wwPDB EM Validation Summary Report (i)

Aug 9, 2026 – 02:15 PM JST

PDB ID	:	9LWI / pdb_00009lwi
EMDB ID	:	EMD-63446
Title	:	The head region of HBx-Smc5/6 ubiquitination complex
Authors	:	Tong, C.; Lili, D.; Hongshuai, L.; Jinhong, Z.; Qian, X.; Lanfeng, W.
Deposited on	:	2025-02-15
Resolution	:	3.12 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:

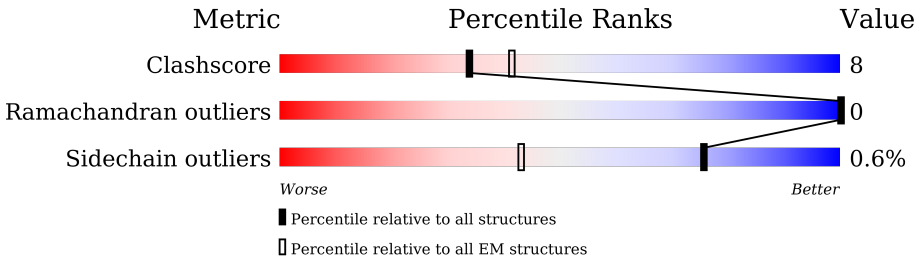
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

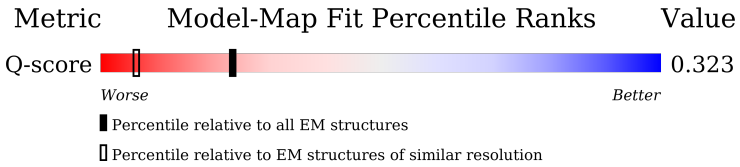
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.12 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.





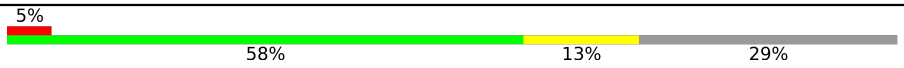
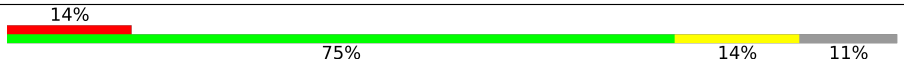
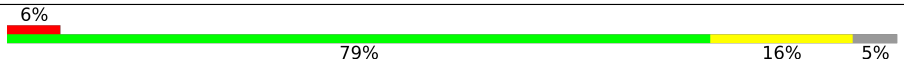
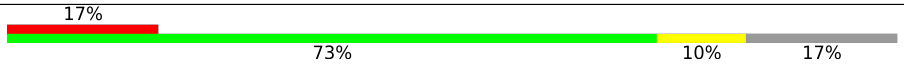
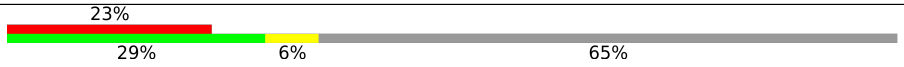
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14478 (2.62 - 3.62)

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	1091	31% 64%
2	B	1140	80% 19%
3	C	154	52% 14% 33%
4	D	333	26% 59% 8% 32%

Continued on next page...

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Mol	Chain	Length	Quality of chain
5	E	304	
6	F	266	
7	G	760	
8	H	108	
9	I	1101	

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 28124 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 Structural maintenance of chromosomes protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	392	3137	1971	557	586	23	0	0

- Molecule 2 is a protein called DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1140	8918	5642	1503	1724	49	0	0

- Molecule 3 is a protein called Protein X.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	103	793	504	143	139	7	0	0

- Molecule 4 is a protein called EP300-interacting inhibitor of differentiation 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	225	1840	1176	307	348	9	0	0

- Molecule 5 is a protein called Non-structural maintenance of chromosomes element 3 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	215	1787	1154	306	322	5	0	0

- Molecule 6 is a protein called Non-structural maintenance of chromosomes element 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	237	1928	1220	333	361	14	0	0

- Molecule 7 is a protein called Cullin-4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	719	Total	C	N	O	S	0	0
			5898	3753	1023	1088	34		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	760	GLY	-	expression tag	UNP Q13619

- Molecule 8 is a protein called E3 ubiquitin-protein ligase RBX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	90	Total	C	N	O	S	0	0
			746	472	137	128	9		

- Molecule 9 is a protein called Structural maintenance of chromosomes protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	381	Total	C	N	O	S	0	0
			3071	1945	523	581	22		

- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	C	1	Total	Zn	0
			1	1	
10	F	2	Total	Zn	0
			2	2	
10	H	3	Total	Zn	0
			3	3	

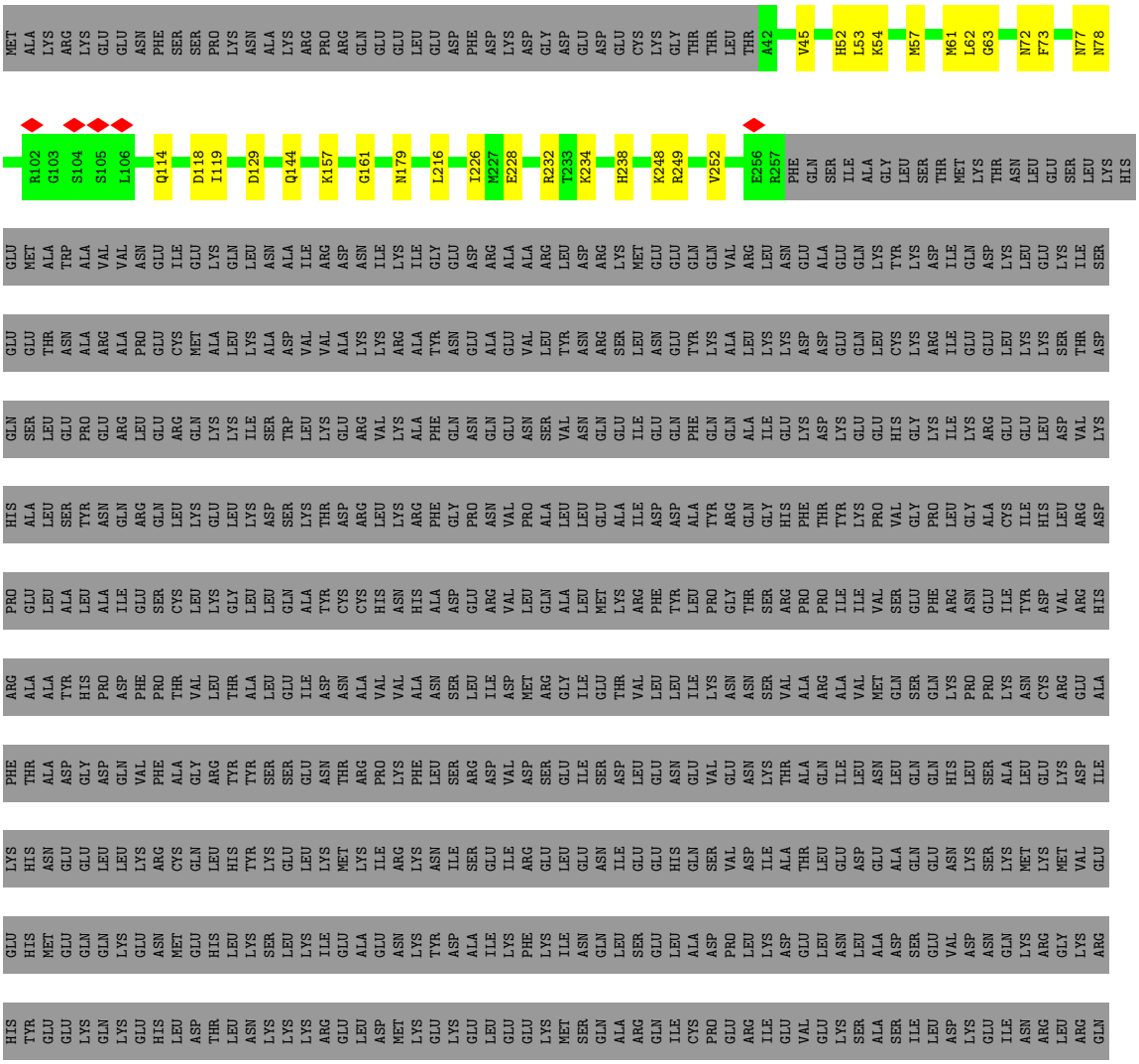
3 Residue-property plots (i)

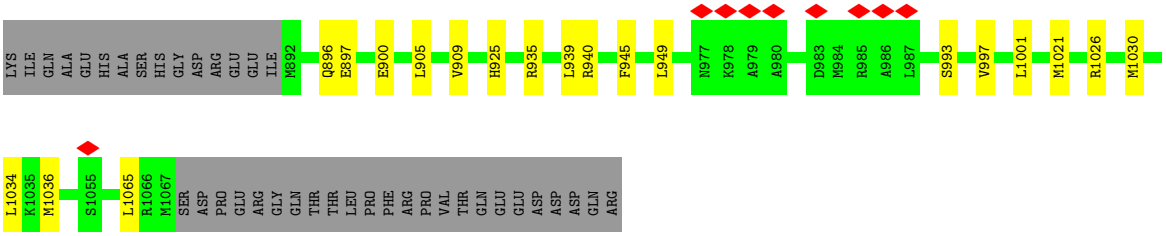
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Structural maintenance of chromosomes protein 6

Chain A:





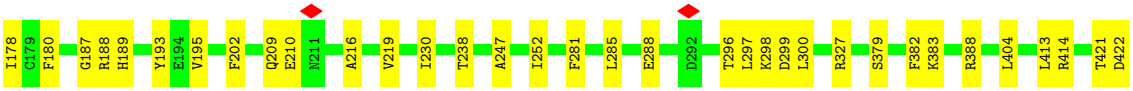


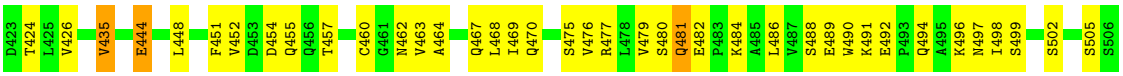
• Molecule 2: DNA damage-binding protein 1

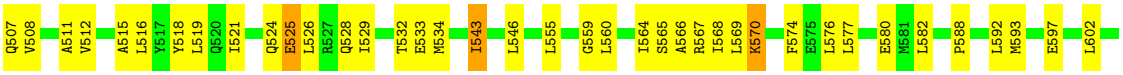
Chain B:

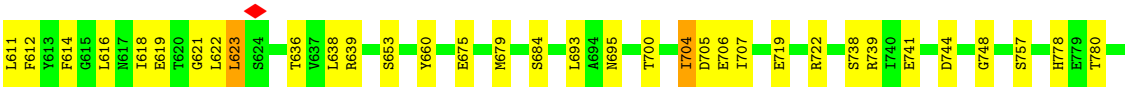




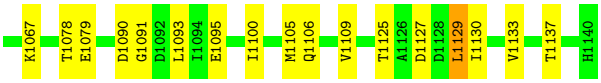








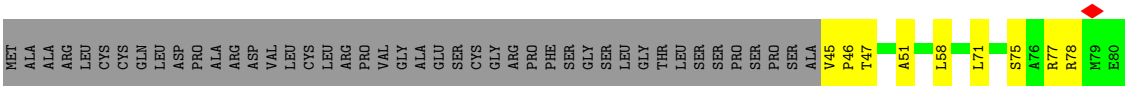


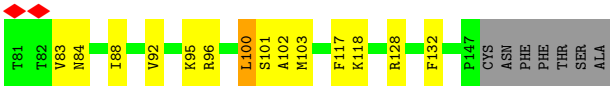


• Molecule 3: Protein X

Chain C:



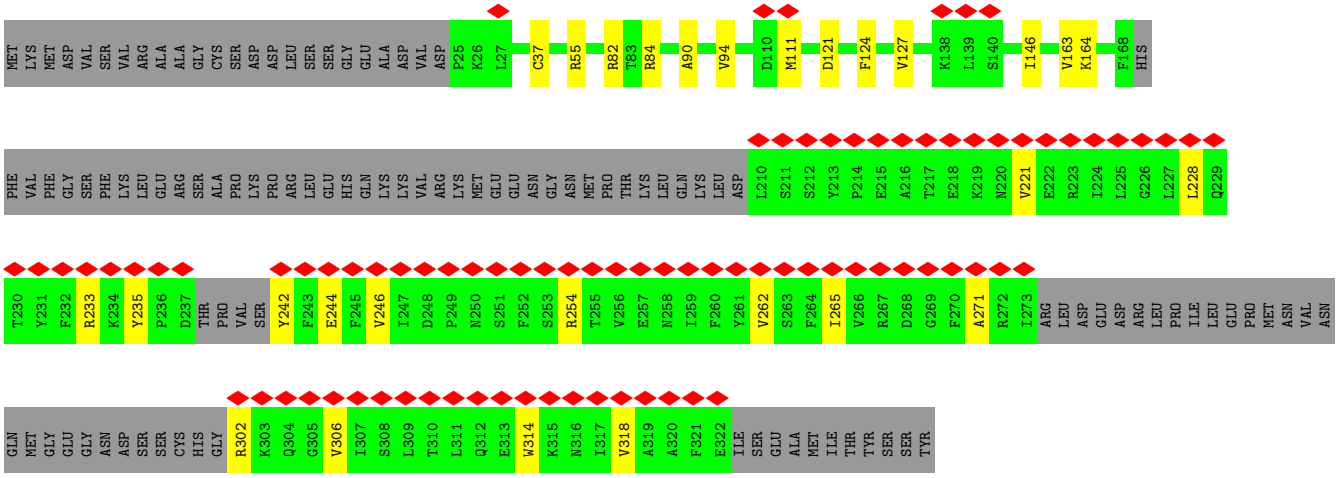




• Molecule 4: EP300-interacting inhibitor of differentiation 3

Chain D:

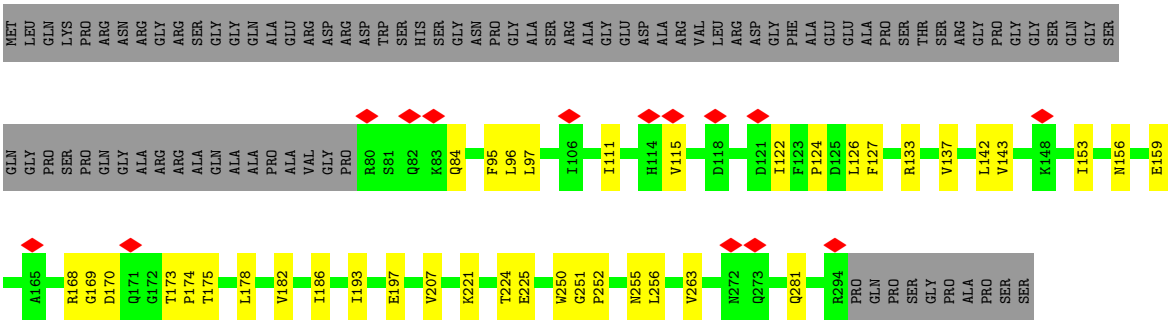




• Molecule 5: Non-structural maintenance of chromosomes element 3 homolog

Chain E:

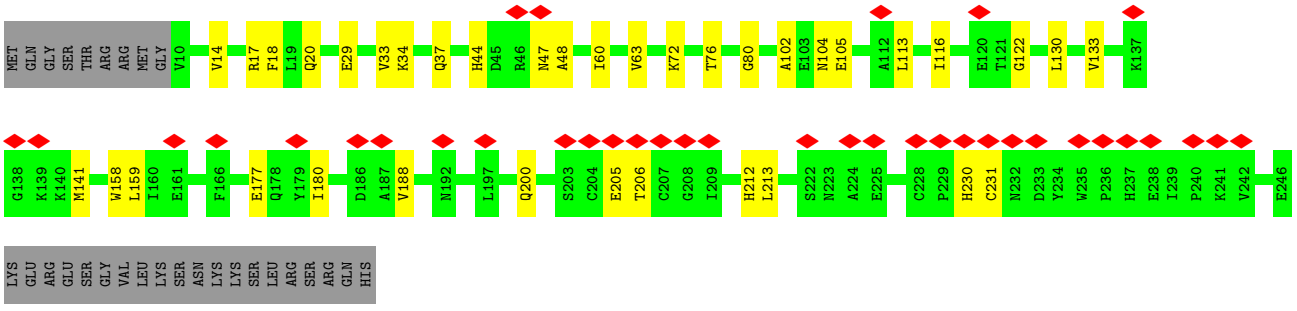




• Molecule 6: Non-structural maintenance of chromosomes element 1 homolog

Chain F:

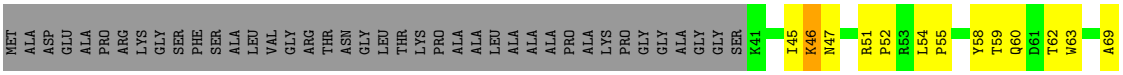


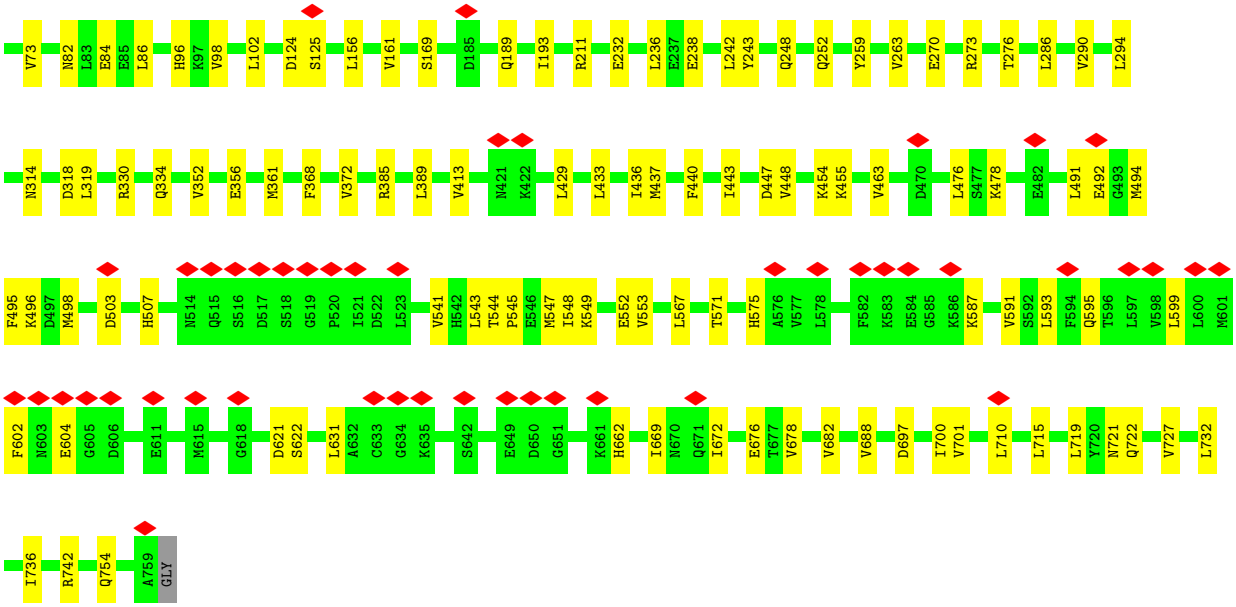


• Molecule 7: Cullin-4A

Chain G:







• Molecule 8: E3 ubiquitin-protein ligase RBX1

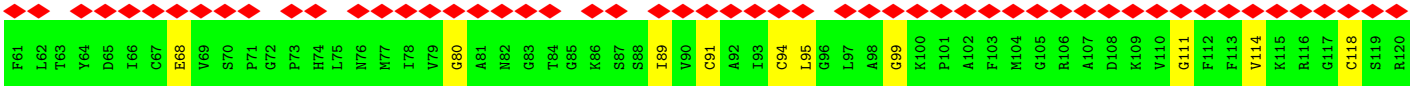


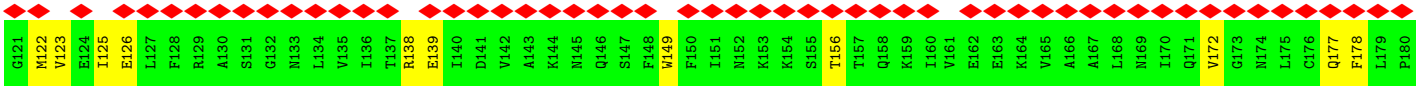


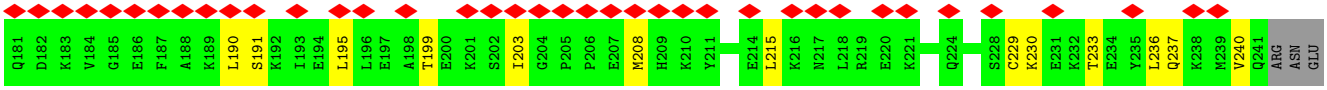
• Molecule 9: Structural maintenance of chromosomes protein 5

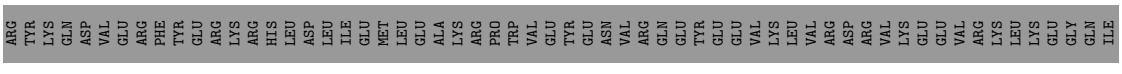


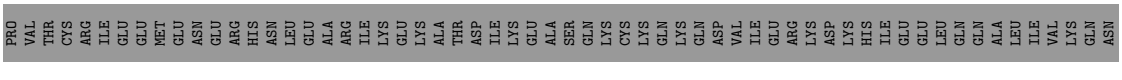




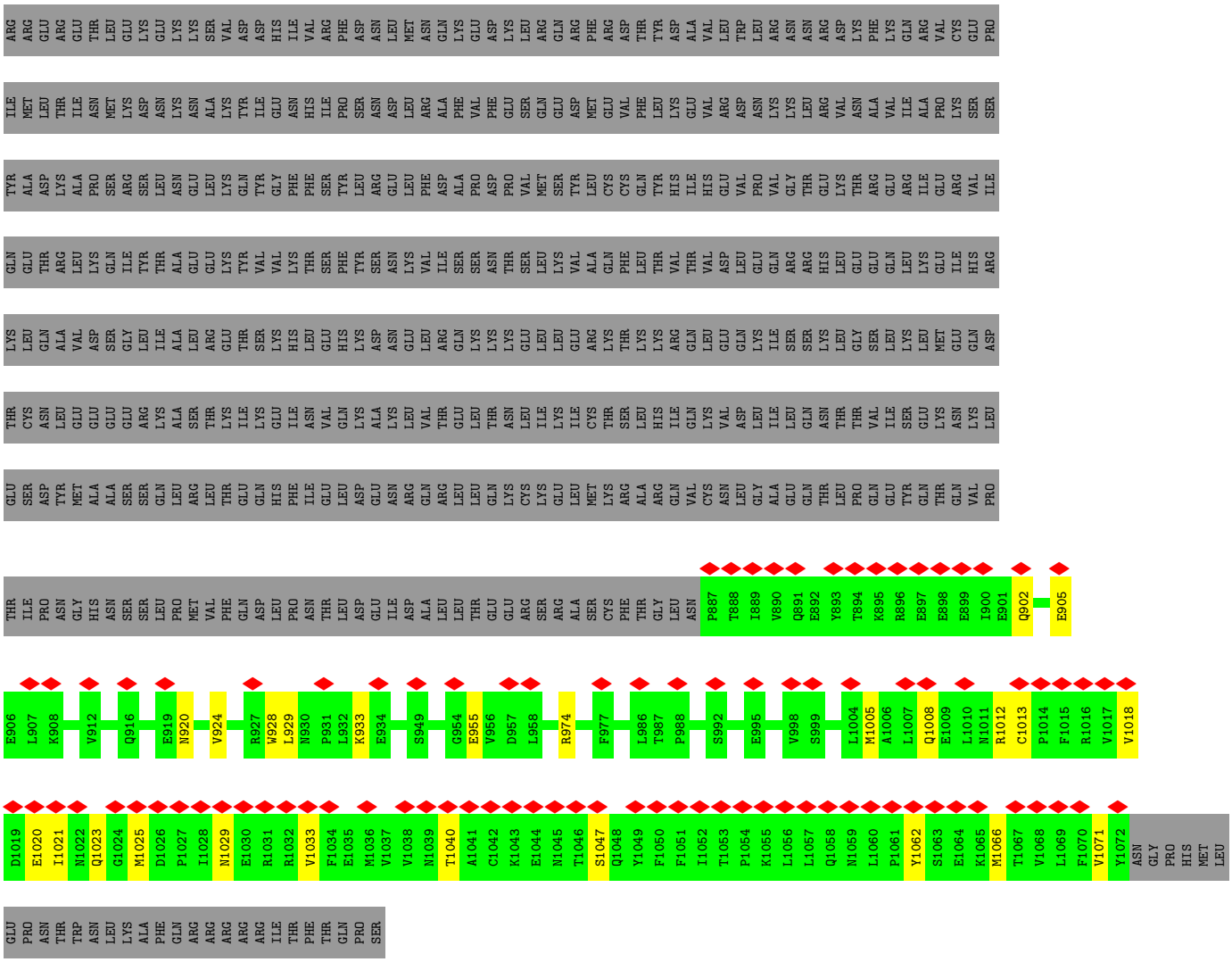











ARG ARG GLU ARG GLU THR LEU GLU LYS GLU LYS LYS SER VAL ASP ASP HIS ILE VAL ARG PHE ASP ASN LEU MET ASN GLN LYS GLU ASP LYS LEU ARG GLN ARG PHE ARG ASP THR TYR ASP ALA VAL LEU TRP LEU ARG ASN ASN ARG ASP LYS PHE LYS GLN ARG VAL CYS GLU PRO
ILE MET LEU THR ILE ASN MET LYS ASP ASN LYS ASN ALA LYS TYR ILE GLU ASN HIS ILE PRO SER ASN ASP LEU ARG ALA PHE VAL PHE GLU SER GLN GLU ASP MET GLU VAL PHE LEU LYS GLU VAL ARG ASP ASN LYS LYS LEU ARG VAL ASN ALA VAL ILE ALA PRO LYS SER SER
TYR ALA ASP LYS ALA PRO SER ARG SER LEU ASN GLU LEU LYS GLN TYR GLY PHE PHE SER TYR LEU ARG GLU LEU PHE ASP ALA PRO ASP PRO VAL MET SER TYR LEU CYS CYS GLN TYR HIS ILE HIS GLU VAL PRO VAL GLY THR GLU LYS THR ARG GLU GLN GLN LEU LYS GLU ARG ILE GLU ARG VAL ILE
GLN GLU THR ARG LEU LYS GLN ILE TYR THR ALA ALA GLU GLU LYS TYR VAL VAL LYS THR SER PHE TYR SER ASN LYS VAL ILE SER SER ASN THR SER LEU LYS VAL ALA GLN PHE LEU THR VAL THR VAL ASP LEU GLU GLN ARG ARG HIS LEU GLU GLN GLN LEU LYS GLU ILE HIS ARG
LYS LEU GLN ALA VAL ASP SER GLY LEU ILE ALA ALA LEU ARG GLU THR SER LYS HIS LEU GLU HIS LYS ASP ASN GLU LEU ARG GLN LYS LYS LYS GLU LEU LEU GLU ARG LYS THR LYS LYS ARG GLN LEU LEU GLU GLN ILE SER SER LYS LEU MET GLU GLN ASP
THR CYS ASN LEU GLU GLU GLU ARG LYS ALA SER THR LYS ILE LYS GLU ILE ASN VAL GLN LYS ALA ALA LYS LEU VAL THR GLU LEU THR ASN LEU GLU ILE LYS ILE CYS THR SER LEU HIS ILE GLN LYS VAL ASP LEU ILE LEU GLN GLN ASN THR THR VAL ILE SER GLU LYS ASN LYS LEU
GLU SER ASP TYR MET ALA ALA SER SER GLN LEU ARG LEU THR GLU GLN HIS PHE ILE GLU LEU ASP GLU ASN ARG GLN ARG LEU LEU GLN LYS CYS LYS GLU LEU MET LYS ARG ALA ARG GLN VAL CYS ASN LEU GLY ALA GLU GLN THR LEU PRO GLN GLU TYR GLN THR GLN VAL PRO
THR ILE PRO ASN GLY HIS ASN SER SER LEU PRO MET VAL PHE GLN ASP LEU PRO ASN THR LEU ASP GLU ILE ASP ALA LEU LEU THR GLU GLU ARG SER ARG ALA SER CYS PHE THR GLY LEU ASN P887 T888 I889 V890 Q891 E892 Y893 T894 K895 R896 E897 E898 E899 I900 E901 Q902 E905
E906 L907 K908 V912 Q916 E919 N920 V924 R927 W928 L929 N930 P931 L932 K933 E934 S949 G954 E955 V956 D957 L958 R974 F977 I986 T987 P988 S992 E995 V998 S999 L1004 M1005 A1006 L1007 Q1008 E1009 L1010 N1011 R1012 C1013 P1014 F1015 R1016 V1017 V1018
D1019 E1020 I1021 N1022 Q1023 G1024 M1025 D1026 P1027 I1028 N1029 E1030 R1031 R1032 V1033 F1034 E1035 M1036 V1037 V1038 N1039 T1040 A1041 C1042 K1043 E1044 N1045 T1046 S1047 Q1048 Y1049 F1050 F1051 I1052 T1053 P1054 K1055 L1056 L1057 Q1058 N1059 L1060 P1061 Y1062 S1063 E1064 K1065 M1066 T1067 V1068 L1069 F1070 V1071 Y1072 ASN GLY PRO HIS MET LEU
GLU PRO ASN THR TRP ASN LEU LYS ALA PHE GLN ARG ARG ARG ARG ARG ILE THR PHE THR GLN PRO SER

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	401828	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 ($e^-/Å^2$)	48.5	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	4.126	Depositor
Minimum map value	-2.523	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	477.184, 477.184, 477.184	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.932, 0.932, 0.932	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.47	1/3183 (0.0%)	0.61	2/4258 (0.0%)
2	B	0.55	0/9083	0.77	7/12306 (0.1%)
3	C	0.95	0/811	1.26	4/1097 (0.4%)
4	D	0.29	0/1874	0.41	0/2522
5	E	0.11	0/1827	0.27	0/2465
6	F	0.29	1/1966 (0.1%)	0.34	1/2656 (0.0%)
7	G	0.27	0/6006	0.43	4/8068 (0.0%)
8	H	0.50	0/768	0.64	1/1040 (0.1%)
9	I	0.19	0/3124	0.32	0/4197
All	All	0.43	2/28642 (0.0%)	0.60	19/38609 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	939	LEU	C-O	-5.86	1.16	1.24
6	F	213	LEU	N-CA	5.24	1.51	1.46

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	619	GLU	N-CA-C	-7.89	102.37	110.97
1	A	216	LEU	N-CA-C	-7.51	103.58	112.89
3	C	84	ASN	N-CA-C	-6.76	104.62	112.86
2	B	525	GLU	N-CA-C	6.53	119.12	108.55
3	C	102	ALA	N-CA-C	-6.38	105.07	112.92

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	3137	0	3173	37	0
2	B	8918	0	8879	214	0
3	C	793	0	804	38	0
4	D	1840	0	1801	21	0
5	E	1787	0	1824	26	0
6	F	1928	0	1910	21	0
7	G	5898	0	5977	86	0
8	H	746	0	699	6	0
9	I	3071	0	3092	47	0
10	C	1	0	0	0	0
10	F	2	0	0	0	0
10	H	3	0	0	0	0
All	All	28124	0	28159	459	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 8.

The worst 5 of 459 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:475:SER:HB3	2:B:491:LYS:HG2	1.45	0.98
2:B:705:ASP:O	2:B:706:GLU:HG3	1.64	0.96
1:A:53:LEU:HD22	1:A:62:LEU:HD13	1.48	0.94
2:B:780:THR:HB	2:B:784:GLU:HB3	1.48	0.94
2:B:475:SER:CB	2:B:491:LYS:HG2	1.96	0.94

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	388/1091 (36%)	378 (97%)	10 (3%)	0	100	100
2	B	1138/1140 (100%)	1086 (95%)	52 (5%)	0	100	100
3	C	101/154 (66%)	96 (95%)	5 (5%)	0	100	100
4	D	217/333 (65%)	206 (95%)	11 (5%)	0	100	100
5	E	213/304 (70%)	205 (96%)	8 (4%)	0	100	100
6	F	235/266 (88%)	230 (98%)	5 (2%)	0	100	100
7	G	717/760 (94%)	700 (98%)	17 (2%)	0	100	100
8	H	88/108 (82%)	84 (96%)	4 (4%)	0	100	100
9	I	377/1101 (34%)	371 (98%)	6 (2%)	0	100	100
All	All	3474/5257 (66%)	3356 (97%)	118 (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	A	348/979 (36%)	348 (100%)	0	100	100
2	B	999/999 (100%)	984 (98%)	15 (2%)	57	73
3	C	86/127 (68%)	84 (98%)	2 (2%)	44	68
4	D	200/296 (68%)	200 (100%)	0	100	100
5	E	195/257 (76%)	195 (100%)	0	100	100
6	F	216/242 (89%)	216 (100%)	0	100	100
7	G	656/679 (97%)	654 (100%)	2 (0%)	86	86
8	H	79/90 (88%)	78 (99%)	1 (1%)	61	75
9	I	346/1023 (34%)	346 (100%)	0	100	100
All	All	3125/4692 (67%)	3105 (99%)	20 (1%)	76	81

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

Mol	Chain	Res	Type
2	B	1129	LEU
7	G	54	LEU
8	H	39	VAL
7	G	62	THR
2	B	497	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	852	GLN
3	C	87	GLN
9	I	1059	ASN
2	B	990	GLN
6	F	25	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)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

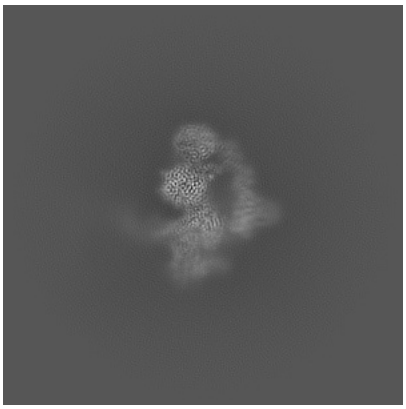
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-63446. These allow visual inspection of the internal detail of the map and identification of artifacts.

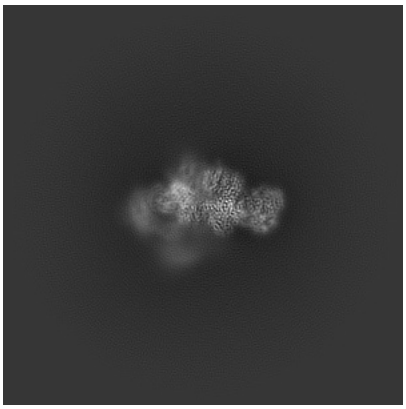
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

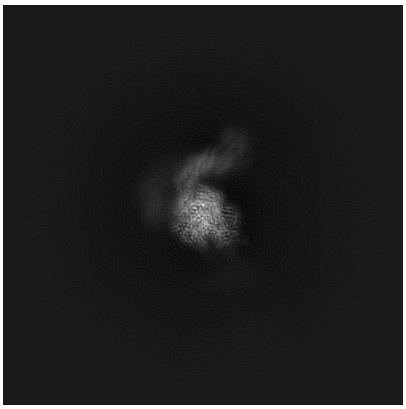
6.1.1 Primary map



X

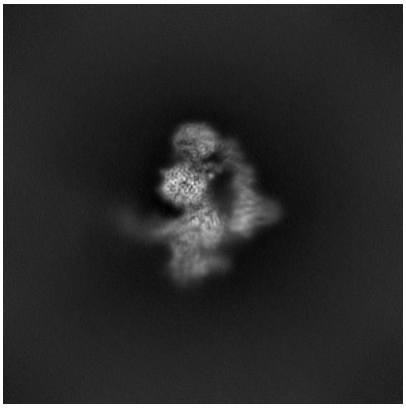


Y

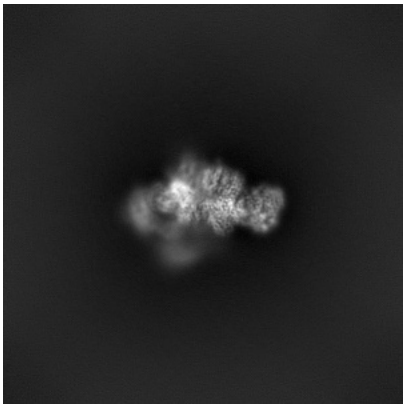


Z

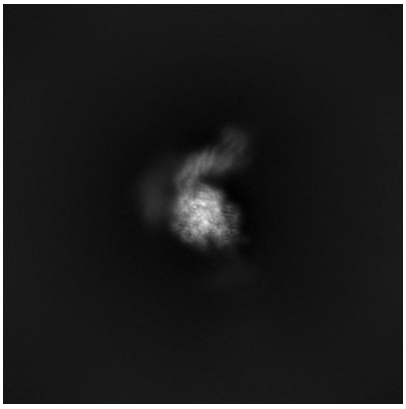
6.1.2 Raw map



X



Y

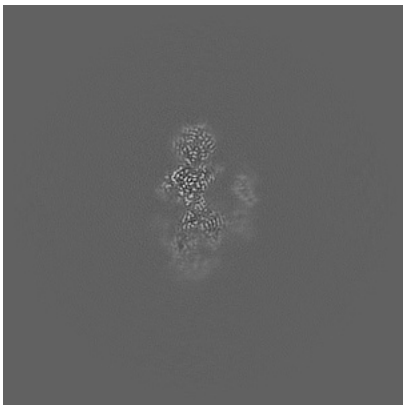


Z

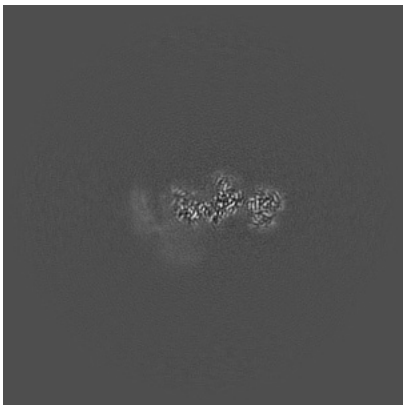
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

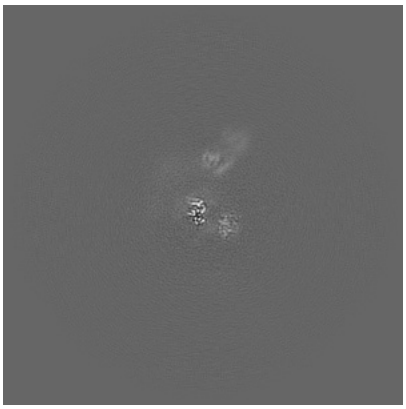
6.2.1 Primary map



X Index: 256

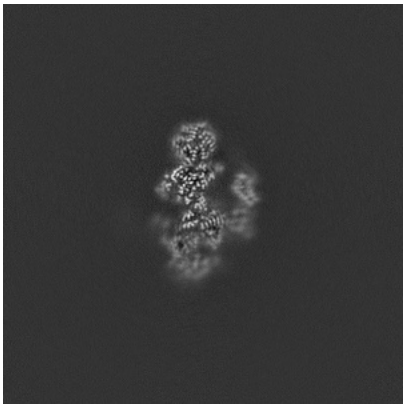


Y Index: 256

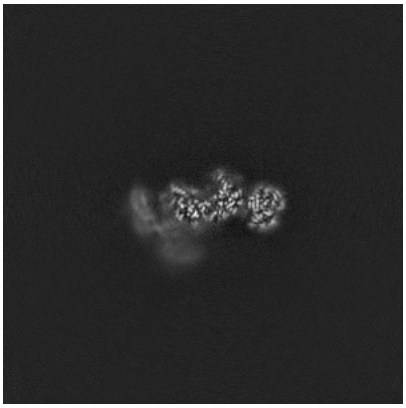


Z Index: 256

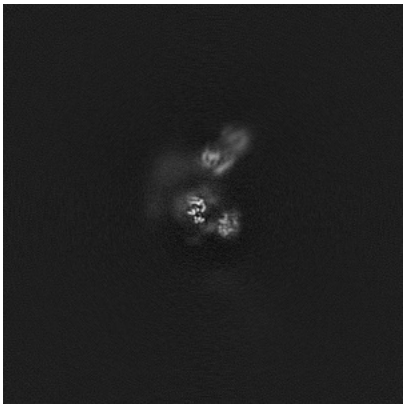
6.2.2 Raw map



X Index: 256



Y Index: 256

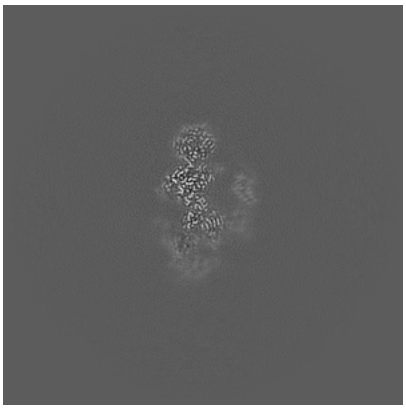


Z Index: 256

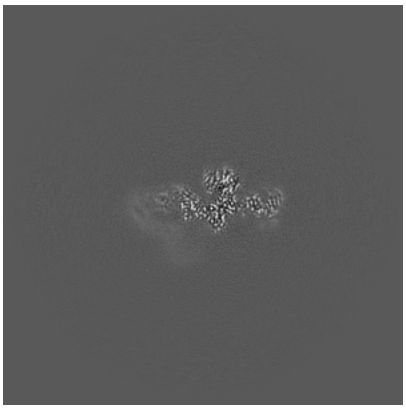
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

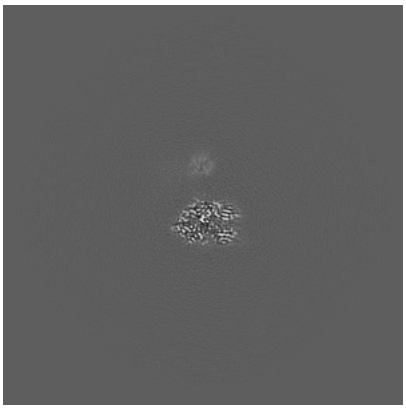
6.3.1 Primary map



X Index: 255

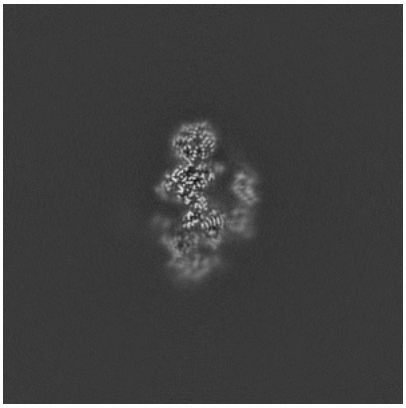


Y Index: 242

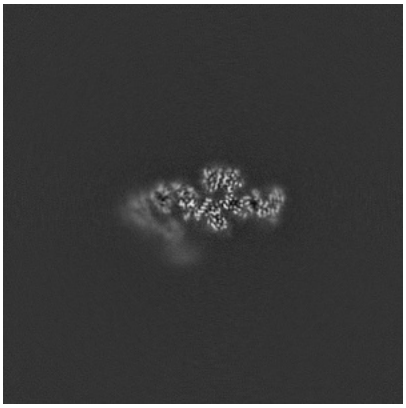


Z Index: 283

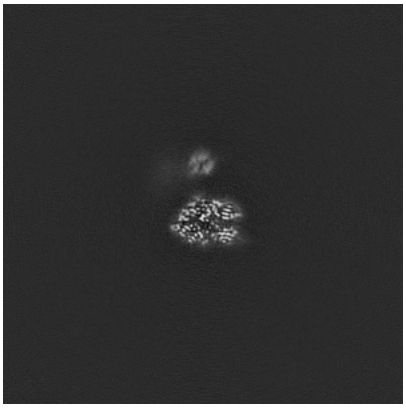
6.3.2 Raw map



X Index: 255



Y Index: 237

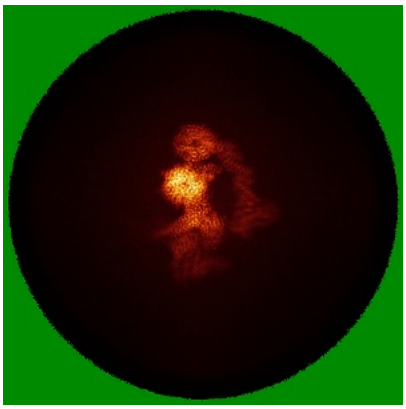


Z Index: 283

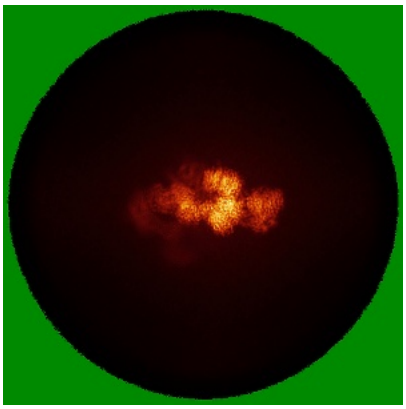
The images above show the largest variance slices of the map in three orthogonal directions.

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

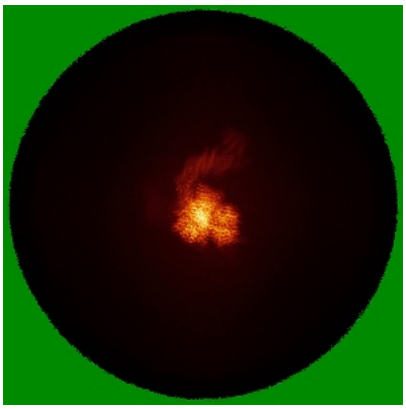
6.4.1 Primary map



X

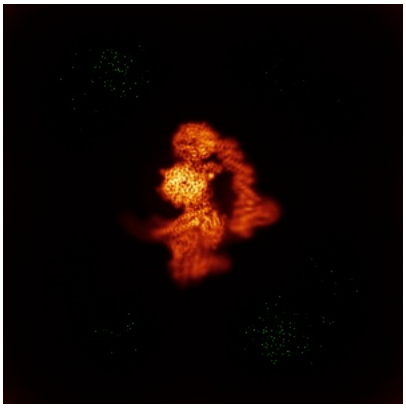


Y

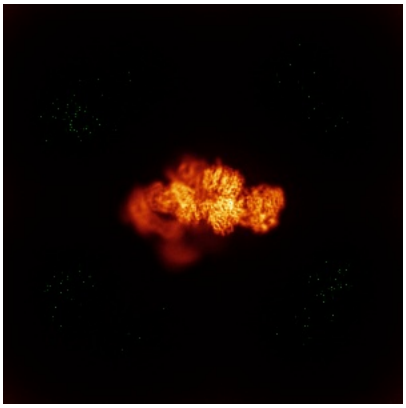


Z

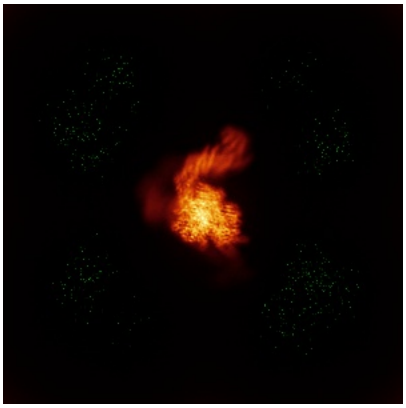
6.4.2 Raw map



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 0.2. 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.

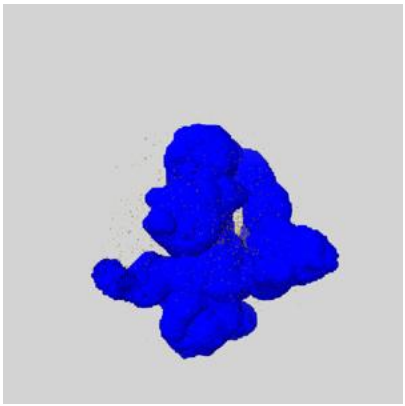
6.6 Mask visualisation (i)

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

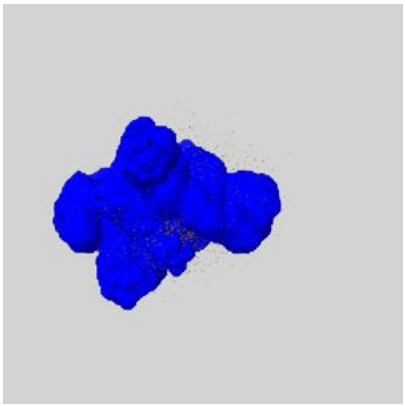
A mask typically either:

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

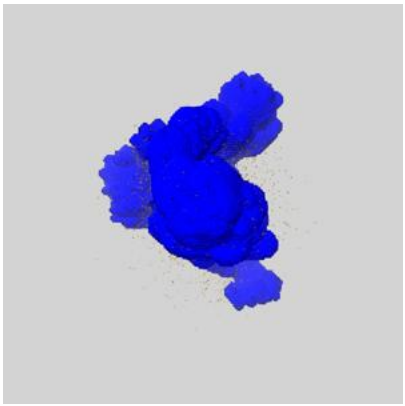
6.6.1 emd_63446_msk_1.map (i)



X



Y

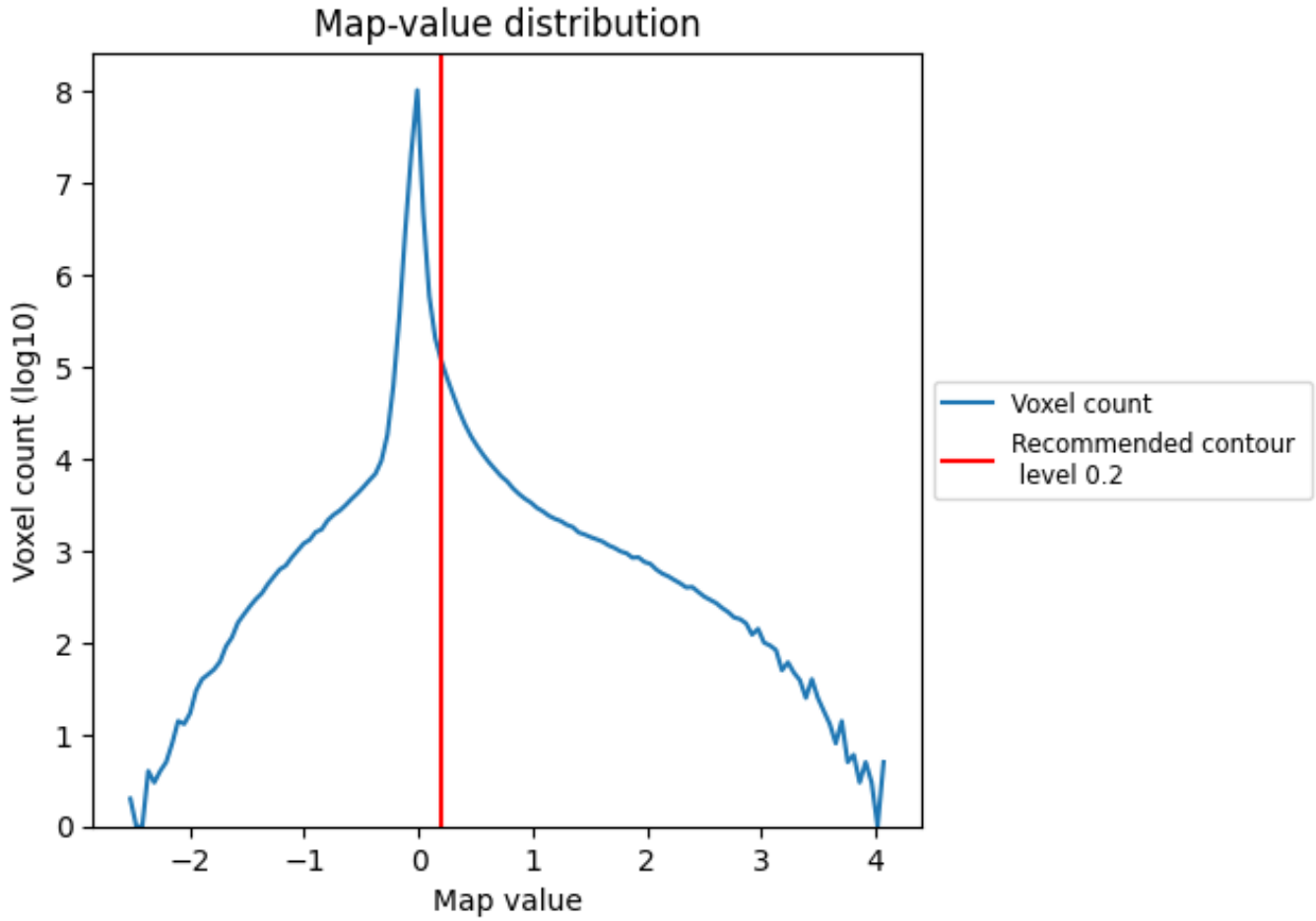


Z

7 Map analysis

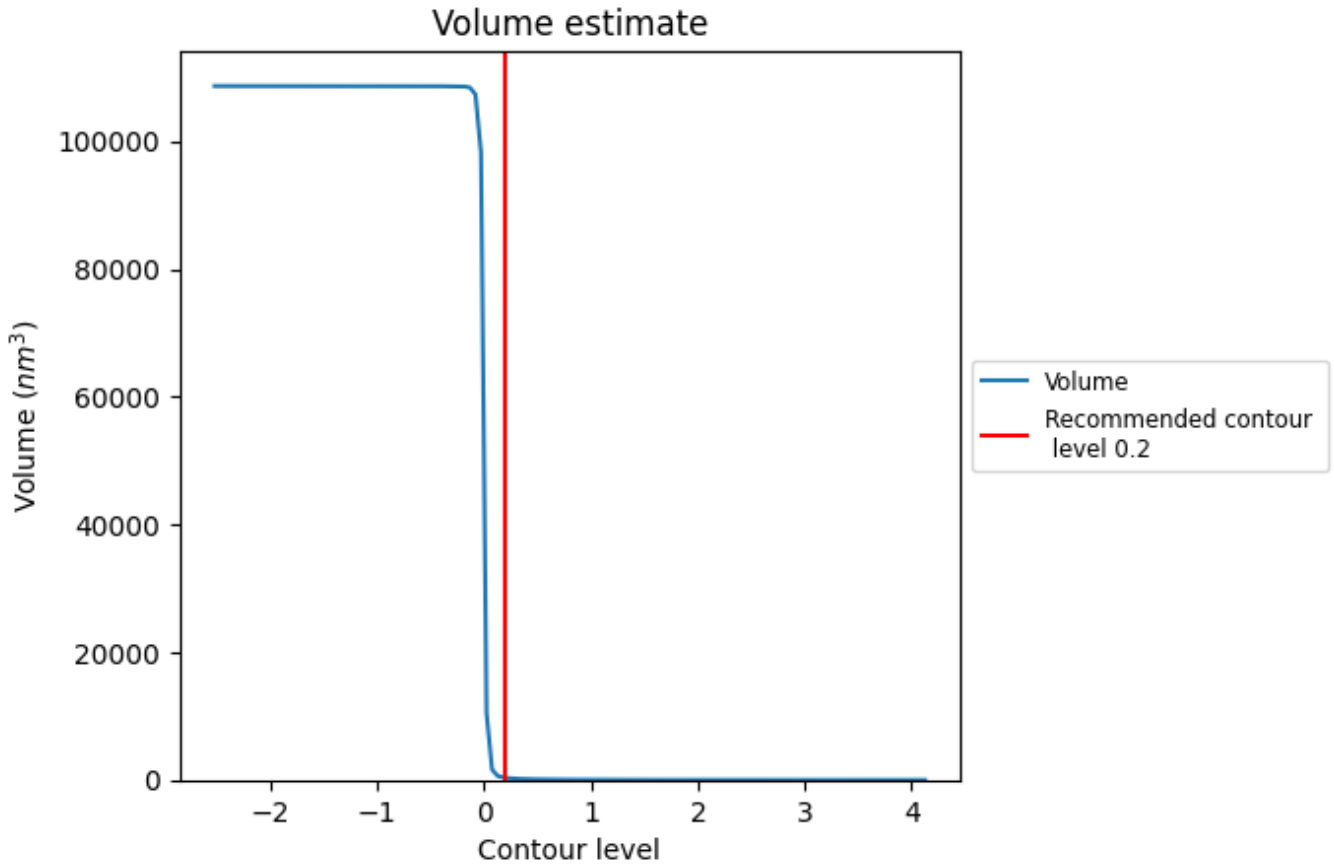
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

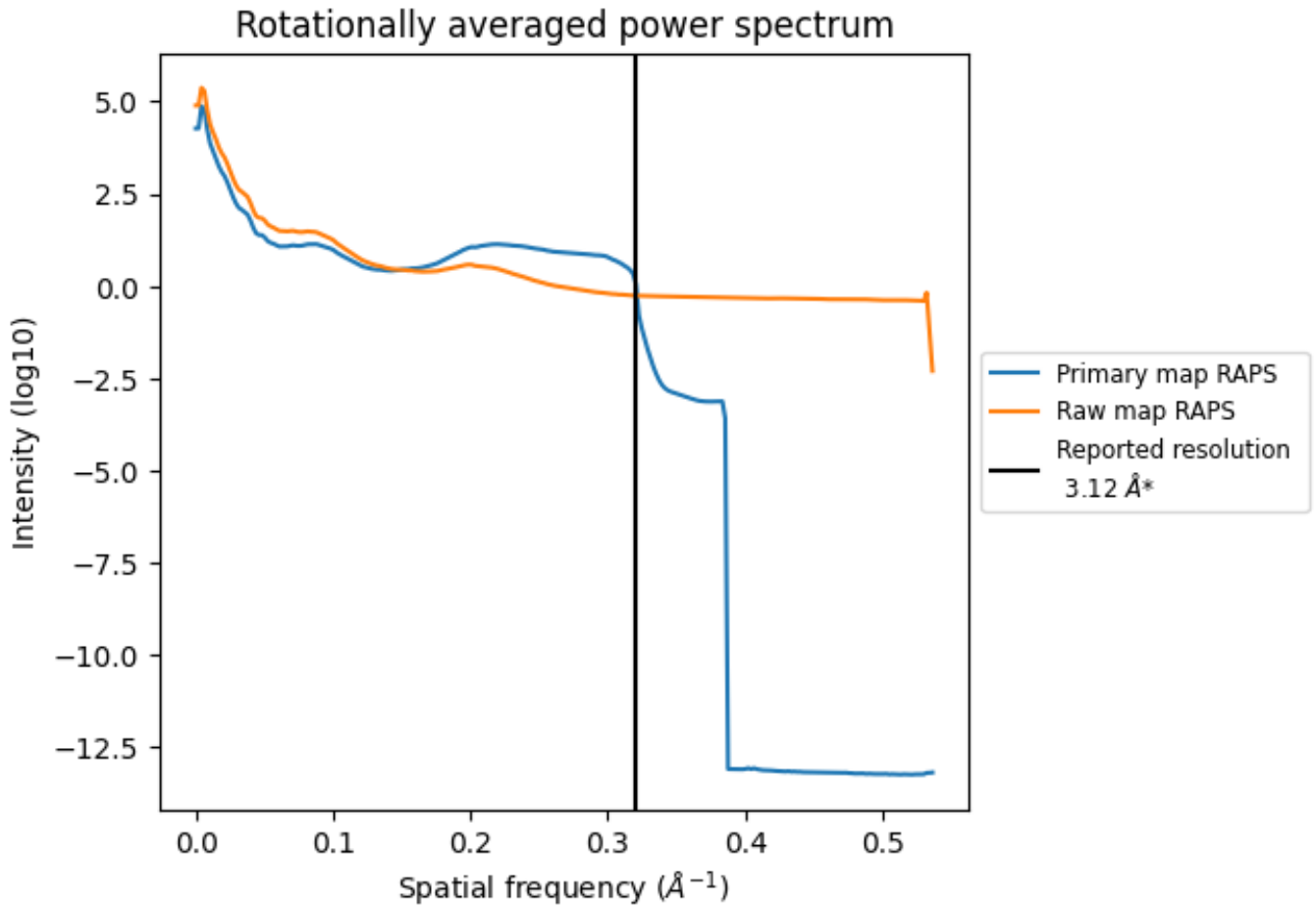
7.2 Volume estimate (i)



The volume at the recommended contour level is 350 nm^3; this corresponds to an approximate mass of 316 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)

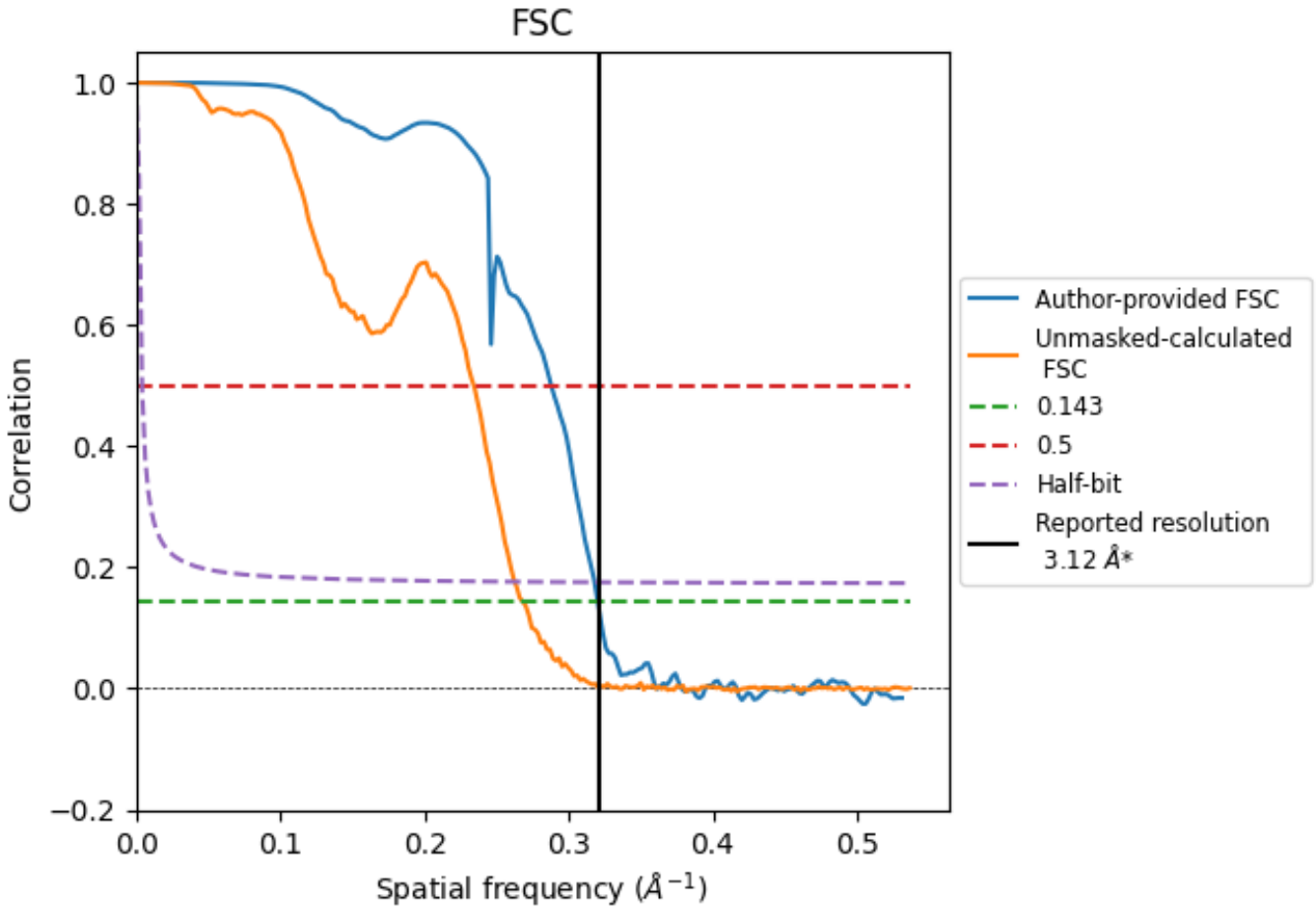


*Reported resolution corresponds to spatial frequency of 0.321 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.321 Å^{-1}

8.2 Resolution estimates (i)

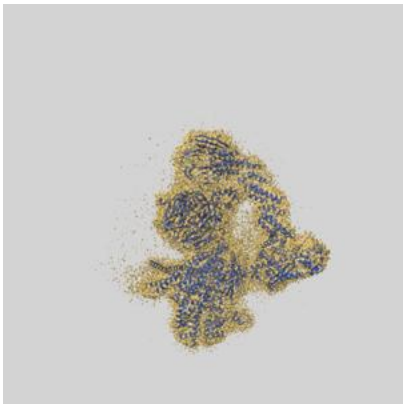
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.12	-	-
Author-provided FSC curve	3.12	3.47	3.15
Unmasked-calculated*	3.73	4.27	3.81

*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 3.73 differs from the reported value 3.12 by more than 10 %

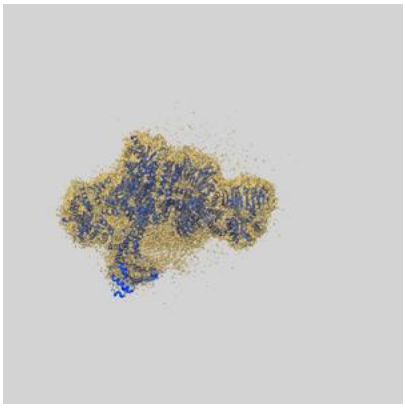
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-63446 and PDB model 9LWI. Per-residue inclusion information can be found in section 3 on page 6.

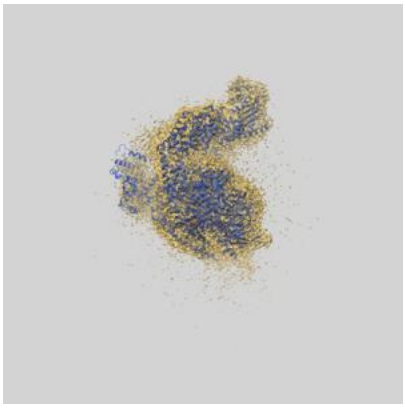
9.1 Map-model overlay



X



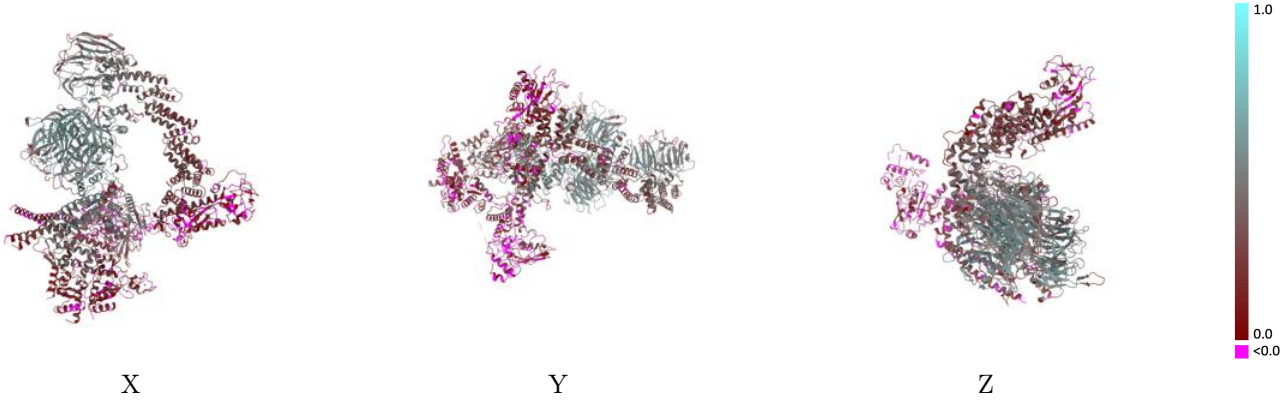
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2 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.

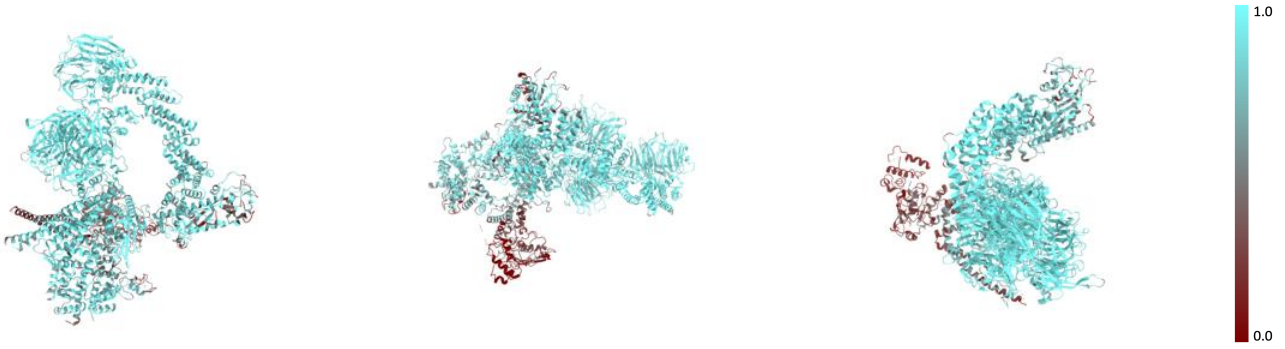
9.2 Q-score mapped to coordinate model (i)



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.

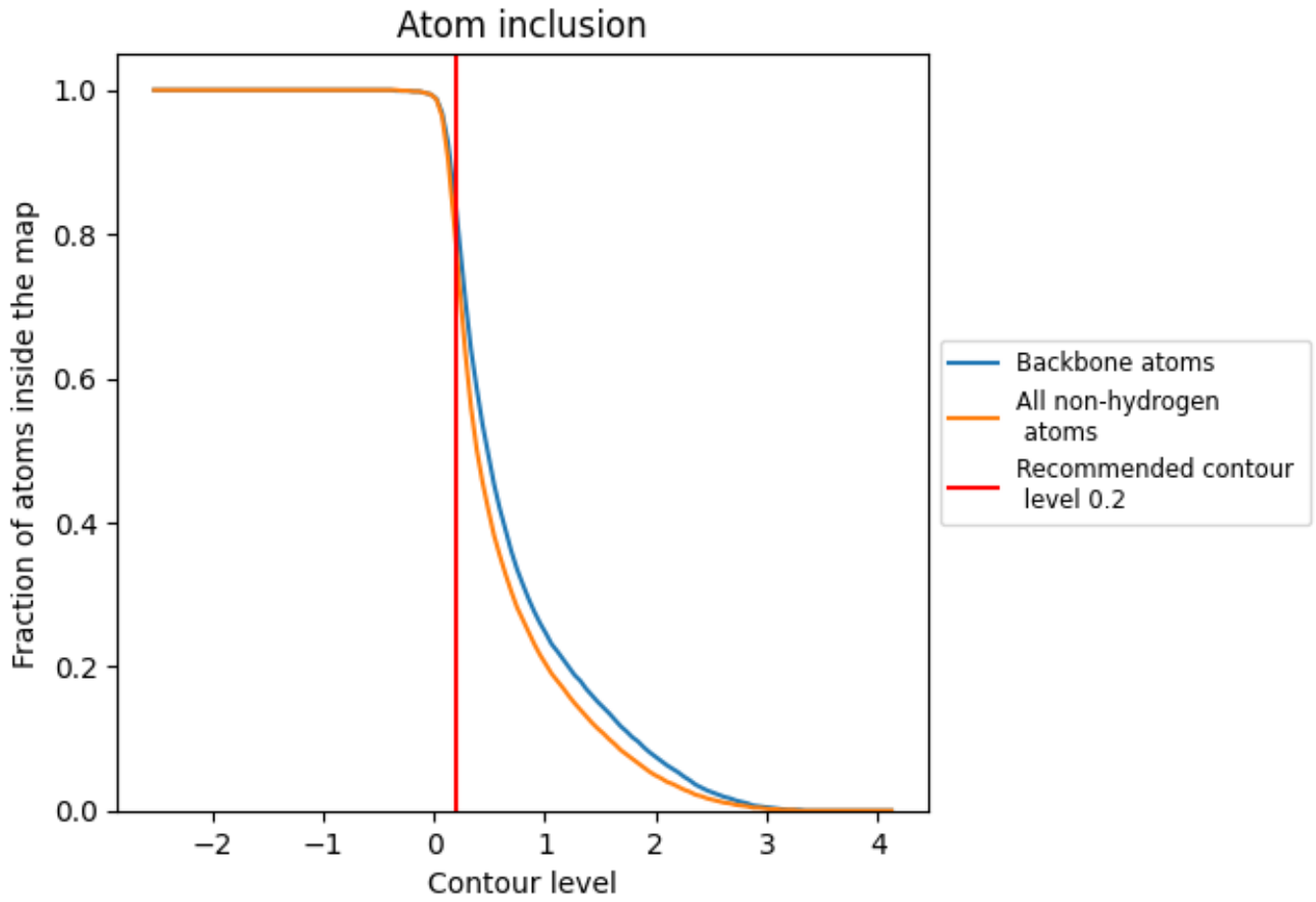
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.2).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 78% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7850	0.3230
A	0.8860	0.3990
B	0.9350	0.4930
C	0.8970	0.4960
D	0.5660	0.2530
E	0.7900	0.2300
F	0.6970	0.1350
G	0.8320	0.2590
H	0.6860	0.1030
I	0.3300	0.0930

