



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:56 AM UTC

PDB ID : 7F5T / pdb_00007f5t
EMDB ID : EMD-31466
Title : Drosophila P5CS filament with glutamate
Authors : Liu, J.L.; Zhong, J.; Guo, C.J.; Zhou, X.
Deposited on : 2021-06-22
Resolution : 4.10 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

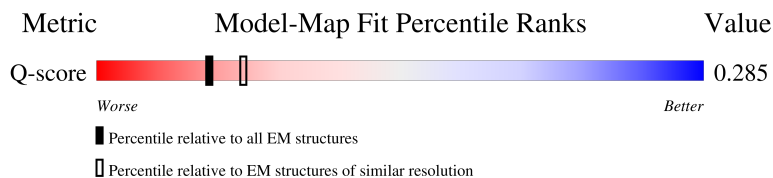
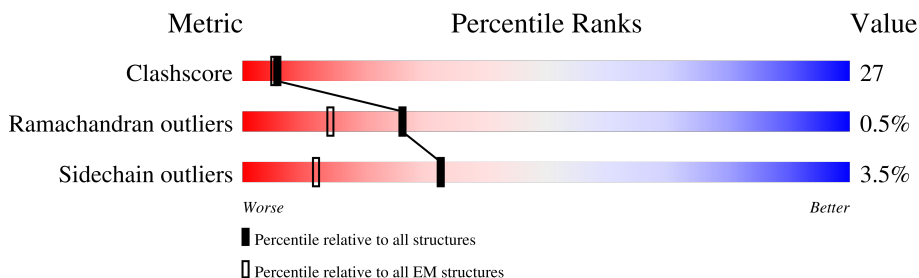
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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	6458 (3.60 - 4.60)

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	776	 5% 42% 44% • 13%
1	B	776	 5% 42% 44% • 13%
1	C	776	 5% 42% 43% • 13%
1	D	776	 5% 42% 43% • 13%

2 Entry composition [i](#)

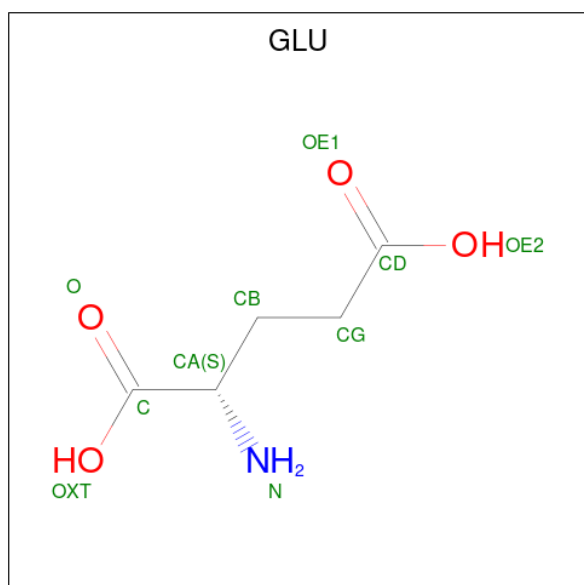
There are 2 unique types of molecules in this entry. The entry contains 20436 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Delta-1-pyrroline-5-carboxylate synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	674	Total	C	N	O	S	0	0
			5099	3195	904	972	28		
1	B	674	Total	C	N	O	S	0	0
			5099	3195	904	972	28		
1	C	674	Total	C	N	O	S	0	0
			5099	3195	904	972	28		
1	D	674	Total	C	N	O	S	0	0
			5099	3195	904	972	28		

- Molecule 2 is GLUTAMIC ACID (CCD ID: GLU) (formula: $C_5H_9NO_4$) (labeled as "Ligand of Interest" by depositor).

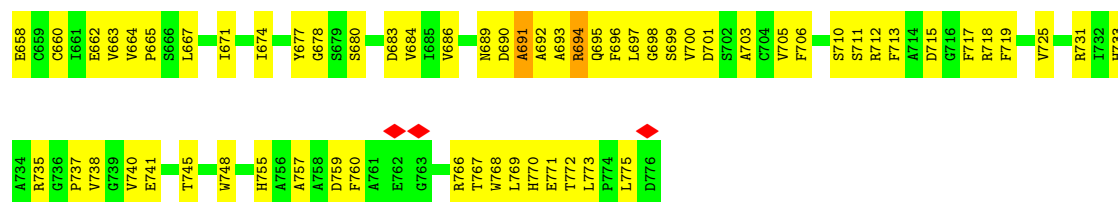


Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			10	5	1	4	
2	B	1	Total	C	N	O	0
			10	5	1	4	

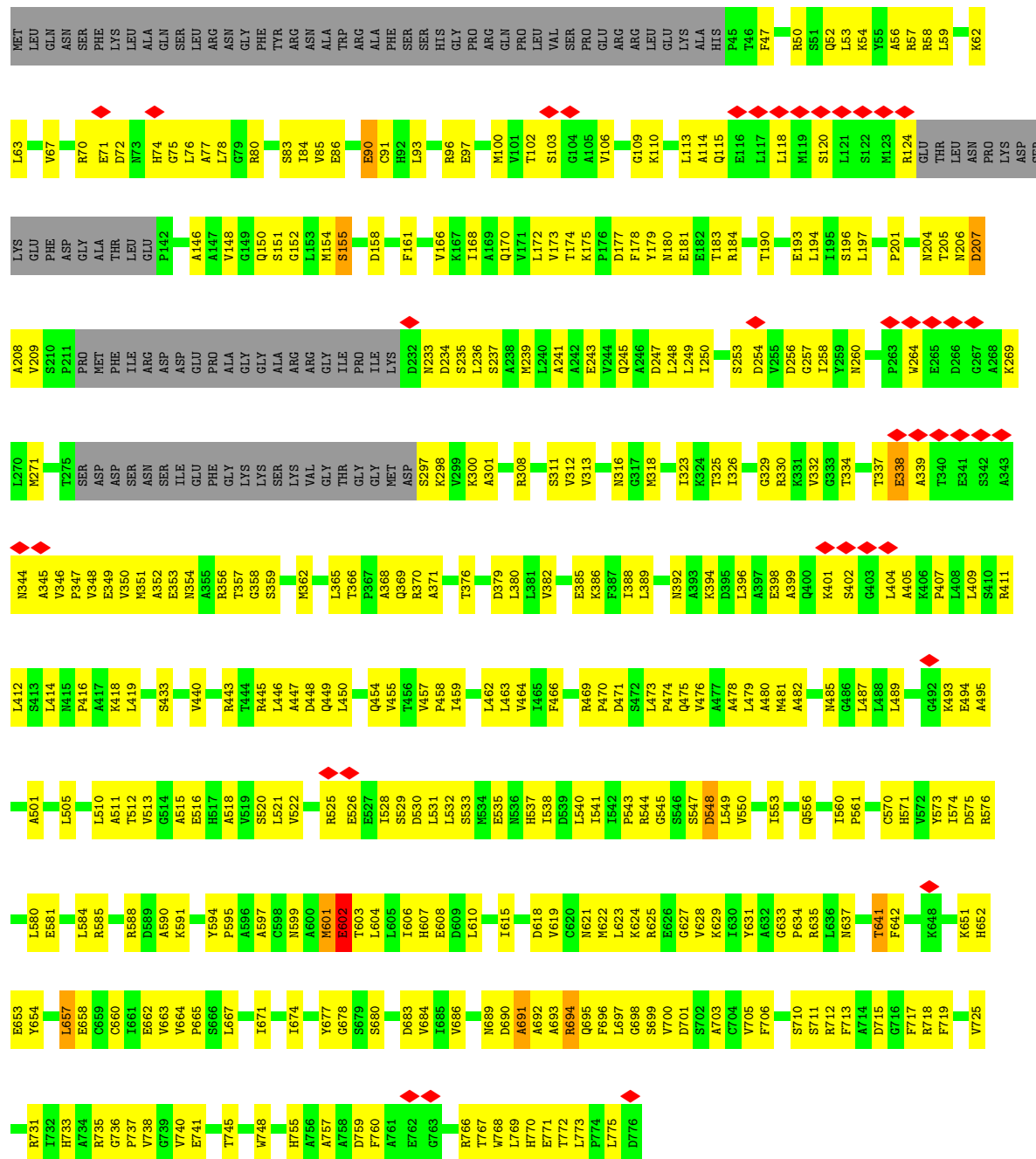
Continued on next page...

Continued from previous page...

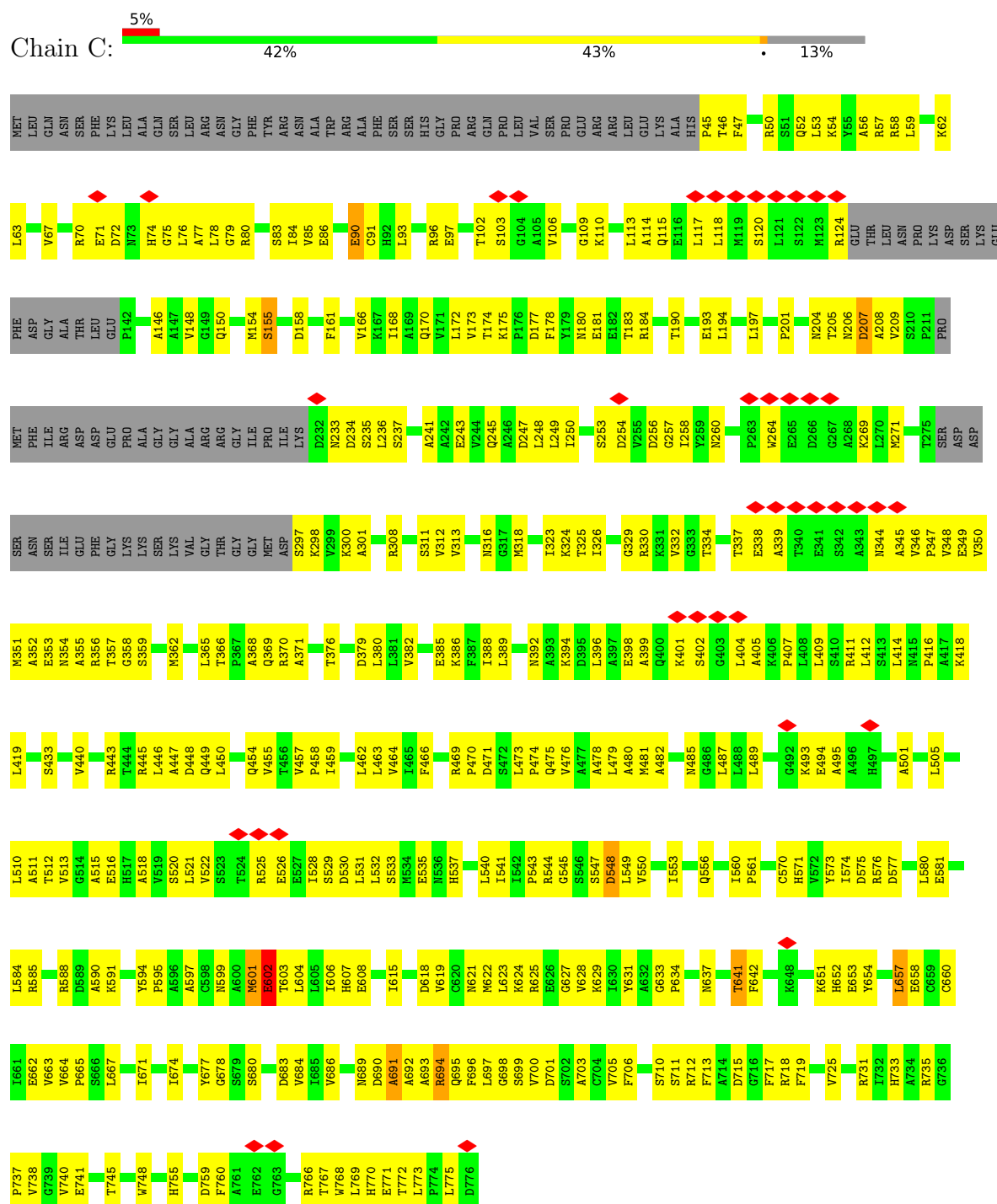
Mol	Chain	Residues	Atoms				AltConf
2	C	1	Total	C	N	O	0
			10	5	1	4	
2	D	1	Total	C	N	O	0
			10	5	1	4	



• Molecule 1: Delta-1-pyrroline-5-carboxylate synthase



• Molecule 1: Delta-1-pyrroline-5-carboxylate synthase



• Molecule 1: Delta-1-pyrroline-5-carboxylate synthase



L63	PHE	S210	V346	L414	L505	E581	E658	A734
V67	ASP	P211	P347	M415	L510	L584	G659	R735
R70	GLY	MET	E349	A417	A511	R585	C660	G736
E71	THR	ILE	V350	K418	T512	R588	I661	P737
D72	LEU	ARG	M351	L419	V513	D589	V663	G738
M73	GLU	ASP	A352	S433	G514	A590	V664	V740
H74	P142	ASP	N354	V440	A515	K591	P665	E741
G75	A146	GLU	A355	R356	H517	Y594	L667	T745
L76	A147	PRO	R357	L365	A518	P595	I671	W748
A77	V148	ALA	G358	T366	V519	A596	I674	H755
L78	G149	GLY	S359	F367	T444	A597	Y677	A756
G79	Q150	GLY	M362	A368	R445	C598	G678	A758
R80	S151	ALA	L365	Q369	L446	N599	R679	D759
S83	G152	ARG	T366	R370	A447	A600	S680	F760
I84	M154	GLY	L365	A371	Q454	M601	D683	A761
V85	S155	ILE	T366	T376	V455	E602	V684	E762
E86	D158	PRO	F367	D379	V456	T603	I685	G763
E90	F161	LYS	A371	L462	L450	L604	V686	R766
C91	V166	D232	A371	L463	Q454	L604	D689	W768
H92	K167	N233	T376	V464	V455	L604	D690	L769
L93	I168	D234	A371	L465	T456	L606	A692	H770
R96	A169	S235	A371	T466	V457	H607	A693	E771
E97	Q170	L236	A371	F466	P458	E608	R694	T772
T102	V171	S237	A371	R469	L459	P609	G695	L773
S103	L172	A238	A371	D471	L462	L610	R696	P774
G104	V173	M239	A371	L473	L463	L615	D697	L775
A105	T174	L240	A371	L477	L465	V619	N621	D776
V106	K175	A241	A371	A477	F466	G620	N622	
G109	P176	E242	A371	L478	R469	G620	N625	
K110	D177	V244	A371	L479	D471	G620	R625	
L113	F178	Q245	A371	L480	S472	G620	E626	
A114	Y179	A246	A371	A480	P474	G627	G627	
Q115	M180	L248	A371	A481	Q475	V628	A703	
E116	E181	L249	A371	A482	V476	K629	V705	
L117	T183	I250	A371	M485	A477	Y631	F706	
L118	R184	S253	A371	G486	L478	A632	S702	
M119	T190	D254	A371	L487	L488	G633	A704	
S120	E193	V255	A371	L489	L489	P634	V705	
L121	E193	D256	A371	G492	G492	N637	S710	
S122	I195	G257	A371	K401	K401	P642	S711	
L121	S196	I258	A371	G403	G403	R648	R712	
S122	L197	N260	A371	L404	L404	K651	F713	
M123	P201	P263	A371	A405	A405	H652	D715	
R124	N204	V264	A371	K406	K406	Y573	G716	
GLU	T205	E265	A371	P407	P407	Y573	R717	
THR	L206	D266	A371	L408	L408	Y573	R718	
LEU	D207	G267	A371	S410	S410	Y573	F719	
ASN	A208	K269	A371	L411	L411	Y573	V725	
PRO	A208	L270	A371	L412	L412	Y573	R731	
LYS	A208	M271	A371	L413	L413	Y573	I732	
LYS	A208		A371	L414	L414	Y573	H733	
GLU	A208		A371	L415	L415	Y573		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	432746	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 ($e^-/\text{\AA}^2$)	72	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.026	Depositor
Minimum map value	-0.006	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	317.99997, 317.99997, 317.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	0/5173	0.56	3/6996 (0.0%)
1	B	0.41	0/5173	0.56	3/6996 (0.0%)
1	C	0.41	0/5173	0.56	3/6996 (0.0%)
1	D	0.41	0/5173	0.56	3/6996 (0.0%)
All	All	0.41	0/20692	0.56	12/27984 (0.0%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	345	ALA	CA-C-N	-5.40	118.63	123.33
1	D	345	ALA	C-N-CA	-5.40	118.63	123.33
1	C	345	ALA	CA-C-N	-5.39	118.64	123.33
1	C	345	ALA	C-N-CA	-5.39	118.64	123.33
1	A	345	ALA	CA-C-N	-5.38	118.65	123.33

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	5099	0	5173	282	0
1	B	5099	0	5173	288	0
1	C	5099	0	5173	278	0
1	D	5099	0	5173	286	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	10	0	5	0	0
2	B	10	0	5	0	0
2	C	10	0	5	0	0
2	D	10	0	5	0	0
All	All	20436	0	20712	1119	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 27.

The worst 5 of 1119 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:733:HIS:HB2	1:D:733:HIS:HB2	1.46	0.97
1:D:346:VAL:HG22	1:D:350:VAL:HG13	1.62	0.81
1:B:346:VAL:HG22	1:B:350:VAL:HG13	1.62	0.81
1:A:346:VAL:HG22	1:A:350:VAL:HG13	1.62	0.80
1:C:346:VAL:HG22	1:C:350:VAL:HG13	1.62	0.80

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	666/776 (86%)	574 (86%)	89 (13%)	3 (0%)	24	61
1	B	666/776 (86%)	575 (86%)	88 (13%)	3 (0%)	24	61
1	C	666/776 (86%)	575 (86%)	88 (13%)	3 (0%)	24	61
1	D	666/776 (86%)	575 (86%)	88 (13%)	3 (0%)	24	61
All	All	2664/3104 (86%)	2299 (86%)	353 (13%)	12 (0%)	26	61

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	602	GLU
1	B	602	GLU
1	C	602	GLU
1	D	602	GLU
1	A	114	ALA

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	545/630 (86%)	526 (96%)	19 (4%)	32	54
1	B	545/630 (86%)	526 (96%)	19 (4%)	32	54
1	C	545/630 (86%)	526 (96%)	19 (4%)	32	54
1	D	545/630 (86%)	526 (96%)	19 (4%)	32	54
All	All	2180/2520 (86%)	2104 (96%)	76 (4%)	32	54

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	90	GLU
1	D	663	VAL
1	D	155	SER
1	D	464	VAL
1	D	772	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	607	HIS
1	D	204	ASN
1	C	637	ASN
1	C	707	HIS
1	D	369	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GLU	D	801	-	8,9,9	1.08	1 (12%)	8,11,11	1.18	1 (12%)
2	GLU	B	801	-	8,9,9	1.10	1 (12%)	8,11,11	1.18	1 (12%)
2	GLU	C	801	-	8,9,9	1.08	1 (12%)	8,11,11	1.18	1 (12%)
2	GLU	A	801	-	8,9,9	1.08	1 (12%)	8,11,11	1.18	1 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLU	D	801	-	-	3/9/9/9	-
2	GLU	B	801	-	-	3/9/9/9	-
2	GLU	C	801	-	-	3/9/9/9	-
2	GLU	A	801	-	-	3/9/9/9	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	GLU	OXT-C	-2.26	1.23	1.30
2	D	801	GLU	OXT-C	-2.17	1.23	1.30
2	A	801	GLU	OXT-C	-2.17	1.23	1.30
2	C	801	GLU	OXT-C	-2.17	1.23	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	GLU	OXT-C-O	-2.62	118.13	124.08
2	A	801	GLU	OXT-C-O	-2.62	118.13	124.08
2	C	801	GLU	OXT-C-O	-2.62	118.13	124.08
2	B	801	GLU	OXT-C-O	-2.62	118.14	124.08

There are no chirality outliers.

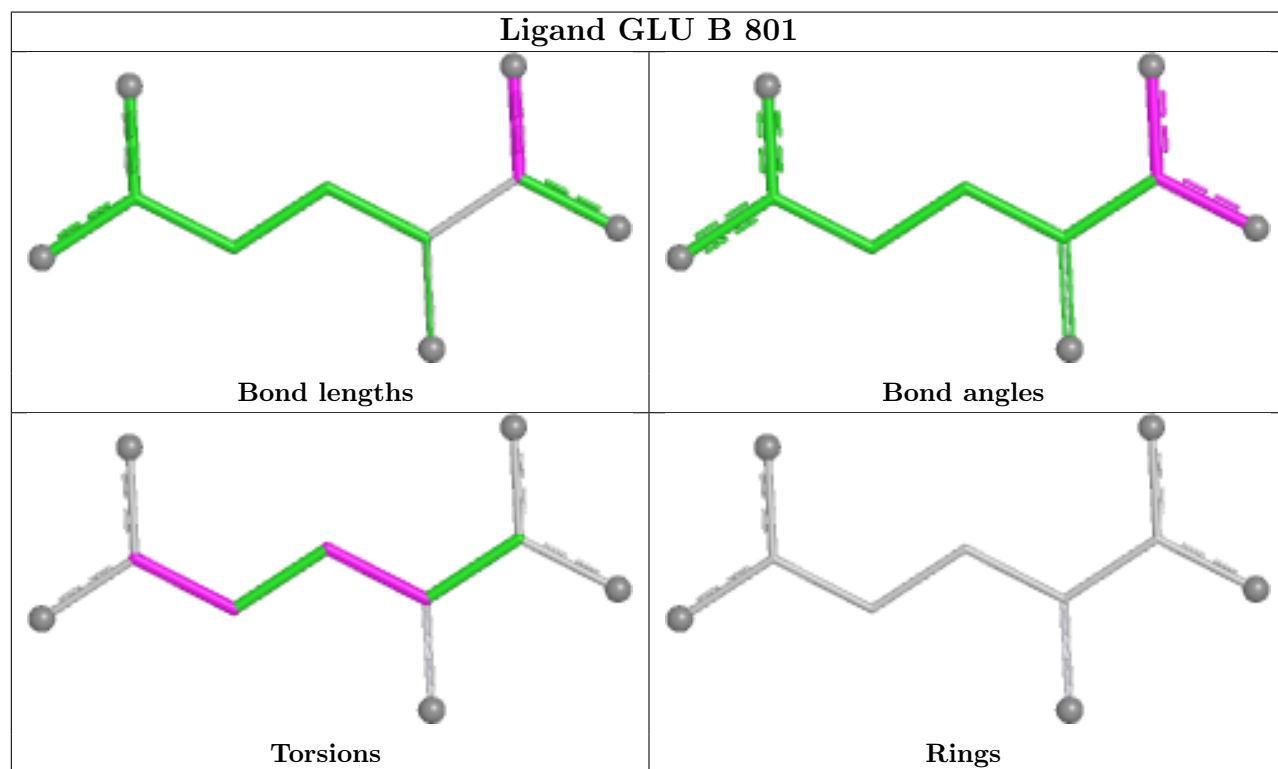
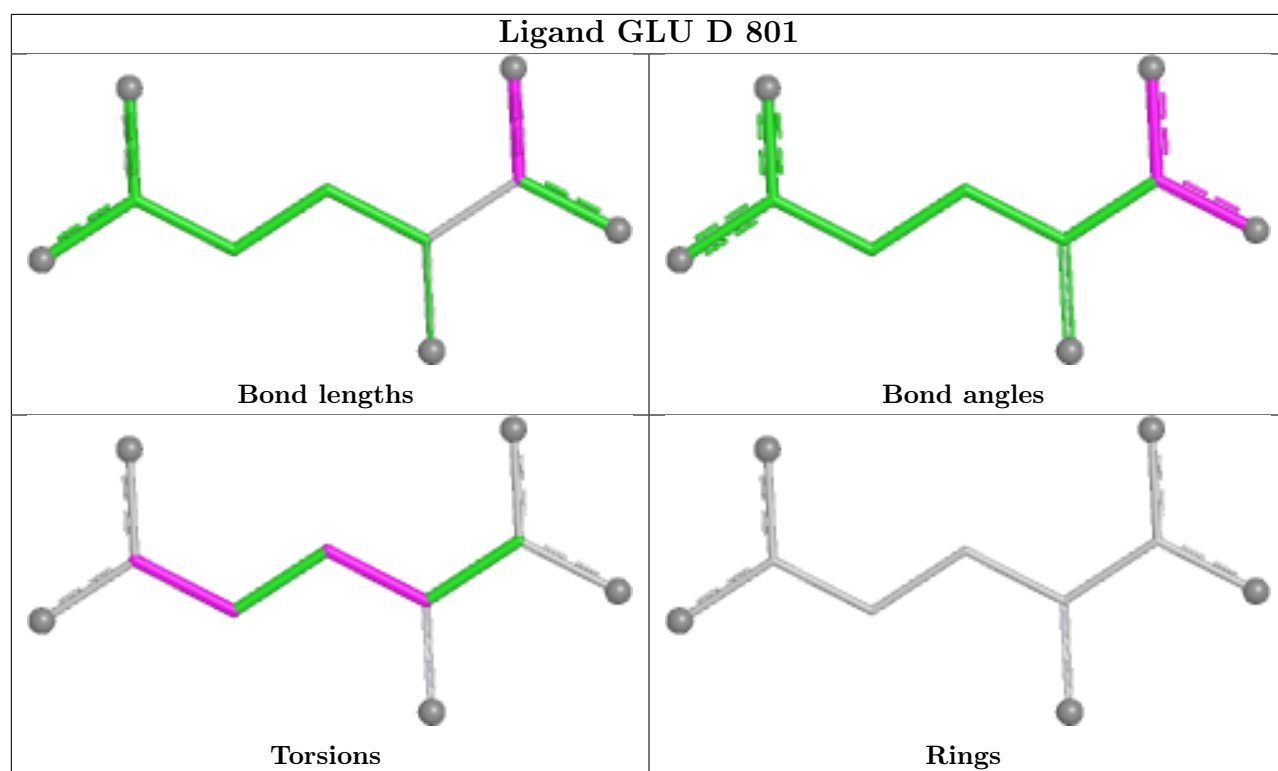
5 of 12 torsion outliers are listed below:

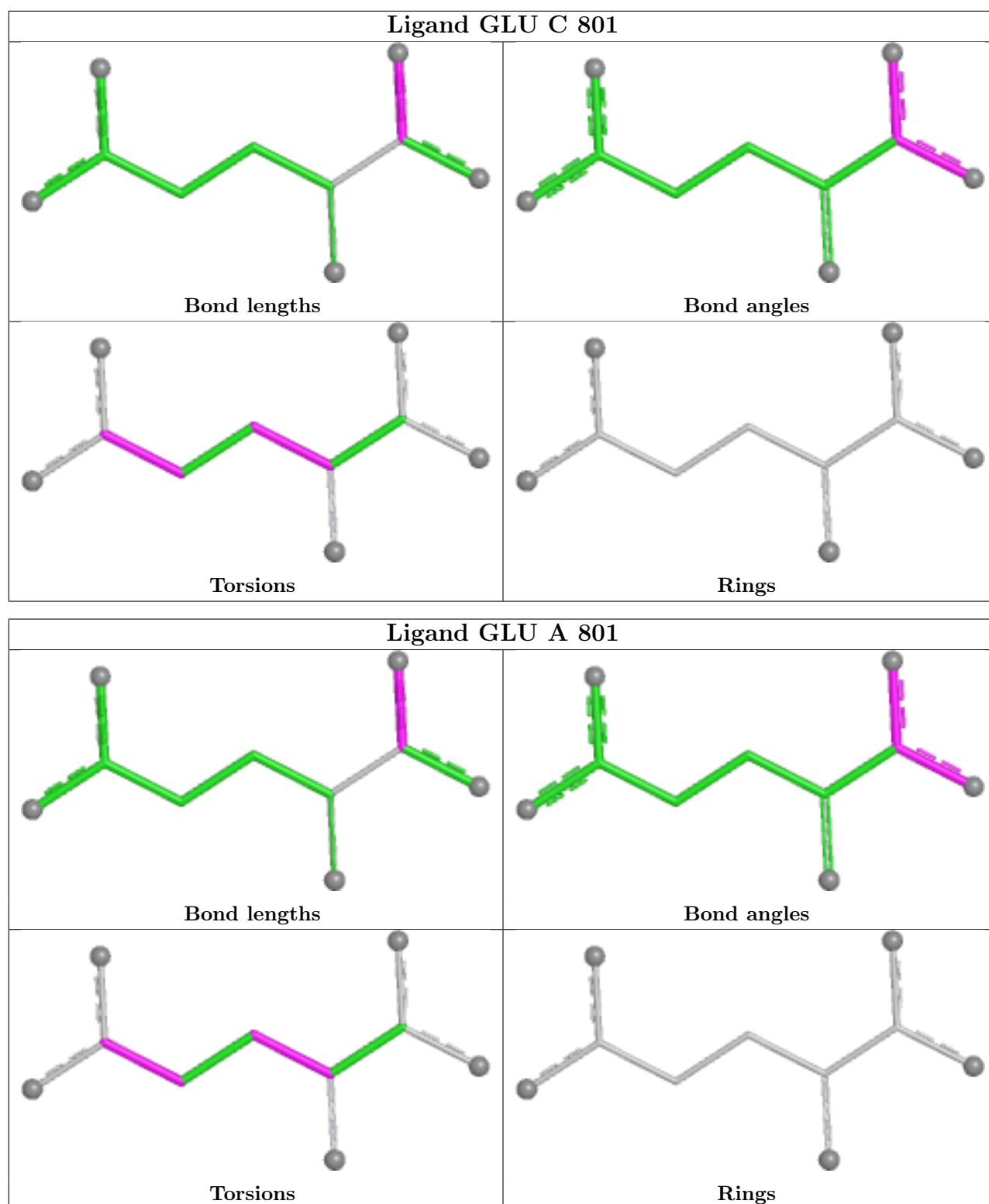
Mol	Chain	Res	Type	Atoms
2	A	801	GLU	OE2-CD-CG-CB
2	C	801	GLU	OE2-CD-CG-CB
2	D	801	GLU	OE2-CD-CG-CB
2	A	801	GLU	OE1-CD-CG-CB
2	C	801	GLU	OE1-CD-CG-CB

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

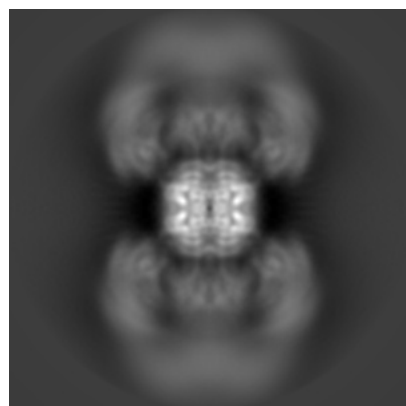
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31466. These allow visual inspection of the internal detail of the map and identification of artifacts.

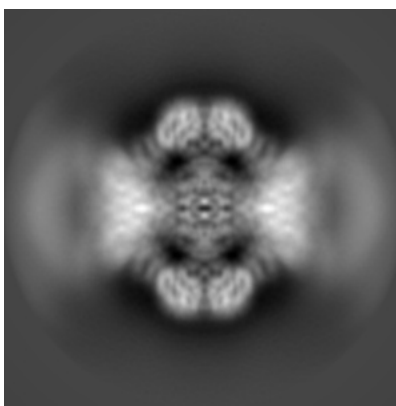
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

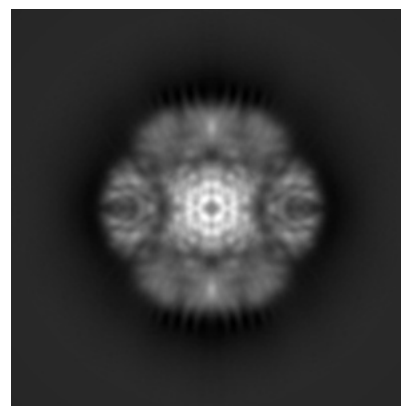
6.1.1 Primary map



X

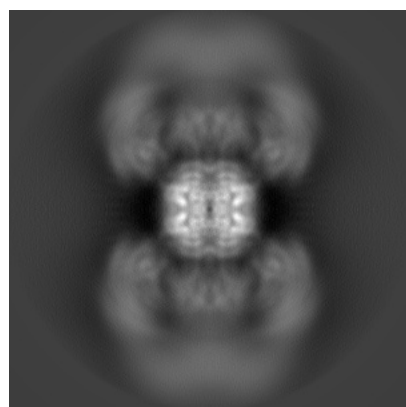


Y

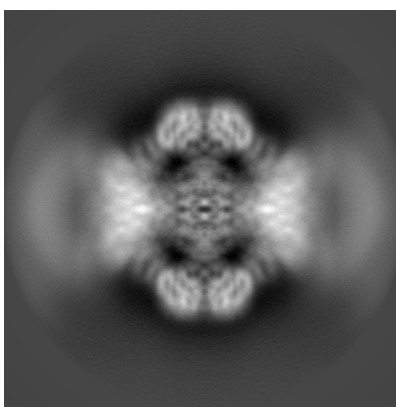


Z

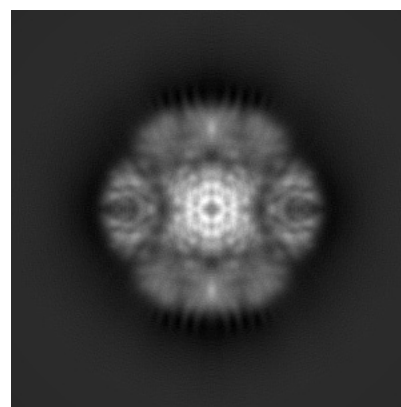
6.1.2 Raw map



X



Y

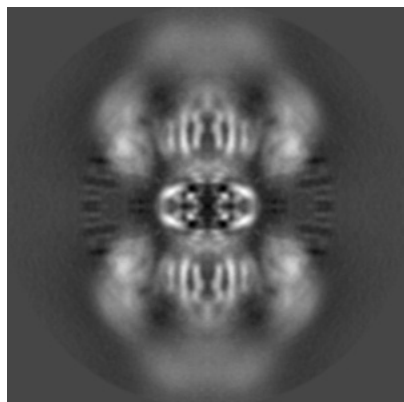


Z

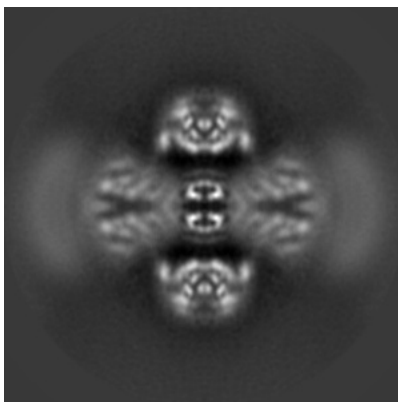
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

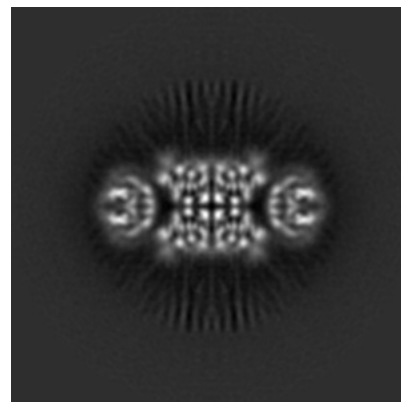
6.2.1 Primary map



X Index: 150

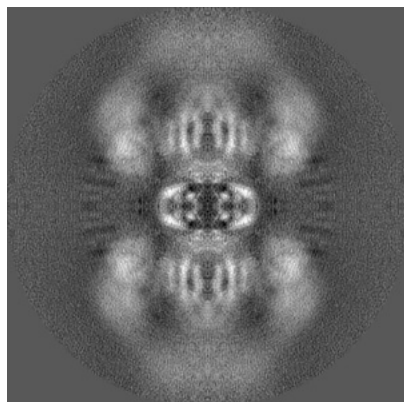


Y Index: 150

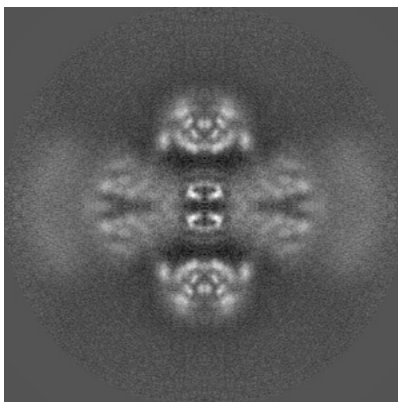


Z Index: 150

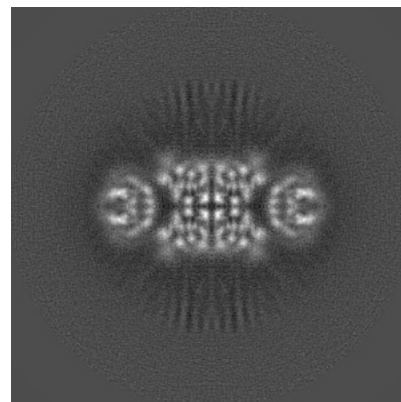
6.2.2 Raw map



X Index: 150



Y Index: 150

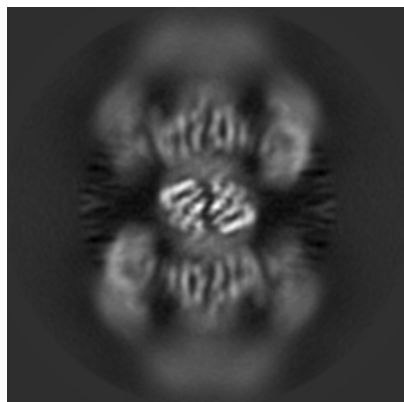


Z Index: 150

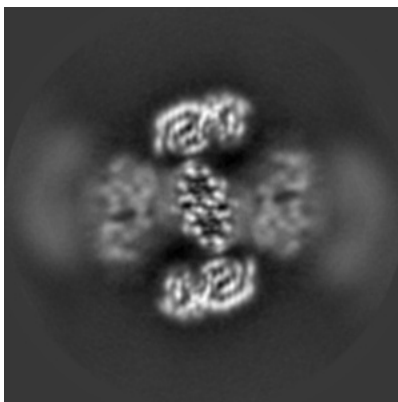
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

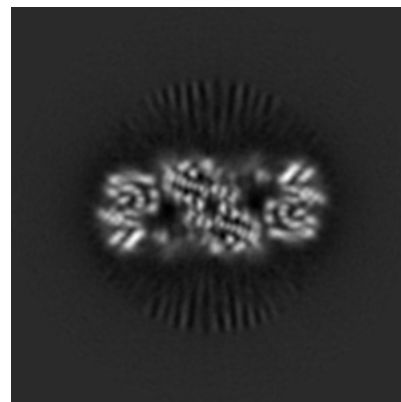
6.3.1 Primary map



X Index: 146

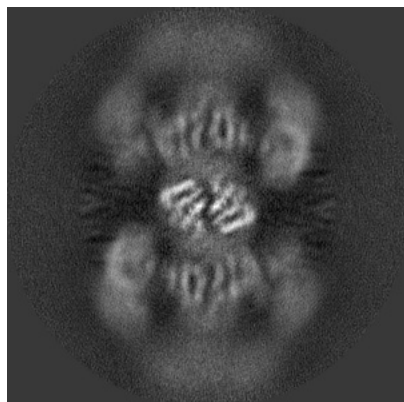


Y Index: 140

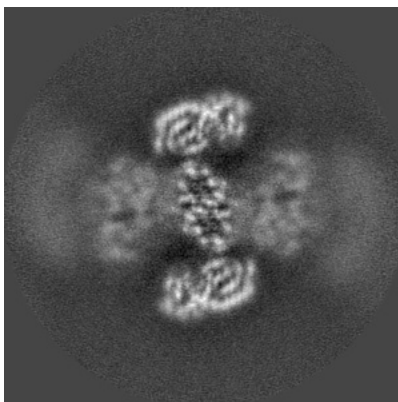


Z Index: 142

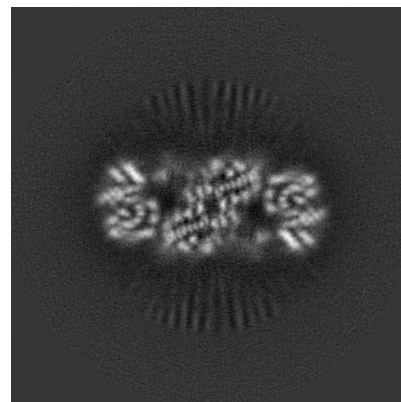
6.3.2 Raw map



X Index: 146



Y Index: 140

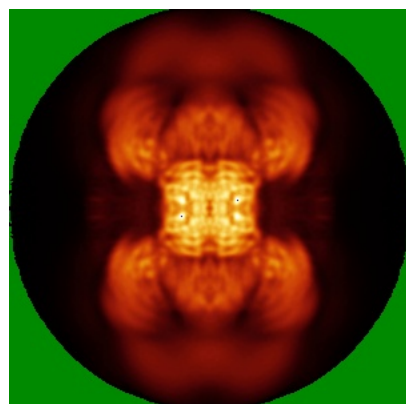


Z Index: 158

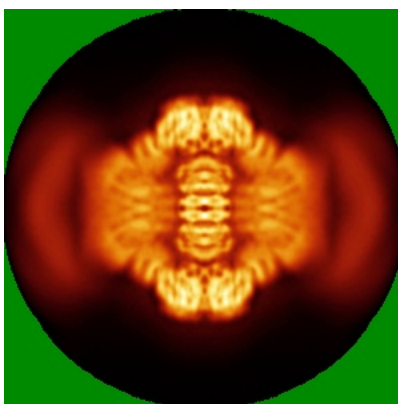
The images above show the largest variance slices of the map in three orthogonal directions.

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

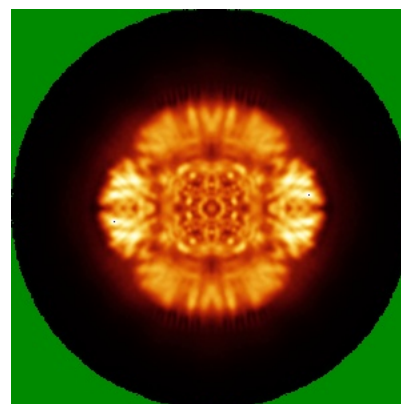
6.4.1 Primary map



X

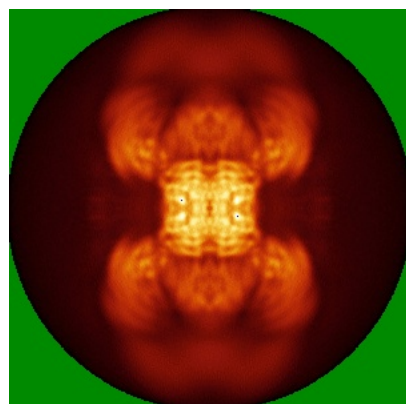


Y

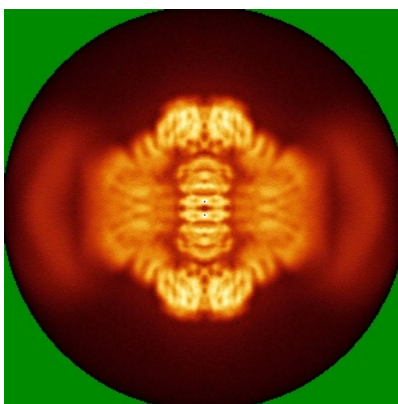


Z

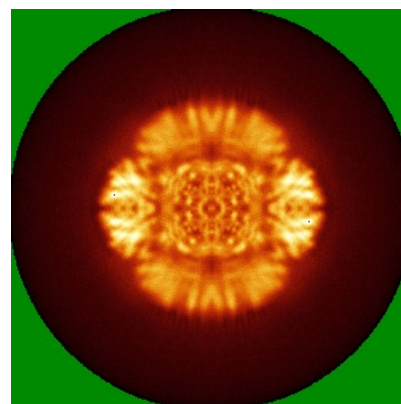
6.4.2 Raw map



X



Y

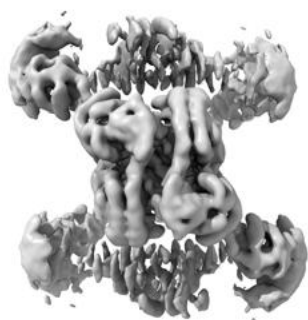


Z

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

6.5 Orthogonal surface views [i](#)

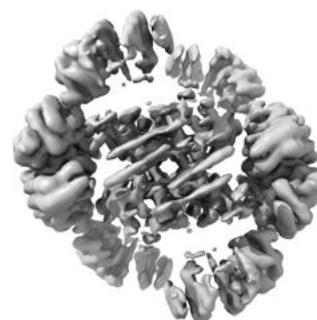
6.5.1 Primary map



X



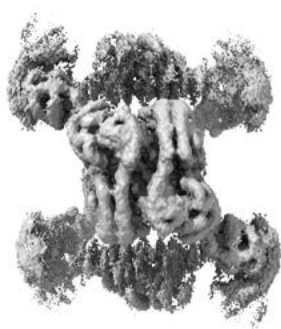
Y



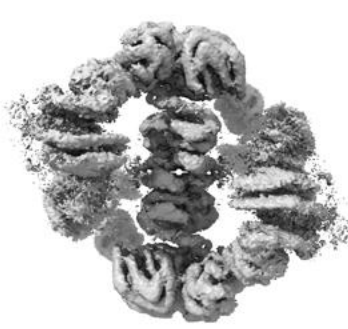
Z

The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

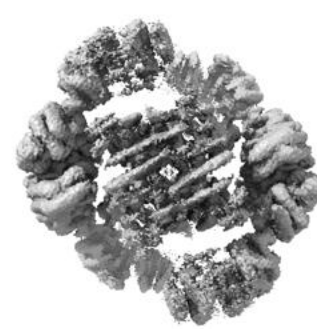
6.5.2 Raw map



X



Y



Z

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

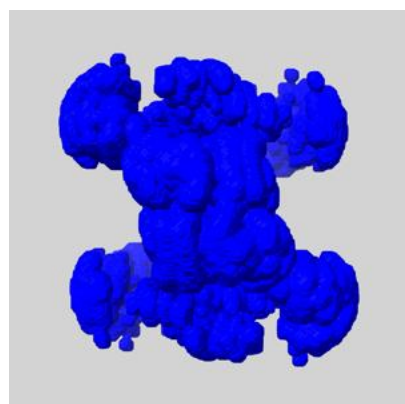
6.6 Mask visualisation [i](#)

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

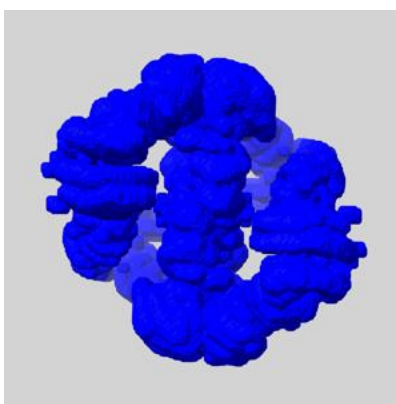
A mask typically either:

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

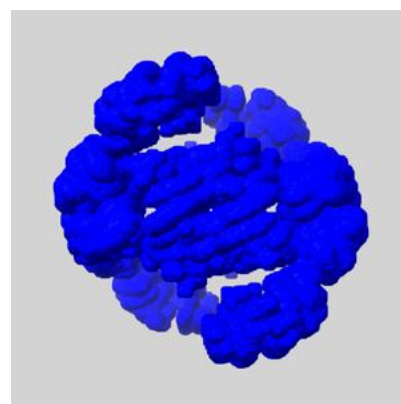
6.6.1 emd_31466_msk_1.map [i](#)



X



Y

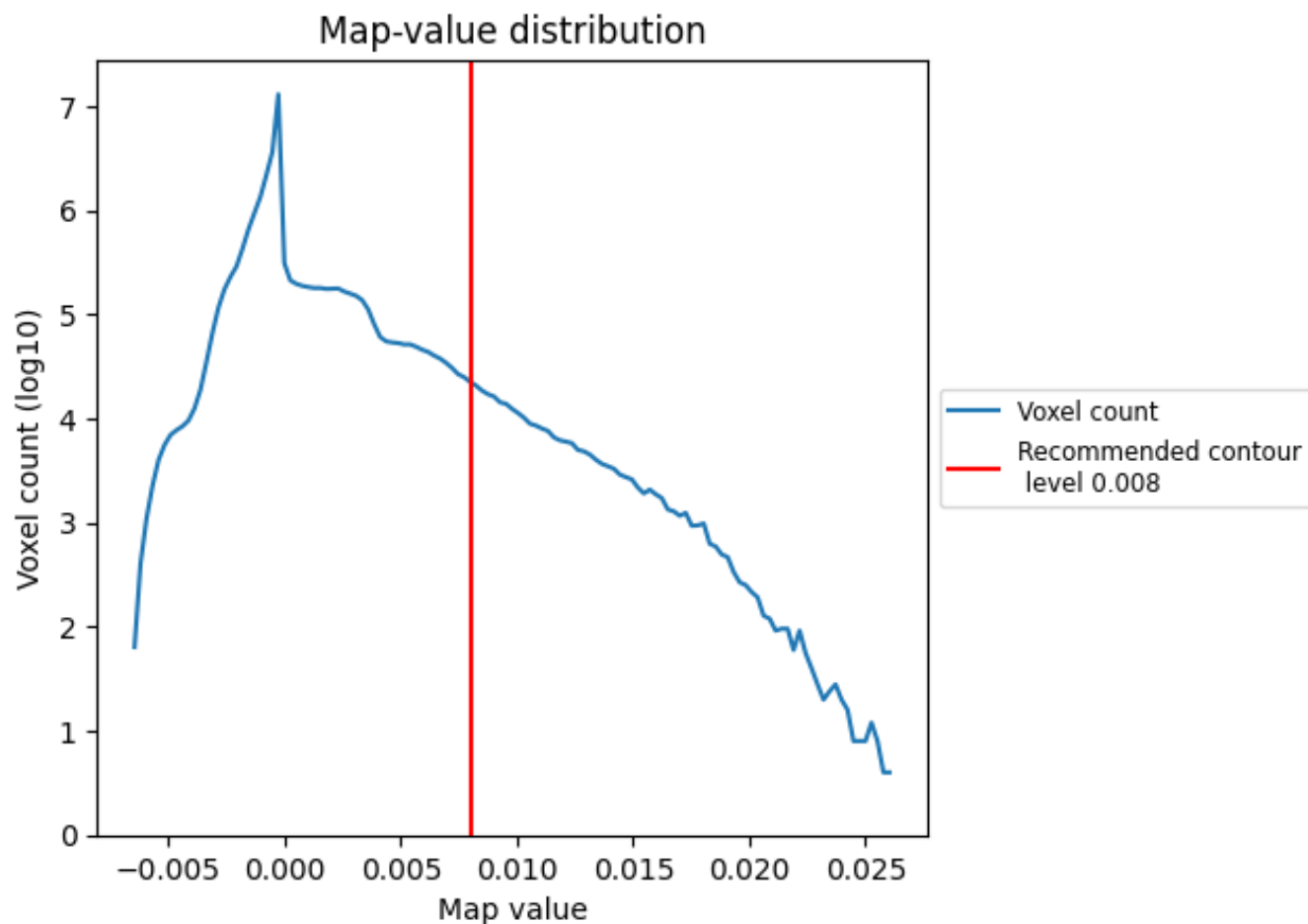


Z

7 Map analysis [i](#)

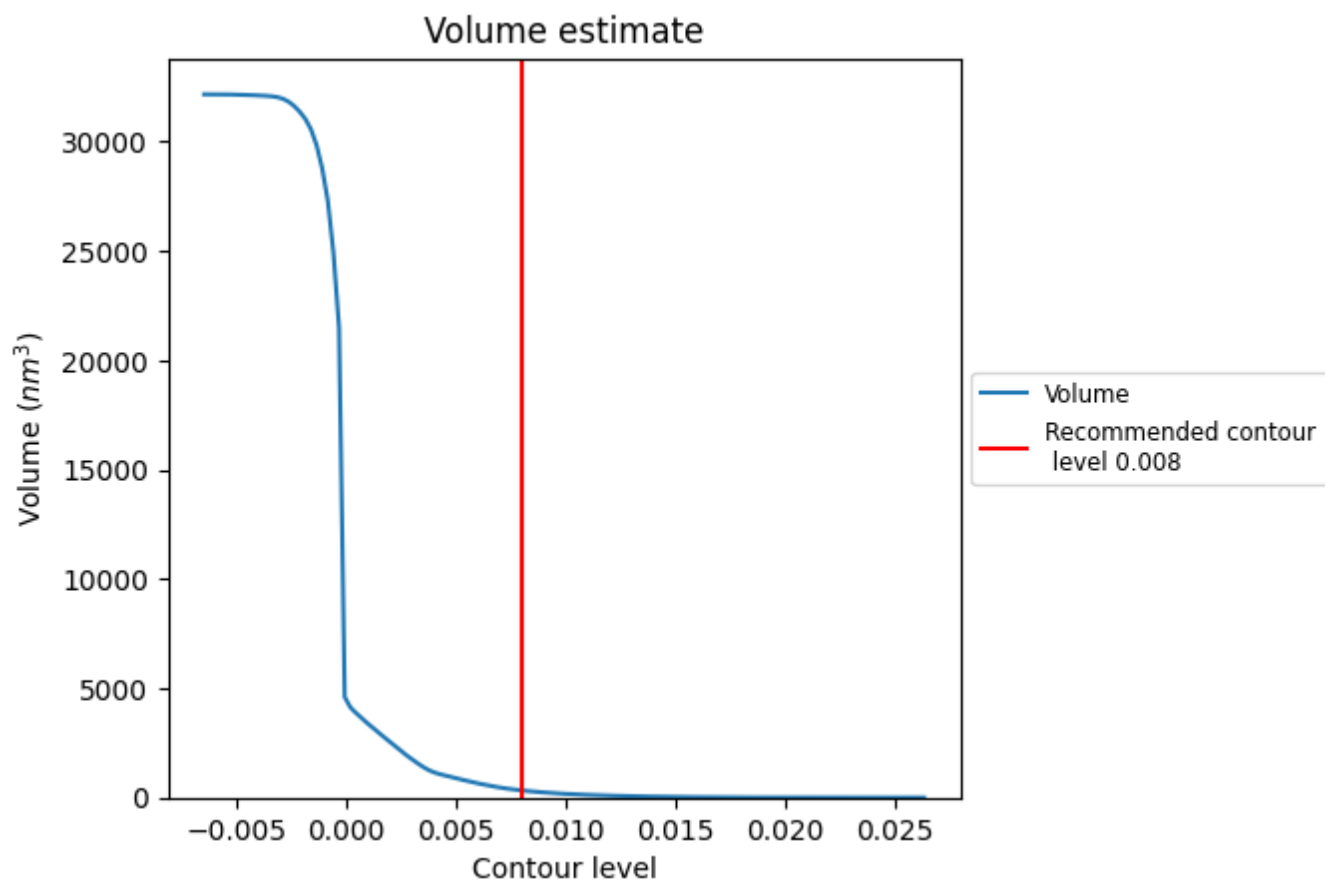
This section contains the results of statistical analysis of the map.

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.

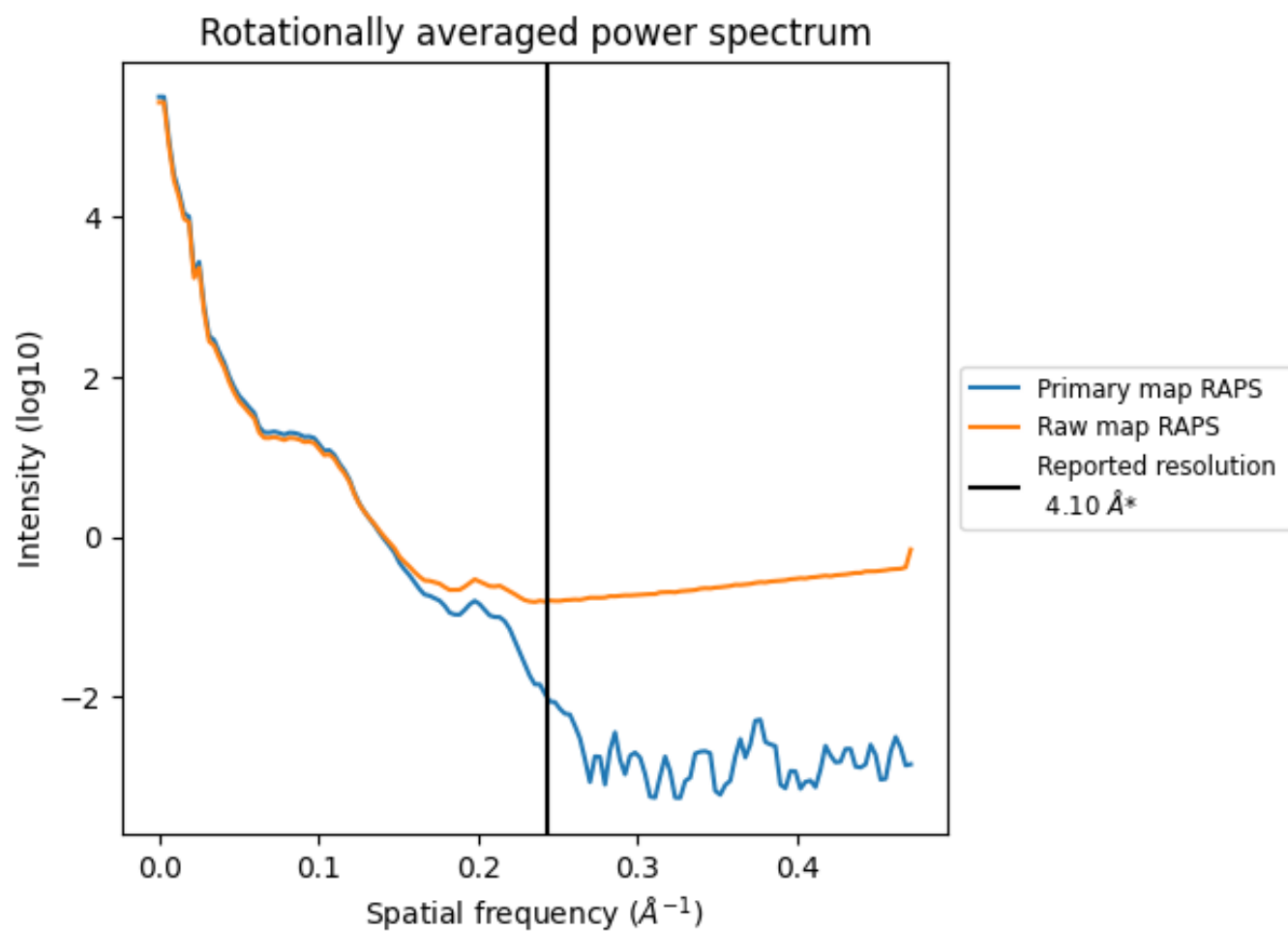
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 325 nm³; this corresponds to an approximate mass of 294 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 ⓘ

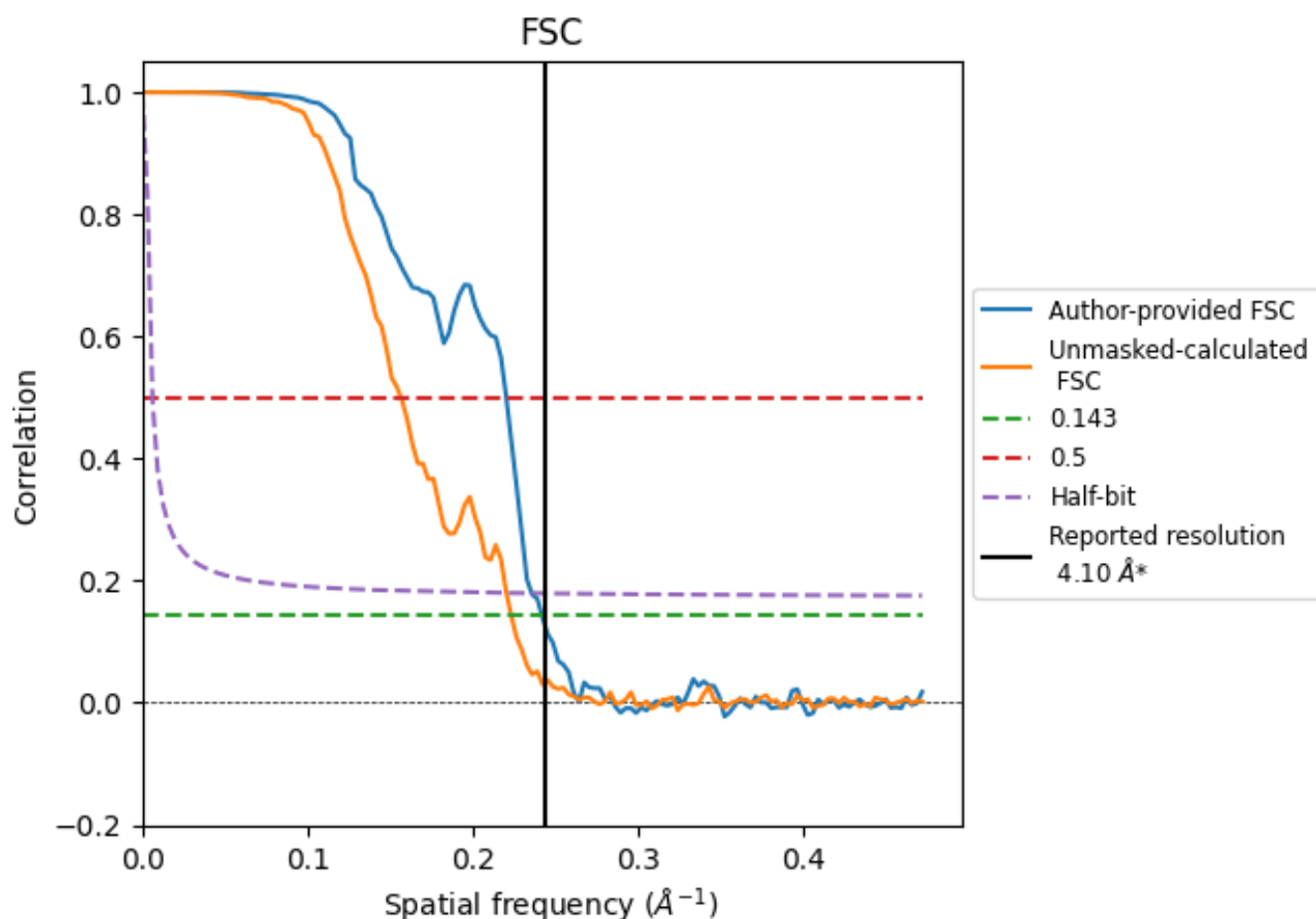


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

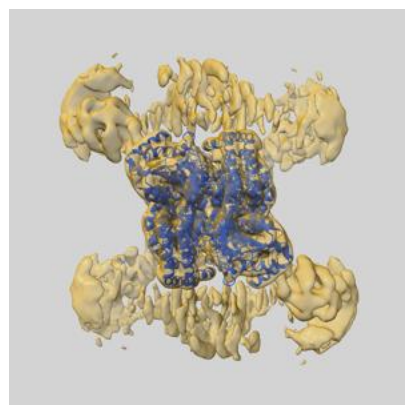
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.14	4.54	4.24
Unmasked-calculated*	4.48	6.39	4.54

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

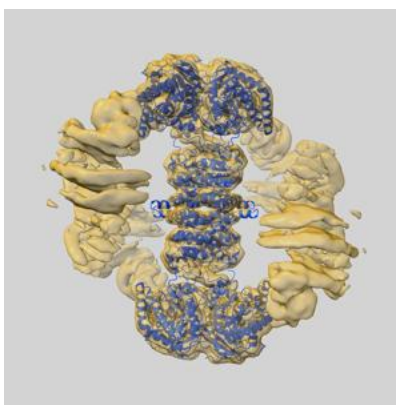
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31466 and PDB model 7F5T. Per-residue inclusion information can be found in section [3](#) on page [5](#).

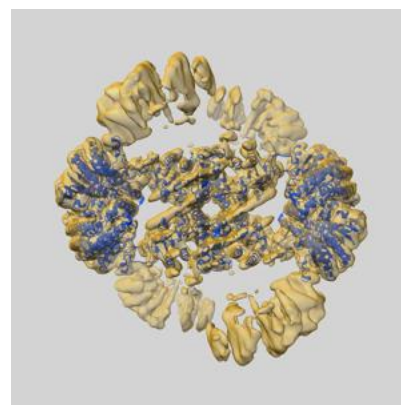
9.1 Map-model overlay [i](#)



X



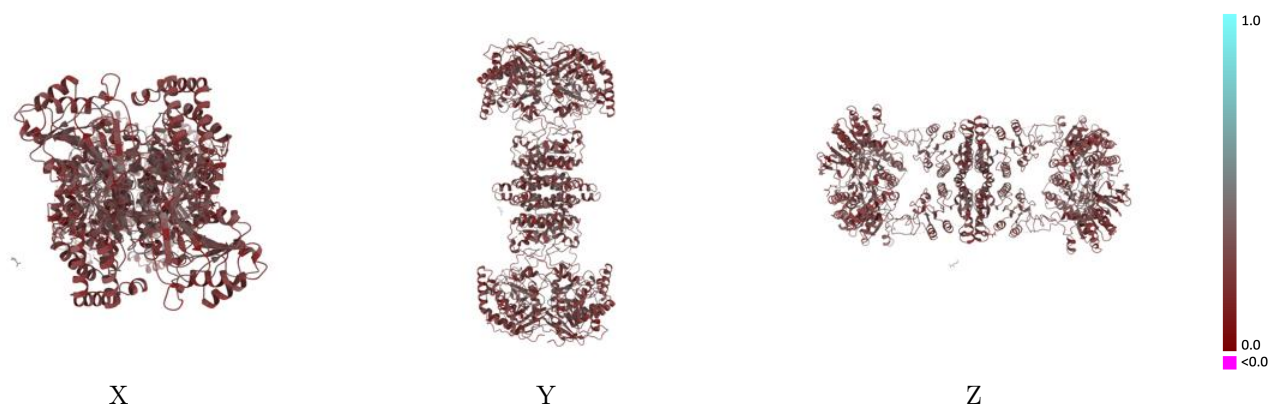
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.008 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](#)

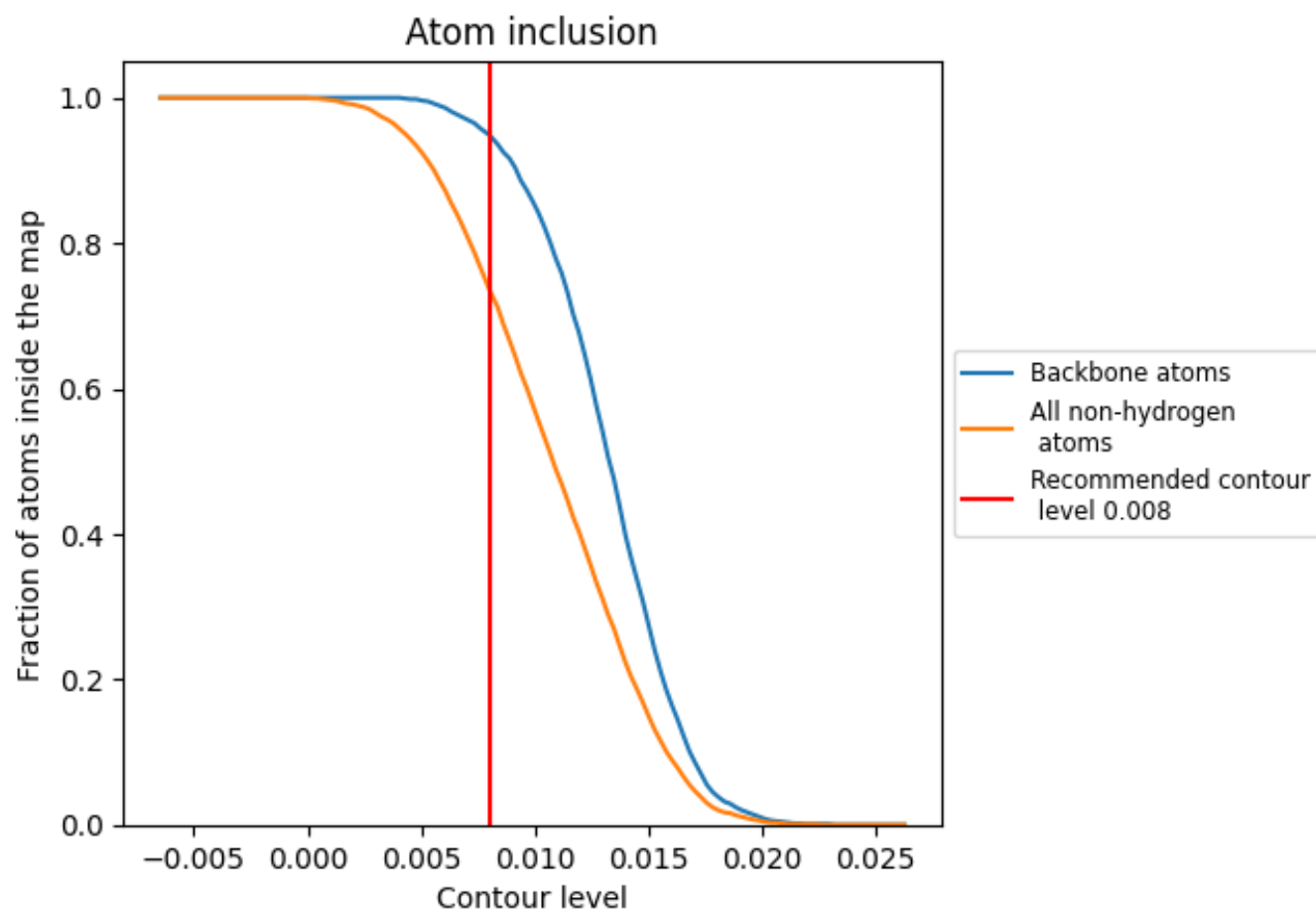


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 74% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7370	0.2850
A	0.7350	0.2850
B	0.7380	0.2840
C	0.7370	0.2860
D	0.7400	0.2850

