:G:O2'	2:I:2744:U:H6	1.98	0.45
2:I:2751:G:H2'	2:I:2752:U:C6	2.52	0.45
2:I:2925:U:H2'	2:I:2926:G:O4'	2.16	0.45
11:E:28:ALA:HB1	11:E:32:ASP:HB3	1.98	0.45
16:K:10:VAL:HG12	16:K:12:ASP:OD2	2.16	0.45
24:S:93:LYS:HG2	24:S:105:ARG:HD2	1.99	0.45
28:Y:5:VAL:HG21	28:Y:21:ARG:NH1	2.27	0.45
2:I:2104:C:H5	2:I:2105:G:H21	1.64	0.45
16:K:64:ARG:HD2	21:P:67:VAL:HG11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1156:A:N1	2:I:1256:U:H5	2.15	0.45
2:I:1177:A:H2'	2:I:1178:C:C6	2.52	0.45
2:I:1715:A:H2'	2:I:1716:G:O4'	2.16	0.45
8:B:2:U:H2'	8:B:3:A:C8	2.51	0.45
11:E:30:LEU:HD23	11:E:125:ALA:HB2	1.98	0.45
12:F:81:ILE:HG22	12:F:83:GLN:HB3	1.98	0.45
2:I:2329:U:P	31:y:36:ARG:HH12	2.40	0.45
2:I:2912:G:H4'	16:K:30:ARG:HD2	1.99	0.45
20:O:72:LYS:CB	20:O:107:ARG:HD3	2.45	0.45
2:I:778:G:H1'	2:I:779:U:H5'	1.97	0.45
2:I:1076:C:H1'	2:I:1113:G:C8	2.52	0.45
2:I:1556:C:N4	2:I:1647:U:OP2	2.50	0.45
2:I:1916:G:N3	2:I:1996:A:H2'	2.32	0.45
2:I:3132:U:O2	15:J:134:ALA:HB1	2.17	0.45
10:D:19:GLU:CD	10:D:19:GLU:H	2.24	0.45
15:J:6:PRO:CB	15:J:48:VAL:HG21	2.47	0.45
2:I:134:A:H2'	2:I:135:C:C6	2.52	0.45
2:I:841:G:C2	2:I:849:C:C4	3.04	0.45
2:I:1516:A:O2'	2:I:1527:U:O2	2.34	0.45
2:I:1722:G:H2'	2:I:1723:C:H6	1.81	0.45
2:I:1767:A:H2'	2:I:1768:G:O4'	2.17	0.45
2:I:2108:A:N3	2:I:2108:A:H2'	2.32	0.45
2:I:568:A:H1'	2:I:569:A:H5''	1.98	0.45
2:I:592:G:N2	2:I:1365:U:H4'	2.32	0.45
2:I:991:G:H2'	2:I:992:A:O4'	2.17	0.45
2:I:1009:U:H2'	2:I:1010:G:C8	2.52	0.45
2:I:1876:A:H2'	2:I:1877:G:O4'	2.17	0.45
2:I:2899:G:H2'	2:I:2900:A:C8	2.52	0.45
10:D:129:ARG:HG3	10:D:170:MET:HB2	1.98	0.45
28:Y:23:ARG:HG2	28:Y:23:ARG:NH1	2.30	0.45
30:b:6:ARG:NH1	30:b:26:ASN:HB2	2.32	0.45
2:I:403:G:H4'	2:I:405:A:C8	2.52	0.45
2:I:668:U:H2'	2:I:669:U:O4'	2.17	0.45
2:I:1581:A:H62	2:I:1623:G:H1'	1.82	0.45
9:C:69:ARG:NH2	9:C:128:GLY:O	2.42	0.45
26:V:46:GLU:HG2	26:V:49:GLY:HA3	1.99	0.45
2:I:808:G:H2'	2:I:809:G:H8	1.81	0.44
2:I:1098:G:H2'	2:I:1099:U:C6	2.52	0.44
2:I:1691:G:OP2	19:N:73:LYS:HE2	2.17	0.44
2:I:2103:C:H2'	2:I:2104:C:C6	2.52	0.44
2:I:2829:C:H2'	2:I:2830:G:H8	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2886:G:H2'	2:I:2887:U:C6	2.51	0.44
2:I:3055:C:N4	2:I:3109:C:OP1	2.50	0.44
8:B:24:A:H2'	8:B:25:A:C8	2.52	0.44
10:D:36:VAL:O	10:D:52:LEU:HA	2.16	0.44
2:I:184:A:H2'	2:I:185:C:C6	2.52	0.44
2:I:304:G:N3	2:I:304:G:H2'	2.31	0.44
2:I:691:C:H2'	2:I:692:A:H8	1.82	0.44
2:I:740:G:N3	17:L:112:LEU:HD11	2.31	0.44
2:I:777:U:OP2	2:I:781:A:N6	2.33	0.44
2:I:2315:C:H2'	2:I:2316:U:C6	2.53	0.44
2:I:2875:U:H2'	2:I:2876:G:O4'	2.17	0.44
3:I:20:PHE:CD2	25:T:24:LEU:HD11	2.52	0.44
12:F:81:ILE:C	12:F:83:GLN:H	2.24	0.44
13:G:35:LEU:HB3	13:G:76:LEU:HD11	2.00	0.44
19:N:55:ALA:HB2	19:N:79:LEU:HG	1.98	0.44
19:N:103:ARG:HG3	19:N:110:MET:SD	2.57	0.44
2:I:328:A:N1	2:I:449:A:C5	2.85	0.44
2:I:1029:A:H3'	2:I:1030:C:H6	1.82	0.44
2:I:1239:A:H8	2:I:1239:A:OP2	2.01	0.44
2:I:1750:C:H2'	2:I:1751:C:C6	2.53	0.44
2:I:1832:G:OP2	25:T:43:LYS:NZ	2.42	0.44
2:I:3023:U:O2	10:D:69:GLN:NE2	2.50	0.44
2:I:3036:G:H3'	2:I:3037:G:H8	1.82	0.44
4:O:27:LEU:HD21	4:O:44:LEU:HD22	1.99	0.44
11:E:161:LEU:HD11	11:E:184:LEU:HG	2.00	0.44
16:K:67:LYS:NZ	16:K:68:GLU:OE2	2.49	0.44
26:V:16:GLU:OE2	26:V:24:ARG:NH2	2.51	0.44
2:I:141:A:H2'	2:I:142:U:C6	2.53	0.44
2:I:309:U:H2'	2:I:310:G:C8	2.52	0.44
2:I:565:G:H4'	2:I:590:A:N1	2.32	0.44
2:I:694:G:H8	11:E:107:ARG:NH2	2.15	0.44
2:I:2616:A:C5	2:I:2617:G:H1'	2.52	0.44
2:I:2636:C:H2'	2:I:2637:A:H8	1.82	0.44
2:I:3028:A:H3'	2:I:3029:C:H5''	1.99	0.44
2:I:3032:A:H2'	2:I:3033:C:C6	2.52	0.44
8:B:28:G:H2'	8:B:29:C:C6	2.53	0.44
9:C:41:GLY:HA2	9:C:55:GLY:HA2	2.00	0.44
2:I:250:G:N3	2:I:2669:U:H4'	2.33	0.44
2:I:2377:C:OP1	2:I:2390:G:N1	2.33	0.44
13:G:9:ILE:HD11	13:G:70:ARG:HD2	1.98	0.44
20:O:49:ASP:N	20:O:49:ASP:OD1	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:352:A:N6	2:I:353:G:O6	2.50	0.44
2:I:858:G:C6	9:C:208:LYS:HB2	2.52	0.44
2:I:1177:A:H1'	2:I:1241:G:H21	1.83	0.44
2:I:2884:C:H2'	2:I:2885:U:O4'	2.17	0.44
3:1:19:LYS:HB3	25:T:97:GLY:HA2	2.00	0.44
12:F:47:VAL:O	12:F:47:VAL:HG23	2.17	0.44
2:I:8:U:H3	2:I:3129:A:H62	1.65	0.44
2:I:131:A:H2'	2:I:132:G:C8	2.52	0.44
2:I:429:A:H5'	2:I:430:A:OP2	2.18	0.44
2:I:1295:A:H2'	2:I:1296:C:H6	1.81	0.44
2:I:287:G:O6	2:I:302:U:H2'	2.18	0.44
2:I:675:G:OP2	23:R:82:LYS:NZ	2.39	0.44
2:I:690:U:H2'	2:I:691:C:C6	2.53	0.44
2:I:1177:A:H2'	2:I:1178:C:H6	1.81	0.44
2:I:2377:C:H1'	2:I:2381:G:N2	2.32	0.44
2:I:2459:A:H2'	2:I:2460:G:O4'	2.18	0.44
8:B:66:G:H2'	8:B:67:C:C6	2.53	0.44
13:G:17:VAL:HB	13:G:45:ARG:HH22	1.83	0.44
13:G:22:GLN:NE2	13:G:41:ILE:O	2.46	0.44
18:M:77:LYS:HB2	18:M:77:LYS:HE3	1.84	0.44
2:I:2058:G:O3'	9:C:249:PRO:HD3	2.17	0.44
2:I:3052:C:OP1	19:N:42:ARG:NH2	2.48	0.44
8:B:65:A:H4'	8:B:66:G:H5'	1.99	0.44
13:G:103:ASN:HB2	13:G:116:ILE:O	2.17	0.44
20:O:13:ARG:HD2	20:O:102:TYR:CZ	2.52	0.44
2:I:56:A:H2'	2:I:57:C:O4'	2.18	0.43
2:I:293:G:H2'	2:I:294:G:H8	1.83	0.43
2:I:849:C:N4	2:I:850:G:O6	2.51	0.43
2:I:986:A:H2'	2:I:987:G:O4'	2.18	0.43
2:I:1968:G:H2'	2:I:1969:U:C6	2.53	0.43
2:I:2309:C:H2'	2:I:2310:C:H6	1.83	0.43
2:I:2381:G:H4'	2:I:2382:C:C5	2.52	0.43
11:E:67:GLY:HA3	11:E:86:ARG:HG2	1.99	0.43
12:F:62:ASN:O	12:F:66:LEU:HD23	2.17	0.43
26:V:46:GLU:CD	26:V:46:GLU:H	2.25	0.43
27:W:50:ASN:HB3	27:W:63:THR:HG22	2.00	0.43
2:I:1242:U:C2	2:I:1243:G:N7	2.87	0.43
2:I:2026:G:C2'	2:I:2027:G:H5'	2.48	0.43
2:I:3084:G:H4'	2:I:3085:A:H5'	2.00	0.43
16:K:68:GLU:CD	16:K:68:GLU:H	2.25	0.43
20:O:13:ARG:HD2	20:O:102:TYR:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:93:C:H2'	2:I:94:C:O4'	2.17	0.43
2:I:485:C:O3'	31:y:31:PRO:HA	2.18	0.43
2:I:682:C:H2'	2:I:683:C:H6	1.82	0.43
2:I:808:G:H2'	2:I:809:G:C8	2.53	0.43
2:I:1001:A:H5'	18:M:69:PHE:CZ	2.53	0.43
2:I:1075:A:H2'	2:I:1076:C:C6	2.52	0.43
2:I:1246:U:H2'	2:I:1247:G:H8	1.81	0.43
2:I:1513:A:H2'	2:I:1514:C:O4'	2.18	0.43
2:I:1572:A:C8	2:I:1573:C:C6	3.06	0.43
2:I:2139:A:H2'	2:I:2140:C:C6	2.52	0.43
2:I:2362:G:N2	2:I:2363:A:O2'	2.50	0.43
2:I:2693:G:H2'	2:I:2694:C:H6	1.83	0.43
10:D:38:ARG:HA	10:D:97:VAL:HG22	1.99	0.43
16:K:112:MET:HE2	16:K:112:MET:HA	2.01	0.43
18:M:54:ILE:CG1	18:M:121:ALA:HB2	2.48	0.43
20:O:47:VAL:HG12	20:O:48:ASN:HB2	1.99	0.43
2:I:178:G:O2'	2:I:179:A:H5'	2.18	0.43
2:I:309:U:H2'	2:I:310:G:H8	1.84	0.43
2:I:992:A:H2'	2:I:993:G:H8	1.82	0.43
2:I:1009:U:C2	2:I:1010:G:N7	2.87	0.43
2:I:1272:A:O2'	2:I:1273:A:H3'	2.18	0.43
2:I:1623:G:HO2'	2:I:1624:C:P	2.42	0.43
2:I:2402:G:H22	2:I:2406:A:H4'	1.83	0.43
2:I:2421:C:N4	2:I:2422:G:C6	2.87	0.43
12:F:23:LEU:HD11	12:F:176:LEU:HD21	2.01	0.43
2:I:35:G:H1'	2:I:543:A:C4	2.54	0.43
2:I:1804:A:OP2	9:C:84:TYR:OH	2.30	0.43
2:I:1962:C:H2'	2:I:1964:U:C5	2.53	0.43
2:I:2569:G:O2'	2:I:2574:A:N1	2.51	0.43
2:I:3018:C:OP2	15:J:120:ARG:HD3	2.18	0.43
9:C:200:GLU:CD	9:C:200:GLU:H	2.26	0.43
2:I:701:U:H2'	2:I:702:C:C6	2.53	0.43
2:I:1656:G:H3'	2:I:1657:A:C2	2.53	0.43
2:I:1689:C:H42	2:I:1697:A:H62	1.66	0.43
2:I:2233:U:OP1	10:D:133:ARG:NH2	2.50	0.43
2:I:2615:A:O2'	20:O:122:PHE:HB3	2.19	0.43
12:F:42:VAL:HG12	12:F:97:THR:HG23	2.01	0.43
29:Z:50:VAL:HG12	29:Z:54:VAL:HG13	2.00	0.43
2:I:274:A:N1	2:I:322:G:O2'	2.50	0.43
2:I:1174:A:N6	2:I:1240:A:N7	2.66	0.43
2:I:2272:U:C2'	2:I:2273:G:H5'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:95:ARG:HG2	12:F:96:VAL:N	2.33	0.43
27:W:80:ILE:HD13	27:W:80:ILE:HA	1.84	0.43
2:I:372:G:O2'	2:I:373:G:H8	2.02	0.43
2:I:689:G:N2	17:L:34:ARG:NH2	2.67	0.43
2:I:1133:C:H2'	2:I:1140:G:H2'	2.00	0.43
2:I:1177:A:N7	2:I:1239:A:C2	2.87	0.43
2:I:1558:A:H2'	2:I:1559:A:C8	2.54	0.43
2:I:1645:A:H2	2:I:1646:G:N2	2.17	0.43
2:I:1771:G:H22	2:I:1776:A:H61	1.65	0.43
2:I:2485:A:H2'	2:I:2486:C:H6	1.83	0.43
2:I:2990:C:H2'	2:I:2991:A:O4'	2.19	0.43
24:S:78:THR:HB	24:S:120:ARG:O	2.19	0.43
2:I:274:A:H8	2:I:275:C:C5	2.37	0.43
2:I:682:C:H4'	22:Q:31:LEU:HD13	2.00	0.43
2:I:776:G:H4'	17:L:116:LYS:HD2	2.00	0.43
2:I:1670:G:H2'	2:I:1671:G:O4'	2.19	0.43
2:I:1734:U:H5''	2:I:1735:C:H5	1.84	0.43
2:I:2185:C:H2'	2:I:2186:G:H8	1.83	0.43
2:I:2693:G:H2'	2:I:2694:C:C6	2.54	0.43
9:C:206:TRP:CD1	9:C:212:MET:HE2	2.53	0.43
10:D:40:ARG:O	10:D:48:SER:HA	2.19	0.43
2:I:429:A:H3'	2:I:430:A:H8	1.84	0.43
2:I:622:U:O2'	22:Q:49:ASP:OD2	2.27	0.43
2:I:772:G:H1'	2:I:773:C:C5	2.54	0.43
2:I:841:G:C2	2:I:842:G:C5	3.07	0.43
2:I:2162:C:H2'	2:I:2163:C:C6	2.54	0.43
12:F:21:ASP:OD1	12:F:21:ASP:N	2.52	0.43
13:G:4:ILE:O	13:G:70:ARG:HG2	2.19	0.43
16:K:71:ARG:NH2	16:K:122:LEU:HD21	2.33	0.43
24:S:51:GLN:C	24:S:53:ALA:H	2.27	0.43
2:I:68:G:H2'	2:I:69:C:O4'	2.18	0.42
2:I:455:U:H2'	2:I:456:C:H6	1.83	0.42
2:I:1267:G:H2'	2:I:1268:G:O4'	2.19	0.42
2:I:1319:G:H5''	23:R:85:TYR:CE1	2.54	0.42
2:I:1399:A:H2'	2:I:1400:G:O4'	2.19	0.42
19:N:45:ARG:O	19:N:49:GLU:HG3	2.19	0.42
2:I:842:G:N7	2:I:843:U:C4	2.87	0.42
2:I:1214:A:H2'	2:I:1215:A:C8	2.54	0.42
2:I:1453:A:C4	2:I:1454:G:C8	3.08	0.42
2:I:1613:G:H2'	2:I:1614:A:C8	2.54	0.42
2:I:2043:A:H2'	2:I:2044:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2658:C:H5''	30:b:8:ILE:CD1	2.43	0.42
2:I:2853:U:H2'	2:I:2854:C:H6	1.84	0.42
2:I:2942:C:H2'	2:I:2943:A:O4'	2.19	0.42
8:B:102:G:H2'	8:B:103:A:O4'	2.19	0.42
12:F:125:SER:O	12:F:127:LYS:HG3	2.19	0.42
14:H:2:LYS:HE3	14:H:20:GLU:HB3	2.01	0.42
18:M:48:GLU:CD	18:M:51:ARG:HH21	2.25	0.42
18:M:51:ARG:HD3	18:M:66:ILE:HD11	2.00	0.42
22:Q:4:VAL:O	22:Q:5:LYS:HB2	2.20	0.42
26:V:9:LEU:HD22	26:V:65:LEU:HD22	2.00	0.42
26:V:119:ASP:O	26:V:181:LYS:HG3	2.19	0.42
2:I:1049:G:H21	2:I:2507:A:H8	1.67	0.42
2:I:1193:C:C5	2:I:1194:U:C4	3.08	0.42
2:I:1605:G:HO2'	2:I:1606:G:P	2.39	0.42
2:I:2012:U:H2'	2:I:2018:A:N6	2.34	0.42
13:G:33:LEU:HB3	13:G:76:LEU:HD22	2.01	0.42
18:M:47:ILE:HD12	18:M:70:PRO:HG3	2.00	0.42
20:O:72:LYS:HG2	20:O:75:ARG:HH12	1.84	0.42
2:I:331:U:O2'	2:I:332:C:O5'	2.37	0.42
2:I:616:A:N1	2:I:2280:A:H2'	2.34	0.42
2:I:1441:G:H2'	2:I:1442:G:O4'	2.19	0.42
2:I:1485:A:H2'	2:I:1486:G:O4'	2.19	0.42
2:I:1892:U:O3'	10:D:143:ALA:HB1	2.19	0.42
2:I:1900:A:H5''	16:K:66:VAL:HG12	2.00	0.42
2:I:2166:A:H2'	2:I:2167:G:O4'	2.19	0.42
2:I:2731:U:O2'	18:M:80:GLU:OE2	2.29	0.42
2:I:3043:U:H5''	2:I:3125:G:O6	2.19	0.42
7:4:14:CYS:HB2	7:4:25:VAL:HG13	2.02	0.42
12:F:76:ARG:HH11	12:F:91:PRO:CD	2.32	0.42
24:S:17:ALA:HB2	24:S:60:VAL:HG22	2.01	0.42
2:I:160:U:H2'	2:I:161:G:O4'	2.19	0.42
2:I:190:G:H5''	31:y:14:PHE:CD1	2.55	0.42
2:I:350:A:H2'	2:I:351:G:C8	2.53	0.42
2:I:1168:G:H2'	2:I:1169:U:C6	2.54	0.42
2:I:1599:C:H42	2:I:1607:G:H22	1.68	0.42
2:I:1664:G:N7	9:C:31:LYS:NZ	2.64	0.42
2:I:1969:U:H2'	2:I:1970:G:C8	2.54	0.42
2:I:2936:U:H2'	2:I:2937:C:H6	1.82	0.42
12:F:31:ASN:HB2	12:F:34:GLN:HE21	1.85	0.42
2:I:617:A:H3'	2:I:618:U:C6	2.54	0.42
2:I:1572:A:N6	2:I:1632:G:H1'	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2036:A:H2'	2:I:2037:A:H8	1.79	0.42
2:I:2252:A:H2'	2:I:2253:A:C8	2.55	0.42
10:D:28:VAL:HG13	10:D:191:VAL:HG13	2.01	0.42
16:K:64:ARG:HB2	16:K:83:ALA:HB3	2.02	0.42
17:L:40:ARG:NH2	17:L:45:VAL:HB	2.34	0.42
26:V:46:GLU:CD	26:V:46:GLU:N	2.77	0.42
30:b:40:ASP:O	30:b:44:ARG:N	2.50	0.42
2:I:283:A:C6	2:I:284:U:C2	3.08	0.42
8:B:41:C:C6	12:F:73:GLU:HB2	2.55	0.42
9:C:28:THR:HB	9:C:29:PRO:HD2	2.01	0.42
10:D:11:LEU:HD12	10:D:28:VAL:HG12	2.02	0.42
13:G:150:ARG:HG3	13:G:151:ARG:H	1.84	0.42
22:Q:27:GLN:OE1	22:Q:34:LYS:HE2	2.19	0.42
2:I:196:G:H2'	2:I:197:A:O4'	2.20	0.42
2:I:357:G:C2	2:I:363:A:N6	2.87	0.42
2:I:454:U:H2'	2:I:455:U:C6	2.54	0.42
2:I:945:C:H2'	2:I:946:C:O2	2.19	0.42
2:I:1565:G:H2'	2:I:1566:G:H8	1.85	0.42
2:I:2874:U:H4'	10:D:83:GLU:OE2	2.20	0.42
2:I:3012:C:H2'	2:I:3013:A:O4'	2.20	0.42
2:I:3023:U:H2'	2:I:3024:U:C6	2.55	0.42
12:F:121:PHE:CE1	12:F:123:GLY:HA2	2.54	0.42
32:U:20:LYS:HD3	32:U:74:VAL:HG11	2.02	0.42
2:I:39:U:H2'	2:I:40:C:C6	2.55	0.42
2:I:289:A:H62	2:I:301:G:H8	1.68	0.42
2:I:374:U:H2'	2:I:375:U:C6	2.55	0.42
2:I:536:A:N1	2:I:543:A:O2'	2.50	0.42
2:I:1198:A:H2	2:I:1226:U:H5'	1.84	0.42
12:F:122:ARG:O	12:F:122:ARG:NH1	2.48	0.42
21:P:47:ILE:HG22	21:P:99:LEU:HD12	2.01	0.42
30:b:8:ILE:HG13	30:b:24:ARG:NH1	2.35	0.42
2:I:946:C:H5	2:I:1322:G:N1	1.98	0.42
2:I:1118:G:OP2	29:Z:11:SER:HB2	2.20	0.42
2:I:2227:A:H2'	2:I:2228:C:O4'	2.19	0.42
2:I:2381:G:H4'	2:I:2382:C:H5	1.84	0.42
2:I:2770:G:N2	2:I:2901:G:O2'	2.52	0.42
9:C:211:ARG:HG3	9:C:214:TRP:CZ3	2.55	0.42
15:J:57:ILE:HD11	15:J:130:HIS:HB3	2.01	0.42
19:N:18:LYS:HE2	19:N:18:LYS:HB3	1.76	0.42
25:T:31:PHE:CE1	25:T:95:LEU:HD21	2.55	0.42
27:W:38:VAL:HB	27:W:59:LEU:HD23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:U:77:ASP:OD1	32:U:101:ASN:ND2	2.52	0.42
2:I:96:A:H4'	28:Y:42:ASN:O	2.20	0.41
2:I:153:C:H2'	2:I:154:C:H6	1.85	0.41
2:I:674:A:H2'	2:I:675:G:O4'	2.19	0.41
2:I:731:A:H2'	17:L:76:ILE:HD11	2.02	0.41
2:I:840:G:C2	2:I:841:G:H1'	2.55	0.41
2:I:1197:G:N2	2:I:1224:A:H2'	2.35	0.41
2:I:1400:G:H2'	2:I:1401:C:C6	2.55	0.41
2:I:2120:A:H2'	2:I:2121:G:O4'	2.20	0.41
2:I:2192:G:O2'	2:I:2194:U:O4	2.34	0.41
2:I:2448:G:H4'	2:I:2449:A:H5''	2.02	0.41
2:I:2827:A:H2'	2:I:2828:A:C8	2.55	0.41
15:J:73:MET:SD	15:J:88:THR:HG22	2.60	0.41
15:J:143:LYS:HE3	15:J:143:LYS:HB2	1.60	0.41
20:O:49:ASP:OD1	20:O:51:ASN:HB2	2.20	0.41
1:7:8:LYS:O	1:7:11:ARG:HG2	2.20	0.41
2:I:648:G:H2'	2:I:649:A:C8	2.55	0.41
2:I:946:C:O2'	2:I:968:U:H5''	2.20	0.41
2:I:1462:C:H2'	2:I:1464:C:H5	1.85	0.41
2:I:1594:A:H2'	2:I:1595:C:H5'	2.02	0.41
2:I:2531:C:H2'	2:I:2532:C:H6	1.84	0.41
2:I:2555:U:H2'	2:I:2556:G:O4'	2.21	0.41
7:4:13:LYS:HB2	7:4:13:LYS:HE3	1.78	0.41
10:D:36:VAL:HG21	10:D:75:VAL:HG11	2.02	0.41
23:R:17:VAL:HB	23:R:100:VAL:HG21	2.01	0.41
30:b:19:TYR:HB2	30:b:42:ILE:HD12	2.01	0.41
31:y:51:VAL:HG22	31:y:52:SER:O	2.20	0.41
2:I:732:G:C2	2:I:740:G:C8	3.08	0.41
2:I:1682:U:H2'	2:I:1683:A:H8	1.85	0.41
2:I:1968:G:H2'	2:I:1969:U:H6	1.85	0.41
2:I:2479:A:H2'	2:I:2480:G:C8	2.55	0.41
2:I:2873:C:H5''	10:D:81:LEU:O	2.20	0.41
4:0:10:ARG:O	4:0:14:ARG:HG3	2.20	0.41
10:D:157:PRO:O	10:D:159:ARG:N	2.45	0.41
12:F:15:TYR:HB3	12:F:19:ILE:HG12	2.02	0.41
2:I:1040:A:N6	18:M:9:HIS:HB3	2.35	0.41
2:I:1101:G:H3'	2:I:1102:A:H2'	2.02	0.41
2:I:2046:A:H2'	2:I:2047:C:C6	2.55	0.41
2:I:2505:A:H5''	2:I:2506:A:H5'	2.02	0.41
2:I:2551:C:H1'	12:F:44:ASN:OD1	2.20	0.41
2:I:3028:A:N7	2:I:3029:C:H3'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:123:ASP:OD1	11:E:124:ARG:NH1	2.53	0.41
12:F:159:MET:HE2	12:F:159:MET:HB2	1.95	0.41
12:F:166:SER:O	12:F:166:SER:OG	2.34	0.41
15:J:36:LEU:O	15:J:51:GLY:HA3	2.20	0.41
16:K:71:ARG:HH12	16:K:122:LEU:HD21	1.85	0.41
2:I:549:A:H2'	2:I:550:C:O4'	2.20	0.41
2:I:842:G:C6	2:I:843:U:C2	3.08	0.41
2:I:1176:G:C4	2:I:1239:A:N6	2.88	0.41
2:I:1220:G:H2'	2:I:1221:C:C6	2.56	0.41
2:I:1386:U:H5''	2:I:1387:G:C5'	2.50	0.41
2:I:1558:A:N7	2:I:1647:U:O4	2.53	0.41
2:I:2163:C:H42	2:I:2167:G:H22	1.68	0.41
2:I:2633:C:OP1	17:L:62:LYS:NZ	2.54	0.41
10:D:36:VAL:HA	10:D:99:GLN:O	2.20	0.41
20:O:68:VAL:HG11	20:O:75:ARG:HG3	2.01	0.41
21:P:2:ASN:OD1	21:P:3:ARG:N	2.41	0.41
24:S:68:ALA:HB1	24:S:74:LEU:HD12	2.01	0.41
2:I:306:G:H2'	2:I:307:U:O4'	2.21	0.41
2:I:331:U:O2'	2:I:332:C:H6	2.04	0.41
2:I:369:C:H2'	2:I:370:G:C8	2.55	0.41
2:I:802:C:H5''	11:E:88:PRO:HD2	2.03	0.41
2:I:1270:U:O2	2:I:1272:A:N6	2.54	0.41
2:I:1749:U:H2'	2:I:1750:C:C6	2.55	0.41
2:I:1766:U:O2'	2:I:1767:A:H8	2.04	0.41
2:I:2364:G:O6	2:I:2398:C:H1'	2.21	0.41
2:I:2810:A:N7	10:D:155:ALA:HB2	2.35	0.41
2:I:3035:U:H3'	2:I:3036:G:C8	2.46	0.41
9:C:72:LYS:HZ3	9:C:190:ARG:NE	2.13	0.41
10:D:126:THR:HB	10:D:132:PHE:CD2	2.56	0.41
10:D:188:GLU:OE1	10:D:188:GLU:N	2.52	0.41
21:P:48:ARG:HD2	21:P:50:GLN:HG3	2.02	0.41
2:I:52:A:H2'	2:I:53:A:H8	1.84	0.41
2:I:492:U:H4'	2:I:493:C:H5'	2.02	0.41
2:I:653:U:H3'	2:I:654:G:H8	1.86	0.41
2:I:746:G:N2	2:I:749:U:C5	2.88	0.41
2:I:1394:U:C4	2:I:1395:G:C6	3.09	0.41
2:I:2341:C:H2'	2:I:2342:G:N7	2.36	0.41
2:I:3044:A:H2'	2:I:3045:A:H8	1.82	0.41
10:D:31:ALA:HB3	10:D:103:ALA:HB2	2.02	0.41
13:G:17:VAL:HG22	13:G:26:VAL:HG13	2.02	0.41
18:M:44:ASN:HB3	18:M:45:ARG:HH21	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:P:42:PHE:CE2	21:P:71:ARG:HG3	2.55	0.41
2:I:184:A:H2'	2:I:185:C:H6	1.86	0.41
2:I:224:A:C2	2:I:235:A:H5''	2.55	0.41
2:I:632:C:H2'	2:I:633:U:O4'	2.20	0.41
2:I:965:G:H2'	2:I:966:C:C6	2.55	0.41
2:I:1332:C:H2'	2:I:1333:C:H6	1.85	0.41
2:I:1525:U:H2'	2:I:1526:A:O4'	2.20	0.41
2:I:2085:U:H2'	2:I:2086:U:O4'	2.21	0.41
2:I:2509:G:OP1	27:W:18:ALA:HB1	2.21	0.41
15:J:92:LEU:O	15:J:96:HIS:N	2.44	0.41
17:L:21:VAL:HG23	17:L:28:LYS:HG3	2.03	0.41
20:O:113:ASP:HA	20:O:116:ARG:HG2	2.02	0.41
32:U:39:ASN:HB3	32:U:64:ALA:HB3	2.01	0.41
2:I:221:A:N3	2:I:236:U:O2'	2.46	0.41
2:I:251:C:O2	6:3:12:LYS:NZ	2.47	0.41
2:I:354:G:H2'	2:I:355:C:O4'	2.21	0.41
2:I:450:U:H2'	2:I:451:C:C6	2.56	0.41
2:I:471:G:N2	2:I:481:U:H3	2.17	0.41
2:I:610:G:H2'	2:I:611:C:C6	2.56	0.41
2:I:626:A:H2'	2:I:627:G:O4'	2.21	0.41
2:I:979:A:H2'	2:I:980:C:O4'	2.21	0.41
2:I:996:A:H2'	2:I:997:C:C6	2.56	0.41
2:I:1155:G:OP2	2:I:1263:G:O2'	2.29	0.41
2:I:1196:A:H3'	2:I:1197:G:C8	2.56	0.41
2:I:1196:A:H5''	2:I:1197:G:N7	2.35	0.41
2:I:1574:C:C2	2:I:1575:A:N7	2.89	0.41
2:I:1576:C:H2'	2:I:1577:C:C6	2.56	0.41
2:I:2542:G:N2	2:I:2550:U:H3	2.10	0.41
2:I:2604:A:H2'	2:I:2605:G:O4'	2.21	0.41
2:I:3119:C:H6	2:I:3119:C:O5'	2.04	0.41
4:O:30:VAL:HG12	4:O:44:LEU:HD12	2.03	0.41
9:C:108:PRO:CD	9:C:111:LEU:HD12	2.49	0.41
10:D:37:THR:HG22	10:D:38:ARG:N	2.36	0.41
13:G:26:VAL:HG12	13:G:80:VAL:HG11	2.01	0.41
15:J:27:ARG:HG2	15:J:142:LEU:HD23	2.03	0.41
32:U:39:ASN:ND2	32:U:66:ILE:HG22	2.35	0.41
32:U:79:LYS:HA	32:U:80:PRO:HD3	1.98	0.41
2:I:94:C:H2'	2:I:95:G:O4'	2.21	0.41
2:I:803:G:H2'	2:I:933:A:H61	1.86	0.41
2:I:1731:A:OP2	2:I:1731:A:H8	2.04	0.41
2:I:1866:G:H1'	2:I:1870:A:N6	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1866:G:H1'	2:I:1870:A:H61	1.86	0.41
2:I:1912:A:H2'	2:I:1913:A:C8	2.56	0.41
2:I:2207:A:O2'	2:I:2210:G:N3	2.41	0.41
2:I:2225:C:H2'	2:I:2226:A:C8	2.56	0.41
2:I:2681:C:OP1	11:E:75:LYS:HD3	2.21	0.41
22:Q:69:ALA:HB1	22:Q:74:ILE:HG23	2.03	0.41
25:T:64:GLY:O	25:T:75:LYS:HE2	2.21	0.41
26:V:41:GLU:HG3	26:V:43:GLN:OE1	2.21	0.41
2:I:1386:U:H3'	2:I:1387:G:H5''	2.02	0.40
2:I:2905:C:H1'	13:G:110:TYR:HD1	1.86	0.40
21:P:71:ARG:HD3	21:P:73:PHE:CZ	2.56	0.40
2:I:84:A:C2	2:I:103:A:C5	3.09	0.40
2:I:267:A:N1	2:I:516:U:O2'	2.53	0.40
2:I:616:A:H2'	2:I:2280:A:N1	2.36	0.40
2:I:1453:A:C5	3:1:38:LYS:HG2	2.56	0.40
2:I:1662:G:H2'	2:I:1663:U:O4'	2.21	0.40
2:I:2225:C:H2'	2:I:2226:A:H8	1.86	0.40
10:D:151:ILE:HD12	10:D:166:MET:HE2	2.04	0.40
23:R:40:VAL:HG23	23:R:56:LEU:HD22	2.03	0.40
26:V:176:VAL:HG12	26:V:177:VAL:HG23	2.03	0.40
2:I:943:C:H1'	2:I:1356:G:N2	2.36	0.40
2:I:963:C:C2	2:I:964:A:C8	3.09	0.40
2:I:1232:A:H8	2:I:1232:A:OP2	2.04	0.40
2:I:1330:U:H2'	2:I:1331:C:C6	2.57	0.40
2:I:1332:C:H2'	2:I:1333:C:C6	2.57	0.40
2:I:1509:A:O2'	2:I:1511:G:N7	2.50	0.40
2:I:1658:A:N6	2:I:1815:U:H3	2.16	0.40
2:I:2585:C:OP1	30:b:38:LYS:NZ	2.52	0.40
2:I:2969:G:H2'	2:I:2970:G:C8	2.56	0.40
11:E:171:GLY:O	11:E:175:VAL:HG22	2.22	0.40
13:G:95:TYR:CE1	13:G:108:LEU:HB2	2.56	0.40
16:K:106:LEU:HB2	16:K:115:ILE:HD11	2.03	0.40
2:I:233:U:H2'	2:I:234:G:O4'	2.22	0.40
2:I:454:U:H2'	2:I:455:U:H6	1.87	0.40
2:I:881:A:N6	3:1:54:ARG:HD3	2.37	0.40
2:I:1728:G:O4'	9:C:99:ASP:HB3	2.22	0.40
2:I:2318:C:H2'	2:I:2319:A:H8	1.86	0.40
2:I:2574:A:H61	27:W:43:THR:CG2	2.20	0.40
27:W:23:VAL:HG22	27:W:38:VAL:HG22	2.02	0.40
29:Z:23:LEU:HD23	29:Z:23:LEU:HA	1.73	0.40
1:7:17:ASN:HB3	1:7:20:LYS:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:36:G:N3	2:I:539:G:O2'	2.54	0.40
2:I:430:A:H2'	2:I:431:A:H8	1.87	0.40
2:I:480:A:H1'	2:I:500:G:O4'	2.22	0.40
2:I:554:G:H2'	2:I:555:A:C8	2.56	0.40
2:I:786:U:H2'	2:I:787:G:C8	2.57	0.40
2:I:1039:A:N3	2:I:2502:C:O2'	2.51	0.40
2:I:1807:A:H2'	2:I:1808:A:C8	2.55	0.40
2:I:1903:A:H4'	2:I:1904:A:O5'	2.22	0.40
2:I:1942:A:H2'	2:I:1943:C:H6	1.86	0.40
2:I:2333:G:H2'	2:I:2334:U:C6	2.57	0.40
10:D:11:LEU:HD11	10:D:30:LYS:HB2	2.04	0.40
12:F:90:MET:HB2	12:F:91:PRO:HD2	2.03	0.40
15:J:5:ALA:HB1	15:J:43:THR:O	2.22	0.40
18:M:108:TYR:HB3	18:M:114:ALA:HB2	2.03	0.40
23:R:31:GLU:O	23:R:34:GLU:HG3	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	7	20/24 (83%)	19 (95%)	1 (5%)	0	100	100
3	1	49/62 (79%)	47 (96%)	2 (4%)	0	100	100
4	0	51/57 (90%)	45 (88%)	6 (12%)	0	100	100
5	2	40/47 (85%)	38 (95%)	2 (5%)	0	100	100
6	3	60/64 (94%)	53 (88%)	7 (12%)	0	100	100
7	4	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
9	C	270/280 (96%)	258 (96%)	12 (4%)	0	100	100
10	D	211/217 (97%)	194 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	E	205/223 (92%)	193 (94%)	12 (6%)	0	100	100
12	F	168/187 (90%)	153 (91%)	15 (9%)	0	100	100
13	G	172/179 (96%)	155 (90%)	17 (10%)	0	100	100
14	H	45/152 (30%)	43 (96%)	2 (4%)	0	100	100
15	J	144/195 (74%)	139 (96%)	5 (4%)	0	100	100
16	K	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
17	L	140/146 (96%)	134 (96%)	6 (4%)	0	100	100
18	M	132/138 (96%)	125 (95%)	7 (5%)	0	100	100
19	N	114/180 (63%)	110 (96%)	4 (4%)	0	100	100
20	O	114/122 (93%)	103 (90%)	11 (10%)	0	100	100
21	P	110/113 (97%)	105 (96%)	5 (4%)	0	100	100
22	Q	120/129 (93%)	116 (97%)	4 (3%)	0	100	100
23	R	96/104 (92%)	93 (97%)	3 (3%)	0	100	100
24	S	111/197 (56%)	109 (98%)	2 (2%)	0	100	100
25	T	93/100 (93%)	92 (99%)	1 (1%)	0	100	100
26	V	175/215 (81%)	148 (85%)	27 (15%)	0	100	100
27	W	72/86 (84%)	63 (88%)	9 (12%)	0	100	100
28	Y	63/77 (82%)	60 (95%)	3 (5%)	0	100	100
29	Z	57/65 (88%)	50 (88%)	7 (12%)	0	100	100
30	b	47/54 (87%)	46 (98%)	1 (2%)	0	100	100
31	y	76/78 (97%)	73 (96%)	2 (3%)	1 (1%)	9	14
32	U	86/105 (82%)	81 (94%)	5 (6%)	0	100	100
All	All	3195/3755 (85%)	2996 (94%)	198 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	y	18	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	7	18/20 (90%)	18 (100%)	0	100	100
3	1	40/50 (80%)	39 (98%)	1 (2%)	42	64
4	0	43/47 (92%)	43 (100%)	0	100	100
5	2	36/40 (90%)	36 (100%)	0	100	100
6	3	53/54 (98%)	53 (100%)	0	100	100
7	4	35/35 (100%)	35 (100%)	0	100	100
9	C	212/219 (97%)	212 (100%)	0	100	100
10	D	163/166 (98%)	163 (100%)	0	100	100
11	E	159/172 (92%)	159 (100%)	0	100	100
12	F	139/155 (90%)	139 (100%)	0	100	100
13	G	143/147 (97%)	143 (100%)	0	100	100
14	H	36/121 (30%)	36 (100%)	0	100	100
15	J	120/161 (74%)	119 (99%)	1 (1%)	73	86
16	K	100/101 (99%)	100 (100%)	0	100	100
17	L	106/110 (96%)	106 (100%)	0	100	100
18	M	110/114 (96%)	110 (100%)	0	100	100
19	N	94/139 (68%)	94 (100%)	0	100	100
20	O	88/93 (95%)	88 (100%)	0	100	100
21	P	98/99 (99%)	96 (98%)	2 (2%)	48	70
22	Q	95/99 (96%)	95 (100%)	0	100	100
23	R	79/83 (95%)	79 (100%)	0	100	100
24	S	87/140 (62%)	87 (100%)	0	100	100
25	T	81/83 (98%)	81 (100%)	0	100	100
26	V	142/164 (87%)	142 (100%)	0	100	100
27	W	54/62 (87%)	53 (98%)	1 (2%)	50	71
28	Y	58/66 (88%)	57 (98%)	1 (2%)	53	74
29	Z	51/55 (93%)	51 (100%)	0	100	100
30	b	46/50 (92%)	46 (100%)	0	100	100
31	y	68/68 (100%)	68 (100%)	0	100	100
32	U	77/88 (88%)	69 (90%)	8 (10%)	7	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2631/3001 (88%)	2617 (100%)	14 (0%)	78 91

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1	51	VAL
15	J	133	SER
21	P	60	VAL
21	P	75	VAL
27	W	56	ASP
28	Y	28	GLU
32	U	3	VAL
32	U	13	SER
32	U	34	LEU
32	U	72	MET
32	U	91	THR
32	U	100	ARG
32	U	103	LYS
32	U	104	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	7	18	HIS
9	C	70	ASN
9	C	122	ASN
9	C	227	ASN
10	D	69	GLN
11	E	82	GLN
11	E	106	GLN
15	J	70	GLN
16	K	3	GLN
16	K	51	ASN
18	M	17	GLN
18	M	28	ASN
19	N	31	HIS
20	O	118	ASN
25	T	27	ASN
25	T	41	GLN
25	T	63	GLN
31	y	4	HIS

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Mol	Chain	Res	Type
31	y	22	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	I	3116/3138 (99%)	566 (18%)	19 (0%)
8	B	114/115 (99%)	12 (10%)	0
All	All	3230/3253 (99%)	578 (17%)	19 (0%)

All (578) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	I	10	U
2	I	12	U
2	I	14	A
2	I	27	G
2	I	34	U
2	I	35	G
2	I	45	G
2	I	50	U
2	I	58	G
2	I	60	G
2	I	71	A
2	I	74	U
2	I	75	G
2	I	91	A
2	I	92	A
2	I	93	C
2	I	102	G
2	I	118	A
2	I	119	A
2	I	120	U
2	I	121	G
2	I	131	A
2	I	142	U
2	I	151	A
2	I	156	C
2	I	165	A
2	I	167	A
2	I	176	G
2	I	183	A

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Mol	Chain	Res	Type
2	I	198	A
2	I	201	A
2	I	217	G
2	I	218	A
2	I	224	A
2	I	230	U
2	I	231	U
2	I	232	G
2	I	250	G
2	I	267	A
2	I	271	U
2	I	282	C
2	I	283	A
2	I	284	U
2	I	285	G
2	I	286	G
2	I	287	G
2	I	288	U
2	I	289	A
2	I	290	A
2	I	293	G
2	I	295	G
2	I	298	G
2	I	299	G
2	I	300	G
2	I	301	G
2	I	302	U
2	I	303	U
2	I	304	G
2	I	305	U
2	I	308	G
2	I	323	A
2	I	329	U
2	I	331	U
2	I	332	C
2	I	334	C
2	I	339	C
2	I	353	G
2	I	359	C
2	I	364	A
2	I	365	G
2	I	367	G

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Mol	Chain	Res	Type
2	I	371	U
2	I	372	G
2	I	373	G
2	I	377	G
2	I	394	U
2	I	413	A
2	I	415	A
2	I	428	A
2	I	429	A
2	I	443	C
2	I	446	A
2	I	447	G
2	I	448	U
2	I	449	A
2	I	453	A
2	I	454	U
2	I	475	G
2	I	500	G
2	I	506	C
2	I	532	A
2	I	540	C
2	I	562	G
2	I	570	G
2	I	582	G
2	I	592	G
2	I	593	A
2	I	595	U
2	I	596	A
2	I	597	C
2	I	617	A
2	I	618	U
2	I	619	C
2	I	620	C
2	I	621	G
2	I	634	U
2	I	637	C
2	I	638	C
2	I	639	U
2	I	643	C
2	I	645	G
2	I	648	G
2	I	655	G

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Mol	Chain	Res	Type
2	I	665	G
2	I	674	A
2	I	675	G
2	I	677	A
2	I	695	G
2	I	703	G
2	I	705	A
2	I	706	A
2	I	707	G
2	I	717	U
2	I	718	G
2	I	719	U
2	I	741	A
2	I	742	G
2	I	749	U
2	I	750	A
2	I	756	A
2	I	757	C
2	I	758	C
2	I	762	A
2	I	763	C
2	I	767	C
2	I	770	A
2	I	771	C
2	I	772	G
2	I	776	G
2	I	779	U
2	I	780	G
2	I	781	A
2	I	783	U
2	I	798	G
2	I	815	U
2	I	841	G
2	I	844	A
2	I	845	A
2	I	856	A
2	I	857	G
2	I	859	C
2	I	869	C
2	I	876	U
2	I	904	G
2	I	905	G

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Mol	Chain	Res	Type
2	I	911	A
2	I	913	G
2	I	914	G
2	I	919	U
2	I	921	A
2	I	922	A
2	I	934	G
2	I	941	C
2	I	956	U
2	I	975	G
2	I	979	A
2	I	988	G
2	I	1001	A
2	I	1007	G
2	I	1009	U
2	I	1010	G
2	I	1025	A
2	I	1028	G
2	I	1029	A
2	I	1031	G
2	I	1034	A
2	I	1039	A
2	I	1043	C
2	I	1059	A
2	I	1060	A
2	I	1074	G
2	I	1086	U
2	I	1089	G
2	I	1096	A
2	I	1103	A
2	I	1112	A
2	I	1114	C
2	I	1118	G
2	I	1125	G
2	I	1138	A
2	I	1142	G
2	I	1150	A
2	I	1155	G
2	I	1162	U
2	I	1163	G
2	I	1174	A
2	I	1180	A

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Mol	Chain	Res	Type
2	I	1186	A
2	I	1187	G
2	I	1189	U
2	I	1191	G
2	I	1192	G
2	I	1193	C
2	I	1194	U
2	I	1196	A
2	I	1197	G
2	I	1198	A
2	I	1200	G
2	I	1201	C
2	I	1207	C
2	I	1209	C
2	I	1210	U
2	I	1211	U
2	I	1212	G
2	I	1213	A
2	I	1214	A
2	I	1216	G
2	I	1217	A
2	I	1219	U
2	I	1225	A
2	I	1227	A
2	I	1232	A
2	I	1234	U
2	I	1236	G
2	I	1239	A
2	I	1240	A
2	I	1241	G
2	I	1242	U
2	I	1247	G
2	I	1251	G
2	I	1257	A
2	I	1259	U
2	I	1261	U
2	I	1262	A
2	I	1264	C
2	I	1271	C
2	I	1272	A
2	I	1300	C
2	I	1301	A

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Mol	Chain	Res	Type
2	I	1302	C
2	I	1306	G
2	I	1308	G
2	I	1378	A
2	I	1380	U
2	I	1386	U
2	I	1387	G
2	I	1402	G
2	I	1403	A
2	I	1404	C
2	I	1406	A
2	I	1432	A
2	I	1437	C
2	I	1453	A
2	I	1456	C
2	I	1475	U
2	I	1477	G
2	I	1480	A
2	I	1496	A
2	I	1497	C
2	I	1499	G
2	I	1510	U
2	I	1513	A
2	I	1515	A
2	I	1526	A
2	I	1527	U
2	I	1553	U
2	I	1556	C
2	I	1558	A
2	I	1560	U
2	I	1568	A
2	I	1571	A
2	I	1574	C
2	I	1575	A
2	I	1579	A
2	I	1582	A
2	I	1585	G
2	I	1589	C
2	I	1591	A
2	I	1592	U
2	I	1596	U
2	I	1597	C

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Mol	Chain	Res	Type
2	I	1598	C
2	I	1599	C
2	I	1601	U
2	I	1606	G
2	I	1613	G
2	I	1617	U
2	I	1622	G
2	I	1623	G
2	I	1624	C
2	I	1627	C
2	I	1628	G
2	I	1646	G
2	I	1651	C
2	I	1653	A
2	I	1657	A
2	I	1666	C
2	I	1681	G
2	I	1687	G
2	I	1690	A
2	I	1691	G
2	I	1692	U
2	I	1693	G
2	I	1696	A
2	I	1698	C
2	I	1699	A
2	I	1705	G
2	I	1712	G
2	I	1720	G
2	I	1721	A
2	I	1727	A
2	I	1731	A
2	I	1734	U
2	I	1741	C
2	I	1744	A
2	I	1748	A
2	I	1767	A
2	I	1773	U
2	I	1796	U
2	I	1803	A
2	I	1806	A
2	I	1807	A
2	I	1815	U

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Mol	Chain	Res	Type
2	I	1820	A
2	I	1833	C
2	I	1842	C
2	I	1843	A
2	I	1845	A
2	I	1881	U
2	I	1883	C
2	I	1884	G
2	I	1888	U
2	I	1892	U
2	I	1909	G
2	I	1948	A
2	I	1950	A
2	I	1951	U
2	I	1952	C
2	I	1958	C
2	I	1961	C
2	I	1962	C
2	I	1963	U
2	I	1964	U
2	I	1965	G
2	I	1966	C
2	I	1992	A
2	I	1993	A
2	I	1998	U
2	I	2007	A
2	I	2010	G
2	I	2020	A
2	I	2034	C
2	I	2035	G
2	I	2043	A
2	I	2050	U
2	I	2051	G
2	I	2082	A
2	I	2105	G
2	I	2106	C
2	I	2107	A
2	I	2108	A
2	I	2109	G
2	I	2110	G
2	I	2147	G
2	I	2149	U

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Mol	Chain	Res	Type
2	I	2150	A
2	I	2152	C
2	I	2153	U
2	I	2155	U
2	I	2156	A
2	I	2158	C
2	I	2159	C
2	I	2160	A
2	I	2161	U
2	I	2162	C
2	I	2167	G
2	I	2168	G
2	I	2175	A
2	I	2176	A
2	I	2179	C
2	I	2180	C
2	I	2193	U
2	I	2201	U
2	I	2202	G
2	I	2203	C
2	I	2205	C
2	I	2208	A
2	I	2209	U
2	I	2210	G
2	I	2229	U
2	I	2231	U
2	I	2258	A
2	I	2261	A
2	I	2269	A
2	I	2270	G
2	I	2274	C
2	I	2281	C
2	I	2293	C
2	I	2294	G
2	I	2296	A
2	I	2298	A
2	I	2299	G
2	I	2300	A
2	I	2313	C
2	I	2314	A
2	I	2337	G
2	I	2338	G

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Mol	Chain	Res	Type
2	I	2339	U
2	I	2341	C
2	I	2342	G
2	I	2344	U
2	I	2348	U
2	I	2349	G
2	I	2352	G
2	I	2353	G
2	I	2355	U
2	I	2356	A
2	I	2357	G
2	I	2358	G
2	I	2359	U
2	I	2360	G
2	I	2361	G
2	I	2362	G
2	I	2363	A
2	I	2364	G
2	I	2365	A
2	I	2366	C
2	I	2367	U
2	I	2368	G
2	I	2369	U
2	I	2370	G
2	I	2371	A
2	I	2372	A
2	I	2376	U
2	I	2377	C
2	I	2380	C
2	I	2382	C
2	I	2383	C
2	I	2384	A
2	I	2386	U
2	I	2388	G
2	I	2390	G
2	I	2391	G
2	I	2392	C
2	I	2393	G
2	I	2394	G
2	I	2395	A
2	I	2396	G
2	I	2397	U

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Mol	Chain	Res	Type
2	I	2398	C
2	I	2400	U
2	I	2401	U
2	I	2403	U
2	I	2410	A
2	I	2412	C
2	I	2413	A
2	I	2414	C
2	I	2416	C
2	I	2417	U
2	I	2419	A
2	I	2428	G
2	I	2435	A
2	I	2440	C
2	I	2441	G
2	I	2447	U
2	I	2448	G
2	I	2449	A
2	I	2450	A
2	I	2460	G
2	I	2463	A
2	I	2476	G
2	I	2488	G
2	I	2506	A
2	I	2517	G
2	I	2521	C
2	I	2525	A
2	I	2543	A
2	I	2546	G
2	I	2548	A
2	I	2557	G
2	I	2560	A
2	I	2563	G
2	I	2573	A
2	I	2585	C
2	I	2588	C
2	I	2599	A
2	I	2621	G
2	I	2623	A
2	I	2640	C
2	I	2641	C
2	I	2644	A

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Mol	Chain	Res	Type
2	I	2648	G
2	I	2660	C
2	I	2661	U
2	I	2663	A
2	I	2667	G
2	I	2668	A
2	I	2669	U
2	I	2673	A
2	I	2679	C
2	I	2685	G
2	I	2686	A
2	I	2697	A
2	I	2702	C
2	I	2713	C
2	I	2714	A
2	I	2725	A
2	I	2729	U
2	I	2730	U
2	I	2740	G
2	I	2743	G
2	I	2751	G
2	I	2756	A
2	I	2758	C
2	I	2767	G
2	I	2781	G
2	I	2794	C
2	I	2795	G
2	I	2802	A
2	I	2804	A
2	I	2805	G
2	I	2811	C
2	I	2820	G
2	I	2823	U
2	I	2824	U
2	I	2840	A
2	I	2844	C
2	I	2847	U
2	I	2848	C
2	I	2851	U
2	I	2853	U
2	I	2868	A
2	I	2883	C

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Mol	Chain	Res	Type
2	I	2901	G
2	I	2952	G
2	I	2962	C
2	I	2964	C
2	I	2971	U
2	I	2986	A
2	I	2990	C
2	I	2995	A
2	I	2999	G
2	I	3016	A
2	I	3018	C
2	I	3023	U
2	I	3028	A
2	I	3029	C
2	I	3030	C
2	I	3034	U
2	I	3035	U
2	I	3039	G
2	I	3043	U
2	I	3047	G
2	I	3057	G
2	I	3058	A
2	I	3069	A
2	I	3107	A
2	I	3108	A
2	I	3115	C
2	I	3119	C
2	I	3120	C
2	I	3121	G
2	I	3125	G
2	I	3126	A
2	I	3128	A
2	I	3129	A
8	B	8	G
8	B	16	C
8	B	34	U
8	B	41	C
8	B	51	A
8	B	52	A
8	B	65	A
8	B	66	G
8	B	85	U

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Mol	Chain	Res	Type
8	B	101	G
8	B	105	A
8	B	115	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	I	91	A
2	I	164	U
2	I	175	C
2	I	855	G
2	I	893	A
2	I	904	G
2	I	913	G
2	I	974	G
2	I	1384	A
2	I	1526	A
2	I	1567	U
2	I	1605	G
2	I	1623	G
2	I	1627	C
2	I	1689	C
2	I	2179	C
2	I	2338	G
2	I	2739	C
2	I	2994	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](#)

There are no ligands in this entry.

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.

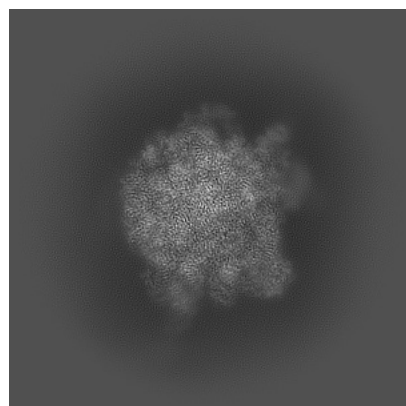
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47419. These allow visual inspection of the internal detail of the map and identification of artifacts.

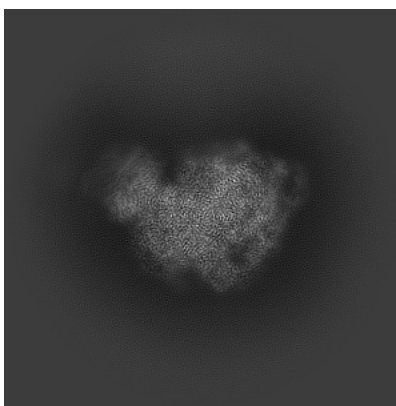
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

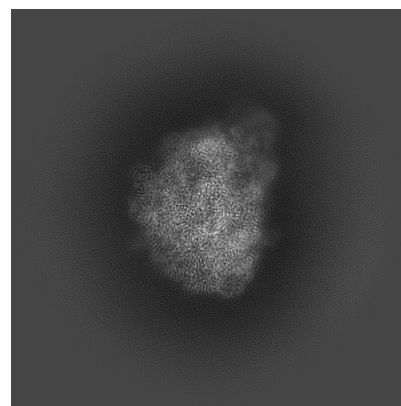
6.1.1 Primary map



X

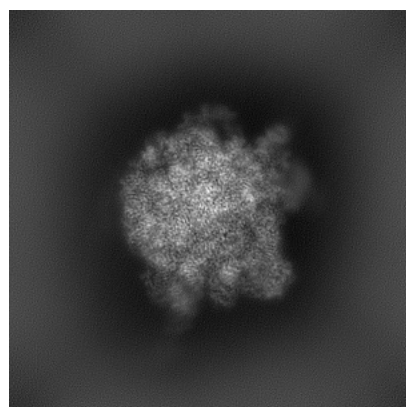


Y

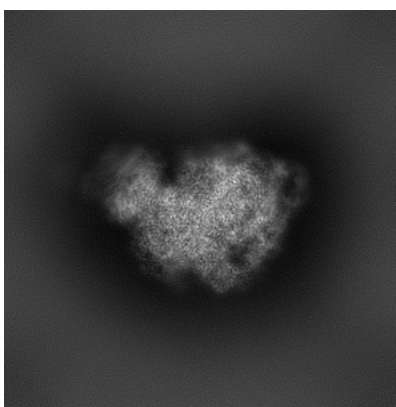


Z

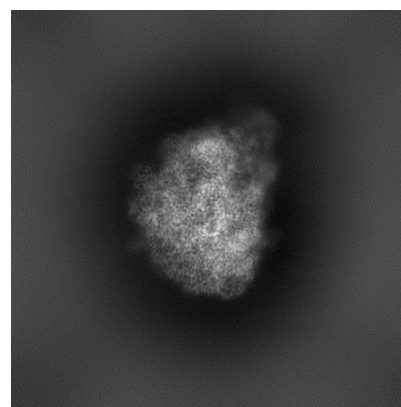
6.1.2 Raw map



X



Y

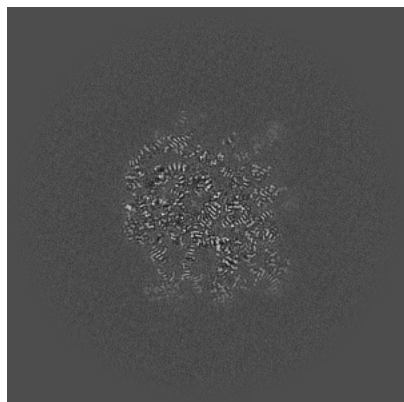


Z

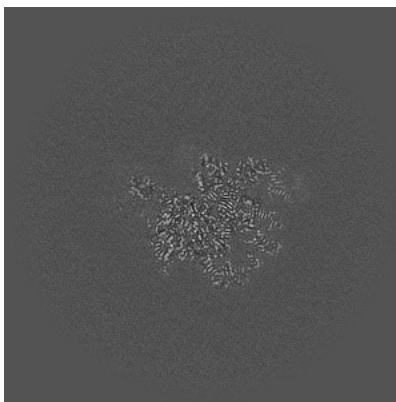
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

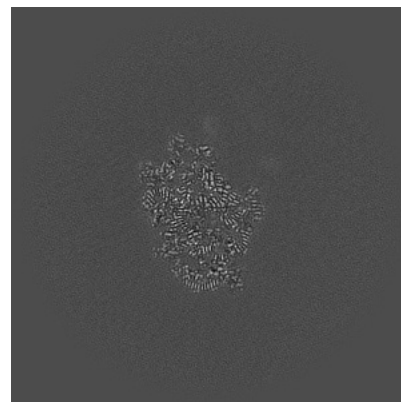
6.2.1 Primary map



X Index: 200

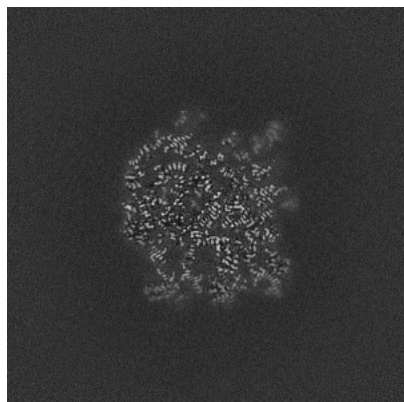


Y Index: 200

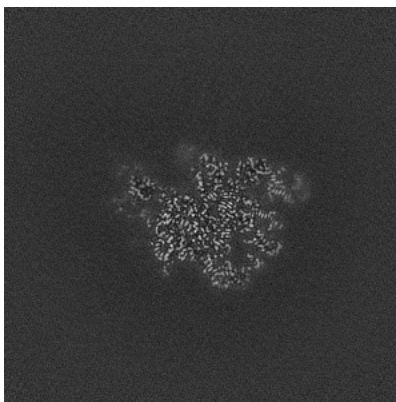


Z Index: 200

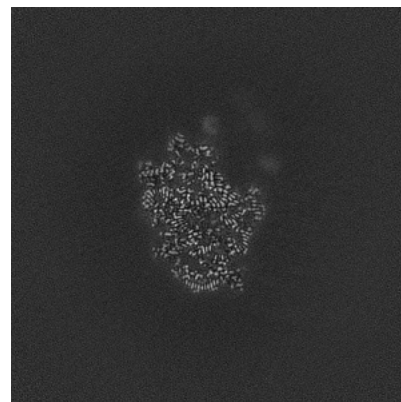
6.2.2 Raw map



X Index: 200



Y Index: 200

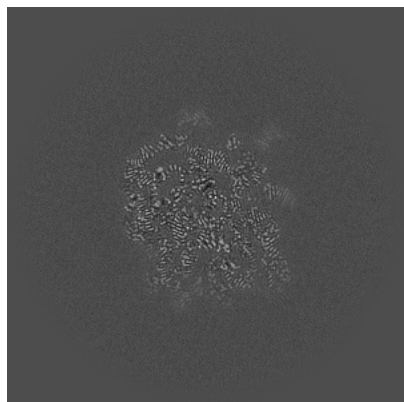


Z Index: 200

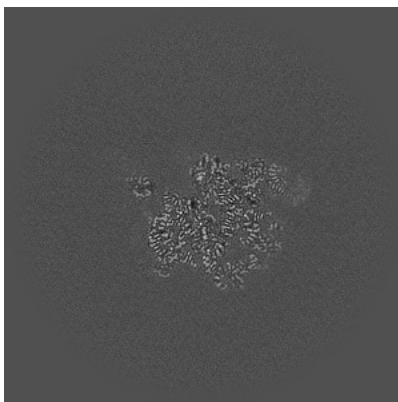
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

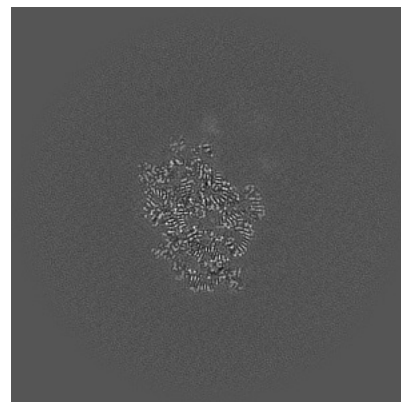
6.3.1 Primary map



X Index: 205

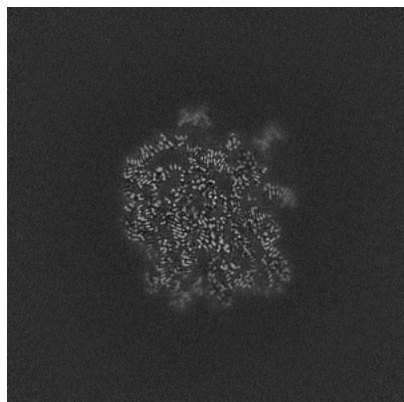


Y Index: 196

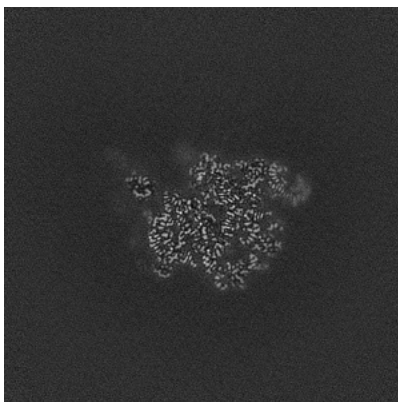


Z Index: 202

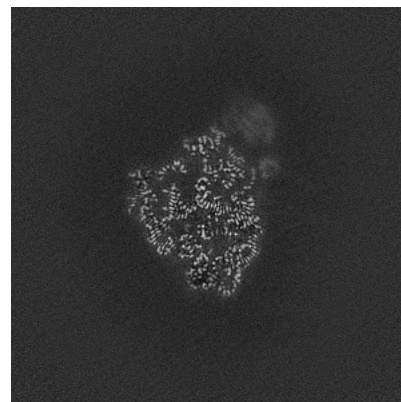
6.3.2 Raw map



X Index: 205



Y Index: 196

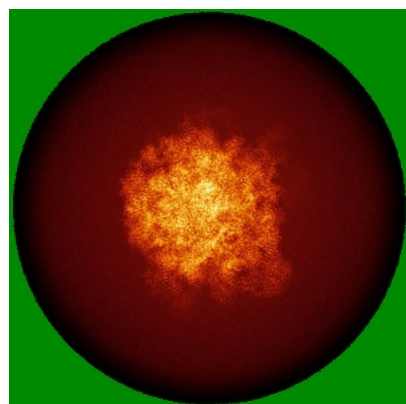


Z Index: 219

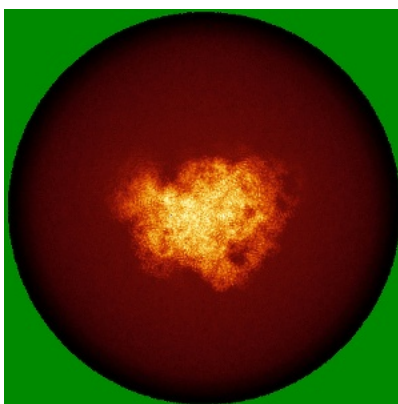
The images above show the largest variance slices of the map in three orthogonal directions.

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

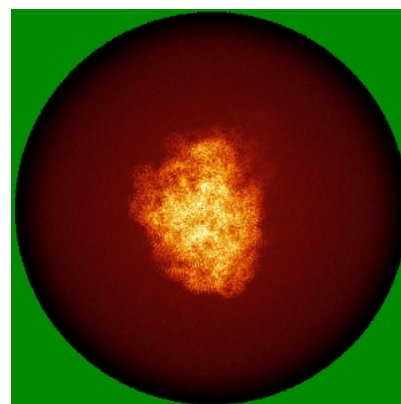
6.4.1 Primary map



X

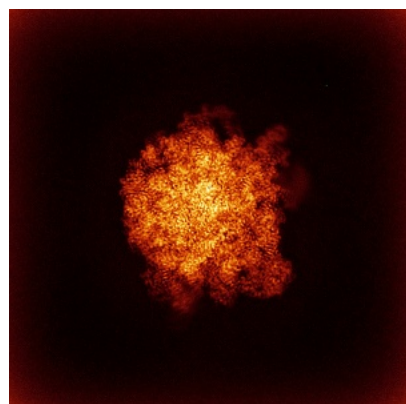


Y

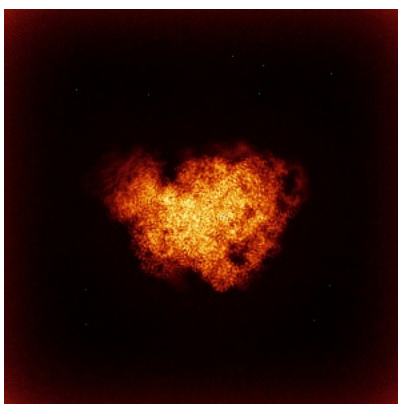


Z

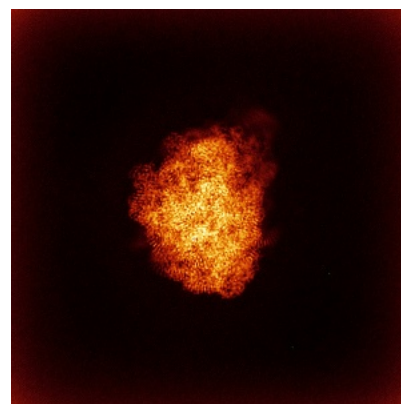
6.4.2 Raw map



X



Y

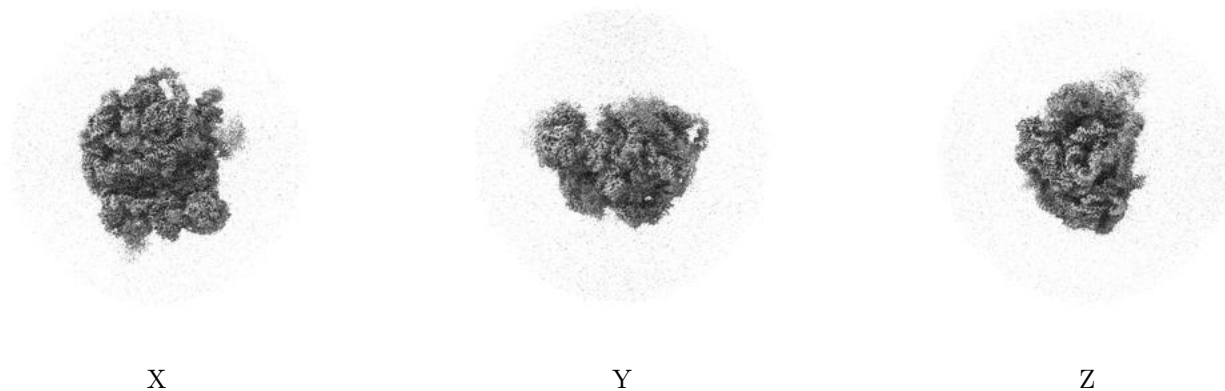


Z

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

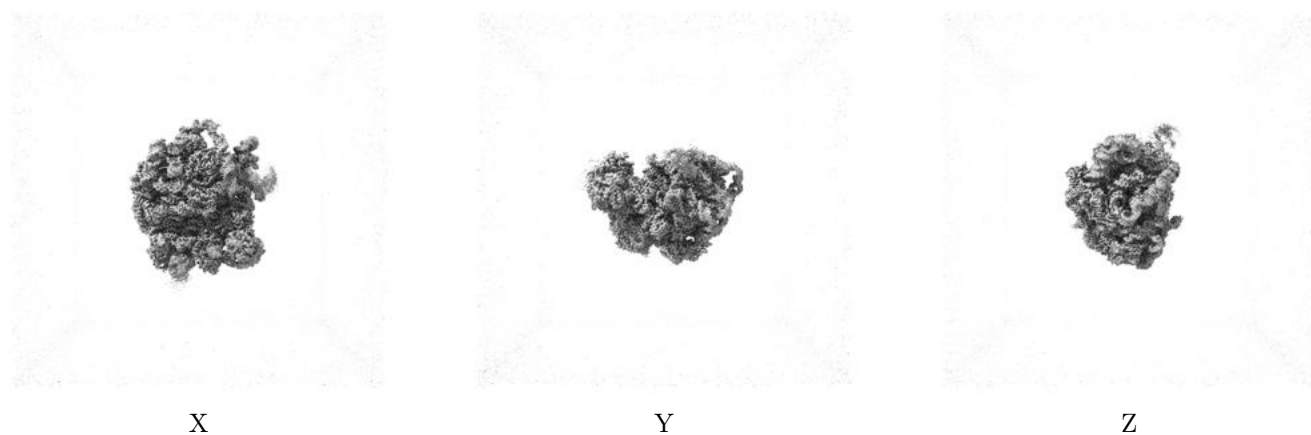
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.377. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

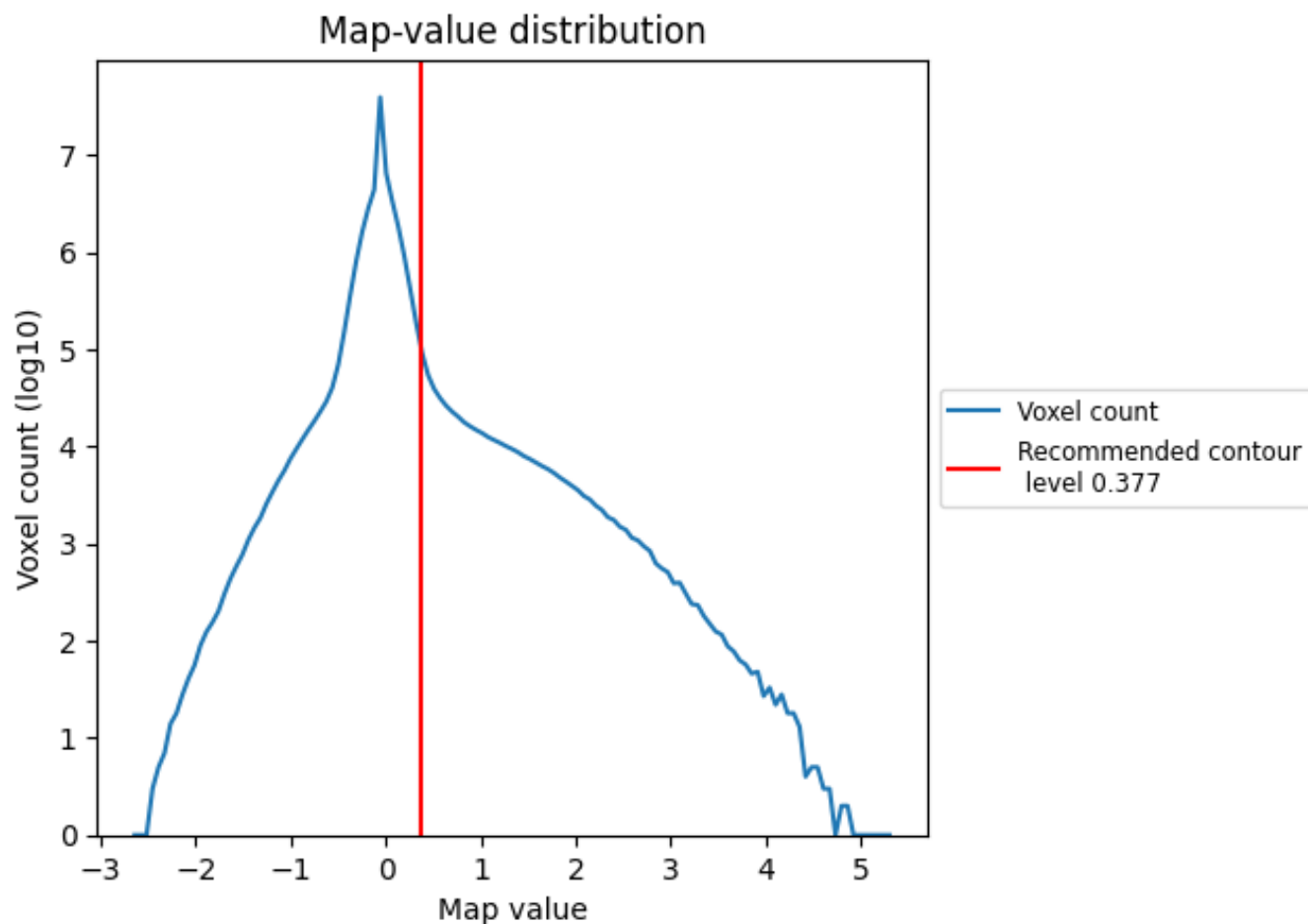
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

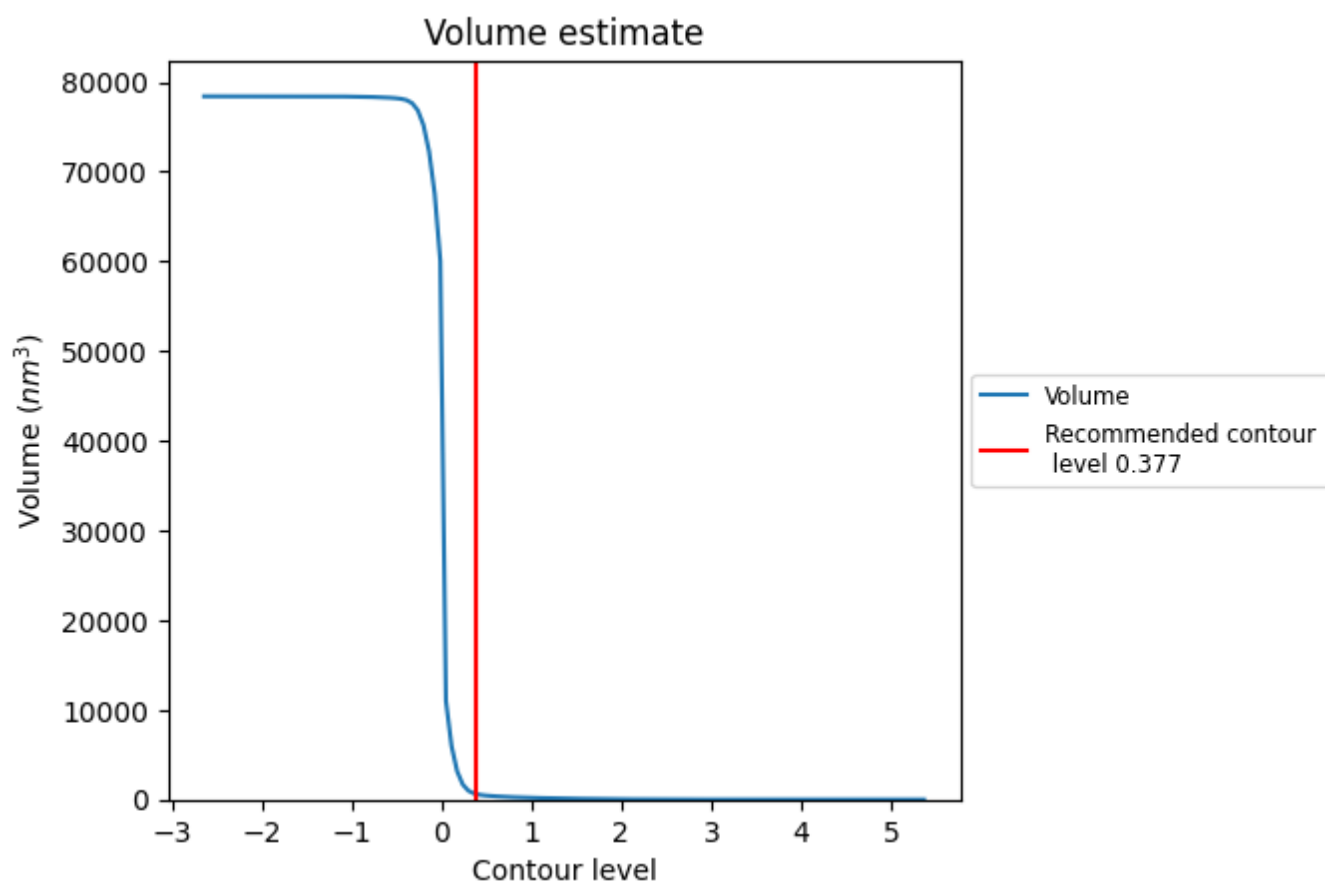
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

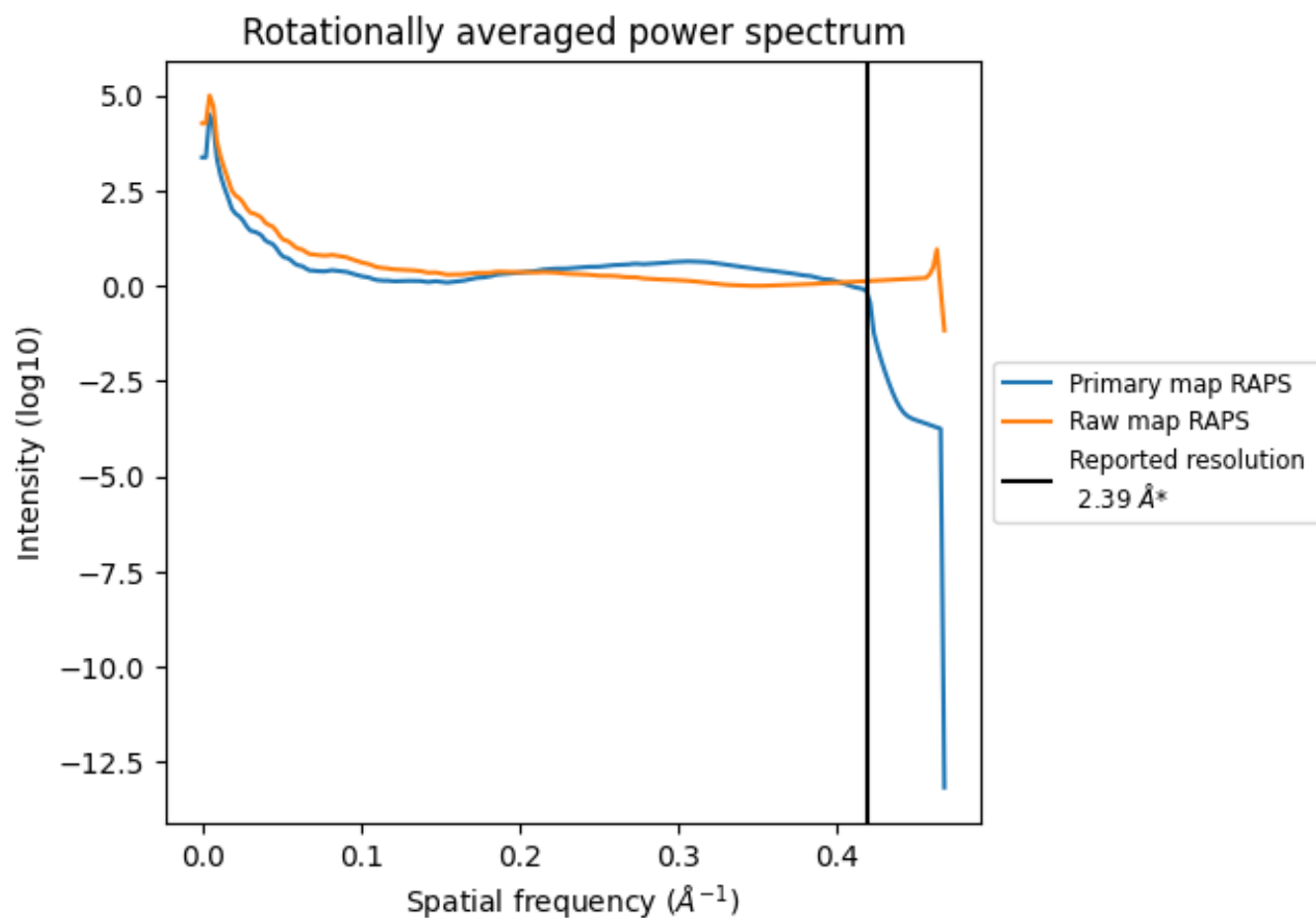
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 635 nm^3 ; this corresponds to an approximate mass of 573 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 ⓘ

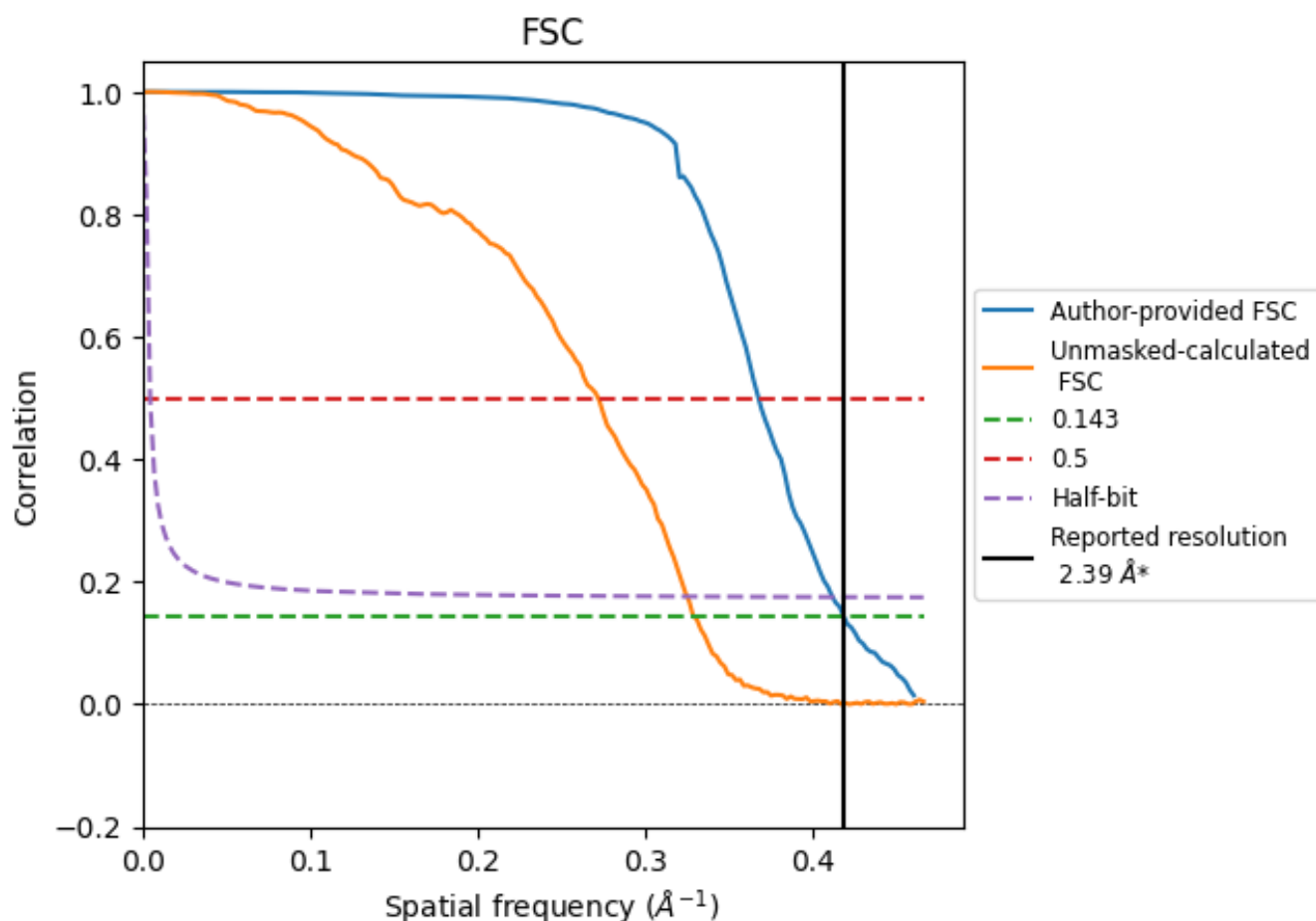


*Reported resolution corresponds to spatial frequency of $0.418 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.418 Å⁻¹

8.2 Resolution estimates [i](#)

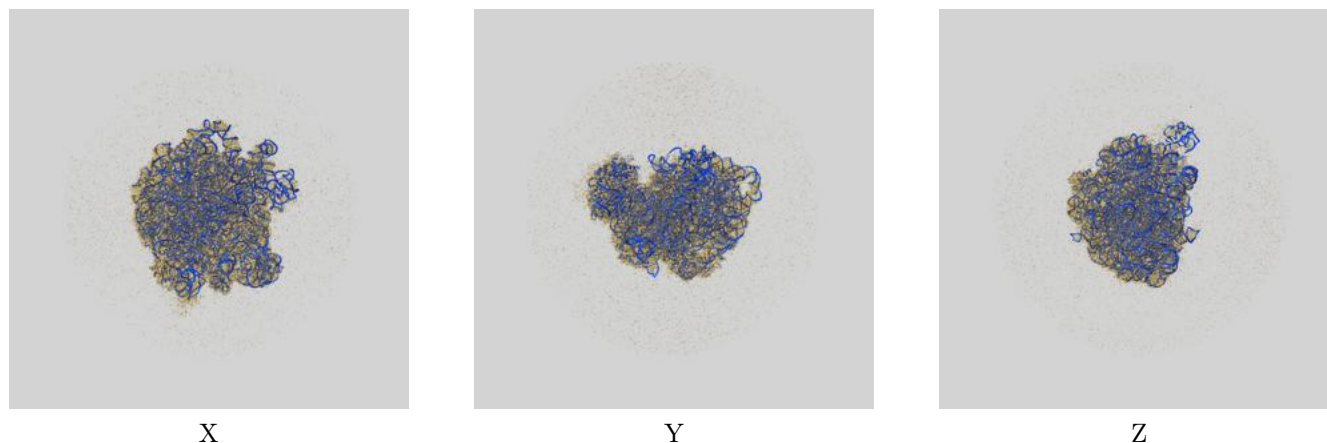
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.39	-	-
Author-provided FSC curve	2.39	2.72	2.43
Unmasked-calculated*	3.04	3.68	3.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.04 differs from the reported value 2.39 by more than 10 %

9 Map-model fit [i](#)

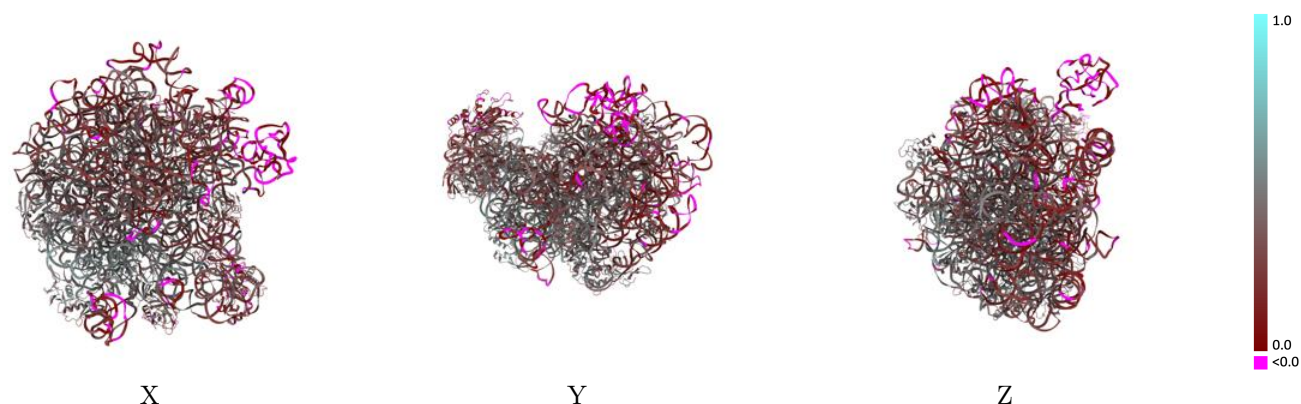
This section contains information regarding the fit between EMDB map EMD-47419 and PDB model 9E1S. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



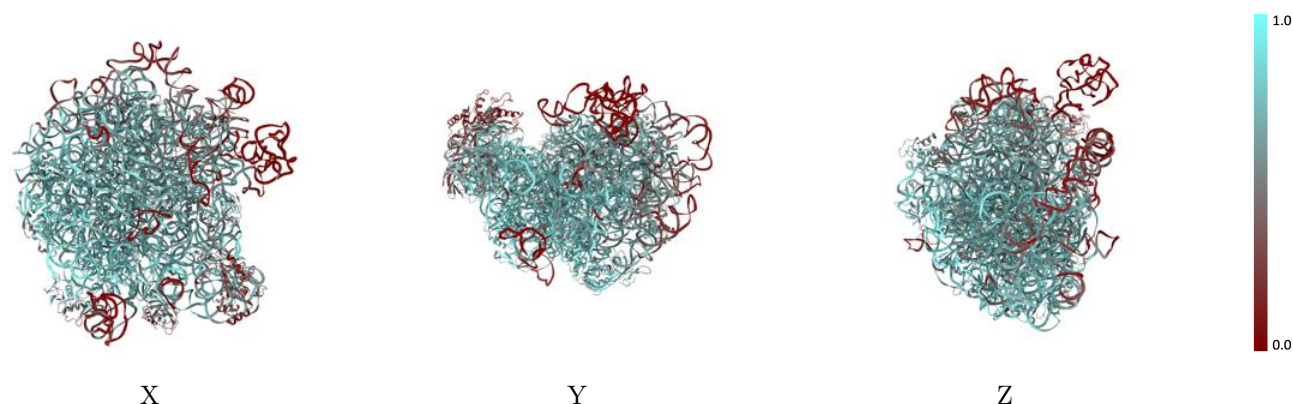
The images above show the 3D surface view of the map at the recommended contour level 0.377 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



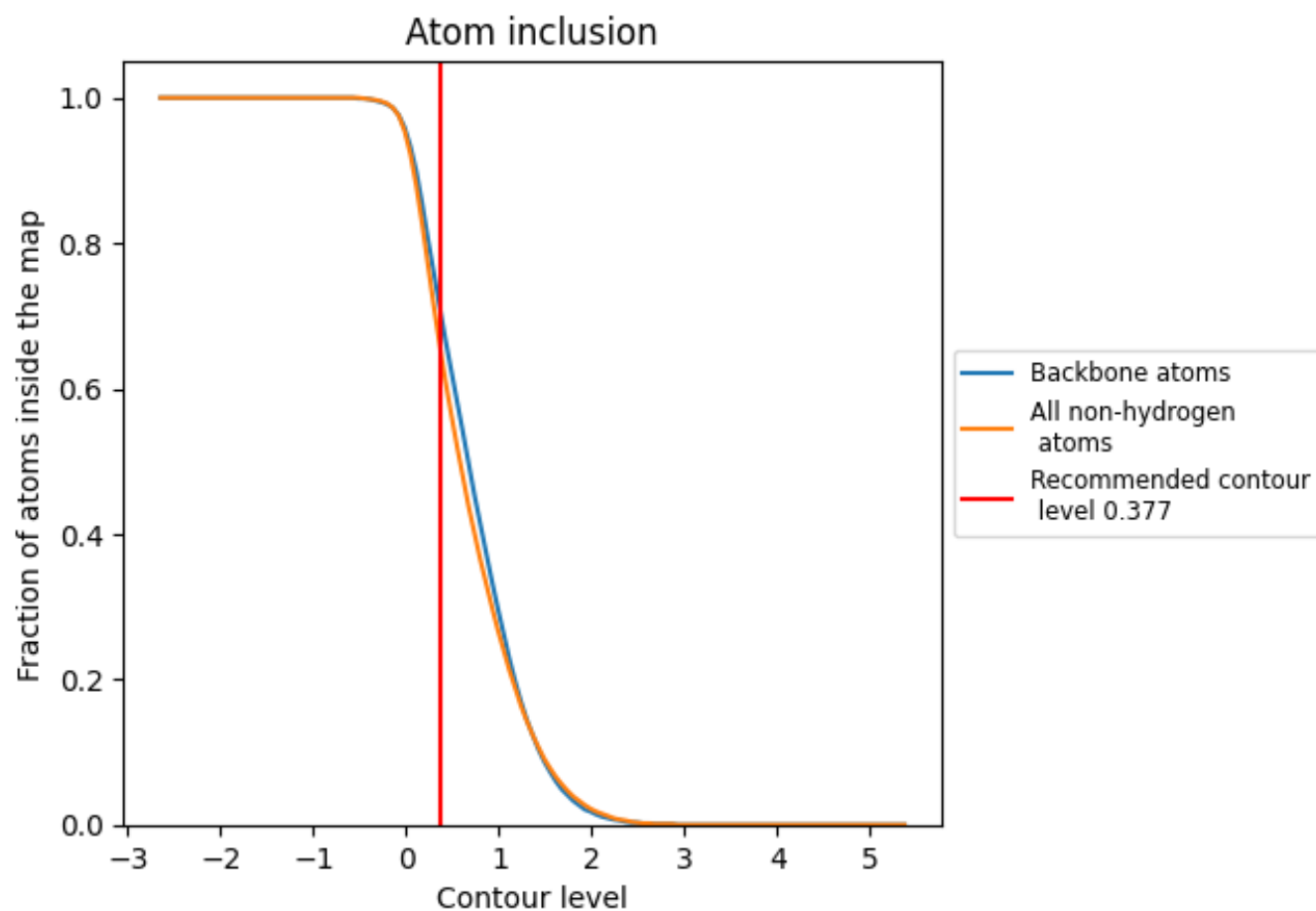
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.377).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.377) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6470	 0.3330
0	 0.7660	 0.4170
1	 0.5220	 0.3390
2	 0.7560	 0.3800
3	 0.7010	 0.3580
4	 0.7460	 0.4430
7	 0.8230	 0.4910
B	 0.6560	 0.3620
C	 0.6570	 0.3190
D	 0.7710	 0.4540
E	 0.7030	 0.3980
F	 0.2330	 0.1770
G	 0.5470	 0.4100
H	 0.3560	 0.1990
I	 0.6430	 0.3130
J	 0.8160	 0.4810
K	 0.6990	 0.4160
L	 0.6860	 0.3750
M	 0.7330	 0.4130
N	 0.7640	 0.4280
O	 0.5700	 0.3340
P	 0.6660	 0.4100
Q	 0.8290	 0.4730
R	 0.7870	 0.4890
S	 0.8280	 0.4580
T	 0.6600	 0.3590
U	 0.6070	 0.3550
V	 0.4740	 0.3370
W	 0.6750	 0.3380
Y	 0.6220	 0.3560
Z	 0.7300	 0.4110
b	 0.6120	 0.3170
y	 0.6290	 0.3180

