



wwPDB EM Validation Summary Report

Dec 10, 2022 – 12:49 pm GMT


PDB ID : 6RD8
EMDB ID : EMD-4809
Title : CryoEM structure of Polytomella F-ATP synthase, c-ring position 2, focussed refinement of Fo and peripheral stalk
Authors : Murphy, B.J.; Klusch, N.; Yildiz, O.; Kuhlbrandt, W.
Deposited on : 2019-04-12
Resolution : 3.08 Å(reported)

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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) : 2.31.3

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Mol	Chain	Length	Quality of chain
8	B	127	 8% 45% 13% 42%
8	C	127	 15% 42% 17% 42%
8	D	127	 20% 47% 11% 42%
8	E	127	 17% 48% 10% 42%
8	F	127	 20% 47% 11% 42%
8	G	127	 22% 52% 6% 42%
8	H	127	 17% 50% 9% 42%
8	I	127	 14% 50% 9% 42%
8	J	127	 10% 48% 10% 42%
9	M	327	 8% 56% 9% 34%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 17312 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 ASA-10: Polytomella F-ATP synthase associated subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	81	605	387	105	110	3	0	0

- Molecule 2 is a protein called ATP synthase associated protein ASA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	595	4661	2958	798	900	5	0	0

- Molecule 3 is a protein called Mitochondrial F1F0 ATP synthase associated 32 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	245	1874	1204	299	370	1	0	0

- Molecule 4 is a protein called Mitochondrial F1F0 ATP synthase associated 14 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	5	123	986	640	172	170	4	0	0

- Molecule 5 is a protein called Mitochondrial ATP synthase subunit ASA6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	6	124	926	599	154	172	1	0	0

- Molecule 6 is a protein called Mitochondrial ATP synthase subunit ASA8.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	8	88	692	456	115	121	0	0

- Molecule 7 is a protein called ASA-9: Polytomella F-ATP synthase associated subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	9	96	768	510	122	130	6	0	0

- Molecule 8 is a protein called Mitochondrial ATP synthase subunit c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	A	74	515	340	83	89	3	0	0
8	B	74	514	340	83	88	3	0	0
8	C	74	514	340	83	88	3	0	0
8	D	74	514	340	83	88	3	0	0
8	E	74	514	340	83	88	3	0	0
8	F	74	514	340	83	88	3	0	0
8	G	74	514	340	83	88	3	0	0
8	H	74	514	340	83	88	3	0	0
8	I	74	514	340	83	88	3	0	0
8	J	74	514	340	83	88	3	0	0

- Molecule 9 is a protein called Mitochondrial ATP synthase subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	M	217	1640	1077	267	288	8	0	0

- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
10	M	1	1	1	0


- Molecule 11 is water.

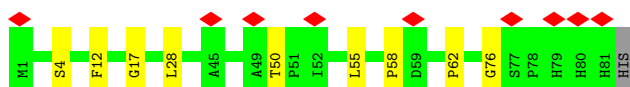
Mol	Chain	Residues	Atoms	AltConf
11	0	2	Total O 2 2	0
11	1	1	Total O 1 1	0
11	3	2	Total O 2 2	0
11	5	2	Total O 2 2	0
11	6	1	Total O 1 1	0
11	A	1	Total O 1 1	0
11	M	9	Total O 9 9	0

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.

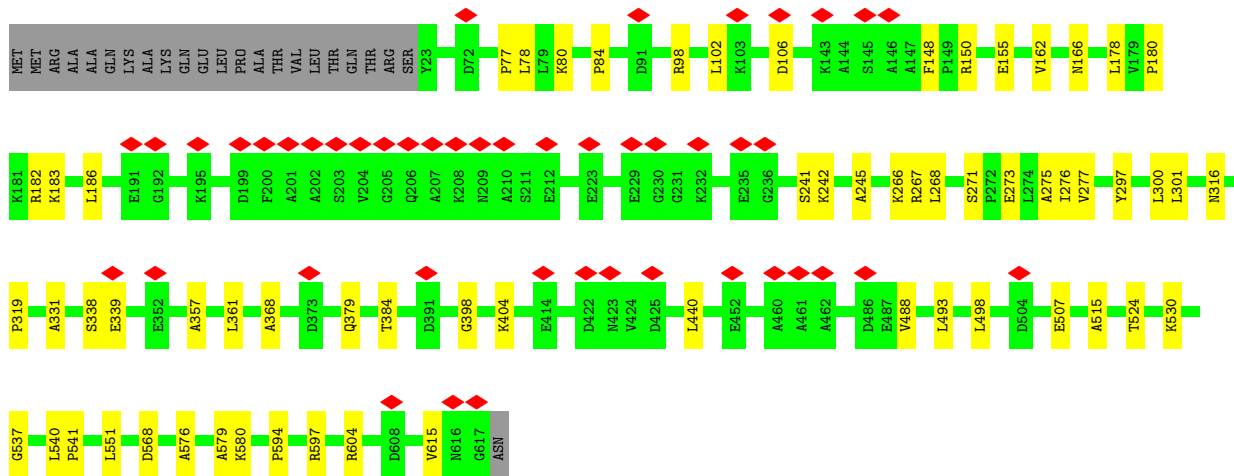
- Molecule 1: ASA-10: Polytomella F-ATP synthase associated subunit 10

Chain 0: 



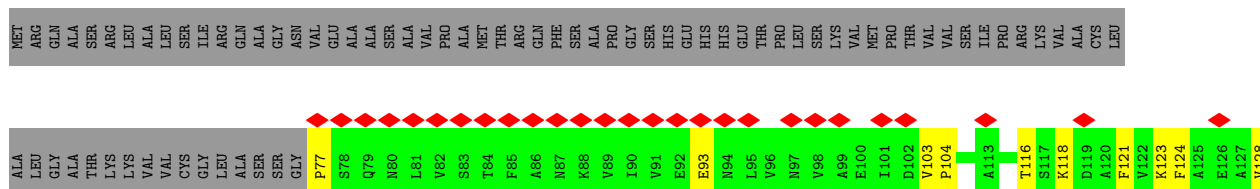
- Molecule 2: ATP synthase associated protein ASA1

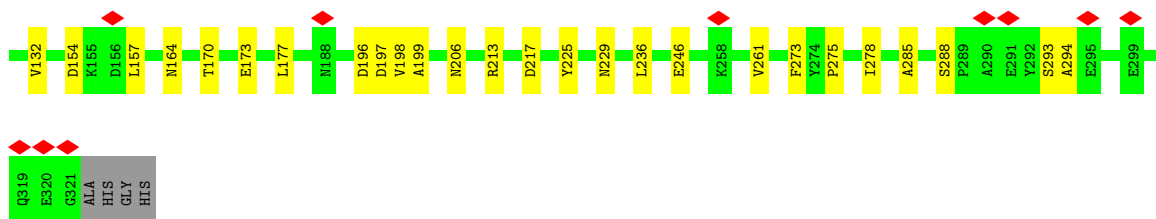
Chain 1: 



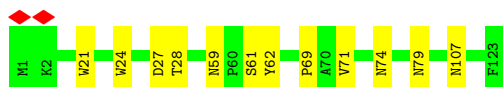
- Molecule 3: Mitochondrial F1F0 ATP synthase associated 32 kDa protein

Chain 3: 

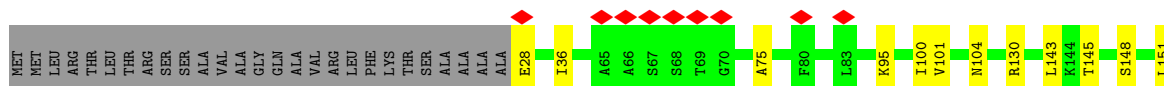
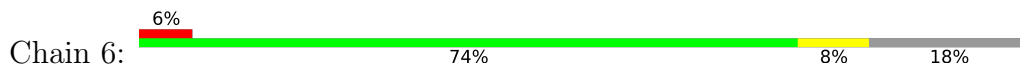




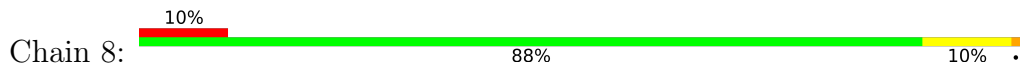
- Molecule 4: Mitochondrial F1F0 ATP synthase associated 14 kDa protein



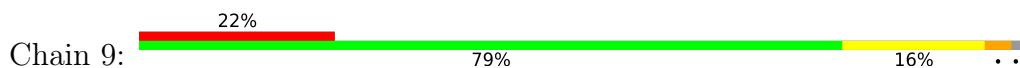
- Molecule 5: Mitochondrial ATP synthase subunit ASA6



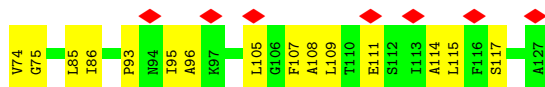
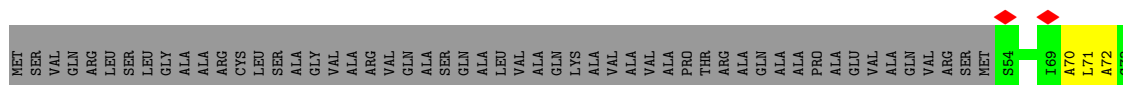
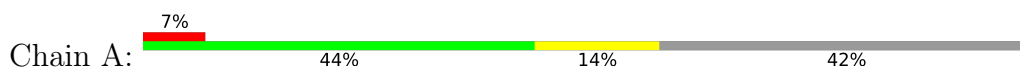
- Molecule 6: Mitochondrial ATP synthase subunit ASA8



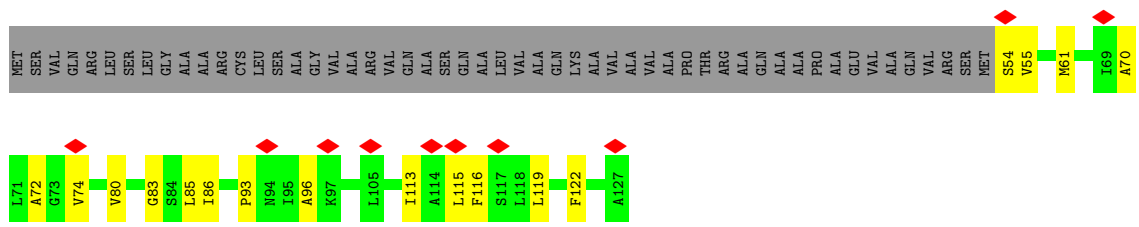
- Molecule 7: ASA-9: Polytomella F-ATP synthase associated subunit 9



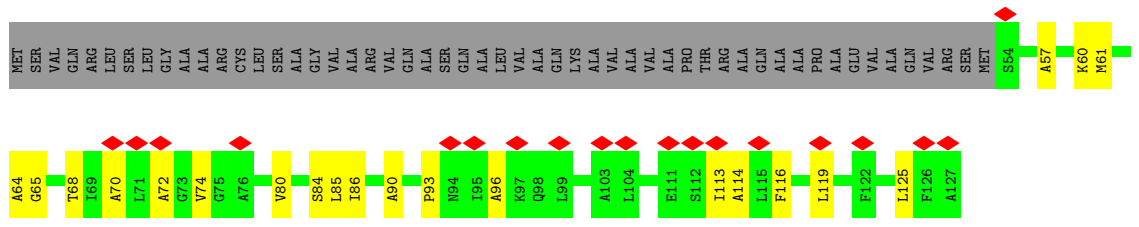
- Molecule 8: Mitochondrial ATP synthase subunit c



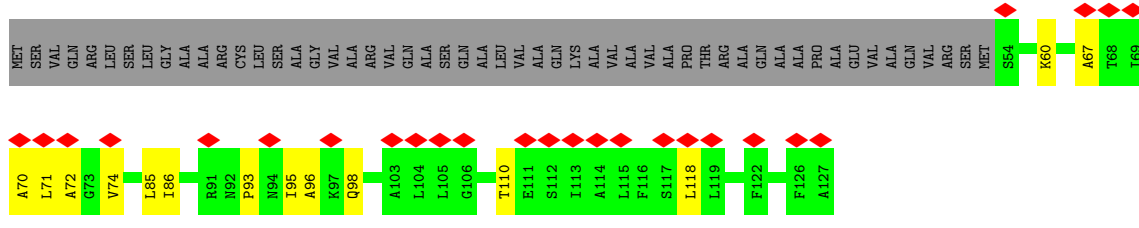
- Molecule 8: Mitochondrial ATP synthase subunit c



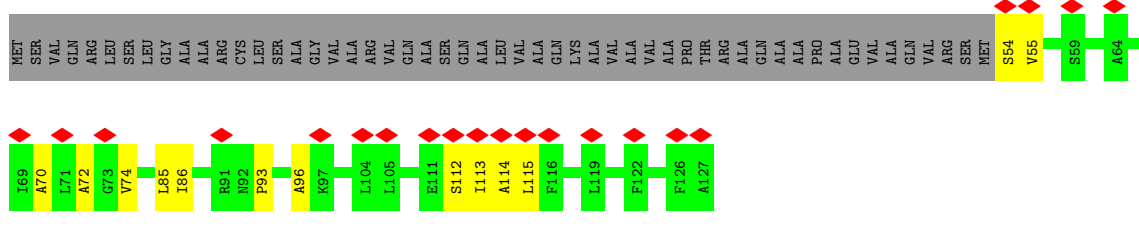
• Molecule 8: Mitochondrial ATP synthase subunit c



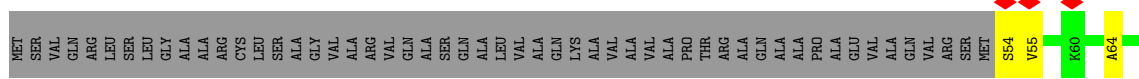
• Molecule 8: Mitochondrial ATP synthase subunit c

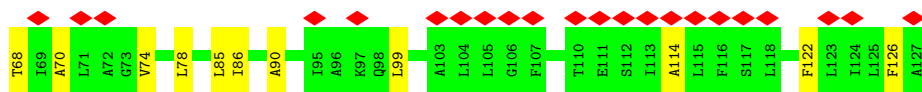


• Molecule 8: Mitochondrial ATP synthase subunit c

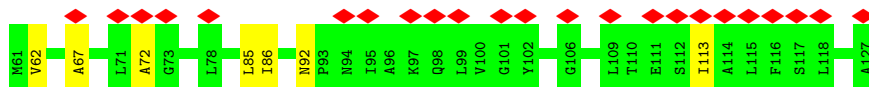
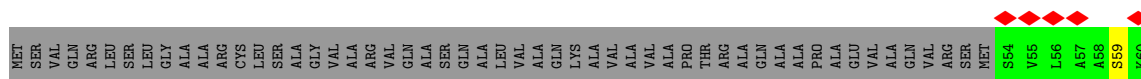


• Molecule 8: Mitochondrial ATP synthase subunit c

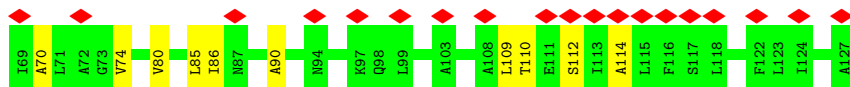
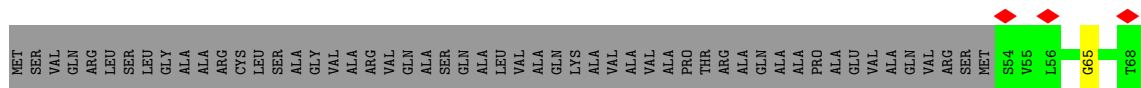




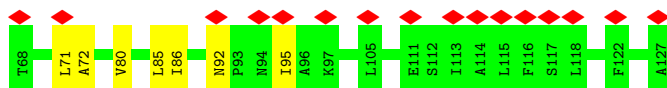
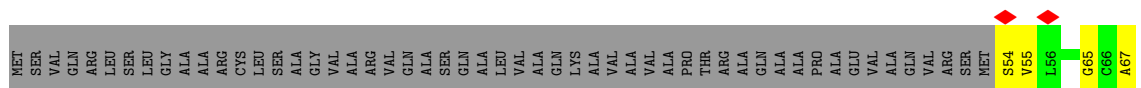
- Molecule 8: Mitochondrial ATP synthase subunit c



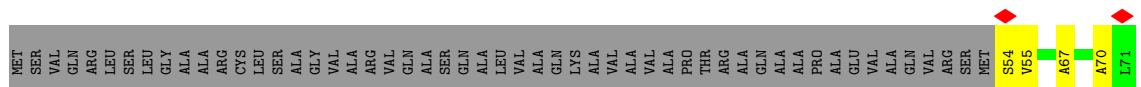
- Molecule 8: Mitochondrial ATP synthase subunit c



- Molecule 8: Mitochondrial ATP synthase subunit c



- Molecule 8: Mitochondrial ATP synthase subunit c



- Molecule 9: Mitochondrial ATP synthase subunit 6



MET SER VAL LEU SER SER VAL MET GLY SER ARG ILE GLY SER LEU LEU LEU GLY ARG SER SER ALA TYR LEU ALA PHE CYS GLY PHE SER THR ARG ASN LEU ASN GLY ILE ASP THR SER SER VAL PHE GLN ALA LEU SER ASP ASN GLU ASN LYS PRO ALA

SER PRO ASN LYS LEU PRO GLY MET SER CYS SER ILE LEU PRO LYS THR SER ARG ILE ALA VAL PRO PHE GLY ASN GLN THR MET ALA MET S95 S96 N121 H127 D128 R133 D143 K144 R145 C162 M163 F172 A173 P174 T175 A181 G201 F202

K203 F204 P205 HIS PHE ILE PRO GLY THR PRO TRP MET ALA F219 I220 F221 V222 P223 L224 E225 V238 R239 L240 W241 V242 N243 M244 T249 L250 I253 L254 M257 A258 L259 A260 P262 F263 S264 L265 G266 F267 F268 S269 M270 A273 L280 L281 L284

A292 G508 N311 K314 V323 K324 LYS ILE HIS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	136422	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	-400	Depositor
Maximum defocus (nm)	-5000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.198	Depositor
Minimum map value	-0.113	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.04	Depositor
Map size (\AA)	505.44, 505.44, 505.44	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.053, 1.053, 1.053	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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	0	0.37	0/625	0.48	0/851
2	1	0.41	0/4750	0.48	0/6434
3	3	0.42	0/1911	0.51	1/2601 (0.0%)
4	5	0.45	0/1011	0.49	0/1376
5	6	0.40	0/946	0.49	0/1287
6	8	0.47	0/715	0.56	1/974 (0.1%)
7	9	0.44	0/794	0.49	0/1073
8	A	0.43	0/521	0.53	0/704
8	B	0.37	0/520	0.44	0/704
8	C	0.36	0/520	0.44	0/704
8	D	0.36	0/520	0.43	0/704
8	E	0.35	0/520	0.49	0/704
8	F	0.34	0/520	0.44	0/704
8	G	0.33	0/520	0.51	0/704
8	H	0.33	0/520	0.52	0/704
8	I	0.32	0/520	0.45	0/704
8	J	0.35	0/520	0.52	0/704
9	M	0.46	0/1683	0.56	0/2295
All	All	0.41	0/17636	0.50	2/23931 (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
7	9	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	77	PRO	N-CA-CB	6.00	110.50	103.30
6	8	8	LEU	CA-CB-CG	5.15	127.14	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	9	57	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	605	0	589	7	0
2	1	4661	0	4695	44	0
3	3	1874	0	1826	26	0
4	5	986	0	1021	11	0
5	6	926	0	941	11	0
6	8	692	0	694	8	0
7	9	768	0	749	16	0
8	A	515	0	554	28	0
8	B	514	0	554	24	0
8	C	514	0	554	17	0
8	D	514	0	554	12	0
8	E	514	0	554	10	0
8	F	514	0	554	11	0
8	G	514	0	554	7	0
8	H	514	0	554	9	0
8	I	514	0	554	10	0
8	J	514	0	554	11	0
9	M	1640	0	1665	48	0
10	M	1	0	0	0	0
11	0	2	0	0	0	0
11	1	1	0	0	0	0
11	3	2	0	0	0	0
11	5	2	0	0	0	0
11	6	1	0	0	0	0
11	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	M	9	0	0	0	0
All	All	17312	0	17720	219	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 219 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:A:115:LEU:HB3	9:M:242:VAL:HG11	1.25	1.16
8:A:115:LEU:HD22	9:M:242:VAL:CG1	1.75	1.15
8:A:115:LEU:HD22	9:M:242:VAL:HG12	1.26	1.14
7:9:56:ASN:OD1	7:9:56:ASN:O	1.79	1.01
8:A:115:LEU:CB	9:M:242:VAL:HG11	2.00	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	
1	0	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
2	1	593/618 (96%)	579 (98%)	14 (2%)	0	100	100
3	3	243/325 (75%)	234 (96%)	9 (4%)	0	100	100
4	5	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
5	6	122/151 (81%)	119 (98%)	3 (2%)	0	100	100
6	8	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
7	9	94/97 (97%)	84 (89%)	7 (7%)	3 (3%)	4	20
8	A	72/127 (57%)	71 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	B	72/127 (57%)	72 (100%)	0	0	100	100
8	C	72/127 (57%)	72 (100%)	0	0	100	100
8	D	72/127 (57%)	72 (100%)	0	0	100	100
8	E	72/127 (57%)	72 (100%)	0	0	100	100
8	F	72/127 (57%)	70 (97%)	2 (3%)	0	100	100
8	G	72/127 (57%)	70 (97%)	2 (3%)	0	100	100
8	H	72/127 (57%)	72 (100%)	0	0	100	100
8	I	72/127 (57%)	71 (99%)	1 (1%)	0	100	100
8	J	72/127 (57%)	71 (99%)	1 (1%)	0	100	100
9	M	213/327 (65%)	210 (99%)	3 (1%)	0	100	100
All	All	2271/3082 (74%)	2215 (98%)	53 (2%)	3 (0%)	54	82

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	9	76	THR
7	9	58	PRO
7	9	66	ILE

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	
1	0	63/64 (98%)	63 (100%)	0	100	100
2	1	493/512 (96%)	493 (100%)	0	100	100
3	3	195/258 (76%)	195 (100%)	0	100	100
4	5	107/107 (100%)	107 (100%)	0	100	100
5	6	96/115 (84%)	96 (100%)	0	100	100
6	8	71/72 (99%)	71 (100%)	0	100	100
7	9	78/79 (99%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	A	50/86 (58%)	50 (100%)	0	100	100
8	B	50/86 (58%)	50 (100%)	0	100	100
8	C	50/86 (58%)	50 (100%)	0	100	100
8	D	50/86 (58%)	50 (100%)	0	100	100
8	E	50/86 (58%)	50 (100%)	0	100	100
8	F	50/86 (58%)	50 (100%)	0	100	100
8	G	50/86 (58%)	50 (100%)	0	100	100
8	H	50/86 (58%)	50 (100%)	0	100	100
8	I	50/86 (58%)	50 (100%)	0	100	100
8	J	50/86 (58%)	50 (100%)	0	100	100
9	M	178/272 (65%)	172 (97%)	6 (3%)	37	67
All	All	1781/2339 (76%)	1775 (100%)	6 (0%)	92	96

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	M	257	MET
9	M	261	LEU
9	M	264	SER
9	M	242	VAL
9	M	240	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
7	9	56	ASN
8	B	94	ASN
7	9	80	GLN
8	I	87	ASN
2	1	482	ASN

5.3.3 RNA ⓘ

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

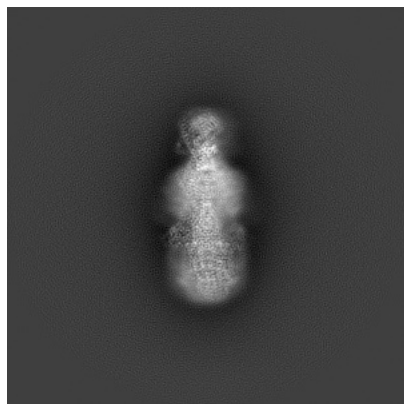
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4809. These allow visual inspection of the internal detail of the map and identification of artifacts.

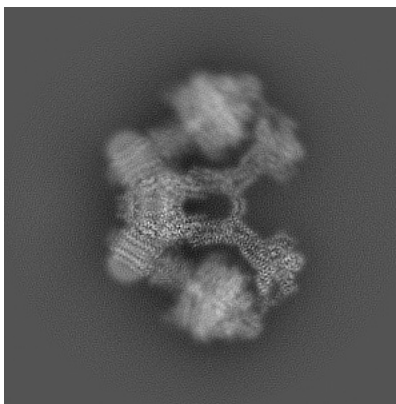
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

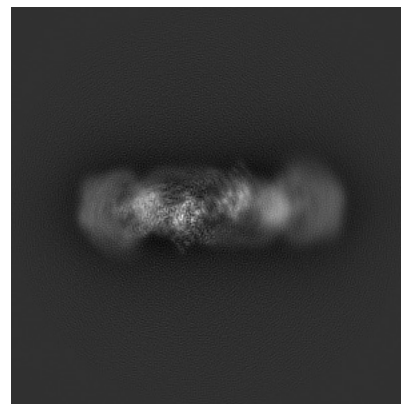
6.1.1 Primary map



X

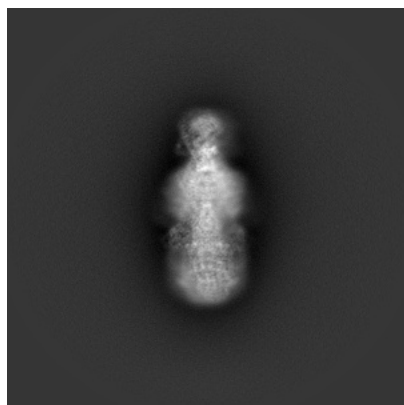


Y

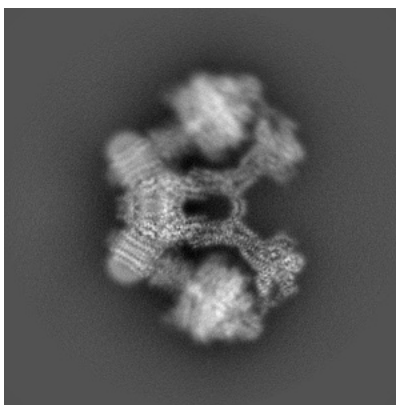


Z

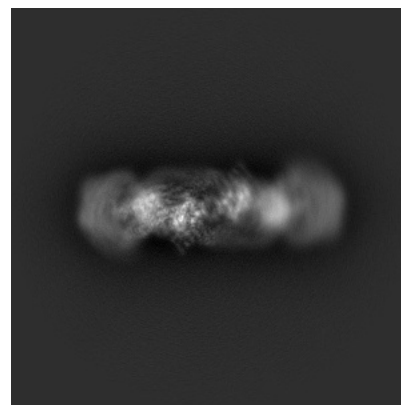
6.1.2 Raw map



X



Y



Z

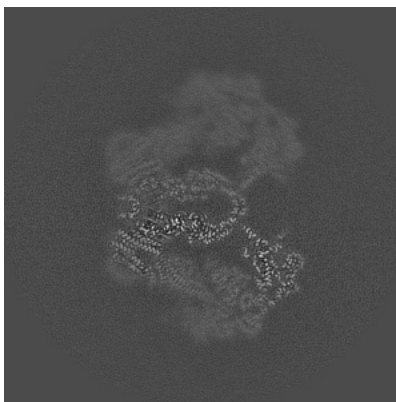
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

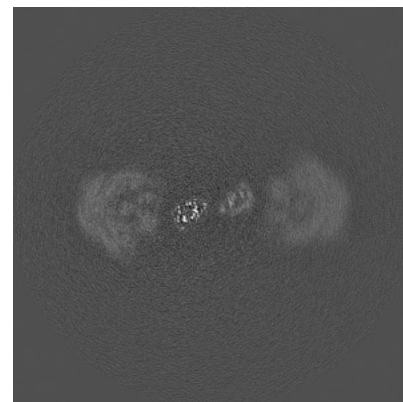
6.2.1 Primary map



X Index: 240

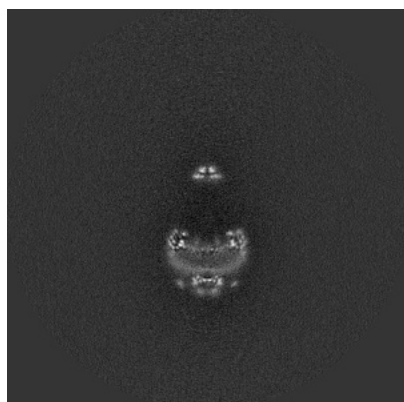


Y Index: 240

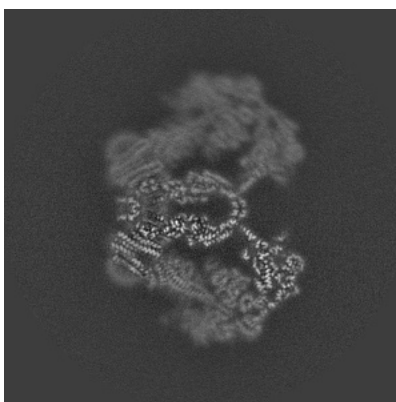


Z Index: 240

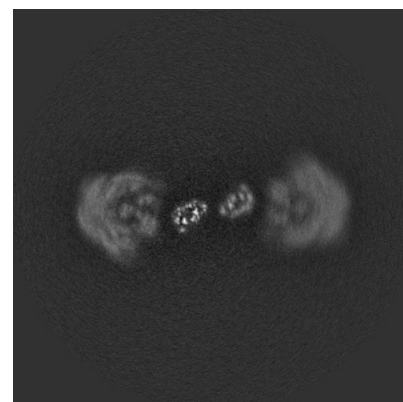
6.2.2 Raw map



X Index: 240



Y Index: 240

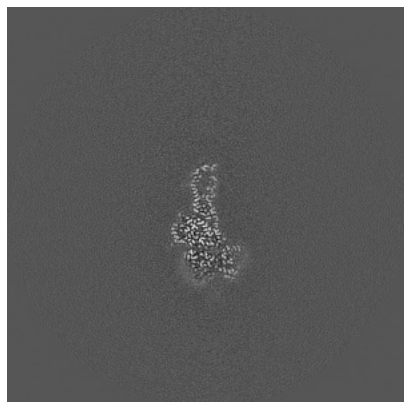


Z Index: 240

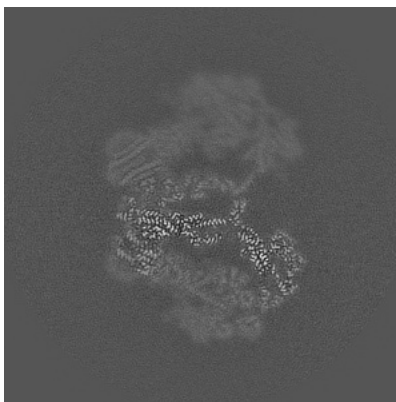
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

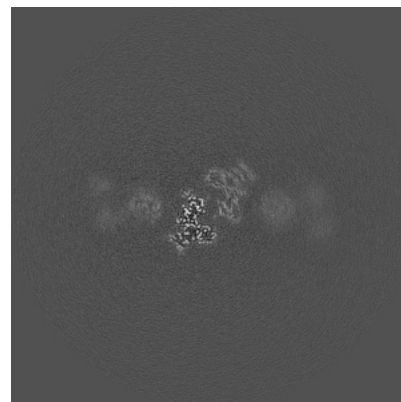
6.3.1 Primary map



X Index: 216

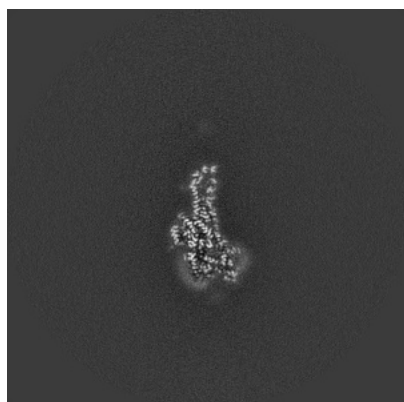


Y Index: 234

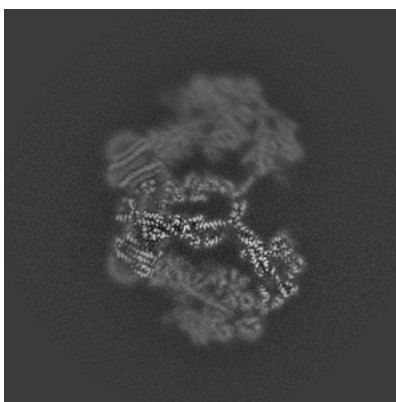


Z Index: 206

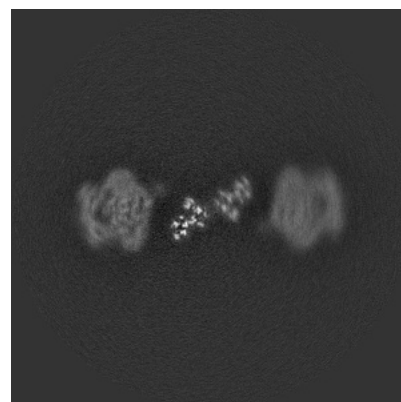
6.3.2 Raw map



X Index: 217



Y Index: 235

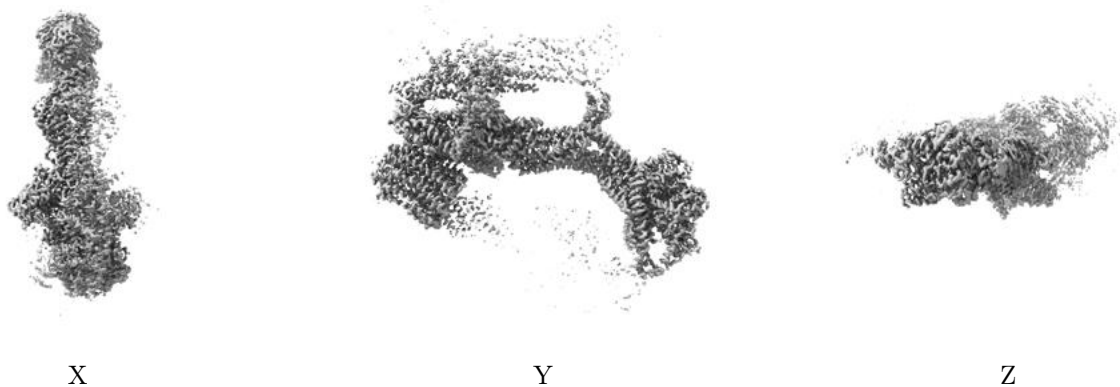


Z Index: 272

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

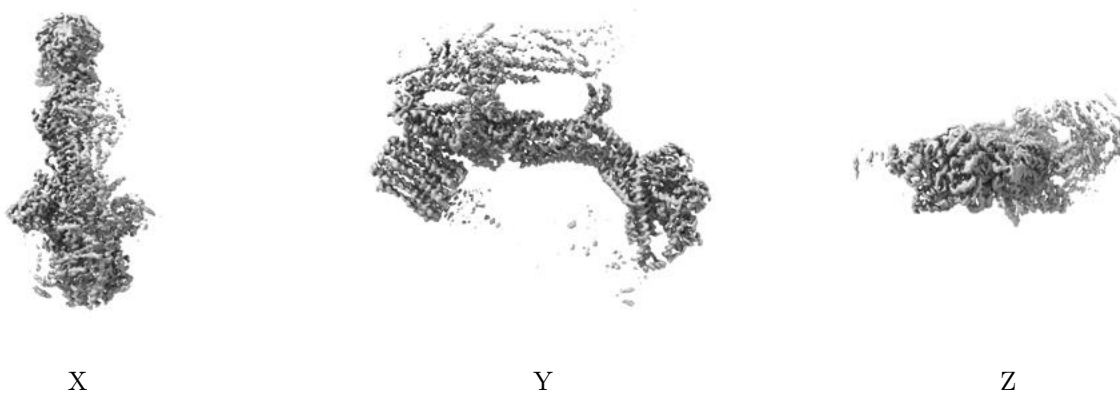
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. 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.

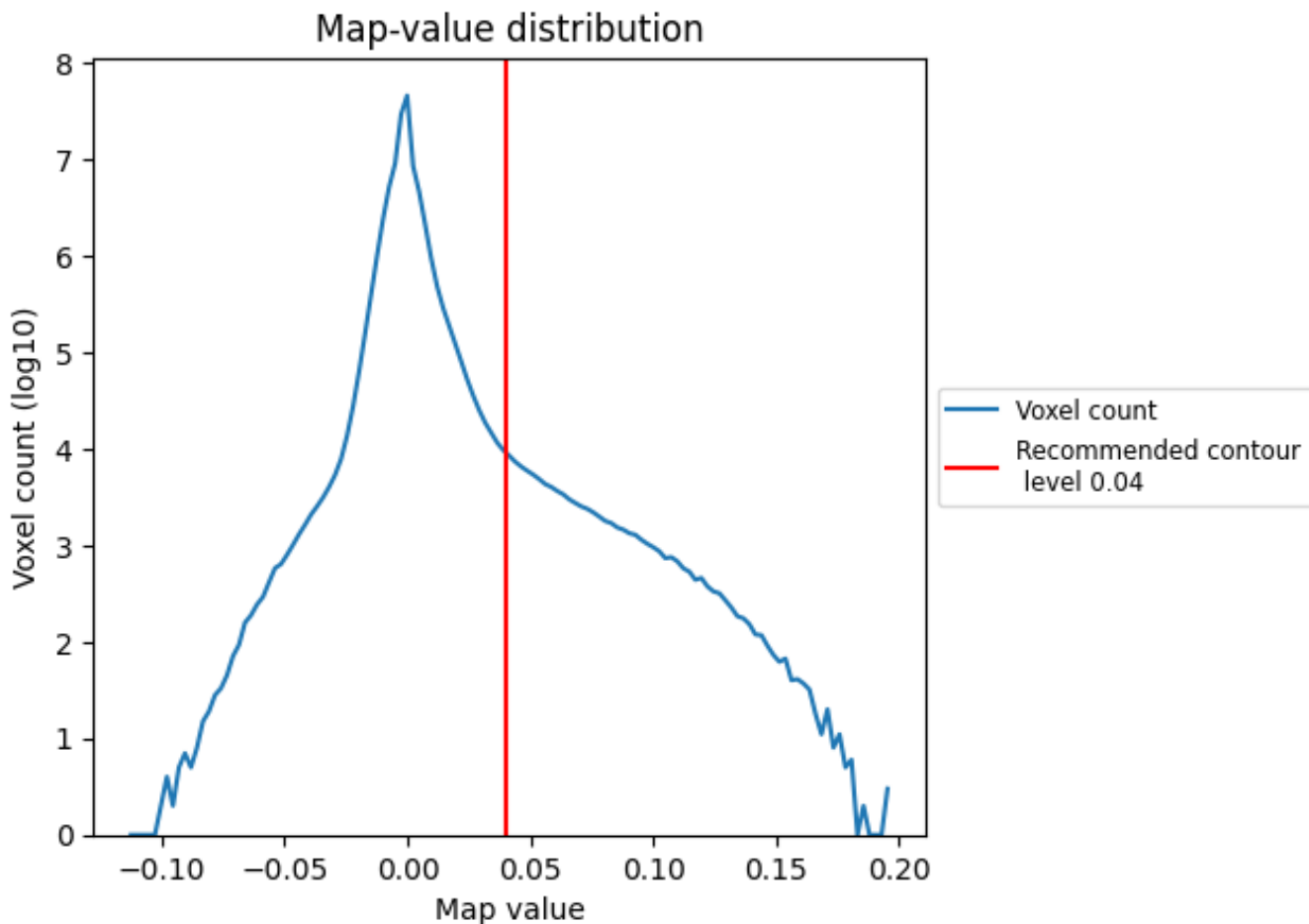
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

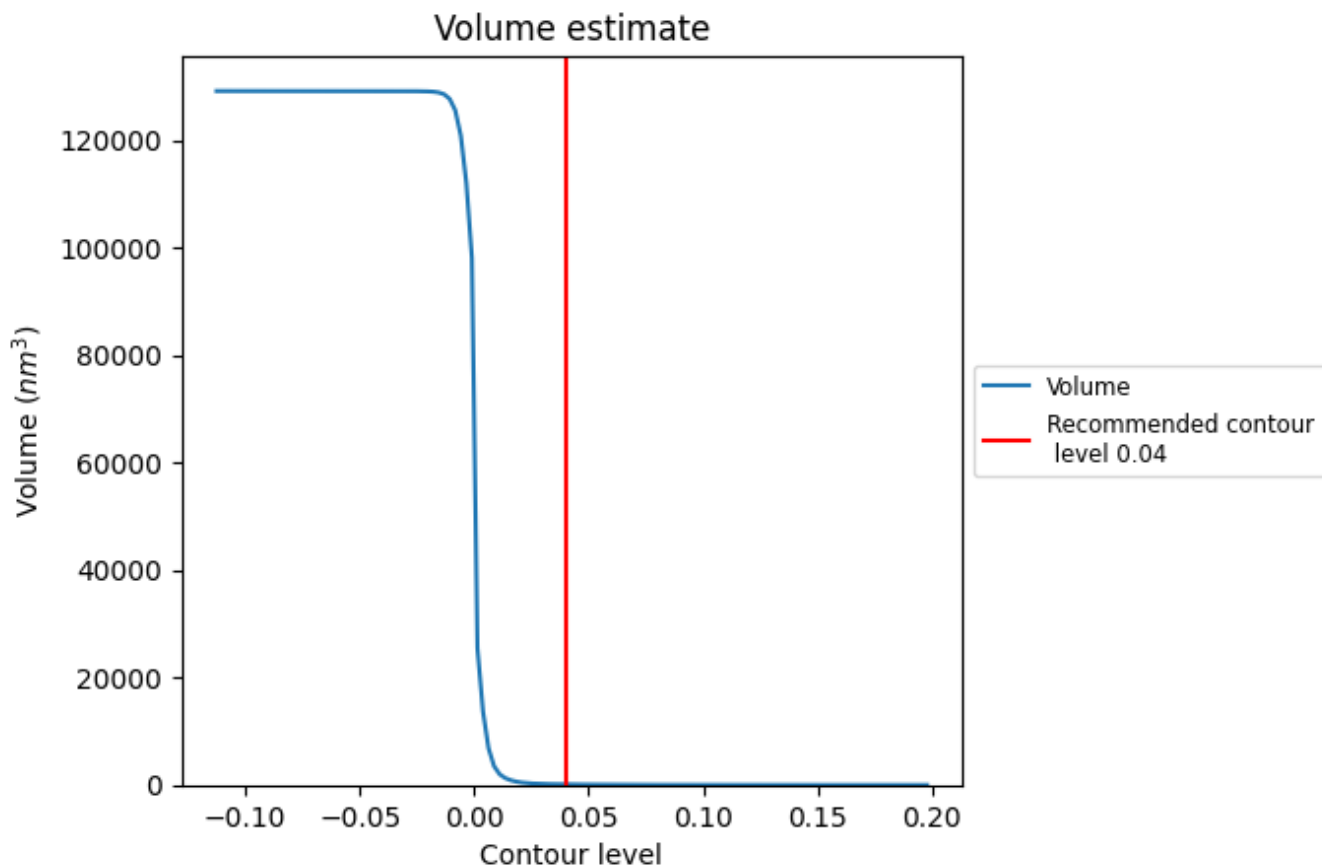
This section contains the results of statistical analysis of the map.

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.

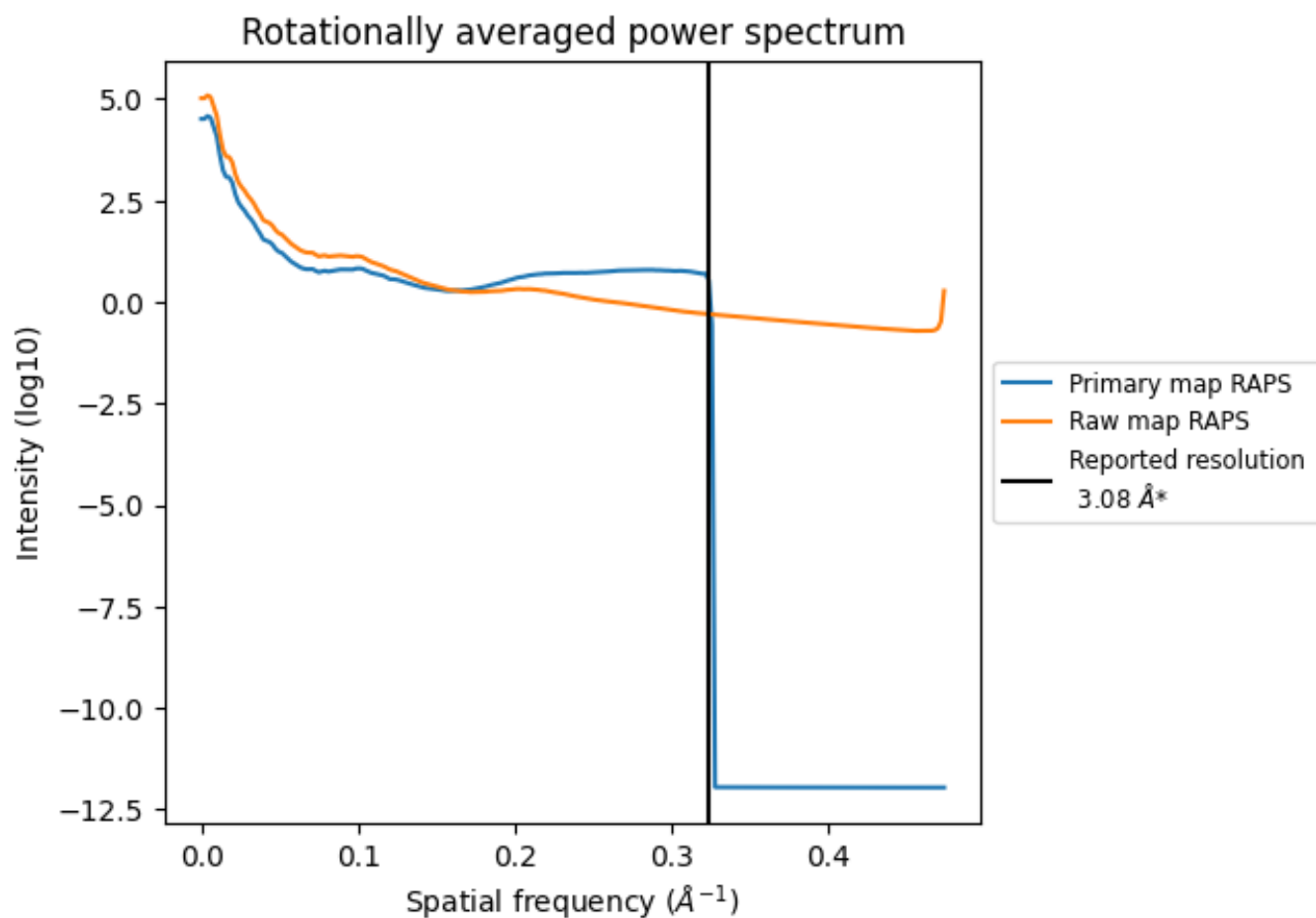
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 110 nm^3 ; this corresponds to an approximate mass of 99 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](#)

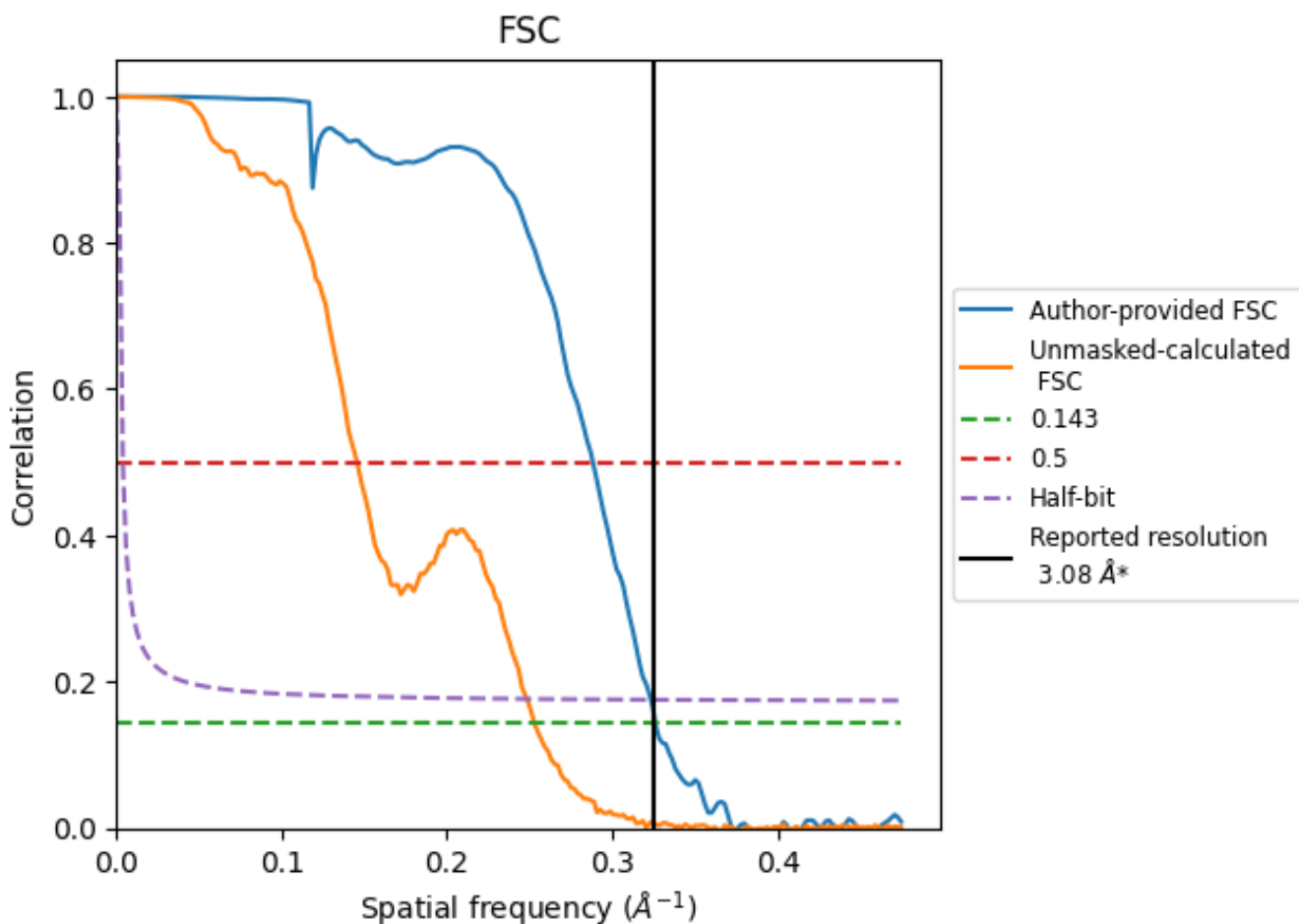


*Reported resolution corresponds to spatial frequency of 0.325 Å⁻¹

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 0.325 Å⁻¹

8.2 Resolution estimates [i](#)

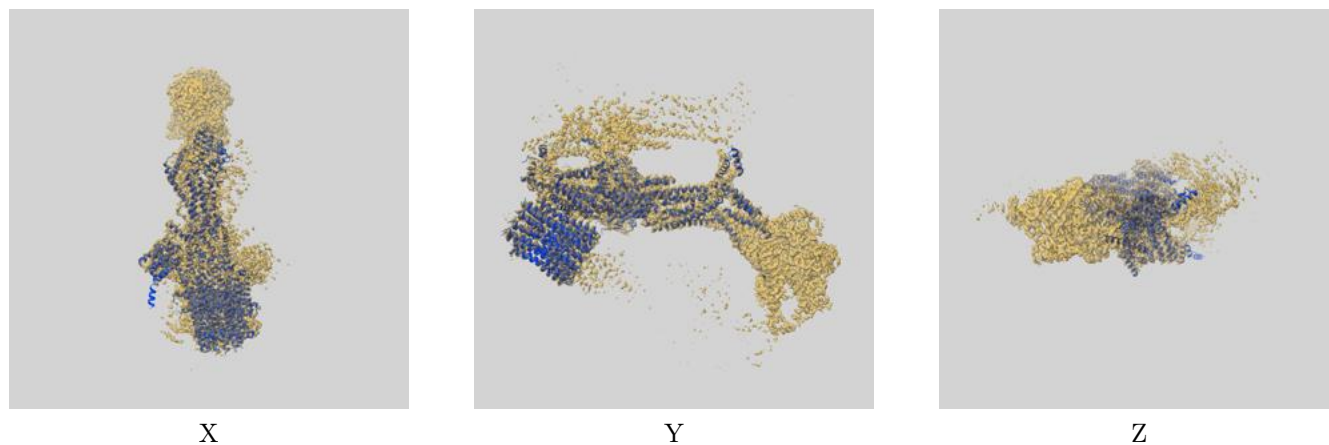
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.08	-	-
Author-provided FSC curve	3.07	3.47	3.09
Unmasked-calculated*	3.95	6.87	4.03

*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 3.95 differs from the reported value 3.08 by more than 10 %

9 Map-model fit [i](#)

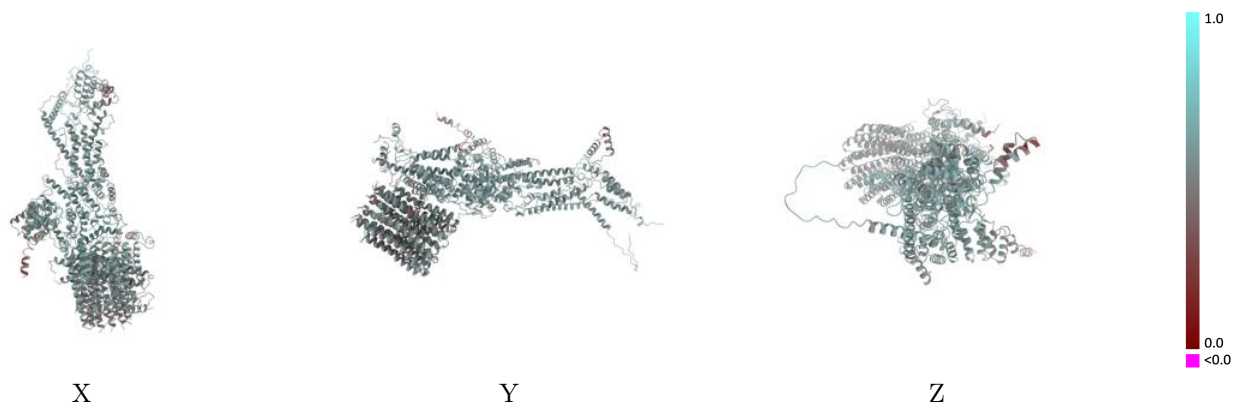
This section contains information regarding the fit between EMDB map EMD-4809 and PDB model 6RD8. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



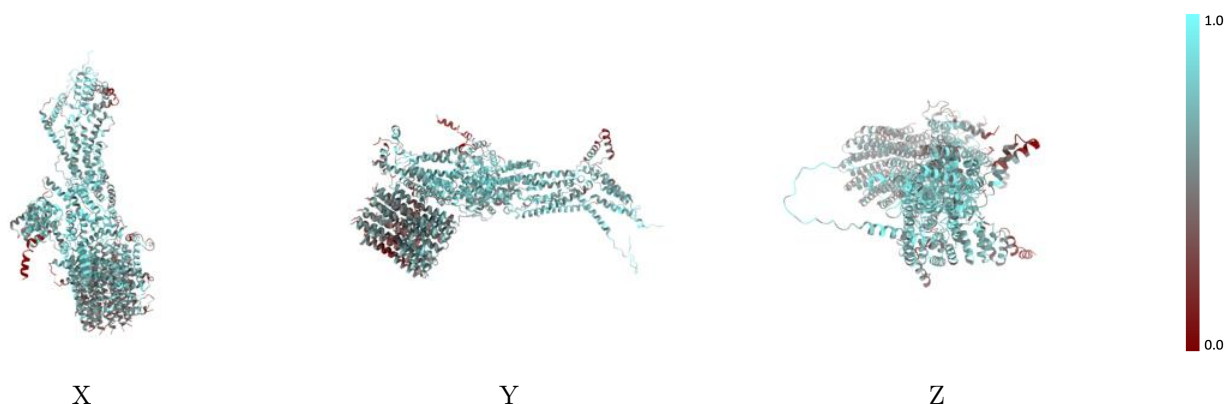
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



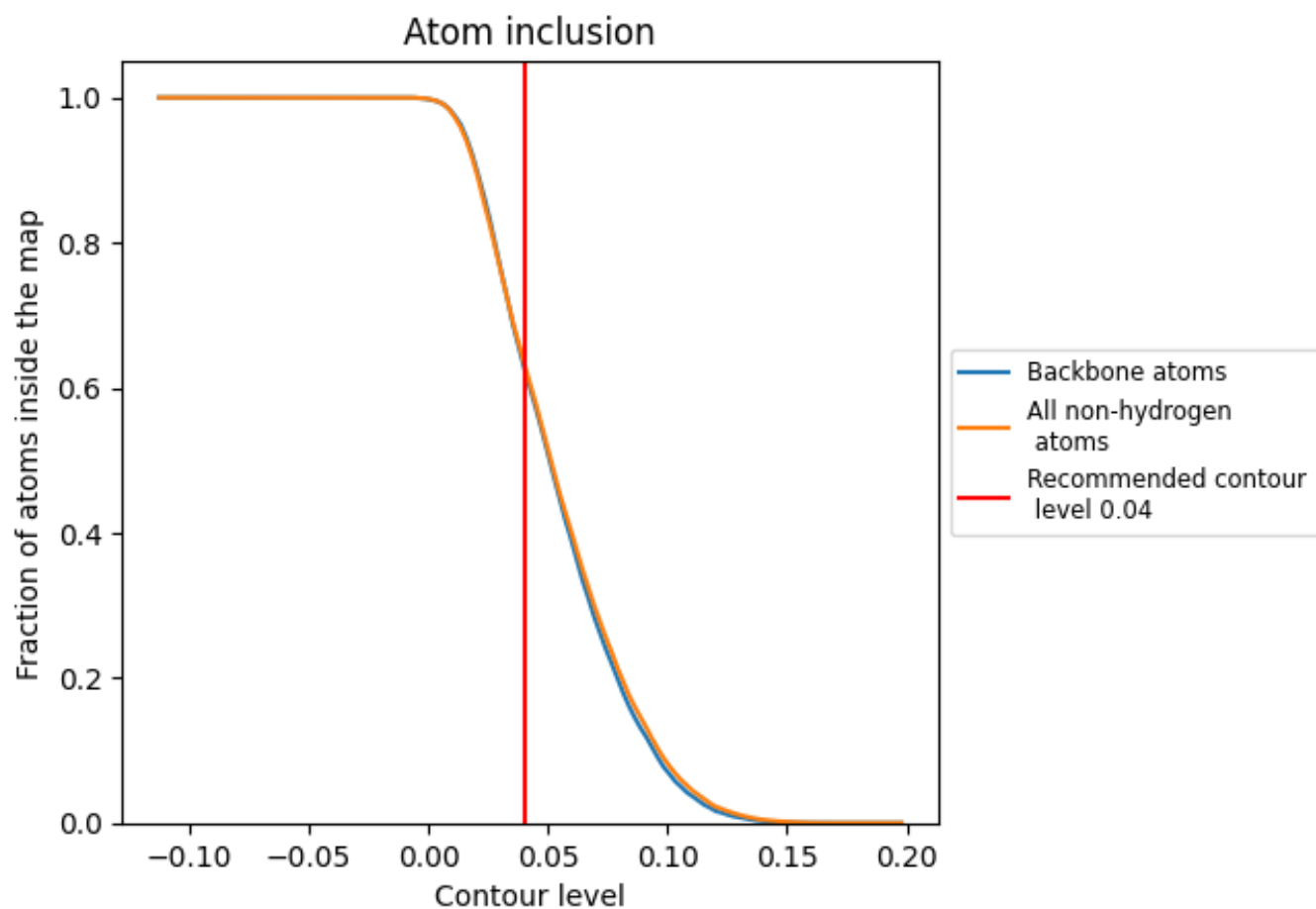
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.04).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 63% 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	 0.6347	 0.5480
0	 0.6578	 0.5590
1	 0.6973	 0.5660
3	 0.6546	 0.5420
5	 0.7734	 0.5880
6	 0.7130	 0.5690
8	 0.7242	 0.5730
9	 0.5794	 0.5190
A	 0.5996	 0.5410
B	 0.5753	 0.5300
C	 0.5068	 0.5110
D	 0.5010	 0.5060
E	 0.5049	 0.5100
F	 0.4834	 0.4890
G	 0.4677	 0.4880
H	 0.4873	 0.5170
I	 0.5362	 0.5240
J	 0.5910	 0.5420
M	 0.6825	 0.5650

