



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:07 PM UTC

PDB ID : 5LQW / pdb_00005lqw
EMDB ID : EMD-4099
Title : yeast activated spliceosome
Authors : Rauhut, R.; Luehrmann, R.
Deposited on : 2016-08-17
Resolution : 5.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

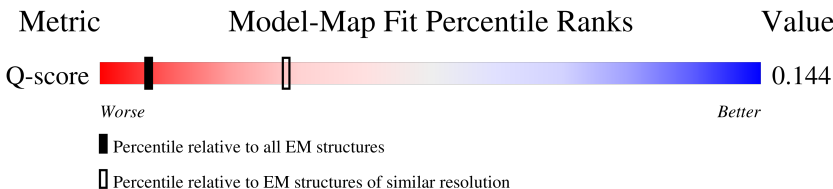
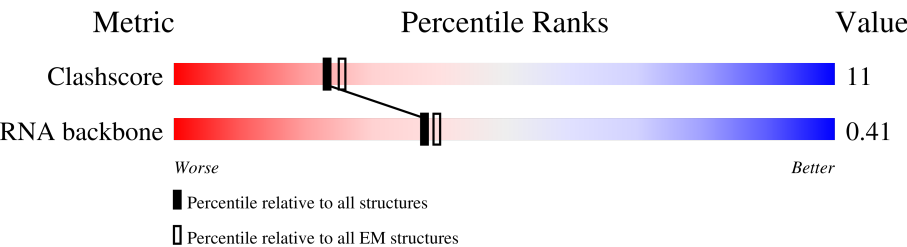
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

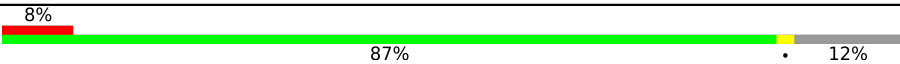
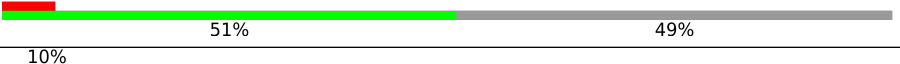
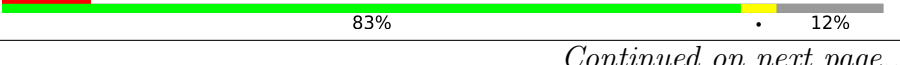
The reported resolution of this entry is 5.80 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	2413	
2	B	1008	
3	C	2163	
4	D	364	
5	E	157	

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Mol	Chain	Length	Quality of chain
6	F	339	
7	H	577	
8	J	148	
9	K	451	
10	L	266	
11	M	379	
12	N	204	
13	O	876	
14	P	859	
15	Q	971	
16	R	687	
17	W	590	
18	X	1361	
19	Y	107	
20	Z	85	
21	b	196	
22	d	101	
23	e	94	
24	f	86	
25	g	77	
26	h	146	
27	j	110	
28	2	1175	
29	5	179	
30	6	112	

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Mol	Chain	Length	Quality of chain
31	9	572	• 5% • 91%

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 18351 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	A	2130	Total	C	0	2130
			2130	2130		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	ASN	MET	conflict	UNP P33334

- Molecule 2 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms		AltConf	Trace
2	B	843	Total	C	0	843
			843	843		

- Molecule 3 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	C	1811	Total	C	0	1811
			1811	1811		

- Molecule 4 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	D	187	Total	C	0	187
			187	187		

- Molecule 5 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms		AltConf	Trace
5	E	138	Total	C	0	138
			138	138		

- Molecule 6 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms		AltConf	Trace
6	F	218	Total	C	0	218
			218	218		

- Molecule 7 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms		AltConf	Trace
7	H	437	Total	C	0	437
			437	437		

- Molecule 8 is a protein called U2 snRNP component IST3.

Mol	Chain	Residues	Atoms		AltConf	Trace
8	J	104	Total	C	0	104
			104	104		

- Molecule 9 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms		AltConf	Trace
9	K	338	Total	C	0	338
			338	338		

- Molecule 10 is a protein called Pre-mRNA-splicing factor CWC26.

Mol	Chain	Residues	Atoms		AltConf	Trace
10	L	32	Total	C	0	32
			32	32		

- Molecule 11 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms		AltConf	Trace
11	M	169	Total	C	0	169
			169	169		

- Molecule 12 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms		AltConf	Trace
12	N	159	Total	C	0	159
			159	159		

- Molecule 13 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase-like protein PRP2.

Mol	Chain	Residues	Atoms		AltConf	Trace
13	O	628	Total	C	0	628
			628	628		

- Molecule 14 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms		AltConf	Trace
14	P	202	Total	C	0	202
			202	202		

- Molecule 15 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms		AltConf	Trace
15	Q	791	Total	C	0	791
			791	791		

- Molecule 16 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms		AltConf	Trace
16	R	219	Total	C	0	219
			219	219		

- Molecule 17 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms		AltConf	Trace
17	W	128	Total	C	0	128
			128	128		

- Molecule 18 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms		AltConf	Trace
18	X	1095	Total	C	0	1095
			1095	1095		

- Molecule 19 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms		AltConf	Trace
19	Y	89	Total	C	0	89
			89	89		

- Molecule 20 is a protein called RDS3 complex subunit 10.

Mol	Chain	Residues	Atoms		AltConf	Trace
20	Z	68	Total	C	0	68
			68	68		

- Molecule 21 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms		AltConf	Trace
21	b	80	Total	C	0	80
			80	80		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
22	d	82	Total	C	0	82
			82	82		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
23	e	75	Total	C	0	75
			75	75		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
24	f	72	Total	C	0	72
			72	72		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
25	g	69	Total	C	0	69
			69	69		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms		AltConf	Trace
26	h	82	Total	C	0	82
			82	82		

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

Mol	Chain	Residues	Atoms	AltConf	Trace
27	j	94	Total C 94 94	0	94

- Molecule 28 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
28	2	81	Total C N O P 1707 764 285 577 81	0	0

- Molecule 29 is a RNA chain called U5 snRNA.

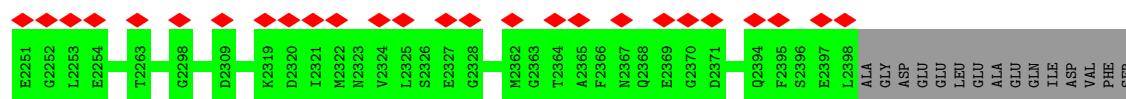
Mol	Chain	Residues	Atoms	AltConf	Trace
29	5	141	Total C N O P 2999 1342 530 986 141	0	0

- Molecule 30 is a RNA chain called U6 snRNA.

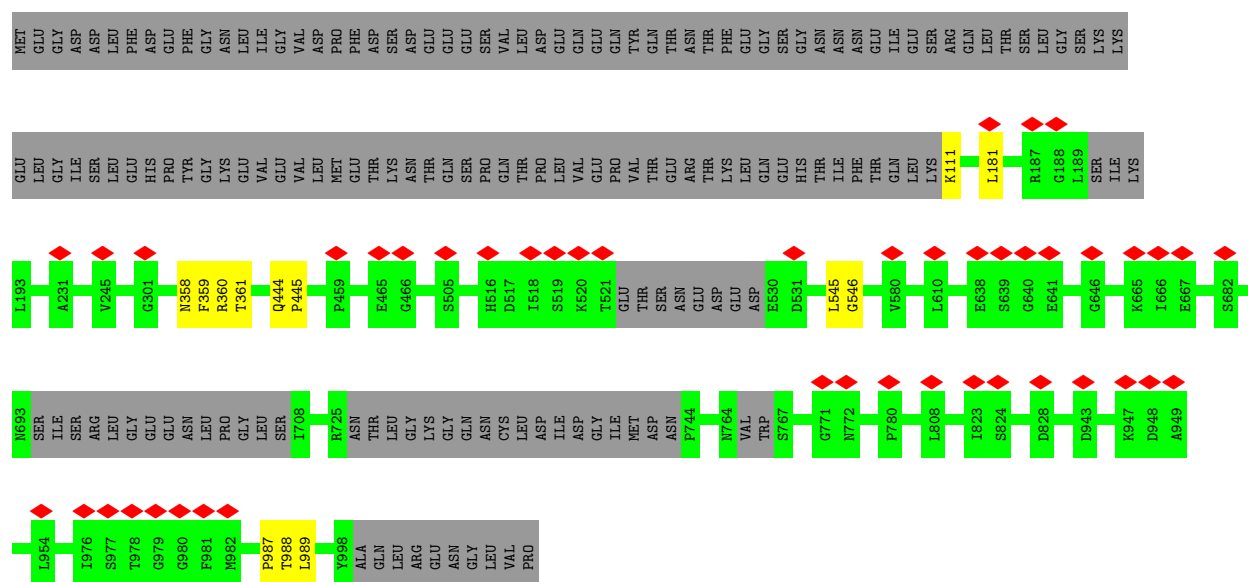
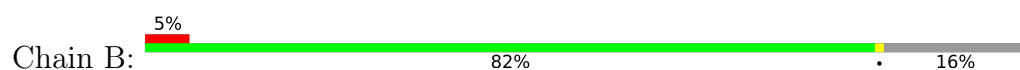
Mol	Chain	Residues	Atoms	AltConf	Trace
30	6	102	Total C N O P 2170 972 386 710 102	0	0

- Molecule 31 is a RNA chain called actin pre-mRNA.

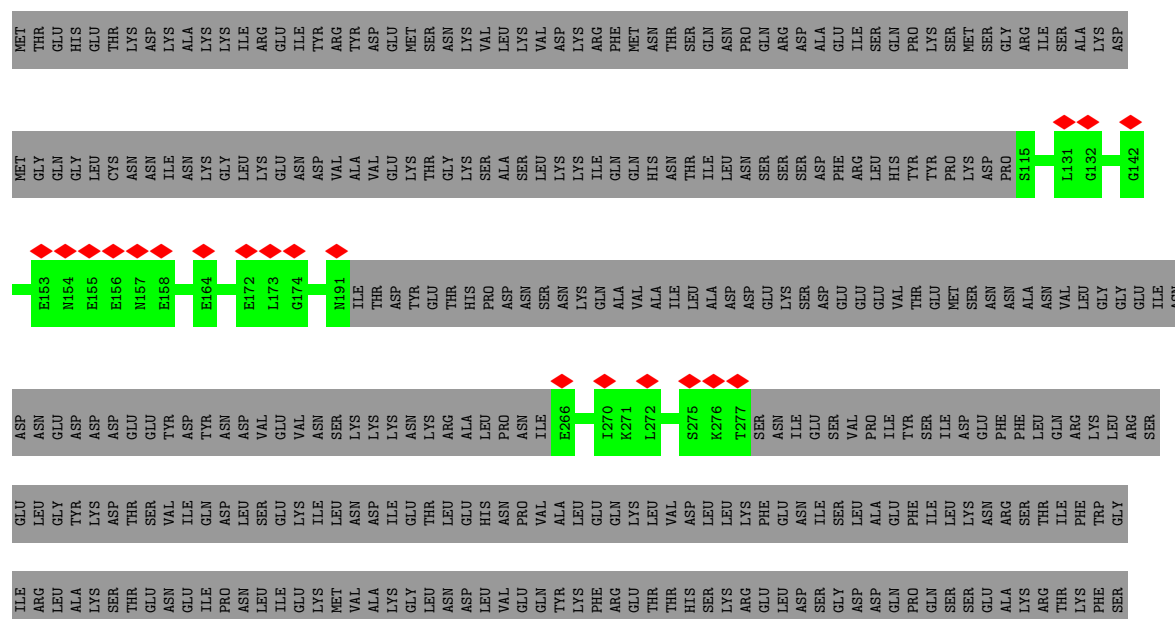
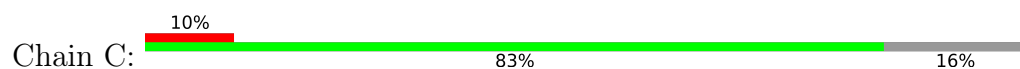
Mol	Chain	Residues	Atoms	AltConf	Trace
31	9	54	Total C N O P 1135 509 187 385 54	0	0

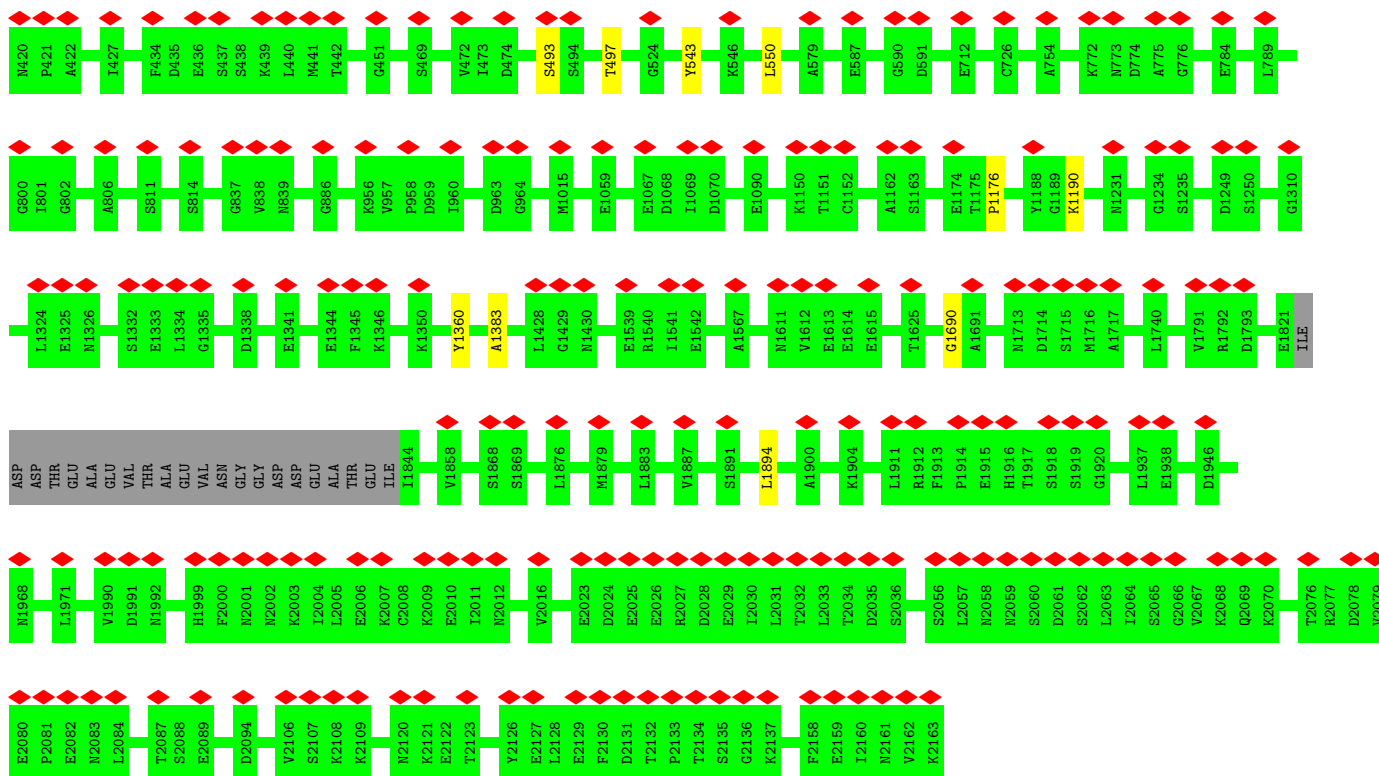


- Molecule 2: Pre-mRNA-splicing factor SNU114

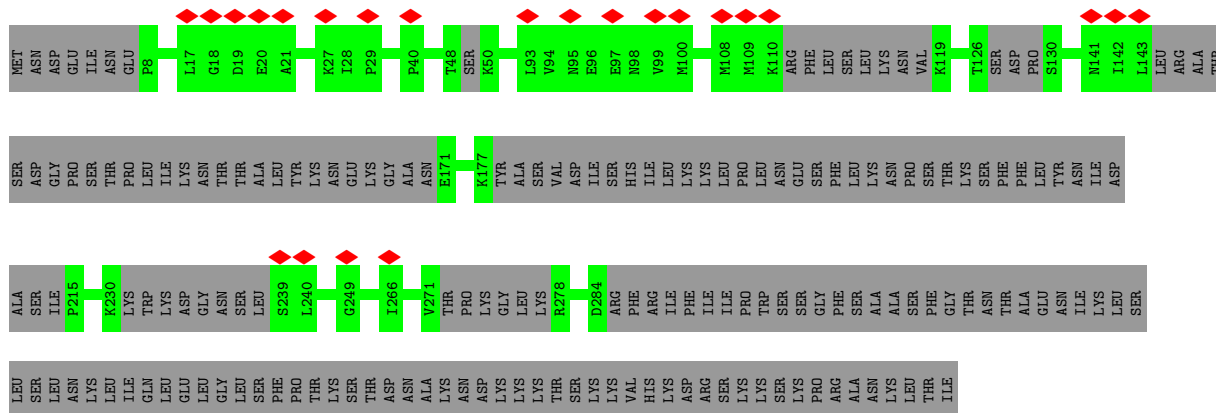


- Molecule 3: Pre-mRNA-splicing helicase BRR2

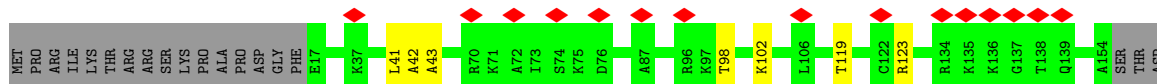
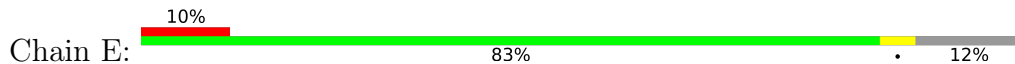




• Molecule 4: Pre-mRNA-splicing factor SLT11



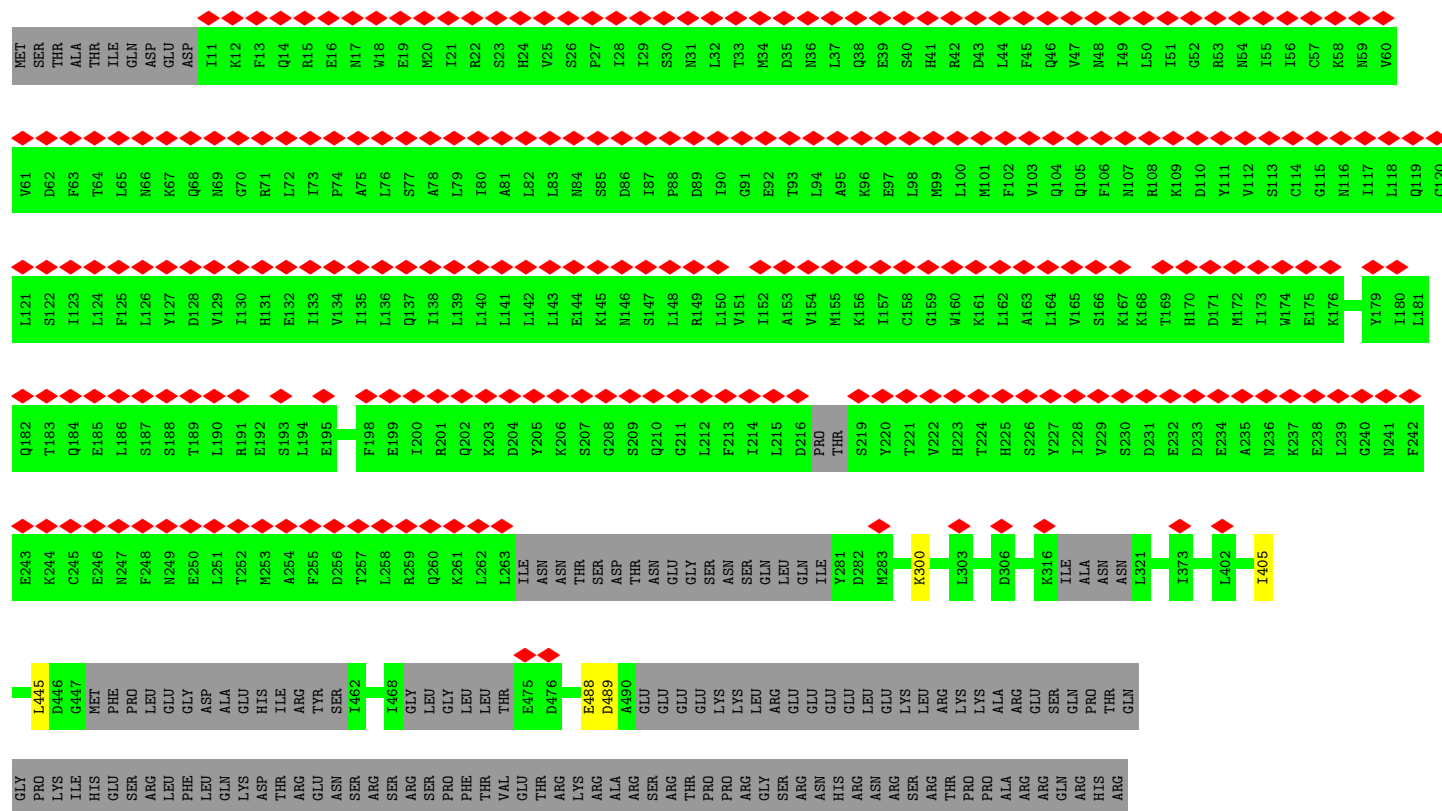
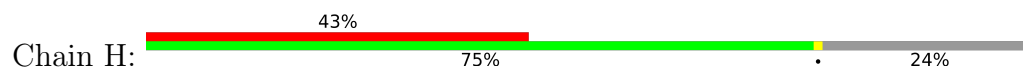
• Molecule 5: Pre-mRNA-splicing factor BUD31



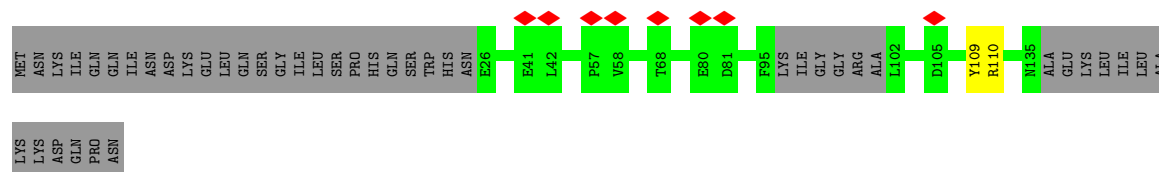
• Molecule 6: Pre-mRNA-splicing factor CWC2

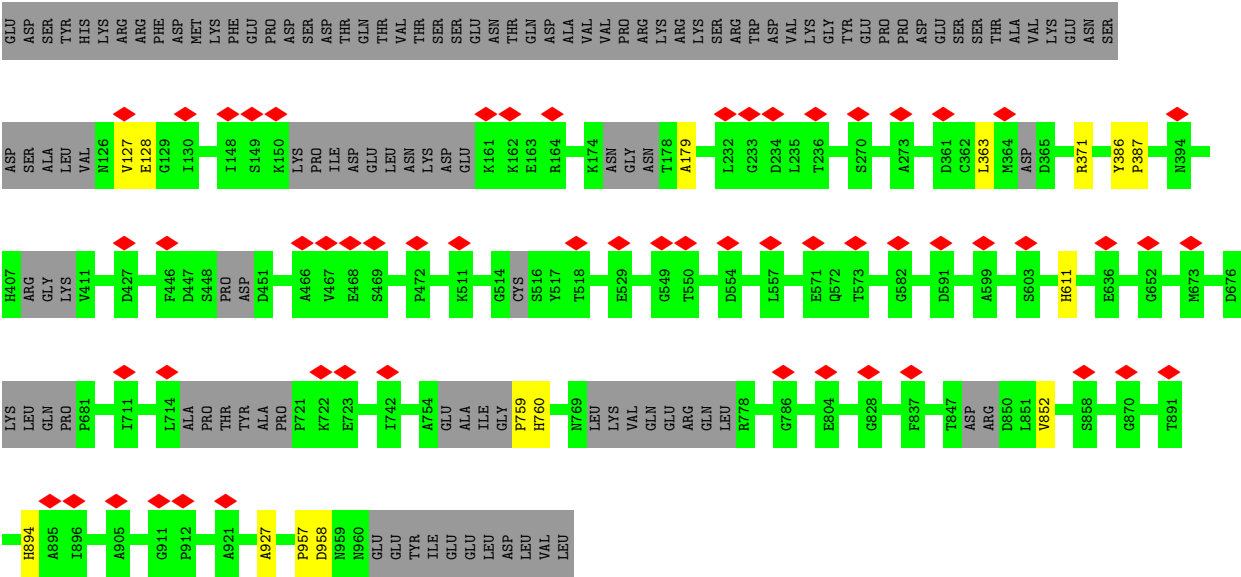


- Molecule 7: Pre-mRNA-splicing factor CWC22

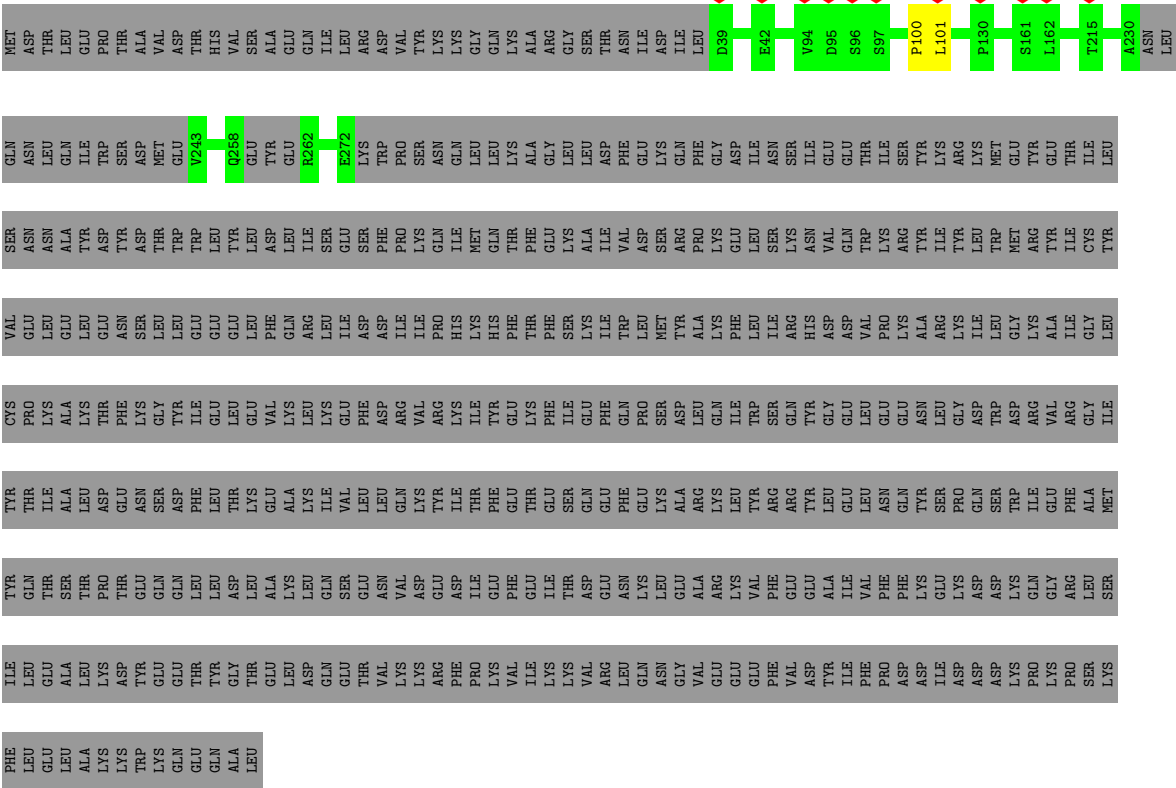


- Molecule 8: U2 snRNP component IST3





• Molecule 16: Pre-mRNA-splicing factor CLF1

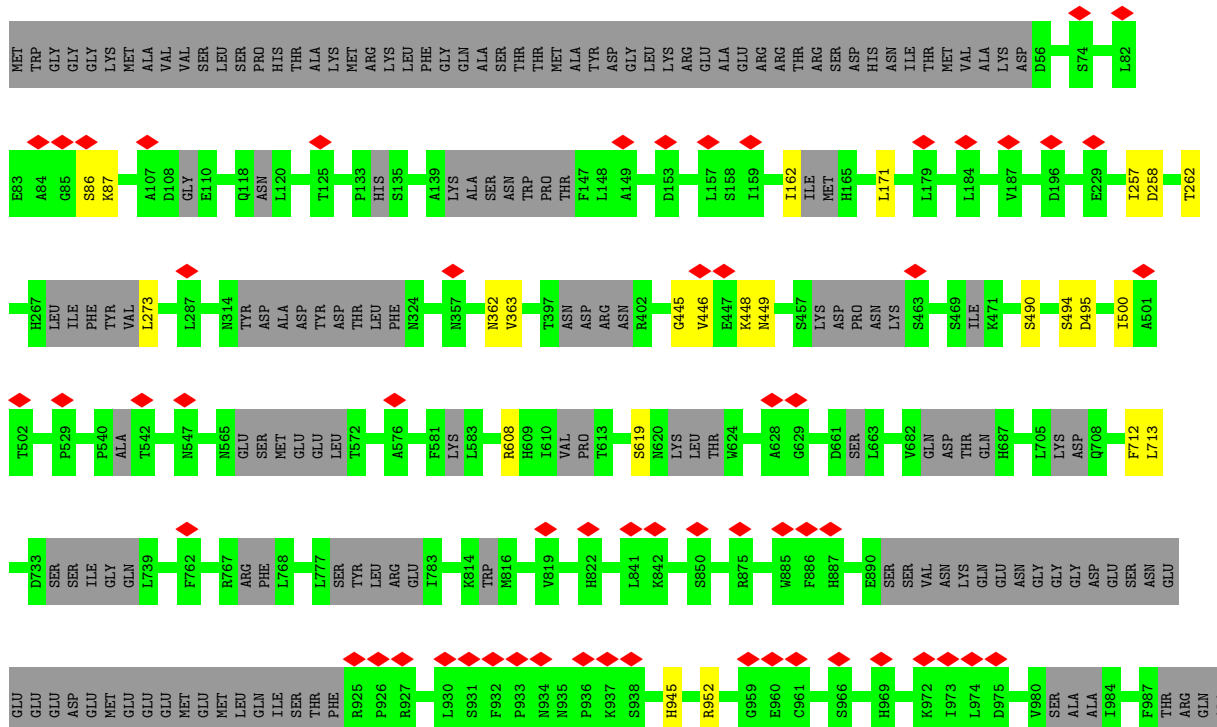
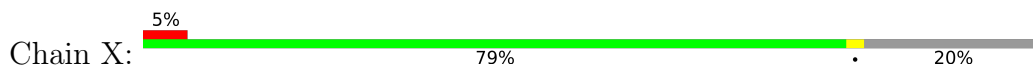


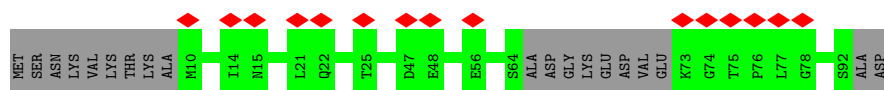
• Molecule 17: Pre-mRNA-splicing factor CEF1



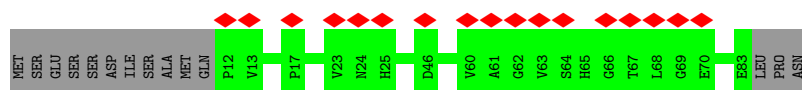
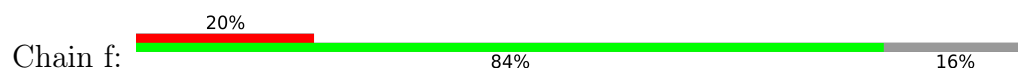


- Molecule 18: Pre-mRNA-splicing factor RSE1

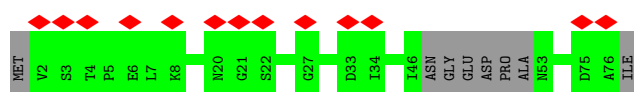
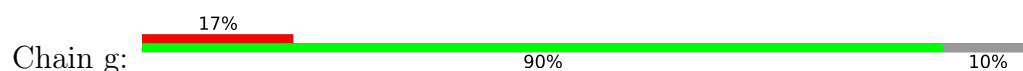




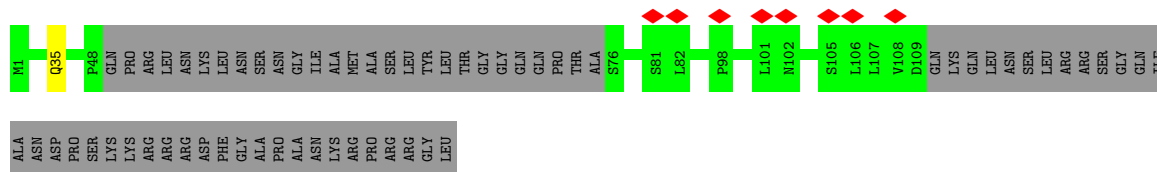
- Molecule 24: Small nuclear ribonucleoprotein F



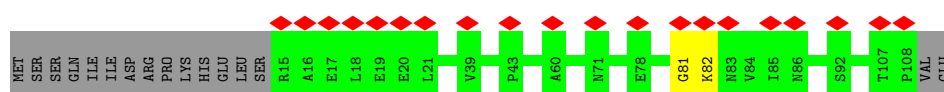
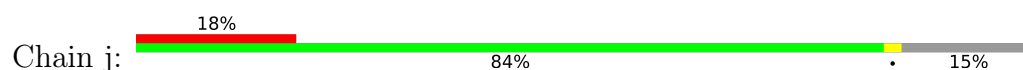
- Molecule 25: Small nuclear ribonucleoprotein G



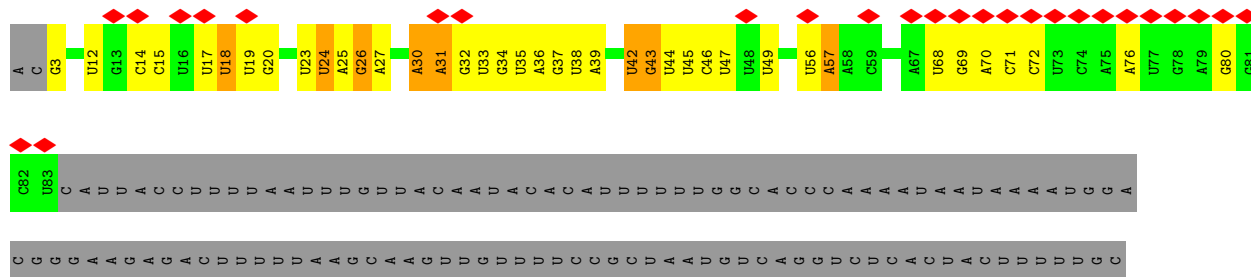
- Molecule 26: Small nuclear ribonucleoprotein Sm D1

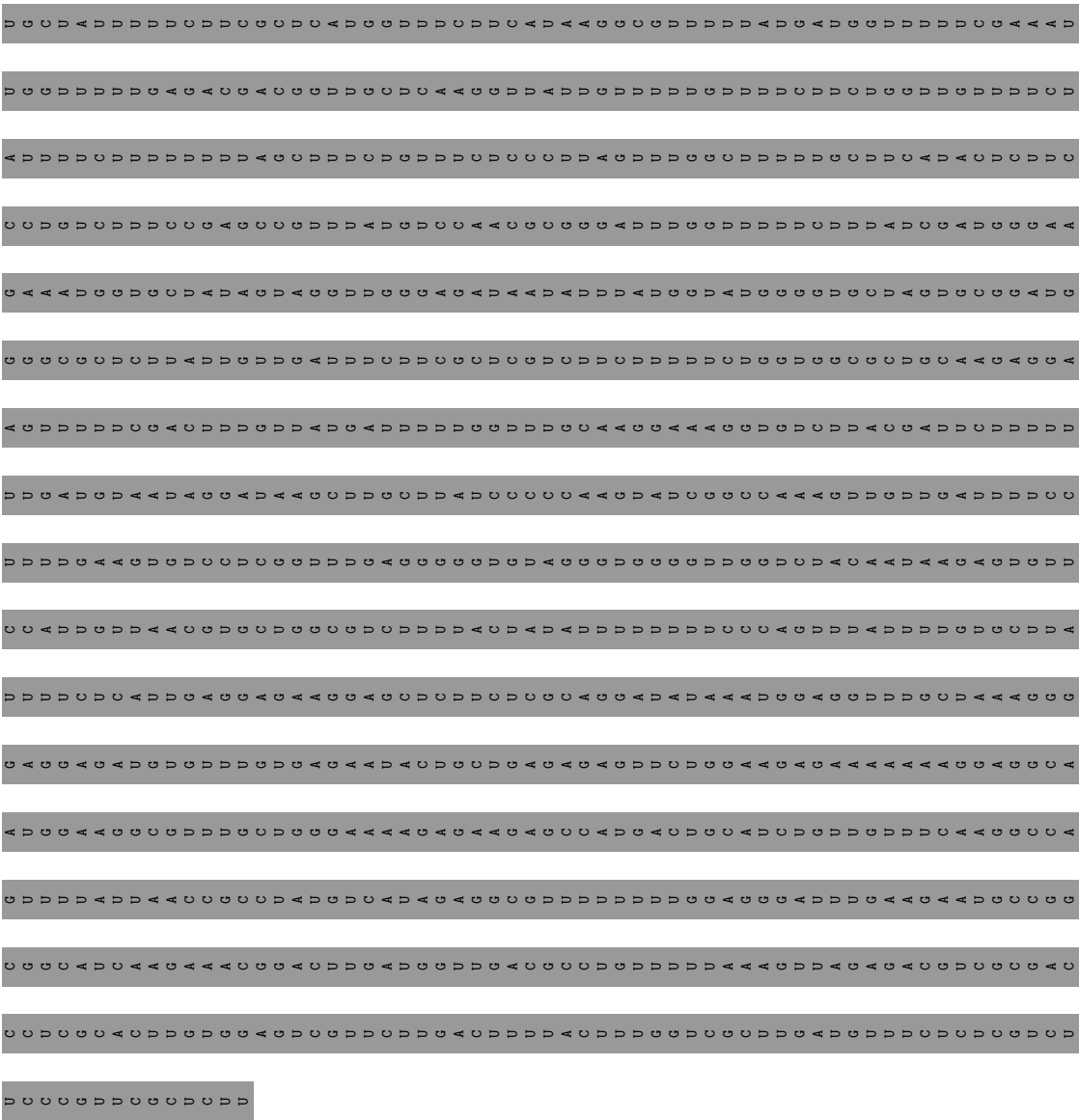


- Molecule 27: Small nuclear ribonucleoprotein Sm D2

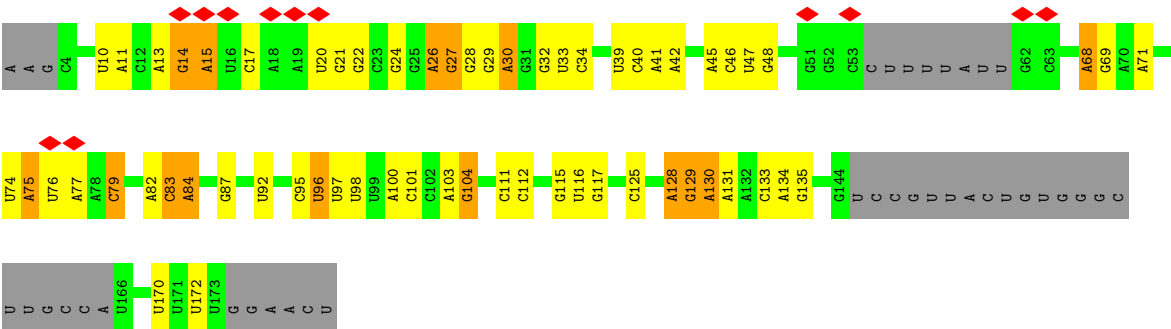


- Molecule 28: U2 snRNA

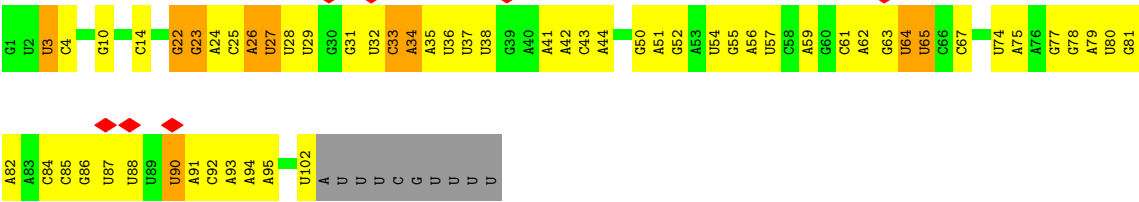




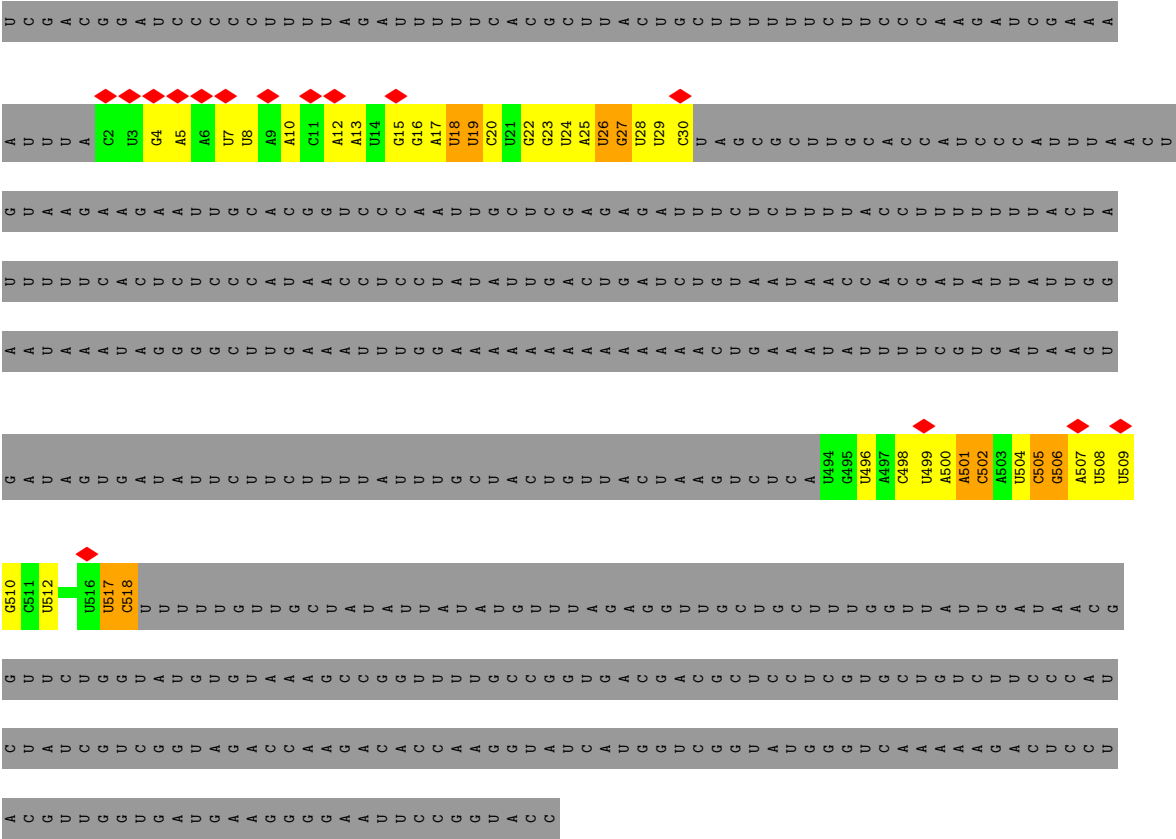
• Molecule 29: U5 snRNA



• Molecule 30: U6 snRNA



• Molecule 31: actin pre-mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	122000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	74000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.343	Depositor
Minimum map value	-0.079	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.11	Depositor
Map size ($\text{\AA}$)	512.0, 512.0, 512.0	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.0, 2.0, 2.0	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	$\# Z > 5$
28	2	0.07	0/1902	0.17	0/2956
29	5	0.06	0/3350	0.17	0/5209
30	6	0.09	0/2427	0.25	0/3778
31	9	0.20	0/1264	0.35	0/1961
All	All	0.10	0/8943	0.23	0/13904

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	A	2130	0	0	48	0
2	B	843	0	0	8	0
3	C	1811	0	0	5	0
4	D	187	0	0	0	0
5	E	138	0	0	17	0
6	F	218	0	0	22	0
7	H	437	0	0	3	0
8	J	104	0	0	1	0
9	K	338	0	0	4	0
10	L	32	0	0	0	0
11	M	169	0	0	10	0
12	N	159	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	O	628	0	0	19	0
14	P	202	0	0	3	0
15	Q	791	0	0	13	0
16	R	219	0	0	4	0
17	W	128	0	0	3	0
18	X	1095	0	0	13	0
19	Y	89	0	0	7	0
20	Z	68	0	0	0	0
21	b	80	0	0	0	0
22	d	82	0	0	1	0
23	e	75	0	0	0	0
24	f	72	0	0	0	0
25	g	69	0	0	0	0
26	h	82	0	0	1	0
27	j	94	0	0	1	0
28	2	1707	0	860	31	0
29	5	2999	0	1515	50	0
30	6	2170	0	1094	53	0
31	9	1135	0	575	31	0
All	All	18351	0	4044	248	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 11.

The worst 5 of 248 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)
1:A:1377:SER:CA	31:9:18:U:C5	1.87	1.56
5:E:98:THR:CA	30:6:4:C:C2	1.88	1.52
15:Q:927:ALA:CA	28:2:57:A:H1'	1.05	1.51
6:F:72:PHE:CA	30:6:34:A:C2	1.94	1.50
6:F:72:PHE:CA	30:6:34:A:H2	1.20	1.49

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	2	80/1175 (6%)	21 (26%)	2 (2%)
29	5	137/179 (76%)	31 (22%)	4 (2%)
30	6	101/112 (90%)	41 (40%)	6 (5%)
31	9	52/572 (9%)	27 (51%)	1 (1%)
All	All	370/2038 (18%)	120 (32%)	13 (3%)

5 of 120 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	2	12	U
28	2	14	C
28	2	15	C
28	2	18	U
28	2	20	G

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	6	26	A
30	6	42	A
31	9	505	C
30	6	64	U
30	6	86	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
29	5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	166:U	O3'	167:A	P	3.66

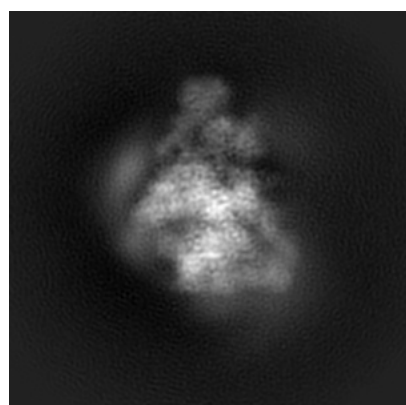
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4099. These allow visual inspection of the internal detail of the map and identification of artifacts.

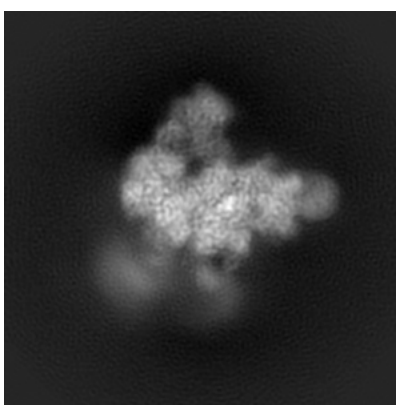
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

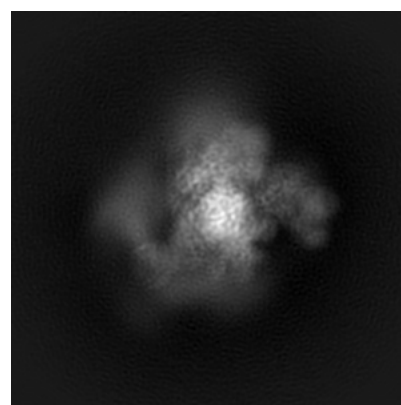
6.1.1 Primary map



X



Y

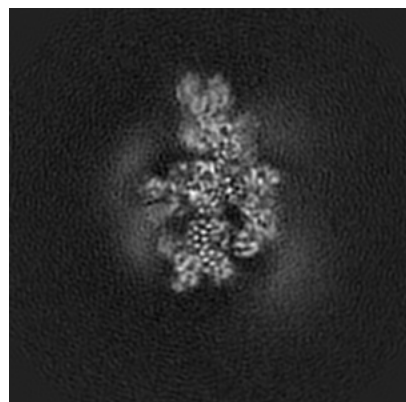


Z

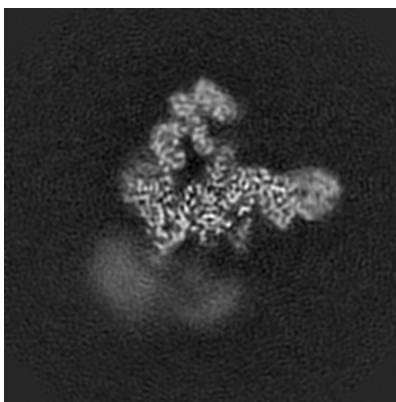
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

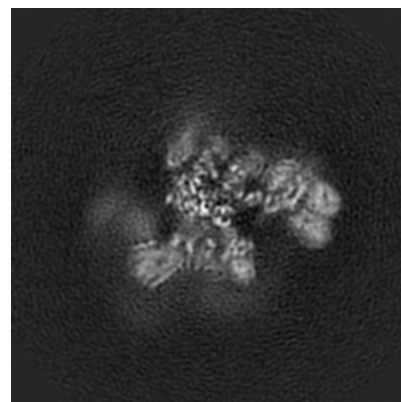
6.2.1 Primary map



X Index: 128



Y Index: 128

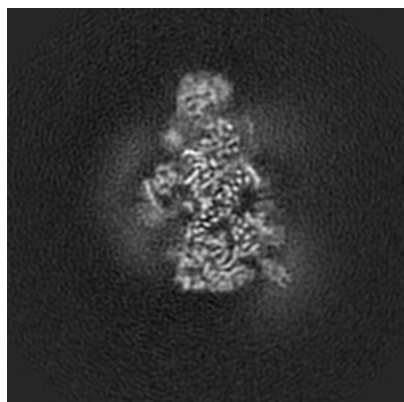


Z Index: 128

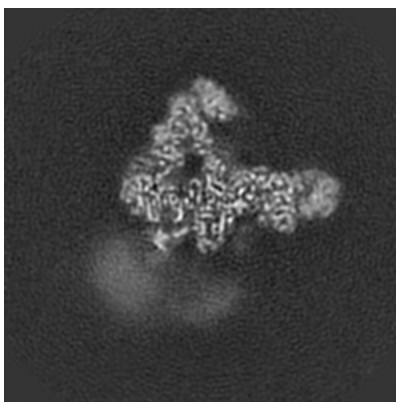
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

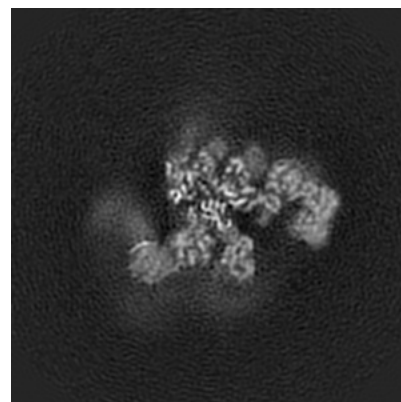
6.3.1 Primary map



X Index: 135



Y Index: 131

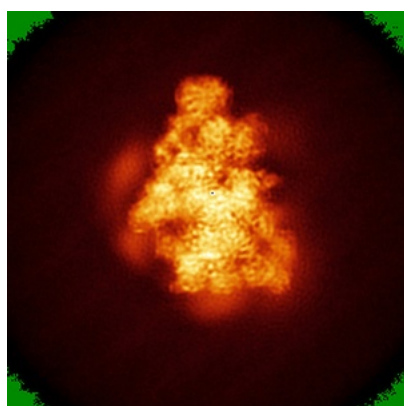


Z Index: 131

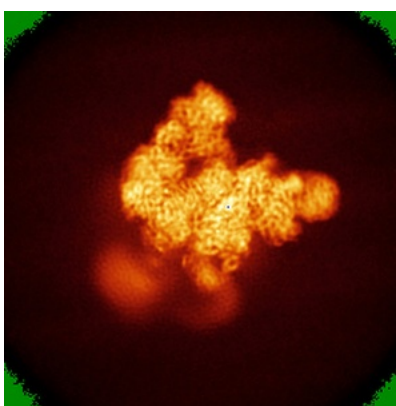
The images above show the largest variance slices of the map in three orthogonal directions.

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

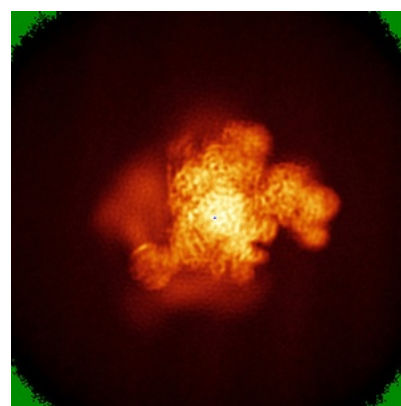
6.4.1 Primary map



X



Y

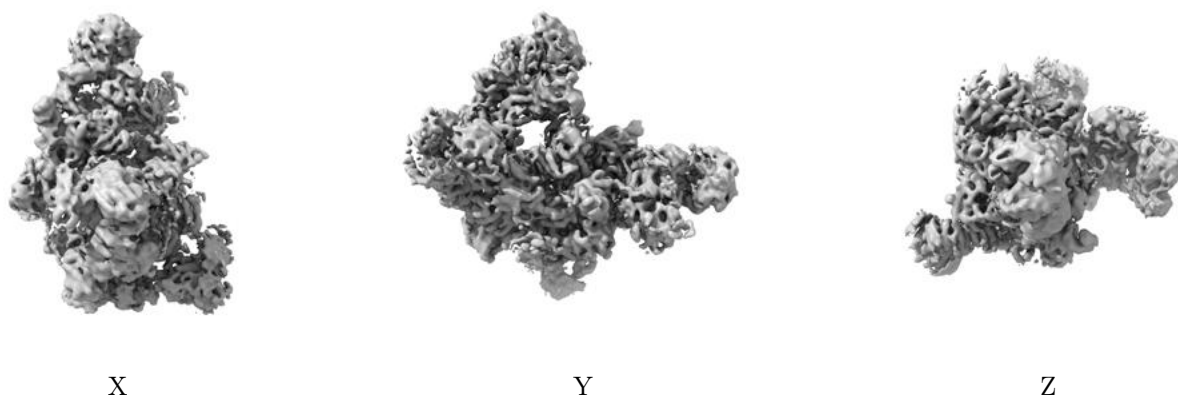


Z

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

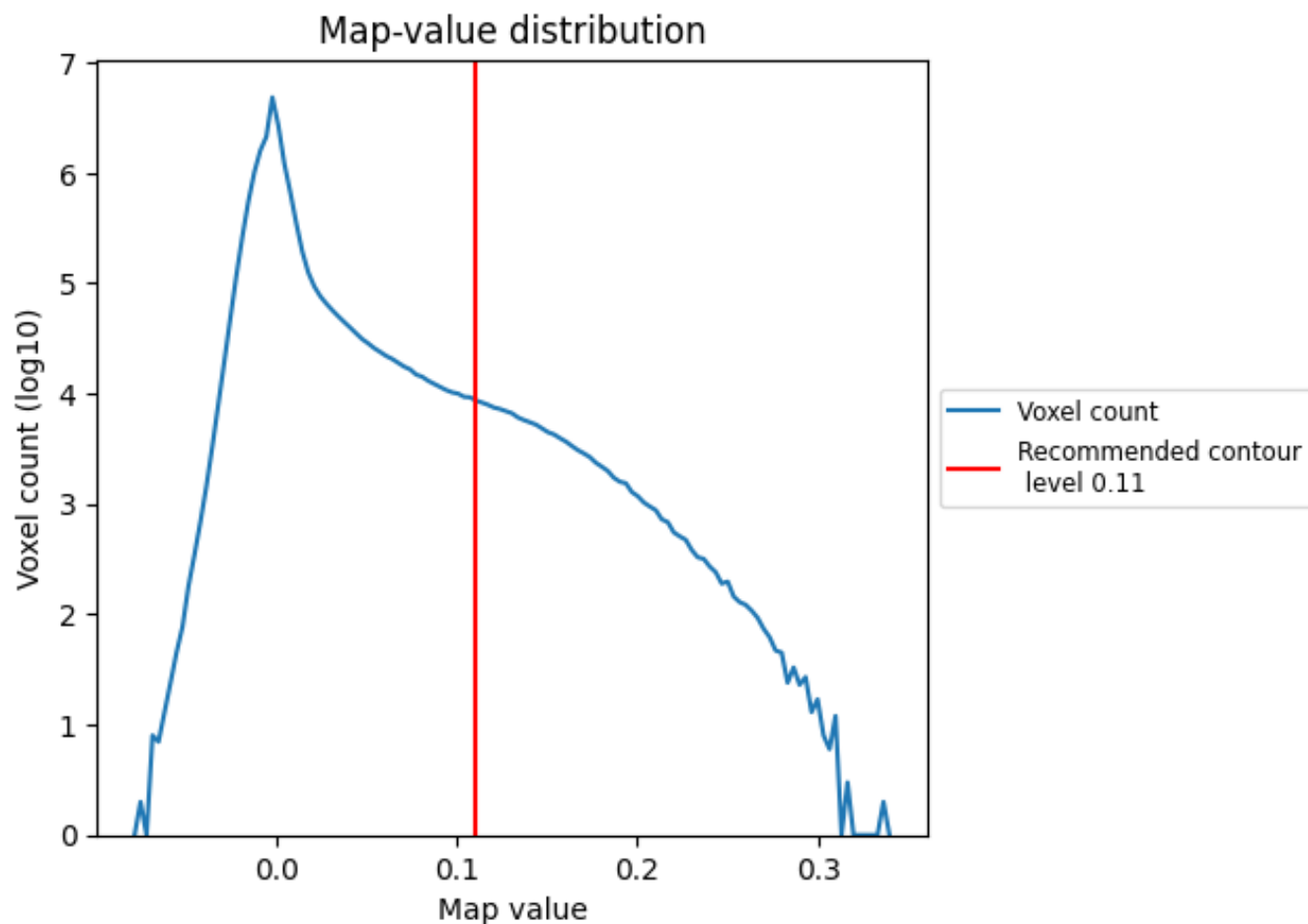
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

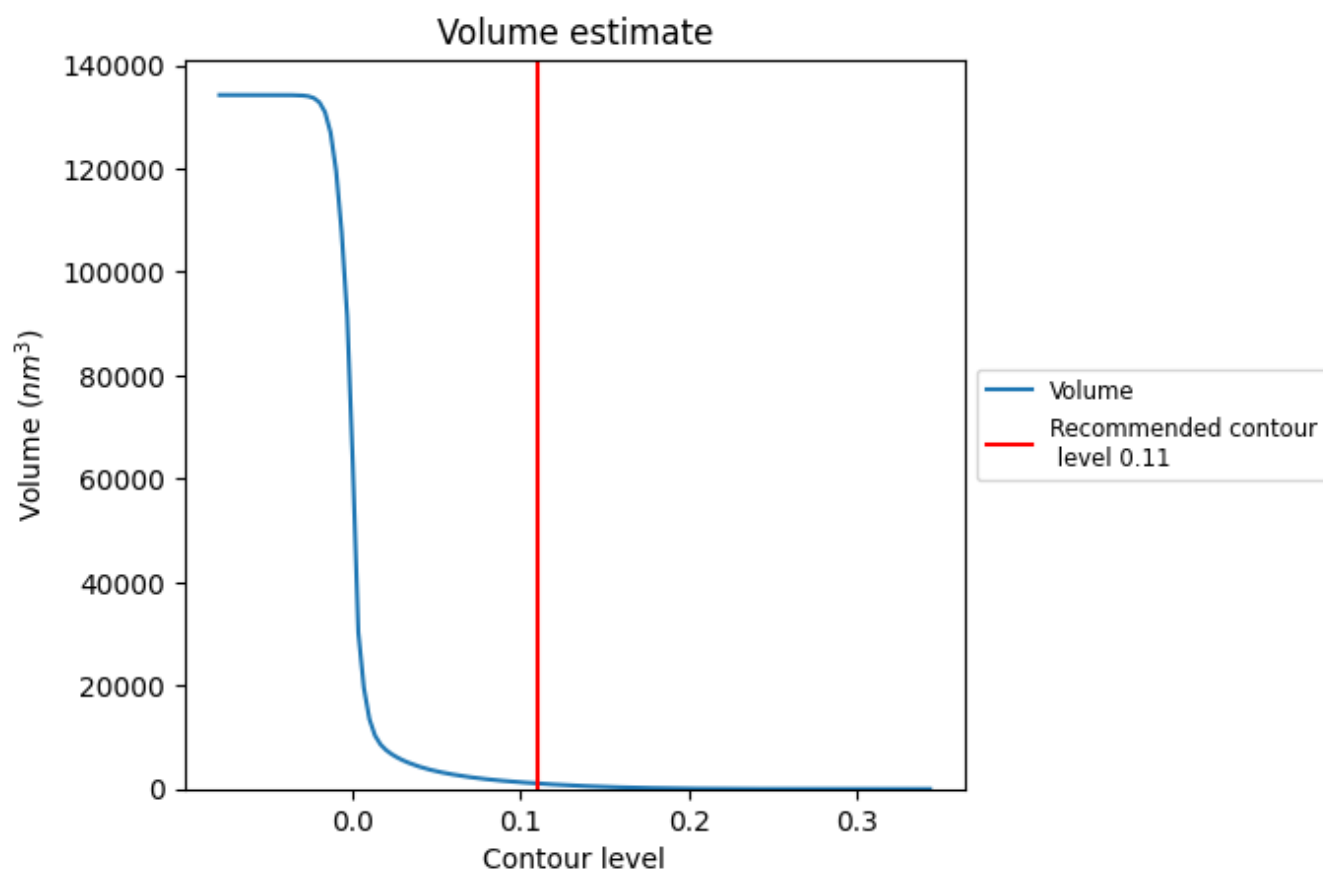
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

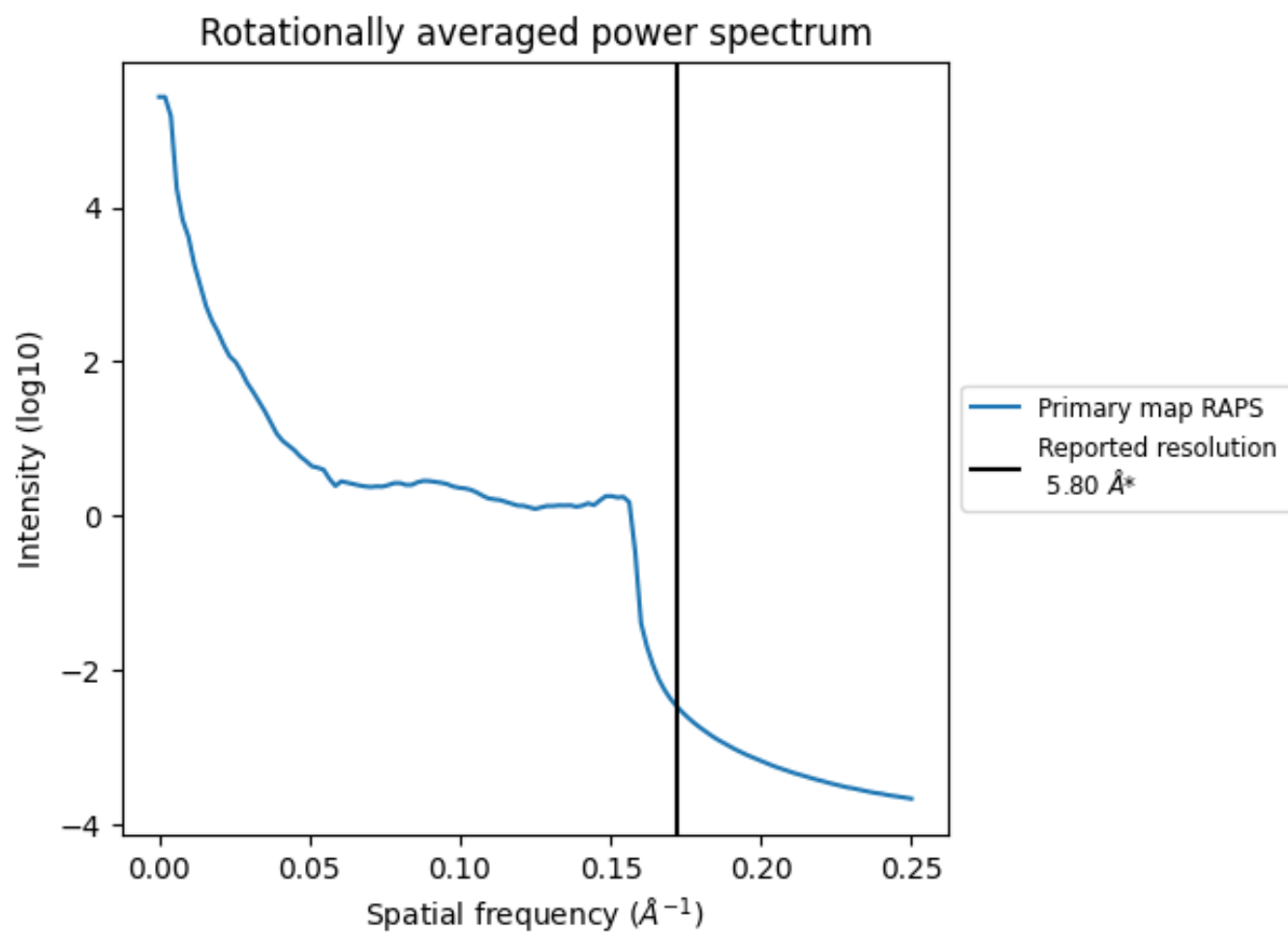
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1066 nm^3 ; this corresponds to an approximate mass of 963 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 0.172 Å⁻¹

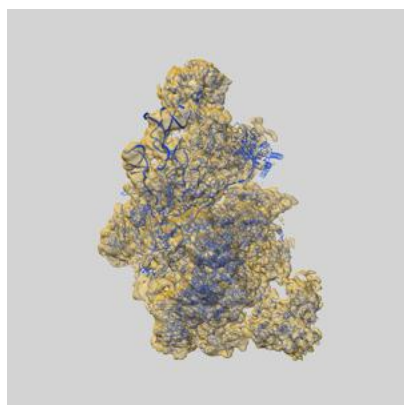
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

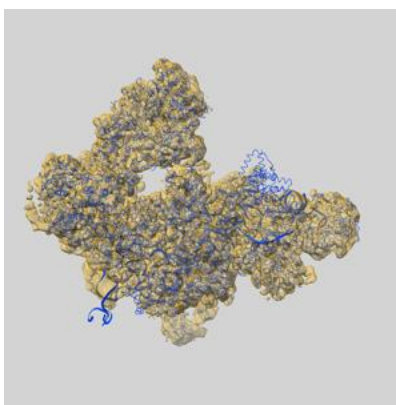
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4099 and PDB model 5LQW. Per-residue inclusion information can be found in section [3](#) on page [10](#).

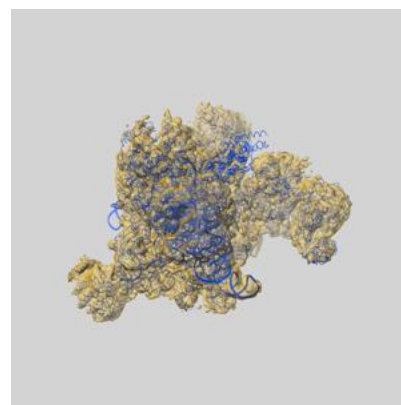
9.1 Map-model overlay [i](#)



X



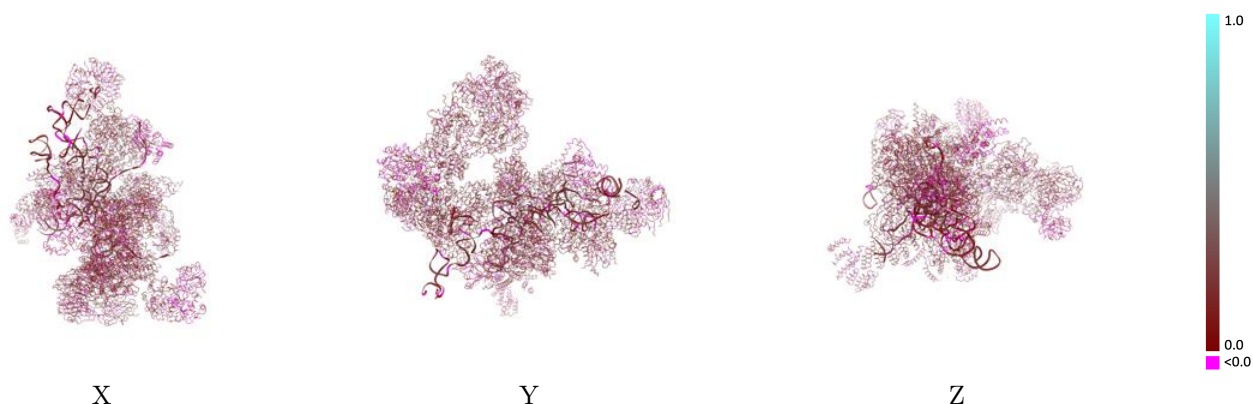
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

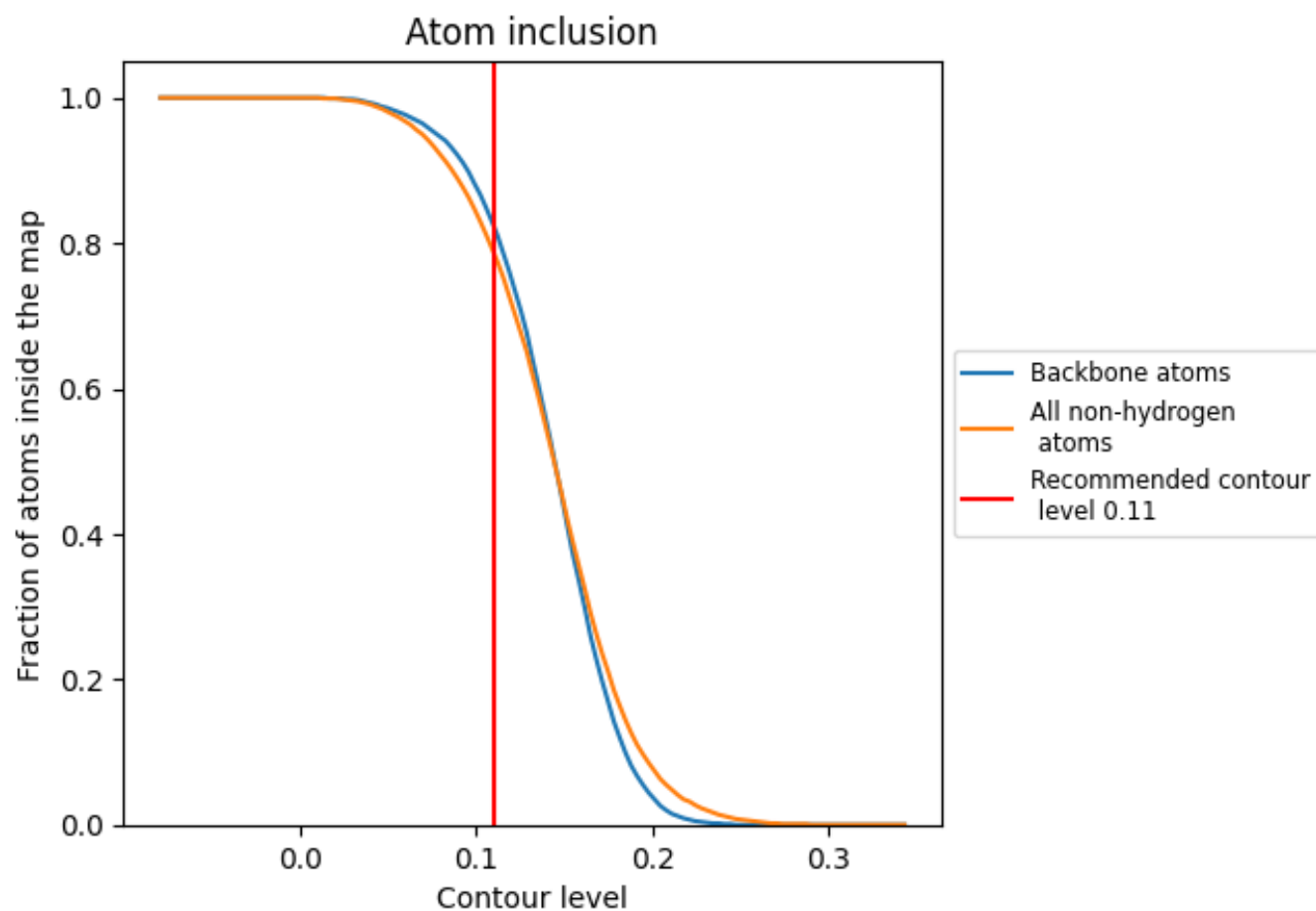


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 79% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7880	 0.1440
2	 0.5240	 0.1370
5	 0.7710	 0.1210
6	 0.7700	 0.1500
9	 0.5890	 0.1550
A	 0.9130	 0.1640
B	 0.9450	 0.1700
C	 0.8770	 0.1370
D	 0.8770	 0.1460
E	 0.8910	 0.1170
F	 0.9080	 0.1660
H	 0.4280	 0.0900
J	 0.9230	 0.1610
K	 0.9440	 0.1790
L	 0.6880	 0.1720
M	 0.7690	 0.2040
N	 0.3150	 0.1200
O	 0.7180	 0.0910
P	 0.7920	 0.1200
Q	 0.9270	 0.1570
R	 0.9500	 0.1360
W	 0.8980	 0.1540
X	 0.9360	 0.1760
Y	 0.9440	 0.2000
Z	 1.0000	 0.1760
b	 0.8870	 0.1220
d	 0.8420	 0.1380
e	 0.8000	 0.0960
f	 0.7640	 0.0760
g	 0.8120	 0.1070
h	 0.9020	 0.1480
j	 0.7870	 0.1020

