



Full wwPDB EM Validation Report ⓘ

Mar 24, 2026 – 01:31 PM UTC

PDB ID : 8E2F / pdb_00008e2f
EMDB ID : EMD-27834
Title : Cryo-EM structure of N-terminal arm of BIRC6 (from local refinement 2)
Authors : Hunkeler, M.; Fischer, E.S.
Deposited on : 2022-08-15
Resolution : 2.47 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

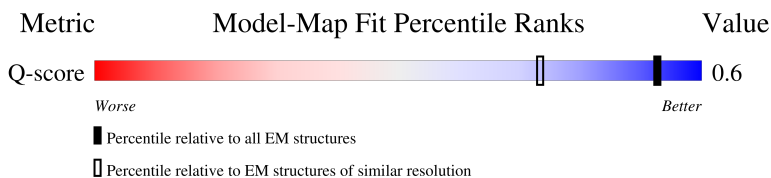
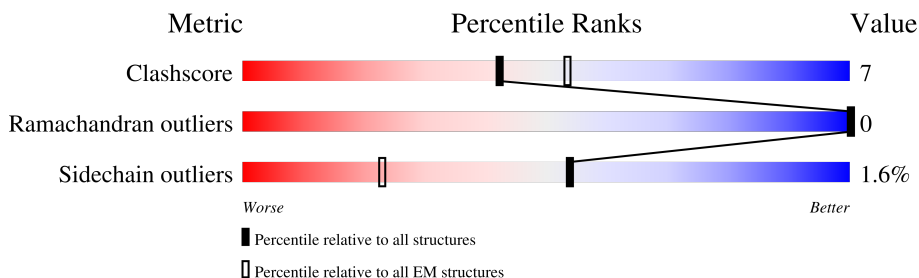
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.47 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	6086 (1.98 - 2.97)

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 is only 1 type of molecule in this entry. The entry contains 12305 atoms, of which 6207 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	771	Total	C	H	N	O	S	0	0
			12305	3905	6207	1046	1107	40		

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







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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	472306	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	5.204	Depositor
Minimum map value	-3.082	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.778	Depositor
Map size ($\text{\AA}$)	422.4, 422.4, 422.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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	0.14	0/6214	0.34	0/8425

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	6098	6207	6207	82	0
All	All	6098	6207	6207	82	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 (82) 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:1501:SER:OG	1:A:2024:ARG:NH2	2.18	0.76
1:A:2106:SER:OG	1:A:2164:ASP:OD1	2.04	0.75
1:A:1105:ASP:OD2	1:A:1304:ARG:NH1	2.24	0.70
1:A:1127:ASN:OD1	1:A:1219:SER:OG	2.08	0.70
1:A:2326:GLU:OE1	1:A:2326:GLU:N	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1783:MET:HE2	1:A:1783:MET:HA	1.75	0.68
1:A:1459:LYS:NZ	1:A:2036:SER:OG	2.27	0.68
1:A:2083:VAL:CG2	1:A:2124:ILE:HD12	2.28	0.63
1:A:1575:ASP:OD2	1:A:1789:ARG:NH2	2.33	0.62
1:A:2124:ILE:O	1:A:2128:SER:OG	2.15	0.62
1:A:1111:ASN:O	1:A:1114:ILE:HG23	2.00	0.61
1:A:2079:GLY:O	1:A:2083:VAL:HG23	2.00	0.61
1:A:2336:VAL:CG2	1:A:2358:LEU:HD11	2.33	0.58
1:A:2336:VAL:HG22	1:A:2358:LEU:HD11	1.86	0.58
1:A:1113:ASN:O	1:A:1113:ASN:OD1	2.23	0.56
1:A:2180:ASP:OD1	1:A:2360:ARG:NH2	2.39	0.56
1:A:1025:LEU:HD22	1:A:1321:MET:HE3	1.89	0.55
1:A:1329:GLU:OE2	1:A:1333:ASN:ND2	2.40	0.55
1:A:1428:LEU:HD23	1:A:1458:VAL:HG21	1.88	0.54
1:A:1193:ASP:OD1	1:A:1194:LEU:N	2.35	0.54
1:A:1512:MET:SD	1:A:1879:TYR:OH	2.66	0.54
1:A:1825:GLU:H	1:A:1825:GLU:CD	2.17	0.53
1:A:1790:PHE:CD1	1:A:1790:PHE:C	2.86	0.53
1:A:1867:THR:HG22	1:A:1867:THR:O	2.10	0.51
1:A:2173:MET:O	1:A:2177:ARG:HG3	2.10	0.51
1:A:1317:GLN:O	1:A:1321:MET:HG3	2.12	0.50
1:A:2049:VAL:HG22	1:A:2050:LEU:H	1.76	0.50
1:A:2333:GLN:O	1:A:2337:LEU:HD12	2.10	0.50
1:A:1484:ARG:NH1	1:A:2018:SER:O	2.46	0.48
1:A:2038:LEU:HD11	1:A:2085:LEU:HG	1.95	0.48
1:A:1319:CYS:O	1:A:1323:GLN:OE1	2.31	0.48
1:A:1825:GLU:OE2	1:A:1825:GLU:N	2.35	0.48
1:A:1345:THR:HG22	1:A:1346:GLU:N	2.28	0.48
1:A:1830:ARG:HD3	1:A:1833:VAL:HG23	1.95	0.48
1:A:1034:LEU:HD12	1:A:1303:ILE:CG2	2.44	0.48
1:A:1038:PHE:CE2	1:A:1093:LEU:HD22	2.49	0.47
1:A:1477:VAL:HG13	1:A:2023:LEU:HD22	1.96	0.47
1:A:1467:SER:CB	1:A:2046:VAL:HG23	2.45	0.46
1:A:2057:GLN:CD	1:A:2057:GLN:H	2.24	0.46
1:A:1117:ILE:HG21	1:A:1192:LEU:HD11	1.96	0.46
1:A:1202:THR:HG21	1:A:2575:LEU:HD23	1.97	0.46
1:A:1429:LEU:HB2	1:A:1458:VAL:HG12	1.98	0.46
1:A:2046:VAL:N	1:A:2047:PRO:CD	2.78	0.46
1:A:1192:LEU:HD23	1:A:1198:ALA:O	2.16	0.45
1:A:2328:CYS:HA	1:A:2331:VAL:HG12	1.98	0.45
1:A:1402:HIS:HB3	1:A:1848:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1799:ILE:C	1:A:1799:ILE:HD12	2.42	0.45
1:A:1385:LEU:O	1:A:1386:SER:C	2.60	0.45
1:A:2145:LEU:HD11	1:A:2167:MET:HE3	1.98	0.45
1:A:1467:SER:HB3	1:A:2046:VAL:HG23	1.98	0.45
1:A:1092:GLU:OE1	1:A:1094:VAL:HG23	2.16	0.44
1:A:1512:MET:O	1:A:1513:SER:OG	2.24	0.44
1:A:2080:LEU:HD12	1:A:2598:LEU:HD22	1.99	0.44
1:A:1108:PHE:HB2	1:A:1296:LEU:HD21	2.00	0.43
1:A:1085:SER:O	1:A:1089:HIS:NE2	2.43	0.43
1:A:1811:ASP:OD1	1:A:1811:ASP:N	2.50	0.43
1:A:1463:LEU:HD22	1:A:2037:LEU:HD23	2.00	0.43
1:A:1813:ALA:N	1:A:1861:ILE:O	2.48	0.43
1:A:1363:HIS:O	1:A:1364:SER:CB	2.67	0.43
1:A:1406:ARG:NH2	1:A:2580:GLU:OE1	2.49	0.43
1:A:2120:LEU:O	1:A:2124:ILE:HG12	2.18	0.43
1:A:2145:LEU:HD21	1:A:2167:MET:HE3	2.01	0.43
1:A:1848:ILE:HD13	1:A:1848:ILE:HA	1.89	0.42
1:A:2035:LEU:HD13	1:A:2598:LEU:HD21	2.01	0.42
1:A:1842:LEU:C	1:A:1842:LEU:HD13	2.44	0.42
1:A:2169:SER:O	1:A:2173:MET:HG3	2.20	0.42
1:A:1403:LYS:HG2	1:A:1848:ILE:HD12	2.01	0.42
1:A:1117:ILE:HD13	1:A:1192:LEU:CD1	2.51	0.41
1:A:1176:ASP:N	1:A:1176:ASP:OD1	2.51	0.41
1:A:1819:ILE:HD12	1:A:1853:CYS:SG	2.60	0.41
1:A:2336:VAL:HG23	1:A:2358:LEU:HD11	2.02	0.41
1:A:2049:VAL:O	1:A:2050:LEU:HB2	2.20	0.41
1:A:1820:TRP:HB3	1:A:1828:GLY:HA2	2.03	0.41
1:A:2138:LEU:HD12	1:A:2178:LEU:HD12	2.02	0.41
1:A:1402:HIS:CG	1:A:1848:ILE:HD11	2.55	0.41
1:A:1035:THR:HB	1:A:1036:PRO:HD3	2.03	0.41
1:A:1182:LEU:HD23	1:A:1208:LEU:HD13	2.03	0.41
1:A:1304:ARG:CD	1:A:2573:VAL:HA	2.51	0.41
1:A:1800:LEU:HD13	1:A:1850:PRO:HB2	2.03	0.41
1:A:1848:ILE:O	1:A:1850:PRO:HD3	2.20	0.41
1:A:2147:SER:HA	1:A:2334:LYS:HD3	2.04	0.40
1:A:1868:ASN:O	1:A:1869:ALA:C	2.64	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	743/4888 (15%)	721 (97%)	22 (3%)	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	695/4242 (16%)	684 (98%)	11 (2%)	55	77

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1112	SER
1	A	1127	ASN
1	A	1205	SER
1	A	1430	LYS
1	A	1481	LEU
1	A	1573	THR
1	A	1811	ASP
1	A	2120	LEU
1	A	2128	SER
1	A	2137	SER
1	A	2330	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1015	GLN
1	A	1051	GLN
1	A	1055	GLN
1	A	1113	ASN
1	A	1127	ASN
1	A	1363	HIS
1	A	2057	GLN
1	A	2577	GLN
1	A	2596	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](#)

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.

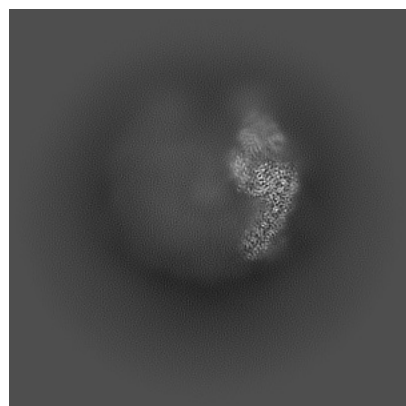
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27834. These allow visual inspection of the internal detail of the map and identification of artifacts.

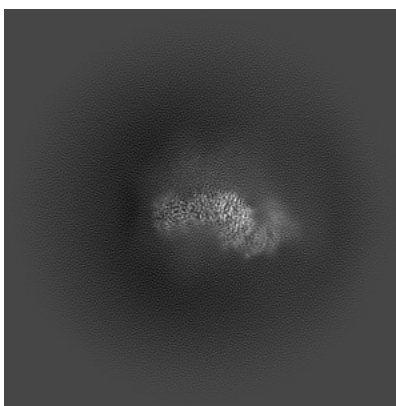
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

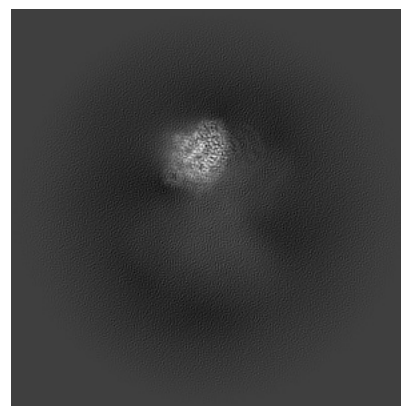
6.1.1 Primary map



X

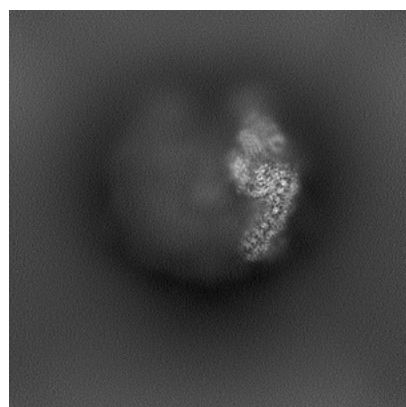


Y

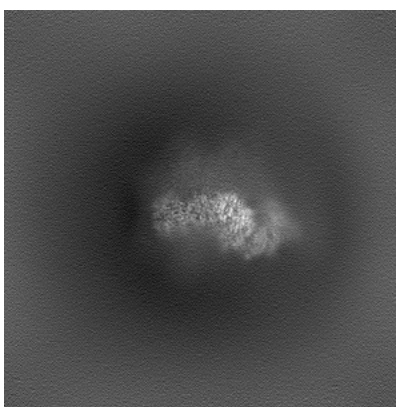


Z

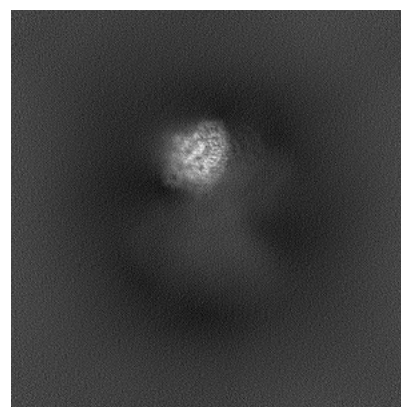
6.1.2 Raw map



X



Y

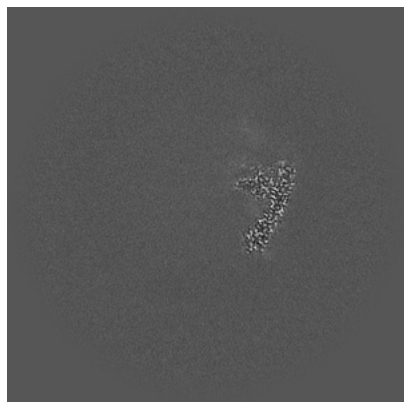


Z

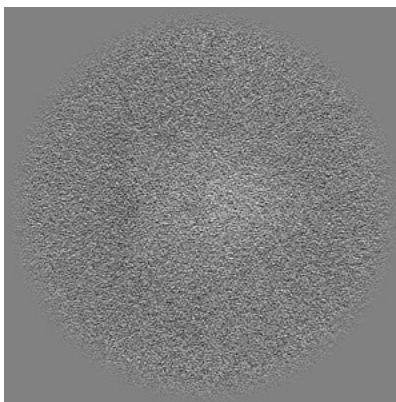
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

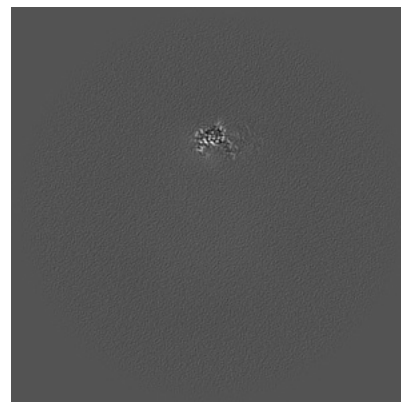
6.2.1 Primary map



X Index: 240



Y Index: 240

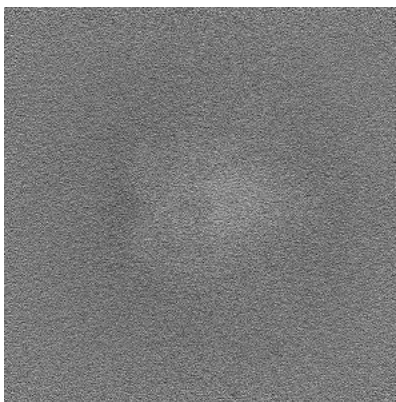


Z Index: 240

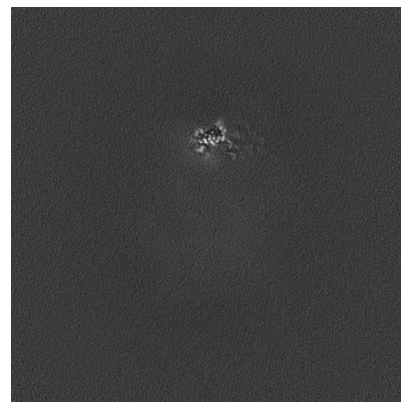
6.2.2 Raw map



X Index: 240



Y Index: 240

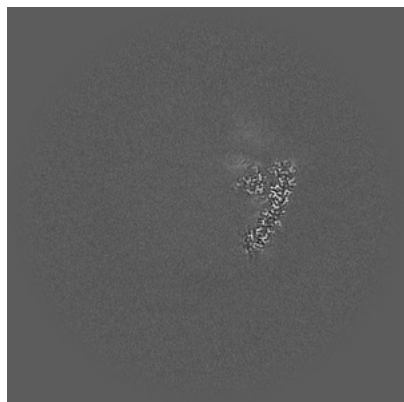


Z Index: 240

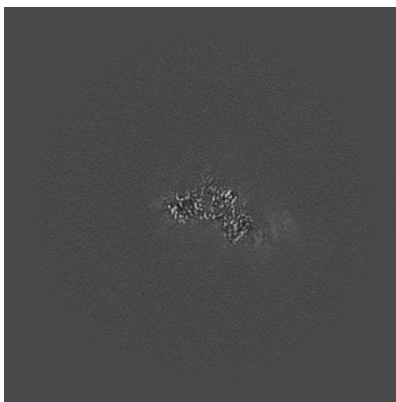
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

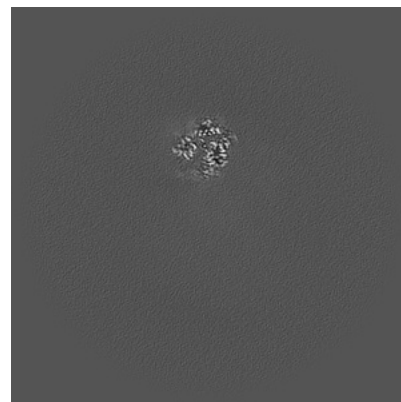
6.3.1 Primary map



X Index: 238

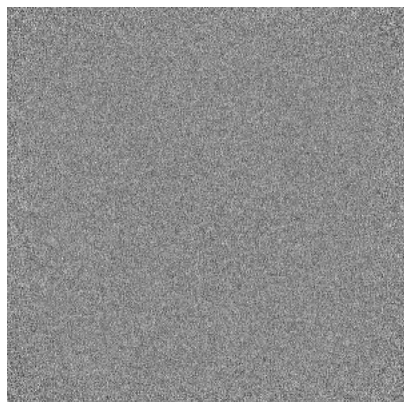


Y Index: 311

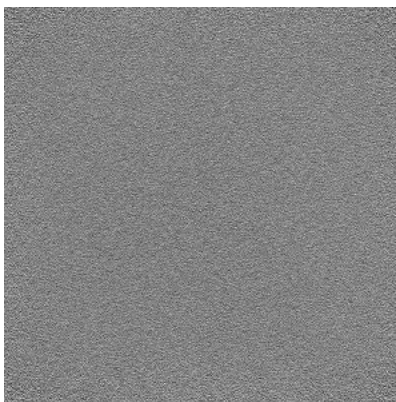


Z Index: 272

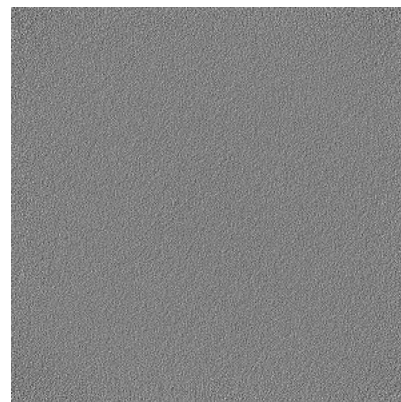
6.3.2 Raw map



X Index: 0



Y Index: 0

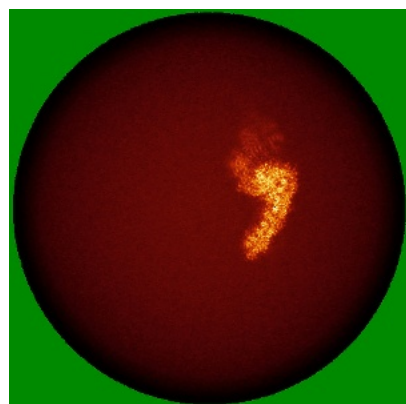


Z Index: 0

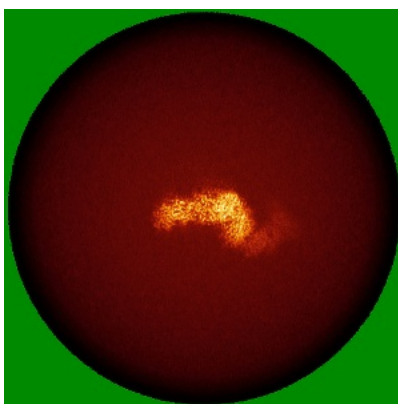
The images above show the largest variance slices of the map in three orthogonal directions.

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

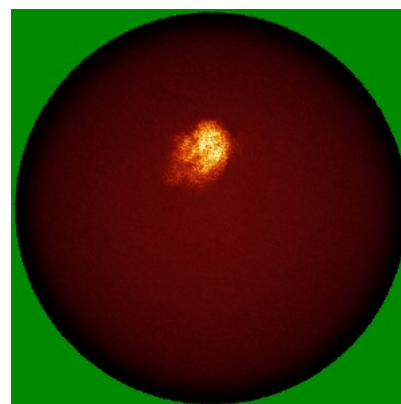
6.4.1 Primary map



X

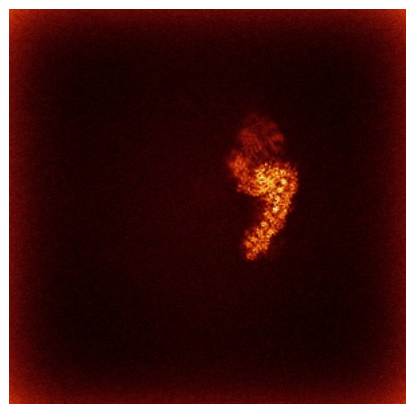


Y

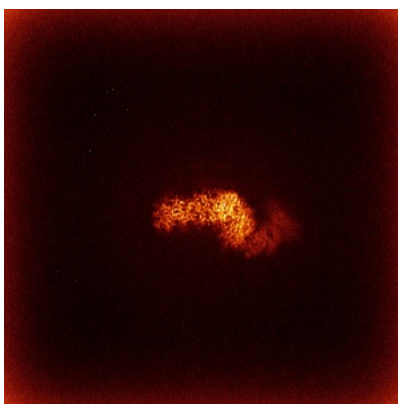


Z

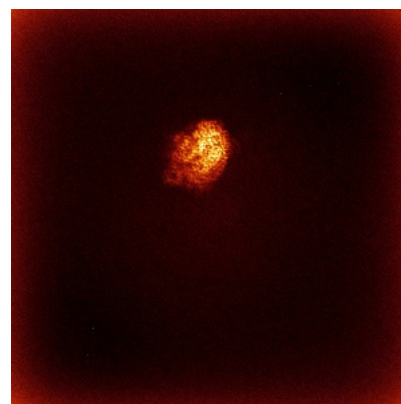
6.4.2 Raw map



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.

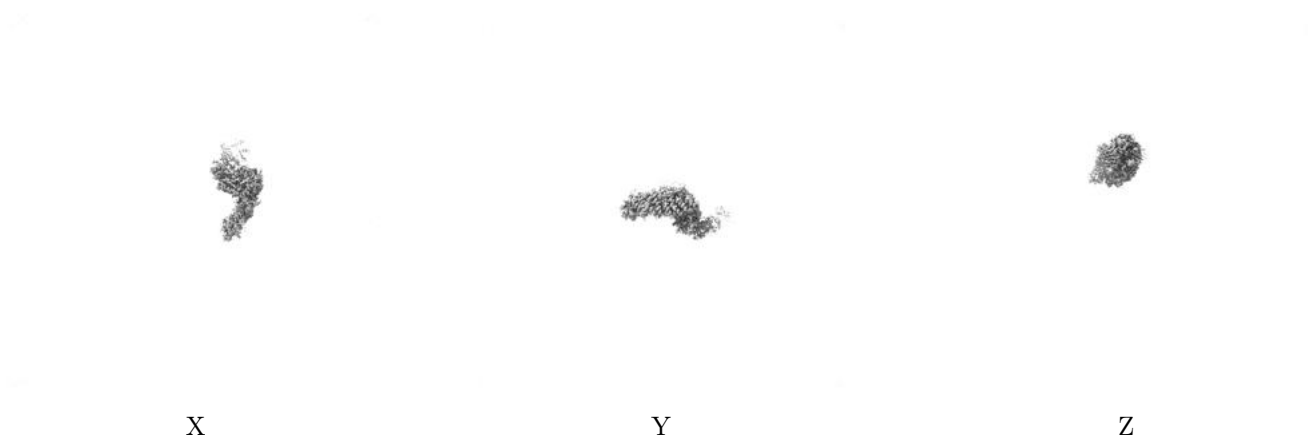
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.778. 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.

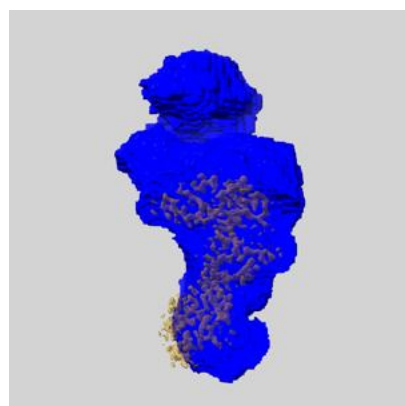
6.6 Mask visualisation [i](#)

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

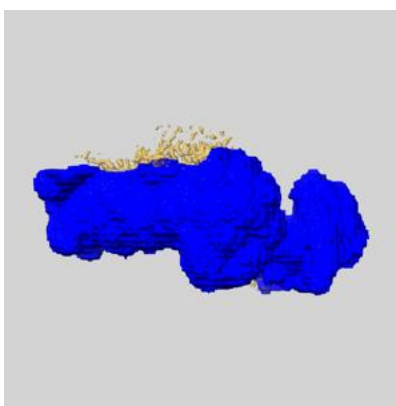
A mask typically either:

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

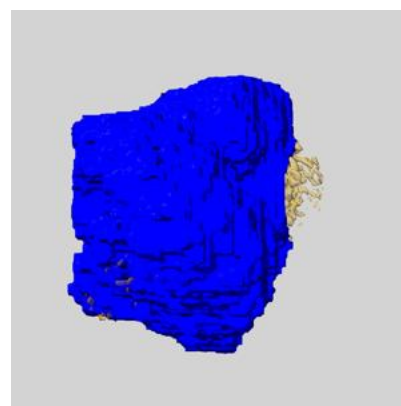
6.6.1 emd_27834_msk_1.map [i](#)



X



Y

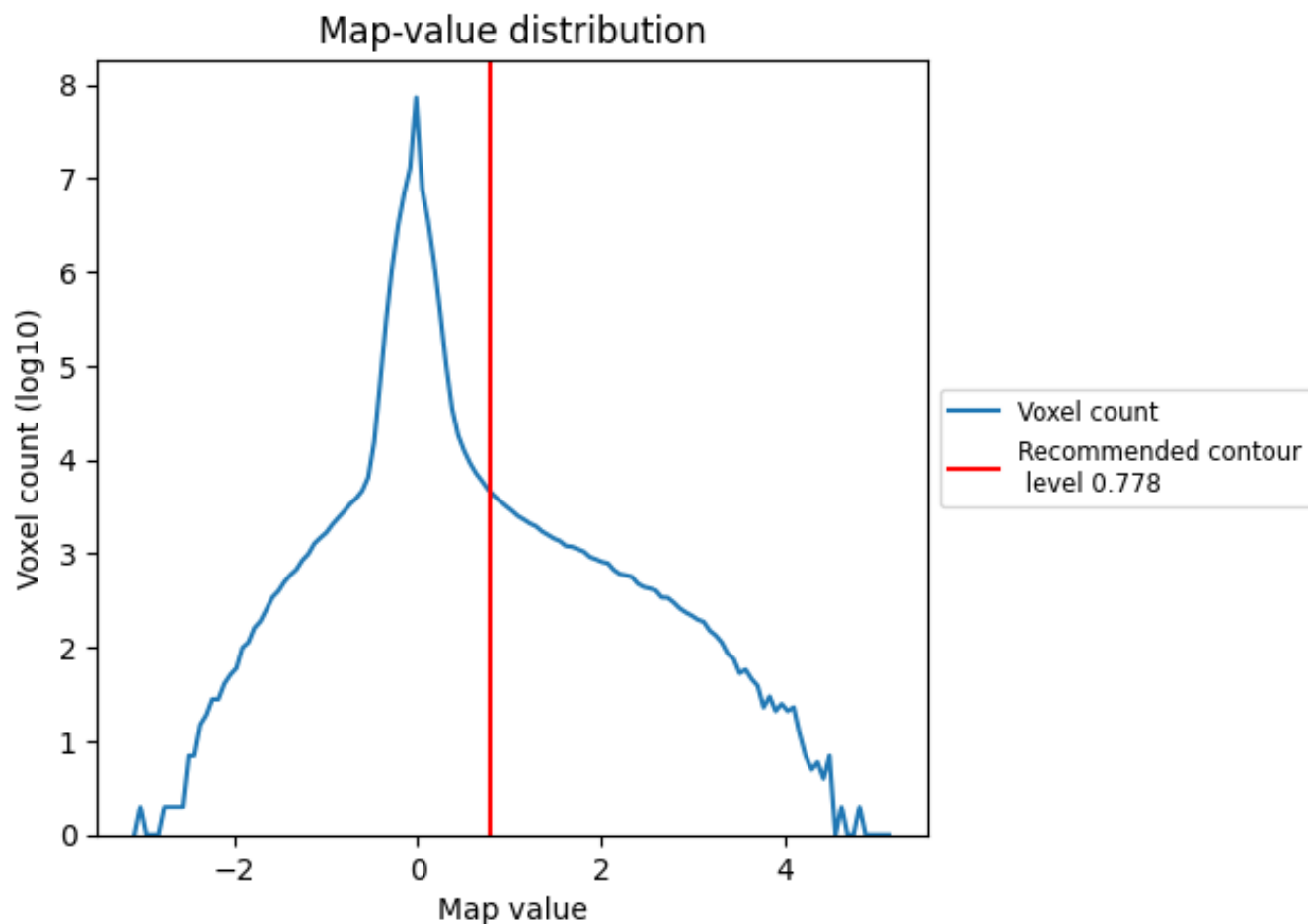


Z

7 Map analysis [i](#)

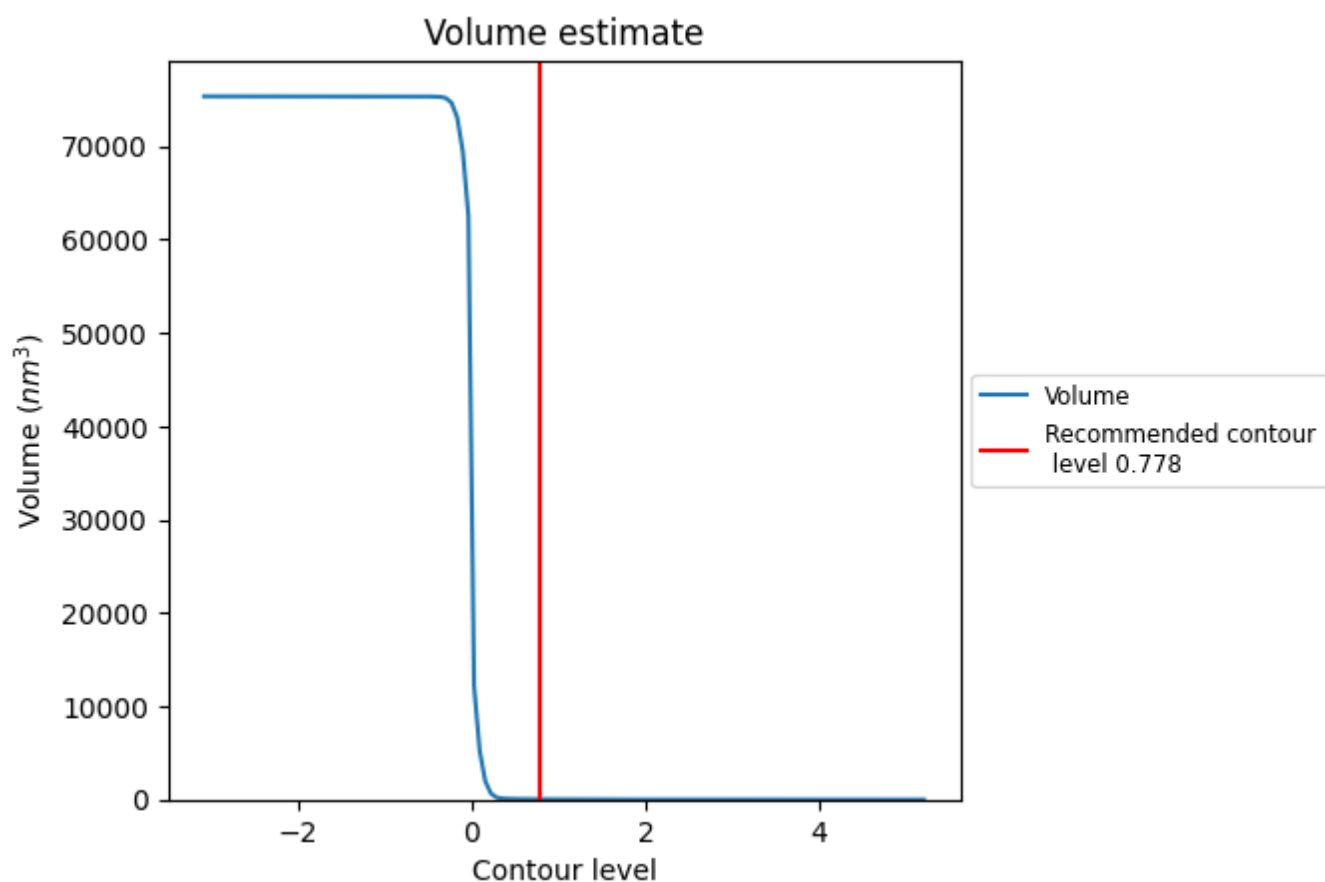
This section contains the results of statistical analysis of the map.

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.

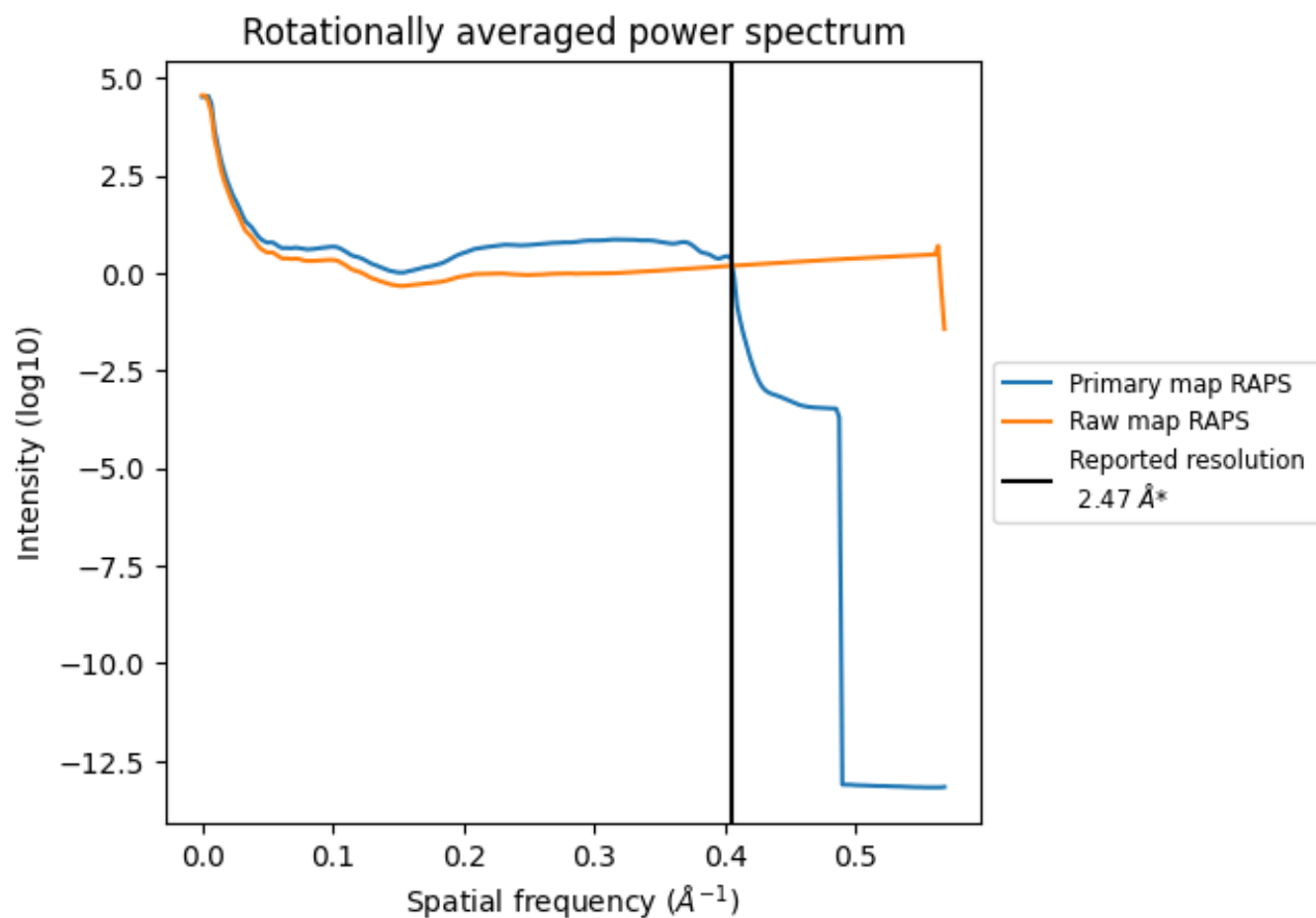
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 33 nm^3 ; this corresponds to an approximate mass of 30 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 ⓘ

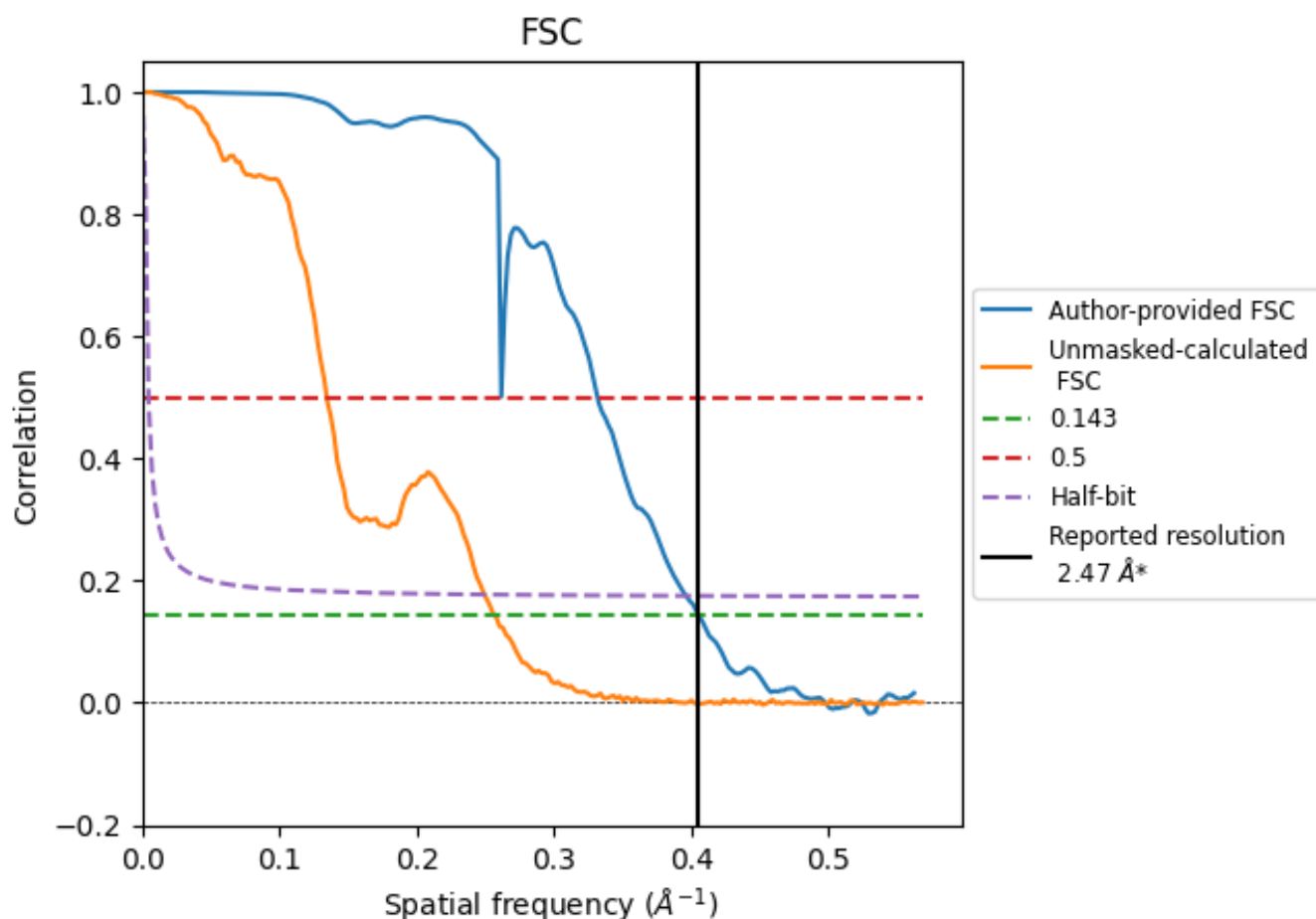


*Reported resolution corresponds to spatial frequency of 0.405 Å⁻¹

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 0.405 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

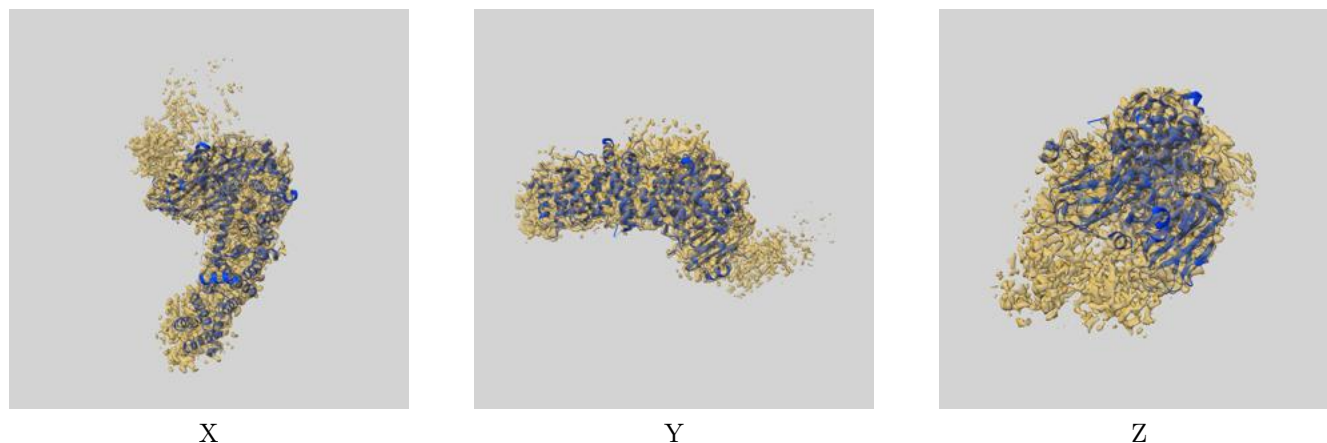
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.47	-	-
Author-provided FSC curve	2.47	3.01	2.52
Unmasked-calculated*	3.90	7.43	4.01

*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 3.90 differs from the reported value 2.47 by more than 10 %

9 Map-model fit [i](#)

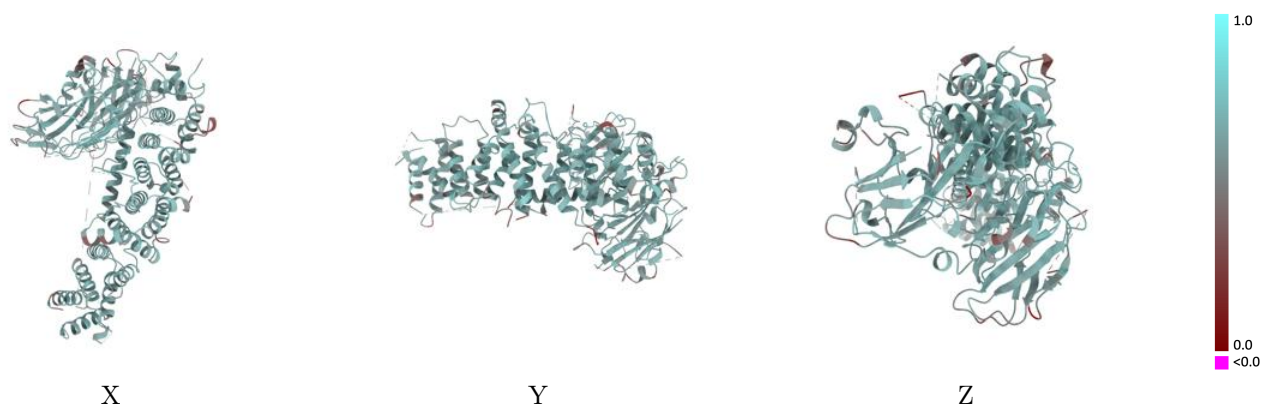
This section contains information regarding the fit between EMDB map EMD-27834 and PDB model 8E2F. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



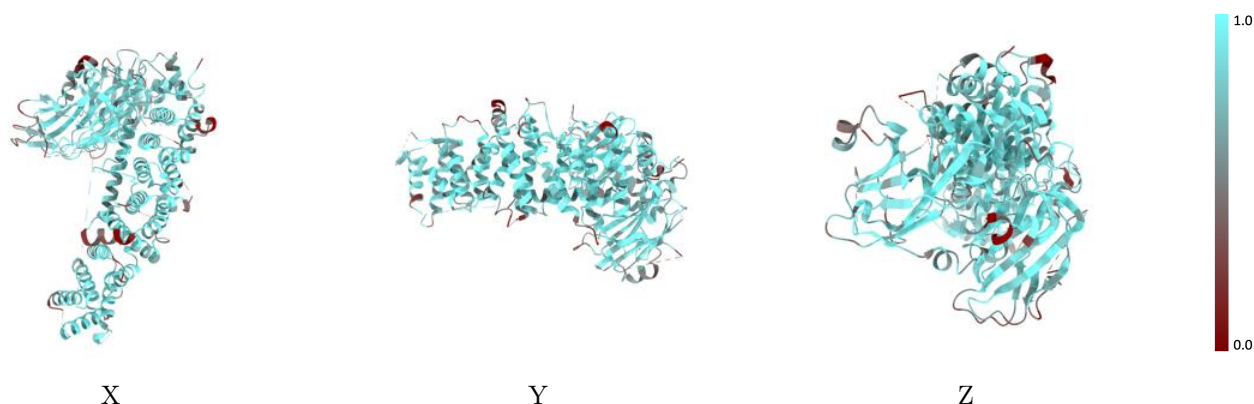
The images above show the 3D surface view of the map at the recommended contour level 0.778 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



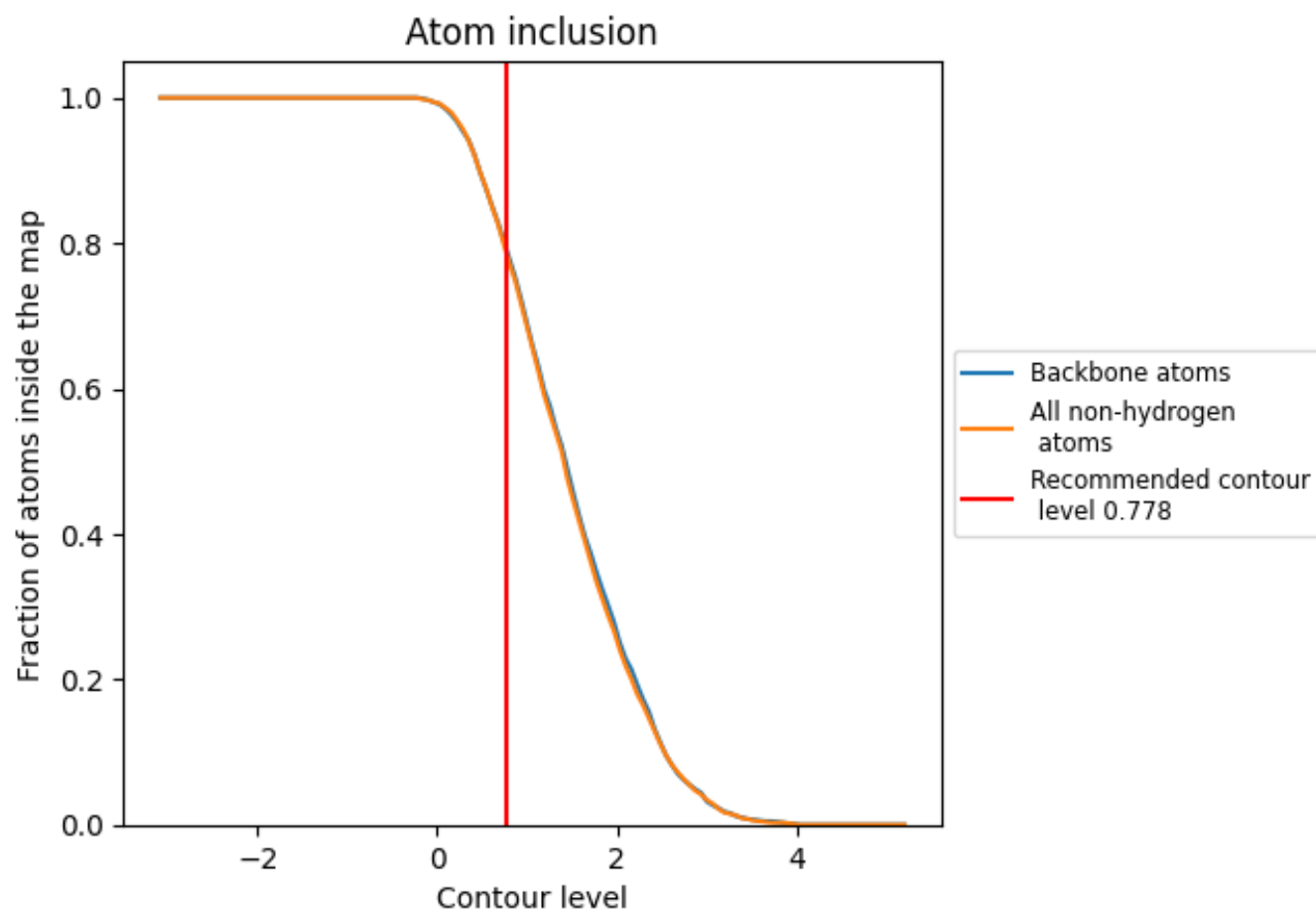
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.778).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 78% 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 (0.778) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7830	0.6000
A	0.7890	0.6000

