



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 04:12 AM UTC

PDB ID : 8T9L / pdb_00008t9l
EMDB ID : EMD-41117
Title : Pom34-Pom152 membrane attachment site yeast NPC
Authors : Akey, C.W.; Echeverria, I.; Ouch, C.; Fernandez-Martinez, J.; Rout, M.P.
Deposited on : 2023-06-24
Resolution : 7.00 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

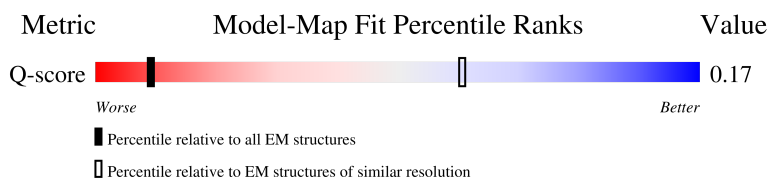
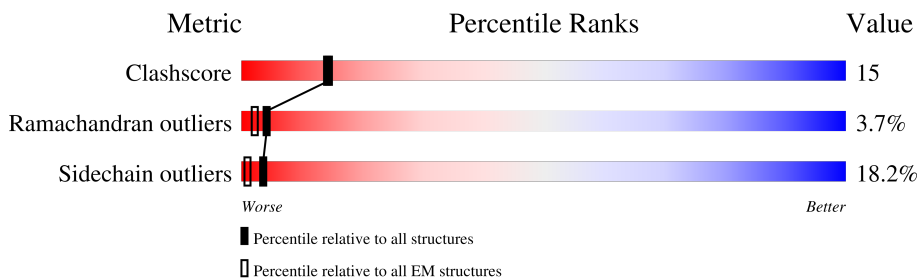
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.00 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	483 (6.50 - 7.50)

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	1337	6% .. 92%
1	D	1337	6% .. 92%
2	A	299	5% 24% 7% . . 64%
2	C	299	6% 23% 7% . . 64%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3718 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 Nucleoporin POM152.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	110	Total	C	N	O	S	0	0
			933	642	140	148	3		
1	D	110	Total	C	N	O	S	0	0
			933	642	140	148	3		

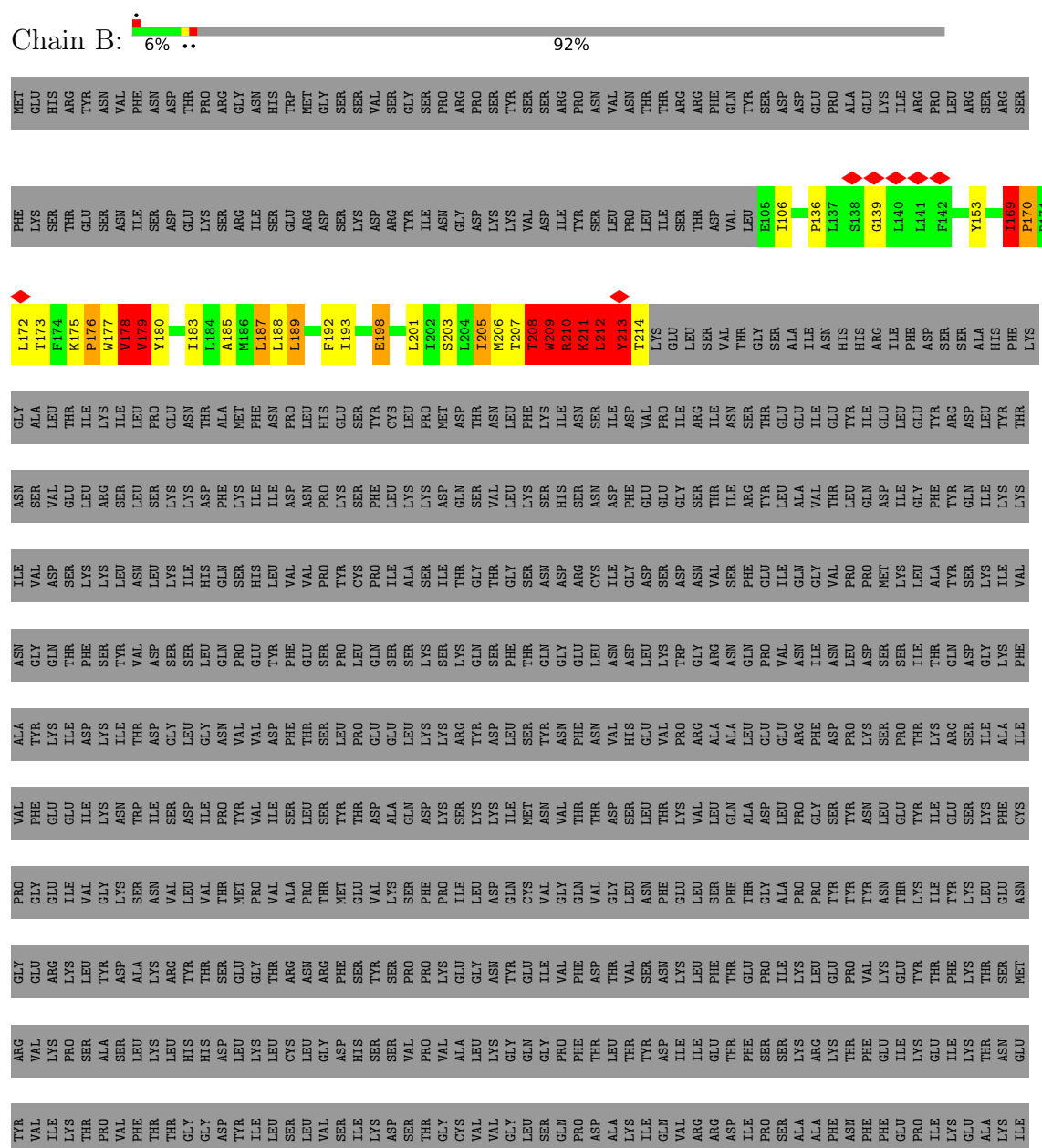
- Molecule 2 is a protein called Nucleoporin POM34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	108	Total	C	N	O	S	0	0
			926	617	158	147	4		
2	C	108	Total	C	N	O	S	0	0
			926	617	158	147	4		

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: Nucleoporin POM152



[illegible]

- Molecule 1: Nucleoporin POM152



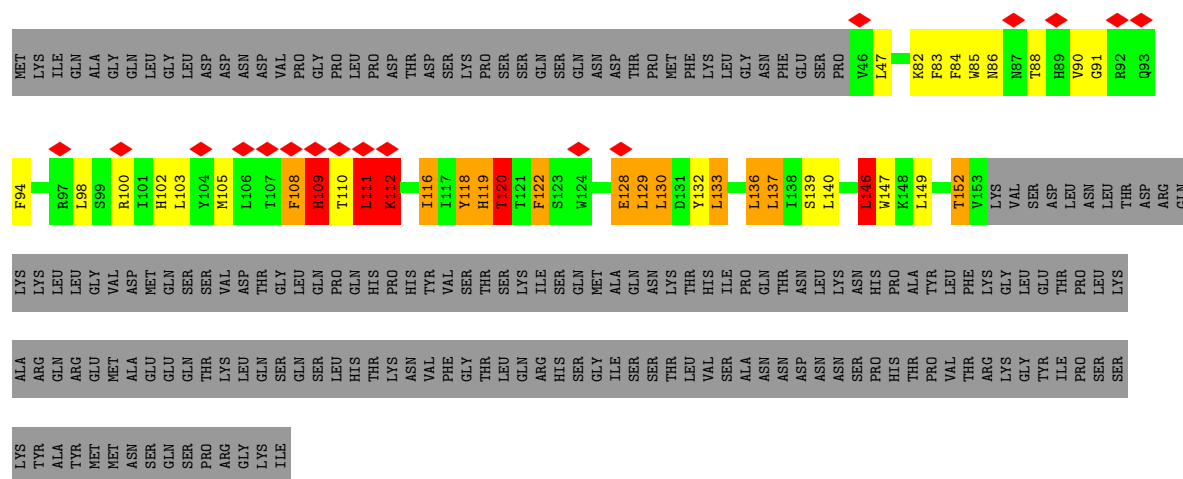
ALA	ILE	PHE	LYS	ILE	VAL	LYS	THR	PHE	PI70	PI71	PI72	PI73	PI74	PI75	PI76	PI77	PI78	PI79	PI80	PI81	PI82	PI83	PI84	PI85	PI86	PI87	PI88	PI89	PI90	PI91	PI92	PI93	PI94	PI95	PI96	PI97	PI98	PI99	PI100	PI101	PI102	PI103	PI104	PI105	PI106	PI107	PI108	PI109	PI110	PI111	PI112	PI113	PI114	PI115	PI116	PI117	PI118	PI119	PI120	PI121	PI122	PI123	PI124	PI125	PI126	PI127	PI128	PI129	PI130	PI131	PI132	PI133	PI134	PI135	PI136	PI137	PI138	PI139	PI140	PI141	PI142	PI143	PI144	PI145	PI146	PI147	PI148	PI149	PI150	PI151	PI152	PI153	PI154	PI155	PI156	PI157	PI158	PI159	PI160	PI161	PI162	PI163	PI164	PI165	PI166	PI167	PI168	PI169	PI170	PI171	PI172	PI173	PI174	PI175	PI176	PI177	PI178	PI179	PI180	PI181	PI182	PI183	PI184	PI185	PI186	PI187	PI188	PI189	PI190	PI191	PI192	PI193	PI194	PI195	PI196	PI197	PI198	PI199	PI200	PI201	PI202	PI203	PI204	PI205	PI206	PI207	PI208	PI209	PI210	PI211	PI212	PI213	PI214	PI215	PI216	PI217	PI218	PI219	PI220	PI221	PI222	PI223	PI224	PI225	PI226	PI227	PI228	PI229	PI230	PI231	PI232	PI233	PI234	PI235	PI236	PI237	PI238	PI239	PI240	PI241	PI242	PI243	PI244	PI245	PI246	PI247	PI248	PI249	PI250	PI251	PI252	PI253	PI254	PI255	PI256	PI257	PI258	PI259	PI260	PI261	PI262	PI263	PI264	PI265	PI266	PI267	PI268	PI269	PI270	PI271	PI272	PI273	PI274	PI275	PI276	PI277	PI278	PI279	PI280	PI281	PI282	PI283	PI284	PI285	PI286	PI287	PI288	PI289	PI290	PI291	PI292	PI293	PI294	PI295	PI296	PI297	PI298	PI299	PI300	PI301	PI302	PI303	PI304	PI305	PI306	PI307	PI308	PI309	PI310	PI311	PI312	PI313	PI314	PI315	PI316	PI317	PI318	PI319	PI320	PI321	PI322	PI323	PI324	PI325	PI326	PI327	PI328	PI329	PI330	PI331	PI332	PI333	PI334	PI335	PI336	PI337	PI338	PI339	PI340	PI341	PI342	PI343	PI344	PI345	PI346	PI347	PI348	PI349	PI350	PI351	PI352	PI353	PI354	PI355	PI356	PI357	PI358	PI359	PI360	PI361	PI362	PI363	PI364	PI365	PI366	PI367	PI368	PI369	PI370	PI371	PI372	PI373	PI374	PI375	PI376	PI377	PI378	PI379	PI380	PI381	PI382	PI383	PI384	PI385	PI386	PI387	PI388	PI389	PI390	PI391	PI392	PI393	PI394	PI395	PI396	PI397	PI398	PI399	PI400	PI401	PI402	PI403	PI404	PI405	PI406	PI407	PI408	PI409	PI410	PI411	PI412	PI413	PI414	PI415	PI416	PI417	PI418	PI419	PI420	PI421	PI422	PI423	PI424	PI425	PI426	PI427	PI428	PI429	PI430	PI431	PI432	PI433	PI434	PI435	PI436	PI437	PI438	PI439	PI440	PI441	PI442	PI443	PI444	PI445	PI446	PI447	PI448	PI449	PI450	PI451	PI452	PI453	PI454	PI455	PI456	PI457	PI458	PI459	PI460	PI461	PI462	PI463	PI464	PI465	PI466	PI467	PI468	PI469	PI470	PI471	PI472	PI473	PI474	PI475	PI476	PI477	PI478	PI479	PI480	PI481	PI482	PI483	PI484	PI485	PI486	PI487	PI488	PI489	PI490	PI491	PI492	PI493	PI494	PI495	PI496	PI497	PI498	PI499	PI500	PI501	PI502	PI503	PI504	PI505	PI506	PI507	PI508	PI509	PI510	PI511	PI512	PI513	PI514	PI515	PI516	PI517	PI518	PI519	PI520	PI521</
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[illegible]

- Molecule 2: Nucleoporin POM34

[illegible]

Chain C: 6% 23% 7% . . 64%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	208392	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF correction applied in RELION during the alignment and reconstruction	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	37651	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.693	Depositor
Minimum map value	-0.601	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.85	Depositor
Map size ($\text{\AA}$)	1276.8, 1276.8, 1276.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.66, 2.66, 2.66	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	B	0.66	0/960	1.50	14/1302 (1.1%)
1	D	0.65	0/960	1.50	14/1302 (1.1%)
2	A	0.58	1/951 (0.1%)	1.00	2/1287 (0.2%)
2	C	0.61	1/951 (0.1%)	1.08	4/1287 (0.3%)
All	All	0.63	2/3822 (0.1%)	1.29	34/5178 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	9
1	D	0	9
All	All	0	18

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	118	TYR	C-O	5.90	1.30	1.24
2	A	118	TYR	C-O	5.73	1.30	1.24

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	212	LEU	O-C-N	-12.05	109.66	122.07
1	D	210	ARG	O-C-N	-12.05	109.66	122.07
1	B	209	TRP	O-C-N	-12.04	109.67	122.07
1	D	209	TRP	O-C-N	-12.03	109.68	122.07
1	D	212	LEU	O-C-N	-12.02	109.69	122.07

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	136	PRO	Peptide
1	B	153	TYR	Sidechain
1	B	170	PRO	Peptide
1	B	208	THR	Mainchain
1	B	209	TRP	Mainchain

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	B	933	0	987	20	0
1	D	933	0	987	20	0
2	A	926	0	957	36	0
2	C	926	0	957	41	0
All	All	3718	0	3888	117	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 15.

The worst 5 of 117 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:82:LYS:O	2:C:86:ASN:HB2	1.58	1.00
2:A:82:LYS:O	2:A:86:ASN:CG	2.19	0.85
2:A:82:LYS:O	2:A:86:ASN:CB	2.25	0.83
2:A:82:LYS:O	2:A:86:ASN:HB2	1.79	0.81
2:C:84:PHE:CD1	2:C:85:TRP:CD1	2.71	0.79

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	108/1337 (8%)	97 (90%)	7 (6%)	4 (4%)	2	20
1	D	108/1337 (8%)	97 (90%)	7 (6%)	4 (4%)	2	20
2	A	106/299 (36%)	96 (91%)	7 (7%)	3 (3%)	4	24
2	C	106/299 (36%)	98 (92%)	3 (3%)	5 (5%)	2	16
All	All	428/3272 (13%)	388 (91%)	24 (6%)	16 (4%)	4	20

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	176	PRO
1	B	179	VAL
1	B	185	ALA
1	D	176	PRO
1	D	179	VAL

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	B	106/1224 (9%)	92 (87%)	14 (13%)	4	15
1	D	106/1224 (9%)	92 (87%)	14 (13%)	4	15
2	A	103/276 (37%)	79 (77%)	24 (23%)	1	5
2	C	103/276 (37%)	79 (77%)	24 (23%)	1	5
All	All	418/3000 (14%)	342 (82%)	76 (18%)	3	9

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	105	MET
2	C	132	TYR
2	C	109	HIS
2	C	119	HIS
2	C	152	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	197	HIS
2	A	86	ASN
1	D	197	HIS
2	C	86	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](#)

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-41117. These allow visual inspection of the internal detail of the map and identification of artifacts.

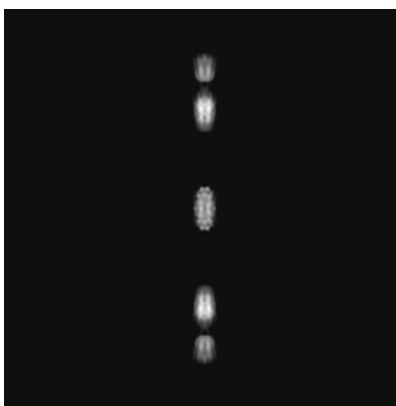
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

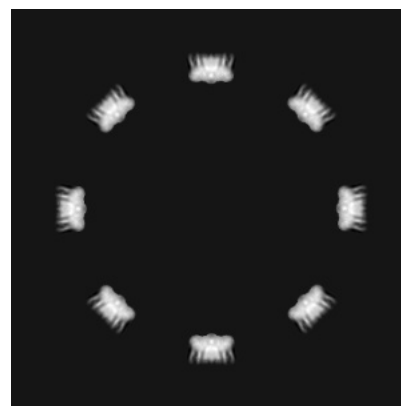
6.1.1 Primary map



X



Y

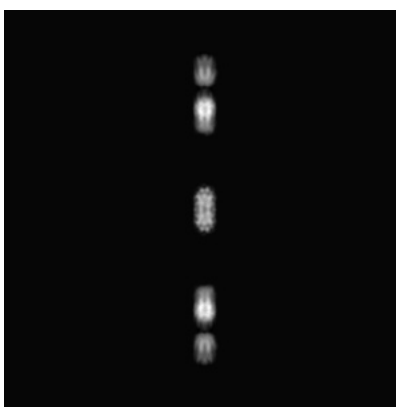


Z

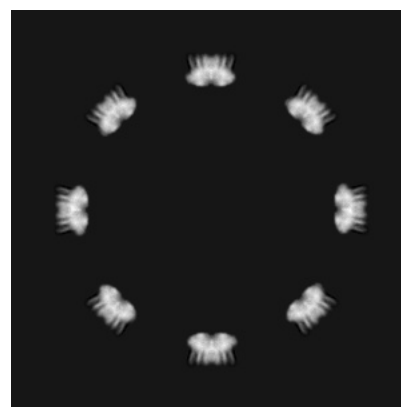
6.1.2 Raw map



X



Y

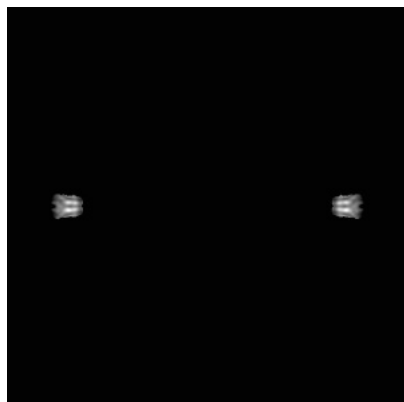


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 240

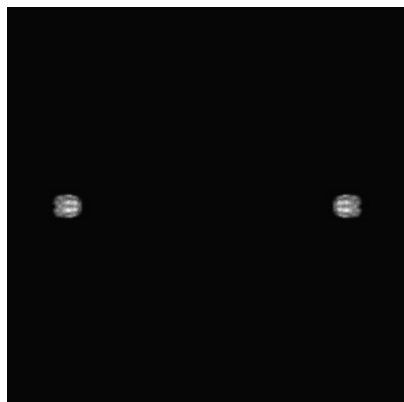


Y Index: 240

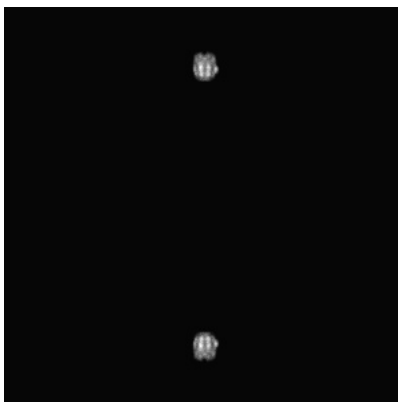


Z Index: 240

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](#)

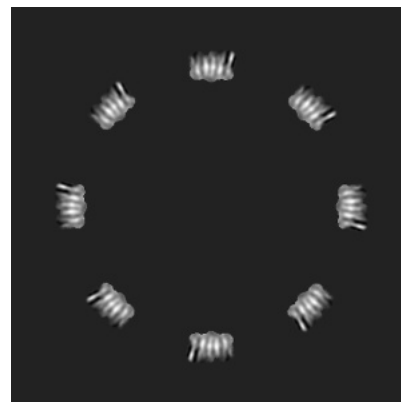
6.3.1 Primary map



X Index: 361



Y Index: 119



Z Index: 236

6.3.2 Raw map



X Index: 123



Y Index: 123

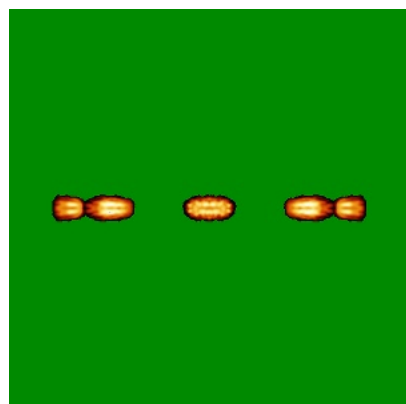


Z Index: 244

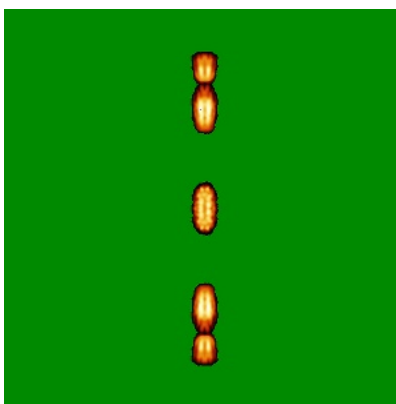
The images above show the largest variance slices of the map in three orthogonal directions.

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

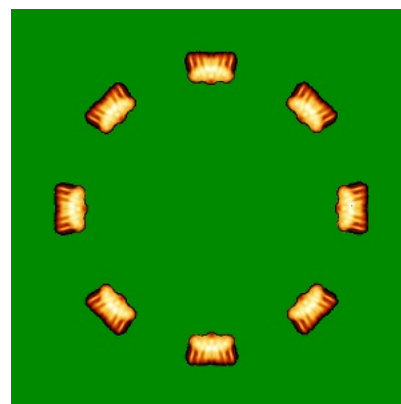
6.4.1 Primary map



X

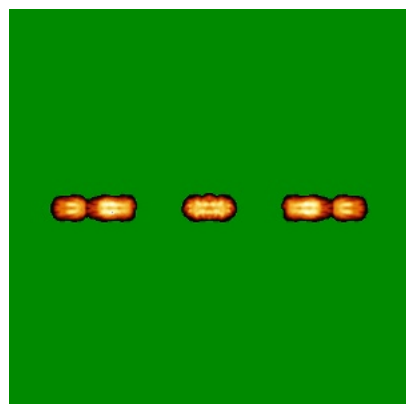


Y

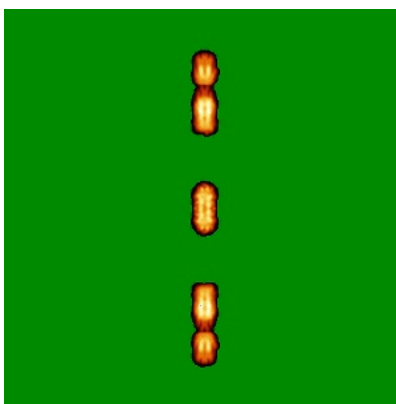


Z

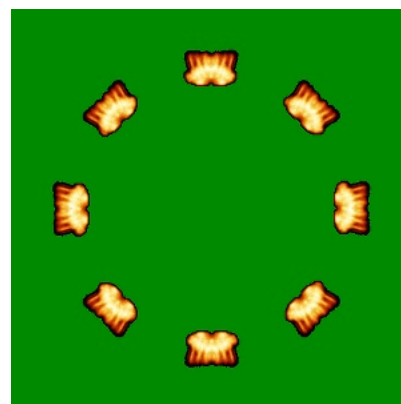
6.4.2 Raw map



X



Y

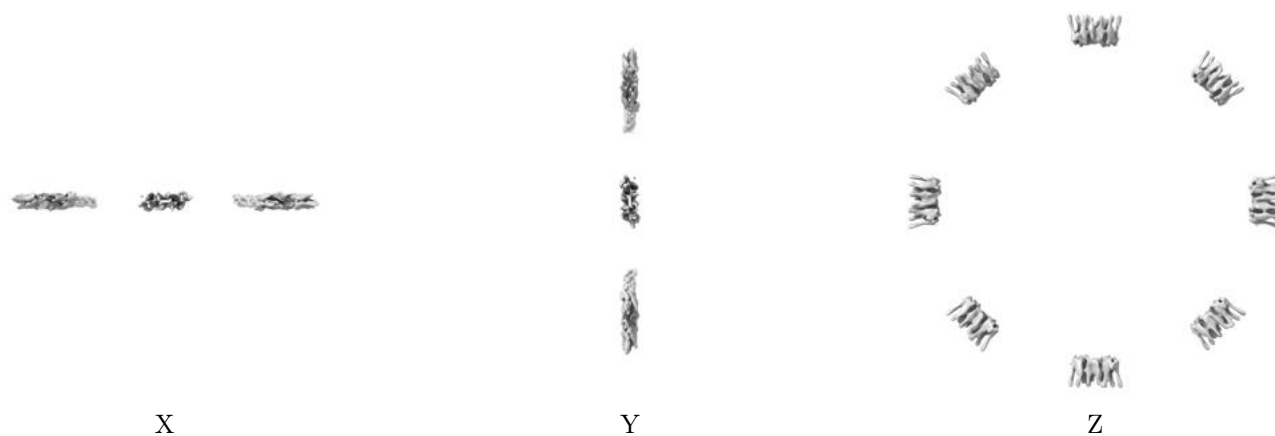


Z

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.

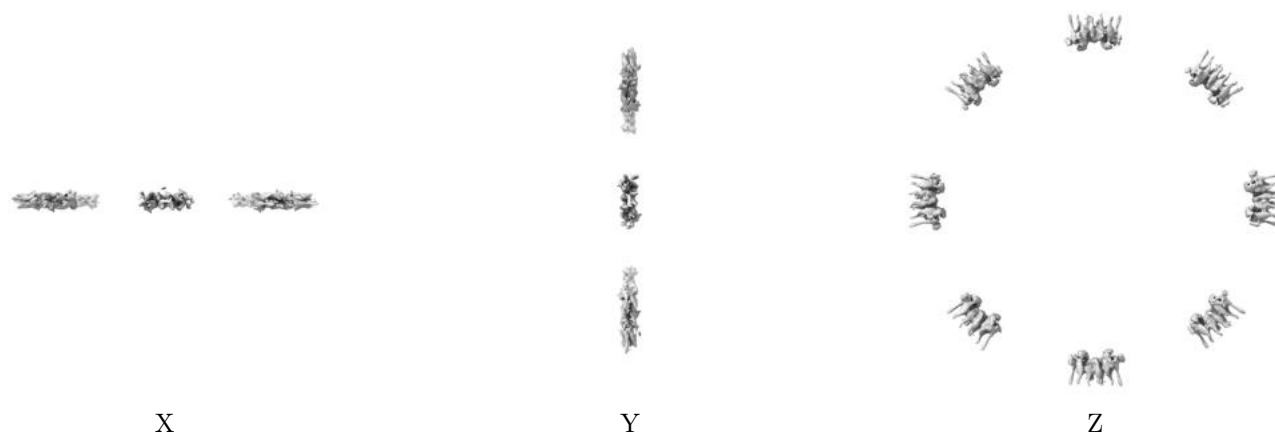
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.85. 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.

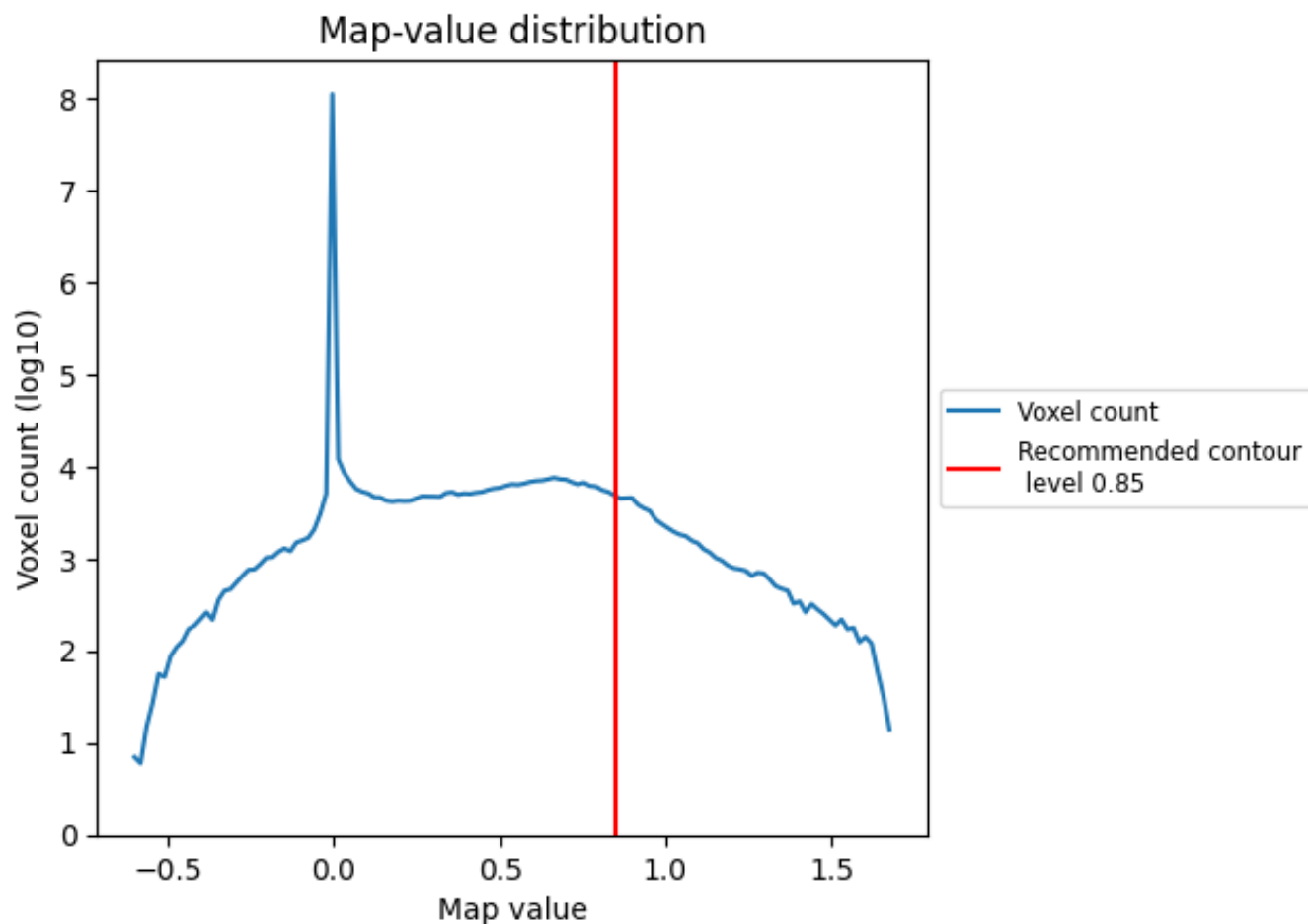
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

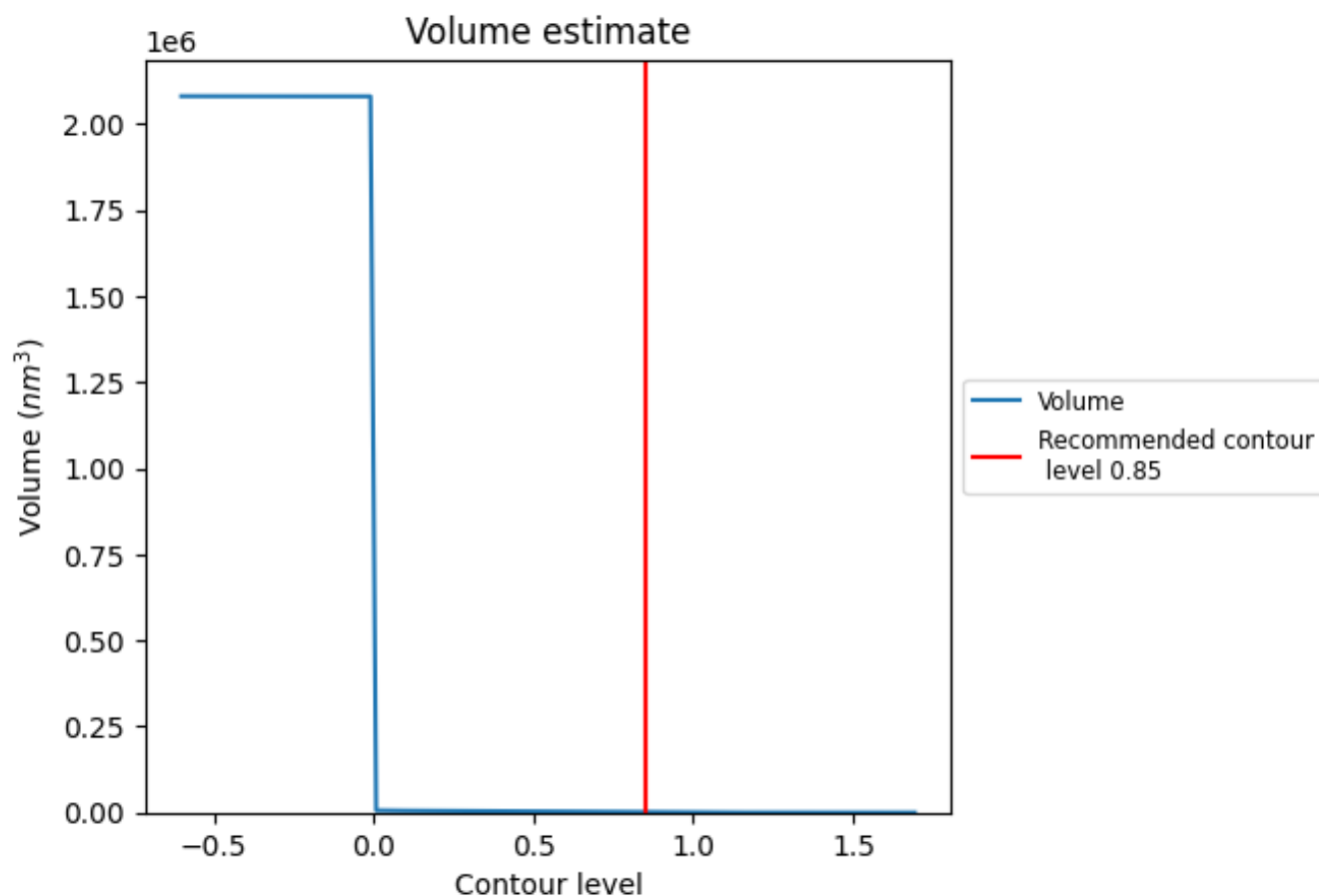
This section contains the results of statistical analysis of the map.

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.

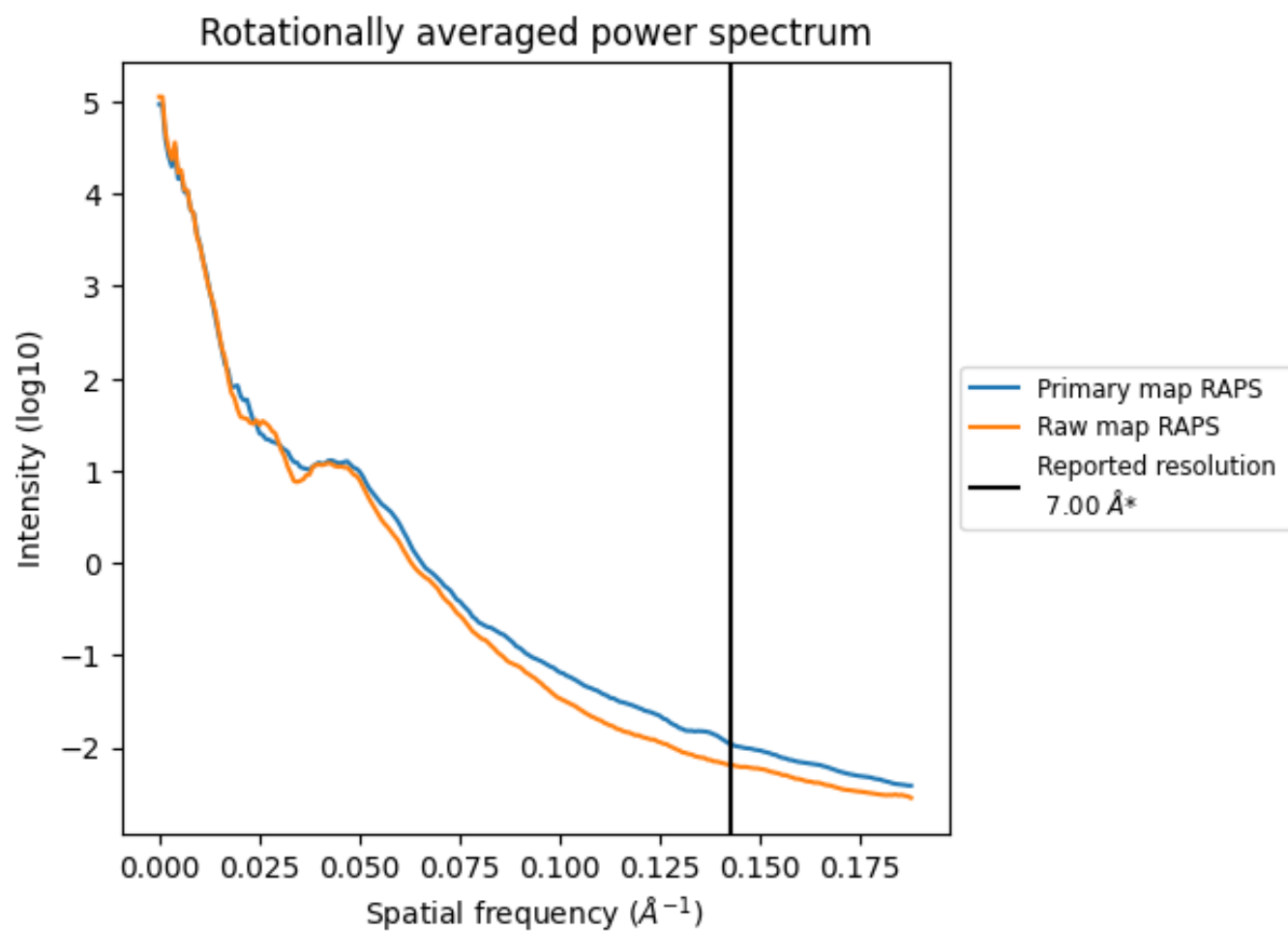
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1093 nm^3 ; this corresponds to an approximate mass of 987 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 ⓘ

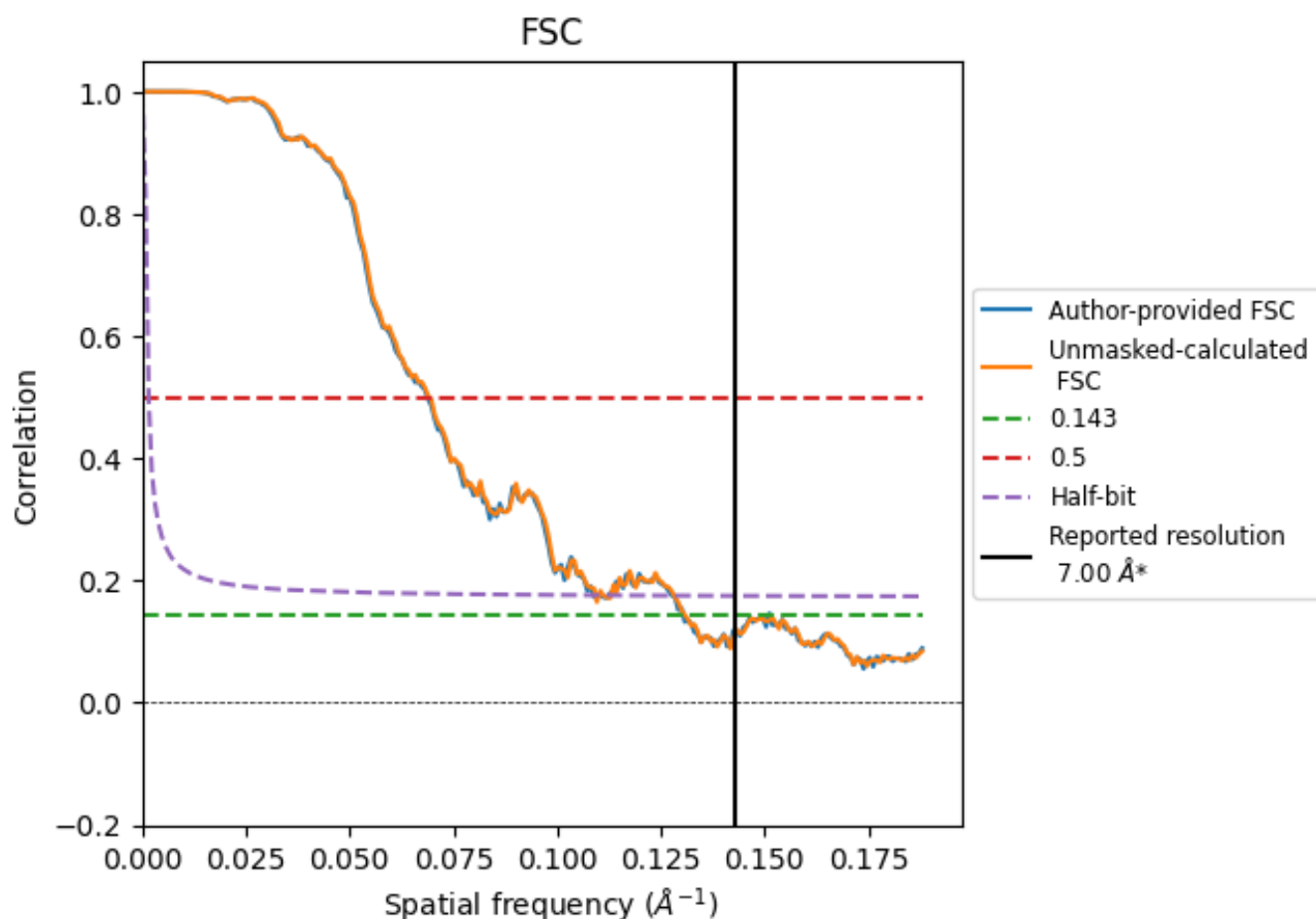


*Reported resolution corresponds to spatial frequency of 0.143 Å⁻¹

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 0.143 Å⁻¹

8.2 Resolution estimates [i](#)

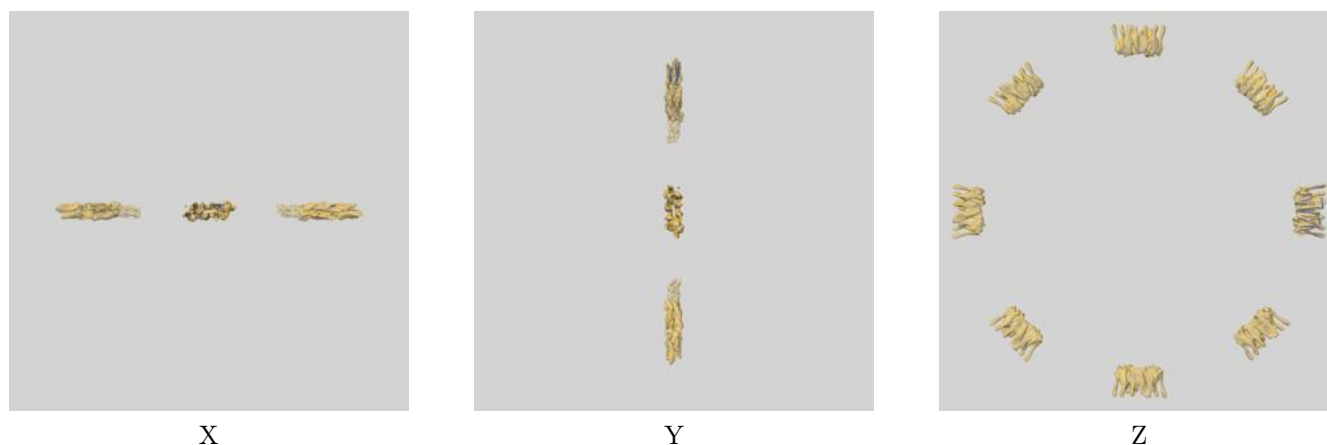
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.00	-	-
Author-provided FSC curve	7.67	14.53	9.20
Unmasked-calculated*	7.64	14.45	9.15

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

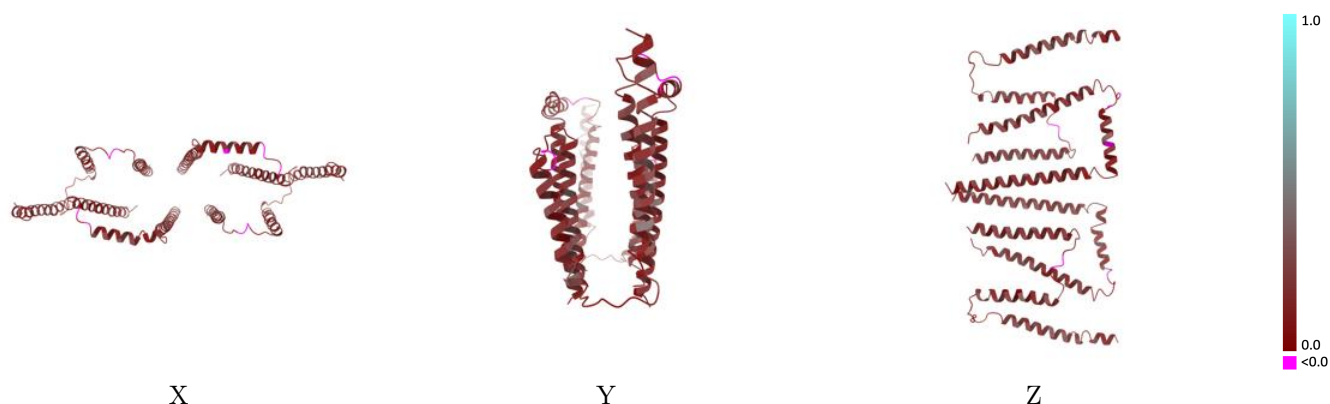
This section contains information regarding the fit between EMDB map EMD-41117 and PDB model 8T9L. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



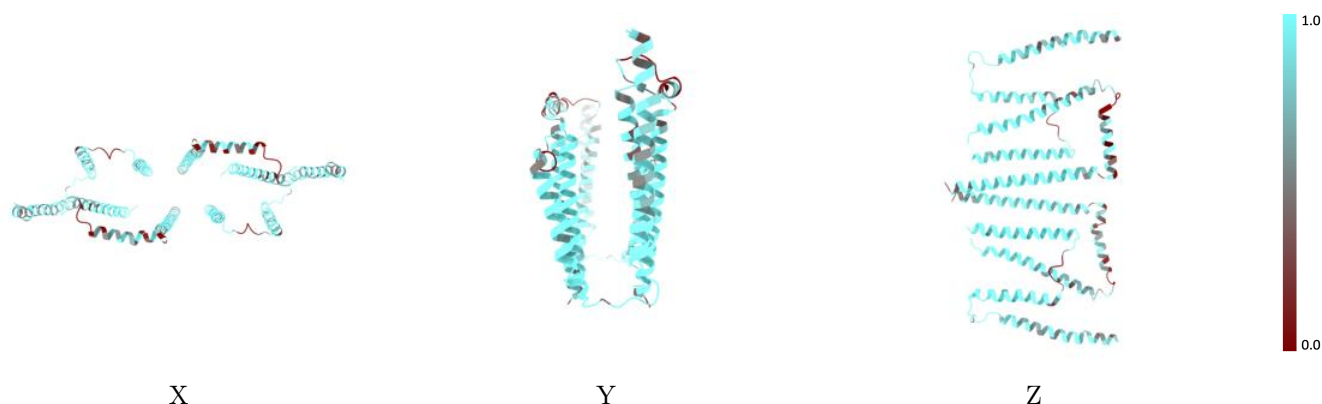
The images above show the 3D surface view of the map at the recommended contour level 0.85 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



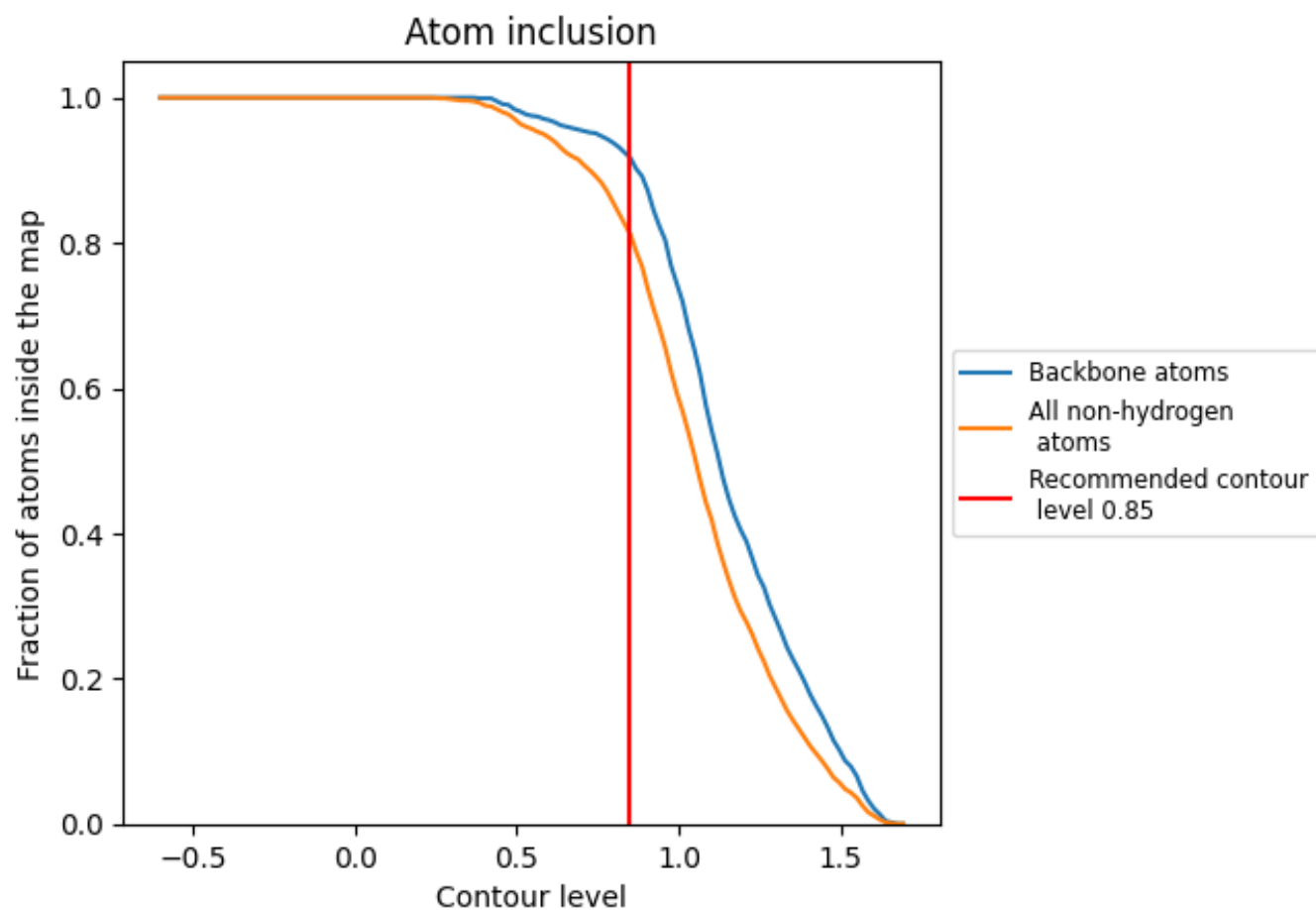
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.85).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 81% 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 (0.85) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8120	0.1700
A	0.7720	0.1690
B	0.8610	0.1800
C	0.7640	0.1620
D	0.8520	0.1720

