



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:37 PM UTC

PDB ID : 7B0Y / pdb_00007b0y
EMDB ID : EMD-11972
Title : Structure of a transcribing RNA polymerase II-U1 snRNP complex
Authors : Zhang, S.; Aibara, S.; Vos, S.M.; Agafonov, D.E.; Luehrmann, R.; Cramer, P.
Deposited on : 2020-11-23
Resolution : 3.60 Å(reported)
Based on initial models : 3PGW, 4PJO, 6GMH, 4PKD

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:

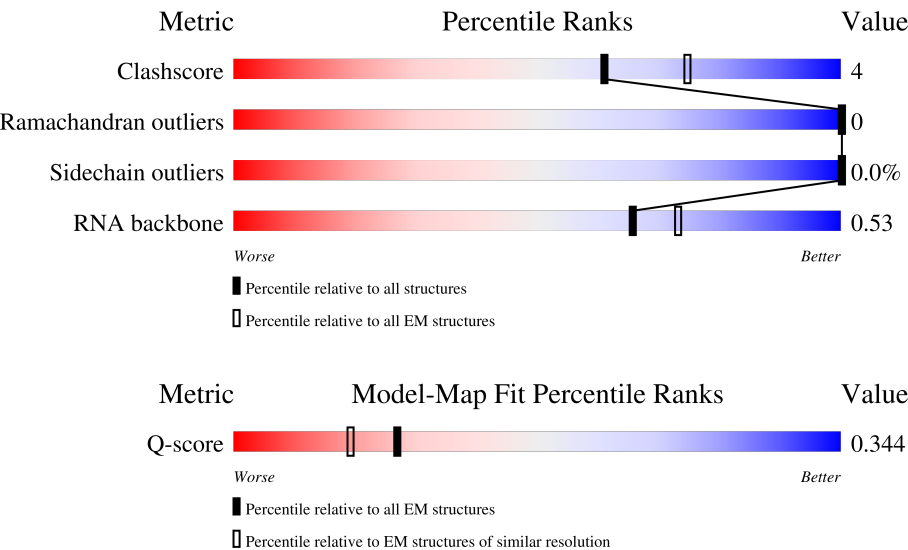
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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	1970	
2	B	1174	
3	C	275	

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Mol	Chain	Length	Quality of chain
4	D	142	
5	E	210	
6	F	127	
7	G	172	
8	H	150	
9	I	125	
10	J	67	
11	K	117	
12	L	58	
13	N	48	
14	P	145	
15	T	48	
16	a	164	
17	b	437	
18	c	282	
19	e	118	
20	f	86	
21	g	92	
22	h	76	
23	i	126	
24	j	231	
25	k	119	

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 43792 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 II subunit RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1422	Total	C	N	O	S	0	0
			11263	7082	2018	2093	70		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1131	Total	C	N	O	S	0	0
			9052	5727	1592	1669	64		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	260	Total	C	N	O	S	0	0
			2089	1309	359	415	6		

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	126	Total	C	N	O	S	0	0
			1030	642	175	209	4		

- 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	0	0
			1720	1089	300	323	8		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	82	Total	C	N	O	S	0	0
			657	418	113	121	5		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1351	875	219	249	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	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	117	Total	C	N	O	S	0	0
			949	587	169	182	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	67	Total	C	N	O	S	0	0
			533	345	90	92	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 RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	46	Total	C	N	O	S	0	0
			388	241	75	66	6		

- Molecule 13 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	37	Total	C	N	O	P	0	0
			769	361	149	222	37		

- Molecule 14 is a RNA chain called 145-nt RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	36	Total	C	N	O	P	0	0
			774	346	147	245	36		

- Molecule 15 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	37	Total	C	N	O	P	0	0
			749	355	128	229	37		

- Molecule 16 is a RNA chain called U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	a	164	Total	C	N	O	P	0	0
			3485	1555	607	1159	164		

- Molecule 17 is a protein called U1 small nuclear ribonucleoprotein 70 kDa.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	b	186	Total	C	N	O	S	0	0
			1543	952	310	276	5		

- Molecule 18 is a protein called U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	c	98	Total	C	N	O	S	0	0
			796	513	136	143	4		

- Molecule 19 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	e	95	Total	C	N	O	S	0	0
			777	486	141	144	6		

- Molecule 20 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	f	74	Total	C	N	O	S	0	0
			576	373	95	103	5		

- Molecule 21 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	g	77	Total	C	N	O	S	0	0
			638	405	113	115	5		

- Molecule 22 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	h	73	Total	C	N	O	S	0	0
			568	358	102	102	6		

- Molecule 23 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	i	81	Total	C	N	O	S	0	0
			637	400	112	119	6		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	j	86	Total	C	N	O	S	0	0
			692	435	126	124	7		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	k	81	Total	C	N	O	S	0	0
			641	408	112	118	3		

- Molecule 26 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

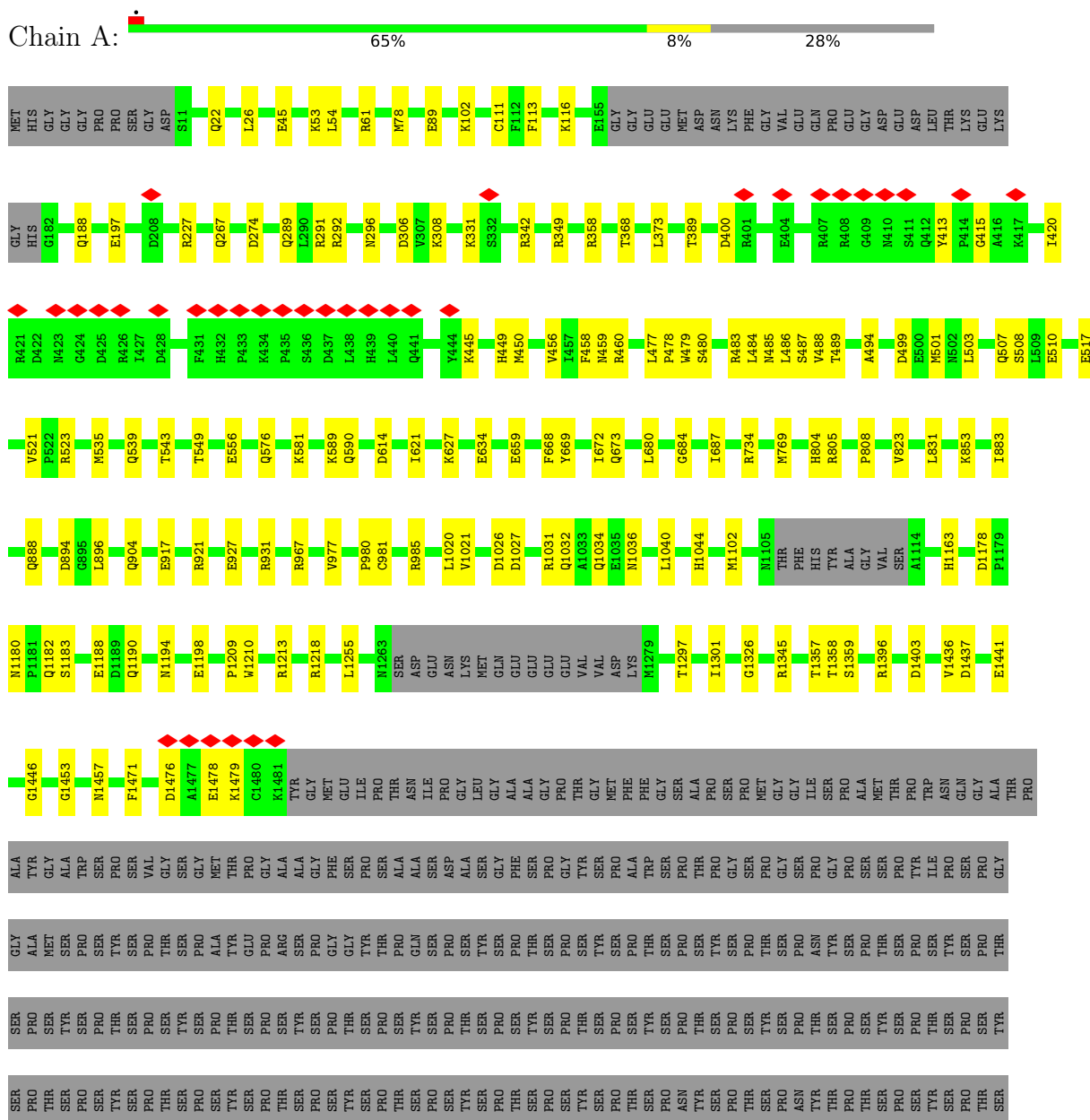
- Molecule 27 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

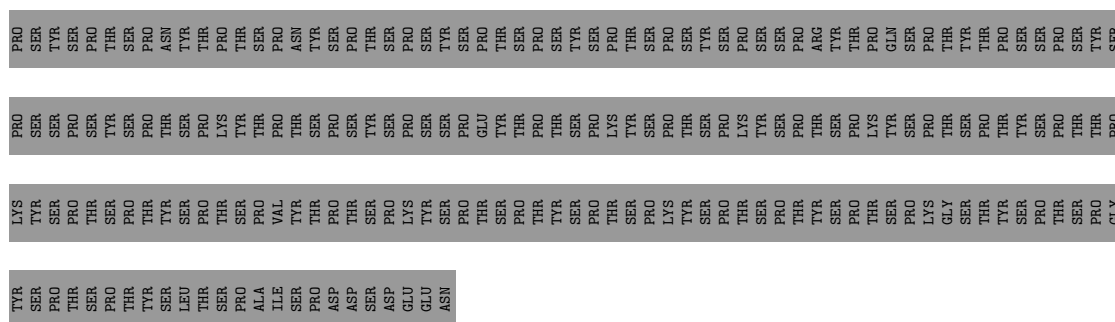
Mol	Chain	Residues	Atoms		AltConf
27	A	1	Total 1	Mg 1	0

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.

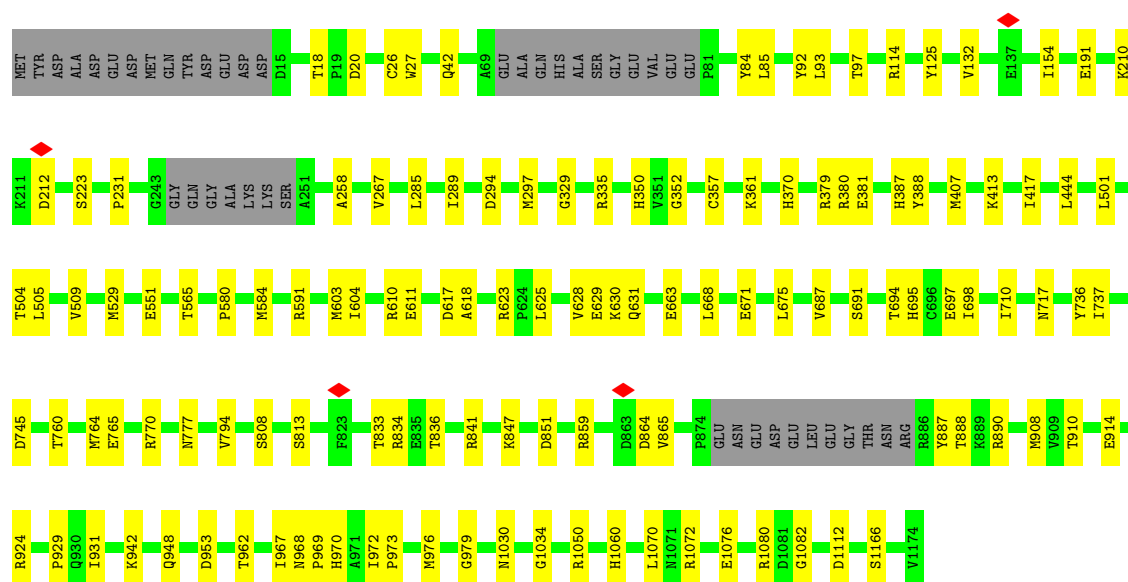
- Molecule 1: DNA-directed RNA polymerase II subunit RPB1



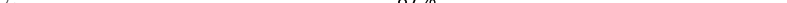


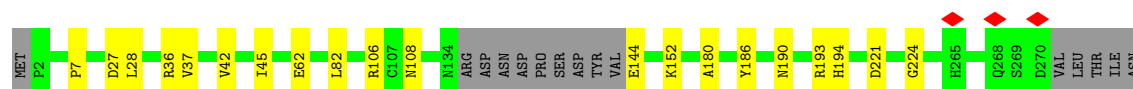
- Molecule 2: DNA-directed RNA polymerase subunit beta

Chain B: 86% 11% .

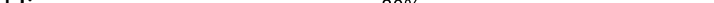


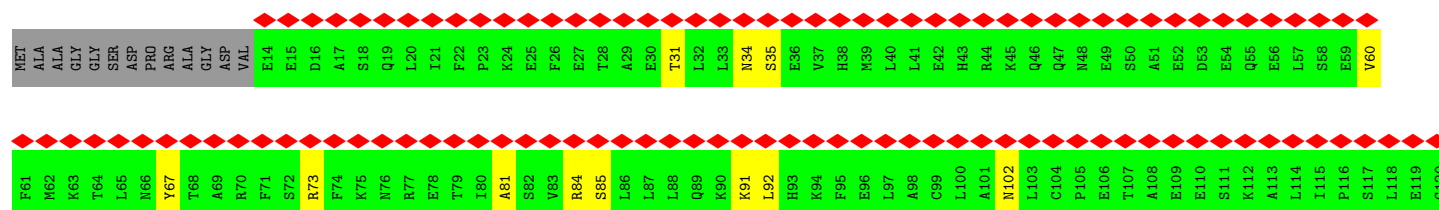
- Molecule 3: DNA-directed RNA polymerase II subunit RPB3

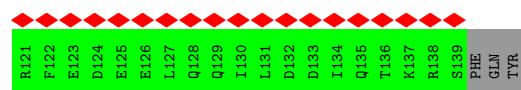
Chain C:  87% 7% 5%



- Molecule 4: DNA-directed RNA polymerase II subunit D

Chain D:  89% 80% 8% 11%





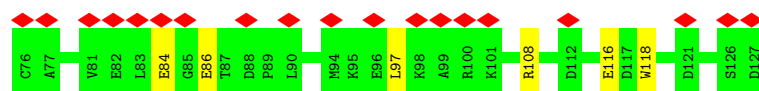
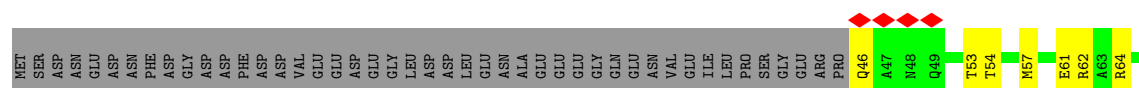
- Molecule 5: DNA-directed RNA polymerase II subunit E

Chain E: 90% 10%



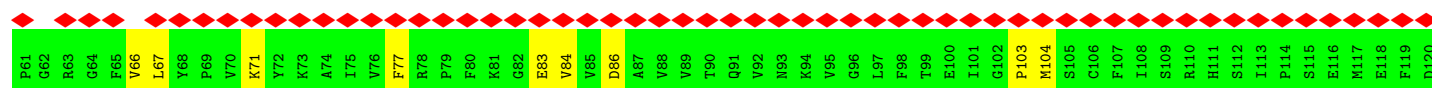
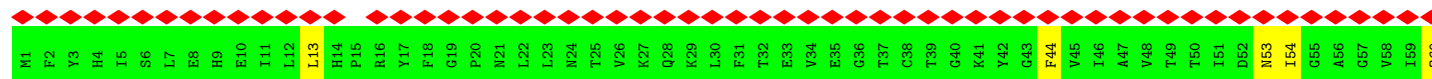
- Molecule 6: DNA-directed RNA polymerase II subunit F

Chain F: 18% 54% 10% 35%



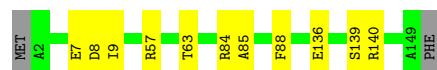
- Molecule 7: DNA-directed RNA polymerase II subunit RPB7

Chain G: 98% 89% 10%



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

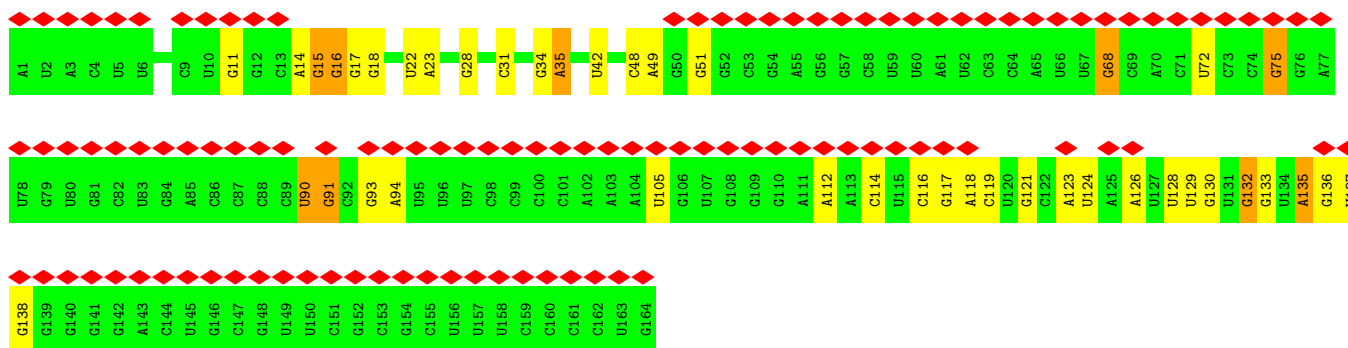
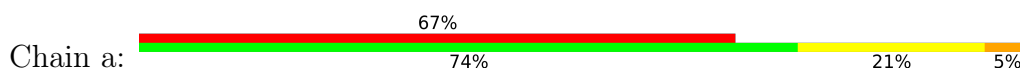
Chain H: 91% 7%



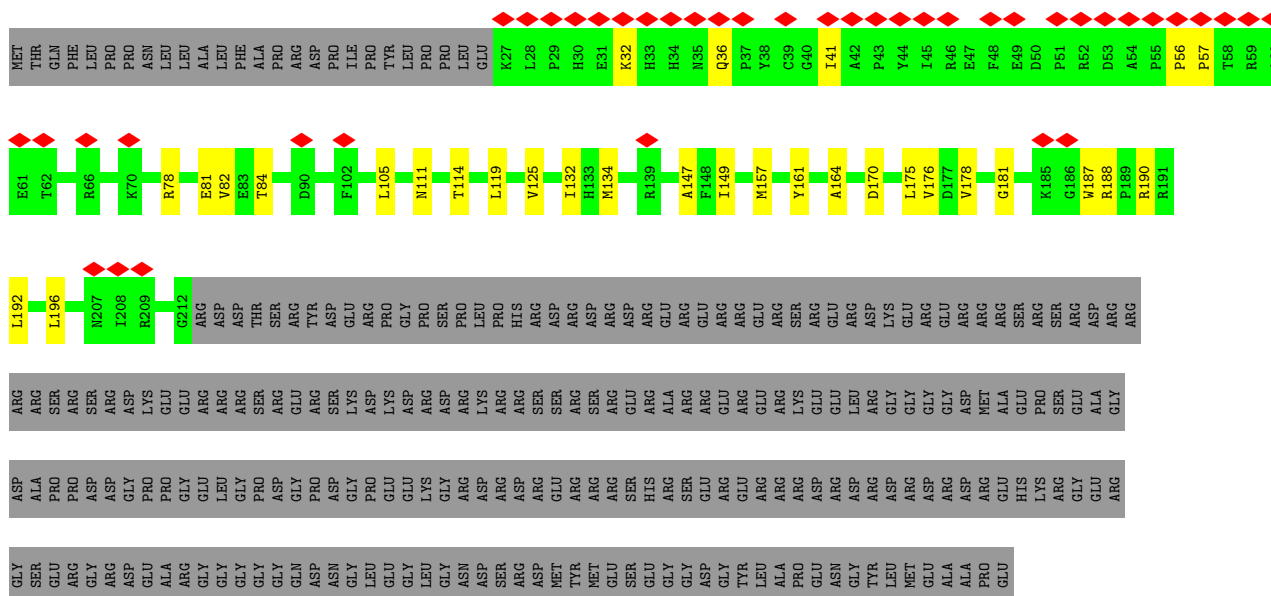
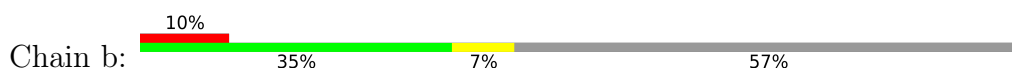
- Molecule 9: DNA-directed RNA polymerase II subunit RPB9

Chain I: 87% 6% 6%

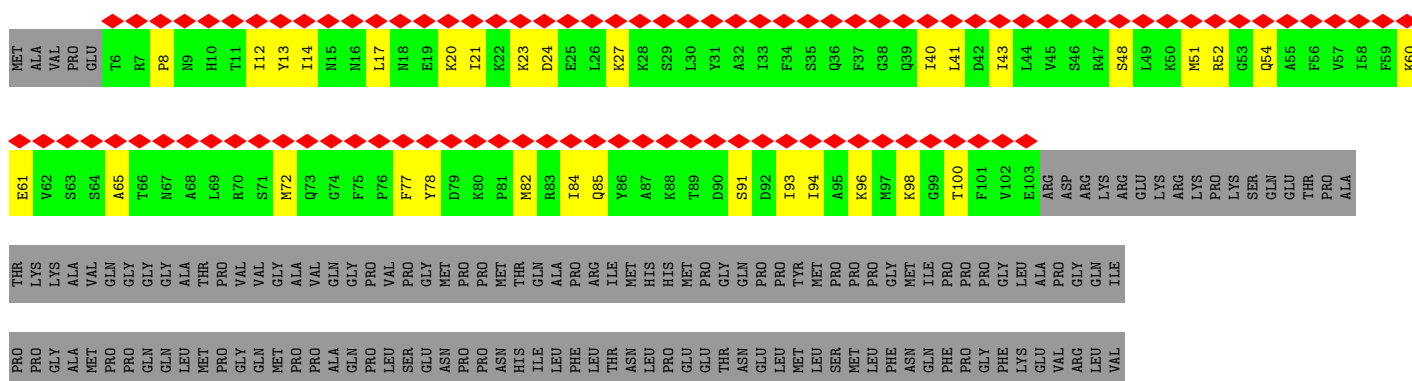




• Molecule 17: U1 small nuclear ribonucleoprotein 70 kDa



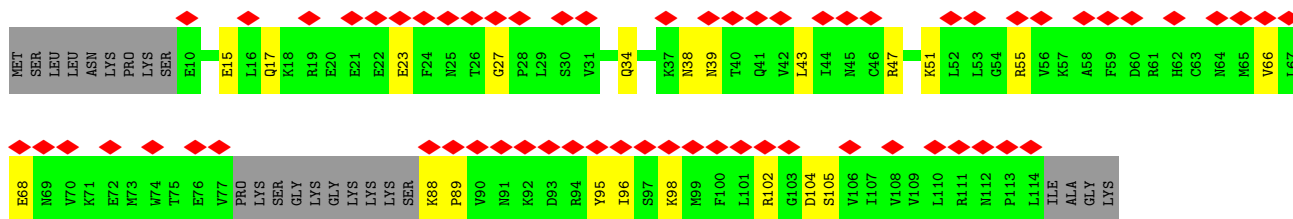
• Molecule 18: U1 small nuclear ribonucleoprotein A



PRO GLY ARG HIS ASP TLE ALA PHE VAL GLU PHE ASP ASN ASP ASN GLU VAL GLN ALA GLY ALA ALA ARG ASP ASP ALA LEU GLN GLY PHE LYS THR GLN ASN ASN ALA MET LYS LYS LYS SER PHE ALA LYS LYS

• Molecule 19: Small nuclear ribonucleoprotein Sm D2

Chain e: 



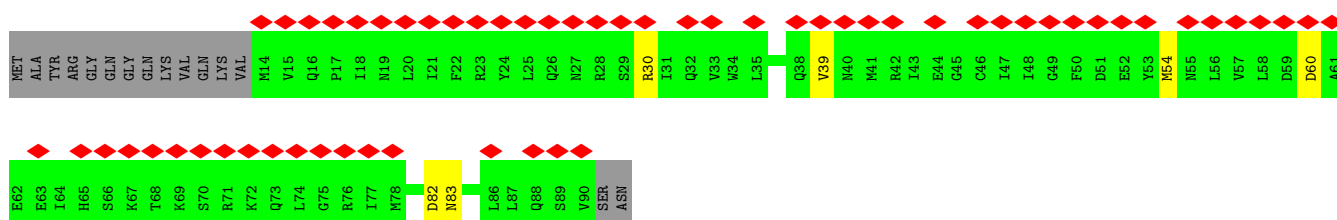
• Molecule 20: Small nuclear ribonucleoprotein F

Chain f: 



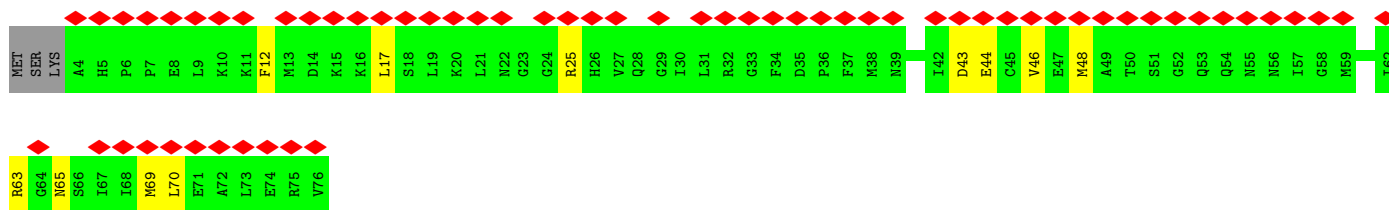
• Molecule 21: Small nuclear ribonucleoprotein E

Chain g: 



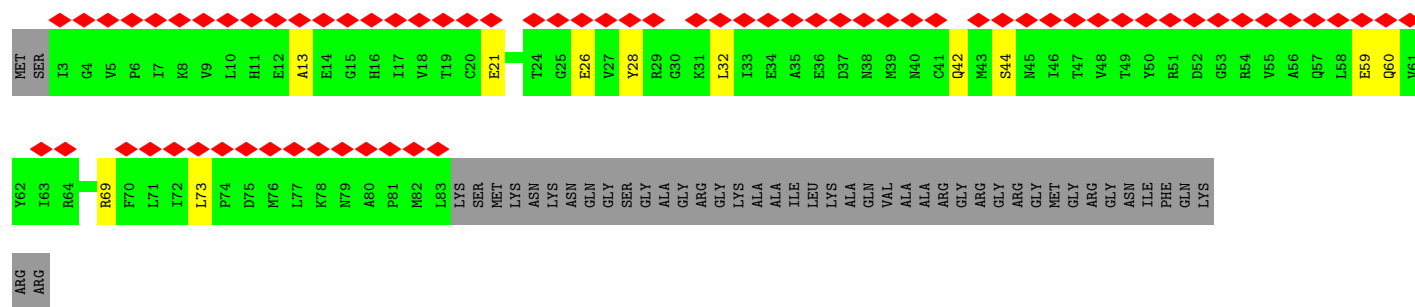
• Molecule 22: Small nuclear ribonucleoprotein G

Chain h: 

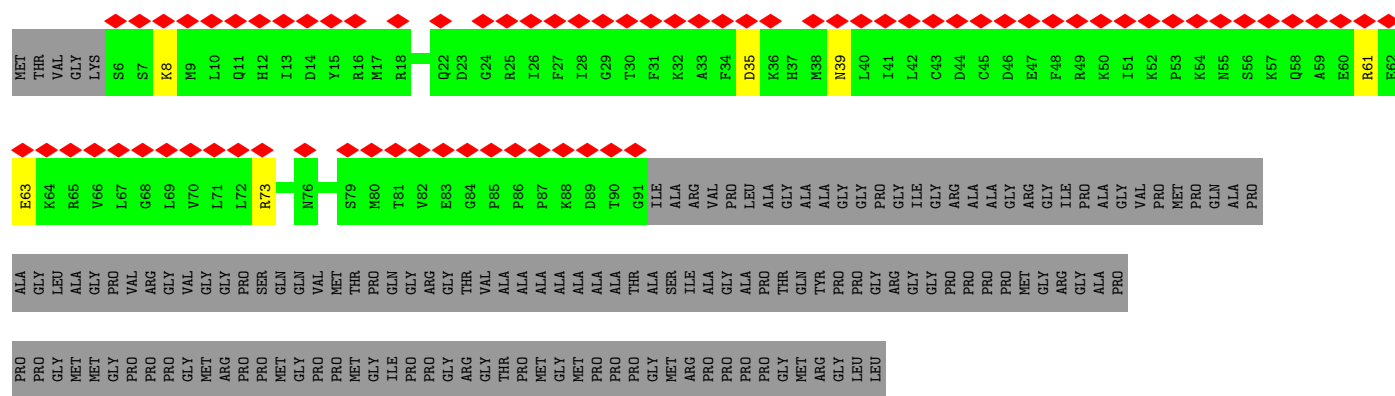


• Molecule 23: Small nuclear ribonucleoprotein Sm D3

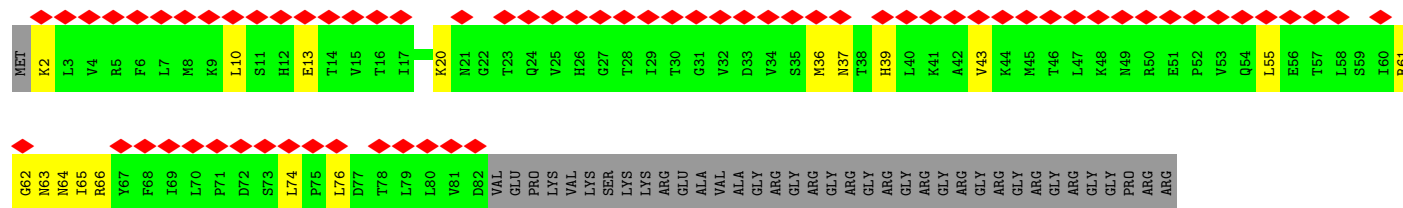
Chain i: 



- Molecule 24: Small nuclear ribonucleoprotein-associated protein



- Molecule 25: Small nuclear ribonucleoprotein Sm D1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	61596	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 ($e^-/\text{\AA}^2$)	1.01	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	41.496	Depositor
Minimum map value	-24.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.8	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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	0.09	0/11468	0.23	0/15484
2	B	0.09	0/9233	0.22	0/12463
3	C	0.09	0/2132	0.23	0/2896
4	D	0.10	0/1043	0.25	0/1400
5	E	0.08	0/1751	0.21	0/2366
6	F	0.08	0/667	0.23	0/901
7	G	0.13	0/1382	0.31	0/1874
8	H	0.10	0/1207	0.20	0/1628
9	I	0.07	0/972	0.22	0/1316
10	J	0.11	0/542	0.21	0/730
11	K	0.10	0/939	0.19	0/1271
12	L	0.12	0/394	0.29	0/524
13	N	0.15	0/864	0.35	0/1334
14	P	0.06	0/867	0.19	0/1350
15	T	0.17	0/835	0.41	0/1285
16	a	0.05	0/3891	0.15	0/6061
17	b	0.11	0/1580	0.27	0/2118
18	c	0.17	0/810	0.48	0/1084
19	e	0.10	0/786	0.30	0/1055
20	f	0.08	0/588	0.23	0/795
21	g	0.09	0/646	0.28	0/867
22	h	0.11	0/575	0.29	0/768
23	i	0.10	0/645	0.29	0/870
24	j	0.11	0/702	0.36	0/936
25	k	0.11	0/649	0.35	0/878
All	All	0.10	0/45168	0.25	0/62254

There are no bond length outliers.

There are no bond angle outliers.

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	11263	0	11391	104	0
2	B	9052	0	9087	86	0
3	C	2089	0	2031	14	0
4	D	1030	0	1016	7	0
5	E	1720	0	1737	13	0
6	F	657	0	684	10	0
7	G	1351	0	1358	13	0
8	H	1186	0	1147	7	0
9	I	949	0	879	5	0
10	J	533	0	553	6	0
11	K	920	0	942	7	0
12	L	388	0	393	5	0
13	N	769	0	414	3	0
14	P	774	0	392	11	0
15	T	749	0	417	2	0
16	a	3485	0	1762	22	0
17	b	1543	0	1514	25	0
18	c	796	0	824	25	0
19	e	777	0	800	14	0
20	f	576	0	589	8	0
21	g	638	0	657	5	0
22	h	568	0	590	9	0
23	i	637	0	652	8	0
24	j	692	0	717	4	0
25	k	641	0	681	13	0
26	A	2	0	0	0	0
26	B	1	0	0	0	0
26	C	1	0	0	0	0
26	I	2	0	0	0	0
26	J	1	0	0	0	0
26	L	1	0	0	0	0
27	A	1	0	0	0	0
All	All	43792	0	41227	362	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 4.

The worst 5 of 362 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)
2:B:223:SER:HG	2:B:350:HIS:HD1	1.04	0.93
16:a:121:G:OP1	25:k:2:LYS:NZ	2.05	0.88
16:a:90:U:O2'	16:a:91:G:OP2	1.95	0.83
2:B:942:LYS:NZ	14:P:145:U:OP1	2.13	0.81
1:A:535:MET:O	1:A:669:TYR:OH	1.98	0.81

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	1414/1970 (72%)	1378 (98%)	36 (2%)	0	100	100
2	B	1123/1174 (96%)	1099 (98%)	24 (2%)	0	100	100
3	C	256/275 (93%)	252 (98%)	4 (2%)	0	100	100
4	D	124/142 (87%)	120 (97%)	4 (3%)	0	100	100
5	E	207/210 (99%)	206 (100%)	1 (0%)	0	100	100
6	F	80/127 (63%)	77 (96%)	3 (4%)	0	100	100
7	G	169/172 (98%)	162 (96%)	7 (4%)	0	100	100
8	H	146/150 (97%)	143 (98%)	3 (2%)	0	100	100
9	I	115/125 (92%)	114 (99%)	1 (1%)	0	100	100
10	J	65/67 (97%)	64 (98%)	1 (2%)	0	100	100
11	K	113/117 (97%)	113 (100%)	0	0	100	100
12	L	44/58 (76%)	41 (93%)	3 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	b	184/437 (42%)	181 (98%)	3 (2%)	0	100	100
18	c	96/282 (34%)	94 (98%)	2 (2%)	0	100	100
19	e	91/118 (77%)	91 (100%)	0	0	100	100
20	f	72/86 (84%)	71 (99%)	1 (1%)	0	100	100
21	g	75/92 (82%)	74 (99%)	1 (1%)	0	100	100
22	h	71/76 (93%)	68 (96%)	3 (4%)	0	100	100
23	i	79/126 (63%)	78 (99%)	1 (1%)	0	100	100
24	j	84/231 (36%)	83 (99%)	1 (1%)	0	100	100
25	k	79/119 (66%)	79 (100%)	0	0	100	100
All	All	4687/6154 (76%)	4588 (98%)	99 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	1252/1749 (72%)	1252 (100%)	0	100	100
2	B	992/1027 (97%)	992 (100%)	0	100	100
3	C	237/252 (94%)	237 (100%)	0	100	100
4	D	116/126 (92%)	116 (100%)	0	100	100
5	E	191/192 (100%)	191 (100%)	0	100	100
6	F	71/111 (64%)	71 (100%)	0	100	100
7	G	152/153 (99%)	152 (100%)	0	100	100
8	H	129/131 (98%)	129 (100%)	0	100	100
9	I	105/112 (94%)	105 (100%)	0	100	100
10	J	56/56 (100%)	56 (100%)	0	100	100
11	K	104/106 (98%)	104 (100%)	0	100	100
12	L	43/55 (78%)	43 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	b	159/373 (43%)	159 (100%)	0	100	100
18	c	88/240 (37%)	87 (99%)	1 (1%)	65	74
19	e	91/110 (83%)	91 (100%)	0	100	100
20	f	63/74 (85%)	63 (100%)	0	100	100
21	g	72/84 (86%)	72 (100%)	0	100	100
22	h	63/66 (96%)	63 (100%)	0	100	100
23	i	71/101 (70%)	71 (100%)	0	100	100
24	j	78/169 (46%)	78 (100%)	0	100	100
25	k	76/101 (75%)	76 (100%)	0	100	100
All	All	4209/5388 (78%)	4208 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	c	8	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
22	h	56	ASN
23	i	45	ASN
24	j	76	ASN
2	B	1160	GLN
2	B	1145	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	P	36/145 (24%)	11 (30%)	5 (13%)
16	a	163/164 (99%)	32 (19%)	0
All	All	199/309 (64%)	43 (21%)	5 (2%)

5 of 43 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
14	P	111	C

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Mol	Chain	Res	Type
14	P	112	G
14	P	124	U
14	P	127	A
14	P	128	C

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	P	110	C
14	P	126	A
14	P	127	A
14	P	135	G
14	P	137	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 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 ⓘ

There are no chain breaks in this entry.

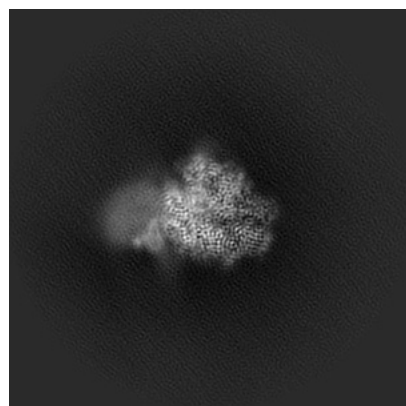
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11972. These allow visual inspection of the internal detail of the map and identification of artifacts.

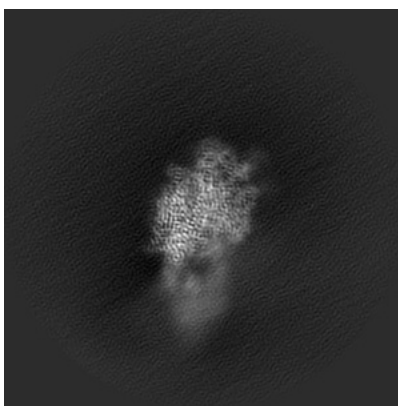
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

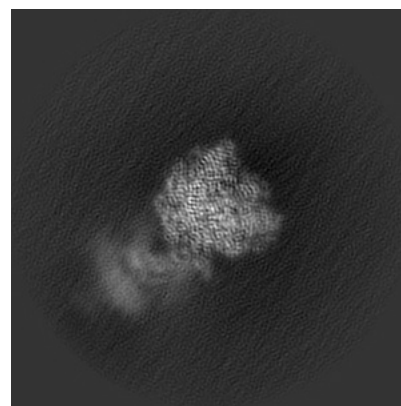
6.1.1 Primary map



X

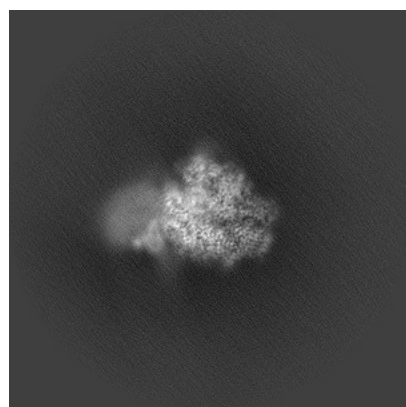


Y

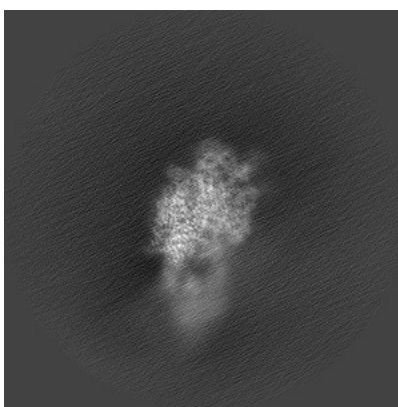


Z

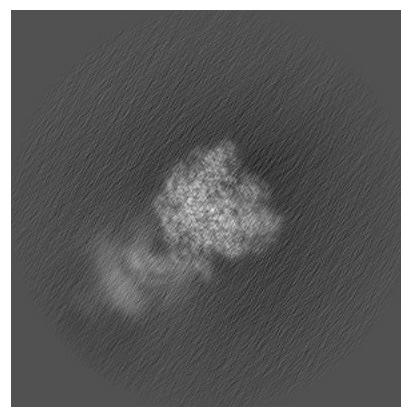
6.1.2 Raw map



X



Y

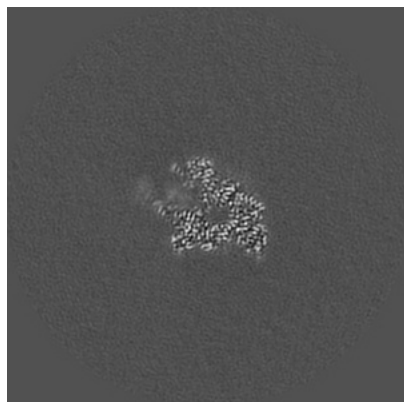


Z

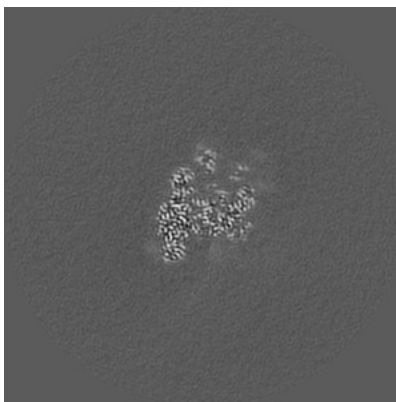
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

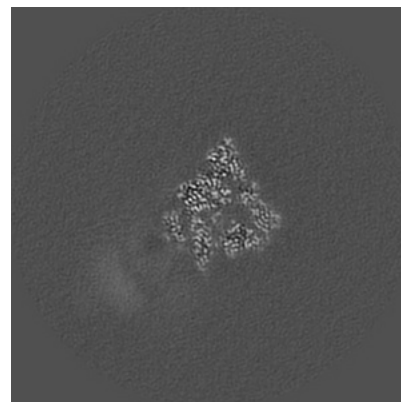
6.2.1 Primary map



X Index: 200

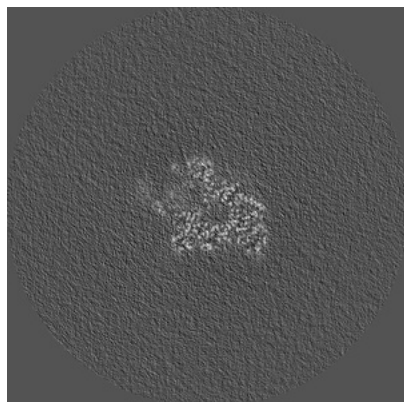


Y Index: 200

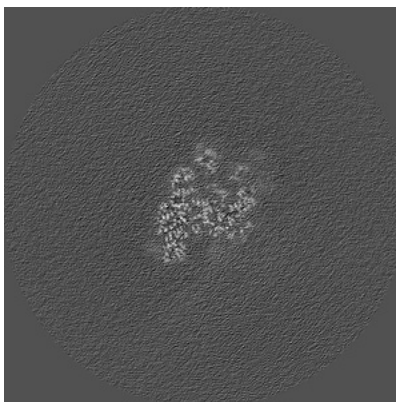


Z Index: 200

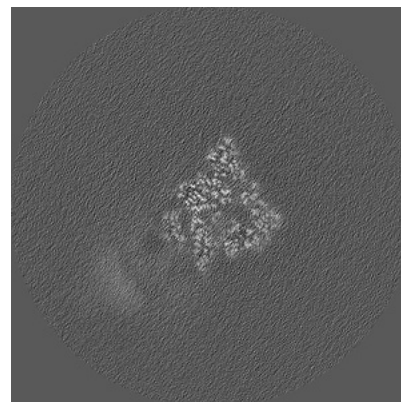
6.2.2 Raw map



X Index: 200



Y Index: 200

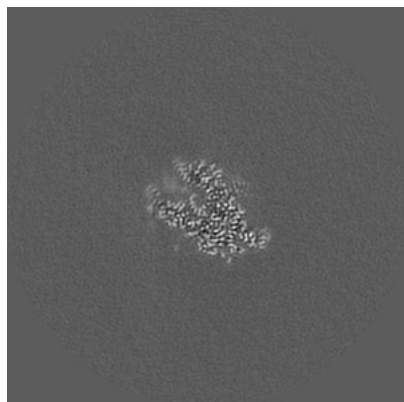


Z Index: 200

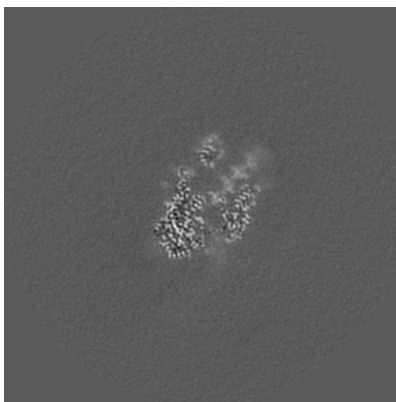
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

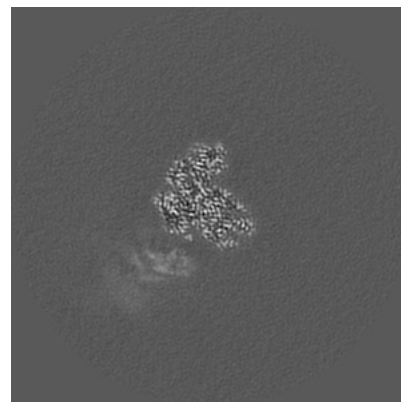
6.3.1 Primary map



X Index: 187

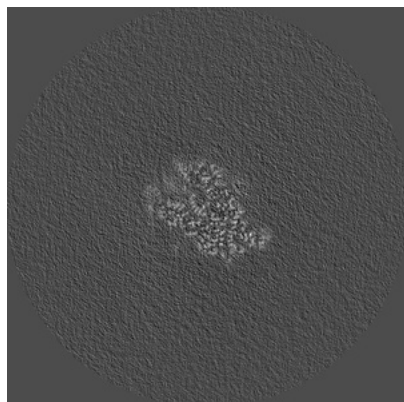


Y Index: 192

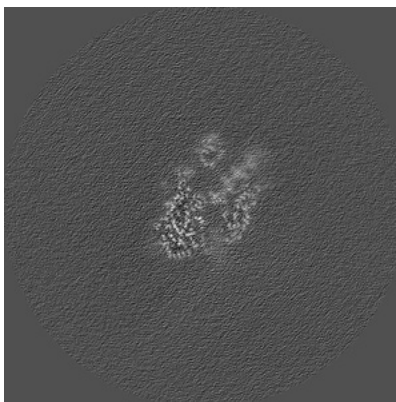


Z Index: 171

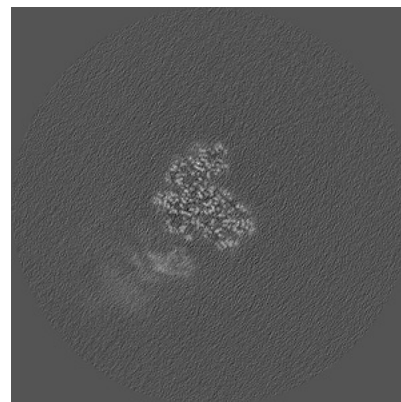
6.3.2 Raw map



X Index: 187



Y Index: 192

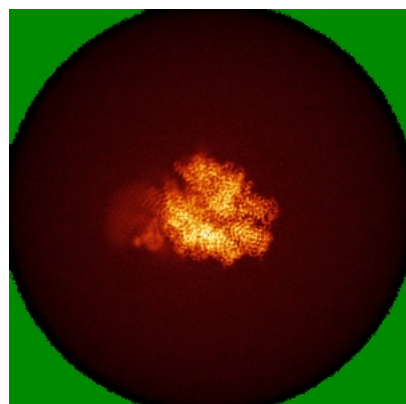


Z Index: 172

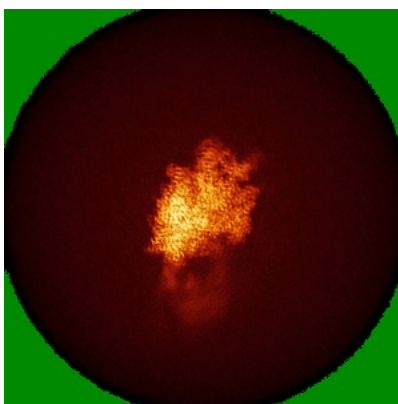
The images above show the largest variance slices of the map in three orthogonal directions.

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

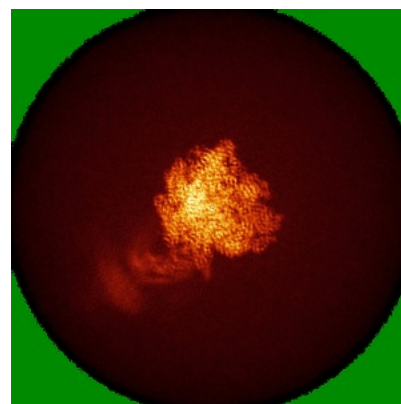
6.4.1 Primary map



X

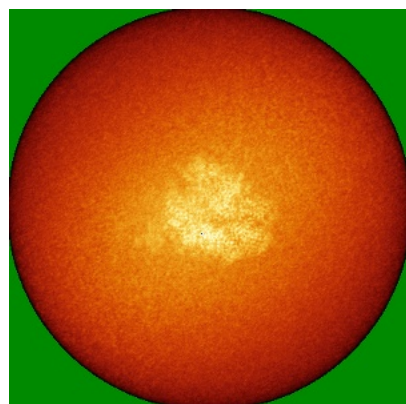


Y

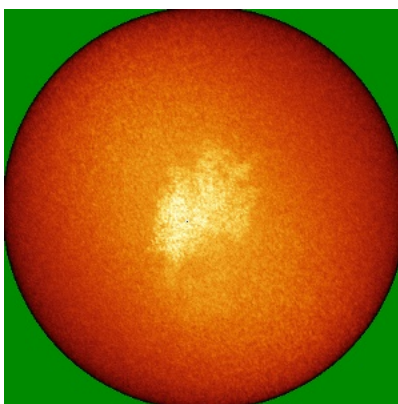


Z

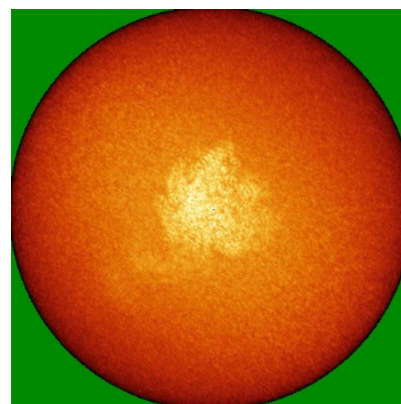
6.4.2 Raw map



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 3.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

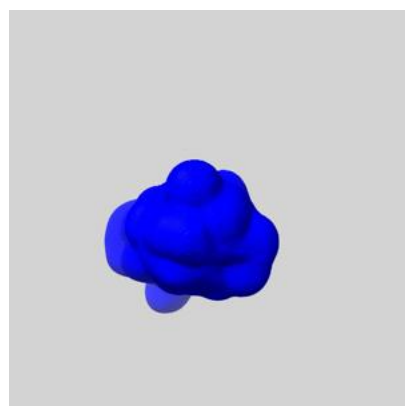
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

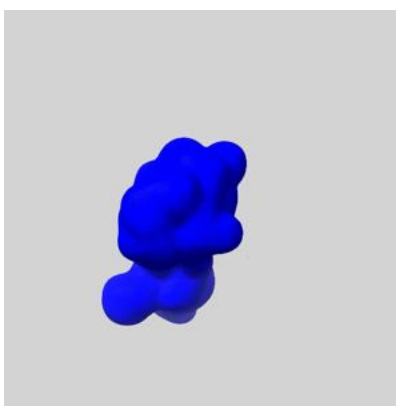
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

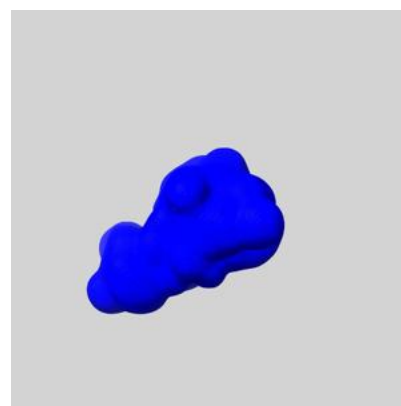
6.6.1 emd_11972_msk_1.map [i](#)



X



Y

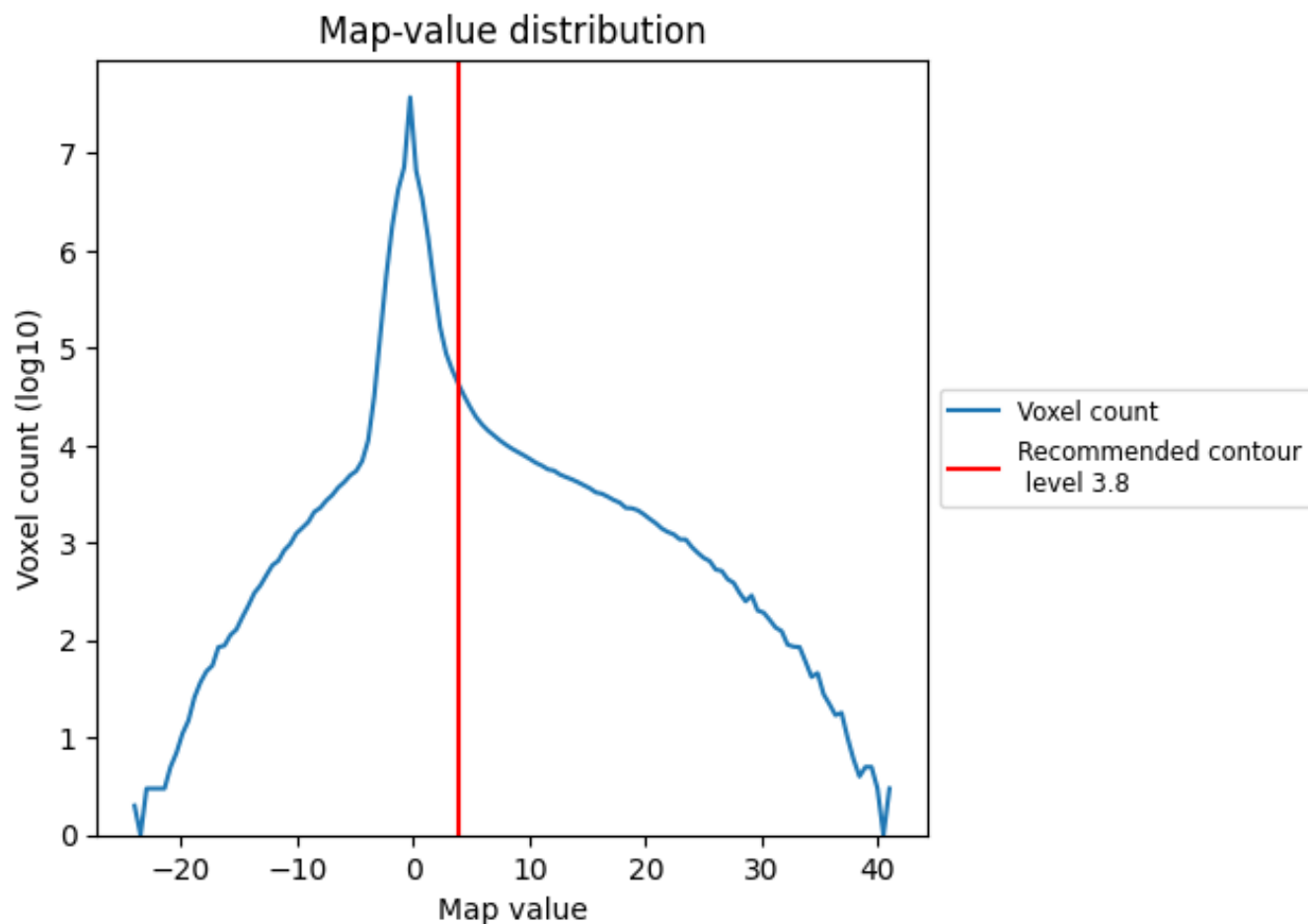


Z

7 Map analysis [i](#)

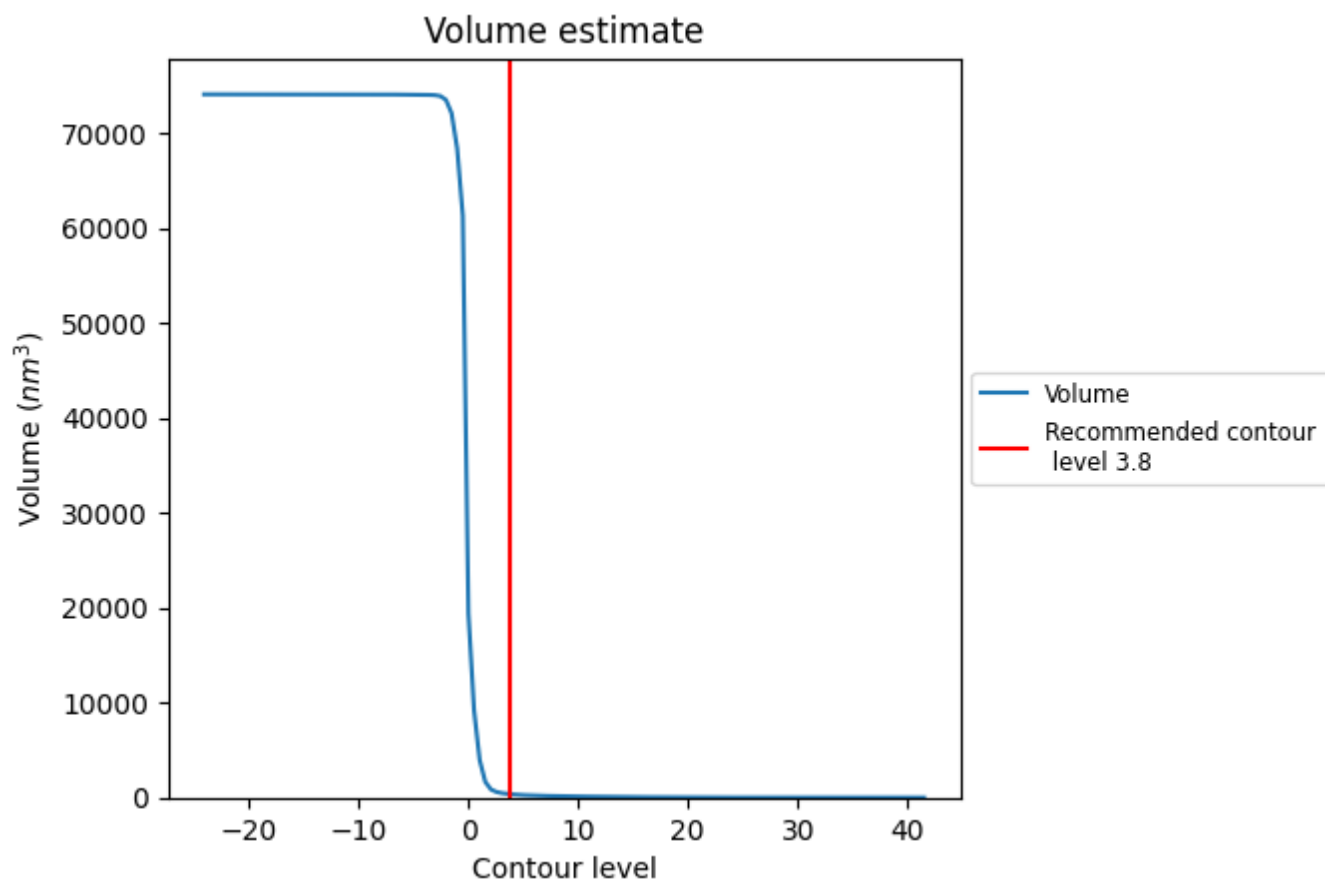
This section contains the results of statistical analysis of the map.

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.

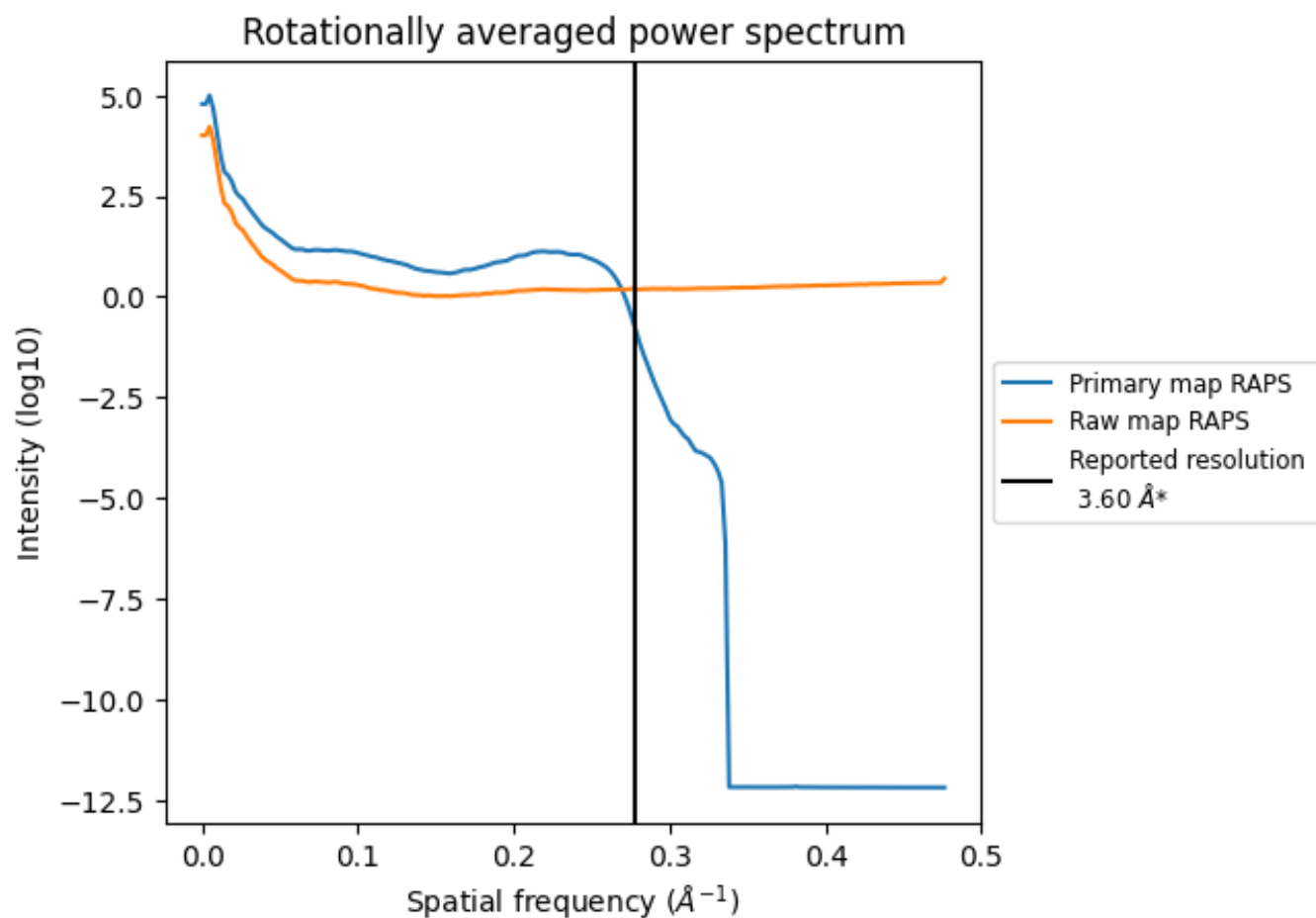
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 363 nm³; this corresponds to an approximate mass of 328 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 ⓘ

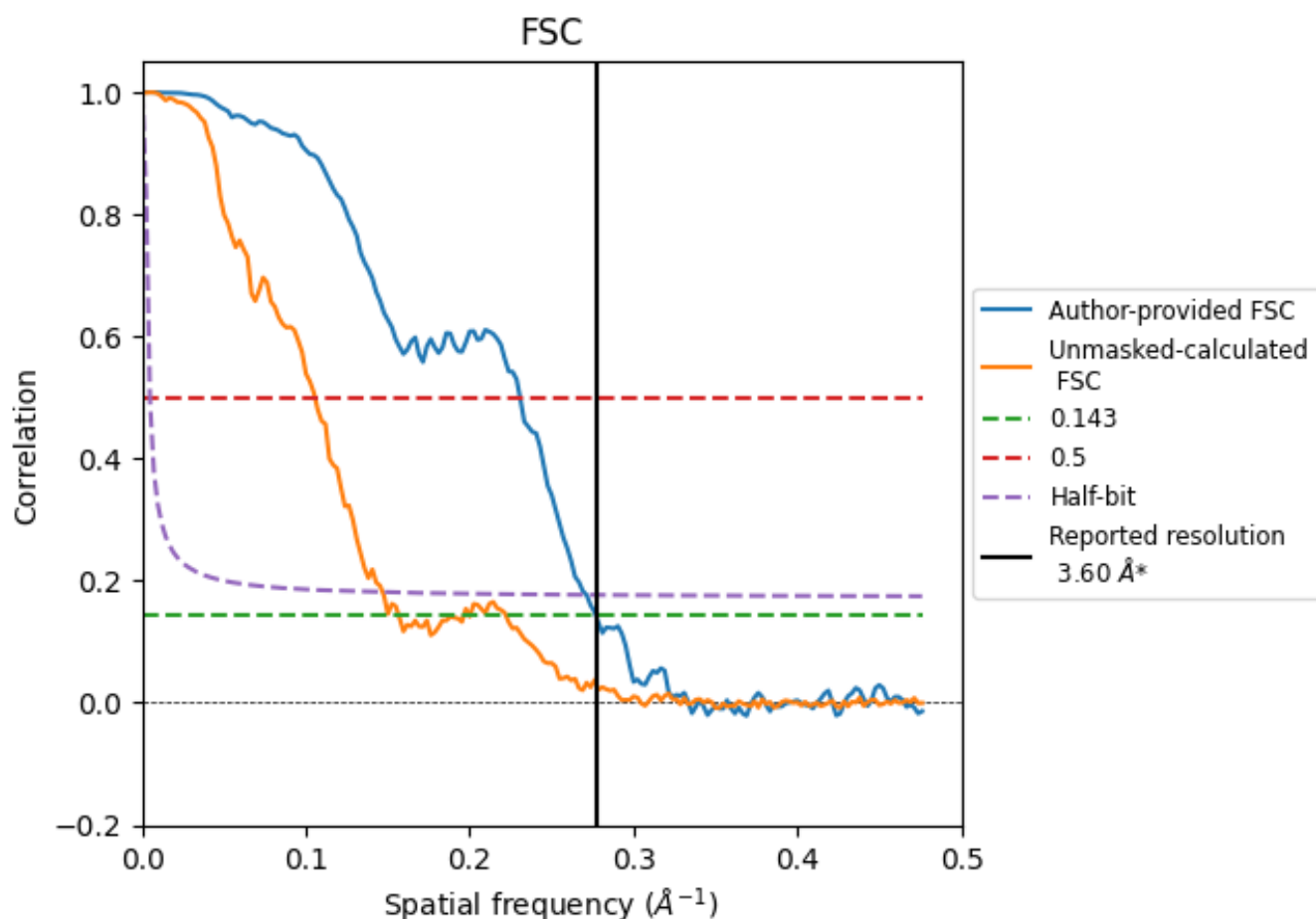


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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](#)

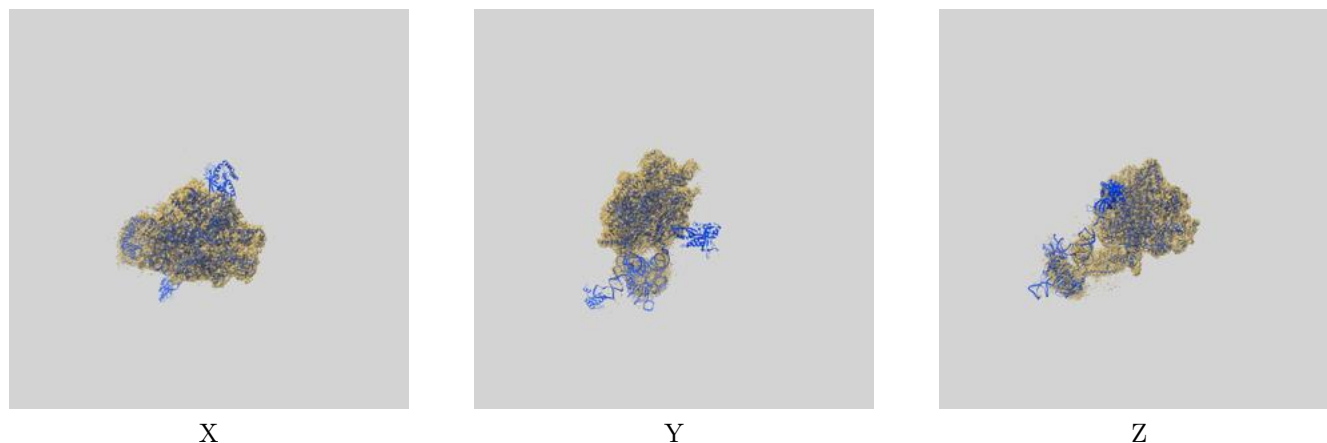
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.61	4.33	3.69
Unmasked-calculated*	6.39	9.48	6.81

*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 6.39 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

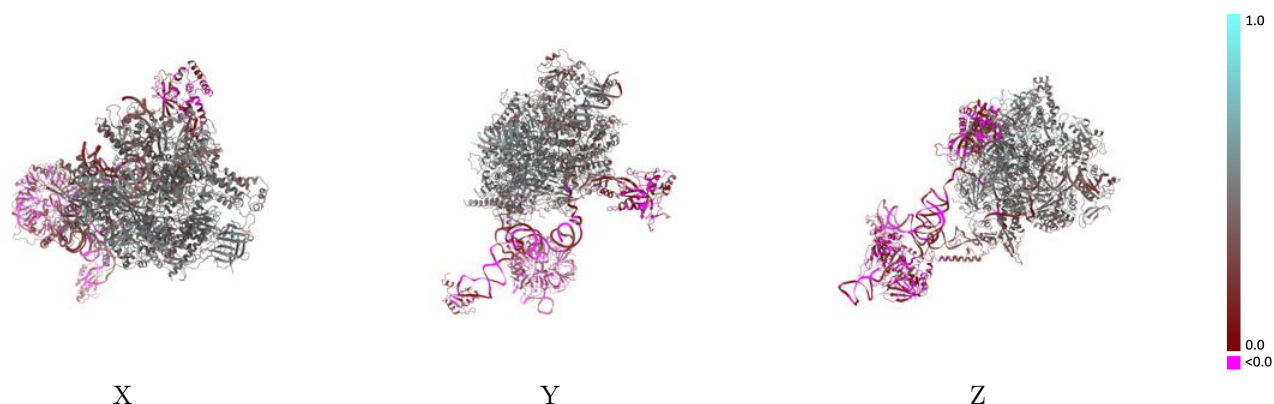
This section contains information regarding the fit between EMDB map EMD-11972 and PDB model 7B0Y. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



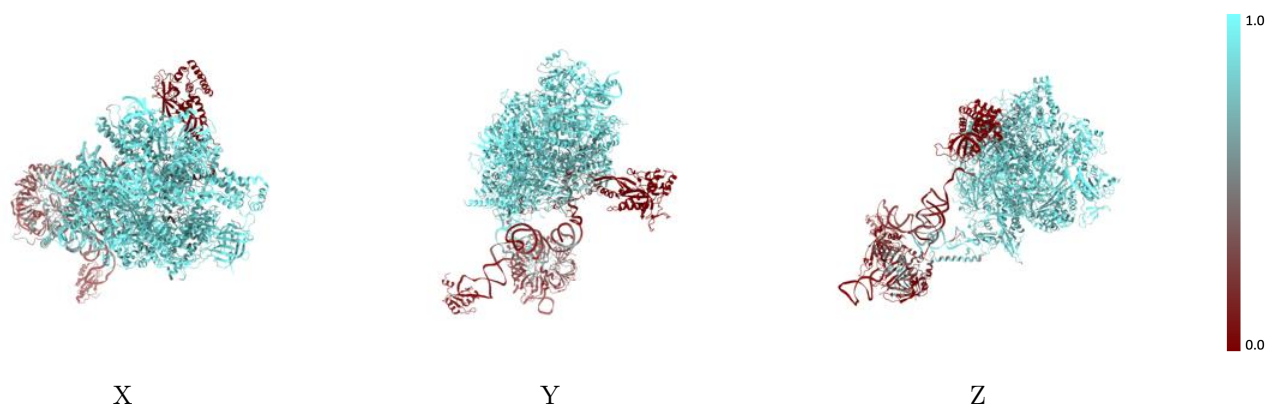
The images above show the 3D surface view of the map at the recommended contour level 3.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



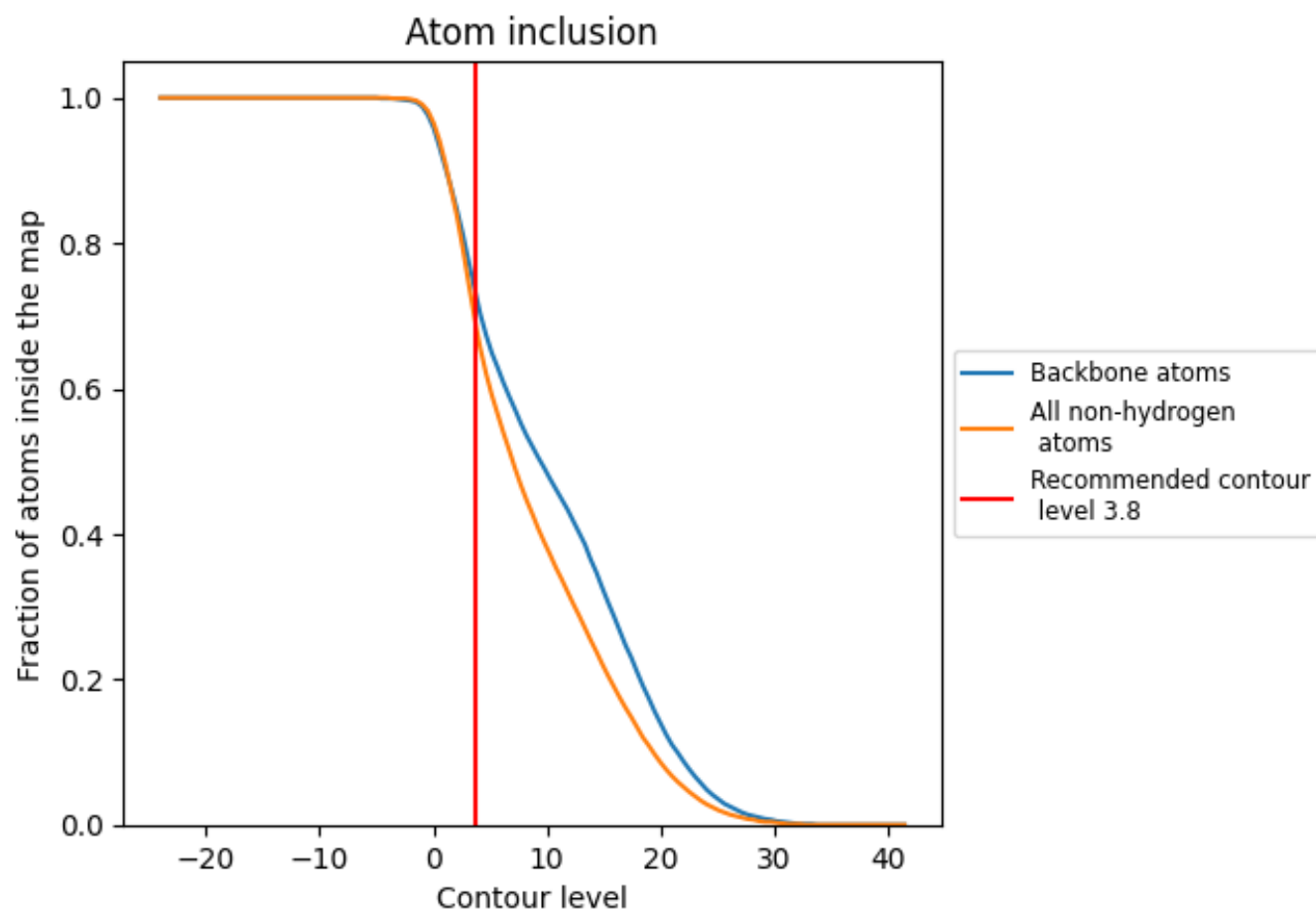
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% 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 (3.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6830	 0.3440
A	 0.8710	 0.4600
B	 0.8900	 0.4630
C	 0.8880	 0.4750
D	 0.0000	 0.1000
E	 0.9150	 0.4650
F	 0.5670	 0.4010
G	 0.0300	 0.1220
H	 0.9080	 0.4750
I	 0.9100	 0.4500
J	 0.8920	 0.4790
K	 0.8010	 0.4350
L	 0.8790	 0.4500
N	 0.8610	 0.2670
P	 0.4500	 0.1810
T	 0.9440	 0.3730
a	 0.2980	 0.0550
b	 0.6780	 0.2420
c	 0.0000	 0.1130
e	 0.2970	 0.0300
f	 0.2440	 0.0190
g	 0.2460	 0.0730
h	 0.1910	 0.0600
i	 0.1590	 0.0640
j	 0.1650	 0.0720
k	 0.1600	 0.0810

