



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 07:59 PM UTC

PDB ID : 9ZIS / pdb_00009zis
EMDB ID : EMD-74281
Title : C. elegans PEZO-1 Isoform G
Authors : Bell, B.; Baker, M.L.; Vasquez, V.
Deposited on : 2025-12-04
Resolution : 3.50 Å(reported)
Based on initial model : .

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

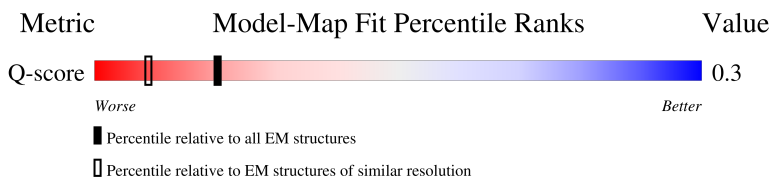
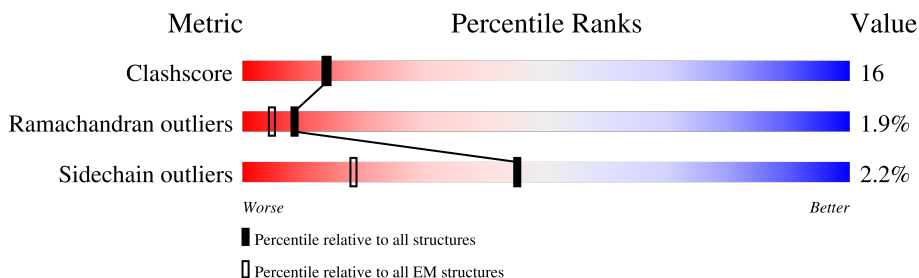
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2442	
1	B	2442	
1	C	2442	

2 Entry composition

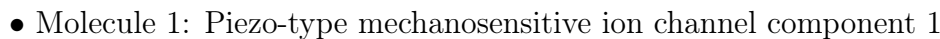
There is only 1 type of molecule in this entry. The entry contains 44505 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1944	Total 14835	C 9697	N 2470	O 2589	S 79	0	0
1	B	1944	Total 14835	C 9697	N 2470	O 2589	S 79	0	0
1	C	1944	Total 14835	C 9697	N 2470	O 2589	S 79	0	0

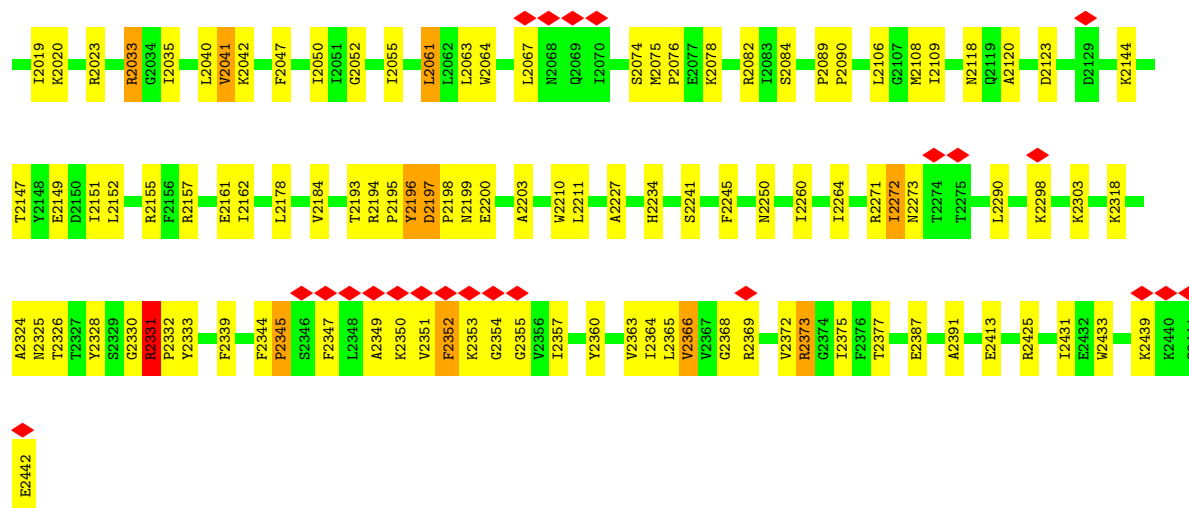




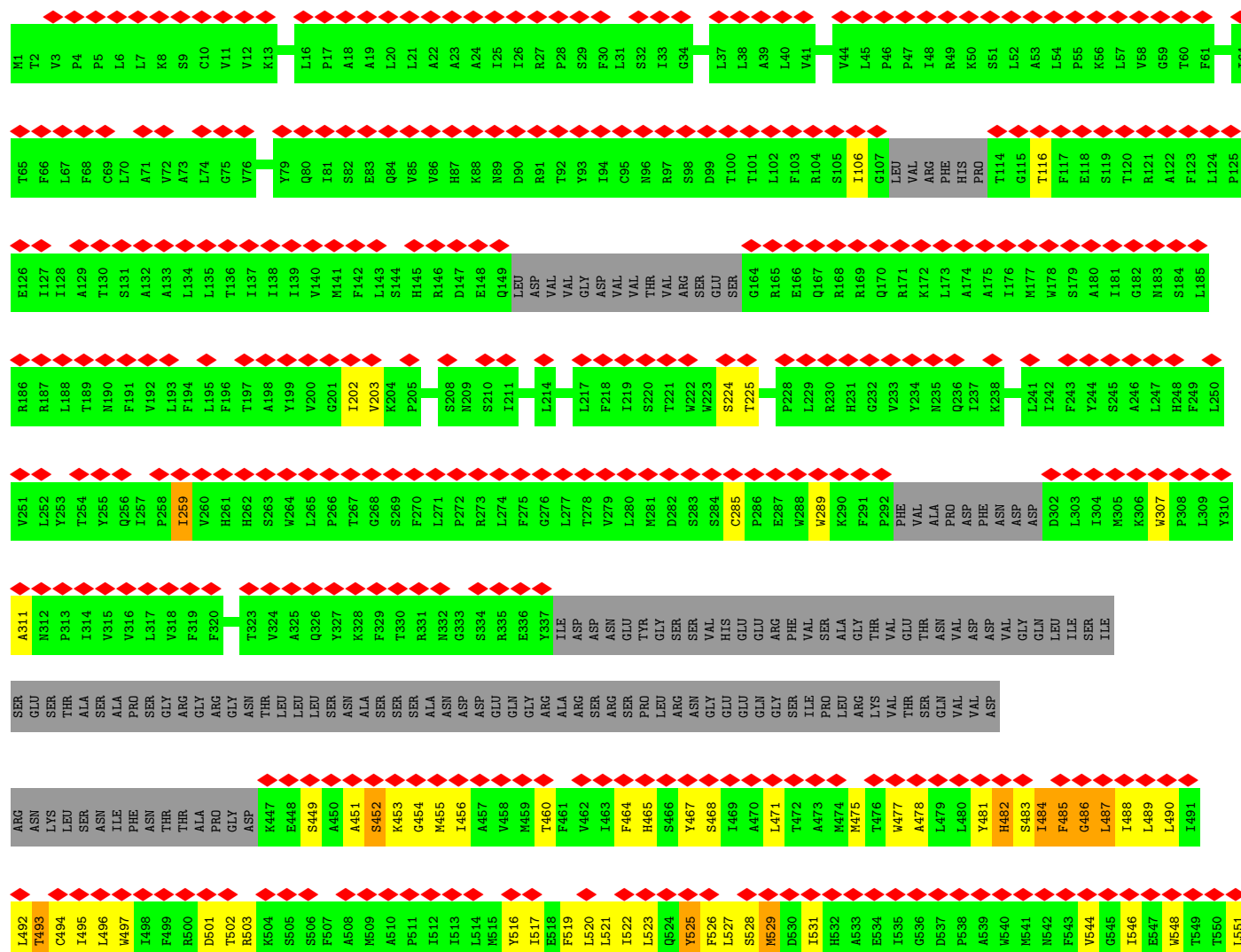
	I64	T2	H1
	T65	V3	
	P66	P4	
	L67	P5	
	F68	L6	
	C69	L7	
	L70	K8	
	A71	S9	
	W72	C10	
	A73	V11	
	L74	V12	
	G75	K13	
	V76		
		L16	
	Y79	P17	
	Q80	A18	
	I81	A19	
	S82	L20	
	E83	L21	
	Q84	A22	
	R85	A23	
	V86	A24	
	H87	T25	
	K88	I26	
	N89	R27	
	D90	P28	
	R91	S29	
	T92	F30	
	Y93	L31	
	I94	S32	
	C95	I33	
	N96	G34	
	R97	T35	
	S98	V36	
	D99	L37	
	T100	L38	
	T101	A39	
	L102	L40	
	F103	V41	
	R104	S42	
	S105	A43	
	I106	V44	
	G107	L45	
	LEU	P46	
	VAL	P47	
	ARG	T48	
	PHE	R49	
	HIS	K50	
	PRO	S51	
	T114	L52	
	G115	L53	
	T116	A53	
	F117	L54	
	E118	P55	
	S119	K56	
	T120	L57	
	R121	V58	
	A122	Q59	
	F123	T60	
		P61	







• Molecule 1: Piezo-type mechanosensitive ion channel component 1



ASP	T1369	E1294	Y1149	L1064	L992	GLU	A867	GLY	R734	L873	ALA	P552
PRO	E1295	T1295	D1150	P1065	I993	PRO	D868	ARG	A735	K674	LYS	V553
GLY	A1371	K1296	F1151	P1066	I994	ILE	G869	ALA	I736	E875	PHE	H554
ILE	E1297	E1297	I1152	I1070	D994	MET	I870	HIS	G737	S676		A555
MET	E1374	E1298	D1153	E1071	Y995	LEU	F871	ALA	E738	F677		V556
TYR	R1375	N1299	T1154	E1072	G996	PHE	F874	GLY	S739	R678		I557
ALA	I1300	N1299	K1155	P1073	Y998	G837	F874	ASP	E740	L879		I558
ALA	G1301	G1301	K1156	W1074	K999	M875	M875	THR	G740	Y880		L559
THR	F1302	F1302	Y1158	W1077	G1001	M876	M876		L742	R621		C560
ALA	D1303	D1303	V1159	I1078	L1002	G876	G876		F743	K622		V561
HIS	I1304	I1304	D1160	P1078	L1002	A877	A877		L744	F623		Q562
ASP	I1305	I1305	P1078	S1080	T1005	Y878	Y878		Q745	A624		T563
LEU	A1306	A1306	Y1081	S1080	M1006	L879	L879		L746	A625		L564
ASP	L1307	L1307	S1082	S1082	I1007	V882	V882		L747	A626		L565
LEU	A1384	A1384	Y1083	Y1083	A1008	V886	V886		L748	F627		T566
ALA	S1308	S1308	D1084	D1084	A1008	M887	M887		A749	E628		L567
LYS	V1311	V1311	L1092	L1092	G1010	I1E	I1E		I750	Y629		P568
THR	R1387	R1387	L1093	L1093	I1013	TYR	TYR		A751	L630		V569
VAL	T1388	T1388	M1176	M1176	R1016	GLN	GLN		L752	S631		F570
GLN	F1389	F1389	S1177	S1177	M1017	LEU	LEU		F753	N632		L571
VAL	E1390	E1390	L1178	L1178	D1018	ASP	ASP		V754	K633		L572
LYS	P1391	P1391	L1179	L1179	A1019	ILE	ILE		V755	V634		L573
LYS	T1393	T1393	A1180	A1180	Q955	VAL	VAL		T756	S635		R574
ASP	Y1394	Y1394	A1181	A1181	R956	PRO	PRO		Q759	V636		R577
THR	G1395	G1395	G1099	G1099	R957	GLU	GLU		L760	Y637		R578
ILE	H1396	H1396	Y1106	Y1106	I1023	LEU	LEU		I761	F638		E579
ASP	R1399	R1399	G1109	G1109	Q1024	SER	SER		F762	I639		K580
PRO	M4005	M4005	Y1113	Y1113	S961	GLN	GLN		H763	F640		F581
ARG	D1409	D1409	L1114	L1114	L962	ASP	ASP		L764	V641		Y582
ALA	N4412	N4412	L1116	L1116	G963	ARG	ARG		R769	V642		E583
ALA	D1413	D1413	C1119	C1119	L964	GLY	GLY		A770	S643		S584
VAL	D1414	D1414	Q1120	Q1120	P965	VAL	VAL		THR	V644		LEU
SER	L1415	L1415	G1121	G1121	E966	ALA	ALA		SER	V645		SER
GLU	L1416	L1416	L1121	L1121	S967	ASP	ASP		ASP	L646		ASP
GLU	E1417	E1417	V1123	V1123	R968	ASN	ASN		PRO	L647		TYR
ALA	PRO	PRO	E1129	E1129	R969	CYS	CYS		ARG	V648		GLU
ARG	VAL	VAL	D1130	D1130	A970	SER	SER		ARG	V649		ARG
LYS	ASP	ASP	ASN	ASN	K971	HIS	HIS		ALA	S650		GLN
PRO	GLY	GLY	ASP	ASP	V972	GLY	GLY		GLY	T651		ARG
PHE	PHE	PHE	ILE	ILE	F973	ASN	ASN		ASN	C652		ARG
VAL	VAL	VAL	SER	SER	F976	SER	SER		PRO	S711		ILE
THR	THR	THR	MET	MET	H977	PRO	PRO		PRO	F653		ASN
GLU	GLU	GLU	ILE	ILE	R978	THR	THR		THR	A654		SER
VAL	VAL	VAL	TYR	TYR	H978	GLU	GLU		SER	P655		TYR
ASP	ASP	ASP	ASN	ASN	I1046	TRP	TRP		THR	N656		GLY
GLY	GLY	GLY	ASN	ASN	Y1049	PHE	PHE		THR	F657		THR
THR	THR	THR	GLY	GLY	M1050	GLY	GLY		GLU	Y658		PHE
ASP	ASP	ASP	LEU	LEU	F981	LEU	LEU		ALA	N659		GLY
GLY	GLY	GLY	ASN	ASN	D982	LYS	LYS		LYS	I660		ALA
ASP	ASP	ASP	PHE	PHE	R983	LYS	LYS		ALA	L661		SER
GLU	GLU	GLU	VAL	VAL	S984	VAL	VAL		ALA	L720		LYS
THR	THR	THR	ILE	ILE	L1056	GLU	GLU		ALA	S721		THR
TYR	TYR	TYR	LYS	LYS	F1059	VAL	VAL		ALA	F663		GLY
ASP	ASP	ASP	PRO	PRO	V1062	GLY	GLY		SER	A664		ALA
ARG	ARG	ARG	E1145	E1145	G1063	THR	THR		THR	L665		GLY
LEU	LEU	LEU							GLN	W666		VAL
										A667		ALA
										L668		VAL
										N669		
										L670		
										I671		
										Y672		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	77342	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)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.545	Depositor
Minimum map value	-0.371	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0561	Depositor
Map size ($\text{\AA}$)	483.84003, 483.84003, 483.84003	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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	0.67	32/15190 (0.2%)	0.95	95/20664 (0.5%)
1	B	0.67	32/15190 (0.2%)	0.95	95/20664 (0.5%)
1	C	0.67	32/15190 (0.2%)	0.95	95/20664 (0.5%)
All	All	0.67	96/45570 (0.2%)	0.95	285/61992 (0.5%)

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	14
1	B	0	14
1	C	0	14
All	All	0	42

The worst 5 of 96 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1330	ARG	C-O	13.70	1.41	1.24
1	B	1330	ARG	C-O	13.66	1.41	1.24
1	A	1330	ARG	C-O	13.65	1.41	1.24
1	A	1079	PRO	N-CD	-13.56	1.28	1.47
1	C	1079	PRO	N-CD	-13.53	1.28	1.47

The worst 5 of 285 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	482	HIS	N-CA-CB	19.06	142.70	110.49
1	B	482	HIS	N-CA-CB	19.05	142.68	110.49
1	C	482	HIS	N-CA-CB	19.03	142.66	110.49
1	C	680	TYR	CB-CA-C	-17.87	82.82	110.88
1	A	680	TYR	CB-CA-C	-17.87	82.82	110.88

There are no chirality outliers.

5 of 42 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1071	GLU	Mainchain
1	A	285	CYS	Peptide
1	A	493	THR	Mainchain
1	A	503	ARG	Sidechain
1	A	681	ARG	Sidechain

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	14835	0	14152	471	0
1	B	14835	0	14152	467	0
1	C	14835	0	14152	466	0
All	All	44505	0	42456	1369	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 16.

The worst 5 of 1369 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:C:477:TRP:HH2	1:C:562:GLN:HE21	1.05	0.99
1:A:477:TRP:HH2	1:A:562:GLN:HE21	1.05	0.99
1:B:495:ILE:C	1:B:497:TRP:H	1.71	0.99
1:B:477:TRP:HH2	1:B:562:GLN:HE21	1.05	0.98
1:A:688:TRP:HA	1:A:760:LEU:HD21	1.45	0.97

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	1918/2442 (78%)	1711 (89%)	171 (9%)	36 (2%)	6	33
1	B	1918/2442 (78%)	1711 (89%)	171 (9%)	36 (2%)	6	33
1	C	1918/2442 (78%)	1712 (89%)	170 (9%)	36 (2%)	6	33
All	All	5754/7326 (78%)	5134 (89%)	512 (9%)	108 (2%)	8	33

5 of 108 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	259	ILE
1	A	289	TRP
1	A	482	HIS
1	A	691	LEU
1	A	983	ARG

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	1449/2141 (68%)	1417 (98%)	32 (2%)	45	65
1	B	1449/2141 (68%)	1418 (98%)	31 (2%)	47	66
1	C	1449/2141 (68%)	1416 (98%)	33 (2%)	44	64
All	All	4347/6423 (68%)	4251 (98%)	96 (2%)	45	65

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	2035	ILE
1	C	1078	ILE
1	B	2042	LYS
1	C	525	TYR
1	C	1196	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2201	ASN
1	C	717	ASN
1	C	2201	ASN
1	C	1931	HIS
1	B	1953	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.

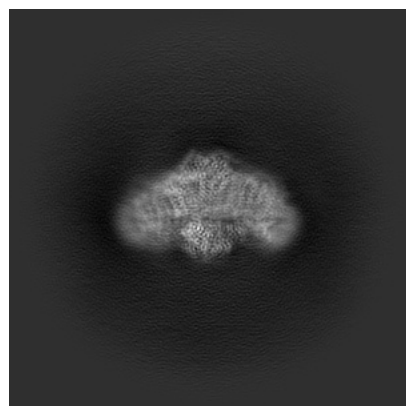
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74281. These allow visual inspection of the internal detail of the map and identification of artifacts.

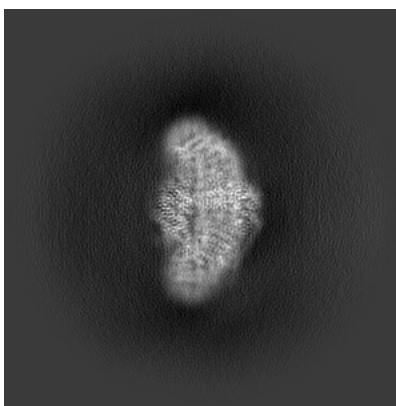
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

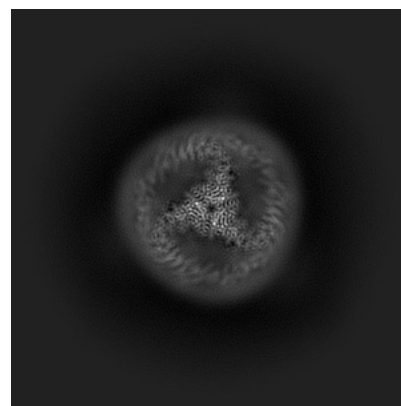
6.1.1 Primary map



X

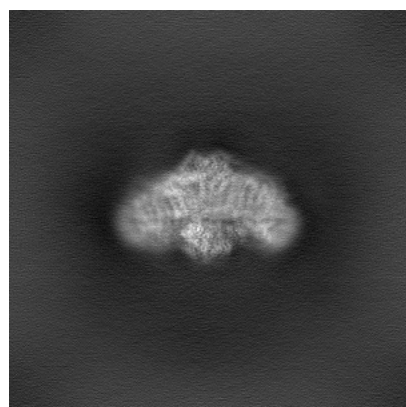


Y

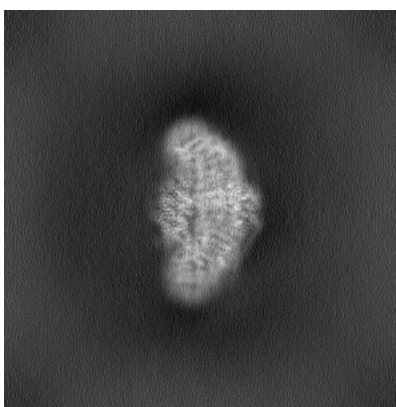


Z

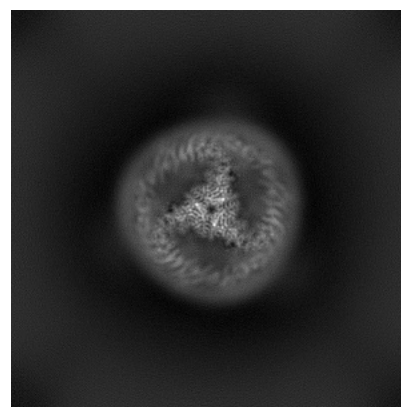
6.1.2 Raw map



X



Y

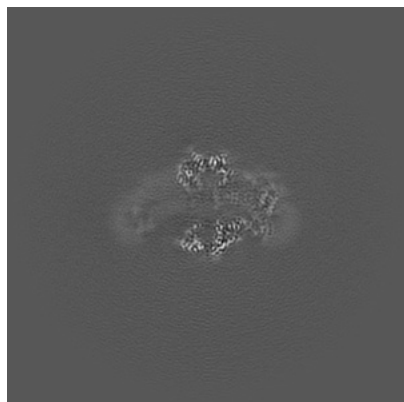


Z

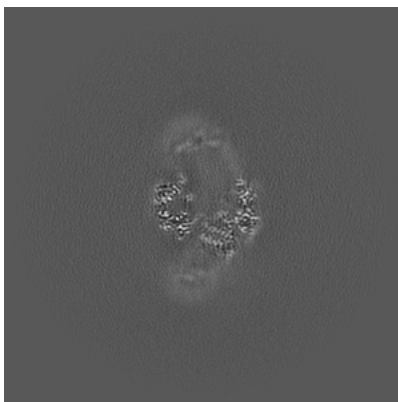
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

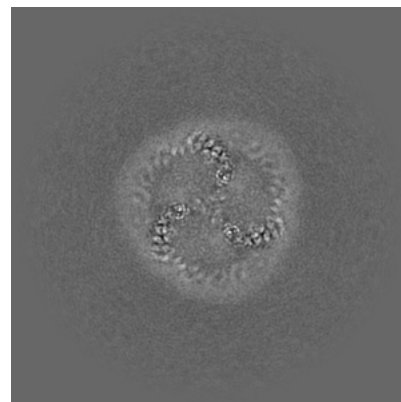
6.2.1 Primary map



X Index: 224

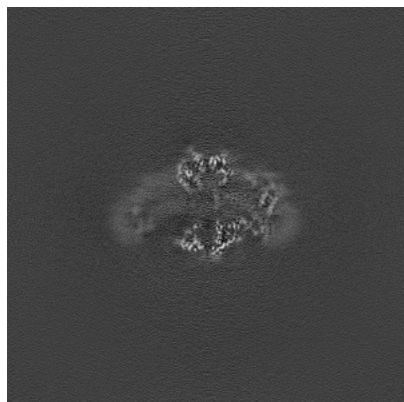


Y Index: 224

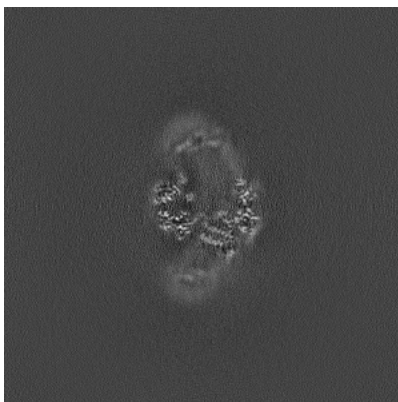


Z Index: 224

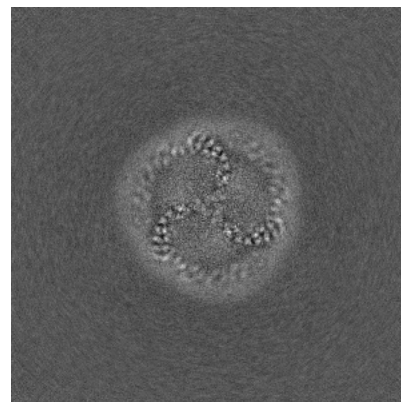
6.2.2 Raw map



X Index: 224



Y Index: 224

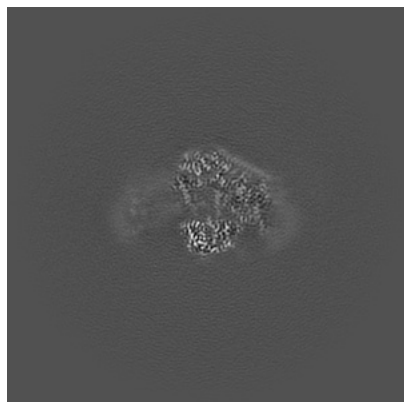


Z Index: 224

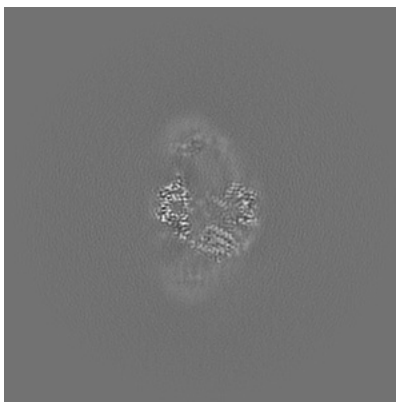
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

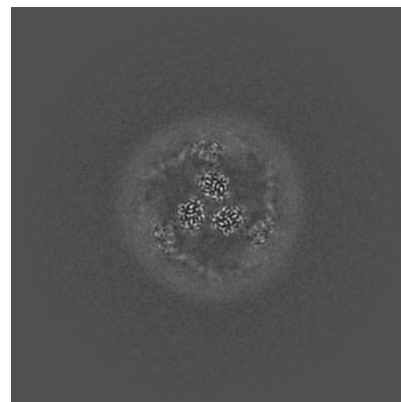
6.3.1 Primary map



X Index: 236

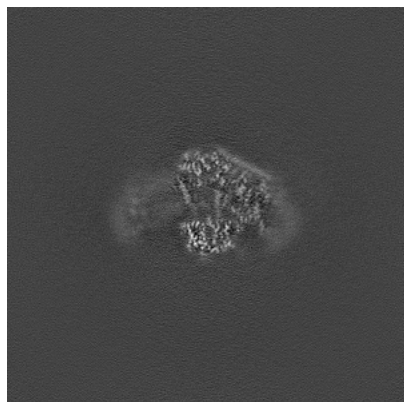


Y Index: 216

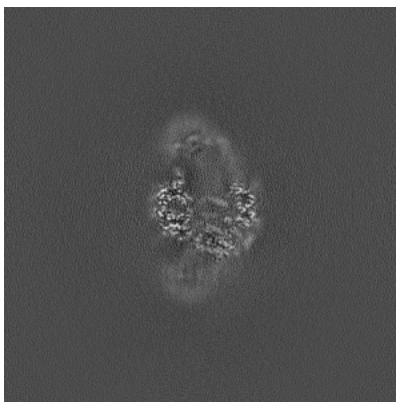


Z Index: 197

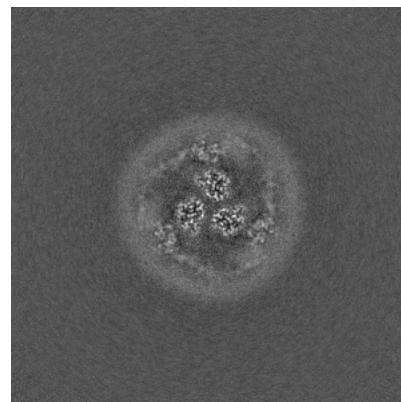
6.3.2 Raw map



X Index: 236



Y Index: 218

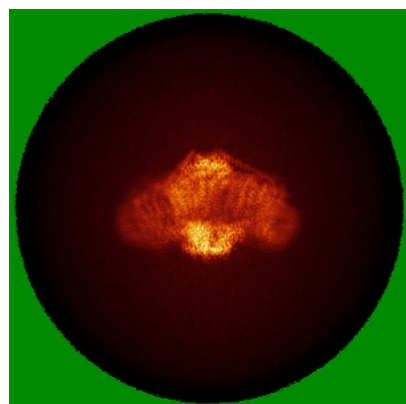


Z Index: 198

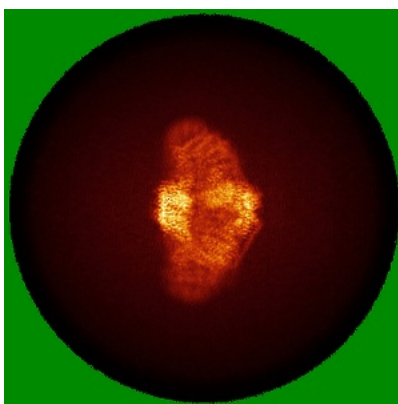
The images above show the largest variance slices of the map in three orthogonal directions.

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

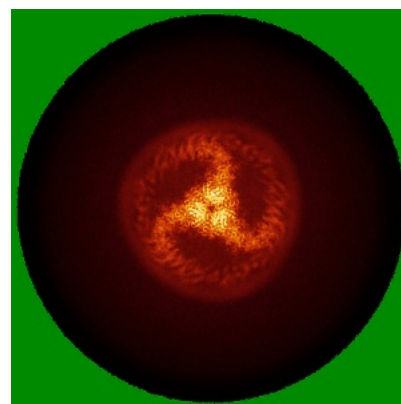
6.4.1 Primary map



X

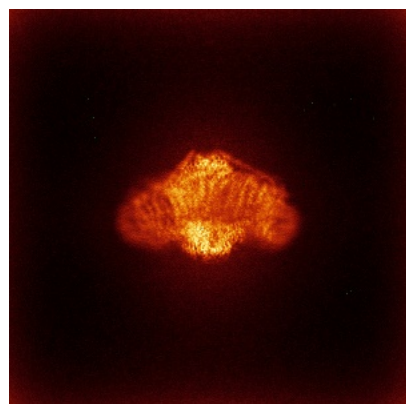


Y

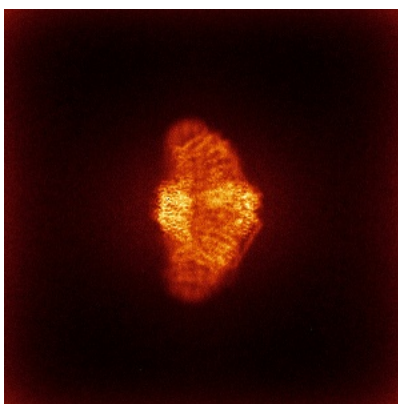


Z

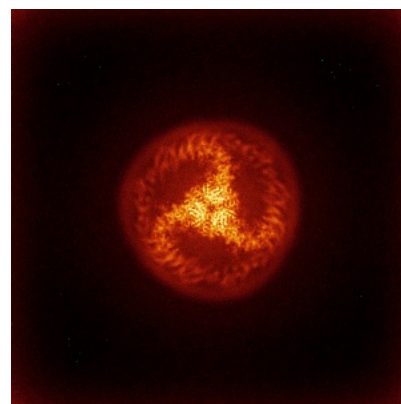
6.4.2 Raw map



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 0.0561. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

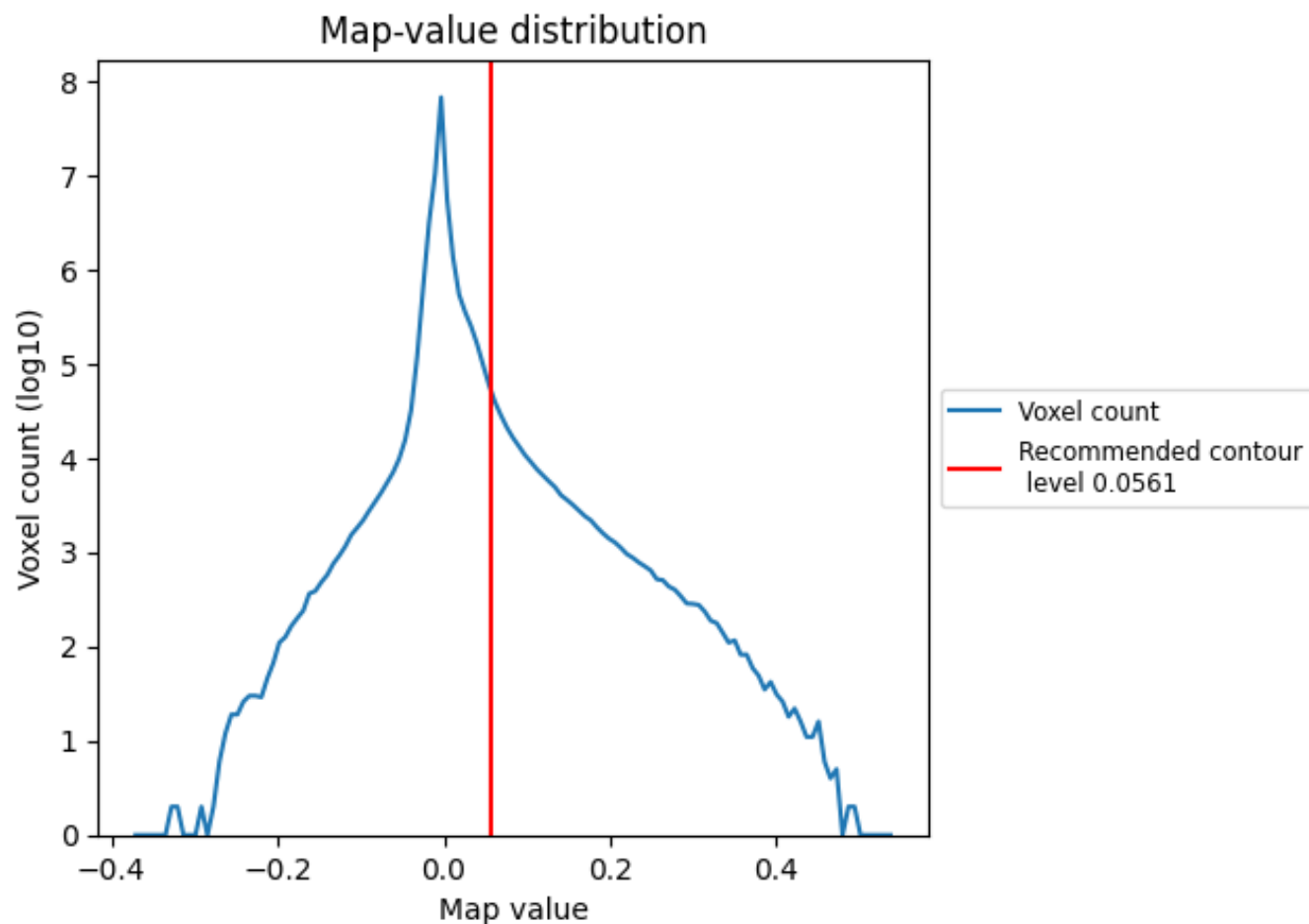
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

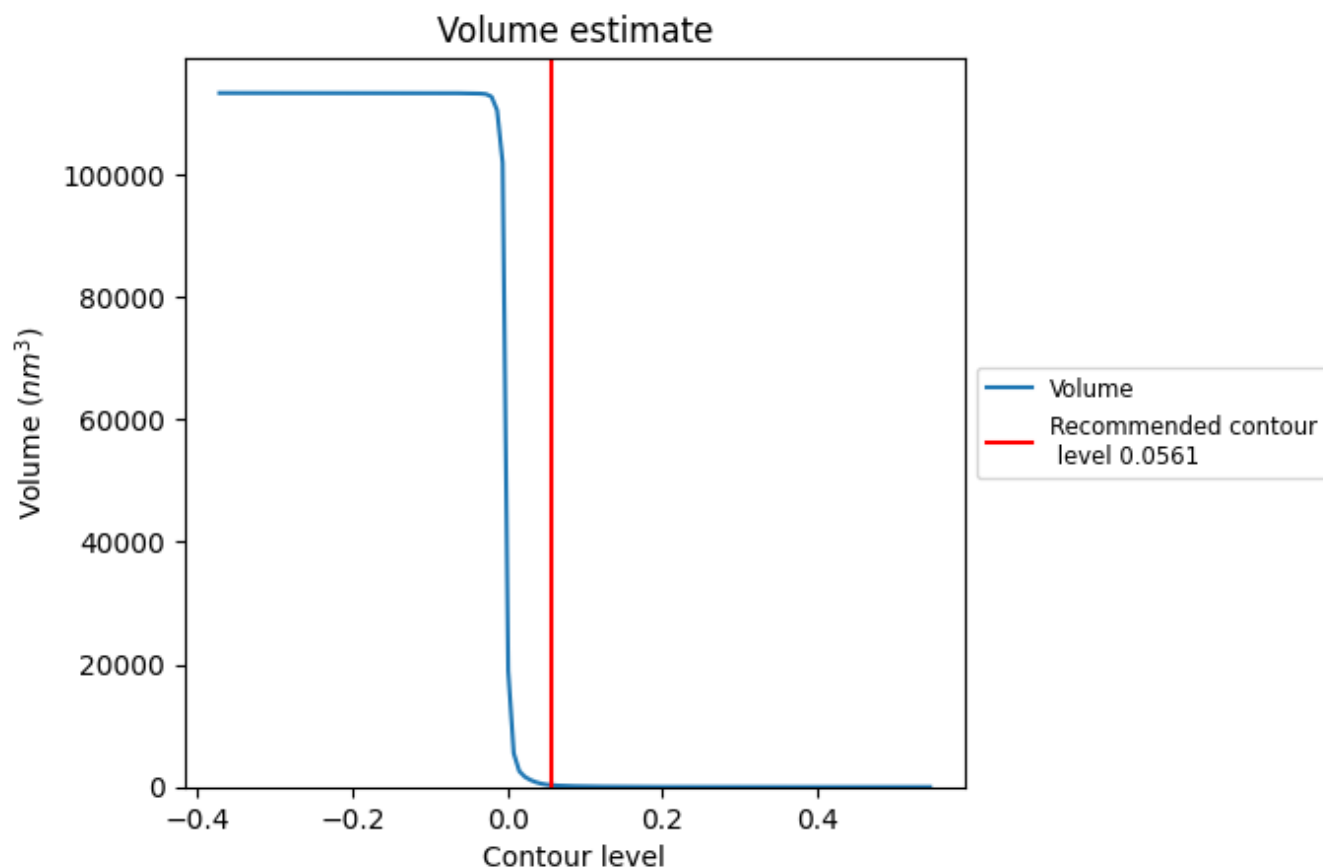
This section contains the results of statistical analysis of the map.

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.

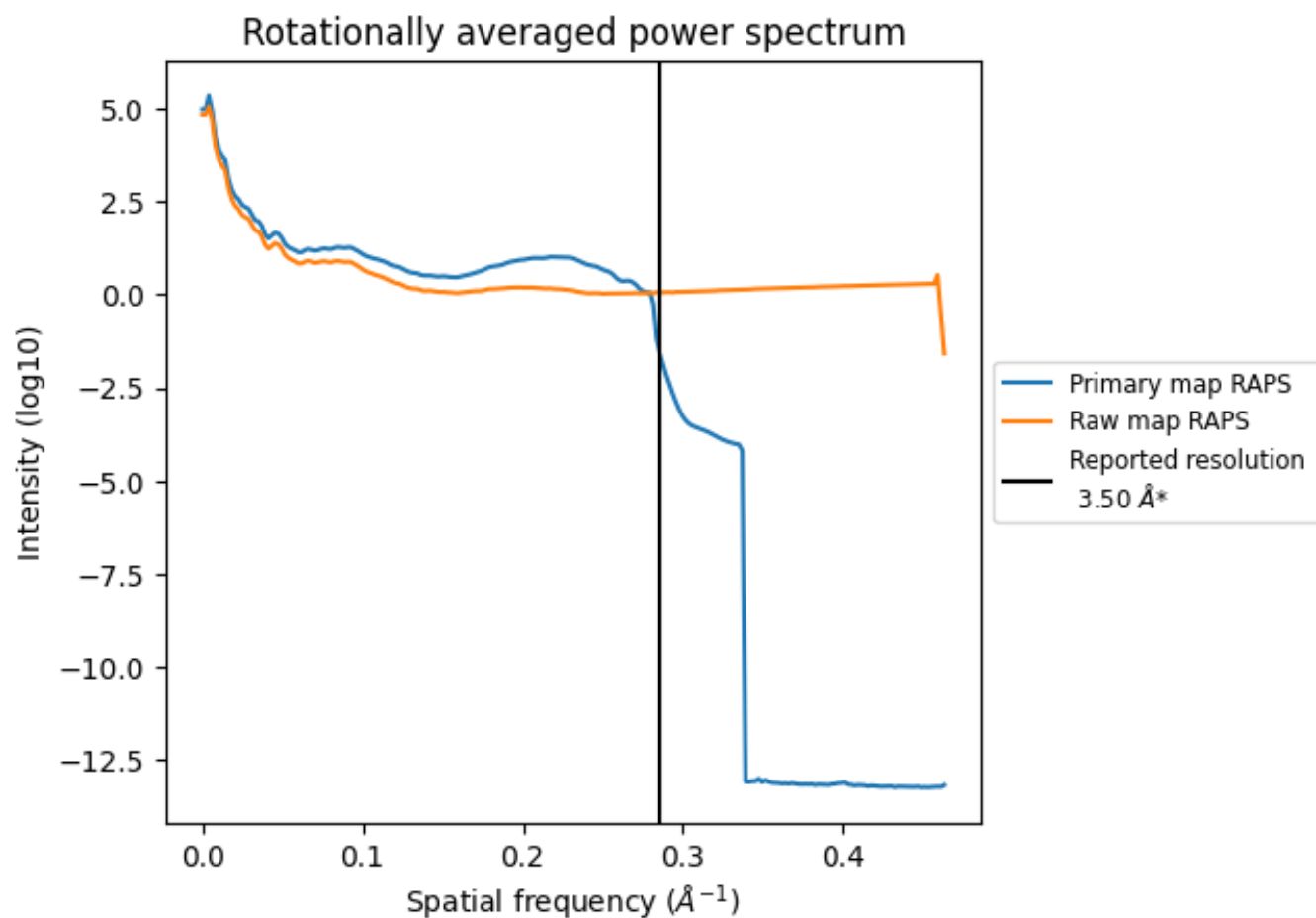
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 305 nm³; this corresponds to an approximate mass of 276 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

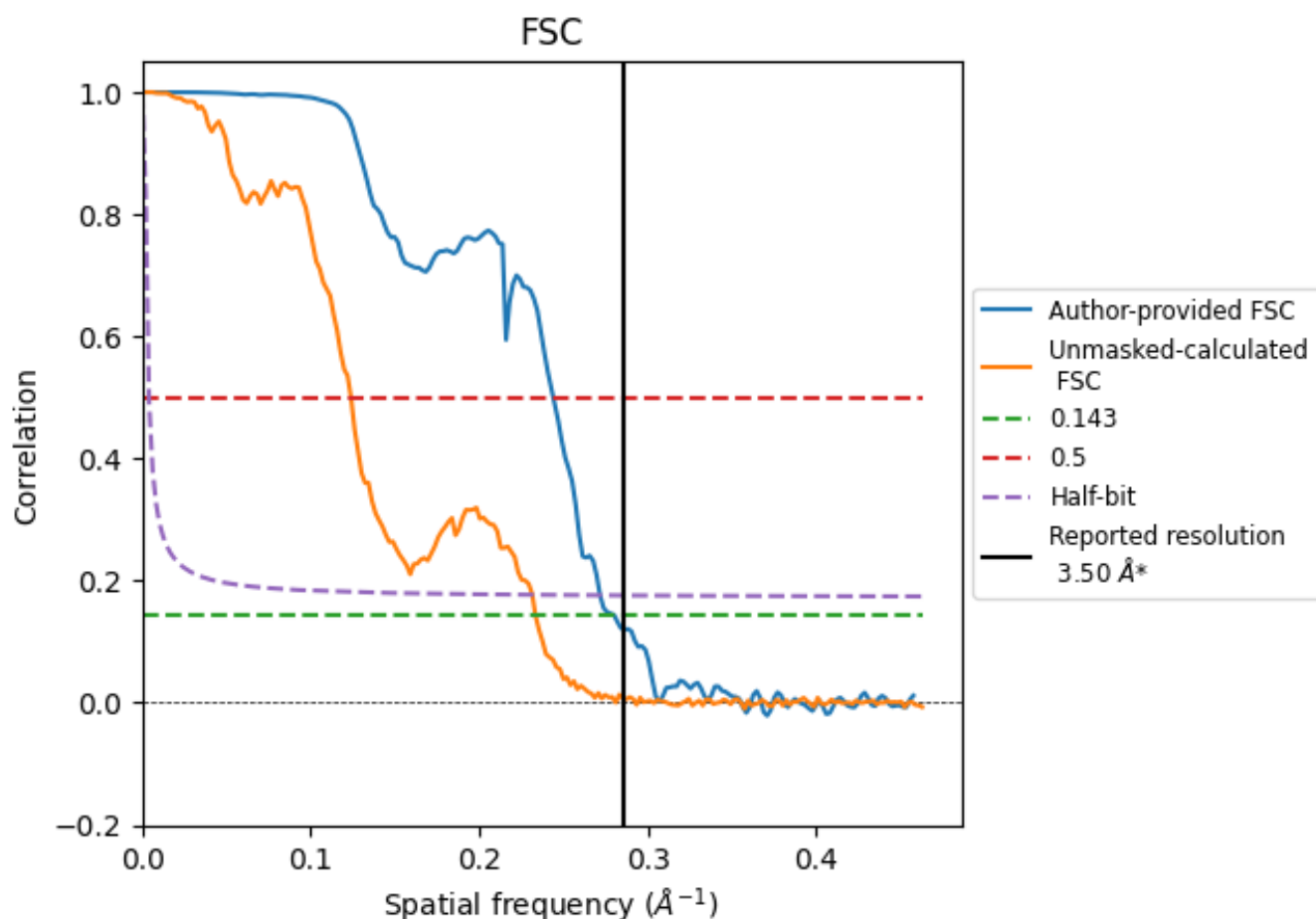


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.286 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

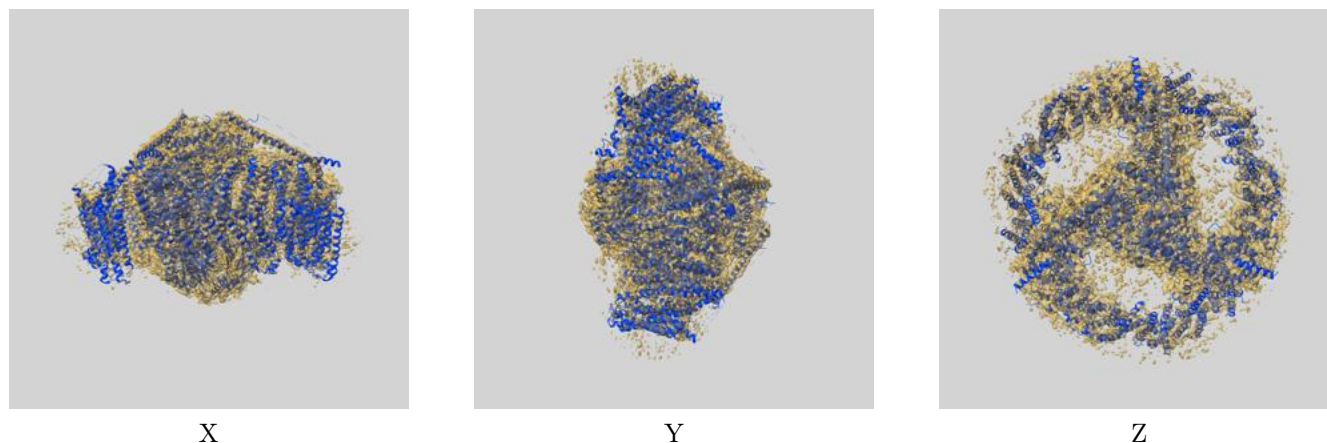
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.57	4.10	3.68
Unmasked-calculated*	4.28	8.06	4.32

*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 4.28 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

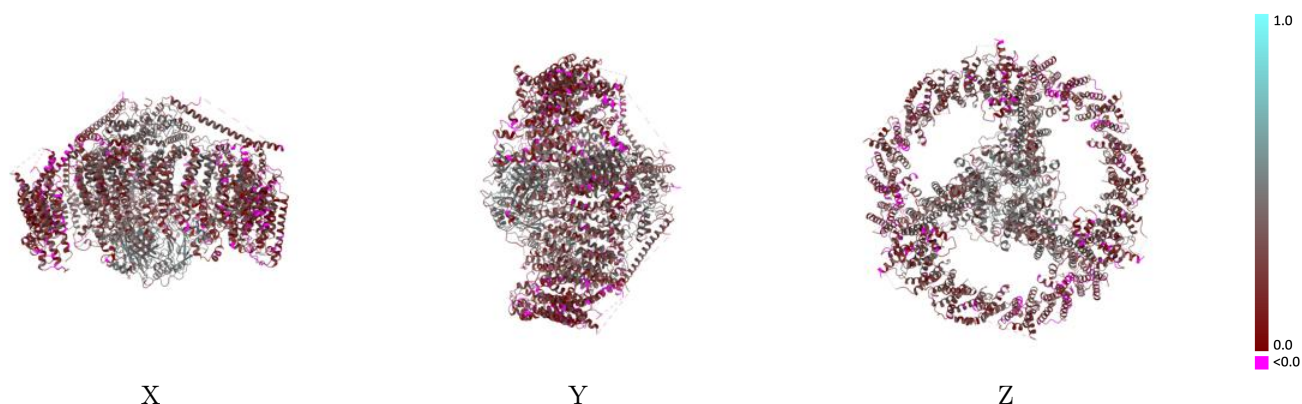
This section contains information regarding the fit between EMDB map EMD-74281 and PDB model 9ZIS. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0561 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](#)

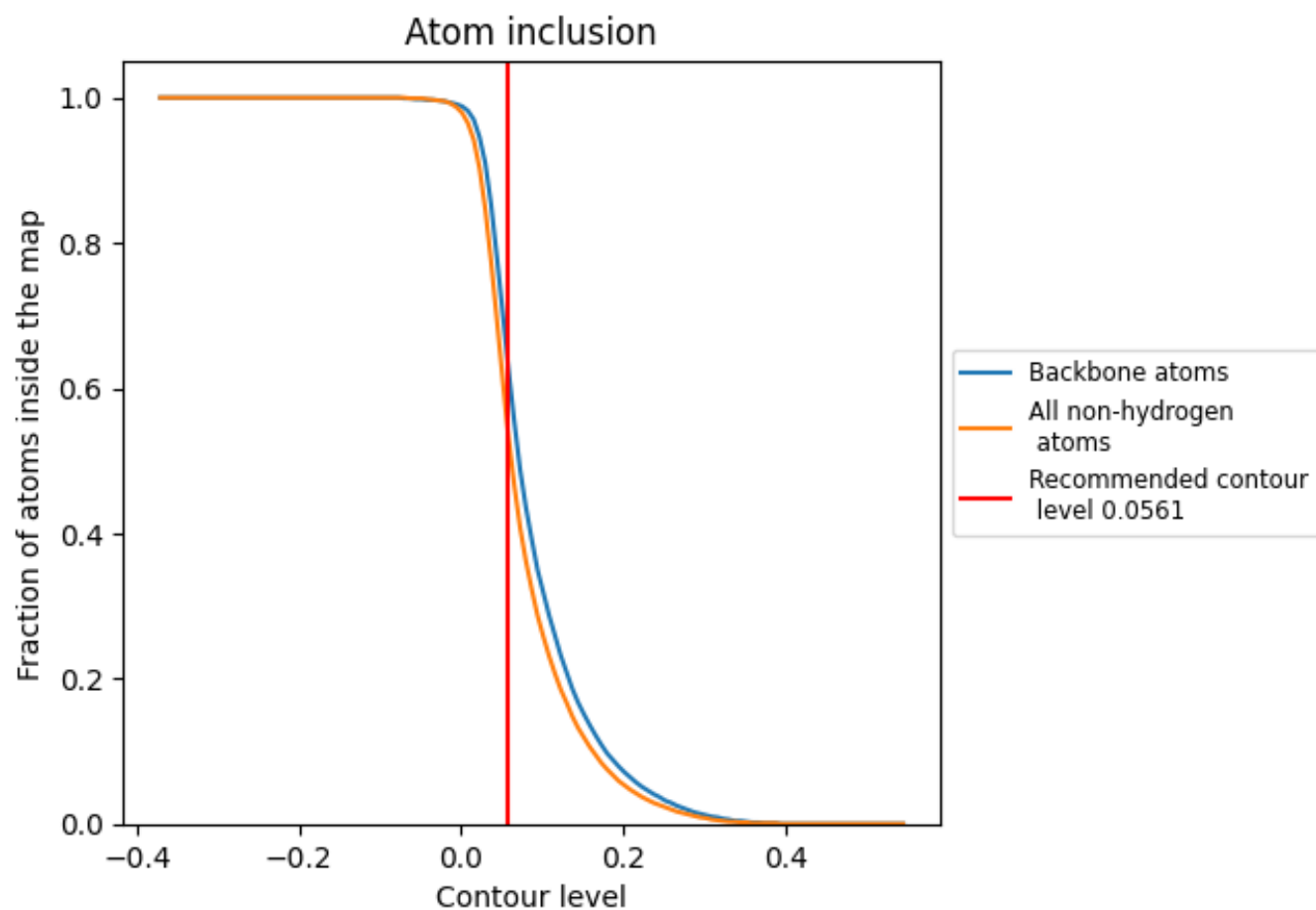


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 55% 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 (0.0561) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5540	0.3000
A	0.5540	0.2990
B	0.5530	0.3010
C	0.5540	0.3000

