



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 09:58 AM UTC

PDB ID : 8HKX / pdb_00008hkk
EMDB ID : EMD-34862
Title : Cryo-EM Structures and Translocation Mechanism of Crenarchaeota Ribosome
Authors : Wang, Y.H.; Zhou, J.
Deposited on : 2022-11-28
Resolution : 3.14 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

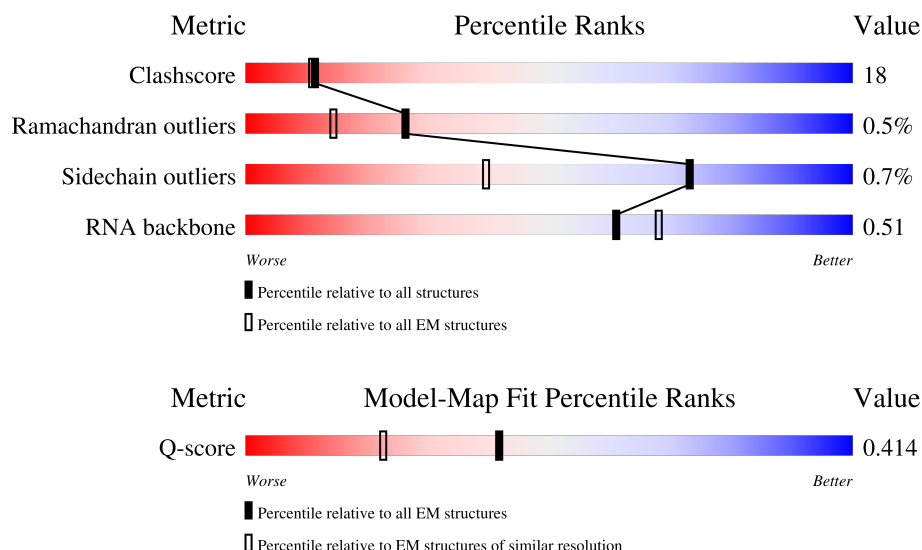
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.14 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	14483 (2.64 - 3.64)

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	A16S	1501	
2	AS2P	196	
3	AS4E	240	

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Mol	Chain	Length	Quality of chain
4	AS4P	166	8% 99%
5	AS5P	204	6% 100%
6	AS6E	105	39% 99%
7	AS8E	126	• 100%
8	AS8P	130	• 100%
9	S11P	128	6% 99%
10	S12P	143	8% 99%
11	S15P	149	5% 98%
12	S17P	111	8% 98%
13	S24E	96	• 100%
14	S27E	59	7% 100%
15	S3AE	189	9% 96%
16	AS3P	201	10% 99%
17	AS7P	193	31% 97%
18	AS9P	136	7% 100%
19	S10P	100	21% 99%
20	S13P	147	31% 98%
21	S14P	52	6% 96%
22	S17E	62	45% 100%
23	S19E	150	23% 100%
24	S19P	115	9% 98%
25	S28E	63	17% 95%
26	SL7A	123	40% 96%
27	S27A	54	15% 63% 35%
28	A	57	16% 93% 7%

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 59656 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 16s rRNA (1491-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A16S	1491	Total	C	N	O	P	0	0
			32023	14261	5925	10346	1491		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AS2P	196	Total	C	N	O	S	0	0
			1587	1022	277	286	2		

- Molecule 3 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AS4E	240	Total	C	N	O	S	0	0
			1925	1238	335	348	4		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AS4P	166	Total	C	N	O	S	0	0
			1370	874	252	241	3		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AS5P	204	Total	C	N	O	S	0	0
			1600	1028	277	287	8		

- Molecule 6 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AS6E	105	Total	C	N	O	S	0	0
			805	506	149	147	3		

- Molecule 7 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	AS8E	126	Total	C	N	O	0	0
			993	619	187	187		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AS8P	130	Total	C	N	O	S	0	0
			1028	661	181	182	4		

- Molecule 9 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	S11P	128	Total	C	N	O	S	0	0
			960	595	190	173	2		

- Molecule 10 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	S12P	143	Total	C	N	O	S	0	0
			1103	701	209	189	4		

- Molecule 11 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	S15P	149	Total	C	N	O	S	0	0
			1225	778	228	214	5		

- Molecule 12 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S17P	111	Total	C	N	O	S	0	0
			885	557	165	160	3		

- Molecule 13 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	S24E	96	Total	C	N	O	0	0
			759	479	133	147		

- Molecule 14 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S27E	59	Total	C	N	O	S	0	0
			458	294	83	76	5		

- Molecule 15 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S3AE	189	Total	C	N	O	S	0	0
			1545	1004	264	276	1		

- Molecule 16 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AS3P	201	Total	C	N	O	S	0	0
			1576	1020	274	278	4		

- Molecule 17 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AS7P	193	Total	C	N	O	S	0	0
			1537	969	285	279	4		

- Molecule 18 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS9P	136	Total	C	N	O	S	0	0
			1096	692	200	197	7		

- Molecule 19 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S10P	100	Total	C	N	O	S	0	0
			824	522	154	142	6		

- Molecule 20 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S13P	147	Total	C	N	O	S	0	0
			1204	753	230	217	4		

- Molecule 21 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S14P	52	Total	C	N	O	S	0	0
			432	273	85	69	5		

- Molecule 22 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S17E	62	Total	C	N	O		0	0
			517	326	92	99			

- Molecule 23 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S19E	150	Total	C	N	O	S	0	0
			1239	801	223	213	2		

- Molecule 24 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S19P	115	Total	C	N	O	S	0	0
			969	620	181	163	5		

- Molecule 25 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S28E	63	Total	C	N	O		0	0
			498	308	99	91			

- Molecule 26 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SL7A	123	Total	C	N	O	S	0	0
			935	593	155	184	3		

- Molecule 27 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S27A	35	Total	C	N	O	S	0	0
			277	174	53	44	6		

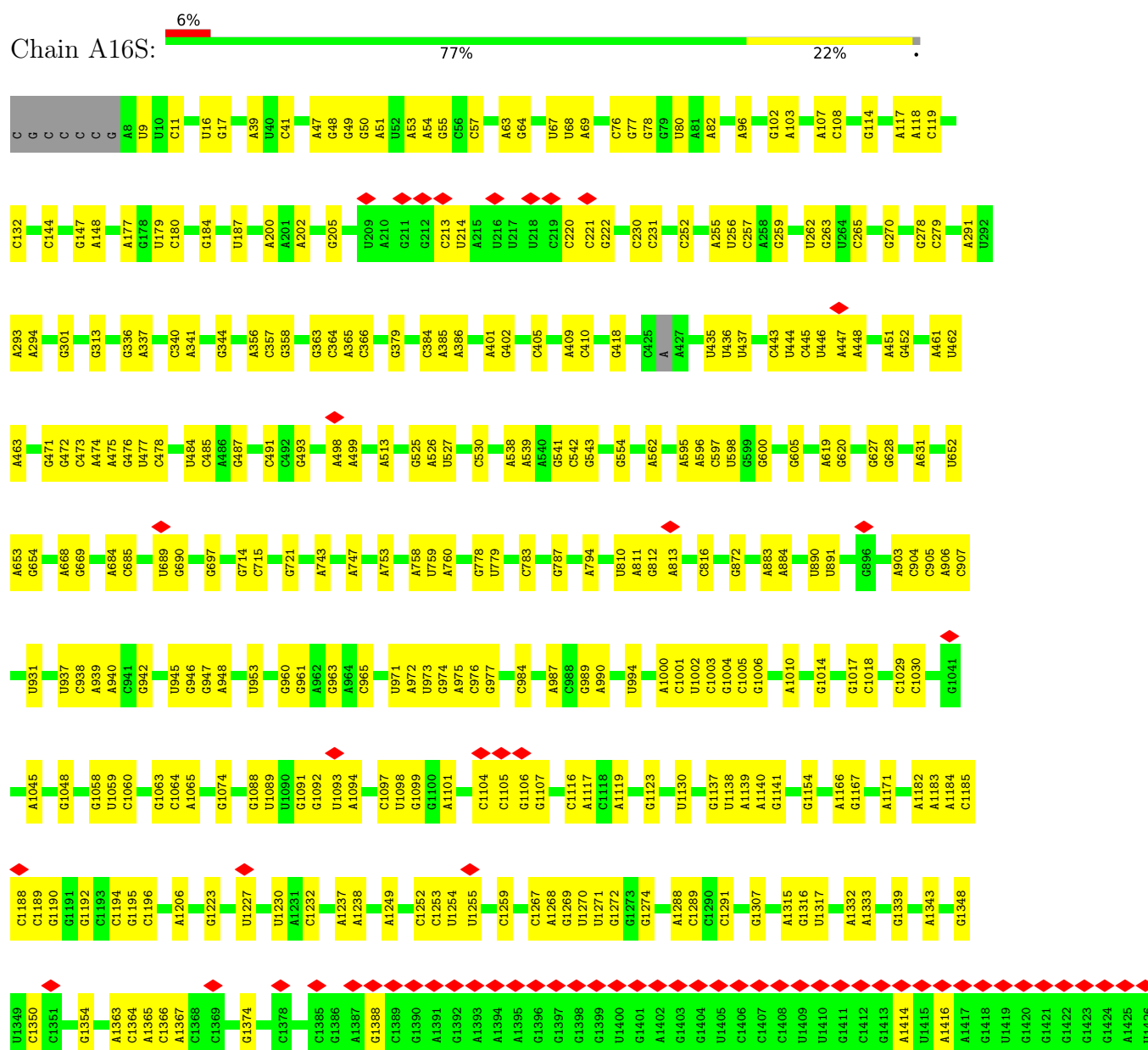
- Molecule 28 is a protein called 30S ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	A	57	Total	C	N	O	0	0
			286	171	57	58		

3 Residue-property plots [i](#)

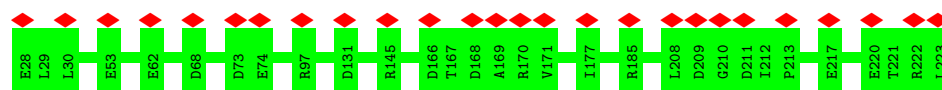
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16s rRNA (1491-MER)

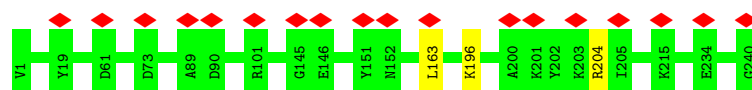




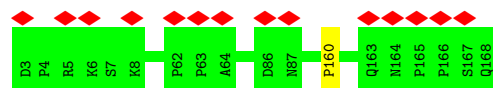
- Molecule 2: 30S ribosomal protein S2



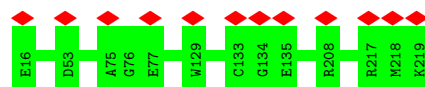
- Molecule 3: 30S ribosomal protein S4e



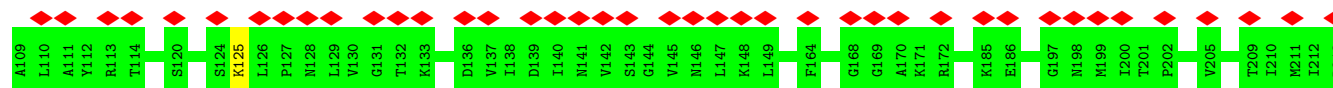
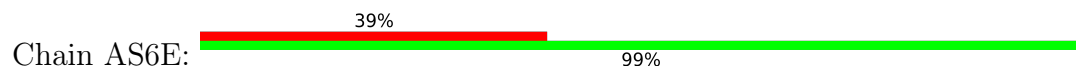
- Molecule 4: 30S ribosomal protein S4



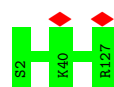
- Molecule 5: 30S ribosomal protein S5



- Molecule 6: 30S ribosomal protein S6e

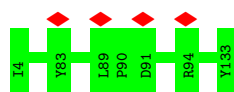


- Molecule 7: 30S ribosomal protein S8e

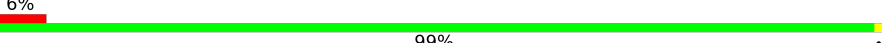


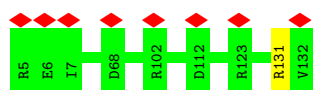
- Molecule 8: 30S ribosomal protein S8

Chain AS8P:  100%

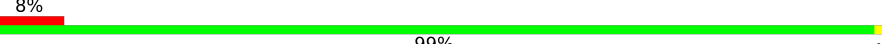


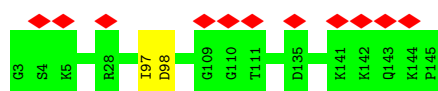
- Molecule 9: 30S ribosomal protein S11

Chain S11P:  99%

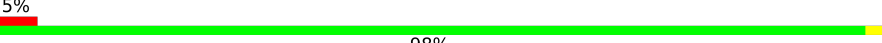


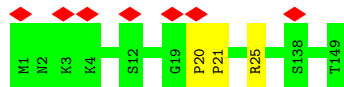
- Molecule 10: 30S ribosomal protein S12

Chain S12P:  99%

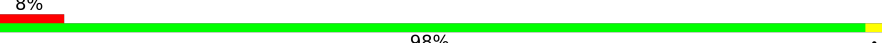


- Molecule 11: 30S ribosomal protein S15

Chain S15P:  98%



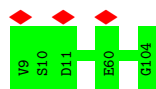
- Molecule 12: 30S ribosomal protein S17

Chain S17P:  98%

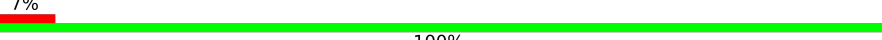


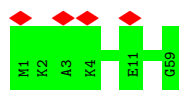
- Molecule 13: 30S ribosomal protein S24e

Chain S24E:  100%

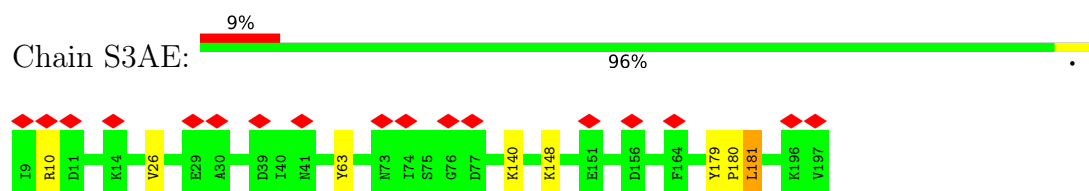


- Molecule 14: 30S ribosomal protein S27e

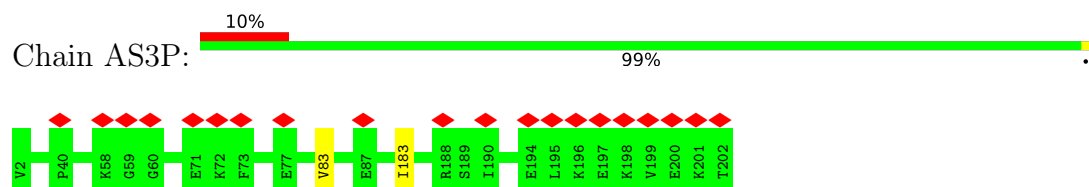
Chain S27E:  100%



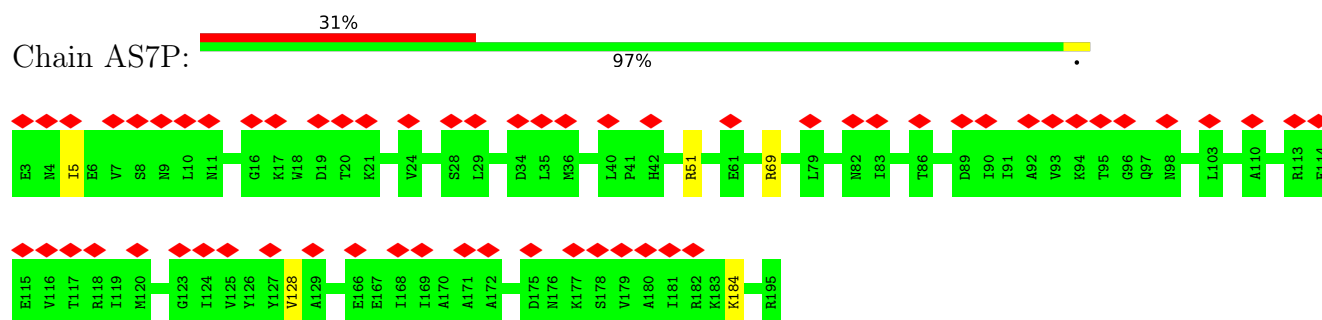
- Molecule 15: 30S ribosomal protein S3Ae



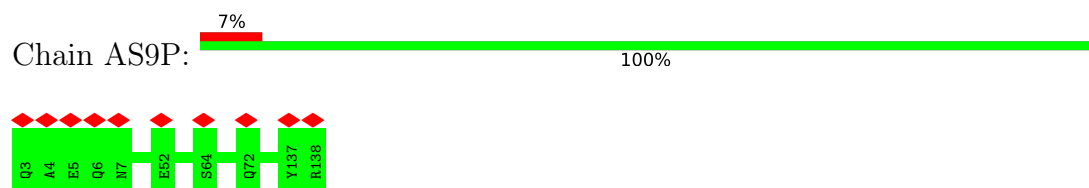
- Molecule 16: 30S ribosomal protein S3



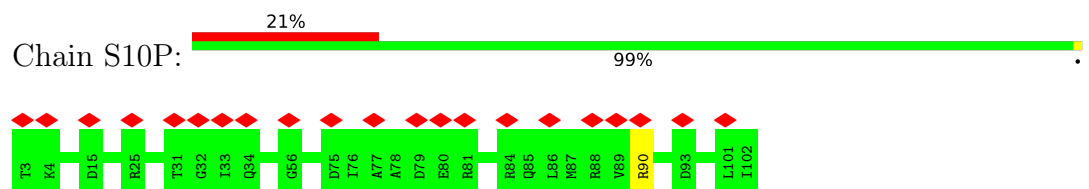
- Molecule 17: 30S ribosomal protein S7



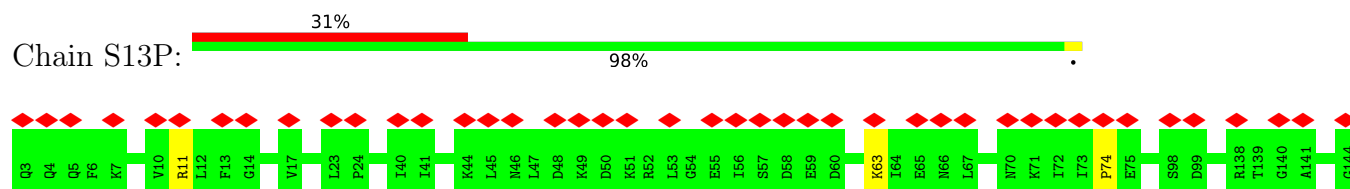
- Molecule 18: 30S ribosomal protein S9



- Molecule 19: 30S ribosomal protein S10

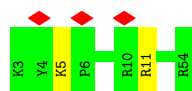


- Molecule 20: 30S ribosomal protein S13

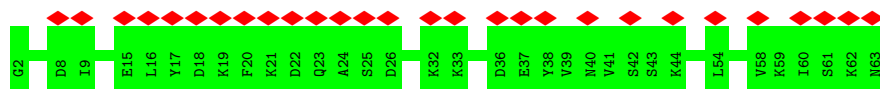




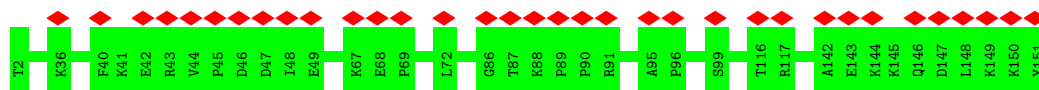
- Molecule 21: 30S ribosomal protein S14 type Z



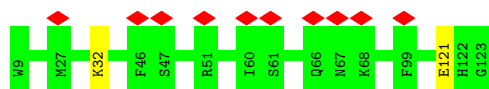
- Molecule 22: 30S ribosomal protein S17e



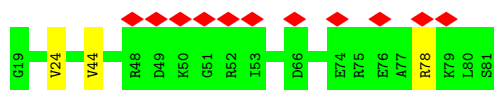
- Molecule 23: 30S ribosomal protein S19e



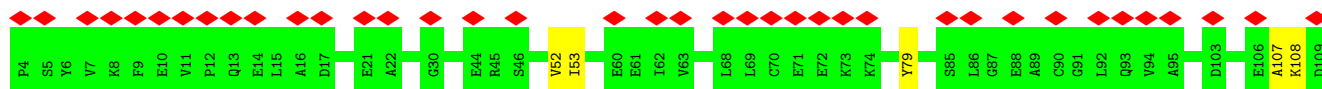
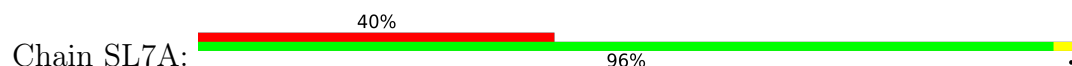
- Molecule 24: 30S ribosomal protein S19

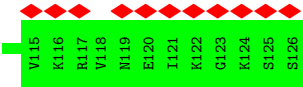


- Molecule 25: 30S ribosomal protein S28e

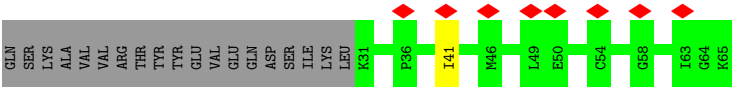


- Molecule 26: 50S ribosomal protein L7Ae

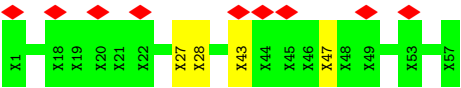
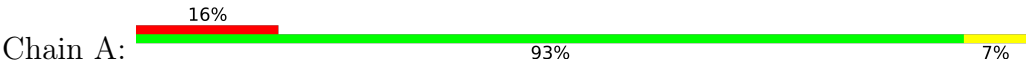




• Molecule 27: 30S ribosomal protein S27ae



• Molecule 28: 30S ribosomal protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	98366	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	26.7	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.666	Depositor
Minimum map value	-2.157	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.46	Depositor
Map size (Å)	413.06, 413.06, 413.06	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.087, 1.087, 1.087	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	A16S	0.19	0/35845	0.33	0/55934
2	AS2P	0.15	0/1621	0.32	0/2202
3	AS4E	0.16	0/1956	0.38	0/2635
4	AS4P	0.19	0/1399	0.43	0/1883
5	AS5P	0.17	0/1631	0.35	0/2200
6	AS6E	0.19	0/815	0.44	0/1093
7	AS8E	0.17	0/1005	0.32	0/1342
8	AS8P	0.16	0/1046	0.32	0/1410
9	S11P	0.16	0/976	0.45	0/1315
10	S12P	0.16	0/1120	0.42	0/1495
11	S15P	0.18	0/1250	0.41	0/1677
12	S17P	0.14	0/899	0.31	0/1203
13	S24E	0.14	0/769	0.26	0/1034
14	S27E	0.16	0/465	0.38	0/618
15	S3AE	0.18	0/1573	0.45	2/2115 (0.1%)
16	AS3P	0.19	0/1599	0.42	0/2147
17	AS7P	0.21	0/1561	0.49	0/2105
18	AS9P	0.20	0/1115	0.49	0/1496
19	S10P	0.19	0/840	0.42	0/1132
20	S13P	0.18	0/1221	0.42	0/1634
21	S14P	0.22	0/441	0.52	0/583
22	S17E	0.17	0/523	0.35	0/696
23	S19E	0.21	0/1267	0.49	0/1705
24	S19P	0.20	0/986	0.44	0/1310
25	S28E	0.23	0/500	0.57	0/669
26	SL7A	0.28	0/946	0.68	0/1272
27	S27A	0.17	0/284	0.38	0/374
All	All	0.19	0/63653	0.37	2/93279 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	AS4E	0	1
10	S12P	0	1
11	S15P	0	1
15	S3AE	0	2
26	SL7A	0	2
All	All	0	7

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	S3AE	181	LEU	CA-CB-CG	5.70	136.25	116.30
15	S3AE	26	VAL	N-CA-C	-5.26	106.75	112.80

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	AS4E	163	LEU	Peptide
10	S12P	98	ASP	Peptide
11	S15P	20	PRO	Peptide
15	S3AE	179	TYR	Peptide
15	S3AE	181	LEU	Peptide
26	SL7A	108	LYS	Peptide
26	SL7A	79	TYR	Peptide

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	A16S	32023	0	0	0	0
2	AS2P	1587	0	0	0	0
3	AS4E	1925	0	0	0	0
4	AS4P	1370	0	0	0	0
5	AS5P	1600	0	0	0	0
6	AS6E	805	0	0	0	0
7	AS8E	993	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	AS8P	1028	0	0	0	0
9	S11P	960	0	0	0	0
10	S12P	1103	0	0	0	0
11	S15P	1225	0	0	0	0
12	S17P	885	0	0	0	0
13	S24E	759	0	0	0	0
14	S27E	458	0	0	0	0
15	S3AE	1545	0	0	0	0
16	AS3P	1576	0	0	0	0
17	AS7P	1537	0	0	0	0
18	AS9P	1096	0	0	0	0
19	S10P	824	0	0	0	0
20	S13P	1204	0	0	0	0
21	S14P	432	0	0	0	0
22	S17E	517	0	0	0	0
23	S19E	1239	0	0	0	0
24	S19P	969	0	0	0	0
25	S28E	498	0	0	0	0
26	SL7A	935	0	0	0	0
27	S27A	277	0	0	0	0
28	A	286	0	71	2	0
All	All	59656	0	71	2	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 18.

All (2) 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)
28:A:43:UNK:O	28:A:47:UNK:N	2.45	0.50
28:A:27:UNK:HA	28:A:28:UNK:HA	1.81	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AS2P	194/196 (99%)	186 (96%)	8 (4%)	0	100	100
3	AS4E	238/240 (99%)	212 (89%)	26 (11%)	0	100	100
4	AS4P	164/166 (99%)	141 (86%)	22 (13%)	1 (1%)	21	50
5	AS5P	202/204 (99%)	186 (92%)	16 (8%)	0	100	100
6	AS6E	103/105 (98%)	89 (86%)	14 (14%)	0	100	100
7	AS8E	124/126 (98%)	108 (87%)	16 (13%)	0	100	100
8	AS8P	128/130 (98%)	124 (97%)	4 (3%)	0	100	100
9	S11P	126/128 (98%)	107 (85%)	19 (15%)	0	100	100
10	S12P	141/143 (99%)	115 (82%)	25 (18%)	1 (1%)	18	47
11	S15P	147/149 (99%)	127 (86%)	19 (13%)	1 (1%)	18	47
12	S17P	109/111 (98%)	105 (96%)	4 (4%)	0	100	100
13	S24E	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
14	S27E	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
15	S3AE	187/189 (99%)	156 (83%)	29 (16%)	2 (1%)	11	36
16	AS3P	199/201 (99%)	171 (86%)	26 (13%)	2 (1%)	12	38
17	AS7P	191/193 (99%)	145 (76%)	45 (24%)	1 (0%)	24	54
18	AS9P	134/136 (98%)	110 (82%)	24 (18%)	0	100	100
19	S10P	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
20	S13P	145/147 (99%)	114 (79%)	30 (21%)	1 (1%)	18	47
21	S14P	50/52 (96%)	43 (86%)	6 (12%)	1 (2%)	6	23
22	S17E	60/62 (97%)	53 (88%)	7 (12%)	0	100	100
23	S19E	148/150 (99%)	122 (82%)	26 (18%)	0	100	100
24	S19P	113/115 (98%)	99 (88%)	13 (12%)	1 (1%)	14	41
25	S28E	61/63 (97%)	47 (77%)	12 (20%)	2 (3%)	3	14
26	SL7A	121/123 (98%)	93 (77%)	26 (22%)	2 (2%)	7	27
27	S27A	33/54 (61%)	29 (88%)	3 (9%)	1 (3%)	3	16
All	All	3367/3438 (98%)	2912 (86%)	439 (13%)	16 (0%)	26	54

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	AS3P	83	VAL
21	S14P	5	LYS
16	AS3P	183	ILE
17	AS7P	128	VAL
25	S28E	44	VAL
15	S3AE	63	TYR
15	S3AE	180	PRO
25	S28E	24	VAL
24	S19P	121	GLU
27	S27A	41	ILE
26	SL7A	107	ALA
4	AS4P	160	PRO
10	S12P	97	ILE
20	S13P	74	PRO
11	S15P	21	PRO
26	SL7A	52	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AS2P	174/174 (100%)	174 (100%)	0	100	100
3	AS4E	210/210 (100%)	208 (99%)	2 (1%)	68	76
4	AS4P	149/149 (100%)	149 (100%)	0	100	100
5	AS5P	174/174 (100%)	174 (100%)	0	100	100
6	AS6E	88/88 (100%)	87 (99%)	1 (1%)	65	75
7	AS8E	106/106 (100%)	106 (100%)	0	100	100
8	AS8P	111/111 (100%)	111 (100%)	0	100	100
9	S11P	94/94 (100%)	93 (99%)	1 (1%)	65	75
10	S12P	116/116 (100%)	116 (100%)	0	100	100
11	S15P	133/133 (100%)	132 (99%)	1 (1%)	73	78
12	S17P	97/97 (100%)	95 (98%)	2 (2%)	47	67
13	S24E	84/84 (100%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	S27E	51/51 (100%)	51 (100%)	0	100	100
15	S3AE	170/170 (100%)	167 (98%)	3 (2%)	51	69
16	AS3P	165/165 (100%)	165 (100%)	0	100	100
17	AS7P	166/166 (100%)	162 (98%)	4 (2%)	43	65
18	AS9P	113/113 (100%)	113 (100%)	0	100	100
19	S10P	92/92 (100%)	91 (99%)	1 (1%)	65	75
20	S13P	129/129 (100%)	127 (98%)	2 (2%)	55	71
21	S14P	45/45 (100%)	44 (98%)	1 (2%)	45	67
22	S17E	57/57 (100%)	57 (100%)	0	100	100
23	S19E	134/134 (100%)	134 (100%)	0	100	100
24	S19P	106/106 (100%)	105 (99%)	1 (1%)	70	77
25	S28E	54/54 (100%)	53 (98%)	1 (2%)	50	69
26	SL7A	104/104 (100%)	103 (99%)	1 (1%)	68	76
27	S27A	29/47 (62%)	29 (100%)	0	100	100
All	All	2951/2969 (99%)	2930 (99%)	21 (1%)	73	79

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	AS4E	196	LYS
3	AS4E	204	ARG
6	AS6E	125	LYS
9	S11P	131	ARG
11	S15P	25	ARG
12	S17P	21	LYS
12	S17P	37	ARG
15	S3AE	10	ARG
15	S3AE	140	LYS
15	S3AE	148	LYS
17	AS7P	5	ILE
17	AS7P	51	ARG
17	AS7P	69	ARG
17	AS7P	184	LYS
19	S10P	90	ARG
20	S13P	11	ARG
20	S13P	63	LYS
21	S14P	11	ARG

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Mol	Chain	Res	Type
24	S19P	32	LYS
25	S28E	78	ARG
26	SL7A	53	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A16S	1489/1501 (99%)	314 (21%)	43 (2%)

All (314) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A16S	9	U
1	A16S	11	C
1	A16S	16	U
1	A16S	17	G
1	A16S	39	A
1	A16S	41	C
1	A16S	47	A
1	A16S	48	G
1	A16S	49	G
1	A16S	50	G
1	A16S	51	A
1	A16S	53	A
1	A16S	54	A
1	A16S	55	G
1	A16S	57	C
1	A16S	64	G
1	A16S	67	U
1	A16S	68	U
1	A16S	69	A
1	A16S	76	C
1	A16S	77	G
1	A16S	78	G
1	A16S	80	U
1	A16S	82	A
1	A16S	96	A
1	A16S	103	A

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Mol	Chain	Res	Type
1	A16S	107	A
1	A16S	108	C
1	A16S	114	G
1	A16S	117	A
1	A16S	118	A
1	A16S	119	C
1	A16S	132	C
1	A16S	144	C
1	A16S	147	G
1	A16S	148	A
1	A16S	177	A
1	A16S	180	C
1	A16S	184	G
1	A16S	187	U
1	A16S	200	A
1	A16S	202	A
1	A16S	205	G
1	A16S	213	C
1	A16S	214	U
1	A16S	220	C
1	A16S	221	C
1	A16S	222	G
1	A16S	230	C
1	A16S	231	C
1	A16S	252	C
1	A16S	256	U
1	A16S	257	C
1	A16S	259	G
1	A16S	263	G
1	A16S	265	C
1	A16S	270	G
1	A16S	278	G
1	A16S	279	C
1	A16S	291	A
1	A16S	294	A
1	A16S	301	G
1	A16S	313	G
1	A16S	336	G
1	A16S	337	A
1	A16S	340	C
1	A16S	341	A
1	A16S	344	G

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Mol	Chain	Res	Type
1	A16S	356	A
1	A16S	357	C
1	A16S	358	G
1	A16S	363	G
1	A16S	364	C
1	A16S	365	A
1	A16S	366	C
1	A16S	379	G
1	A16S	385	A
1	A16S	386	A
1	A16S	401	A
1	A16S	402	G
1	A16S	405	C
1	A16S	409	A
1	A16S	410	C
1	A16S	418	G
1	A16S	435	U
1	A16S	436	U
1	A16S	437	U
1	A16S	443	C
1	A16S	444	U
1	A16S	445	C
1	A16S	446	U
1	A16S	447	A
1	A16S	448	A
1	A16S	451	A
1	A16S	452	G
1	A16S	461	A
1	A16S	462	U
1	A16S	463	A
1	A16S	471	G
1	A16S	472	G
1	A16S	473	C
1	A16S	474	A
1	A16S	475	A
1	A16S	476	G
1	A16S	477	U
1	A16S	478	C
1	A16S	484	U
1	A16S	485	C
1	A16S	487	G
1	A16S	491	C

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Mol	Chain	Res	Type
1	A16S	493	G
1	A16S	498	A
1	A16S	499	A
1	A16S	513	A
1	A16S	525	G
1	A16S	526	A
1	A16S	527	U
1	A16S	530	C
1	A16S	538	A
1	A16S	539	A
1	A16S	542	C
1	A16S	543	G
1	A16S	554	G
1	A16S	562	A
1	A16S	596	A
1	A16S	597	C
1	A16S	598	U
1	A16S	600	G
1	A16S	605	G
1	A16S	619	A
1	A16S	620	G
1	A16S	627	G
1	A16S	628	G
1	A16S	631	A
1	A16S	652	U
1	A16S	653	A
1	A16S	654	G
1	A16S	668	A
1	A16S	669	G
1	A16S	685	C
1	A16S	689	U
1	A16S	690	G
1	A16S	697	G
1	A16S	714	G
1	A16S	715	C
1	A16S	721	G
1	A16S	743	A
1	A16S	747	A
1	A16S	753	A
1	A16S	759	U
1	A16S	760	A
1	A16S	779	U

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Mol	Chain	Res	Type
1	A16S	783	C
1	A16S	787	G
1	A16S	794	A
1	A16S	810	U
1	A16S	811	A
1	A16S	812	G
1	A16S	813	A
1	A16S	816	C
1	A16S	872	G
1	A16S	884	A
1	A16S	891	U
1	A16S	903	A
1	A16S	904	C
1	A16S	905	C
1	A16S	906	A
1	A16S	907	C
1	A16S	931	U
1	A16S	937	U
1	A16S	938	C
1	A16S	939	A
1	A16S	940	A
1	A16S	942	G
1	A16S	945	U
1	A16S	946	G
1	A16S	947	G
1	A16S	948	A
1	A16S	953	U
1	A16S	960	G
1	A16S	961	G
1	A16S	963	G
1	A16S	965	C
1	A16S	971	U
1	A16S	972	A
1	A16S	973	U
1	A16S	974	G
1	A16S	975	A
1	A16S	976	C
1	A16S	977	G
1	A16S	984	C
1	A16S	987	A
1	A16S	989	G
1	A16S	990	A

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Mol	Chain	Res	Type
1	A16S	994	U
1	A16S	1000	A
1	A16S	1001	C
1	A16S	1002	U
1	A16S	1003	C
1	A16S	1004	G
1	A16S	1005	C
1	A16S	1006	G
1	A16S	1010	A
1	A16S	1014	G
1	A16S	1017	G
1	A16S	1018	C
1	A16S	1029	C
1	A16S	1030	C
1	A16S	1045	A
1	A16S	1048	G
1	A16S	1058	G
1	A16S	1059	U
1	A16S	1060	C
1	A16S	1063	G
1	A16S	1064	C
1	A16S	1065	A
1	A16S	1074	G
1	A16S	1088	G
1	A16S	1089	U
1	A16S	1091	G
1	A16S	1092	G
1	A16S	1093	U
1	A16S	1094	A
1	A16S	1097	C
1	A16S	1098	U
1	A16S	1099	G
1	A16S	1101	A
1	A16S	1104	C
1	A16S	1105	C
1	A16S	1106	G
1	A16S	1107	G
1	A16S	1116	C
1	A16S	1117	A
1	A16S	1119	A
1	A16S	1123	G
1	A16S	1130	U

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Mol	Chain	Res	Type
1	A16S	1137	G
1	A16S	1138	U
1	A16S	1139	A
1	A16S	1140	A
1	A16S	1141	G
1	A16S	1154	G
1	A16S	1166	A
1	A16S	1167	G
1	A16S	1171	A
1	A16S	1182	A
1	A16S	1183	A
1	A16S	1185	C
1	A16S	1188	C
1	A16S	1189	C
1	A16S	1190	G
1	A16S	1192	G
1	A16S	1194	C
1	A16S	1195	G
1	A16S	1196	C
1	A16S	1206	A
1	A16S	1223	G
1	A16S	1227	U
1	A16S	1230	U
1	A16S	1232	C
1	A16S	1237	A
1	A16S	1238	A
1	A16S	1249	A
1	A16S	1252	C
1	A16S	1253	C
1	A16S	1254	U
1	A16S	1255	U
1	A16S	1259	C
1	A16S	1267	C
1	A16S	1268	A
1	A16S	1269	G
1	A16S	1270	U
1	A16S	1271	U
1	A16S	1272	G
1	A16S	1274	G
1	A16S	1288	A
1	A16S	1289	C
1	A16S	1291	C

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Mol	Chain	Res	Type
1	A16S	1307	G
1	A16S	1315	A
1	A16S	1316	G
1	A16S	1317	U
1	A16S	1332	A
1	A16S	1333	A
1	A16S	1339	G
1	A16S	1343	A
1	A16S	1348	G
1	A16S	1350	C
1	A16S	1354	G
1	A16S	1363	A
1	A16S	1364	C
1	A16S	1365	A
1	A16S	1366	C
1	A16S	1367	A
1	A16S	1374	G
1	A16S	1388	G
1	A16S	1414	A
1	A16S	1416	A
1	A16S	1430	A
1	A16S	1443	G
1	A16S	1451	A
1	A16S	1460	A
1	A16S	1463	A
1	A16S	1465	G
1	A16S	1466	G
1	A16S	1467	U
1	A16S	1468	A
1	A16S	1481	C
1	A16S	1490	G
1	A16S	1491	G
1	A16S	1492	A
1	A16S	1493	U
1	A16S	1497	C
1	A16S	1501	U

All (43) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A16S	47	A
1	A16S	49	G

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Mol	Chain	Res	Type
1	A16S	54	A
1	A16S	63	A
1	A16S	102	G
1	A16S	117	A
1	A16S	179	U
1	A16S	220	C
1	A16S	255	A
1	A16S	262	U
1	A16S	278	G
1	A16S	293	A
1	A16S	340	C
1	A16S	384	C
1	A16S	444	U
1	A16S	471	G
1	A16S	475	A
1	A16S	484	U
1	A16S	526	A
1	A16S	541	G
1	A16S	595	A
1	A16S	653	A
1	A16S	684	A
1	A16S	758	A
1	A16S	778	G
1	A16S	883	A
1	A16S	890	U
1	A16S	903	A
1	A16S	973	U
1	A16S	974	G
1	A16S	1088	G
1	A16S	1093	U
1	A16S	1116	C
1	A16S	1138	U
1	A16S	1184	A
1	A16S	1254	U
1	A16S	1270	U
1	A16S	1315	A
1	A16S	1316	G
1	A16S	1442	C
1	A16S	1459	U
1	A16S	1466	G
1	A16S	1489	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

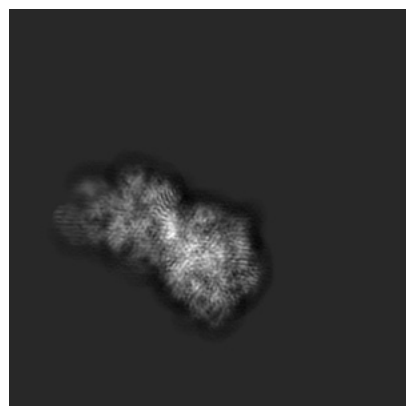
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34862. These allow visual inspection of the internal detail of the map and identification of artifacts.

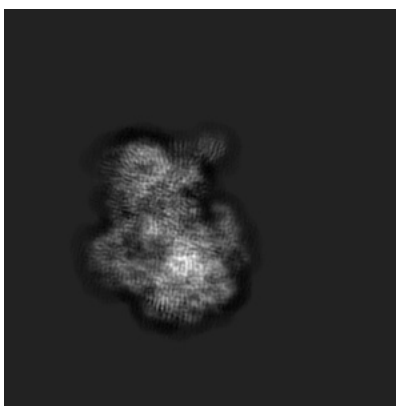
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

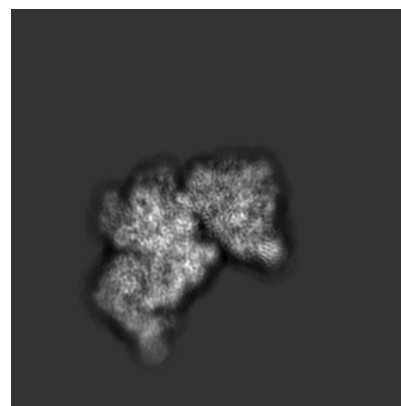
6.1.1 Primary map



X

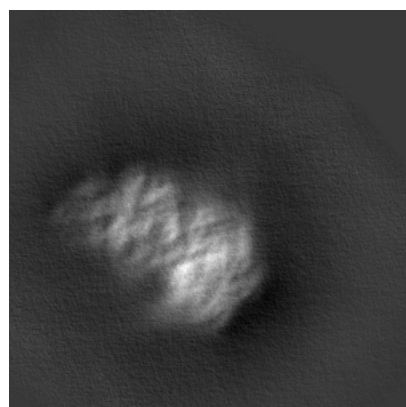


Y

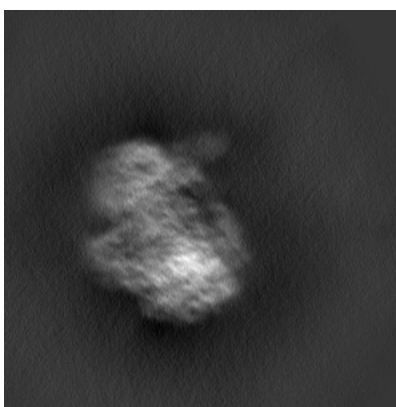


Z

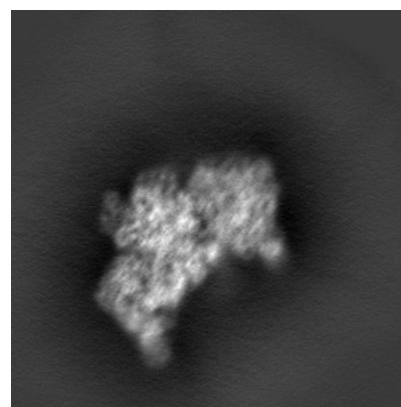
6.1.2 Raw map



X



Y

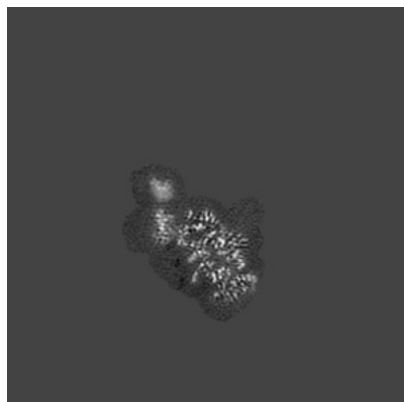


Z

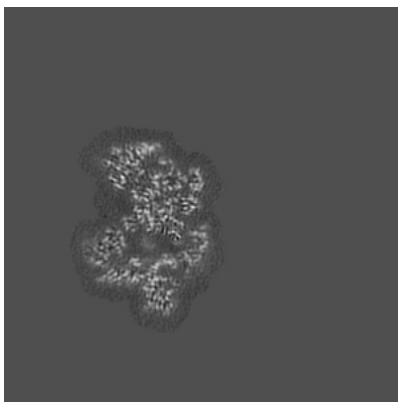
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

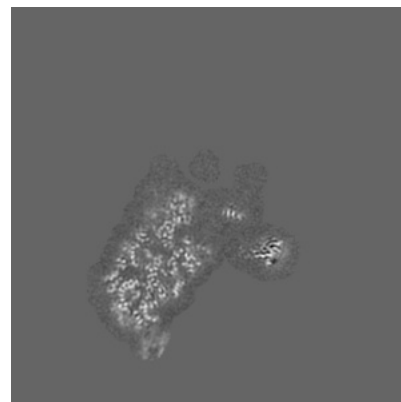
6.2.1 Primary map



X Index: 190

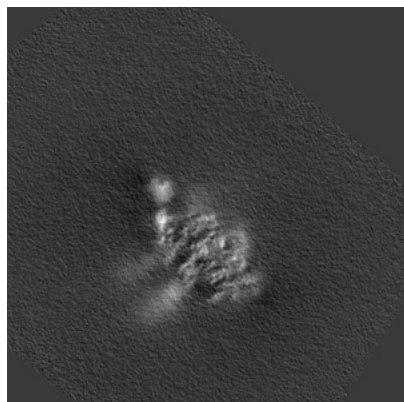


Y Index: 190

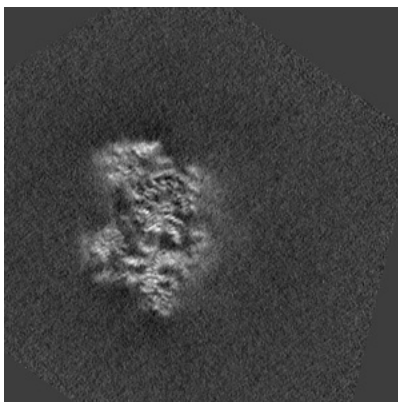


Z Index: 190

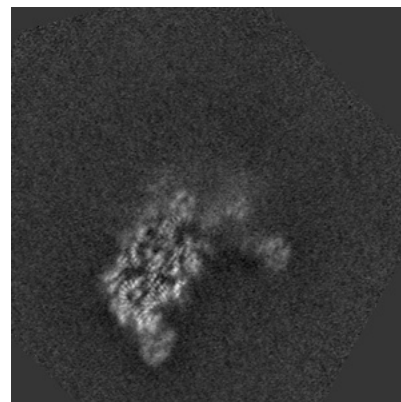
6.2.2 Raw map



X Index: 190



Y Index: 190

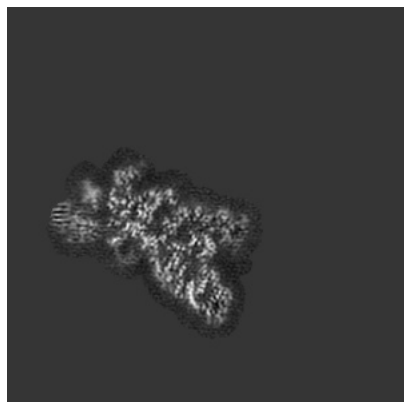


Z Index: 190

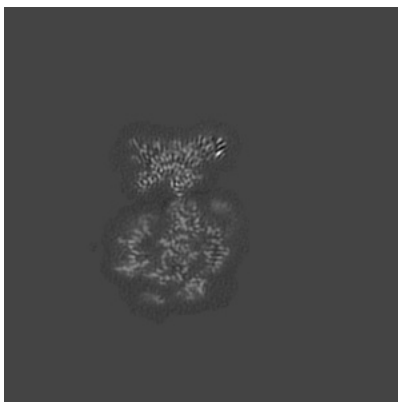
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

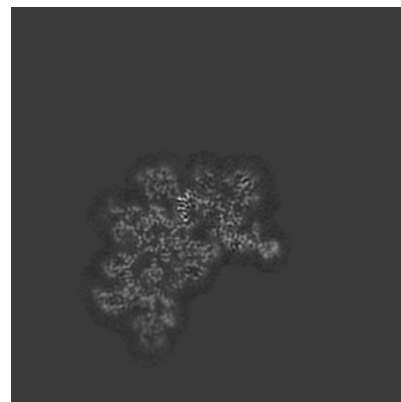
6.3.1 Primary map



X Index: 137

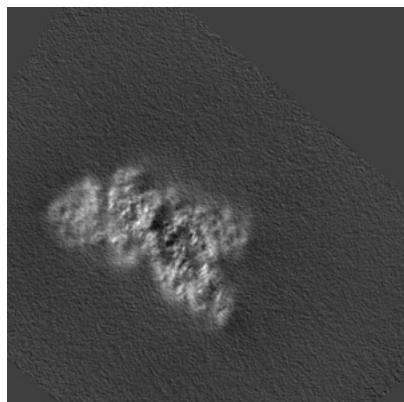


Y Index: 154

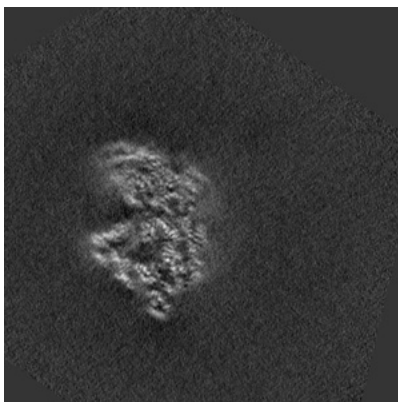


Z Index: 162

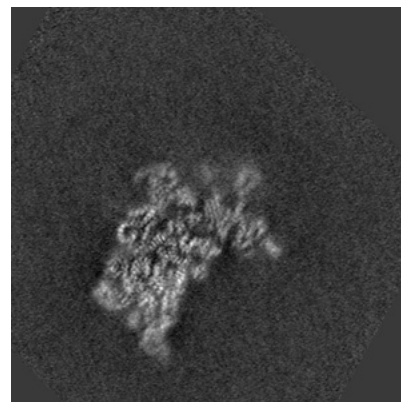
6.3.2 Raw map



X Index: 136



Y Index: 180

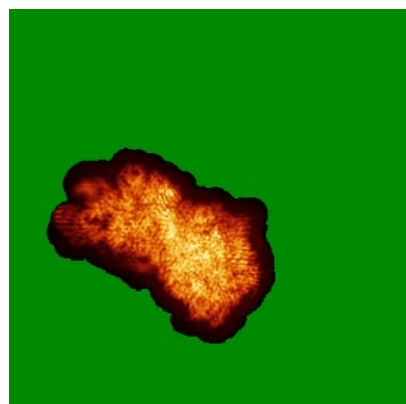


Z Index: 170

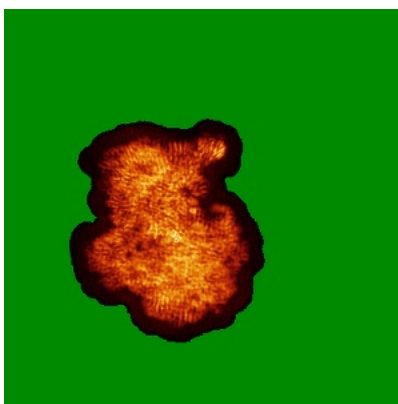
The images above show the largest variance slices of the map in three orthogonal directions.

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

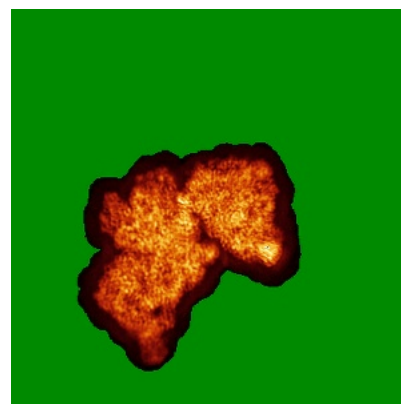
6.4.1 Primary map



X

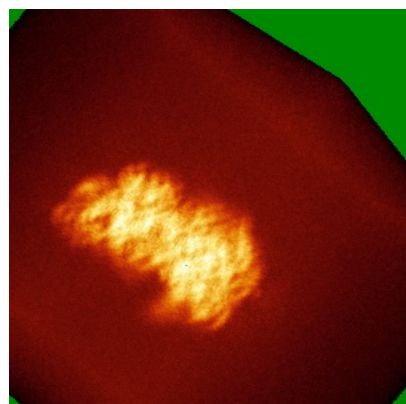


Y

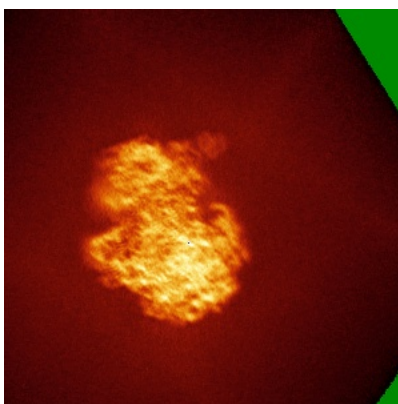


Z

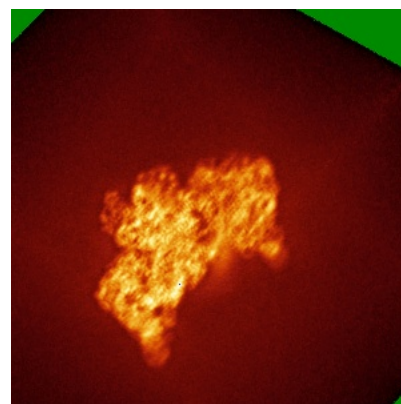
6.4.2 Raw map



X



Y

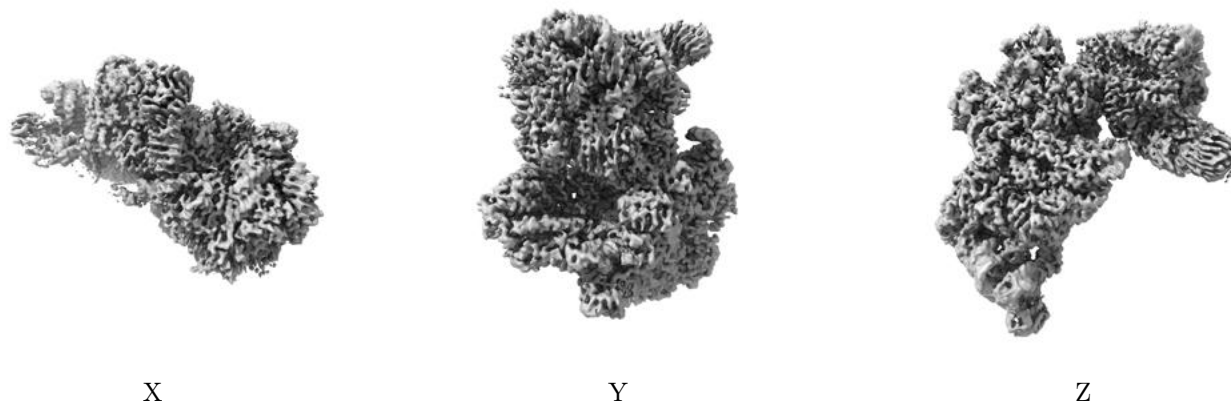


Z

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.

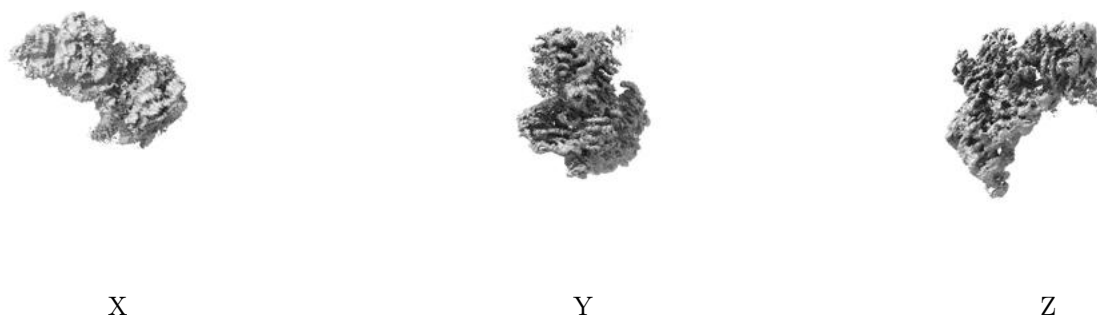
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.46. 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.

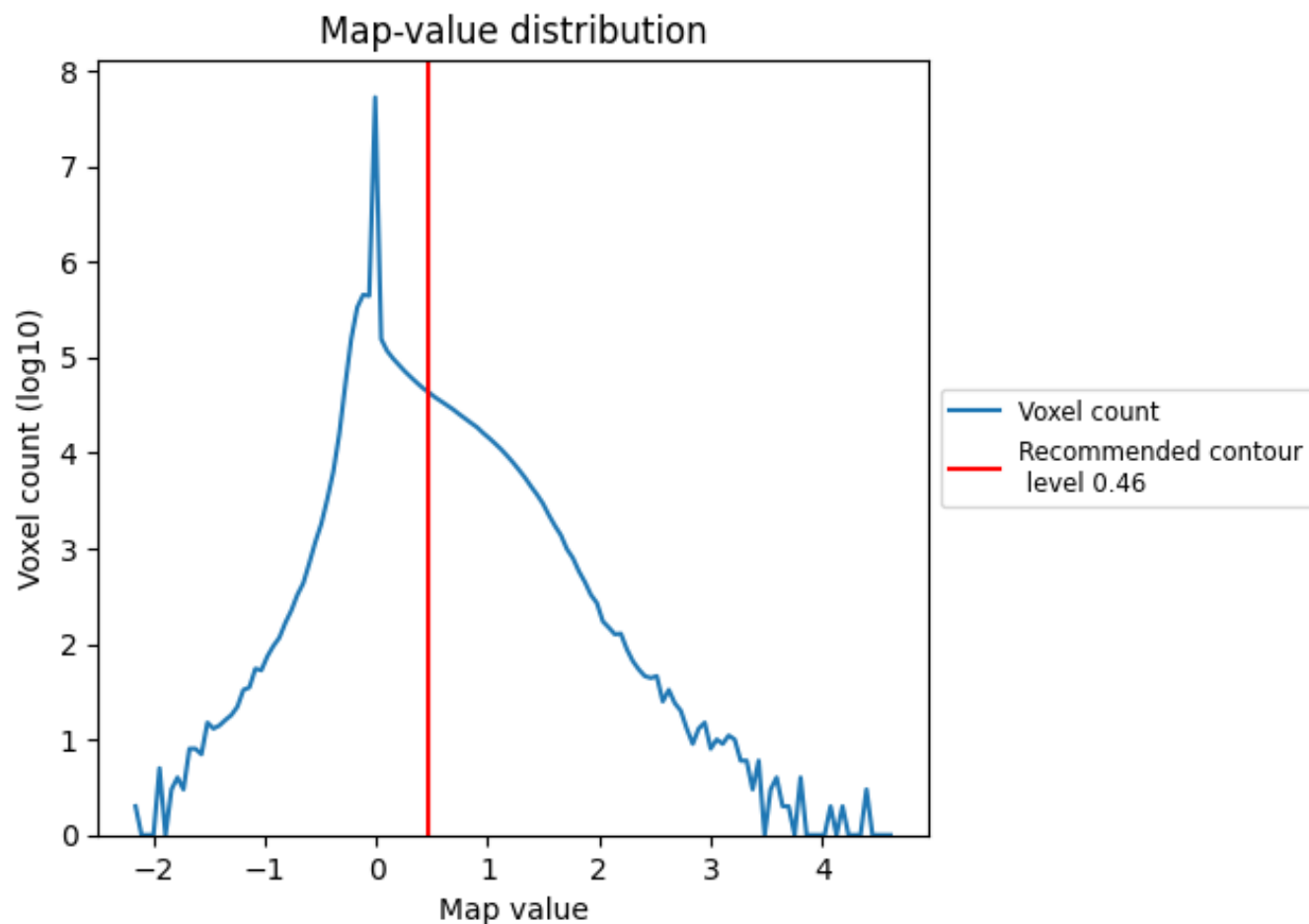
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

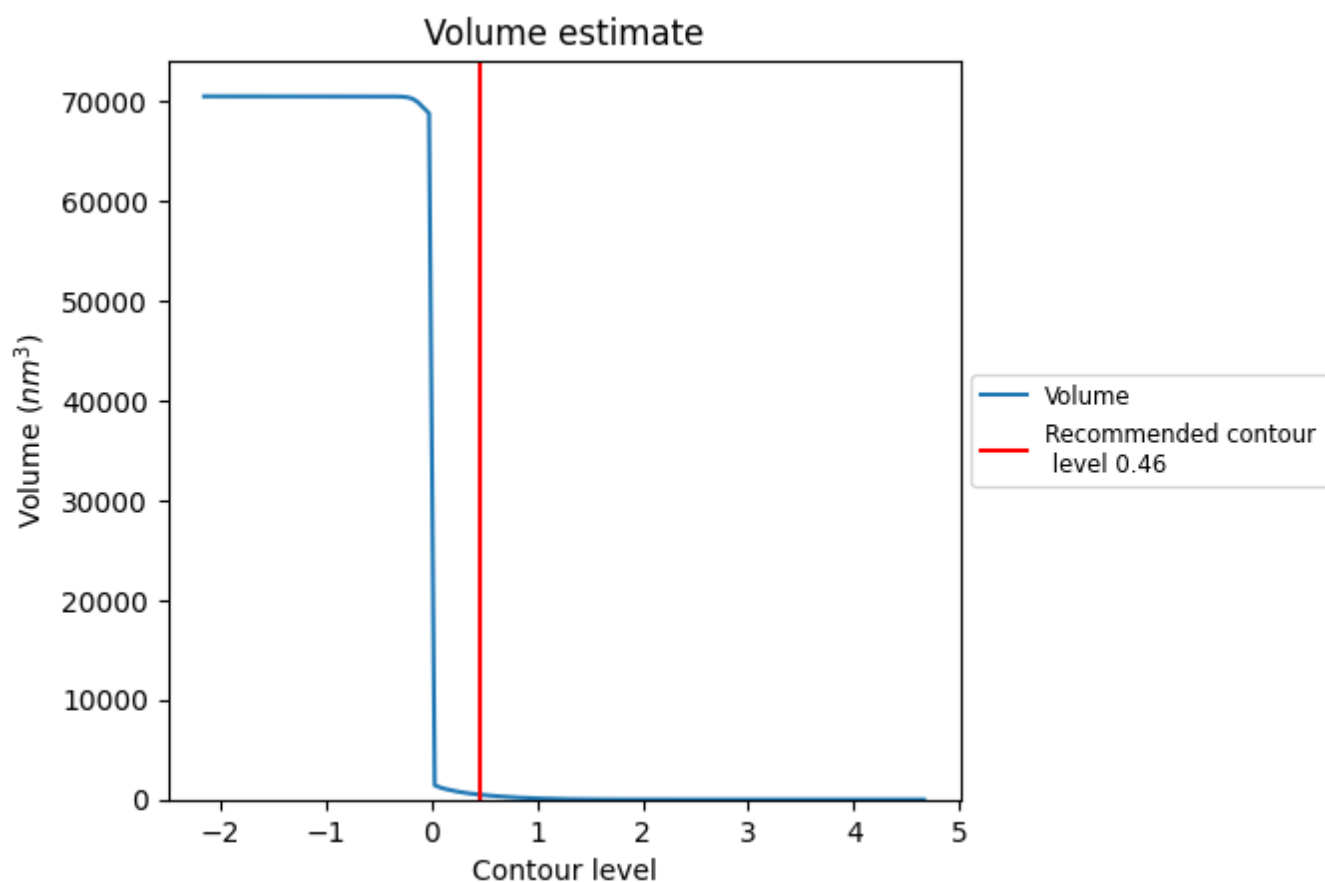
This section contains the results of statistical analysis of the map.

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.

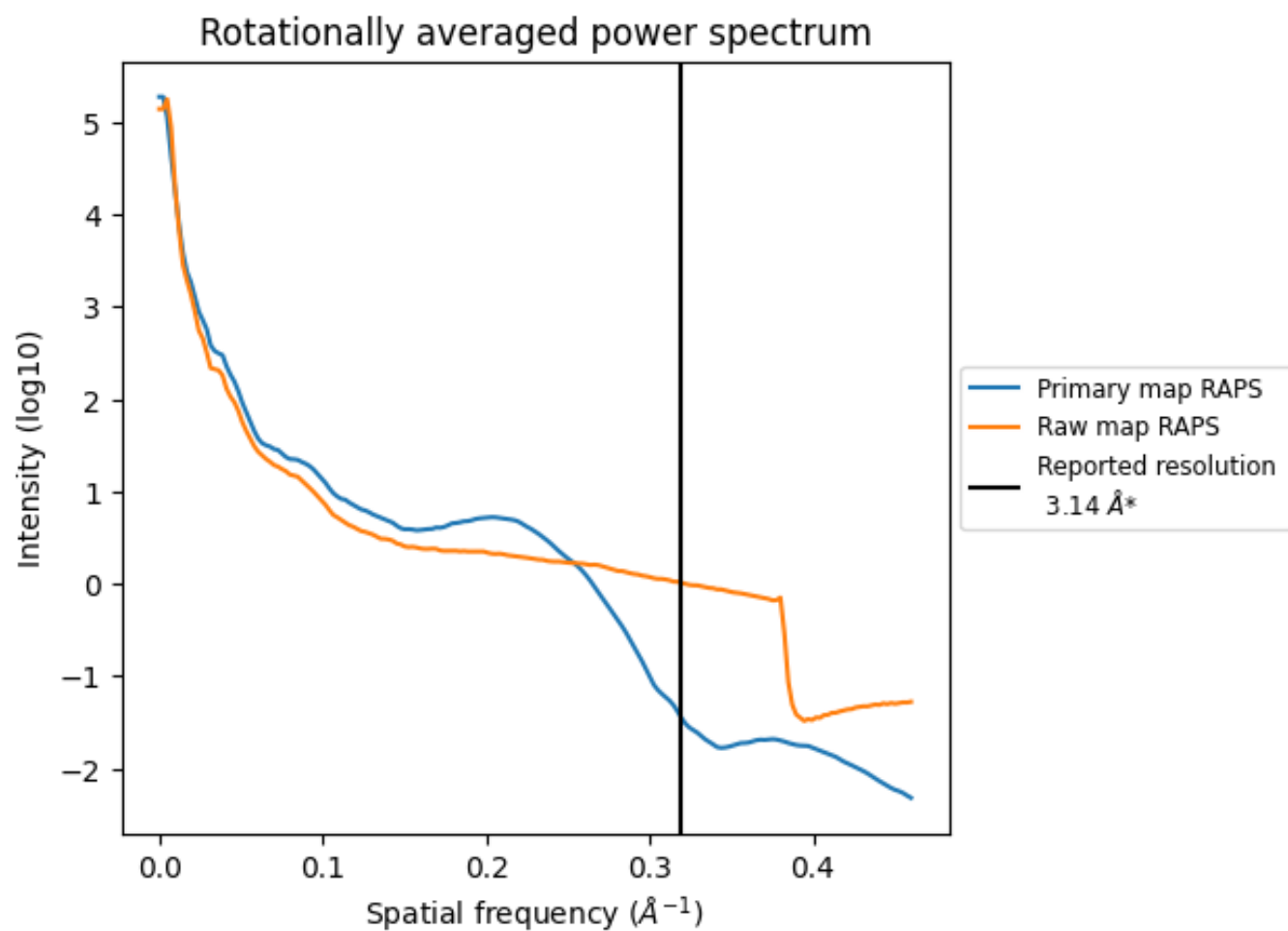
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 487 nm³; this corresponds to an approximate mass of 440 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](#)

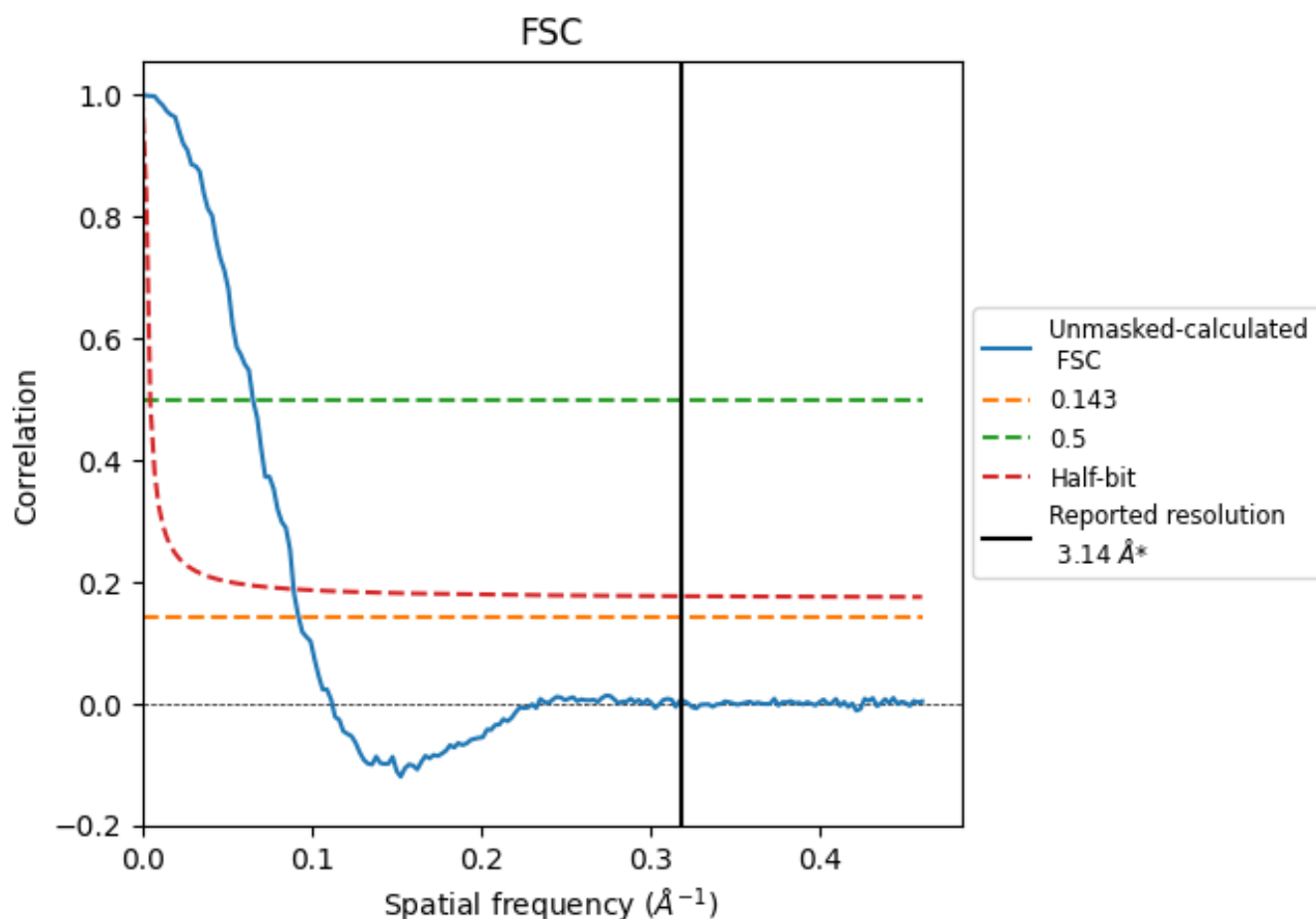


*Reported resolution corresponds to spatial frequency of $0.318 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.318 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

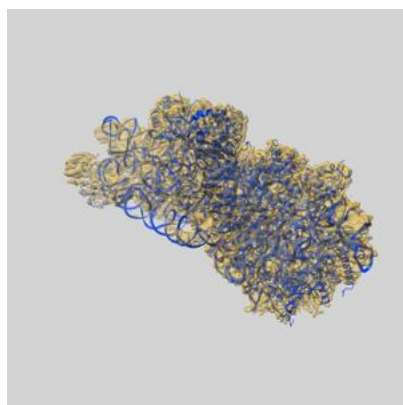
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.14	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	10.86	15.34	11.20

*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 10.86 differs from the reported value 3.14 by more than 10 %

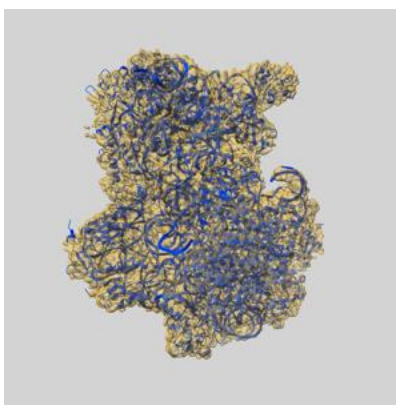
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34862 and PDB model 8HKX. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

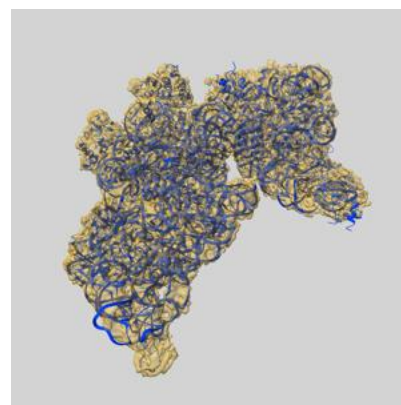
9.1 Map-model overlay [i](#)



X



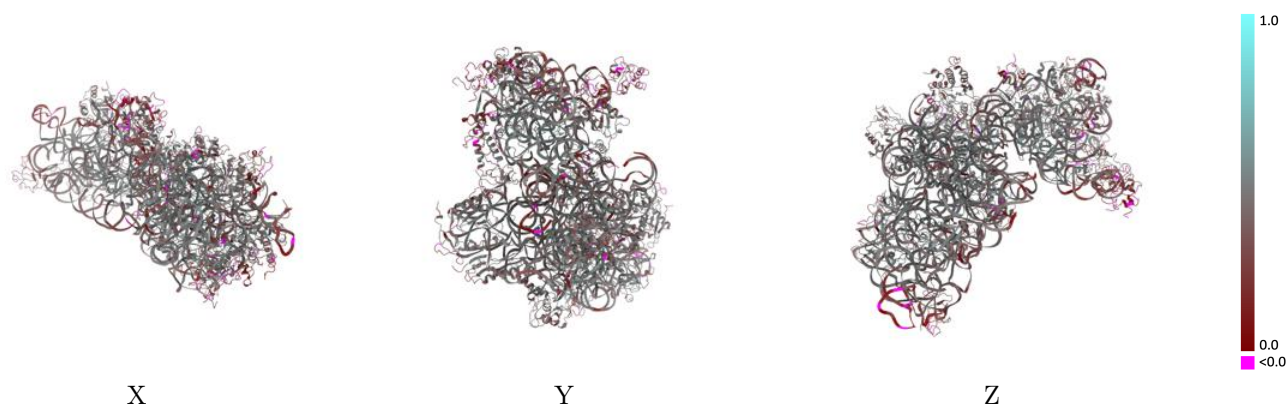
Y



Z

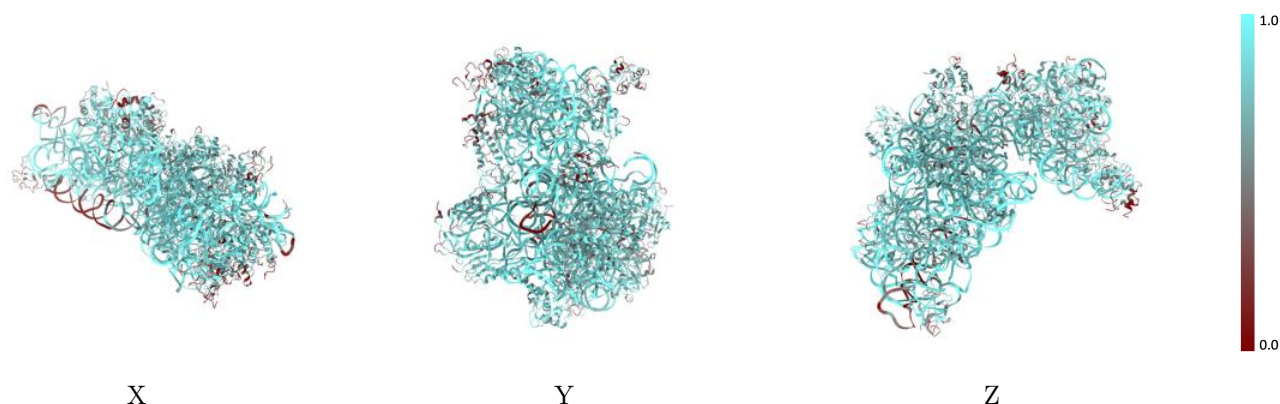
The images above show the 3D surface view of the map at the recommended contour level 0.46 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



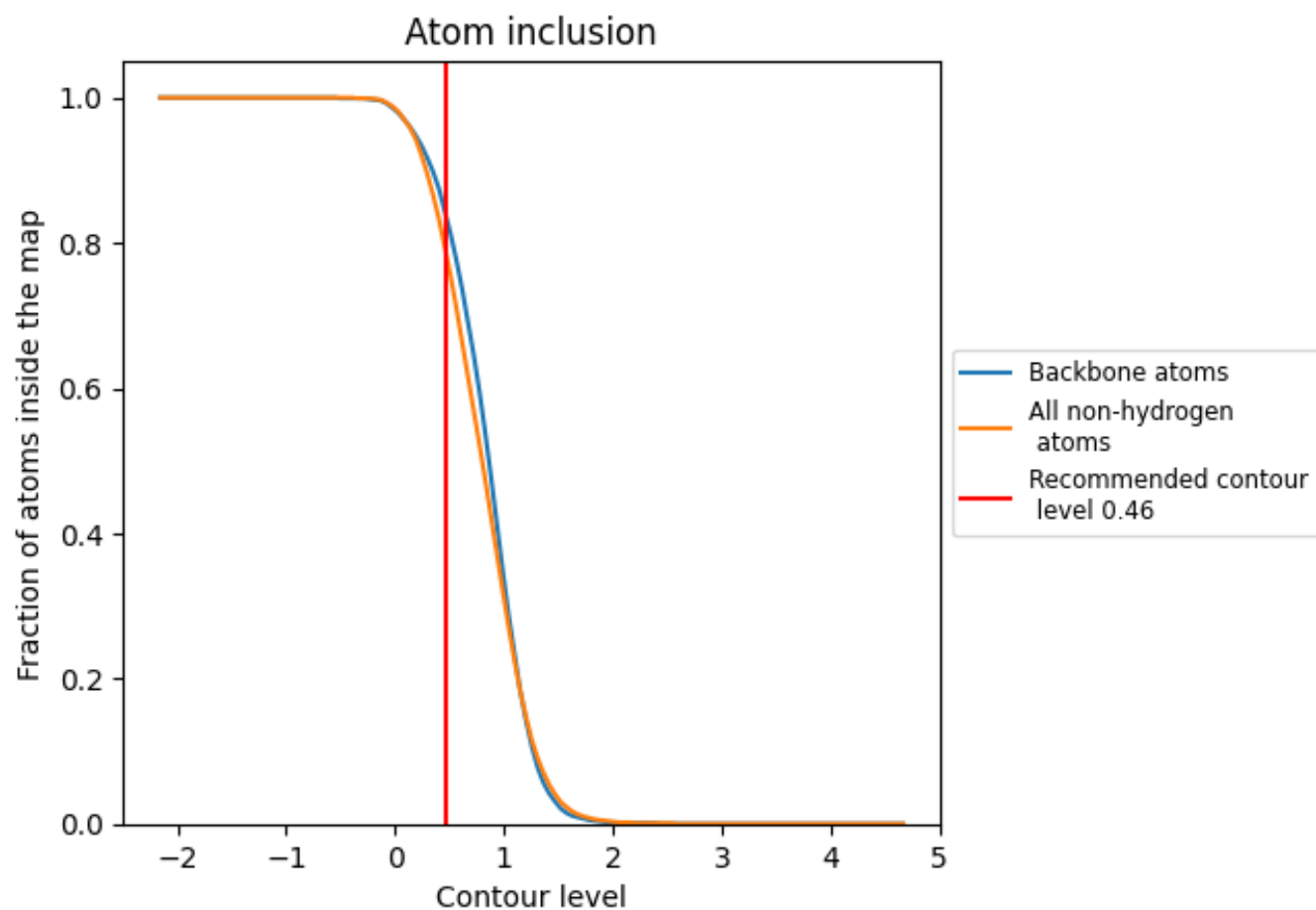
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.46).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 79% 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 (0.46) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7910	 0.4140
A	 0.7800	 0.3860
A16S	 0.8770	 0.4220
AS2P	 0.6660	 0.4120
AS3P	 0.7030	 0.4260
AS4E	 0.7200	 0.4540
AS4P	 0.7270	 0.4330
AS5P	 0.7470	 0.4480
AS6E	 0.4860	 0.3370
AS7P	 0.5830	 0.3240
AS8E	 0.7890	 0.4510
AS8P	 0.7950	 0.4640
AS9P	 0.7280	 0.4530
S10P	 0.6790	 0.3920
S11P	 0.7230	 0.4450
S12P	 0.7670	 0.4670
S13P	 0.5460	 0.3200
S14P	 0.7840	 0.4360
S15P	 0.7630	 0.4270
S17E	 0.4510	 0.3190
S17P	 0.7510	 0.4700
S19E	 0.6380	 0.3480
S19P	 0.7350	 0.4120
S24E	 0.7330	 0.4440
S27A	 0.6130	 0.2630
S27E	 0.7540	 0.4300
S28E	 0.6530	 0.3930
S3AE	 0.7260	 0.4120
SL7A	 0.4690	 0.2030

