wwPDB EM Validation Summary Report (i)

Oct 8, 2026 – 03:06 PM EDT

PDB ID	:	9ZTR / pdb_00009ztr
EMDB ID	:	EMD-74770
Title	:	Nucleosome with an SSB at SHL +5.3 in complex with human PARP2 and HPF1, Class 4
Authors	:	Kim, T.H.; Jayathilake, C.; Virk, R.K.; Gregory-Lott, E.R.
Deposited on	:	2025-12-23
Resolution	:	2.33 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 (i) 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 (i)) were used in the production of this report:

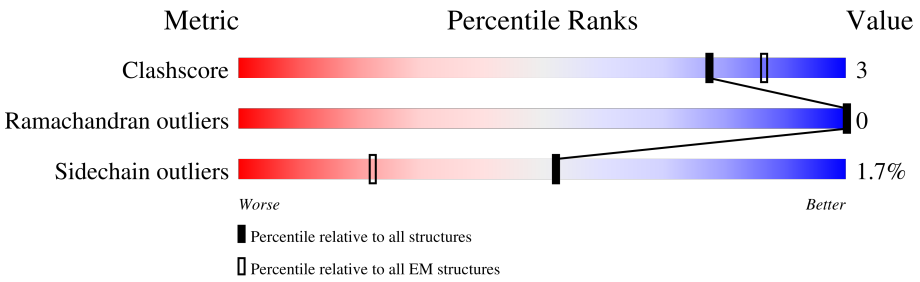
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

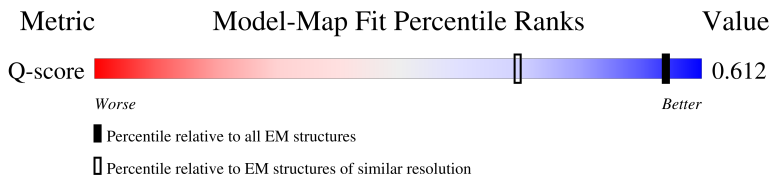
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.33 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	4434 (1.83 - 2.83)

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 <=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	124	82% • 14%
1	B	124	85% • 14%
2	C	125	74% • 22%
2	D	125	76% • 22%

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Mol	Chain	Length	Quality of chain
3	E	136	68% 27%
3	F	136	70% 27%
4	G	104	75% 5% 20%
4	H	104	73% 7% 20%
5	I	274	11% 78% 6% 16%
5	J	274	74% 9% 16%
6	K	130	72% 28%
7	L	23	70% 30%
8	M	153	80% 20%
9	P	494	21% 77%

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 31341 atoms, of which 14375 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 Histone H2A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	107	1701	518	880	160	142	1	0	0
1	B	107	1701	518	880	160	142	1	0	0

- Molecule 2 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	C	97	1584	486	813	141	142	2	0	0
2	D	97	1583	486	812	141	142	2	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	GLY	-	expression tag	UNP P02283
C	2	ILE	-	insertion	UNP P02283
D	0	GLY	-	expression tag	UNP P02283
D	2	ILE	-	insertion	UNP P02283

- Molecule 3 is a protein called Histone H3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	E	99	1673	514	857	158	142	2	0	0
3	F	99	1673	514	857	158	142	2	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	111	SER	CYS	engineered mutation	UNP P02299

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Chain	Residue	Modelled	Actual	Comment	Reference
F	111	SER	CYS	engineered mutation	UNP P02299

- Molecule 4 is a protein called Histone H4.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	G	83	1372	418	710	129	114	1	0	0
4	H	83	1372	418	710	129	114	1	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	2	ILE	-	insertion	UNP P84040
H	2	ILE	-	insertion	UNP P84040

- Molecule 5 is a protein called PL2-6 scFv.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	I	230	3543	1132	1743	296	363	9	0	0
5	J	230	3542	1132	1742	296	363	9	0	0

- Molecule 6 is a DNA chain called DNA 130-mer.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
6	K	130	4103	1255	1458	479	781	130	0	0

- Molecule 7 is a DNA chain called DNA 23-mer.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
7	L	23	734	226	262	83	140	23	0	0

- Molecule 8 is a DNA chain called DNA 153-mer.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
8	M	153	4874	1494	1717	594	916	153	0	0

- Molecule 9 is a protein called Poly [ADP-ribose] polymerase 2.

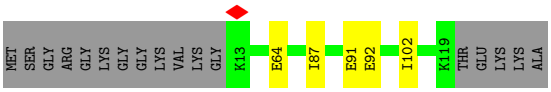
Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
9	P	116	1886	602	934	167	175	8	0	0

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.

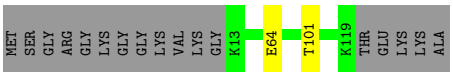
- Molecule 1: Histone H2A

Chain A:



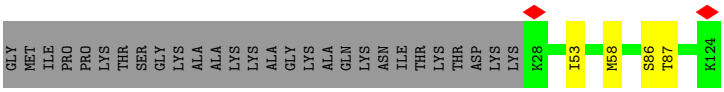
- Molecule 1: Histone H2A

Chain B:



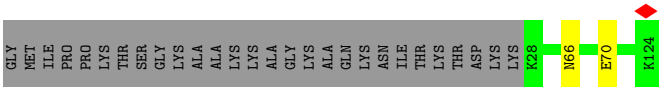
- Molecule 2: Histone H2B

Chain C:



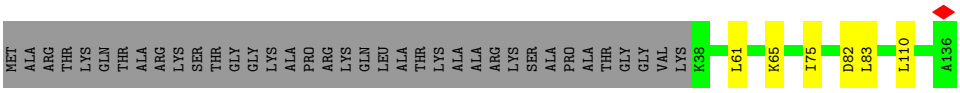
- Molecule 2: Histone H2B

Chain D:



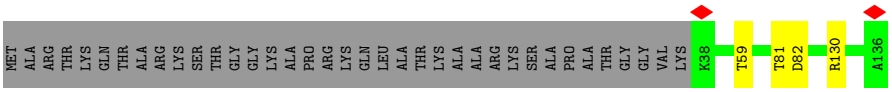
- Molecule 3: Histone H3

Chain E:



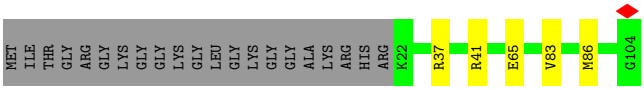
- Molecule 3: Histone H3

Chain F:



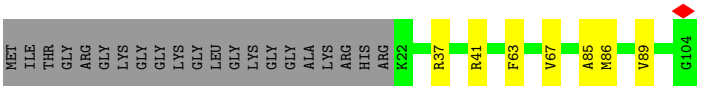
• Molecule 4: Histone H4

Chain G:



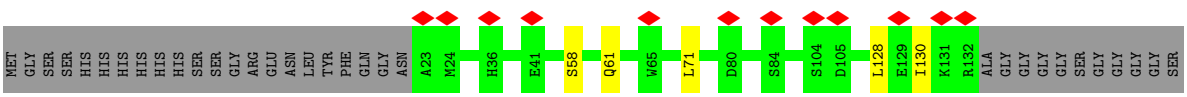
• Molecule 4: Histone H4

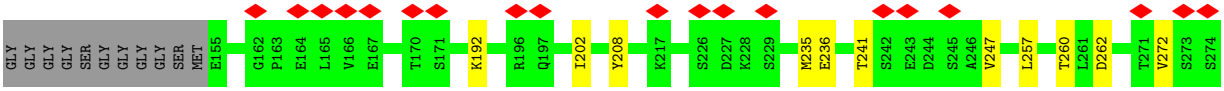
Chain H:



• Molecule 5: PL2-6 scFv

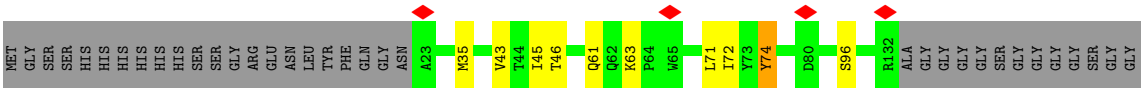
Chain I:

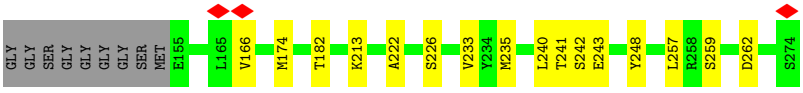




• Molecule 5: PL2-6 scFv

Chain J:





• Molecule 6: DNA 130-mer

Chain K:

• Molecule 7: DNA 23-mer

Chain L: 70% 30%

G1 T2 C3 A4 G5 A22 T23

• Molecule 8: DNA 153-mer

Chain M: 80% 20%

A1 T2 G24 G25 C29 C30 T53 T54 T60 T61 C84 G85 T90 T91 C101 T102 C107 T108 T112 A113 C114 G115 C118 A119 C126 G127 G140 G141 C145 T146 C147 C148 A149 A152 T153

• Molecule 9: Poly [ADP-ribose] polymerase 2

Chain P: 21% 77%

GLY K91 G103 H106 N112 M118 L119 L133 L136 F145 M157 L162 V163 A164 C165 A172 L181 K185 V197 M206 ASP TYR ALA THR ASN THR GLN ASP GLU GLU GLU THR LYS LYS GLU GLU SER LEU LYS SER PRO LEU LYS PRO GLU SER

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

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

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

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

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

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

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	184658	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.784	Depositor
Minimum map value	-0.479	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.042	Depositor
Map size (Å)	331.2, 331.2, 331.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.828, 0.828, 0.828	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	0.14	0/831	0.27	0/1119
1	B	0.14	0/831	0.29	0/1119
2	C	0.14	0/782	0.28	0/1046
2	D	0.14	0/782	0.29	0/1046
3	E	0.14	0/828	0.28	0/1109
3	F	0.15	0/828	0.31	0/1109
4	G	0.14	0/669	0.29	0/894
4	H	0.14	0/669	0.29	0/894
5	I	0.11	0/1842	0.27	0/2493
5	J	0.12	0/1842	0.28	0/2493
6	K	0.78	0/2962	0.88	0/4564
7	L	0.79	0/528	0.96	0/811
8	M	0.75	0/3546	0.87	0/5476
9	P	0.12	0/972	0.30	0/1305
All	All	0.49	0/17912	0.61	0/25478

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	821	880	879	4	0
1	B	821	880	879	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	771	813	811	2	0
2	D	771	812	811	1	0
3	E	816	857	856	4	0
3	F	816	857	856	3	0
4	G	662	710	709	4	0
4	H	662	710	709	3	0
5	I	1800	1743	1740	13	0
5	J	1800	1742	1740	10	0
6	K	2645	1458	1458	25	0
7	L	472	262	262	4	0
8	M	3157	1717	1717	18	0
9	P	952	934	933	6	0
All	All	16966	14375	14360	90	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 3.

The worst 5 of 90 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)
5:I:202:ILE:HG21	5:I:235:MET:HE1	1.69	0.73
6:K:107:DT:H2'	6:K:108:DT:H71	1.78	0.64
6:K:114:DC:H2"	6:K:115:DT:H71	1.79	0.64
9:P:181:LEU:O	9:P:181:LEU:HD13	2.01	0.61
2:C:87:THR:HG22	6:K:43:DG:OP1	2.01	0.59

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	105/124 (85%)	103 (98%)	2 (2%)	0	100	100
1	B	105/124 (85%)	103 (98%)	2 (2%)	0	100	100
2	C	95/125 (76%)	94 (99%)	1 (1%)	0	100	100
2	D	95/125 (76%)	95 (100%)	0	0	100	100
3	E	97/136 (71%)	96 (99%)	1 (1%)	0	100	100
3	F	97/136 (71%)	97 (100%)	0	0	100	100
4	G	81/104 (78%)	79 (98%)	2 (2%)	0	100	100
4	H	81/104 (78%)	80 (99%)	1 (1%)	0	100	100
5	I	226/274 (82%)	217 (96%)	9 (4%)	0	100	100
5	J	226/274 (82%)	218 (96%)	8 (4%)	0	100	100
9	P	114/494 (23%)	110 (96%)	4 (4%)	0	100	100
All	All	1322/2020 (65%)	1292 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	83/94 (88%)	82 (99%)	1 (1%)	63	75
1	B	83/94 (88%)	82 (99%)	1 (1%)	63	75
2	C	84/105 (80%)	83 (99%)	1 (1%)	63	75
2	D	84/105 (80%)	84 (100%)	0	100	100
3	E	86/111 (78%)	85 (99%)	1 (1%)	63	75
3	F	86/111 (78%)	86 (100%)	0	100	100
4	G	68/80 (85%)	68 (100%)	0	100	100
4	H	68/80 (85%)	67 (98%)	1 (2%)	57	69
5	I	202/226 (89%)	201 (100%)	1 (0%)	81	88
5	J	202/226 (89%)	194 (96%)	8 (4%)	28	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	P	103/433 (24%)	97 (94%)	6 (6%)	18	22
All	All	1149/1665 (69%)	1129 (98%)	20 (2%)	52	66

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	P	106	HIS
9	P	157	MET
9	P	197	VAL
9	P	162	LEU
5	J	63	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	104	GLN
2	C	46	GLN
3	F	86	GLN
5	I	61	GLN
9	P	144	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.

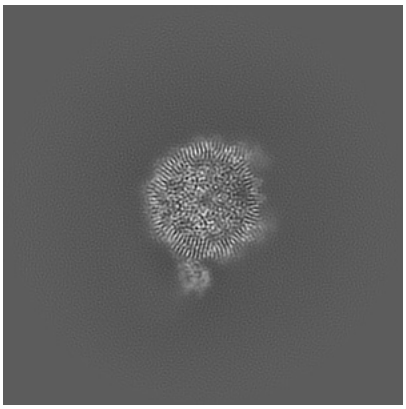
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-74770. These allow visual inspection of the internal detail of the map and identification of artifacts.

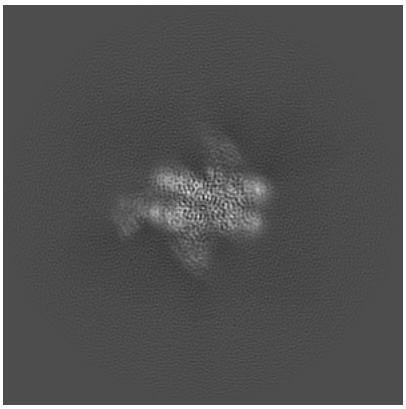
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

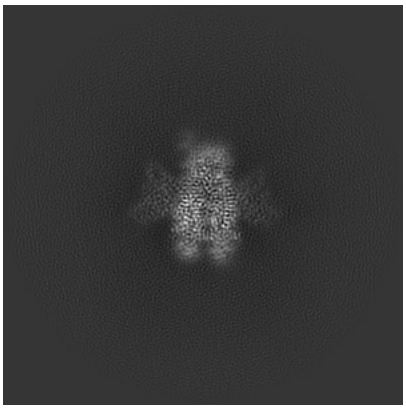
6.1.1 Primary map



X

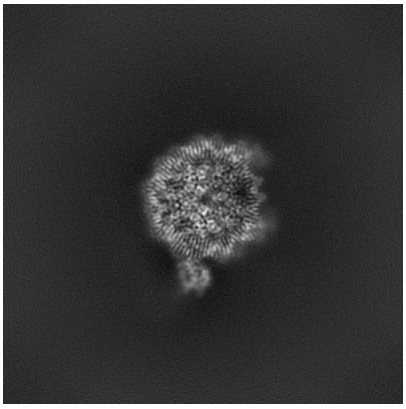


Y

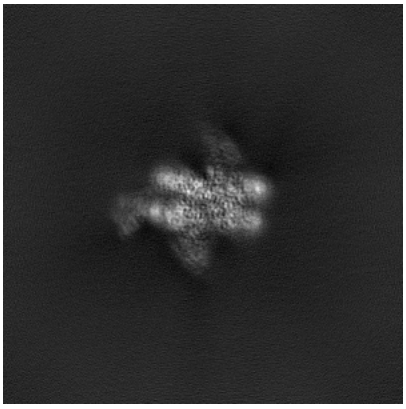


Z

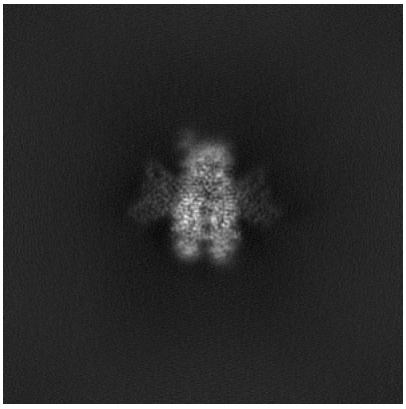
6.1.2 Raw map



X



Y

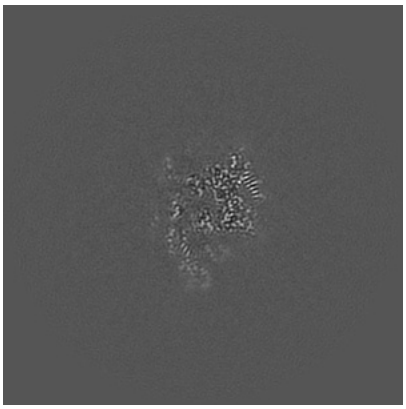


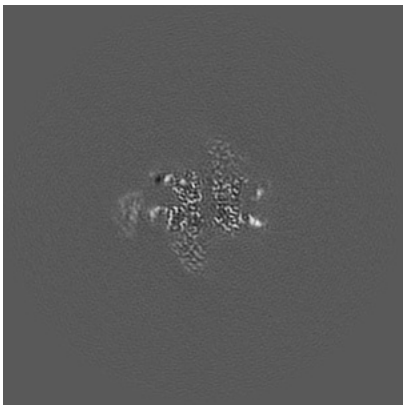
Z

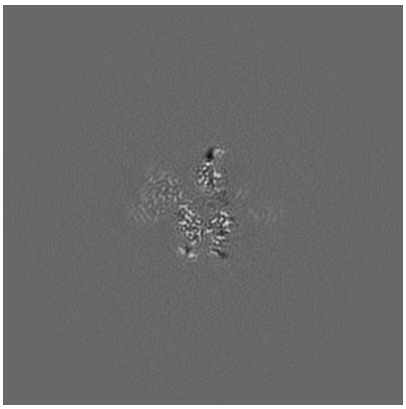
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

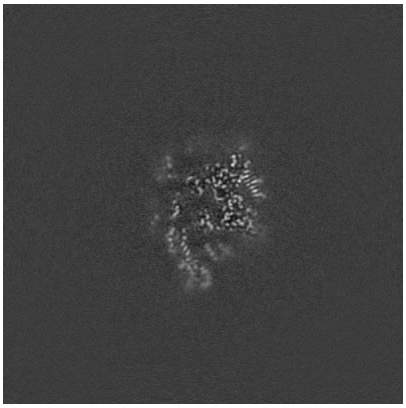
6.2.1 Primary map

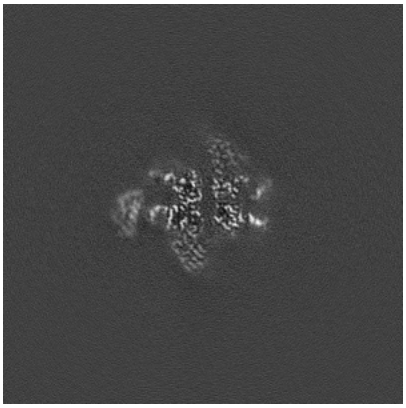

X Index: 200

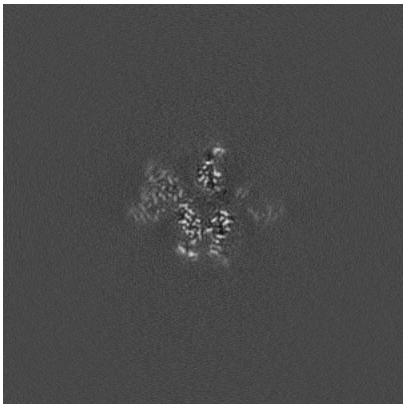

Y Index: 200


Z Index: 200

6.2.2 Raw map


X Index: 200

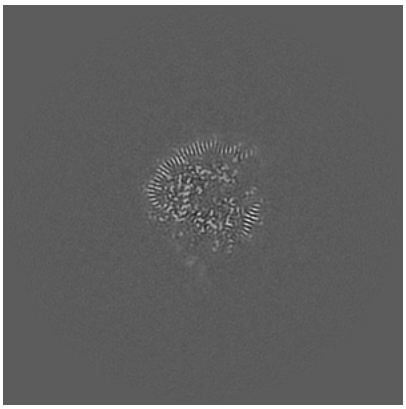

Y Index: 200

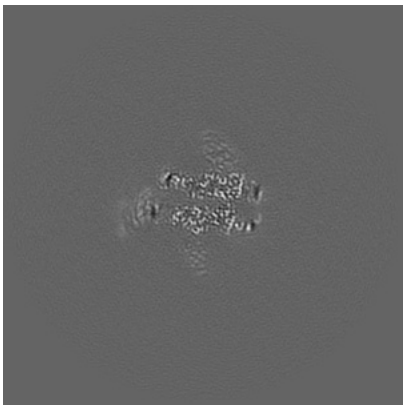

Z Index: 200

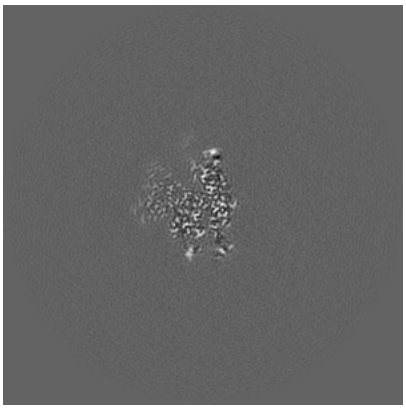
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

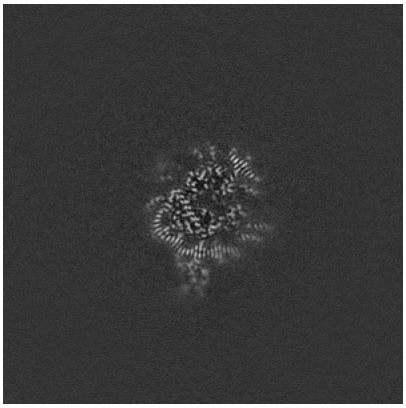
6.3.1 Primary map

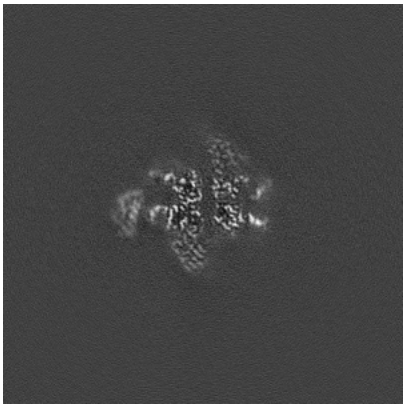

X Index: 213

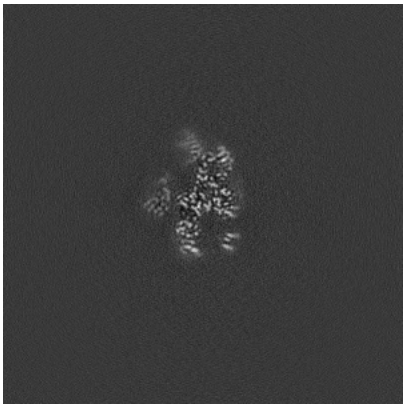

Y Index: 186


Z Index: 190

6.3.2 Raw map


X Index: 192

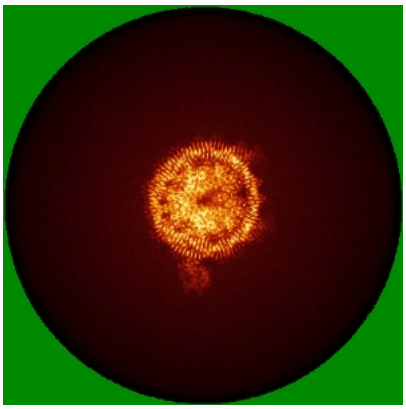

Y Index: 200

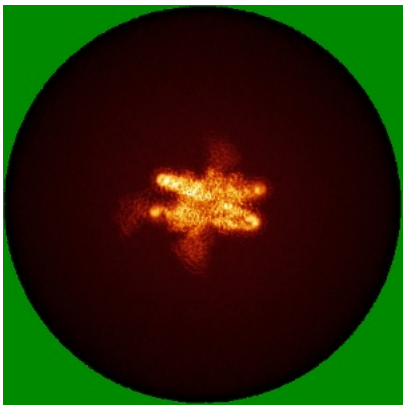

Z Index: 178

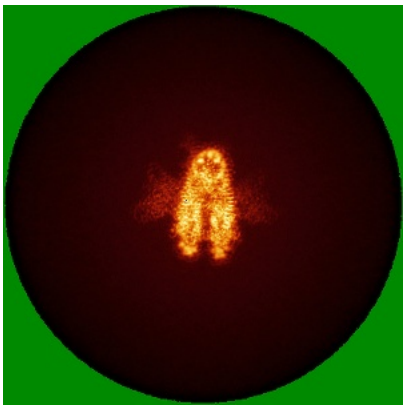
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

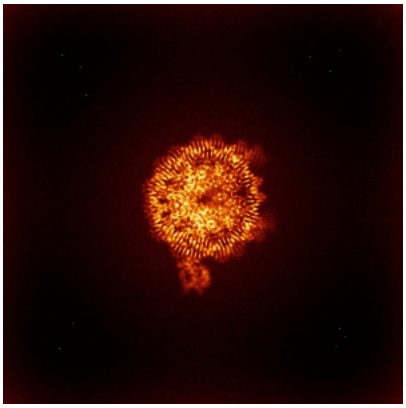
6.4.1 Primary map

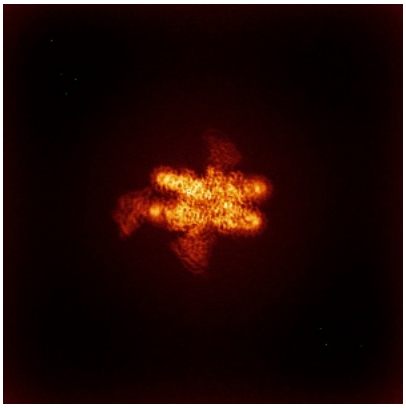

X

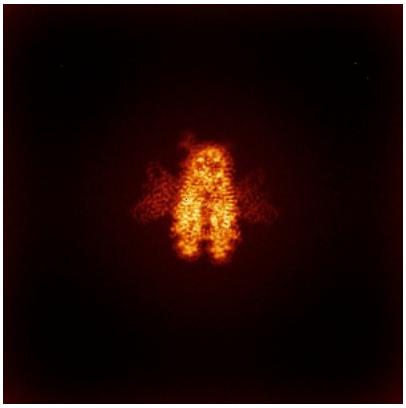

Y


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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.042. 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

X Y Z

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.

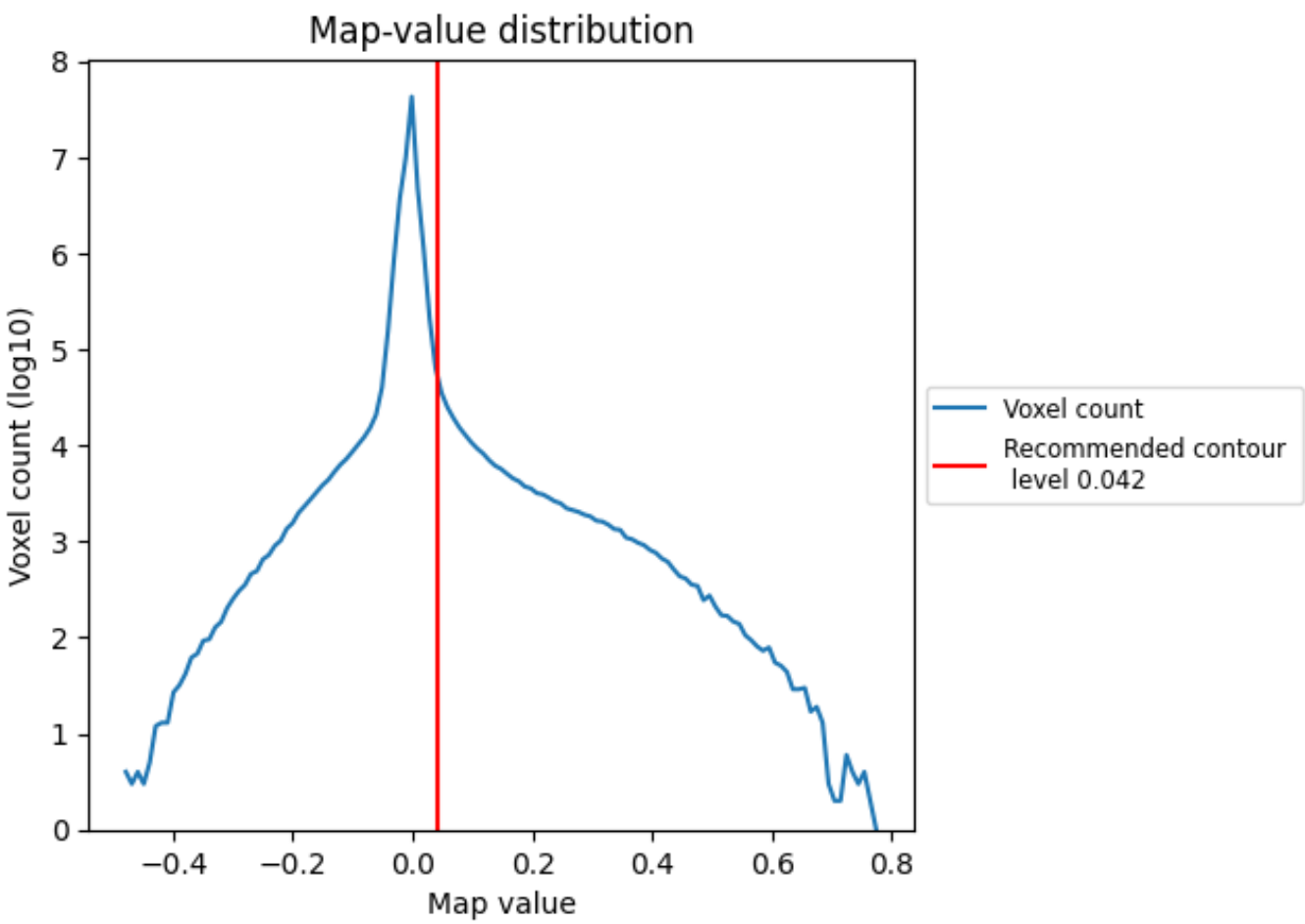
6.6 Mask visualisation (i)

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

7 Map analysis (i)

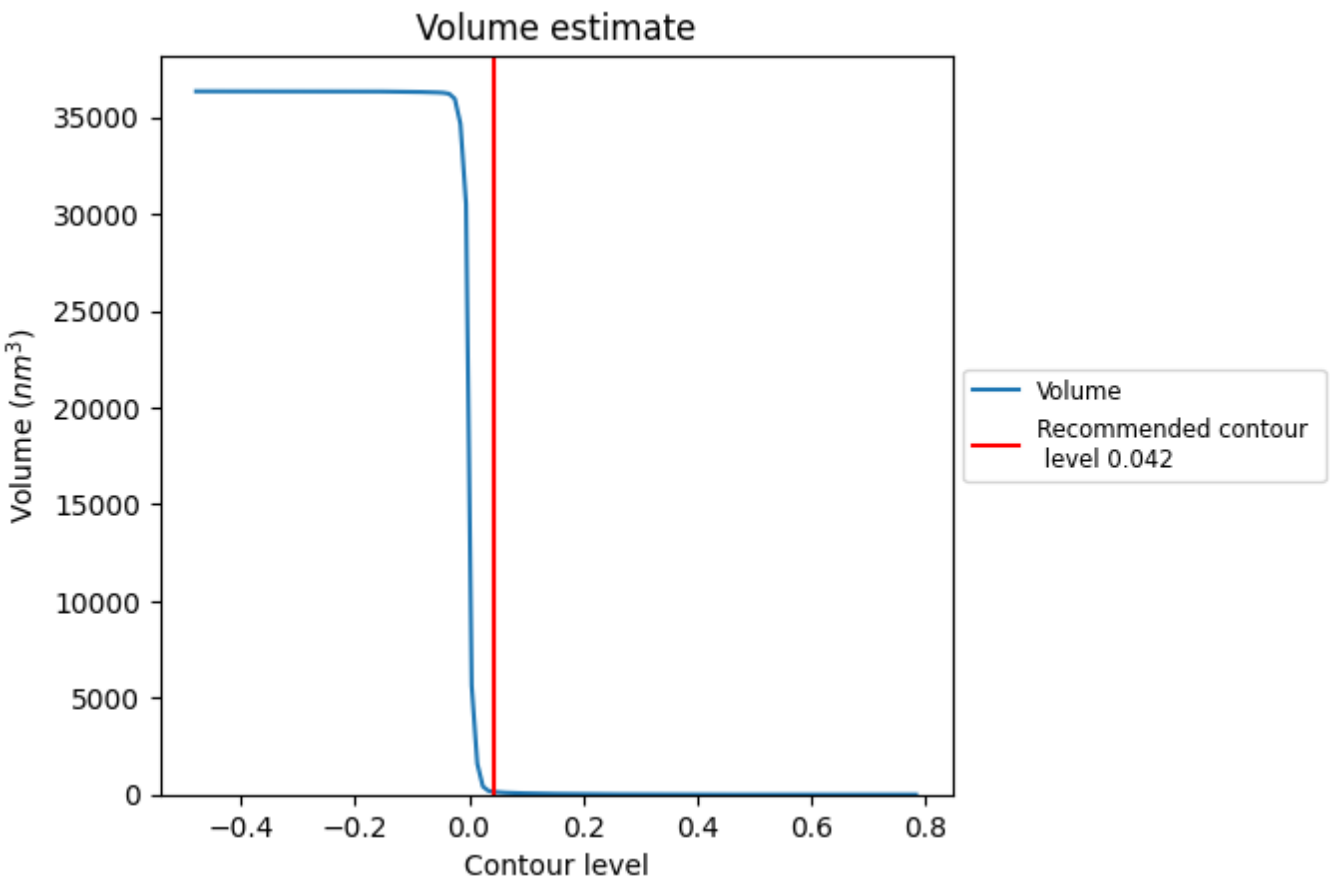
This section contains the results of statistical analysis of the map.

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.

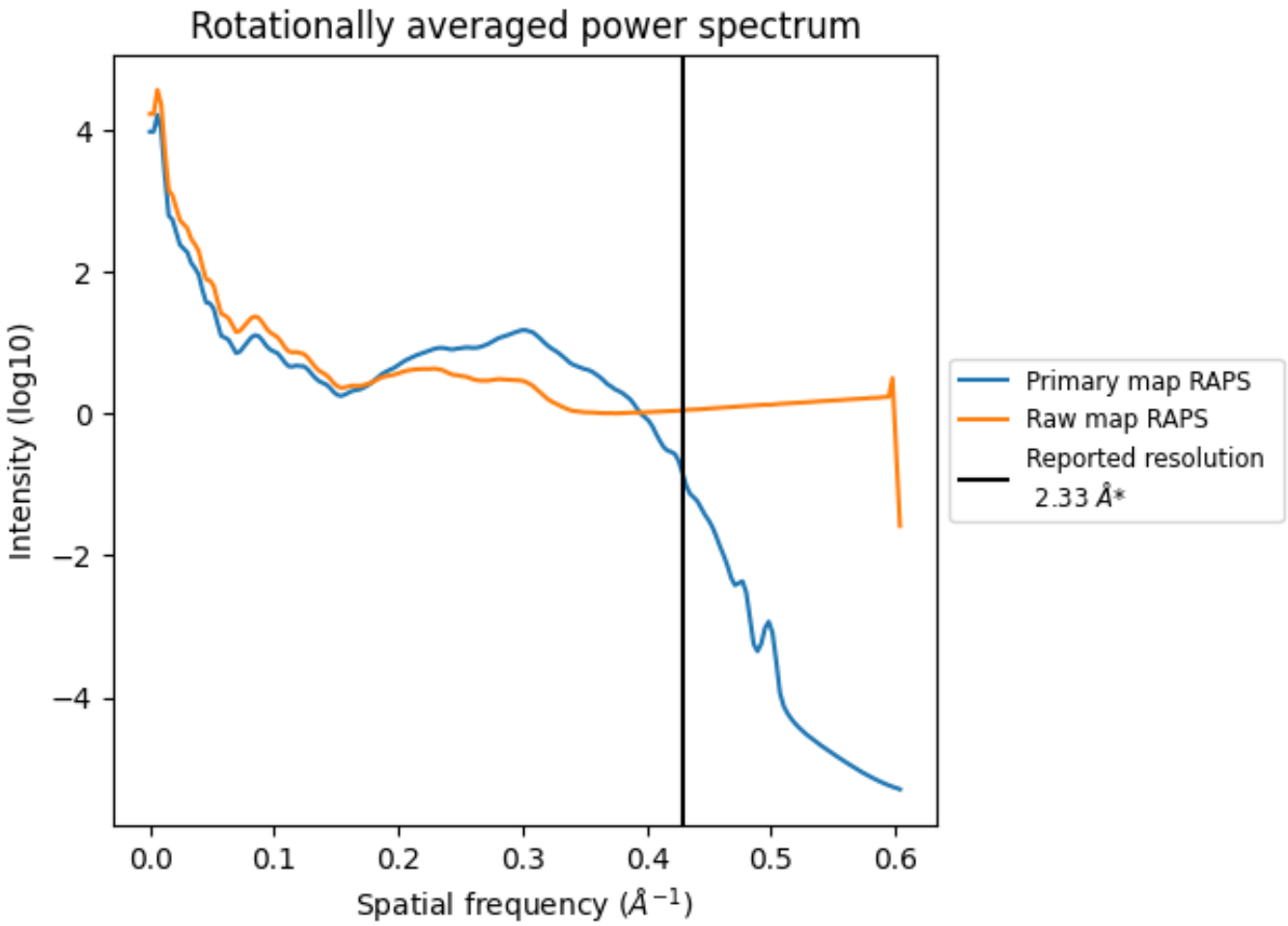
7.2 Volume estimate (i)



The volume at the recommended contour level is 148 nm^3; this corresponds to an approximate mass of 134 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)

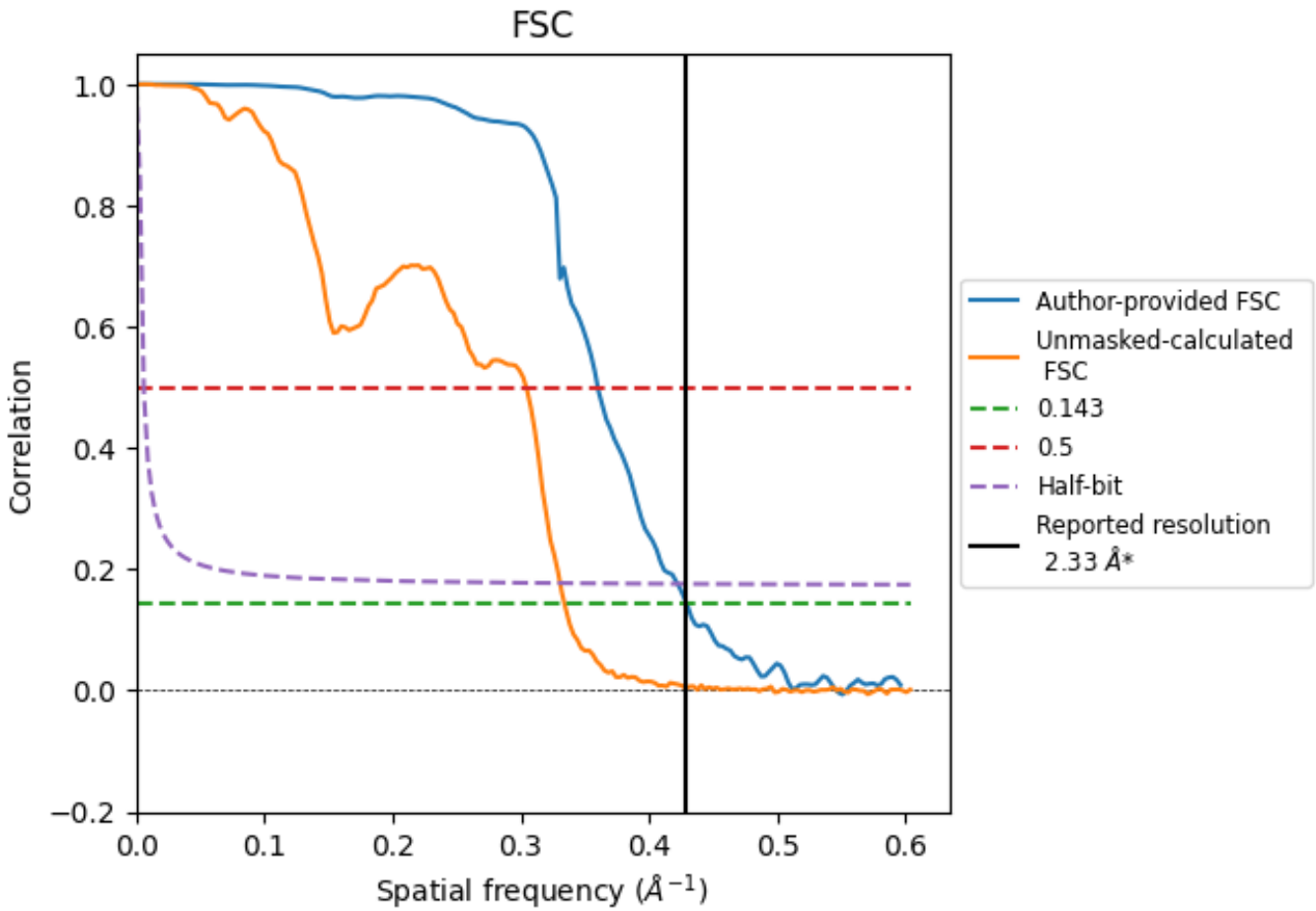


*Reported resolution corresponds to spatial frequency of 0.429 Å^{-1}

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 0.429 Å^{-1}

8.2 Resolution estimates (i)

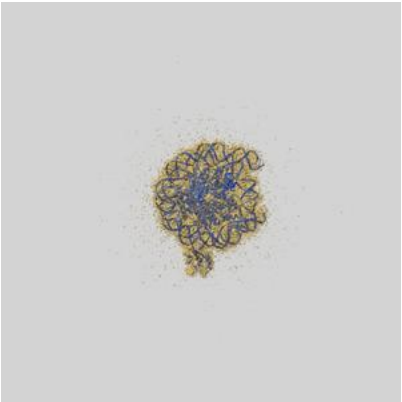
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.33	-	-
Author-provided FSC curve	2.33	2.78	2.37
Unmasked-calculated*	2.99	3.29	3.02

*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 2.99 differs from the reported value 2.33 by more than 10 %

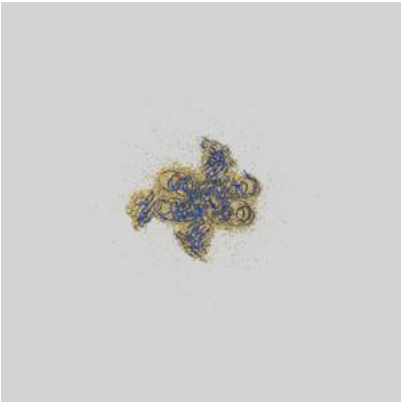
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-74770 and PDB model 9ZTR. Per-residue inclusion information can be found in section 3 on page 7.

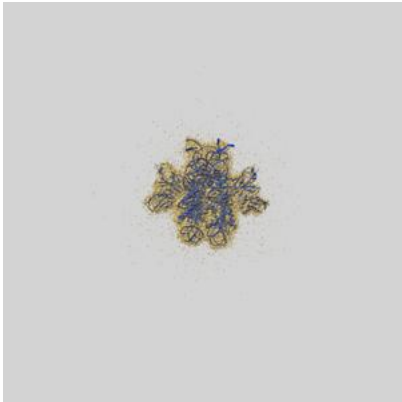
9.1 Map-model overlay (i)



X



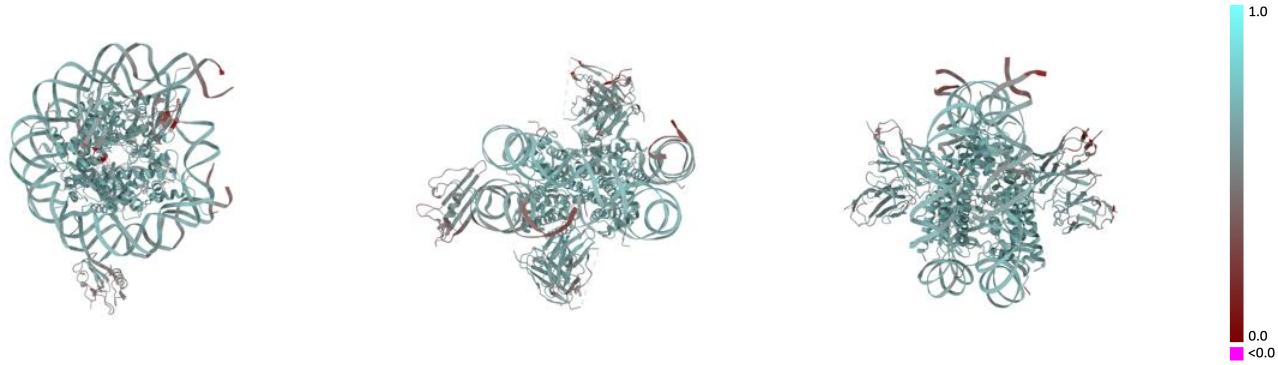
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.042 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.

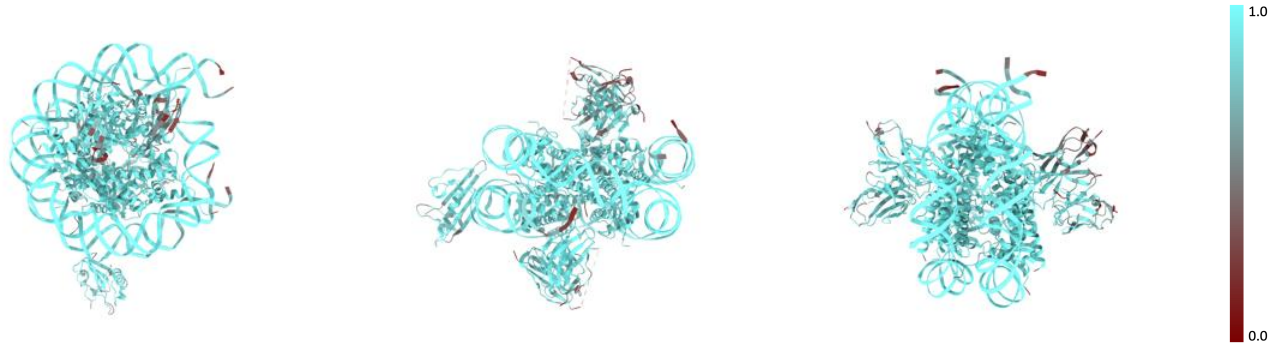
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

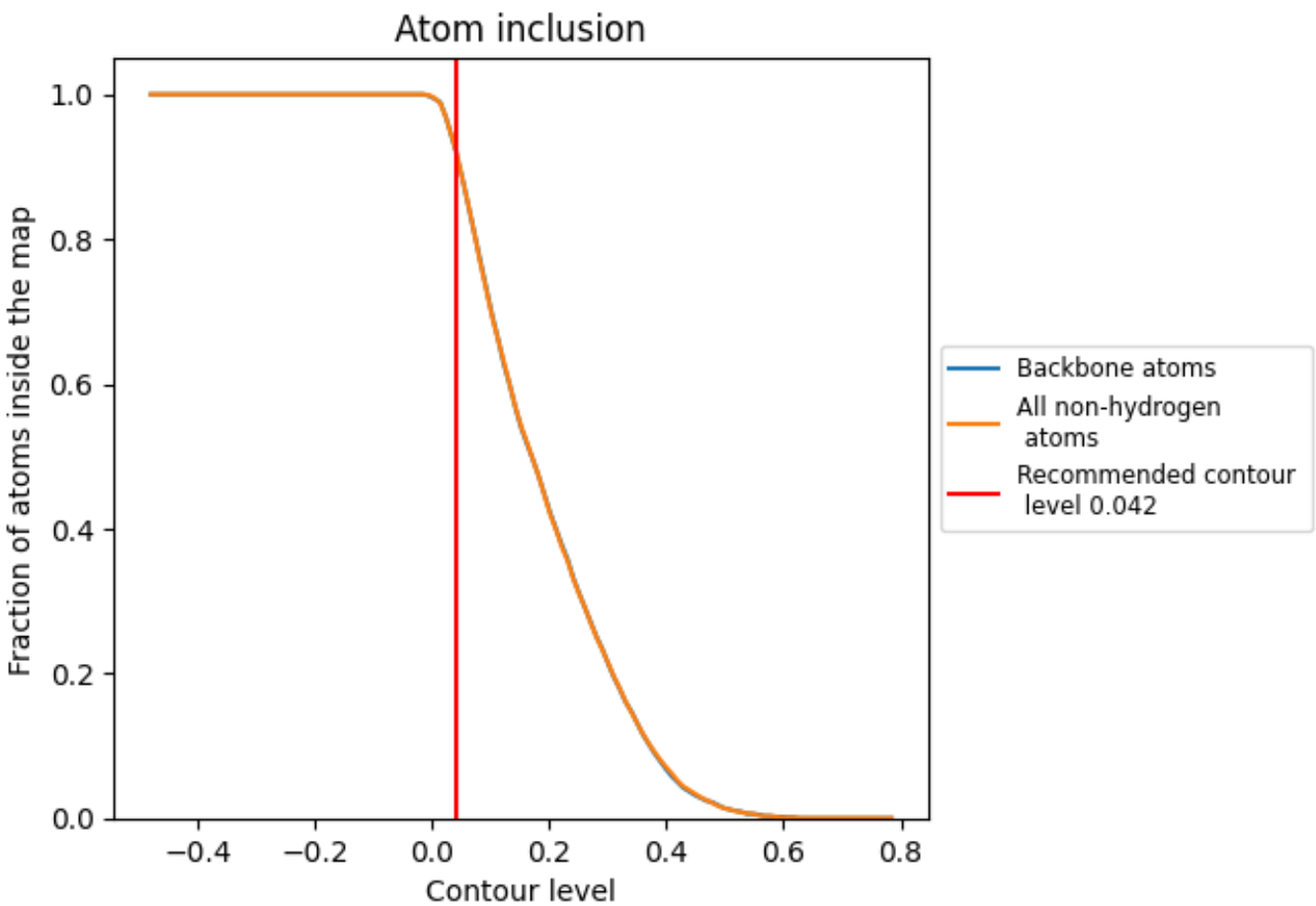
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.042).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.042) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9210	0.6120
A	0.9770	0.6740
B	0.9790	0.6720
C	0.9630	0.6580
D	0.9630	0.6620
E	0.9690	0.6710
F	0.9710	0.6690
G	0.9730	0.6750
H	0.9760	0.6740
I	0.7260	0.5490
J	0.8720	0.5890
K	0.9770	0.6130
L	0.8830	0.5300
M	0.9500	0.6000
P	0.8570	0.4790