



wwPDB EM Validation Summary Report ⓘ

Jun 9, 2025 – 04:44 PM JST

PDB ID : 7YUU / pdb_00007yuu
EMDB ID : EMD-34111
Title : MtaLon-ADP for the spiral oligomers of trimer
Authors : Li, S.; Hsieh, K.; Kuo, C.; Lee, S.; Ho, M.; Wang, C.; Zhang, K.; Chang, C.I.
Deposited on : 2022-08-17
Resolution : 5.80 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.43.1

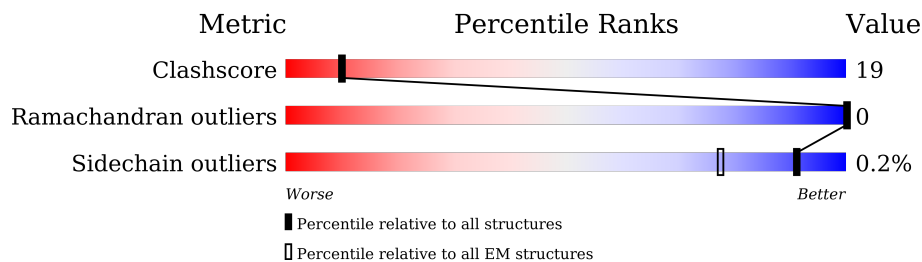
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	A	793	<div> <div>10%</div> <div>37%</div> <div>29%</div> <div>33%</div> </div>
1	B	793	<div> <div>5%</div> <div>37%</div> <div>29%</div> <div>33%</div> </div>
1	C	793	<div> <div>8%</div> <div>36%</div> <div>31%</div> <div>33%</div> </div>

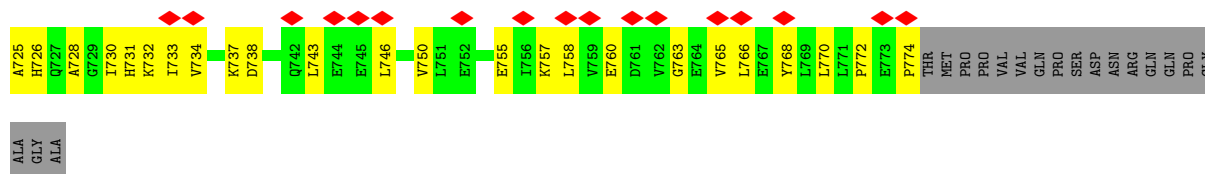
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12432 atoms, of which 0 are hydrogens and 0 are deuteriums.

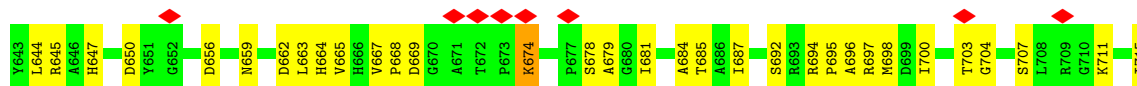
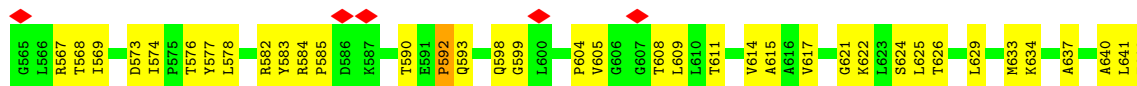
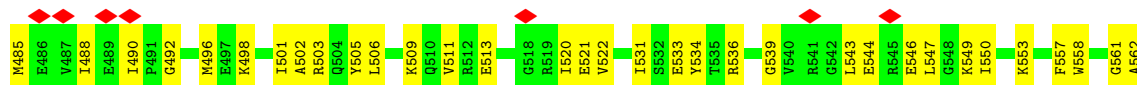
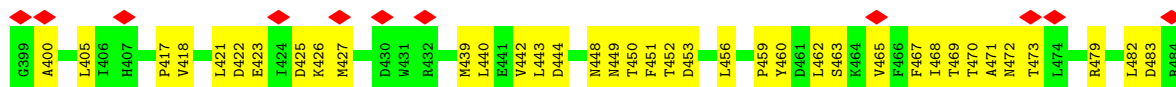
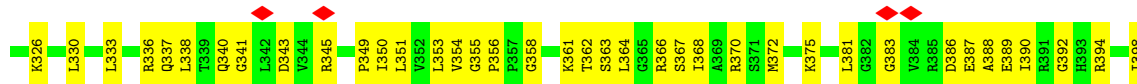
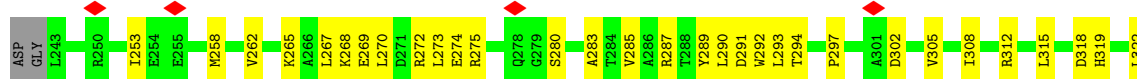
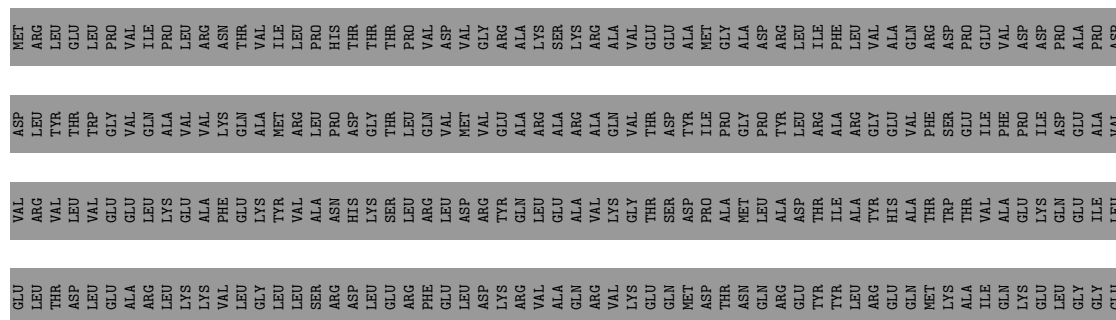
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Lon protease.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	532	Total	C	N	O	S	0	0
			4144	2620	726	783	15		
1	B	532	Total	C	N	O	S	0	0
			4144	2620	726	783	15		
1	C	532	Total	C	N	O	S	0	0
			4144	2620	726	783	15		



• Molecule 1: Lon protease



• Molecule 1: Lon protease



ASN	ARG	GLN	PRO	GLY	ALA	GLY	ALA	ASP	ASP	GLY	L243	L244	D245	L246	L249	R250	K251	K252	E255	V256	G257	M258	A261	V262	K265	E269	R272	L273	E274	R275	M276	Q277	Q278	P281	E282	A283	T284	V285	A286	R287	T288	Y289	L290	D291	W292	L293	T294	S299	K300	A301	D302	P303	V305	L306	D307	I308	N309	H310	T311												
ASP	LEU	THR	THR	LEU	TRP	GLU	VAL	GLN	LEU	ALA	ARG	LEU	LEU	VAL	LYS	ALA	VAL	LYS	THR	VAL	LEU	ASP	THR	GLY	THR	LEU	ARG	VAL	GLY	ALA	ARG	GLN	ALA	VAL	GLN	SER	ASP	PRO	ILE	PRO	GLY	ASP	LEU	ARG	ILE	ALA	THR	GLY	ARG	GLU	VAL	GLN	THR	LYS	ASP	LEU	THR	ALA	VAL	GLN	LYS	GLU	LEU	GLY	ILE	LEU	VAL				
GLU	LEU	THR	ASP	LEU	GLU	ALA	ALA	ARG	LEU	LYS	GLY	LEU	LEU	VAL	LEU	SER	ASN	HIS	ASP	LEU	GLY	THR	GLY	THR	PRO	VAL	GLN	LEU	ASP	VAL	GLY	ARG	GLN	ALA	GLY	THR	GLY	THR	ASP	PRO	ILE	THR	ASN	GLN	ARG	ALA	GLU	THR	ILE	ALA	ARG	GLY	GLU	GLN	MET	THR	TRP	LYS	ASP	LEU	THR	ALA	VAL	GLN	LYS	GLU	LEU	GLY	ILE	GLY	GLU
R312	Q313	E317	D318	H319	K323	D324	V325	K326	E327	R328	I329	L330	Q337	Q340	D343	V344	R345	N346	K347	A348	P349	I350	L351	V354	G355	P356	V359	S371	K375	F376	H377	R378	I379	S380	L381	G382	D386	E389	I390	R391	G392	H393	R394	R395	T396	Y397	I398	G399																							
A400	M401	P402	G403	L405	I406	H407	A408	M409	K410	Q411	Q412	I415	N416	P417	V418	I419	L420	L421	D422	E423	I424	D425	K426	M427	S428	W431	R432	G433	M439	L440	E441	V442	L443	D444	Q447	N448	M449	T450	F451	T452	D453	H454	Y455	L456	D457	V458	D461	L462	S463	K464	V465	F466																			
T469	I470	A471	P478	L481	R484	M485	A486	V487	I488	E489	I490	P491	T494	W495	M496	E497	K498	Q499	A500	I501	A502	R503	Q504	Y505	L506	Q510	V511	S514	G515	M516	E517	G518	R519	I520	E521	V522	R529	V530	I531	S532	E533	Y534	T535	R536	G539	E544	L547	I550																							
A551	W558	W563	E564	G565	L566	R567	T568	I569	D573	I574	Y577	L578	Y583	R584	P585	D586	K587	A588	E589	T590	E591	T596	G599	L600	A601	W602	T603	P604	V605	G606	G607	T608	L609	I612	E613	V614	A615	A616	V617	G621	S624	L625	Q628	L629	M633	K634																									
Y643	L644	R645	A646	H647	T648	Q649	D650	D656	N659	K660	V661	D662	L663	H664	V665	H666	V667	P668	D669	G670	A671	T672	P673	K674	D675	G676	P677	S678	T682	M683	A684	T685	S689	R693	R694	P695	A696	R697	M698	A701	M702	T703	G704	E705	V706	S707	L708	R709	G710	K711	V712	M713	P714																		
I715	G716	G717	V718	K719	E720	K721	L722	L723	A724	A725	H726	Q727	A728	G729	K732	I733	V734	L735	P736	G737	D738	N739	E740	A741	Q742	L743	P747	L754	K757	L758	V759	E760	G763	E764	V765	L766	E767	L769	L770	L771	P772	E773	P774	THR	MET	PRO	PRO	VAL	VAL	GLN	PRO	PRO	ASP																		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	17690	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 ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.826	Depositor
Minimum map value	-0.405	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.203	Depositor
Map size (\AA)	275.52, 275.52, 275.52	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.82, 0.82, 0.82	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.41	0/4221	0.80	4/5721 (0.1%)
1	B	0.45	0/4221	0.85	2/5721 (0.0%)
1	C	0.44	0/4221	0.81	7/5721 (0.1%)
All	All	0.44	0/12663	0.82	13/17163 (0.1%)

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
1	A	0	3
1	B	0	5
1	C	0	1
All	All	0	9

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	605	VAL	N-CA-C	-7.88	105.51	113.47
1	C	670	GLY	N-CA-C	-7.22	105.71	114.66
1	B	341	GLY	N-CA-C	-6.55	105.47	114.64
1	A	657	PHE	N-CA-C	-6.13	103.50	113.19
1	C	591	GLU	CA-C-N	5.81	127.10	119.84

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	350	ILE	Peptide
1	A	454	HIS	Peptide

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Mol	Chain	Res	Type	Group
1	A	591	GLU	Peptide
1	B	322	LEU	Peptide
1	B	422	ASP	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	A	4144	0	4226	160	0
1	B	4144	0	4226	155	0
1	C	4144	0	4226	166	0
All	All	12432	0	12678	477	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 19.

The worst 5 of 477 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)
1:B:599:GLY:O	1:B:609:LEU:HA	1.80	0.81
1:A:500:ALA:O	1:A:504:GLN:HB2	1.84	0.78
1:C:265:LYS:HE3	1:C:457:ASP:HB2	1.69	0.74
1:A:246:LEU:O	1:A:250:ARG:HB2	1.89	0.72
1:C:737:LYS:HB3	1:C:760:GLU:HB2	1.71	0.71

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	A	530/793 (67%)	479 (90%)	51 (10%)	0	100	100
1	B	530/793 (67%)	483 (91%)	47 (9%)	0	100	100
1	C	530/793 (67%)	485 (92%)	45 (8%)	0	100	100
All	All	1590/2379 (67%)	1447 (91%)	143 (9%)	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	A	443/665 (67%)	443 (100%)	0	100	100
1	B	443/665 (67%)	442 (100%)	1 (0%)	92	94
1	C	443/665 (67%)	442 (100%)	1 (0%)	92	94
All	All	1329/1995 (67%)	1327 (100%)	2 (0%)	91	94

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	765	VAL
1	C	715	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	373	ASN
1	B	638	GLN
1	C	742	GLN
1	C	340	GLN
1	C	510	GLN

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.

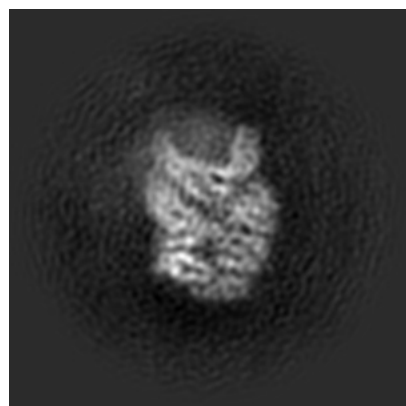
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34111. These allow visual inspection of the internal detail of the map and identification of artifacts.

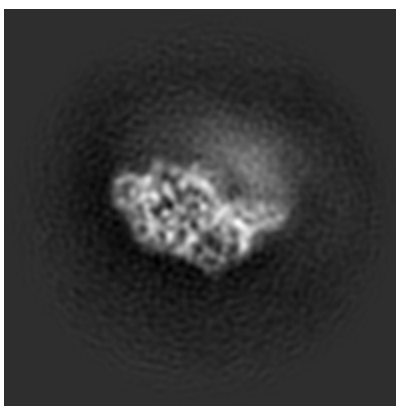
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

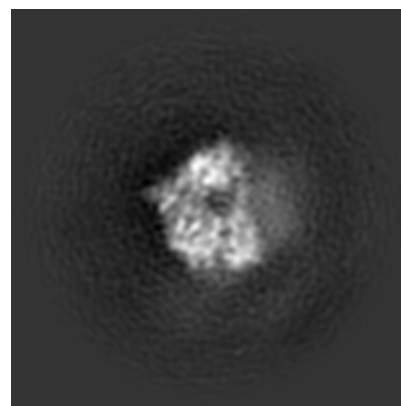
6.1.1 Primary map



X

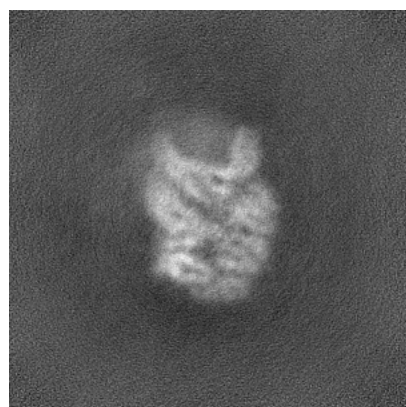


Y

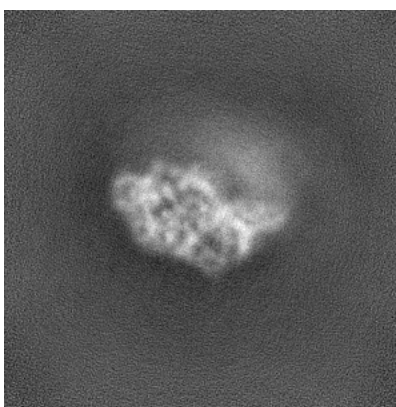


Z

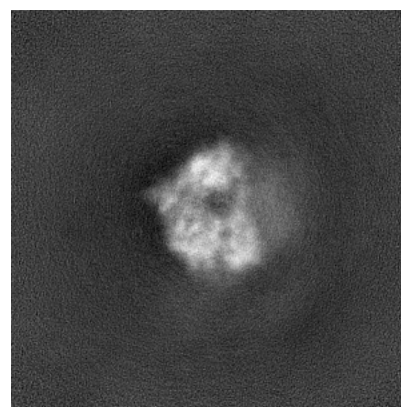
6.1.2 Raw map



X



Y

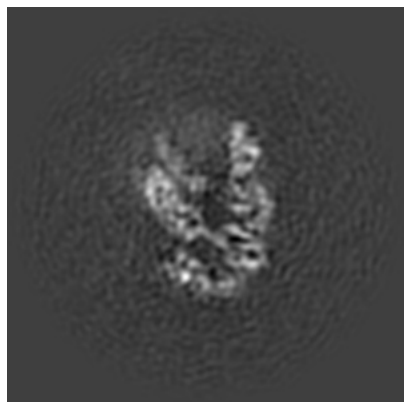


Z

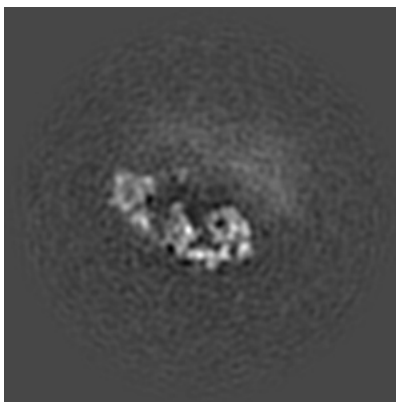
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

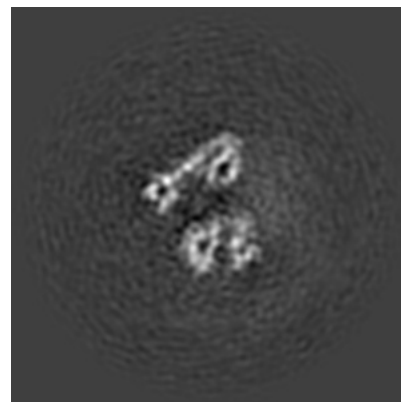
6.2.1 Primary map



X Index: 168

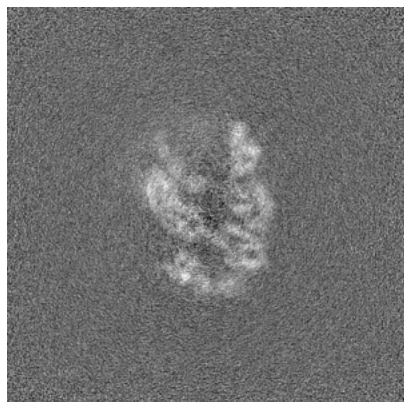


Y Index: 168

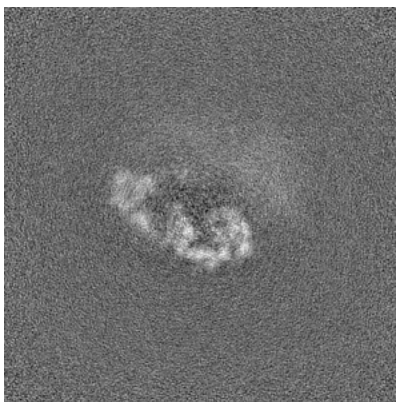


Z Index: 168

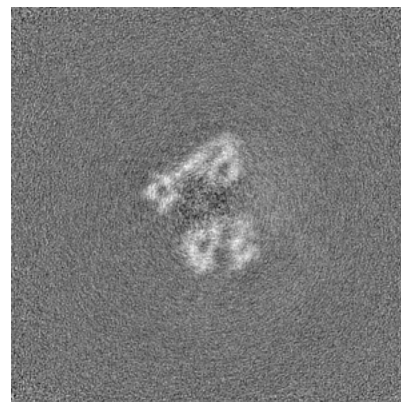
6.2.2 Raw map



X Index: 168



Y Index: 168

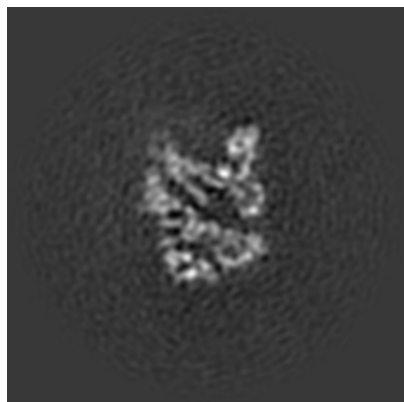


Z Index: 168

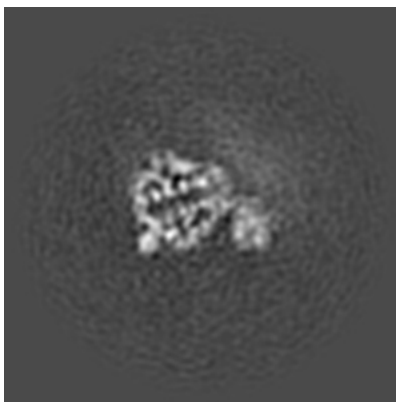
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

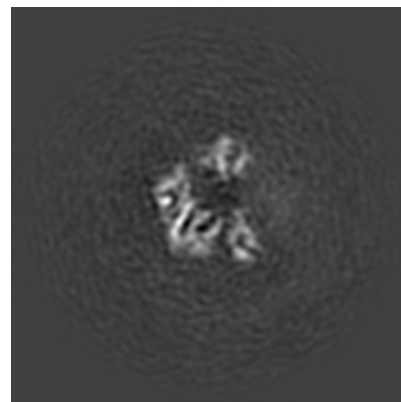
6.3.1 Primary map



X Index: 155

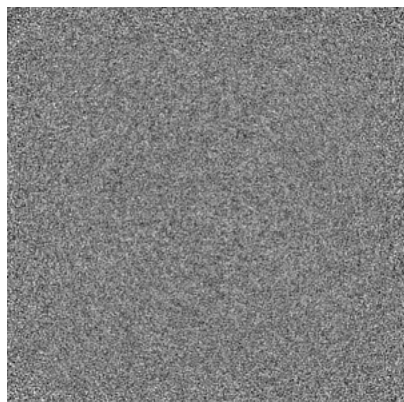


Y Index: 137

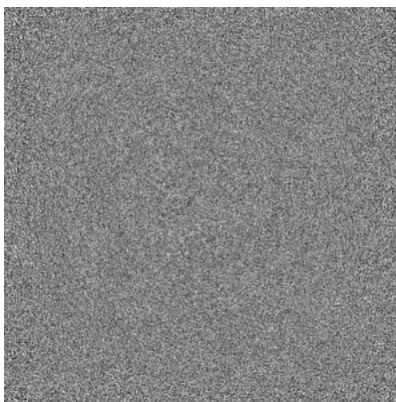


Z Index: 155

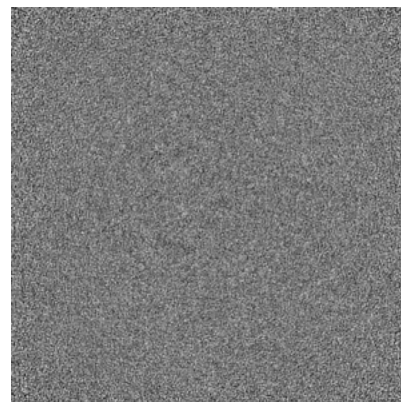
6.3.2 Raw map



X Index: 0



Y Index: 0

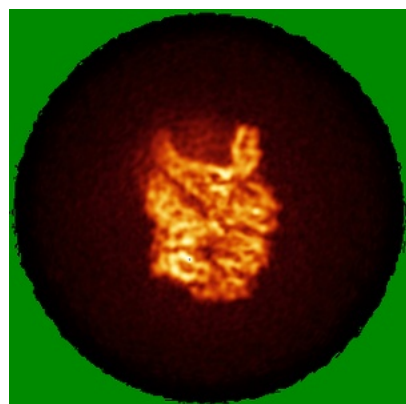


Z Index: 0

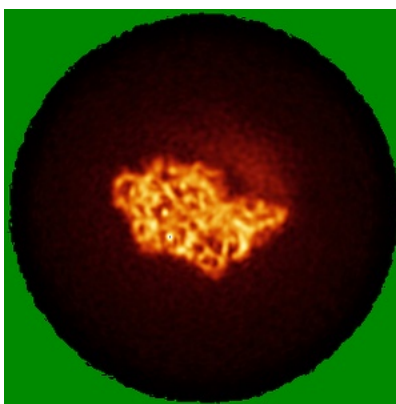
The images above show the largest variance slices of the map in three orthogonal directions.

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

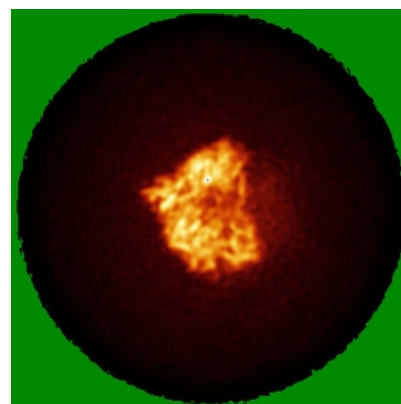
6.4.1 Primary map



X

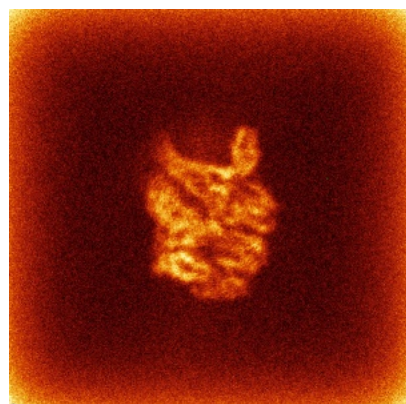


Y

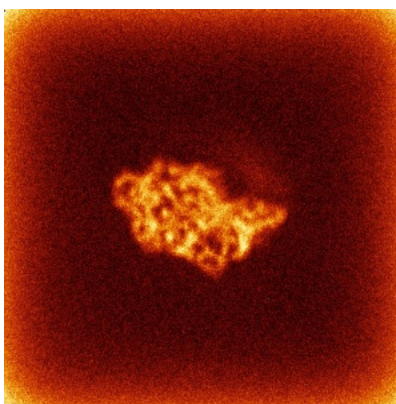


Z

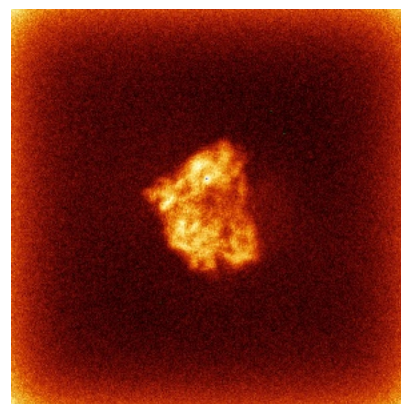
6.4.2 Raw map



X



Y

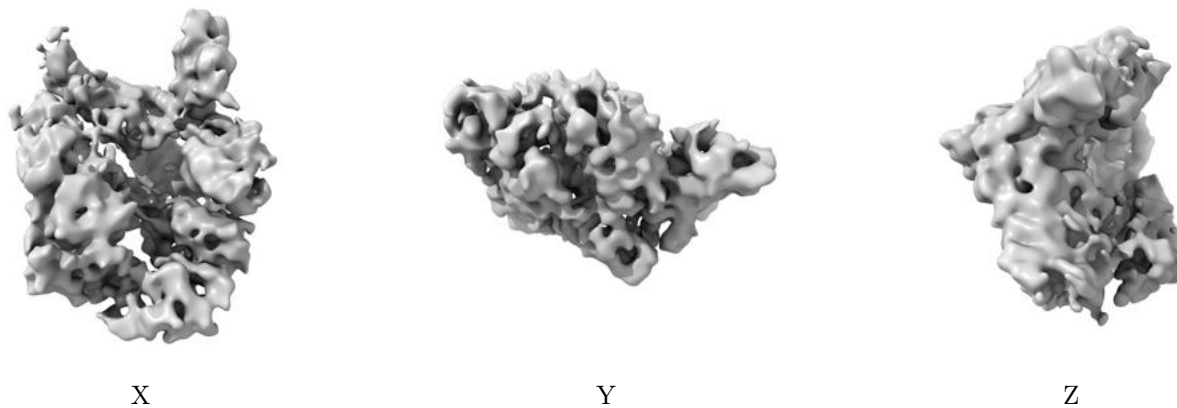


Z

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.

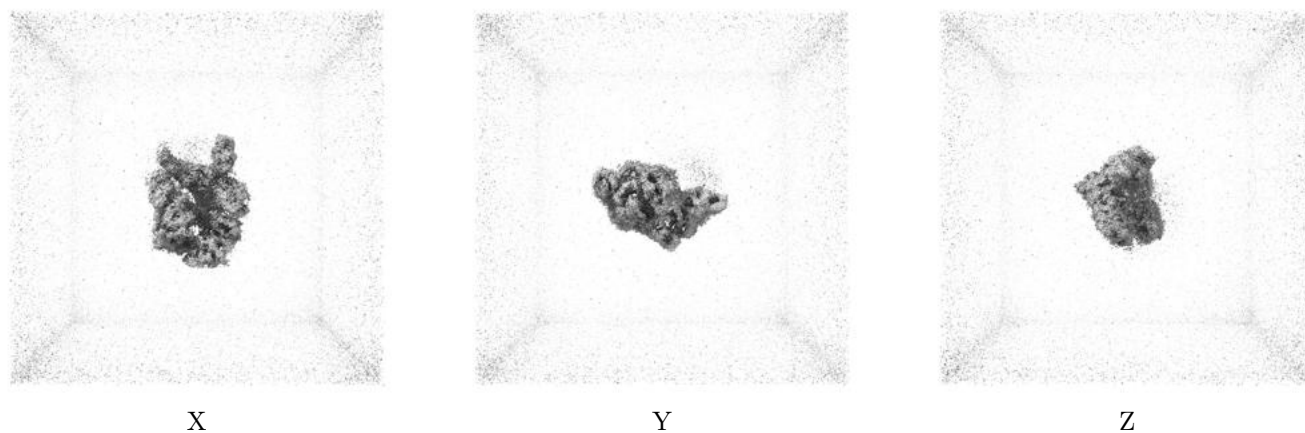
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.203. 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.

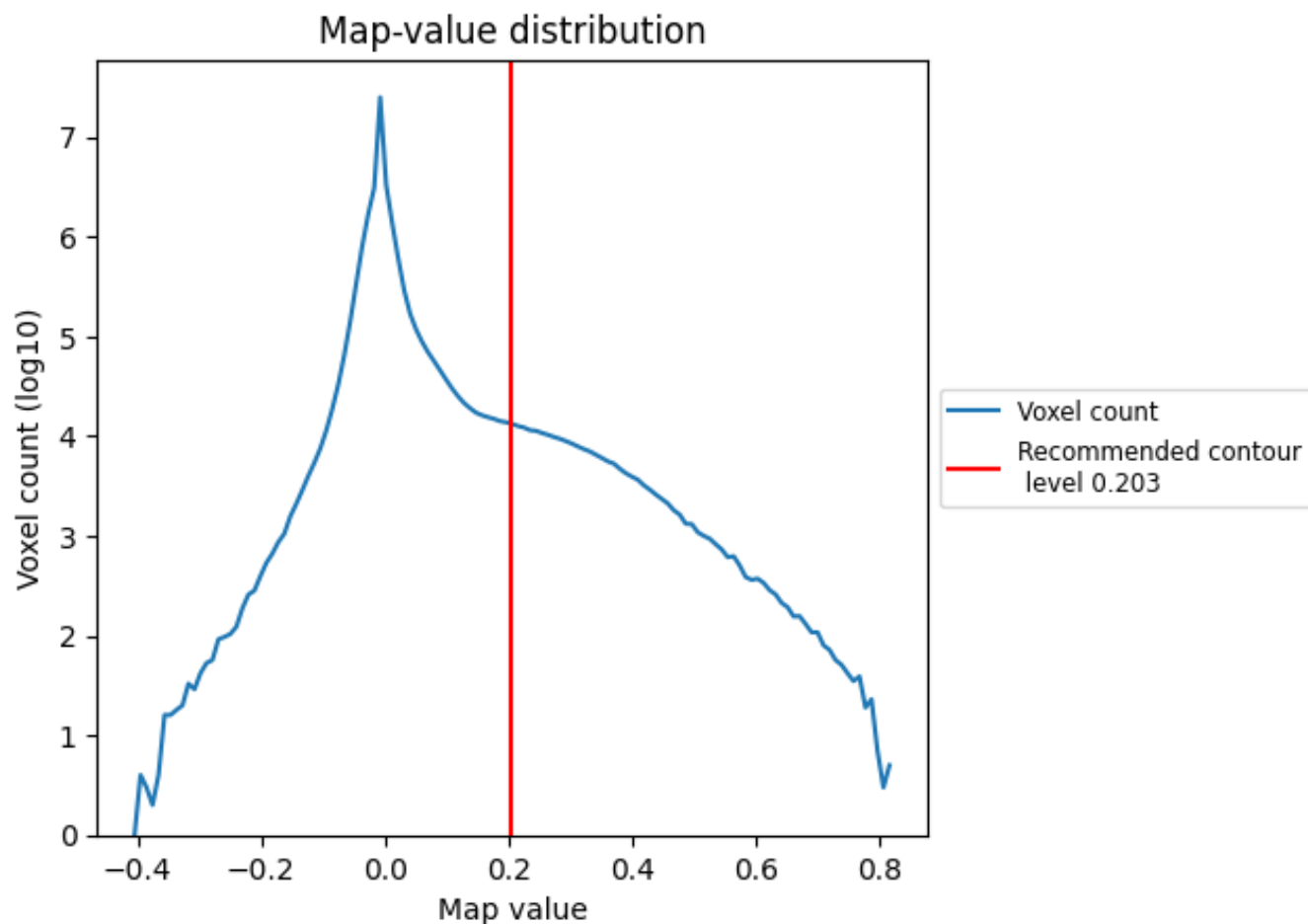
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

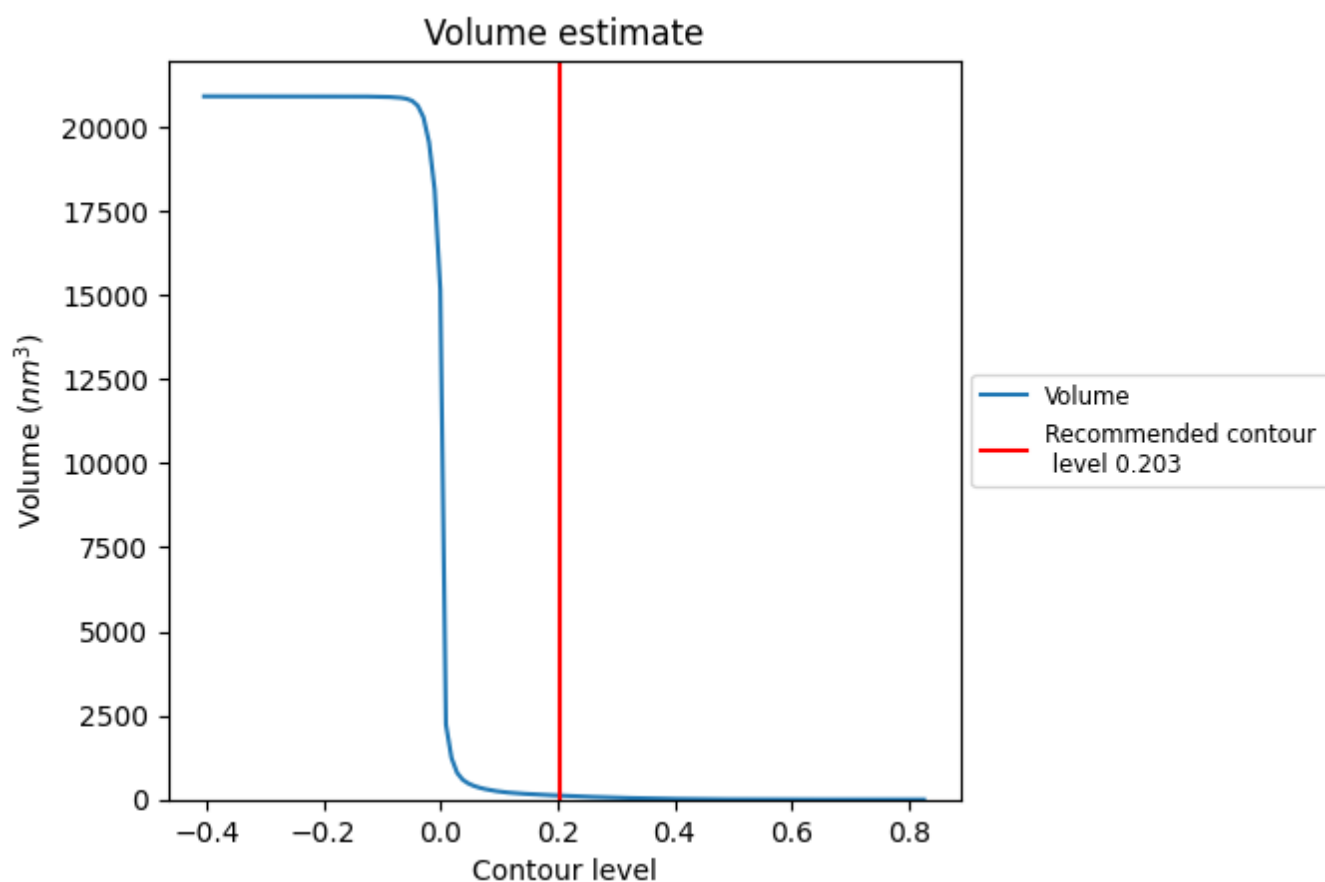
This section contains the results of statistical analysis of the map.

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.

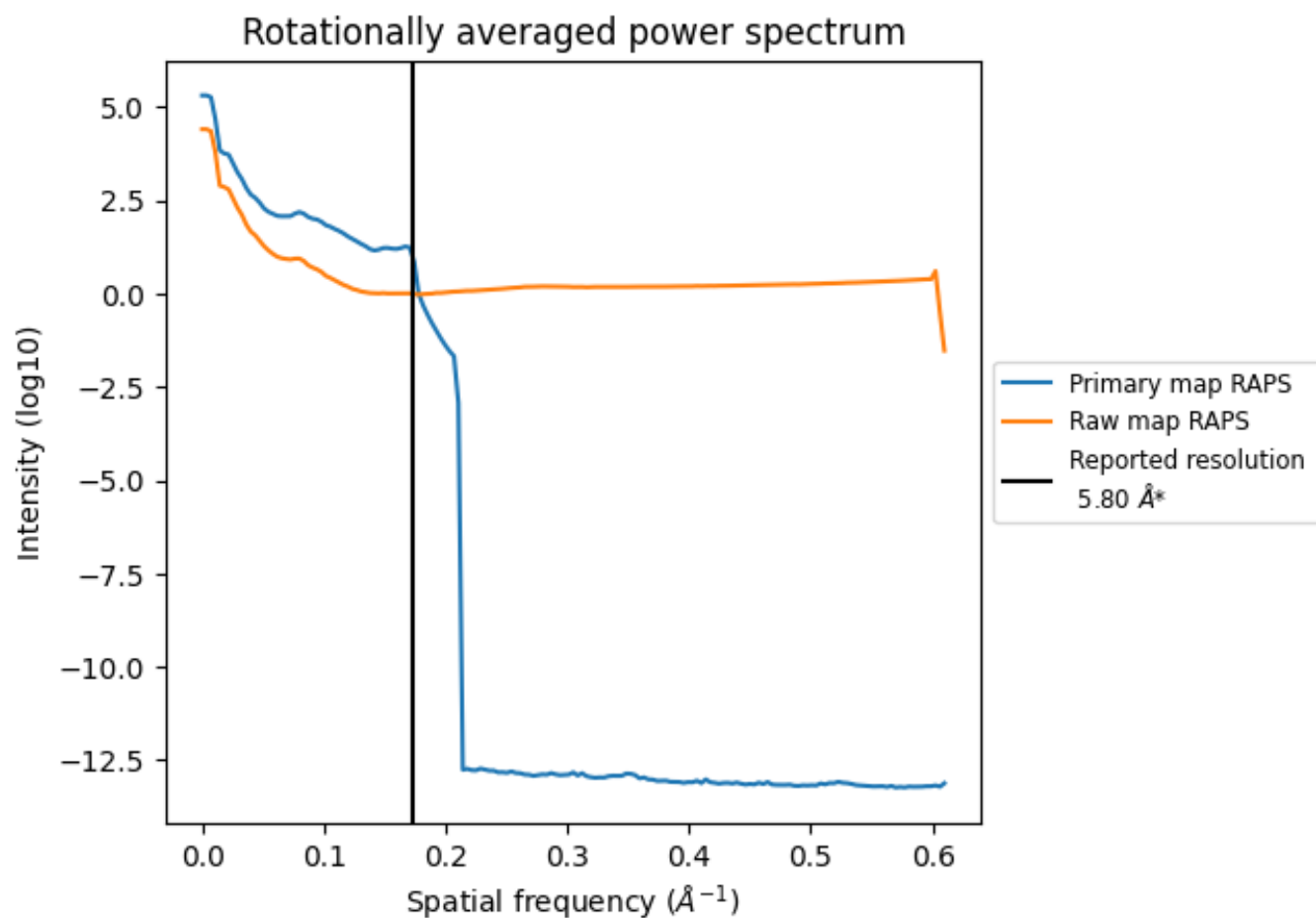
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 118 nm^3 ; this corresponds to an approximate mass of 107 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 ⓘ

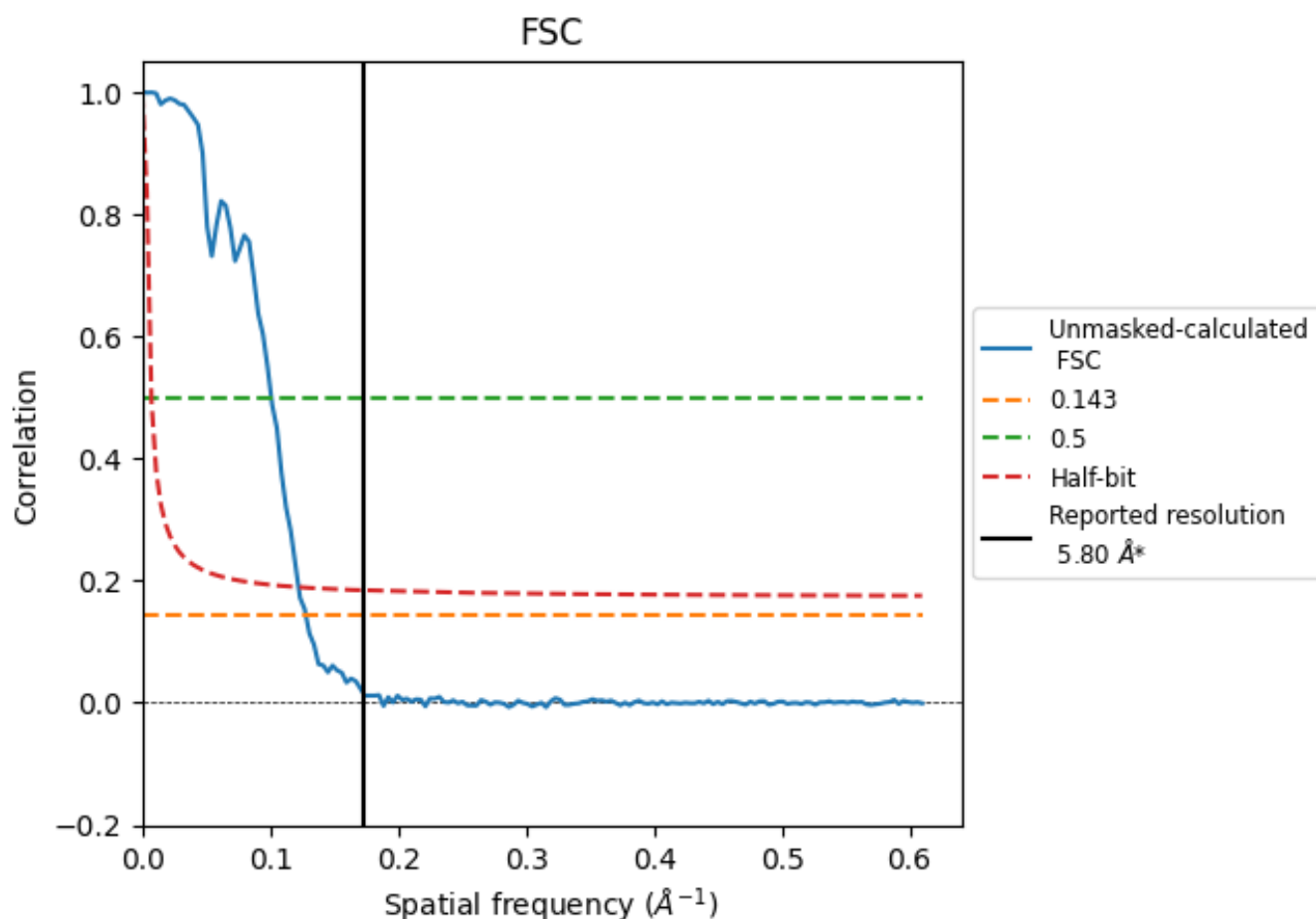


*Reported resolution corresponds to spatial frequency of 0.172 Å⁻¹

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 0.172 Å⁻¹

8.2 Resolution estimates [i](#)

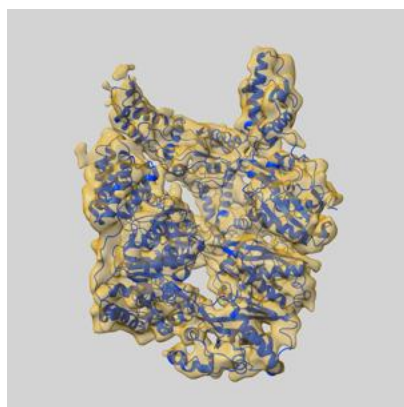
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.81	9.91	8.18

*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 7.81 differs from the reported value 5.8 by more than 10 %

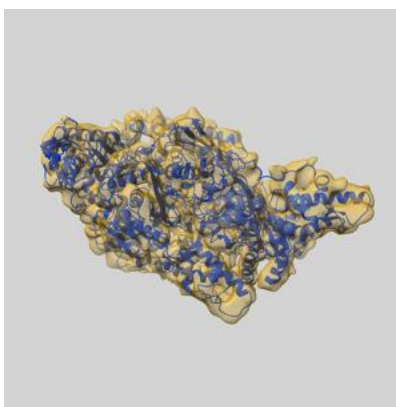
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34111 and PDB model 7YUU. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

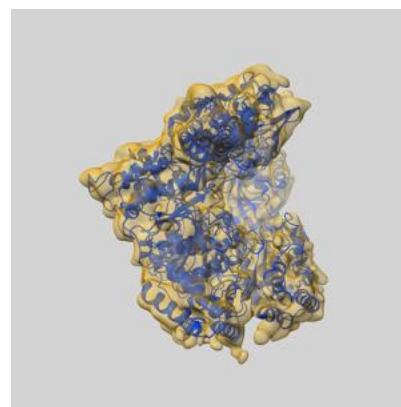
9.1 Map-model overlay [i](#)



X



Y



Z

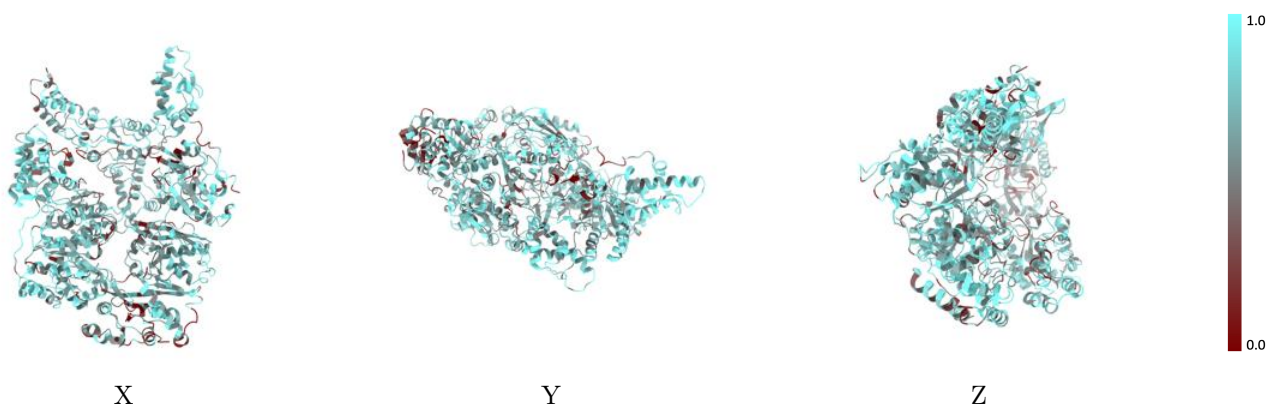
The images above show the 3D surface view of the map at the recommended contour level 0.203 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



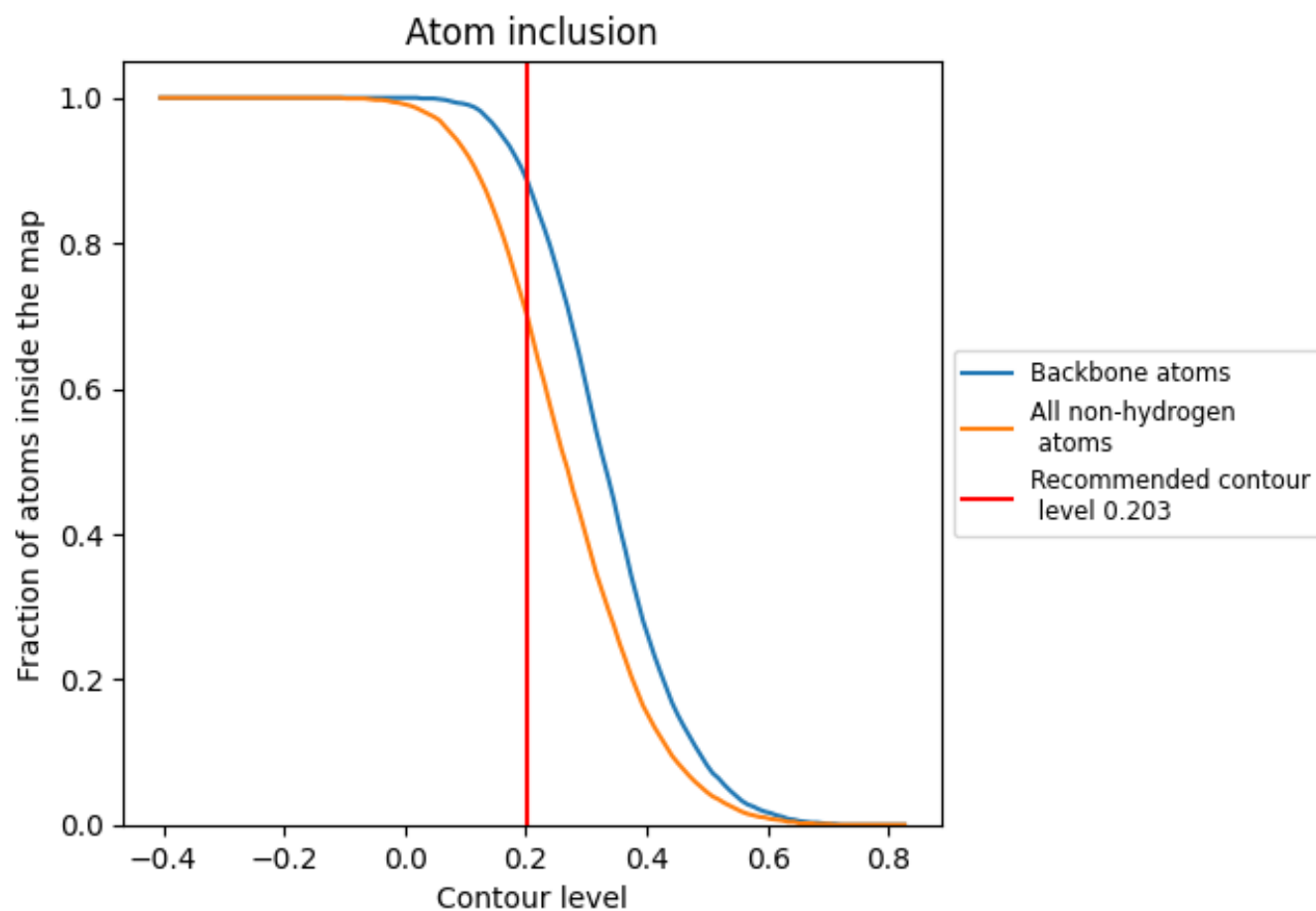
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.203).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 70% 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 (0.203) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6970	<div></div> 0.1940
A	<div></div> 0.6740	<div></div> 0.1870
B	<div></div> 0.7180	<div></div> 0.2060
C	<div></div> 0.7000	<div></div> 0.1880

