



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 03:35 PM UTC

PDB ID : 7F5X / pdb_00007f5x
EMDB ID : EMD-31469
Title : GK domain of Drosophila P5CS filament with glutamate
Authors : Liu, J.L.; Zhong, J.; Guo, C.J.; Zhou, X.
Deposited on : 2021-06-23
Resolution : 3.50 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

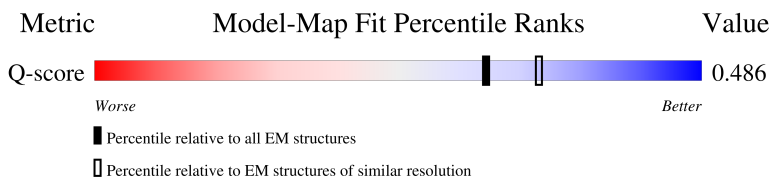
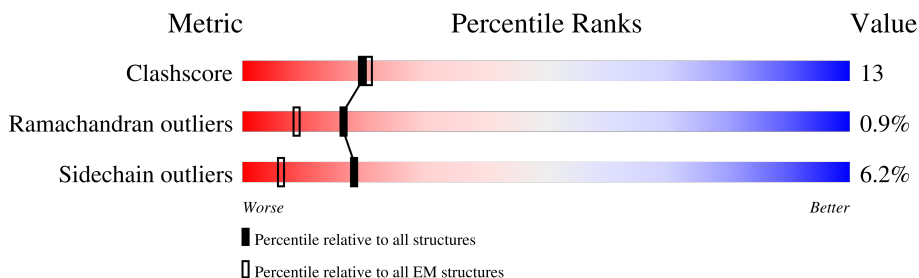
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	
1	B	776	
1	C	776	
1	D	776	

2 Entry composition [i](#)

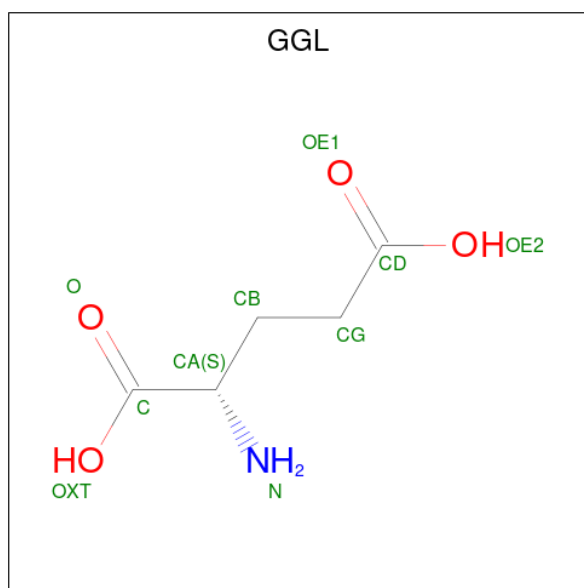
There are 2 unique types of molecules in this entry. The entry contains 7244 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	236	Total	C	N	O	S	0	0
			1801	1138	309	341	13		
1	B	236	Total	C	N	O	S	0	0
			1801	1138	309	341	13		
1	C	236	Total	C	N	O	S	0	0
			1801	1138	309	341	13		
1	D	236	Total	C	N	O	S	0	0
			1801	1138	309	341	13		

- Molecule 2 is GAMMA-L-GLUTAMIC ACID (CCD ID: GGL) (formula: C₅H₉NO₄) (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	

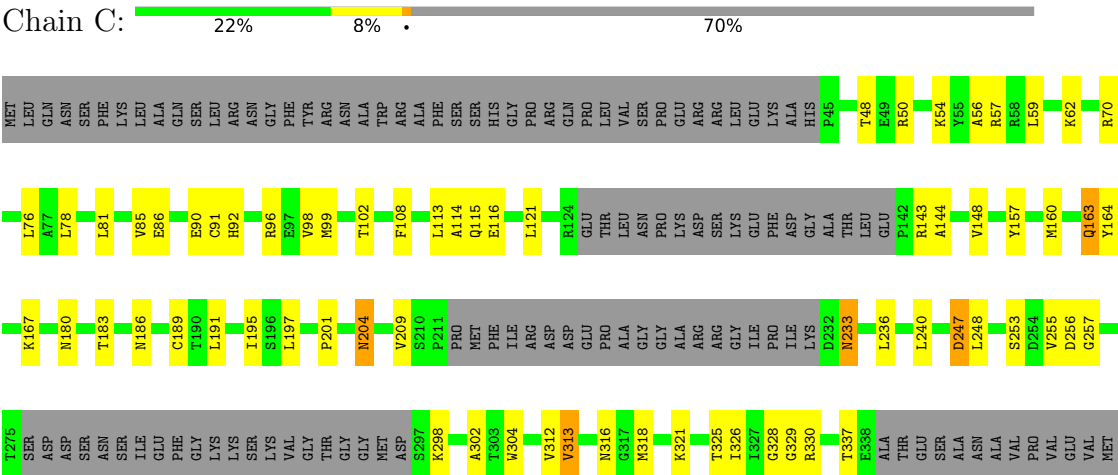
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Mol	Chain	Residues	Atoms				AltConf
2	C	1	Total	C	N	O	0
			10	5	1	4	
2	D	1	Total	C	N	O	0
			10	5	1	4	



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



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



ALA	ALA	ILE	GLU	PHE	LYS	VAL	S253	Q163		
ALA	ALA	ARG	GLU	GLU	PRO	VAL	D254	Y164	L76	LEU
SER	SER	ASP	ILE	SER	LEU	PRO	D255	A77	A77	GLN
ALA	ASP	ALA	ASP	PRO	LEU	GLU	D256	K167	L78	ASN
LYS	LYS	LYS	LEU	ASP	SER	MET	G257	I168		ASN
HIS	CYS	CYS	LEU	LEU	LEU	ALA	T275	L172	L81	PHE
GLU	ASP	ASP	SER	SER	GLU	GLU	SER			LYS
GLU	TRR	GLU	MET	PRO	ASN	ASN	ASP	N180	V85	LEU
LYS	PRO	PRO	GLU	GLN	ASN	ALA	ASP		E86	ALA
ALA	ALA	VAL	VAL	VAL	PRO	ARG	SER	T183	E90	SER
LEU	LEU	ALA	HIS	ALA	ALA	THR	ASN		C91	LEU
GLU	GLU	CYS	ILE	ALA	LYS	GLY	SER	N186	H92	ARG
CYS	ASN	ASN	ASP	LEU	LEU	SER	ILE			ASN
CYS	CYS	ALA	GLU	ALA	LYS	ARG	GLU	C189	R96	GLY
ILE	ILE	MET	ILE	MET	ASN	GLN	PHE	T190	E97	PHE
GLU	GLU	GLU	ILE	ALA	LEU	MET	GLY	L191	V98	TYR
VAL	VAL	THR	PRO	SER	SER	GLN	LYS		N99	ARG
VAL	VAL	LEU	ARG	ALA	VAL	ALA	LYS	T195		ASN
PRO	PRO	LEU	GLY	ASN	GLY	LEU	SER	S196	T102	ALA
SER	SER	ILE	SER	GLY	LYS	THR	VAL	L197		TRP
LEU	LEU	HIS	SER	LEU	LYS	PRO	VAL		F108	ARG
GLU	ASP	GLU	ASP	LEU	GLN	ALA	GLY	P201	L113	ALA
ASP	GLU	LEU	LEU	LEU	ILE	GLN	THR	I202	L113	PHE
ALA	ALA	VAL	VAL	LYS	ALA	ARG	GLY	T203	A114	SER
ILE	ILE	MET	ARG	GLY	GLU	ALA	GLY	N204	Q115	SER
ASN	ASN	GLY	SER	GLY	SER	SER	MET		E116	HIS
GLY	GLY	ILE	ILE	LYS	ALA	ALA	ASP	V209		GLY
ILE	ILE	ALA	GLN	GLU	HIS	VAL	S297	S210	L121	PRO
HIS	HIS	ILE	GLN	ALA	LYS	ASN	K298	P211		ARG
THR	THR	PHE	GLN	ALA	ASN	THR		PRO	R124	GLN
GLY	GLY	SER	SER	HIS	VAL	LEU	A302	MET	GLU	PRO
SER	SER	ASP	LEU	ARG	GLY	THR	T303	PHE	THR	LEU
VAL	VAL	ASP	LEU	ASN	GLY	ALA	W304	ILE	LEU	VAL
SER	SER	VAL	ILE	LYS	VAL	LEU		ARG	ASN	SER
HIS	ASN	CYS	ILE	LYS	LEU	LEU	V312	ASP	PRO	PRO
THR	THR	MET	VAL	LEU	ARG	VAL	V313	ASP	LYS	GLU
ASP	ASP	LEU	LEU	MET	THR	SER		GLU	ARG	ARG
VAL	VAL	LYS	GLY	GLY	THR	ARG	N316	PRO	SER	LEU
ILE	ILE	ARG	HIS	LEU	ARG	GLU	G317	ALA	LYS	LEU
VAL	VAL	GLU	HIS	VAL	LEU	LYS	M318	GLY	GLU	GLU
THR	THR	GLY	GLY	LYS	ALA	PHE		GLY	PHE	LYS
GLN	GLN	VAL	GLY	GLU	ASP	ILE	K321	ALA	ASP	ALA
ASN	ASN	LYS	VAL	ALA	GLN	LEU		ARG	GLY	HIS
ASP	ASP	ILE	CYS	LEU	VAL	ASP	T325	ARG	ALA	ALA
ALA	ALA	ALA	HIS	ALA	GLU	ALA	I326	GLY	THR	THR
ALA	ALA	ALA	VAL	THR	LEU	ASN	I327	ILE	LEU	LEU
ALA	GLY	GLY	TYR	VAL	LYS	ALA	G328	PRO	GLU	GLU
ARG	ARG	PRO	ILE	GLY	LYS	LYS	G329	ILE	LEU	LEU
GLN	GLN	ARG	ASP	GLU	VAL	VAL	R330	LYS	P142	HIS
PHE	PHE	LEU	ARG	GLU	THR	LEU	S330	THR		
GLY	GLY	LEU	THR	HIS	VAL	ALA	T337	ILE	GLU	ALA
GLY	GLY	GLN	ALA	ALA	PRO	GLU	S336	N233	V148	ASN
SER	SER	GLN	ASP	VAL	ILE	ALA	ALA			
VAL	VAL	GLY	LEU	SER	ILE	ALA	THR	L236	L153	ASN
ASP	ASP	THR	GLU	GLY	VAL	GLN	GLU	L240	Y157	ASN
SER	SER	PHE	LYS	VAL	VAL	LYS	SER			
ALA	ALA	GLY	ALA	SER	LEU	GLY	ALA	D247	Y157	ASN
CYS	CYS	PRO	LEU	THR	VAL	LEU	ALA	L248	M150	ASN
ALA	ALA	PRO	ARG	ARG	ILE	ALA	ALA			ALA

PHE	ARG
HIS	THR
ASN	TRP
ALA	LEU
SER	HIS
SER	GLU
ARG	THR
PHE	LEU
ALA	PRO
ASP	LEU
GLY	ASP
PHE	
ARG	
PHE	
GLY	
LEU	
GLY	
ALA	
GLU	
VAL	
GLY	
ILE	
SER	
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ARG
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LEU
PRO
LEU
ASP

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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.115	Depositor
Minimum map value	-0.083	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.22	0/1824	0.35	0/2460
1	B	0.22	0/1824	0.35	0/2460
1	C	0.22	0/1824	0.35	0/2460
1	D	0.22	0/1824	0.35	0/2460
All	All	0.22	0/7296	0.35	0/9840

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 [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	1801	0	1840	58	0
1	B	1801	0	1840	59	0
1	C	1801	0	1840	58	0
1	D	1801	0	1840	61	0
2	A	10	0	7	2	0
2	B	10	0	7	2	0
2	C	10	0	7	2	0
2	D	10	0	7	2	0
All	All	7244	0	7388	183	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 13.

The worst 5 of 183 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:A:164:TYR:CE1	1:C:70:ARG:NH2	1.85	1.45
1:A:70:ARG:NH2	1:C:164:TYR:CE1	1.85	1.44
1:B:70:ARG:NH2	1:D:164:TYR:CE1	1.85	1.43
1:B:164:TYR:CE1	1:D:70:ARG:NH2	1.85	1.43
1:B:108:PHE:CE2	1:D:163:GLN:OE1	1.90	1.25

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	228/776 (29%)	209 (92%)	17 (8%)	2 (1%)	14	47
1	B	228/776 (29%)	209 (92%)	17 (8%)	2 (1%)	14	47
1	C	228/776 (29%)	209 (92%)	17 (8%)	2 (1%)	14	47
1	D	228/776 (29%)	209 (92%)	17 (8%)	2 (1%)	14	47
All	All	912/3104 (29%)	836 (92%)	68 (8%)	8 (1%)	16	47

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	114	ALA
1	A	233	ASN
1	B	114	ALA
1	B	233	ASN
1	C	114	ALA

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	195/630 (31%)	183 (94%)	12 (6%)	16	43
1	B	195/630 (31%)	183 (94%)	12 (6%)	16	43
1	C	195/630 (31%)	183 (94%)	12 (6%)	16	43
1	D	195/630 (31%)	183 (94%)	12 (6%)	16	43
All	All	780/2520 (31%)	732 (94%)	48 (6%)	18	43

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	195	ILE
1	C	313	VAL
1	C	197	LEU
1	C	240	LEU
1	D	90	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	186	ASN
1	D	111	GLN
1	C	87	GLN
1	D	87	GLN
1	B	204	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](#)

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	GGL	D	801	-	8,9,9	1.09	1 (12%)	8,11,11	0.74	0
2	GGL	A	801	-	8,9,9	1.10	1 (12%)	8,11,11	0.74	0
2	GGL	C	801	-	8,9,9	1.09	1 (12%)	8,11,11	0.74	0
2	GGL	B	801	-	8,9,9	1.10	1 (12%)	8,11,11	0.74	0

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	GGL	D	801	-	-	2/9/9/9	-
2	GGL	A	801	-	-	2/9/9/9	-
2	GGL	C	801	-	-	2/9/9/9	-
2	GGL	B	801	-	-	2/9/9/9	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	GGL	OXT-C	-2.24	1.23	1.30
2	B	801	GGL	OXT-C	-2.24	1.23	1.30
2	C	801	GGL	OXT-C	-2.20	1.23	1.30
2	D	801	GGL	OXT-C	-2.20	1.23	1.30

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

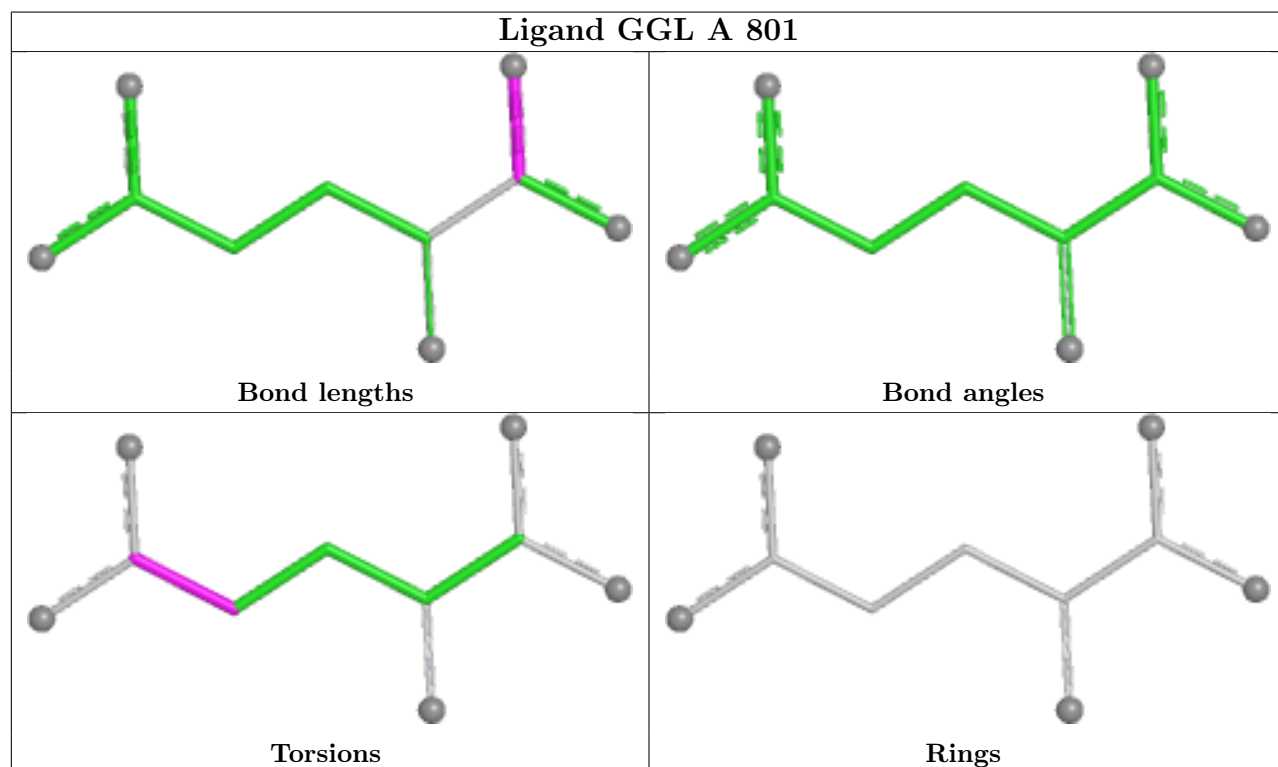
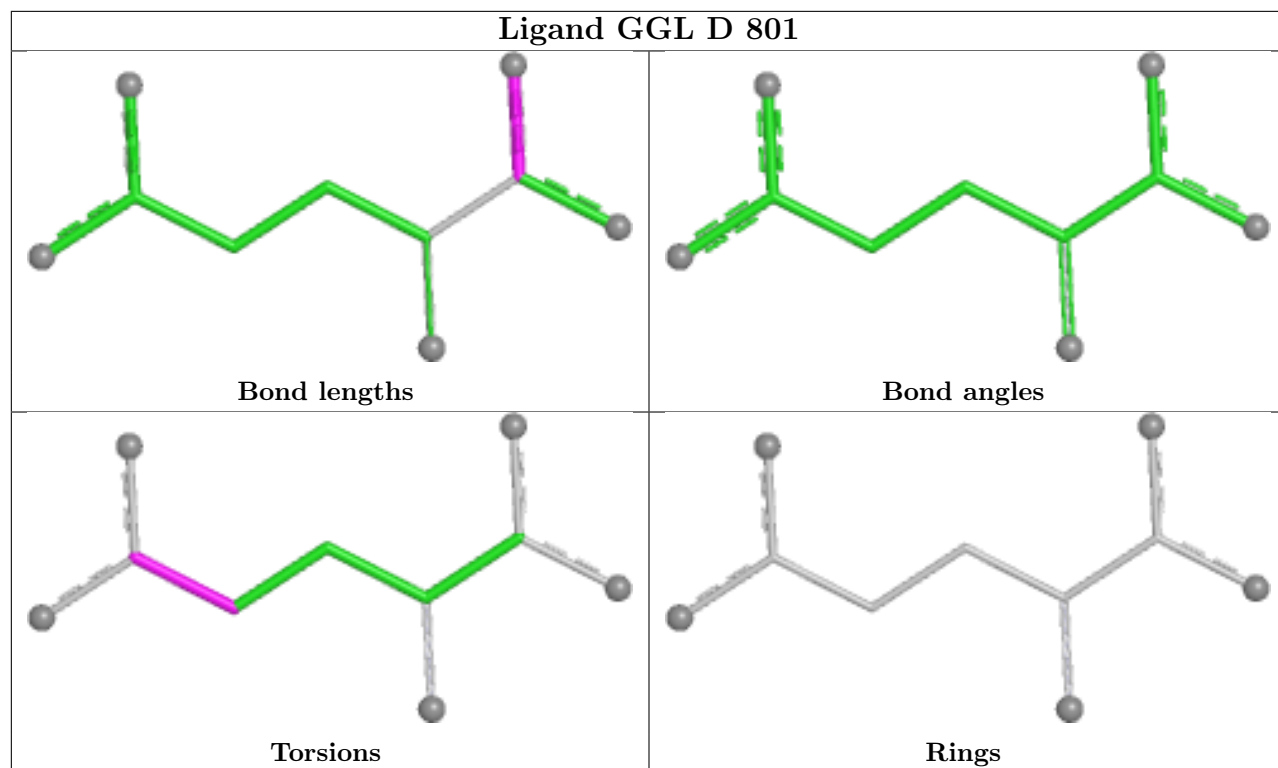
Mol	Chain	Res	Type	Atoms
2	C	801	GGL	OE2-CD-CG-CB
2	D	801	GGL	OE2-CD-CG-CB
2	A	801	GGL	OE2-CD-CG-CB
2	B	801	GGL	OE2-CD-CG-CB
2	A	801	GGL	OE1-CD-CG-CB

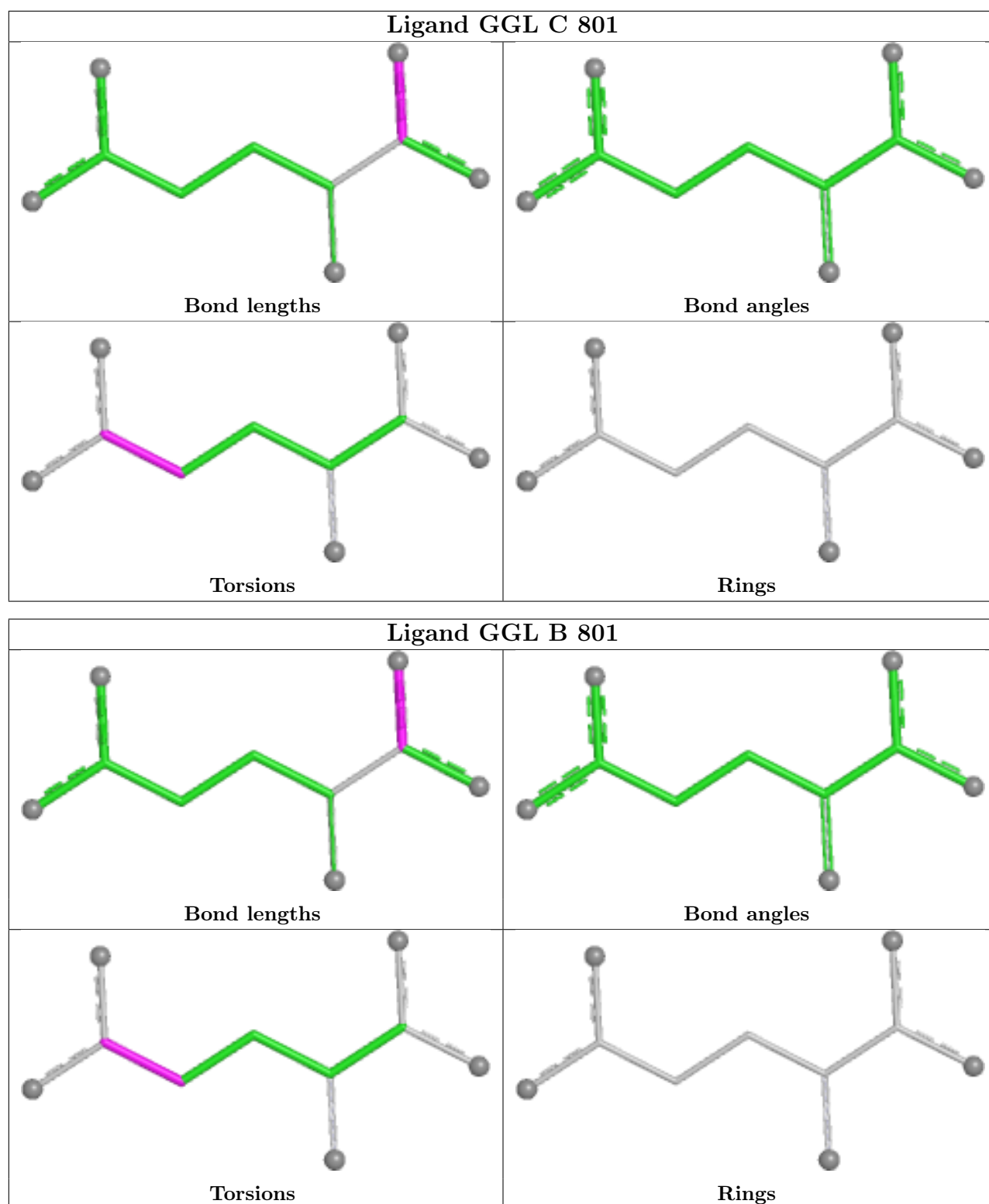
There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	801	GGL	2	0
2	A	801	GGL	2	0
2	C	801	GGL	2	0
2	B	801	GGL	2	0

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.

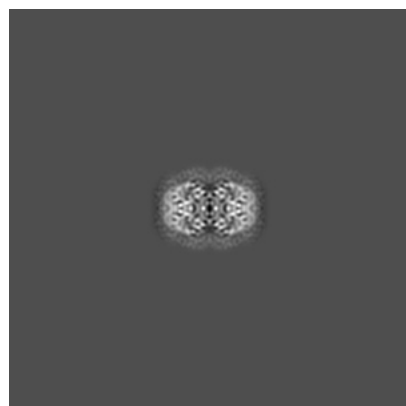
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31469. 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

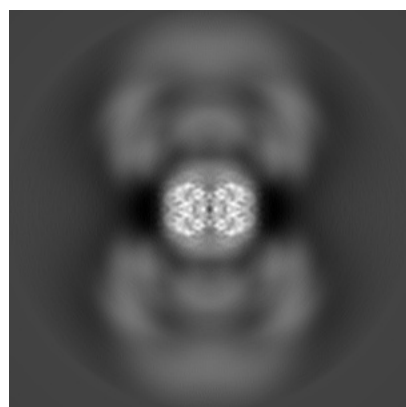


Y

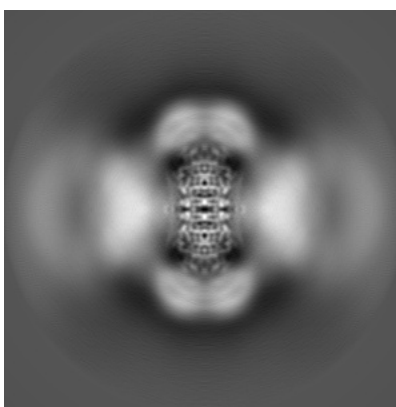


Z

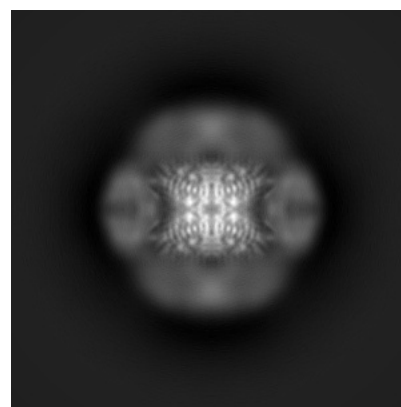
6.1.2 Raw map



X



Y

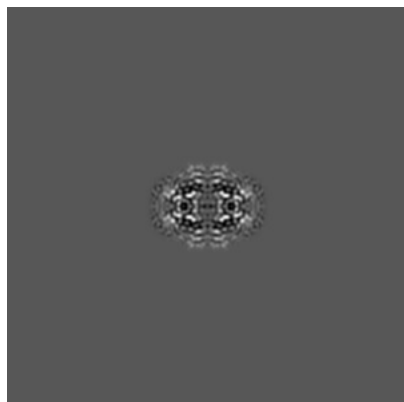


Z

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

6.2 Central slices [i](#)

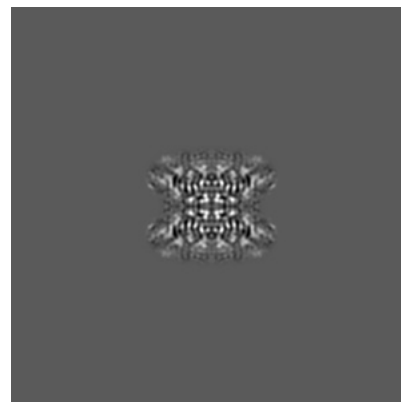
6.2.1 Primary map



X Index: 150

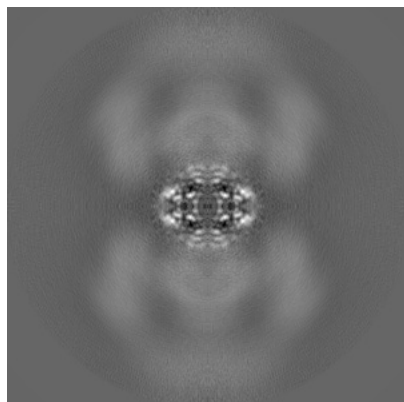


Y Index: 150

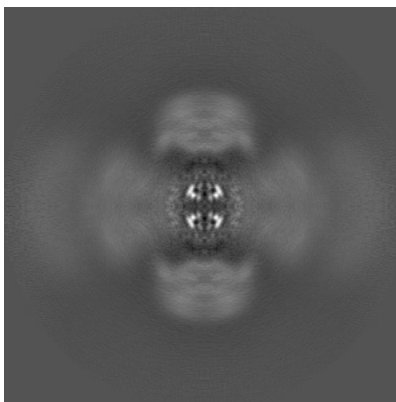


Z Index: 150

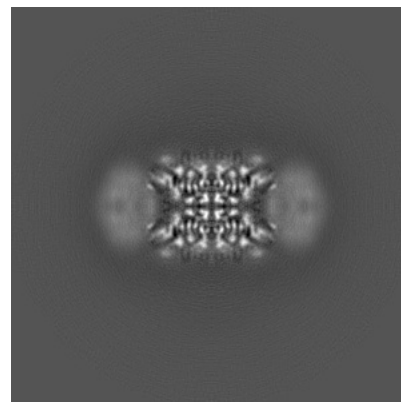
6.2.2 Raw map



X Index: 150



Y Index: 150

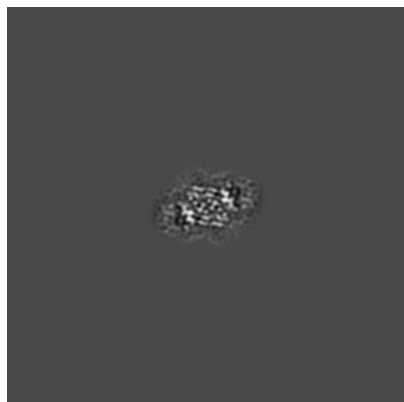


Z Index: 150

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

6.3 Largest variance slices [i](#)

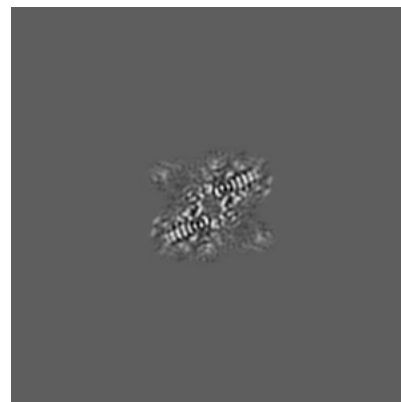
6.3.1 Primary map



X Index: 158

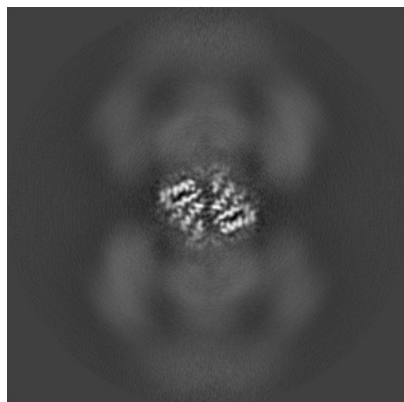


Y Index: 165

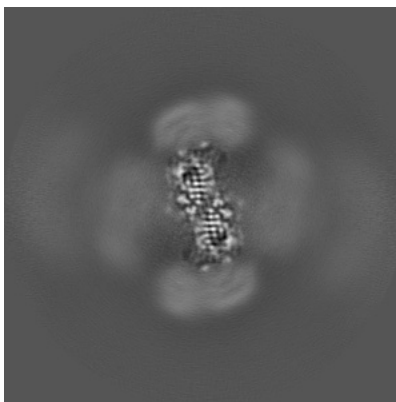


Z Index: 158

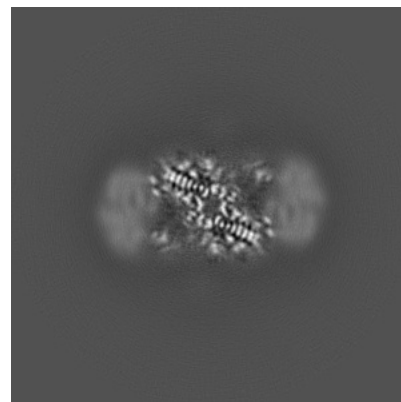
6.3.2 Raw map



X Index: 146



Y Index: 135

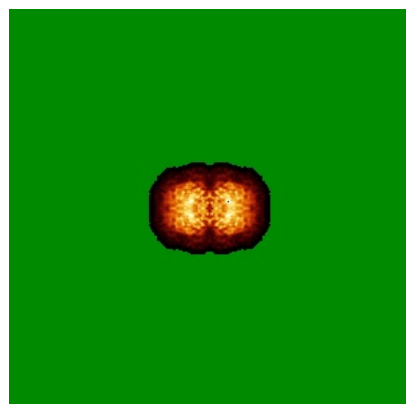


Z Index: 142

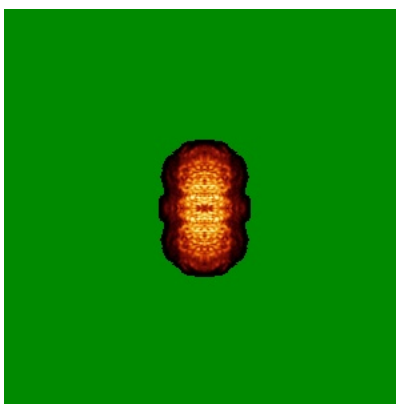
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

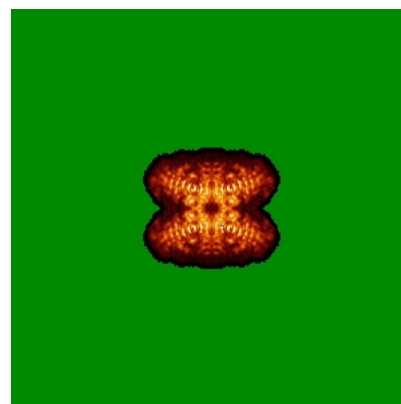
6.4.1 Primary map



X

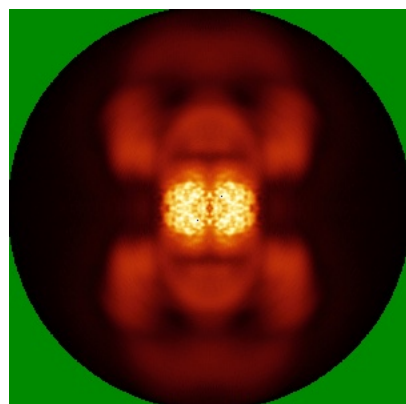


Y

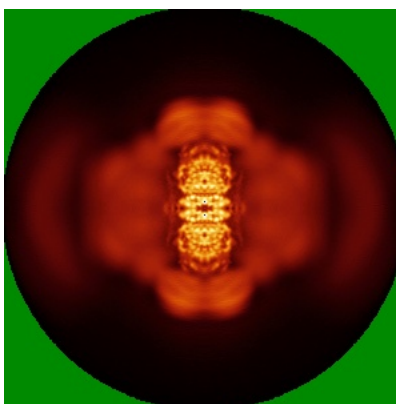


Z

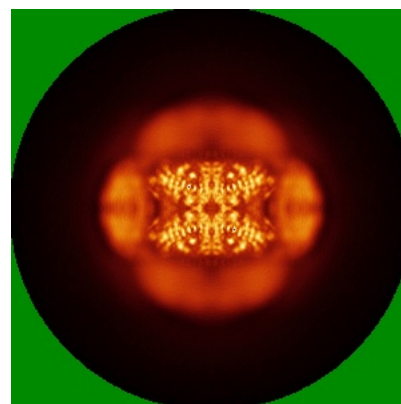
6.4.2 Raw map



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.

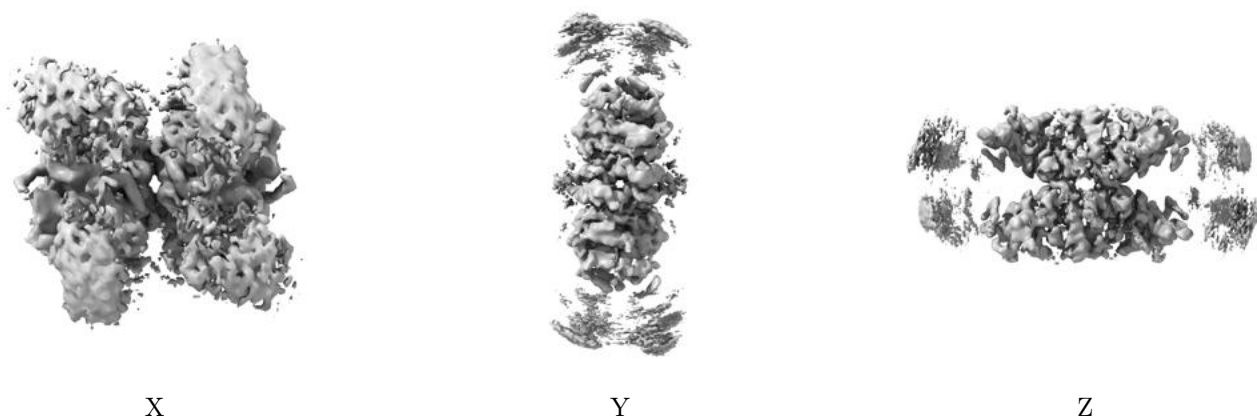
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

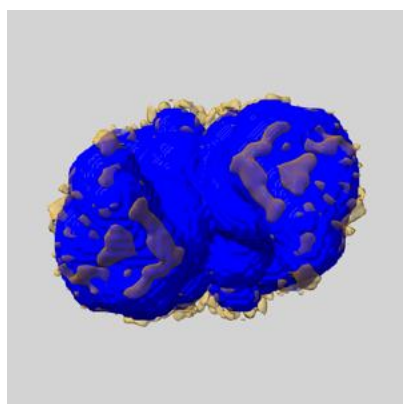
6.6 Mask visualisation [i](#)

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

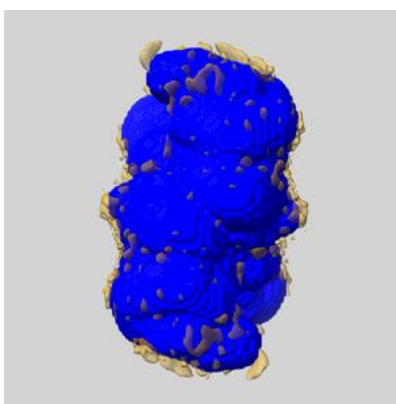
A mask typically either:

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

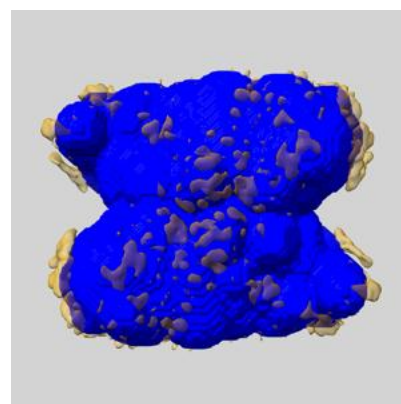
6.6.1 emd_31469_msk_1.map [i](#)



X



Y

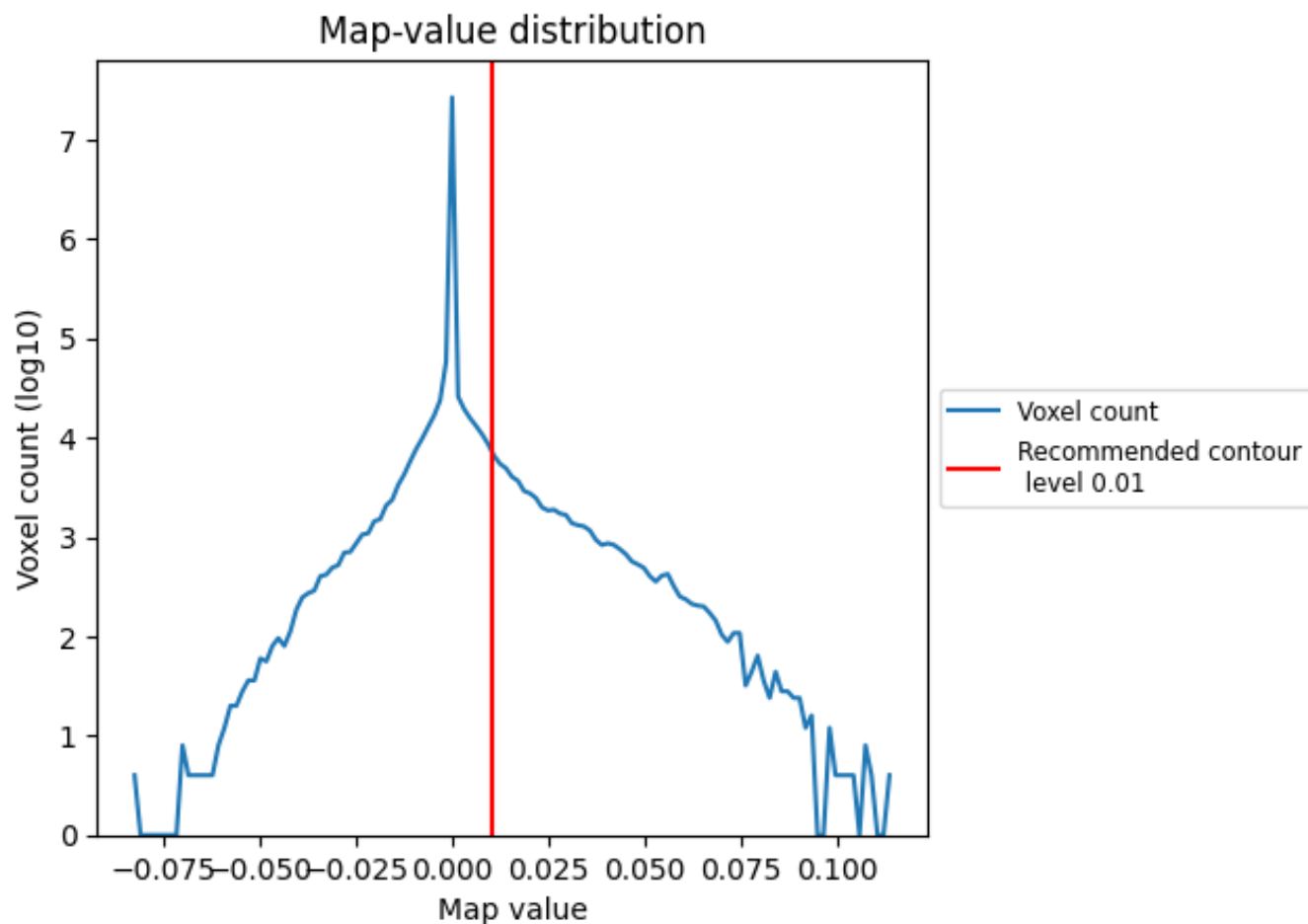


Z

7 Map analysis [i](#)

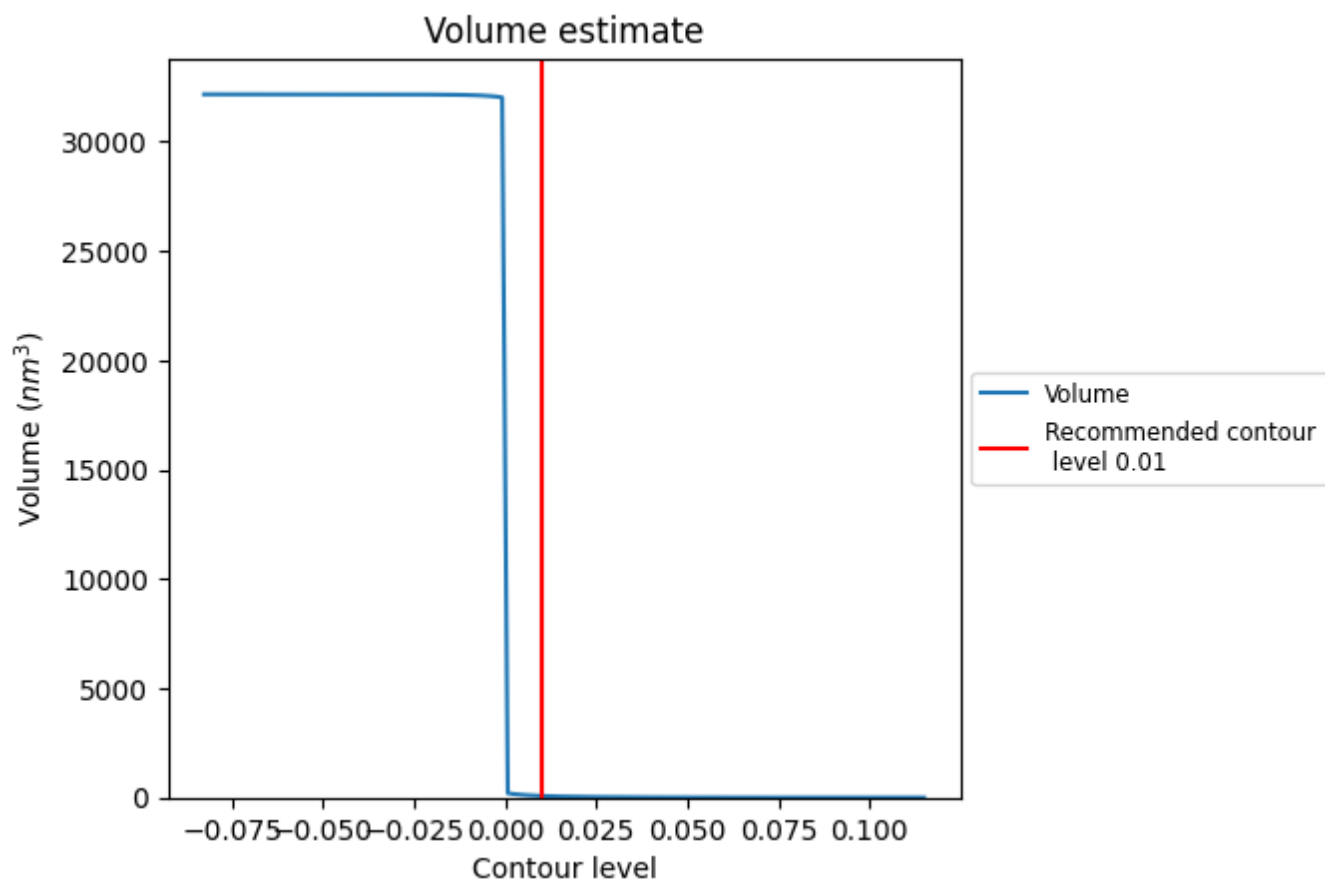
This section contains the results of statistical analysis of the map.

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.

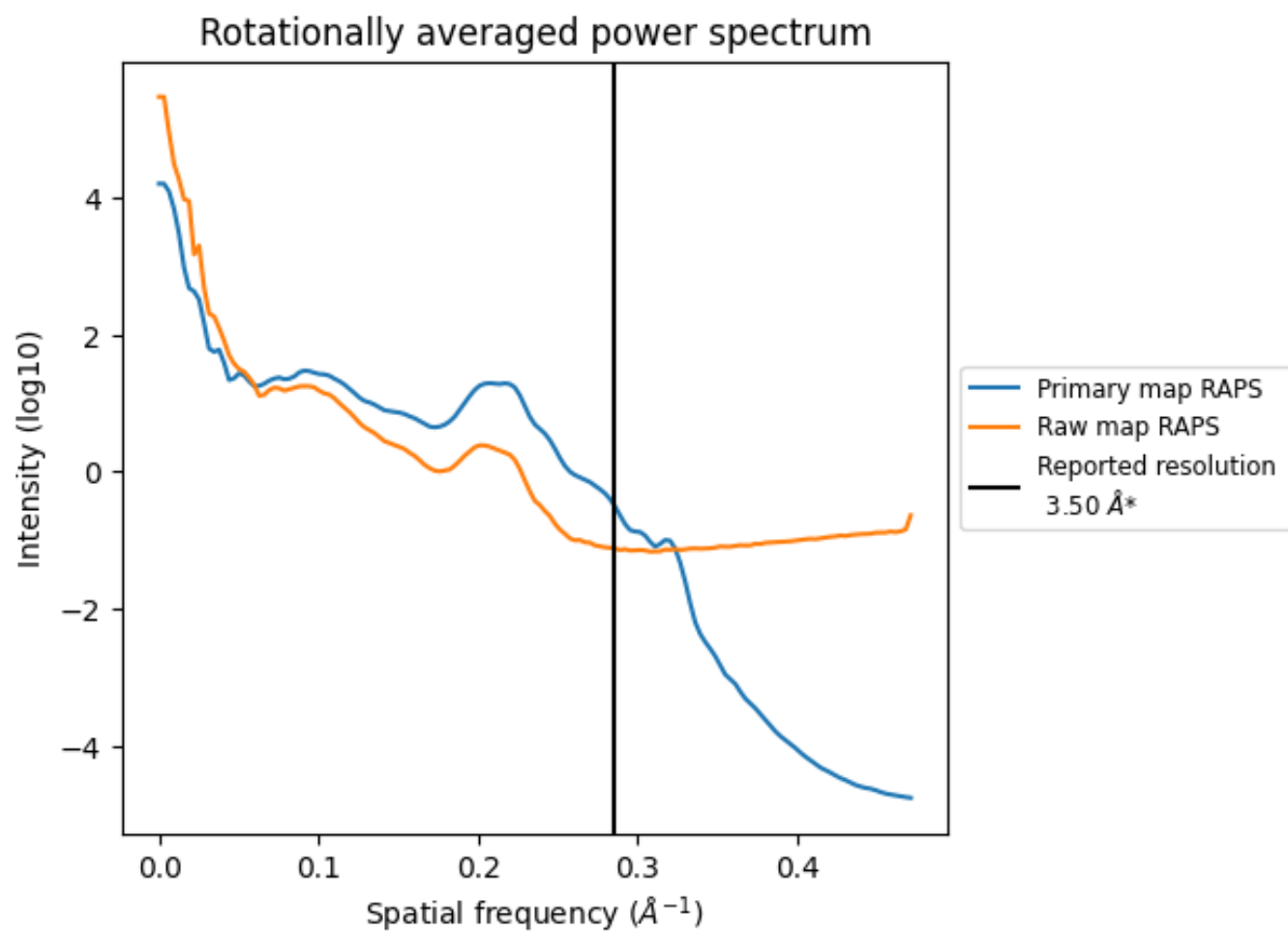
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 73 nm^3 ; this corresponds to an approximate mass of 66 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 ⓘ

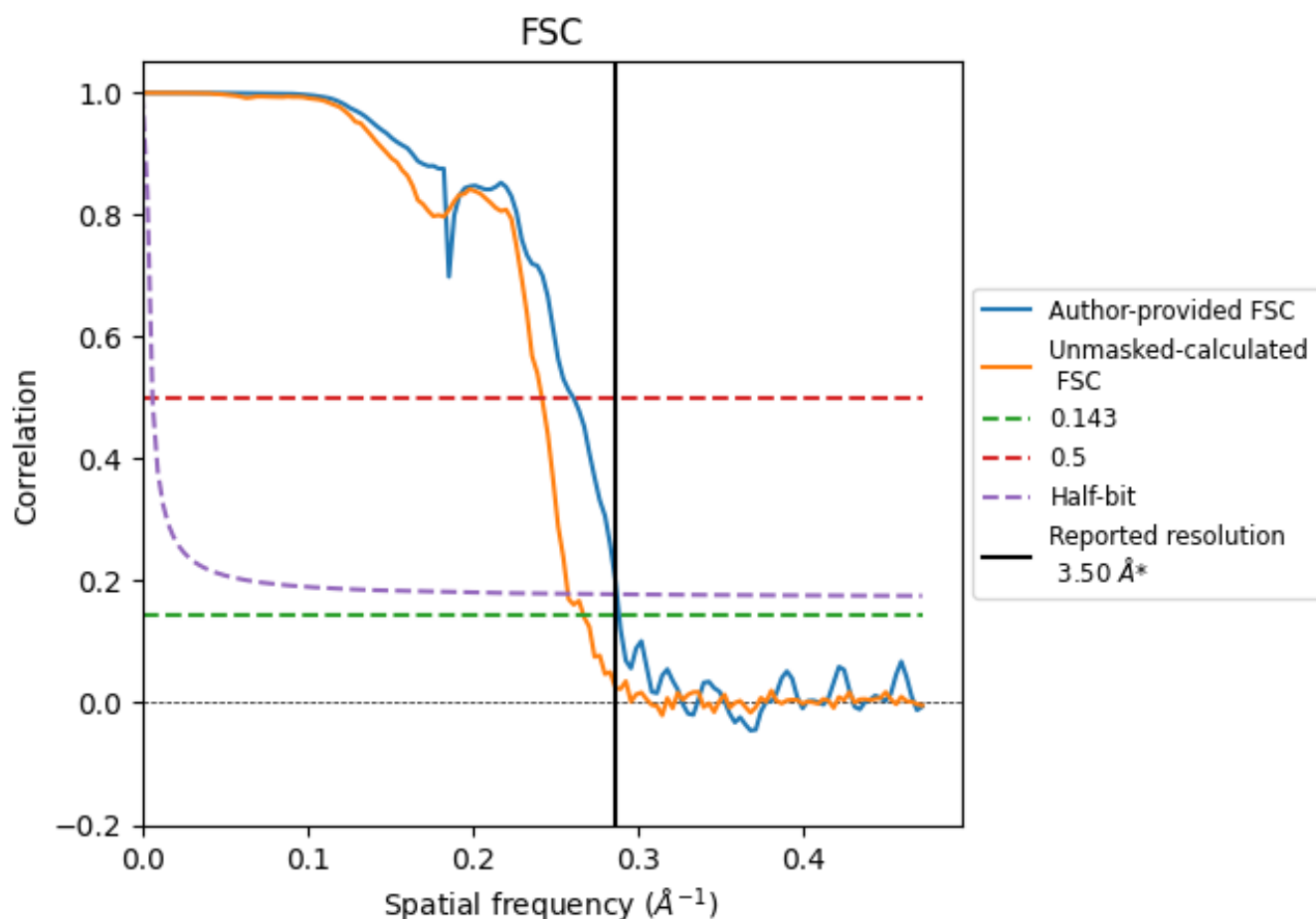


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

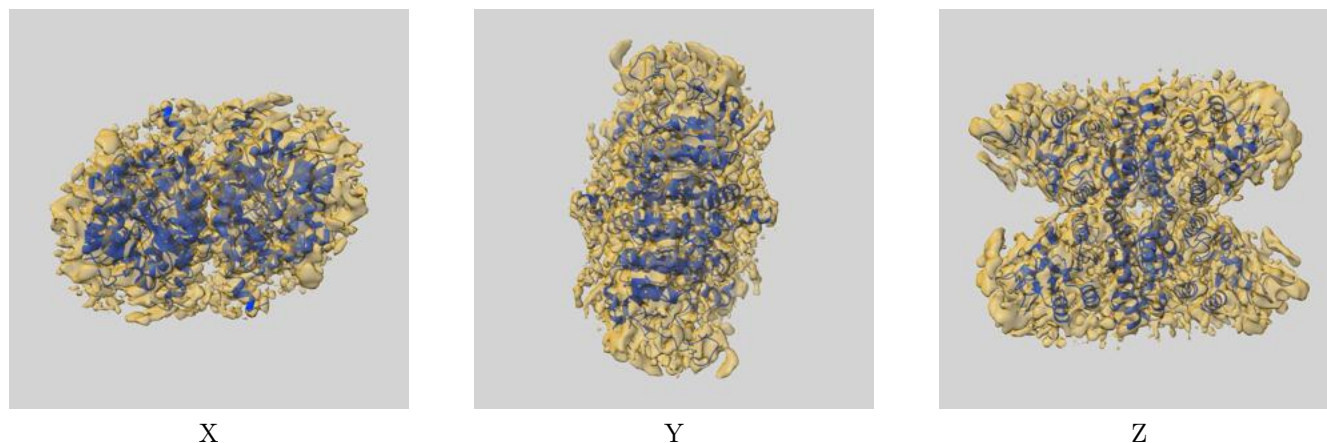
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.47	3.83	3.48
Unmasked-calculated*	3.75	4.14	3.88

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

9 Map-model fit [i](#)

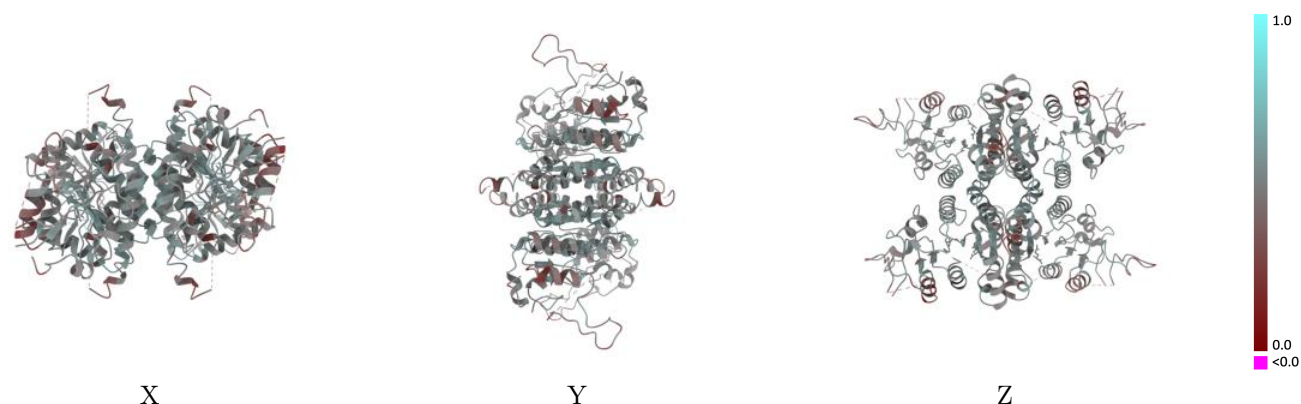
This section contains information regarding the fit between EMDB map EMD-31469 and PDB model 7F5X. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



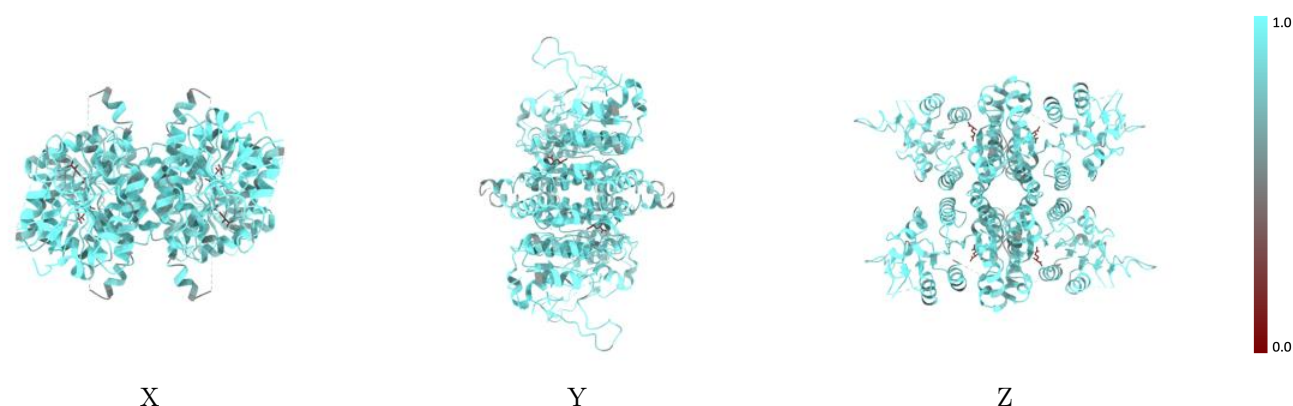
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



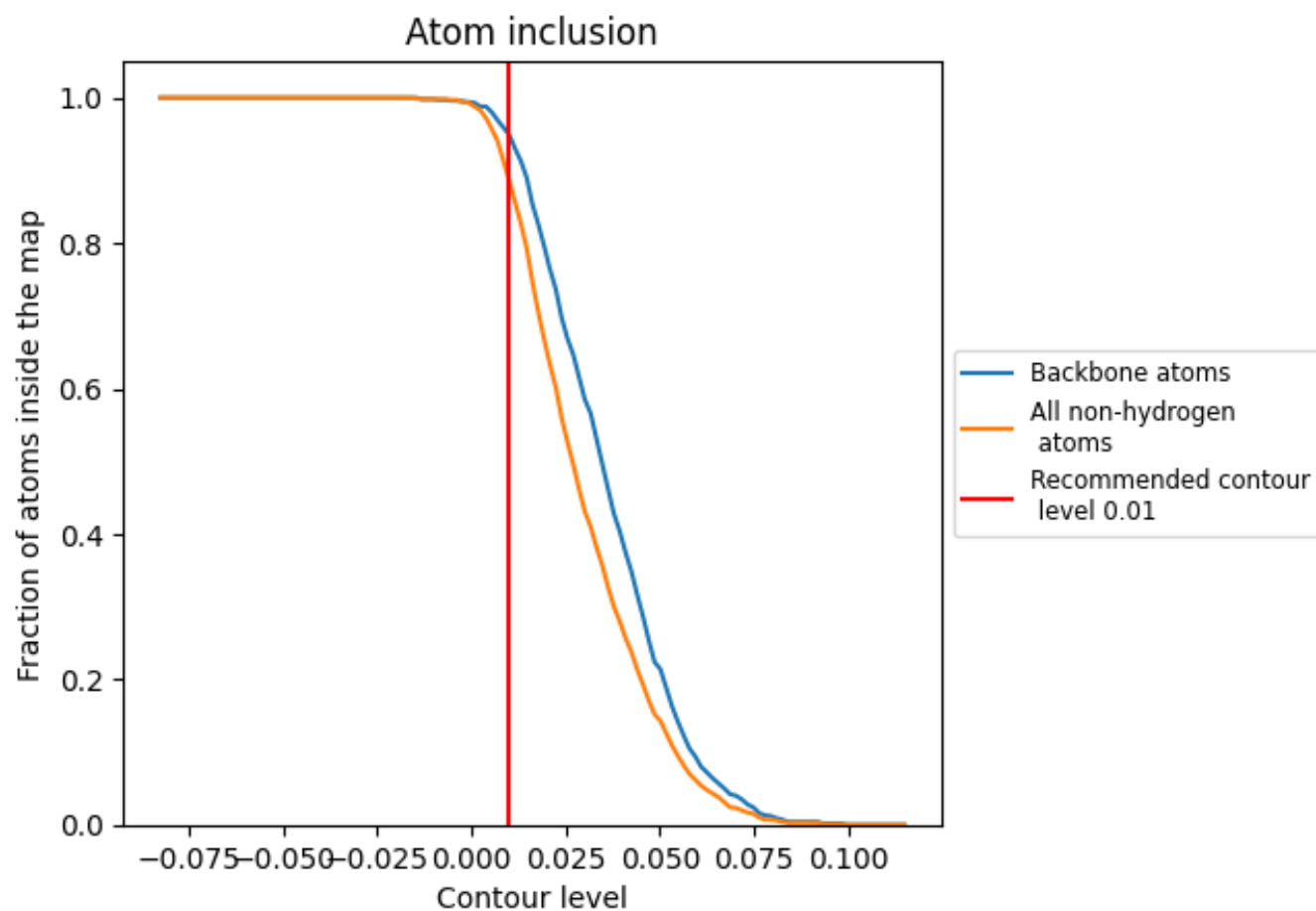
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 89% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8870	0.4860
A	0.8870	0.4860
B	0.8870	0.4870
C	0.8870	0.4880
D	0.8870	0.4850

