



Full wwPDB EM Validation Report ⓘ

Jul 2, 2026 – 02:56 PM JST

PDB ID : 9L95 / pdb_00009195
EMDB ID : EMD-62894
Title : State F of archaeal pre-50S ribosome
Authors : Li, Z.Q.; Yang, X.Y.
Deposited on : 2024-12-29
Resolution : 2.43 Å (reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

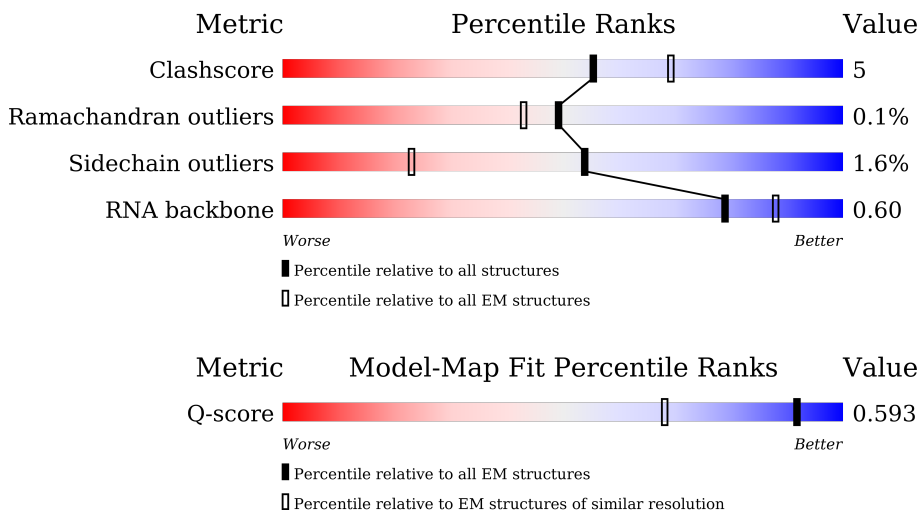
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.43 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	5787 (1.94 - 2.93)

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

Mol	Chain	Length	Quality of chain
1	0	2916	
2	9	122	
3	e	58	

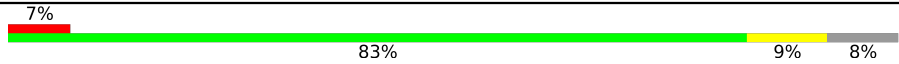

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Mol	Chain	Length	Quality of chain
4	A	50	14% 82% 12% . . .
5	E	120	87% 12% ..
6	F	176	5% 78% 15% 7%
7	G	196	90% 9%
8	H	116	88% 11%
9	I	184	7% 80% 20%
10	J	151	83% 11%
11	K	96	92% 7%
12	L	153	82% 16% ..
13	M	67	6% 75% 10% 13%
14	N	118	86% 11%
15	O	154	90% 9%
16	P	92	8% 77% 17%
17	Q	234	56% 39%
18	R	89	6% 72% 18% 10%
19	S	58	91% 7%
20	T	93	87% 13%
21	U	241	89% 8%
22	V	338	91% 9%
23	W	248	92% 8%
24	X	172	41% 71% 26% ..
25	Y	178	6% 81% 16% ..
26	b	145	80% 18% ..
27	c	83	10% 81% 18%
28	d	70	27% 79% 19% ..

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Mol	Chain	Length	Quality of chain
29	i	168	 <p>7% 83% 9% 8%</p>
30	f	132	 <p>80% 19%</p>

2 Entry composition [i](#)

There are 32 unique types of molecules in this entry. The entry contains 91437 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	0	2750	58947	26310	10851	19036	2750	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	9	120	2551	1138	453	840	120	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	e	57	435	269	76	90	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	49	414	252	89	71	2	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	119	880	546	141	192	1	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	164	1310	817	238	247	8	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	194	1579	963	338	276	2	0	0

- Molecule 8 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	H	115	887	544	167	176	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	183	1417	880	258	278	1	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	147	1179	712	243	223	1	0	0

- Molecule 11 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	95	736	451	150	133	2	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	151	1174	730	214	226	4	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	58	466	287	83	94	2	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	114	Total	C	N	O	0	0
			903	545	171	187		

- Molecule 15 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	154	Total	C	N	O	S	0	0
			1200	731	220	245	4		

- Molecule 16 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	89	Total	C	N	O	S	0	0
			726	448	138	139	1		

- Molecule 17 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	142	Total	C	N	O	S	0	0
			1146	698	231	216	1		

- Molecule 18 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	80	Total	C	N	O	S	0	0
			617	374	125	117	1		

- Molecule 19 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	57	Total	C	N	O	S	0	0
			439	265	90	80	4		

- Molecule 20 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	93	Total	C	N	O	S	0	0
			746	457	152	129	8		

- Molecule 21 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	235	Total	C	N	O	S	0	0
			1766	1089	349	323	5		

- Molecule 22 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	337	Total	C	N	O	S	0	0
			2619	1623	484	502	10		

- Molecule 23 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	248	Total	C	N	O	S	0	0
			1898	1164	354	377	3		

- Molecule 24 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	169	Total	C	N	O	S	0	0
			1308	808	229	268	3		

- Molecule 25 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	174	Total	C	N	O	S	0	0
			1346	832	228	283	3		

- Molecule 26 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	144	Total	C	N	O	S	0	0
			1127	701	201	220	5		

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	82	Total	C	N	O	S	0	0
			651	403	112	133	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	d	69	529	324	89	115	1	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	i	154	1166	699	231	236	0	0

- Molecule 30 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	f	132	996	612	188	191	5	0	0

- Molecule 31 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
31	0	260	Total 260	Mg 260	0
31	9	1	Total 1	Mg 1	0
31	F	1	Total 1	Mg 1	0
31	G	3	Total 3	Mg 3	0
31	K	1	Total 1	Mg 1	0
31	O	3	Total 3	Mg 3	0
31	Q	1	Total 1	Mg 1	0
31	T	1	Total 1	Mg 1	0
31	U	3	Total 3	Mg 3	0
31	V	1	Total 1	Mg 1	0
31	i	1	Total 1	Mg 1	0
31	f	1	Total 1	Mg 1	0

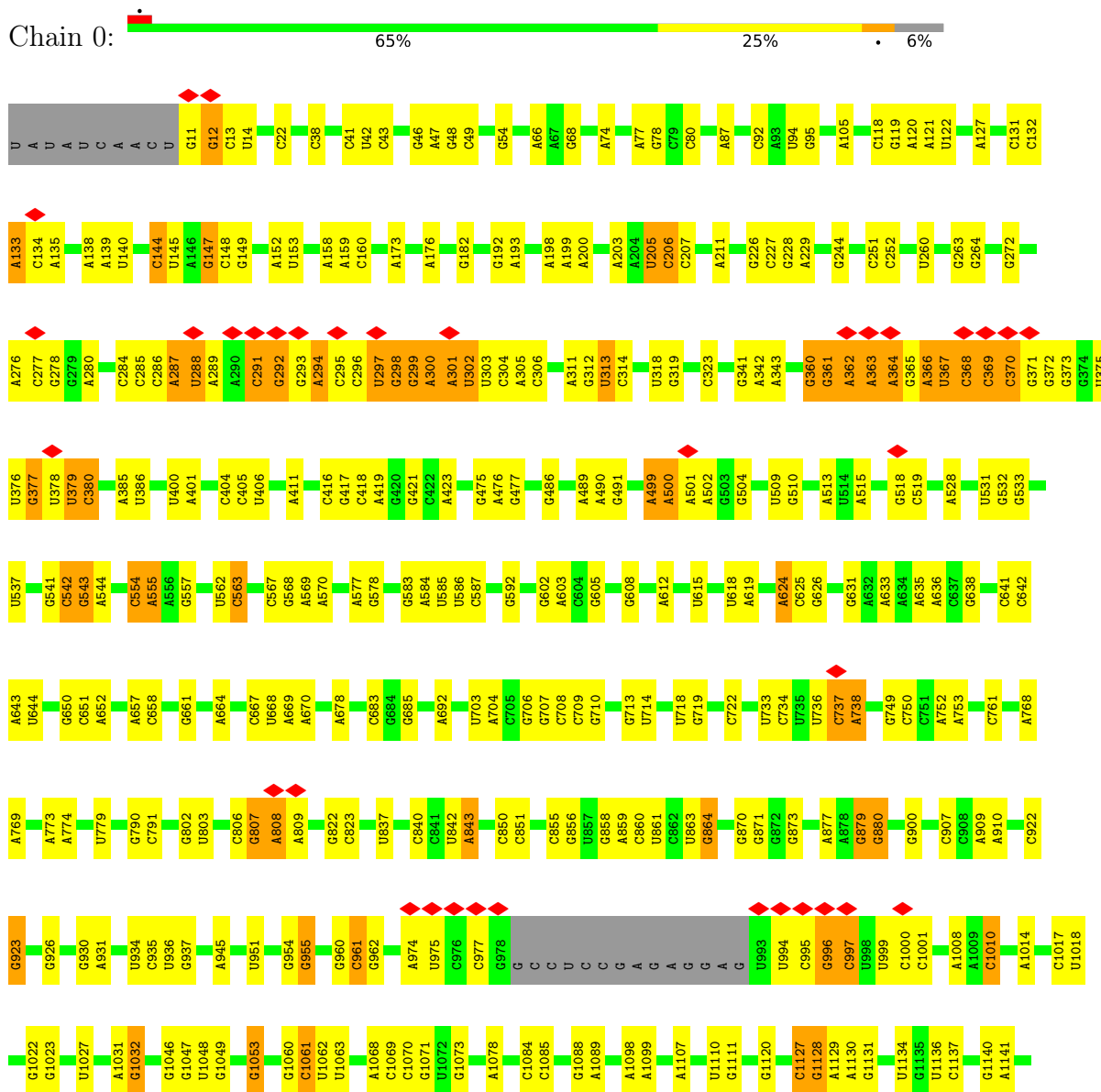
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

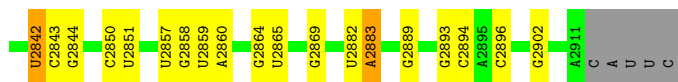
Mol	Chain	Residues	Atoms		AltConf
32	S	1	Total 1	Zn 1	0
32	T	1	Total 1	Zn 1	0

3 Residue-property plots [i](#)

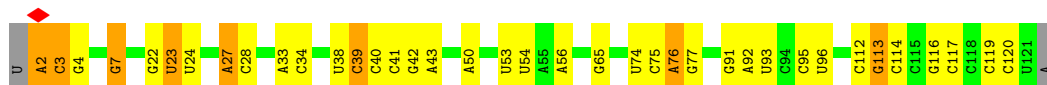
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 23S RNA

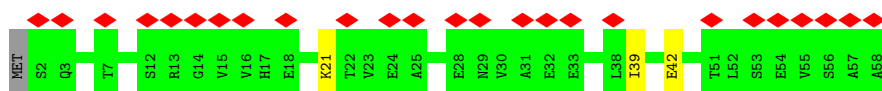




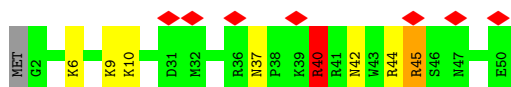
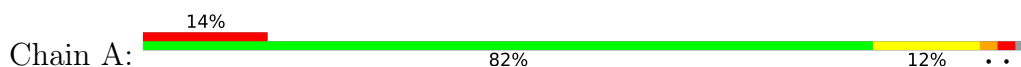
• Molecule 2: 5S RNA



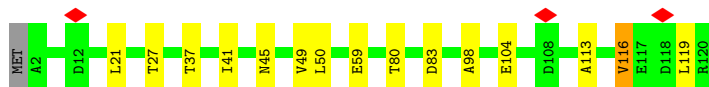
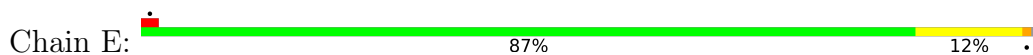
• Molecule 3: Large ribosomal subunit protein eL20



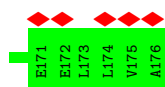
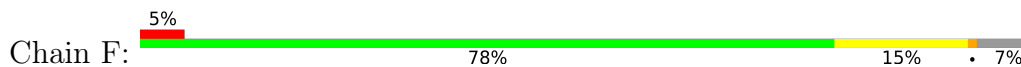
• Molecule 4: Large ribosomal subunit protein eL39



• Molecule 5: Large ribosomal subunit protein eL8



• Molecule 6: Large ribosomal subunit protein uL16

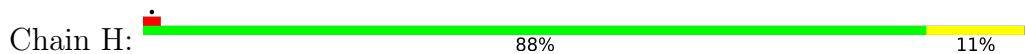


• Molecule 7: Large ribosomal subunit protein eL15

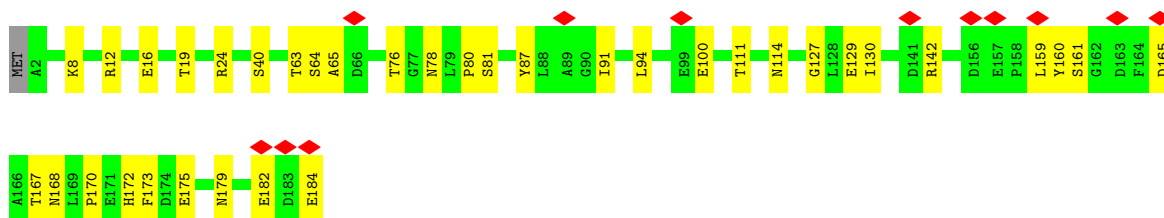




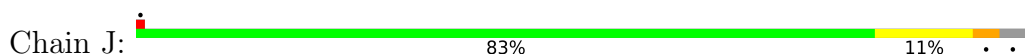
- Molecule 8: Large ribosomal subunit protein eL18



- Molecule 9: Large ribosomal subunit protein uL18



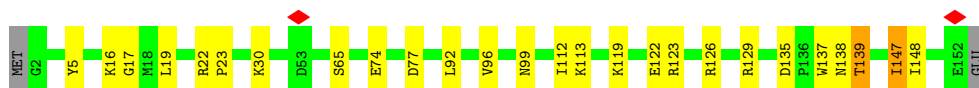
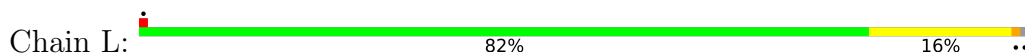
- Molecule 10: Large ribosomal subunit protein eL19



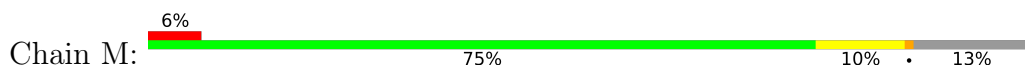
- Molecule 11: Large ribosomal subunit protein eL21



- Molecule 12: Large ribosomal subunit protein uL22

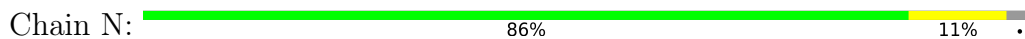


- Molecule 13: Large ribosomal subunit protein eL24

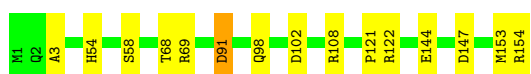
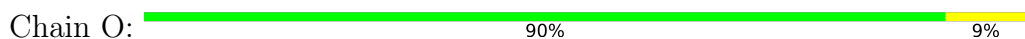




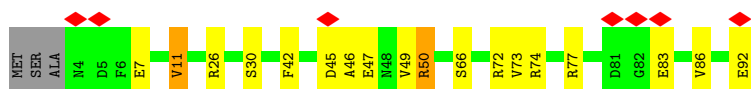
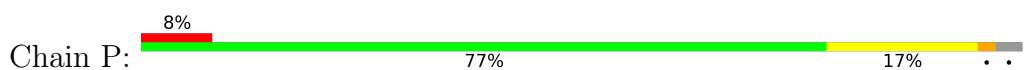
• Molecule 14: Large ribosomal subunit protein uL24



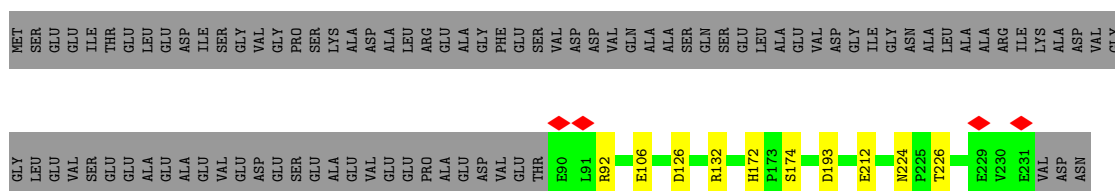
• Molecule 15: Large ribosomal subunit protein uL30



• Molecule 16: Large ribosomal subunit protein eL31



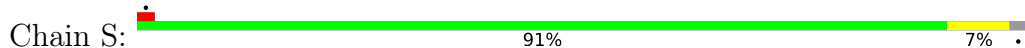
• Molecule 17: Large ribosomal subunit protein eL32



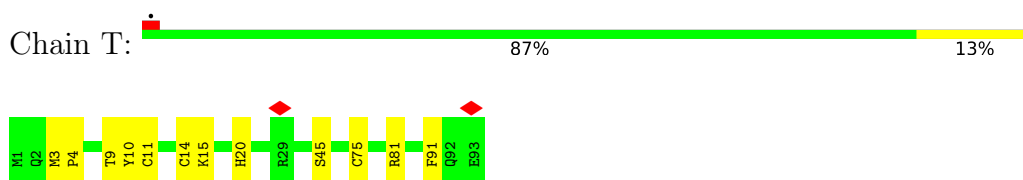
• Molecule 18: Large ribosomal subunit protein eL43



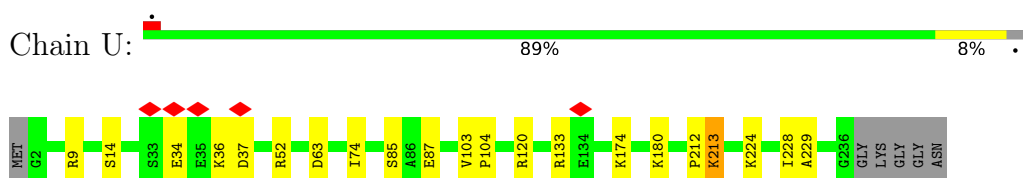
• Molecule 19: Large ribosomal subunit protein eL37



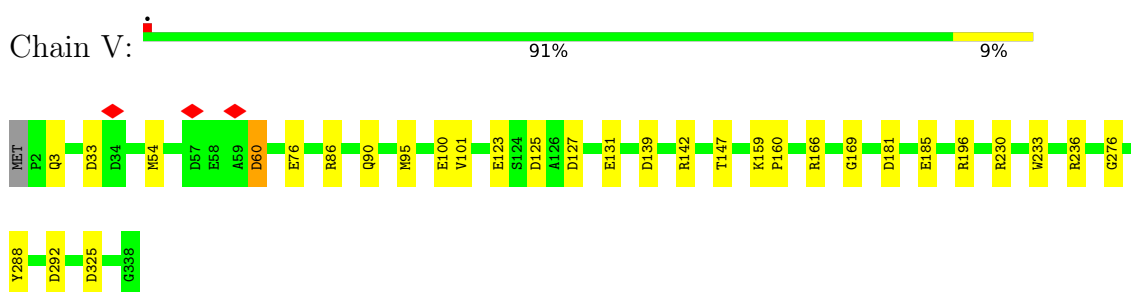
- Molecule 20: Large ribosomal subunit protein eL42



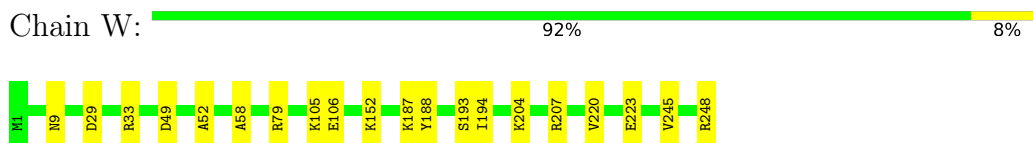
- Molecule 21: Large ribosomal subunit protein uL2



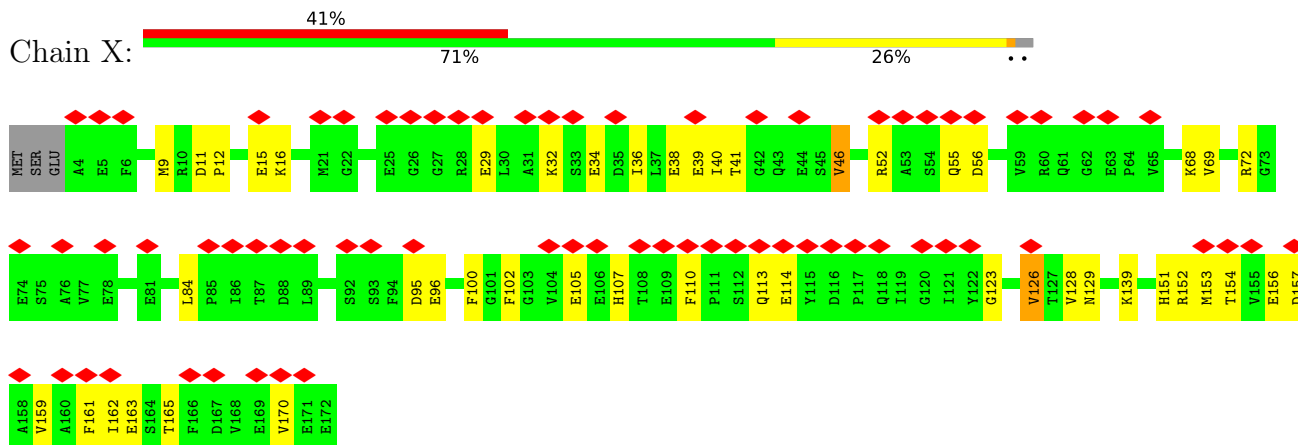
- Molecule 22: Large ribosomal subunit protein uL3



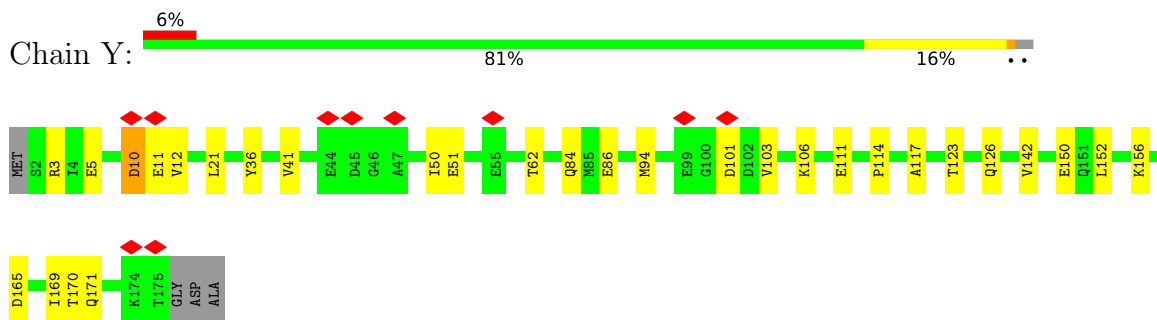
- Molecule 23: Large ribosomal subunit protein uL4



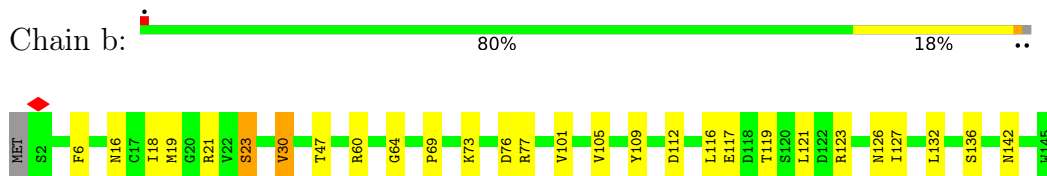
- Molecule 24: Large ribosomal subunit protein uL5



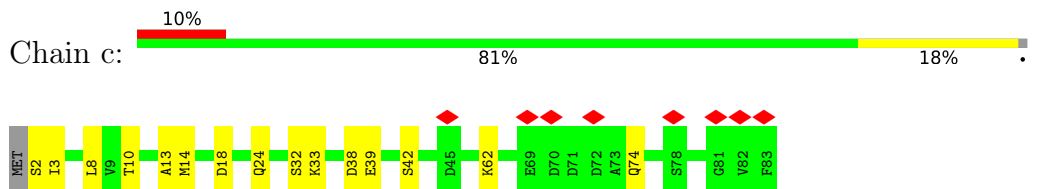
- Molecule 25: Large ribosomal subunit protein uL6



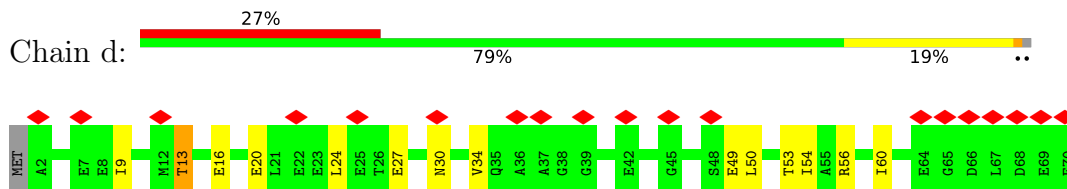
• Molecule 26: Large ribosomal subunit protein uL13



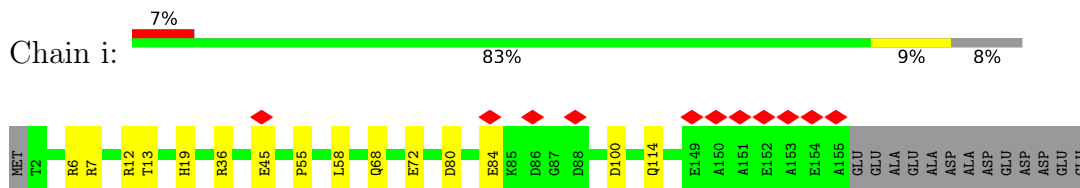
• Molecule 27: Large ribosomal subunit protein uL23



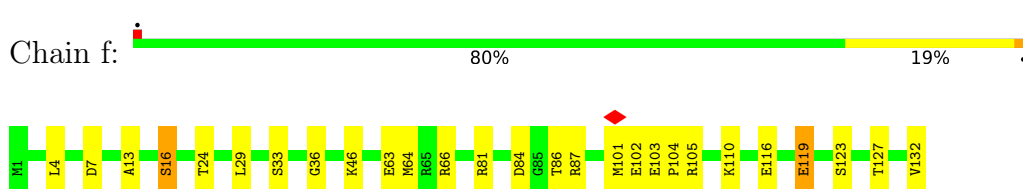
• Molecule 28: Large ribosomal subunit protein uL29



• Molecule 29: Large ribosomal subunit protein uL15



• Molecule 30: Large ribosomal subunit protein uL14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	918876	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.075	Depositor
Minimum map value	-1.440	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.111	Depositor
Recommended contour level	0.35	Depositor
Map size (\AA)	427.52, 427.52, 427.52	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.668, 0.668, 0.668	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.13	0/66003	0.28	0/102938
2	9	0.12	0/2848	0.27	0/4436
3	e	0.09	0/441	0.27	0/594
4	A	0.22	0/419	0.41	0/553
5	E	0.13	0/889	0.33	0/1209
6	F	0.14	0/1332	0.38	0/1788
7	G	0.12	0/1606	0.27	0/2145
8	H	0.14	0/895	0.31	0/1210
9	I	0.14	0/1447	0.36	0/1969
10	J	0.21	0/1191	0.45	2/1587 (0.1%)
11	K	0.12	0/750	0.31	0/1001
12	L	0.13	0/1199	0.33	0/1619
13	M	0.14	0/474	0.39	0/634
14	N	0.13	0/911	0.34	0/1232
15	O	0.12	0/1218	0.29	0/1651
16	P	0.18	0/741	0.42	0/998
17	Q	0.11	0/1165	0.28	0/1561
18	R	0.12	0/624	0.29	0/835
19	S	0.10	0/446	0.24	0/586
20	T	0.15	0/764	0.35	0/1015
21	U	0.14	0/1800	0.36	0/2420
22	V	0.11	0/2677	0.29	0/3617
23	W	0.11	0/1925	0.31	0/2598
24	X	0.19	0/1329	0.54	0/1793
25	Y	0.13	0/1368	0.32	0/1859
26	b	0.12	0/1144	0.30	0/1541
27	c	0.11	0/657	0.29	0/881
28	d	0.15	0/532	0.38	0/716
29	i	0.13	0/1181	0.32	0/1584
30	f	0.19	0/1004	0.43	1/1347 (0.1%)
All	All	0.13	0/98980	0.30	3/147917 (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
4	A	0	1
16	P	0	1
24	X	0	1
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	147	GLN	CA-CB-CG	8.91	131.92	114.10
10	J	147	GLN	CB-CG-CD	6.07	122.91	112.60
30	f	102	GLU	CB-CG-CD	5.62	122.16	112.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	40	ARG	Sidechain
16	P	50	ARG	Sidechain
24	X	52	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	58947	0	29734	456	0
2	9	2551	0	1298	21	0
3	e	435	0	426	1	0
4	A	414	0	442	6	0
5	E	880	0	852	9	0
6	F	1310	0	1311	19	0
7	G	1579	0	1606	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	887	0	907	8	0
9	I	1417	0	1365	24	0
10	J	1179	0	1183	16	0
11	K	736	0	745	6	0
12	L	1174	0	1146	19	0
13	M	466	0	443	6	0
14	N	903	0	886	9	0
15	O	1200	0	1159	11	0
16	P	726	0	703	10	0
17	Q	1146	0	1146	10	0
18	R	617	0	618	10	0
19	S	439	0	445	2	0
20	T	746	0	737	8	0
21	U	1766	0	1799	12	0
22	V	2619	0	2572	20	0
23	W	1898	0	1895	12	0
24	X	1308	0	1251	31	0
25	Y	1346	0	1292	18	0
26	b	1127	0	1118	18	0
27	c	651	0	652	8	0
28	d	529	0	525	8	0
29	i	1166	0	1113	9	0
30	f	996	0	1046	19	0
31	0	260	0	0	0	0
31	9	1	0	0	0	0
31	F	1	0	0	0	0
31	G	3	0	0	0	0
31	K	1	0	0	0	0
31	O	3	0	0	0	0
31	Q	1	0	0	0	0
31	T	1	0	0	0	0
31	U	3	0	0	0	0
31	V	1	0	0	0	0
31	f	1	0	0	0	0
31	i	1	0	0	0	0
32	S	1	0	0	0	0
32	T	1	0	0	0	0
All	All	91437	0	60415	756	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 5.

All (756) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1941:G:H1	1:0:1957:U:H3	1.13	0.96
9:I:111:THR:H	9:I:114:ASN:HD21	1.16	0.93
1:0:280:A:N1	1:0:379:U:C4	2.48	0.82
24:X:102:PHE:HB2	24:X:126:VAL:HG22	1.64	0.80
1:0:1148:A:HO2'	1:0:1211:G:H1	1.28	0.79
1:0:1902:A:H2'	1:0:1903:A:H8	1.47	0.78
1:0:2083:A:H2'	1:0:2084:G:C8	2.20	0.77
1:0:280:A:N1	1:0:379:U:O4	2.19	0.75
1:0:1947:A:H2'	1:0:1948:C:H4'	1.68	0.75
27:c:18:ASP:OD1	27:c:74:GLN:NE2	2.18	0.75
24:X:55:GLN:OE1	24:X:56:ASP:N	2.17	0.74
6:F:82:GLU:HG2	6:F:83:LYS:HG2	1.69	0.74
7:G:182:GLU:N	7:G:182:GLU:OE2	2.21	0.74
16:P:45:ASP:OD1	16:P:46:ALA:N	2.21	0.73
1:0:300:A:H62	1:0:360:G:N2	1.87	0.73
12:L:113:LYS:HD3	12:L:147:ILE:HD11	1.70	0.72
7:G:48:ASP:OD1	7:G:49:LYS:N	2.23	0.72
15:O:121:PRO:HG3	15:O:153:MET:HE2	1.69	0.72
20:T:14:CYS:HB2	20:T:75:CYS:HB2	1.73	0.71
1:0:528:A:H5''	12:L:30:LYS:HD2	1.72	0.70
30:f:101:MET:HE3	30:f:101:MET:HA	1.73	0.70
16:P:74:ARG:NH2	16:P:92:GLU:OE1	2.25	0.70
1:0:2730:C:OP2	10:J:62:ARG:NH2	2.25	0.69
25:Y:84:GLN:HB2	25:Y:171:GLN:HB3	1.72	0.69
1:0:2713:C:O2	30:f:87:ARG:NH2	2.26	0.69
9:I:111:THR:OG1	9:I:114:ASN:OD1	2.11	0.69
1:0:379:U:HO2'	1:0:380:C:H6	1.42	0.68
1:0:2540:C:H41	22:V:3:GLN:HE22	1.41	0.68
10:J:109:LEU:HD23	10:J:115:LEU:HD11	1.74	0.68
26:b:116:LEU:O	26:b:119:THR:OG1	2.12	0.68
1:0:312:G:OP2	14:N:39:ARG:NH2	2.27	0.68
1:0:2553:C:OP1	25:Y:156:LYS:NZ	2.27	0.68
1:0:1902:A:H2'	1:0:1903:A:C8	2.29	0.68
15:O:91:ASP:OD1	15:O:91:ASP:N	2.27	0.68
9:I:100:GLU:N	9:I:100:GLU:OE1	2.27	0.67
4:A:37:ASN:HB3	4:A:40:ARG:HG3	1.76	0.67
1:0:293:G:O6	1:0:369:C:N4	2.27	0.67
1:0:975:U:C4	1:0:997:C:N4	2.63	0.67
2:9:50:A:H5''	9:I:161:SER:HB2	1.77	0.67
9:I:63:THR:HG22	9:I:65:ALA:H	1.60	0.67
21:U:87:GLU:OE1	21:U:87:GLU:N	2.22	0.67
16:P:47:GLU:OE1	16:P:47:GLU:N	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2129:G:H2'	1:0:2130:A:H8	1.61	0.66
30:f:24:THR:HG23	30:f:64:MET:HE1	1.76	0.66
1:0:1534:U:H2'	1:0:1535:A:H8	1.61	0.66
12:L:74:GLU:N	12:L:74:GLU:OE1	2.28	0.66
18:R:33:GLU:OE1	18:R:67:ARG:NH1	2.29	0.66
1:0:1027:U:OP1	15:O:108:ARG:NH1	2.29	0.66
1:0:1129:A:H2'	1:0:1130:A:C8	2.30	0.66
30:f:103:GLU:N	30:f:103:GLU:OE1	2.28	0.66
24:X:110:PHE:O	24:X:113:GLN:NE2	2.28	0.65
2:9:53:U:H1'	24:X:9:MET:HE1	1.78	0.65
1:0:1961:A:H2'	1:0:1962:A:C8	2.32	0.65
1:0:1902:A:OP2	1:0:1922:G:N2	2.29	0.65
6:F:84:GLN:N	6:F:84:GLN:OE1	2.30	0.65
13:M:4:LYS:HG2	13:M:16:PRO:HG3	1.79	0.64
26:b:64:GLY:HA2	26:b:69:PRO:HD2	1.79	0.64
1:0:300:A:N6	1:0:360:G:H21	1.95	0.64
7:G:140:PRO:O	7:G:144:ASN:ND2	2.28	0.64
26:b:16:ASN:OD1	26:b:123:ARG:NH1	2.29	0.64
13:M:4:LYS:HE2	13:M:16:PRO:HD3	1.80	0.64
1:0:2335:G:O6	1:0:2338:A:N6	2.31	0.64
6:F:44:GLU:N	6:F:44:GLU:OE1	2.30	0.64
1:0:376:U:H2'	1:0:377:G:C8	2.33	0.63
1:0:1963:G:OP2	1:0:1963:G:N2	2.23	0.63
2:9:38:U:H1'	2:9:43:A:H61	1.62	0.63
8:H:98:THR:H	8:H:101:GLN:HE21	1.46	0.63
1:0:2355:A:H2'	1:0:2356:G:C8	2.34	0.63
1:0:1516:C:H2'	1:0:1517:A:H8	1.64	0.63
16:P:83:GLU:OE1	16:P:83:GLU:N	2.32	0.62
1:0:642:C:H2'	1:0:643:A:H8	1.63	0.62
1:0:510:G:N1	1:0:513:A:OP2	2.31	0.62
1:0:1679:A:H1'	4:A:44:ARG:HH22	1.64	0.62
16:P:26:ARG:O	16:P:30:SER:OG	2.16	0.62
1:0:1459:U:H2'	1:0:1460:A:H8	1.65	0.62
1:0:1802:G:N2	1:0:1805:G:OP2	2.30	0.62
1:0:300:A:H62	1:0:360:G:H21	1.45	0.62
1:0:2619:C:H2'	1:0:2620:G:H8	1.65	0.62
1:0:1567:A:H2'	1:0:1568:A:C8	2.34	0.62
1:0:2729:C:OP2	10:J:62:ARG:NH1	2.33	0.62
1:0:2859:U:C4	13:M:51:GLU:HG2	2.35	0.62
1:0:661:G:OP2	8:H:38:ARG:NH2	2.33	0.61
4:A:42:ASN:HB3	4:A:45:ARG:HG2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:122:ARG:NH1	15:O:154:ARG:O	2.31	0.61
1:0:752:A:H2'	1:0:753:A:C8	2.36	0.61
1:0:1987:A:OP2	30:f:66:ARG:NH2	2.33	0.61
1:0:2105:A:H2'	1:0:2106:G:H8	1.66	0.61
1:0:2501:C:OP1	1:0:2503:C:N4	2.34	0.60
22:V:86:ARG:HG3	22:V:100:GLU:HG2	1.84	0.60
1:0:1239:A:OP2	26:b:60:ARG:NH2	2.32	0.60
24:X:36:ILE:O	24:X:40:ILE:HG13	2.00	0.60
1:0:1701:G:N1	1:0:1704:U:OP2	2.31	0.60
10:J:90:ASN:HD22	10:J:93:ASP:H	1.48	0.60
10:J:119:GLN:HE21	10:J:146:TYR:HD2	1.49	0.60
1:0:996:G:O2'	1:0:997:C:OP1	2.18	0.60
1:0:1518:A:H4'	1:0:1519:U:OP1	2.01	0.60
28:d:50:LEU:O	28:d:54:ILE:HG13	2.02	0.60
30:f:104:PRO:HG3	30:f:127:THR:HG21	1.81	0.60
15:O:58:SER:OG	15:O:147:ASP:OD2	2.20	0.60
24:X:95:ASP:OD1	24:X:96:GLU:N	2.35	0.60
24:X:152:ARG:HG2	24:X:154:THR:HG23	1.84	0.60
1:0:1534:U:H2'	1:0:1535:A:C8	2.36	0.59
17:Q:172:HIS:ND1	17:Q:174:SER:OG	2.35	0.59
1:0:583:G:H2'	1:0:584:A:C8	2.36	0.59
3:e:21:LYS:NZ	3:e:42:GLU:OE2	2.34	0.59
1:0:1098:A:H2'	1:0:1099:A:C8	2.38	0.59
1:0:2619:C:H2'	1:0:2620:G:C8	2.38	0.59
1:0:1267:C:H2'	1:0:1268:G:H8	1.67	0.59
1:0:1541:C:H2'	1:0:1542:A:C8	2.38	0.59
1:0:1454:A:H2'	1:0:1455:A:C8	2.37	0.59
1:0:1901:G:N1	1:0:1923:A:OP2	2.32	0.59
1:0:280:A:C2	1:0:379:U:C5	2.91	0.58
8:H:8:LEU:O	8:H:12:ILE:HG13	2.03	0.58
1:0:295:C:N3	1:0:366:A:N6	2.51	0.58
5:E:27:THR:HG21	5:E:104:GLU:H	1.68	0.58
6:F:113:ASP:OD1	6:F:113:ASP:N	2.36	0.58
24:X:156:GLU:HG2	24:X:161:PHE:HE1	1.67	0.58
1:0:11:G:O2'	1:0:12:G:O4'	2.22	0.58
8:H:98:THR:H	8:H:101:GLN:NE2	2.02	0.58
1:0:304:C:H2'	1:0:305:A:H8	1.69	0.58
1:0:1541:C:H2'	1:0:1542:A:H8	1.68	0.58
1:0:2098:C:H2'	1:0:2099:C:H6	1.69	0.58
1:0:642:C:H2'	1:0:643:A:C8	2.39	0.58
1:0:2105:A:H2'	1:0:2106:G:C8	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1148:A:O2'	1:0:1211:G:N1	2.23	0.58
9:I:87:TYR:O	9:I:91:ILE:HG13	2.03	0.58
24:X:41:THR:HG21	24:X:69:VAL:HG21	1.85	0.57
30:f:63:GLU:OE2	30:f:63:GLU:N	2.33	0.57
1:0:960:G:H2'	1:0:961:C:C6	2.39	0.57
1:0:311:A:OP2	14:N:39:ARG:NE	2.37	0.57
1:0:737:C:H3'	1:0:738:A:C8	2.40	0.57
2:9:75:C:H3'	2:9:76:A:H5''	1.86	0.57
30:f:13:ALA:O	30:f:16:SER:OG	2.21	0.57
1:0:1736:A:H61	1:0:2030:C:H42	1.51	0.57
1:0:2361:A:N6	9:I:19:THR:O	2.38	0.57
24:X:153:MET:HE2	24:X:153:MET:HA	1.86	0.57
1:0:68:G:H1	1:0:92:C:H5	1.51	0.57
1:0:2098:C:H2'	1:0:2099:C:C6	2.39	0.57
1:0:299:G:H1	1:0:361:G:H8	1.53	0.57
25:Y:41:VAL:HG12	25:Y:50:ILE:HG23	1.87	0.57
1:0:486:G:N1	1:0:489:A:OP2	2.38	0.57
1:0:1022:G:H2'	1:0:1023:G:H8	1.70	0.57
1:0:1520:A:N3	1:0:1520:A:H2'	2.20	0.57
1:0:1653:A:H2'	1:0:1654:A:C8	2.40	0.57
7:G:157:ASP:O	7:G:162:ARG:NH1	2.38	0.57
9:I:87:TYR:OH	9:I:184:GLU:OE1	2.22	0.57
27:c:38:ASP:OD1	27:c:39:GLU:N	2.37	0.57
1:0:38:C:OP2	14:N:9:ARG:NH1	2.38	0.56
1:0:2497:A:OP1	6:F:154:ARG:NH1	2.37	0.56
26:b:30:VAL:HG21	26:b:101:VAL:HB	1.88	0.56
16:P:49:VAL:HG22	16:P:86:VAL:HB	1.87	0.56
1:0:1063:U:O2'	1:0:2300:A:N3	2.39	0.56
1:0:1129:A:H2'	1:0:1130:A:H8	1.70	0.56
1:0:144:C:OP1	1:0:264:G:O2'	2.23	0.56
1:0:1647:C:OP1	21:U:174:LYS:NZ	2.39	0.56
16:P:72:ARG:HH11	16:P:72:ARG:HG2	1.71	0.56
1:0:293:G:O6	1:0:294:A:N6	2.38	0.56
1:0:975:U:N3	1:0:997:C:C4	2.73	0.56
1:0:1942:G:H2'	1:0:1943:G:C8	2.40	0.56
24:X:165:THR:HG22	24:X:170:VAL:HA	1.88	0.56
1:0:667:C:OP2	23:W:105:LYS:NZ	2.39	0.56
6:F:49:GLU:OE1	6:F:168:GLU:HB2	2.06	0.56
1:0:1210:C:H2'	1:0:1211:G:C4	2.41	0.55
1:0:773:A:H2'	1:0:774:A:C8	2.41	0.55
8:H:19:SER:HB2	8:H:27:TRP:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:7:GLU:N	16:P:7:GLU:OE2	2.40	0.55
18:R:11:SER:OG	18:R:31:GLU:OE1	2.17	0.55
1:0:1048:U:H2'	1:0:1049:G:H8	1.71	0.55
1:0:1942:G:C6	1:0:1943:G:O6	2.59	0.55
1:0:2226:C:H4'	1:0:2227:U:C4	2.41	0.55
1:0:2668:A:O2'	26:b:77:ARG:NH1	2.39	0.55
1:0:543:G:H2'	1:0:544:A:C8	2.42	0.55
5:E:59:GLU:OE2	7:G:13:TRP:NE1	2.27	0.55
1:0:13:C:H2'	1:0:14:U:C6	2.42	0.55
1:0:1791:U:H3'	1:0:1792:A:H8	1.71	0.55
21:U:212:PRO:O	21:U:213:LYS:HB2	2.07	0.55
1:0:22:C:O2'	1:0:615:U:OP1	2.25	0.54
1:0:1607:A:H2'	1:0:1608:A:C8	2.42	0.54
24:X:55:GLN:CD	24:X:56:ASP:H	2.11	0.54
1:0:298:G:N2	1:0:362:A:N3	2.56	0.54
1:0:873:G:OP2	21:U:9:ARG:NH1	2.40	0.54
12:L:123:ARG:HB2	12:L:139:THR:HG23	1.89	0.54
17:Q:193:ASP:OD1	17:Q:193:ASP:N	2.38	0.54
10:J:119:GLN:HA	10:J:122:THR:HG22	1.89	0.54
1:0:863:U:O2'	1:0:1483:A:N6	2.40	0.54
24:X:105:GLU:HA	24:X:123:GLY:HA2	1.90	0.54
9:I:170:PRO:O	9:I:173:PHE:HB3	2.06	0.54
17:Q:106:GLU:OE1	17:Q:106:GLU:N	2.32	0.54
27:c:32:SER:OG	27:c:33:LYS:N	2.40	0.54
1:0:954:G:N3	1:0:2295:A:H2'	2.23	0.54
21:U:37:ASP:OD1	21:U:85:SER:OG	2.22	0.54
26:b:19:MET:O	26:b:23:SER:OG	2.19	0.54
28:d:30:ASN:O	28:d:34:VAL:HG23	2.08	0.54
1:0:2677:U:H2'	1:0:2678:U:C6	2.42	0.54
1:0:1031:A:N3	1:0:1269:U:O2'	2.38	0.54
1:0:624:A:O2'	17:Q:126:ASP:OD2	2.26	0.54
1:0:704:A:N6	29:i:114:GLN:O	2.36	0.54
1:0:1127:C:H4'	1:0:1128:G:O5'	2.07	0.54
14:N:110:GLU:O	14:N:114:LYS:HG2	2.08	0.54
1:0:1803:C:OP1	13:M:45:ARG:NH1	2.39	0.53
1:0:1509:C:H2'	1:0:1510:U:H6	1.73	0.53
7:G:45:THR:OG1	7:G:131:GLU:OE1	2.18	0.53
18:R:76:VAL:HG22	21:U:104:PRO:HG2	1.90	0.53
15:O:68:THR:HG22	15:O:69:ARG:HG2	1.91	0.53
21:U:34:GLU:HG2	21:U:36:LYS:HG2	1.89	0.53
1:0:2136:U:H2'	1:0:2137:C:C6	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:f:7:ASP:OD2	30:f:81:ARG:NH2	2.39	0.53
1:0:1010:C:OP1	6:F:19:ARG:NH1	2.41	0.53
2:9:39:C:H5'	2:9:40:C:H5''	1.89	0.53
1:0:159:A:H2'	1:0:160:C:H6	1.74	0.53
26:b:142:ASN:OD1	26:b:142:ASN:N	2.40	0.53
1:0:366:A:O2'	1:0:367:U:O5'	2.20	0.53
1:0:2426:U:H2'	1:0:2427:A:H8	1.74	0.53
6:F:43:PRO:HB3	6:F:139:TYR:CE2	2.43	0.53
24:X:156:GLU:HG2	24:X:161:PHE:CE1	2.43	0.53
1:0:286:C:O2'	1:0:287:A:H8	1.91	0.52
1:0:2099:C:H2'	1:0:2100:U:H6	1.75	0.52
1:0:2238:C:OP1	7:G:33:ARG:NH1	2.41	0.52
1:0:2761:G:H2'	1:0:2762:C:C6	2.44	0.52
1:0:2812:U:H2'	1:0:2813:U:C6	2.44	0.52
1:0:1418:U:H2'	1:0:1419:C:C6	2.44	0.52
1:0:228:G:H2'	1:0:229:A:C8	2.45	0.52
1:0:955:G:O2'	1:0:1014:A:N6	2.36	0.52
1:0:291:C:C4	1:0:292:G:H1'	2.44	0.52
1:0:1516:C:H2'	1:0:1517:A:C8	2.43	0.52
1:0:2269:U:H2'	1:0:2270:U:C6	2.45	0.52
1:0:2426:U:H2'	1:0:2427:A:C8	2.44	0.52
10:J:115:LEU:HB3	10:J:119:GLN:HG3	1.91	0.52
18:R:44:VAL:HG12	18:R:54:ASN:HA	1.91	0.52
26:b:18:ILE:HD11	26:b:121:LEU:HD13	1.91	0.52
1:0:280:A:N1	1:0:379:U:C5	2.78	0.52
1:0:1512:C:H2'	1:0:1513:U:C6	2.45	0.52
1:0:2099:C:H2'	1:0:2100:U:C6	2.45	0.52
1:0:975:U:N3	1:0:997:C:N4	2.58	0.52
6:F:130:PRO:HD2	6:F:133:GLU:HG3	1.90	0.52
1:0:418:C:H2'	1:0:419:A:H8	1.75	0.52
18:R:56:GLU:OE1	18:R:56:GLU:N	2.43	0.52
1:0:737:C:H3'	1:0:738:A:H8	1.75	0.52
21:U:52:ARG:NH1	21:U:120:ARG:O	2.43	0.52
1:0:42:U:H2'	1:0:43:C:C6	2.44	0.51
23:W:49:ASP:HB3	23:W:52:ALA:HB2	1.92	0.51
1:0:417:G:H2'	1:0:418:C:C6	2.46	0.51
1:0:542:C:H5''	1:0:543:G:C8	2.45	0.51
2:9:34:C:H2'	9:I:142:ARG:HH12	1.74	0.51
1:0:840:C:HO2'	1:0:843:A:HO2'	1.55	0.51
25:Y:86:GLU:HB2	25:Y:170:THR:HG21	1.92	0.51
25:Y:126:GLN:OE1	25:Y:126:GLN:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:569:A:H2'	1:0:570:A:C8	2.46	0.51
2:9:41:C:O2	24:X:72:ARG:NH1	2.43	0.51
1:0:1323:G:N2	1:0:1326:A:OP2	2.36	0.51
23:W:29:ASP:OD1	23:W:29:ASP:N	2.43	0.51
1:0:1145:C:O2'	1:0:1212:A:N1	2.44	0.51
1:0:2589:A:O2'	30:f:33:SER:OG	2.24	0.51
1:0:1946:A:H4'	1:0:1947:A:H5'	1.93	0.51
9:I:165:ASP:OD2	9:I:167:THR:OG1	2.26	0.51
12:L:119:LYS:NZ	12:L:122:GLU:OE2	2.36	0.51
24:X:34:GLU:O	24:X:38:GLU:HG2	2.11	0.51
1:0:499:A:O2'	1:0:500:A:OP1	2.26	0.51
1:0:1459:U:H2'	1:0:1460:A:C8	2.46	0.51
20:T:11:CYS:O	20:T:15:LYS:N	2.44	0.50
1:0:1136:U:H2'	1:0:1137:C:C6	2.45	0.50
7:G:16:PRO:HA	7:G:21:LEU:HD23	1.92	0.50
15:O:154:ARG:HH11	15:O:154:ARG:HG2	1.75	0.50
20:T:9:THR:OG1	20:T:81:ARG:NH2	2.43	0.50
1:0:1270:G:H2'	1:0:1271:C:C6	2.47	0.50
1:0:2108:U:H2'	1:0:2109:U:C6	2.46	0.50
1:0:2354:A:H2'	1:0:2355:A:C8	2.47	0.50
1:0:2678:U:H2'	1:0:2679:C:C6	2.46	0.50
20:T:45:SER:O	20:T:45:SER:OG	2.29	0.50
24:X:15:GLU:HB3	24:X:129:ASN:HB3	1.93	0.50
1:0:1739:G:O2'	1:0:2025:U:O4	2.26	0.50
1:0:2318:U:H2'	1:0:2319:U:C6	2.47	0.50
1:0:2850:C:H2'	1:0:2851:U:C6	2.46	0.50
1:0:300:A:H2	1:0:301:A:H62	1.59	0.50
1:0:1570:C:H2'	1:0:1571:A:H8	1.75	0.50
1:0:2244:G:H2'	1:0:2245:C:C6	2.47	0.50
1:0:205:U:H4'	1:0:206:C:H5'	1.92	0.50
1:0:423:A:H1'	1:0:1914:A:C2	2.47	0.50
1:0:360:G:O2'	1:0:361:G:H2'	2.12	0.50
1:0:2259:A:H2'	1:0:2260:G:C8	2.46	0.50
19:S:43:SER:OG	19:S:45:LYS:O	2.30	0.50
23:W:193:SER:OG	23:W:194:ILE:N	2.45	0.50
1:0:80:C:OP1	28:d:56:ARG:NH1	2.38	0.50
1:0:1274:U:H5'	8:H:20:ARG:HH21	1.76	0.50
1:0:2336:G:H1'	1:0:2337:A:C8	2.47	0.50
17:Q:106:GLU:H	17:Q:106:GLU:CD	2.19	0.50
1:0:41:C:H2'	1:0:42:U:C6	2.47	0.49
1:0:618:U:H2'	1:0:619:A:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1908:C:H2'	1:0:1909:A:H8	1.77	0.49
11:K:72:PHE:HE1	11:K:89:PRO:HG3	1.77	0.49
12:L:112:ILE:HA	12:L:148:ILE:HG22	1.93	0.49
26:b:76:ASP:N	26:b:76:ASP:OD1	2.44	0.49
26:b:112:ASP:OD1	26:b:112:ASP:N	2.38	0.49
1:0:313:U:H2'	14:N:52:LEU:HD13	1.93	0.49
1:0:1471:G:H2'	1:0:1472:A:C8	2.48	0.49
1:0:1653:A:H2'	1:0:1654:A:H8	1.77	0.49
17:Q:212:GLU:OE2	17:Q:226:THR:HG23	2.13	0.49
22:V:142:ARG:HG2	22:V:166:ARG:HA	1.93	0.49
1:0:1302:U:H2'	1:0:1303:G:H8	1.77	0.49
1:0:1504:A:H2'	1:0:1505:G:C8	2.48	0.49
1:0:1662:A:H2'	1:0:1663:A:C8	2.48	0.49
1:0:2319:U:H2'	1:0:2320:U:C6	2.48	0.49
1:0:2882:U:H4'	1:0:2883:A:H5'	1.94	0.49
23:W:204:LYS:HA	23:W:207:ARG:HG3	1.94	0.49
24:X:159:VAL:O	24:X:162:ILE:HG13	2.13	0.49
1:0:554:C:HO2'	1:0:555:A:P	2.35	0.49
5:E:37:THR:HG23	5:E:98:ALA:HB2	1.95	0.49
22:V:127:ASP:O	22:V:131:GLU:HG2	2.12	0.49
1:0:251:C:OP1	7:G:2:ALA:N	2.46	0.49
1:0:499:A:HO2'	1:0:500:A:P	2.35	0.49
24:X:15:GLU:OE2	24:X:139:LYS:NZ	2.46	0.49
1:0:297:U:H1'	1:0:365:G:H22	1.77	0.49
1:0:1267:C:H2'	1:0:1268:G:C8	2.47	0.49
1:0:2813:U:H2'	1:0:2814:C:C6	2.48	0.49
23:W:33:ARG:NH1	23:W:106:GLU:OE2	2.46	0.49
1:0:1136:U:H2'	1:0:1137:C:H6	1.77	0.49
1:0:1514:U:H2'	1:0:1515:G:H8	1.77	0.49
1:0:1542:A:H2'	1:0:1543:C:H6	1.77	0.49
1:0:2230:G:H2'	1:0:2231:A:O4'	2.13	0.49
1:0:2678:U:H2'	1:0:2679:C:H6	1.77	0.49
1:0:2761:G:H2'	1:0:2762:C:H6	1.78	0.49
20:T:9:THR:OG1	20:T:10:TYR:N	2.46	0.49
22:V:233:TRP:CD1	22:V:236:ARG:HD2	2.48	0.49
1:0:1941:G:O6	1:0:1957:U:O4	2.31	0.48
1:0:145:U:O2'	1:0:147:G:OP2	2.29	0.48
1:0:1567:A:H2'	1:0:1568:A:H8	1.75	0.48
1:0:1828:U:H5	1:0:1833:A:N7	2.12	0.48
10:J:99:ILE:O	10:J:103:ARG:HG2	2.13	0.48
26:b:117:GLU:H	26:b:117:GLU:CD	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1509:C:H2'	1:0:1510:U:C6	2.49	0.48
6:F:99:GLU:HG2	6:F:101:LYS:HG2	1.95	0.48
1:0:1878:A:C5	1:0:1879:A:C8	3.01	0.48
26:b:21:ARG:HB2	26:b:119:THR:HG22	1.94	0.48
1:0:2313:A:H4'	1:0:2314:A:O4'	2.14	0.48
9:I:64:SER:HB2	9:I:76:THR:HB	1.95	0.48
12:L:77:ASP:OD1	12:L:77:ASP:N	2.40	0.48
22:V:101:VAL:HG22	22:V:125:ASP:HB3	1.95	0.48
1:0:2758:A:H2'	1:0:2759:C:C6	2.48	0.48
24:X:100:PHE:CZ	24:X:128:VAL:HG11	2.48	0.48
1:0:2334:G:H5''	1:0:2335:G:N7	2.29	0.48
1:0:2842:U:C4	1:0:2844:G:N2	2.81	0.48
6:F:30:LYS:HG3	6:F:62:HIS:CE1	2.48	0.48
10:J:105:ARG:NH1	10:J:109:LEU:HD12	2.28	0.48
24:X:114:GLU:HA	24:X:114:GLU:OE2	2.14	0.48
1:0:1516:C:O2'	1:0:1517:A:O5'	2.31	0.48
1:0:1752:U:N3	1:0:1813:G:OP2	2.46	0.48
1:0:2319:U:H2'	1:0:2320:U:H6	1.78	0.48
1:0:2704:U:H2'	1:0:2705:G:H8	1.79	0.48
28:d:9:ILE:HG22	28:d:60:ILE:HG21	1.96	0.48
1:0:2731:G:C2	1:0:2732:A:C8	3.01	0.48
1:0:2824:C:C2	1:0:2825:A:C8	3.02	0.48
24:X:151:HIS:O	24:X:151:HIS:ND1	2.46	0.48
1:0:669:A:H2'	1:0:670:A:C8	2.49	0.48
1:0:1511:U:H2'	1:0:1512:C:H6	1.78	0.48
1:0:1512:C:H2'	1:0:1513:U:H6	1.78	0.48
1:0:2422:A:H2'	1:0:2423:A:H8	1.79	0.48
1:0:2784:U:H1'	1:0:2785:A:H5''	1.96	0.48
2:9:113:G:H2'	2:9:114:C:C6	2.49	0.48
1:0:960:G:H2'	1:0:961:C:H6	1.79	0.47
1:0:1662:A:H2'	1:0:1663:A:H8	1.79	0.47
1:0:1747:C:O2	22:V:230:ARG:NH2	2.42	0.47
25:Y:106:LYS:HG2	25:Y:114:PRO:HB3	1.95	0.47
1:0:1587:G:O2'	1:0:1588:C:O4'	2.30	0.47
1:0:1851:A:H2'	1:0:1852:A:H8	1.77	0.47
24:X:84:LEU:HD13	24:X:102:PHE:HZ	1.79	0.47
1:0:318:U:H2'	1:0:319:G:O4'	2.14	0.47
1:0:418:C:H2'	1:0:419:A:C8	2.48	0.47
1:0:1270:G:H2'	1:0:1271:C:H6	1.79	0.47
1:0:1923:A:H2'	1:0:1924:A:C8	2.49	0.47
25:Y:123:THR:HG23	25:Y:142:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:42:U:H2'	1:0:43:C:H6	1.78	0.47
1:0:1530:G:H2'	1:0:1531:C:H6	1.78	0.47
1:0:2046:G:OP1	12:L:139:THR:HB	2.13	0.47
1:0:2623:G:N2	1:0:2626:A:OP2	2.37	0.47
9:I:172:HIS:O	9:I:175:GLU:HB3	2.14	0.47
12:L:19:LEU:HG	12:L:92:LEU:HD13	1.96	0.47
25:Y:117:ALA:HB2	25:Y:152:LEU:HD22	1.96	0.47
1:0:733:U:H2'	1:0:734:C:C6	2.50	0.47
1:0:1457:U:H2'	1:0:1458:C:H6	1.79	0.47
1:0:2677:U:H2'	1:0:2678:U:H6	1.78	0.47
30:f:116:GLU:O	30:f:119:GLU:HB2	2.14	0.47
1:0:362:A:O2'	1:0:363:A:N3	2.36	0.47
1:0:995:C:H2'	1:0:996:G:C8	2.49	0.47
1:0:651:C:H2'	1:0:652:A:H8	1.79	0.47
1:0:930:G:C2	1:0:931:A:C8	3.02	0.47
22:V:196:ARG:NH2	22:V:325:ASP:OD2	2.48	0.47
25:Y:3:ARG:NE	25:Y:5:GLU:OE2	2.33	0.47
30:f:105:ARG:HE	30:f:105:ARG:HB3	1.50	0.47
1:0:475:G:H2'	1:0:476:A:C8	2.49	0.47
1:0:650:G:H2'	1:0:651:C:C6	2.50	0.47
1:0:1048:U:H2'	1:0:1049:G:C8	2.50	0.47
1:0:1652:A:H2'	1:0:1653:A:C8	2.50	0.47
1:0:1667:G:H5''	1:0:1668:C:H5'	1.97	0.47
5:E:45:ASN:OD1	5:E:45:ASN:N	2.47	0.47
13:M:24:LYS:HB2	13:M:28:THR:HB	1.97	0.47
20:T:3:MET:O	20:T:91:PHE:HA	2.14	0.47
22:V:123:GLU:OE2	22:V:123:GLU:N	2.45	0.47
29:i:12:ARG:HG2	29:i:13:THR:HG23	1.97	0.47
1:0:1022:G:H2'	1:0:1023:G:C8	2.47	0.47
1:0:1672:U:OP2	4:A:9:LYS:NZ	2.47	0.47
1:0:1904:C:C2	1:0:1905:A:C8	3.02	0.47
11:K:11:THR:HB	11:K:15:LEU:HD12	1.97	0.47
1:0:1272:U:H2'	1:0:1273:A:C4	2.50	0.47
1:0:1457:U:H2'	1:0:1458:C:C6	2.50	0.47
1:0:1511:U:H2'	1:0:1512:C:C6	2.51	0.47
9:I:179:ASN:O	9:I:182:GLU:HG3	2.15	0.47
1:0:2320:U:H2'	1:0:2321:C:C6	2.50	0.46
1:0:554:C:O2'	1:0:555:A:OP1	2.27	0.46
1:0:2289:C:OP2	11:K:4:SER:OG	2.25	0.46
22:V:233:TRP:HD1	22:V:236:ARG:HD2	1.79	0.46
1:0:543:G:H2'	1:0:544:A:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1098:A:H2'	1:0:1099:A:H8	1.78	0.46
1:0:1276:U:H1'	1:0:1277:A:C8	2.51	0.46
1:0:1919:G:H2'	1:0:1920:A:C8	2.50	0.46
29:i:68:GLN:O	29:i:72:GLU:HG3	2.14	0.46
1:0:1515:G:H2'	1:0:1516:C:O4'	2.15	0.46
1:0:1542:A:H2'	1:0:1543:C:C6	2.50	0.46
1:0:2252:C:C2	1:0:2253:A:C8	3.04	0.46
1:0:2394:G:H2'	1:0:2395:U:C6	2.50	0.46
15:O:98:GLN:NE2	15:O:102:ASP:OD2	2.41	0.46
20:T:11:CYS:HB2	20:T:20:HIS:CE1	2.51	0.46
28:d:49:GLU:O	28:d:53:THR:OG1	2.34	0.46
1:0:934:U:H2'	1:0:935:C:C6	2.50	0.46
1:0:1362:C:H2'	1:0:1363:U:C6	2.51	0.46
1:0:2338:A:H5'	1:0:2339:C:H5	1.79	0.46
1:0:1268:G:H2'	1:0:1269:U:C6	2.49	0.46
1:0:280:A:C6	1:0:379:U:O4	2.68	0.46
1:0:641:C:H2'	1:0:642:C:C6	2.51	0.46
1:0:643:A:H2'	1:0:644:U:C6	2.51	0.46
1:0:657:A:H2'	1:0:658:C:C6	2.50	0.46
1:0:668:U:C5	1:0:685:G:C5	3.04	0.46
24:X:12:PRO:HB2	24:X:163:GLU:HG3	1.96	0.46
1:0:47:A:H2'	1:0:48:G:C8	2.51	0.46
1:0:182:G:H2'	7:G:192:ARG:HD2	1.97	0.46
1:0:532:G:H2'	1:0:533:G:H8	1.81	0.46
1:0:1295:G:N7	29:i:7:ARG:NH1	2.63	0.46
1:0:2440:A:H2'	1:0:2441:U:C6	2.51	0.46
1:0:2620:G:H2'	1:0:2621:U:C6	2.51	0.46
1:0:1839:U:H2'	1:0:1840:A:C8	2.50	0.46
1:0:531:U:H2'	1:0:532:G:H8	1.81	0.46
1:0:2355:A:H2'	1:0:2356:G:H8	1.80	0.46
22:V:181:ASP:O	22:V:185:GLU:HG2	2.15	0.46
1:0:132:C:O2'	1:0:133:A:H5''	2.16	0.45
1:0:490:A:OP2	14:N:82:LYS:NZ	2.47	0.45
1:0:806:C:H2'	1:0:807:G:O4'	2.16	0.45
1:0:1299:U:H2'	1:0:1300:A:H8	1.80	0.45
21:U:63:ASP:OD1	21:U:63:ASP:N	2.49	0.45
1:0:1299:U:H2'	1:0:1300:A:C8	2.52	0.45
1:0:1791:U:H3'	1:0:1792:A:C8	2.49	0.45
1:0:1947:A:O2'	1:0:1950:A:N6	2.34	0.45
1:0:2320:U:H2'	1:0:2321:C:H6	1.81	0.45
2:9:95:C:H2'	2:9:96:U:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:220:VAL:O	23:W:248:ARG:NH2	2.49	0.45
28:d:13:THR:HG23	28:d:16:GLU:OE2	2.15	0.45
1:0:159:A:H2'	1:0:160:C:C6	2.51	0.45
1:0:879:G:H5'	1:0:880:G:OP1	2.16	0.45
1:0:1317:A:H2'	1:0:1318:C:C6	2.52	0.45
1:0:1375:A:O2'	1:0:1717:G:N7	2.43	0.45
7:G:42:GLU:OE1	7:G:42:GLU:HA	2.16	0.45
12:L:5:TYR:CZ	12:L:16:LYS:HD3	2.51	0.45
1:0:252:C:N4	1:0:272:G:O6	2.50	0.45
1:0:404:C:H2'	1:0:405:C:H6	1.81	0.45
1:0:713:G:H2'	1:0:714:U:C6	2.51	0.45
1:0:1570:C:H2'	1:0:1571:A:C8	2.52	0.45
12:L:126:ARG:HA	12:L:126:ARG:HD2	1.86	0.45
1:0:11:G:O2'	1:0:12:G:O5'	2.33	0.45
1:0:1467:A:H2'	1:0:1468:U:C6	2.52	0.45
1:0:2859:U:H4'	1:0:2860:A:H5'	1.99	0.45
6:F:72:ALA:HB3	6:F:87:MET:HE1	1.99	0.45
1:0:379:U:O2'	1:0:380:C:H6	1.98	0.45
1:0:2489:C:H2'	1:0:2490:A:H8	1.82	0.45
2:9:116:G:H2'	2:9:117:C:C6	2.52	0.45
4:A:6:LYS:O	4:A:10:LYS:HG3	2.17	0.45
17:Q:224:ASN:OD1	17:Q:224:ASN:N	2.50	0.45
1:0:2508:C:H2'	1:0:2509:G:O4'	2.17	0.45
22:V:90:GLN:N	22:V:139:ASP:OD2	2.49	0.45
24:X:105:GLU:OE1	24:X:105:GLU:N	2.45	0.45
30:f:63:GLU:H	30:f:63:GLU:CD	2.24	0.45
1:0:1870:G:O2'	1:0:1871:G:H5'	2.17	0.45
24:X:9:MET:HE3	24:X:9:MET:HB2	1.61	0.45
25:Y:165:ASP:N	25:Y:165:ASP:OD1	2.50	0.45
1:0:1510:U:H2'	1:0:1511:U:C6	2.52	0.45
22:V:76:GLU:OE1	22:V:288:TYR:OH	2.22	0.45
23:W:187:LYS:HD3	23:W:188:TYR:CE2	2.52	0.45
26:b:73:LYS:O	26:b:136:SER:OG	2.29	0.45
1:0:1634:G:H2'	1:0:1635:G:O4'	2.17	0.45
1:0:2134:G:N2	1:0:2229:C:OP2	2.49	0.45
1:0:2704:U:H2'	1:0:2705:G:C8	2.51	0.45
23:W:58:ALA:O	23:W:79:ARG:NH2	2.49	0.45
28:d:20:GLU:OE1	28:d:24:LEU:HG	2.16	0.45
30:f:84:ASP:OD1	30:f:86:THR:HG22	2.17	0.45
1:0:288:U:H4'	1:0:289:A:H5'	1.98	0.44
10:J:5:LYS:HE2	10:J:5:LYS:HB2	1.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:11:G:H2'	1:0:11:G:N3	2.31	0.44
1:0:532:G:H2'	1:0:533:G:C8	2.52	0.44
1:0:1761:A:H2'	1:0:1762:A:C8	2.53	0.44
1:0:2313:A:C2	20:T:4:PRO:HG3	2.52	0.44
1:0:2366:A:H2'	1:0:2367:A:H8	1.82	0.44
1:0:304:C:H2'	1:0:305:A:C8	2.49	0.44
1:0:1678:G:HO2'	1:0:1717:G:HO2'	1.65	0.44
15:O:154:ARG:HG2	15:O:154:ARG:NH1	2.31	0.44
1:0:2342:G:OP1	24:X:16:LYS:NZ	2.47	0.44
2:9:27:A:H2'	2:9:28:C:C6	2.51	0.44
23:W:187:LYS:HD3	23:W:188:TYR:CZ	2.52	0.44
1:0:417:G:H2'	1:0:418:C:H6	1.80	0.44
1:0:1710:A:H4'	10:J:56:LYS:HG2	2.00	0.44
1:0:1749:A:H2'	1:0:1750:G:O4'	2.17	0.44
1:0:2048:A:H2'	1:0:2049:C:H6	1.83	0.44
1:0:2717:U:H2'	1:0:2718:G:O4'	2.18	0.44
5:E:41:ILE:HD11	5:E:49:VAL:HG21	1.98	0.44
24:X:157:ASP:HA	24:X:161:PHE:CD1	2.53	0.44
1:0:1017:C:H2'	1:0:1018:U:C6	2.52	0.44
1:0:1589:C:OP2	10:J:121:ARG:HD2	2.17	0.44
1:0:1649:U:H3	18:R:48:GLU:HG2	1.82	0.44
1:0:713:G:H2'	1:0:714:U:H6	1.81	0.44
1:0:2366:A:H2'	1:0:2367:A:C8	2.53	0.44
1:0:2385:C:H2'	1:0:2386:C:O4'	2.18	0.44
9:I:80:PRO:HB3	9:I:173:PHE:HD2	1.82	0.44
22:V:54:MET:HE3	22:V:54:MET:HB2	1.83	0.44
1:0:1530:G:H2'	1:0:1531:C:C6	2.52	0.44
1:0:1843:U:H2'	1:0:1844:G:H8	1.82	0.44
1:0:2259:A:H2'	1:0:2260:G:H8	1.82	0.44
1:0:2696:A:H2	25:Y:111:GLU:HG2	1.83	0.44
1:0:2893:G:H2'	1:0:2894:C:O4'	2.17	0.44
2:9:23:U:H3'	2:9:24:U:O2	2.17	0.44
6:F:62:HIS:H	6:F:62:HIS:CD2	2.34	0.44
9:I:159:LEU:HD23	9:I:160:TYR:CD1	2.53	0.44
14:N:67:ASP:OD1	14:N:69:THR:N	2.51	0.44
1:0:2799:C:H2'	1:0:2800:A:H8	1.82	0.44
1:0:635:A:N3	1:0:2066:G:O2'	2.50	0.43
1:0:1418:U:H2'	1:0:1419:C:H6	1.81	0.43
1:0:1955:C:O2'	1:0:1956:C:H5'	2.18	0.43
1:0:2658:A:N3	1:0:2658:A:H2'	2.32	0.43
22:V:33:ASP:HB3	22:V:169:GLY:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:276:GLY:O	22:V:292:ASP:HA	2.18	0.43
1:0:87:A:C2	1:0:105:A:C5	3.06	0.43
1:0:638:G:O2'	1:0:1354:A:OP1	2.36	0.43
1:0:1961:A:H2'	1:0:1962:A:H8	1.82	0.43
1:0:2053:A:H2'	1:0:2054:C:C6	2.54	0.43
6:F:78:LYS:HE3	6:F:78:LYS:HB2	1.87	0.43
10:J:144:ASN:OD1	10:J:144:ASN:C	2.60	0.43
15:O:3:ALA:O	15:O:54:HIS:HA	2.17	0.43
29:i:80:ASP:OD1	29:i:80:ASP:C	2.61	0.43
1:0:1366:G:OP1	12:L:65:SER:HB3	2.19	0.43
2:9:119:C:H2'	2:9:120:C:O4'	2.19	0.43
25:Y:150:GLU:OE2	25:Y:169:ILE:HG13	2.18	0.43
1:0:509:U:H2'	1:0:510:G:O4'	2.18	0.43
1:0:1272:U:H2'	1:0:1273:A:N3	2.33	0.43
1:0:1559:C:H2'	1:0:1560:C:H6	1.82	0.43
1:0:1796:C:H2'	1:0:1797:A:C8	2.53	0.43
1:0:2496:A:H5''	1:0:2504:A:C6	2.52	0.43
5:E:113:ALA:O	5:E:116:VAL:HG12	2.17	0.43
6:F:153:ARG:HA	6:F:156:TYR:CE2	2.54	0.43
9:I:129:GLU:C	9:I:130:ILE:HD13	2.44	0.43
1:0:1377:A:N6	1:0:1398:A:H4'	2.33	0.43
1:0:1958:C:H2'	1:0:1959:U:C6	2.53	0.43
1:0:2000:A:N3	1:0:2620:G:O2'	2.51	0.43
24:X:107:HIS:O	24:X:113:GLN:NE2	2.51	0.43
1:0:1490:C:H2'	1:0:1491:U:C6	2.53	0.43
1:0:2407:A:H2'	1:0:2408:A:C8	2.54	0.43
1:0:2728:U:H2'	1:0:2729:C:C6	2.53	0.43
19:S:5:GLY:O	19:S:9:GLN:HG2	2.19	0.43
22:V:60:ASP:OD1	22:V:60:ASP:N	2.52	0.43
24:X:29:GLU:O	24:X:32:LYS:HG3	2.18	0.43
27:c:2:SER:OG	27:c:3:ILE:N	2.51	0.43
1:0:297:U:O2	1:0:365:G:N1	2.52	0.43
12:L:22:ARG:HA	12:L:23:PRO:HD3	1.90	0.43
12:L:147:ILE:O	12:L:147:ILE:HG13	2.19	0.43
26:b:126:ASN:HD22	26:b:127:ILE:N	2.16	0.43
28:d:27:GLU:HG2	28:d:50:LEU:HD11	2.01	0.43
1:0:11:G:H2'	1:0:12:G:H8	1.83	0.43
1:0:562:U:H2'	1:0:563:C:C6	2.54	0.43
1:0:1796:C:H2'	1:0:1797:A:H8	1.83	0.43
18:R:54:ASN:OD1	18:R:55:GLU:N	2.51	0.43
1:0:802:G:H2'	1:0:803:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:50:ILE:HG12	6:F:167:VAL:HG22	2.01	0.43
1:0:642:C:OP2	17:Q:132:ARG:NH1	2.49	0.42
1:0:709:C:H2'	1:0:710:G:O4'	2.18	0.42
1:0:1084:C:H2'	1:0:1085:C:H6	1.84	0.42
1:0:2489:C:H2'	1:0:2490:A:C8	2.54	0.42
2:9:116:G:H2'	2:9:117:C:H6	1.84	0.42
17:Q:92:ARG:HG3	17:Q:92:ARG:HH11	1.84	0.42
29:i:6:ARG:HE	29:i:6:ARG:HB3	1.69	0.42
1:0:860:C:H2'	1:0:861:U:H6	1.84	0.42
1:0:1068:A:H2'	1:0:1069:C:C6	2.54	0.42
1:0:2850:C:H2'	1:0:2851:U:H6	1.84	0.42
1:0:612:A:O2'	1:0:1320:G:OP1	2.34	0.42
1:0:768:A:HO2'	1:0:769:A:H8	1.59	0.42
1:0:1206:C:H2'	1:0:1207:G:H8	1.83	0.42
1:0:1895:G:H2'	1:0:1896:U:O4'	2.20	0.42
1:0:2762:C:H2'	1:0:2763:A:O4'	2.19	0.42
2:9:7:G:OP1	9:I:24:ARG:NH1	2.52	0.42
1:0:297:U:O2'	1:0:364:A:N1	2.44	0.42
1:0:855:C:H2'	1:0:856:G:O4'	2.19	0.42
1:0:1520:A:O2'	1:0:1521:A:N3	2.44	0.42
1:0:2466:U:O2'	1:0:2468:C:OP1	2.31	0.42
1:0:2768:A:H2'	1:0:2769:A:C8	2.54	0.42
16:P:42:PHE:O	16:P:77:ARG:NH1	2.52	0.42
1:0:131:C:O2'	1:0:132:C:H5'	2.19	0.42
1:0:951:U:H4'	11:K:96:GLN:HB2	2.02	0.42
1:0:1131:G:C6	1:0:1226:G:N2	2.88	0.42
1:0:2046:G:H4'	12:L:137:TRP:CE2	2.55	0.42
1:0:2229:C:H4'	1:0:2230:G:OP1	2.18	0.42
12:L:17:GLY:HA3	12:L:96:VAL:HG22	2.01	0.42
12:L:122:GLU:HG2	12:L:138:ASN:HB3	2.00	0.42
24:X:46:VAL:HG23	24:X:68:LYS:O	2.20	0.42
25:Y:10:ASP:HB2	25:Y:11:GLU:H	1.76	0.42
1:0:305:A:H2'	1:0:306:C:C6	2.55	0.42
1:0:368:C:C2	1:0:369:C:C5	3.08	0.42
1:0:651:C:H2'	1:0:652:A:C8	2.54	0.42
1:0:1790:A:H5''	1:0:1790:A:H8	1.85	0.42
1:0:1828:U:OP2	1:0:1833:A:N6	2.44	0.42
1:0:1857:C:OP1	7:G:76:GLN:HG2	2.20	0.42
18:R:26:ARG:HD2	18:R:26:ARG:HA	1.75	0.42
1:0:2057:U:H2'	1:0:2058:C:H6	1.84	0.42
1:0:2318:U:H2'	1:0:2319:U:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2416:C:H2'	1:0:2417:U:C6	2.55	0.42
1:0:2425:C:H2'	1:0:2426:U:C6	2.55	0.42
2:9:2:A:H1'	2:9:3:C:OP2	2.19	0.42
8:H:61:VAL:HG12	8:H:115:ILE:O	2.19	0.42
25:Y:10:ASP:HB2	25:Y:11:GLU:OE2	2.19	0.42
1:0:909:A:H2'	1:0:910:A:H8	1.85	0.42
1:0:936:U:H2'	1:0:937:G:H8	1.84	0.42
1:0:1032:G:H8	1:0:1032:G:OP2	2.02	0.42
14:N:16:PRO:O	14:N:20:ARG:HG3	2.20	0.42
22:V:95:MET:HE3	22:V:95:MET:HB3	1.83	0.42
29:i:84:GLU:OE1	29:i:84:GLU:N	2.53	0.42
1:0:860:C:H2'	1:0:861:U:C6	2.55	0.42
1:0:2857:U:H2'	1:0:2858:G:O4'	2.19	0.42
18:R:84:LEU:HD12	18:R:84:LEU:HA	1.90	0.42
29:i:36:ARG:NH2	29:i:45:GLU:O	2.49	0.42
1:0:303:U:H2'	1:0:304:C:C6	2.55	0.41
1:0:369:C:H1'	1:0:370:C:H5	1.85	0.41
1:0:1061:C:H2'	1:0:1062:U:C6	2.55	0.41
1:0:1520:A:O2'	1:0:1521:A:H5'	2.19	0.41
2:9:76:A:H8	2:9:76:A:OP1	2.02	0.41
2:9:95:C:H2'	2:9:96:U:C6	2.55	0.41
5:E:80:THR:OG1	5:E:83:ASP:OD2	2.27	0.41
9:I:78:ASN:O	9:I:81:SER:OG	2.37	0.41
9:I:168:ASN:OD1	9:I:168:ASN:N	2.46	0.41
14:N:67:ASP:OD1	14:N:67:ASP:C	2.63	0.41
1:0:631:G:H2'	1:0:2064:C:C5	2.56	0.41
1:0:1140:G:H2'	1:0:1141:A:H8	1.84	0.41
1:0:1458:C:H2'	1:0:1459:U:C6	2.55	0.41
1:0:1671:G:OP1	4:A:9:LYS:HE2	2.21	0.41
1:0:2577:G:C2	1:0:2578:G:N7	2.89	0.41
10:J:81:ARG:HG2	10:J:88:ARG:CZ	2.49	0.41
16:P:11:VAL:HG22	16:P:73:VAL:HG12	2.01	0.41
25:Y:3:ARG:NH1	25:Y:51:GLU:OE1	2.51	0.41
1:0:1018:U:O2'	1:0:2296:A:N7	2.48	0.41
1:0:1241:U:OP2	26:b:47:THR:OG1	2.36	0.41
1:0:1936:C:O4'	21:U:212:PRO:HA	2.20	0.41
1:0:2591:U:H5''	30:f:36:GLY:HA2	2.02	0.41
6:F:99:GLU:HG2	6:F:101:LYS:CG	2.50	0.41
11:K:22:ARG:H	11:K:22:ARG:HG2	1.67	0.41
13:M:54:GLU:HG3	13:M:58:ARG:HH22	1.83	0.41
22:V:147:THR:O	22:V:160:PRO:HB3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:9:ASN:OD1	23:W:9:ASN:C	2.62	0.41
1:0:139:A:H2'	1:0:140:U:C6	2.55	0.41
1:0:625:C:H2'	1:0:626:G:C8	2.55	0.41
1:0:863:U:H2'	1:0:864:G:N7	2.35	0.41
1:0:934:U:H2'	1:0:935:C:H6	1.85	0.41
1:0:1519:U:C2	1:0:1520:A:O4'	2.72	0.41
1:0:1996:U:H4'	1:0:1997:U:H5	1.85	0.41
1:0:2825:A:C4	1:0:2826:C:C5	3.08	0.41
15:O:144:GLU:OE1	15:O:144:GLU:N	2.39	0.41
26:b:132:LEU:HD23	26:b:132:LEU:HA	1.87	0.41
27:c:10:THR:H	27:c:13:ALA:HB3	1.84	0.41
30:f:46:LYS:HA	30:f:46:LYS:HD3	1.69	0.41
1:0:577:A:H2'	1:0:578:G:H8	1.85	0.41
1:0:1047:G:H2'	1:0:1048:U:C6	2.56	0.41
1:0:1790:A:H5''	1:0:1790:A:C8	2.55	0.41
1:0:2757:C:H2'	1:0:2758:A:H8	1.85	0.41
9:I:94:LEU:HD23	9:I:94:LEU:HA	1.89	0.41
21:U:224:LYS:HD2	21:U:228:ILE:HG23	2.02	0.41
27:c:24:GLN:NE2	27:c:62:LYS:HD3	2.36	0.41
1:0:11:G:H2'	1:0:12:G:C8	2.54	0.41
1:0:1070:C:H2'	1:0:1071:G:O4'	2.19	0.41
27:c:8:LEU:HD12	27:c:8:LEU:HA	1.86	0.41
29:i:55:PRO:HD2	29:i:58:LEU:HD12	2.03	0.41
1:0:923:G:H4'	1:0:926:G:N1	2.35	0.41
1:0:1053:G:O2'	1:0:2293:A:OP2	2.39	0.41
1:0:1417:C:H2'	1:0:1418:U:C6	2.56	0.41
1:0:2658:A:O3'	1:0:2659:A:H3'	2.21	0.41
6:F:42:ASP:OD1	6:F:42:ASP:C	2.64	0.41
10:J:106:LEU:HD23	10:J:106:LEU:HA	1.92	0.41
22:V:159:LYS:HA	22:V:160:PRO:HD3	1.91	0.41
1:0:790:G:H2'	1:0:791:C:C6	2.55	0.41
1:0:822:G:O2'	1:0:858:G:H4'	2.20	0.41
1:0:1243:A:O2'	1:0:1244:A:H3'	2.21	0.41
1:0:1888:A:C2	1:0:1889:G:C8	3.09	0.41
1:0:2129:G:H2'	1:0:2130:A:C8	2.48	0.41
1:0:2245:C:C5	1:0:2246:G:H1'	2.56	0.41
1:0:2538:U:H2'	1:0:2539:U:C6	2.56	0.41
1:0:2864:G:H2'	1:0:2865:U:C6	2.55	0.41
25:Y:101:ASP:OD1	25:Y:101:ASP:C	2.63	0.41
1:0:586:U:H2'	1:0:587:C:H6	1.86	0.41
1:0:602:G:H2'	1:0:603:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:707:G:H2'	1:0:708:C:H6	1.85	0.41
1:0:749:G:H2'	1:0:750:C:C6	2.56	0.41
1:0:1149:A:N3	1:0:1149:A:H2'	2.36	0.41
1:0:1519:U:C4	1:0:1520:A:H1'	2.55	0.41
1:0:1755:U:H2'	1:0:1756:C:H6	1.84	0.41
2:9:91:G:H2'	2:9:92:A:C8	2.56	0.41
11:K:72:PHE:CE1	11:K:89:PRO:HG3	2.54	0.41
27:c:10:THR:O	27:c:14:MET:HG2	2.21	0.41
1:0:577:A:H2'	1:0:578:G:C8	2.56	0.41
1:0:1452:C:H2'	1:0:1453:U:C6	2.56	0.41
1:0:1517:A:O2'	1:0:1518:A:H5'	2.21	0.41
2:9:74:U:H2'	2:9:75:C:O4'	2.20	0.41
30:f:4:LEU:HA	30:f:119:GLU:OE1	2.21	0.41
1:0:118:C:H2'	1:0:119:G:O4'	2.21	0.40
1:0:1472:A:H2'	1:0:1473:A:H8	1.85	0.40
1:0:1951:U:O2'	1:0:1952:G:H5'	2.21	0.40
1:0:2135:G:H2'	1:0:2136:U:C5	2.55	0.40
1:0:2336:G:H1'	1:0:2337:A:N7	2.37	0.40
1:0:2620:G:H2'	1:0:2621:U:H6	1.86	0.40
5:E:119:LEU:HD23	5:E:119:LEU:HA	1.83	0.40
6:F:17:TYR:H	6:F:95:HIS:CE1	2.39	0.40
17:Q:92:ARG:HG3	17:Q:92:ARG:NH1	2.35	0.40
1:0:152:A:H2'	1:0:153:U:C6	2.57	0.40
1:0:291:C:C5	1:0:292:G:H1'	2.56	0.40
1:0:625:C:H2'	1:0:626:G:H8	1.86	0.40
1:0:1498:U:H2'	1:0:1499:A:O4'	2.22	0.40
1:0:2630:A:N3	1:0:2630:A:H3'	2.36	0.40
1:0:2809:A:H5''	1:0:2810:A:H5'	2.01	0.40
8:H:21:GLU:C	8:H:21:GLU:OE2	2.64	0.40
9:I:12:ARG:O	9:I:16:GLU:HG3	2.21	0.40
23:W:152:LYS:HB3	23:W:152:LYS:HE2	1.84	0.40
25:Y:94:MET:H	25:Y:94:MET:HG2	1.61	0.40
30:f:110:LYS:H	30:f:110:LYS:HG2	1.79	0.40
30:f:123:SER:O	30:f:127:THR:HG22	2.21	0.40
1:0:13:C:H2'	1:0:14:U:H6	1.85	0.40
1:0:504:G:H21	12:L:99:ASN:HD21	1.69	0.40
1:0:1632:G:H2'	1:0:1633:C:C6	2.56	0.40
1:0:1735:U:O2'	1:0:2716:G:H4'	2.21	0.40
1:0:2728:U:H2'	1:0:2729:C:H6	1.86	0.40
2:9:27:A:OP2	9:I:40:SER:HB2	2.21	0.40
5:E:21:LEU:HD22	5:E:50:LEU:HD22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:37:ALA:HB1	18:R:68:PRO:HG3	2.03	0.40
21:U:133:ARG:HG2	21:U:133:ARG:HH11	1.87	0.40
25:Y:36:TYR:CG	25:Y:62:THR:HG21	2.56	0.40
1:0:808:A:N3	1:0:808:A:H2'	2.37	0.40
1:0:1571:A:H2'	1:0:1572:C:H6	1.86	0.40
1:0:2289:C:H2'	1:0:2290:U:H6	1.85	0.40
9:I:94:LEU:HD11	9:I:127:GLY:HA3	2.02	0.40
10:J:90:ASN:HD21	10:J:92:LYS:HB3	1.86	0.40
26:b:6:PHE:O	26:b:109:TYR:OH	2.32	0.40
1:0:298:G:O2'	1:0:299:G:OP2	2.35	0.40
1:0:300:A:H2'	1:0:302:U:H5''	2.03	0.40
1:0:405:C:H2'	1:0:406:U:C6	2.56	0.40
1:0:567:C:H2'	1:0:568:G:O4'	2.21	0.40
1:0:773:A:H2'	1:0:774:A:H8	1.82	0.40
1:0:850:C:H2'	1:0:851:C:C6	2.56	0.40
1:0:1919:G:H2'	1:0:1920:A:H8	1.87	0.40
12:L:129:ARG:HG3	12:L:135:ASP:OD2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	e	55/58 (95%)	55 (100%)	0	0	100	100
4	A	47/50 (94%)	45 (96%)	2 (4%)	0	100	100
5	E	117/120 (98%)	116 (99%)	1 (1%)	0	100	100
6	F	160/176 (91%)	158 (99%)	2 (1%)	0	100	100
7	G	192/196 (98%)	188 (98%)	4 (2%)	0	100	100
8	H	113/116 (97%)	113 (100%)	0	0	100	100
9	I	181/184 (98%)	178 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	145/151 (96%)	143 (99%)	2 (1%)	0	100	100
11	K	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
12	L	149/153 (97%)	147 (99%)	2 (1%)	0	100	100
13	M	56/67 (84%)	55 (98%)	1 (2%)	0	100	100
14	N	112/118 (95%)	109 (97%)	3 (3%)	0	100	100
15	O	152/154 (99%)	151 (99%)	1 (1%)	0	100	100
16	P	87/92 (95%)	87 (100%)	0	0	100	100
17	Q	140/234 (60%)	140 (100%)	0	0	100	100
18	R	78/89 (88%)	75 (96%)	3 (4%)	0	100	100
19	S	55/58 (95%)	54 (98%)	1 (2%)	0	100	100
20	T	91/93 (98%)	90 (99%)	1 (1%)	0	100	100
21	U	233/241 (97%)	217 (93%)	14 (6%)	2 (1%)	14	16
22	V	335/338 (99%)	331 (99%)	4 (1%)	0	100	100
23	W	246/248 (99%)	240 (98%)	6 (2%)	0	100	100
24	X	167/172 (97%)	156 (93%)	11 (7%)	0	100	100
25	Y	172/178 (97%)	170 (99%)	2 (1%)	0	100	100
26	b	142/145 (98%)	140 (99%)	2 (1%)	0	100	100
27	c	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
28	d	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
29	i	152/168 (90%)	149 (98%)	3 (2%)	0	100	100
30	f	130/132 (98%)	127 (98%)	3 (2%)	0	100	100
All	All	3747/3980 (94%)	3669 (98%)	76 (2%)	2 (0%)	49	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	U	213	LYS
21	U	229	ALA

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	e	48/49 (98%)	47 (98%)	1 (2%)	47	60
4	A	45/46 (98%)	43 (96%)	2 (4%)	25	35
5	E	93/94 (99%)	92 (99%)	1 (1%)	65	75
6	F	140/147 (95%)	139 (99%)	1 (1%)	76	83
7	G	161/163 (99%)	161 (100%)	0	100	100
8	H	98/99 (99%)	96 (98%)	2 (2%)	48	62
9	I	144/145 (99%)	143 (99%)	1 (1%)	76	83
10	J	117/121 (97%)	112 (96%)	5 (4%)	26	36
11	K	77/78 (99%)	77 (100%)	0	100	100
12	L	122/124 (98%)	120 (98%)	2 (2%)	55	68
13	M	48/55 (87%)	47 (98%)	1 (2%)	47	60
14	N	98/102 (96%)	95 (97%)	3 (3%)	35	47
15	O	132/132 (100%)	131 (99%)	1 (1%)	73	81
16	P	78/80 (98%)	75 (96%)	3 (4%)	29	41
17	Q	120/191 (63%)	120 (100%)	0	100	100
18	R	61/68 (90%)	59 (97%)	2 (3%)	33	45
19	S	48/49 (98%)	48 (100%)	0	100	100
20	T	77/77 (100%)	77 (100%)	0	100	100
21	U	183/186 (98%)	179 (98%)	4 (2%)	45	59
22	V	277/278 (100%)	276 (100%)	1 (0%)	84	89
23	W	198/198 (100%)	196 (99%)	2 (1%)	68	77
24	X	141/147 (96%)	137 (97%)	4 (3%)	38	51
25	Y	149/151 (99%)	145 (97%)	4 (3%)	39	52
26	b	122/123 (99%)	119 (98%)	3 (2%)	42	54
27	c	75/76 (99%)	74 (99%)	1 (1%)	61	72
28	d	55/56 (98%)	54 (98%)	1 (2%)	51	64
29	i	112/123 (91%)	110 (98%)	2 (2%)	51	64
30	f	106/106 (100%)	102 (96%)	4 (4%)	29	41
All	All	3125/3264 (96%)	3074 (98%)	51 (2%)	54	68

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	e	39	ILE
4	A	40	ARG
4	A	45	ARG
5	E	116	VAL
6	F	49	GLU
8	H	68	SER
8	H	104	GLU
9	I	8	LYS
10	J	56	LYS
10	J	71	SER
10	J	109	LEU
10	J	115	LEU
10	J	147	GLN
12	L	139	THR
12	L	147	ILE
13	M	28	THR
14	N	63	VAL
14	N	66	VAL
14	N	95	SER
15	O	91	ASP
16	P	11	VAL
16	P	50	ARG
16	P	66	SER
18	R	40	ASP
18	R	57	THR
21	U	14	SER
21	U	74	ILE
21	U	103	VAL
21	U	180	LYS
22	V	60	ASP
23	W	223	GLU
23	W	245	VAL
24	X	11	ASP
24	X	39	GLU
24	X	46	VAL
24	X	126	VAL
25	Y	10	ASP
25	Y	12	VAL
25	Y	21	LEU
25	Y	103	VAL
26	b	23	SER
26	b	30	VAL
26	b	105	VAL

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Mol	Chain	Res	Type
27	c	42	SER
28	d	13	THR
29	i	19	HIS
29	i	100	ASP
30	f	16	SER
30	f	29	LEU
30	f	119	GLU
30	f	132	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	42	ASN
6	F	100	ASN
7	G	123	GLN
7	G	153	ASN
8	H	101	GLN
8	H	111	ASN
9	I	108	ASN
9	I	114	ASN
9	I	120	GLN
10	J	89	GLN
10	J	90	ASN
10	J	147	GLN
11	K	68	GLN
12	L	95	ASN
12	L	99	ASN
12	L	103	GLN
12	L	114	HIS
14	N	4	GLN
14	N	23	GLN
14	N	44	ASN
14	N	93	GLN
15	O	12	ASN
15	O	49	ASN
15	O	54	HIS
16	P	24	HIS
16	P	37	HIS
16	P	62	HIS
17	Q	113	GLN
17	Q	121	GLN
19	S	9	GLN

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Mol	Chain	Res	Type
19	S	52	GLN
20	T	40	GLN
21	U	111	GLN
21	U	151	ASN
22	V	3	GLN
22	V	107	HIS
22	V	222	GLN
23	W	73	GLN
23	W	90	HIS
23	W	208	ASN
24	X	43	GLN
24	X	99	ASN
25	Y	75	HIS
25	Y	151	GLN
26	b	40	ASN
26	b	67	GLN
26	b	126	ASN
27	c	6	HIS
27	c	24	GLN
29	i	8	GLN
29	i	14	HIS
29	i	19	HIS
29	i	43	HIS
29	i	68	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2746/2916 (94%)	374 (13%)	20 (0%)
2	9	120/122 (98%)	16 (13%)	2 (1%)
All	All	2866/3038 (94%)	390 (13%)	22 (0%)

All (390) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	12	G
1	0	46	G
1	0	49	C
1	0	54	G
1	0	66	A
1	0	74	A

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Mol	Chain	Res	Type
1	0	77	A
1	0	78	G
1	0	94	U
1	0	95	G
1	0	120	A
1	0	121	A
1	0	122	U
1	0	127	A
1	0	133	A
1	0	134	C
1	0	135	A
1	0	138	A
1	0	144	C
1	0	147	G
1	0	148	C
1	0	149	G
1	0	158	A
1	0	173	A
1	0	176	A
1	0	192	G
1	0	193	A
1	0	198	A
1	0	199	A
1	0	200	A
1	0	203	A
1	0	205	U
1	0	206	C
1	0	207	C
1	0	211	A
1	0	226	G
1	0	227	C
1	0	244	G
1	0	260	U
1	0	263	G
1	0	276	A
1	0	277	C
1	0	278	G
1	0	284	C
1	0	285	C
1	0	287	A
1	0	288	U
1	0	291	C

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Mol	Chain	Res	Type
1	0	292	G
1	0	294	A
1	0	296	C
1	0	297	U
1	0	298	G
1	0	299	G
1	0	300	A
1	0	301	A
1	0	302	U
1	0	313	U
1	0	314	C
1	0	323	C
1	0	341	G
1	0	342	A
1	0	343	A
1	0	361	G
1	0	362	A
1	0	363	A
1	0	364	A
1	0	366	A
1	0	367	U
1	0	368	C
1	0	369	C
1	0	370	C
1	0	371	G
1	0	372	G
1	0	373	G
1	0	375	U
1	0	377	G
1	0	378	U
1	0	379	U
1	0	380	C
1	0	385	A
1	0	386	U
1	0	400	U
1	0	401	A
1	0	411	A
1	0	416	C
1	0	421	G
1	0	477	G
1	0	491	G
1	0	500	A

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Mol	Chain	Res	Type
1	0	501	A
1	0	502	A
1	0	515	A
1	0	518	G
1	0	519	C
1	0	537	U
1	0	541	G
1	0	542	C
1	0	543	G
1	0	555	A
1	0	557	G
1	0	563	C
1	0	585	U
1	0	592	G
1	0	605	G
1	0	608	G
1	0	624	A
1	0	633	A
1	0	636	A
1	0	664	A
1	0	678	A
1	0	683	C
1	0	692	A
1	0	703	U
1	0	706	G
1	0	718	U
1	0	719	G
1	0	722	C
1	0	736	U
1	0	737	C
1	0	738	A
1	0	761	C
1	0	779	U
1	0	807	G
1	0	808	A
1	0	809	A
1	0	823	C
1	0	837	U
1	0	842	U
1	0	843	A
1	0	859	A
1	0	864	G

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Mol	Chain	Res	Type
1	0	870	G
1	0	871	G
1	0	877	A
1	0	879	G
1	0	880	G
1	0	900	G
1	0	907	C
1	0	922	C
1	0	923	G
1	0	945	A
1	0	955	G
1	0	962	G
1	0	974	A
1	0	977	C
1	0	994	U
1	0	996	G
1	0	997	C
1	0	999	U
1	0	1000	C
1	0	1001	C
1	0	1008	A
1	0	1010	C
1	0	1032	G
1	0	1046	G
1	0	1053	G
1	0	1060	G
1	0	1061	C
1	0	1073	G
1	0	1078	A
1	0	1088	G
1	0	1089	A
1	0	1107	A
1	0	1110	U
1	0	1111	G
1	0	1120	G
1	0	1128	G
1	0	1134	U
1	0	1148	A
1	0	1206	C
1	0	1210	C
1	0	1211	G
1	0	1212	A

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Mol	Chain	Res	Type
1	0	1213	G
1	0	1235	C
1	0	1236	G
1	0	1239	A
1	0	1242	C
1	0	1273	A
1	0	1274	U
1	0	1276	U
1	0	1277	A
1	0	1278	G
1	0	1285	U
1	0	1286	C
1	0	1287	C
1	0	1288	G
1	0	1338	C
1	0	1355	U
1	0	1356	C
1	0	1391	C
1	0	1402	U
1	0	1403	A
1	0	1408	C
1	0	1431	U
1	0	1447	C
1	0	1481	A
1	0	1483	A
1	0	1487	A
1	0	1499	A
1	0	1500	U
1	0	1516	C
1	0	1517	A
1	0	1518	A
1	0	1519	U
1	0	1520	A
1	0	1521	A
1	0	1522	A
1	0	1523	A
1	0	1529	C
1	0	1584	G
1	0	1587	G
1	0	1595	G
1	0	1612	U
1	0	1621	A

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Mol	Chain	Res	Type
1	0	1629	U
1	0	1631	G
1	0	1636	U
1	0	1642	G
1	0	1648	G
1	0	1651	A
1	0	1677	A
1	0	1680	U
1	0	1685	C
1	0	1687	C
1	0	1688	A
1	0	1704	U
1	0	1705	A
1	0	1716	U
1	0	1717	G
1	0	1718	U
1	0	1719	C
1	0	1724	U
1	0	1725	C
1	0	1746	G
1	0	1747	C
1	0	1784	C
1	0	1790	A
1	0	1791	U
1	0	1792	A
1	0	1812	G
1	0	1813	G
1	0	1822	A
1	0	1825	G
1	0	1849	C
1	0	1860	G
1	0	1866	G
1	0	1872	U
1	0	1882	C
1	0	1903	A
1	0	1912	A
1	0	1943	G
1	0	1944	G
1	0	1946	A
1	0	1947	A
1	0	1948	C
1	0	1949	U

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Mol	Chain	Res	Type
1	0	1951	U
1	0	1952	G
1	0	1953	A
1	0	1955	C
1	0	1956	C
1	0	1957	U
1	0	1958	C
1	0	1959	U
1	0	1960	U
1	0	1961	A
1	0	1964	G
1	0	1971	A
1	0	1972	G
1	0	1974	A
1	0	1988	G
1	0	1989	U
1	0	1997	U
1	0	1998	G
1	0	2001	U
1	0	2004	A
1	0	2006	G
1	0	2027	U
1	0	2057	U
1	0	2065	G
1	0	2066	G
1	0	2067	A
1	0	2073	G
1	0	2085	G
1	0	2089	A
1	0	2094	A
1	0	2095	G
1	0	2096	A
1	0	2103	A
1	0	2130	A
1	0	2132	G
1	0	2133	U
1	0	2134	G
1	0	2136	U
1	0	2227	U
1	0	2228	G
1	0	2229	C
1	0	2230	G

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Mol	Chain	Res	Type
1	0	2236	C
1	0	2244	G
1	0	2246	G
1	0	2251	A
1	0	2264	G
1	0	2265	G
1	0	2284	A
1	0	2296	A
1	0	2306	C
1	0	2310	C
1	0	2314	A
1	0	2332	U
1	0	2333	C
1	0	2334	G
1	0	2335	G
1	0	2336	G
1	0	2338	A
1	0	2347	A
1	0	2349	A
1	0	2353	C
1	0	2362	A
1	0	2378	G
1	0	2413	G
1	0	2415	U
1	0	2432	G
1	0	2455	G
1	0	2460	A
1	0	2463	A
1	0	2469	C
1	0	2473	G
1	0	2476	A
1	0	2496	A
1	0	2501	C
1	0	2502	A
1	0	2526	C
1	0	2530	G
1	0	2531	A
1	0	2546	A
1	0	2548	C
1	0	2557	G
1	0	2563	G
1	0	2582	U

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Mol	Chain	Res	Type
1	0	2594	A
1	0	2595	G
1	0	2601	C
1	0	2606	G
1	0	2610	G
1	0	2627	G
1	0	2643	U
1	0	2658	A
1	0	2659	A
1	0	2674	A
1	0	2675	C
1	0	2691	G
1	0	2709	G
1	0	2740	G
1	0	2741	U
1	0	2743	G
1	0	2761	G
1	0	2776	A
1	0	2785	A
1	0	2793	A
1	0	2804	A
1	0	2807	A
1	0	2812	U
1	0	2818	U
1	0	2820	A
1	0	2830	U
1	0	2843	C
1	0	2869	G
1	0	2883	A
1	0	2889	G
1	0	2896	C
1	0	2902	G
2	9	3	C
2	9	4	G
2	9	7	G
2	9	23	U
2	9	27	A
2	9	33	A
2	9	39	C
2	9	42	G
2	9	54	U
2	9	56	A

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Mol	Chain	Res	Type
2	9	65	G
2	9	76	A
2	9	77	G
2	9	93	U
2	9	112	C
2	9	113	G

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	360	G
1	0	372	G
1	0	499	A
1	0	500	A
1	0	554	C
1	0	736	U
1	0	808	A
1	0	879	G
1	0	961	C
1	0	996	G
1	0	1127	C
1	0	1272	U
1	0	1518	A
1	0	1520	A
1	0	2133	U
1	0	2229	C
1	0	2243	G
1	0	2337	A
1	0	2784	U
1	0	2842	U
2	9	2	A
2	9	22	G

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

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

5.5 Carbohydrates [\(i\)](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 279 ligands modelled in this entry, 279 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

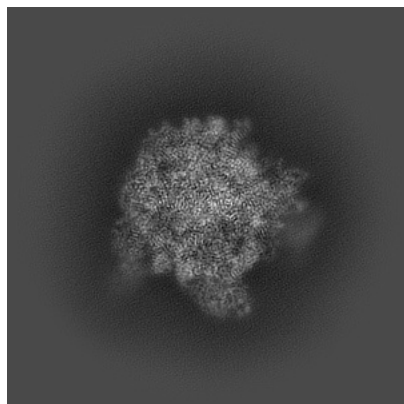
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62894. These allow visual inspection of the internal detail of the map and identification of artifacts.

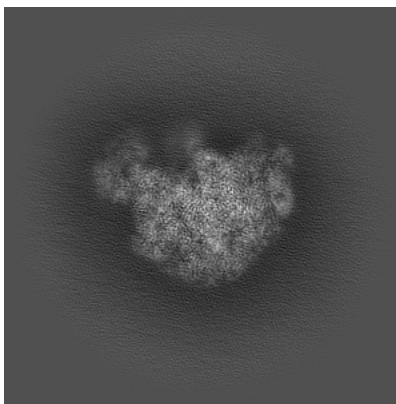
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

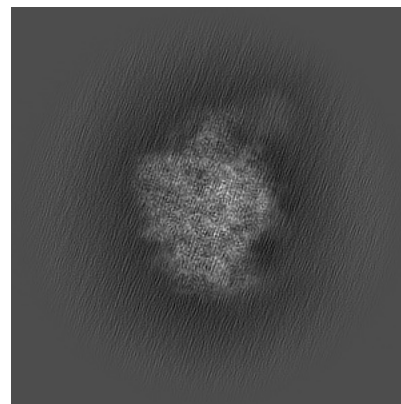
6.1.1 Primary map



X

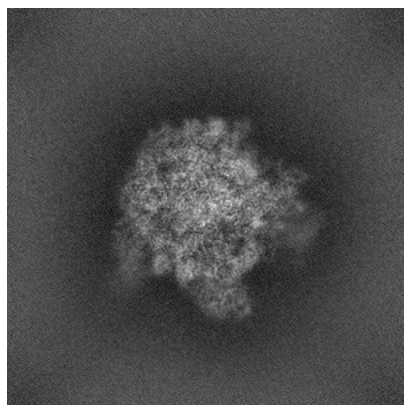


Y

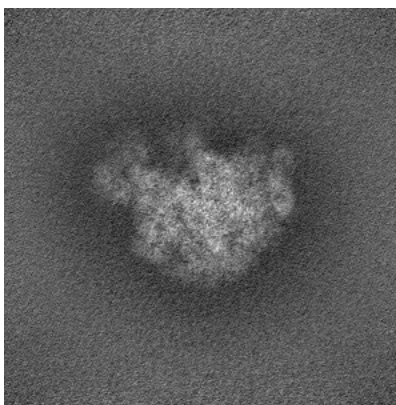


Z

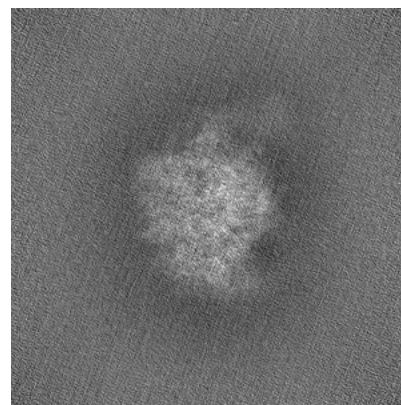
6.1.2 Raw map



X



Y

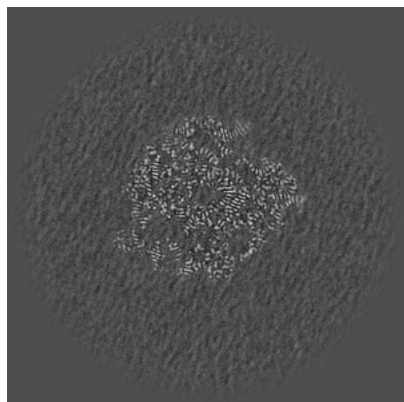


Z

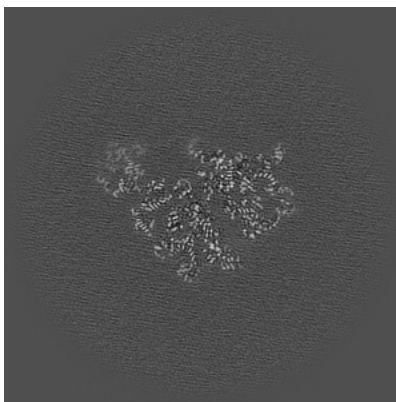
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

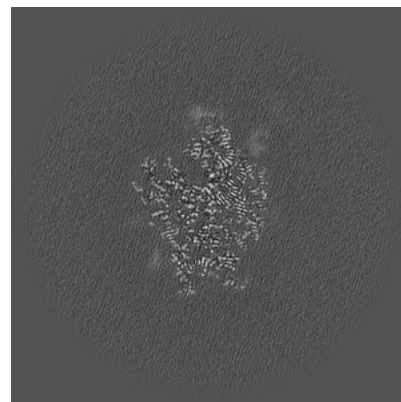
6.2.1 Primary map



X Index: 320

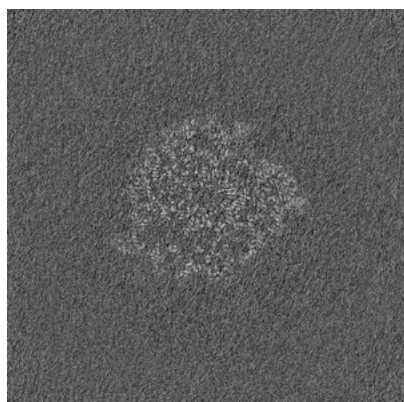


Y Index: 320

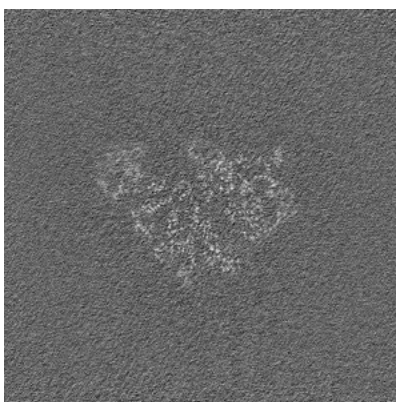


Z Index: 320

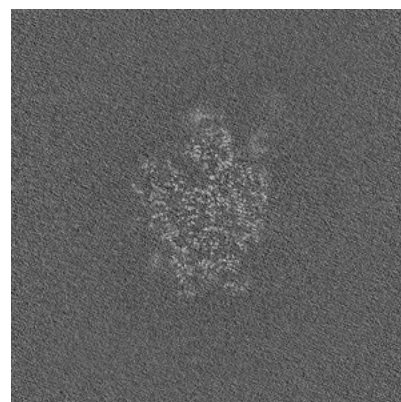
6.2.2 Raw map



X Index: 320



Y Index: 320

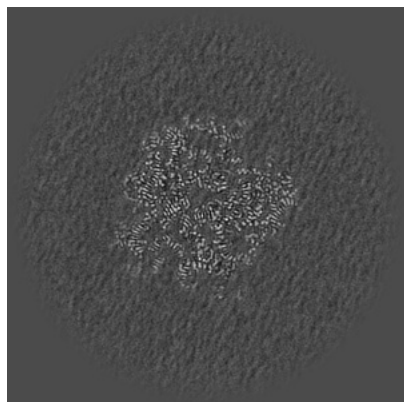


Z Index: 320

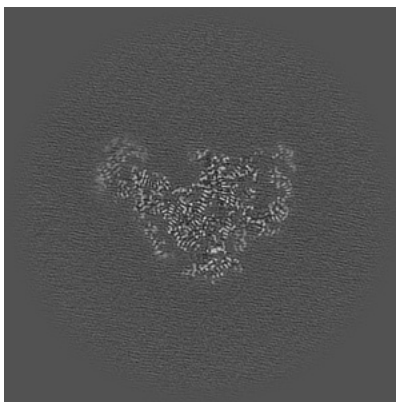
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

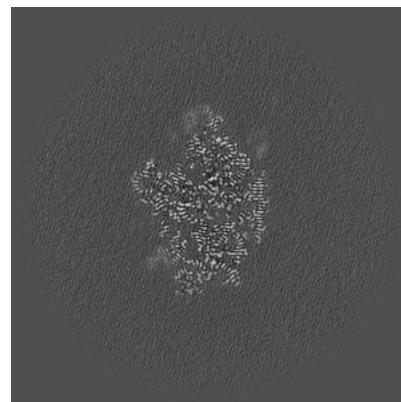
6.3.1 Primary map



X Index: 327

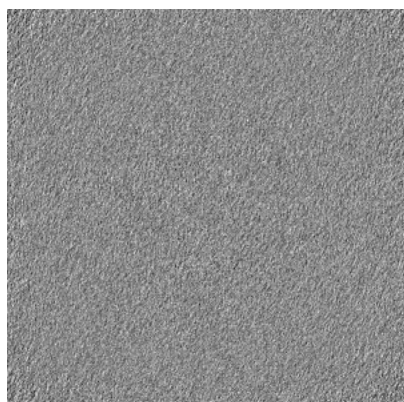


Y Index: 335

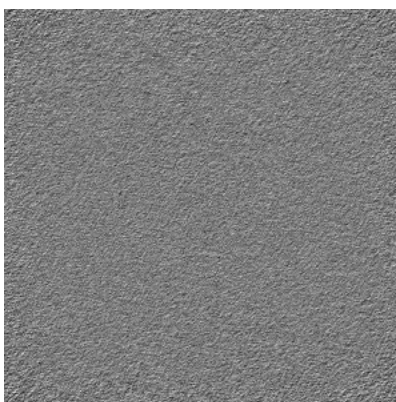


Z Index: 327

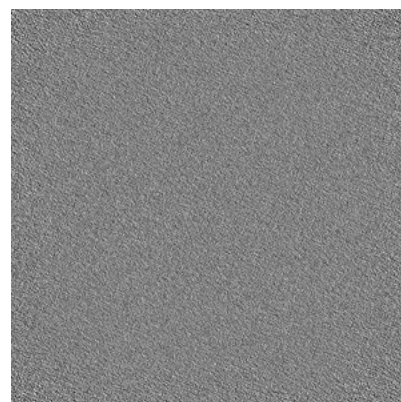
6.3.2 Raw map



X Index: 0



Y Index: 0

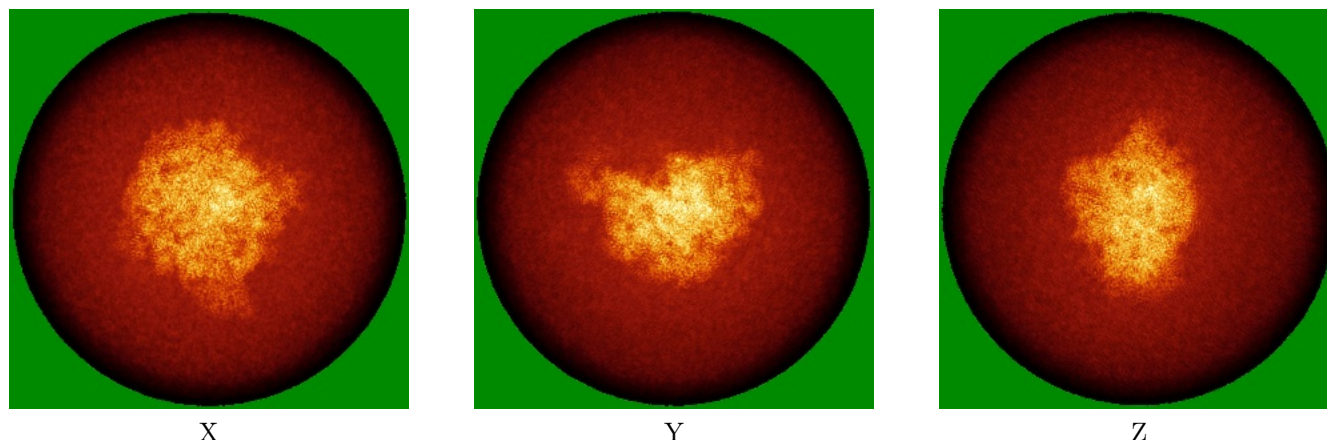


Z Index: 639

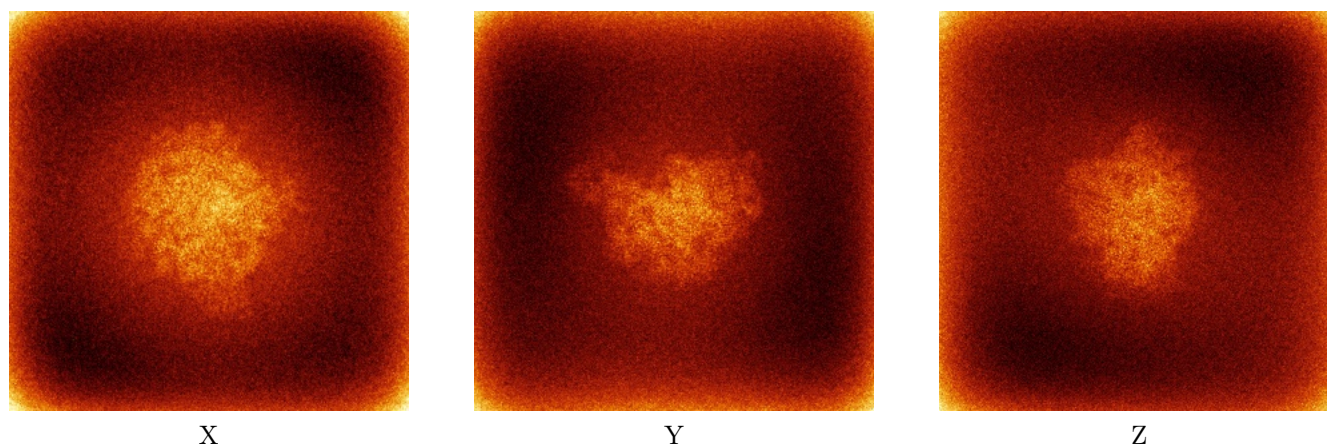
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



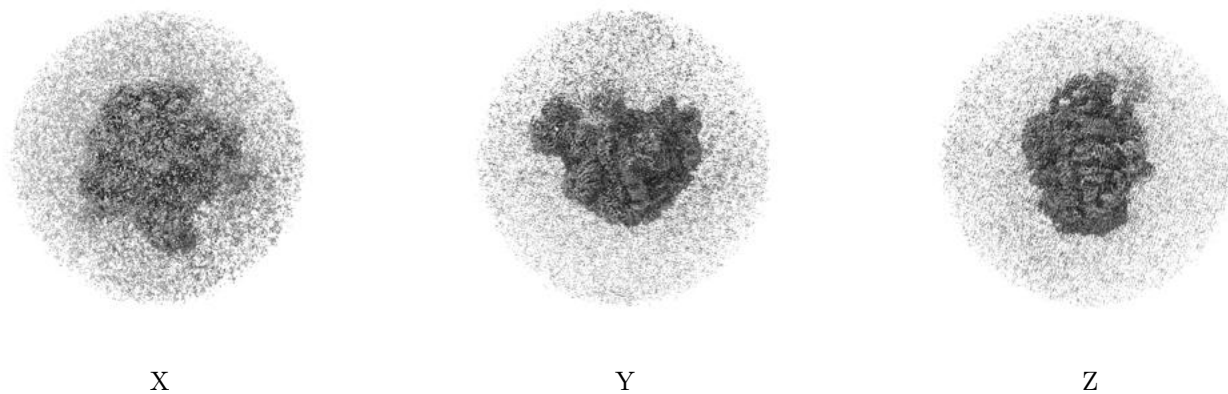
6.4.2 Raw map



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.

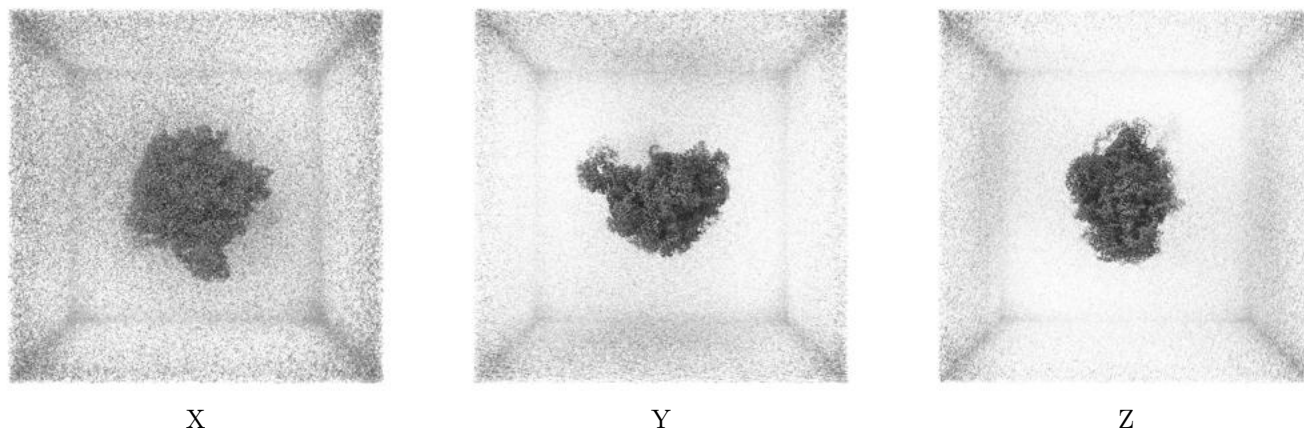
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. 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.

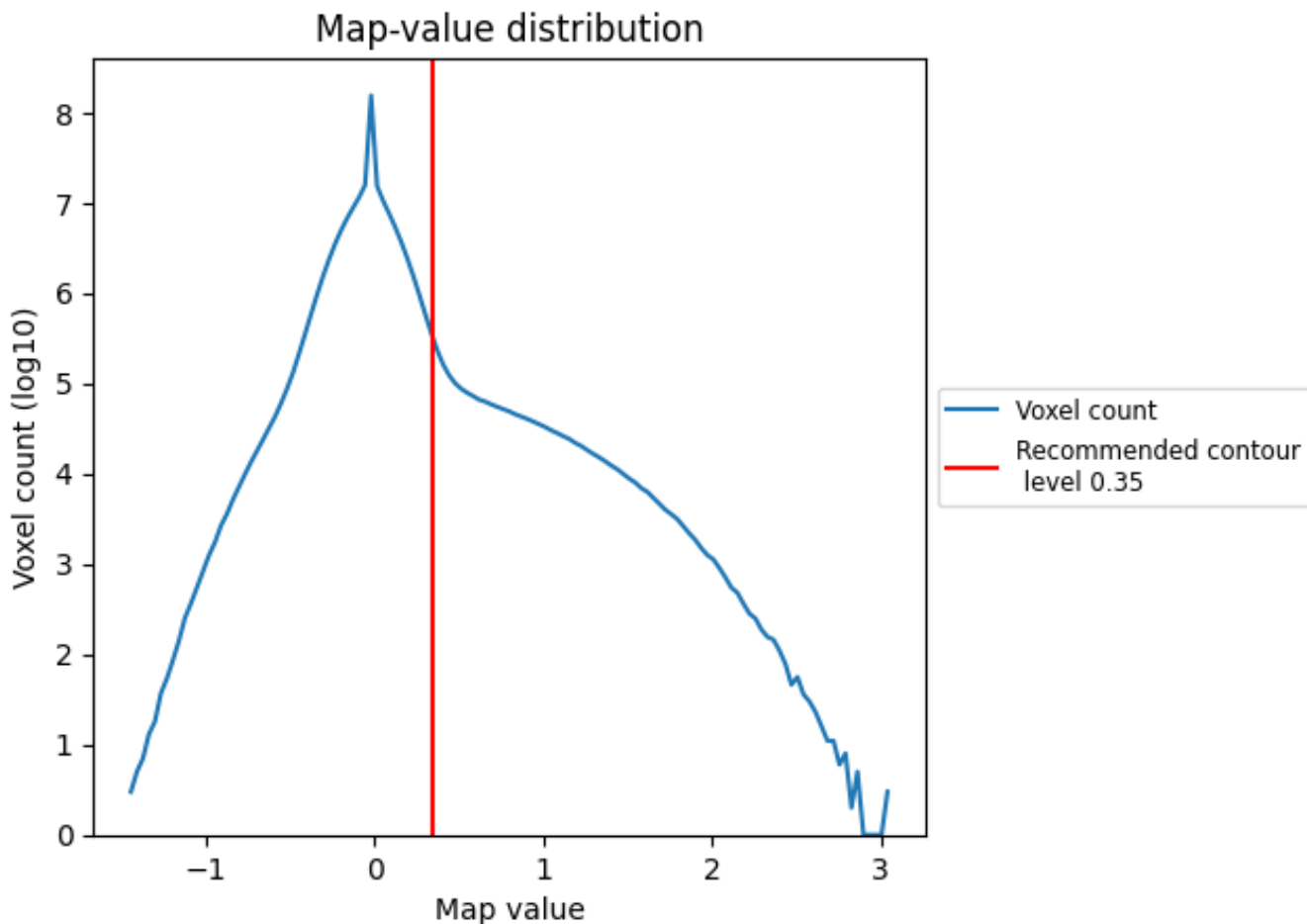
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

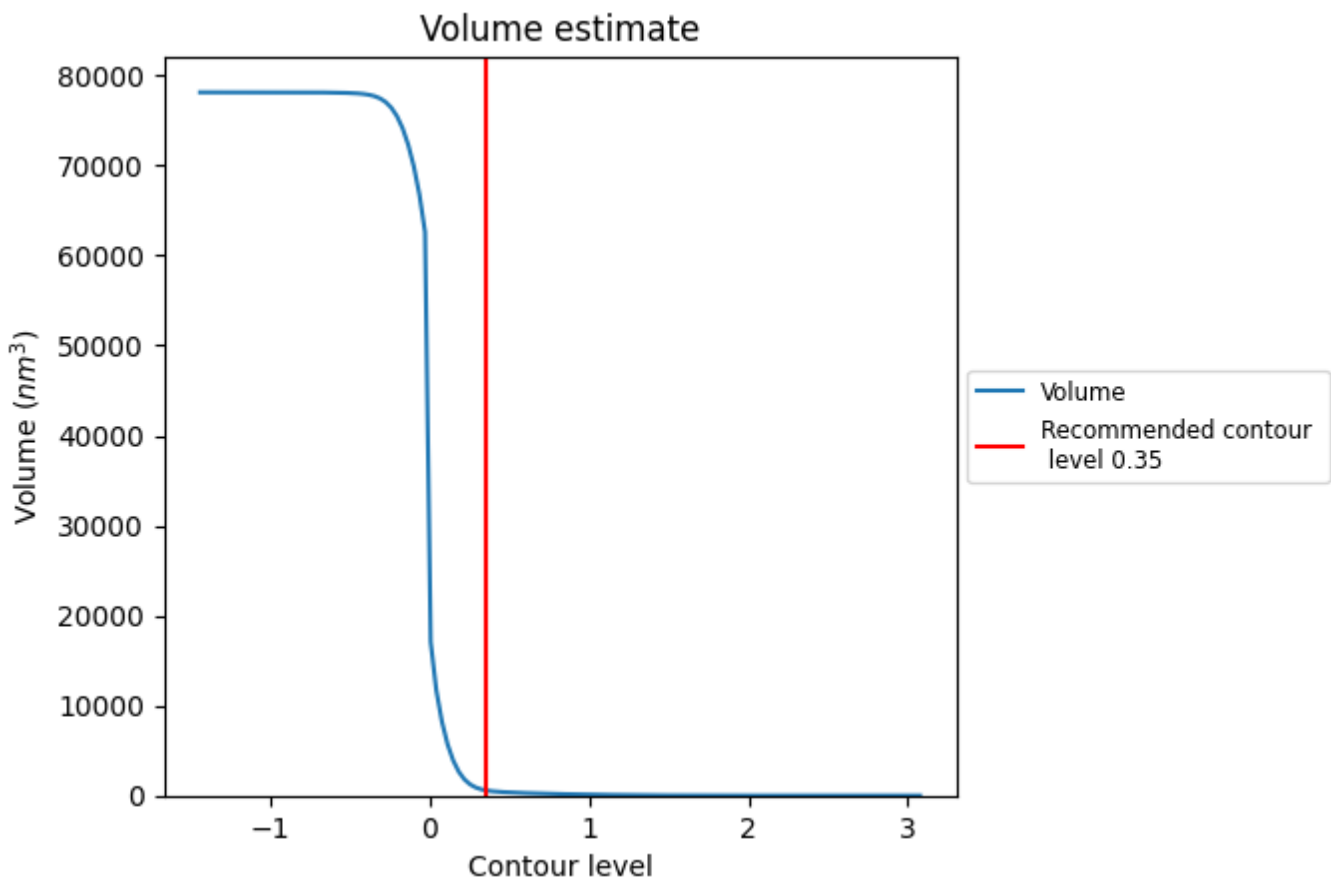
This section contains the results of statistical analysis of the map.

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.

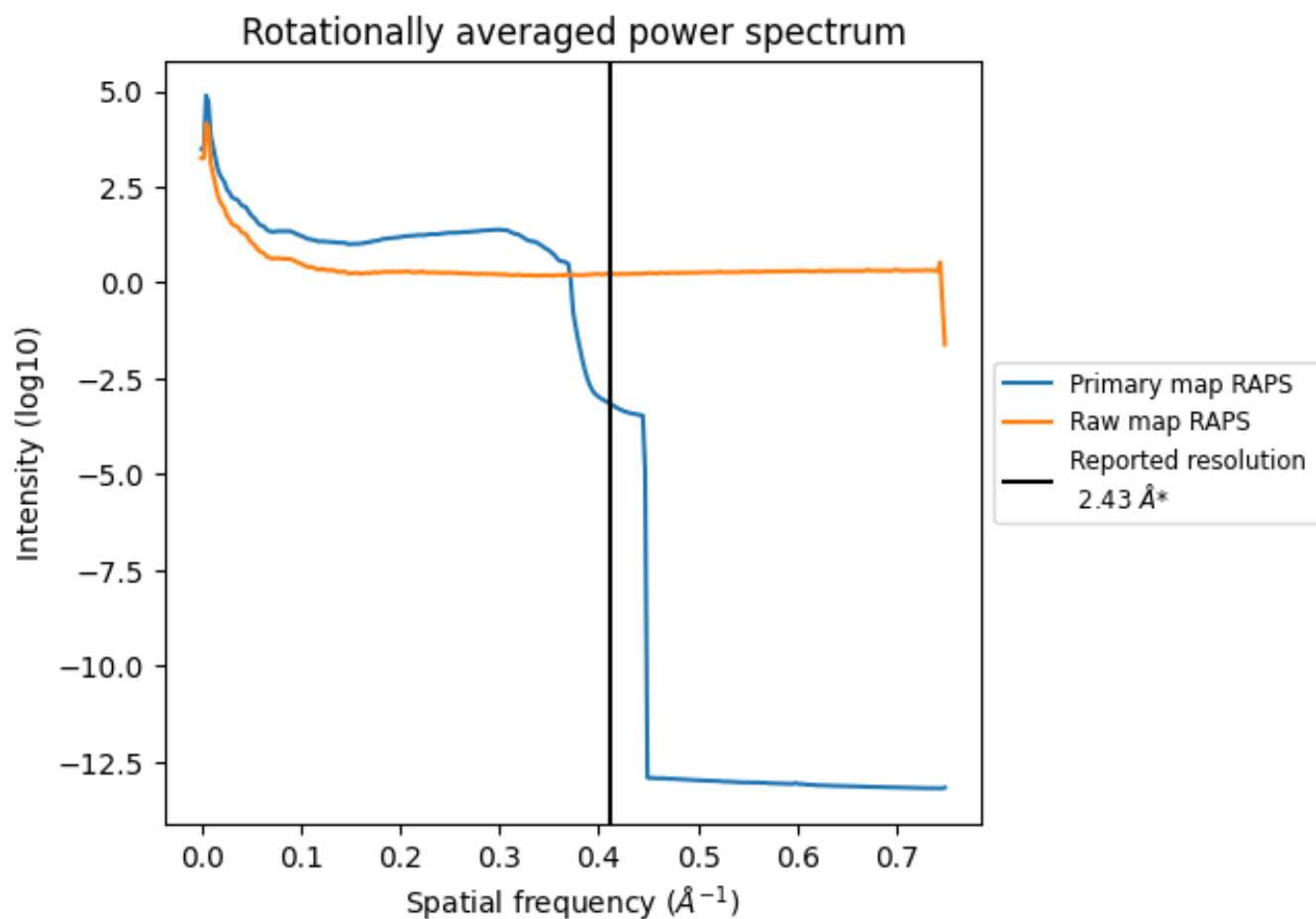
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 591 nm³; this corresponds to an approximate mass of 534 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 [i](#)

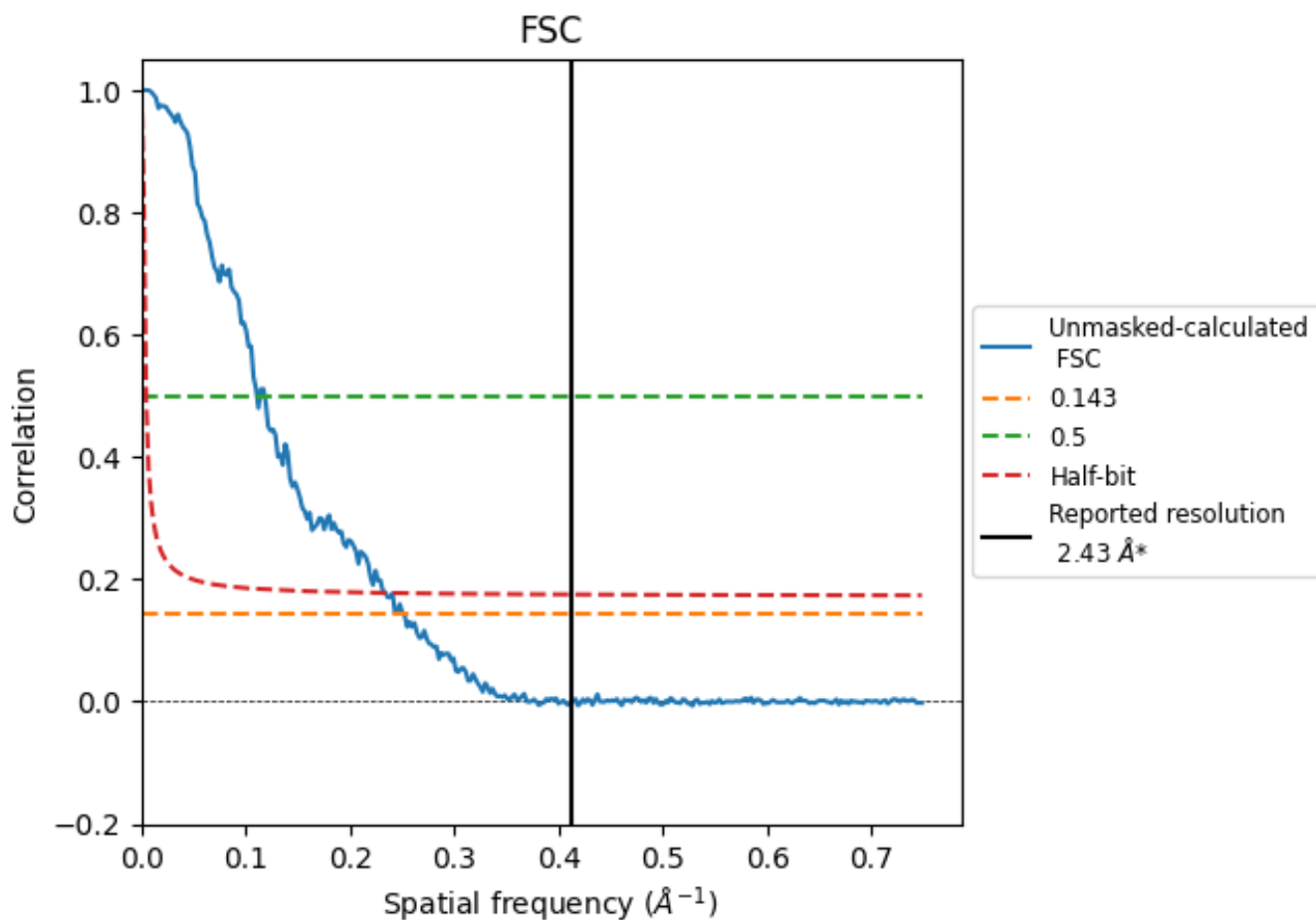


*Reported resolution corresponds to spatial frequency of 0.412 Å⁻¹

8 Fourier-Shell correlation [\(i\)](#)

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

8.1 FSC [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.412 Å⁻¹

8.2 Resolution estimates [i](#)

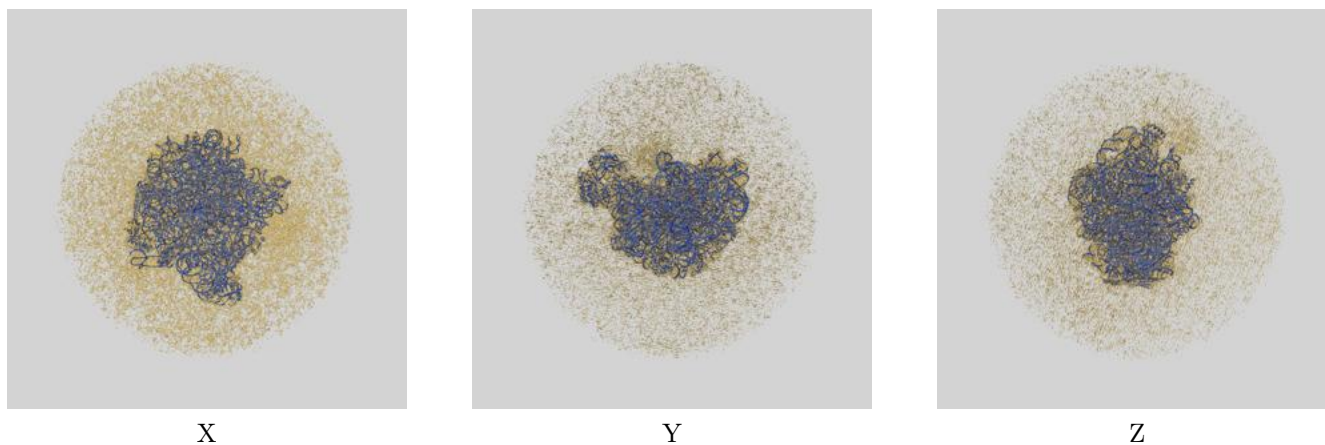
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.43	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.98	9.03	4.27

*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 3.98 differs from the reported value 2.43 by more than 10 %

9 Map-model fit [i](#)

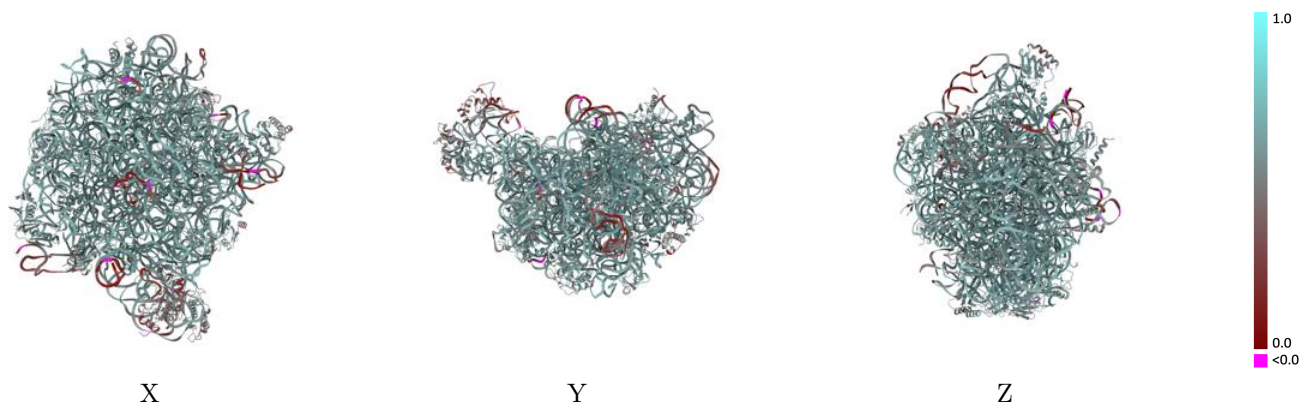
This section contains information regarding the fit between EMDB map EMD-62894 and PDB model 9L95. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



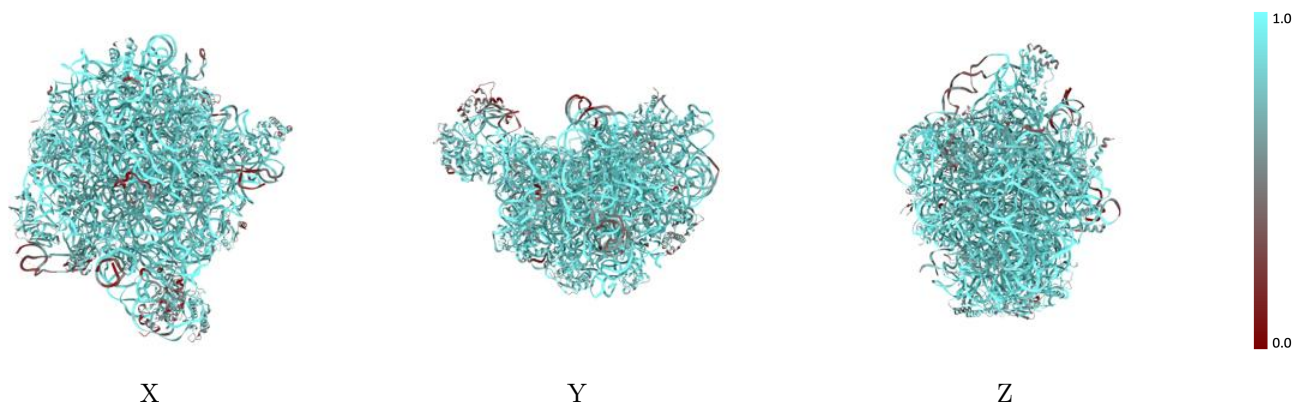
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



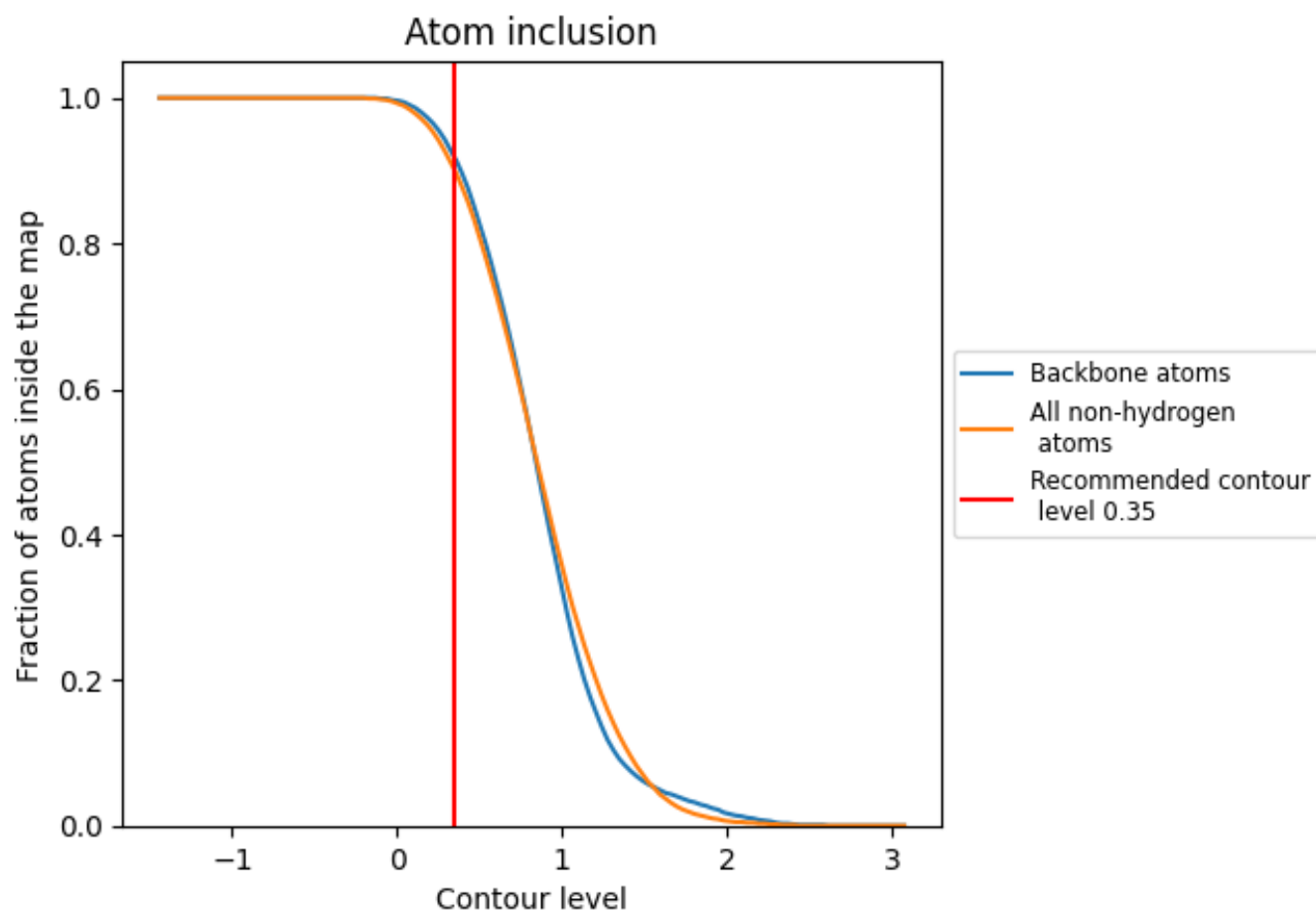
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).































































9.4 Atom inclusion [i](#)



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

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9000	 0.5930
0	 0.9380	 0.6020
9	 0.9050	 0.5670
A	 0.7320	 0.5630
E	 0.7850	 0.5570
F	 0.8300	 0.5870
G	 0.9350	 0.6360
H	 0.8520	 0.5940
I	 0.7800	 0.5380
J	 0.8590	 0.5860
K	 0.8870	 0.6130
L	 0.9010	 0.6130
M	 0.7990	 0.5680
N	 0.8510	 0.5920
O	 0.8980	 0.6110
P	 0.7790	 0.5480
Q	 0.8500	 0.5930
R	 0.8100	 0.5630
S	 0.9320	 0.6370
T	 0.8800	 0.6030
U	 0.8840	 0.5970
V	 0.8900	 0.6150
W	 0.8800	 0.6050
X	 0.4750	 0.3630
Y	 0.7740	 0.5530
b	 0.8800	 0.6070
c	 0.7330	 0.5340
d	 0.5540	 0.4330
e	 0.4510	 0.4930
f	 0.8690	 0.5980
i	 0.7840	 0.5640

