wwPDB EM Validation Summary Report ⓘ

Jan 16, 2025 – 01:17 am GMT

PDB ID	:	9HA1
EMDB ID	:	EMD-51973
Title	:	Pooled 50S subunit C_(L22)- precursor states supplemented with Api137 - Canonical PET exit Api137
Authors	:	Lauer, S.; Nikolay, R.; Spahn, C.M.T.
Deposited on	:	2024-11-01
Resolution	:	4.17 Å(reported)

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

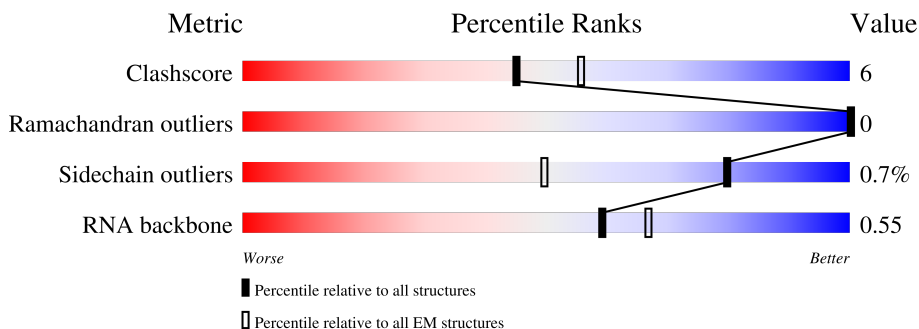|		
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 4.17 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.
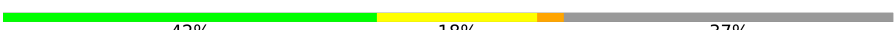
Metric	Percentile Ranks	Value
Clashscore		6
Ramachandran outliers		0
Sidechain outliers		0.7%
RNA backbone		0.55

Worse *Better*

▌ Percentile relative to all structures

▯ Percentile relative to all EM structures

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	46	65% 20% 15%
2	J	142	84% 16%
3	K	122	84% 16%
4	N	120	90% 10%
5	P	114	85% 14% •
6	Q	117	88% 12%
7	R	103	84% 16%

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Mol	Chain	Length	Quality of chain
8	T	93	87% 13%
9	U	102	86% 14%
10	Y	63	83% 17%
11	A	2904	42% 18% 37%
12	D	209	69% 14% 16%
13	E	201	73% 9% 18%
14	L	143	15% 66% 10% 24%
15	y	17	35% 94% 6%

2   Entry composition ⓘ

There are 15 unique types of molecules in this entry. The entry contains 50932 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 protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	39	Total 312	C 187	N 77	O 47	S 1	0	0

- Molecule 2 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	142	Total 1129	C 714	N 212	O 199	S 4	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	122	Total 939	C 587	N 180	O 166	S 6	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	120	Total 961	C 593	N 196	O 167	S 5	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	114	Total 917	C 574	N 179	O 163	S 1	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	Q	117	Total 947	C 604	N 192	O 151	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 8 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	T	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 9 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	U	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 10 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 11 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	1832	Total	C	N	O	P	0	0
			39369	17562	7293	12682	1832		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	827	A	U	conflict	GB 1897866982
A	830	A	G	conflict	GB 1897866982

- Molecule 12 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	175	Total	C	N	O	S	0	0
			1306	820	235	247	4		

- Molecule 13 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	165	Total 1282	C 809	N 225	O 243	S 5	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	L	109	Total 778	C 483	N 149	O 146	0	0

- Molecule 15 is a protein called Apidaecins type 137.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	y	17	Total 148	C 94	N 33	O 21	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	10	ARG	GLN	conflict	UNP P35581

3   Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Large ribosomal subunit protein bL34

Chain 2:

• Molecule 2: Large ribosomal subunit protein uL13

Chain J:
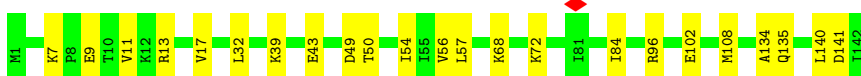
• Molecule 3: Large ribosomal subunit protein uL14

Chain K:

• Molecule 4: Large ribosomal subunit protein bL17

Chain N:
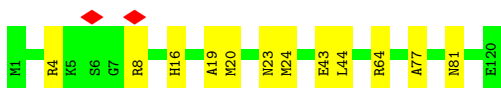
• Molecule 5: Large ribosomal subunit protein bL19

Chain P:

• Molecule 6: Large ribosomal subunit protein bL20

Chain Q:

88% 12%

A1 Q19 R27 R32 Y46 R47 R54 Q55 F56 R57 I79 N80 D101 K102 V103 A104 L108 A117

• Molecule 7: Large ribosomal subunit protein bL21

Chain R:

84% 16%

M1 K10 Q11 E16 R21 L22 A28 E31 E34 I59 H66 K73 I74 R78 H82 Q86 T94 A103

• Molecule 8: Large ribosomal subunit protein uL23

Chain T:

87% 13%

M1 E4 E18 E25 D37 K40 I43 E54 V58 G65 D79 W80 K81 L87 L93

• Molecule 9: Large ribosomal subunit protein uL24

Chain U:

86% 14%

A1 I4 E9 K32 G37 I38 N39 V48 P49 A50 E61 Q65 V66 S67 R81 E87 K96 S97 I102

• Molecule 10: Large ribosomal subunit protein uL29

Chain Y:

83% 17%

M1 L14 L18 R23 E24 Q25 R29 M30 Q31 K44 R48 R52 N58 A63

• Molecule 11: 23S ribosomal RNA

Chain A:

42% 18% 37%

G1 G9 A10 C11 U12 A13 A14 U18 U19 U25 G26 G27 A28 A29 G30 C31 G35 G43 A44 G45 G46 C47 G48 G51 A52 A53 G54 U59 G60 G68 C69 U72 A73 A74 G75 C76 G81 U82 A83 U87 C96 U100 A101 A102 A103 U114

G117 A118 A119 U120 A125 A131 U138 U139 C140 G141 A142 C143 C151 A152 C164 A165 U166 G175 A176 G177 A181 A191 A195 A196 A213 G214 G215 A216 A221 A222 A223 U224 C225 A226 A227 C228 C229 G230 A231 G232 A233 U234 U235 C238 C239 A244

G245 C246 G247 G248 C249 G254 A255 G259 G260 G261 A262 G263 C264 A265 G266 C267 C268 C269 A270 G271 A272 A278 U284 G291 G295 G301 C302 G307 G308 A309 A310 A311 G312 G313 C316 G319 A320 U321 A324 G329 A330 C331 C335 A340 A345
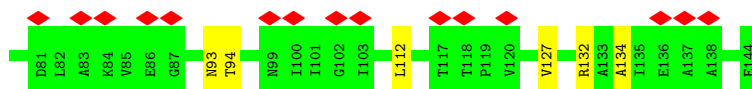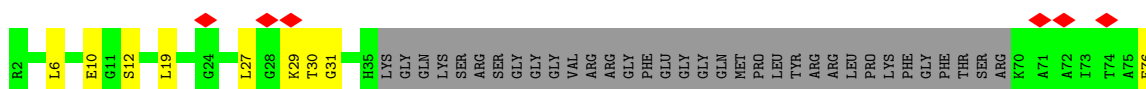
• Molecule 12: 50S ribosomal protein L3
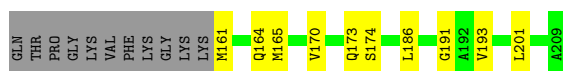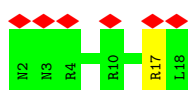
Chain D:

• Molecule 13: Large ribosomal subunit protein uL4

Chain E:
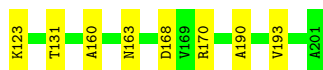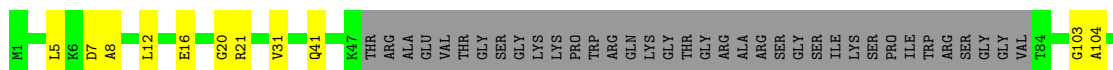
• Molecule 14: Large ribosomal subunit protein uL15

Chain L:

• Molecule 15: Apidaecins type 137

Chain y:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29868	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	46.2	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.448	Depositor
Minimum map value	-0.156	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	399.6, 399.6, 399.6	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.332, 1.332, 1.332	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	2	0.23	0/314	0.65	0/413
2	J	0.24	0/1152	0.50	0/1551
3	K	0.25	0/948	0.54	0/1268
4	N	0.24	0/974	0.57	0/1301
5	P	0.24	0/929	0.55	0/1242
6	Q	0.24	0/960	0.51	0/1278
7	R	0.26	0/829	0.53	0/1107
8	T	0.24	0/745	0.50	0/994
9	U	0.26	0/788	0.49	0/1051
10	Y	0.25	0/510	0.51	0/677
11	A	0.15	0/44100	0.72	8/68792 (0.0%)
12	D	0.25	0/1320	0.50	0/1776
13	E	0.24	0/1294	0.47	0/1741
14	L	0.25	0/780	0.55	0/1041
15	y	0.48	0/155	0.65	0/212
All	All	0.18	0/55798	0.68	8/84444 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	269	C	N3-C2-O2	-6.61	117.27	121.90
11	A	2772	C	N3-C2-O2	-6.50	117.35	121.90
11	A	1675	C	C2-N1-C1'	6.39	125.83	118.80
11	A	635	C	N3-C2-O2	-6.08	117.64	121.90
11	A	1734	G	N1-C2-N2	-5.67	111.09	116.20

There are no chirality outliers.

There are no planarity outliers.

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	312	0	344	8	0
2	J	1129	0	1162	18	0
3	K	939	0	1012	12	0
4	N	961	0	1000	8	0
5	P	917	0	965	12	0
6	Q	947	0	1022	13	0
7	R	816	0	839	14	0
8	T	739	0	807	10	0
9	U	780	0	834	8	0
10	Y	509	0	543	9	0
11	A	39369	0	19807	301	0
12	D	1306	0	1355	23	0
13	E	1282	0	1336	13	0
14	L	778	0	841	11	0
15	y	148	0	152	0	0
All	All	50932	0	32019	411	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 6.

The worst 5 of 411 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)
11:A:513:A:O2'	11:A:514:A:O5'	1.76	1.00
11:A:1437:C:HO2'	11:A:1516:G:HO2'	1.00	0.99
11:A:175:G:O2'	11:A:176:A:O5'	1.87	0.91
11:A:1666:G:O2'	11:A:1667:G:O4'	1.88	0.89
11:A:475:C:O2	11:A:479:A:N6	2.09	0.86

There are no symmetry-related clashes.

5.3   Torsion angles ⓘ

5.3.1   Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	37/46 (80%)	35 (95%)	2 (5%)	0	100	100
2	J	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
3	K	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
4	N	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
5	P	112/114 (98%)	112 (100%)	0	0	100	100
6	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
7	R	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
8	T	91/93 (98%)	81 (89%)	10 (11%)	0	100	100
9	U	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
10	Y	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
12	D	171/209 (82%)	166 (97%)	5 (3%)	0	100	100
13	E	161/201 (80%)	159 (99%)	2 (1%)	0	100	100
14	L	105/143 (73%)	97 (92%)	8 (8%)	0	100	100
15	y	15/17 (88%)	11 (73%)	4 (27%)	0	100	100
All	All	1447/1592 (91%)	1389 (96%)	58 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	2	31/38 (82%)	31 (100%)	0	100	100
2	J	116/116 (100%)	115 (99%)	1 (1%)	75	83
3	K	103/103 (100%)	103 (100%)	0	100	100
4	N	100/100 (100%)	98 (98%)	2 (2%)	50	68
5	P	99/99 (100%)	97 (98%)	2 (2%)	50	68
6	Q	89/89 (100%)	89 (100%)	0	100	100
7	R	84/84 (100%)	84 (100%)	0	100	100
8	T	80/80 (100%)	80 (100%)	0	100	100
9	U	83/83 (100%)	81 (98%)	2 (2%)	44	63
10	Y	55/55 (100%)	55 (100%)	0	100	100
12	D	136/164 (83%)	136 (100%)	0	100	100
13	E	138/165 (84%)	137 (99%)	1 (1%)	81	87
14	L	76/102 (74%)	76 (100%)	0	100	100
15	y	17/17 (100%)	16 (94%)	1 (6%)	16	40
All	All	1207/1295 (93%)	1198 (99%)	9 (1%)	80	87

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	E	123	LYS
15	y	17	ARG
5	P	81	ASP
5	P	113	LEU
9	U	39	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
15	y	3	ASN

5.3.3   RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1825/2904 (62%)	293 (16%)	11 (0%)

5 of 293 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	10	A
11	A	12	U
11	A	14	A
11	A	25	U
11	A	27	G

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	1737	G
11	A	1738	G
11	A	2834	G
11	A	2763	G
11	A	1198	U

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

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

5.5　Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6　Ligand geometry ⓘ

There are no ligands in this entry.

5.7　Other polymers ⓘ

There are no such residues in this entry.

5.8　Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-51973. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections ⓘ
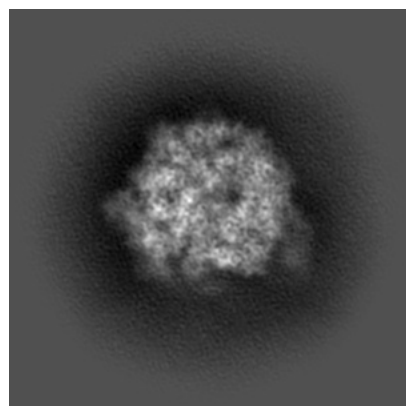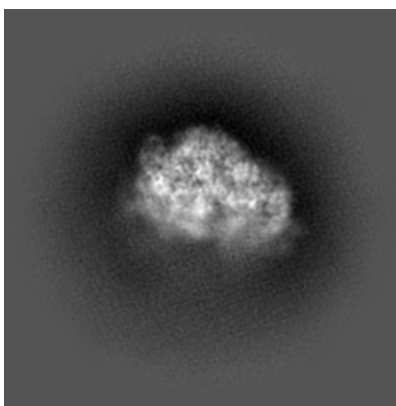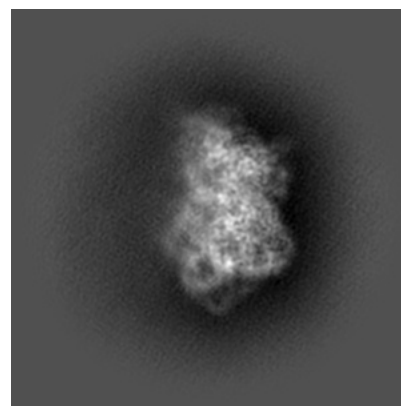
6.1.1 Primary map

X   Y   Z

6.1.2 Raw map

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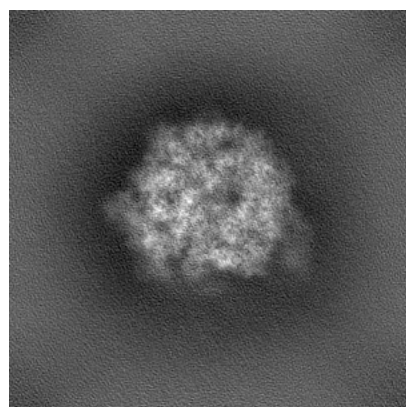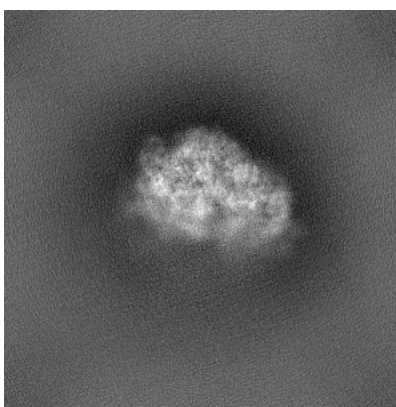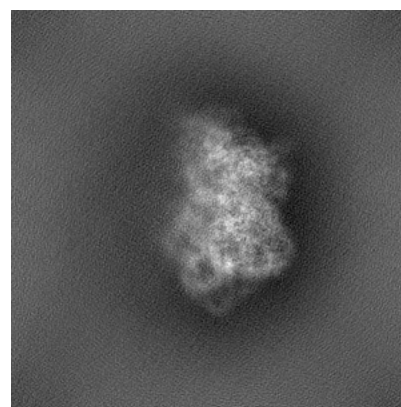
The images above show the map projected in three orthogonal directions.

6.2   Central slices ⓘ
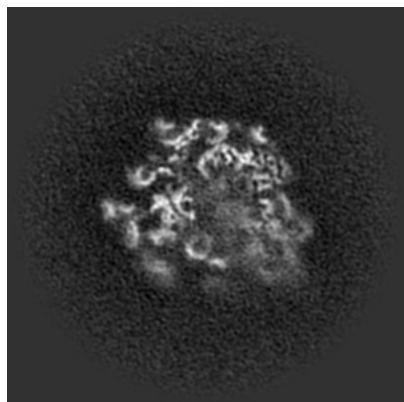
6.2.1   Primary map
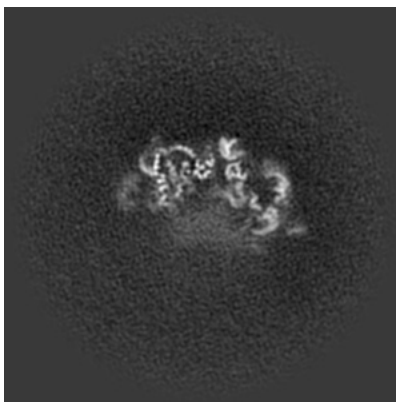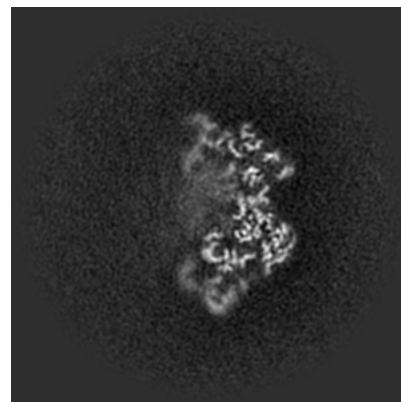
| X Index: 150 | Y Index: 150 | Z Index: 150 |

6.2.2   Raw map
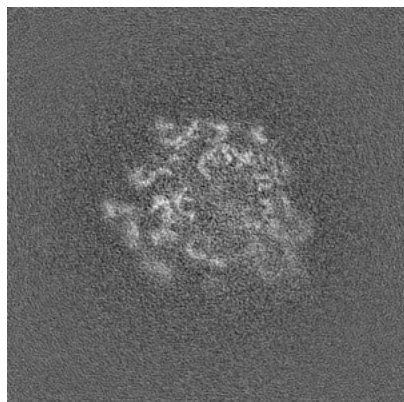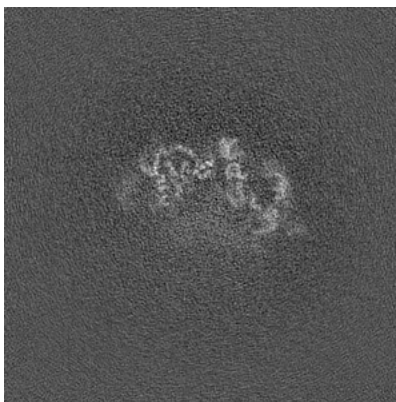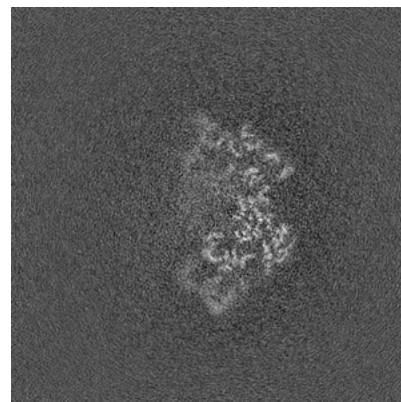
| X Index: 150 | Y Index: 150 | Z Index: 150 |

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

6.3 Largest variance slices (i)

6.3.1 Primary map
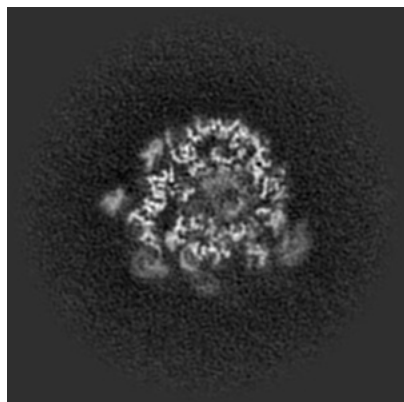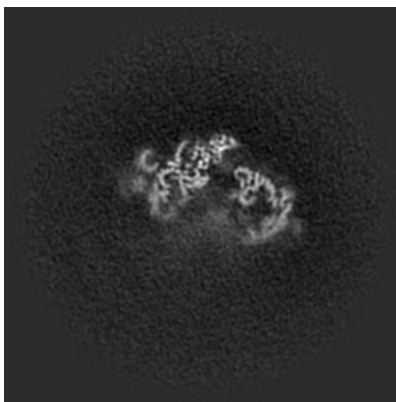
| X Index: 161 | Y Index: 142 | Z Index: 146 |
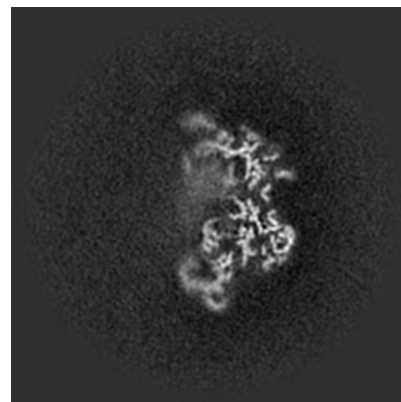
6.3.2 Raw map
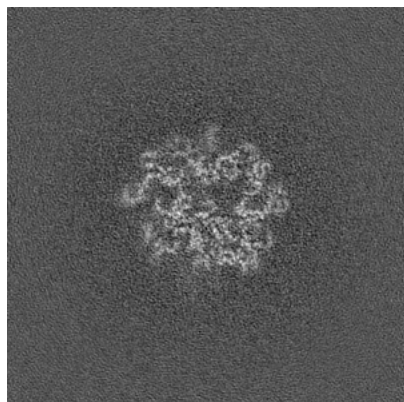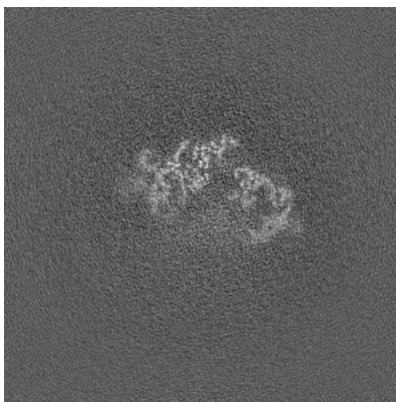
| X Index: 177 | Y Index: 143 | Z Index: 146 |
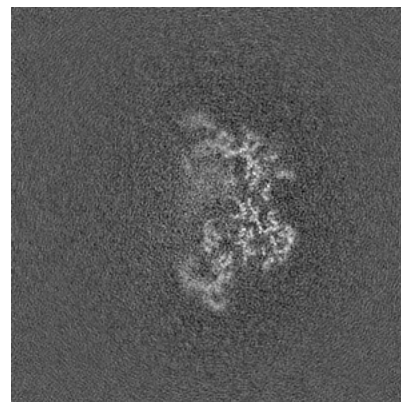
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map
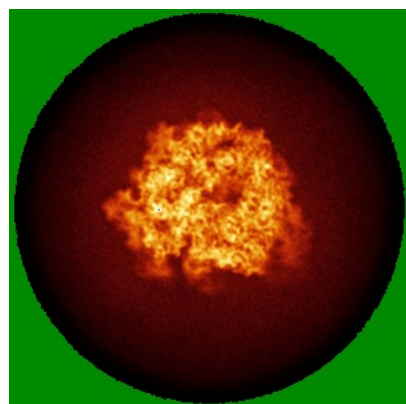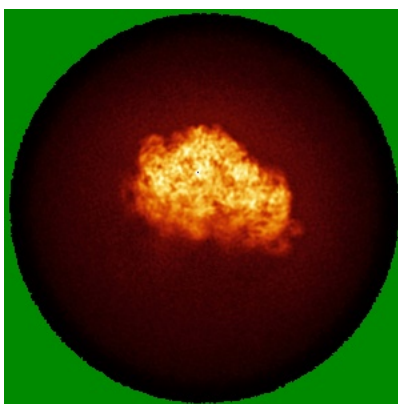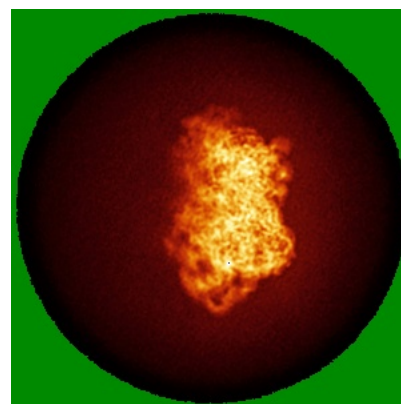
X   Y   Z

6.4.2 Raw map

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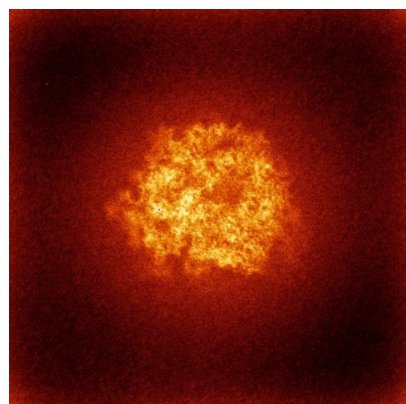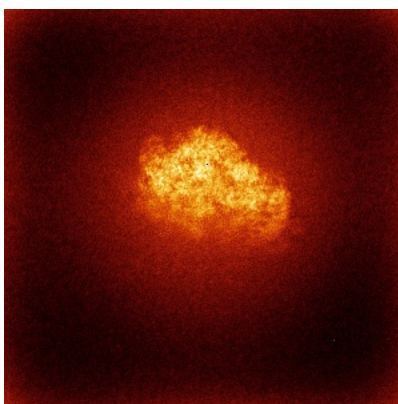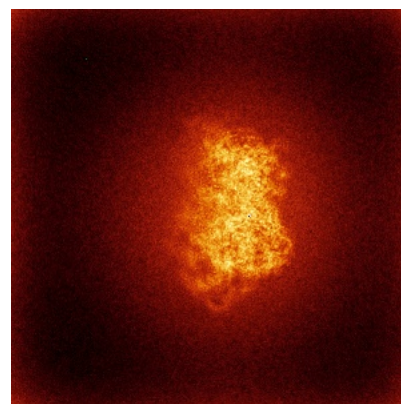
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

| X | Y | Z |

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map
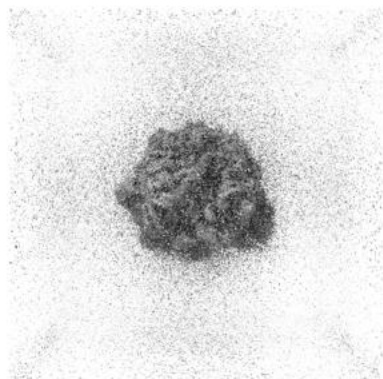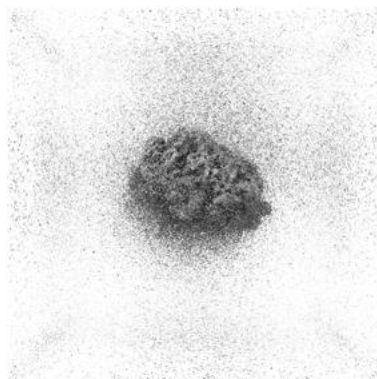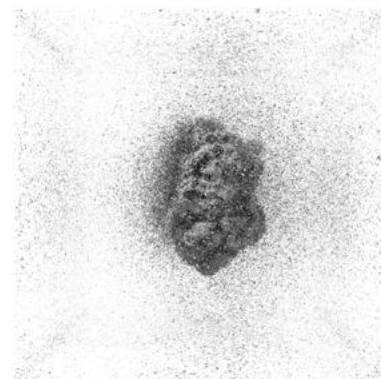
| X | Y | Z |

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

6.6   Mask visualisation ⓘ

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

A mask typically either:

- Encompasses the whole structure

- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure
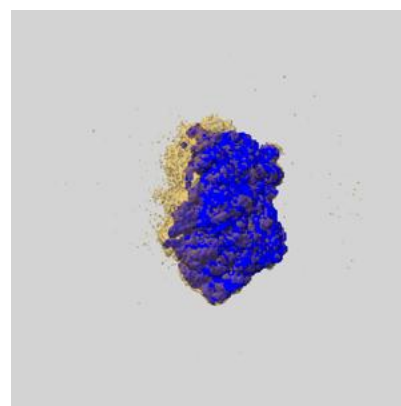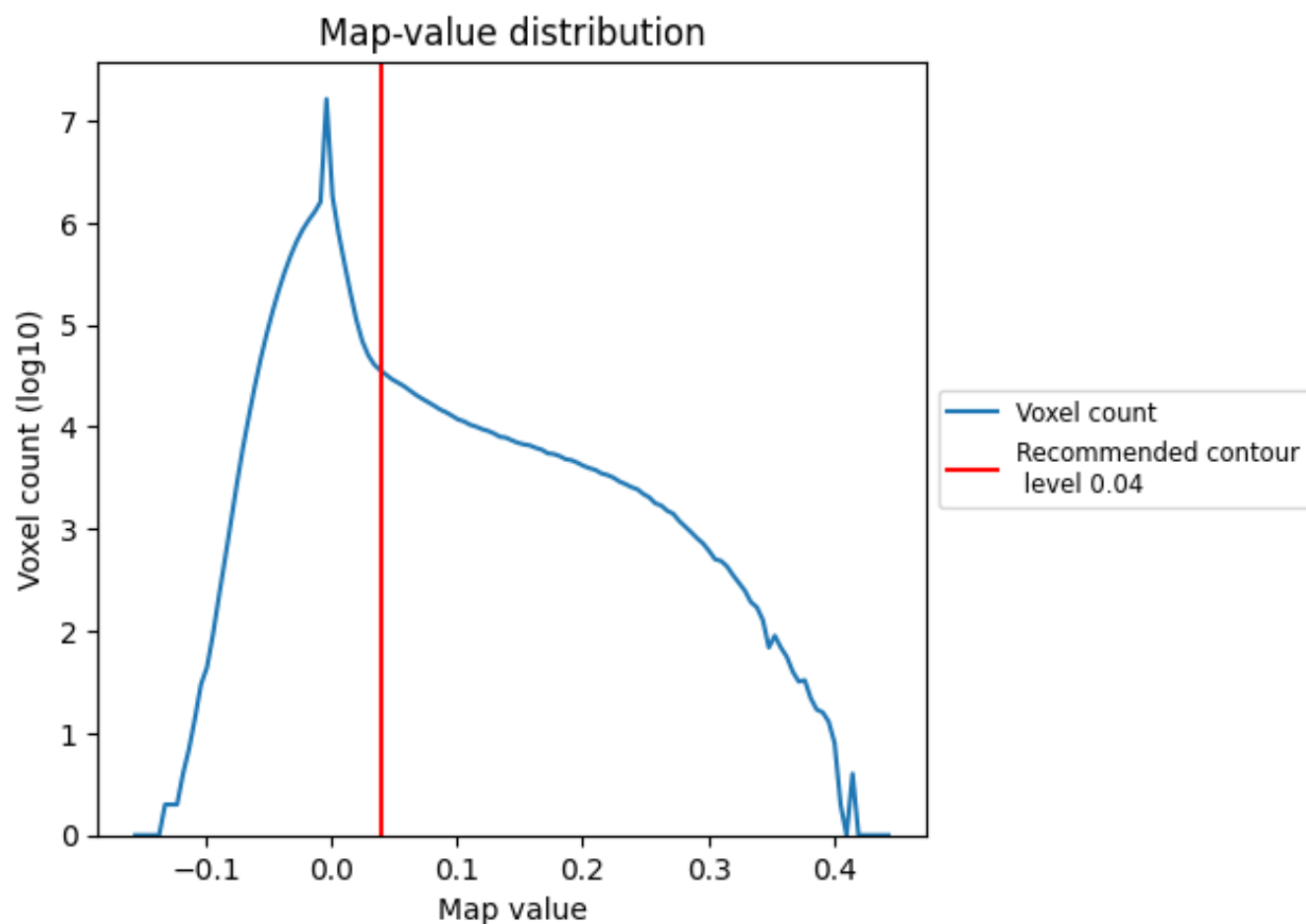
6.6.1   emd_51973_msk_1.map ⓘ
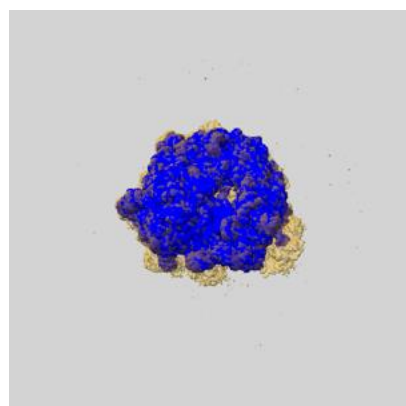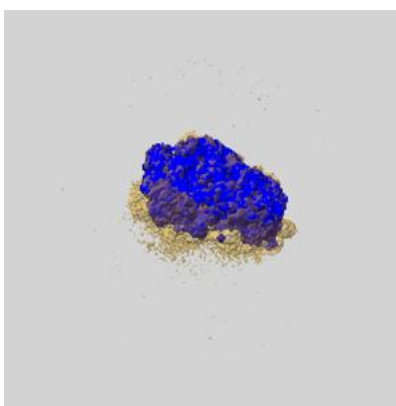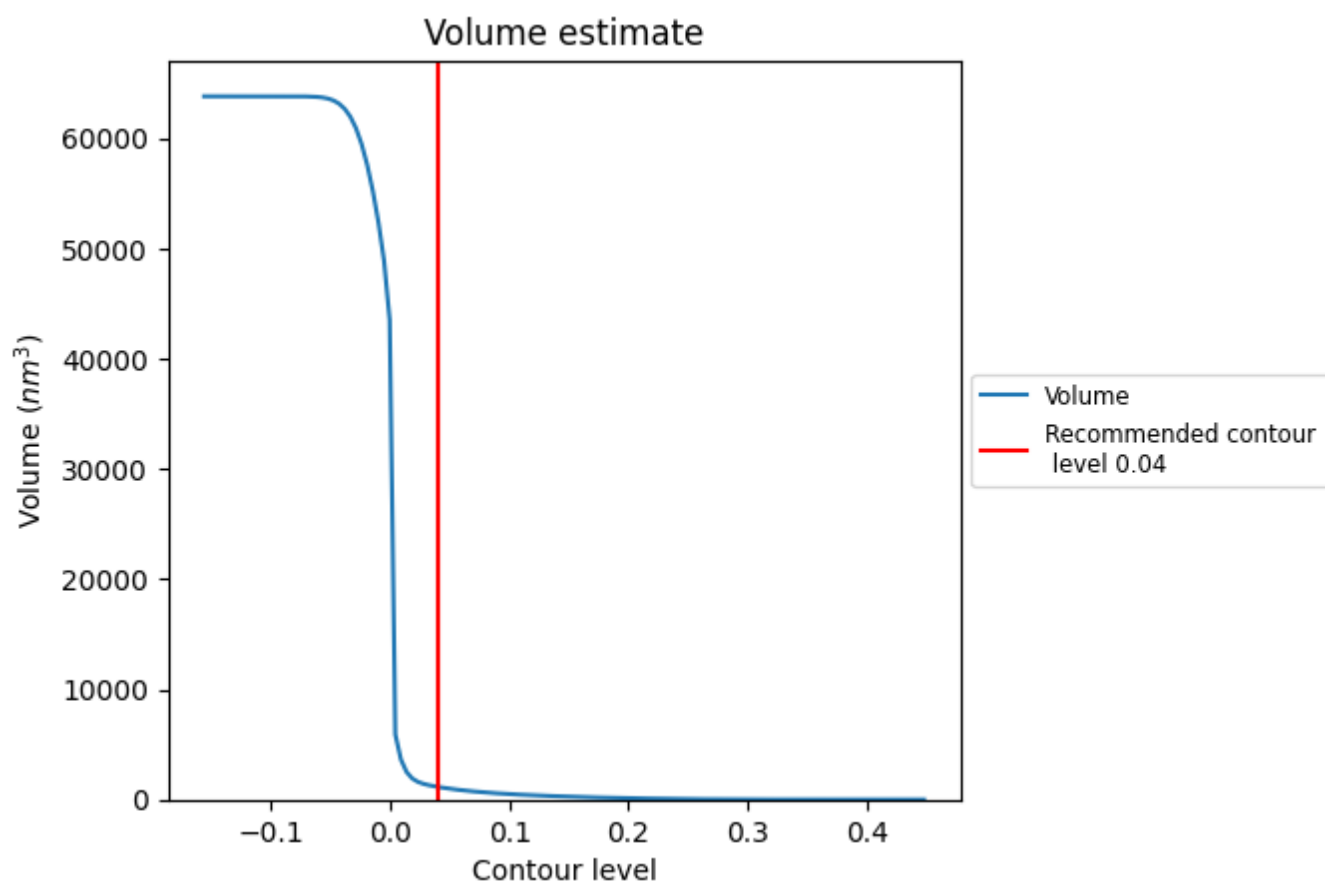

X   Y   Z

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 ⓘ

The volume at the recommended contour level is 1149 nm^3; this corresponds to an approximate mass of 1038 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 ⓘ
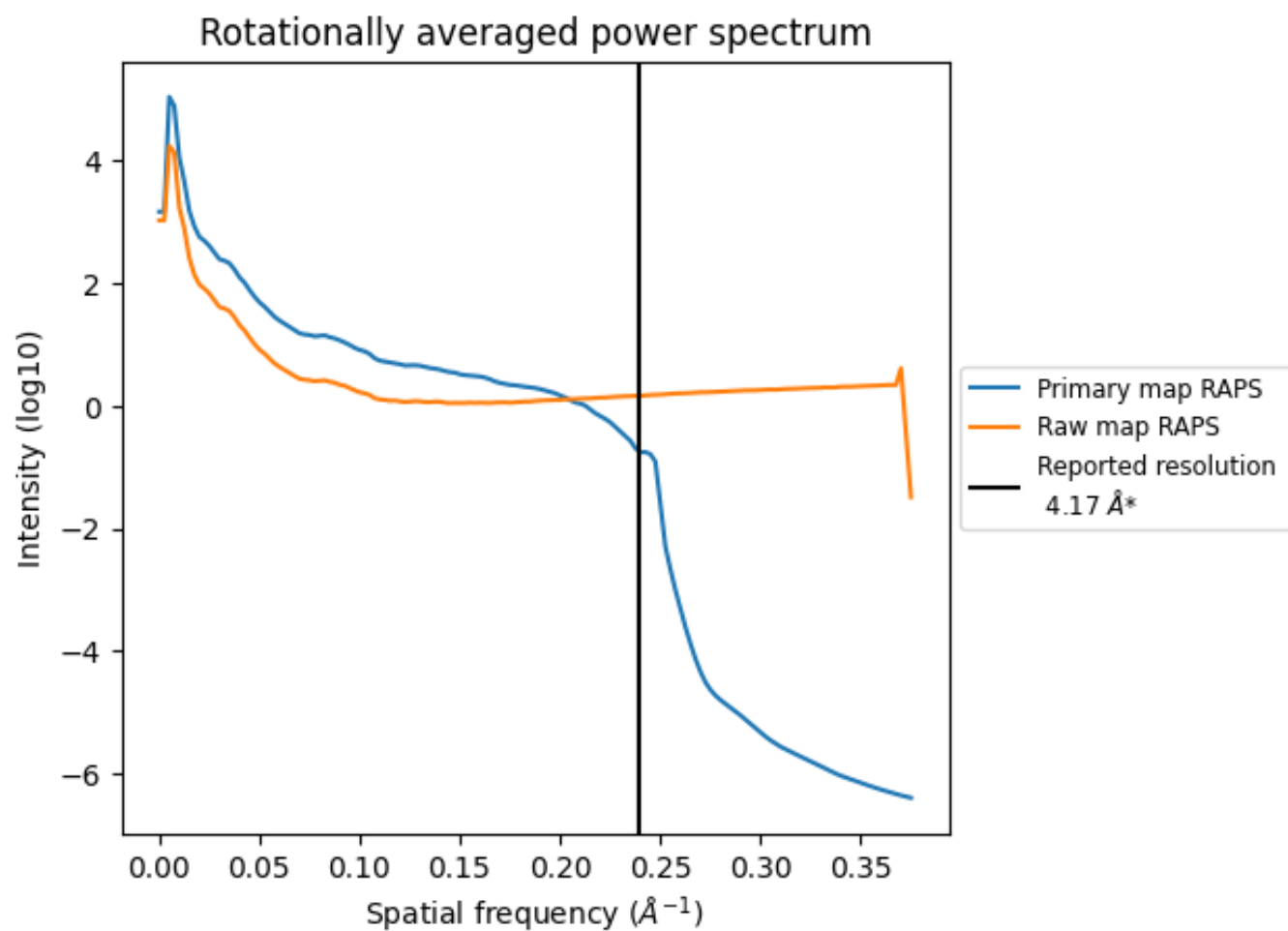
*Reported resolution corresponds to spatial frequency of 0.240 Å^{-1}

8   Fourier-Shell correlation ⓘ

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

8.1   FSC ⓘ
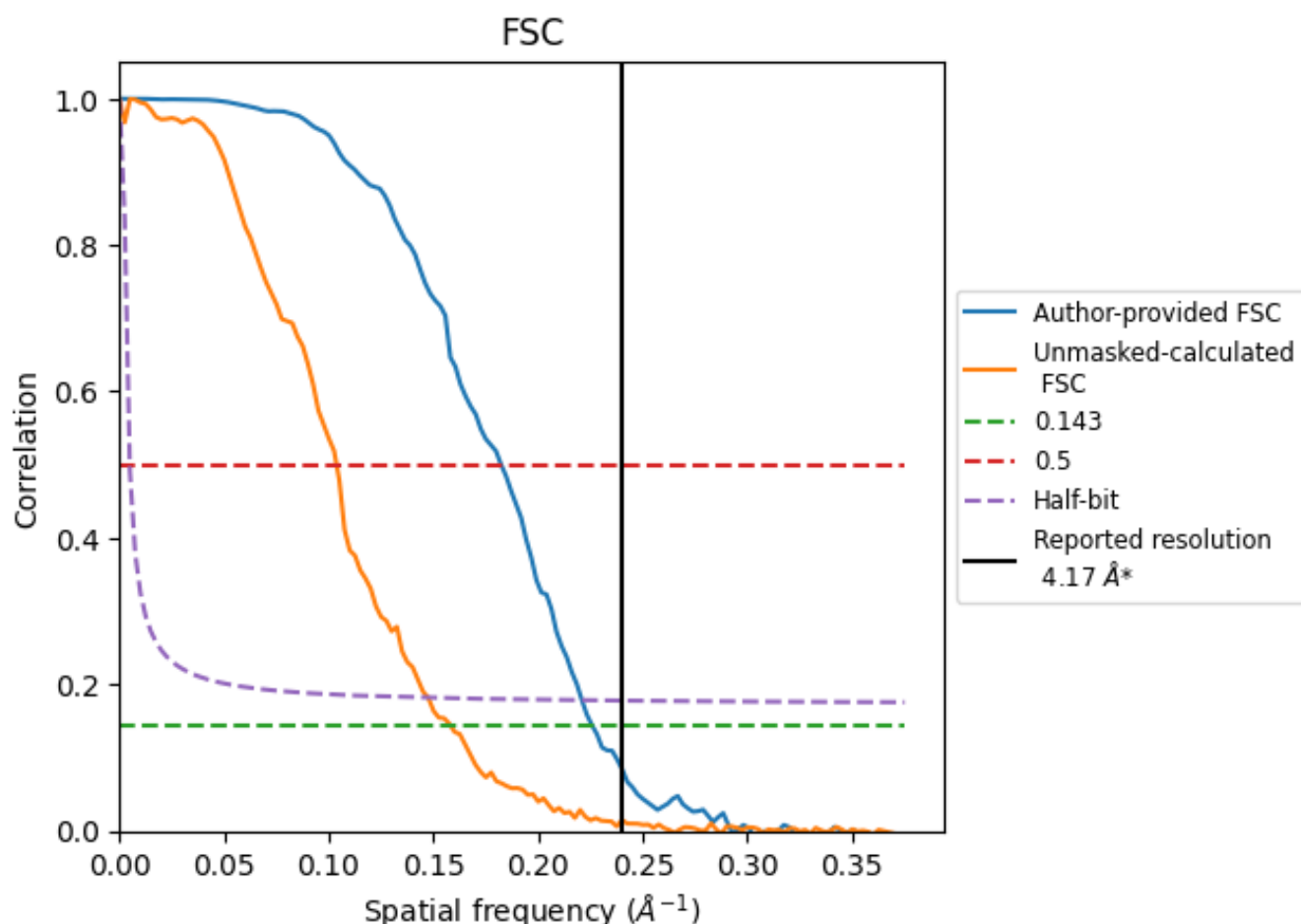
*Reported resolution corresponds to spatial frequency of 0.240 Å^{-1}

8.2   Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.17	-	-
Author-provided FSC curve	4.42	5.48	4.52
Unmasked-calculated*	6.32	9.63	6.77

*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 6.32 differs from the reported value 4.17 by more than 10 %

9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-51973 and PDB model 9HA1. Per-residue inclusion information can be found in section 3 on page 7.

## 9.1 Map-model overlay ⓘ

| X | Y | Z |
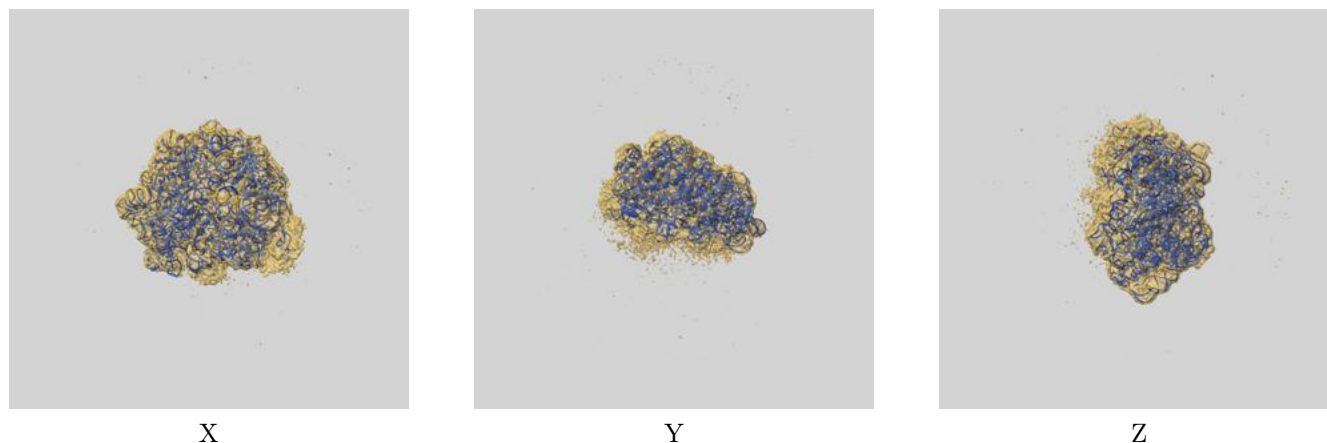
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model ⓘ

X
Y
Z
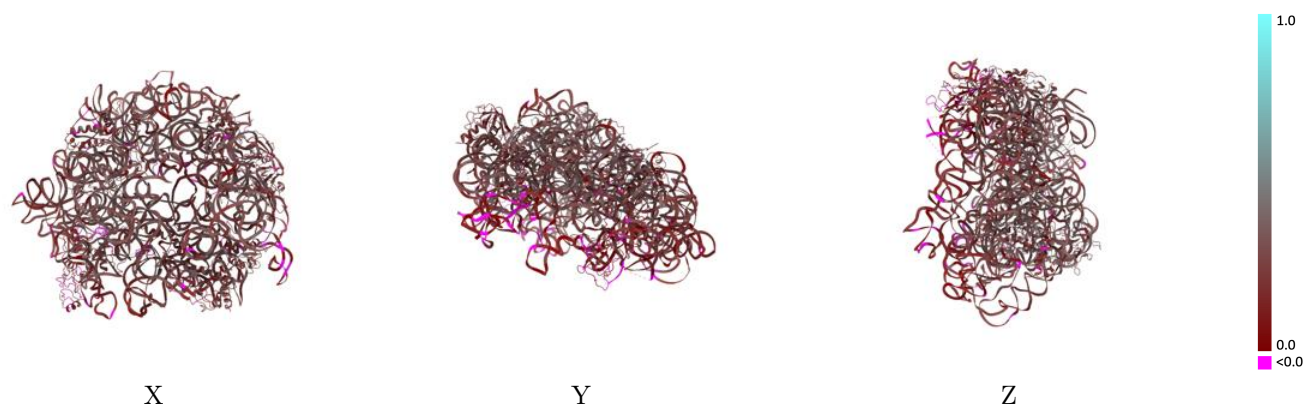
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model ⓘ

X
Y
Z
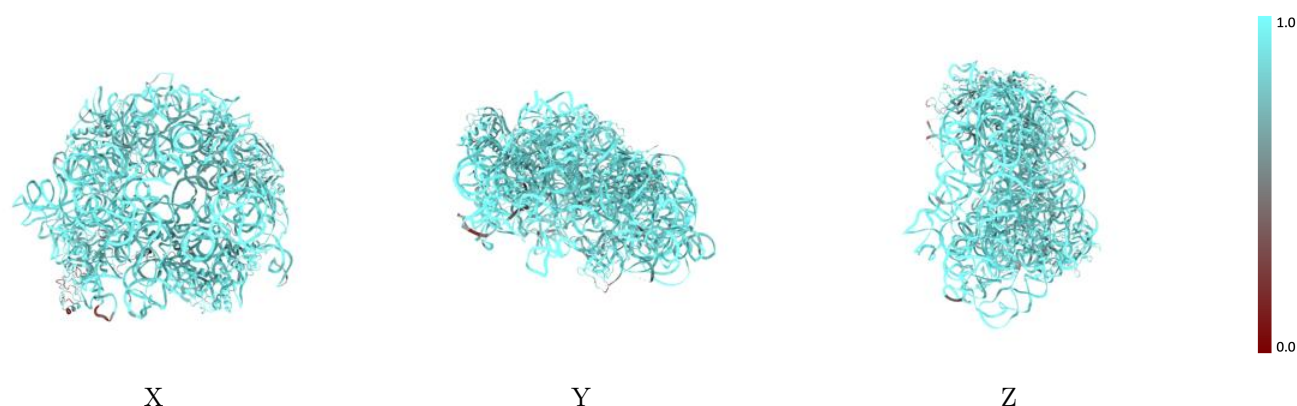
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4   Atom inclusion ⓘ
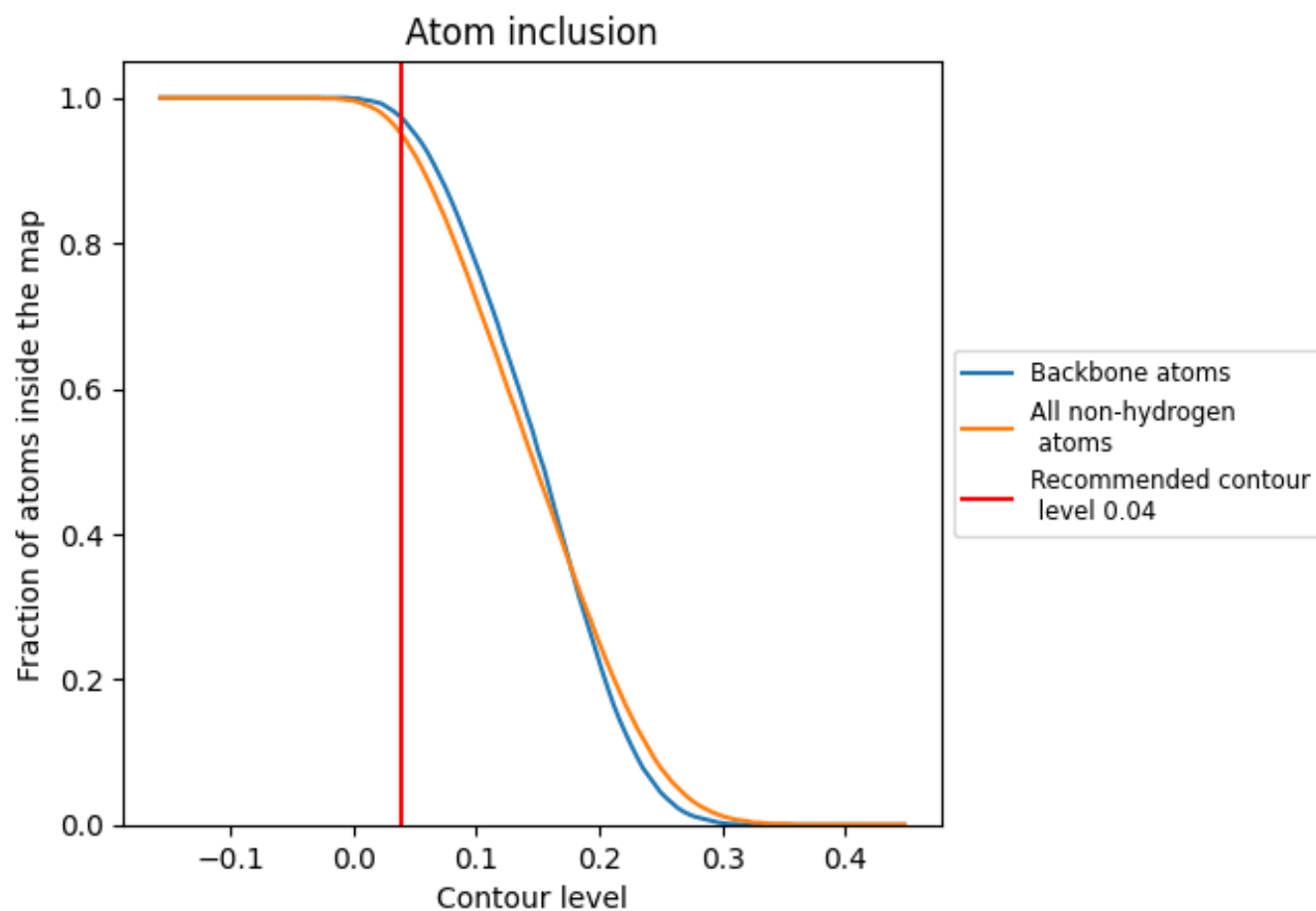
At the recommended contour level, 97% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5　Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9490	0.2470
2	0.9210	0.2860
A	0.9680	0.2510
D	0.9180	0.2740
E	0.8920	0.2620
J	0.9190	0.2830
K	0.8500	0.1300
L	0.6970	0.1090
N	0.9110	0.2460
P	0.8670	0.1870
Q	0.9310	0.2710
R	0.8790	0.2230
T	0.9140	0.2940
U	0.9400	0.3130
Y	0.8870	0.2100
y	0.5180	0.0840

1.0

0.0
<0.0