wwPDB EM Validation Summary Report ⓘ

Nov 9, 2026 – 10:42 PM JST

PDB ID	:	9XP5 / pdb_00009xp5
EMDB ID	:	EMD-66879
Title	:	Cryo-EM structure of the 50S ribosomal subunit from stationary-phase Methanolobus
Authors	:	Zhu, L.; Yi, C.; Li, W.
Deposited on	:	2025-11-15
Resolution	:	2.10 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:

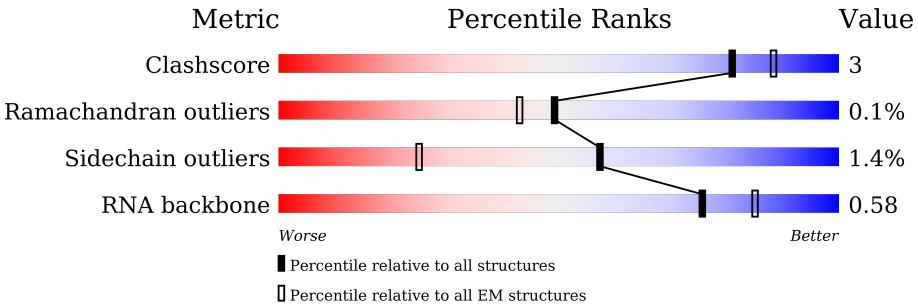
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

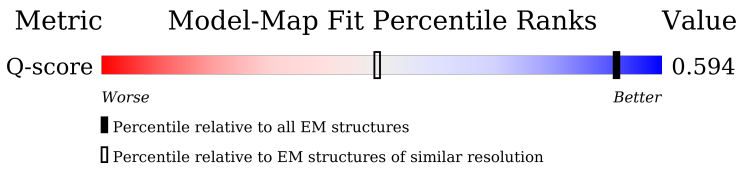
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.10 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.





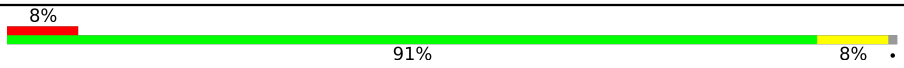
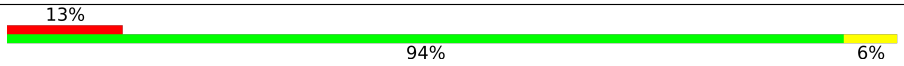
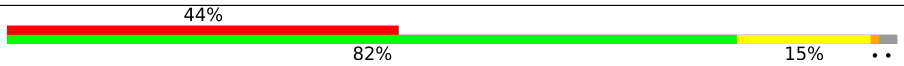
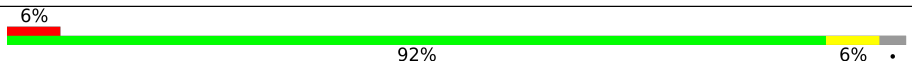
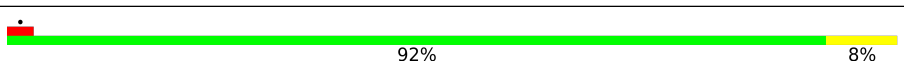
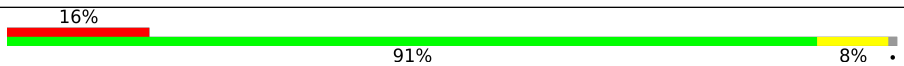
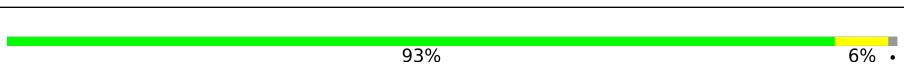
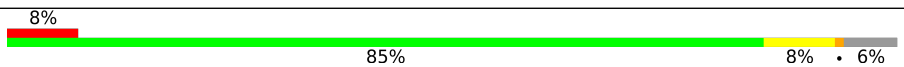
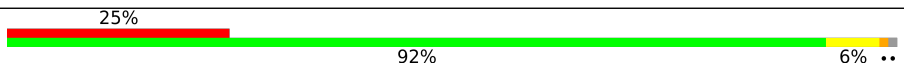
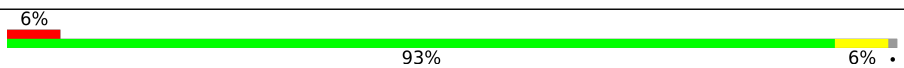
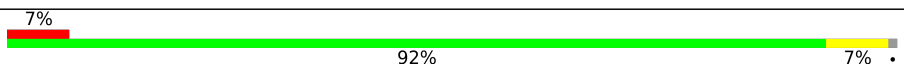
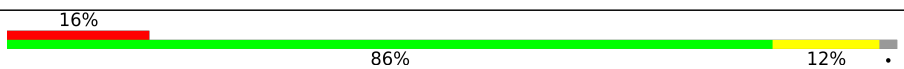
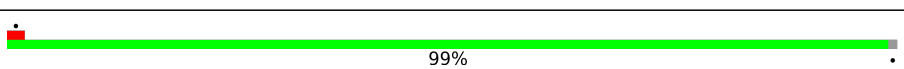
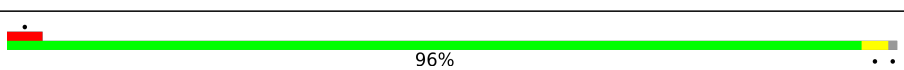
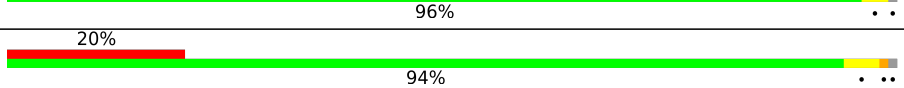
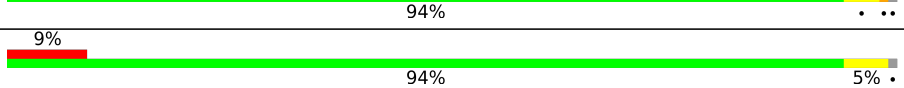
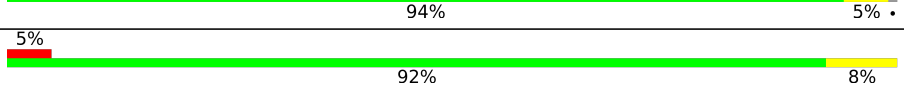
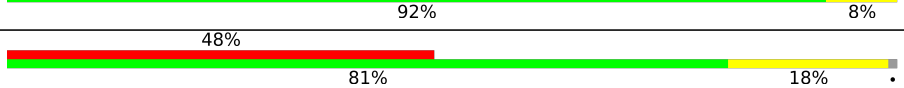
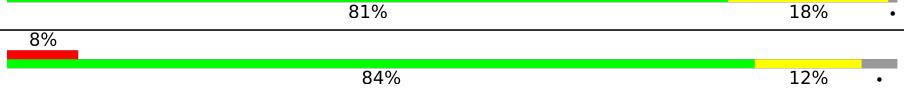
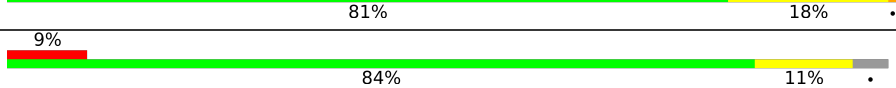
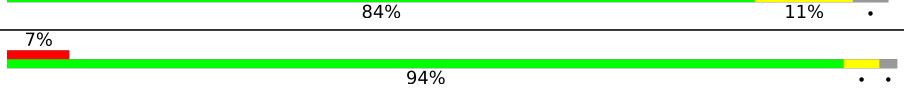
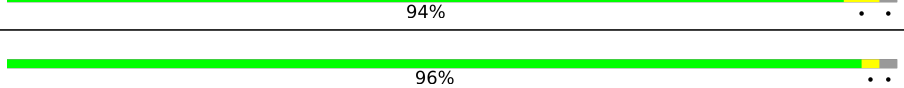
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 (1.71 - 2.70)

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 <=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	1	2910	11% 77% 20%
2	2	126	9% 79% 19%
3	AA	237	8% 95% 5%

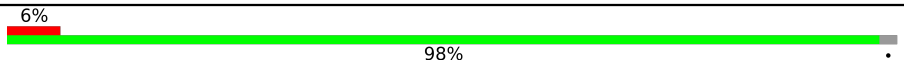
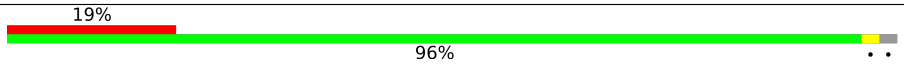
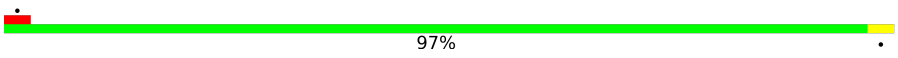
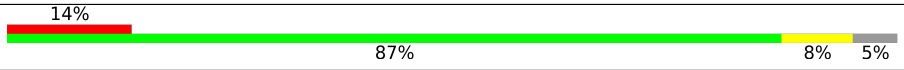
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Mol	Chain	Length	Quality of chain
4	AB	337	
5	AC	253	
6	AD	165	
7	AE	177	
8	AF	130	
9	AG	142	
10	AI	132	
11	AL	147	
12	AM	196	
13	AN	172	
14	AO	173	
15	AP	126	
16	AQ	150	
17	AR	58	
18	AS	97	
19	AT	151	
20	AU	82	
21	AV	117	
22	AW	62	
23	AX	67	
24	AY	160	
25	AZ	95	
26	Aa	90	
27	Ab	129	
28	Ad	56	

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Mol	Chain	Length	Quality of chain
29	Af	51	
30	Ag	47	
31	Ah	92	
32	Ai	97	

2 Entry composition (i)

There are 33 unique types of molecules in this entry. The entry contains 95592 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2910	62358	27842	11402	20204	2910	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	126	2683	1199	479	879	126	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AA	236	1783	1114	345	317	7	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AB	335	2570	1620	460	482	8	0	0

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AC	252	1914	1183	365	359	7	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AD	165	1305	829	230	241	5	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AE	174	Total	C	N	O	S	0	0
			1358	868	228	255	7		

- Molecule 8 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AF	117	Total	C	N	O	S	0	0
			858	538	143	174	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AG	138	Total	C	N	O	S	0	0
			1088	691	196	195	6		

- Molecule 10 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AI	132	Total	C	N	O	S	0	0
			1005	623	194	181	7		

- Molecule 11 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	146	Total	C	N	O	S	0	0
			1092	666	207	216	3		

- Molecule 12 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AM	195	Total	C	N	O	S	0	0
			1600	985	332	277	6		

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AN	161	Total	C	N	O	S	0	0
			1265	789	251	218	7		

- Molecule 14 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AO	172	Total	C	N	O	S	0	0
			1344	844	237	261	2		

- Molecule 15 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AP	125	Total	C	N	O	S	0	0
			957	604	171	179	3		

- Molecule 16 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	149	Total	C	N	O	S	0	0
			1190	733	246	206	5		

- Molecule 17 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	AR	57	Total	C	N	O	0	0
			454	290	78	86		

- Molecule 18 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	96	Total	C	N	O	S	0	0
			761	472	146	138	5		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AT	150	Total	C	N	O	S	0	0
			1157	717	222	209	9		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	81	Total	C	N	O	S	0	0
			629	404	103	114	8		

- Molecule 21 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AV	116	Total	C	N	O	S	0	0
			900	558	171	168	3		

- Molecule 22 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AW	62	Total	C	N	O	S	0	0
			504	319	88	92	5		

- Molecule 23 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	66	Total	C	N	O	S	0	0
			528	318	103	102	5		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AY	153	Total	C	N	O	S	0	0
			1199	746	228	219	6		

- Molecule 25 is a protein called Ribosomal protein L30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AZ	95	Total	C	N	O	S	0	0
			683	429	116	133	5		

- Molecule 26 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Aa	86	Total	C	N	O	S	0	0
			716	460	126	128	2		

- Molecule 27 is a protein called 50S ribosomal protein L23e.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ab	126	Total	C	N	O	S	0	0
			993	626	195	171	1		

- Molecule 28 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ad	55	Total	C	N	O	S	0	0
			435	264	91	73	7		

- Molecule 29 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	Af	50	Total	C	N	O	0	0
			422	261	97	64		

- Molecule 30 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ag	46	Total	C	N	O	S	0	0
			362	218	77	61	6		

- Molecule 31 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ah	92	Total	C	N	O	S	0	0
			758	472	157	123	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ai	92	Total	C	N	O	S	0	0
			716	439	146	125	6		

- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
33	AW	1	Total	Zn	0
			1	1	
33	Ad	1	Total	Zn	0
			1	1	
33	Ag	1	Total	Zn	0
			1	1	
33	Ah	1	Total	Zn	0
			1	1	
33	Ai	1	Total	Zn	0
			1	1	

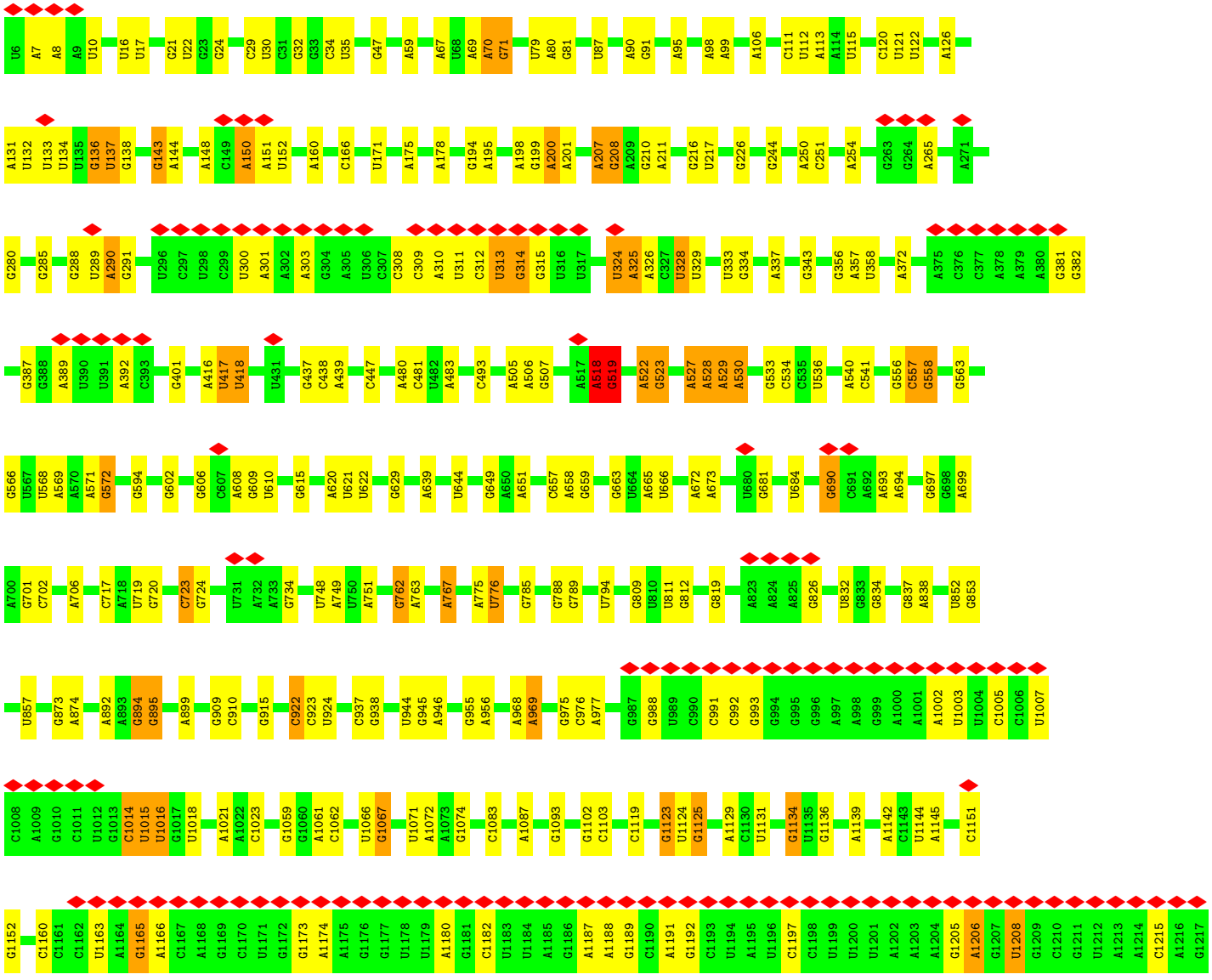
3 Residue-property plots (i)

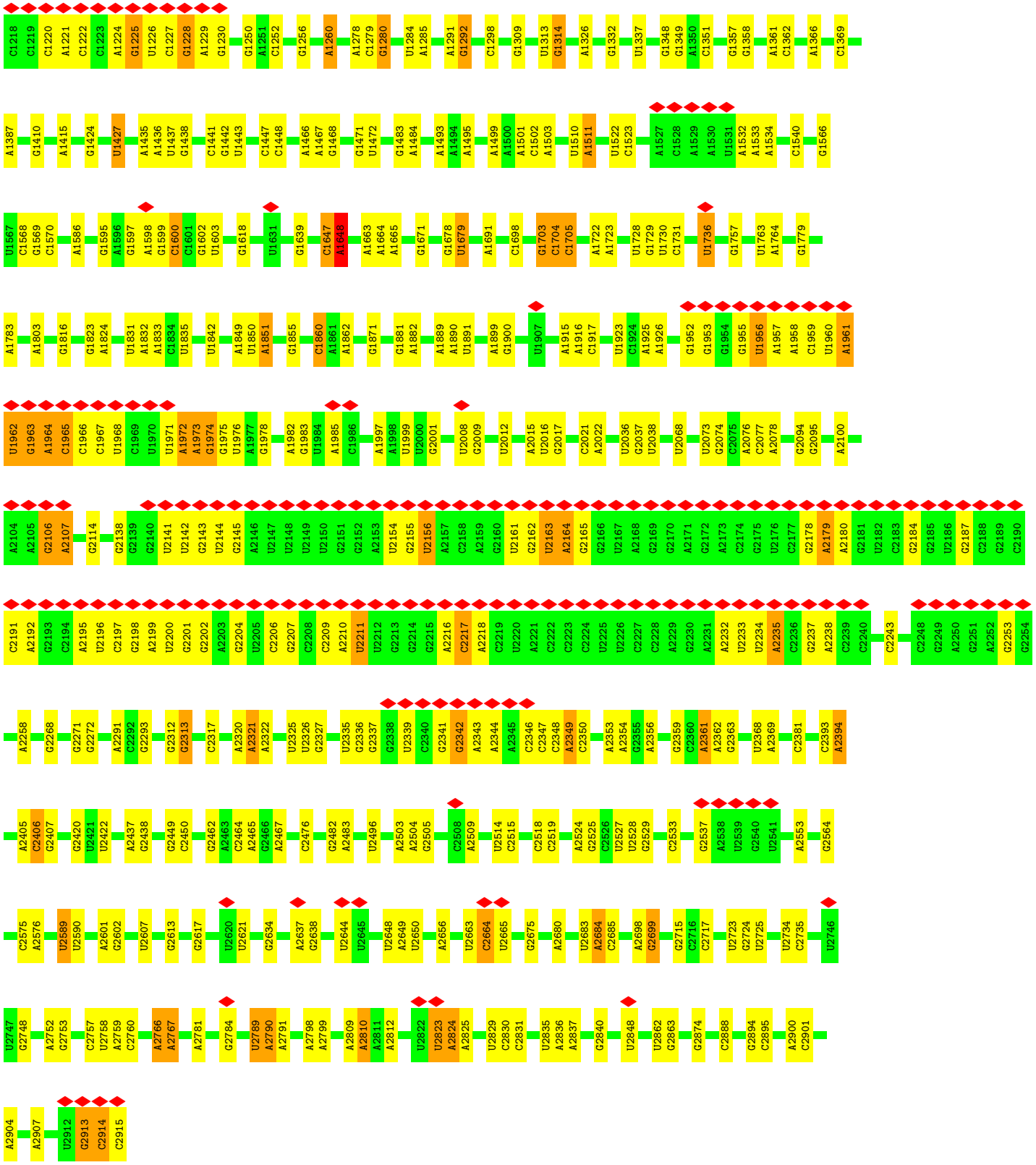
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 rRNA

Chain 1:



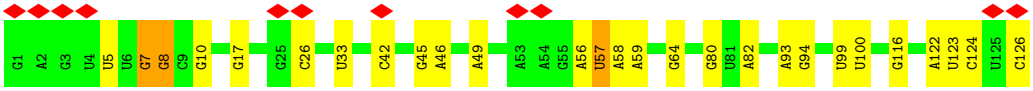




• Molecule 2: 5S rRNA

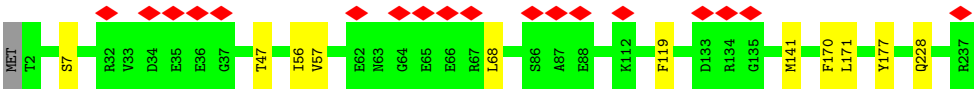
Chain 2:



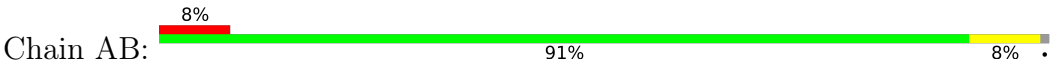


• Molecule 3: Large ribosomal subunit protein uL2





• Molecule 4: Large ribosomal subunit protein uL3

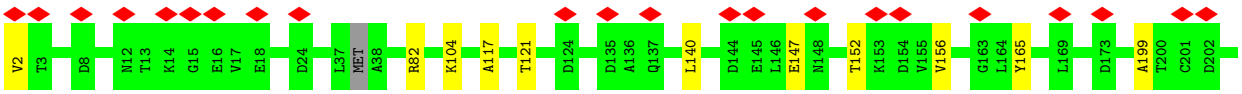


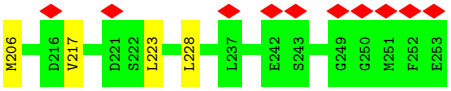




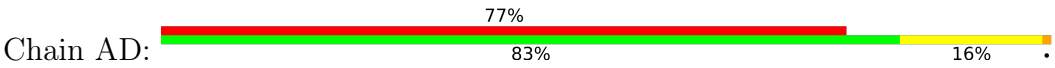
• Molecule 5: 50S ribosomal protein L4

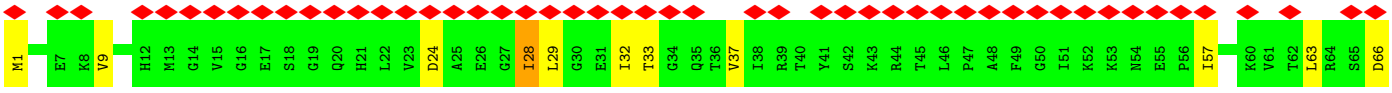


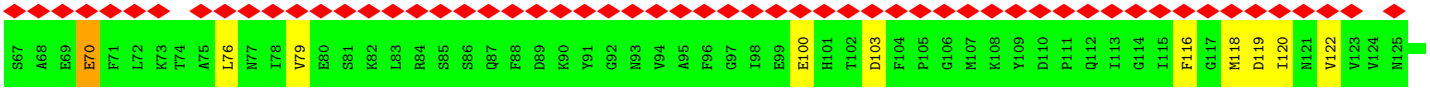




• Molecule 6: Large ribosomal subunit protein uL5



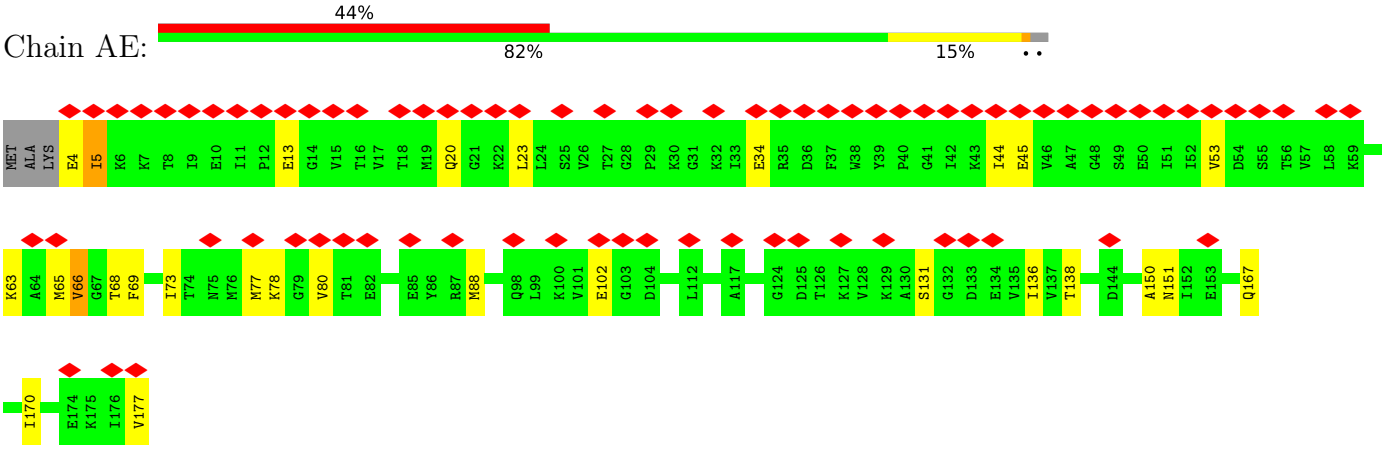






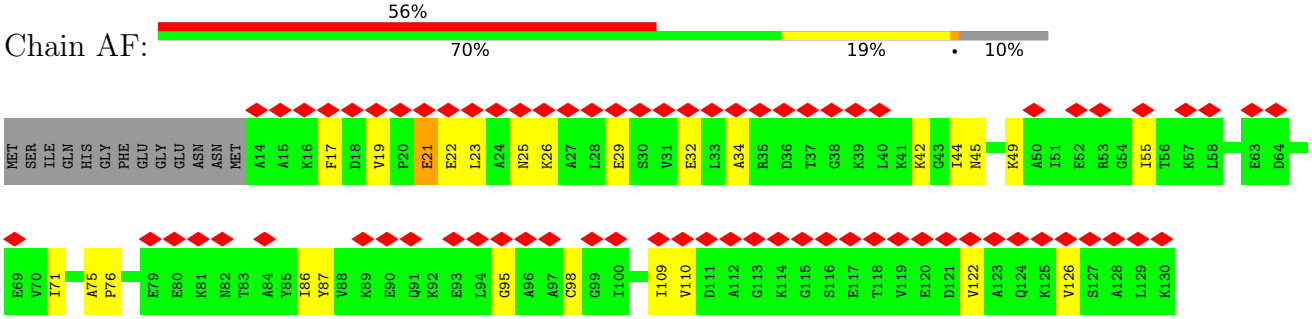
• Molecule 7: Large ribosomal subunit protein uL6

Chain AE:



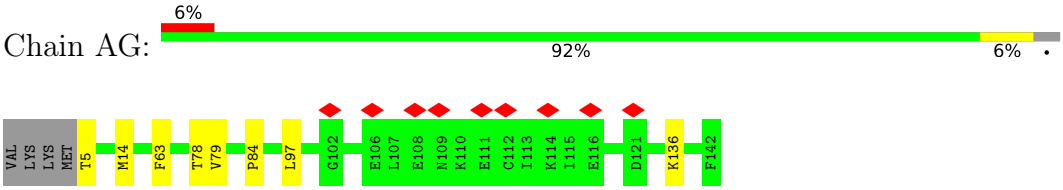
• Molecule 8: 50S ribosomal protein L7Ae

Chain AF:



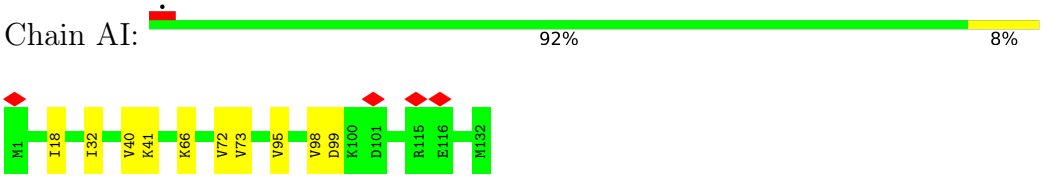
• Molecule 9: 50S ribosomal protein L13

Chain AG:



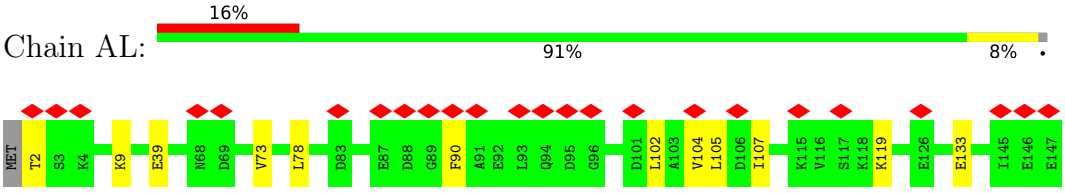
• Molecule 10: Large ribosomal subunit protein uL14

Chain AI:



• Molecule 11: Large ribosomal subunit protein uL15

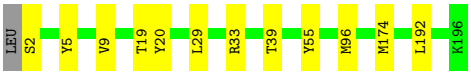
Chain AL:



• Molecule 12: 50S ribosomal protein L15e

Chain AM:

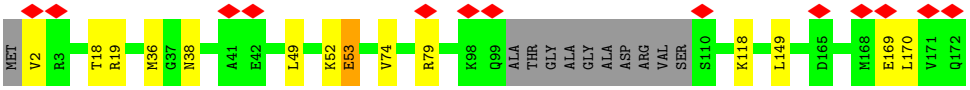




• Molecule 13: Large ribosomal subunit protein uL16

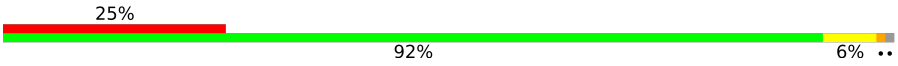
Chain AN:

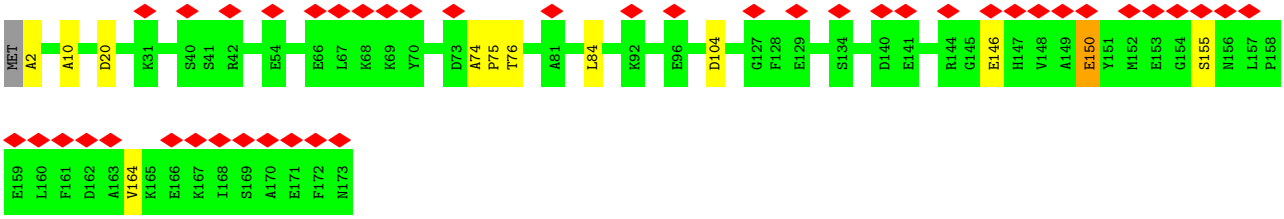




• Molecule 14: Large ribosomal subunit protein uL18

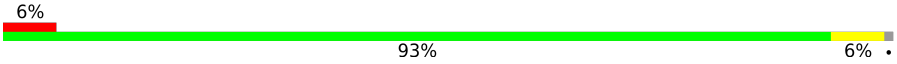
Chain AO:

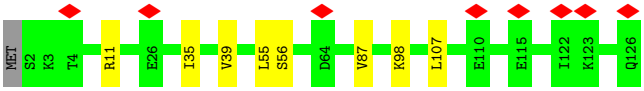




• Molecule 15: Large ribosomal subunit protein eL18

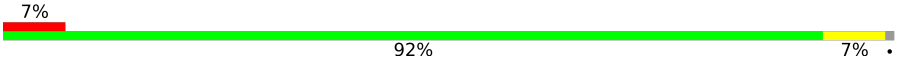
Chain AP:

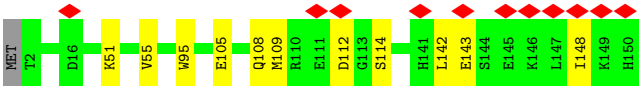




• Molecule 16: Large ribosomal subunit protein eL19

Chain AQ:

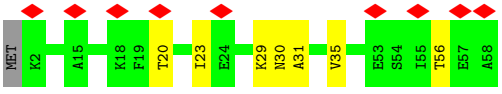




• Molecule 17: Large ribosomal subunit protein eL20

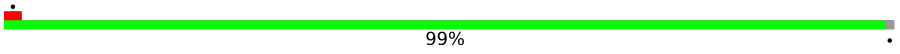
Chain AR:

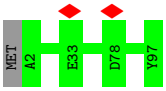




• Molecule 18: Large ribosomal subunit protein eL21

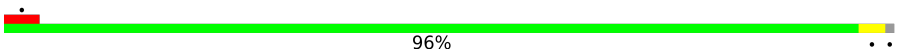
Chain AS:

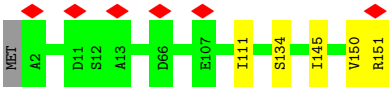




• Molecule 19: 50S ribosomal protein L22

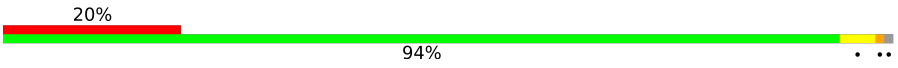
Chain AT:

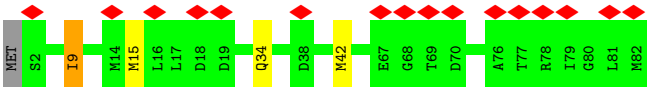




• Molecule 20: 50S ribosomal protein L23

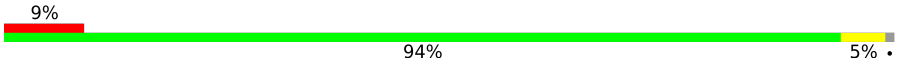
Chain AU:

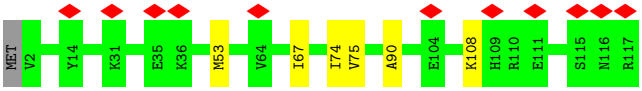




• Molecule 21: Large ribosomal subunit protein uL24

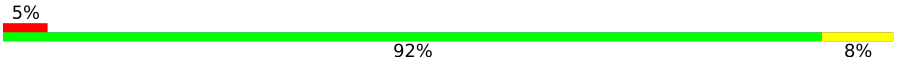
Chain AV:

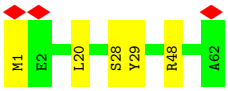




• Molecule 22: Large ribosomal subunit protein eL24

Chain AW:

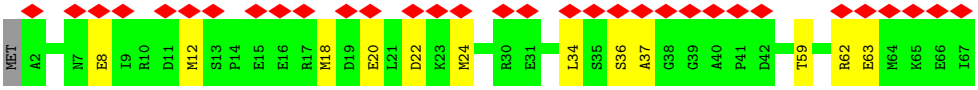




• Molecule 23: Large ribosomal subunit protein uL29

Chain AX:

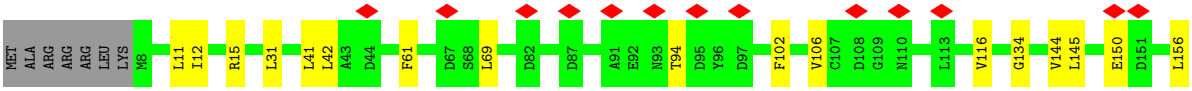




• Molecule 24: 50S ribosomal protein L30

Chain AY:



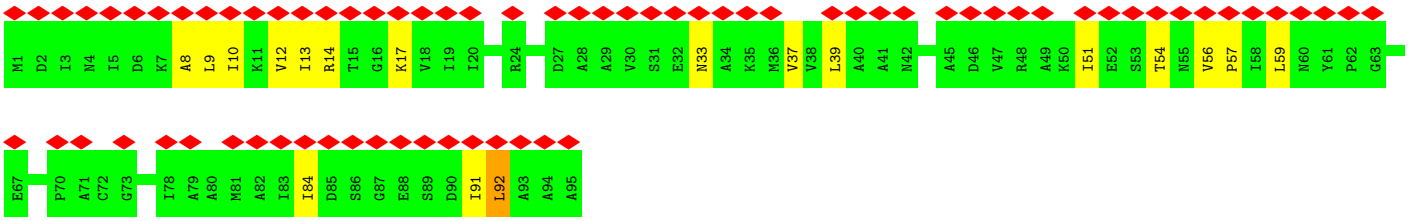




• Molecule 25: Ribosomal protein L30E

Chain AZ:

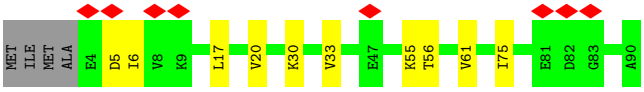




• Molecule 26: 50S ribosomal protein L31e

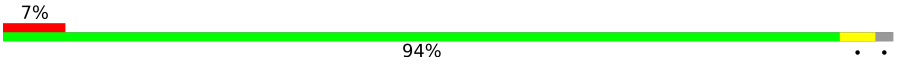
Chain Aa:

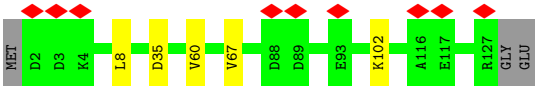




• Molecule 27: 50S ribosomal protein L23e

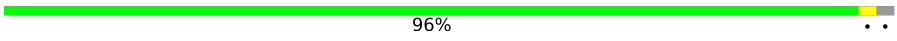
Chain Ab:

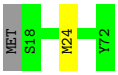




• Molecule 28: Large ribosomal subunit protein eL37

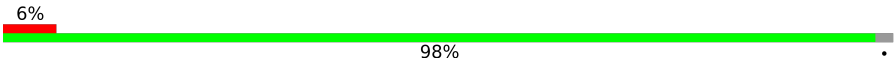
Chain Ad:

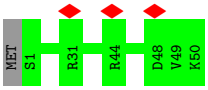




• Molecule 29: Large ribosomal subunit protein eL39

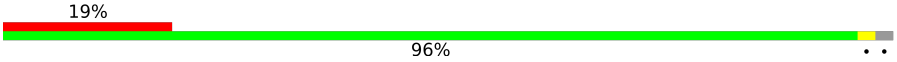
Chain Af:

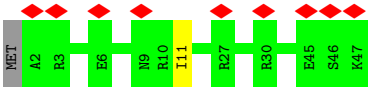




• Molecule 30: Large ribosomal subunit protein eL40

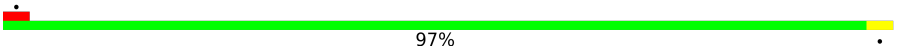
Chain Ag:

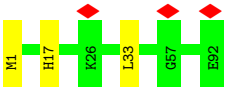




• Molecule 31: Large ribosomal subunit protein eL42

Chain Ah:

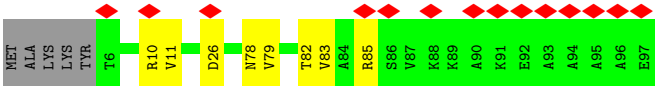




• Molecule 32: Large ribosomal subunit protein eL43

Chain Ai:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	482027	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.733	Depositor
Minimum map value	-0.926	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	446.4, 446.4, 446.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	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

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	1	0.27	0/69829	0.67	8/108904 (0.0%)
2	2	0.24	0/2999	0.66	0/4671
3	AA	0.13	0/1821	0.34	0/2454
4	AB	0.13	0/2620	0.34	0/3541
5	AC	0.13	0/1943	0.33	0/2620
6	AD	0.16	0/1328	0.41	0/1784
7	AE	0.16	0/1378	0.38	0/1849
8	AF	0.14	0/864	0.38	0/1165
9	AG	0.13	0/1102	0.32	0/1472
10	AI	0.13	0/1016	0.34	0/1363
11	AL	0.14	0/1102	0.35	0/1470
12	AM	0.14	0/1628	0.35	0/2173
13	AN	0.13	0/1285	0.34	0/1720
14	AO	0.13	0/1369	0.33	0/1846
15	AP	0.13	0/966	0.30	0/1299
16	AQ	0.16	0/1204	0.34	0/1598
17	AR	0.13	0/460	0.32	0/614
18	AS	0.12	0/775	0.27	0/1033
19	AT	0.14	0/1176	0.35	0/1575
20	AU	0.15	0/637	0.38	0/852
21	AV	0.14	0/911	0.35	0/1224
22	AW	0.14	0/514	0.30	0/683
23	AX	0.14	0/530	0.38	0/704
24	AY	0.15	0/1216	0.38	0/1634
25	AZ	0.19	0/689	0.46	0/934
26	Aa	0.14	0/730	0.34	0/980
27	Ab	0.14	0/1007	0.34	0/1344
28	Ad	0.12	0/442	0.32	0/582
29	Af	0.16	0/432	0.30	0/578
30	Ag	0.13	0/363	0.38	0/476
31	Ah	0.14	0/774	0.30	0/1027
32	Ai	0.15	0/727	0.37	0/968

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
All	All	0.23	0/103837	0.60	8/155137 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	518	A	O4'-C1'-N9	6.11	113.09	108.20
1	1	519	G	O5'-C5'-C4'	6.01	114.21	109.40
1	1	1427	U	C2-N1-C1'	6.00	124.90	117.70
1	1	1647	C	O4'-C1'-N1	5.92	112.93	108.20
1	1	1648	A	O5'-C5'-C4'	5.89	114.11	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	62358	0	31379	235	0
2	2	2683	0	1358	8	0
3	AA	1783	0	1844	6	0
4	AB	2570	0	2632	16	0
5	AC	1914	0	1949	8	0
6	AD	1305	0	1344	18	0
7	AE	1358	0	1414	17	0
8	AF	858	0	889	15	0
9	AG	1088	0	1161	4	0
10	AI	1005	0	1067	6	0
11	AL	1092	0	1097	9	0
12	AM	1600	0	1648	9	0
13	AN	1265	0	1312	6	0
14	AO	1344	0	1337	8	0
15	AP	957	0	1022	5	0
16	AQ	1190	0	1257	8	0
17	AR	454	0	468	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	AS	761	0	778	0	0
19	AT	1157	0	1188	2	0
20	AU	629	0	666	4	0
21	AV	900	0	941	3	0
22	AW	504	0	503	3	0
23	AX	528	0	546	7	0
24	AY	1199	0	1227	14	0
25	AZ	683	0	721	12	0
26	Aa	716	0	751	4	0
27	Ab	993	0	1069	4	0
28	Ad	435	0	449	0	0
29	Af	422	0	451	0	0
30	Ag	362	0	388	1	0
31	Ah	758	0	793	1	0
32	Ai	716	0	739	5	0
33	AW	1	0	0	0	0
33	Ad	1	0	0	0	0
33	Ag	1	0	0	0	0
33	Ah	1	0	0	0	0
33	Ai	1	0	0	0	0
All	All	95592	0	64388	417	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 3.

The worst 5 of 417 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)
25:AZ:8:ALA:O	25:AZ:12:VAL:HG23	1.81	0.80
1:1:1314:G:H1	1:1:1358:G:H22	1.36	0.71
6:AD:24:ASP:O	6:AD:28:ILE:HD12	1.91	0.70
20:AU:9:ILE:HD11	23:AX:37:ALA:HB2	1.73	0.70
1:1:1314:G:H22	1:1:1358:G:N2	1.90	0.69

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	AA	234/237 (99%)	226 (97%)	8 (3%)	0	100	100
4	AB	333/337 (99%)	327 (98%)	5 (2%)	1 (0%)	36	36
5	AC	250/253 (99%)	241 (96%)	9 (4%)	0	100	100
6	AD	163/165 (99%)	155 (95%)	8 (5%)	0	100	100
7	AE	172/177 (97%)	166 (96%)	5 (3%)	1 (1%)	21	18
8	AF	115/130 (88%)	109 (95%)	6 (5%)	0	100	100
9	AG	136/142 (96%)	134 (98%)	2 (2%)	0	100	100
10	AI	130/132 (98%)	130 (100%)	0	0	100	100
11	AL	144/147 (98%)	136 (94%)	8 (6%)	0	100	100
12	AM	193/196 (98%)	190 (98%)	3 (2%)	0	100	100
13	AN	157/172 (91%)	143 (91%)	13 (8%)	1 (1%)	21	18
14	AO	170/173 (98%)	169 (99%)	1 (1%)	0	100	100
15	AP	123/126 (98%)	123 (100%)	0	0	100	100
16	AQ	147/150 (98%)	146 (99%)	1 (1%)	0	100	100
17	AR	55/58 (95%)	54 (98%)	1 (2%)	0	100	100
18	AS	94/97 (97%)	94 (100%)	0	0	100	100
19	AT	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
20	AU	79/82 (96%)	78 (99%)	1 (1%)	0	100	100
21	AV	114/117 (97%)	114 (100%)	0	0	100	100
22	AW	60/62 (97%)	60 (100%)	0	0	100	100
23	AX	64/67 (96%)	64 (100%)	0	0	100	100
24	AY	151/160 (94%)	147 (97%)	4 (3%)	0	100	100
25	AZ	93/95 (98%)	90 (97%)	2 (2%)	1 (1%)	11	8
26	Aa	84/90 (93%)	83 (99%)	1 (1%)	0	100	100
27	Ab	124/129 (96%)	124 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Ad	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
29	Af	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
30	Ag	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
31	Ah	90/92 (98%)	90 (100%)	0	0	100	100
32	Ai	90/97 (93%)	88 (98%)	2 (2%)	0	100	100
All	All	3858/3988 (97%)	3765 (98%)	89 (2%)	4 (0%)	49	50

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AB	322	MET
13	AN	53	GLU
25	AZ	54	THR
7	AE	5	ILE

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	AA	184/185 (100%)	181 (98%)	3 (2%)	55	64
4	AB	277/278 (100%)	275 (99%)	2 (1%)	76	83
5	AC	199/200 (100%)	197 (99%)	2 (1%)	68	76
6	AD	145/145 (100%)	141 (97%)	4 (3%)	38	43
7	AE	149/151 (99%)	147 (99%)	2 (1%)	61	69
8	AF	89/100 (89%)	87 (98%)	2 (2%)	45	53
9	AG	115/119 (97%)	113 (98%)	2 (2%)	53	62
10	AI	108/108 (100%)	107 (99%)	1 (1%)	70	78
11	AL	113/114 (99%)	111 (98%)	2 (2%)	51	60
12	AM	166/167 (99%)	165 (99%)	1 (1%)	78	86
13	AN	130/136 (96%)	127 (98%)	3 (2%)	44	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
14	AO	143/144 (99%)	139 (97%)	4 (3%)	38 43
15	AP	103/104 (99%)	102 (99%)	1 (1%)	68 76
16	AQ	120/121 (99%)	119 (99%)	1 (1%)	73 81
17	AR	49/50 (98%)	48 (98%)	1 (2%)	48 56
18	AS	82/83 (99%)	82 (100%)	0	100 100
19	AT	122/123 (99%)	121 (99%)	1 (1%)	73 81
20	AU	70/71 (99%)	68 (97%)	2 (3%)	37 42
21	AV	99/100 (99%)	98 (99%)	1 (1%)	68 76
22	AW	55/55 (100%)	54 (98%)	1 (2%)	51 60
23	AX	57/58 (98%)	55 (96%)	2 (4%)	32 35
24	AY	129/135 (96%)	129 (100%)	0	100 100
25	AZ	73/73 (100%)	72 (99%)	1 (1%)	59 67
26	Aa	78/81 (96%)	75 (96%)	3 (4%)	29 32
27	Ab	104/106 (98%)	104 (100%)	0	100 100
28	Ad	49/50 (98%)	48 (98%)	1 (2%)	48 56
29	Af	46/47 (98%)	46 (100%)	0	100 100
30	Ag	39/40 (98%)	39 (100%)	0	100 100
31	Ah	82/82 (100%)	80 (98%)	2 (2%)	43 49
32	Ai	73/77 (95%)	73 (100%)	0	100 100
All	All	3248/3303 (98%)	3203 (99%)	45 (1%)	57 67

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	AP	11	ARG
22	AW	1	MET
16	AQ	51	LYS
20	AU	9	ILE
23	AX	36	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
15	AP	31	ASN

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Mol	Chain	Res	Type
18	AS	5	HIS
17	AR	5	GLN
21	AV	22	GLN
5	AC	148	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2909/2910 (99%)	413 (14%)	14 (0%)
2	2	125/126 (99%)	16 (12%)	1 (0%)
All	All	3034/3036 (99%)	429 (14%)	15 (0%)

5 of 429 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	7	A
1	1	8	A
1	1	10	U
1	1	24	G
1	1	47	G

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	894	G
1	1	2914	C
1	1	1703	G
2	2	7	G
1	1	2789	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 5 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.

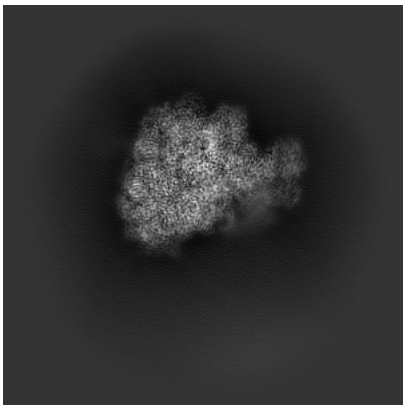
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-66879. These allow visual inspection of the internal detail of the map and identification of artifacts.

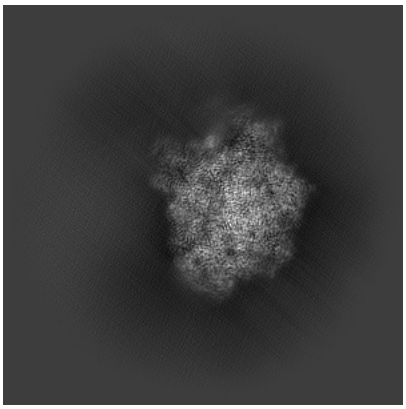
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

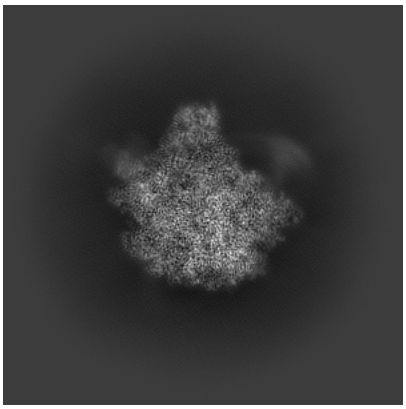
6.1.1 Primary map



X

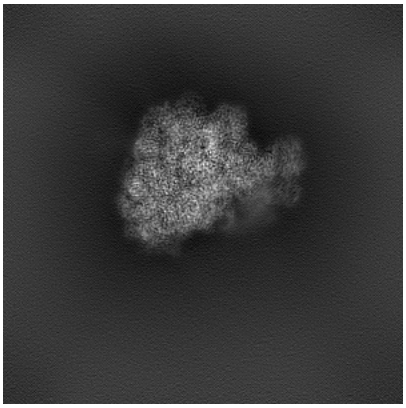


Y

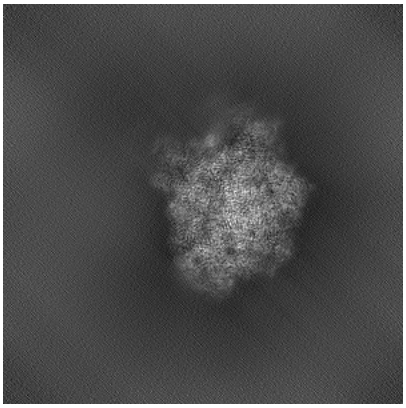


Z

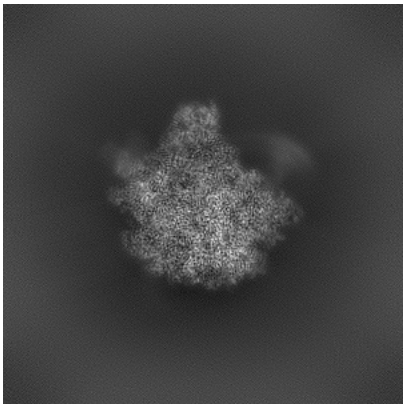
6.1.2 Raw map



X



Y

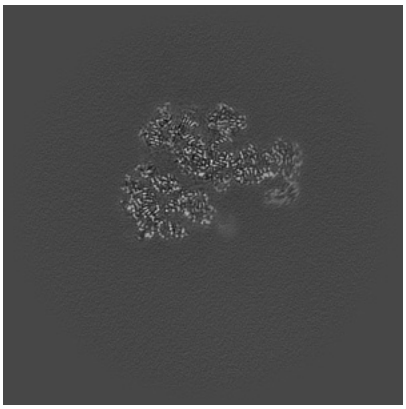


Z

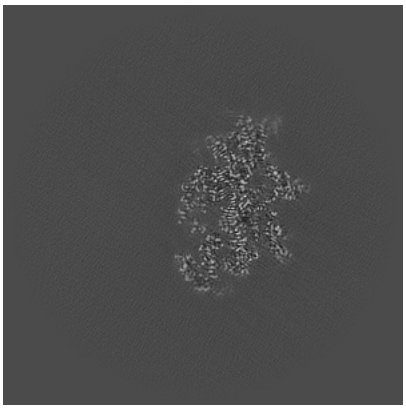
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

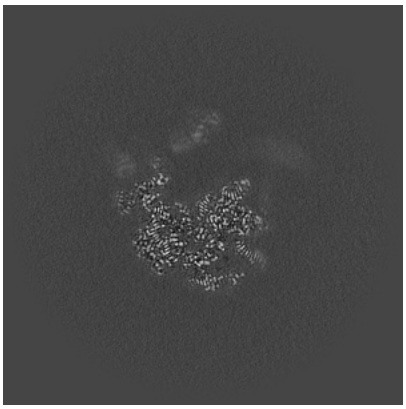
6.2.1 Primary map



X Index: 240

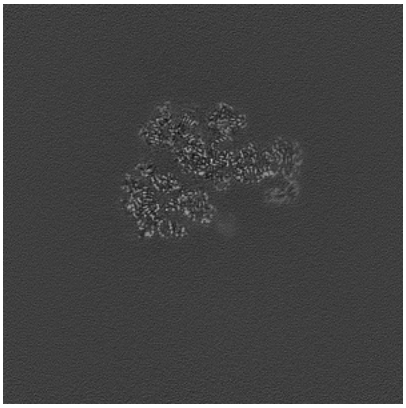


Y Index: 240

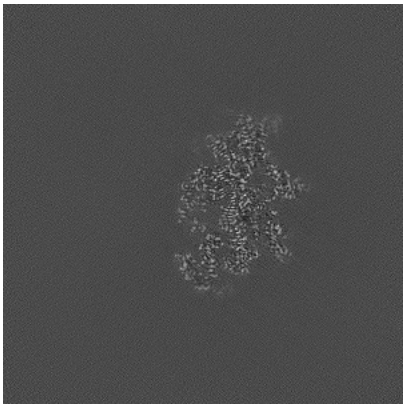


Z Index: 240

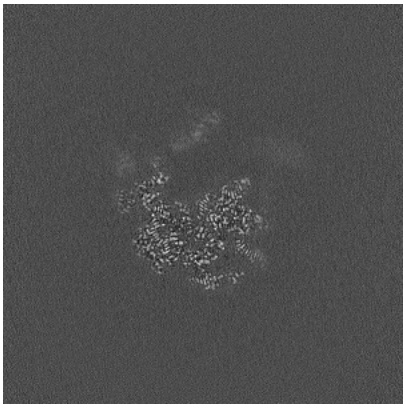
6.2.2 Raw map



X Index: 240



Y Index: 240

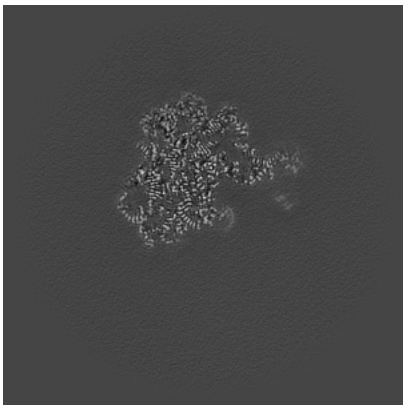


Z Index: 240

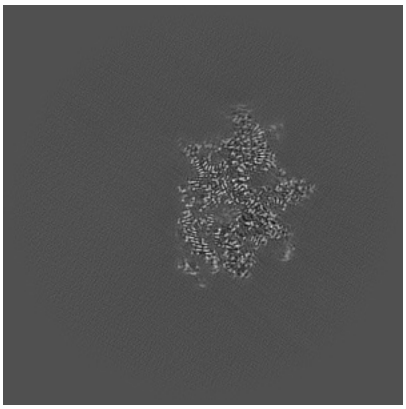
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

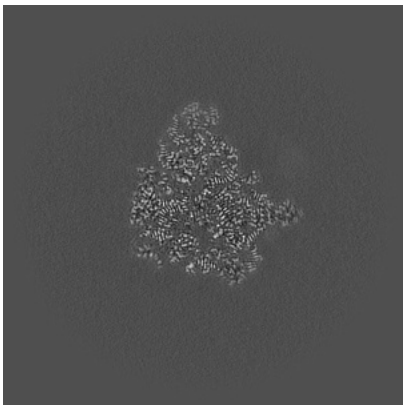
6.3.1 Primary map



X Index: 256

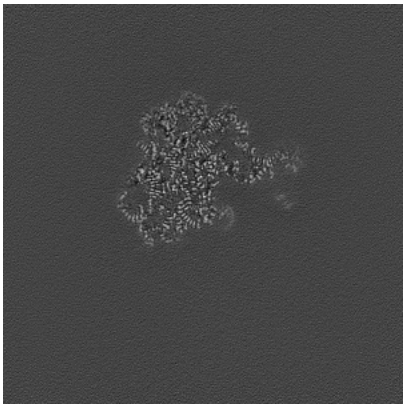


Y Index: 229

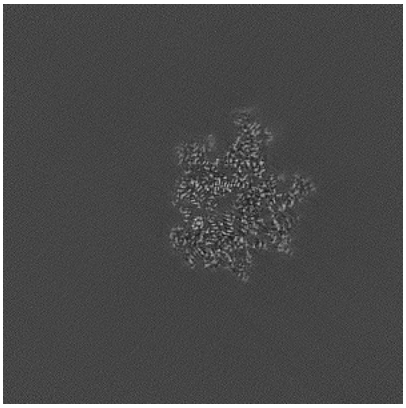


Z Index: 283

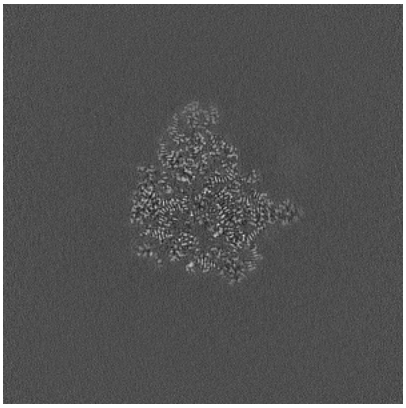
6.3.2 Raw map



X Index: 256



Y Index: 219

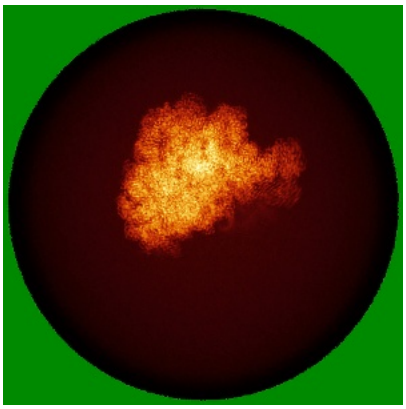


Z Index: 283

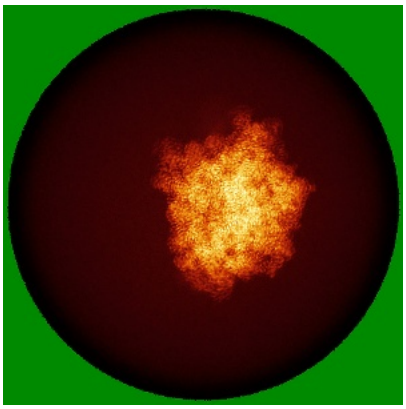
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

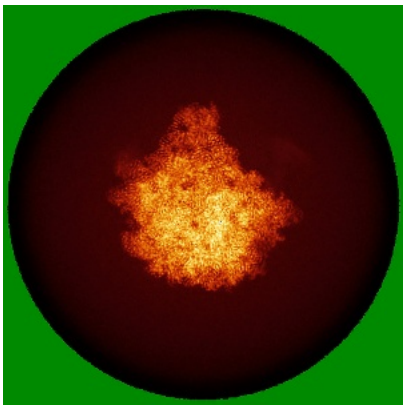
6.4.1 Primary map



X

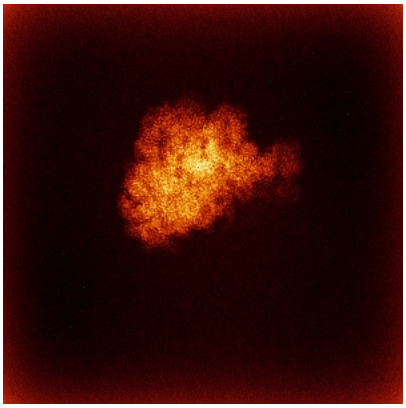


Y

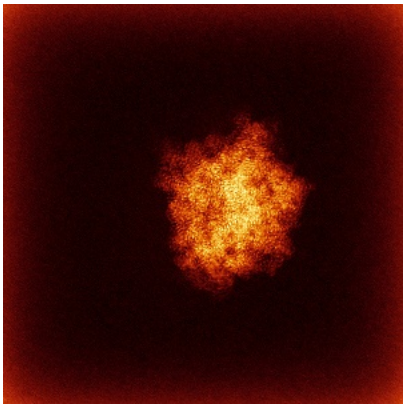


Z

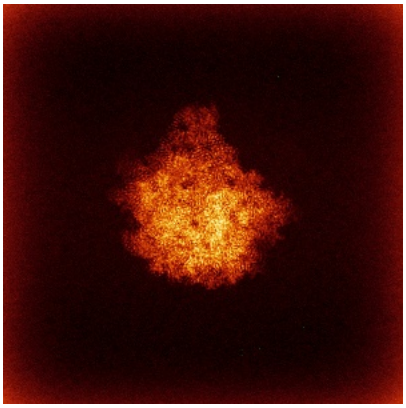
6.4.2 Raw map



X



Y

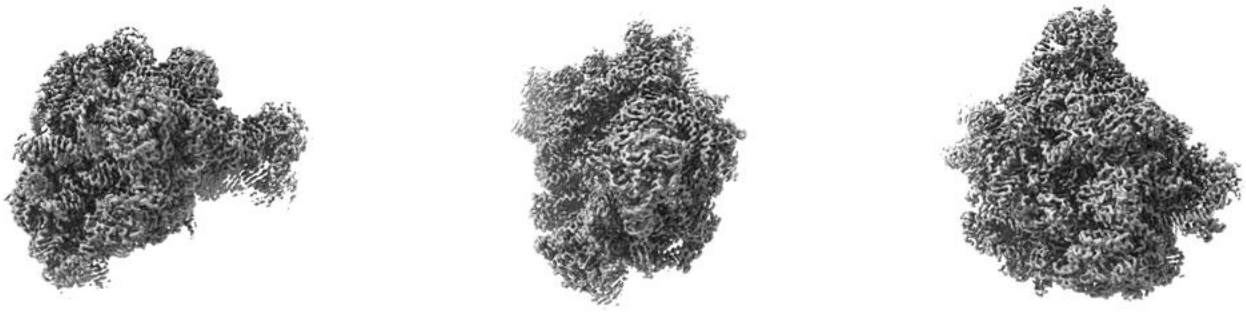


Z

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

6.5 Orthogonal surface views (i)

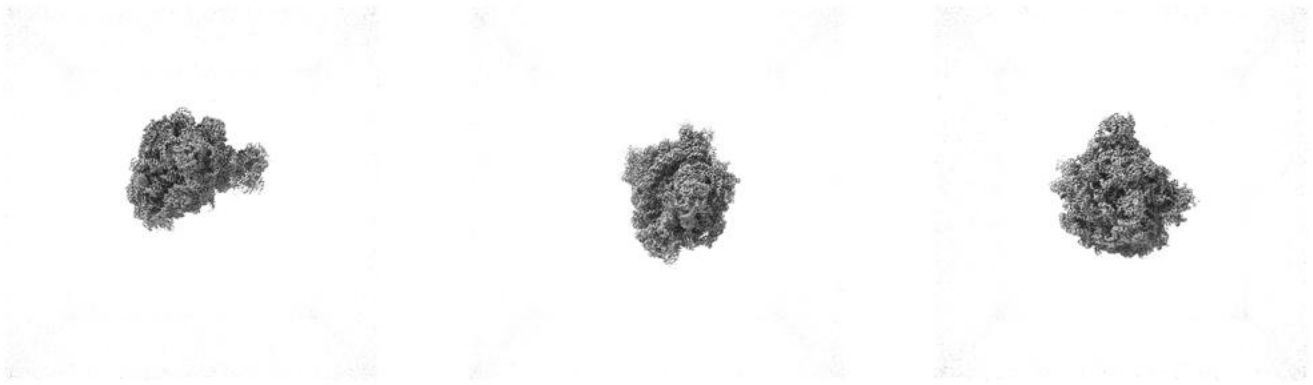
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. 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



X Y Z

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.

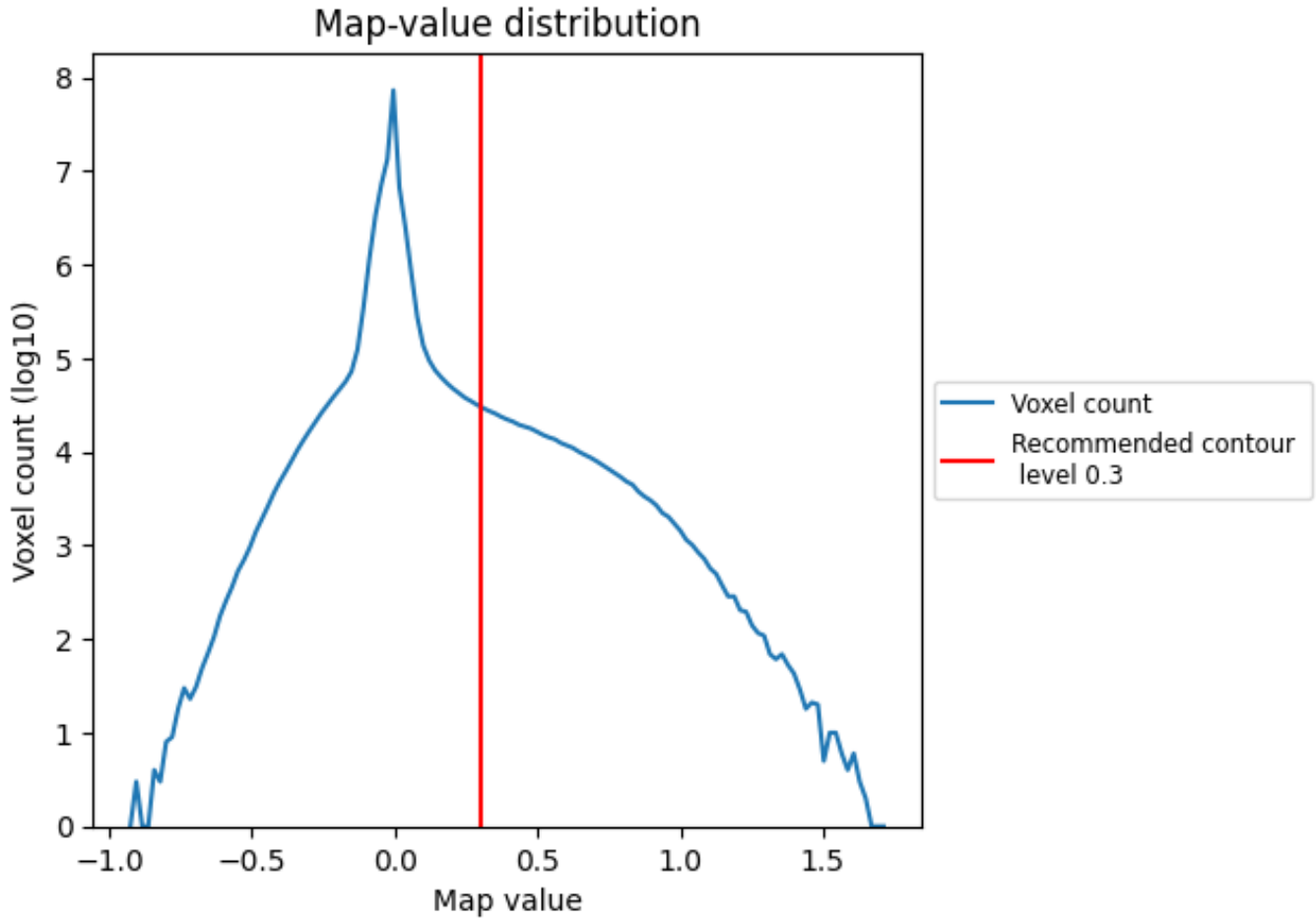
6.6 Mask visualisation (i)

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

7 Map analysis

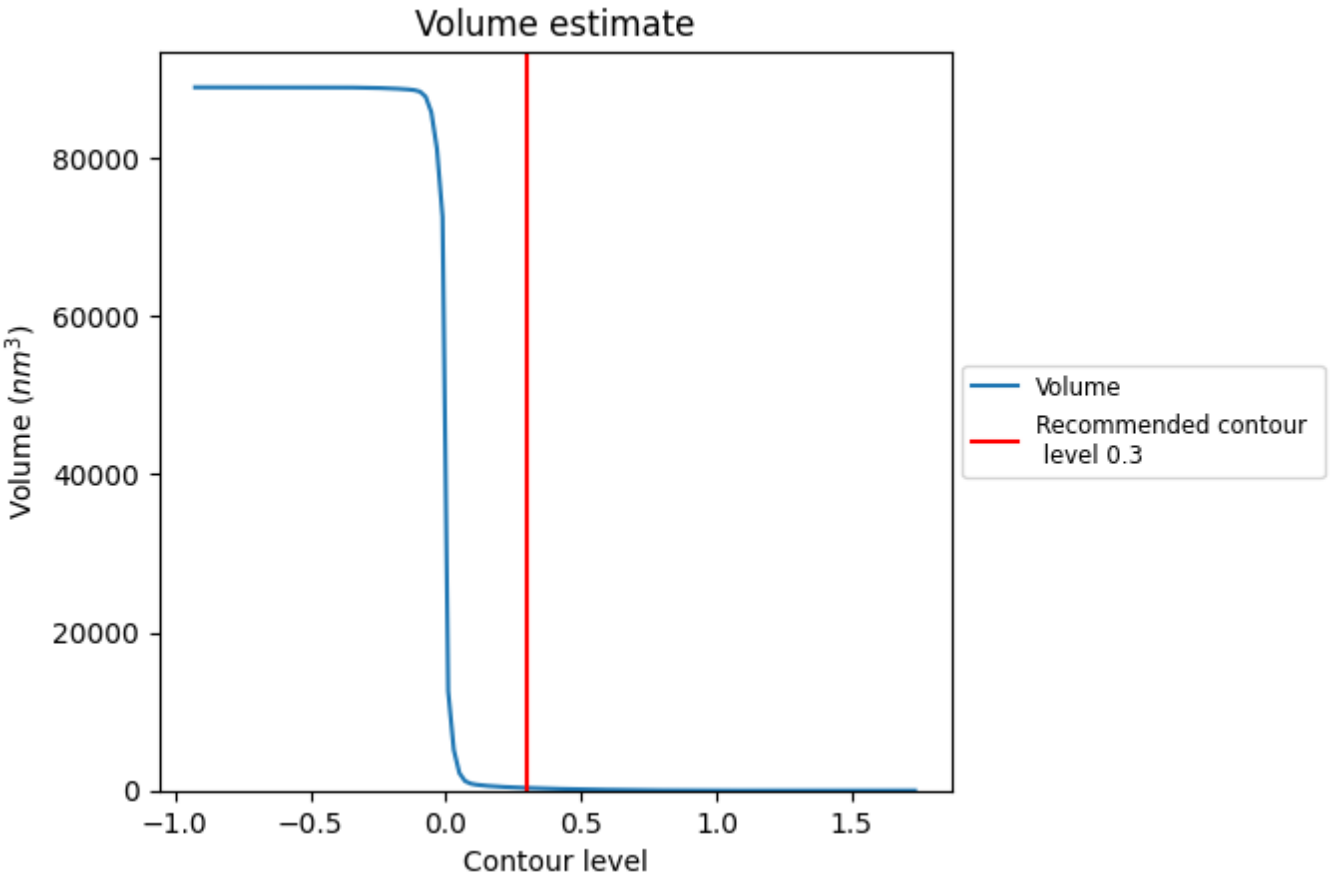
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

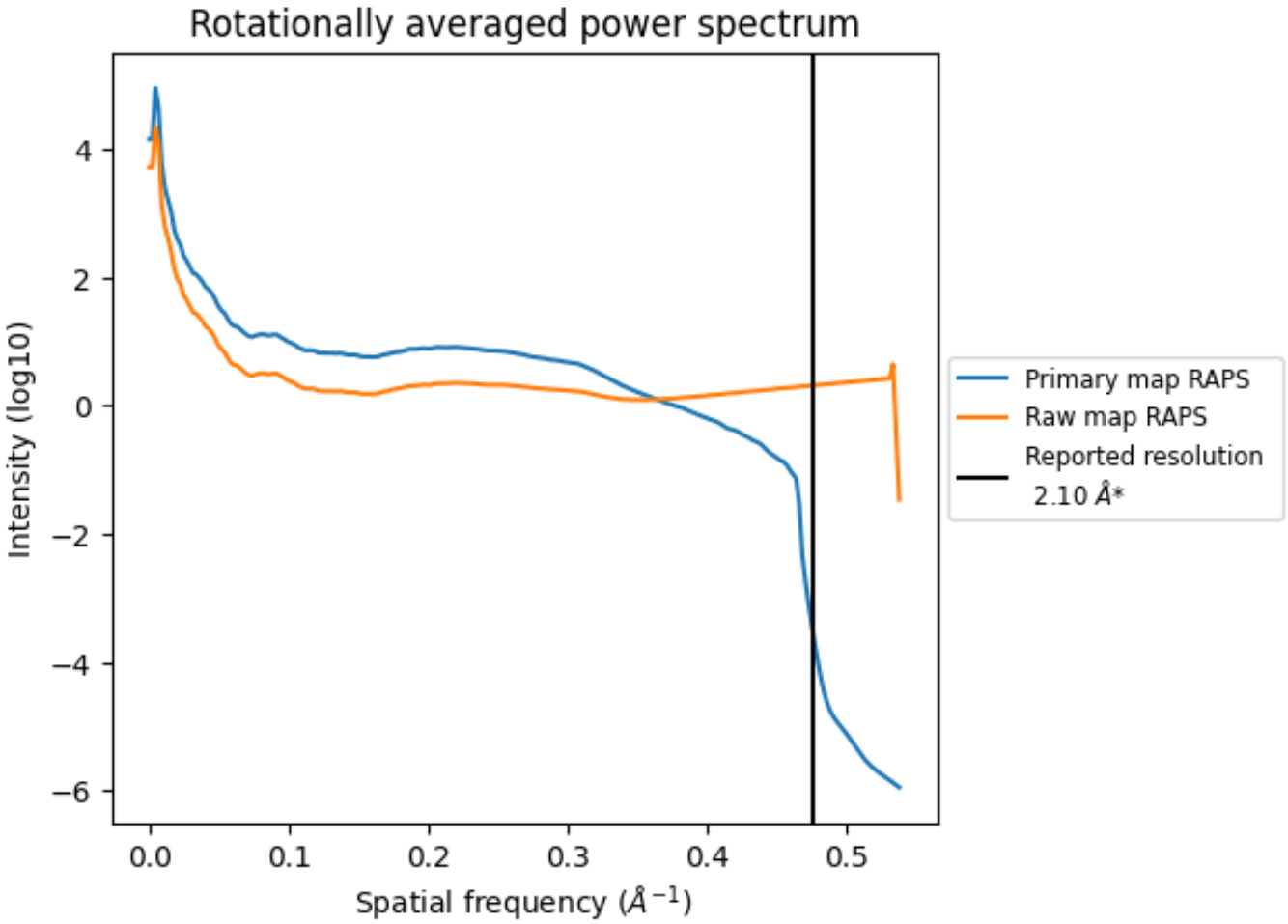
7.2 Volume estimate (i)



The volume at the recommended contour level is 331 nm^3; this corresponds to an approximate mass of 299 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)

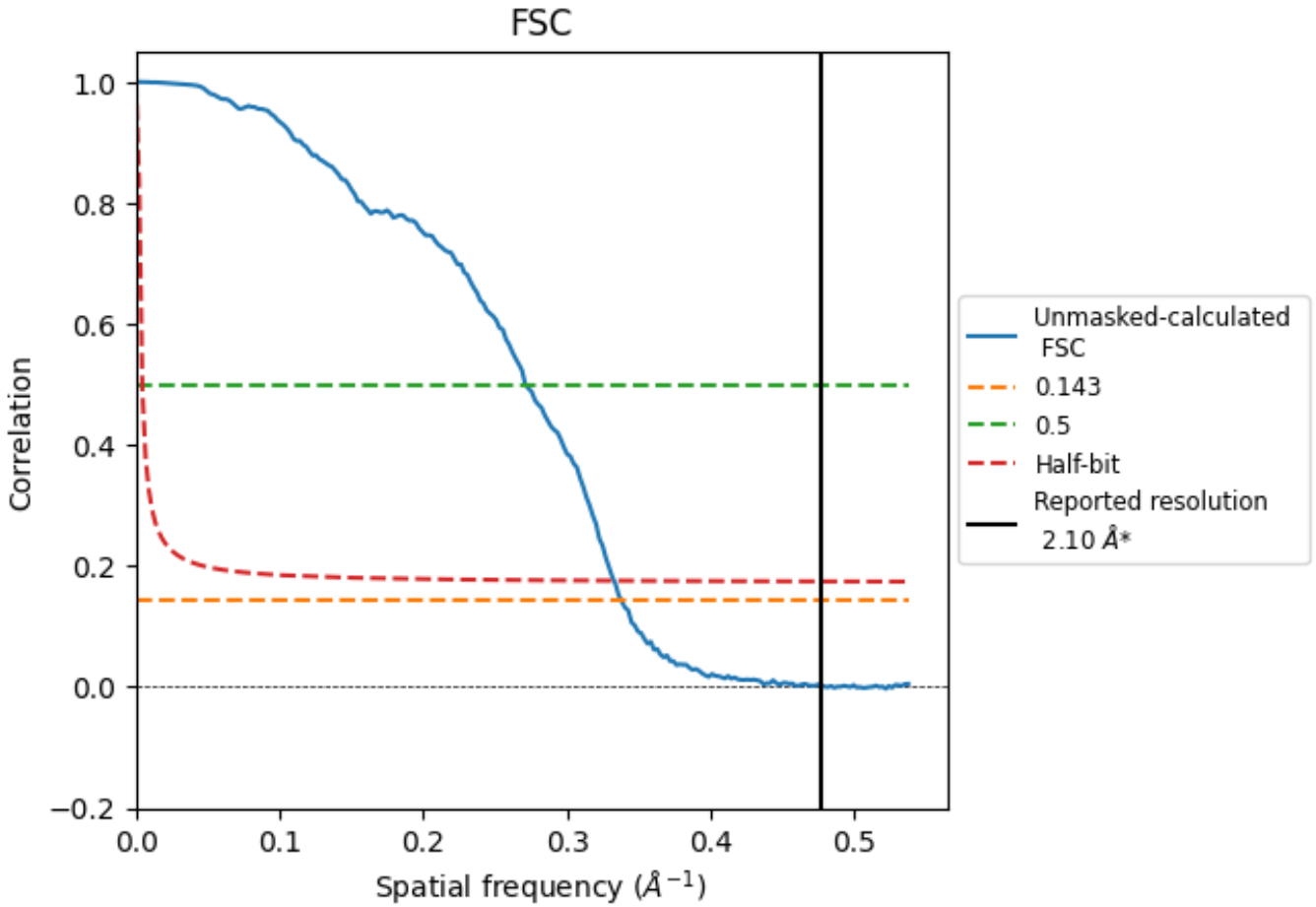


*Reported resolution corresponds to spatial frequency of 0.476 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.476 Å^{-1}

8.2 Resolution estimates (i)

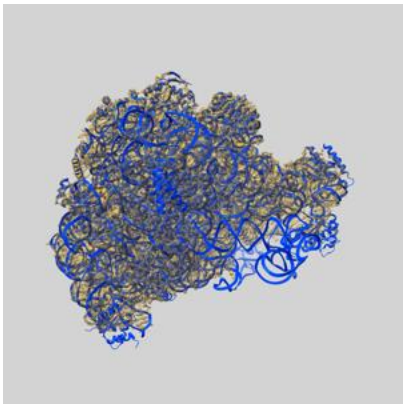
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.96	3.69	3.00

*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 2.96 differs from the reported value 2.1 by more than 10 %

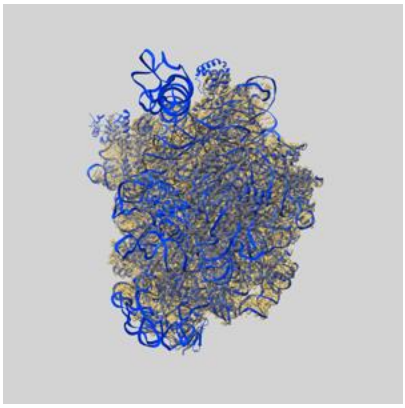
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-66879 and PDB model 9XP5. Per-residue inclusion information can be found in section 3 on page 10.

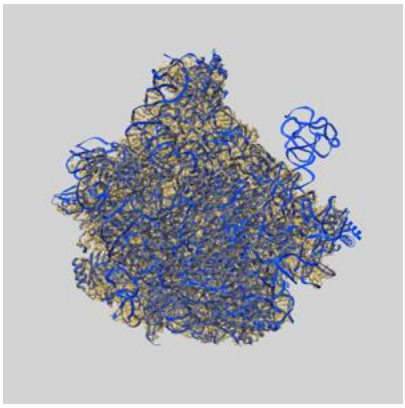
9.1 Map-model overlay



X



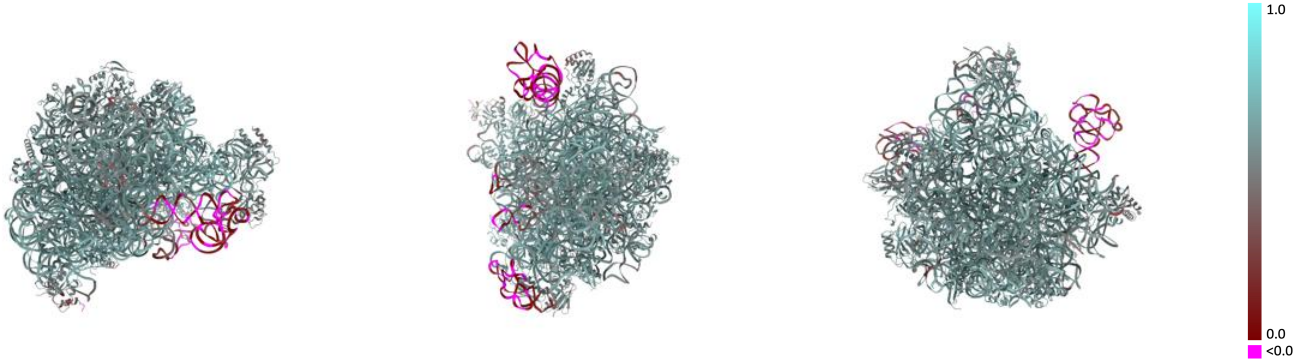
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3 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.

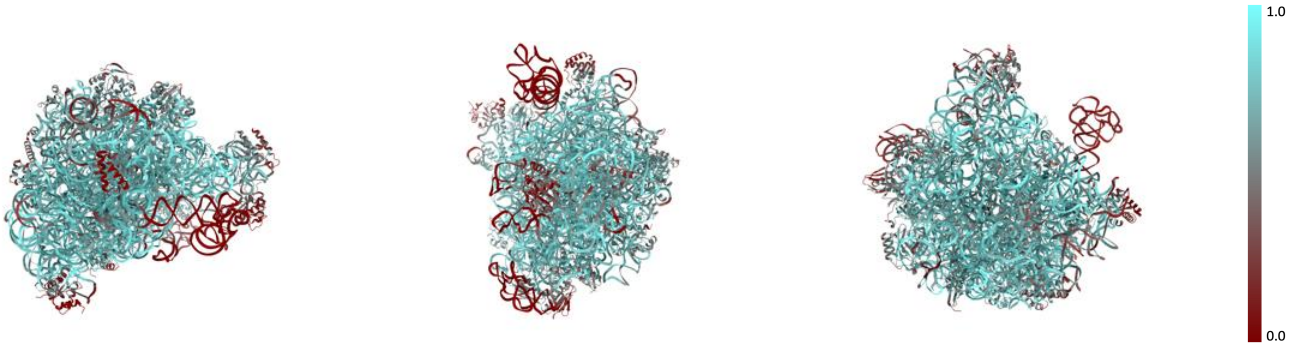
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

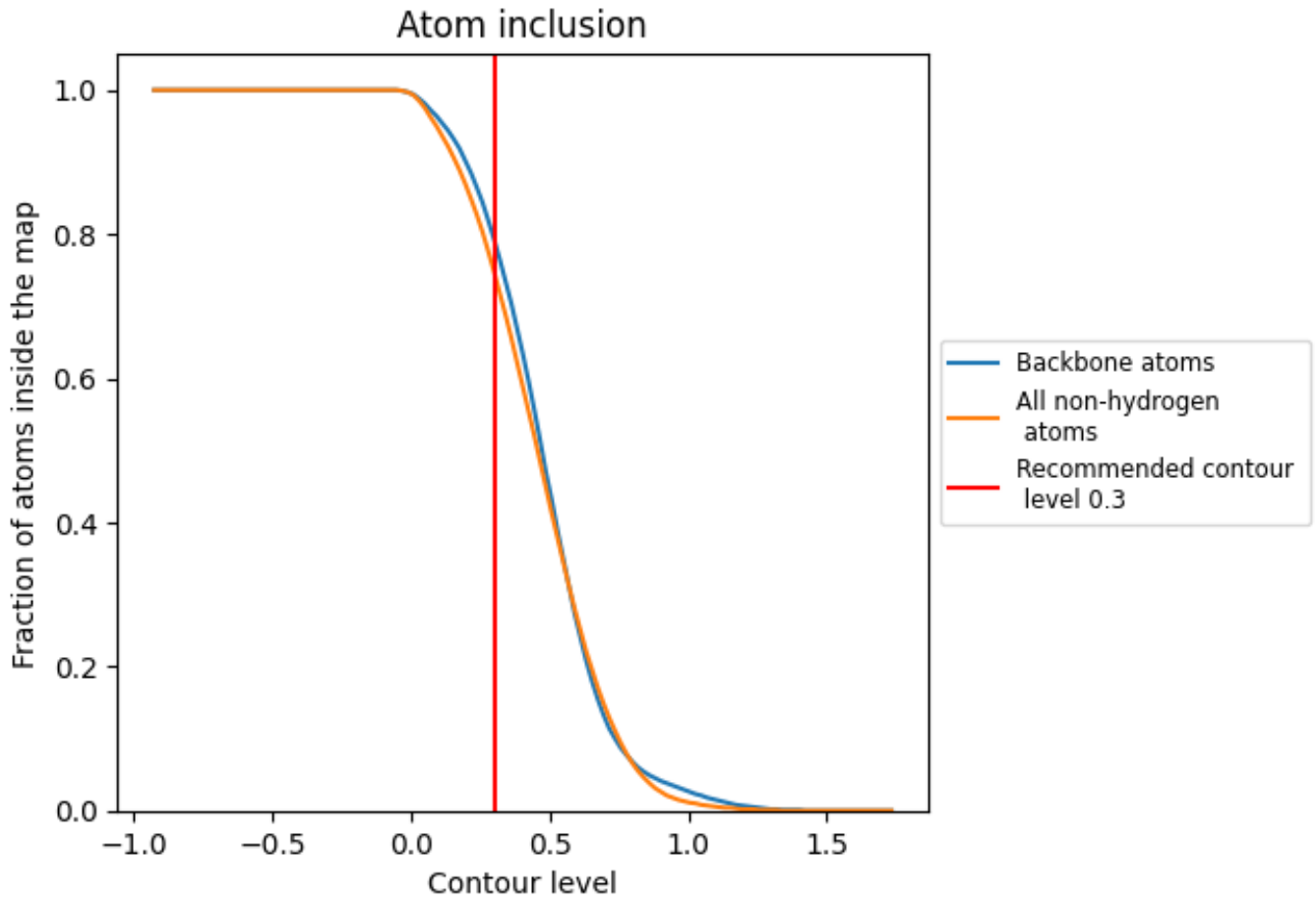
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.3).

9.4 Atom inclusion (i)



At the recommended contour level, 79% of all backbone atoms, 75% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7470	0.5940
1	0.7890	0.5840
2	0.7240	0.5850
AA	0.7640	0.6470
AB	0.7640	0.6400
AC	0.6710	0.6040
AD	0.2270	0.5120
AE	0.4420	0.5750
AF	0.3120	0.5020
AG	0.7120	0.6180
AI	0.7650	0.6650
AL	0.6590	0.6180
AM	0.8090	0.6400
AN	0.7560	0.6480
AO	0.5720	0.5910
AP	0.6820	0.6030
AQ	0.7450	0.6450
AR	0.6090	0.6020
AS	0.7960	0.6550
AT	0.7590	0.6290
AU	0.6260	0.6170
AV	0.6610	0.5950
AW	0.7640	0.6580
AX	0.4760	0.5790
AY	0.7220	0.6080
AZ	0.2100	0.4590
Aa	0.7040	0.6440
Ab	0.7130	0.6130
Ad	0.9100	0.6800
Af	0.7770	0.6480
Ag	0.5930	0.6200
Ah	0.7970	0.6540
Ai	0.6900	0.6240

