



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 02:05 AM UTC

PDB ID : 8R0A / pdb_00008r0a
EMDB ID : EMD-18788
Title : Cryo-EM structure of the cross-exon pre-B+5'ss 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 : 5.80 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

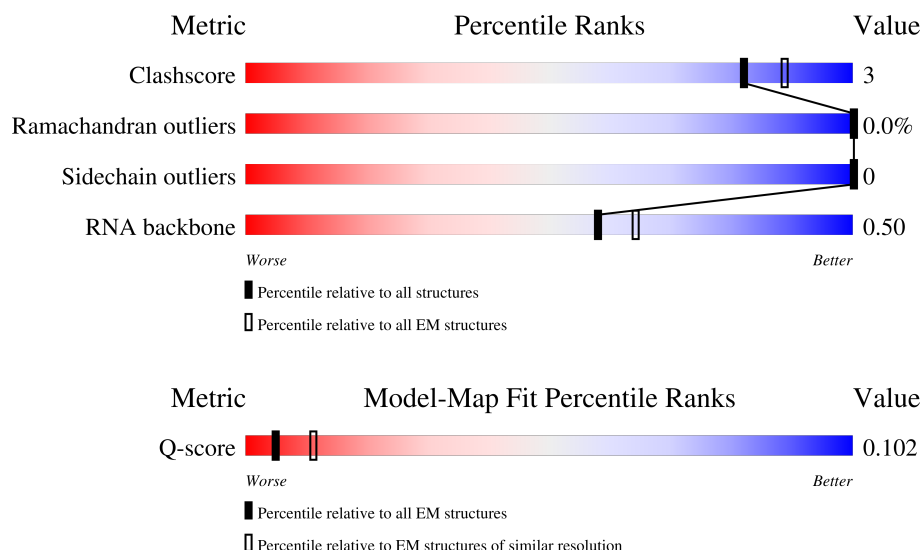
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 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.



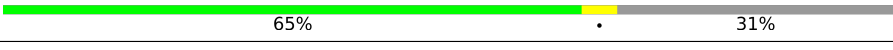
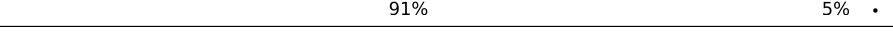
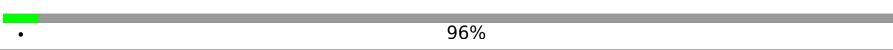
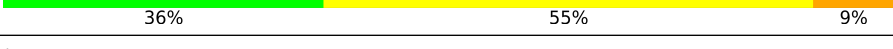
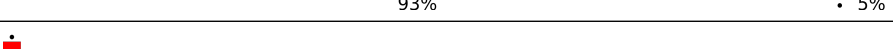
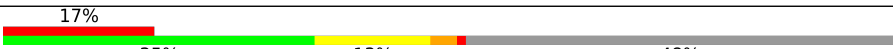
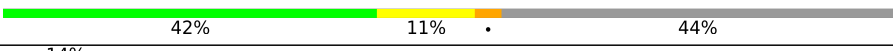
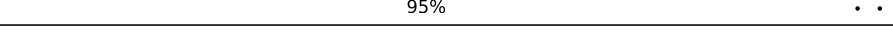
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	511 (5.30 - 6.30)

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	5	117	
2	C	972	
3	D	142	

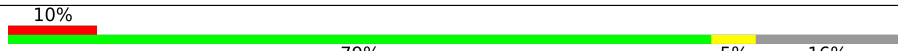
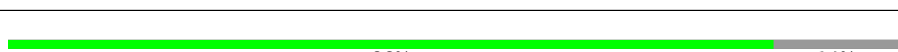
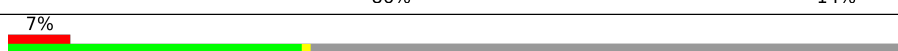
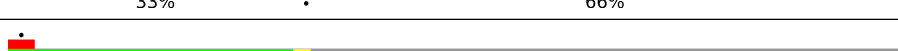
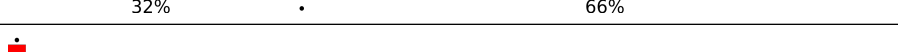
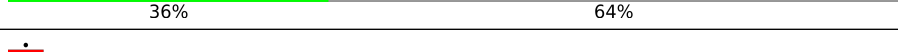
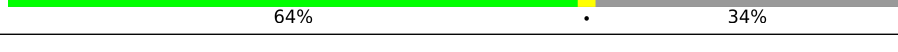
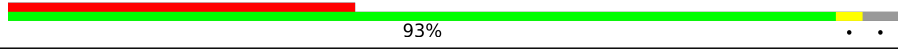
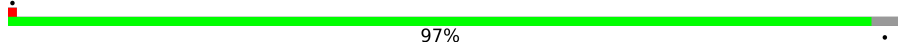
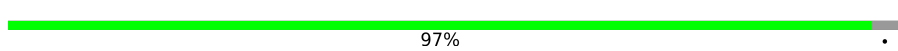
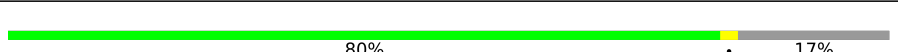
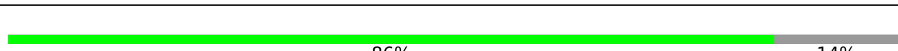
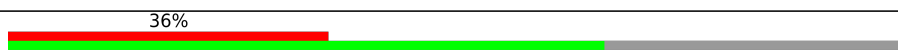
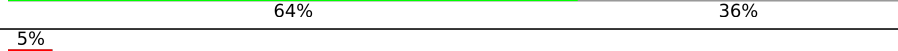
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Mol	Chain	Length	Quality of chain
4	E	357	
5	F	522	
6	M	128	
7	R	480	
8	U	565	
9	X	155	
10	Z	347	
11	z	11	
12	A	2335	
13	B	2136	
14	2	188	
15	4	144	
16	6	106	
17	7	793	
18	8	464	
19	B4	424	
20	9	501	
21	B2	895	
22	B5	86	
23	B3	1217	
24	BP	110	
25	B1	1304	
26	B6	125	
27	22	118	
27	42	118	

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Mol	Chain	Length	Quality of chain
27	52	118	
28	2B	225	
29	2f	86	
29	4f	86	
29	5f	86	
30	2b	240	
30	4b	240	
30	5b	240	
31	23	126	
31	43	126	
31	53	126	
32	2g	76	
32	4g	76	
32	5g	76	
33	2e	92	
33	4e	92	
33	5e	92	
34	21	119	
34	41	119	
34	51	119	
35	2A	255	
36	66	80	
37	67	103	
38	62	95	
39	63	102	

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Mol	Chain	Length	Quality of chain
40	68	96	
41	64	139	
42	65	91	
43	J	683	
44	K	1007	
45	G	820	
46	L	499	
47	S	800	
48	N	941	

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 80982 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 RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	115	Total	C	N	O	P	0	0
			2420	1084	403	818	115		

- Molecule 2 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

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

- Molecule 3 is a protein called Thioredoxin-like protein 4A.

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

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

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

- Molecule 5 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	F	359	Total	C	N	O	0	0
			1795	1077	359	359		

- Molecule 6 is a protein called NHP2-like protein 1, N-terminally processed.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	M	123	Total	C	N	O	0	0
			622	376	123	123		

- Molecule 7 is a protein called RNA-binding protein 42.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	R	106	Total	C	N	O	0	0
			531	319	106	106		

- Molecule 8 is a protein called Ubiquitin carboxyl-terminal hydrolase 39.

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

- Molecule 9 is a protein called U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	X	22	Total	C	N	O	0	0
			110	66	22	22		

- Molecule 10 is a RNA chain called pre-mRNA.

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

- Molecule 11 is a RNA chain called 5'ss oligo.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	z	11	Total	C	N	O	P	0	0
			239	107	46	75	11		

- Molecule 12 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	A	2210	Total	C	N	O	0	0
			11208	6788	2210	2210		

- Molecule 13 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	B	1981	Total	C	N	O	0	0
			9980	6018	1981	1981		

- Molecule 14 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2	97	Total	C	N	O	P	0	0
			2052	917	346	692	97		

- Molecule 15 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	4	124	Total	C	N	O	P	0	0
			2636	1179	466	868	123		

- Molecule 16 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	6	59	Total	C	N	O	P	0	0
			1265	565	230	411	59		

- Molecule 17 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	7	159	Total	C	N	O	0	0
			799	481	159	159		

- Molecule 18 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	8	144	Total	C	N	O	0	0
			729	441	144	144		

- Molecule 19 is a protein called Splicing factor 3B subunit 4.

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

- Molecule 20 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	9	383	Total	C	N	O	0	0
			1920	1154	383	383		

- Molecule 21 is a protein called Splicing factor 3B subunit 2.

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

- Molecule 22 is a protein called Splicing factor 3B subunit 5.

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

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

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

- Molecule 24 is a protein called PHD finger-like domain-containing protein 5A.

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

- Molecule 25 is a protein called Splicing factor 3B subunit 1.

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

- Molecule 26 is a protein called Splicing factor 3B subunit 6.

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

- Molecule 27 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	22	95	Total	C	N	O	0	0
			482	292	95	95		
27	52	97	Total	C	N	O	0	0
			388	194	97	97		
27	42	92	Total	C	N	O	0	0
			463	279	92	92		

- Molecule 28 is a protein called U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	2B	92	Total	C	N	O	0	0
			461	277	92	92		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	2f	72	Total	C	N	O	0	0
			359	215	72	72		
29	5f	74	Total	C	N	O	0	0
			296	148	74	74		
29	4f	72	Total	C	N	O	0	0
			359	215	72	72		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	2b	82	Total	C	N	O	0	0
			413	249	82	82		
30	5b	86	Total	C	N	O	0	0
			344	172	86	86		
30	4b	82	Total	C	N	O	0	0
			413	249	82	82		

- Molecule 31 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	23	83	Total	C	N	O	0	0
			415	249	83	83		
31	53	77	Total	C	N	O	0	0
			308	154	77	77		
31	43	83	Total	C	N	O	0	0
			415	249	83	83		

- Molecule 32 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	2g	73	Total	C	N	O	0	0
			364	218	73	73		
32	5g	74	Total	C	N	O	0	0
			296	148	74	74		

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Mol	Chain	Residues	Atoms				AltConf	Trace
32	4g	74	Total	C	N	O	0	0
			369	221	74	74		

- Molecule 33 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	2e	81	Total	C	N	O	0	0
			403	241	81	81		
33	5e	79	Total	C	N	O	0	0
			316	158	79	79		
33	4e	76	Total	C	N	O	0	0
			378	226	76	76		

- Molecule 34 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	21	80	Total	C	N	O	0	0
			402	242	80	80		
34	51	82	Total	C	N	O	0	0
			328	164	82	82		
34	41	81	Total	C	N	O	0	0
			407	245	81	81		

- Molecule 35 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	2A	162	Total	C	N	O	0	0
			816	492	162	162		

- Molecule 36 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	66	72	Total	C	N	O	0	0
			357	213	72	72		

- Molecule 37 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	67	77	Total	C	N	O	0	0
			384	230	77	77		

- Molecule 38 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	62	95	Total	C	N	O	0	0
			478	288	95	95		

- Molecule 39 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	63	85	Total	C	N	O	0	0
			429	259	85	85		

- Molecule 40 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	68	95	Total	C	N	O	0	0
			469	279	95	95		

- Molecule 41 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	64	73	Total	C	N	O	0	0
			369	223	73	73		

- Molecule 42 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	65	76	Total	C	N	O	0	0
			378	226	76	76		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
43	J	159	Total	C	N	O	0	0
			792	474	159	159		

- Molecule 44 is a protein called Serine/threonine-protein kinase PRP4 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	K	322	Total	C	N	O	0	0
			1615	971	322	322		

- Molecule 45 is a protein called Probable ATP-dependent RNA helicase DDX23.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	G	415	Total	C	N	O	6	0
			2128	1286	421	421		

- Molecule 46 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	L	292	Total	C	N	O	0	0
			1464	880	292	292		

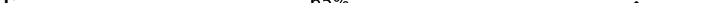
- Molecule 47 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

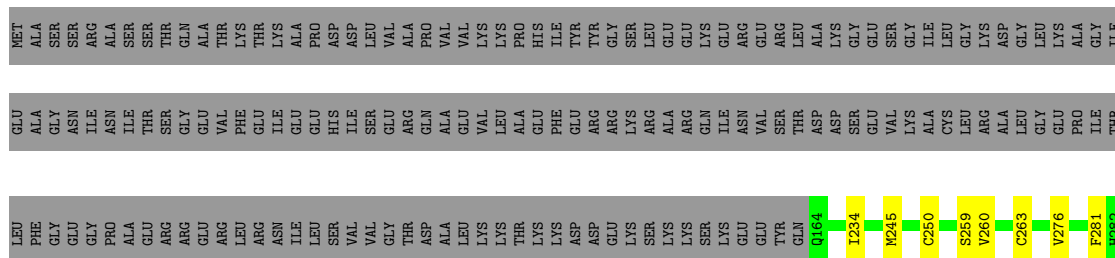
Mol	Chain	Residues	Atoms				AltConf	Trace
47	S	86	Total	C	N	O	0	0
			428	256	86	86		

- Molecule 48 is a protein called Pre-mRNA-processing factor 6.

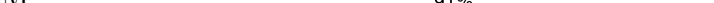
Mol	Chain	Residues	Atoms				AltConf	Trace
48	N	792	Total	C	N	O	0	0
			3991	2407	792	792		

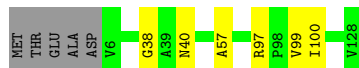
- Molecule 5: U4/U6 small nuclear ribonucleoprotein Prp4

Chain F:  65% . 31%

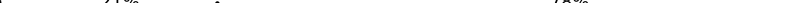


- Molecule 6: NHP2-like protein 1, N-terminally processed

Chain M:  91% 5%



- Molecule 7: RNA-binding protein 42

Chain R:  21% 78%



Chain U:

Chain	Residue	Value	Color
MET	SER	1164	Green
	GLY	1185	Green
	ARG	1166	Yellow
	SER	1171	Yellow
	LYS	1172	Green
	ARG	1173	Green
	GLU	1180	Yellow
	SER	1190	Yellow
	GLY	1198	Yellow
	THR	1202	Yellow
GLU	ARG	1206	Yellow
	LYS	1267	Green
	ASP	1353	Yellow
	GLU	1354	Yellow
	SER	1357	Yellow
	GLY	1382	Yellow
	ARG	1399	Yellow
	VAL	1403	Yellow
	ALA	1411	Yellow
	ASN	1416	Yellow
ASP	GLY	1420	Yellow
	VAL	1424	Green
	SER	1425	Green
	GLU	1426	Green
	ASP	1429	Yellow
	ALA	1438	Yellow
	SER	1439	Green
	ARG	1440	Yellow
	GLY	1441	Green
	SER	1442	Yellow
PRO	VAL	1443	Yellow
	ARG	1459	Yellow
	LYS	1464	Yellow
	ARG	1465	Green
	GLU	1466	Yellow
	PHE	1467	Yellow
	GLU	1468	Yellow
	PRO	1469	Yellow
	ALA	1470	Yellow
	SER	1471	Yellow
ALA	ARG	1472	Yellow
	GLU	1473	Yellow
	ASP	1474	Yellow
	GLY	1475	Yellow
	VAL	1476	Yellow
	ARG	1477	Yellow
	LYS	1478	Yellow
	THR	1479	Yellow
	GLY	1480	Yellow
	ASP	1481	Yellow

Chain X: 14% 86%

Met	THR	ARG	GLU	ASP	LEU	GLY	VAL	ASN	ALA	TYR	ILE	M130	V131	L151	ASP	PHE	ILE	ALA	THR	LYS	THR	ASP	LEU	GLY	VAL	ASN	ALA	TYR	ILE	M130	V131	L151	ASP	PHE	ILE	ALA
ARG	GLU	ASP	LEU	GLY	VAL	ASN	ALA	TYR	ILE	M130	V131	L151	ASP	PHE	ILE	ALA	THR	LYS	THR	ASP	LEU	GLY	VAL	ASN	ALA	TYR	ILE	M130	V131	L151	ASP	PHE	ILE	ALA		

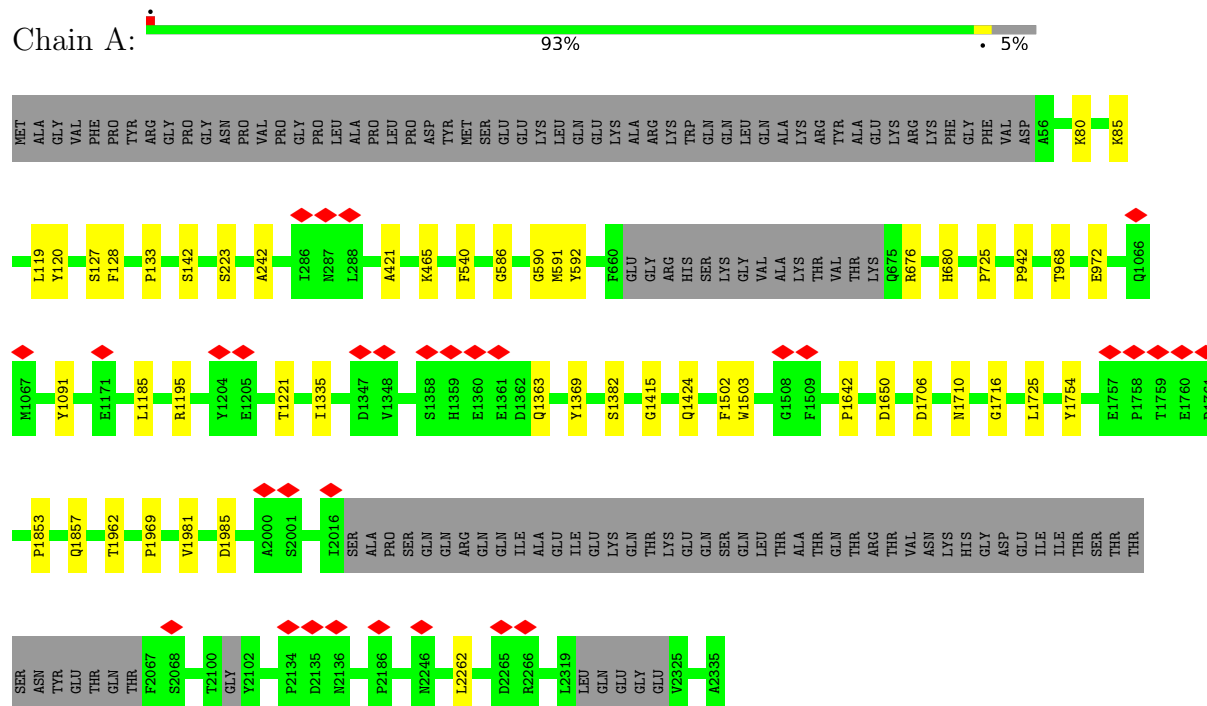
Chain Z: . 96%

Sequence logo for Chain Z, showing nucleotide conservation across 100 positions. The y-axis represents information content in bits. Nucleotides are color-coded: A (green), C (blue), G (red), and U (orange). Positions 629, 641, 642, and 643 are highlighted with colored boxes and labels: 629 (green), 641 (yellow), 642 (orange), and 643 (blue).

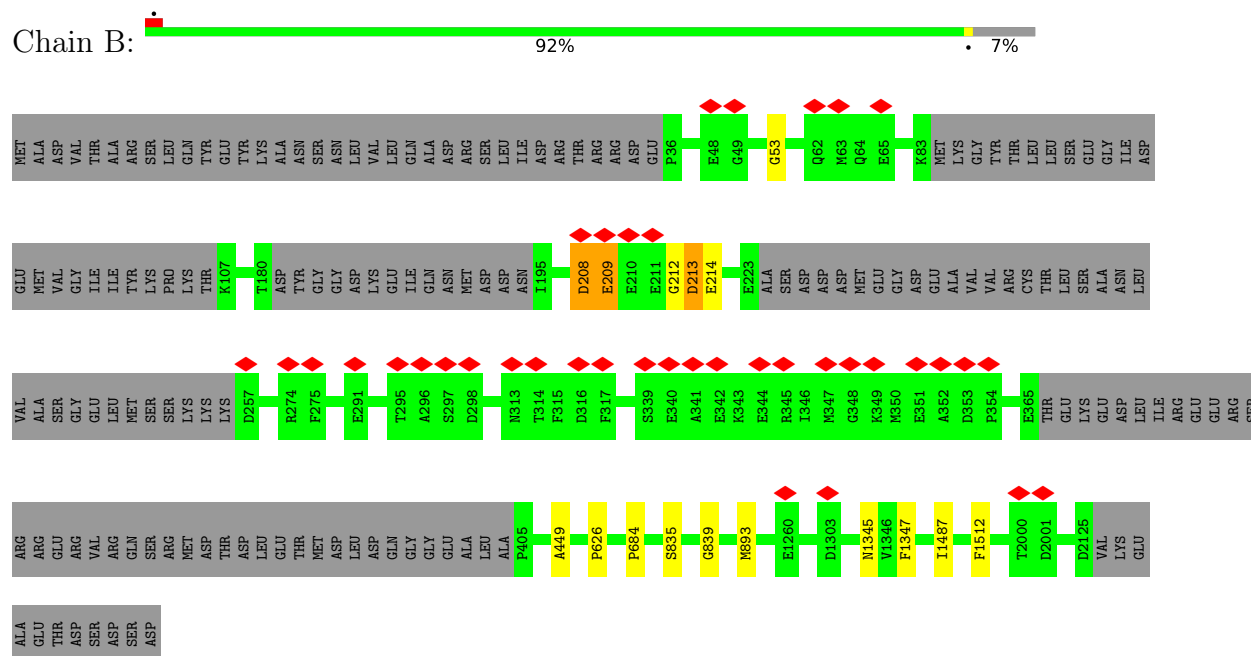
Chain z: 36% 55% 9%



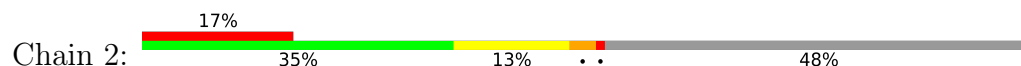
• Molecule 12: Pre-mRNA-processing-splicing factor 8

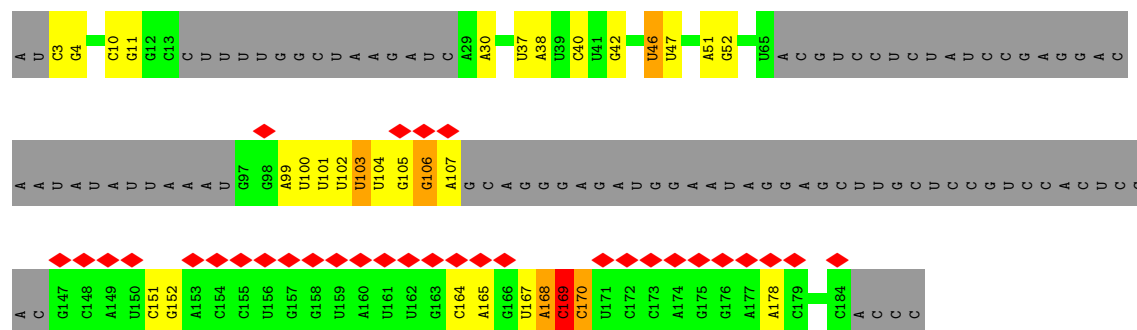


• Molecule 13: U5 small nuclear ribonucleoprotein 200 kDa helicase

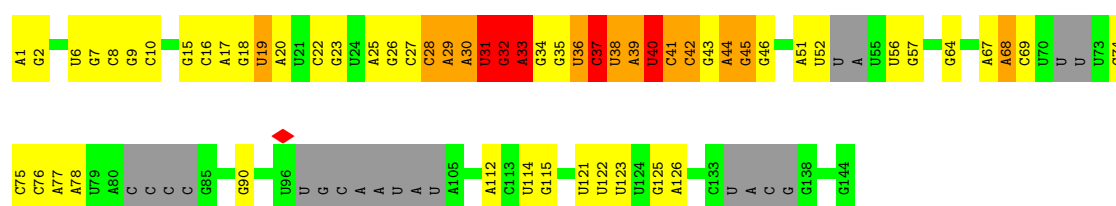


• Molecule 14: U2 snRNA

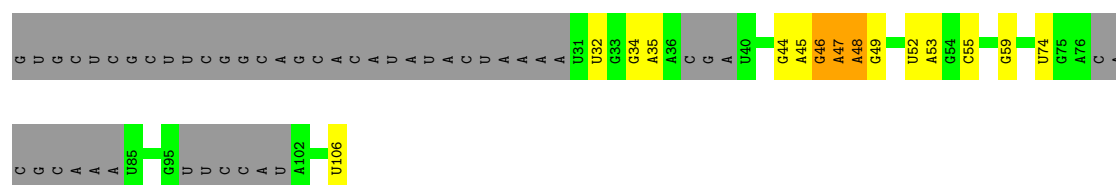




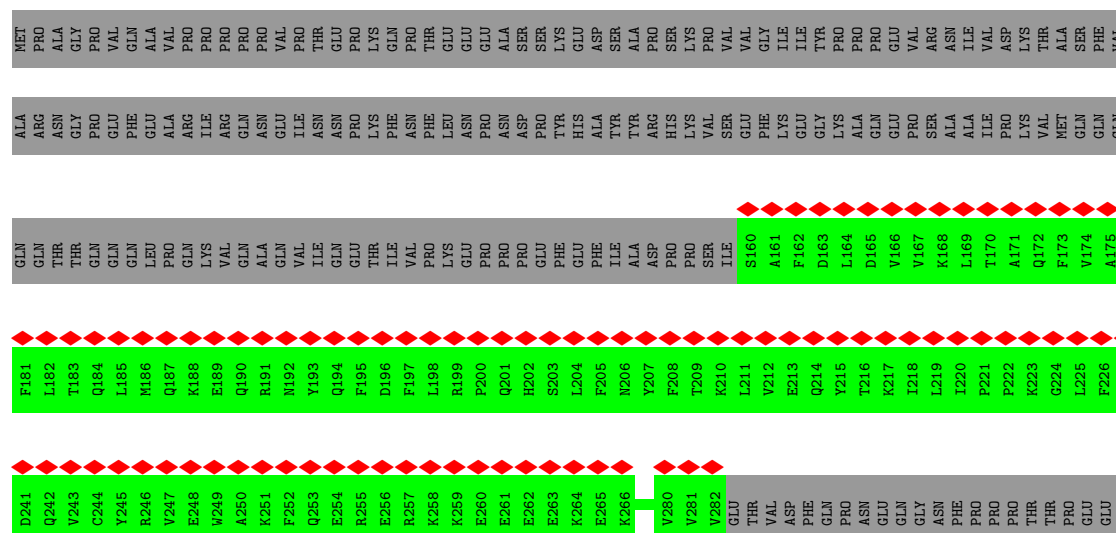
• Molecule 15: U4 snRNA

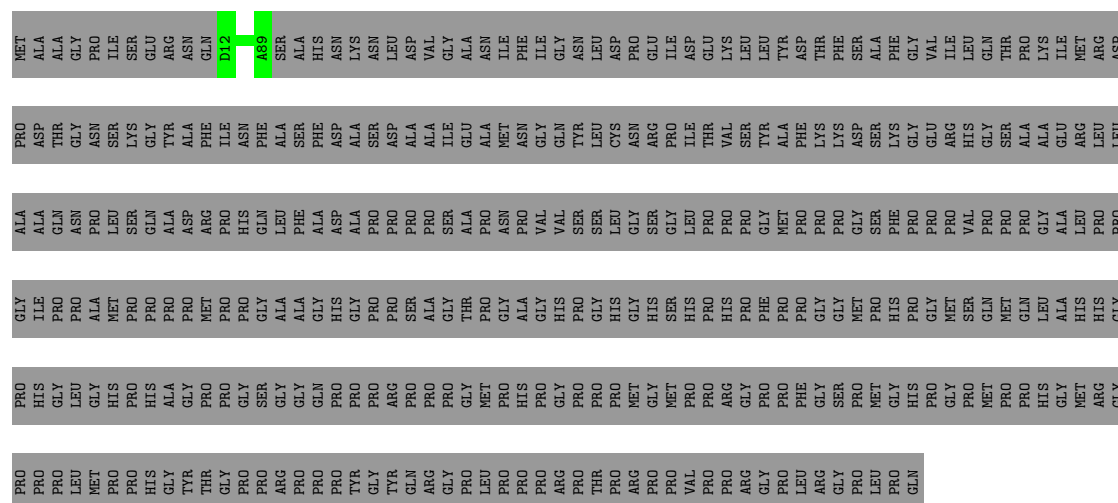


• Molecule 16: U6 snRNA

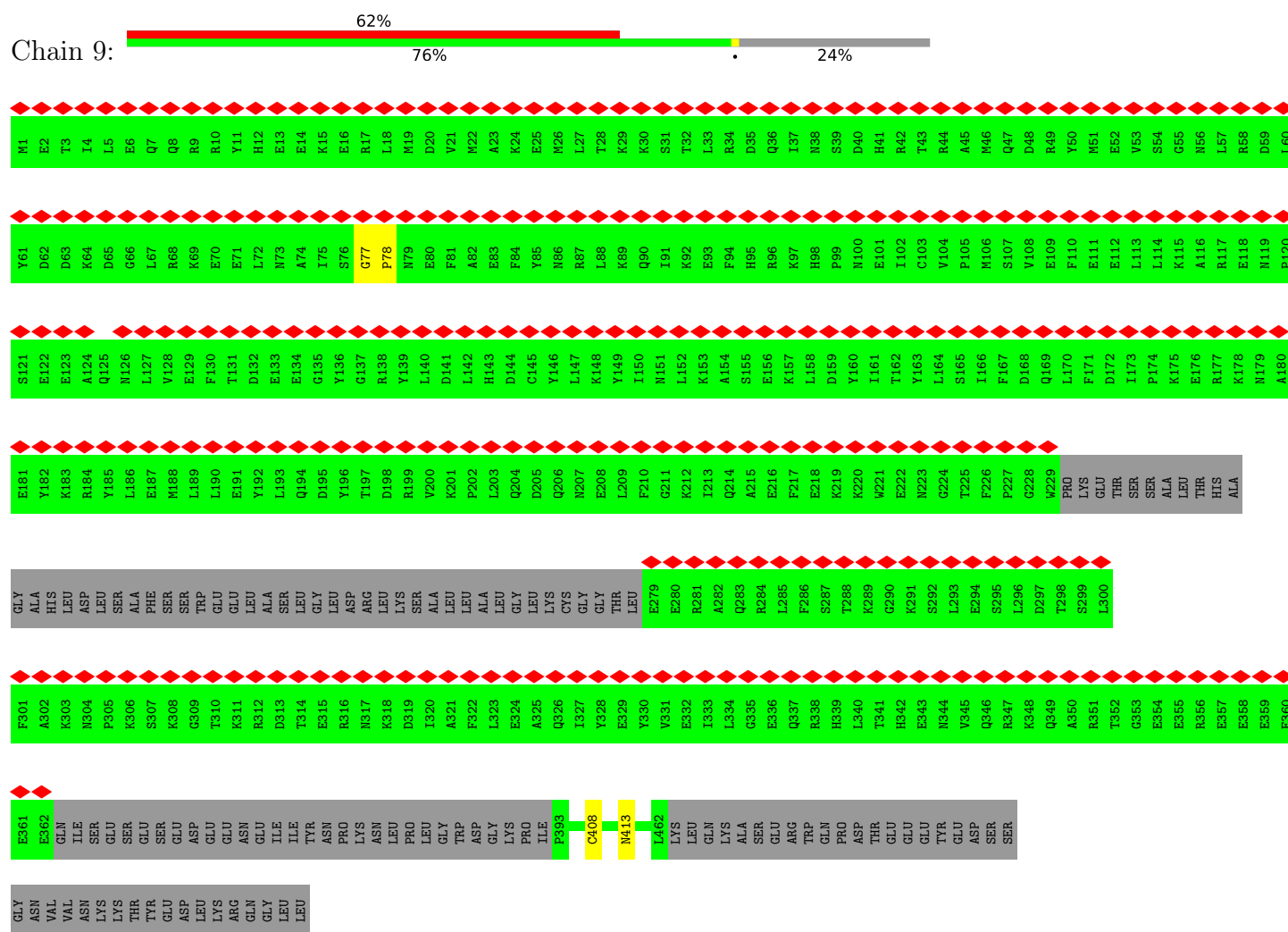


• Molecule 17: Splicing factor 3A subunit 1





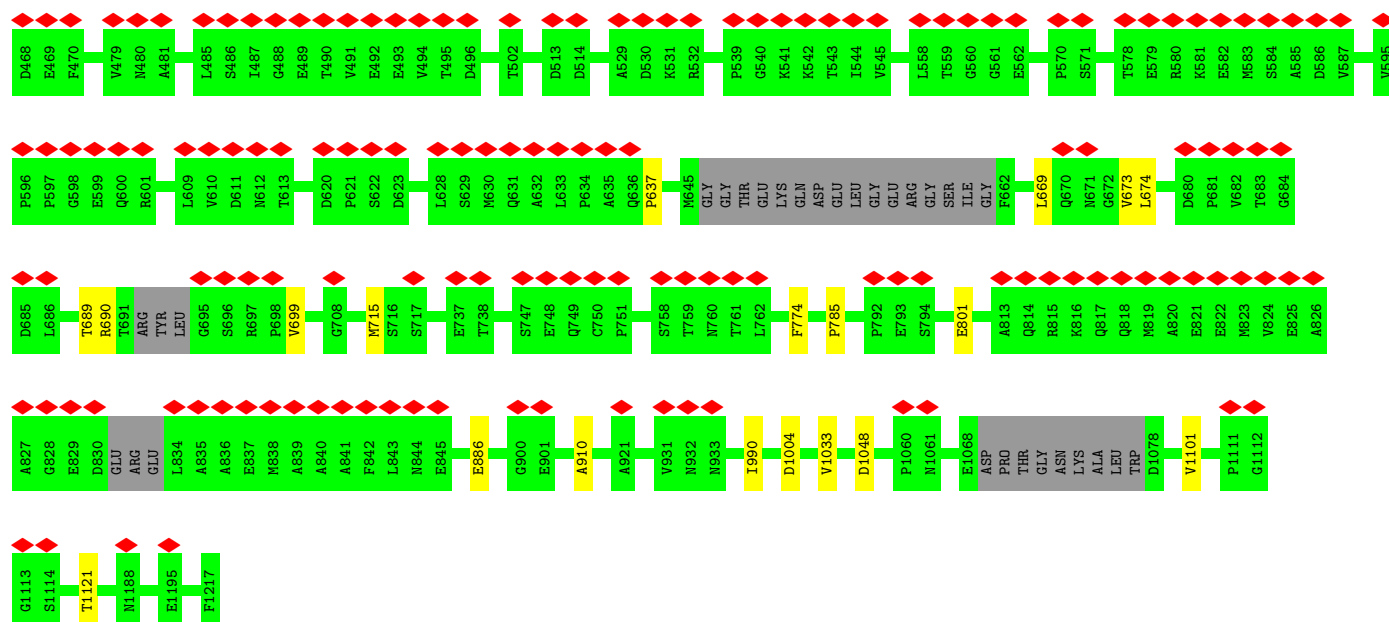
- Molecule 20: Splicing factor 3A subunit 3



- Molecule 21: Splicing factor 3B subunit 2

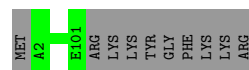






- Molecule 24: PHD finger-like domain-containing protein 5A

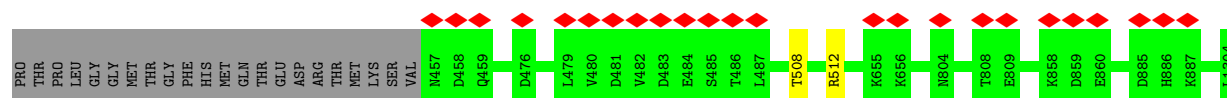
Chain BP: 91% 9%



- Molecule 25: Splicing factor 3B subunit 1

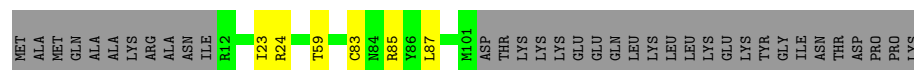
Chain B1: 67% 33%





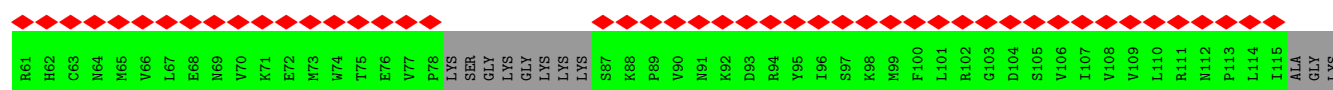
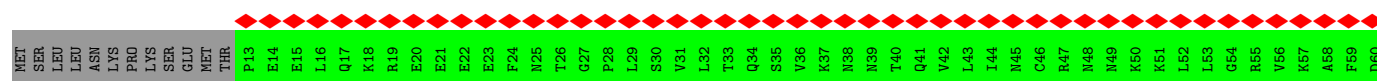
- Molecule 26: Splicing factor 3B subunit 6

Chain B6: 67% 5% 28%



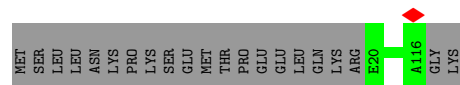
- Molecule 27: Small nuclear ribonucleoprotein Sm D2

Chain 22: 81% 81% 19%



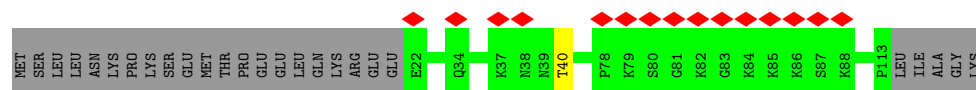
- Molecule 27: Small nuclear ribonucleoprotein Sm D2

Chain 52: 82% 18%



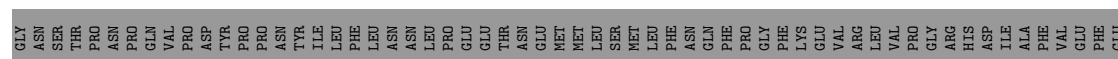
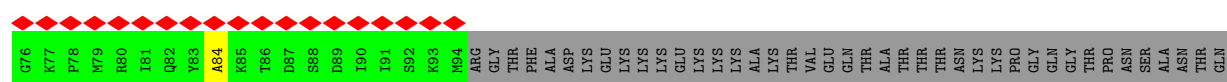
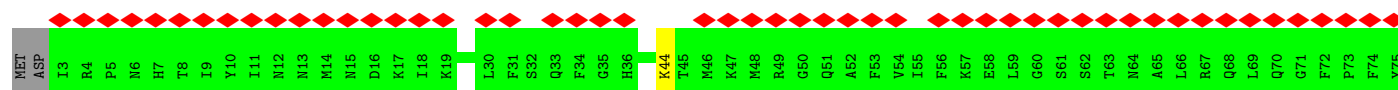
- Molecule 27: Small nuclear ribonucleoprotein Sm D2

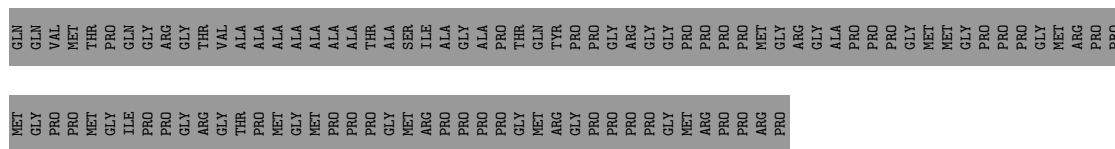
Chain 42: 13% 77% 22%



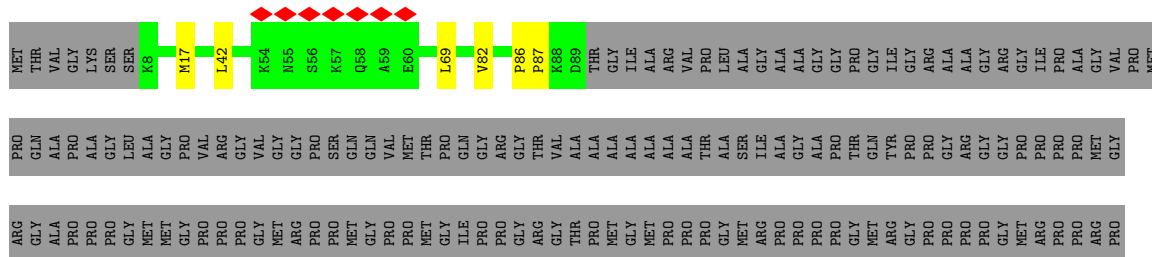
- Molecule 28: U2 small nuclear ribonucleoprotein B"

Chain 2B: 32% 40% 59%

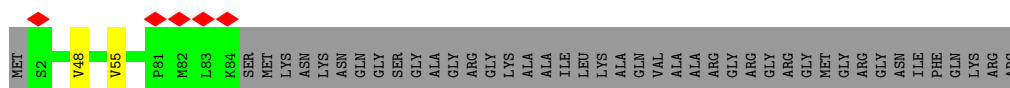




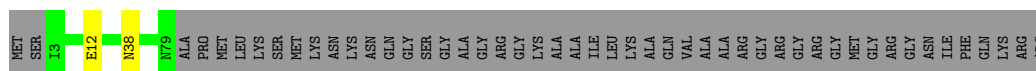
- Molecule 30: Small nuclear ribonucleoprotein-associated proteins B and B'



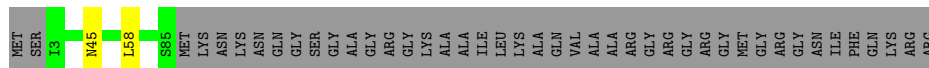
- Molecule 31: Small nuclear ribonucleoprotein Sm D3



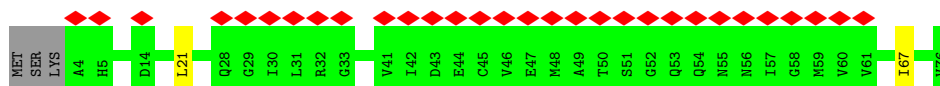
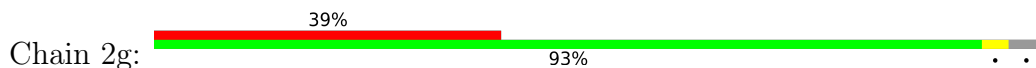
- Molecule 31: Small nuclear ribonucleoprotein Sm D3



- Molecule 31: Small nuclear ribonucleoprotein Sm D3



- Molecule 32: Small nuclear ribonucleoprotein G

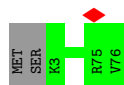


- Molecule 32: Small nuclear ribonucleoprotein G

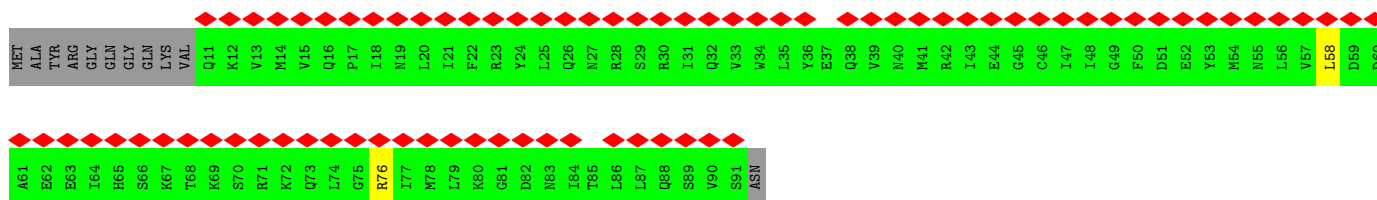
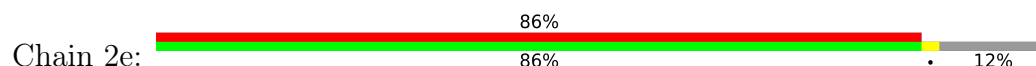




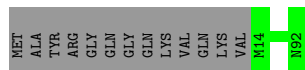
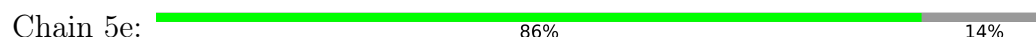
- Molecule 32: Small nuclear ribonucleoprotein G



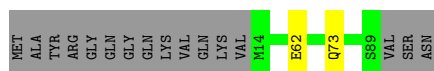
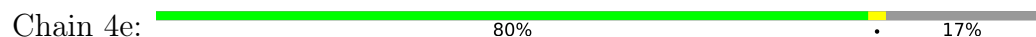
- Molecule 33: Small nuclear ribonucleoprotein E



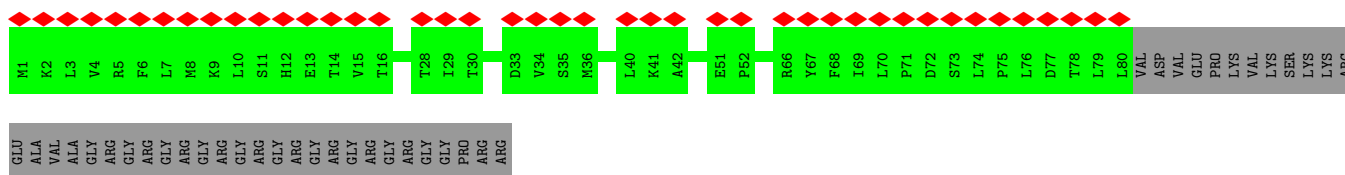
- Molecule 33: Small nuclear ribonucleoprotein E



- Molecule 33: Small nuclear ribonucleoprotein E



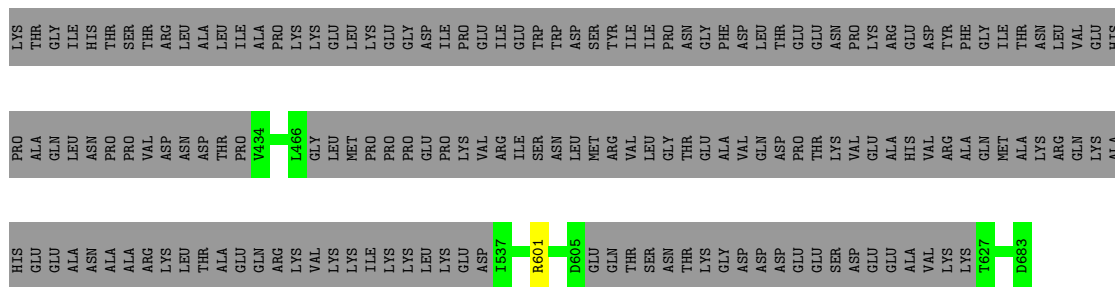
- Molecule 34: Small nuclear ribonucleoprotein Sm D1



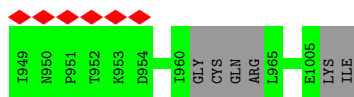
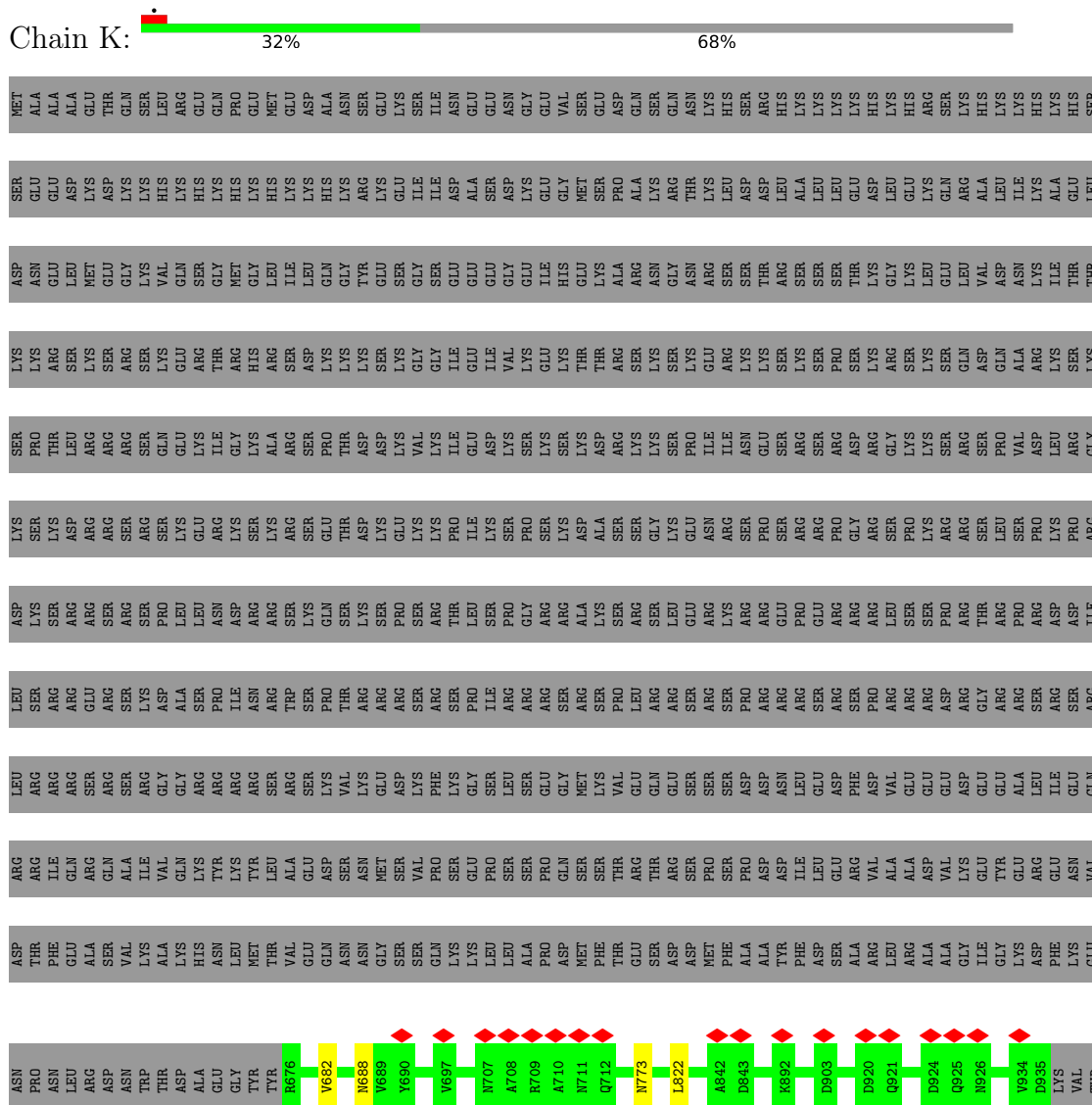
- Molecule 34: Small nuclear ribonucleoprotein Sm D1



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



- Molecule 44: Serine/threonine-protein kinase PRP4 homolog



- Molecule 45: Probable ATP-dependent RNA helicase DDX23





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	176879	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	0.034	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	580.0, 580.0, 580.0	wwPDB
Map dimensions	500, 500, 500	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	5	0.19	0/2698	0.38	6/4195 (0.1%)
2	C	0.10	0/4270	0.28	0/5983
3	D	0.10	0/712	0.28	0/995
4	E	0.24	0/1540	0.46	0/2148
5	F	0.15	0/1809	0.39	0/2525
6	M	0.41	0/627	0.55	0/878
7	R	0.08	0/534	0.26	0/745
8	U	0.09	0/2330	0.25	0/3268
9	X	0.57	0/110	0.56	0/152
10	Z	0.12	0/349	0.24	0/540
11	z	0.08	0/268	0.17	0/416
12	A	0.14	0/11329	0.32	1/15897 (0.0%)
13	B	0.17	0/10059	0.34	0/14084
14	2	0.22	0/2286	0.46	7/3550 (0.2%)
15	4	0.24	0/2941	0.49	12/4569 (0.3%)
16	6	0.08	0/1413	0.13	0/2194
17	7	0.13	0/802	0.30	0/1120
18	8	0.15	0/734	0.39	0/1025
19	B4	0.13	0/394	0.29	0/549
20	9	0.14	0/1928	0.31	0/2692
21	B2	0.14	0/1092	0.35	0/1536
22	B5	0.10	0/349	0.26	0/487
23	B3	0.14	0/6024	0.35	0/8425
24	BP	0.13	0/501	0.39	0/697
25	B1	0.19	0/4421	0.40	0/6190
26	B6	0.12	0/459	0.30	0/642
27	22	0.12	0/485	0.35	0/677
27	42	0.39	0/466	0.56	0/651
27	52	0.09	0/387	0.23	0/482
28	2B	0.11	0/463	0.27	0/646
29	2f	0.16	0/362	0.39	0/502
29	4f	0.16	0/362	0.38	0/502
29	5f	0.09	0/295	0.22	0/367
30	2b	0.12	0/416	0.36	0/581

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	4b	0.16	0/416	0.36	0/581
30	5b	0.11	0/343	0.20	0/427
31	23	0.16	0/417	0.43	0/581
31	43	0.14	0/417	0.35	0/581
31	53	0.09	0/307	0.21	0/382
32	2g	0.13	0/366	0.37	0/509
32	4g	0.14	0/371	0.36	0/516
32	5g	0.10	0/295	0.22	0/367
33	2e	0.13	0/403	0.38	0/561
33	4e	0.14	0/378	0.42	0/526
33	5e	0.10	0/315	0.21	0/392
34	21	0.13	0/404	0.35	0/564
34	41	0.13	0/409	0.33	0/571
34	51	0.11	0/327	0.21	0/407
35	2A	0.16	0/821	0.42	0/1149
36	66	0.16	0/358	0.38	0/497
37	67	0.11	0/386	0.28	0/537
38	62	0.15	0/480	0.37	0/671
39	63	0.14	0/432	0.42	0/604
40	68	0.14	0/469	0.34	0/651
41	64	0.16	0/372	0.40	0/520
42	65	0.14	0/380	0.33	0/528
43	J	0.20	0/792	0.35	0/1101
44	K	0.14	0/1622	0.38	0/2265
45	G	0.24	0/2146	0.40	0/3003
46	L	0.38	0/1469	0.55	0/2049
47	S	0.09	0/427	0.21	0/591
48	N	0.18	0/4017	0.36	0/5620
All	All	0.17	0/82554	0.36	26/116661 (0.0%)

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	4	37	C	P-O3'-C3'	-8.13	108.00	120.20
15	4	32	G	P-O3'-C3'	-8.01	108.19	120.20
15	4	41	C	P-O3'-C3'	-7.94	108.29	120.20
15	4	30	A	P-O3'-C3'	-7.92	108.32	120.20
1	5	76	A	P-O3'-C3'	-7.86	108.42	120.20

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	5	2420	0	1226	29	0
2	C	4223	0	2099	17	0
3	D	708	0	328	1	0
4	E	1531	0	747	8	0
5	F	1795	0	891	10	0
6	M	622	0	313	8	0
7	R	531	0	253	3	0
8	U	2308	0	1104	23	0
9	X	110	0	50	1	0
10	Z	314	0	160	0	0
11	z	239	0	119	4	0
12	A	11208	0	5481	29	0
13	B	9980	0	4817	10	0
14	2	2052	0	1038	12	0
15	4	2636	0	1339	65	0
16	6	1265	0	638	18	0
17	7	799	0	377	0	0
18	8	729	0	356	2	0
19	B4	391	0	197	0	0
20	9	1920	0	902	2	0
21	B2	1072	0	563	0	0
22	B5	347	0	171	1	0
23	B3	5969	0	2985	13	0
24	BP	498	0	241	0	0
25	B1	4383	0	2195	1	0
26	B6	455	0	227	3	0
27	22	482	0	220	0	0
27	42	463	0	211	1	0
27	52	388	0	102	0	0
28	2B	461	0	218	2	0
29	2f	359	0	179	2	0
29	4f	359	0	179	2	0
29	5f	296	0	87	0	0
30	2b	413	0	194	1	0
30	4b	413	0	194	3	0
30	5b	344	0	93	0	0
31	23	415	0	198	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	43	415	0	198	1	0
31	53	308	0	86	2	0
32	2g	364	0	176	1	0
32	4g	369	0	178	0	0
32	5g	296	0	84	0	0
33	2e	403	0	173	1	0
33	4e	378	0	163	1	0
33	5e	316	0	85	0	0
34	21	402	0	184	0	0
34	41	407	0	183	0	0
34	51	328	0	89	0	0
35	2A	816	0	386	0	0
36	66	357	0	169	1	0
37	67	384	0	178	0	0
38	62	478	0	222	0	0
39	63	429	0	199	2	0
40	68	469	0	220	3	0
41	64	369	0	172	1	0
42	65	378	0	174	1	0
43	J	792	0	366	4	0
44	K	1615	0	754	2	0
45	G	2128	0	1038	2	0
46	L	1464	0	708	28	0
47	S	428	0	200	2	0
48	N	3991	0	2047	1	0
All	All	80982	0	39124	280	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 280 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)
46:L:251:LEU:HA	46:L:272:GLY:HA3	1.27	1.08
46:L:251:LEU:HA	46:L:272:GLY:CA	1.85	1.04
31:23:48:VAL:O	31:23:55:VAL:HA	1.74	0.87
4:E:56:GLN:H	4:E:96:TYR:HA	1.39	0.87
23:B3:886:GLU:HA	23:B3:910:ALA:O	1.76	0.83

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	
2	C	834/972 (86%)	813 (98%)	21 (2%)	0	100	100
3	D	139/142 (98%)	136 (98%)	3 (2%)	0	100	100
4	E	305/357 (85%)	301 (99%)	4 (1%)	0	100	100
5	F	357/522 (68%)	348 (98%)	9 (2%)	0	100	100
6	M	121/128 (94%)	121 (100%)	0	0	100	100
7	R	104/480 (22%)	101 (97%)	3 (3%)	0	100	100
8	U	454/565 (80%)	441 (97%)	13 (3%)	0	100	100
9	X	20/155 (13%)	20 (100%)	0	0	100	100
12	A	2200/2335 (94%)	2116 (96%)	83 (4%)	1 (0%)	100	100
13	B	1971/2136 (92%)	1940 (98%)	28 (1%)	3 (0%)	43	78
17	7	155/793 (20%)	155 (100%)	0	0	100	100
18	8	138/464 (30%)	135 (98%)	3 (2%)	0	100	100
19	B4	76/424 (18%)	76 (100%)	0	0	100	100
20	9	377/501 (75%)	372 (99%)	5 (1%)	0	100	100
21	B2	204/895 (23%)	200 (98%)	4 (2%)	0	100	100
22	B5	67/86 (78%)	66 (98%)	1 (2%)	0	100	100
23	B3	1176/1217 (97%)	1144 (97%)	32 (3%)	0	100	100
24	BP	98/110 (89%)	96 (98%)	2 (2%)	0	100	100
25	B1	866/1304 (66%)	847 (98%)	19 (2%)	0	100	100
26	B6	88/125 (70%)	84 (96%)	4 (4%)	0	100	100
27	22	91/118 (77%)	91 (100%)	0	0	100	100
27	42	90/118 (76%)	89 (99%)	1 (1%)	0	100	100
27	52	95/118 (80%)	88 (93%)	7 (7%)	0	100	100
28	2B	90/225 (40%)	90 (100%)	0	0	100	100
29	2f	70/86 (81%)	68 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	4f	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
29	5f	72/86 (84%)	72 (100%)	0	0	100	100
30	2b	80/240 (33%)	80 (100%)	0	0	100	100
30	4b	80/240 (33%)	79 (99%)	1 (1%)	0	100	100
30	5b	84/240 (35%)	78 (93%)	6 (7%)	0	100	100
31	23	81/126 (64%)	78 (96%)	3 (4%)	0	100	100
31	43	81/126 (64%)	81 (100%)	0	0	100	100
31	53	75/126 (60%)	72 (96%)	3 (4%)	0	100	100
32	2g	71/76 (93%)	71 (100%)	0	0	100	100
32	4g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
32	5g	72/76 (95%)	69 (96%)	3 (4%)	0	100	100
33	2e	79/92 (86%)	79 (100%)	0	0	100	100
33	4e	74/92 (80%)	74 (100%)	0	0	100	100
33	5e	77/92 (84%)	77 (100%)	0	0	100	100
34	21	78/119 (66%)	75 (96%)	3 (4%)	0	100	100
34	41	79/119 (66%)	78 (99%)	1 (1%)	0	100	100
34	51	80/119 (67%)	76 (95%)	4 (5%)	0	100	100
35	2A	160/255 (63%)	158 (99%)	2 (1%)	0	100	100
36	66	70/80 (88%)	69 (99%)	1 (1%)	0	100	100
37	67	75/103 (73%)	74 (99%)	1 (1%)	0	100	100
38	62	93/95 (98%)	89 (96%)	4 (4%)	0	100	100
39	63	83/102 (81%)	82 (99%)	1 (1%)	0	100	100
40	68	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
41	64	71/139 (51%)	70 (99%)	1 (1%)	0	100	100
42	65	74/91 (81%)	71 (96%)	3 (4%)	0	100	100
43	J	153/683 (22%)	151 (99%)	2 (1%)	0	100	100
44	K	316/1007 (31%)	307 (97%)	9 (3%)	0	100	100
45	G	413/820 (50%)	405 (98%)	6 (2%)	2 (0%)	24	63
46	L	284/499 (57%)	280 (99%)	4 (1%)	0	100	100
47	S	80/800 (10%)	79 (99%)	1 (1%)	0	100	100
48	N	780/941 (83%)	769 (99%)	11 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	14236/22218 (64%)	13911 (98%)	319 (2%)	6 (0%)	100	100

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
45	G	355	ARG
12	A	80	LYS
13	B	208	ASP
13	B	213	ASP
45	G	366	THR

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	
2	C	48/866 (6%)	48 (100%)	0	100	100
3	D	5/130 (4%)	5 (100%)	0	100	100
4	E	10/300 (3%)	10 (100%)	0	100	100
5	F	15/442 (3%)	15 (100%)	0	100	100
6	M	6/111 (5%)	6 (100%)	0	100	100
7	R	4/369 (1%)	4 (100%)	0	100	100
8	U	23/511 (4%)	23 (100%)	0	100	100
9	X	1/144 (1%)	1 (100%)	0	100	100
12	A	126/2108 (6%)	126 (100%)	0	100	100
13	B	84/1908 (4%)	84 (100%)	0	100	100
17	7	5/709 (1%)	5 (100%)	0	100	100
18	8	8/382 (2%)	8 (100%)	0	100	100
19	B4	4/336 (1%)	4 (100%)	0	100	100
20	9	11/446 (2%)	11 (100%)	0	100	100
21	B2	22/776 (3%)	22 (100%)	0	100	100
22	B5	3/77 (4%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	B3	60/1051 (6%)	60 (100%)	0	100	100
24	BP	4/95 (4%)	4 (100%)	0	100	100
25	B1	40/1104 (4%)	40 (100%)	0	100	100
26	B6	5/109 (5%)	5 (100%)	0	100	100
27	22	5/110 (4%)	5 (100%)	0	100	100
27	42	4/110 (4%)	4 (100%)	0	100	100
28	2B	3/195 (2%)	3 (100%)	0	100	100
29	2f	4/74 (5%)	4 (100%)	0	100	100
29	4f	4/74 (5%)	4 (100%)	0	100	100
30	2b	4/177 (2%)	4 (100%)	0	100	100
30	4b	4/177 (2%)	4 (100%)	0	100	100
31	23	3/101 (3%)	3 (100%)	0	100	100
31	43	3/101 (3%)	3 (100%)	0	100	100
32	2g	3/66 (4%)	3 (100%)	0	100	100
32	4g	3/66 (4%)	3 (100%)	0	100	100
33	2e	1/84 (1%)	1 (100%)	0	100	100
33	4e	1/84 (1%)	1 (100%)	0	100	100
34	21	3/101 (3%)	3 (100%)	0	100	100
34	41	3/101 (3%)	3 (100%)	0	100	100
35	2A	6/218 (3%)	6 (100%)	0	100	100
36	66	2/70 (3%)	2 (100%)	0	100	100
37	67	3/91 (3%)	3 (100%)	0	100	100
38	62	3/88 (3%)	3 (100%)	0	100	100
39	63	4/94 (4%)	4 (100%)	0	100	100
40	68	1/82 (1%)	1 (100%)	0	100	100
41	64	4/111 (4%)	4 (100%)	0	100	100
42	65	3/80 (4%)	3 (100%)	0	100	100
43	J	3/599 (0%)	3 (100%)	0	100	100
44	K	10/919 (1%)	10 (100%)	0	100	100
45	G	22/721 (3%)	22 (100%)	0	100	100
46	L	9/424 (2%)	9 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	S	2/681 (0%)	2 (100%)	0	100	100
48	N	32/792 (4%)	32 (100%)	0	100	100
All	All	636/18565 (3%)	636 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	114/117 (97%)	42 (36%)	1 (0%)
10	Z	14/347 (4%)	1 (7%)	0
11	z	10/11 (90%)	5 (50%)	0
14	2	93/188 (49%)	16 (17%)	4 (4%)
15	4	119/144 (82%)	21 (17%)	3 (2%)
16	6	55/106 (51%)	6 (10%)	0
All	All	405/913 (44%)	91 (22%)	8 (1%)

5 of 91 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	8	G
1	5	9	G
1	5	10	U
1	5	12	U
1	5	14	U

5 of 8 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
15	4	114	U
15	4	68	A
14	2	106	G
14	2	103	U
15	4	1	A

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.

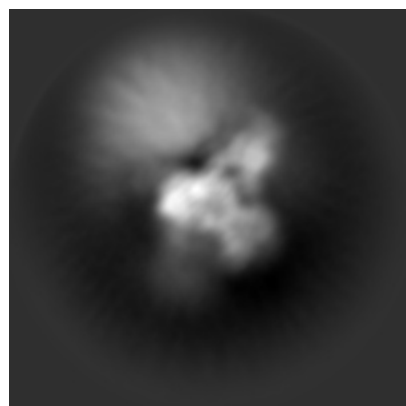
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18788. These allow visual inspection of the internal detail of the map and identification of artifacts.

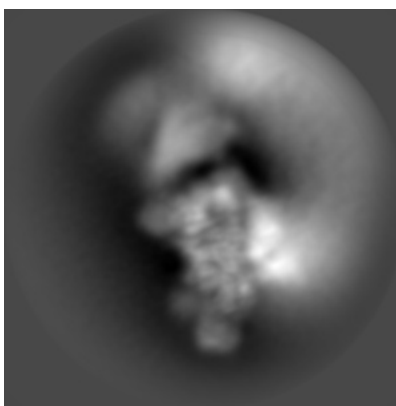
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

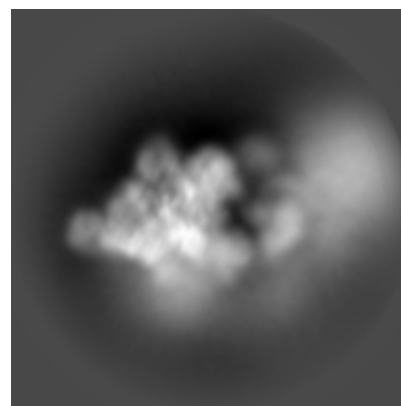
6.1.1 Primary map



X

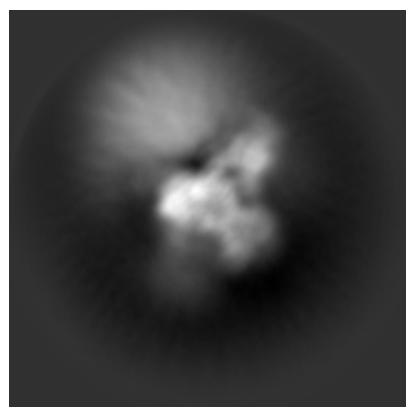


Y

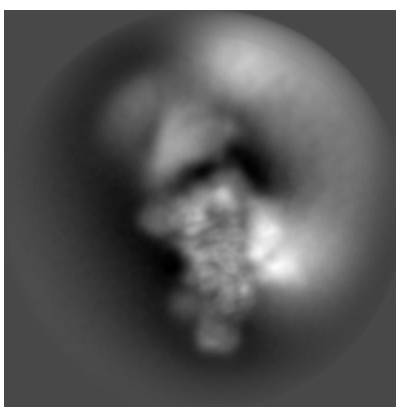


Z

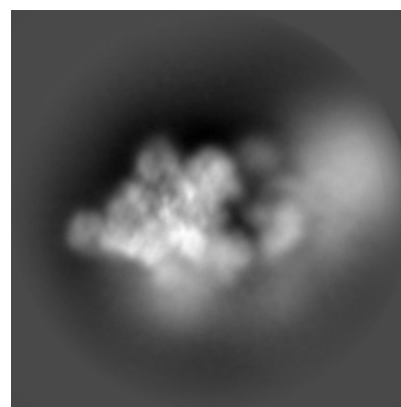
6.1.2 Raw map



X



Y

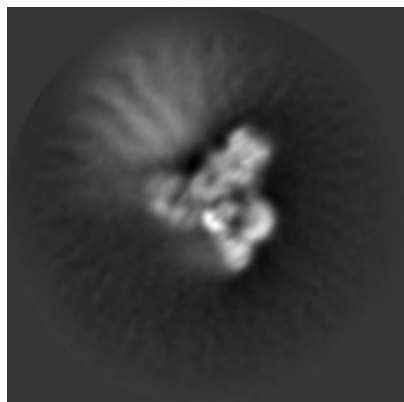


Z

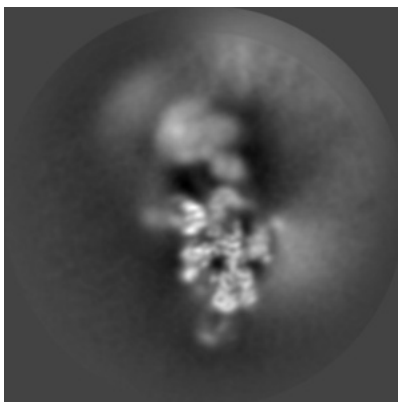
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

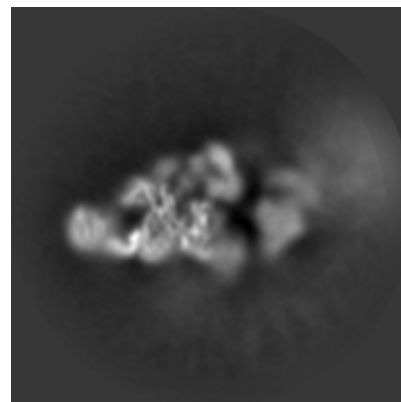
6.2.1 Primary map



X Index: 250

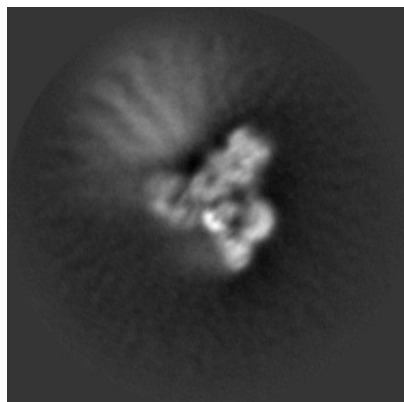


Y Index: 250

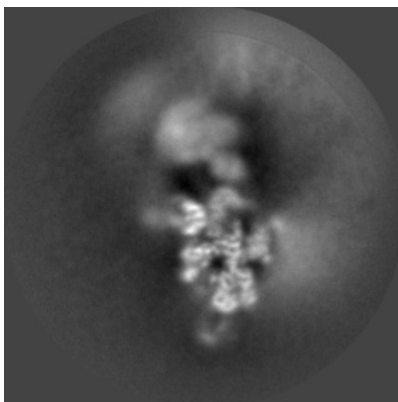


Z Index: 250

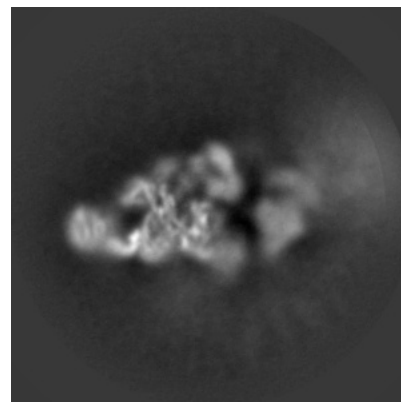
6.2.2 Raw map



X Index: 250



Y Index: 250

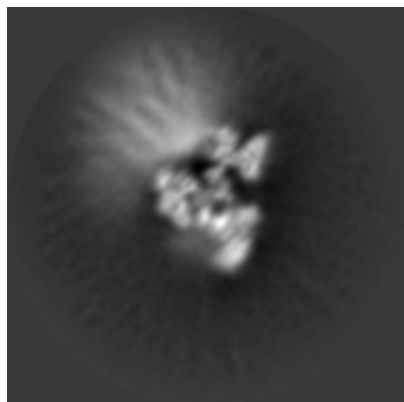


Z Index: 250

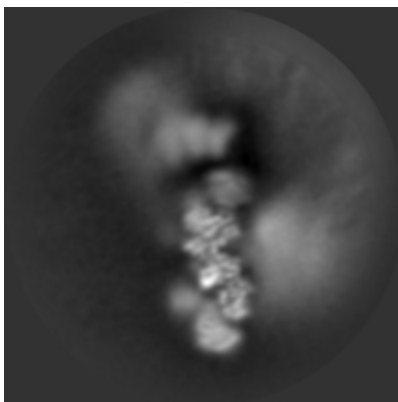
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

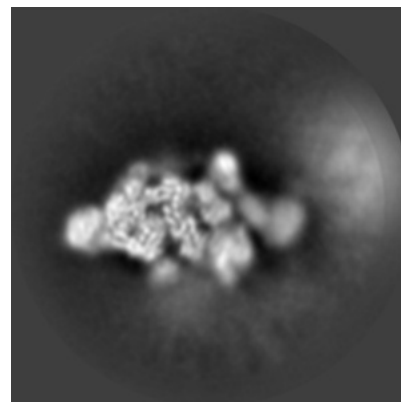
6.3.1 Primary map



X Index: 225

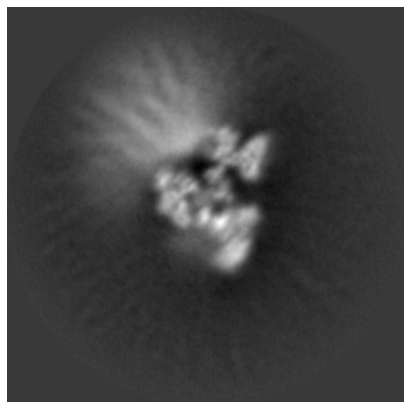


Y Index: 214

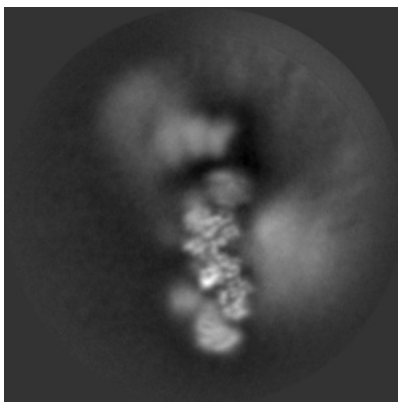


Z Index: 275

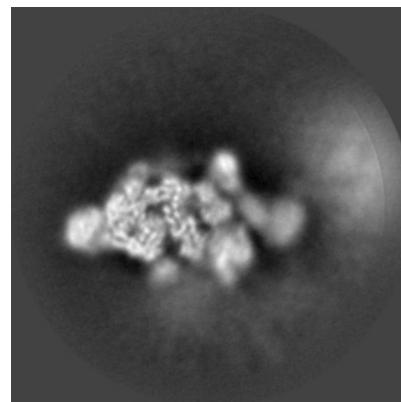
6.3.2 Raw map



X Index: 225



Y Index: 214

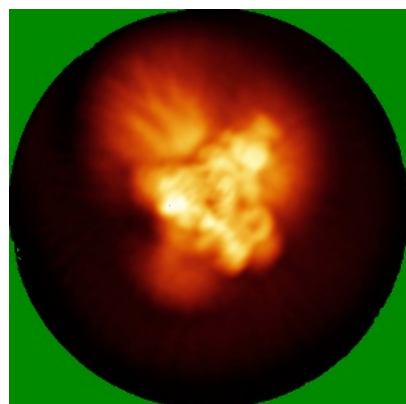


Z Index: 275

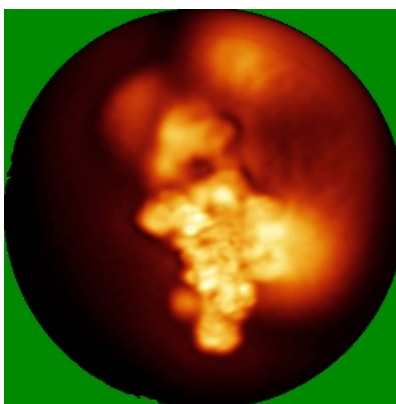
The images above show the largest variance slices of the map in three orthogonal directions.

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

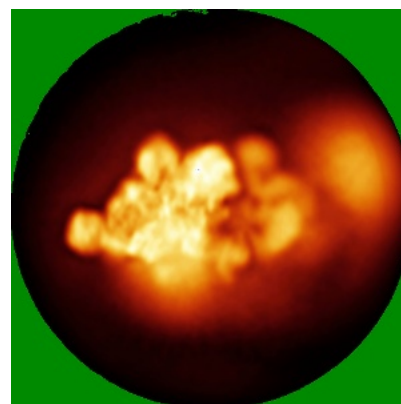
6.4.1 Primary map



X

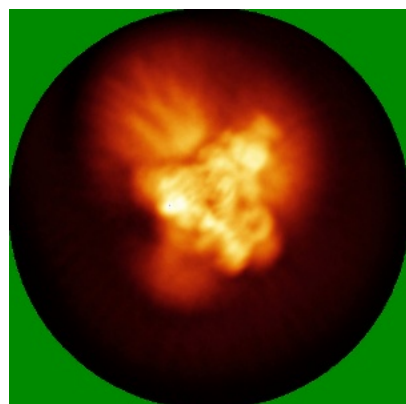


Y

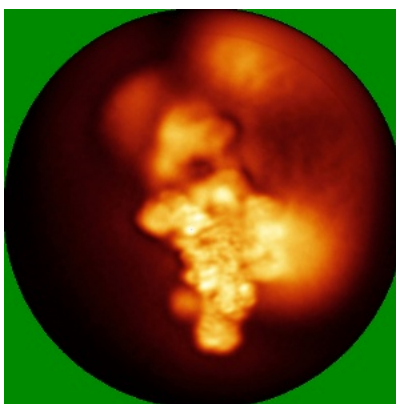


Z

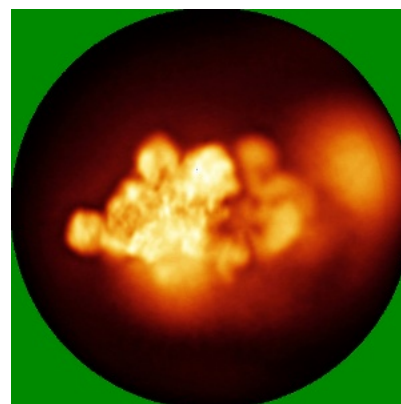
6.4.2 Raw map



X



Y

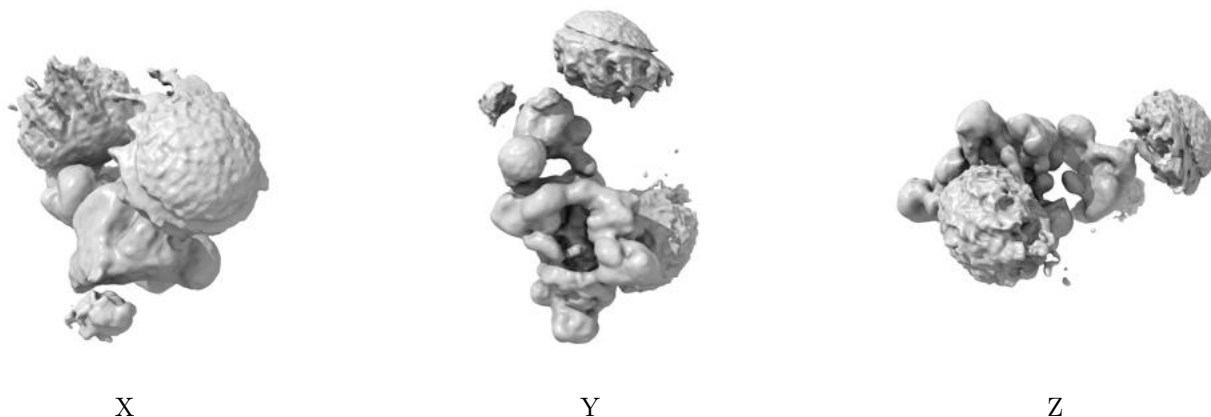


Z

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

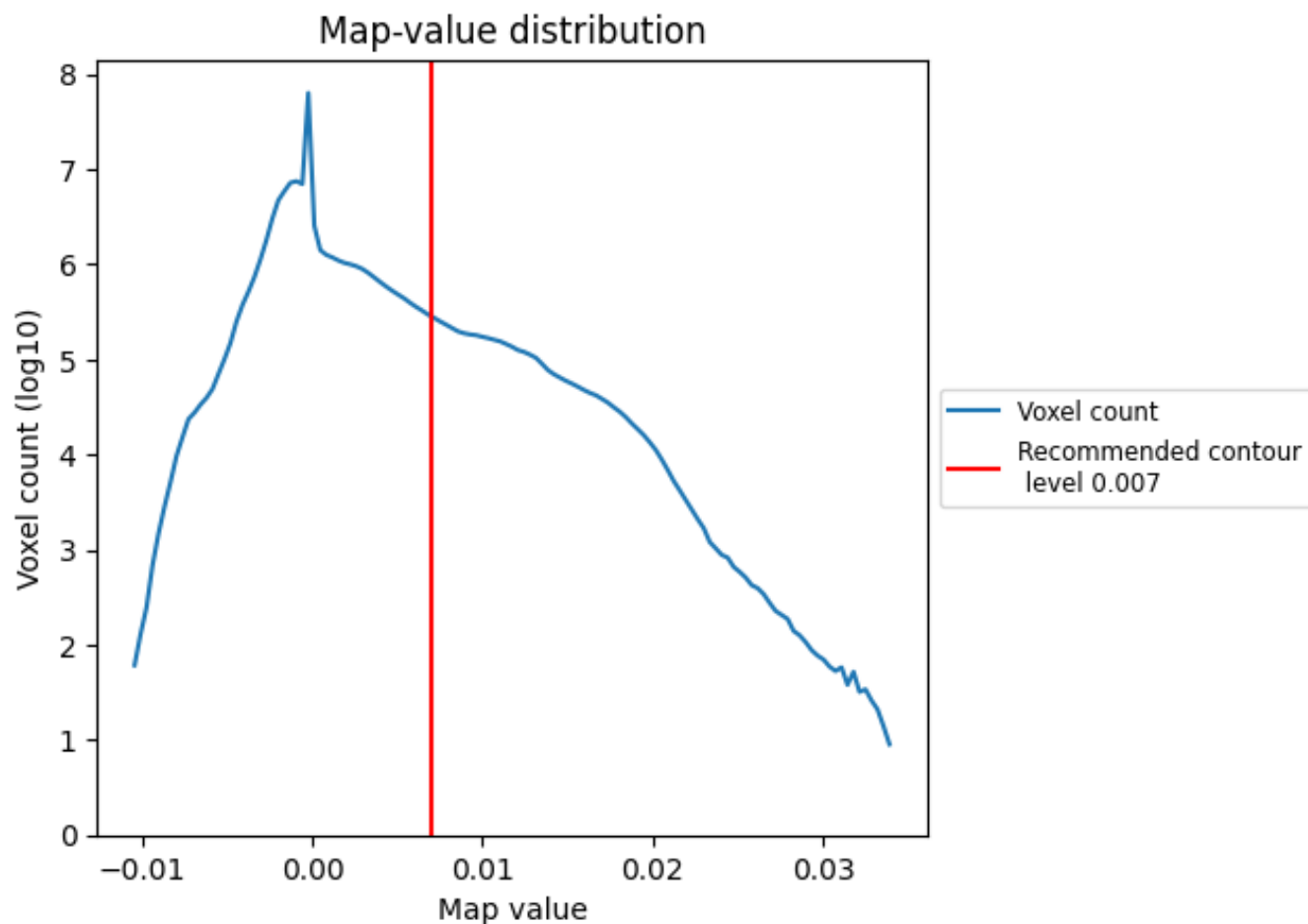
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

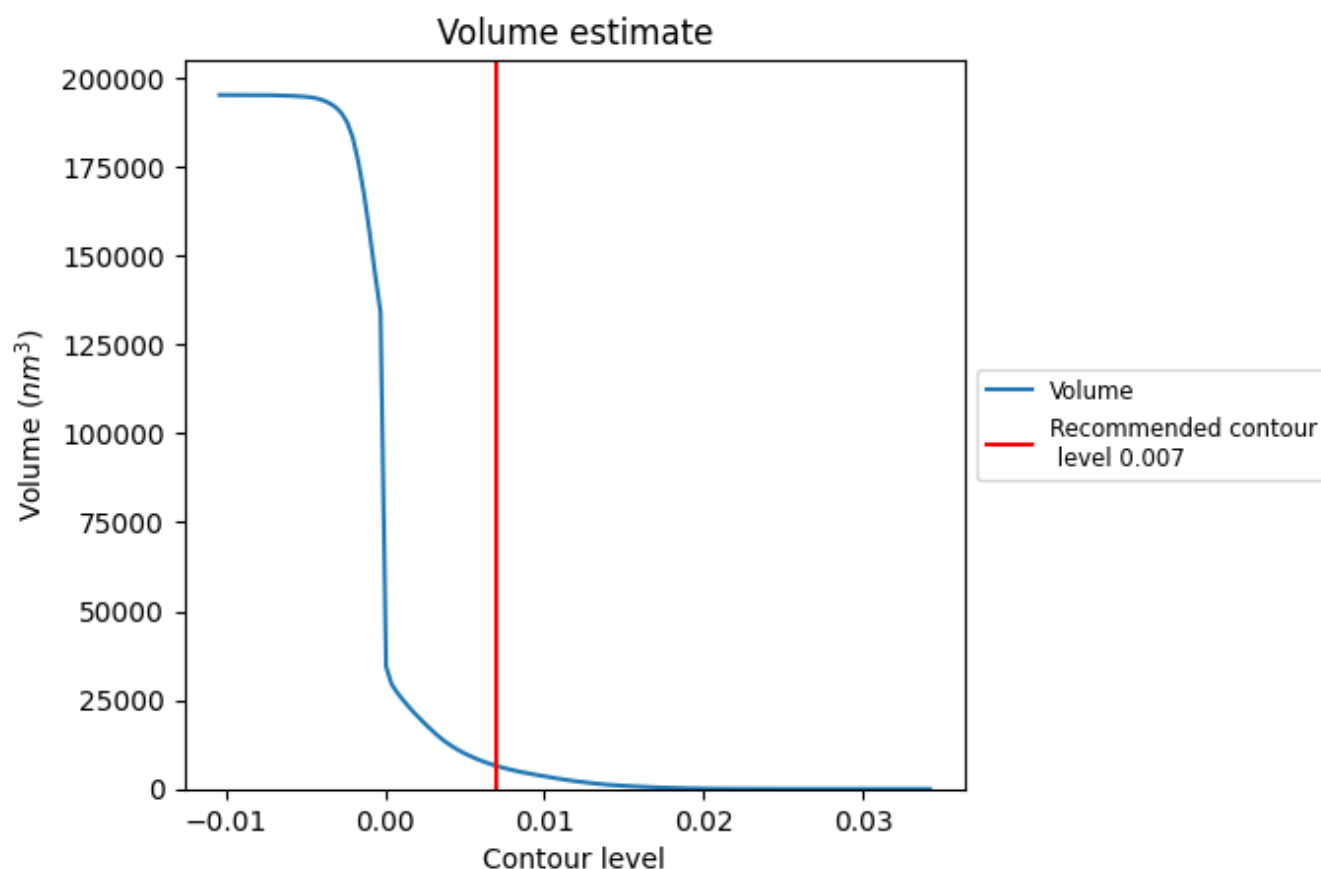
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

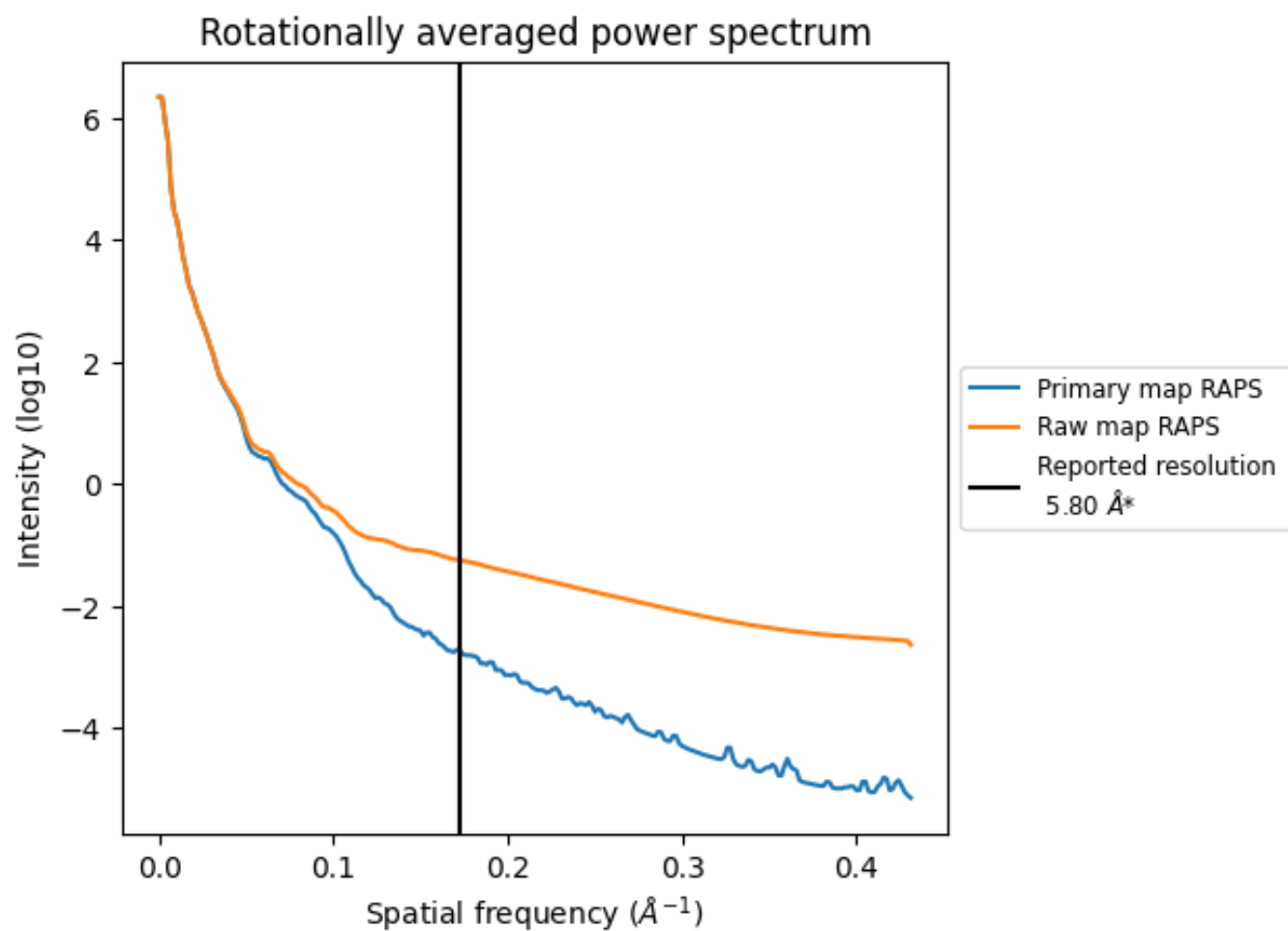
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6461 nm^3 ; this corresponds to an approximate mass of 5837 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 ⓘ

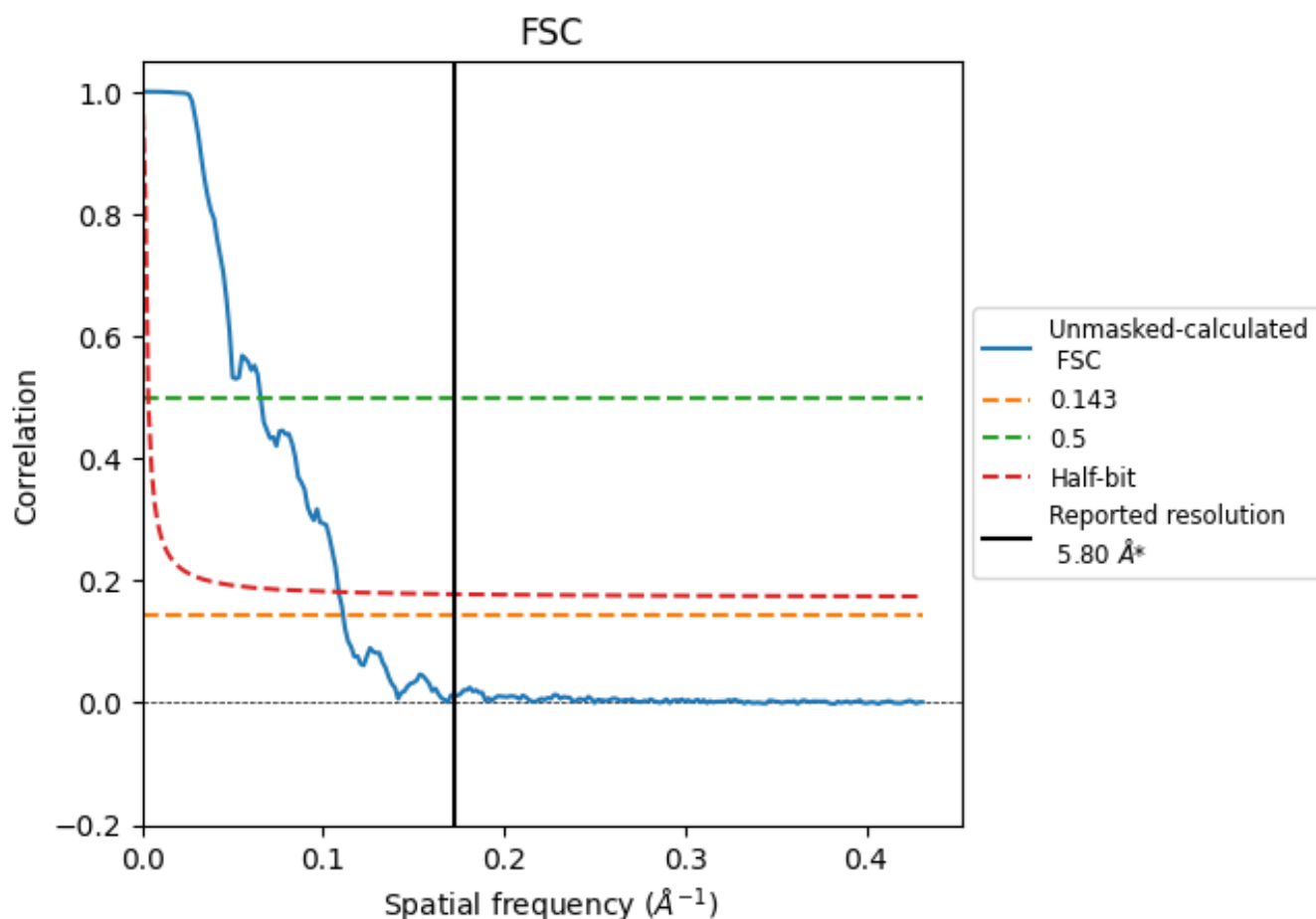


*Reported resolution corresponds to spatial frequency of 0.172 Å⁻¹

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 0.172 Å⁻¹

8.2 Resolution estimates [i](#)

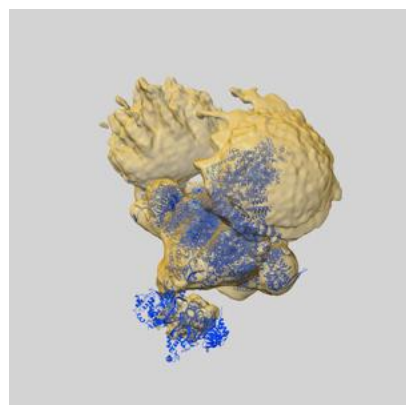
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.00	15.29	9.21

*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 9.00 differs from the reported value 5.8 by more than 10 %

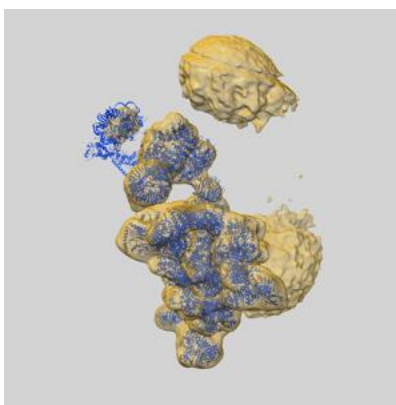
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18788 and PDB model 8R0A. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

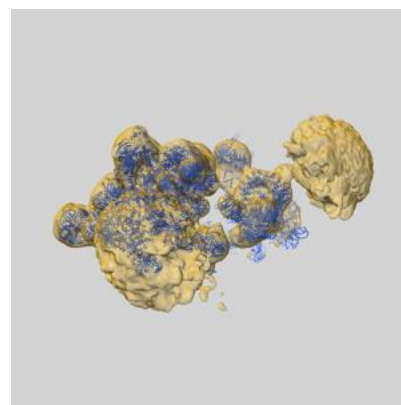
9.1 Map-model overlay [i](#)



X



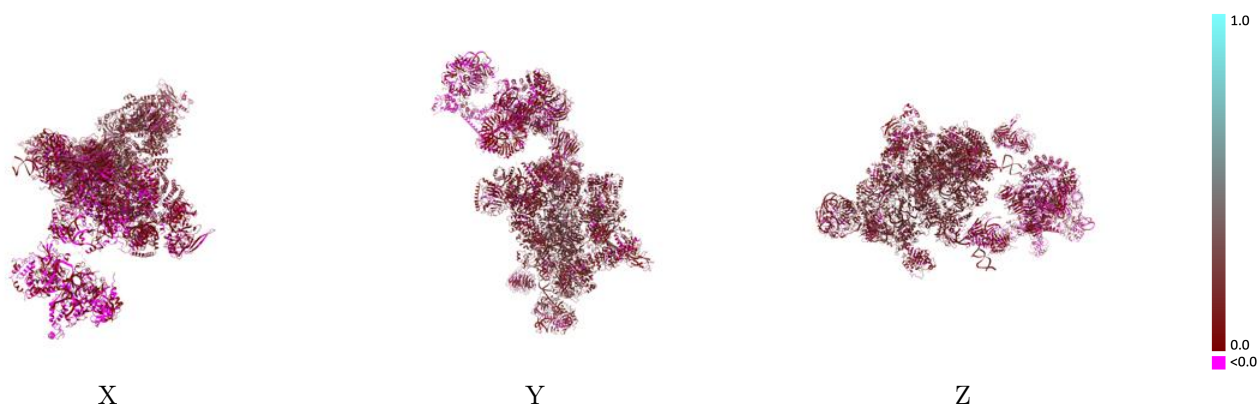
Y



Z

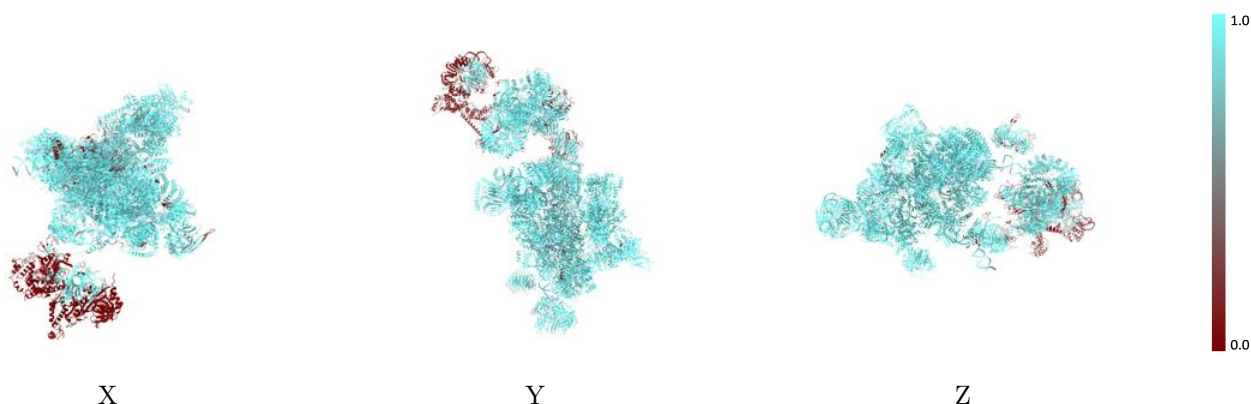
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



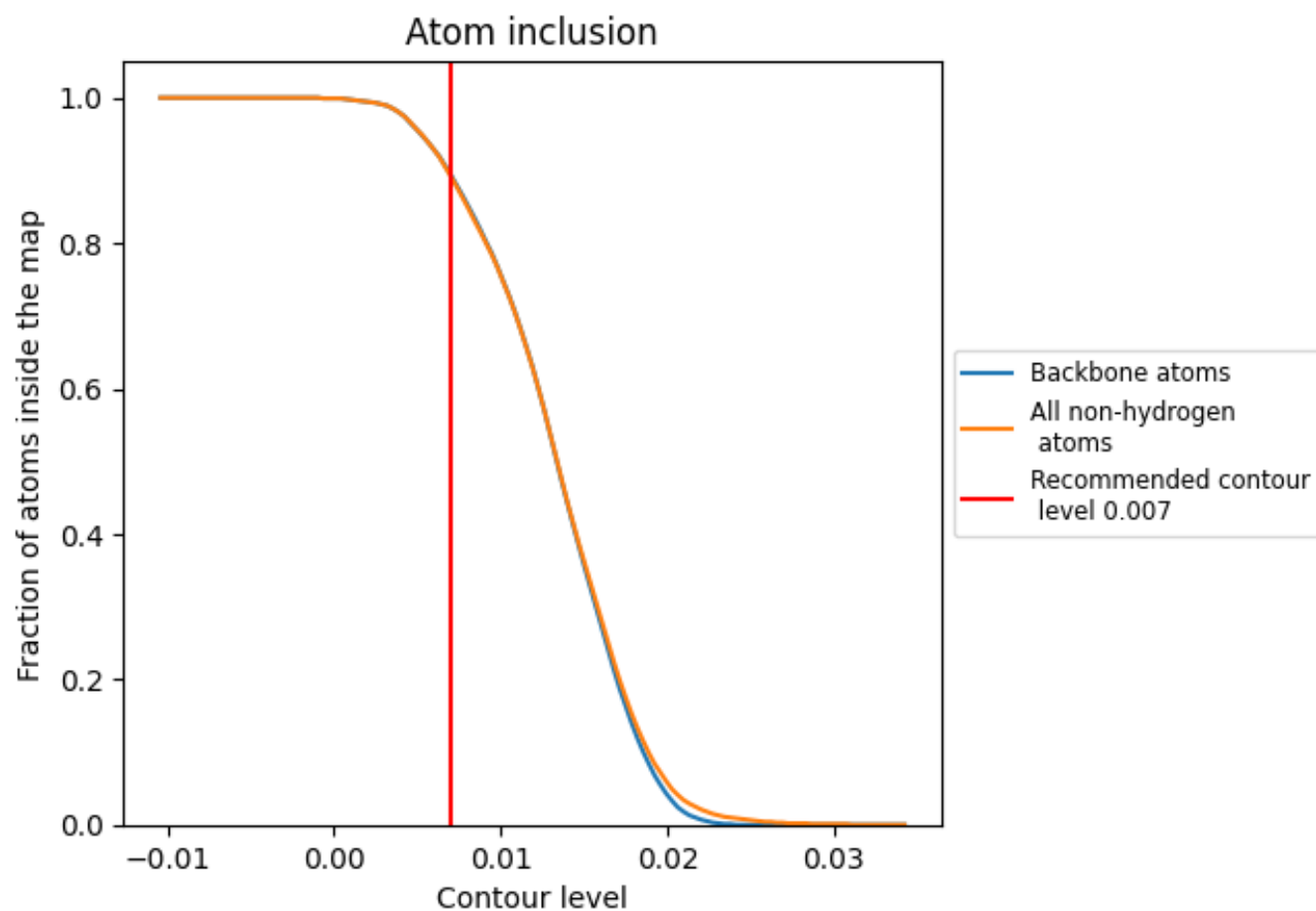
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 89% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8920	 0.1020
2	 0.6380	 0.0370
21	 0.4280	 0.0200
22	 0.0000	 0.0180
23	 0.9320	 0.0480
2A	 0.2590	 0.0420
2B	 0.2360	 0.0590
2b	 0.7840	 0.0540
2e	 0.0420	 0.0060
2f	 0.0000	 0.0250
2g	 0.5520	 0.0420
4	 0.9890	 0.1110
41	 0.9980	 0.0310
42	 0.8380	 0.0320
43	 1.0000	 0.0640
4b	 0.9150	 0.0410
4e	 0.9970	 0.0560
4f	 0.8610	 0.0550
4g	 0.9760	 0.0550
5	 0.9990	 0.1350
51	 1.0000	 0.1270
52	 0.9850	 0.1190
53	 1.0000	 0.1820
5b	 0.9420	 0.1270
5e	 1.0000	 0.1160
5f	 1.0000	 0.0940
5g	 1.0000	 0.1230
6	 0.9950	 0.1250
62	 0.9750	 0.0290
63	 0.8580	 0.0350
64	 0.9840	 0.0430
65	 0.9130	 0.0530
66	 0.9470	 0.0610
67	 0.8960	 0.0520
68	 0.7570	 0.0270



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Chain	Atom inclusion	Q-score
7	 0.2980	 0.0330
8	 0.4110	 0.0230
9	 0.1850	 0.0270
A	 0.9810	 0.1670
B	 0.9780	 0.1280
B1	 0.9650	 0.0470
B2	 0.9830	 0.0530
B3	 0.7940	 0.0540
B4	 1.0000	 0.0620
B5	 1.0000	 0.0440
B6	 0.9960	 0.0690
BP	 1.0000	 0.0400
C	 0.9980	 0.1670
D	 1.0000	 0.1670
E	 0.9650	 0.0430
F	 0.9990	 0.0850
G	 0.9950	 0.1320
J	 1.0000	 0.1420
K	 0.9110	 0.0690
L	 0.9300	 0.1040
M	 1.0000	 0.1130
N	 0.9980	 0.1300
R	 0.9980	 0.1140
S	 0.9210	 0.1450
U	 0.9920	 0.1450
X	 1.0000	 0.0610
Z	 1.0000	 0.0800
z	 1.0000	 0.1530