



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:28 PM UTC

PDB ID : 7UNC / pdb\_00007unc  
EMDB ID : EMD-26620  
Title : Pol II-DSIF-SPT6-PAF1c-TFIIS complex with rewrapped nucleosome  
Authors : Filipovski, M.; Vos, S.M.; Farnung, L.  
Deposited on : 2022-04-10  
Resolution : 3.00 Å(reported)  
Based on initial models : 6TED, 3LZ0

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

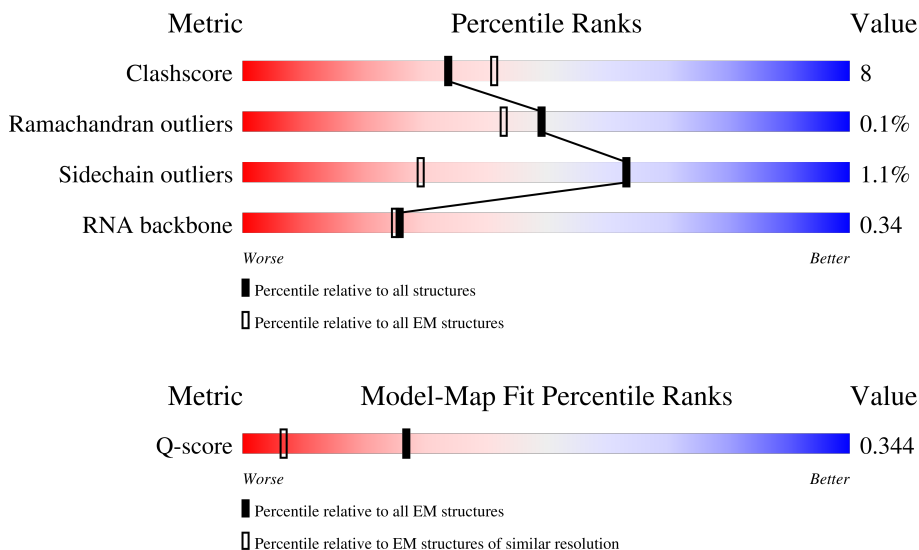
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 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.



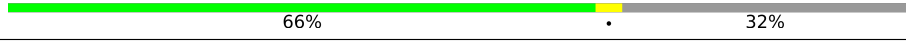









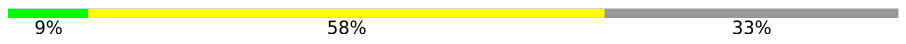




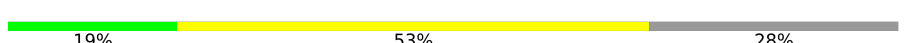


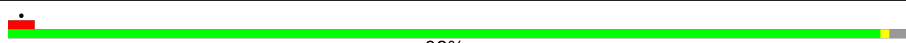





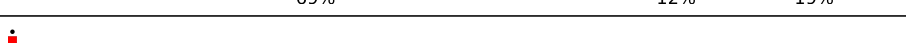
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 ( 2.50 - 3.50 )

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1984	
2	B	1251	
3	C	275	





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Mol	Chain	Length	Quality of chain
4	D	184	
5	E	210	
6	F	127	
7	G	172	
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	M	1729	
14	N	209	
15	O	304	
16	P	16	
17	Q	1179	
18	R	713	
19	T	215	
20	U	666	
21	V	531	
22	W	305	
23	X	531	
24	Z	1087	
25	a	136	
25	e	136	
26	b	103	
26	f	103	

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Mol	Chain	Length	Quality of chain
27	c	130	 70% 9% 21%
27	g	130	 69% 12% 19%
28	d	123	 69% 8% 23%
28	h	123	 63% 12% 24%

## 2 Entry composition [i](#)

There are 30 unique types of molecules in this entry. The entry contains 105742 atoms, of which 48112 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 DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P S		
1	A	1426	22643	7074	11388	2014	2095	2 70	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	B	1117	17949	5665	9002	1571	1647	64	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	C	258	4096	1300	2024	356	410	6	0	0

- Molecule 4 is a protein called RPOL4c domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
4	D	126	1985	630	981	170	200	4	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
5	E	209	3458	1089	1738	300	323	8	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
6	F	78	1284	401	658	106	114	5	0	0

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace	
7	G	171	Total	C	H	N	O	S	0	0
			2654	866	1321	214	245	8		

- Molecule 8 is a protein called RPB8.

Mol	Chain	Residues	Atoms					AltConf	Trace	
8	H	149	Total	C	H	N	O	S	0	0
			2354	759	1157	195	238	5		

- Molecule 9 is a protein called RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace	
9	I	116	Total	C	H	N	O	S	0	0
			1822	582	880	168	181	11		

- Molecule 10 is a protein called RPB10.

Mol	Chain	Residues	Atoms					AltConf	Trace	
10	J	66	Total	C	H	N	O	S	0	0
			1068	339	544	88	91	6		

- Molecule 11 is a protein called RPB11.

Mol	Chain	Residues	Atoms					AltConf	Trace	
11	K	115	Total	C	H	N	O	S	0	0
			1862	593	942	152	173	2		

- Molecule 12 is a protein called RNA polymerase II subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace	
12	L	47	Total	C	H	N	O	S	0	0
			803	246	406	77	68	6		

- Molecule 13 is a protein called Transcription elongation factor SPT6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	1002	Total	C	H	N	O	0	0
			5267	2004	1259	1002	1002		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	SER	-	expression tag	UNP Q7KZ85
M	-1	ASN	-	expression tag	UNP Q7KZ85
M	0	ALA	-	expression tag	UNP Q7KZ85

- Molecule 14 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
14	N	140	4480	1376	1594	490	880	140	0	0

- Molecule 15 is a protein called Transcription elongation factor A protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	O	161	645	322	161	162	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	-2	SER	-	expression tag	UNP P23193
O	-1	ASN	-	expression tag	UNP P23193
O	0	ALA	-	expression tag	UNP P23193

- Molecule 16 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
16	P	16	502	148	170	49	119	16	0	0

- Molecule 17 is a protein called RNA polymerase-associated protein CTR9 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
17	Q	890	5356	1780	1796	890	890	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	1174	GLU	-	expression tag	UNP Q6PD62
Q	1175	ASN	-	expression tag	UNP Q6PD62
Q	1176	LEU	-	expression tag	UNP Q6PD62
Q	1177	TYR	-	expression tag	UNP Q6PD62

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	1178	PHE	-	expression tag	UNP Q6PD62
Q	1179	GLN	-	expression tag	UNP Q6PD62

- Molecule 18 is a protein called RNA polymerase-associated protein RTF1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
18	R	244	1467	488	491	244	244	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-2	SER	-	expression tag	UNP Q92541
R	-1	ASN	-	expression tag	UNP Q92541
R	0	ALA	-	expression tag	UNP Q92541

- Molecule 19 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
19	T	155	4885	1498	1719	629	884	155	0	0

- Molecule 20 is a protein called RNA polymerase-associated protein LEO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
20	U	104	626	208	210	104	104	0	0

- Molecule 21 is a protein called RNA polymerase II-associated factor 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
21	V	244	1457	488	481	244	244	0	0

- Molecule 22 is a protein called WDR61.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
22	W	300	1817	600	617	300	300	0	0

- Molecule 23 is a protein called Parafibromin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
23	X	43	259	86	87	43	43	0	0

- Molecule 24 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms						AltConf	Trace	
			Total	C	H	N	O	P			S
24	Z	307	4751	1495	2363	430	450	1	12	0	0

- Molecule 25 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
25	a	97	1643	506	841	155	138	3	0	0
25	e	97	1640	504	839	155	139	3	0	0

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 26 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
26	b	83	1372	418	710	129	114	1	0	0
26	f	78	1279	391	660	120	107	1	0	0

- Molecule 27 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace	
			Total	C	H	N			O
27	c	103	1642	501	847	155	139	0	0
27	g	105	1674	510	865	158	141	0	0

- Molecule 28 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	d	95	1519	469	774	134	140	2	0	0
28	h	93	1474	457	748	130	137	2	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	0	MET	-	initiating methionine	UNP P02281
d	29	THR	SER	engineered mutation	UNP P02281
h	0	MET	-	initiating methionine	UNP P02281
h	29	THR	SER	engineered mutation	UNP P02281

- Molecule 29 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
29	A	2	Total 2	Zn 2	0
29	B	1	Total 1	Zn 1	0
29	C	1	Total 1	Zn 1	0
29	I	2	Total 2	Zn 2	0
29	J	1	Total 1	Zn 1	0
29	R	1	Total 1	Zn 1	0

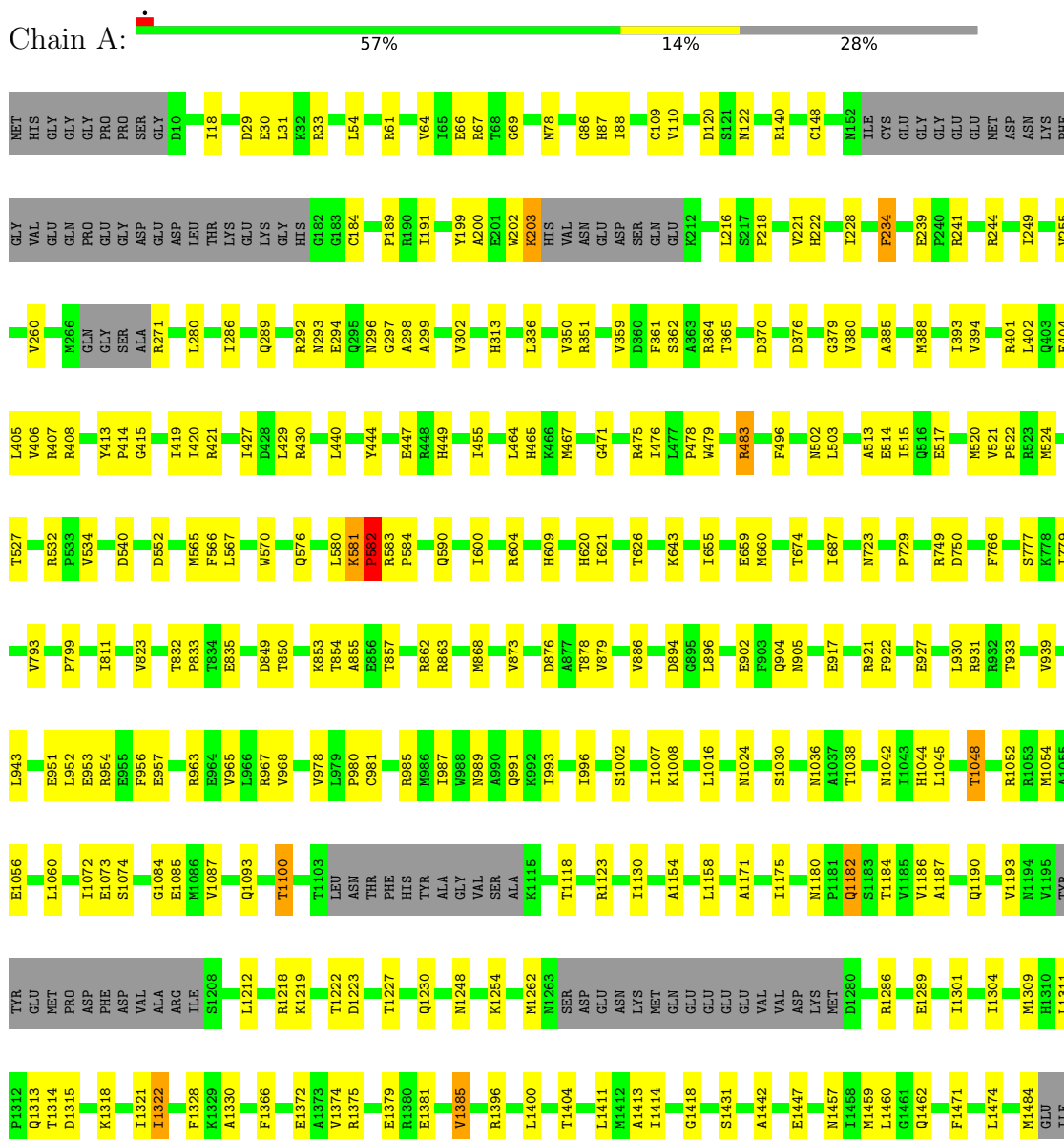
- Molecule 30 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
30	A	1	Total 1	Mg 1	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

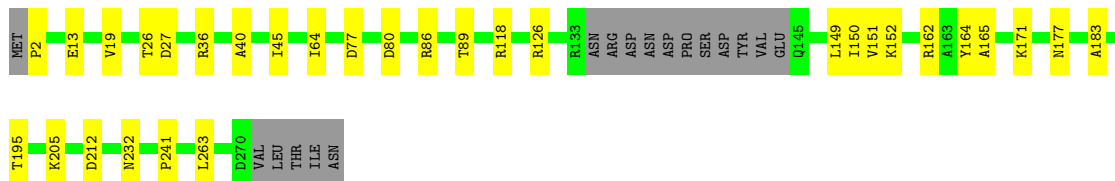
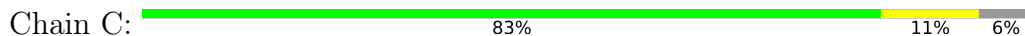
- Molecule 1: DNA-directed RNA polymerase subunit



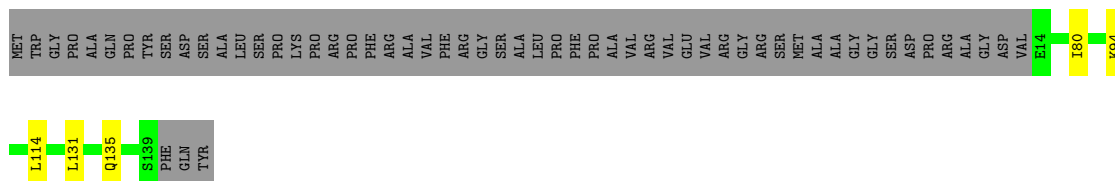




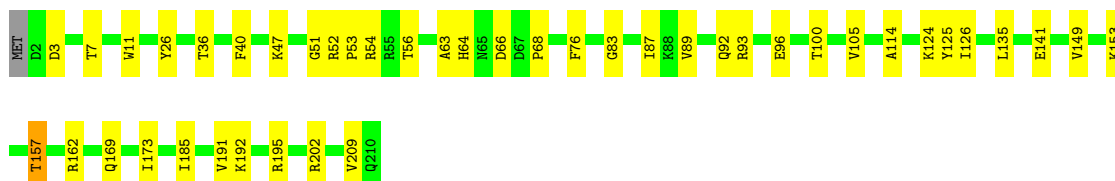
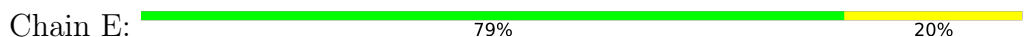
• Molecule 3: DNA-directed RNA polymerase II subunit RPB3



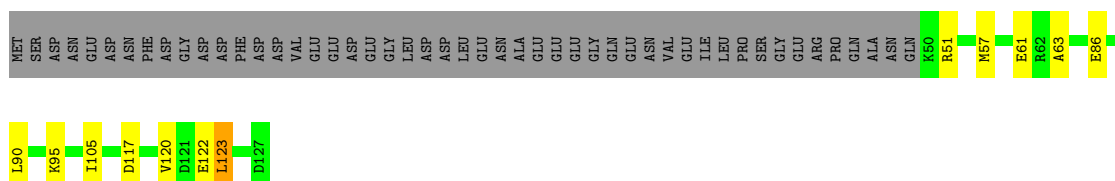
• Molecule 4: RPOL4c domain-containing protein



• Molecule 5: DNA-directed RNA polymerase II subunit E



• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2



• Molecule 7: DNA-directed RNA polymerase II subunit RPB7











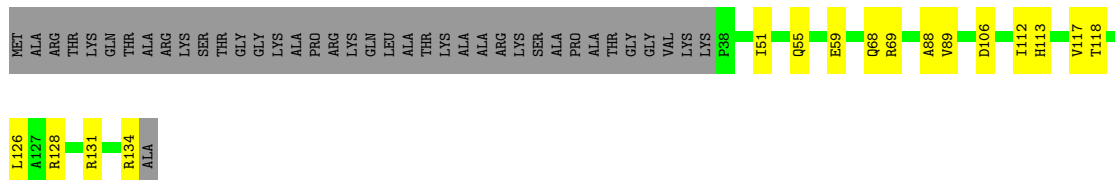




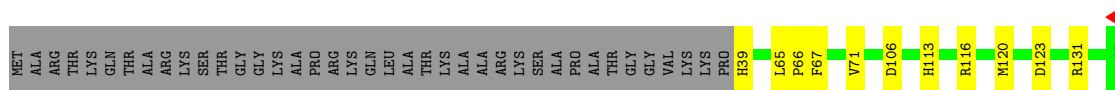




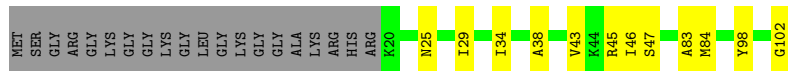
• Molecule 25: Histone H3.2



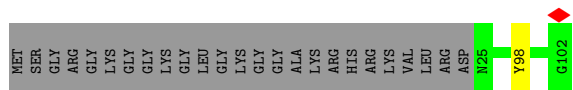
• Molecule 25: Histone H3.2



• Molecule 26: Histone H4



• Molecule 26: Histone H4



• Molecule 27: Histone H2A

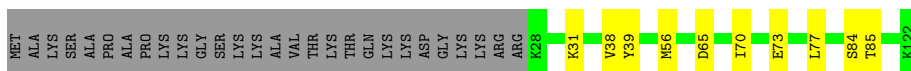


• Molecule 27: Histone H2A



• Molecule 28: Histone H2B 1.1





• Molecule 28: Histone H2B 1.1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	105420	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	52	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.466	Depositor
Minimum map value	-0.485	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.106	Depositor
Map size ( $\text{\AA}$ )	373.5, 373.5, 373.5	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.83, 0.83, 0.83	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.33	0/11437	0.49	4/15433 (0.0%)
2	B	0.35	0/9124	0.48	1/12313 (0.0%)
3	C	0.35	0/2115	0.39	0/2873
4	D	0.13	0/1017	0.35	0/1368
5	E	0.25	0/1751	0.45	0/2366
6	F	0.37	0/636	0.44	0/859
7	G	0.15	0/1364	0.35	0/1853
8	H	0.26	0/1219	0.38	0/1644
9	I	0.21	0/964	0.41	0/1305
10	J	0.41	0/533	0.47	0/719
11	K	0.36	0/939	0.43	0/1271
12	L	0.28	0/403	0.42	0/536
13	M	0.25	6/3995 (0.2%)	0.31	2/4971 (0.0%)
14	N	0.36	0/3226	0.89	0/4986
15	O	0.70	0/643	1.32	0/799
16	P	0.36	0/367	0.71	0/568
17	Q	0.15	0/3559	0.40	0/4447
18	R	0.16	0/974	0.42	0/1214
19	T	0.36	0/3564	0.82	0/5487
20	U	0.15	0/413	0.28	0/511
21	V	0.26	0/972	0.52	0/1208
22	W	0.10	0/1199	0.38	0/1497
23	X	0.16	0/171	0.35	0/212
24	Z	0.13	0/2414	0.33	0/3250
25	a	0.22	0/814	0.52	0/1092
25	e	0.20	0/812	0.35	0/1088
26	b	0.26	0/669	0.39	0/894
26	f	0.24	0/626	0.36	0/837
27	c	0.21	0/805	0.41	0/1088
27	g	0.22	0/819	0.43	0/1106
28	d	0.21	0/756	0.36	0/1015
28	h	0.25	0/737	0.42	0/993

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
All	All	0.30	6/59037 (0.0%)	0.52	7/79803 (0.0%)

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	A	0	2
2	B	0	3
7	G	0	1
10	J	0	1
13	M	0	1
14	N	0	1
21	V	0	1
All	All	0	10

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	M	1335	ILE	N-CA	7.65	1.55	1.46
13	M	1334	ASN	CA-C	6.24	1.61	1.52
13	M	1335	ILE	C-N	5.51	1.41	1.33
13	M	1335	ILE	CA-C	5.39	1.59	1.52
13	M	1333	HIS	C-N	5.38	1.41	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	581	LYS	C-N-CD	-16.57	57.08	125.00
1	A	581	LYS	CA-C-N	10.09	132.45	119.84
1	A	581	LYS	C-N-CA	10.09	132.45	119.84
1	A	582	PRO	CA-N-CD	-7.79	101.09	112.00
13	M	1335	ILE	N-CA-C	6.15	122.14	109.34

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	244	ARG	Sidechain
1	A	430	ARG	Sidechain

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Mol	Chain	Res	Type	Group
2	B	491	ARG	Sidechain
2	B	743	ARG	Sidechain
2	B	859	ARG	Sidechain

## 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	11255	11388	11374	234	0
2	B	8947	9002	8994	124	0
3	C	2072	2024	2019	23	0
4	D	1004	981	980	4	0
5	E	1720	1738	1737	29	0
6	F	626	658	657	10	0
7	G	1333	1321	1321	18	0
8	H	1197	1157	1156	10	0
9	I	942	880	872	17	0
10	J	524	544	540	11	0
11	K	920	942	942	19	0
12	L	397	406	405	4	0
13	M	4008	1259	1035	9	0
14	N	2886	1594	1596	163	0
15	O	645	0	171	30	0
16	P	332	170	169	3	0
17	Q	3560	1796	940	4	0
18	R	976	491	255	1	0
19	T	3166	1719	1720	142	0
20	U	416	210	111	2	0
21	V	976	481	240	3	0
22	W	1200	617	341	1	0
23	X	172	87	44	0	0
24	Z	2388	2363	2360	43	0
25	a	802	841	841	16	0
25	e	801	839	838	8	0
26	b	662	710	709	10	0
26	f	619	660	659	1	0
27	c	795	847	846	7	0
27	g	809	865	864	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	d	745	774	773	8	0
28	h	726	748	747	11	0
29	A	2	0	0	0	0
29	B	1	0	0	0	0
29	C	1	0	0	0	0
29	I	2	0	0	0	0
29	J	1	0	0	0	0
29	R	1	0	0	0	0
30	A	1	0	0	0	0
All	All	57630	48112	46256	842	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 842 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:A:729:PRO:CG	15:O:249:GLN:O	1.79	1.27
1:A:1314:THR:C	15:O:295:GLY:HA3	1.56	1.27
1:A:729:PRO:HB3	15:O:247:GLU:O	1.38	1.21
1:A:203:LYS:NZ	19:T:-67:DC:OP1	1.75	1.20
1:A:729:PRO:CB	15:O:247:GLU:O	1.90	1.17

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	1408/1984 (71%)	1297 (92%)	109 (8%)	2 (0%)	48 80
2	B	1107/1251 (88%)	1022 (92%)	85 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	254/275 (92%)	241 (95%)	13 (5%)	0	100	100
4	D	124/184 (67%)	118 (95%)	6 (5%)	0	100	100
5	E	207/210 (99%)	199 (96%)	8 (4%)	0	100	100
6	F	76/127 (60%)	71 (93%)	5 (7%)	0	100	100
7	G	169/172 (98%)	160 (95%)	9 (5%)	0	100	100
8	H	147/150 (98%)	138 (94%)	8 (5%)	1 (1%)	18	53
9	I	114/125 (91%)	100 (88%)	14 (12%)	0	100	100
10	J	64/67 (96%)	60 (94%)	3 (5%)	1 (2%)	7	34
11	K	113/117 (97%)	106 (94%)	7 (6%)	0	100	100
12	L	45/58 (78%)	39 (87%)	6 (13%)	0	100	100
13	M	976/1729 (56%)	903 (92%)	72 (7%)	1 (0%)	48	80
15	O	157/304 (52%)	154 (98%)	3 (2%)	0	100	100
17	Q	888/1179 (75%)	832 (94%)	56 (6%)	0	100	100
18	R	240/713 (34%)	227 (95%)	13 (5%)	0	100	100
20	U	98/666 (15%)	87 (89%)	11 (11%)	0	100	100
21	V	236/531 (44%)	200 (85%)	34 (14%)	2 (1%)	16	50
22	W	298/305 (98%)	271 (91%)	27 (9%)	0	100	100
23	X	41/531 (8%)	38 (93%)	3 (7%)	0	100	100
24	Z	300/1087 (28%)	274 (91%)	25 (8%)	1 (0%)	36	70
25	a	95/136 (70%)	90 (95%)	5 (5%)	0	100	100
25	e	95/136 (70%)	92 (97%)	3 (3%)	0	100	100
26	b	81/103 (79%)	80 (99%)	1 (1%)	0	100	100
26	f	76/103 (74%)	72 (95%)	4 (5%)	0	100	100
27	c	101/130 (78%)	97 (96%)	4 (4%)	0	100	100
27	g	103/130 (79%)	99 (96%)	4 (4%)	0	100	100
28	d	93/123 (76%)	88 (95%)	5 (5%)	0	100	100
28	h	91/123 (74%)	87 (96%)	4 (4%)	0	100	100
All	All	7797/12749 (61%)	7242 (93%)	547 (7%)	8 (0%)	49	80

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	582	PRO

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Mol	Chain	Res	Type
13	M	1334	ASN
21	V	300	ASN
8	H	77	PRO
1	A	478	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1245/1761 (71%)	1222 (98%)	23 (2%)	51	77
2	B	983/1084 (91%)	977 (99%)	6 (1%)	78	88
3	C	235/252 (93%)	233 (99%)	2 (1%)	70	85
4	D	109/160 (68%)	109 (100%)	0	100	100
5	E	191/192 (100%)	187 (98%)	4 (2%)	47	75
6	F	68/111 (61%)	66 (97%)	2 (3%)	37	70
7	G	146/153 (95%)	144 (99%)	2 (1%)	59	80
8	H	130/131 (99%)	130 (100%)	0	100	100
9	I	104/112 (93%)	103 (99%)	1 (1%)	68	84
10	J	55/56 (98%)	55 (100%)	0	100	100
11	K	104/106 (98%)	103 (99%)	1 (1%)	68	84
12	L	44/55 (80%)	44 (100%)	0	100	100
24	Z	257/939 (27%)	254 (99%)	3 (1%)	63	82
25	a	85/111 (77%)	85 (100%)	0	100	100
25	e	84/111 (76%)	83 (99%)	1 (1%)	63	82
26	b	68/79 (86%)	68 (100%)	0	100	100
26	f	63/79 (80%)	63 (100%)	0	100	100
27	c	82/102 (80%)	82 (100%)	0	100	100
27	g	83/102 (81%)	83 (100%)	0	100	100
28	d	81/103 (79%)	80 (99%)	1 (1%)	63	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	h	79/103 (77%)	79 (100%)	0	100	100
All	All	4296/5902 (73%)	4250 (99%)	46 (1%)	63	83

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1150	ARG
6	F	90	LEU
3	C	13	GLU
5	E	141	GLU
7	G	86	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	32	ASN
27	c	38	ASN
11	K	2	ASN
24	Z	642	HIS
26	f	64	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	P	15/16 (93%)	4 (26%)	2 (13%)

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	P	41	U
16	P	42	U
16	P	44	U
16	P	46	C

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	P	43	U
16	P	45	C

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

3 non-standard protein/DNA/RNA residues are modelled in this entry.

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
1	TPO	A	1525	1	8,10,11	1.64	1 (12%)	10,14,16	2.08	1 (10%)
24	TPO	Z	775	24	8,10,11	1.66	1 (12%)	10,14,16	1.70	1 (10%)
1	SEP	A	1547	1	8,9,10	1.62	1 (12%)	7,12,14	1.35	1 (14%)

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
1	TPO	A	1525	1	-	2/9/11/13	-
24	TPO	Z	775	24	-	4/9/11/13	-
1	SEP	A	1547	1	-	0/6/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1547	SEP	P-O1P	3.54	1.61	1.50
24	Z	775	TPO	P-O1P	3.53	1.61	1.50
1	A	1525	TPO	P-O1P	3.51	1.61	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1525	TPO	P-OG1-CB	-5.80	107.56	123.33
24	Z	775	TPO	P-OG1-CB	-4.44	111.27	123.33
1	A	1547	SEP	OG-CB-CA	2.94	111.00	108.14

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1525	TPO	C-CA-CB-CG2
24	Z	775	TPO	CB-OG1-P-O2P
1	A	1525	TPO	N-CA-CB-CG2
24	Z	775	TPO	CB-OG1-P-O1P
24	Z	775	TPO	CB-OG1-P-O3P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	Z	775	TPO	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 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.

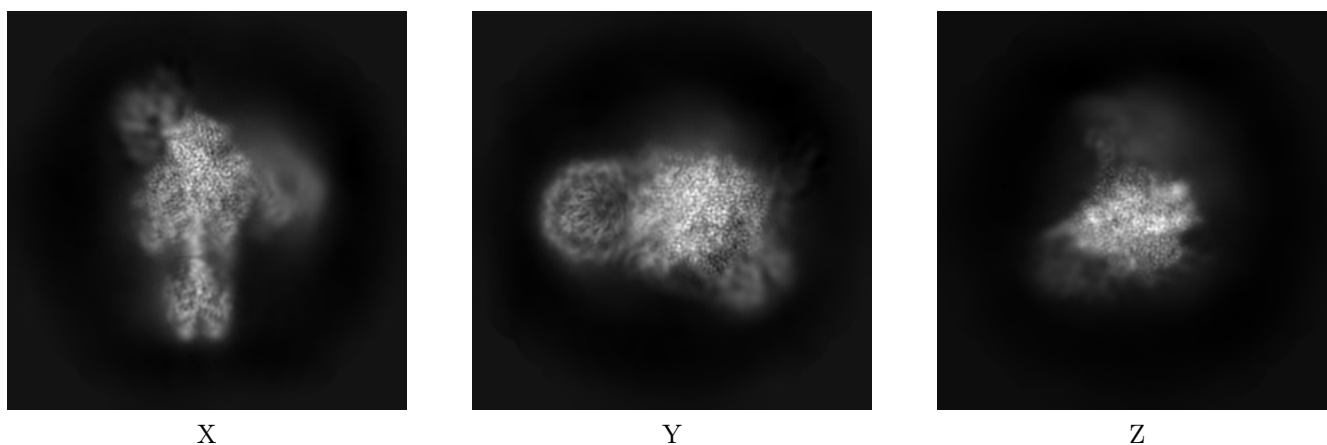
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26620. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

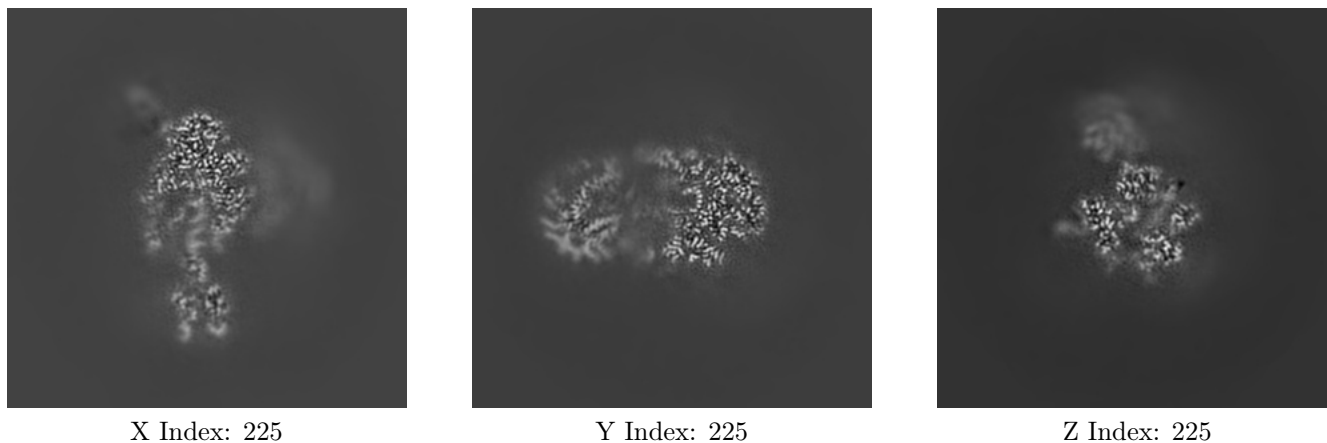
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

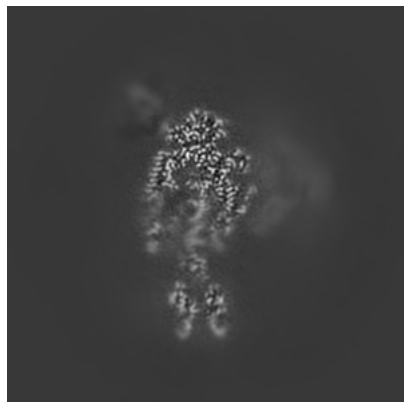
#### 6.2.1 Primary map



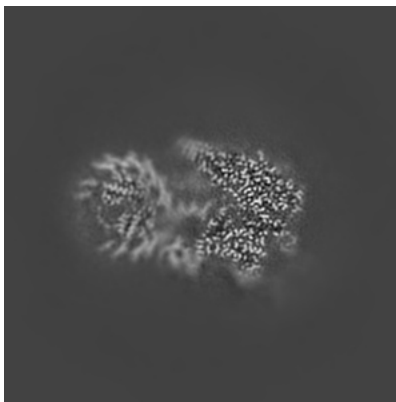
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

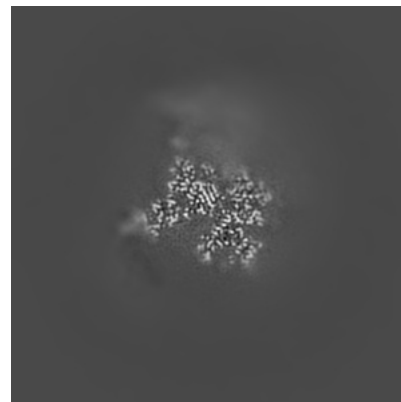
### 6.3.1 Primary map



X Index: 222



Y Index: 214

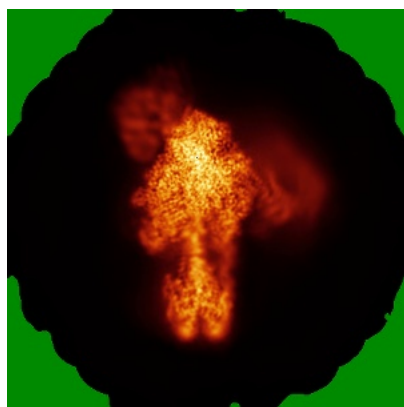


Z Index: 266

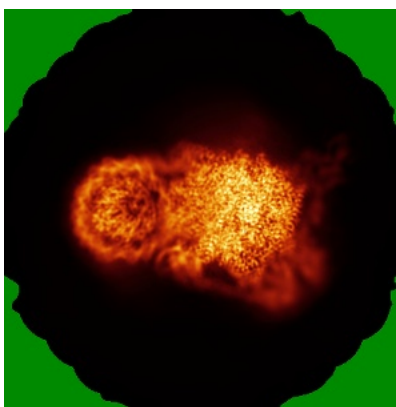
The images above show the largest variance slices of the map in three orthogonal directions.

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

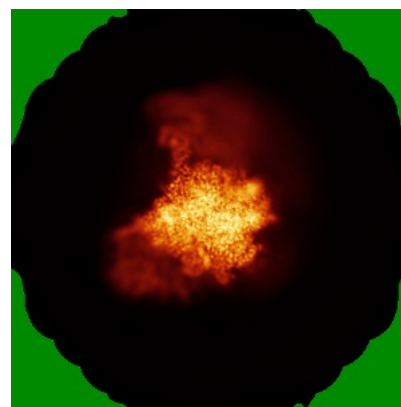
### 6.4.1 Primary map



X



Y



Z

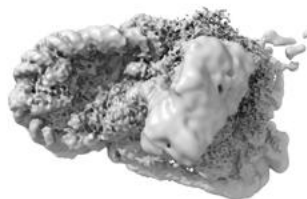
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

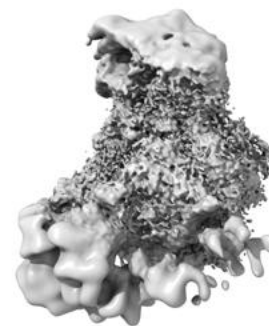
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.106. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

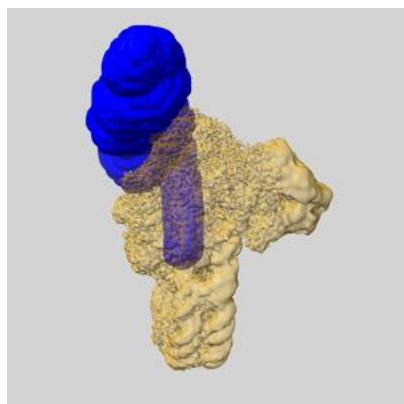
## 6.6 Mask visualisation [i](#)

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

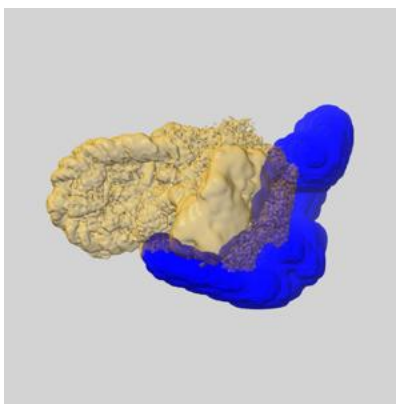
A mask typically either:

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

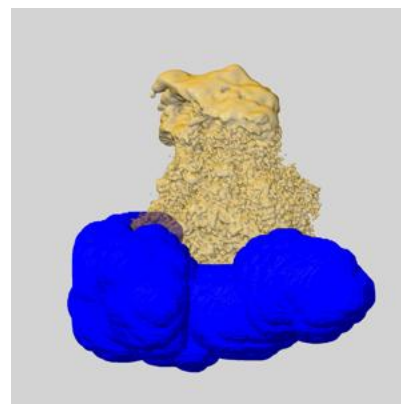
### 6.6.1 emd\_26620\_msk\_1.map [i](#)



X

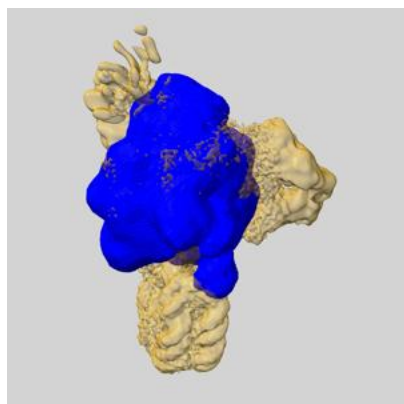


Y

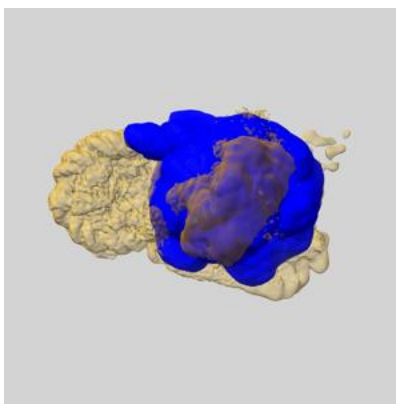


Z

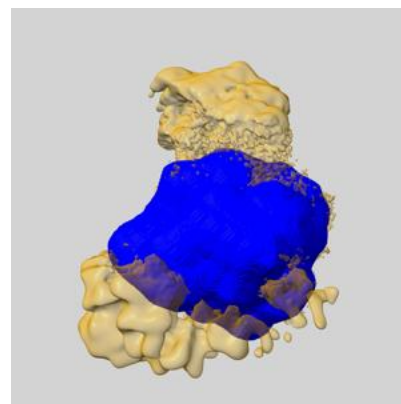
### 6.6.2 emd\_26620\_msk\_2.map [i](#)



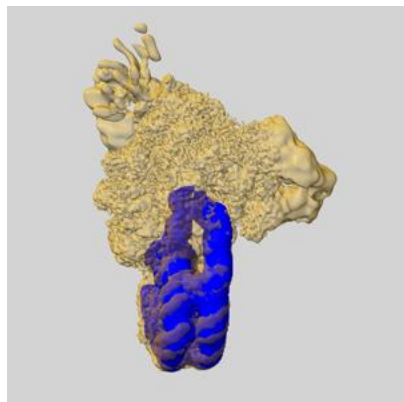
X



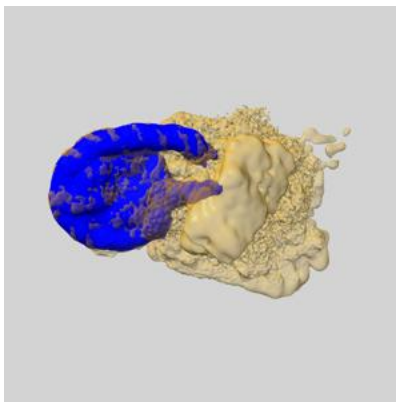
Y



Z

6.6.3 emd\_26620\_msk\_3.map [i](#)

X



Y

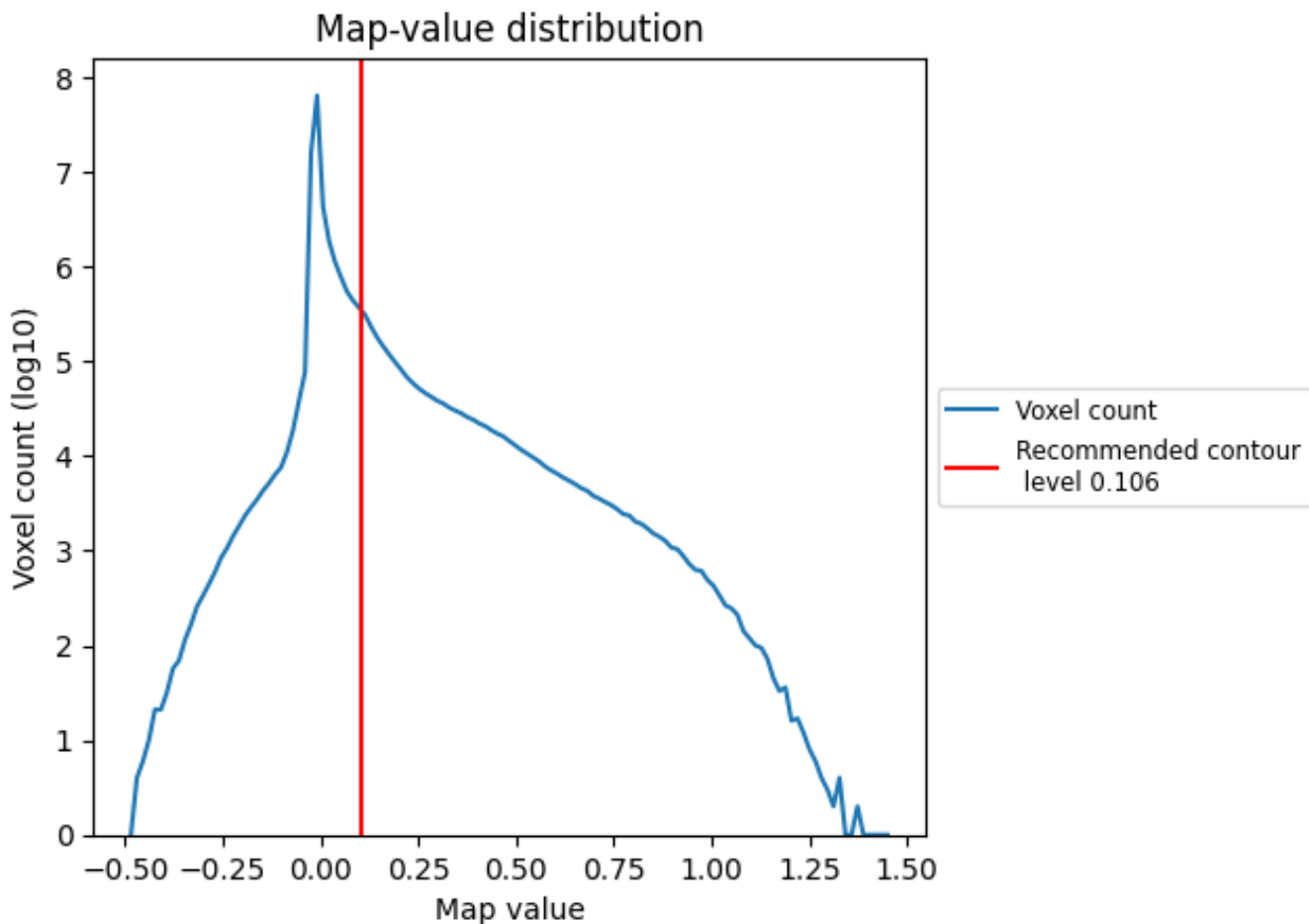


Z

## 7 Map analysis [i](#)

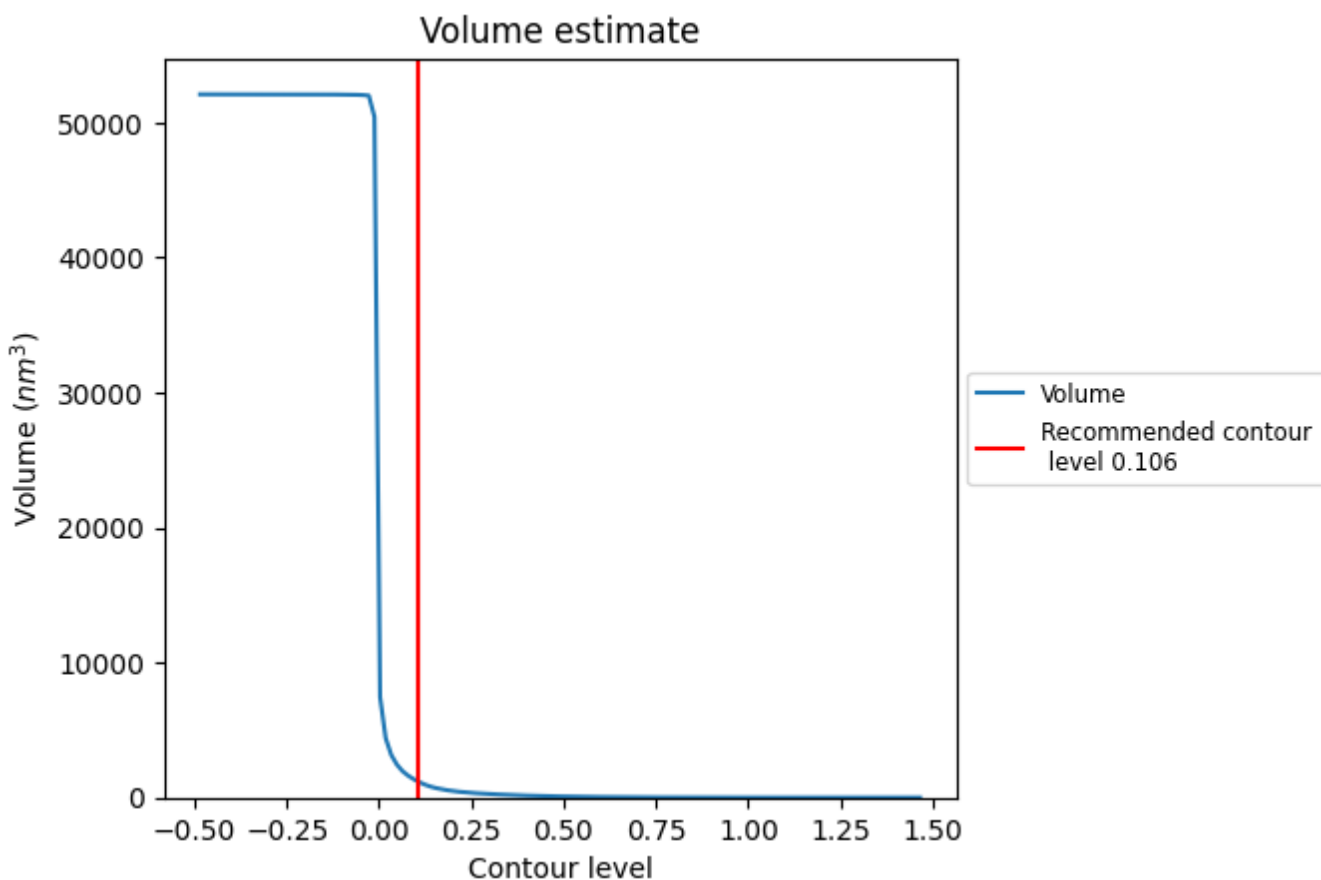
This section contains the results of statistical analysis of the map.

### 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.

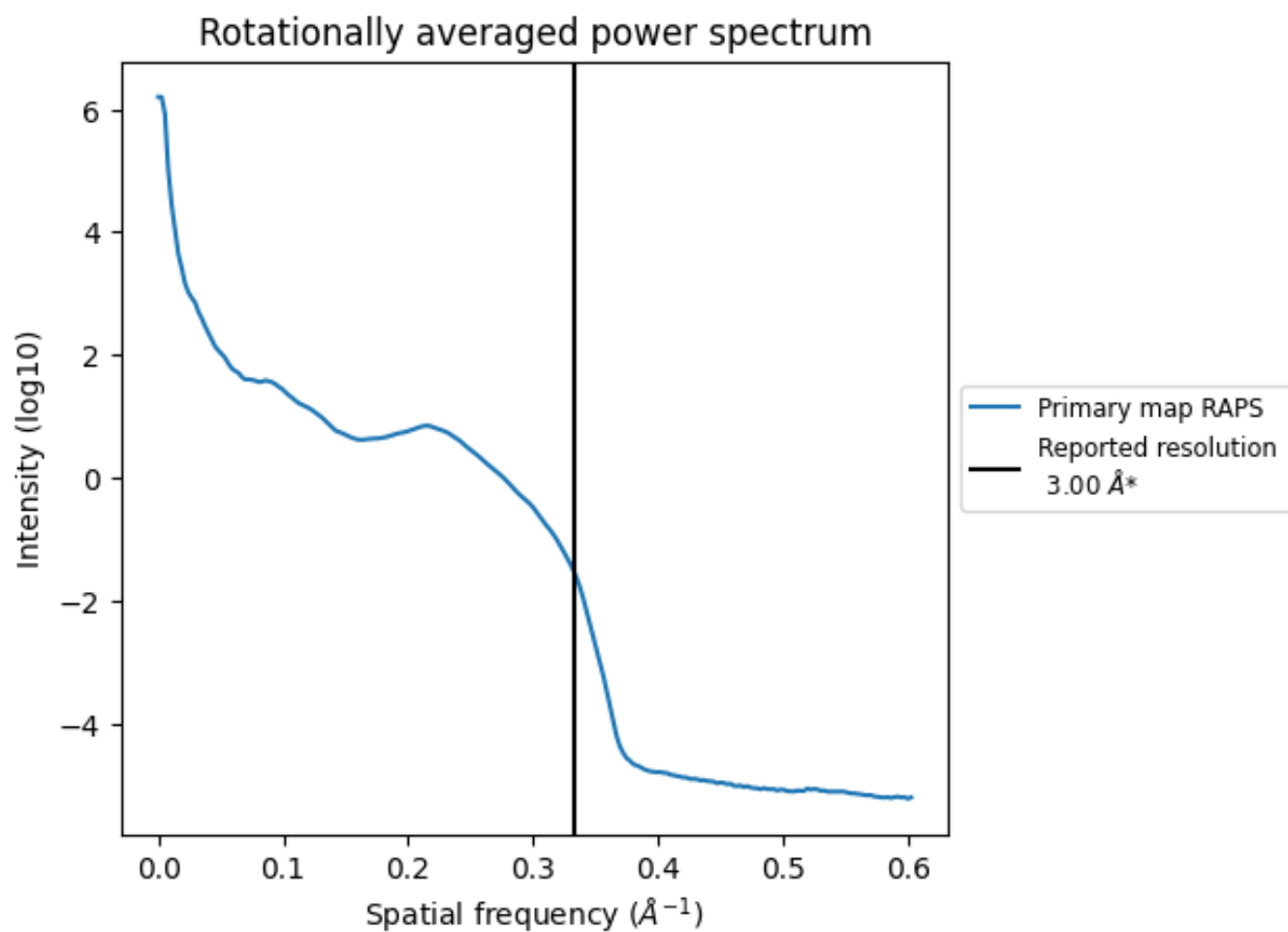
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is  $1190 \text{ nm}^3$ ; this corresponds to an approximate mass of 1075 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 0.333 Å<sup>-1</sup>

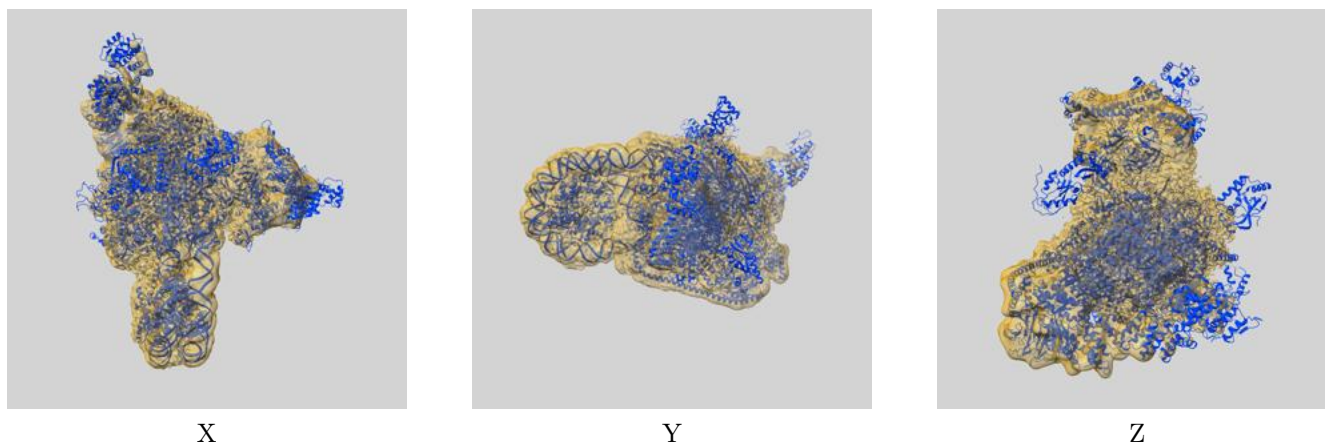
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

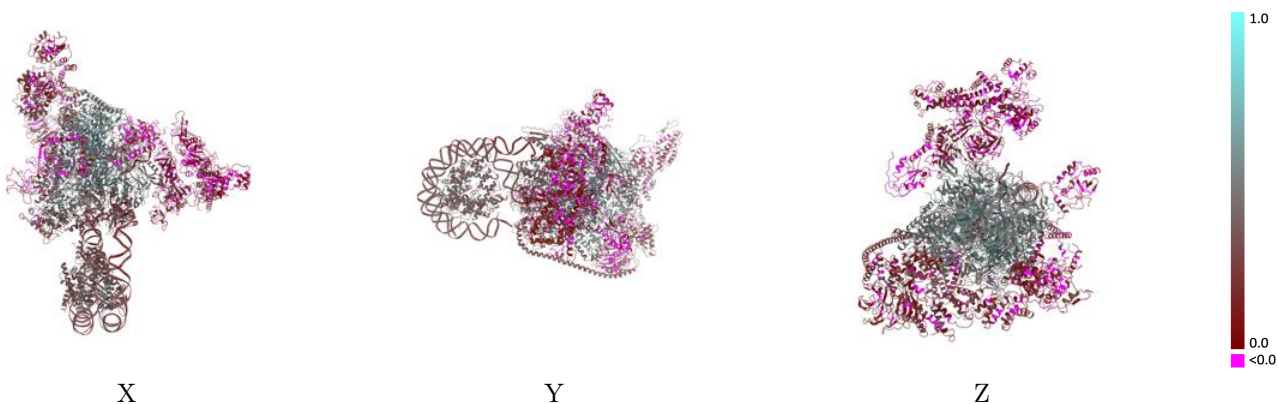
This section contains information regarding the fit between EMDB map EMD-26620 and PDB model 7UNC. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlay [i](#)



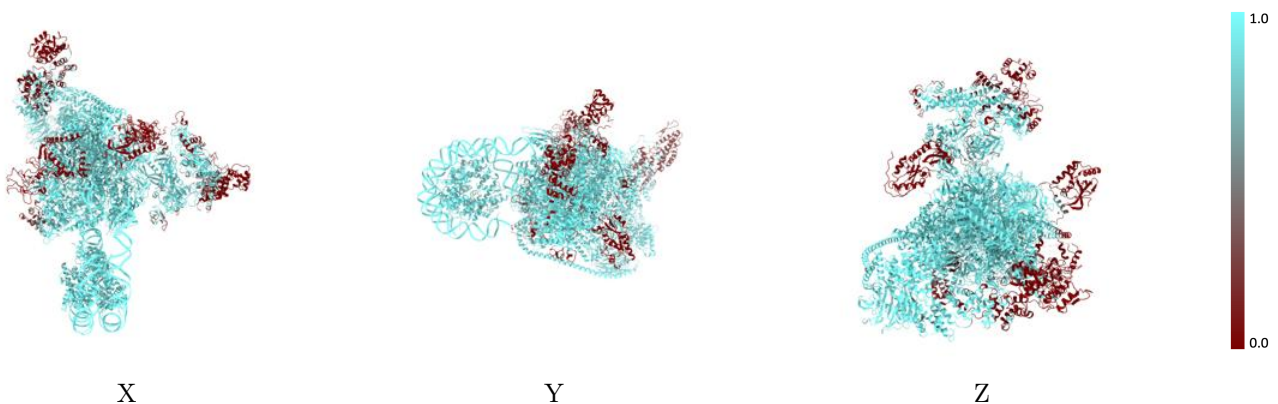
The images above show the 3D surface view of the map at the recommended contour level 0.106 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



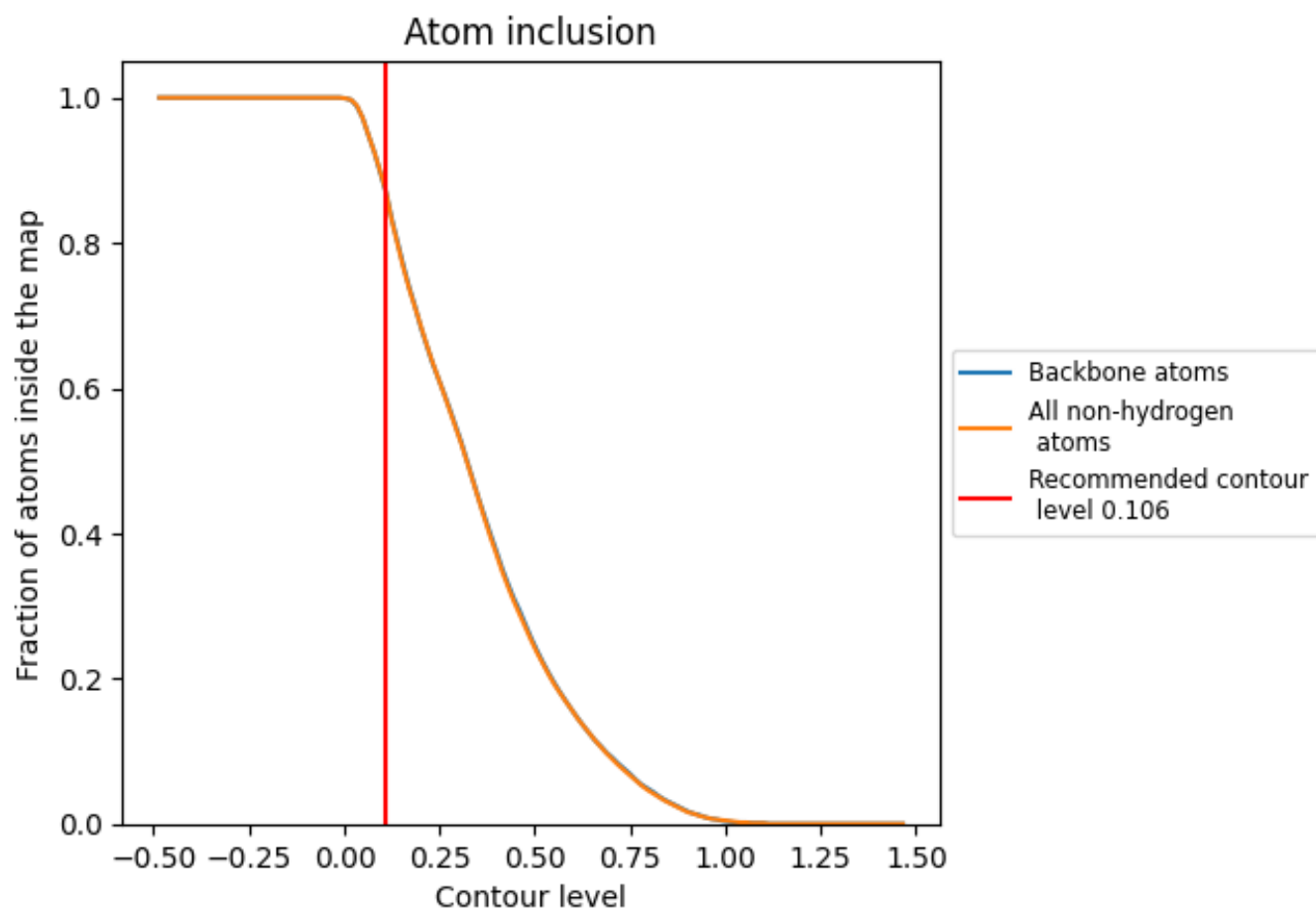
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.106).



































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 88% 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 (0.106) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8780	 0.3440
A	 0.9760	 0.4790
B	 0.9910	 0.4950
C	 0.9950	 0.5280
D	 0.9570	 0.1580
E	 0.9910	 0.3560
F	 0.9920	 0.5280
G	 0.9770	 0.2300
H	 0.9830	 0.4160
I	 0.9970	 0.3840
J	 0.9820	 0.5340
K	 0.9920	 0.5250
L	 0.9760	 0.4380
M	 0.4380	 0.0470
N	 0.9980	 0.2890
O	 0.2820	 0.1330
P	 1.0000	 0.4100
Q	 0.6660	 0.1610
R	 0.1910	 0.0900
T	 1.0000	 0.3130
U	 0.0050	 0.0230
V	 0.2770	 0.1000
W	 0.9510	 0.1380
X	 0.9830	 0.2460
Z	 0.7620	 0.1280
a	 0.9870	 0.3510
b	 0.9890	 0.3960
c	 0.9700	 0.3650
d	 0.9740	 0.3460
e	 0.9730	 0.3290
f	 0.9830	 0.3670
g	 0.9750	 0.3930
h	 0.9890	 0.3890

