



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 10:49 AM UTC

PDB ID : 9Q3A / pdb_00009q3a
EMDB ID : EMD-72189
Title : Structure of the Borna Disease Virus 1 L and co-factor P Protein in an apo state
Authors : Ogino, T.; Chakrapani, S.; Gibbs, E.; Ogino, M.
Deposited on : 2025-08-18
Resolution : 2.77 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

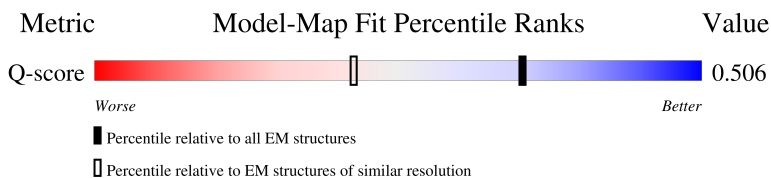
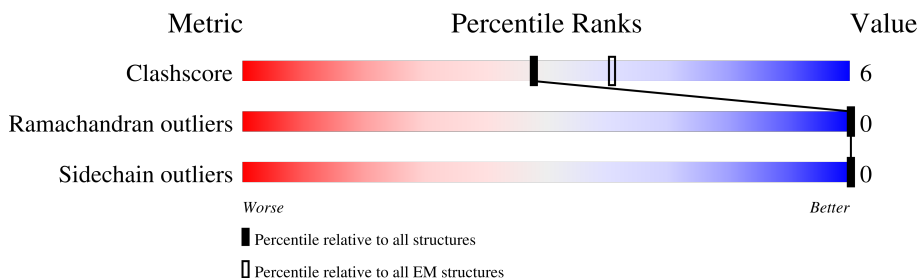
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.77 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	10695 (2.27 - 3.27)

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	1721	 79% 12% 8%
2	B	201	 30% 6% 64%
2	C	201	 20% 6% 74%
2	D	201	 16% 80%

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Mol	Chain	Length	Quality of chain
2	E	201	20%6%73%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14223 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1579	Total	C	N	O	S	0	0
			12506	8023	2138	2270	75		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	428	GLY	SER	conflict	UNP Q8JMN0
A	1116	ARG	LEU	conflict	UNP Q8JMN0
A	1398	ASP	ASN	conflict	UNP Q8JMN0
A	1620	LEU	VAL	conflict	UNP Q8JMN0
A	1712	GLY	-	expression tag	UNP Q8JMN0
A	1713	THR	-	expression tag	UNP Q8JMN0
A	1714	HIS	-	expression tag	UNP Q8JMN0
A	1715	HIS	-	expression tag	UNP Q8JMN0
A	1716	HIS	-	expression tag	UNP Q8JMN0
A	1717	HIS	-	expression tag	UNP Q8JMN0
A	1718	HIS	-	expression tag	UNP Q8JMN0
A	1719	HIS	-	expression tag	UNP Q8JMN0
A	1720	HIS	-	expression tag	UNP Q8JMN0
A	1721	HIS	-	expression tag	UNP Q8JMN0

- Molecule 2 is a protein called Isoform p24 of Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	41	Total	C	N	O	S	0	0
			320	201	52	61	6		
2	B	73	Total	C	N	O	S	0	0
			554	344	94	108	8		
2	C	53	Total	C	N	O	S	0	0
			420	258	72	83	7		
2	E	54	Total	C	N	O	S	0	0
			422	260	72	83	7		

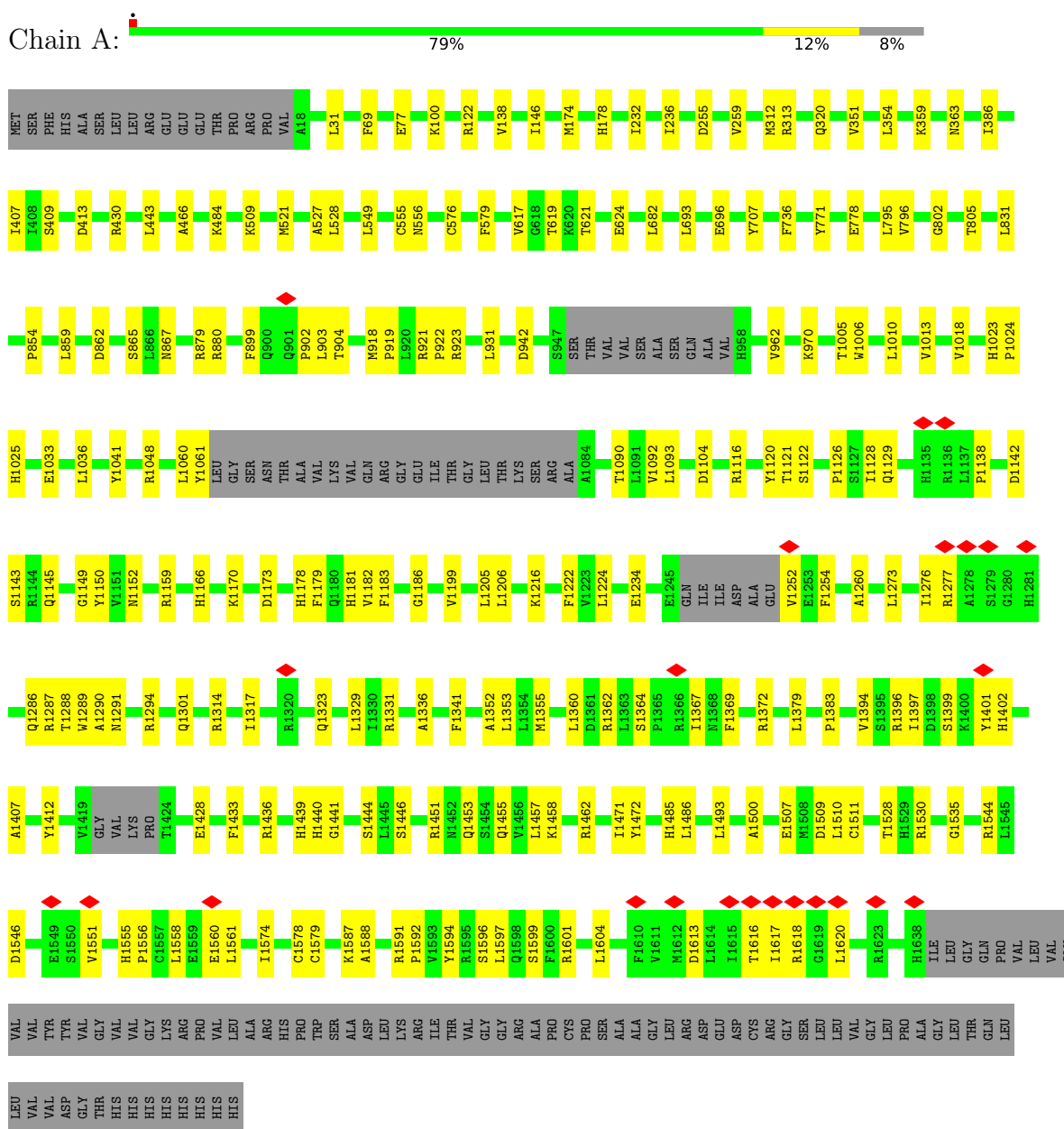
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: RNA-directed RNA polymerase L



[illegible][illegible]

Chain C:

MET ALA THR ARG PRO SER SER LEU LEU ASP VAL SER ASP PRO GLN THR ARG ARG GLU ARG ASP PRO GLN THR ARG ARG GLY SER PRO ARG PRO ARG LYS ILE PRO ARG ASN ALA LEU THR GLN PRO VAL ASP GLN LEU LEU LYS ASP LEU ARG LYS ASN PRO SER MET ILE SER ASP PRO

ASP GLN ARG THR GLY ARG GLU GLN LEU SER ASN ASP GLN ILE LYS LYS LEU VAL THR THR LEU GLU GLU ALA GLU ASN MET SER ILE GLU ALA GLU VAL ARG GLY THR LEU GLY ASP ILE SER ALA ARG ILE GLU ALA ALA PHE GLU SER LEU SER ALA LEU Q115 Q125 D126 H127 H128

D129 S130 I133 E136 K139 I140 R143 S144 T147 L162 T166 I167 VAL GLY THR SER ALA PRO MET LEU PRO SER HIS PRO ALA PRO PRO ARG ILE TYR PRO GLN LEU PRO SER ALA PRO THR ALA ASP GLU TRP ILE ILE PRO

Chain E: 20% 6% 73%

Position	Residue	Position	Residue	Position	Residue
1	MET	101	GLN	201	ASP
2	ALA	102	ARG	202	GLN
3	THR	103	THR	203	ARG
4	ARG	104	GLY	204	GLY
5	PRO	105	ARG	205	ARG
6	SER	106	GLU	206	GLU
7	SER	107	GLN	207	GLN
8	LEU	108	LEU	208	LEU
9	VAL	109	LEU	209	SER
10	ASP	110	ASN	210	ASP
11	ASP	111	ASP	211	ASN
12	LEU	112	ASP	212	LEU
13	LEU	113	GLU	213	LEU
14	GLU	114	LEU	214	GLU
15	ASP	115	ILE	215	ASP
16	GLU	116	LYS	216	GLU
17	GLU	117	LYS	217	LYS
18	ASP	118	LEU	218	ASP
19	PRO	119	VAL	219	LEU
20	GLN	120	THR	220	VAL
21	THR	121	GLU	221	THR
22	LEU	122	GLU	222	GLU
23	ARG	123	ALA	223	ALA
24	ARG	124	GLU	224	GLU
25	GLU	125	ASN	225	ASN
26	ARG	126	SER	226	SER
27	SER	127	MET	227	MET
28	GLY	128	ILE	228	ILE
29	GLY	129	GLU	229	GLU
30	PRO	130	ALA	230	ALA
31	PRO	131	ALA	231	ALA
32	ARG	132	GLU	232	GLU
33	ARG	133	VAL	233	VAL
34	ILE	134	ARG	234	ARG
35	ILE	135	GLY	235	GLY
36	PRO	136	THR	236	THR
37	ARG	137	LEU	237	LEU
38	ASN	138	LEU	238	LEU
39	ALA	139	ASP	239	ASP
40	ALA	140	GLN	240	GLN
41	LEU	141	LEU	241	LEU
42	PRO	142	PRO	242	PRO
43	SER	143	SER	243	SER
44	HIS	144	THR	244	THR
45	PRO	145	ALA	245	ALA
46	PRO	146	ALA	246	ALA
47	PRO	147	PRO	247	PRO
48	PRO	148	PRO	248	PRO
49	ARG	149	ARG	249	ARG
50	ILE	150	ILE	250	ILE
51	TYR	151	PRO	251	PRO
52	PRO	152	GLN	252	GLN
53	PRO	153	LEU	253	LEU
54	ASP	154	ASP	254	ASP
55	ASP	155	ASP	255	ASP
56	TRP	156	TRP	256	TRP
57	ILE	157	ILE	257	ILE
58	ILE	158	ILE	258	ILE
59	PRO	159	PRO	259	PRO

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	224617	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	8000	Depositor
Maximum defocus (nm)	16000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.031	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	251.99998, 251.99998, 251.99998	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	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: ZN

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	0.34	0/12797	0.49	0/17382
2	B	0.38	0/561	0.50	0/757
2	C	0.11	0/421	0.36	0/561
2	D	0.36	0/320	0.59	0/424
2	E	0.96	0/423	1.31	0/564
All	All	0.37	0/14522	0.53	0/19688

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	12506	0	12614	139	0
2	B	554	0	574	8	0
2	C	420	0	436	9	0
2	D	320	0	345	9	0
2	E	422	0	440	15	0
3	A	1	0	0	0	0
All	All	14223	0	14409	169	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 6.

The worst 5 of 169 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:1510:LEU:HD11	1:A:1587:LYS:HB3	1.73	0.70
2:D:152:MET:HE3	2:E:155:MET:HE2	1.77	0.67
2:E:148:MET:HG3	2:E:152:MET:CE	2.24	0.67
1:A:1116:ARG:NH1	1:A:1234:GLU:OE2	2.29	0.64
1:A:1485:HIS:NE2	1:A:1511:CYS:SG	2.69	0.64

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	1569/1721 (91%)	1514 (96%)	55 (4%)	0	100	100
2	B	71/201 (35%)	69 (97%)	2 (3%)	0	100	100
2	C	51/201 (25%)	50 (98%)	1 (2%)	0	100	100
2	D	39/201 (19%)	37 (95%)	2 (5%)	0	100	100
2	E	52/201 (26%)	47 (90%)	5 (10%)	0	100	100
All	All	1782/2525 (71%)	1717 (96%)	65 (4%)	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	1388/1504 (92%)	1388 (100%)	0	100	100
2	B	65/180 (36%)	65 (100%)	0	100	100
2	C	49/180 (27%)	49 (100%)	0	100	100
2	D	37/180 (21%)	37 (100%)	0	100	100
2	E	49/180 (27%)	49 (100%)	0	100	100
All	All	1588/2224 (71%)	1588 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1440	HIS
2	C	120	GLN
1	A	901	GLN
1	A	987	GLN
1	A	1166	HIS

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

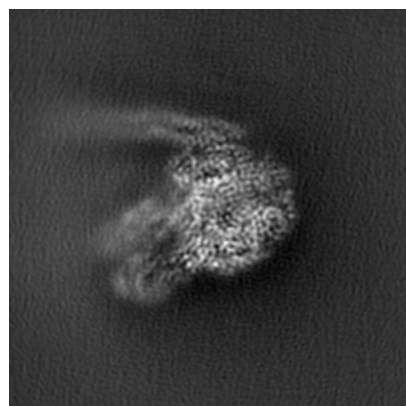
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72189. These allow visual inspection of the internal detail of the map and identification of artifacts.

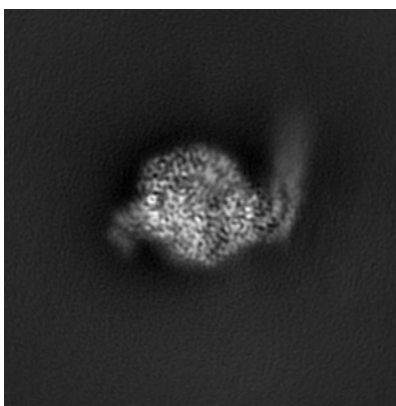
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

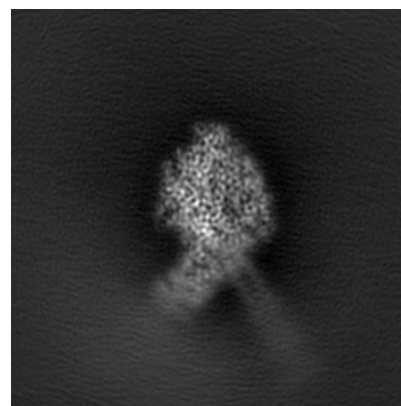
6.1.1 Primary map



X

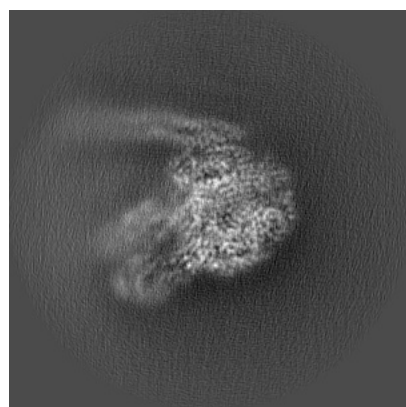


Y

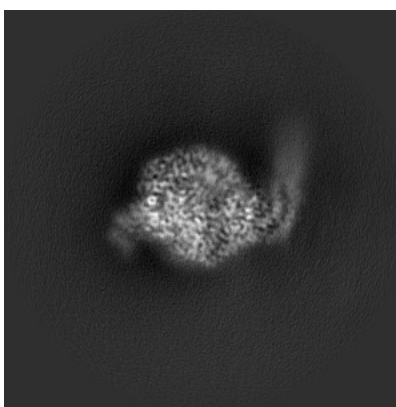


Z

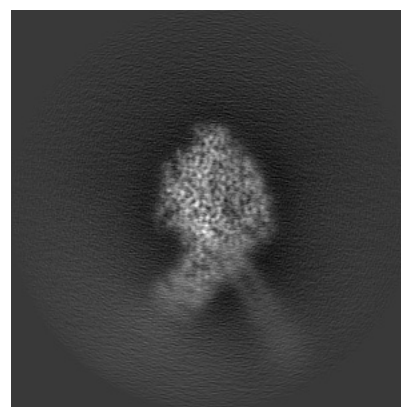
6.1.2 Raw map



X



Y

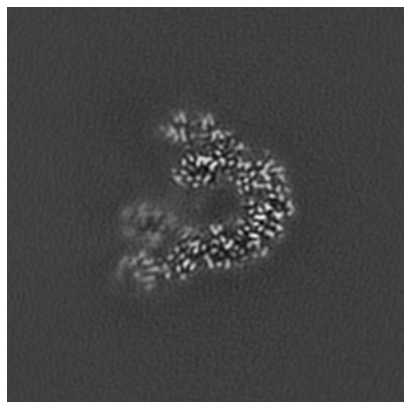


Z

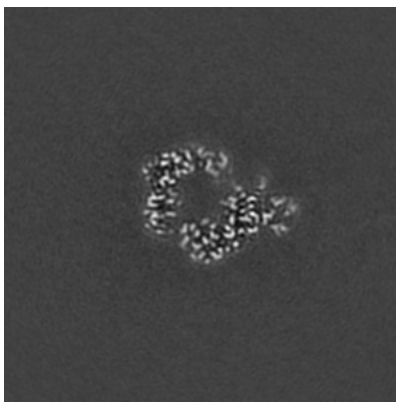
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

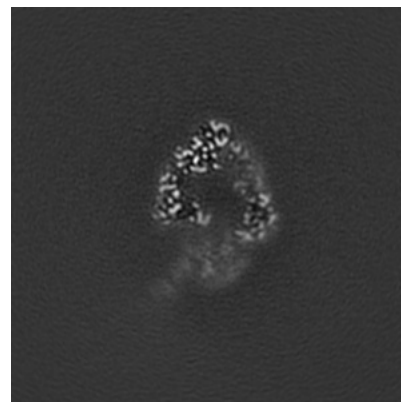
6.2.1 Primary map



X Index: 150

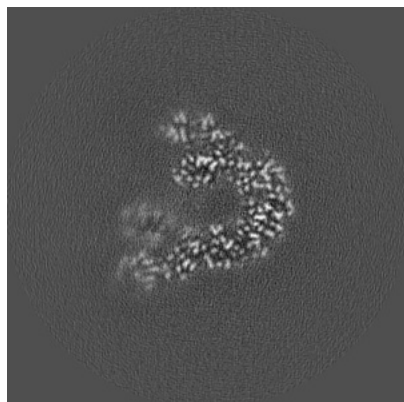


Y Index: 150

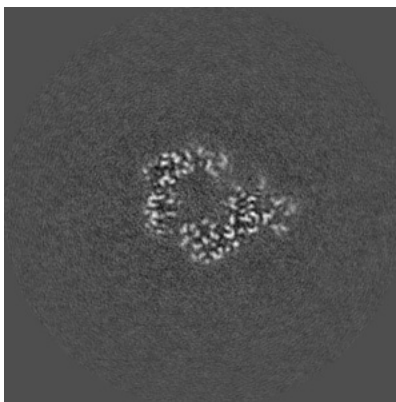


Z Index: 150

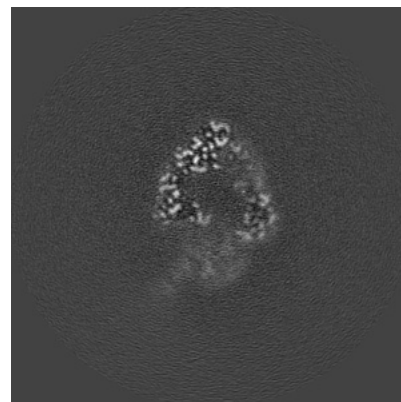
6.2.2 Raw map



X Index: 150



Y Index: 150

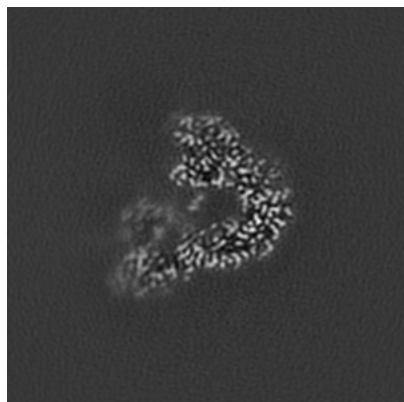


Z Index: 150

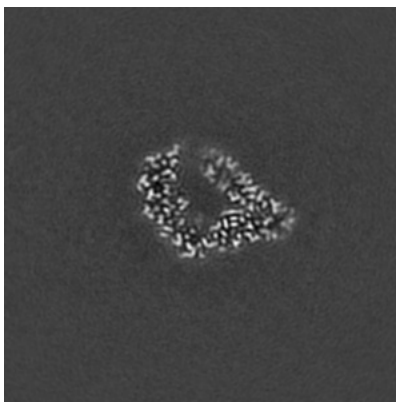
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

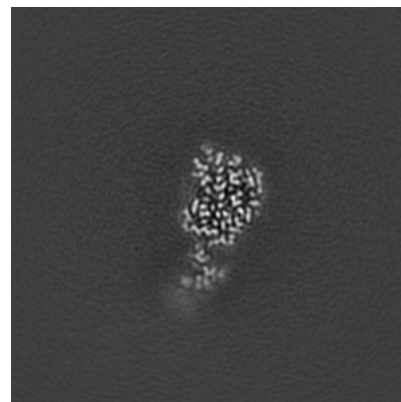
6.3.1 Primary map



X Index: 146

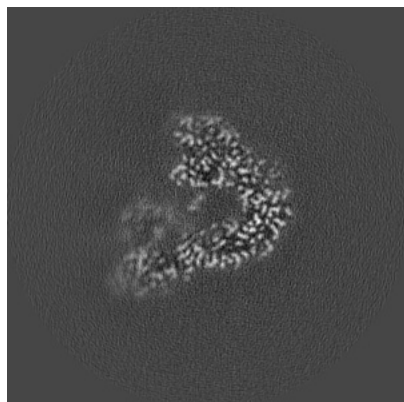


Y Index: 160

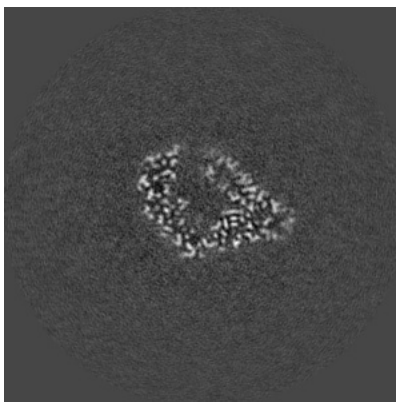


Z Index: 113

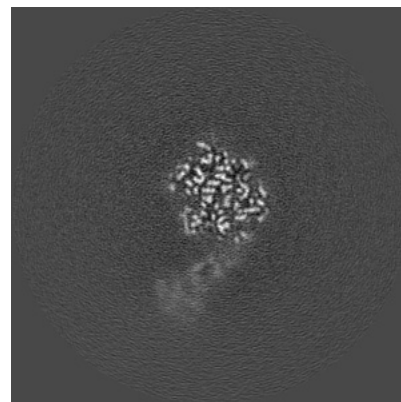
6.3.2 Raw map



X Index: 146



Y Index: 160

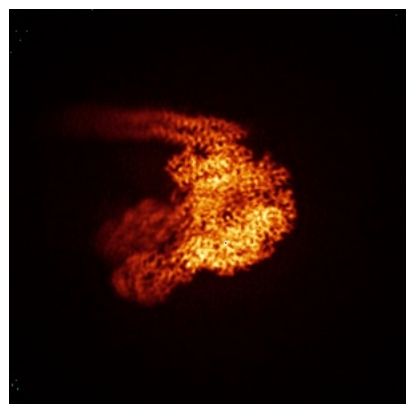


Z Index: 124

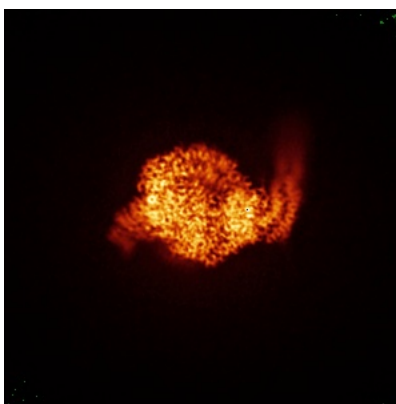
The images above show the largest variance slices of the map in three orthogonal directions.

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

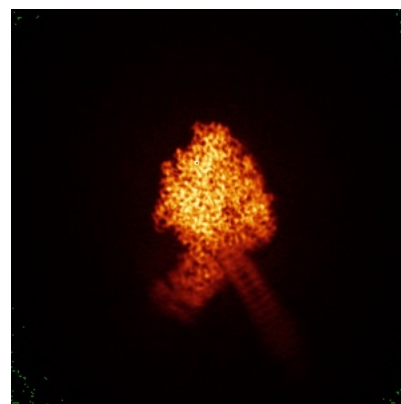
6.4.1 Primary map



X

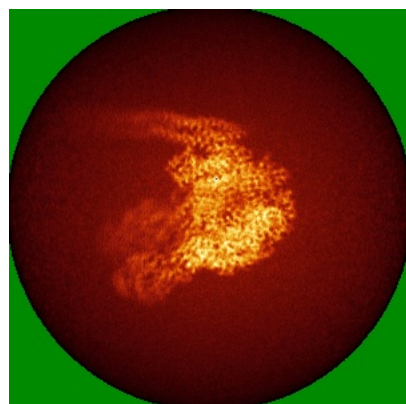


Y

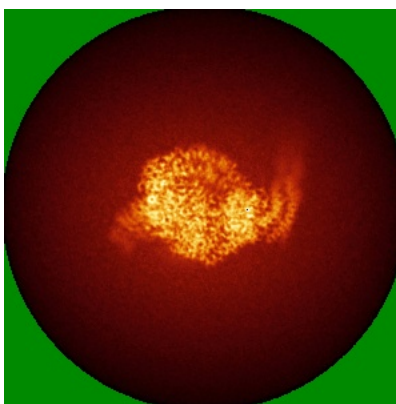


Z

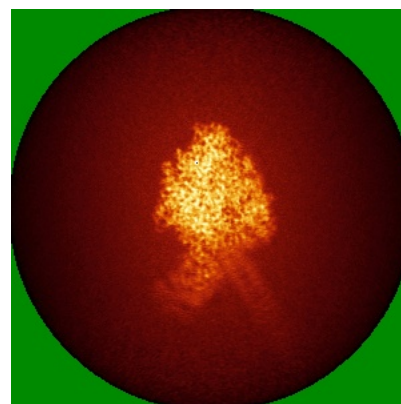
6.4.2 Raw map



X



Y

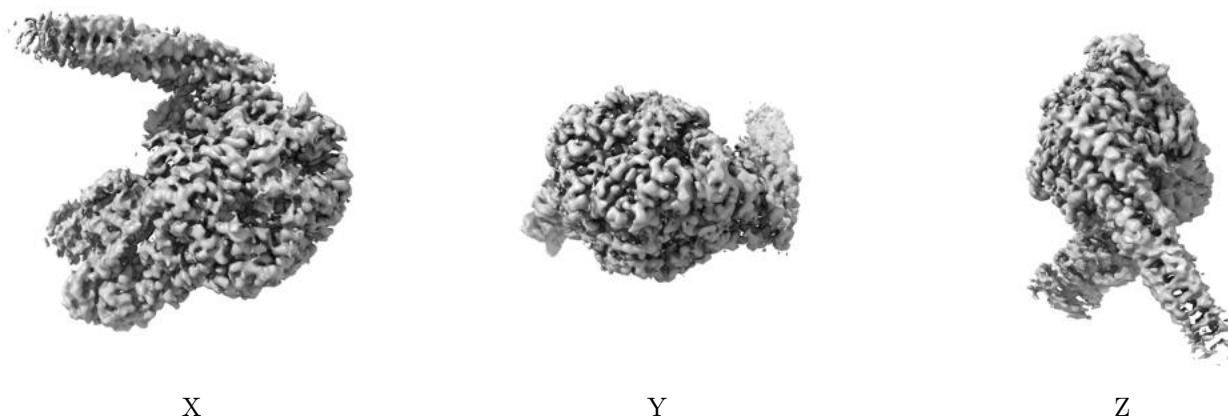


Z

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.

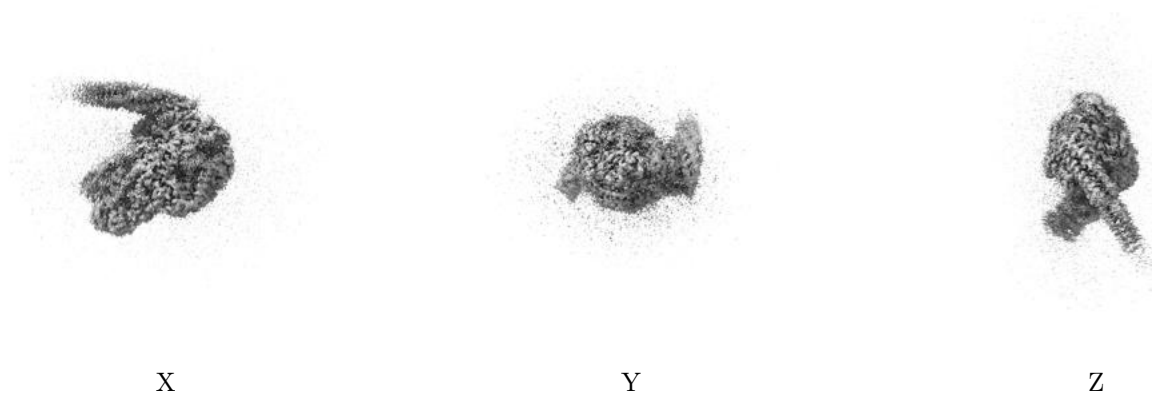
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.003. 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.

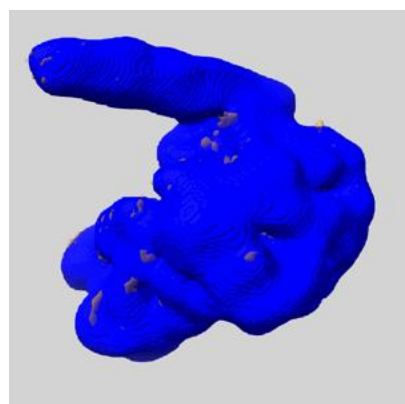
6.6 Mask visualisation [i](#)

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

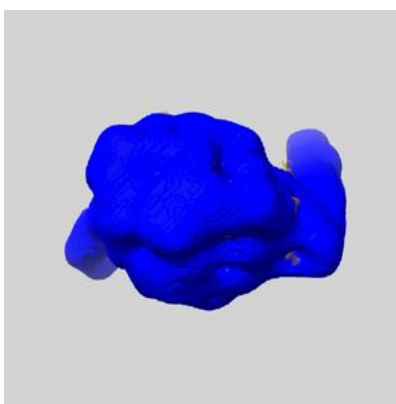
A mask typically either:

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

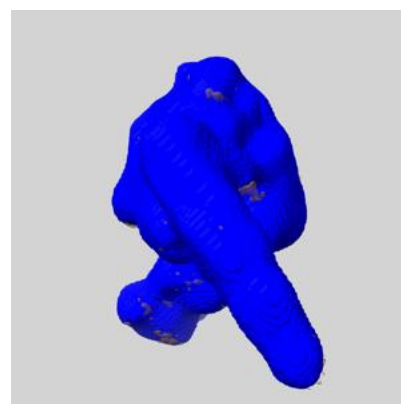
6.6.1 emd_72189_msk_1.map [i](#)



X



Y

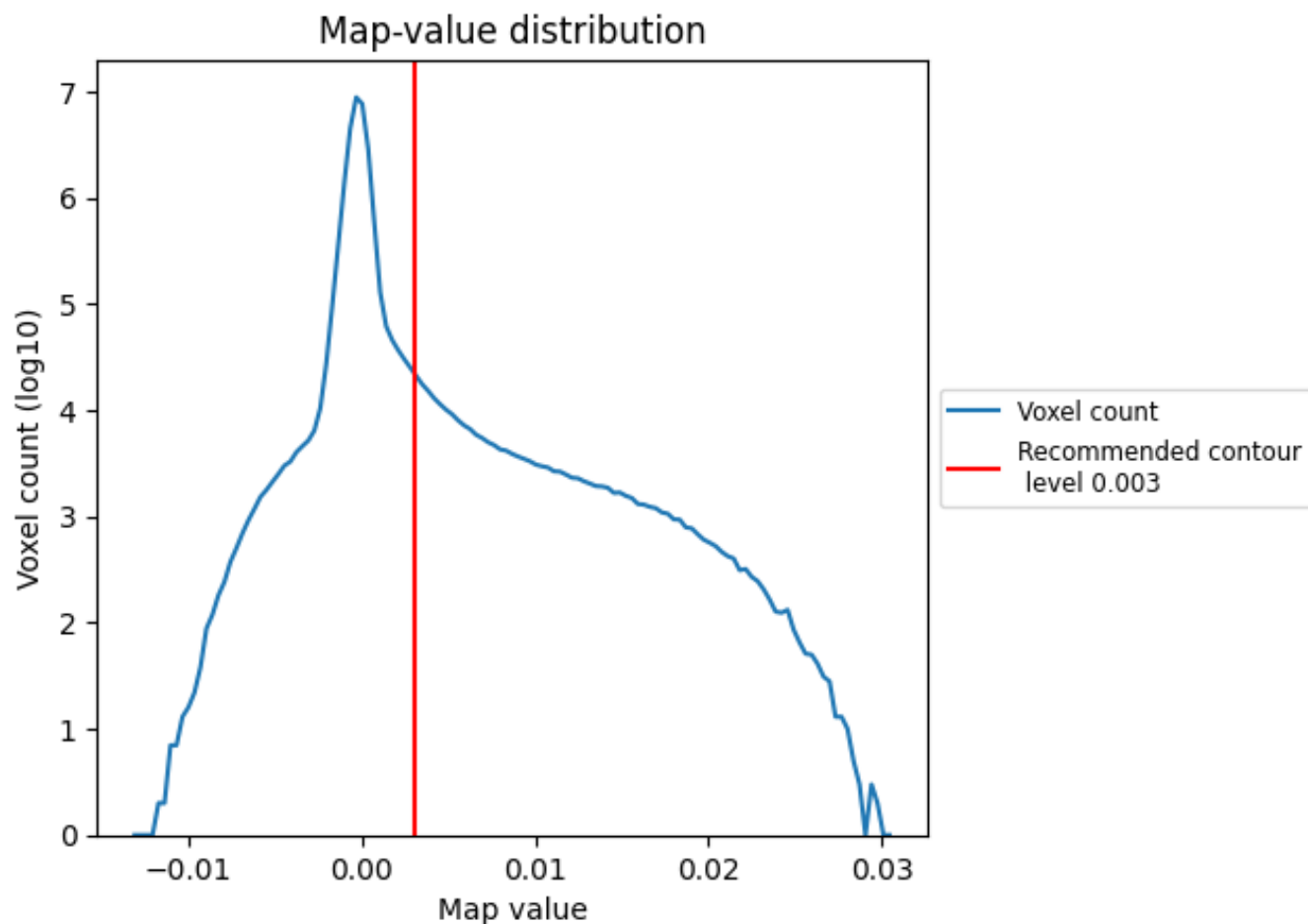


Z

7 Map analysis [i](#)

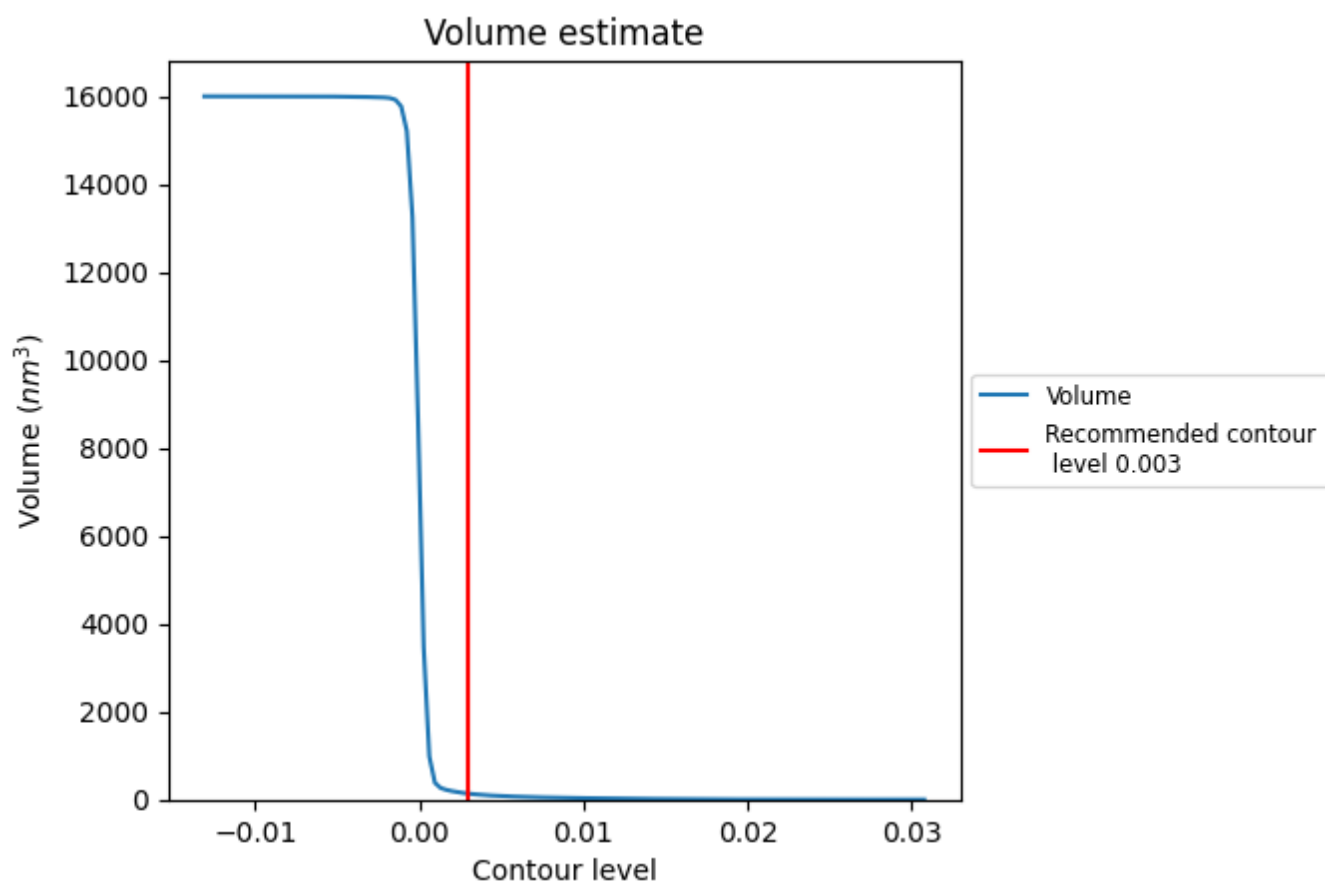
This section contains the results of statistical analysis of the map.

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.

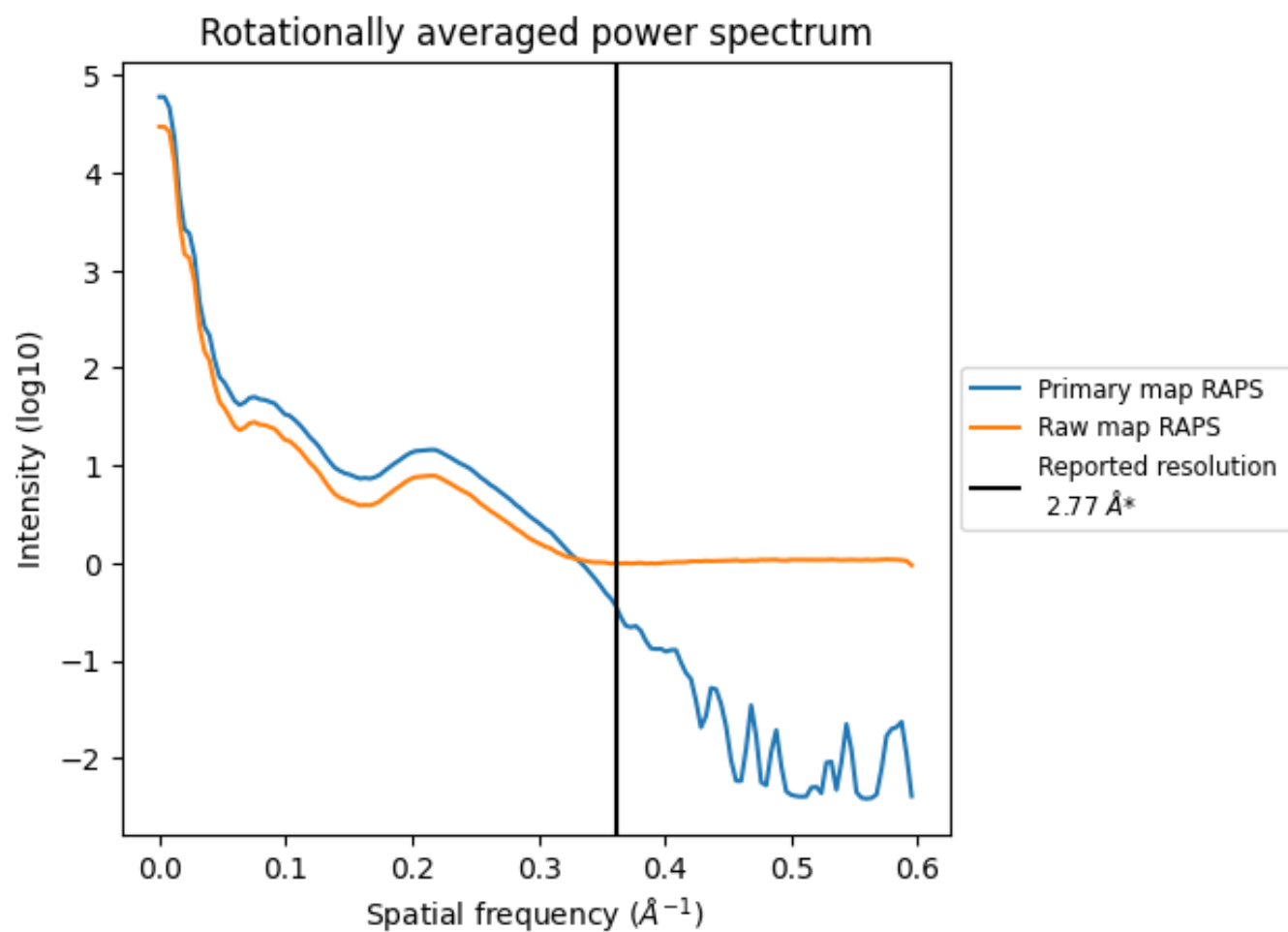
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 135 nm^3 ; this corresponds to an approximate mass of 122 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 ⓘ

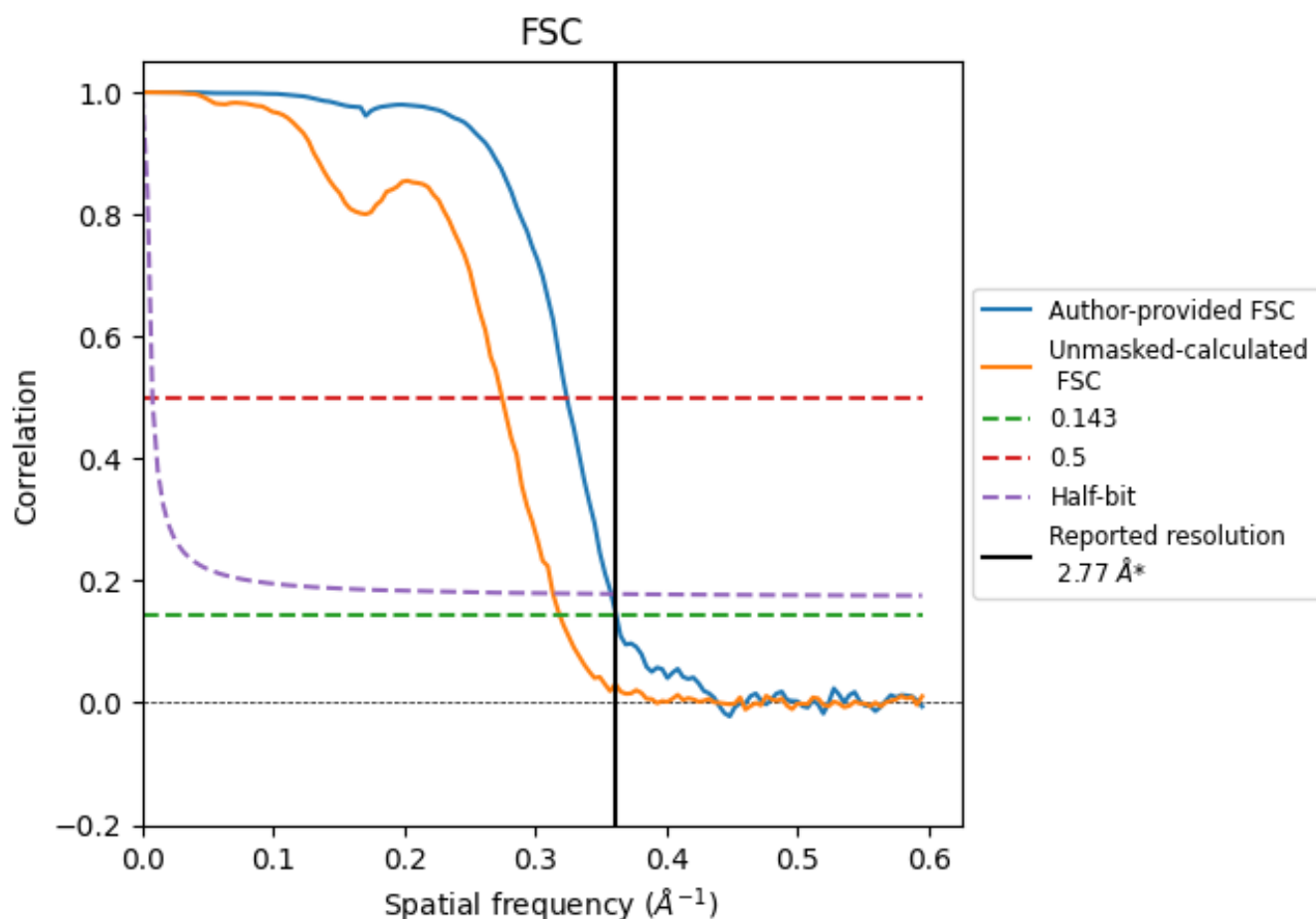


*Reported resolution corresponds to spatial frequency of 0.361 Å⁻¹

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 0.361 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

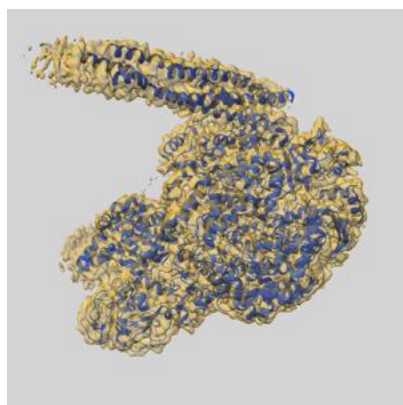
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.77	-	-
Author-provided FSC curve	2.76	3.09	2.79
Unmasked-calculated*	3.14	3.64	3.19

*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 3.14 differs from the reported value 2.77 by more than 10 %

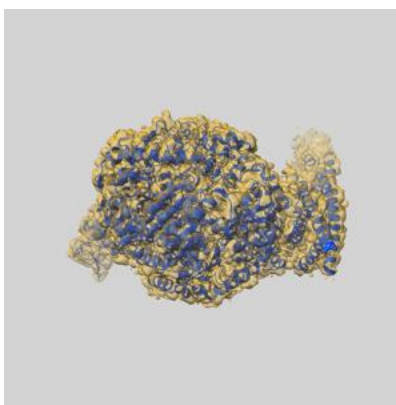
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72189 and PDB model 9Q3A. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

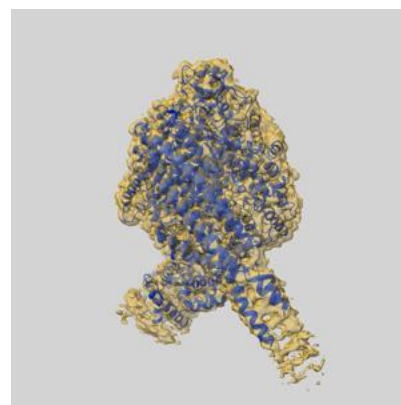
9.1 Map-model overlay [i](#)



X



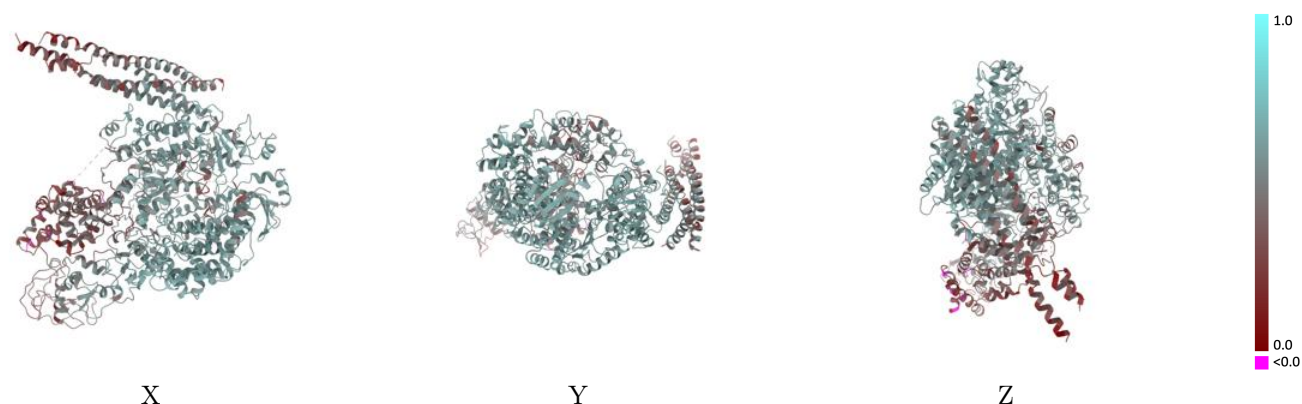
Y



Z

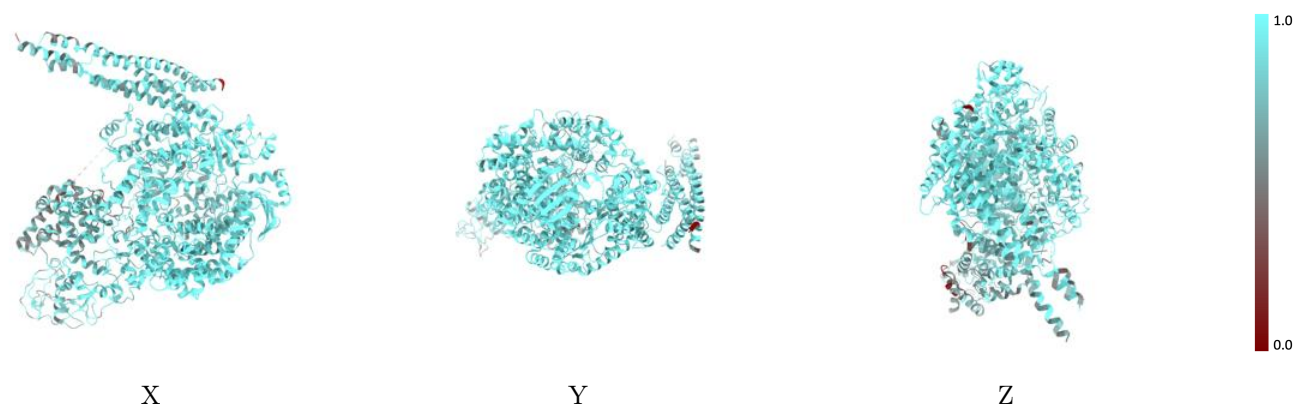
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



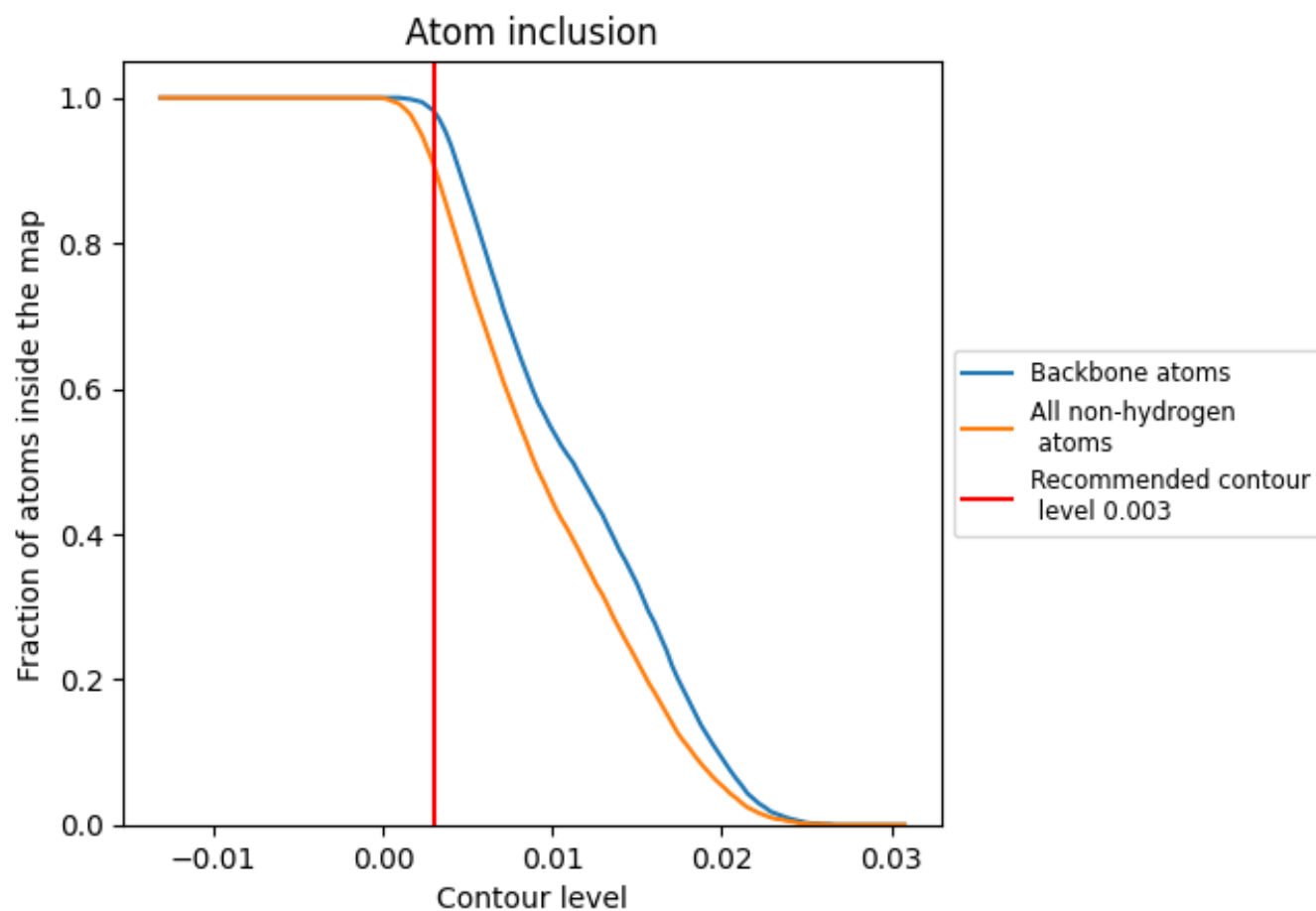
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9090	0.5060
A	0.9150	0.5160
B	0.9030	0.4720
C	0.8670	0.4200
D	0.8380	0.4350
E	0.8340	0.4080

