



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 05:29 AM UTC

PDB ID : 8VJB / pdb_00008vjb
EMDB ID : EMD-43279
Title : Cryo-EM structure of short form insulin receptor (IR-A) with four IGF2 bound, symmetric conformation.
Authors : An, W.; Hall, C.; Li, J.; Huang, A.; Wu, J.; Park, J.; Bai, X.C.; Choi, E.
Deposited on : 2024-01-06
Resolution : 3.60 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

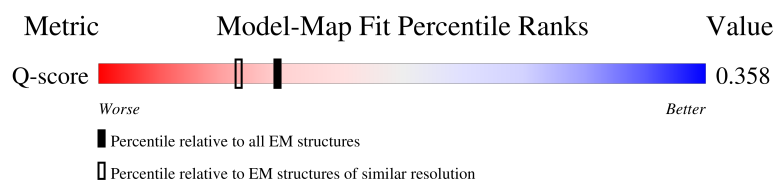
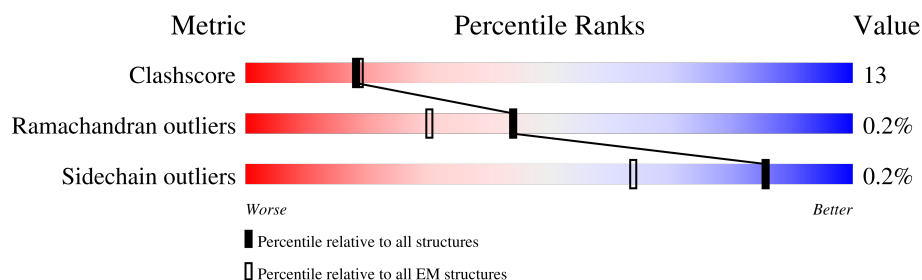
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	12797 (3.10 - 4.10)

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	1370	
1	B	1370	
2	C	180	
2	D	180	

Continued on next page...

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Mol	Chain	Length	Quality of chain
2	E	180	16%8%77%
2	F	180	16%13%70%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14688 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Isoform Short of Insulin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	816	Total	C	N	O	S	0	0
			6601	4191	1142	1220	48		
1	B	816	Total	C	N	O	S	0	0
			6601	4191	1142	1220	48		

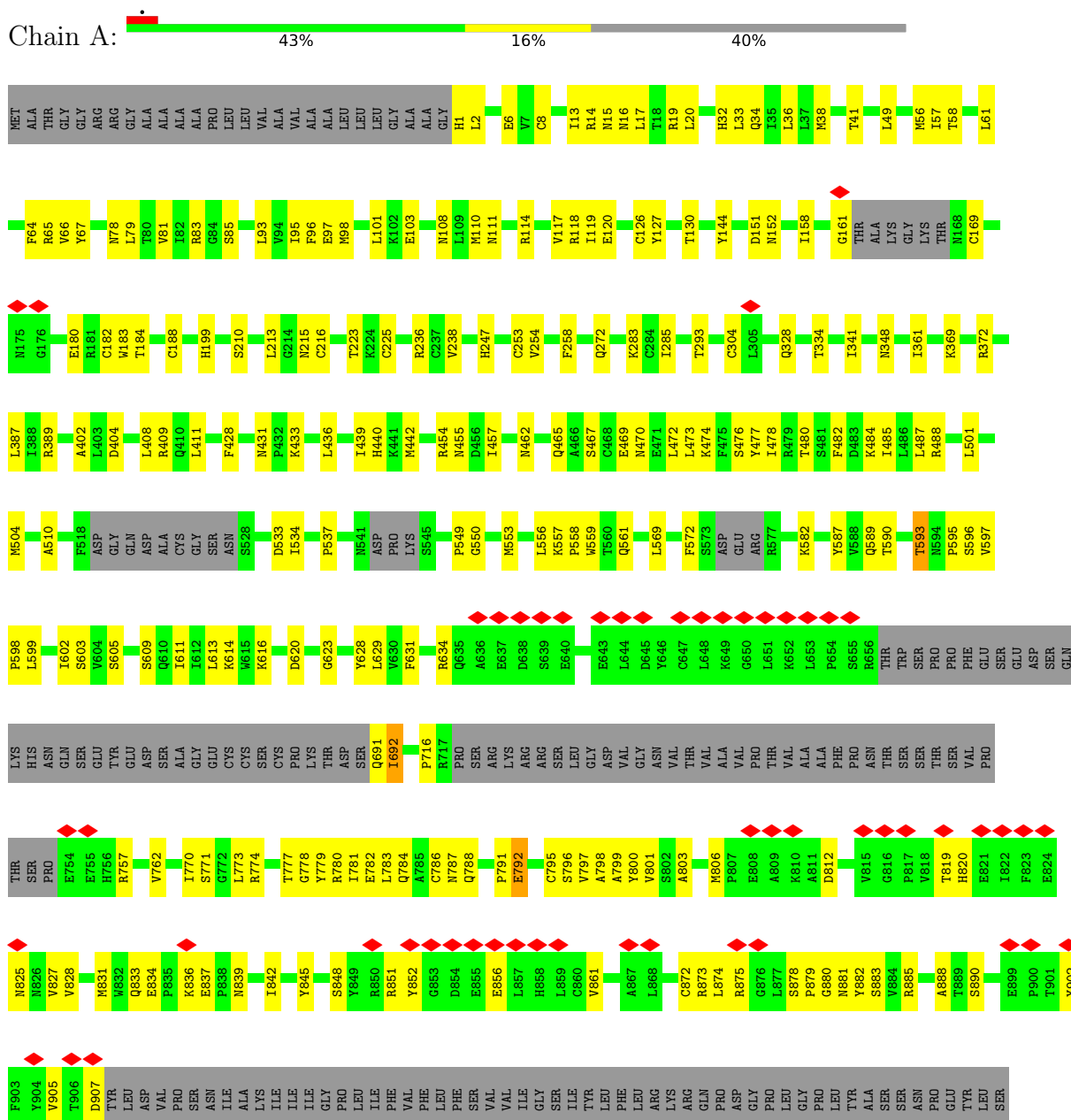
- Molecule 2 is a protein called Insulin-like growth factor II.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	42	Total	C	N	O	S	0	0
			323	204	49	64	6		
2	D	54	Total	C	N	O	S	0	0
			420	261	73	80	6		
2	E	42	Total	C	N	O	S	0	0
			323	204	49	64	6		
2	F	54	Total	C	N	O	S	0	0
			420	261	73	80	6		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

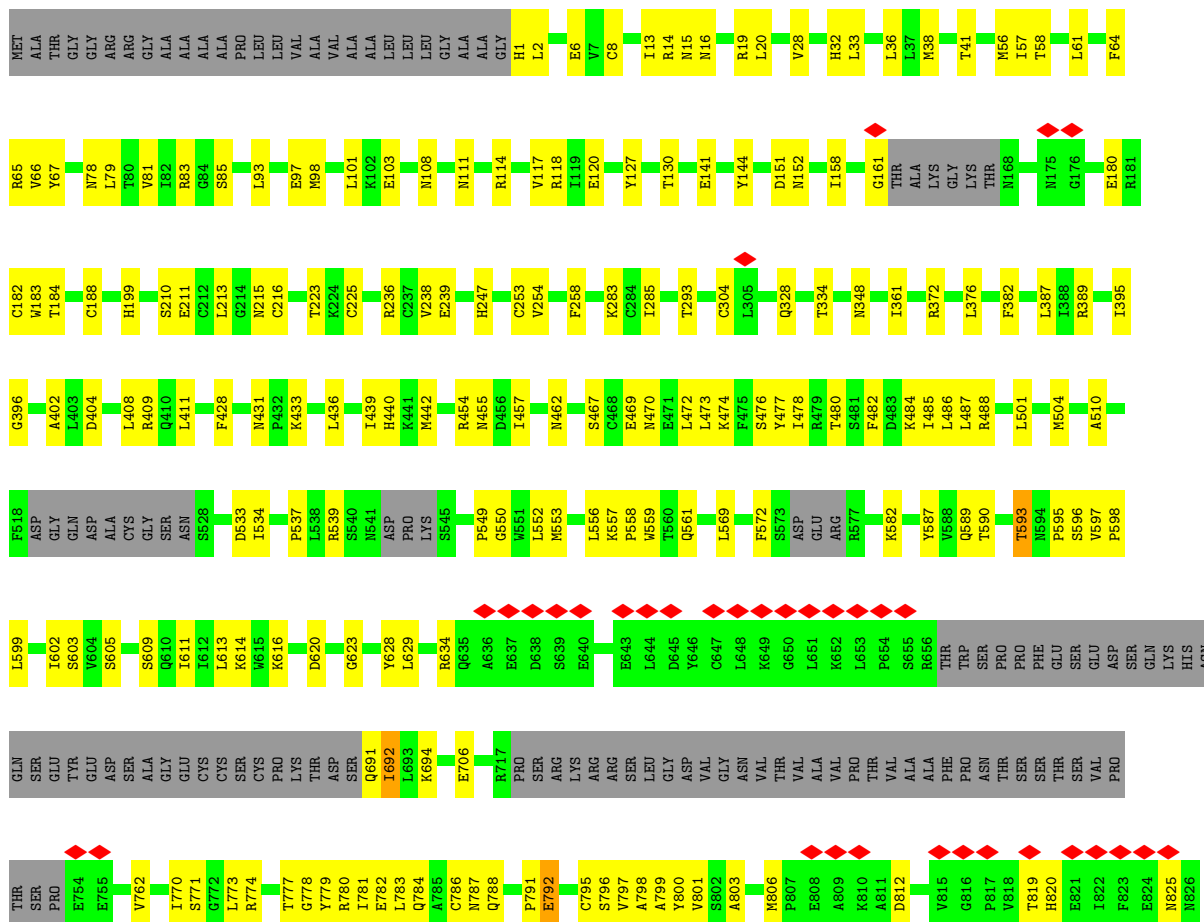
• Molecule 1: Isoform Short of Insulin receptor



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

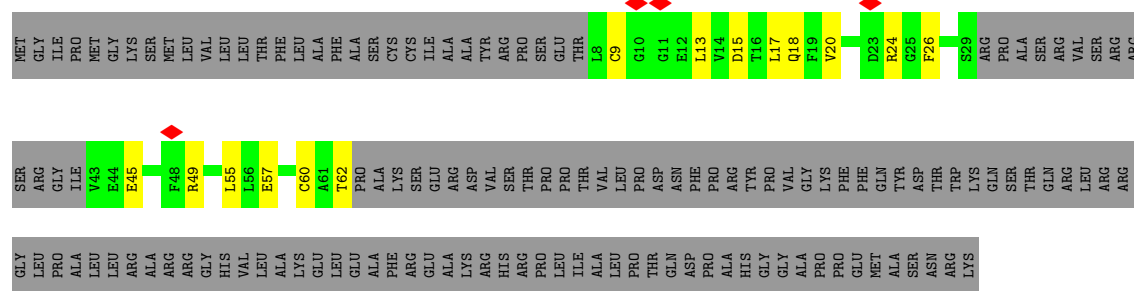
- Molecule 1: Isoform Short of Insulin receptor

Chain B:

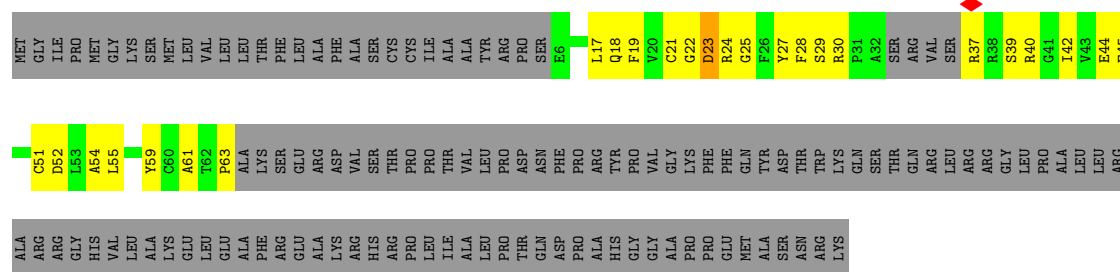




Chain E: 16% 8% 77%



Chain F: 16% 13% 70%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	66937	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	0.039	Depositor
Minimum map value	-0.022	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	291.6, 291.6, 291.6	wwPDB
Map dimensions	270, 270, 270	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	0.12	0/6762	0.32	1/9165 (0.0%)
1	B	0.12	0/6762	0.31	1/9165 (0.0%)
2	C	0.15	0/327	0.49	0/439
2	D	0.14	0/426	0.41	0/572
2	E	0.13	0/327	0.46	0/439
2	F	0.15	0/426	0.43	0/572
All	All	0.13	0/15030	0.33	2/20352 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	692	ILE	N-CA-C	-5.38	108.26	113.53
1	B	692	ILE	N-CA-C	-5.37	108.27	113.53

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	6601	0	6421	164	0
1	B	6601	0	6421	159	0
2	C	323	0	292	13	0
2	D	420	0	395	19	0
2	E	323	0	292	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	420	0	395	19	0
All	All	14688	0	14216	381	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 381 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:28:VAL:HG23	1:B:56:MET:HB3	1.64	0.77
1:B:784:GLN:NE2	1:B:786:CYS:SG	2.63	0.71
1:A:784:GLN:NE2	1:A:786:CYS:SG	2.63	0.70
1:A:57:ILE:HG12	1:A:79:LEU:HD11	1.72	0.70
1:B:780:ARG:HH22	1:B:800:TYR:HB3	1.57	0.70

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	802/1370 (58%)	750 (94%)	51 (6%)	1 (0%)	48	79
1	B	802/1370 (58%)	749 (93%)	52 (6%)	1 (0%)	48	79
2	C	38/180 (21%)	35 (92%)	3 (8%)	0	100	100
2	D	50/180 (28%)	40 (80%)	9 (18%)	1 (2%)	6	32
2	E	38/180 (21%)	35 (92%)	3 (8%)	0	100	100
2	F	50/180 (28%)	40 (80%)	9 (18%)	1 (2%)	6	32
All	All	1780/3460 (51%)	1649 (93%)	127 (7%)	4 (0%)	44	72

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	23	ASP
2	F	23	ASP
1	A	792	GLU
1	B	792	GLU

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	743/1215 (61%)	742 (100%)	1 (0%)	88	87
1	B	743/1215 (61%)	741 (100%)	2 (0%)	86	83
2	C	36/151 (24%)	35 (97%)	1 (3%)	38	60
2	D	46/151 (30%)	46 (100%)	0	100	100
2	E	36/151 (24%)	36 (100%)	0	100	100
2	F	46/151 (30%)	46 (100%)	0	100	100
All	All	1650/3034 (54%)	1646 (100%)	4 (0%)	85	85

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	593	THR
1	B	593	THR
1	B	841	LEU
2	C	51	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	111	ASN
1	B	282	ASN
2	D	18	GLN
1	B	276	GLN
1	B	431	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

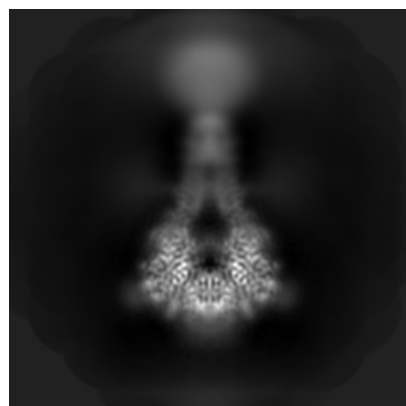
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43279. These allow visual inspection of the internal detail of the map and identification of artifacts.

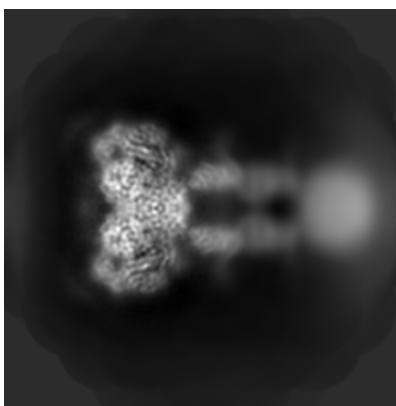
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

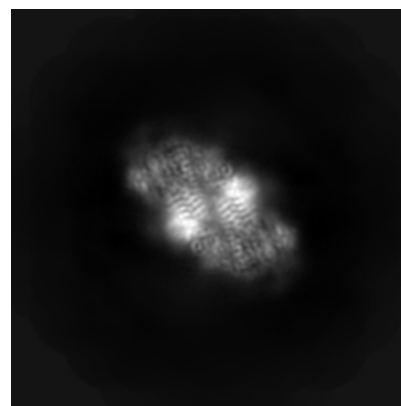
6.1.1 Primary map



X

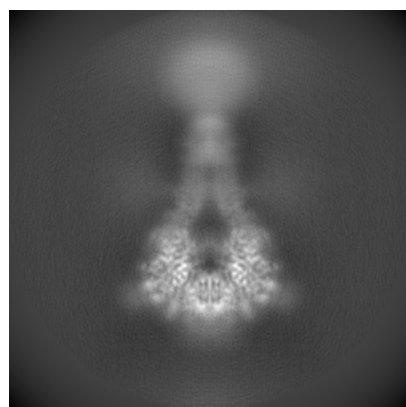


Y

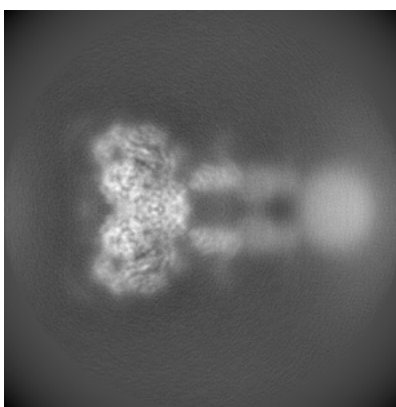


Z

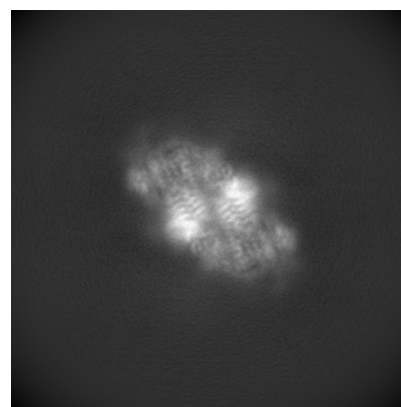
6.1.2 Raw map



X



Y

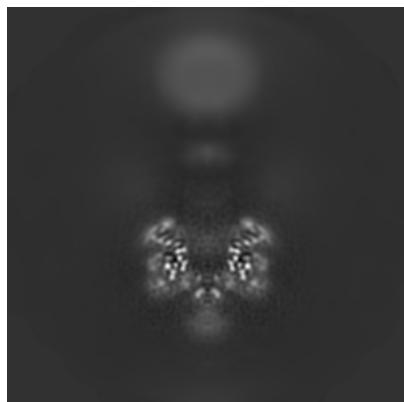


Z

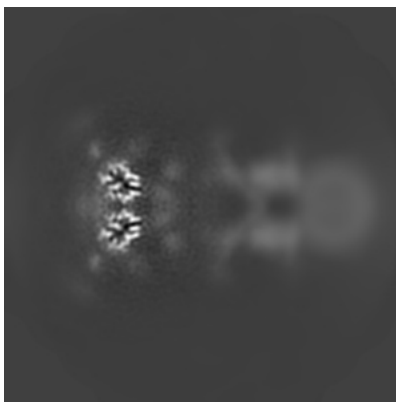
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

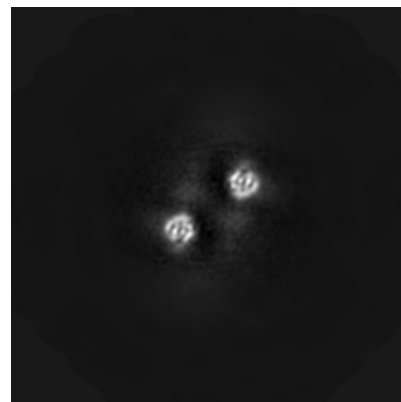
6.2.1 Primary map



X Index: 135

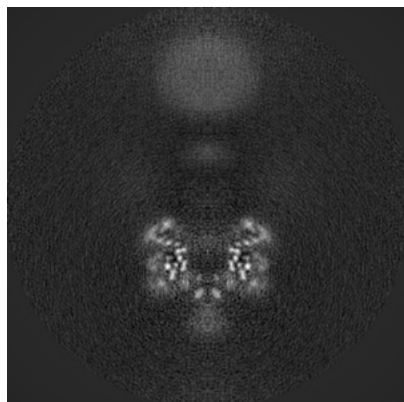


Y Index: 135

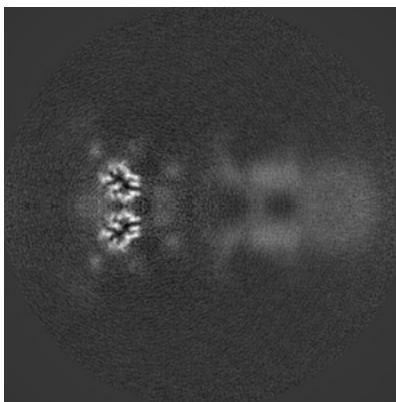


Z Index: 135

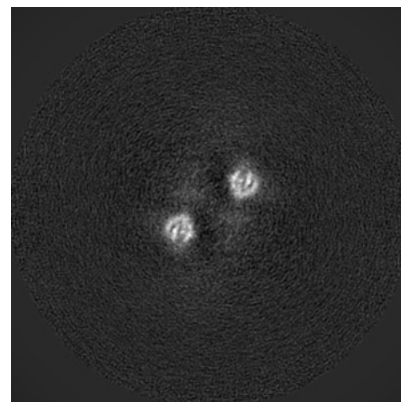
6.2.2 Raw map



X Index: 135



Y Index: 135

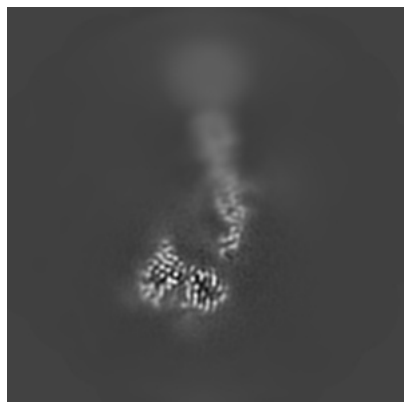


Z Index: 135

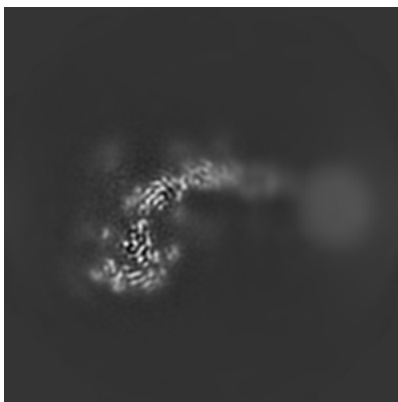
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

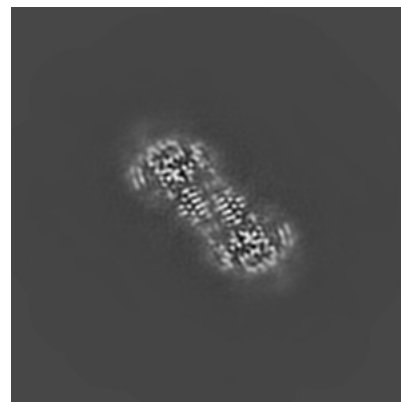
6.3.1 Primary map



X Index: 153

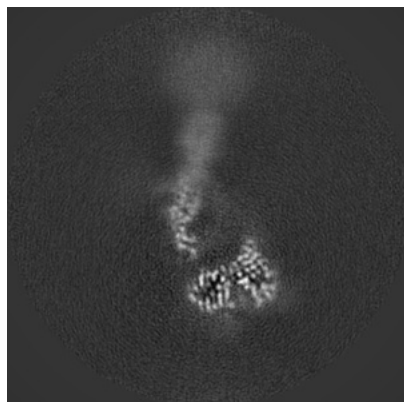


Y Index: 152

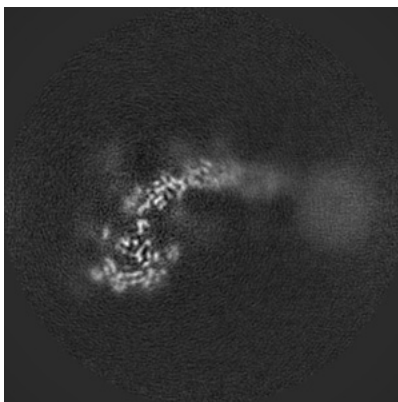


Z Index: 86

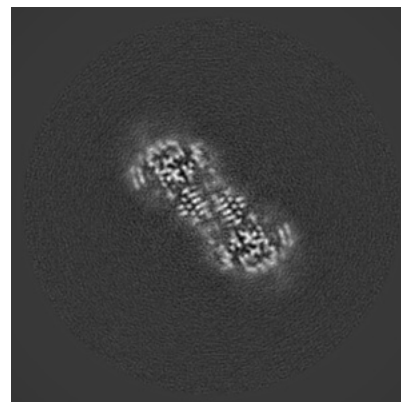
6.3.2 Raw map



X Index: 117



Y Index: 151

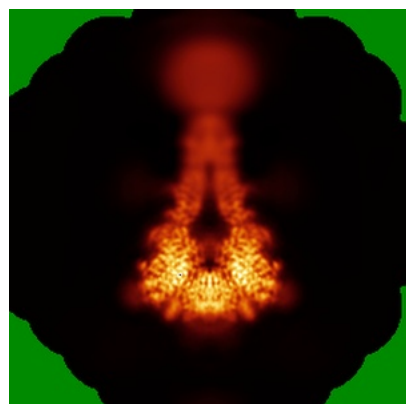


Z Index: 86

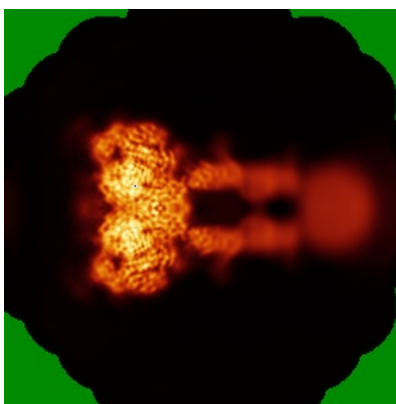
The images above show the largest variance slices of the map in three orthogonal directions.

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

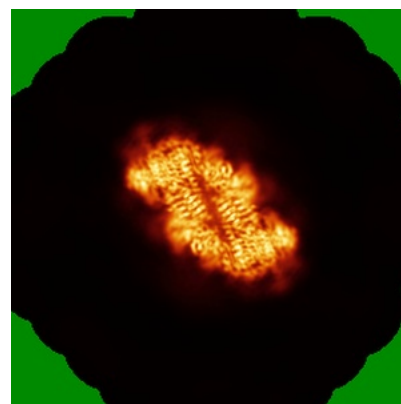
6.4.1 Primary map



X

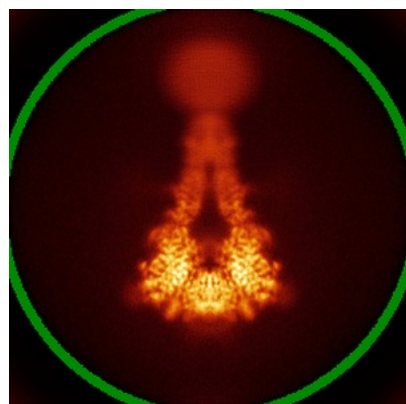


Y

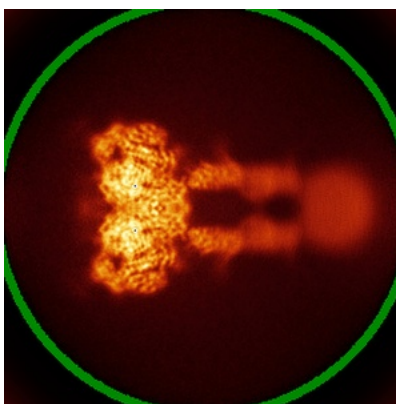


Z

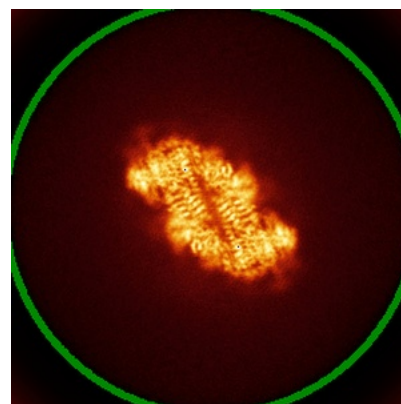
6.4.2 Raw map



X



Y

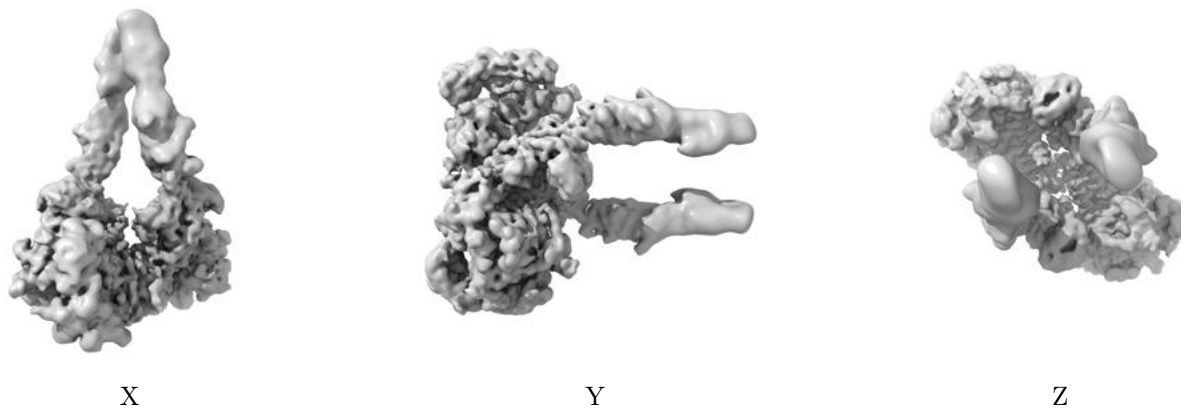


Z

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.

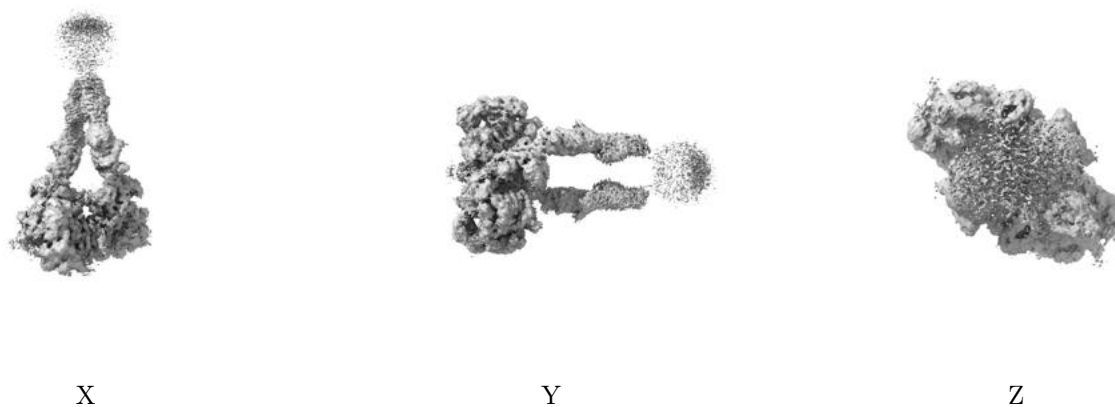
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. 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.

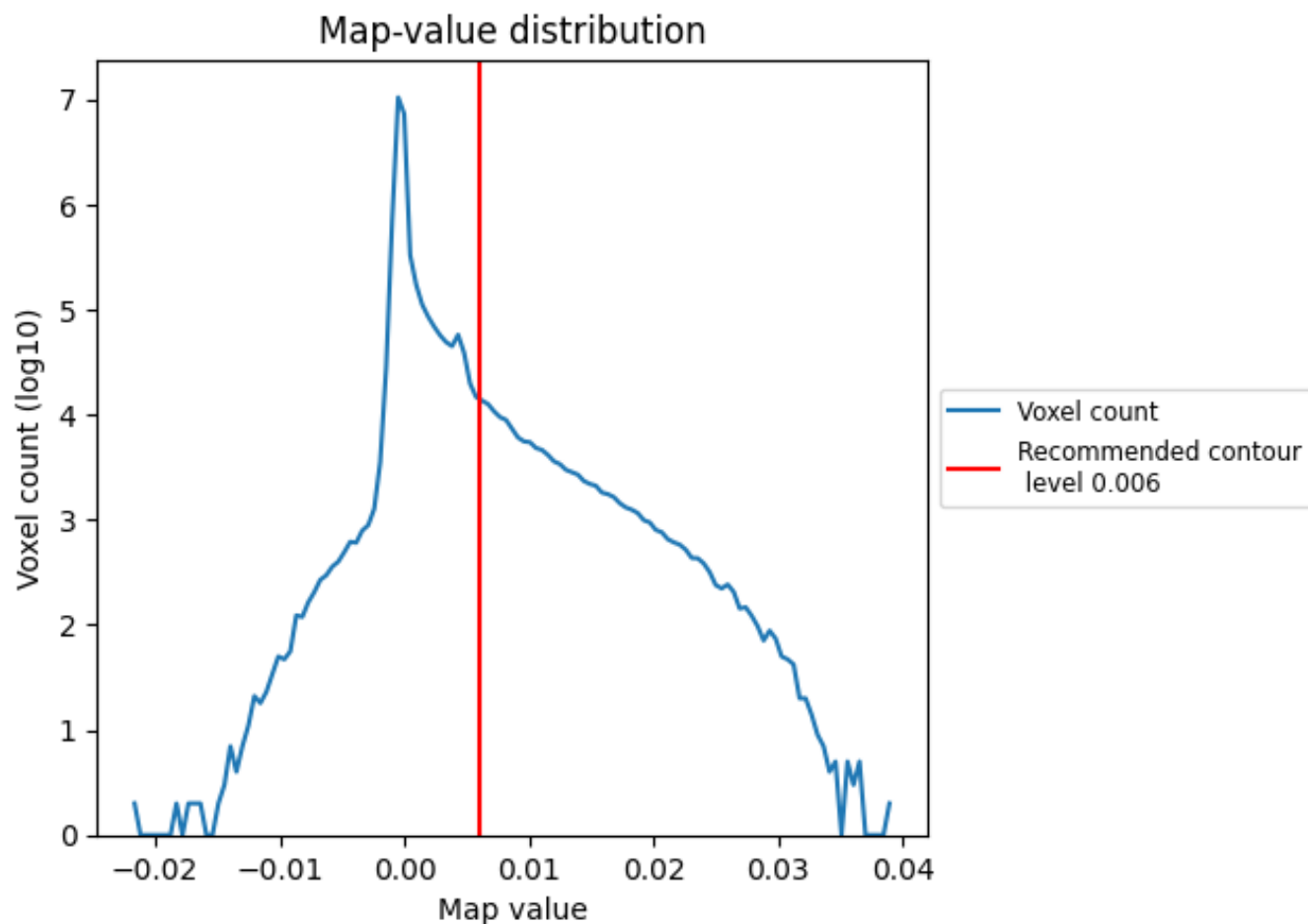
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

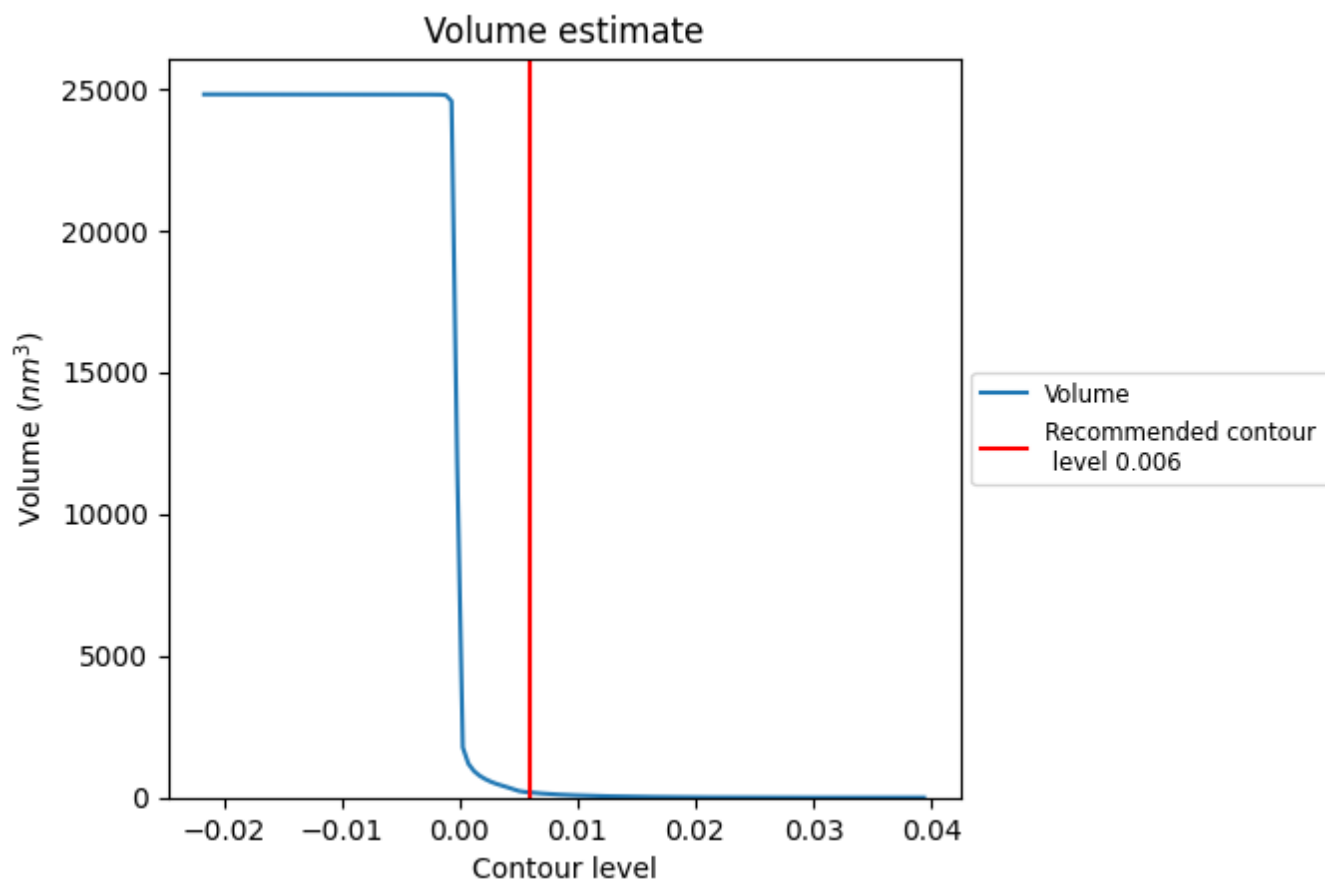
This section contains the results of statistical analysis of the map.

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.

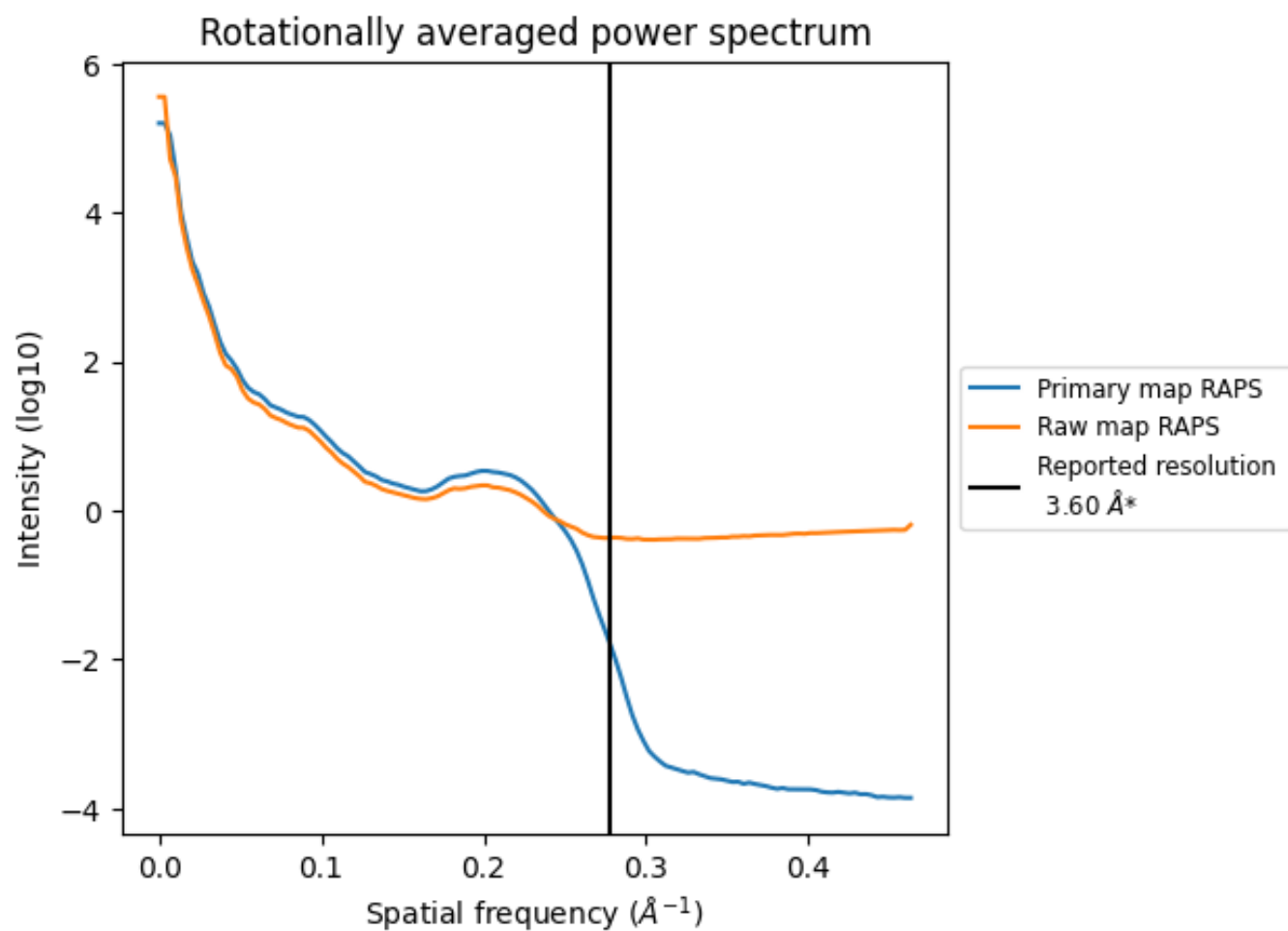
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 178 nm³; this corresponds to an approximate mass of 161 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 ⓘ

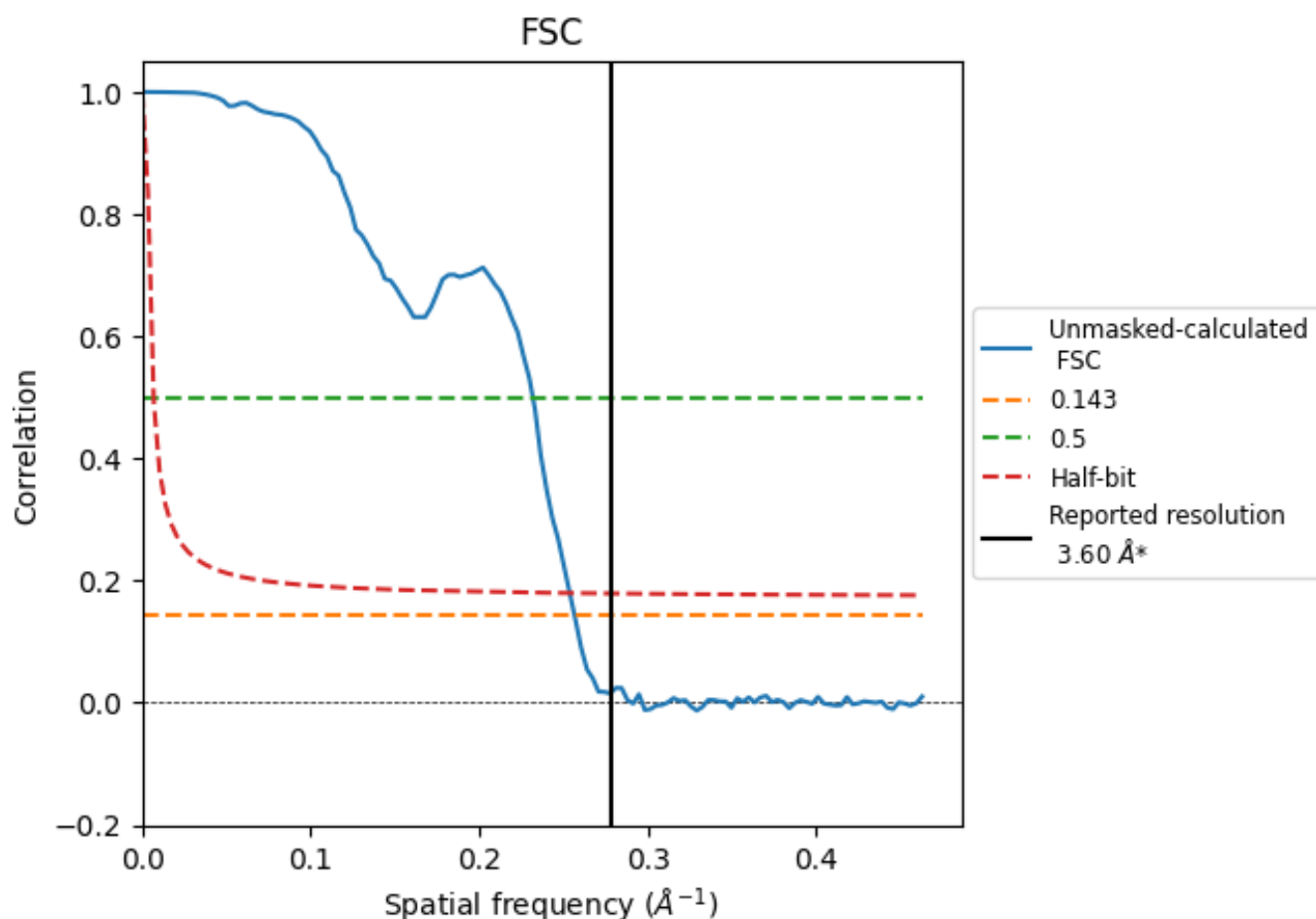


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

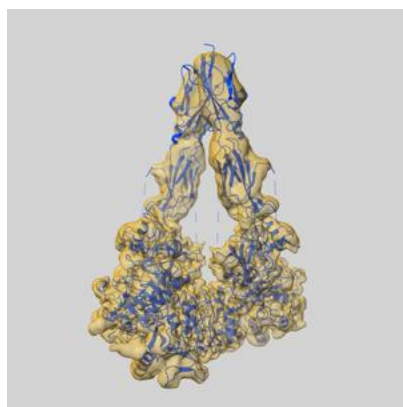
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.90	4.31	3.94

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

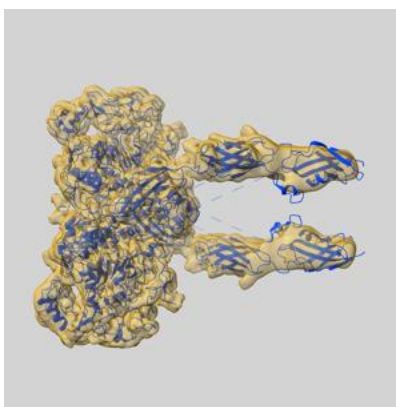
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43279 and PDB model 8VJB. Per-residue inclusion information can be found in section [3](#) on page [5](#).

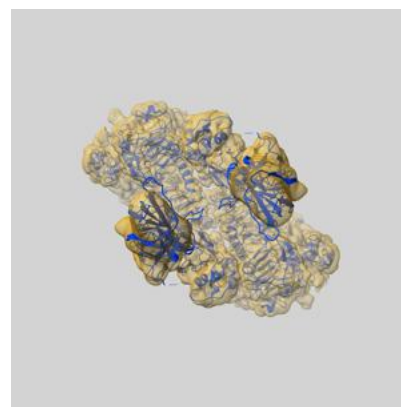
9.1 Map-model overlay [i](#)



X



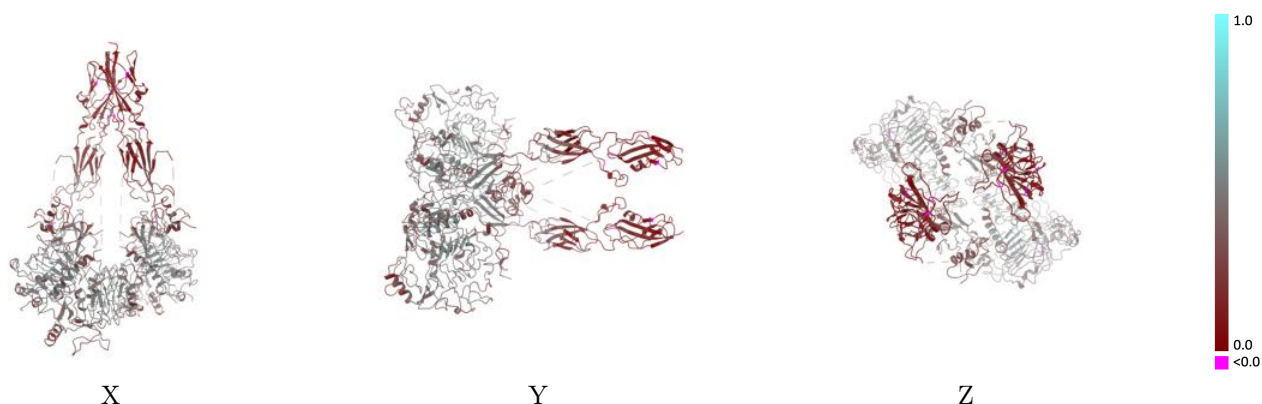
Y



Z

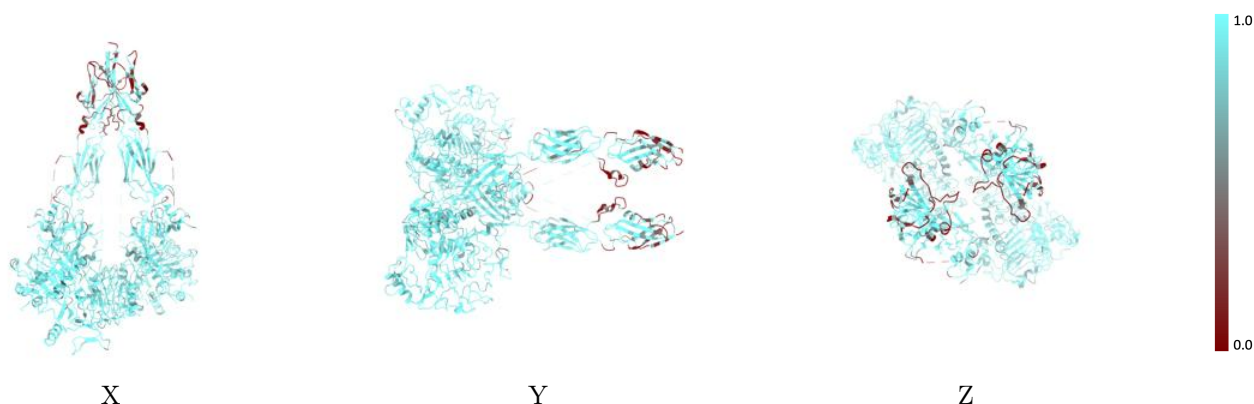
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



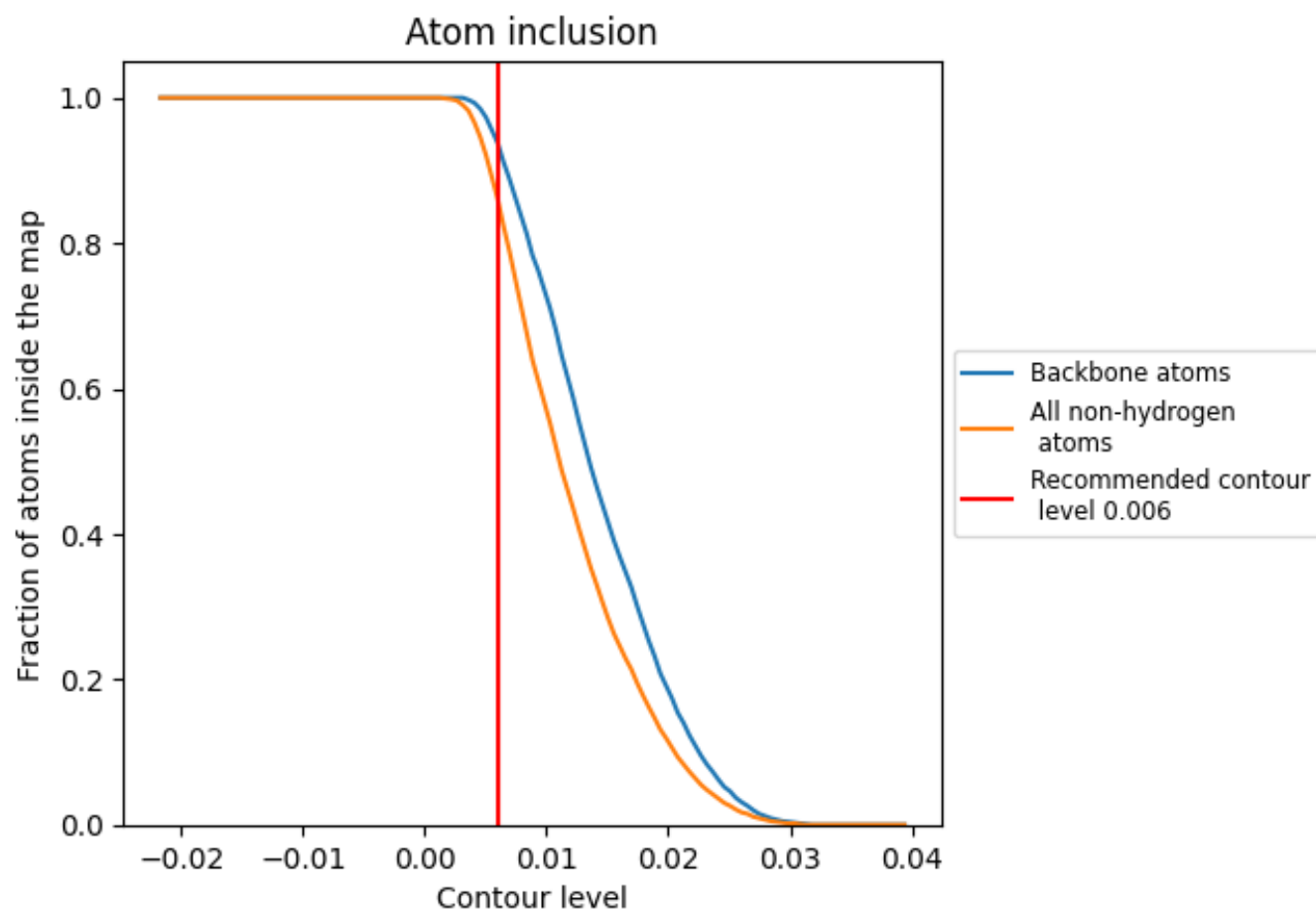
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 86% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8610	0.3580
A	0.8590	0.3600
B	0.8590	0.3590
C	0.8040	0.2680
D	0.9310	0.3980
E	0.8140	0.2690
F	0.9310	0.3940

1.0

0.0

<0.0