



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 09:21 AM UTC

PDB ID : 8SNO / pdb_00008sno
EMDB ID : EMD-40631
Title : Structure of mature human ADAM17/iRhom2 sheddase complex, conformation 2
Authors : Zhao, H.; Dai, Y.; Wang, Y.; Lee, C.H.
Deposited on : 2023-04-27
Resolution : 2.78 Å(reported)

This is a Full wwPDB EM Validation 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

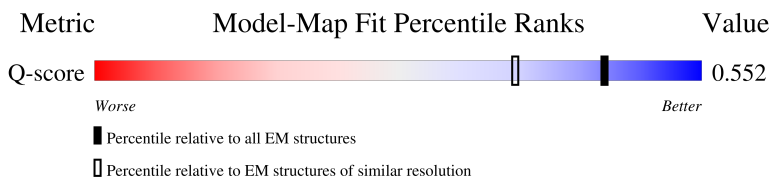
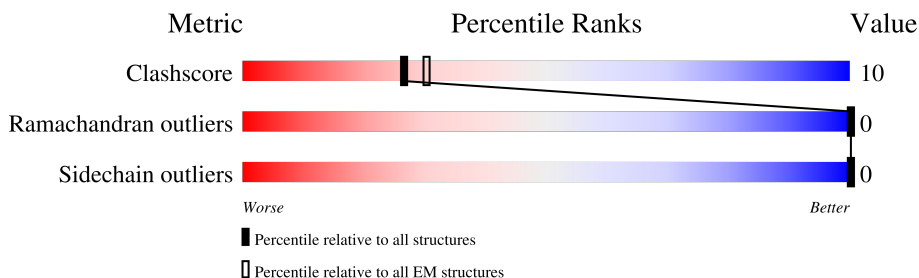
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.78 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	10754 (2.28 - 3.28)

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	610	 6% 25% 12% 63%
2	B	827	 48% 11% 41%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5685 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 Disintegrin and metalloproteinase domain-containing protein 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	227	Total	C	N	O	S	0	0
			1745	1071	298	347	29		

- Molecule 2 is a protein called Inactive rhomboid protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	491	Total	C	N	O	S	0	0
			3939	2564	663	686	26		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Ca	0
			1	1	

ARG	PRO	ARG	ASP	E418	D523	L698
TYR	PRO	SER	GLY	E423	E528	L712
GLY	THR	PHE	VAL	I423	E529	L715
ARG	PRO	ARG	ALA	E426	P530	K718
LEU	GLY	PHE	ILE	A531	A531	
LYS	VAL	PRO	LEU	I435	D540	L728
ALA	SER	PHE	LYS	G441	P546	I732
SER	LEU	GLU	GLY	P446	E550	L736
CYS	THR	GLN	TYR	K450	R553	P737
ARG	PHE	ASP	ARG	K450	L560	K738
LEU	THR	VAL	ALA	Q453	E561	I742
GLU	SER	ASP	PRO	E455	H562	I762
LEU	THR	VAL	PRO	V458	I566	K769
GLY	SER	THR	PRO	R462	G568	K772
ALA	TYR	ASP	ARG	E465	R569	R773
PRO	SER	PHE	GLY	V472	K576	T808
PRO	GLN	ARG	ARG	Q473	E580	S814
ALA	THR	SER	SER	N474	I581	R815
PRO	ARG	THR	LYS	D475	T582	V825
GLY	LEU	PHE	ILE	I480	H590	L826
GLY	PRO	GLN	ALA	Q481	F594	H827
THR	ARG	ARG	ALA	T482	S602	
GLY	ARG	SER	LYS	D486	K609	
THR	ARG	THR	LYS	V497	L613	
GLU	LYS	GLU	VAL	Q498	L614	
ARG	ARG	SER	VAL	D499	P615	
LEU	MET	GLU	GLU	D500	L628	
PRO	GLY	PRO	PRO	T501	F647	
LYS	VAL	SER	PRO	G502	Q648	
PRO	ALA	ALA	LEU	M505	D654	
LYS	LEU	LEU	LEU	D506	L685	
ILE	GLY	ARG	SER	K507	E656	
VAL	ARG	ALA	ALA	S508	N676	
ASP	PHE	ARG	TYR	L510	L683	
PRO	VAL	ARG	PHE	D509	P684	
GLY	ASP	GLY	GLY	L510	P691	
ARG	ALA	ILE	ILE	G511	Q695	
GLU	THR	PRO	PRO	Q512		
LEU	GLY	HIS	HIS	R513		
MET	GLN	SER	R514	T515		
ASP	ARG	ALA	S516	G517		
ARG	CYS	SER	A518	V519		
PRO	ARG	PRO	H404	C520		
HIS	VAL	VAL	V405	H521		
PRO	VAL	SER	R412	Q522		
LYS	LYS	PRO				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	325764	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	66.6	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.664	Depositor
Minimum map value	-2.852	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.55	Depositor
Map size ($\text{\AA}$)	343.3248, 343.3248, 343.3248	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8253, 0.8253, 0.8253	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.31	0/1773	0.57	1/2390 (0.0%)
2	B	0.20	0/4055	0.36	1/5517 (0.0%)
All	All	0.24	0/5828	0.43	2/7907 (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	483	VAL	CB-CA-C	-7.28	101.24	111.28
2	B	518	ALA	N-CA-C	-7.10	95.13	107.20

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	1745	0	1637	57	0
2	B	3939	0	3875	63	0
3	A	1	0	0	0	0
All	All	5685	0	5512	112	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 10.

All (112) 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)
2:B:506:ASP:HB3	2:B:509:ASP:HB2	1.60	0.84
1:A:651:ARG:HH12	2:B:615:PRO:HB2	1.52	0.74
1:A:672:ILE:HD12	1:A:672:ILE:H	1.56	0.70
2:B:712:LEU:HD11	2:B:762:ILE:HD11	1.75	0.68
2:B:465:GLU:OE2	2:B:602:SER:OG	2.13	0.64
1:A:697:LYS:O	1:A:701:GLN:HG2	1.97	0.64
2:B:502:GLY:HA3	2:B:514:ARG:O	1.98	0.63
2:B:522:GLN:N	2:B:562:MET:HE1	2.14	0.63
1:A:584:ARG:NH1	1:A:585:GLU:OE2	2.33	0.61
2:B:502:GLY:O	2:B:513:LYS:HE3	2.01	0.61
1:A:694:VAL:HA	1:A:697:LYS:HE2	1.84	0.59
1:A:699:ASP:O	1:A:703:GLU:HG2	2.03	0.59
1:A:625:ARG:NH2	2:B:550:GLU:OE1	2.35	0.58
2:B:520:CYS:O	2:B:562:MET:HE2	2.03	0.57
1:A:651:ARG:NH2	2:B:615:PRO:O	2.36	0.56
2:B:376:THR:OG1	2:B:656:GLU:OE1	2.20	0.56
2:B:523:ASP:HB2	2:B:562:MET:HE3	1.87	0.56
1:A:501:CYS:HA	1:A:509:LYS:HD2	1.88	0.55
1:A:549:THR:HB	1:A:552:SER:HB3	1.87	0.55
2:B:441:GLY:HA2	2:B:613:LEU:HD11	1.87	0.55
1:A:501:CYS:HB2	1:A:512:VAL:HG21	1.88	0.55
1:A:696:LYS:O	1:A:700:LYS:HD3	2.07	0.55
2:B:338:ARG:NE	2:B:654:ASP:OD1	2.39	0.55
2:B:522:GLN:NE2	2:B:546:PRO:O	2.32	0.54
2:B:383:HIS:CE1	2:B:648:GLN:HE22	2.26	0.54
1:A:569:ASP:OD2	2:B:531:ALA:HB3	2.08	0.54
2:B:715:ARG:HE	2:B:718:LYS:HD2	1.72	0.54
1:A:678:VAL:O	1:A:682:ILE:HG13	2.09	0.53
1:A:580:PRO:HB2	1:A:583:GLU:OE1	2.10	0.52
2:B:458:VAL:O	2:B:462:ARG:HG2	2.09	0.52
2:B:580:GLU:HG3	2:B:582:THR:HG23	1.90	0.52
1:A:693:CYS:O	1:A:697:LYS:HG3	2.10	0.52
2:B:401:PHE:HB3	2:B:738:TRP:CZ2	2.45	0.52
2:B:762:ILE:O	2:B:772:LYS:NZ	2.42	0.52
2:B:516:SER:HB3	2:B:540:ASP:O	2.10	0.51
2:B:529:GLU:HB3	2:B:550:GLU:HB3	1.91	0.51
2:B:505:MET:N	2:B:512:GLN:O	2.41	0.51
1:A:568:LEU:HD12	2:B:528:GLU:HG2	1.94	0.50
1:A:694:VAL:O	1:A:698:LEU:HD23	2.12	0.49
1:A:485:GLU:H	1:A:485:GLU:CD	2.20	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:483:VAL:CG2	1:A:518:ASN:CG	2.85	0.49
2:B:446:PRO:HD3	2:B:684:PRO:O	2.12	0.49
2:B:472:VAL:HG11	2:B:560:LEU:HG	1.94	0.49
2:B:691:PRO:O	2:B:695:GLN:HG3	2.13	0.49
1:A:546:SER:OG	1:A:555:CYS:SG	2.71	0.48
1:A:480:ASN:HB2	2:B:474:ASN:HD22	1.78	0.48
1:A:483:VAL:HG13	1:A:489:CYS:HA	1.95	0.48
2:B:647:PHE:HE1	2:B:698:LEU:HD12	1.79	0.47
1:A:483:VAL:CG1	1:A:489:CYS:HA	2.44	0.47
1:A:491:PRO:HB2	1:A:496:LEU:HA	1.97	0.47
1:A:652:PHE:O	1:A:656:ILE:HG12	2.15	0.47
1:A:636:ASP:OD1	1:A:640:LYS:N	2.46	0.47
1:A:527:PHE:CE1	1:A:553:SER:HB2	2.50	0.47
1:A:685:ILE:HB	1:A:686:PRO:HD3	1.96	0.46
2:B:728:LEU:O	2:B:732:ILE:HG12	2.15	0.46
1:A:603:CYS:HA	1:A:613:PRO:HA	1.96	0.46
2:B:480:ILE:HG23	2:B:482:THR:HG23	1.97	0.46
1:A:484:ASP:H	1:A:487:GLU:CD	2.24	0.46
2:B:510:LEU:H	2:B:510:LEU:HD22	1.80	0.46
2:B:412:ARG:HG3	2:B:418:GLU:HB2	1.98	0.46
2:B:628:LEU:O	2:B:676:ASN:ND2	2.35	0.46
1:A:480:ASN:HD22	2:B:474:ASN:ND2	2.14	0.45
1:A:591:CYS:SG	1:A:592:ALA:N	2.89	0.45
2:B:609:LYS:HE3	2:B:609:LYS:HB3	1.77	0.45
2:B:505:MET:O	2:B:505:MET:HG2	2.17	0.45
1:A:487:GLU:HB2	1:A:506:CYS:SG	2.57	0.45
2:B:736:LEU:HB3	2:B:738:TRP:HE3	1.82	0.45
1:A:483:VAL:HG22	1:A:518:ASN:OD1	2.17	0.45
1:A:491:PRO:HG3	1:A:502:CYS:HB3	1.98	0.44
2:B:522:GLN:C	2:B:562:MET:HE1	2.42	0.44
1:A:513:GLN:NE2	1:A:526:GLN:OE1	2.50	0.44
1:A:597:ASP:OD1	1:A:597:ASP:N	2.51	0.44
2:B:497:TRP:CD2	2:B:517:GLY:O	2.69	0.44
1:A:485:GLU:HG2	1:A:486:GLY:N	2.32	0.44
1:A:490:ASP:HA	1:A:491:PRO:HD3	1.86	0.44
2:B:769:LYS:HG2	2:B:773:ARG:NH1	2.33	0.44
1:A:567:CYS:HB3	1:A:568:LEU:H	1.55	0.44
1:A:479:GLY:H	1:A:490:ASP:CG	2.26	0.43
1:A:656:ILE:O	1:A:659:LEU:HD23	2.19	0.43
2:B:435:ILE:H	2:B:435:ILE:HD12	1.83	0.43
1:A:619:GLN:HG3	1:A:620:LYS:H	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:482:THR:HB	2:B:486:ASP:HB2	2.01	0.43
2:B:576:LYS:HG3	2:B:826:LEU:HD11	2.01	0.43
1:A:584:ARG:HG3	1:A:585:GLU:OE1	2.18	0.43
1:A:578:CYS:SG	1:A:579:ILE:N	2.92	0.42
2:B:405:VAL:HG22	2:B:423:ILE:HG23	2.00	0.42
2:B:475:ASP:OD1	2:B:475:ASP:N	2.52	0.42
2:B:683:LEU:HD21	2:B:808:THR:HG21	2.01	0.42
2:B:355:ARG:HA	2:B:355:ARG:HD2	1.71	0.42
2:B:453:GLN:HE22	2:B:825:VAL:HA	1.85	0.42
1:A:564:ASP:HA	1:A:572:LYS:HB3	2.02	0.42
1:A:565:THR:HG22	1:A:573:CYS:HB3	2.01	0.42
1:A:482:ARG:NE	2:B:474:ASN:HD21	2.17	0.42
2:B:590:MET:HE3	2:B:590:MET:HB3	1.91	0.41
1:A:634:PHE:O	1:A:642:GLU:HG2	2.19	0.41
2:B:404:HIS:HB2	2:B:426:GLU:HG2	2.01	0.41
1:A:483:VAL:HG12	1:A:484:ASP:O	2.21	0.41
2:B:344:VAL:N	2:B:654:ASP:OD2	2.53	0.41
2:B:498:GLN:N	2:B:501:THR:OG1	2.52	0.41
1:A:491:PRO:HG2	1:A:496:LEU:HD12	2.02	0.41
2:B:742:ILE:HG12	2:B:808:THR:HB	2.02	0.41
2:B:387:THR:O	2:B:391:ILE:HG12	2.20	0.41
2:B:736:LEU:HB3	2:B:738:TRP:CE3	2.55	0.41
1:A:478:CYS:HA	1:A:490:ASP:OD2	2.21	0.41
1:A:589:GLU:HG2	1:A:605:ARG:HB3	2.02	0.41
2:B:498:GLN:C	2:B:515:THR:HG22	2.45	0.41
2:B:566:ILE:O	2:B:568:GLY:N	2.54	0.41
2:B:569:ARG:HB2	2:B:594:PHE:CZ	2.56	0.41
1:A:480:ASN:O	1:A:481:SER:C	2.65	0.40
1:A:488:GLU:OE1	1:A:508:LEU:HB2	2.21	0.40
1:A:698:LEU:HD13	1:A:698:LEU:HA	1.96	0.40
2:B:450:LYS:HE2	2:B:455:GLU:OE1	2.21	0.40

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	225/610 (37%)	212 (94%)	13 (6%)	0	100	100
2	B	489/827 (59%)	463 (95%)	26 (5%)	0	100	100
All	All	714/1437 (50%)	675 (94%)	39 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	202/539 (38%)	202 (100%)	0	100	100
2	B	429/721 (60%)	429 (100%)	0	100	100
All	All	631/1260 (50%)	631 (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. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	701	GLN
2	B	347	ASN
2	B	362	GLN
2	B	371	HIS
2	B	383	HIS
2	B	404	HIS
2	B	474	ASN
2	B	551	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

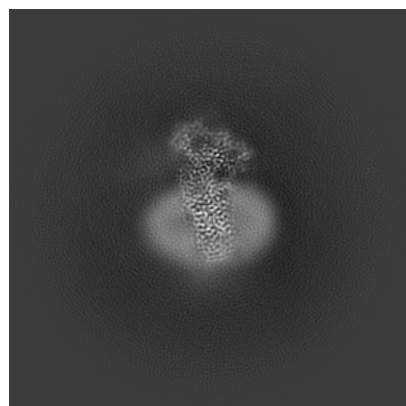
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40631. These allow visual inspection of the internal detail of the map and identification of artifacts.

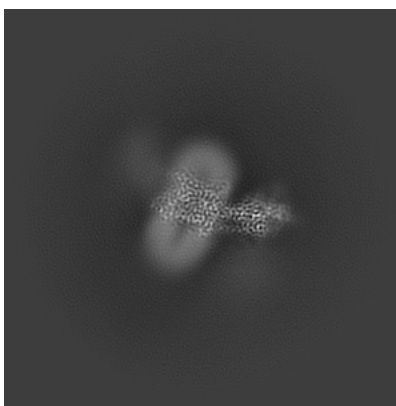
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

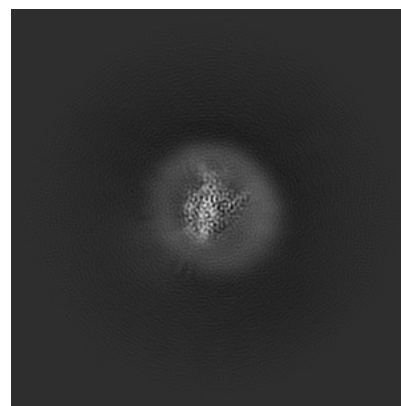
6.1.1 Primary map



X

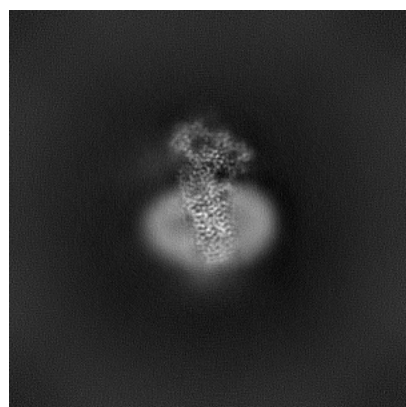


Y

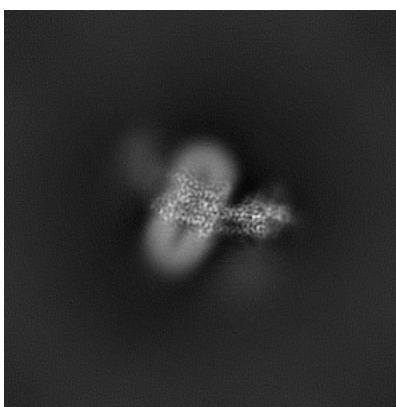


Z

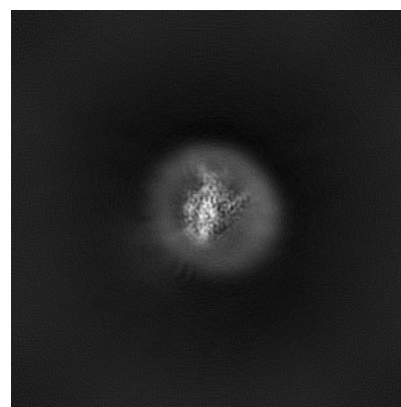
6.1.2 Raw map



X



Y

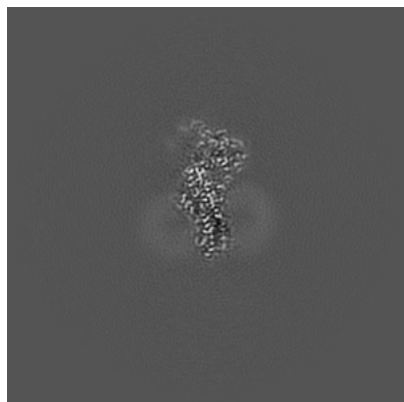


Z

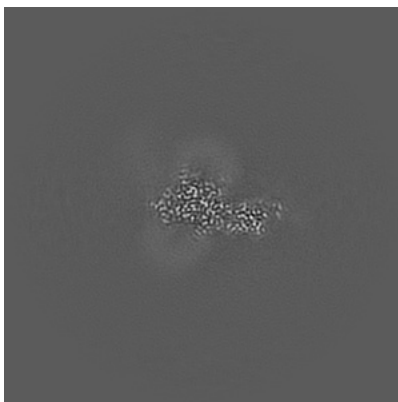
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

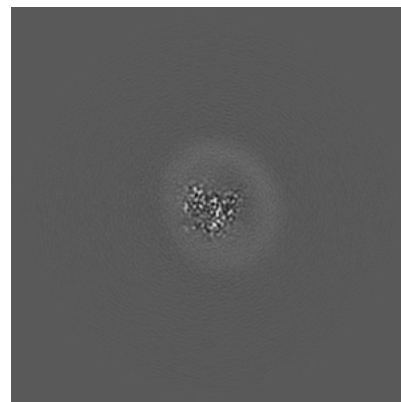
6.2.1 Primary map



X Index: 208

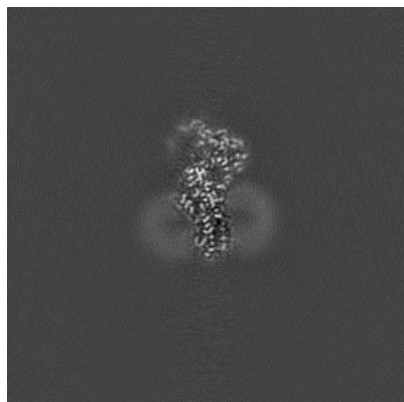


Y Index: 208

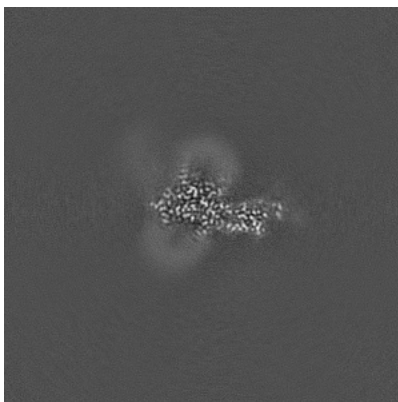


Z Index: 208

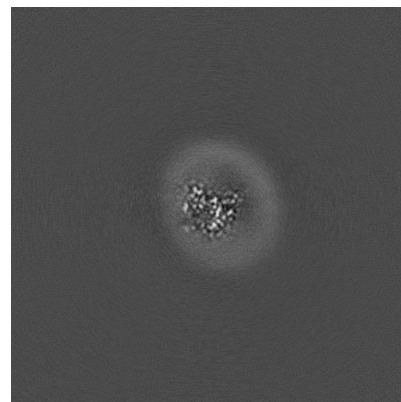
6.2.2 Raw map



X Index: 208



Y Index: 208

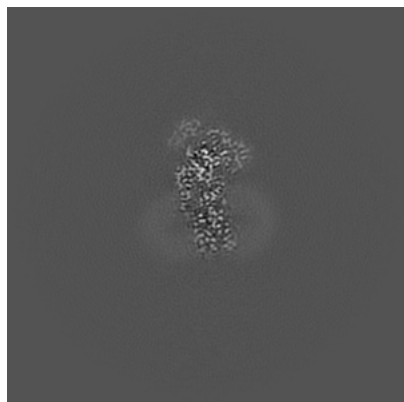


Z Index: 208

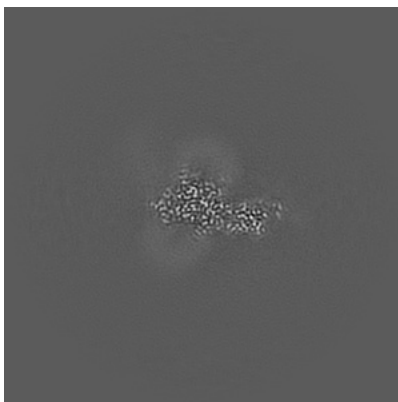
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

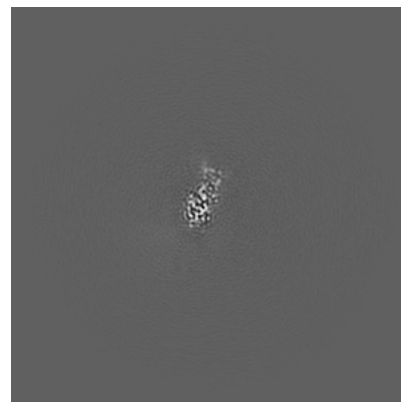
6.3.1 Primary map



X Index: 202

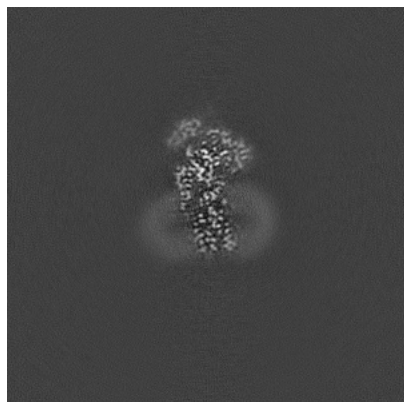


Y Index: 208

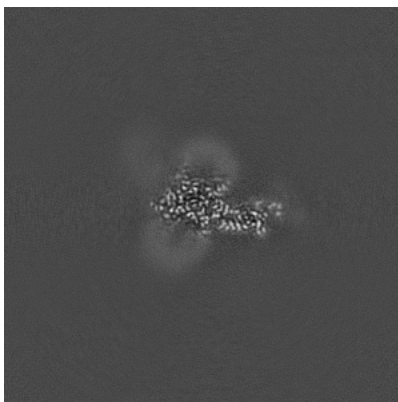


Z Index: 259

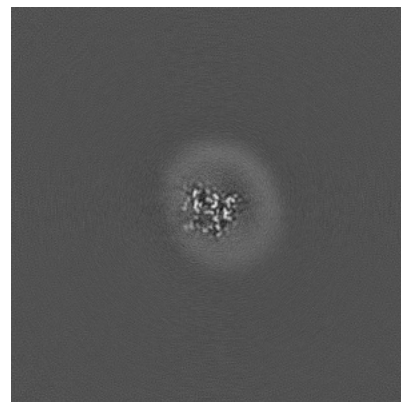
6.3.2 Raw map



X Index: 202



Y Index: 210

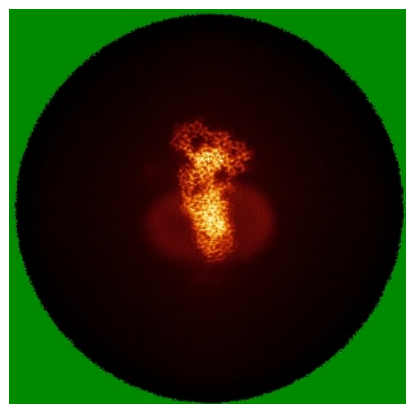


Z Index: 210

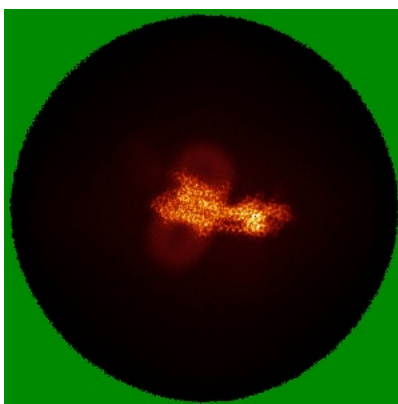
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

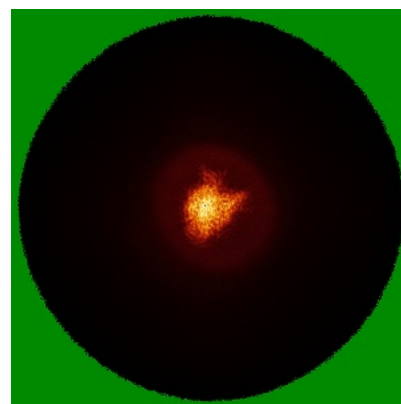
6.4.1 Primary map



X

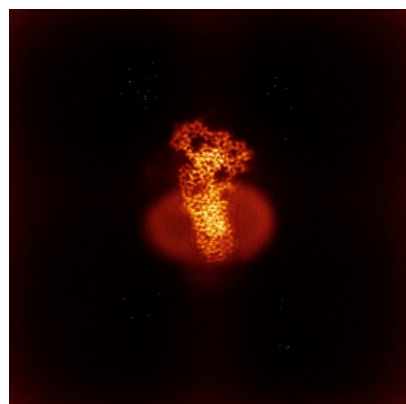


Y

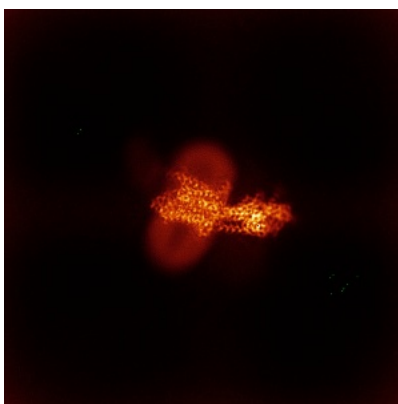


Z

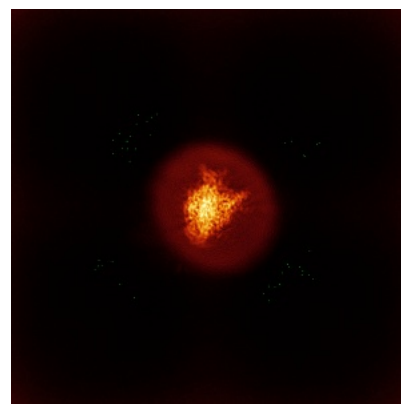
6.4.2 Raw map



X



Y

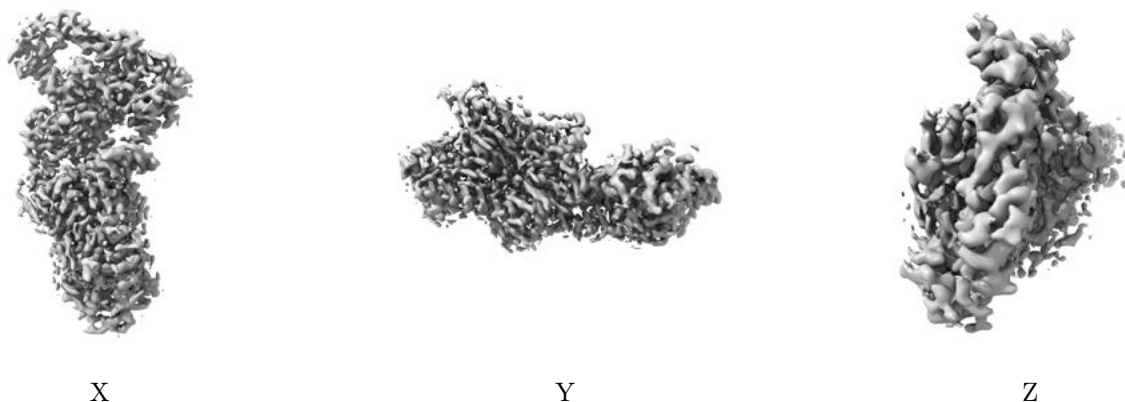


Z

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

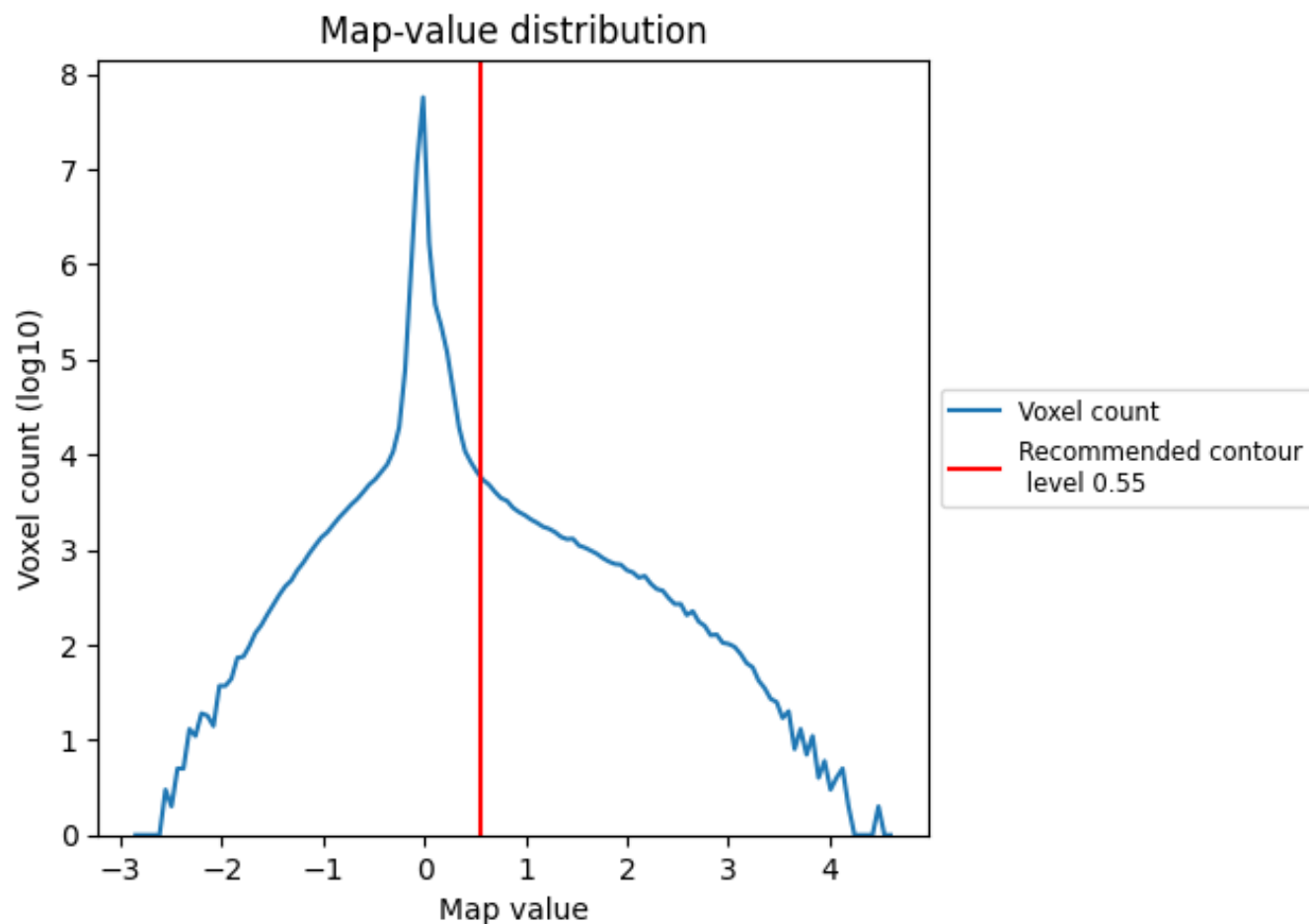
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

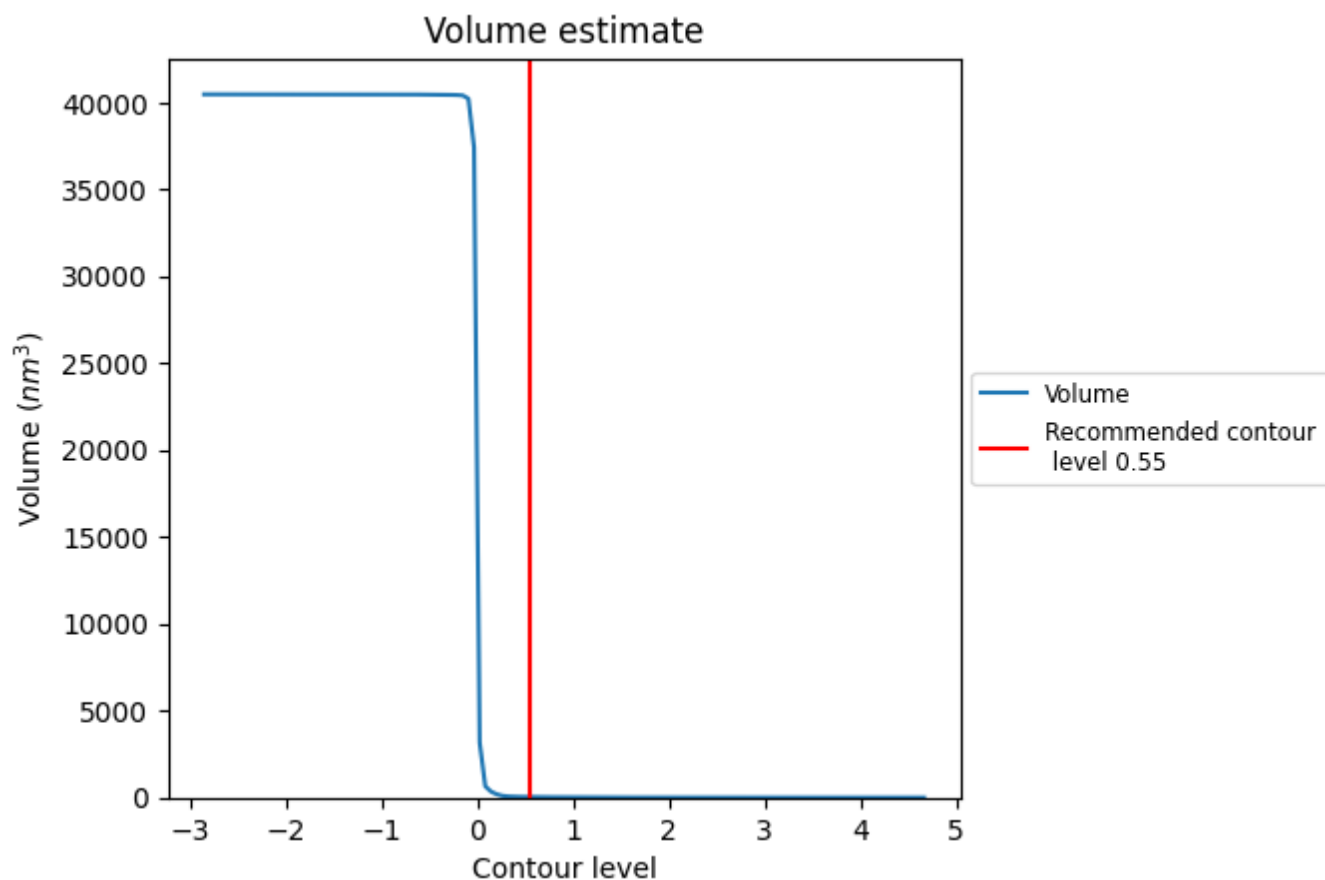
This section contains the results of statistical analysis of the map.

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.

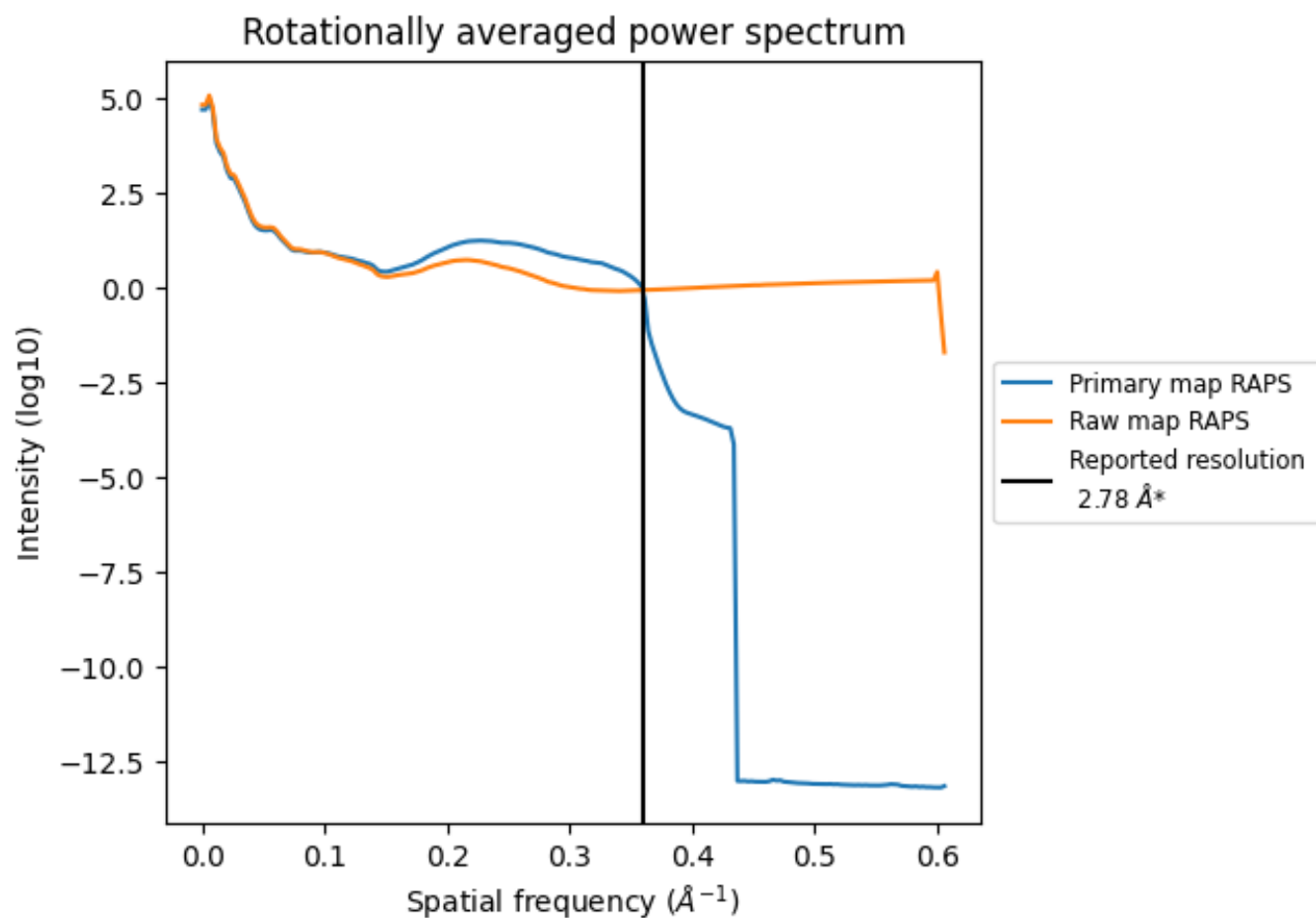
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 32 nm³; this corresponds to an approximate mass of 29 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 ⓘ

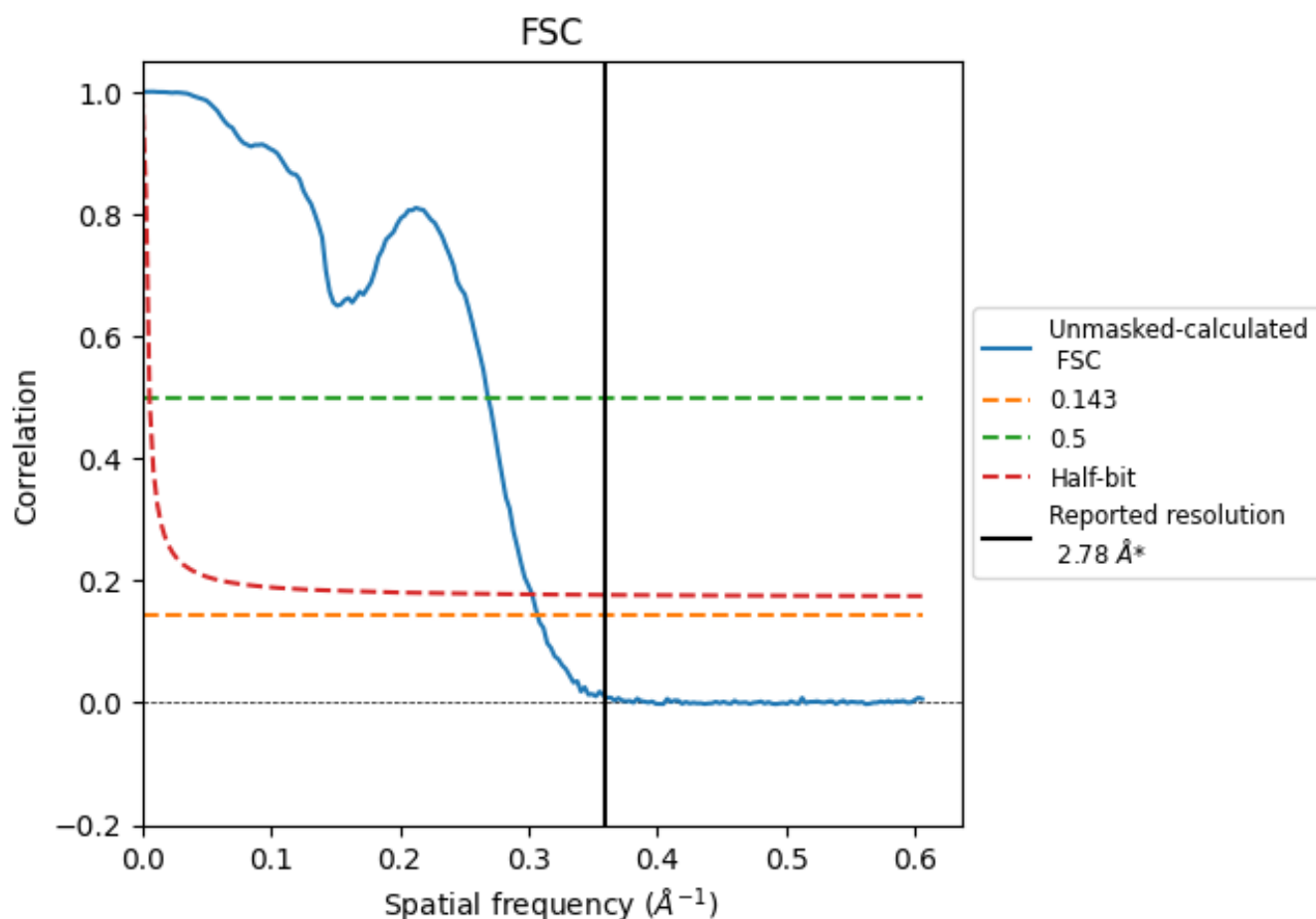


*Reported resolution corresponds to spatial frequency of 0.360 Å⁻¹

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 0.360 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.78	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.26	3.72	3.30

*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 3.26 differs from the reported value 2.78 by more than 10 %

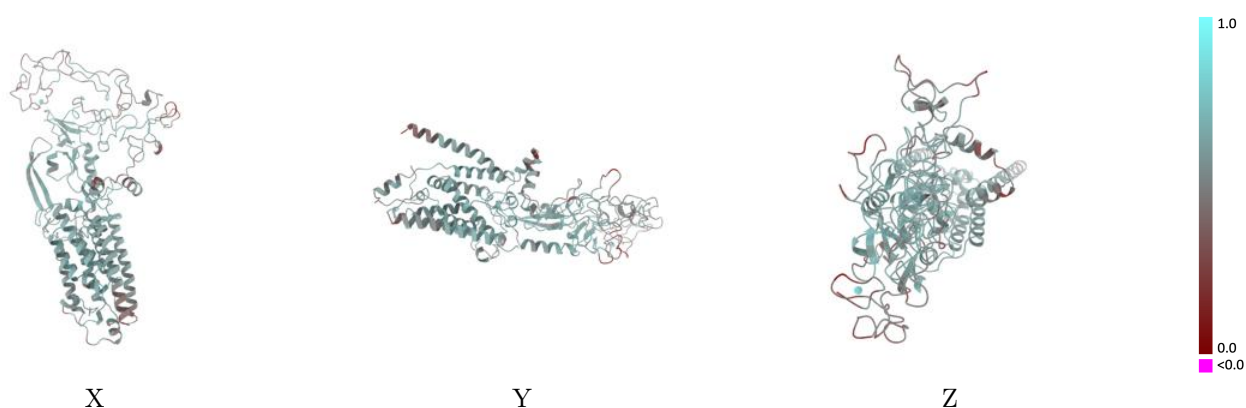
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-40631 and PDB model 8SNO. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

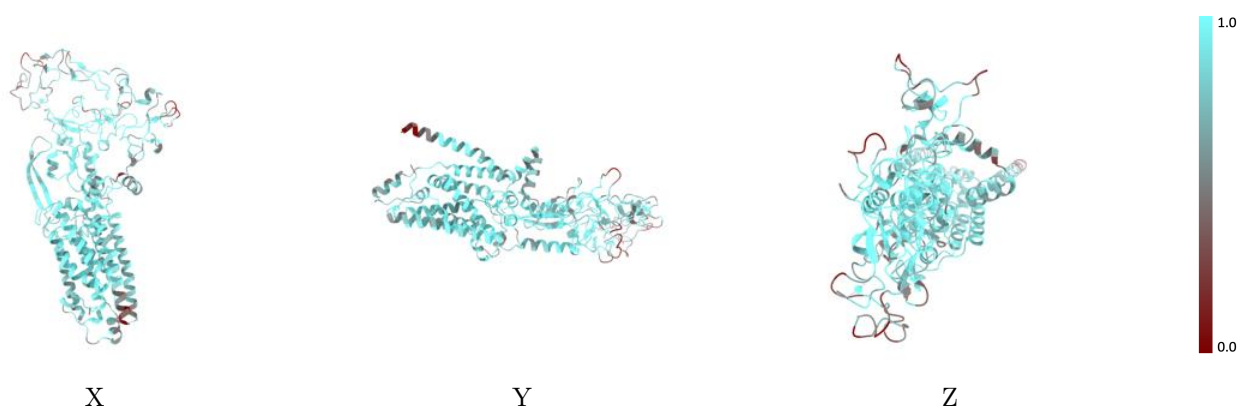
This section was not generated.

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



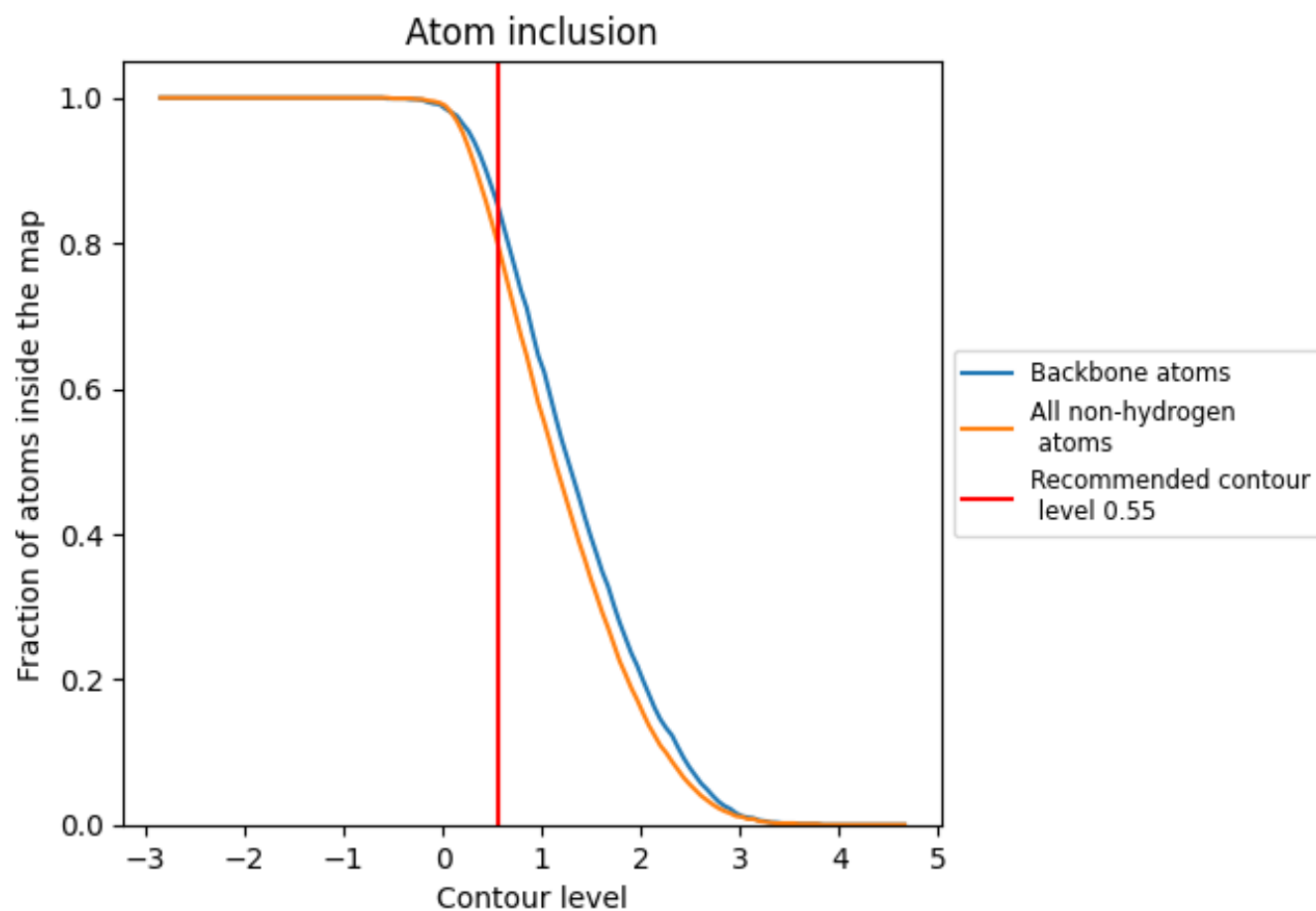
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.55).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8010	0.5520
A	0.6520	0.4820
B	0.8680	0.5830

