



wwPDB EM Validation Summary Report ⓘ

Mar 18, 2026 – 12:58 AM UTC

PDB ID : 9WMW / pdb_00009wmw
EMDB ID : EMD-66107
Title : Co-transcriptional histone H3K36 methylation complex containing RNA polymerase II elongation complex, Set2, and the upstream nucleosome. (temp115, FACT-hexamer)
Authors : Kujirai, T.; Ehara, H.; Ito, T.; Henmi, M.; Sekine, S.; Kurumizaka, H.
Deposited on : 2025-09-03
Resolution : 3.62 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

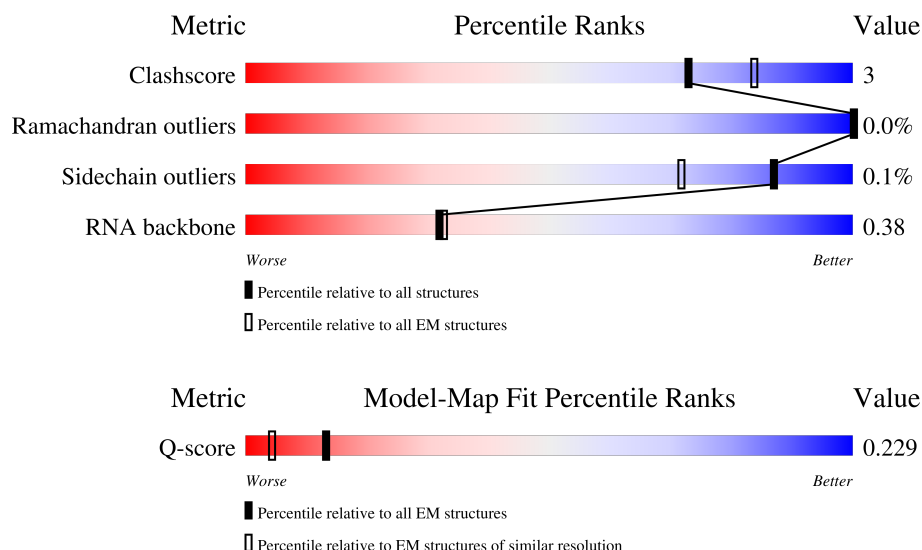
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.62 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	11773 (3.12 - 4.12)

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	

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Mol	Chain	Length	Quality of chain
4	D	186	
5	E	214	
6	F	155	
7	G	171	
8	H	145	
9	I	115	
10	J	72	
11	K	118	
12	L	72	
13	M	113	
14	N	198	
15	P	20	
16	T	198	
17	V	108	
18	W	911	
19	m	1503	
20	n	417	
21	q	1084	
22	r	544	
23	s	725	
24	u	459	
25	v	396	
26	x	395	
27	a	139	
27	e	139	

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Mol	Chain	Length	Quality of chain
28	b	106	
28	f	106	
29	g	133	
30	h	129	
31	j	965	
32	k	531	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 78756 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 DNA-directed RNA polymerases I, II, and III subunit RPABC2.

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	75	Total	C	N	O	P	0	0
			1548	732	276	465	75		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	20	Total	C	N	O	P	0	0
			417	186	64	147	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	86	Total	C	N	O	P	0	0
			1758	828	348	496	86		

- 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	-	initiating methionine	UNP C4R0E6

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	W	535	Total	C	N	O	S	0	0
			4250	2680	754	814	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	1178	Total	C	N	O	S	0	0
			9653	6112	1648	1866	27		

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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 Histone-lysine N-methyltransferase, H3 lysine-36 specific.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	s	11	Total	C	N	O	0	0
			91	60	14	17		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	-2	GLY	-	expression tag	UNP C4QY01
s	-1	PRO	-	expression tag	UNP C4QY01
s	0	GLY	-	expression tag	UNP C4QY01

- Molecule 24 is a protein called Leo1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	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

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Chain	Residue	Modelled	Actual	Comment	Reference
u	-1	SER	-	expression tag	UNP C4R3K1
u	0	GLY	-	expression tag	UNP C4R3K1

- Molecule 25 is a protein called RNAP II-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	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
v	-1	SER	-	expression tag	UNP C4R997
v	0	ALA	-	expression tag	UNP C4R997

- Molecule 26 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
26	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

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

- Molecule 27 is a protein called Histone H3.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	75	Total	C	N	O	S	0	0
			606	385	114	105	2		
27	e	77	Total	C	N	O	S	0	0
			620	393	116	109	2		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	-3	GLY	-	expression tag	UNP P84243
a	-2	SER	-	expression tag	UNP P84243
a	-1	HIS	-	expression tag	UNP P84243
a	36	MET	LYS	variant	UNP P84243
e	-3	GLY	-	expression tag	UNP P84243
e	-2	SER	-	expression tag	UNP P84243
e	-1	HIS	-	expression tag	UNP P84243
e	36	MET	LYS	variant	UNP P84243

- Molecule 28 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	83	Total	C	N	O	S	0	0
			662	418	129	114	1		
28	f	78	Total	C	N	O	S	0	0
			619	391	120	107	1		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	-3	GLY	-	expression tag	UNP P62805
b	-2	SER	-	expression tag	UNP P62805
b	-1	HIS	-	expression tag	UNP P62805
f	-3	GLY	-	expression tag	UNP P62805
f	-2	SER	-	expression tag	UNP P62805
f	-1	HIS	-	expression tag	UNP P62805

- Molecule 29 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	g	92	Total	C	N	O	0	0
			715	447	142	126		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	-3	GLY	-	expression tag	UNP P04908
g	-2	SER	-	expression tag	UNP P04908
g	-1	HIS	-	expression tag	UNP P04908

- Molecule 30 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	h	93	Total	C	N	O	S	0	0
			722	453	129	137	3		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	-3	GLY	-	expression tag	UNP P06899
h	-2	SER	-	expression tag	UNP P06899
h	-1	HIS	-	expression tag	UNP P06899
h	120	CYS	LYS	engineered mutation	UNP P06899

- Molecule 31 is a protein called FACT complex subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	471	Total	C	N	O	S	0	0
			3794	2406	663	712	13		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	-2	GLY	-	expression tag	UNP C4QYQ8
j	-1	PRO	-	expression tag	UNP C4QYQ8
j	0	GLY	-	expression tag	UNP C4QYQ8
j	939	UNK	-	expression tag	UNP C4QYQ8
j	940	UNK	-	expression tag	UNP C4QYQ8
j	941	UNK	-	expression tag	UNP C4QYQ8
j	942	UNK	-	expression tag	UNP C4QYQ8
j	943	UNK	-	expression tag	UNP C4QYQ8
j	944	UNK	-	expression tag	UNP C4QYQ8
j	945	UNK	-	expression tag	UNP C4QYQ8
j	946	UNK	-	expression tag	UNP C4QYQ8
j	947	UNK	-	expression tag	UNP C4QYQ8
j	948	UNK	-	expression tag	UNP C4QYQ8
j	949	UNK	-	expression tag	UNP C4QYQ8
j	950	UNK	-	expression tag	UNP C4QYQ8
j	951	UNK	-	expression tag	UNP C4QYQ8
j	952	UNK	-	expression tag	UNP C4QYQ8
j	953	UNK	-	expression tag	UNP C4QYQ8
j	954	UNK	-	expression tag	UNP C4QYQ8
j	955	UNK	-	expression tag	UNP C4QYQ8
j	956	UNK	-	expression tag	UNP C4QYQ8
j	957	UNK	-	expression tag	UNP C4QYQ8
j	958	UNK	-	expression tag	UNP C4QYQ8
j	959	UNK	-	expression tag	UNP C4QYQ8
j	960	UNK	-	expression tag	UNP C4QYQ8
j	961	UNK	-	expression tag	UNP C4QYQ8
j	962	UNK	-	expression tag	UNP C4QYQ8

- Molecule 32 is a protein called FACT complex subunit POB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	k	434	Total	C	N	O	S	0	0
			3535	2233	619	673	10		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	-2	GLY	-	expression tag	UNP F2QNN8
k	-1	PRO	-	expression tag	UNP F2QNN8
k	0	GLY	-	expression tag	UNP F2QNN8

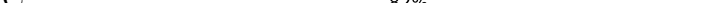
- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn).

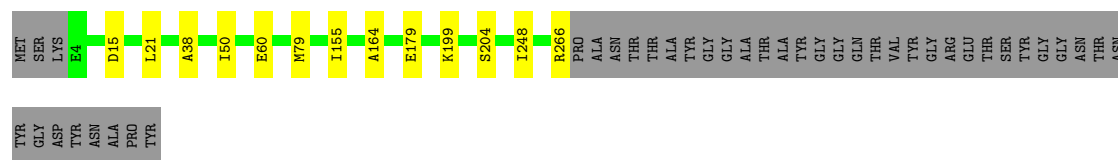
Mol	Chain	Residues	Atoms		AltConf
33	A	2	Total 2	Zn 2	0
33	B	1	Total 1	Zn 1	0
33	C	1	Total 1	Zn 1	0
33	I	2	Total 2	Zn 2	0
33	J	1	Total 1	Zn 1	0
33	L	1	Total 1	Zn 1	0
33	M	1	Total 1	Zn 1	0
33	V	1	Total 1	Zn 1	0

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

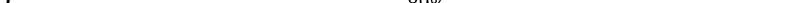
Mol	Chain	Residues	Atoms		AltConf
34	A	1	Total 1	Mg 1	0

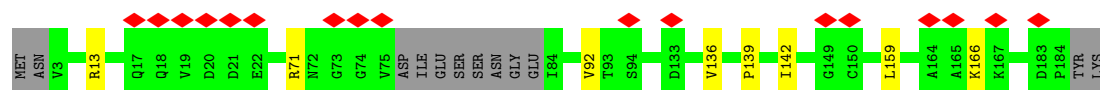
- Molecule 3: RNA polymerase II third largest subunit B44, part of central core

Chain C:  82% • 13%



- Molecule 4: RNA polymerase II subunit B32

Chain D:  9% 89% 6%

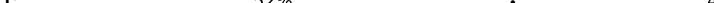


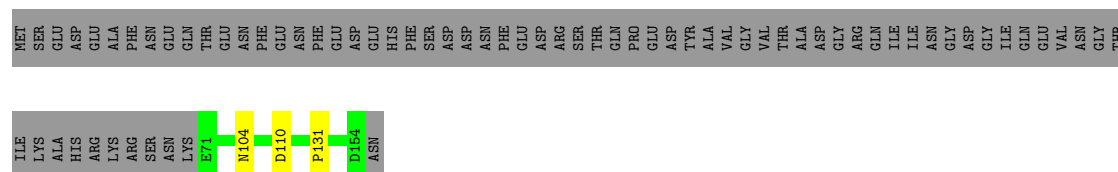
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E:  92% 7%



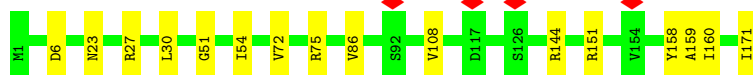
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F:  52% . 46%



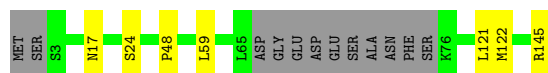
- Molecule 7: RNA polymerase II subunit

Chain G:  91% 9%



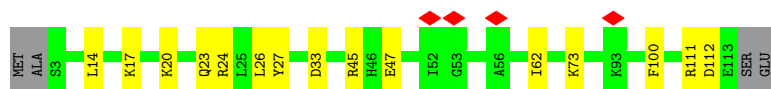
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H:  87% 5% 8%



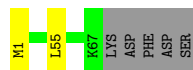
- Molecule 9: DNA-directed RNA polymerase subunit

Chain I:  83% 13% •



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

Chain J:  90% • 7%



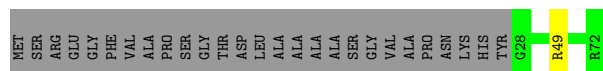
- Molecule 11: RNA polymerase II subunit B12.5

Chain K:  84% 12% •



- Molecule 12: RNA polymerase subunit ABC10-alpha

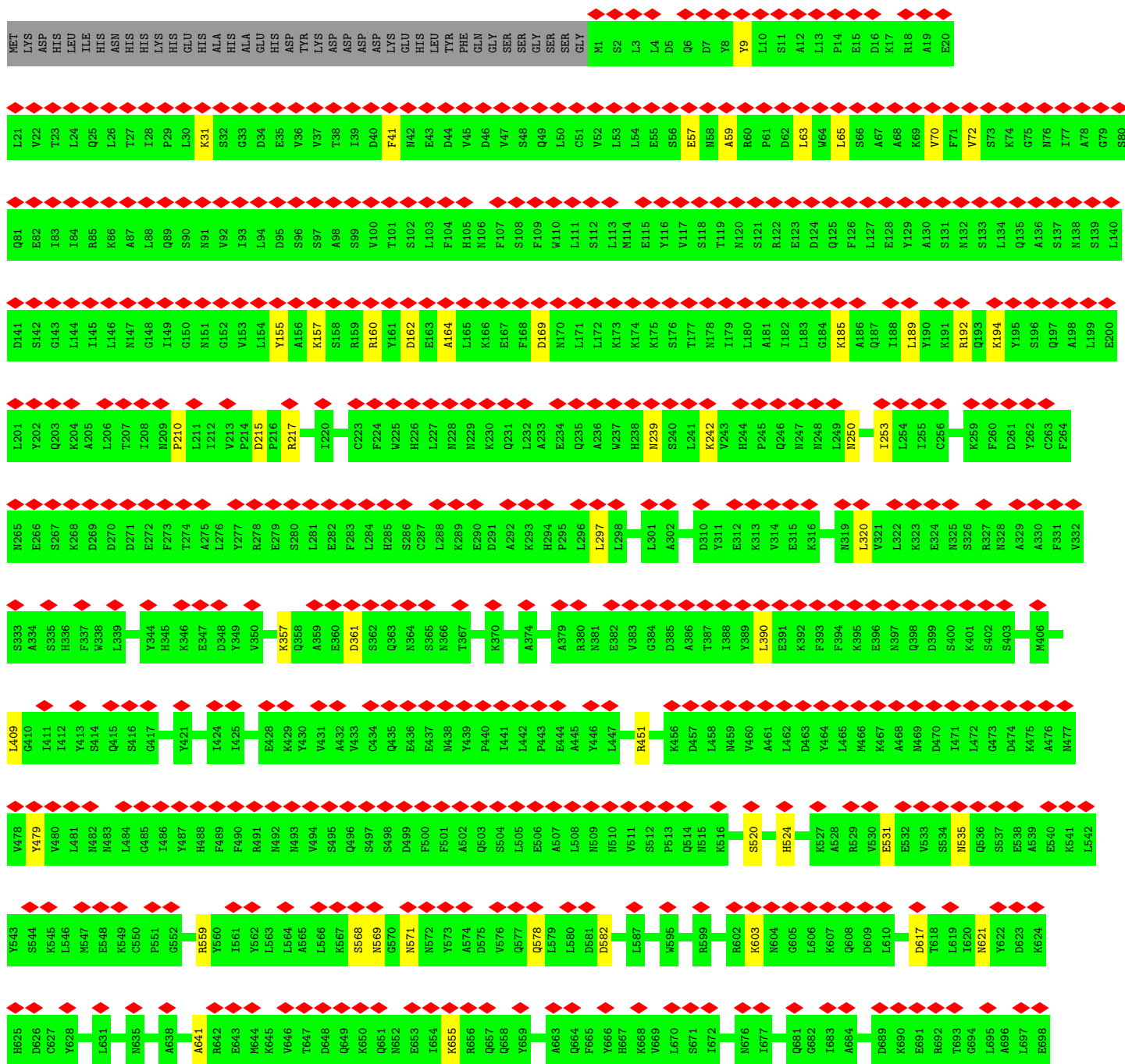
Chain L:  61% • 38%

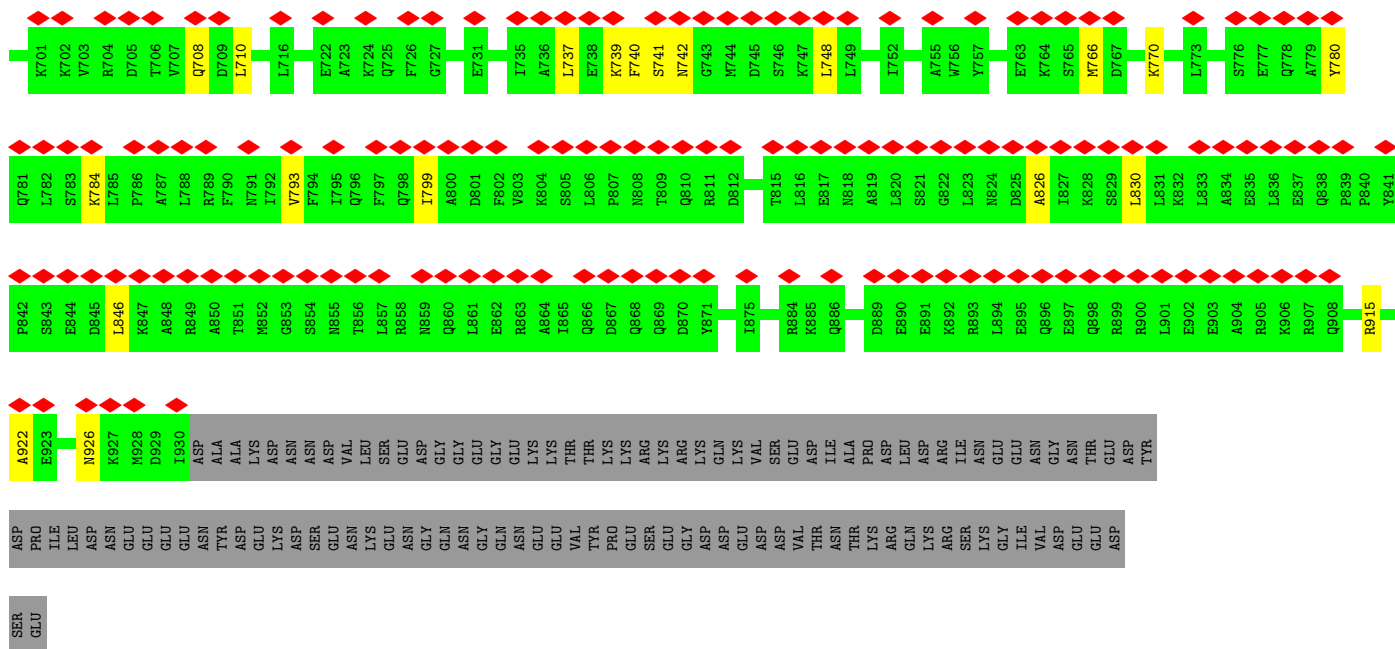


- Molecule 13: Transcription elongation factor 1 homolog

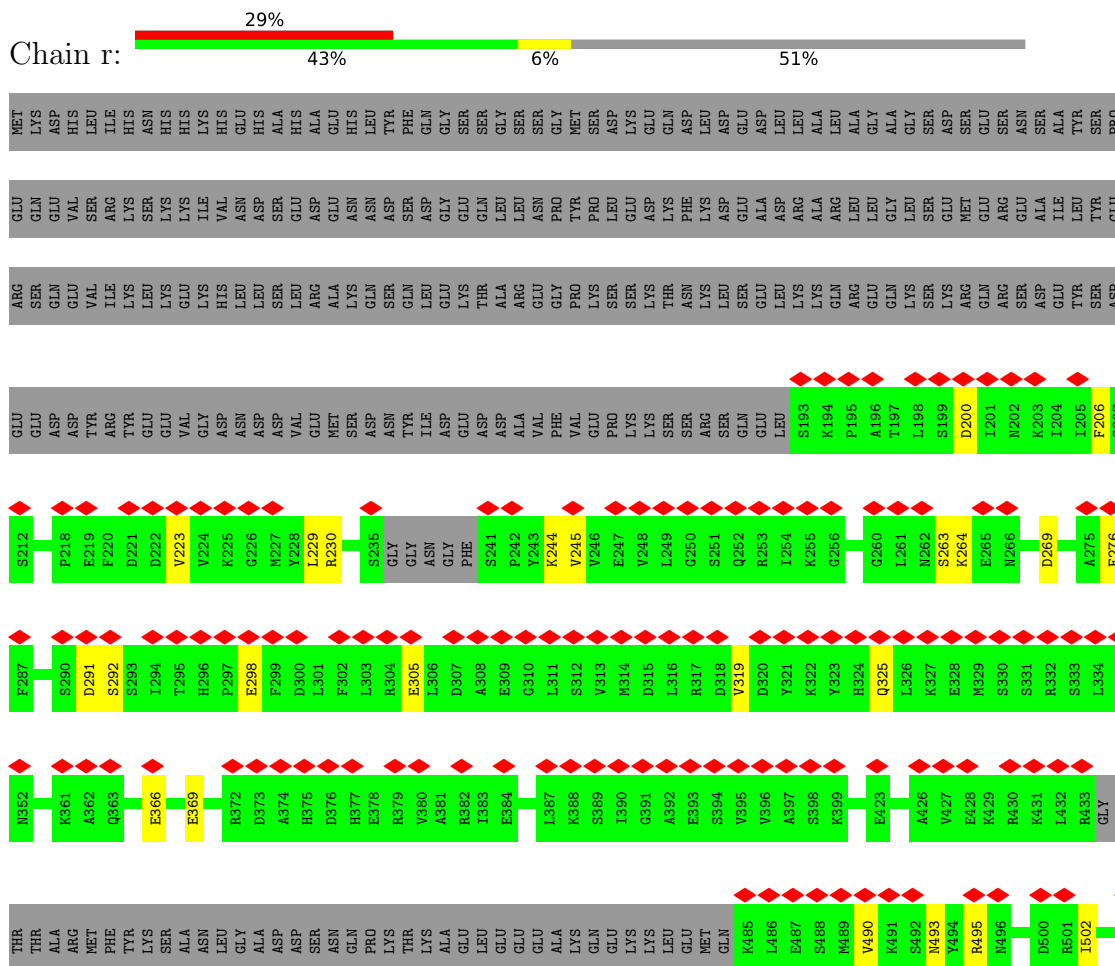
Chain M:  5% 51% 5% 43%



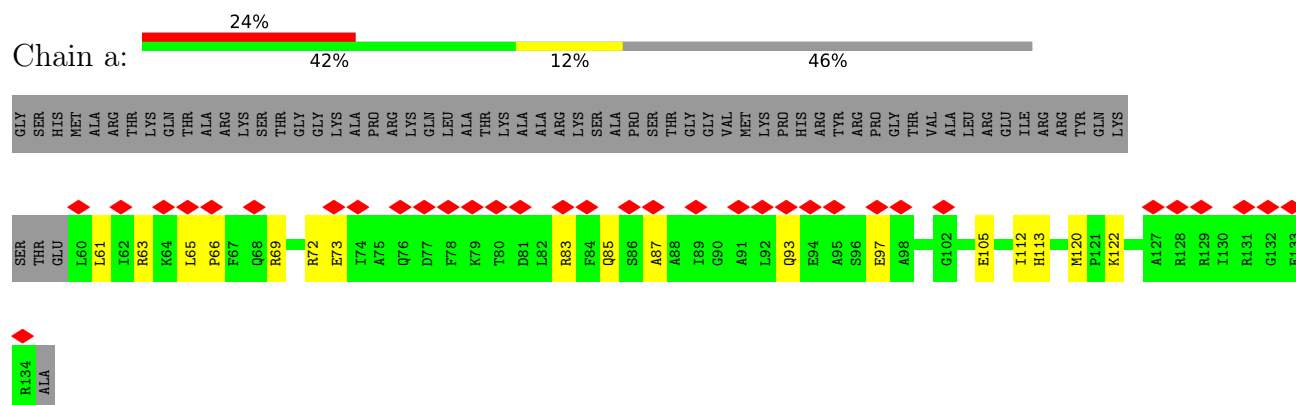
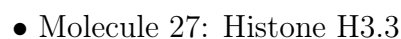




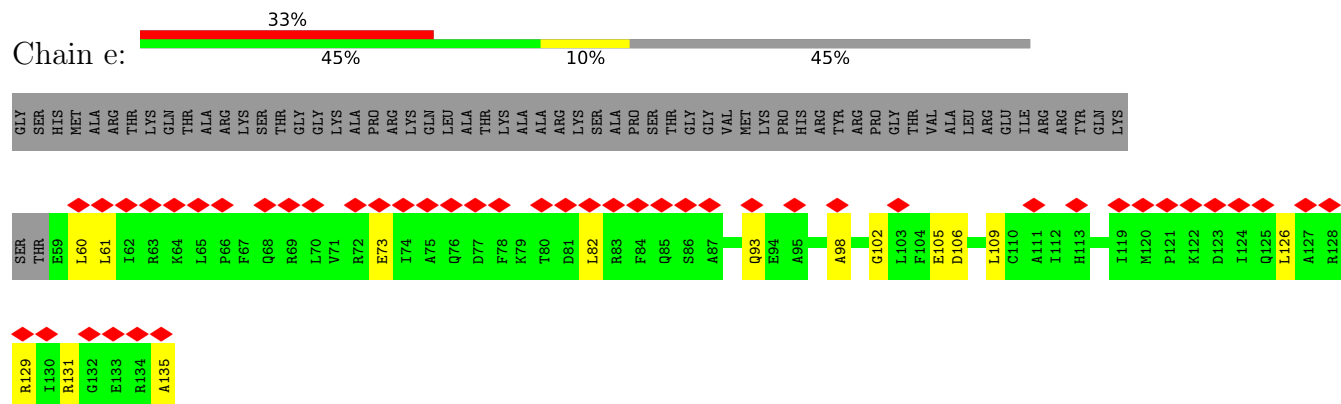
• Molecule 22: RNAPII-associated chromatin remodeling Paf1 complex subunit



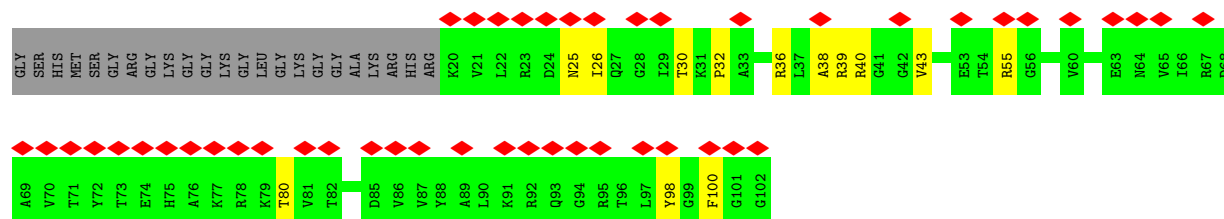
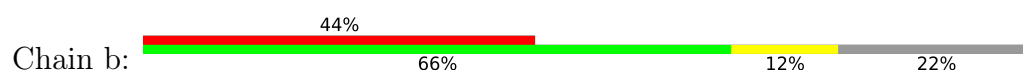




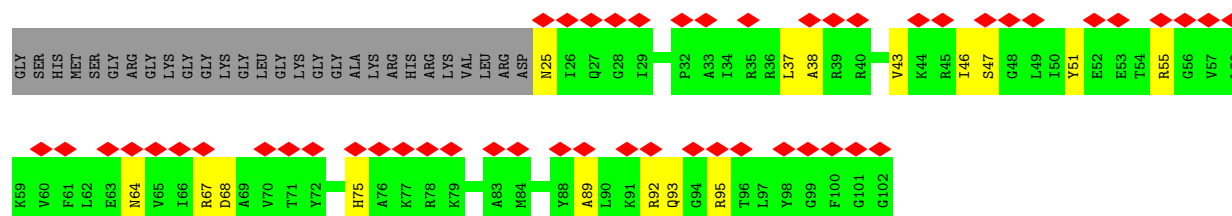
- Molecule 27: Histone H3.3



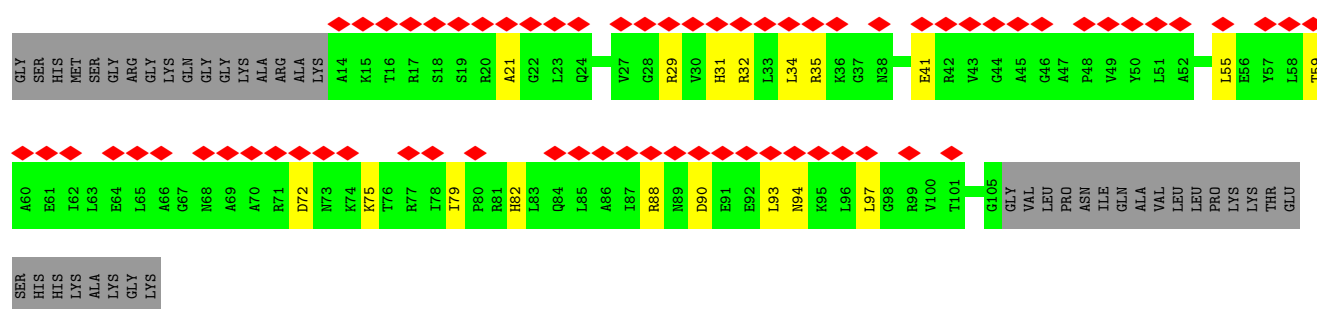
- Molecule 28: Histone H4



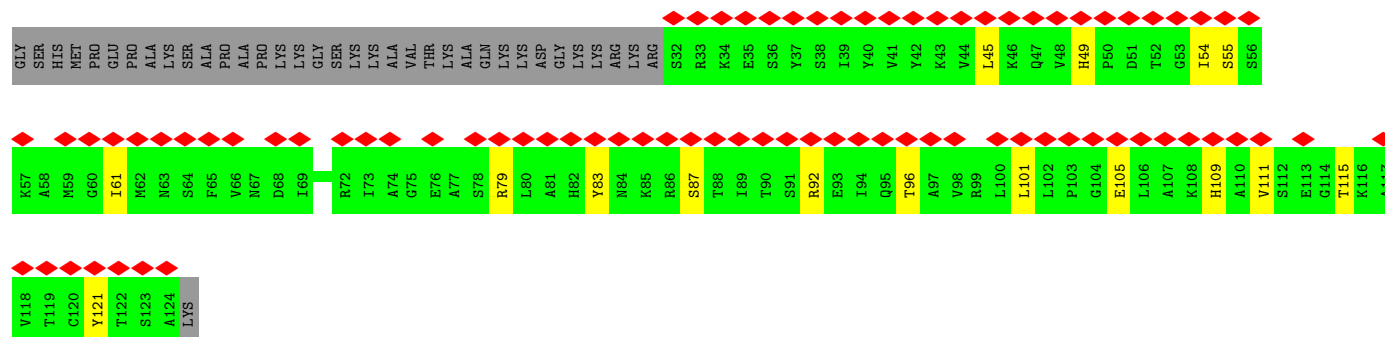
- Molecule 28: Histone H4



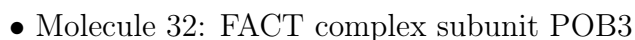
- Molecule 29: Histone H2A type 1-B/E

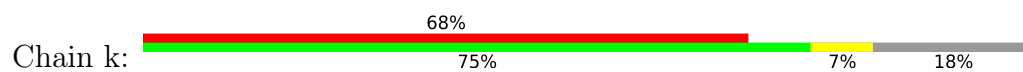


- Molecule 30: Histone H2B type 1-J



- Molecule 31: FACT complex subunit





GLY	PRO	GLY	M1	S2	T3	V4	D5	F6	D7	I8	I9	F10	L11	N12	Q13	S14	K15	A16	P17	G18	R19	F20	R21	I22	T23	S24	S25	G26	L27	G28	W29	K30	P31	S32	S33	Q34	V35	P36	T37	K38	G39	K40	T41	D42	P43	F44	L45	S106	P47	S48	G49	D50	I51	L52	S53	V54	S55	W56	S57
R58	G59	Y60	R61	G62	W63	F124	E64	L65	R66	V67	Y68	T69	R70	N71	D72	K73	V74	I75	M76	L77	D78	G79	F80	E81	Q82	Q83	D84	F85	Q86	Q87	L88	K89	N90	E91	I92	Q93	R94	T95	F96	N97	V98	N99	L100	E101	H102	K103	E104	H105	S106	L107	G108	G109	W110	N111	W112	T115	Q116	L117	T118
R119	A120	E121	L122	V123	F124	N125	V126	N127	N128	R129	P130	P135	Y136	S137	E138	S140	N141	S142	N143	L144	T145	G146	R147	E153	P156	K157	T158	V159	D160	E161	N162	H163	Y164	E165	T166	L167	G168	D169	E170	L171	V172	E173	L176	Y177	V178	P179	G180	Q181	I182	ASP	LYS	ASP	GLU	ASP					
SER	THR	GLU	GLN	ASP	THR	THR	GLU	ALA	LYS	SER	K201	S202	Q203	L204	F205	Y206	Q207	Q208	L209	K210	D211	K212	A213	D214	F215	D216	T217	T218	S219	E220	A221	I222	V223	S224	F225	E226	D227	F230	L231	T232	G235	R236	T239	S240	N241	Y242	A243	N244	N245	L246	R247	L248	R249	G250					
Q251	S252	Y255	K256	I257	Q258	N259	K260	N261	V262	L263	R264	L265	F266	S267	L268	P269	R270	L271	D272	D273	R274	H275	H276	L277	V278	I279	L280	Q281	V282	D283	P284	P285	L286	R287	Q288	G289	Q290	T291	R292	Y293	P294	F295	L296	V297	H298	Q299	F300	D301	K302	N303	E304	E305	L306	E307	V308	E309	L310	N311	
L312	S313	D314	E315	E316	Y317	K318	S319	K320	Y321	E322	G323	K324	L325	N326	R327	S328	Y329	G330	T331	D332	S333	T334	Y335	K336	S339	H340	C341	L342	R343	G344	L345	T346	E347	R348	R349	V350	I351	T352	P353	G354	S355	F356	Q357	S358	Q359	H360	K361	Q362	P363	G364	S368	L369	K370	A371	S372	E373	G374		
Q375	I376	Y377	L378	L379	D380	K381	C382	L383	F384	F385	A386	T387	K388	P389	C390	V391	Y392	L393	F394	Y395	S396	G397	I398	I399	S400	V401	V402	T403	S404	R405	G406	S410	T411	S412	D416	I417	E418	V419	Q420	F421	S422	G423	G424	S425	H426	T427	F428	A429	N430	I431	N432	K433	D434	E435	Q436	K437			
P438	T439	E440	D441	F442	L443	K444	G445	Q446	F384	V448	ASP	GLU	ASP	SER	ALA	SER	LYS	PRO	GLY	ALA	GLU	PHE	LEU	GLY	ASN	ALA	LEU	VAL	ASP	ASP	ASP	ASP	SER	GLY	GLU	ASP	ASP	GLU	SER	LYS	VAL	ASP	GLU	ASP	ASP	PHE	ASN	ALA	GLY	SER	ASP	SER							
ASP	VAL	ALA	GLU	GLU	TYR	ASP	SER	ASN	ALA	G445	GLY	SER	GLU	ASP	ASP	ALA	SER	LYS	PRO	GLY	ALA	GLU	PHE	LEU	GLY	ASN	ALA	LEU	VAL	ASP	ASP	ASP	SER	GLY	GLU	ASP	ASP	GLU	SER	LYS	VAL	ASP	GLU	ASP	ASP	PHE	ASN	ALA	GLY	SER	ASP	SER							

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29821	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 ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.147	Depositor
Minimum map value	-0.059	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.016	Depositor
Map size ($\text{\AA}$)	398.25, 398.25, 398.25	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.475, 1.475, 1.475	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, 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	0.21	0/11267	0.43	0/15222
2	B	0.21	0/9464	0.43	0/12763
3	C	0.21	0/2139	0.41	0/2895
4	D	0.15	0/1361	0.33	0/1837
5	E	0.20	0/1773	0.44	0/2385
6	F	0.20	0/687	0.38	0/931
7	G	0.15	0/1354	0.33	0/1837
8	H	0.21	0/1070	0.38	0/1444
9	I	0.12	0/934	0.28	0/1257
10	J	0.20	0/563	0.41	0/753
11	K	0.21	0/953	0.41	0/1291
12	L	0.20	0/365	0.45	0/484
13	M	0.17	0/513	0.37	0/693
14	N	0.51	0/1732	0.92	0/2674
15	P	0.26	0/462	0.60	0/716
16	T	0.51	0/1977	0.80	0/3044
17	V	0.15	0/840	0.33	0/1140
18	W	0.18	0/4319	0.43	1/5838 (0.0%)
19	m	0.18	0/9847	0.38	0/13321
20	n	0.18	0/1132	0.38	0/1526
21	q	0.17	0/7689	0.34	0/10368
22	r	0.17	0/2169	0.35	0/2901
23	s	0.12	0/92	0.29	0/122
24	u	0.15	0/1740	0.31	0/2347
25	v	0.16	0/2944	0.33	0/3973
26	x	0.15	0/1716	0.31	0/2310
27	a	0.47	0/613	0.64	0/822
27	e	0.25	0/627	0.43	0/841
28	b	0.43	0/669	0.64	0/894
28	f	0.29	0/626	0.46	0/837
29	g	0.21	0/723	0.36	0/973
30	h	0.31	0/733	0.39	0/987

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	j	0.84	0/3748	1.16	0/5044
32	k	0.80	0/3613	1.12	0/4881
All	All	0.33	0/80454	0.54	1/109351 (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
14	N	0	3
16	T	0	1
31	j	0	1
32	k	0	1
All	All	0	6

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	W	435	LEU	N-CA-C	5.14	117.20	109.23

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	N	-21	DG	Sidechain
14	N	-6	DG	Sidechain
14	N	14	DT	Sidechain
16	T	-2	DC	Sidechain
31	j	616	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	11064	0	11090	61	0
2	B	9284	0	9282	61	0
3	C	2098	0	2057	10	0
4	D	1349	0	1345	5	0
5	E	1741	0	1754	11	0
6	F	677	0	693	3	0
7	G	1325	0	1342	10	0
8	H	1053	0	1050	4	0
9	I	917	0	864	10	0
10	J	554	0	573	1	0
11	K	932	0	944	11	0
12	L	359	0	358	1	0
13	M	505	0	495	3	0
14	N	1548	0	848	13	0
15	P	417	0	213	1	0
16	T	1758	0	953	13	0
17	V	824	0	795	11	0
18	W	4250	0	4296	55	0
19	m	9653	0	9500	64	0
20	n	1115	0	1186	16	0
21	q	7552	0	7545	43	0
22	r	2139	0	2155	18	0
23	s	91	0	98	2	0
24	u	1707	0	1676	23	0
25	v	2878	0	2873	26	0
26	x	1682	0	1731	8	0
27	a	606	0	639	20	0
27	e	620	0	650	13	0
28	b	662	0	709	14	0
28	f	619	0	659	12	0
29	g	715	0	755	13	0
30	h	722	0	737	13	0
31	j	3794	0	3700	34	0
32	k	3535	0	3467	32	0
33	A	2	0	0	0	0
33	B	1	0	0	0	0
33	C	1	0	0	0	0
33	I	2	0	0	0	0
33	J	1	0	0	0	0
33	L	1	0	0	0	0
33	M	1	0	0	0	0
33	V	1	0	0	0	0
34	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	78756	0	77032	508	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 3.

The worst 5 of 508 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)
32:k:374:GLY:HA2	32:k:387:THR:HG21	1.71	0.72
1:A:445:PHE:CE2	1:A:471:LEU:HD21	2.24	0.72
31:j:919:THR:HG23	31:j:920:ILE:N	2.07	0.70
18:W:461:LEU:HD13	19:m:278:THR:HA	1.74	0.70
29:g:88:ARG:NH2	29:g:97:LEU:O	2.24	0.70

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	1392/1743 (80%)	1357 (98%)	34 (2%)	1 (0%)	48	78
2	B	1154/1227 (94%)	1127 (98%)	27 (2%)	0	100	100
3	C	261/304 (86%)	259 (99%)	2 (1%)	0	100	100
4	D	170/186 (91%)	168 (99%)	2 (1%)	0	100	100
5	E	211/214 (99%)	207 (98%)	4 (2%)	0	100	100
6	F	82/155 (53%)	79 (96%)	3 (4%)	0	100	100
7	G	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
8	H	129/145 (89%)	125 (97%)	4 (3%)	0	100	100
9	I	109/115 (95%)	105 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	65/72 (90%)	65 (100%)	0	0	100	100
11	K	111/118 (94%)	109 (98%)	2 (2%)	0	100	100
12	L	43/72 (60%)	41 (95%)	2 (5%)	0	100	100
13	M	62/113 (55%)	61 (98%)	1 (2%)	0	100	100
17	V	104/108 (96%)	102 (98%)	2 (2%)	0	100	100
18	W	529/911 (58%)	506 (96%)	23 (4%)	0	100	100
19	m	1170/1503 (78%)	1152 (98%)	18 (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	s	9/725 (1%)	9 (100%)	0	0	100	100
24	u	206/459 (45%)	206 (100%)	0	0	100	100
25	v	341/396 (86%)	330 (97%)	11 (3%)	0	100	100
26	x	201/395 (51%)	200 (100%)	1 (0%)	0	100	100
27	a	73/139 (52%)	67 (92%)	6 (8%)	0	100	100
27	e	75/139 (54%)	73 (97%)	2 (3%)	0	100	100
28	b	81/106 (76%)	77 (95%)	4 (5%)	0	100	100
28	f	76/106 (72%)	73 (96%)	3 (4%)	0	100	100
29	g	90/133 (68%)	87 (97%)	3 (3%)	0	100	100
30	h	91/129 (70%)	89 (98%)	2 (2%)	0	100	100
31	j	444/965 (46%)	428 (96%)	14 (3%)	2 (0%)	24	55
32	k	430/531 (81%)	409 (95%)	21 (5%)	0	100	100
All	All	9203/13425 (69%)	8989 (98%)	211 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	960	VAL
31	j	544	ASN
31	j	866	GLY

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%)	1219 (100%)	0	100	100
2	B	1018/1077 (94%)	1014 (100%)	4 (0%)	84	79
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%)	196 (100%)	0	100	100
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%)	61 (100%)	0	100	100
17	V	90/92 (98%)	90 (100%)	0	100	100
18	W	482/796 (61%)	482 (100%)	0	100	100
19	m	1079/1354 (80%)	1078 (100%)	1 (0%)	88	87
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	s	11/649 (2%)	11 (100%)	0	100	100
24	u	192/406 (47%)	192 (100%)	0	100	100
25	v	325/369 (88%)	325 (100%)	0	100	100
26	x	190/354 (54%)	190 (100%)	0	100	100
27	a	63/112 (56%)	63 (100%)	0	100	100
27	e	64/112 (57%)	64 (100%)	0	100	100
28	b	68/81 (84%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	f	63/81 (78%)	63 (100%)	0	100	100
29	g	72/102 (71%)	71 (99%)	1 (1%)	59	68
30	h	79/107 (74%)	79 (100%)	0	100	100
31	j	412/852 (48%)	408 (99%)	4 (1%)	68	72
32	k	396/474 (84%)	395 (100%)	1 (0%)	86	81
All	All	8305/11829 (70%)	8294 (100%)	11 (0%)	87	87

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	j	865	PHE
31	j	867	LEU
32	k	388	LYS
31	j	888	THR
19	m	770	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
21	q	187	GLN
25	v	64	ASN
21	q	397	ASN
22	r	279	GLN
25	v	381	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	19/20 (95%)	8 (42%)	0

5 of 8 RNA backbone outliers are listed below:

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

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

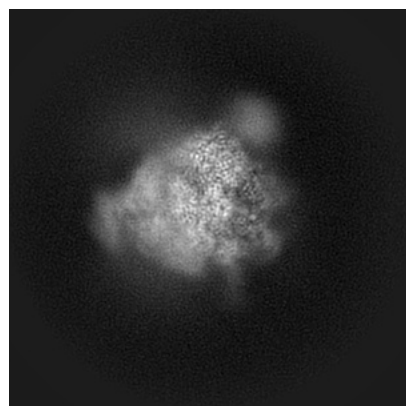
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66107. These allow visual inspection of the internal detail of the map and identification of artifacts.

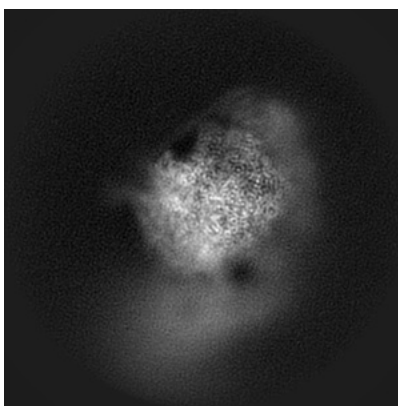
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

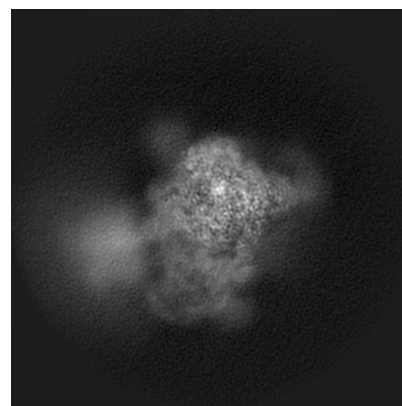
6.1.1 Primary map



X

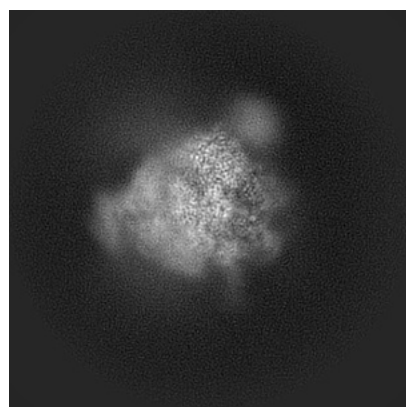


Y

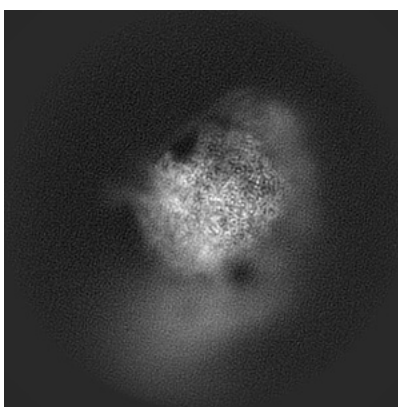


Z

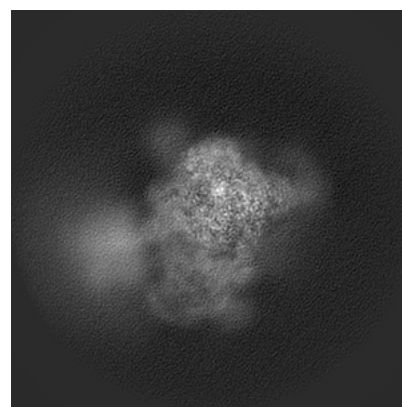
6.1.2 Raw map



X



Y

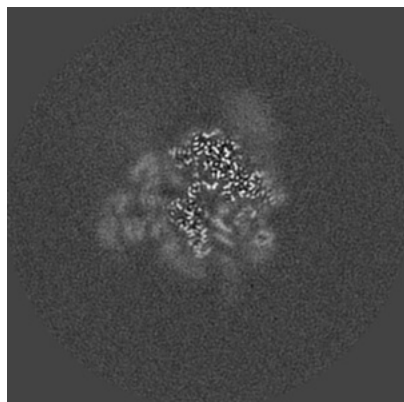


Z

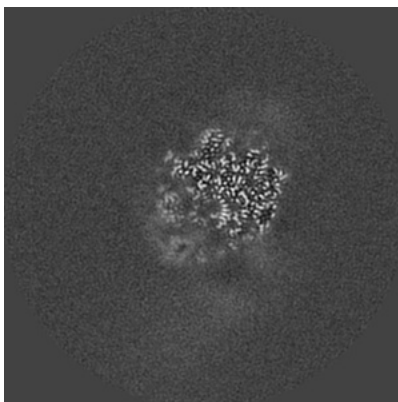
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

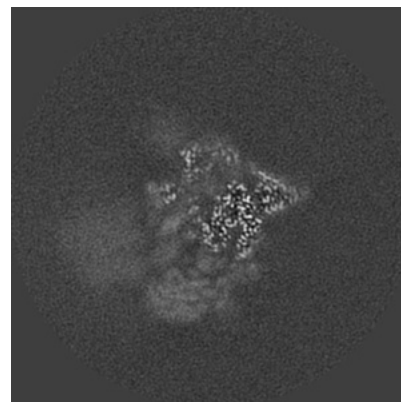
6.2.1 Primary map



X Index: 135

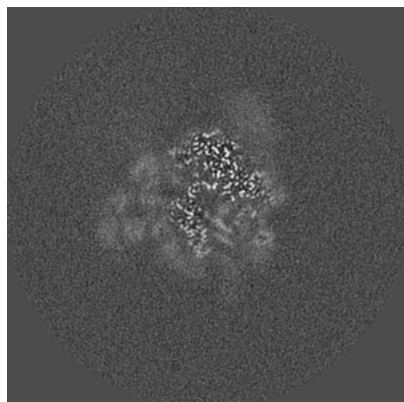


Y Index: 135

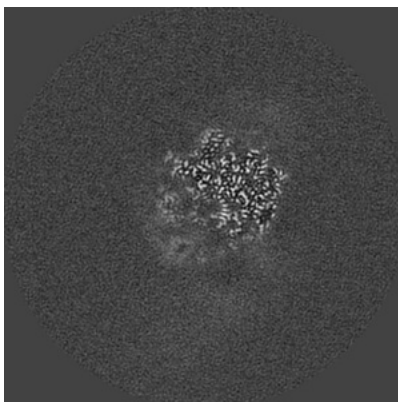


Z Index: 135

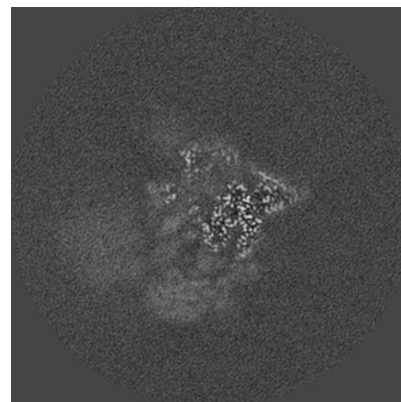
6.2.2 Raw map



X Index: 135



Y Index: 135

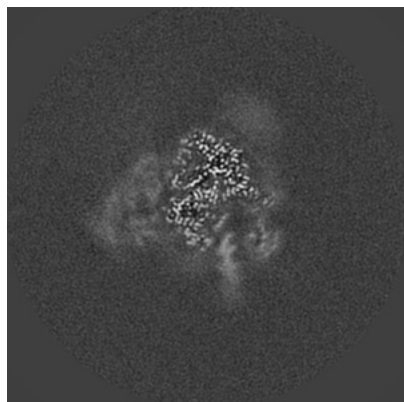


Z Index: 135

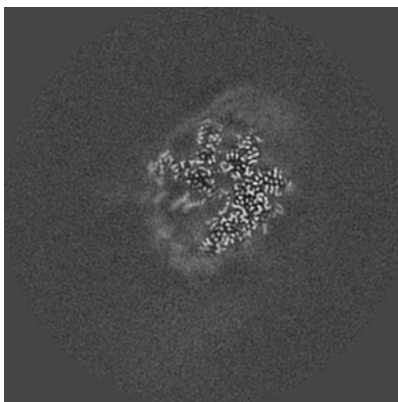
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

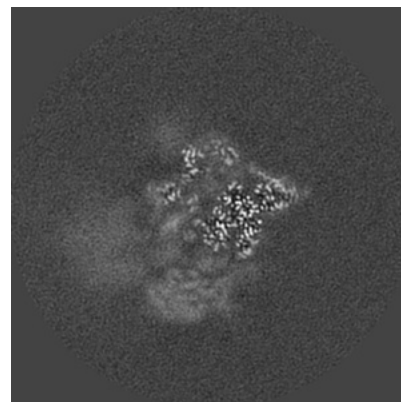
6.3.1 Primary map



X Index: 141

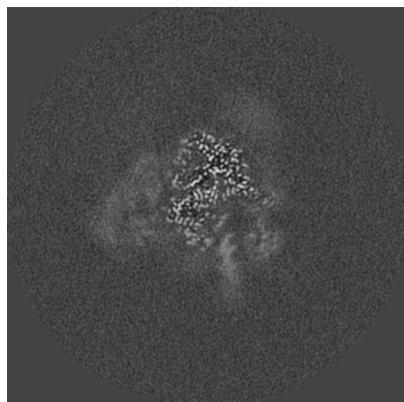


Y Index: 142

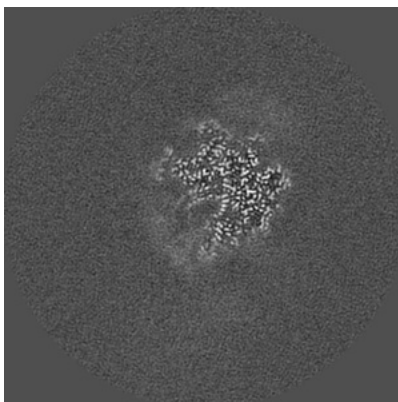


Z Index: 136

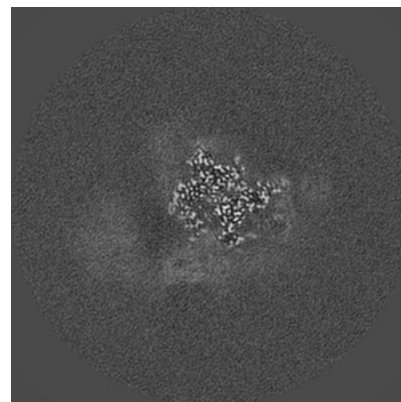
6.3.2 Raw map



X Index: 141



Y Index: 139

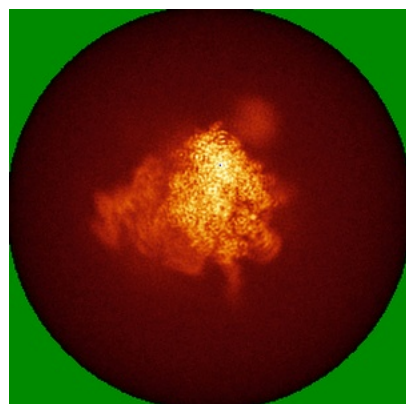


Z Index: 154

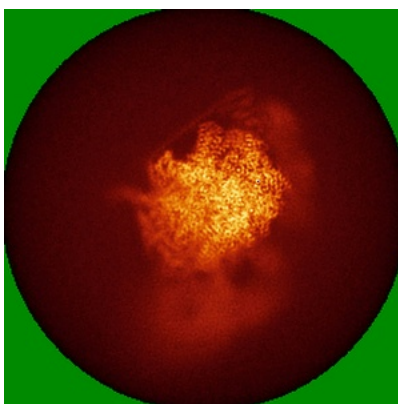
The images above show the largest variance slices of the map in three orthogonal directions.

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

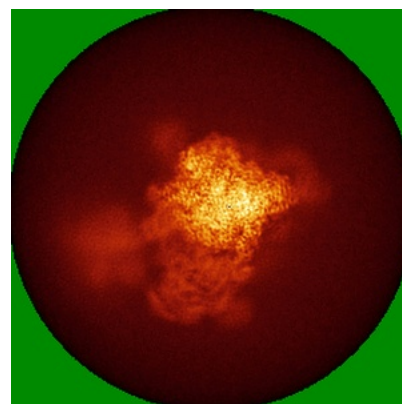
6.4.1 Primary map



X

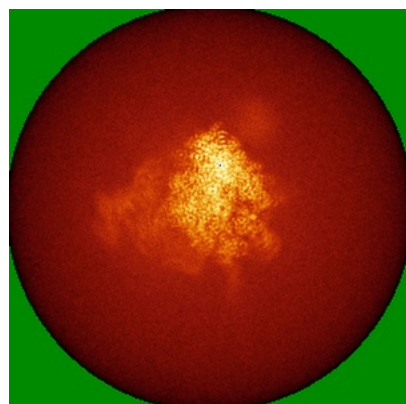


Y

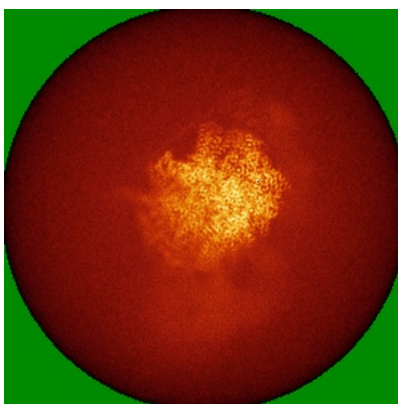


Z

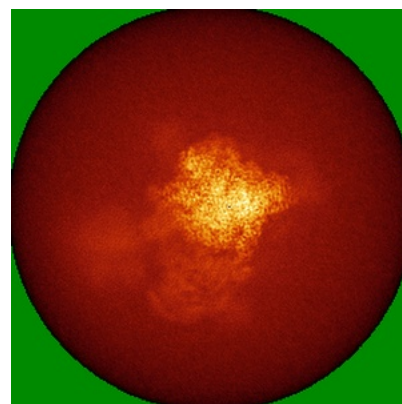
6.4.2 Raw map



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.

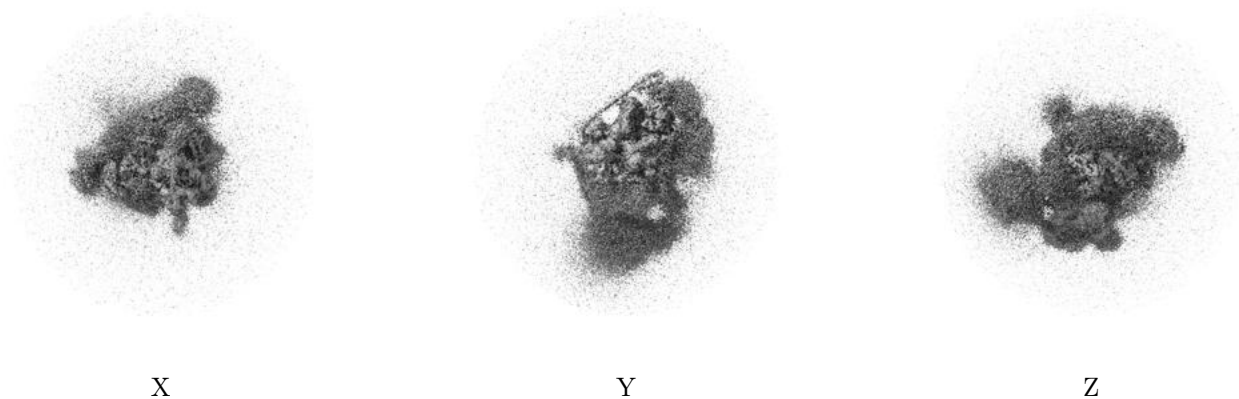
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. 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.

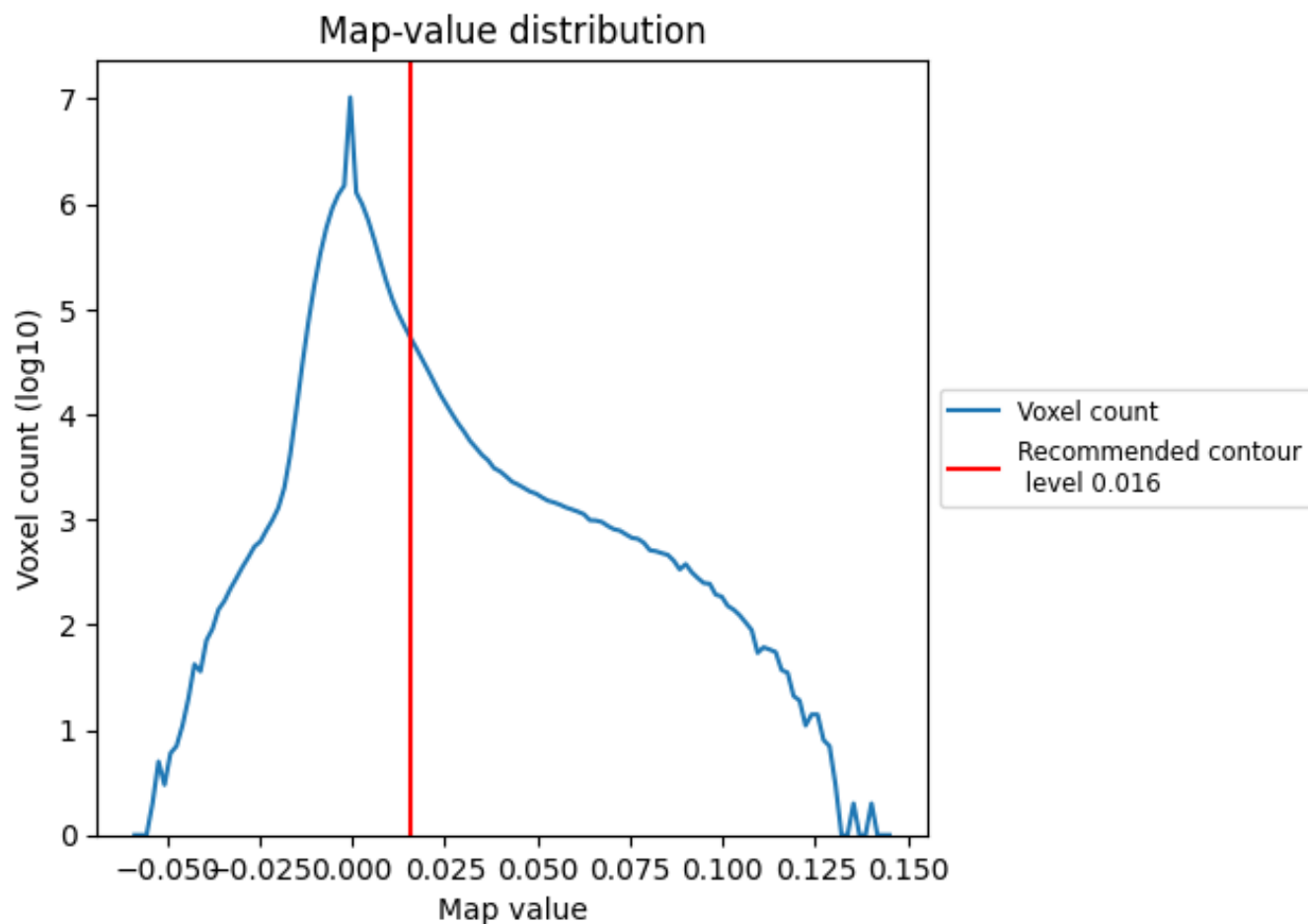
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

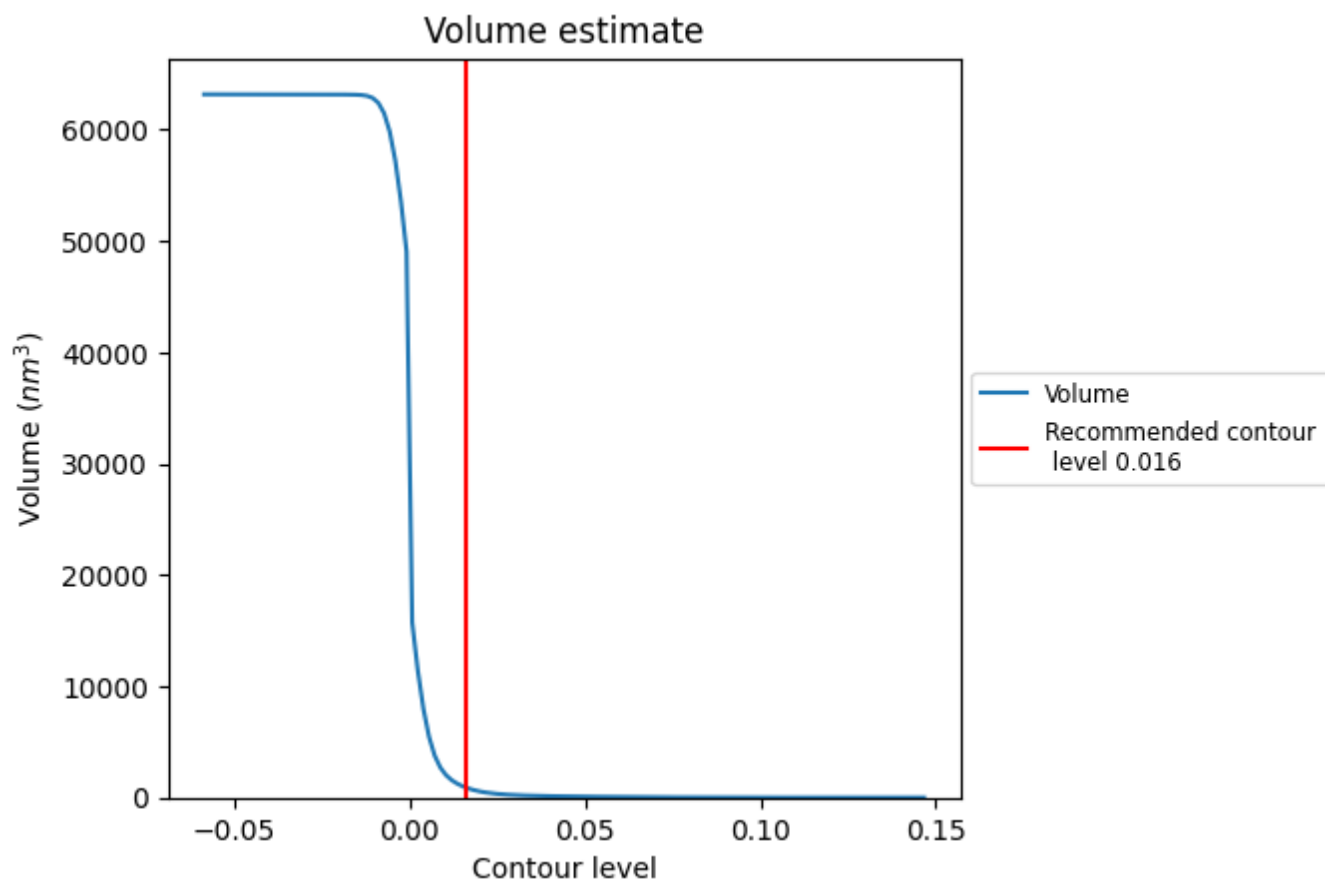
This section contains the results of statistical analysis of the map.

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.

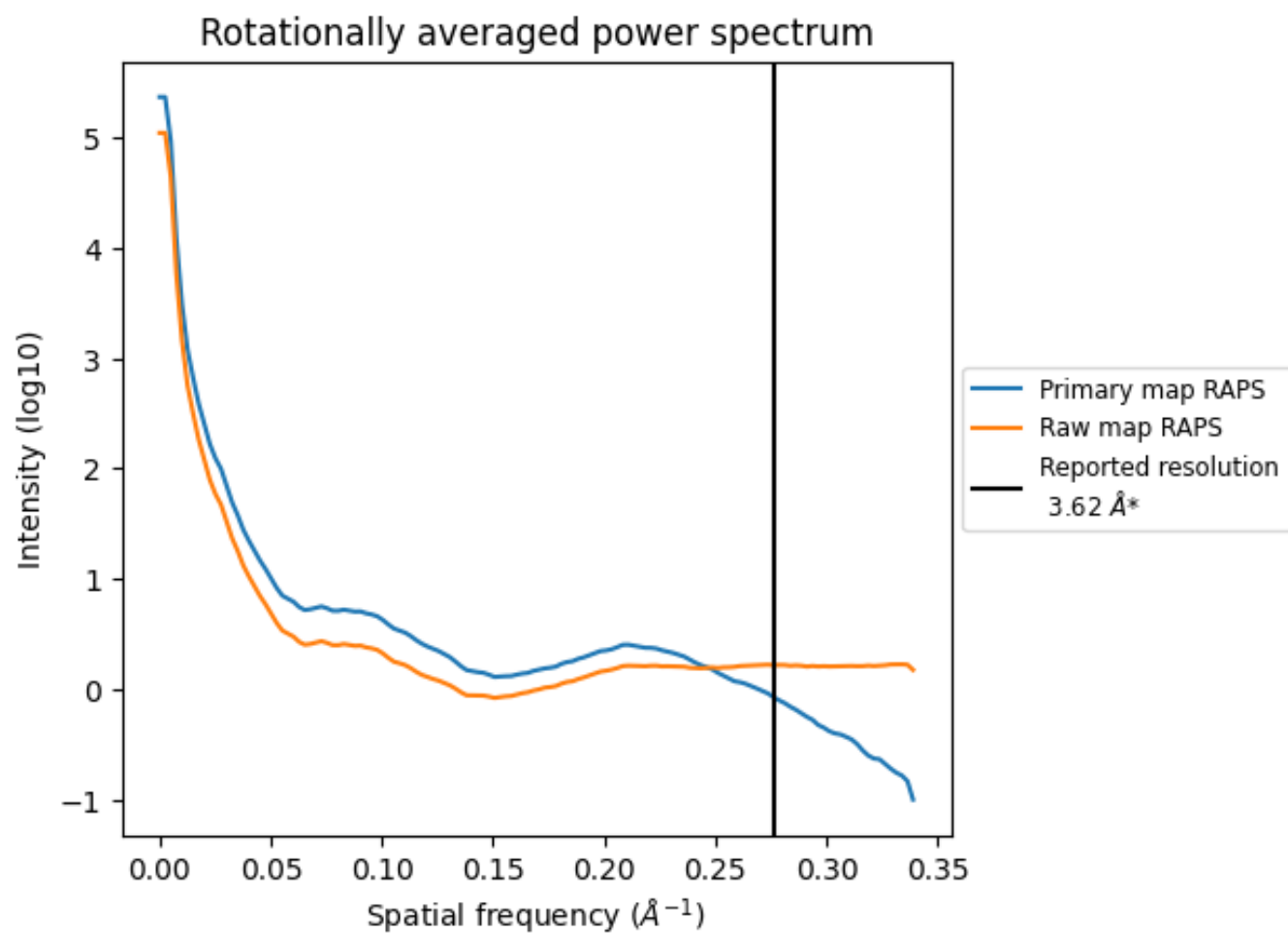
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 903 nm³; this corresponds to an approximate mass of 815 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 ⓘ

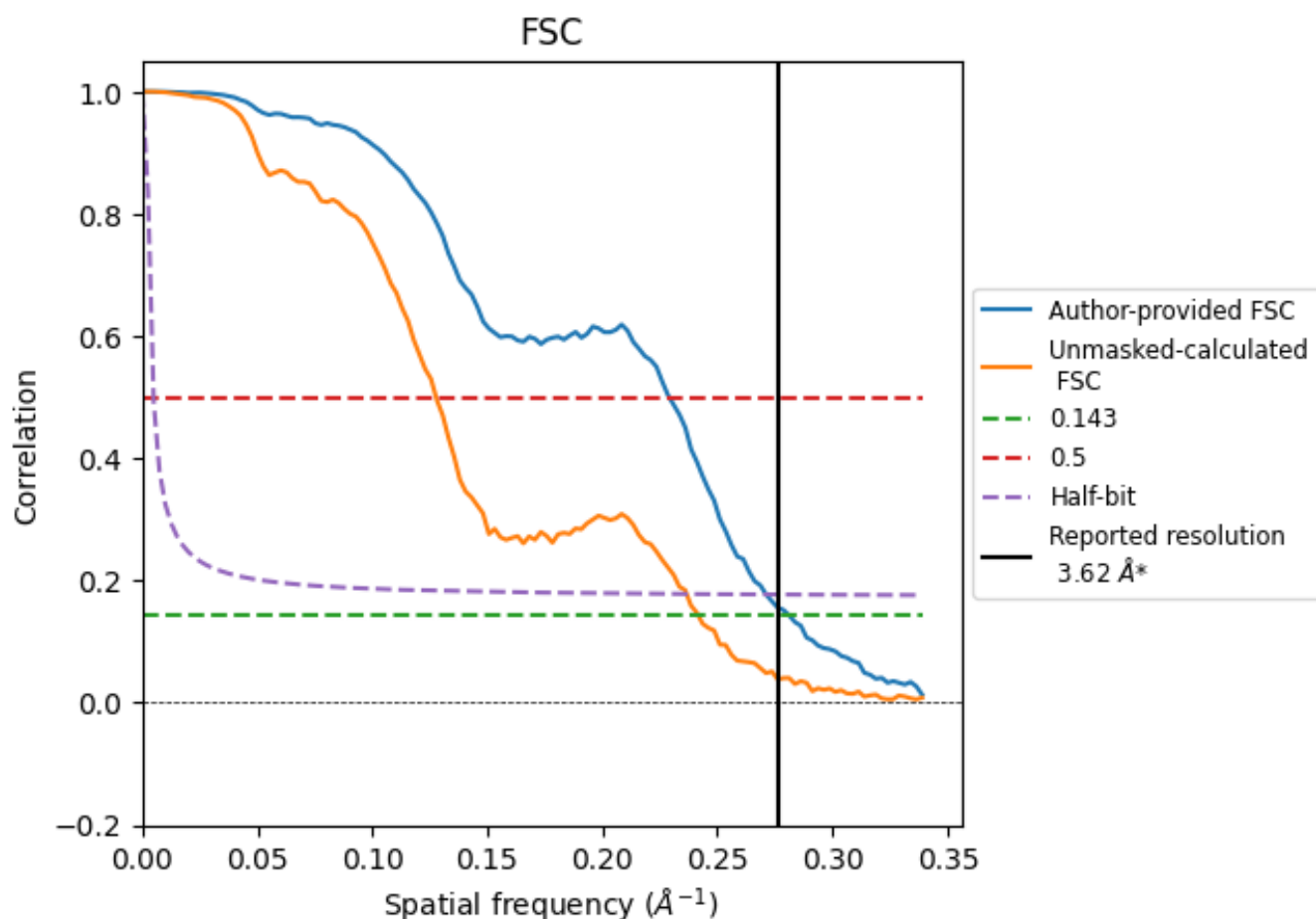


*Reported resolution corresponds to spatial frequency of 0.276 $\text{\AA}^{-1}$

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 0.276 Å⁻¹

8.2 Resolution estimates [i](#)

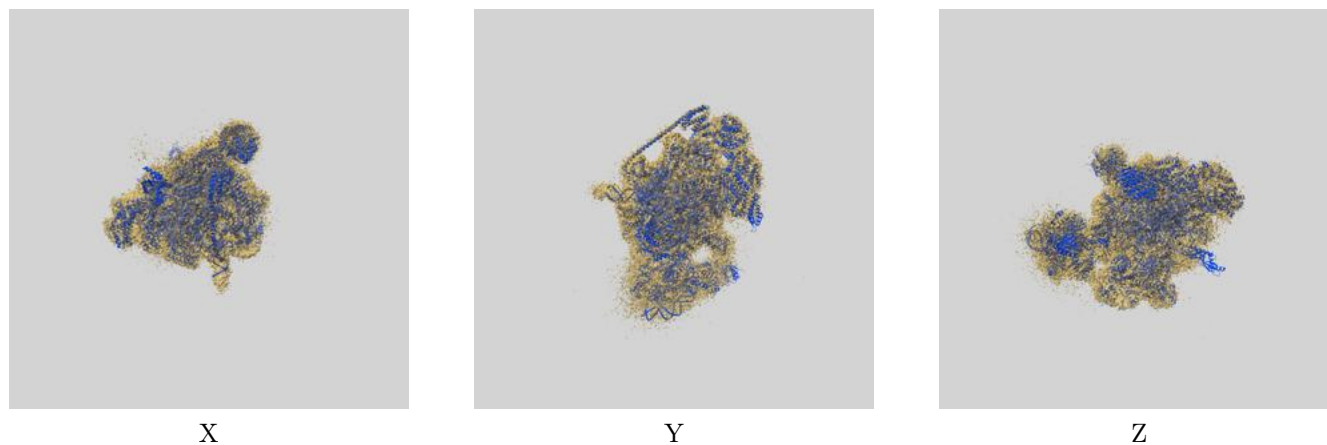
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.62	-	-
Author-provided FSC curve	3.56	4.36	3.69
Unmasked-calculated*	4.14	7.83	4.22

*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 4.14 differs from the reported value 3.62 by more than 10 %

9 Map-model fit [i](#)

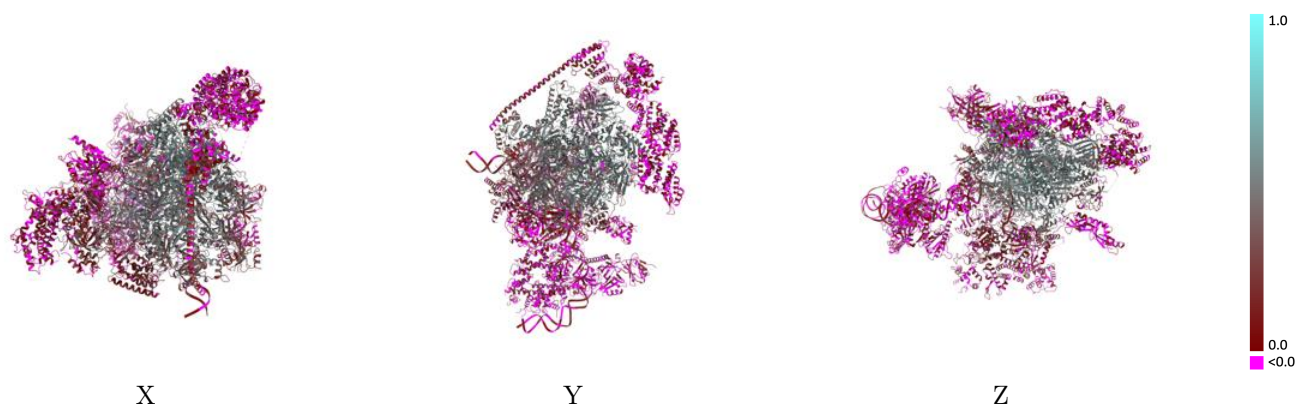
This section contains information regarding the fit between EMDB map EMD-66107 and PDB model 9WMW. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



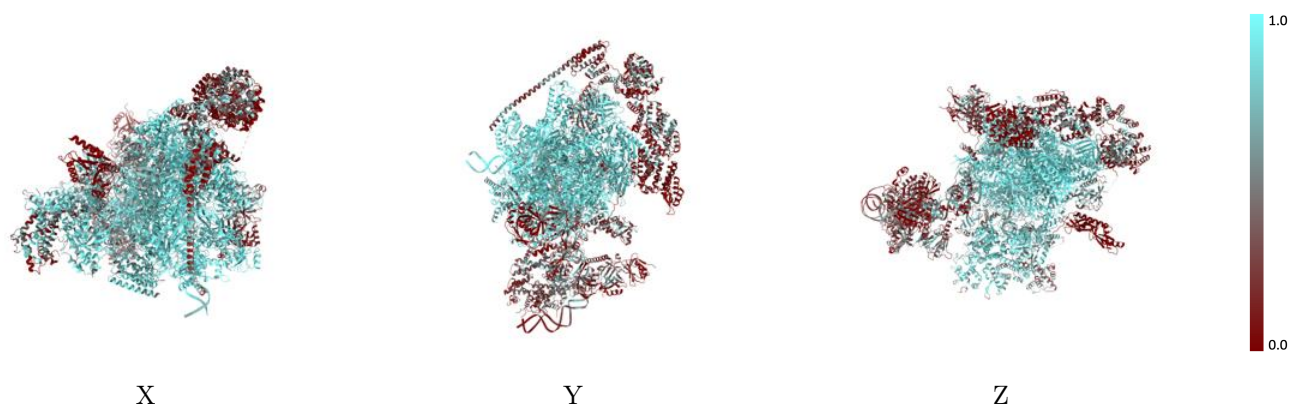
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



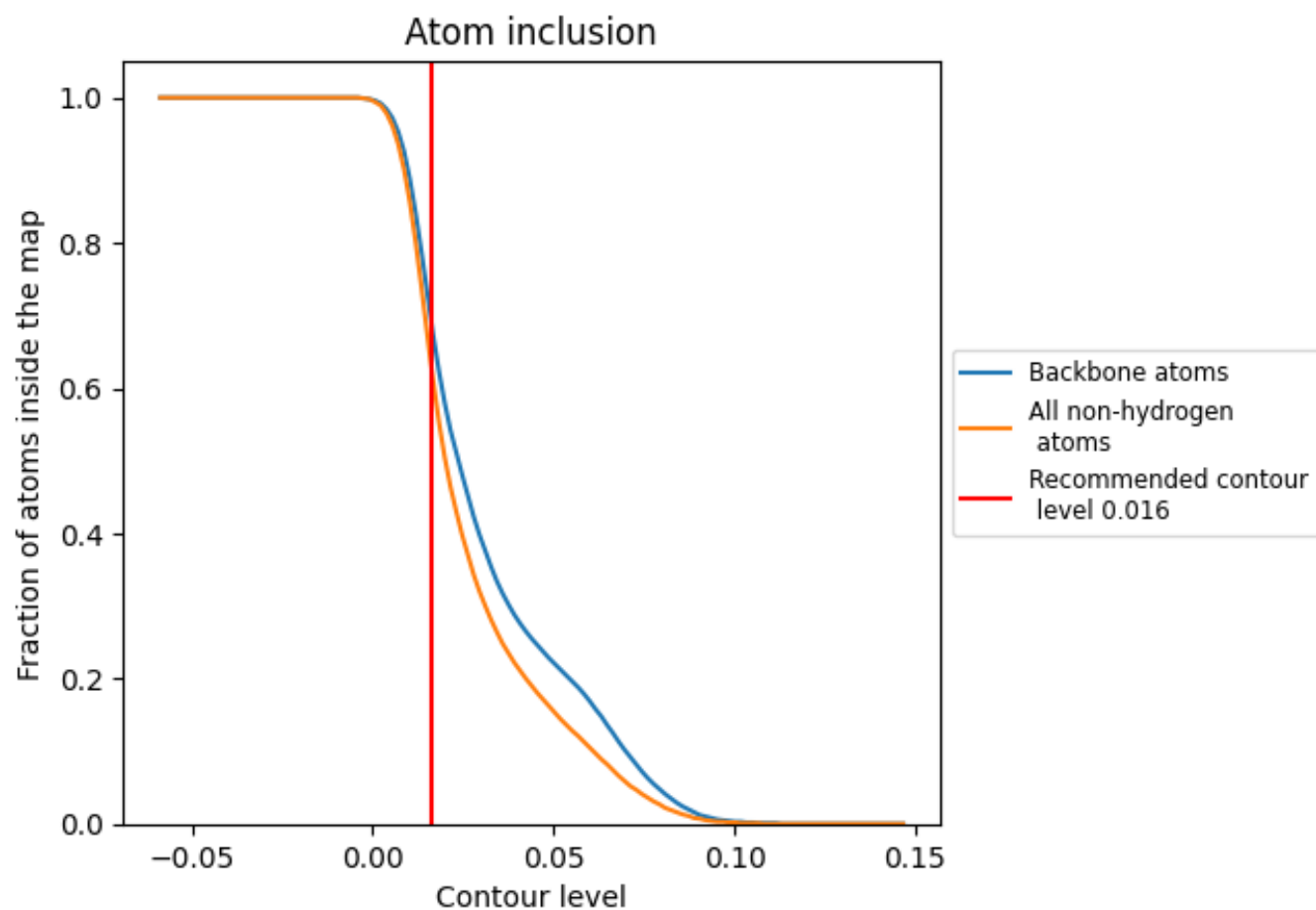
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 64% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6370	 0.2290
A	 0.9330	 0.4680
B	 0.9290	 0.4740
C	 0.9390	 0.5000
D	 0.7730	 0.2030
E	 0.9460	 0.4450
F	 0.9540	 0.5060
G	 0.8470	 0.3080
H	 0.9520	 0.4850
I	 0.8810	 0.3290
J	 0.9500	 0.5150
K	 0.9550	 0.5040
L	 0.9570	 0.4610
M	 0.7640	 0.1520
N	 0.6340	 0.1100
P	 0.8420	 0.3260
T	 0.6860	 0.1610
V	 0.8310	 0.1080
W	 0.7330	 0.1850
a	 0.4790	 0.0130
b	 0.3730	 0.0110
e	 0.3860	 0.0120
f	 0.3530	 0.0550
g	 0.2160	 0.0290
h	 0.1650	 -0.0500
j	 0.3280	 0.0050
k	 0.1830	 0.0000
m	 0.6060	 0.0810
n	 0.8170	 0.1630
q	 0.2720	 0.0400
r	 0.3490	 0.1160
s	 0.2780	 0.0340
u	 0.2470	 0.1020
v	 0.1900	 0.0570
x	 0.4610	 0.2300

