



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 08:12 PM UTC

PDB ID : 8JO2 / pdb_00008jo2
EMDB ID : EMD-36453
Title : Structural basis of transcriptional activation by the OmpR/PhoB-family response regulator PmrA
Authors : Lou, Y.-C.; Huang, H.-Y.; Chen, C.; Wu, K.-P.
Deposited on : 2023-06-06
Resolution : 2.74 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:

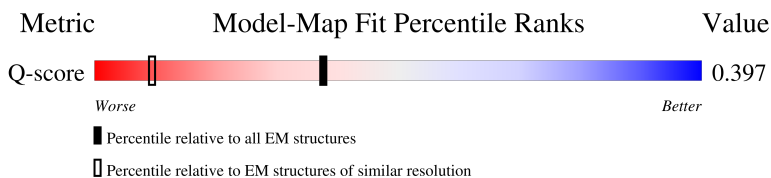
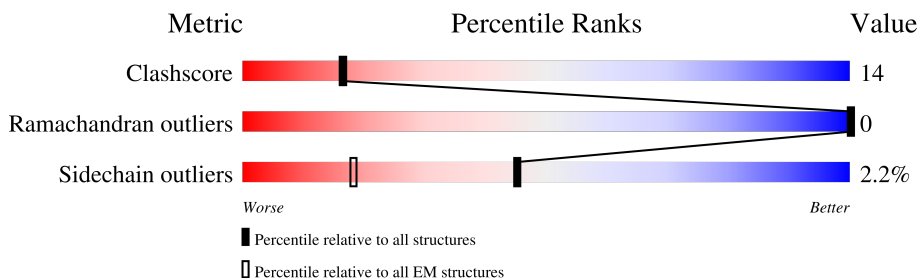
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.74 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10492 (2.24 - 3.24)

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	1	65	74% 46% 54%
2	2	65	82% 58% 40%
3	A	329	51% 19% 30%
3	B	329	9% 48% 21% 31%

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Mol	Chain	Length	Quality of chain
4	C	1342	
5	D	1407	
6	E	91	
7	F	613	
8	H	226	
8	I	226	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 35368 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 DNA chain called DNA (65-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	65	1338	640	242	391	65	0	0

- Molecule 2 is a DNA chain called DNA (65-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	65	1332	638	238	391	65	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	A	230	1786	1112	317	351	6	0	0
3	B	228	1767	1100	312	349	6	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	1340	10570	6631	1841	2055	43	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	1351	10474	6575	1867	1982	50	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerase subunit omega.

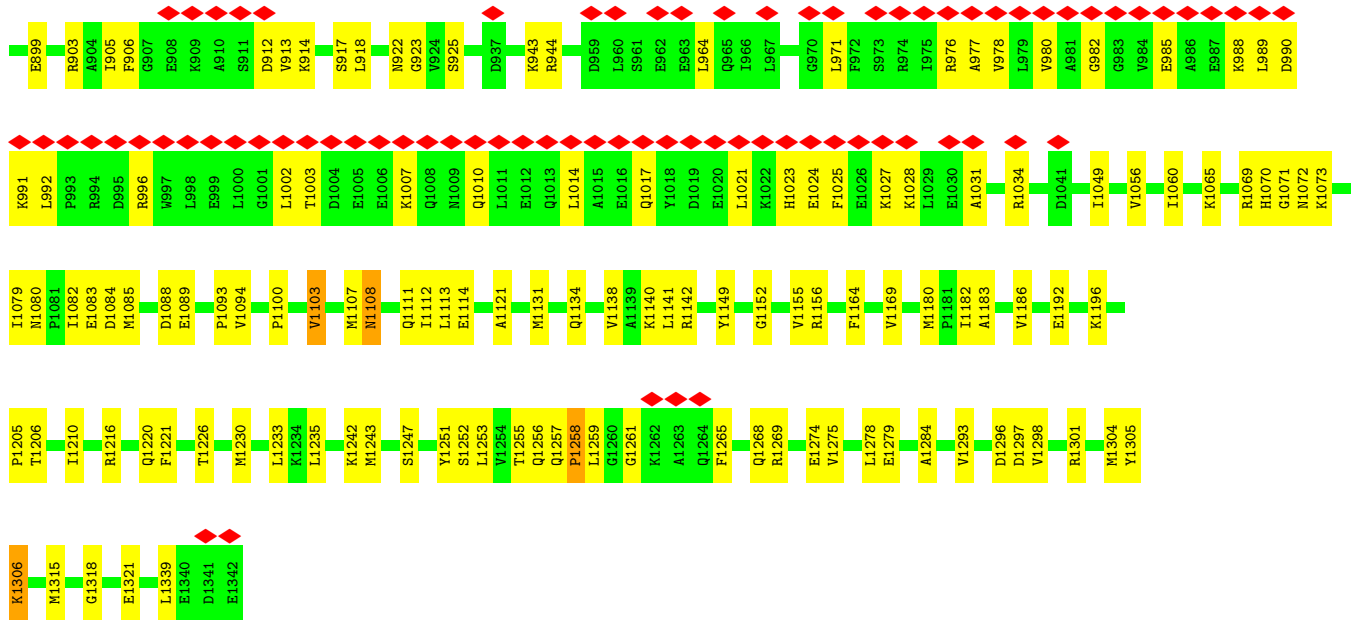
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	79	627	382	118	126	1	0	0

- Molecule 7 is a protein called RNA polymerase sigma factor RpoD.

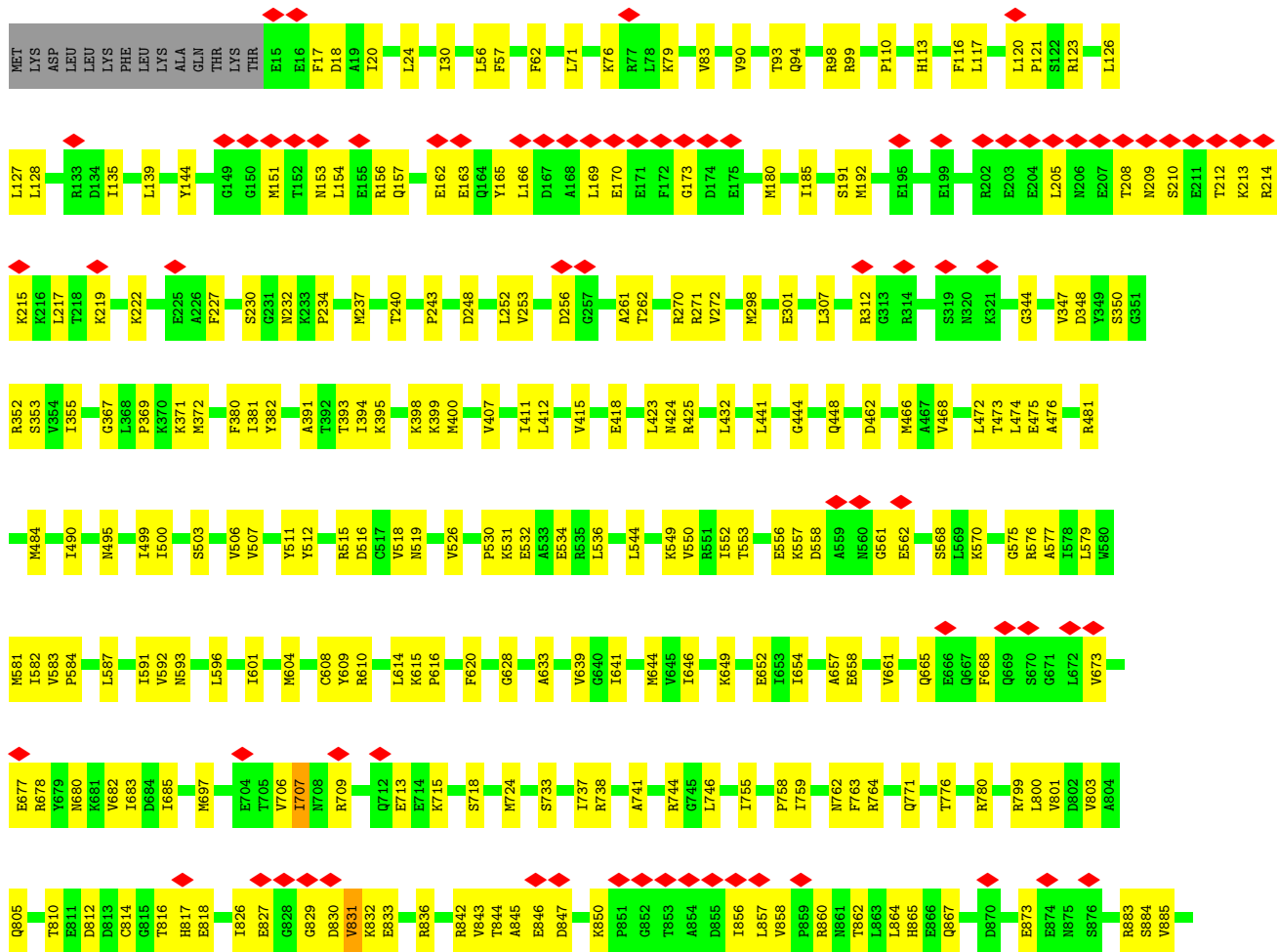
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	F	497	4022	2512	719	768	23	0	0

- Molecule 8 is a protein called DNA-binding transcriptional regulator BasR.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	219	1726	1080	312	326	8	0	0
8	I	219	1726	1080	312	326	8	0	0



● Molecule 5: DNA-directed RNA polymerase subunit beta'



H61	F62	L63	S64	R65	M66	R67	R68	E69	K70	M71	T72	Q73	P74	V75	L76	I77	L78	T79	A80	R81	D82	T83	L84	E85	D86	R87	I88	S89	G90	L91	D92	T93	G94	A95	D96	D97	Y98	L99	V100	K101	P102	F103	A104	L105	E106	E107	L108	N109	A110	R111	I112	R113	A114	L115	L116	R117	R118	H119	N120
N121	Q122	G123	D124	M125	E126	I127	S128	V129	G130	M131	L132	R133	L134	N135	V136	T137	R138	R139	L140	V141	W142	L143	G144	E145	T146	A147	L148	D149	L150	T151	P152	K153	E154	Y155	A156	L157	L158	S159	R160	L161	M162	M163	K164	A165	G166	S167	P168	V169	H170	R171	E172	I173	L174	Y175	N176	D177	I178	Y179	S180
G181	D182	N183	E184	P185	A186	T187	N188	T189	L190	E191	V192	H193	I194	H195	N196	L197	R198	E199	K200	I201	G202	K203	S204	R205	I206	R207	T208	V209	R210	G211	F212	G213	Y214	M215	L216	A217	N218	N219	ASP	ASP	THR	GLU	HIS	LEU	GLU														

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	219627	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	57.1	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.294	Depositor
Minimum map value	-0.936	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.16	Depositor
Map size (\AA)	394.56, 394.56, 394.56	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.82199997, 0.82199997, 0.82199997	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	1	0.39	0/1501	0.62	0/2316
2	2	0.39	0/1493	0.68	1/2302 (0.0%)
3	A	0.63	1/1808 (0.1%)	0.72	1/2450 (0.0%)
3	B	0.62	1/1789 (0.1%)	0.77	0/2425
4	C	0.57	0/10739	0.70	6/14489 (0.0%)
5	D	0.56	0/10632	0.70	3/14357 (0.0%)
6	E	0.35	0/629	0.40	0/847
7	F	0.43	0/4076	0.66	2/5482 (0.0%)
8	H	0.47	0/1750	0.71	2/2366 (0.1%)
8	I	0.53	0/1750	0.74	1/2366 (0.0%)
All	All	0.54	2/36167 (0.0%)	0.70	16/49400 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	52	PRO	C-O	-6.03	1.17	1.23
3	B	223	ILE	C-O	5.64	1.30	1.24

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1079	ILE	CA-C-N	8.57	132.16	120.67
4	C	1079	ILE	C-N-CA	8.57	132.16	120.67
4	C	519	ASN	CB-CA-C	-7.01	100.96	110.22
7	F	401	PHE	CA-CB-CG	6.58	120.38	113.80
5	D	503	SER	CA-C-N	-6.15	109.80	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1338	0	737	37	0
2	2	1332	0	737	29	0
3	A	1786	0	1813	53	0
3	B	1767	0	1789	53	0
4	C	10570	0	10582	275	0
5	D	10474	0	10678	336	0
6	E	627	0	634	22	0
7	F	4022	0	4083	148	0
8	H	1726	0	1755	58	0
8	I	1726	0	1755	59	0
All	All	35368	0	34563	983	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 14.

The worst 5 of 983 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)
8:H:117:ARG:HD2	8:H:125:ASN:OD1	1.49	1.11
5:D:826:ILE:HG12	5:D:831:VAL:HG13	1.48	0.95
8:H:126:GLU:HG2	8:H:135:ASN:OD1	1.66	0.94
7:F:309:ASN:HD22	7:F:315:TRP:HB3	1.32	0.94
3:A:22:THR:CG2	3:A:207:THR:H	1.81	0.92

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	
3	A	228/329 (69%)	207 (91%)	21 (9%)	0	100	100
3	B	226/329 (69%)	213 (94%)	13 (6%)	0	100	100
4	C	1338/1342 (100%)	1253 (94%)	85 (6%)	0	100	100
5	D	1347/1407 (96%)	1249 (93%)	98 (7%)	0	100	100
6	E	77/91 (85%)	77 (100%)	0	0	100	100
7	F	493/613 (80%)	455 (92%)	38 (8%)	0	100	100
8	H	217/226 (96%)	209 (96%)	8 (4%)	0	100	100
8	I	217/226 (96%)	203 (94%)	14 (6%)	0	100	100
All	All	4143/4563 (91%)	3866 (93%)	277 (7%)	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	
3	A	198/286 (69%)	194 (98%)	4 (2%)	48	67
3	B	196/286 (68%)	191 (97%)	5 (3%)	40	62
4	C	1155/1157 (100%)	1128 (98%)	27 (2%)	44	65
5	D	1124/1168 (96%)	1096 (98%)	28 (2%)	42	63
6	E	67/75 (89%)	67 (100%)	0	100	100
7	F	439/540 (81%)	432 (98%)	7 (2%)	55	72
8	H	188/195 (96%)	183 (97%)	5 (3%)	39	61
8	I	188/195 (96%)	185 (98%)	3 (2%)	55	72
All	All	3555/3902 (91%)	3476 (98%)	79 (2%)	45	65

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	D	1152	GLU
8	H	50	LEU
5	D	1180	VAL
7	F	110	LEU
8	H	127	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
5	D	186	GLN
7	F	600	HIS
5	D	929	GLN
8	I	121	ASN
7	F	309	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

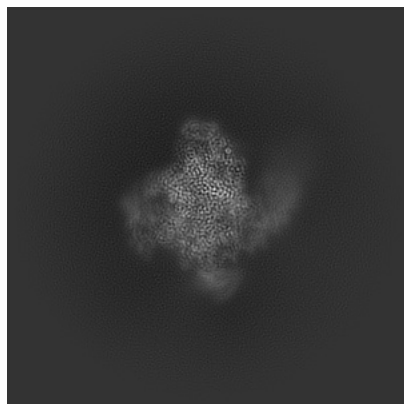
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36453. These allow visual inspection of the internal detail of the map and identification of artifacts.

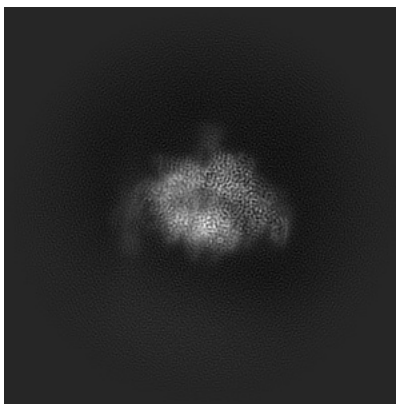
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

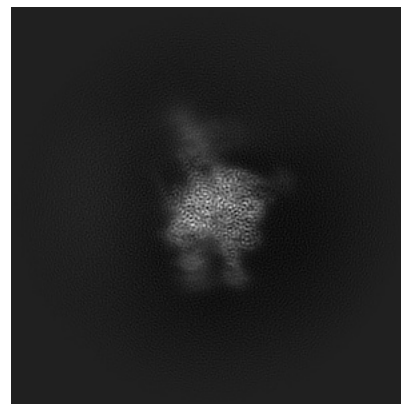
6.1.1 Primary map



X

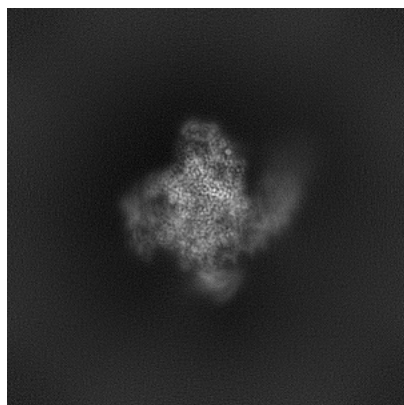


Y

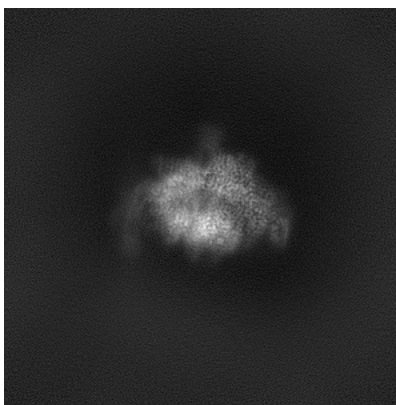


Z

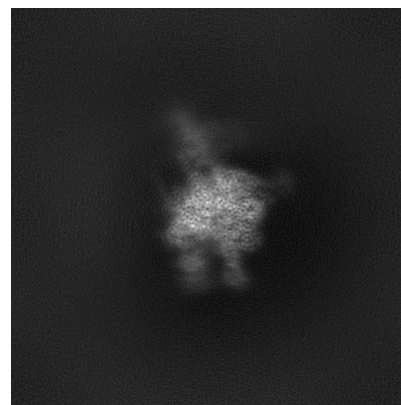
6.1.2 Raw map



X



Y

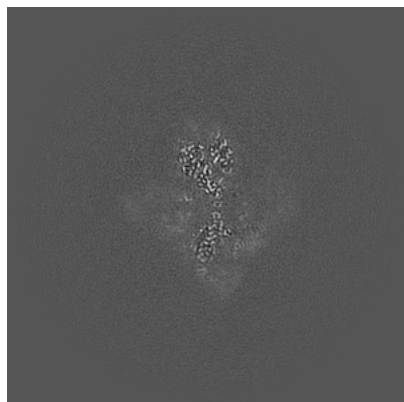


Z

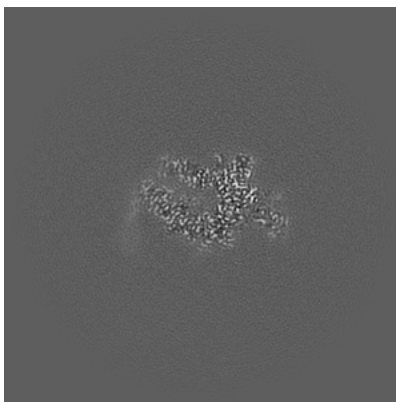
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

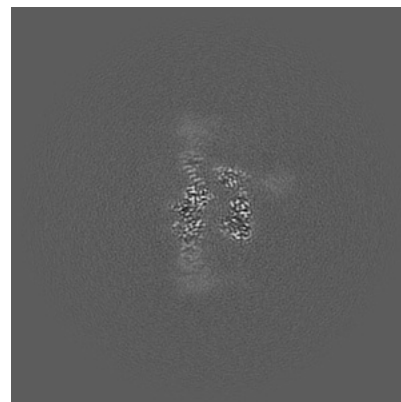
6.2.1 Primary map



X Index: 240

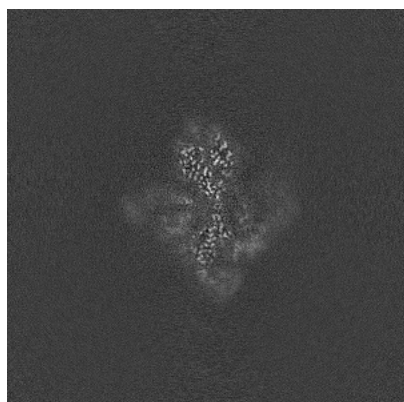


Y Index: 240

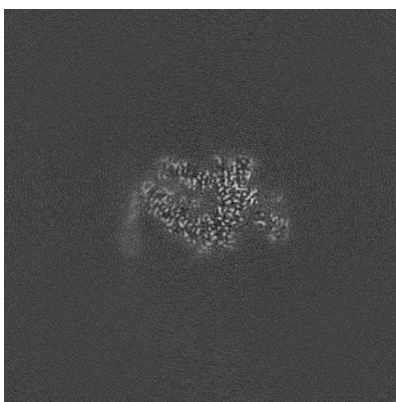


Z Index: 240

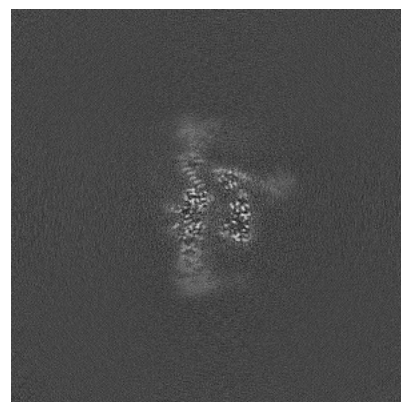
6.2.2 Raw map



X Index: 240



Y Index: 240

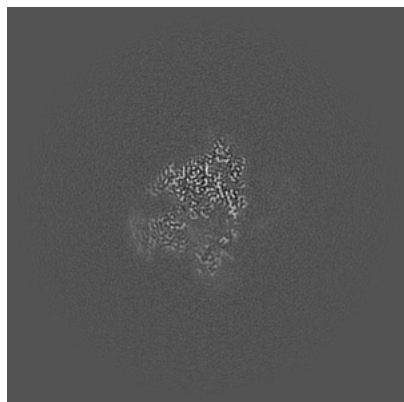


Z Index: 240

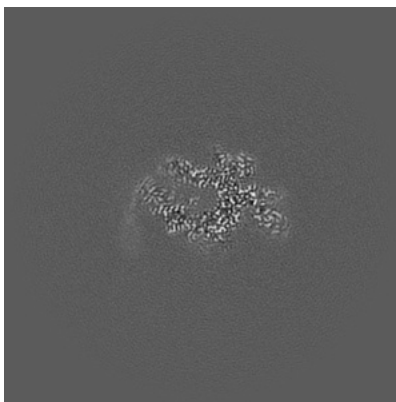
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

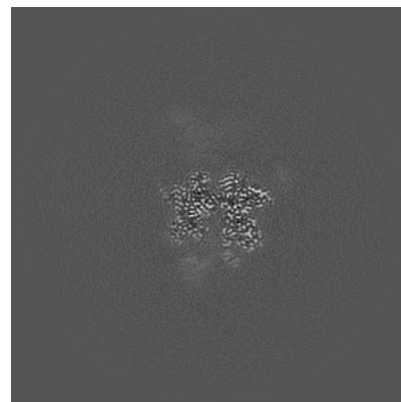
6.3.1 Primary map



X Index: 263

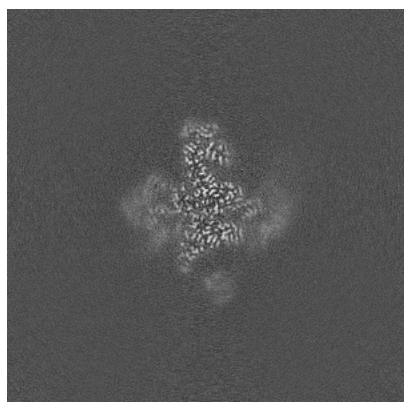


Y Index: 243

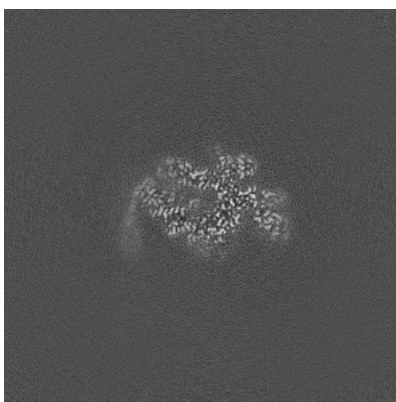


Z Index: 258

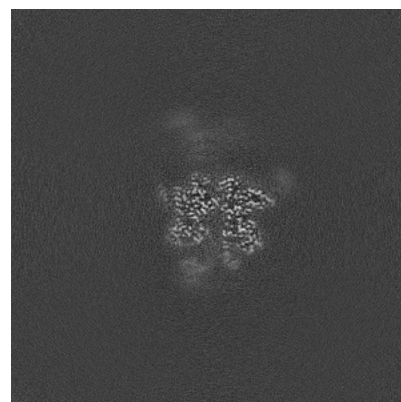
6.3.2 Raw map



X Index: 223



Y Index: 243

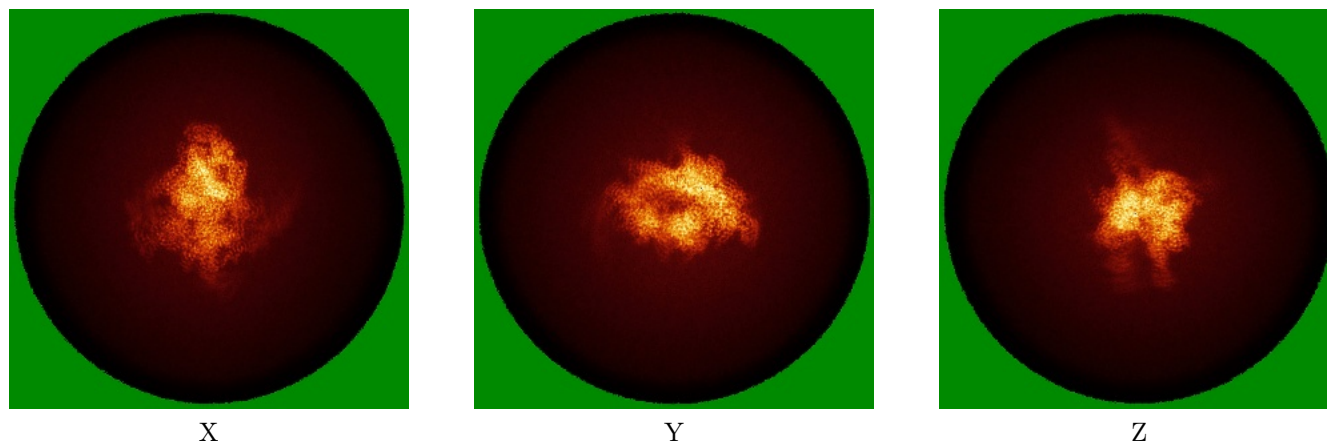


Z Index: 257

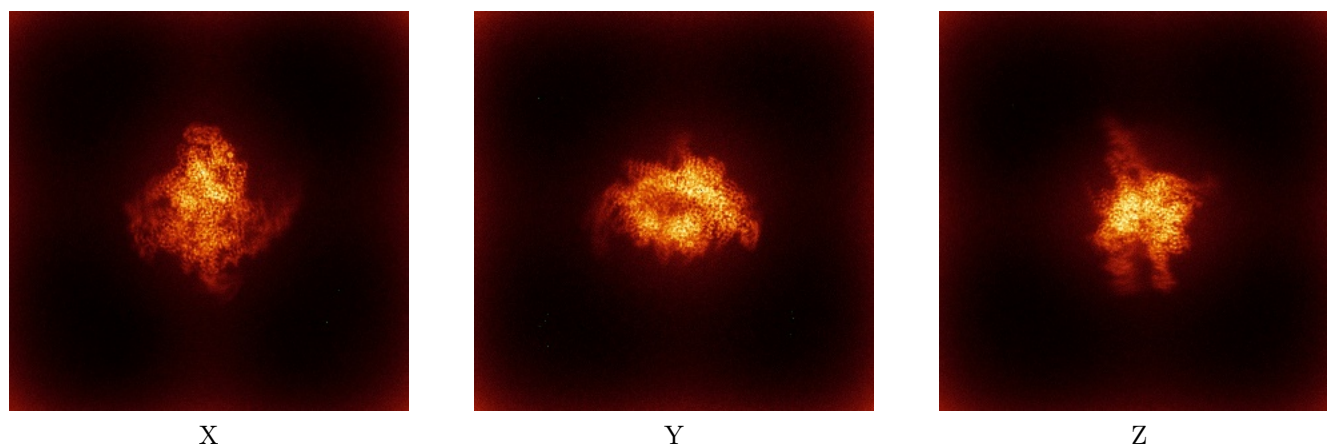
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



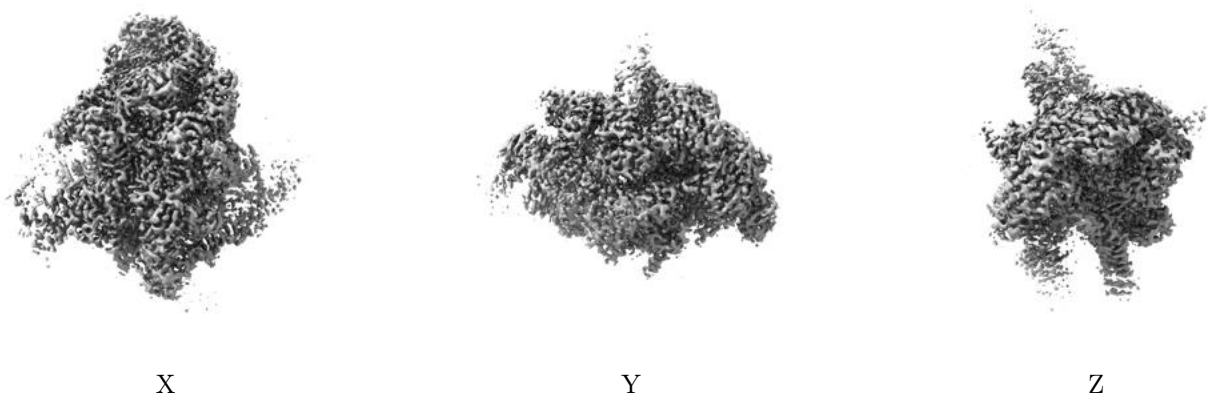
6.4.2 Raw map



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.

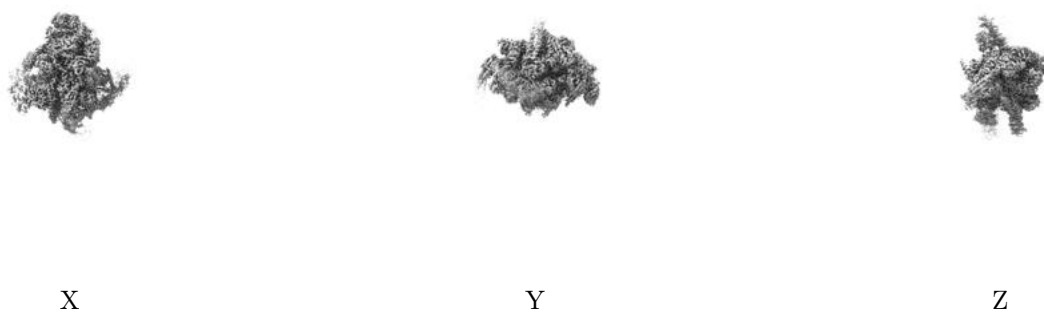
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

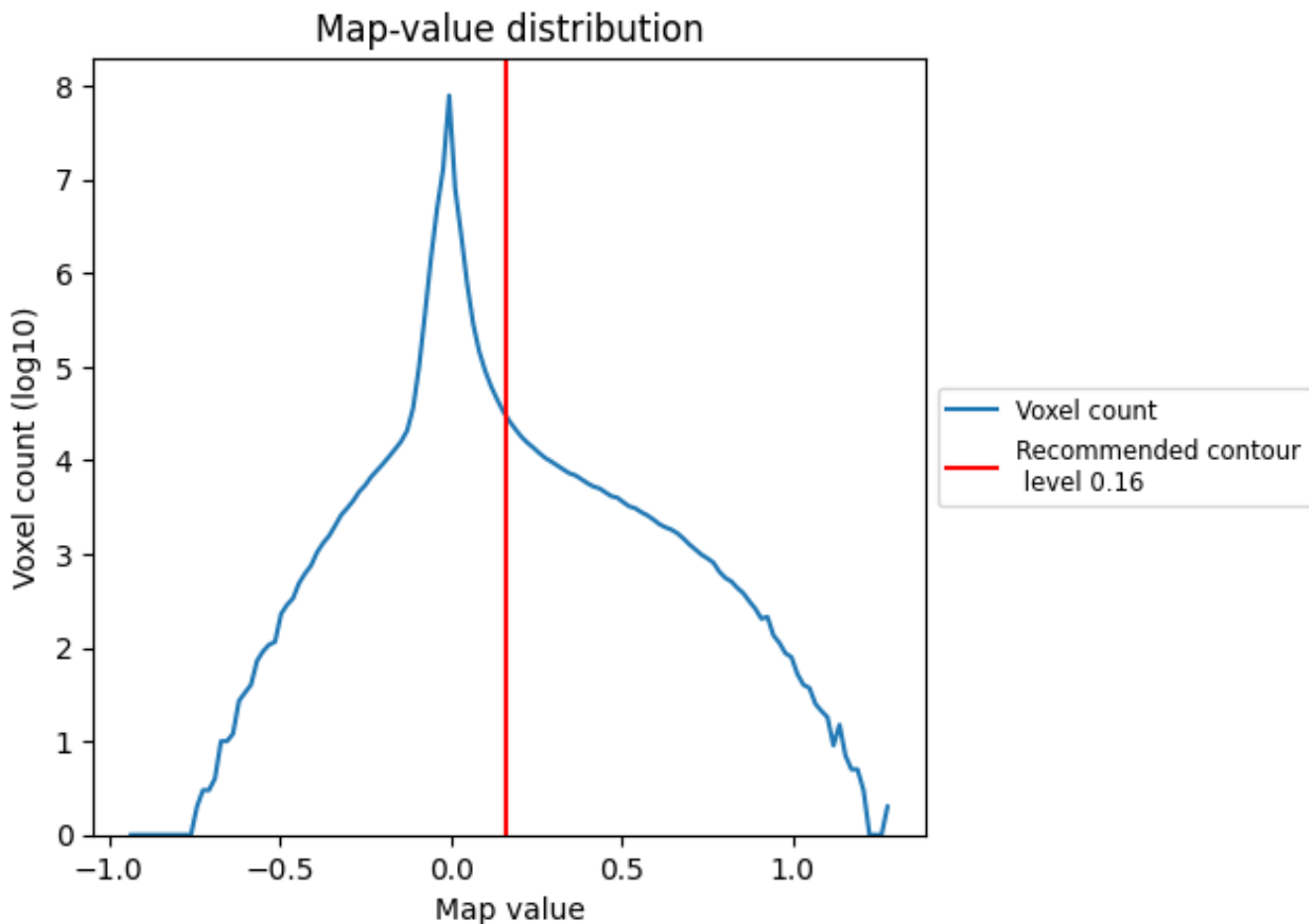
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

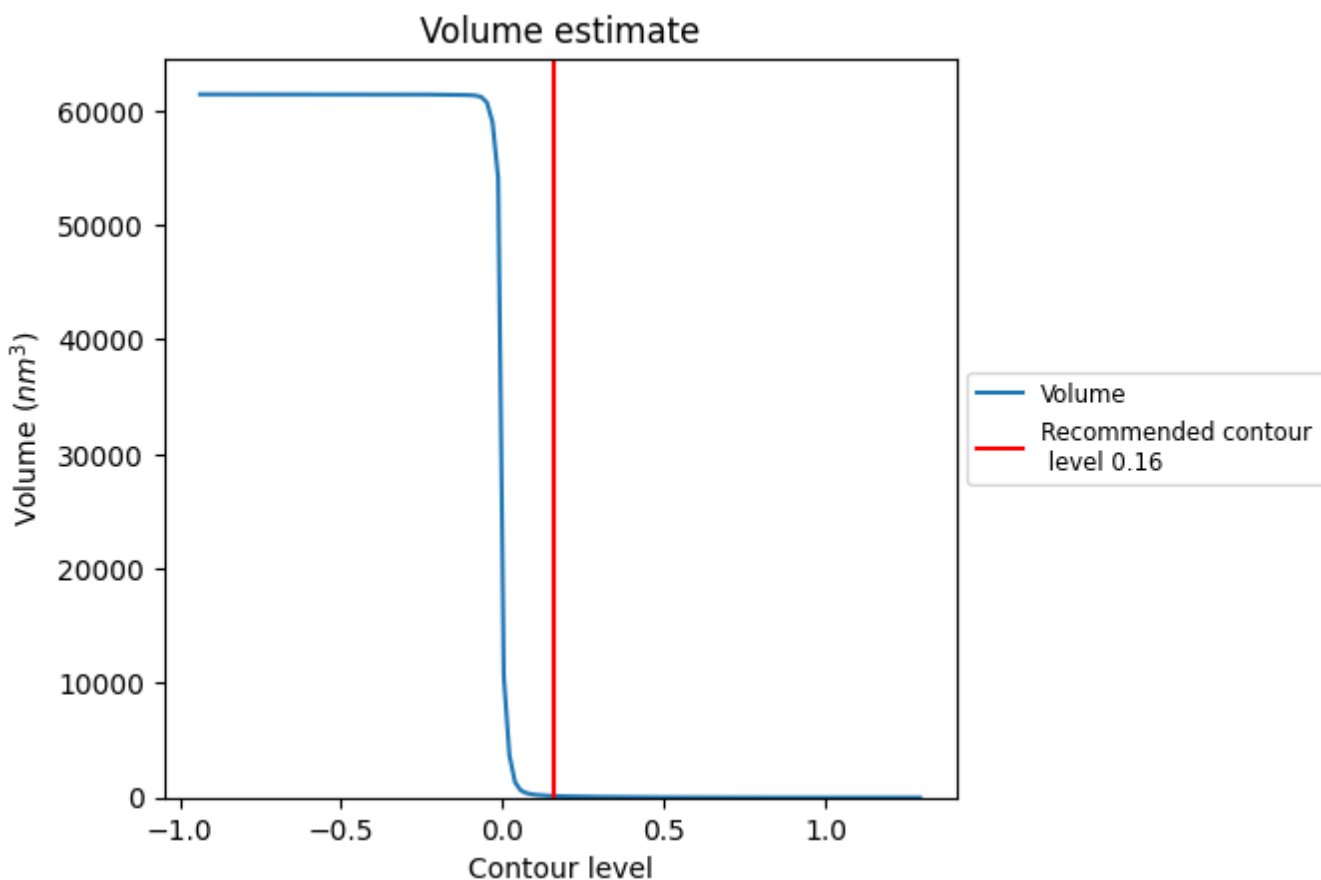
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

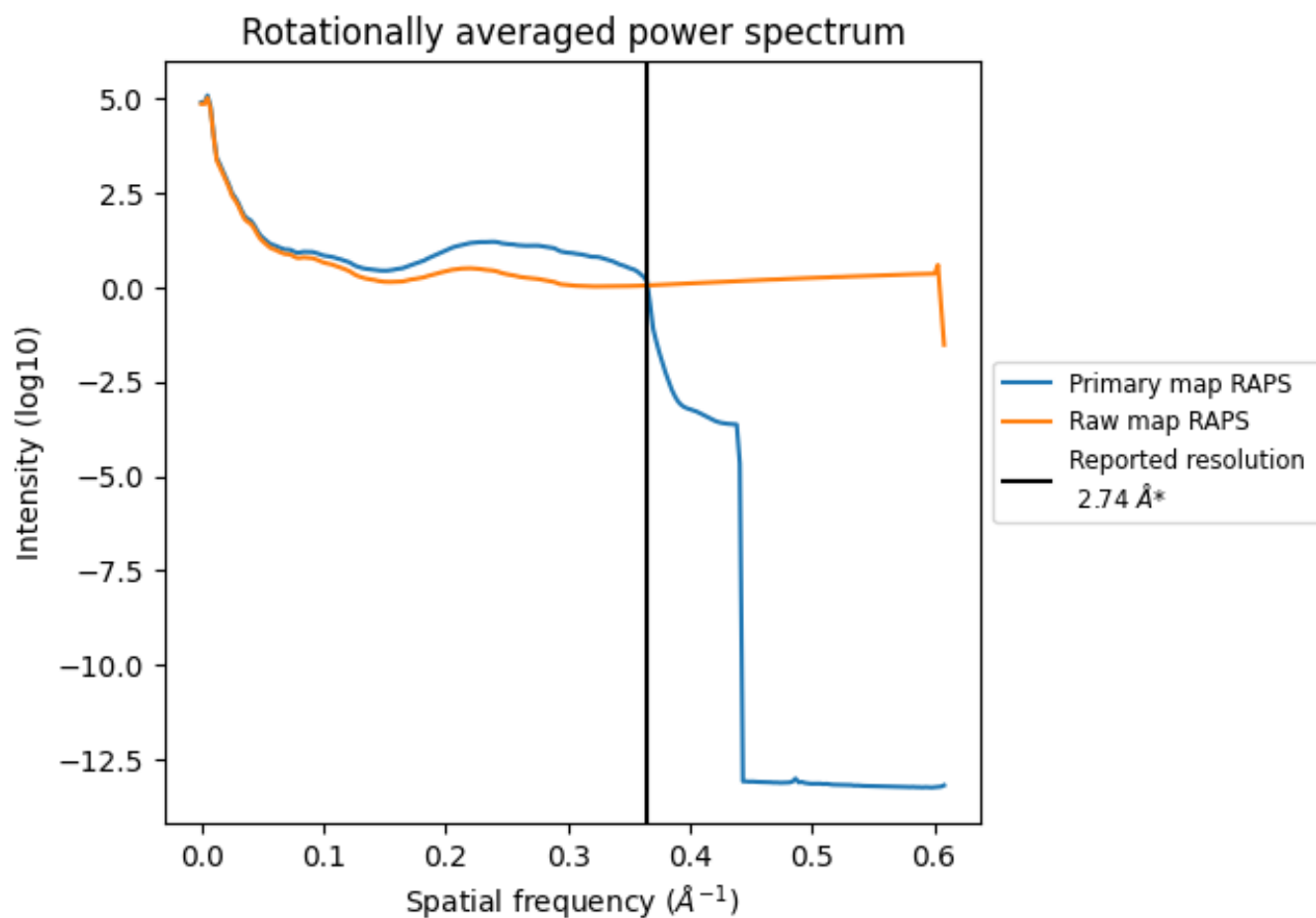
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 137 nm³; this corresponds to an approximate mass of 124 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](#)

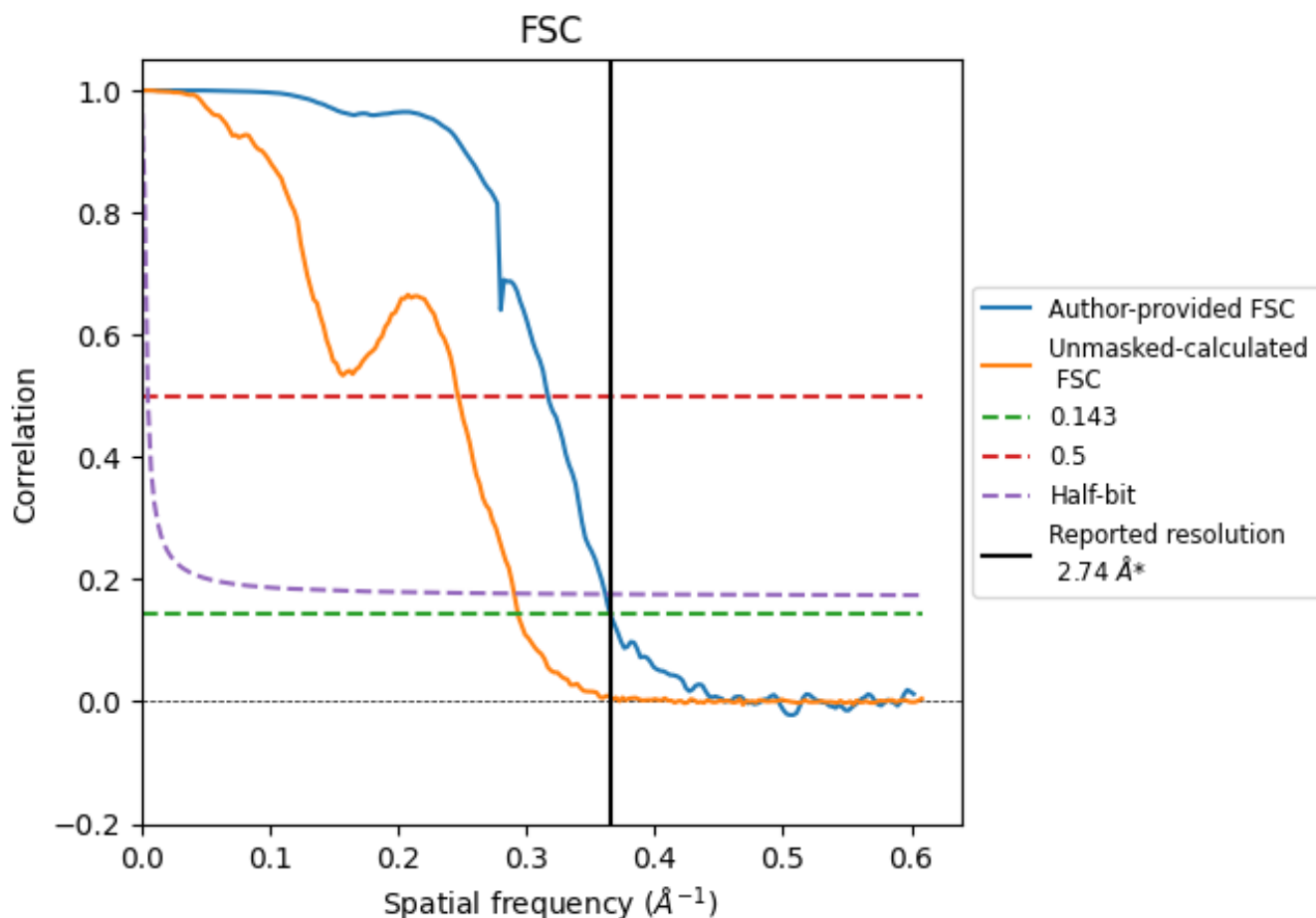


*Reported resolution corresponds to spatial frequency of 0.365 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.365 Å⁻¹

8.2 Resolution estimates

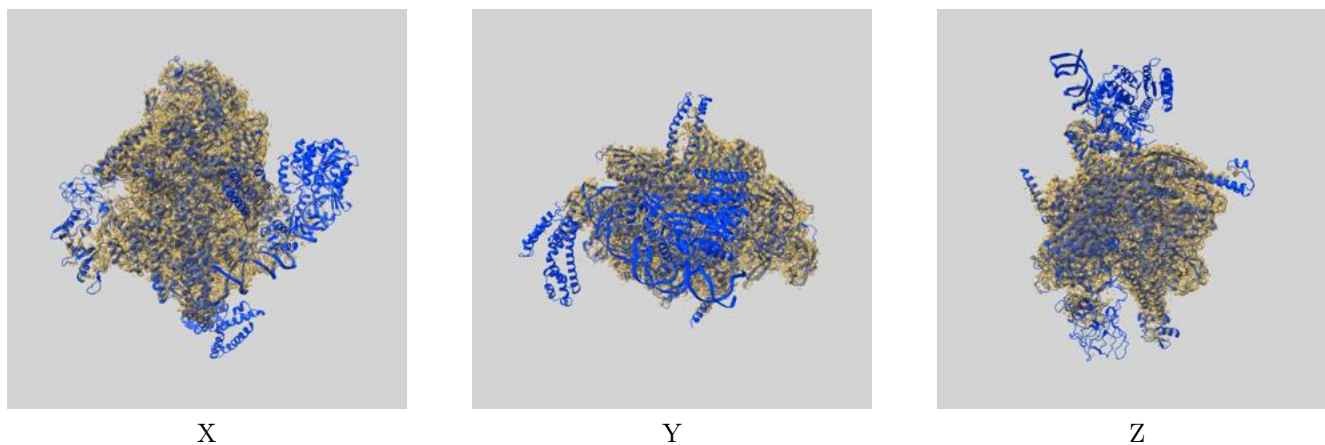
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.74	-	-
Author-provided FSC curve	2.74	3.16	2.77
Unmasked-calculated*	3.41	4.05	3.44

*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 3.41 differs from the reported value 2.74 by more than 10 %

9 Map-model fit [i](#)

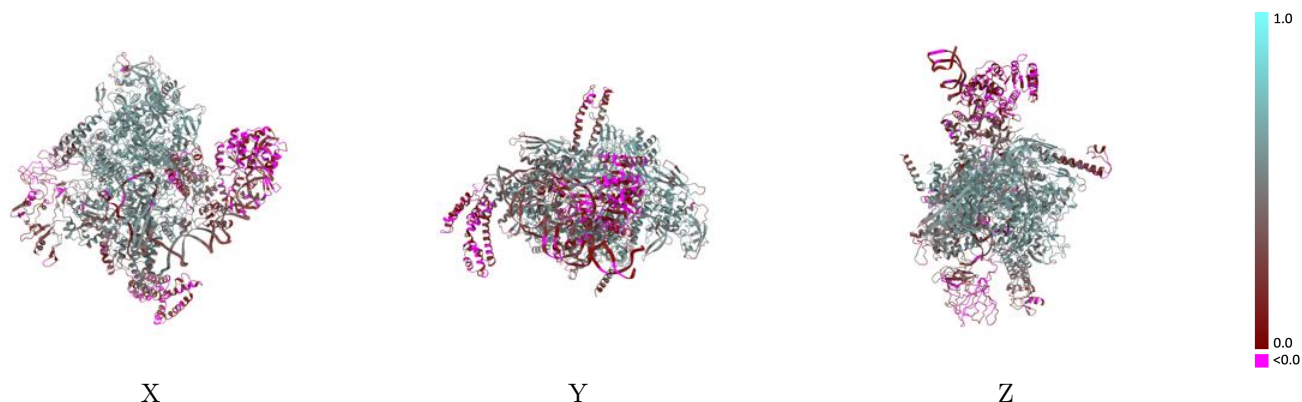
This section contains information regarding the fit between EMDB map EMD-36453 and PDB model 8JO2. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



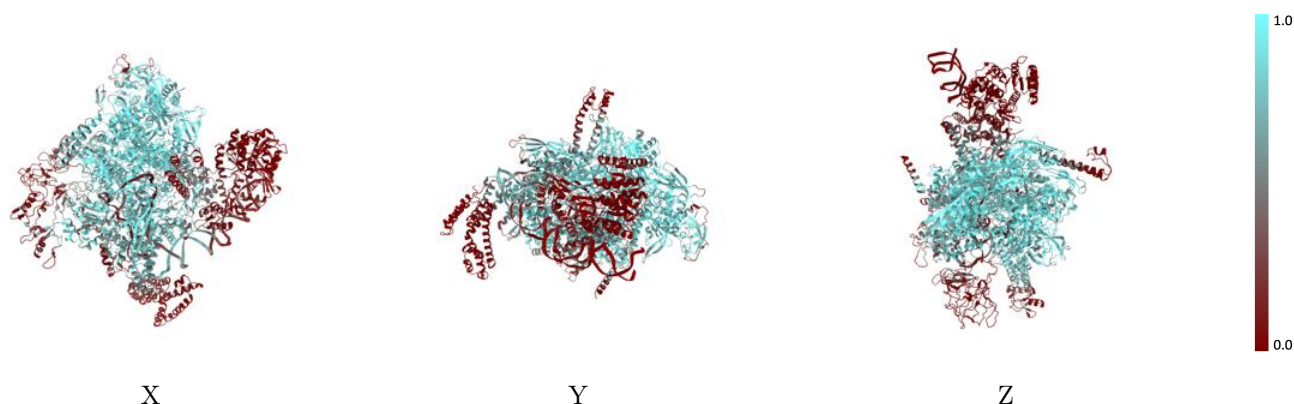
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



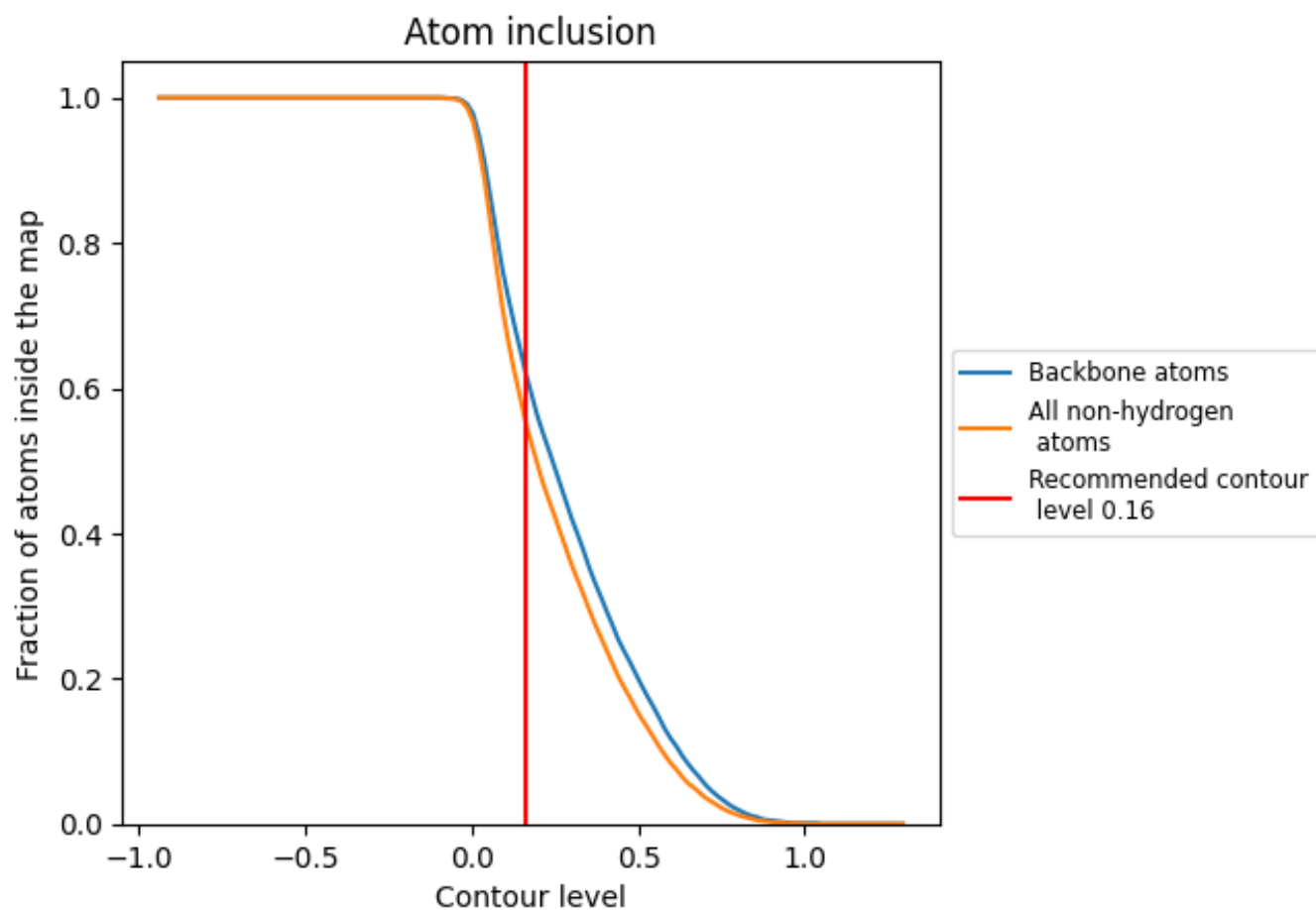
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.16).























9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 56% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5580	 0.3970
1	 0.2620	 0.2230
2	 0.1850	 0.1860
A	 0.8280	 0.5480
B	 0.7130	 0.4890
C	 0.7330	 0.5000
D	 0.6610	 0.4540
E	 0.6630	 0.4980
F	 0.3090	 0.2440
H	 0.0060	 0.0740
I	 0.0320	 0.1060

