wwPDB EM Validation Summary Report

May 25, 2024 – 10:21 am BST

PDB ID	:	8RM5
EMDB ID	:	EMD-19349
Title	:	Cryo-EM structure of the cross-exon pre-B+5'ssLNG+ATPyS 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	:	2024-01-05
Resolution	:	6.90 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 (i) 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 (i)) were used in the production of this report:

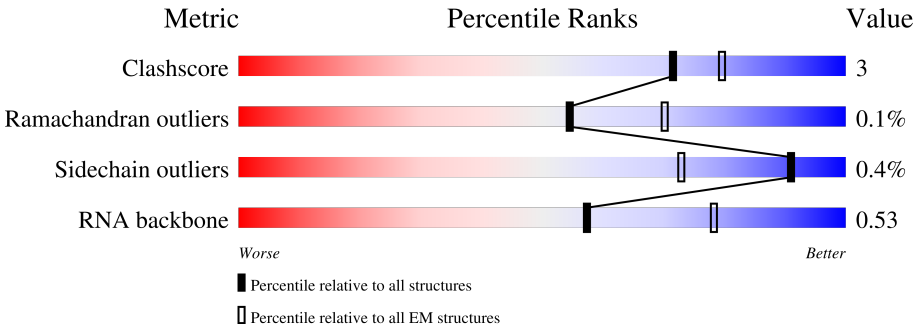
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 6.90 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	66	80	88% · 10%
2	67	103	75% 25%
3	62	95	34% 100%
4	63	102	15% 81% · 17%
5	68	96	22% 94% 5% ·
6	64	139	· 51% · 47%
7	65	91	· 81% · 16%

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Mol	Chain	Length	Quality of chain
8	E	357	80% 6% 14%
9	B4	424	18% 82%
10	Z	347	96%
11	8	464	18% 30% 69%
12	9	501	60% 76% 24%
13	B2	895	23% 77%
14	B5	86	78% 20%
15	2	188	26% 28% 19% 5% 48%
16	B3	1217	38% 94%
17	BP	110	89% 9%
18	B1	1304	11% 66% 33%
19	B6	125	29% 67% 5% 28%
20	22	118	64% 81% 19%
20	42	118	19% 78% 22%
20	52	118	82% 18%
21	2B	225	41% 40% 59%
22	2f	86	84% 84% 16%
22	4f	86	84% 16%
22	5f	86	86% 14%
23	2b	240	21% 34% 66%
23	4b	240	33% 67%
23	5b	240	36% 64%
24	23	126	48% 64% 34%
24	43	126	60% 5% 34%
24	53	126	61% 39%

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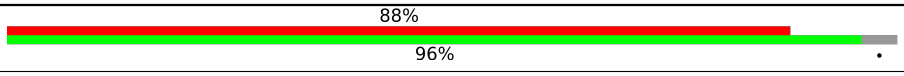
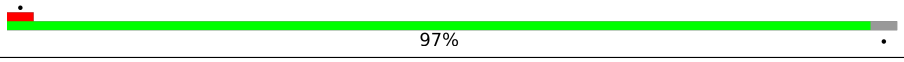
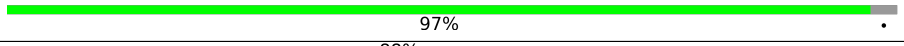
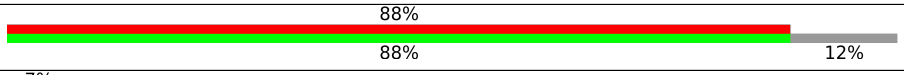
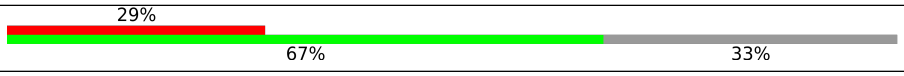
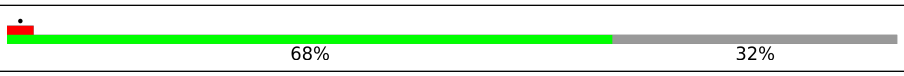
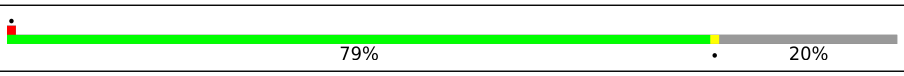
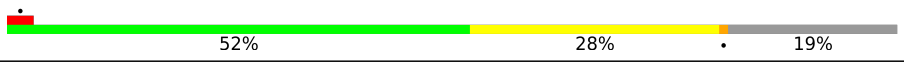
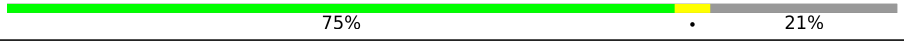
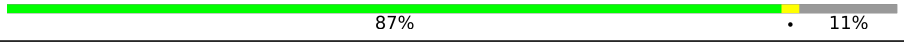
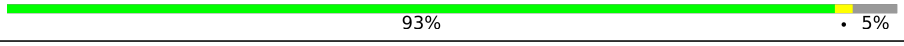
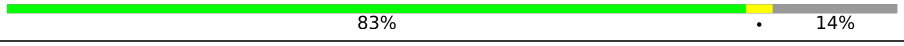
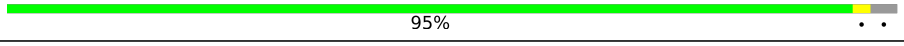
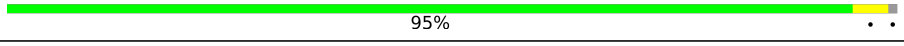
Mol	Chain	Length	Quality of chain
25	2g	76	
25	4g	76	
25	5g	76	
26	2e	92	
26	4e	92	
26	5e	92	
27	21	119	
27	41	119	
27	51	119	
28	2A	255	
29	B	2136	
30	W	177	
31	U	565	
32	z	18	
33	G	820	
34	J	683	
35	L	499	
36	F	522	
37	N	941	
38	A	2335	
39	S	800	
40	C	972	
41	M	128	
42	D	142	
43	5	117	

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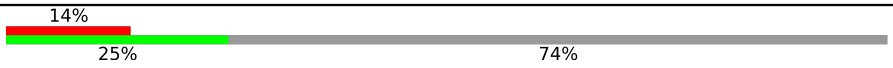
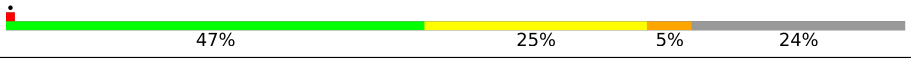
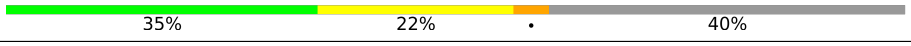
Mol	Chain	Length	Quality of chain
44	7	793	
45	4	144	
46	6	106	

2 Entry composition (i)

There are 46 unique types of molecules in this entry. The entry contains 80921 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	66	72	357	213	72	72	0	0

- Molecule 2 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	67	77	384	230	77	77	0	0

- Molecule 3 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	62	95	478	288	95	95	0	0

- Molecule 4 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	63	85	429	259	85	85	0	0

- Molecule 5 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	68	95	469	279	95	95	0	0

- Molecule 6 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	64	73	369	223	73	73	0	0

- Molecule 7 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	65	76	Total 378	C 226	N 76	O 76	0	0

- Molecule 8 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

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

- Molecule 9 is a protein called Splicing factor 3B subunit 4.

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

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

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

- Molecule 11 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	8	144	Total 729	C 441	N 144	O 144	0	0

- Molecule 12 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	9	383	Total 1920	C 1154	N 383	O 383	0	0

- Molecule 13 is a protein called Splicing factor 3B subunit 2.

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

- Molecule 14 is a protein called Splicing factor 3B subunit 5.

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

- Molecule 15 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2	98	Total 2072	C 926	N 349	O 699	P 98	0	0

- Molecule 16 is a protein called Splicing factor 3B subunit 3.

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

- Molecule 17 is a protein called PHD finger-like domain-containing protein 5A.

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

- Molecule 18 is a protein called Splicing factor 3B subunit 1.

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

- Molecule 19 is a protein called Splicing factor 3B subunit 6.

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

- Molecule 20 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	22	95	Total 482	C 292	N 95	O 95	0	0
20	52	97	Total 388	C 194	N 97	O 97	0	0
20	42	92	Total 463	C 279	N 92	O 92	0	0

- Molecule 21 is a protein called U2 small nuclear ribonucleoprotein B".

Mol	Chain	Residues	Atoms				AltConf	Trace
21	2B	92	Total	C	N	O	0	0
			461	277	92	92		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
22	2f	72	Total	C	N	O	0	0
			359	215	72	72		
22	5f	74	Total	C	N	O	0	0
			296	148	74	74		
22	4f	72	Total	C	N	O	0	0
			359	215	72	72		

- Molecule 23 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	2b	82	Total	C	N	O	0	0
			413	249	82	82		
23	5b	86	Total	C	N	O	0	0
			344	172	86	86		
23	4b	79	Total	C	N	O	0	0
			396	238	79	79		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	23	83	Total	C	N	O	0	0
			415	249	83	83		
24	53	77	Total	C	N	O	0	0
			308	154	77	77		
24	43	83	Total	C	N	O	0	0
			415	249	83	83		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	2g	73	Total	C	N	O	0	0
			364	218	73	73		
25	5g	74	Total	C	N	O	0	0
			296	148	74	74		

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Mol	Chain	Residues	Atoms				AltConf	Trace
25	4g	74	Total 369	C 221	N 74	O 74	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
26	2e	81	Total 403	C 241	N 81	O 81	0	0
26	5e	79	Total 316	C 158	N 79	O 79	0	0
26	4e	76	Total 378	C 226	N 76	O 76	0	0

- Molecule 27 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	21	80	Total 402	C 242	N 80	O 80	0	0
27	51	82	Total 328	C 164	N 82	O 82	0	0
27	41	81	Total 407	C 245	N 81	O 81	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
28	2A	162	Total 816	C 492	N 162	O 162	0	0

- Molecule 29 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

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

- Molecule 30 is a protein called Peptidyl-prolyl cis-trans isomerase H.

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

- Molecule 31 is a protein called Ubiquitin carboxyl-terminal hydrolase 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	456	Total	C	N	O	S	0	0
			3749	2427	635	673	14		

- Molecule 32 is a RNA chain called 5'SS oligo.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	z	18	Total	C	N	O	P	0	0
			384	172	69	125	18		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
33	G	376	Total	C	N	O	6	0
			1930	1166	382	382		

- Molecule 34 is a protein called U4/U6 small nuclear ribonucleoprotein Prp3.

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

- Molecule 35 is a protein called U4/U6 small nuclear ribonucleoprotein Prp31.

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

- Molecule 36 is a protein called U4/U6 small nuclear ribonucleoprotein Prp4.

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

- Molecule 37 is a protein called Pre-mRNA-processing factor 6.

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

- Molecule 38 is a protein called Pre-mRNA-processing-splicing factor 8.

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

- Molecule 39 is a protein called U4/U6.U5 tri-snRNP-associated protein 1.

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

- Molecule 40 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

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

- Molecule 41 is a protein called NHP2-like protein 1, N-terminally processed.

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

- Molecule 42 is a protein called Thioredoxin-like protein 4A.

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

- Molecule 43 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5	112	Total 2356	C 1055	N 390	O 799	P 112	0	0

- Molecule 44 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	7	204	Total 1028	C 620	N 204	O 204	0	0

- Molecule 45 is a RNA chain called U4 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	4	110	Total	C	N	O	P	0	0
			2341	1046	413	773	109		

- Molecule 46 is a RNA chain called U6 snRNA.

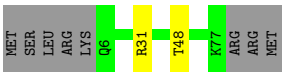
Mol	Chain	Residues	Atoms					AltConf	Trace
46	6	64	Total	C	N	O	P	0	0
			1368	613	251	441	63		

3 Residue-property plots (i)

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.

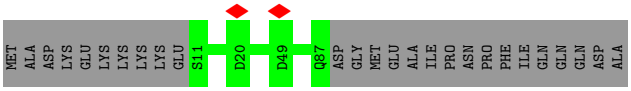
• Molecule 1: U6 snRNA-associated Sm-like protein LSm6

Chain 66:



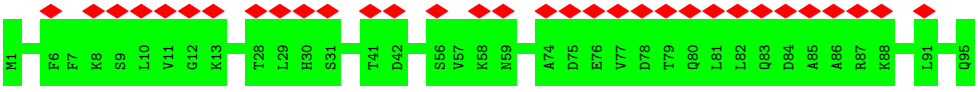
• Molecule 2: U6 snRNA-associated Sm-like protein LSm7

Chain 67:



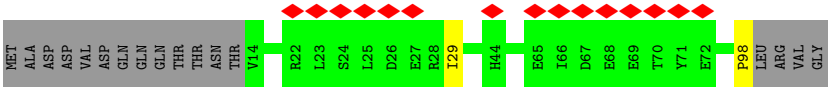
• Molecule 3: U6 snRNA-associated Sm-like protein LSm2

Chain 62:



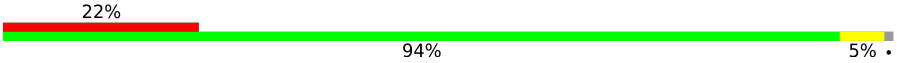
• Molecule 4: U6 snRNA-associated Sm-like protein LSm3

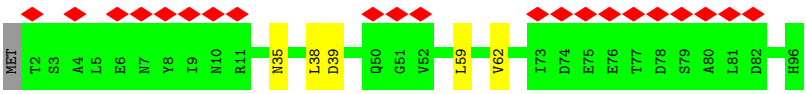
Chain 63:



• Molecule 5: U6 snRNA-associated Sm-like protein LSm8

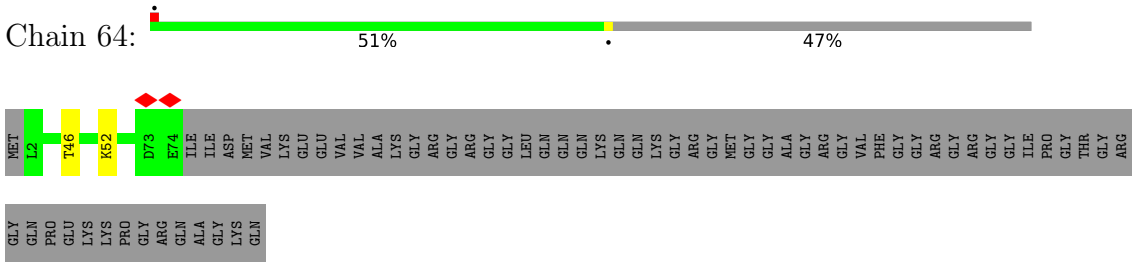
Chain 68:





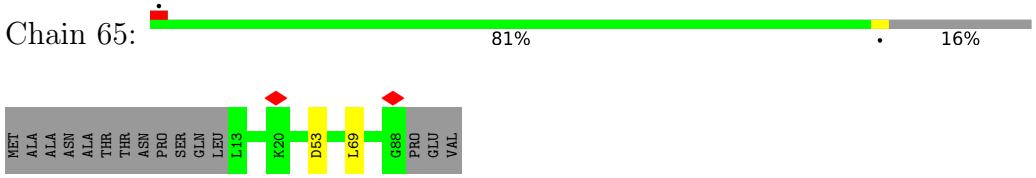
• Molecule 6: U6 snRNA-associated Sm-like protein LSm4

Chain 64:



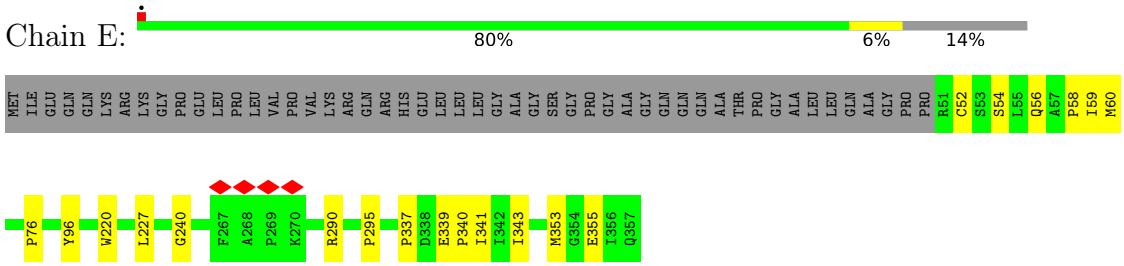
• Molecule 7: U6 snRNA-associated Sm-like protein LSm5

Chain 65:



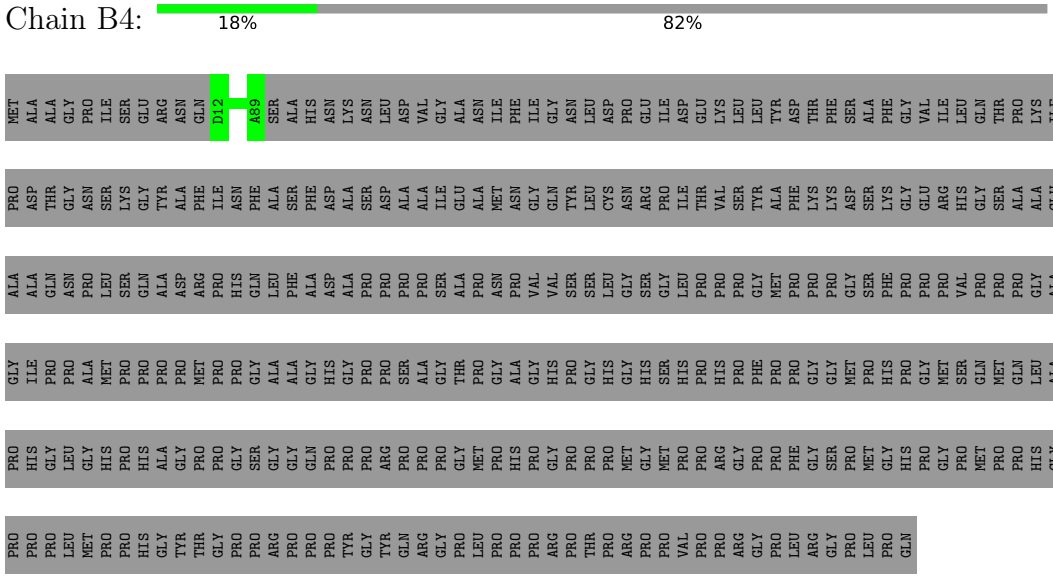
• Molecule 8: U5 small nuclear ribonucleoprotein 40 kDa protein

Chain E:



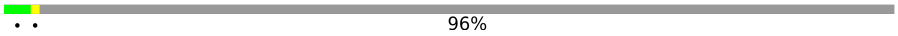
• Molecule 9: Splicing factor 3B subunit 4

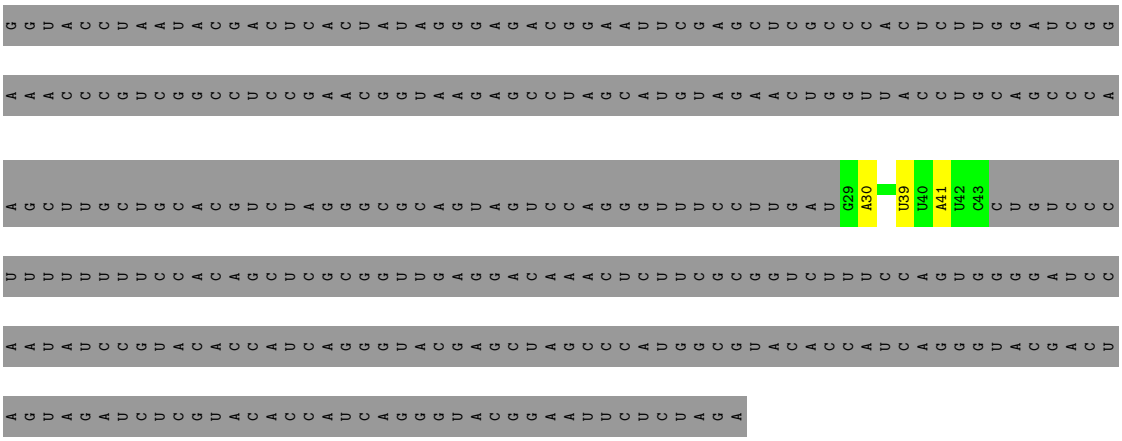
Chain B4:



• Molecule 10: pre-mRNA

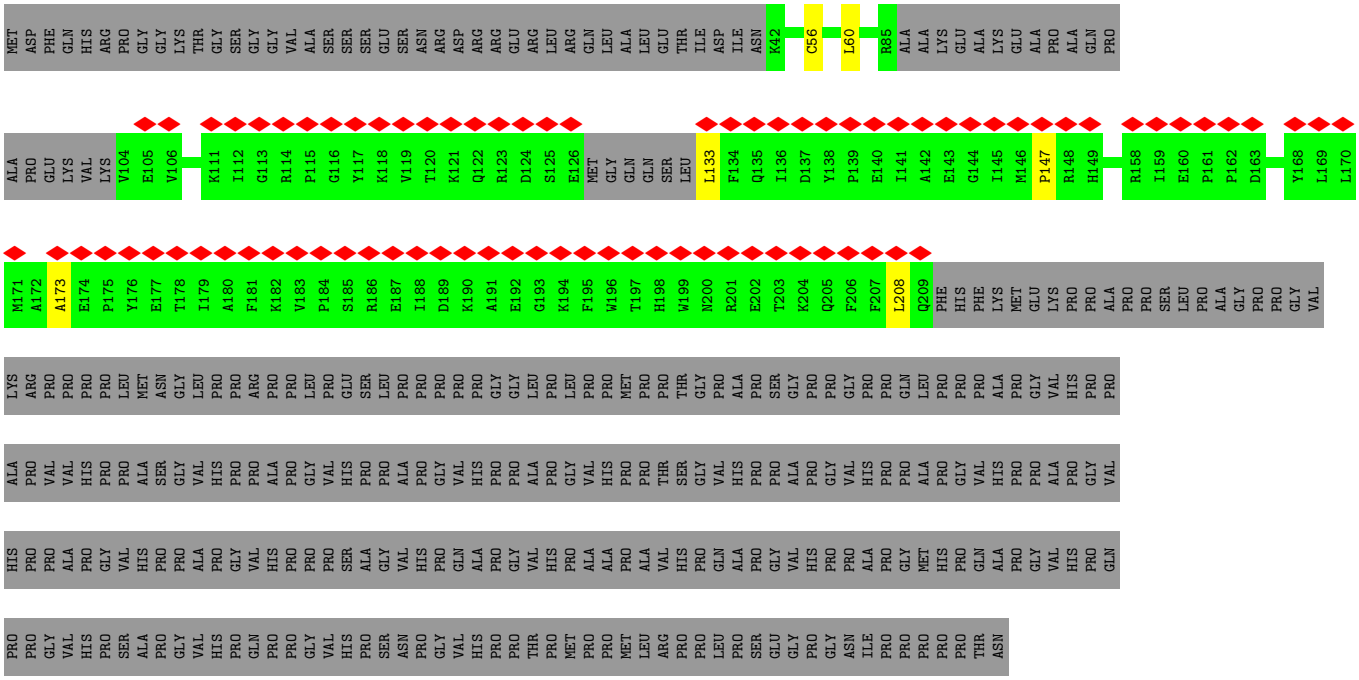
Chain Z:





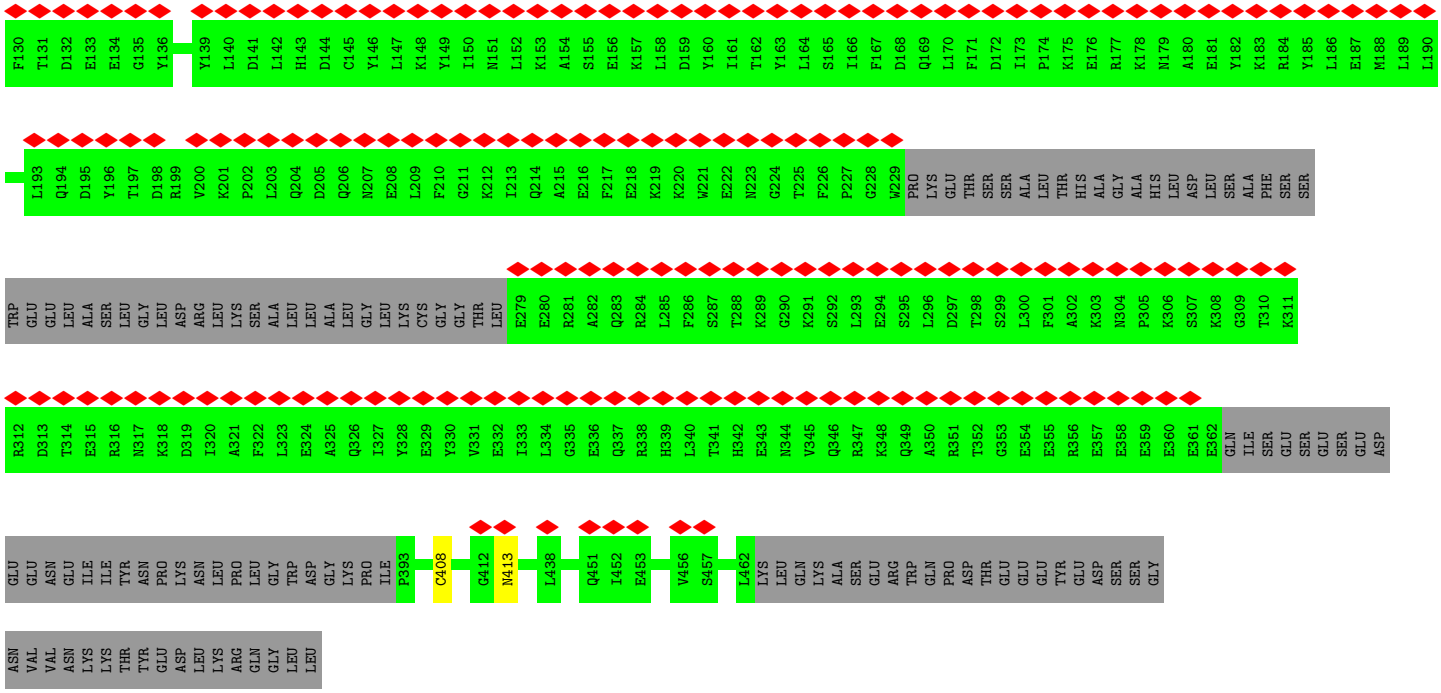
• Molecule 11: Splicing factor 3A subunit 2

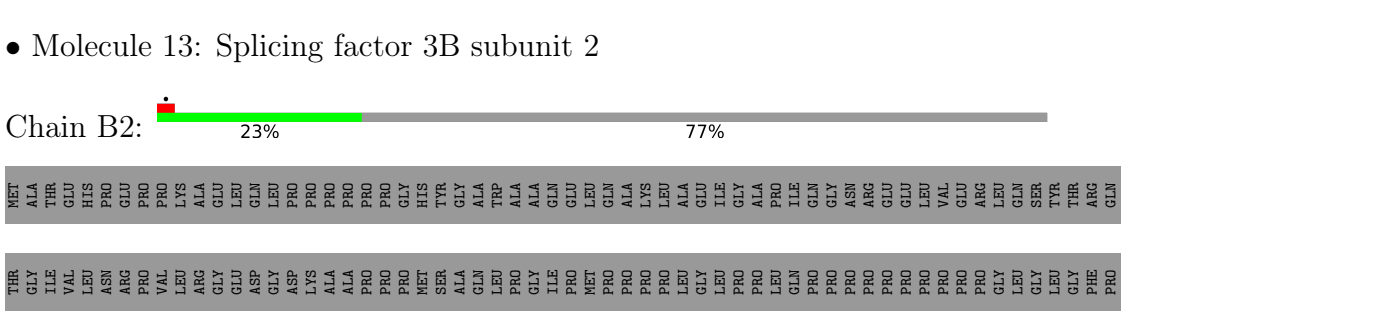
Chain 8:

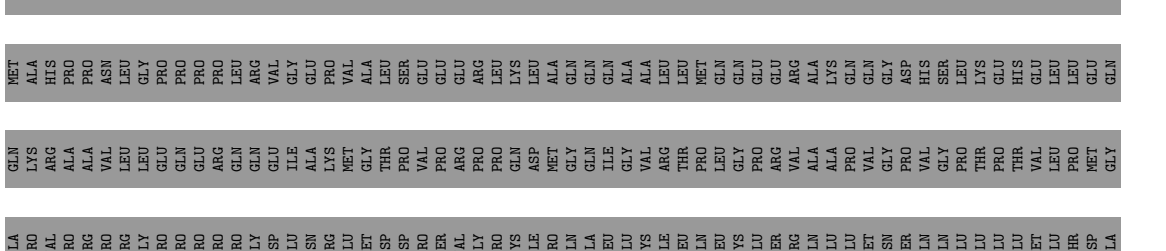


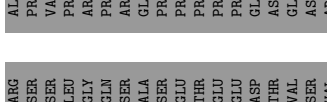
• Molecule 12: Splicing factor 3A subunit 3

Chain 9:



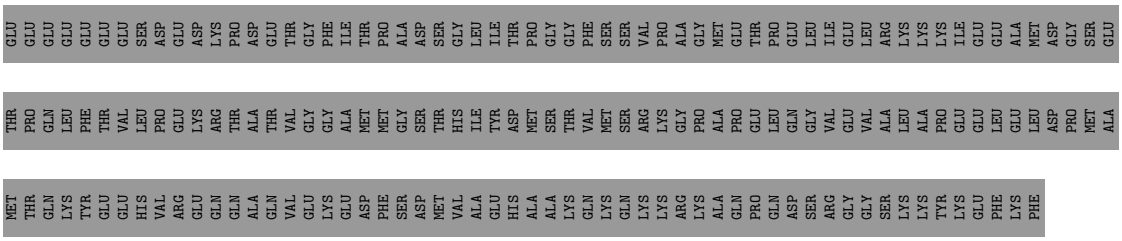






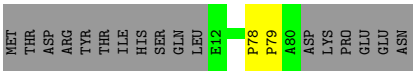
• Molecule 13: Splicing factor 3B subunit 2

Chain B2:



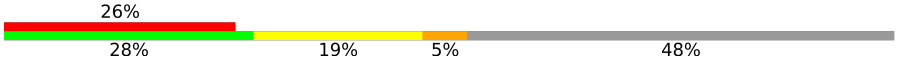
• Molecule 14: Splicing factor 3B subunit 5

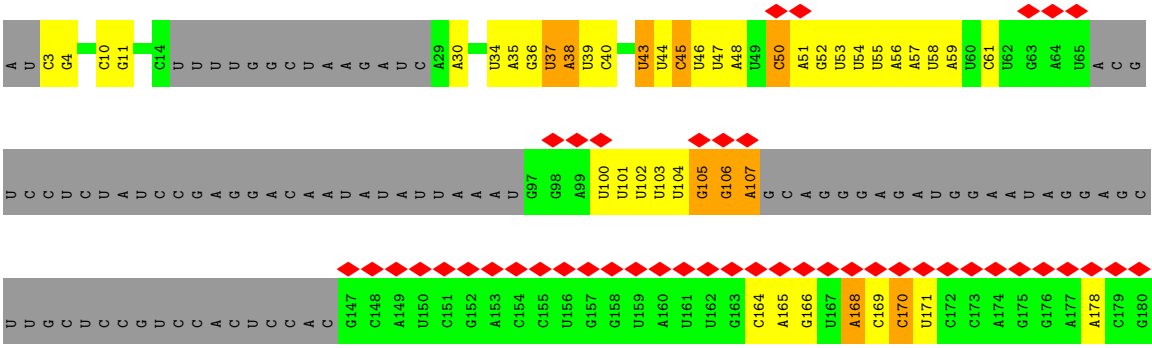
Chain B5:



• Molecule 15: U2 snRNA

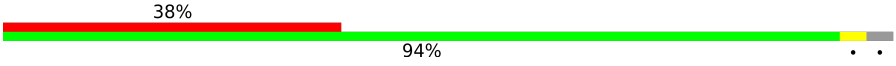
Chain 2:

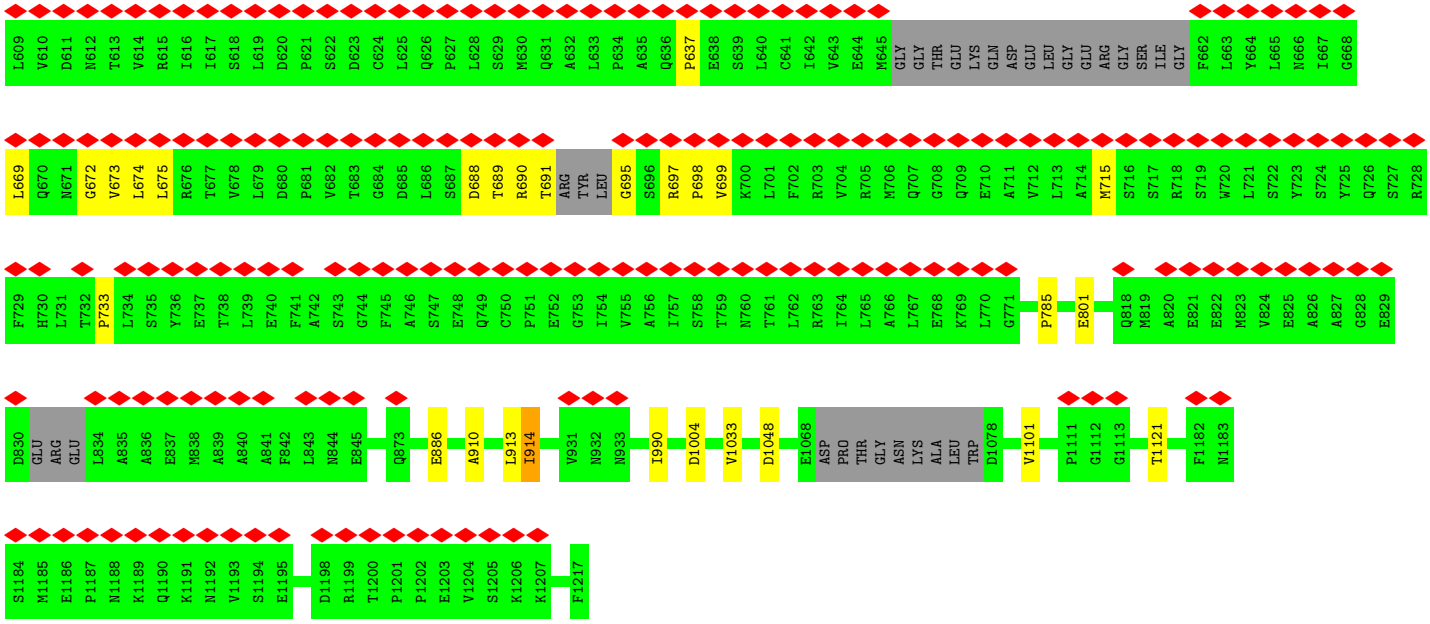




• Molecule 16: Splicing factor 3B subunit 3

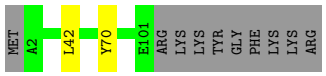
Chain B3:





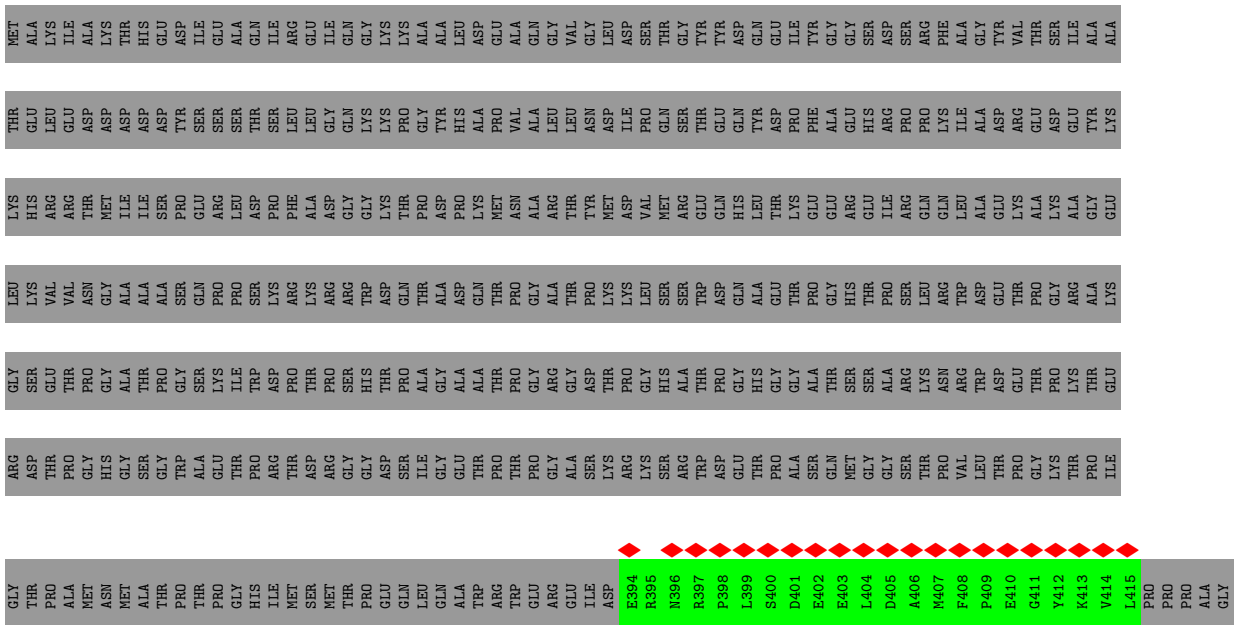
• Molecule 17: PHD finger-like domain-containing protein 5A

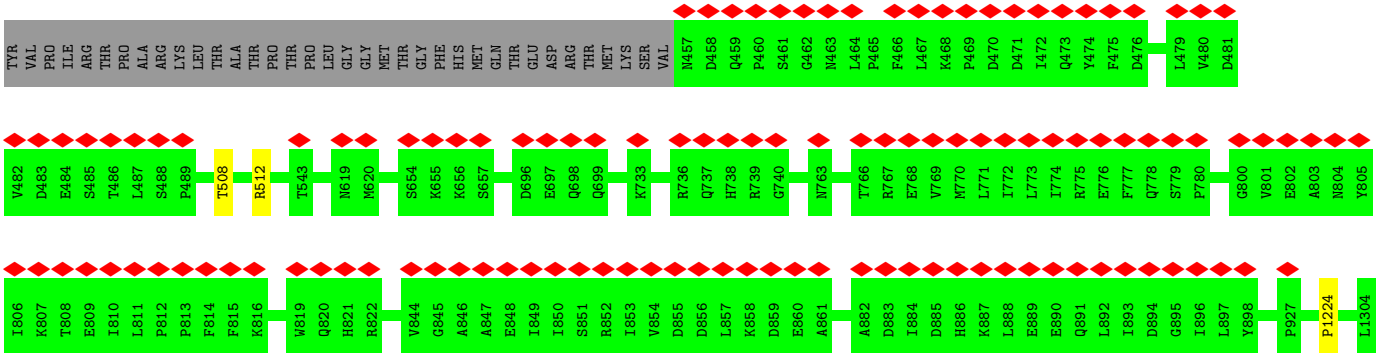
Chain BP:



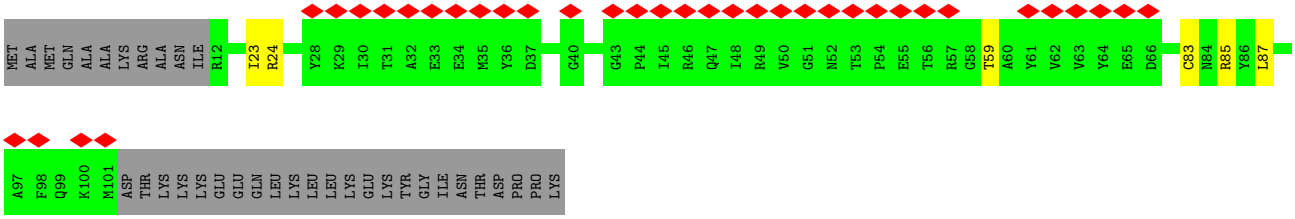
• Molecule 18: Splicing factor 3B subunit 1

Chain B1:

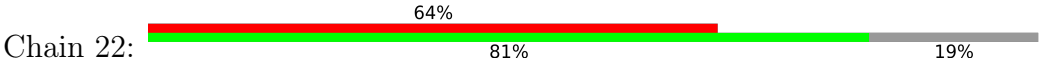


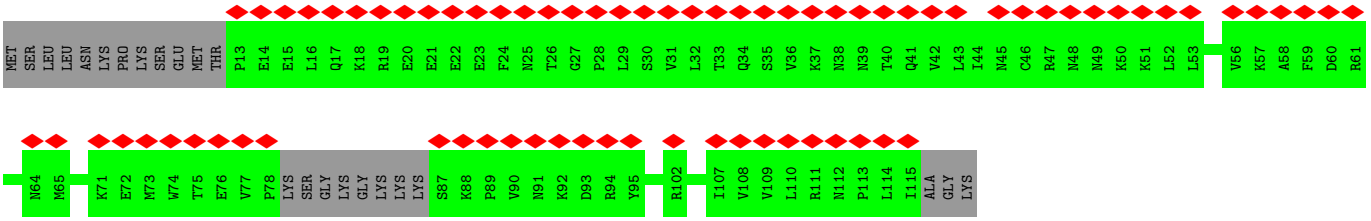


• Molecule 19: Splicing factor 3B subunit 6

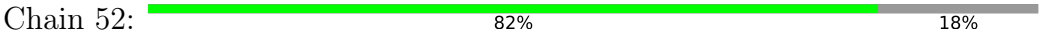


• Molecule 20: Small nuclear ribonucleoprotein Sm D2

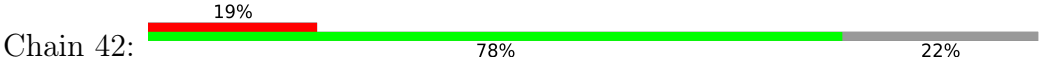


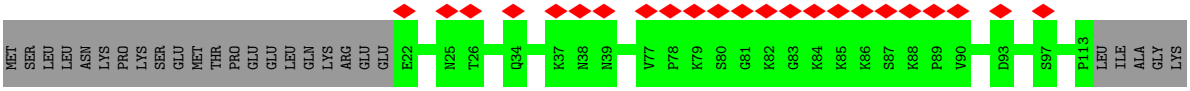


• Molecule 20: Small nuclear ribonucleoprotein Sm D2



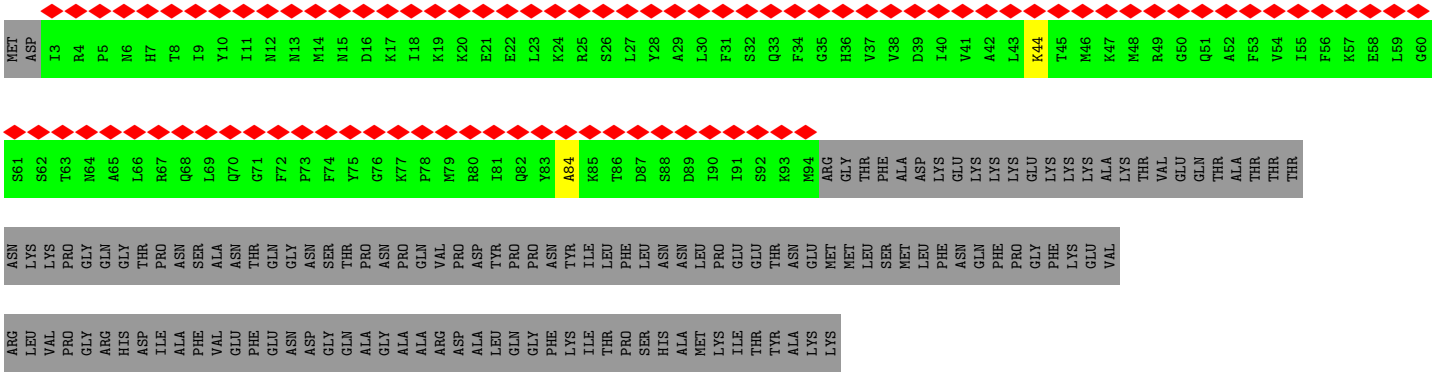
• Molecule 20: Small nuclear ribonucleoprotein Sm D2





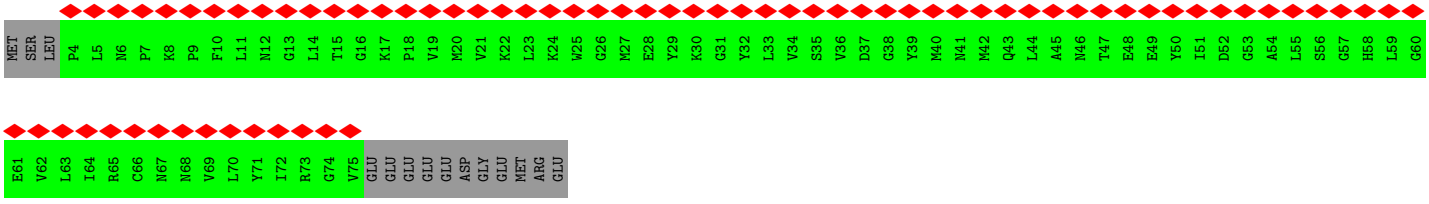
• Molecule 21: U2 small nuclear ribonucleoprotein B"

Chain 2B:



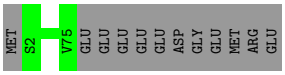
• Molecule 22: Small nuclear ribonucleoprotein F

Chain 2f:



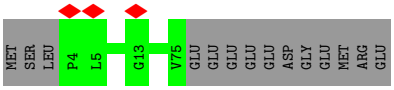
• Molecule 22: Small nuclear ribonucleoprotein F

Chain 5f:



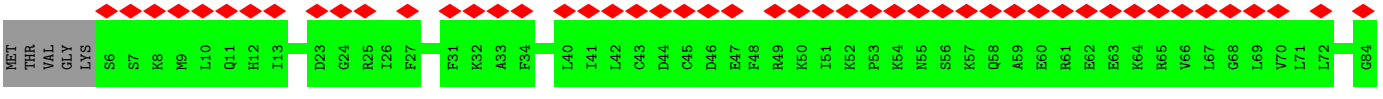
• Molecule 22: Small nuclear ribonucleoprotein F

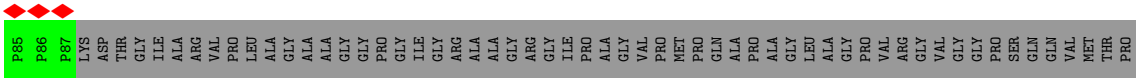
Chain 4f:

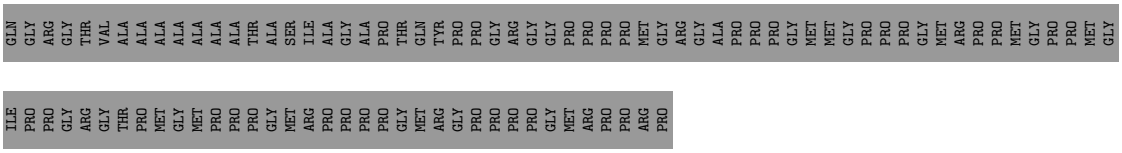


• Molecule 23: Small nuclear ribonucleoprotein-associated proteins B and B'

Chain 2b:

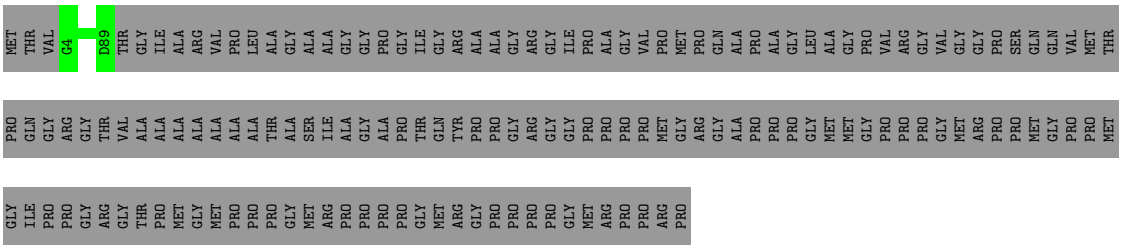






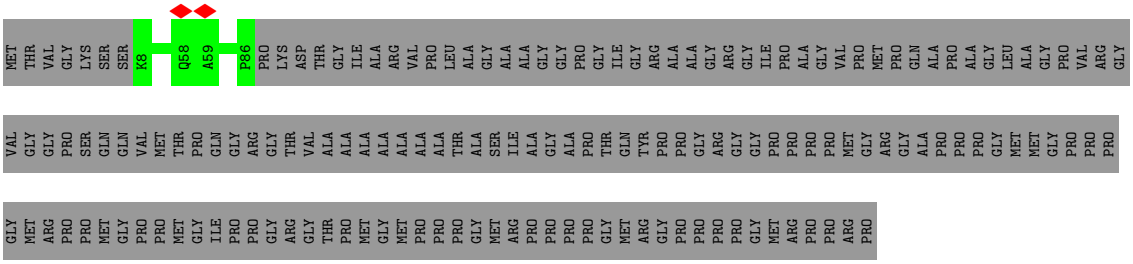
• Molecule 23: Small nuclear ribonucleoprotein-associated proteins B and B'

Chain 5b:



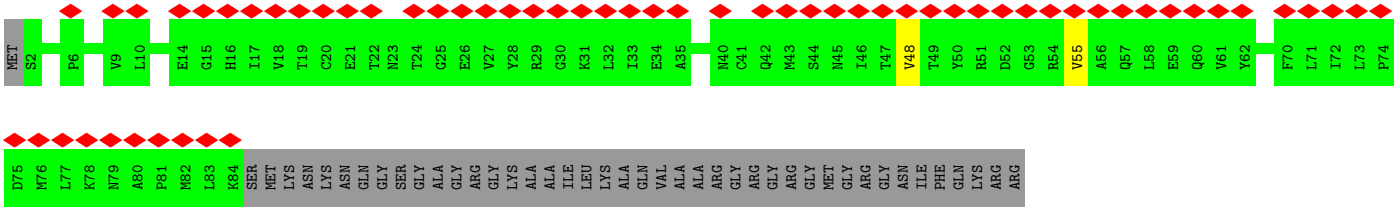
• Molecule 23: Small nuclear ribonucleoprotein-associated proteins B and B'

Chain 4b:



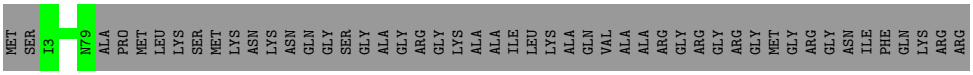
• Molecule 24: Small nuclear ribonucleoprotein Sm D3

Chain 23:



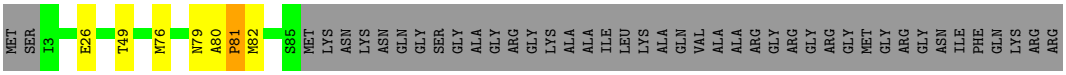
• Molecule 24: Small nuclear ribonucleoprotein Sm D3

Chain 53:



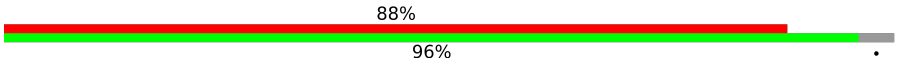
• Molecule 24: Small nuclear ribonucleoprotein Sm D3

Chain 43:



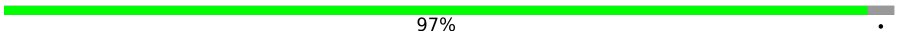
• Molecule 25: Small nuclear ribonucleoprotein G

Chain 2g:



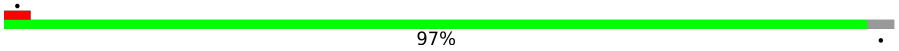
• Molecule 25: Small nuclear ribonucleoprotein G

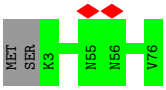
Chain 5g:



• Molecule 25: Small nuclear ribonucleoprotein G

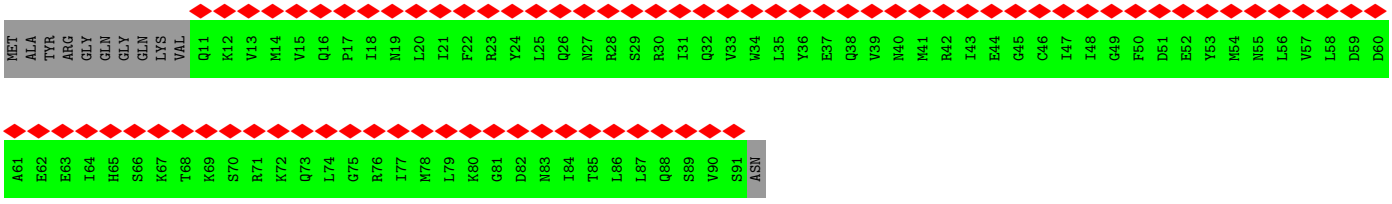
Chain 4g:





• Molecule 26: Small nuclear ribonucleoprotein E

Chain 2e:

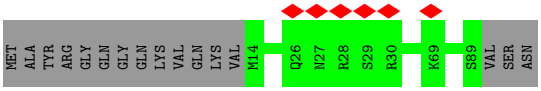


• Molecule 26: Small nuclear ribonucleoprotein E

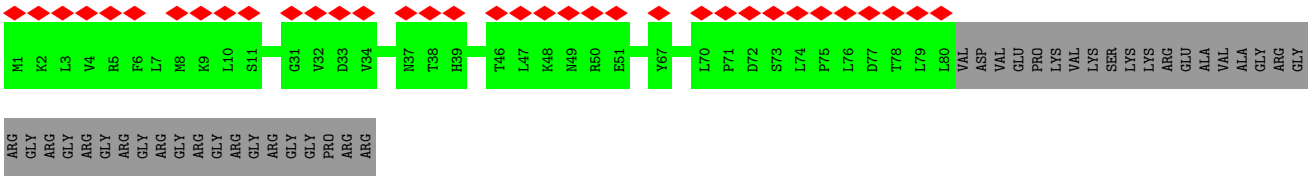
Chain 5e:

• Molecule 26: Small nuclear ribonucleoprotein E

Chain 4e:

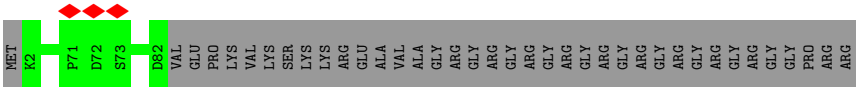


• Molecule 27: Small nuclear ribonucleoprotein Sm D1

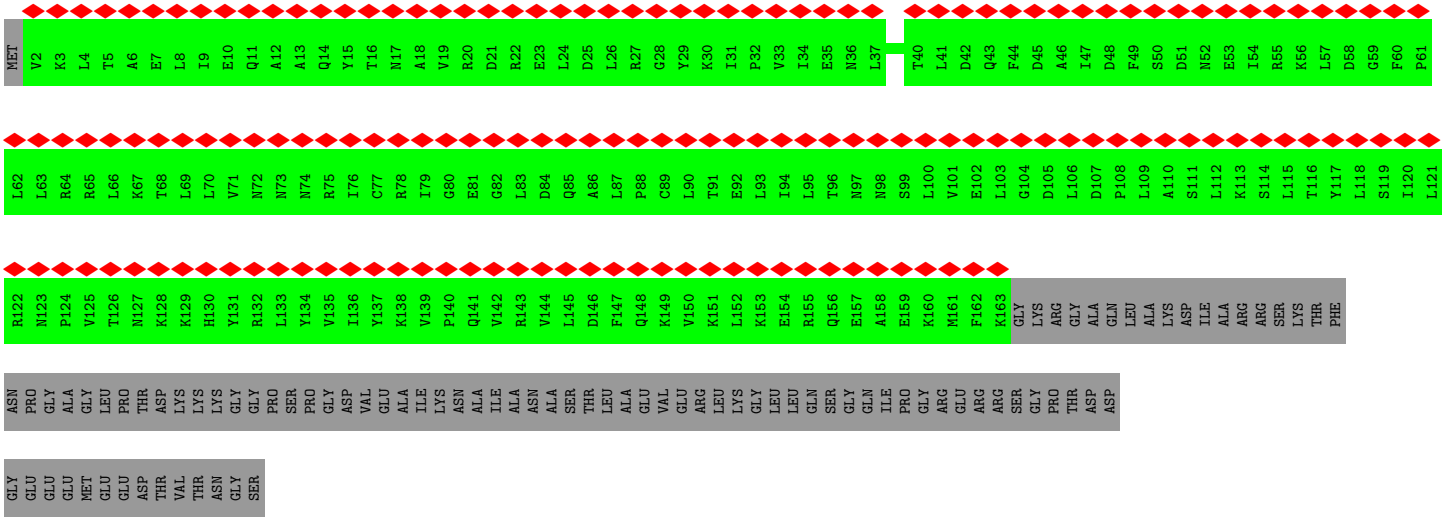


• Molecule 27: Small nuclear ribonucleoprotein Sm D1

• Molecule 27: Small nuclear ribonucleoprotein Sm D1

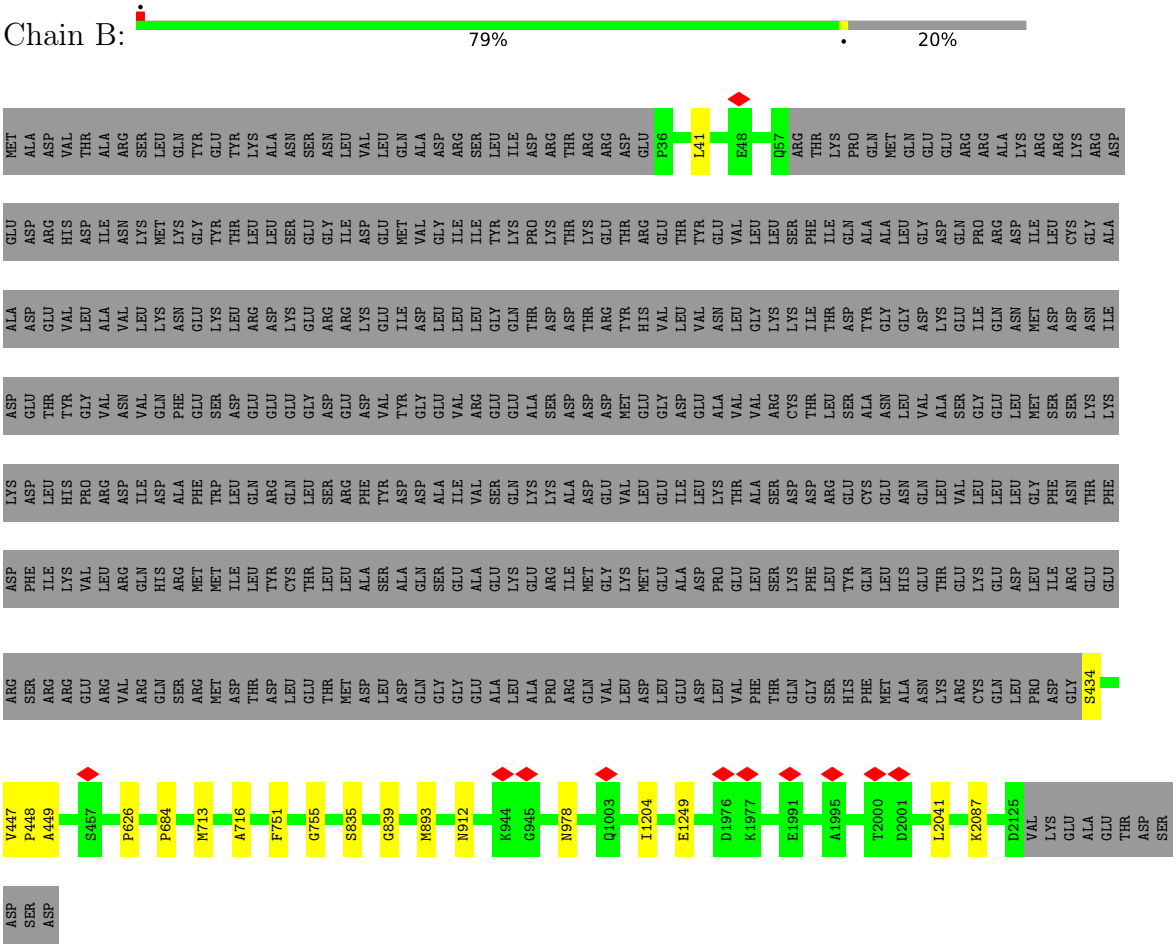


• Molecule 28: U2 small nuclear ribonucleoprotein A'



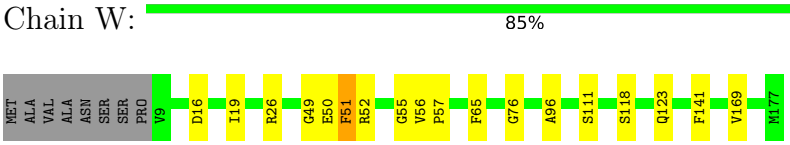
• Molecule 29: U5 small nuclear ribonucleoprotein 200 kDa helicase

Chain B:



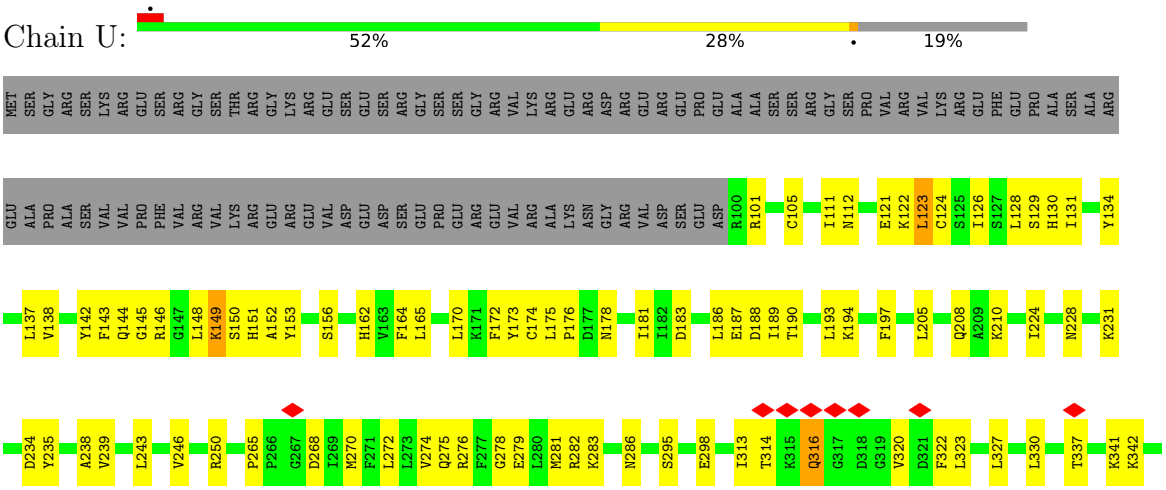
• Molecule 30: Peptidyl-prolyl cis-trans isomerase H

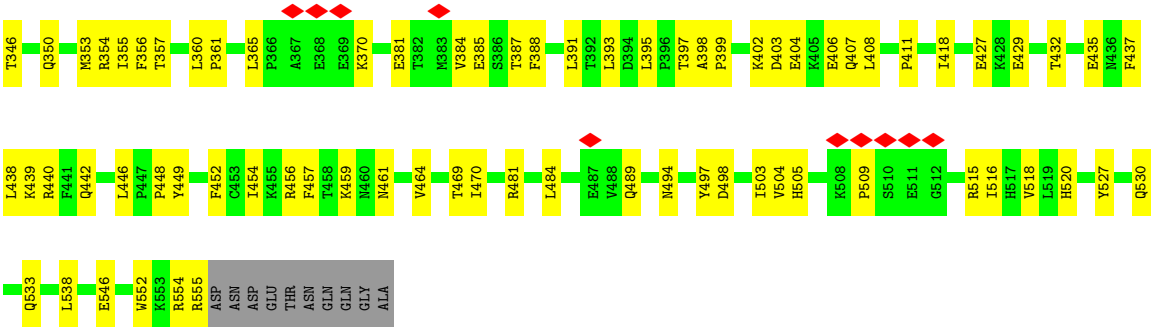
Chain W:



• Molecule 31: Ubiquitin carboxyl-terminal hydrolase 39

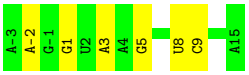
Chain U:





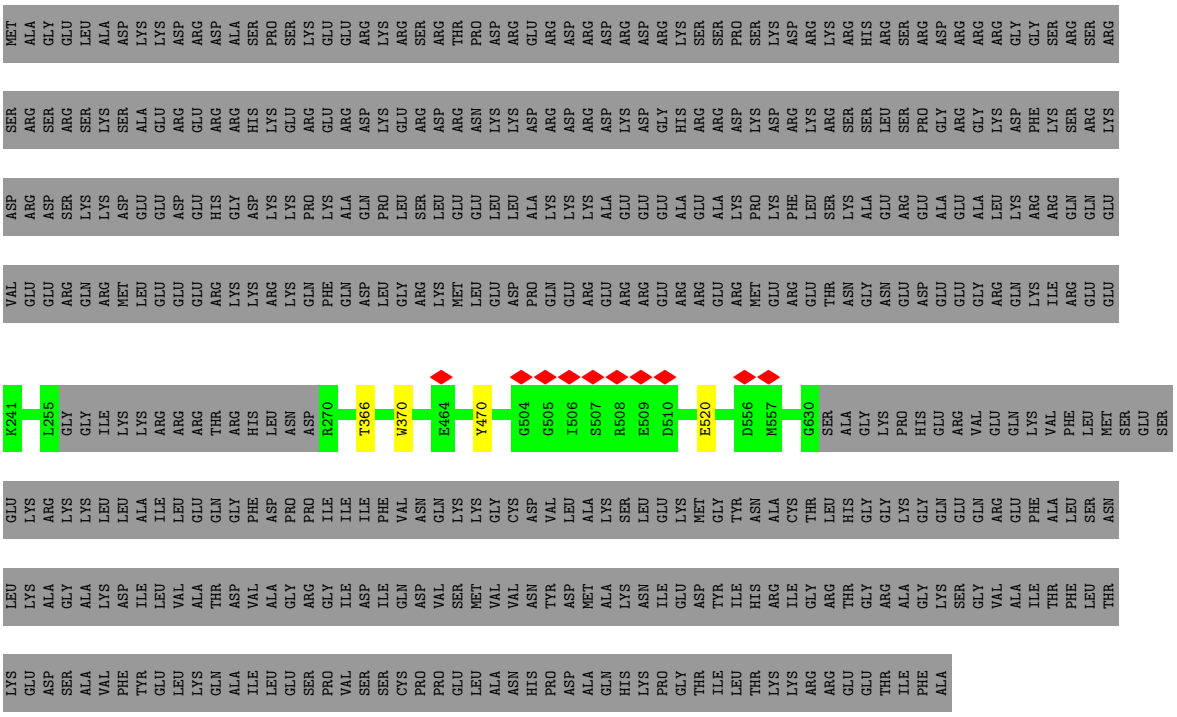
• Molecule 32: 5'SS oligo

Chain z:



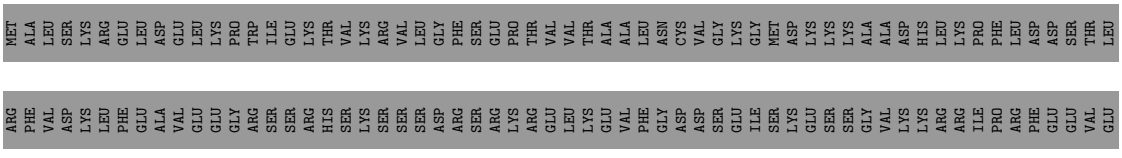
• Molecule 33: Probable ATP-dependent RNA helicase DDX23

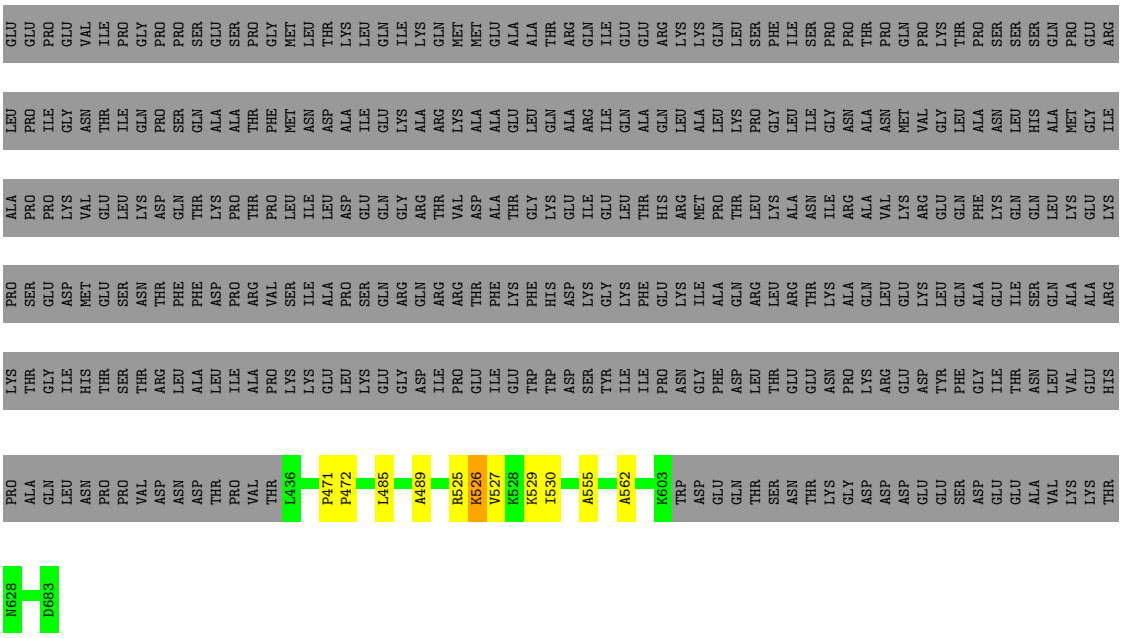
Chain G:



• Molecule 34: U4/U6 small nuclear ribonucleoprotein Prp3

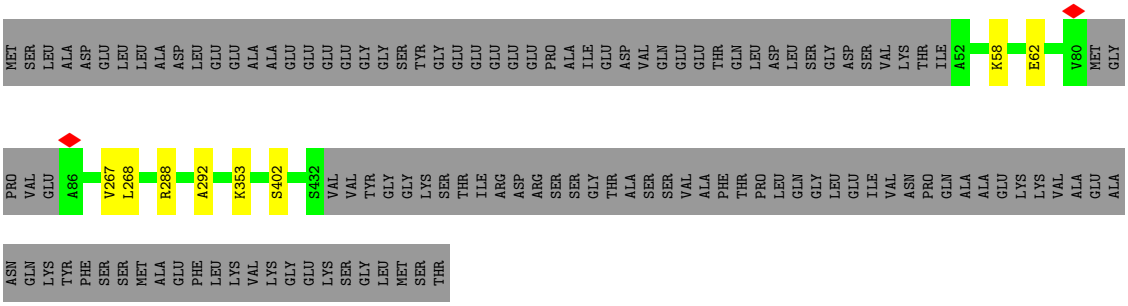
Chain J:





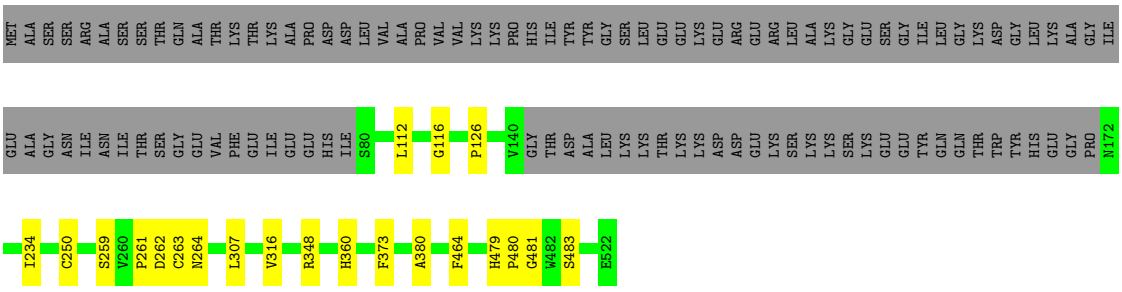
• Molecule 35: U4/U6 small nuclear ribonucleoprotein Prp31

Chain L:



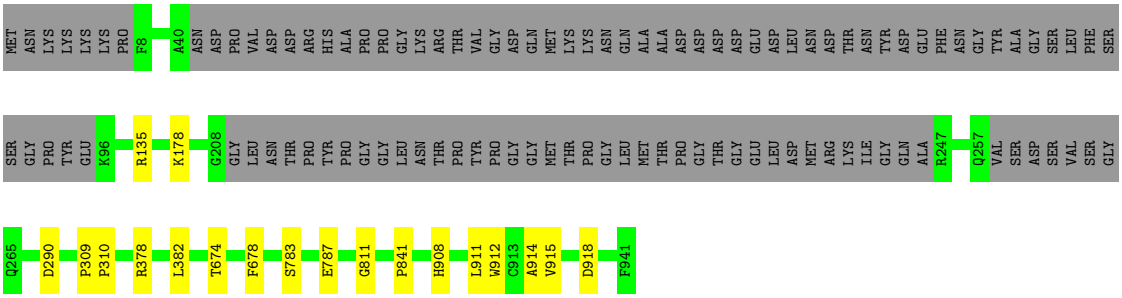
• Molecule 36: U4/U6 small nuclear ribonucleoprotein Prp4

Chain F:



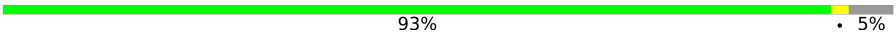
• Molecule 37: Pre-mRNA-processing factor 6

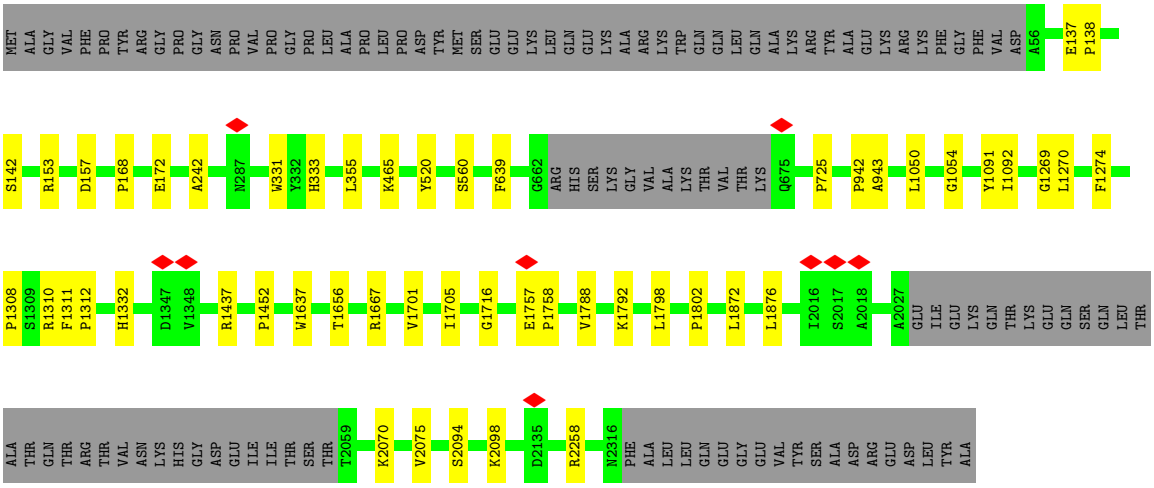
Chain N:



• Molecule 38: Pre-mRNA-processing-splicing factor 8

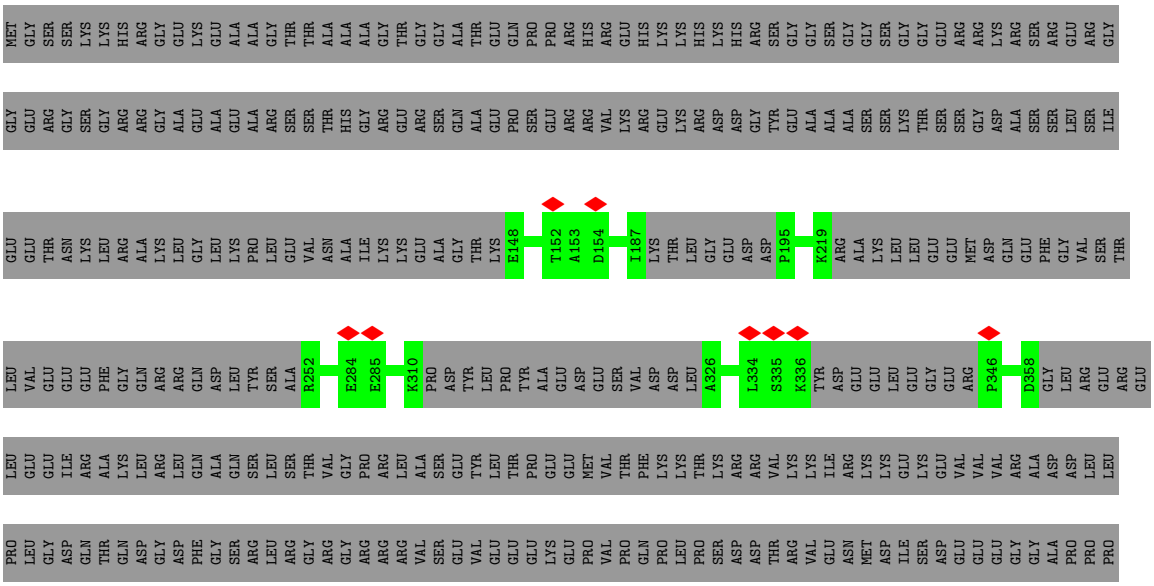
Chain A:

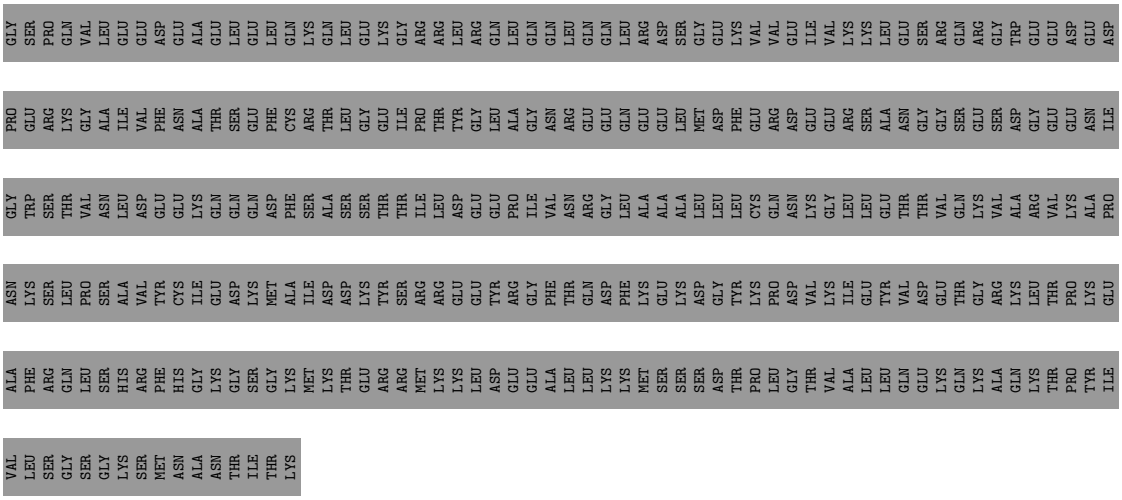




• Molecule 39: U4/U6.U5 tri-snRNP-associated protein 1

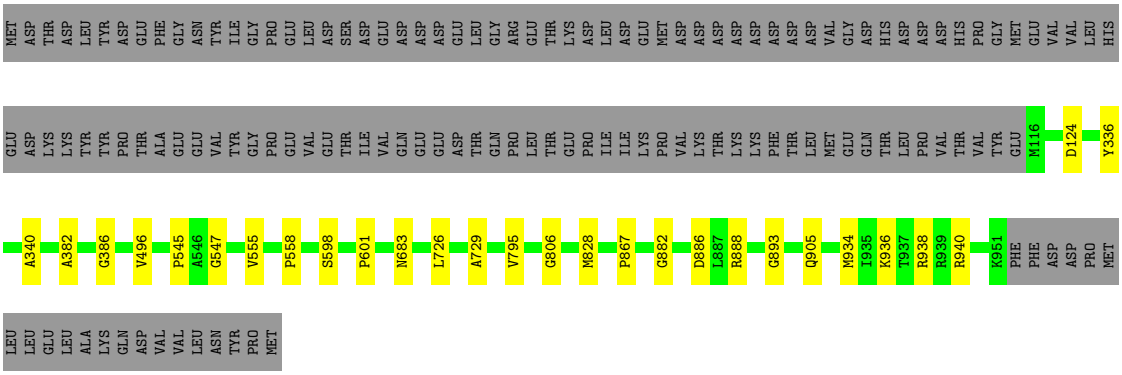
Chain S:





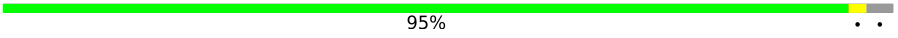
• Molecule 40: 116 kDa U5 small nuclear ribonucleoprotein component

Chain C:



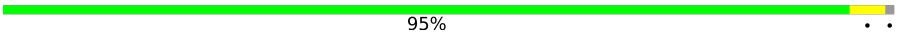
• Molecule 41: NHP2-like protein 1, N-terminally processed

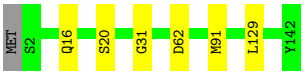
Chain M:



• Molecule 42: Thioredoxin-like protein 4A

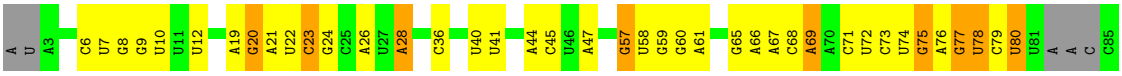
Chain D:

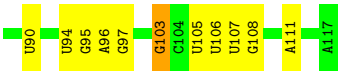




• Molecule 43: U5 snRNA

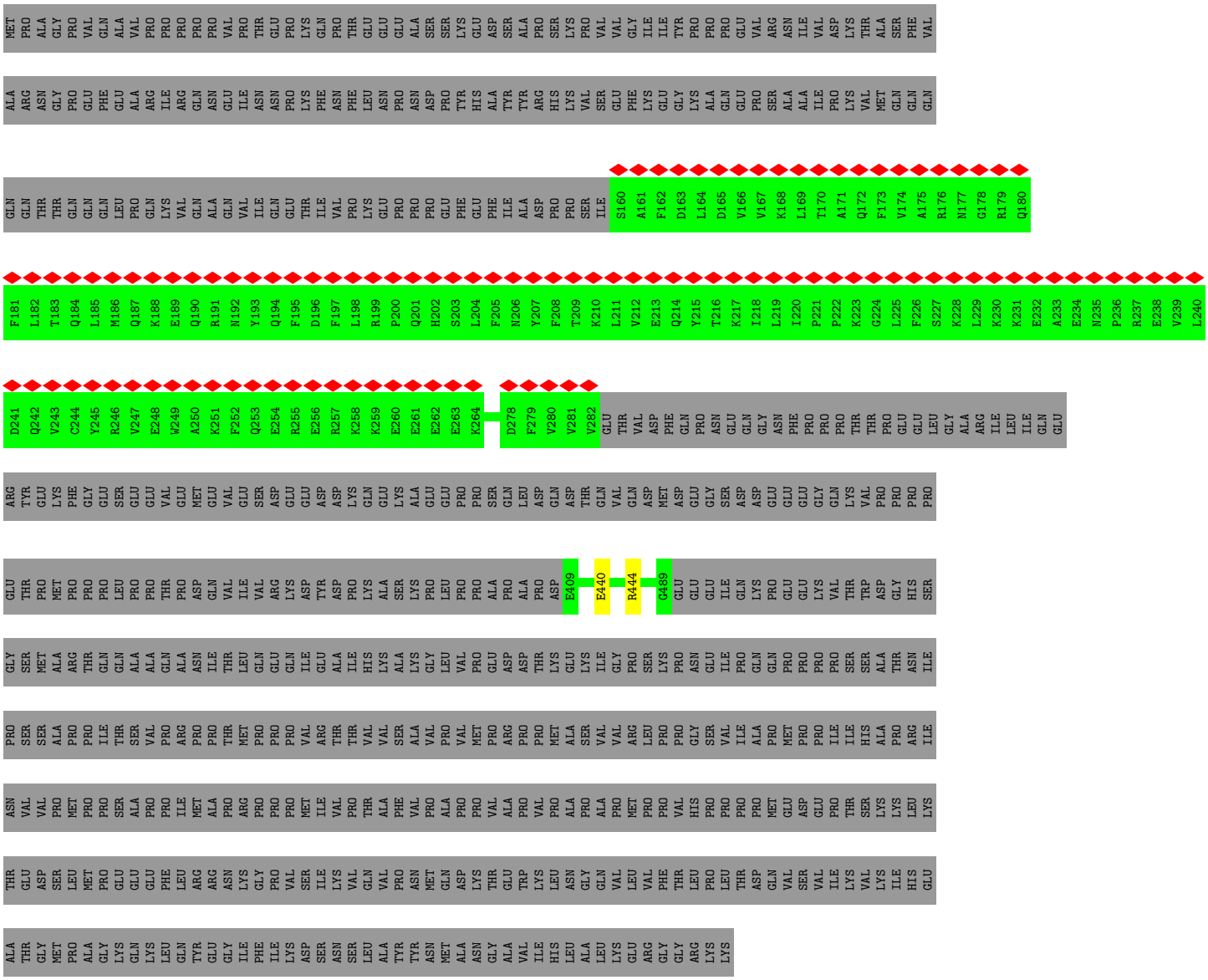
Chain 5:





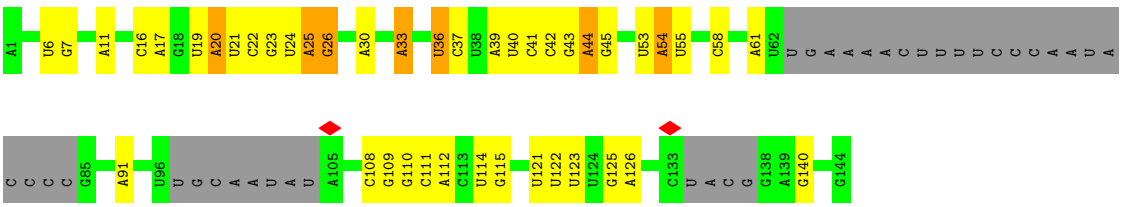
• Molecule 44: Splicing factor 3A subunit 1

Chain 7:



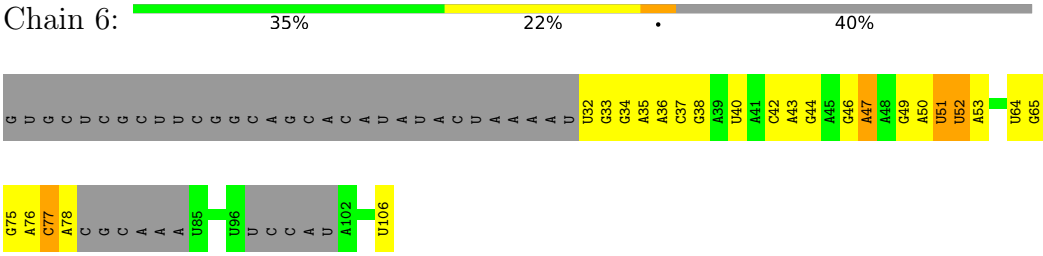
• Molecule 45: U4 snRNA

Chain 4:



• Molecule 46: U6 snRNA

Chain 6:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	136333	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 ($e^-/Å^2$)	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	0.044	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0075	Depositor
Map size (Å)	556.8, 556.8, 556.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	66	0.25	0/358	0.45	0/497
2	67	0.24	0/386	0.47	0/537
3	62	0.25	0/480	0.44	0/671
4	63	0.25	0/432	0.47	0/604
5	68	0.24	0/469	0.48	0/651
6	64	0.25	0/372	0.47	0/520
7	65	0.24	0/380	0.48	0/528
8	E	0.25	0/1540	0.47	0/2148
9	B4	0.26	0/394	0.44	0/549
10	Z	0.24	0/349	0.96	0/540
11	8	0.24	0/734	0.46	0/1025
12	9	0.24	0/1928	0.39	0/2692
13	B2	0.25	0/1092	0.42	0/1536
14	B5	0.24	0/349	0.36	0/487
15	2	0.25	0/2308	0.83	0/3584
16	B3	0.25	0/6024	0.47	0/8425
17	BP	0.25	0/501	0.45	0/697
18	B1	0.26	0/4421	0.41	0/6190
19	B6	0.23	0/459	0.41	0/642
20	22	0.24	0/485	0.43	0/677
20	42	0.25	0/466	0.48	0/651
20	52	0.24	0/387	0.48	0/482
21	2B	0.23	0/463	0.41	0/646
22	2f	0.26	0/362	0.48	0/502
22	4f	0.26	0/362	0.48	0/502
22	5f	0.24	0/295	0.51	0/367
23	2b	0.24	0/416	0.46	0/581
23	4b	0.24	0/398	0.49	0/555
23	5b	0.24	0/343	0.51	0/427
24	23	0.26	0/417	0.48	0/581
24	43	0.25	0/417	0.48	0/581
24	53	0.24	0/307	0.50	0/382
25	2g	0.25	0/366	0.49	0/509
25	4g	0.24	0/371	0.47	0/516

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
25	5g	0.24	0/295	0.52	0/367
26	2e	0.24	0/403	0.44	0/561
26	4e	0.24	0/378	0.47	0/526
26	5e	0.23	0/315	0.49	0/392
27	21	0.23	0/404	0.48	0/564
27	41	0.23	0/409	0.48	0/571
27	51	0.23	0/327	0.50	0/407
28	2A	0.24	0/821	0.45	0/1149
29	B	0.24	0/8720	0.42	0/12217
30	W	0.26	0/853	0.44	0/1188
31	U	0.25	0/3845	0.47	0/5208
32	z	0.20	0/429	0.67	0/666
33	G	0.27	0/1949	0.45	0/2729
34	J	0.28	0/1127	0.44	0/1572
35	L	0.25	0/1899	0.41	0/2654
36	F	0.25	0/2074	0.45	0/2894
37	N	0.26	0/4239	0.41	0/5936
38	A	0.25	0/11081	0.44	0/15398
39	S	0.23	0/744	0.41	0/1032
40	C	0.25	0/4270	0.45	0/5983
41	M	0.24	0/632	0.44	0/885
42	D	0.24	0/712	0.44	0/995
43	5	0.21	0/2625	0.80	0/4079
44	7	0.24	0/1034	0.40	0/1446
45	4	0.23	0/2613	0.78	0/4064
46	6	0.20	0/1530	0.72	0/2379
All	All	0.25	0/82559	0.50	0/116344

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	66	357	0	169	1	0
2	67	384	0	178	0	0
3	62	478	0	222	0	0
4	63	429	0	199	1	0
5	68	469	0	220	3	0
6	64	369	0	172	1	0
7	65	378	0	174	1	0
8	E	1531	0	747	11	0
9	B4	391	0	197	0	0
10	Z	314	0	160	4	0
11	8	729	0	356	3	0
12	9	1920	0	902	2	0
13	B2	1072	0	563	0	0
14	B5	347	0	171	1	0
15	2	2072	0	1049	39	0
16	B3	5969	0	2985	20	0
17	BP	498	0	241	1	0
18	B1	4383	0	2195	2	0
19	B6	455	0	227	3	0
20	22	482	0	220	0	0
20	42	463	0	211	0	0
20	52	388	0	102	0	0
21	2B	461	0	218	2	0
22	2f	359	0	179	0	0
22	4f	359	0	179	0	0
22	5f	296	0	87	0	0
23	2b	413	0	194	0	0
23	4b	396	0	183	0	0
23	5b	344	0	93	0	0
24	23	415	0	198	1	0
24	43	415	0	198	3	0
24	53	308	0	86	0	0
25	2g	364	0	176	0	0
25	4g	369	0	178	0	0
25	5g	296	0	84	0	0
26	2e	403	0	173	0	0
26	4e	378	0	163	0	0
26	5e	316	0	85	0	0
27	21	402	0	184	0	0
27	41	407	0	183	0	0
27	51	328	0	89	0	0
28	2A	816	0	386	0	0
29	B	8644	0	4199	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	W	844	0	426	15	0
31	U	3749	0	3769	131	0
32	z	384	0	194	0	0
33	G	1930	0	946	2	0
34	J	1121	0	547	9	0
35	L	1887	0	934	5	0
36	F	2060	0	1021	10	0
37	N	4207	0	2161	11	0
38	A	10977	0	5122	35	0
39	S	744	0	360	0	0
40	C	4223	0	2099	18	0
41	M	627	0	315	1	0
42	D	708	0	328	3	0
43	5	2356	0	1194	18	0
44	7	1028	0	487	1	0
45	4	2341	0	1186	17	0
46	6	1368	0	693	16	0
All	All	80921	0	40957	371	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 371 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)
31:U:404:GLU:HA	38:A:725:PRO:CB	1.95	0.97
31:U:404:GLU:HA	38:A:725:PRO:HB3	1.46	0.94
31:U:231:LYS:HD2	40:C:598:SER:CB	1.98	0.93
24:23:48:VAL:O	24:23:55:VAL:HA	1.71	0.90
16:B3:886:GLU:HA	16:B3:910:ALA:O	1.74	0.88

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	66	70/80 (88%)	70 (100%)	0	0	100	100
2	67	75/103 (73%)	74 (99%)	1 (1%)	0	100	100
3	62	93/95 (98%)	92 (99%)	1 (1%)	0	100	100
4	63	83/102 (81%)	83 (100%)	0	0	100	100
5	68	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
6	64	71/139 (51%)	70 (99%)	1 (1%)	0	100	100
7	65	74/91 (81%)	73 (99%)	1 (1%)	0	100	100
8	E	305/357 (85%)	301 (99%)	3 (1%)	1 (0%)	41	77
9	B4	76/424 (18%)	76 (100%)	0	0	100	100
11	8	138/464 (30%)	134 (97%)	4 (3%)	0	100	100
12	9	377/501 (75%)	370 (98%)	7 (2%)	0	100	100
13	B2	204/895 (23%)	199 (98%)	5 (2%)	0	100	100
14	B5	67/86 (78%)	66 (98%)	1 (2%)	0	100	100
16	B3	1176/1217 (97%)	1135 (96%)	38 (3%)	3 (0%)	41	77
17	BP	98/110 (89%)	96 (98%)	2 (2%)	0	100	100
18	B1	866/1304 (66%)	848 (98%)	18 (2%)	0	100	100
19	B6	88/125 (70%)	85 (97%)	3 (3%)	0	100	100
20	22	91/118 (77%)	91 (100%)	0	0	100	100
20	42	90/118 (76%)	88 (98%)	2 (2%)	0	100	100
20	52	95/118 (80%)	90 (95%)	5 (5%)	0	100	100
21	2B	90/225 (40%)	90 (100%)	0	0	100	100
22	2f	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
22	4f	70/86 (81%)	68 (97%)	2 (3%)	0	100	100
22	5f	72/86 (84%)	72 (100%)	0	0	100	100
23	2b	80/240 (33%)	80 (100%)	0	0	100	100
23	4b	77/240 (32%)	76 (99%)	1 (1%)	0	100	100
23	5b	84/240 (35%)	79 (94%)	5 (6%)	0	100	100
24	23	81/126 (64%)	80 (99%)	1 (1%)	0	100	100
24	43	81/126 (64%)	79 (98%)	0	2 (2%)	5	32
24	53	75/126 (60%)	73 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	2g	71/76 (93%)	71 (100%)	0	0	100	100
25	4g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
25	5g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
26	2e	79/92 (86%)	79 (100%)	0	0	100	100
26	4e	74/92 (80%)	74 (100%)	0	0	100	100
26	5e	77/92 (84%)	75 (97%)	2 (3%)	0	100	100
27	21	78/119 (66%)	76 (97%)	2 (3%)	0	100	100
27	41	79/119 (66%)	77 (98%)	2 (2%)	0	100	100
27	51	80/119 (67%)	75 (94%)	5 (6%)	0	100	100
28	2A	160/255 (63%)	157 (98%)	3 (2%)	0	100	100
29	B	1710/2136 (80%)	1690 (99%)	19 (1%)	1 (0%)	51	86
30	W	167/177 (94%)	164 (98%)	2 (1%)	1 (1%)	25	66
31	U	454/565 (80%)	435 (96%)	18 (4%)	1 (0%)	47	81
33	G	378/820 (46%)	371 (98%)	7 (2%)	0	100	100
34	J	220/683 (32%)	217 (99%)	2 (1%)	1 (0%)	29	69
35	L	372/499 (74%)	364 (98%)	8 (2%)	0	100	100
36	F	408/522 (78%)	395 (97%)	11 (3%)	2 (0%)	29	69
37	N	826/941 (88%)	786 (95%)	40 (5%)	0	100	100
38	A	2212/2335 (95%)	2141 (97%)	70 (3%)	1 (0%)	100	100
39	S	138/800 (17%)	138 (100%)	0	0	100	100
40	C	834/972 (86%)	804 (96%)	30 (4%)	0	100	100
41	M	122/128 (95%)	118 (97%)	4 (3%)	0	100	100
42	D	139/142 (98%)	131 (94%)	8 (6%)	0	100	100
44	7	200/793 (25%)	199 (100%)	1 (0%)	0	100	100
All	All	14032/20753 (68%)	13675 (98%)	344 (2%)	13 (0%)	54	86

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	43	76	MET
31	U	397	THR
34	J	526	LYS
16	B3	914	ILE
38	A	2094	SER

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	66	2/70 (3%)	2 (100%)	0	100	100
2	67	3/91 (3%)	3 (100%)	0	100	100
3	62	3/88 (3%)	3 (100%)	0	100	100
4	63	4/94 (4%)	4 (100%)	0	100	100
5	68	1/82 (1%)	1 (100%)	0	100	100
6	64	4/111 (4%)	4 (100%)	0	100	100
7	65	3/80 (4%)	3 (100%)	0	100	100
8	E	10/300 (3%)	10 (100%)	0	100	100
9	B4	4/336 (1%)	4 (100%)	0	100	100
11	8	8/382 (2%)	8 (100%)	0	100	100
12	9	11/446 (2%)	11 (100%)	0	100	100
13	B2	22/776 (3%)	22 (100%)	0	100	100
14	B5	3/77 (4%)	3 (100%)	0	100	100
16	B3	60/1051 (6%)	60 (100%)	0	100	100
17	BP	4/95 (4%)	4 (100%)	0	100	100
18	B1	40/1104 (4%)	40 (100%)	0	100	100
19	B6	5/109 (5%)	5 (100%)	0	100	100
20	22	5/110 (4%)	5 (100%)	0	100	100
20	42	4/110 (4%)	4 (100%)	0	100	100
21	2B	3/195 (2%)	3 (100%)	0	100	100
22	2f	4/74 (5%)	4 (100%)	0	100	100
22	4f	4/74 (5%)	4 (100%)	0	100	100
23	2b	4/177 (2%)	4 (100%)	0	100	100
23	4b	3/177 (2%)	3 (100%)	0	100	100
24	23	3/101 (3%)	3 (100%)	0	100	100
24	43	3/101 (3%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	2g	3/66 (4%)	3 (100%)	0	100	100
25	4g	3/66 (4%)	3 (100%)	0	100	100
26	2e	1/84 (1%)	1 (100%)	0	100	100
26	4e	1/84 (1%)	1 (100%)	0	100	100
27	21	3/101 (3%)	3 (100%)	0	100	100
27	41	3/101 (3%)	3 (100%)	0	100	100
28	2A	6/218 (3%)	6 (100%)	0	100	100
29	B	78/1908 (4%)	78 (100%)	0	100	100
30	W	10/148 (7%)	10 (100%)	0	100	100
31	U	418/511 (82%)	414 (99%)	4 (1%)	76	86
33	G	21/721 (3%)	21 (100%)	0	100	100
34	J	8/599 (1%)	8 (100%)	0	100	100
35	L	14/424 (3%)	14 (100%)	0	100	100
36	F	16/442 (4%)	16 (100%)	0	100	100
37	N	36/792 (4%)	36 (100%)	0	100	100
38	A	107/2108 (5%)	107 (100%)	0	100	100
39	S	5/681 (1%)	5 (100%)	0	100	100
40	C	48/866 (6%)	48 (100%)	0	100	100
41	M	6/111 (5%)	6 (100%)	0	100	100
42	D	5/130 (4%)	5 (100%)	0	100	100
44	7	8/709 (1%)	8 (100%)	0	100	100
All	All	1020/17281 (6%)	1016 (100%)	4 (0%)	91	94

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	U	123	LEU
31	U	149	LYS
31	U	270	MET
31	U	316	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
31	U	144	GLN
31	U	151	HIS
31	U	162	HIS
31	U	316	GLN
31	U	372	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	Z	14/347 (4%)	1 (7%)	0
15	2	94/188 (50%)	23 (24%)	6 (6%)
32	z	17/18 (94%)	6 (35%)	0
43	5	110/117 (94%)	34 (30%)	3 (2%)
45	4	106/144 (73%)	25 (23%)	1 (0%)
46	6	61/106 (57%)	11 (18%)	3 (4%)
All	All	402/920 (43%)	100 (24%)	13 (3%)

5 of 100 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	Z	41	A
15	2	30	A
15	2	38	A
15	2	40	C
15	2	43	U

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
43	5	78	U
43	5	105	U
46	6	77	C
46	6	46	G
46	6	51	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 monosaccharides 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.

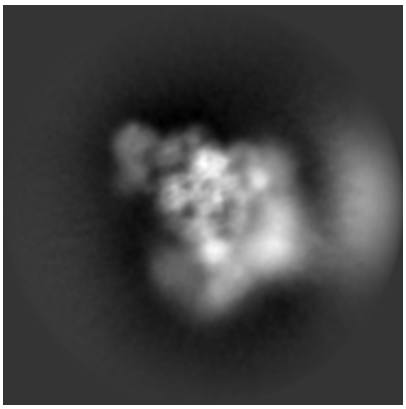
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-19349. These allow visual inspection of the internal detail of the map and identification of artifacts.

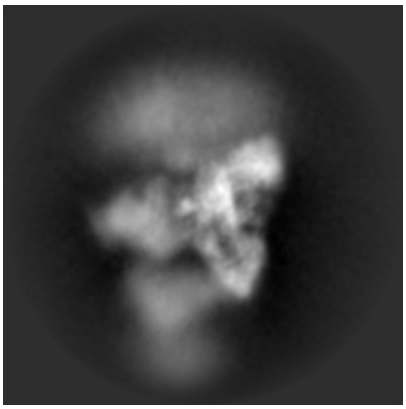
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

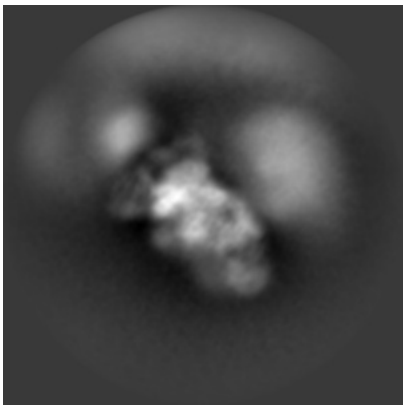
6.1.1 Primary map



X

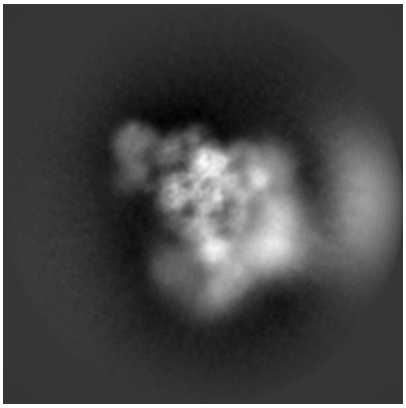


Y

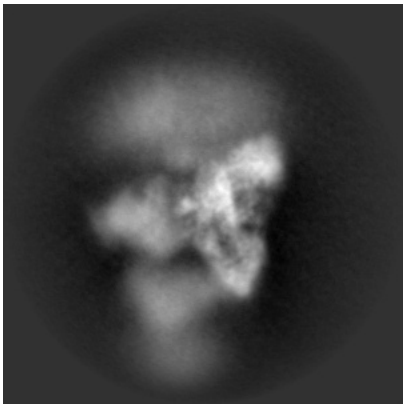


Z

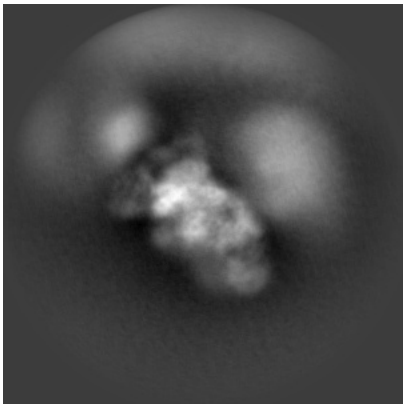
6.1.2 Raw map



X



Y

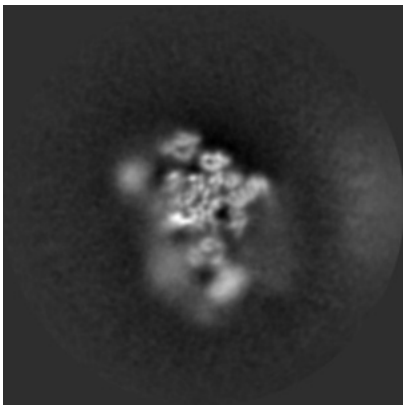


Z

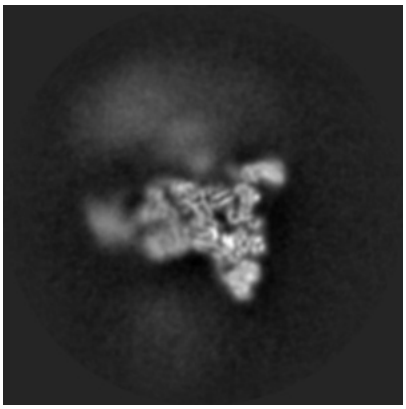
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

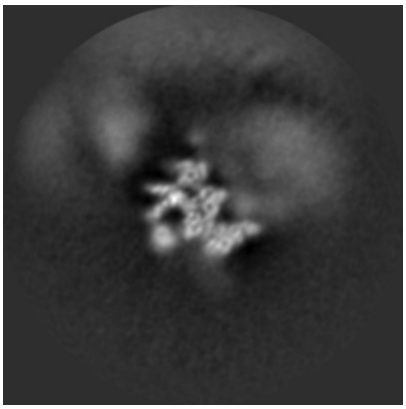
6.2.1 Primary map



X Index: 240

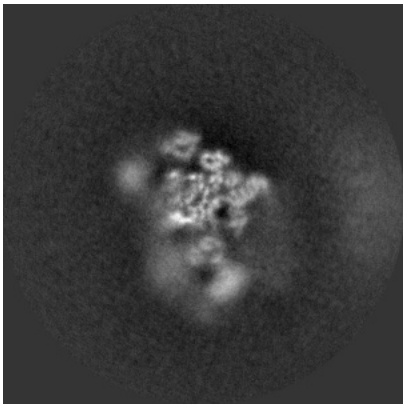


Y Index: 240

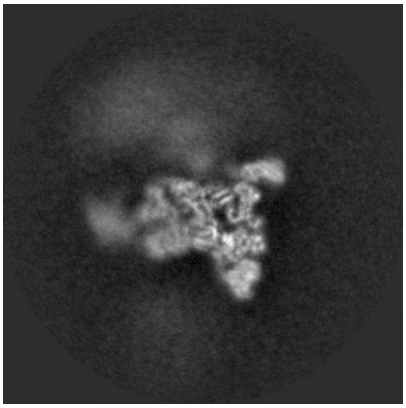


Z Index: 240

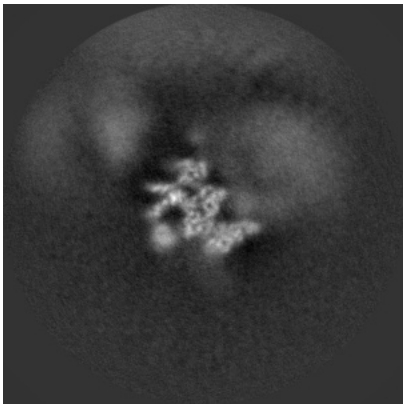
6.2.2 Raw map



X Index: 240



Y Index: 240

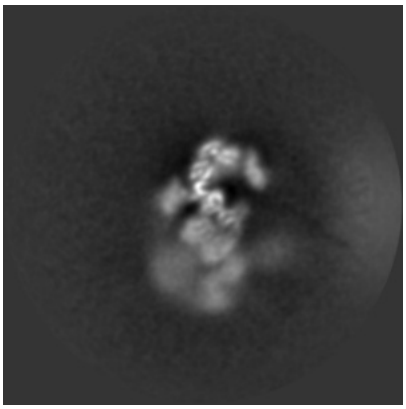


Z Index: 240

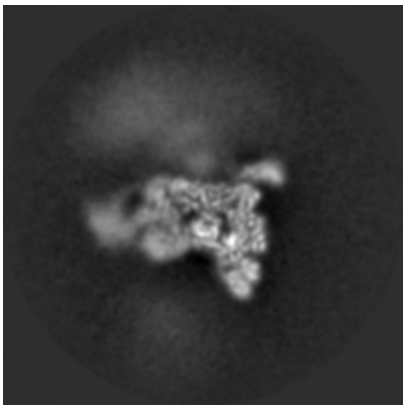
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

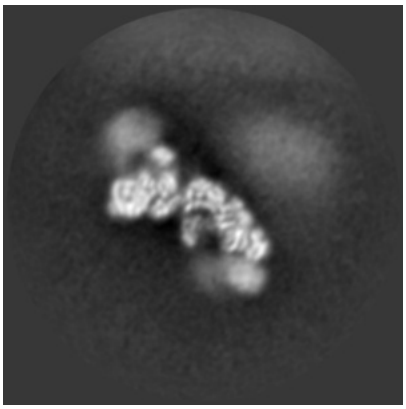
6.3.1 Primary map



X Index: 201

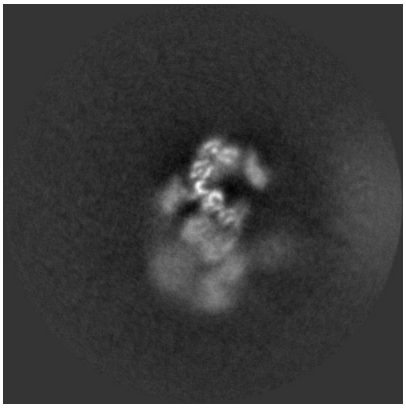


Y Index: 244

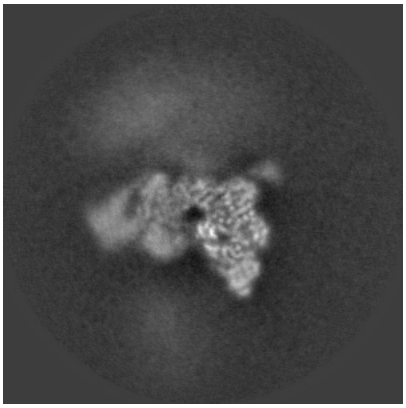


Z Index: 292

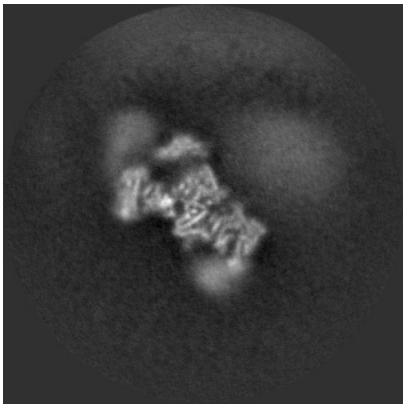
6.3.2 Raw map



X Index: 202



Y Index: 252

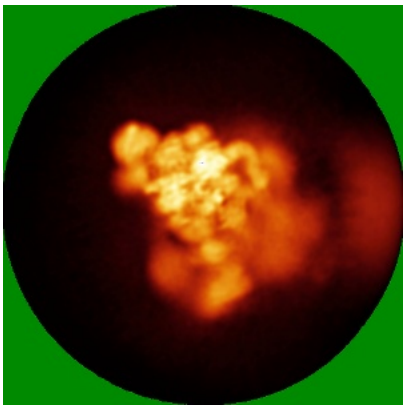


Z Index: 273

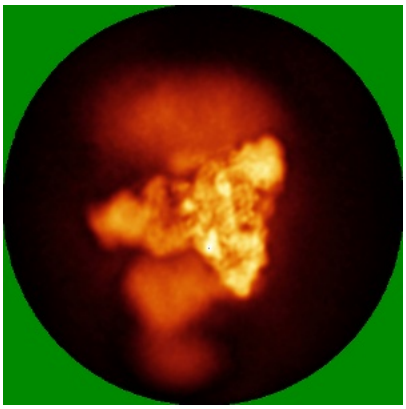
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

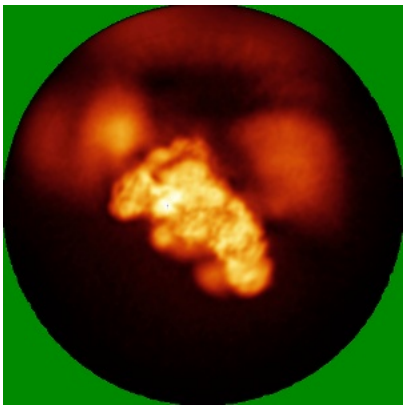
6.4.1 Primary map



X

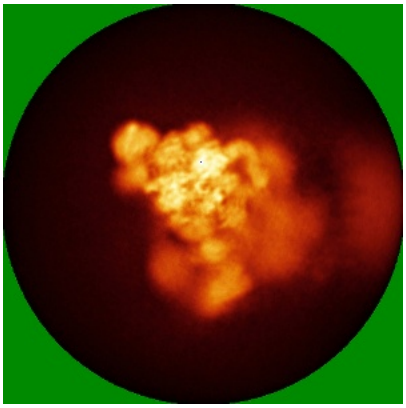


Y

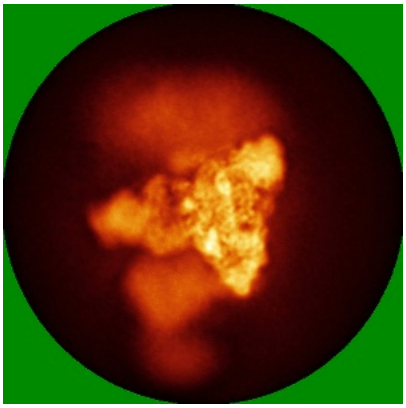


Z

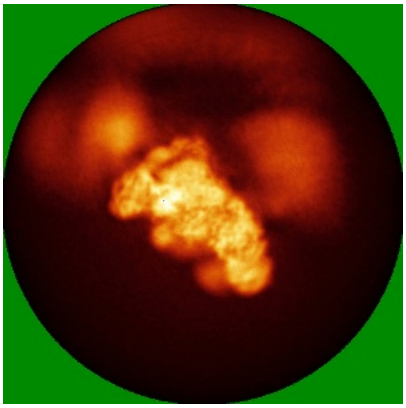
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

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

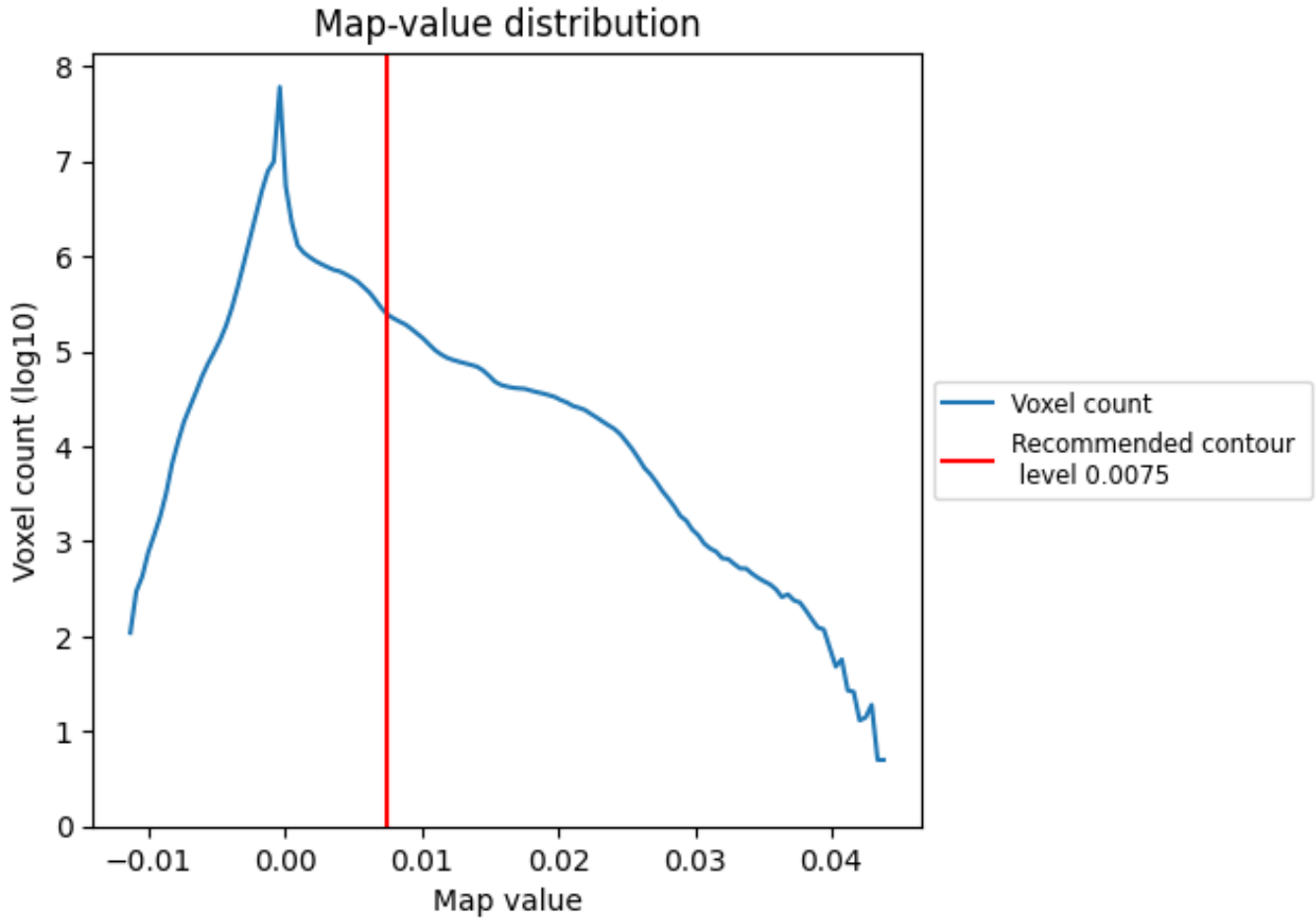
6.6 Mask visualisation (i)

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

7 Map analysis

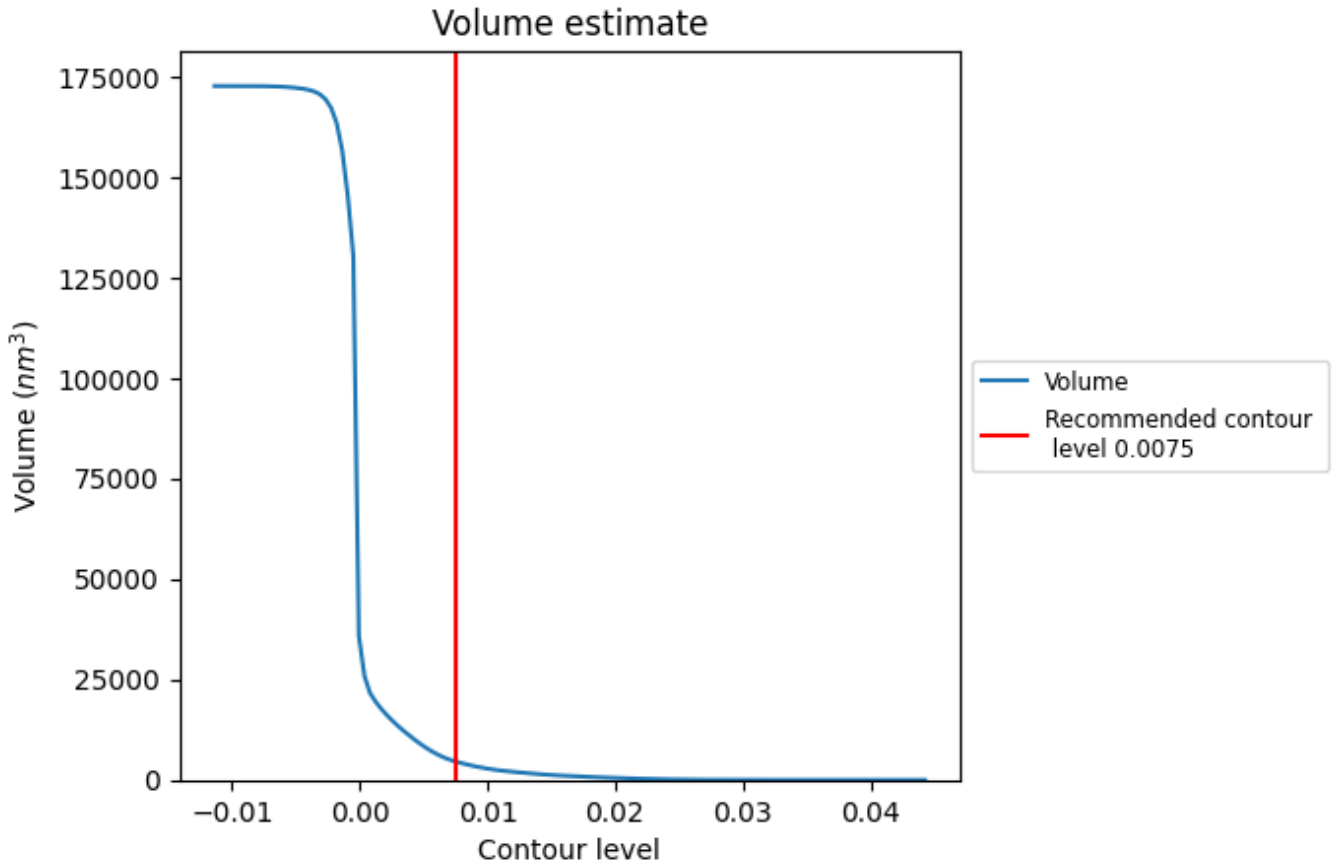
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

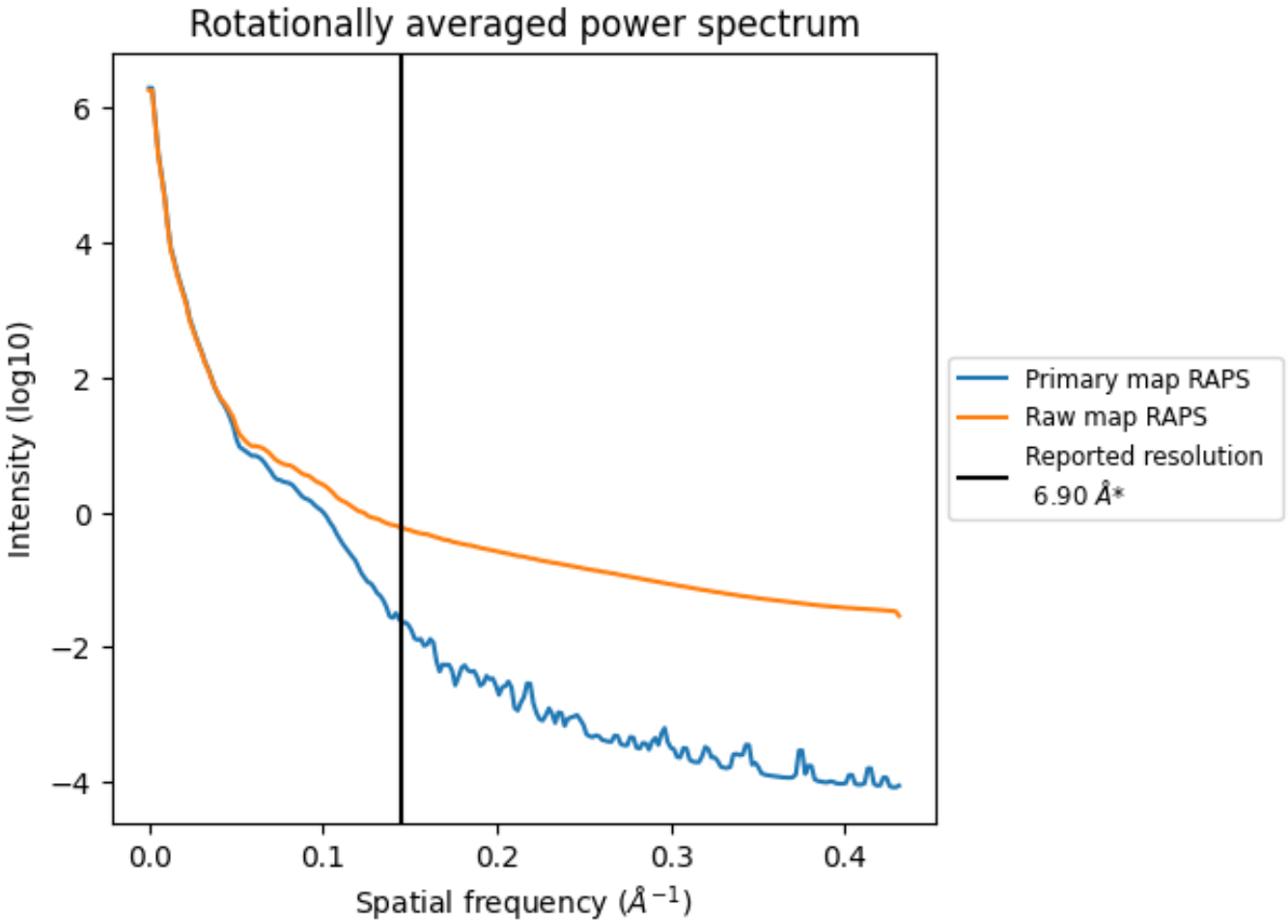
7.2 Volume estimate (i)



The volume at the recommended contour level is 4594 nm^3; this corresponds to an approximate mass of 4150 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 (i)

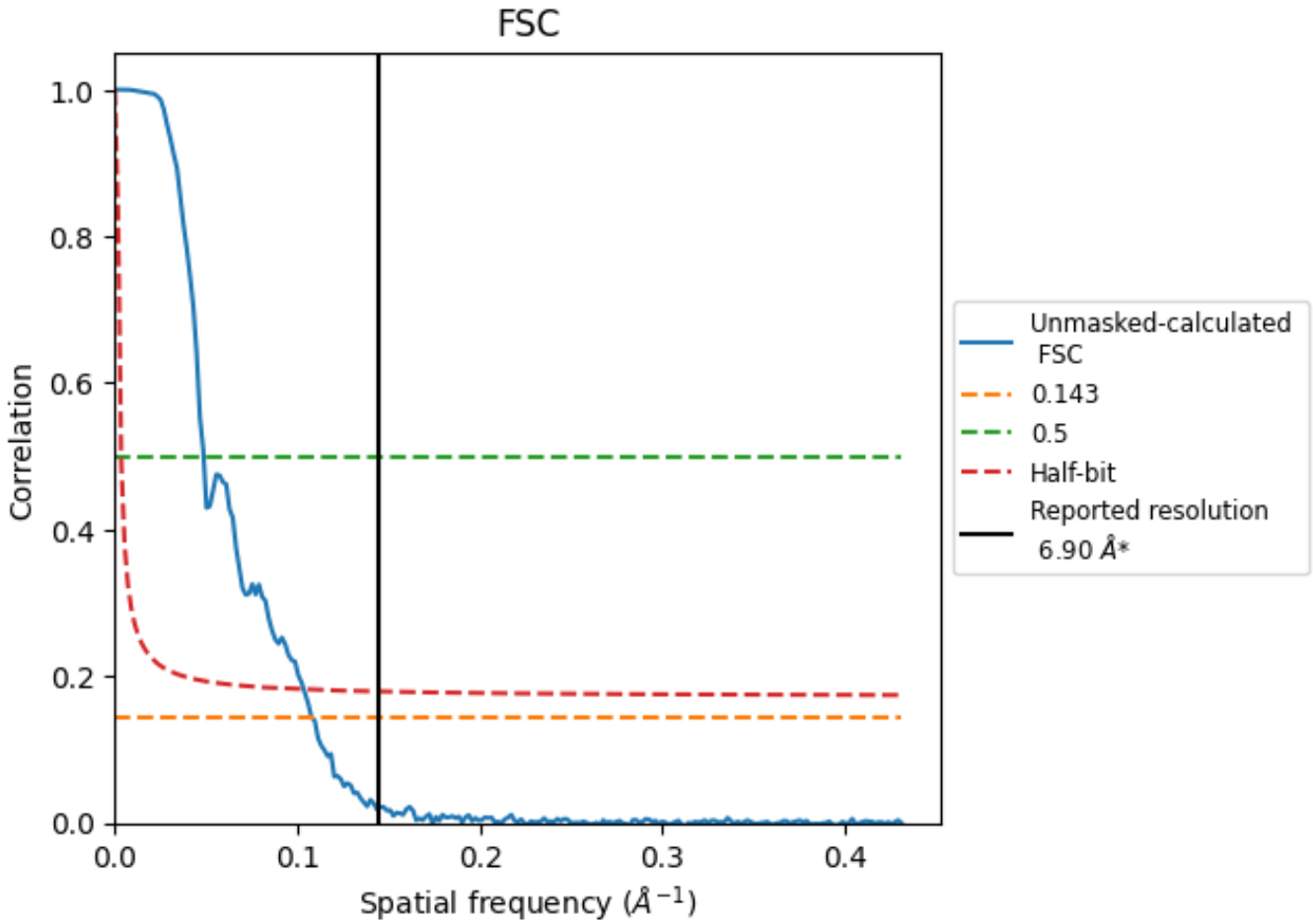


*Reported resolution corresponds to spatial frequency of 0.145 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.145 Å^{-1}

8.2 Resolution estimates (i)

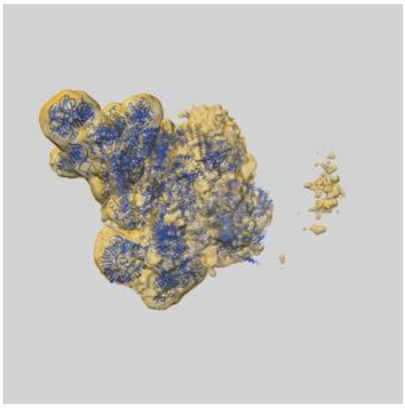
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.26	20.53	9.66

*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 9.26 differs from the reported value 6.9 by more than 10 %

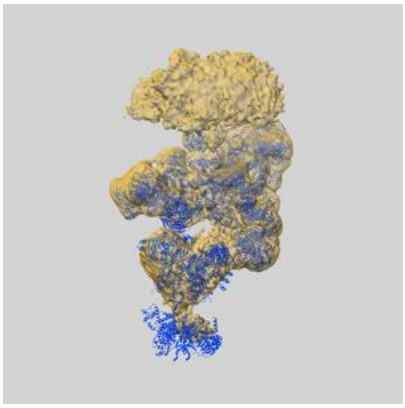
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-19349 and PDB model 8RM5. Per-residue inclusion information can be found in section 3 on page 14.

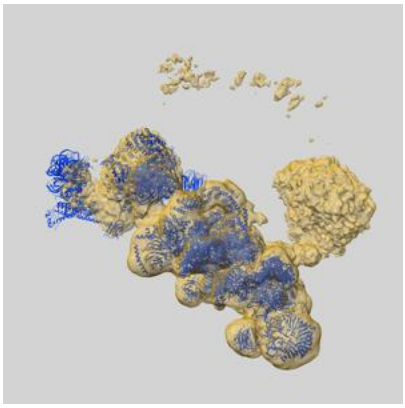
9.1 Map-model overlay



X



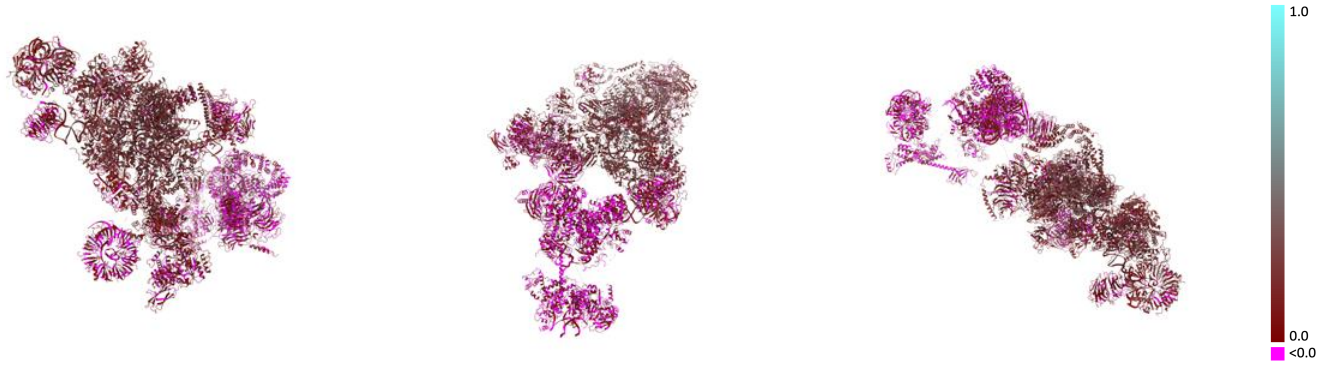
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0075 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.

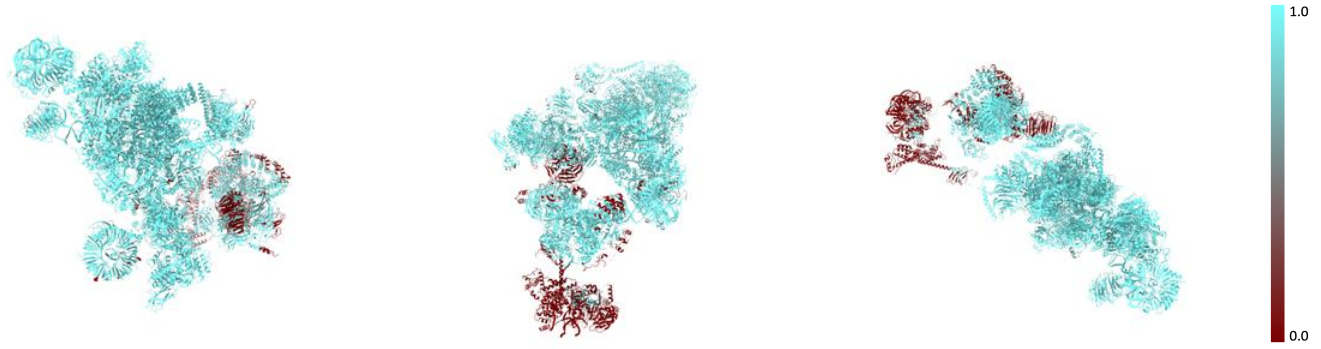
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

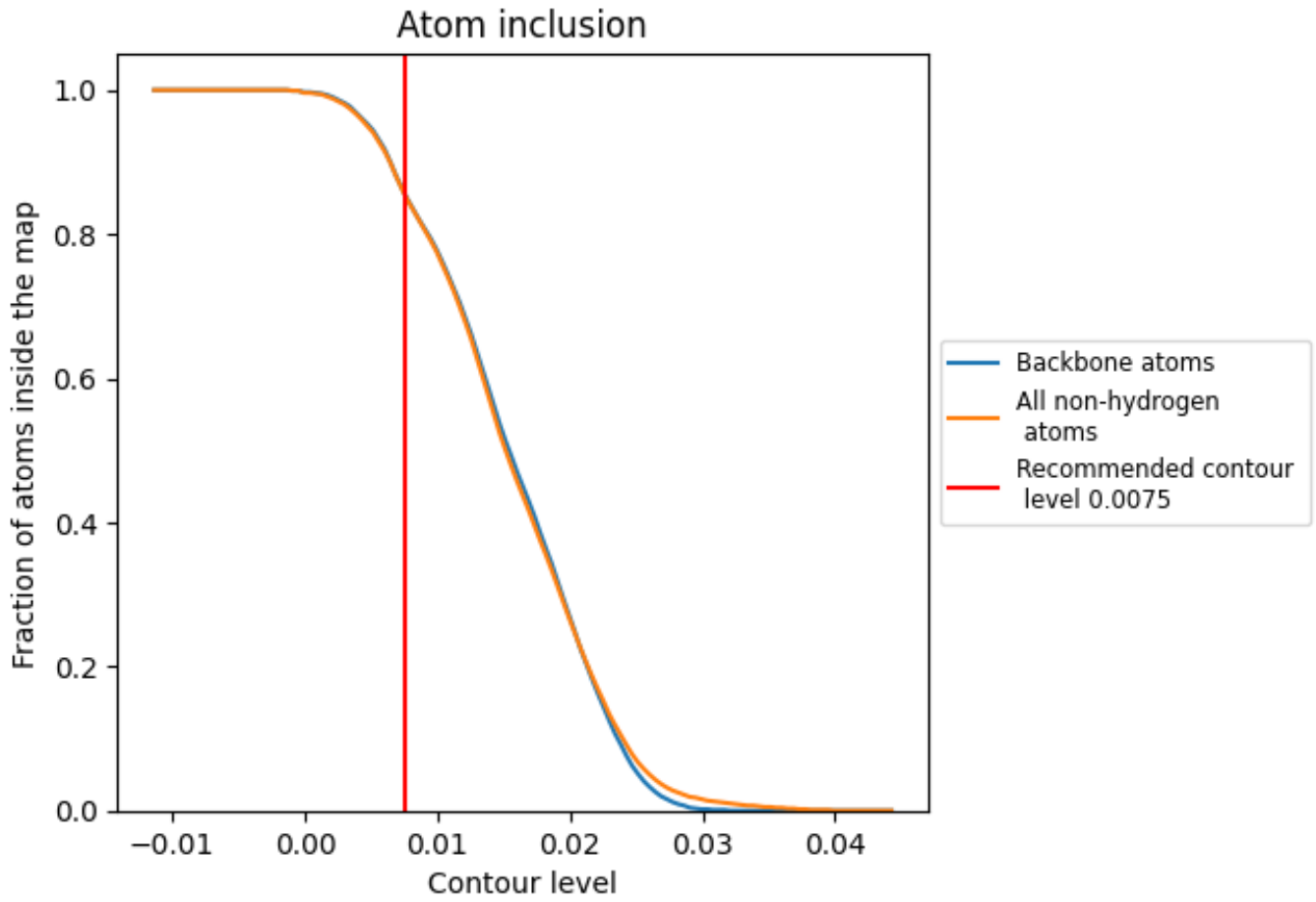
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0075).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.0075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8560	0.1090
2	0.4860	0.0290
21	0.5450	0.0300
22	0.1910	0.0280
23	0.2700	0.0420
2A	0.0070	0.0020
2B	0.0000	-0.0040
2b	0.3560	0.0600
2e	0.0000	0.0370
2f	0.0000	-0.0010
2g	0.0850	0.0360
4	0.9680	0.1010
41	0.9530	-0.0160
42	0.7580	0.0140
43	1.0000	0.0920
4b	0.9770	0.0630
4e	0.8860	0.0220
4f	0.9470	0.0310
4g	0.9620	0.0670
5	1.0000	0.1570
51	1.0000	0.1540
52	1.0000	0.1440
53	1.0000	0.1790
5b	0.9970	0.1390
5e	1.0000	0.1460
5f	1.0000	0.1090
5g	1.0000	0.1570
6	0.9990	0.1560
62	0.6480	-0.0050
63	0.8090	0.0400
64	0.9700	0.0550
65	0.9550	0.0550
66	0.9970	0.0710
67	0.9580	0.0550
68	0.7760	0.0230

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
7	0.4570	0.0700
8	0.4290	0.0360
9	0.2120	0.0070
A	0.9930	0.2080
B	0.9910	0.1140
B1	0.8320	0.0180
B2	0.9160	0.0080
B3	0.6100	0.0190
B4	1.0000	0.0380
B5	1.0000	0.0250
B6	0.6020	0.0360
BP	1.0000	0.0280
C	1.0000	0.1880
D	1.0000	0.2170
E	0.9820	0.0440
F	1.0000	0.1420
G	0.9670	0.1280
J	0.9960	0.1890
L	0.9940	0.2130
M	1.0000	0.1730
N	0.9990	0.1610
S	0.9420	0.1790
U	0.9350	0.1130
W	0.9990	0.1200
Z	1.0000	0.0340
z	1.0000	0.1560