



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:18 PM UTC

PDB ID : 8R0B / pdb_00008r0b
EMDB ID : EMD-18789
Title : Cryo-EM structure of the cross-exon pre-B+ATP complex
Authors : Zhang, Z.; Kumar, V.; Dybkov, O.; Will, C.L.; Zhong, J.; Ludwig, S.; Urlaub, H.; Kastner, B.; Stark, H.; Luehrmann, R.
Deposited on : 2023-10-31
Resolution : 4.40 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:

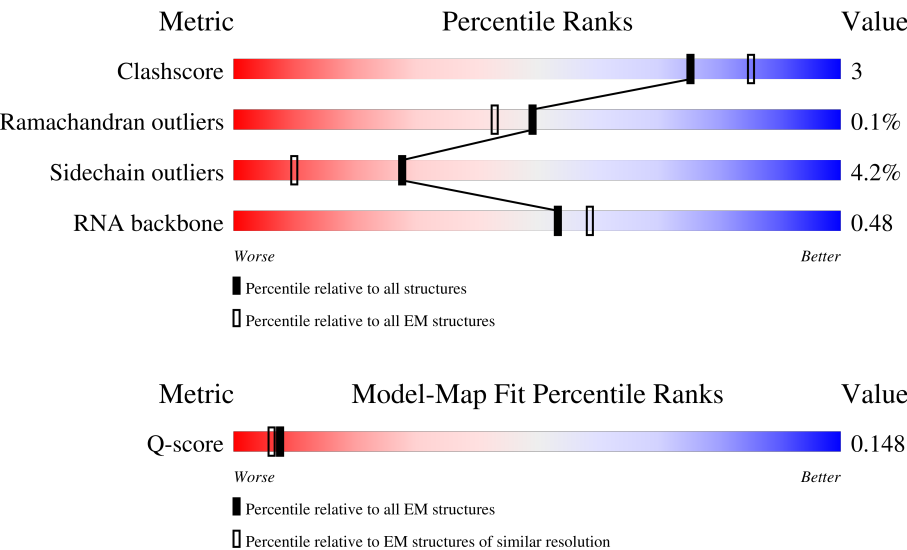
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.40 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.



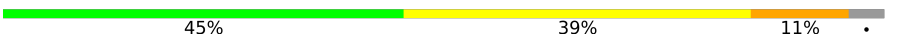
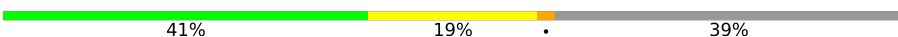
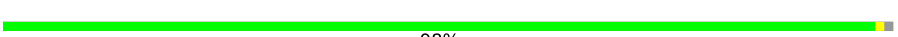
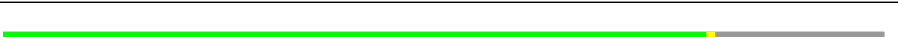
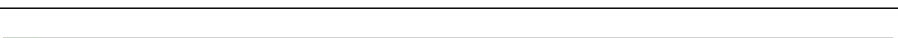
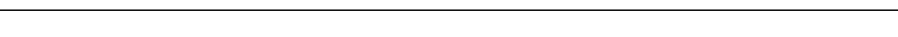
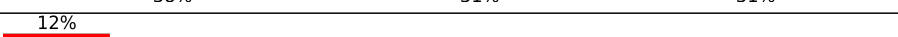
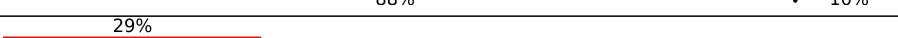
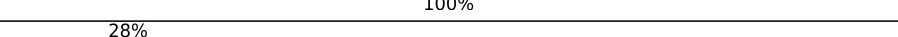
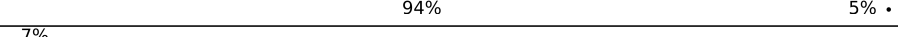
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3132 (3.91 - 4.90)

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	2335	94% 5%
2	B	2136	79% 20%
3	2	188	26% 37% 14% 48%

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Mol	Chain	Length	Quality of chain
4	4	144	
5	5	117	
6	6	106	
7	7	793	
8	8	464	
9	C	972	
10	D	142	
11	E	357	
12	G	820	
13	M	128	
14	U	565	
15	W	177	
16	Z	347	
17	z	13	
18	66	80	
19	67	103	
20	62	95	
21	63	102	
22	68	96	
23	64	139	
24	65	91	
25	B4	424	
26	9	501	
27	B2	895	
28	B5	86	

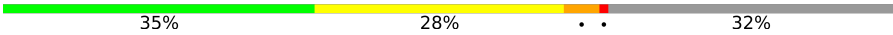
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Mol	Chain	Length	Quality of chain
29	B3	1217	
30	BP	110	
31	B1	1304	
32	B6	125	
33	22	118	
33	42	118	
33	52	118	
34	2B	225	
35	2f	86	
35	4f	86	
35	5f	86	
36	2b	240	
36	4b	240	
36	5b	240	
37	23	126	
37	43	126	
37	53	126	
38	2g	76	
38	4g	76	
38	5g	76	
39	2e	92	
39	4e	92	
39	5e	92	
40	21	119	
40	41	119	

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Mol	Chain	Length	Quality of chain
40	51	119	 35% 28% 32%
41	2A	255	 64% 36%
42	F	522	 75% 21%
43	J	683	 31% 67%
44	L	499	 74% 25%
45	N	941	 87% 11%
46	S	800	 18% 82%

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 80460 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 Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	2218	Total	C	N	O	0	0
			10977	6541	2218	2218		

- Molecule 2 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	1714	Total	C	N	O	0	0
			8644	5216	1714	1714		

- Molecule 3 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	98	Total	C	N	O	P	0	0
			2072	926	349	699	98		

- Molecule 4 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	128	Total	C	N	O	P	0	0
			2718	1216	477	898	127		

- Molecule 5 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	112	Total	C	N	O	P	0	0
			2356	1055	390	799	112		

- Molecule 6 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	65	Total	C	N	O	P	0	0
			1392	622	253	452	65		

- Molecule 7 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	7	230	Total	C	N	O	0	0
			1158	698	230	230		

- Molecule 8 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	8	144	Total	C	N	O	0	0
			729	441	144	144		

- Molecule 9 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	C	836	Total	C	N	O	0	0
			4223	2551	836	836		

- Molecule 10 is a protein called Thioredoxin-like protein 4A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	D	141	Total	C	N	O	0	0
			708	426	141	141		

- Molecule 11 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	E	307	Total	C	N	O	0	0
			1531	917	307	307		

- Molecule 12 is a protein called Probable ATP-dependent RNA helicase DDX23.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	G	57	Total	C	N	O	0	0
			283	169	57	57		

- Molecule 13 is a protein called NHP2-like protein 1, N-terminally processed.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	124	Total	C	N	O	0	0
			627	379	124	124		

- Molecule 14 is a protein called Ubiquitin carboxyl-terminal hydrolase 39.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	U	456	Total	C	N	O	0	0
			2308	1396	456	456		

- Molecule 15 is a protein called Peptidyl-prolyl cis-trans isomerase H.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	W	169	Total	C	N	O	0	0
			844	506	169	169		

- Molecule 16 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Z	15	Total	C	N	O	P	0	0
			314	141	51	107	15		

- Molecule 17 is a RNA chain called 5'ss oligo.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	z	13	Total	C	N	O	P	0	0
			286	127	57	89	13		

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	66	72	Total	C	N	O	0	0
			357	213	72	72		

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	67	77	Total	C	N	O	0	0
			384	230	77	77		

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	62	95	Total	C	N	O	0	0
			478	288	95	95		

- Molecule 21 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	63	85	Total	C	N	O	0	0
			429	259	85	85		

- Molecule 22 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	68	95	Total	C	N	O	0	0
			469	279	95	95		

- Molecule 23 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	64	73	Total	C	N	O	0	0
			369	223	73	73		

- Molecule 24 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	65	76	Total	C	N	O	0	0
			378	226	76	76		

- Molecule 25 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	B4	78	Total	C	N	O	0	0
			391	235	78	78		

- Molecule 26 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	9	383	Total	C	N	O	0	0
			1920	1154	383	383		

- Molecule 27 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	B2	208	Total	C	N	O	0	0
			1072	656	208	208		

- Molecule 28 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	B5	69	Total	C	N	O	0	0
			347	209	69	69		

- Molecule 29 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	B3	1186	Total	C	N	O	0	0
			5969	3597	1186	1186		

- Molecule 30 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	BP	100	Total	C	N	O	0	0
			498	298	100	100		

- Molecule 31 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	B1	870	Total	C	N	O	0	0
			4383	2643	870	870		

- Molecule 32 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	B6	90	Total	C	N	O	0	0
			455	275	90	90		

- Molecule 33 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	22	95	Total	C	N	O	0	0
			482	292	95	95		
33	42	92	Total	C	N	O	0	0
			463	279	92	92		
33	52	98	Total	C	N	O	S	0
			796	498	144	148	6	0

- Molecule 34 is a protein called U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	2B	92	Total	C	N	O	0	0
			461	277	92	92		

- Molecule 35 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace	
35	2f	72	Total	C	N	O	0	0	
			359	215	72	72			
35	4f	72	Total	C	N	O	0	0	
			359	215	72	72			
35	5f	73	Total	C	N	O	S	0	0
			567	367	94	101	5		

- Molecule 36 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	2b	82	Total	C	N	O		0	0
			413	249	82	82			
36	4b	79	Total	C	N	O		0	0
			396	238	79	79			
36	5b	73	Total	C	N	O	S	0	0
			594	376	108	103	7		

- Molecule 37 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	23	83	Total	C	N	O		0	0
			415	249	83	83			
37	43	83	Total	C	N	O		0	0
			415	249	83	83			
37	53	84	Total	C	N	O	S	0	0
			657	412	116	123	6		

- Molecule 38 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2g	73	Total	C	N	O		0	0
			364	218	73	73			
38	4g	74	Total	C	N	O		0	0
			369	221	74	74			
38	5g	74	Total	C	N	O	S	0	0
			577	364	104	103	6		

- Molecule 39 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace	
39	2e	81	Total	C	N	O	0	0	
			403	241	81	81			
39	4e	76	Total	C	N	O	0	0	
			378	226	76	76			
39	5e	77	Total	C	N	O	S	0	0
			638	405	113	115	5		

- Molecule 40 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	21	80	Total	C	N	O		0	0
			402	242	80	80			
40	41	81	Total	C	N	O		0	0
			407	245	81	81			
40	51	81	Total	C	N	O	S	0	0
			641	408	112	118	3		

- Molecule 41 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	2A	162	Total	C	N	O	0	0
			816	492	162	162		

- Molecule 42 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	F	412	Total	C	N	O	0	0
			2060	1236	412	412		

- Molecule 43 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	J	224	Total	C	N	O	0	0
			1121	673	224	224		

- Molecule 44 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

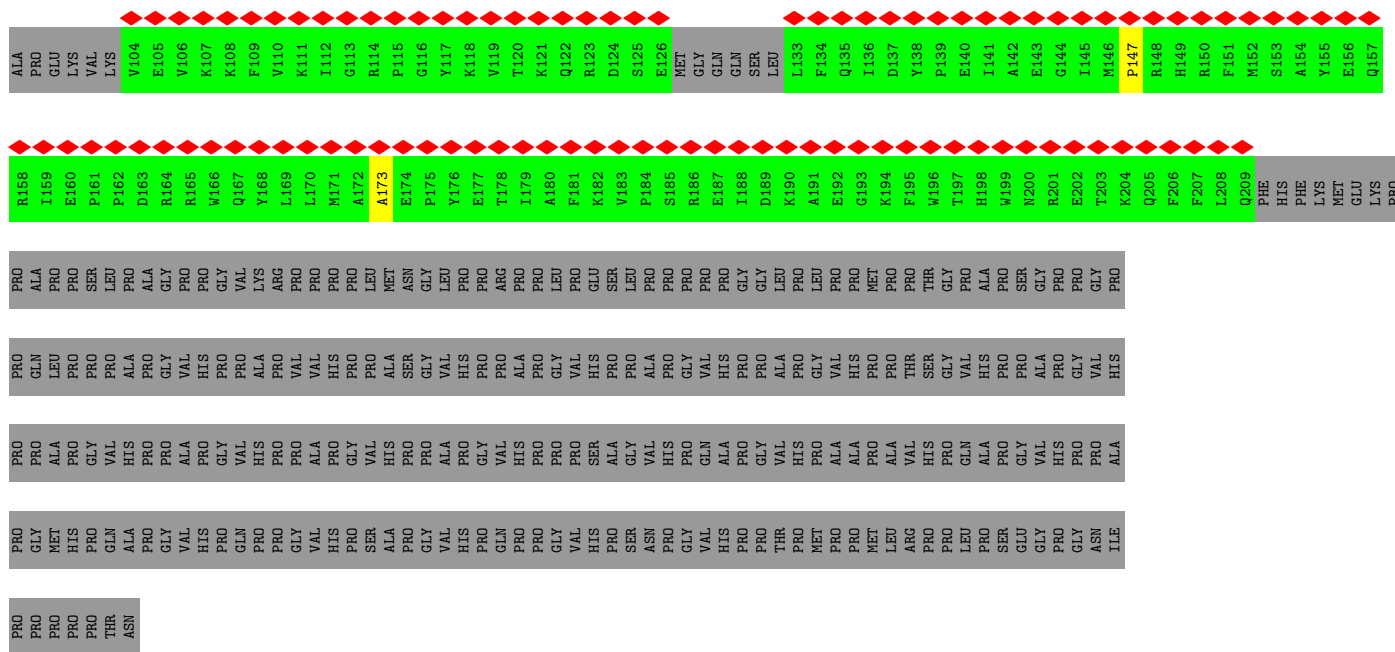
Mol	Chain	Residues	Atoms				AltConf	Trace
44	L	376	Total	C	N	O	0	0
			1887	1135	376	376		

- Molecule 45 is a protein called Pre-mRNA-processing factor 6.

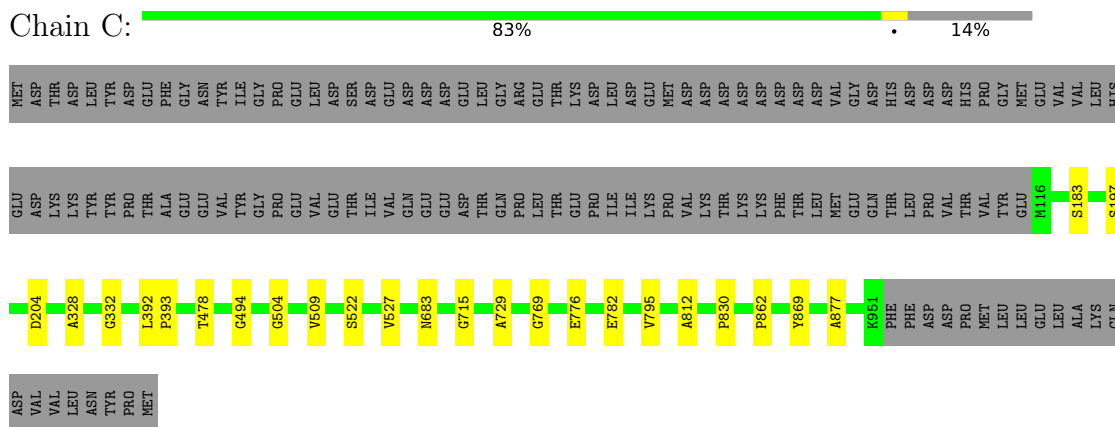
Mol	Chain	Residues	Atoms				AltConf	Trace
45	N	834	Total	C	N	O	0	0
			4207	2539	834	834		

- Molecule 46 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

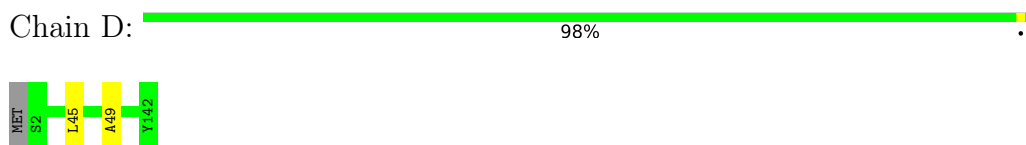
Mol	Chain	Residues	Atoms				AltConf	Trace
46	S	148	Total	C	N	O	0	0
			744	448	148	148		



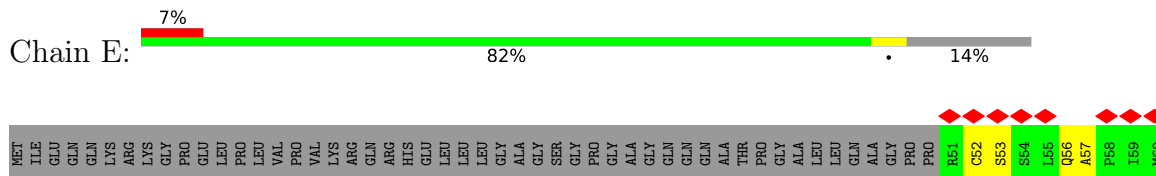
- Molecule 9: 116 kDa U5 small nuclear ribonucleoprotein component

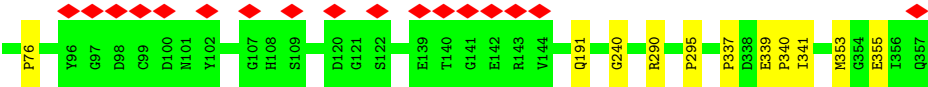


- Molecule 10: Thioredoxin-like protein 4A

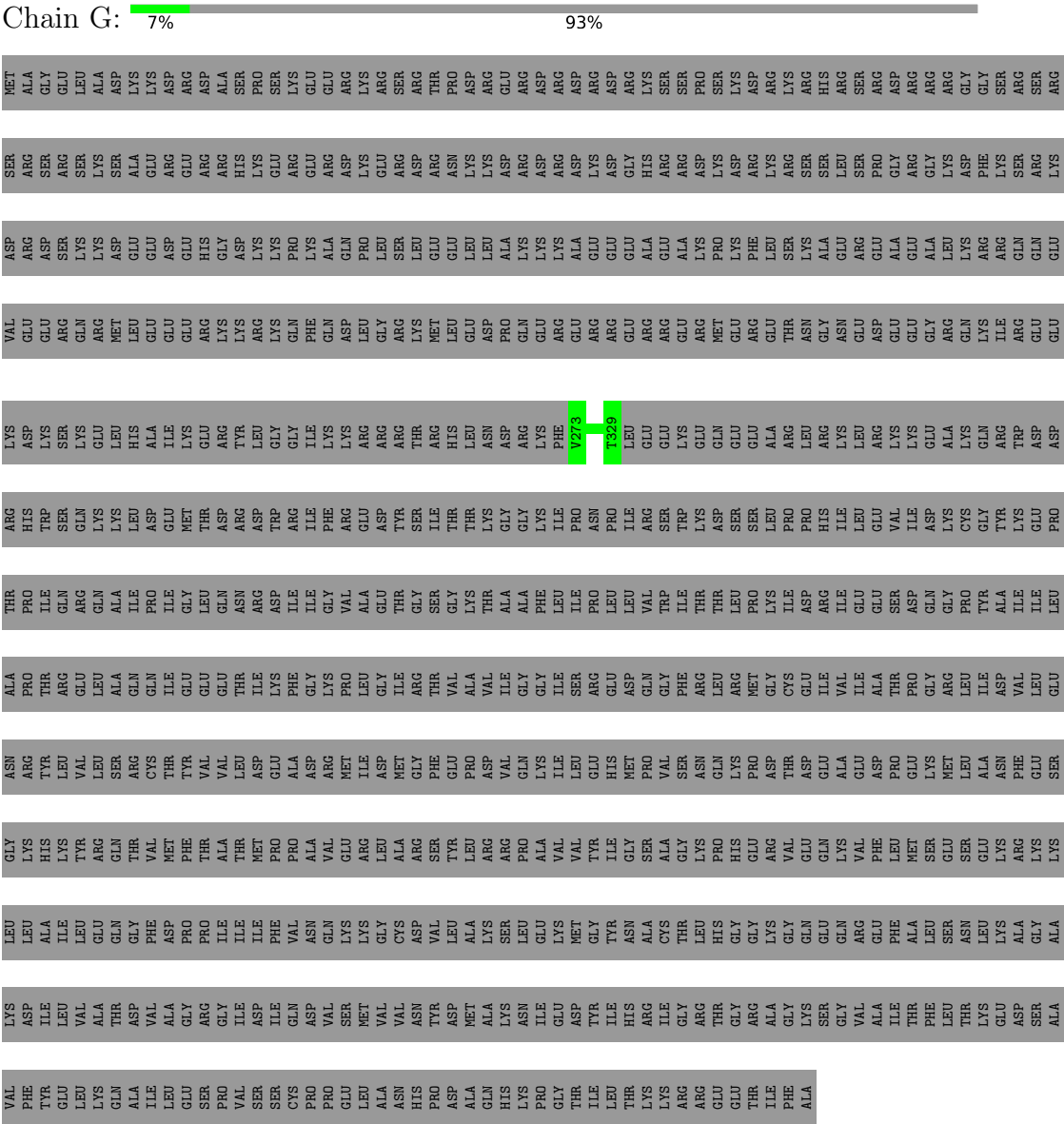


- Molecule 11: U5 small nuclear ribonucleoprotein 40 kDa protein

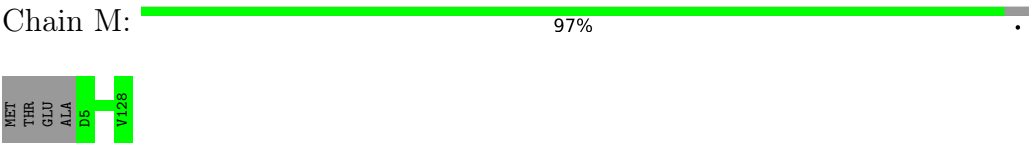




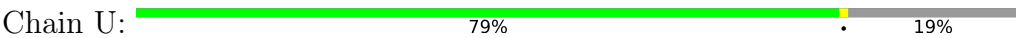
● Molecule 12: Probable ATP-dependent RNA helicase DDX23

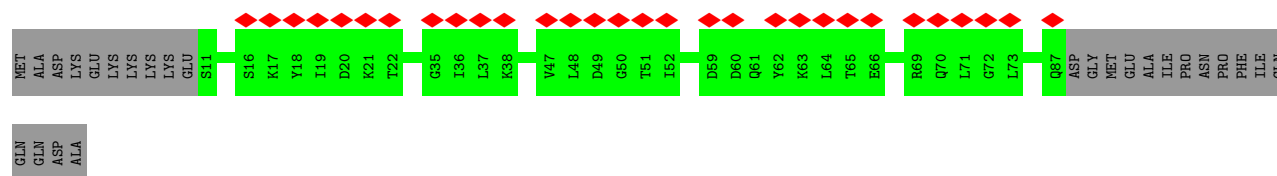


● Molecule 13: NHP2-like protein 1, N-terminally processed

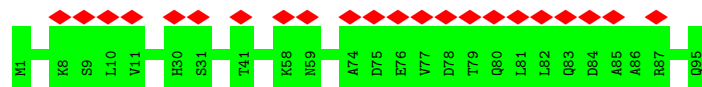


● Molecule 14: Ubiquitin carboxyl-terminal hydrolase 39

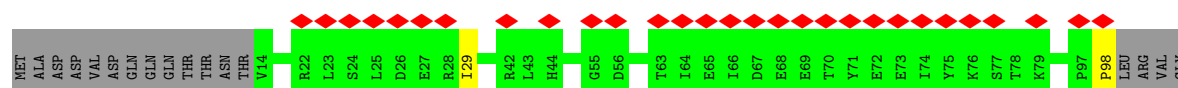
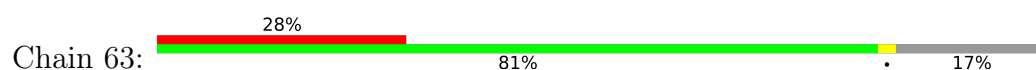




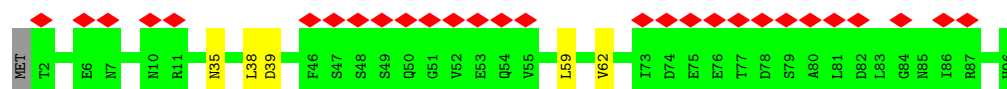
- Molecule 20: U6 snRNA-associated Sm-like protein LSm2



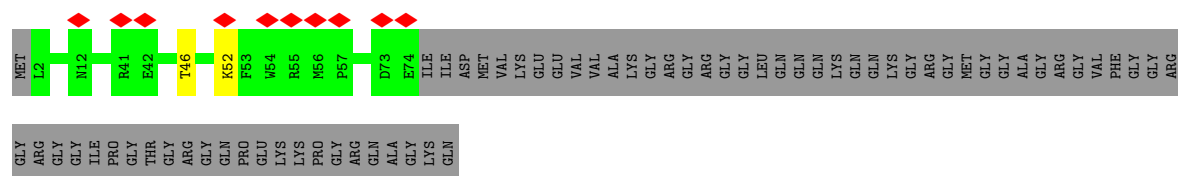
- Molecule 21: U6 snRNA-associated Sm-like protein LSm3



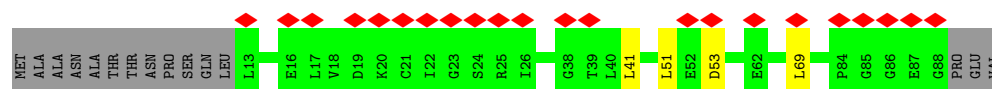
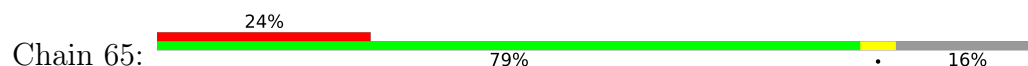
- Molecule 22: U6 snRNA-associated Sm-like protein LSm8



- Molecule 23: U6 snRNA-associated Sm-like protein LSm4



- Molecule 24: U6 snRNA-associated Sm-like protein LSm5

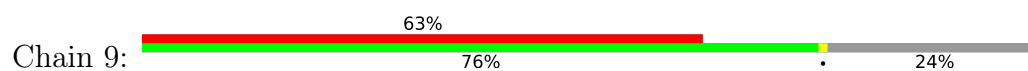


- Molecule 25: Splicing factor 3B subunit 4



PRO	PRO	PRO	PRO	LEU	MET	PRO	PRO	HIS	GLY	GLY	TYR	THR	GLY	PRO	PRO	GLY	PRO	GLY	GLY	PRO	PRO	GLN	ARG	PRO	GLY	GLY	PRO	GLY	GLY	THR	PRO	PRO	PRO	PRO	ARG	GLY	PRO	PRO	GLN	LEU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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• Molecule 26: Splicing factor 3A subunit 3

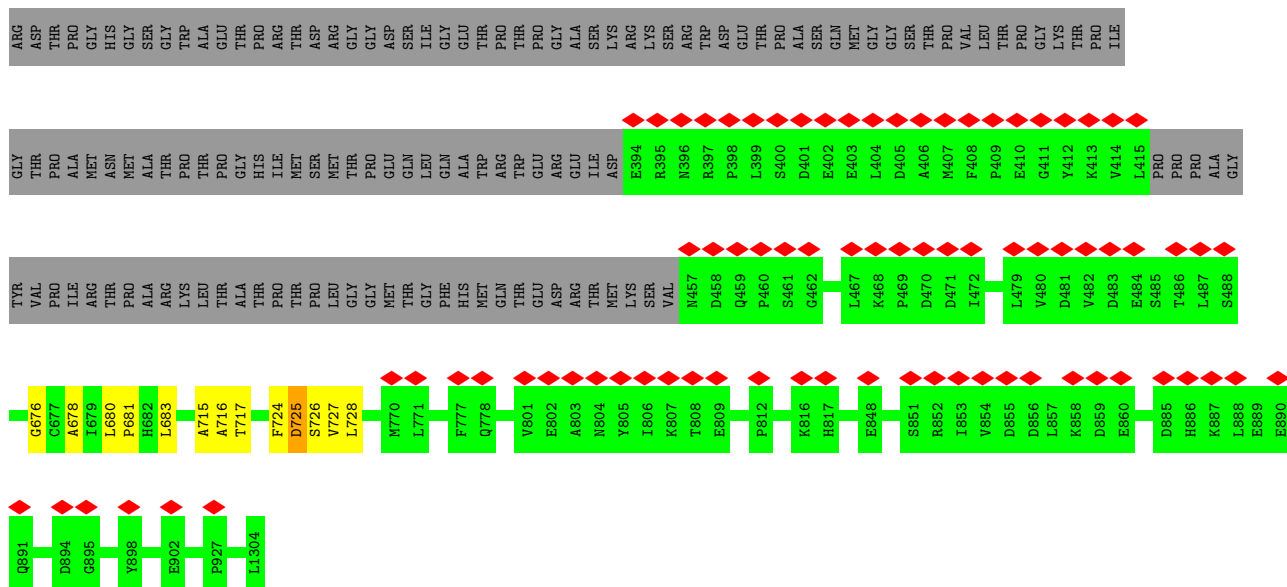


M1	E2	T3	I4	L5	E6	Q7	Q8	R9	R10	Y11	H12	E13	E14	K15	E16	R17	L18	M19	D20	V21	M22	A23	K24	E25	M26	L27	T28	K29	K30	S31	T32	L33	R34	D35	Q36	I37	N38	S39	D40	H41	R42	T43	R44	A45	M46	Q47	D48	R49	Y50	M51	E52	V53	S54	G55	N56	L57	R58	D59	L60
Y61	D62	D63	K64	D65	G66	L67	R68	K69	E70	E71	L72	M73	A74	I75	S76	G77	P78	M79	E80	F81	A82	E83	F84	Y85	N86	R87	L88	K89	Q90	I91	K92	E93	F94	H95	R96	K97	H98	P99	N100	E101	I102	C103	V104	P105	M106	S107	V108	E109	F110	E111	E112	L113	L114	K115	A116	R117	E118	N119	P120
S121	E122	E123	A124	Q125	N126	L127	V128	E129	F130	T131	D132	E133	E134	G135	Y136	G137	R138	Y139	L140	D141	L142	H143	D144	C145	Y146	L147	K148	Y149	I150	N151	L152	K153	A154	S155	E156	K157	L158	D159	Y160	I161	T162	Y163	L164	S165	T166	F167	D168	Q169	L170	F171	D172	I173	P174	K175	E176	R177	N178	A179	
E181	Y182	K183	R184	Y185	L186	E187	M188	L189	L190	E191	Y192	L193	Q194	D195	Y196	T197	D198	R199	V200	K201	P202	L203	Q204	D205	Q206	N207	E208	L209	F210	G211	K212	I213	Q214	A215	E216	F217	E218	K219	K220	W221	E222	N223	G224	T225	F226	P227	G228	W229	PRO	LYS	GLU	THR	SER	SER	ALA	LEU	THR	HIS	ALA
GLY	ALA	HIS	LEU	ASP	LEU	SER	PHE	SER	TRP	GLU	GLU	LEU	ALA	SER	LEU	GLY	ASP	ARG	LYS	SER	LEU	ALA	GLY	LEU	LYS	CYS	GLY	THR	LEU	E279	E280	R281	A282	Q283	R284	L285	F286	S287	T288	K289	Q290	S292	L293	E294	S295	L296	D297	T298	S299	L300									
F301	A302	K303	N304	P305	K306	S307	K308	G309	T310	K311	R312	D313	T314	E315	R316	R317	K318	D319	I320	A321	F322	L323	E324	A325	Q326	I327	Y328	E329	Y330	V331	E332	I333	L334	G335	E336	Q337	R338	H339	L340	T341	H342	E343	N344	V345	Q346	R347	K348	Q349	A350	R351	T352	G353	E354	E355	R356	E357	E358	E359	T360
E361	E362	GLN	ILE	SER	GLU	SER	GLU	ASN	GLU	SER	VAL	VAL	ASN	GLU	ASP	GLU	GLU	GLU	ASN	TYR	ASN	GLY	TRP	ASP	GLY	LYS	PRO	ILE	F393	C408	N413	I452	E453	V456	S457	L462	LYS	LEU	GLN	LYS	ALA	SER	GLU	ARG	TRP	GLN	PRO	ASP	THR	GLU	GLU								
GLU	TYR	GLU	ASP	SER	SER	GLY	ASN	VAL	VAL	ASN	LYS	THR	TYR	GLU	ASP	LYS	ARG	GLN	GLY	LEU	LEU	TRP	ASP	GLY	LYS	PRO	ILE	F393	C408	N413	I452	E453	V456	S457	L462	LYS	LEU	GLN	LYS	ALA	SER	GLU	ARG	TRP	GLN	PRO	ASP	THR	GLU	GLU									

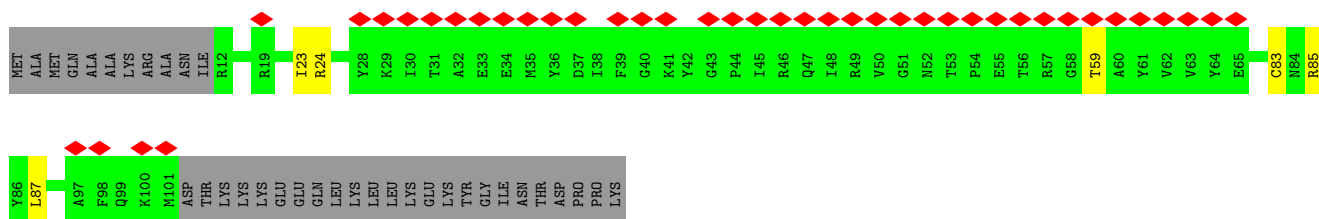
• Molecule 27: Splicing factor 3B subunit 2



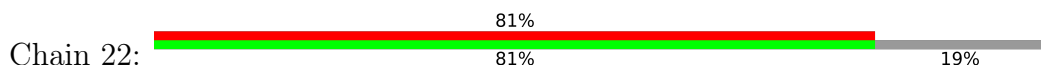




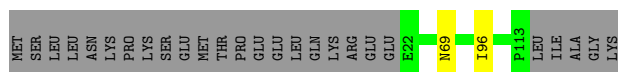
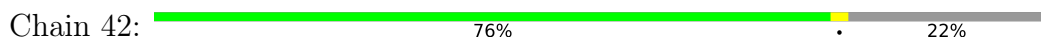
- Molecule 32: Splicing factor 3B subunit 6



- Molecule 33: Small nuclear ribonucleoprotein Sm D2

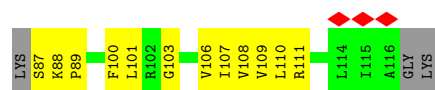
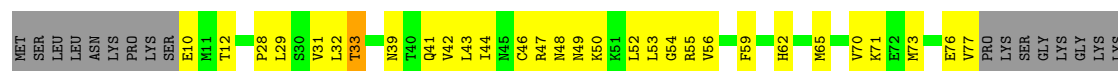


- Molecule 33: Small nuclear ribonucleoprotein Sm D2

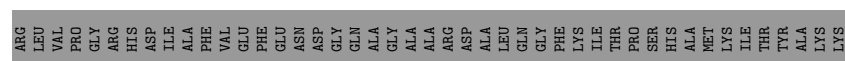
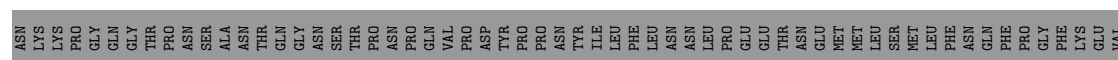
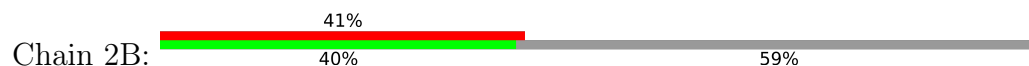


- Molecule 33: Small nuclear ribonucleoprotein Sm D2

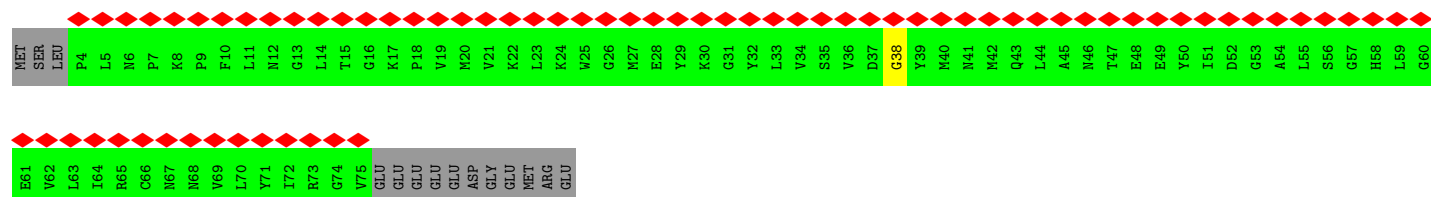
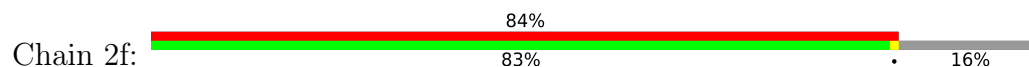




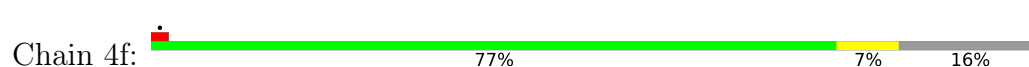
• Molecule 34: U2 small nuclear ribonucleoprotein B''



• Molecule 35: Small nuclear ribonucleoprotein F



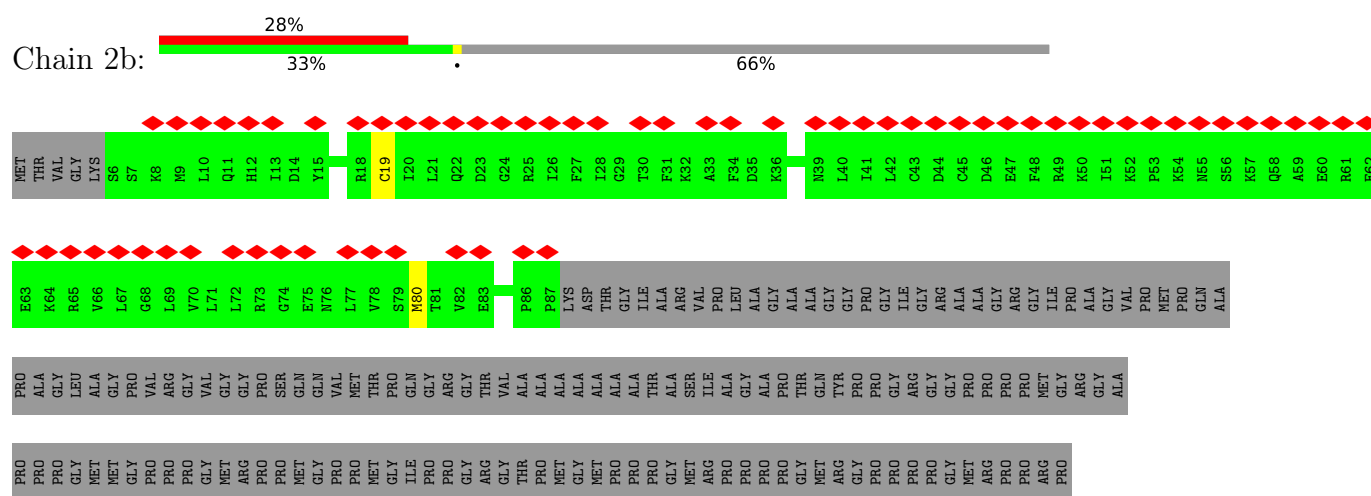
• Molecule 35: Small nuclear ribonucleoprotein F



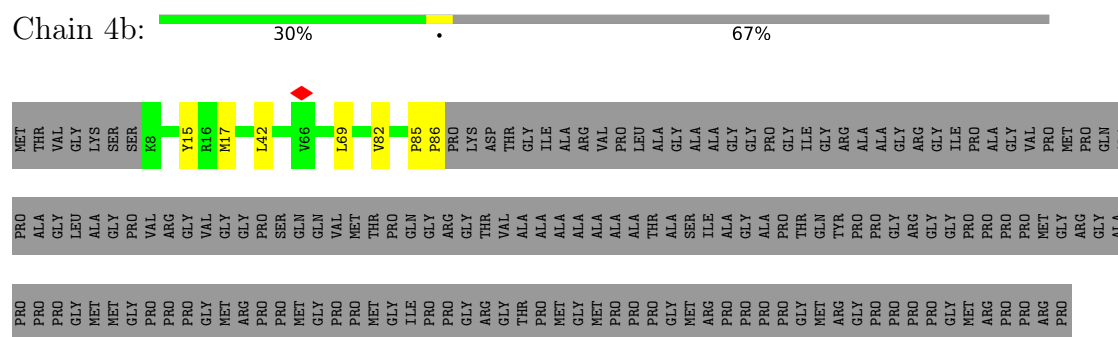
• Molecule 35: Small nuclear ribonucleoprotein F



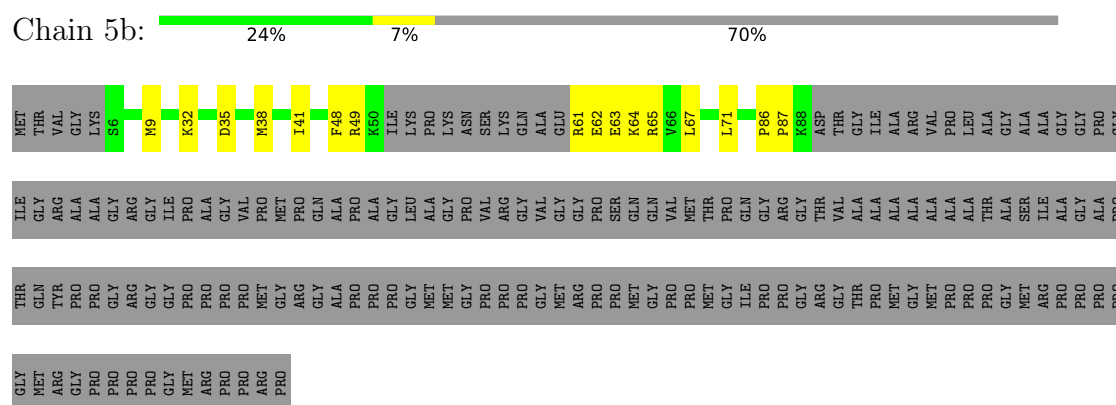
• Molecule 36: Small nuclear ribonucleoprotein-associated proteins B and B'



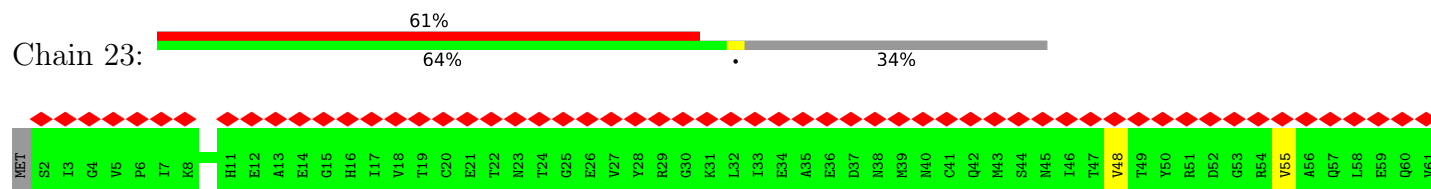
- Molecule 36: Small nuclear ribonucleoprotein-associated proteins B and B'

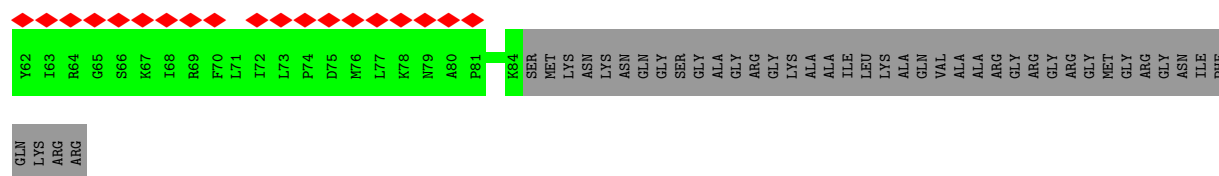


- Molecule 36: Small nuclear ribonucleoprotein-associated proteins B and B'



- Molecule 37: Small nuclear ribonucleoprotein Sm D3





• Molecule 37: Small nuclear ribonucleoprotein Sm D3



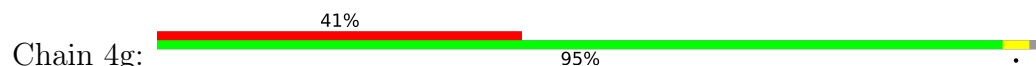
• Molecule 37: Small nuclear ribonucleoprotein Sm D3



• Molecule 38: Small nuclear ribonucleoprotein G



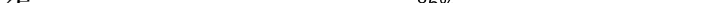
• Molecule 38: Small nuclear ribonucleoprotein G



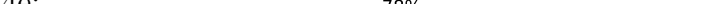
• Molecule 38: Small nuclear ribonucleoprotein G



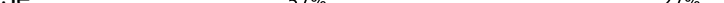


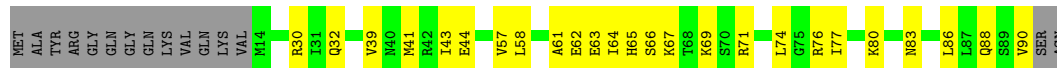
- Chain 2e:  88% 86% 12%

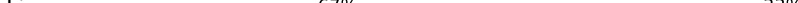


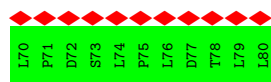
- Chain 4e:  29% 78% 17%

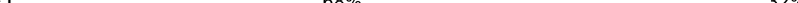


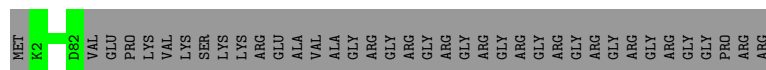
- Chain 5e:  57% 27% 16%



- Chain 21:  56% 67% 33%



- Chain 41:  68% 32%



- WORLDWIDE
PDB
PROTEIN DATA BANK

- Molecule 41: U2 small nuclear ribonucleoprotein A'

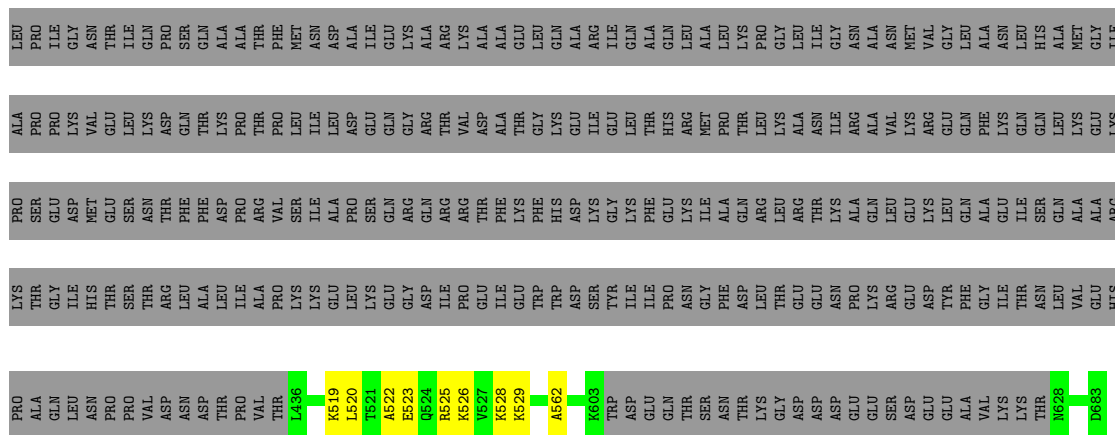
[illegible]

- Molecule 42: U4/U6 small nuclear ribonucleoprotein Prp4

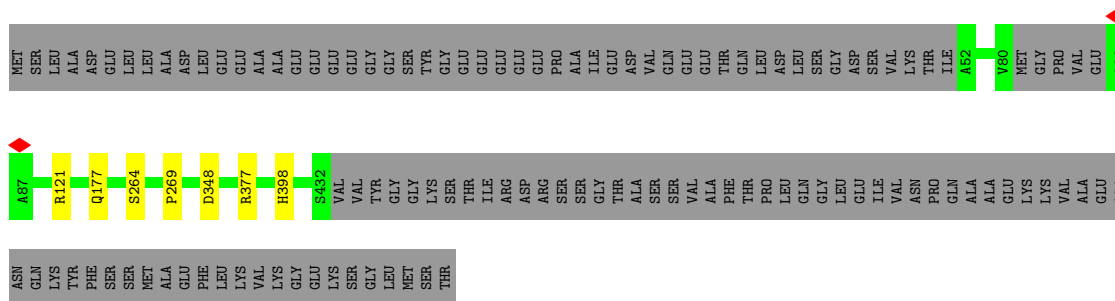
GLU	ALA	GLY	ASN	ARG	ASN	THR	GLY	VAL	PHE	GLU	ILE	GLU	GLU	GLU	GLU	HIS	ILE	S90	G123	V140	GLY	THR	ASP	ALA	ALA	ALA	PRO	VAL	VAL	LYS	LYS	LYS	LYS	LYS	ASP	LYS	LYS	LYS	LYS	GLY	TYR	ILE	HIS	PRO	ALA	LYS	LYS	LYS	LYS	GLY	GLU	ASP	GLU	LEU	LEU	ALA	ALA	MET
ALA	ALA	GLY	ASN	ARG	ASN	THR	GLY	VAL	PHE	GLU	ILE	GLU	GLU	GLU	GLU	HIS	ILE	S90	G123	V140	GLY	THR	ASP	ALA	ALA	ALA	PRO	VAL	VAL	LYS	LYS	LYS	LYS	LYS	ASP	LYS	LYS	LYS	LYS	GLY	TYR	ILE	HIS	PRO	ALA	LYS	LYS	LYS	LYS	GLY	GLU	ASP	GLU	LEU	LEU	ALA	ALA	MET

- Molecule 43: U4/U6 small nuclear ribonucleoprotein Prp3

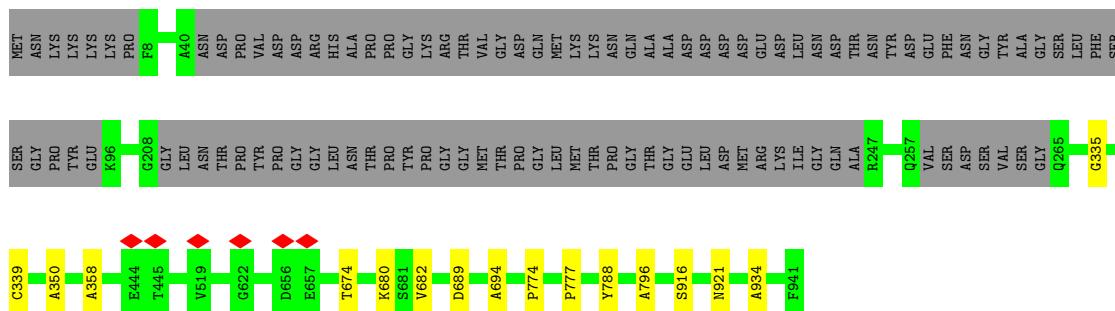
[illegible]



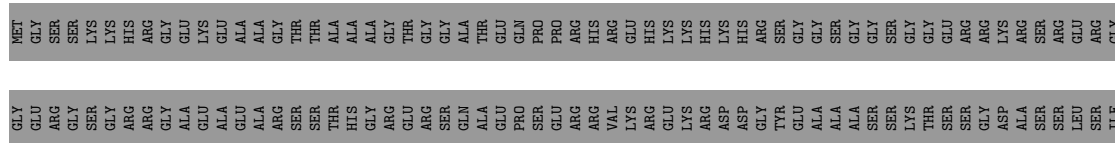
- Molecule 44: U4/U6 small nuclear ribonucleoprotein Prp31



- Molecule 45: Pre-mRNA-processing factor 6



- Molecule 46: U4/U6.U5 tri-snRNP-associated protein 1



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94460	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	556.8, 556.8, 556.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.14	0/11081	0.34	0/15398
2	B	0.14	0/8720	0.32	0/12217
3	2	0.17	0/2308	0.36	2/3584 (0.1%)
4	4	0.12	0/3034	0.19	0/4718
5	5	0.17	0/2625	0.33	0/4079
6	6	0.14	0/1556	0.25	0/2419
7	7	0.13	0/1164	0.31	0/1625
8	8	0.14	0/734	0.40	0/1025
9	C	0.14	0/4270	0.37	0/5983
10	D	0.13	0/712	0.30	0/995
11	E	0.24	0/1540	0.42	0/2148
12	G	0.09	0/283	0.27	0/393
13	M	0.15	0/632	0.37	0/885
14	U	0.12	0/2330	0.34	0/3268
15	W	0.12	0/853	0.35	0/1188
16	Z	0.13	0/349	0.24	0/540
17	z	0.12	0/321	0.14	0/500
18	66	0.15	0/358	0.38	0/497
19	67	0.10	0/386	0.27	0/537
20	62	0.15	0/480	0.41	0/671
21	63	0.14	0/432	0.41	0/604
22	68	0.13	0/469	0.33	0/651
23	64	0.16	0/372	0.39	0/520
24	65	0.14	0/380	0.35	0/528
25	B4	0.13	0/394	0.29	0/549
26	9	0.13	0/1928	0.30	0/2692
27	B2	0.15	0/1092	0.36	0/1536
28	B5	0.11	0/349	0.26	0/487
29	B3	0.20	0/6024	0.37	0/8425
30	BP	0.13	0/501	0.37	0/697
31	B1	0.20	0/4421	0.41	0/6190
32	B6	0.11	0/459	0.30	0/642
33	22	0.13	0/485	0.35	0/677
33	42	0.13	0/466	0.38	0/651

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	52	0.32	0/805	0.78	0/1081
34	2B	0.11	0/463	0.26	0/646
35	2f	0.16	0/362	0.38	0/502
35	4f	0.16	0/362	0.37	0/502
35	5f	0.38	0/579	0.87	1/783 (0.1%)
36	2b	0.12	0/416	0.36	0/581
36	4b	0.13	0/398	0.36	0/555
36	5b	0.34	0/602	0.56	0/801
37	23	0.16	0/417	0.43	0/581
37	43	0.32	0/417	0.46	0/581
37	53	0.37	0/665	0.55	0/896
38	2g	0.14	0/366	0.36	0/509
38	4g	0.13	0/371	0.38	0/516
38	5g	0.38	0/584	0.78	0/779
39	2e	0.13	0/403	0.38	0/561
39	4e	0.14	0/378	0.40	0/526
39	5e	0.34	0/646	0.75	0/867
40	21	0.12	0/404	0.34	0/564
40	41	0.14	0/409	0.35	0/571
40	51	0.37	0/649	0.79	1/878 (0.1%)
41	2A	0.16	0/821	0.42	0/1149
42	F	0.24	0/2074	0.38	0/2894
43	J	0.41	0/1127	0.55	1/1572 (0.1%)
44	L	0.13	0/1899	0.30	0/2654
45	N	0.25	0/4239	0.43	0/5936
46	S	0.16	0/744	0.32	0/1032
All	All	0.18	0/82108	0.38	5/116036 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	J	520	LEU	N-CA-C	-6.11	104.70	111.36
3	2	106	G	P-O3'-C3'	5.35	128.22	120.20
3	2	103	U	P-O3'-C3'	5.16	127.94	120.20
35	5f	38	GLY	N-CA-C	-5.10	108.33	114.66
40	51	51	GLU	CB-CG-CD	5.03	121.15	112.60

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	10977	0	5122	14	0
2	B	8644	0	4199	11	0
3	2	2072	0	1049	8	0
4	4	2718	0	1378	20	0
5	5	2356	0	1194	27	0
6	6	1392	0	702	26	0
7	7	1158	0	558	0	0
8	8	729	0	356	2	0
9	C	4223	0	2099	16	0
10	D	708	0	328	1	0
11	E	1531	0	747	10	0
12	G	283	0	128	0	0
13	M	627	0	315	0	0
14	U	2308	0	1104	6	0
15	W	844	0	426	16	0
16	Z	314	0	160	0	0
17	z	286	0	142	6	0
18	66	357	0	169	1	0
19	67	384	0	178	0	0
20	62	478	0	222	0	0
21	63	429	0	199	1	0
22	68	469	0	220	3	0
23	64	369	0	172	1	0
24	65	378	0	174	2	0
25	B4	391	0	197	0	0
26	9	1920	0	902	2	0
27	B2	1072	0	563	0	0
28	B5	347	0	171	0	0
29	B3	5969	0	2985	19	0
30	BP	498	0	241	1	0
31	B1	4383	0	2195	13	0
32	B6	455	0	227	3	0
33	22	482	0	220	0	0
33	42	463	0	211	1	0
33	52	796	0	821	34	0
34	2B	461	0	218	1	0
35	2f	359	0	179	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	4f	359	0	179	3	0
35	5f	567	0	575	26	0
36	2b	413	0	194	1	0
36	4b	396	0	183	4	0
36	5b	594	0	615	14	0
37	23	415	0	198	1	0
37	43	415	0	198	4	0
37	53	657	0	675	18	0
38	2g	364	0	176	1	0
38	4g	369	0	178	1	0
38	5g	577	0	603	20	0
39	2e	403	0	173	1	0
39	4e	378	0	163	2	0
39	5e	638	0	657	24	0
40	21	402	0	184	0	0
40	41	407	0	183	0	0
40	51	641	0	681	17	0
41	2A	816	0	386	0	0
42	F	2060	0	1021	19	0
43	J	1121	0	547	8	0
44	L	1887	0	934	4	0
45	N	4207	0	2161	7	0
46	S	744	0	360	0	0
All	All	80460	0	41695	361	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 361 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)
39:5e:58:LEU:O	39:5e:76:ARG:HA	1.63	0.98
11:E:53:SER:CB	11:E:56:GLN:CB	2.45	0.94
37:23:48:VAL:O	37:23:55:VAL:HA	1.73	0.89
31:B1:676:GLY:HA2	31:B1:715:ALA:HB1	1.57	0.87
29:B3:886:GLU:HA	29:B3:910:ALA:O	1.75	0.85

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	2212/2335 (95%)	2128 (96%)	84 (4%)	0	100	100
2	B	1710/2136 (80%)	1689 (99%)	21 (1%)	0	100	100
7	7	224/793 (28%)	219 (98%)	5 (2%)	0	100	100
8	8	138/464 (30%)	134 (97%)	4 (3%)	0	100	100
9	C	834/972 (86%)	817 (98%)	17 (2%)	0	100	100
10	D	139/142 (98%)	138 (99%)	1 (1%)	0	100	100
11	E	305/357 (85%)	302 (99%)	3 (1%)	0	100	100
12	G	55/820 (7%)	53 (96%)	2 (4%)	0	100	100
13	M	122/128 (95%)	114 (93%)	8 (7%)	0	100	100
14	U	454/565 (80%)	441 (97%)	13 (3%)	0	100	100
15	W	167/177 (94%)	166 (99%)	1 (1%)	0	100	100
18	66	70/80 (88%)	70 (100%)	0	0	100	100
19	67	75/103 (73%)	74 (99%)	1 (1%)	0	100	100
20	62	93/95 (98%)	91 (98%)	2 (2%)	0	100	100
21	63	83/102 (81%)	82 (99%)	1 (1%)	0	100	100
22	68	93/96 (97%)	92 (99%)	1 (1%)	0	100	100
23	64	71/139 (51%)	70 (99%)	1 (1%)	0	100	100
24	65	74/91 (81%)	72 (97%)	2 (3%)	0	100	100
25	B4	76/424 (18%)	76 (100%)	0	0	100	100
26	9	377/501 (75%)	369 (98%)	8 (2%)	0	100	100
27	B2	204/895 (23%)	200 (98%)	4 (2%)	0	100	100
28	B5	67/86 (78%)	66 (98%)	1 (2%)	0	100	100
29	B3	1176/1217 (97%)	1137 (97%)	38 (3%)	1 (0%)	48	83
30	BP	98/110 (89%)	96 (98%)	2 (2%)	0	100	100
31	B1	866/1304 (66%)	843 (97%)	21 (2%)	2 (0%)	43	77

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	B6	88/125 (70%)	85 (97%)	3 (3%)	0	100	100
33	22	91/118 (77%)	91 (100%)	0	0	100	100
33	42	90/118 (76%)	89 (99%)	1 (1%)	0	100	100
33	52	94/118 (80%)	88 (94%)	6 (6%)	0	100	100
34	2B	90/225 (40%)	90 (100%)	0	0	100	100
35	2f	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
35	4f	70/86 (81%)	68 (97%)	2 (3%)	0	100	100
35	5f	71/86 (83%)	62 (87%)	9 (13%)	0	100	100
36	2b	80/240 (33%)	80 (100%)	0	0	100	100
36	4b	77/240 (32%)	76 (99%)	1 (1%)	0	100	100
36	5b	69/240 (29%)	65 (94%)	4 (6%)	0	100	100
37	23	81/126 (64%)	79 (98%)	2 (2%)	0	100	100
37	43	81/126 (64%)	78 (96%)	1 (1%)	2 (2%)	4	26
37	53	82/126 (65%)	77 (94%)	5 (6%)	0	100	100
38	2g	71/76 (93%)	71 (100%)	0	0	100	100
38	4g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
38	5g	72/76 (95%)	66 (92%)	6 (8%)	0	100	100
39	2e	79/92 (86%)	79 (100%)	0	0	100	100
39	4e	74/92 (80%)	73 (99%)	1 (1%)	0	100	100
39	5e	75/92 (82%)	72 (96%)	3 (4%)	0	100	100
40	21	78/119 (66%)	76 (97%)	2 (3%)	0	100	100
40	41	79/119 (66%)	77 (98%)	2 (2%)	0	100	100
40	51	79/119 (66%)	75 (95%)	4 (5%)	0	100	100
41	2A	160/255 (63%)	158 (99%)	2 (1%)	0	100	100
42	F	408/522 (78%)	398 (98%)	6 (2%)	4 (1%)	12	47
43	J	220/683 (32%)	216 (98%)	3 (1%)	1 (0%)	24	62
44	L	372/499 (74%)	366 (98%)	6 (2%)	0	100	100
45	N	826/941 (88%)	786 (95%)	38 (5%)	2 (0%)	43	77
46	S	138/800 (17%)	136 (99%)	2 (1%)	0	100	100
All	All	13720/20753 (66%)	13355 (97%)	353 (3%)	12 (0%)	49	83

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	43	78	LYS
42	F	480	PRO
42	F	261	PRO
31	B1	726	SER
37	43	81	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	107/2108 (5%)	107 (100%)	0	100	100
2	B	78/1908 (4%)	78 (100%)	0	100	100
7	7	9/709 (1%)	9 (100%)	0	100	100
8	8	8/382 (2%)	8 (100%)	0	100	100
9	C	48/866 (6%)	48 (100%)	0	100	100
10	D	5/130 (4%)	5 (100%)	0	100	100
11	E	10/300 (3%)	10 (100%)	0	100	100
12	G	1/721 (0%)	1 (100%)	0	100	100
13	M	6/111 (5%)	6 (100%)	0	100	100
14	U	23/511 (4%)	23 (100%)	0	100	100
15	W	10/148 (7%)	10 (100%)	0	100	100
18	66	2/70 (3%)	2 (100%)	0	100	100
19	67	3/91 (3%)	3 (100%)	0	100	100
20	62	3/88 (3%)	3 (100%)	0	100	100
21	63	4/94 (4%)	4 (100%)	0	100	100
22	68	1/82 (1%)	1 (100%)	0	100	100
23	64	4/111 (4%)	4 (100%)	0	100	100
24	65	3/80 (4%)	3 (100%)	0	100	100
25	B4	4/336 (1%)	4 (100%)	0	100	100
26	9	11/446 (2%)	11 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	B2	22/776 (3%)	22 (100%)	0	100	100
28	B5	3/77 (4%)	3 (100%)	0	100	100
29	B3	60/1051 (6%)	60 (100%)	0	100	100
30	BP	4/95 (4%)	4 (100%)	0	100	100
31	B1	40/1104 (4%)	40 (100%)	0	100	100
32	B6	5/109 (5%)	5 (100%)	0	100	100
33	22	5/110 (4%)	5 (100%)	0	100	100
33	42	4/110 (4%)	4 (100%)	0	100	100
33	52	93/110 (84%)	92 (99%)	1 (1%)	65	74
34	2B	3/195 (2%)	3 (100%)	0	100	100
35	2f	4/74 (5%)	4 (100%)	0	100	100
35	4f	4/74 (5%)	4 (100%)	0	100	100
35	5f	61/74 (82%)	59 (97%)	2 (3%)	33	55
36	2b	4/177 (2%)	4 (100%)	0	100	100
36	4b	3/177 (2%)	3 (100%)	0	100	100
36	5b	67/177 (38%)	67 (100%)	0	100	100
37	23	3/101 (3%)	3 (100%)	0	100	100
37	43	3/101 (3%)	3 (100%)	0	100	100
37	53	73/101 (72%)	73 (100%)	0	100	100
38	2g	3/66 (4%)	3 (100%)	0	100	100
38	4g	3/66 (4%)	3 (100%)	0	100	100
38	5g	64/66 (97%)	43 (67%)	21 (33%)	0	2
39	2e	1/84 (1%)	1 (100%)	0	100	100
39	4e	1/84 (1%)	1 (100%)	0	100	100
39	5e	72/84 (86%)	72 (100%)	0	100	100
40	21	3/101 (3%)	3 (100%)	0	100	100
40	41	3/101 (3%)	3 (100%)	0	100	100
40	51	76/101 (75%)	53 (70%)	23 (30%)	0	2
41	2A	6/218 (3%)	6 (100%)	0	100	100
42	F	16/442 (4%)	16 (100%)	0	100	100
43	J	8/599 (1%)	8 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	L	14/424 (3%)	14 (100%)	0	100	100
45	N	36/792 (4%)	36 (100%)	0	100	100
46	S	5/681 (1%)	5 (100%)	0	100	100
All	All	1112/17994 (6%)	1065 (96%)	47 (4%)	28	48

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	5g	11	LYS
38	5g	47	GLU
38	5g	15	LYS
38	5g	43	ASP
38	5g	51	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
33	52	91	ASN
38	5g	55	ASN
38	5g	28	GLN
35	5f	41	ASN
33	52	41	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	Z	14/347 (4%)	1 (7%)	0
17	z	12/13 (92%)	6 (50%)	0
3	2	94/188 (50%)	18 (19%)	4 (4%)
4	4	124/144 (86%)	31 (25%)	1 (0%)
5	5	110/117 (94%)	39 (35%)	4 (3%)
6	6	62/106 (58%)	9 (14%)	1 (1%)
All	All	416/915 (45%)	104 (25%)	10 (2%)

5 of 104 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	2	30	A
3	2	38	A

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Mol	Chain	Res	Type
3	2	40	C
3	2	43	U
3	2	47	U

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	5	96	A
5	5	105	U
6	6	77	C
3	2	106	G
4	4	114	U

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](#)

There are no ligands in this entry.

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.

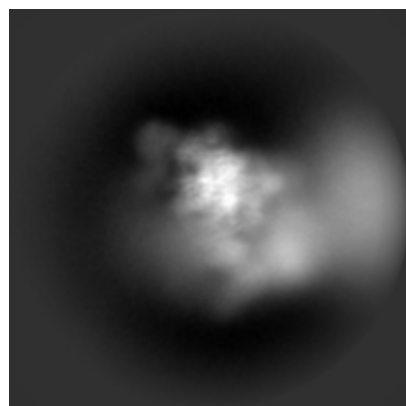
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18789. These allow visual inspection of the internal detail of the map and identification of artifacts.

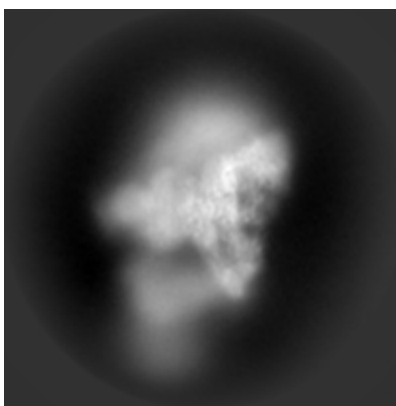
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

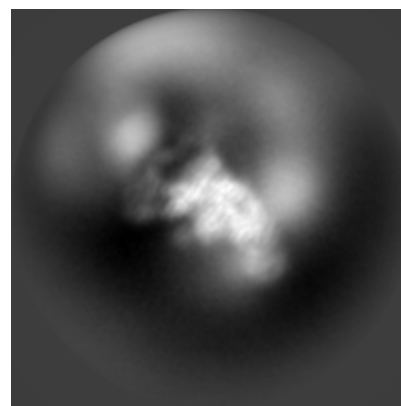
6.1.1 Primary map



X

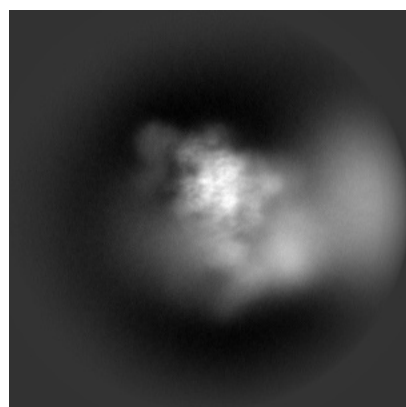


Y

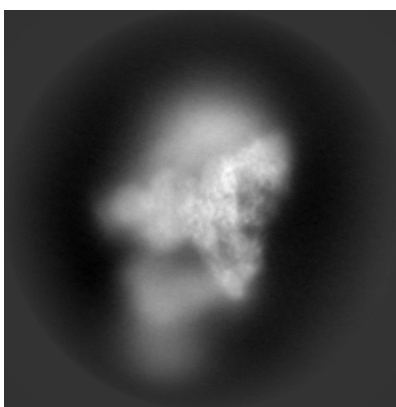


Z

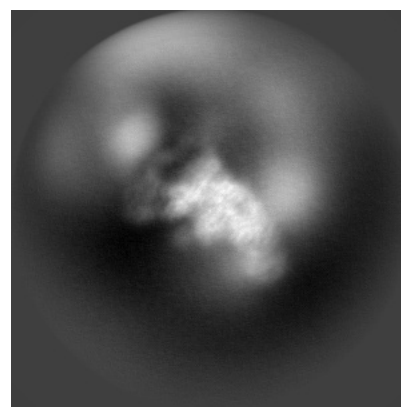
6.1.2 Raw map



X



Y

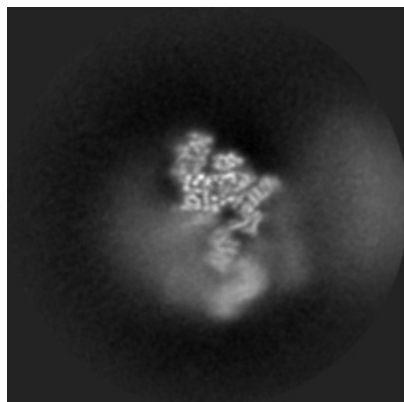


Z

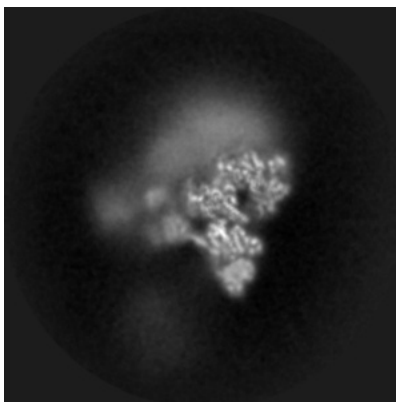
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

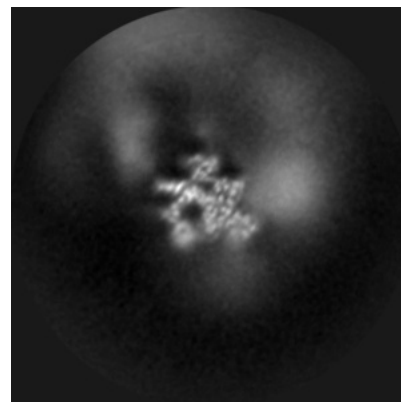
6.2.1 Primary map



X Index: 240

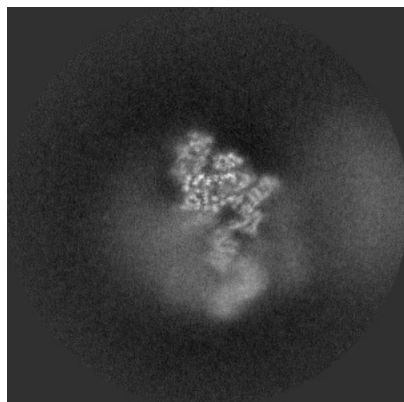


Y Index: 240

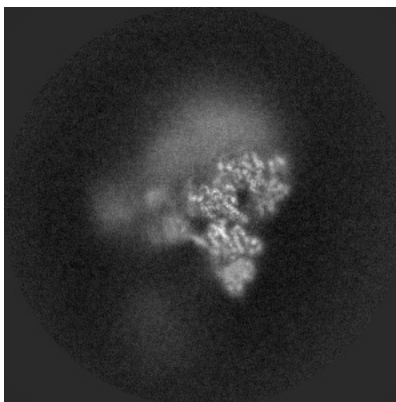


Z Index: 240

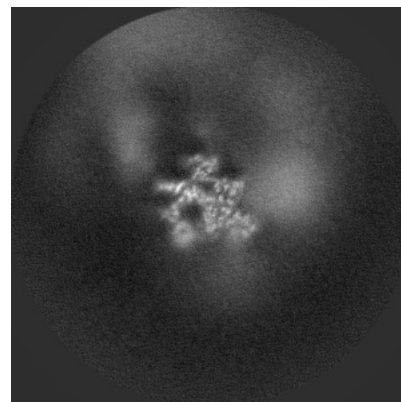
6.2.2 Raw map



X Index: 240



Y Index: 240

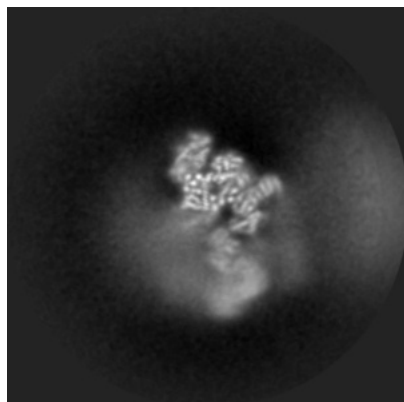


Z Index: 240

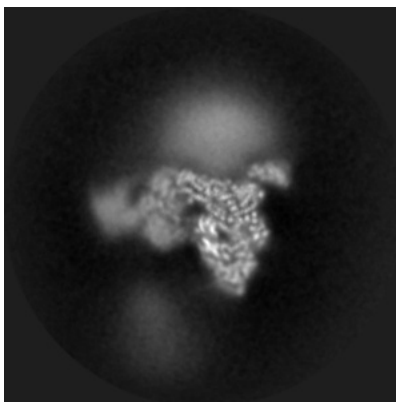
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

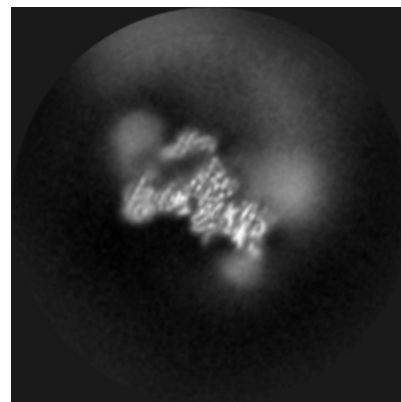
6.3.1 Primary map



X Index: 237

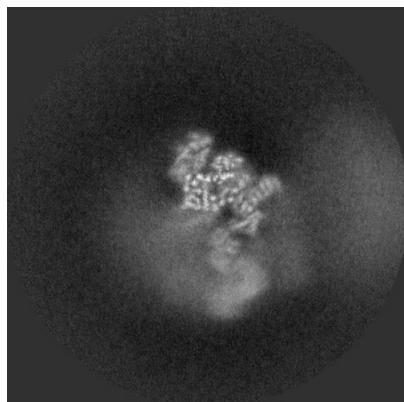


Y Index: 260

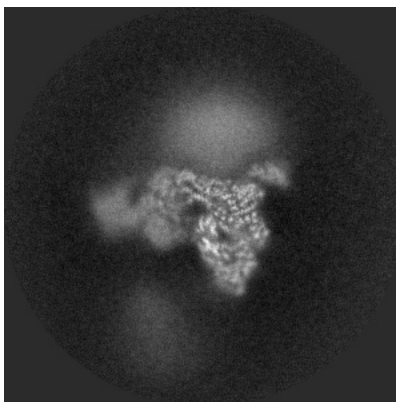


Z Index: 273

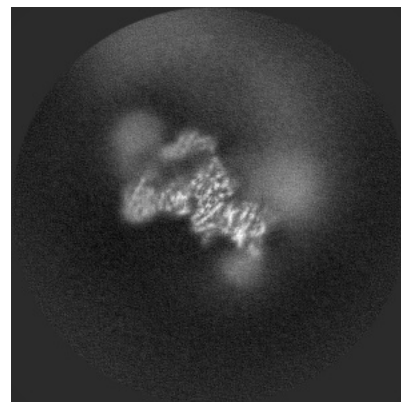
6.3.2 Raw map



X Index: 238



Y Index: 261

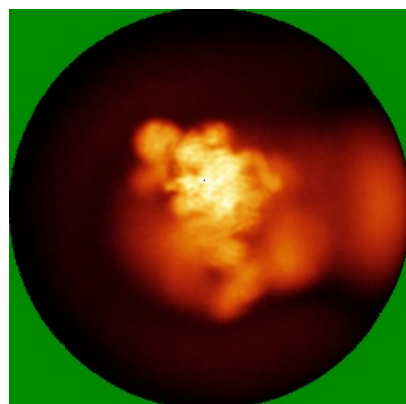


Z Index: 274

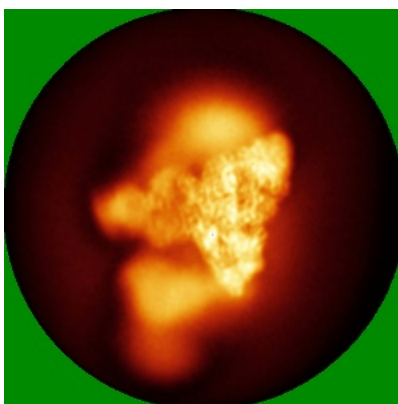
The images above show the largest variance slices of the map in three orthogonal directions.

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

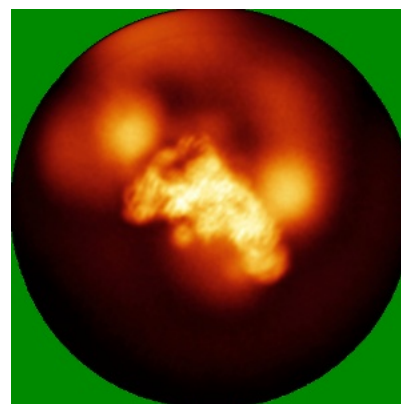
6.4.1 Primary map



X

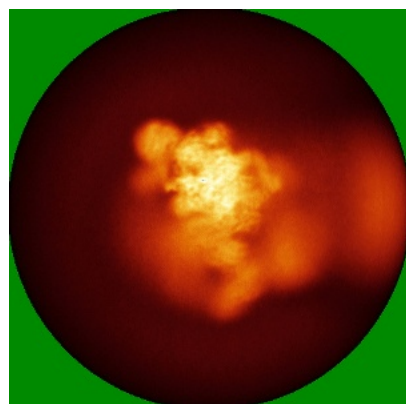


Y

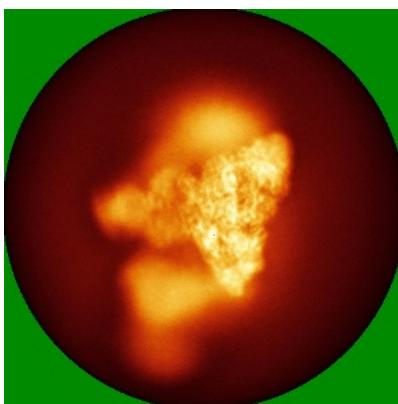


Z

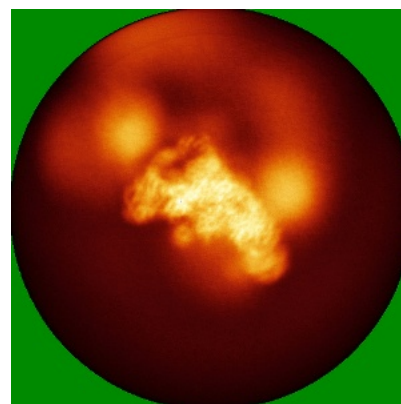
6.4.2 Raw map



X



Y



Z

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

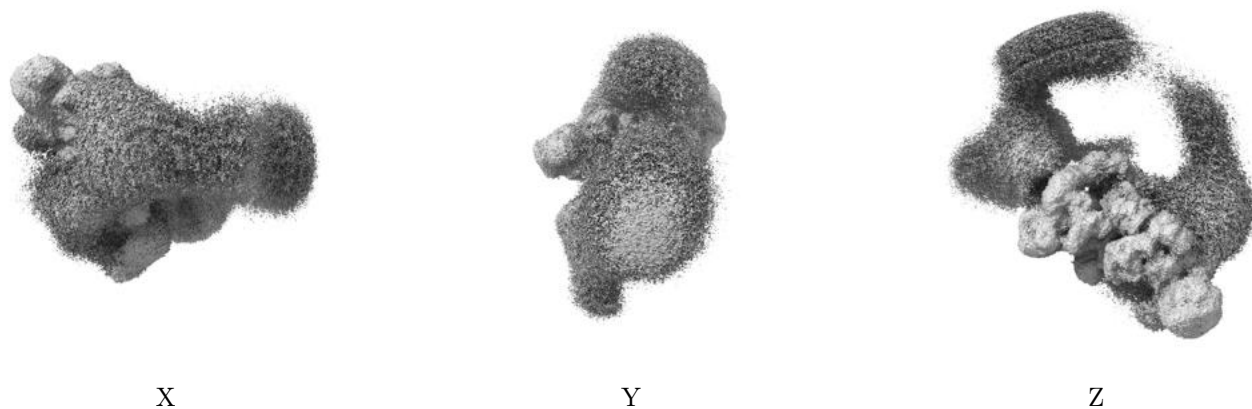
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

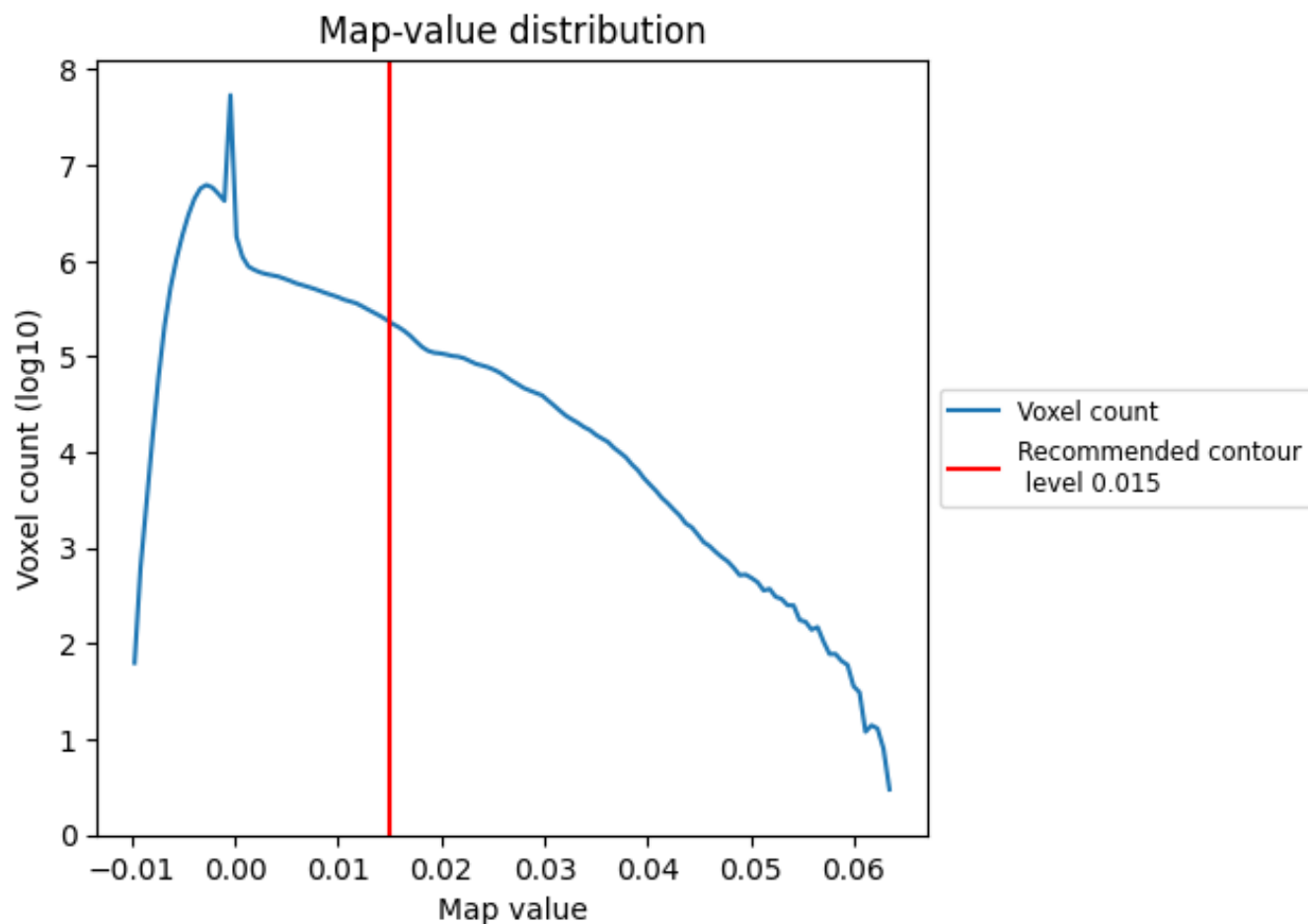
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

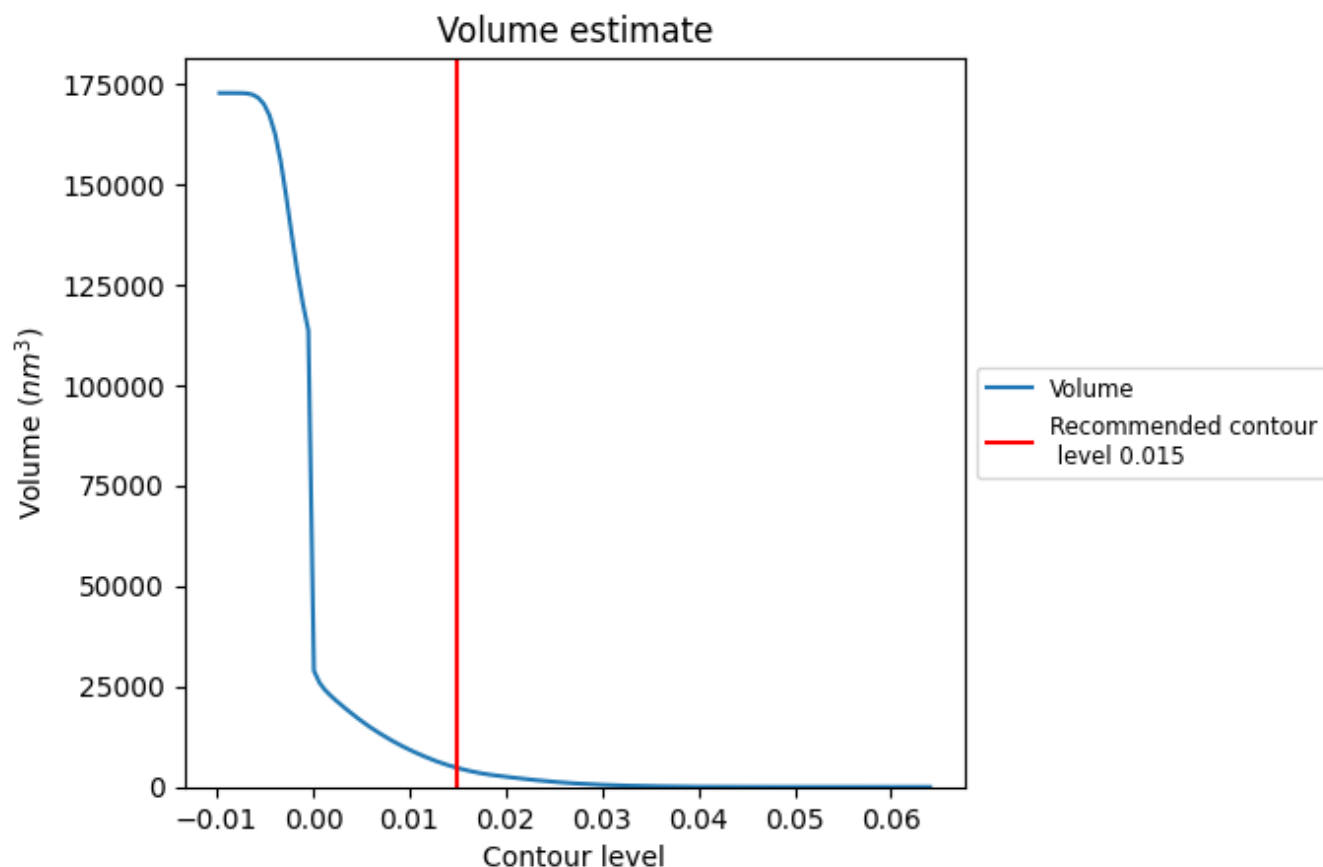
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

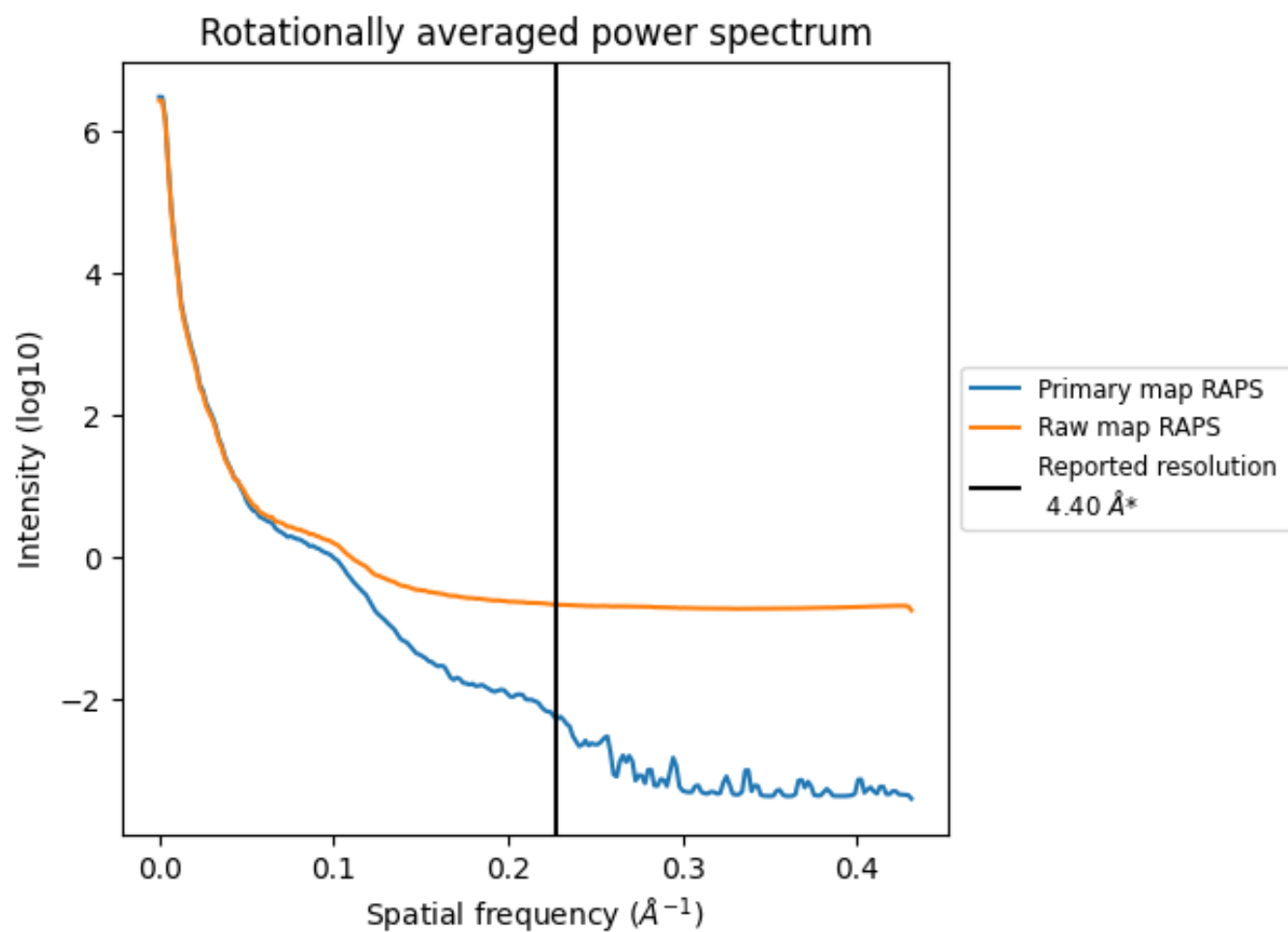
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4716 nm^3 ; this corresponds to an approximate mass of 4260 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 ⓘ

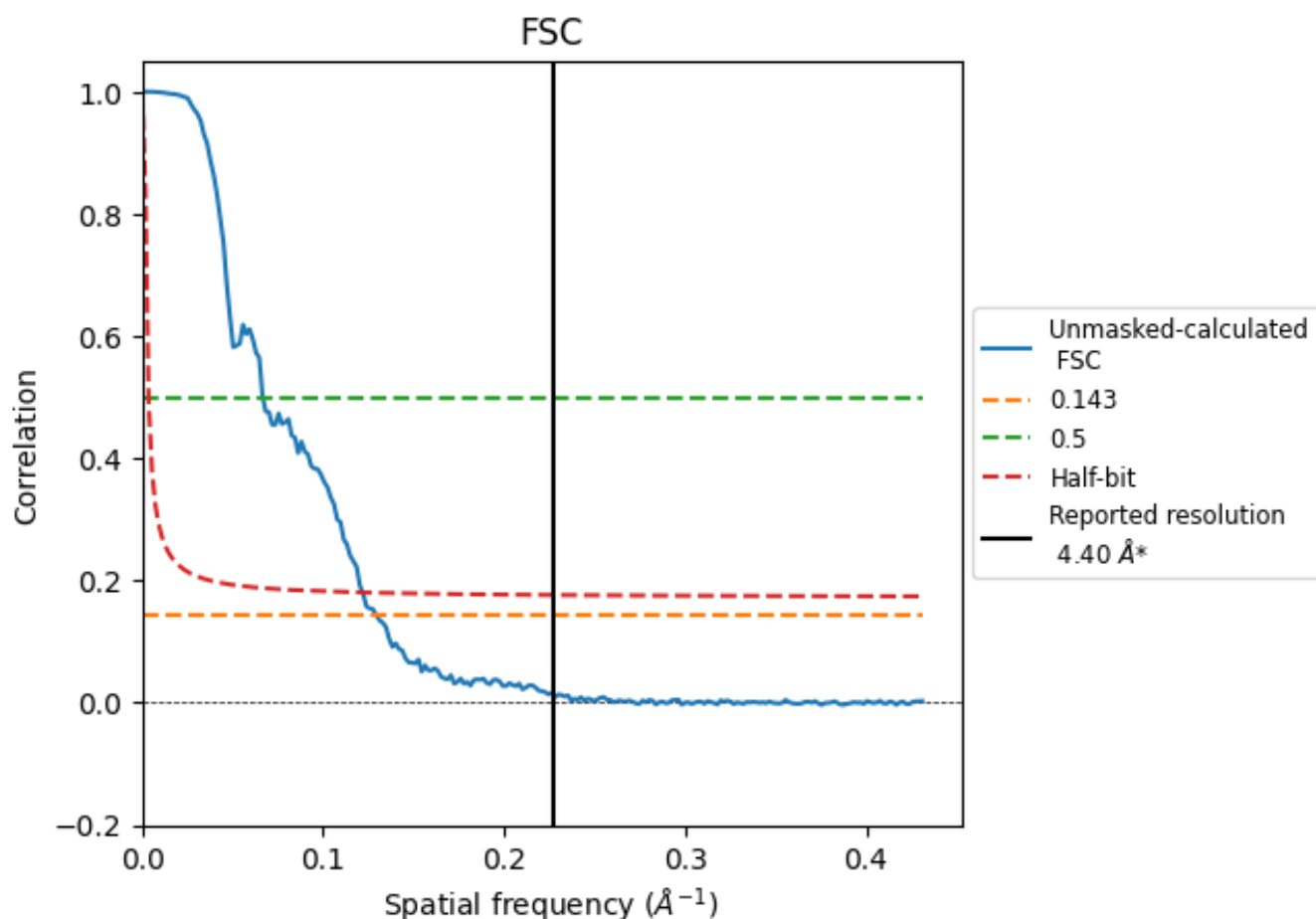


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

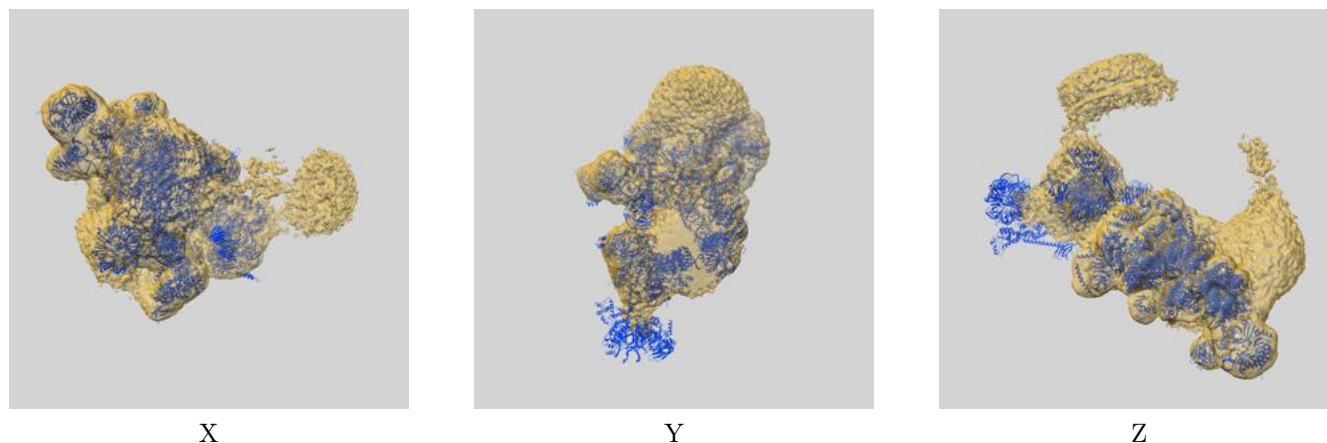
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.73	15.02	8.21

*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 7.73 differs from the reported value 4.4 by more than 10 %

9 Map-model fit [i](#)

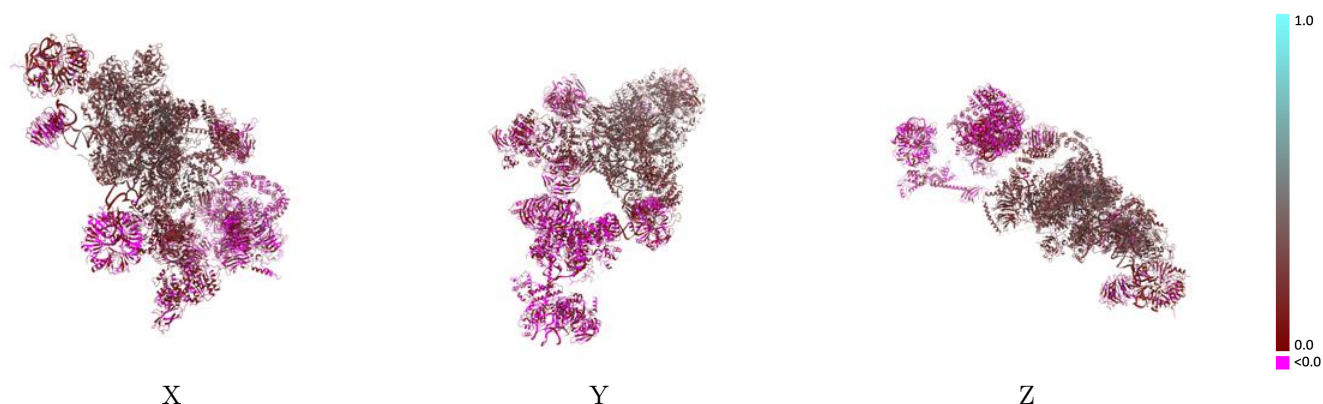
This section contains information regarding the fit between EMDB map EMD-18789 and PDB model 8R0B. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



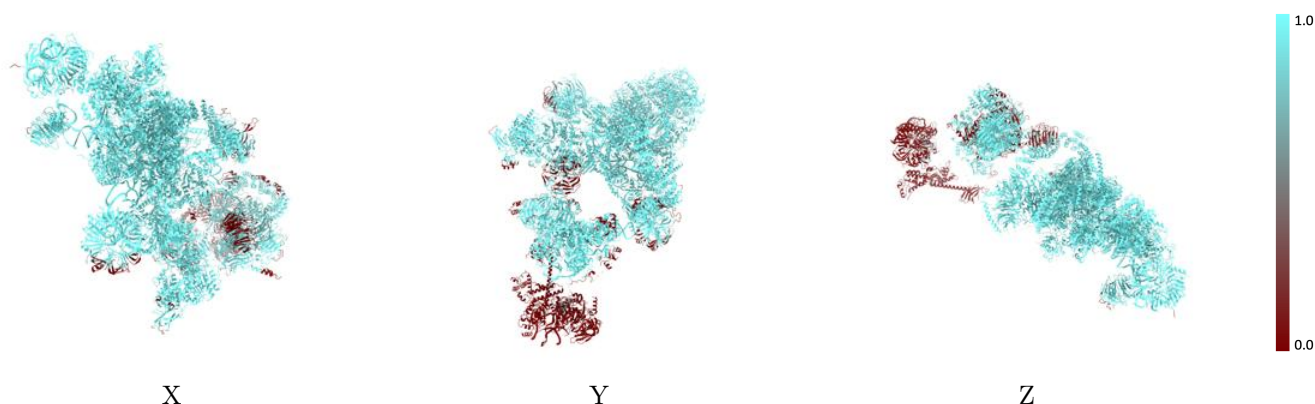
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



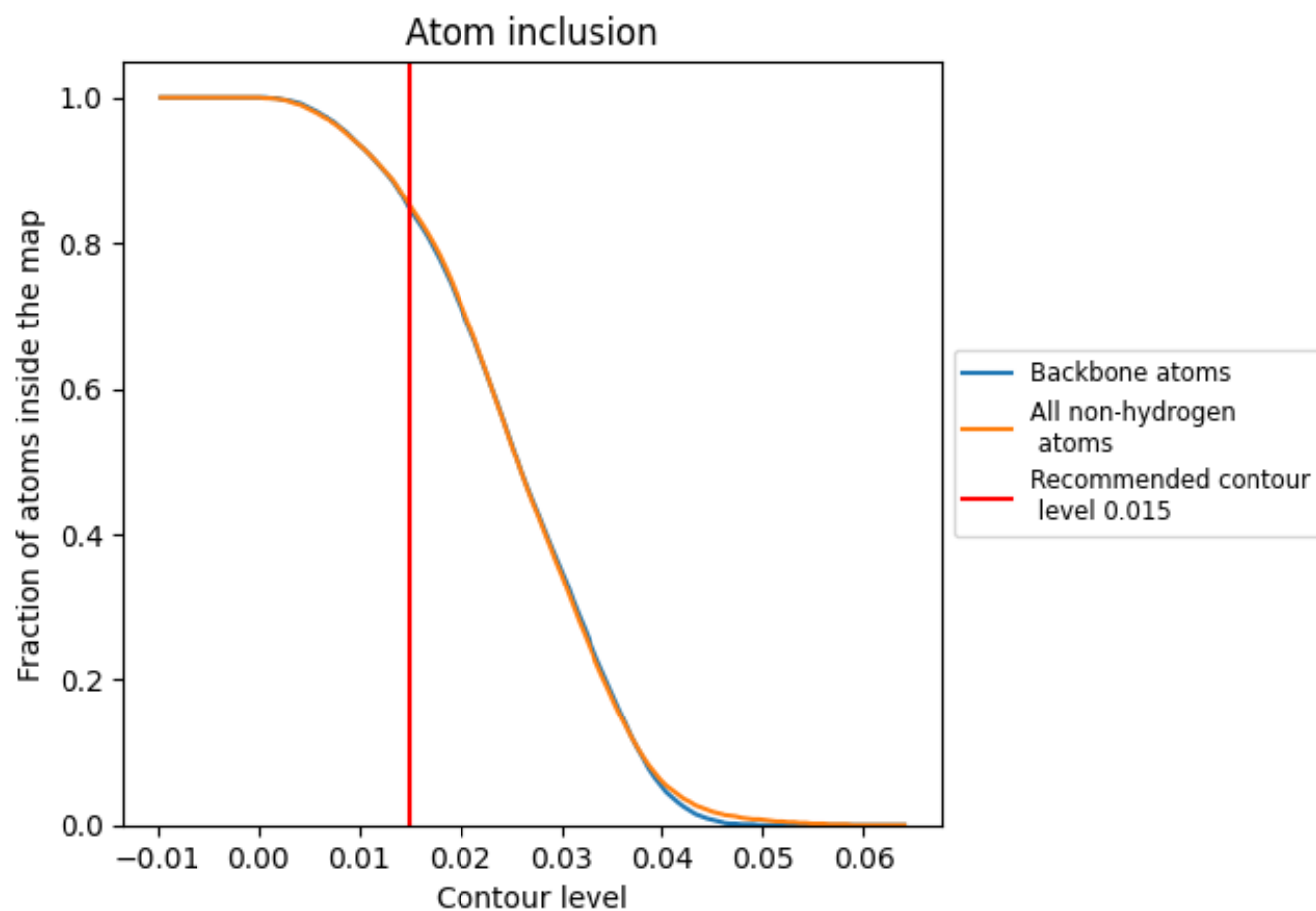
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 85% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8510	 0.1480
2	 0.4870	 0.0350
21	 0.1520	 0.0210
22	 0.0000	 -0.0070
23	 0.0870	 0.0350
2A	 0.0030	 0.0010
2B	 0.0000	 -0.0000
2b	 0.1720	 0.0090
2e	 0.0000	 0.0190
2f	 0.0000	 0.0410
2g	 0.0000	 0.0450
4	 1.0000	 0.1420
41	 1.0000	 0.0480
42	 1.0000	 0.0230
43	 0.7830	 -0.0220
4b	 0.9770	 0.0230
4e	 0.6480	 0.0200
4f	 0.9640	 0.0080
4g	 0.5830	 0.0130
5	 0.9960	 0.2080
51	 0.9940	 0.1070
52	 0.9640	 0.0900
53	 1.0000	 0.1530
5b	 0.9930	 0.1280
5e	 1.0000	 0.1100
5f	 0.9980	 0.1010
5g	 0.9930	 0.1010
6	 1.0000	 0.1980
62	 0.7680	 0.0500
63	 0.6570	 0.0290
64	 0.8180	 0.0830
65	 0.7090	 0.0110
66	 0.8740	 0.0430
67	 0.6220	 0.0410
68	 0.7080	 0.0440



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Chain	Atom inclusion	Q-score
7	 0.4540	 0.1390
8	 0.2920	 0.0180
9	 0.1730	 0.0250
A	 0.9990	 0.2920
B	 0.9690	 0.1280
B1	 0.9060	 0.0260
B2	 0.8620	 0.0220
B3	 0.7050	 0.0250
B4	 1.0000	 0.0440
B5	 1.0000	 0.0300
B6	 0.5450	 0.0410
BP	 1.0000	 -0.0030
C	 1.0000	 0.2810
D	 1.0000	 0.3290
E	 0.9090	 0.0360
F	 1.0000	 0.2310
G	 1.0000	 0.1960
J	 1.0000	 0.2600
L	 0.9950	 0.3020
M	 1.0000	 0.2980
N	 0.9910	 0.2350
S	 0.9920	 0.2510
U	 0.9920	 0.2670
W	 0.9960	 0.1610
Z	 1.0000	 0.0360
z	 1.0000	 0.2670