



wwPDB EM Validation Summary Report ⓘ

Sep 22, 2025 – 09:03 pm BST

PDB ID : 9SLJ / pdb_00009slj
EMDB ID : EMD-55003
Title : Chromosomal Passenger Complex in complex with H3T3ph Nucleosome (Double Occupancy)
Authors : Gireesh, A.; Abad, M.A.; Sotelo-Parrilla, P.; Jeyaprakash, A.A.
Deposited on : 2025-09-04
Resolution : 3.80 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:

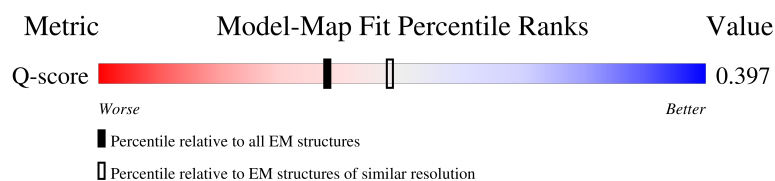
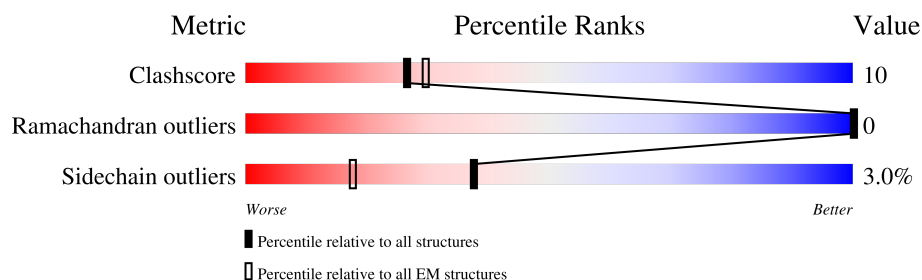
EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

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 3.80 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.



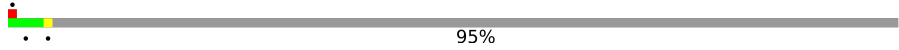
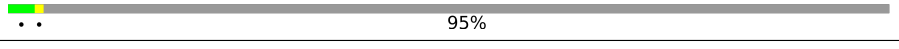
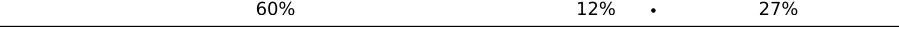
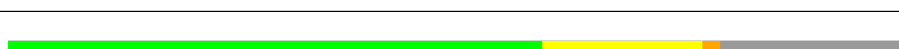


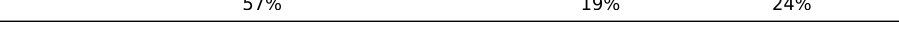




Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	L	280	 23% 73%
1	O	280	 22% 73%
2	M	142	 23% 76% 19%
2	P	142	 15% 70% 26%

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Mol	Chain	Length	Quality of chain
3	N	918	 95%
3	Q	918	 95%
4	A	135	 60%12%27%
4	E	135	 59%16%25%
5	B	102	 60%18%21%
5	F	102	 59%21%20%
6	C	129	 68%19%13%
6	G	129	 71%17%12%
7	D	125	 57%19%24%
7	H	125	 66%10%24%
8	I	147	 47%53%
9	J	147	 50%50%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 16390 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 Borealin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L	75	Total	C	N	O	S	0	0
			633	400	120	112	1		
1	O	75	Total	C	N	O	S	0	0
			633	400	120	112	1		

- Molecule 2 is a protein called Baculoviral IAP repeat-containing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	137	Total	C	N	O	S	0	0
			1118	712	191	207	8		
2	P	137	Total	C	N	O	S	0	0
			1118	712	191	207	8		

- Molecule 3 is a protein called Inner centromere protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	42	Total	C	N	O	S	0	0
			346	220	54	67	5		
3	Q	42	Total	C	N	O	S	0	0
			346	220	54	67	5		

- Molecule 4 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	98	Total	C	N	O	S	0	0
			811	512	157	139	3		
4	E	101	Total	C	N	O	S	0	0
			831	525	161	142	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	102	ALA	GLY	engineered mutation	UNP P84233

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Chain	Residue	Modelled	Actual	Comment	Reference
E	102	ALA	GLY	engineered mutation	UNP P84233

- Molecule 5 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	81	Total 648	C 410	N 126	O 111	S 1	0	0
5	F	82	Total 657	C 416	N 128	O 112	S 1	0	0

- Molecule 6 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	C	112	Total 862	C 545	N 169	O 148	0	0
6	G	113	Total 871	C 550	N 170	O 151	0	0

- Molecule 7 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	95	Total 746	C 468	N 136	O 140	S 2	0	0
7	H	95	Total 746	C 468	N 136	O 140	S 2	0	0

- Molecule 8 is a DNA chain called DNA (147-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	147	Total	C	N	O	P	0	0
			3034	1435	572	880	147		

- Molecule 9 is a DNA chain called DNA (147-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	147	Total	C	N	O	P	0	0
			2990	1422	540	882	146		



Tyr	Tyr	His	Pro	Pro	Asn	Leu	Leu	Leu	Glu	Gly	Phe	Thr	Leu	Leu	Pro	Leu	Leu	Asp	Leu	Glu	Asp	Leu	Ile	Ile	Phe	Lys	Ser	Lys	Arg	Tyr	His	Lys	Arg	Ser	Ser	Ala	Ala	Val	Trp	Asn	Ser	Ser	Pro	Pro	Leu	Gly	Gly	Ala	Arg	Val	Pro	Ser	Ser	Lys	Lys	His
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- Molecule 3: Inner centromere protein

Chain Q: 95%

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

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THR	THR	TYR	GLN	MET	THR	PRO	GLN	HIS	ARG	ALA	PRO	PRO	LYS	ILE	ASN	ASP	ASN	TYR	GLY	MET	ASP	LEU	ASN	SER	ASP	SER	THR	ASP	ASP	GLU	ALA	HIS	PRO	PRO	ARG	LYS	ILE	PRO	PRO	THR	TRP	ALA	ARG	GLY	THR	PRO	LEU	SER	GLN	ALA	ILE	ILE	HIS	GLN	TYR	TYR	HIS
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PRO	PRO	ASN	ASN	LEU	LEU	GLU	GLU	PHE	GLY	THR	LEU	LEU	PRO	PRO	ASP	ASP	GLU	GLU	ASP	ILE	PHE	LYS	LYS	SER	SER	LYS	PRO	PRO	ARG	ARG	TYR	HIS	HIS	LYS	ARG	THR	THR	SER	SER	ALA	ALA	TRP	ASN	PRO	SER	PRO	PRO	PRO	LEU	GLN	GLY	ALA	ALA	ARG	VAL	VAL	SER	SER	LEU	TYR	LEU	LEU	LYS	LYS	HIS
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- Molecule 4: Histone H3.2

- Molecule 4: Histone H3.2

- Molecule 5: Histone H4

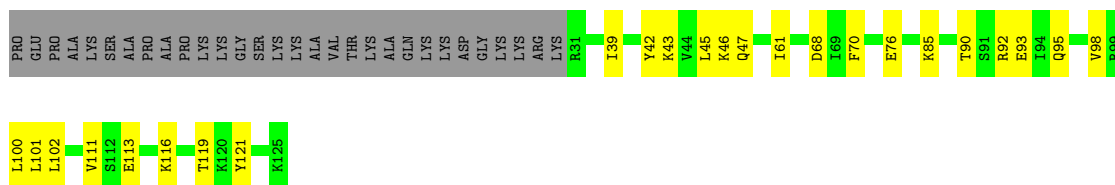
- Molecule 5: Histone H4

- Molecule 6: Histone H2A type 1

- Molecule 6: Histone H2A type 1

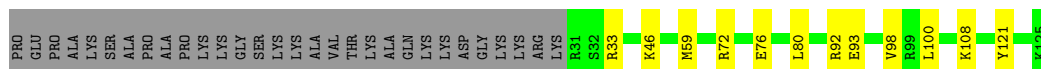
- Molecule 7: Histone H2B type 1-J

Chain D:  57% 19% 24%



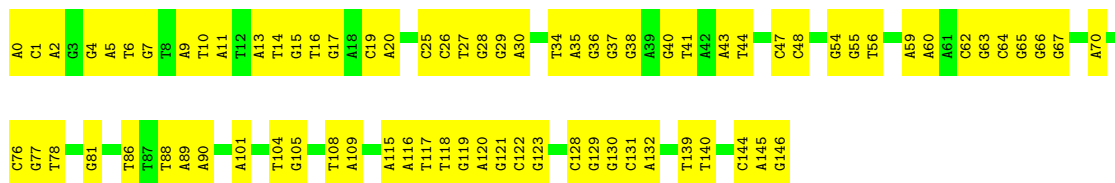
• Molecule 7: Histone H2B type 1-J

Chain H:  66% 10% 24%



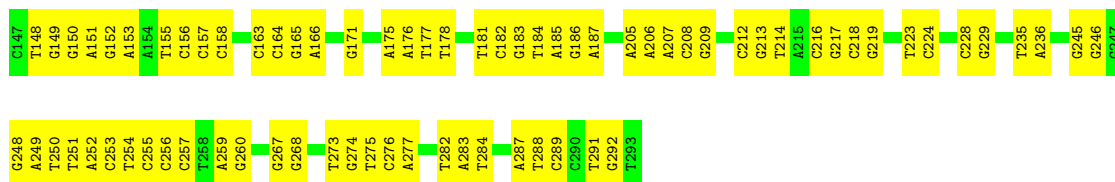
• Molecule 8: DNA (147-MER)

Chain I:  47% 53%



• Molecule 9: DNA (147-MER)

Chain J:  50% 50%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75653	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.025	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.001	Depositor
Map size (Å)	279.168, 279.168, 279.168	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	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	L	0.10	0/641	0.28	0/857
1	O	0.13	0/641	0.38	0/857
2	M	0.11	0/1147	0.30	0/1542
2	P	0.14	0/1147	0.44	0/1542
3	N	0.11	0/352	0.33	0/474
3	Q	0.13	0/352	0.40	0/474
4	A	0.18	0/823	0.38	0/1104
4	E	0.19	0/843	0.35	0/1130
5	B	0.18	0/655	0.41	0/878
5	F	0.17	0/664	0.39	0/889
6	C	0.18	0/872	0.36	0/1174
6	G	0.17	0/881	0.37	0/1186
7	D	0.19	0/757	0.43	0/1015
7	H	0.17	0/757	0.37	0/1015
8	I	0.21	0/3408	0.39	0/5263
9	J	0.20	0/3349	0.36	0/5162
All	All	0.18	0/17289	0.37	0/24562

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	L	633	0	663	6	0
1	O	633	0	663	12	0
2	M	1118	0	1091	23	0
2	P	1118	0	1091	26	0
3	N	346	0	334	6	0
3	Q	346	0	334	7	0
4	A	811	0	853	15	0
4	E	831	0	878	17	0
5	B	648	0	693	19	0
5	F	657	0	706	21	0
6	C	862	0	935	19	0
6	G	871	0	941	18	0
7	D	746	0	771	20	0
7	H	746	0	771	11	0
8	I	3034	0	1649	68	0
9	J	2990	0	1652	55	0
All	All	16390	0	14025	299	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 10.

The worst 5 of 299 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)
4:A:112:ILE:HD13	6:G:114:VAL:HG11	1.67	0.76
6:G:79:ILE:HD12	6:G:81:ARG:H	1.56	0.71
6:C:65:LEU:HB3	6:C:86:ALA:HB1	1.73	0.70
6:G:118:LYS:HD3	6:G:120:THR:H	1.60	0.67
1:L:68:MET:HE1	1:L:73:TYR:HB2	1.77	0.67

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	L	73/280 (26%)	71 (97%)	2 (3%)	0	100	100
1	O	73/280 (26%)	71 (97%)	2 (3%)	0	100	100
2	M	135/142 (95%)	132 (98%)	3 (2%)	0	100	100
2	P	135/142 (95%)	130 (96%)	5 (4%)	0	100	100
3	N	40/918 (4%)	38 (95%)	2 (5%)	0	100	100
3	Q	40/918 (4%)	37 (92%)	3 (8%)	0	100	100
4	A	96/135 (71%)	94 (98%)	2 (2%)	0	100	100
4	E	99/135 (73%)	98 (99%)	1 (1%)	0	100	100
5	B	79/102 (78%)	77 (98%)	2 (2%)	0	100	100
5	F	80/102 (78%)	77 (96%)	3 (4%)	0	100	100
6	C	110/129 (85%)	108 (98%)	2 (2%)	0	100	100
6	G	111/129 (86%)	106 (96%)	5 (4%)	0	100	100
7	D	93/125 (74%)	88 (95%)	5 (5%)	0	100	100
7	H	93/125 (74%)	91 (98%)	2 (2%)	0	100	100
All	All	1257/3662 (34%)	1218 (97%)	39 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	L	69/242 (28%)	68 (99%)	1 (1%)	62	75
1	O	69/242 (28%)	68 (99%)	1 (1%)	62	75
2	M	120/123 (98%)	117 (98%)	3 (2%)	42	62
2	P	120/123 (98%)	117 (98%)	3 (2%)	42	62
3	N	39/817 (5%)	38 (97%)	1 (3%)	41	61
3	Q	39/817 (5%)	38 (97%)	1 (3%)	41	61
4	A	86/110 (78%)	83 (96%)	3 (4%)	31	54

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Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	88/110 (80%)	85 (97%)	3 (3%)	32	55
5	B	67/78 (86%)	64 (96%)	3 (4%)	23	47
5	F	68/78 (87%)	66 (97%)	2 (3%)	37	58
6	C	87/98 (89%)	84 (97%)	3 (3%)	32	55
6	G	88/98 (90%)	83 (94%)	5 (6%)	17	43
7	D	81/104 (78%)	78 (96%)	3 (4%)	29	53
7	H	81/104 (78%)	80 (99%)	1 (1%)	67	77
All	All	1102/3144 (35%)	1069 (97%)	33 (3%)	37	58

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	21	LEU
2	P	58	PHE
3	Q	38	GLN
6	C	101	THR
6	C	64	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	P	17	HIS
2	P	80	HIS
3	Q	38	GLN
3	Q	25	ASN
4	E	85	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.

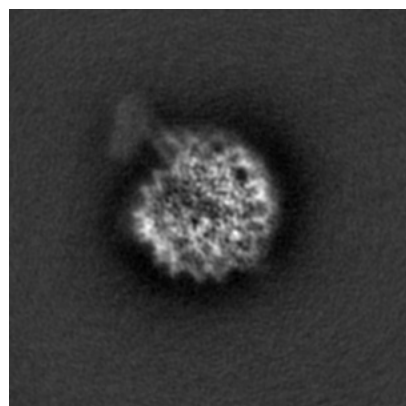
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55003. These allow visual inspection of the internal detail of the map and identification of artifacts.

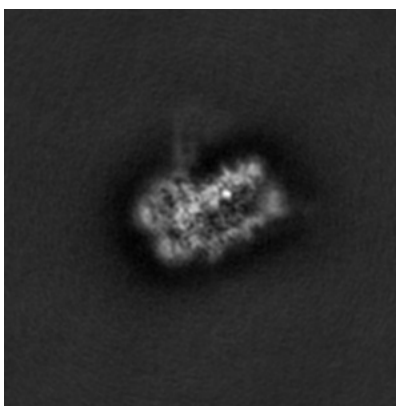
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

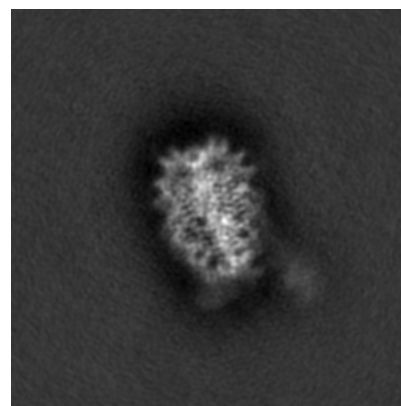
6.1.1 Primary map



X

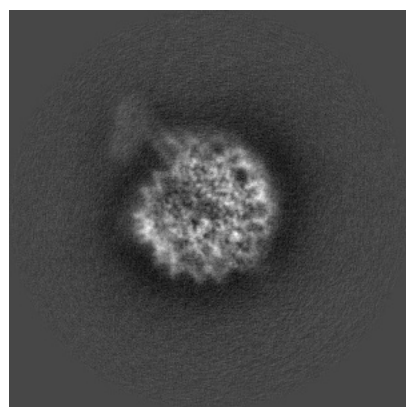


Y

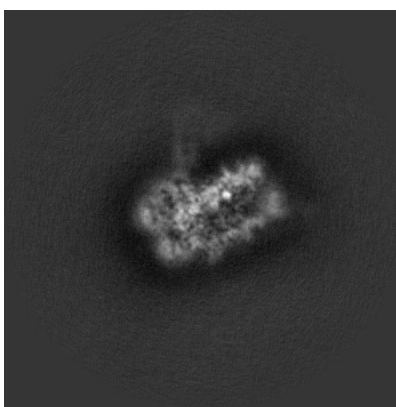


Z

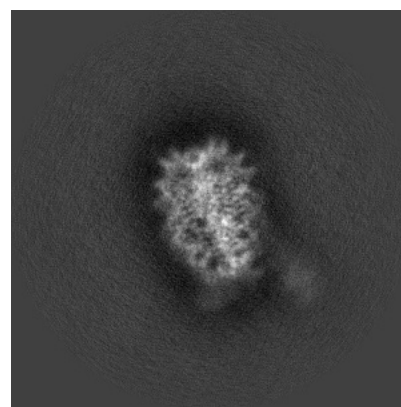
6.1.2 Raw map



X



Y

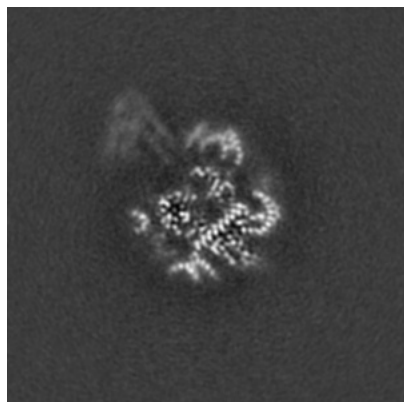


Z

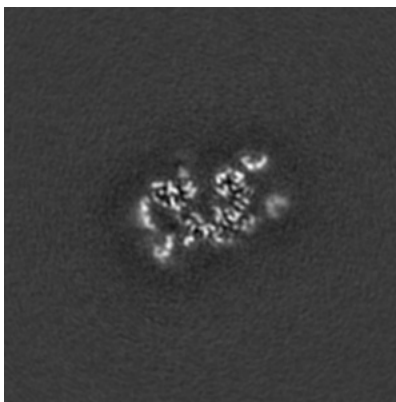
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

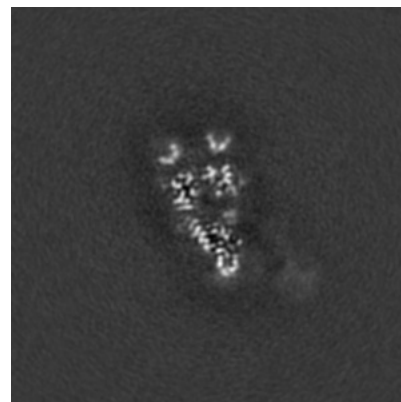
6.2.1 Primary map



X Index: 192

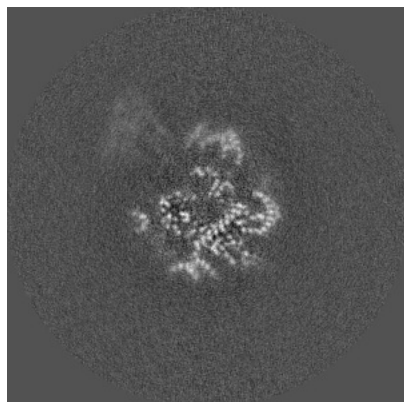


Y Index: 192

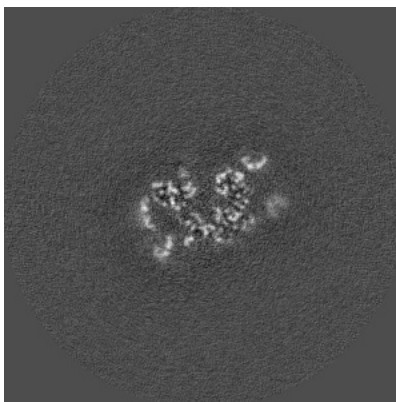


Z Index: 192

6.2.2 Raw map



X Index: 192



Y Index: 192

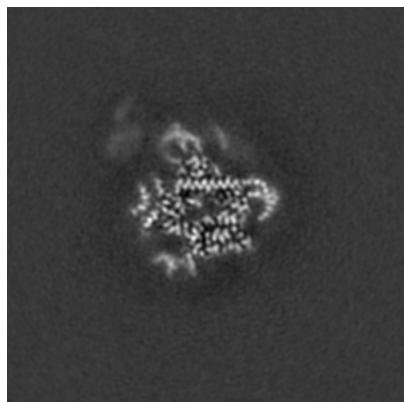


Z Index: 192

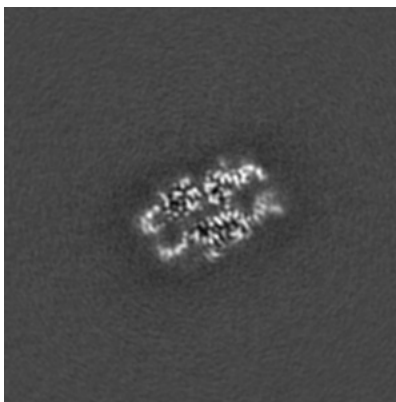
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

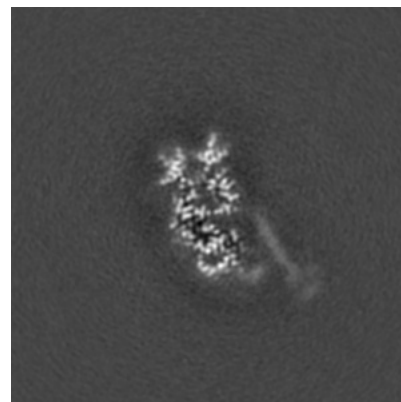
6.3.1 Primary map



X Index: 205

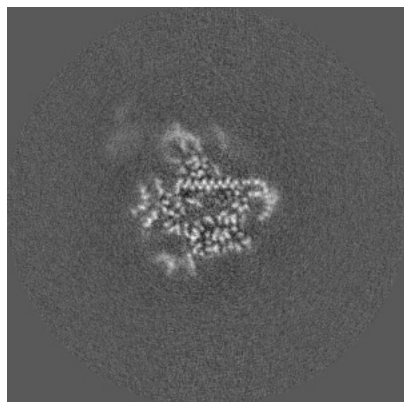


Y Index: 210

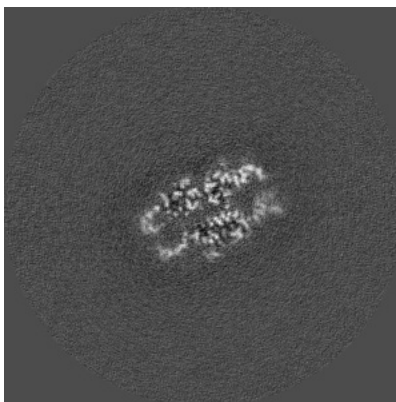


Z Index: 181

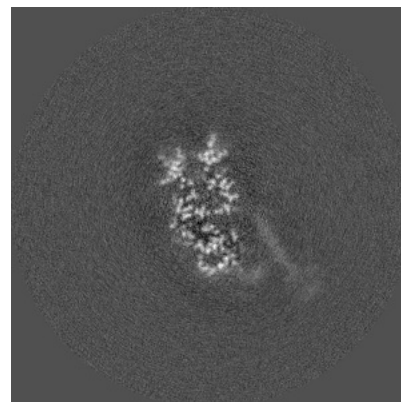
6.3.2 Raw map



X Index: 205



Y Index: 210

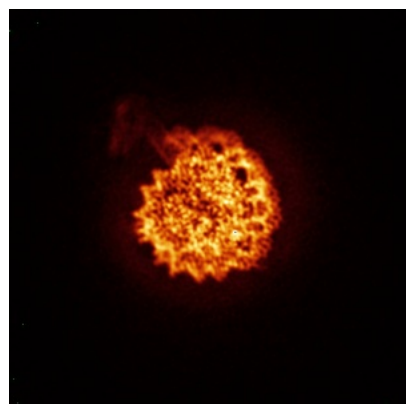


Z Index: 181

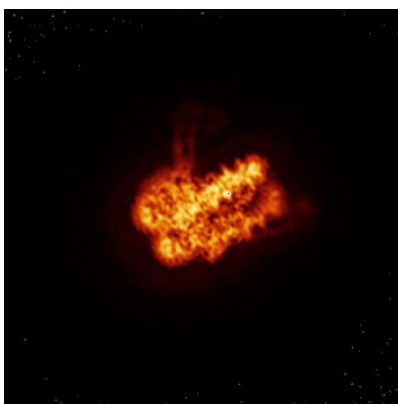
The images above show the largest variance slices of the map in three orthogonal directions.

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

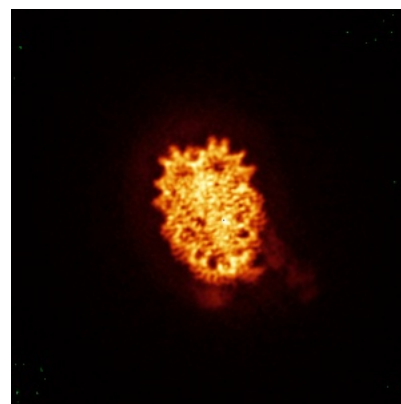
6.4.1 Primary map



X

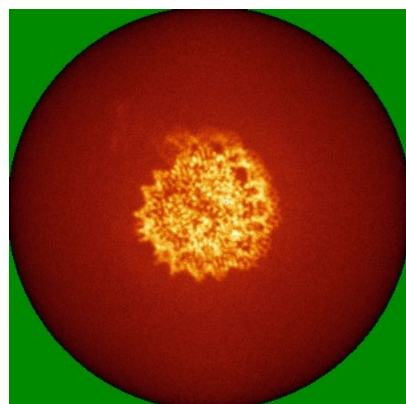


Y

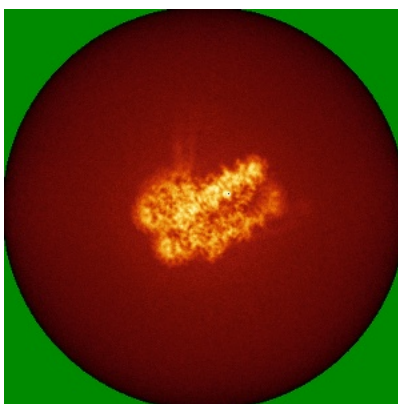


Z

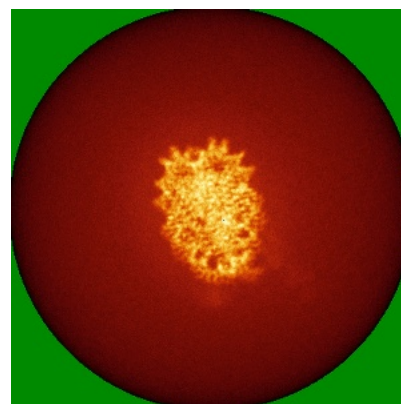
6.4.2 Raw map



X



Y

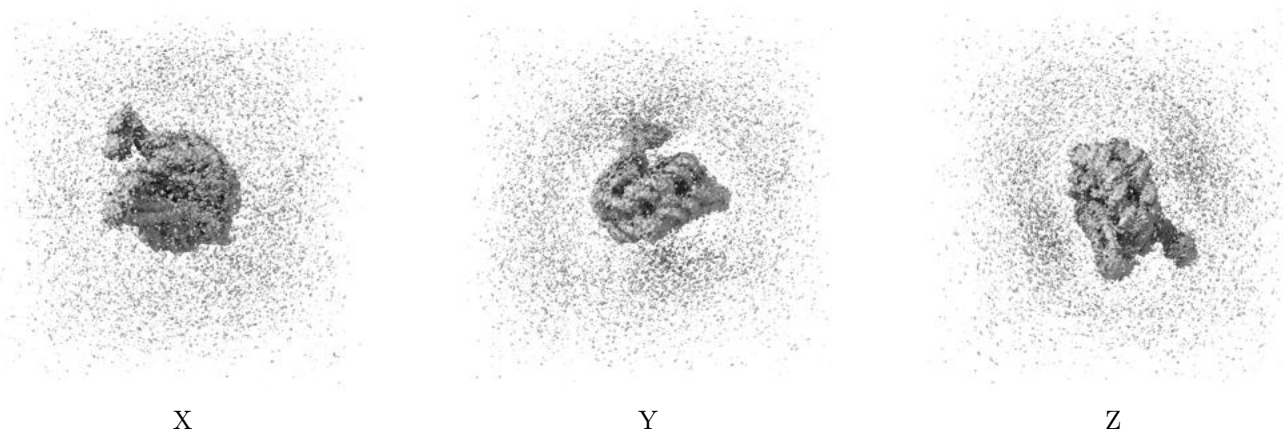


Z

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.

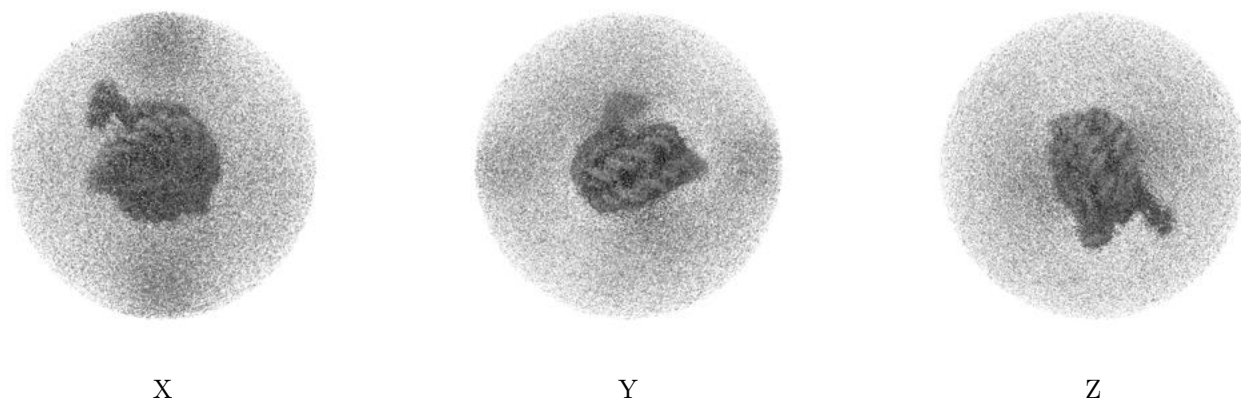
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.001. 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.

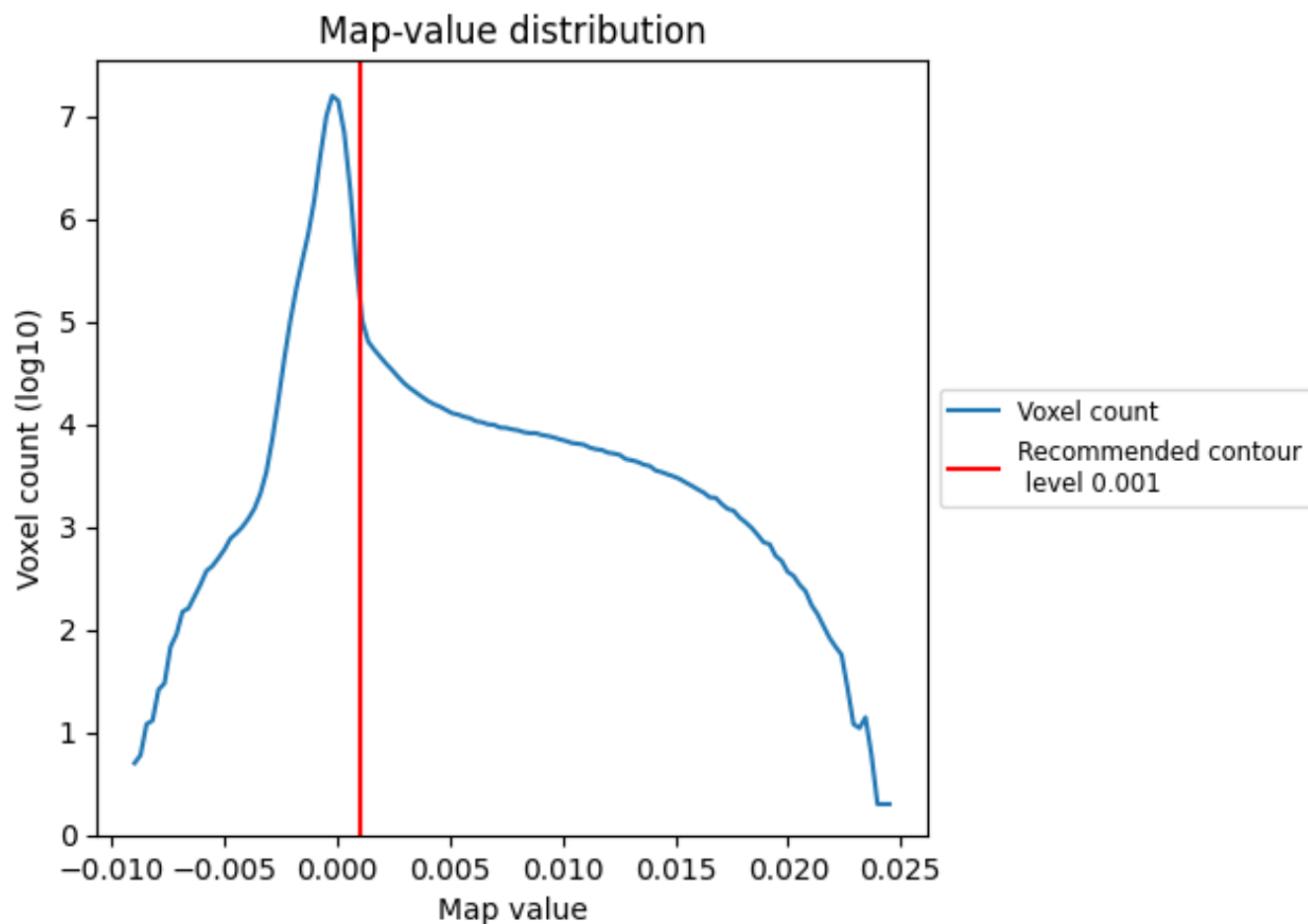
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

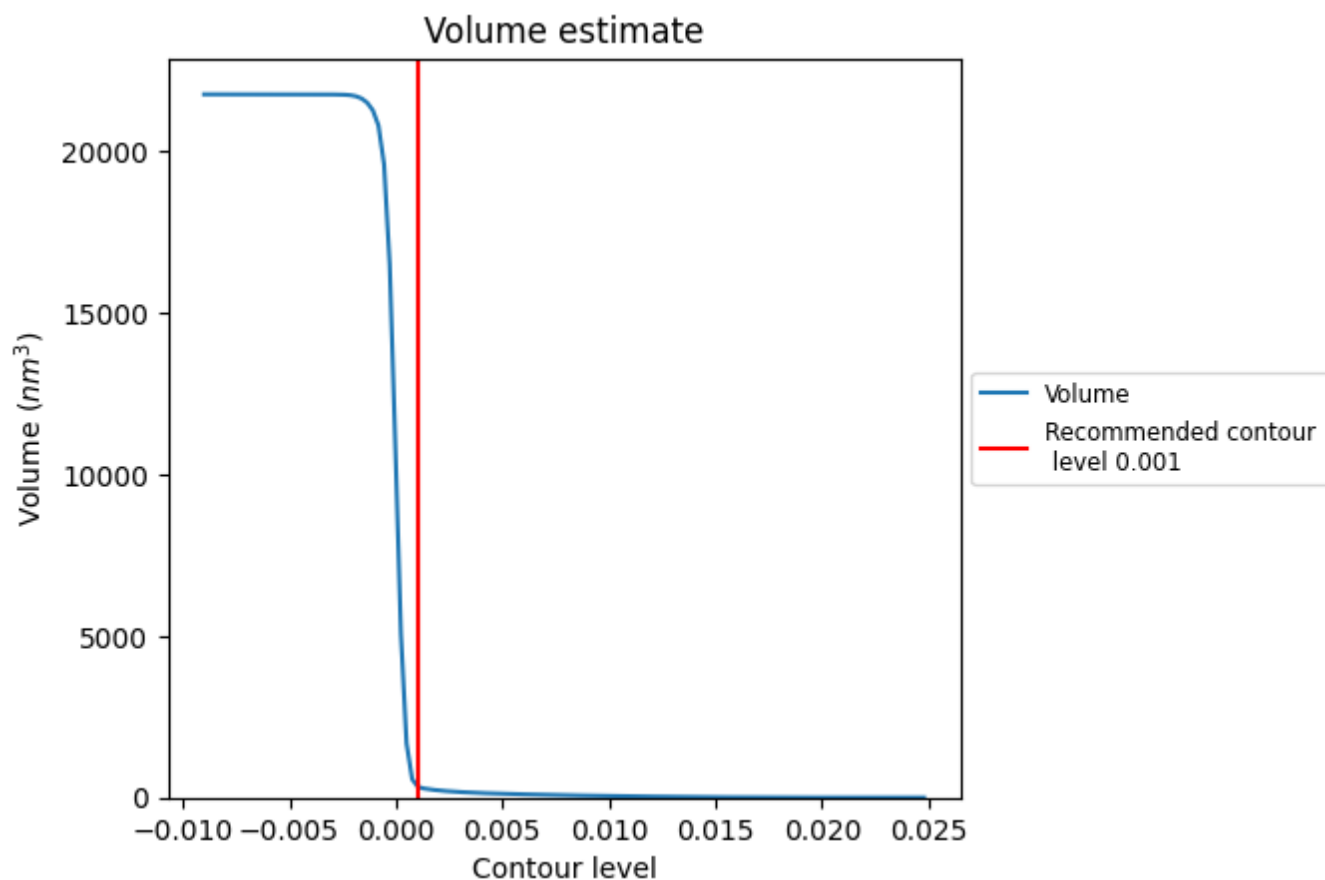
This section contains the results of statistical analysis of the map.

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.

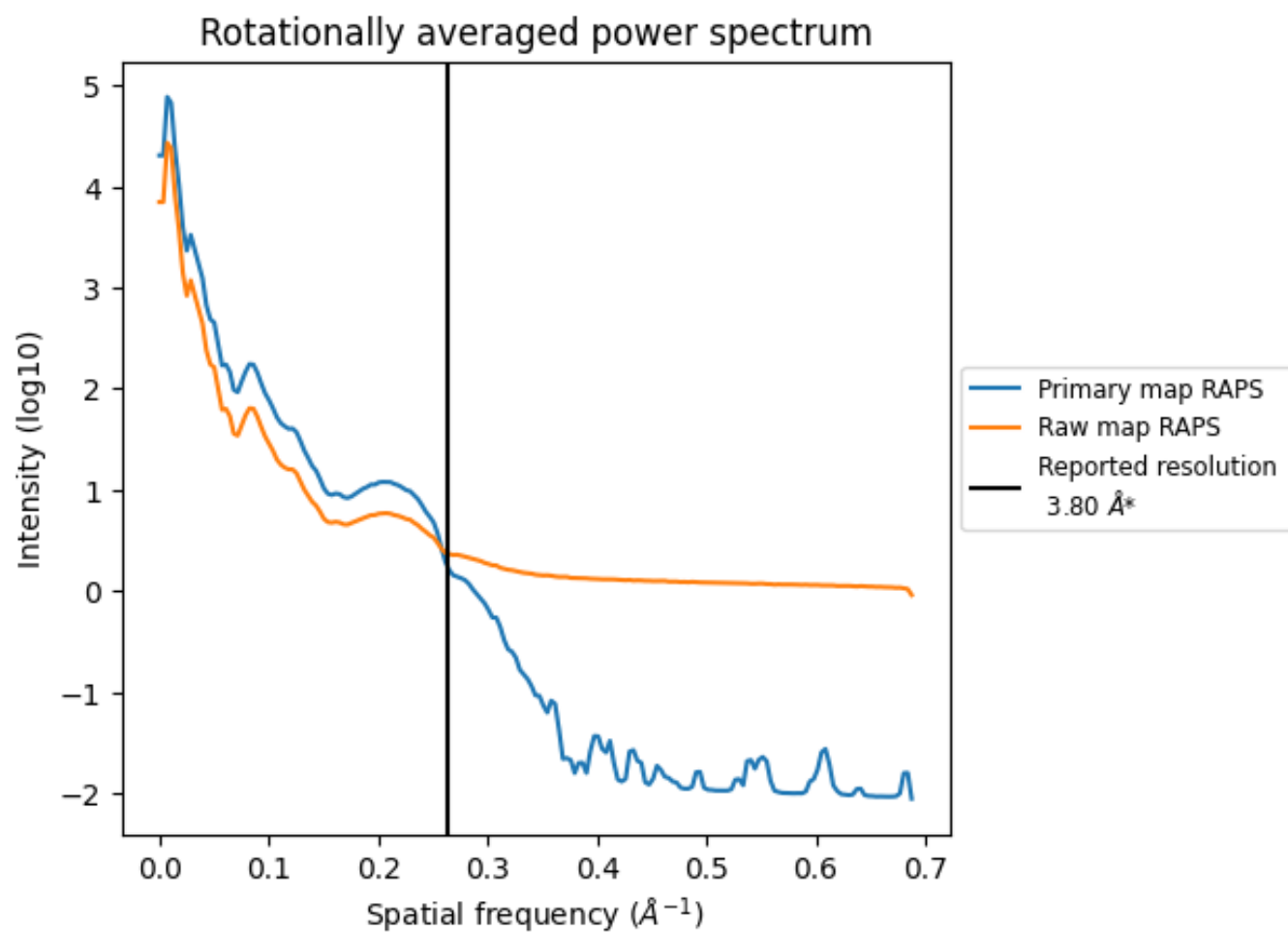
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 359 nm^3 ; this corresponds to an approximate mass of 324 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 ⓘ

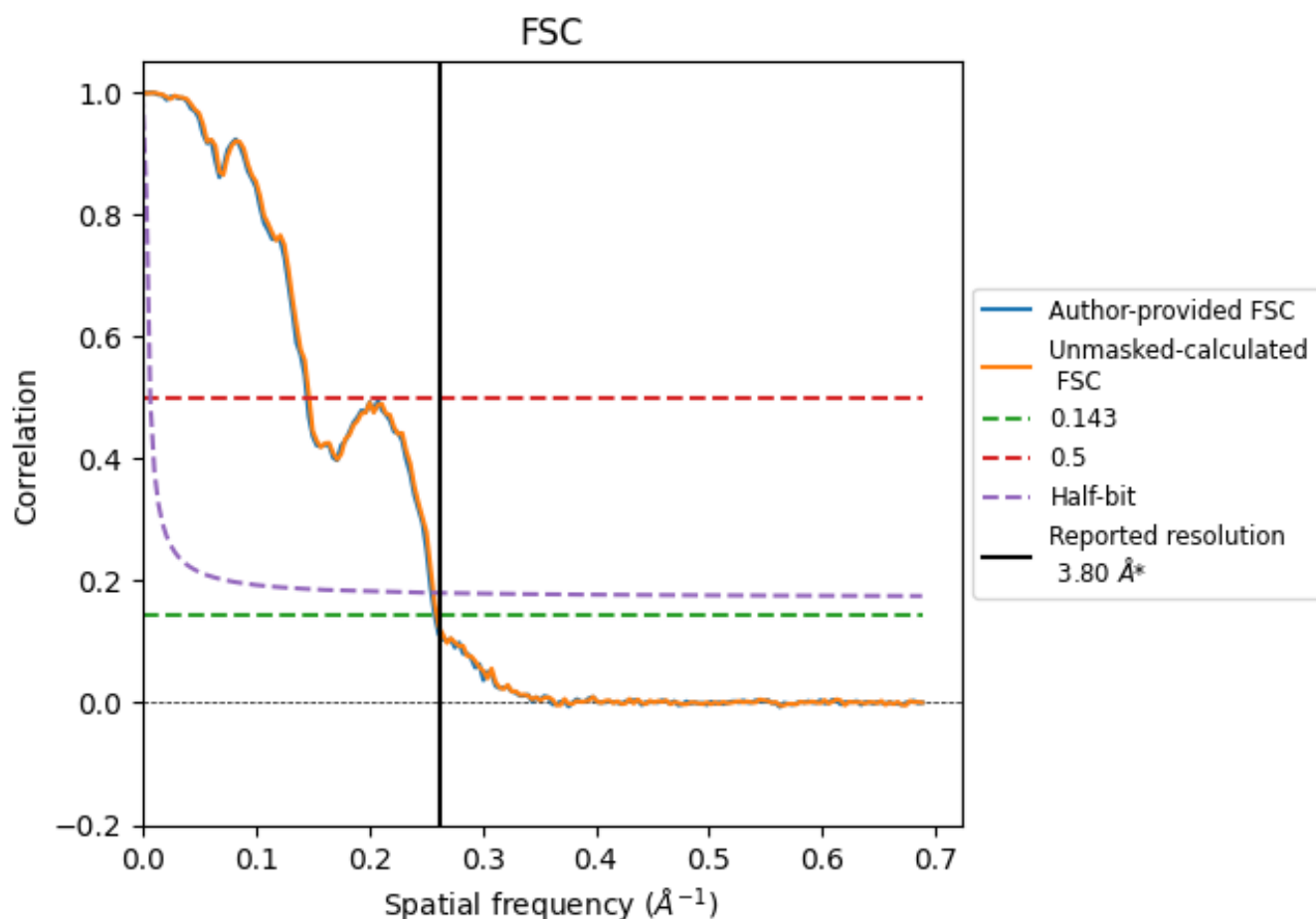


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.88	6.89	3.92
Unmasked-calculated*	3.85	6.79	3.89

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

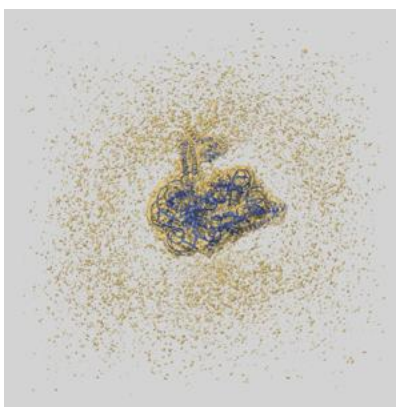
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55003 and PDB model 9SLJ. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



X



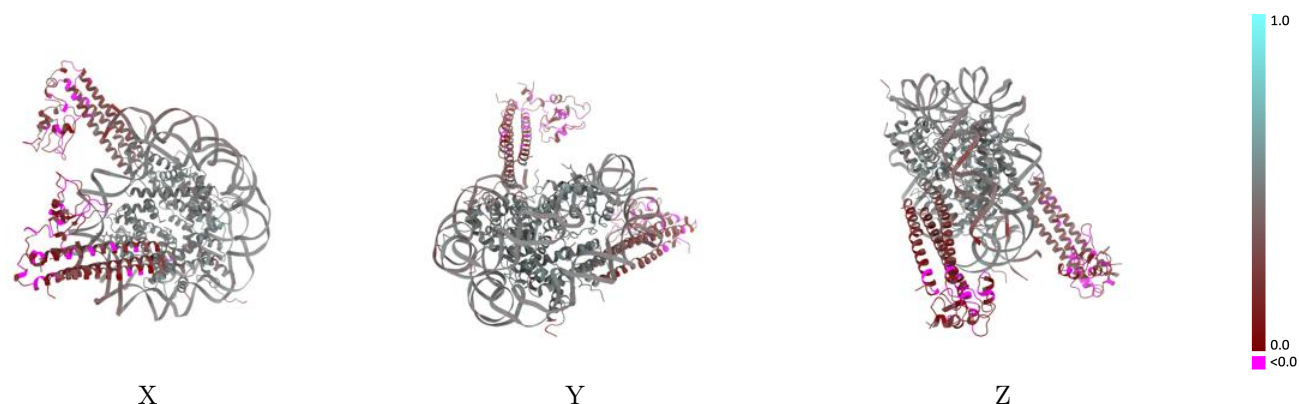
Y



Z

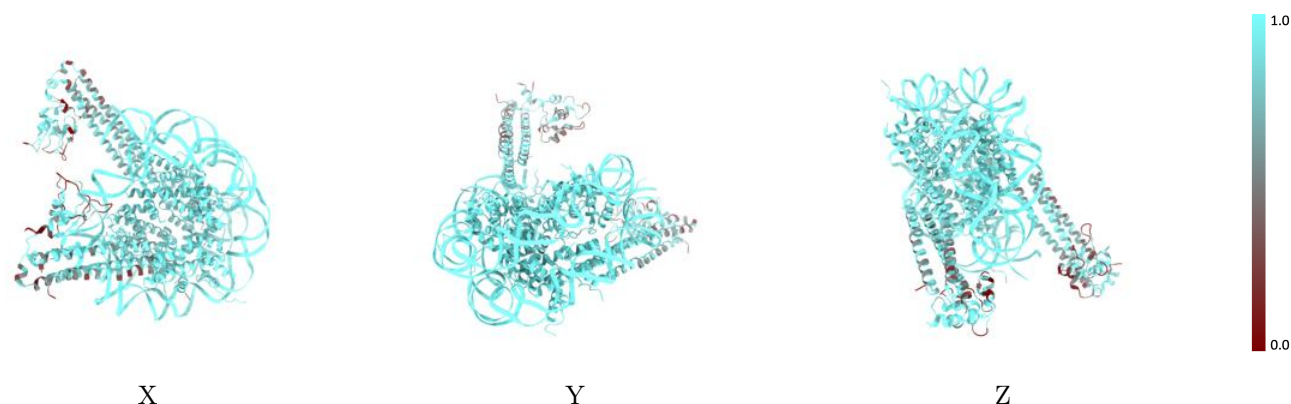
The images above show the 3D surface view of the map at the recommended contour level 0.001 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



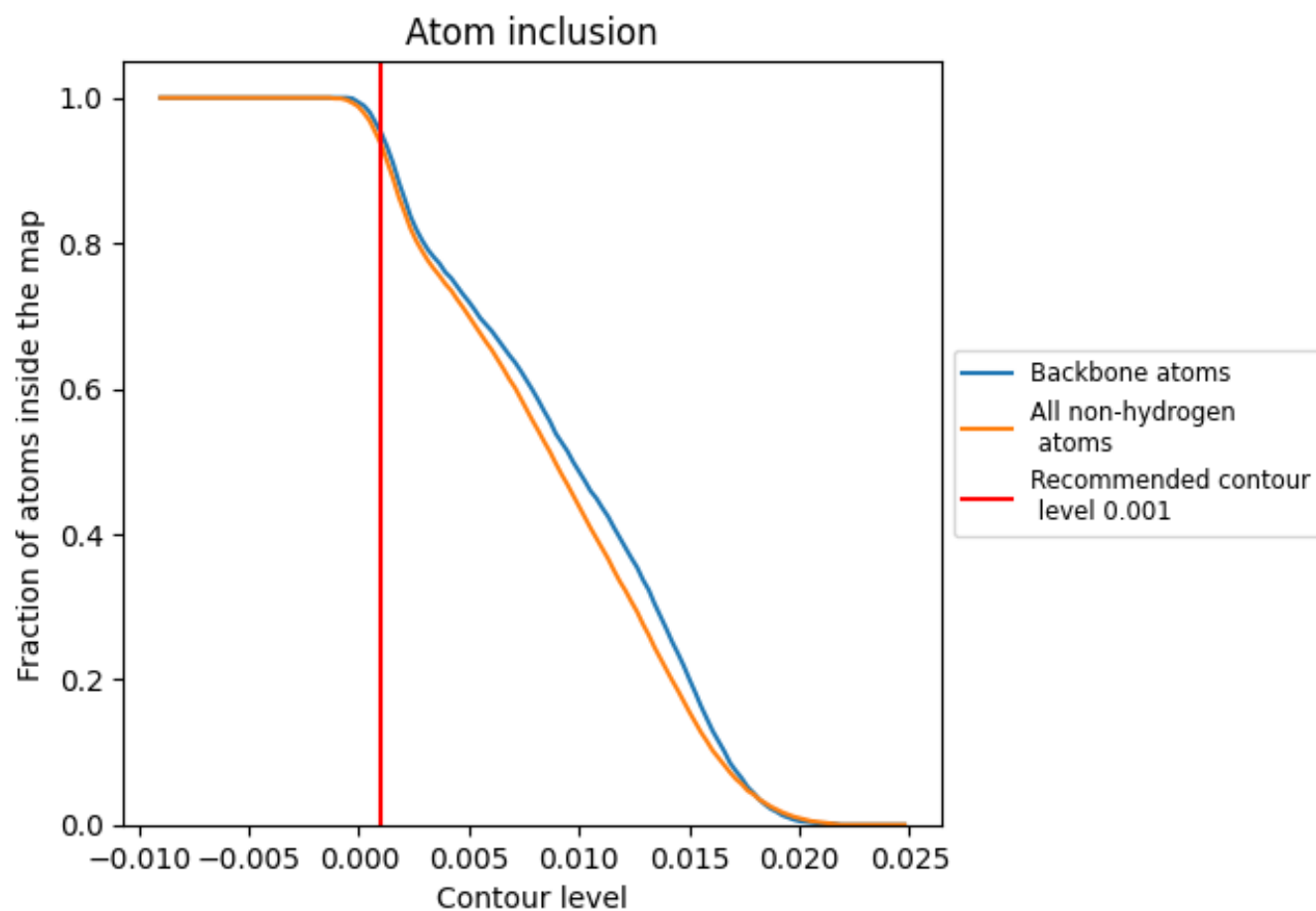
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.001).



































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (0.001) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9360	 0.3970
A	 0.9960	 0.5020
B	 1.0000	 0.5050
C	 0.9920	 0.4920
D	 0.9970	 0.4880
E	 0.9840	 0.4910
F	 0.9940	 0.5000
G	 0.9930	 0.5010
H	 0.9970	 0.4900
I	 0.9980	 0.4550
J	 1.0000	 0.4570
L	 0.8080	 0.2230
M	 0.6650	 0.1200
N	 0.6880	 0.1790
O	 0.8460	 0.2610
P	 0.7880	 0.1320
Q	 0.8050	 0.1550

