



wwPDB EM Validation Summary Report ⓘ

Jun 26, 2024 – 11:30 AM JST

PDB ID : 7XN7
EMDB ID : EMD-33313
Title : RNA polymerase II elongation complex containing Spt4/5, Elf1, Spt6, Spn1 and Paf1C
Authors : Ehara, H.; Kujirai, T.; Shirouzu, M.; Kurumizaka, H.; Sekine, S.
Deposited on : 2022-04-28
Resolution : 3.10 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

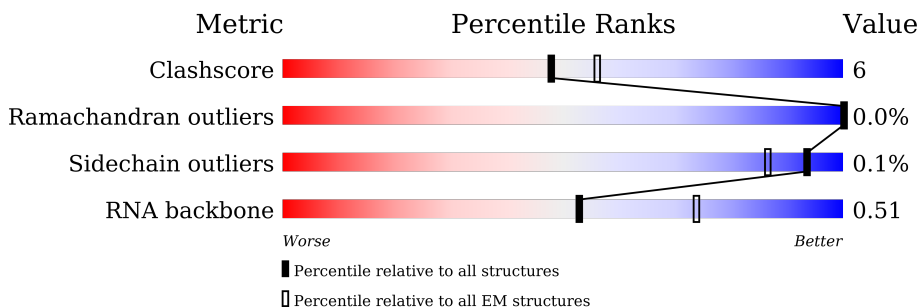
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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.








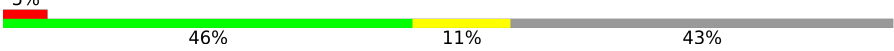

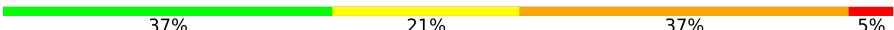









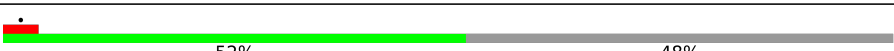
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1743	
2	B	1227	
3	C	304	
4	D	186	
5	E	214	
6	F	155	
7	G	171	

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Mol	Chain	Length	Quality of chain
8	H	145	
9	I	115	
10	J	72	
11	K	118	
12	L	72	
13	M	113	
14	N	198	
15	P	19	
16	T	198	
17	V	108	
18	W	911	
19	m	1503	
20	n	417	
21	q	1084	
22	r	544	
23	u	459	
24	v	396	
25	x	395	

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 66076 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 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1404	Total	C	N	O	S	0	0
			11064	6975	1930	2089	70		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1164	Total	C	N	O	S	0	0
			9284	5848	1639	1739	58		

- Molecule 3 is a protein called RNA polymerase II third largest subunit B44, part of central core.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	263	Total	C	N	O	S	0	0
			2098	1319	354	413	12		

- Molecule 4 is a protein called RNA polymerase II subunit B32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	174	Total	C	N	O	S	0	0
			1349	828	244	274	3		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	213	Total	C	N	O	S	0	0
			1741	1094	312	325	10		

- Molecule 6 is a protein called RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	84	Total	C	N	O	S	0	0
			677	429	114	131	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1325	858	214	248	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	133	Total	C	N	O	S	0	0
			1053	671	169	209	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	111	Total	C	N	O	S	0	0
			917	565	161	180	11		

- Molecule 10 is a protein called RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	67	Total	C	N	O	S	0	0
			554	355	97	96	6		

- Molecule 11 is a protein called RNA polymerase II subunit B12.5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	113	Total	C	N	O	S	0	0
			932	599	160	169	4		

- Molecule 12 is a protein called RNA polymerase subunit ABC10-alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			359	221	72	61	5		

- Molecule 13 is a protein called Transcription elongation factor 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	64	Total	C	N	O	S	0	0
			505	318	82	99	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	GLY	-	expression tag	UNP C4QZ45
M	-1	PRO	-	expression tag	UNP C4QZ45
M	0	GLY	-	expression tag	UNP C4QZ45

- Molecule 14 is a DNA chain called DNA (198-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	42	Total	C	N	O	P	0	0
			854	408	144	260	42		

- Molecule 15 is a RNA chain called RNA (5'-R(P*AP*AP*GP*CP*CP*UP*GP*GP*UP*GP*UP*CP*UP*UP*GP*GP*GP*UP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	19	Total	C	N	O	P	0	0
			404	179	65	141	19		

- Molecule 16 is a DNA chain called DNA (198-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	53	Total	C	N	O	P	0	0
			1090	515	217	305	53		

- Molecule 17 is a protein called Transcription elongation factor SPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	V	106	Total	C	N	O	S	0	0
			824	512	150	155	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	7	MET	VAL	conflict	UNP C4R0E6

- Molecule 18 is a protein called Chromatin elongation factor SPT5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	W	533	Total	C	N	O	S	0	0
			4232	2666	752	812	2		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	-2	GLY	-	expression tag	UNP C4R370
W	-1	PRO	-	expression tag	UNP C4R370
W	0	GLY	-	expression tag	UNP C4R370

- Molecule 19 is a protein called Transcription elongation factor Spt6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	m	1187	Total	C	N	O	S	0	0
			9730	6162	1663	1877	28		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	-2	GLY	-	expression tag	UNP C4R7H2
m	-1	PRO	-	expression tag	UNP C4R7H2
m	0	GLY	-	expression tag	UNP C4R7H2

- Molecule 20 is a protein called Protein that interacts with Spt6p and copurifies with Spt5p and RNA polymerase II.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	n	139	Total	C	N	O	S	0	0
			1115	716	193	202	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	-2	GLY	-	expression tag	UNP C4R7L8
n	-1	PRO	-	expression tag	UNP C4R7L8
n	0	GLY	-	expression tag	UNP C4R7L8

- Molecule 21 is a protein called Component of the Paf1p complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	q	930	Total	C	N	O	S	0	0
			7552	4805	1283	1439	25		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
q	-39	MET	-	initiating methionine	UNP C4R6B2
q	-38	LYS	-	expression tag	UNP C4R6B2
q	-37	ASP	-	expression tag	UNP C4R6B2
q	-36	HIS	-	expression tag	UNP C4R6B2
q	-35	LEU	-	expression tag	UNP C4R6B2
q	-34	ILE	-	expression tag	UNP C4R6B2
q	-33	HIS	-	expression tag	UNP C4R6B2
q	-32	ASN	-	expression tag	UNP C4R6B2
q	-31	HIS	-	expression tag	UNP C4R6B2
q	-30	HIS	-	expression tag	UNP C4R6B2
q	-29	LYS	-	expression tag	UNP C4R6B2
q	-28	HIS	-	expression tag	UNP C4R6B2
q	-27	GLU	-	expression tag	UNP C4R6B2
q	-26	HIS	-	expression tag	UNP C4R6B2
q	-25	ALA	-	expression tag	UNP C4R6B2
q	-24	HIS	-	expression tag	UNP C4R6B2
q	-23	ALA	-	expression tag	UNP C4R6B2
q	-22	GLU	-	expression tag	UNP C4R6B2
q	-21	HIS	-	expression tag	UNP C4R6B2
q	-20	ASP	-	expression tag	UNP C4R6B2
q	-19	TYR	-	expression tag	UNP C4R6B2
q	-18	LYS	-	expression tag	UNP C4R6B2
q	-17	ASP	-	expression tag	UNP C4R6B2
q	-16	ASP	-	expression tag	UNP C4R6B2
q	-15	ASP	-	expression tag	UNP C4R6B2
q	-14	ASP	-	expression tag	UNP C4R6B2
q	-13	LYS	-	expression tag	UNP C4R6B2
q	-12	GLU	-	expression tag	UNP C4R6B2
q	-11	HIS	-	expression tag	UNP C4R6B2
q	-10	LEU	-	expression tag	UNP C4R6B2
q	-9	TYR	-	expression tag	UNP C4R6B2
q	-8	PHE	-	expression tag	UNP C4R6B2
q	-7	GLN	-	expression tag	UNP C4R6B2
q	-6	GLY	-	expression tag	UNP C4R6B2
q	-5	SER	-	expression tag	UNP C4R6B2
q	-4	SER	-	expression tag	UNP C4R6B2
q	-3	GLY	-	expression tag	UNP C4R6B2
q	-2	SER	-	expression tag	UNP C4R6B2
q	-1	SER	-	expression tag	UNP C4R6B2
q	0	GLY	-	expression tag	UNP C4R6B2

- Molecule 22 is a protein called RNAPII-associated chromatin remodeling Paf1 complex sub-

unit.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	r	266	Total	C	N	O	S	0	0
			2139	1342	374	412	11		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	-29	MET	-	initiating methionine	UNP F2QQ42
r	-28	LYS	-	expression tag	UNP F2QQ42
r	-27	ASP	-	expression tag	UNP F2QQ42
r	-26	HIS	-	expression tag	UNP F2QQ42
r	-25	LEU	-	expression tag	UNP F2QQ42
r	-24	ILE	-	expression tag	UNP F2QQ42
r	-23	HIS	-	expression tag	UNP F2QQ42
r	-22	ASN	-	expression tag	UNP F2QQ42
r	-21	HIS	-	expression tag	UNP F2QQ42
r	-20	HIS	-	expression tag	UNP F2QQ42
r	-19	LYS	-	expression tag	UNP F2QQ42
r	-18	HIS	-	expression tag	UNP F2QQ42
r	-17	GLU	-	expression tag	UNP F2QQ42
r	-16	HIS	-	expression tag	UNP F2QQ42
r	-15	ALA	-	expression tag	UNP F2QQ42
r	-14	HIS	-	expression tag	UNP F2QQ42
r	-13	ALA	-	expression tag	UNP F2QQ42
r	-12	GLU	-	expression tag	UNP F2QQ42
r	-11	HIS	-	expression tag	UNP F2QQ42
r	-10	LEU	-	expression tag	UNP F2QQ42
r	-9	TYR	-	expression tag	UNP F2QQ42
r	-8	PHE	-	expression tag	UNP F2QQ42
r	-7	GLN	-	expression tag	UNP F2QQ42
r	-6	GLY	-	expression tag	UNP F2QQ42
r	-5	SER	-	expression tag	UNP F2QQ42
r	-4	SER	-	expression tag	UNP F2QQ42
r	-3	GLY	-	expression tag	UNP F2QQ42
r	-2	SER	-	expression tag	UNP F2QQ42
r	-1	SER	-	expression tag	UNP F2QQ42
r	0	GLY	-	expression tag	UNP F2QQ42

- Molecule 23 is a protein called Leo1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	u	208	Total	C	N	O	S	0	0
			1707	1063	304	337	3		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	-29	MET	-	initiating methionine	UNP C4R3K1
u	-28	LYS	-	expression tag	UNP C4R3K1
u	-27	ASP	-	expression tag	UNP C4R3K1
u	-26	HIS	-	expression tag	UNP C4R3K1
u	-25	LEU	-	expression tag	UNP C4R3K1
u	-24	ILE	-	expression tag	UNP C4R3K1
u	-23	HIS	-	expression tag	UNP C4R3K1
u	-22	ASN	-	expression tag	UNP C4R3K1
u	-21	HIS	-	expression tag	UNP C4R3K1
u	-20	HIS	-	expression tag	UNP C4R3K1
u	-19	LYS	-	expression tag	UNP C4R3K1
u	-18	HIS	-	expression tag	UNP C4R3K1
u	-17	GLU	-	expression tag	UNP C4R3K1
u	-16	HIS	-	expression tag	UNP C4R3K1
u	-15	ALA	-	expression tag	UNP C4R3K1
u	-14	HIS	-	expression tag	UNP C4R3K1
u	-13	ALA	-	expression tag	UNP C4R3K1
u	-12	GLU	-	expression tag	UNP C4R3K1
u	-11	HIS	-	expression tag	UNP C4R3K1
u	-10	LEU	-	expression tag	UNP C4R3K1
u	-9	TYR	-	expression tag	UNP C4R3K1
u	-8	PHE	-	expression tag	UNP C4R3K1
u	-7	GLN	-	expression tag	UNP C4R3K1
u	-6	GLY	-	expression tag	UNP C4R3K1
u	-5	SER	-	expression tag	UNP C4R3K1
u	-4	SER	-	expression tag	UNP C4R3K1
u	-3	GLY	-	expression tag	UNP C4R3K1
u	-2	SER	-	expression tag	UNP C4R3K1
u	-1	SER	-	expression tag	UNP C4R3K1
u	0	GLY	-	expression tag	UNP C4R3K1

- Molecule 24 is a protein called RNAP II-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	v	349	Total	C	N	O	S	0	0
			2878	1835	510	528	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	-2	GLY	-	expression tag	UNP C4R997

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Chain	Residue	Modelled	Actual	Comment	Reference
v	-1	SER	-	expression tag	UNP C4R997
v	0	ALA	-	expression tag	UNP C4R997

- Molecule 25 is a protein called Constituent of Paf1 complex with RNA polymerase II, Paf1p, Hpr1p, Ctr9, Leo1, Rtf1 and Ccr4p.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	x	205	Total	C	N	O	S	0	0
			1682	1086	287	307	2		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	-29	MET	-	initiating methionine	UNP C4R1E6
x	-28	LYS	-	expression tag	UNP C4R1E6
x	-27	ASP	-	expression tag	UNP C4R1E6
x	-26	HIS	-	expression tag	UNP C4R1E6
x	-25	LEU	-	expression tag	UNP C4R1E6
x	-24	ILE	-	expression tag	UNP C4R1E6
x	-23	HIS	-	expression tag	UNP C4R1E6
x	-22	ASN	-	expression tag	UNP C4R1E6
x	-21	HIS	-	expression tag	UNP C4R1E6
x	-20	HIS	-	expression tag	UNP C4R1E6
x	-19	LYS	-	expression tag	UNP C4R1E6
x	-18	HIS	-	expression tag	UNP C4R1E6
x	-17	GLU	-	expression tag	UNP C4R1E6
x	-16	HIS	-	expression tag	UNP C4R1E6
x	-15	ALA	-	expression tag	UNP C4R1E6
x	-14	HIS	-	expression tag	UNP C4R1E6
x	-13	ALA	-	expression tag	UNP C4R1E6
x	-12	GLU	-	expression tag	UNP C4R1E6
x	-11	HIS	-	expression tag	UNP C4R1E6
x	-10	LEU	-	expression tag	UNP C4R1E6
x	-9	TYR	-	expression tag	UNP C4R1E6
x	-8	PHE	-	expression tag	UNP C4R1E6
x	-7	GLN	-	expression tag	UNP C4R1E6
x	-6	GLY	-	expression tag	UNP C4R1E6
x	-5	SER	-	expression tag	UNP C4R1E6
x	-4	SER	-	expression tag	UNP C4R1E6
x	-3	GLY	-	expression tag	UNP C4R1E6
x	-2	SER	-	expression tag	UNP C4R1E6
x	-1	SER	-	expression tag	UNP C4R1E6

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Chain	Residue	Modelled	Actual	Comment	Reference
x	0	GLY	-	expression tag	UNP C4R1E6

- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

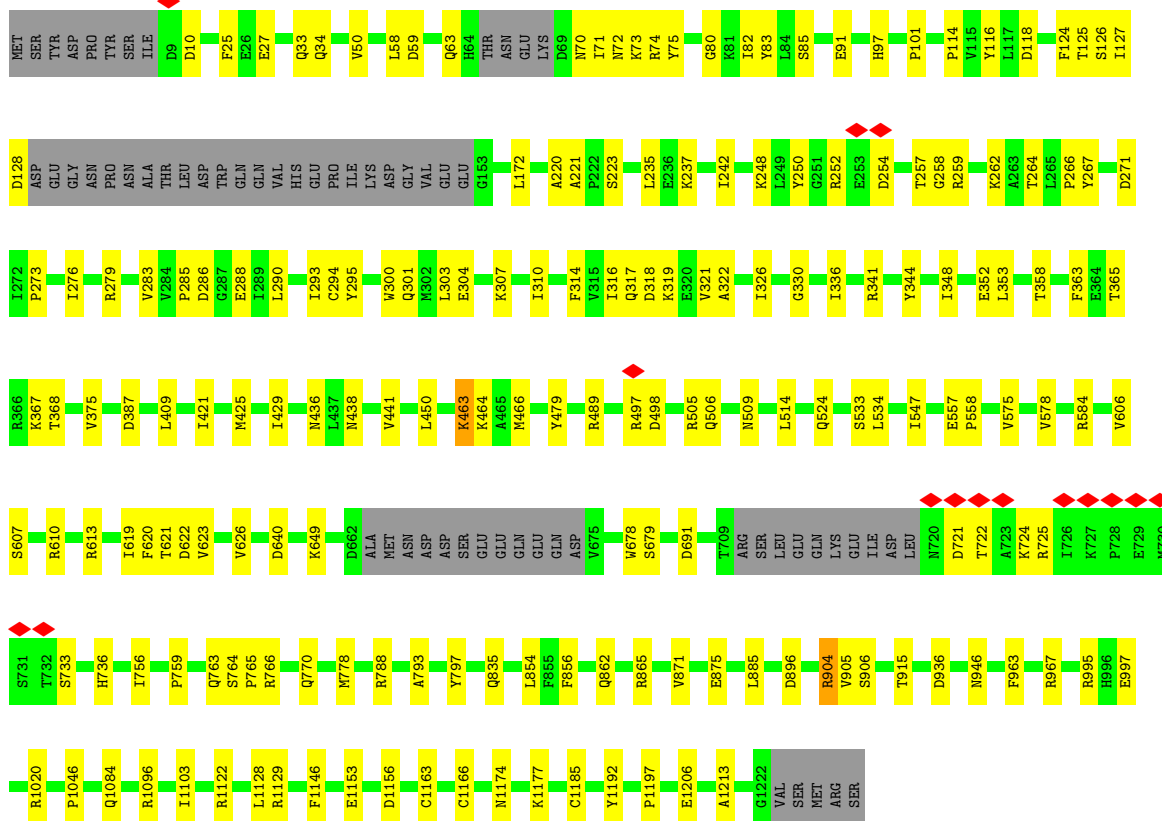
Mol	Chain	Residues	Atoms		AltConf
26	A	2	Total 2	Zn 2	0
26	B	1	Total 1	Zn 1	0
26	C	1	Total 1	Zn 1	0
26	I	2	Total 2	Zn 2	0
26	J	1	Total 1	Zn 1	0
26	L	1	Total 1	Zn 1	0
26	M	1	Total 1	Zn 1	0
26	V	1	Total 1	Zn 1	0

- Molecule 27 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

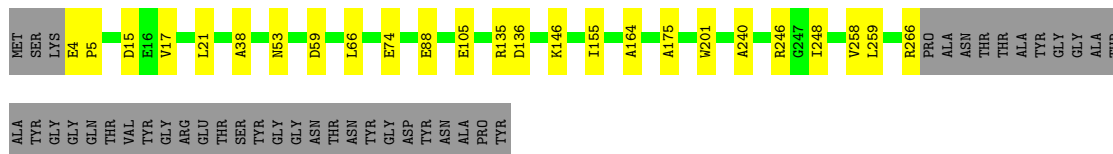
- Molecule 2: DNA-directed RNA polymerase subunit beta

Chain B:



- Molecule 3: RNA polymerase II third largest subunit B44, part of central core

Chain C:




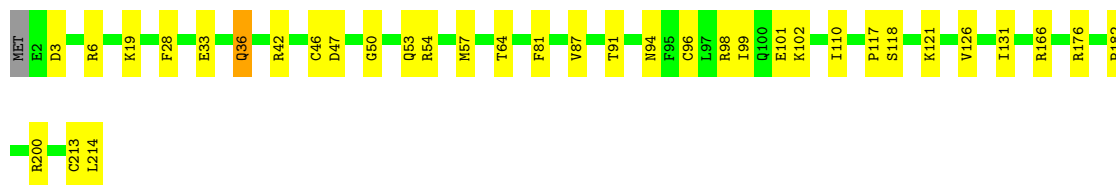
- Molecule 4: RNA polymerase II subunit B32

Chain D:



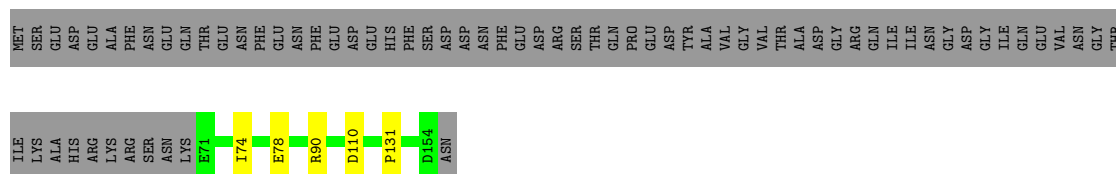
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E:  83% 16%




- Molecule 6: RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III

Chain F:  51% 46%




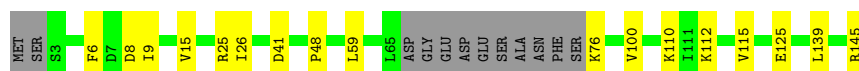
- Molecule 7: RNA polymerase II subunit

Chain G:  82% 18%




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

Chain H:  80% 12% 8%




- Molecule 9: DNA-directed RNA polymerase subunit

Chain I:  6% 81% 16%



- Molecule 10: RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III

Chain J:  82% 11% 7%



- Molecule 11: RNA polymerase II subunit B12.5

#1	I11	N29	L42	R47	D55	V56	T57	Y61	K62	V63	E64	H65	F68	Q76	T77	E78	K84	R89	A90	C91	L101	D102	H103	E107	N113	PHE	SER	LEU	ASN	ASP
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- Chain L:  56% 7% 38%

MET	SER	ARG	GLU	GLY	PHE	VAL	ALA	PRO	PRO	SER	GLY	THR	ASP	LEU	ALA	ALA	ALA	ALA	SER	SER	GLY	VAL	ALA	ALA	PRO	ASN	LYS	HIS	TYR	G28	V29	K30	Y31	T32	C33	G34		D70	A71	R72
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- Chain M: 

[illegible]

- Chain N: 6% 12% 79%

[illegible]

- Chain P:  37% 21% 37% 5%

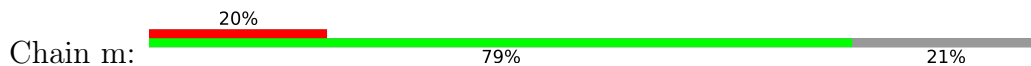
Category	Count
U-7	1
G-6	1
C-5	1
C-4	2
U-3	1
G-2	1
G-1	1
U0	1
G1	1
U2	1
G6	1
G10	1
U11	1

- Chain T: 9% 14% 73%

[illegible]

[illegible]

- Molecule 19: Transcription elongation factor Spt6



GLY	PRO	GLY	MET	SER	ALA	PRO	SER	PRO	SER	VAL	SER	GLU	ASP	TLE	ASN	THR	ARG	ASN	SER	SER	TLE	ASP	ALA	ALA	ALA	SER	THR	THR	GLN	ASP	LEU	LEU	ASP	GLN	ASP	GLN	GLN	GLY	SER	GLY	SER	ASP	ASN	GLY	SER	VAL	ASP	ASN	GLU	GLY	ASP
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[illegible]

ASN	SER	GLY	ALA	VAL	PRO	GLY	GLN	GLN	GLN	ASN	VAL	LYS	PHE	LYS	ARG	LEU	LYS	ARG	ALA	GLU	GLN	ASP	GLU	LYS	ALA	GLN	ASP	SER	ASP	SER	ARG	GLY	LEU	ASN	ASP	MET	PHE	SER	SER	ASP	GLU	GLU	GLY	GLY	VAL	VAL	GLU	GLU	GLY	LEU	GLU	ASP	ASN
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[illegible]

P260	GLN	GLN	ASP	GLN	GLU	TYR	ASP	GLU	ALA	GLY	GLU	ILE	LYS	GLY	THR	THR	T278	S279	K290	K291	K292	M293	L294	A312	S316	I317	K318	D399	M400	M401	M402	D442	L443	D444	V445	V446	M480	L481	T482	A483	V484	ALA	GLU	LEU	SER	ILE	GLY	GLY	ASN	GLY	SER	GLY
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[illegible]

T693	S694	E695	A702	L712	D713	K714	L715	I716	P717	L718	S815	D853	N854	GLU	TYR	GLY	TYR	ASP	ARG	GLU	GLU	ASP	GLY	ARG	S866	R839	R966	I995	G996	S997	E1008	Q1009	L1010	V1026	F1027	D1028	P1029	D1030	V1031	E1032	R1033	N1034	P1035	G1036	G1037	E1038	D1064	I1065	S1066	L1067	E1068	S1069	L1070	E1071	S1072	L1073	E1074	S1075	L1076	E1077	S1078	L1079	E1079	S1080	L1081	E1082	S1083	L1084	E1085	S1086	L1087	E1088	S1089	L1089	E1089	S1090	L1091	E1091	S1092	L1092	E1092	S1093	L1093	E1093	S1094	L1094	E1094	S1095	L1095	E1095	S1096	L1096	E1096	S1097	L1097	E1097	S1098	L1098	E1098	S1099	L1099	E1099	S1100	L1100	E1100	S1101	L1101	E1101	S1102	L1102	E1102	S1103	L1103	E1103	S1104	L1104	E1104	S1105	L1105	E1105	S1106	L1106	E1106	S1107	L1107	E1107	S1108	L1108	E1108	S1109	L1109	E1109	S1110	L1110	E1110	S1111	L1111	E1111	S1112	L1112	E1112	S1113	L1113	E1113	S1114	L1114	E1114	S1115	L1115	E1115	S1116	L1116	E1116	S1117	L1117	E1117	S1118	L1118	E1118	S1119	L1119	E1119	S1120	L1120	E1120	S1121	L1121	E1121	S1122	L1122	E1122	S1123	L1123	E1123	S1124	L1124	E1124	S1125	L1125	E1125	S1126	L1126	E1126	S1127	L1127	E1127	S1128	L1128	E1128	S1129	L1129	E1129	S1130	L1130	E1130	S1131	L1131	E1131	S1132	L1132	E1132	S1133	L1133	E1133	S1134	L1134	E1134	S1135	L1135	E1135	S1136	L1136	E1136	S1137	L1137	E1137	S1138	L1138	E1138	S1139	L1139	E1139	S1140	L1140	E1140	S1141	L1141	E1141	S1142	L1142	E1142	S1143	L1143	E1143	S1144	L1144	E1144	S1145	L1145	E1145	S1146	L1146	E1146	S1147	L1147	E1147	S1148	L1148	E1148	S1149	L1149	E1149	S1150	L1150	E1150	S1151	L1151	E1151	S1152	L1152	E1152	S1153	L1153	E1153	S1154	L1154	E1154	S1155	L1155	E1155	S1156	L1156	E1156	S1157	L1157	E1157	S1158	L1158	E1158	S1159	L1159	E1159	S1160	L1160	E1160	S1161	L1161	E1161	S1162	L1162	E1162	S1163	L1163	E1163	S1164	L1164	E1164	S1165	L1165	E1165	S1166	L1166	E1166	S1167	L1167	E1167	S1168	L1168	E1168	S1169	L1169	E1169	S1170	L1170	E1170	S1171	L1171	E1171	S1172	L1172	E1172	S1173	L1173	E1173	S1174	L1174	E1174	S1175	L1175	E1175	S1176	L1176	E1176	S1177	L1177	E1177	S1178	L1178	E1178	S1179	L1179	E1179	S1180	L1180	E1180	S1181	L1181	E1181	S1182	L1182	E1182	S1183	L1183	E1183	S1184	L1184	E1184	S1185	L1185	E1185	S1186	L1186	E1186	S1187	L1187	E1187	S1188	L1188	E1188	S1189	L1189	E1189	S1190	L1190	E1190	S1191	L1191	E1191	S1192	L1192	E1192	S1193	L1193	E1193	S1194	L1194	E1194	S1195	L1195	E1195	S1196	L1196	E1196	S1197	L1197	E1197	S1198	L1198	E1198	S1199	L1199	E1199	S1200	L1200	E1200	S1201	L1201	E1201	S1202	L1202	E1202	S1203	L1203	E1203	S1204	L1204	E1204	S1205	L1205	E1205	S1206	L1206	E1206	S1207	L1207	E1207	S1208	L1208	E1208	S1209	L1209	E1209	S1210	L1210	E1210	S1211	L1211	E1211	S1212	L1212	E1212	S1213	L1213	E1213	S1214	L1214	E1214	S1215	L1215	E1215	S1216	L1216	E1216	S1217	L1217	E1217	S1218	L1218	E1218	S1219	L1219	E1219	S1220	L1220	E1220	S1221	L1221	E1221	S1222	L1222	E1222	S1223	L1223	E1223	S1224	L1224	E1224	S1225	L1225	E1225	S1226	L1226	E1226	S1227	L1227	E1227	S1228	L1228	E1228	S1229	L1229	E1229	S1230	L1230	E1230	S1231	L1231	E1231	S1232	L1232	E1232	S1233	L1233	E1233	S1234	L1234	E1234	S1235	L1235	E1235	S1236	L1236	E1236	S1237	L1237	E1237	S1238	L1238	E1238	S1239	L1239	E1239	S1240	L1240	E1240	S1241	L1241	E1241	S1242	L1242	E1242	S1243	L1243	E1243	S1244	L1244	E1244	S1245	L1245	E1245	S1246	L1246	E1246	S1247	L1247	E1247	S1248	L1248	E1248	S1249	L1249	E1249	S1250	L1250	E1250	S1251	L1251	E1251	S1252	L1252	E1252	S1253	L1253	E1253	S1254	L1254	E1254	S1255	L1255	E1255	S1256	L1256	E1256	S1257	L1257	E1257	S1258	L1258	E1258	S1259	L1259	E1259	S1260	L1260	E1260	S1261	L1261	E1261	S1262	L1262	E1262	S1263	L1263	E1263	S1264	L1264	E1264	S1265	L1265	E1265	S1266	L1266	E1266	S1267	L1267	E1267	S1268	L1268	E1268	S1269	L1269	E1269	S1270	L1270	E1270	S1271	L1271	E1271	S1272	L1272	E1272	S1273	L1273	E1273	S1274	L1274	E1274	S1275	L1275	E1275	S1276	L1276	E1276	S1277	L1277	E1277	S1278	L1278	E1278	S1279	L1279	E1279	S1280	L1280	E1280	S1281	L1281	E1281	S1282	L1282	E1282	S1283	L1283	E1283	S1284	L1284	E1284	S1285	L1285	E1285	S1286	L1286	E1286	S1287	L1287	E1287	S1288	L1288	E1288	S1289	L1289	E1289	S1290	L1290	E1290	S1291	L1291	E1291	S1292	L1292	E1292	S1293	L1293	E1293	S1294	L1294	E1294	S1295	L1295	E1295	S1296	L1296	E1296	S1297	L1297	E1297	S1298	L1298	E1298	S1299	L1299	E1299	S1300	L1300	E1300	S1301	L1301	E1301	S1302	L1302	E1302	S1303	L1303	E1303	S1304	L1304	E1304	S1305	L1305	E1305	S1306	L1306	E1306	S1307	L1307	E1307	S1308	L1308	E1308	S1309	L1309	E1309	S1310	L1310	E1310	S1311	L1311	E1311	S1312	L1312	E1312	S1313	L1313	E1313	S1314	L1314	E1314	S1315	L1315	E1315	S1316	L1316	E1316	S1317	L1317	E1317	S1318	L1318	E1318	S1319	L1319	E1319	S1320	L1320	E1320	S1321	L1321	E1321	S1322	L1322	E1322	S1323	L1323	E1323	S1324	L1324	E1324	S1325	L1325	E1325	S1326	L1326	E1326	S1327	L1327	E1327	S1328	L1328	E1328	S1329	L1329	E1329	S1330	L1330	E1330	S1331	L1331	E1331	S1332	L1332	E1332	S1333	L1333	E1333	S1334	L1334	E1334	S1335	L1335	E1335	S1336	L1336	E1336	S1337	L1337	E1337	S1338	L1338	E1338	S1339	L1339	E1339	S1340	L1340	E1340	S1341	L1341	E1341	S1342	L1342	E1342	S1343	L1343	E1343	S1344	L1344	E1344	S1345	L1345	E1345	S1346	L1346	E1346	S1347	L1347	E1347	S1348	L1348	E1348	S1349	L1349	E1349	S1350	L1350	E1350	S1351	L1351	E1351	S1352	L1352	E1352	S1353	L1353	E1353	S1354	L1354	E1354	S1355	L1355	E1355	S1356	L1356	E1356	S1357	L1357	E1357	S1358	L1358	E1358	S1359	L1359	E1359	S1360	L1360	E1360	S1361	L1361	E1361	S1362	L1362	E1362	S1363	L1363	E1363	S1364	L1364	E1364	S1365	L1365	E1365	S1366	L1366	E1366	S1367	L1367	E1367	S1368	L1368	E1368	S1369	L1369	E1369	S1370	L1370	E1370	S1371	L1371	E1371	S1372	L1372	E1372	S1373	L1373	E1373	S1374	L1374	E1374	S1375	L1375	E1375	S1376	L1376	E1376	S1377	L1377	E1377	S1378	L1378	E1378	S1379	L1379	E1379	S1380	L1380	E1380	S1381	L1381	E1381	S1382	L1382	E1382	S1383	L1383	E1383	S1384	L1384	E1384	S1385	L1385	E1385	S1386	L1386	E1386	S1387	L1387	E1387	S1388	L1388	E1388	S1389	L1389	E1389	S1390	L1390	E1390	S1391	L1391	E1391	S1392	L1392	E1392	S1393	L1393	E1393	S1394	L1394	E1394	S1395	L1395	E1395	S1396	L1396	E1396	S1397	L1397	E1397	S1398	L1398	E1398	S1399	L1399	E1399	S1400	L1400	E1400	S1401	L1401	E1401	S1402	L1402	E1402	S1403	L1403	E1403	S1404	L1404	E1404	S1405	L1405	E1405	S1406	L1406	E1406	S1407	L1407	E1407	S1408	L1408	E1408	S1409	L1409	E1409	S1410	L1410	E1410	S1411	L1411	E1411	S1412	L1412	E1412	S1413	L1413	E1413	S1414	L1414	E1414	S1415	L1415	E1415	S1416	L1416	E1416	S1417	L1417	E1417	S1418	L1418	E1418	S1419	L1419	E1419	S1420	L1420	E1420	S1421	L1421	E1421	S1422	L1422	E1422	S1423	L1423	E1423	S1424	L1424	E1424	S1425	L1425	E1425	S1426	L1426	E1426	S1427	L1427	E1427	S1428	L1428	E1428	S1429	L1429	E1429	S1430	L1430	E1430	S1431	L1431	E1431	S1432	L1432	E1432	S1433	L1433	E1433	S1434	L1434	E1434	S1435	L1435	E1435	S1436	L1436	E1436	S1437	L1437	E1437	S1438	L1438	E1438	S1439	L1439	E1439	S1440	L1440	E1440	S1441	L1441	E1441	S1442	L1442	E1442	S1443	L1443	E1443	S1444	L1444	E1444	S1445	L1445	E1445	S1446	L1446	E1446	S1447	L1447	E1447	S1448	L1448	E1448	S1449	L1449	E1449	S1450	L1450	E1450	S1451	L1451	E1451	S1452	L1452	E1452	S1453	L1453	E1453	S1454	L1454	E1454	S1455	L1455	E1455	S1456	L1456	E1456	S1457	L1457	E1457	S1458	L1458	E1458	S1459	L1459	E1459	S1460	L1460	E1460	S1461	L1461	E1461	S1462	L1462	E1462	S1463	L1463	E1463	S1464	L1464	E1464	S1465	L1465	E1465	S1466	L1466	E1466	S1467	L1467	E1467	S1468	L1468	E1468	S1469	L1469	E1469	S1470	L1470	E1470	S1471	L1471	E1471	S1472	L1472	E1472	S1473	L1473	E1473	S1474	L1474	E1474	S1475	L1475	E1475	S1476	L1476	E1476	S1477	L1477	E1477	S1478	L1478	E1478	S1479	L1479	E1479	S1480	L1480	E1480	S1481	L1481	E1481	S1482	L1482	E1482	S1483	L1483	E1483	S1484	L1484	E1484	S1485	L1485	E1485	S1486	L1486	E1486	S1487	L1487	E1487	S1488	L1488	E1488	S1489	L1489	E1489	S1490	L1490	E1490	S1491	L1491	E1491	S1492	L1492	E1492	S1493	L1493	E1493	S1494	L1494	E1494	S1495	L1495	E1495	S1496	L1496	E1496	S1497	L1497	E1497	S1498	L1498	E1498	S1499	L1499	E1499	S1500	L1500	E1500	S1501	L1501	E1501	S1502	L1502	E1502	S1503	L1503	E1503	S1504	L1504	E1504	S1505	L1505	E1505	S1506	L1506	E1506	S1507	L1507	E1507	S1508	L1508	E1508	S1509	L1509	E1509	S1510	L1510	E1510	S1511	L1511	E1511	S1512	L1512	E1512	S1513	L1513	E1513	S1514	L1514	E1514	S1515	L1515	E1515	S1516	L1516	E1516	S1517	L1517	E1517	S1518	L1518	E1518	S1519	L1519	E1519	S1520	L1520	E1520	S1521	L1521	E1521	S1522	L1522	E1522	S1523	L1523	E1523	S1524	L1524	E1524	S1525	L1525	E152
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D1067	I1068	D1069	D1070	D1071	D1072	R1087	S1088	P1089	P1090	K1091	E1092	E1093	R1114	P1200	M1201	D1202	R1203	A1244	G1245	L1246	M1247	E1274	S1275	R1276	E1277	S1278	R1279	V1280	I1281	K1282	H1283	P1284	F1285	F1286	H1287	M1288	M1289	K1290	S1291	K1292	E1293	A1294	E1295	D1296	V1297	L1298	A1299	A1300	R1301	P1302	V1303	G1304	D1305	V1306
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V1307	I1308	I1309	P1310	S1311	S1312	I1318	T1319	I1320	S1321	K1323	S1324	A1325	P1326	Q1327	L1328	I1329	Q1330	H1331	I1332	V1334	L1335	E1337	M1338	D1340	D1341	A1342	M1343	A1344	I1345	G1346	I1347	V1348	L1349	L1350	V1351	K1352	K1353	V1354	I1355	Y1356	H1357	D1358	L1359	D1360	E1361	L1362	L1363	V1364	E1365	Y1366	V1367	M1368	V1370
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A1371	M1372	K1373	V1374	E1375	L1376	M1377	V1378	S1379	H1380	D1381	K1382	F1383	M1384	S1385	L1386	S1387	L1388	L1389	V1390	V1391	K1392	S1393	V1394	L1395	E1396	R1397	V1398	S1399	K1400	A1401	M1402	G1403	N1404	R1405	S1406	H1407	V1408	L1409	F1410	T1411	F1412	M1413	K1414	A1415	P1417	G1418	M1419	F1420	F1421	L1422	L1423	F1424	K1425	L1426	M1427	P1428	T1429
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E1431	I1432	I1433	I1434	W1435	M1436	I1437	K1438	A1439	L1440	P1441	D1442	G1443	I1444	L1445	L1446	A1447	M1448	N1449	V1450	Y1451	D1452	D1453	T1454	M1455	S1456	L1457	C1458	M1459	G1460	F1461	K1462	T1463	L1464	M1465	S1466	S1467	R1468	R1469	GLN	ILE	LYS	GLN	ARG	SER	ASN	ARG	ALA	GLY	GLY	GLU	TYR	ASN	ASN	SER	HIS	ALA	GLY	ALA	TYR
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ASP
ASN
GLY
TYR
SER
ASN
ALA
PRO
ARG
TYR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	444232	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.127	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.015	Depositor
Map size (\AA)	356.16, 356.16, 356.16	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.484, 1.484, 1.484	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, 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	0.31	0/11267	0.49	0/15222
2	B	0.33	0/9464	0.52	0/12763
3	C	0.33	0/2139	0.49	0/2895
4	D	0.23	0/1361	0.46	0/1837
5	E	0.30	0/1773	0.49	0/2385
6	F	0.33	0/687	0.50	0/931
7	G	0.28	0/1354	0.48	0/1837
8	H	0.33	0/1070	0.49	0/1444
9	I	0.24	0/934	0.50	0/1257
10	J	0.36	0/563	0.50	0/753
11	K	0.32	0/953	0.50	0/1291
12	L	0.32	0/365	0.56	0/484
13	M	0.24	0/513	0.41	0/693
14	N	0.96	6/952 (0.6%)	0.95	0/1464
15	P	1.17	5/449 (1.1%)	1.57	8/698 (1.1%)
16	T	1.06	13/1227 (1.1%)	0.98	0/1890
17	V	0.24	0/840	0.50	0/1140
18	W	0.24	0/4300	0.49	0/5812
19	m	0.24	0/9925	0.45	0/13424
20	n	0.23	0/1132	0.42	0/1526
21	q	0.24	0/7689	0.40	0/10368
22	r	0.24	0/2169	0.45	0/2901
23	u	0.24	0/1740	0.48	0/2347
24	v	0.25	0/2944	0.47	0/3973
25	x	0.25	0/1716	0.45	0/2310
All	All	0.34	24/67526 (0.0%)	0.52	8/91645 (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
15	P	0	1

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	P	10	G	C1'-N9	-6.75	1.37	1.46
15	P	6	G	C1'-N9	-6.44	1.37	1.46
16	T	34	DA	C1'-N9	-6.22	1.38	1.47
16	T	53	DA	C1'-N9	-6.03	1.38	1.47
14	N	-21	DG	C1'-N9	-5.90	1.39	1.47

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	P	-4	C	N3-C2-O2	-7.11	116.93	121.90
15	P	11	U	OP1-P-OP2	-6.44	109.93	119.60
15	P	-4	C	N1-C2-O2	6.32	122.69	118.90
15	P	-1	G	N3-C2-N2	-6.30	115.49	119.90
15	P	-3	U	N3-C2-O2	-6.09	117.94	122.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	P	-4	C	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	11064	0	11090	120	0
2	B	9284	0	9282	118	0
3	C	2098	0	2057	18	0
4	D	1349	0	1345	11	0
5	E	1741	0	1754	22	0
6	F	677	0	693	4	0
7	G	1325	0	1342	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1053	0	1050	10	0
9	I	917	0	867	14	0
10	J	554	0	573	5	0
11	K	932	0	944	14	0
12	L	359	0	358	4	0
13	M	505	0	495	6	0
14	N	854	0	478	43	0
15	P	404	0	202	7	0
16	T	1090	0	590	36	0
17	V	824	0	795	17	0
18	W	4232	0	4278	57	0
19	m	9730	0	9588	0	0
20	n	1115	0	1186	0	0
21	q	7552	0	7545	0	0
22	r	2139	0	2155	0	0
23	u	1707	0	1676	0	0
24	v	2878	0	2873	0	0
25	x	1682	0	1731	0	0
26	A	2	0	0	0	0
26	B	1	0	0	0	0
26	C	1	0	0	0	0
26	I	2	0	0	0	0
26	J	1	0	0	0	0
26	L	1	0	0	0	0
26	M	1	0	0	0	0
26	V	1	0	0	0	0
27	A	1	0	0	0	0
All	All	66076	0	64947	463	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 6.

The worst 5 of 463 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)
14:N:-48:DC:H2''	14:N:-47:DC:C5	2.03	0.92
16:T:13:DT:H2''	16:T:14:DT:C7	1.99	0.92
16:T:13:DT:H2''	16:T:14:DT:H71	1.51	0.88
1:A:318:LYS:HE3	16:T:43:DA:C6	2.13	0.83
16:T:19:DC:H2'	16:T:20:DG:C8	2.17	0.80

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	1392/1743 (80%)	1354 (97%)	37 (3%)	1 (0%)	51	83
2	B	1154/1227 (94%)	1118 (97%)	36 (3%)	0	100	100
3	C	261/304 (86%)	259 (99%)	2 (1%)	0	100	100
4	D	170/186 (91%)	166 (98%)	4 (2%)	0	100	100
5	E	211/214 (99%)	205 (97%)	6 (3%)	0	100	100
6	F	82/155 (53%)	80 (98%)	2 (2%)	0	100	100
7	G	169/171 (99%)	167 (99%)	2 (1%)	0	100	100
8	H	129/145 (89%)	125 (97%)	4 (3%)	0	100	100
9	I	109/115 (95%)	106 (97%)	3 (3%)	0	100	100
10	J	65/72 (90%)	65 (100%)	0	0	100	100
11	K	111/118 (94%)	110 (99%)	1 (1%)	0	100	100
12	L	43/72 (60%)	41 (95%)	2 (5%)	0	100	100
13	M	62/113 (55%)	62 (100%)	0	0	100	100
17	V	104/108 (96%)	100 (96%)	4 (4%)	0	100	100
18	W	527/911 (58%)	508 (96%)	19 (4%)	0	100	100
19	m	1179/1503 (78%)	1157 (98%)	22 (2%)	0	100	100
20	n	137/417 (33%)	136 (99%)	1 (1%)	0	100	100
21	q	928/1084 (86%)	922 (99%)	6 (1%)	0	100	100
22	r	260/544 (48%)	254 (98%)	6 (2%)	0	100	100
23	u	206/459 (45%)	204 (99%)	2 (1%)	0	100	100
24	v	341/396 (86%)	327 (96%)	14 (4%)	0	100	100
25	x	201/395 (51%)	200 (100%)	1 (0%)	0	100	100
All	All	7841/10452 (75%)	7666 (98%)	174 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	960	VAL

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	1219/1528 (80%)	1216 (100%)	3 (0%)	93	97
2	B	1018/1077 (94%)	1016 (100%)	2 (0%)	93	97
3	C	236/264 (89%)	236 (100%)	0	100	100
4	D	149/160 (93%)	149 (100%)	0	100	100
5	E	196/197 (100%)	194 (99%)	2 (1%)	76	90
6	F	75/137 (55%)	75 (100%)	0	100	100
7	G	148/148 (100%)	148 (100%)	0	100	100
8	H	120/130 (92%)	120 (100%)	0	100	100
9	I	106/109 (97%)	106 (100%)	0	100	100
10	J	61/66 (92%)	61 (100%)	0	100	100
11	K	104/109 (95%)	104 (100%)	0	100	100
12	L	38/56 (68%)	38 (100%)	0	100	100
13	M	61/99 (62%)	60 (98%)	1 (2%)	62	84
17	V	90/92 (98%)	90 (100%)	0	100	100
18	W	480/796 (60%)	480 (100%)	0	100	100
19	m	1087/1354 (80%)	1086 (100%)	1 (0%)	93	98
20	n	125/361 (35%)	125 (100%)	0	100	100
21	q	824/962 (86%)	824 (100%)	0	100	100
22	r	239/485 (49%)	239 (100%)	0	100	100
23	u	192/406 (47%)	191 (100%)	1 (0%)	88	94
24	v	325/369 (88%)	325 (100%)	0	100	100
25	x	190/354 (54%)	190 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	7083/9259 (76%)	7073 (100%)	10 (0%)	93 98

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	40	LYS
19	m	514	LYS
23	u	124	ARG
2	B	463	LYS
2	B	904	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
25	x	296	ASN
21	q	147	ASN
19	m	955	ASN
18	W	644	ASN
20	n	232	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	19/19 (100%)	7 (36%)	3 (15%)

5 of 7 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	P	-6	G
15	P	-5	C
15	P	-4	C
15	P	-3	U
15	P	-2	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	P	-7	U
15	P	-3	U
15	P	-2	G

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 11 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.

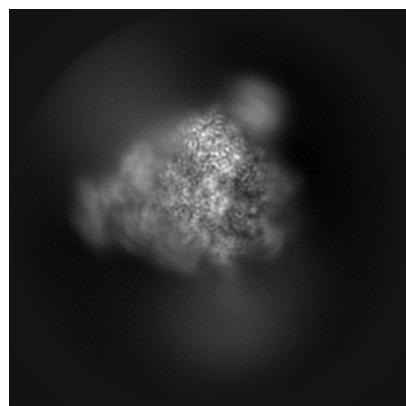
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33313. These allow visual inspection of the internal detail of the map and identification of artifacts.

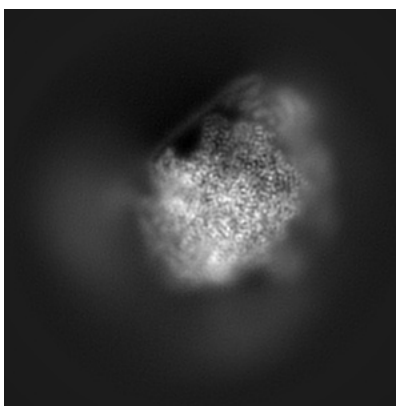
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

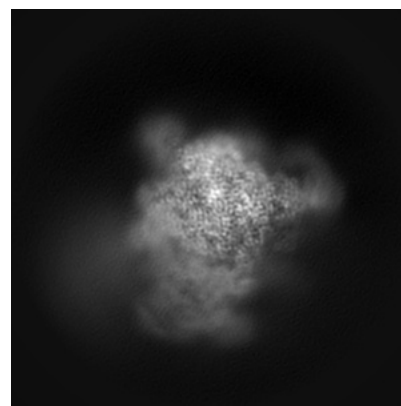
6.1.1 Primary map



X

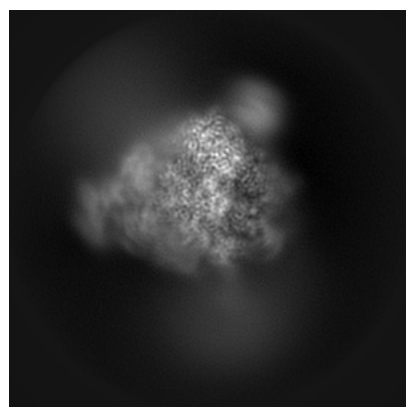


Y

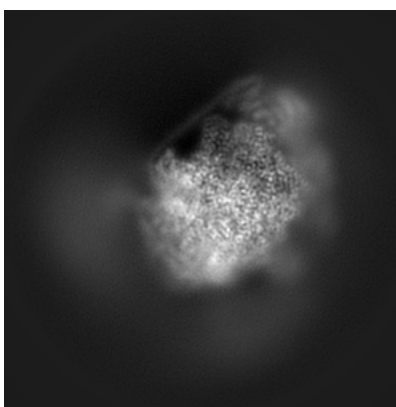


Z

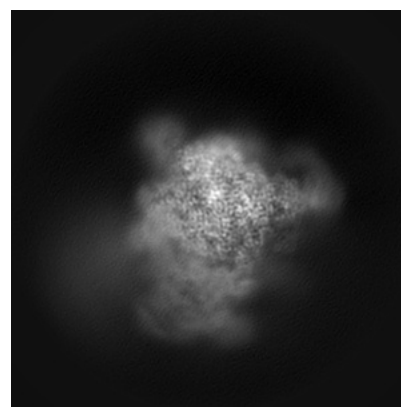
6.1.2 Raw map



X



Y

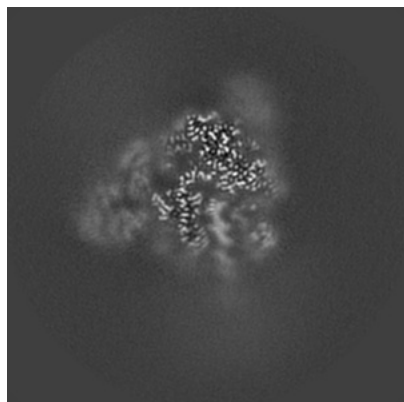


Z

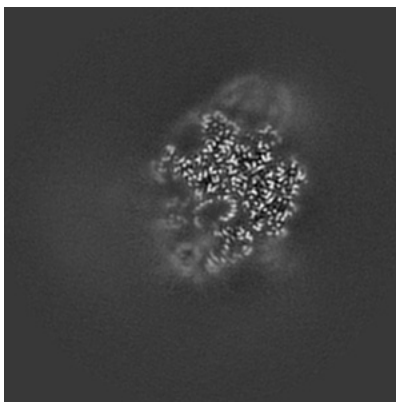
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

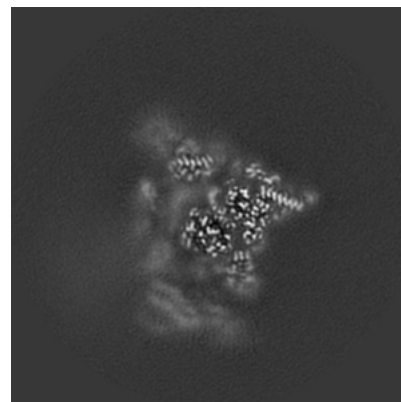
6.2.1 Primary map



X Index: 120

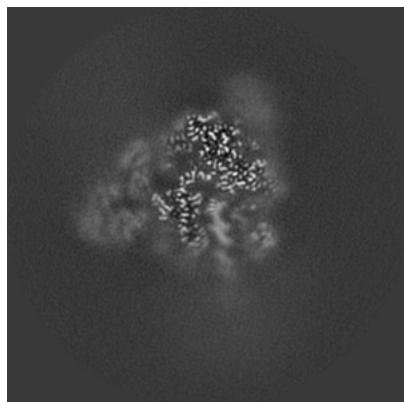


Y Index: 120

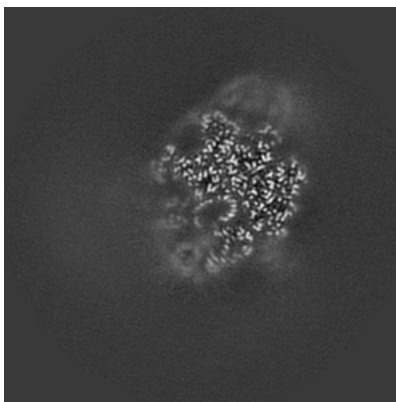


Z Index: 120

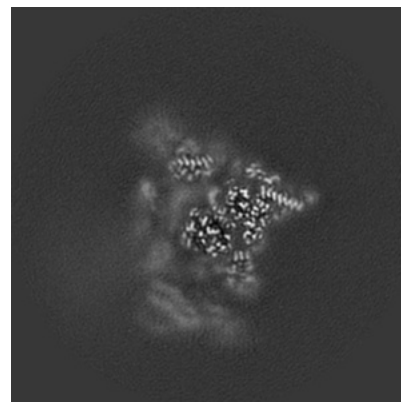
6.2.2 Raw map



X Index: 120



Y Index: 120

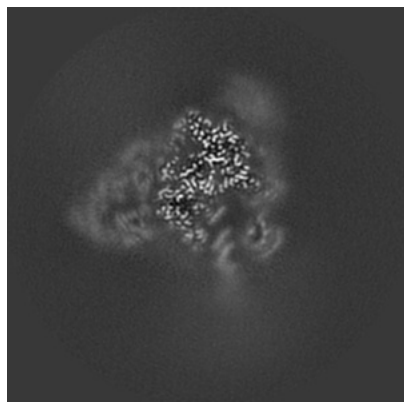


Z Index: 120

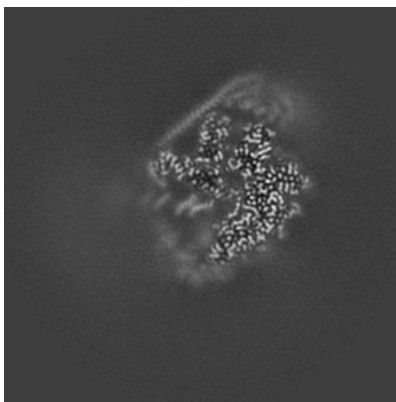
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

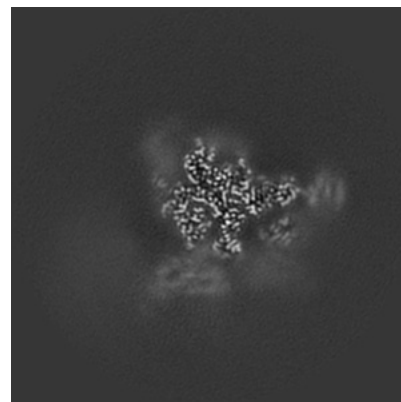
6.3.1 Primary map



X Index: 125

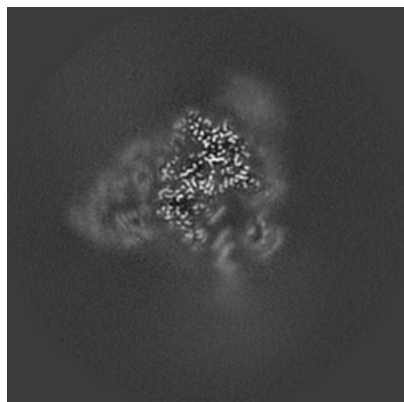


Y Index: 124

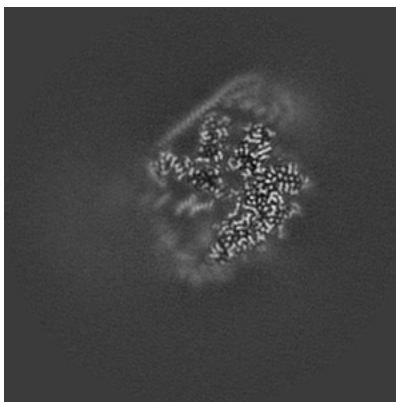


Z Index: 146

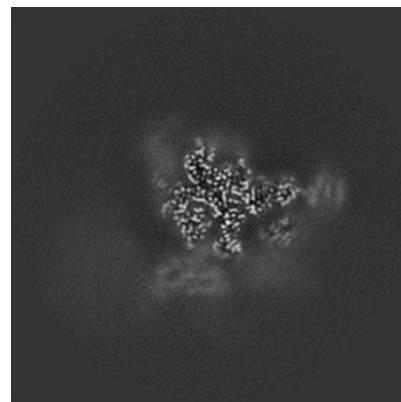
6.3.2 Raw map



X Index: 125



Y Index: 124

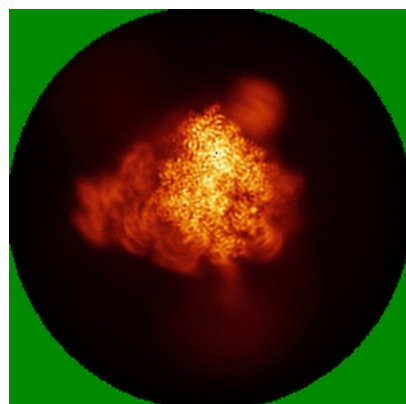


Z Index: 146

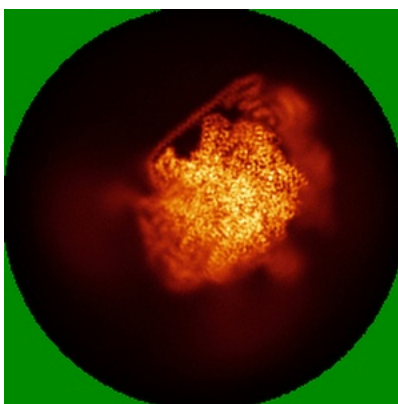
The images above show the largest variance slices of the map in three orthogonal directions.

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

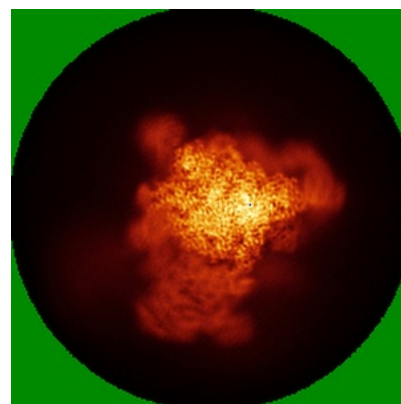
6.4.1 Primary map



X

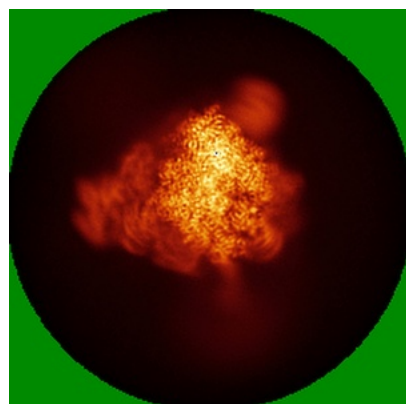


Y

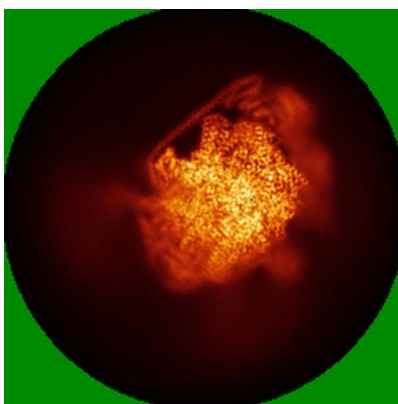


Z

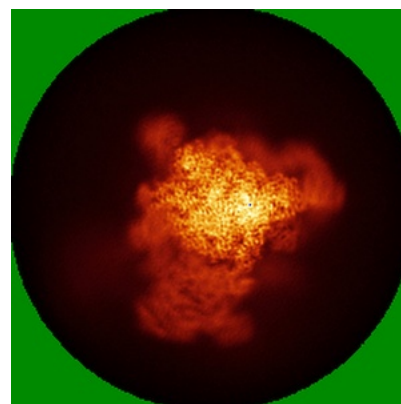
6.4.2 Raw map



X



Y

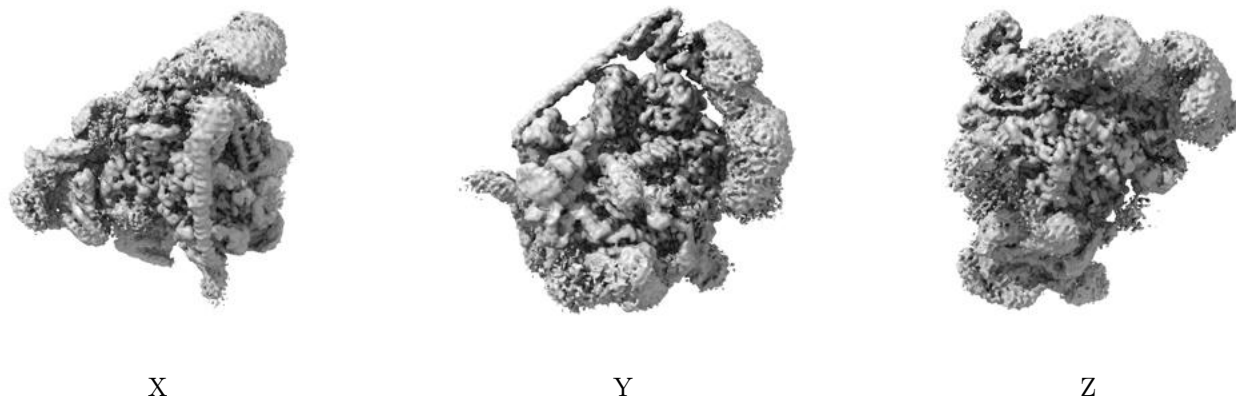


Z

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.

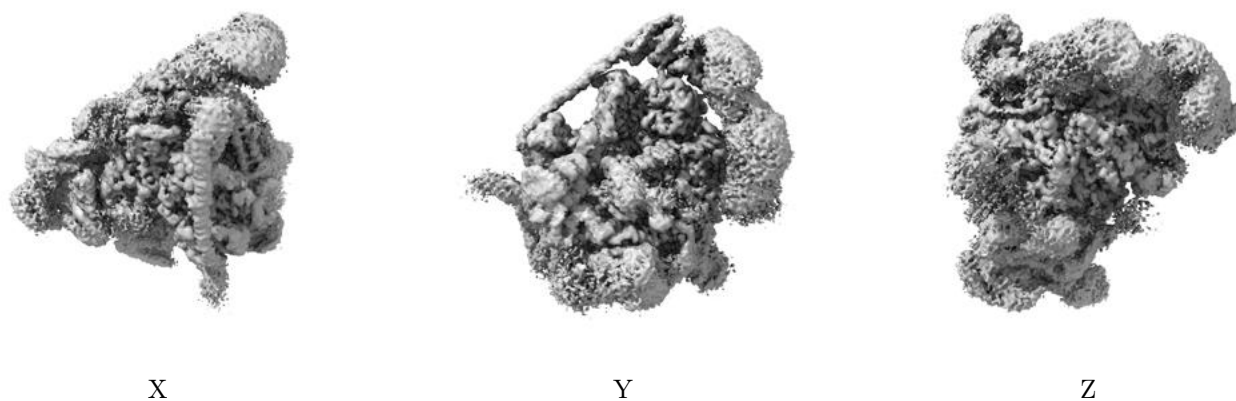
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. 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.

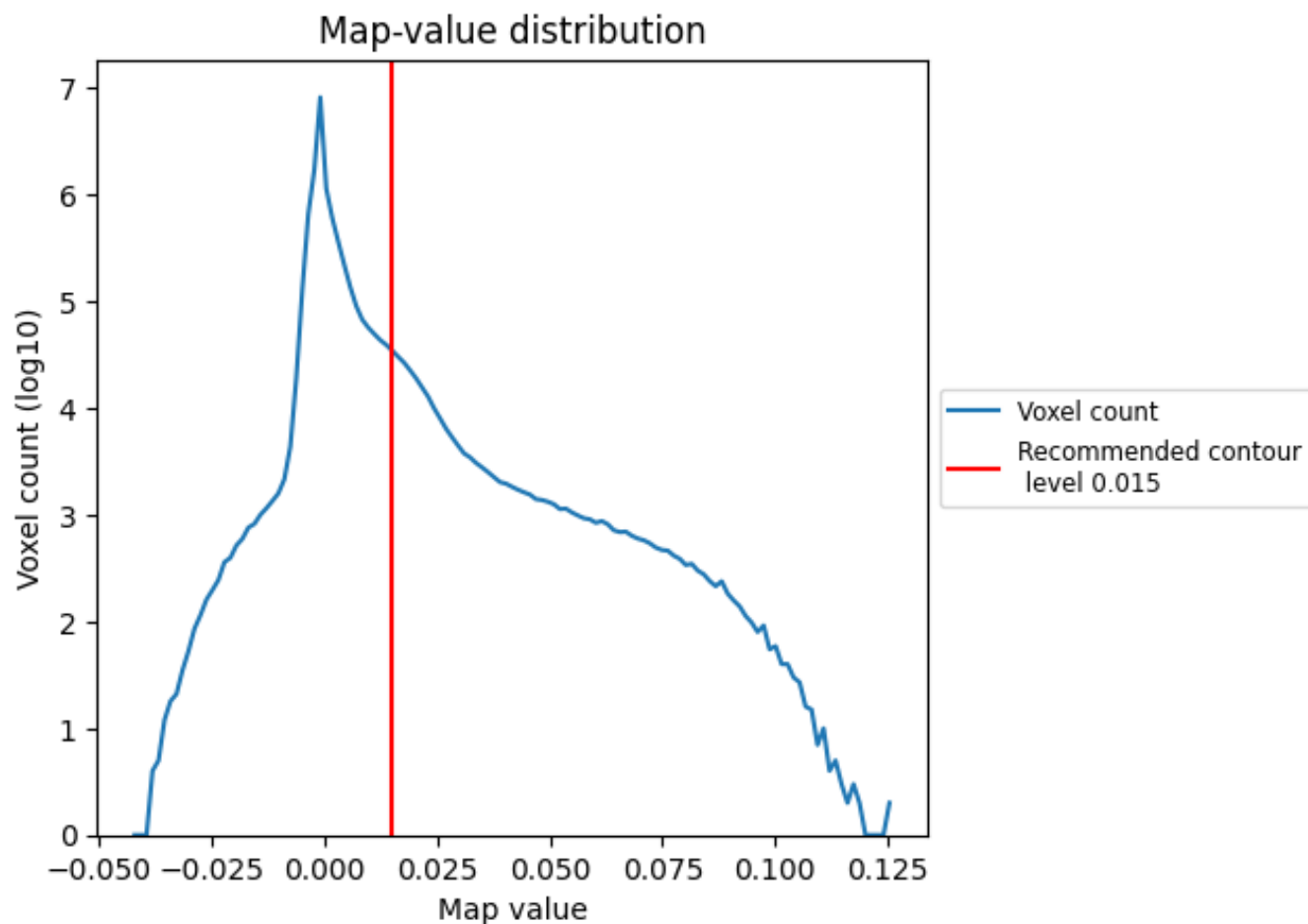
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

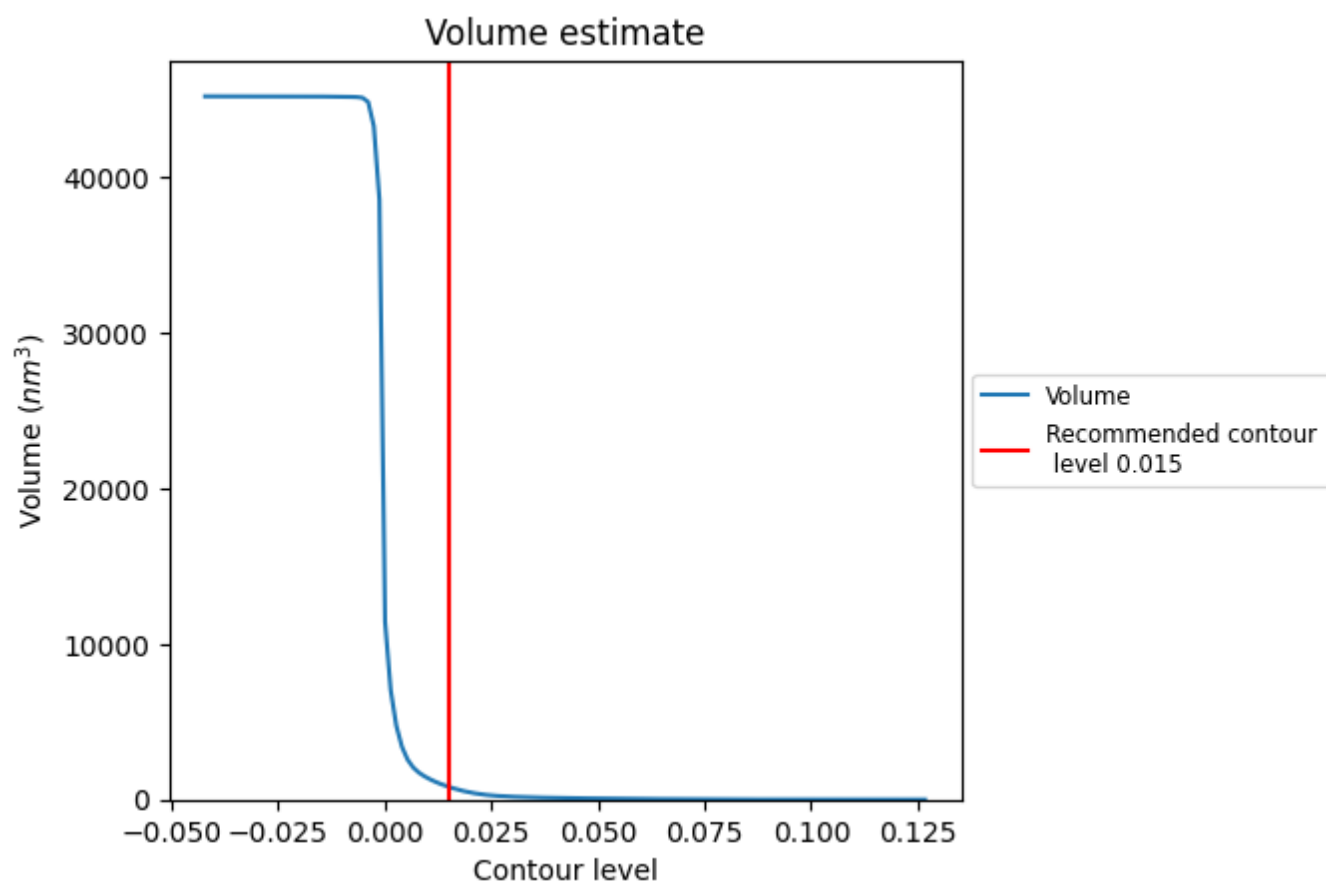
This section contains the results of statistical analysis of the map.

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.

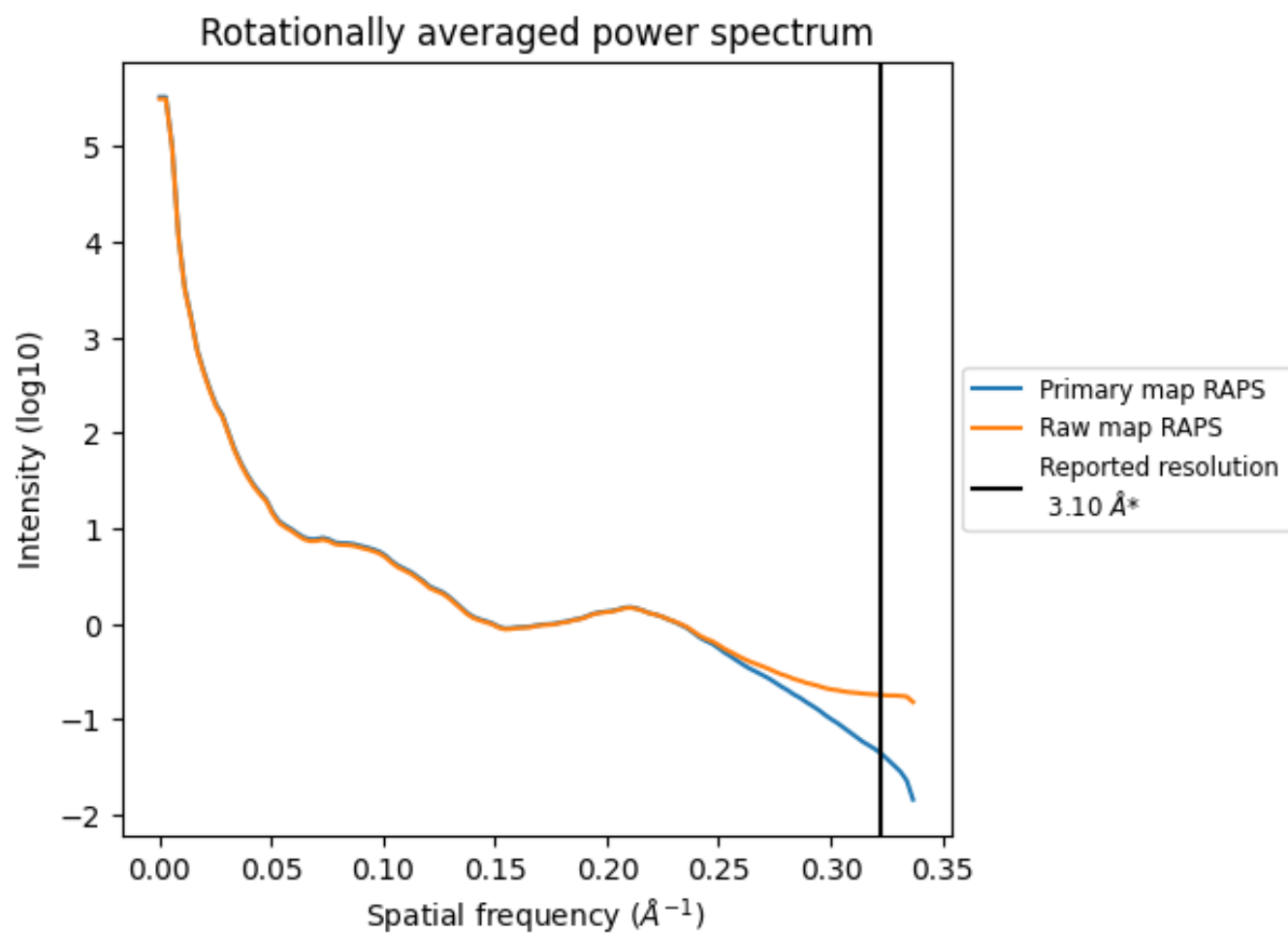
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 824 nm^3 ; this corresponds to an approximate mass of 744 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 ⓘ

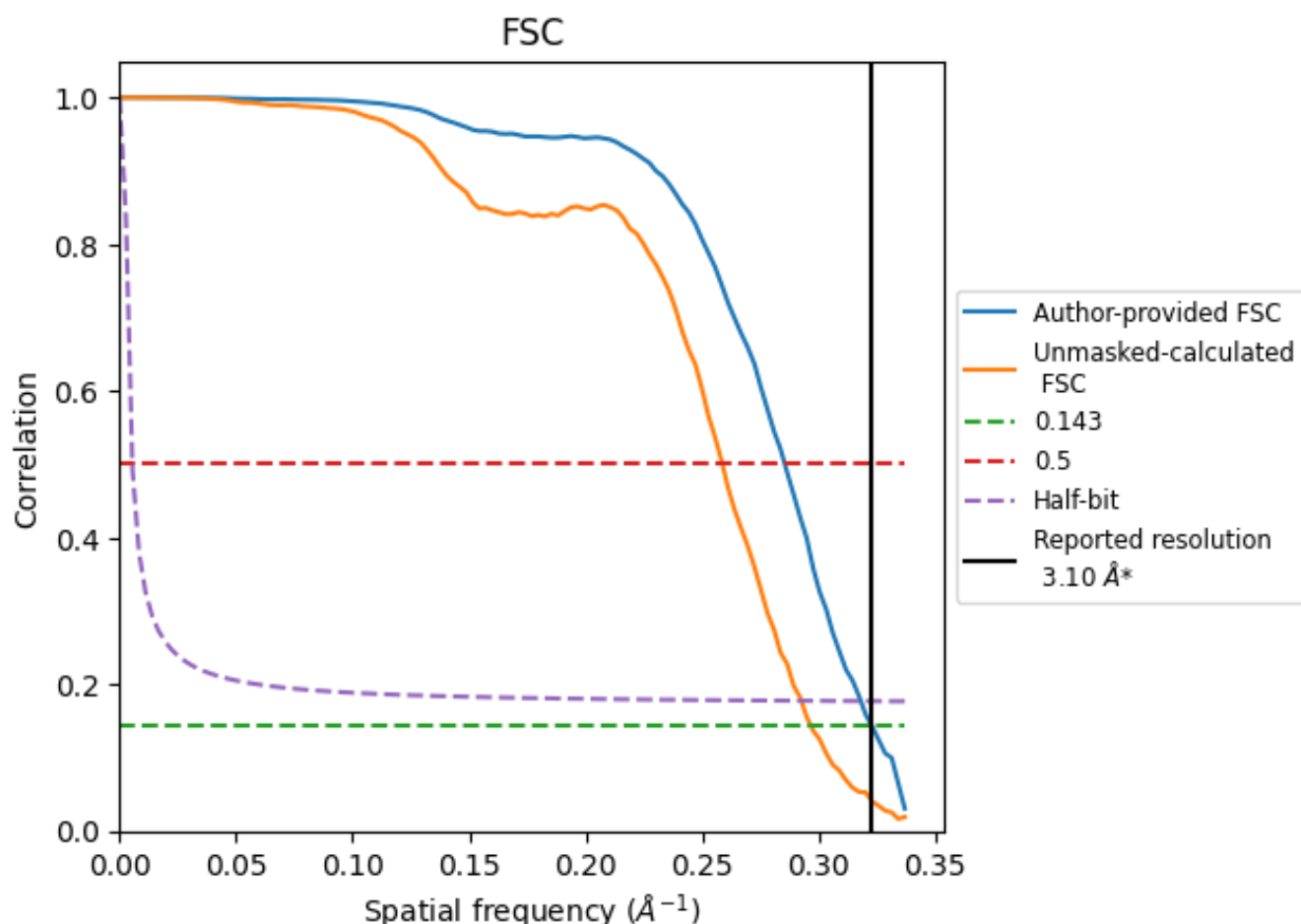


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

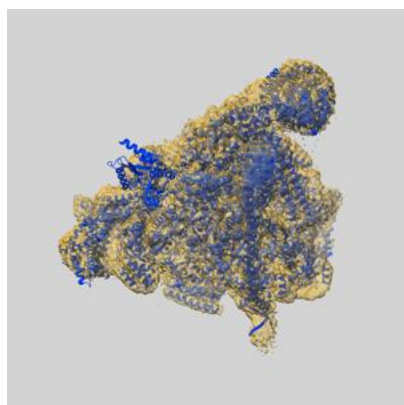
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.10	3.50	3.14
Unmasked-calculated*	3.37	3.87	3.42

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

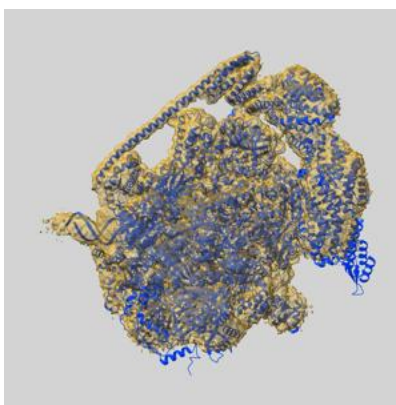
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33313 and PDB model 7XN7. Per-residue inclusion information can be found in section [3](#) on page [13](#).

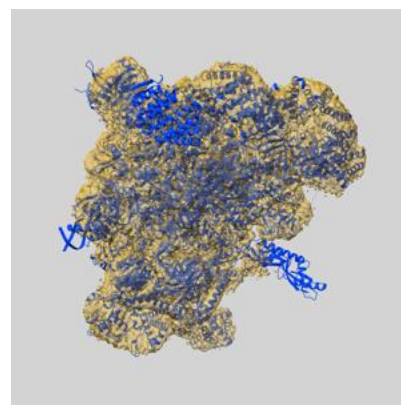
9.1 Map-model overlay [i](#)



X



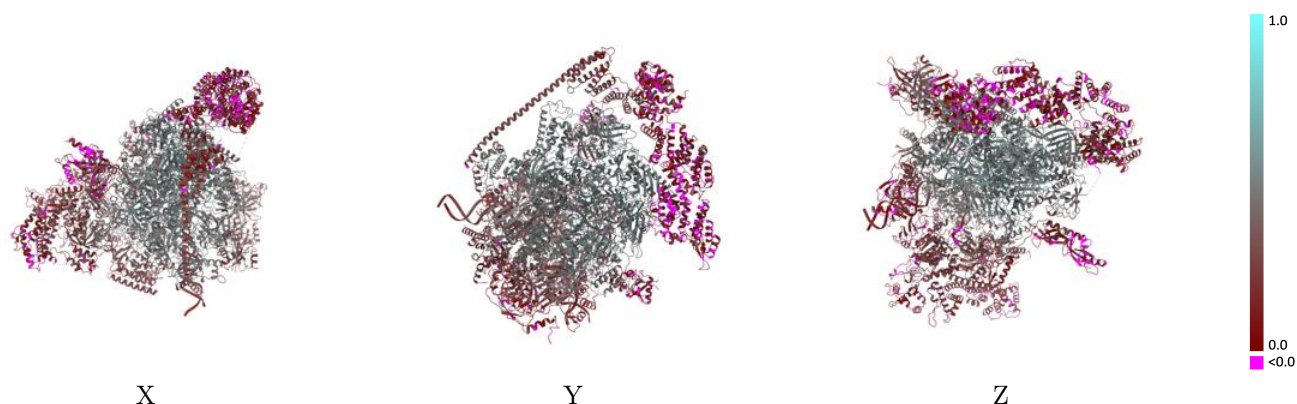
Y



Z

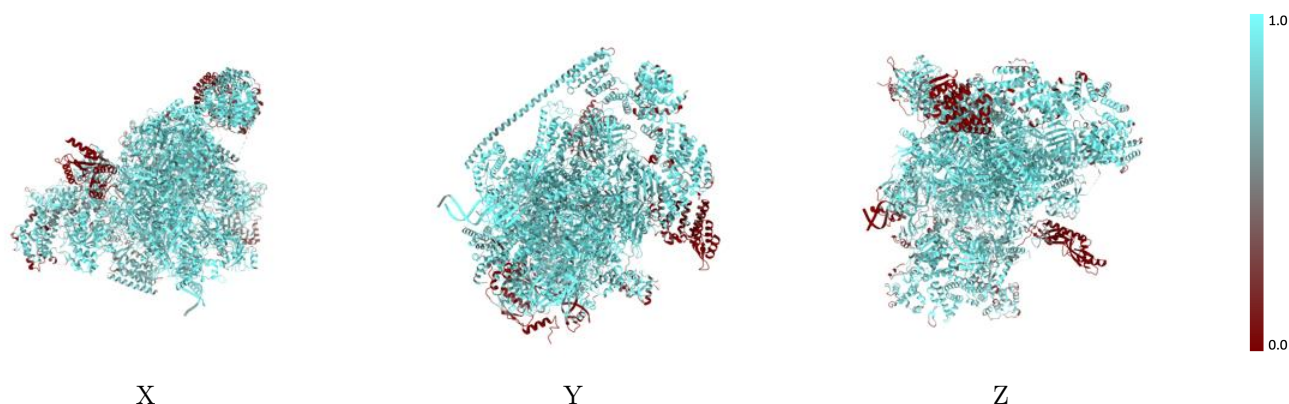
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



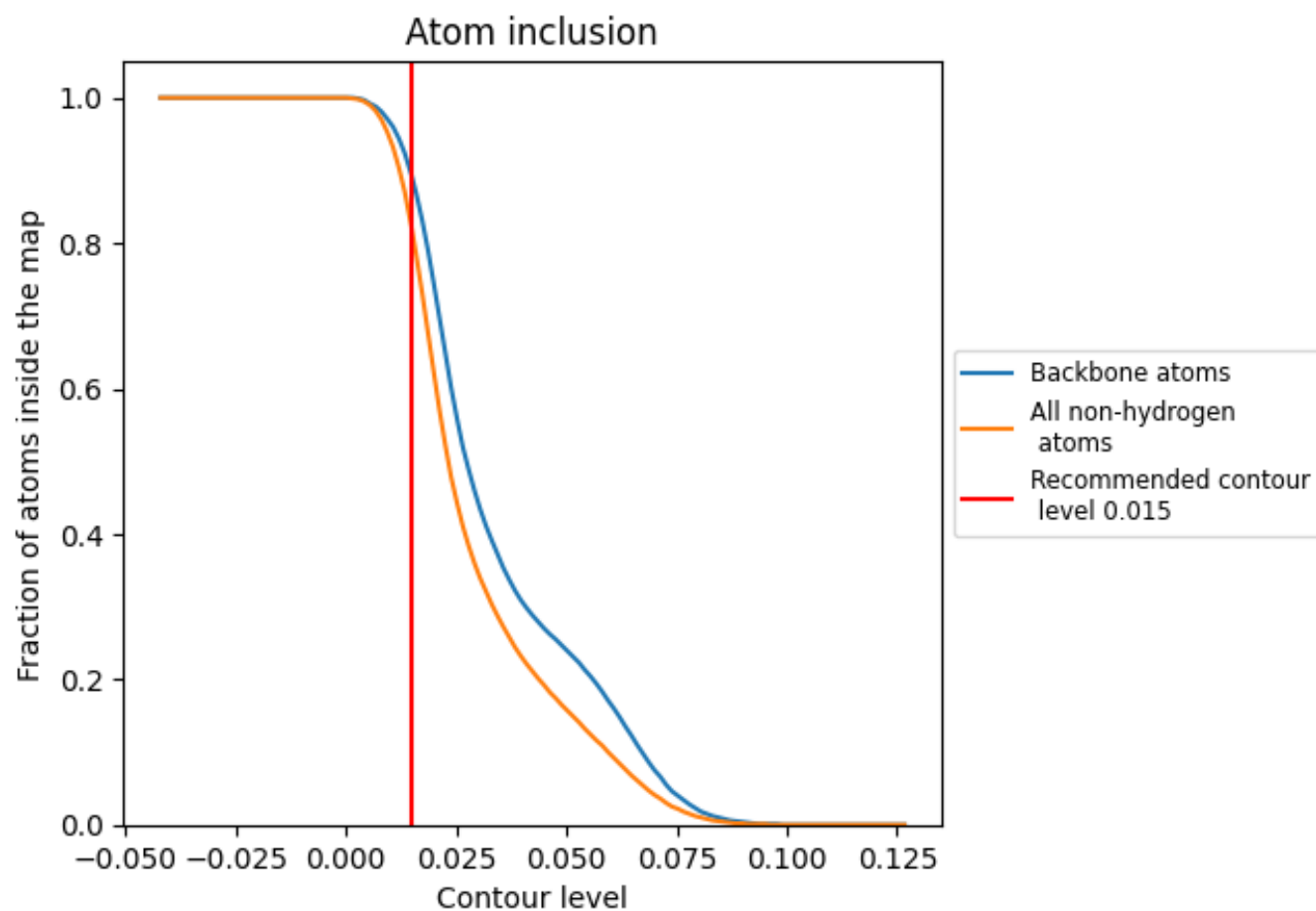
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).





















































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 82% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.3380
A	 0.9470	 0.4890
B	 0.9460	 0.4960
C	 0.9470	 0.5170
D	 0.8800	 0.2810
E	 0.9620	 0.4750
F	 0.9740	 0.5280
G	 0.9110	 0.3780
H	 0.9480	 0.5050
I	 0.8610	 0.3750
J	 0.9560	 0.5230
K	 0.9630	 0.5200
L	 0.9630	 0.4870
M	 0.7880	 0.2360
N	 0.8000	 0.2410
P	 0.9410	 0.3480
T	 0.8140	 0.2970
V	 0.9060	 0.1830
W	 0.7800	 0.2680
m	 0.6700	 0.1780
n	 0.8020	 0.2350
q	 0.6820	 0.1390
r	 0.6800	 0.2310
u	 0.6610	 0.2960
v	 0.5700	 0.2150
x	 0.7940	 0.3550

