



wwPDB EM Validation Summary Report ⓘ

Oct 8, 2026 – 02:10 PM EDT

PDB ID : 9PBY / pdb_00009pby
EMDB ID : EMD-71493
Title : TFIID of PIC-Med-SWI/SNF-Nucleosome
Authors : Yang, C.; Nagai, S.; Chen, D.-H.
Deposited on : 2025-06-26
Resolution : 4.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

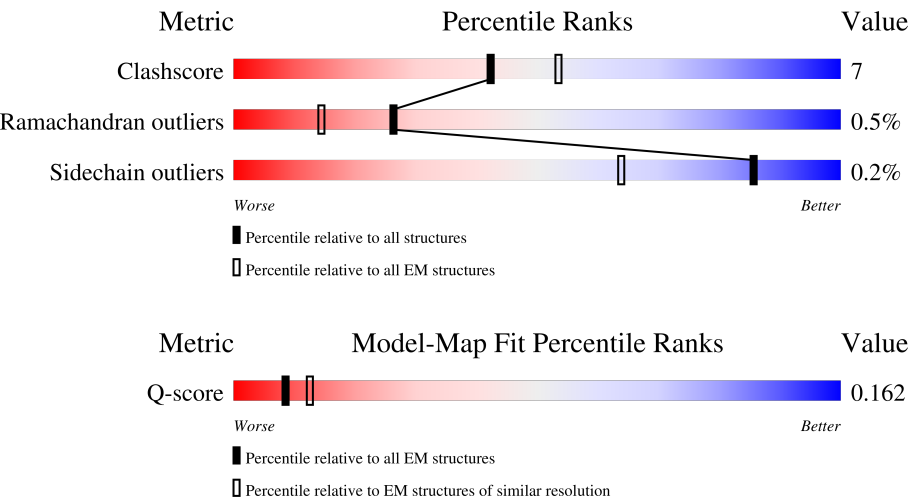
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 4.70 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	1989 (4.20 - 5.20)

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	0	778	
2	3	321	
3	5	72	
4	8	905	

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Mol	Chain	Length	Quality of chain
5	9	244	
6	N	26	
7	T	26	
8	1	642	
9	2	513	
10	4	338	
11	6	461	
12	7	843	

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 26523 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 General transcription and DNA repair factor IIH helicase subunit XPD/RAD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	752	Total	C	N	O	S	0	0
			6091	3882	1029	1142	38		

- Molecule 2 is a protein called RNA polymerase II transcription factor B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	131	Total	C	N	O	S	0	0
			1089	692	180	209	8		

- Molecule 3 is a protein called General transcription and DNA repair factor IIH subunit TFB5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	65	Total	C	N	O	S	0	0
			514	326	90	95	3		

- Molecule 4 is a protein called SWI/SNF chromatin-remodeling complex subunit SNF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	17	Total	C	N	O	S	0	0
			134	89	22	22	1		

- Molecule 5 is a protein called Transcription initiation factor TFIID subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	9	68	Total	C	N	O	S	0	0
			542	345	82	113	2		

- Molecule 6 is a DNA chain called promoter DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	26	Total	C	N	O	P	0	0
			534	257	91	160	26		

- Molecule 7 is a DNA chain called promoter DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	26	Total	C	N	O	P	0	0
			532	255	99	152	26		

- Molecule 8 is a protein called General transcription and DNA repair factor IIH subunit TFB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1	416	Total	C	N	O	S	0	0
			3374	2133	586	639	16		

- Molecule 9 is a protein called General transcription and DNA repair factor IIH subunit TFB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	2	445	Total	C	N	O	S	0	0
			3597	2327	591	663	16		

- Molecule 10 is a protein called General transcription and DNA repair factor IIH subunit TFB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	4	293	Total	C	N	O	S	0	0
			2274	1454	377	429	14		

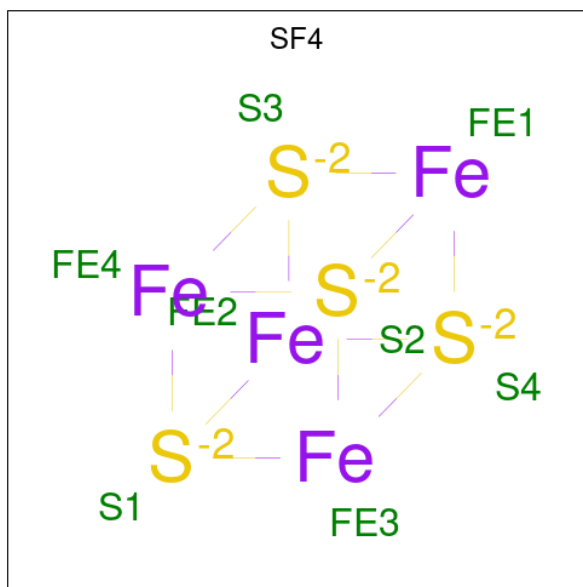
- Molecule 11 is a protein called General transcription and DNA repair factor IIH subunit SSL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	6	374	Total	C	N	O	S	0	0
			2946	1870	507	541	28		

- Molecule 12 is a protein called General transcription and DNA repair factor IIH helicase subunit XPB.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	7	607	Total	C	N	O	S	0	0
			4881	3104	846	905	26		

- Molecule 13 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
13	0	1	Total	Fe	S	0
			8	4	4	

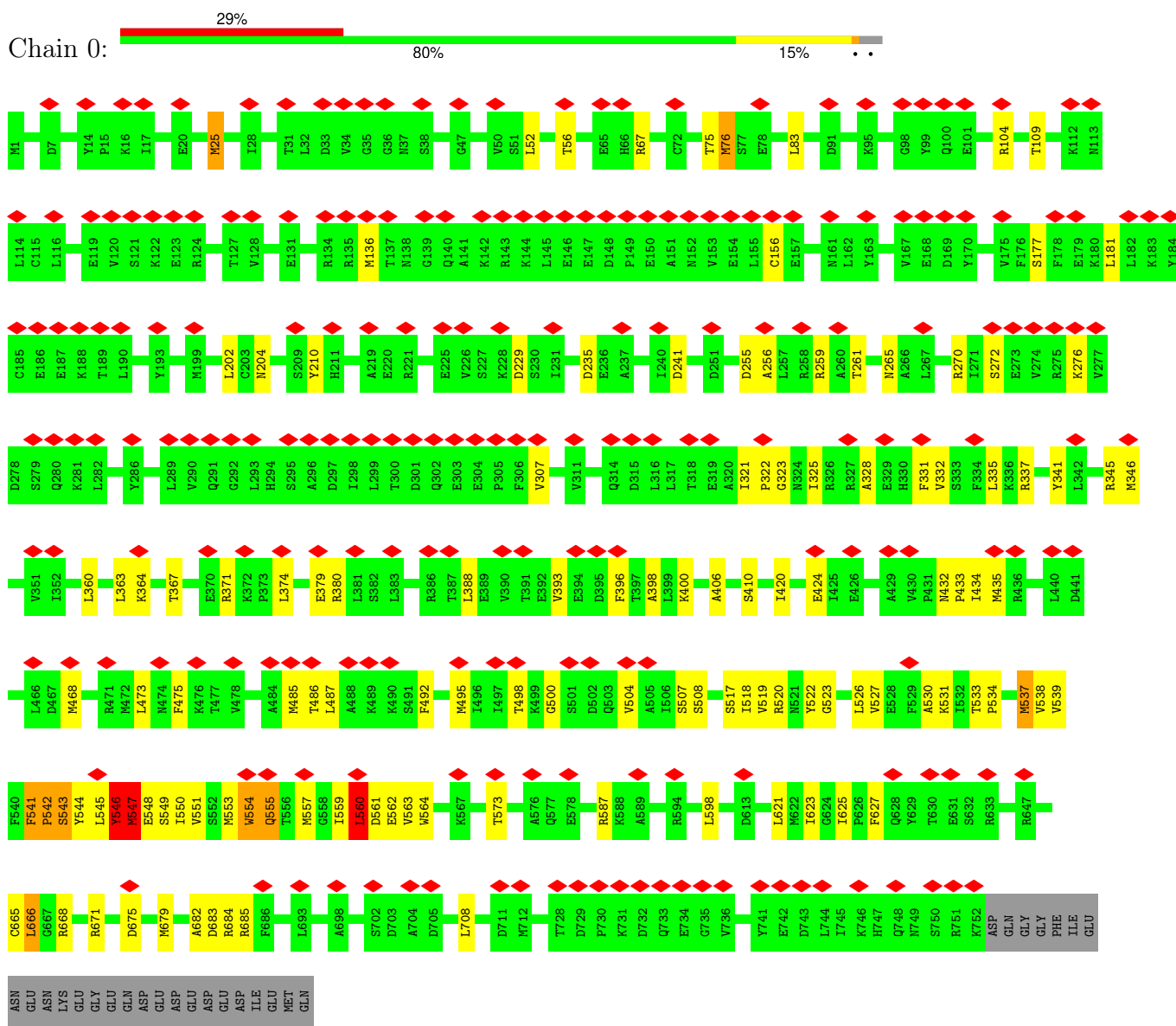
- Molecule 14 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
14	3	2	Total	Zn	0
			2	2	
14	4	1	Total	Zn	0
			1	1	
14	6	4	Total	Zn	0
			4	4	

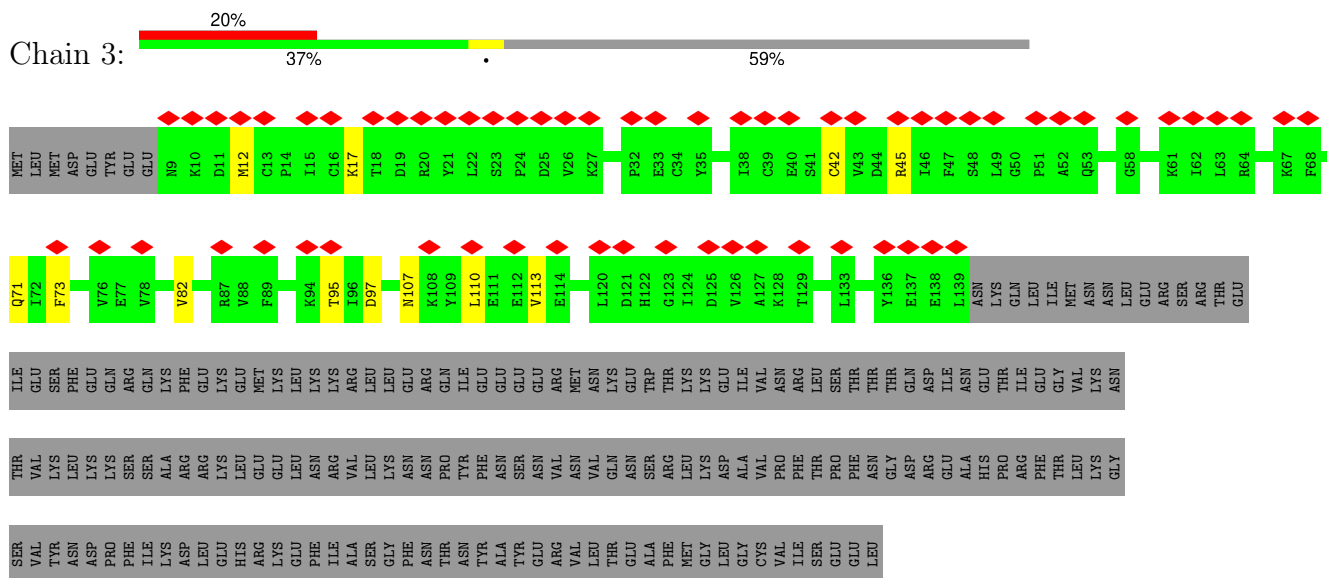
3 Residue-property plots

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.

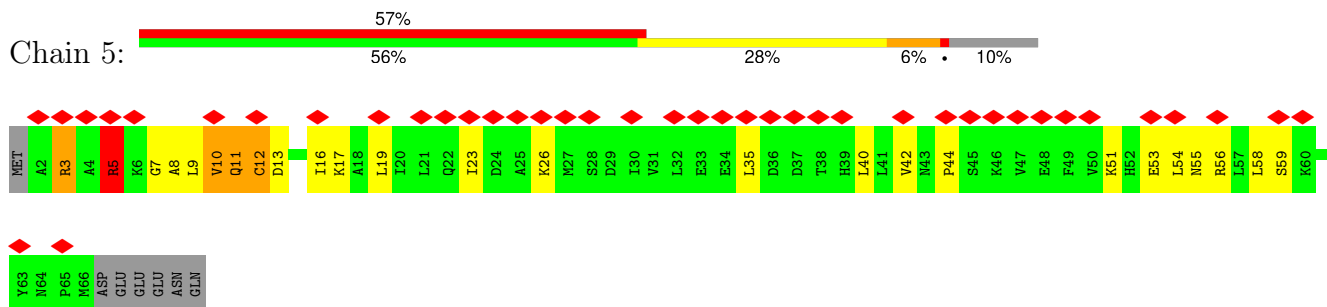
- Molecule 1: General transcription and DNA repair factor IIH helicase subunit XPD/RAD3



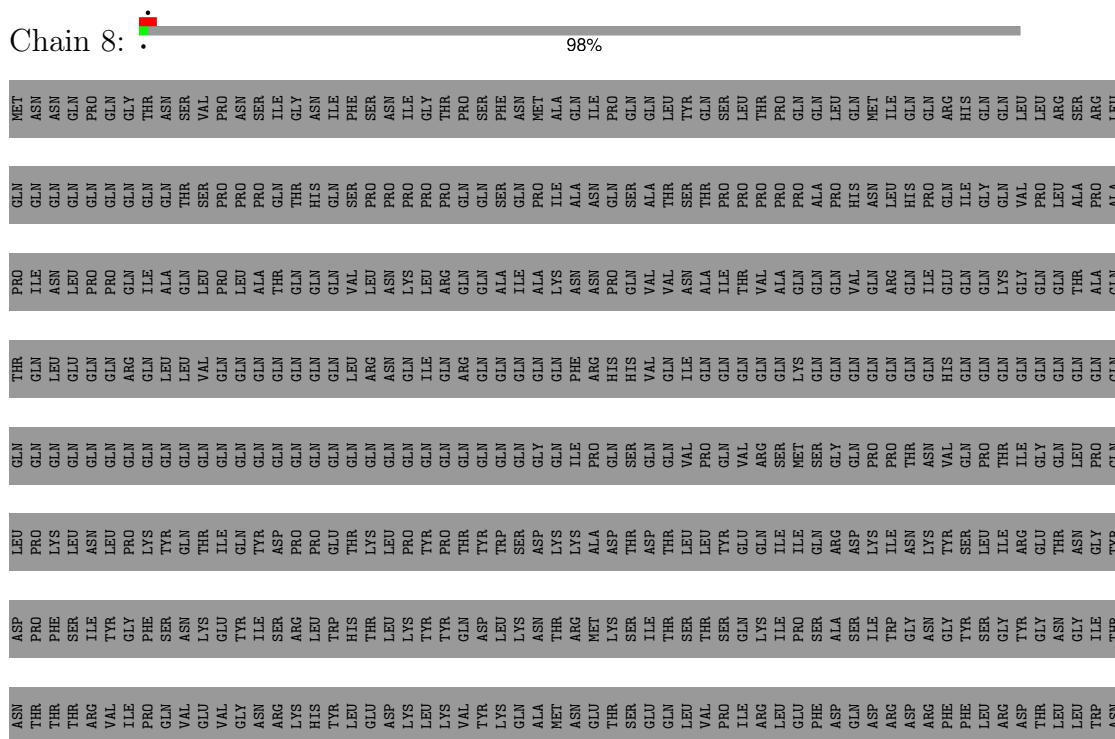
- Molecule 2: RNA polymerase II transcription factor B subunit 3

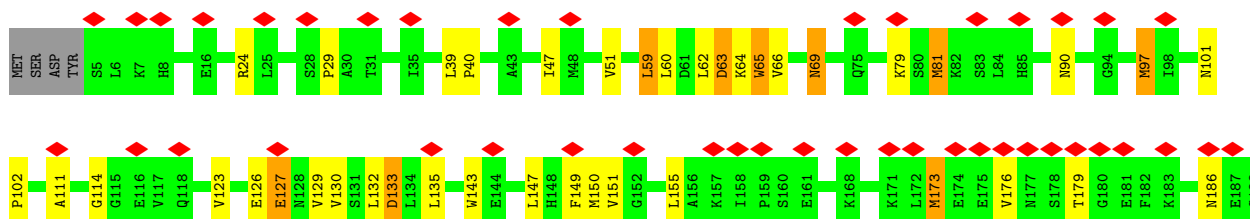
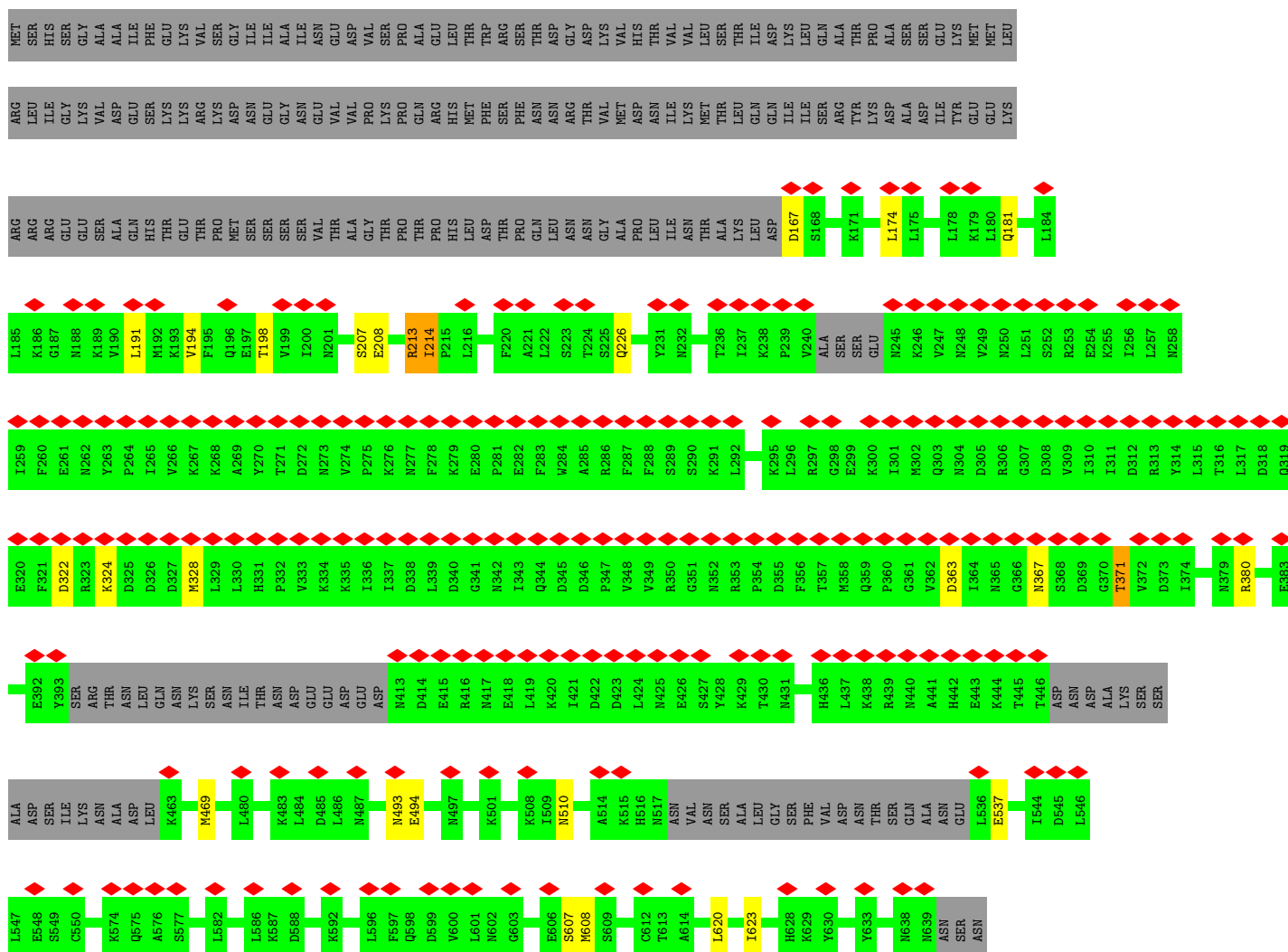
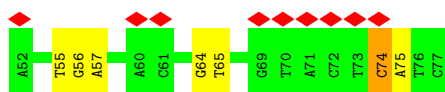


- Molecule 3: General transcription and DNA repair factor IIH subunit TFB5



- Molecule 4: SWI/SNF chromatin-remodeling complex subunit SNF5





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

TYR
TYR
LYS
ASN
LYS
LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	470400	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 ($e^-/\text{\AA}^2$)	40.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.098	Depositor
Minimum map value	-0.068	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0175	Depositor
Map size (Å)	537.6, 537.6, 537.6	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4, 1.4, 1.4	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, 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	0	1.16	32/6209 (0.5%)	1.15	43/8384 (0.5%)
2	3	0.20	0/1109	0.39	0/1492
3	5	0.72	0/520	1.43	9/701 (1.3%)
4	8	2.06	5/137 (3.6%)	3.02	11/185 (5.9%)
5	9	1.93	10/549 (1.8%)	2.42	27/743 (3.6%)
6	N	1.57	13/597 (2.2%)	1.36	9/920 (1.0%)
7	T	1.25	6/597 (1.0%)	1.32	11/918 (1.2%)
8	1	0.33	2/3425 (0.1%)	0.54	5/4609 (0.1%)
9	2	0.83	19/3664 (0.5%)	1.17	36/4952 (0.7%)
10	4	0.29	0/2312	0.51	0/3127
11	6	0.48	3/3007 (0.1%)	0.75	5/4066 (0.1%)
12	7	0.27	1/4982 (0.0%)	0.42	0/6736
All	All	0.81	91/27108 (0.3%)	0.97	156/36833 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	8
3	5	0	4
4	8	0	1
5	9	2	2
8	1	0	1
9	2	0	4
11	6	0	4
All	All	2	24

The worst 5 of 91 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	546	TYR	CD1-CE1	49.19	2.86	1.38
1	0	547	MET	CB-CG	25.34	2.28	1.52
1	0	546	TYR	CB-CG	-25.20	0.96	1.51
5	9	181	LYS	CA-C	20.46	1.80	1.52
1	0	546	TYR	CG-CD2	20.21	1.81	1.39

The worst 5 of 156 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	546	TYR	CG-CD1-CE1	-35.24	68.34	121.20
1	0	547	MET	CA-CB-CG	31.03	176.17	114.10
5	9	209	MET	CA-CB-CG	28.07	170.24	114.10
9	2	97	MET	CB-CG-SD	22.42	179.96	112.70
1	0	546	TYR	CA-C-N	20.78	161.22	121.54

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	9	202	THR	CA,CB

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	337	ARG	Sidechain
1	0	542	PRO	Peptide
1	0	545	LEU	Peptide
1	0	546	TYR	Sidechain,Peptide
1	0	560	LEU	Mainchain

5.2 Too-close contacts

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	0	6091	0	6155	114	0
2	3	1089	0	1069	7	0
3	5	514	0	541	16	0
4	8	134	0	141	31	0
5	9	542	0	537	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	N	534	0	298	5	0
7	T	532	0	294	2	0
8	1	3374	0	3423	15	0
9	2	3597	0	3687	91	0
10	4	2274	0	2332	20	0
11	6	2946	0	2958	45	0
12	7	4881	0	4865	35	0
13	0	8	0	0	1	0
14	3	2	0	0	0	0
14	4	1	0	0	0	0
14	6	4	0	0	0	0
All	All	26523	0	26300	353	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 353 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:546:TYR:CG	1:0:546:TYR:CD2	1.81	1.67
1:0:546:TYR:CD2	1:0:546:TYR:CE2	1.79	1.65
1:0:560:LEU:CG	1:0:560:LEU:CB	1.77	1.59
5:9:181:LYS:C	5:9:181:LYS:CA	1.80	1.53
4:8:786:LEU:CD2	4:8:786:LEU:CG	1.92	1.47

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	0	750/778 (96%)	714 (95%)	31 (4%)	5 (1%)	18 55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	3	129/321 (40%)	126 (98%)	3 (2%)	0	100	100
3	5	63/72 (88%)	56 (89%)	7 (11%)	0	100	100
4	8	15/905 (2%)	12 (80%)	3 (20%)	0	100	100
5	9	66/244 (27%)	61 (92%)	4 (6%)	1 (2%)	8	38
8	1	404/642 (63%)	385 (95%)	18 (4%)	1 (0%)	43	78
9	2	435/513 (85%)	403 (93%)	27 (6%)	5 (1%)	11	45
10	4	287/338 (85%)	279 (97%)	7 (2%)	1 (0%)	36	72
11	6	368/461 (80%)	324 (88%)	42 (11%)	2 (0%)	24	63
12	7	599/843 (71%)	577 (96%)	22 (4%)	0	100	100
All	All	3116/5117 (61%)	2937 (94%)	164 (5%)	15 (0%)	26	63

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	543	SER
1	0	546	TYR
1	0	547	MET
8	1	214	ILE
9	2	231	LEU

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	0	684/707 (97%)	683 (100%)	1 (0%)	88	88
2	3	125/303 (41%)	125 (100%)	0	100	100
3	5	59/66 (89%)	59 (100%)	0	100	100
4	8	16/823 (2%)	16 (100%)	0	100	100
5	9	63/219 (29%)	61 (97%)	2 (3%)	34	56
8	1	388/589 (66%)	388 (100%)	0	100	100
9	2	408/468 (87%)	406 (100%)	2 (0%)	81	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	4	260/300 (87%)	260 (100%)	0	100	100
11	6	338/418 (81%)	338 (100%)	0	100	100
12	7	539/737 (73%)	539 (100%)	0	100	100
All	All	2880/4630 (62%)	2875 (100%)	5 (0%)	85	86

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	547	MET
5	9	181	LYS
5	9	202	THR
9	2	81	MET
9	2	464	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
9	2	365	HIS
10	4	303	ASN
9	2	372	ASN
9	2	500	GLN
11	6	248	HIS

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 7 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
13	SF4	0	801	1	0,12,12	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	SF4	0	801	1	-	-	0/6/5/5

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	0	801	SF4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	7	2
8	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	7	538:ALA	C	539:ASN	N	4.12
1	7	628:TYR	C	629:GLY	N	3.15
1	1	229:GLY	C	230:PRO	N	3.13

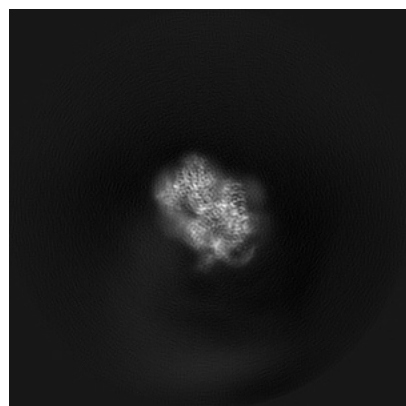
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71493. These allow visual inspection of the internal detail of the map and identification of artifacts.

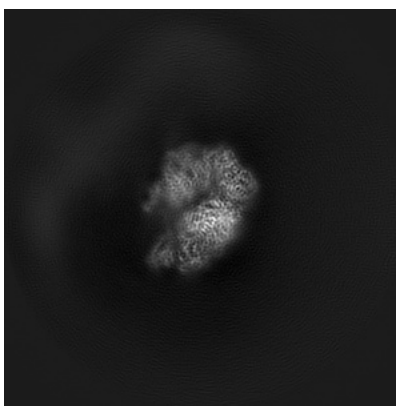
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

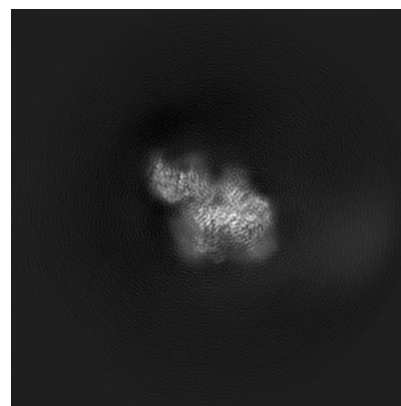
6.1.1 Primary map



X

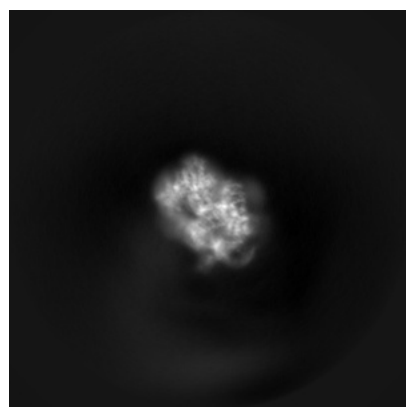


Y

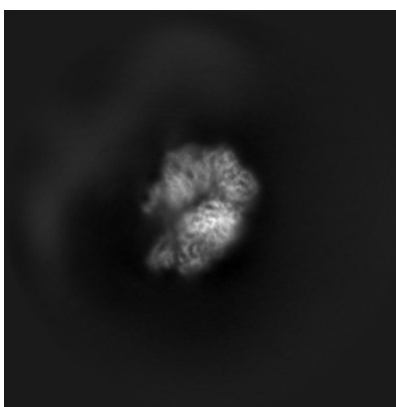


Z

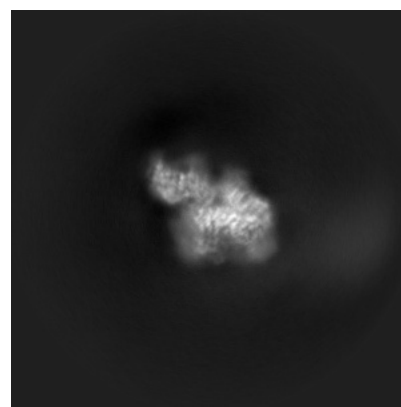
6.1.2 Raw map



X



Y

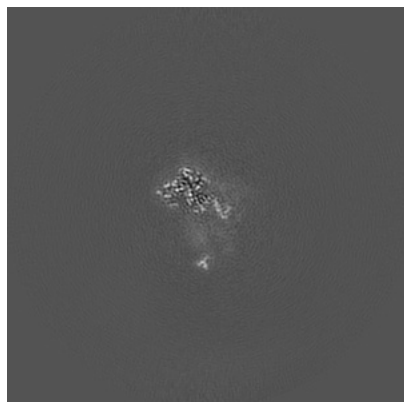


Z

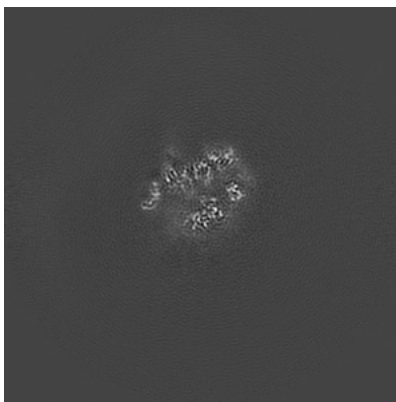
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

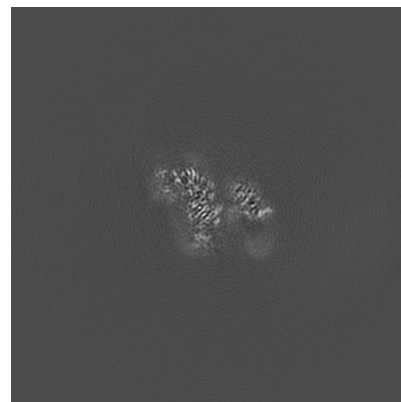
6.2.1 Primary map



X Index: 192

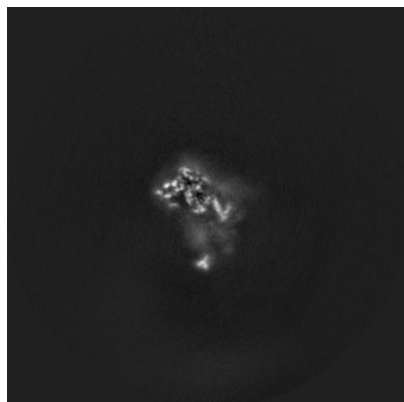


Y Index: 192

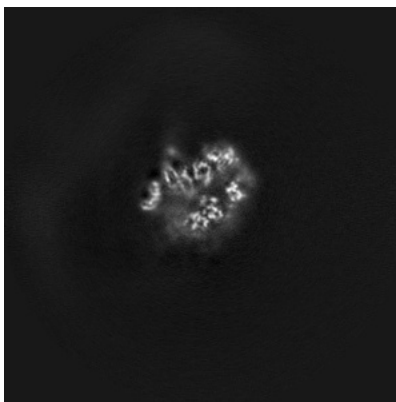


Z Index: 192

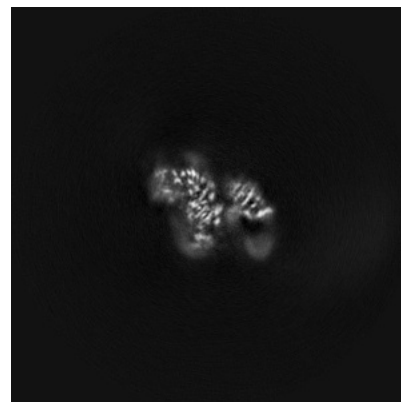
6.2.2 Raw map



X Index: 192



Y Index: 192

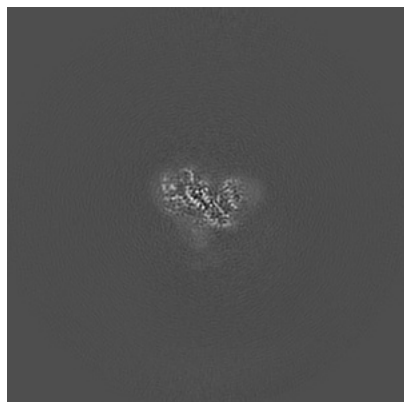


Z Index: 192

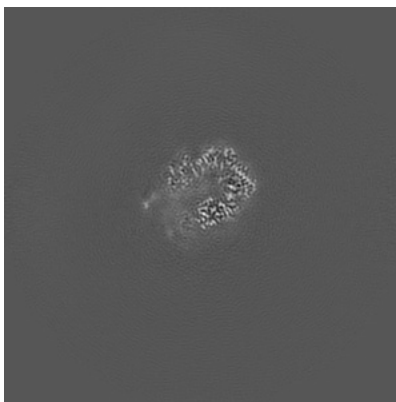
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

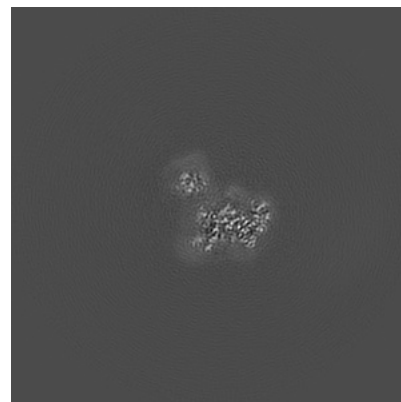
6.3.1 Primary map



X Index: 183

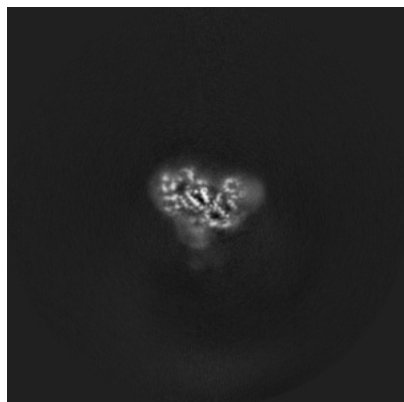


Y Index: 184

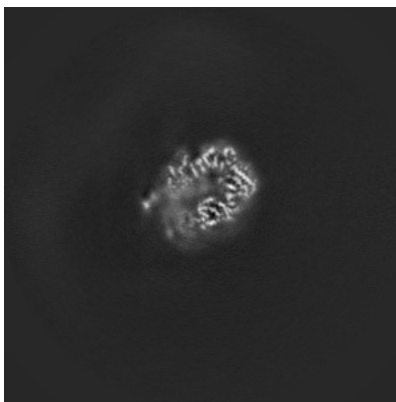


Z Index: 214

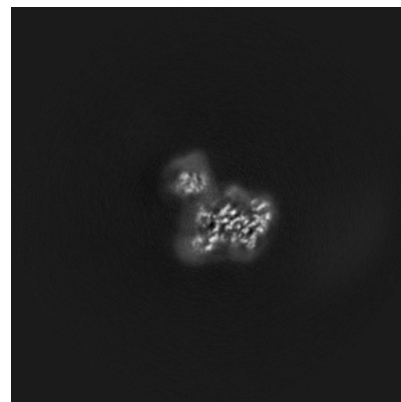
6.3.2 Raw map



X Index: 182



Y Index: 184

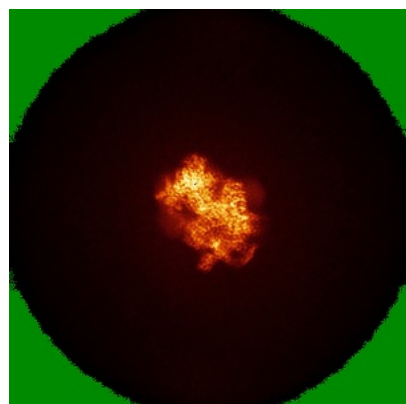


Z Index: 214

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

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

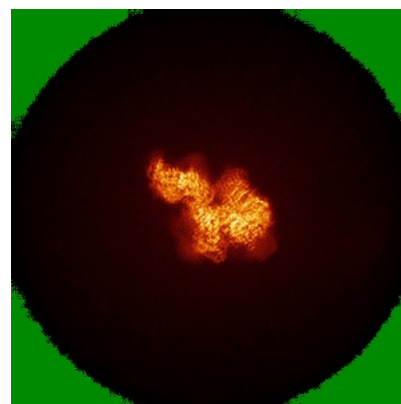
6.4.1 Primary map



X

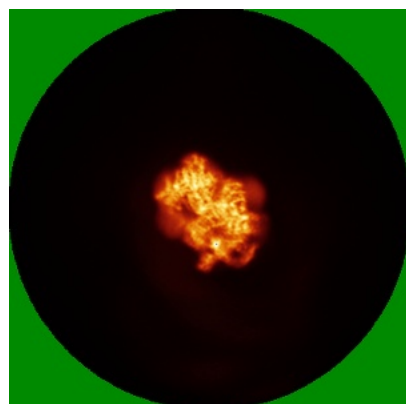


Y



Z

6.4.2 Raw map



X



Y

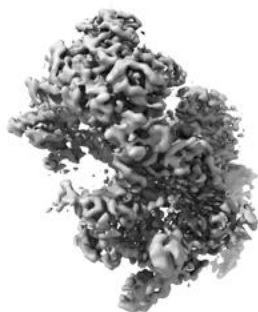


Z

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](#)

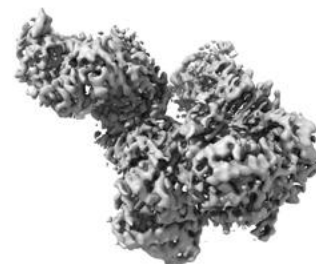
6.5.1 Primary map



X



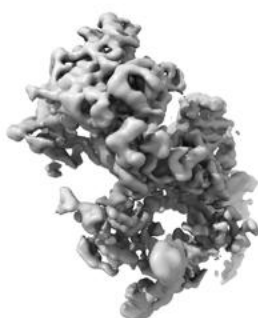
Y



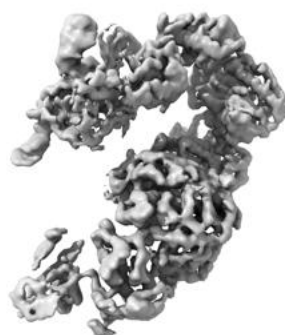
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0175. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

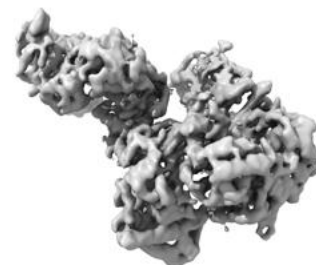
6.5.2 Raw map



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.

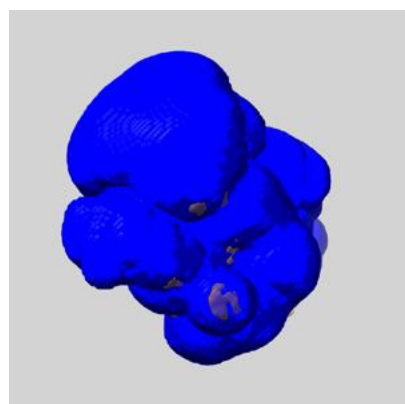
6.6 Mask visualisation [i](#)

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

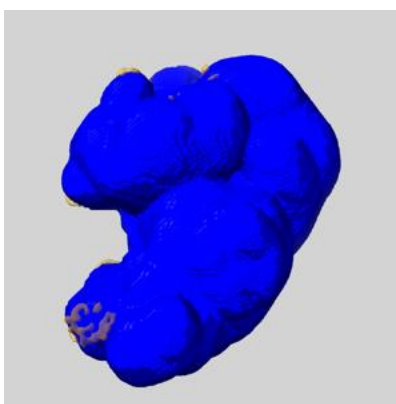
A mask typically either:

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

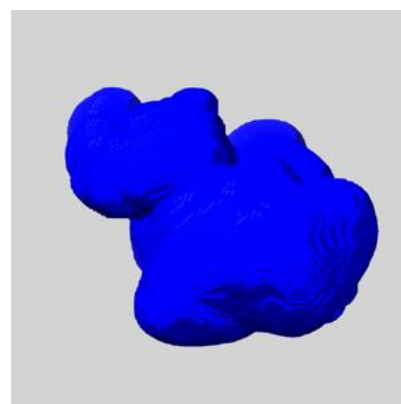
6.6.1 emd_71493_msk_1.map [i](#)



X



Y

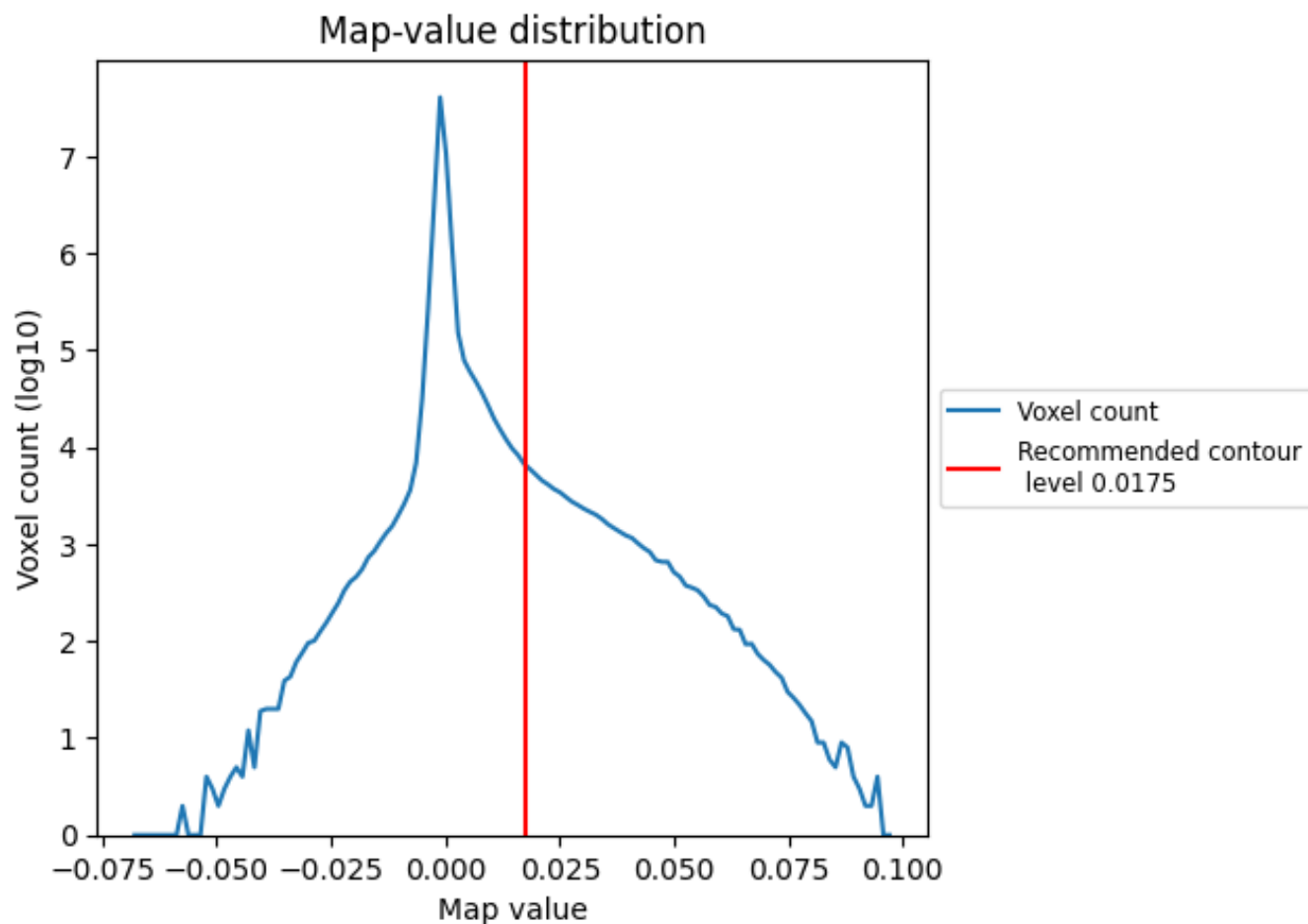


Z

7 Map analysis [i](#)

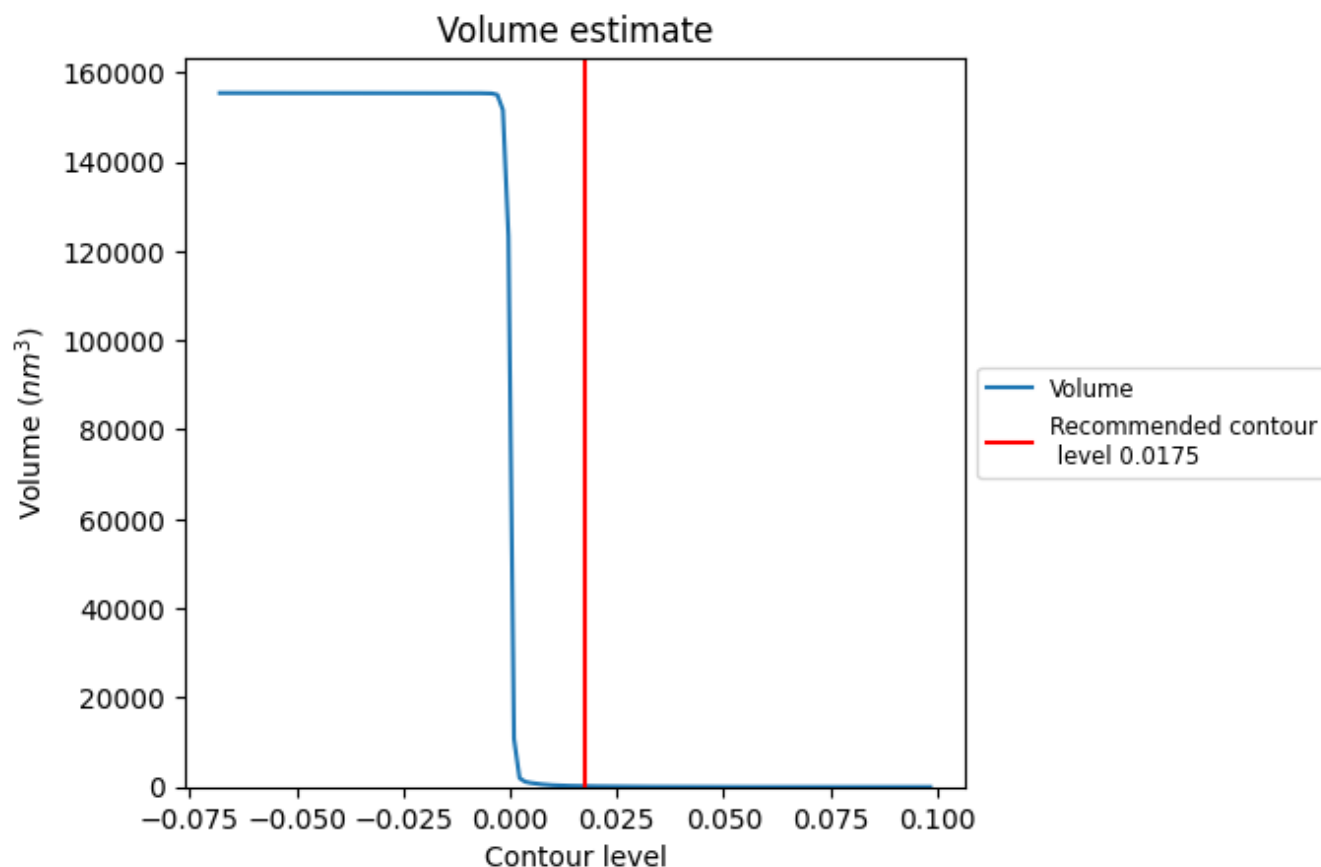
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

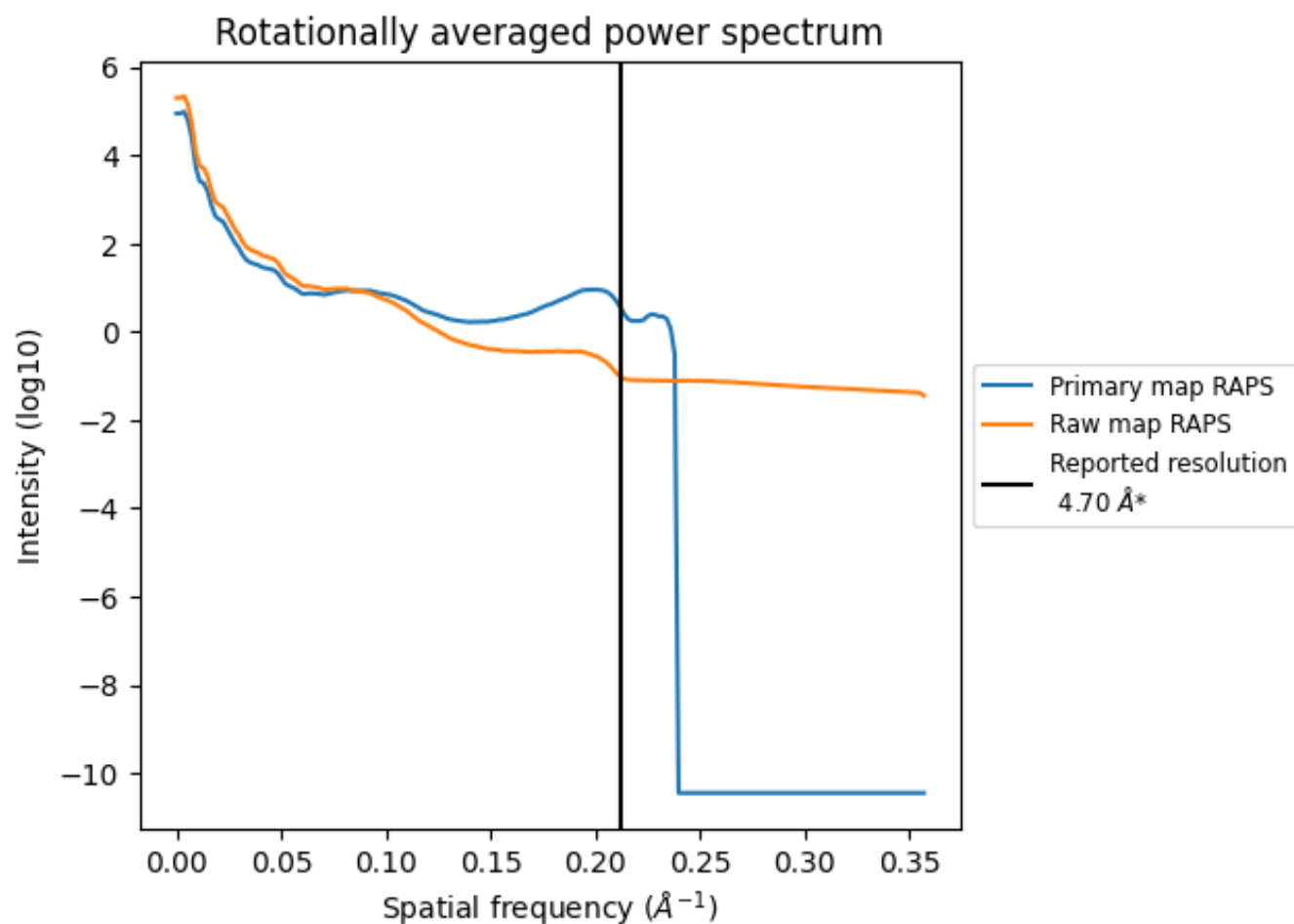
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 177 nm³; this corresponds to an approximate mass of 160 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 ⓘ

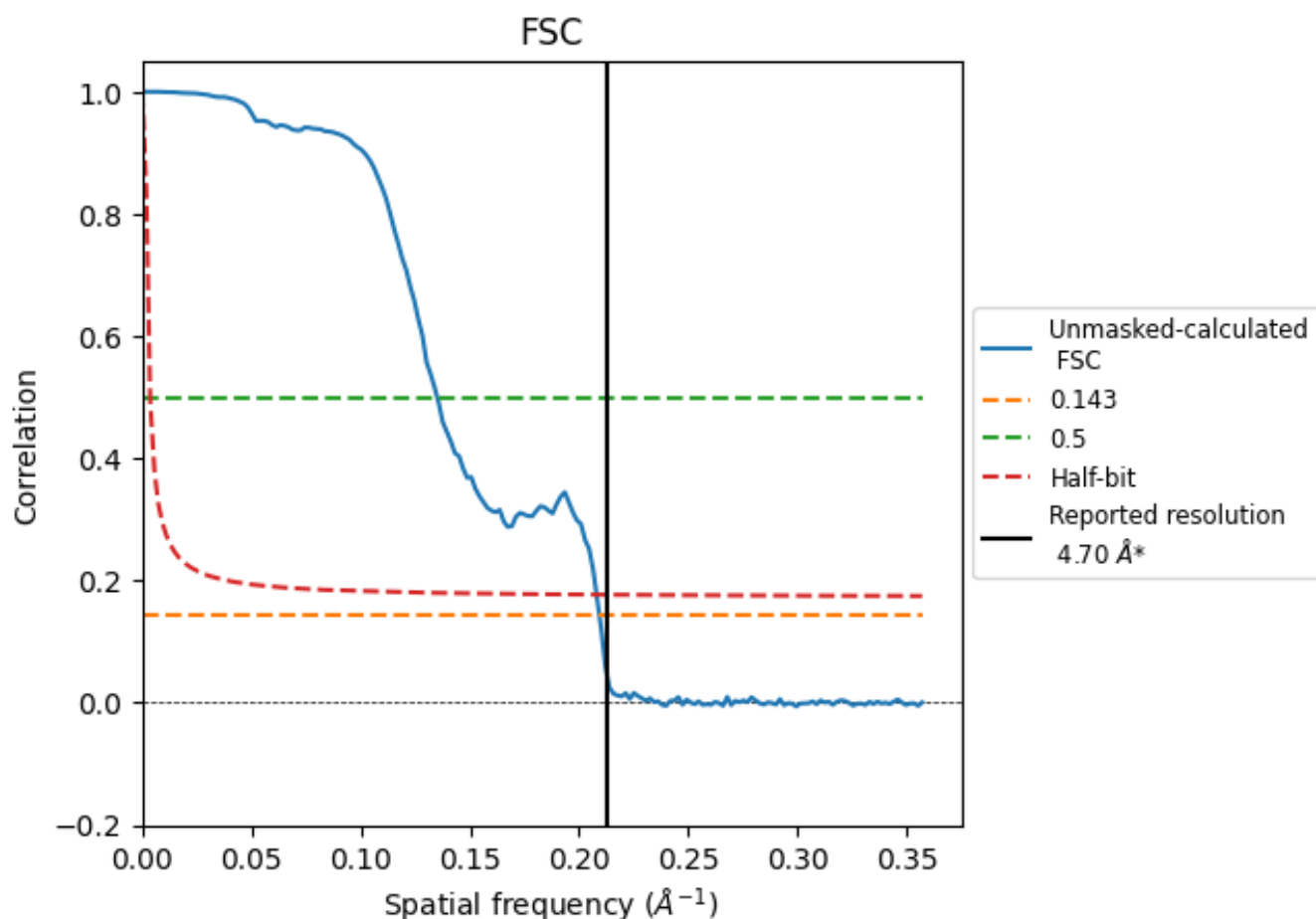


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

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 0.213 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

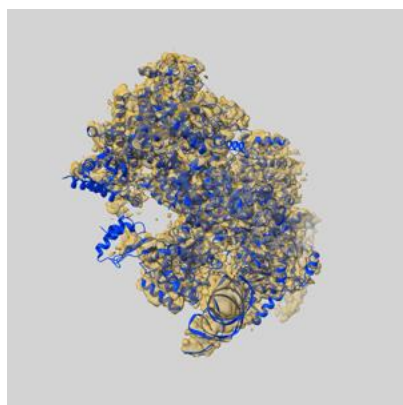
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.78	7.40	4.81

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

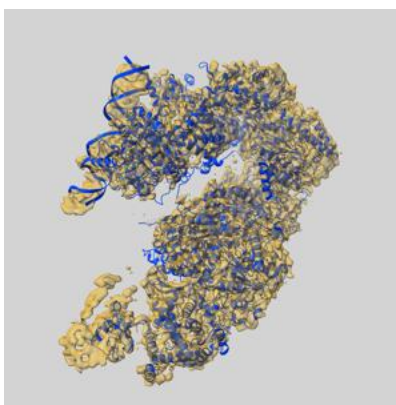
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-71493 and PDB model 9PBY. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

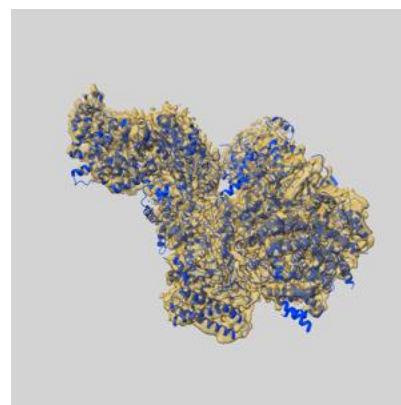
9.1 Map-model overlay [i](#)



X



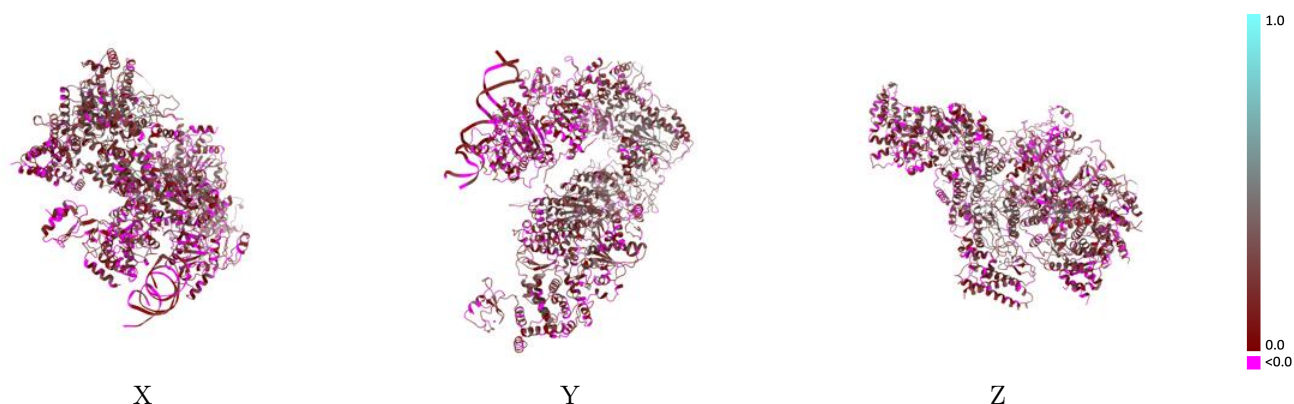
Y



Z

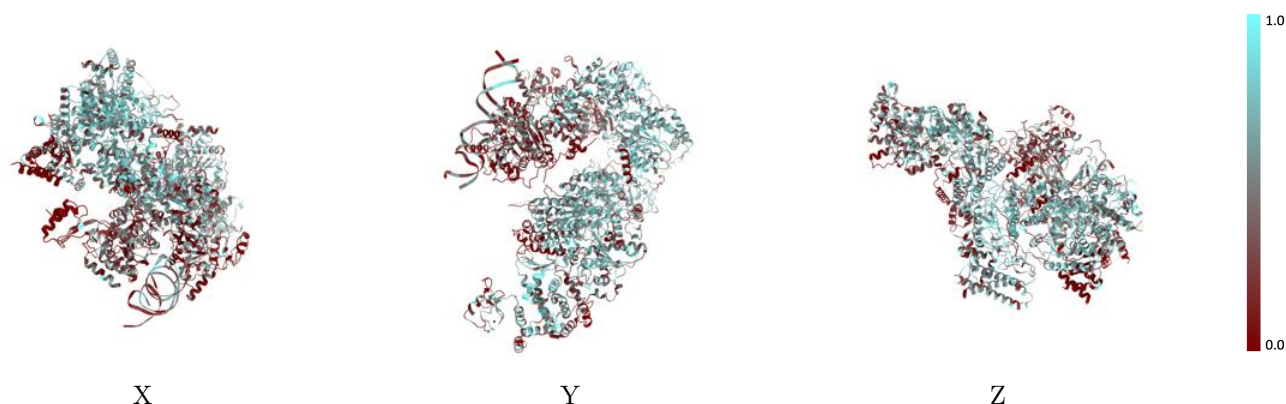
The images above show the 3D surface view of the map at the recommended contour level 0.0175 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



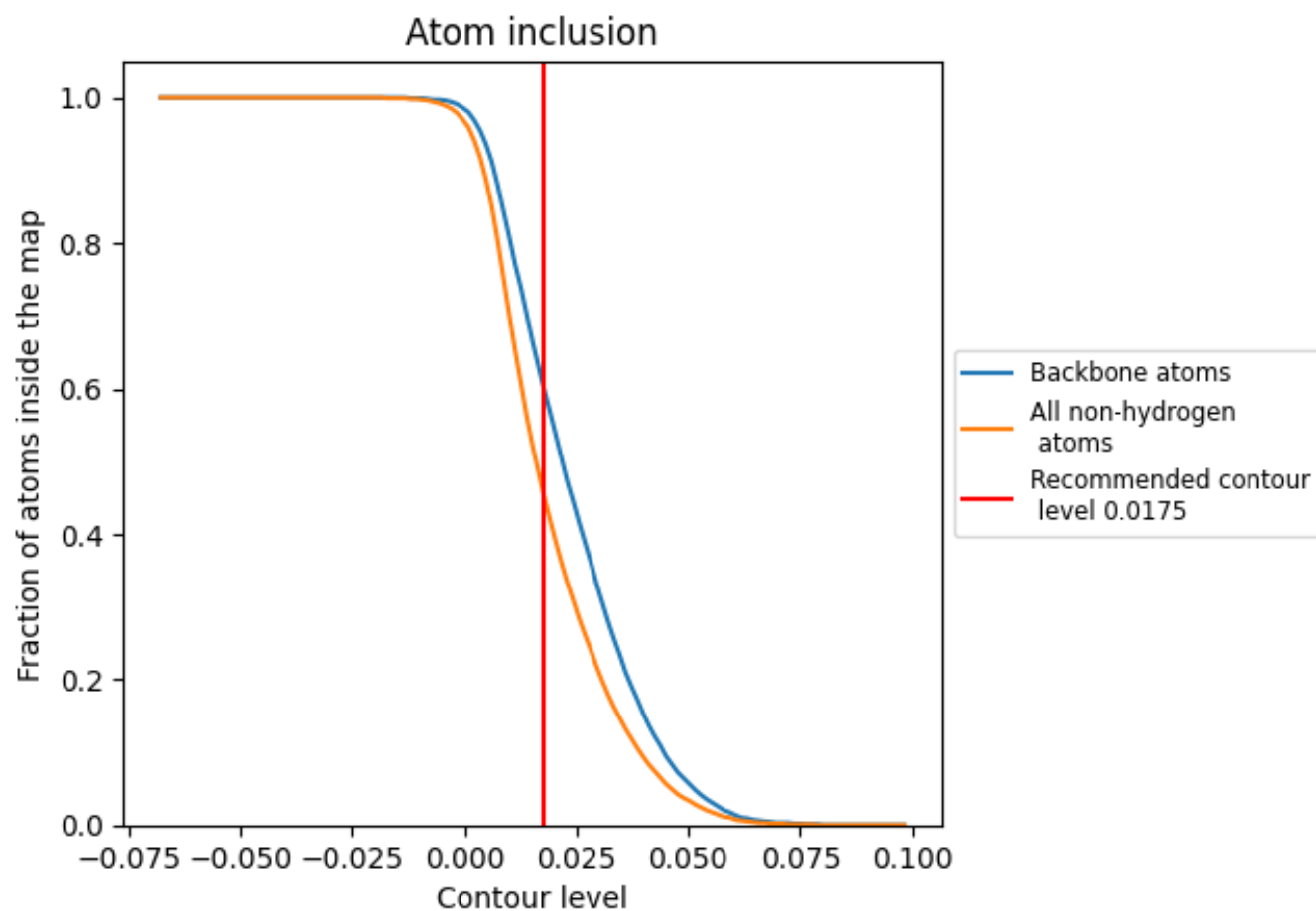
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0175).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 46% 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 (0.0175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4590	0.1620
0	0.5430	0.1870
1	0.3460	0.1250
2	0.4900	0.1580
3	0.4290	0.1510
4	0.6480	0.2670
5	0.3180	0.1020
6	0.6380	0.2860
7	0.3080	0.0840
8	0.0070	0.0130
9	0.0000	0.0430
N	0.3350	0.0350
T	0.4700	0.0840

1.0

0.0

<0.0