



wwPDB EM Validation Summary Report ⓘ

Jul 2, 2026 – 11:29 PM JST

PDB ID : 9WXF / pdb_00009wxf
EMDB ID : EMD-66345
Title : cryo-electron microscopy structure of Dandelion
Authors : Yu, Y.; Chen, Q.; Tang, Y.
Deposited on : 2025-09-25
Resolution : 3.33 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:

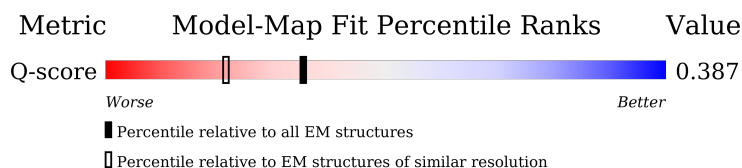
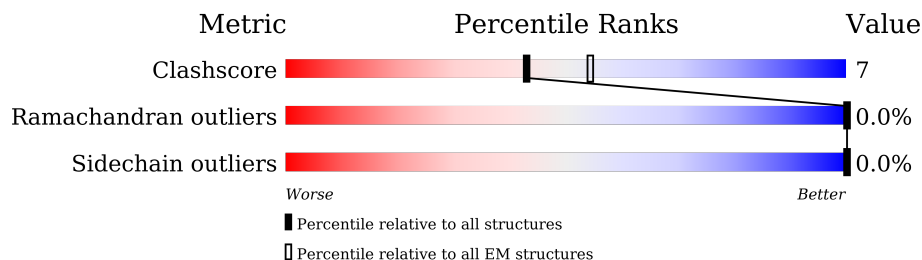
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 3.33 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	14484 (2.83 - 3.83)

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	460	 80% 15% 5%
1	B	460	 83% 13% .
1	C	460	 82% 13% 5%
1	D	460	 82% 13% 6%

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Mol	Chain	Length	Quality of chain
1	E	460	 77% 19%
1	F	460	 78% 17%
1	G	460	 28% 6% 66%
1	H	460	 30% 66%
1	I	460	 82% 13% 5%
1	J	460	 78% 17% 5%
1	K	460	 76% 20%
1	L	460	 78% 18%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 77260 atoms, of which 38424 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 Dandelion.

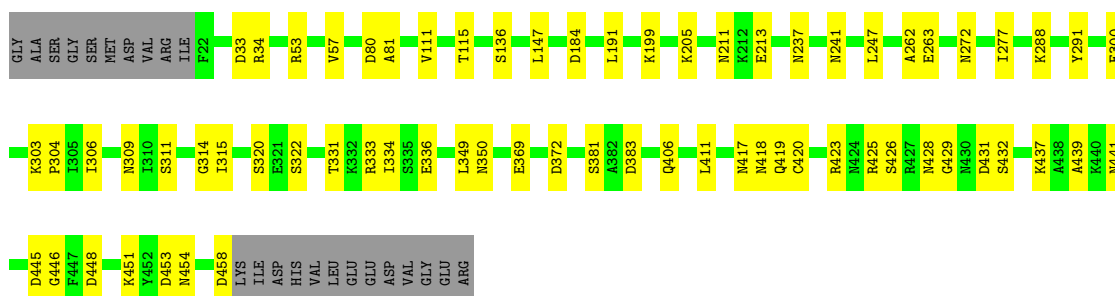
Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	437	7199	2308	3589	610	680	12	0	0
1	B	442	7276	2335	3624	618	687	12	0	0
1	C	437	7208	2308	3598	610	680	12	0	0
1	D	433	7143	2285	3567	606	673	12	0	0
1	E	441	7263	2326	3622	617	686	12	0	0
1	F	441	7256	2326	3615	617	686	12	0	0
1	G	155	2526	818	1239	223	241	5	0	0
1	H	155	2526	818	1239	223	241	5	0	0
1	I	438	7229	2312	3611	614	680	12	0	0
1	J	437	7199	2308	3589	610	680	12	0	0
1	K	442	7236	2334	3584	618	687	13	0	0
1	L	442	7199	2334	3547	618	687	13	0	0

3 Residue-property plots [i](#)


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.

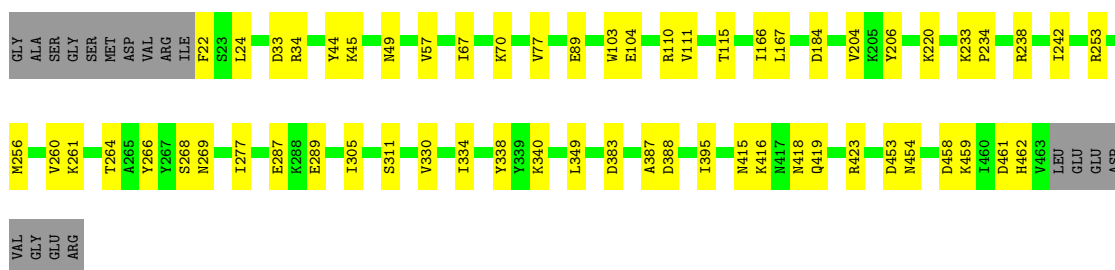
- Molecule 1: Dandelion

Chain A: 




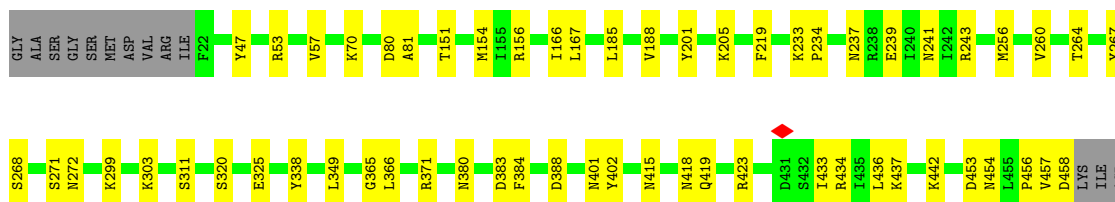
- Molecule 1: Dandelion

Chain B: 



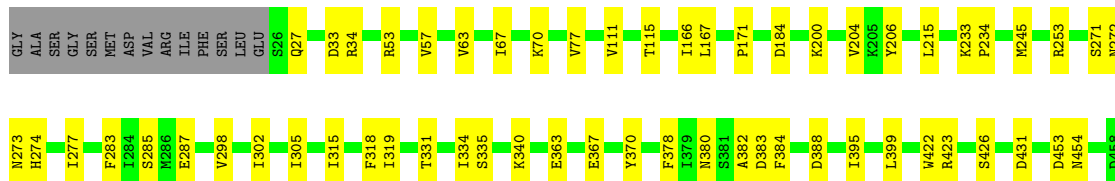
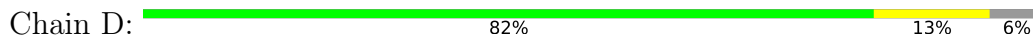
- Molecule 1: Dandelion

Chain C: 



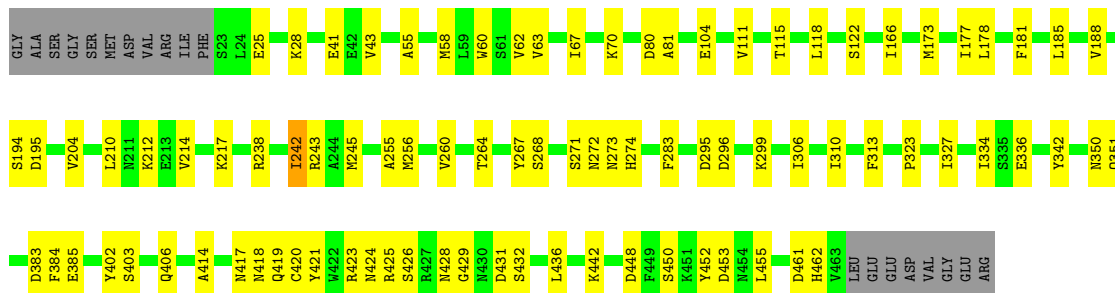
HIS
VAL
LEU
GLY
GLU
ASP
VAL
GLY
ARG

● Molecule 1: Dandelion

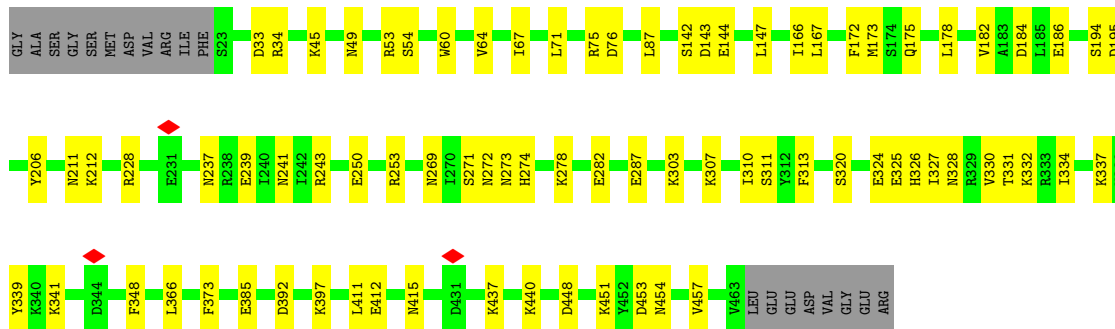
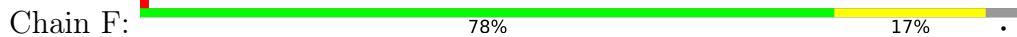


LYS
ILE
ASP
HIS
VAL
LEU
GLU
ASP
GLY
GLY
ARG

● Molecule 1: Dandelion

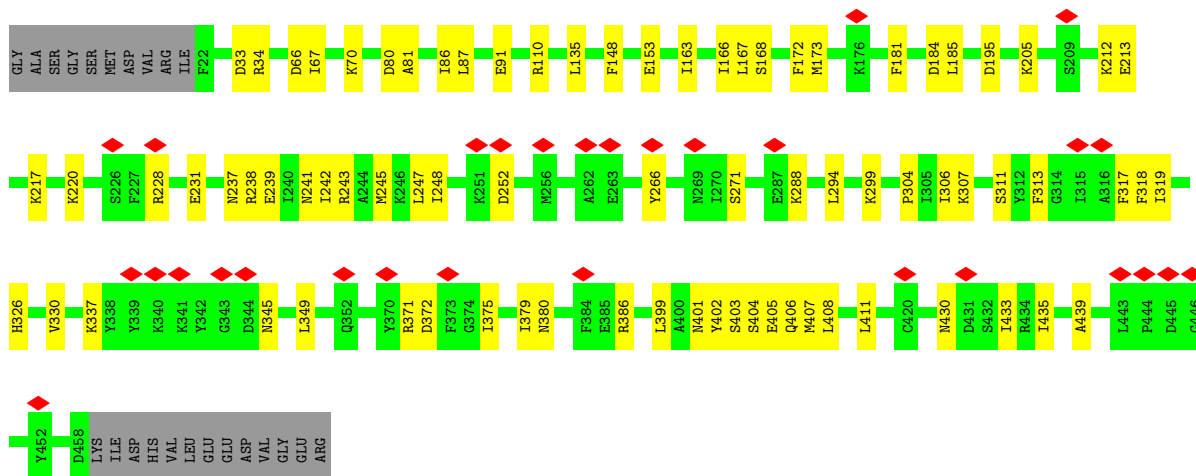


● Molecule 1: Dandelion

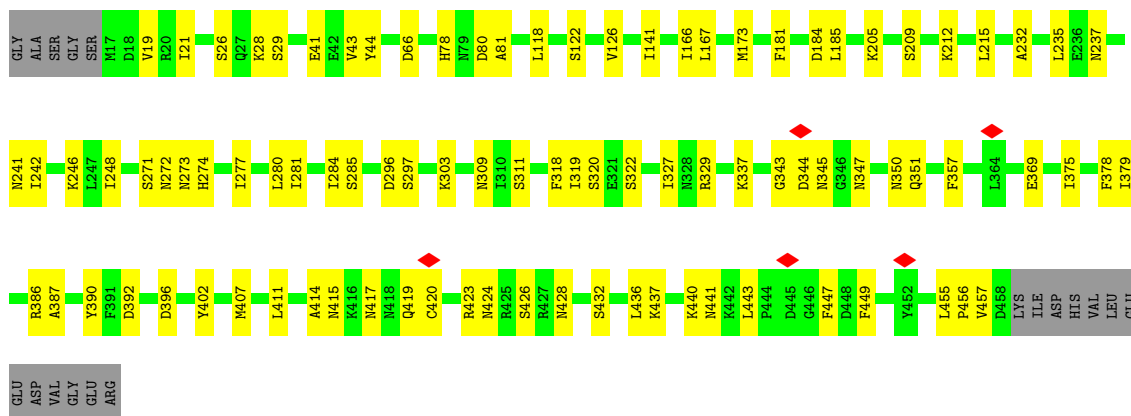
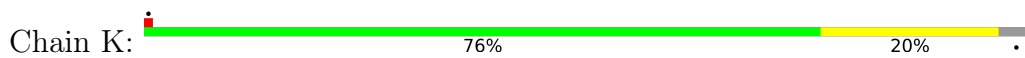


● Molecule 1: Dandelion

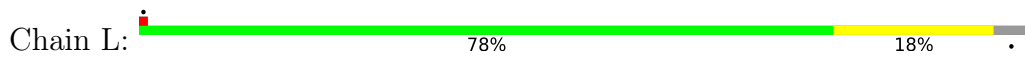




• Molecule 1: Dandelion



• Molecule 1: Dandelion



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	70976	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55.68	Depositor
Minimum defocus (nm)	404	Depositor
Maximum defocus (nm)	4966	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	2.072	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.0225	Depositor
Map size (\AA)	435.2, 435.2, 435.2	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.85, 0.85, 0.85	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	0.23	0/3683	0.37	0/4957
1	B	0.29	0/3726	0.35	0/5015
1	C	0.23	0/3683	0.34	0/4957
1	D	0.28	0/3648	0.40	2/4910 (0.0%)
1	E	0.27	0/3714	0.40	2/4999 (0.0%)
1	F	0.20	0/3714	0.34	0/4999
1	G	0.24	0/1312	0.38	0/1772
1	H	0.26	0/1312	0.34	0/1772
1	I	0.23	0/3691	0.35	0/4968
1	J	0.20	0/3683	0.33	0/4957
1	K	0.21	0/3725	0.33	0/5013
1	L	0.21	0/3725	0.39	0/5013
All	All	0.24	0/39616	0.36	4/53332 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	171	PRO	CA-C-N	8.20	133.72	120.60
1	D	171	PRO	C-N-CA	8.20	133.72	120.60
1	E	336	GLU	CA-C-N	7.55	135.55	122.56
1	E	336	GLU	C-N-CA	7.55	135.55	122.56

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	3610	3589	3597	39	0
1	B	3652	3624	3641	40	0
1	C	3610	3598	3597	35	0
1	D	3576	3567	3566	41	0
1	E	3641	3622	3632	59	0
1	F	3641	3615	3632	52	0
1	G	1287	1239	1298	23	0
1	H	1287	1239	1298	8	0
1	I	3618	3611	3610	47	0
1	J	3610	3589	3597	52	0
1	K	3652	3584	3643	66	0
1	L	3652	3547	3643	60	0
All	All	38836	38424	38754	508	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.

The worst 5 of 508 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:70:LYS:NZ	1:D:166:ILE:O	2.05	0.90
1:E:402:TYR:O	1:E:442:LYS:NZ	2.06	0.89
1:C:402:TYR:O	1:C:442:LYS:NZ	2.08	0.87
1:F:250:GLU:O	1:F:253:ARG:NH2	2.09	0.86
1:F:172:PHE:O	1:F:173:MET:HG2	1.74	0.86

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	435/460 (95%)	419 (96%)	16 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	440/460 (96%)	425 (97%)	15 (3%)	0	100	100
1	C	435/460 (95%)	418 (96%)	17 (4%)	0	100	100
1	D	431/460 (94%)	407 (94%)	24 (6%)	0	100	100
1	E	439/460 (95%)	414 (94%)	25 (6%)	0	100	100
1	F	439/460 (95%)	421 (96%)	18 (4%)	0	100	100
1	G	153/460 (33%)	150 (98%)	3 (2%)	0	100	100
1	H	153/460 (33%)	148 (97%)	5 (3%)	0	100	100
1	I	436/460 (95%)	427 (98%)	9 (2%)	0	100	100
1	J	435/460 (95%)	425 (98%)	10 (2%)	0	100	100
1	K	440/460 (96%)	429 (98%)	11 (2%)	0	100	100
1	L	440/460 (96%)	434 (99%)	4 (1%)	2 (0%)	24	55
All	All	4676/5520 (85%)	4517 (97%)	157 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	171	PRO
1	L	172	PHE

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	401/420 (96%)	401 (100%)	0	100	100
1	B	406/420 (97%)	406 (100%)	0	100	100
1	C	401/420 (96%)	401 (100%)	0	100	100
1	D	397/420 (94%)	397 (100%)	0	100	100
1	E	405/420 (96%)	404 (100%)	1 (0%)	87	87
1	F	405/420 (96%)	405 (100%)	0	100	100
1	G	147/420 (35%)	147 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	147/420 (35%)	147 (100%)	0	100	100
1	I	402/420 (96%)	402 (100%)	0	100	100
1	J	401/420 (96%)	401 (100%)	0	100	100
1	K	406/420 (97%)	406 (100%)	0	100	100
1	L	406/420 (97%)	406 (100%)	0	100	100
All	All	4324/5040 (86%)	4323 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	242	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	138	HIS
1	J	430	ASN
1	I	196	ASN
1	J	78	HIS
1	K	132	HIS

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.

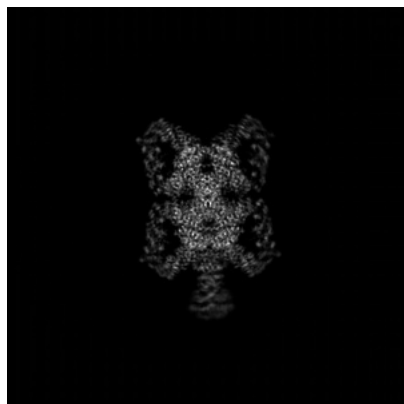
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66345. These allow visual inspection of the internal detail of the map and identification of artifacts.

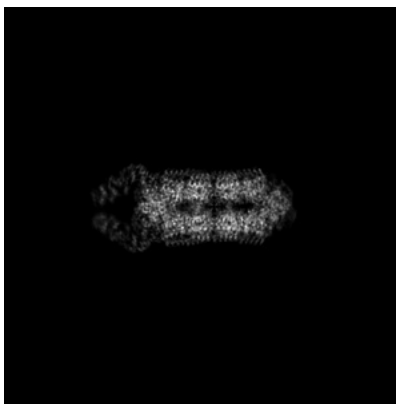
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

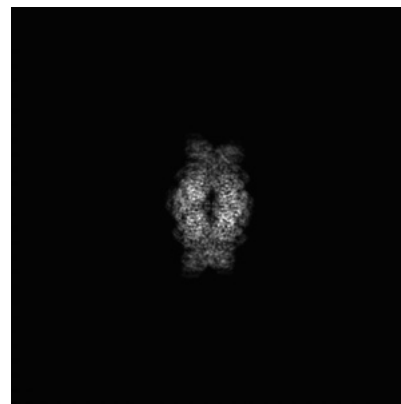
6.1.1 Primary map



X

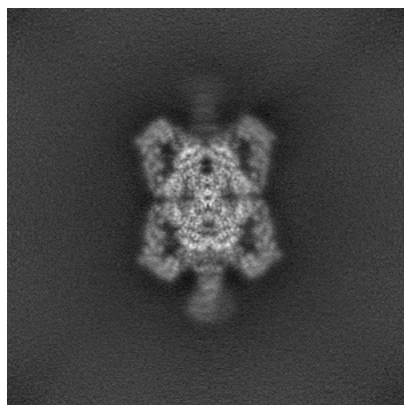


Y

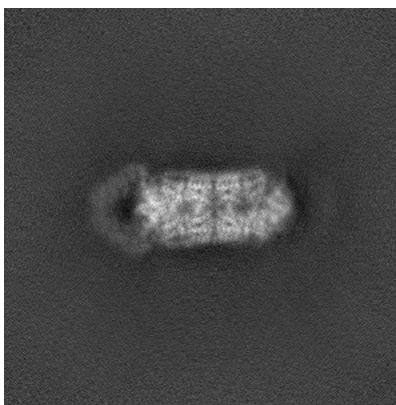


Z

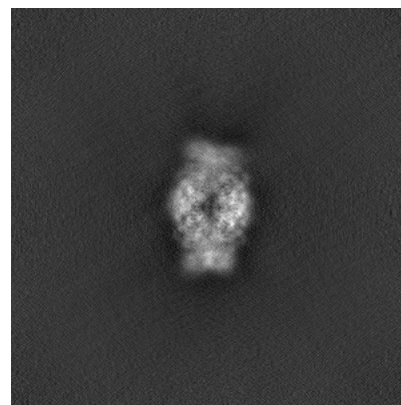
6.1.2 Raw map



X



Y

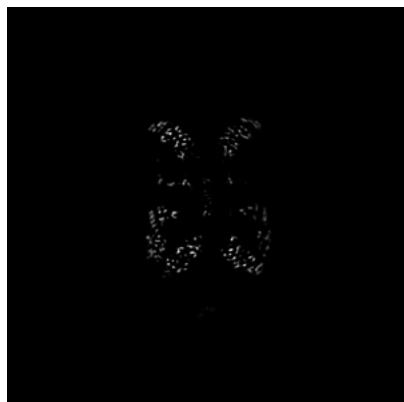


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 256

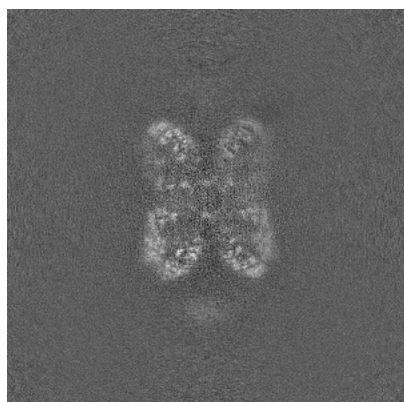


Y Index: 256

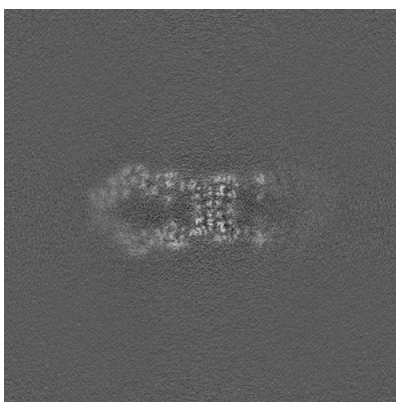


Z Index: 256

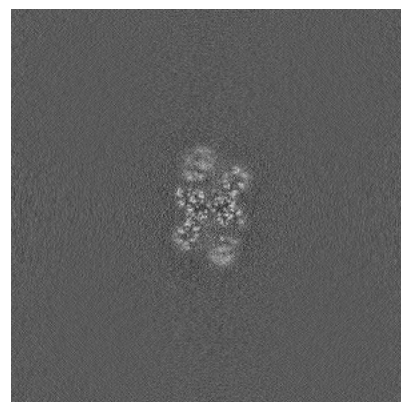
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

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: 240

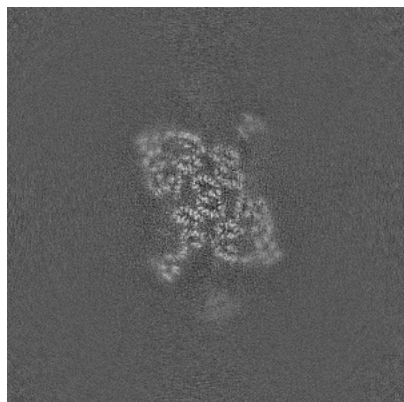


Y Index: 238

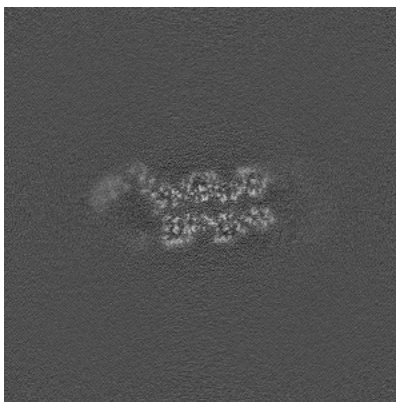


Z Index: 291

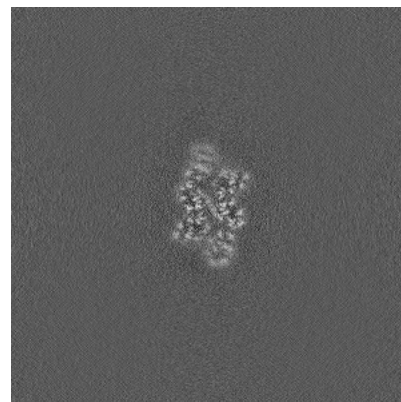
6.3.2 Raw map



X Index: 240



Y Index: 243



Z Index: 246

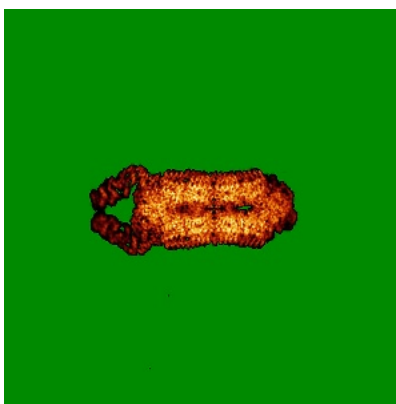
The images above show the largest variance slices of the map in three orthogonal directions.

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

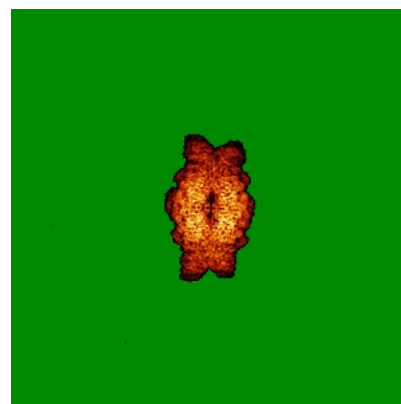
6.4.1 Primary map



X

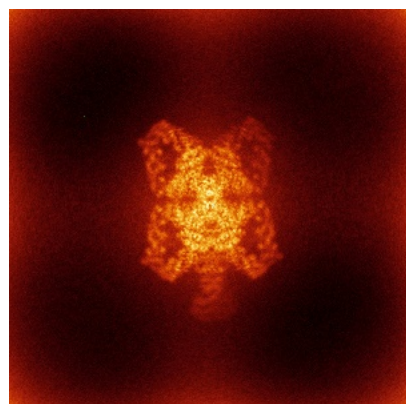


Y

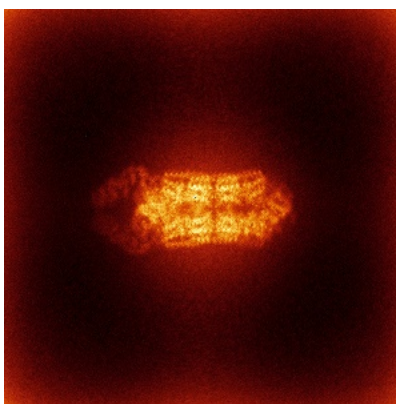


Z

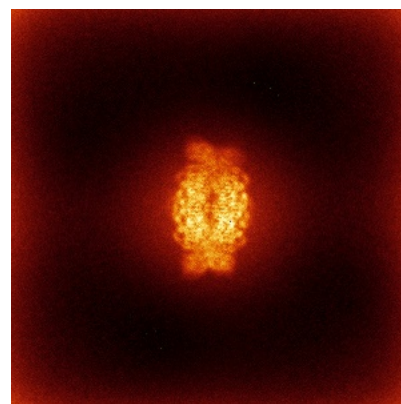
6.4.2 Raw map



X



Y

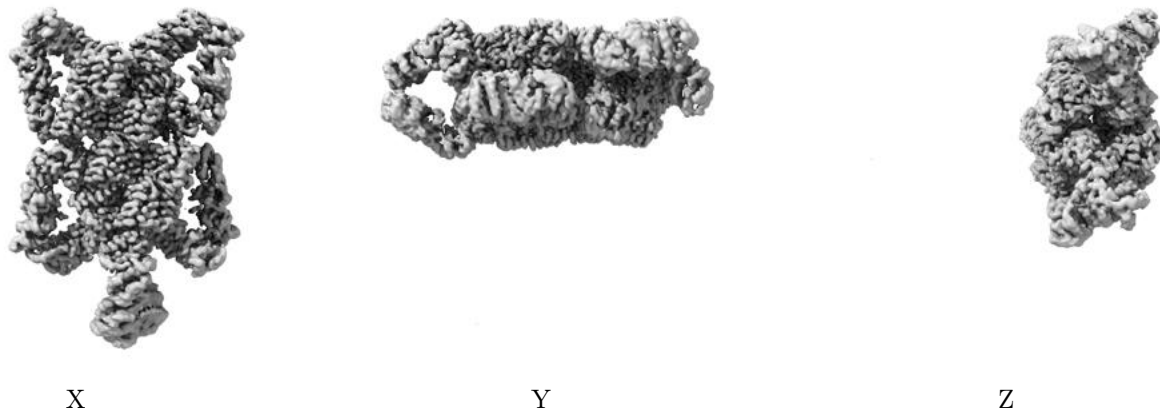


Z

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.

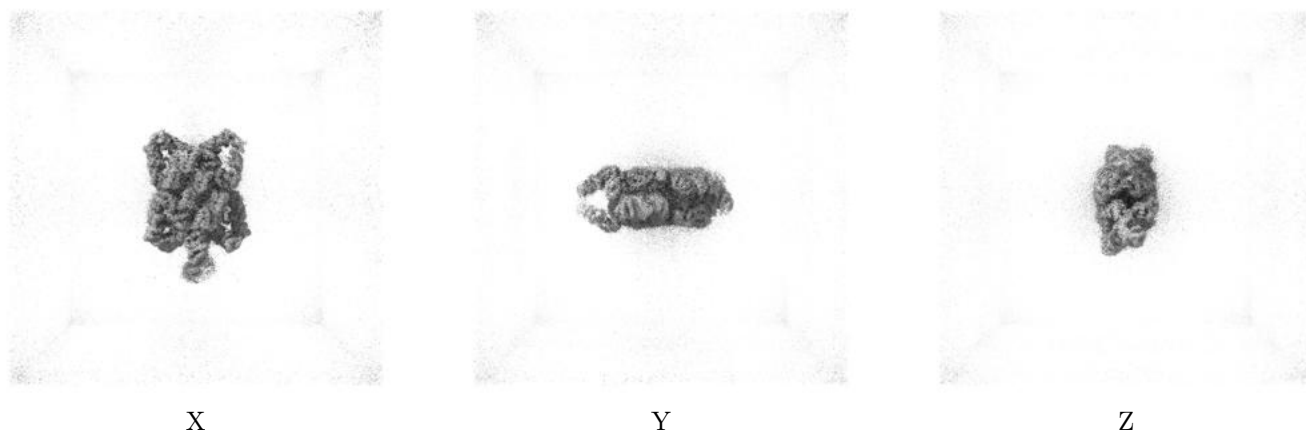
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0225. 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.

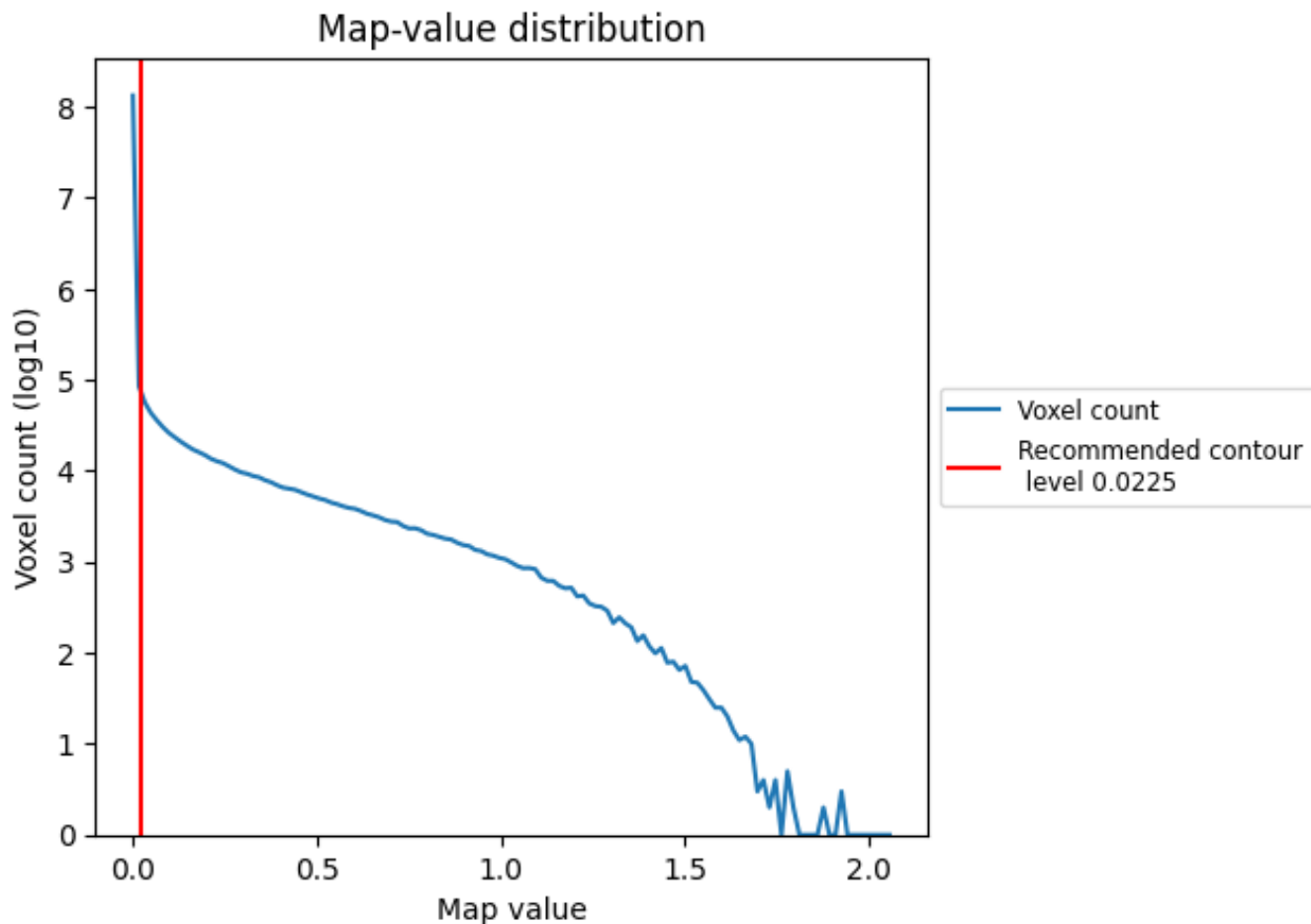
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

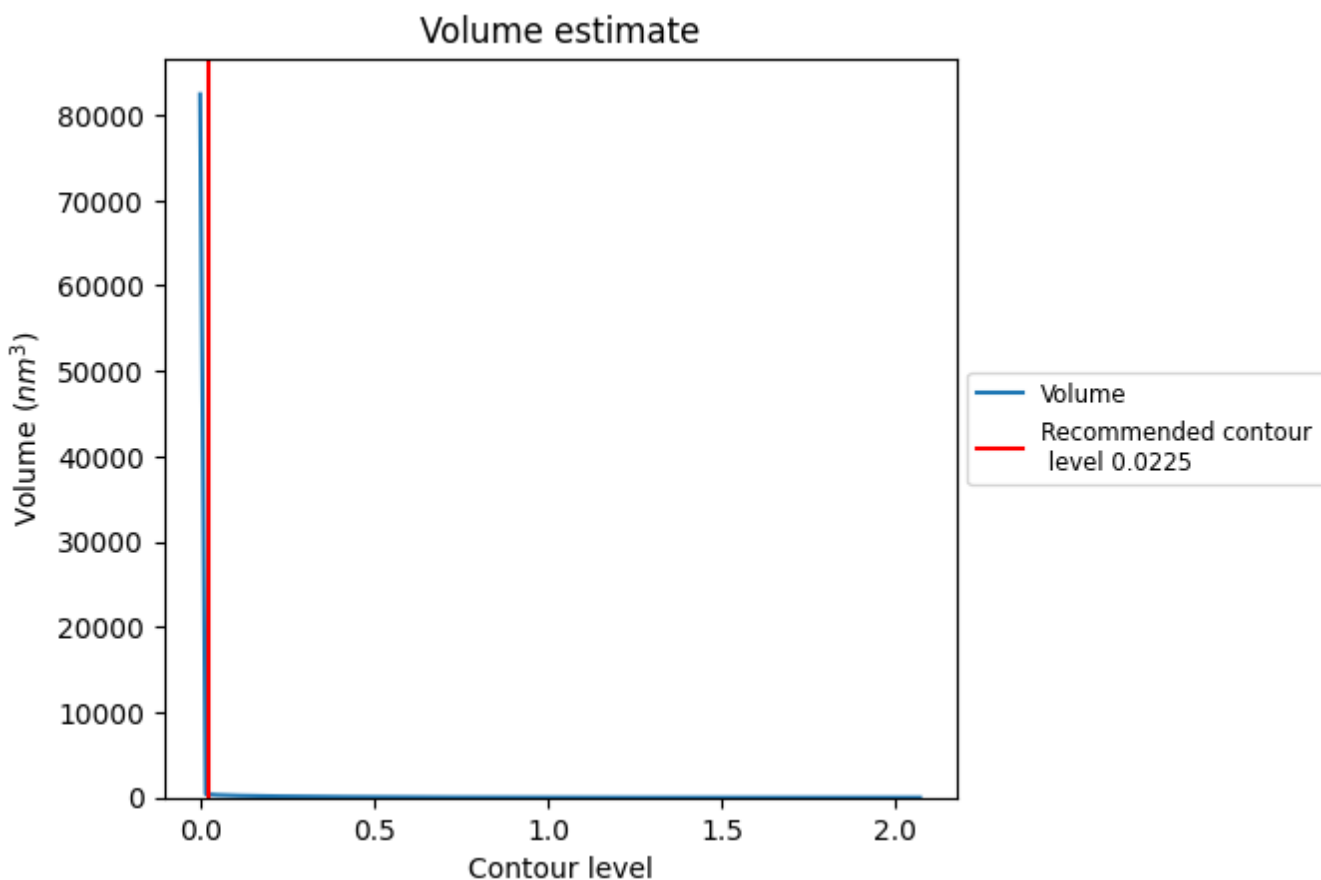
This section contains the results of statistical analysis of the map.

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.

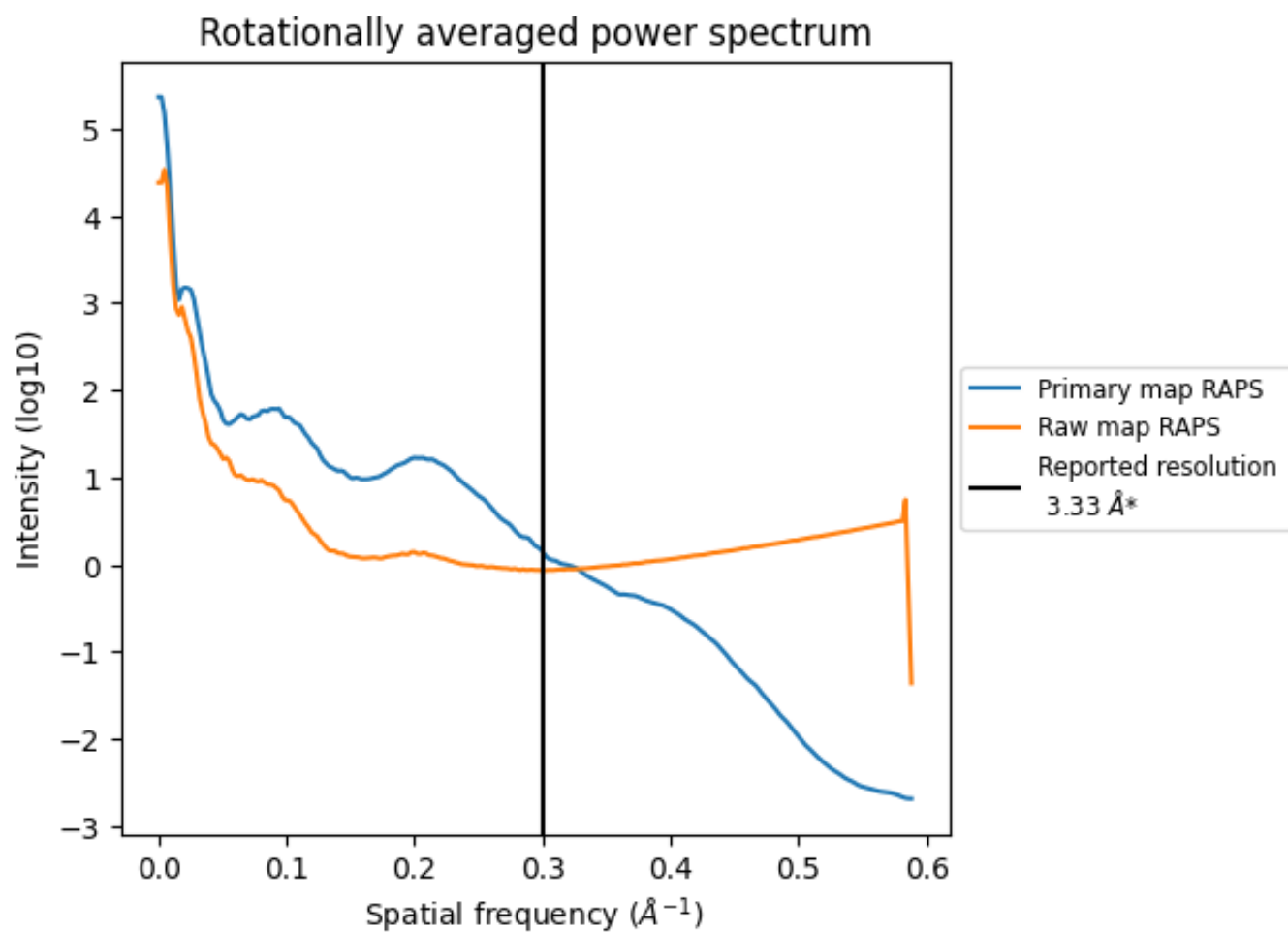
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 367 nm³; this corresponds to an approximate mass of 331 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 i

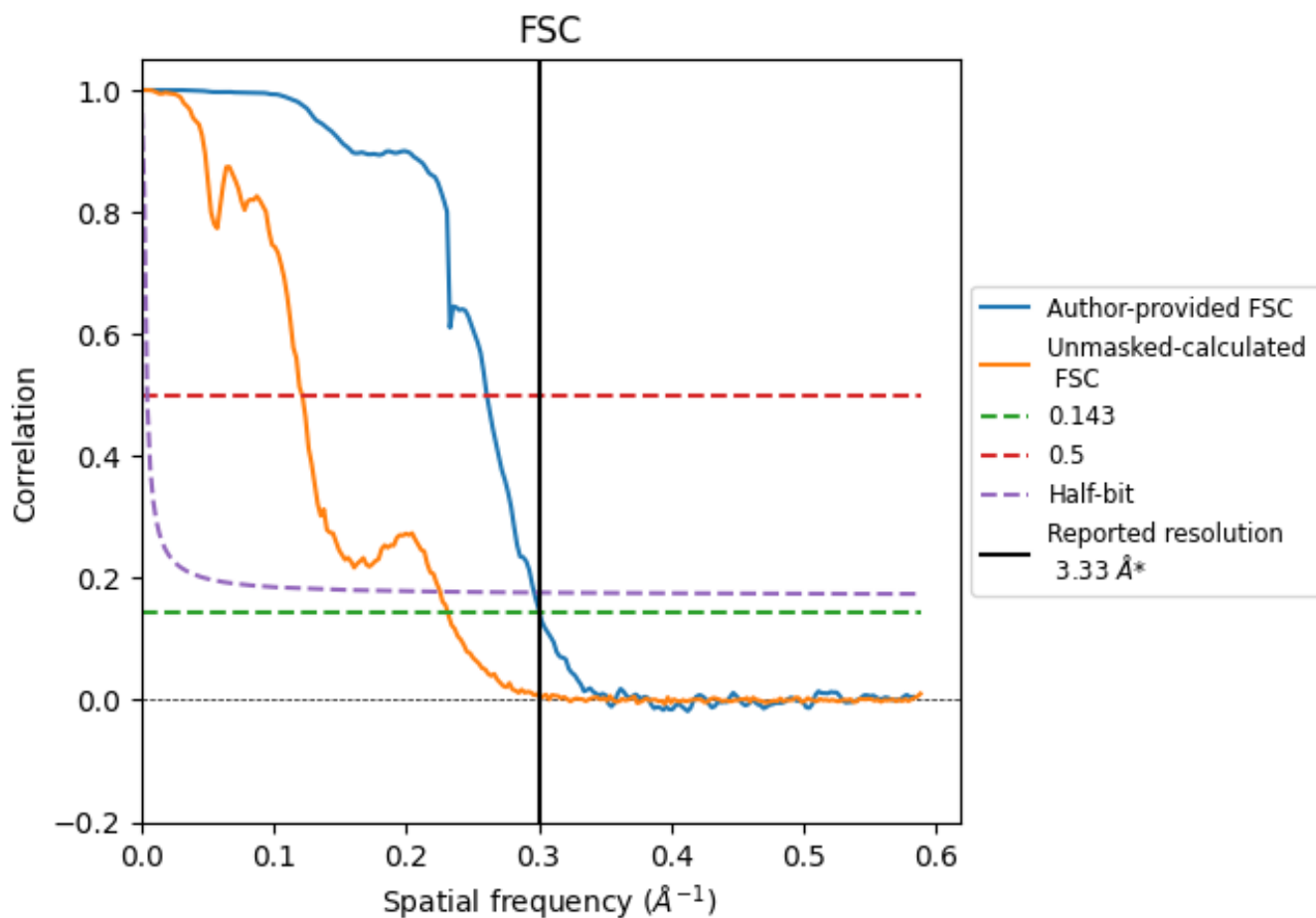


*Reported resolution corresponds to spatial frequency of 0.300 Å⁻¹

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 0.300 Å⁻¹

8.2 Resolution estimates [i](#)

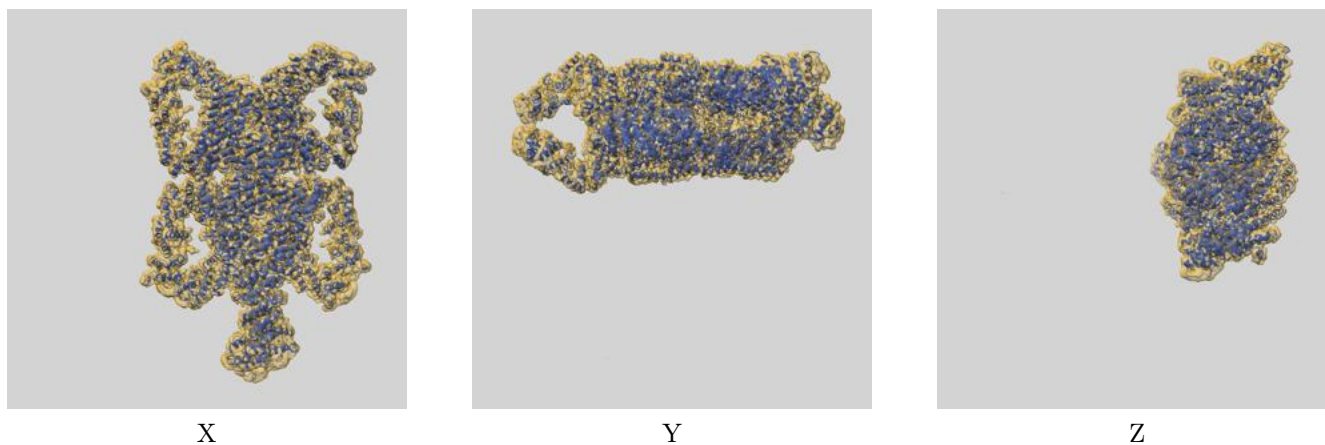
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.33	-	-
Author-provided FSC curve	3.33	3.83	3.37
Unmasked-calculated*	4.32	8.23	4.43

*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 4.32 differs from the reported value 3.33 by more than 10 %

9 Map-model fit [i](#)

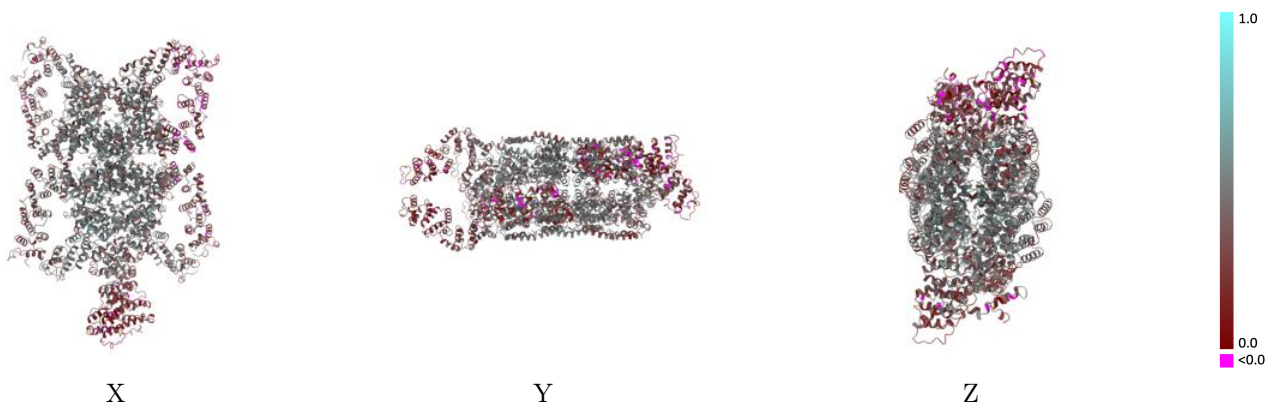
This section contains information regarding the fit between EMDB map EMD-66345 and PDB model 9WXF. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



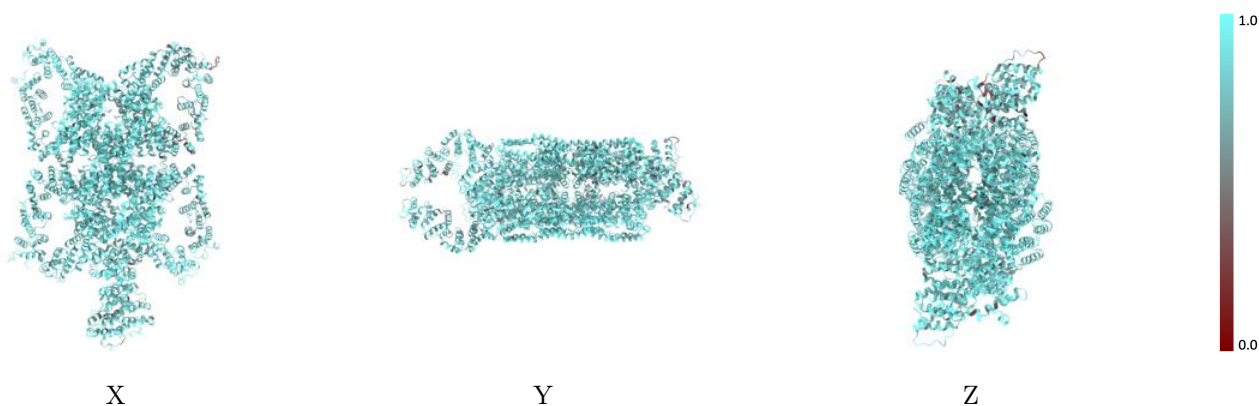
The images above show the 3D surface view of the map at the recommended contour level 0.0225 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



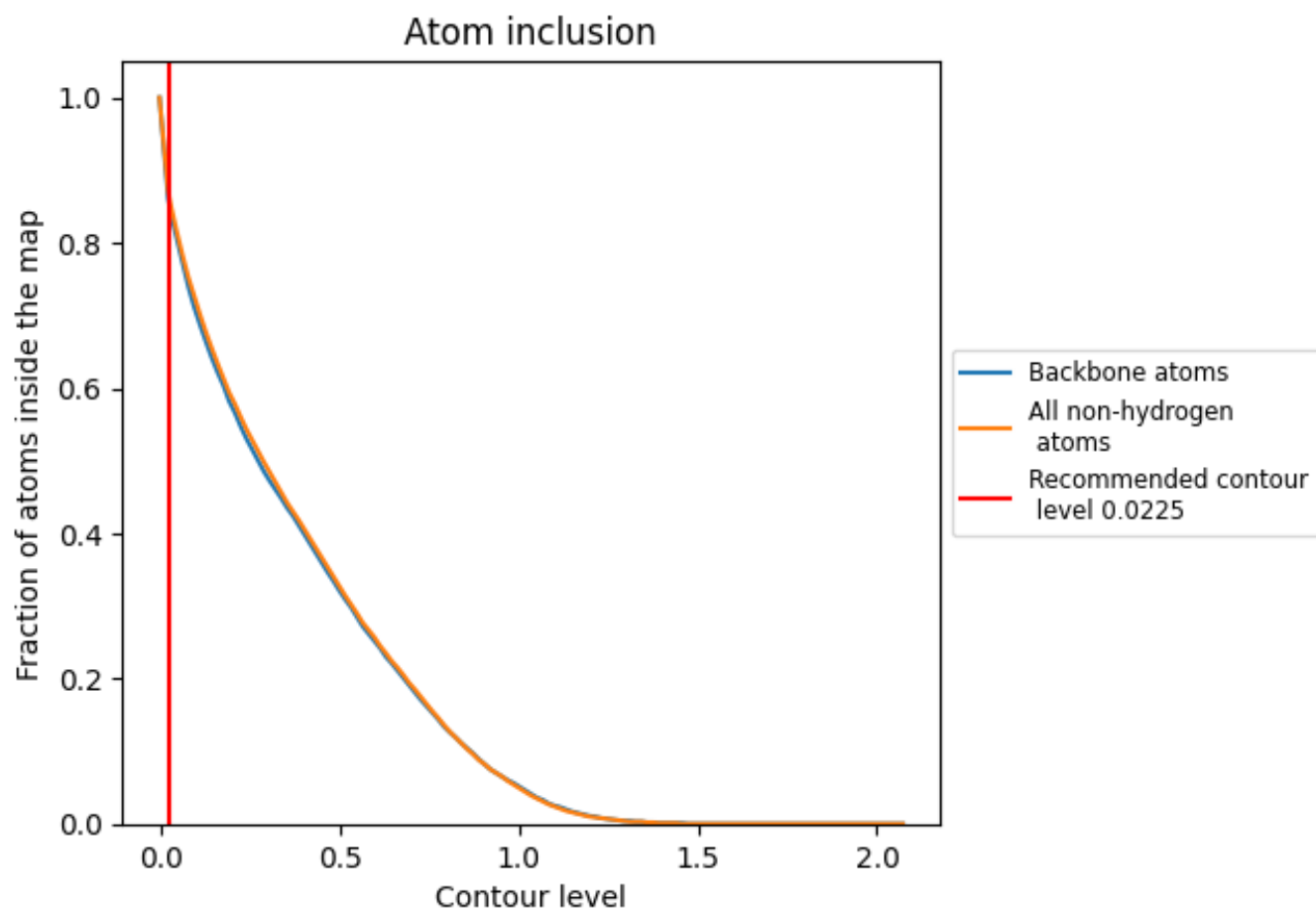
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0225).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 87% 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 (0.0225) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8710	 0.3870
A	 0.8770	 0.3870
B	 0.9100	 0.4560
C	 0.8840	 0.4030
D	 0.9140	 0.4580
E	 0.9100	 0.4400
F	 0.8490	 0.3340
G	 0.8790	 0.3890
H	 0.9130	 0.4400
I	 0.8590	 0.3860
J	 0.7990	 0.3050
K	 0.8600	 0.3410
L	 0.8650	 0.3370

