



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 12:28 AM UTC

PDB ID : 8OEV / pdb_00008oev
EMDB ID : EMD-16837
Title : Structure of the mammalian Pol II-SPT6-Elongin complex, lacking ELOA latch (composite structure, structure 3)
Authors : Chen, Y.; Kokic, G.; Dienemann, C.; Dybkov, O.; Urlaub, H.; Cramer, P.
Deposited on : 2023-03-13
Resolution : 2.86 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:

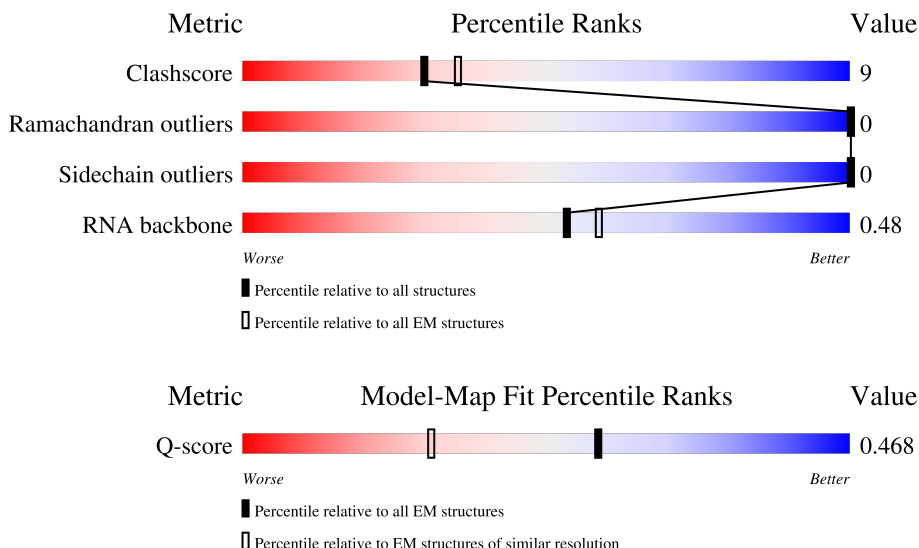
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.86 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.



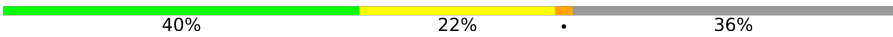
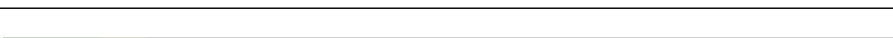
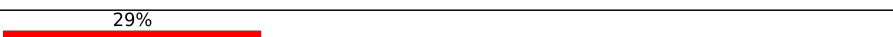
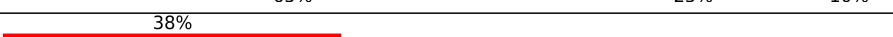
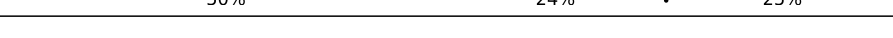
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12017 (2.36 - 3.36)

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	1970	
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	N	48	
14	P	46	
15	T	48	
16	M	801	
17	O	112	
18	Q	118	
19	S	1729	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 41781 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	1409	Total	C	N	O	S	0	0
			11159	7024	2000	2064	71		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1131	Total	C	N	O	S	0	0
			9047	5721	1592	1670	64		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	258	Total	C	N	O	S	0	0
			2072	1300	356	410	6		

- Molecule 4 is a protein called RNA polymerase II subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	118	Total	C	N	O	S	0	0
			967	608	167	188	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	209	Total	C	N	O	S	0	0
			1721	1089	300	324	8		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	78	Total	C	N	O	S	0	0
			626	401	106	114	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1347	872	218	249	8		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	116	Total	C	N	O	S	0	0
			932	577	165	179	11		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	66	Total	C	N	O	S	0	0
			524	339	88	91	6		

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	115	Total	C	N	O	S	0	0
			920	593	152	173	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	44	Total	C	N	O	S	0	0
			367	228	69	64	6		

- Molecule 13 is a DNA chain called Non-Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	26	Total	C	N	O	P	0	0
			549	255	117	151	26		

- Molecule 14 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	13	Total	C	N	O	P	0	0
			280	125	54	88	13		

- Molecule 15 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	38	Total	C	N	O	P	0	0
			769	365	130	236	38		

- Molecule 16 is a protein called Elongin-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	128	Total	C	N	O	S	0	0
			1074	680	195	192	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	SER	-	expression tag	UNP Q14241
M	-1	ASN	-	expression tag	UNP Q14241
M	0	ALA	-	expression tag	UNP Q14241

- Molecule 17 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	101	Total	C	N	O	S	0	0
			792	506	127	153	6		

- Molecule 18 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	88	Total	C	N	O	S	0	0
			696	437	121	135	3		

- Molecule 19 is a protein called Transcription elongation factor SPT6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	825	Total	C	N	O	S	0	0
			6744	4289	1168	1253	34		

There are 3 discrepancies between the modelled and reference sequences:

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

- Molecule 20 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

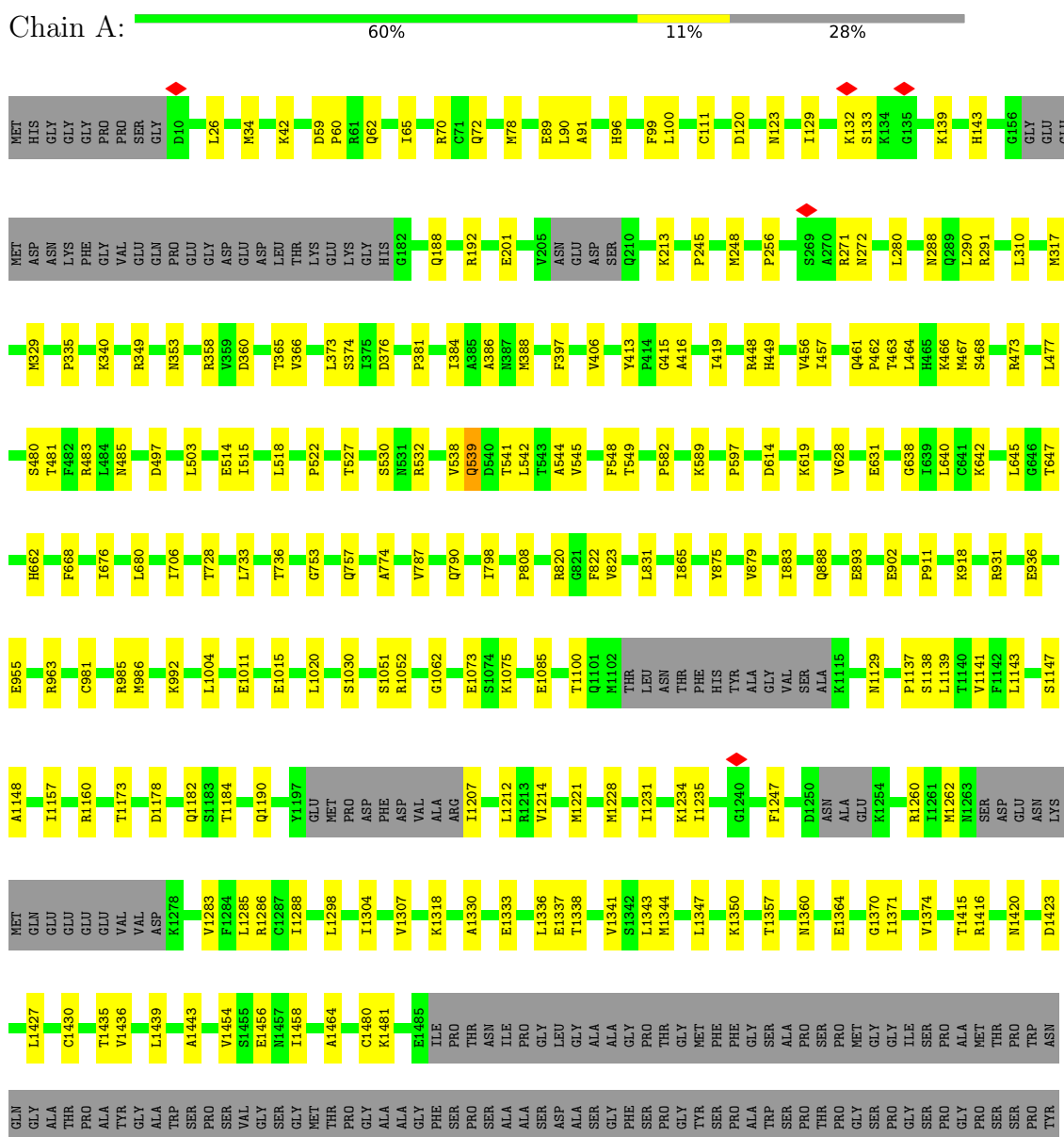
- Molecule 21 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

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



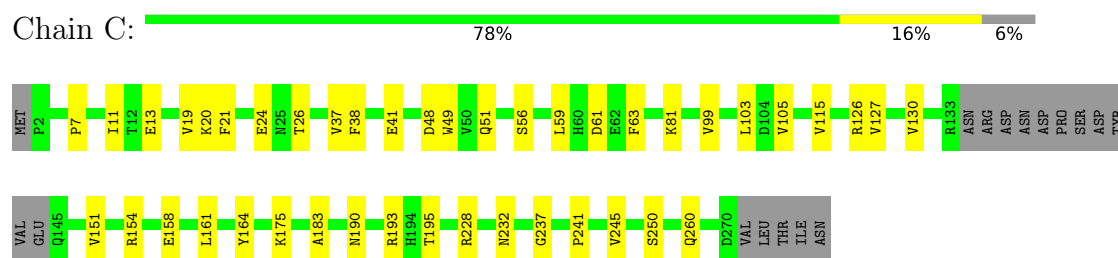
[illegible]

- Molecule 2: DNA-directed RNA polymerase subunit beta

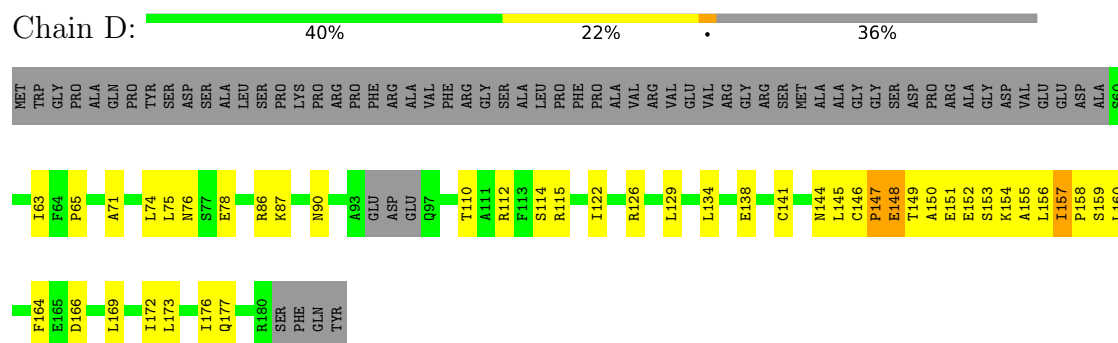
Chain B:  75% 16% 10%

I1244	T1054	C699	G474	W313	Y169	VAL
A1245	E1060	R700	L480	G320	L170	SER
V1253	E893	L702	W484	GLN	S171	CYS
	Q894	L703		GLY	K172	THR
	E895					ASN
	S896	E706	I512		H175	LEU
	K897	L711	L521	LYS	W176	SER
	K898	L712		SER	R178	GLN
	G899			LYS	D179	LEU
	F900	I717	A526	A328		ALA
					P182	ALA
	E904	E722	T551	T336		PRO
	I1114		S557	K341	M185	GLY
	C914	Y725				SER
T1115	Q915				A190	ARG
S1116	G916	D743	L562	T346		GLY
Q1117	M917		N563	T347		ALA
V1132	R918	L752	R568	R351	N194	ASN
	H919		D569		L195	LEU
					T196	THR
R1139	E763	E763	D358	D358	Y197	ALA
A1140	V764	V764	R359	R360	P200	ALA
			K571		L201	ASP
					Y202	GLU
R1149	D928	I775	L578	H364		LEU
						TRP
D1158	D941	P791	L582	D371	T208	ASP
E1167	I944	D792			W209	GLN
R1168			E590	K375	I210	THR
D1169	L950	R805	L599		K211	ARG
C1170	P951	A809		A385	E212	GLY
Q1171	GLU	M810	R606	F386	G213	SER
	ASN	G811		V387	E214	ARG
H1174	GLU	H812	E623	I388		ILE
	ASP				L217	PHI
	GLU					TRP
L1180	GLU	W819	M627	A403	I226	GLY
E1186	LEU	R820	E628			ARG
	GLU	M821	N628	Q421	W232	ARG
	GLY	D822			L233	LYS
D1189	THR	T823	E632	H427	R234	ARG
P1190	ASN	L824			S235	ARG
Y1191	ARG	A825	I644	D432		LYS
Q1192	R963	H826			L248	SER
				K438		LEU
C1196	T971	P831	H654			LEU
N1197				L442	N252	CYS
L1198	Q883	P834	L664		E253	ALA
C1199				M445	C254	LEU
	K994	M841	Q670		G266	ARG
R1208	F995		M671	R456	S267	GLY
		P850	D672	R457	W268	PRO
R1215	H1016		L673	E458		VAL
	G1017		I674		K269	GLY
Q1018	Q1018					ALA
K1019			M680	D461	S300	CYS
		A860		H464	C301	TRP
L1225	P1032	N866	R690			TRP
			L691	L470	T309	LEU
R1239						ALA
W1240	T1044	N874				

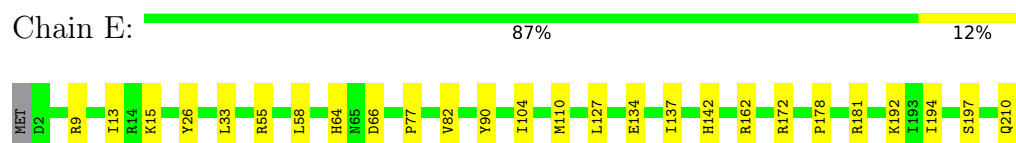
- Molecule 3: DNA-directed RNA polymerase II subunit RPB3



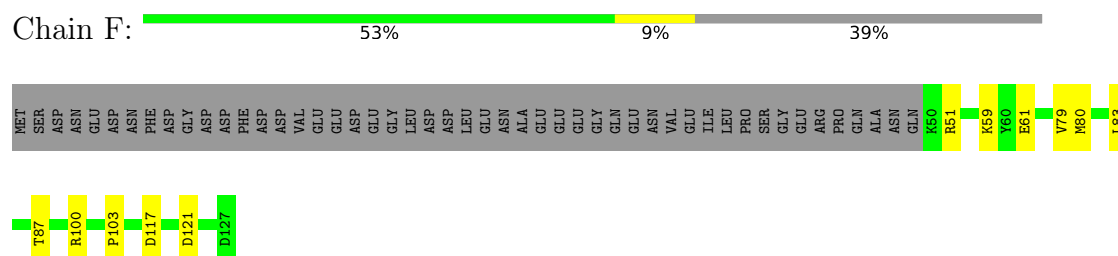
- Molecule 4: RNA polymerase II subunit D



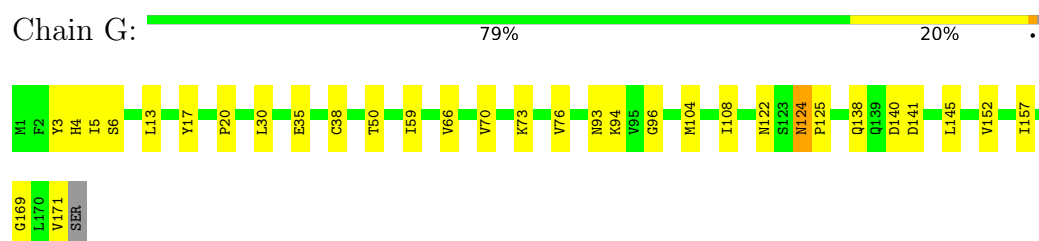
- Molecule 5: DNA-directed RNA polymerase II subunit E



- Molecule 6: DNA-directed RNA polymerase II subunit F

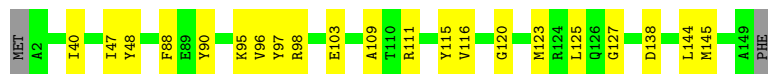


- Molecule 7: DNA-directed RNA polymerase II subunit RPB7



- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H:  85% 14%



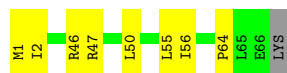
- Molecule 9: DNA-directed RNA polymerase II subunit RPB9

Chain I:  80% 13% 7%



- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J:  87% 12%



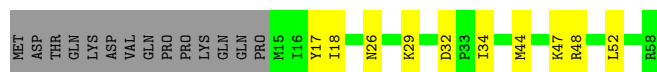
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11-a

Chain K:  87% 11%

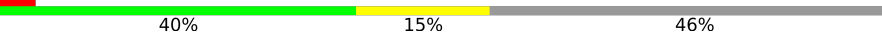


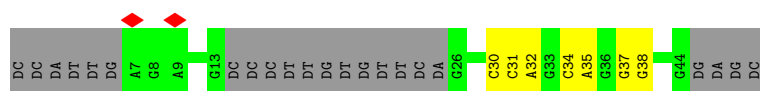
- Molecule 12: RNA polymerase II subunit K

Chain L:  59% 17% 24%



- Molecule 13: Non-Template DNA

Chain N:  40% 15% 46%



- Molecule 14: RNA

Chain P:  22% 72%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	118642	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 ($e^-/\text{\AA}^2$)	40.09	Depositor
Minimum defocus (nm)	350	Depositor
Maximum defocus (nm)	7500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	39.253	Depositor
Minimum map value	-16.528	Depositor
Average map value	0.015	Depositor
Map value standard deviation	1.086	Depositor
Recommended contour level	3.5	Depositor
Map size (Å)	461.99997, 461.99997, 461.99997	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.20	0/11360	0.45	2/15328 (0.0%)
2	B	0.22	0/9227	0.44	0/12454
3	C	0.21	0/2115	0.39	0/2873
4	D	0.43	0/979	0.84	2/1312 (0.2%)
5	E	0.19	0/1752	0.44	0/2366
6	F	0.19	0/636	0.45	0/859
7	G	0.24	0/1378	0.60	0/1870
8	H	0.18	0/1207	0.41	0/1628
9	I	0.17	0/954	0.43	0/1293
10	J	0.20	0/533	0.41	0/719
11	K	0.22	0/939	0.41	0/1271
12	L	0.21	0/372	0.49	0/493
13	N	0.18	0/619	0.31	0/954
14	P	0.13	0/313	0.21	0/486
15	T	0.23	0/857	0.43	0/1319
16	M	0.24	0/1098	0.58	0/1481
17	O	0.24	0/810	0.68	2/1097 (0.2%)
18	Q	0.26	0/707	0.73	2/952 (0.2%)
19	S	0.24	0/6868	0.51	1/9250 (0.0%)
All	All	0.22	0/42724	0.48	9/58005 (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	1
4	D	0	1
7	G	0	1
19	S	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	4

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	538	VAL	CA-C-N	6.43	133.83	121.54
1	A	538	VAL	C-N-CA	6.43	133.83	121.54
18	Q	10	HIS	CA-C-N	5.94	136.66	126.32
18	Q	10	HIS	C-N-CA	5.94	136.66	126.32
4	D	147	PRO	N-CA-C	-5.86	102.25	111.34

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	539	GLN	Mainchain
4	D	157	ILE	Mainchain
7	G	124	ASN	Peptide
19	S	415	ARG	Sidechain

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	11159	0	11304	148	0
2	B	9047	0	9080	127	0
3	C	2072	0	2019	28	0
4	D	967	0	973	54	0
5	E	1721	0	1737	17	0
6	F	626	0	657	8	0
7	G	1347	0	1347	72	0
8	H	1186	0	1147	13	0
9	I	932	0	856	12	0
10	J	524	0	540	5	0
11	K	920	0	942	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	367	0	367	10	0
13	N	549	0	289	4	0
14	P	280	0	142	2	0
15	T	769	0	429	13	0
16	M	1074	0	1070	27	0
17	O	792	0	774	18	0
18	Q	696	0	694	16	0
19	S	6744	0	6723	272	0
20	A	1	0	0	0	0
21	A	2	0	0	0	0
21	B	1	0	0	0	0
21	C	1	0	0	0	0
21	I	2	0	0	0	0
21	J	1	0	0	0	0
21	L	1	0	0	0	0
All	All	41781	0	41090	743	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 9.

The worst 5 of 743 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)
7:G:171:VAL:HG22	19:S:518:ALA:CB	1.43	1.48
7:G:171:VAL:CG2	19:S:518:ALA:HB1	1.58	1.32
7:G:171:VAL:CG2	19:S:518:ALA:CB	2.07	1.32
19:S:815:THR:O	19:S:829:LYS:HD2	1.11	1.24
7:G:122:ASN:HB2	19:S:405:GLN:NE2	1.57	1.18

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	1395/1970 (71%)	1365 (98%)	30 (2%)	0	100	100
2	B	1123/1251 (90%)	1088 (97%)	35 (3%)	0	100	100
3	C	254/275 (92%)	247 (97%)	7 (3%)	0	100	100
4	D	114/184 (62%)	106 (93%)	8 (7%)	0	100	100
5	E	207/210 (99%)	201 (97%)	6 (3%)	0	100	100
6	F	76/127 (60%)	76 (100%)	0	0	100	100
7	G	169/172 (98%)	156 (92%)	13 (8%)	0	100	100
8	H	146/150 (97%)	142 (97%)	4 (3%)	0	100	100
9	I	114/125 (91%)	111 (97%)	3 (3%)	0	100	100
10	J	64/67 (96%)	63 (98%)	1 (2%)	0	100	100
11	K	113/117 (97%)	111 (98%)	2 (2%)	0	100	100
12	L	42/58 (72%)	39 (93%)	3 (7%)	0	100	100
16	M	126/801 (16%)	119 (94%)	7 (6%)	0	100	100
17	O	99/112 (88%)	90 (91%)	9 (9%)	0	100	100
18	Q	86/118 (73%)	73 (85%)	13 (15%)	0	100	100
19	S	799/1729 (46%)	770 (96%)	29 (4%)	0	100	100
All	All	4927/7466 (66%)	4757 (96%)	170 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1239/1749 (71%)	1239 (100%)	0	100	100
2	B	953/1084 (88%)	953 (100%)	0	100	100
3	C	235/252 (93%)	235 (100%)	0	100	100
4	D	109/160 (68%)	109 (100%)	0	100	100
5	E	191/192 (100%)	191 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	68/111 (61%)	68 (100%)	0	100	100
7	G	151/153 (99%)	151 (100%)	0	100	100
8	H	129/131 (98%)	129 (100%)	0	100	100
9	I	102/112 (91%)	102 (100%)	0	100	100
10	J	55/56 (98%)	55 (100%)	0	100	100
11	K	104/106 (98%)	104 (100%)	0	100	100
12	L	40/55 (73%)	40 (100%)	0	100	100
16	M	118/706 (17%)	118 (100%)	0	100	100
17	O	88/96 (92%)	88 (100%)	0	100	100
18	Q	75/103 (73%)	75 (100%)	0	100	100
19	S	731/1524 (48%)	731 (100%)	0	100	100
All	All	4388/6590 (67%)	4388 (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 42 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	116	GLN
17	O	68	HIS
8	H	131	ASN
11	K	89	ASN
19	S	465	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	12/46 (26%)	3 (25%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	P	35	A
14	P	36	G
14	P	37	G

There are no RNA pucker outliers to report.

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 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.

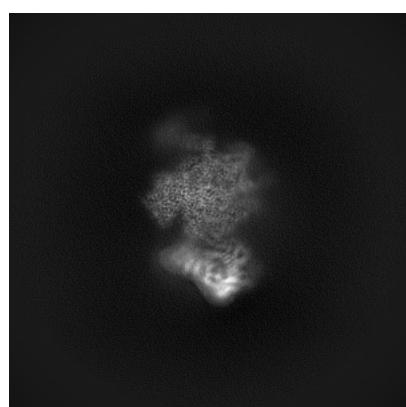
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16837. These allow visual inspection of the internal detail of the map and identification of artifacts.

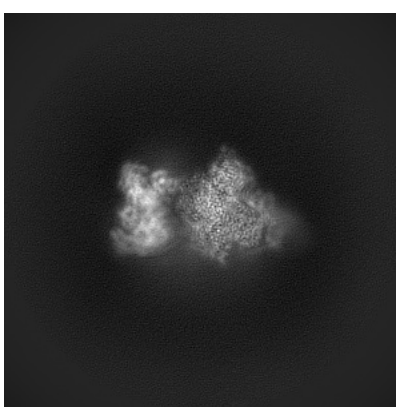
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

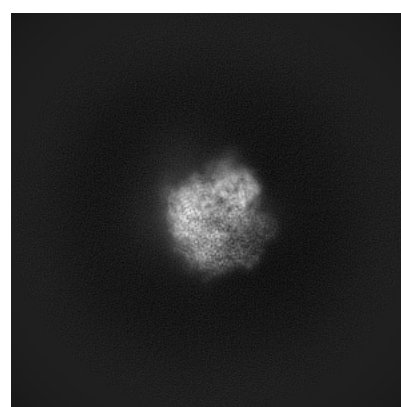
6.1.1 Primary map



X



Y

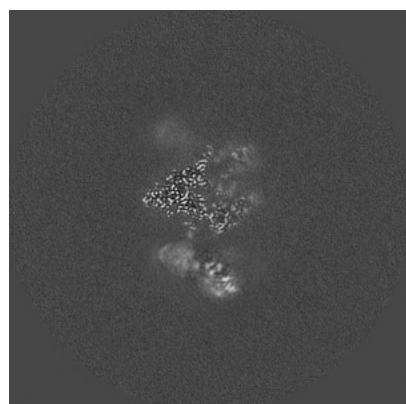


Z

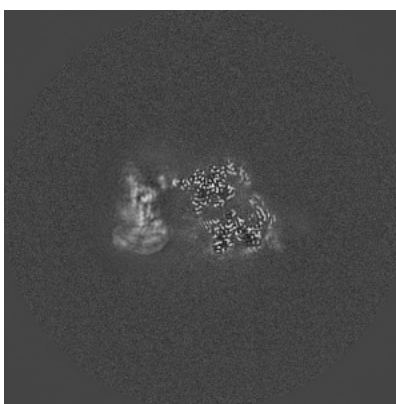
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

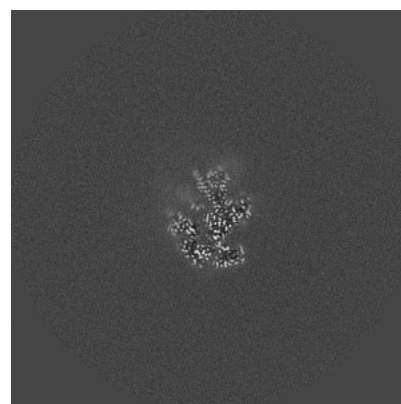
6.2.1 Primary map



X Index: 220



Y Index: 220

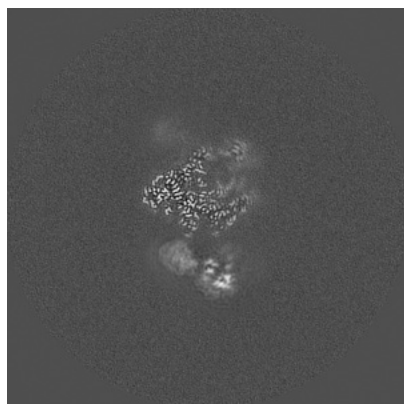


Z Index: 220

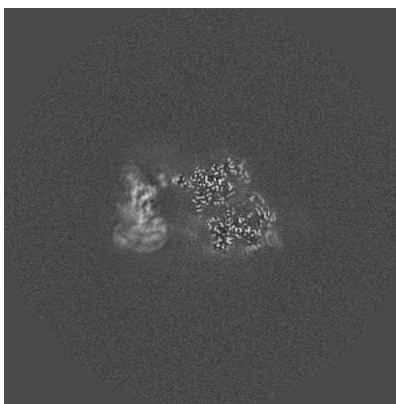
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

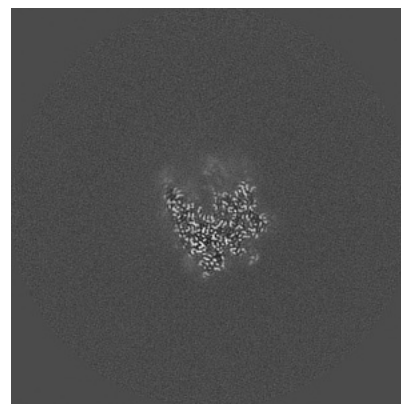
6.3.1 Primary map



X Index: 223



Y Index: 219

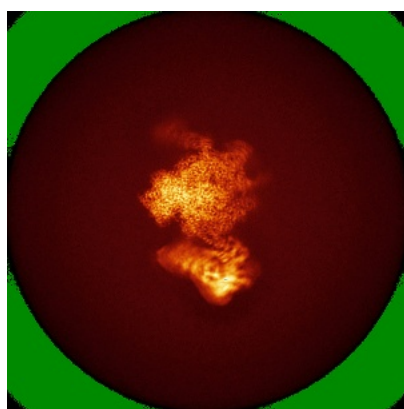


Z Index: 235

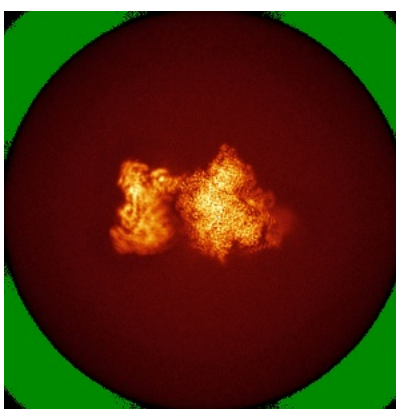
The images above show the largest variance slices of the map in three orthogonal directions.

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

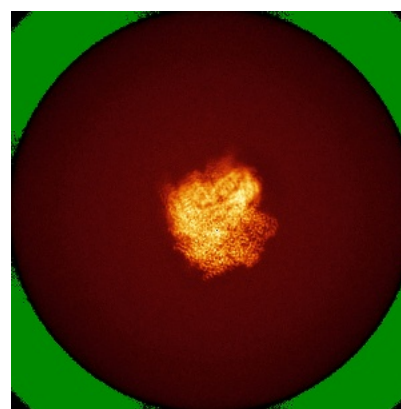
6.4.1 Primary map



X



Y

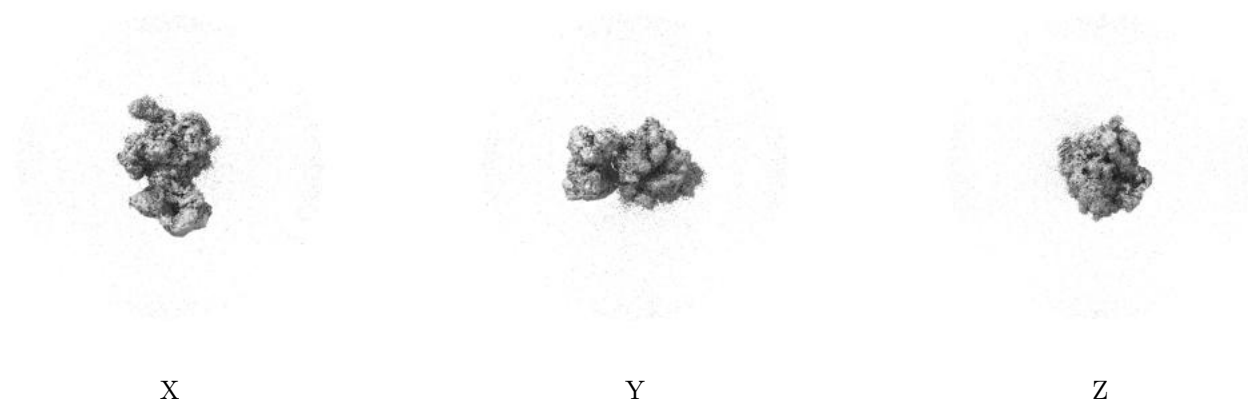


Z

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



The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

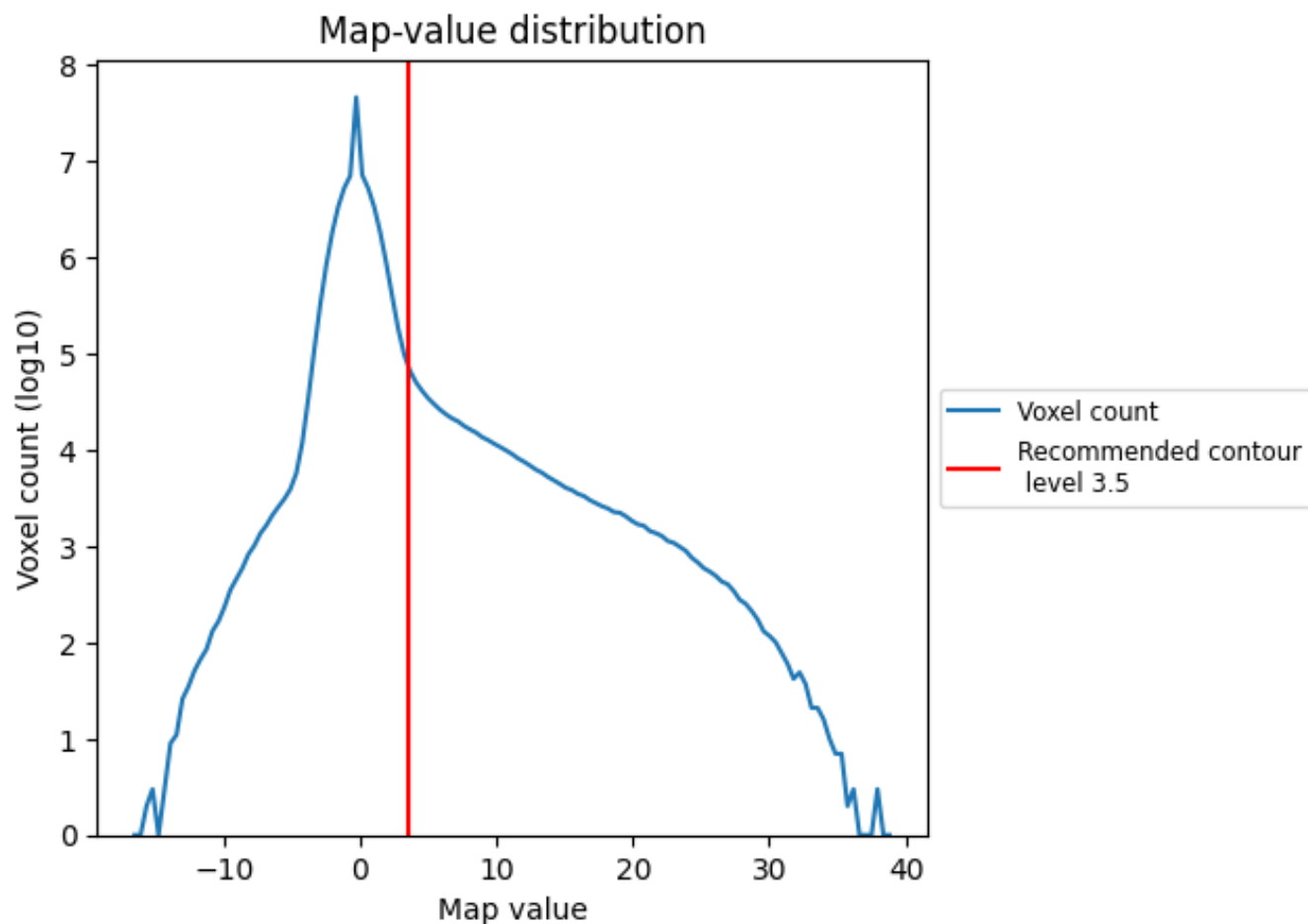
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

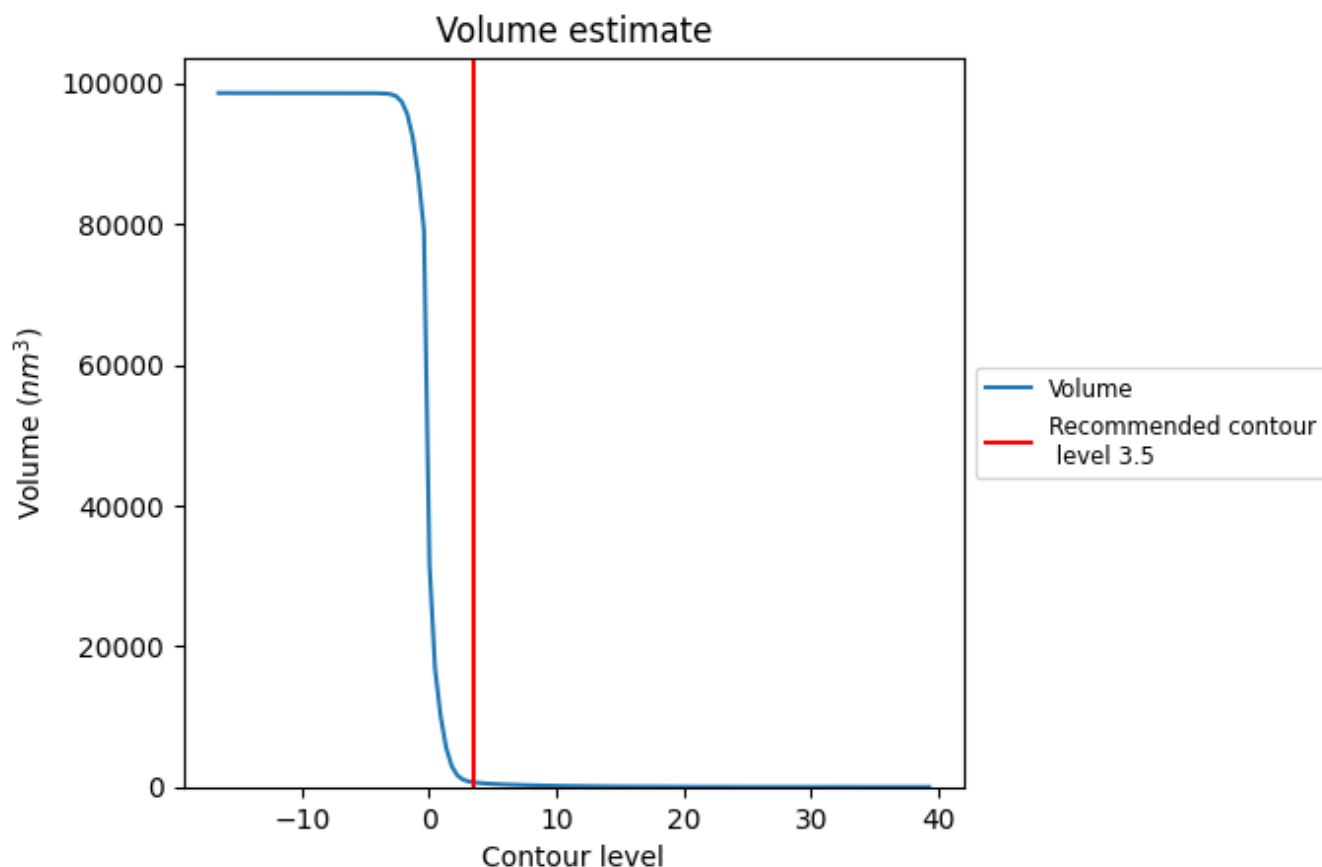
This section contains the results of statistical analysis of the map.

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.

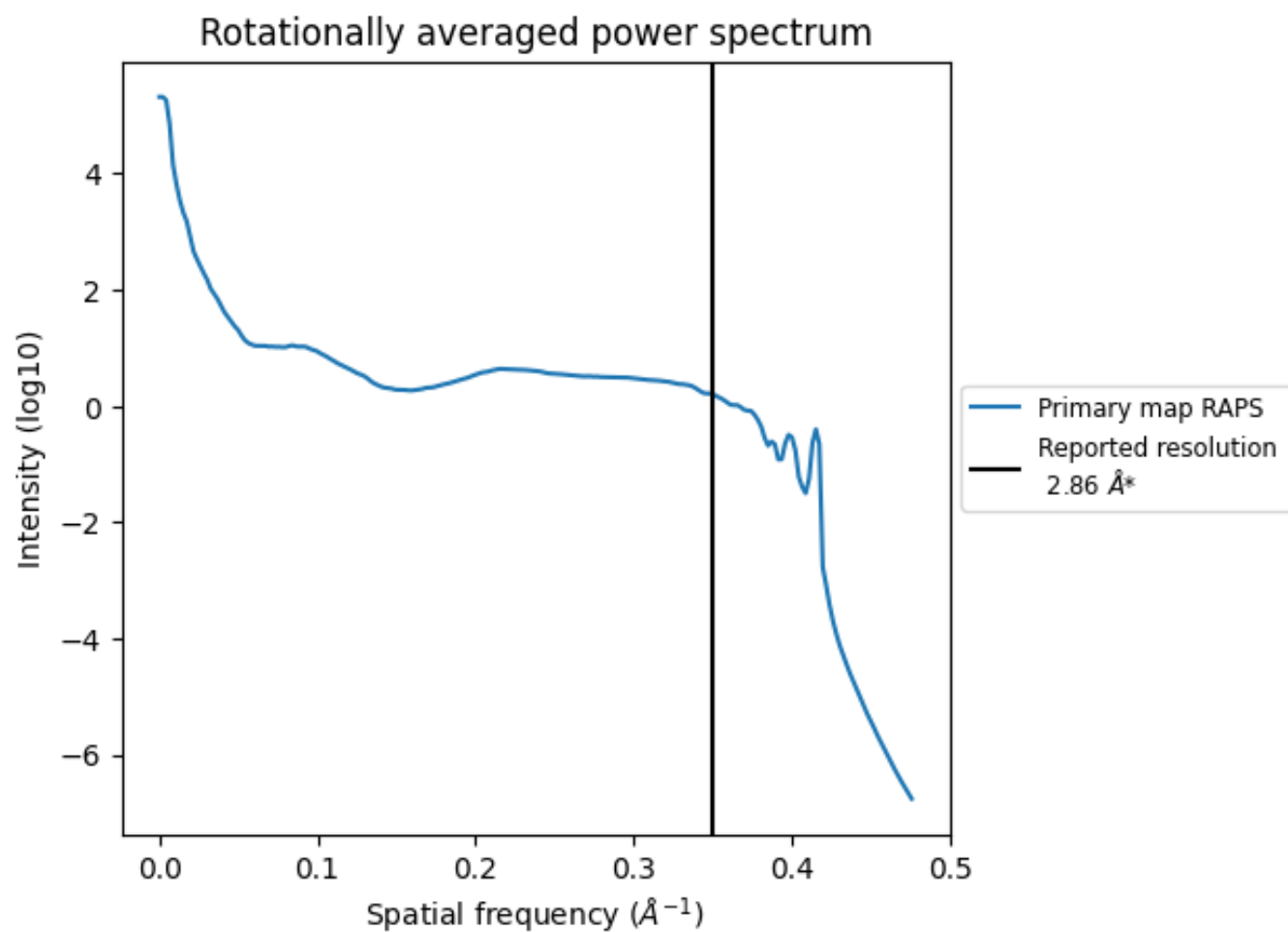
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 656 nm³; this corresponds to an approximate mass of 593 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 0.350 Å⁻¹

8 Fourier-Shell correlation

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

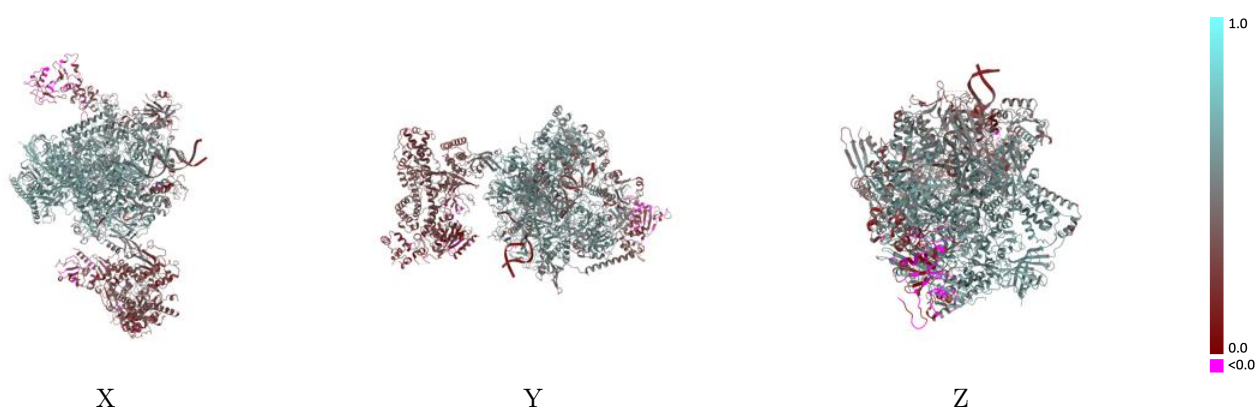
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16837 and PDB model 80EV. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

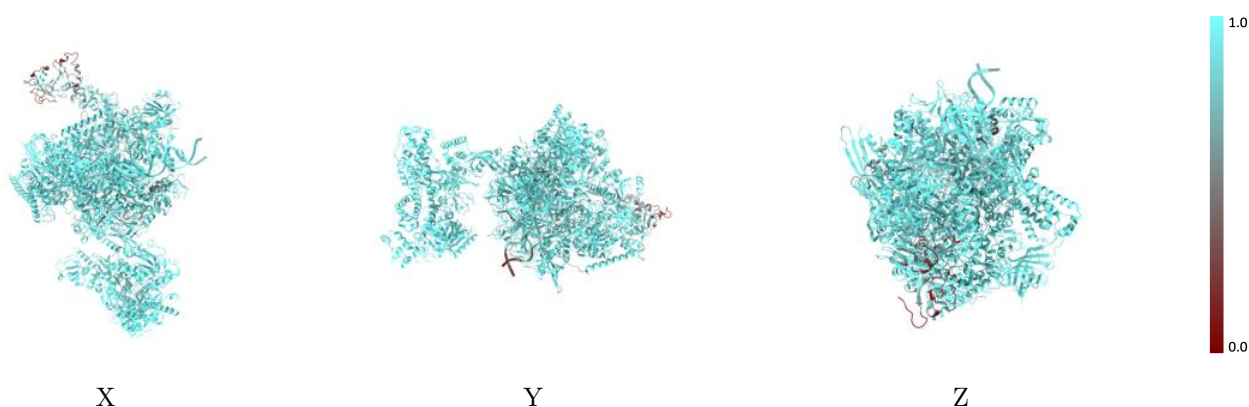
This section was not generated.

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



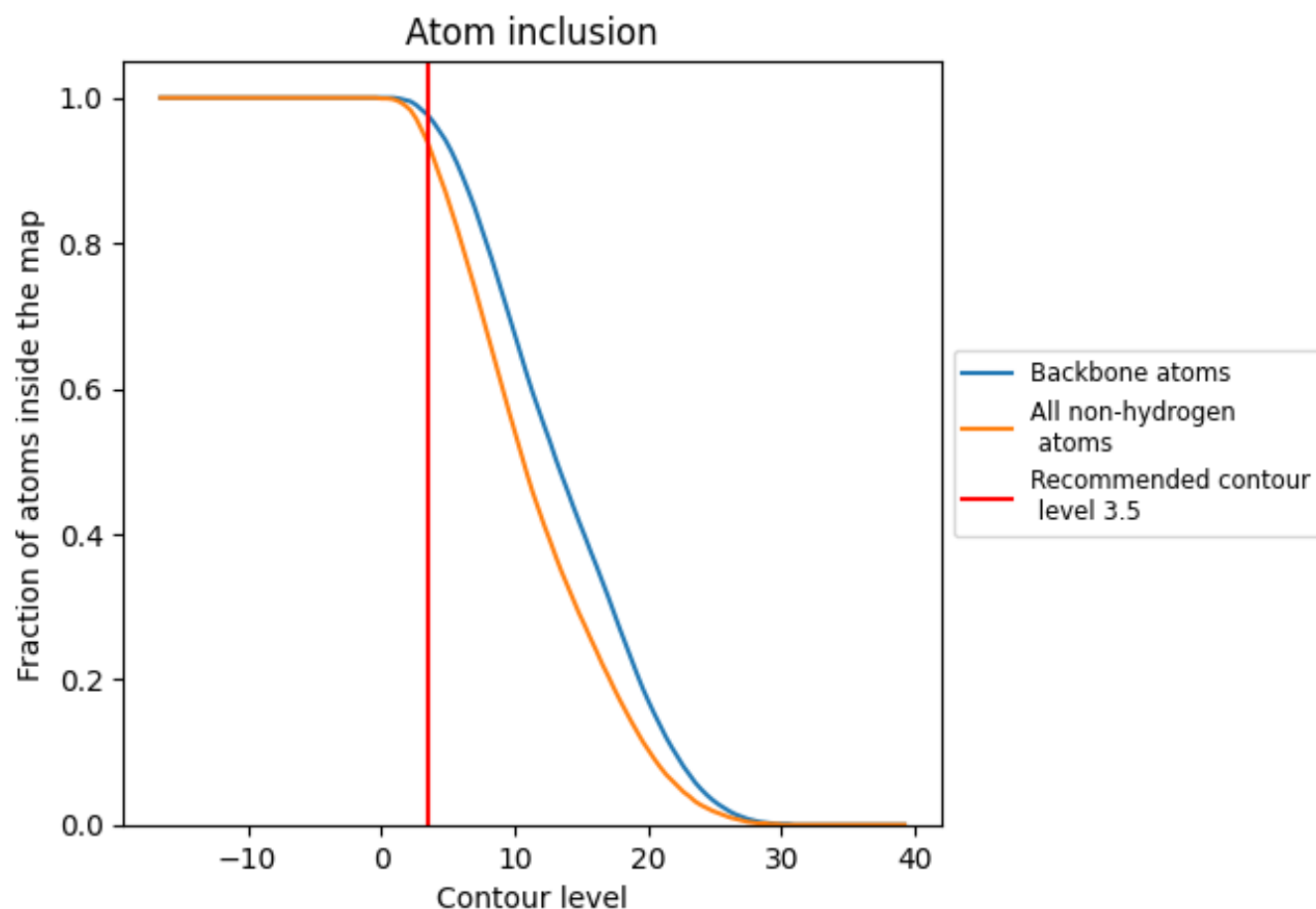
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9390	 0.4680
A	 0.9550	 0.5510
B	 0.9600	 0.5650
C	 0.9690	 0.5950
D	 0.9610	 0.3040
E	 0.9520	 0.5160
F	 0.9620	 0.5790
G	 0.9500	 0.4070
H	 0.9650	 0.5760
I	 0.9310	 0.4670
J	 0.9750	 0.6040
K	 0.9670	 0.5950
L	 0.9410	 0.5120
M	 0.8590	 0.3090
N	 0.8140	 0.2840
O	 0.5700	 0.1210
P	 0.8820	 0.4980
Q	 0.4420	 0.0670
S	 0.9830	 0.2530
T	 0.8450	 0.3850

