



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 04:09 AM UTC

PDB ID : 8E2H / pdb_00008e2h
EMDB ID : EMD-27836
Title : Cryo-EM structure of C-terminal arm of BIRC6 (from local refinement 4)
Authors : Hunkeler, M.; Fischer, E.S.
Deposited on : 2022-08-15
Resolution : 2.30 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

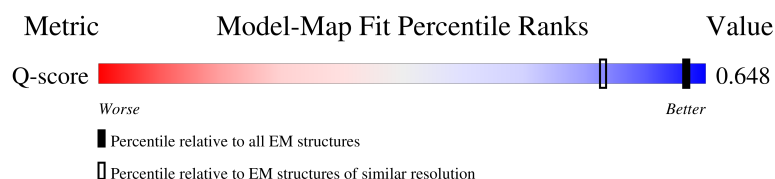
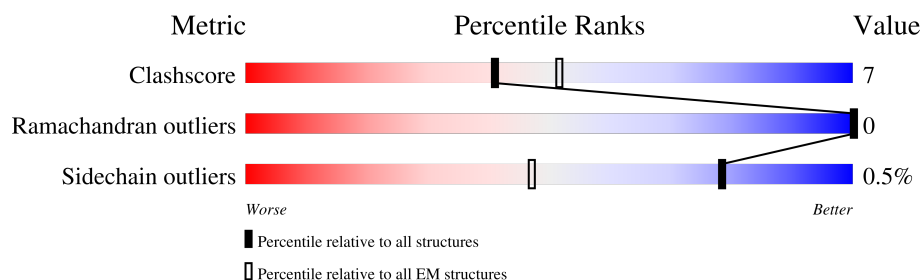
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4254 (1.80 - 2.80)

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

Mol	Chain	Length	Quality of chain
1	A	4888	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10412 atoms, of which 5280 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 Baculoviral IAP repeat-containing protein 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	656	Total	C	H	N	O	S	0	0
			10372	3280	5280	863	912	37		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-30	MET	-	expression tag	UNP Q9NR09
A	-29	ASP	-	expression tag	UNP Q9NR09
A	-28	TYR	-	expression tag	UNP Q9NR09
A	-27	LYS	-	expression tag	UNP Q9NR09
A	-26	ASP	-	expression tag	UNP Q9NR09
A	-25	ASP	-	expression tag	UNP Q9NR09
A	-24	ASP	-	expression tag	UNP Q9NR09
A	-23	ASP	-	expression tag	UNP Q9NR09
A	-22	LYS	-	expression tag	UNP Q9NR09
A	-21	LEU	-	expression tag	UNP Q9NR09
A	-20	ALA	-	expression tag	UNP Q9NR09
A	-19	ALA	-	expression tag	UNP Q9NR09
A	-18	ALA	-	expression tag	UNP Q9NR09
A	-17	ASN	-	expression tag	UNP Q9NR09
A	-16	SER	-	expression tag	UNP Q9NR09
A	-15	SER	-	expression tag	UNP Q9NR09
A	-14	ILE	-	expression tag	UNP Q9NR09
A	-13	ASP	-	expression tag	UNP Q9NR09
A	-12	LEU	-	expression tag	UNP Q9NR09
A	-11	ILE	-	expression tag	UNP Q9NR09
A	-10	SER	-	expression tag	UNP Q9NR09
A	-9	THR	-	expression tag	UNP Q9NR09
A	-8	SER	-	expression tag	UNP Q9NR09
A	-7	LEU	-	expression tag	UNP Q9NR09
A	-6	TYR	-	expression tag	UNP Q9NR09
A	-5	LYS	-	expression tag	UNP Q9NR09
A	-4	LYS	-	expression tag	UNP Q9NR09
A	-3	ALA	-	expression tag	UNP Q9NR09

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q9NR09
A	-1	LEU	-	expression tag	UNP Q9NR09
A	0	THR	-	expression tag	UNP Q9NR09
A	1332	VAL	LEU	conflict	UNP Q9NR09

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	AltConf
2	A	40	Total O 40 40	0







LEU	LEU	PRO	LEU	ASP	ALA	LYS	R4441
LYS	LYS	CYS	GLN	VAL	ASN	LYS	T4442
LEU	VAL	PHE	VAL	TYR	SER	ALA	C4443
PRO	LEU	LYS	LEU	PHE	ALA	MET	V4444
CYS	VAL	GLU	VAL	PRO	ALA	LYS	T4445
PRO	SER	VAL	SER	GLN	ARG	LYS	D4446
GLY	VAL	ILE	GLN	ASP	ARG	LYS	R4450
GLU	GLY	HIS	GLN	TYR	ALA	LYS	L4451
LEU	LEU	LYS	SER	PRO	ARG	PRO	R4452
ASP	LEU	HIS	LEU	SER	LEU	LEU	S4453
PRO	ILE	PHE	SER	SER	ALA	SER	R4454
ASP	TYR	TYR	PRO	PRO	GLN	VAL	K4454
THR	VAL	LYS	VAL	PRO	GLN	LEU	R4455
ASP	GLU	LYS	LEU	VAL	ALA	LYS	GLU
ASP	ALA	ARG	PRO	ASN	THR	SER	ASN
ALA	VAL	GLU	TYR	LEU	LEU	GLU	VAL
PRO	GLU	ILE	PHE	GLU	SER	GLU	LYS
VAL	VAL	MET	ASN	THR	THR	LYS	LYS
CYS	CYS	ALA	GLU	THR	SER	TYR	GLY
ARG	ARG	GLN	PRO	GLY	LEU	VAL	VAL
ALA	ALA	CYS	GLY	GLY	PRO	ALA	LYS
THR	THR	GLU	TYR	HIS	LEU	VAL	ASP
THR	GLY	GLU	GLU	SER	SER	MET	PRO
GLY	ALA	TRP	ARG	VAL	SER	LYS	ASP
ALA	ALA	ILE	SER	ARG	SER	LYS	ALA
GLU	GLU	ALA	GLY	PHE	SER	LEU	SER
THR	THR	ASP	GLY	ASN	GLN	PHE	ASP
GLU	GLU	ILE	THR	PRO	VAL	GLN	GLN
THR	THR	ILE	GLN	ASN	PHE	ASP	GLU
LEU	LEU	GLN	PRO	ASN	VAL	THR	PRO
MET	GLN	GLN	SER	LEU	VAL	THR	GLU
HIS	HIS	TYR	GLY	TYR	ARG	PHE	GLU
ASP	ASP	SER	THR	ASN	GLU	ASP	C4473
GLN	GLN	LYS	GLN	ASP	ASP	MET	GLU
VAL	VAL	ASP	SER	GLY	GLU	VAL	L4476
LYS	LYS	LYS	SER	LYS	GLU	SER	T4477
PRO	PRO	ARG	ARG	VAL	ARG	GLU	V4478
SER	SER	VAL	GLU	CYS	LEU	ASP	P4479
SER	SER	GLY	TYR	LEU	LEU	GLU	D4480
LYS	LYS	ARG	ASP	SER	ILE	ASP	I4481
SER	SER	THR	GLY	ILE	MET	GLY	LYS
LEU	LEU	MET	ASN	LEU	LYS	LYS	T4484
GLU	GLU	SER	ILE	ASN	VAL	LEU	GLU
PRO	PRO	HIS	ARG	THR	THR	GLY	V4488
SER	SER	HIS	GLN	TRP	ILE	PHE	Y4489
ASP	ASP	ALA	ALA	HIS	THR	LYS	T4493
PHE	PHE	ALA	THR	GLY	GLY	VAL	S4494
GLN	GLN	ALA	VAL	ARG	PRO	ASN	L4495
LEU	LEU	LYS	LYS	PRO	ALA	TYR	R4496
LYS	LYS	TRP	TRP	GLU	ASP	THR	Q4497
ARG	ARG	ALA	GLU	GLU	THR	TYR	SER
HIS	HIS	MET	LEU	LYS	PRO	SER	A4498
THR	THR	THR	GLU	ASN	ALA	GLN	R4499
ALA	ALA	ALA	GLN	PRO	ASN	VAL	GLN
GLN	GLN	GLN	ILE	GLN	GLY	LYS	LYS
LEU	LEU	LEU	ARG	THR	CYS	ASN	GLU
ARG	ARG	ARG	ASN	THR	PHE	ALA	LYS
GLU	GLU	GLU	SER	SER	ALA	LYS	LYS
GLU	GLU	GLU	PRO	SER	GLU	ASP	LEU
LEU	LEU	LEU	SER	PHE	PHE	ASP	GLY
							GLU
							TYR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	2232961	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 ($e^-/\text{\AA}^2$)	52.5	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	6.219	Depositor
Minimum map value	-4.074	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.068	Depositor
Recommended contour level	0.825	Depositor
Map size (Å)	422.4, 422.4, 422.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.88, 0.88, 0.88	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	0.16	0/5186	0.33	0/7039

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5092	5280	5279	71	0
2	A	40	0	0	3	0
All	All	5132	5280	5279	71	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 7.

All (71) 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:A:3826:LEU:HD12	1:A:3873:VAL:HG11	1.54	0.87
1:A:3981:MET:O	1:A:3982:THR:OG1	1.98	0.81
1:A:4063:GLU:OE1	1:A:4063:GLU:N	2.19	0.74
1:A:4489:TYR:O	1:A:4493:THR:HG23	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3975:GLN:OE1	1:A:4061:LEU:HD11	1.96	0.66
1:A:4311:THR:OG1	1:A:4314:ARG:NH2	2.28	0.66
1:A:4230:ASP:OD2	1:A:4231:GLY:N	2.30	0.64
1:A:4442:THR:O	1:A:4446:THR:HG23	1.99	0.62
1:A:3809:ARG:NH1	1:A:4189:LEU:O	2.32	0.60
1:A:4412:LEU:HD13	1:A:4488:VAL:HG13	1.83	0.60
1:A:4484:THR:HG21	2:A:4932:HOH:O	2.01	0.59
1:A:3624:LYS:NZ	1:A:3628:ASP:OD2	2.33	0.58
1:A:3716:LEU:HD12	1:A:3784:VAL:HG12	1.86	0.58
1:A:4254:LEU:HD13	1:A:4319:HIS:HB3	1.85	0.58
1:A:3824:MET:SD	1:A:3983:LEU:HD22	2.44	0.58
1:A:3870:LEU:O	1:A:3874:SER:N	2.36	0.57
1:A:4396:LEU:HD11	1:A:4481:ILE:HG13	1.88	0.56
1:A:3642:PHE:CE2	1:A:3683:VAL:HG21	2.42	0.54
1:A:3693:VAL:HG23	1:A:3699:MET:HG2	1.89	0.54
1:A:4440:MET:O	1:A:4444:VAL:HG23	2.07	0.54
1:A:3443:ASP:HB2	1:A:3444:PRO:HD2	1.90	0.53
1:A:4399:LEU:HB2	2:A:4932:HOH:O	2.08	0.53
1:A:4157:SER:OG	1:A:4210:PRO:O	2.26	0.52
1:A:4224:THR:O	1:A:4235:ARG:NH1	2.42	0.52
1:A:4495:LEU:C	1:A:4495:LEU:HD23	2.35	0.51
1:A:3676:MET:HE2	1:A:3678:ILE:HD11	1.91	0.51
1:A:4441:LYS:O	1:A:4445:ASP:OD2	2.29	0.50
1:A:3965:PHE:HE1	1:A:4008:LEU:HD22	1.77	0.50
1:A:3837:ILE:HG22	1:A:3839:ALA:H	1.77	0.50
1:A:3564:MET:HB2	1:A:3566:ILE:HD12	1.93	0.49
1:A:4218:ARG:NH2	1:A:4397:GLU:OE2	2.43	0.49
1:A:4080:LEU:HD12	1:A:4171:ALA:HB1	1.94	0.48
1:A:3451:GLN:HG2	1:A:3516:LEU:HD22	1.95	0.48
1:A:3689:PHE:O	1:A:3693:VAL:HG22	2.13	0.47
1:A:3462:ARG:HG3	1:A:3524:LEU:HD11	1.97	0.47
1:A:4400:ARG:HD3	1:A:4484:THR:HG23	1.97	0.47
1:A:3448:ASP:OD2	1:A:3448:ASP:N	2.49	0.45
1:A:4161:PHE:HD2	1:A:4188:VAL:HG11	1.81	0.45
1:A:4226:LEU:H	1:A:4226:LEU:HD22	1.81	0.45
1:A:3981:MET:O	1:A:3982:THR:CB	2.64	0.45
1:A:4409:VAL:N	1:A:4410:PRO:HD2	2.32	0.45
1:A:3638:SER:HB3	1:A:3678:ILE:HG12	1.98	0.45
1:A:3443:ASP:O	1:A:3446:THR:HG22	2.16	0.45
1:A:3525:LEU:HD12	1:A:3549:MET:SD	2.57	0.45
1:A:4209:LEU:N	1:A:4210:PRO:HD2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3713:THR:HG22	1:A:3784:VAL:HG13	1.98	0.44
1:A:3867:SER:HB3	1:A:3979:ALA:HB1	1.98	0.44
1:A:3848:MET:HE1	1:A:4000:ARG:NE	2.32	0.44
1:A:4008:LEU:N	1:A:4008:LEU:HD23	2.32	0.44
1:A:3804:ILE:HD11	1:A:3809:ARG:HA	2.00	0.44
1:A:4160:ALA:HB2	1:A:4246:LEU:HD21	2.00	0.44
1:A:3760:GLU:O	1:A:3764:VAL:HG23	2.18	0.43
1:A:4413:LEU:HD12	1:A:4413:LEU:C	2.43	0.43
1:A:4478:VAL:N	1:A:4479:PRO:CD	2.82	0.43
1:A:4484:THR:CG2	2:A:4932:HOH:O	2.60	0.43
1:A:3432:ILE:HD11	1:A:3492:SER:HB3	2.01	0.43
1:A:3819:ASP:OD2	1:A:3820:GLU:N	2.52	0.43
1:A:3462:ARG:O	1:A:3466:MET:HG3	2.19	0.42
1:A:4362:GLU:O	1:A:4366:GLN:HG2	2.19	0.41
1:A:3865:THR:HA	1:A:3982:THR:HA	2.01	0.41
1:A:4400:ARG:HG3	1:A:4484:THR:HG23	2.02	0.41
1:A:4153:ILE:HG23	1:A:4153:ILE:O	2.20	0.41
1:A:3518:ASP:OD1	1:A:3518:ASP:N	2.51	0.41
1:A:4478:VAL:CG1	1:A:4479:PRO:HD3	2.51	0.41
1:A:3709:ASN:OD1	1:A:3710:PRO:HD3	2.20	0.41
1:A:4377:LEU:HD12	1:A:4433:VAL:HG13	2.02	0.41
1:A:3848:MET:HE1	1:A:4000:ARG:CD	2.51	0.40
1:A:4256:HIS:NE2	1:A:4316:GLU:OE1	2.53	0.40
1:A:4445:ASP:OD2	1:A:4445:ASP:N	2.54	0.40
1:A:3684:ALA:HB3	1:A:3685:PRO:HD3	2.03	0.40
1:A:3631:LEU:HB3	1:A:3632:PRO:HD3	2.03	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	630/4888 (13%)	623 (99%)	7 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	576/4242 (14%)	573 (100%)	3 (0%)	81	90

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

Mol	Chain	Res	Type
1	A	3787	GLU
1	A	4083	ILE
1	A	4191	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4182	GLN
1	A	4308	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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.

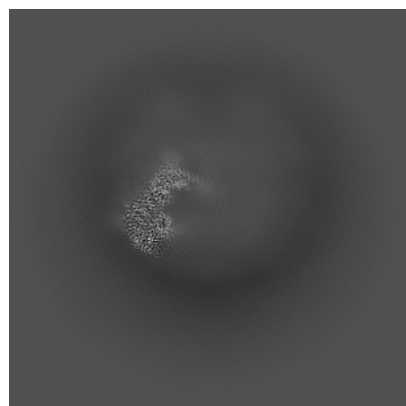
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27836. These allow visual inspection of the internal detail of the map and identification of artifacts.

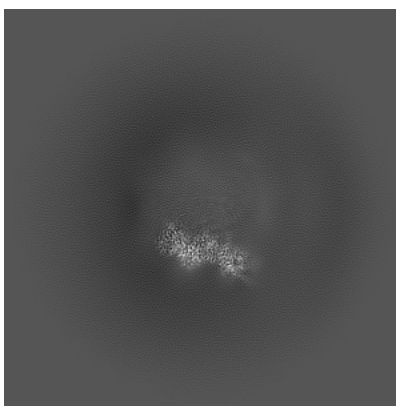
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

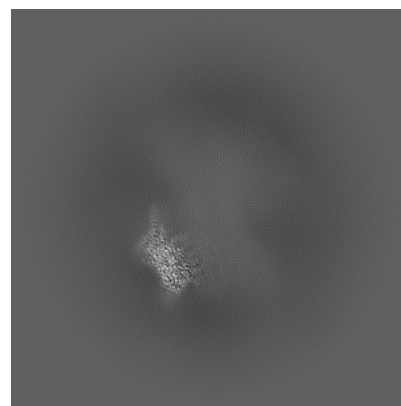
6.1.1 Primary map



X

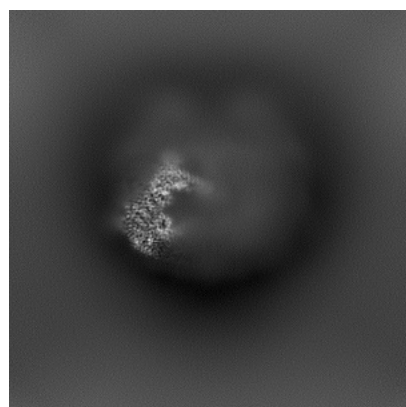


Y

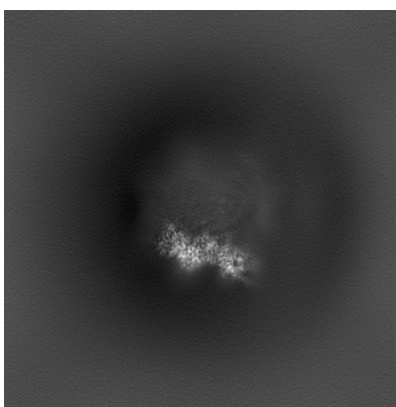


Z

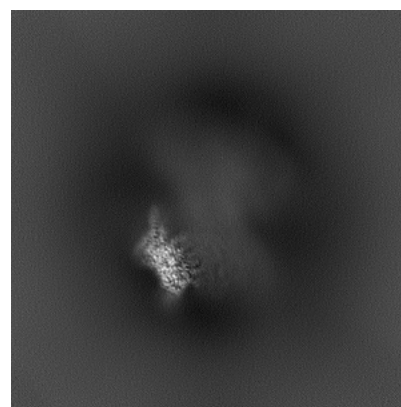
6.1.2 Raw map



X



Y

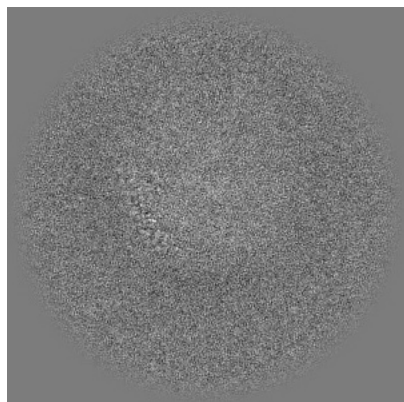


Z

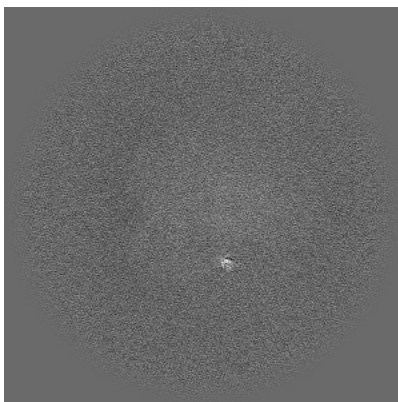
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

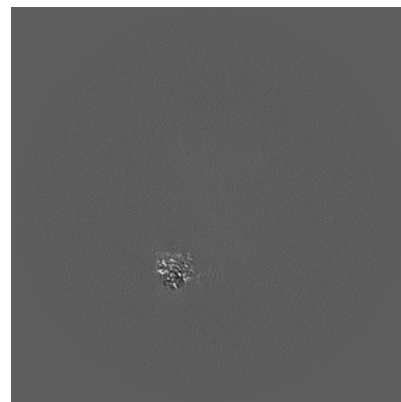
6.2.1 Primary map



X Index: 240

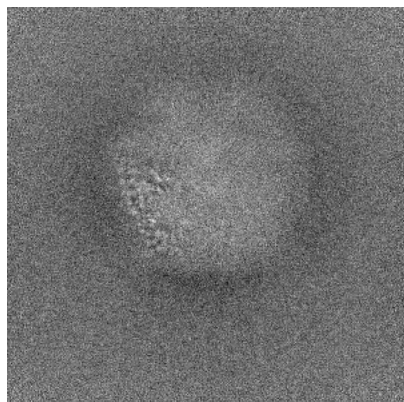


Y Index: 240

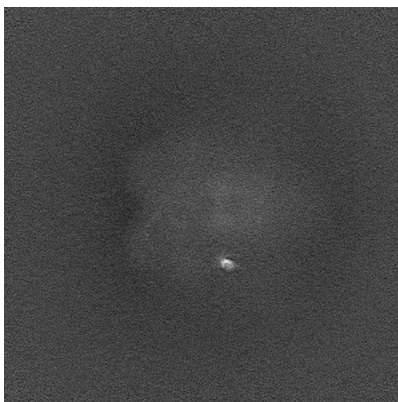


Z Index: 240

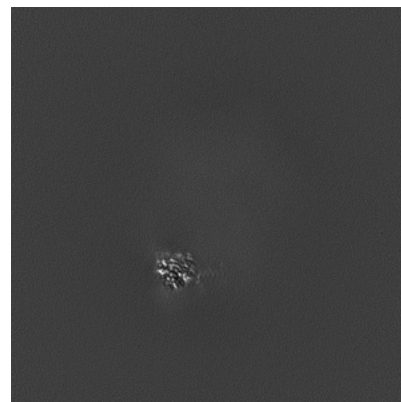
6.2.2 Raw map



X Index: 240



Y Index: 240

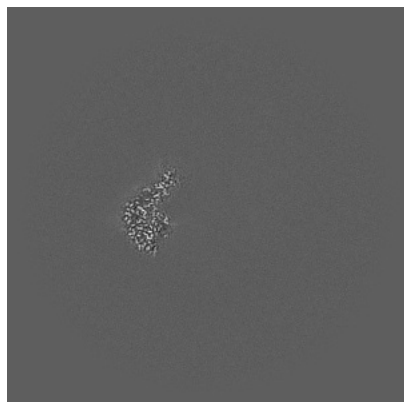


Z Index: 240

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

6.3 Largest variance slices [i](#)

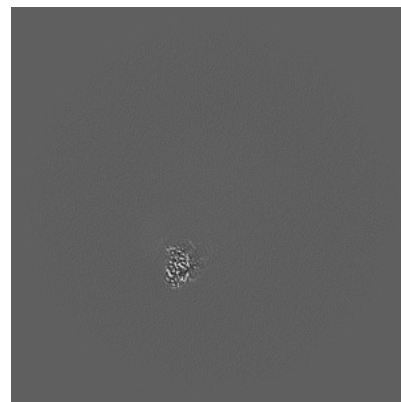
6.3.1 Primary map



X Index: 191

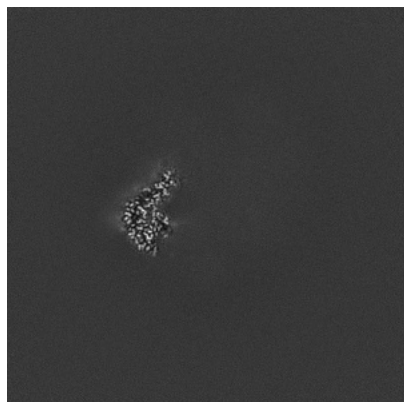


Y Index: 168

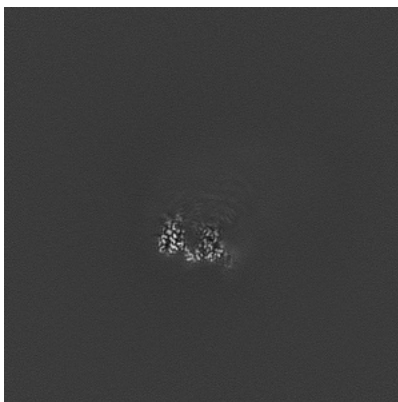


Z Index: 205

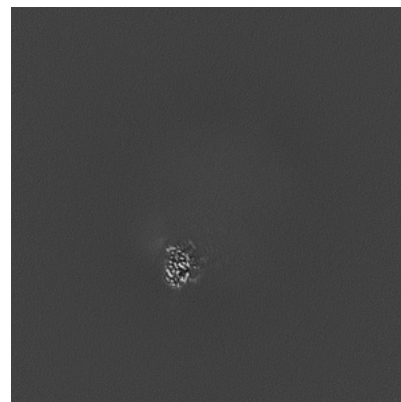
6.3.2 Raw map



X Index: 191



Y Index: 168

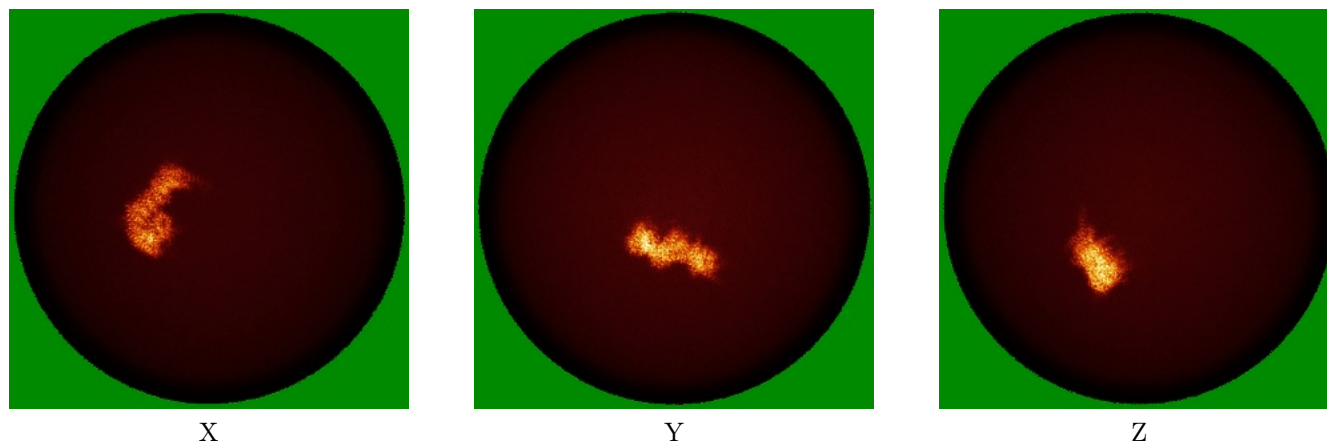


Z Index: 205

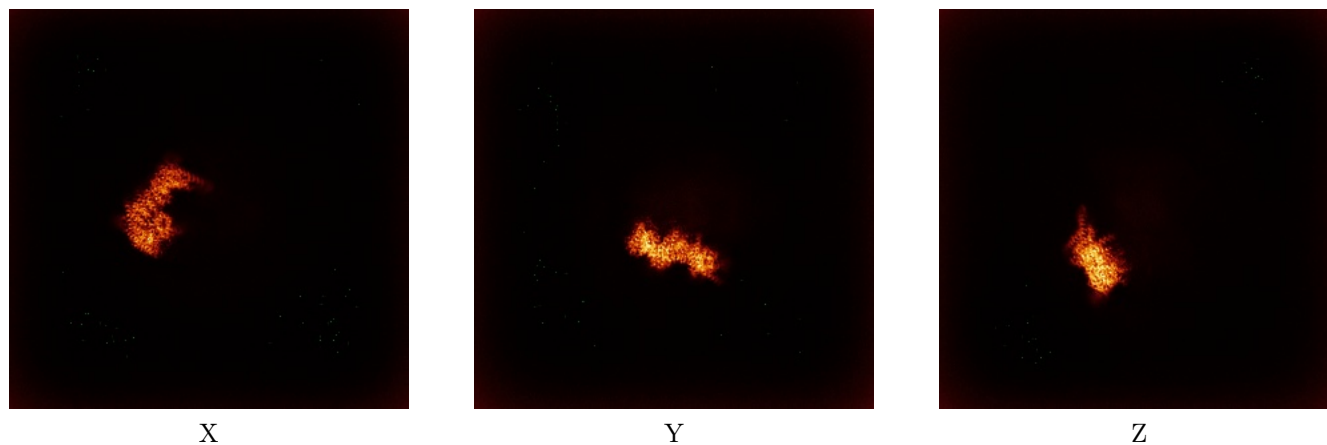
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



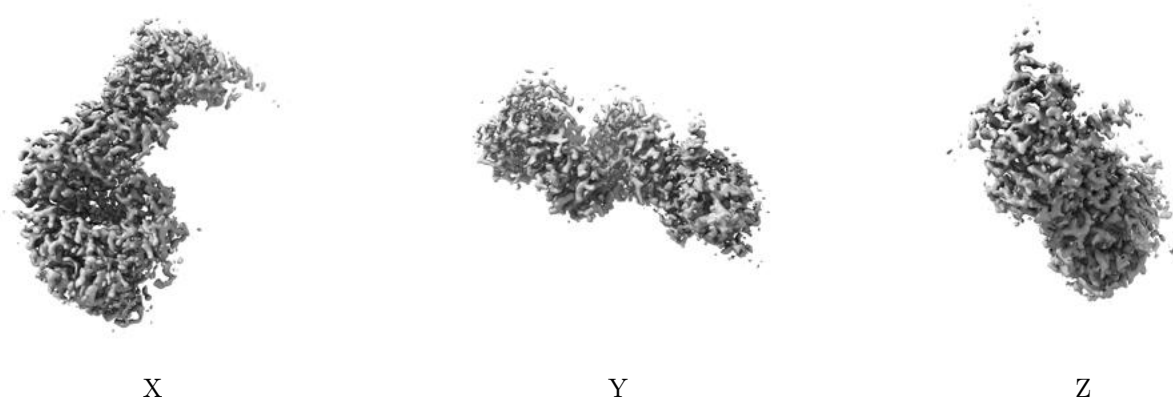
6.4.2 Raw map



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.

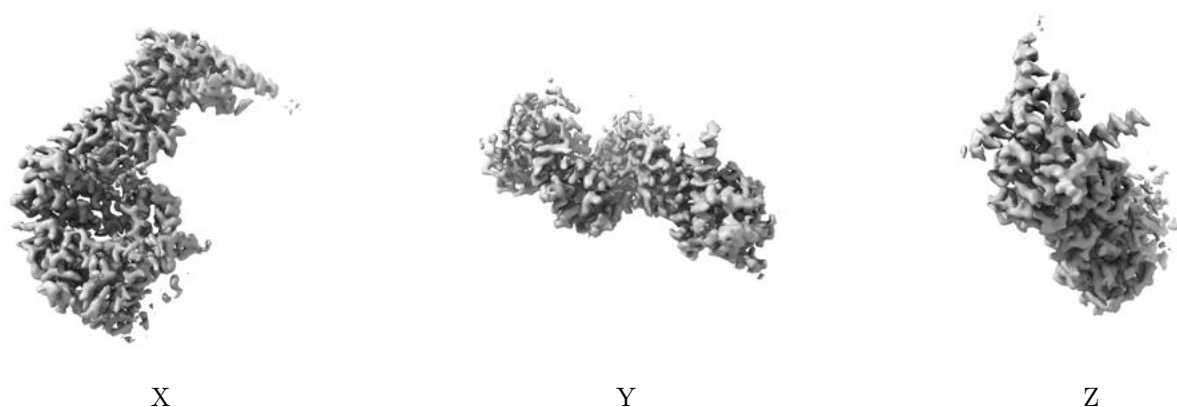
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.825. 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.

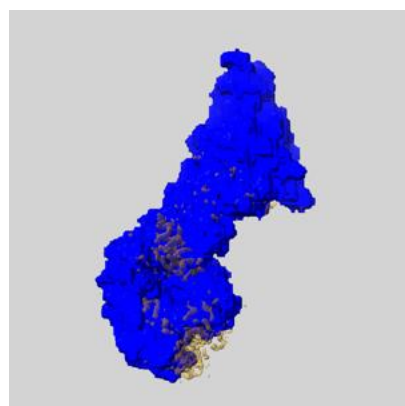
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

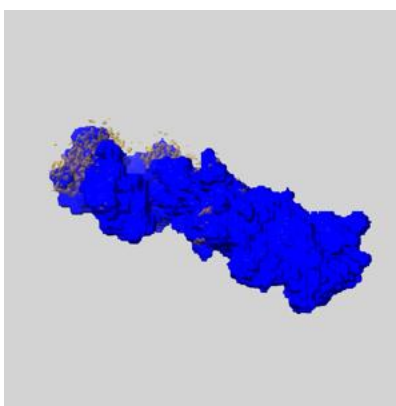
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

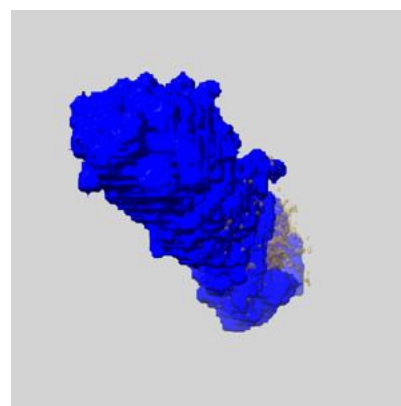
6.6.1 emd_27836_msk_1.map [i](#)



X



Y

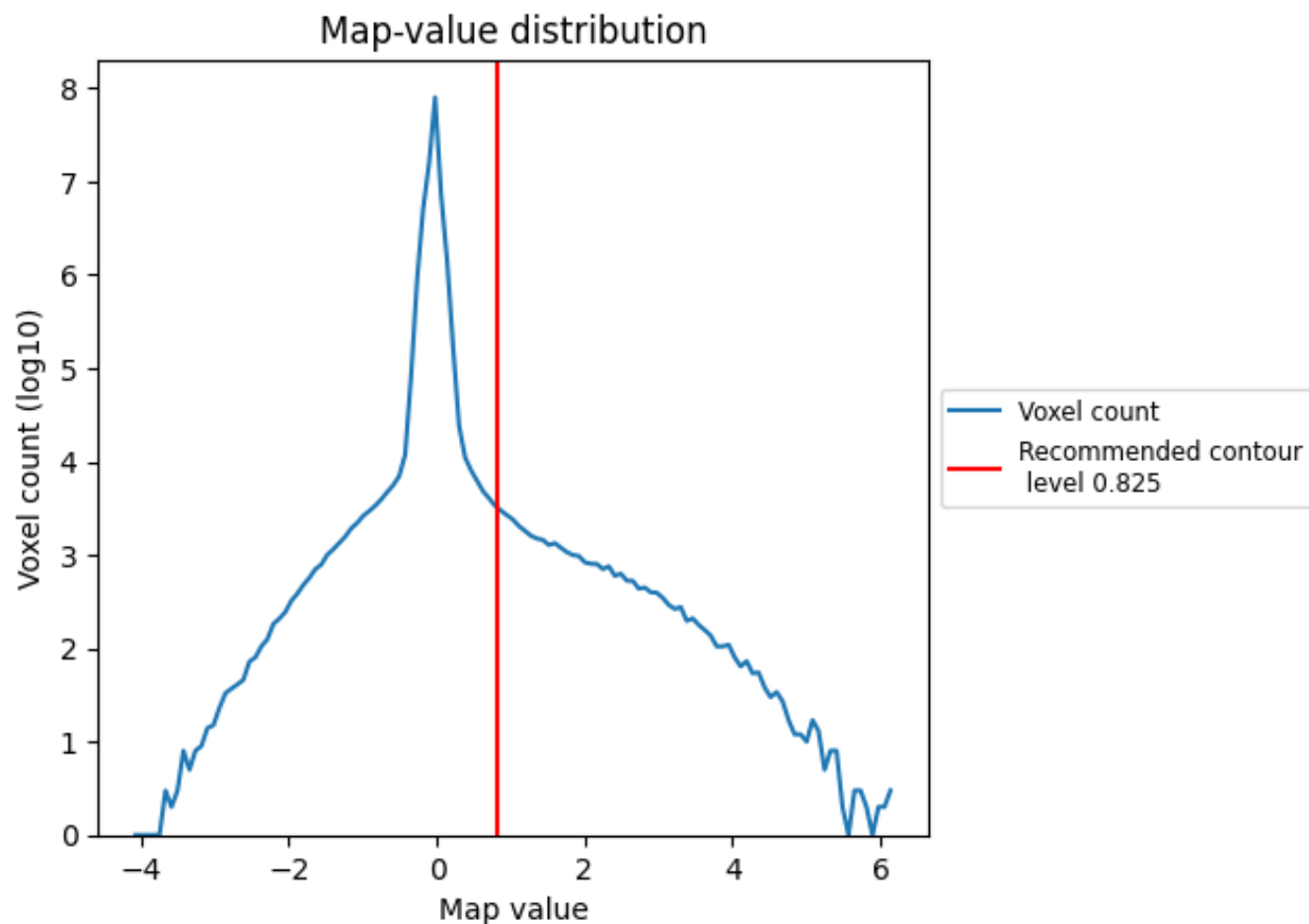


Z

7 Map analysis [i](#)

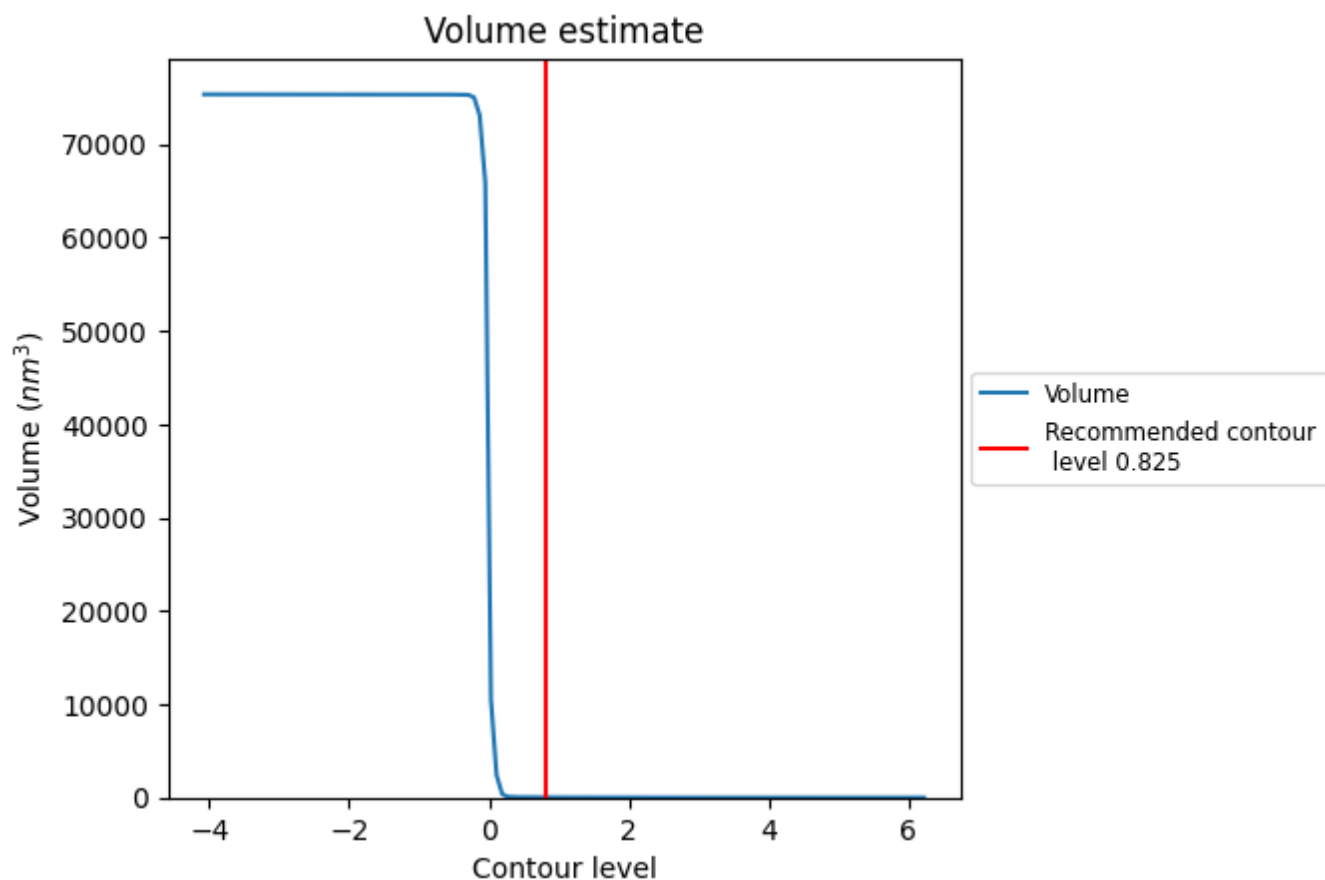
This section contains the results of statistical analysis of the map.

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.

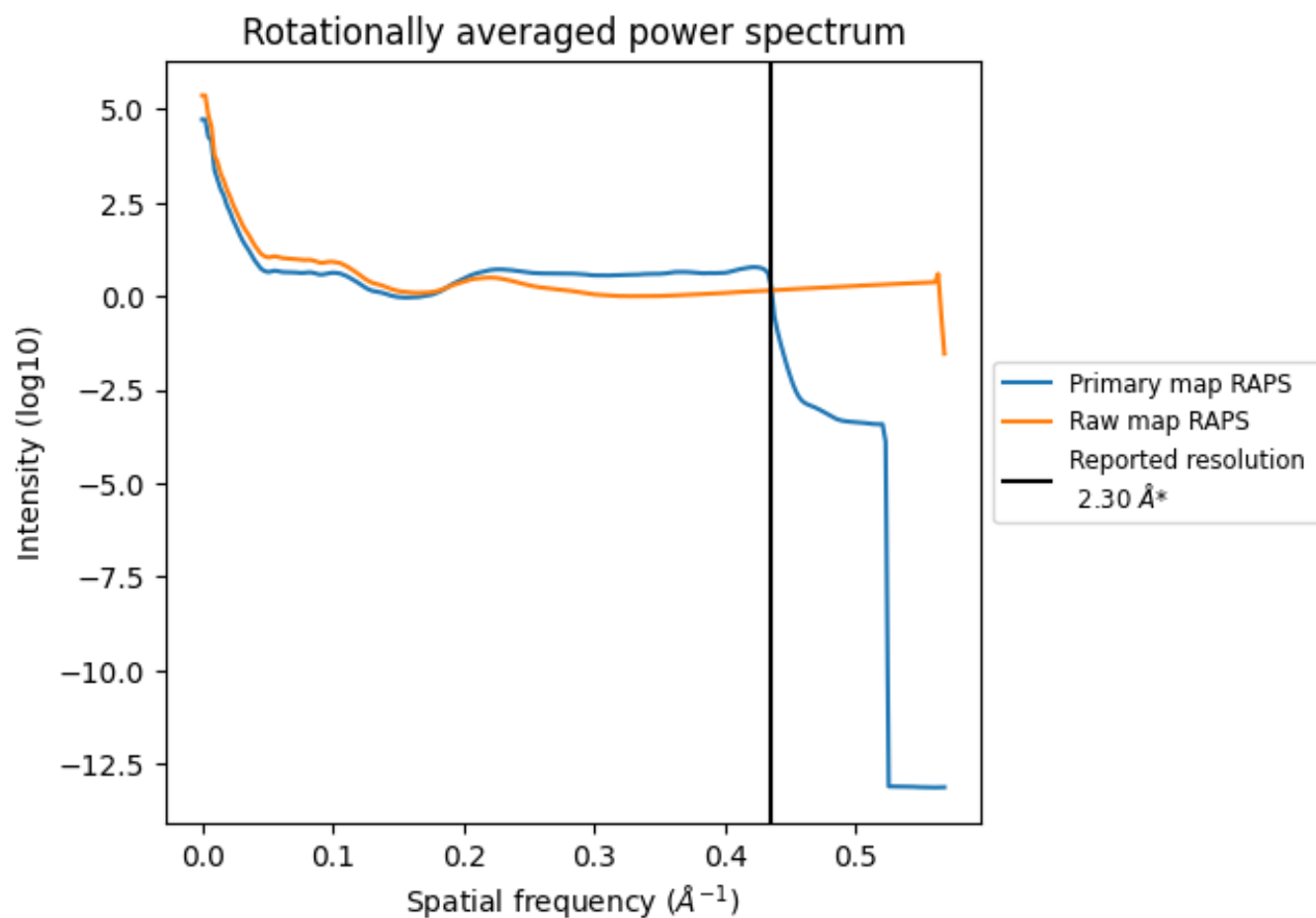
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 24 nm³; this corresponds to an approximate mass of 22 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 ⓘ

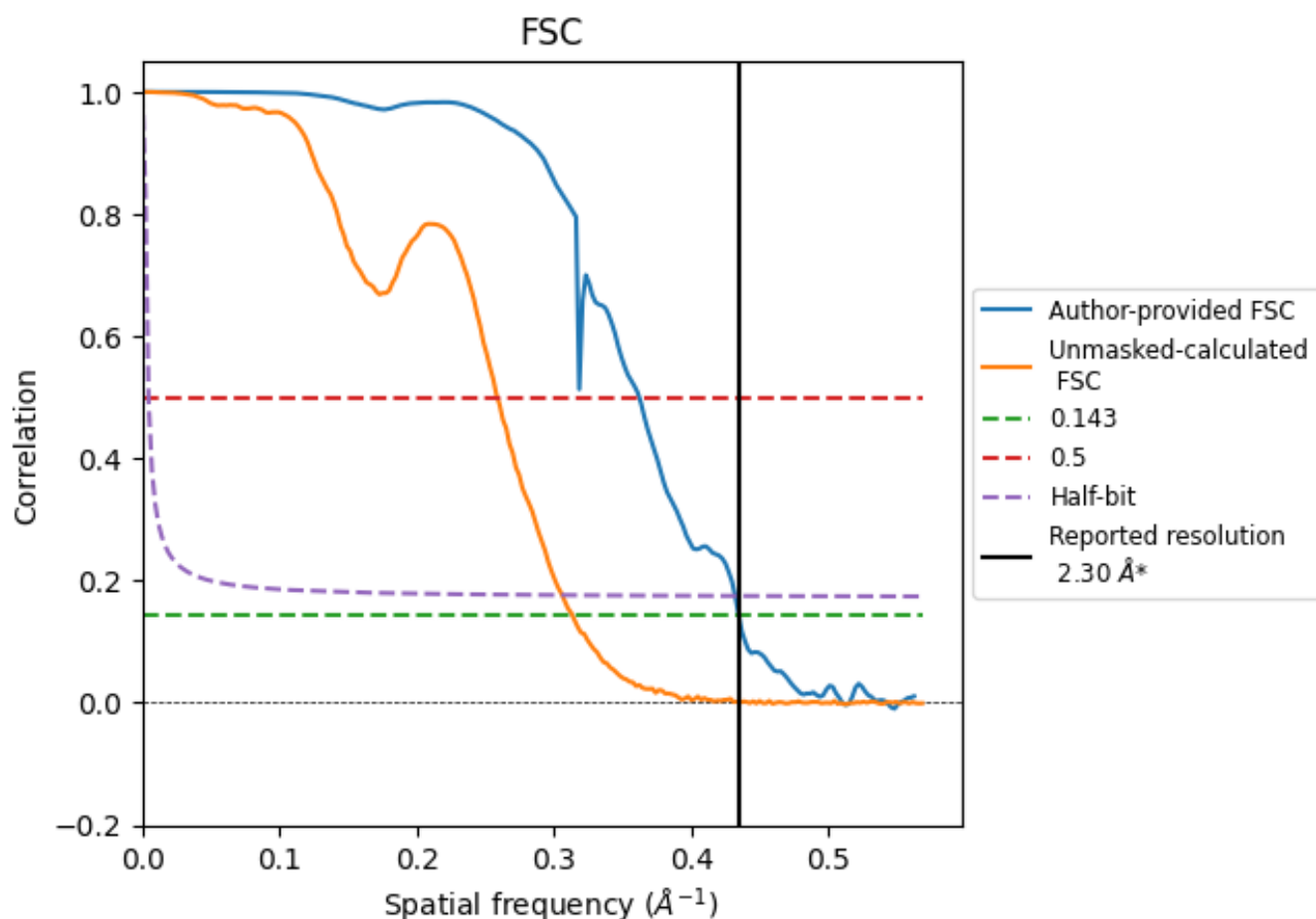


*Reported resolution corresponds to spatial frequency of 0.435 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.435 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

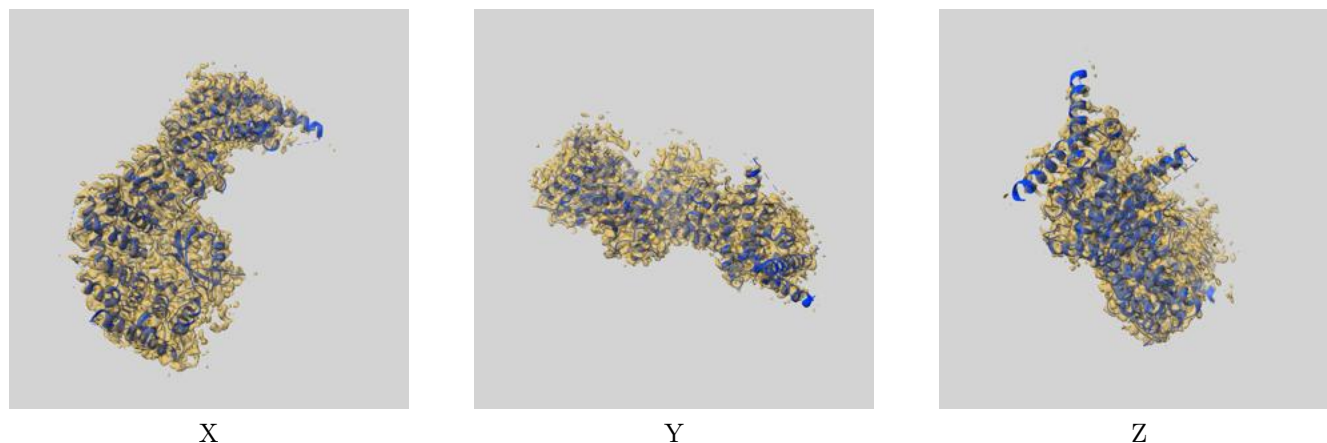
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.30	-	-
Author-provided FSC curve	2.30	2.76	2.32
Unmasked-calculated*	3.19	3.87	3.27

*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 3.19 differs from the reported value 2.3 by more than 10 %

9 Map-model fit [i](#)

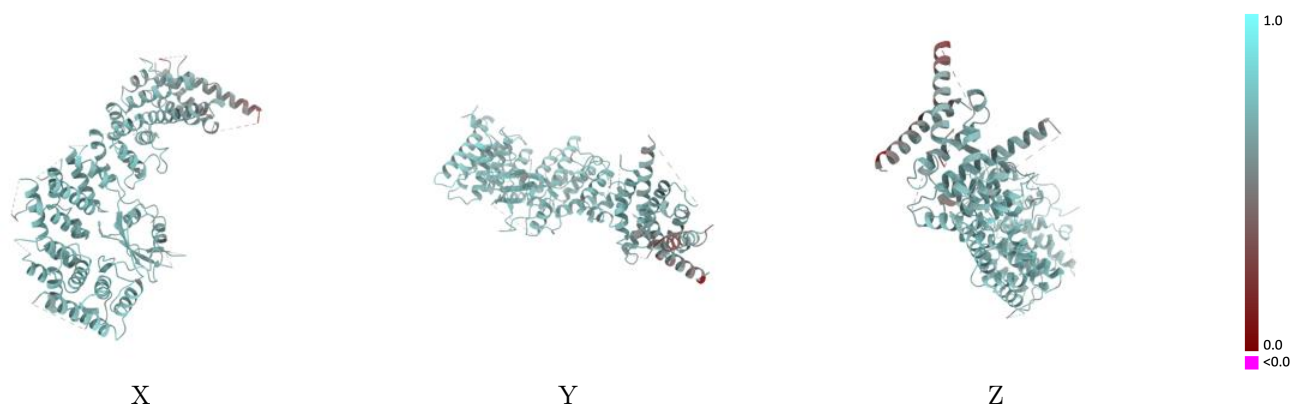
This section contains information regarding the fit between EMDB map EMD-27836 and PDB model 8E2H. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



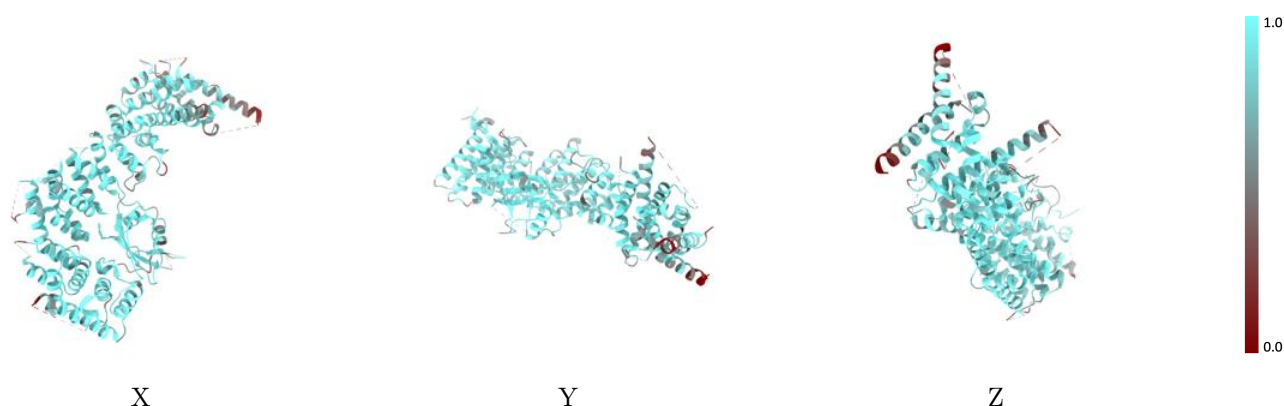
The images above show the 3D surface view of the map at the recommended contour level 0.825 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



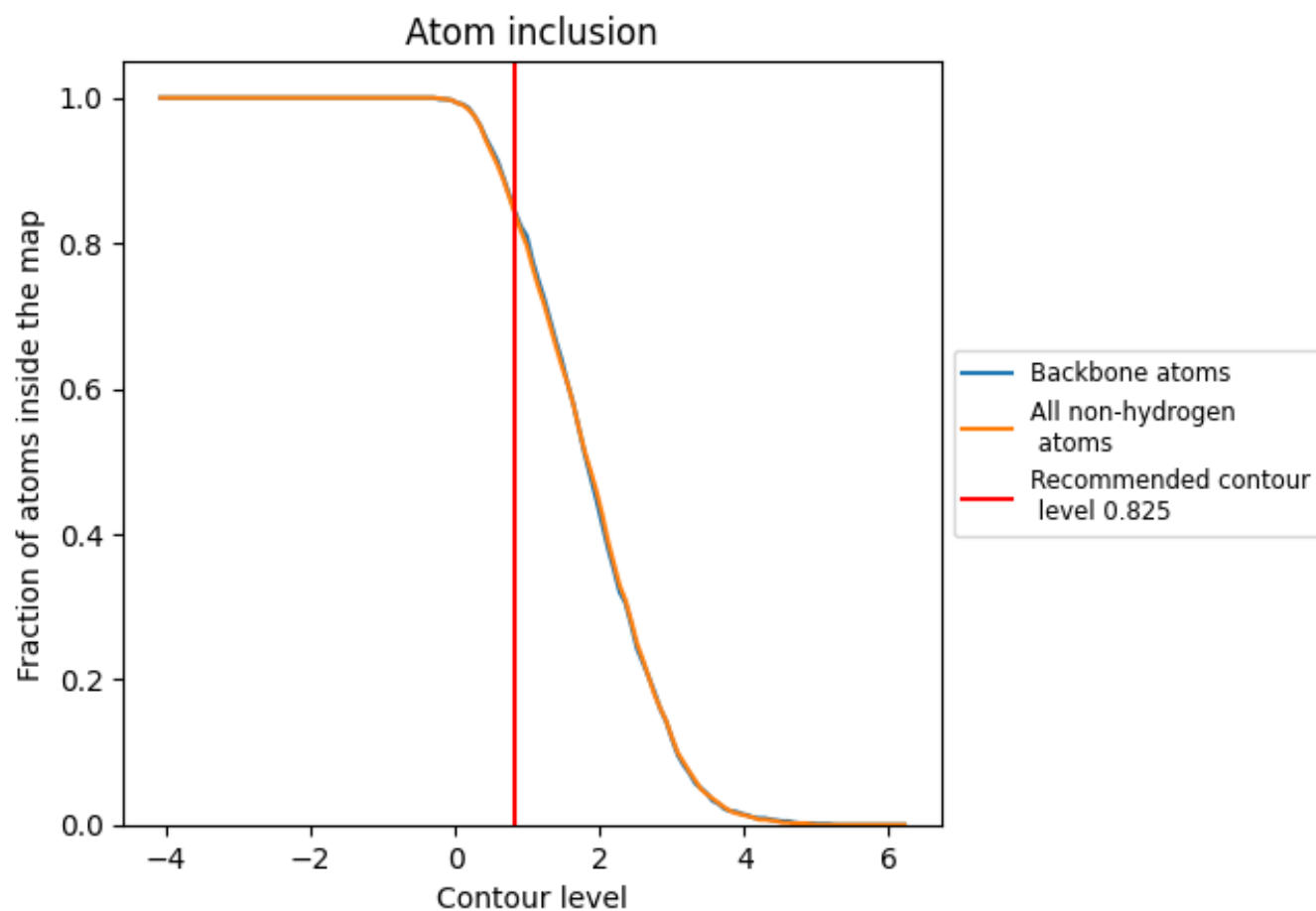
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.825).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 84% 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 (0.825) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8410	0.6480
A	0.8550	0.6480

