



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 03:35 PM UTC

PDB ID : 9G8Q / pdb_00009g8q
EMDB ID : EMD-51136
Title : 40S-bound human SKI238 complex in the open state (Gatekeeping module)
Authors : Koegel, A.; Keidel, A.; Loukeri, M.J.; Kuhn, C.C.; Langer, L.M.; Schaefer, I.B.; Conti, E.
Deposited on : 2024-07-23
Resolution : 4.10 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:

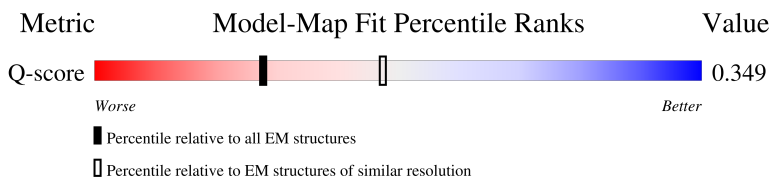
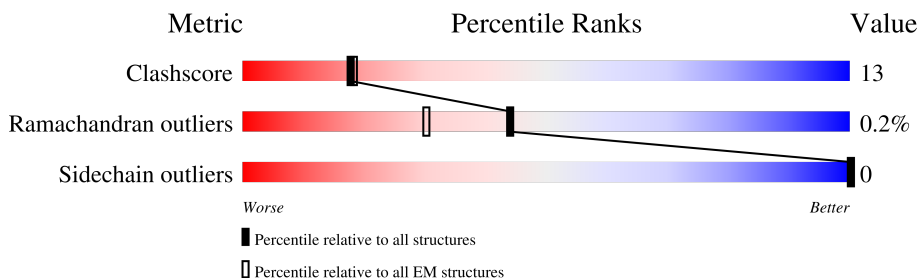
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.10 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	6458 (3.60 - 4.60)

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	1246	 9% 9% 87%
2	B	1568	 9% 42% 18% 40%
3	C	305	 10% 72% 28%
3	D	305	 10% 67% 33%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13313 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 Helicase SKI2W.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	163	Total	C	N	O	S	0	0
			1268	809	210	243	6		

- Molecule 2 is a protein called Superkiller complex protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	934	Total	C	N	O	S	0	0
			7299	4637	1259	1359	44		

There are 4 discrepancies between the modelled and reference sequences:

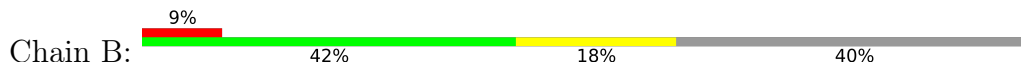
Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP Q6PGP7
B	-2	PRO	-	expression tag	UNP Q6PGP7
B	-1	ASP	-	expression tag	UNP Q6PGP7
B	0	SER	-	expression tag	UNP Q6PGP7

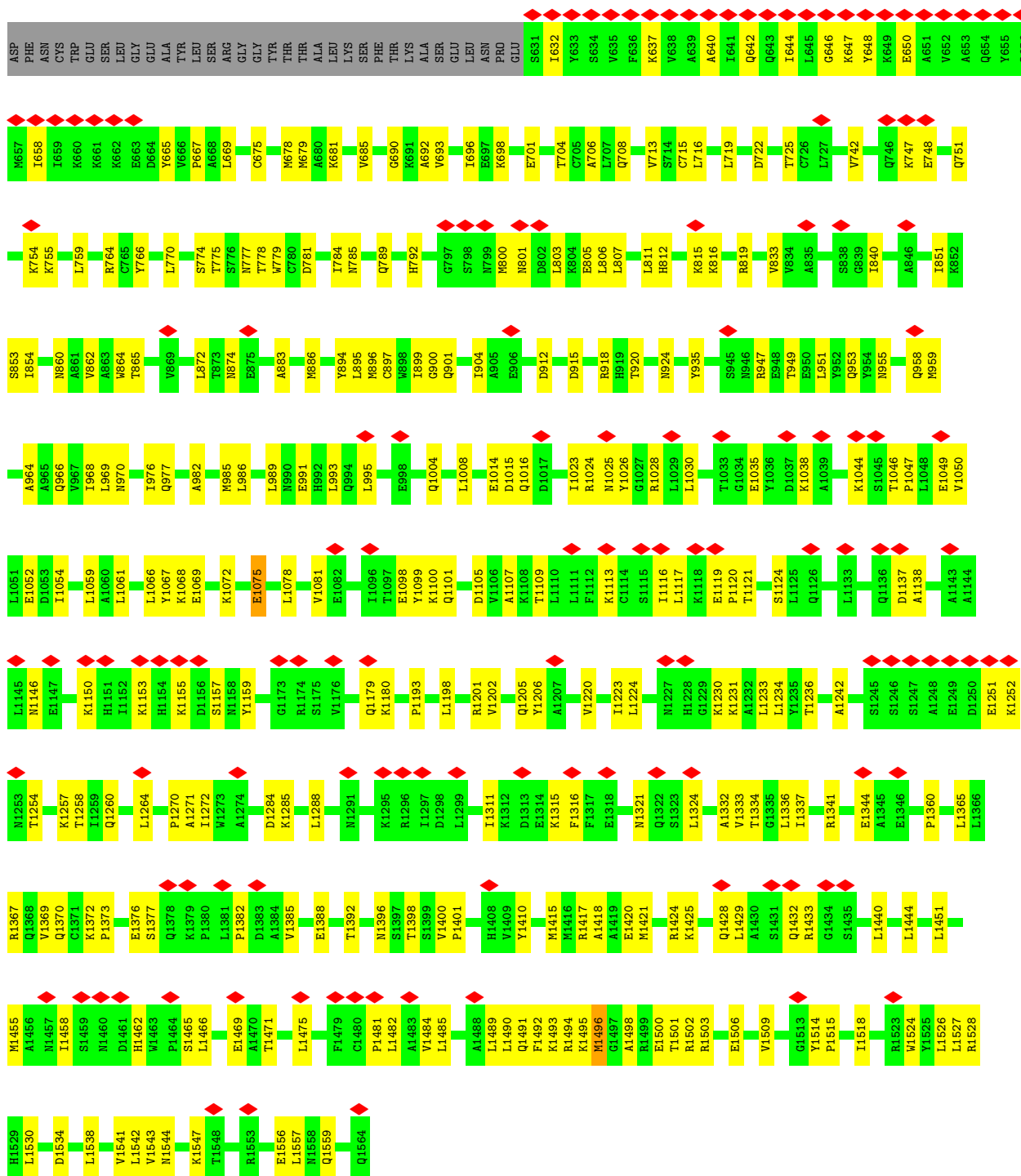
- Molecule 3 is a protein called WD repeat-containing protein 61.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	305	Total	C	N	O	S	0	0
			2373	1507	399	462	5		
3	D	305	Total	C	N	O	S	0	0
			2373	1507	399	462	5		

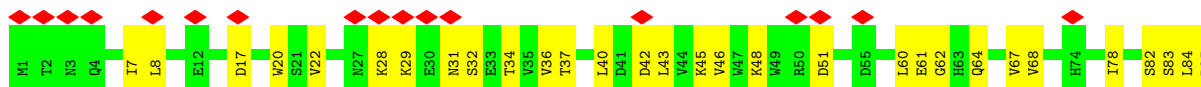
PHE	GLY	SER	VAL	GLY	LYS	THR	ALA
ALA	MET	PRO	GLU	LEU	ILE	LYS	LEU
ALA	PRO	GLY	VAL	ARG	LEU	LEU	ARG
SER	PHE	ASP	LEU	ARG	GLU	GLN	VAL
LEU	SER	ALA	ARG	ARG	ASP	GLN	GLU
THR	GLU	GLY	THR	LYS	PHE	MET	ASP
GLN	LEU	ASP	LEU	LEU	SER	ILE	MET
	ALA	GLN	GLY	GLU	GLN	GLM	GLM
	GLY	LEU	TYR	LEU	ARG	ARG	LYS
	LEU	PRO	VAL	LEU	GLN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

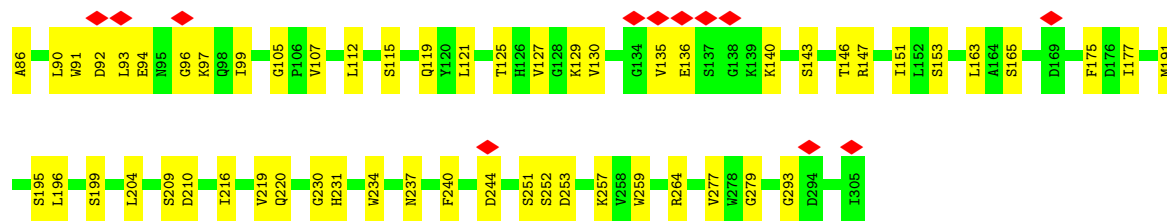
- Molecule 2: Supercollider complex protein 3

[illegible]

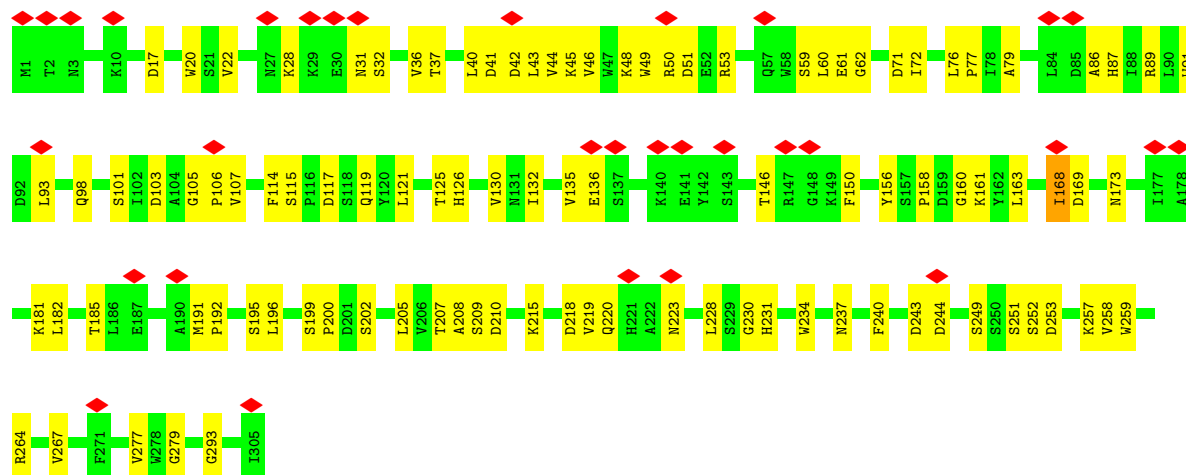


• Molecule 3: WD repeat-containing protein 61





• Molecule 3: WD repeat-containing protein 61



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53460	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 ($e^-/\text{\AA}^2$)	64.2	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.033	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	708.19836, 708.19836, 708.19836	wwPDB
Map dimensions	832, 832, 832	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8512, 0.8512, 0.8512	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	0.18	0/1304	0.64	0/1782
2	B	0.18	0/7429	0.49	3/10058 (0.0%)
3	C	0.15	0/2432	0.51	0/3311
3	D	0.15	0/2432	0.48	2/3311 (0.1%)
All	All	0.17	0/13597	0.51	5/18462 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1120	PRO	CA-N-CD	-6.79	102.49	112.00
2	B	1120	PRO	N-CD-CG	-6.30	93.75	103.20
2	B	1075	GLU	N-CA-CB	5.58	118.42	110.16
3	D	168	ILE	CA-C-N	5.23	135.34	125.66
3	D	168	ILE	C-N-CA	5.23	135.34	125.66

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	1268	0	1246	49	0
2	B	7299	0	7423	211	0
3	C	2373	0	2290	60	0
3	D	2373	0	2290	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	13313	0	13249	356	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 13.

The worst 5 of 356 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:B:895:LEU:HD22	2:B:924:ASN:HB2	1.60	0.82
2:B:800:MET:HE3	2:B:801:ASN:H	1.46	0.80
2:B:1524:TRP:HE1	2:B:1557:LEU:HD13	1.47	0.79
3:D:115:SER:HB3	3:D:119:GLN:H	1.47	0.77
3:D:48:LYS:HE3	3:D:50:ARG:HH12	1.51	0.75

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	159/1246 (13%)	149 (94%)	8 (5%)	2 (1%)	9	41
2	B	932/1568 (59%)	915 (98%)	16 (2%)	1 (0%)	48	81
3	C	303/305 (99%)	288 (95%)	15 (5%)	0	100	100
3	D	303/305 (99%)	287 (95%)	16 (5%)	0	100	100
All	All	1697/3424 (50%)	1639 (97%)	55 (3%)	3 (0%)	44	76

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	ASP

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Mol	Chain	Res	Type
2	B	1496	MET
1	A	109	THR

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	140/1062 (13%)	140 (100%)	0	100	100
2	B	780/1316 (59%)	780 (100%)	0	100	100
3	C	260/260 (100%)	260 (100%)	0	100	100
3	D	260/260 (100%)	260 (100%)	0	100	100
All	All	1440/2898 (50%)	1440 (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 23 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1404	GLN
2	B	1545	ASN
2	B	1432	GLN
2	B	1549	HIS
2	B	966	GLN

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 [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.

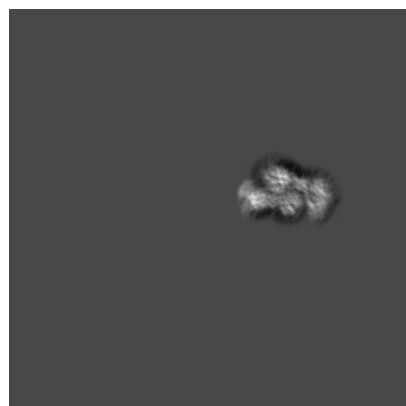
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51136. These allow visual inspection of the internal detail of the map and identification of artifacts.

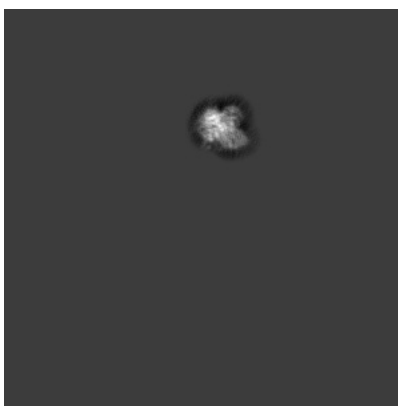
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

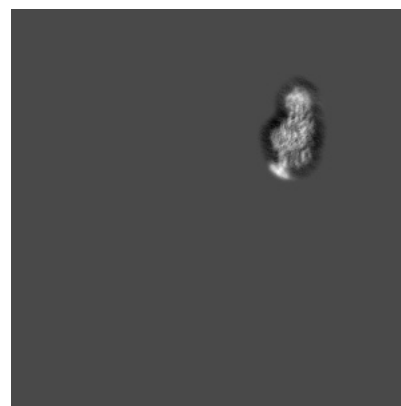
6.1.1 Primary map



X

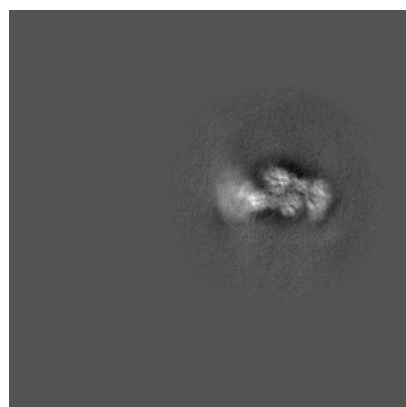


Y

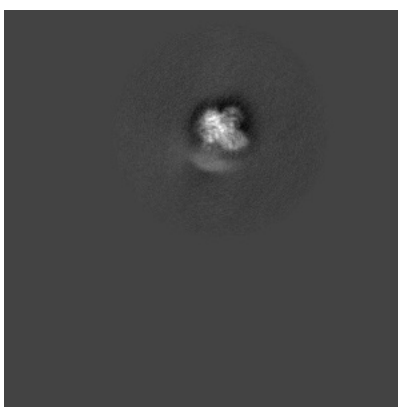


Z

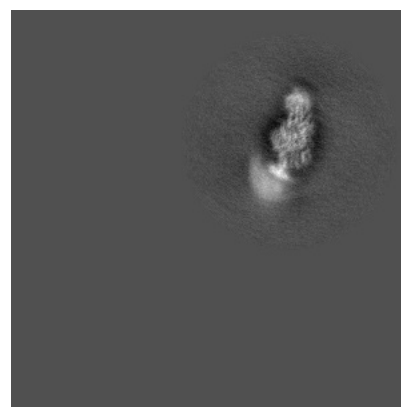
6.1.2 Raw map



X



Y

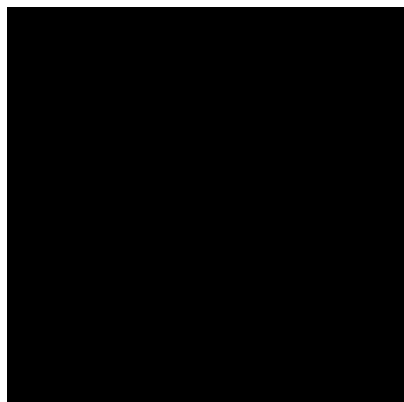


Z

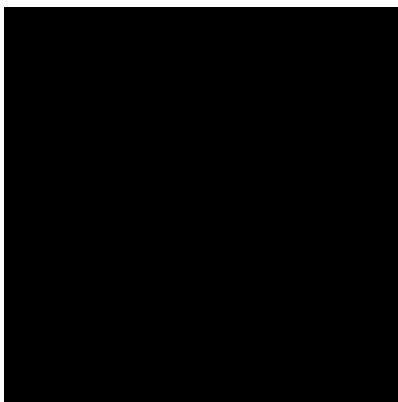
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

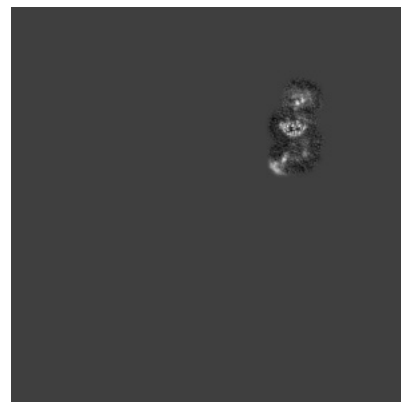
6.2.1 Primary map



X Index: 416

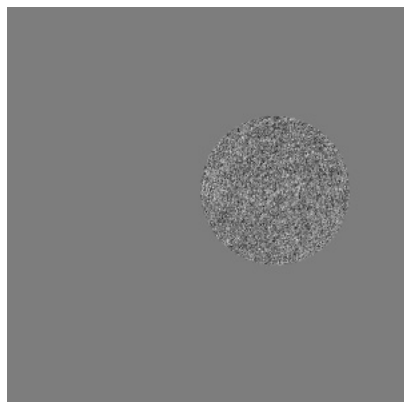


Y Index: 416

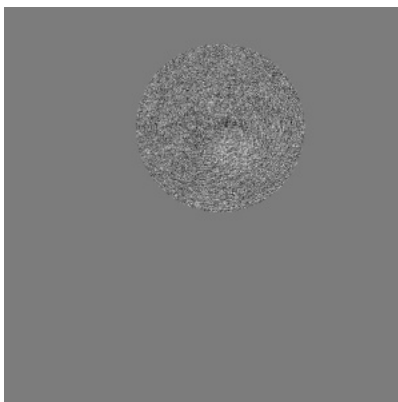


Z Index: 416

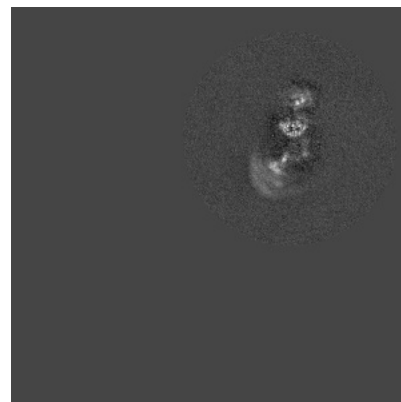
6.2.2 Raw map



X Index: 416



Y Index: 416

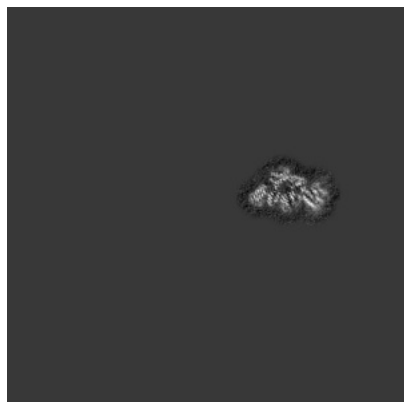


Z Index: 416

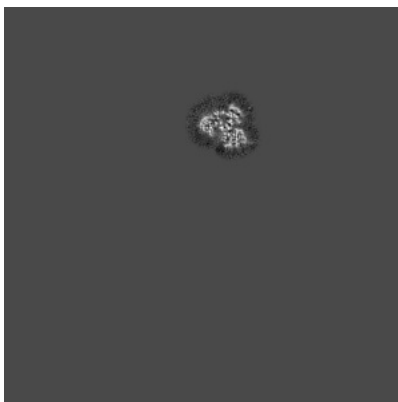
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

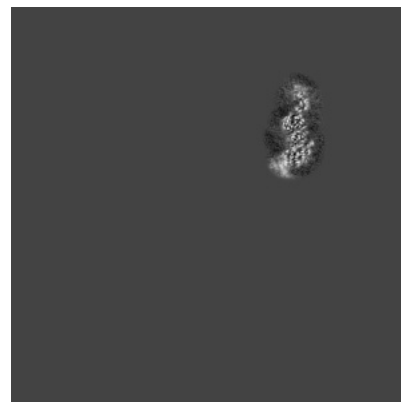
6.3.1 Primary map



X Index: 605

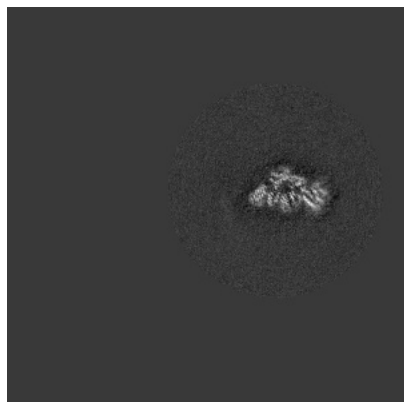


Y Index: 568

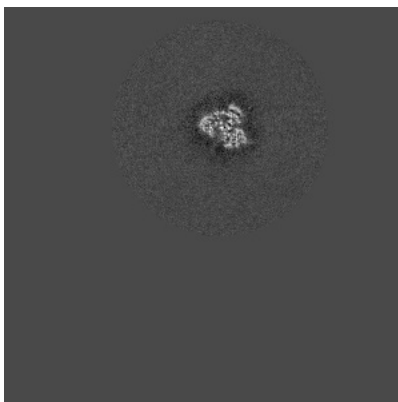


Z Index: 441

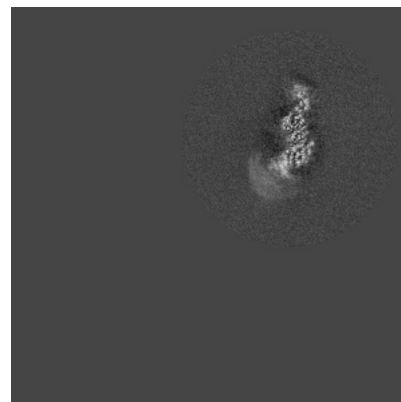
6.3.2 Raw map



X Index: 605



Y Index: 568

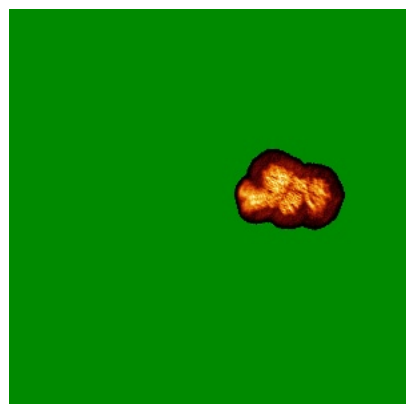


Z Index: 441

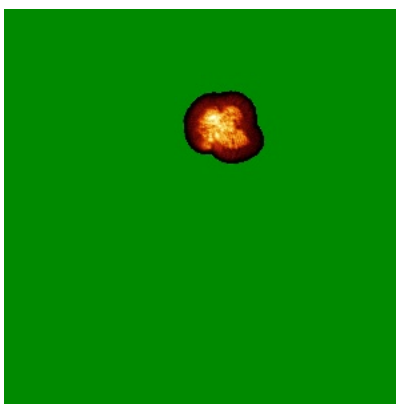
The images above show the largest variance slices of the map in three orthogonal directions.

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

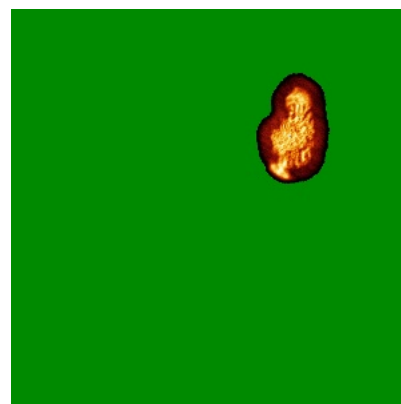
6.4.1 Primary map



X

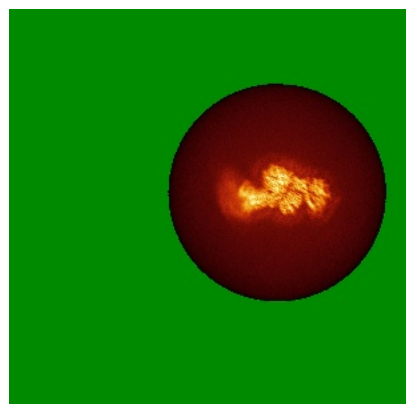


Y

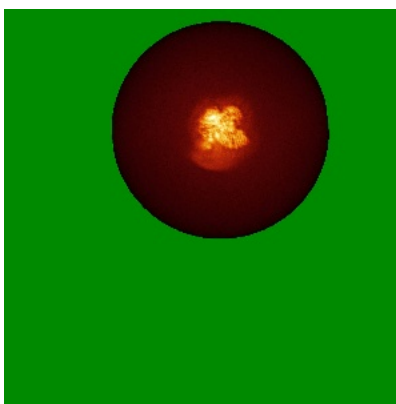


Z

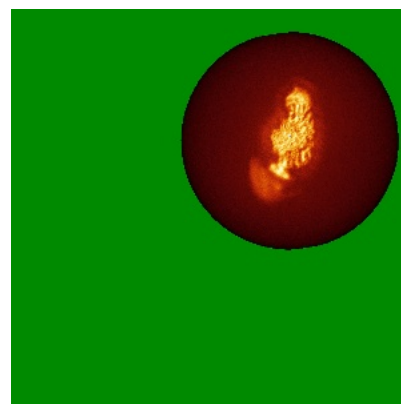
6.4.2 Raw map



X



Y

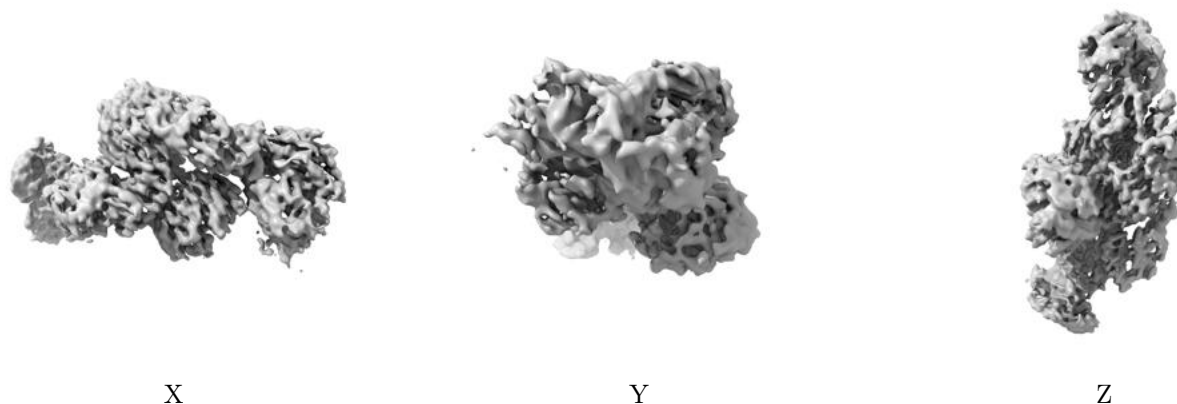


Z

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 0.01. 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.

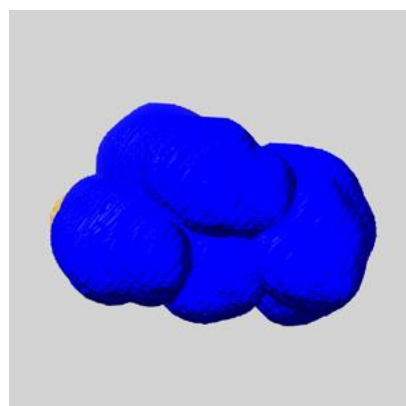
6.6 Mask visualisation [i](#)

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

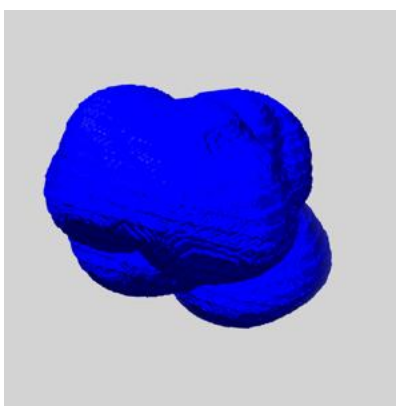
A mask typically either:

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

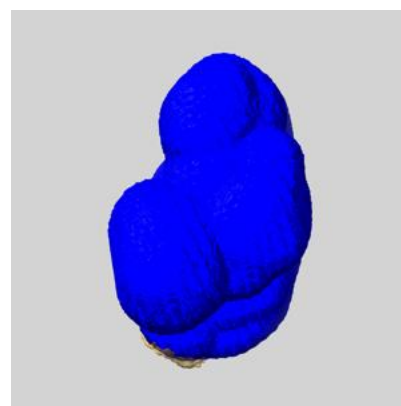
6.6.1 emd_51136_msk_1.map [i](#)



X



Y

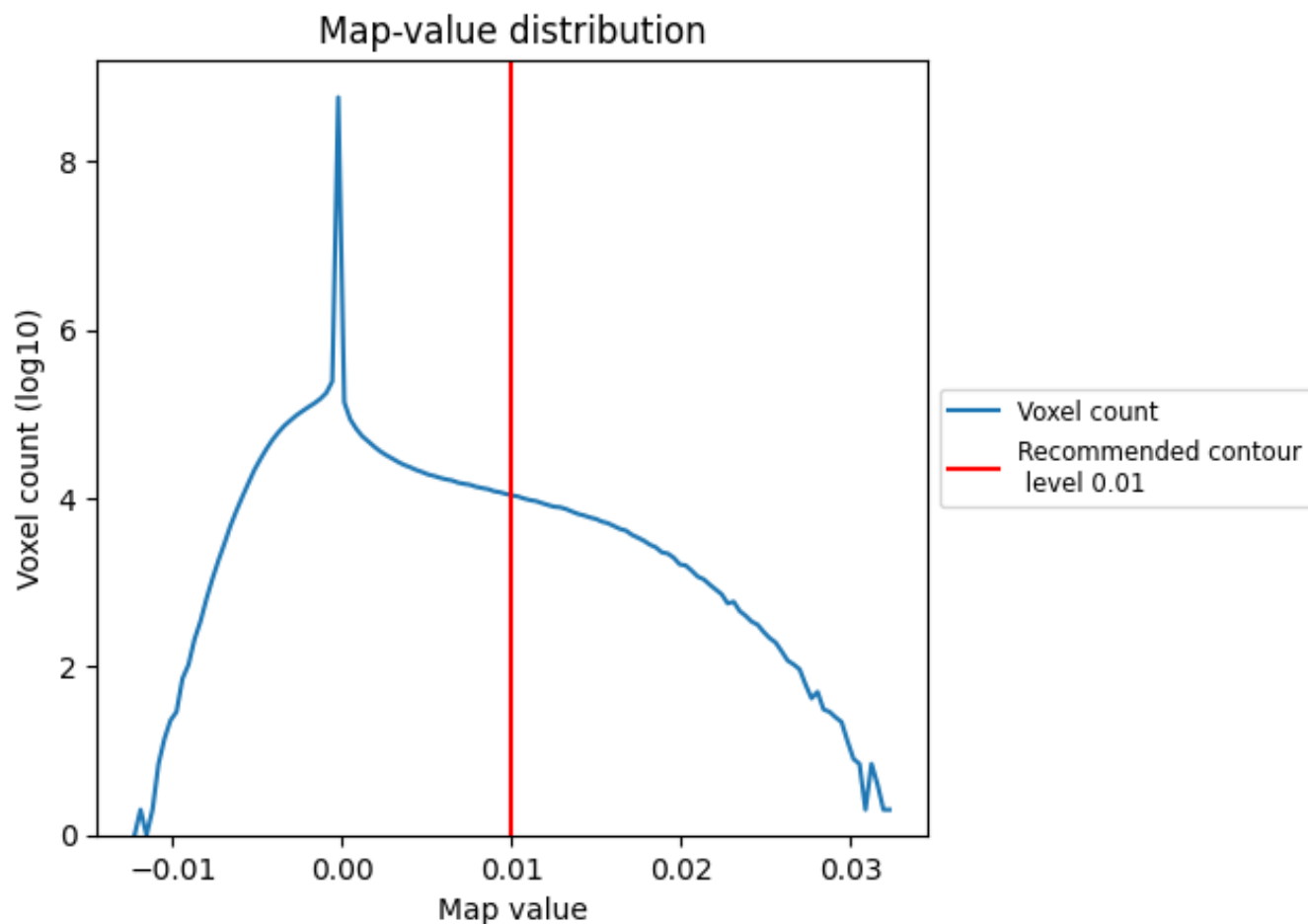


Z

7 Map analysis [i](#)

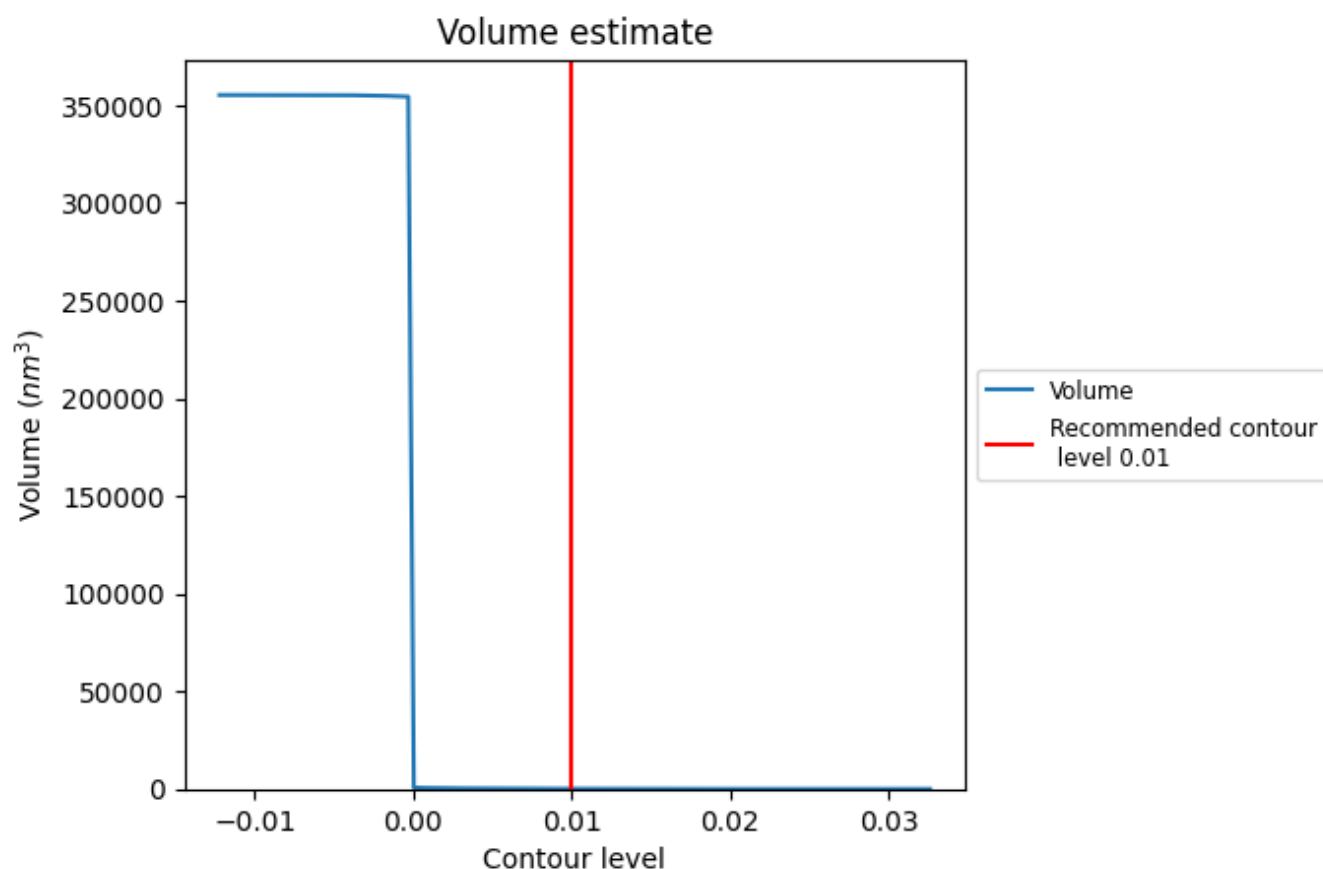
This section contains the results of statistical analysis of the map.

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.

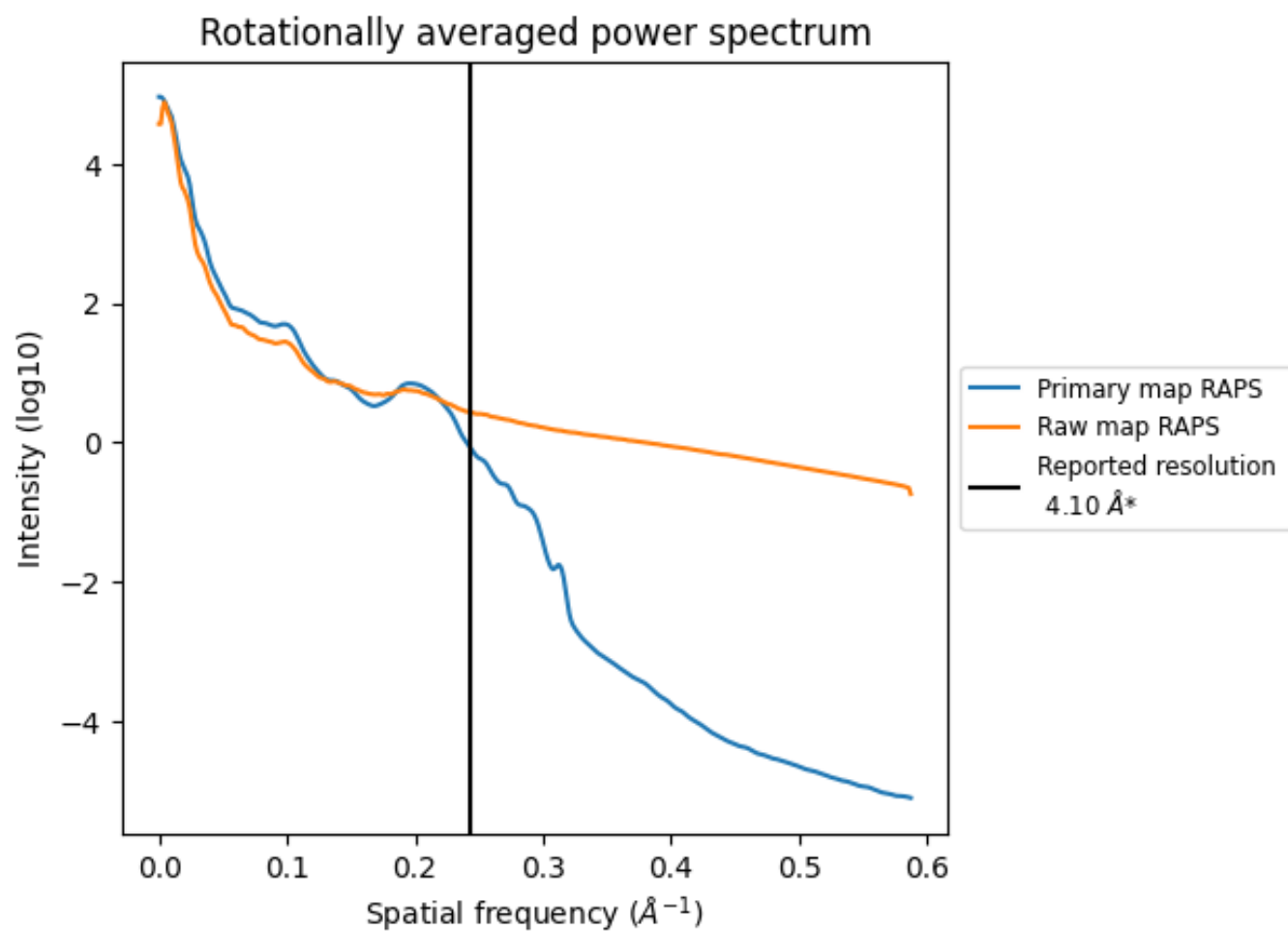
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 112 nm^3 ; this corresponds to an approximate mass of 101 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 ⓘ

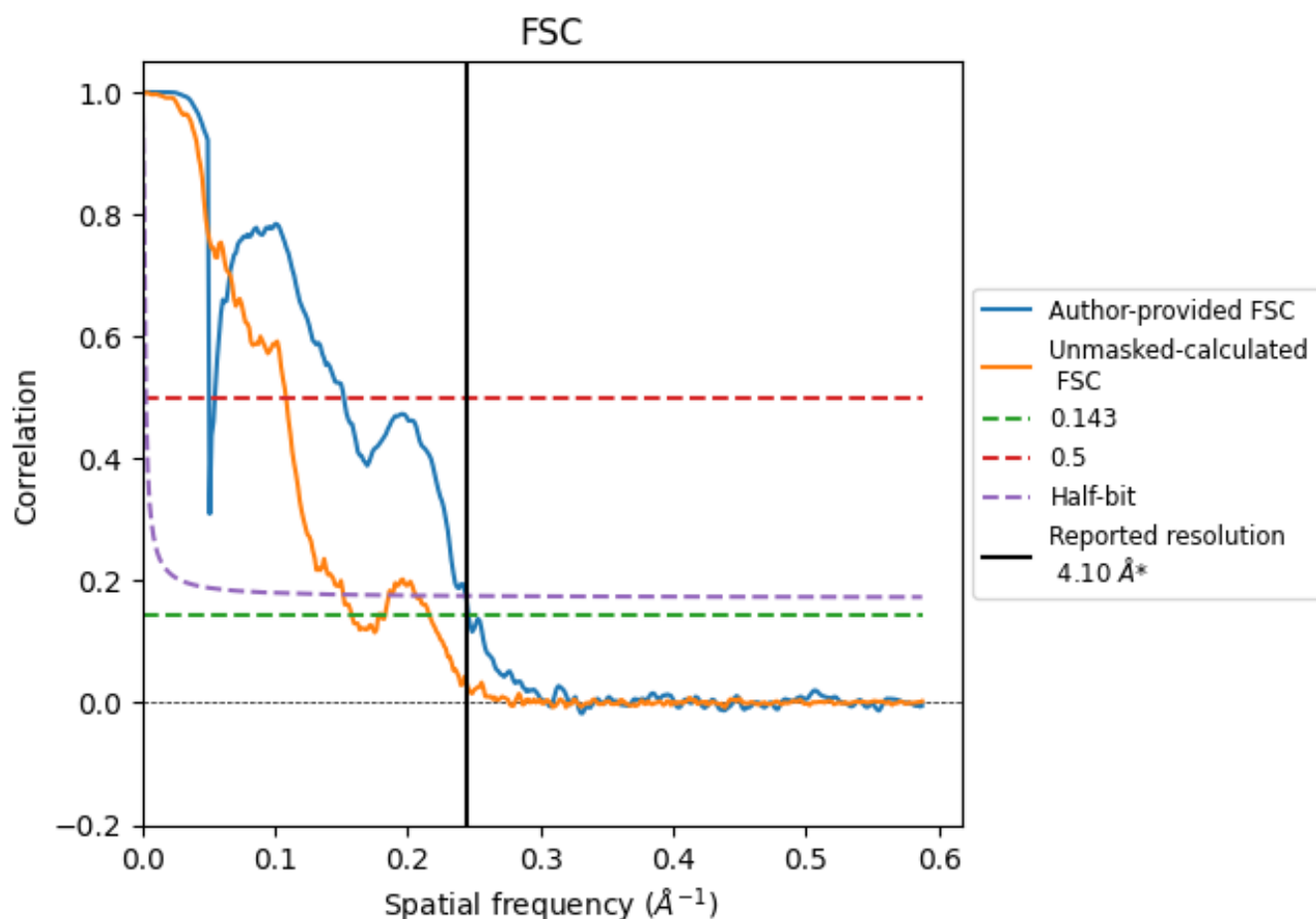


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 $0.244 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

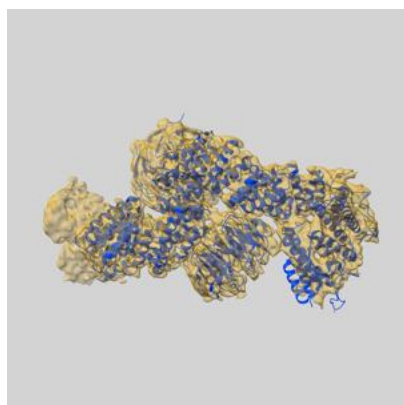
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.07	19.84	4.10
Unmasked-calculated*	6.33	9.23	6.61

*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 6.33 differs from the reported value 4.1 by more than 10 %

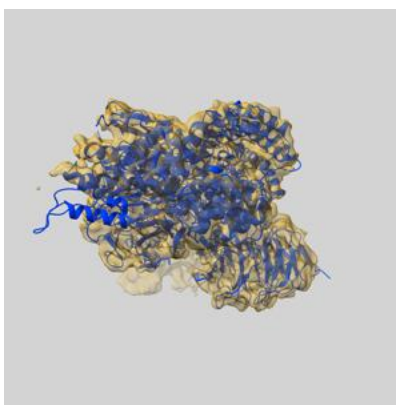
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51136 and PDB model 9G8Q. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

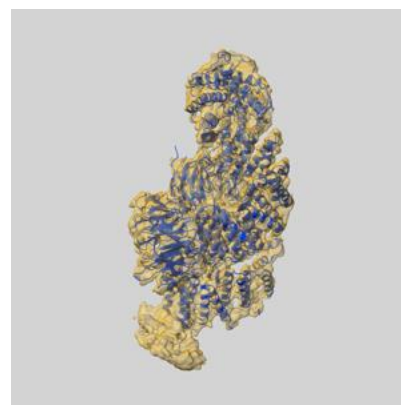
9.1 Map-model overlay [i](#)



X



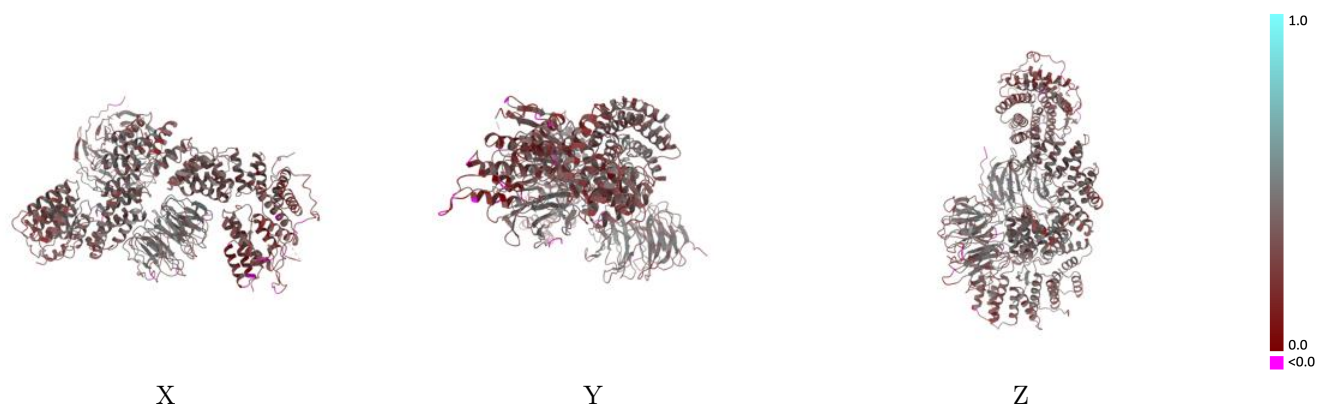
Y



Z

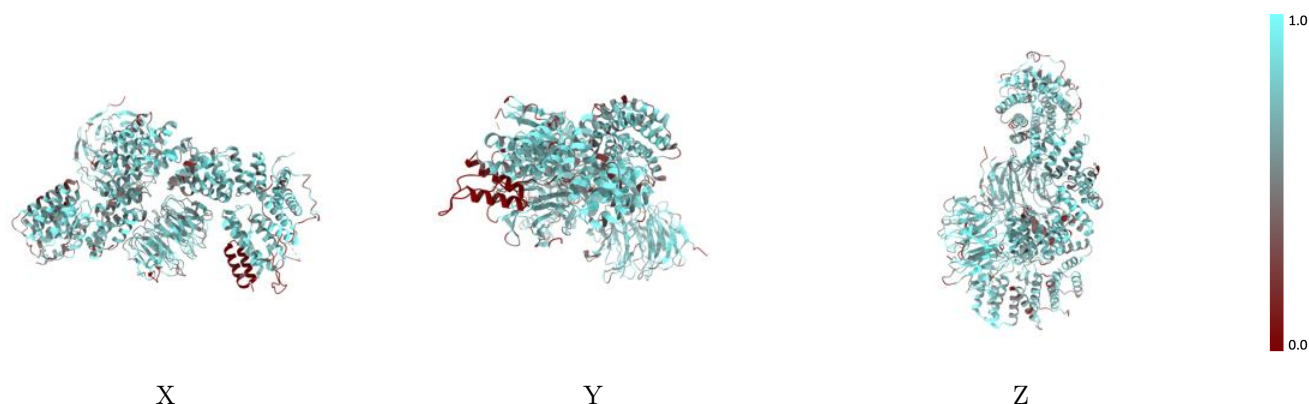
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



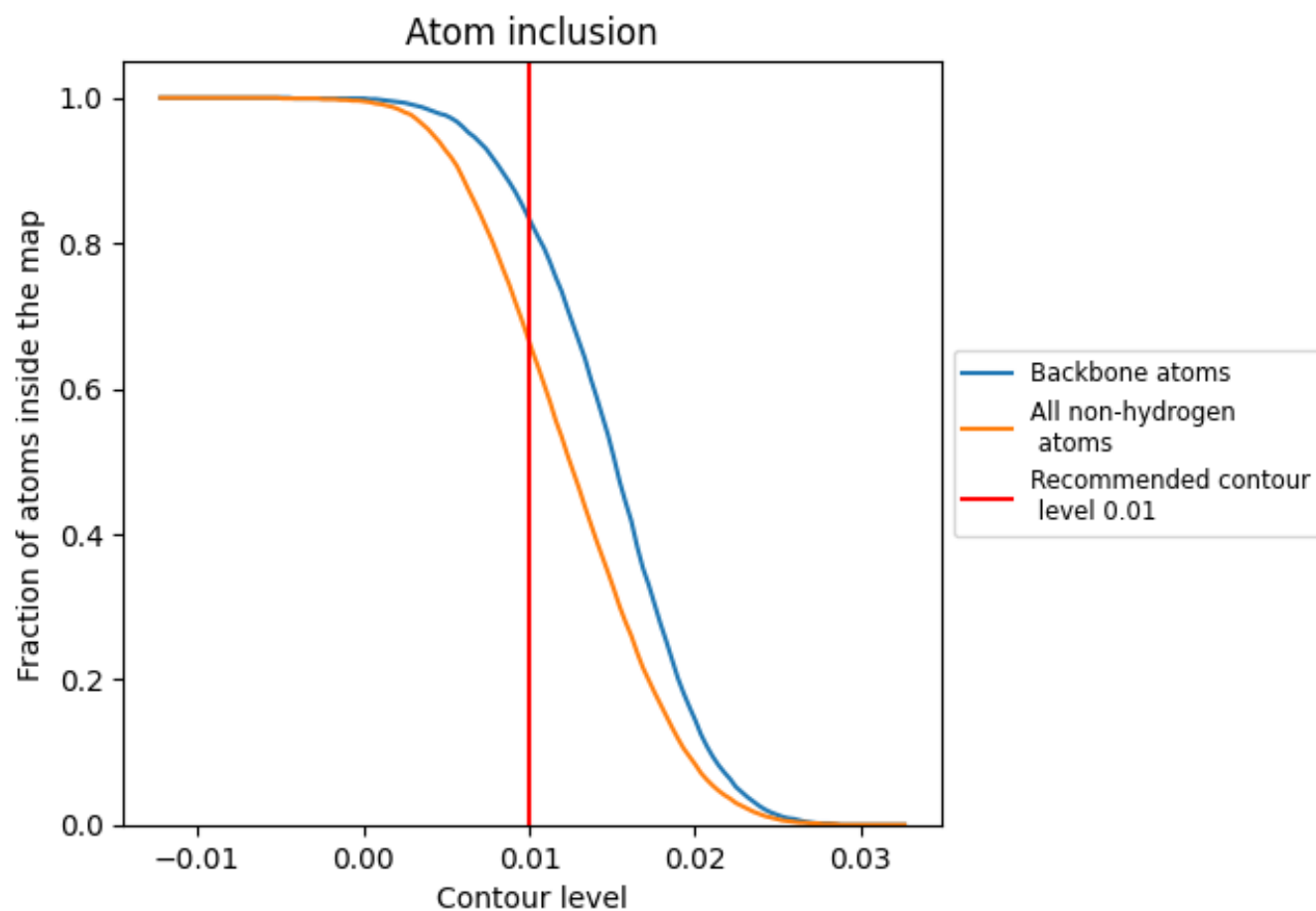
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 66% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6640	0.3490
A	0.5460	0.3220
B	0.6640	0.3290
C	0.6810	0.4060
D	0.7080	0.3650

