



wwPDB EM Validation Summary Report ⓘ

Sep 2, 2026 – 02:12 PM EDT

PDB ID : 36RS / pdb_000036rs
EMDB ID : EMD-77811
Title : Cryo-EM structure of *Saccharomyces cerevisiae* RNA polymerase II without stalk (no Rpb4/Rpb7)
Authors : Fordjour, G.N.R.; Murakami, K.; Armache, J.-P.; Murakami, K.S.
Deposited on : 2026-06-29
Resolution : 6.75 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
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

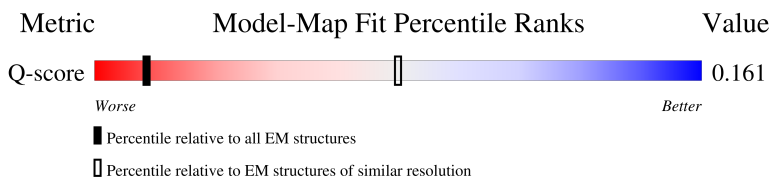
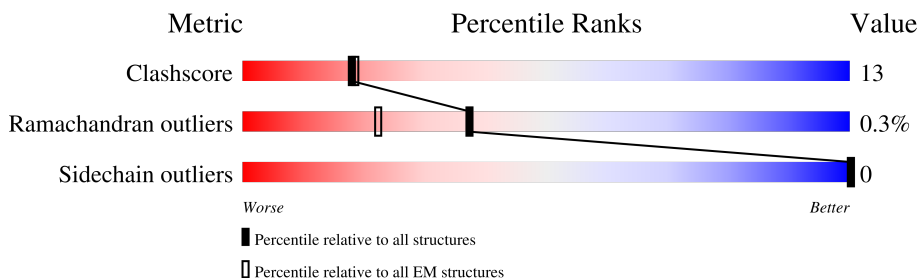
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.75 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.



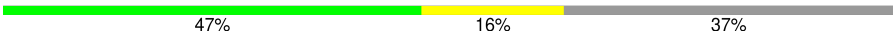
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	480 (6.25 - 7.25)

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	A	1733	
2	B	1224	
3	C	318	
4	E	215	

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Mol	Chain	Length	Quality of chain
5	F	155	
6	H	146	
7	I	122	
8	J	70	
9	K	120	
10	L	70	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 28625 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 DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1419	Total	C	N	O	S	0	0
			11135	7014	1944	2115	62		

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1148	Total	C	N	O	S	0	0
			9107	5755	1592	1705	55		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	265	Total	C	N	O	S	0	0
			2086	1312	347	414	13		

- Molecule 4 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	214	Total	C	N	O	S	0	0
			1752	1111	309	321	11		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	87	Total	C	N	O	S	0	0
			705	451	119	132	3		

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	136	Total	C	N	O	S	0	0
			1089	685	184	215	5		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	114	Total	C	N	O	S	0	0
			927	571	168	178	10		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	66	Total	C	N	O	S	0	0
			540	345	94	95	6		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	115	Total	C	N	O	S	0	0
			924	593	157	172	2		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	44	Total	C	N	O	S	0	0
			352	217	70	61	4		

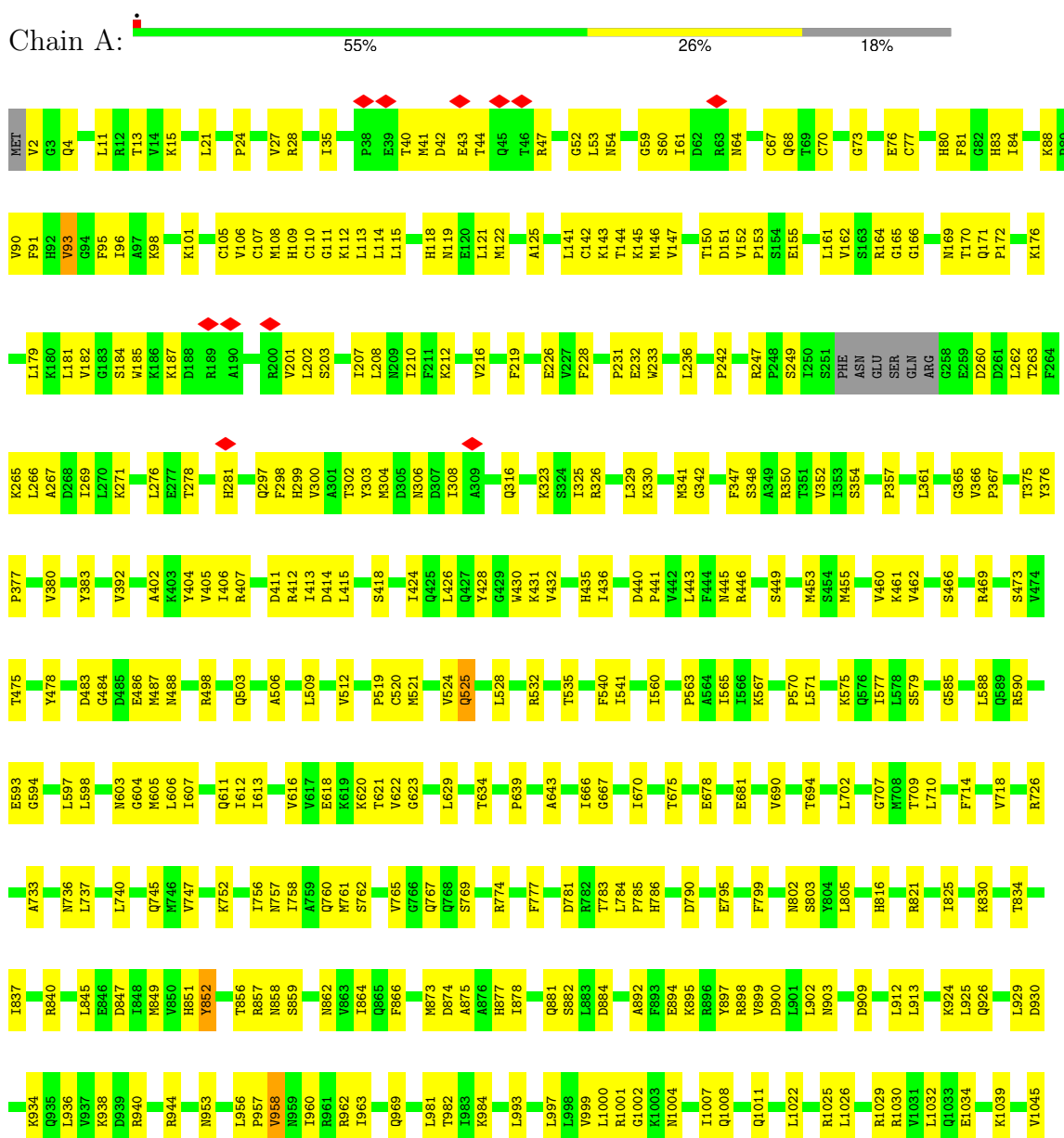
- Molecule 11 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
11	A	2	Total	Zn	0
			2	2	
11	B	1	Total	Zn	0
			1	1	
11	C	1	Total	Zn	0
			1	1	
11	I	2	Total	Zn	0
			2	2	
11	J	1	Total	Zn	0
			1	1	
11	L	1	Total	Zn	0
			1	1	

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: DNA-directed RNA polymerase II subunit RPB1

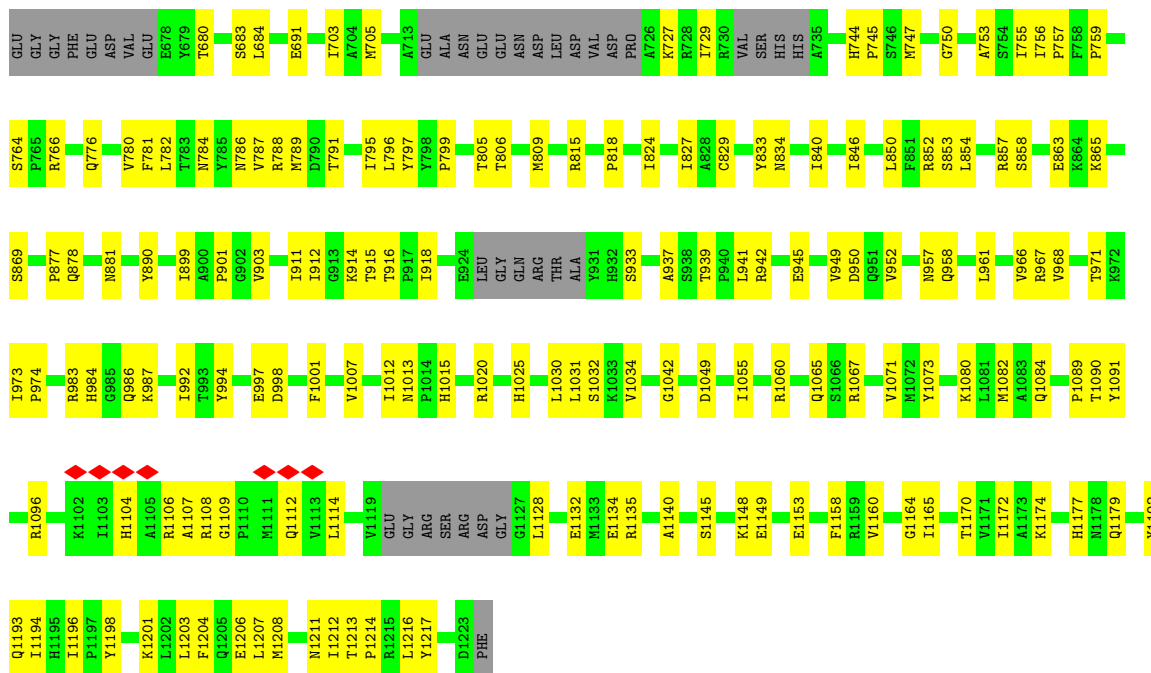


L1046	T1142	C1240		VAL	SER		HIS
E1050	S1145	R1241	T1377	LYS	PRO	PRO	ASN
A1051	V1146	V1242	L1381	GLU	THR	THR	GLU
Q1052	T1147	V1243	L1381	ASP	TYR	TYR	ASN
F1053		V1244	V1384	LEU	SER	PRO	ASN
S1056	I1152	P1245		MET	PRO	PRO	GLN
V1057	Y1153	LYS	L1397	PHE	THR	THR	SER
V1058	Y1154	SER	M1398	SER	SER	SER	ARG
H1059	Y1155	LEU	M1399	PRO	PRO	PRO	
P1060	P1156	ASP	C1400	ALA	ALA	TYR	
V1066	T1161	GLU	E1404	SER	SER	PRO	
A1069	V1162	THR	T1405	THR	THR	THR	
I1072	I1163	GLU	V1406	GLY	THR	THR	
T1077	D1166	A1254	E1407	SER	SER	PRO	
L1081	D1170	E1255	L1408	ASN	PRO	PRO	
THR	S1175	E1256	L1409	ASP	SER	PRO	
PHE	LEU	M1259	A1416	MET	SER	PRO	
HIS	ASP	K1262	S1425	ALA	THR	THR	
ALA	GLU	I1263	M1433	GLY	THR	THR	
GLY	GLU	E1264	M1444	PHE	PRO	PRO	
VAL	GLN	R1261	I1445	THR	SER	PRO	
ALA	SER	V1282	M1454	TYR	PRO	PRO	
ALA	F1185	K1290	PRO	ALA	THR	THR	
LYS	Q1188	Y1298	GLU	ASP	PRO	PRO	
K1093	S1189	E1307	GLN	GLY	THR	THR	
V1094	P1190	T1308	LYS	GLY	PRO	PRO	
T1095	W1191	D1309	ILE	ALA	SER	PRO	
S1096	L1192	G1310	THR	THR	THR	THR	
G1097	L1193	V1311	SER	SER	SER	PRO	
V1098	R1194	N1312	ILE	PRO	PRO	THR	
R1100	L1195	L1313	GLU	PHE	SER	THR	
V1107	E1196	S1314	ASP	GLY	THR	THR	
M1111	L1197	T1318	GLY	ALA	PRO	PRO	
K1112	D1198	I1327	GLY	GLY	PRO	PRO	
P1114	R1199	Y1328	VAL	PRO	THR	THR	
S1115	G1210	T1329	THR	THR	THR	THR	
L1116	M1209	N1330	PRO	SER	TYR	TYR	
T1117	G1214	S1331	PRO	SER	PRO	PRO	
V1118	E1214	I1335	TYR	GLY	THR	THR	
Y1119	K1217	M1336	ASN	PHE	SER	PRO	
Q1128	L1224	E1337	GLU	GLY	PRO	PRO	
K1132	W1228	V1338	VAL	VAL	ALA	LYS	
R1135	S1229	G1340	GLY	THR	GLN	ASP	
	I1237	E1342	ALA	THR	GLY	GLY	
	I1238	L1371	ASP	PRO	GLU	GLN	
	R1239	V1372	LEU	THR	THR	THR	
		D1373	ASP	TYR	SER	LYS	

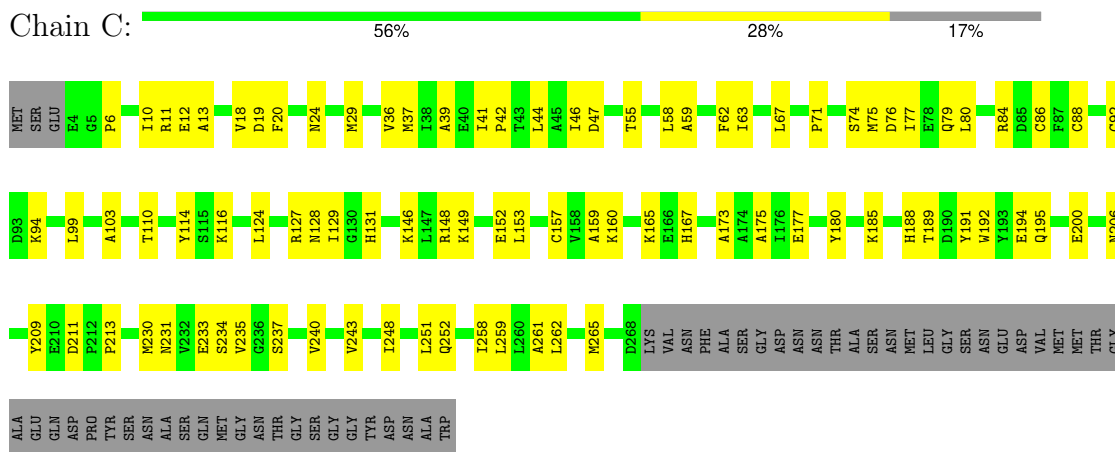
● Molecule 2: DNA-directed RNA polymerase II subunit RPB2



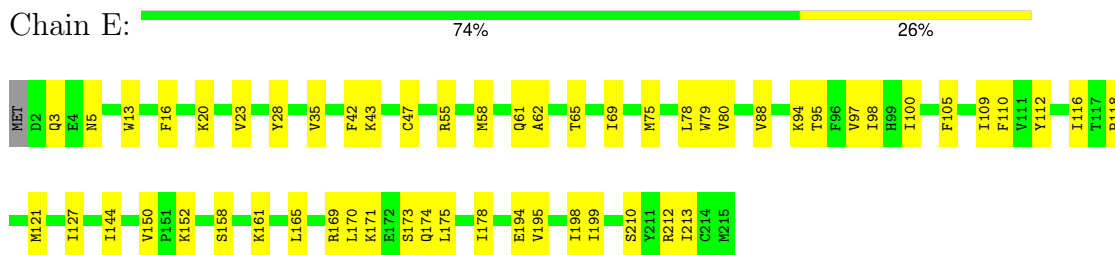
MET	K99	L189	T292	I428	V570
SER	K99	L189	P293	F429	P571
ASP	P100	E194	D294	R430	
LEU	M101	C195	G295	Y431	
ALA	V102	P196	E296	M432	
ASN	N103	Y202	I297	T435	
SER	E104		L298	V581	
GLY	L112		T301	V582	
TYR	A117		C302	N583	
ASP	R118		Y303	G584	
GLU	R119		R310	V585	
ASP	R120		V318	N449	
PRO	M121		I334	I453	
THR	L122		G335	R601	
GLY	T123		R336	T602	
PHE	Y124		R337	L603	
GLU	S125		T339	R604	
D20	V130		G342	E467	
E21	D131		I343	E468	
S22	V132		K344	K471	
A23	K133		R348	S474	
P24	LYS		I349	V479	
I25	ARG		Q350	T500	
D29	T136		Y351	P501	
R39	Y137		H363	L502	
Q46	E138		T364	GLY	
Q60	A139		T365	ARG	
D66	Y142		R261	ASP	
G67	P143		GLY	GLY	
T68	G144		E371	LYS	
L69	R145		S372	LEU	
I70	E146		R373	A509	
L71	L147		K374	R512	
E72	K148		A271	E544	
Q73	E150		L272	S517	
L74	ILE		L273	L521	
H77	GLU		P274	G534	
E80	SER		Y275	I545	
S81	ASP		I276	M552	
D82	D159		R277	I555	
R83	K164		T280	S559	
I84	I167		P281	M563	
K87	G168		I282	D668	
Y88	R169		V283	ILE	
E89	M173		I284		
I90	R175		L285		
S91	F92		F286		
G93	S176		L289		
K94			G290		
			I291		



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

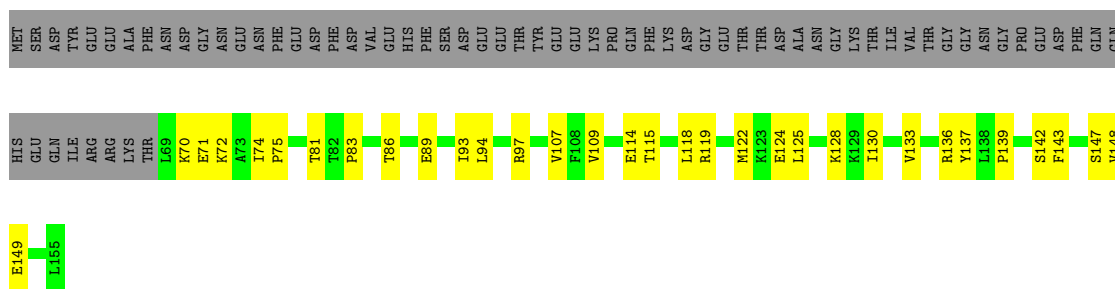


• Molecule 4: DNA-directed RNA polymerases I, II, and III subunit RPABC1

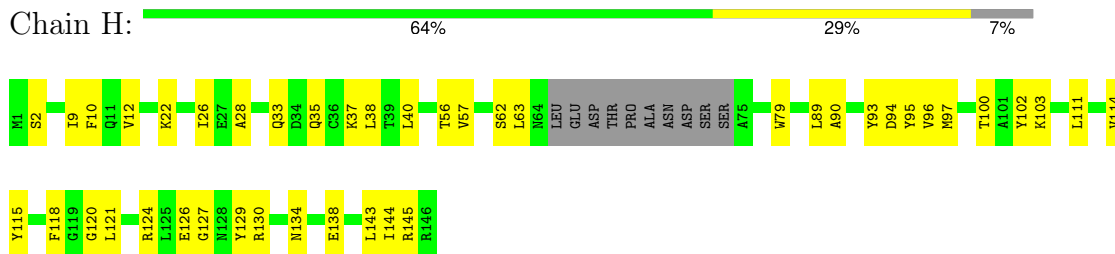


• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC2

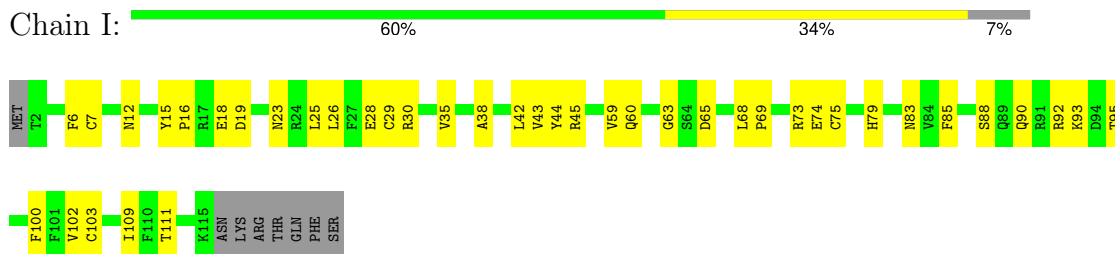




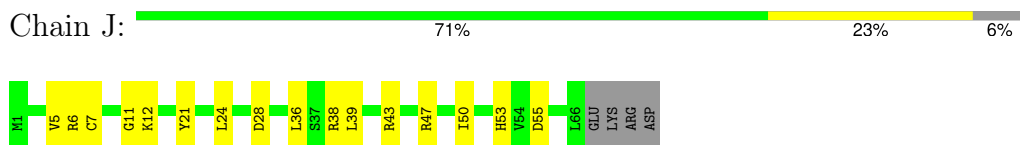
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC3



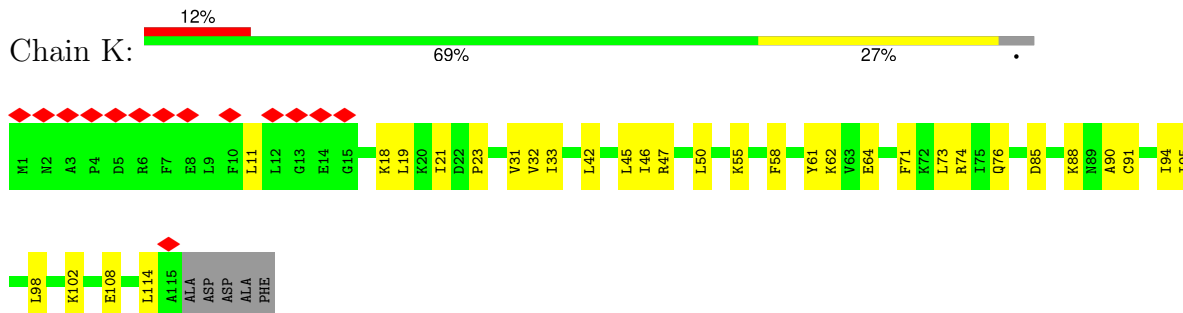
- Molecule 7: DNA-directed RNA polymerase II subunit RPB9



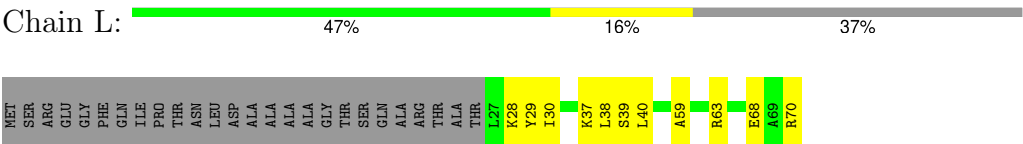
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC5



- Molecule 9: DNA-directed RNA polymerase II subunit RPB11



- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39868	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.582	Depositor
Minimum map value	-0.121	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	377.6, 377.6, 377.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.944, 0.944, 0.944	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	0.15	0/11334	0.44	2/15332 (0.0%)
2	B	0.13	0/9280	0.38	0/12516
3	C	0.12	0/2124	0.34	0/2879
4	E	0.12	0/1788	0.36	0/2406
5	F	0.14	0/717	0.45	0/967
6	H	0.13	0/1107	0.39	0/1498
7	I	0.11	0/945	0.32	0/1273
8	J	0.12	0/549	0.35	0/738
9	K	0.11	0/942	0.30	0/1272
10	L	0.14	0/354	0.46	0/468
All	All	0.14	0/29140	0.40	2/39349 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	CYS	CA-C-N	5.04	131.17	121.54
1	A	67	CYS	C-N-CA	5.04	131.17	121.54

There are no chirality outliers.

There are no planarity outliers.

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	A	11135	0	11177	354	0
2	B	9107	0	9091	245	0
3	C	2086	0	2045	66	0
4	E	1752	0	1776	39	0
5	F	705	0	731	23	0
6	H	1089	0	1063	36	0
7	I	927	0	880	30	0
8	J	540	0	553	12	0
9	K	924	0	934	26	0
10	L	352	0	374	9	0
11	A	2	0	0	0	0
11	B	1	0	0	0	0
11	C	1	0	0	0	0
11	I	2	0	0	0	0
11	J	1	0	0	0	0
11	L	1	0	0	0	0
All	All	28625	0	28624	759	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 13.

The worst 5 of 759 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:583:ASN:HD21	2:B:628:THR:H	1.26	0.83
4:E:43:LYS:O	4:E:47:CYS:HB2	1.78	0.82
1:A:607:ILE:HG12	1:A:612:ILE:HG22	1.62	0.81
2:B:117:ALA:O	2:B:121:ASN:HA	1.84	0.78
1:A:326:ARG:O	1:A:330:LYS:HB3	1.86	0.76

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1409/1733 (81%)	1244 (88%)	158 (11%)	7 (0%)	24	63
2	B	1128/1224 (92%)	1000 (89%)	123 (11%)	5 (0%)	30	67
3	C	263/318 (83%)	245 (93%)	18 (7%)	0	100	100
4	E	212/215 (99%)	200 (94%)	12 (6%)	0	100	100
5	F	85/155 (55%)	79 (93%)	6 (7%)	0	100	100
6	H	132/146 (90%)	115 (87%)	17 (13%)	0	100	100
7	I	112/122 (92%)	107 (96%)	5 (4%)	0	100	100
8	J	64/70 (91%)	58 (91%)	6 (9%)	0	100	100
9	K	113/120 (94%)	109 (96%)	4 (4%)	0	100	100
10	L	42/70 (60%)	36 (86%)	6 (14%)	0	100	100
All	All	3560/4173 (85%)	3193 (90%)	355 (10%)	12 (0%)	37	72

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	GLN
1	A	525	GLN
1	A	1107	VAL
2	B	364	ILE
1	A	93	VAL

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	1234/1520 (81%)	1234 (100%)	0	100	100
2	B	991/1061 (93%)	991 (100%)	0	100	100
3	C	233/274 (85%)	233 (100%)	0	100	100
4	E	196/197 (100%)	196 (100%)	0	100	100
5	F	77/137 (56%)	77 (100%)	0	100	100
6	H	119/128 (93%)	119 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	I	108/116 (93%)	108 (100%)	0	100	100
8	J	61/65 (94%)	61 (100%)	0	100	100
9	K	99/102 (97%)	99 (100%)	0	100	100
10	L	39/57 (68%)	39 (100%)	0	100	100
All	All	3157/3657 (86%)	3157 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	986	GLN
7	I	114	GLN
2	B	1176	ASN
4	E	106	GLN
1	A	935	GLN

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 8 ligands modelled in this entry, 8 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

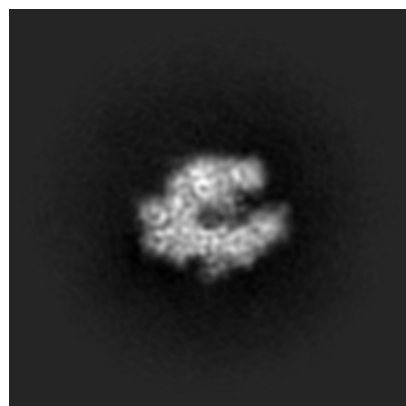
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-77811. These allow visual inspection of the internal detail of the map and identification of artifacts.

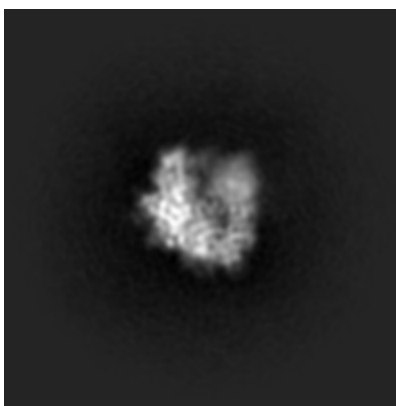
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

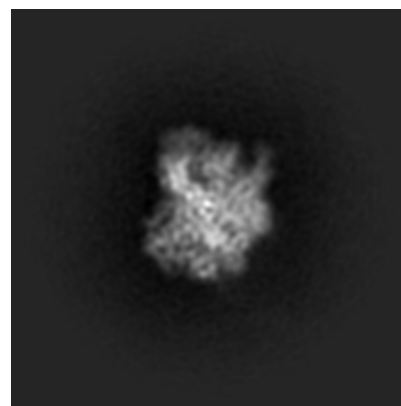
6.1.1 Primary map



X

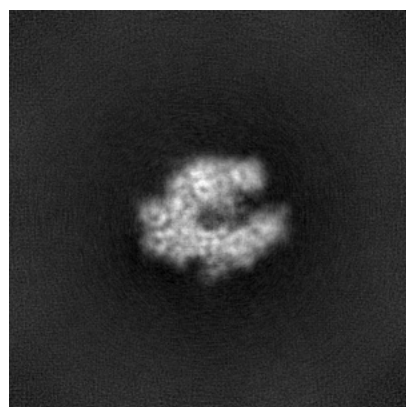


Y

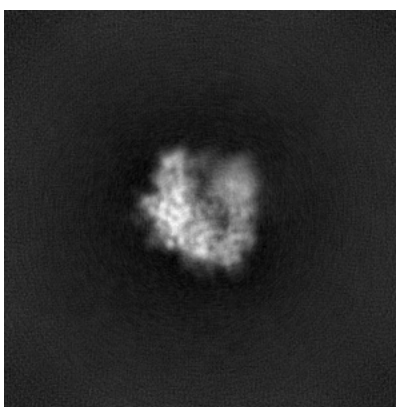


Z

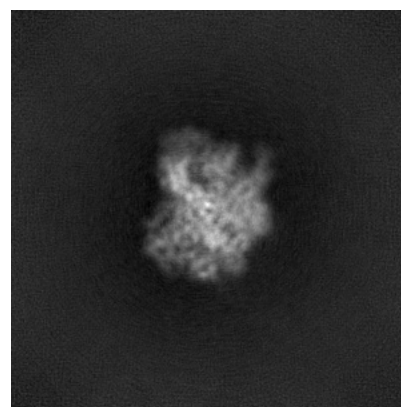
6.1.2 Raw map



X



Y



Z

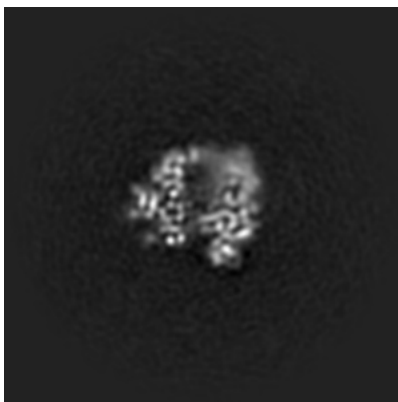
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

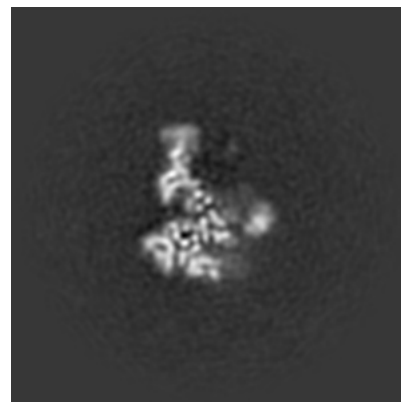
6.2.1 Primary map



X Index: 200

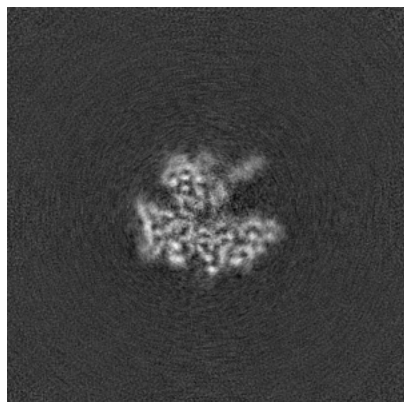


Y Index: 200

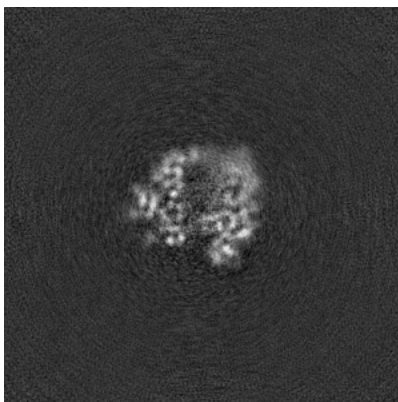


Z Index: 200

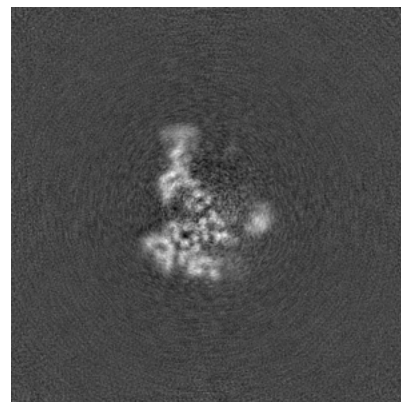
6.2.2 Raw map



X Index: 200



Y Index: 200

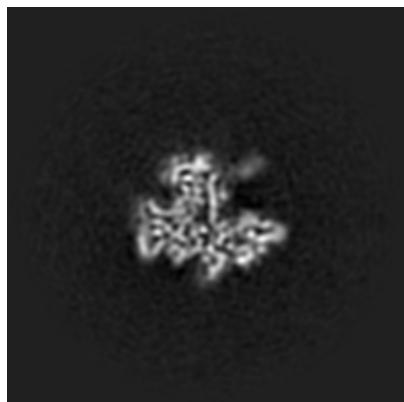


Z Index: 200

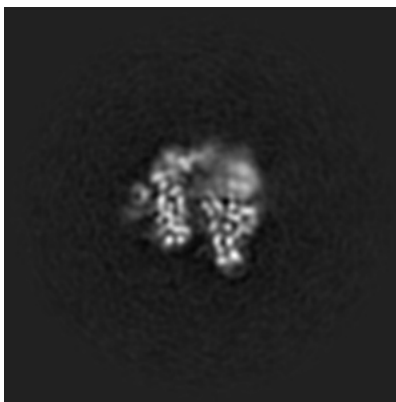
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

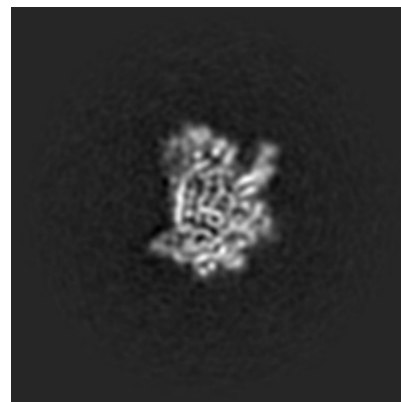
6.3.1 Primary map



X Index: 196

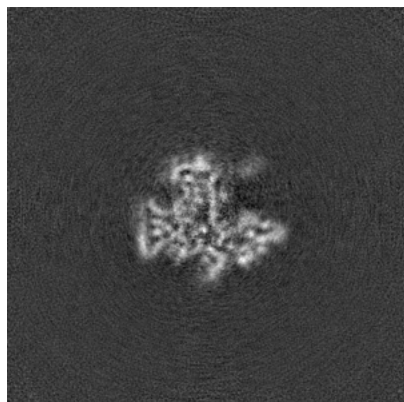


Y Index: 193

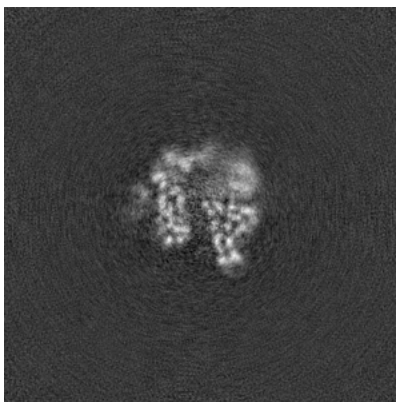


Z Index: 176

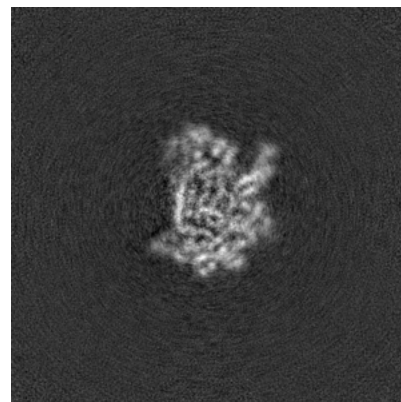
6.3.2 Raw map



X Index: 195



Y Index: 192

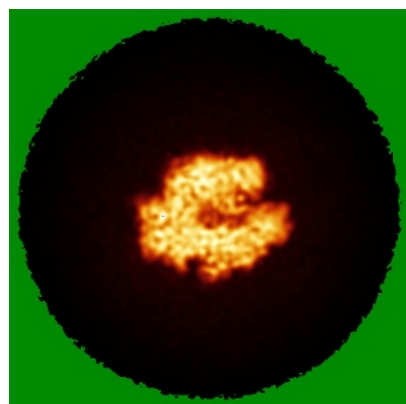


Z Index: 176

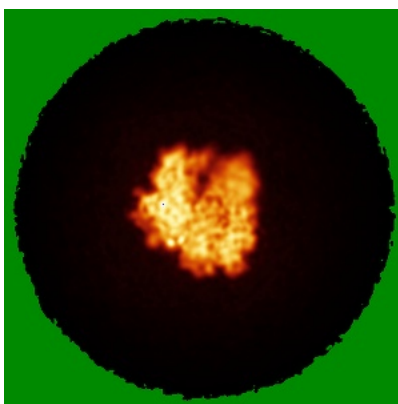
The images above show the largest variance slices of the map in three orthogonal directions.

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

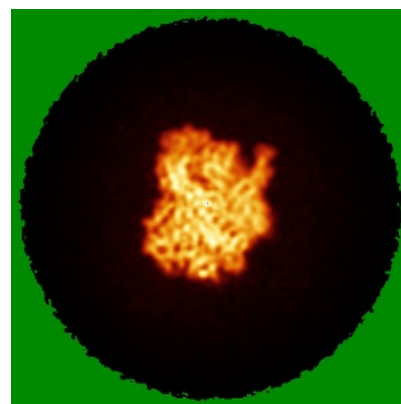
6.4.1 Primary map



X

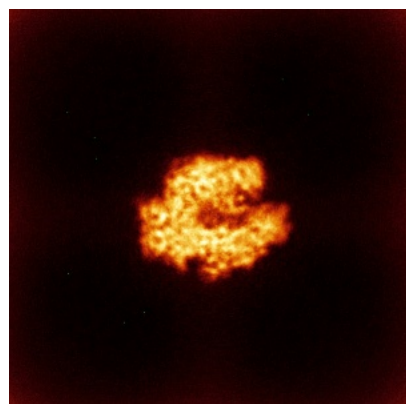


Y

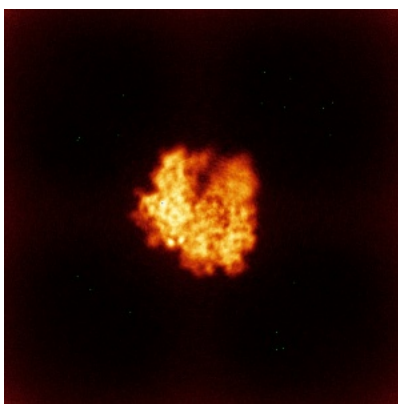


Z

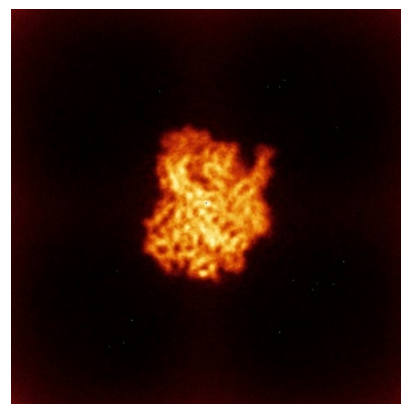
6.4.2 Raw map



X



Y

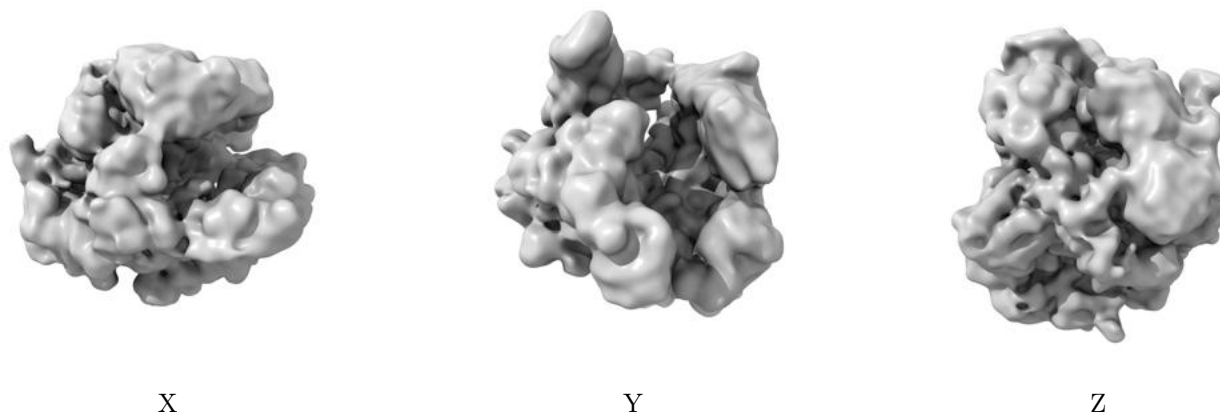


Z

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

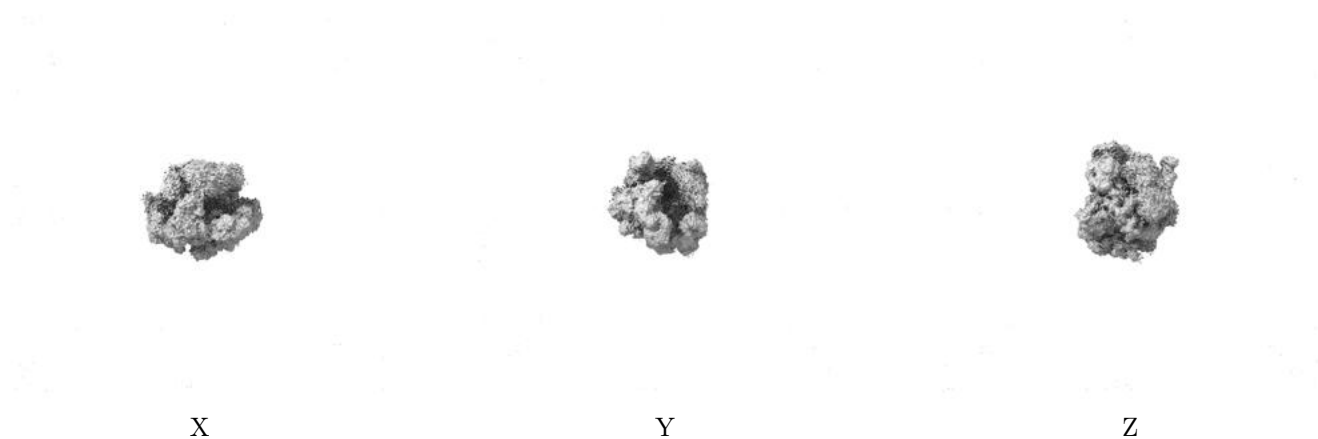
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

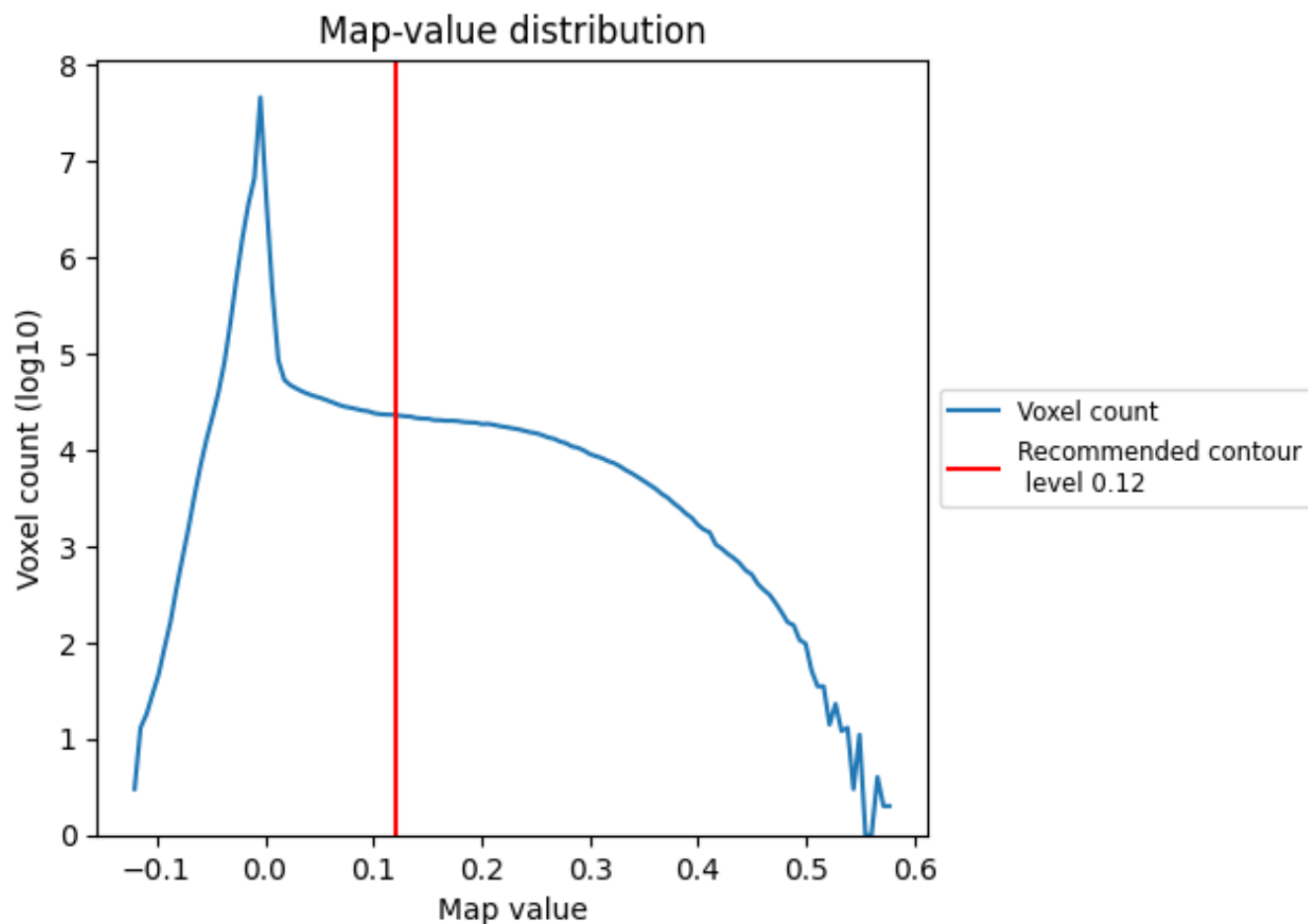
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

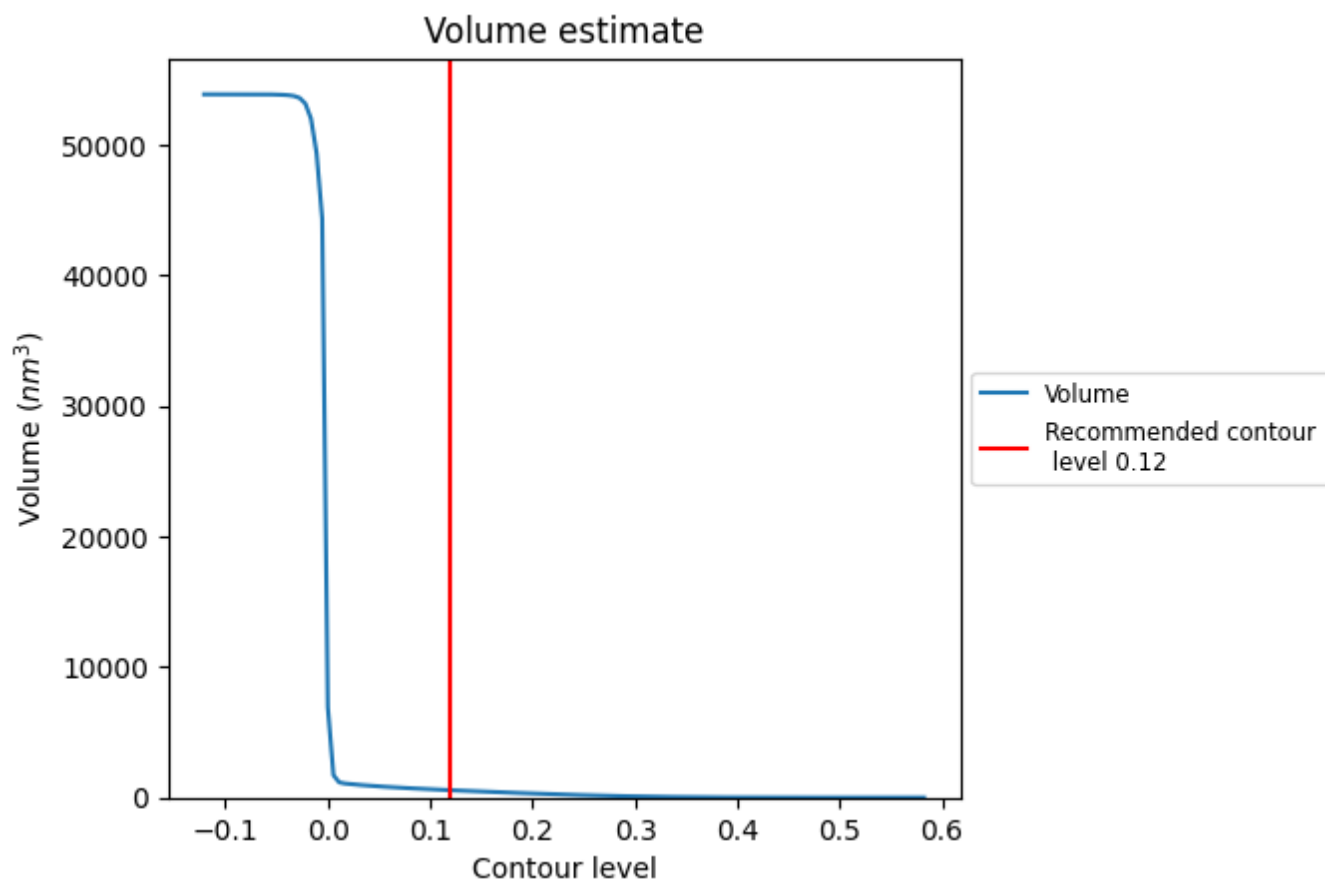
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

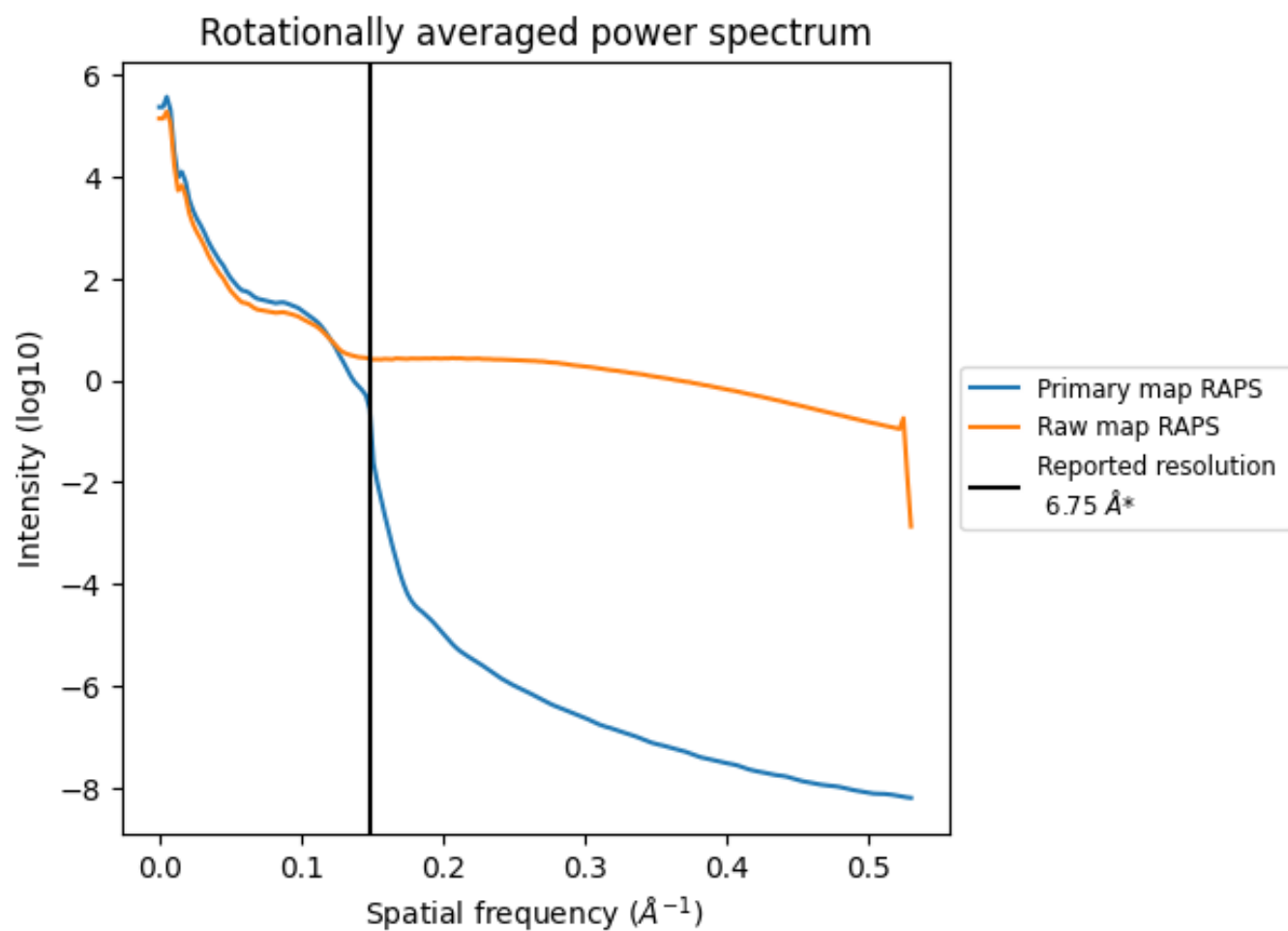
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 565 nm³; this corresponds to an approximate mass of 510 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 ⓘ

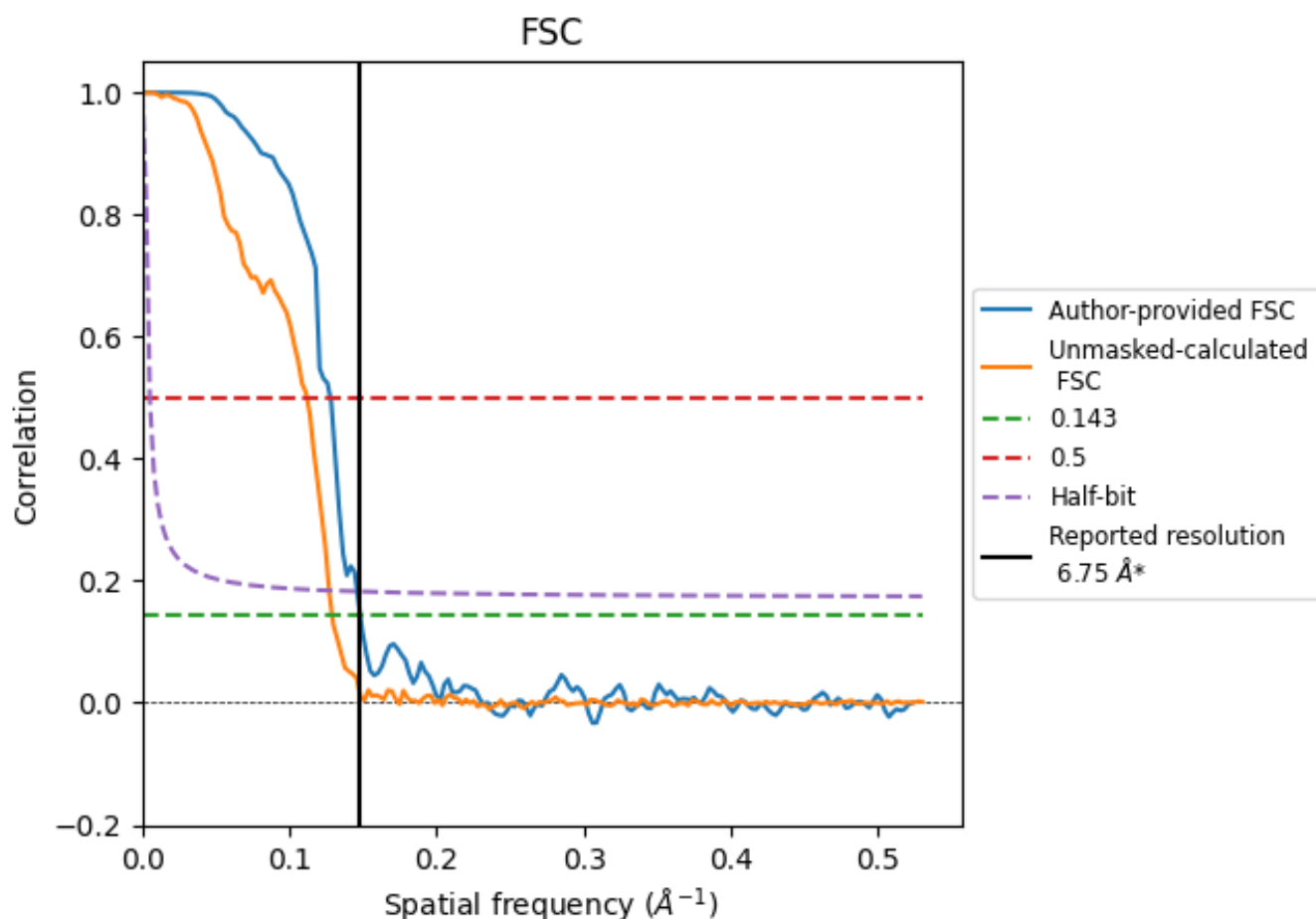


*Reported resolution corresponds to spatial frequency of $0.148 \text{ \AA}^{-1}$

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 $0.148 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

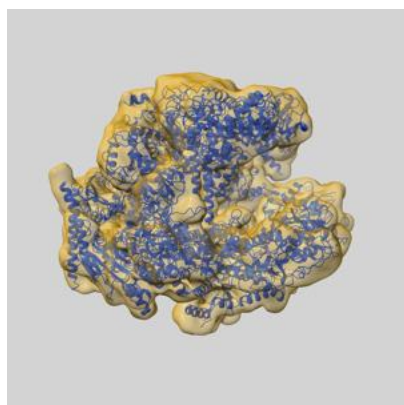
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.75	-	-
Author-provided FSC curve	6.75	7.82	6.84
Unmasked-calculated*	7.75	8.94	7.87

*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 7.75 differs from the reported value 6.75 by more than 10 %

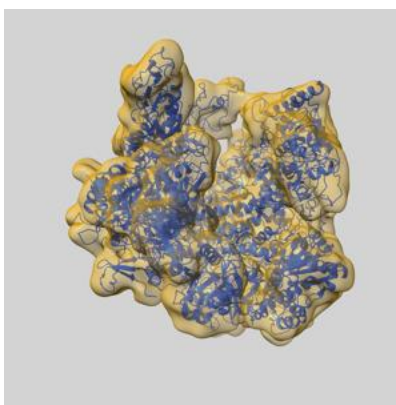
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-77811 and PDB model 36RS. Per-residue inclusion information can be found in section [3](#) on page [6](#).

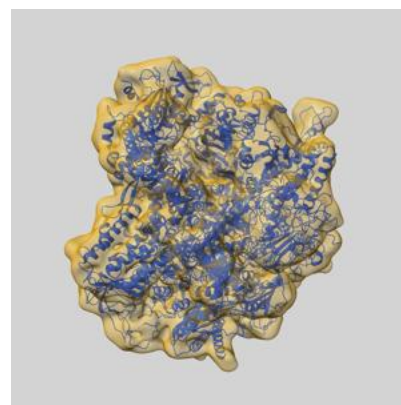
9.1 Map-model overlay [i](#)



X



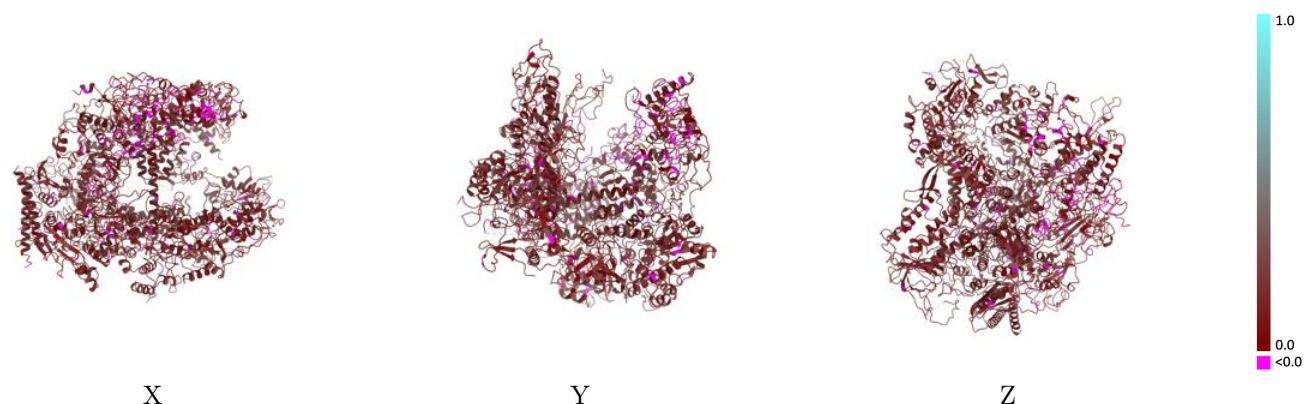
Y



Z

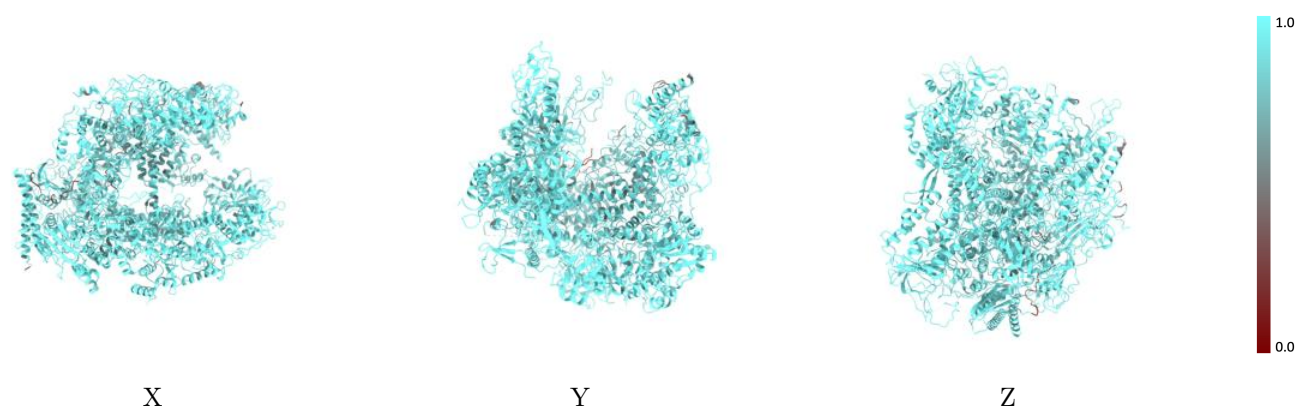
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



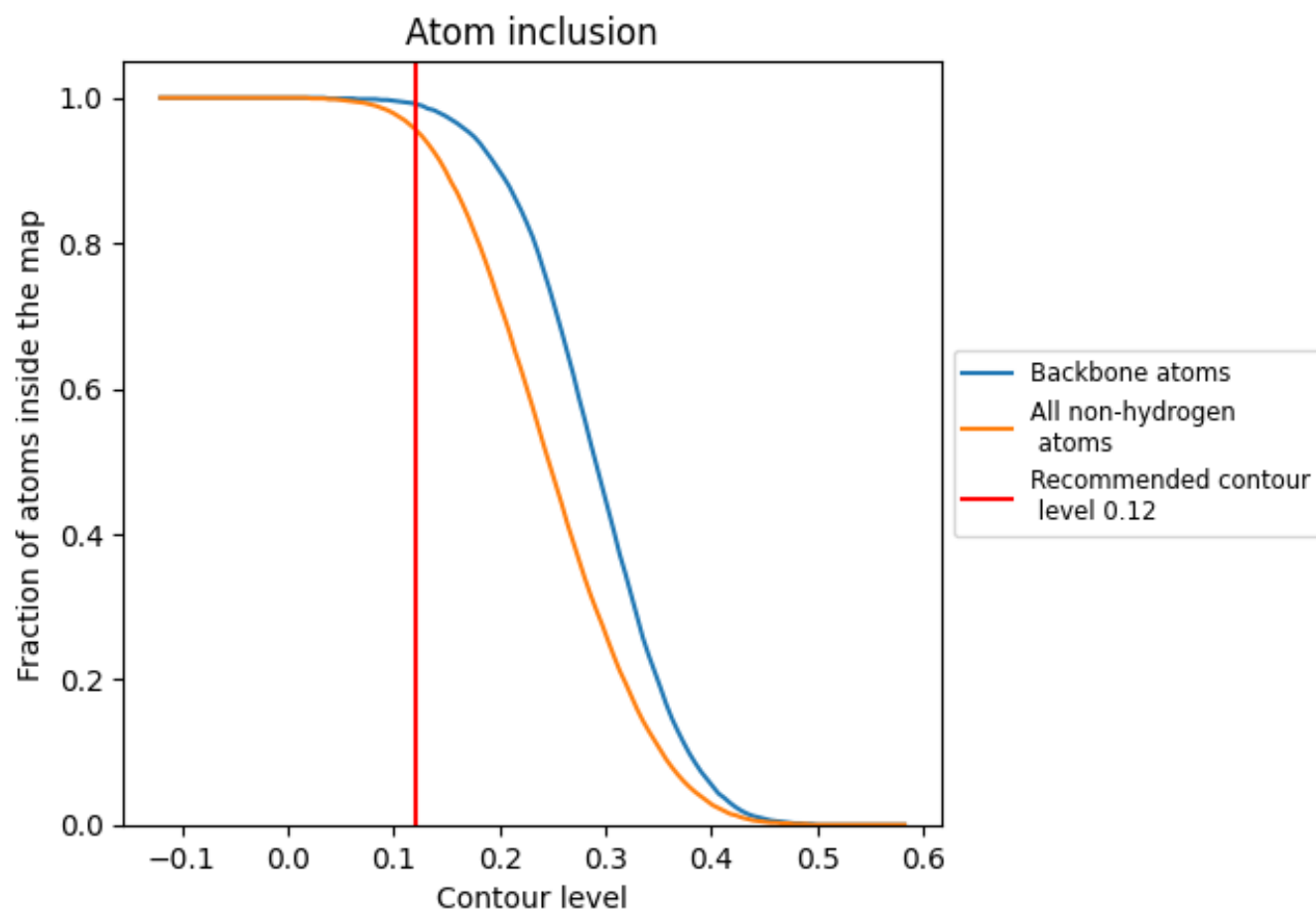
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 96% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9570	0.1610
A	0.9580	0.1510
B	0.9550	0.1620
C	0.9630	0.1830
E	0.9780	0.1720
F	0.9670	0.1850
H	0.9760	0.1890
I	0.9740	0.1610
J	0.9620	0.1590
K	0.8570	0.1610
L	0.9850	0.1600

1.0

0.0

<0.0