



wwPDB EM Validation Summary Report ⓘ

Jul 6, 2026 – 03:55 PM JST

PDB ID : 9L9C / pdb_00009l9c
EMDB ID : EMD-62900
Title : StateB of archaeal pre-50S ribosome
Authors : Li, Z.Q.; Yang, X.Y.
Deposited on : 2024-12-30
Resolution : 3.00 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

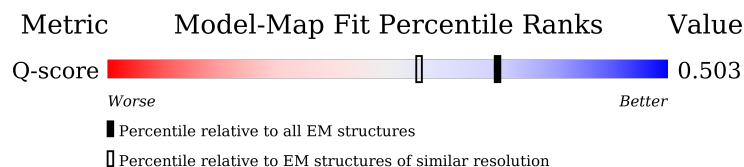
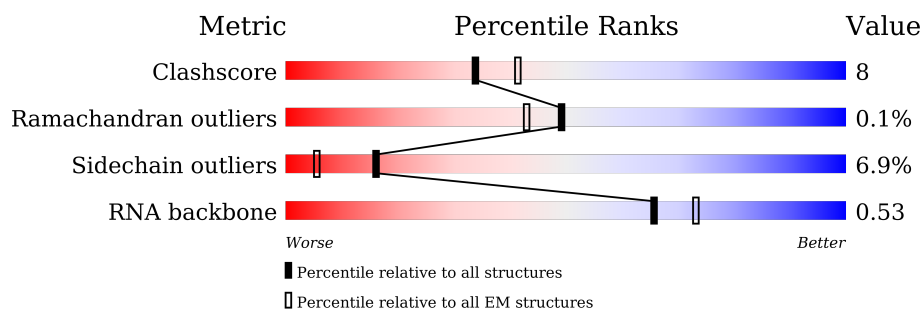
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	1	122	
3	A	50	

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Mol	Chain	Length	Quality of chain
4	B	221	
5	E	120	
6	F	176	
7	G	196	
8	H	116	
9	I	184	
10	J	151	
11	K	96	
12	L	153	
13	M	67	
14	N	118	
15	O	154	
16	P	92	
17	Q	234	
18	R	89	
19	S	58	
20	T	93	
21	U	241	
22	V	338	
23	W	248	
24	X	172	
25	Y	178	
26	Z	344	
27	b	145	
28	c	83	

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Mol	Chain	Length	Quality of chain
29	d	70	17% 76% 21%
30	e	58	16% 88% 10%
31	f	132	70% 29%
32	a	406	33% 47% 20% 31%

2 Entry composition [i](#)

There are 35 unique types of molecules in this entry. The entry contains 94993 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
1	0	2802	Total	C	N	O	P	0	0
			60067	26811	11065	19389	2802		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	120	Total	C	N	O	P	0	0
			2551	1138	453	840	120		

- Molecule 3 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	31	Total	C	N	O	S	0	0
			252	159	51	40	2		

- Molecule 4 is a protein called Translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	219	Total	C	N	O	S	0	0
			1576	972	267	336	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	119	Total	C	N	O	S	0	0
			868	539	138	190	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	174	Total	C	N	O	S	0	0
			1364	847	249	260	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	194	Total	C	N	O	S	0	0
			1562	957	336	267	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	115	Total	C	N	O	S	0	0
			880	541	164	175			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	183	Total	C	N	O	S	0	0
			1403	872	255	275	1		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	151	Total	C	N	O	S	0	0
			1170	728	214	224	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	59	Total	C	N	O	S	0	0
			473	292	84	95	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	114	Total	C	N	O		
			899	543	171	185	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	154	Total	C	N	O	S		
			1195	728	220	243	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	89	Total	C	N	O	S		
			712	439	137	135	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	142	Total	C	N	O	S		
			1124	686	225	212	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	80	Total	C	N	O	S		
			610	369	125	115	1	0	0

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	235	Total	C	N	O	S	0	0
			1747	1074	346	322	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	337	Total	C	N	O	S	0	0
			2601	1615	484	492	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	248	Total	C	N	O	S	0	0
			1887	1159	353	372	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	168	Total	C	N	O	S	0	0
			853	507	176	169	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	174	Total	C	N	O	S	0	0
			1321	815	221	282	3		

- Molecule 26 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	100	Total	C	N	O	S	0	0
			765	483	132	148	2		

- Molecule 27 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	144	Total	C	N	O	S	0	0
			1120	697	201	217	5		

- Molecule 28 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	82	Total	C	N	O	S	0	0
			648	401	112	133	2		

- Molecule 29 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	68	Total	C	N	O	S	0	0
			508	310	87	110	1		

- Molecule 30 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	e	57	Total	C	N	O	0	0
			433	269	76	88		

- Molecule 31 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	132	Total	C	N	O	S	0	0
			990	609	185	191	5		

- Molecule 32 is a protein called CBS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	279	Total	C	N	O	S	0	0
			2061	1287	355	416	3		

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
33	0	183	Total	Mg	0
			183	183	
33	1	7	Total	Mg	0
			7	7	
33	A	1	Total	Mg	0
			1	1	
33	G	4	Total	Mg	0
			4	4	
33	M	1	Total	Mg	0
			1	1	
33	O	1	Total	Mg	0
			1	1	

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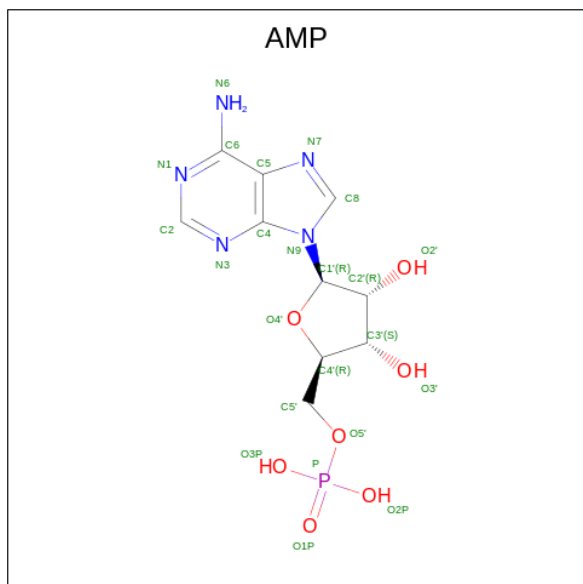
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Mol	Chain	Residues	Atoms		AltConf
33	P	1	Total	Mg	0
			1	1	
33	Q	1	Total	Mg	0
			1	1	
33	U	2	Total	Mg	0
			2	2	
33	V	2	Total	Mg	0
			2	2	
33	W	1	Total	Mg	0
			1	1	
33	f	1	Total	Mg	0
			1	1	

- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 35 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P) (labeled as "Ligand of Interest" by depositor).

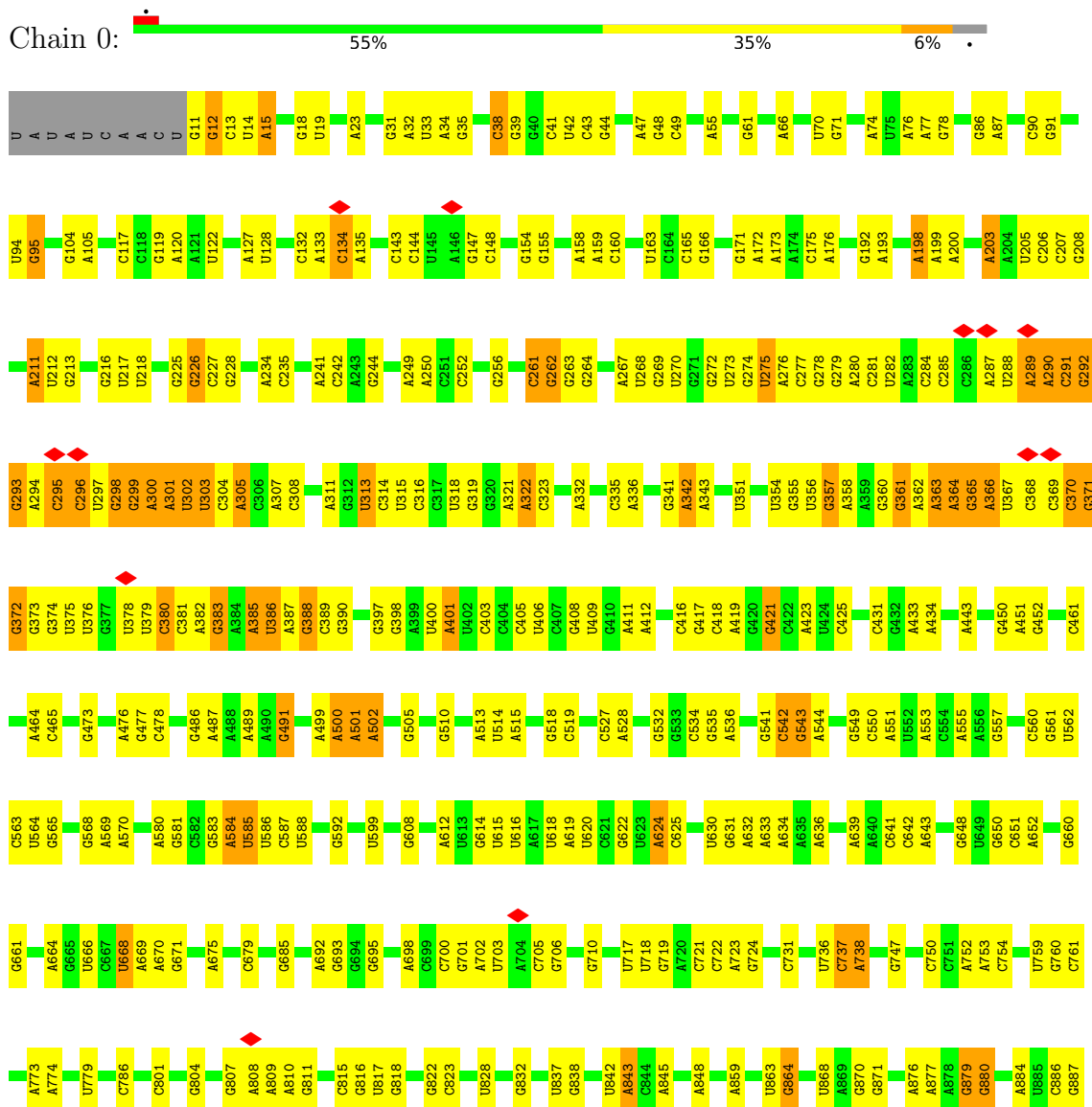


Mol	Chain	Residues	Atoms					AltConf
35	a	1	Total 23	C 10	N 5	O 7	P 1	0
35	a	1	Total 23	C 10	N 5	O 7	P 1	0

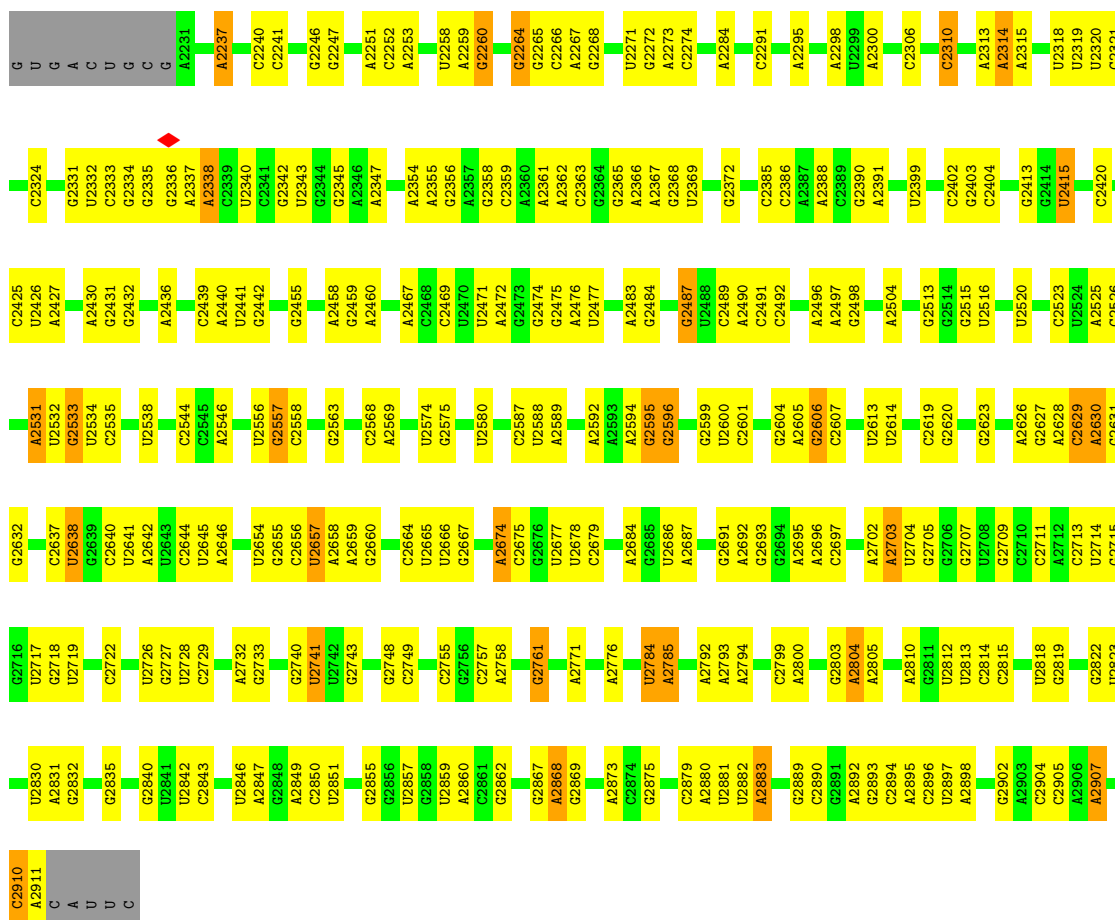
3 Residue-property plots

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

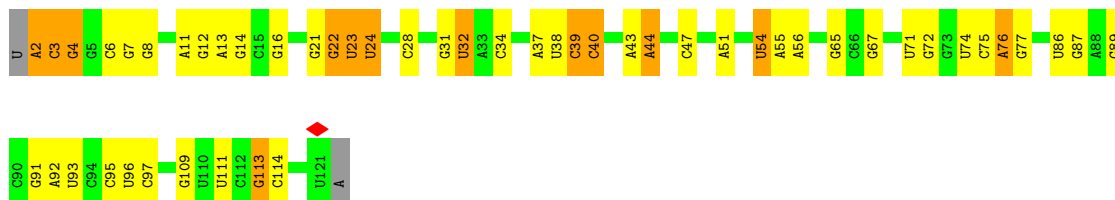






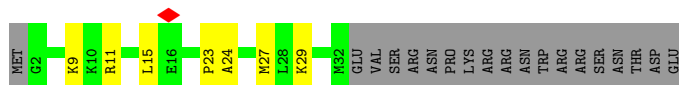
• Molecule 2: 5S RNA

Chain 1: 57% 31% 11%



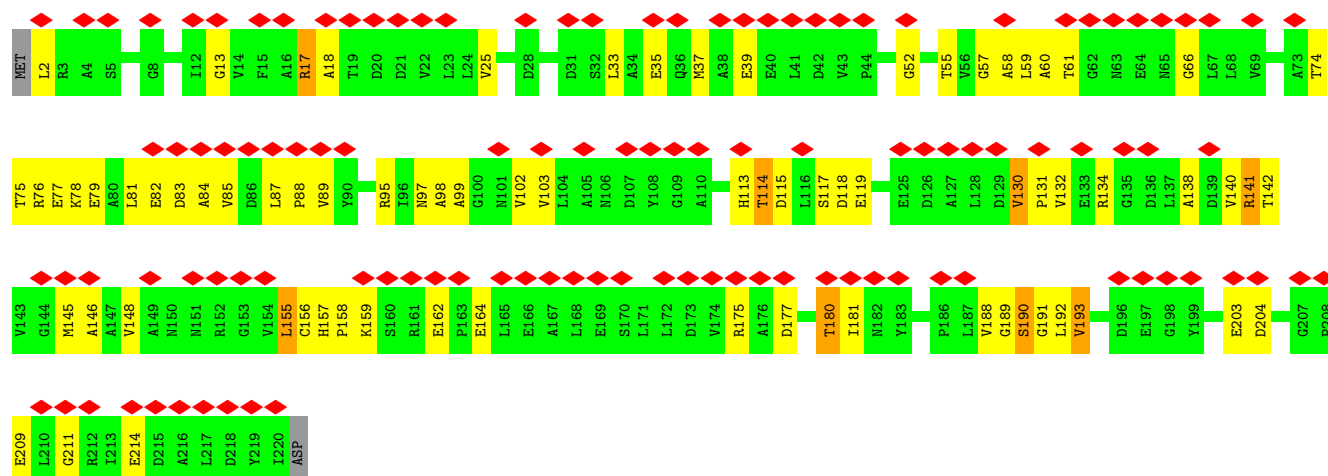
• Molecule 3: Large ribosomal subunit protein eL39

Chain A: 48% 14% 38%

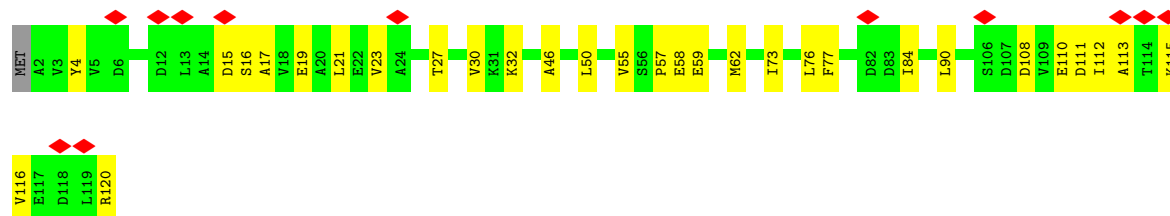
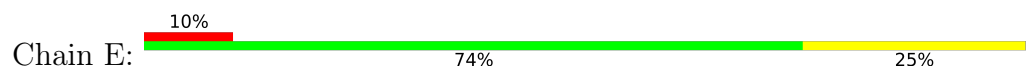


• Molecule 4: Translation initiation factor 6

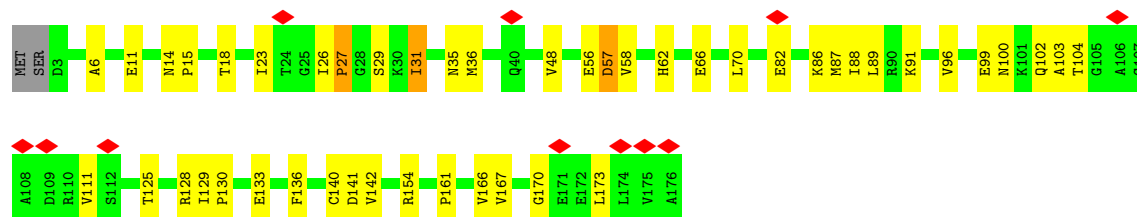
Chain B: 52% 65% 31%



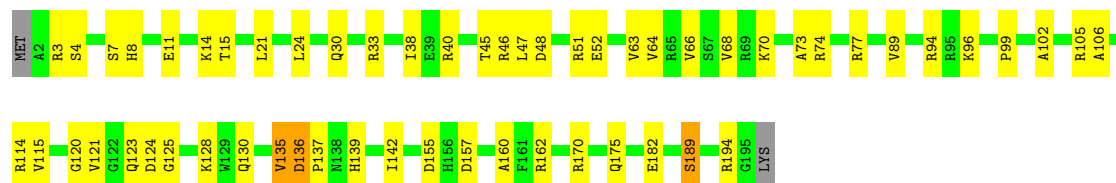
- Molecule 5: Large ribosomal subunit protein eL8



- Molecule 6: Large ribosomal subunit protein uL16

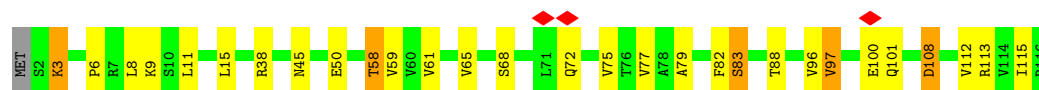


- Molecule 7: Large ribosomal subunit protein eL15

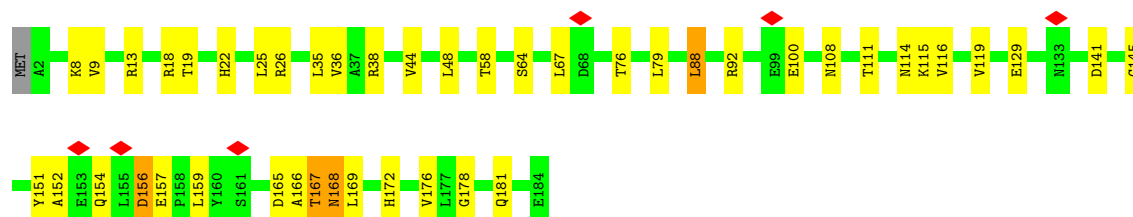


- Molecule 8: Large ribosomal subunit protein eL18

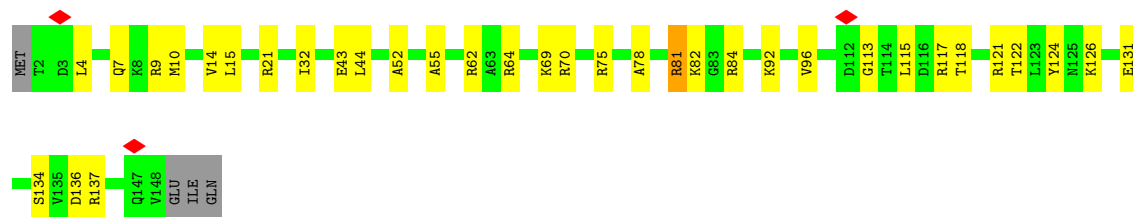




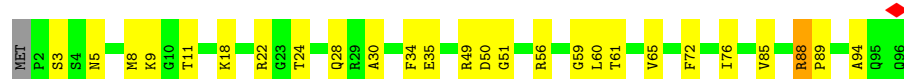
- Molecule 9: Large ribosomal subunit protein uL18



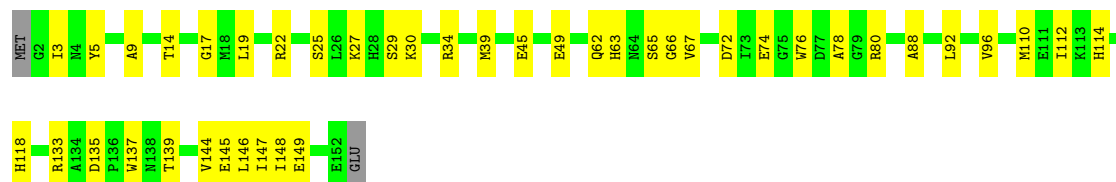
- Molecule 10: Large ribosomal subunit protein eL19



- Molecule 11: Large ribosomal subunit protein eL21



- Molecule 12: Large ribosomal subunit protein uL22

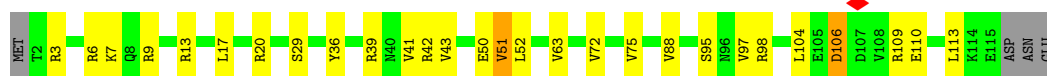


- Molecule 13: Large ribosomal subunit protein eL24

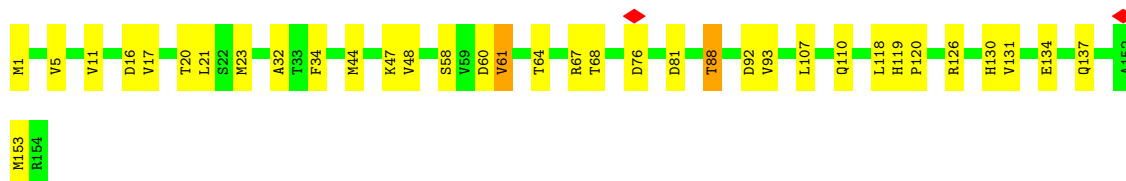
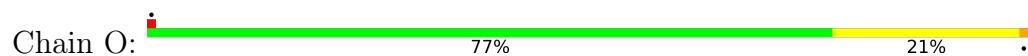




- Molecule 14: Large ribosomal subunit protein uL24



- Molecule 15: Large ribosomal subunit protein uL30



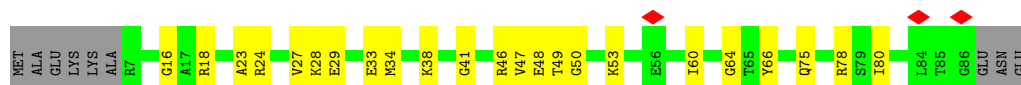
- Molecule 16: Large ribosomal subunit protein eL31



- Molecule 17: Large ribosomal subunit protein eL32



- Molecule 18: Large ribosomal subunit protein eL43



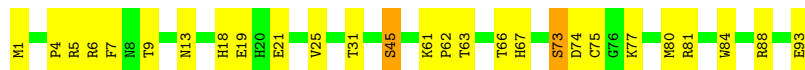
- Molecule 19: Large ribosomal subunit protein eL37

Chain S:  84% 14%



- Molecule 20: Large ribosomal subunit protein eL42

Chain T:  71% 27%



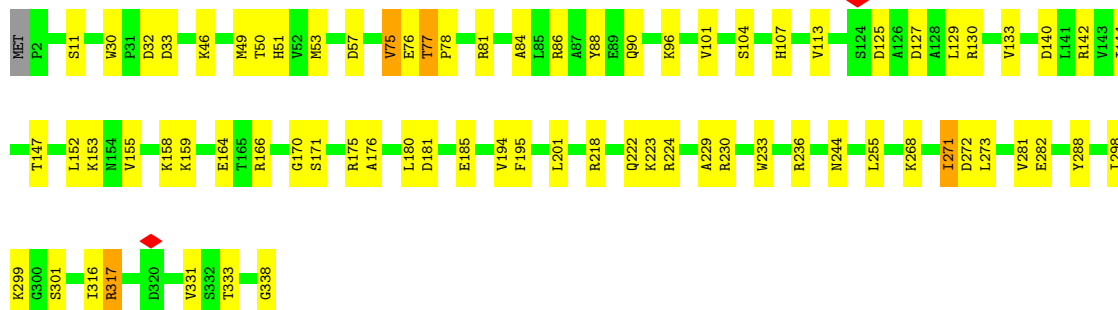
- Molecule 21: Large ribosomal subunit protein uL2

Chain U:  71% 24%



- Molecule 22: Large ribosomal subunit protein uL3

Chain V:  78% 21%



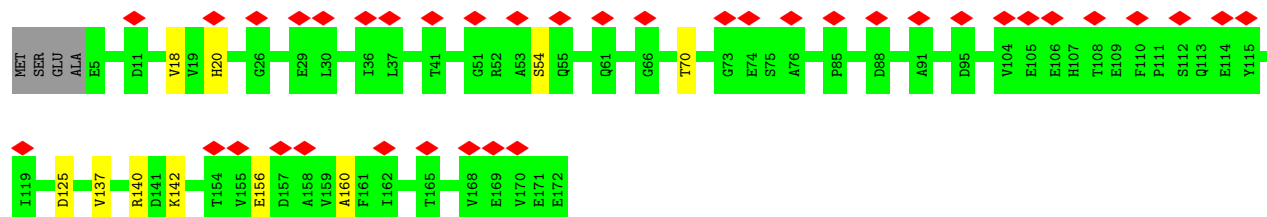
- Molecule 23: Large ribosomal subunit protein uL4

Chain W:  77% 22%

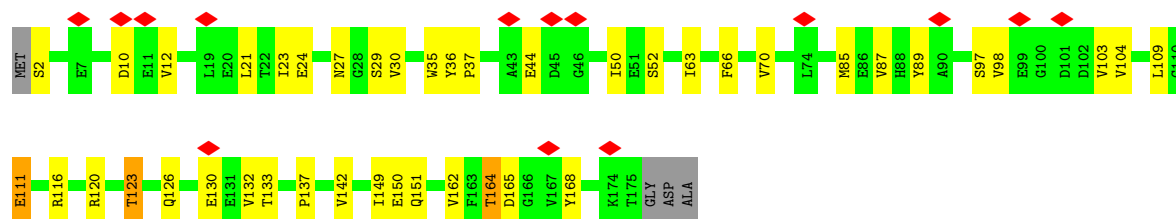
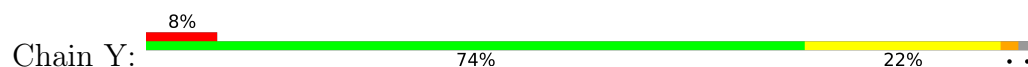




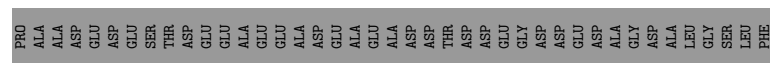
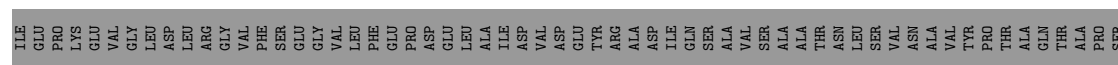
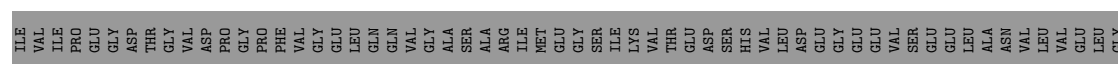
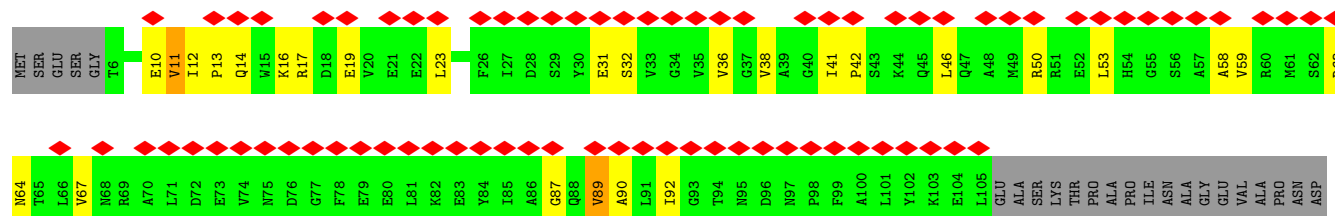
- Molecule 24: Large ribosomal subunit protein uL5



- Molecule 25: Large ribosomal subunit protein uL6

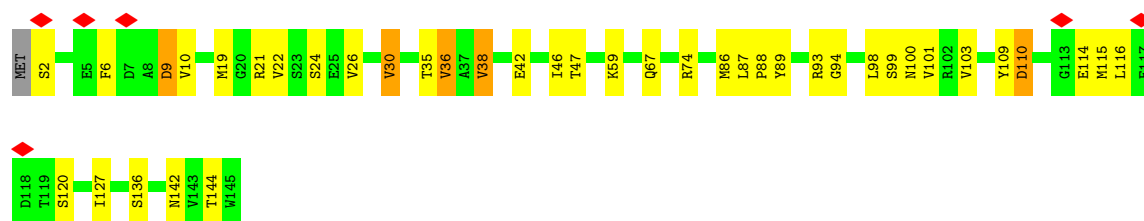


- Molecule 26: Large ribosomal subunit protein uL10



- Molecule 27: Large ribosomal subunit protein uL13

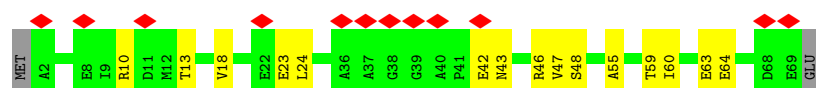
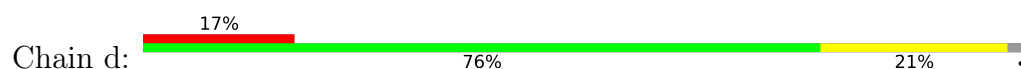




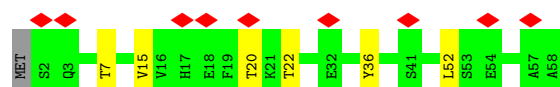
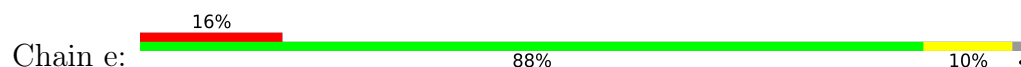
- Molecule 28: Large ribosomal subunit protein uL23



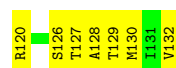
- Molecule 29: Large ribosomal subunit protein uL29



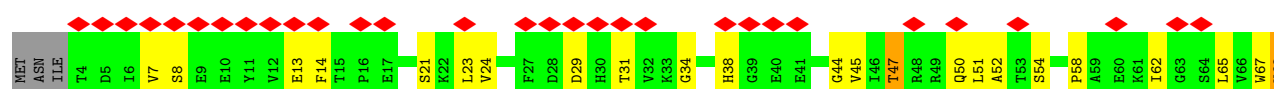
- Molecule 30: Large ribosomal subunit protein eL20

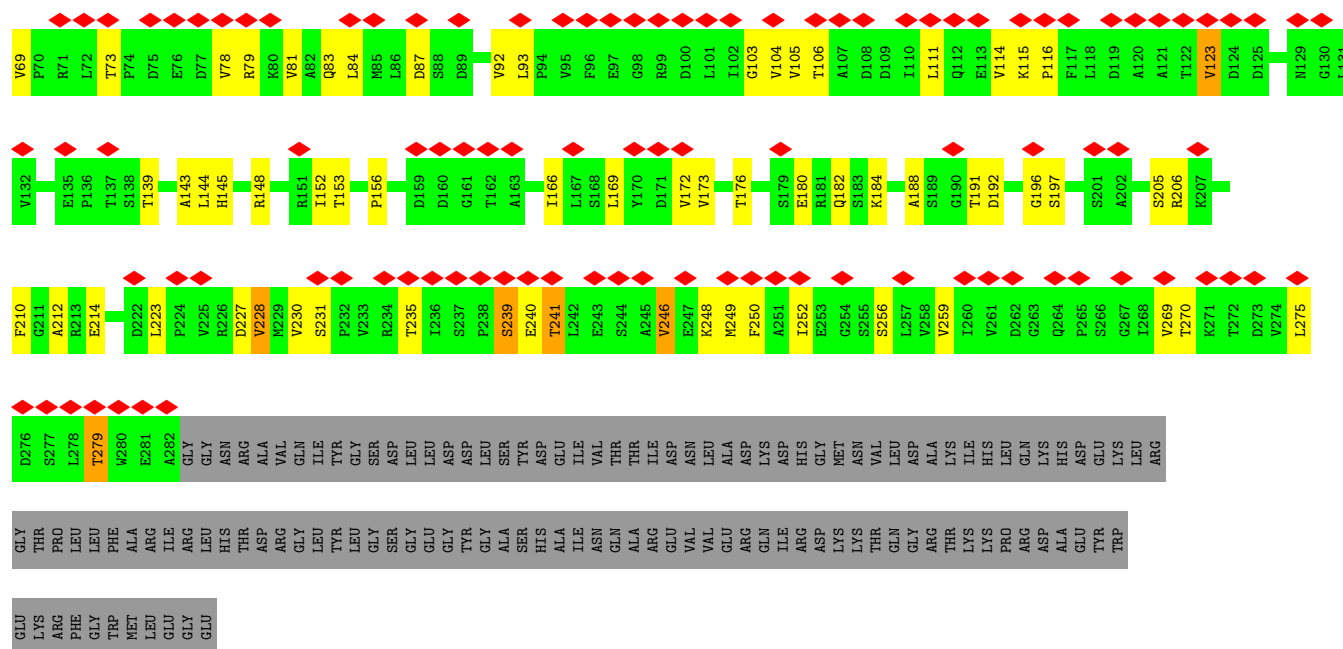


- Molecule 31: Large ribosomal subunit protein uL14



- Molecule 32: CBS domain-containing protein





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	0.444	Depositor
Minimum map value	-0.244	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.056	Depositor
Map size (Å)	427.52, 427.52, 427.52	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.668, 0.668, 0.668	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.14	0/67262	0.29	0/104907
2	1	0.13	0/2848	0.28	0/4436
3	A	0.11	0/254	0.28	0/333
4	B	0.13	0/1595	0.37	0/2178
5	E	0.13	0/877	0.32	0/1194
6	F	0.18	0/1387	0.40	1/1866 (0.1%)
7	G	0.15	0/1589	0.30	0/2121
8	H	0.13	0/888	0.28	0/1201
9	I	0.13	0/1433	0.33	0/1951
10	J	0.14	0/1191	0.30	0/1587
11	K	0.15	0/750	0.36	0/1001
12	L	0.13	0/1195	0.33	0/1614
13	M	0.16	0/481	0.41	0/644
14	N	0.13	0/907	0.34	0/1226
15	O	0.15	0/1213	0.34	0/1644
16	P	0.19	0/727	0.43	1/981 (0.1%)
17	Q	0.13	0/1143	0.30	0/1534
18	R	0.14	0/617	0.37	0/826
19	S	0.14	0/446	0.29	0/586
20	T	0.14	0/764	0.31	0/1015
21	U	0.16	0/1781	0.38	0/2398
22	V	0.14	0/2659	0.32	0/3594
23	W	0.14	0/1914	0.33	0/2585
24	X	0.11	0/855	0.31	0/1180
25	Y	0.13	0/1343	0.33	0/1828
26	Z	0.13	0/776	0.33	0/1048
27	b	0.14	0/1137	0.35	0/1532
28	c	0.11	0/654	0.32	0/878
29	d	0.14	0/511	0.35	0/690
30	e	0.11	0/439	0.26	0/590
31	f	0.14	0/998	0.32	0/1340
32	a	0.14	0/2096	0.45	1/2860 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.14	0/102730	0.31	3/153368 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	27	PRO	CA-N-CD	-7.25	101.84	112.00
16	P	67	PRO	CA-N-CD	-6.30	103.18	112.00
32	a	228	VAL	N-CA-C	-5.18	108.23	113.20

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	0	60067	0	30297	713	0
2	1	2551	0	1298	36	0
3	A	252	0	287	5	0
4	B	1576	0	1493	52	0
5	E	868	0	824	17	0
6	F	1364	0	1354	28	0
7	G	1562	0	1590	38	0
8	H	880	0	896	16	0
9	I	1403	0	1341	30	0
10	J	1179	0	1183	23	0
11	K	736	0	745	22	0
12	L	1170	0	1142	31	0
13	M	473	0	452	13	0
14	N	899	0	876	15	0
15	O	1195	0	1150	22	0
16	P	712	0	677	14	0
17	Q	1124	0	1109	11	0
18	R	610	0	605	16	0
19	S	439	0	445	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	T	746	0	736	15	0
21	U	1747	0	1745	46	0
22	V	2601	0	2555	43	0
23	W	1887	0	1877	33	0
24	X	853	0	415	6	0
25	Y	1321	0	1234	22	0
26	Z	765	0	744	19	0
27	b	1120	0	1104	25	0
28	c	648	0	645	13	0
29	d	508	0	490	7	0
30	e	433	0	426	2	0
31	f	990	0	1035	22	0
32	a	2061	0	1990	49	0
33	0	183	0	0	0	0
33	1	7	0	0	0	0
33	A	1	0	0	0	0
33	G	4	0	0	0	0
33	M	1	0	0	0	0
33	O	1	0	0	0	0
33	P	1	0	0	0	0
33	Q	1	0	0	0	0
33	U	2	0	0	0	0
33	V	2	0	0	0	0
33	W	1	0	0	0	0
33	f	1	0	0	0	0
34	S	1	0	0	0	0
34	T	1	0	0	0	0
35	a	46	0	20	2	0
All	All	94993	0	62780	1267	0

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

The worst 5 of 1267 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1194:G:N2	1:0:1199:A:H62	1.59	1.01
1:0:2862:G:H1	1:0:2881:U:H3	1.06	1.01
1:0:1194:G:H21	1:0:1199:A:N6	1.66	0.92
1:0:1911:U:O2'	1:0:1914:A:N6	2.03	0.92
1:0:973:A:H2'	1:0:974:A:H8	1.42	0.84

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	29/50 (58%)	28 (97%)	1 (3%)	0	100	100
4	B	217/221 (98%)	199 (92%)	18 (8%)	0	100	100
5	E	117/120 (98%)	110 (94%)	7 (6%)	0	100	100
6	F	172/176 (98%)	160 (93%)	12 (7%)	0	100	100
7	G	192/196 (98%)	187 (97%)	4 (2%)	1 (0%)	24	60
8	H	113/116 (97%)	110 (97%)	3 (3%)	0	100	100
9	I	181/184 (98%)	174 (96%)	7 (4%)	0	100	100
10	J	145/151 (96%)	143 (99%)	2 (1%)	0	100	100
11	K	93/96 (97%)	90 (97%)	3 (3%)	0	100	100
12	L	149/153 (97%)	145 (97%)	4 (3%)	0	100	100
13	M	57/67 (85%)	54 (95%)	3 (5%)	0	100	100
14	N	112/118 (95%)	107 (96%)	5 (4%)	0	100	100
15	O	152/154 (99%)	147 (97%)	5 (3%)	0	100	100
16	P	87/92 (95%)	84 (97%)	3 (3%)	0	100	100
17	Q	140/234 (60%)	139 (99%)	1 (1%)	0	100	100
18	R	78/89 (88%)	74 (95%)	4 (5%)	0	100	100
19	S	55/58 (95%)	55 (100%)	0	0	100	100
20	T	91/93 (98%)	91 (100%)	0	0	100	100
21	U	233/241 (97%)	210 (90%)	21 (9%)	2 (1%)	14	48
22	V	335/338 (99%)	326 (97%)	9 (3%)	0	100	100
23	W	246/248 (99%)	238 (97%)	8 (3%)	0	100	100
24	X	166/172 (96%)	153 (92%)	13 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	Y	172/178 (97%)	167 (97%)	4 (2%)	1 (1%)	21	56
26	Z	98/344 (28%)	96 (98%)	2 (2%)	0	100	100
27	b	142/145 (98%)	138 (97%)	4 (3%)	0	100	100
28	c	80/83 (96%)	79 (99%)	1 (1%)	0	100	100
29	d	66/70 (94%)	66 (100%)	0	0	100	100
30	e	55/58 (95%)	53 (96%)	2 (4%)	0	100	100
31	f	130/132 (98%)	125 (96%)	5 (4%)	0	100	100
32	a	277/406 (68%)	232 (84%)	44 (16%)	1 (0%)	30	65
All	All	4180/4783 (87%)	3980 (95%)	195 (5%)	5 (0%)	49	80

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	U	213	LYS
21	U	229	ALA
25	Y	10	ASP
7	G	4	SER
32	a	241	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	27/46 (59%)	27 (100%)	0	100	100
4	B	159/171 (93%)	144 (91%)	15 (9%)	8	32
5	E	89/94 (95%)	85 (96%)	4 (4%)	24	59
6	F	143/147 (97%)	134 (94%)	9 (6%)	16	48
7	G	157/163 (96%)	150 (96%)	7 (4%)	24	59
8	H	97/99 (98%)	88 (91%)	9 (9%)	8	32
9	I	141/145 (97%)	131 (93%)	10 (7%)	13	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	117/121 (97%)	111 (95%)	6 (5%)	21	55
11	K	77/78 (99%)	70 (91%)	7 (9%)	9	33
12	L	121/124 (98%)	119 (98%)	2 (2%)	53	78
13	M	49/55 (89%)	46 (94%)	3 (6%)	17	49
14	N	96/102 (94%)	86 (90%)	10 (10%)	7	28
15	O	130/132 (98%)	124 (95%)	6 (5%)	24	58
16	P	74/80 (92%)	69 (93%)	5 (7%)	14	45
17	Q	115/191 (60%)	110 (96%)	5 (4%)	26	60
18	R	59/68 (87%)	58 (98%)	1 (2%)	53	78
19	S	48/49 (98%)	46 (96%)	2 (4%)	26	61
20	T	77/77 (100%)	71 (92%)	6 (8%)	11	39
21	U	177/186 (95%)	163 (92%)	14 (8%)	11	39
22	V	272/278 (98%)	254 (93%)	18 (7%)	15	46
23	W	194/198 (98%)	177 (91%)	17 (9%)	9	35
24	X	6/147 (4%)	6 (100%)	0	100	100
25	Y	143/151 (95%)	132 (92%)	11 (8%)	12	40
26	Z	81/277 (29%)	79 (98%)	2 (2%)	42	72
27	b	119/123 (97%)	106 (89%)	13 (11%)	6	26
28	c	74/76 (97%)	68 (92%)	6 (8%)	11	38
29	d	51/56 (91%)	47 (92%)	4 (8%)	11	39
30	e	48/49 (98%)	46 (96%)	2 (4%)	26	61
31	f	105/106 (99%)	95 (90%)	10 (10%)	8	31
32	a	222/344 (64%)	202 (91%)	20 (9%)	9	34
All	All	3268/3933 (83%)	3044 (93%)	224 (7%)	16	45

5 of 224 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	U	144	GLU
32	a	259	VAL
23	W	80	VAL
32	a	239	SER
31	f	73	ILE

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	U	92	ASN
22	V	90	GLN
22	V	3	GLN
23	W	103	ASN
9	I	108	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2800/2916 (96%)	483 (17%)	25 (0%)
2	1	120/122 (98%)	21 (17%)	2 (1%)
All	All	2920/3038 (96%)	504 (17%)	27 (0%)

5 of 504 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	12	G
1	0	13	C
1	0	15	A
1	0	18	G
1	0	38	C

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1273	A
1	0	1941	G
1	0	2842	U
1	0	1659	A
1	0	1956	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 209 ligands modelled in this entry, 207 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	AMP	a	502	-	25,25,25	1.39	4 (16%)	38,38,38	1.92	8 (21%)
35	AMP	a	501	-	25,25,25	1.34	4 (16%)	38,38,38	2.08	9 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	AMP	a	502	-	-	0/10/26/26	0/3/3/3
35	AMP	a	501	-	-	0/10/26/26	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	a	502	AMP	C5-C4	4.51	1.47	1.39
35	a	501	AMP	C5-C4	4.31	1.47	1.39
35	a	502	AMP	C5-C6	2.78	1.48	1.41
35	a	501	AMP	C5-C6	2.70	1.48	1.41
35	a	501	AMP	C8-N7	2.62	1.36	1.31

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	a	501	AMP	C5-C4-N3	-6.35	118.46	126.75
35	a	502	AMP	C5-C4-N3	-6.30	118.54	126.75
35	a	502	AMP	N3-C4-N9	4.76	134.93	127.08
35	a	501	AMP	N3-C4-N9	4.74	134.89	127.08
35	a	501	AMP	C2-N3-C4	3.96	121.11	111.75

There are no chirality outliers.

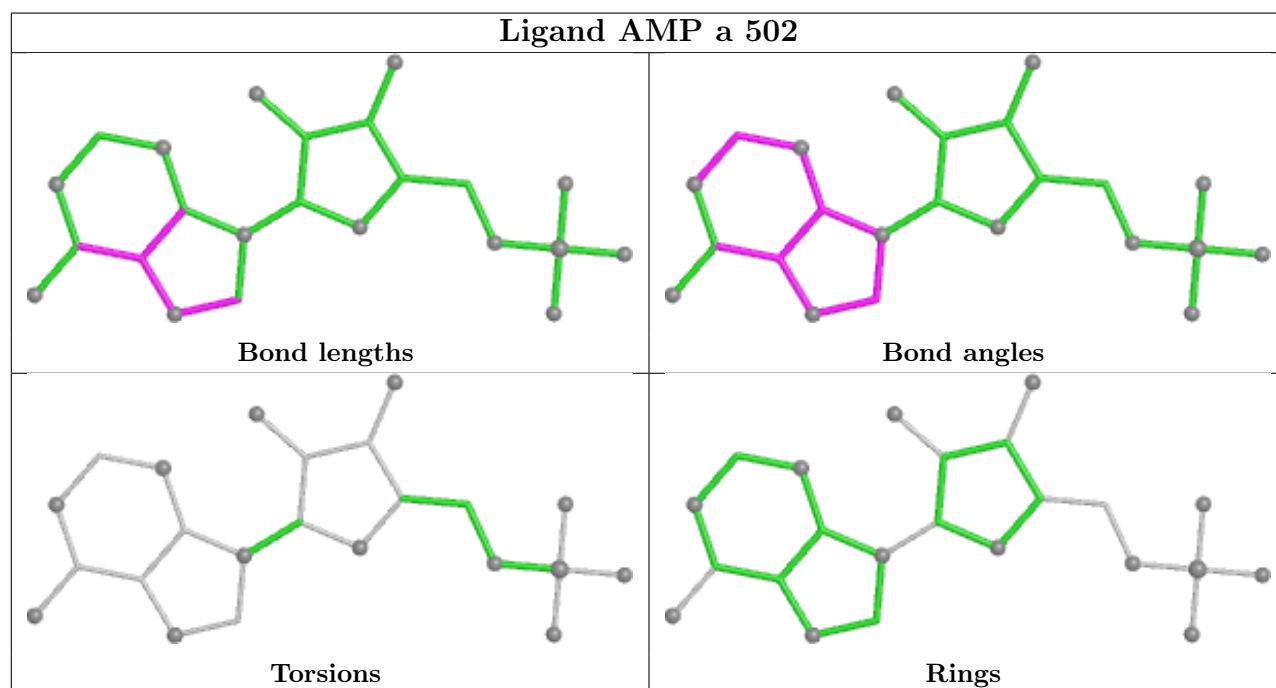
There are no torsion outliers.

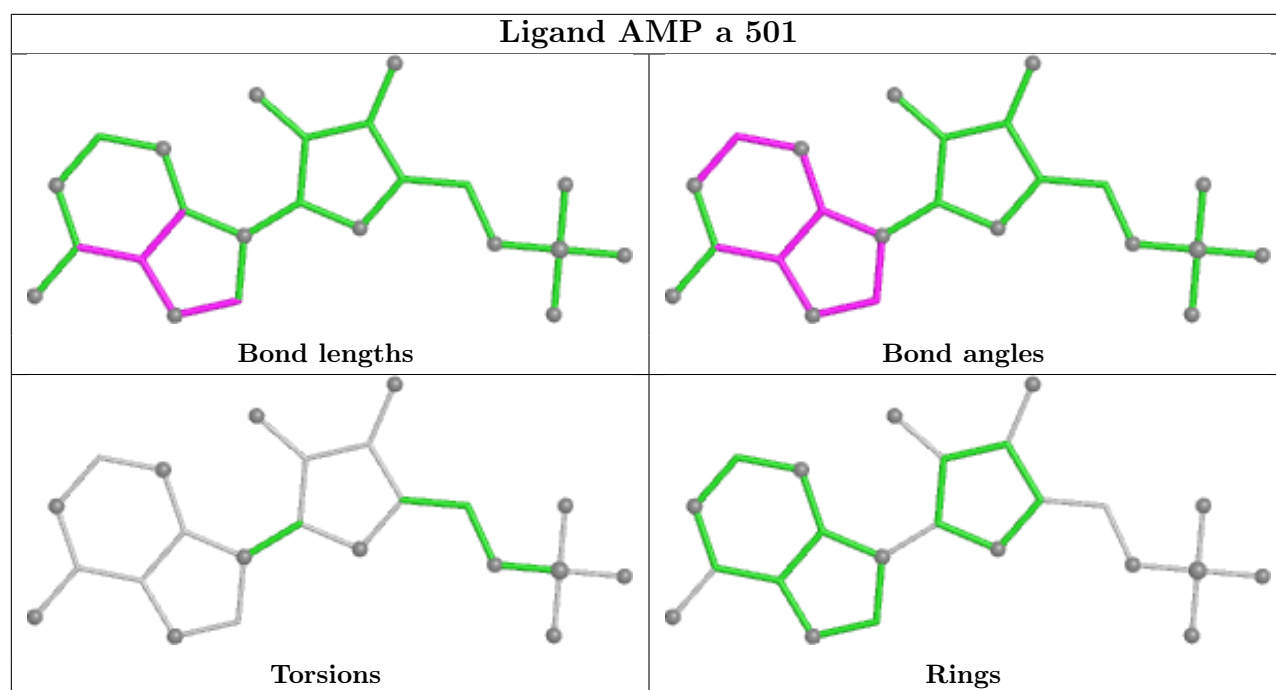
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	a	502	AMP	1	0
35	a	501	AMP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

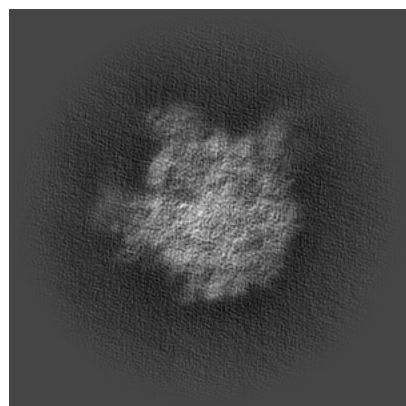
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62900. These allow visual inspection of the internal detail of the map and identification of artifacts.

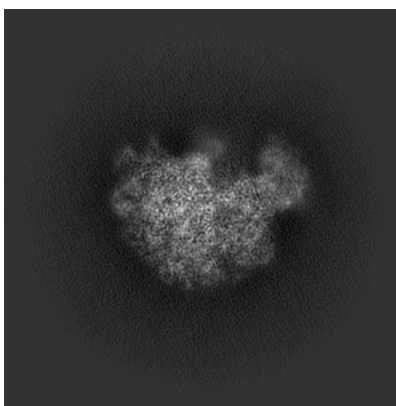
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

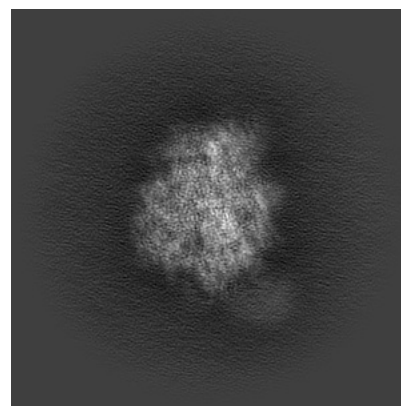
6.1.1 Primary map



X

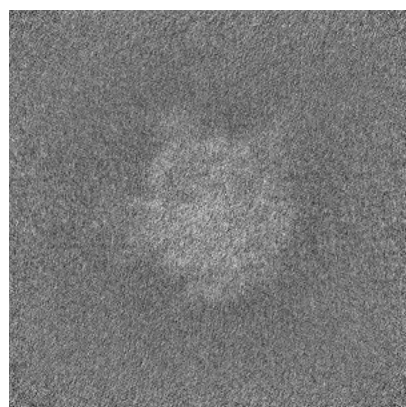


Y

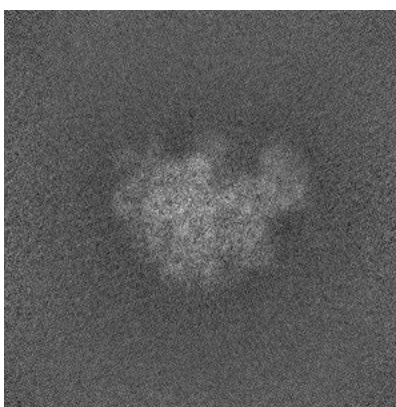


Z

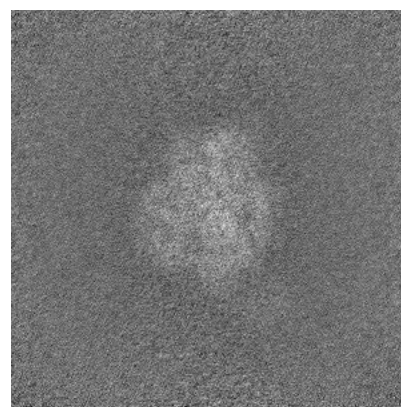
6.1.2 Raw map



X



Y

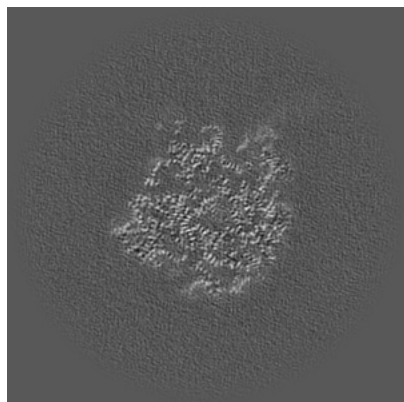


Z

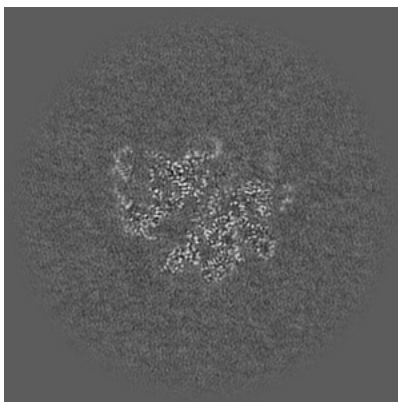
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

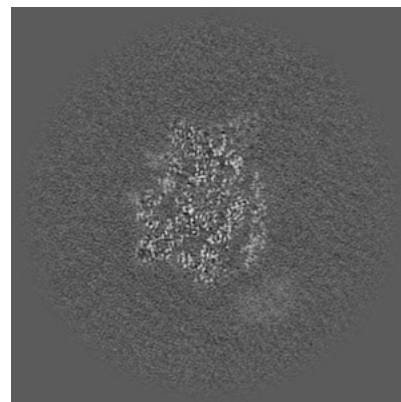
6.2.1 Primary map



X Index: 320

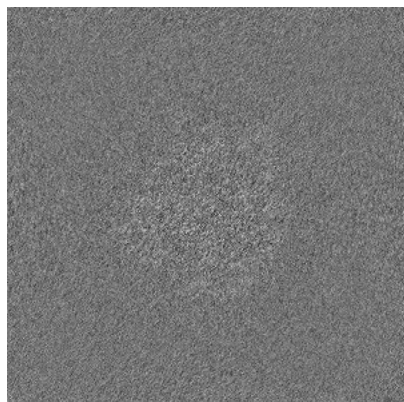


Y Index: 320

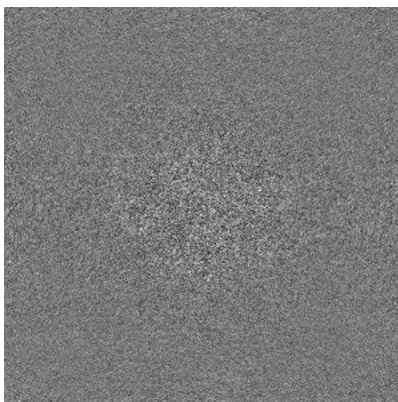


Z Index: 320

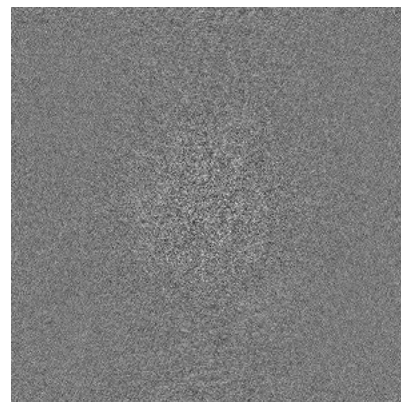
6.2.2 Raw map



X Index: 320



Y Index: 320

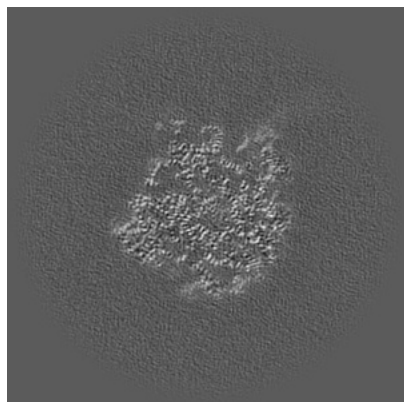


Z Index: 320

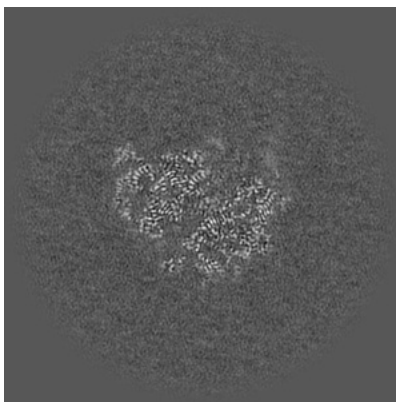
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

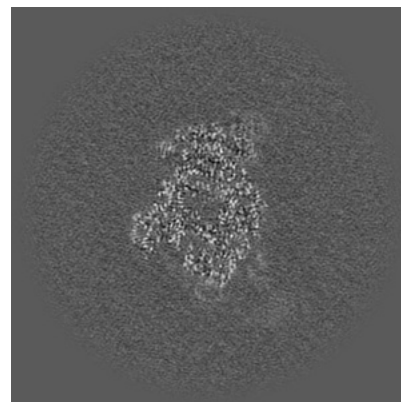
6.3.1 Primary map



X Index: 321

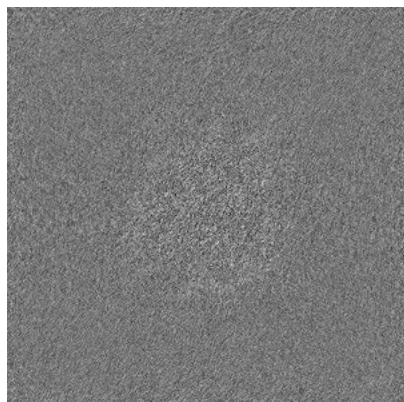


Y Index: 330

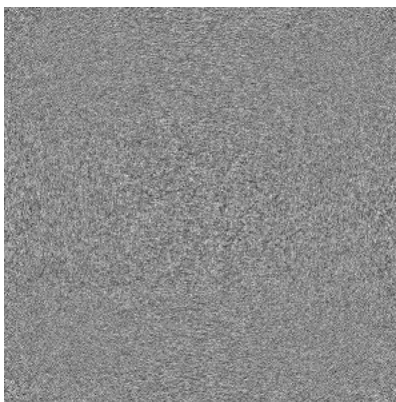


Z Index: 297

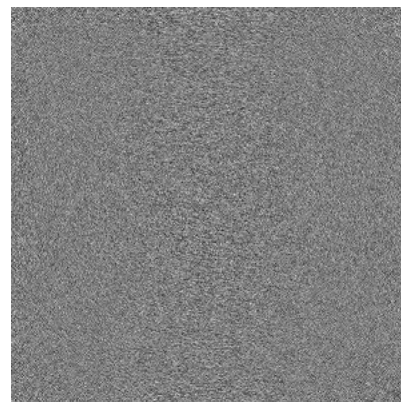
6.3.2 Raw map



X Index: 325



Y Index: 0

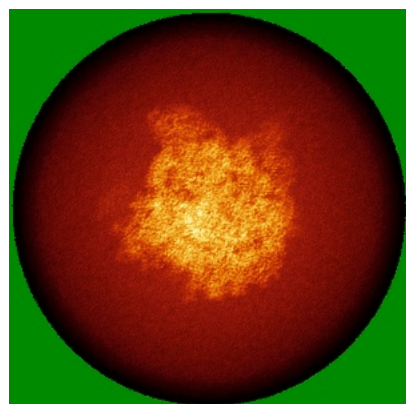


Z Index: 639

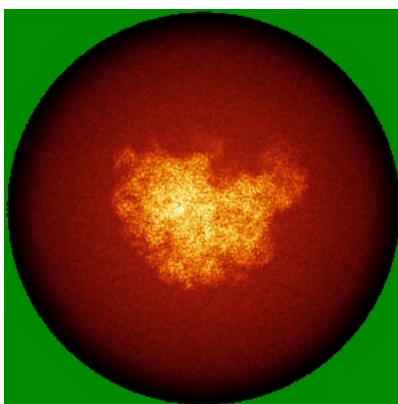
The images above show the largest variance slices of the map in three orthogonal directions.

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

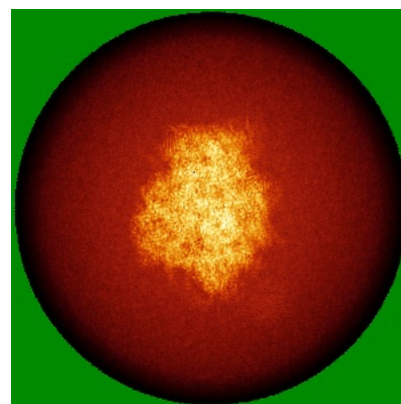
6.4.1 Primary map



X

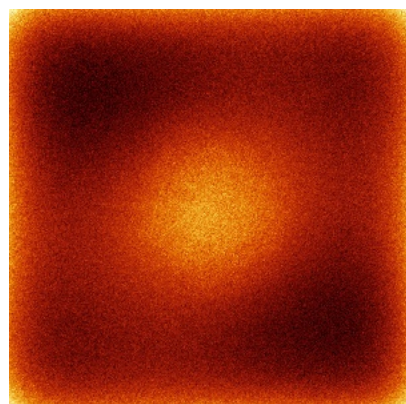


Y

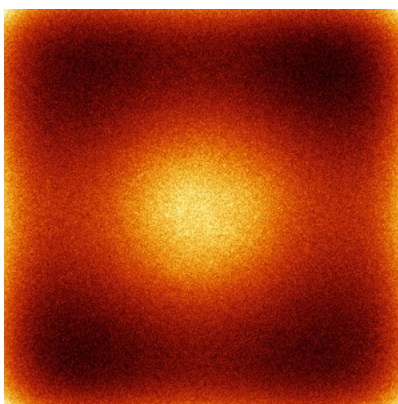


Z

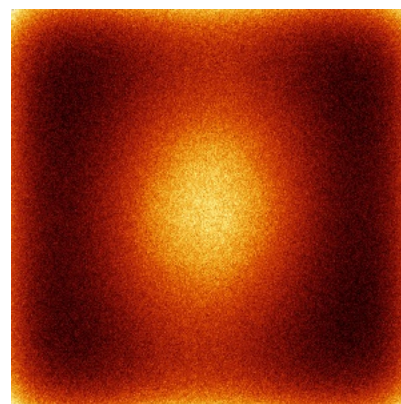
6.4.2 Raw map



X



Y

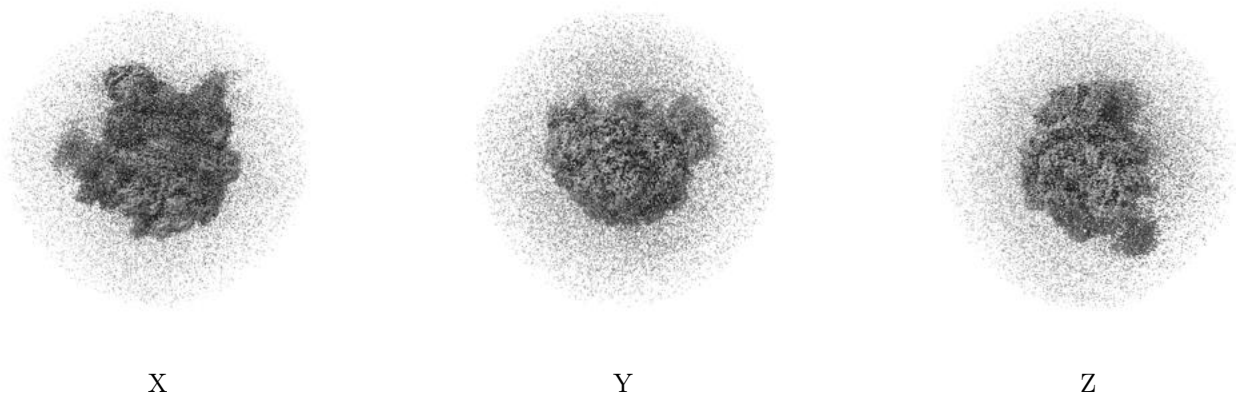


Z

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

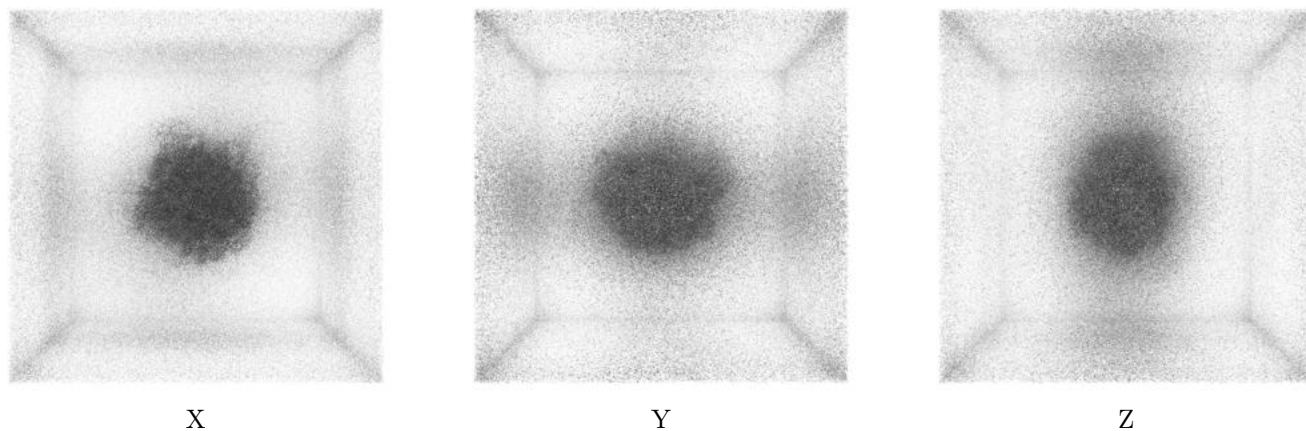
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.056. 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.

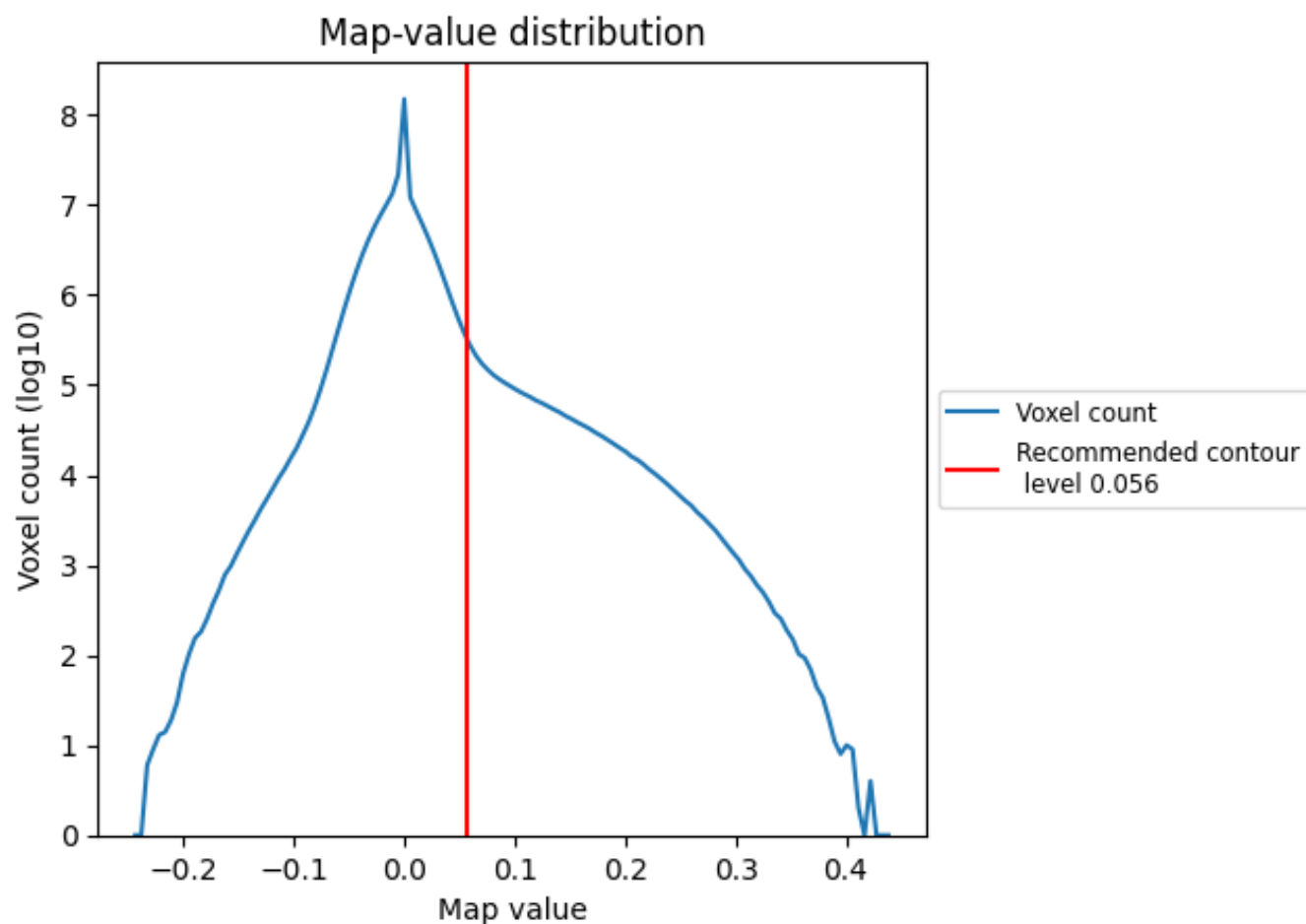
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

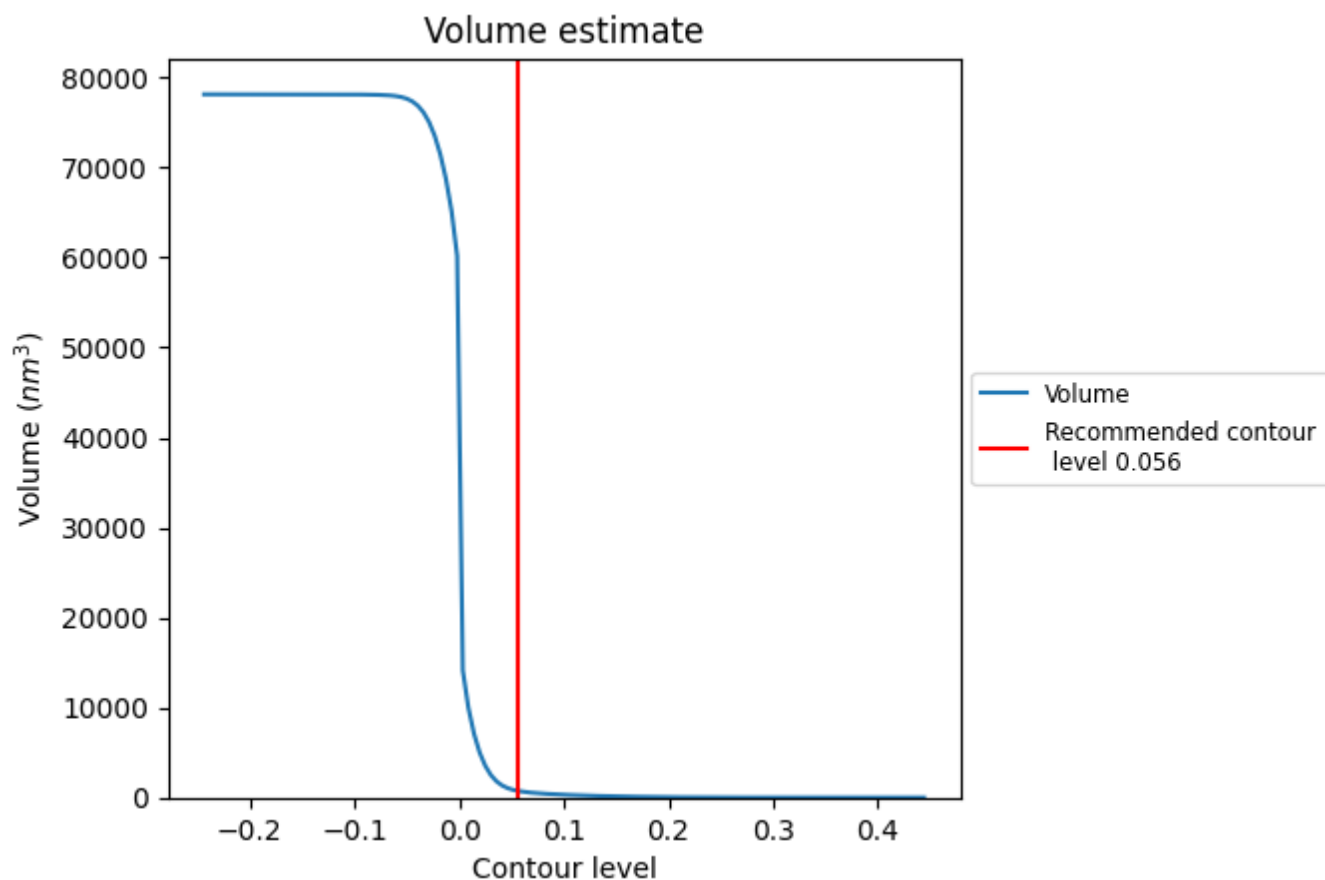
This section contains the results of statistical analysis of the map.

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.

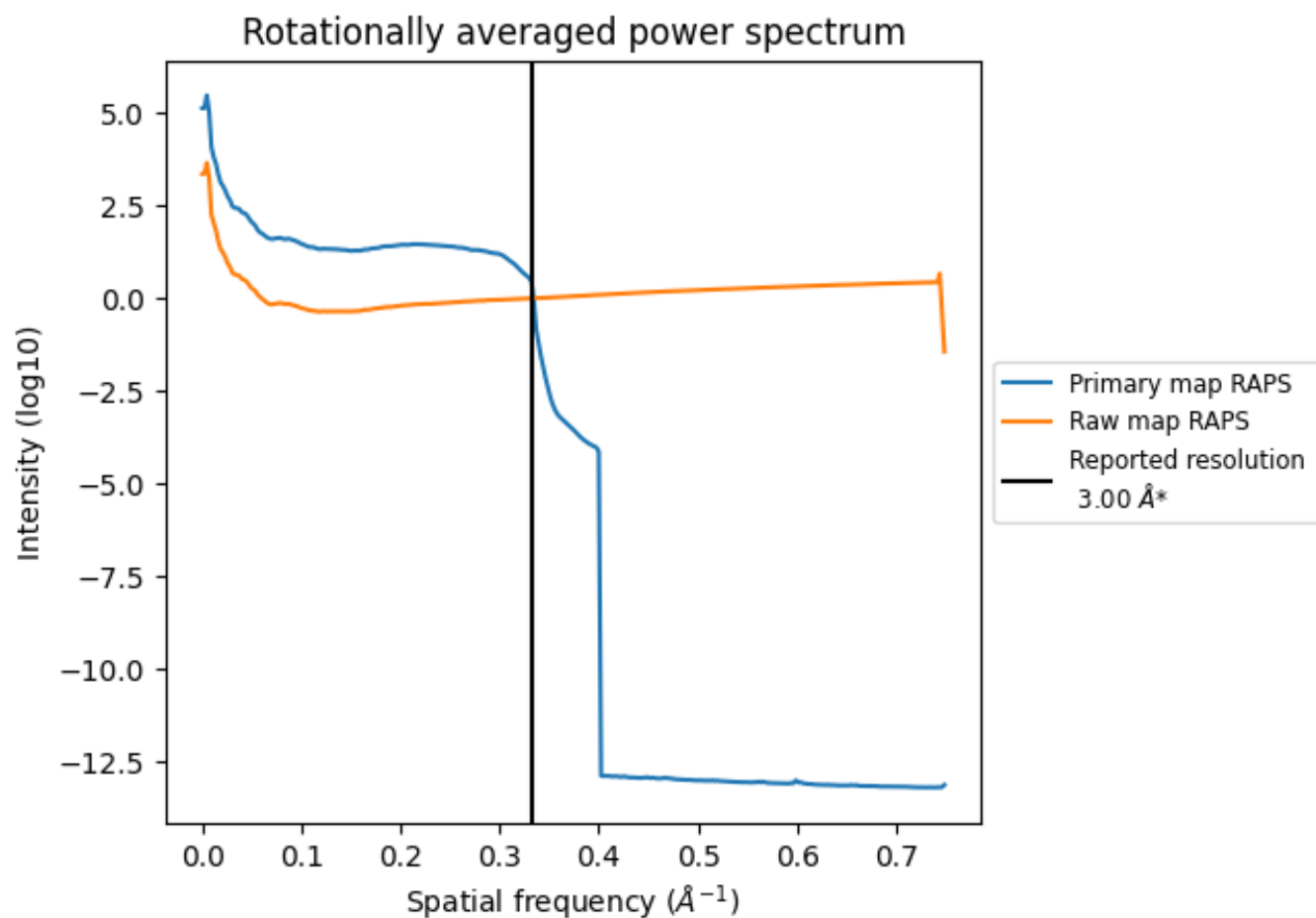
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 743 nm³; this corresponds to an approximate mass of 671 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](#)

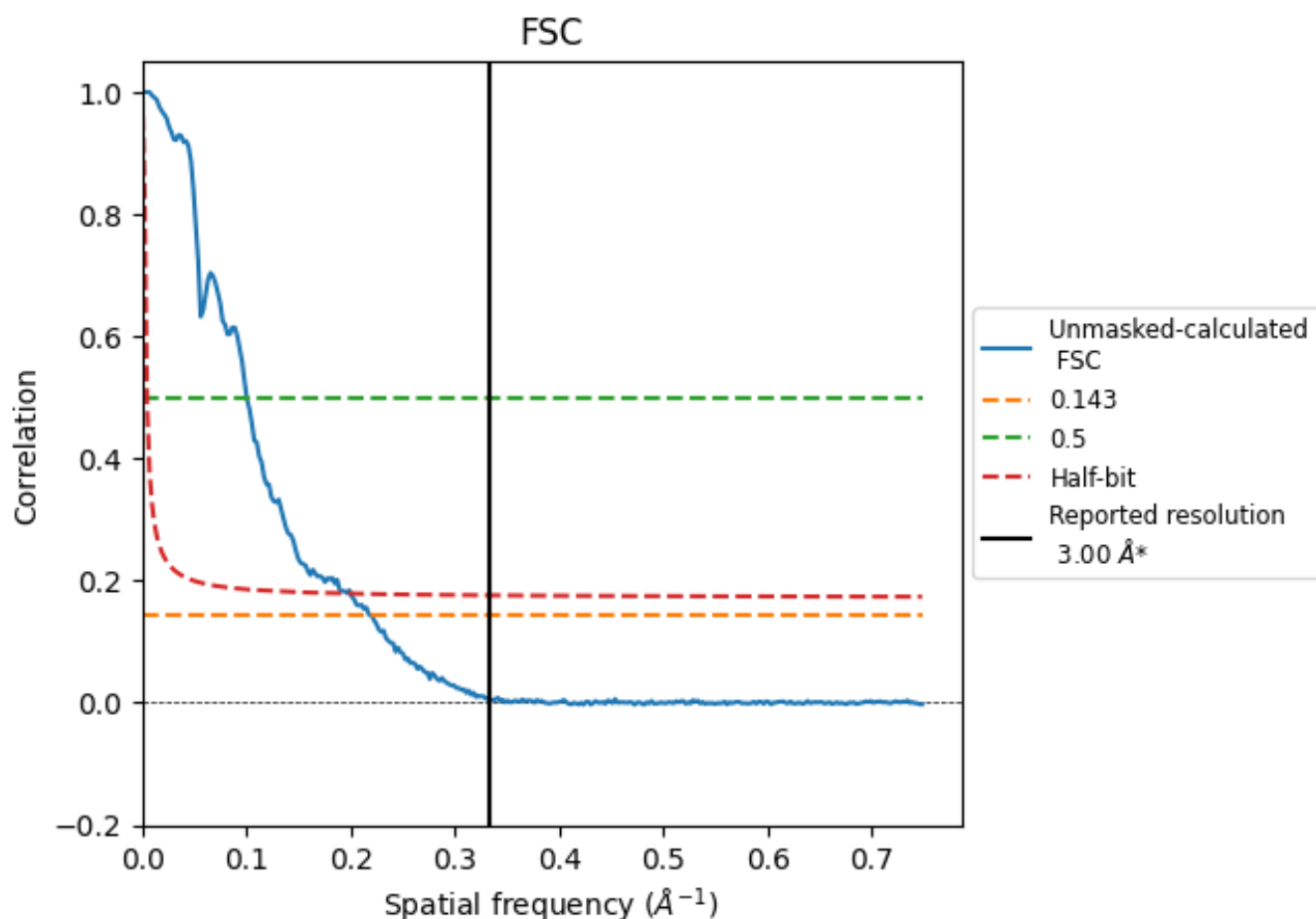


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

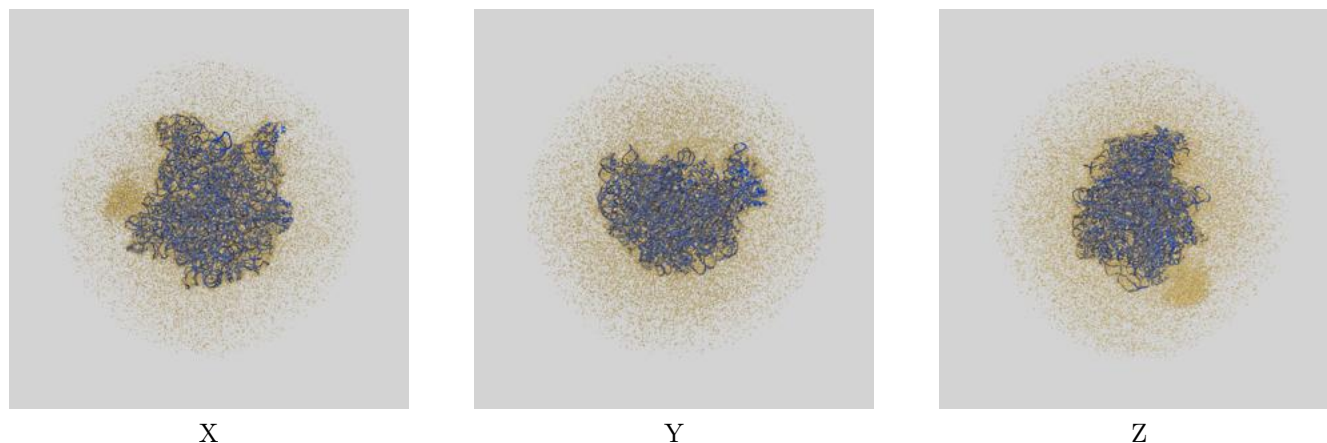
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.55	9.97	5.00

*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 4.55 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

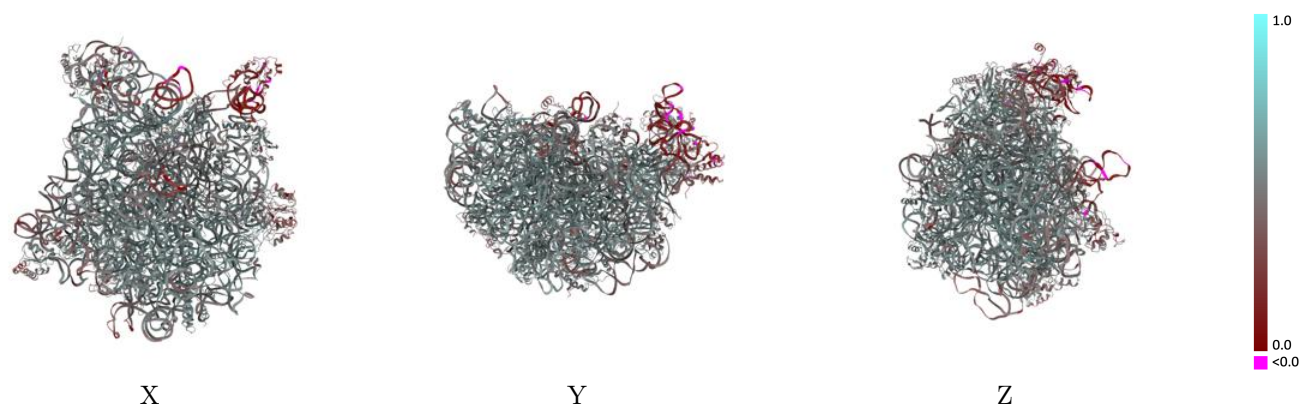
This section contains information regarding the fit between EMDB map EMD-62900 and PDB model 9L9C. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



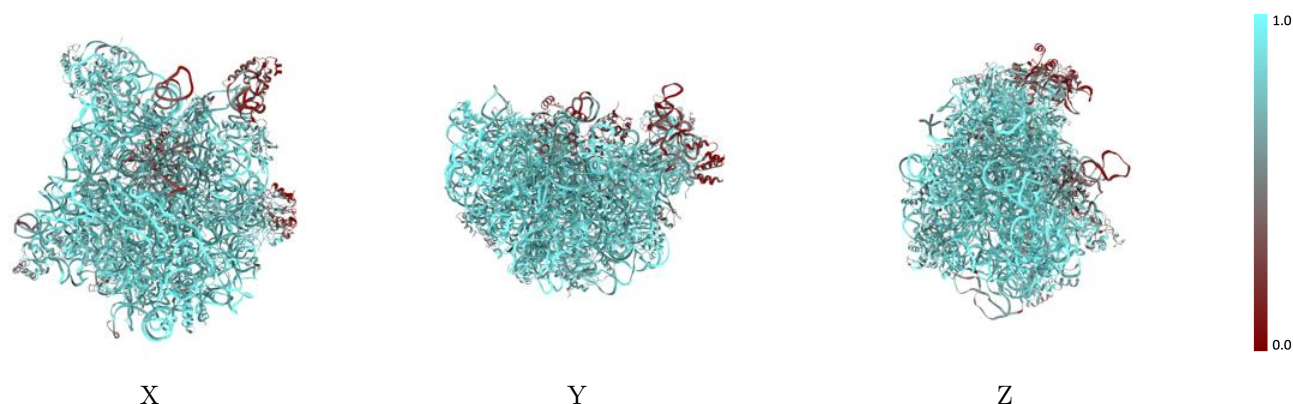
The images above show the 3D surface view of the map at the recommended contour level 0.056 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



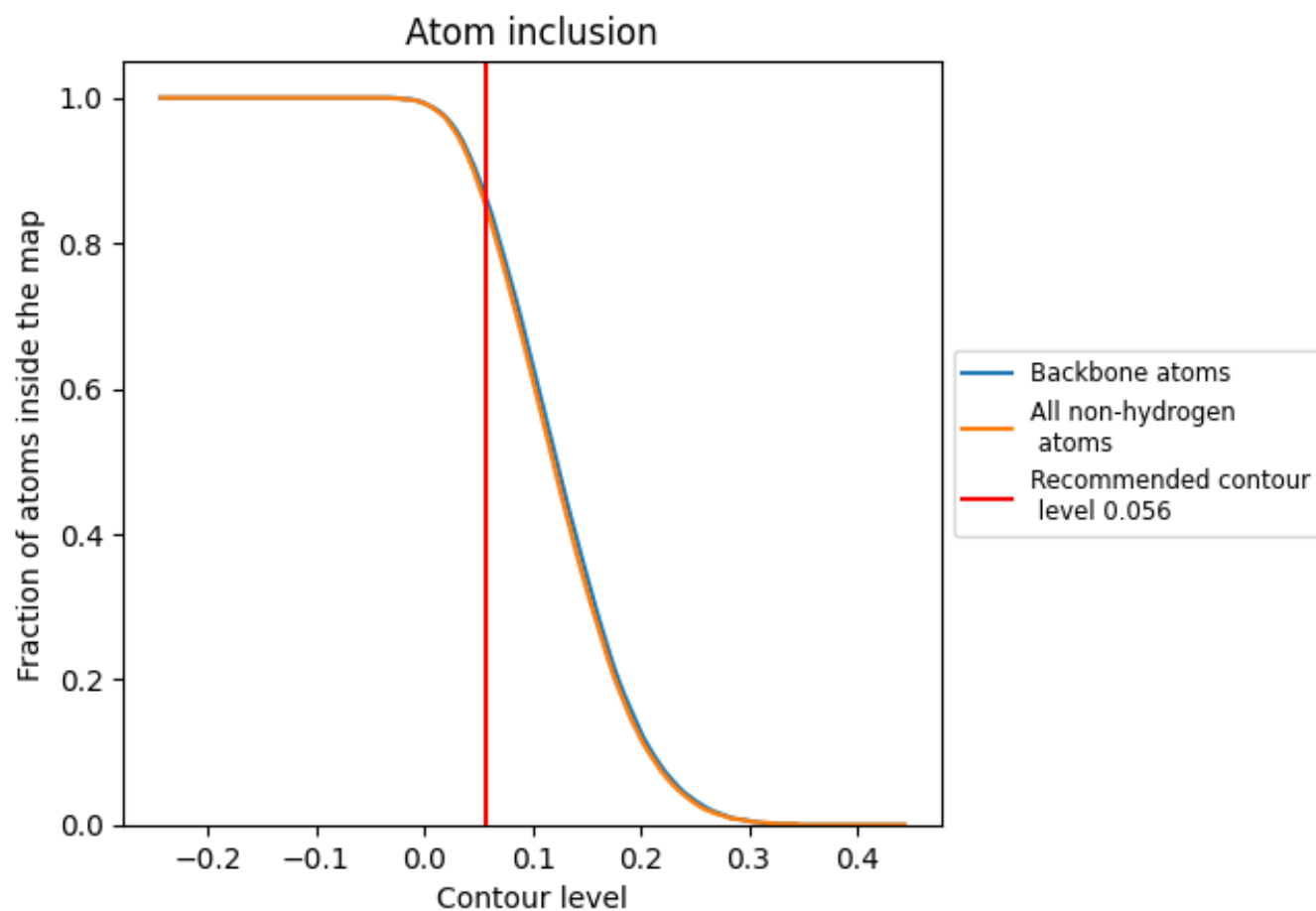
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.056).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 86% 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 (0.056) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8550	 0.5030
0	 0.8970	 0.5030
1	 0.8900	 0.4950
A	 0.8700	 0.5400
B	 0.4160	 0.3770
E	 0.7120	 0.4600
F	 0.8290	 0.5310
G	 0.9160	 0.5510
H	 0.8370	 0.5370
I	 0.7950	 0.5020
J	 0.8480	 0.5290
K	 0.9050	 0.5620
L	 0.8790	 0.5510
M	 0.8480	 0.5090
N	 0.8440	 0.5420
O	 0.8580	 0.5360
P	 0.8180	 0.5240
Q	 0.8630	 0.5460
R	 0.8080	 0.5020
S	 0.9250	 0.5780
T	 0.8880	 0.5470
U	 0.8510	 0.5300
V	 0.8760	 0.5410
W	 0.8510	 0.5470
X	 0.6980	 0.4180
Y	 0.7360	 0.4930
Z	 0.2500	 0.2430
a	 0.4340	 0.4500
b	 0.8580	 0.5300
c	 0.7500	 0.4900
d	 0.6450	 0.4270
e	 0.6080	 0.4730
f	 0.8400	 0.5240

