



wwPDB EM Validation Summary Report ⓘ

Nov 17, 2024 – 12:43 AM JST

PDB ID : 8ZYN
EMDB ID : EMD-60573
Title : Cryo-EM Structure of inhibitor-free hERG Channel
Authors : Miyashita, Y.; Moriya, T.; Kato, T.; Kawasaki, M.; Yasuda, Y.; Adachi, N.;
Suzuki, K.; Ogasawara, S.; Saito, T.; Senda, T.; Murata, T.
Deposited on : 2024-06-18
Resolution : 3.27 Å(reported)

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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.dev113
MolProbity : 4.02b-467
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) : 2.39

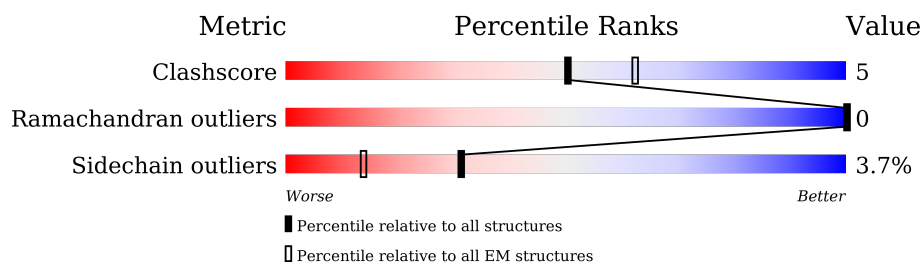
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY





The reported resolution of this entry is 3.27 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	820	
1	B	820	
1	C	820	
1	D	820	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6640 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 Potassium voltage-gated channel subfamily H member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	210	Total	C	N	O	S	0	0
			1658	1114	266	270	8		
1	B	210	Total	C	N	O	S	0	0
			1662	1117	267	270	8		
1	C	210	Total	C	N	O	S	0	0
			1662	1117	267	270	8		
1	D	210	Total	C	N	O	S	0	0
			1658	1114	266	270	8		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1025	LEU	-	expression tag	UNP Q12809
A	1026	GLU	-	expression tag	UNP Q12809
A	1027	VAL	-	expression tag	UNP Q12809
A	1028	LEU	-	expression tag	UNP Q12809
A	1029	PHE	-	expression tag	UNP Q12809
A	1030	GLN	-	expression tag	UNP Q12809
B	1025	LEU	-	expression tag	UNP Q12809
B	1026	GLU	-	expression tag	UNP Q12809
B	1027	VAL	-	expression tag	UNP Q12809
B	1028	LEU	-	expression tag	UNP Q12809
B	1029	PHE	-	expression tag	UNP Q12809
B	1030	GLN	-	expression tag	UNP Q12809
C	1025	LEU	-	expression tag	UNP Q12809
C	1026	GLU	-	expression tag	UNP Q12809
C	1027	VAL	-	expression tag	UNP Q12809
C	1028	LEU	-	expression tag	UNP Q12809
C	1029	PHE	-	expression tag	UNP Q12809
C	1030	GLN	-	expression tag	UNP Q12809
D	1025	LEU	-	expression tag	UNP Q12809
D	1026	GLU	-	expression tag	UNP Q12809
D	1027	VAL	-	expression tag	UNP Q12809
D	1028	LEU	-	expression tag	UNP Q12809

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1029	PHE	-	expression tag	UNP Q12809
D	1030	GLN	-	expression tag	UNP Q12809



GLY	GLY	PRO	THR	THR	ARG	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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● Molecule 1: Potassium voltage-gated channel subfamily H member 2



MET	PRO	VAL	ARG	ARG	GLY	HIS	VAL	ALA	PRO	GLN	ASN	THR	PHE	LEU	ASP	THR	ILE	ILE	ARG	LYS	PHE	GLY	GLN	SER	ARG	ILE	ALA	ALA	ASN	CYS	VAL	VAL	TYR	CYS	ASN	ASP	PHE	CYS	VAL	LEU	CYS	GLY	TYR	SER	ARG	ALA	GLU	VAL	MET		
GLN	ARG	PRO	CYS	THR	CYS	ASP	PHE	LEU	HIS	GLY	VAL	PRO	ARG	THR	GLN	ARG	ARG	ALA	ALA	GLN	ILE	ALA	GLN	LEU	LEU	GLY	GLU	GLU	ILE	ARG	LYS	VAL	GLU	LYS	PHE	THR	ARG	VAL	LEU	VAL	ASP	VAL	VAL	VAL	PRO	VAL	VAL	ASN	GLU	ASP	GLY
ALA	VAL	ILE	MET	PHE	ILE	LEU	ASN	PHE	GLU	GLY	VAL	MET	GLU	LYS	ASP	MET	VAL	GLY	SER	PRO	THR	ASP	ARG	GLU	ILE	ILE	ALA	PRO	LYS	ILE	LYS	GLU	THR	GLN	VAL	LEU	SER	LEU	GLY	ALA	ASP	VAL	VAL	VAL	PRO	GLY	TYR	LYS	LEU		
GLN	ALA	PRO	ARG	ILE	HIS	ARG	TRP	THR	ILE	LEU	HIS	TYR	SER	PHE	K407	L413	I414	L415	L416	L417	V418	I419	Y420	T421	L433	K434	GLY	THR	GLU	GLY	GLY	PRO	PRO	ALA	THR	THR	THR	GLY	PRO	L452	D456	L457	I458	V459	D460	I461	V465	D466	I469		

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	254567	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)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.075	Depositor
Minimum map value	-1.849	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.35	Depositor
Map size (\AA)	298.8, 298.8, 298.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.24	0/1698	0.42	0/2305
1	B	0.25	0/1702	0.45	0/2309
1	C	0.27	0/1702	0.44	0/2309
1	D	0.25	0/1698	0.46	0/2305
All	All	0.25	0/6800	0.44	0/9228

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	1658	0	1706	19	0
1	B	1662	0	1717	18	0
1	C	1662	0	1717	17	0
1	D	1658	0	1706	23	0
All	All	6640	0	6846	73	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 5.

The worst 5 of 73 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:466:ASP:OD2	1:A:534:ARG:NH1	2.26	0.69
1:B:656:PHE:HA	1:B:659:VAL:HG22	1.77	0.66
1:D:576:GLN:OE1	1:D:587:HIS:NE2	2.30	0.64
1:B:658:ASN:O	1:B:662:ILE:HD12	1.98	0.63
1:C:632:PRO:O	1:D:629:ASN:ND2	2.32	0.62

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	198/820 (24%)	196 (99%)	2 (1%)	0	100	100
1	B	198/820 (24%)	193 (98%)	5 (2%)	0	100	100
1	C	198/820 (24%)	191 (96%)	7 (4%)	0	100	100
1	D	198/820 (24%)	195 (98%)	3 (2%)	0	100	100
All	All	792/3280 (24%)	775 (98%)	17 (2%)	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	173/706 (24%)	167 (96%)	6 (4%)	31	57
1	B	174/706 (25%)	172 (99%)	2 (1%)	70	82

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	174/706 (25%)	167 (96%)	7 (4%)	27	54
1	D	173/706 (24%)	162 (94%)	11 (6%)	14	40
All	All	694/2824 (25%)	668 (96%)	26 (4%)	31	56

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	616	TYR
1	D	493	TYR
1	D	576	GLN
1	D	456	ASP
1	D	497	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no chain breaks in this entry.

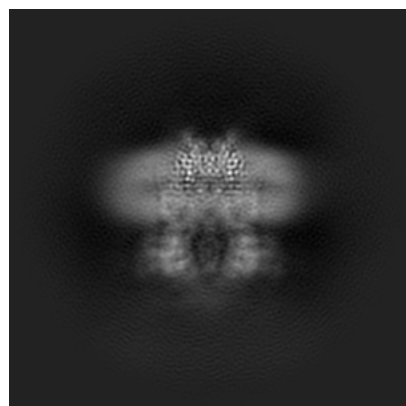
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60573. These allow visual inspection of the internal detail of the map and identification of artifacts.

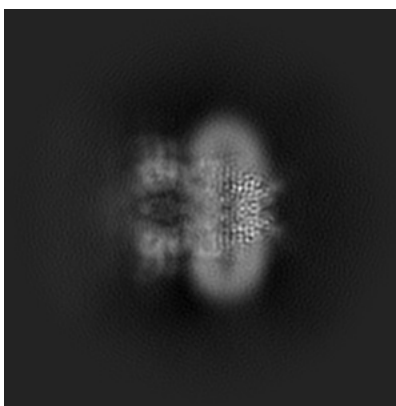
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

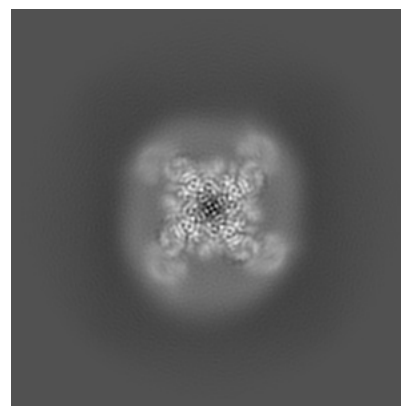
6.1.1 Primary map



X

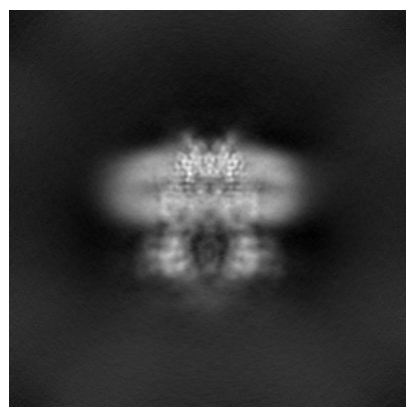


Y

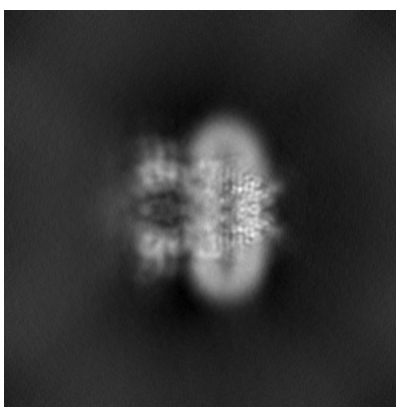


Z

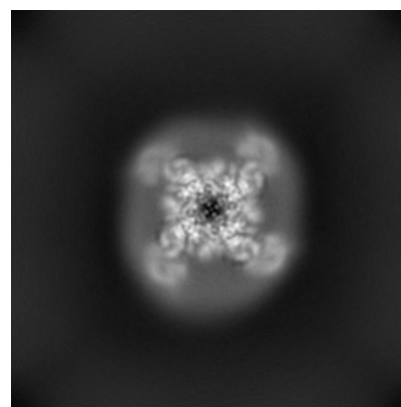
6.1.2 Raw map



X



Y

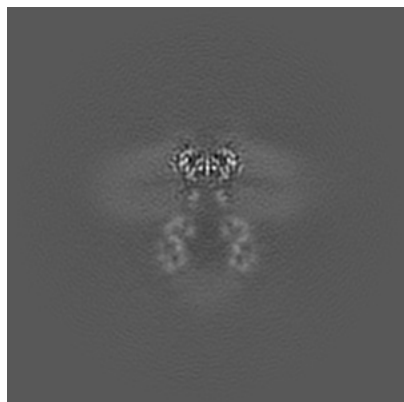


Z

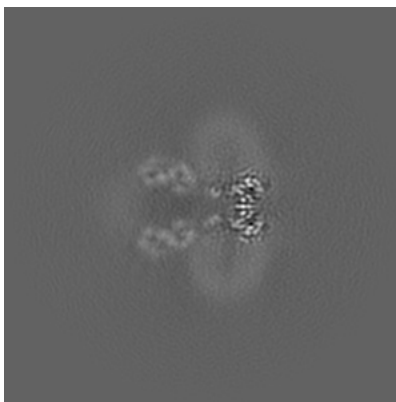
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

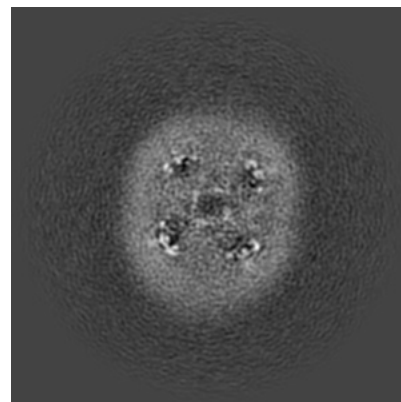
6.2.1 Primary map



X Index: 180

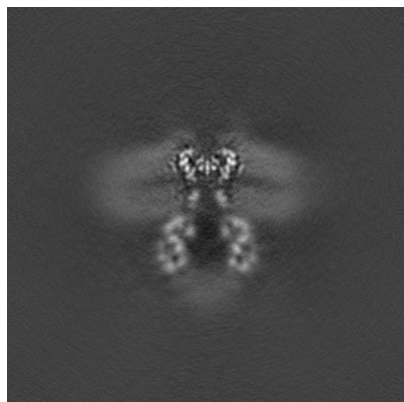


Y Index: 180

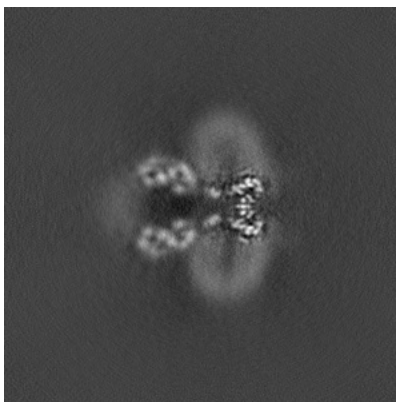


Z Index: 180

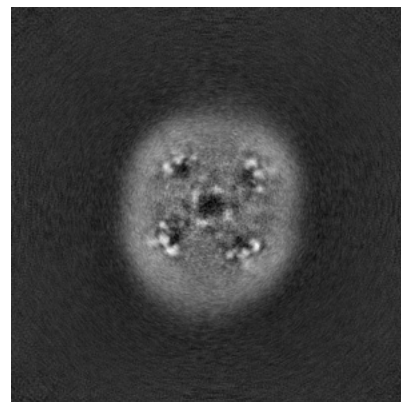
6.2.2 Raw map



X Index: 180



Y Index: 180

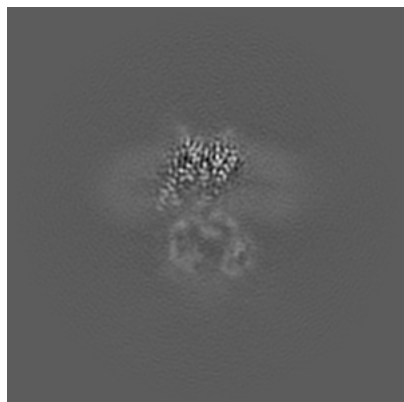


Z Index: 180

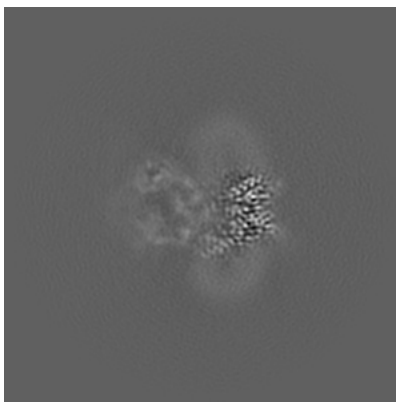
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

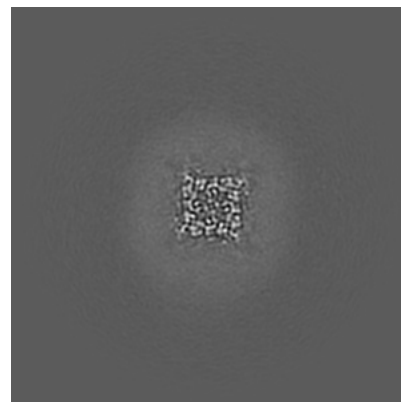
6.3.1 Primary map



X Index: 196

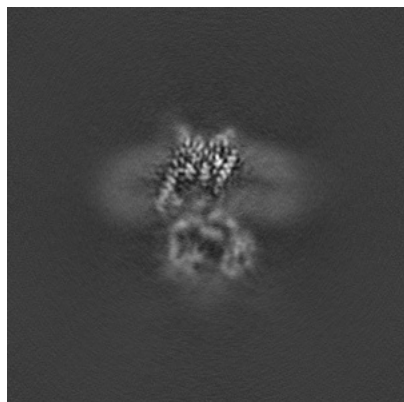


Y Index: 164

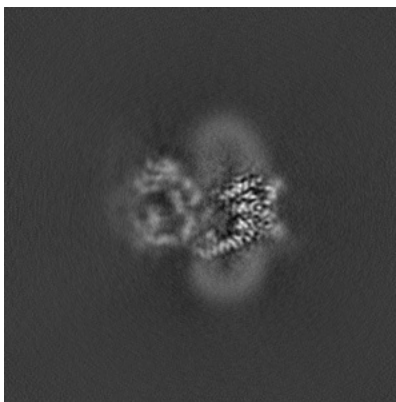


Z Index: 223

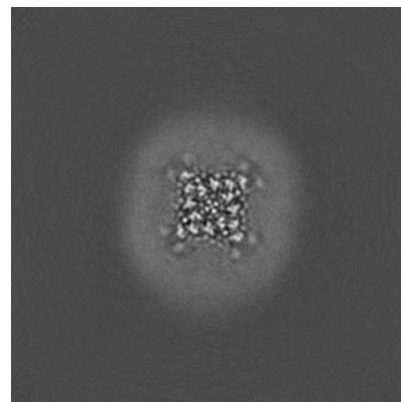
6.3.2 Raw map



X Index: 197



Y Index: 162

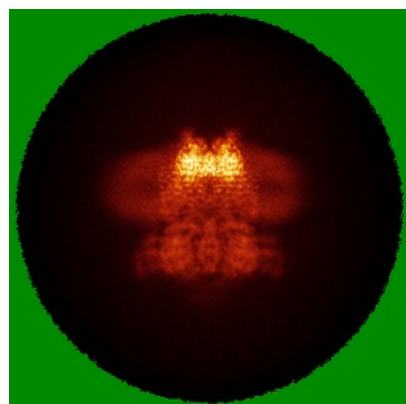


Z Index: 218

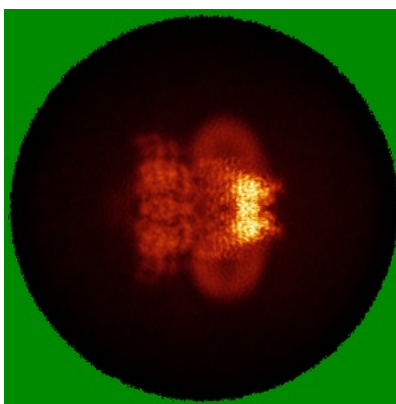
The images above show the largest variance slices of the map in three orthogonal directions.

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

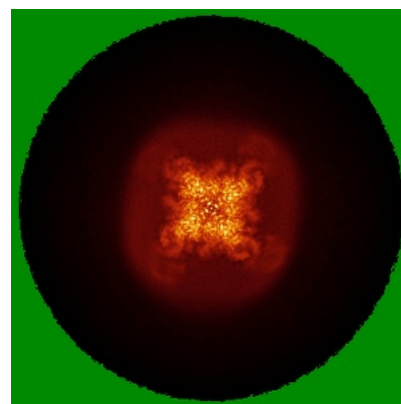
6.4.1 Primary map



X

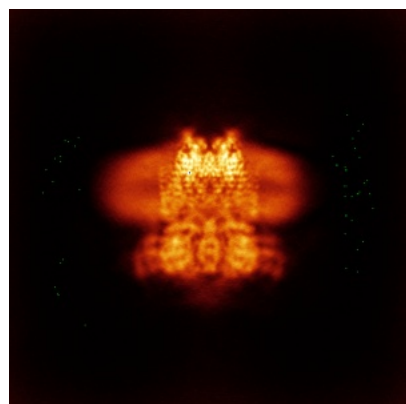


Y

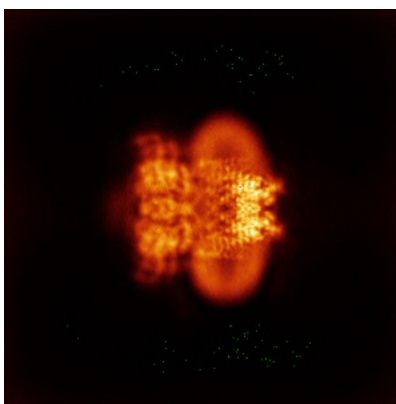


Z

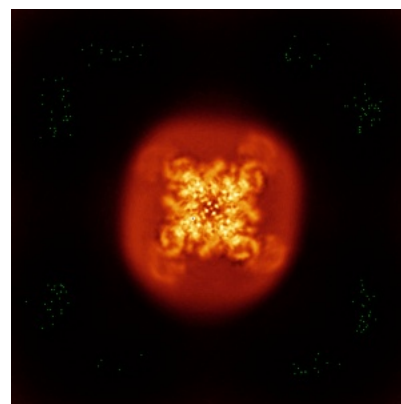
6.4.2 Raw map



X



Y

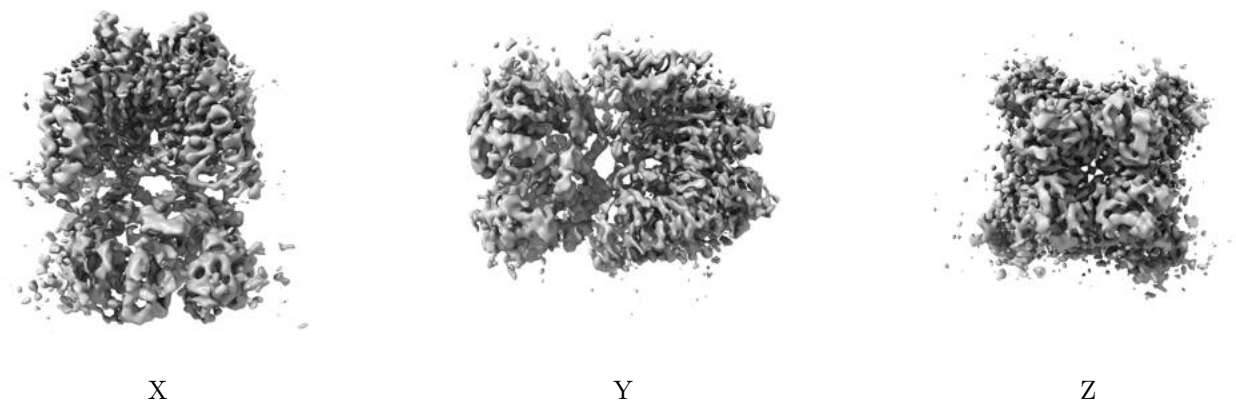


Z

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.

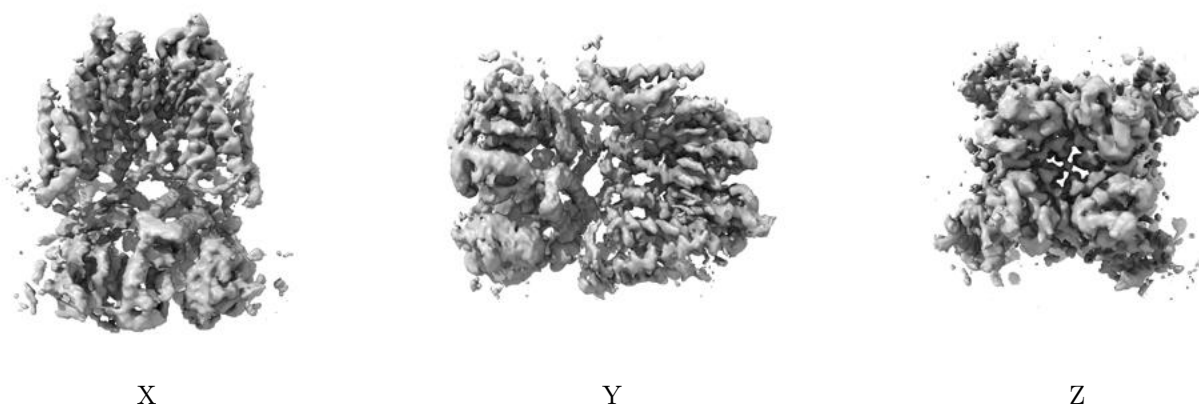
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. 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.

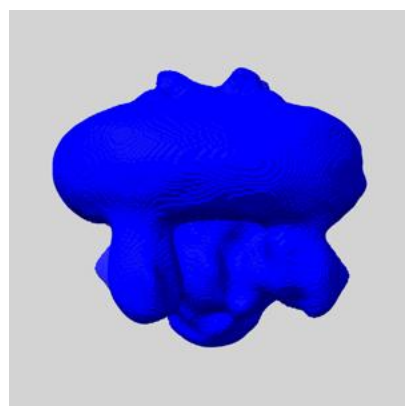
6.6 Mask visualisation [i](#)

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

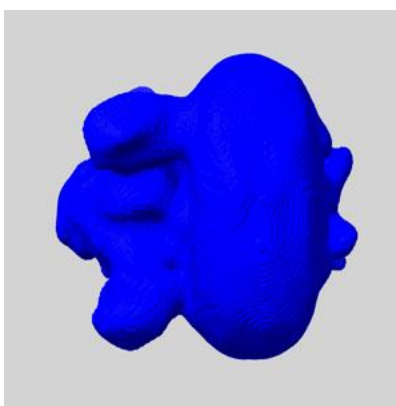
A mask typically either:

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

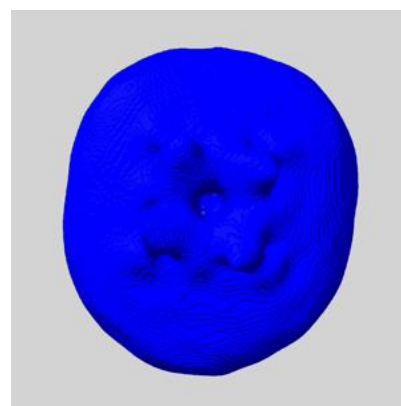
6.6.1 emd_60573_msk_1.map [i](#)



X



Y

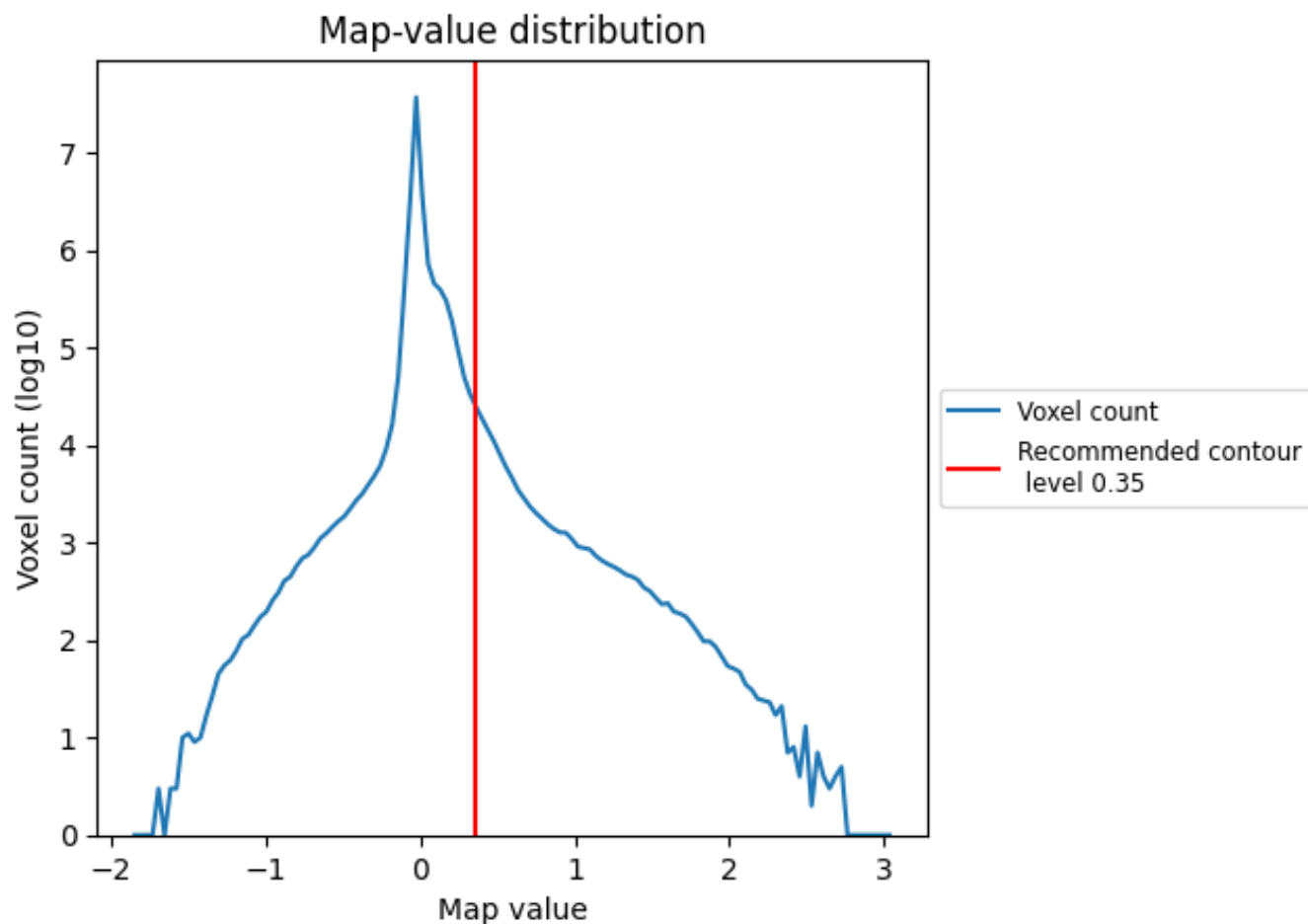


Z

7 Map analysis [i](#)

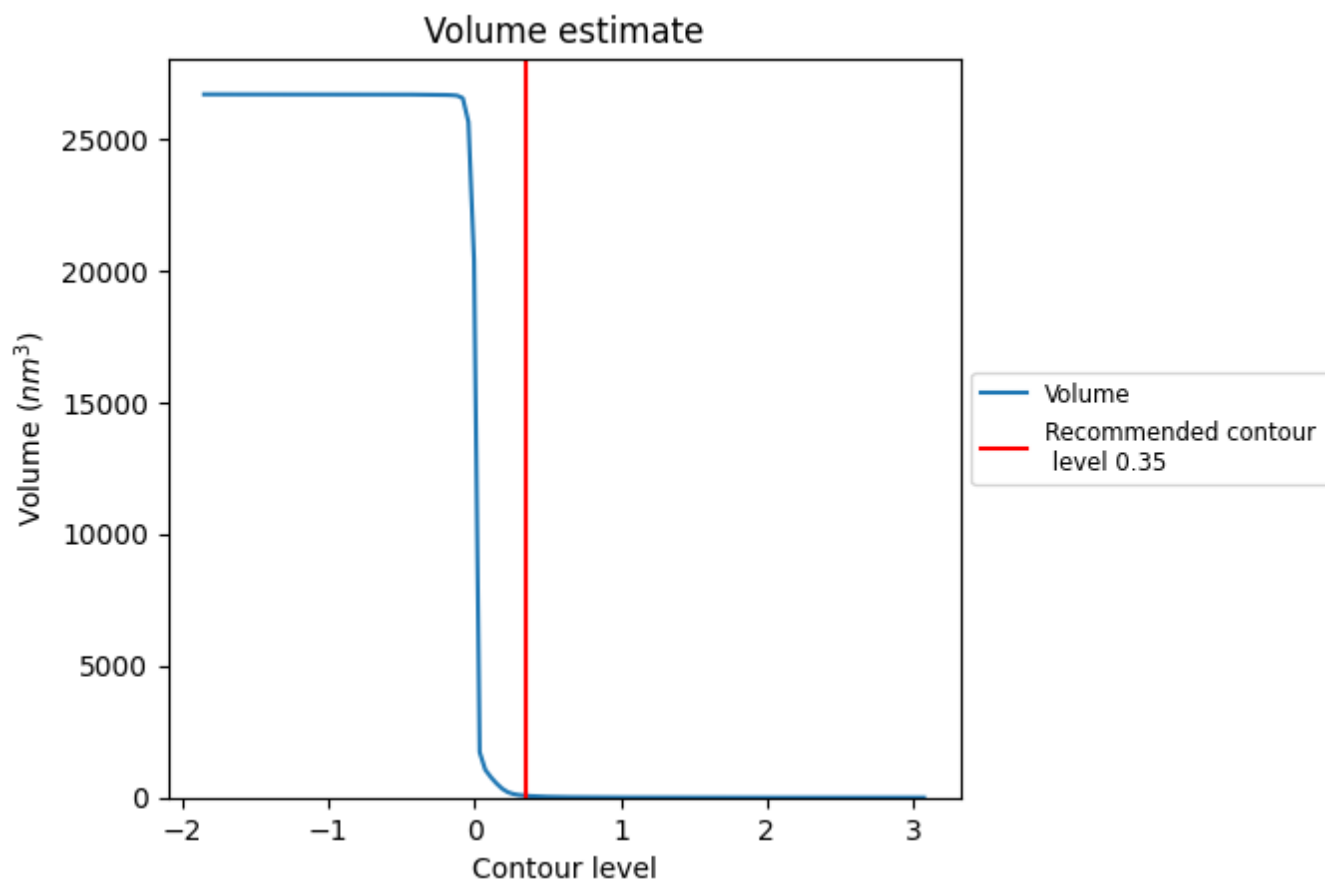
This section contains the results of statistical analysis of the map.

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.

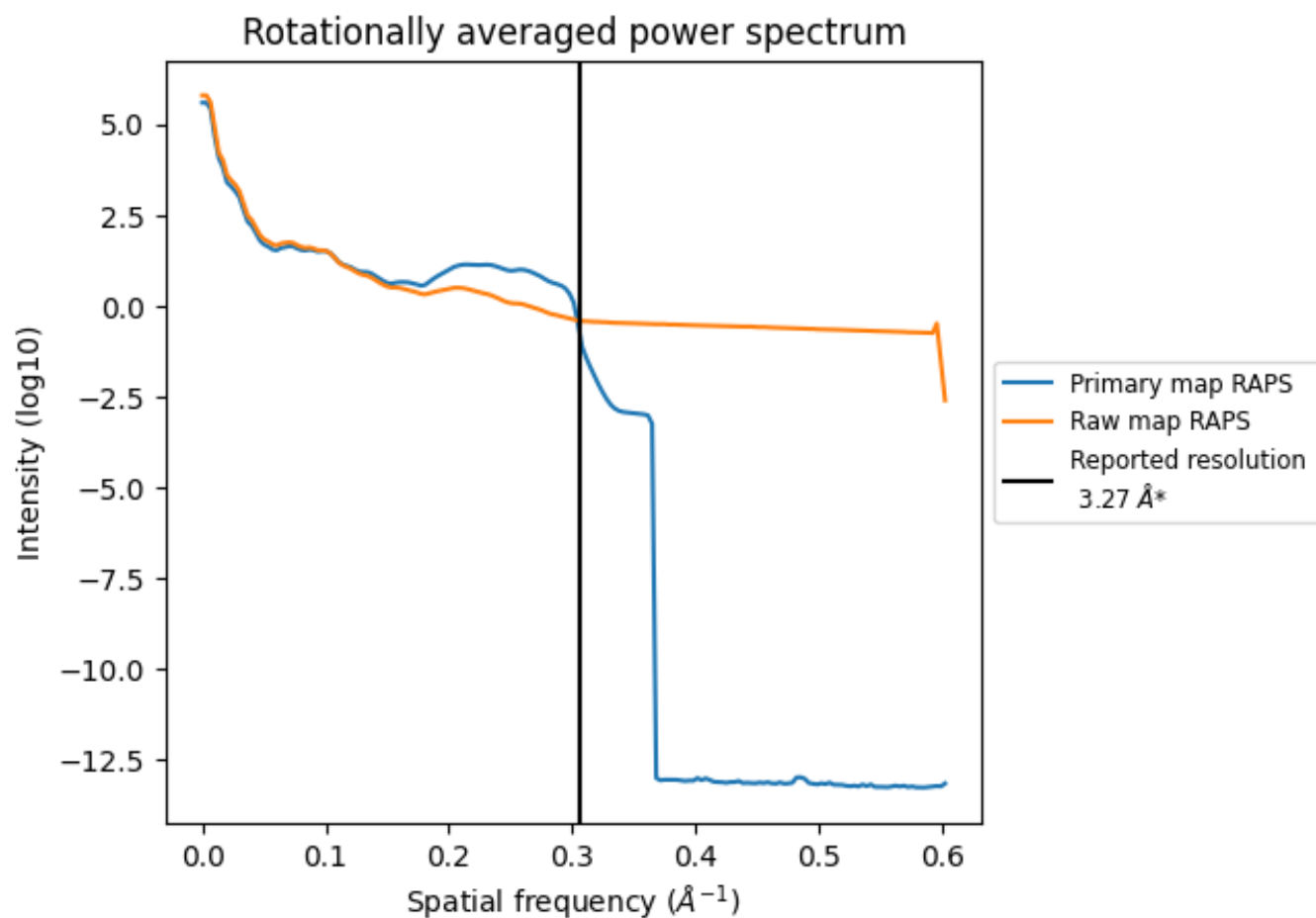
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 71 nm³; this corresponds to an approximate mass of 64 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 ⓘ

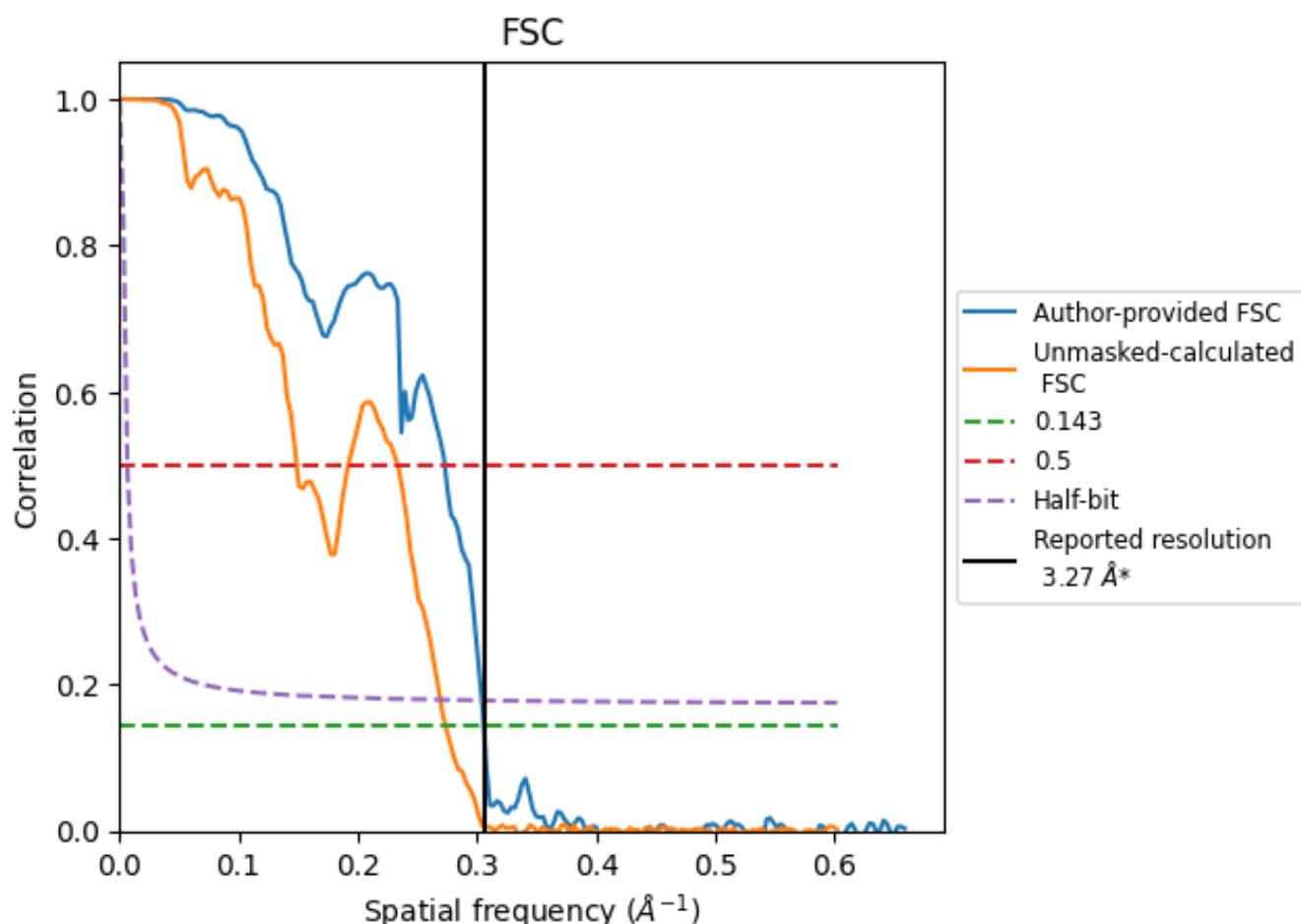


*Reported resolution corresponds to spatial frequency of 0.306 Å⁻¹

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 0.306 Å⁻¹

8.2 Resolution estimates [i](#)

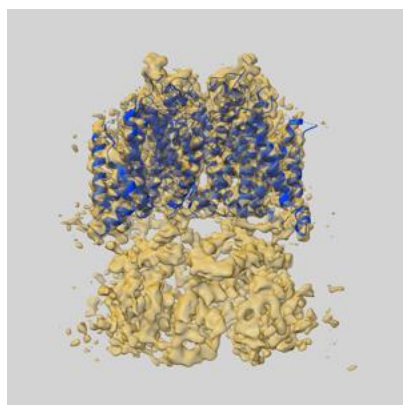
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.27	-	-
Author-provided FSC curve	3.27	3.66	3.29
Unmasked-calculated*	3.65	6.72	3.71

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.65 differs from the reported value 3.27 by more than 10 %

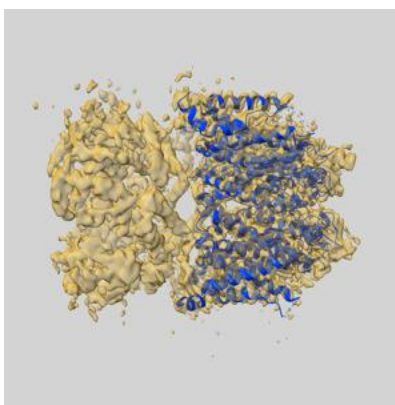
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60573 and PDB model 8ZYN. Per-residue inclusion information can be found in section [3](#) on page [5](#).

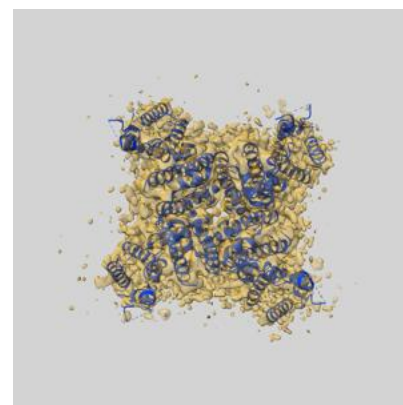
9.1 Map-model overlay [i](#)



X



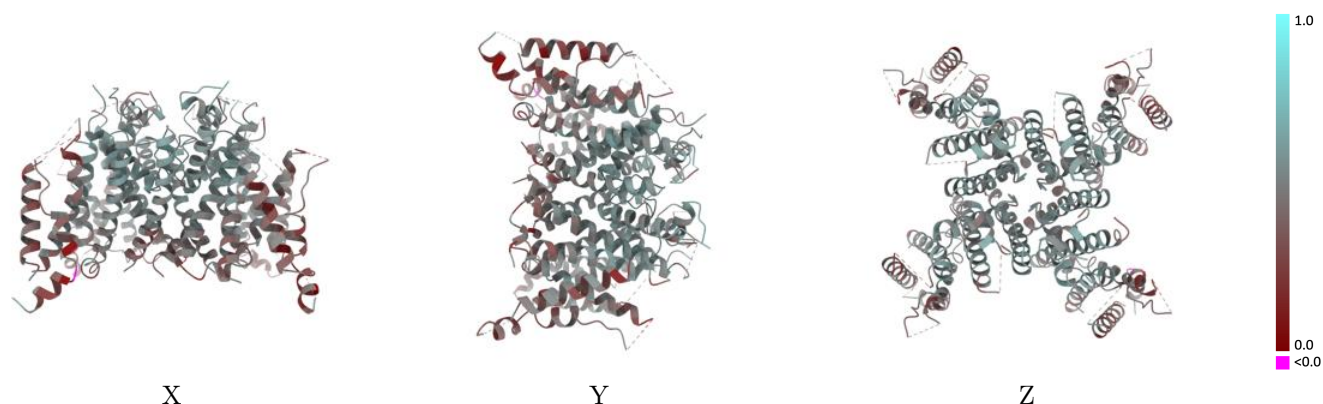
Y



Z

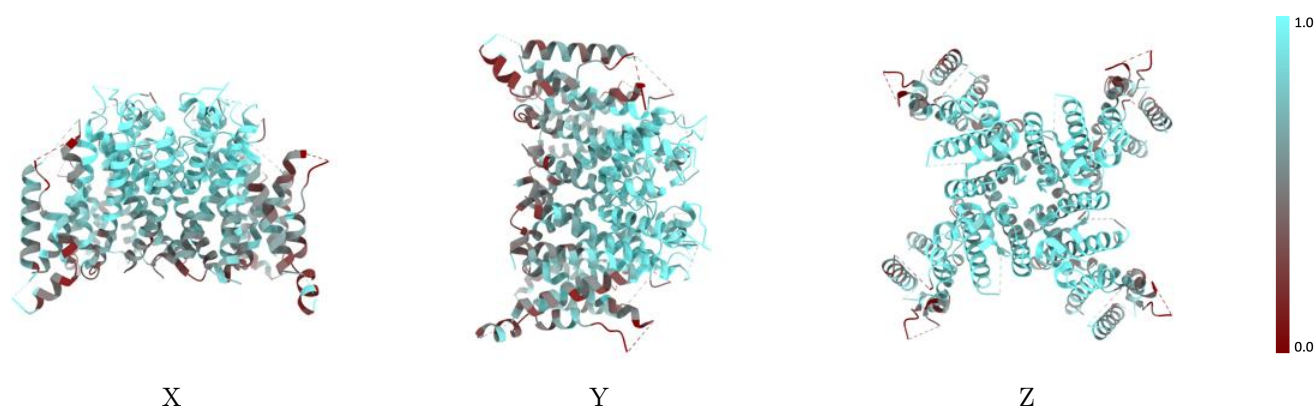
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



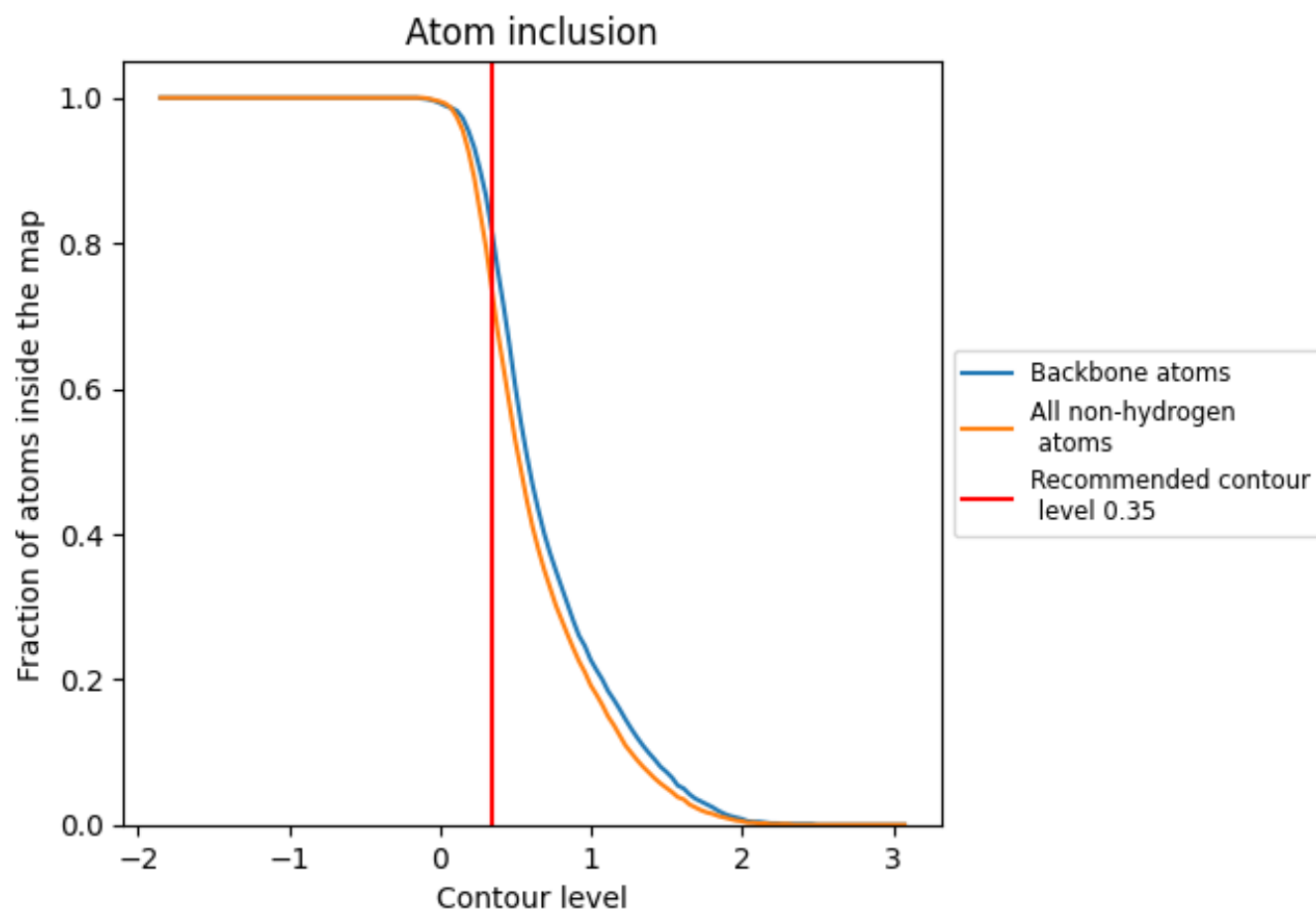
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 73% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7260	<div></div> 0.4690
A	<div></div> 0.7150	<div></div> 0.4720
B	<div></div> 0.7510	<div></div> 0.4770
C	<div></div> 0.7380	<div></div> 0.4660
D	<div></div> 0.6990	<div></div> 0.4590

