



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 09:50 AM UTC

PDB ID : 8R08 / pdb_00008r08
EMDB ID : EMD-18786
Title : Cryo-EM structure of the cross-exon pre-B+AMPPNP 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 : 6.10 Å(reported)

This is a Full wwPDB EM Validation 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

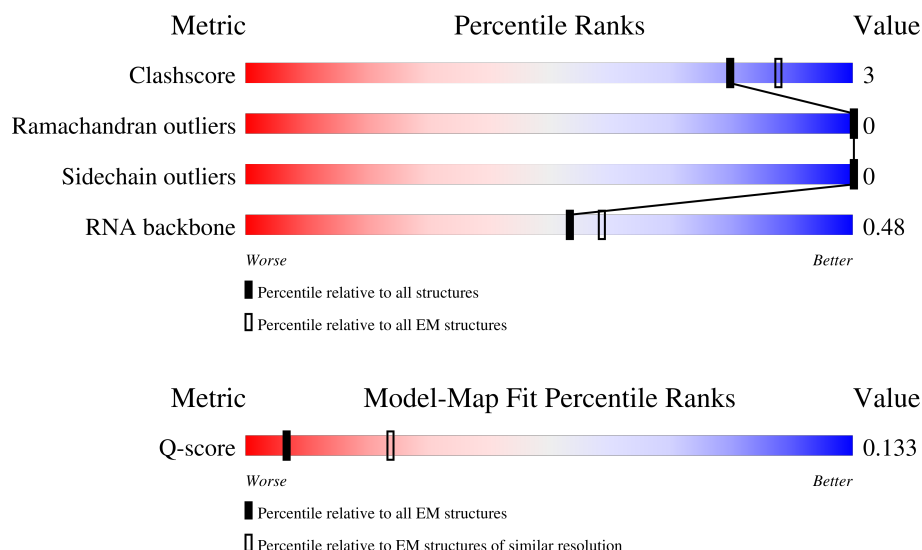
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.10 Å.

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



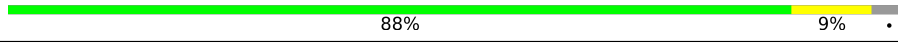
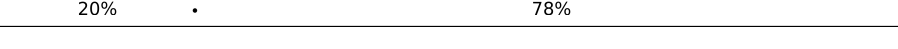
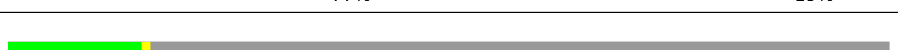
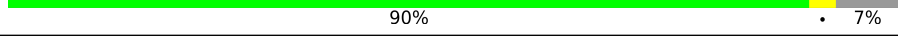
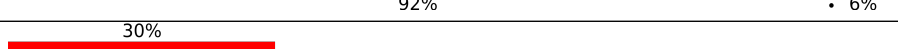
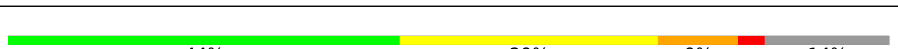
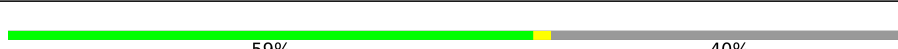
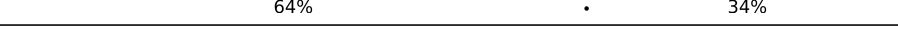
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	531 (5.60 - 6.60)

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

Mol	Chain	Length	Quality of chain
1	1	163	11% 67% 23% 6%
2	C	972	84% 12%
3	D	142	96%

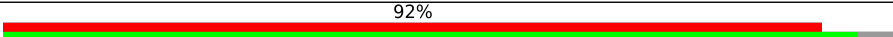
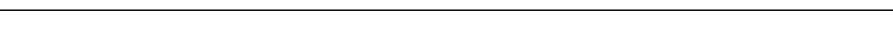
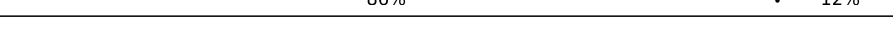
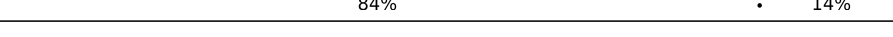
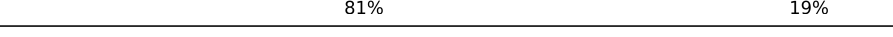
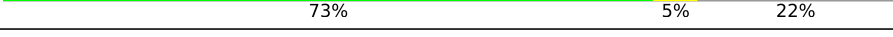
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Mol	Chain	Length	Quality of chain
4	E	357	
5	M	128	
6	R	480	
7	U	565	
8	X	155	
9	Z	15	
10	K	1007	
11	A	2335	
12	B	2136	
13	2	188	
14	4	144	
15	5	117	
16	6	106	
17	7	793	
18	8	464	
19	J	683	
20	L	499	
21	Z1	6	
22	13	126	
22	23	126	
22	43	126	
22	53	126	
23	1f	86	
23	2f	86	
23	4f	86	

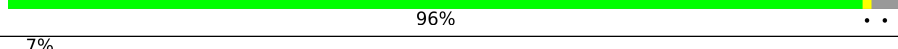
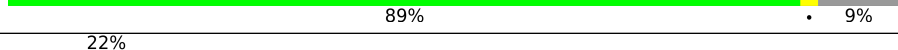
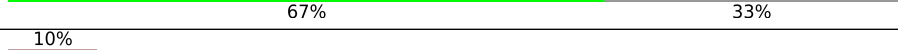
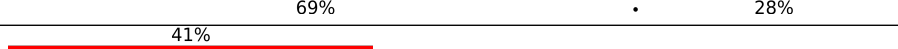
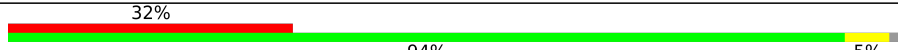
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Mol	Chain	Length	Quality of chain
23	5f	86	
24	11	119	
24	21	119	
24	41	119	
24	51	119	
25	1b	240	
25	2b	240	
25	4b	240	
25	5b	240	
26	1g	76	
26	2g	76	
26	4g	76	
26	5g	76	
27	1e	92	
27	2e	92	
27	4e	92	
27	5e	92	
28	12	118	
28	22	118	
28	42	118	
28	52	118	
29	1K	437	
30	S	800	
31	4B	522	
32	N	941	

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Mol	Chain	Length	Quality of chain
33	G	820	
34	B4	424	
35	9	501	
36	B2	895	
37	B5	86	
38	B3	1217	
39	BP	110	
40	B1	1304	
41	B6	125	
42	2B	225	
43	2A	255	
44	66	80	
45	67	103	
46	62	95	
47	63	102	
48	68	96	
49	64	139	
50	65	91	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 88763 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 U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	153	Total	C	N	O	P	0	0
			3256	1452	570	1081	153		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	C	852	Total	C	N	O	0	0
			4307	2603	852	852		

- 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 NHP2-like protein 1, N-terminally processed.

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

- Molecule 6 is a protein called RNA-binding protein 42.

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

- Molecule 7 is a protein called Ubiquitin carboxyl-terminal hydrolase 39.

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

- Molecule 8 is a protein called U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	X	26	Total	C	N	O	0	0
			130	78	26	26		

- Molecule 9 is a RNA chain called pre-mRNA.

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

- Molecule 10 is a protein called Serine/threonine-protein kinase PRP4 homolog.

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

- Molecule 11 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	A	2178	Total	C	N	O	0	0
			11050	6694	2178	2178		

- Molecule 12 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	B	2001	Total	C	N	O	0	0
			10078	6076	2001	2001		

- Molecule 13 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	2	97	Total	C	N	O	P	0	0
			2052	917	346	692	97		

- Molecule 14 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	4	124	Total	C	N	O	P	0	0
			2636	1179	466	868	123		

- Molecule 15 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	5	104	Total	C	N	O	P	0	0
			2192	983	372	734	103		

- Molecule 16 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	6	53	Total	C	N	O	P	0	0
			1133	506	203	371	53		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	7	136	Total	C	N	O		0	0
			686	414	136	136			

- 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 U4/U6 small nuclear ribonucleoprotein Prp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J	196	Total	C	N	O		0	0
			991	599	196	196			

- Molecule 20 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	301	Total	C	N	O		0	0
			1510	908	301	301			

- Molecule 21 is a RNA chain called oligo 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Z1	5	Total	C	N	O	P	
			100	45	10	40	5	
							0	0

- Molecule 22 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	13	81	Total	C	N	O		
			405	243	81	81	0	0
22	23	83	Total	C	N	O		
			415	249	83	83	0	0
22	43	83	Total	C	N	O		
			415	249	83	83	0	0
22	53	77	Total	C	N	O		
			308	154	77	77	0	0

- Molecule 23 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	1f	74	Total	C	N	O		
			369	221	74	74	0	0
23	2f	72	Total	C	N	O		
			359	215	72	72	0	0
23	4f	72	Total	C	N	O		
			359	215	72	72	0	0
23	5f	74	Total	C	N	O		
			296	148	74	74	0	0

- Molecule 24 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	11	81	Total	C	N	O		
			407	245	81	81	0	0
24	21	80	Total	C	N	O		
			402	242	80	80	0	0
24	41	81	Total	C	N	O		
			407	245	81	81	0	0
24	51	82	Total	C	N	O		
			328	164	82	82	0	0

- Molecule 25 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	1b	86	Total	C	N	O	0	0
			432	260	86	86		
25	2b	82	Total	C	N	O	0	0
			413	249	82	82		
25	4b	82	Total	C	N	O	0	0
			413	249	82	82		
25	5b	86	Total	C	N	O	0	0
			344	172	86	86		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	1g	73	Total	C	N	O	0	0
			364	218	73	73		
26	2g	73	Total	C	N	O	0	0
			364	218	73	73		
26	4g	74	Total	C	N	O	0	0
			369	221	74	74		
26	5g	74	Total	C	N	O	0	0
			296	148	74	74		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	1e	77	Total	C	N	O	0	0
			383	229	77	77		
27	2e	81	Total	C	N	O	0	0
			403	241	81	81		
27	4e	76	Total	C	N	O	0	0
			378	226	76	76		
27	5e	79	Total	C	N	O	0	0
			316	158	79	79		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	12	95	Total	C	N	O	0	0
			480	290	95	95		
28	22	95	Total	C	N	O	0	0
			482	292	95	95		
28	42	92	Total	C	N	O	0	0
			463	279	92	92		

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Mol	Chain	Residues	Atoms				AltConf	Trace
28	52	97	Total	C	N	O	0	0
			388	194	97	97		

- Molecule 29 is a protein called U1 small nuclear ribonucleoprotein 70 kDa.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	1K	201	Total	C	N	O	0	0
			1028	626	201	201		

- Molecule 30 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	S	108	Total	C	N	O	0	0
			539	323	108	108		

- Molecule 31 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	4B	359	Total	C	N	O	0	0
			1795	1077	359	359		

- Molecule 32 is a protein called Pre-mRNA-processing factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	N	801	Total	C	N	O	0	0
			4030	2428	801	801		

- Molecule 33 is a protein called Probable ATP-dependent RNA helicase DDX23.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	G	579	Total	C	N	O	7	0
			2958	1786	586	586		

- Molecule 34 is a protein called Splicing factor 3B subunit 4.

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

- Molecule 35 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	9	383	Total	C	N	O	0	0
			1920	1154	383	383		

- Molecule 36 is a protein called Splicing factor 3B subunit 2.

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

- Molecule 37 is a protein called Splicing factor 3B subunit 5.

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

- Molecule 38 is a protein called Splicing factor 3B subunit 3.

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

- Molecule 39 is a protein called PHD finger-like domain-containing protein 5A.

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

- Molecule 40 is a protein called Splicing factor 3B subunit 1.

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

- Molecule 41 is a protein called Splicing factor 3B subunit 6.

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

- Molecule 42 is a protein called U2 small nuclear ribonucleoprotein B”.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	2B	92	Total	C	N	O	0	0
			461	277	92	92		

- Molecule 43 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	2A	162	Total	C	N	O	0	0
			816	492	162	162		

- Molecule 44 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	66	72	Total	C	N	O	0	0
			357	213	72	72		

- Molecule 45 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	67	77	Total	C	N	O	0	0
			384	230	77	77		

- Molecule 46 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	62	95	Total	C	N	O	0	0
			478	288	95	95		

- Molecule 47 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	63	85	Total	C	N	O	0	0
			429	259	85	85		

- Molecule 48 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	68	95	Total	C	N	O	0	0
			469	279	95	95		

- Molecule 49 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	64	73	Total	C	N	O	0	0
			369	223	73	73		

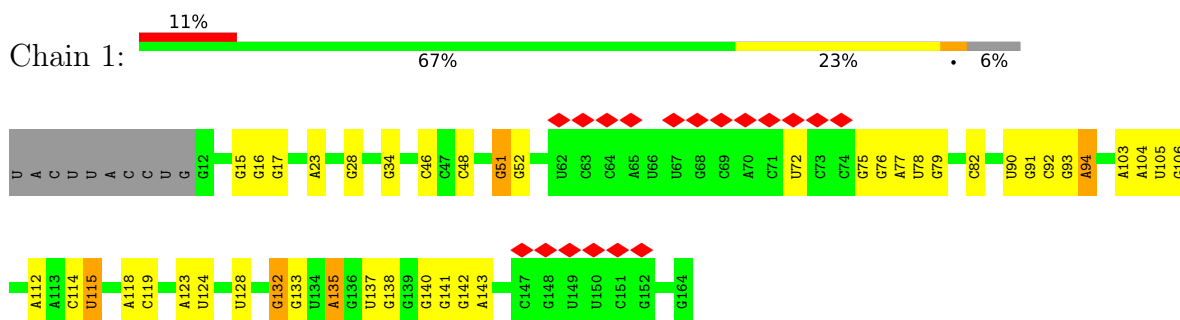
- Molecule 50 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	65	76	Total	C	N	O	0	0
			378	226	76	76		

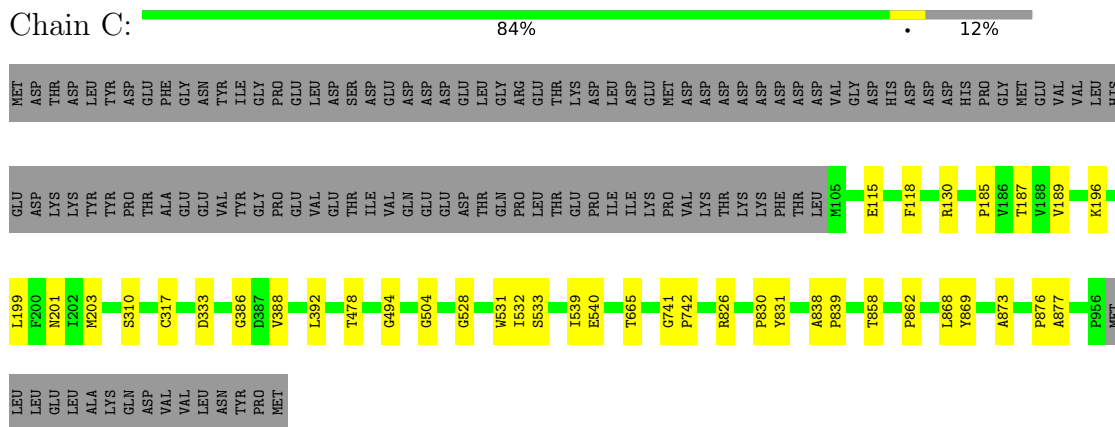
3 Residue-property plots

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

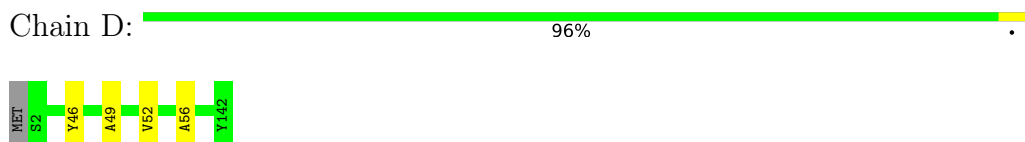
• Molecule 1: U1 snRNA



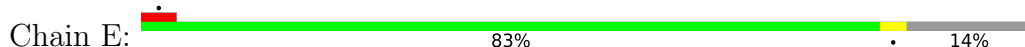
• Molecule 2: 116 kDa U5 small nuclear ribonucleoprotein component



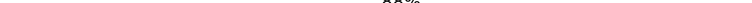
• Molecule 3: Thioredoxin-like protein 4A

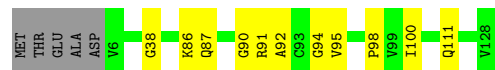


• Molecule 4: U5 small nuclear ribonucleoprotein 40 kDa protein



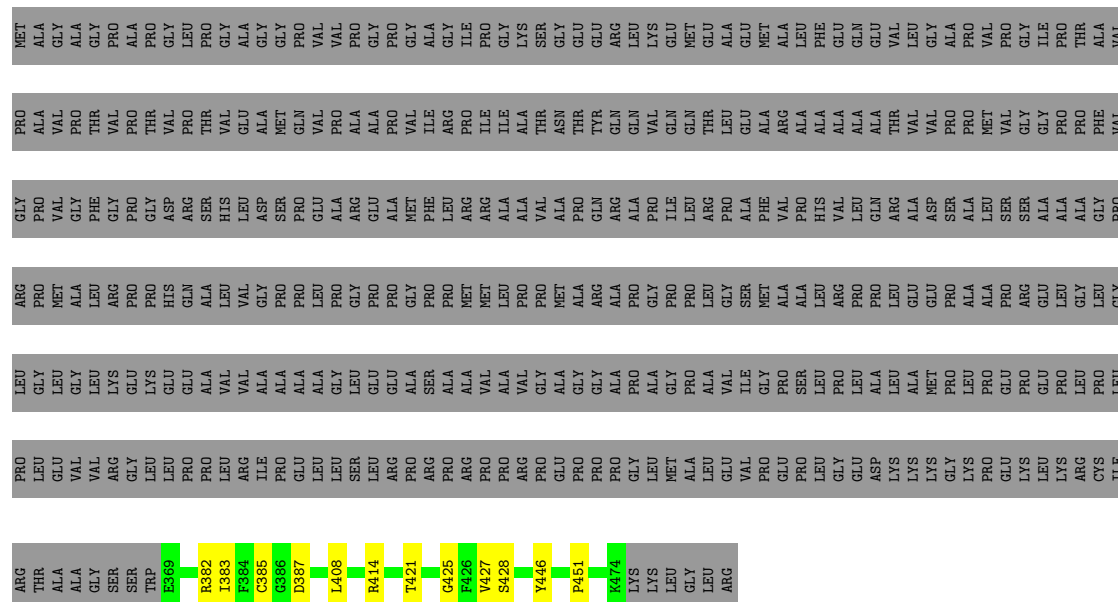
- Molecule 5: NHP2-like protein 1, N-terminally processed

Chain M:  88% 9% .

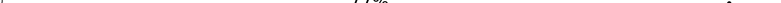


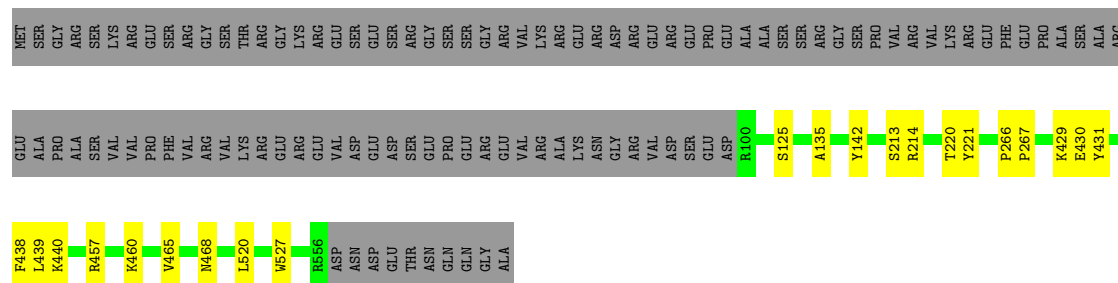
- Molecule 6: RNA-binding protein 42

Chain R: 20% 78%



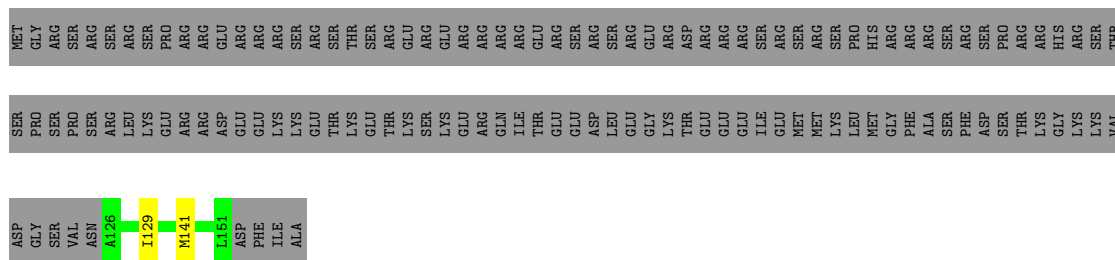
- Molecule 7: Ubiquitin carboxyl-terminal hydrolase 39

Chain U:  77% . 19%



- Molecule 8: U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein

Chain X: 15% . 83%

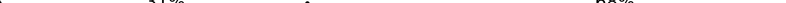


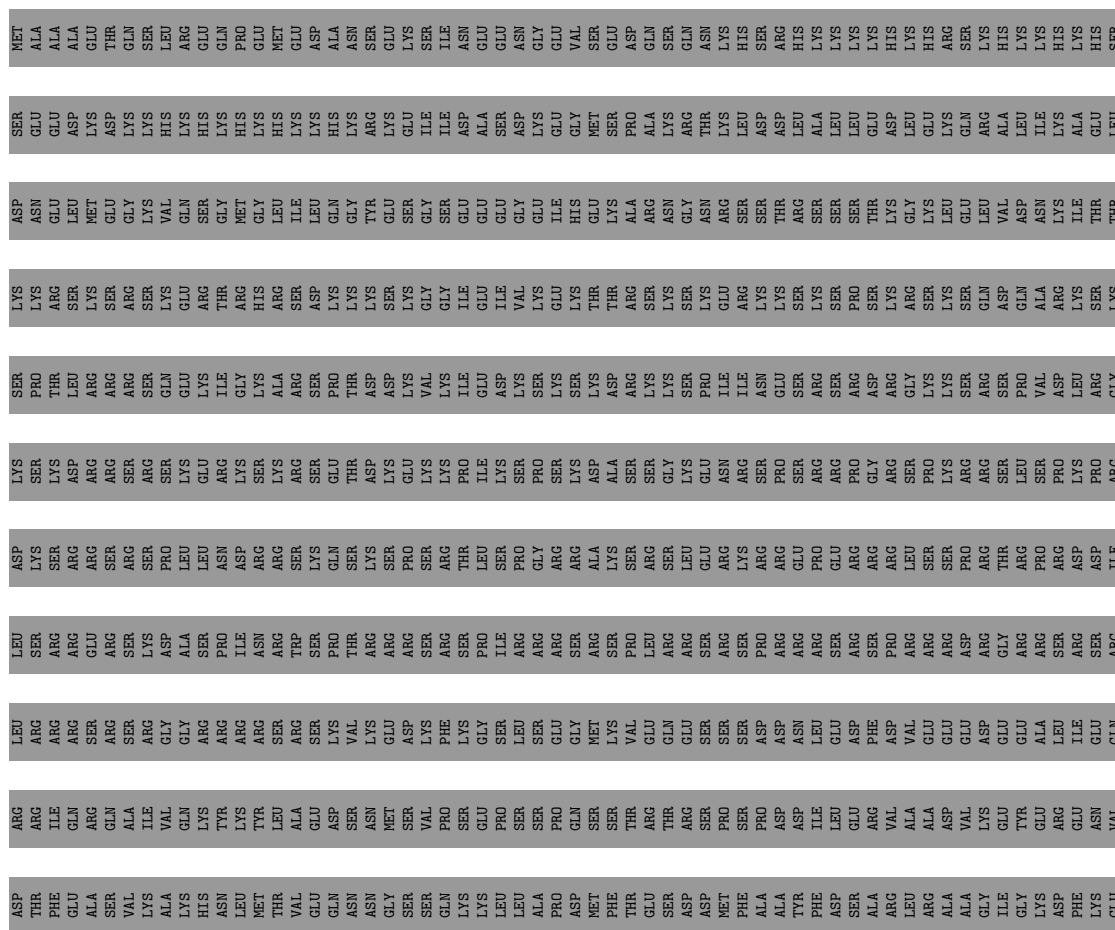
- Molecule 9: pre-mRNA

Chain Z: 87% 13%

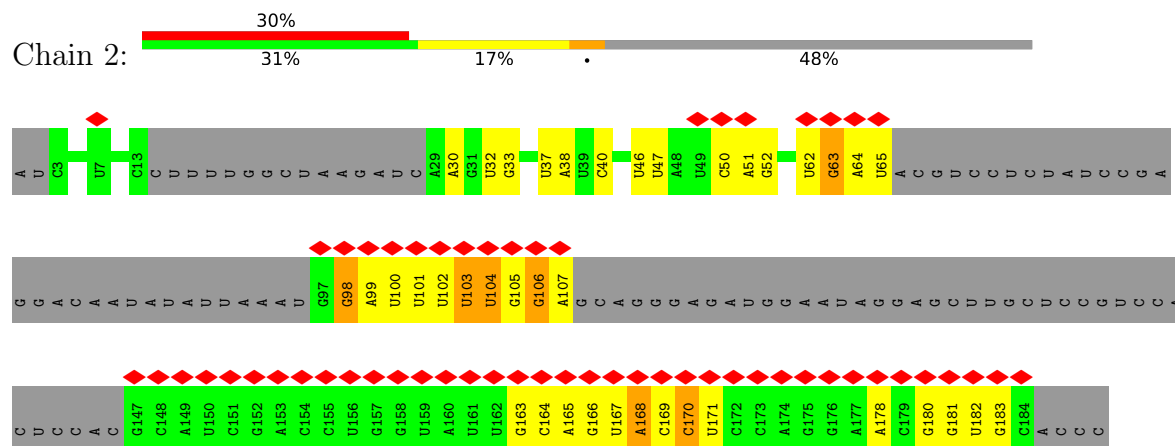


- Molecule 10: Serine/threonine-protein kinase PRP4 homolog

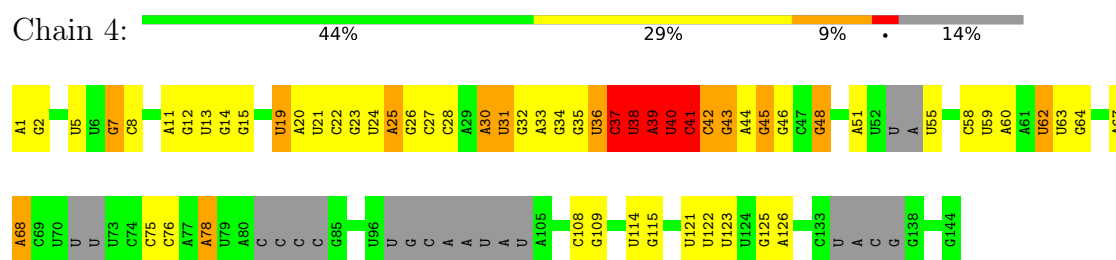
Chain K:  31% 68%



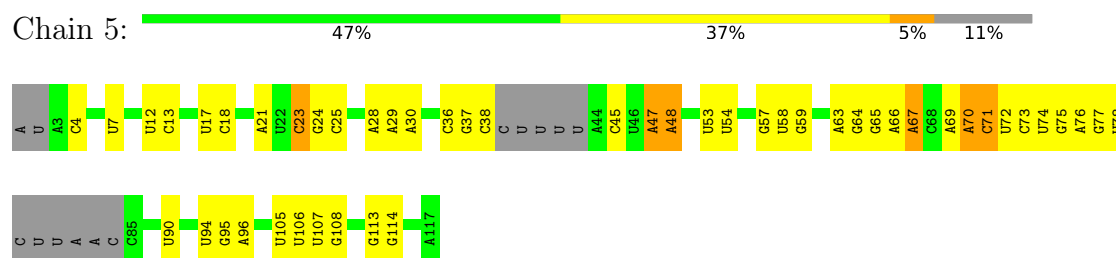
- Molecule 13: U2 snRNA



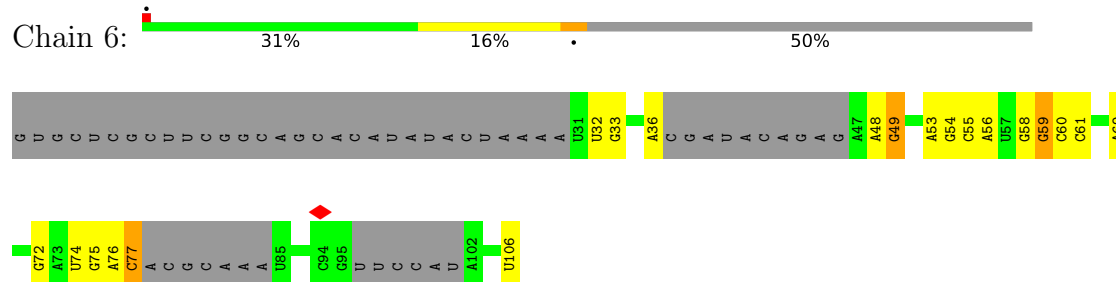
- Molecule 14: U4 snRNA



- Molecule 15: U5 snRNA



- Molecule 16: U6 snRNA

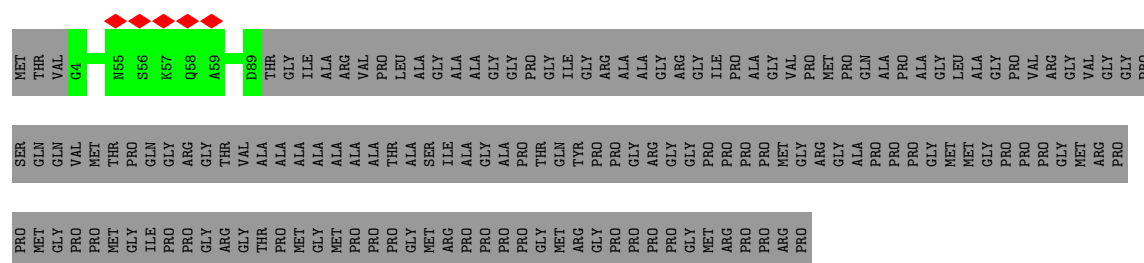


- Molecule 17: Splicing factor 3A subunit 1





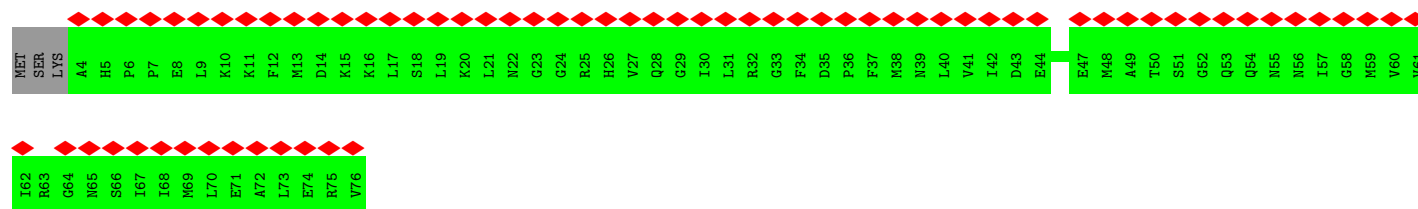
- Molecule 25: Small nuclear ribonucleoprotein-associated proteins B and B'



- Molecule 26: Small nuclear ribonucleoprotein G



- Molecule 26: Small nuclear ribonucleoprotein G



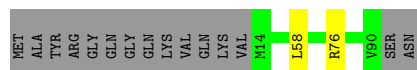
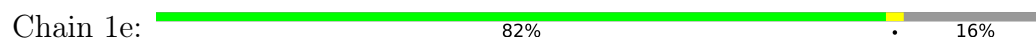
- Molecule 26: Small nuclear ribonucleoprotein G



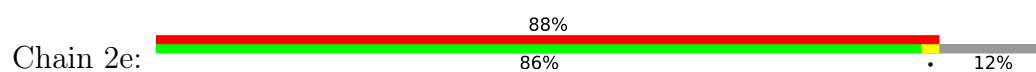
- Molecule 26: Small nuclear ribonucleoprotein G



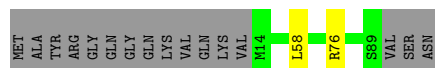
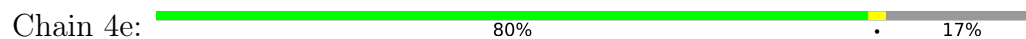
- Molecule 27: Small nuclear ribonucleoprotein E



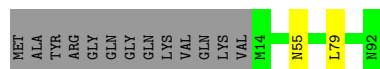
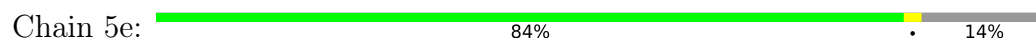
- Molecule 27: Small nuclear ribonucleoprotein E



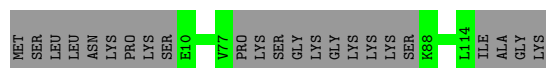
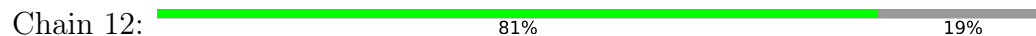
- Molecule 27: Small nuclear ribonucleoprotein E



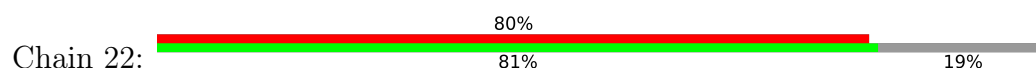
- Molecule 27: Small nuclear ribonucleoprotein E



- Molecule 28: Small nuclear ribonucleoprotein Sm D2

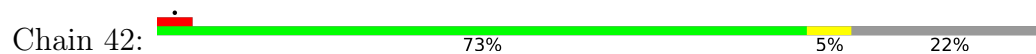


- Molecule 28: Small nuclear ribonucleoprotein Sm D2

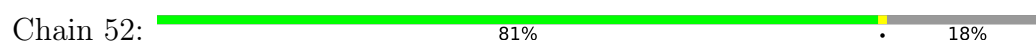




• Molecule 28: Small nuclear ribonucleoprotein Sm D2



• Molecule 28: Small nuclear ribonucleoprotein Sm D2



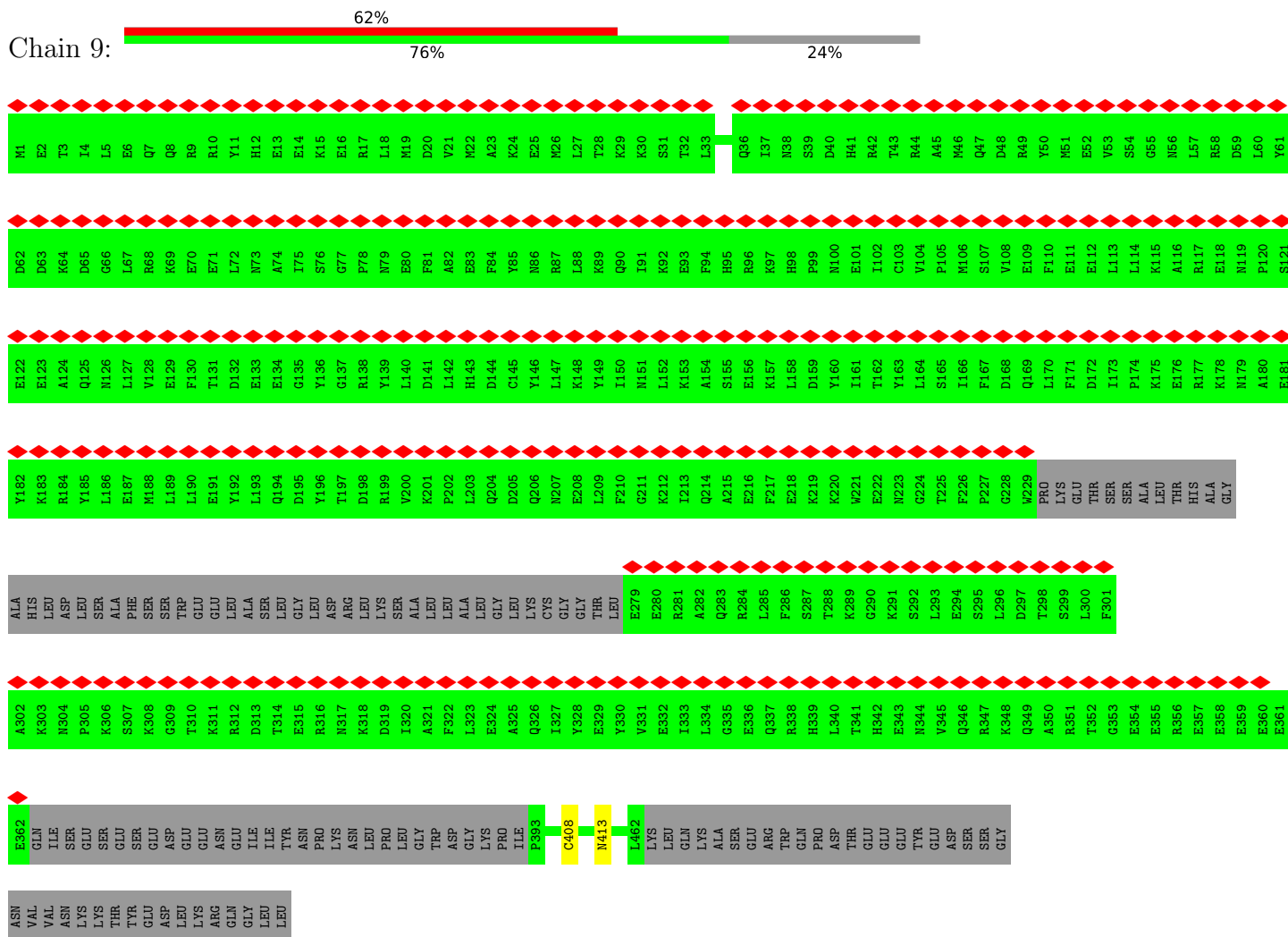
• Molecule 29: U1 small nuclear ribonucleoprotein 70 kDa



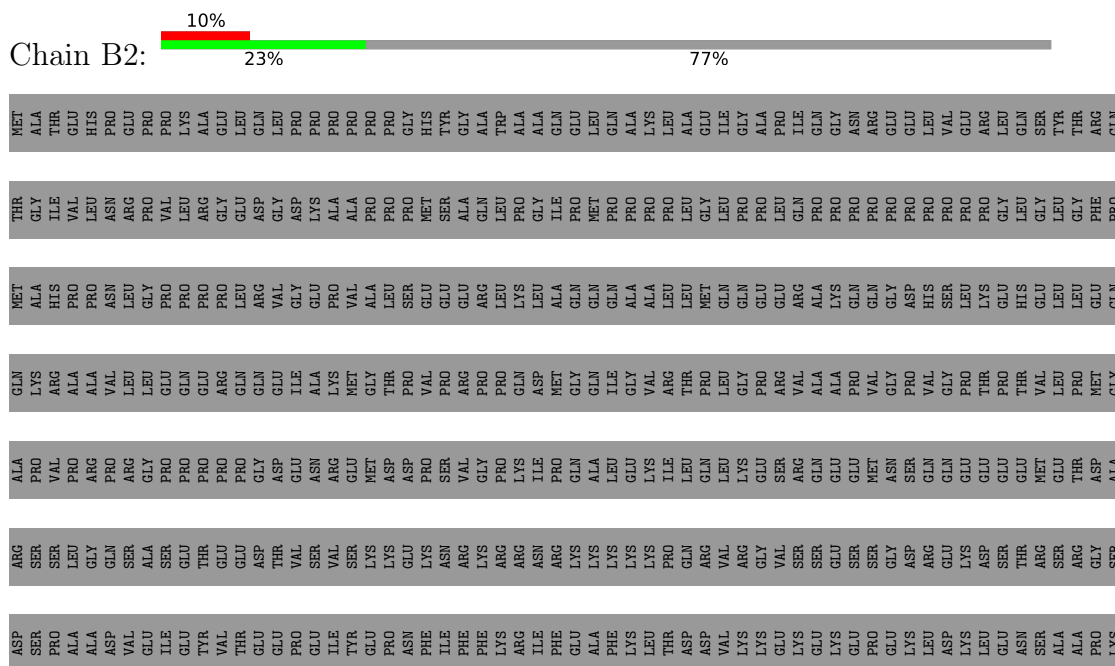
• Molecule 30: U4/U6.U5 tri-snRNP-associated protein 1

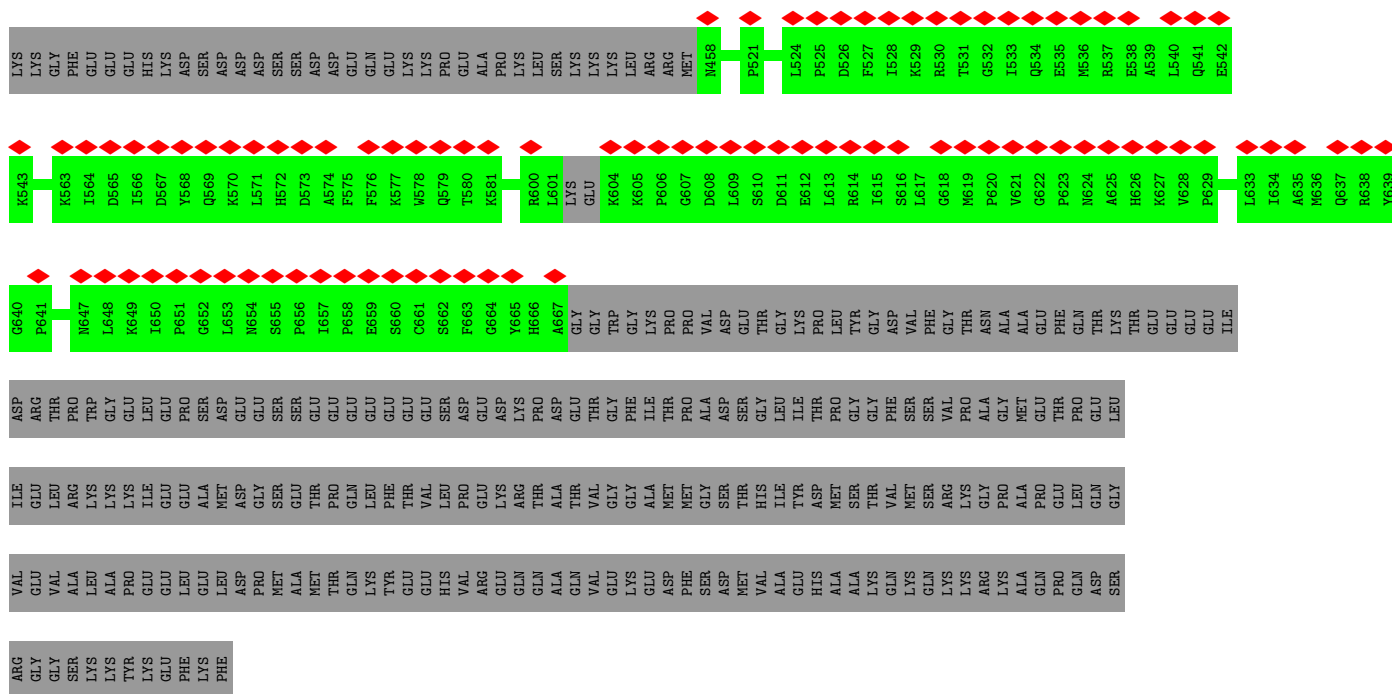




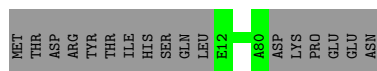
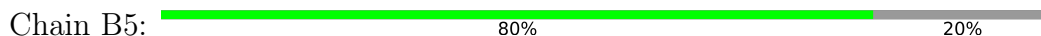


- Molecule 36: Splicing factor 3B subunit 2

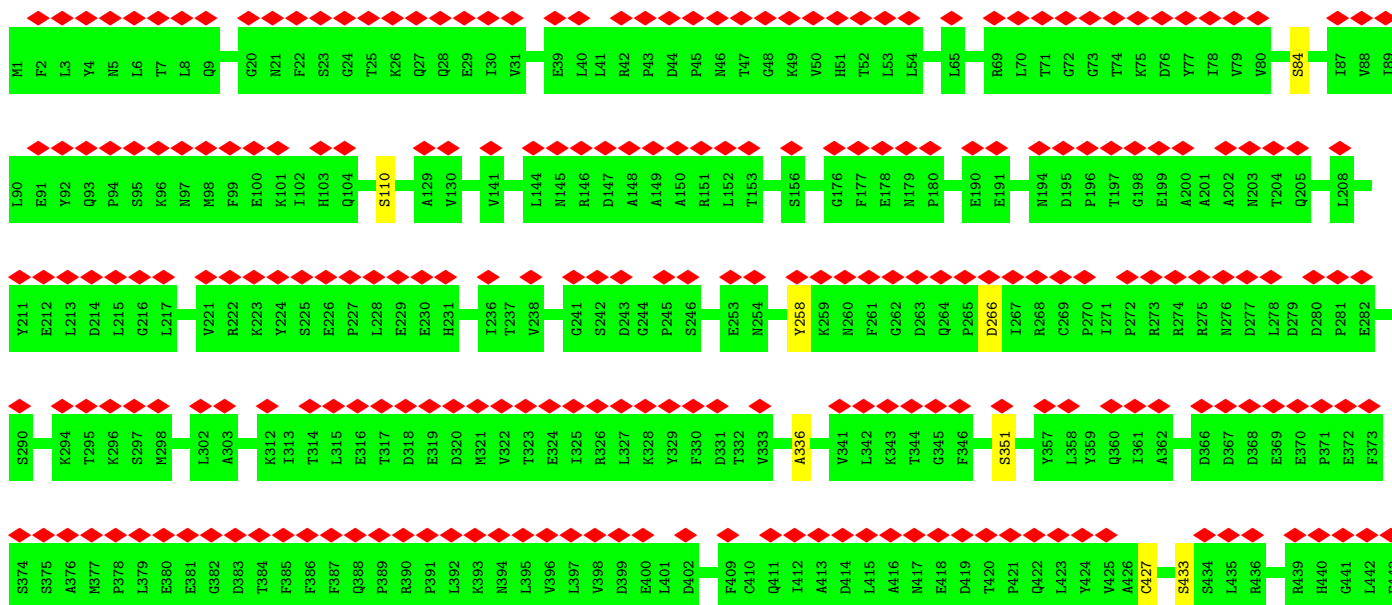


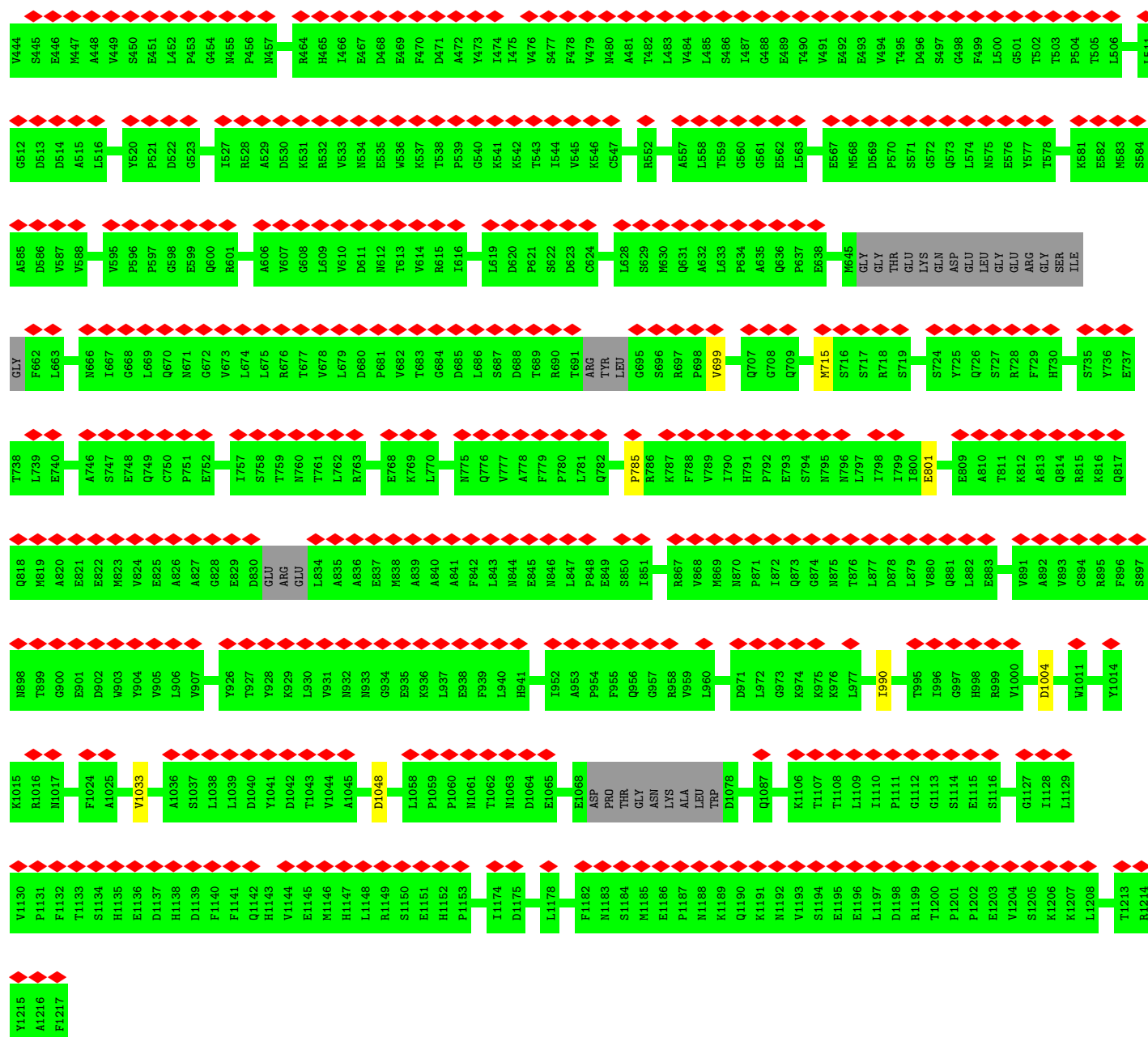


- Molecule 37: Splicing factor 3B subunit 5

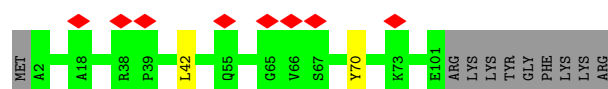


- Molecule 38: Splicing factor 3B subunit 3

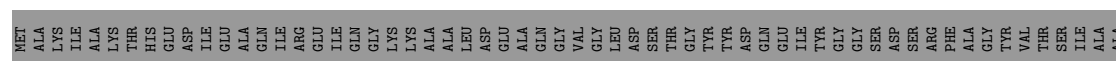


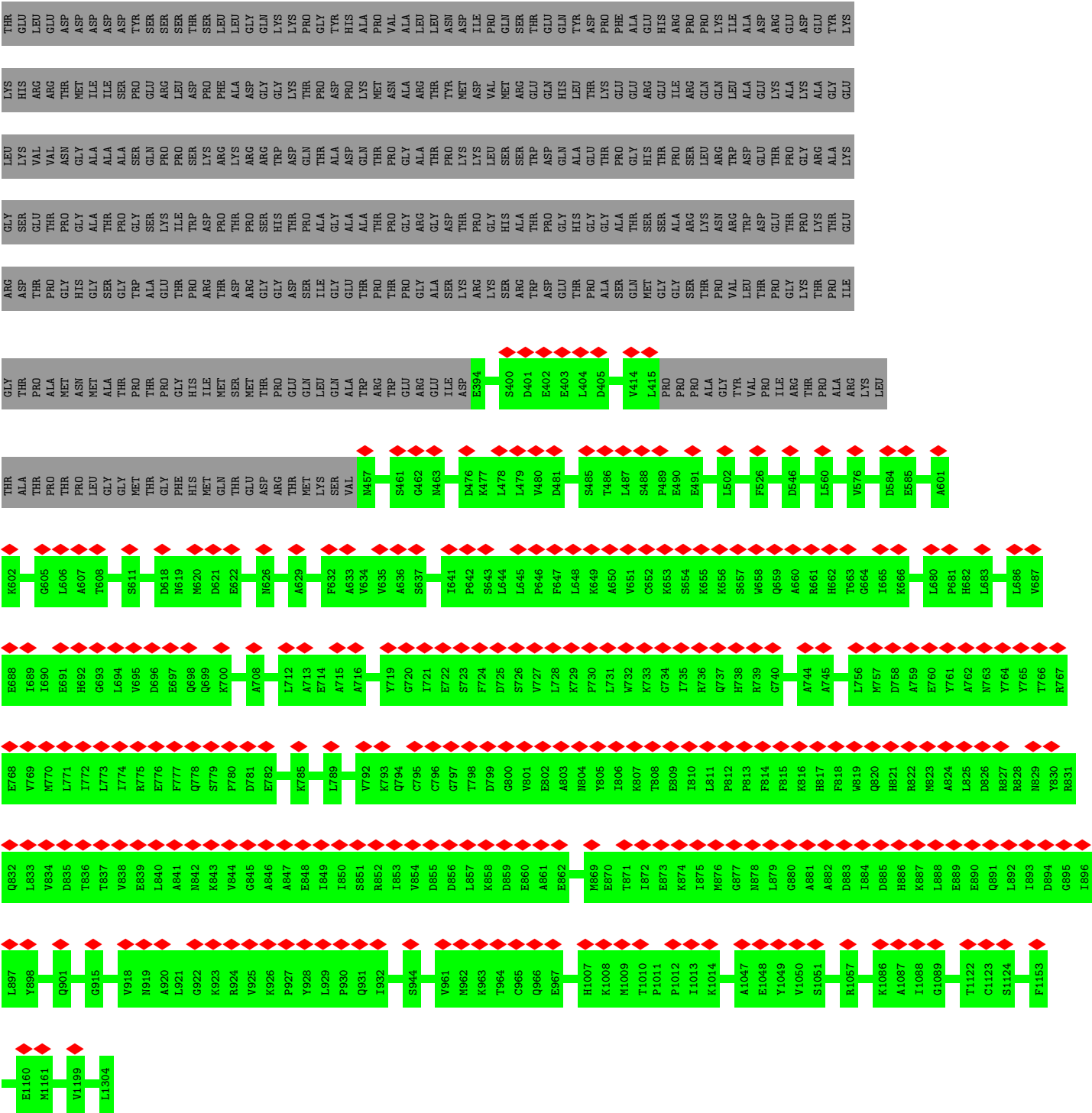


- Molecule 39: PHD finger-like domain-containing protein 5A



- Molecule 40: Splicing factor 3B subunit 1





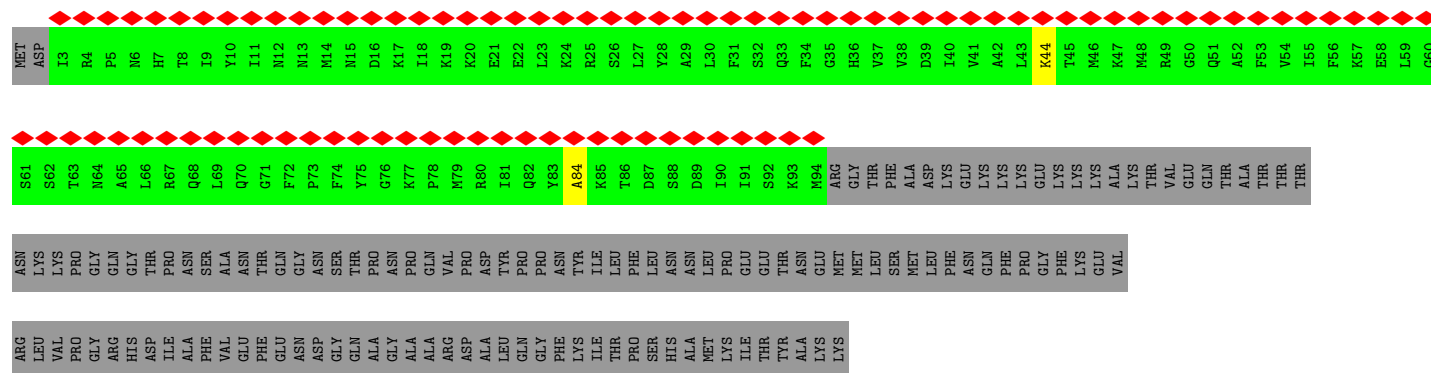
● Molecule 41: Splicing factor 3B subunit 6



PRO
LYS

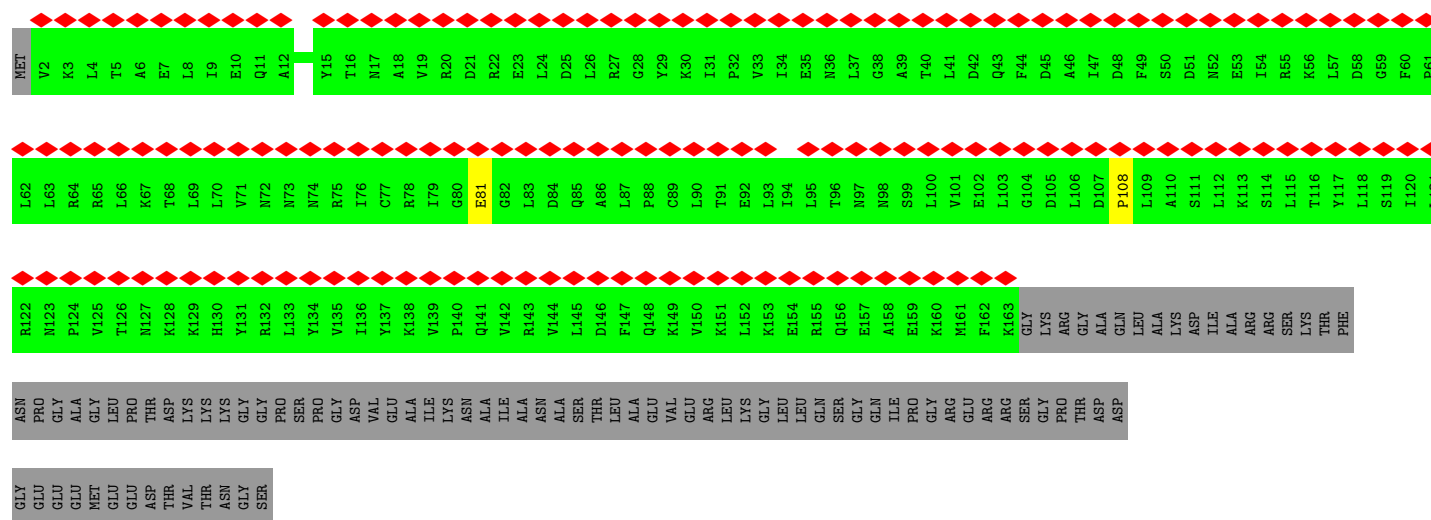
- Molecule 42: U2 small nuclear ribonucleoprotein B''

Chain 2B: 

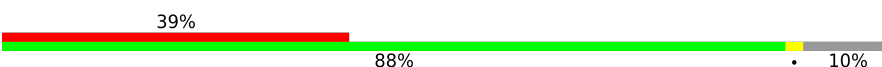


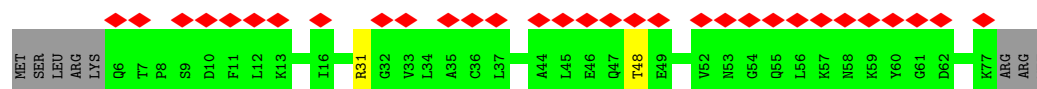
- Molecule 43: U2 small nuclear ribonucleoprotein A'

Chain 2A: 



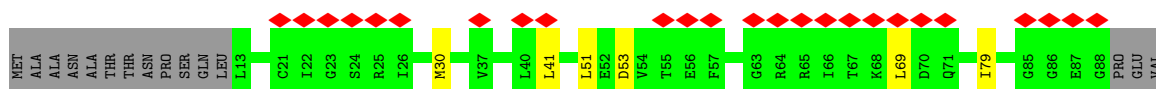
- Molecule 44: U6 snRNA-associated Sm-like protein LSm6

Chain 66: 



- Molecule 45: U6 snRNA-associated Sm-like protein LSm7

Chain 67: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53422	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	0.065	Depositor
Minimum map value	-0.021	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0078	Depositor
Map size (Å)	648.0, 648.0, 648.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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	1	0.14	0/3636	0.29	0/5665
2	C	0.13	0/4356	0.30	0/6105
3	D	0.12	0/712	0.26	0/995
4	E	0.25	0/1540	0.40	0/2148
5	M	0.50	0/627	0.71	0/878
6	R	0.13	0/534	0.34	0/745
7	U	0.10	0/2330	0.27	0/3268
8	X	0.24	0/130	0.67	0/180
9	Z	0.12	0/349	0.24	0/540
10	K	0.14	0/1622	0.37	0/2265
11	A	0.12	0/11168	0.29	0/15668
12	B	0.19	0/10156	0.34	0/14217
13	2	0.19	0/2286	0.39	2/3550 (0.1%)
14	4	0.20	0/2941	0.39	7/4569 (0.2%)
15	5	0.11	0/2444	0.23	0/3798
16	6	0.07	0/1264	0.14	0/1961
17	7	0.14	0/688	0.32	0/962
18	8	0.14	0/734	0.37	0/1025
19	J	0.31	0/997	0.47	0/1389
20	L	0.35	0/1516	0.49	0/2115
21	Z1	0.33	0/109	0.73	0/166
22	13	0.17	0/407	0.44	0/567
22	23	0.17	0/417	0.42	0/581
22	43	0.14	0/417	0.33	0/581
22	53	0.09	0/307	0.15	0/382
23	1f	0.21	0/372	0.49	0/517
23	2f	0.15	0/362	0.38	0/502
23	4f	0.16	0/362	0.37	0/502
23	5f	0.08	0/295	0.15	0/367
24	11	0.16	0/409	0.47	0/571
24	21	0.12	0/404	0.34	0/564
24	41	0.12	0/409	0.32	0/571
24	51	0.07	0/327	0.17	0/407
25	1b	0.15	0/435	0.38	0/607

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
25	2b	0.14	0/416	0.34	0/581
25	4b	0.14	0/416	0.38	0/581
25	5b	0.07	0/343	0.16	0/427
26	1g	0.18	0/366	0.52	0/509
26	2g	0.14	0/366	0.37	0/509
26	4g	0.14	0/371	0.36	0/516
26	5g	0.08	0/295	0.20	0/367
27	1e	0.16	0/383	0.49	0/533
27	2e	0.13	0/403	0.36	0/561
27	4e	0.14	0/378	0.35	0/526
27	5e	0.09	0/315	0.16	0/392
28	12	0.17	0/482	0.48	0/673
28	22	0.13	0/485	0.32	0/677
28	42	0.44	0/466	0.68	0/651
28	52	0.08	0/387	0.19	0/482
29	1K	0.21	0/1046	0.51	0/1469
30	S	0.10	0/539	0.26	0/746
31	4B	0.14	0/1809	0.35	0/2525
32	N	0.15	0/4054	0.34	0/5669
33	G	0.36	0/2978	0.53	0/4156
34	B4	0.13	0/394	0.28	0/549
35	9	0.13	0/1928	0.28	0/2692
36	B2	0.13	0/1092	0.32	0/1536
37	B5	0.10	0/349	0.24	0/487
38	B3	0.13	0/6024	0.32	0/8425
39	BP	0.13	0/501	0.36	0/697
40	B1	0.18	0/4421	0.38	0/6190
41	B6	0.10	0/459	0.26	0/642
42	2B	0.10	0/463	0.26	0/646
43	2A	0.16	0/821	0.41	0/1149
44	66	0.14	0/358	0.35	0/497
45	67	0.09	0/386	0.26	0/537
46	62	0.14	0/480	0.39	0/671
47	63	0.14	0/432	0.39	0/604
48	68	0.12	0/469	0.30	0/651
49	64	0.16	0/372	0.36	0/520
50	65	0.13	0/380	0.32	0/528
All	All	0.18	0/90689	0.35	9/128499 (0.0%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	4	41	C	P-O3'-C3'	-7.70	108.64	120.20
14	4	37	C	P-O3'-C3'	-7.57	108.85	120.20
14	4	42	C	P-O3'-C3'	-7.50	108.95	120.20
14	4	39	A	P-O3'-C3'	-7.31	109.23	120.20
14	4	38	U	P-O3'-C3'	-6.87	109.90	120.20
14	4	43	G	P-O3'-C3'	-6.46	110.50	120.20
14	4	40	U	P-O3'-C3'	-6.46	110.51	120.20
13	2	106	G	P-O3'-C3'	5.32	128.19	120.20
13	2	103	U	P-O3'-C3'	5.10	127.85	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	1	3256	0	1645	10	0
2	C	4307	0	2141	25	0
3	D	708	0	328	2	0
4	E	1531	0	747	7	0
5	M	622	0	313	15	0
6	R	531	0	253	7	0
7	U	2308	0	1104	11	0
8	X	130	0	64	4	0
9	Z	314	0	160	0	0
10	K	1615	0	754	4	0
11	A	11050	0	5409	43	0
12	B	10078	0	4861	21	0
13	2	2052	0	1038	16	0
14	4	2636	0	1339	46	0
15	5	2192	0	1111	20	0
16	6	1133	0	573	18	0
17	7	686	0	316	0	0
18	8	729	0	356	4	0
19	J	991	0	484	13	0
20	L	1510	0	735	6	0
21	Z1	100	0	51	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	13	405	0	194	0	0
22	23	415	0	198	1	0
22	43	415	0	198	2	0
22	53	308	0	86	5	0
23	1f	369	0	182	1	0
23	2f	359	0	179	1	0
23	4f	359	0	179	2	0
23	5f	296	0	87	0	0
24	11	407	0	183	2	0
24	21	402	0	184	0	0
24	41	407	0	183	0	0
24	51	328	0	89	1	0
25	1b	432	0	203	1	0
25	2b	413	0	194	0	0
25	4b	413	0	194	3	0
25	5b	344	0	93	0	0
26	1g	364	0	176	2	0
26	2g	364	0	176	0	0
26	4g	369	0	178	1	0
26	5g	296	0	84	2	0
27	1e	383	0	165	1	0
27	2e	403	0	173	1	0
27	4e	378	0	163	1	0
27	5e	316	0	85	1	0
28	12	480	0	214	0	0
28	22	482	0	220	0	0
28	42	463	0	211	5	0
28	52	388	0	102	1	0
29	1K	1028	0	544	2	0
30	S	539	0	265	2	0
31	4B	1795	0	891	9	0
32	N	4030	0	2054	6	0
33	G	2958	0	1458	18	0
34	B4	391	0	197	0	0
35	9	1920	0	902	1	0
36	B2	1072	0	563	0	0
37	B5	347	0	171	0	0
38	B3	5969	0	2985	8	0
39	BP	498	0	241	1	0
40	B1	4383	0	2195	0	0
41	B6	455	0	227	2	0
42	2B	461	0	218	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	2A	816	0	386	1	0
44	66	357	0	169	1	0
45	67	384	0	178	0	0
46	62	478	0	222	0	0
47	63	429	0	199	1	0
48	68	469	0	220	3	0
49	64	369	0	172	1	0
50	65	378	0	174	3	0
All	All	88763	0	42986	317	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.

All (317) 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)
5:M:90:GLY:HA2	5:M:98:PRO:CA	1.76	1.15
5:M:94:GLY:HA2	19:J:441:THR:HA	1.10	1.09
5:M:90:GLY:CA	5:M:98:PRO:HA	1.83	1.08
8:X:129:ILE:HA	28:42:58:ALA:HA	1.37	1.04
5:M:94:GLY:HA2	19:J:441:THR:CA	1.96	0.95
11:A:823:SER:HA	12:B:239:THR:HA	1.48	0.94
5:M:90:GLY:HA2	5:M:98:PRO:HA	0.94	0.93
22:23:48:VAL:O	22:23:55:VAL:HA	1.71	0.90
33:G:643:VAL:HA	33:G:766:THR:H	1.36	0.89
25:1b:47:GLU:O	25:1b:64:LYS:HA	1.77	0.84
13:2:168:A:H3'	13:2:169:C:H6	1.44	0.82
14:4:39:A:H4'	14:4:40:U:H5''	1.64	0.79
24:11:45:MET:O	24:11:52:PRO:HA	1.84	0.77
12:B:1345:ASN:HA	12:B:1487:ILE:O	1.85	0.77
12:B:1204:ILE:O	12:B:1249:GLU:HA	1.87	0.75
16:6:77:C:H5''	19:J:555:ALA:HA	1.69	0.75
2:C:196:LYS:CB	22:53:11:HIS:O	2.36	0.74
2:C:386:GLY:HA2	11:A:401:GLY:HA3	1.70	0.74
14:4:35:G:H2'	14:4:36:U:H5''	1.70	0.73
2:C:333:ASP:HA	26:5g:3:LYS:N	2.03	0.73
13:2:98:G:H4'	13:2:104:U:H2'	1.71	0.72
5:M:94:GLY:CA	19:J:441:THR:HA	2.05	0.71
13:2:168:A:H3'	13:2:169:C:C6	2.25	0.71
14:4:64:G:H22	14:4:67:A:H5'	1.54	0.71
16:6:76:A:N1	19:J:563:ASN:HA	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1e:58:LEU:O	27:1e:76:ARG:HA	1.92	0.69
14:4:41:C:H2'	14:4:42:C:C6	2.29	0.68
38:B3:427:CYS:O	38:B3:433:SER:HA	1.94	0.67
14:4:40:U:H5'	20:L:251:LEU:CB	2.25	0.67
11:A:1424:GLN:HA	12:B:214:GLU:HA	1.78	0.66
11:A:142:SER:HA	11:A:242:ALA:HB2	1.78	0.65
5:M:87:GLN:HA	5:M:98:PRO:HB3	1.77	0.65
21:Z1:5:U:H3'	21:Z1:6:U:C6	2.32	0.65
21:Z1:6:U:H4'	21:Z1:7:U:H3'	1.79	0.64
14:4:5:U:O4	16:6:69:A:N6	2.30	0.64
21:Z1:5:U:H3'	21:Z1:6:U:H6	1.62	0.64
1:1:94:A:N1	1:1:115:U:C4	2.66	0.64
23:1f:44:LEU:O	23:1f:61:GLU:HA	1.98	0.63
14:4:37:C:H3'	14:4:39:A:N7	2.13	0.63
48:68:38:LEU:O	48:68:59:LEU:HA	1.98	0.63
2:C:187:THR:N	2:C:533:SER:O	2.32	0.62
16:6:76:A:C2	19:J:563:ASN:HA	2.34	0.62
15:5:71:C:O2'	15:5:73:C:N4	2.30	0.61
15:5:74:U:H2'	15:5:75:G:C8	2.34	0.61
32:N:78:TYR:HA	32:N:84:TYR:HA	1.81	0.61
14:4:36:U:H2'	14:4:37:C:H5'	1.81	0.61
14:4:22:C:H2'	14:4:23:G:C8	2.35	0.61
41:B6:23:ILE:O	41:B6:59:THR:HA	2.00	0.61
13:2:98:G:C4'	13:2:104:U:H2'	2.30	0.61
2:C:118:PHE:HA	22:53:76:MET:O	2.00	0.60
38:B3:699:VAL:HA	38:B3:715:MET:O	2.00	0.60
1:1:103:A:H8	1:1:106:G:H1	1.49	0.60
11:A:1788:VAL:HA	11:A:1802:PRO:HA	1.83	0.59
35:9:408:CYS:O	35:9:413:ASN:HA	2.01	0.59
2:C:830:PRO:HG2	2:C:877:ALA:HB3	1.83	0.59
5:M:91:ARG:HA	5:M:95:VAL:O	2.02	0.59
14:4:58:C:N4	20:L:353:LYS:O	2.34	0.59
2:C:310:SER:HA	2:C:317:CYS:HA	1.85	0.59
38:B3:990:ILE:HA	38:B3:1004:ASP:HA	1.85	0.58
15:5:76:A:H2'	15:5:77:G:H8	1.69	0.58
10:K:863:GLY:HA3	10:K:918:PHE:H	1.69	0.58
27:2e:58:LEU:O	27:2e:76:ARG:HA	2.04	0.58
13:2:62:U:H2'	13:2:63:G:C8	2.39	0.57
14:4:24:U:O2'	14:4:48:G:N2	2.31	0.57
11:A:1334:LEU:HA	11:A:1364:LEU:HA	1.85	0.57
33:G:348:ALA:O	33:G:352:TRP:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:57:ALA:HB3	4:E:60:MET:CB	2.35	0.57
11:A:1217:GLN:HA	11:A:1224:ARG:HA	1.85	0.56
13:2:168:A:H5''	13:2:169:C:H5	1.71	0.56
13:2:165:A:H61	42:2B:84:ALA:HB1	1.69	0.56
14:4:13:U:H2'	14:4:14:G:H8	1.70	0.56
12:B:242:ALA:HA	32:N:262:VAL:HA	1.86	0.56
2:C:478:THR:HA	2:C:494:GLY:HA3	1.88	0.56
2:C:839:PRO:HA	2:C:868:LEU:HA	1.88	0.56
15:5:47:A:O2'	15:5:48:A:O5'	2.23	0.56
14:4:35:G:H1'	14:4:37:C:H5	1.71	0.55
13:2:170:C:H2'	42:2B:44:LYS:O	2.06	0.55
11:A:897:GLU:O	11:A:908:VAL:N	2.35	0.55
11:A:1425:LYS:H	12:B:213:ASP:C	2.14	0.55
13:2:51:A:H2'	13:2:52:G:H8	1.71	0.55
14:4:36:U:H3'	14:4:39:A:N6	2.21	0.55
5:M:38:GLY:HA3	14:4:32:G:N1	2.22	0.55
4:E:240:GLY:HA3	4:E:290:ARG:HA	1.88	0.54
30:S:721:THR:O	30:S:725:ALA:N	2.32	0.54
2:C:115:GLU:CB	22:53:79:ASN:C	2.80	0.54
2:C:388:VAL:O	2:C:392:LEU:CB	2.56	0.54
33:G:644:PHE:N	33:G:766:THR:O	2.41	0.54
11:A:1733:ILE:O	11:A:1737:ASN:N	2.40	0.53
38:B3:84:SER:HA	38:B3:110:SER:HA	1.90	0.53
31:4B:350:TRP:HA	31:4B:357:GLU:HA	1.91	0.53
4:E:52:CYS:O	4:E:340:PRO:HD2	2.09	0.52
16:6:74:U:H2'	16:6:75:G:H8	1.73	0.52
7:U:135:ALA:HA	7:U:142:TYR:HA	1.89	0.52
7:U:520:LEU:HA	7:U:527:TRP:HA	1.92	0.52
38:B3:1033:VAL:HA	38:B3:1048:ASP:HA	1.91	0.52
47:63:29:ILE:HA	47:63:98:PRO:HD3	1.91	0.51
13:2:50:C:H42	13:2:63:G:H1	1.59	0.51
41:B6:24:ARG:O	41:B6:87:LEU:HA	2.10	0.51
1:1:137:U:H3	29:1K:34:HIS:HA	1.74	0.51
11:A:1789:THR:O	11:A:1790:ILE:C	2.53	0.51
12:B:463:PRO:HA	12:B:480:THR:HA	1.93	0.51
13:2:63:G:H2'	13:2:64:A:C8	2.46	0.51
14:4:41:C:H2'	14:4:42:C:H6	1.73	0.51
31:4B:236:TYR:HA	31:4B:497:GLY:HA3	1.91	0.51
33:G:357:TRP:HA	33:G:365:MET:CB	2.42	0.50
5:M:111:GLN:O	16:6:72:G:H5'	2.11	0.50
21:Z1:5:U:H4'	33:G:504:GLY:CA	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:135:A:N6	29:1K:36:GLN:O	2.44	0.50
19:J:569:LEU:HA	19:J:585:GLU:O	2.12	0.50
28:42:33:THR:O	28:42:37:LYS:N	2.45	0.50
11:A:1310:ARG:CB	12:B:37:THR:HA	2.42	0.50
50:65:41:LEU:H	50:65:51:LEU:HA	1.77	0.50
7:U:429:LYS:O	7:U:440:LYS:N	2.40	0.50
14:4:39:A:H5'	14:4:41:C:O4'	2.11	0.49
15:5:12:U:H3	15:5:65:G:H1	1.59	0.49
2:C:831:TYR:HA	2:C:876:PRO:HA	1.94	0.49
11:A:1417:PRO:O	11:A:1418:ARG:C	2.53	0.49
38:B3:258:TYR:O	38:B3:266:ASP:HA	2.12	0.49
14:4:59:U:H2'	14:4:60:A:C8	2.48	0.49
1:1:51:G:H2'	1:1:52:G:H8	1.78	0.49
14:4:7:G:H2'	14:4:8:C:C6	2.48	0.49
33:G:648:GLU:O	33:G:652:ARG:N	2.45	0.49
23:4f:19:VAL:HA	23:4f:75:VAL:H	1.78	0.49
2:C:862:PRO:HA	2:C:869:TYR:HA	1.94	0.49
4:E:59:ILE:O	4:E:60:MET:C	2.55	0.49
13:2:168:A:H5''	13:2:169:C:C5	2.48	0.49
8:X:129:ILE:CA	28:42:58:ALA:HA	2.27	0.49
7:U:457:ARG:O	7:U:468:ASN:N	2.45	0.49
11:A:1639:VAL:N	11:A:1655:THR:O	2.46	0.49
14:4:35:G:C5	14:4:39:A:C2	3.01	0.49
15:5:66:A:O2'	15:5:67:A:H8	1.96	0.48
6:R:446:TYR:HA	6:R:451:PRO:HB3	1.94	0.48
14:4:76:C:H2'	16:6:33:G:H22	1.78	0.48
19:J:569:LEU:O	19:J:570:THR:C	2.56	0.48
14:4:37:C:O5'	14:4:39:A:N6	2.47	0.48
2:C:858:THR:H	2:C:873:ALA:HA	1.78	0.48
16:6:76:A:H2	19:J:566:GLN:CB	2.27	0.48
28:42:69:ASN:HA	28:42:96:ILE:O	2.13	0.48
7:U:430:GLU:HA	7:U:439:LEU:HA	1.96	0.48
12:B:449:ALA:HB1	12:B:684:PRO:HB2	1.96	0.48
2:C:531:TRP:HA	2:C:540:GLU:HA	1.95	0.48
11:A:1637:TRP:N	11:A:1657:THR:O	2.47	0.48
20:L:289:ARG:O	20:L:292:ALA:HB3	2.14	0.48
48:68:39:ASP:HA	48:68:59:LEU:H	1.79	0.48
50:65:53:ASP:HA	50:65:69:LEU:HA	1.95	0.48
11:A:822:PHE:O	12:B:240:LEU:N	2.41	0.48
14:4:19:U:O2'	14:4:20:A:O4'	2.30	0.48
18:8:147:PRO:HB3	18:8:173:ALA:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:460:LYS:HA	7:U:465:VAL:HA	1.95	0.48
33:G:671:VAL:O	33:G:721:THR:HA	2.14	0.48
19:J:564:ALA:O	19:J:569:LEU:N	2.44	0.47
10:K:682:VAL:HA	10:K:688:ASN:HA	1.95	0.47
14:4:11:A:H2'	14:4:12:G:H8	1.78	0.47
16:6:55:C:H2'	16:6:56:A:C8	2.49	0.47
33:G:436:GLU:H	33:G:633:GLY:HA2	1.80	0.47
3:D:52:VAL:O	3:D:56:ALA:N	2.47	0.47
11:A:1404:THR:HA	12:B:219:GLU:HA	1.96	0.47
7:U:125:SER:N	7:U:142:TYR:O	2.47	0.47
26:1g:19:LEU:HA	26:1g:70:LEU:HA	1.96	0.47
33:G:776:PHE:O	33:G:780:LYS:N	2.47	0.47
11:A:274:PRO:HB3	33:G:283:SER:HA	1.97	0.47
33:G:355:ARG:HA	33:G:359:GLN:CB	2.44	0.47
50:65:30:MET:HA	50:65:79:ILE:HA	1.97	0.47
11:A:1644:LEU:HA	11:A:1715:TYR:HA	1.96	0.46
14:4:78:A:N6	16:6:32:U:O2	2.48	0.46
31:4B:281:PHE:HA	31:4B:296:LEU:HA	1.97	0.46
38:B3:336:ALA:HA	38:B3:351:SER:HA	1.97	0.46
11:A:1505:LYS:N	20:L:376:ASN:O	2.38	0.46
2:C:118:PHE:CB	22:53:79:ASN:O	2.62	0.46
11:A:518:LEU:HA	11:A:524:LEU:HA	1.97	0.46
2:C:532:ILE:N	2:C:539:ILE:O	2.40	0.46
11:A:115:ASP:HA	11:A:488:ASP:HA	1.97	0.46
14:4:64:G:N2	14:4:67:A:H5'	2.28	0.46
32:N:255:LEU:O	32:N:259:SER:N	2.40	0.46
3:D:46:TYR:HA	3:D:49:ALA:HB2	1.98	0.46
12:B:835:SER:O	12:B:839:GLY:N	2.49	0.46
14:4:55:U:N3	16:6:58:G:N3	2.56	0.46
15:5:63:A:H2'	15:5:64:G:C8	2.51	0.46
2:C:504:GLY:H	2:C:528:GLY:HA2	1.81	0.46
11:A:1665:GLN:N	11:A:1703:ILE:O	2.46	0.45
11:A:1793:THR:H	11:A:1798:LEU:HA	1.81	0.45
31:4B:234:ILE:HA	31:4B:250:CYS:HA	1.97	0.45
12:B:243:ASN:N	32:N:261:SER:O	2.49	0.45
16:6:48:A:H5''	16:6:49:G:H21	1.80	0.45
20:L:254:ALA:HB1	20:L:271:THR:N	2.32	0.45
1:1:132:G:H22	1:1:135:A:H4'	1.81	0.45
14:4:35:G:C4	14:4:39:A:C2	3.04	0.45
15:5:23:C:H5''	15:5:24:G:H2'	1.99	0.45
23:4f:23:LEU:HA	23:4f:69:VAL:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R:387:ASP:N	14:4:68:A:N1	2.64	0.45
11:A:1789:THR:N	11:A:1801:LYS:O	2.44	0.45
14:4:33:A:H62	14:4:43:G:H21	1.64	0.45
11:A:1817:LEU:O	11:A:1917:PHE:N	2.50	0.45
31:4B:452:VAL:HA	31:4B:469:ALA:HA	1.98	0.45
2:C:189:VAL:HA	2:C:199:LEU:HA	1.99	0.45
5:M:100:ILE:N	14:4:31:U:OP1	2.50	0.45
6:R:383:ILE:N	6:R:427:VAL:O	2.34	0.44
14:4:35:G:H1'	14:4:37:C:C5	2.50	0.44
15:5:75:G:H2'	15:5:76:A:O4'	2.17	0.44
44:66:31:ARG:O	44:66:48:THR:HA	2.17	0.44
12:B:498:ASN:HA	12:B:648:LEU:O	2.17	0.44
14:4:35:G:C2'	14:4:36:U:H5''	2.44	0.44
33:G:499:THR:HA	33:G:521:ILE:O	2.17	0.44
39:BP:42:LEU:HA	39:BP:70:TYR:HA	1.99	0.44
1:1:76:G:H2'	1:1:77:A:H8	1.83	0.44
5:M:91:ARG:O	5:M:92:ALA:C	2.61	0.44
15:5:12:U:H2'	15:5:13:C:C6	2.53	0.44
4:E:295:PRO:HG2	4:E:337:PRO:HA	1.99	0.44
16:6:77:C:OP2	19:J:559:LYS:N	2.50	0.44
33:G:654:LYS:O	33:G:658:ILE:N	2.45	0.44
11:A:1663:ASP:O	11:A:1703:ILE:N	2.47	0.44
14:4:11:A:H2'	14:4:12:G:C8	2.51	0.44
33:G:242:ASP:O	33:G:246:GLU:N	2.46	0.44
6:R:382:ARG:HA	6:R:428:SER:HA	2.00	0.44
11:A:531:THR:O	11:A:535:ARG:N	2.46	0.44
20:L:299:CYS:O	20:L:302:ALA:HB3	2.18	0.44
38:B3:785:PRO:HA	38:B3:801:GLU:HA	1.99	0.44
14:4:15:G:H1	16:6:60:C:H42	1.66	0.44
16:6:60:C:H2'	16:6:61:C:C6	2.52	0.44
14:4:45:G:H2'	14:4:46:G:C8	2.51	0.44
15:5:70:A:O2'	15:5:71:C:O4'	2.31	0.44
11:A:1786:TYR:CB	12:B:203:VAL:H	2.31	0.43
26:4g:46:VAL:HA	26:4g:56:ASN:HA	2.00	0.43
6:R:385:CYS:O	6:R:425:GLY:N	2.41	0.43
14:4:62:U:H2'	14:4:63:U:C6	2.53	0.43
15:5:12:U:O2	15:5:65:G:N2	2.34	0.43
31:4B:259:SER:O	31:4B:263:CYS:N	2.51	0.43
2:C:185:PRO:HA	2:C:203:MET:HA	1.99	0.43
12:B:1349:GLY:H	12:B:1513:ASN:HA	1.84	0.43
11:A:1609:VAL:HA	11:A:1631:LEU:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:5:17:U:H2'	15:5:18:C:C6	2.53	0.43
16:6:53:A:H2'	16:6:54:G:C8	2.54	0.43
16:6:59:G:H2'	16:6:60:C:C6	2.53	0.43
19:J:564:ALA:HB1	19:J:569:LEU:O	2.19	0.43
2:C:130:ARG:O	2:C:201:ASN:N	2.43	0.43
11:A:824:PRO:HD3	12:B:240:LEU:N	2.34	0.43
14:4:42:C:H2'	14:4:43:G:O4'	2.18	0.43
11:A:2130:GLY:HA3	11:A:2142:ILE:HA	2.01	0.43
24:11:23:THR:HA	24:11:47:LEU:HA	2.01	0.43
5:M:95:VAL:HA	14:4:30:A:C5	2.54	0.42
26:1g:42:ILE:O	26:1g:59:MET:HA	2.19	0.42
14:4:38:U:OP2	14:4:38:U:H3'	2.19	0.42
33:G:356:HIS:H	33:G:359:GLN:CB	2.33	0.42
48:68:35:ASN:HA	48:68:62:VAL:O	2.20	0.42
11:A:1554:GLN:HA	11:A:1561:PHE:HA	2.00	0.42
12:B:656:PRO:HB2	12:B:888:PRO:HG3	2.00	0.42
14:4:108:C:H2'	14:4:109:G:H8	1.84	0.42
15:5:53:U:H2'	15:5:54:U:C6	2.54	0.42
11:A:1928:SER:O	11:A:1932:ALA:N	2.44	0.42
22:43:26:GLU:HA	22:43:49:THR:O	2.19	0.42
14:4:27:C:H2'	14:4:28:C:C6	2.55	0.42
1:1:51:G:H2'	1:1:52:G:C8	2.55	0.42
13:2:32:U:H2'	13:2:33:G:H8	1.85	0.42
14:4:24:U:H5''	14:4:25:A:O5'	2.19	0.42
15:5:63:A:H2'	15:5:64:G:H8	1.84	0.42
2:C:741:GLY:HA2	2:C:742:PRO:HD3	1.86	0.42
23:2f:23:LEU:HA	23:2f:69:VAL:HA	2.02	0.42
13:2:182:U:H2'	13:2:183:G:C8	2.54	0.42
15:5:113:G:H2'	15:5:114:G:H8	1.85	0.42
31:4B:373:PHE:HA	31:4B:380:ALA:HA	2.01	0.42
7:U:213:SER:N	7:U:221:TYR:O	2.53	0.42
7:U:431:TYR:N	7:U:438:PHE:O	2.42	0.42
11:A:1706:ASP:N	11:A:1711:LEU:O	2.42	0.42
11:A:912:GLU:O	11:A:916:LYS:N	2.40	0.41
11:A:1806:ALA:HA	11:A:1821:ILE:HA	2.01	0.41
18:8:133:LEU:HA	18:8:208:LEU:O	2.20	0.41
15:5:47:A:O2'	15:5:48:A:H8	2.04	0.41
31:4B:276:VAL:HA	31:4B:300:ALA:HA	2.02	0.41
32:N:415:GLU:O	32:N:419:ALA:N	2.49	0.41
25:4b:86:PRO:HA	25:4b:87:PRO:HD3	1.93	0.41
49:64:46:THR:HA	49:64:52:LYS:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:X:129:ILE:CB	28:42:59:PHE:H	2.33	0.41
11:A:824:PRO:HD3	12:B:239:THR:HA	2.01	0.41
2:C:665:THR:O	2:C:826:ARG:N	2.53	0.41
11:A:2214:ILE:HA	11:A:2227:ALA:HA	2.02	0.41
25:4b:28:ILE:O	25:4b:45:CYS:HA	2.21	0.41
18:8:171:MET:O	18:8:178:THR:HA	2.20	0.41
25:4b:42:LEU:O	25:4b:69:LEU:HA	2.20	0.41
5:M:86:LYS:CB	5:M:98:PRO:HB2	2.50	0.41
8:X:141:MET:N	30:S:733:PHE:O	2.37	0.41
31:4B:495:VAL:HA	31:4B:511:SER:HA	2.02	0.41
43:2A:81:GLU:HA	43:2A:108:PRO:HB3	2.02	0.41
13:2:180:G:H2'	13:2:181:G:H8	1.85	0.41
15:5:45:C:N4	33:G:271:LYS:O	2.46	0.41
33:G:492:GLY:O	33:G:496:GLY:N	2.54	0.41
22:43:45:ASN:HA	22:43:58:LEU:O	2.21	0.41
5:M:38:GLY:HA3	14:4:32:G:H1	1.85	0.41
6:R:408:LEU:N	6:R:428:SER:O	2.53	0.41
10:K:714:VAL:HA	10:K:769:PRO:HD3	2.03	0.41
10:K:773:ASN:HA	10:K:822:LEU:HA	2.03	0.41
11:A:1218:ASN:N	11:A:1223:GLU:O	2.54	0.41
12:B:912:ASN:HA	12:B:978:ASN:HA	2.02	0.41
13:2:32:U:H2'	13:2:33:G:C8	2.56	0.41
14:4:41:C:P	14:4:41:C:H3'	2.61	0.41
15:5:29:A:H2'	15:5:30:A:C8	2.56	0.41
16:6:56:A:O2'	19:J:474:PRO:O	2.39	0.41
33:G:646:MET:O	33:G:647:SER:C	2.64	0.41
24:51:68:PHE:O	28:52:100:PHE:N	2.53	0.41
27:5e:55:ASN:CA	27:5e:79:LEU:O	2.69	0.41
2:C:838:ALA:O	2:C:869:TYR:N	2.54	0.41
11:A:1413:ASP:O	11:A:1419:ILE:HA	2.20	0.41
12:B:834:TYR:HA	12:B:841:TRP:HA	2.03	0.41
27:4e:58:LEU:O	27:4e:76:ARG:HA	2.21	0.40
1:1:140:G:H2'	1:1:141:G:H8	1.85	0.40
11:A:978:GLU:O	11:A:1174:PHE:N	2.54	0.40
14:4:37:C:C6	14:4:39:A:N6	2.89	0.40
18:8:56:CYS:O	18:8:60:LEU:HA	2.21	0.40
6:R:414:ARG:HA	6:R:421:THR:HA	2.04	0.40
7:U:214:ARG:HA	7:U:220:THR:HA	2.03	0.40
1:1:78:U:H2'	1:1:79:G:C8	2.57	0.40
26:5g:42:ILE:O	26:5g:59:MET:CA	2.69	0.40
2:C:196:LYS:HA	22:53:12:GLU:CA	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:76:PRO:HA	4:E:337:PRO:HG3	2.04	0.40
4:E:290:ARG:N	4:E:331:ASN:O	2.55	0.40
7:U:266:PRO:HA	7:U:267:PRO:HD3	1.96	0.40
11:A:734:PRO:HB2	32:N:149:LEU:HA	2.02	0.40
15:5:76:A:H2'	15:5:77:G:C8	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	850/972 (87%)	822 (97%)	28 (3%)	0	100	100
3	D	139/142 (98%)	138 (99%)	1 (1%)	0	100	100
4	E	305/357 (85%)	299 (98%)	6 (2%)	0	100	100
5	M	121/128 (94%)	117 (97%)	4 (3%)	0	100	100
6	R	104/480 (22%)	99 (95%)	5 (5%)	0	100	100
7	U	454/565 (80%)	434 (96%)	20 (4%)	0	100	100
8	X	24/155 (16%)	22 (92%)	2 (8%)	0	100	100
10	K	316/1007 (31%)	312 (99%)	4 (1%)	0	100	100
11	A	2162/2335 (93%)	2109 (98%)	53 (2%)	0	100	100
12	B	1989/2136 (93%)	1965 (99%)	24 (1%)	0	100	100
17	7	132/793 (17%)	132 (100%)	0	0	100	100
18	8	138/464 (30%)	135 (98%)	3 (2%)	0	100	100
19	J	186/683 (27%)	181 (97%)	5 (3%)	0	100	100
20	L	293/499 (59%)	286 (98%)	7 (2%)	0	100	100
22	13	79/126 (63%)	79 (100%)	0	0	100	100
22	23	81/126 (64%)	81 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	43	81/126 (64%)	81 (100%)	0	0	100	100
22	53	75/126 (60%)	75 (100%)	0	0	100	100
23	1f	72/86 (84%)	71 (99%)	1 (1%)	0	100	100
23	2f	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
23	4f	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
23	5f	72/86 (84%)	71 (99%)	1 (1%)	0	100	100
24	11	79/119 (66%)	78 (99%)	1 (1%)	0	100	100
24	21	78/119 (66%)	75 (96%)	3 (4%)	0	100	100
24	41	79/119 (66%)	77 (98%)	2 (2%)	0	100	100
24	51	80/119 (67%)	75 (94%)	5 (6%)	0	100	100
25	1b	84/240 (35%)	84 (100%)	0	0	100	100
25	2b	80/240 (33%)	80 (100%)	0	0	100	100
25	4b	80/240 (33%)	79 (99%)	1 (1%)	0	100	100
25	5b	84/240 (35%)	80 (95%)	4 (5%)	0	100	100
26	1g	71/76 (93%)	70 (99%)	1 (1%)	0	100	100
26	2g	71/76 (93%)	70 (99%)	1 (1%)	0	100	100
26	4g	72/76 (95%)	71 (99%)	1 (1%)	0	100	100
26	5g	72/76 (95%)	69 (96%)	3 (4%)	0	100	100
27	1e	75/92 (82%)	74 (99%)	1 (1%)	0	100	100
27	2e	79/92 (86%)	79 (100%)	0	0	100	100
27	4e	74/92 (80%)	73 (99%)	1 (1%)	0	100	100
27	5e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
28	12	91/118 (77%)	90 (99%)	1 (1%)	0	100	100
28	22	91/118 (77%)	91 (100%)	0	0	100	100
28	42	90/118 (76%)	87 (97%)	3 (3%)	0	100	100
28	52	95/118 (80%)	88 (93%)	7 (7%)	0	100	100
29	1K	199/437 (46%)	195 (98%)	4 (2%)	0	100	100
30	S	100/800 (12%)	98 (98%)	2 (2%)	0	100	100
31	4B	357/522 (68%)	346 (97%)	11 (3%)	0	100	100
32	N	789/941 (84%)	779 (99%)	10 (1%)	0	100	100
33	G	567/820 (69%)	552 (97%)	15 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	B4	76/424 (18%)	76 (100%)	0	0	100	100
35	9	377/501 (75%)	370 (98%)	7 (2%)	0	100	100
36	B2	204/895 (23%)	202 (99%)	2 (1%)	0	100	100
37	B5	67/86 (78%)	66 (98%)	1 (2%)	0	100	100
38	B3	1176/1217 (97%)	1153 (98%)	23 (2%)	0	100	100
39	BP	98/110 (89%)	96 (98%)	2 (2%)	0	100	100
40	B1	866/1304 (66%)	847 (98%)	19 (2%)	0	100	100
41	B6	88/125 (70%)	84 (96%)	4 (4%)	0	100	100
42	2B	90/225 (40%)	90 (100%)	0	0	100	100
43	2A	160/255 (63%)	158 (99%)	2 (1%)	0	100	100
44	66	70/80 (88%)	70 (100%)	0	0	100	100
45	67	75/103 (73%)	74 (99%)	1 (1%)	0	100	100
46	62	93/95 (98%)	91 (98%)	2 (2%)	0	100	100
47	63	83/102 (81%)	82 (99%)	1 (1%)	0	100	100
48	68	93/96 (97%)	93 (100%)	0	0	100	100
49	64	71/139 (51%)	70 (99%)	1 (1%)	0	100	100
50	65	74/91 (81%)	72 (97%)	2 (3%)	0	100	100
All	All	15188/23512 (65%)	14877 (98%)	311 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	50/866 (6%)	50 (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	M	6/111 (5%)	6 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	R	4/369 (1%)	4 (100%)	0	100	100
7	U	23/511 (4%)	23 (100%)	0	100	100
8	X	1/144 (1%)	1 (100%)	0	100	100
10	K	10/919 (1%)	10 (100%)	0	100	100
11	A	126/2108 (6%)	126 (100%)	0	100	100
12	B	84/1908 (4%)	84 (100%)	0	100	100
17	7	4/709 (1%)	4 (100%)	0	100	100
18	8	8/382 (2%)	8 (100%)	0	100	100
19	J	11/599 (2%)	11 (100%)	0	100	100
20	L	10/424 (2%)	10 (100%)	0	100	100
22	13	3/101 (3%)	3 (100%)	0	100	100
22	23	3/101 (3%)	3 (100%)	0	100	100
22	43	3/101 (3%)	3 (100%)	0	100	100
23	1f	4/74 (5%)	4 (100%)	0	100	100
23	2f	4/74 (5%)	4 (100%)	0	100	100
23	4f	4/74 (5%)	4 (100%)	0	100	100
24	11	3/101 (3%)	3 (100%)	0	100	100
24	21	3/101 (3%)	3 (100%)	0	100	100
24	41	3/101 (3%)	3 (100%)	0	100	100
25	1b	4/177 (2%)	4 (100%)	0	100	100
25	2b	4/177 (2%)	4 (100%)	0	100	100
25	4b	4/177 (2%)	4 (100%)	0	100	100
26	1g	3/66 (4%)	3 (100%)	0	100	100
26	2g	3/66 (4%)	3 (100%)	0	100	100
26	4g	3/66 (4%)	3 (100%)	0	100	100
27	1e	1/84 (1%)	1 (100%)	0	100	100
27	2e	1/84 (1%)	1 (100%)	0	100	100
27	4e	1/84 (1%)	1 (100%)	0	100	100
28	12	4/110 (4%)	4 (100%)	0	100	100
28	22	5/110 (4%)	5 (100%)	0	100	100
28	42	4/110 (4%)	4 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	1K	19/373 (5%)	19 (100%)	0	100	100
30	S	4/681 (1%)	4 (100%)	0	100	100
31	4B	15/442 (3%)	15 (100%)	0	100	100
32	N	30/792 (4%)	30 (100%)	0	100	100
33	G	30/721 (4%)	30 (100%)	0	100	100
34	B4	4/336 (1%)	4 (100%)	0	100	100
35	9	11/446 (2%)	11 (100%)	0	100	100
36	B2	22/776 (3%)	22 (100%)	0	100	100
37	B5	3/77 (4%)	3 (100%)	0	100	100
38	B3	60/1051 (6%)	60 (100%)	0	100	100
39	BP	4/95 (4%)	4 (100%)	0	100	100
40	B1	40/1104 (4%)	40 (100%)	0	100	100
41	B6	5/109 (5%)	5 (100%)	0	100	100
42	2B	3/195 (2%)	3 (100%)	0	100	100
43	2A	6/218 (3%)	6 (100%)	0	100	100
44	66	2/70 (3%)	2 (100%)	0	100	100
45	67	3/91 (3%)	3 (100%)	0	100	100
46	62	3/88 (3%)	3 (100%)	0	100	100
47	63	4/94 (4%)	4 (100%)	0	100	100
48	68	1/82 (1%)	1 (100%)	0	100	100
49	64	4/111 (4%)	4 (100%)	0	100	100
50	65	3/80 (4%)	3 (100%)	0	100	100
All	All	695/19651 (4%)	695 (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	1	152/163 (93%)	31 (20%)	2 (1%)
13	2	93/188 (49%)	24 (25%)	6 (6%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	4	119/144 (82%)	30 (25%)	3 (2%)
15	5	101/117 (86%)	28 (27%)	3 (2%)
16	6	49/106 (46%)	5 (10%)	0
21	Z1	4/6 (66%)	2 (50%)	0
9	Z	14/15 (93%)	2 (14%)	0
All	All	532/739 (71%)	122 (22%)	14 (2%)

All (122) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	16	G
1	1	17	G
1	1	23	A
1	1	28	G
1	1	34	G
1	1	46	C
1	1	48	C
1	1	51	G
1	1	72	U
1	1	75	G
1	1	82	C
1	1	90	U
1	1	91	G
1	1	93	G
1	1	94	A
1	1	104	A
1	1	105	U
1	1	112	A
1	1	114	C
1	1	115	U
1	1	118	A
1	1	119	C
1	1	123	A
1	1	124	U
1	1	128	U
1	1	132	G
1	1	133	G
1	1	135	A
1	1	138	G
1	1	142	G
1	1	143	A
9	Z	33	U

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Mol	Chain	Res	Type
9	Z	41	A
13	2	30	A
13	2	38	A
13	2	40	C
13	2	47	U
13	2	63	G
13	2	65	U
13	2	98	G
13	2	99	A
13	2	100	U
13	2	101	U
13	2	102	U
13	2	103	U
13	2	104	U
13	2	105	G
13	2	106	G
13	2	107	A
13	2	163	G
13	2	164	C
13	2	166	G
13	2	167	U
13	2	168	A
13	2	170	C
13	2	171	U
13	2	178	A
14	4	2	G
14	4	7	G
14	4	19	U
14	4	21	U
14	4	25	A
14	4	26	G
14	4	30	A
14	4	31	U
14	4	34	G
14	4	36	U
14	4	37	C
14	4	38	U
14	4	39	A
14	4	40	U
14	4	41	C
14	4	44	A
14	4	45	G

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Mol	Chain	Res	Type
14	4	48	G
14	4	51	A
14	4	62	U
14	4	68	A
14	4	75	C
14	4	78	A
14	4	114	U
14	4	115	G
14	4	121	U
14	4	122	U
14	4	123	U
14	4	125	G
14	4	126	A
15	5	4	C
15	5	7	U
15	5	21	A
15	5	23	C
15	5	25	C
15	5	28	A
15	5	36	C
15	5	37	G
15	5	38	C
15	5	47	A
15	5	48	A
15	5	57	G
15	5	58	U
15	5	59	G
15	5	67	A
15	5	69	A
15	5	70	A
15	5	71	C
15	5	72	U
15	5	78	U
15	5	90	U
15	5	94	U
15	5	95	G
15	5	96	A
15	5	105	U
15	5	106	U
15	5	107	U
15	5	108	G
16	6	36	A

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Mol	Chain	Res	Type
16	6	49	G
16	6	59	G
16	6	77	C
16	6	106	U
21	Z1	5	U
21	Z1	7	U

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	15	G
1	1	92	C
13	2	37	U
13	2	46	U
13	2	103	U
13	2	106	G
13	2	167	U
13	2	170	C
14	4	1	A
14	4	37	C
14	4	114	U
15	5	57	G
15	5	58	U
15	5	105	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 ⓘ

There are no chain breaks in this entry.

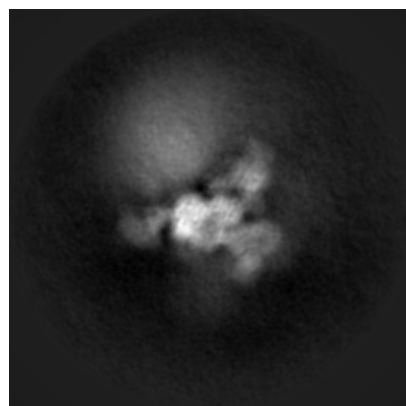
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18786. These allow visual inspection of the internal detail of the map and identification of artifacts.

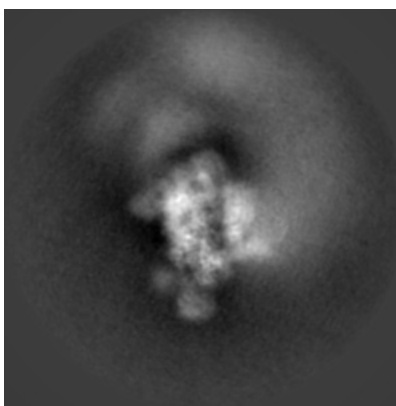
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

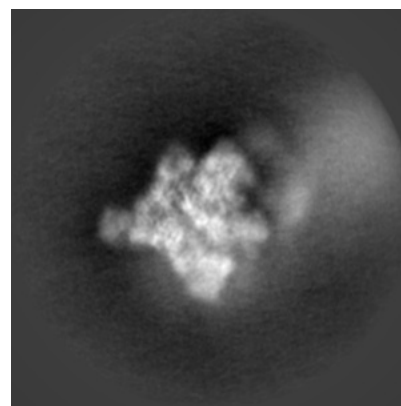
6.1.1 Primary map



X

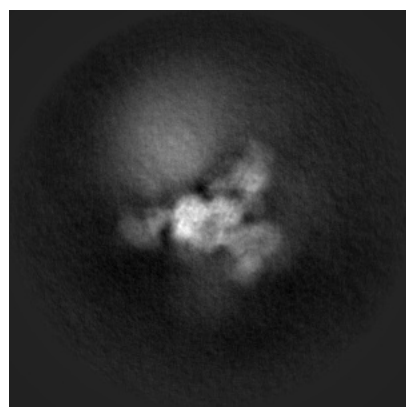


Y

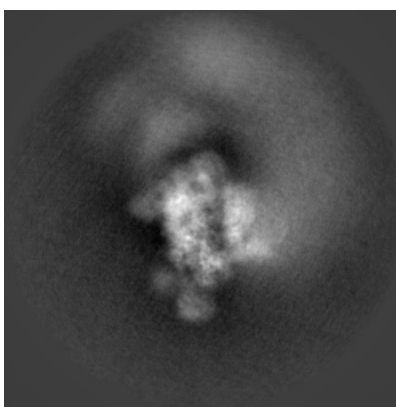


Z

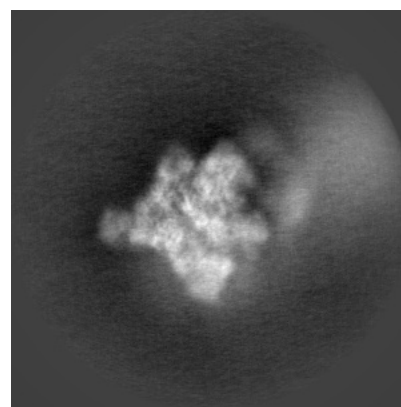
6.1.2 Raw map



X



Y

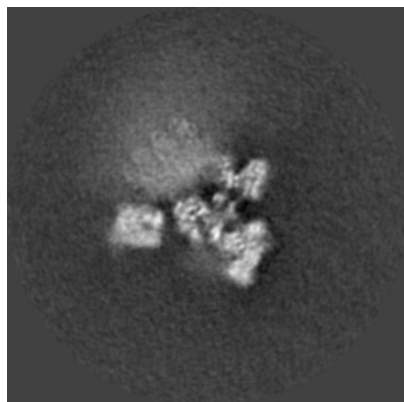


Z

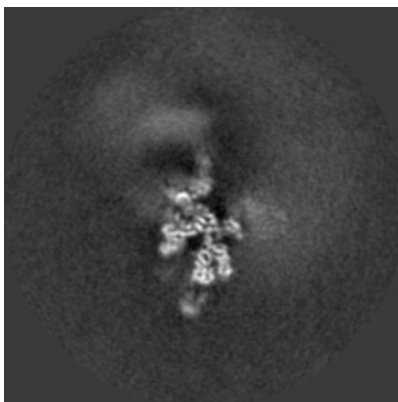
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

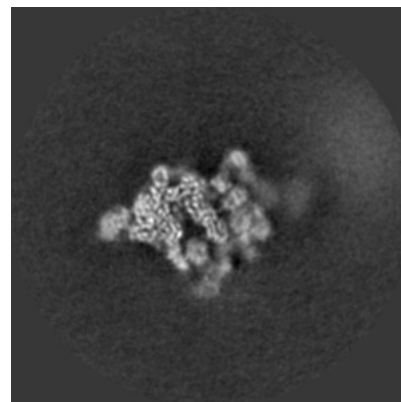
6.2.1 Primary map



X Index: 240

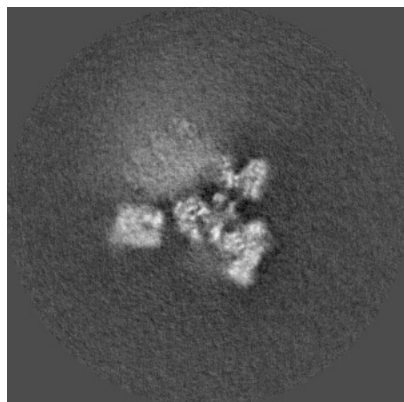


Y Index: 240

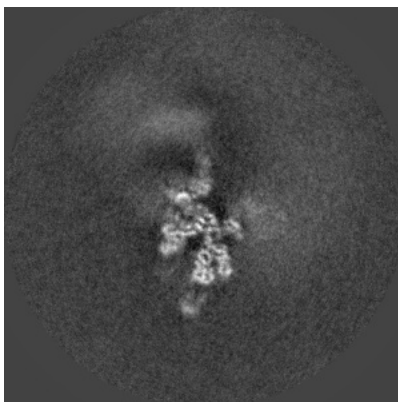


Z Index: 240

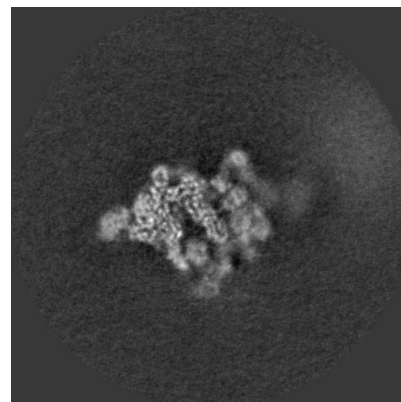
6.2.2 Raw map



X Index: 240



Y Index: 240

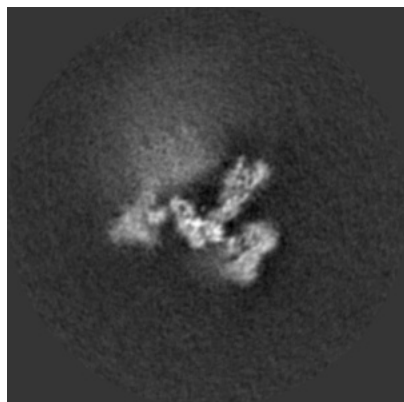


Z Index: 240

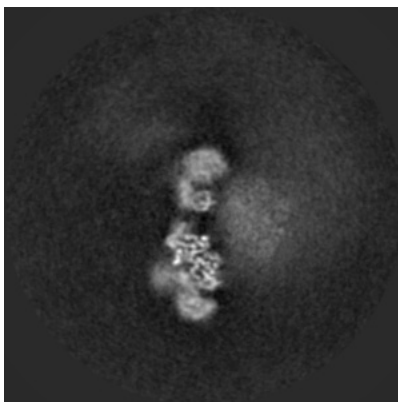
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

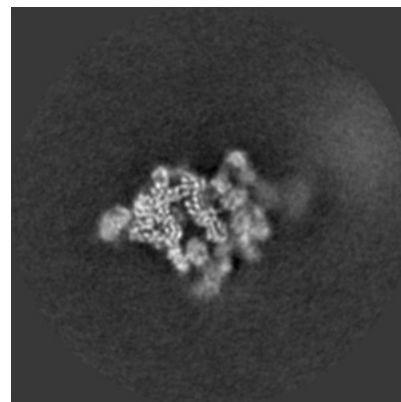
6.3.1 Primary map



X Index: 249

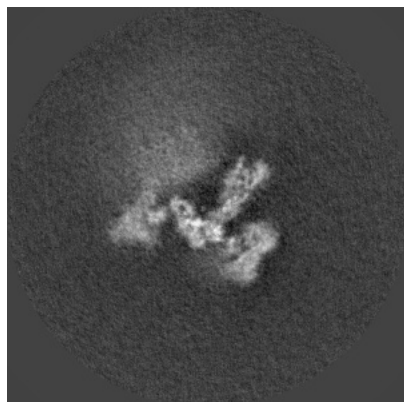


Y Index: 208

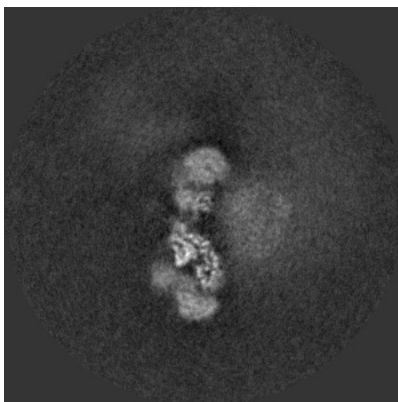


Z Index: 238

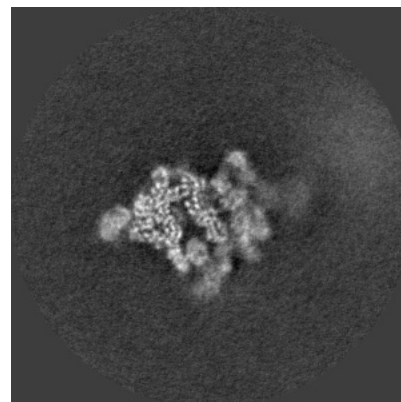
6.3.2 Raw map



X Index: 249



Y Index: 213

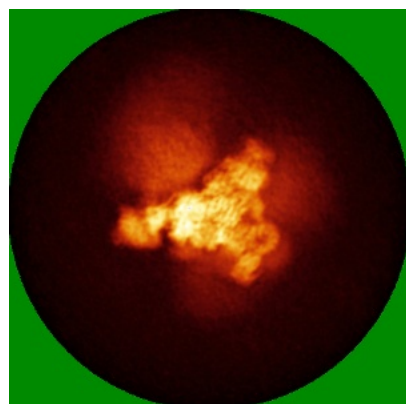


Z Index: 238

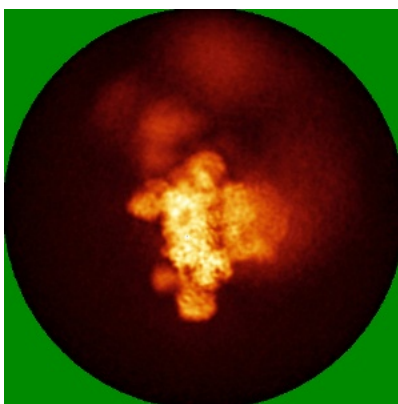
The images above show the largest variance slices of the map in three orthogonal directions.

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

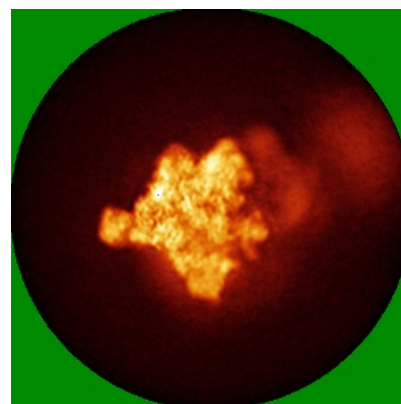
6.4.1 Primary map



X

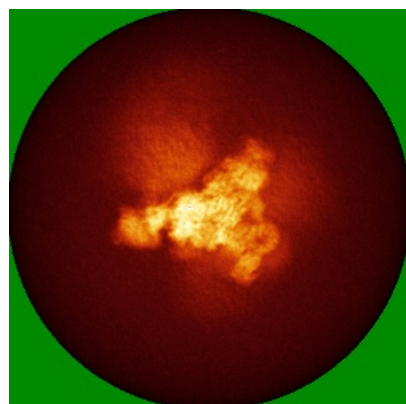


Y

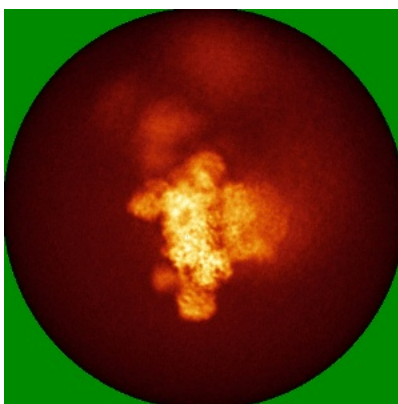


Z

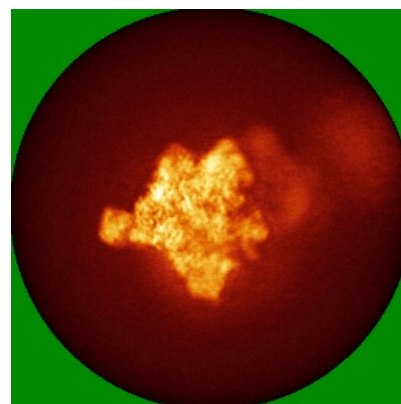
6.4.2 Raw map



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.

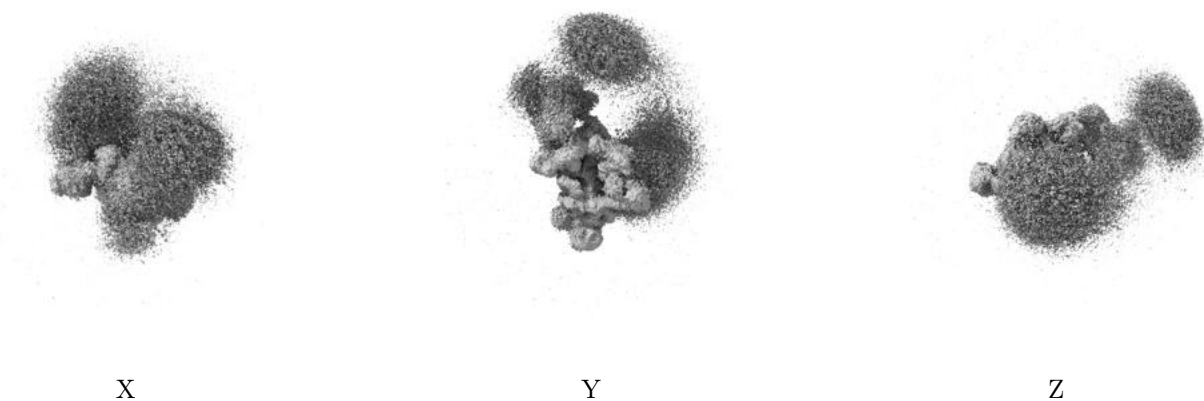
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0078. 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.

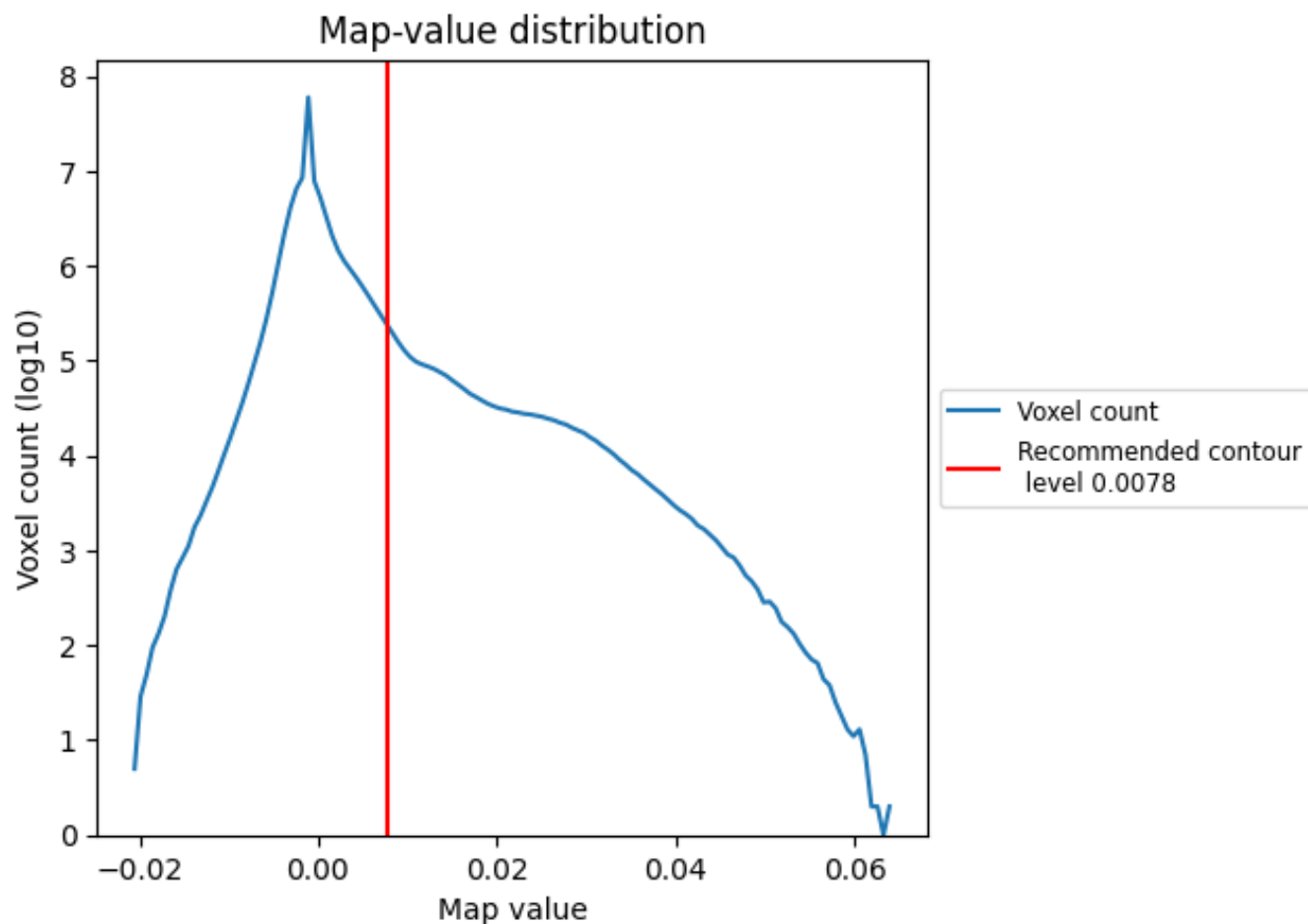
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

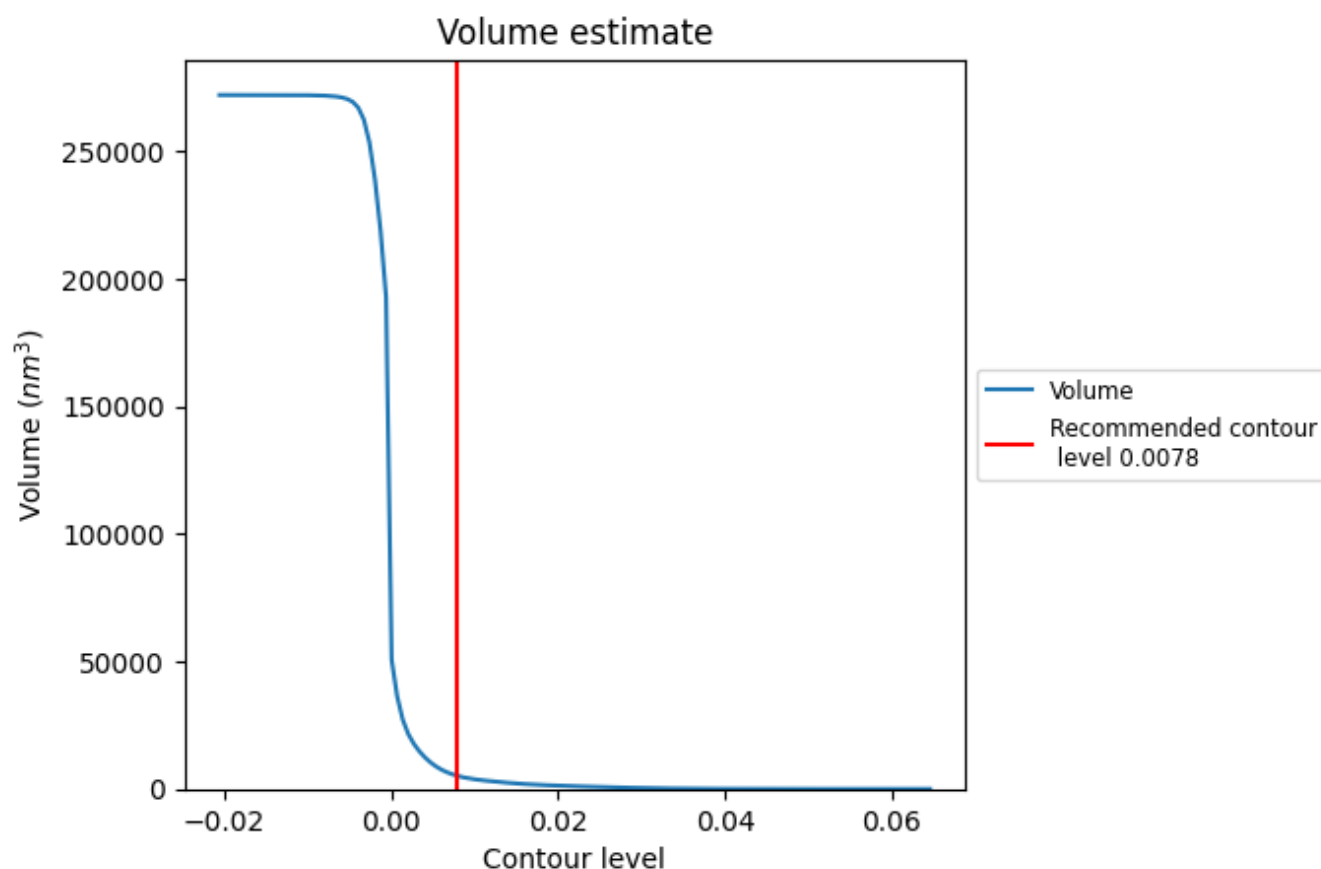
This section contains the results of statistical analysis of the map.

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.

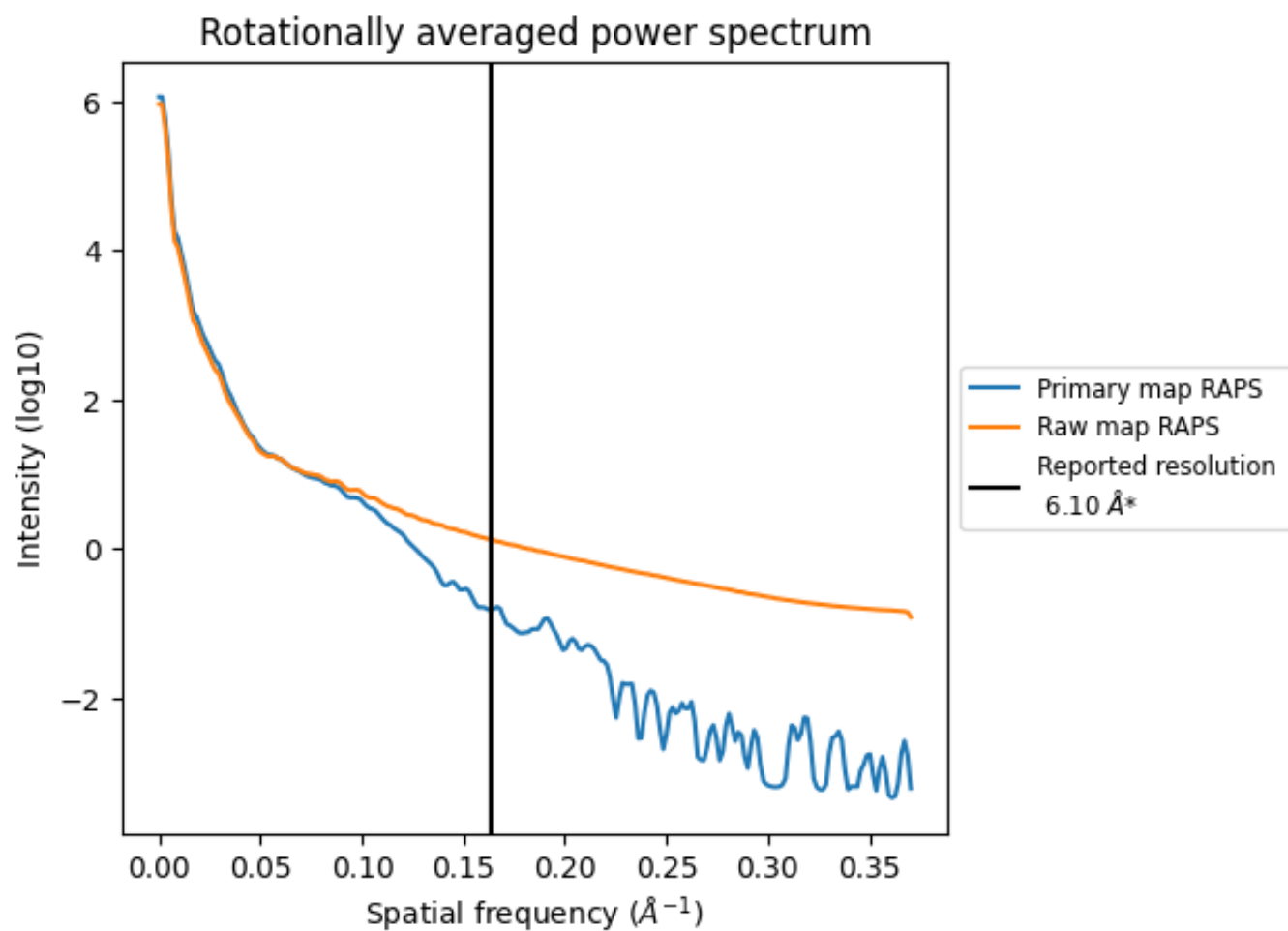
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5316 nm^3 ; this corresponds to an approximate mass of 4802 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 ⓘ

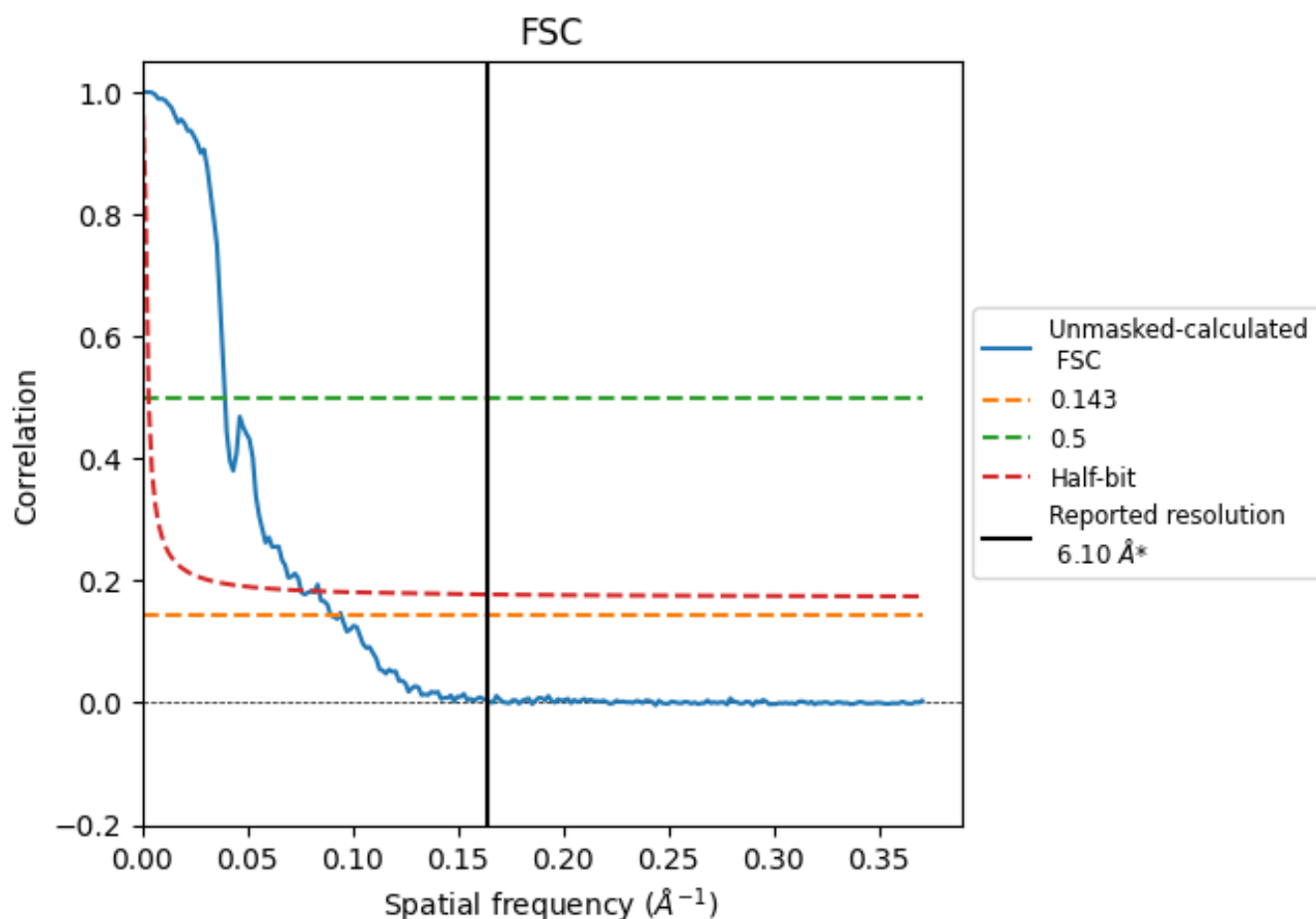


*Reported resolution corresponds to spatial frequency of 0.164 Å^{-1}

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 0.164 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

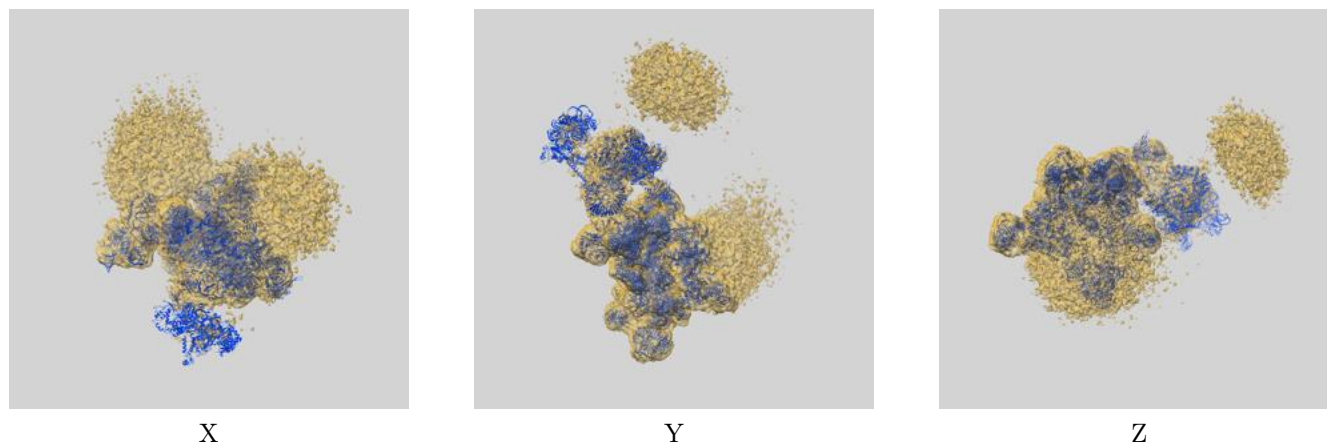
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	11.17	25.45	13.26

*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 11.17 differs from the reported value 6.1 by more than 10 %

9 Map-model fit [i](#)

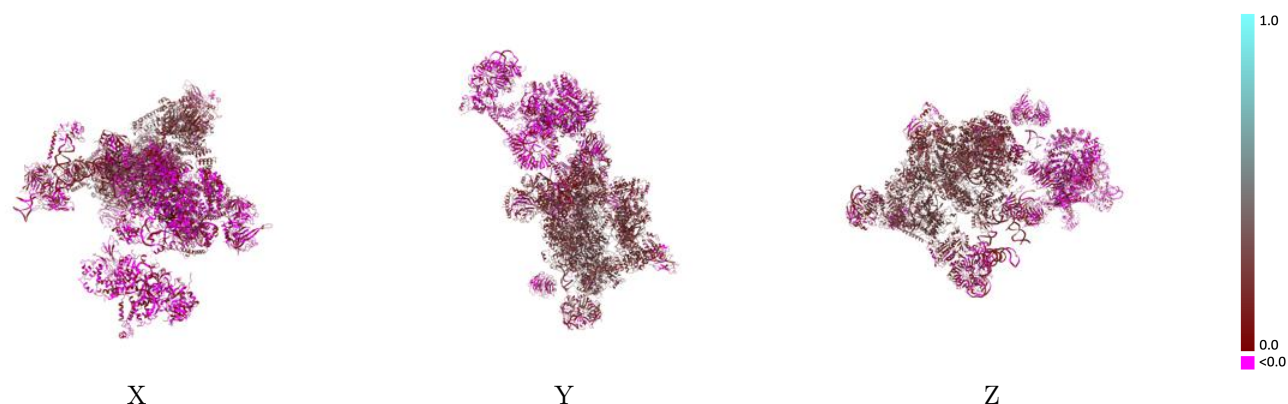
This section contains information regarding the fit between EMDB map EMD-18786 and PDB model 8R08. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



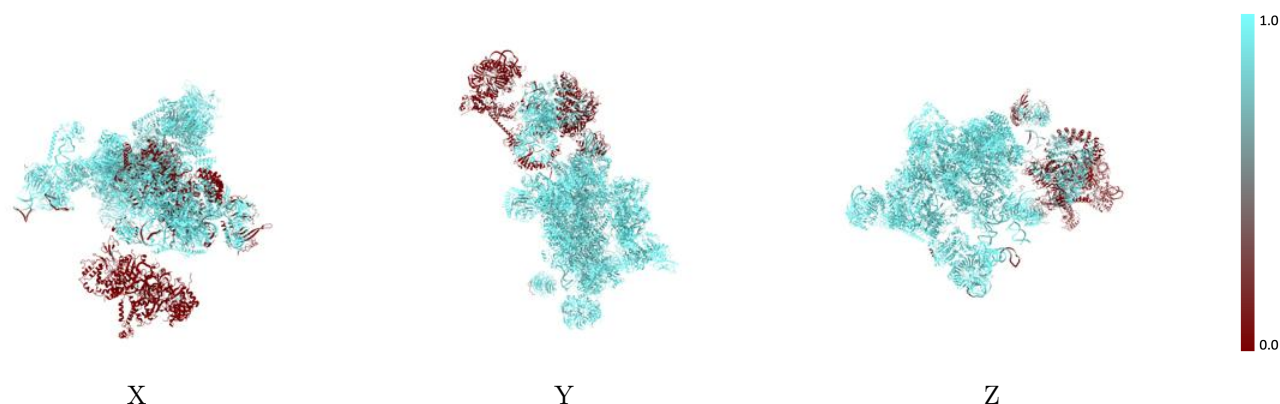
The images above show the 3D surface view of the map at the recommended contour level 0.0078 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



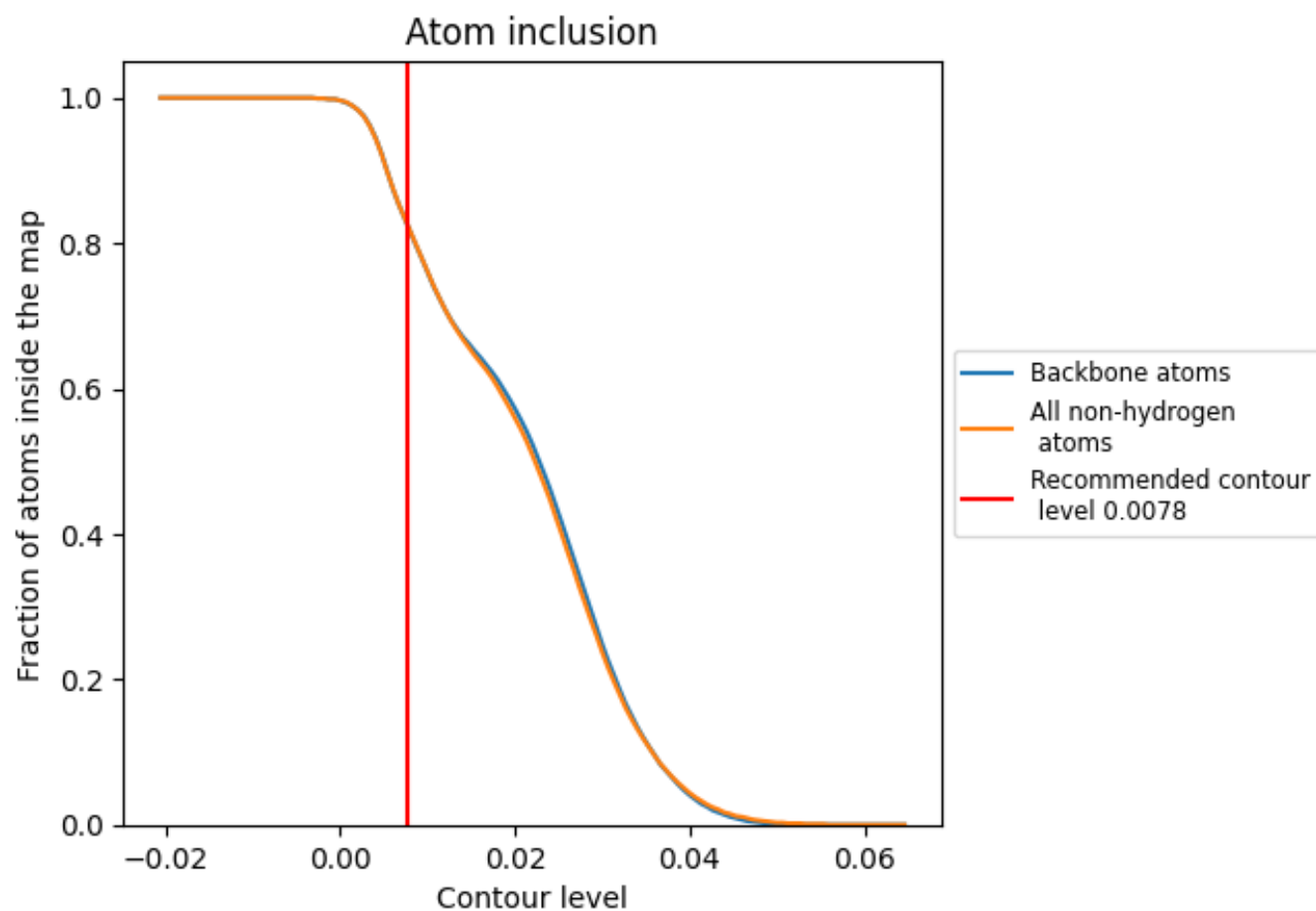
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0078).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 82% 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 (0.0078) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8230	 0.1330
1	 0.8370	 0.0540
11	 0.9930	 0.0870
12	 0.9920	 0.0980
13	 1.0000	 0.0360
1K	 0.9740	 0.0140
1b	 0.9490	 0.0650
1e	 1.0000	 0.0860
1f	 0.9920	 0.0950
1g	 0.9970	 0.0800
2	 0.4080	 0.0180
21	 0.0400	 -0.0220
22	 0.0120	 0.0100
23	 0.0220	 -0.0080
2A	 0.0200	 0.0020
2B	 0.0020	 0.0060
2b	 0.0480	 0.0110
2e	 0.0050	 -0.0140
2f	 0.0030	 -0.0090
2g	 0.0600	 0.0340
4	 0.9990	 0.1490
41	 0.9780	 0.1640
42	 0.9420	 0.1210
43	 0.9980	 0.0510
4B	 0.9990	 0.1390
4b	 0.8860	 0.0610
4e	 1.0000	 0.0880
4f	 0.9940	 0.1040
4g	 0.9840	 0.0720
5	 1.0000	 0.1800
51	 1.0000	 0.1580
52	 0.9970	 0.1250
53	 1.0000	 0.2210
5b	 0.9330	 0.1390
5e	 1.0000	 0.1540



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Chain	Atom inclusion	Q-score
5f	 1.0000	 0.0850
5g	 0.9870	 0.1910
6	 0.9310	 0.1130
62	 0.6340	 0.0250
63	 0.3010	 0.0120
64	 0.9020	 -0.0100
65	 0.6480	 0.0490
66	 0.5290	 0.0380
67	 0.8910	 0.0400
68	 0.6440	 0.0050
7	 0.1020	 0.0230
8	 0.3240	 0.0360
9	 0.1910	 0.0160
A	 0.9960	 0.2650
B	 0.9970	 0.2010
B1	 0.6620	 0.0000
B2	 0.5550	 0.0260
B3	 0.4050	 0.0270
B4	 0.8210	 -0.0060
B5	 0.9910	 0.0390
B6	 0.8240	 0.0110
BP	 0.9140	 -0.0100
C	 1.0000	 0.2690
D	 1.0000	 0.2480
E	 0.9450	 0.0430
G	 0.9900	 0.1840
J	 0.9970	 0.1750
K	 0.9440	 0.1040
L	 0.9920	 0.2110
M	 1.0000	 0.1850
N	 0.9970	 0.1860
R	 1.0000	 0.1710
S	 0.9870	 0.1880
U	 0.9990	 0.2690
X	 0.9920	 0.1590
Z	 1.0000	 0.0080
Z1	 1.0000	 0.1260