



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:29 PM UTC

PDB ID : 8IZM / pdb_00008izm
EMDB ID : EMD-35865
Title : Structure of the Mumps Virus L Protein (state2) Bound by Phosphoprotein Tetramer
Authors : Li, T.H.; Shen, Q.T.
Deposited on : 2023-04-07
Resolution : 3.01 Å(reported)

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:

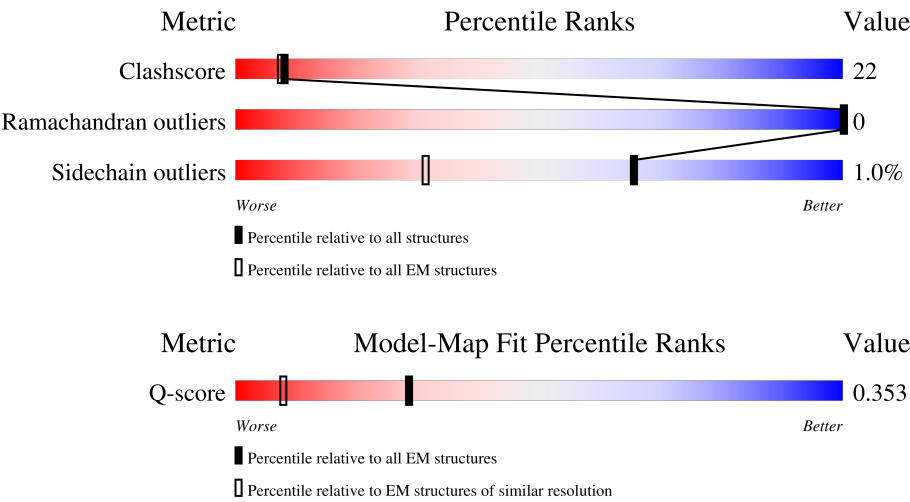
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.01 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	13882 (2.51 - 3.51)

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	B	391	
1	C	391	
1	D	391	
1	E	391	

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Mol	Chain	Length	Quality of chain
2	A	2261	43% 17% 40%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12742 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 Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	69	Total	C	N	O	S	0	0
			517	321	89	101	6		
1	C	85	Total	C	N	O	S	0	0
			642	398	112	126	6		
1	D	50	Total	C	N	O	S	0	0
			387	239	68	77	3		
1	E	54	Total	C	N	O	S	0	0
			412	254	72	81	5		

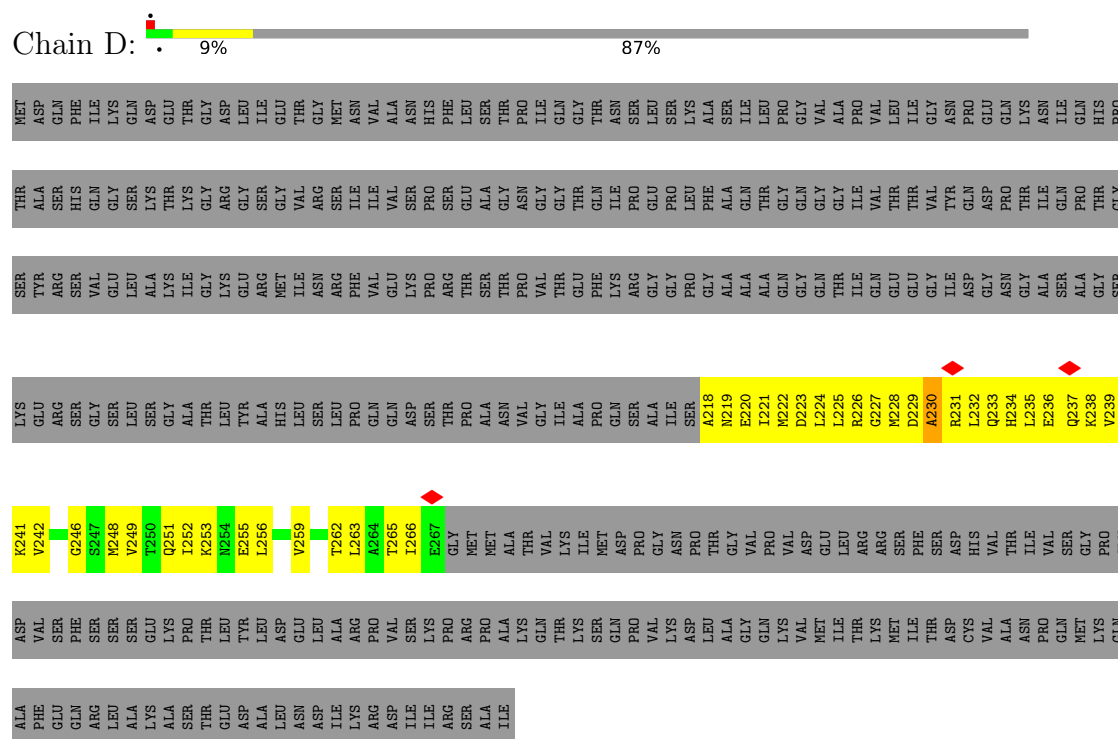
- Molecule 2 is a protein called RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1350	Total	C	N	O	S	0	0
			10782	6893	1841	1987	61		

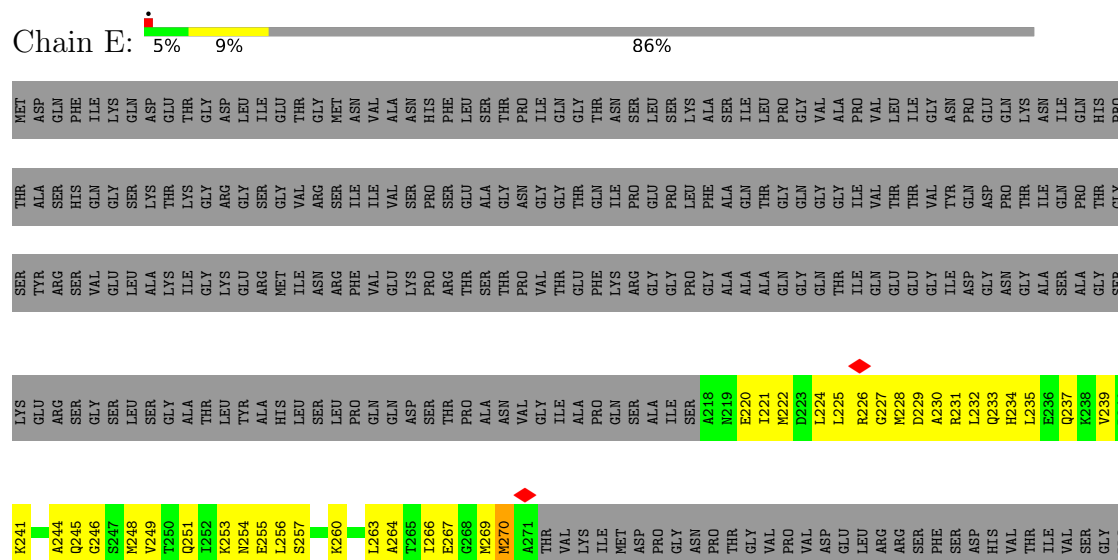
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

- Molecule 1: Phosphoprotein

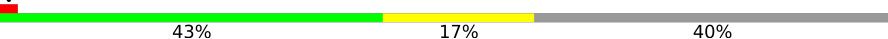


- Molecule 1: Phosphoprotein



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

● Molecule 2: RNA-directed RNA polymerase L

Chain A:  43% 17% 40%

MET	ALA	GLY	L4	I7	L8	E11	V12	L23	H29	G30	L36	L44	W49	I52	H60	L63	R73	I74	L77	R81	I88	L89	I90	W91	I94	I97	Y101	M107	P110	W113	L116	T120	L128	V131																		
S136	L139	T140	L145	R150	A151	GLY	ASP	THR	LYS	ASP	Y158	I160	P161	L166	I169	M173	M184	I185	K186	L192	E200	L201	T202	D203	L204	V205	D209	T210	T213	T218	P219	L224	L232	T233	Y234	L235	W239	W242	T244													
L247	L256	C257	T258	K267	M284	G285	S293	F298	A301	V309	I312	I320	C321	I333	L343	K347	D356	L364	L367	H370	K381	V382	E384	S385	F394	Q395	T396	K398	K399	T400	F404	R410	G411	Y412	R413	R414																
S415	H416	G418	I419	W420	P421	P422	T423	L425	H426	G427	M428	A429	R437	K450	N451	W452	K453	S456	W457	L458	R459	L460	H461	K462	C463	P464	P468	L474	P475	W476	K477	A480	I481	S482	Q486	D487	W488	M489	P492	R493	R494	S495										
L496	L497	R500	Y501	L508	P509	R514	L517	F520	L521	R525	P526	N527	P528	V535	Y540	P546	Y550	K558	A559	R562	L563	F564	A565	K566	M571	Q575	L582	H585	M590	E591	N593	G594	V595	W596	L597	D598	Q599	L600	K601	L602	T603											
K604	S605	L606	L614	L615	E617	H618	SER	ARG	ARG	SER	THR	ALA	ASP	ASN	MET	THR	LEU	ALA	HIS	SER	GLY	R705	L706	M707	R708	S709	T710	L711	D715	P716	N717	P718	P723	L724	Q725	L726	A731	P741	R742	I745	L748	K751	M755	I756	A662	A663	G664	F665	L666	T667	K672	Y673
C674	W677	D779	W780	I785	L793	E797	S806	F809	R812	L813	R814	R815	R816	H822	E826	Q827	T829	F836	I837	R847	L848	L849	K854	N855	W856	S857	K858	L861	T862	D864	L866	A878	W881	H882	R883	E890	L893	E1046	E1047	E1048												
L897	N898	T902	Q905	V911	F912	L927	I933	L936	C937	L943	R957	L963	I967	A968	D969	V970	K971	R972	L973	D980	I981	W982	N986	I987	R990	I1009	T1017	K1020	L1027	M1028	E1029	R1030	P1034	M1035	L1036	V1039	E1046	E1047	E1048													
L1051	L1055	L1056	D1057	R1058	V1061	M1062	P1063	R1064	V1065	V1068	I1069	L1070	C1075	G1076	Y1084	L1085	R1089	S1225	F1317	S1318	V1321	N1325	D1326	C1327	L1328	Q1329	I1330	GLU	ARG	V1232	A1233	S1234	M1235	A1236	Y1237	S1244	A1248	L1249	R1250	L1251	A1252	G1253	Y1254	L1255	P1170	D1171	P1172	I1173	V1176	L1177	G1178	
C1179	L1180	I1181	C1187	E1188	H1189	C1190	F1197	T1198	W1199	L1202	P1203	I1206	R1207	L1208	D1209	P1216	I1223	G1224	S1225	K1226	T1227	D1228	GLU	ARG	V1232	A1233	S1234	M1235	A1236	Y1237	S1244	A1248	L1249	R1250	L1251	A1252	G1253	Y1254	L1255	P1170	D1171	P1172	I1173	V1176	L1177	G1178						
A1269	A1273	P1289	M1295	L1296	V1297	H1298	H1299	LEU	ASP	ASP	GLY	THR	THR	GLN	LEU	K1308	F1309	T1310	Y1315	A1316	F1317	S1318	V1321	N1325	D1326	C1327	L1328	Q1329	I1330	GLU	ILE	ASP	ASP	GLN	VAL	T1337	D1338	S1339	I1342	L1351	A1352	L1353	T1356	M1359	P1360	P1361	T1369	D1268				



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	477568	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.682	Depositor
Minimum map value	-0.006	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	233.19998, 233.19998, 233.19998	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.53, 0.53, 0.53	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	B	0.80	0/520	0.97	2/701 (0.3%)
1	C	0.67	1/648 (0.2%)	1.03	2/874 (0.2%)
1	D	0.67	0/387	1.17	2/519 (0.4%)
1	E	0.72	0/412	0.87	0/551
2	A	0.44	8/11010 (0.1%)	0.70	18/14946 (0.1%)
All	All	0.49	9/12977 (0.1%)	0.76	24/17591 (0.1%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	444	LYS	C-N	8.16	1.45	1.34
2	A	443	LEU	C-N	7.68	1.44	1.33
2	A	285	GLY	C-N	6.36	1.43	1.33
2	A	672	LYS	C-N	-6.25	1.25	1.33
2	A	364	ILE	C-N	6.11	1.41	1.33

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	414	ARG	N-CA-C	-7.54	102.25	113.72
1	C	228	MET	CA-C-N	6.98	132.52	120.58
1	C	228	MET	C-N-CA	6.98	132.52	120.58
2	A	412	TYR	N-CA-C	-6.78	103.89	111.28
2	A	415	SER	N-CA-C	-6.61	100.12	108.45

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	517	0	544	92	0
1	C	642	0	665	122	0
1	D	387	0	408	125	0
1	E	412	0	434	79	0
2	A	10782	0	10909	296	0
3	A	2	0	0	0	0
All	All	12742	0	12960	567	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 22.

The worst 5 of 567 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:D:252:ILE:HD12	1:E:256:LEU:CG	1.26	1.57
1:C:259:VAL:CG2	1:D:256:LEU:HD13	1.07	1.54
1:C:259:VAL:HG21	1:D:256:LEU:CD1	1.15	1.53
1:D:252:ILE:HD12	1:E:256:LEU:CD2	1.62	1.29
1:D:252:ILE:CD1	1:E:256:LEU:HG	1.61	1.29

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	B	67/391 (17%)	63 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	83/391 (21%)	81 (98%)	2 (2%)	0	100	100
1	D	48/391 (12%)	48 (100%)	0	0	100	100
1	E	52/391 (13%)	51 (98%)	1 (2%)	0	100	100
2	A	1338/2261 (59%)	1296 (97%)	42 (3%)	0	100	100
All	All	1588/3825 (42%)	1539 (97%)	49 (3%)	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	B	59/324 (18%)	54 (92%)	5 (8%)	10	35
1	C	74/324 (23%)	71 (96%)	3 (4%)	27	60
1	D	44/324 (14%)	44 (100%)	0	100	100
1	E	46/324 (14%)	45 (98%)	1 (2%)	45	73
2	A	1214/2037 (60%)	1209 (100%)	5 (0%)	84	89
All	All	1437/3333 (43%)	1423 (99%)	14 (1%)	65	83

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	295	ASP
1	E	270	MET
2	A	1384	VAL
2	A	972	ARG
2	A	1190	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	780	ASN
2	A	905	GLN
2	A	1298	HIS
2	A	1215	ASN
2	A	5	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are 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.

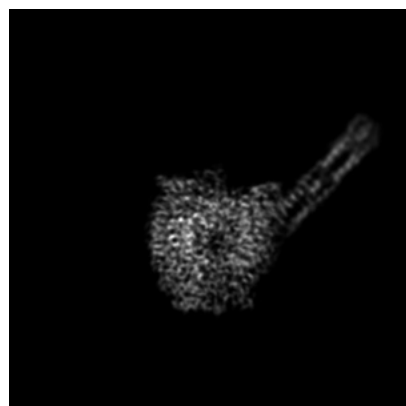
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35865. These allow visual inspection of the internal detail of the map and identification of artifacts.

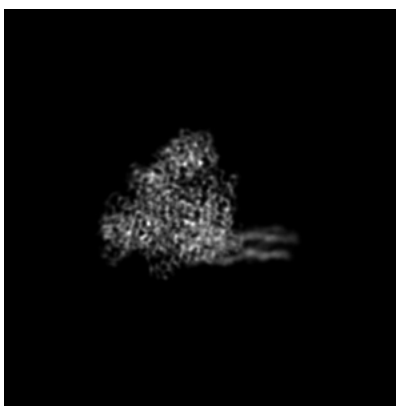
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

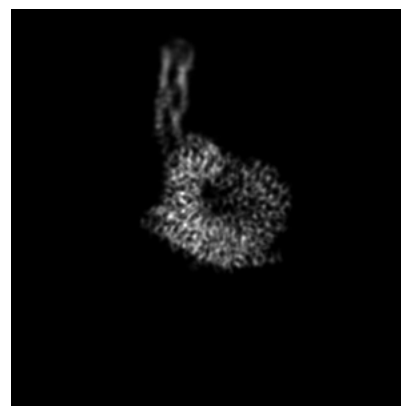
6.1.1 Primary map



X

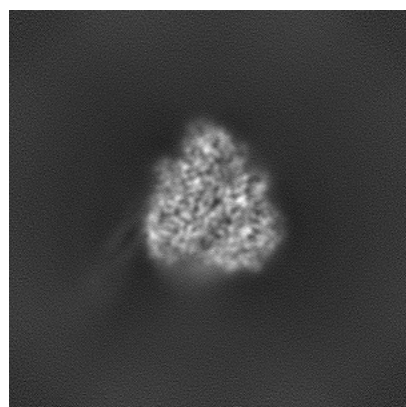


Y

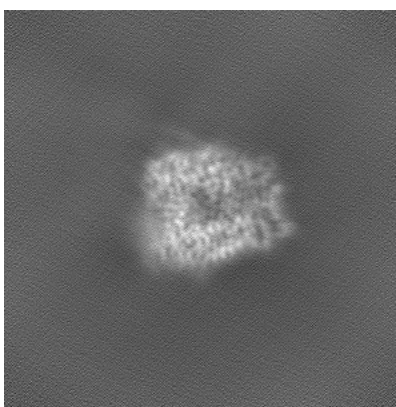


Z

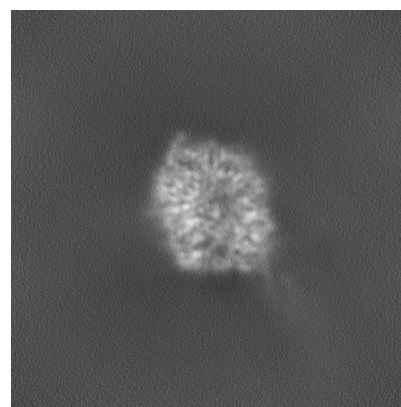
6.1.2 Raw map



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: 220

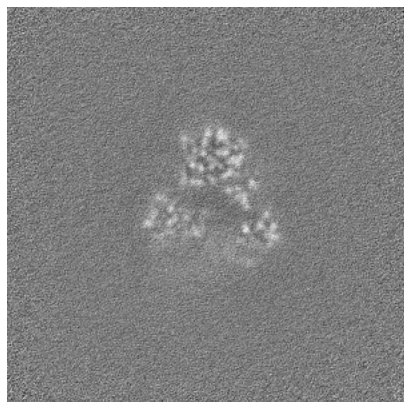


Y Index: 220

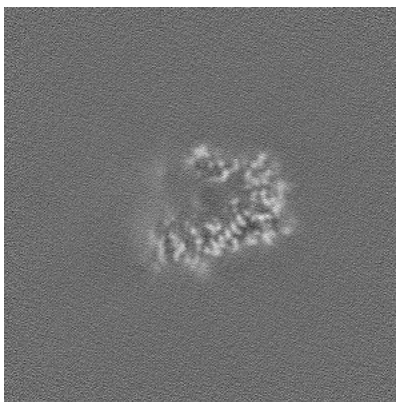


Z Index: 220

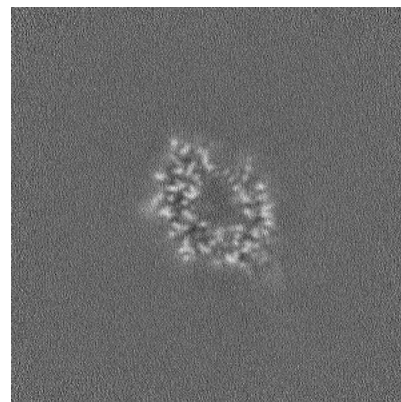
6.2.2 Raw map



X Index: 220



Y Index: 220



Z Index: 220

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: 189

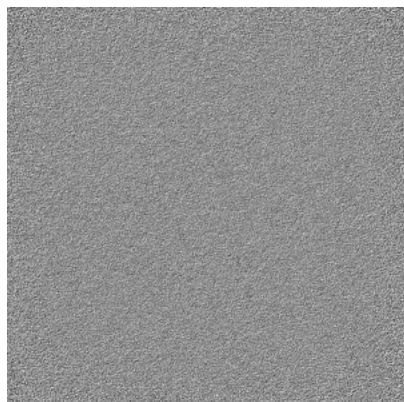


Y Index: 198

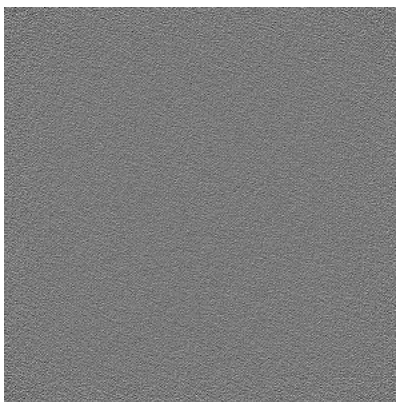


Z Index: 206

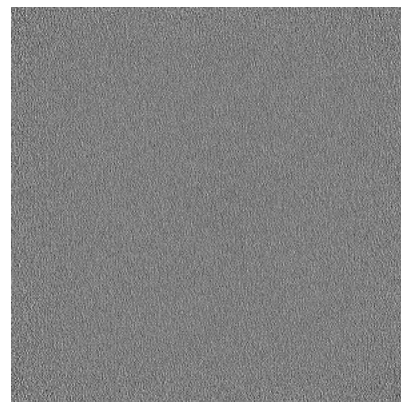
6.3.2 Raw map



X Index: 0



Y Index: 0



Z Index: 0

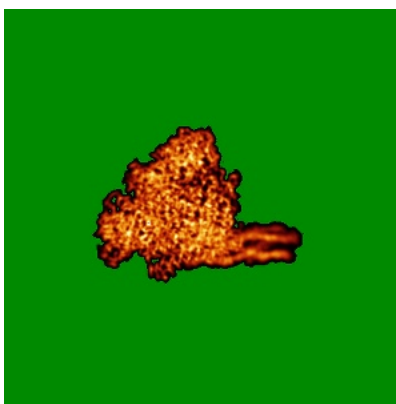
The images above show the largest variance slices of the map in three orthogonal directions.

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

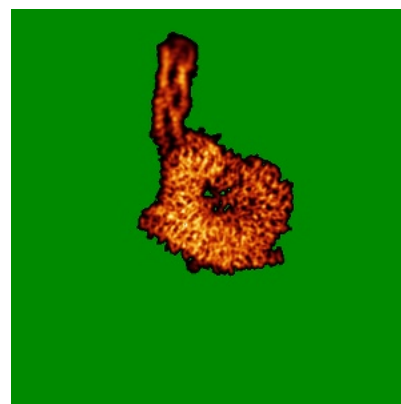
6.4.1 Primary map



X

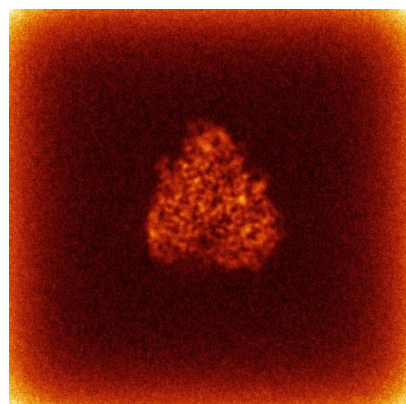


Y

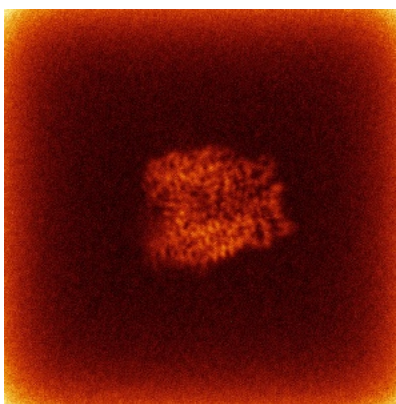


Z

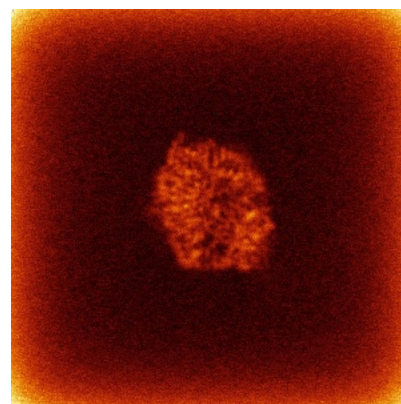
6.4.2 Raw map



X



Y

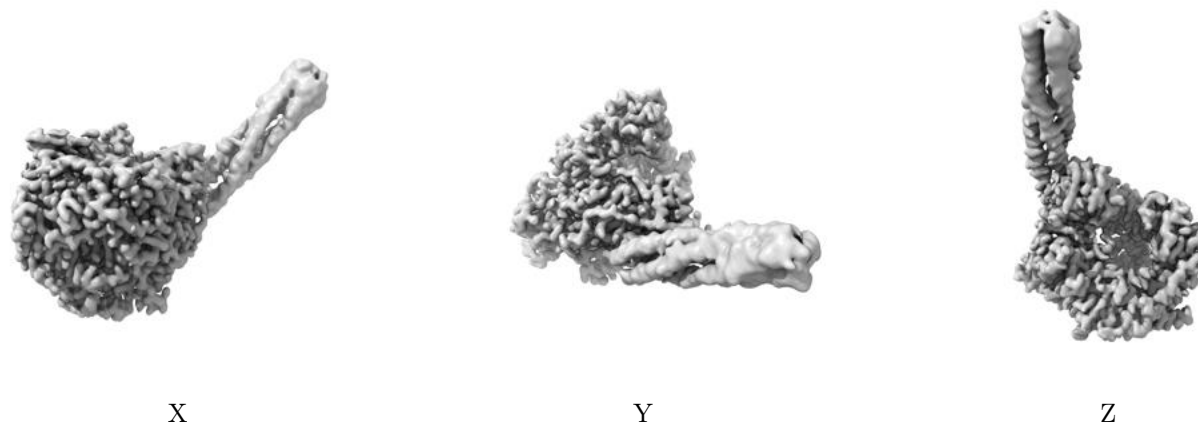


Z

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.

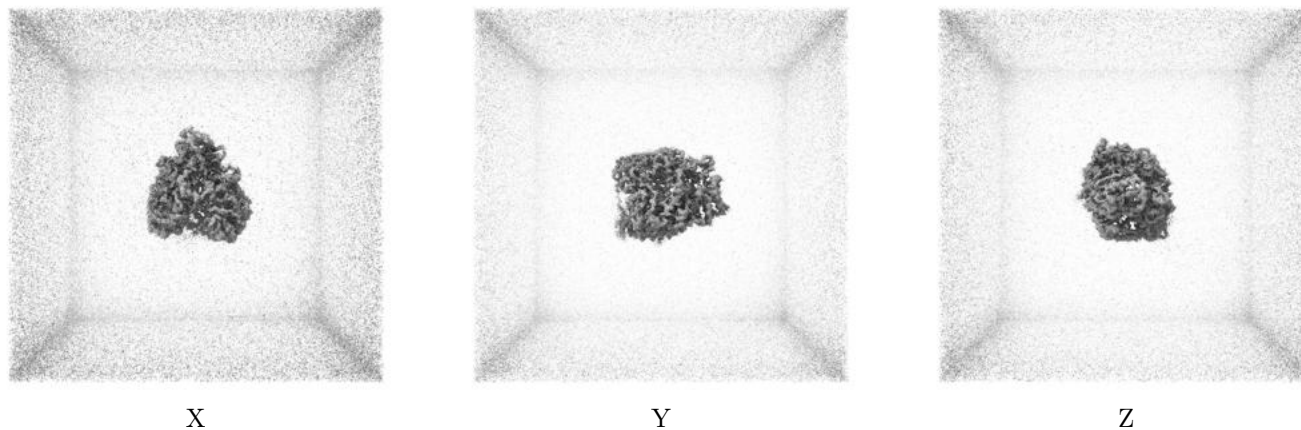
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. 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.

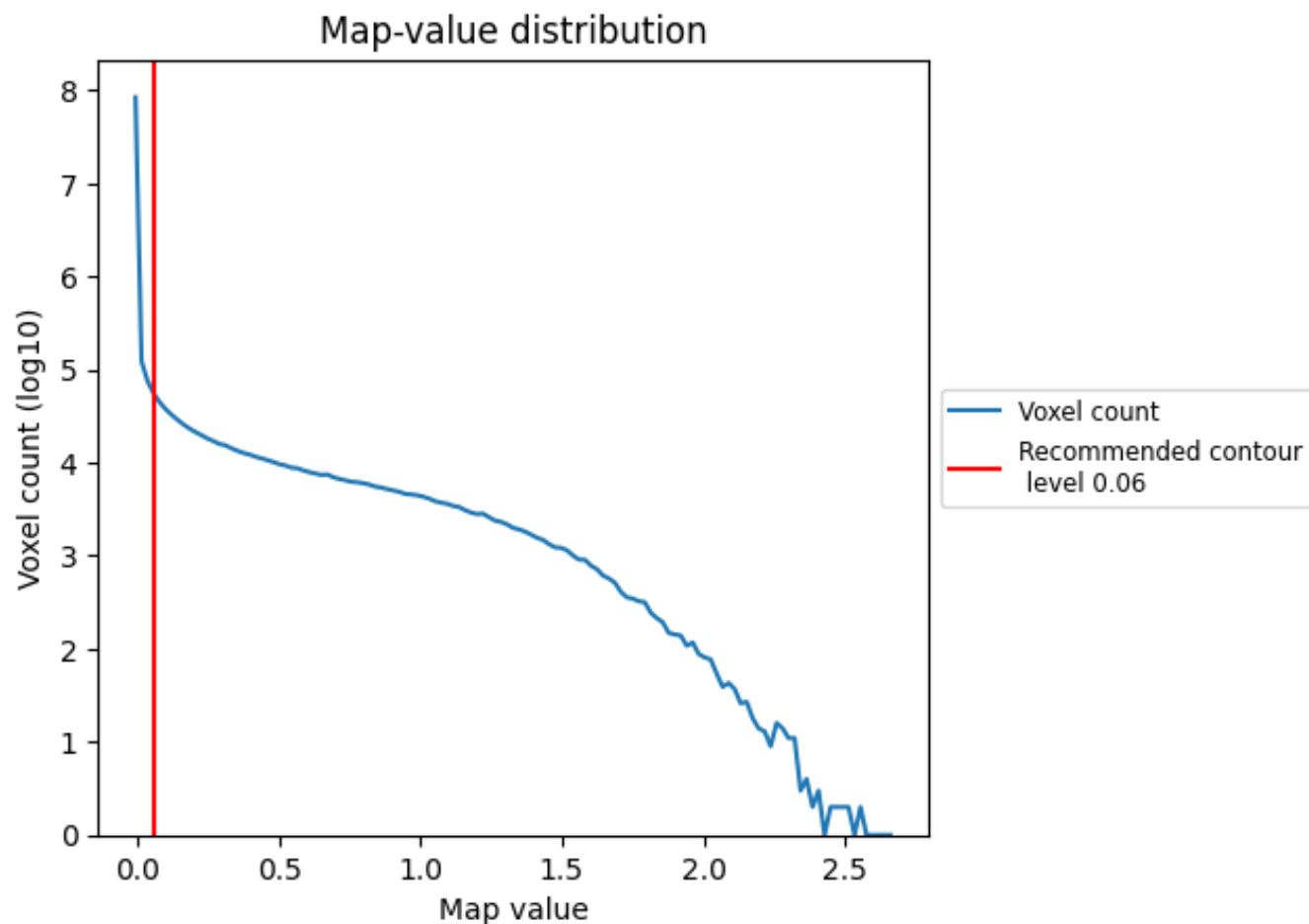
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

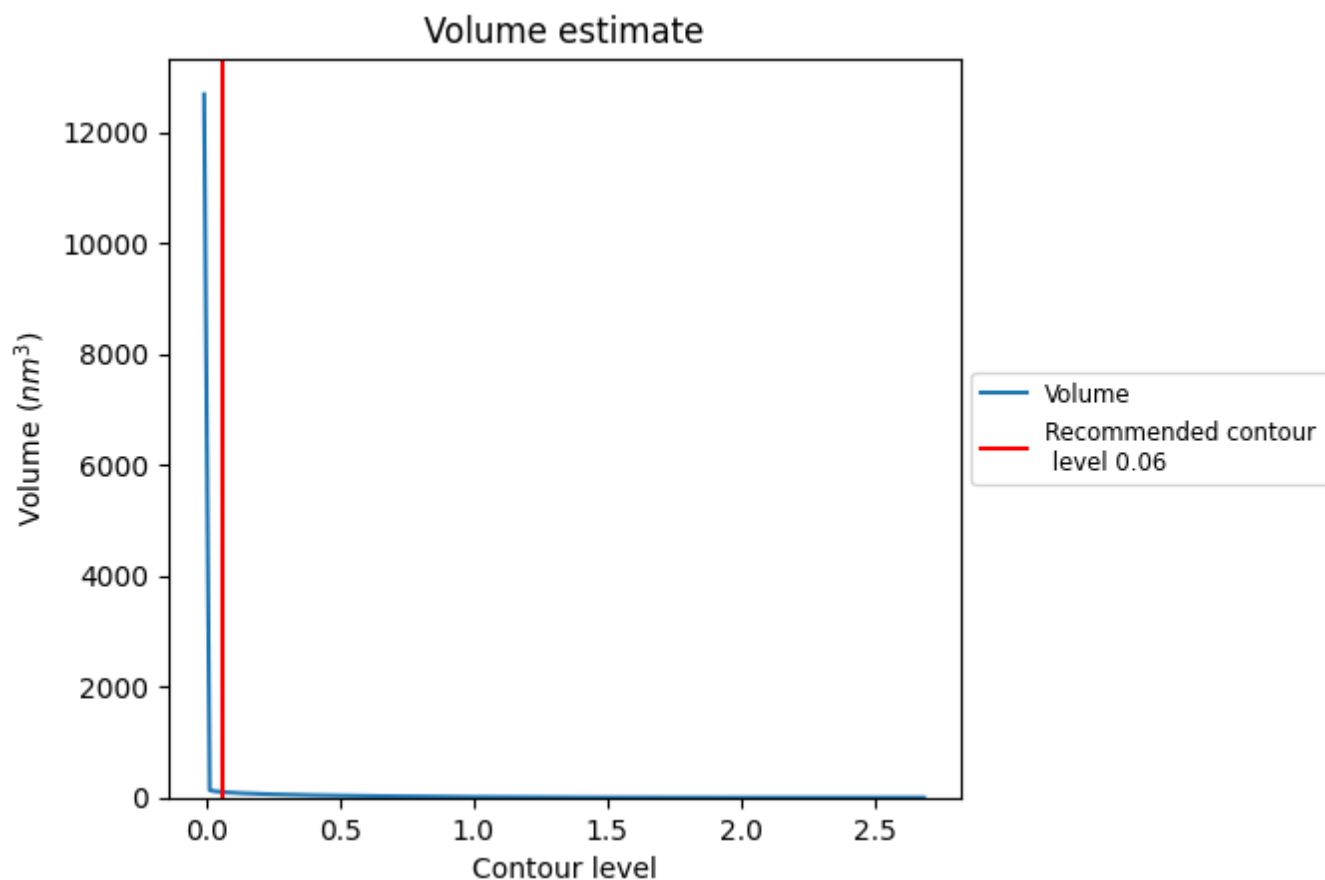
This section contains the results of statistical analysis of the map.

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.

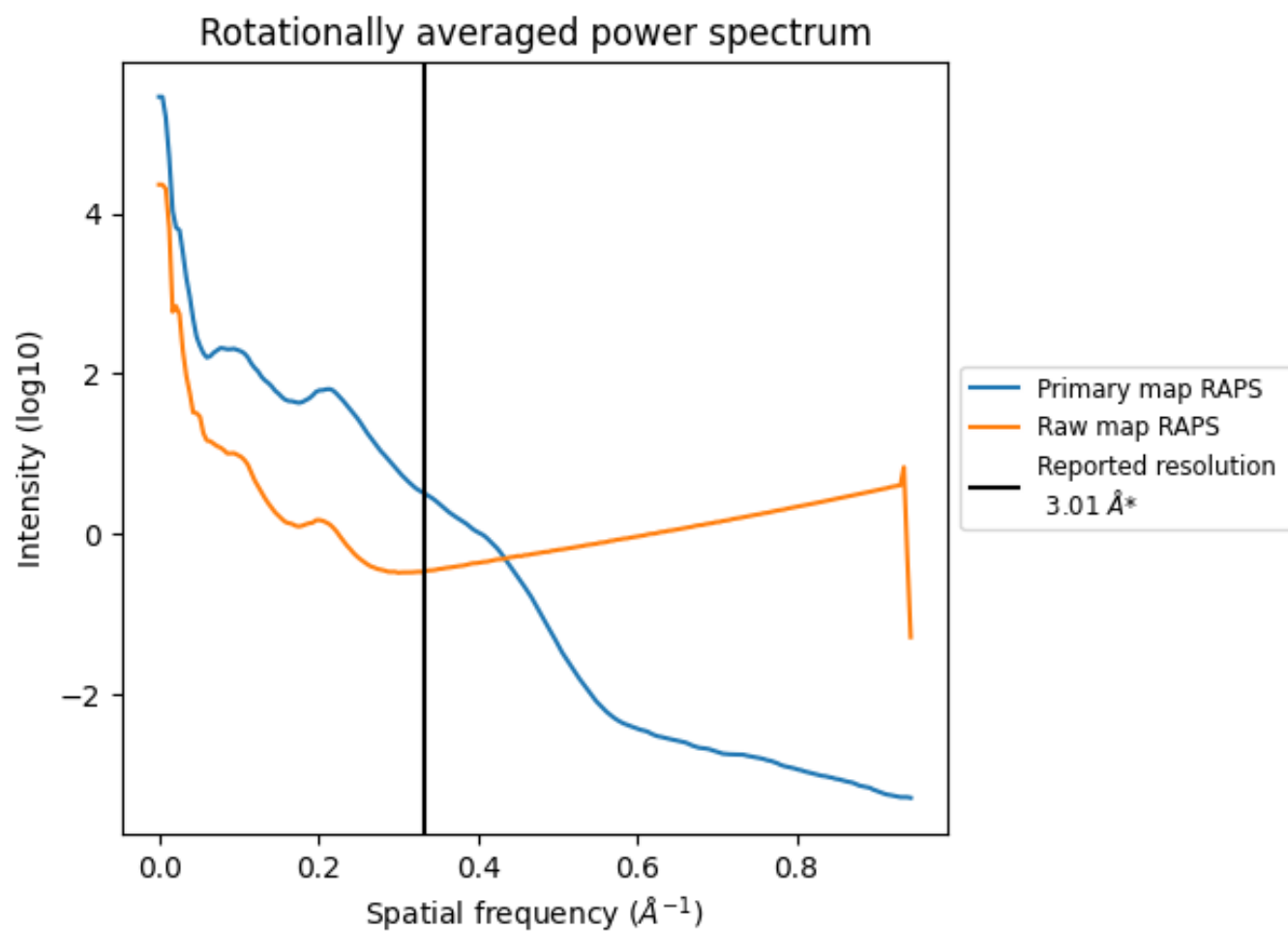
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 101 nm^3 ; this corresponds to an approximate mass of 91 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 ⓘ

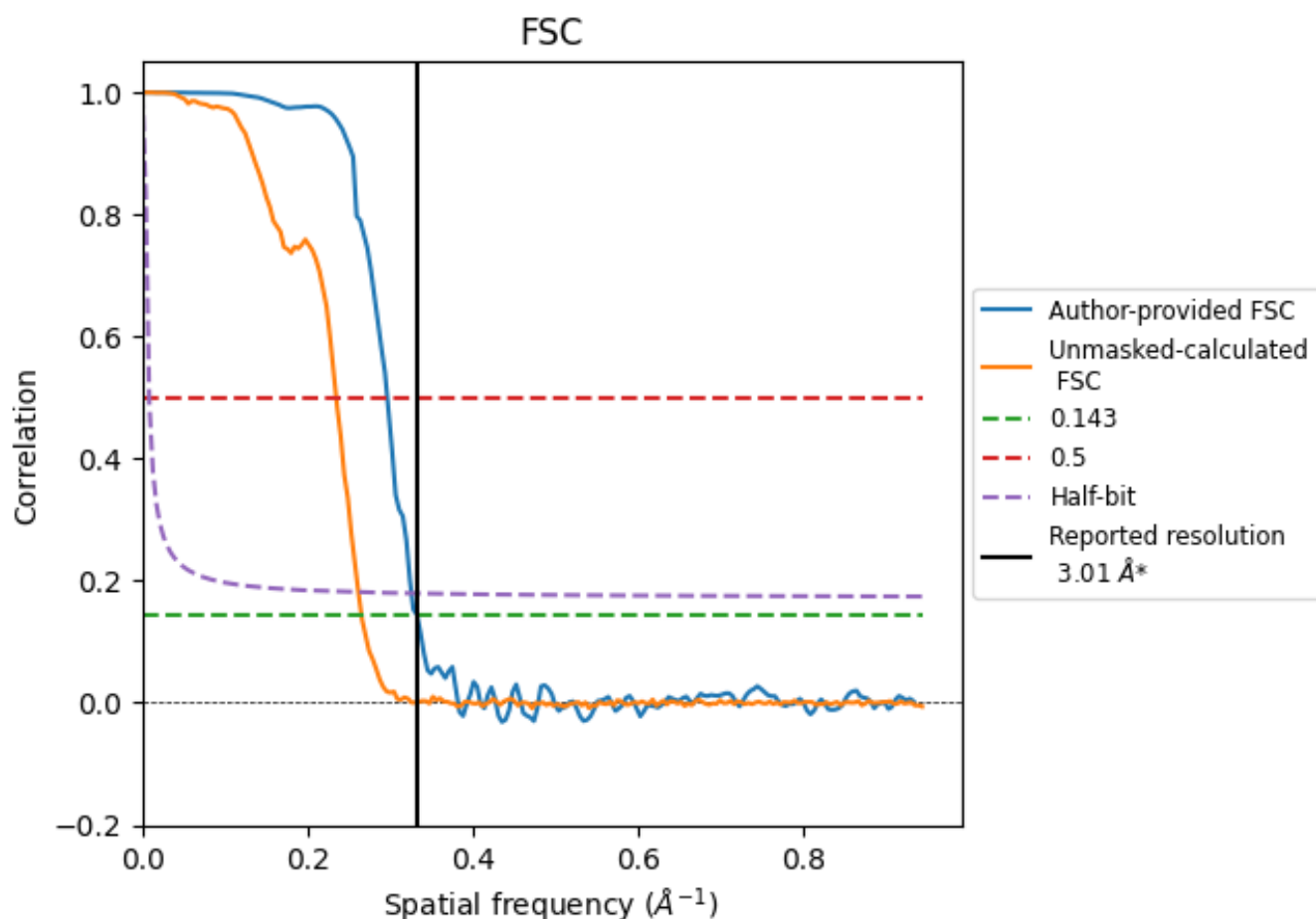


*Reported resolution corresponds to spatial frequency of 0.332 $\text{\AA}^{-1}$

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 0.332 Å⁻¹

8.2 Resolution estimates [i](#)

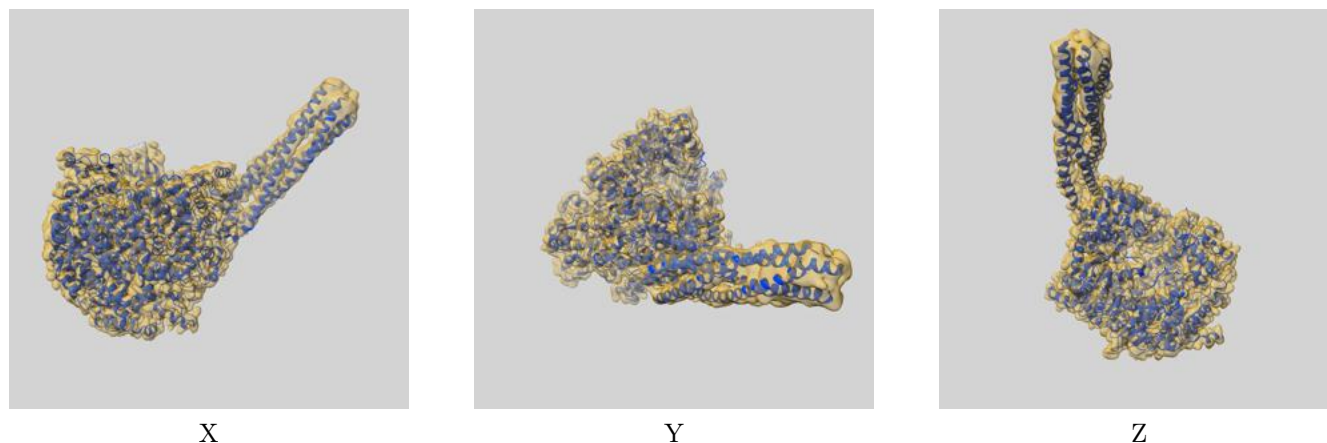
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.01	-	-
Author-provided FSC curve	3.01	3.37	3.07
Unmasked-calculated*	3.77	4.26	3.82

*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 3.77 differs from the reported value 3.01 by more than 10 %

9 Map-model fit [i](#)

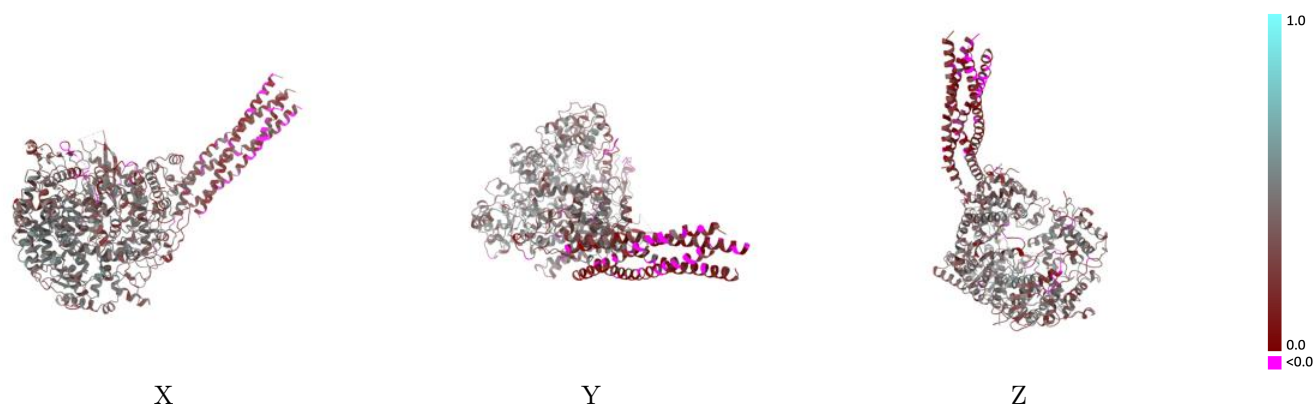
This section contains information regarding the fit between EMDB map EMD-35865 and PDB model 8IZM. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



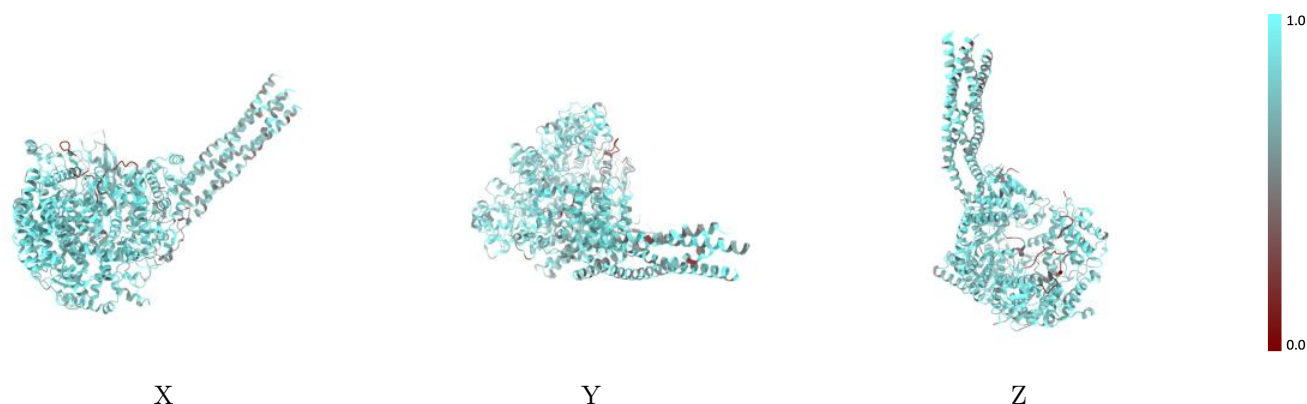
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



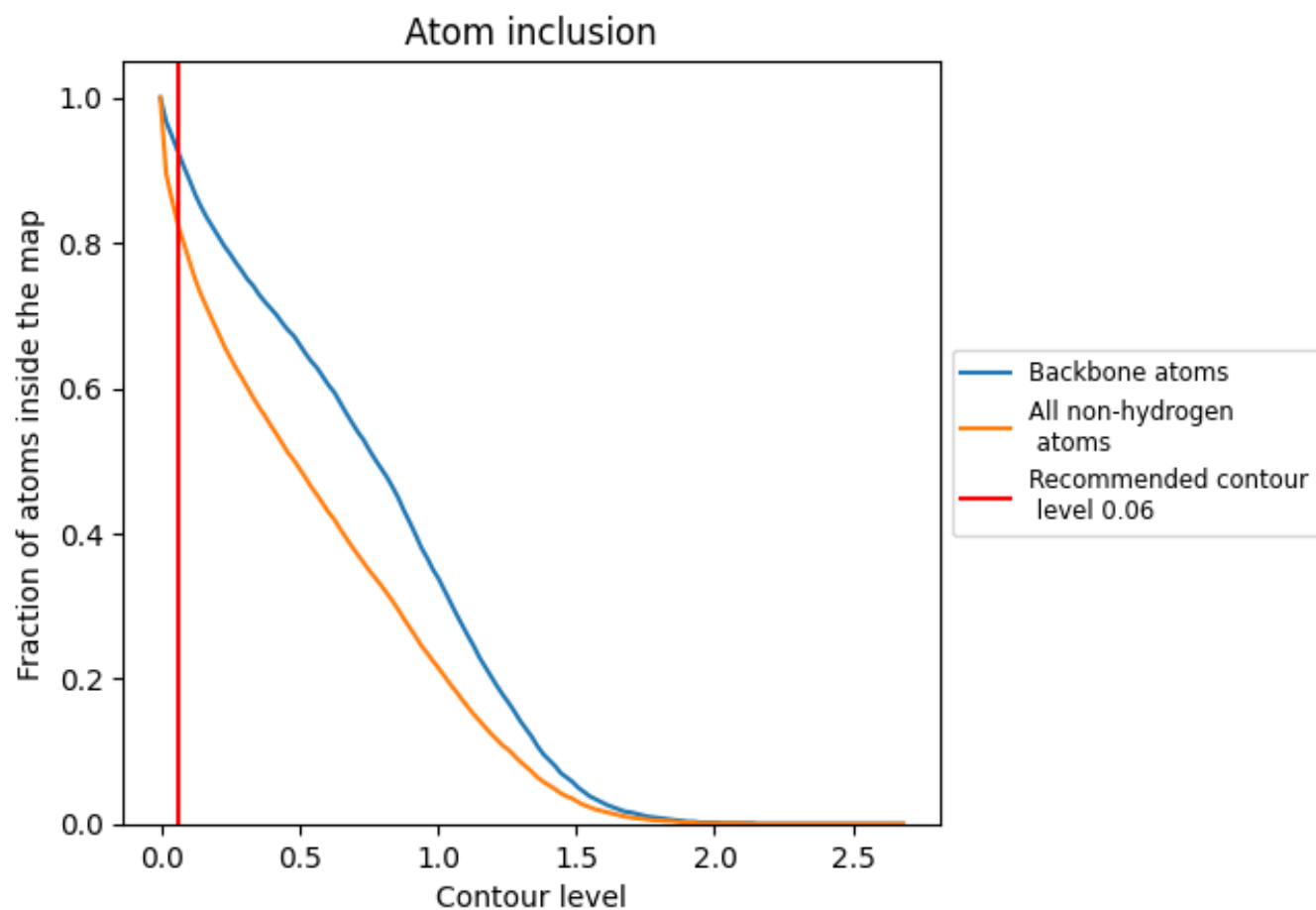
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 82% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8220	0.3530
A	0.8430	0.3890
B	0.7540	0.2050
C	0.6920	0.1710
D	0.6660	0.0930
E	0.7080	0.1360

