



Full wwPDB EM Validation Report ⓘ

Dec 19, 2022 – 12:29 PM EST

PDB ID : 7R6Q
EMDB ID : EMD-24286
Title : State E2 nucleolar 60S ribosome biogenesis intermediate - Foot region model
Authors : Cruz, V.E.; Sekulski, K.; Peddada, N.; Erzberger, J.P.
Deposited on : 2021-06-23
Resolution : 2.98 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:

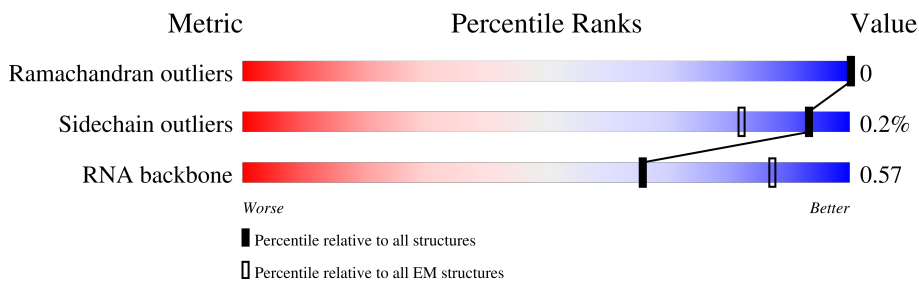
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 2.98 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	6	87	
2	D	505	
3	G	256	
4	K	376	
5	n	605	
6	o	220	
7	t	322	
8	X	142	

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Mol	Chain	Length	Quality of chain
9	m	807	22% 78%
10	1	295	14% 83% 17%
11	v	231	23% 77%
12	2	57	12% 89% 11%
13	N	204	15% 64% 36%
14	h	18	33% 100%
15	Z	16	38% 100%
16	g	39	49% 90% 10%
17	w	68	21% 100%
18	i	100	7% 58% 42%
19	L	199	16% 84%

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 29033 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 ITS-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	6	87	1838	823	309	619	87	0	0

- Molecule 2 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	437	3486	2247	600	627	12	0	0

- Molecule 3 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	199	1560	1004	275	278	3	0	0

- Molecule 4 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	K	286	2291	1472	378	437	4	0	0

- Molecule 5 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	n	425	3467	2242	600	611	14	0	0

- Molecule 6 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	o	133	1107	716	198	189	4	0	0

- Molecule 7 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	t	290	2328	1472	431	422	3	0	0

- Molecule 8 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	X	62	465	297	92	76	0	0

- Molecule 9 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	m	180	1513	961	266	282	4	0	0

- Molecule 10 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
10	1	295	6301	2816	1129	2061	295	0	0

- Molecule 11 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	v	53	475	300	90	84	1	0	0

- Molecule 12 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
12	2	57	1206	538	204	407	57	0	0

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	131	1131	710	236	184	1	0	0

- Molecule 14 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	h	18	Total	C	N	O	0	0
			151	96	30	25		

- Molecule 15 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	Z	16	Total	C	N	O	0	0
			125	80	27	18		

- Molecule 16 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	g	35	Total	C	N	O	0	0
			284	177	60	47		

- Molecule 17 is a protein called 60S ribosome biogenesis factor Spb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	w	68	Total	C	N	O	S	0	0
			574	352	99	121	2		

- Molecule 18 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	i	58	Total	C	N	O	S	0	0
			468	290	96	81	1		

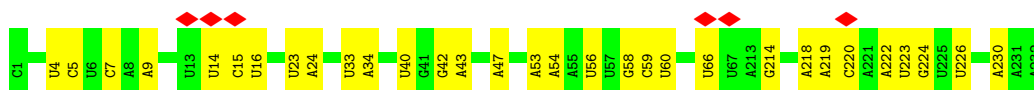
- Molecule 19 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	L	32	Total	C	N	O	0	0
			263	162	54	47		

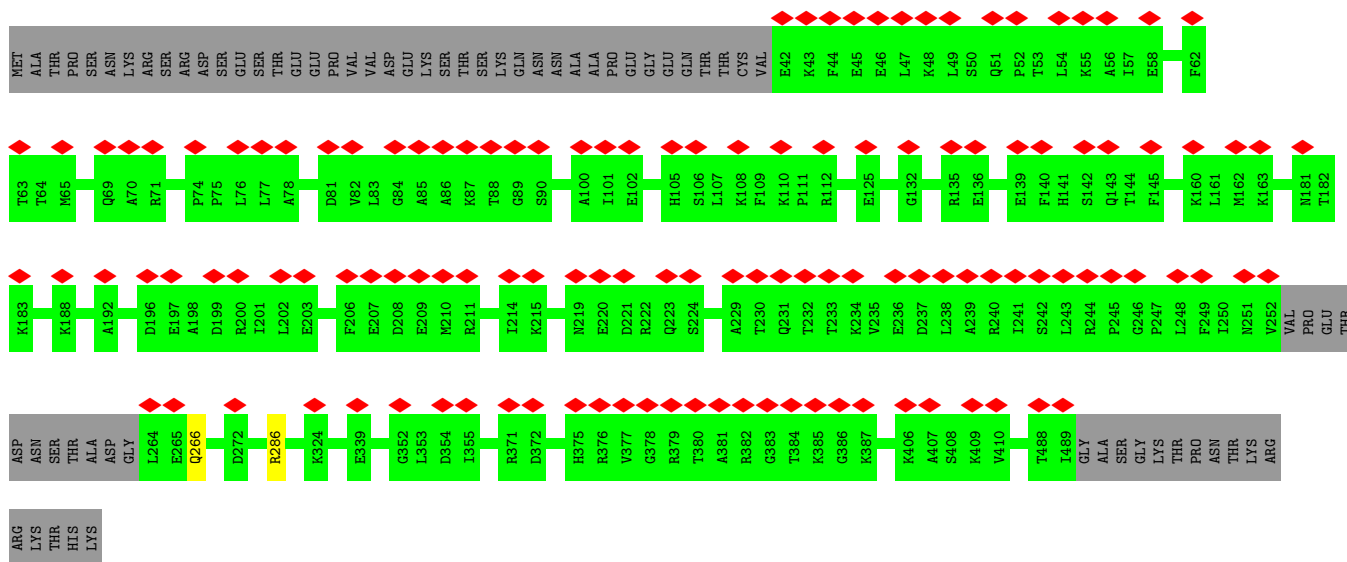
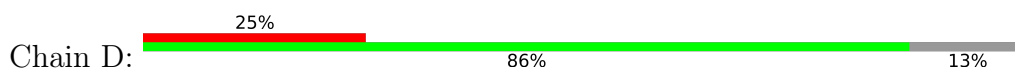
3 Residue-property plots [i](#)

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.

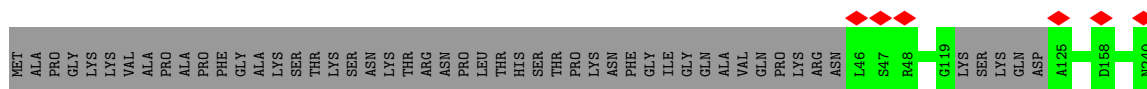
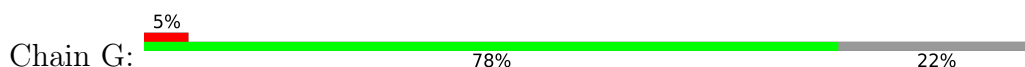
- Molecule 1: ITS-2

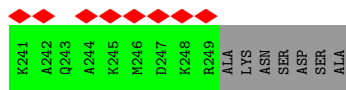


- Molecule 2: ATP-dependent RNA helicase HAS1



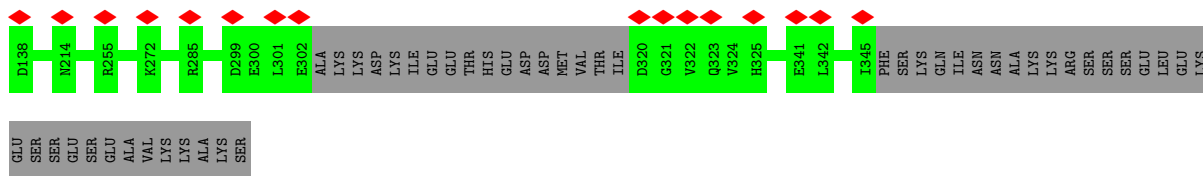
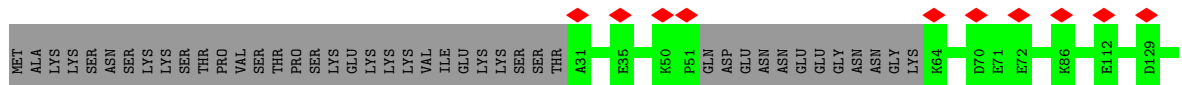
- Molecule 3: 60S ribosomal protein L8-A





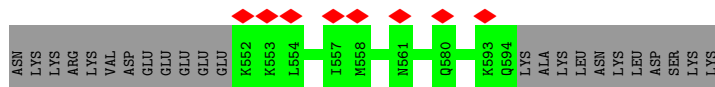
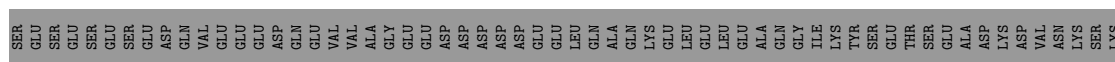
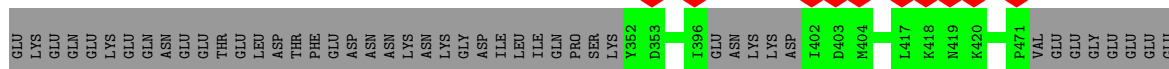
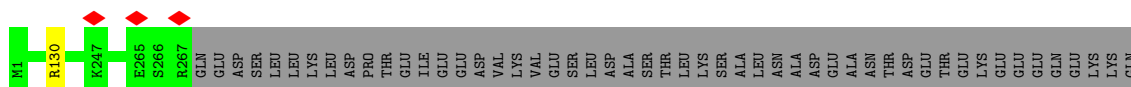
- Molecule 4: Proteasome-interacting protein CIC1

Chain K: 7% 76% 24%



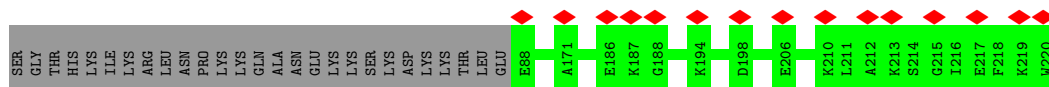
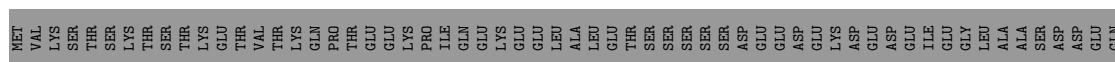
- Molecule 5: Pescadillo homolog

Chain n: 7% 70% 30%



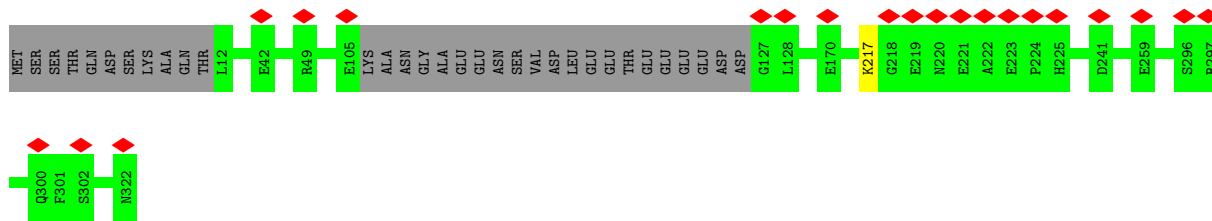
- Molecule 6: Ribosome biogenesis protein 15

Chain o: 7% 60% 40%

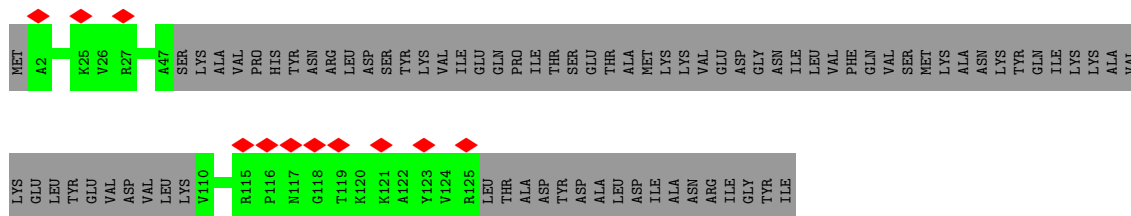
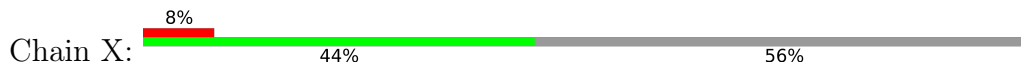


- Molecule 7: Ribosome biogenesis protein RLP7

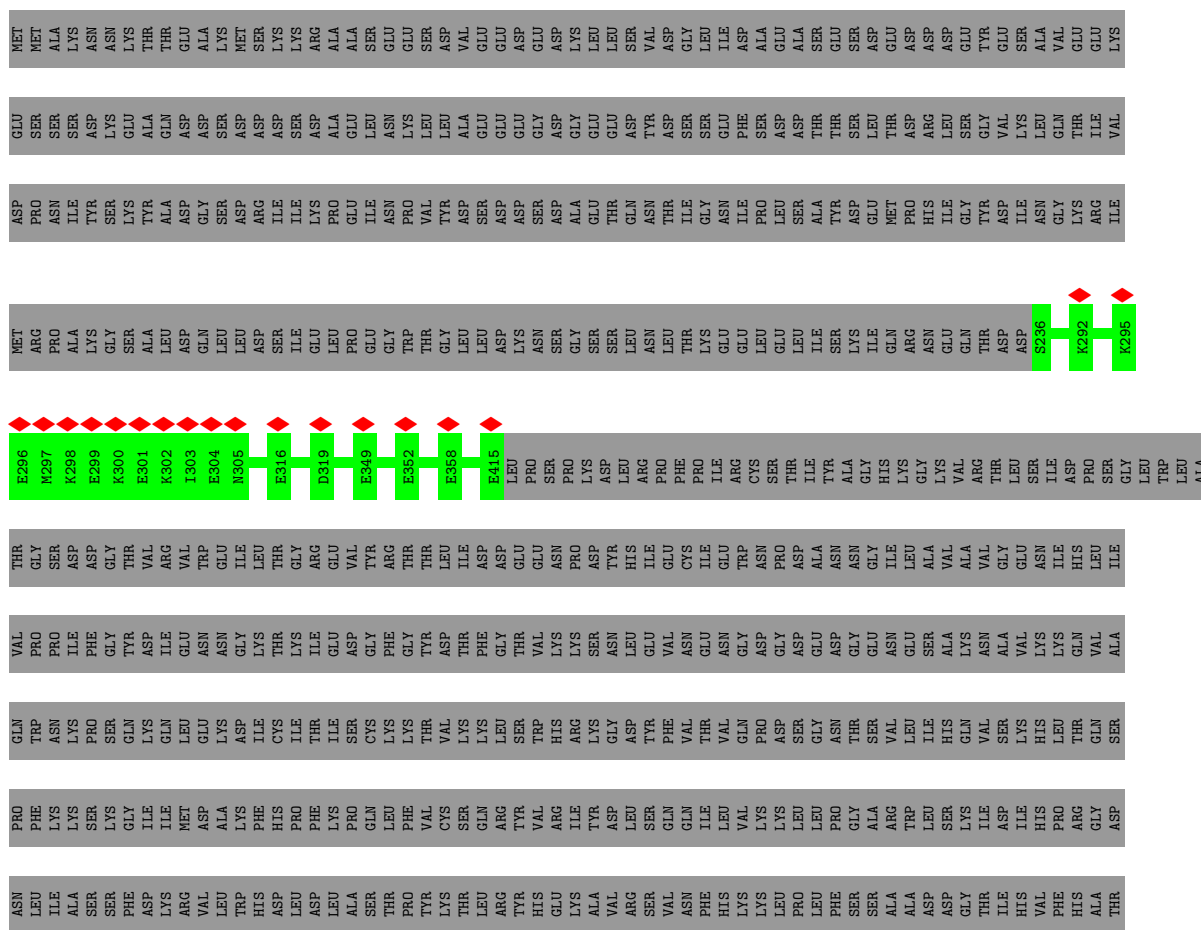
Chain t: 7% 90% 10%



• Molecule 8: 60S ribosomal protein L25

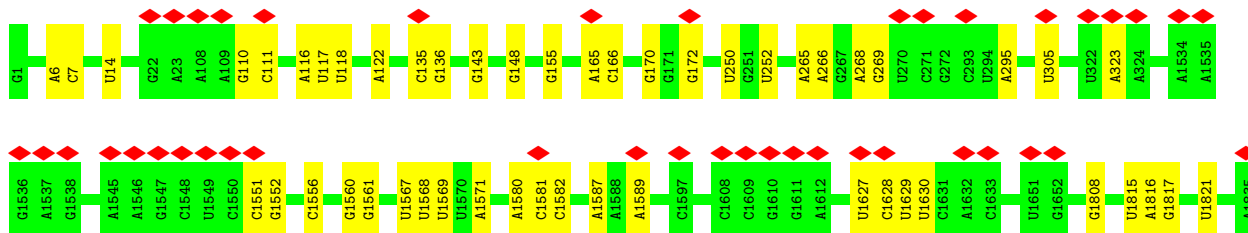
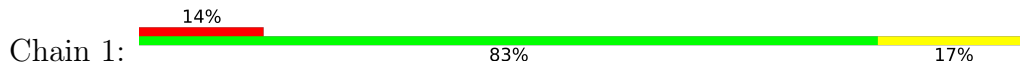


• Molecule 9: Ribosome biogenesis protein ERB1

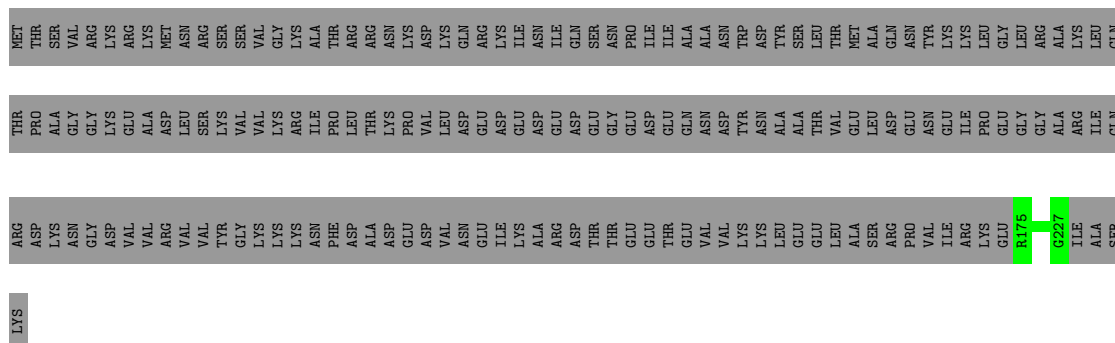


VAL TYR ASP ASP MET MET LYS ASN PRO PRO MET ILE VAL PRO LEU LYS LYS LEU THR THR THR THR THR THR THR THR THR THR

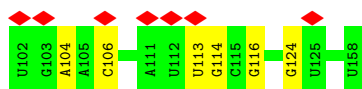
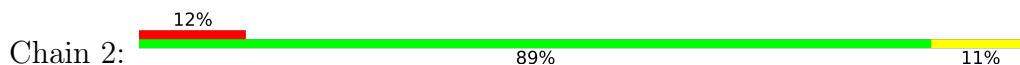
Molecule 10: 25S rRNA



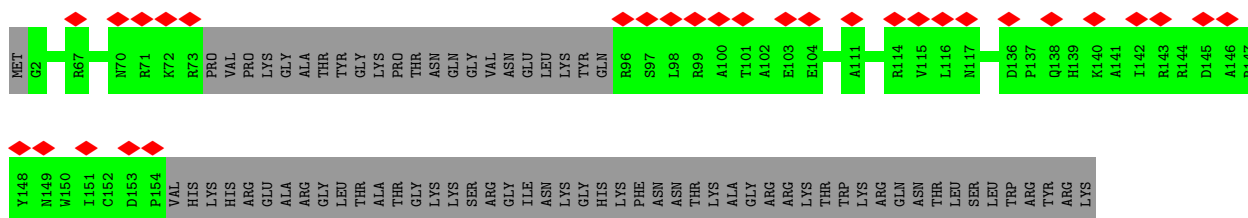
Molecule 11: Nucleolar protein 16



Molecule 12: 5.8S rRNA



Molecule 13: 60S ribosomal protein L15-A



Molecule 14: 60S ribosomal protein L35



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	198000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.119	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	453.6, 453.6, 453.6	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	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	6	0.22	0/2050	0.75	0/3186
2	D	0.25	0/3552	0.48	0/4789
3	G	0.26	0/1586	0.47	0/2139
4	K	0.25	0/2327	0.47	0/3140
5	n	0.26	0/3542	0.47	0/4765
6	o	0.25	0/1129	0.50	0/1502
7	t	0.25	0/2355	0.51	0/3158
8	X	0.24	0/470	0.55	0/629
9	m	0.25	0/1554	0.50	0/2104
10	1	0.23	0/7043	0.73	0/10957
11	v	0.25	0/484	0.49	0/638
12	2	0.22	0/1344	0.73	0/2091
13	N	0.26	0/1153	0.58	0/1545
14	h	0.24	0/151	0.44	0/195
15	Z	0.22	0/125	0.46	0/162
16	g	0.23	0/286	0.56	0/377
17	w	0.25	0/583	0.50	0/779
18	i	0.25	0/471	0.54	0/626
19	L	0.24	0/264	0.51	0/351
All	All	0.24	0/30469	0.60	0/43133

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	D	433/505 (86%)	425 (98%)	8 (2%)	0	100	100
3	G	195/256 (76%)	192 (98%)	3 (2%)	0	100	100
4	K	280/376 (74%)	271 (97%)	9 (3%)	0	100	100
5	n	417/605 (69%)	400 (96%)	17 (4%)	0	100	100
6	o	131/220 (60%)	126 (96%)	5 (4%)	0	100	100
7	t	286/322 (89%)	278 (97%)	8 (3%)	0	100	100
8	X	58/142 (41%)	57 (98%)	1 (2%)	0	100	100
9	m	178/807 (22%)	174 (98%)	4 (2%)	0	100	100
11	v	51/231 (22%)	50 (98%)	1 (2%)	0	100	100
13	N	127/204 (62%)	126 (99%)	1 (1%)	0	100	100
14	h	14/18 (78%)	14 (100%)	0	0	100	100
15	Z	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
16	g	27/39 (69%)	27 (100%)	0	0	100	100
17	w	64/68 (94%)	59 (92%)	5 (8%)	0	100	100
18	i	54/100 (54%)	51 (94%)	3 (6%)	0	100	100
19	L	28/199 (14%)	27 (96%)	1 (4%)	0	100	100
All	All	2357/4108 (57%)	2290 (97%)	67 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	381/440 (87%)	379 (100%)	2 (0%)	88	95
3	G	162/208 (78%)	162 (100%)	0	100	100
4	K	263/346 (76%)	263 (100%)	0	100	100
5	n	381/548 (70%)	380 (100%)	1 (0%)	92	97
6	o	118/199 (59%)	118 (100%)	0	100	100
7	t	259/287 (90%)	258 (100%)	1 (0%)	91	97
8	X	47/118 (40%)	47 (100%)	0	100	100
9	m	169/723 (23%)	169 (100%)	0	100	100
11	v	50/205 (24%)	50 (100%)	0	100	100
13	N	115/176 (65%)	115 (100%)	0	100	100
14	h	16/16 (100%)	16 (100%)	0	100	100
15	Z	13/13 (100%)	13 (100%)	0	100	100
16	g	30/33 (91%)	30 (100%)	0	100	100
17	w	62/62 (100%)	62 (100%)	0	100	100
18	i	49/82 (60%)	49 (100%)	0	100	100
19	L	27/159 (17%)	27 (100%)	0	100	100
All	All	2142/3615 (59%)	2138 (100%)	4 (0%)	93	98

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	266	GLN
2	D	286	ARG
5	n	130	ARG
7	t	217	LYS

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	6	85/87 (97%)	29 (34%)	2 (2%)
10	1	286/295 (96%)	49 (17%)	2 (0%)
12	2	56/57 (98%)	6 (10%)	0
All	All	427/439 (97%)	84 (19%)	4 (0%)

All (84) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	6	4	U
1	6	5	C
1	6	7	C
1	6	9	A
1	6	14	U
1	6	15	C
1	6	16	U
1	6	23	U
1	6	24	A
1	6	33	U
1	6	34	A
1	6	40	U
1	6	42	G
1	6	43	A
1	6	47	A
1	6	53	A
1	6	54	A
1	6	56	U
1	6	58	G
1	6	60	U
1	6	66	U
1	6	214	G
1	6	218	A
1	6	219	A
1	6	220	C
1	6	223	U
1	6	224	G
1	6	226	U
1	6	230	A
10	1	6	A
10	1	7	C
10	1	14	U
10	1	110	G
10	1	111	C
10	1	116	A
10	1	117	U
10	1	118	U
10	1	122	A
10	1	135	C
10	1	136	G
10	1	143	G
10	1	148	G

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Mol	Chain	Res	Type
10	1	155	G
10	1	165	A
10	1	166	C
10	1	170	G
10	1	172	G
10	1	250	U
10	1	252	U
10	1	265	A
10	1	266	A
10	1	268	A
10	1	269	G
10	1	295	A
10	1	305	U
10	1	323	A
10	1	1552	G
10	1	1556	C
10	1	1560	G
10	1	1561	G
10	1	1567	U
10	1	1568	U
10	1	1569	U
10	1	1571	A
10	1	1580	A
10	1	1581	C
10	1	1582	C
10	1	1587	A
10	1	1589	A
10	1	1627	U
10	1	1628	C
10	1	1629	U
10	1	1630	U
10	1	1808	G
10	1	1815	U
10	1	1816	A
10	1	1817	G
10	1	1821	U
12	2	104	A
12	2	106	C
12	2	113	U
12	2	114	G
12	2	116	G
12	2	124	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	6	59	C
1	6	222	A
10	1	165	A
10	1	1551	C

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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
10	1	8
16	g	2
17	w	1
14	h	1
1	6	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	324:A	O3'	1523:U	P	75.16
1	w	485:ARG	C	680:VAL	N	43.26
1	1	23:A	O3'	108:A	P	38.37

Continued on next page...

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	h	78:LYS	C	100:VAL	N	30.74
1	1	272:G	O3'	293:C	P	17.26
1	1	305:U	O3'	311:C	P	17.18
1	1	1633:C	O3'	1643:A	P	16.79
1	1	172:G	O3'	248:U	P	14.30
1	6	67:U	O3'	213:A	P	14.09
1	1	1597:C	O3'	1606:U	P	13.76
1	g	11:ASN	C	34:HIS	N	11.31
1	g	40:THR	C	54:ILE	N	10.64
1	1	1656:A	O3'	1798:A	P	9.69

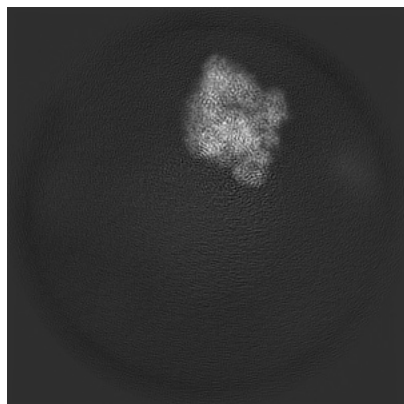
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24286. These allow visual inspection of the internal detail of the map and identification of artifacts.

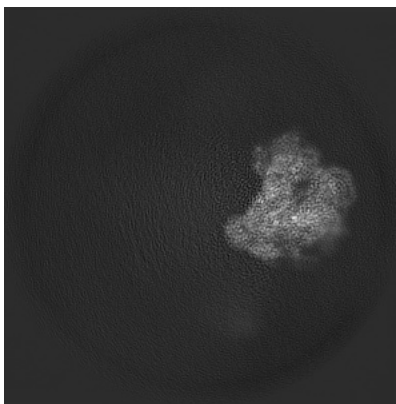
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

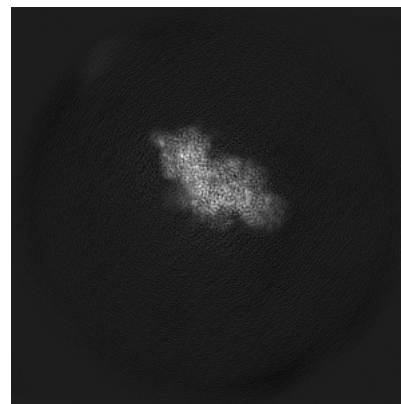
6.1.1 Primary map



X

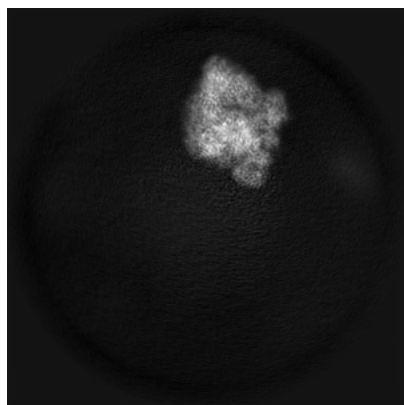


Y

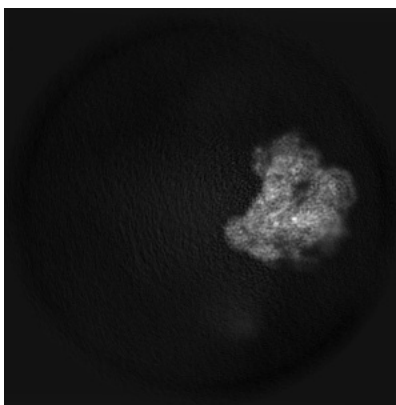


Z

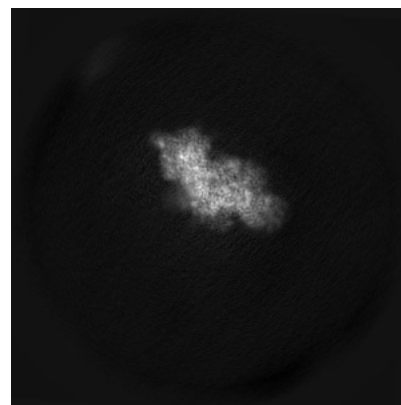
6.1.2 Raw map



X



Y

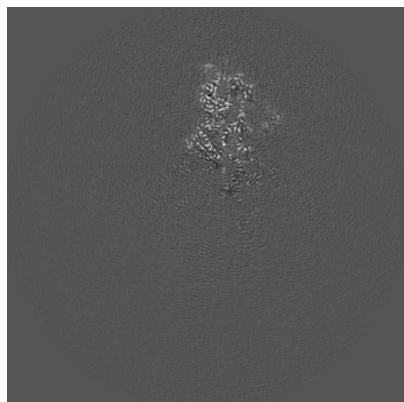


Z

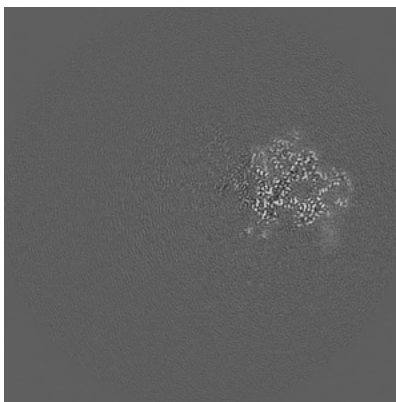
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

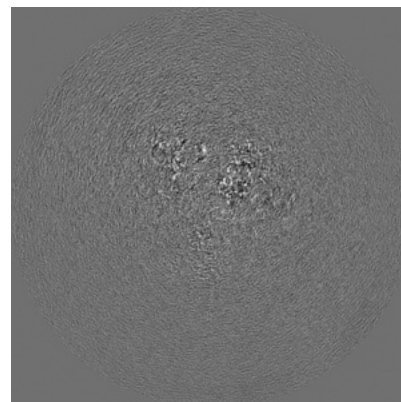
6.2.1 Primary map



X Index: 210

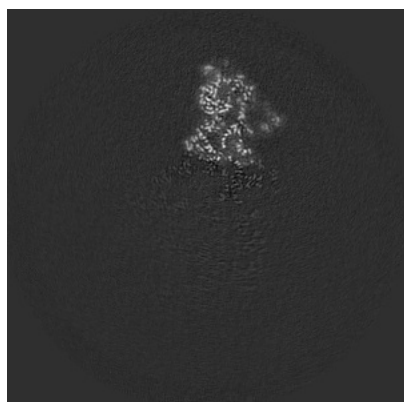


Y Index: 210

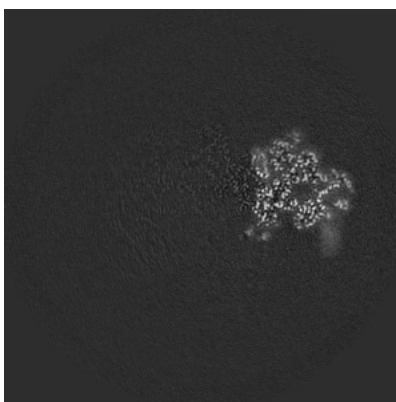


Z Index: 210

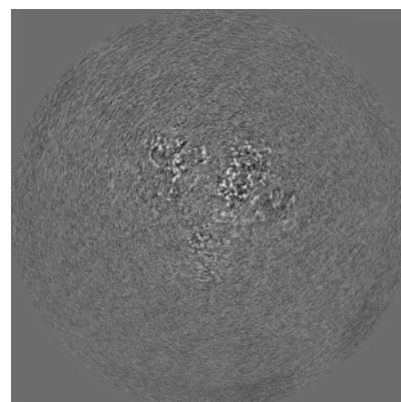
6.2.2 Raw map



X Index: 210



Y Index: 210

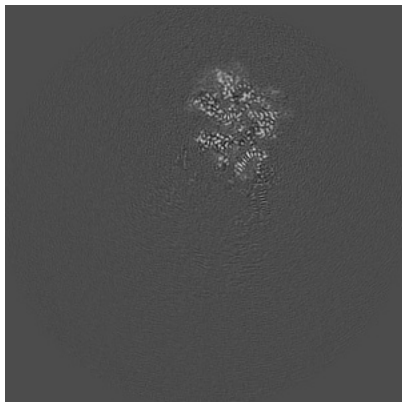


Z Index: 210

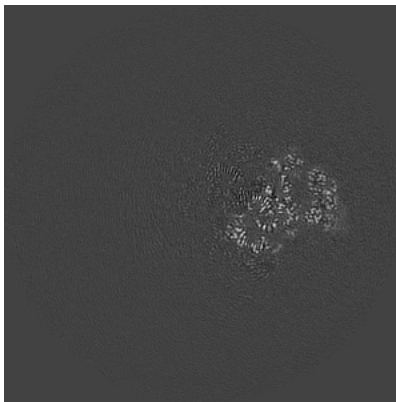
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

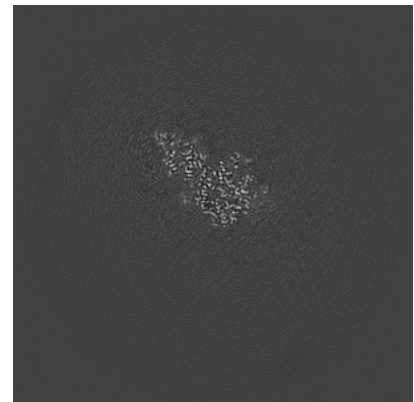
6.3.1 Primary map



X Index: 199

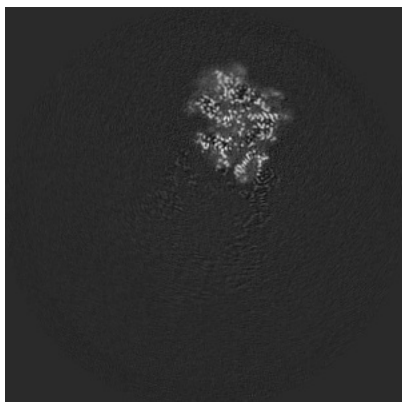


Y Index: 243

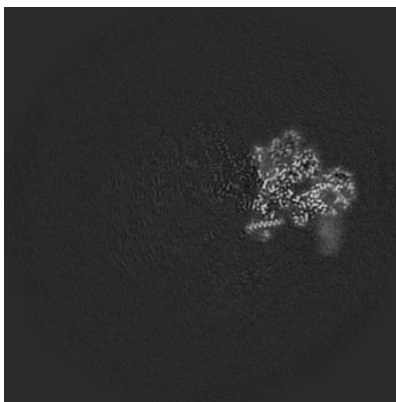


Z Index: 276

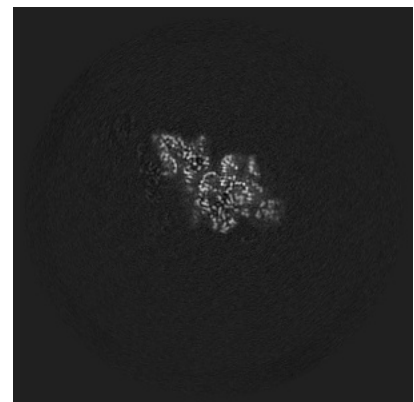
6.3.2 Raw map



X Index: 198



Y Index: 214

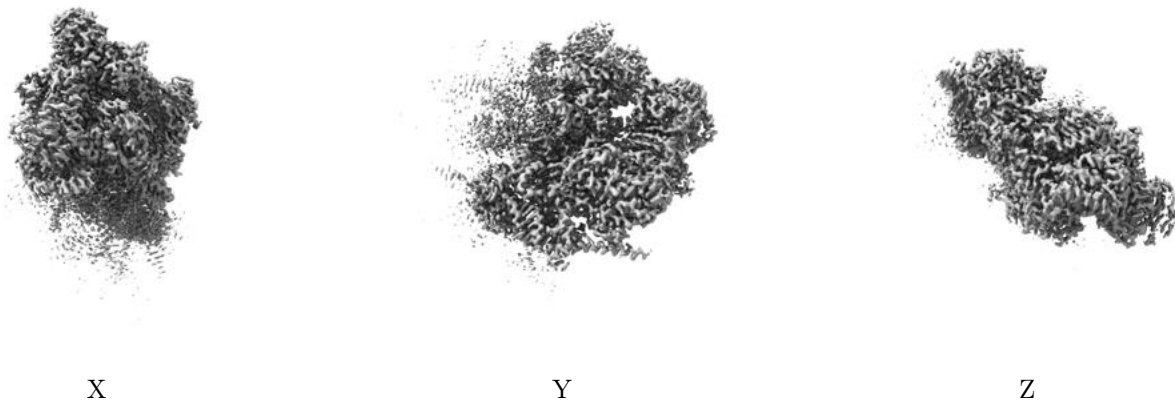


Z Index: 281

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

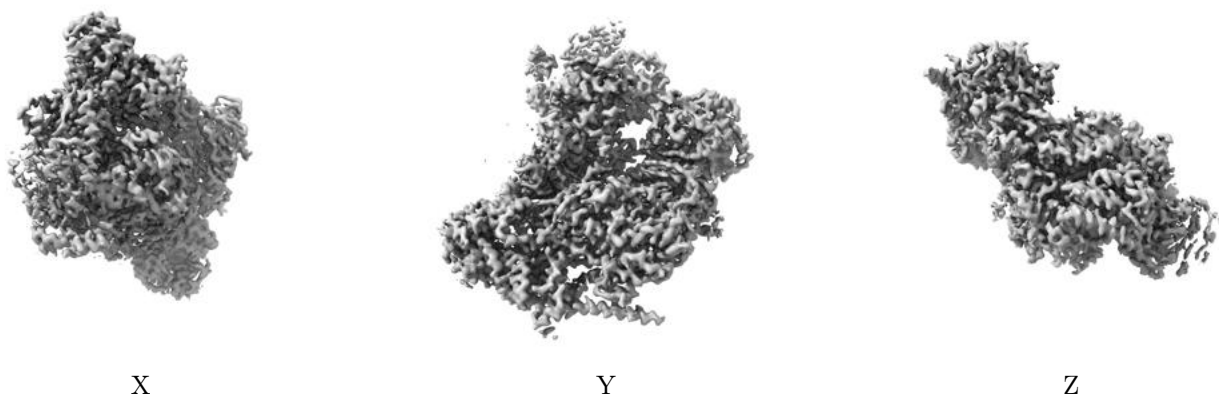
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

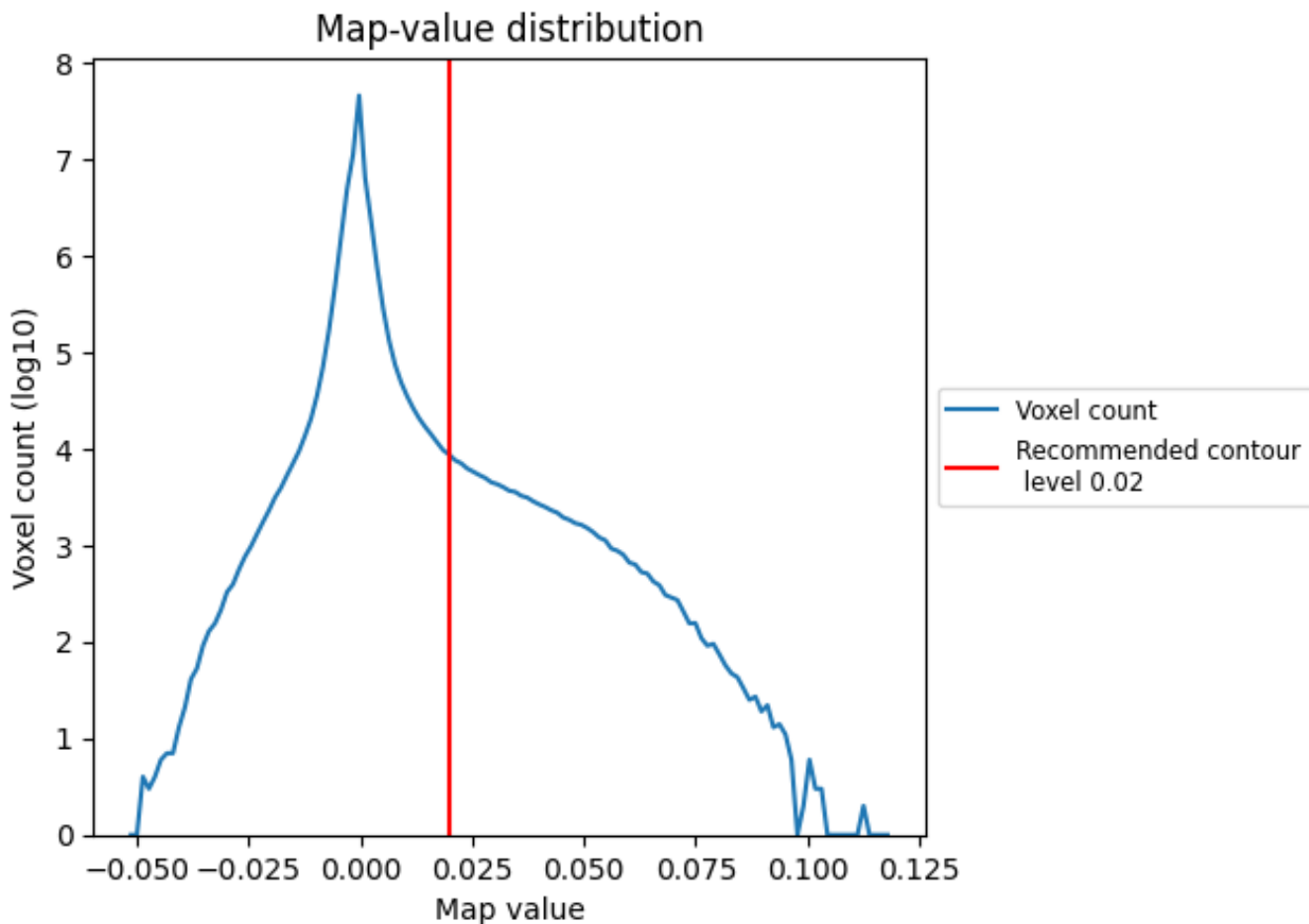
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

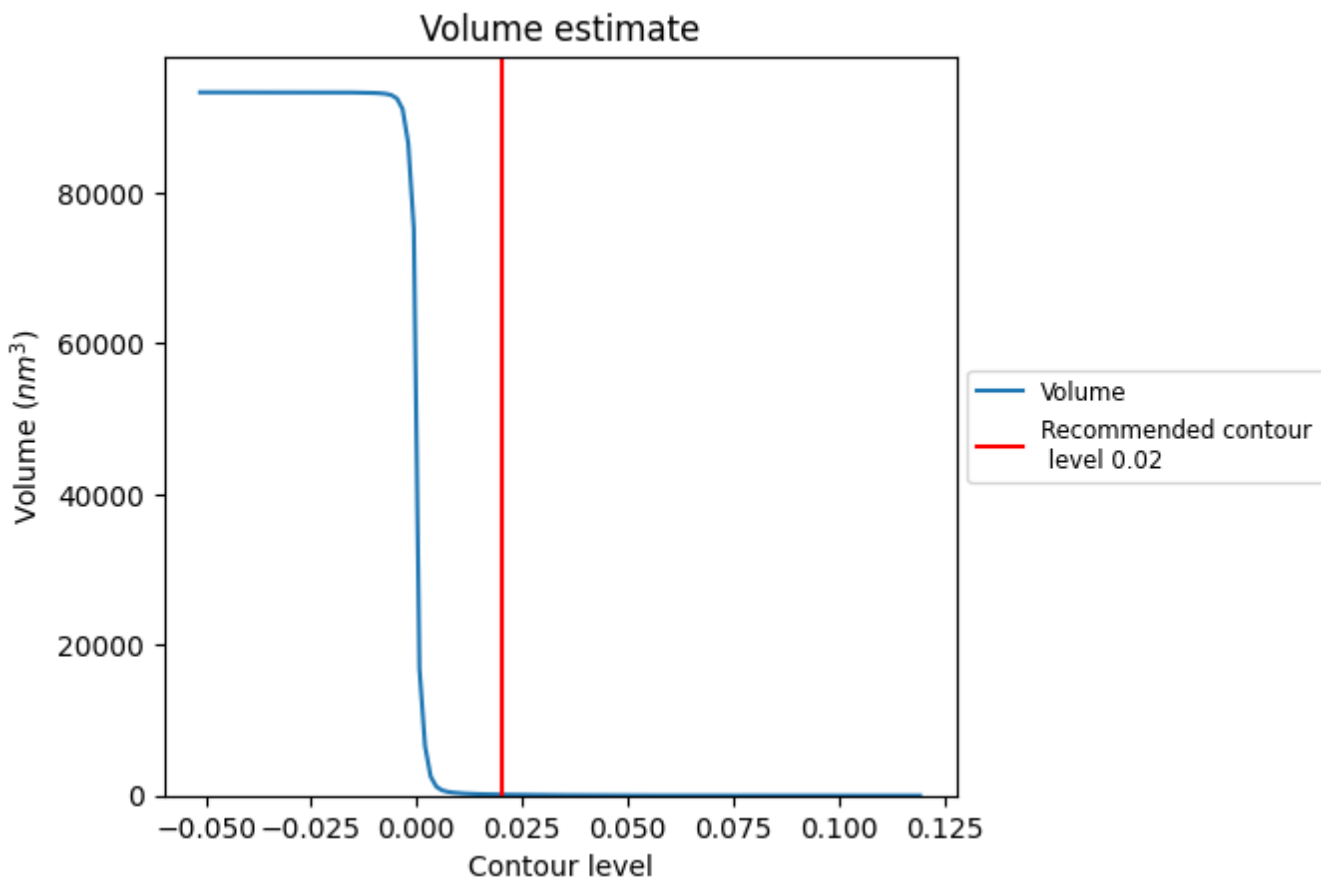
This section contains the results of statistical analysis of the map.

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.

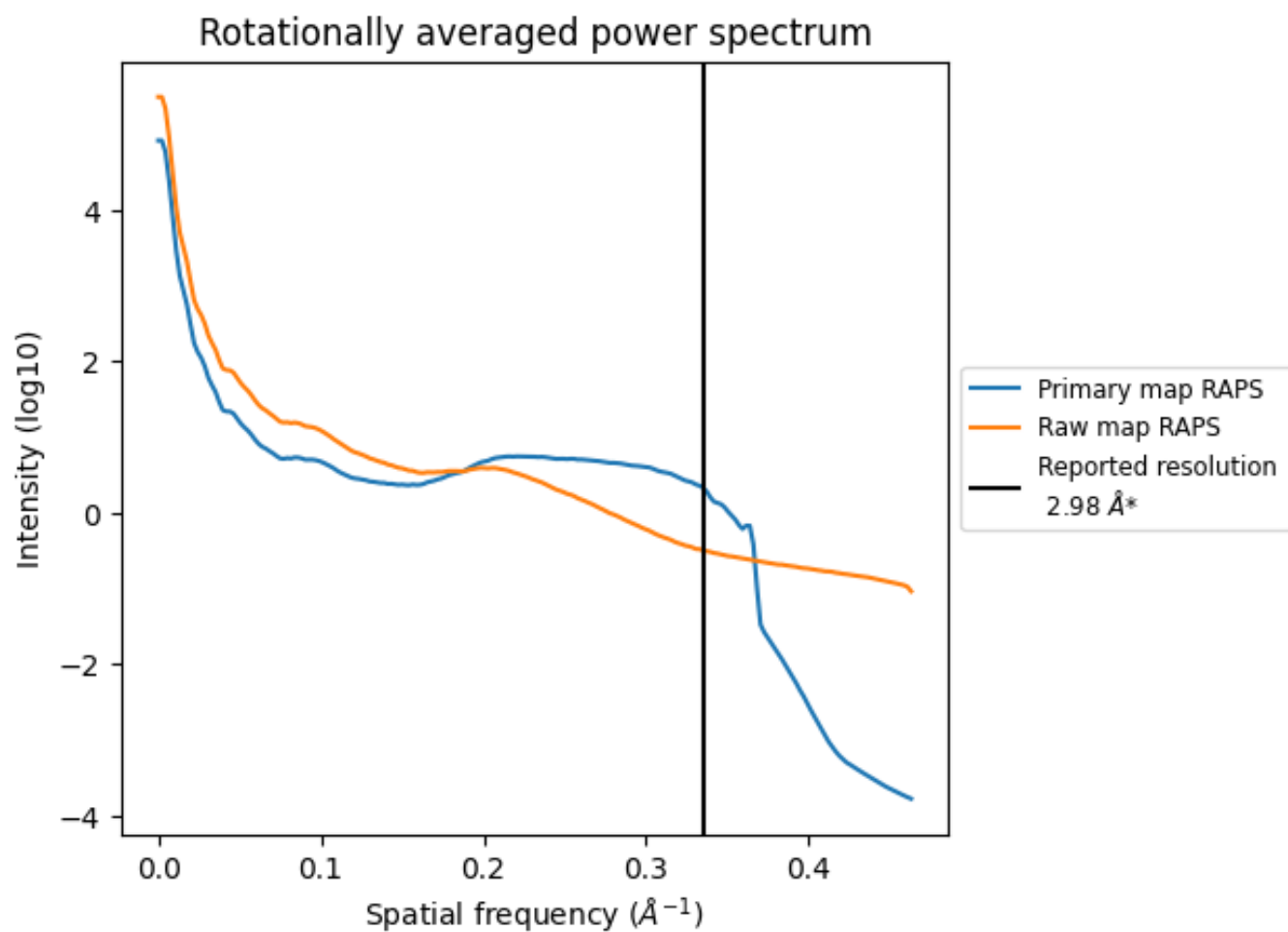
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 131 nm^3 ; this corresponds to an approximate mass of 118 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](#)

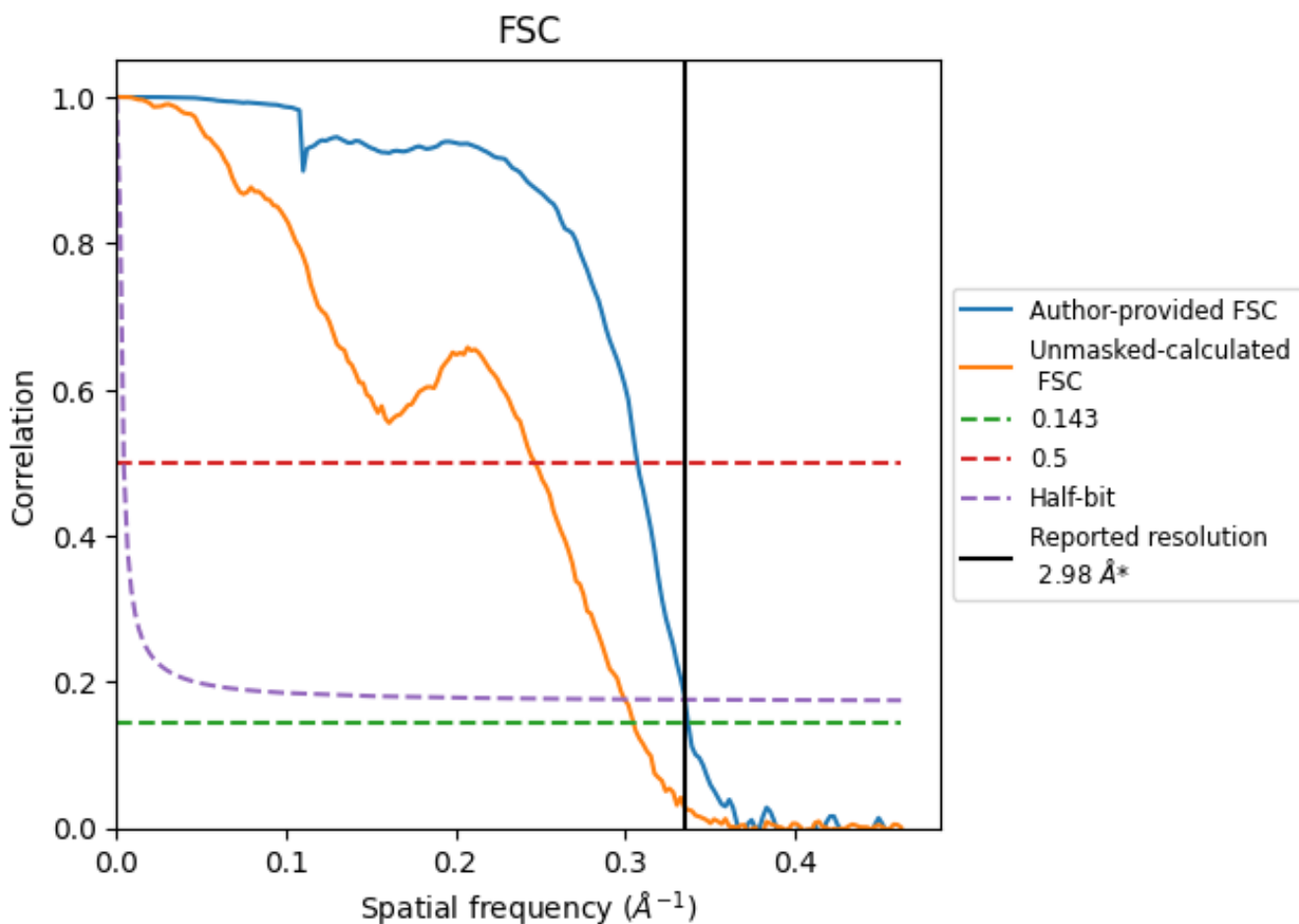


*Reported resolution corresponds to spatial frequency of 0.336 Å⁻¹

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 0.336 Å⁻¹

8.2 Resolution estimates [i](#)

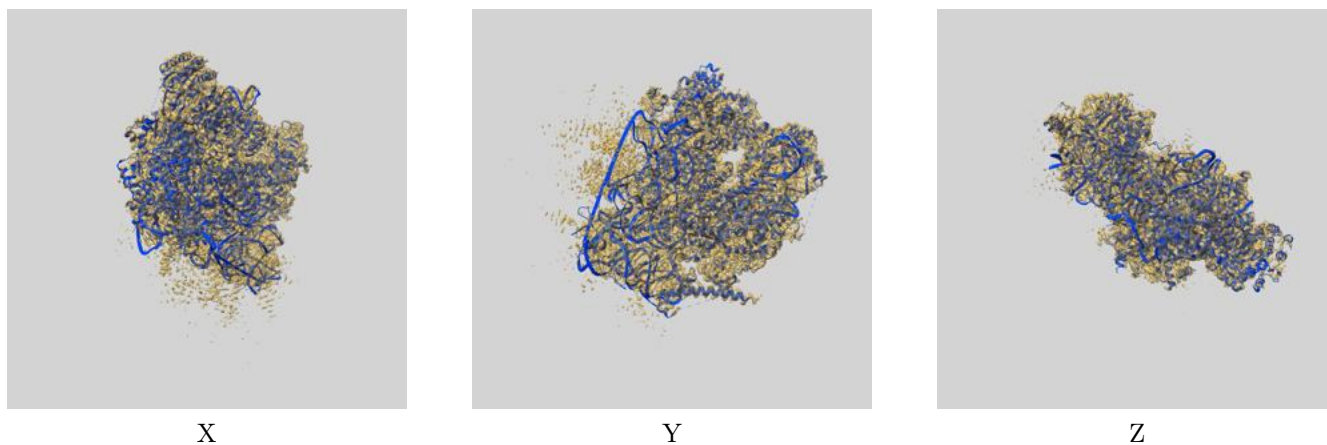
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.98	-	-
Author-provided FSC curve	2.96	3.25	2.98
Unmasked-calculated*	3.28	4.05	3.34

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.28 differs from the reported value 2.98 by more than 10 %

9 Map-model fit [i](#)

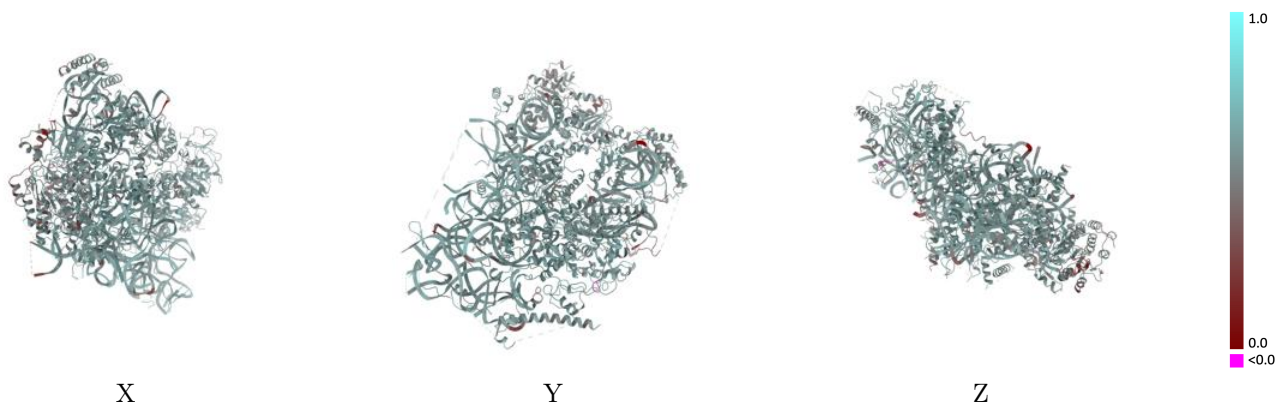
This section contains information regarding the fit between EMDB map EMD-24286 and PDB model 7R6Q. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



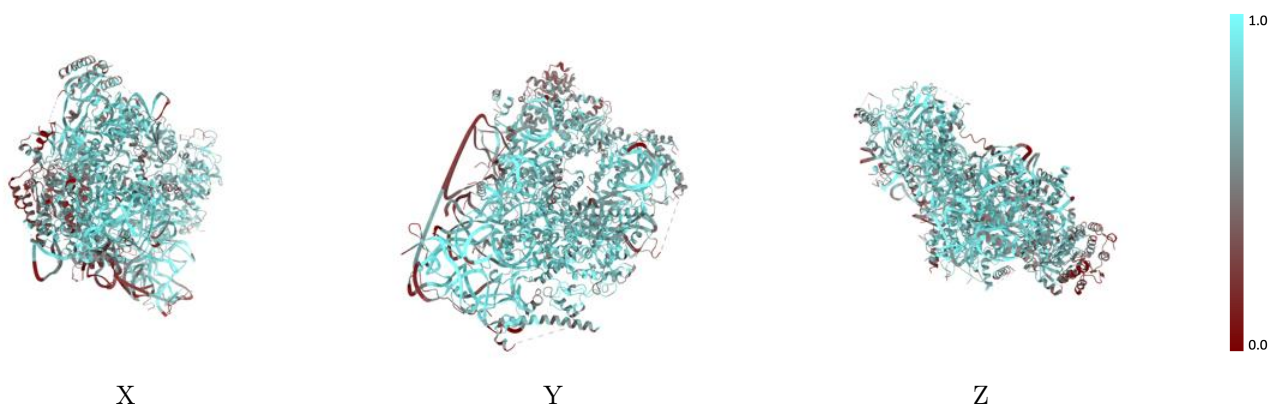
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



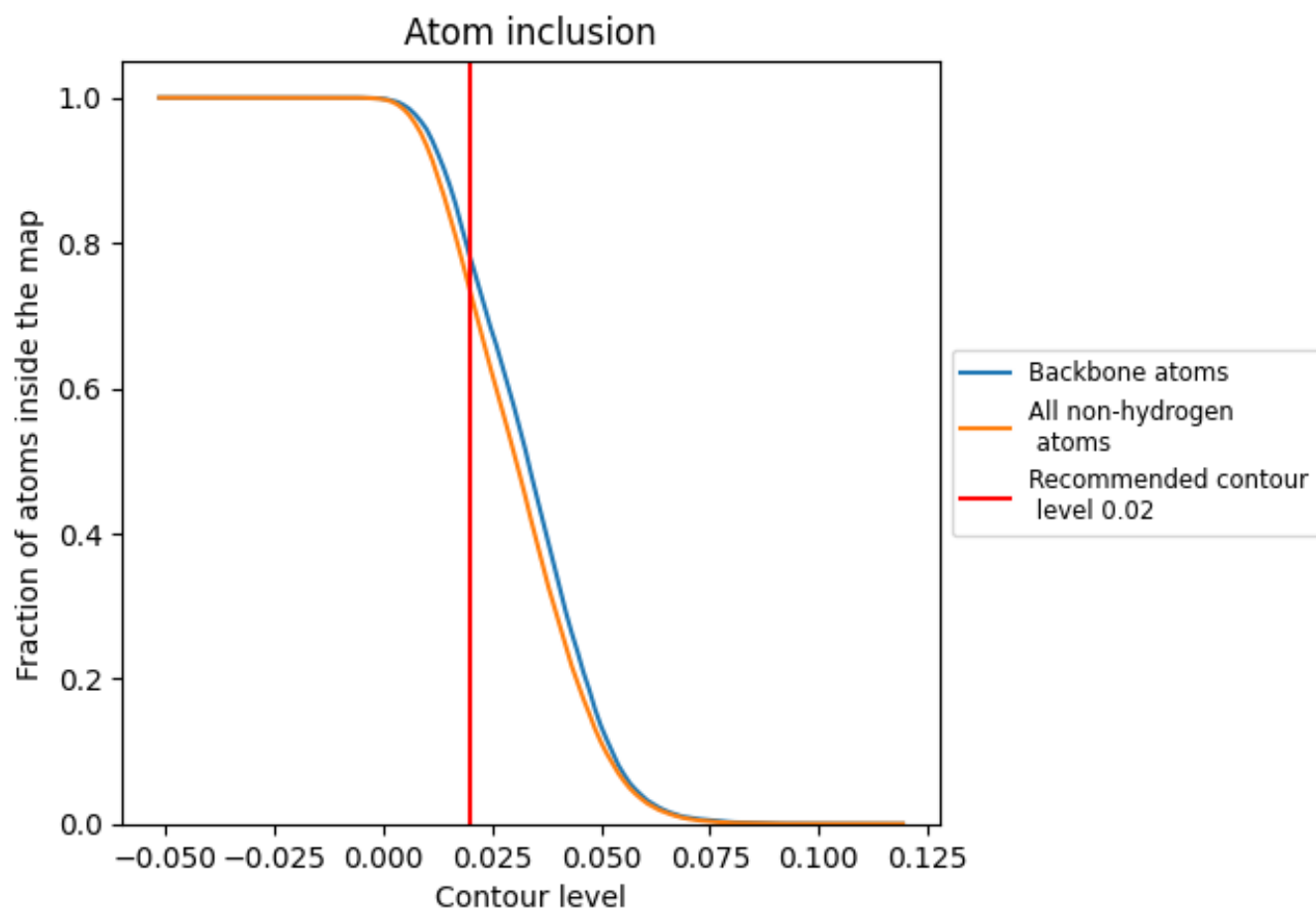
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).









































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 73% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7328	 0.5760
1	 0.7678	 0.5870
2	 0.8192	 0.5910
6	 0.8215	 0.5600
D	 0.5717	 0.5370
G	 0.8150	 0.5970
K	 0.7227	 0.5670
L	 0.6392	 0.5880
N	 0.7184	 0.6210
X	 0.6556	 0.5810
Z	 0.5041	 0.4940
g	 0.4522	 0.6010
h	 0.5743	 0.5880
i	 0.7254	 0.5620
m	 0.7502	 0.5820
n	 0.7824	 0.5830
o	 0.7429	 0.5710
t	 0.7331	 0.5720
v	 0.7707	 0.5830
w	 0.6308	 0.5590

