



wwPDB EM Validation Summary Report ⓘ

May 18, 2026 – 12:24 PM EDT

PDB ID : 10ET / pdb_000010et
EMDB ID : EMD-75118
Title : Chloroplast Glutamyl Peptidase D855N in open-closed conformation
Authors : Ehrlich, J.J.; Routray, P.; van Wijk, K.J.; Kawate, T.
Deposited on : 2026-01-15
Resolution : 3.00 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

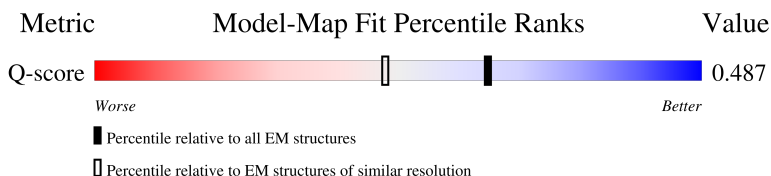
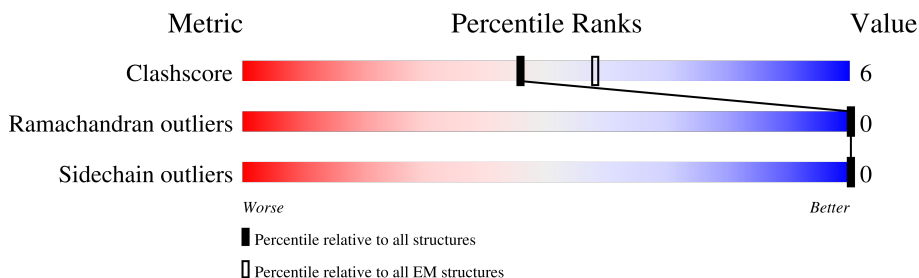
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	907	
1	B	907	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12659 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 Isoform 2 of Probable glutamyl endopeptidase, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	807	Total	C	N	O	S	0	0
			6366	4046	1092	1207	21		
1	A	797	Total	C	N	O	S	0	0
			6293	4003	1076	1193	21		

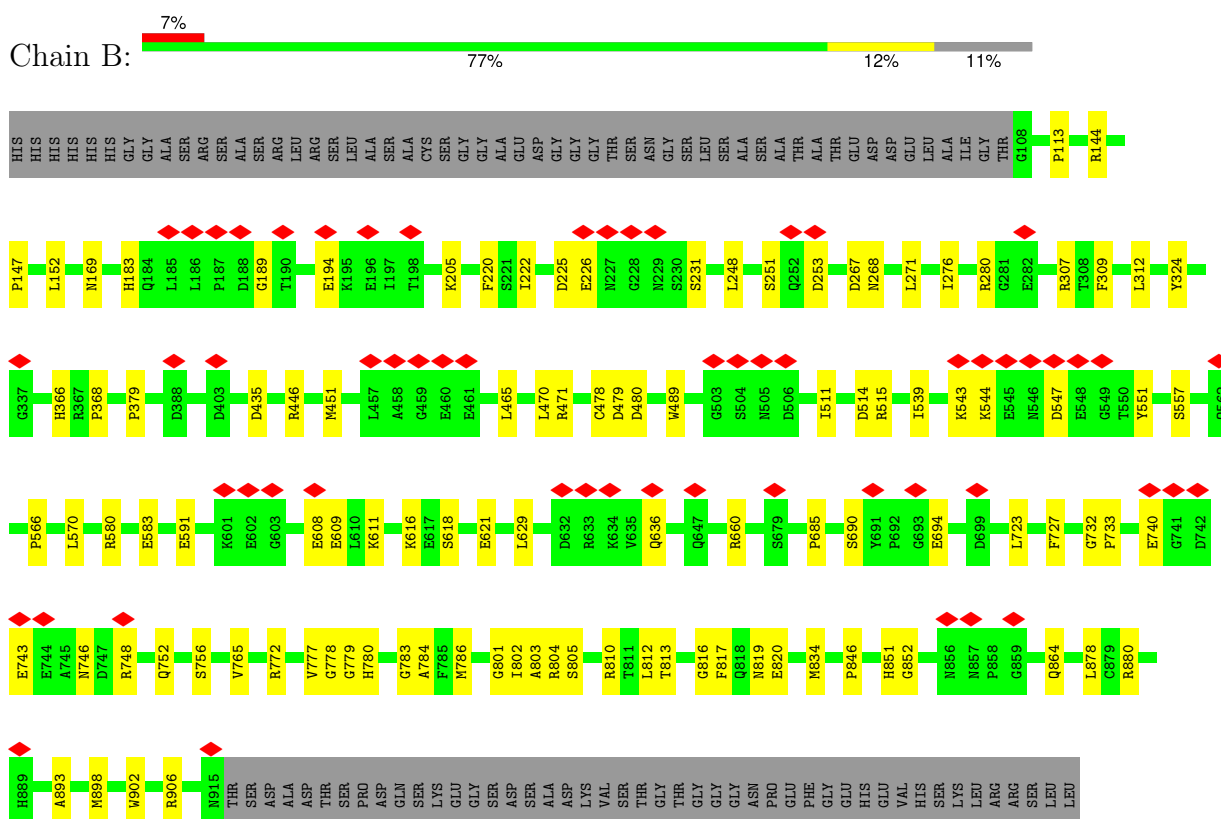
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	54	HIS	-	expression tag	UNP Q8VZF3
B	55	HIS	-	expression tag	UNP Q8VZF3
B	56	HIS	-	expression tag	UNP Q8VZF3
B	57	HIS	-	expression tag	UNP Q8VZF3
B	58	HIS	-	expression tag	UNP Q8VZF3
B	59	HIS	-	expression tag	UNP Q8VZF3
B	60	GLY	-	expression tag	UNP Q8VZF3
B	61	GLY	-	expression tag	UNP Q8VZF3
B	855	ASN	ASP	engineered mutation	UNP Q8VZF3
A	55	HIS	-	expression tag	UNP Q8VZF3
A	56	HIS	-	expression tag	UNP Q8VZF3
A	57	HIS	-	expression tag	UNP Q8VZF3
A	58	HIS	-	expression tag	UNP Q8VZF3
A	59	HIS	-	expression tag	UNP Q8VZF3
A	60	HIS	-	expression tag	UNP Q8VZF3
A	61	GLY	-	expression tag	UNP Q8VZF3
A	62	GLY	-	expression tag	UNP Q8VZF3
A	855	ASN	ASP	engineered mutation	UNP Q8VZF3

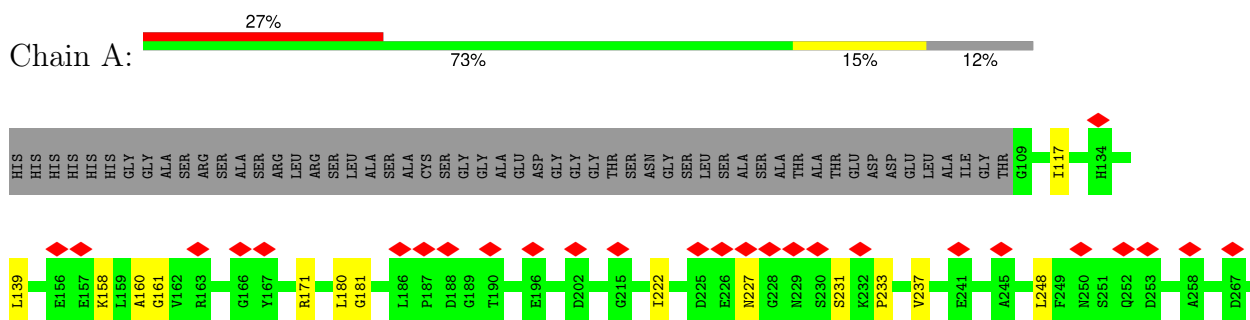
3 Residue-property plots

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: Isoform 2 of Probable glutamyl endopeptidase, chloroplastic



- Molecule 1: Isoform 2 of Probable glutamyl endopeptidase, chloroplastic



GLY	G801	I638	V552	W489	L428	S354	L272
GLY	T639	L553	L554	Y490	W430	T355	L275
ASN	R804	N555	G556	K491	A431	T355	L276
PRO	A807	H643	S557	T492	E432	H357	P277
PHE	Y645	P644	G558	R493	T433	K358	S278
GLY	L812	Y645	S557	R493	Q434	Y359	S279
GLU	Q652	Q652	G558	R494	D435	L365	R280
HIS	E820	M655	T560	R496	G436	L365	G281
GLU	P651	P561	P561	T497	G437	S370	E282
VAL	K844	Q562	Q562	W498	D438	F371	P283
HIS	K845	G563	G563	V499	A439	I372	P284
SER	P846	N564	N564	I500	K440	V373	K285
LYS	H851	L672	V565	S501	M441	G376	K286
LEU		K690	P566	P502	E442		P287
ARG	N856	F567	F567	G503	V443		L288
ARG	N857	L568	L568	S504	S444		V289
LEU	P858	D569	D569	S504	S444	K380	P290
LEU	G859	L570	L570	N505	P445	K381	S291
	T860	LYS	F571	D506	R446	V382	
		SER	D572	V507	D447	E383	T295
	T860	LYS	D572	V507	D447	E383	
	Q864	ASP	I573	S508	I448		
	S865	ALA	N574	P509	Y449	T387	T300
		ALA	N574	P509	Y449	D388	K301
	S888	ALA	T575	R510	Y450	G389	
	H889	GLY	G576	R510	Y450		
		GLN	N577	L512	M451	R390	
	I897	VAL	N577	L512	M451	F391	
		ARG	K578	F513	Q452	V392	V303
		G706	E579	D514	S453	R393	V304
			R580	R515	A454	Q394	Q305
		T717	R580	R515	E455	Q394	V306
	N915	S718	I581	S516	E455	L395	R307
THR	SER	A719	W582	S517	P456	C596	T308
SER	ASP	L720	E583	E518	L457	D397	F309
ALA	ASP	L721		D519	A458	L398	
ALA	G732		E587	V520	G459		Q310
P733				V520	E460	E402	D311
THR		S598	S598	Y521	E461	D403	L312
SER		D599	D599	S522	E461	D403	L313
PRO		Q600	Q600	D523	E462	I404	K314
ASP		K601	K601	P524	E463	P405	D315
GLN	E740	E602	E602	G525	L465	I406	E316
SER	G741	G603	G603	S526	H466	A407	E317
LYS	D742	D604	D604	T527	K467	S408	Y317
GLU	E743	L605	L605	M528	L468	N409	D318
GLY	E744	L605	L605	M528	L468	N409	A319
SER	A745	K606	K606	R530	D469	S410	D320
ASP	N746	M607	M607	R531	L470	V411	
SER		E763	E763	T532	R471	R412	D323
ALA		E608	E608	D533	Y472	K413	
ASP	R767	E609	E609	D533	G473	G414	Q329
LYS	G768	L610	L610	A534	G474	M415	L330
VAL	V769	K611	K611		I475	R416	V331
SER		L612	L612	I539	S476	S417	L332
THR				A540	W477	I418	
GLY	H780	N622	N622	A540	C478	I418	L335
THR				K541	D479		D336
	L791	Q628	Q628	I542	D479	R421	
		L629	L629	K543	D480	A422	
		W630	W630	K544	T481	D423	K340
		P631	P631	E545	L482	K424	E341
		D632	D632	N546		P425	
		R633	R633	D547	V485	S426	A346
		K634	K634	E548	Y486	T427	
				G549	E487		L351
				T550	S488		
				Y551			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70609	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	0.666	Depositor
Minimum map value	-0.387	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	284.96, 284.96, 284.96	wwPDB
Map dimensions	208, 208, 208	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	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	0.10	0/6455	0.28	0/8781
1	B	0.11	0/6529	0.29	0/8880
All	All	0.11	0/12984	0.29	0/17661

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	6293	0	6194	91	0
1	B	6366	0	6273	66	0
All	All	12659	0	12467	156	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 156 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:479:ASP:OD1	1:B:480:ASP:N	2.17	0.78
1:A:421:ARG:HH22	1:A:451:MET:HG2	1.47	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:690:SER:OG	1:B:786:MET:SD	2.48	0.71
1:A:780:HIS:HD2	1:A:804:ARG:HE	1.39	0.71
1:A:421:ARG:HH21	1:A:429:TYR:HB3	1.56	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	793/907 (87%)	769 (97%)	24 (3%)	0	100	100
1	B	805/907 (89%)	778 (97%)	27 (3%)	0	100	100
All	All	1598/1814 (88%)	1547 (97%)	51 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	691/772 (90%)	691 (100%)	0	100	100
1	B	698/772 (90%)	698 (100%)	0	100	100
All	All	1389/1544 (90%)	1389 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	329	GLN
1	A	643	HIS
1	A	577	ASN
1	A	659	GLN
1	B	789	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.

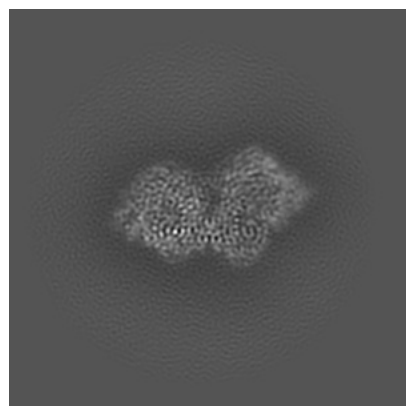
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75118. These allow visual inspection of the internal detail of the map and identification of artifacts.

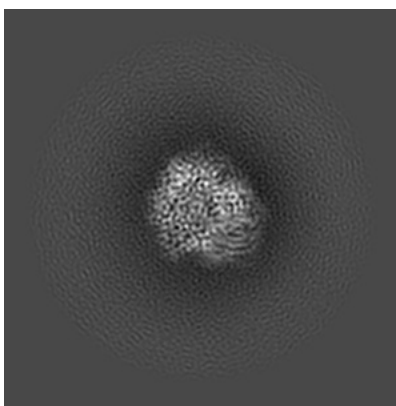
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

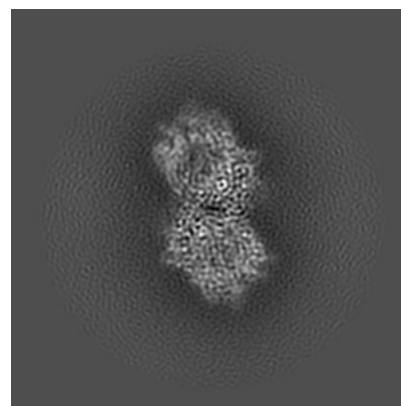
6.1.1 Primary map



X

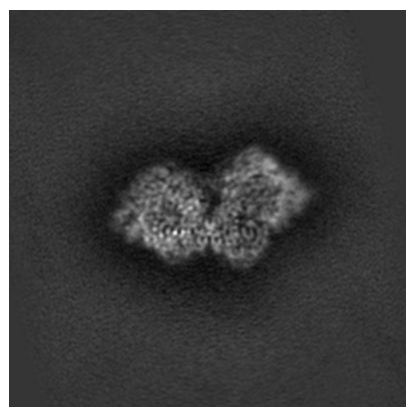


Y

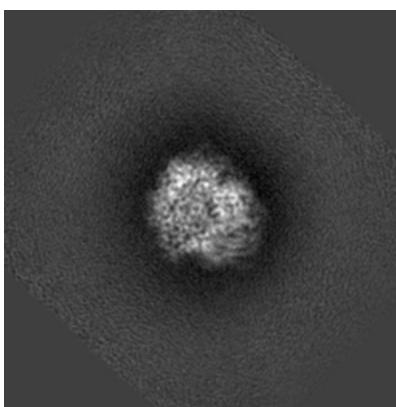


Z

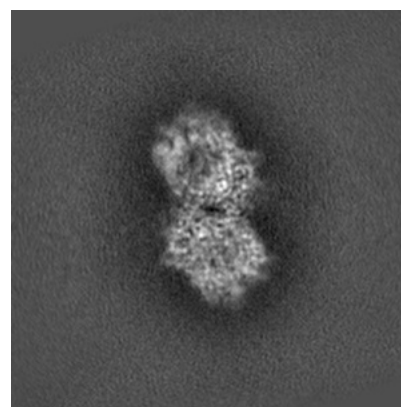
6.1.2 Raw map



X



Y

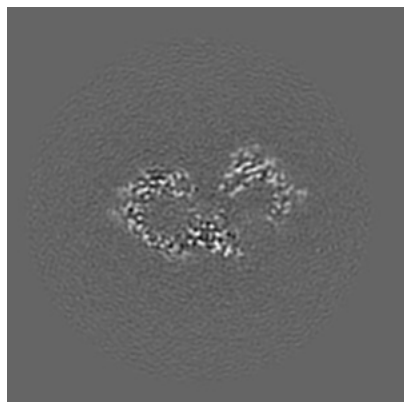


Z

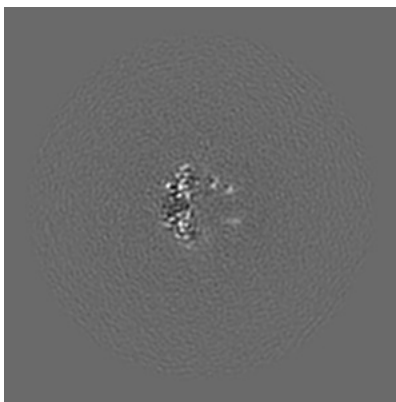
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

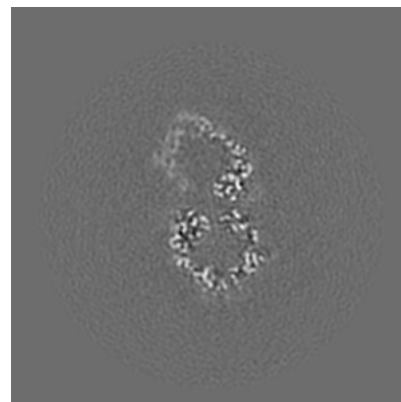
6.2.1 Primary map



X Index: 104



Y Index: 104

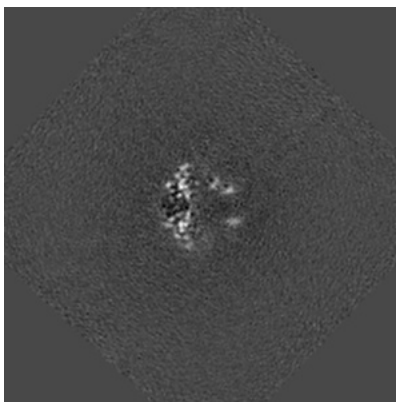


Z Index: 104

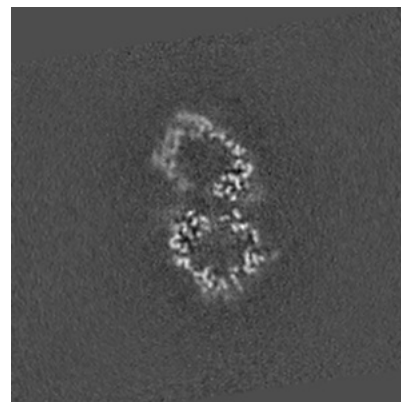
6.2.2 Raw map



X Index: 104



Y Index: 104

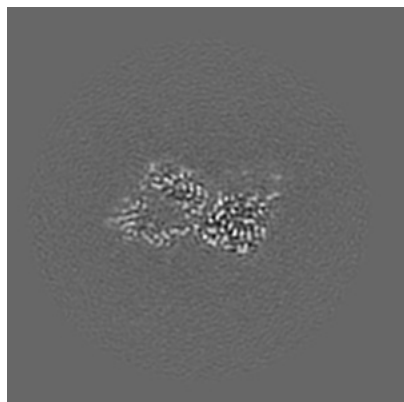


Z Index: 104

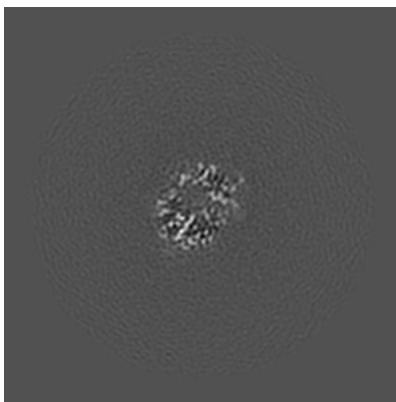
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

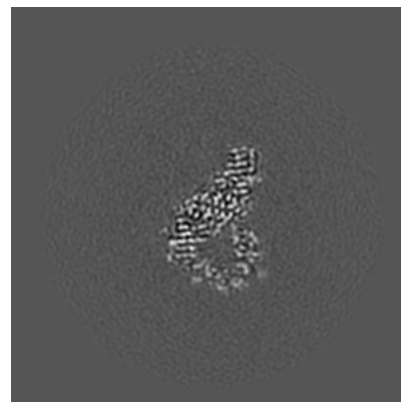
6.3.1 Primary map



X Index: 116

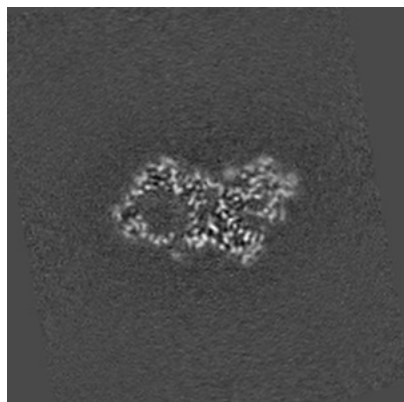


Y Index: 93

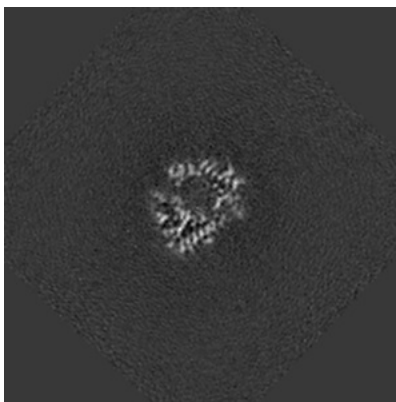


Z Index: 91

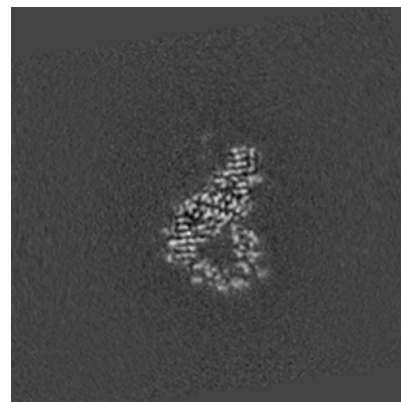
6.3.2 Raw map



X Index: 112



Y Index: 90

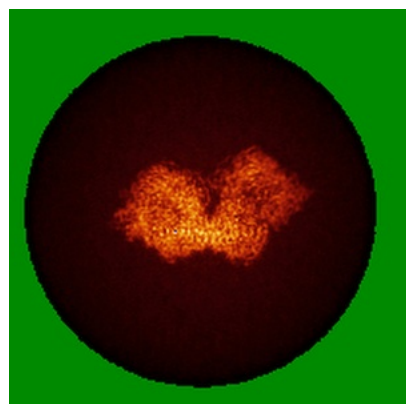


Z Index: 91

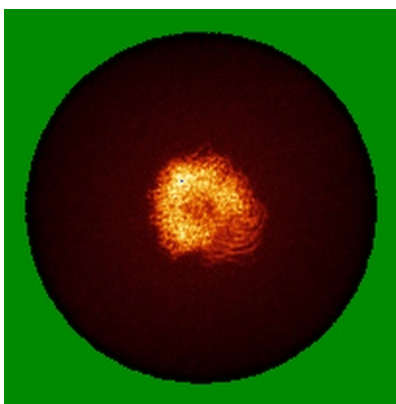
The images above show the largest variance slices of the map in three orthogonal directions.

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

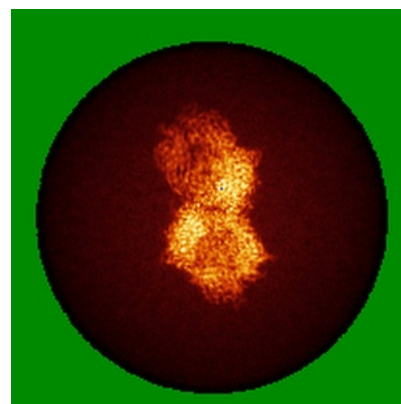
6.4.1 Primary map



X

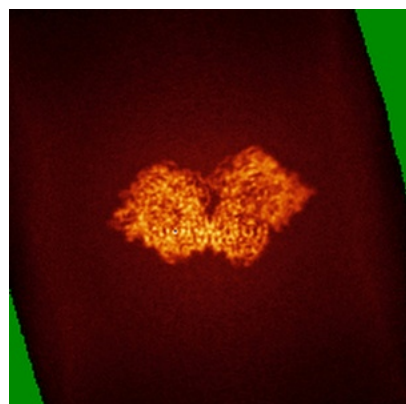


Y

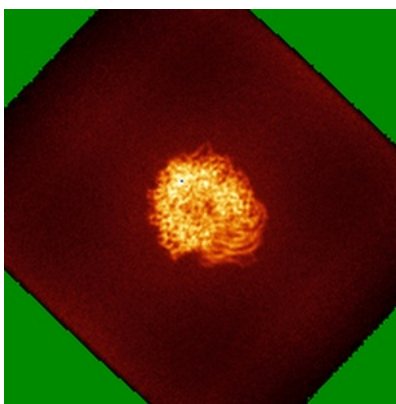


Z

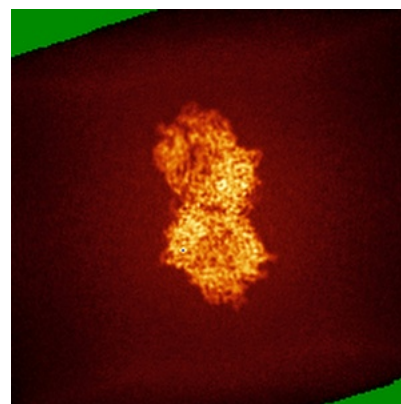
6.4.2 Raw map



X



Y

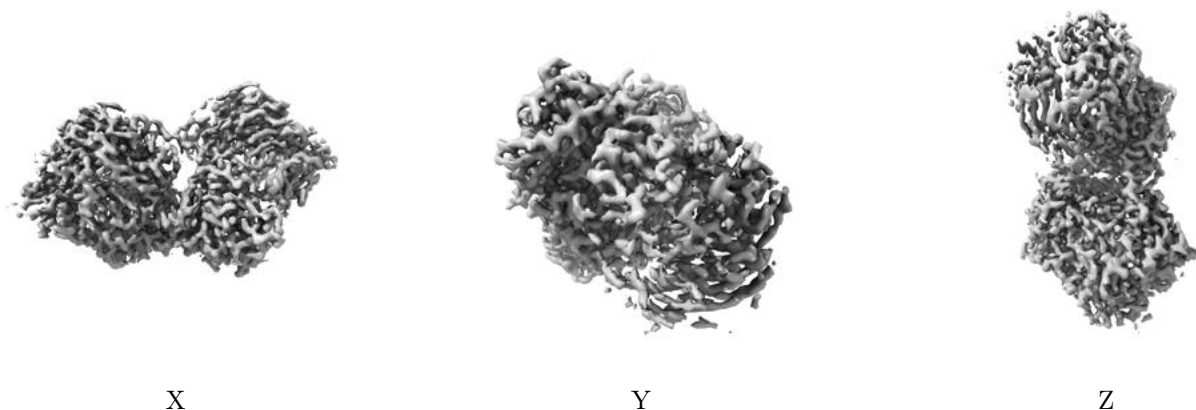


Z

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.

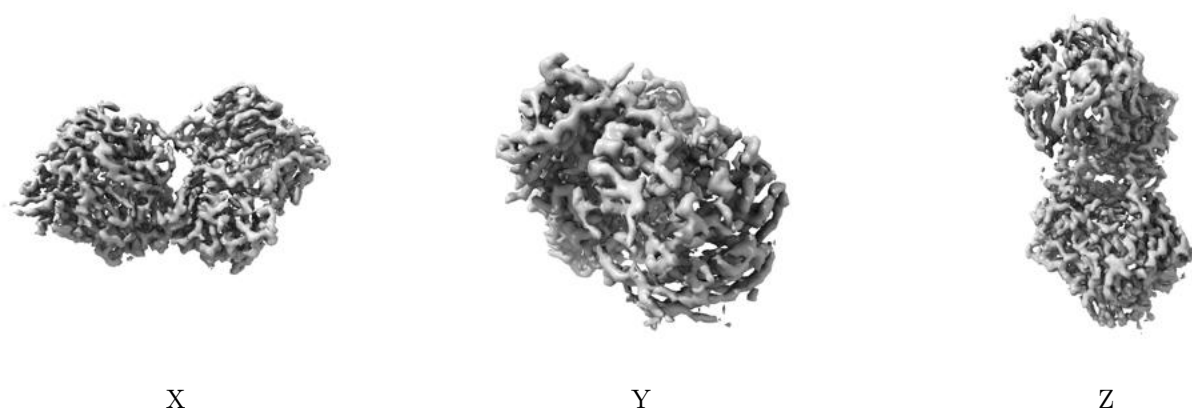
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

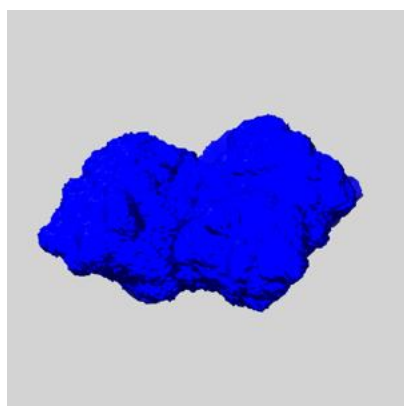
6.6 Mask visualisation [i](#)

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

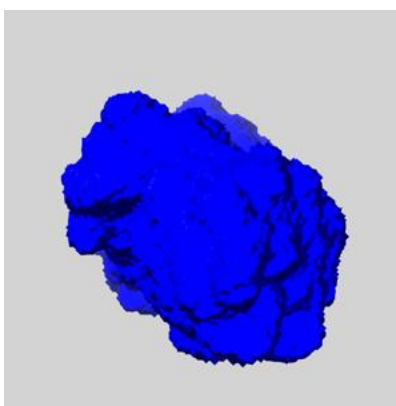
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

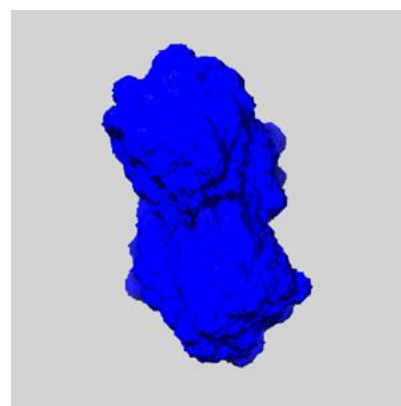
6.6.1 emd_75118_msk_1.map [i](#)



X



Y

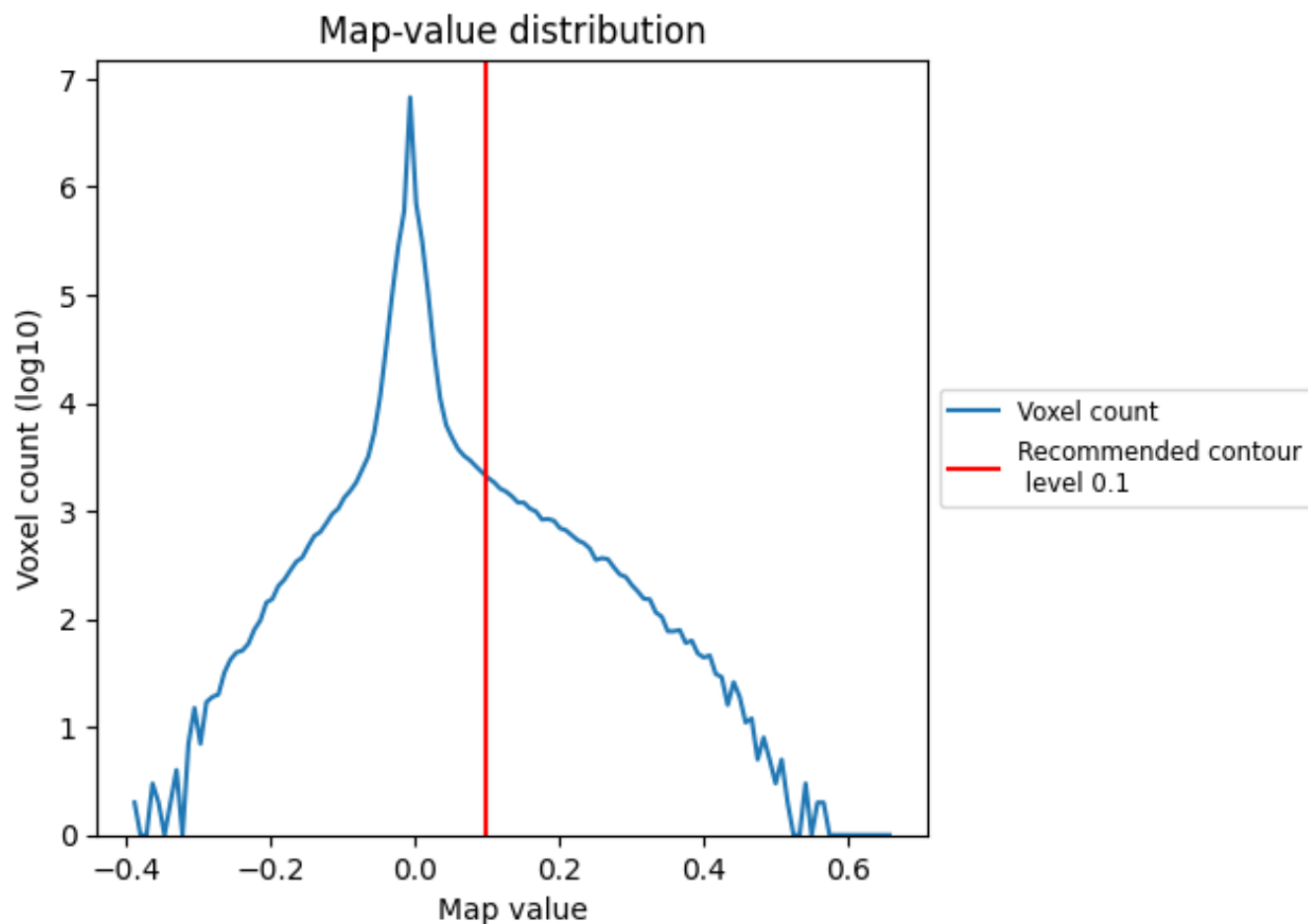


Z

7 Map analysis [i](#)

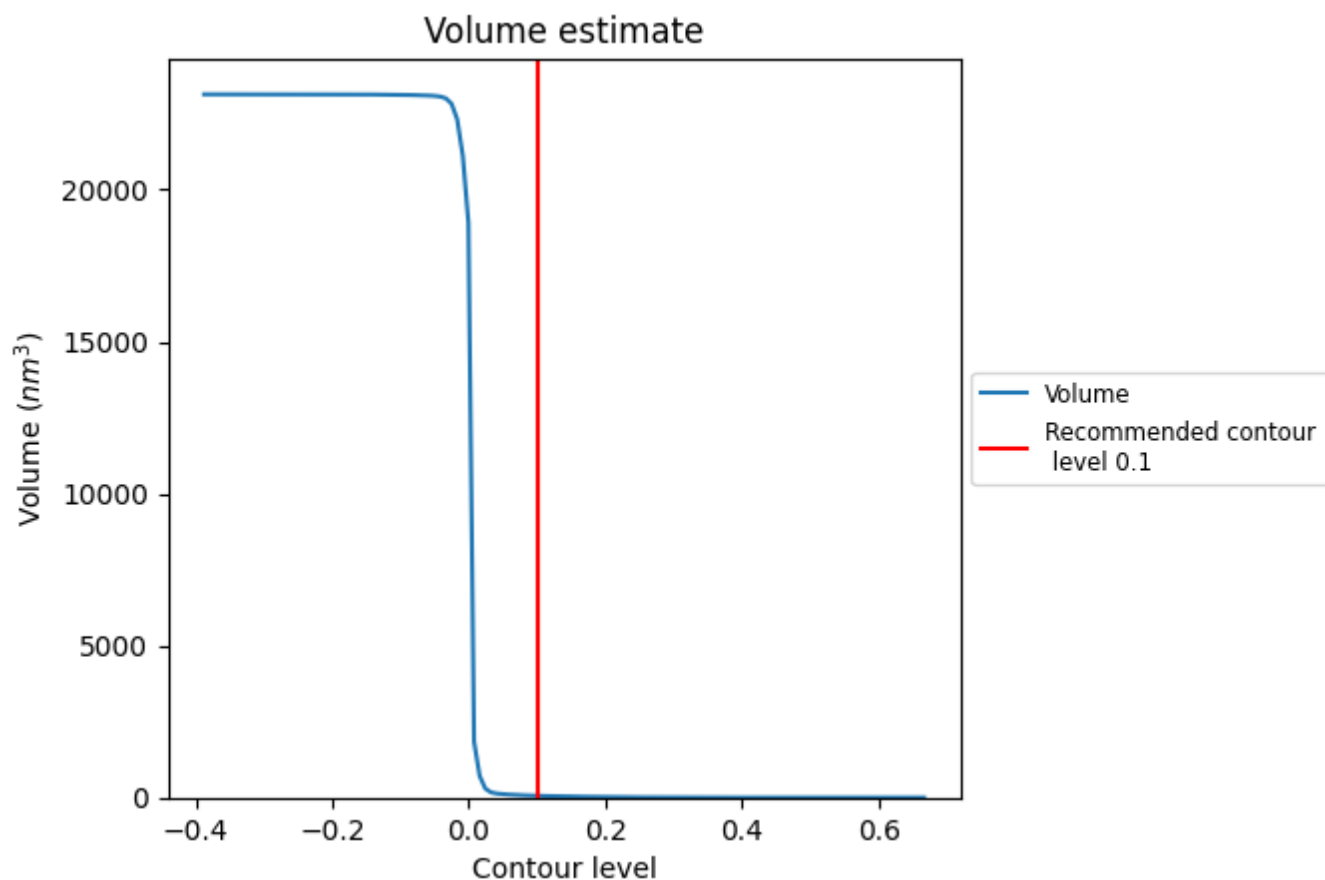
This section contains the results of statistical analysis of the map.

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.

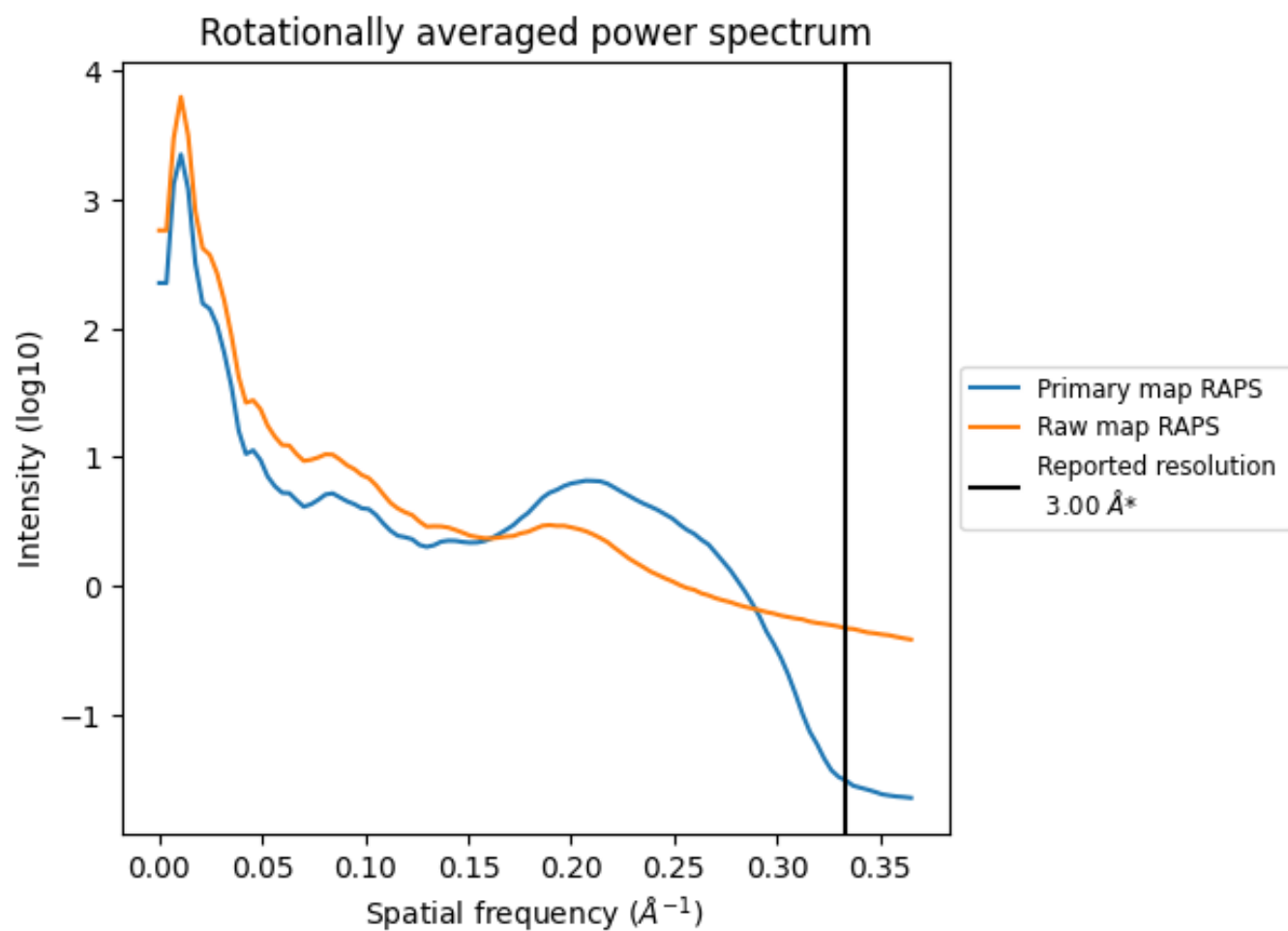
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 58 nm³; this corresponds to an approximate mass of 53 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 ⓘ

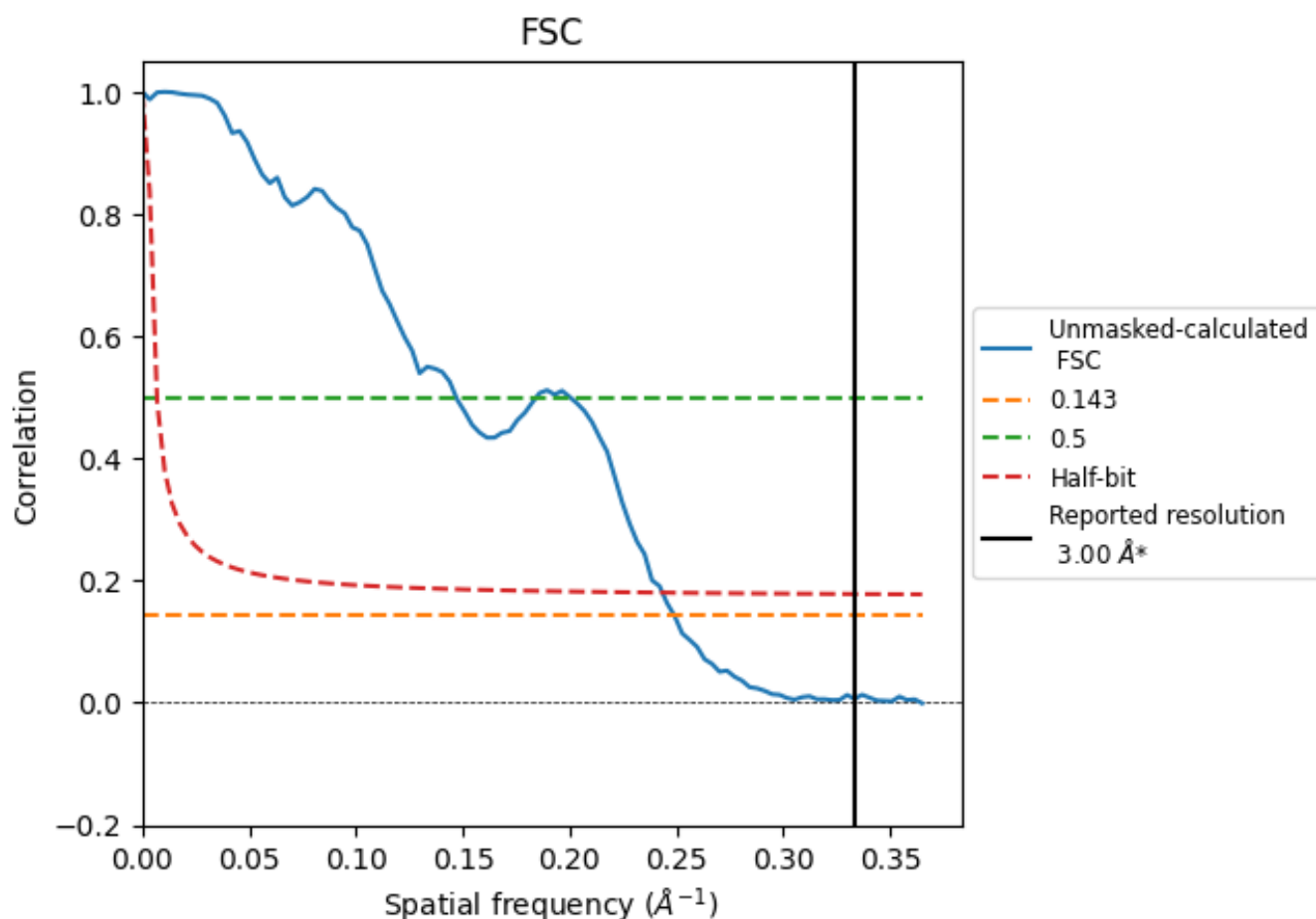


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

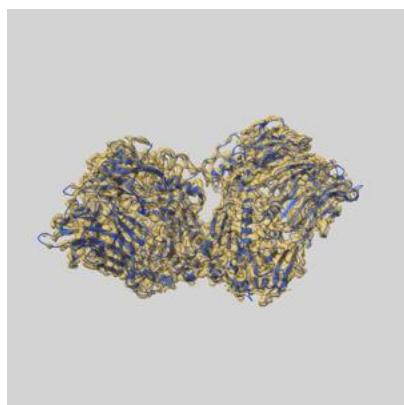
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.02	6.81	4.11

*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 4.02 differs from the reported value 3.0 by more than 10 %

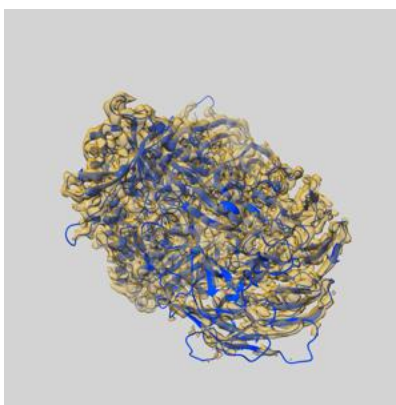
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75118 and PDB model 10ET. Per-residue inclusion information can be found in section [3](#) on page [4](#).

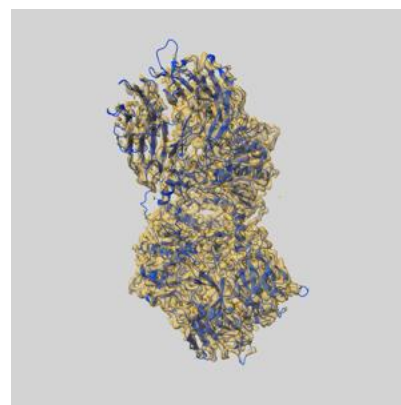
9.1 Map-model overlay [i](#)



X



Y



Z

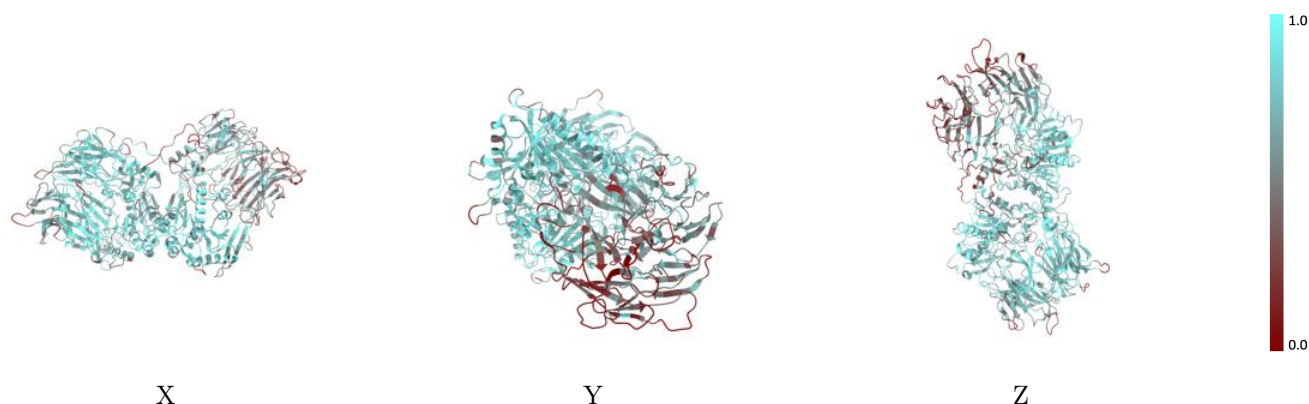
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



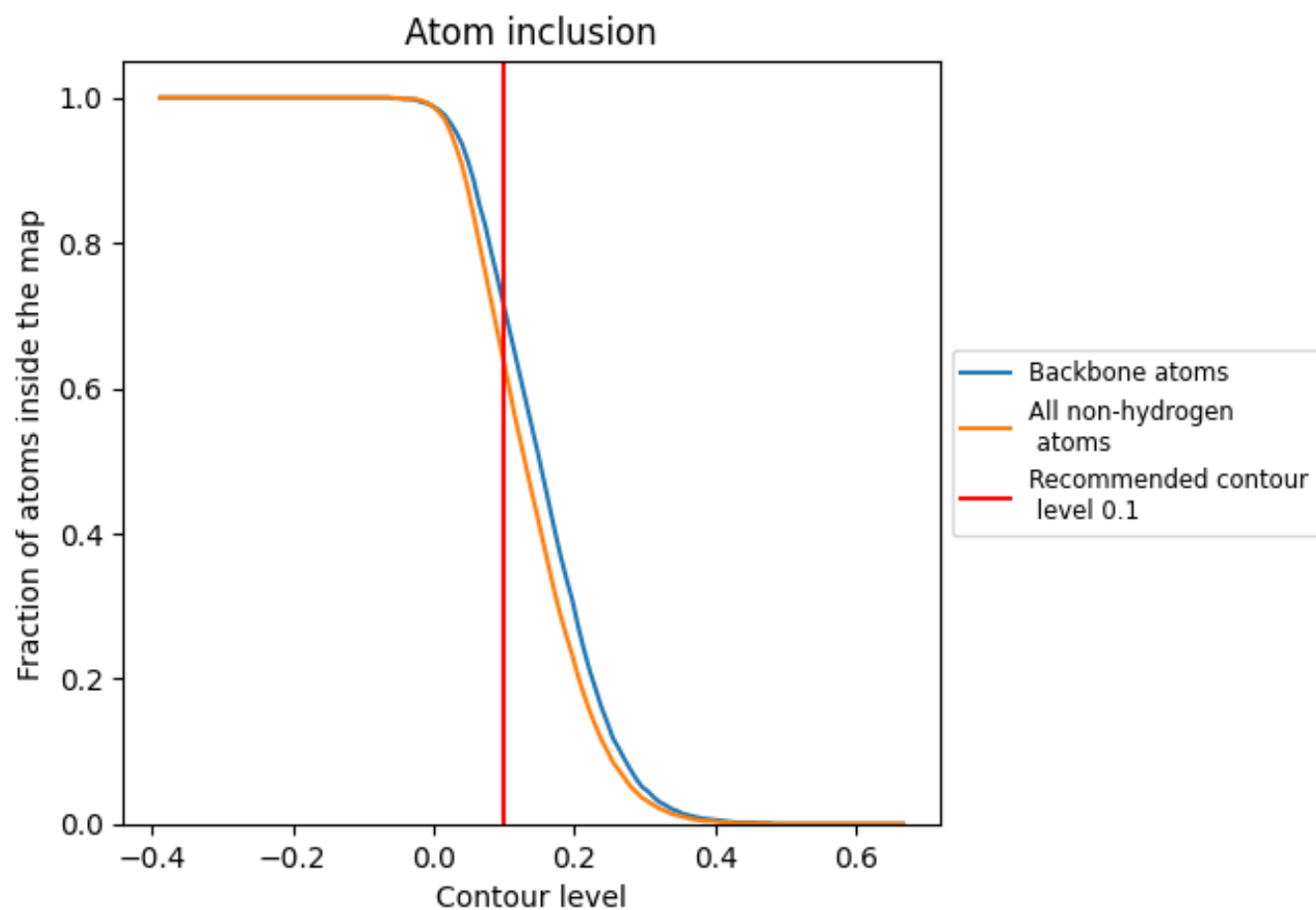
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6340	<div></div> 0.4870
A	<div></div> 0.5480	<div></div> 0.4590
B	<div></div> 0.7200	<div></div> 0.5140

