



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:49 PM UTC

PDB ID : 9EH1 / pdb_00009eh1
EMDB ID : EMD-48043
Title : RNA polymerase II-DSIF-SPT6-PAF1c-TFIIS-IWS1-SETD2-nucleosome, 20 bp upstream
Authors : Markert, J.; Farnung, L.
Deposited on : 2024-11-21
Resolution : 3.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

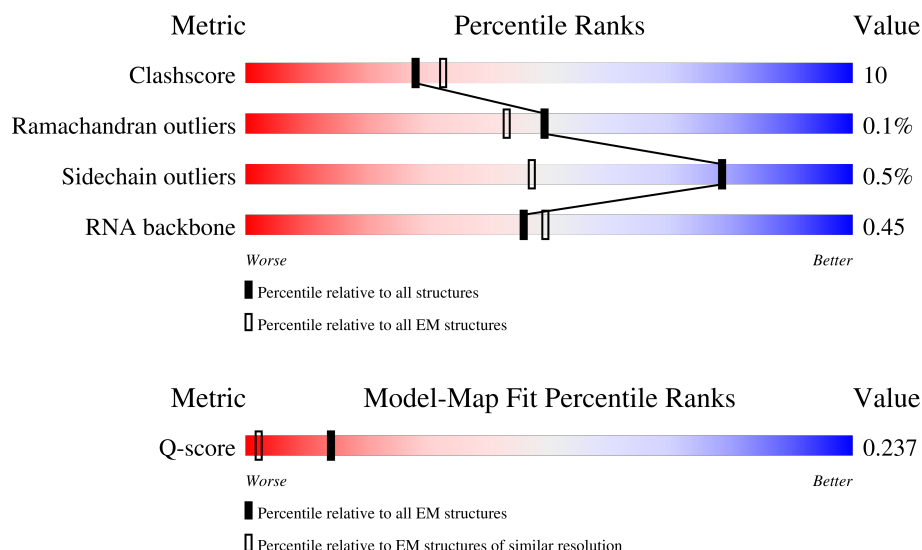
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



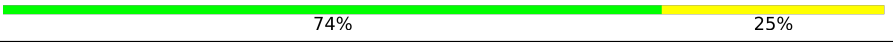
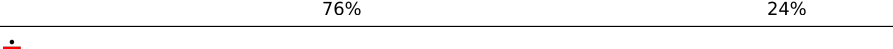
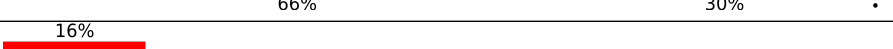
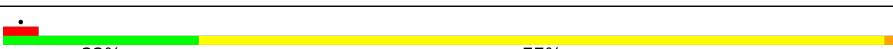
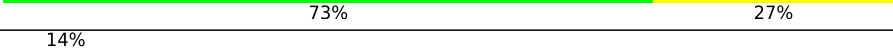
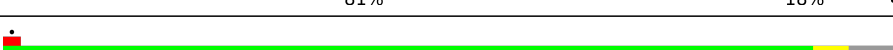
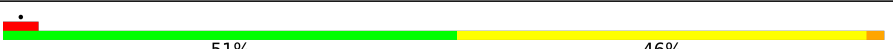
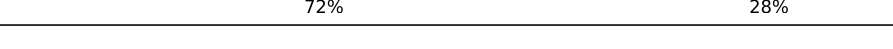
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	1544	
2	B	1159	
3	C	269	

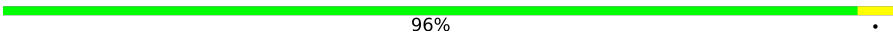
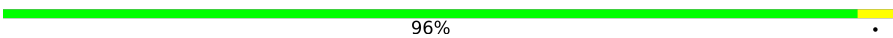
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Mol	Chain	Length	Quality of chain
4	D	126	
5	E	209	
6	F	78	
7	G	171	
8	H	149	
9	I	116	
10	J	66	
11	K	115	
12	L	47	
13	M	1002	
14	N	170	
15	O	132	
16	P	11	
17	Q	890	
18	R	248	
19	S	170	
20	T	181	
21	U	125	
22	V	244	
23	W	300	
24	X	43	
25	Y	116	
26	Z	510	
27	a	136	
27	e	136	

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Mol	Chain	Length	Quality of chain
28	b	78	 96% .
28	f	78	 96% .
29	c	130	 77% . 20%
29	g	130	 75% . 21%
30	d	123	 73% . 25%
30	h	123	 69% . 28%
31	l	589	 37% 7% 55% .

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 72243 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	1426	Total	C	N	O	P	S	
			11255	7074	2014	2095	2	70	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1122	Total	C	N	O	S		
			8980	5684	1576	1656	64	0	0

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

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

- Molecule 4 is a protein called RNA polymerase Rpb4/RPC9 core domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	126	Total	C	N	O	S		
			1004	630	170	200	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	209	Total	C	N	O	S		
			1720	1089	300	323	8	0	0

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1333	866	214	245	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	149	Total	C	N	O	S	0	0
			1197	759	195	238	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	116	Total	C	N	O	S	0	0
			942	582	168	181	11		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	47	Total	C	N	O	S	0	0
			397	246	77	68	6		

- Molecule 13 is a protein called Transcription elongation factor SPT6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	1002	Total	C	N	O	S	0	0
			4883	2708	1072	1096	7		

- Molecule 14 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	170	Total	C	N	O	P	0	0
			3474	1651	626	1027	170		

- Molecule 15 is a protein called Protein IWS1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	132	Total	C	N	O	S	0	0
			1046	663	181	196	6		

- Molecule 16 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	11	Total	C	N	O	P	0	0
			233	105	42	75	11		

- Molecule 17 is a protein called RNA polymerase-associated protein CTR9 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	890	Total	C	N	O	S	0	0
			7226	4579	1264	1352	31		

- Molecule 18 is a protein called RNA polymerase-associated protein RTF1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	244	Total	C	N	O	S	0	0
			1836	1152	340	337	7		

- Molecule 19 is a protein called Transcription elongation factor A protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	161	Total	C	N	O	0	0
			657	334	161	162		

- Molecule 20 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	181	Total	C	N	O	P	0	0
			3725	1765	701	1078	181		

- Molecule 21 is a protein called RNA polymerase-associated protein LEO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	125	Total	C	N	O	S	0	0
			856	538	151	166	1		

- Molecule 22 is a protein called RNA polymerase II-associated factor 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	244	Total	C	N	O	S	0	0
			1703	1061	305	333	4		

- Molecule 23 is a protein called Superkiller complex protein 8, N-terminally processed.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	300	Total	C	N	O	S	0	0
			2333	1483	392	454	4		

- Molecule 24 is a protein called Parafibromin.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	43	Total	C	N	O	0	0
			353	220	69	64		

- Molecule 25 is a protein called Transcription elongation factor SPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	116	Total	C	N	O	S	0	0
			911	570	159	173	9		

- Molecule 26 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Z	510	Total	C	N	O	P	S	0	0
			4025	2552	709	745	1	18		

- Molecule 27 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	101	Total	C	N	O	S	0	0
			823	520	157	142	4		
27	e	94	Total	C	N	O	S	0	0
			776	491	149	133	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	36	MET	LYS	engineered mutation	UNP A0A310TTQ1
e	36	MET	LYS	engineered mutation	UNP A0A310TTQ1

- Molecule 28 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	78	Total	C	N	O	S	0	0
			622	393	120	108	1		
28	f	78	Total	C	N	O	S	0	0
			622	393	120	108	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	104	Total	C	N	O		0	0
			800	504	156	140			
29	g	103	Total	C	N	O		0	0
			795	501	155	139			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	99	ARG	GLY	conflict	UNP P06897
c	123	SER	ALA	conflict	UNP P06897
g	99	ARG	GLY	conflict	UNP P06897
g	123	SER	ALA	conflict	UNP P06897

- Molecule 30 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	92	Total	C	N	O	S	0	0
			721	454	129	136	2		
30	h	89	Total	C	N	O	S	0	0
			694	438	122	132	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	3	MET	-	initiating methionine	UNP P02281
d	32	THR	SER	engineered mutation	UNP P02281
h	3	MET	-	initiating methionine	UNP P02281
h	32	THR	SER	engineered mutation	UNP P02281

- Molecule 31 is a protein called Histone-lysine N-methyltransferase SETD2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	1	263	Total	C	N	O	S	0	0
			2149	1329	393	406	21		

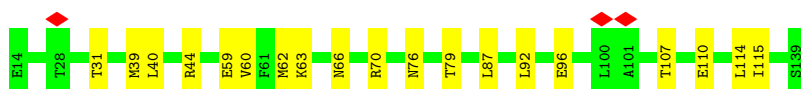
- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

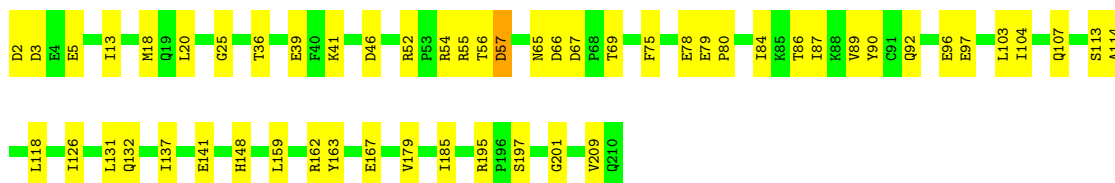
Mol	Chain	Residues	Atoms		AltConf
33	A	1	Total	Mg	0
			1	1	

Chain D:  85% 15%



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

Chain E:  74% 25%



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

Chain F:  76% 24%



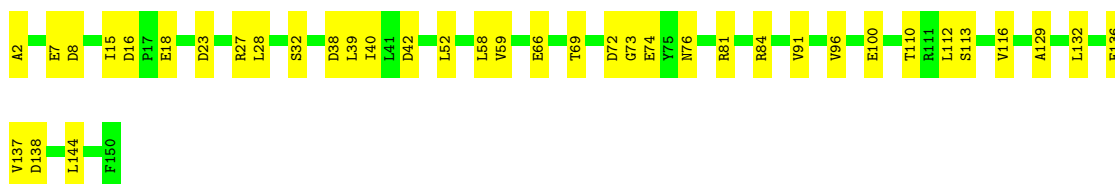
- Molecule 7: DNA-directed RNA polymerase subunit

Chain G:  79% 21%



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

Chain H:  74% 26%



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

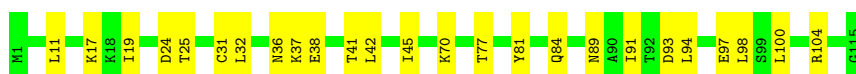
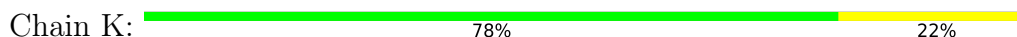
Chain I:  73% 26%



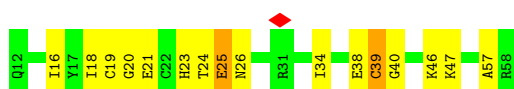
- Molecule 10: DNA-directed RNA polymerase I, II, and III subunit RPABC5



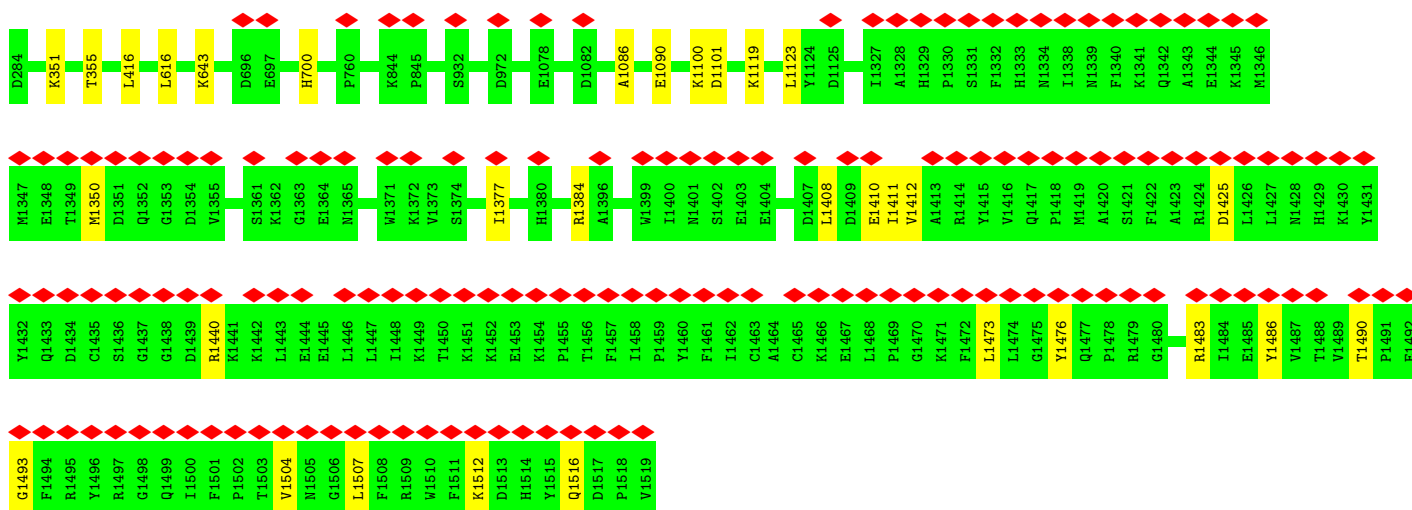
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11-a



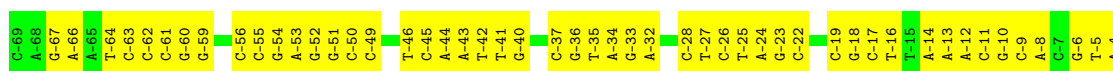
- Molecule 12: RNA polymerase II subunit K

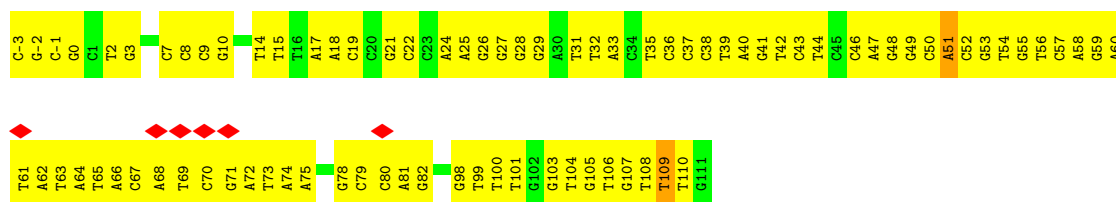


- Molecule 13: Transcription elongation factor SPT6

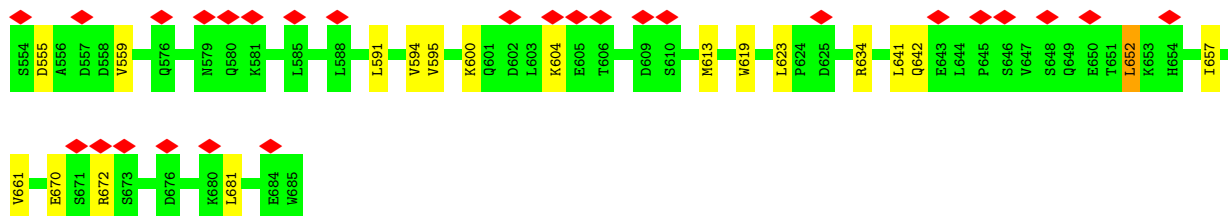
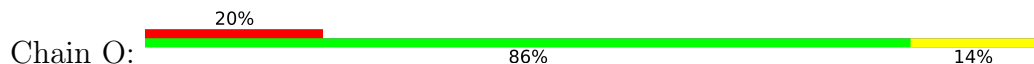


- Molecule 14: Non-template DNA

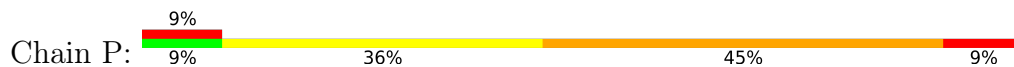




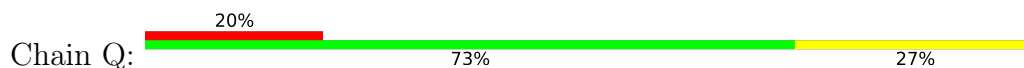
• Molecule 15: Protein IWS1 homolog

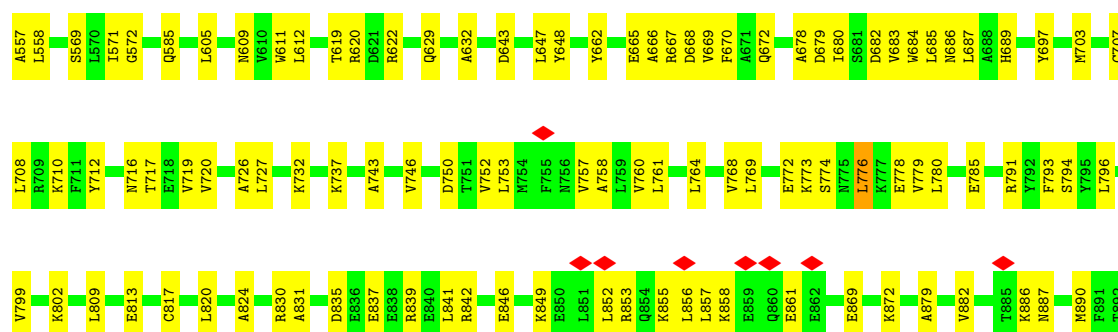


• Molecule 16: RNA

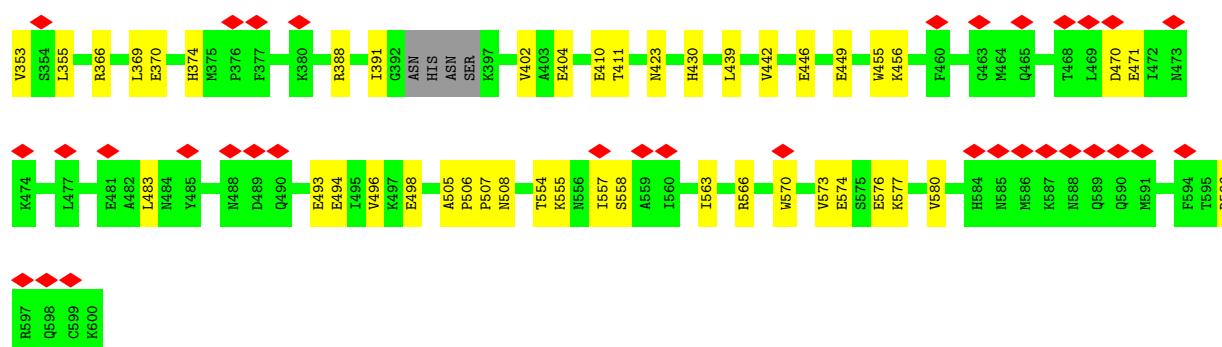
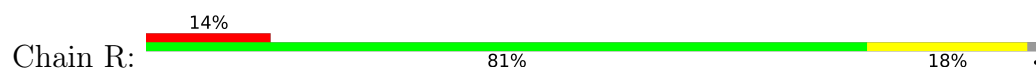


• Molecule 17: RNA polymerase-associated protein CTR9 homolog

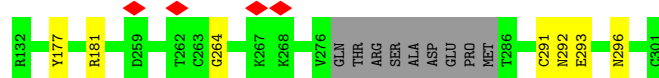




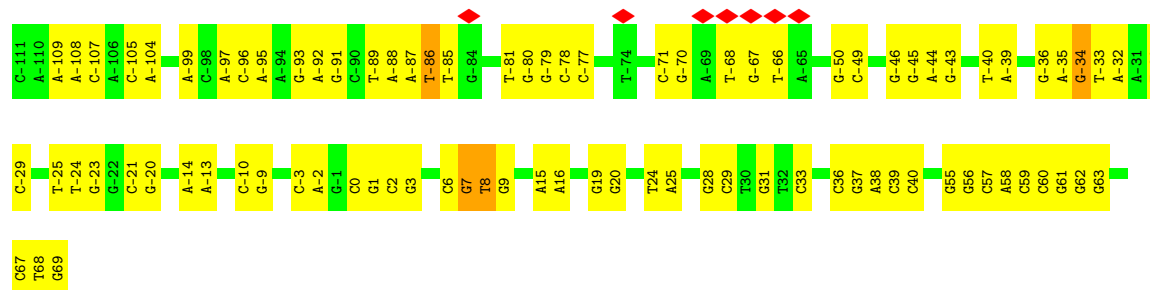
- Molecule 18: RNA polymerase-associated protein RTF1 homolog



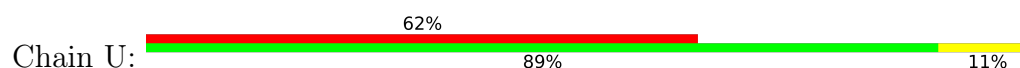
- Molecule 19: Transcription elongation factor A protein 1

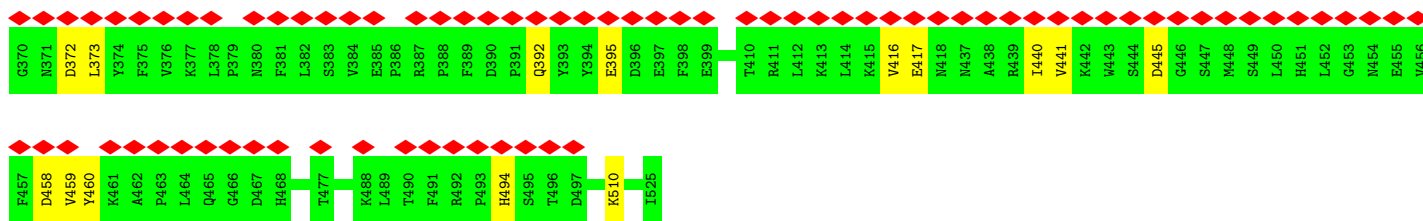


- Molecule 20: Template DNA

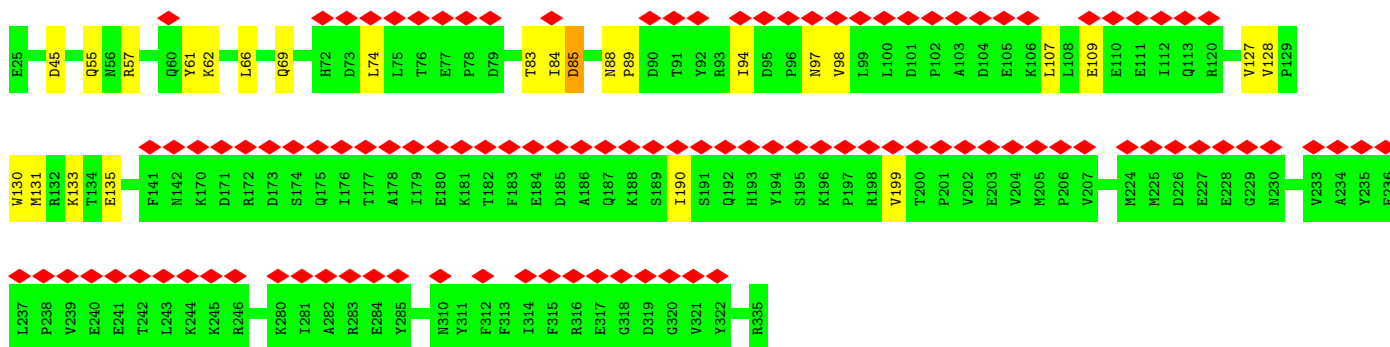
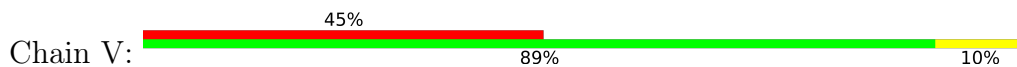


- Molecule 21: RNA polymerase-associated protein LEO1

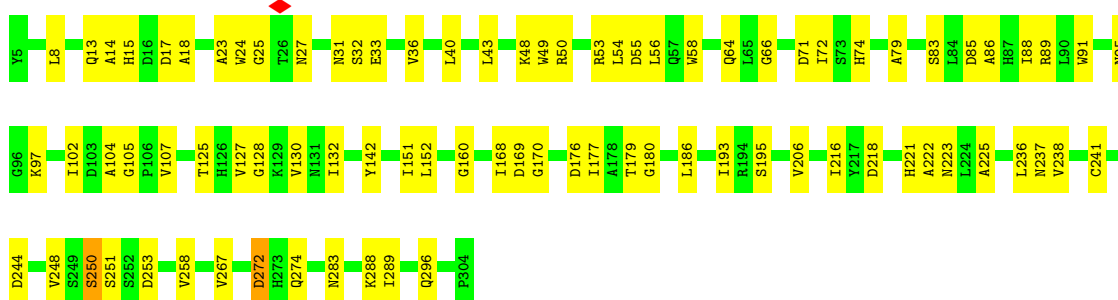




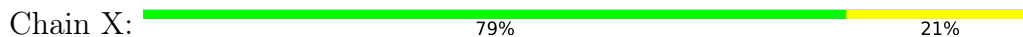
• Molecule 22: RNA polymerase II-associated factor 1 homolog



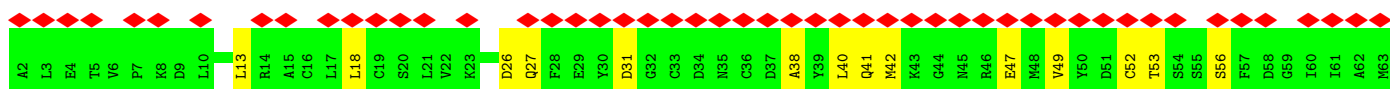
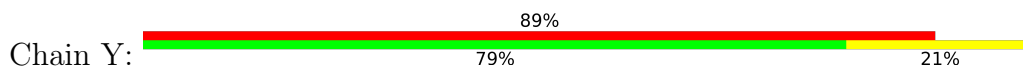
• Molecule 23: Superskiller complex protein 8, N-terminally processed

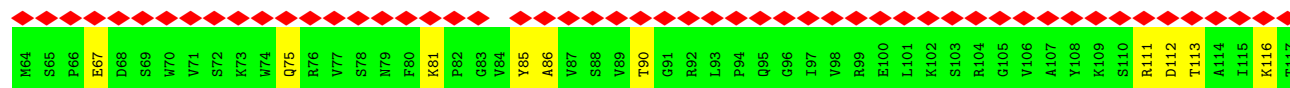


• Molecule 24: Parafibromin

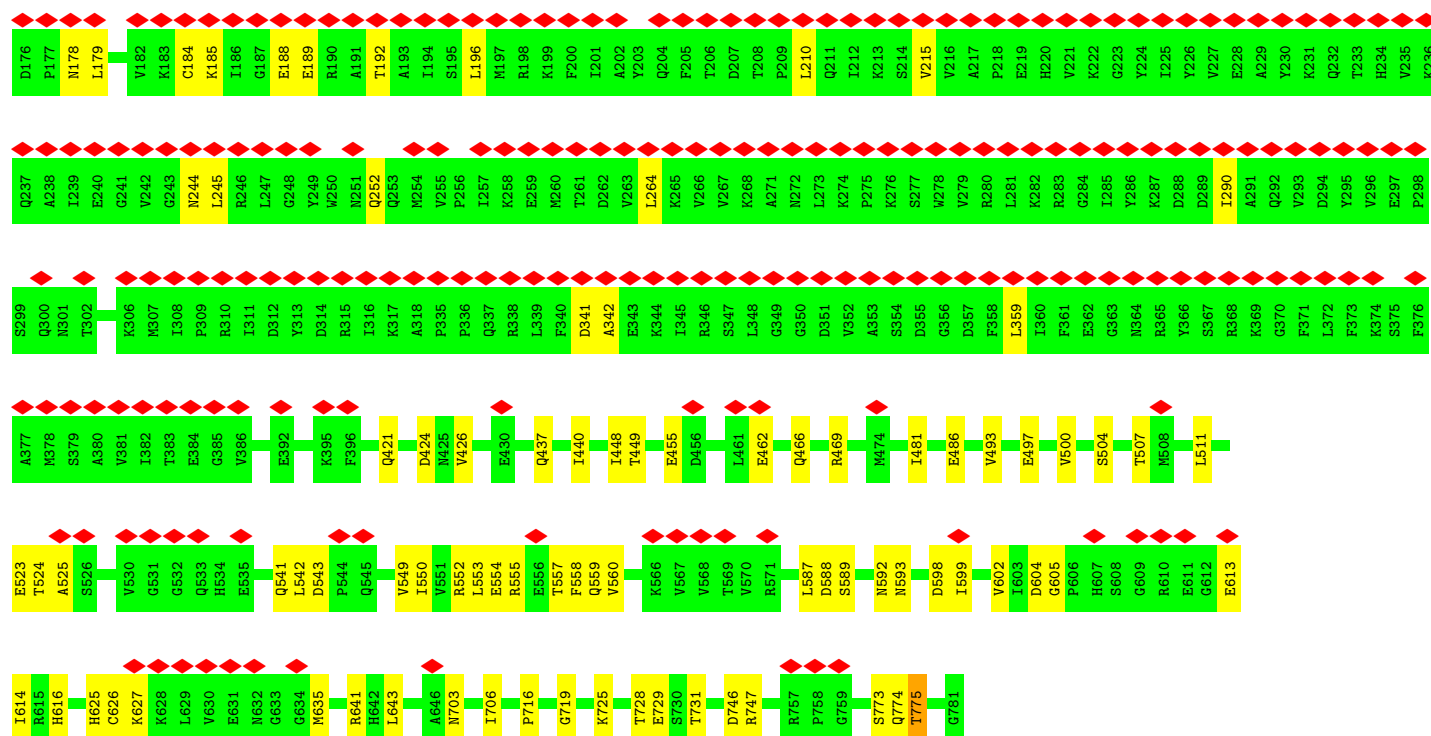
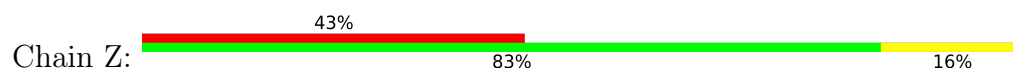


• Molecule 25: Transcription elongation factor SPT4

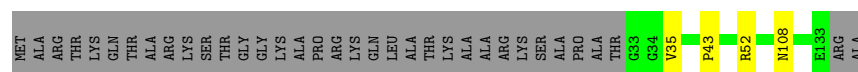




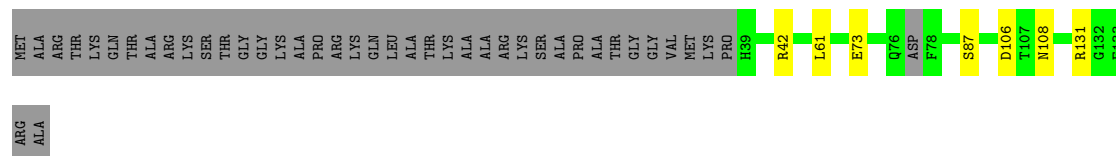
• Molecule 26: Transcription elongation factor SPT5



• Molecule 27: Histone H3



• Molecule 27: Histone H3



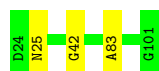
• Molecule 28: Histone H4





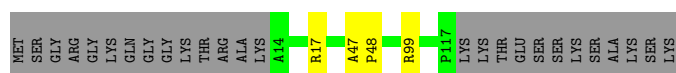
- Molecule 28: Histone H4

Chain f: 96%



- Molecule 29: Histone H2A type 1

Chain c: 77% 20%



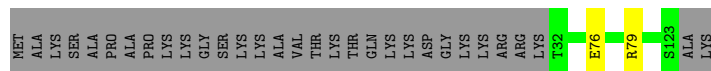
- Molecule 29: Histone H2A type 1

Chain g: 75% 21%



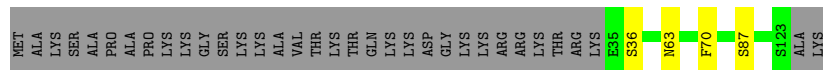
- Molecule 30: Histone H2B 1.1

Chain d: 73% 25%



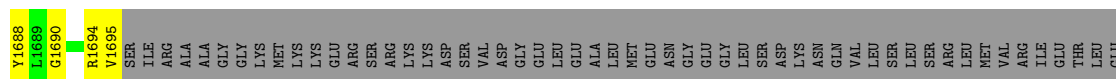
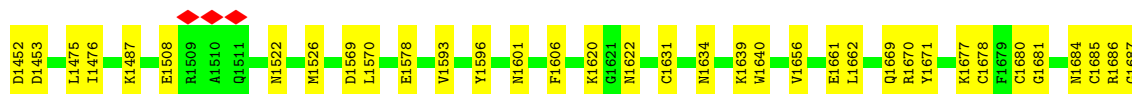
- Molecule 30: Histone H2B 1.1

Chain h: 69% 28%



- Molecule 31: Histone-lysine N-methyltransferase SETD2

Chain l: 37% 7% 55%



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	121657	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.541	Depositor
Minimum map value	-0.191	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	550.0, 550.0, 550.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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, TPO, SEP, 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	0.22	0/11437	0.32	0/15433
2	B	0.24	0/9158	0.33	0/12360
3	C	0.29	0/2115	0.35	0/2873
4	D	0.17	0/1017	0.25	0/1368
5	E	0.22	0/1751	0.31	0/2366
6	F	0.26	0/636	0.31	0/859
7	G	0.17	0/1364	0.27	0/1853
8	H	0.26	0/1219	0.35	0/1644
9	I	0.23	0/964	0.31	0/1305
10	J	0.28	0/533	0.35	0/719
11	K	0.26	0/939	0.32	0/1271
12	L	0.27	0/403	0.32	0/536
13	M	0.11	0/4944	0.23	0/6387
14	N	0.37	0/3891	0.99	3/5999 (0.1%)
15	O	0.12	0/1062	0.23	0/1428
16	P	0.58	0/260	1.53	3/402 (0.7%)
17	Q	0.16	0/7365	0.30	0/9927
18	R	0.11	0/1866	0.24	0/2519
19	S	0.13	0/659	0.18	0/827
20	T	0.37	0/4184	0.98	8/6458 (0.1%)
21	U	0.13	0/870	0.24	0/1183
22	V	0.13	0/1728	0.31	0/2357
23	W	0.16	0/2392	0.28	0/3257
24	X	0.17	0/356	0.28	0/478
25	Y	0.11	0/927	0.21	0/1250
26	Z	0.10	0/4084	0.22	0/5498
27	a	0.21	0/835	0.33	0/1120
27	e	0.23	0/786	0.35	0/1053
28	b	0.21	0/629	0.34	0/843
28	f	0.21	0/629	0.32	0/843
29	c	0.20	0/810	0.30	0/1095
29	g	0.22	0/805	0.31	0/1088

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	d	0.24	0/732	0.33	0/986
30	h	0.24	0/705	0.35	0/951
31	l	0.14	0/2189	0.31	0/2930
All	All	0.22	0/74244	0.46	14/101466 (0.0%)

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	109	DT	OP1-P-O3'	-21.64	43.08	108.00
20	T	-86	DT	OP1-P-O3'	7.08	129.24	108.00
16	P	16	A	N9-C1'-C2'	6.78	124.17	114.00
20	T	-99	DA	OP1-P-O3'	6.68	128.03	108.00
20	T	-34	DG	OP2-P-O3'	6.53	127.58	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	11255	0	11374	234	0
2	B	8980	0	9019	179	0
3	C	2072	0	2020	53	0
4	D	1004	0	980	16	0
5	E	1720	0	1737	42	0
6	F	626	0	657	13	0
7	G	1333	0	1321	29	0
8	H	1197	0	1156	26	0
9	I	942	0	872	28	0
10	J	524	0	541	16	0
11	K	920	0	942	22	0
12	L	397	0	405	17	0
13	M	4883	0	2550	22	0
14	N	3474	0	1914	157	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	O	1046	0	1096	11	0
16	P	233	0	119	11	0
17	Q	7226	0	7169	186	0
18	R	1836	0	1699	31	0
19	S	657	0	199	5	0
20	T	3725	0	2030	86	0
21	U	856	0	680	11	0
22	V	1703	0	1426	26	0
23	W	2333	0	2246	55	0
24	X	353	0	371	7	0
25	Y	911	0	907	17	0
26	Z	4025	0	4041	62	0
27	a	823	0	864	7	0
27	e	776	0	815	6	0
28	b	622	0	660	3	0
28	f	622	0	660	3	0
29	c	800	0	851	3	0
29	g	795	0	846	4	0
30	d	721	0	742	1	0
30	h	694	0	709	3	0
31	l	2149	0	2089	30	0
32	A	2	0	0	0	0
32	B	1	0	0	0	0
32	C	1	0	0	0	0
32	I	2	0	0	0	0
32	J	1	0	0	0	0
32	L	1	0	0	0	0
32	Y	1	0	0	0	0
33	A	1	0	0	0	0
All	All	72243	0	65707	1313	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 10.

The worst 5 of 1313 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)
17:Q:276:ALA:HB1	17:Q:288:VAL:HG23	1.30	1.12
17:Q:353:TYR:OH	22:V:57:ARG:O	1.79	1.00
3:C:36:ARG:NH1	11:K:41:THR:OG1	1.99	0.95
31:l:1677:LYS:HA	31:l:1688:TYR:HA	1.49	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:534:TYR:OH	17:Q:556:GLU:OE1	1.87	0.92

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	1408/1544 (91%)	1295 (92%)	112 (8%)	1 (0%)	48	78
2	B	1112/1159 (96%)	1024 (92%)	88 (8%)	0	100	100
3	C	254/269 (94%)	228 (90%)	26 (10%)	0	100	100
4	D	124/126 (98%)	118 (95%)	6 (5%)	0	100	100
5	E	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
6	F	76/78 (97%)	72 (95%)	4 (5%)	0	100	100
7	G	169/171 (99%)	161 (95%)	8 (5%)	0	100	100
8	H	147/149 (99%)	132 (90%)	15 (10%)	0	100	100
9	I	114/116 (98%)	104 (91%)	10 (9%)	0	100	100
10	J	64/66 (97%)	57 (89%)	7 (11%)	0	100	100
11	K	113/115 (98%)	112 (99%)	1 (1%)	0	100	100
12	L	45/47 (96%)	41 (91%)	3 (7%)	1 (2%)	5	24
13	M	976/1002 (97%)	937 (96%)	38 (4%)	1 (0%)	48	78
15	O	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
17	Q	888/890 (100%)	851 (96%)	37 (4%)	0	100	100
18	R	240/248 (97%)	233 (97%)	7 (3%)	0	100	100
19	S	157/170 (92%)	154 (98%)	3 (2%)	0	100	100
21	U	117/125 (94%)	105 (90%)	11 (9%)	1 (1%)	14	44
22	V	234/244 (96%)	219 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	W	298/300 (99%)	288 (97%)	10 (3%)	0	100	100
24	X	41/43 (95%)	40 (98%)	1 (2%)	0	100	100
25	Y	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
26	Z	497/510 (98%)	474 (95%)	22 (4%)	1 (0%)	43	73
27	a	99/136 (73%)	98 (99%)	1 (1%)	0	100	100
27	e	90/136 (66%)	90 (100%)	0	0	100	100
28	b	76/78 (97%)	75 (99%)	1 (1%)	0	100	100
28	f	76/78 (97%)	75 (99%)	1 (1%)	0	100	100
29	c	102/130 (78%)	101 (99%)	1 (1%)	0	100	100
29	g	101/130 (78%)	100 (99%)	1 (1%)	0	100	100
30	d	90/123 (73%)	90 (100%)	0	0	100	100
30	h	87/123 (71%)	85 (98%)	2 (2%)	0	100	100
31	l	259/589 (44%)	237 (92%)	22 (8%)	0	100	100
All	All	8505/9352 (91%)	8024 (94%)	476 (6%)	5 (0%)	49	78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	L	39	CYS
13	M	700	HIS
1	A	1343	LEU
21	U	510	LYS
26	Z	774	GLN

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	1245/1341 (93%)	1240 (100%)	5 (0%)	84	86
2	B	986/1013 (97%)	981 (100%)	5 (0%)	81	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	235/246 (96%)	234 (100%)	1 (0%)	84	86
4	D	109/116 (94%)	109 (100%)	0	100	100
5	E	191/191 (100%)	189 (99%)	2 (1%)	68	79
6	F	68/68 (100%)	68 (100%)	0	100	100
7	G	146/152 (96%)	146 (100%)	0	100	100
8	H	130/130 (100%)	130 (100%)	0	100	100
9	I	104/104 (100%)	102 (98%)	2 (2%)	50	73
10	J	55/55 (100%)	55 (100%)	0	100	100
11	K	104/104 (100%)	104 (100%)	0	100	100
12	L	44/44 (100%)	43 (98%)	1 (2%)	44	70
13	M	196/894 (22%)	196 (100%)	0	100	100
15	O	118/118 (100%)	116 (98%)	2 (2%)	53	74
17	Q	761/763 (100%)	751 (99%)	10 (1%)	61	77
18	R	170/222 (77%)	169 (99%)	1 (1%)	78	83
19	S	4/148 (3%)	4 (100%)	0	100	100
21	U	65/112 (58%)	65 (100%)	0	100	100
22	V	144/227 (63%)	143 (99%)	1 (1%)	76	82
23	W	255/255 (100%)	252 (99%)	3 (1%)	63	78
24	X	40/40 (100%)	40 (100%)	0	100	100
25	Y	102/102 (100%)	102 (100%)	0	100	100
26	Z	435/444 (98%)	435 (100%)	0	100	100
27	a	87/111 (78%)	87 (100%)	0	100	100
27	e	82/111 (74%)	82 (100%)	0	100	100
28	b	64/64 (100%)	64 (100%)	0	100	100
28	f	64/64 (100%)	64 (100%)	0	100	100
29	c	82/102 (80%)	82 (100%)	0	100	100
29	g	82/102 (80%)	82 (100%)	0	100	100
30	d	79/103 (77%)	79 (100%)	0	100	100
30	h	76/103 (74%)	76 (100%)	0	100	100
31	l	235/534 (44%)	233 (99%)	2 (1%)	70	80
All	All	6558/8183 (80%)	6523 (100%)	35 (0%)	78	85

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	R	576	GLU
22	V	85	ASP
23	W	272	ASP
5	E	57	ASP
5	E	18	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
17	Q	40	GLN
26	Z	272	ASN
17	Q	407	GLN
26	Z	244	ASN
29	c	24	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	P	11/11 (100%)	2 (18%)	2 (18%)

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	P	17	A
16	P	19	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	P	16	A
16	P	18	A

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
26	TPO	Z	775	26	8,10,11	1.12	0	10,14,16	1.95	1 (10%)
1	TPO	A	1525	1	8,10,11	1.11	0	10,14,16	2.14	1 (10%)
1	SEP	A	1547	1	8,9,10	1.61	1 (12%)	7,12,14	1.39	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	TPO	Z	775	26	-	1/9/11/13	-
1	TPO	A	1525	1	-	0/9/11/13	-
1	SEP	A	1547	1	-	0/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1547	SEP	P-O1P	3.53	1.61	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1525	TPO	P-OG1-CB	-6.11	106.73	123.33
26	Z	775	TPO	P-OG1-CB	-5.44	108.55	123.33
1	A	1547	SEP	OG-CB-CA	3.05	111.12	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
26	Z	775	TPO	C-CA-CB-CG2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	Z	775	TPO	2	0
1	A	1525	TPO	1	0
1	A	1547	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
13	M	12
26	Z	5
22	V	4
21	U	3
14	N	1

The worst 5 of 25 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	1287:MET	C	1327:ILE	N	44.24
1	Z	646:ALA	C	703:ASN	N	38.49

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	V	142:ASN	C	170:LYS	N	36.57
1	N	83:DT	O3'	95:DT	P	32.16
1	M	477:LYS	C	538:LYS	N	29.12

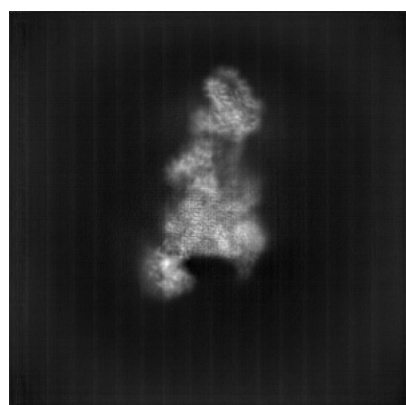
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48043. These allow visual inspection of the internal detail of the map and identification of artifacts.

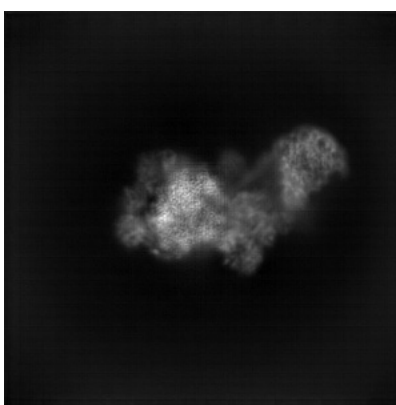
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

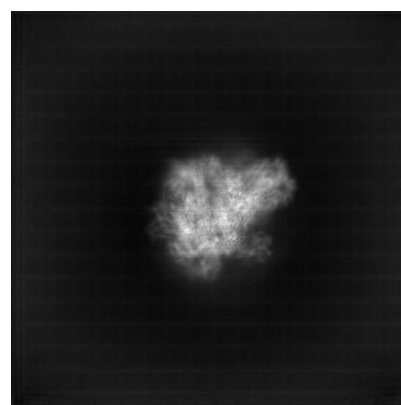
6.1.1 Primary map



X



Y

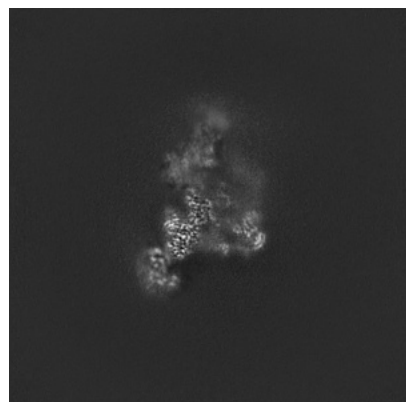


Z

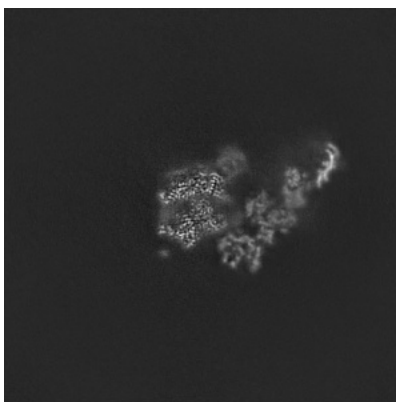
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

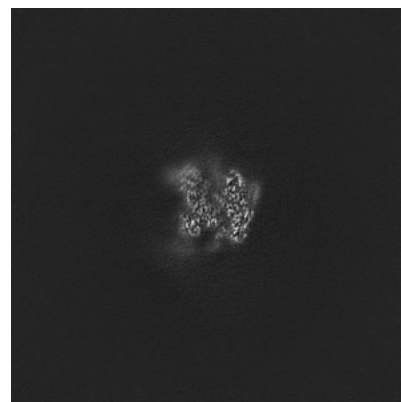
6.2.1 Primary map



X Index: 250



Y Index: 250

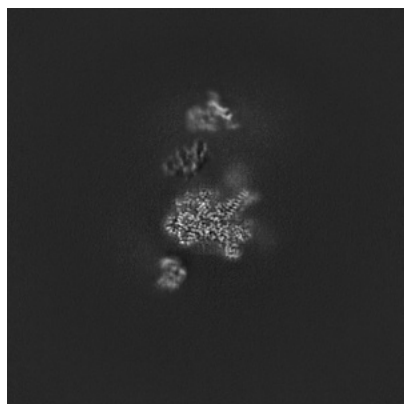


Z Index: 250

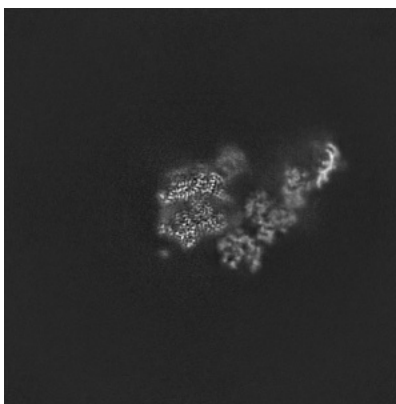
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

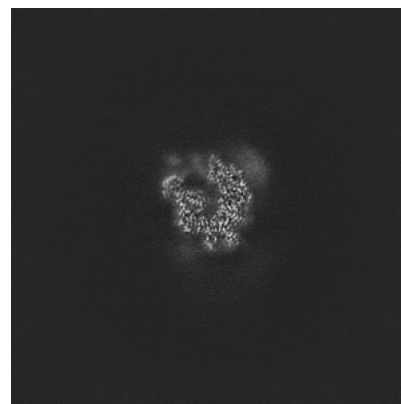
6.3.1 Primary map



X Index: 273



Y Index: 251



Z Index: 219

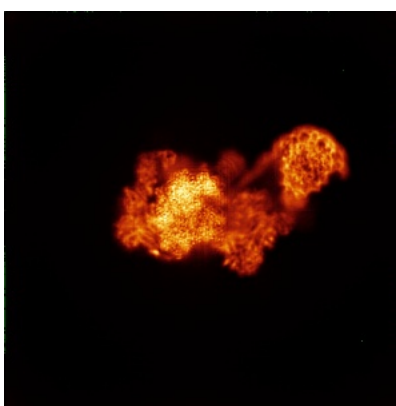
The images above show the largest variance slices of the map in three orthogonal directions.

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

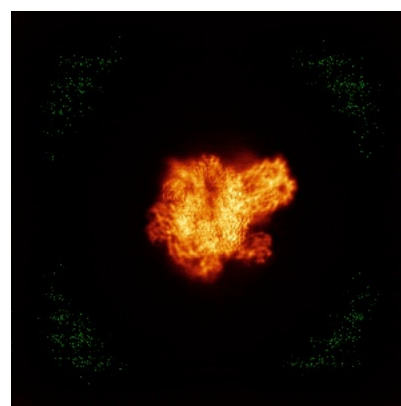
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

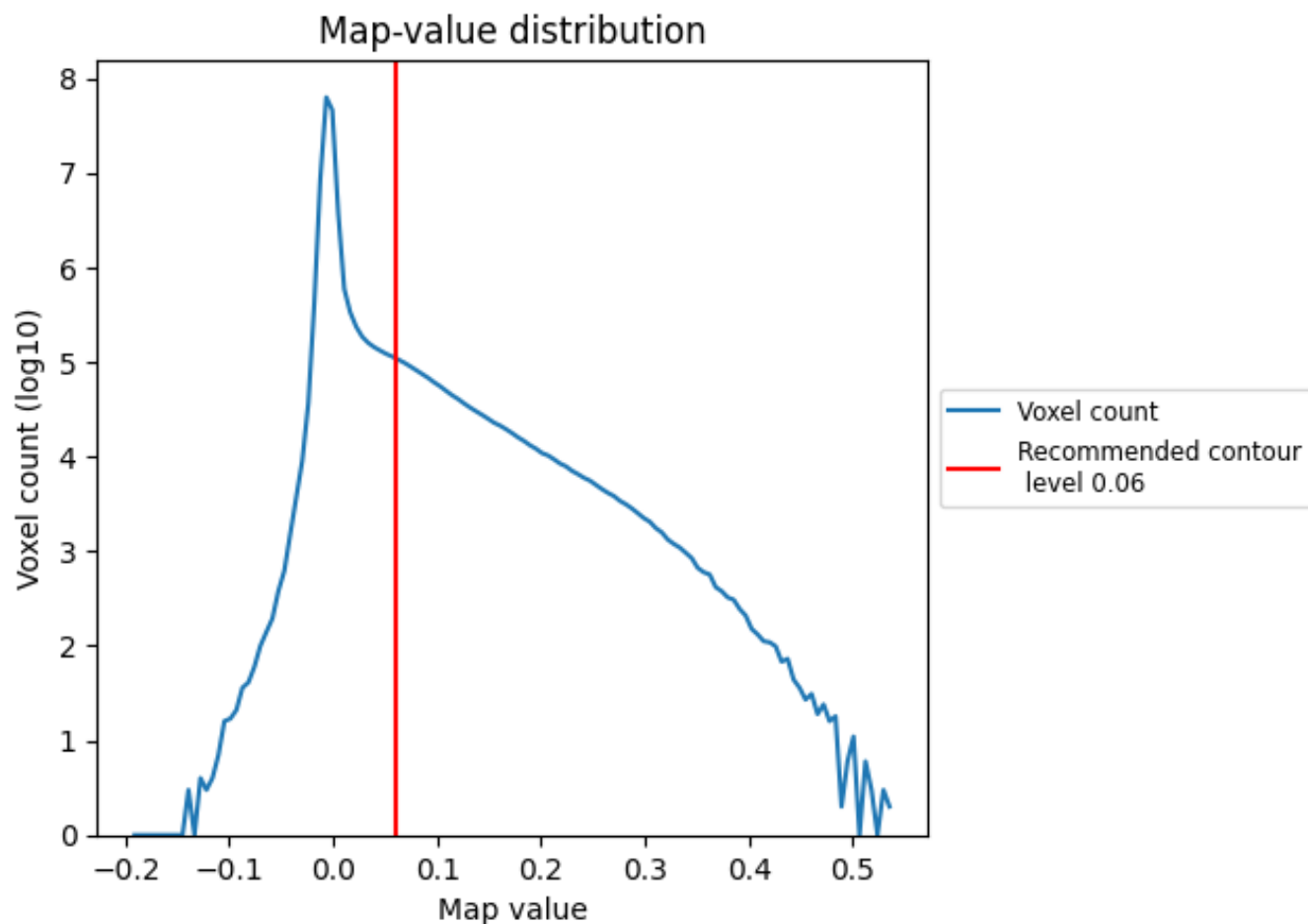
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

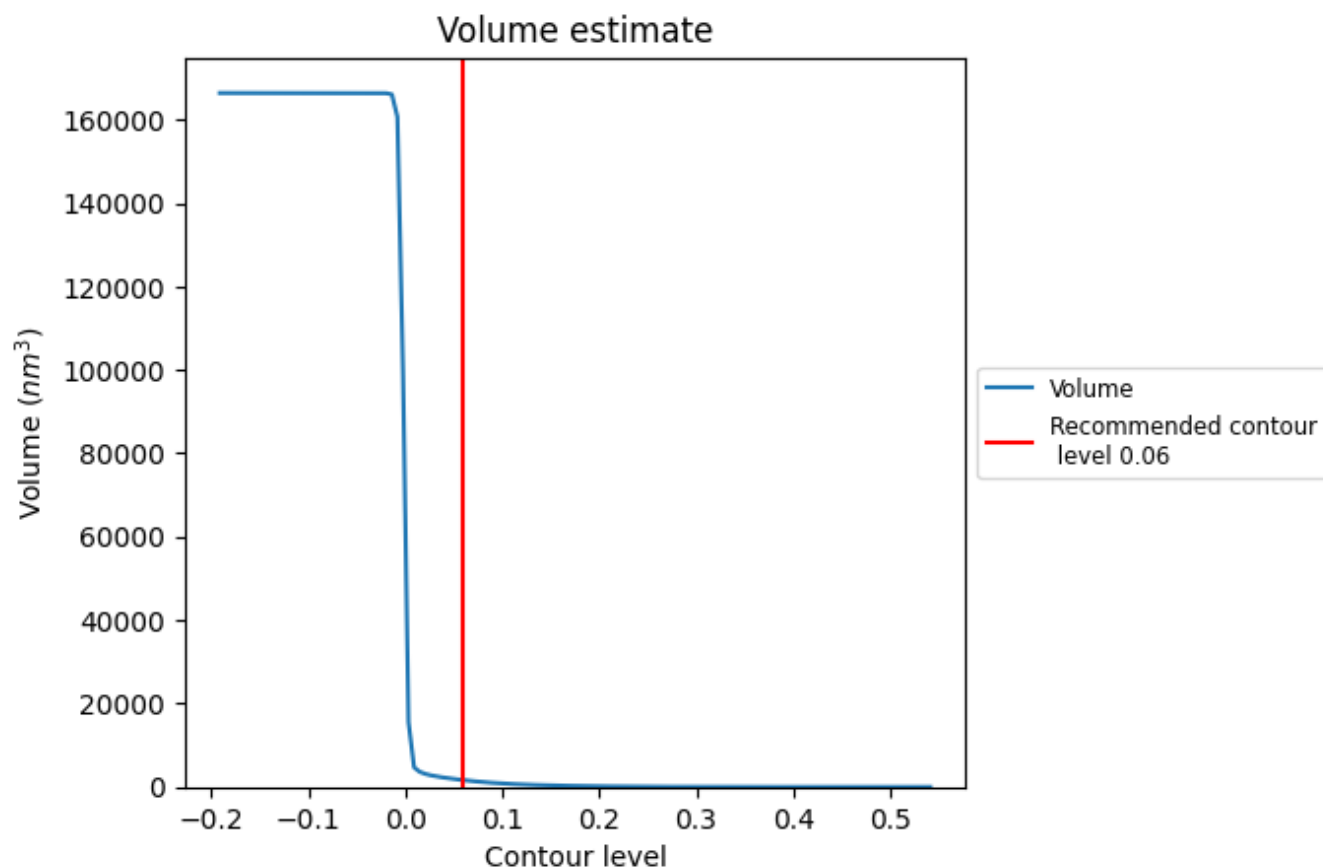
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

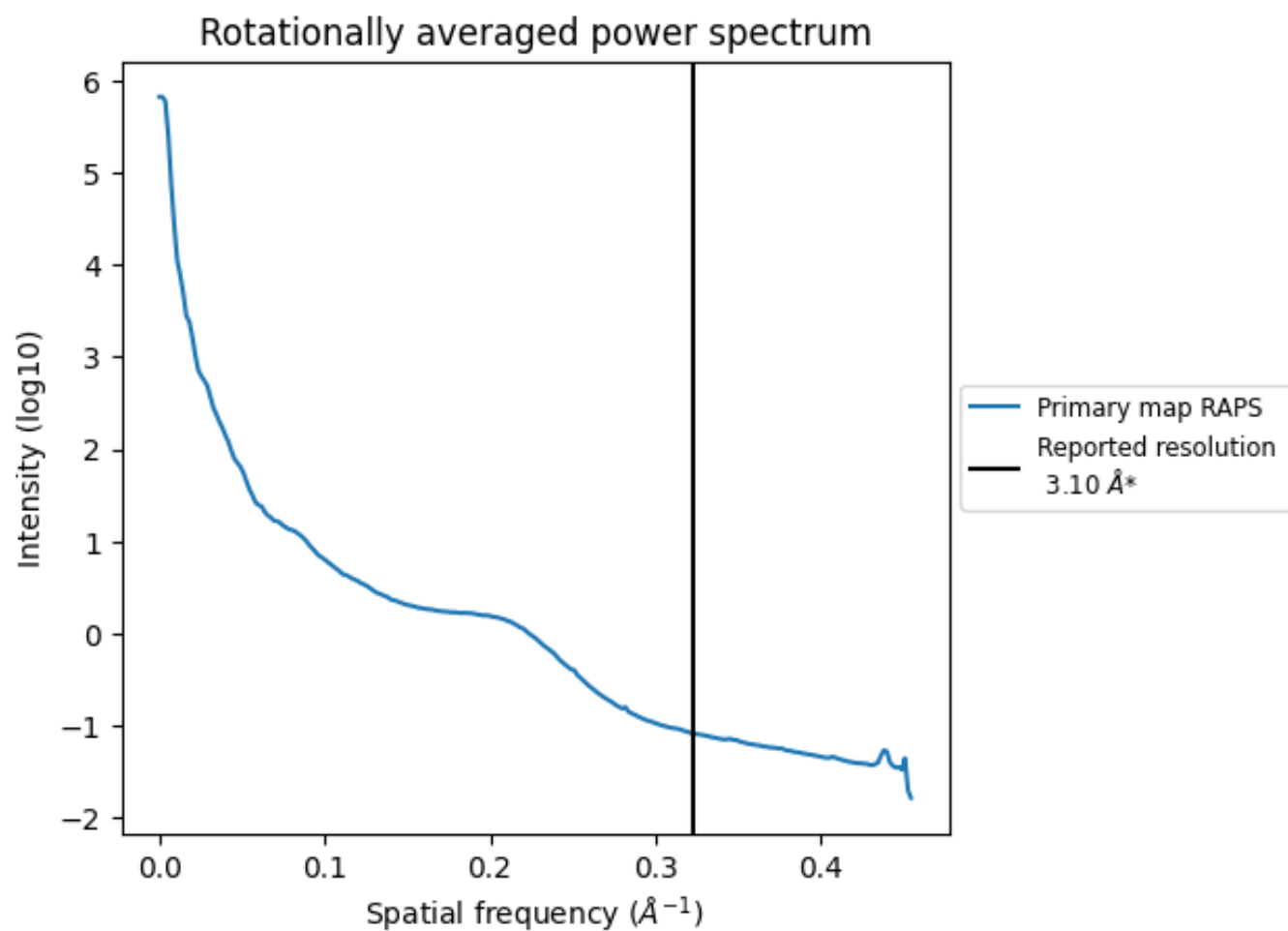
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1637 nm^3 ; this corresponds to an approximate mass of 1479 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



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

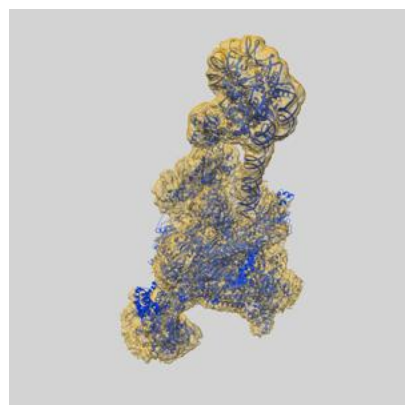
8 Fourier-Shell correlation

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

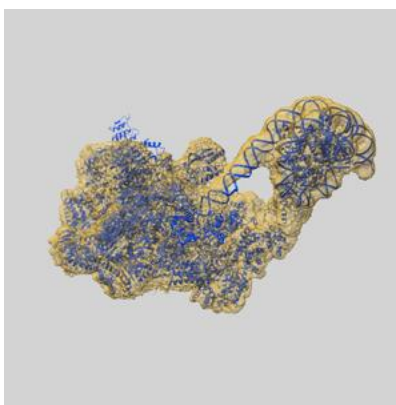
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48043 and PDB model 9EH1. Per-residue inclusion information can be found in section [3](#) on page [11](#).

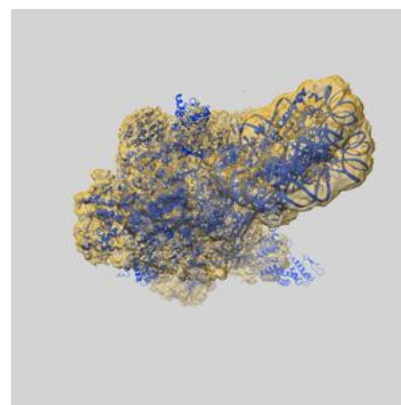
9.1 Map-model overlay [i](#)



X



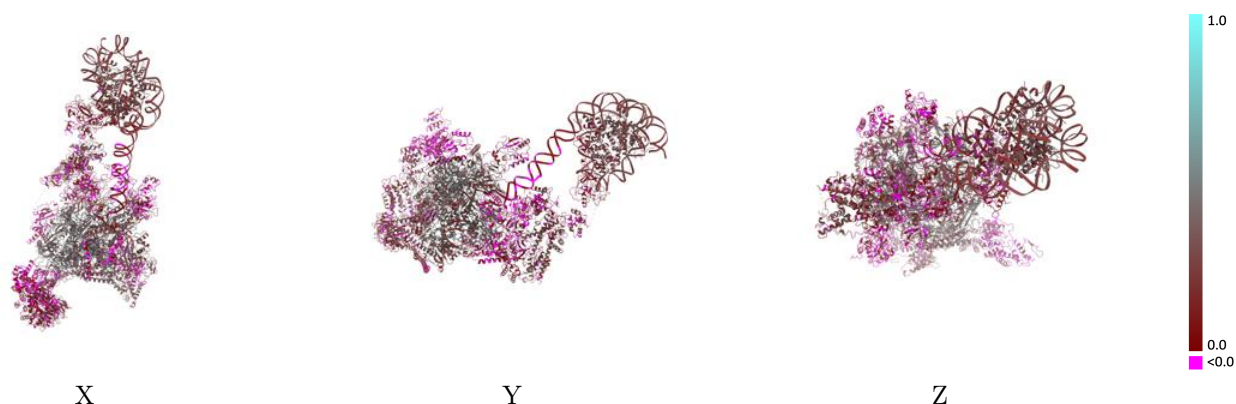
Y



Z

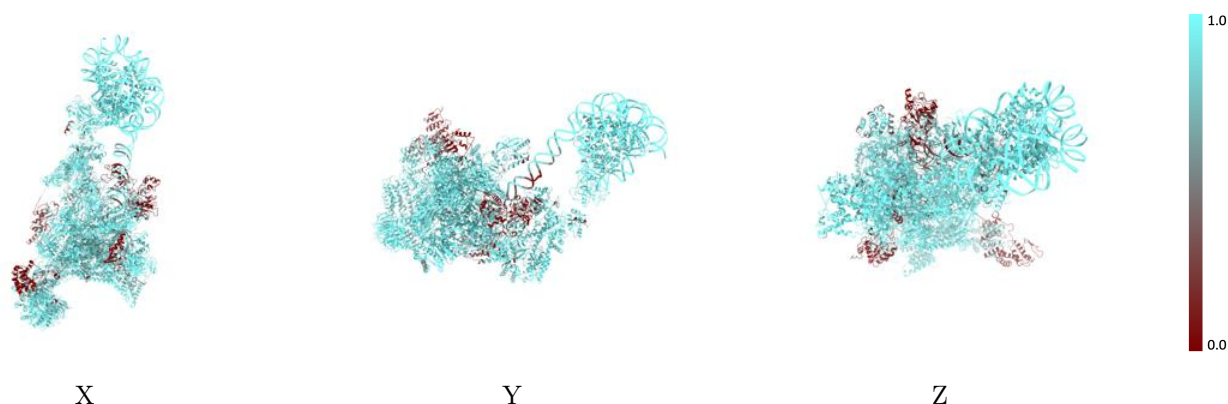
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



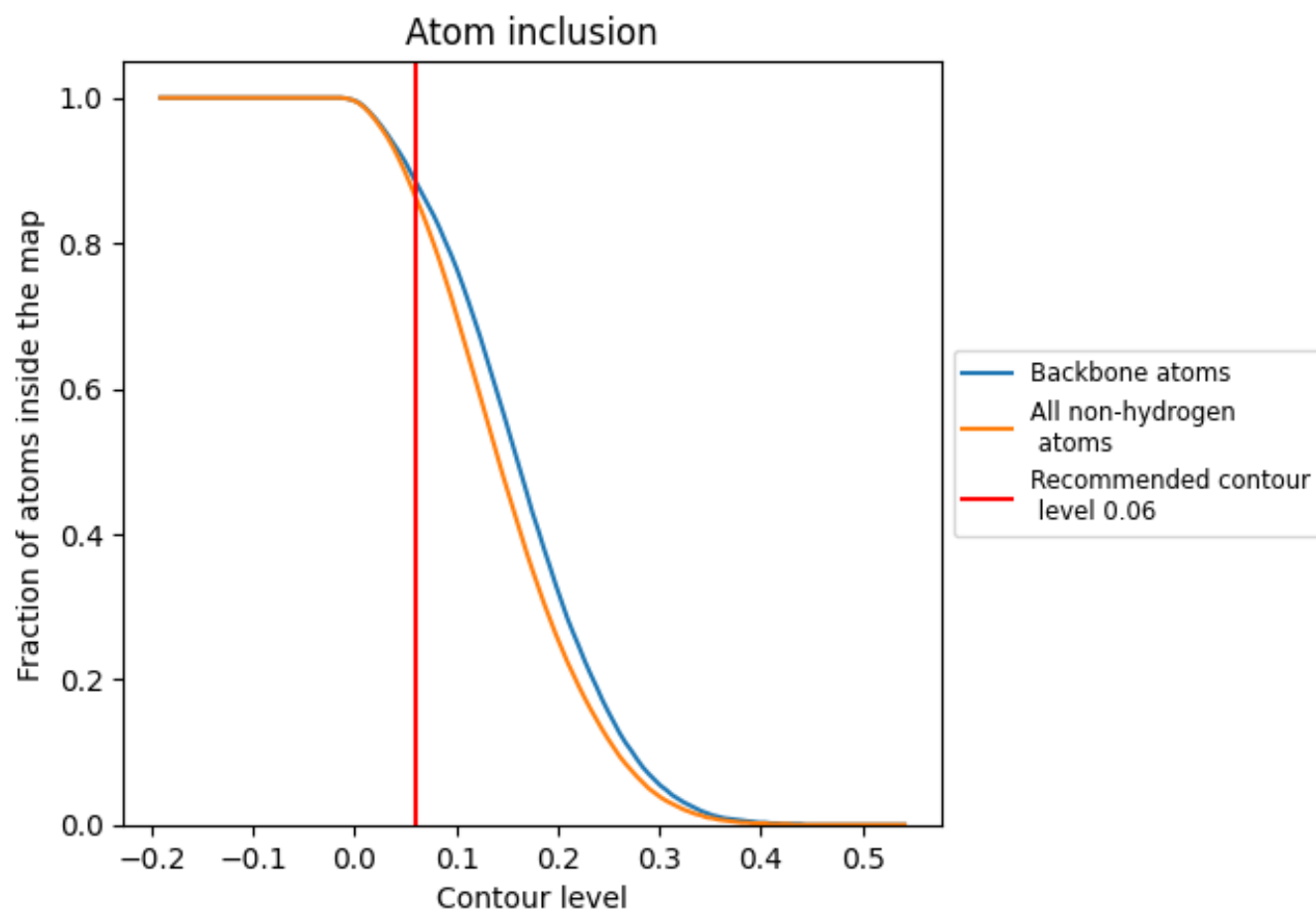
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8630	 0.2370
A	 0.9620	 0.3750
B	 0.9810	 0.3880
C	 0.9810	 0.4090
D	 0.8910	 0.1570
E	 0.9820	 0.3570
F	 0.9700	 0.4160
G	 0.9310	 0.2010
H	 0.9620	 0.3890
I	 0.9750	 0.3110
J	 0.9900	 0.4130
K	 0.9890	 0.3960
L	 0.9630	 0.3620
M	 0.7290	 0.1230
N	 0.9360	 0.2050
O	 0.7340	 0.0310
P	 0.9060	 0.2330
Q	 0.7450	 0.0870
R	 0.8020	 0.1050
S	 0.9440	 0.2190
T	 0.9260	 0.2130
U	 0.2970	 0.0170
V	 0.5100	 0.0470
W	 0.9700	 0.1190
X	 0.9820	 0.1770
Y	 0.1140	 -0.0010
Z	 0.5390	 0.0810
a	 0.9700	 0.2300
b	 0.9650	 0.2710
c	 0.9810	 0.3290
d	 0.9800	 0.3090
e	 0.9830	 0.2920
f	 0.9830	 0.3410
g	 0.9490	 0.2390
h	 0.9620	 0.2450
l	 0.9160	 0.1130

