



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:03 AM UTC

PDB ID : 6G4S / pdb_00006g4s
EMDB ID : EMD-4348
Title : Cryo-EM structure of a late human pre-40S ribosomal subunit - State B
Authors : Ameismeier, M.; Cheng, J.; Berninghausen, O.; Beckmann, R.
Deposited on : 2018-03-28
Resolution : 4.00 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:

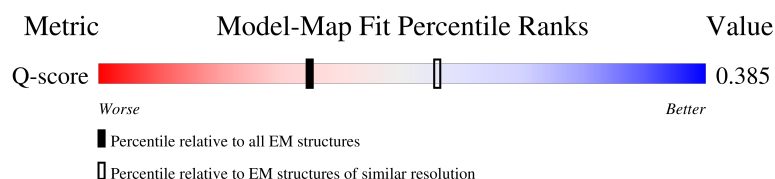
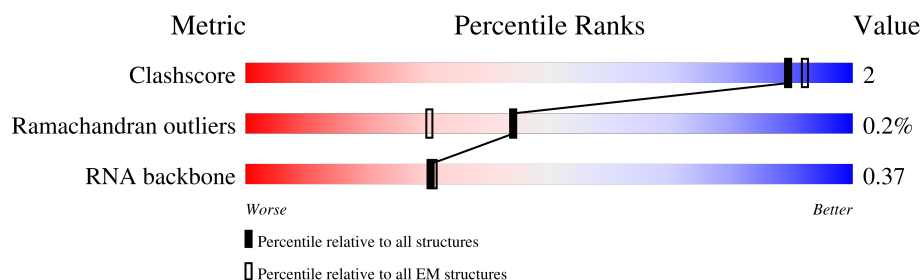
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.00 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.



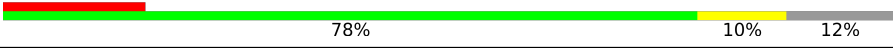
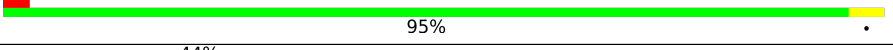
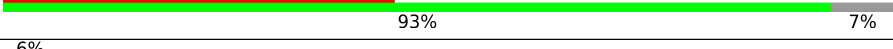
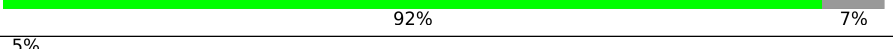
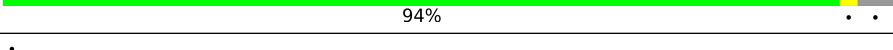
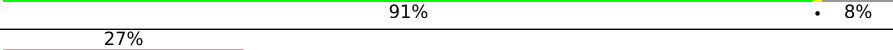
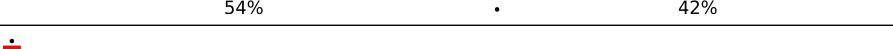
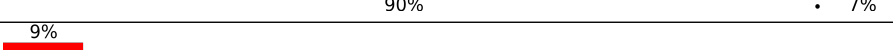
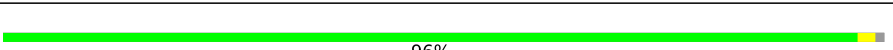
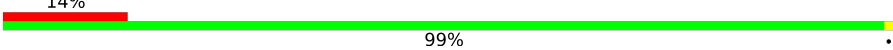
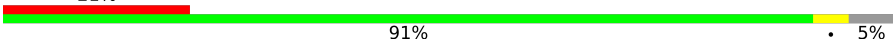
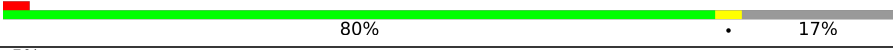
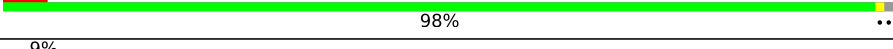
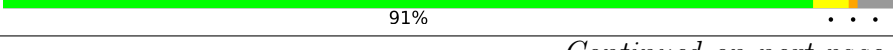
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	2	1882	
2	R	135	
3	A	295	
4	b	84	

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Mol	Chain	Length	Quality of chain
5	B	264	
6	C	293	
7	c	69	
8	E	263	
9	e	59	
10	F	204	
11	H	194	
12	G	249	
13	Z	125	
14	Y	133	
15	y	412	
16	x	252	
17	X	143	
18	w	437	
19	W	130	
20	V	83	
21	u	804	
22	t	475	
23	T	145	
24	S	152	
25	Q	146	
26	P	145	
27	O	151	
28	N	151	
29	L	158	

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Mol	Chain	Length	Quality of chain
30	J	194	91% 7%
31	I	208	91% 7%
32	s	800	38% 94%
33	k	39	31% 92% 8%

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 48967 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 pre-18S ribosomal RNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	1613	Total	C	O	P	0	0
			19353	8065	9676	1612		

- Molecule 2 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	R	120	Total	C	N	O	0	0
			595	355	120	120		

- Molecule 3 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	A	216	Total	C	N	O	0	0
			1068	636	216	216		

- Molecule 4 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	b	82	Total	C	N	O	0	0
			405	241	82	82		

- Molecule 5 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	B	213	Total	C	N	O	0	0
			1054	628	213	213		

- Molecule 6 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	C	218	Total	C	N	O	0	0
			1072	636	218	218		

- Molecule 7 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	c	61	Total	C	N	O	0	0
			300	178	61	61		

- Molecule 8 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	E	262	Total	C	N	O	0	0
			1287	763	262	262		

- Molecule 9 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	e	55	Total	C	N	O	0	0
			270	160	55	55		

- Molecule 10 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	F	189	Total	C	N	O	0	0
			935	557	189	189		

- Molecule 11 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	H	186	Total	C	N	O	0	0
			920	548	186	186		

- Molecule 12 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	G	230	Total	C	N	O	0	0
			1135	675	230	230		

- Molecule 13 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	Z	72	Total	C	N	O	0	0
			358	214	72	72		

- Molecule 14 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	Y	124	Total	C	N	O	0	0
			610	362	124	124		

- Molecule 15 is a protein called RNA-binding protein NOB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	y	317	Total	C	N	O	0	0
			1566	932	317	317		

- Molecule 16 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	x	175	Total	C	N	O	0	0
			865	515	175	175		

- Molecule 17 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	X	141	Total	C	N	O	0	0
			690	408	141	141		

- Molecule 18 is a protein called Bystin.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	w	248	Total	C	N	O	0	0
			1232	736	248	248		

- Molecule 19 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	W	129	Total	C	N	O	0	0
			634	376	129	129		

- Molecule 20 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	V	82	Total	C	N	O	0	0
			403	239	82	82		

- Molecule 21 is a protein called Pre-rRNA-processing protein TSR1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	u	628	Total	C	N	O	0	0
			3106	1850	628	628		

- Molecule 22 is a protein called Protein LTV1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	t	71	Total	C	N	O	0	0
			355	213	71	71		

- Molecule 23 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	T	144	Total	C	N	O	0	0
			705	417	144	144		

- Molecule 24 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	S	143	Total	C	N	O	0	0
			704	418	143	143		

- Molecule 25 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Q	139	Total	C	N	O	0	0
			683	405	139	139		

- Molecule 26 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	P	120	Total	C	N	O	0	0
			590	350	120	120		

- Molecule 27 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	O	135	Total	C	N	O	0	0
			659	389	135	135		

- Molecule 28 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	N	149	Total	C	N	O	0	0
			737	439	149	149		

- Molecule 29 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	L	151	Total	C	N	O	0	0
			744	442	151	151		

- Molecule 30 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	J	180	Total	C	N	O	0	0
			888	528	180	180		

- Molecule 31 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	I	205	Total	C	N	O	0	0
			1009	599	205	205		

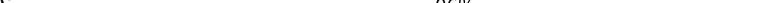
- Molecule 32 is a protein called RRP12.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	s	768	Total	C	N	O	0	0
			3840	2304	768	768		

- Molecule 33 is a protein called Unknown.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	k	39	Total	C	N	O	0	0
			195	117	39	39		

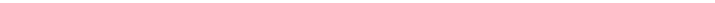
Sequence logo for the 12th position. The y-axis represents information content in bits, ranging from 0 to 0.4. The x-axis shows amino acids. The most conserved amino acid is Aspartic acid (D), with a value of approximately 0.35 bits. Other significant amino acids include Asparagine (N) at ~0.15 bits, Glutamine (Q) at ~0.1 bits, and Glutamic acid (E) at ~0.08 bits. The background is a light gray bar with a red diamond above the 'D' and 'N' positions.

- Chain b:  96%

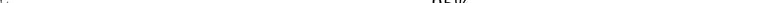
- Chain B: 79% 1% 20%

- Chain C:  72% 26%

[illegible]

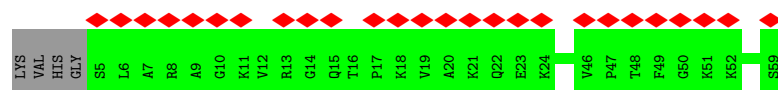
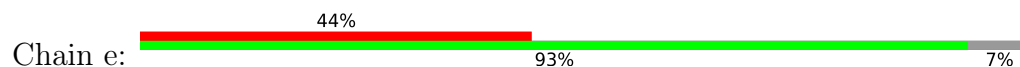
- Chain c: 

NET
ASP
THR
SER
ARG
VAL
GLN
P8
K16
V17
L18
G19
G22
Q29
V32
M35
D36
D37
T38
S39
R40
S41
S61
E62
R66
R67
L68
ARG

- Chain E:  95%



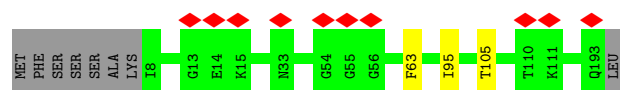
- Molecule 9: 40S ribosomal protein S30



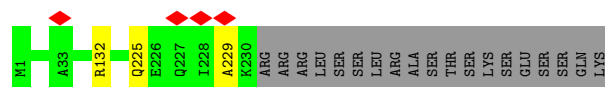
- Molecule 10: 40S ribosomal protein S5



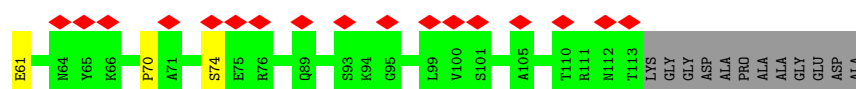
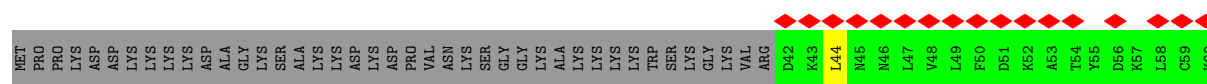
- Molecule 11: 40S ribosomal protein S7



- Molecule 12: 40S ribosomal protein S6

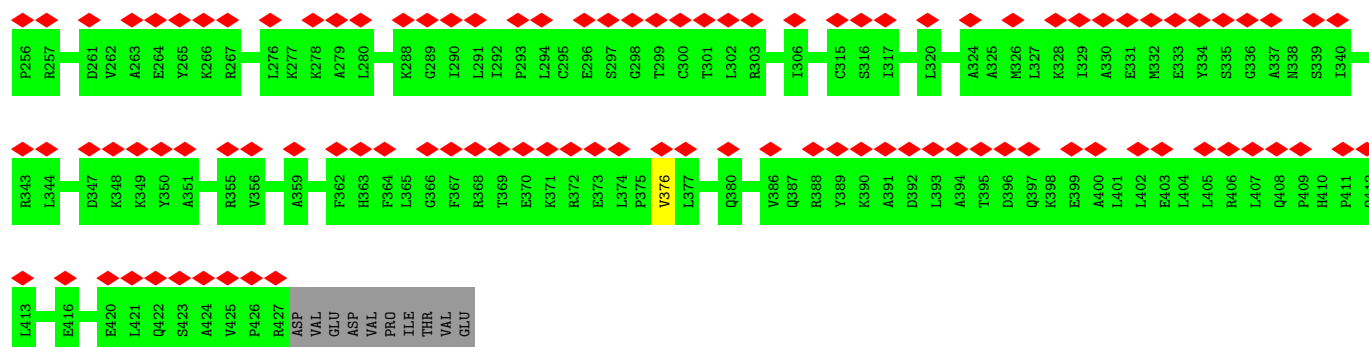


- Molecule 13: 40S ribosomal protein S25



- Molecule 14: 40S ribosomal protein S24





- Molecule 19: 40S ribosomal protein S15a

Chain W: 98% ..



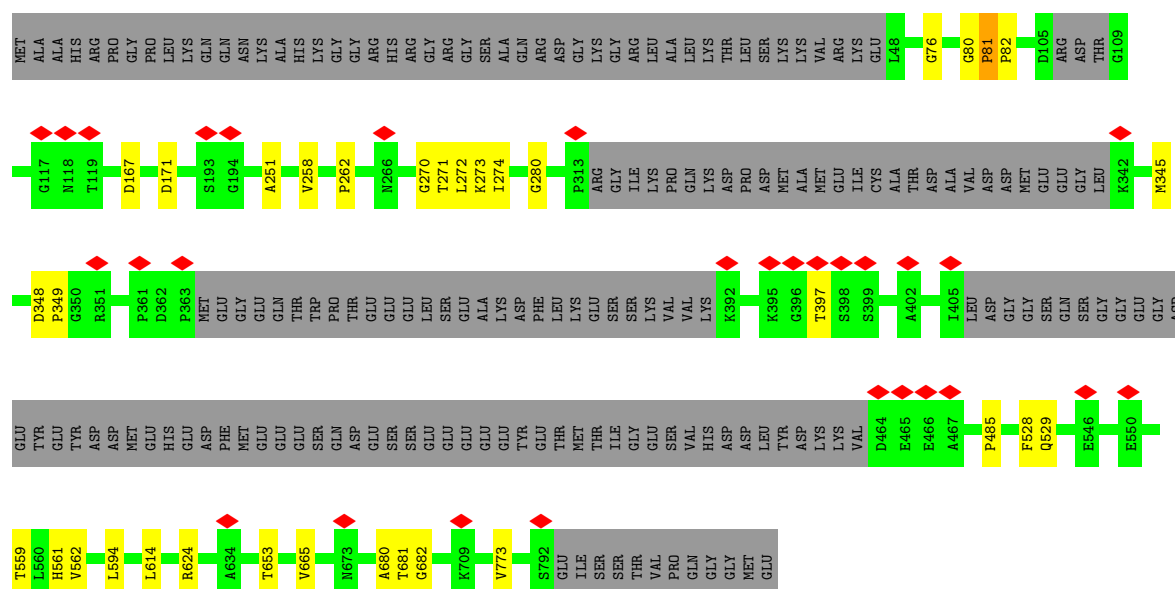
- Molecule 20: 40S ribosomal protein S21

Chain V: 96% ..



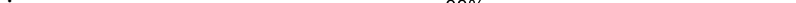
- Molecule 21: Pre-rRNA-processing protein TSR1 homolog

Chain u: 74% 22%

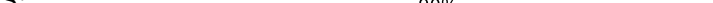


- Molecule 22: Protein LTV1 homolog

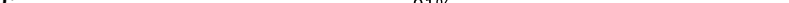
Chain t: 14% 85%

- Chain T:  14% 99%

Category	Number of Genes
MET	10
P2	15
G3	15
V4	15
T5	15
K24	25
S25	25
G26	25
K27	25
L28	25
K29	25
G68	35
G69	35
A70	35
G86	10
G109	25
D118	25
G127	25
G136	25
A139	45
A140	45
A141	45
N142	45
K143	45
K144	45
H145	45

- Chain S:  24% 90% 6%

[illegible]

- Chain Q:  21% 91% 5%

[illegible]



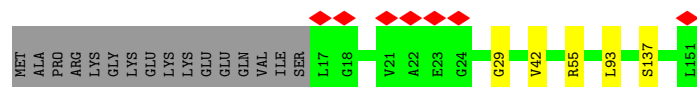
- Molecule 26: 40S ribosomal protein S15

Chain P: 80% 17%



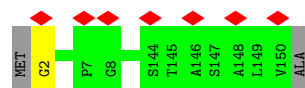
- Molecule 27: 40S ribosomal protein S14

Chain O: 5% 86% 11%



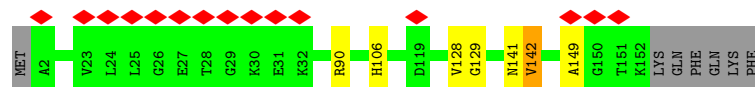
- Molecule 28: 40S ribosomal protein S13

Chain N: 5% 98% ..



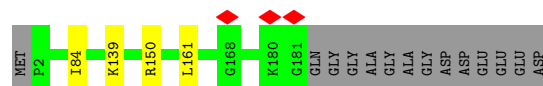
- Molecule 29: 40S ribosomal protein S11

Chain L: 9% 91% ..



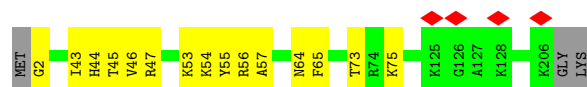
- Molecule 30: 40S ribosomal protein S9

Chain J: 91% 7%

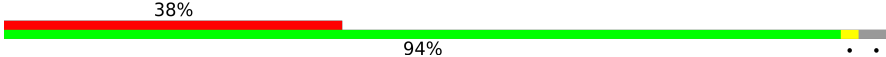


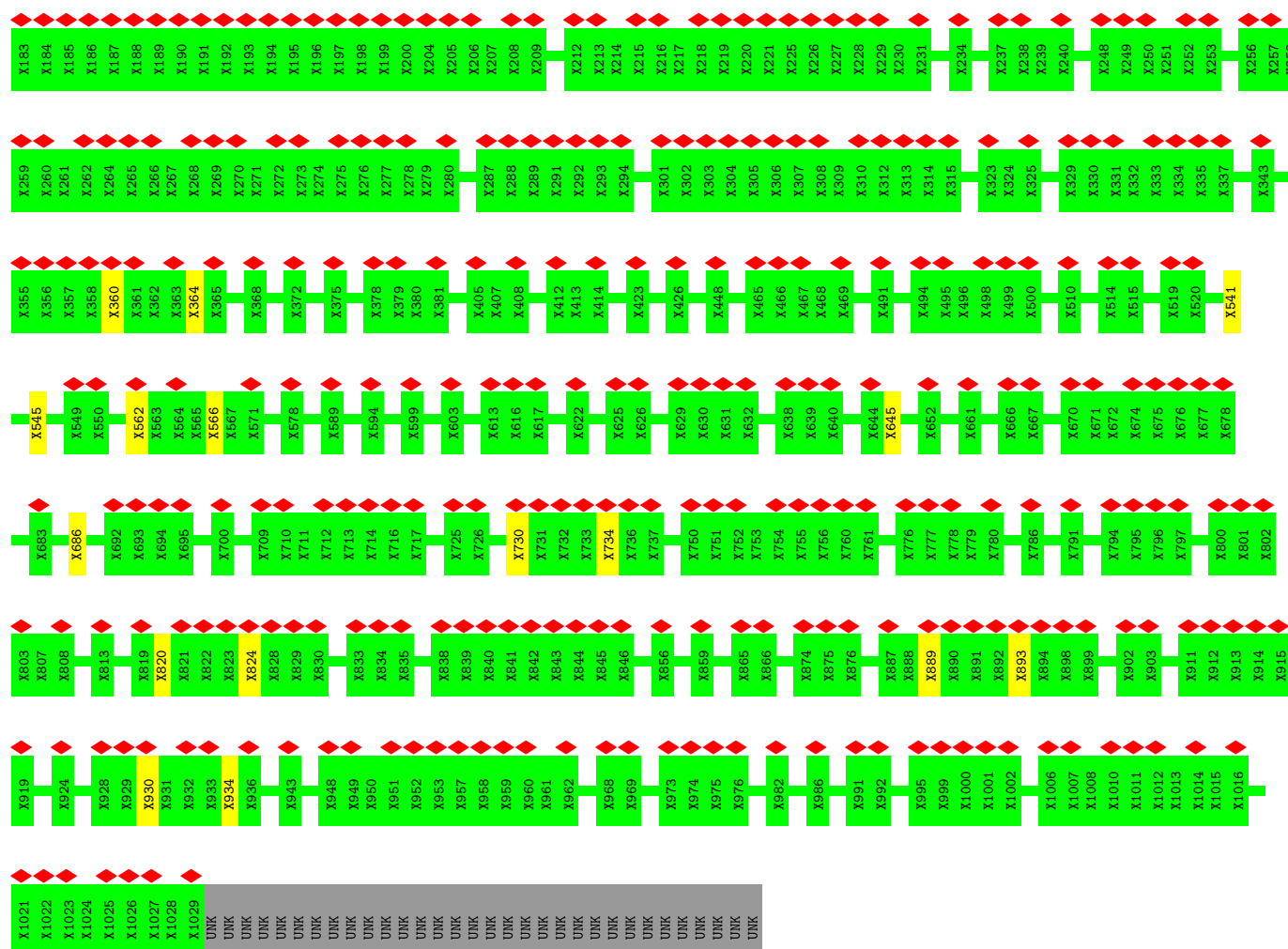
- Molecule 31: 40S ribosomal protein S8

Chain I: 91% 7%

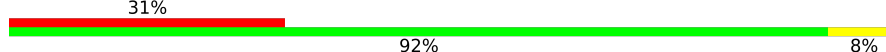


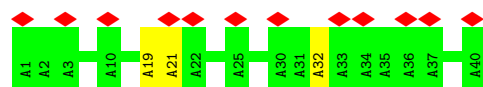
- Molecule 32: RRP12

Chain s:  38% 94%



• Molecule 33: Unknown

Chain k:  31% 92% 8%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73661	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 ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.203	Depositor
Minimum map value	-0.075	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	2	0.34	0/20941	0.69	3/32156 (0.0%)
2	R	0.31	0/592	0.90	1/821 (0.1%)
3	A	0.42	0/1067	0.75	0/1485
4	b	0.39	0/404	0.77	0/561
5	B	0.35	0/1053	0.78	2/1466 (0.1%)
6	C	0.39	0/1071	0.78	0/1487
7	c	0.33	0/299	1.00	4/414 (1.0%)
8	E	0.41	0/1286	0.81	0/1785
9	e	0.33	0/269	0.81	0/372
10	F	0.26	0/934	0.69	2/1300 (0.2%)
11	H	0.30	0/919	0.66	0/1279
12	G	0.32	0/1134	0.68	0/1577
13	Z	0.31	0/357	0.84	2/497 (0.4%)
14	Y	0.36	0/609	0.78	1/845 (0.1%)
15	y	0.37	0/1563	0.78	0/2172
16	x	0.36	0/864	0.80	0/1202
17	X	0.42	0/689	0.96	0/954
18	w	0.28	0/1231	0.77	0/1717
19	W	0.49	0/633	0.85	0/878
20	V	0.49	1/402 (0.2%)	0.61	0/557
21	u	0.35	0/3101	0.77	2/4313 (0.0%)
22	t	0.31	0/353	0.82	0/491
23	T	0.29	0/704	0.67	0/975
24	S	0.28	0/703	0.70	0/976
25	Q	0.30	0/682	0.78	2/946 (0.2%)
26	P	0.34	0/589	0.60	0/817
27	O	0.35	0/658	0.75	1/910 (0.1%)
28	N	0.32	0/736	0.59	0/1024
29	L	0.40	0/743	0.76	0/1032
30	J	0.36	0/887	0.77	0/1233
31	I	0.33	0/1008	0.73	0/1400
33	k	1.07	0/193	1.57	0/267
All	All	0.36	1/46674 (0.0%)	0.74	20/67909 (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
2	R	0	2
4	b	0	1
8	E	0	2
14	Y	0	1
15	y	0	3
17	X	0	1
21	u	0	4
24	S	0	1
26	P	0	1
30	J	0	1
All	All	0	17

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	V	33	GLN	CA-CB	-5.39	1.44	1.53

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	c	16	LYS	CA-C-N	6.10	132.95	121.97
7	c	16	LYS	C-N-CA	6.10	132.95	121.97
25	Q	16	LYS	CA-C-N	5.97	130.68	121.19
25	Q	16	LYS	C-N-CA	5.97	130.68	121.19
2	R	67	ARG	N-CA-C	-5.79	107.45	114.75

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	E	228	ILE	Mainchain,Peptide
2	R	26	ASN	Peptide
2	R	73	LEU	Peptide
14	Y	118	ARG	Peptide
4	b	52	THR	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	19353	0	9704	40	0
2	R	595	0	249	3	0
3	A	1068	0	503	3	0
4	b	405	0	172	0	0
5	B	1054	0	455	2	0
6	C	1072	0	489	4	0
7	c	300	0	131	4	0
8	E	1287	0	577	6	0
9	e	270	0	126	0	0
10	F	935	0	442	0	0
11	H	920	0	399	2	0
12	G	1135	0	512	3	0
13	Z	358	0	161	2	0
14	Y	610	0	271	2	0
15	y	1566	0	693	2	0
16	x	865	0	394	3	0
17	X	690	0	330	5	0
18	w	1232	0	562	2	0
19	W	634	0	283	2	0
20	V	403	0	199	1	0
21	u	3106	0	1357	16	0
22	t	355	0	151	3	0
23	T	705	0	343	1	0
24	S	704	0	317	4	0
25	Q	683	0	320	3	0
26	P	590	0	251	2	0
27	O	659	0	321	2	0
28	N	737	0	330	1	0
29	L	744	0	321	5	0
30	J	888	0	389	1	0
31	I	1009	0	451	8	0
32	s	3840	0	848	8	0
33	k	195	0	196	8	0
All	All	48967	0	22247	128	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 2.

The worst 5 of 128 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)
33:k:19:ALA:HB2	33:k:21:ALA:CB	1.26	1.57
33:k:19:ALA:CB	33:k:21:ALA:HB2	1.35	1.55
33:k:19:ALA:CB	33:k:21:ALA:CB	1.91	1.41
8:E:131:VAL:HA	8:E:136:ILE:O	1.28	1.26
19:W:101:PHE:O	19:W:128:PHE:HA	1.49	1.09

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	R	114/135 (84%)	98 (86%)	16 (14%)	0	100	100
3	A	214/295 (72%)	197 (92%)	17 (8%)	0	100	100
4	b	80/84 (95%)	72 (90%)	8 (10%)	0	100	100
5	B	211/264 (80%)	196 (93%)	15 (7%)	0	100	100
6	C	216/293 (74%)	203 (94%)	13 (6%)	0	100	100
7	c	59/69 (86%)	53 (90%)	6 (10%)	0	100	100
8	E	260/263 (99%)	235 (90%)	24 (9%)	1 (0%)	30	65
9	e	53/59 (90%)	41 (77%)	12 (23%)	0	100	100
10	F	187/204 (92%)	173 (92%)	14 (8%)	0	100	100
11	H	184/194 (95%)	172 (94%)	12 (6%)	0	100	100
12	G	228/249 (92%)	210 (92%)	18 (8%)	0	100	100
13	Z	70/125 (56%)	63 (90%)	7 (10%)	0	100	100
14	Y	122/133 (92%)	111 (91%)	11 (9%)	0	100	100
15	y	311/412 (76%)	271 (87%)	40 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	x	173/252 (69%)	165 (95%)	8 (5%)	0	100	100
17	X	139/143 (97%)	129 (93%)	8 (6%)	2 (1%)	9	39
18	w	246/437 (56%)	226 (92%)	20 (8%)	0	100	100
19	W	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
20	V	80/83 (96%)	73 (91%)	7 (9%)	0	100	100
21	u	618/804 (77%)	550 (89%)	64 (10%)	4 (1%)	21	57
22	t	67/475 (14%)	58 (87%)	6 (9%)	3 (4%)	2	20
23	T	142/145 (98%)	136 (96%)	6 (4%)	0	100	100
24	S	141/152 (93%)	131 (93%)	10 (7%)	0	100	100
25	Q	137/146 (94%)	119 (87%)	18 (13%)	0	100	100
26	P	118/145 (81%)	111 (94%)	7 (6%)	0	100	100
27	O	133/151 (88%)	120 (90%)	13 (10%)	0	100	100
28	N	147/151 (97%)	138 (94%)	9 (6%)	0	100	100
29	L	149/158 (94%)	138 (93%)	10 (7%)	1 (1%)	18	54
30	J	178/194 (92%)	163 (92%)	14 (8%)	1 (1%)	21	57
31	I	203/208 (98%)	184 (91%)	19 (9%)	0	100	100
33	k	35/39 (90%)	35 (100%)	0	0	100	100
All	All	5142/6592 (78%)	4688 (91%)	442 (9%)	12 (0%)	44	75

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	u	81	PRO
22	t	353	ILE
30	J	161	LEU
21	u	82	PRO
21	u	485	PRO

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1592/1882 (84%)	506 (31%)	0

5 of 506 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	4	C
1	2	5	U
1	2	8	U

There are no RNA pucker outliers to report.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	s	39
1	2	8
33	k	1

The worst 5 of 48 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	s	915:UNK	C	919:UNK	N	17.96
1	s	688:UNK	C	692:UNK	N	17.29
1	s	358:UNK	C	360:UNK	N	16.52
1	s	803:UNK	C	807:UNK	N	16.48
1	s	381:UNK	C	383:UNK	N	15.07

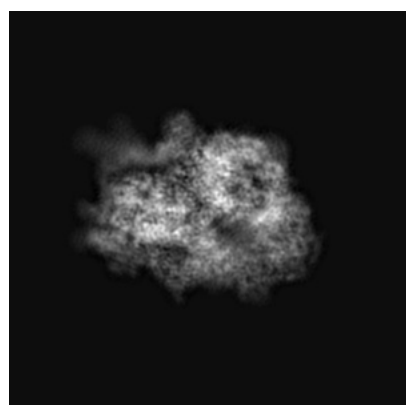
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4348. These allow visual inspection of the internal detail of the map and identification of artifacts.

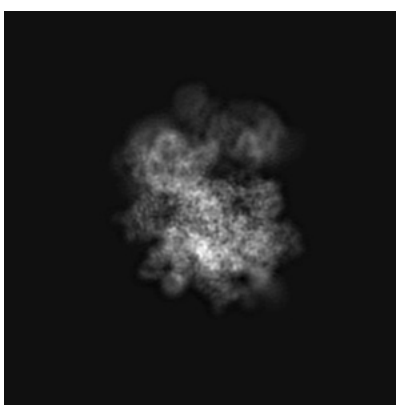
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

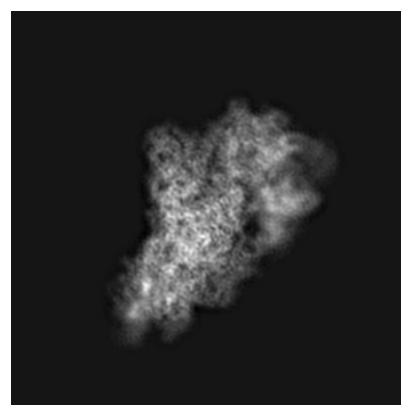
6.1.1 Primary map



X



Y

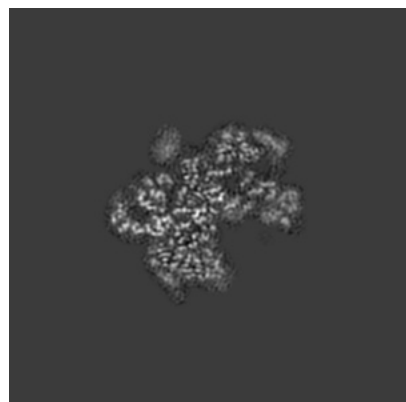


Z

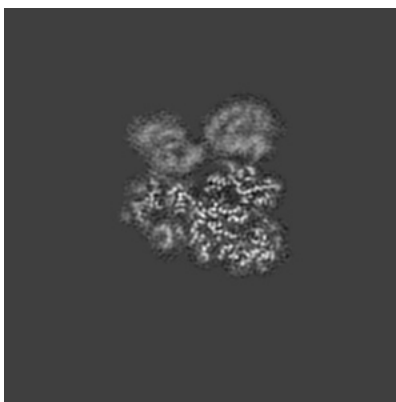
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

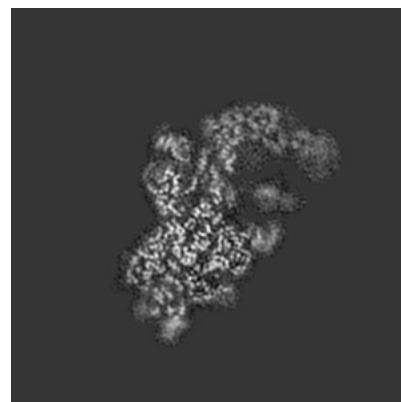
6.2.1 Primary map



X Index: 180



Y Index: 180

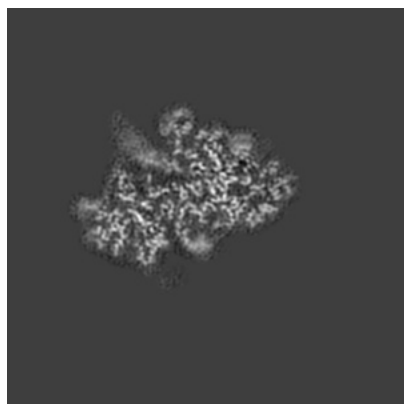


Z Index: 180

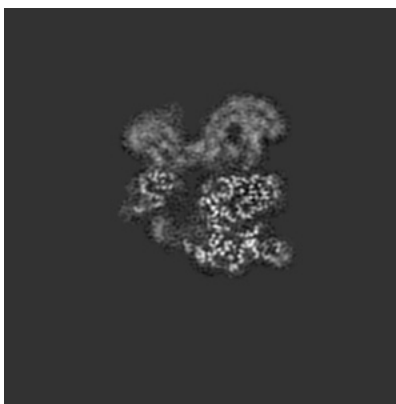
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

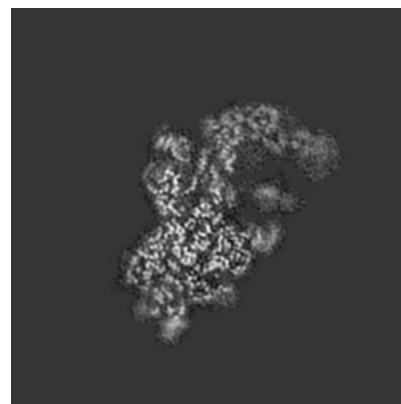
6.3.1 Primary map



X Index: 146



Y Index: 189

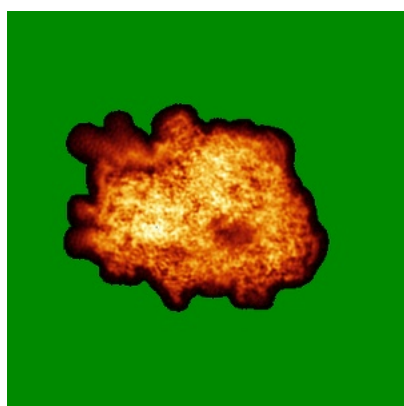


Z Index: 180

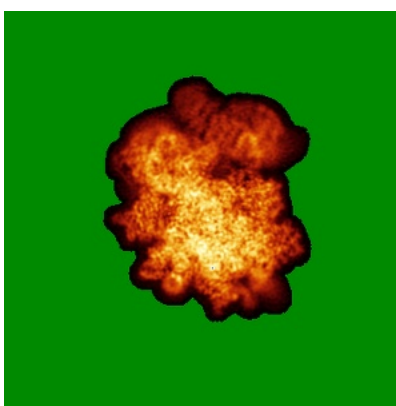
The images above show the largest variance slices of the map in three orthogonal directions.

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

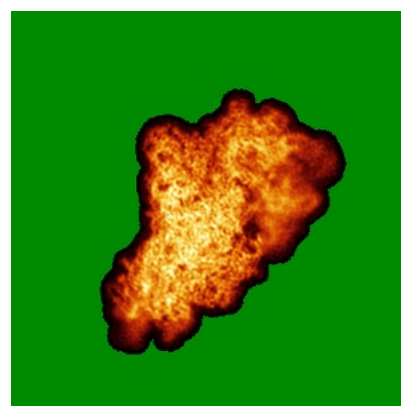
6.4.1 Primary map



X



Y

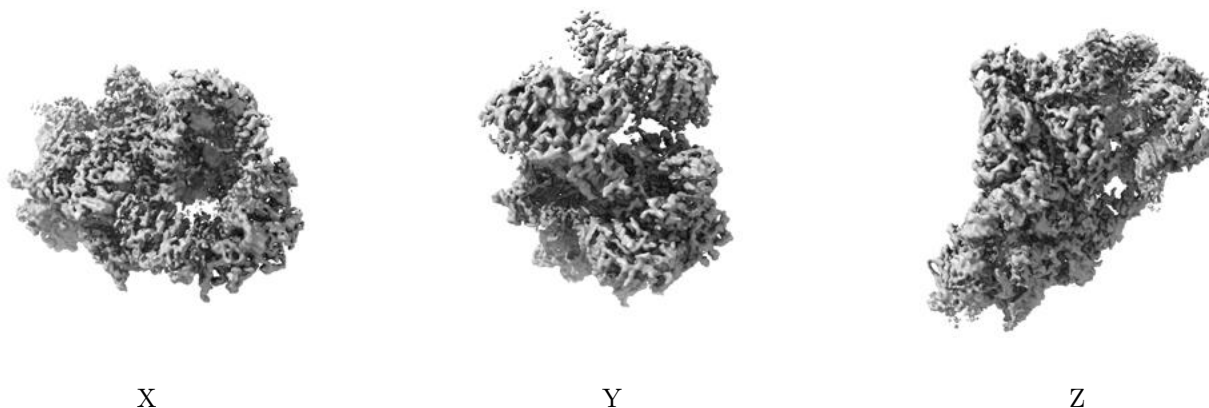


Z

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

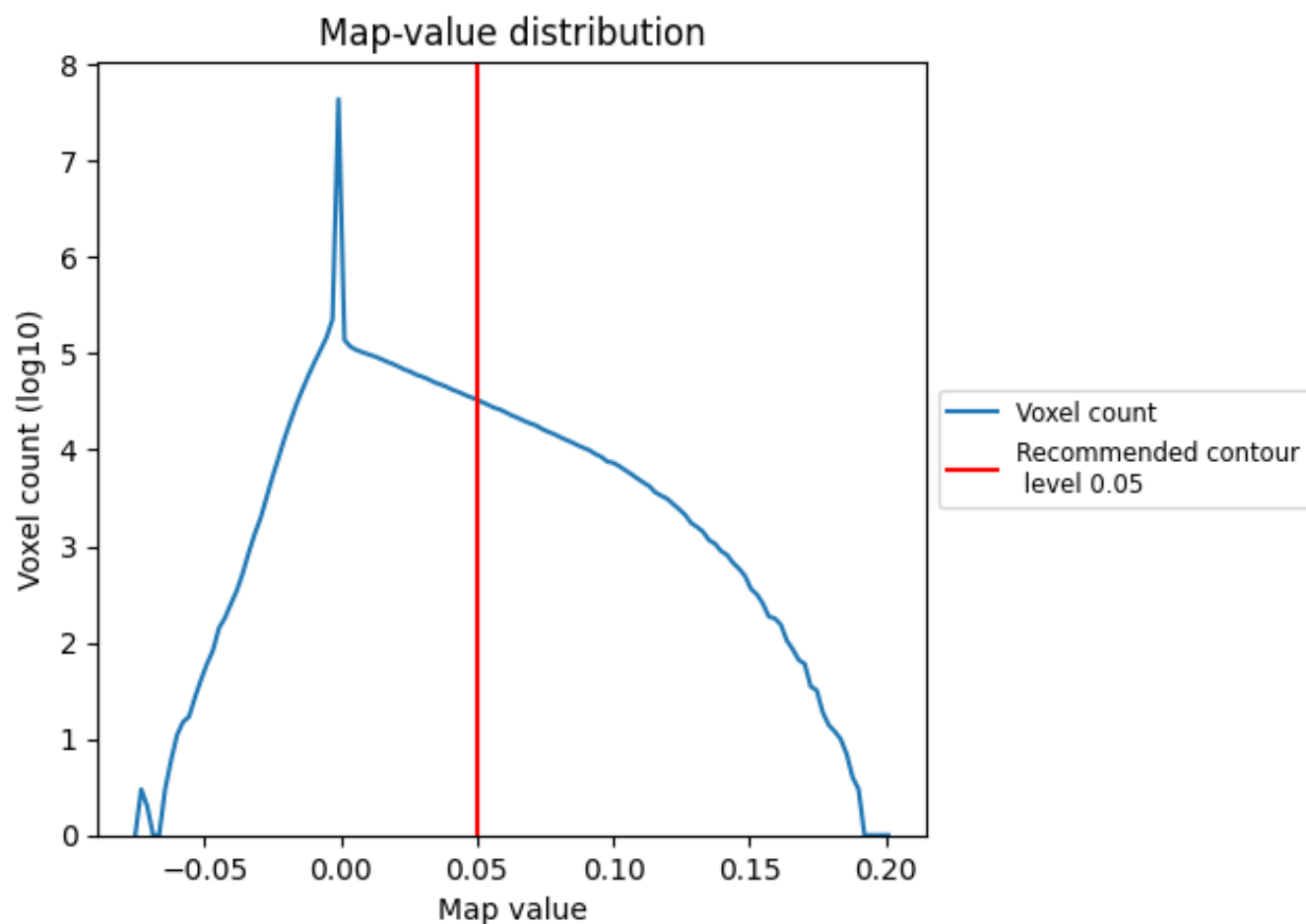
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

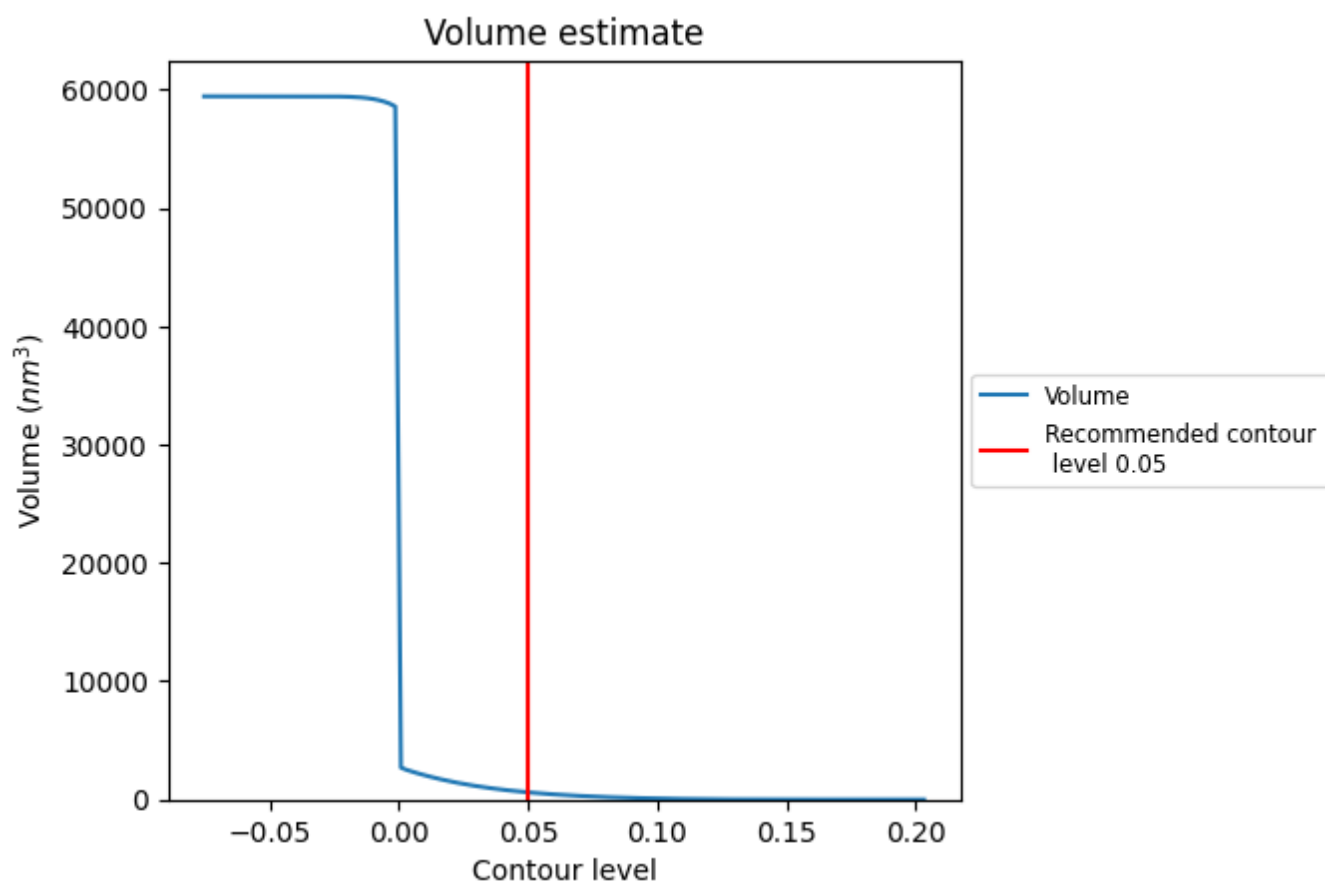
This section contains the results of statistical analysis of the map.

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.

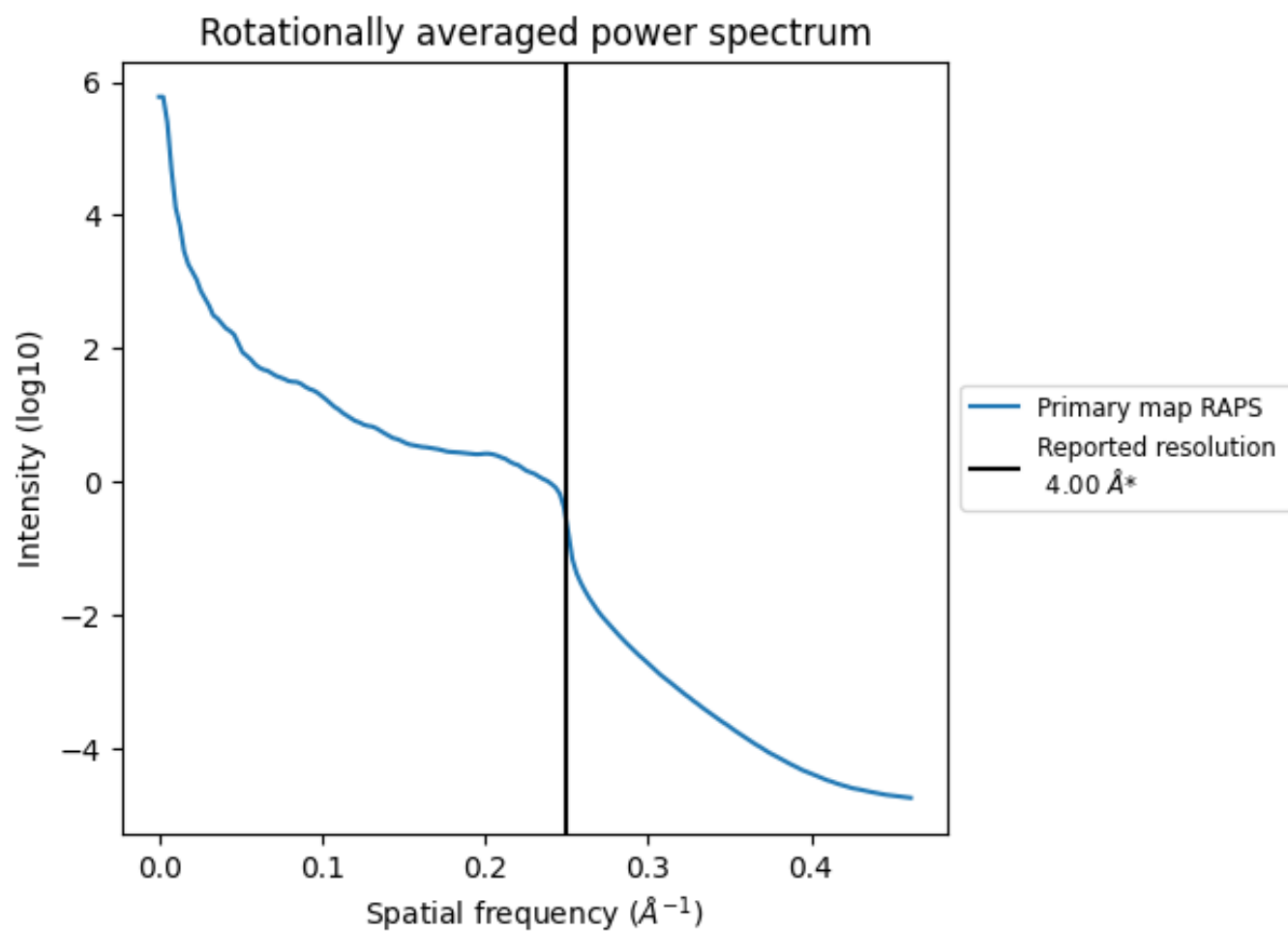
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 611 nm³; this corresponds to an approximate mass of 552 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 ⓘ

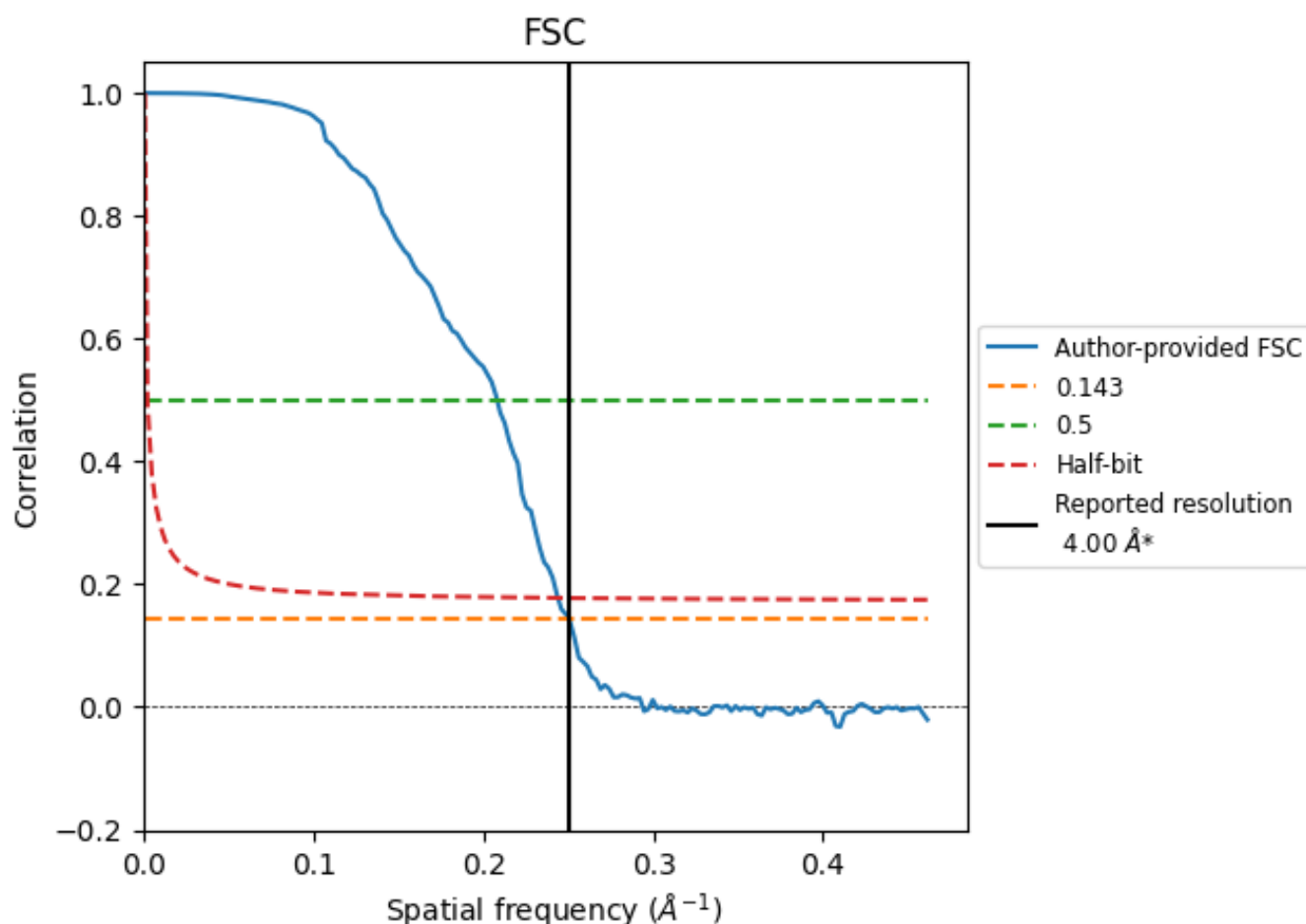


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

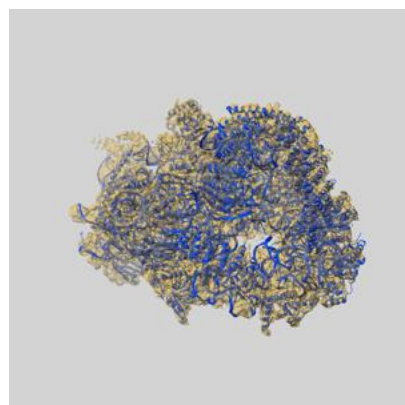
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.00	4.80	4.10
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

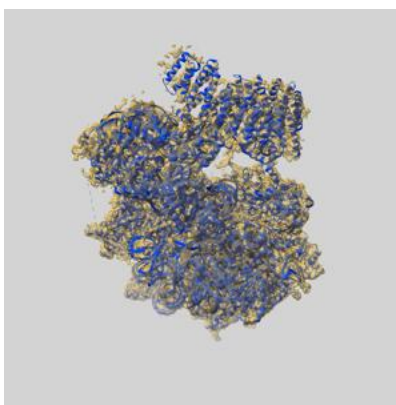
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4348 and PDB model 6G4S. Per-residue inclusion information can be found in section [3](#) on page [10](#).

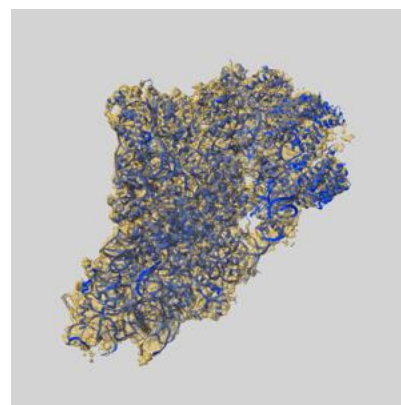
9.1 Map-model overlay [i](#)



X



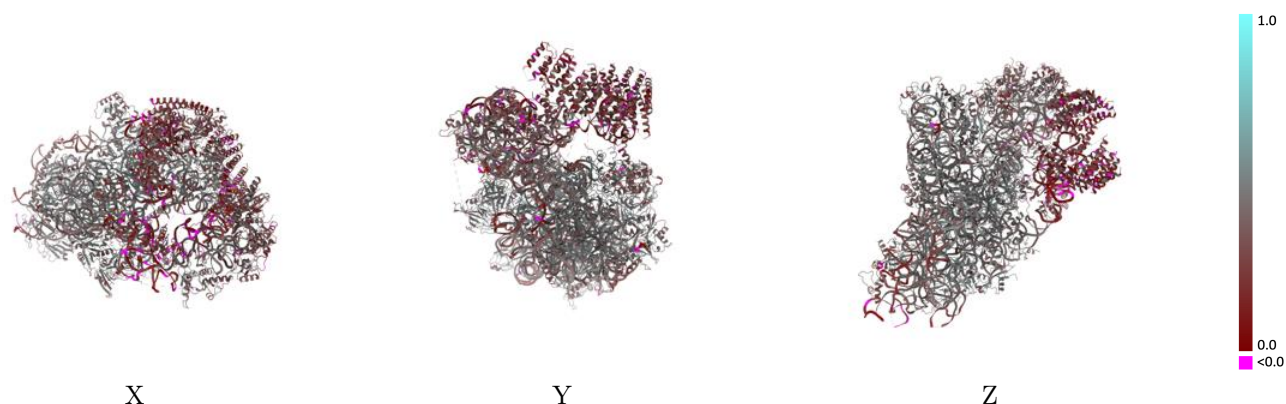
Y



Z

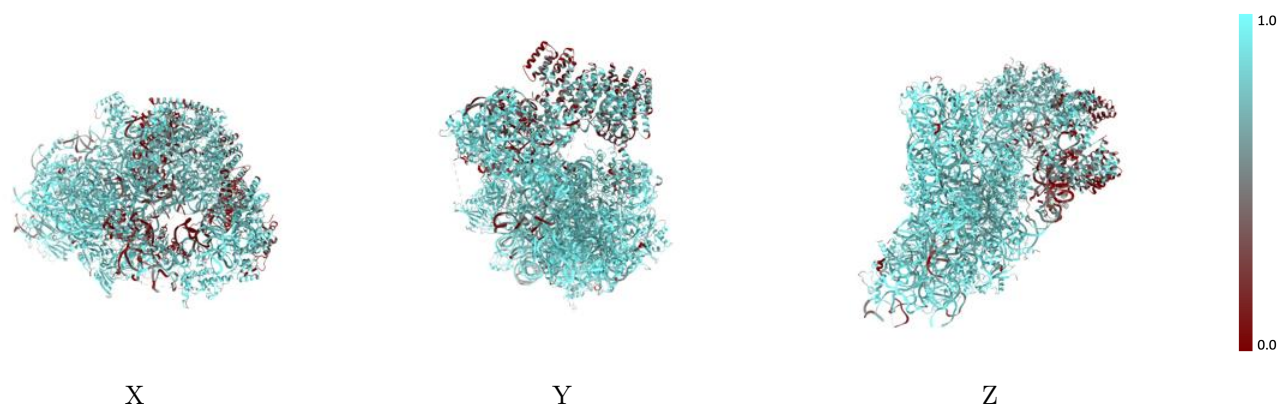
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



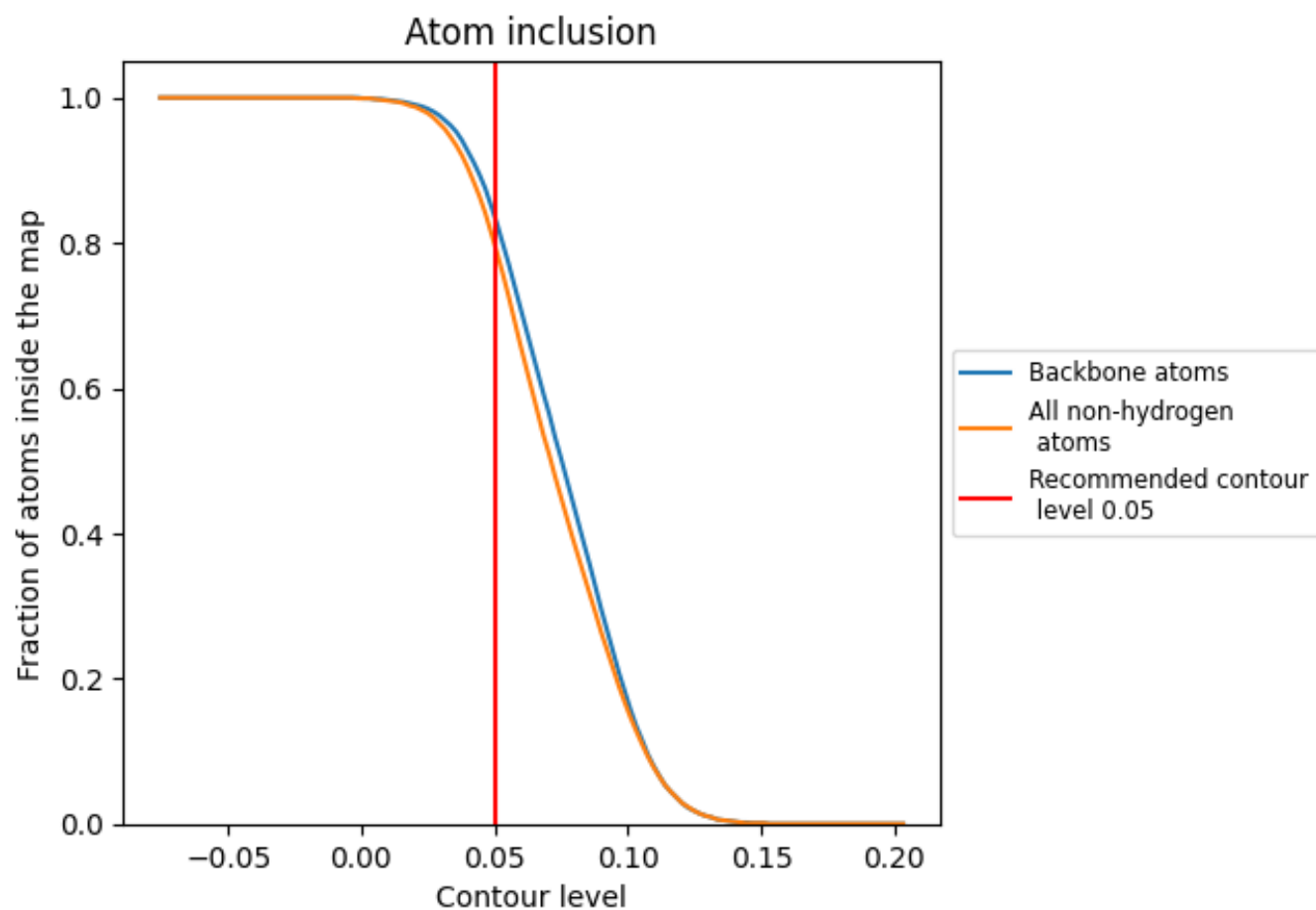
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 84% of all backbone atoms, 80% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7980	 0.3850
2	 0.8170	 0.3770
A	 0.8760	 0.4510
B	 0.9030	 0.4470
C	 0.8740	 0.4710
E	 0.8870	 0.4670
F	 0.8160	 0.3810
G	 0.9120	 0.4200
H	 0.8850	 0.4230
I	 0.9160	 0.4230
J	 0.9040	 0.4460
L	 0.8330	 0.4630
N	 0.8970	 0.4280
O	 0.8360	 0.4360
P	 0.8850	 0.4160
Q	 0.6840	 0.3290
R	 0.6760	 0.3130
S	 0.6860	 0.3170
T	 0.7620	 0.3500
V	 0.8830	 0.4660
W	 0.8970	 0.4710
X	 0.9040	 0.4770
Y	 0.9160	 0.4510
Z	 0.4940	 0.2940
b	 0.8620	 0.4580
c	 0.7800	 0.4240
e	 0.4960	 0.3790
k	 0.5900	 0.2590
s	 0.5540	 0.2410
t	 0.7440	 0.3890
u	 0.8780	 0.4400
w	 0.4030	 0.2070
x	 0.9010	 0.4470
y	 0.7680	 0.4040

