



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 01:14 PM UTC

PDB ID : 8JH4 / pdb_00008jh4
EMDB ID : EMD-36253
Title : RNA polymerase II elongation complex containing 60 bp upstream DNA loop, stalled at SHL(-1) of the nucleosome
Authors : Akatsu, M.; Fujita, R.; Ogasawara, M.; Ehara, H.; Kujirai, T.; Takizawa, Y.; Sekine, S.; Kurumizaka, H.
Deposited on : 2023-05-22
Resolution : 3.20 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:

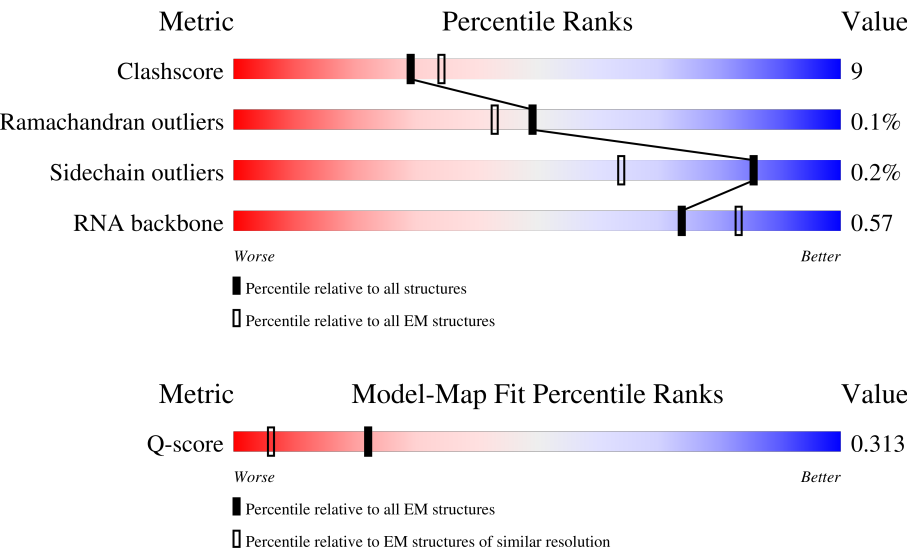
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.20 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	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1743	
2	B	1227	
3	C	304	

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Mol	Chain	Length	Quality of chain
4	D	186	
5	E	214	
6	F	155	
7	G	171	
8	H	145	
9	I	115	
10	J	72	
11	K	118	
12	L	72	
13	N	198	
14	P	10	
15	T	198	
16	a	136	
16	e	136	
17	b	103	
17	f	103	
18	c	130	
18	g	130	
19	d	126	
19	h	126	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 44415 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	1400	Total	C	N	O	S	0	0
			11038	6966	1920	2082	70		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1161	Total	C	N	O	S	0	0
			9261	5835	1636	1732	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	168	Total	C	N	O	S	0	0
			1314	812	237	263	2		

- 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	66	Total	C	N	O	S	0	0
			545	349	95	95	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 DNA chain called DNA (198-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	166	Total	C	N	O	P	0	0
			3415	1624	596	1029	166		

- Molecule 14 is a RNA chain called RNA (5'-R(P*GP*UP*CP*UP*UP*GP*GP*GP*UP*GP)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	10	Total	C	N	O	P	0	0
			215	95	36	74	10		

- Molecule 15 is a DNA chain called DNA (198-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	178	Total	C	N	O	P	0	0
			3631	1720	707	1027	177		

- Molecule 16 is a protein called Histone H3.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	a	96	Total	C	N	O	S	0	0
			786	497	151	136	2		
16	e	99	Total	C	N	O	S	0	0
			815	515	159	139	2		

- Molecule 17 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	b	77	Total	C	N	O	S	0	0
			614	389	119	105	1		
17	f	79	Total	C	N	O	S	0	0
			627	395	121	110	1		

- Molecule 18 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	c	105	Total	C	N	O	0	0
			810	511	158	141		
18	g	105	Total	C	N	O	0	0
			810	511	158	141		

- Molecule 19 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	d	92	Total	C	N	O	S	0	0
			720	453	129	136	2		
19	h	90	Total	C	N	O	S	0	0
			703	444	124	133	2		

- Molecule 20 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

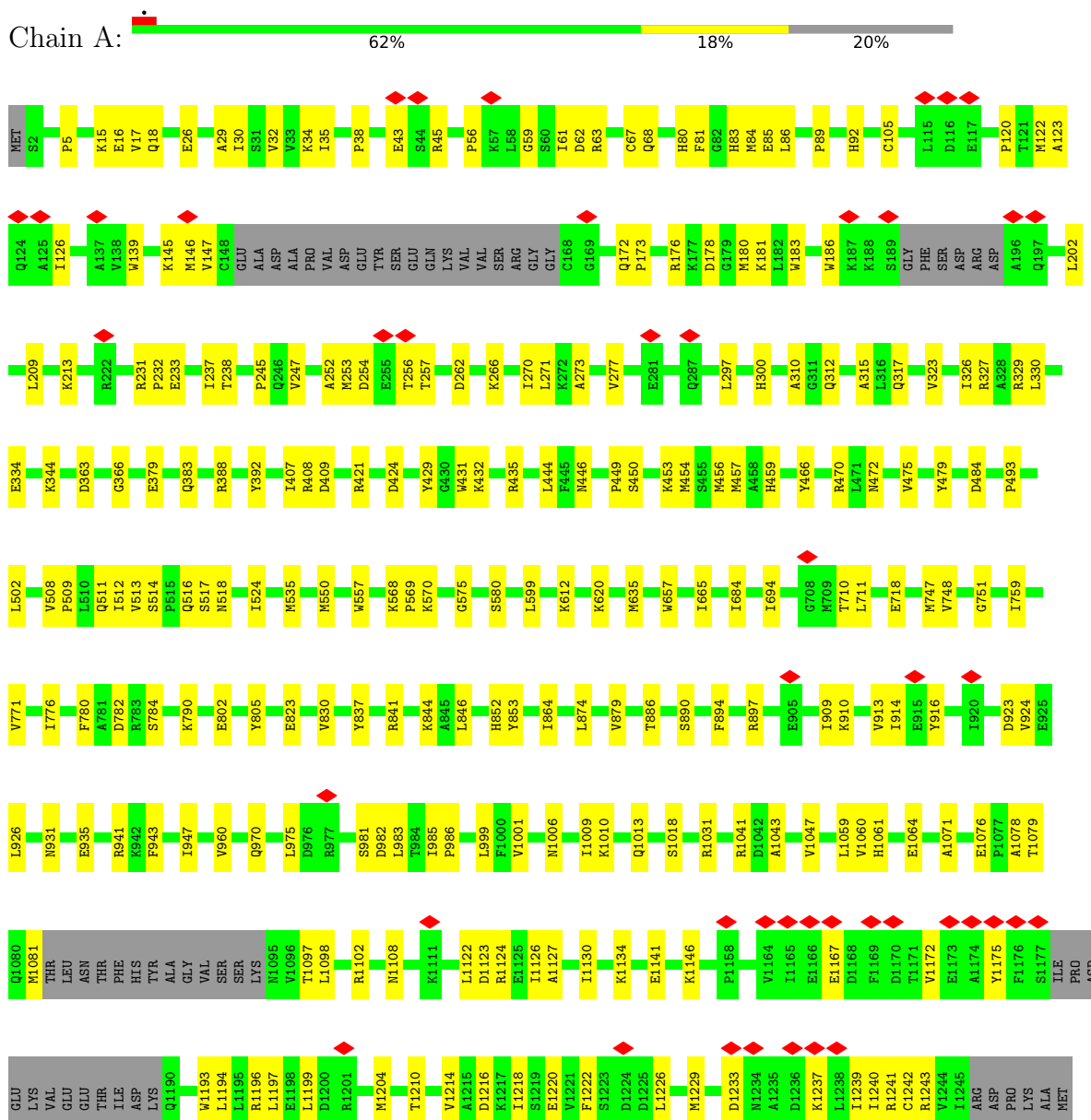
- Molecule 21 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

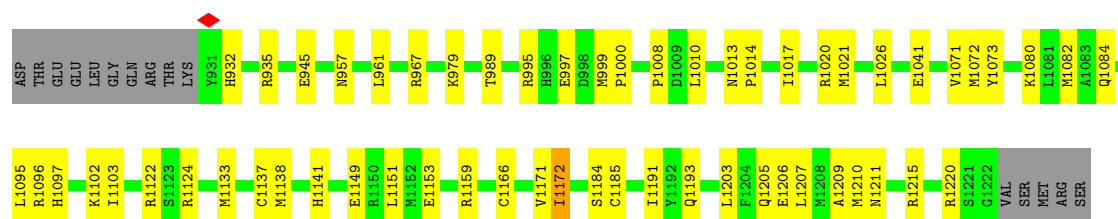
Mol	Chain	Residues	Atoms		AltConf
21	A	1	Total	Mg	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

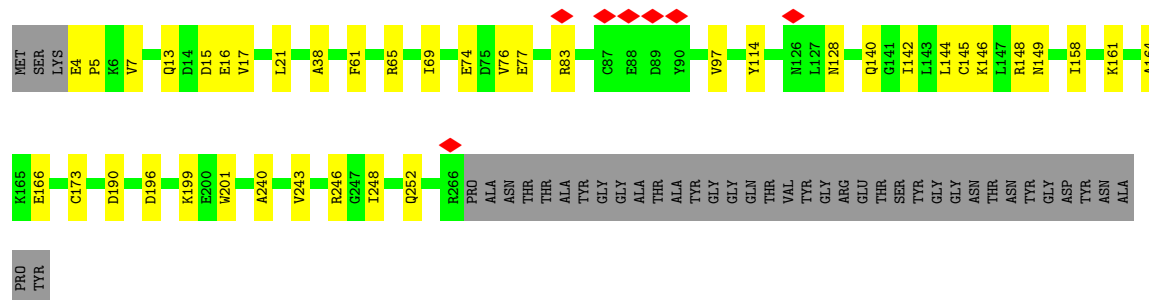
• Molecule 1: DNA-directed RNA polymerase subunit





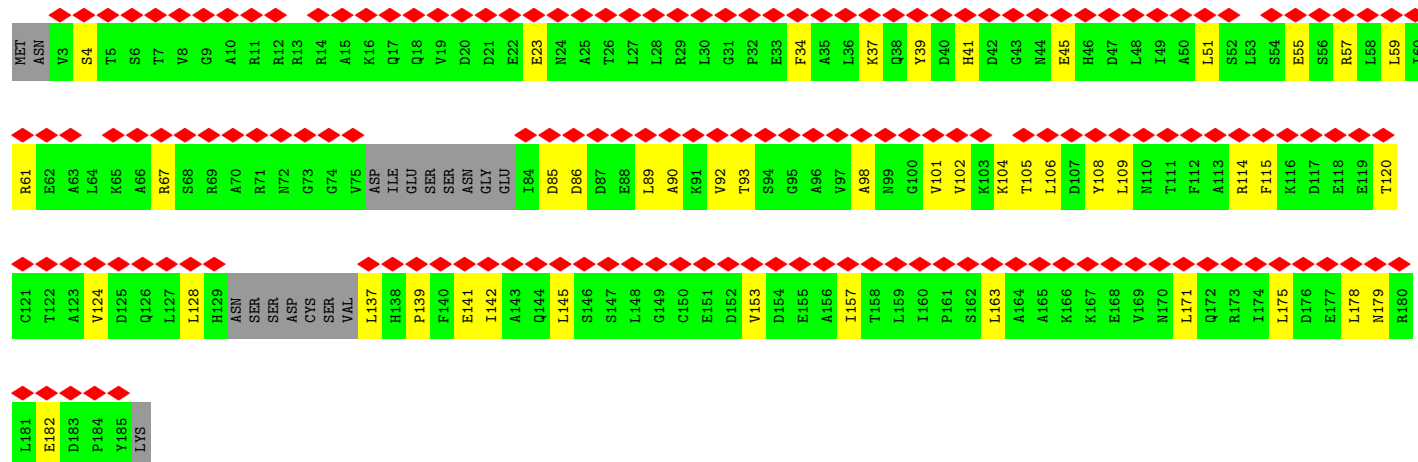
- Molecule 3: RNA polymerase II third largest subunit B44, part of central core

Chain C: 73% 13% 13%



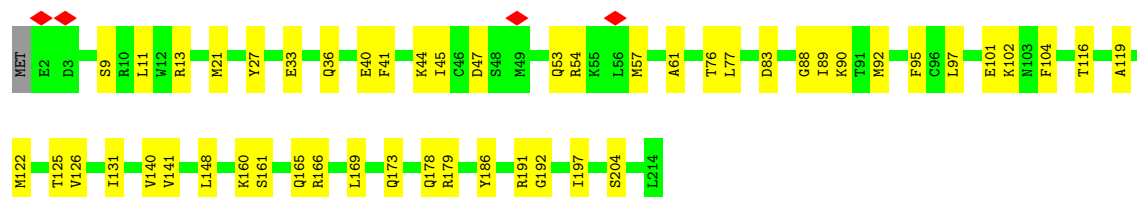
- Molecule 4: RNA polymerase II subunit B32

Chain D: 66% 24% 10%

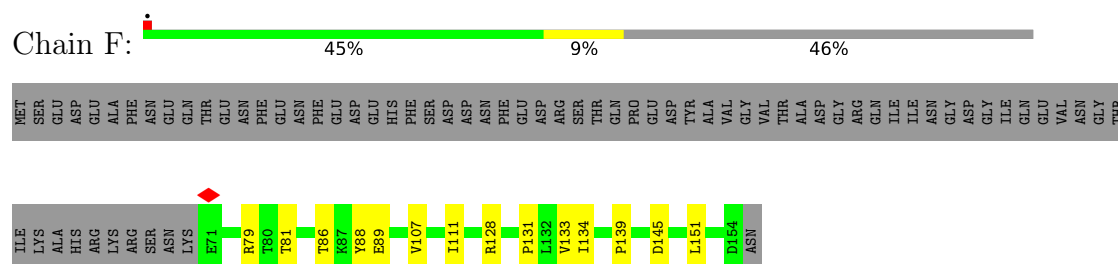


- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

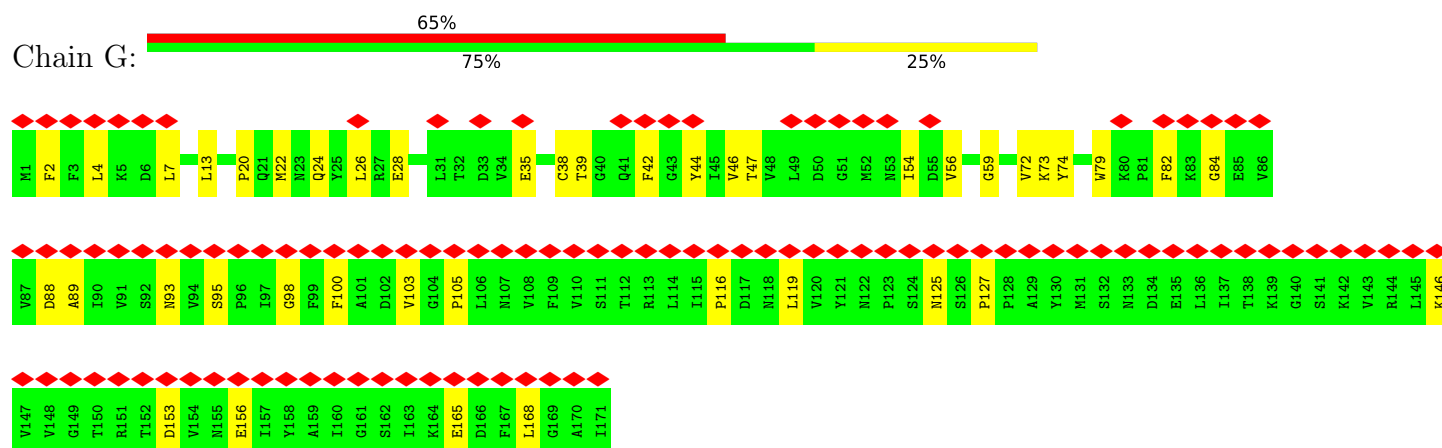
Chain E: 76% 23%



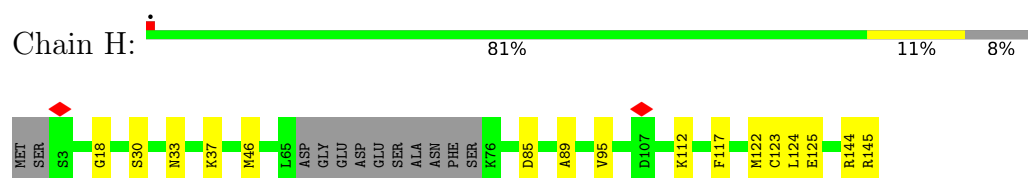
- Molecule 6: RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III



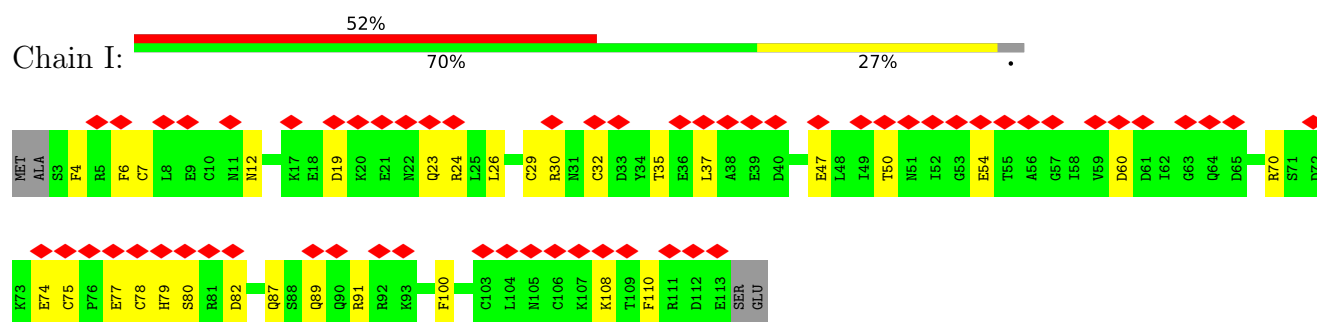
- Molecule 7: RNA polymerase II subunit



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



- Molecule 9: DNA-directed RNA polymerase subunit

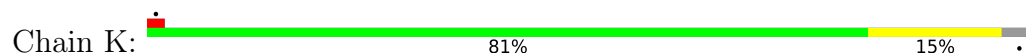


- Molecule 10: RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III

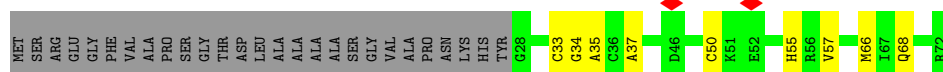




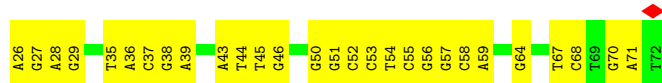
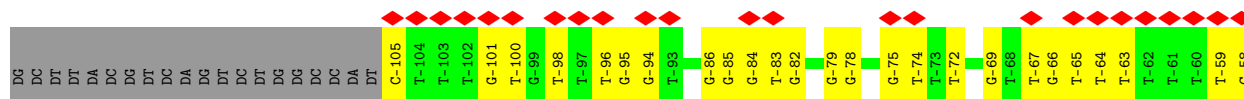
- Molecule 11: RNA polymerase II subunit B12.5



- Molecule 12: RNA polymerase subunit ABC10-alpha



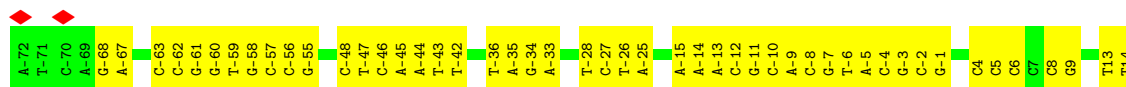
- Molecule 13: DNA (198-MER)

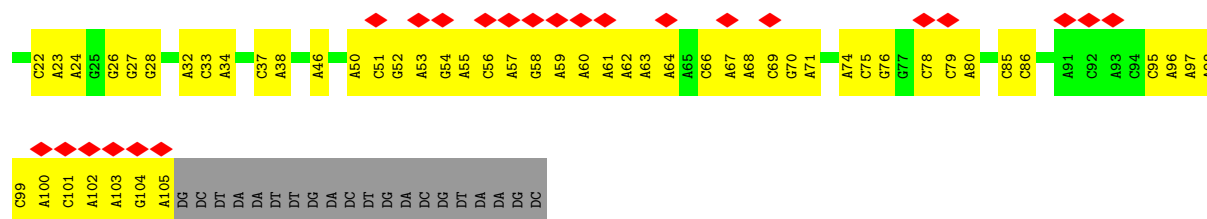


- Molecule 14: RNA (5'-R(P*GP*UP*CP*UP*UP*GP*GP*GP*UP*GP)-3')

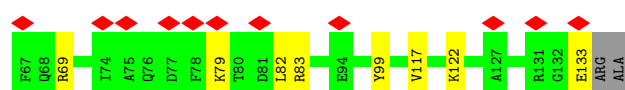
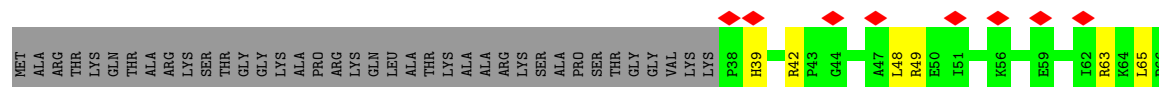


- Molecule 15: DNA (198-MER)

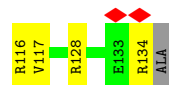
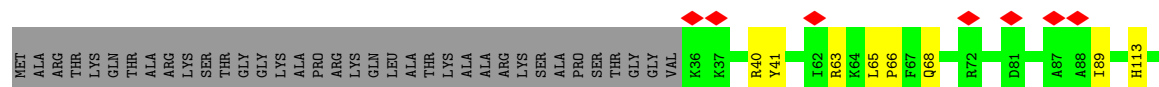




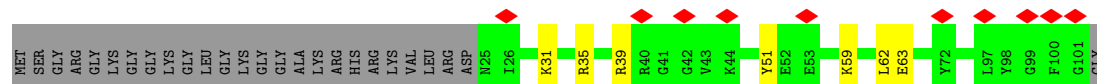
• Molecule 16: Histone H3.3



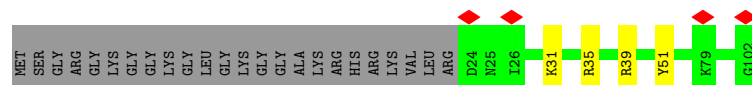
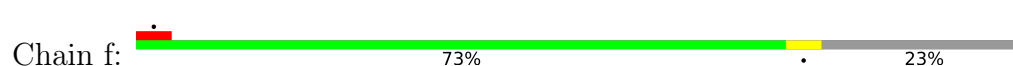
• Molecule 16: Histone H3.3



• Molecule 17: Histone H4



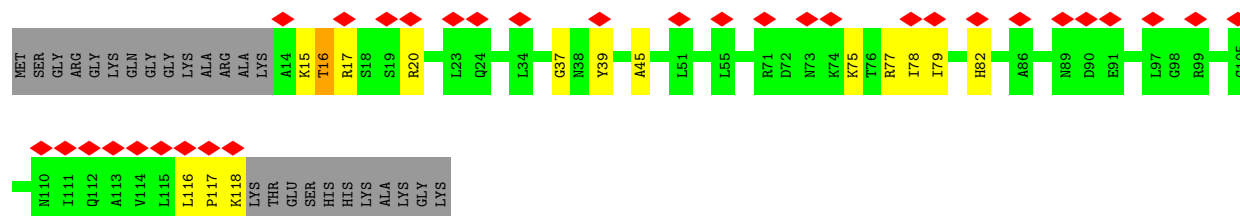
• Molecule 17: Histone H4



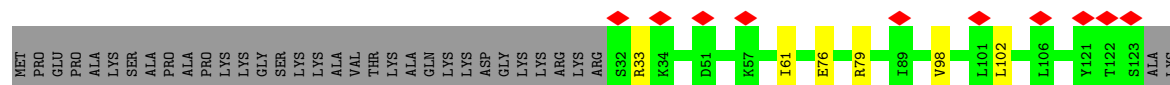
• Molecule 18: Histone H2A type 1-B/E



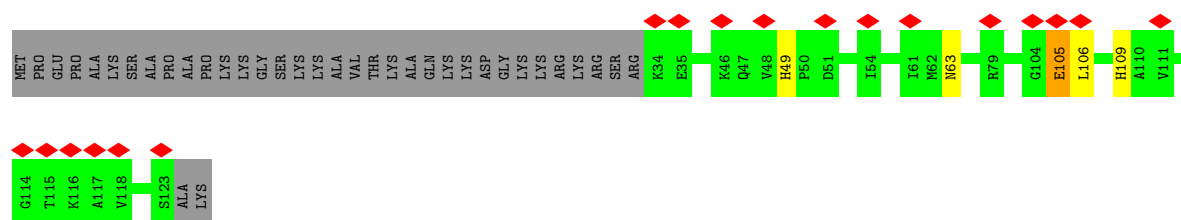
- Molecule 18: Histone H2A type 1-B/E



- Molecule 19: Histone H2B type 1-J



- Molecule 19: Histone H2B type 1-J



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97768	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59.84	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	0.082	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0149	Depositor
Map size (Å)	381.59998, 381.59998, 381.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	0.26	0/11243	0.49	1/15194 (0.0%)
2	B	0.24	0/9441	0.44	0/12732
3	C	0.28	0/2139	0.50	0/2895
4	D	0.28	0/1326	0.52	0/1788
5	E	0.21	0/1773	0.44	0/2385
6	F	0.17	0/687	0.36	0/931
7	G	0.31	0/1354	0.55	0/1837
8	H	0.25	0/1070	0.48	0/1444
9	I	0.16	0/934	0.42	0/1257
10	J	0.23	0/554	0.41	0/742
11	K	0.19	0/953	0.39	0/1291
12	L	0.17	0/365	0.42	0/484
13	N	0.17	0/3821	0.37	0/5902
14	P	0.21	0/239	0.28	0/371
15	T	0.17	0/4083	0.34	0/6289
16	a	0.32	0/798	0.76	1/1071 (0.1%)
16	e	0.38	0/827	0.79	1/1108 (0.1%)
17	b	0.36	0/621	0.86	0/832
17	f	0.35	0/634	0.81	0/848
18	c	0.42	0/820	0.81	0/1107
18	g	0.45	0/820	0.84	1/1107 (0.1%)
19	d	0.35	0/731	0.78	0/983
19	h	0.33	0/714	0.78	2/961 (0.2%)
All	All	0.26	0/45947	0.50	6/63559 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	a	117	VAL	N-CA-C	-7.11	106.29	113.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1311	THR	N-CA-C	6.76	119.45	109.24
16	e	117	VAL	N-CA-C	-5.83	107.58	113.47
18	g	16	THR	N-CA-C	5.19	118.16	110.48
19	h	49	HIS	CA-C-N	5.03	125.31	119.47

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	11038	0	11069	246	0
2	B	9261	0	9266	191	0
3	C	2098	0	2057	32	0
4	D	1314	0	1314	54	0
5	E	1741	0	1754	40	0
6	F	677	0	693	12	0
7	G	1325	0	1342	53	0
8	H	1053	0	1050	12	0
9	I	917	0	869	26	0
10	J	545	0	560	15	0
11	K	932	0	944	14	0
12	L	359	0	359	6	0
13	N	3415	0	1882	92	0
14	P	215	0	106	5	0
15	T	3631	0	1981	122	0
16	a	786	0	822	32	0
16	e	815	0	860	9	0
17	b	614	0	656	5	0
17	f	627	0	663	2	0
18	c	810	0	866	17	0
18	g	810	0	866	19	0
19	d	720	0	740	4	0
19	h	703	0	722	2	0
20	A	2	0	0	0	0
20	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	C	1	0	0	0	0
20	I	2	0	0	0	0
20	J	1	0	0	0	0
20	L	1	0	0	0	0
21	A	1	0	0	0	0
All	All	44415	0	41441	795	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 795 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)
15:T:99:DC:H5'	16:a:42:ARG:HH21	1.17	1.06
15:T:99:DC:OP1	16:a:42:ARG:HG2	1.58	1.02
15:T:98:DA:H2	16:a:39:HIS:HE2	1.10	0.98
1:A:5:PRO:O	2:B:1159:ARG:NH2	1.98	0.95
1:A:61:ILE:HD13	1:A:245:PRO:HB2	1.47	0.91

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	1388/1743 (80%)	1332 (96%)	53 (4%)	3 (0%)	43	73
2	B	1151/1227 (94%)	1115 (97%)	35 (3%)	1 (0%)	48	79
3	C	261/304 (86%)	254 (97%)	7 (3%)	0	100	100
4	D	162/186 (87%)	153 (94%)	9 (6%)	0	100	100
5	E	211/214 (99%)	205 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	82/155 (53%)	80 (98%)	2 (2%)	0	100	100
7	G	169/171 (99%)	162 (96%)	7 (4%)	0	100	100
8	H	129/145 (89%)	122 (95%)	6 (5%)	1 (1%)	16	50
9	I	109/115 (95%)	106 (97%)	3 (3%)	0	100	100
10	J	64/72 (89%)	64 (100%)	0	0	100	100
11	K	111/118 (94%)	108 (97%)	3 (3%)	0	100	100
12	L	43/72 (60%)	41 (95%)	2 (5%)	0	100	100
16	a	94/136 (69%)	93 (99%)	1 (1%)	0	100	100
16	e	97/136 (71%)	97 (100%)	0	0	100	100
17	b	75/103 (73%)	73 (97%)	2 (3%)	0	100	100
17	f	77/103 (75%)	76 (99%)	1 (1%)	0	100	100
18	c	103/130 (79%)	102 (99%)	1 (1%)	0	100	100
18	g	103/130 (79%)	102 (99%)	1 (1%)	0	100	100
19	d	90/126 (71%)	90 (100%)	0	0	100	100
19	h	88/126 (70%)	88 (100%)	0	0	100	100
All	All	4607/5512 (84%)	4463 (97%)	139 (3%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	18	GLY
1	A	43	GLU
1	A	466	TYR
1	A	960	VAL
2	B	61	PRO

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	1217/1528 (80%)	1217 (100%)	0	100	100
2	B	1016/1077 (94%)	1015 (100%)	1 (0%)	88	91
3	C	236/264 (89%)	236 (100%)	0	100	100
4	D	143/160 (89%)	143 (100%)	0	100	100
5	E	196/197 (100%)	196 (100%)	0	100	100
6	F	75/137 (55%)	75 (100%)	0	100	100
7	G	148/148 (100%)	148 (100%)	0	100	100
8	H	120/130 (92%)	120 (100%)	0	100	100
9	I	106/109 (97%)	106 (100%)	0	100	100
10	J	60/66 (91%)	60 (100%)	0	100	100
11	K	104/109 (95%)	104 (100%)	0	100	100
12	L	38/56 (68%)	38 (100%)	0	100	100
16	a	82/110 (74%)	82 (100%)	0	100	100
16	e	85/110 (77%)	85 (100%)	0	100	100
17	b	63/79 (80%)	63 (100%)	0	100	100
17	f	64/79 (81%)	64 (100%)	0	100	100
18	c	83/100 (83%)	81 (98%)	2 (2%)	43	70
18	g	83/100 (83%)	83 (100%)	0	100	100
19	d	79/105 (75%)	78 (99%)	1 (1%)	61	78
19	h	77/105 (73%)	74 (96%)	3 (4%)	28	62
All	All	4075/4769 (85%)	4068 (100%)	7 (0%)	85	89

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	d	61	ILE
19	h	63	ASN
19	h	106	LEU
19	h	105	GLU
18	c	84	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	31	ASN

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Mol	Chain	Res	Type
19	d	95	GLN
9	I	90	GLN
18	c	24	GLN
16	e	113	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	9/10 (90%)	1 (11%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	P	2	U

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

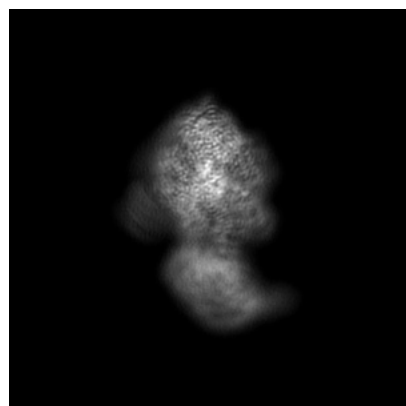
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36253. These allow visual inspection of the internal detail of the map and identification of artifacts.

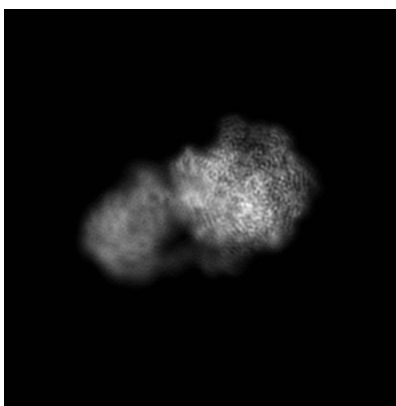
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

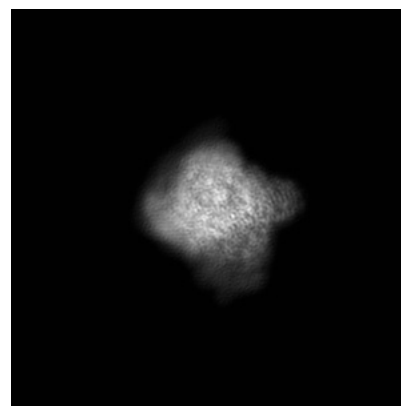
6.1.1 Primary map



X

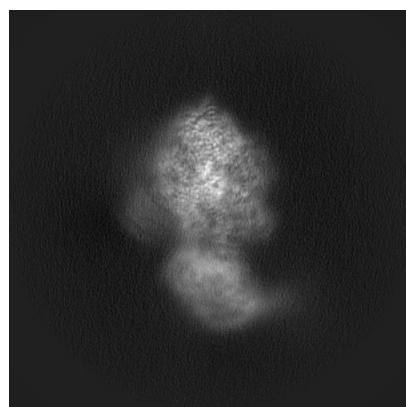


Y

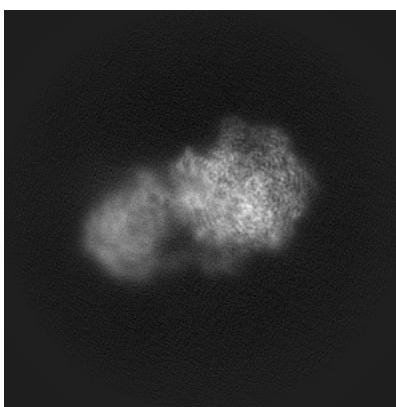


Z

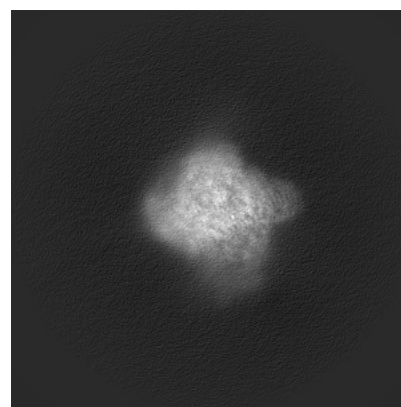
6.1.2 Raw map



X



Y

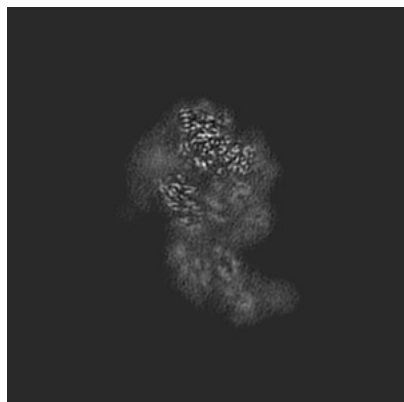


Z

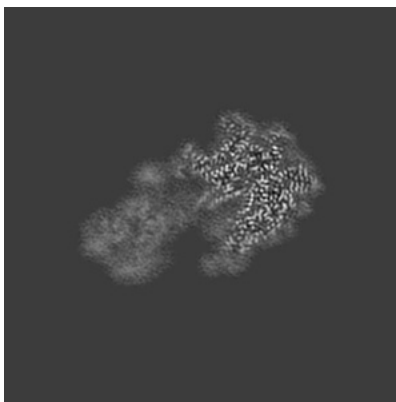
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

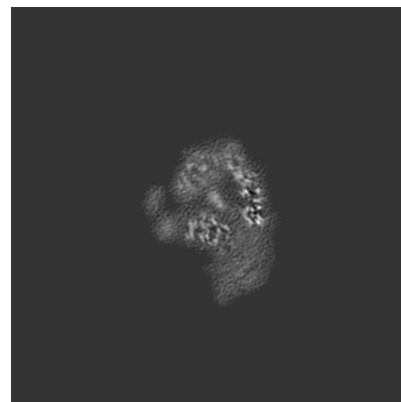
6.2.1 Primary map



X Index: 180

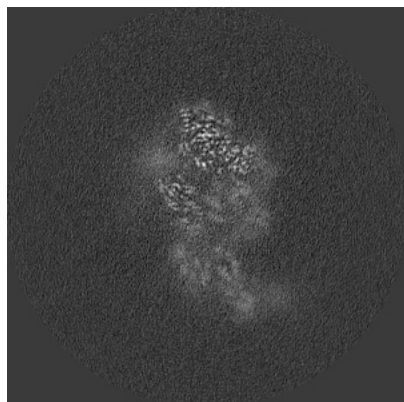


Y Index: 180

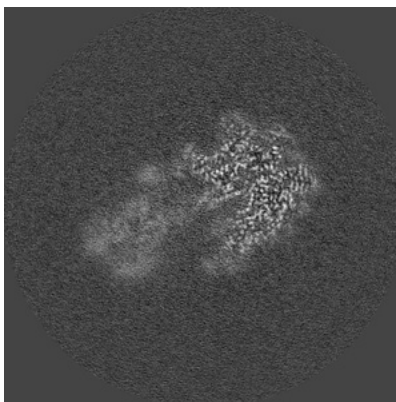


Z Index: 180

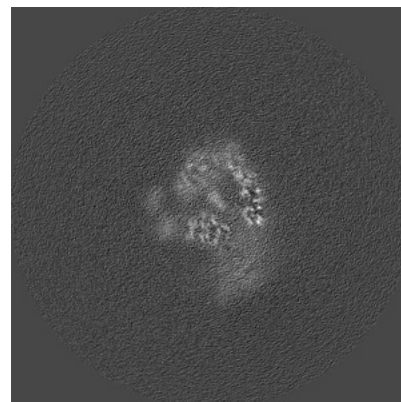
6.2.2 Raw map



X Index: 180



Y Index: 180

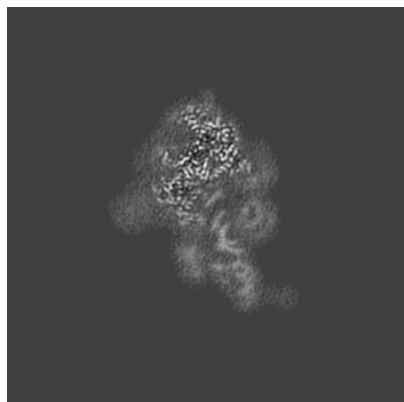


Z Index: 180

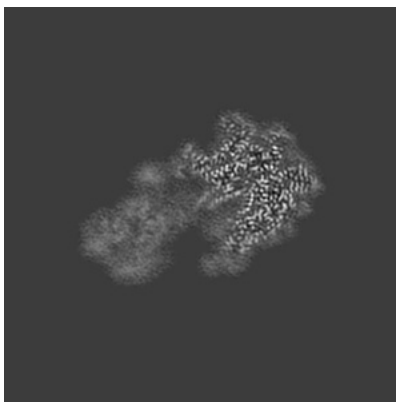
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

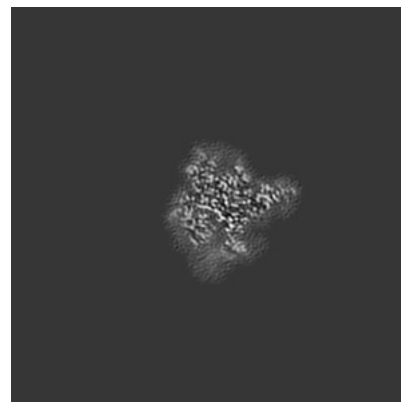
6.3.1 Primary map



X Index: 192

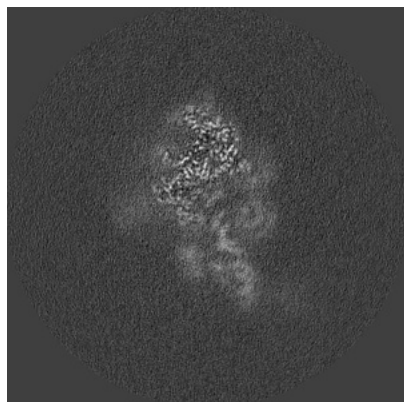


Y Index: 180

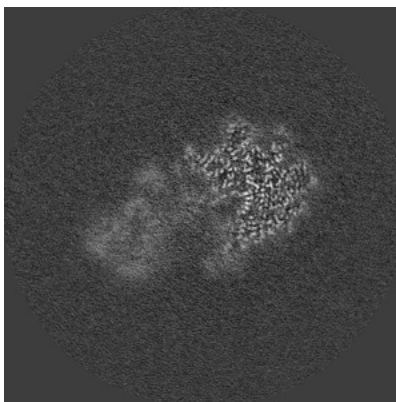


Z Index: 230

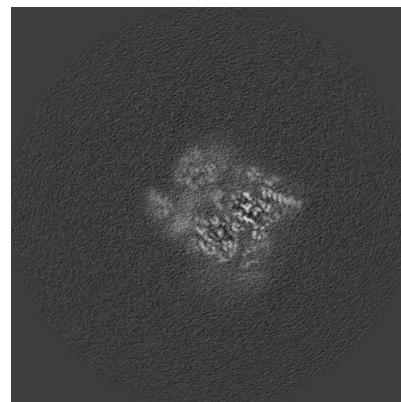
6.3.2 Raw map



X Index: 192



Y Index: 178

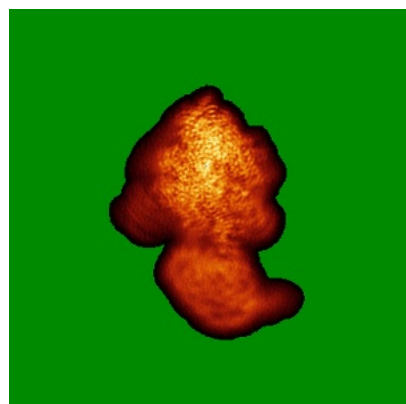


Z Index: 196

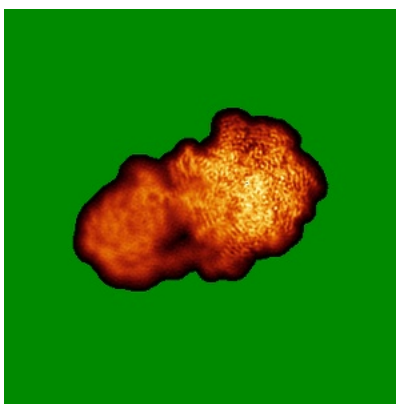
The images above show the largest variance slices of the map in three orthogonal directions.

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

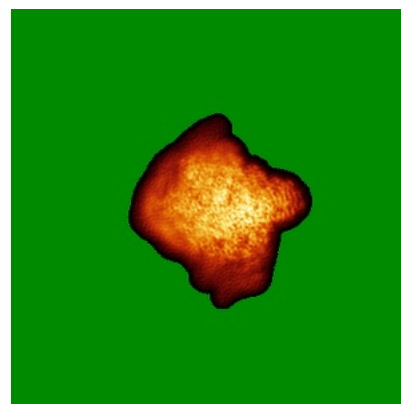
6.4.1 Primary map



X

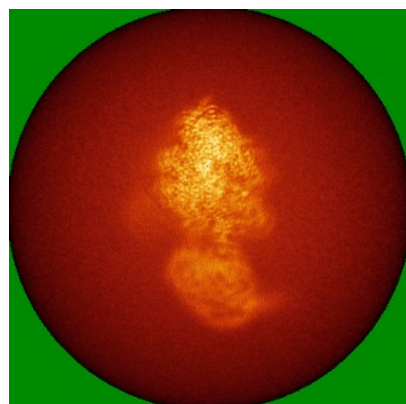


Y

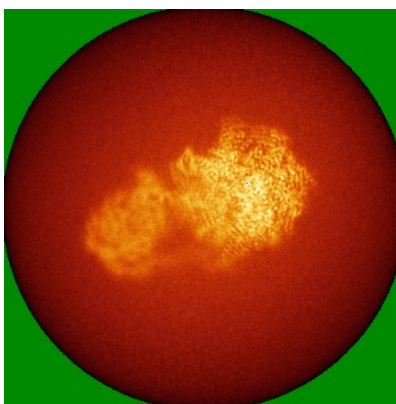


Z

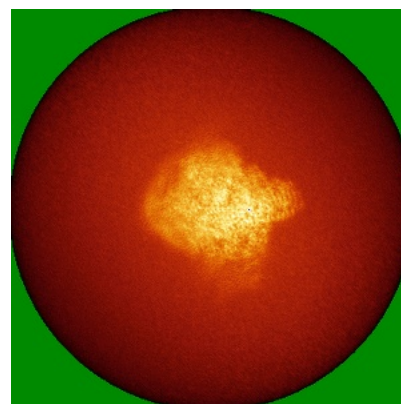
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0149. 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



X



Y



Z

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.

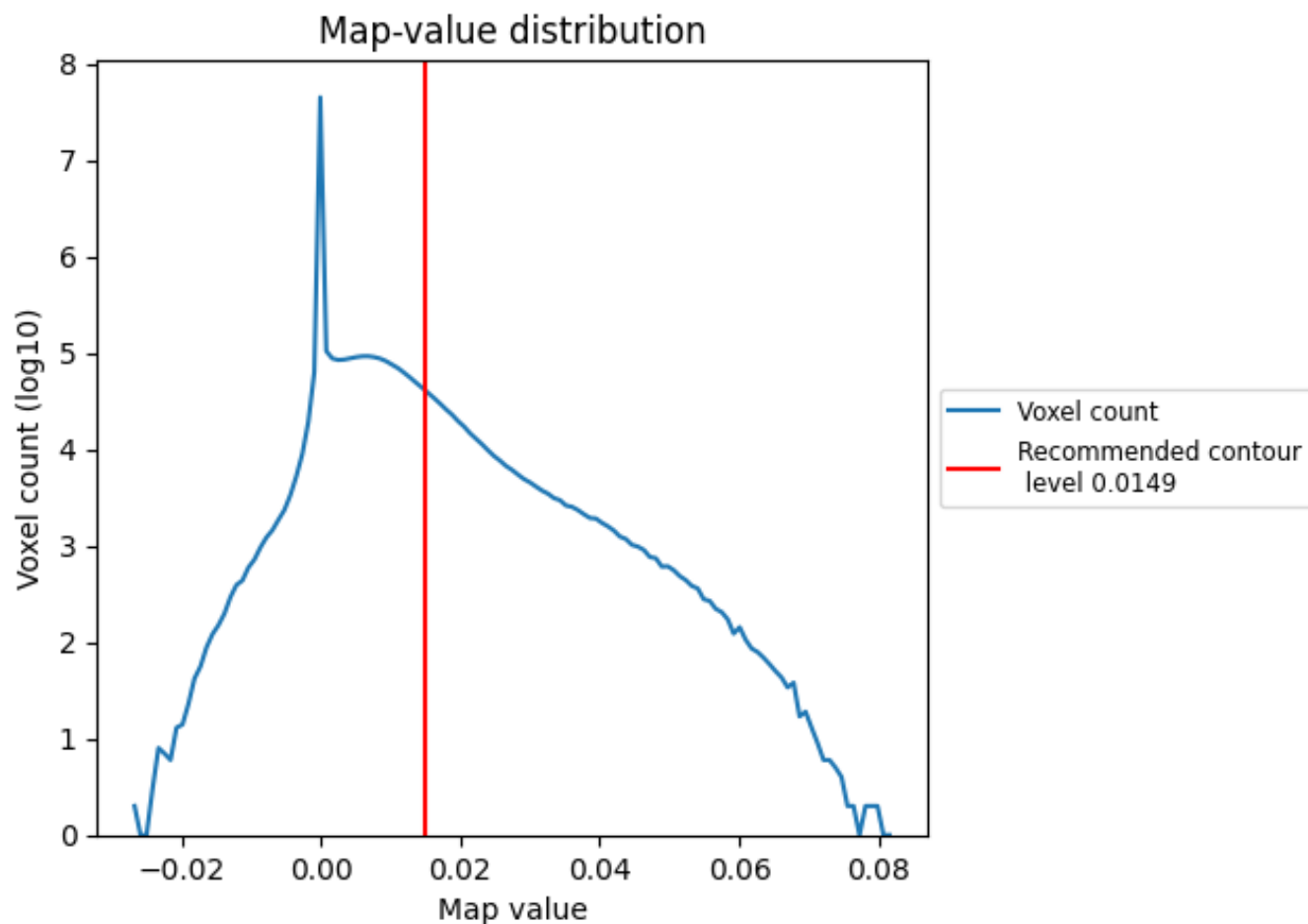
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

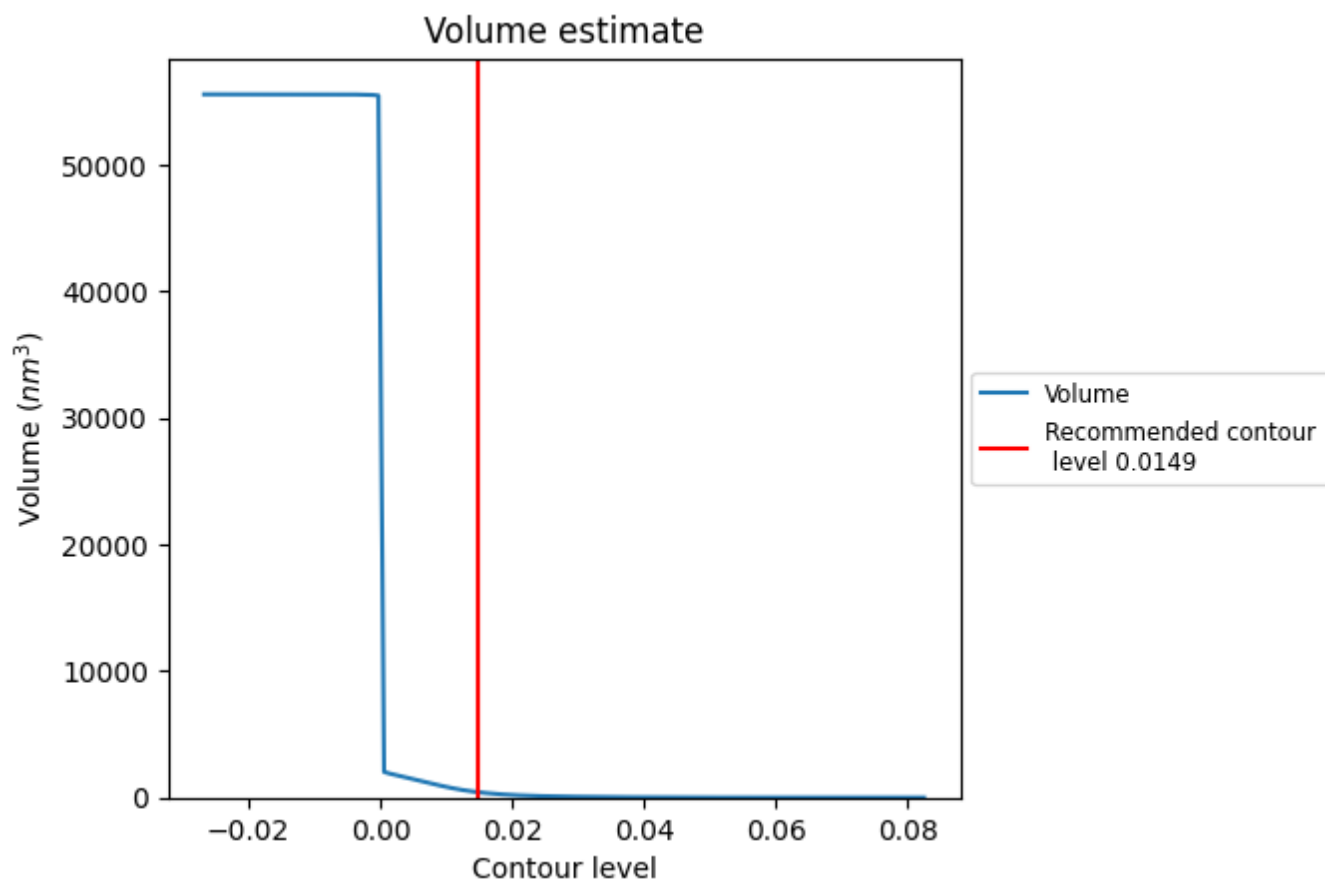
This section contains the results of statistical analysis of the map.

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.

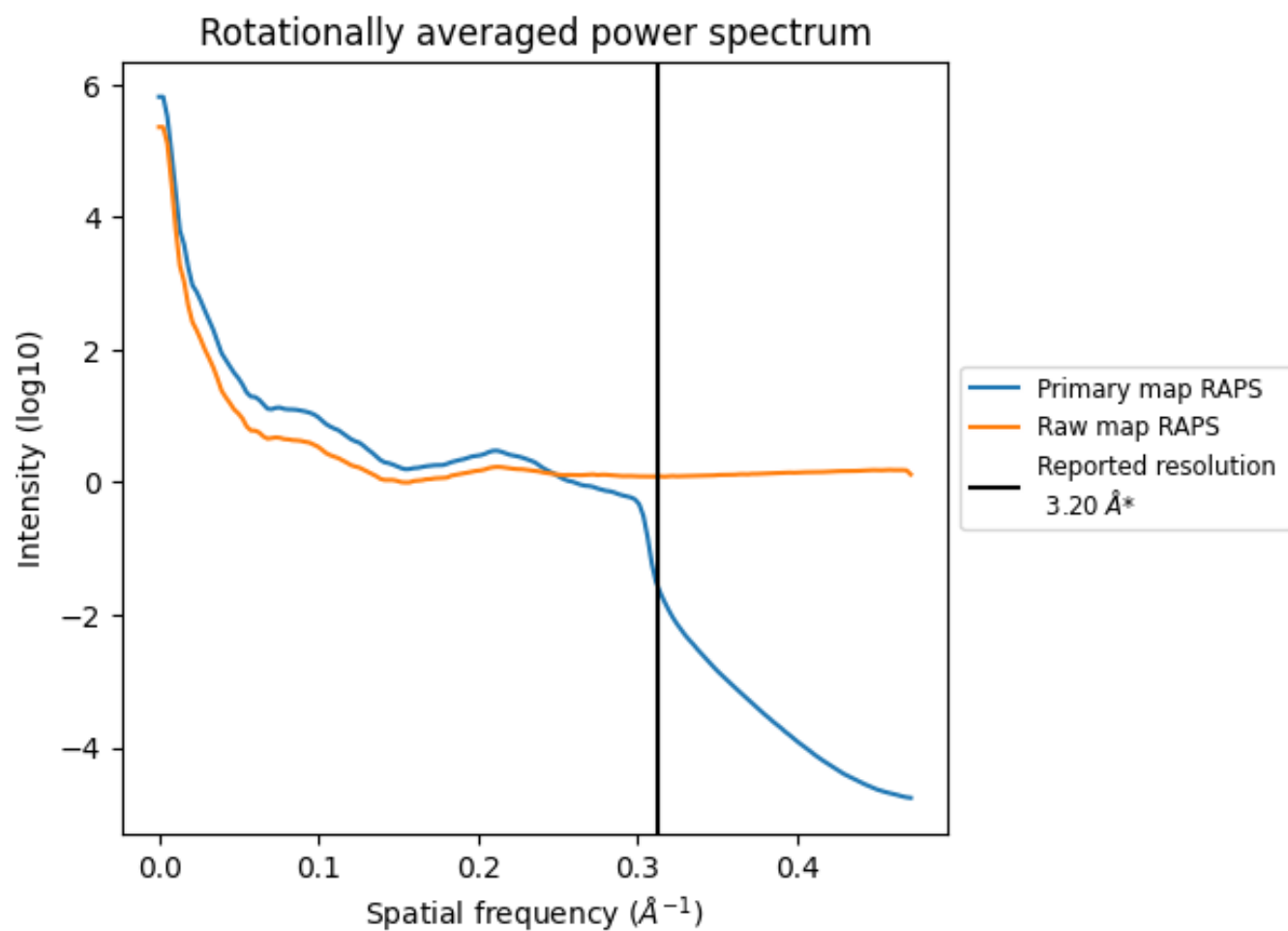
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 420 nm³; this corresponds to an approximate mass of 380 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 ⓘ

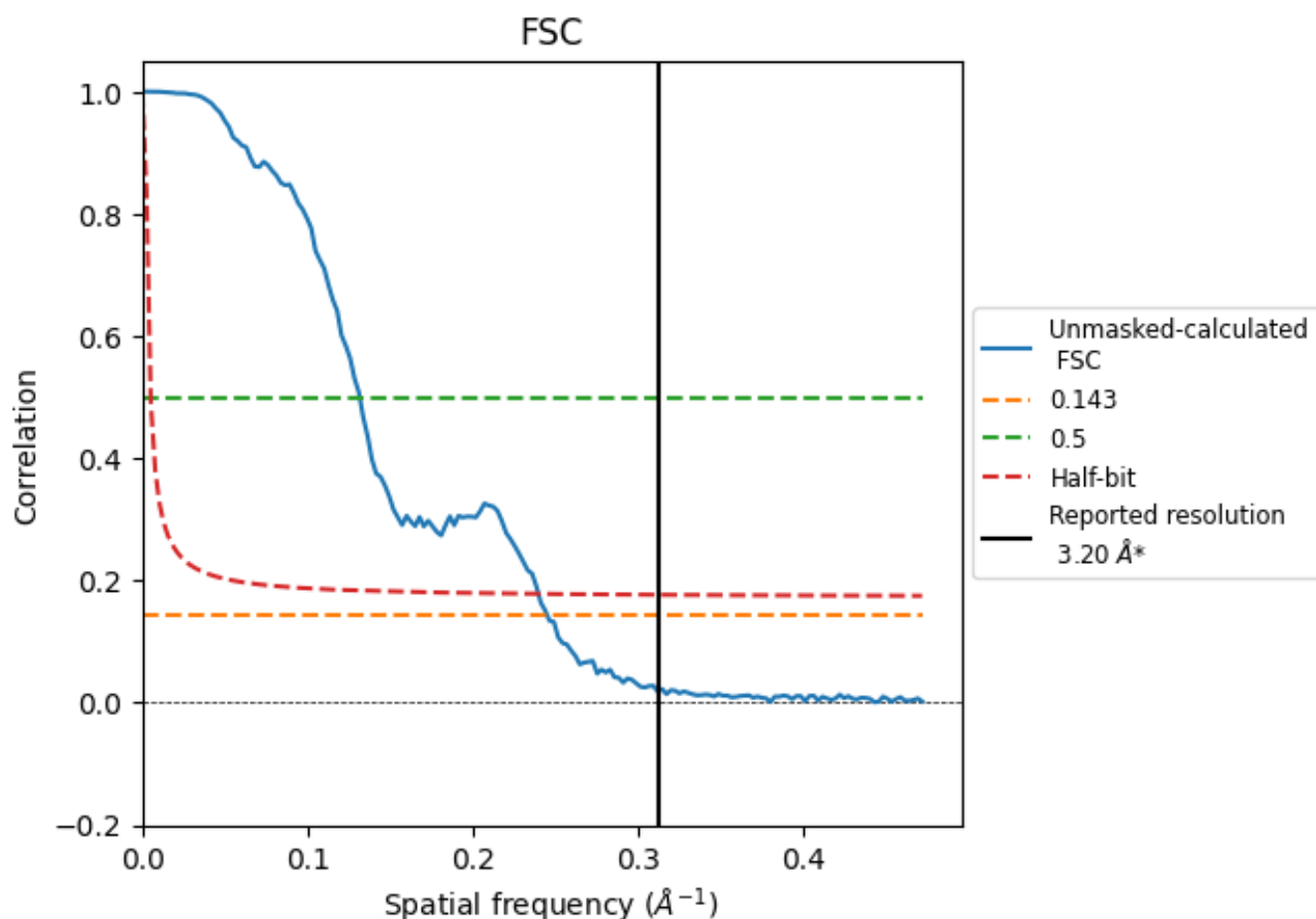


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

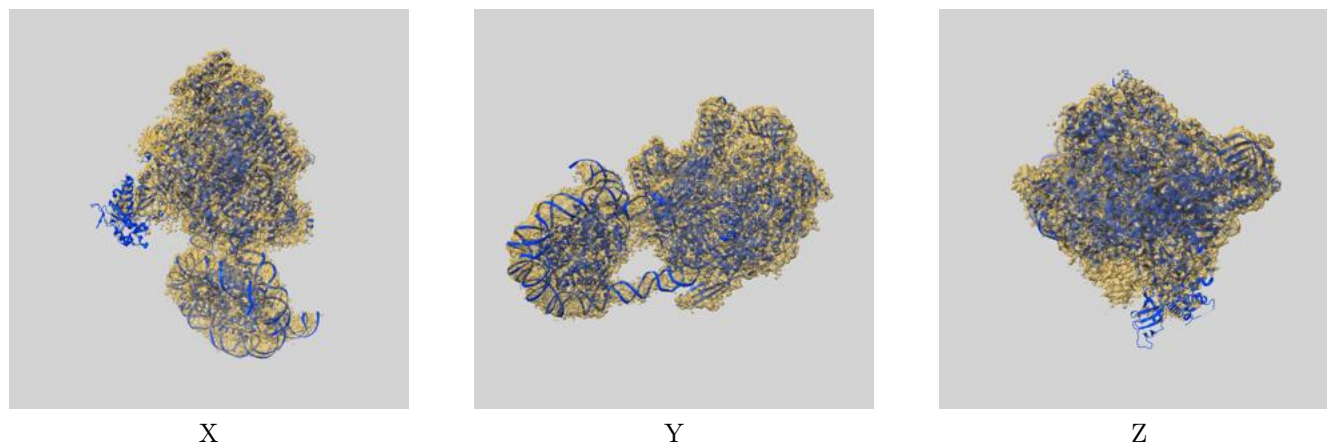
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.08	7.60	4.17

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.08 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

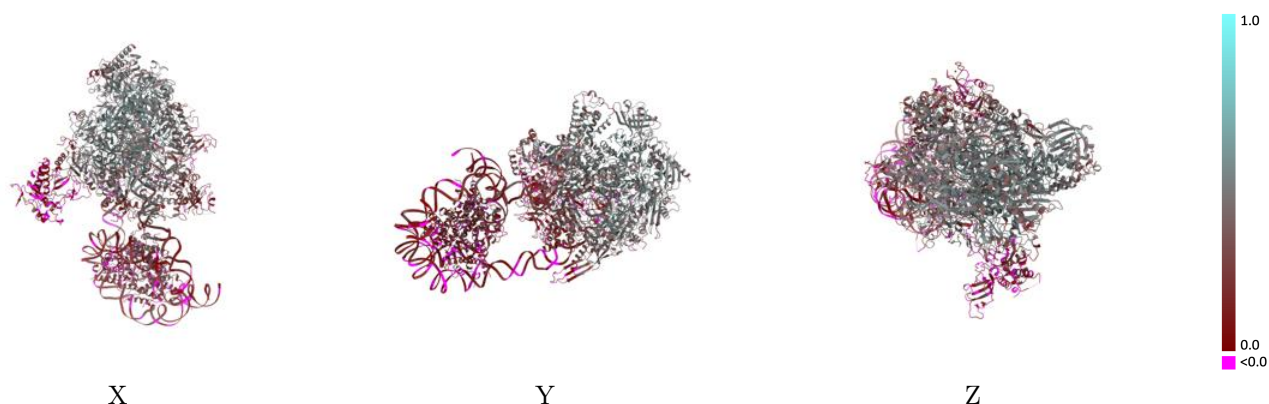
This section contains information regarding the fit between EMDB map EMD-36253 and PDB model 8JH4. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



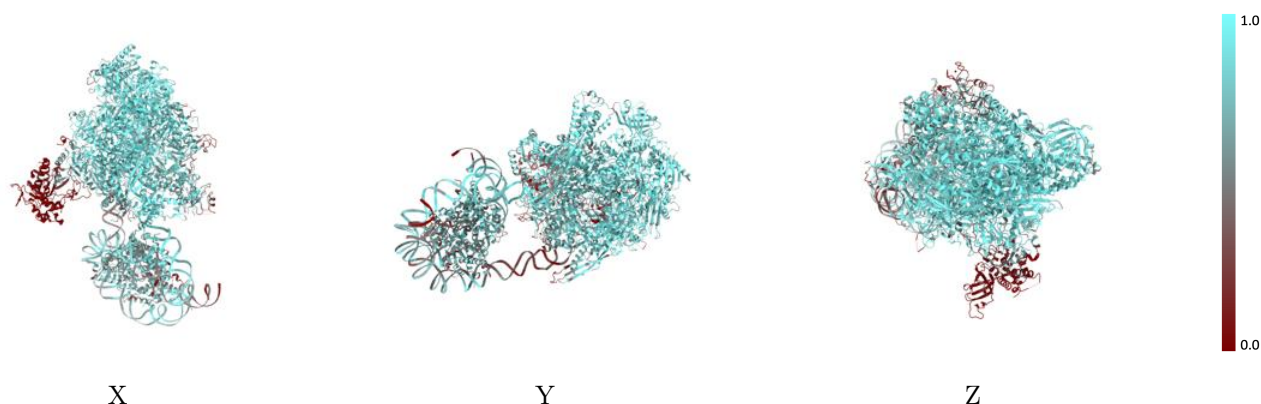
The images above show the 3D surface view of the map at the recommended contour level 0.0149 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



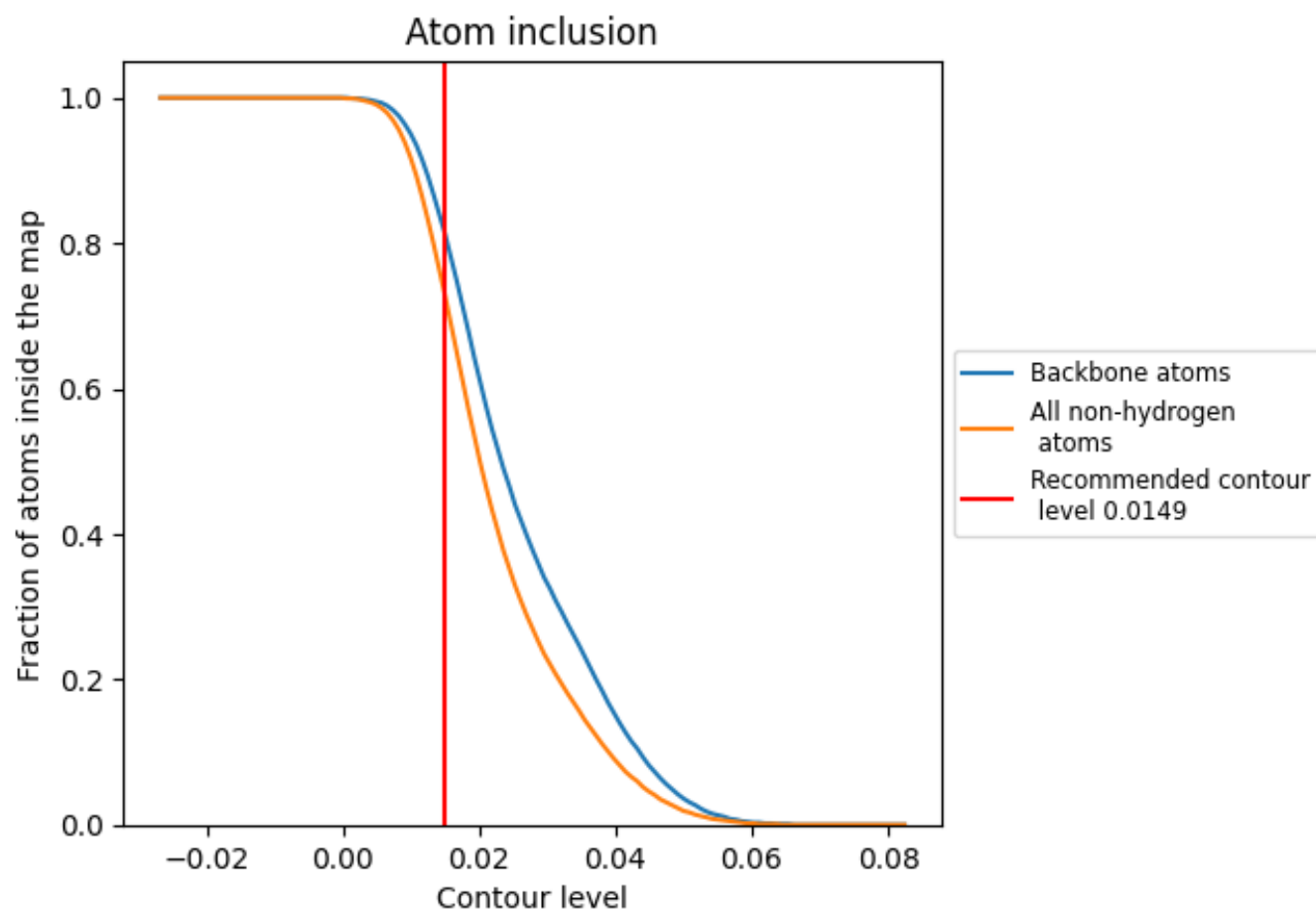
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0149).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 73% 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 (0.0149) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7330	 0.3130
A	 0.8350	 0.4170
B	 0.8210	 0.4110
C	 0.8330	 0.4350
D	 0.0530	 0.0490
E	 0.8370	 0.4020
F	 0.8830	 0.4630
G	 0.2910	 0.1700
H	 0.8310	 0.4460
I	 0.3830	 0.1610
J	 0.8740	 0.4550
K	 0.8560	 0.4490
L	 0.7930	 0.3380
N	 0.6600	 0.1170
P	 0.9720	 0.4710
T	 0.6700	 0.1420
a	 0.6130	 0.1300
b	 0.6710	 0.1250
c	 0.6610	 0.1460
d	 0.6610	 0.1280
e	 0.6730	 0.1910
f	 0.7300	 0.2350
g	 0.5400	 0.1190
h	 0.6160	 0.1100

