



# wwPDB EM Validation Summary Report ⓘ

Apr 9, 2026 – 12:01 AM UTC

PDB ID : 9VEF / pdb\_00009vef  
EMDB ID : EMD-65006  
Title : The cryo-EM structure of human Piezo2-MDFIC complex (composite map)  
Authors : Zhang, Y.; Dai, F.  
Deposited on : 2025-06-09  
Resolution : 3.75 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

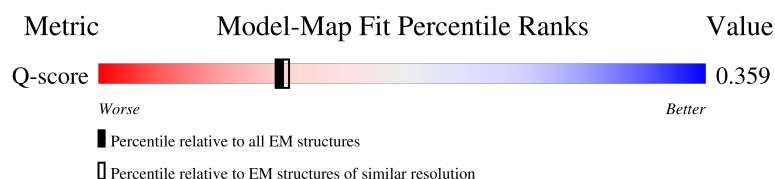
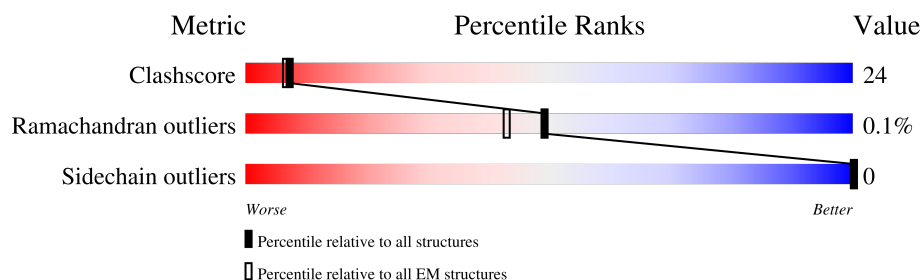
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 3.75 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.



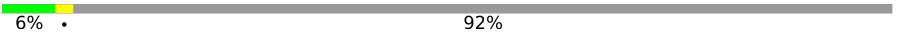

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10301 ( 3.25 - 4.25 )

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  $\geq 3$ , 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	3020	 26% 20% 54%
1	C	3020	 26% 20% 54%
1	E	3020	 26% 20% 54%
2	B	267	 6% 92%

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Mol	Chain	Length	Quality of chain
2	D	267	 6% • 92%
2	F	267	 6% • 92%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 34857 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 Piezo-type mechanosensitive ion channel component 2, Green fluorescent protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1396	Total	C	N	O	S	0	0
			11465	7568	1851	1969	77		
1	C	1396	Total	C	N	O	S	0	0
			11465	7568	1851	1969	77		
1	E	1396	Total	C	N	O	S	0	0
			11465	7568	1851	1969	77		

There are 105 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2753	SER	-	linker	UNP Q9H5I5
A	2754	ASN	-	linker	UNP Q9H5I5
A	2755	SER	-	linker	UNP Q9H5I5
A	2756	LEU	-	linker	UNP Q9H5I5
A	2757	GLU	-	linker	UNP Q9H5I5
A	2758	VAL	-	linker	UNP Q9H5I5
A	2759	LEU	-	linker	UNP Q9H5I5
A	2760	PHE	-	linker	UNP Q9H5I5
A	2761	GLN	-	linker	UNP Q9H5I5
A	2762	GLY	-	linker	UNP Q9H5I5
A	2763	PRO	-	linker	UNP Q9H5I5
A	2764	THR	-	linker	UNP Q9H5I5
A	2765	ALA	-	linker	UNP Q9H5I5
A	2766	ALA	-	linker	UNP Q9H5I5
A	2767	ALA	-	linker	UNP Q9H5I5
A	2768	ALA	-	linker	UNP Q9H5I5
A	2769	VAL	-	linker	UNP Q9H5I5
A	2832	LEU	PHE	conflict	UNP P42212
A	2833	THR	SER	conflict	UNP P42212
A	2974	LYS	ALA	conflict	UNP P42212
A	2999	LEU	HIS	conflict	UNP P42212
A	3007	SER	-	expression tag	UNP P42212
A	3008	GLY	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	3009	GLY	-	expression tag	UNP P42212
A	3010	GLY	-	expression tag	UNP P42212
A	3011	HIS	-	expression tag	UNP P42212
A	3012	HIS	-	expression tag	UNP P42212
A	3013	HIS	-	expression tag	UNP P42212
A	3014	HIS	-	expression tag	UNP P42212
A	3015	HIS	-	expression tag	UNP P42212
A	3016	HIS	-	expression tag	UNP P42212
A	3017	HIS	-	expression tag	UNP P42212
A	3018	HIS	-	expression tag	UNP P42212
A	3019	HIS	-	expression tag	UNP P42212
A	3020	HIS	-	expression tag	UNP P42212
C	2753	SER	-	linker	UNP Q9H5I5
C	2754	ASN	-	linker	UNP Q9H5I5
C	2755	SER	-	linker	UNP Q9H5I5
C	2756	LEU	-	linker	UNP Q9H5I5
C	2757	GLU	-	linker	UNP Q9H5I5
C	2758	VAL	-	linker	UNP Q9H5I5
C	2759	LEU	-	linker	UNP Q9H5I5
C	2760	PHE	-	linker	UNP Q9H5I5
C	2761	GLN	-	linker	UNP Q9H5I5
C	2762	GLY	-	linker	UNP Q9H5I5
C	2763	PRO	-	linker	UNP Q9H5I5
C	2764	THR	-	linker	UNP Q9H5I5
C	2765	ALA	-	linker	UNP Q9H5I5
C	2766	ALA	-	linker	UNP Q9H5I5
C	2767	ALA	-	linker	UNP Q9H5I5
C	2768	ALA	-	linker	UNP Q9H5I5
C	2769	VAL	-	linker	UNP Q9H5I5
C	2832	LEU	PHE	conflict	UNP P42212
C	2833	THR	SER	conflict	UNP P42212
C	2974	LYS	ALA	conflict	UNP P42212
C	2999	LEU	HIS	conflict	UNP P42212
C	3007	SER	-	expression tag	UNP P42212
C	3008	GLY	-	expression tag	UNP P42212
C	3009	GLY	-	expression tag	UNP P42212
C	3010	GLY	-	expression tag	UNP P42212
C	3011	HIS	-	expression tag	UNP P42212
C	3012	HIS	-	expression tag	UNP P42212
C	3013	HIS	-	expression tag	UNP P42212
C	3014	HIS	-	expression tag	UNP P42212
C	3015	HIS	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
C	3016	HIS	-	expression tag	UNP P42212
C	3017	HIS	-	expression tag	UNP P42212
C	3018	HIS	-	expression tag	UNP P42212
C	3019	HIS	-	expression tag	UNP P42212
C	3020	HIS	-	expression tag	UNP P42212
E	2753	SER	-	linker	UNP Q9H5I5
E	2754	ASN	-	linker	UNP Q9H5I5
E	2755	SER	-	linker	UNP Q9H5I5
E	2756	LEU	-	linker	UNP Q9H5I5
E	2757	GLU	-	linker	UNP Q9H5I5
E	2758	VAL	-	linker	UNP Q9H5I5
E	2759	LEU	-	linker	UNP Q9H5I5
E	2760	PHE	-	linker	UNP Q9H5I5
E	2761	GLN	-	linker	UNP Q9H5I5
E	2762	GLY	-	linker	UNP Q9H5I5
E	2763	PRO	-	linker	UNP Q9H5I5
E	2764	THR	-	linker	UNP Q9H5I5
E	2765	ALA	-	linker	UNP Q9H5I5
E	2766	ALA	-	linker	UNP Q9H5I5
E	2767	ALA	-	linker	UNP Q9H5I5
E	2768	ALA	-	linker	UNP Q9H5I5
E	2769	VAL	-	linker	UNP Q9H5I5
E	2832	LEU	PHE	conflict	UNP P42212
E	2833	THR	SER	conflict	UNP P42212
E	2974	LYS	ALA	conflict	UNP P42212
E	2999	LEU	HIS	conflict	UNP P42212
E	3007	SER	-	expression tag	UNP P42212
E	3008	GLY	-	expression tag	UNP P42212
E	3009	GLY	-	expression tag	UNP P42212
E	3010	GLY	-	expression tag	UNP P42212
E	3011	HIS	-	expression tag	UNP P42212
E	3012	HIS	-	expression tag	UNP P42212
E	3013	HIS	-	expression tag	UNP P42212
E	3014	HIS	-	expression tag	UNP P42212
E	3015	HIS	-	expression tag	UNP P42212
E	3016	HIS	-	expression tag	UNP P42212
E	3017	HIS	-	expression tag	UNP P42212
E	3018	HIS	-	expression tag	UNP P42212
E	3019	HIS	-	expression tag	UNP P42212
E	3020	HIS	-	expression tag	UNP P42212

- Molecule 2 is a protein called MyoD family inhibitor domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	22	Total 154	C 91	N 22	O 33	S 8	0	0
2	D	22	Total 154	C 91	N 22	O 33	S 8	0	0
2	F	22	Total 154	C 91	N 22	O 33	S 8	0	0

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	MET	-	initiating methionine	UNP Q9P1T7
B	-19	ASP	-	expression tag	UNP Q9P1T7
B	-18	TYR	-	expression tag	UNP Q9P1T7
B	-17	LYS	-	expression tag	UNP Q9P1T7
B	-16	ASP	-	expression tag	UNP Q9P1T7
B	-15	ASP	-	expression tag	UNP Q9P1T7
B	-14	ASP	-	expression tag	UNP Q9P1T7
B	-13	ASP	-	expression tag	UNP Q9P1T7
B	-12	LYS	-	expression tag	UNP Q9P1T7
B	-11	GLY	-	expression tag	UNP Q9P1T7
B	-10	LEU	-	expression tag	UNP Q9P1T7
B	-9	GLU	-	expression tag	UNP Q9P1T7
B	-8	VAL	-	expression tag	UNP Q9P1T7
B	-7	LEU	-	expression tag	UNP Q9P1T7
B	-6	PHE	-	expression tag	UNP Q9P1T7
B	-5	GLN	-	expression tag	UNP Q9P1T7
B	-4	GLY	-	expression tag	UNP Q9P1T7
B	-3	PRO	-	expression tag	UNP Q9P1T7
B	-2	GLY	-	expression tag	UNP Q9P1T7
B	-1	SER	-	expression tag	UNP Q9P1T7
B	0	SER	-	expression tag	UNP Q9P1T7
D	-20	MET	-	initiating methionine	UNP Q9P1T7
D	-19	ASP	-	expression tag	UNP Q9P1T7
D	-18	TYR	-	expression tag	UNP Q9P1T7
D	-17	LYS	-	expression tag	UNP Q9P1T7
D	-16	ASP	-	expression tag	UNP Q9P1T7
D	-15	ASP	-	expression tag	UNP Q9P1T7
D	-14	ASP	-	expression tag	UNP Q9P1T7
D	-13	ASP	-	expression tag	UNP Q9P1T7
D	-12	LYS	-	expression tag	UNP Q9P1T7
D	-11	GLY	-	expression tag	UNP Q9P1T7
D	-10	LEU	-	expression tag	UNP Q9P1T7
D	-9	GLU	-	expression tag	UNP Q9P1T7

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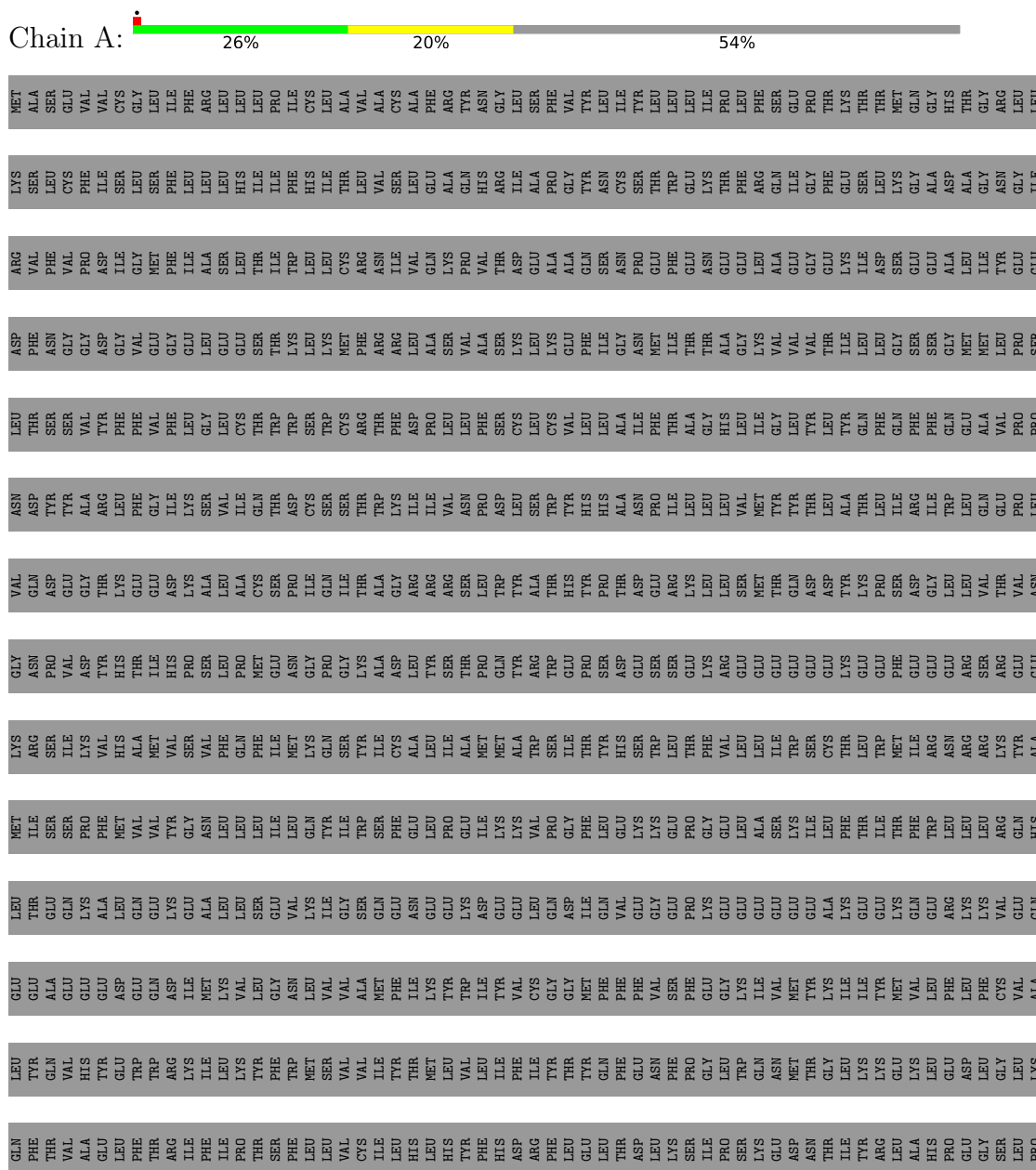
Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	VAL	-	expression tag	UNP Q9P1T7
D	-7	LEU	-	expression tag	UNP Q9P1T7
D	-6	PHE	-	expression tag	UNP Q9P1T7
D	-5	GLN	-	expression tag	UNP Q9P1T7
D	-4	GLY	-	expression tag	UNP Q9P1T7
D	-3	PRO	-	expression tag	UNP Q9P1T7
D	-2	GLY	-	expression tag	UNP Q9P1T7
D	-1	SER	-	expression tag	UNP Q9P1T7
D	0	SER	-	expression tag	UNP Q9P1T7
F	-20	MET	-	initiating methionine	UNP Q9P1T7
F	-19	ASP	-	expression tag	UNP Q9P1T7
F	-18	TYR	-	expression tag	UNP Q9P1T7
F	-17	LYS	-	expression tag	UNP Q9P1T7
F	-16	ASP	-	expression tag	UNP Q9P1T7
F	-15	ASP	-	expression tag	UNP Q9P1T7
F	-14	ASP	-	expression tag	UNP Q9P1T7
F	-13	ASP	-	expression tag	UNP Q9P1T7
F	-12	LYS	-	expression tag	UNP Q9P1T7
F	-11	GLY	-	expression tag	UNP Q9P1T7
F	-10	LEU	-	expression tag	UNP Q9P1T7
F	-9	GLU	-	expression tag	UNP Q9P1T7
F	-8	VAL	-	expression tag	UNP Q9P1T7
F	-7	LEU	-	expression tag	UNP Q9P1T7
F	-6	PHE	-	expression tag	UNP Q9P1T7
F	-5	GLN	-	expression tag	UNP Q9P1T7
F	-4	GLY	-	expression tag	UNP Q9P1T7
F	-3	PRO	-	expression tag	UNP Q9P1T7
F	-2	GLY	-	expression tag	UNP Q9P1T7
F	-1	SER	-	expression tag	UNP Q9P1T7
F	0	SER	-	expression tag	UNP Q9P1T7



### 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: Piezo-type mechanosensitive ion channel component 2, Green fluorescent protein







WORLDWIDE  
PDB  
PROTEIN DATA BANK





[illegible]









CYS	GLY	ILE	MET	ASP	A225	S229	S230	D231	C232	L233	F234	I235	E238	S246
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83949	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 ( $e^-/\text{\AA}^2$ )	49.41	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.940	Depositor
Minimum map value	-0.120	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.238	Depositor
Map size (Å)	421.99997, 421.99997, 421.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.055, 1.055, 1.055	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	0.45	0/11775	0.55	0/15965
1	C	0.45	0/11775	0.55	0/15965
1	E	0.45	0/11775	0.55	0/15965
2	B	0.30	0/155	0.55	0/207
2	D	0.31	0/155	0.55	0/207
2	F	0.30	0/155	0.55	0/207
All	All	0.45	0/35790	0.55	0/48516

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	C	0	3
1	E	0	3
All	All	0	9

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2477	SER	Peptide
1	A	2624	THR	Peptide
1	A	2653	PHE	Peptide
1	C	2477	SER	Peptide
1	C	2624	THR	Peptide

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11465	0	11592	577	0
1	C	11465	0	11592	570	0
1	E	11465	0	11592	577	0
2	B	154	0	137	6	0
2	D	154	0	137	7	0
2	F	154	0	137	7	0
All	All	34857	0	35187	1648	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 24.

The worst 5 of 1648 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:E:2430:ALA:N	1:E:2658:SER:HG	1.44	1.15
1:C:2430:ALA:N	1:C:2658:SER:HG	1.43	1.15
1:A:2430:ALA:N	1:A:2658:SER:HG	1.45	1.14
1:E:2468:SER:HB2	1:E:2472:PHE:HB3	1.46	0.95
1:A:2468:SER:HB2	1:A:2472:PHE:HB3	1.46	0.94

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	1378/3020 (46%)	1187 (86%)	190 (14%)	1 (0%)	48 79

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	1378/3020 (46%)	1187 (86%)	190 (14%)	1 (0%)	48	79
1	E	1378/3020 (46%)	1187 (86%)	190 (14%)	1 (0%)	48	79
2	B	20/267 (8%)	17 (85%)	3 (15%)	0	100	100
2	D	20/267 (8%)	17 (85%)	3 (15%)	0	100	100
2	F	20/267 (8%)	17 (85%)	3 (15%)	0	100	100
All	All	4194/9861 (42%)	3612 (86%)	579 (14%)	3 (0%)	49	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2487	GLU
1	C	2487	GLU
1	E	2487	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	1268/2707 (47%)	1268 (100%)	0	100	100
1	C	1268/2707 (47%)	1268 (100%)	0	100	100
1	E	1268/2707 (47%)	1268 (100%)	0	100	100
2	B	20/221 (9%)	20 (100%)	0	100	100
2	D	20/221 (9%)	20 (100%)	0	100	100
2	F	20/221 (9%)	20 (100%)	0	100	100
All	All	3864/8784 (44%)	3864 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	1027	ASN
1	E	1713	ASN
1	E	2488	ASN
1	E	2263	GLN
1	E	1674	HIS

### 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.

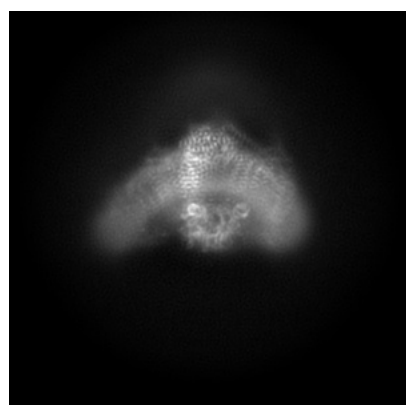
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-65006. These allow visual inspection of the internal detail of the map and identification of artifacts.

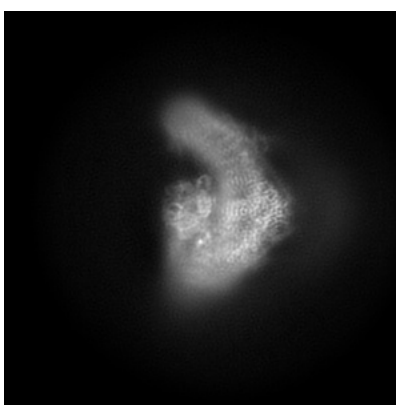
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

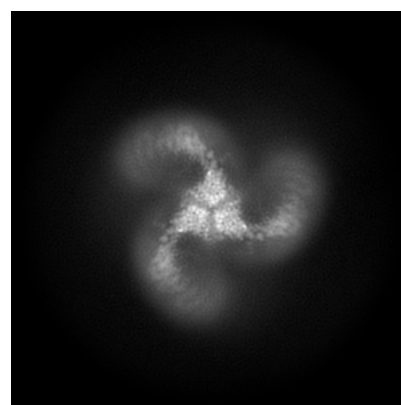
#### 6.1.1 Primary map



X



Y

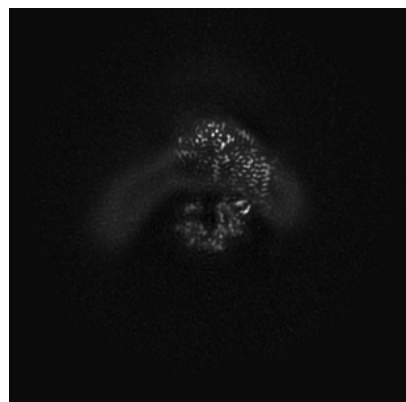


Z

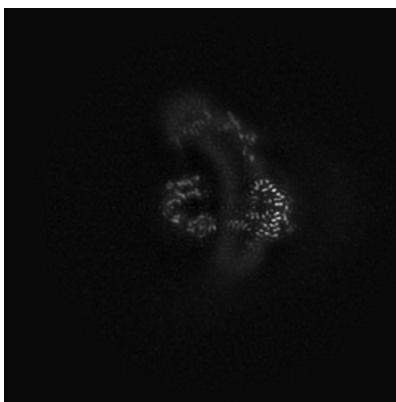
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

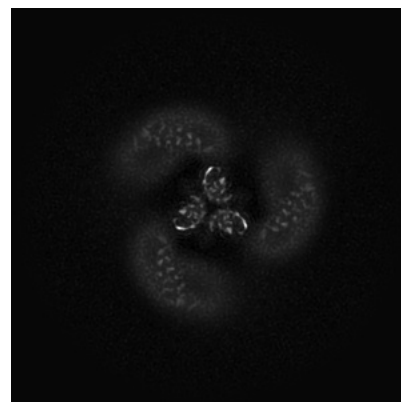
#### 6.2.1 Primary map



X Index: 200



Y Index: 200



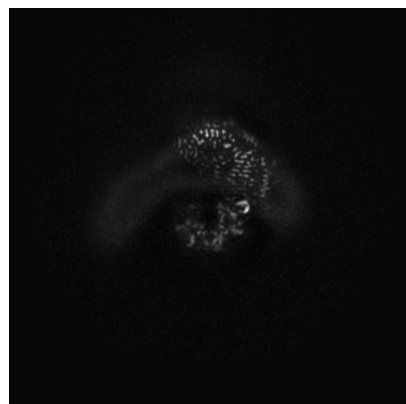
Z Index: 200



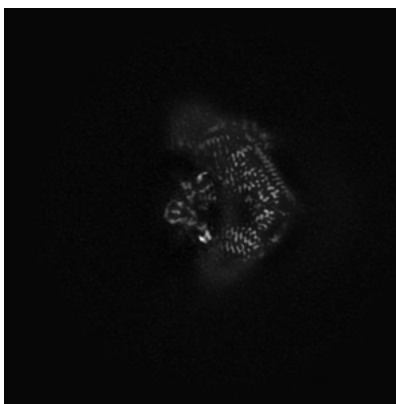
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

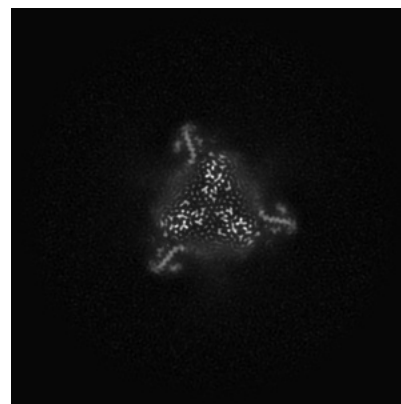
### 6.3.1 Primary map



X Index: 198



Y Index: 180

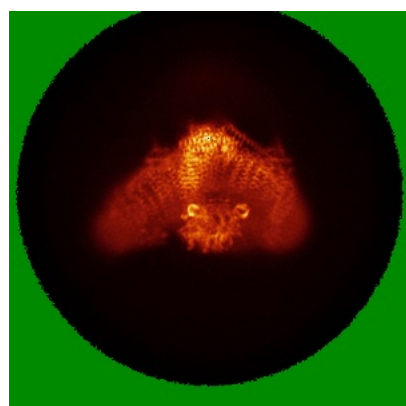


Z Index: 250

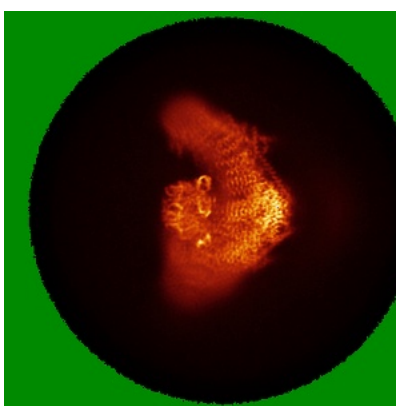
The images above show the largest variance slices of the map in three orthogonal directions.

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

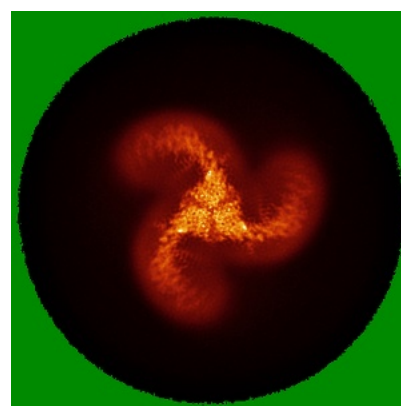
### 6.4.1 Primary map



X



Y



Z

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 0.238. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

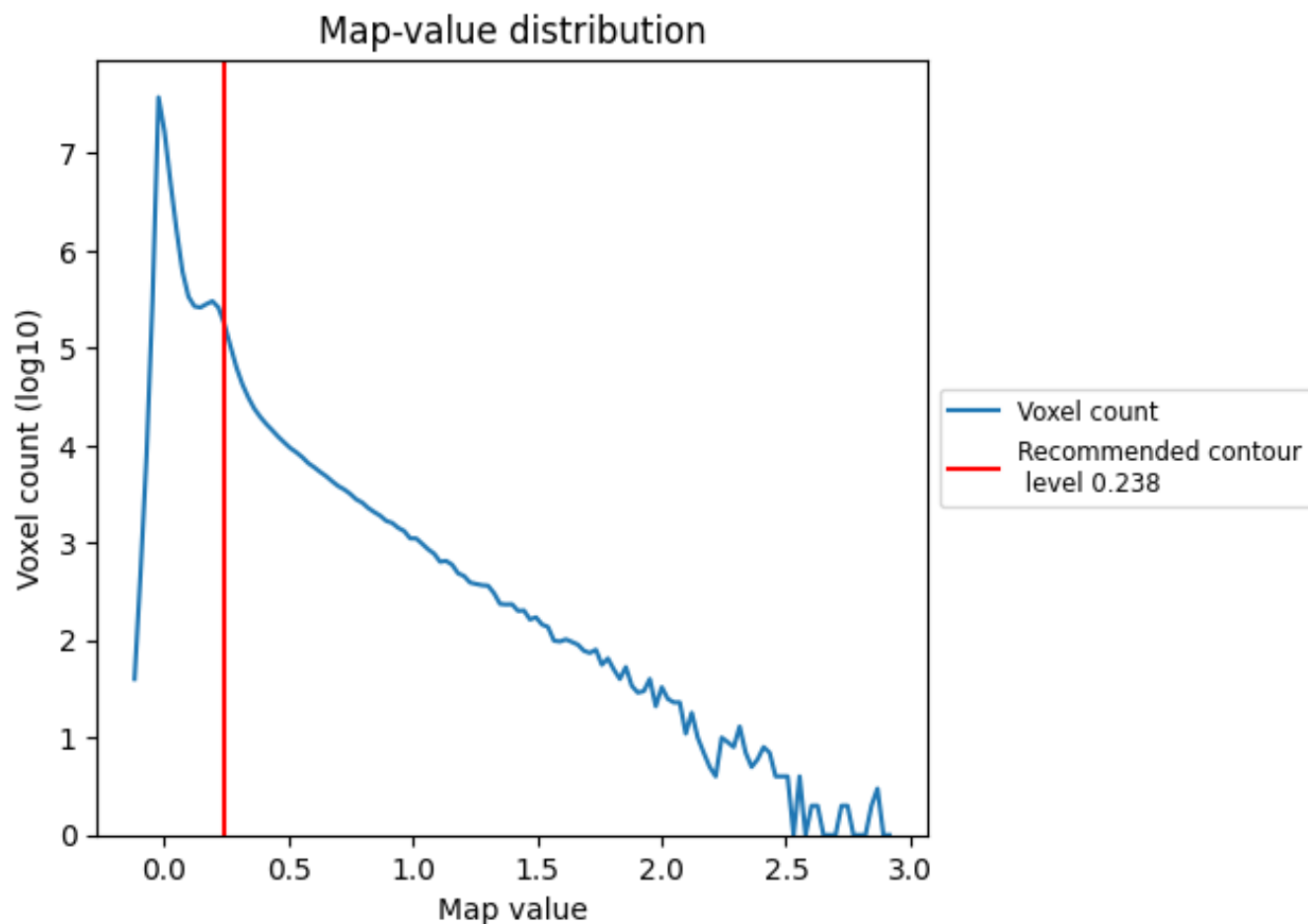
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

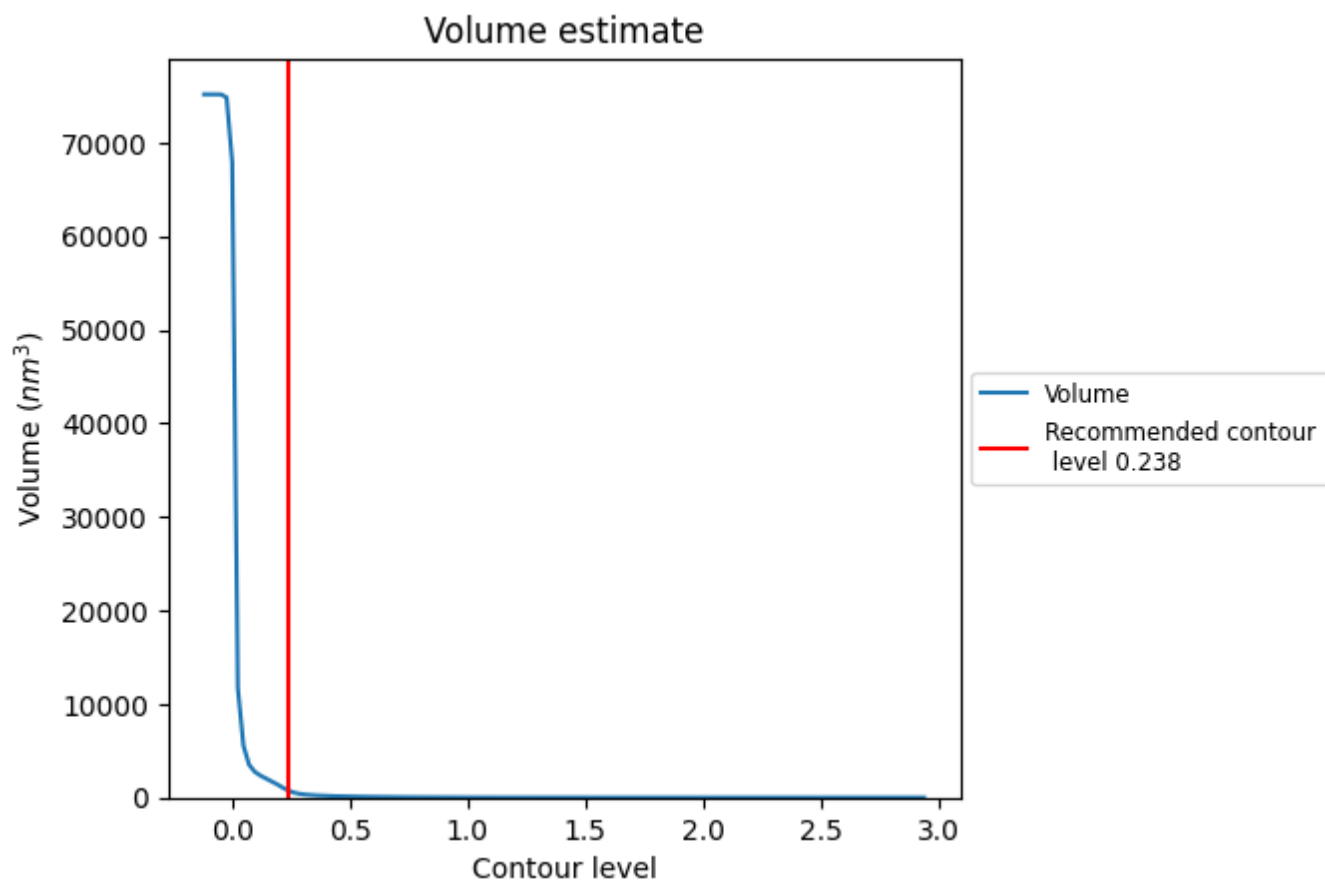
This section contains the results of statistical analysis of the map.

### 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.

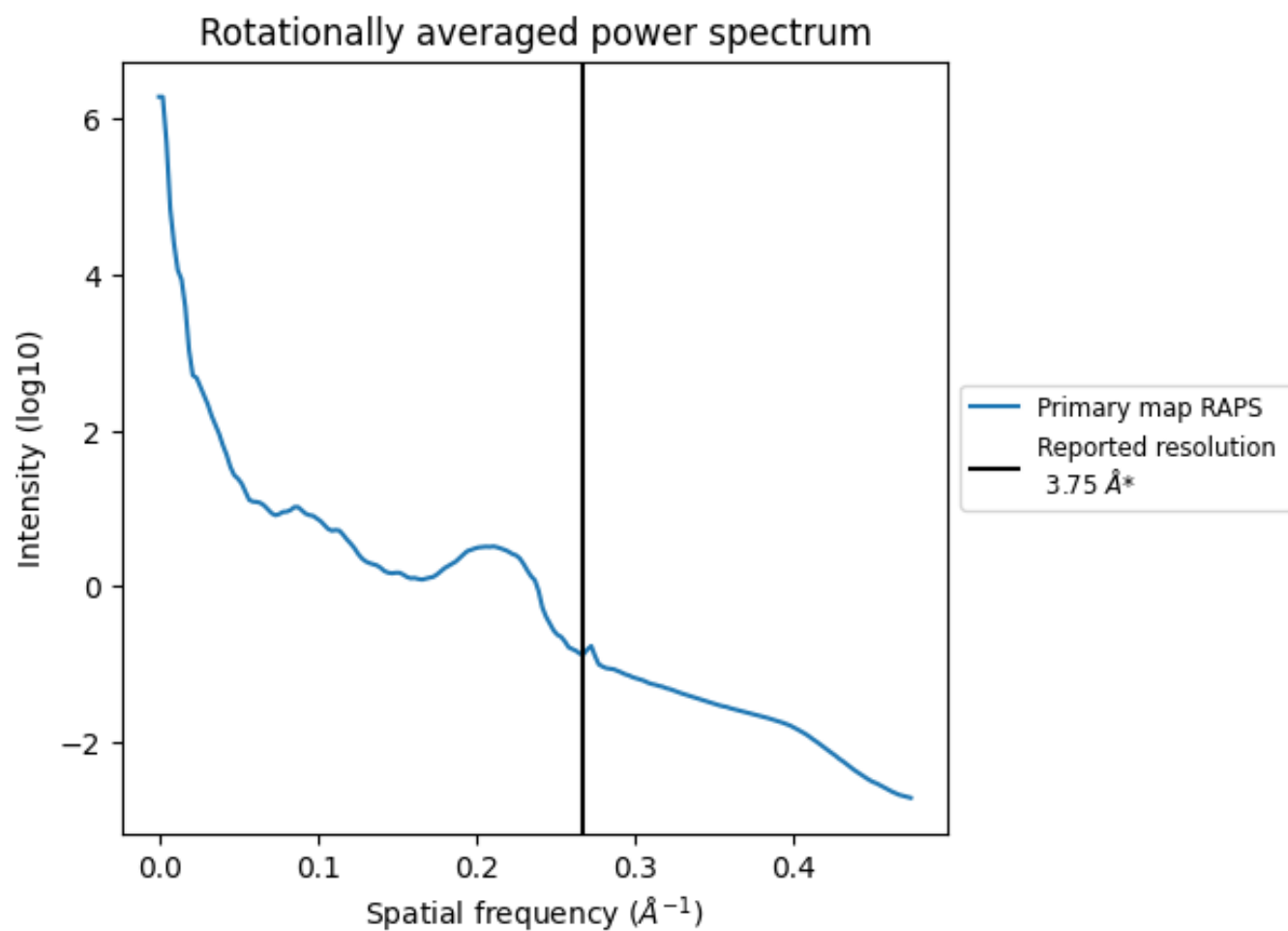
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 750  $\text{nm}^3$ ; this corresponds to an approximate mass of 678 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 0.267 Å<sup>-1</sup>

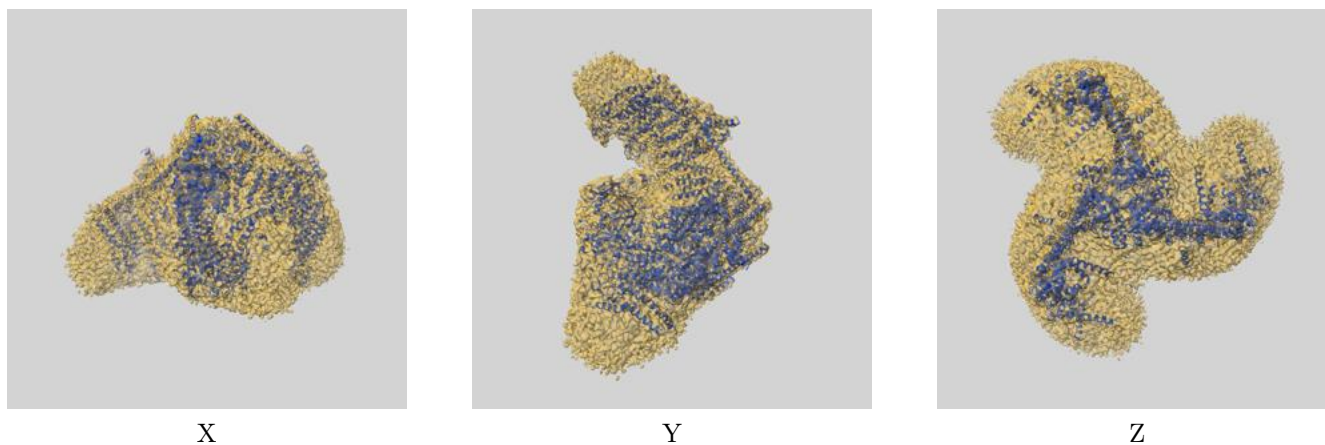
## 8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

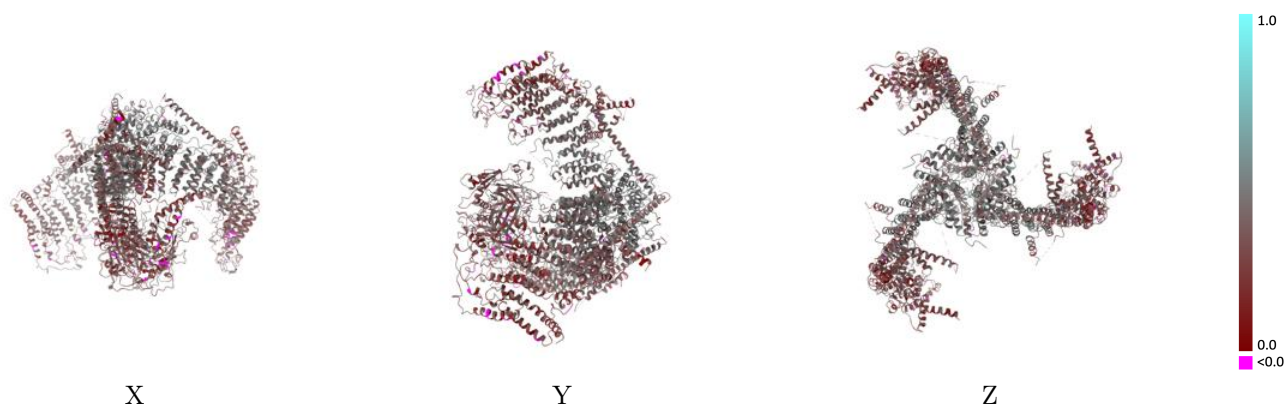
This section contains information regarding the fit between EMDB map EMD-65006 and PDB model 9VEF. Per-residue inclusion information can be found in section 3 on page 9.

### 9.1 Map-model overlay [i](#)



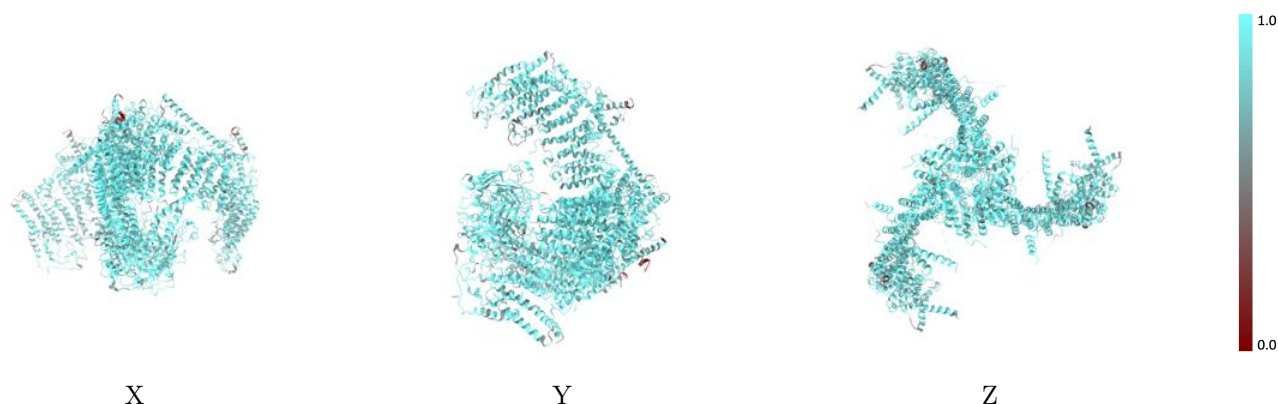
The images above show the 3D surface view of the map at the recommended contour level 0.238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

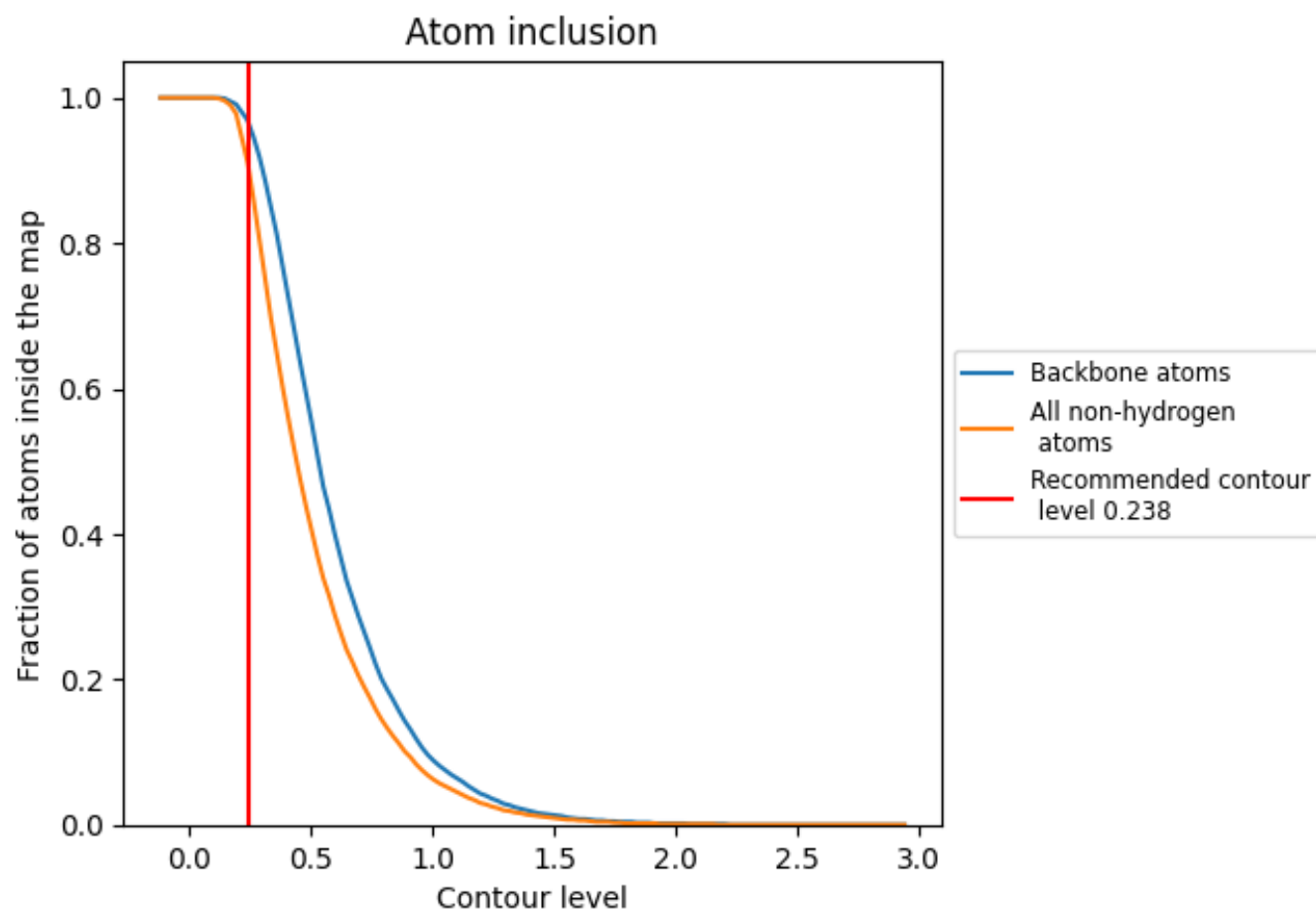
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.238).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 91% 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 (0.238) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9110	<div><div></div></div> 0.3590
A	<div><div></div></div> 0.9100	<div><div></div></div> 0.3580
B	<div><div></div></div> 0.9680	<div><div></div></div> 0.4200
C	<div><div></div></div> 0.9090	<div><div></div></div> 0.3580
D	<div><div></div></div> 0.9740	<div><div></div></div> 0.4230
E	<div><div></div></div> 0.9100	<div><div></div></div> 0.3570
F	<div><div></div></div> 0.9740	<div><div></div></div> 0.4240

1.0

0.0

<0.0