



wwPDB EM Validation Summary Report ⓘ

Jul 2, 2026 – 06:07 PM JST

PDB ID : 9L9V / pdb_0000919v
EMDB ID : EMD-62914
Title : State A of archaeal pre-50S ribosome
Authors : Li, Z.Q.; Yang, X.Y.
Deposited on : 2024-12-31
Resolution : 2.77 Å (reported)

This is a wwPDB EM Validation Summary 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:

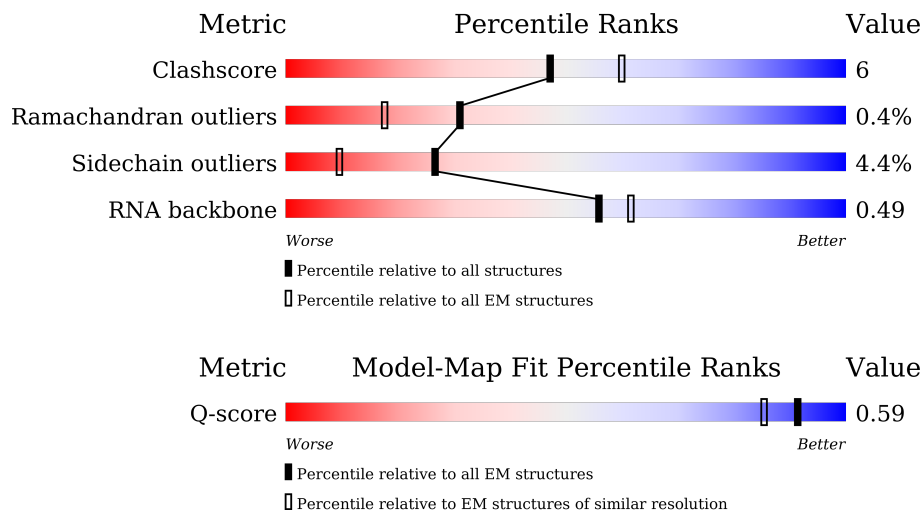
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.77 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	10695 (2.27 - 3.27)

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	B	221	

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Mol	Chain	Length	Quality of chain
4	E	120	71% 27% ..
5	F	176	79% 19% ..
6	G	196	80% 16% ...
7	H	116	76% 22% ..
8	I	184	81% 18% .
9	J	151	83% 16% .
10	K	96	85% 14% .
11	L	153	84% 15% .
12	M	67	72% 15% 13%
13	N	118	71% 25% ..
14	O	154	78% 21% .
15	P	92	82% 15% .
16	Q	234	50% 11% 39%
17	R	89	71% 18% • 10%
18	S	58	83% 16% .
19	T	93	88% 12%
20	U	241	76% 20% ..
21	V	338	87% 12% .
22	W	248	79% 19% .
23	X	172	15% 60% 37% ..
24	Y	178	75% 21% ..
25	b	145	84% 12% ..
26	f	132	78% 22%
27	i	406	40% 23% 6% 31%

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 92125 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	2758	59124	26388	10885	19093	2758	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 Translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	220	1612	993	273	342	4	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	174	1372	852	251	261	8	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	193	1575	961	337	275	2	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 9 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	150	1205	728	247	229	1	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein eL21.

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

- Molecule 11 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 12 is a protein called Large ribosomal subunit protein eL24.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 15 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 16 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 17 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 18 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 19 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 20 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 21 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 22 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 23 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 25 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 27 is a protein called CBS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	i	281	2131	1331	364	432	4	1	0

- Molecule 28 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
28	0	140	Total 140	Mg 140	0
28	9	7	Total 7	Mg 7	0
28	G	3	Total 3	Mg 3	0
28	U	1	Total 1	Mg 1	0
28	V	3	Total 3	Mg 3	0
28	W	1	Total 1	Mg 1	0
28	f	1	Total 1	Mg 1	0

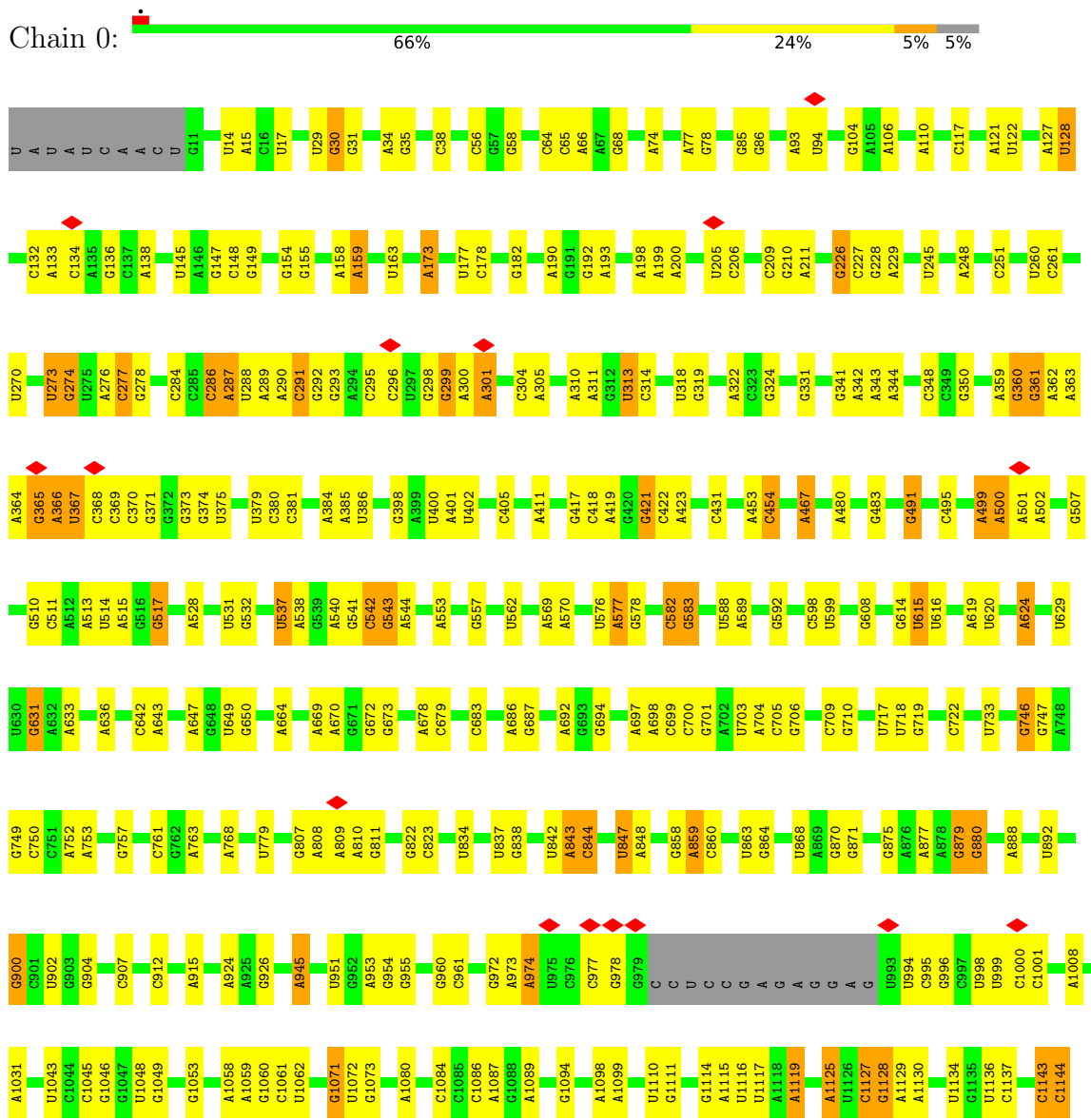
- Molecule 29 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

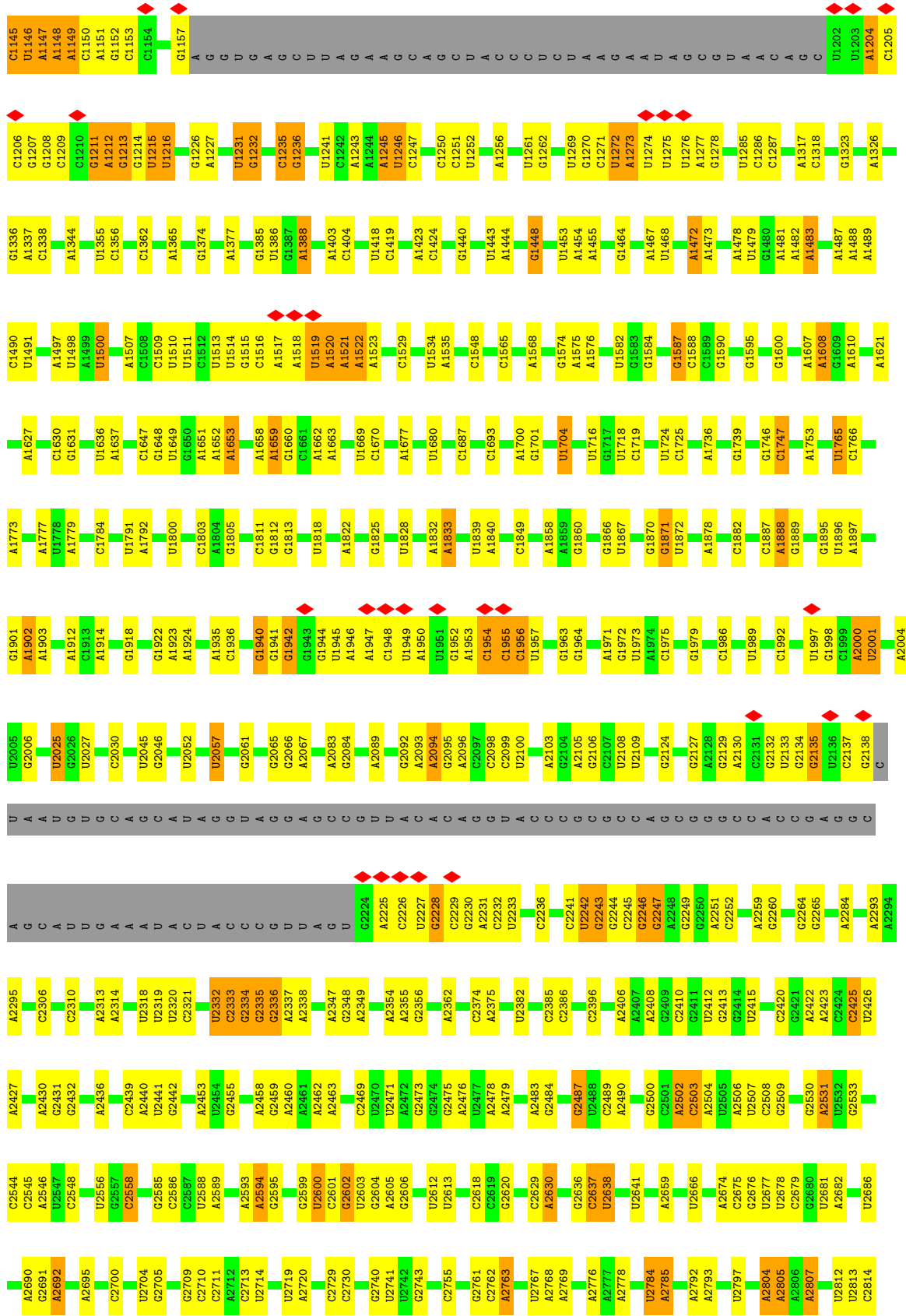
Mol	Chain	Residues	Atoms		AltConf
29	S	1	Total 1	Zn 1	0
29	T	1	Total 1	Zn 1	0

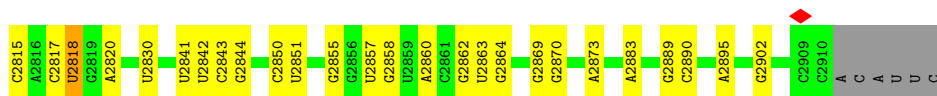
3 Residue-property plots

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

- Molecule 1: 23S RNA







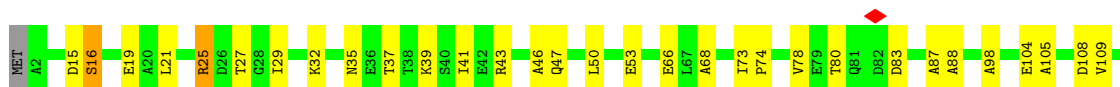
- Molecule 2: 5S RNA



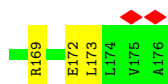
- Molecule 3: Translation initiation factor 6



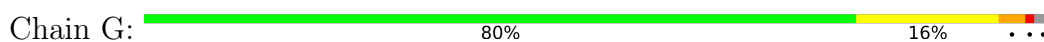
- Molecule 4: Large ribosomal subunit protein eL8



- Molecule 5: Large ribosomal subunit protein uL16

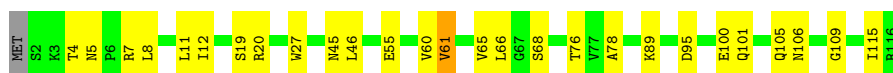


- Molecule 6: Large ribosomal subunit protein eL15

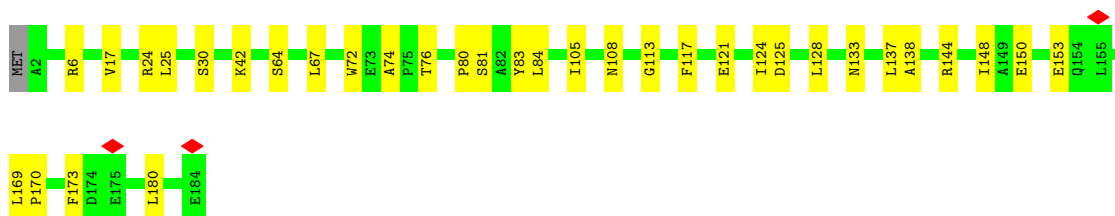
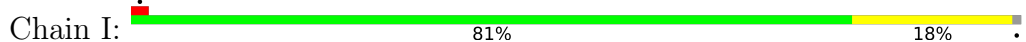




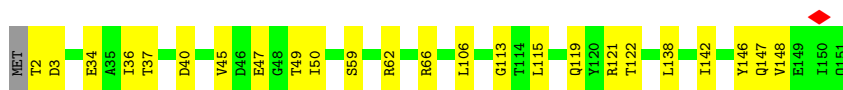
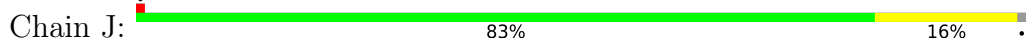
• Molecule 7: Large ribosomal subunit protein eL18



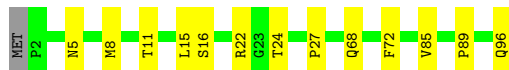
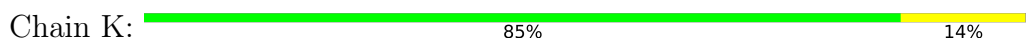
• Molecule 8: Large ribosomal subunit protein uL18



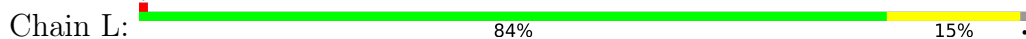
• Molecule 9: Large ribosomal subunit protein eL19



• Molecule 10: Large ribosomal subunit protein eL21



• Molecule 11: Large ribosomal subunit protein uL22

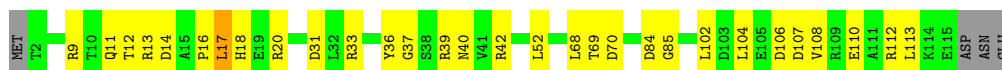


• Molecule 12: Large ribosomal subunit protein eL24

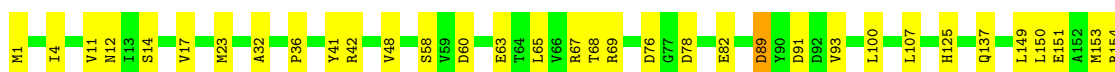
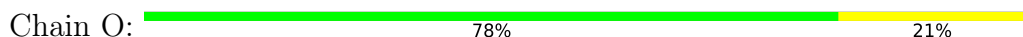




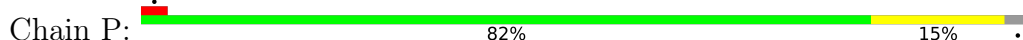
- Molecule 13: Large ribosomal subunit protein uL24



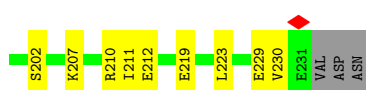
- Molecule 14: Large ribosomal subunit protein uL30



- Molecule 15: Large ribosomal subunit protein eL31



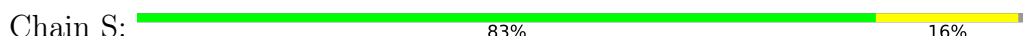
- Molecule 16: Large ribosomal subunit protein eL32



- Molecule 17: Large ribosomal subunit protein eL43

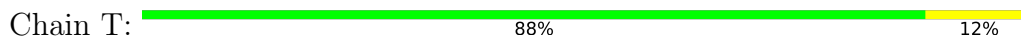


- Molecule 18: Large ribosomal subunit protein eL37

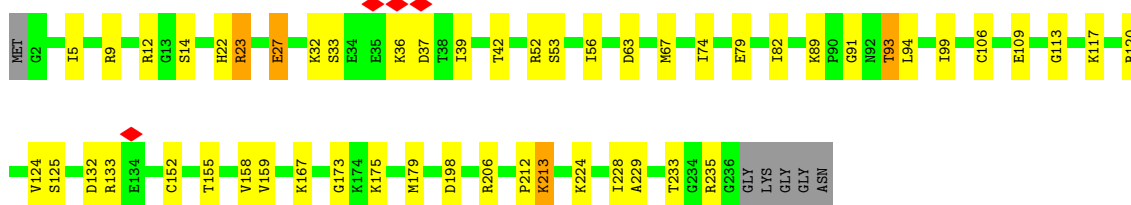
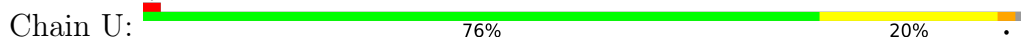




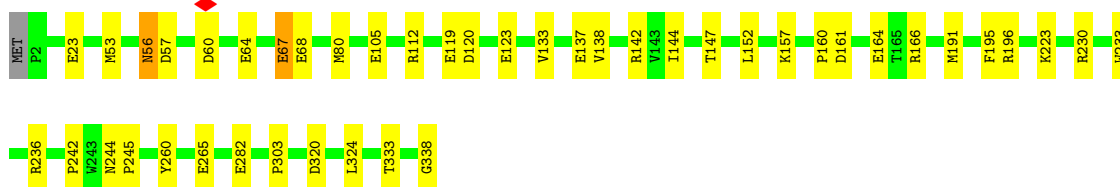
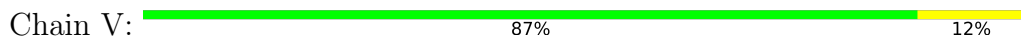
- Molecule 19: Large ribosomal subunit protein eL42



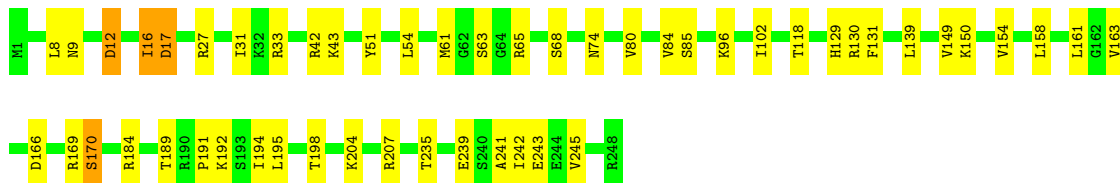
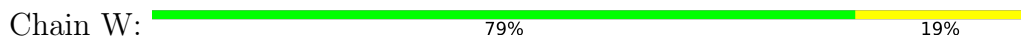
- Molecule 20: Large ribosomal subunit protein uL2



- Molecule 21: Large ribosomal subunit protein uL3



- Molecule 22: Large ribosomal subunit protein uL4

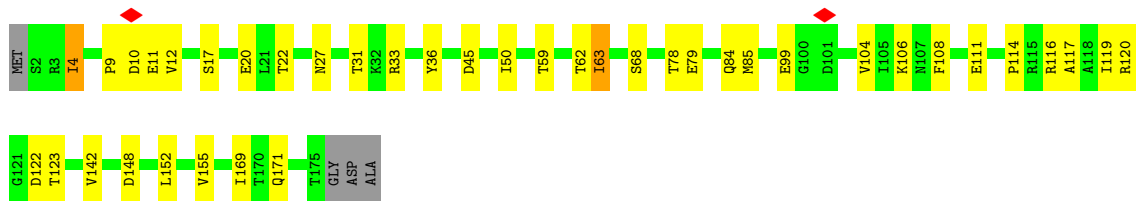
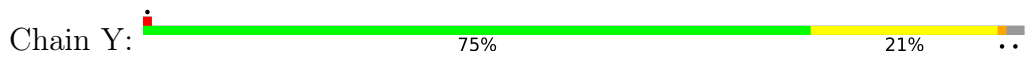


- Molecule 23: Large ribosomal subunit protein uL5

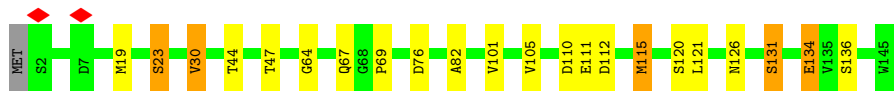
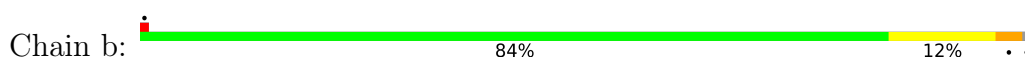




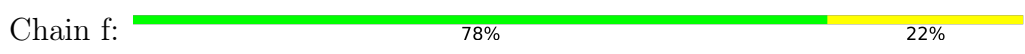
• Molecule 24: Large ribosomal subunit protein uL6



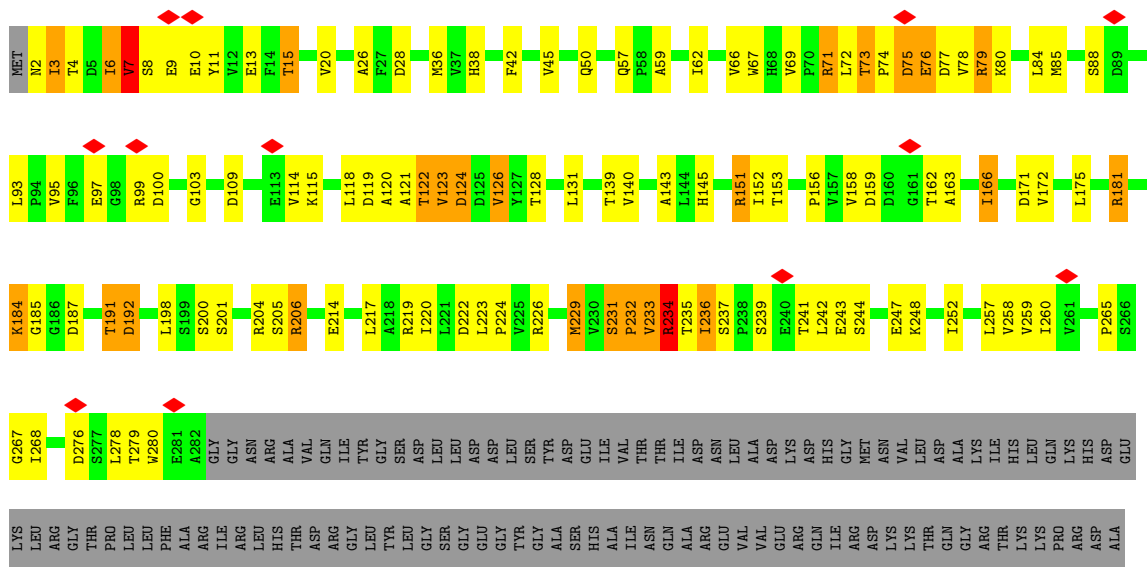
• Molecule 25: Large ribosomal subunit protein uL13



• Molecule 26: Large ribosomal subunit protein uL14



• Molecule 27: CBS domain-containing protein



GLU
TYR
TRP
GLU
LYS
ARG
PHE
GLY
TRP
MET
LEU
GLU
GLY
GLU

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	1.697	Depositor
Minimum map value	-0.986	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.16	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	0.33	0/66202	0.37	0/103250
2	9	0.28	0/2848	0.33	0/4436
3	B	0.20	0/1631	0.40	0/2225
4	E	0.25	0/889	0.41	0/1209
5	F	0.29	0/1395	0.44	0/1875
6	G	0.31	0/1602	0.37	0/2140
7	H	0.27	0/895	0.43	0/1210
8	I	0.22	0/1447	0.38	0/1969
9	J	0.28	0/1217	0.41	0/1622
10	K	0.31	0/750	0.39	0/1001
11	L	0.29	0/1199	0.42	0/1619
12	M	0.27	0/474	0.35	0/634
13	N	0.27	0/911	0.36	0/1232
14	O	0.29	0/1218	0.41	0/1651
15	P	0.27	0/741	0.40	0/998
16	Q	0.29	0/1165	0.37	0/1561
17	R	0.30	0/624	0.45	0/835
18	S	0.30	0/446	0.47	0/586
19	T	0.25	0/764	0.36	0/1015
20	U	0.32	0/1800	0.47	0/2420
21	V	0.30	0/2677	0.39	0/3617
22	W	0.28	0/1925	0.39	0/2598
23	X	0.25	0/1329	0.55	0/1793
24	Y	0.24	0/1368	0.40	0/1859
25	b	0.30	0/1144	0.42	0/1541
26	f	0.27	0/1004	0.40	0/1347
27	i	0.60	2/2169 (0.1%)	0.83	4/2951 (0.1%)
All	All	0.33	2/99834 (0.0%)	0.39	4/149194 (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
19	T	0	1
20	U	0	2
27	i	0	8
All	All	0	11

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	i	181[A]	ARG	C-O	6.35	1.31	1.23
27	i	181[B]	ARG	C-O	6.35	1.31	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	i	181[A]	ARG	CA-C-O	8.62	130.68	121.45
27	i	181[B]	ARG	CA-C-O	8.62	130.68	121.45
27	i	126	VAL	N-CA-C	-5.31	106.69	112.80
27	i	185	GLY	N-CA-C	-5.00	105.88	111.63

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	T	42	ARG	Sidechain
20	U	23	ARG	Sidechain
20	U	235	ARG	Sidechain
27	i	71	ARG	Sidechain
27	i	79	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	0	59124	0	29819	374	0
2	9	2551	0	1298	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1612	0	1567	51	0
4	E	880	0	852	24	0
5	F	1372	0	1371	30	0
6	G	1575	0	1603	27	0
7	H	887	0	907	19	0
8	I	1417	0	1365	27	0
9	J	1205	0	1208	18	0
10	K	736	0	745	8	0
11	L	1174	0	1146	13	0
12	M	466	0	443	7	0
13	N	903	0	886	17	0
14	O	1200	0	1159	24	0
15	P	726	0	703	11	0
16	Q	1146	0	1146	16	0
17	R	617	0	618	10	0
18	S	439	0	445	7	0
19	T	746	0	736	5	0
20	U	1766	0	1799	31	0
21	V	2619	0	2572	33	0
22	W	1898	0	1895	33	0
23	X	1308	0	1251	44	0
24	Y	1346	0	1292	21	0
25	b	1127	0	1118	13	0
26	f	996	0	1046	25	0
27	i	2131	0	2117	93	0
28	0	140	0	0	0	0
28	9	7	0	0	0	0
28	G	3	0	0	0	0
28	U	1	0	0	0	0
28	V	3	0	0	0	0
28	W	1	0	0	0	0
28	f	1	0	0	0	0
29	S	1	0	0	0	0
29	T	1	0	0	0	0
All	All	92125	0	61107	906	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 6.

The worst 5 of 906 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)
27:i:234:ARG:NH2	27:i:252:ILE:HG21	1.42	1.33
5:F:27:PRO:HA	27:i:234:ARG:NH1	1.47	1.26
5:F:27:PRO:CA	27:i:234:ARG:HH12	1.48	1.25
27:i:11:TYR:CE1	27:i:13:GLU:OE2	1.94	1.20
27:i:115:LYS:HG3	27:i:243:GLU:HG3	1.30	1.11

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	B	218/221 (99%)	204 (94%)	14 (6%)	0	100	100
4	E	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
5	F	172/176 (98%)	161 (94%)	11 (6%)	0	100	100
6	G	191/196 (97%)	185 (97%)	4 (2%)	2 (1%)	12	35
7	H	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
8	I	181/184 (98%)	175 (97%)	6 (3%)	0	100	100
9	J	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
10	K	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
11	L	149/153 (97%)	146 (98%)	3 (2%)	0	100	100
12	M	56/67 (84%)	55 (98%)	1 (2%)	0	100	100
13	N	112/118 (95%)	106 (95%)	6 (5%)	0	100	100
14	O	152/154 (99%)	146 (96%)	6 (4%)	0	100	100
15	P	87/92 (95%)	85 (98%)	2 (2%)	0	100	100
16	Q	140/234 (60%)	137 (98%)	3 (2%)	0	100	100
17	R	78/89 (88%)	74 (95%)	4 (5%)	0	100	100
18	S	55/58 (95%)	53 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	T	91/93 (98%)	88 (97%)	3 (3%)	0	100	100
20	U	233/241 (97%)	213 (91%)	18 (8%)	2 (1%)	14	37
21	V	335/338 (99%)	325 (97%)	10 (3%)	0	100	100
22	W	246/248 (99%)	235 (96%)	11 (4%)	0	100	100
23	X	167/172 (97%)	150 (90%)	17 (10%)	0	100	100
24	Y	172/178 (97%)	163 (95%)	8 (5%)	1 (1%)	21	47
25	b	142/145 (98%)	135 (95%)	7 (5%)	0	100	100
26	f	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
27	i	280/406 (69%)	227 (81%)	44 (16%)	9 (3%)	3	10
All	All	3858/4178 (92%)	3648 (95%)	196 (5%)	14 (0%)	31	57

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	i	75	ASP
27	i	191	THR
27	i	192	ASP
20	U	213	LYS
6	G	192	ARG

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	B	170/171 (99%)	161 (95%)	9 (5%)	20	49
4	E	93/94 (99%)	91 (98%)	2 (2%)	45	75
5	F	145/147 (99%)	139 (96%)	6 (4%)	27	59
6	G	161/163 (99%)	155 (96%)	6 (4%)	30	62
7	H	98/99 (99%)	96 (98%)	2 (2%)	48	77
8	I	144/145 (99%)	143 (99%)	1 (1%)	76	90
9	J	120/121 (99%)	117 (98%)	3 (2%)	42	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	K	77/78 (99%)	73 (95%)	4 (5%)	21	50
11	L	122/124 (98%)	120 (98%)	2 (2%)	55	81
12	M	48/55 (87%)	48 (100%)	0	100	100
13	N	98/102 (96%)	90 (92%)	8 (8%)	10	30
14	O	132/132 (100%)	130 (98%)	2 (2%)	57	81
15	P	78/80 (98%)	78 (100%)	0	100	100
16	Q	120/191 (63%)	117 (98%)	3 (2%)	42	73
17	R	61/68 (90%)	56 (92%)	5 (8%)	10	30
18	S	48/49 (98%)	48 (100%)	0	100	100
19	T	77/77 (100%)	75 (97%)	2 (3%)	40	72
20	U	183/186 (98%)	174 (95%)	9 (5%)	22	52
21	V	277/278 (100%)	275 (99%)	2 (1%)	76	90
22	W	198/198 (100%)	188 (95%)	10 (5%)	21	50
23	X	141/147 (96%)	131 (93%)	10 (7%)	13	36
24	Y	149/151 (99%)	141 (95%)	8 (5%)	20	48
25	b	122/123 (99%)	113 (93%)	9 (7%)	13	34
26	f	106/106 (100%)	105 (99%)	1 (1%)	70	87
27	i	241/344 (70%)	203 (84%)	38 (16%)	2	7
All	All	3209/3429 (94%)	3067 (96%)	142 (4%)	27	56

5 of 142 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	i	78	VAL
27	i	119	ASP
27	i	184	LYS
17	R	8	SER
16	Q	202	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
21	V	231	GLN
22	W	44	GLN
21	V	306	ASN

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Mol	Chain	Res	Type
23	X	107	HIS
13	N	4	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2754/2916 (94%)	485 (17%)	10 (0%)
2	9	119/122 (97%)	20 (16%)	2 (1%)
All	All	2873/3038 (94%)	505 (17%)	12 (0%)

5 of 505 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	17	U
1	0	30	G
1	0	31	G
1	0	58	G
1	0	66	A

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1272	U
1	0	2784	U
2	9	120	C
1	0	2842	U
1	0	582	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 158 ligands modelled in this entry, 158 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

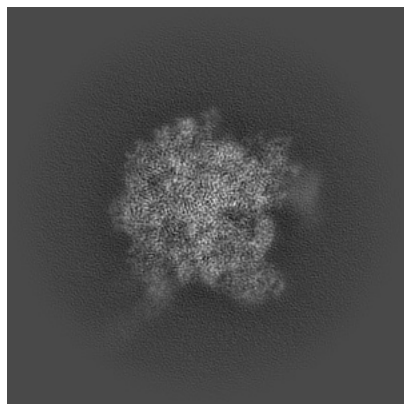
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62914. These allow visual inspection of the internal detail of the map and identification of artifacts.

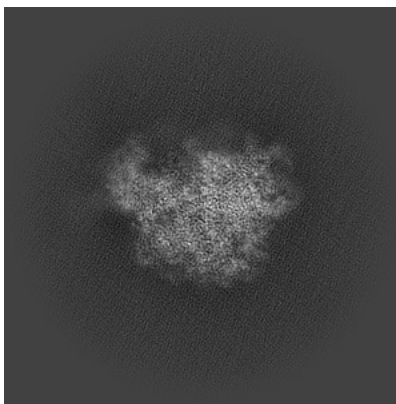
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

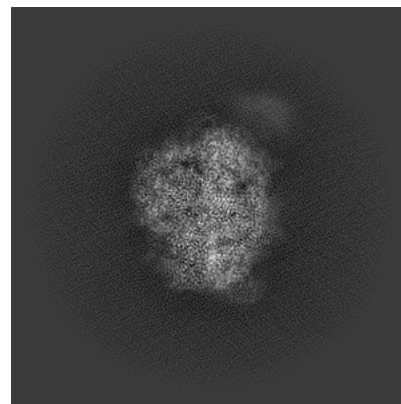
6.1.1 Primary map



X

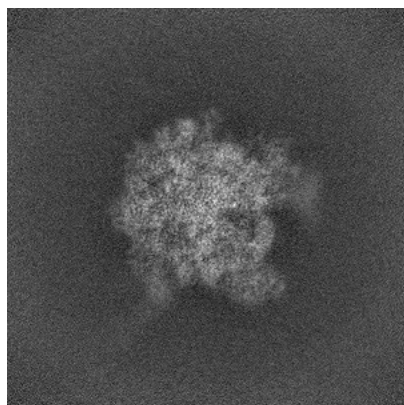


Y

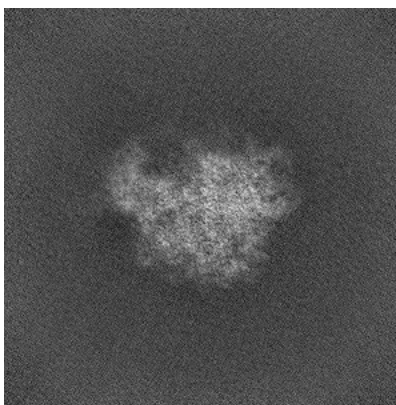


Z

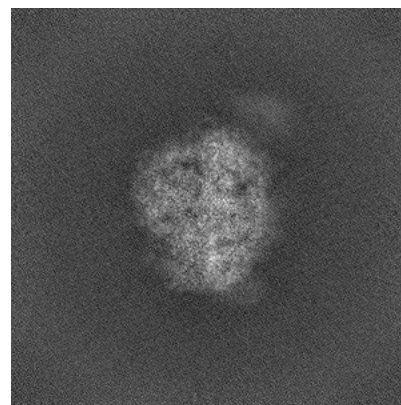
6.1.2 Raw map



X



Y

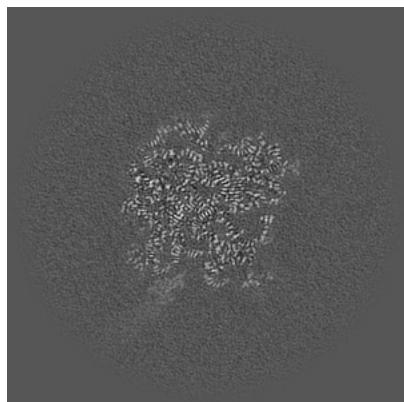


Z

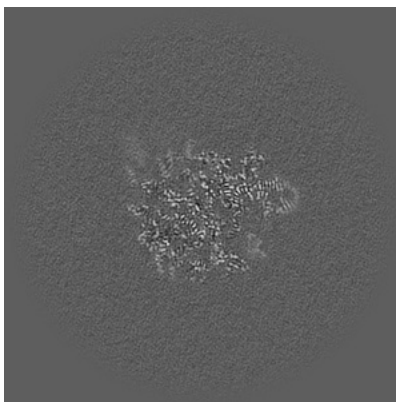
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

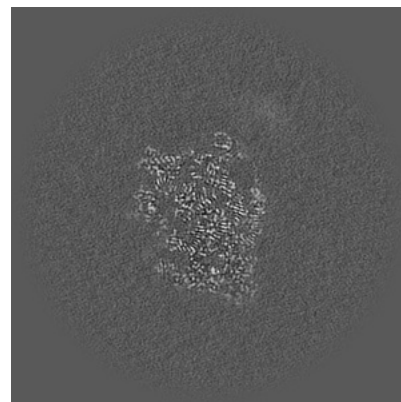
6.2.1 Primary map



X Index: 320

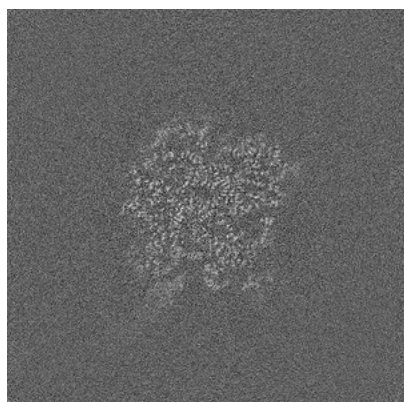


Y Index: 320

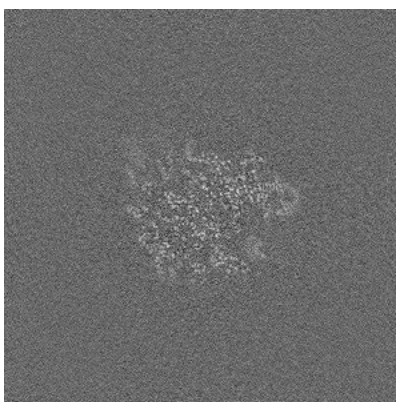


Z Index: 320

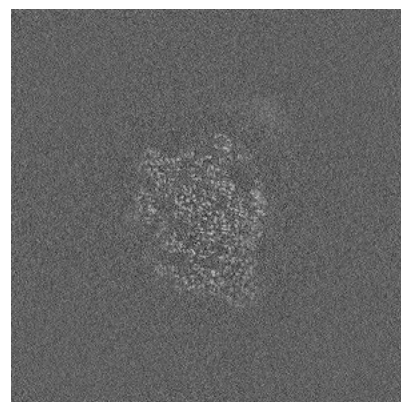
6.2.2 Raw map



X Index: 320



Y Index: 320

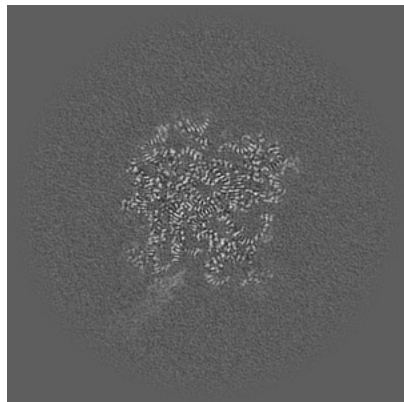


Z Index: 320

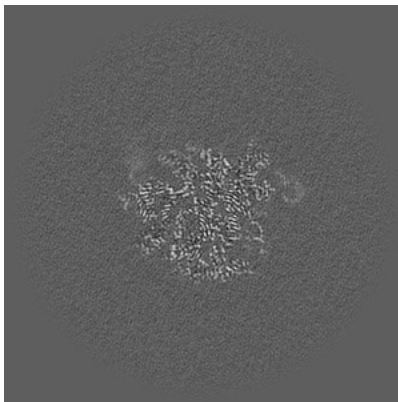
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

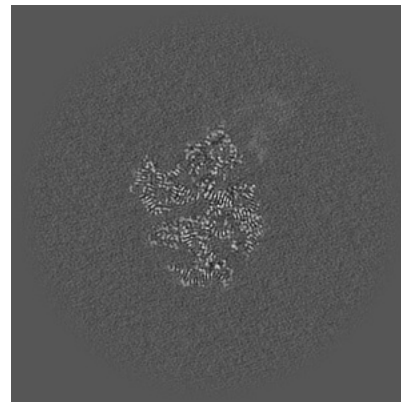
6.3.1 Primary map



X Index: 321

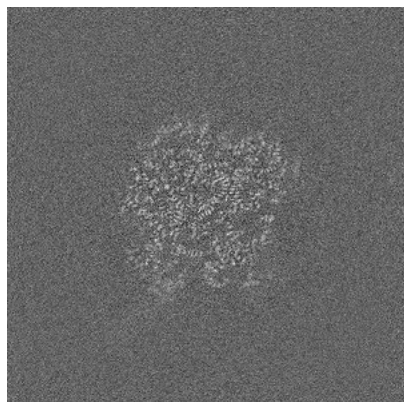


Y Index: 331

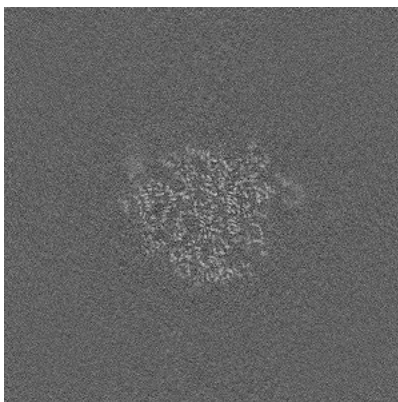


Z Index: 361

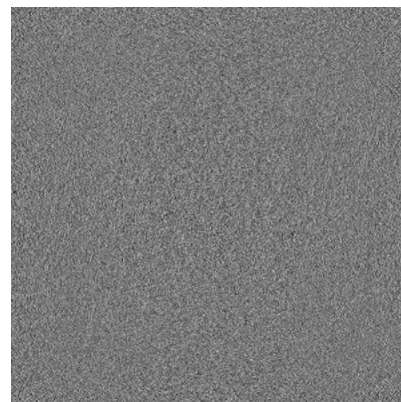
6.3.2 Raw map



X Index: 319



Y Index: 332

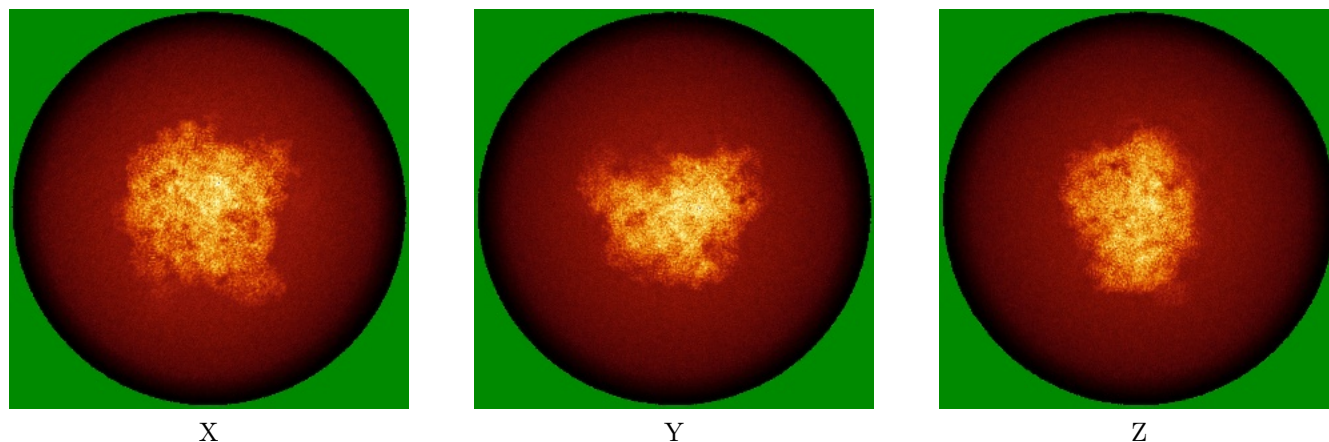


Z Index: 0

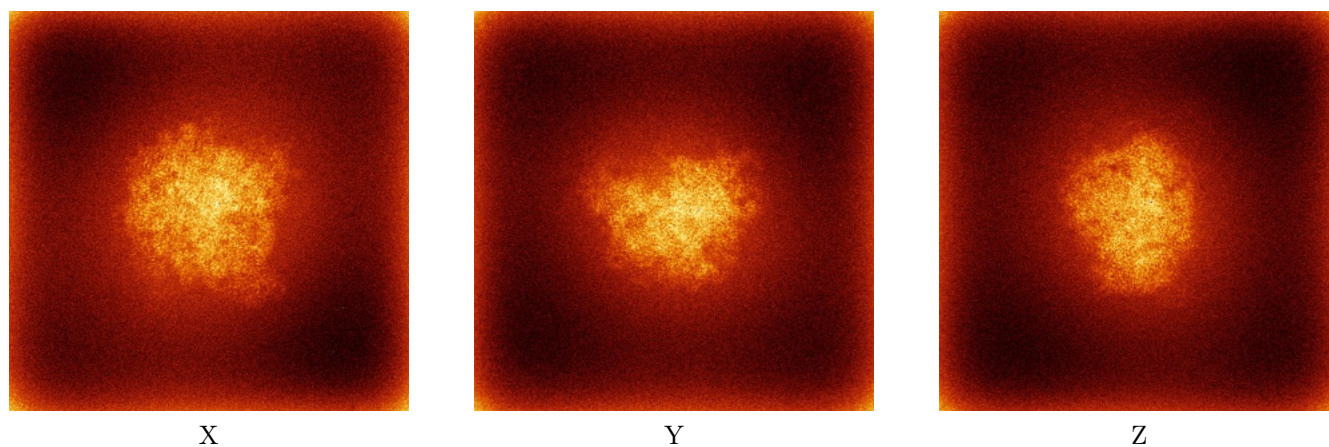
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



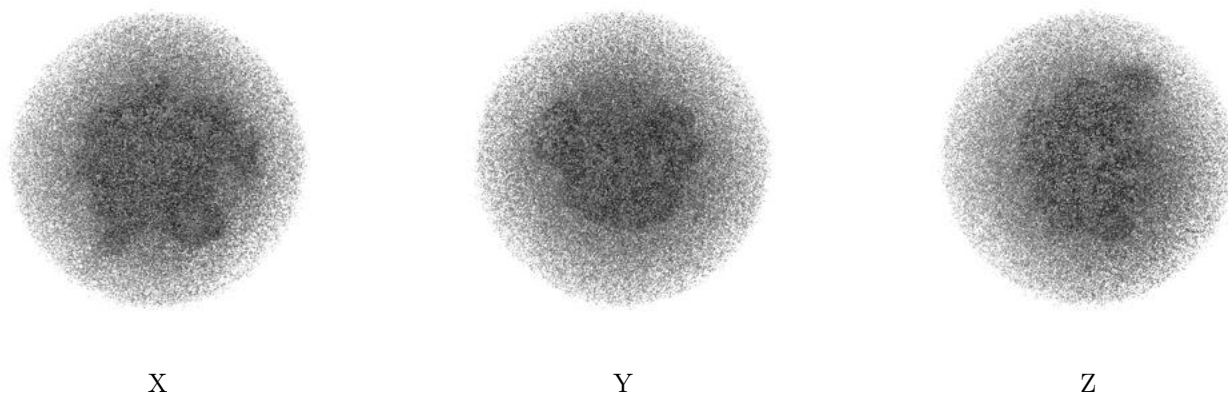
6.4.2 Raw map



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.

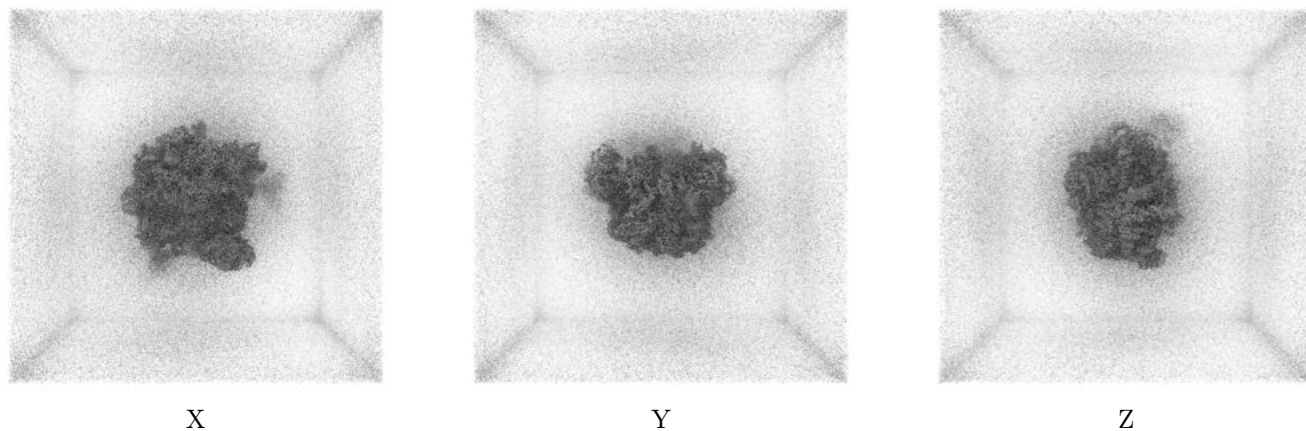
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.16. 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.

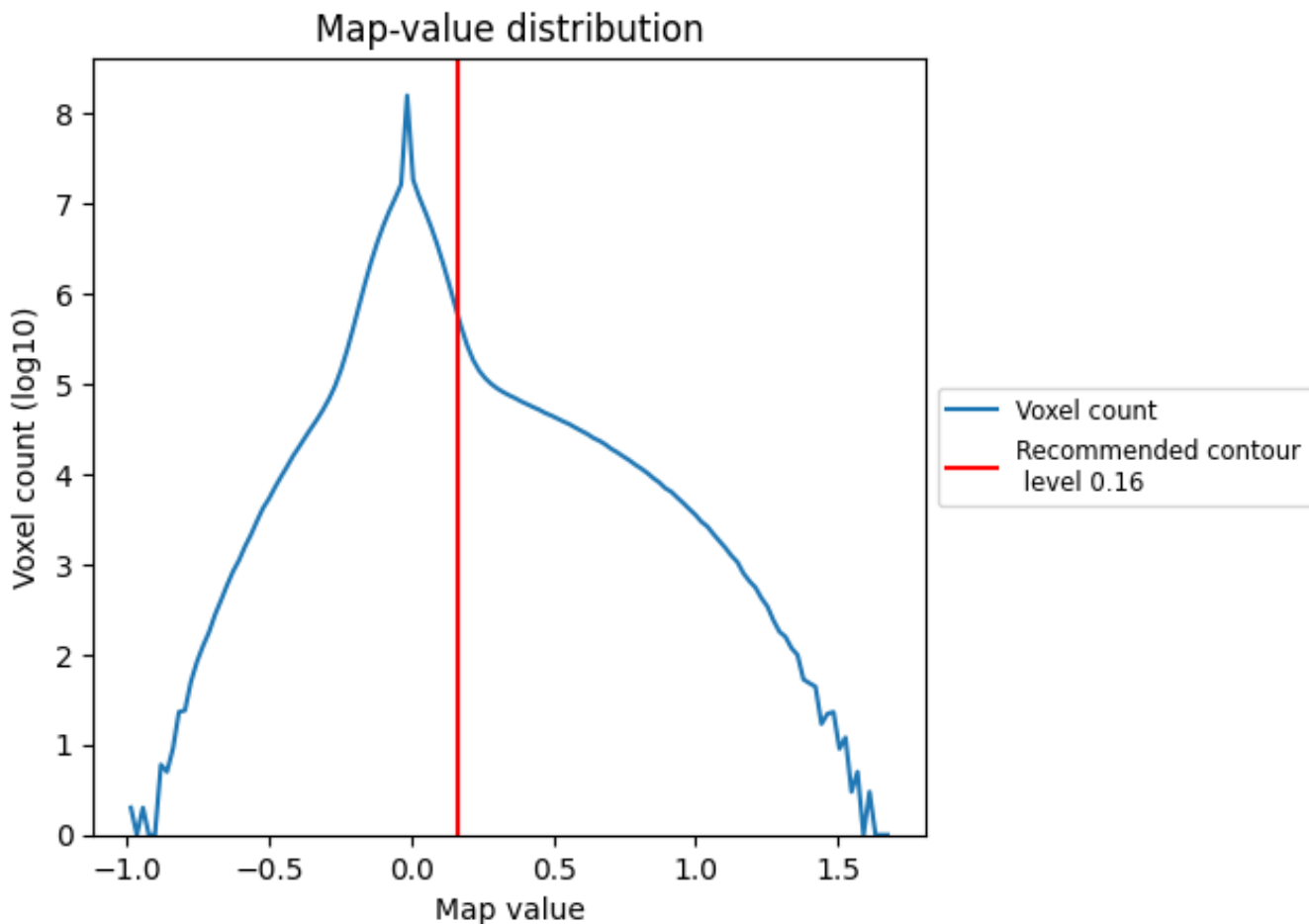
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

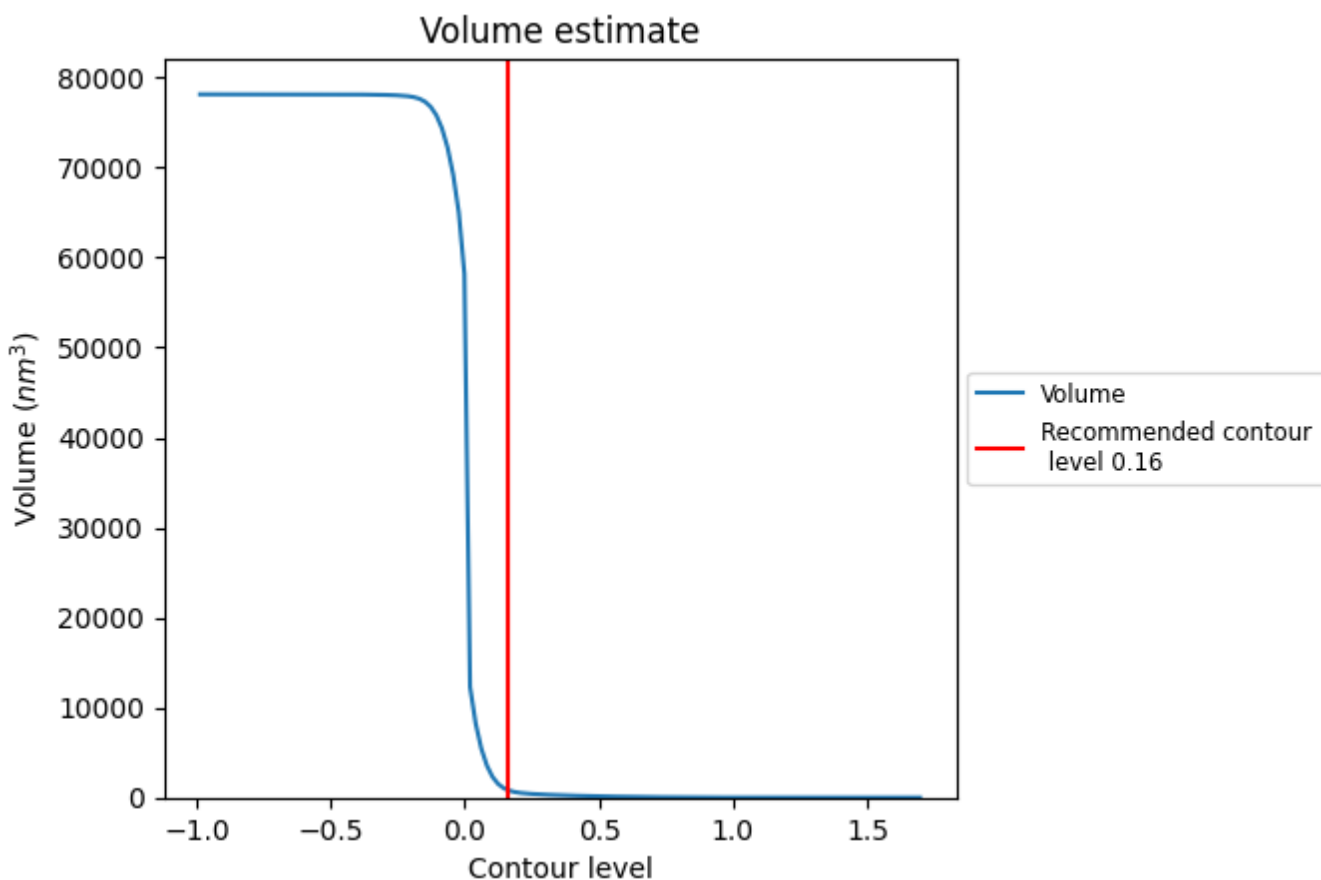
This section contains the results of statistical analysis of the map.

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.

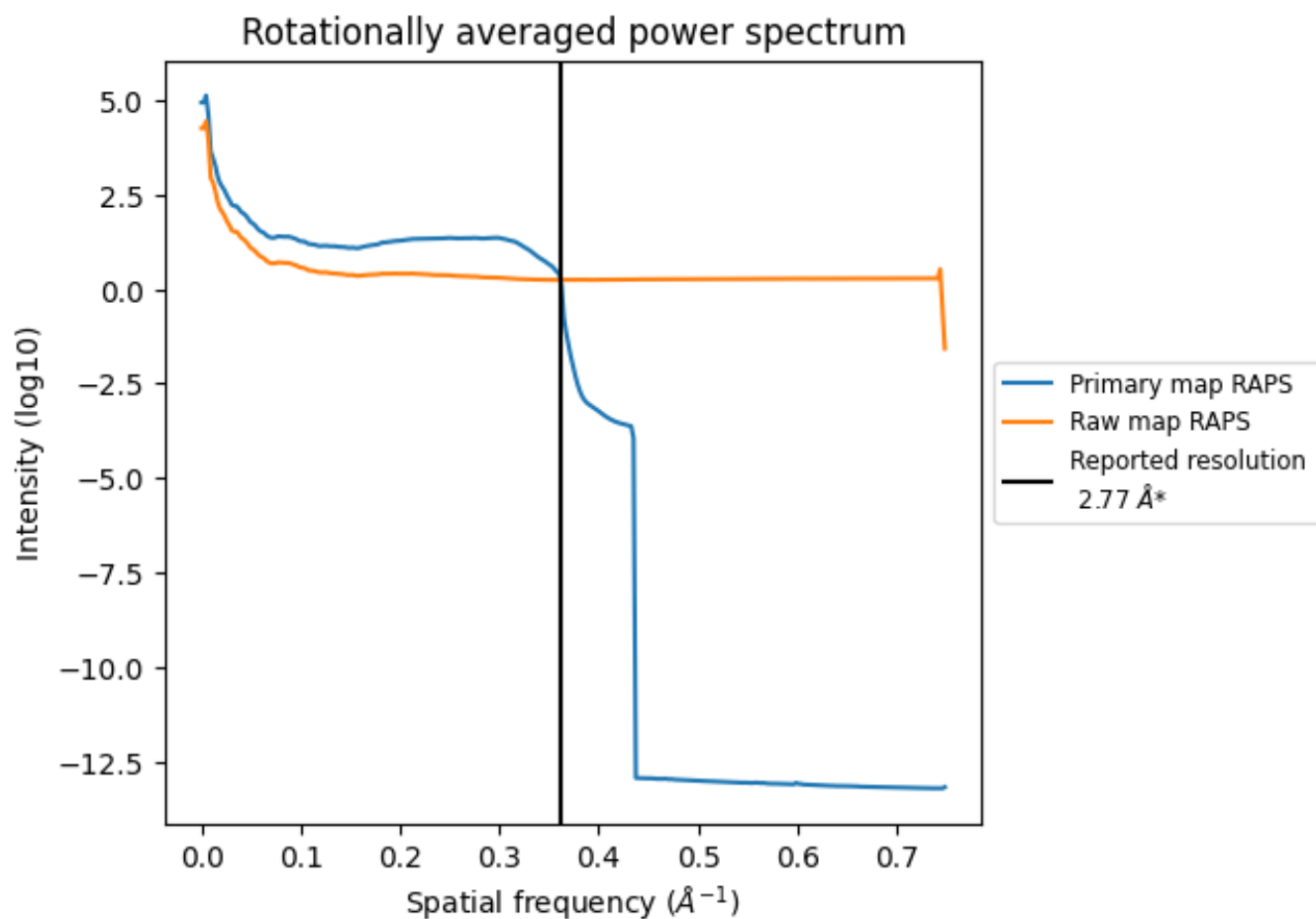
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 854 nm³; this corresponds to an approximate mass of 772 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](#)

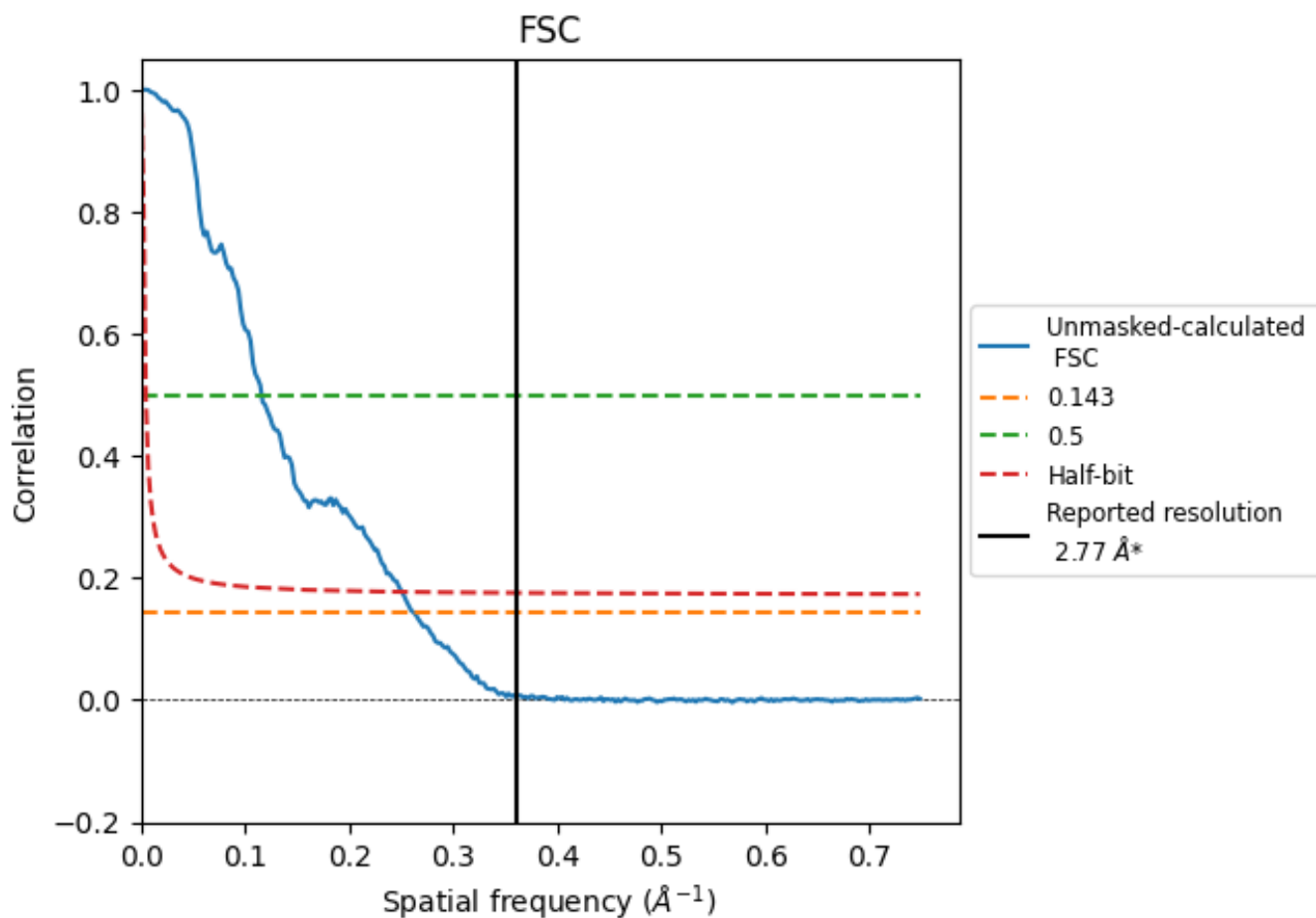


*Reported resolution corresponds to spatial frequency of 0.361 Å⁻¹

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 0.361 Å⁻¹

8.2 Resolution estimates [i](#)

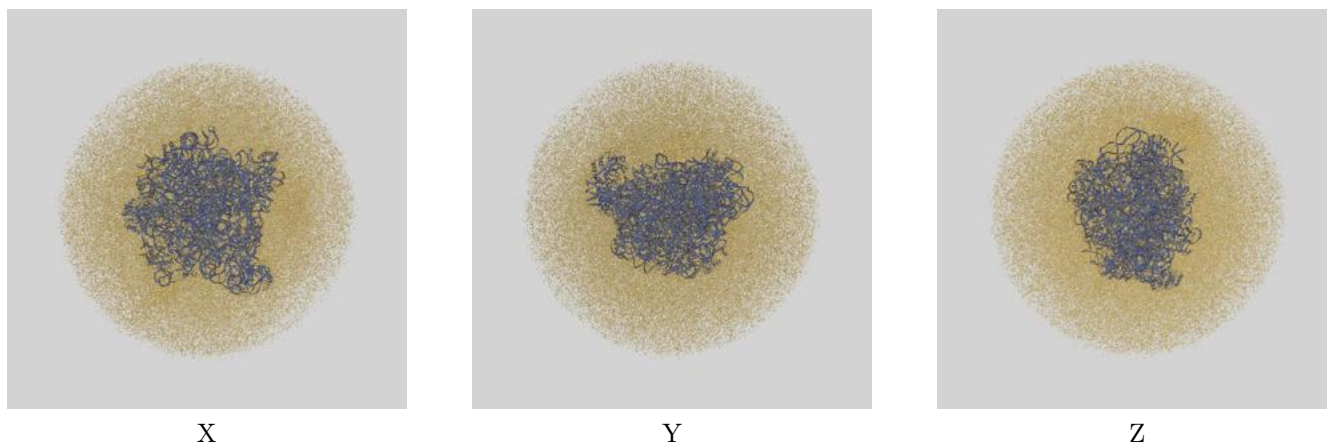
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.77	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	8.63	3.99

*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 3.82 differs from the reported value 2.77 by more than 10 %

9 Map-model fit [i](#)

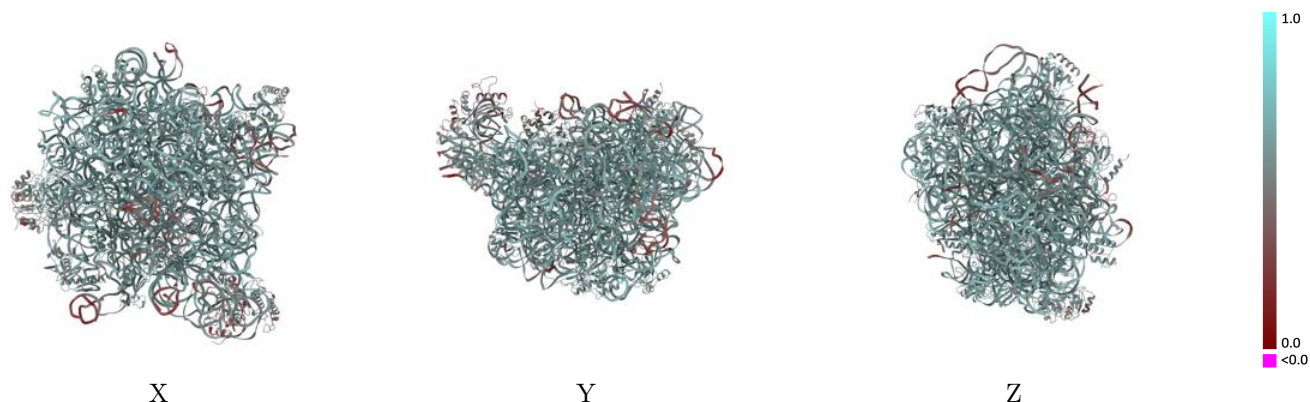
This section contains information regarding the fit between EMDB map EMD-62914 and PDB model 9L9V. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



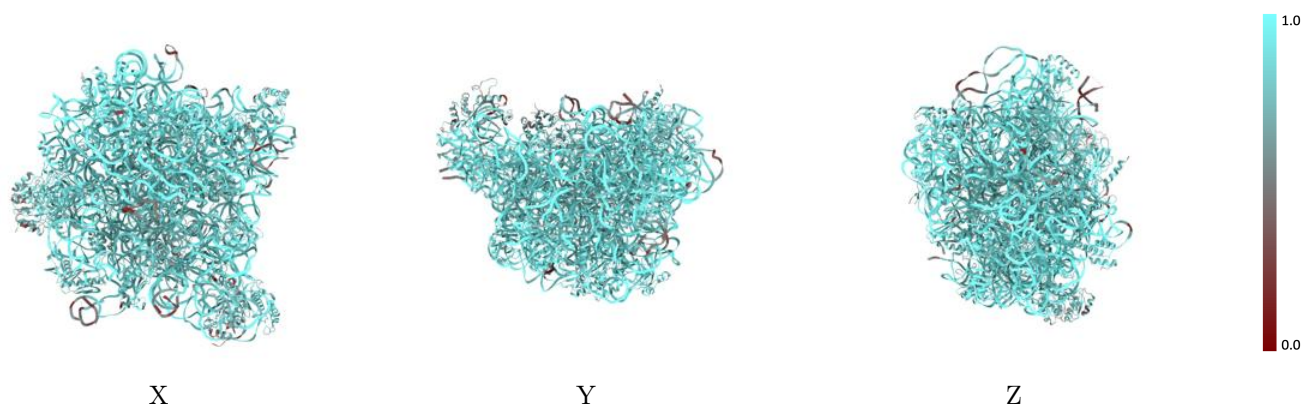
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



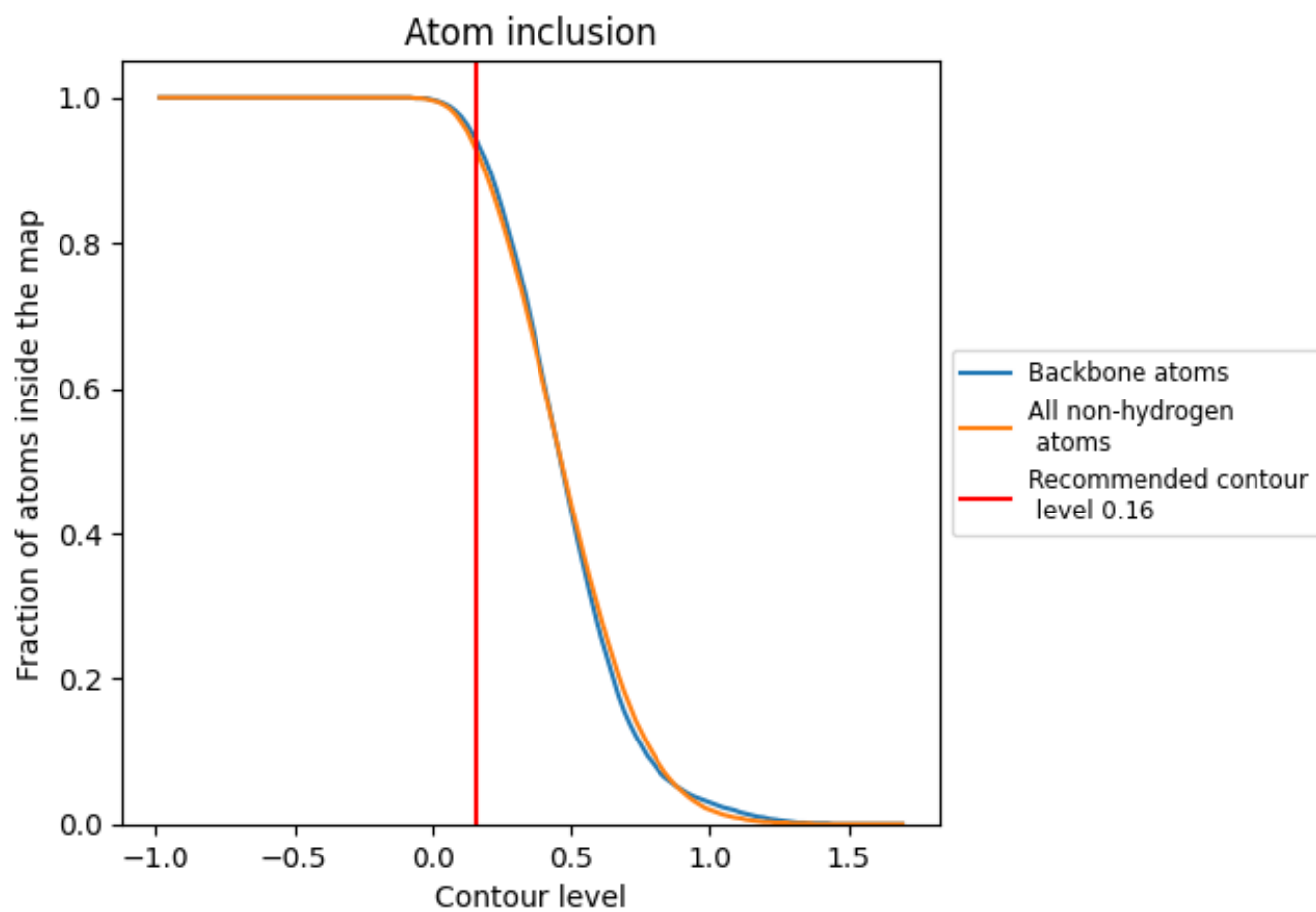
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.16).

























































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9260	 0.5900
0	 0.9490	 0.5950
9	 0.9390	 0.5690
B	 0.7210	 0.5060
E	 0.8440	 0.5530
F	 0.9180	 0.6040
G	 0.9620	 0.6300
H	 0.8890	 0.5870
I	 0.8770	 0.5600
J	 0.9100	 0.5930
K	 0.9440	 0.6180
L	 0.9310	 0.6190
M	 0.9110	 0.6040
N	 0.9070	 0.5950
O	 0.9230	 0.6040
P	 0.8740	 0.5840
Q	 0.9160	 0.6000
R	 0.8760	 0.5780
S	 0.9580	 0.6320
T	 0.9060	 0.6130
U	 0.9300	 0.6020
V	 0.9410	 0.6170
W	 0.9190	 0.6080
X	 0.6440	 0.4270
Y	 0.8300	 0.5570
b	 0.9190	 0.6060
f	 0.9200	 0.6040
i	 0.7790	 0.5090

