



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 11:50 PM UTC

PDB ID : 7TYJ / pdb_00007tyj
EMDB ID : EMD-26181
Title : Cryo-EM Structure of insulin receptor-related receptor (IRR) in apo-state captured at pH 7. The 3D refinement was focused on one of two halves with C1 symmetry applied
Authors : Wang, L.W.; Hall, C.; Li, J.; Choi, E.; Bai, X.C.
Deposited on : 2022-02-13
Resolution : 3.30 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

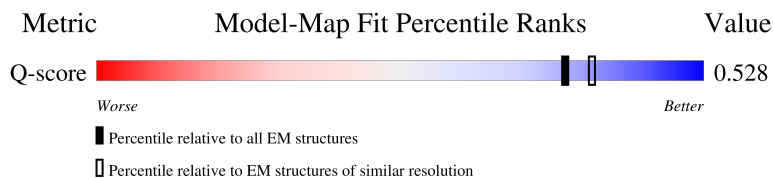
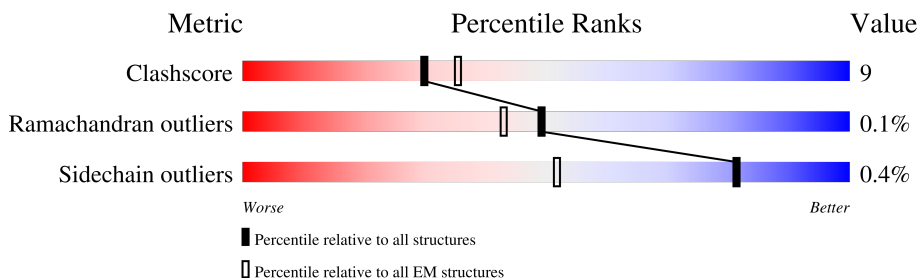
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	1297	 26% 9% 66%
1	B	1297	 22% 6% 72%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6338 atoms, of which 0 are hydrogens and 0 are deuteriums.

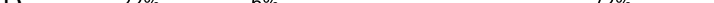
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Insulin receptor-related protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	447	Total	C	N	O	S	0	0
			3437	2163	611	630	33		
1	B	361	Total	C	N	O	S	0	0
			2901	1845	518	532	6		

Tyr	Tyr	Gln	Val	Asn	Ser	Tyr
Tyr	Tyr	Val	Tyr	Asn	Ser	Phe
Ser	Ser	Leu	Glu	Pro	Arg	Pro
Pro	Glu	Phe	Thr	Gly	Glu	Ala
Cys	Val	Lys	Asp	Leu	Cys	Ser
Cys	Val	Val	Tyr	Pro	Ile	Asp
Arg	Met	Met	Tyr	Gln	Glu	Met
Gly	Asp	Asp	Arg	Pro	Phe	Tyr
Ala	Gly	Gly	Lys	Leu	Leu	Val
Arg	Gly	Gly	Gly	Ala	Lys	Pro
Gly	Val	Val	Gly	Gly	Glu	Asp
Ser	Ser	Leu	Lys	Met	Ser	Trp
Leu	Leu	Glu	Gly	Met	Ala	Glu
Pro	Pro	Glu	Leu	Ile	Val	Glu
Thr	Thr	Leu	Leu	Gln	Met	Val
Thr	Thr	Gly	Pro	Met	Lys	Arg
Asp	Asp	Gly	Val	Ala	Ala	Pro
Ala	Ala	Cys	Arg	Gly	Phe	Glu
Glu	Glu	Pro	Trp	Glu	Lys	Gln
Pro	Pro	Leu	Met	Ile	Cys	Ile
Asp	Asp	Gln	Ala	Ala	Ser	Ile
Ser	Ser	Leu	Pro	Asp	His	Ile
Ser	Ser	Gln	Glu	Gly	Val	Ile
Pro	Pro	Glu	Ser	Met	Val	Arg
Thr	Thr	Leu	Leu	Ala	Arg	Glu
Pro	Pro	Met	Lys	Tyr	Leu	Leu
Arg	Arg	Ser	Asp	Leu	Leu	Gly
Asp	Asp	Arg	Gly	Ala	Gln	Gln
Cys	Cys	Cys	Ile	Ala	Val	Gly
Ser	Ser	Trp	Phe	Asn	Val	Ser
Pro	Pro	Gln	Thr	Lys	Ser	Phe
Gln	Gln	Pro	Thr	Phe	Gln	Gly
Asn	Asn	Asn	His	Val	Gly	Met
Gly	Gly	Pro	Ser	His	Gln	Val
Gly	Gly	Arg	Asp	Arg	Pro	Tyr
Pro	Pro	Leu	Val	Asp	Thr	Glu
Gly	Gly	Arg	Trp	Leu	Leu	Gly
His	His	Pro	Ser	Ala	Val	Leu
		Ser	Phe	Ala	Ile	Ala
		Phe	Gly	Ser	Met	Arg
		Thr	Val	Asn	Glu	Gly
		His	Val	Cys	Leu	Leu
		Ile	Leu	Met	Met	Glu
		Leu	Trp	Val	Thr	Ala
		Asp	Glu	Ser	Arg	Gly
		Ser	Ile	Gln	Gly	Glu
		Ile	Val	Asp	Asp	Glu
		Gln	Thr	Phe	Leu	Ser
		Glu	Leu	Thr	Lys	Thr
		Glu	Ala	Val	Ser	Pro
		Leu	Glu	Lys	His	Ala
		Arg	Gln	Ile	Leu	Leu
		Pro	Pro	Gly	Arg	Leu
		Ser	Tyr	Asp	Ser	Lys
		Arg	Gln	Phe	Leu	Thr
		Phe	Gly	Gly	Arg	Val
		Leu	Leu	Met	Pro	Glu
		Leu	Ser	Thr	Glu	Leu
		Ser	Asn	Arg	Ala	Leu
		Phe	Glu	Asp	Cys	Ala

- Molecule 1: Insulin receptor-related protein

Chain B:  22% 6% 72%

I695	S591	C456	ASN	GLY	LEU	GLU	PRO	PRO	PRO	PHE	MET
	S592	V467	LEU	TYR	ALA	ASP	GLY	GLY	HIS	THR	ALA
I699	P602	T468	GLN	ASN	GLN	PRO	VAL	VAL	LEU	PRO	VAL
		E469	LEU	LEU	CYS	ARG	LEU	GLY	THR	THR	THR
			GLY	GLU	PRO	ALA	ALA	GLY	ASP	GLU	GLU
			SER	GLN	SER	CYS	ALA	ALA	VAL	ASP	TRP
			TRP	GLN	PHE	VAL	GLY	GLY	LEU	PRO	GLY
			LYS	LEU	THR	ALA	ALA	ALA	PRO	TRP	GLY
			VAL	GLN	THR	ARG	GLU	PRO	ALA	GLY	GLY
			THR	HIS	ARG	ARG	PRO	ALA	GLY	TRP	TRP
			SER	HIS	ASN	HIS	CYS	LEU	LEU	ALA	ALA
			ILE	LEU	SER	LEU	ALA	ALA	GLY	SER	CYS
			ASN	LEU	SER	LEU	ALA	LYS	ALA	PHE	LEU
			LYS	GLY	SER	TYR	LYS	VAL	PHE	PRO	VAL
			THR	GLY	SER	PHE	THR	THR	ARG	PRO	ARG
			SER	VAL	SER	GLN	THR	THR	GLY	VAL	VAL
			D629	ILE	ILE	GLN	PHE	THR	LEU	ARG	GLY
			Y630	VAL	VAL	GLY	VAL	THR	GLY	GLY	THR
			GLN	THR	THR	CYS	ALA	SER	GLY	THR	THR
			ARG	GLU	VAL	CYS	ALA	ALA	GLN	VAL	PHE
			ASP	ILE	GLY	LEU	ILE	GLY	ALA	LEU	LEU
			SER	THR	LYS	LEU	THR	CYS	VAL	SER	SER
			GLY	GLY	ILE	TRP	ARG	TRP	HIS	VAL	LEU
			L635	GLY	CYS	TRP	THR	THR	ARG	VAL	SER
				GLY	GLY	ALA	ALA	ALA	GLY	THR	THR
				LEU	GLU	ALA	ALA	ASP	GLY	THR	THR
				ARG	GLY	ALA	GLY	GLY	VAL	THR	THR
				GLY	PHE	LEU	PHE	CYS	THR	GLY	GLY
				HIS	THR	CYS	ALA	LYS	HIS	TYR	VAL
				ARG	PHE	LEU	VAL	VAL	CYS	GLY	CYS
				ARG	ALA	CYS	ILE	CYS	LEU	SER	PRO
				ARG	PHE	ILE	LYS	PRO	ASN	GLN	ASP
				ALA	ASN	LYS	LYS	GLY	LEU	LEU	LEU
				ALA	PRO	GLY	HIS	THR	GLY	PHE	THR
				ALA	LEU	GLY	ASN	GLY	VAL	THR	VAL
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	VAL	GLY	LEU
				LEU	GLY	ASP	PHE	ILE	GLY	GLY	LEU
				ARG	GLY	PRO	LEU	VAL	GLY	GLY	LEU
				ARG	GLY	GLY	LEU	GLY	GLY	GLY	LEU
				ARG	GLY	GLY	LEU	GLY	GLY	GLY	LEU
				ALA	ASN	LYS	LYS	PRO	ASN	GLN	MET
				ALA	PRO	GLY	HIS	THR	GLY	VAL	GLY
				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				LEU	GLY	ASP	PHE	ILE	GLY	GLY	GLY
				ARG	GLY	PRO	LEU	VAL	GLY	GLY	GLY
				ARG	GLY	GLY	LEU	GLY	GLY	GLY	GLY
				ARG	GLY	GLY	LEU	GLY	GLY	GLY	GLY
				ALA	ASN	LYS	LYS	PRO	ASN	GLN	MET
				ALA	PRO	GLY	HIS	THR	GLY	VAL	GLY
				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				LEU	GLY	ASP	PHE	ILE	GLY	GLY	GLY
				ARG	GLY	PRO	LEU	VAL	GLY	GLY	GLY
				ARG	GLY	GLY	LEU	GLY	GLY	GLY	GLY
				ALA	ASN	LYS	LYS	PRO	ASN	GLN	MET
				ALA	PRO	GLY	HIS	THR	GLY	VAL	GLY
				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				LEU	GLY	ASP	PHE	ILE	GLY	GLY	GLY
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				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
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				ALA	ASN	LYS	LYS	PRO	ASN	GLN	MET
				ALA	PRO	GLY	HIS	THR	GLY	VAL	GLY
				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				LEU	GLY	ASP	PHE	ILE	GLY	GLY	GLY
				ARG	GLY	PRO	LEU	VAL	GLY	GLY	GLY
				ARG	GLY	GLY	LEU	GLY	GLY	GLY	GLY
				ALA	ASN	LYS	LYS	PRO	ASN	GLN	MET
				ALA	PRO	GLY	HIS	THR	GLY	VAL	GLY
				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
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				ALA	ASN	LYS	LYS	PRO	ASN	GLN	MET
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				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
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				ALA	ASN	LYS	LYS	PRO	ASN	GLN	MET
				ALA	PRO	GLY	HIS	THR	GLY	VAL	GLY
				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				LEU	GLY	ASP	PHE	ILE	GLY	GLY	GLY
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				ALA	PRO	GLY	HIS	THR	GLY	VAL	GLY
				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				LEU	GLY	ASP	PHE	ILE	GLY	GLY	GLY
				ARG	GLY	PRO	LEU	VAL	GLY	GLY	GLY
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				ARG	GLY	GLY	LEU	GLY	GLY	GLY	GLY
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				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
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				LEU	GLY	ASP	PHE	ILE	GLY	GLY	GLY
				ARG	GLY	PRO	LEU	VAL	GLY	GLY	GLY
				ARG	GLY	GLY	LEU	GLY	GLY	GLY	GLY
				ALA	ASN	LYS	LYS	PRO	ASN	GLN	MET
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				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				LEU	GLY	ASP	PHE	ILE	GLY	GLY	GLY
				ARG	GLY	PRO	LEU	VAL	GLY	GLY	GLY
				ARG	GLY	GLY	LEU	GLY	GLY	GLY	GLY
				ALA	ASN	LYS	LYS	PRO	ASN	GLN	MET
				ALA	PRO	GLY	HIS	THR	GLY	VAL	GLY
				ALA	LEU	GLY	ASN	GLY	VAL	THR	THR
				GLY	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				PRO	LEU	GLY	ASN	GLY	GLY	GLY	GLY
				LEU	GLY	ASP	PHE	ILE	GLY	GLY	GLY
				ARG	GLY	PRO	LEU	VAL	GLY	GLY	GLY
				ARG	GLY						



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	129384	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.196	Depositor
Minimum map value	-0.119	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	259.2, 259.2, 259.2	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	0.17	0/3512	0.36	0/4764
1	B	0.16	0/2975	0.31	0/4053
All	All	0.16	0/6487	0.34	0/8817

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	3437	0	3369	67	0
1	B	2901	0	2853	48	0
All	All	6338	0	6222	114	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 9.

The worst 5 of 114 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:759:ILE:O	1:B:778:PHE:HA	1.73	0.88
1:B:475:LEU:O	1:B:533:GLY:HA2	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:456:CYS:HB2	1:B:562:HIS:HB2	1.77	0.66
1:A:424:LEU:HD11	1:A:447:PRO:HG3	1.78	0.66
1:A:196:CYS:HA	1:A:202:CYS:HA	1.79	0.64

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	443/1297 (34%)	395 (89%)	47 (11%)	1 (0%)	43	71
1	B	353/1297 (27%)	318 (90%)	35 (10%)	0	100	100
All	All	796/2594 (31%)	713 (90%)	82 (10%)	1 (0%)	49	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	157	VAL

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	375/1097 (34%)	373 (100%)	2 (0%)	81	83
1	B	313/1097 (28%)	312 (100%)	1 (0%)	86	86

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Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	688/2194 (31%)	685 (100%)	3 (0%)	81	84

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	270	HIS
1	A	391	LEU
1	B	488	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	515	GLN
1	B	689	ASN
1	A	133	GLN
1	A	192	HIS
1	A	334	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

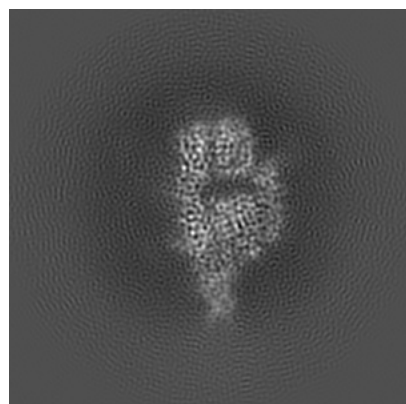
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26181. These allow visual inspection of the internal detail of the map and identification of artifacts.

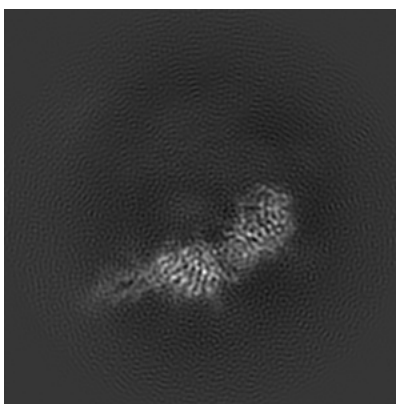
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

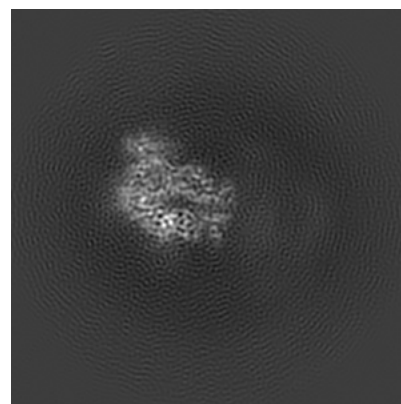
6.1.1 Primary map



X

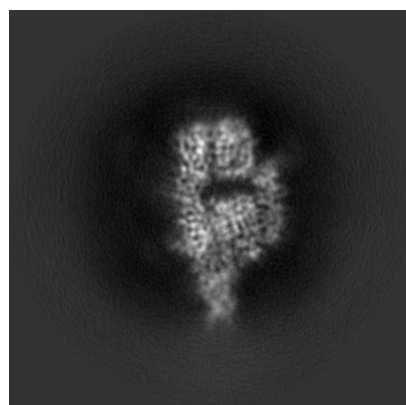


Y

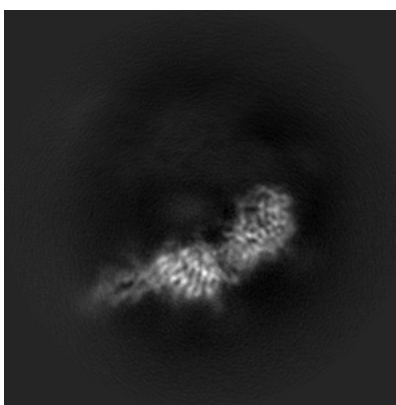


Z

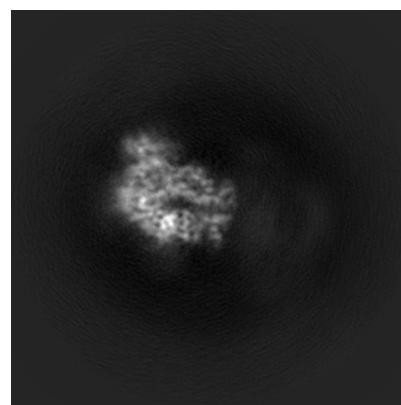
6.1.2 Raw map



X



Y

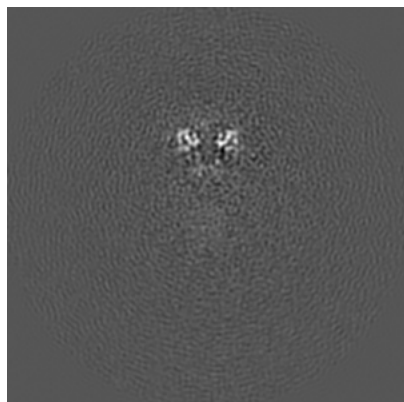


Z

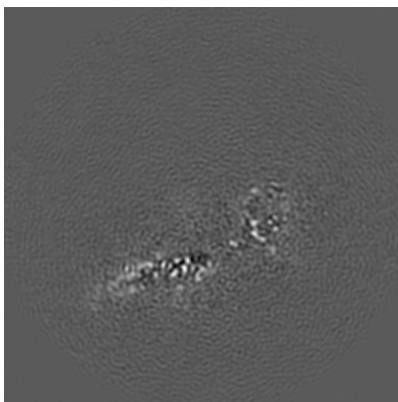
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

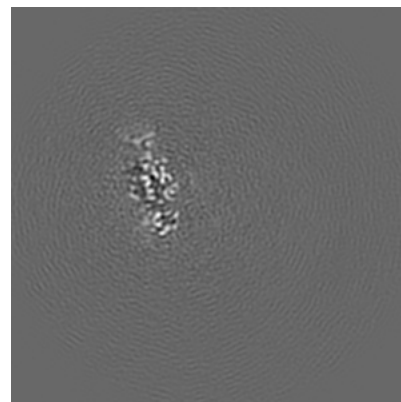
6.2.1 Primary map



X Index: 120

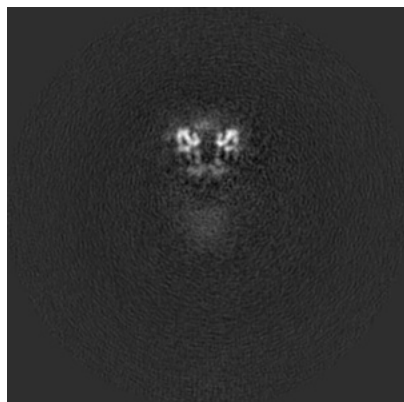


Y Index: 120

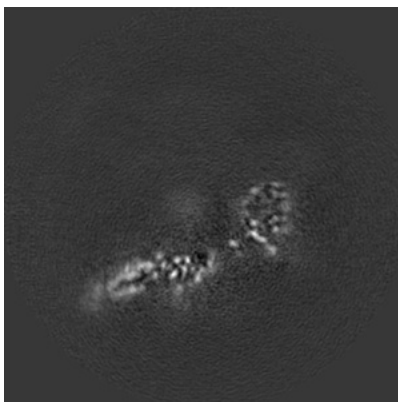


Z Index: 120

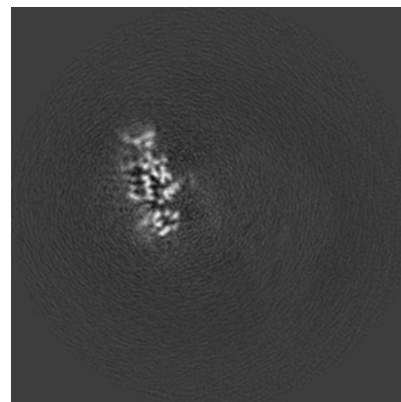
6.2.2 Raw map



X Index: 120



Y Index: 120

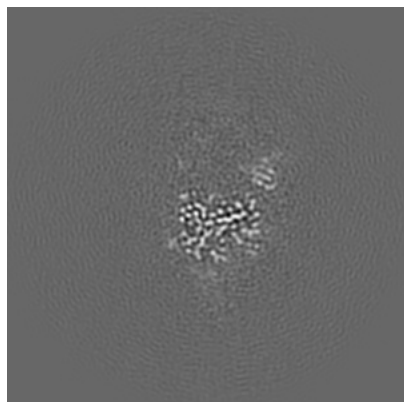


Z Index: 120

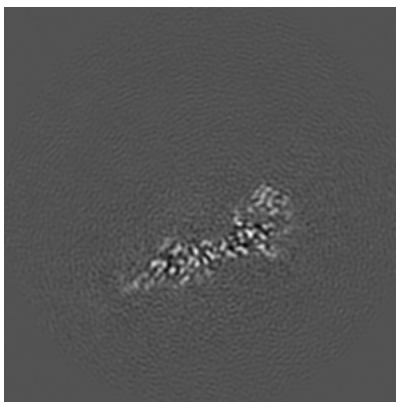
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

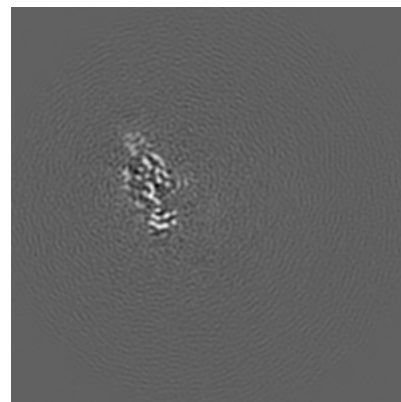
6.3.1 Primary map



X Index: 87

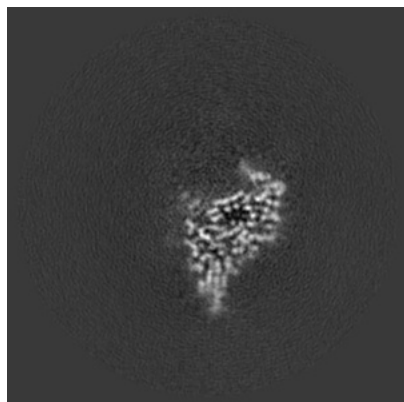


Y Index: 114

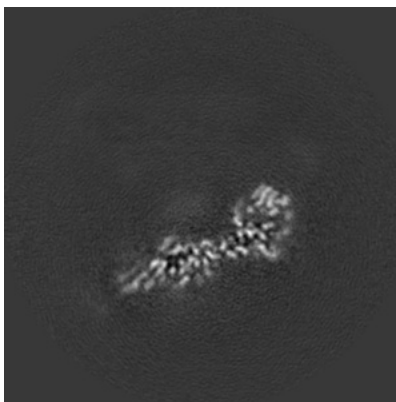


Z Index: 115

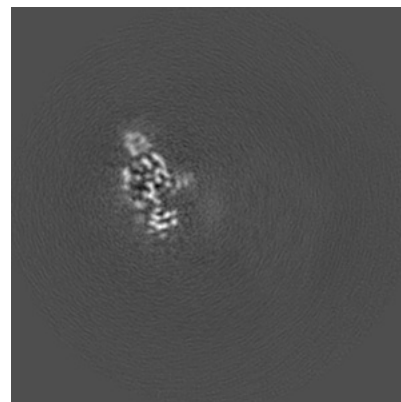
6.3.2 Raw map



X Index: 79



Y Index: 114

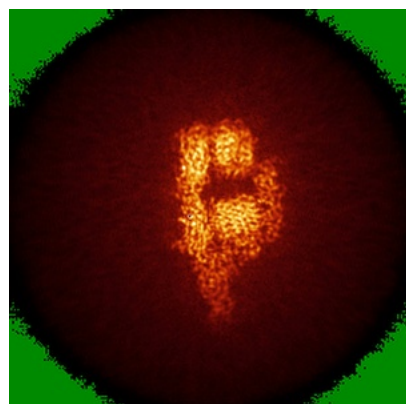


Z Index: 115

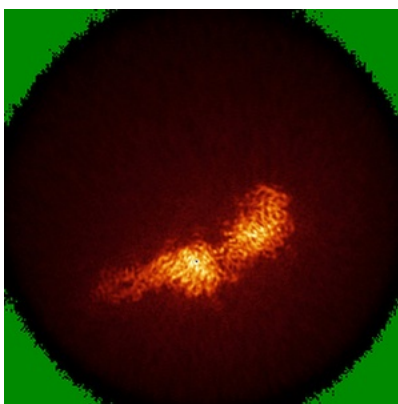
The images above show the largest variance slices of the map in three orthogonal directions.

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

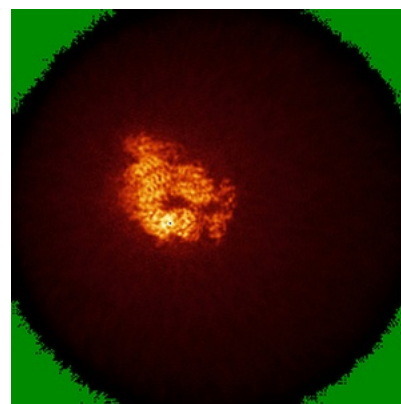
6.4.1 Primary map



X

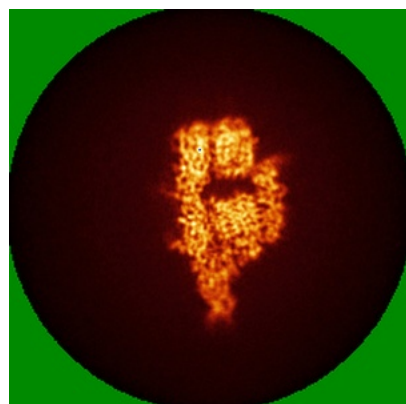


Y



Z

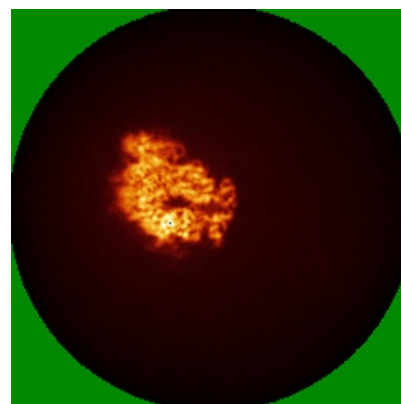
6.4.2 Raw map



X



Y

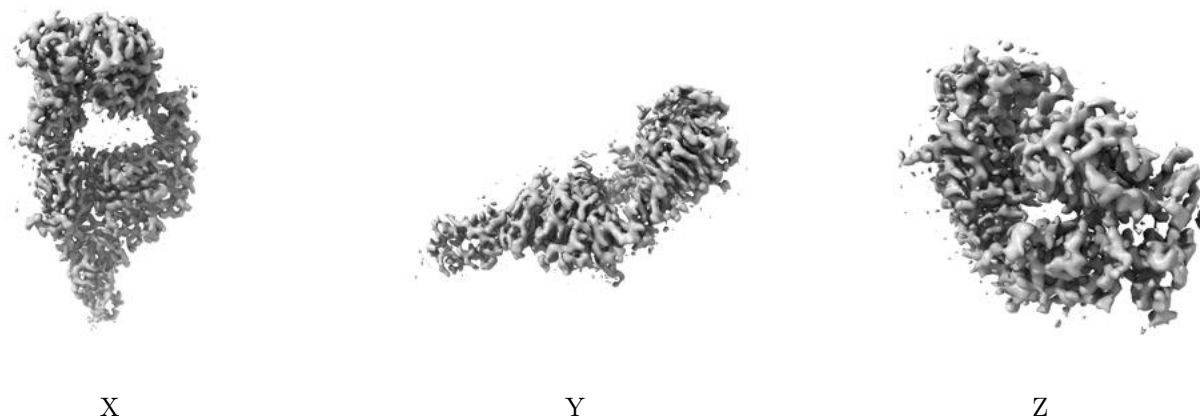


Z

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.

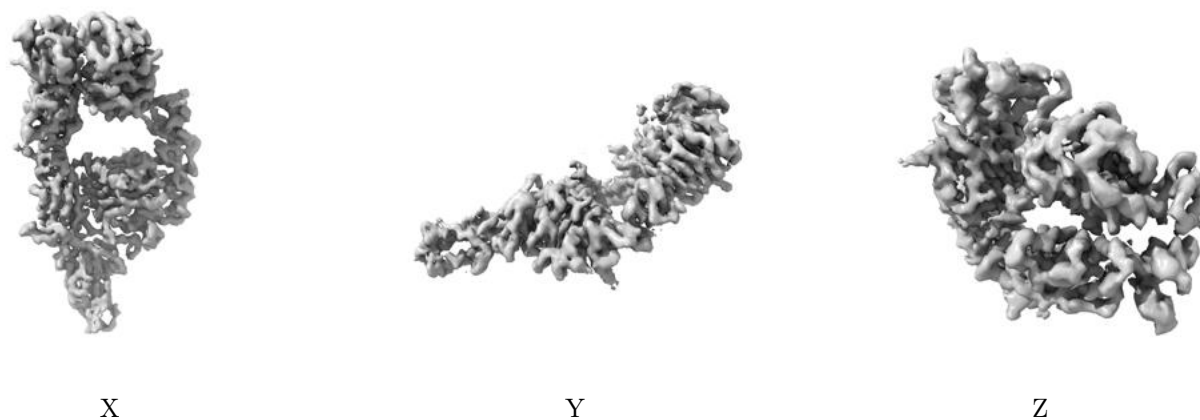
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

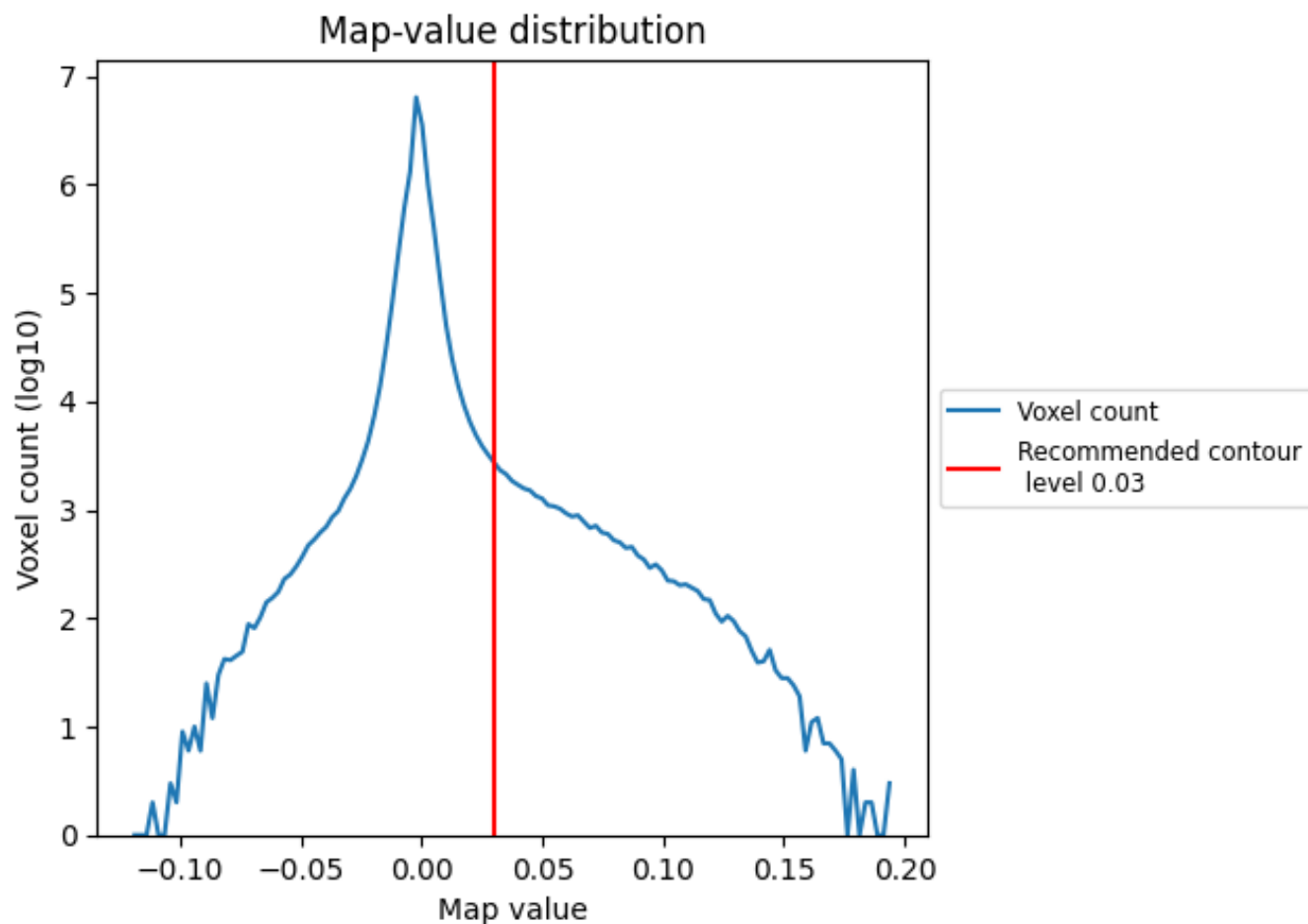
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

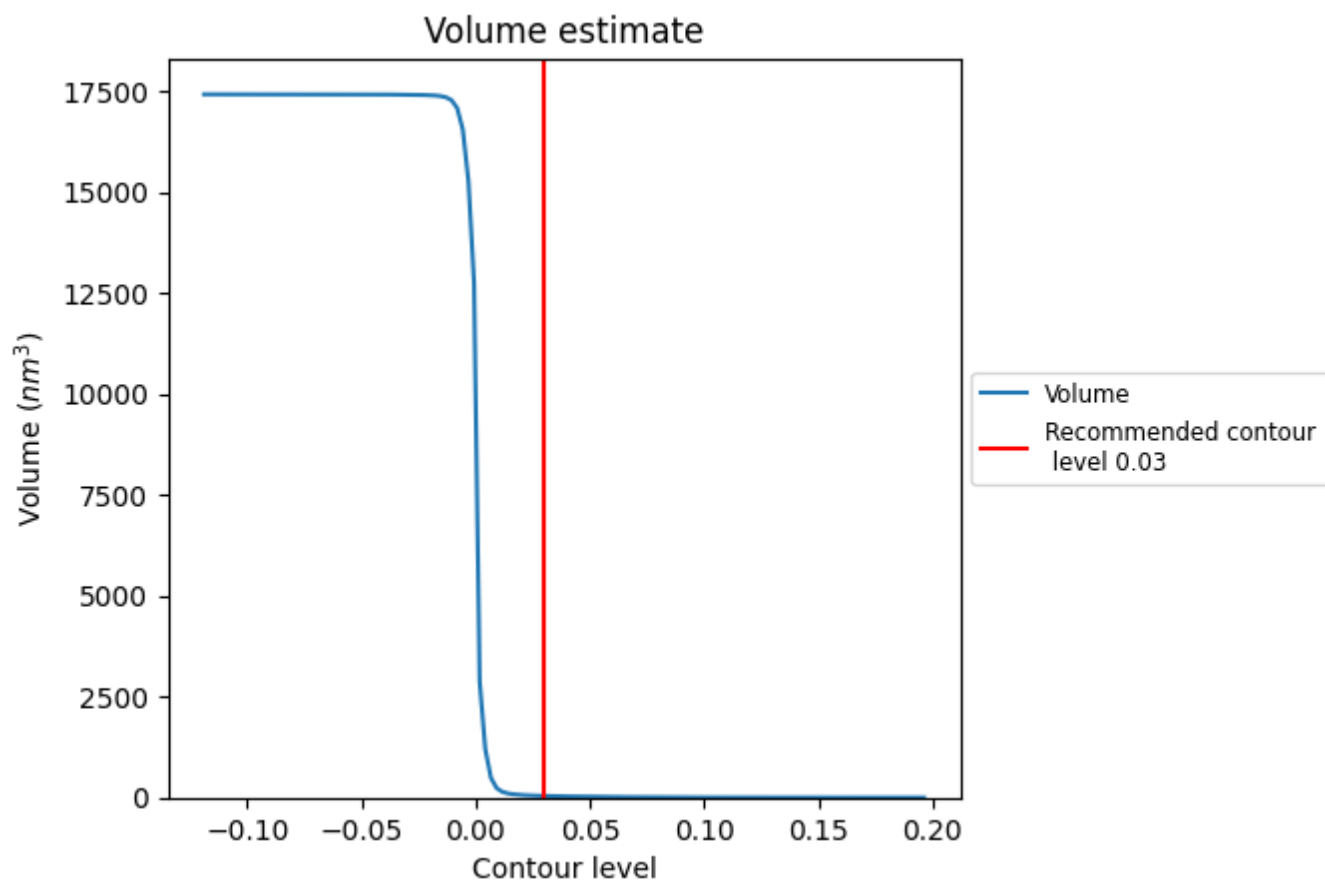
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

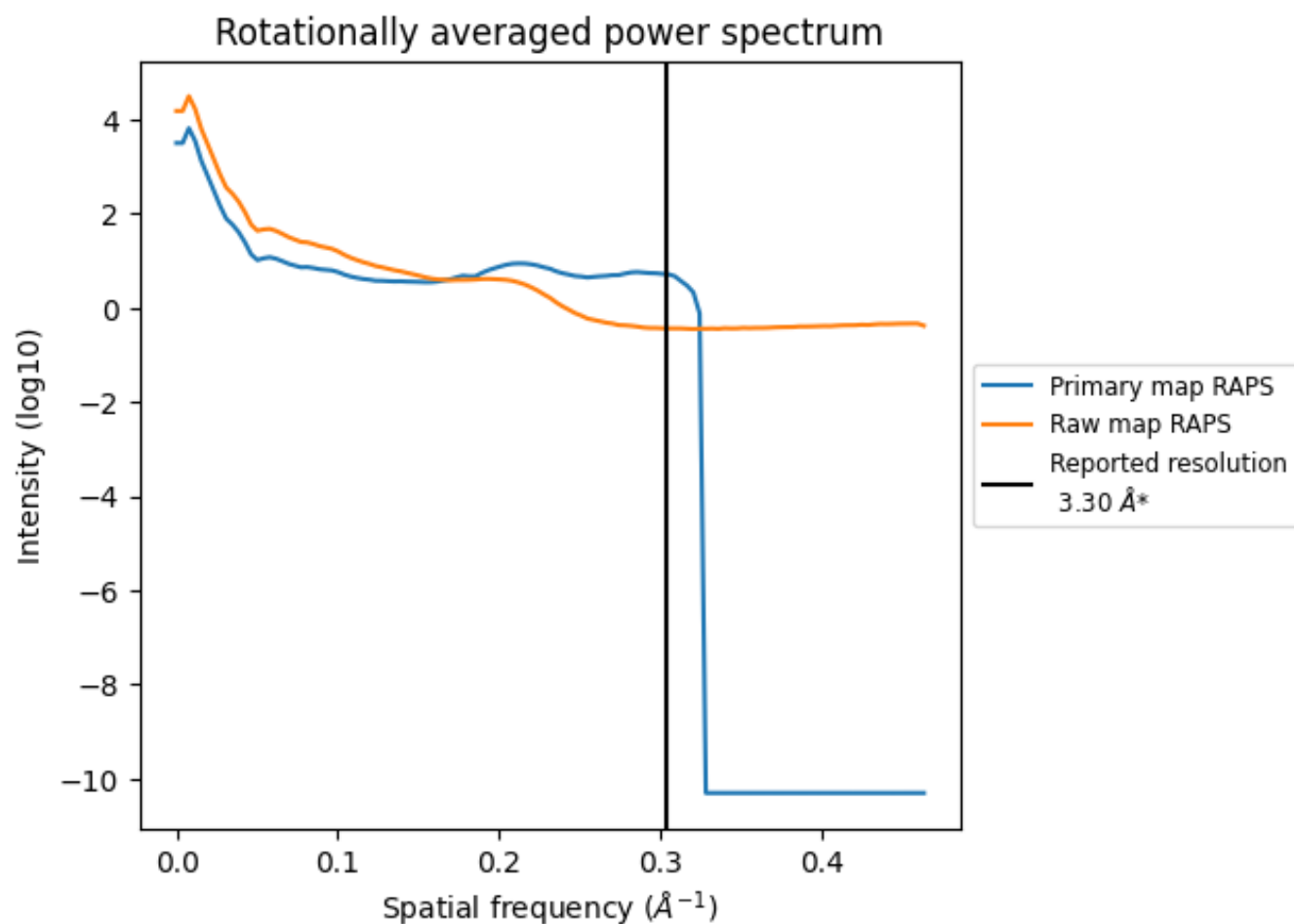
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 40 nm³; this corresponds to an approximate mass of 36 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 ⓘ

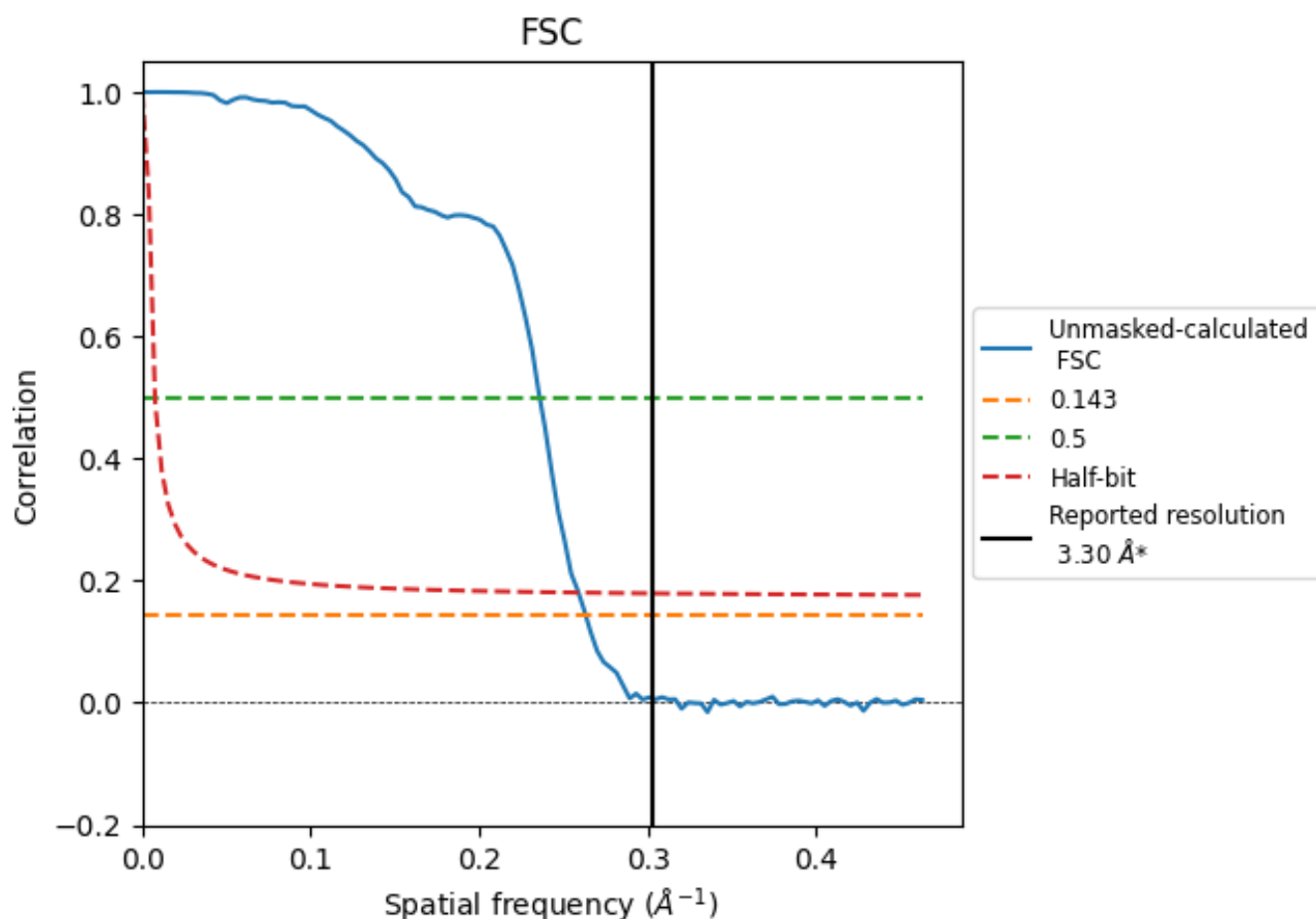


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

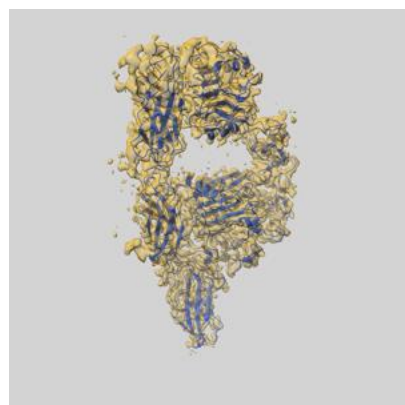
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.80	4.24	3.86

*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 3.80 differs from the reported value 3.3 by more than 10 %

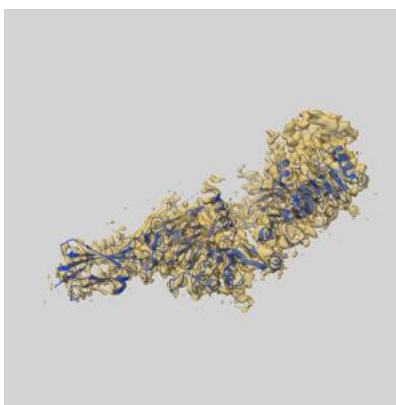
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26181 and PDB model 7TYJ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

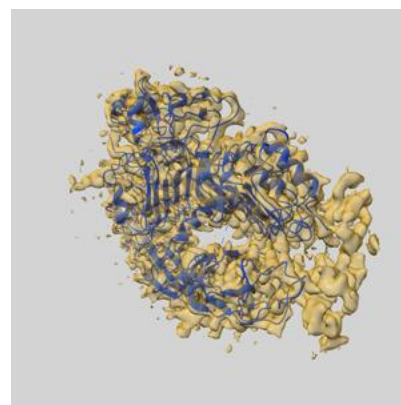
9.1 Map-model overlay [i](#)



X



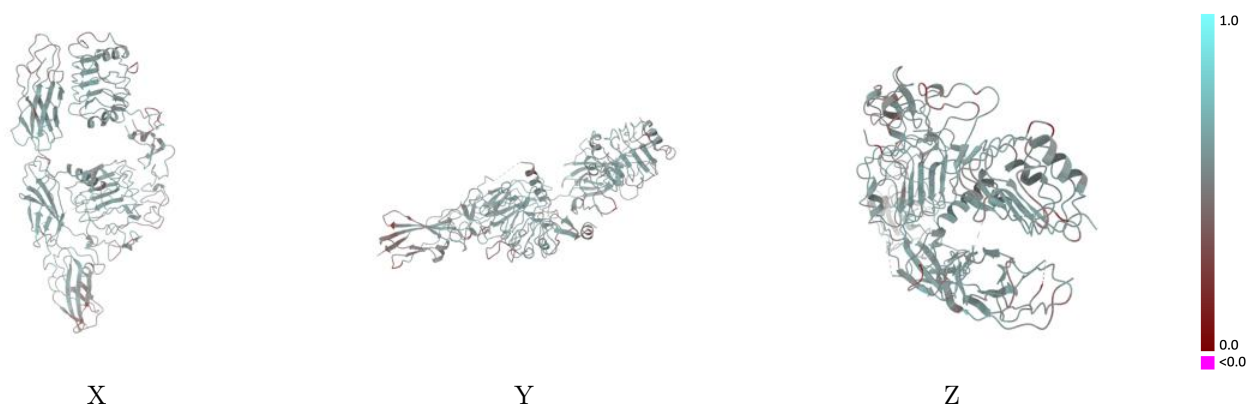
Y



Z

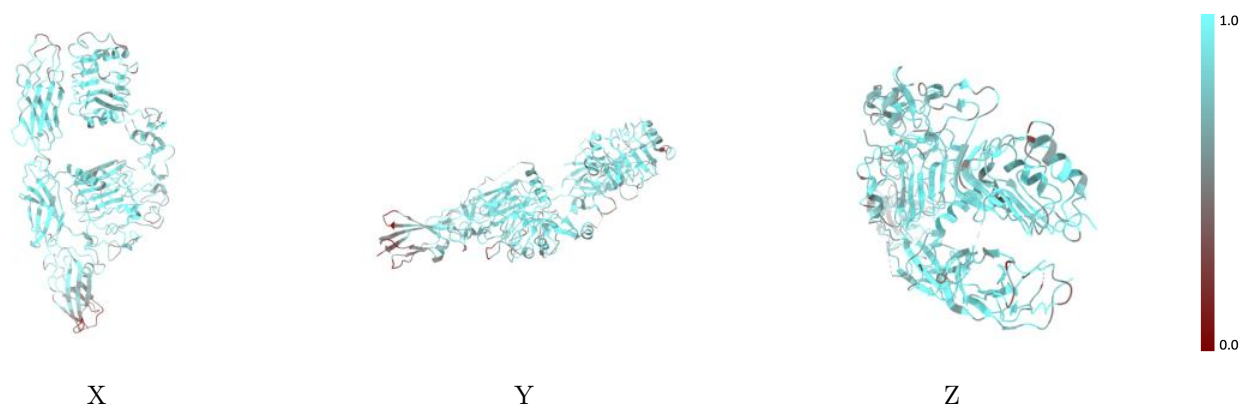
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



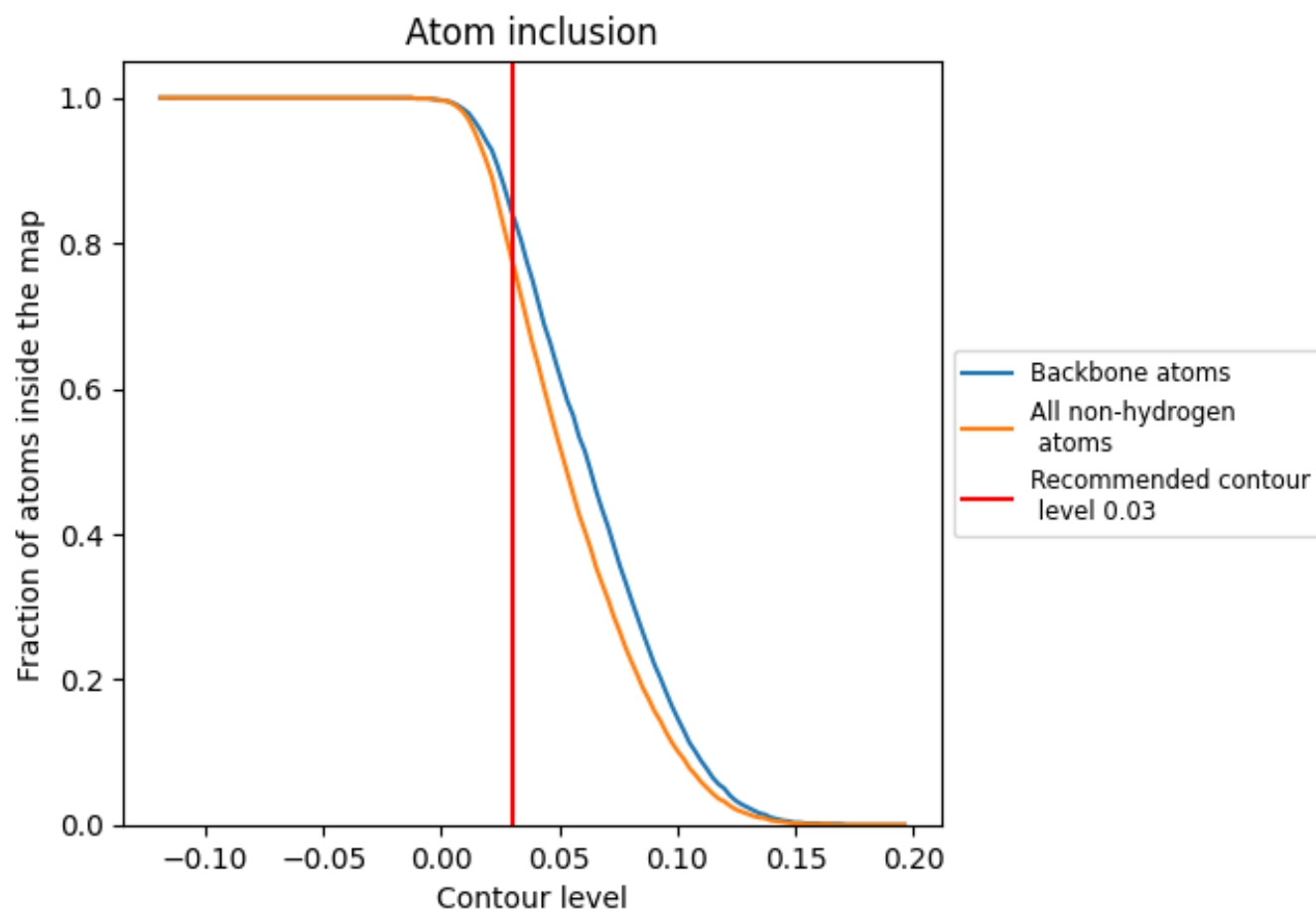
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 78% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7760	0.5280
A	0.7940	0.5330
B	0.7540	0.5220

