



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 02:46 PM UTC

PDB ID : 7XSE / pdb_00007xse
EMDB ID : EMD-33424
Title : RNA polymerase II elongation complex transcribing a nucleosome (EC42)
Authors : Ehara, H.; Kujirai, T.; Shirouzu, M.; Kurumizaka, H.; Sekine, S.
Deposited on : 2022-05-13
Resolution : 3.60 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:

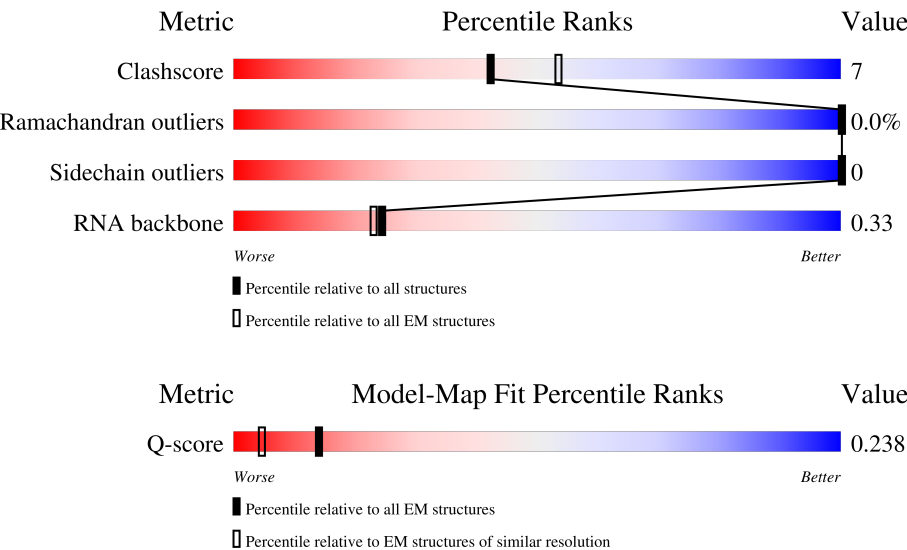
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.60 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.



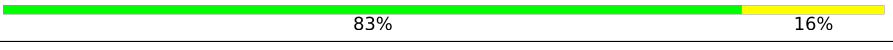
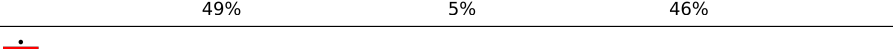
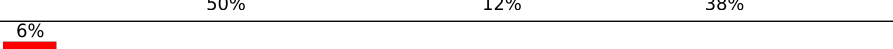
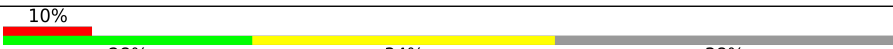
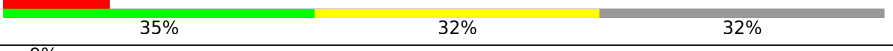
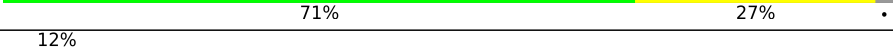
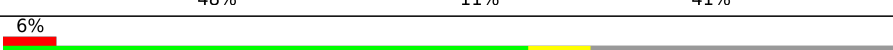
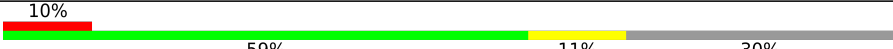
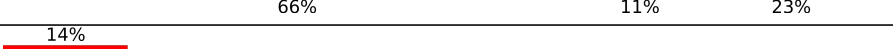
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	70%11%19%
2	B	1227	78%17%5%
3	C	304	77%10%13%

Continued on next page...

Continued from previous page...

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	19	
16	T	198	
17	V	108	
18	W	911	
19	a	139	
19	e	139	
20	b	106	
20	f	106	
21	c	133	
21	g	133	
22	d	129	
22	h	129	
23	m	1503	
24	n	417	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
25	q	1084	
26	r	544	
27	u	459	
28	v	396	
29	x	395	

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 75229 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	123	Total	C	N	O	P	0	0
			2527	1198	458	748	123		

- Molecule 15 is a RNA chain called RNA (5'-R(P*UP*GP*CP*CP*UP*GP*GP*UP*GP*UP*CP*UP*UP*GP*GP*GP*UP*GP*U)-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	134	Total	C	N	O	P	0	0
			2735	1296	519	787	133		

- 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	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 Histone H3.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	a	92	Total	C	N	O	S	0	0
			746	471	142	131	2		
19	e	97	Total	C	N	O	S	0	0
			795	501	155	137	2		

There are 6 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
e	-3	GLY	-	expression tag	UNP P84243
e	-2	SER	-	expression tag	UNP P84243
e	-1	HIS	-	expression tag	UNP P84243

- Molecule 20 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	b	83	Total	C	N	O	S	0	0
			662	418	129	114	1		
20	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

Continued on next page...

Continued from previous page...

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

- Molecule 21 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	c	103	Total	C	N	O	0	0
			796	502	155	139		
21	g	98	Total	C	N	O	0	0
			757	475	149	133		

There are 6 discrepancies between the modelled and reference sequences:

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

- Molecule 22 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	94	Total	C	N	O	S	0	0
			735	462	132	139	2		
22	h	93	Total	C	N	O	S	0	0
			725	456	130	137	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	-6	GLY	-	expression tag	UNP P06899
d	-5	SER	-	expression tag	UNP P06899
d	-4	HIS	-	expression tag	UNP P06899
h	-6	GLY	-	expression tag	UNP P06899
h	-5	SER	-	expression tag	UNP P06899
h	-4	HIS	-	expression tag	UNP P06899

- Molecule 23 is a protein called Transcription elongation factor Spt6.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	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 24 is a protein called Protein that interacts with Spt6p and copurifies with Spt5p and RNA polymerase II.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	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 25 is a protein called Component of the Paf1p complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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 26 is a protein called RNAPII-associated chromatin remodeling Paf1 complex sub-unit.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	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 27 is a protein called Leo1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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 28 is a protein called RNAP II-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	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 29 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
29	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
x	0	GLY	-	expression tag	UNP C4R1E6

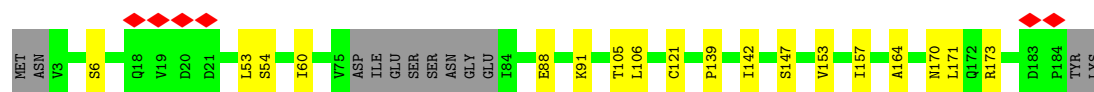
- Molecule 30 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 31 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

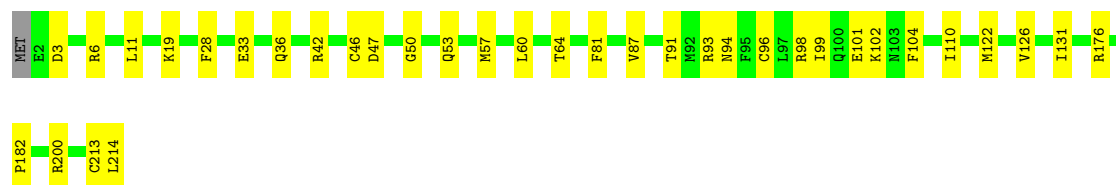
Mol	Chain	Residues	Atoms		AltConf
31	A	1	Total 1	Mg 1	0





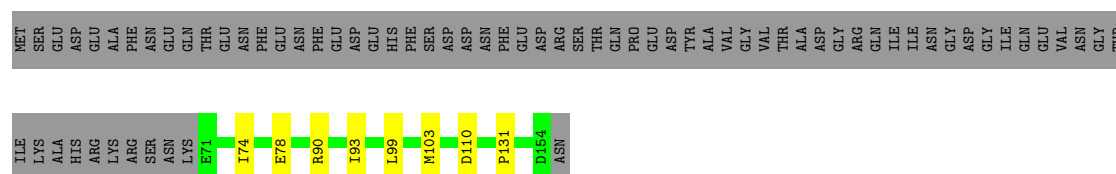
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 83% 16%



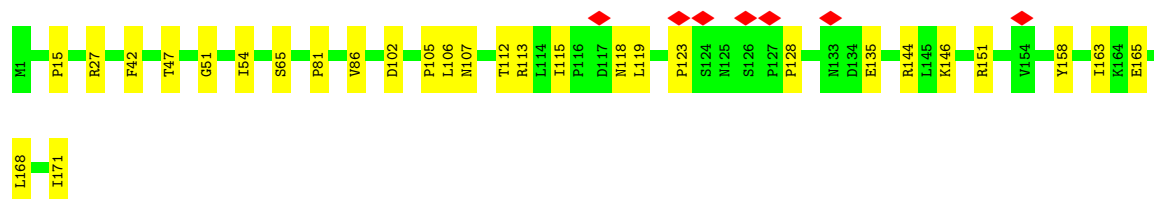
- Molecule 6: RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III

Chain F: 49% 5% 46%



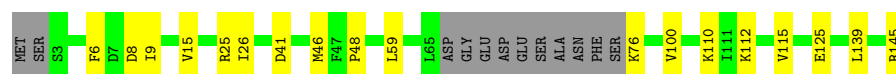
- Molecule 7: RNA polymerase II subunit

Chain G: 83% 17%



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

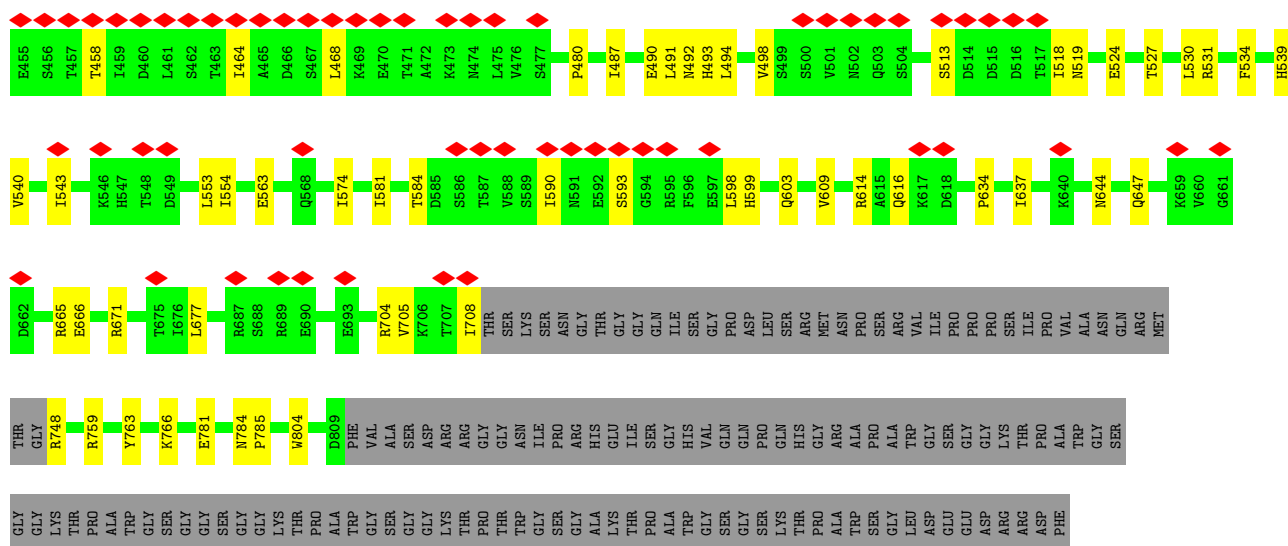
Chain H: 79% 12% 8%



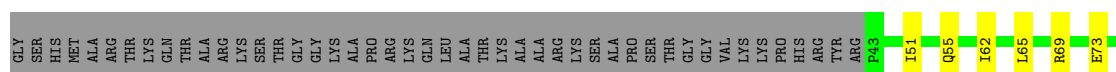
- Molecule 9: DNA-directed RNA polymerase subunit

Chain I: 7% 80% 17%

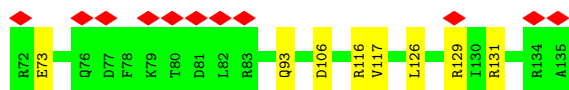
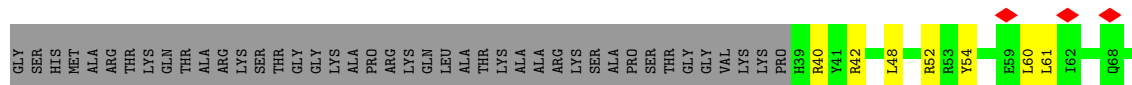




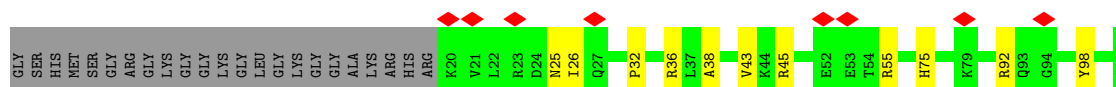
• Molecule 19: Histone H3.3



• Molecule 19: Histone H3.3



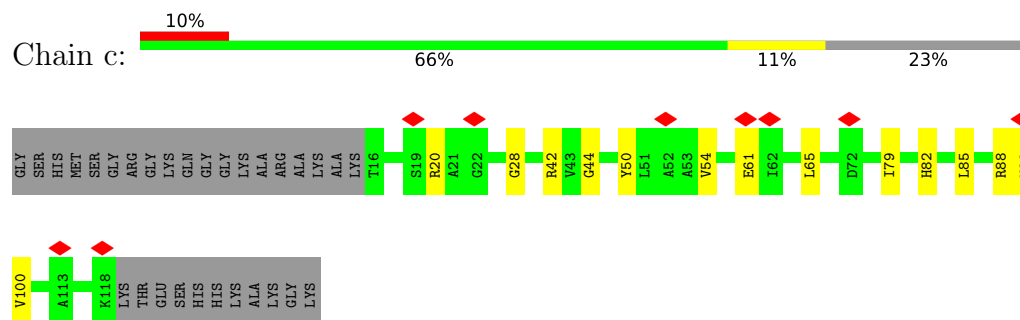
• Molecule 20: Histone H4



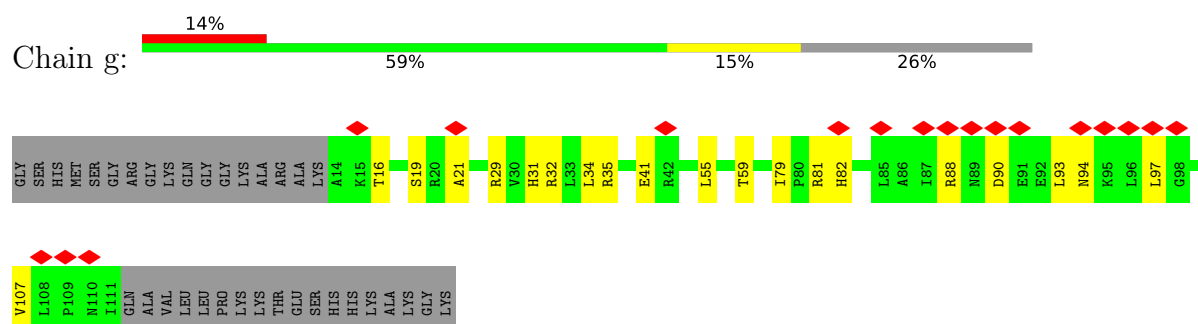
• Molecule 20: Histone H4



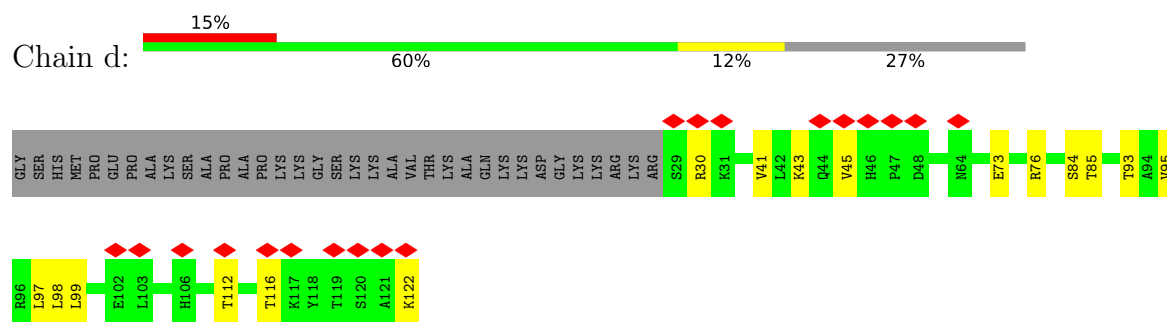
- Molecule 21: Histone H2A type 1-B/E



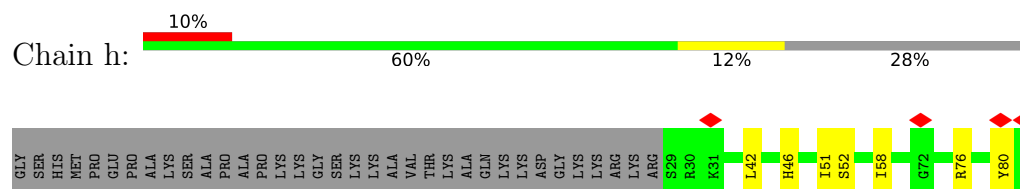
- Molecule 21: Histone H2A type 1-B/E



- Molecule 22: Histone H2B type 1-J

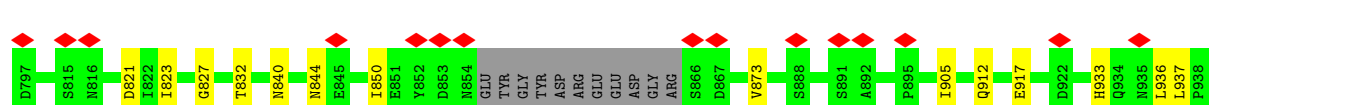
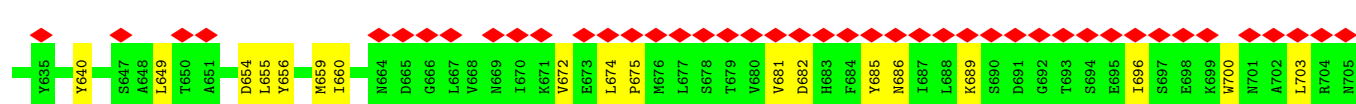
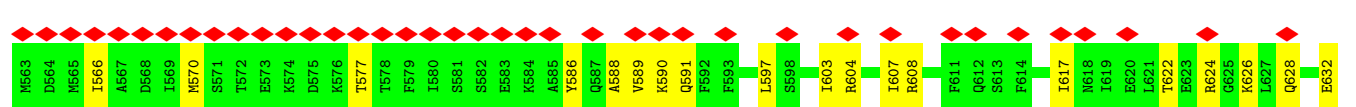
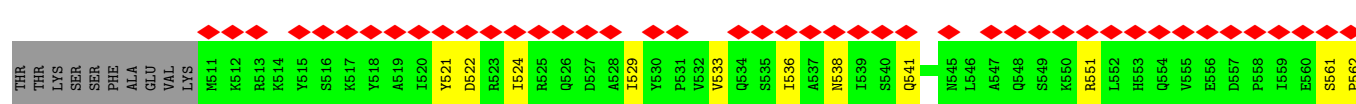
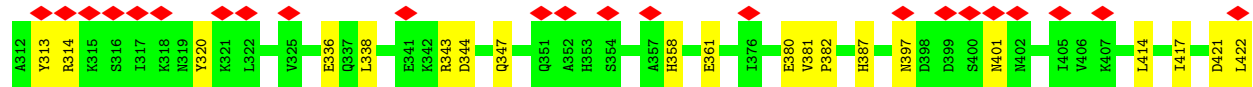
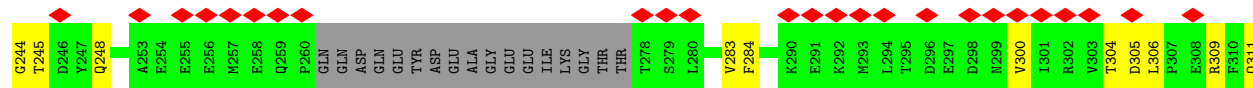
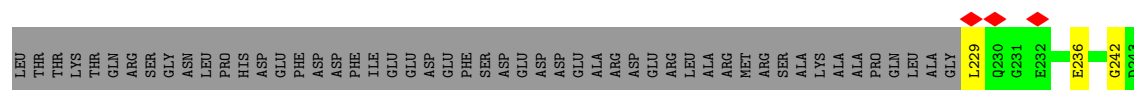


- Molecule 22: Histone H2B type 1-J



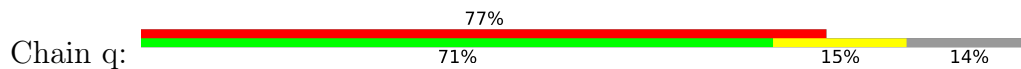


• Molecule 23: Transcription elongation factor Spt6

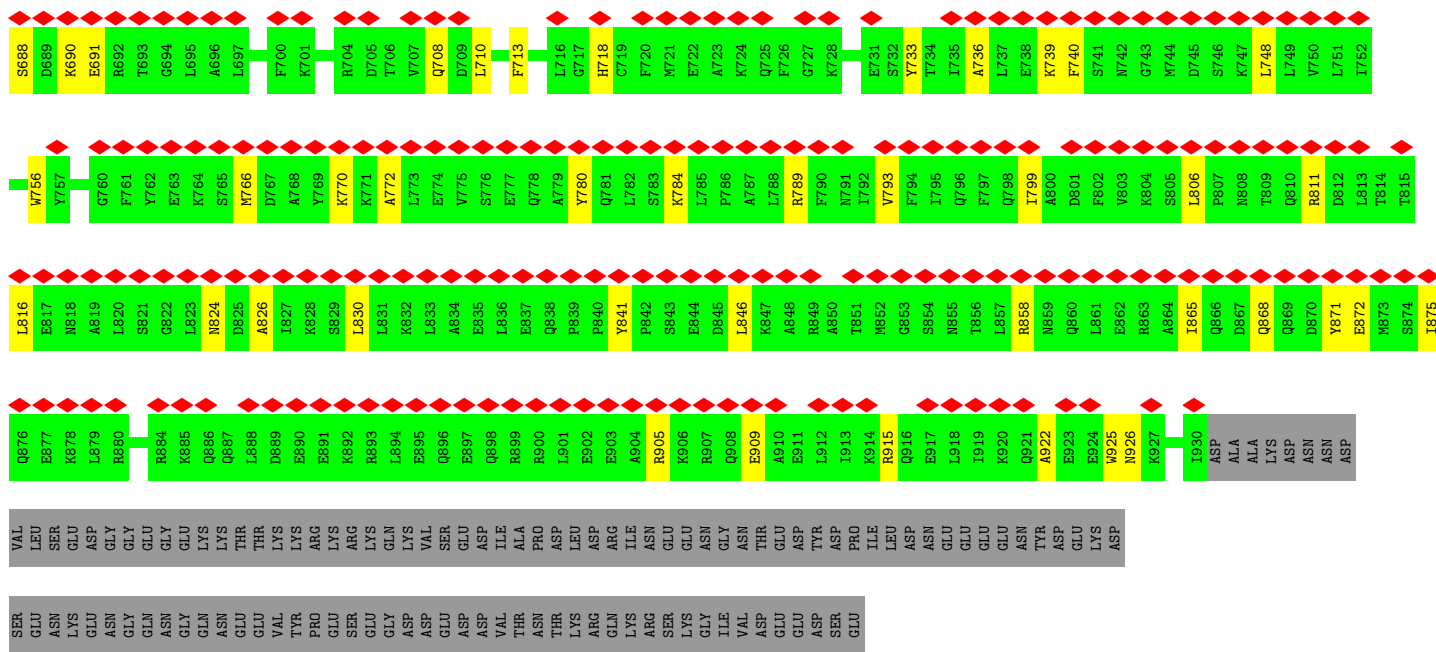


GLU	LEU	LEU	MET	HIS	SER	SER	ALA	ARG	ARG	THR	HIS	LEU	PRO	SER	GLY	VAL	GLY	SER	SER	SER	LEU	SER	GLY	GLU	ASP	GLN	TYR	LYS	ARG	GLU	ASN	SER	ARG	LEU	ASN	GLN	THR	THR	GLY	MET	GLY	THR	LYS	LYS	SER	SER	ALA	ALA	LYS	LYS	GLY	GLY	ILE	ILE	GLY	GLY	ARG	GLY	PRO	GLN
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

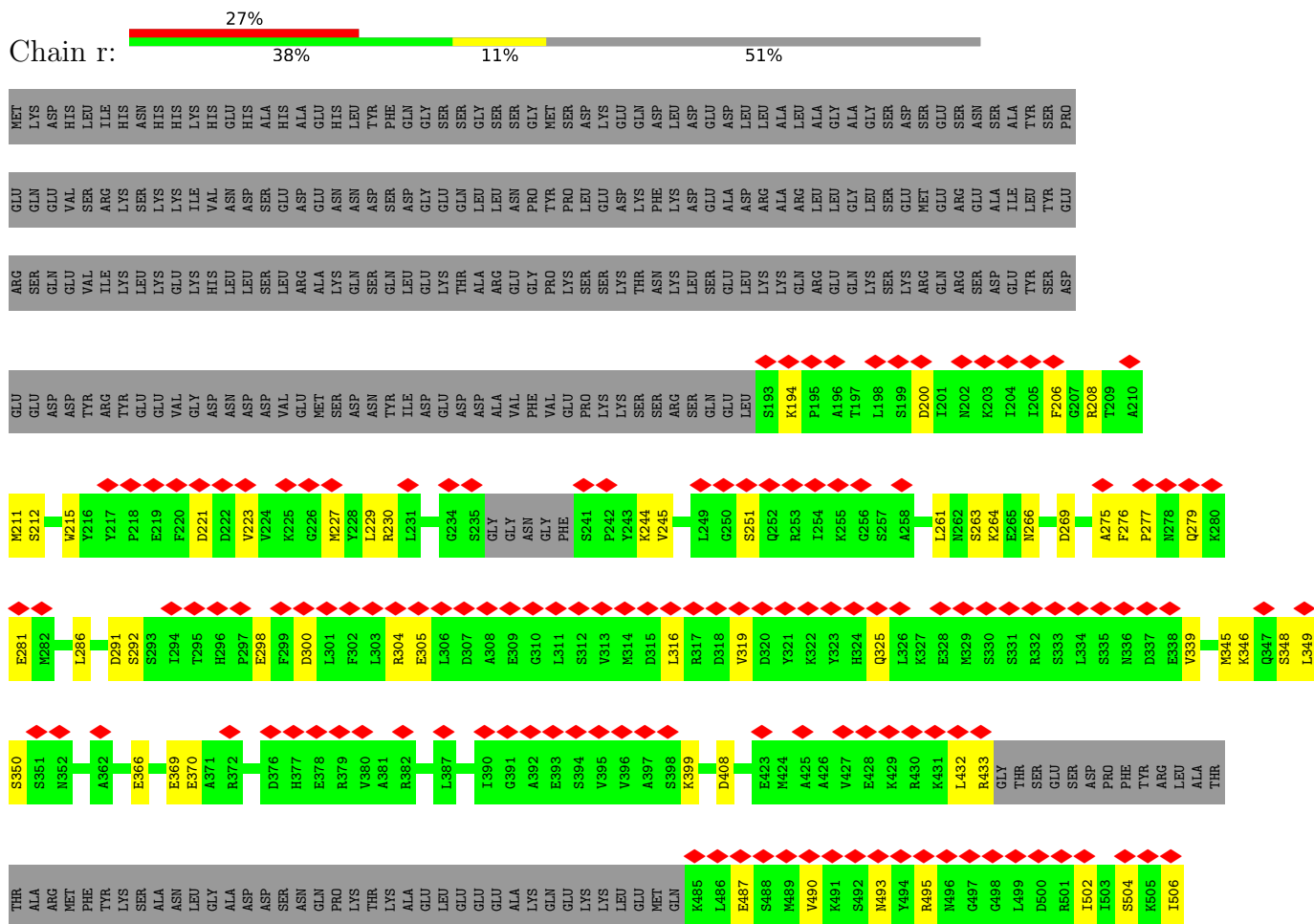
● Molecule 25: Component of the Paf1p complex



MET	LYS	ASP	HIS	LEU	ILE	HIS	ASN	HIS	HIS	LYS	HIS	GLU	HIS	ALA	ALA	GLU	HIS	ASP	ASP	ASP	ASP	LYS	GLU	HIS	LEU	TYR	PHE	GLN	GLY	SER	SER	SER	GLY	SER	SER	GLY	HIS	S2	L3	L4	D5	D6	D7	Y8	Y9	L10	S11	A12	L13	P14	E15	D16	K17	R18	A19	E20			
L21	V22	T23	L24	Q25	L26	T27	T28	P29	L30	K31	S32	G33	D34	E35	V36	V37	T38	I39	D40	F41	N42	E43	D44	V45	D46	V47	S48	Q49	L50	C51	V52	L53	L54	E55	S56	E57	N58	A59	R60	P61	D62	L63	W64	L65	S66	A67	A68	K69	V70	F71	V72	S73	K74	G75	N76	I77	A78	G79	S80
Q81	E82	I83	T84	R85	K86	A87	L88	Q89	S90	N91	V92	I93	L94	D95	S96	S97	A98	S99	V100	T101	S102	L103	F104	H105	N106	F107	S108	F109	W110	L111	S112	L113	M114	E115	Y116	I117	S118	T119	N120	S121	R122	E123	D124	Q125	F126	S127	L128	A129	I130	K131	V132	W133	L134	Q135	A136	S137	N138	S139	L140
D141	S142	G143	L144	T145	L146	M147	G148	I149	G150	M151	G152	V153	L154	Y155	A156	K157	S158	R159	R160	Y161	D162	E163	A164	L165	K166	E167	F168	D169	M170	L171	L172	K173	K174	K175	S176	T177	I178	I179	L180	A181	S182	L183	G184	K185	A186	Q187	L188	Y189	K190	R191	R192	Q193	K194	Y195	S196	Q197	A198	L199	F200
L201	Y202	Q203	K204	A205	L206	T207	I208	N209	P210	L211	T212	V213	P214	D215	P216	R217	L218	G219	I220	G221	L222	C223	F224	W225	H226	L227	N228	N229	K230	Q231	L232	A233	E234	Q235	L236	W237	H238	N239	S240	L241	K242	W243	P245	Q246	N247	N248	L249	N250	T251	K252	L253	L254	I255	C256	L257	K258	F259		
D261	Y262	C263	F264	N265	E266	S267	N268	D269	D270	D271	E272	F273	T274	A275	L276	Y277	R278	E279	S280	L281	E282	F283	L284	H285	S286	C287	L288	K289	E290	D291	A292	H294	P295	L296	L297	L298	N299	V300	L301	A302	S303	Y304	Y305	F306	K307	G308	E309	D310	Y311	E312	K313	V314	E315	K316	L317	C318	N319	L320	
V321	K323	E324	N325	S326	R327	N328	A329	A330	F331	F332	S333	A334	S335	H336	F337	W338	L339	A340	R341	V342	K346	E347	D348	Y349	V350	Q351	A352	Q353	A354	Q355	F356	K357	Q358	V359	E360	D361	S362	Q363	N364	S365	N366	A369	K370	L371	G372	Y373	A374	Q375	C376	L377	I378	A379	R380	N381	E382	V383			
G384	D385	A386	T387	V388	L389	L390	E391	K392	F393	F394	K395	E396	N397	Q398	D399	S400	K401	S402	E403	E404	M405	M406	L407	A408	L409	G410	I411	I412	Y413	S414	Q415	S416	G417	K418	S419	Y420	Y421	K422	A423	I424	I425	F426	E428	K429	Y430	R431	A432	D433	C434	Q435	E436	E437	N438	Y439	P440	I441	L442	P443	
E444	A445	Y446	L447	V448	L449	S450	R451	W452	Y453	E454	M455	K456	D457	L458	M459	W460	A461	L462	D463	Y464	L465	M466	K467	A468	M469	D470	I471	L472	G473	D474	K475	A476	W477	W478	Y479	V480	L481	M482	M483	L484	G485	I486	Y487	H488	F489	F490	R491	M492	M493	V494	S495	Q496	S497	S498	D499	F500	F501	A502	Q503
S504	L505	E506	A507	L508	N509	N510	V511	S512	P513	Q514	M515	K516	E517	A518	L519	S520	I521	T522	L523	H524	N526	K527	A528	R529	V530	E531	E532	V533	S534	N535	Q536	S537	G601	R602	K603	N604	G605	L606	K607	Q608	D609	L610	E611	S612	Q613	H614	H615	K616	D617	T618	L619	I620	N621	I683	A684	I685	I686	F687	
L566	K567	S568	N569	G570	N571	N572	Y573	A574	D575	V576	Q577	Q578	I640	A641	R642	E643	M644	V645	T647	D648	Q649	K650	V589	R590	S591	G594	W595	F596	L597	K598	R599	Y600	G601	A662	A663	Q664	F665	Y666	H667	K668	S671	I672	D673	P674	K675	N676	I677	Y678	A679	A680	Q681	G682	I683	A684	I685	I686	F687		



• Molecule 26: RNAPII-associated chromatin remodeling Paf1 complex subunit

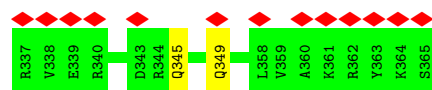
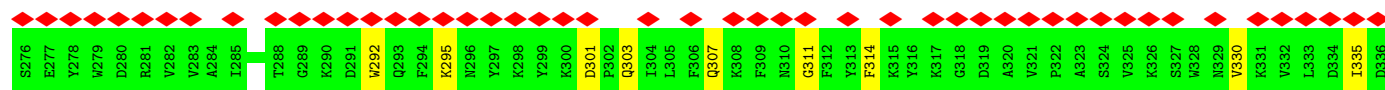
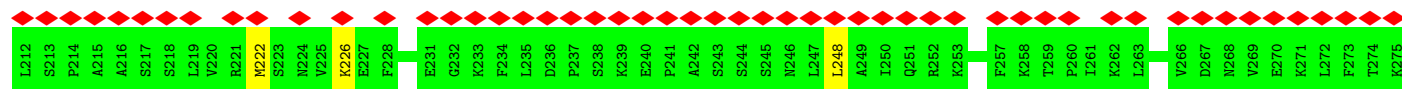
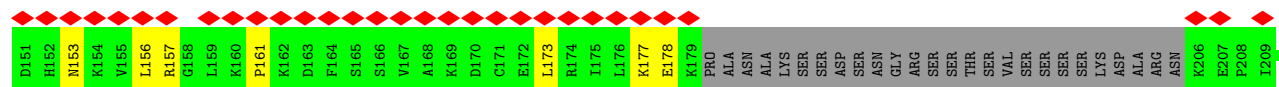
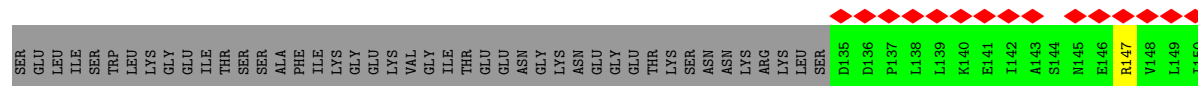
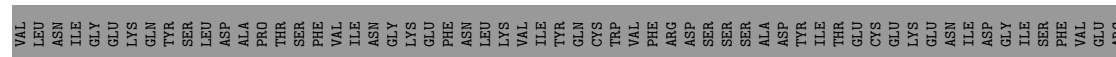
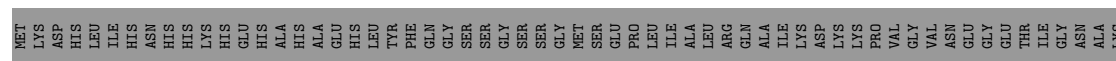
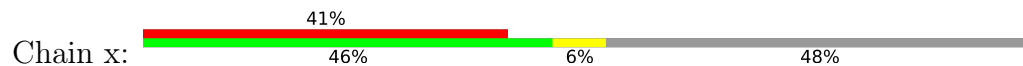


Chain u:





- Molecule 29: Constituent of Paf1 complex with RNA polymerase II, Paf1p, Hpr1p, Ctr9, Leo1, Rtf1 and Ccr4p



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76913	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	0.120	Depositor
Minimum map value	-0.040	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.014	Depositor
Map size ($\text{\AA}$)	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 ($\text{\AA}$)	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: MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.22	0/11267	0.31	1/15222 (0.0%)
2	B	0.23	0/9464	0.29	0/12763
3	C	0.25	0/2139	0.30	0/2895
4	D	0.09	0/1361	0.24	0/1837
5	E	0.21	0/1773	0.31	0/2385
6	F	0.23	0/687	0.28	0/931
7	G	0.14	0/1354	0.27	0/1837
8	H	0.22	0/1070	0.28	0/1444
9	I	0.09	0/934	0.25	0/1257
10	J	0.25	0/563	0.28	0/753
11	K	0.23	0/953	0.29	0/1291
12	L	0.19	0/365	0.26	0/484
13	M	0.09	0/513	0.25	0/693
14	N	0.44	0/2831	0.64	0/4368
15	P	0.50	0/449	0.73	1/698 (0.1%)
16	T	0.48	0/3071	0.64	0/4733
17	V	0.09	0/840	0.21	0/1140
18	W	0.10	0/4300	0.26	0/5812
19	a	0.19	0/755	0.35	0/1012
19	e	0.31	0/806	0.49	0/1081
20	b	0.22	0/669	0.46	0/894
20	f	0.41	0/626	0.63	0/837
21	c	0.19	0/806	0.36	0/1089
21	g	0.16	0/766	0.34	0/1033
22	d	0.20	0/746	0.34	0/1001
22	h	0.26	0/736	0.39	0/990
23	m	0.10	0/9925	0.25	0/13424
24	n	0.19	0/1132	0.37	0/1526
25	q	0.09	0/7689	0.21	0/10368
26	r	0.10	0/2169	0.24	0/2901
27	u	0.10	0/1740	0.23	0/2347
28	v	0.10	0/2944	0.24	0/3973

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
29	x	0.12	0/1716	0.25	0/2310
All	All	0.22	0/77159	0.34	2/105329 (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

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1001	VAL	N-CA-C	-5.72	107.24	112.96
15	P	10	G	OP1-P-O3'	5.36	124.07	108.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	N	-17	DT	Sidechain
14	N	-18	DG	Sidechain
14	N	-23	DT	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	121	0
2	B	9284	0	9282	136	0
3	C	2098	0	2057	21	0
4	D	1349	0	1345	11	0
5	E	1741	0	1754	24	0
6	F	677	0	693	8	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	1325	0	1342	19	0
8	H	1053	0	1050	11	0
9	I	917	0	867	17	0
10	J	554	0	573	6	0
11	K	932	0	944	14	0
12	L	359	0	358	8	0
13	M	505	0	495	6	0
14	N	2527	0	1386	68	0
15	P	404	0	202	13	0
16	T	2735	0	1497	63	0
17	V	824	0	795	17	0
18	W	4232	0	4278	69	0
19	a	746	0	786	9	0
19	e	795	0	832	16	0
20	b	662	0	709	11	0
20	f	619	0	659	16	0
21	c	796	0	848	11	0
21	g	757	0	802	14	0
22	d	735	0	758	12	0
22	h	725	0	745	11	0
23	m	9730	0	9588	143	0
24	n	1115	0	1186	25	0
25	q	7552	0	7545	112	0
26	r	2139	0	2155	43	0
27	u	1707	0	1676	26	0
28	v	2878	0	2873	58	0
29	x	1682	0	1731	16	0
30	A	2	0	0	0	0
30	B	1	0	0	0	0
30	C	1	0	0	0	0
30	I	2	0	0	0	0
30	J	1	0	0	0	0
30	L	1	0	0	0	0
30	M	1	0	0	0	0
30	V	1	0	0	0	0
31	A	1	0	0	0	0
All	All	75229	0	72901	984	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 7.

The worst 5 of 984 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
1:A:318:LYS:HE3	16:T:43:DA:C6	2.13	0.83
25:q:793:VAL:HG11	25:q:830:LEU:HG	1.64	0.79
14:N:-61:DT:C2'	14:N:-60:DT:H72	2.13	0.78
14:N:-45:DG:N2	16:T:45:DC:O2	2.16	0.78

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%)	1355 (97%)	36 (3%)	1 (0%)	48	79
2	B	1154/1227 (94%)	1119 (97%)	35 (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%)	166 (98%)	3 (2%)	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	a	90/139 (65%)	86 (96%)	4 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	e	95/139 (68%)	95 (100%)	0	0	100	100
20	b	81/106 (76%)	78 (96%)	3 (4%)	0	100	100
20	f	76/106 (72%)	73 (96%)	3 (4%)	0	100	100
21	c	101/133 (76%)	100 (99%)	1 (1%)	0	100	100
21	g	96/133 (72%)	93 (97%)	3 (3%)	0	100	100
22	d	92/129 (71%)	88 (96%)	4 (4%)	0	100	100
22	h	91/129 (70%)	90 (99%)	1 (1%)	0	100	100
23	m	1179/1503 (78%)	1157 (98%)	22 (2%)	0	100	100
24	n	137/417 (33%)	136 (99%)	1 (1%)	0	100	100
25	q	928/1084 (86%)	922 (99%)	6 (1%)	0	100	100
26	r	260/544 (48%)	254 (98%)	6 (2%)	0	100	100
27	u	206/459 (45%)	203 (98%)	3 (2%)	0	100	100
28	v	341/396 (86%)	327 (96%)	14 (4%)	0	100	100
29	x	201/395 (51%)	200 (100%)	1 (0%)	0	100	100
All	All	8563/11466 (75%)	8369 (98%)	193 (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%)	1219 (100%)	0	100	100
2	B	1018/1077 (94%)	1018 (100%)	0	100	100
3	C	236/264 (89%)	236 (100%)	0	100	100
4	D	149/160 (93%)	149 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	480/796 (60%)	480 (100%)	0	100	100
19	a	78/112 (70%)	78 (100%)	0	100	100
19	e	82/112 (73%)	82 (100%)	0	100	100
20	b	68/81 (84%)	68 (100%)	0	100	100
20	f	63/81 (78%)	63 (100%)	0	100	100
21	c	82/102 (80%)	82 (100%)	0	100	100
21	g	77/102 (76%)	77 (100%)	0	100	100
22	d	80/107 (75%)	80 (100%)	0	100	100
22	h	79/107 (74%)	79 (100%)	0	100	100
23	m	1087/1354 (80%)	1087 (100%)	0	100	100
24	n	125/361 (35%)	125 (100%)	0	100	100
25	q	824/962 (86%)	824 (100%)	0	100	100
26	r	239/485 (49%)	239 (100%)	0	100	100
27	u	192/406 (47%)	192 (100%)	0	100	100
28	v	325/369 (88%)	325 (100%)	0	100	100
29	x	190/354 (54%)	190 (100%)	0	100	100
All	All	7692/10063 (76%)	7692 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
25	q	132	ASN
26	r	493	ASN
25	q	187	GLN
25	q	621	ASN
28	v	305	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	19/19 (100%)	8 (42%)	2 (10%)

5 of 8 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 (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	P	-7	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 oligosaccharides 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

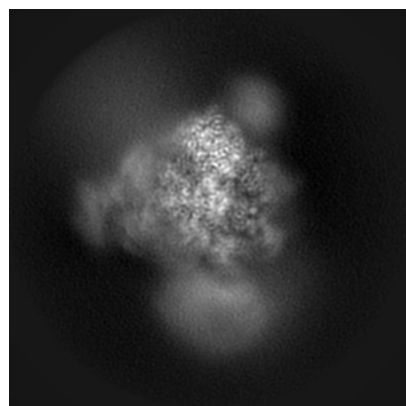
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33424. These allow visual inspection of the internal detail of the map and identification of artifacts.

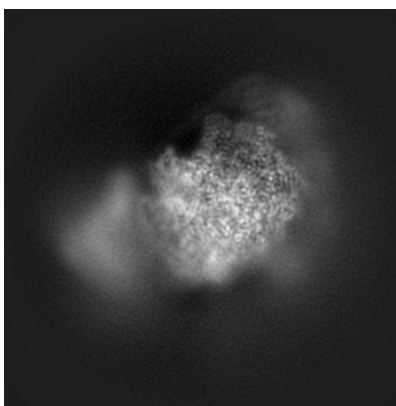
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

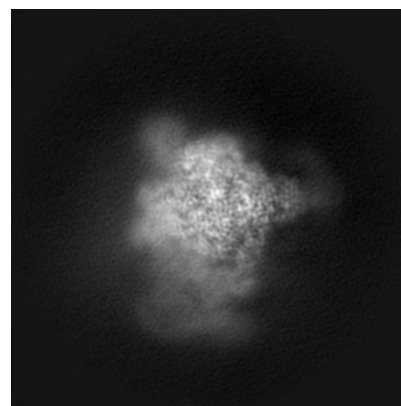
6.1.1 Primary map



X

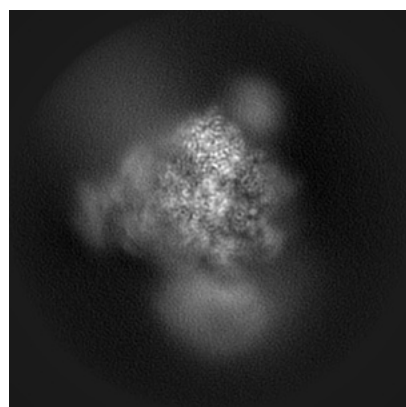


Y

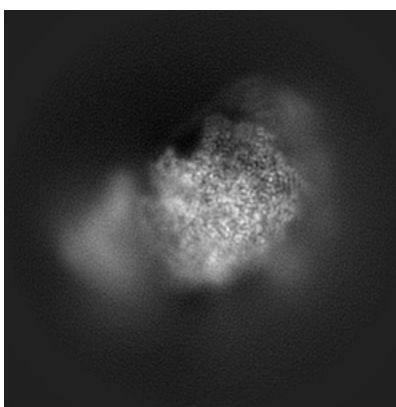


Z

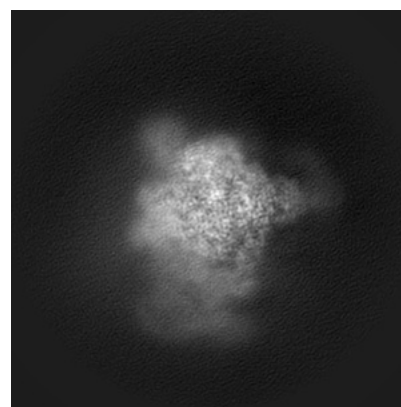
6.1.2 Raw map



X



Y

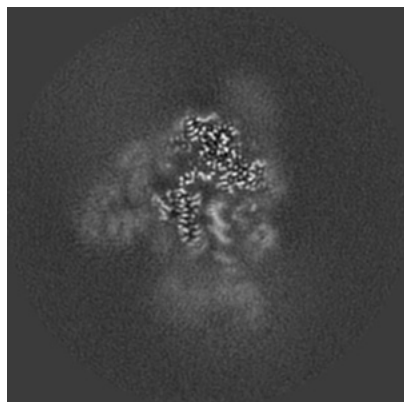


Z

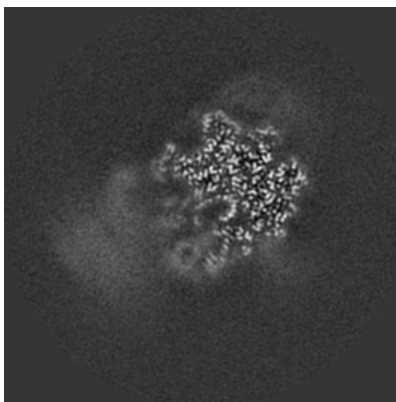
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

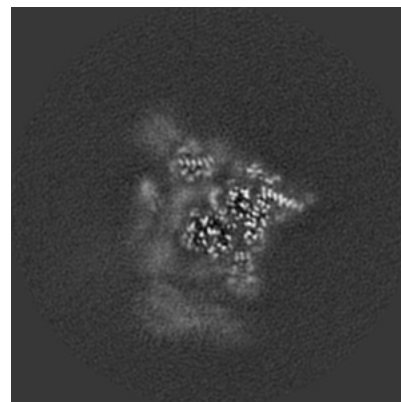
6.2.1 Primary map



X Index: 120

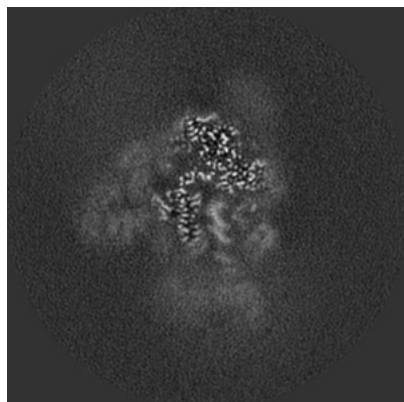


Y Index: 120

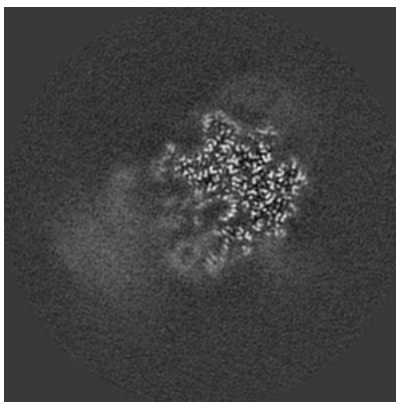


Z Index: 120

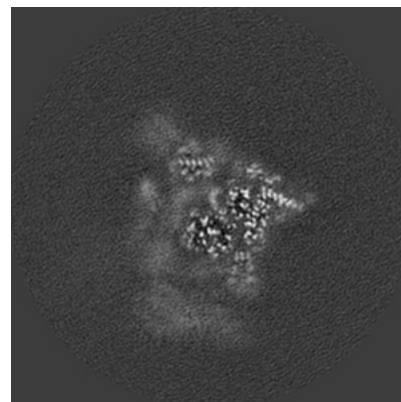
6.2.2 Raw map



X Index: 120



Y Index: 120

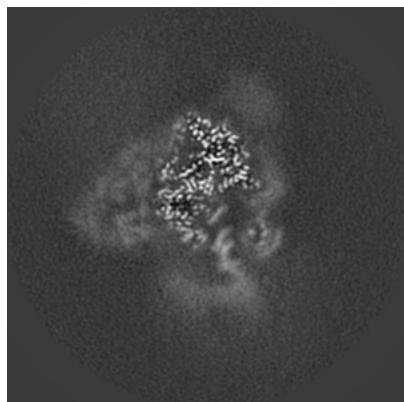


Z Index: 120

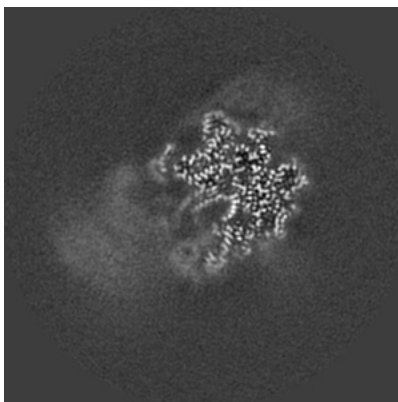
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

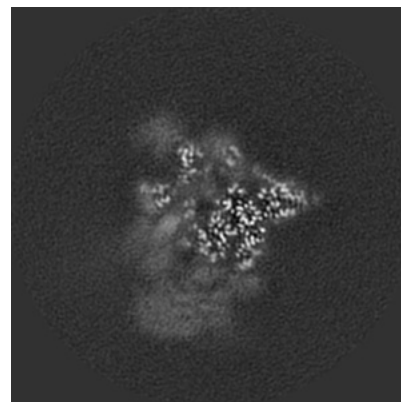
6.3.1 Primary map



X Index: 125

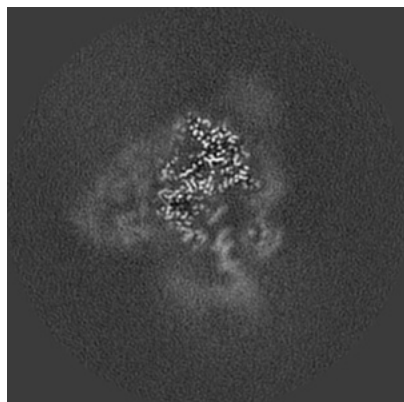


Y Index: 121

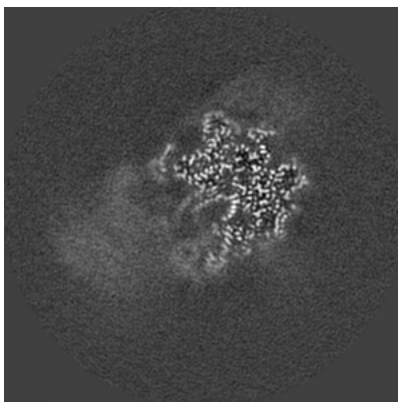


Z Index: 125

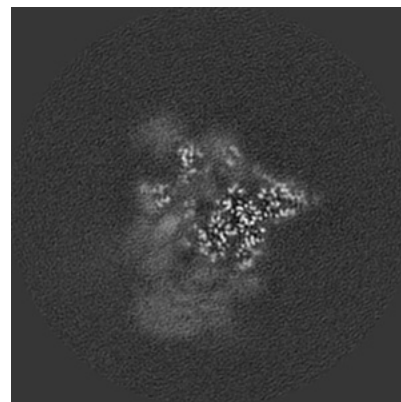
6.3.2 Raw map



X Index: 125



Y Index: 121

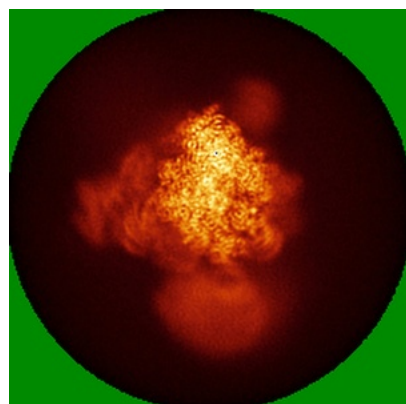


Z Index: 125

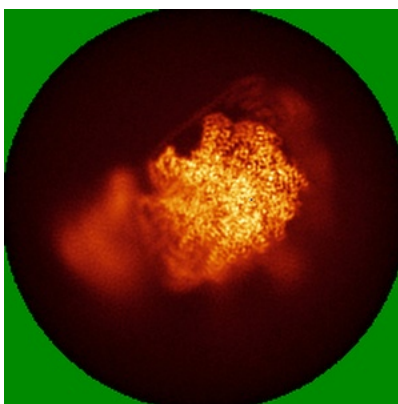
The images above show the largest variance slices of the map in three orthogonal directions.

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

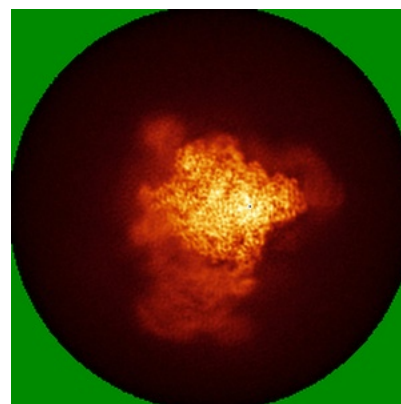
6.4.1 Primary map



X

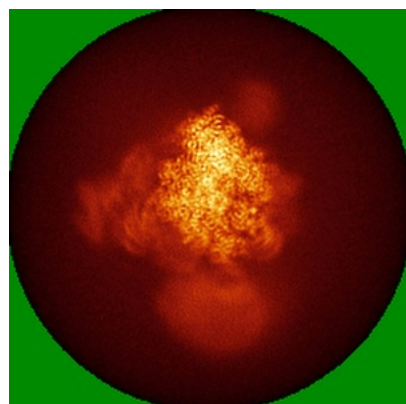


Y

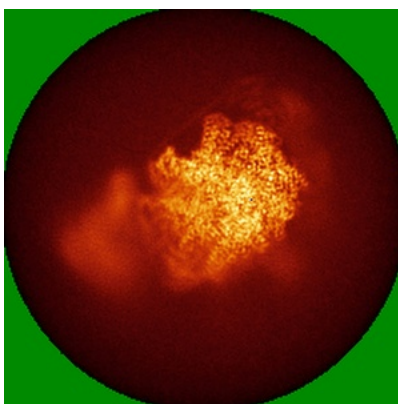


Z

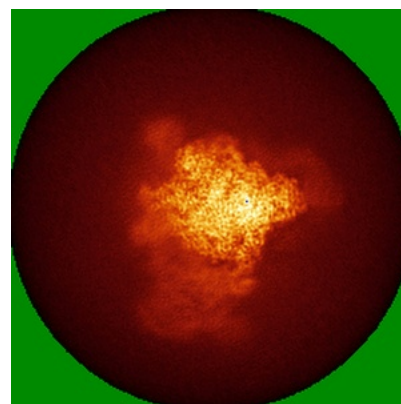
6.4.2 Raw map



X



Y

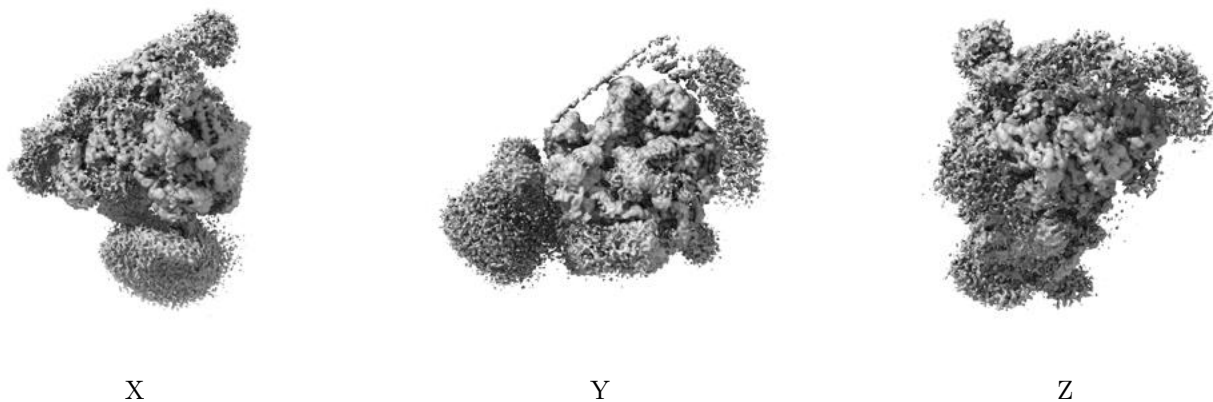


Z

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.

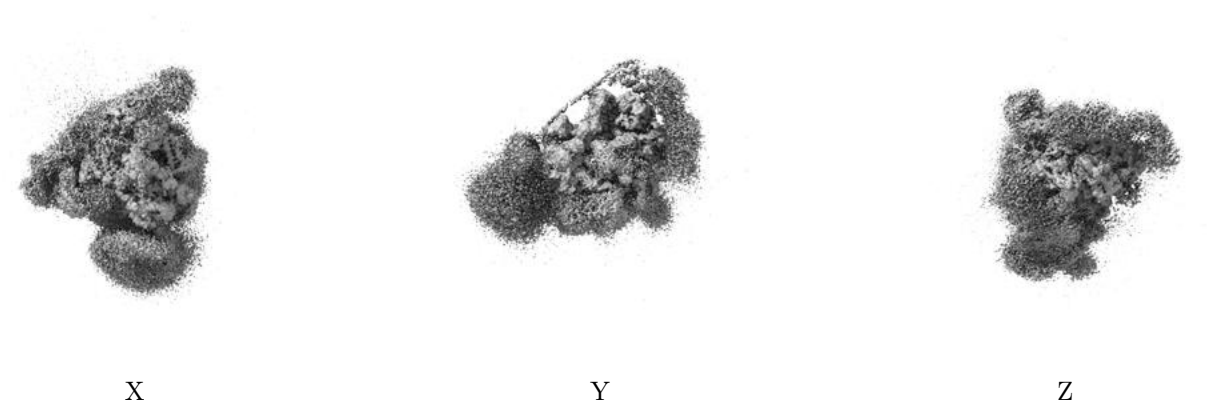
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.014. 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.

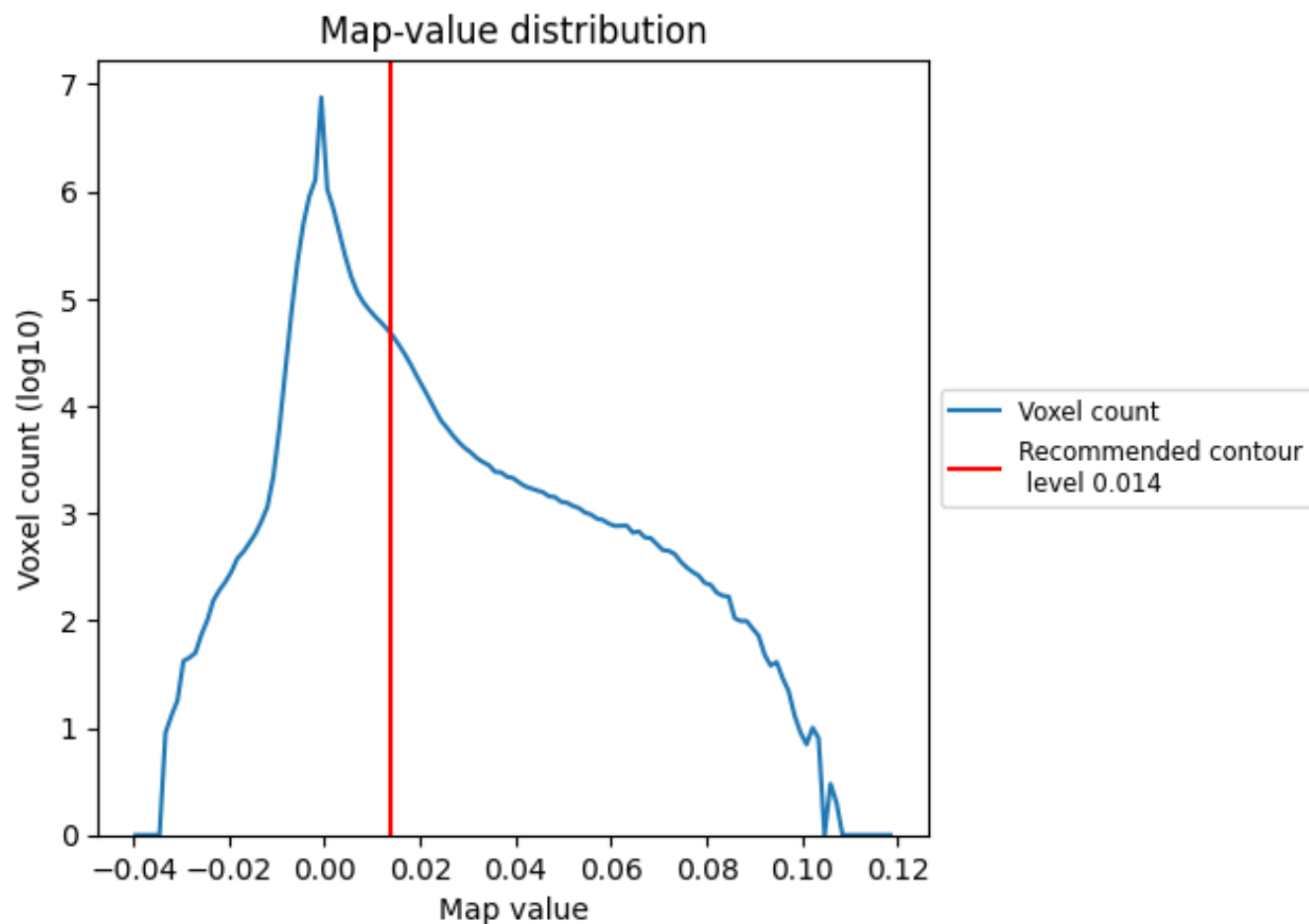
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

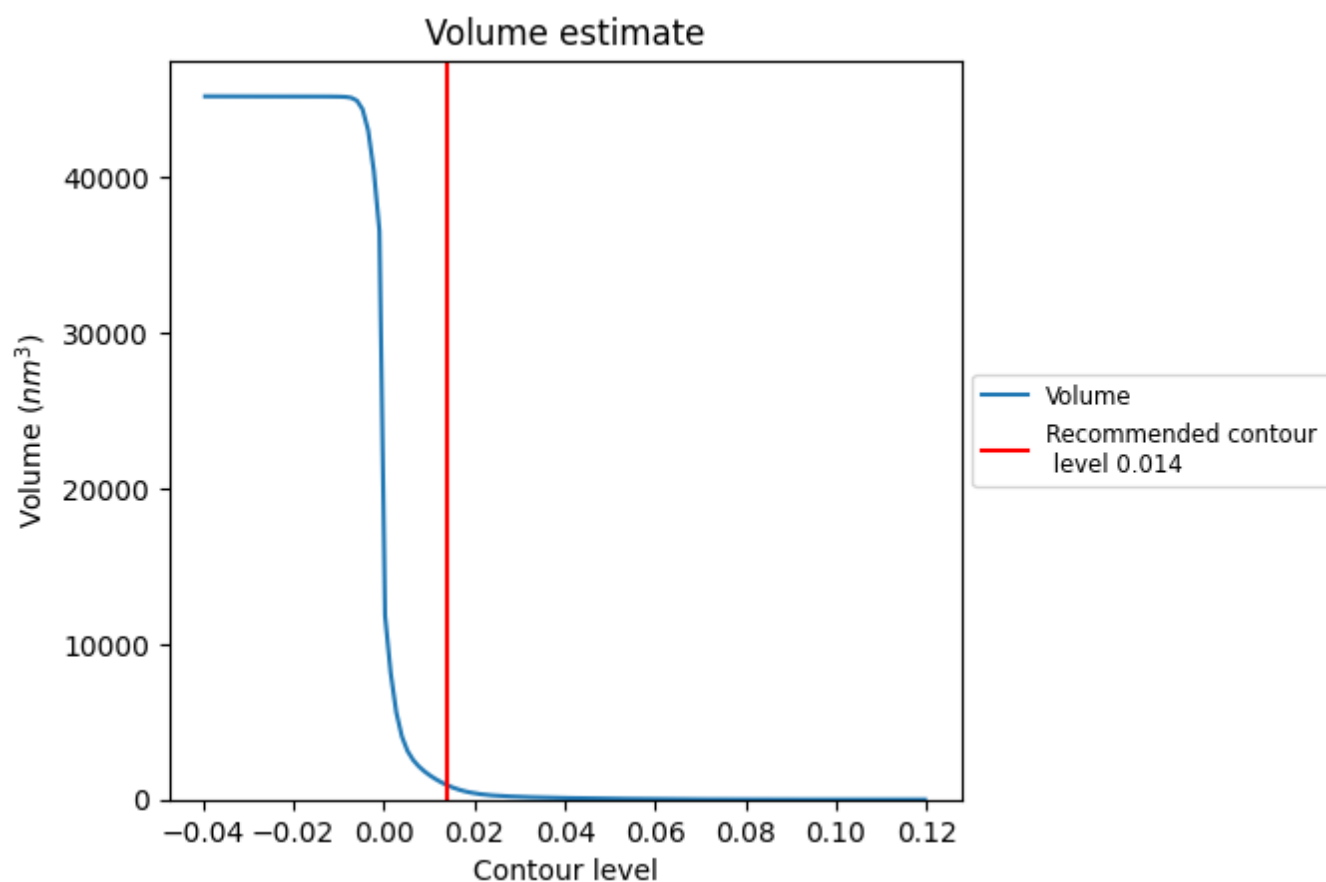
This section contains the results of statistical analysis of the map.

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.

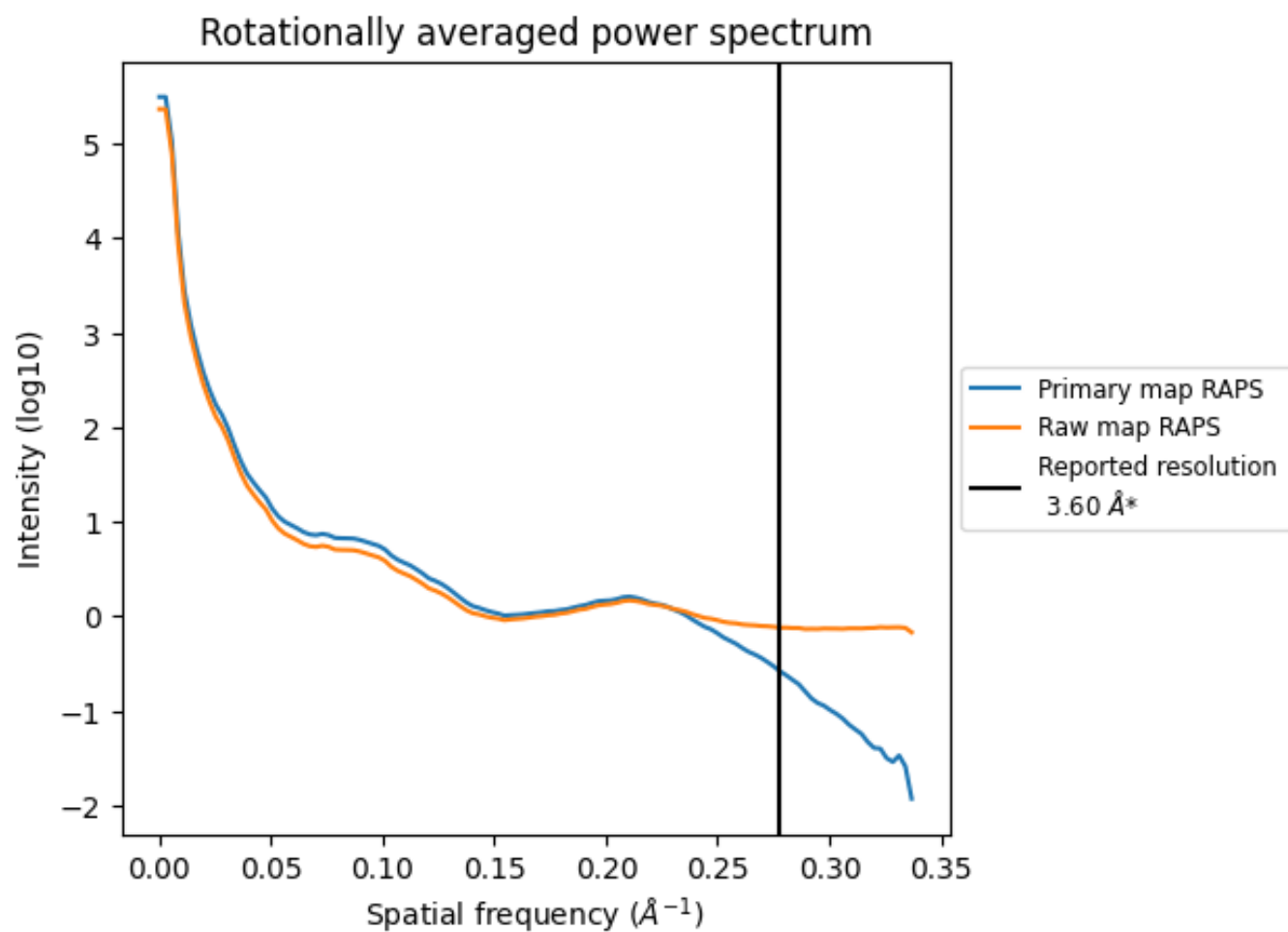
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 927 nm³; this corresponds to an approximate mass of 837 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 ⓘ

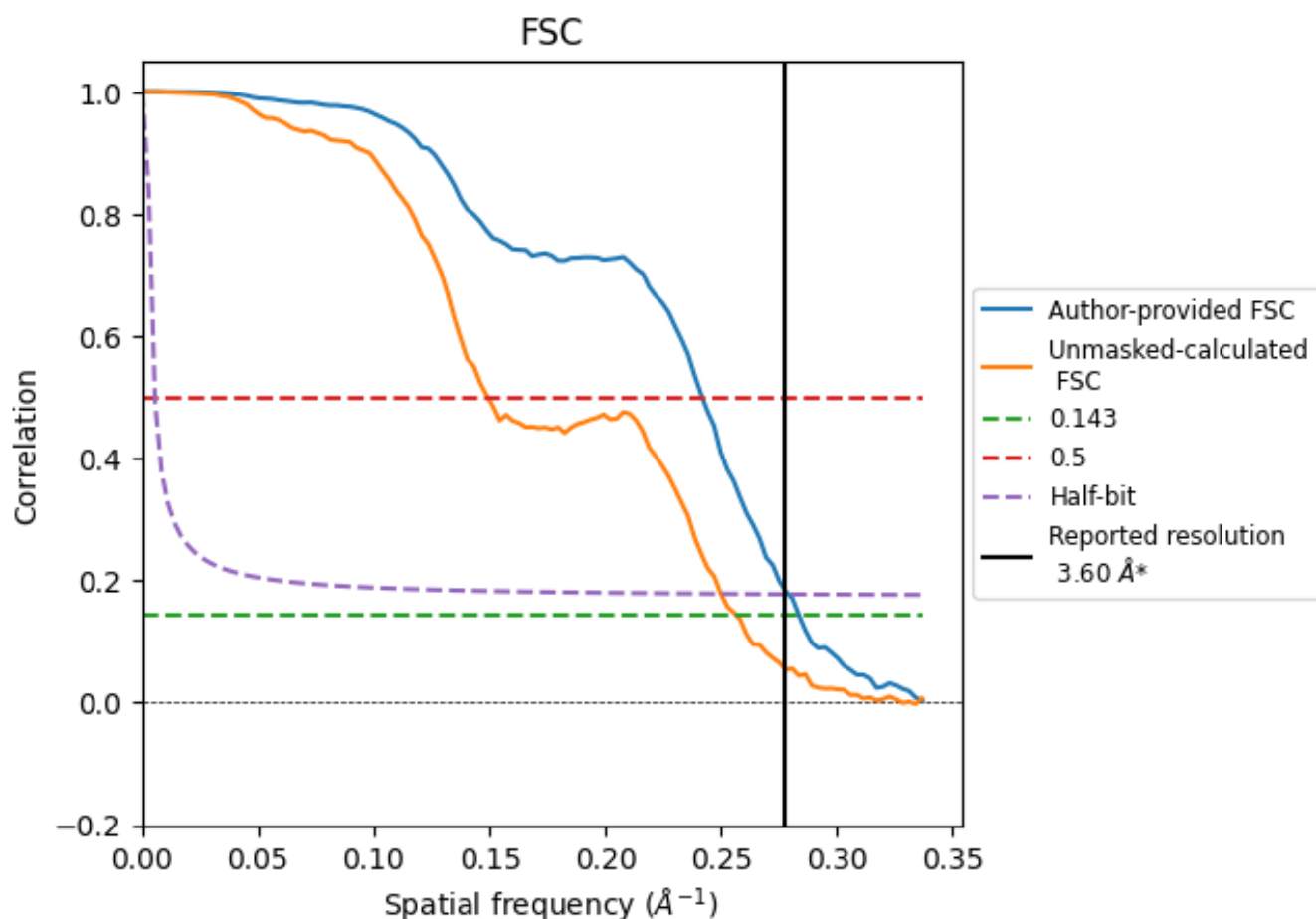


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

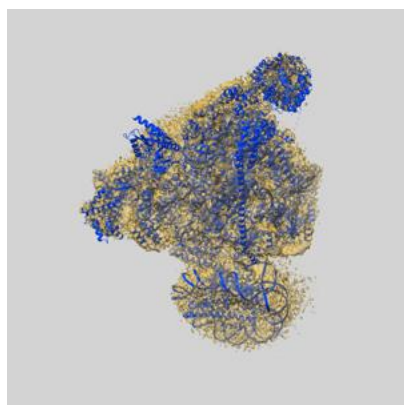
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.53	4.13	3.58
Unmasked-calculated*	3.90	6.70	4.00

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

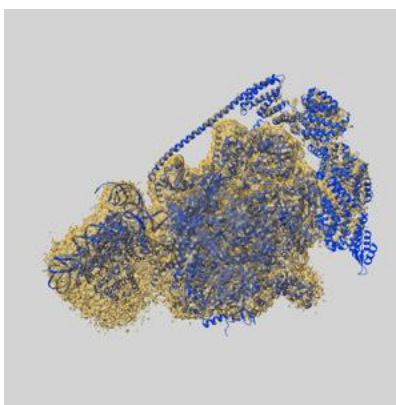
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33424 and PDB model 7XSE. Per-residue inclusion information can be found in section [3](#) on page [16](#).

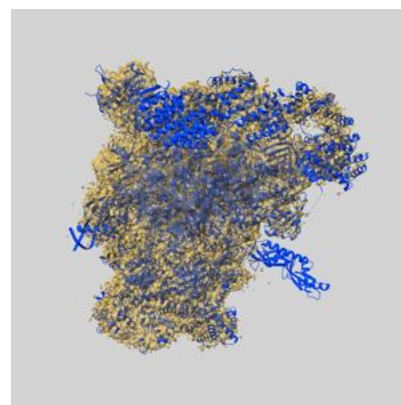
9.1 Map-model overlay [i](#)



X



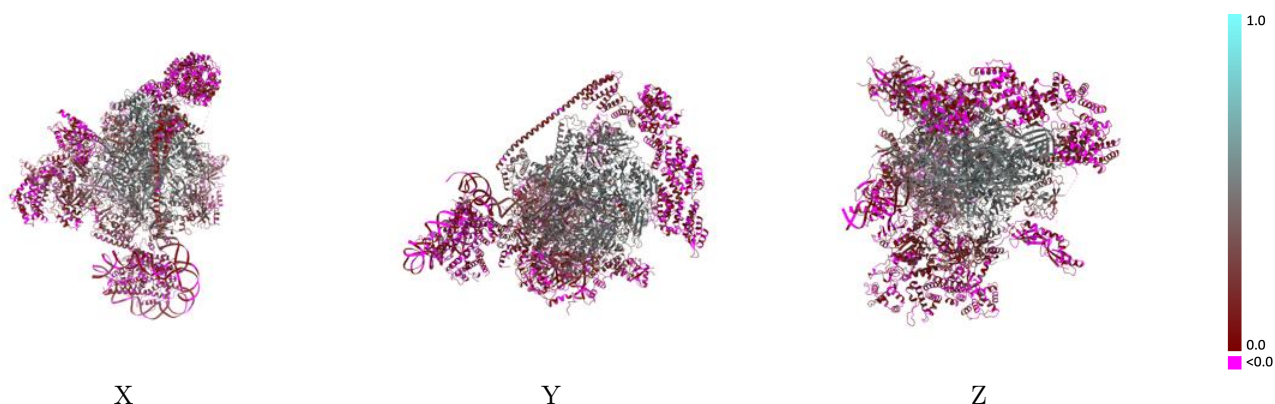
Y



Z

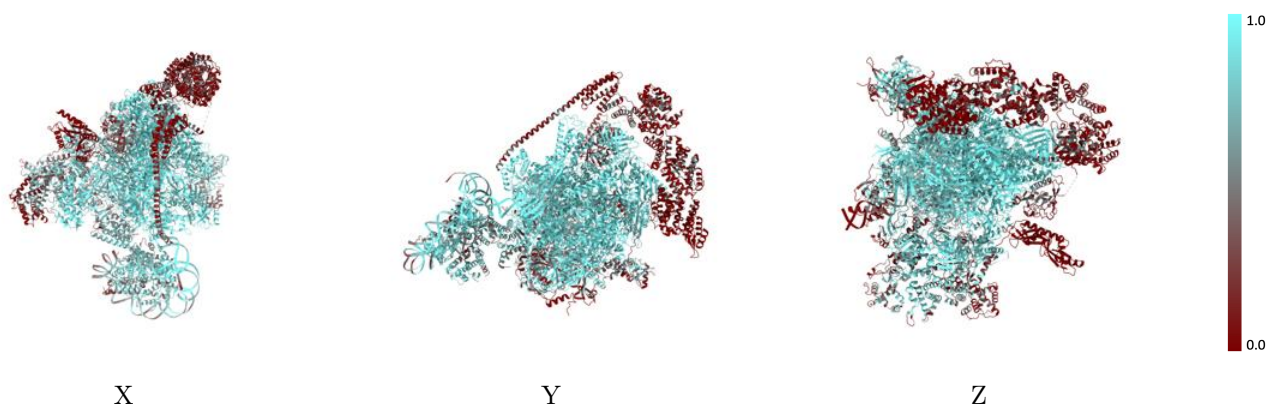
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



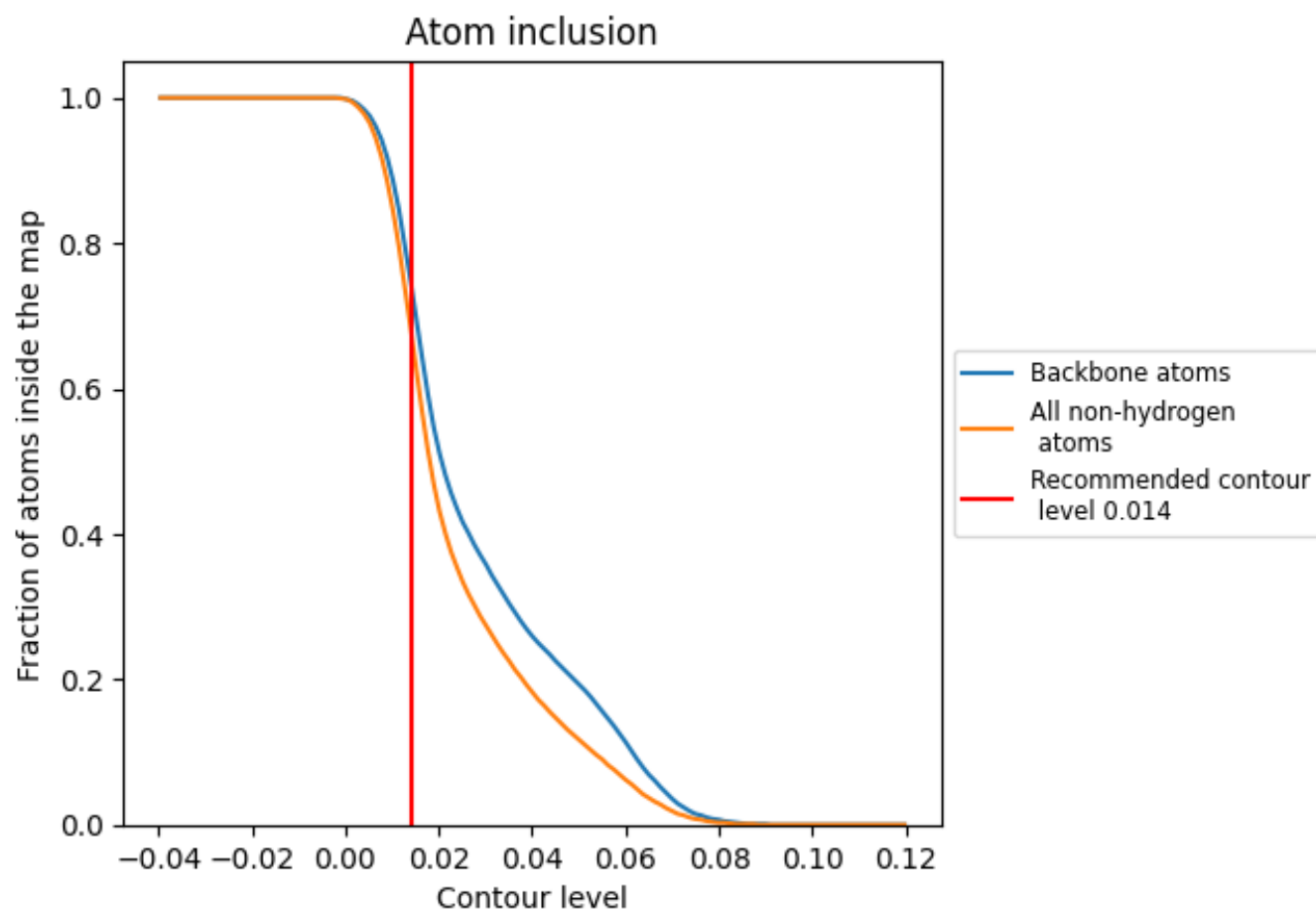
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 68% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6820	 0.2380
A	 0.9430	 0.4470
B	 0.9380	 0.4540
C	 0.9540	 0.4810
D	 0.8580	 0.1860
E	 0.9620	 0.4200
F	 0.9730	 0.4860
G	 0.8680	 0.2860
H	 0.9660	 0.4760
I	 0.8330	 0.2790
J	 0.9500	 0.4800
K	 0.9690	 0.4810
L	 0.9570	 0.4190
M	 0.7660	 0.1840
N	 0.7060	 0.0780
P	 0.9430	 0.3110
T	 0.7280	 0.1290
V	 0.8440	 0.1010
W	 0.6980	 0.1730
a	 0.7400	 0.0460
b	 0.7850	 0.0500
c	 0.7290	 0.0080
d	 0.7020	 0.0360
e	 0.7500	 0.0180
f	 0.8100	 0.0840
g	 0.7130	 0.0030
h	 0.7290	 0.0330
m	 0.4660	 0.0730
n	 0.7040	 0.1690
q	 0.1300	 0.0660
r	 0.3750	 0.1360
u	 0.5830	 0.1740
v	 0.3470	 0.0980
x	 0.2340	 0.2380

