



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 04:14 AM UTC

PDB ID : 5GM6 / pdb_00005gm6
EMDB ID : EMD-9524
Title : Cryo-EM structure of the activated spliceosome (Bact complex) at 3.5 angstrom resolution
Authors : Yan, C.; Wan, R.; Bai, R.; Huang, G.; Shi, Y.
Deposited on : 2016-07-12
Resolution : 3.50 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:

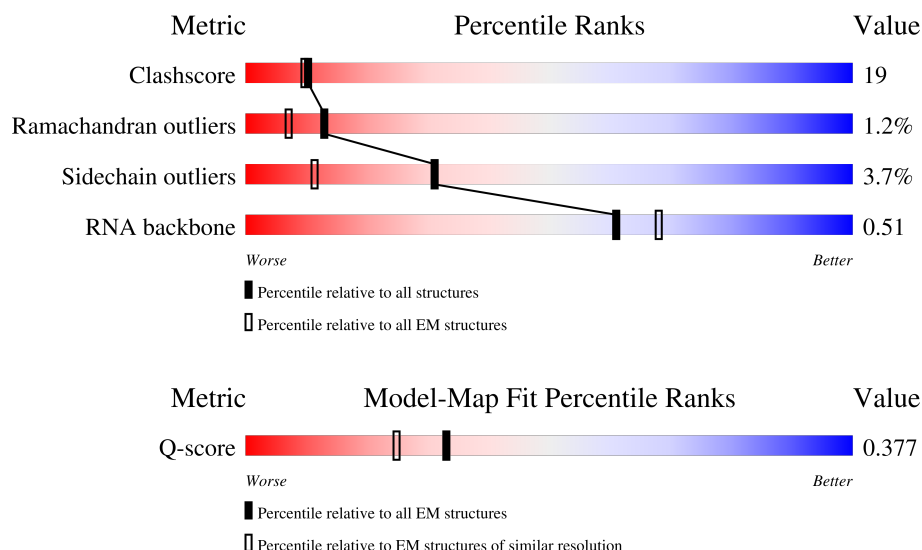
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	2287	
2	B	2163	
3	C	1008	

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Mol	Chain	Length	Quality of chain
4	D	214	
5	E	112	
6	F	1361	
7	H	436	
8	I	266	
9	J	107	
10	K	85	
11	L	1175	
12	N	25	
13	M	61	
14	O	451	
15	P	379	
16	Q	364	
17	R	339	
18	S	175	
19	T	157	
20	U	207	
21	V	148	
22	W	266	
23	Y	876	
24	Z	577	
25	a	259	
26	b	301	
27	c	587	
28	G	971	

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Mol	Chain	Length	Quality of chain
29	d	687	
30	X	135	
31	v	859	
32	e	213	
33	f	215	
34	o	503	
34	p	503	
34	q	503	
34	r	503	
35	t	175	
36	n	455	
37	k	196	
38	i	94	
39	h	86	
40	j	77	
41	l	101	
42	m	146	
43	g	94	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 112064 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	2200	Total	C	N	O	S	0	0
			18101	11636	3086	3315	64		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	ALA	-	insertion	UNP P33334

- Molecule 2 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1809	Total	C	N	O	S	0	0
			14504	9283	2414	2750	57		

- Molecule 3 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	878	Total	C	N	O	S	0	0
			7014	4526	1166	1293	29		

- Molecule 4 is a RNA chain called *Saccharomyces cerevisiae* strain CDRDR_sf_H chromosome VII sequence.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	117	Total	C	N	O	P	0	0
			2465	1104	414	830	117		

- Molecule 5 is a RNA chain called *Saccharomyces cerevisiae* strain T.52_2H chromosome XII sequence.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	103	Total	C	N	O	P	0	0
			2192	982	391	716	103		

- Molecule 6 is a protein called Pre-mRNA-splicing factor RSE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	1180	Total	C	N	O	S	0	0
			9380	5996	1580	1753	51		

- Molecule 7 is a protein called Cold sensitive U2 snRNA suppressor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	151	Total	C	N	O	S	0	0
			1248	804	217	221	6		

- Molecule 8 is a protein called Pre-mRNA-splicing factor PRP11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	102	Total	C	N	O	S	0	0
			800	495	150	150	5		

- Molecule 9 is a protein called Pre-mRNA-splicing factor RDS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	103	Total	C	N	O	S	0	0
			814	503	154	143	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	84	Total	C	N	O	S	0	0
			693	429	130	132	2		

- Molecule 11 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	66	Total	C	N	O	P	0	0
			1388	622	228	472	66		

- Molecule 12 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	25	Total	C	N	O	P	0	0
			521	234	77	185	25		

- Molecule 13 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	50	Total	C	N	O	P	0	0
			1057	479	191	338	49		

- Molecule 14 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	337	Total	C	N	O	S	0	0
			2646	1669	466	501	10		

- Molecule 15 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	246	Total	C	N	O	S	0	0
			1978	1233	359	380	6		

- Molecule 16 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	185	Total	C	N	O	S	0	0
			1472	930	256	271	15		

- Molecule 17 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	261	Total	C	N	O	S	0	0
			2089	1320	369	388	12		

- Molecule 18 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	71	Total	C	N	O	S	0	0
			578	361	117	99	1		

- Molecule 19 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	157	Total	C	N	O	S	0	0
			1291	808	240	232	11		

- Molecule 20 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	176	Total	C	N	O	S	0	0
			1401	877	237	277	10		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	205	HIS	-	insertion	UNP Q07930
U	206	HIS	-	insertion	UNP Q07930
U	207	HIS	-	insertion	UNP Q07930

- Molecule 21 is a protein called U2 snRNP component IST3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	128	Total	C	N	O	S	0	0
			1051	662	181	208			

- Molecule 22 is a protein called Pre-mRNA-splicing factor CWC26.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	104	Total	C	N	O	S	0	0
			842	528	145	167	2		

- Molecule 23 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase-like protein PRP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	598	Total	C	N	O	S	0	0
			4047	2590	690	752	15		

- Molecule 24 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	447	Total	C	N	O	S	0	0
			3651	2343	602	688	18		

- Molecule 25 is a protein called Pre-mRNA-splicing factor CWC24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	123	Total	C	N	O	S	0	0
			988	621	171	183	13		

- Molecule 26 is a protein called Peptidyl-prolyl isomerase CWC27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	150	Total	C	N	O	S	0	0
			1224	789	206	223	6		

- Molecule 27 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	415	Total	C	N	O	S	0	0
			2803	1741	518	537	7		

- Molecule 28 is a protein called U2 snRNP component HSH155.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	875	Total	C	N	O	S	0	0
			6970	4467	1196	1265	42		

- Molecule 29 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	545	Total	C	N	O	S	0	0
			3558	2212	671	667	8		

- Molecule 30 is a protein called Pre-mRNA-splicing factor CWC21.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	X	27	Total	C	N	O	0	0
			190	112	38	40		

- Molecule 31 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	566	Total	C	N	O	S	0	0
			3047	1871	576	599	1		

- Molecule 32 is a protein called Protein HSH49.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	149	Total	C	N	O	S	0	0
			947	617	154	174	2		

- Molecule 33 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	102	Total	C	N	O	S	0	0
			822	504	152	165	1		

- Molecule 34 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	o	124	Total	C	N	O	S	0	0
			819	518	132	167	2		
34	p	128	Total	C	N	O	S	0	0
			843	533	136	172	2		
34	q	381	Total	C	N	O	S	0	0
			2315	1456	396	455	8		
34	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		

- Molecule 35 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	t	155	Total	C	N	O	S	0	0
			921	582	159	179	1		

- Molecule 36 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	n	23	Total	C	N	O	0	0
			195	122	41	32		

- Molecule 37 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	80	Total	C	N	O	S	0	0
			631	403	114	111	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 40 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 41 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	82	Total	C	N	O	S	0	0
			625	399	109	115	2		

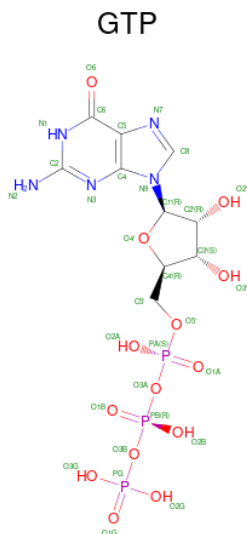
- Molecule 42 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 43 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	94	Total	C	N	O	S	0	0
			741	477	141	119	4		

- Molecule 44 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
44	C	1	Total 32	C 10	N 5	O 14	P 3	0

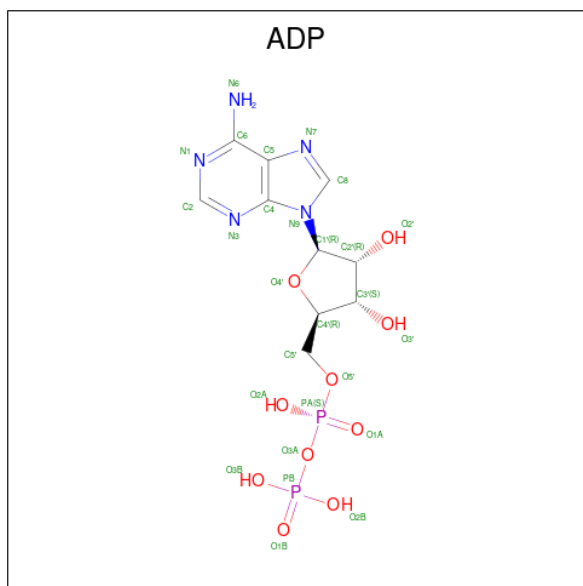
- Molecule 45 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
45	E	4	Total 4	Mg 4	0
45	Y	1	Total 1	Mg 1	0

- Molecule 46 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
46	I	1	Total 1	Zn 1	0
46	J	3	Total 3	Zn 3	0
46	Q	2	Total 2	Zn 2	0
46	R	1	Total 1	Zn 1	0
46	T	3	Total 3	Zn 3	0
46	a	3	Total 3	Zn 3	0

- Molecule 47 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
47	Y	1	27	10	5	10	2	0

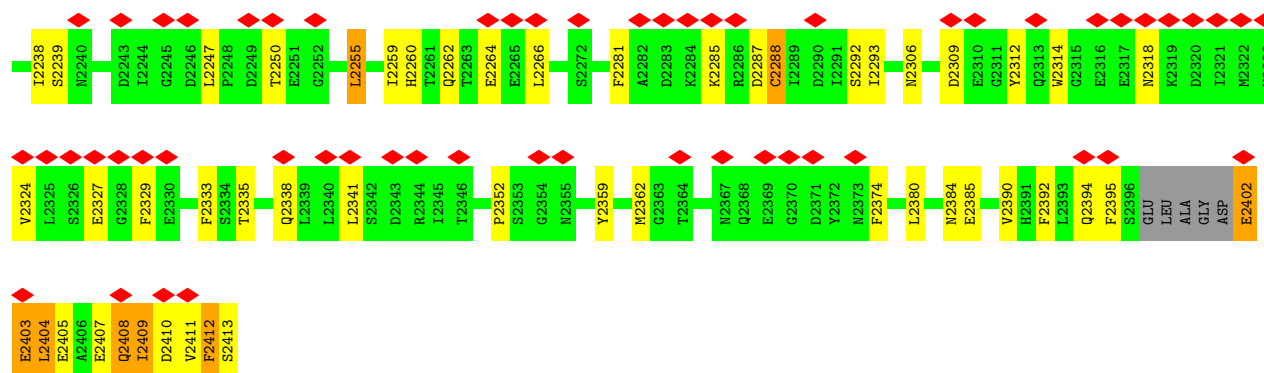
3 Residue-property plots

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

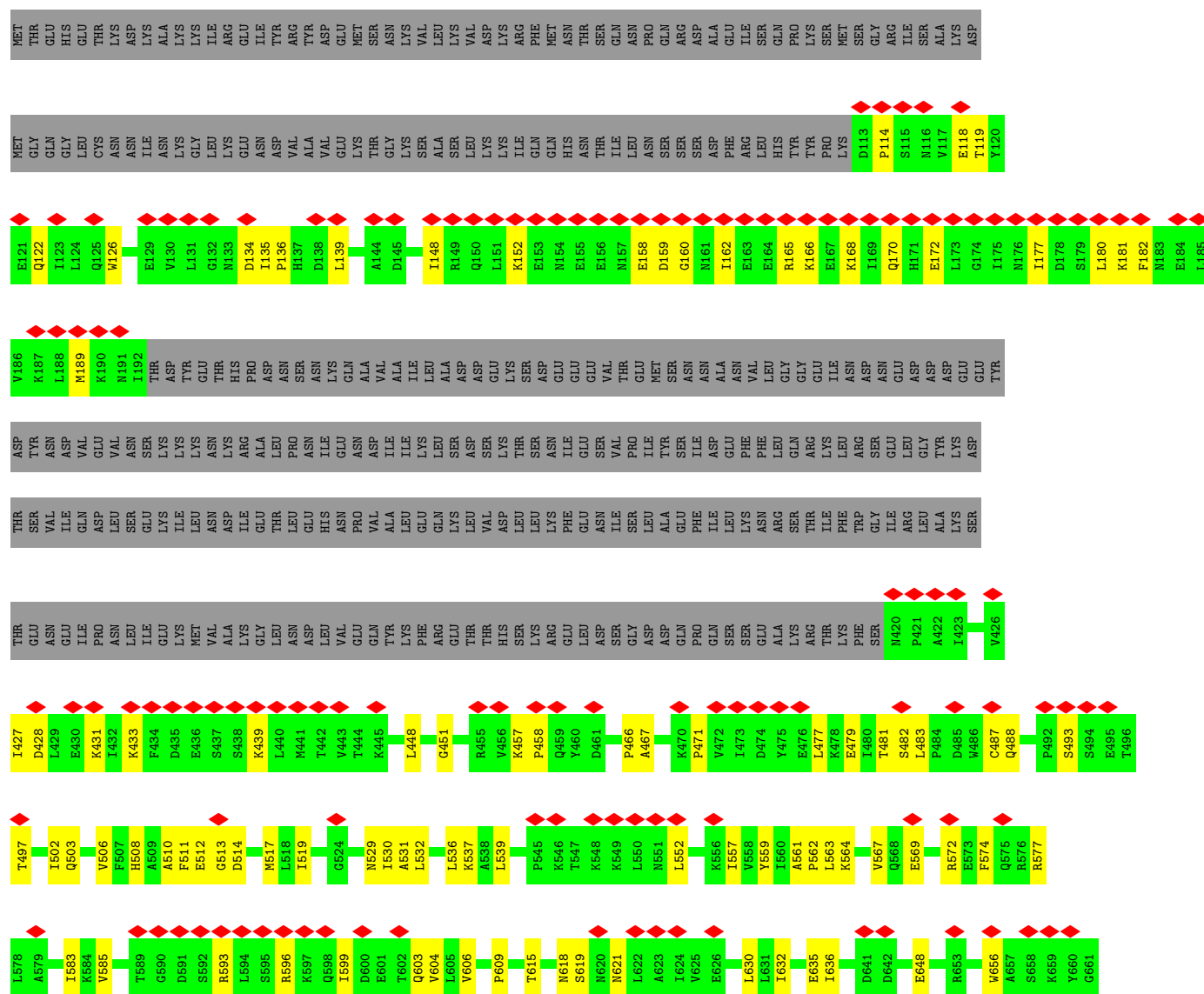
• Molecule 1: Pre-mRNA-splicing factor 8

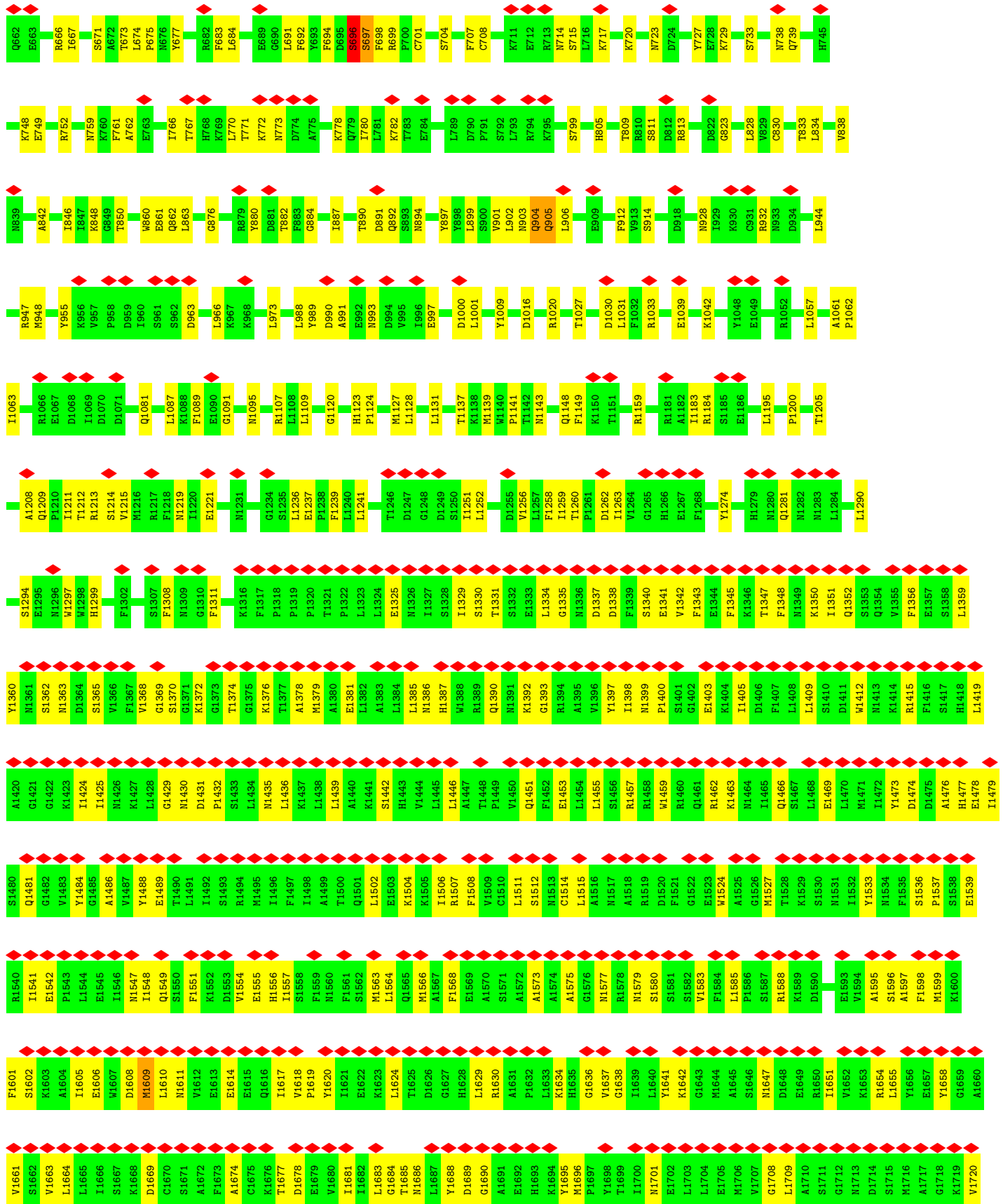


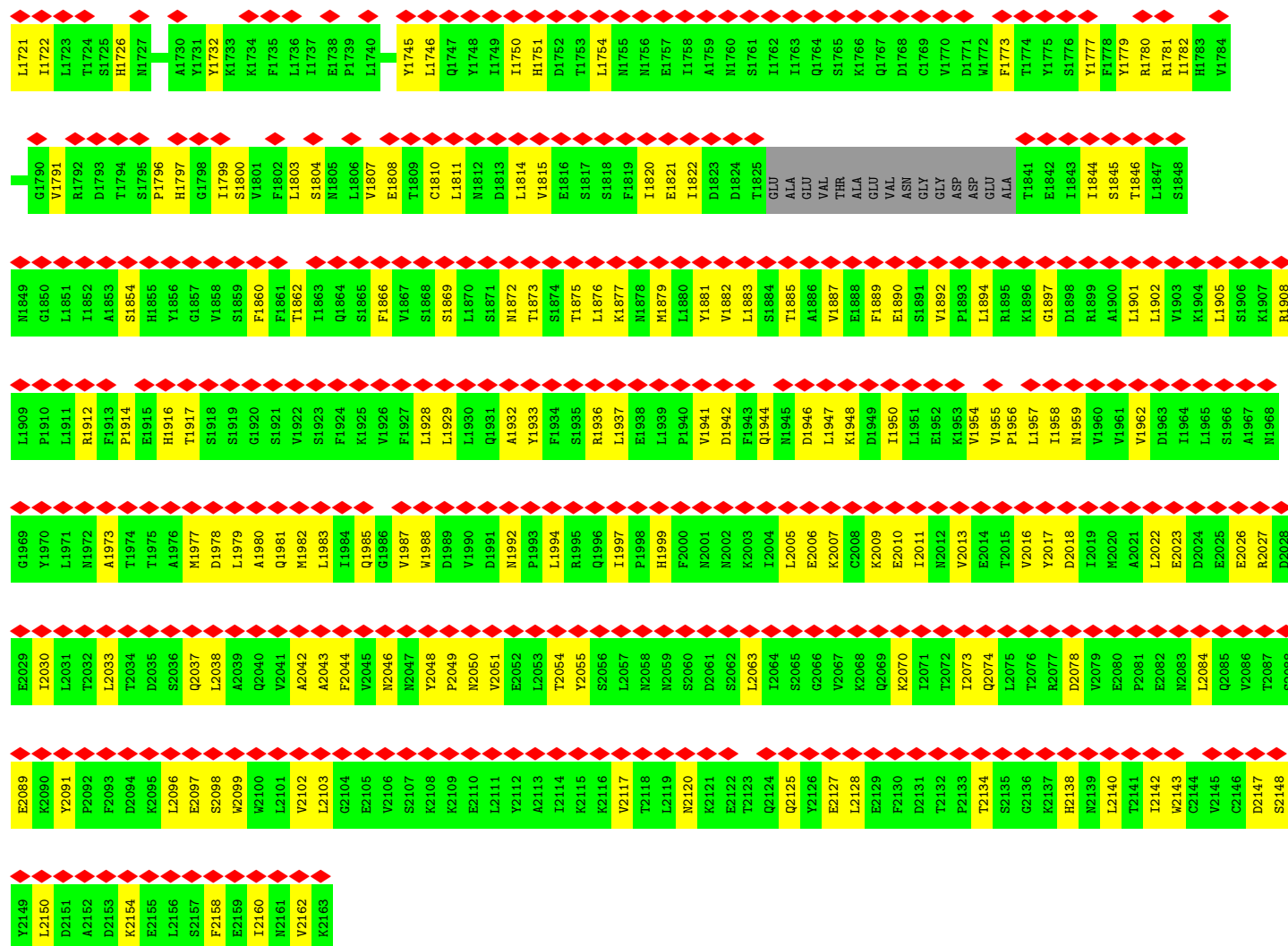




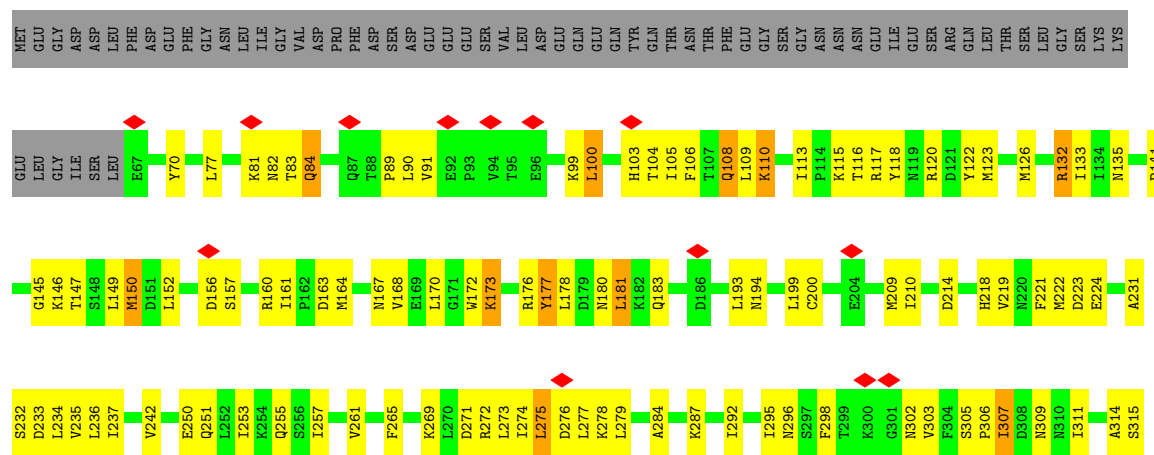
● Molecule 2: Pre-mRNA-splicing helicase BRR2



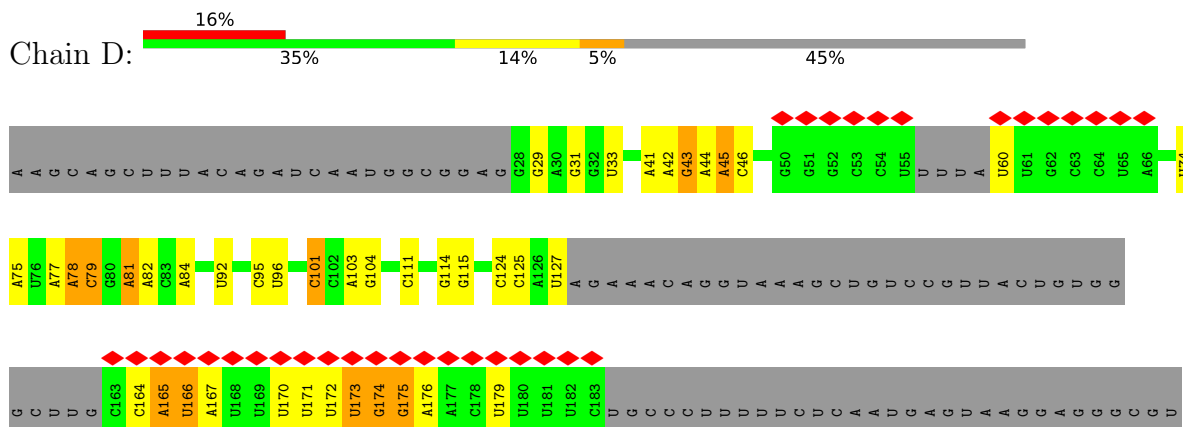




● Molecule 3: Pre-mRNA-splicing factor SNU114

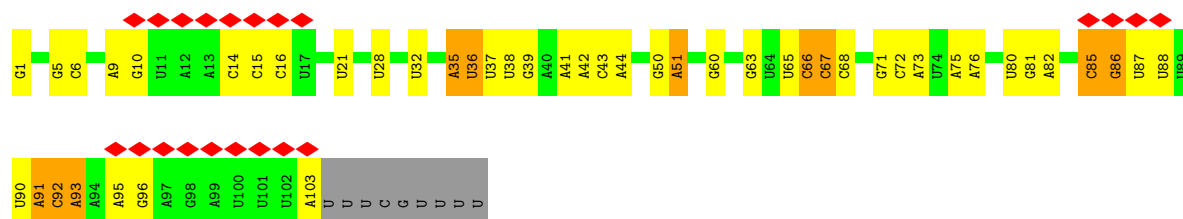


- Molecule 4: *Saccharomyces cerevisiae* strain CDRDR_sf_H chromosome VII sequence

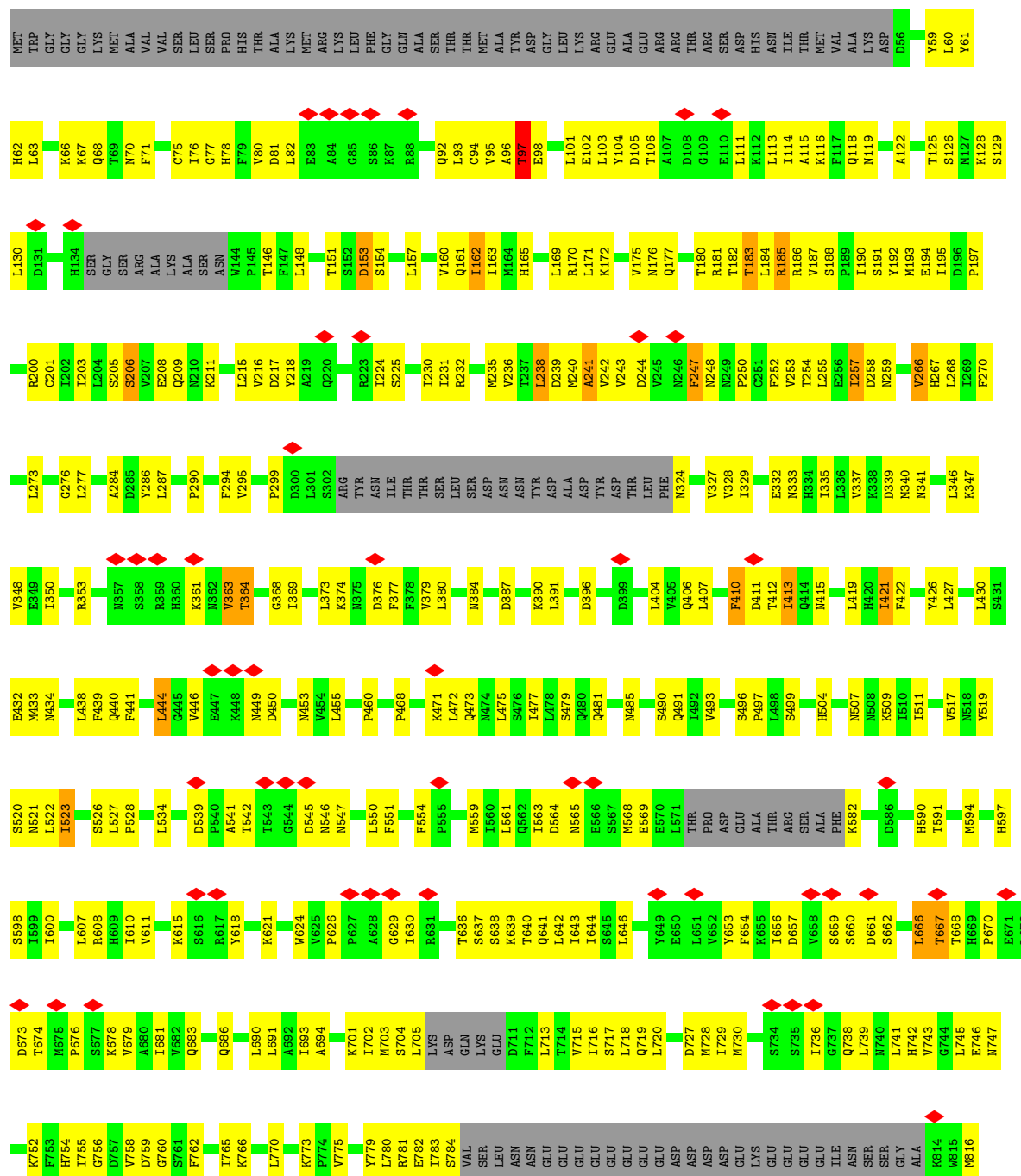


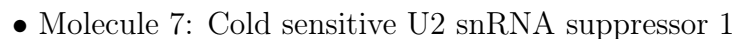
- Molecule 5: *Saccharomyces cerevisiae* strain T.52_2H chromosome XII sequence





• Molecule 6: Pre-mRNA-splicing factor RSE1

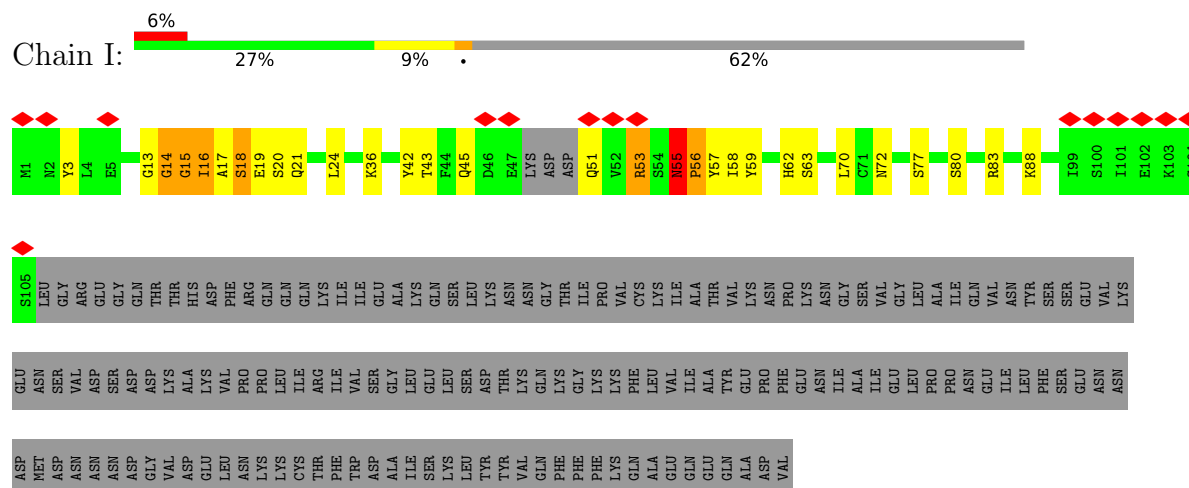




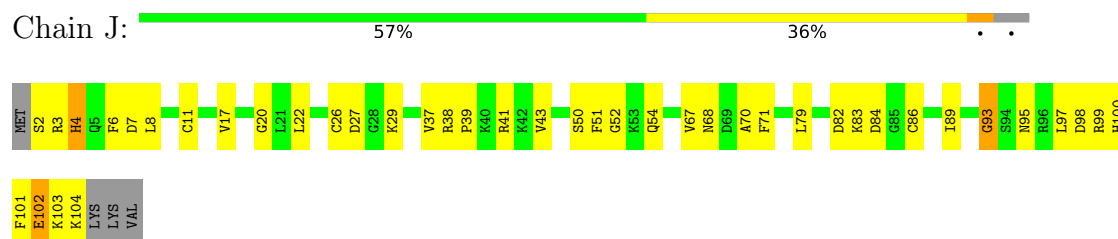
Chain H: 18% 13% . 65%



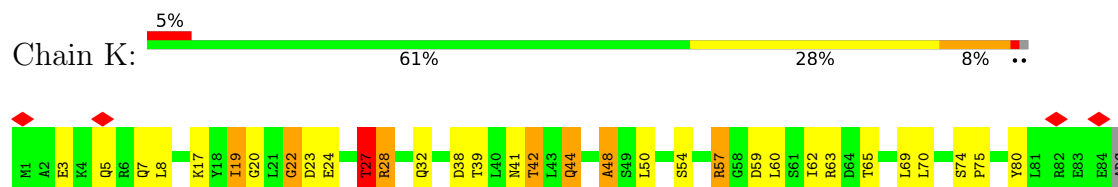
● Molecule 8: Pre-mRNA-splicing factor PRP11



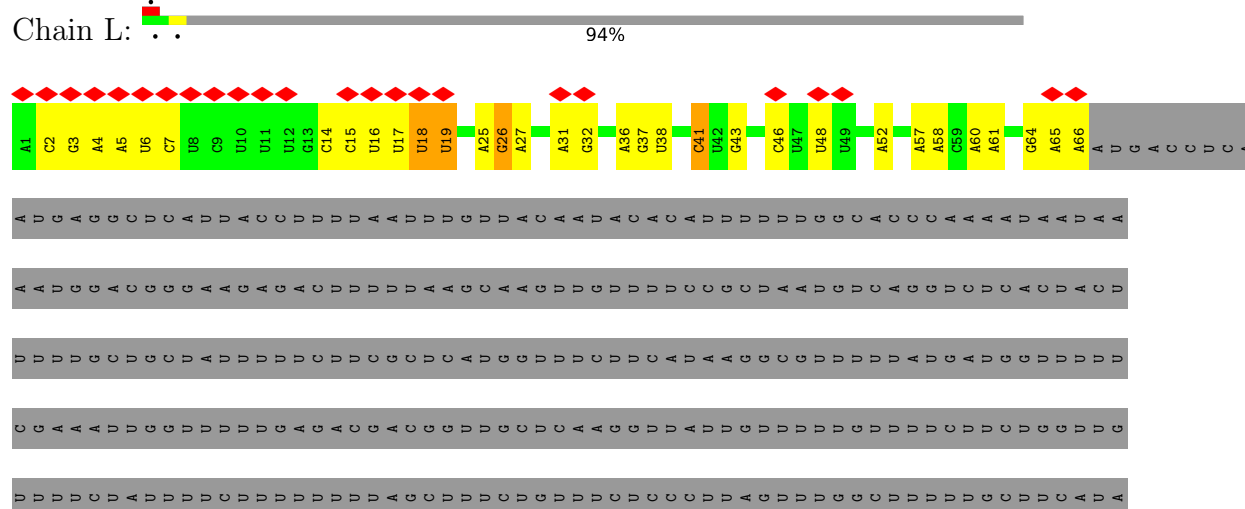
● Molecule 9: Pre-mRNA-splicing factor RDS3

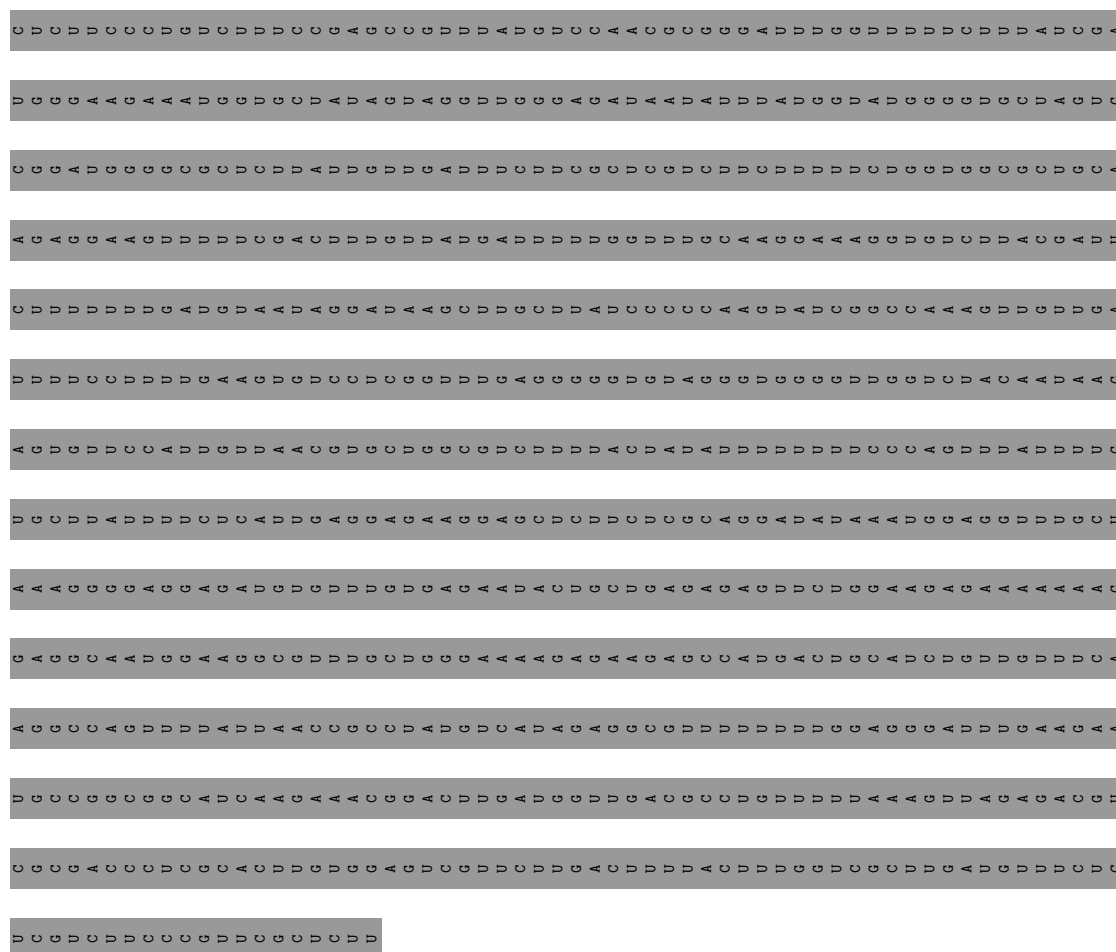


● Molecule 10: RDS3 complex subunit 10

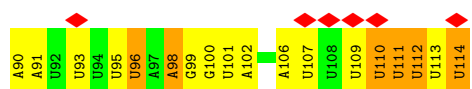


● Molecule 11: U2 snRNA

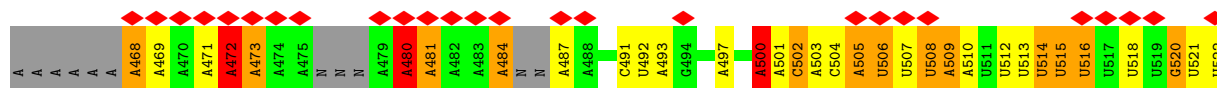
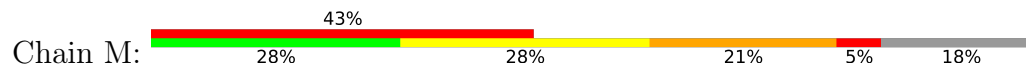




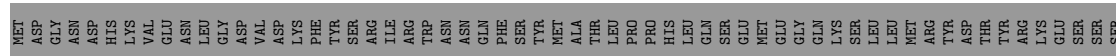
- Molecule 12: Pre-mRNA

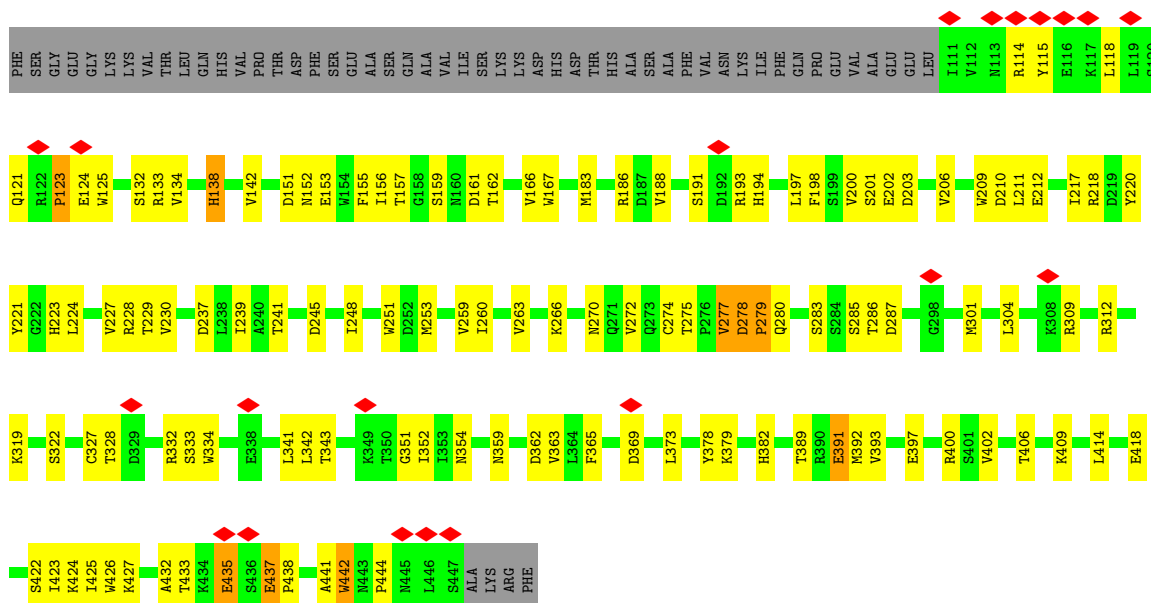


- Molecule 13: Pre-mRNA

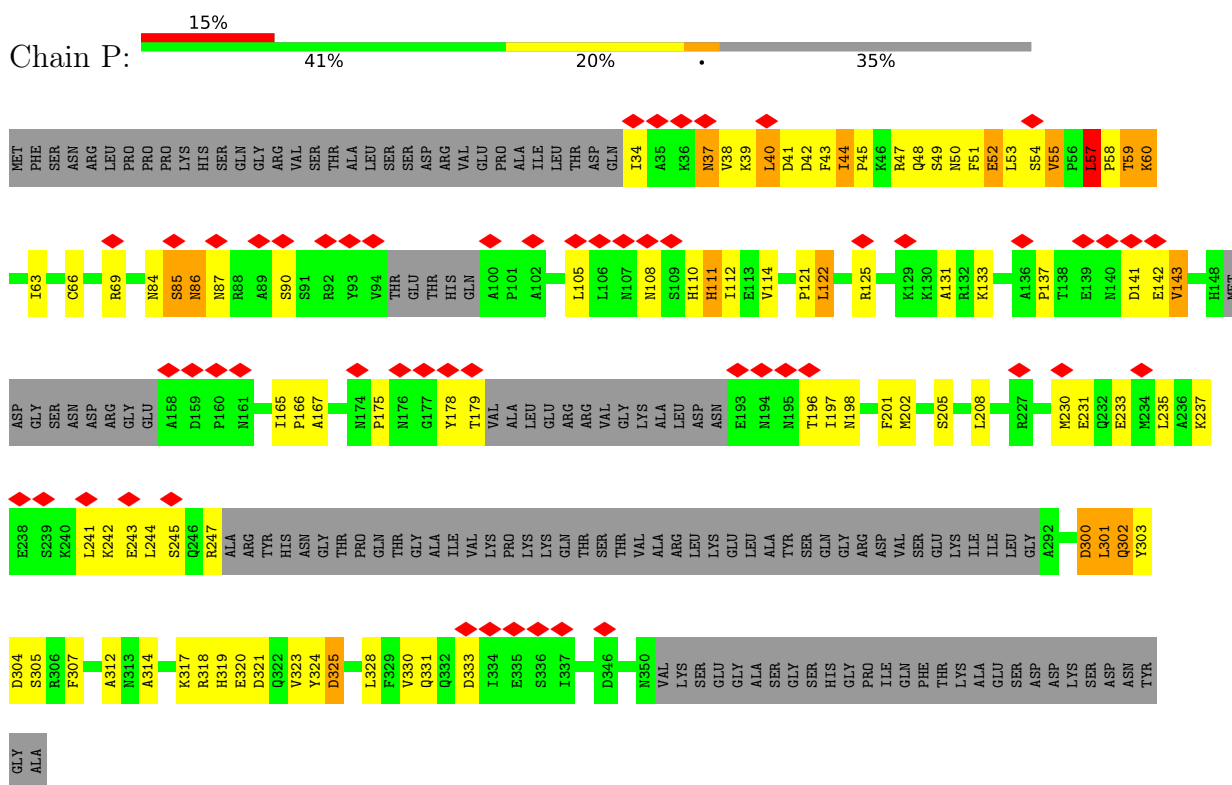


- Molecule 14: Pre-mRNA-splicing factor PRP46

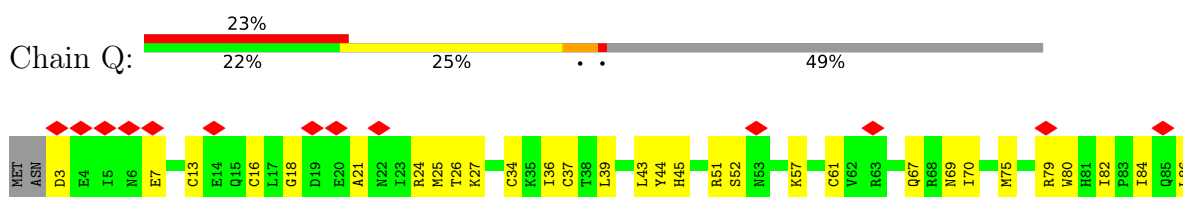


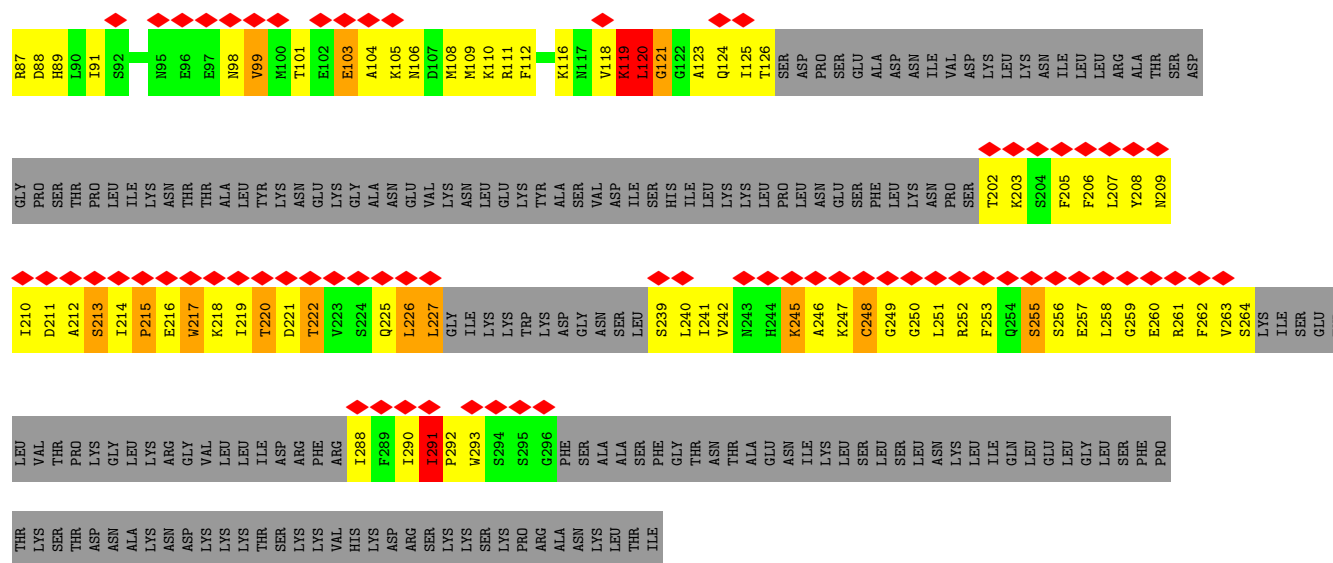


- Molecule 15: Pre-mRNA-processing protein 45

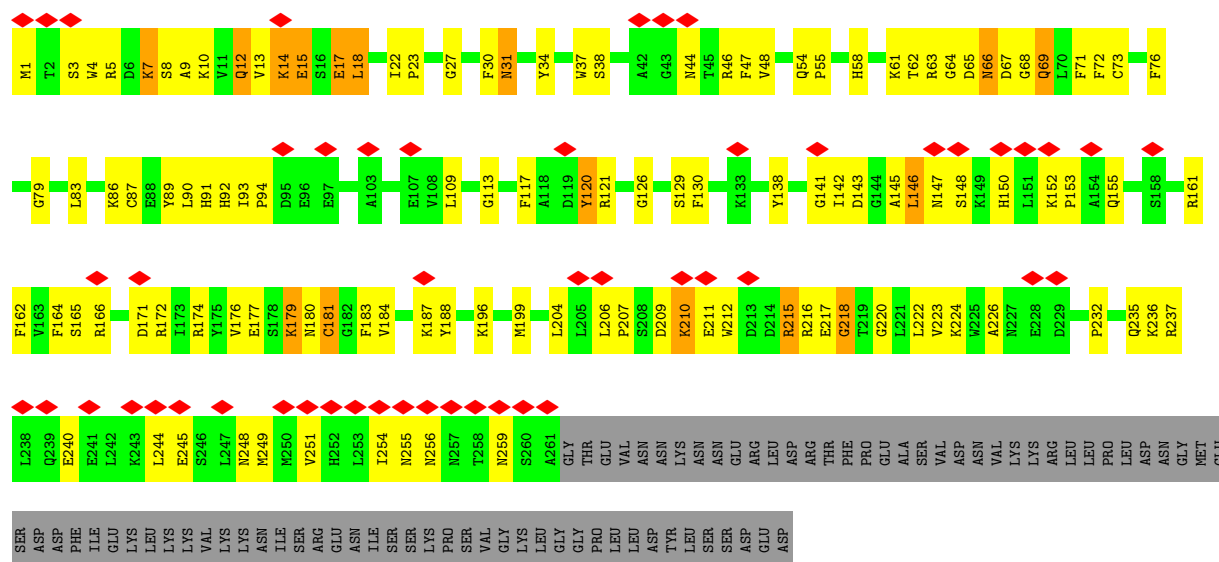


- Molecule 16: Pre-mRNA-splicing factor SLT11

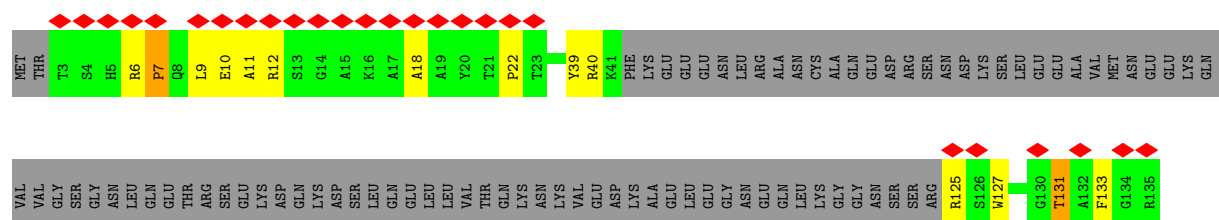


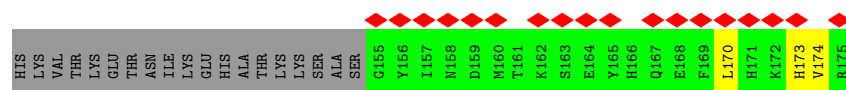


• Molecule 17: Pre-mRNA-splicing factor CWC2

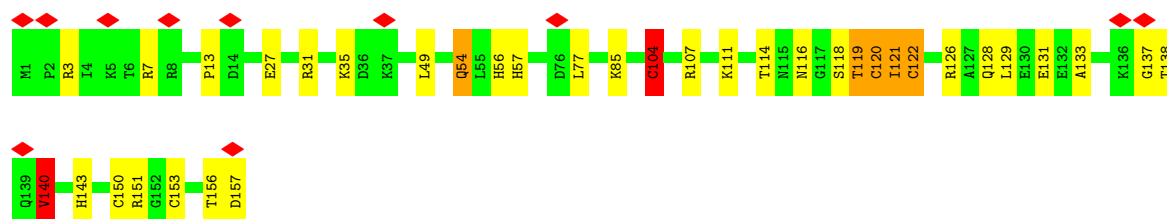
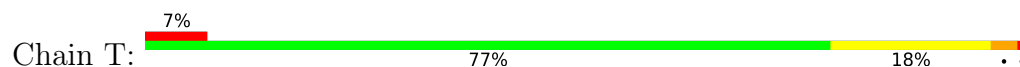


• Molecule 18: Pre-mRNA-splicing factor CWC15

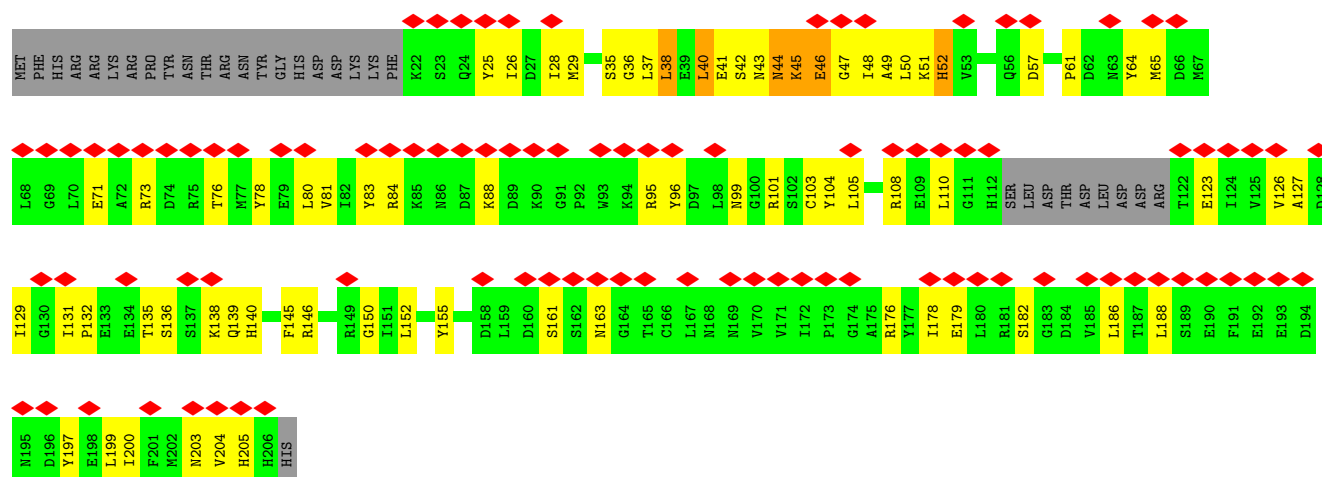




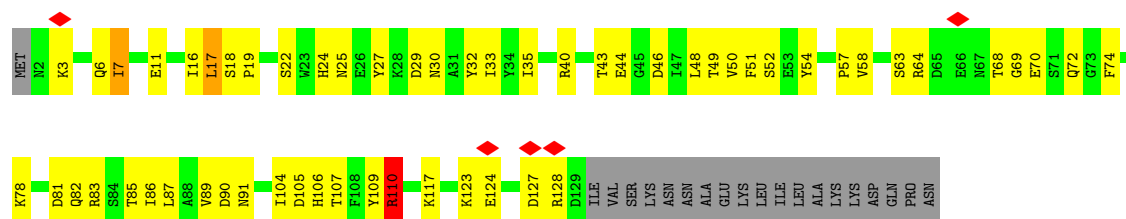
• Molecule 19: Pre-mRNA-splicing factor BUD31



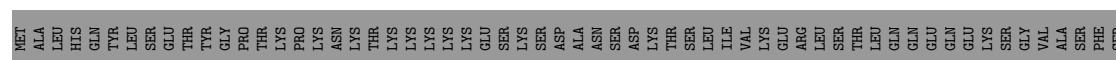
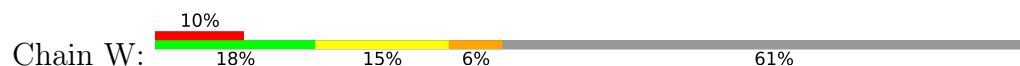
• Molecule 20: Pre-mRNA leakage protein 1

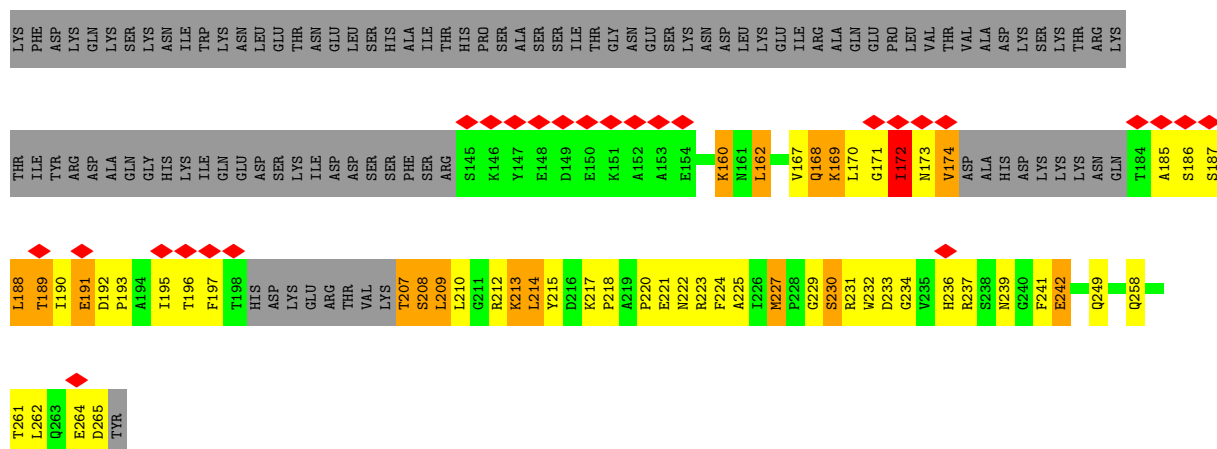


• Molecule 21: U2 snRNP component IST3

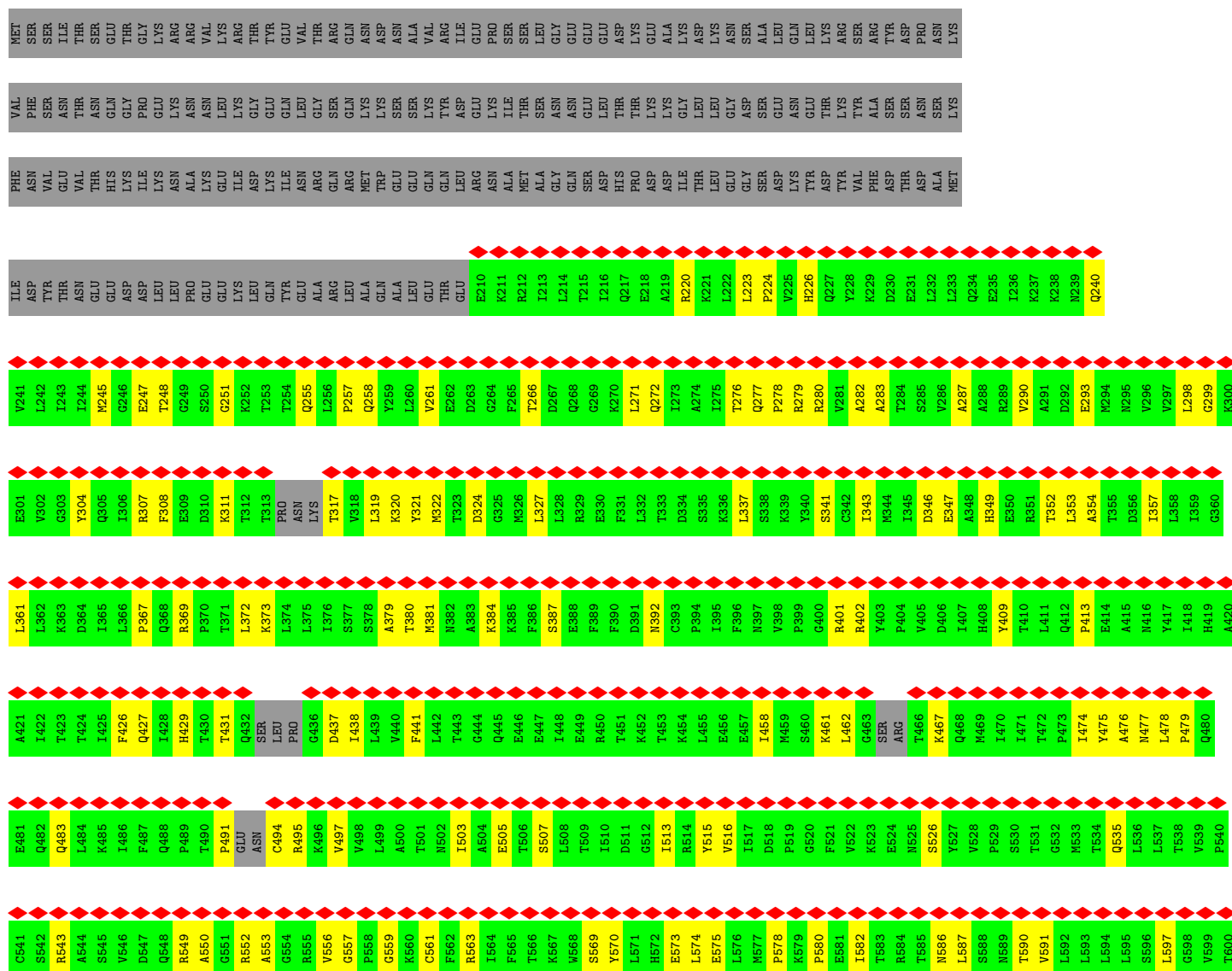


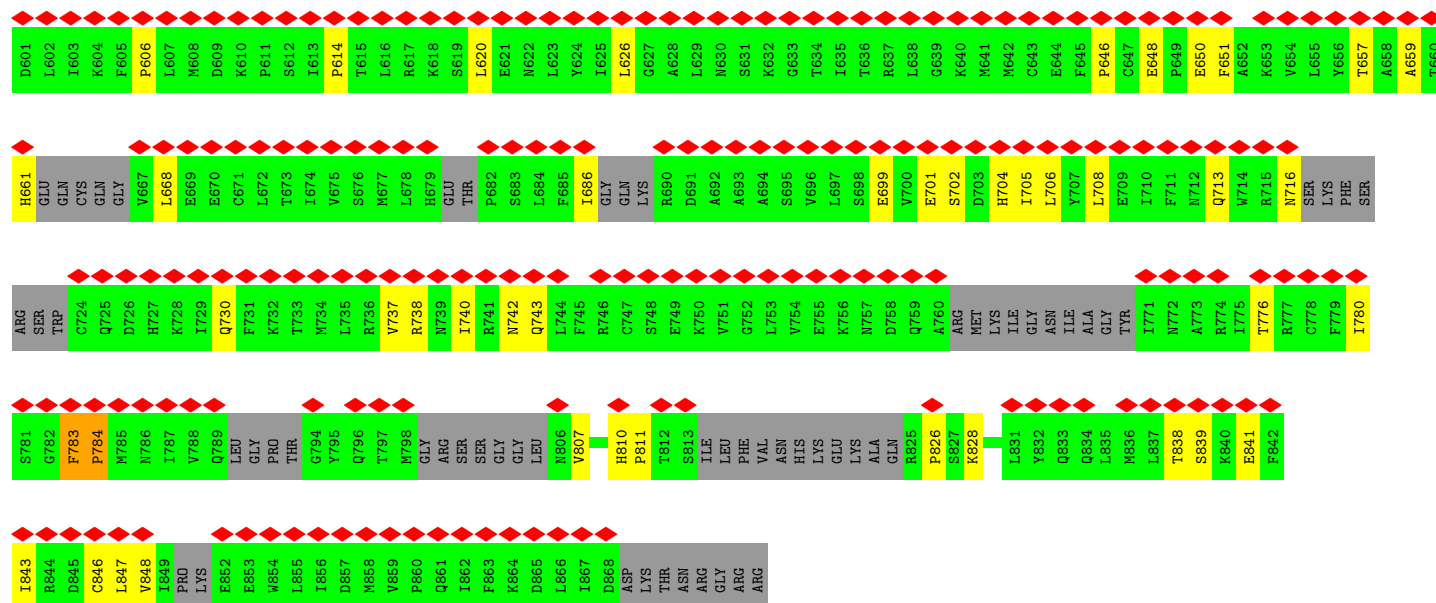
• Molecule 22: Pre-mRNA-splicing factor CWC26



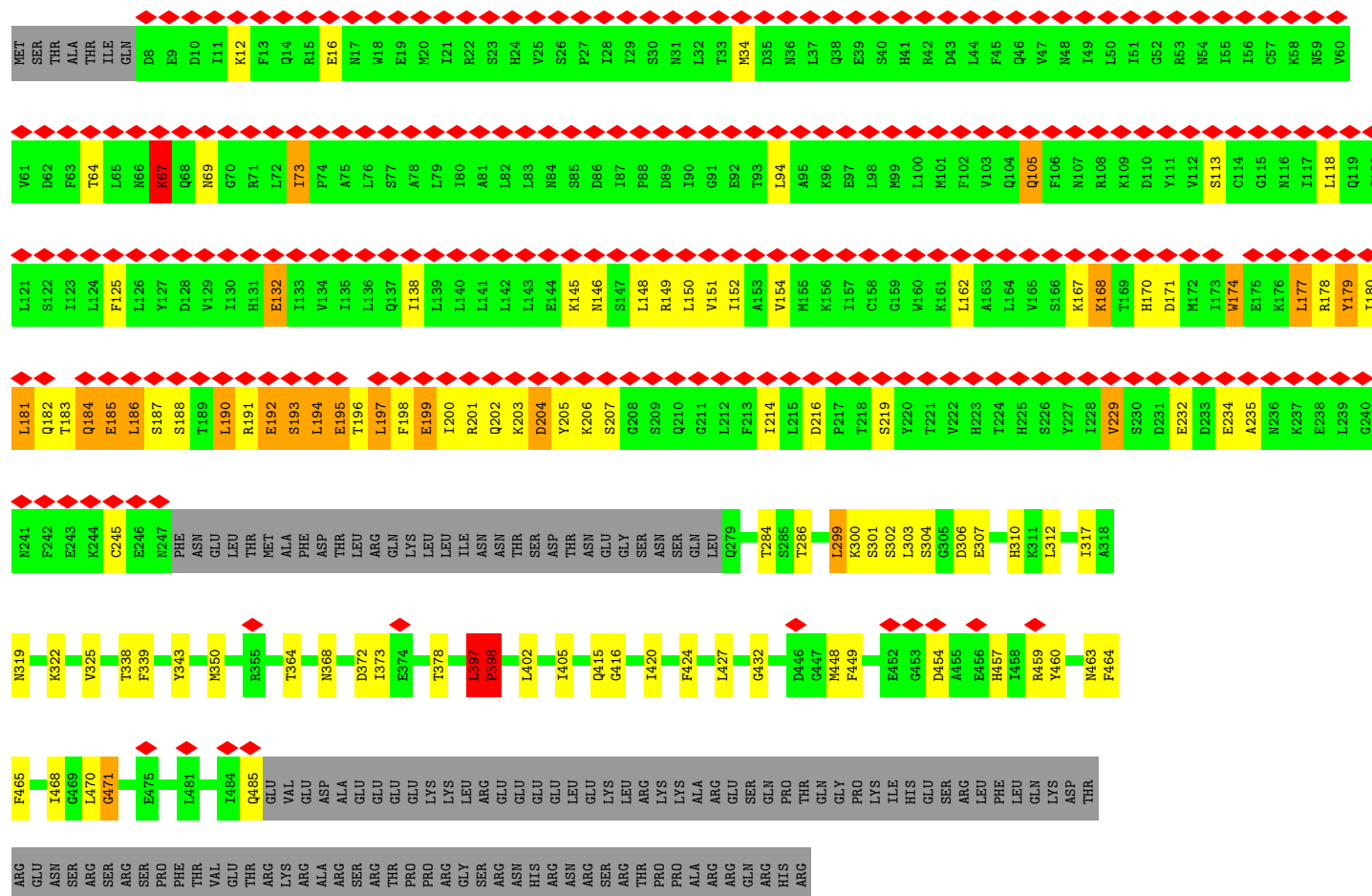
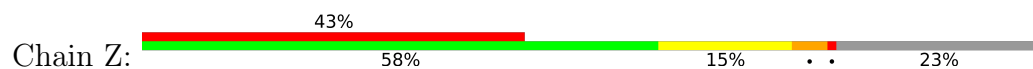


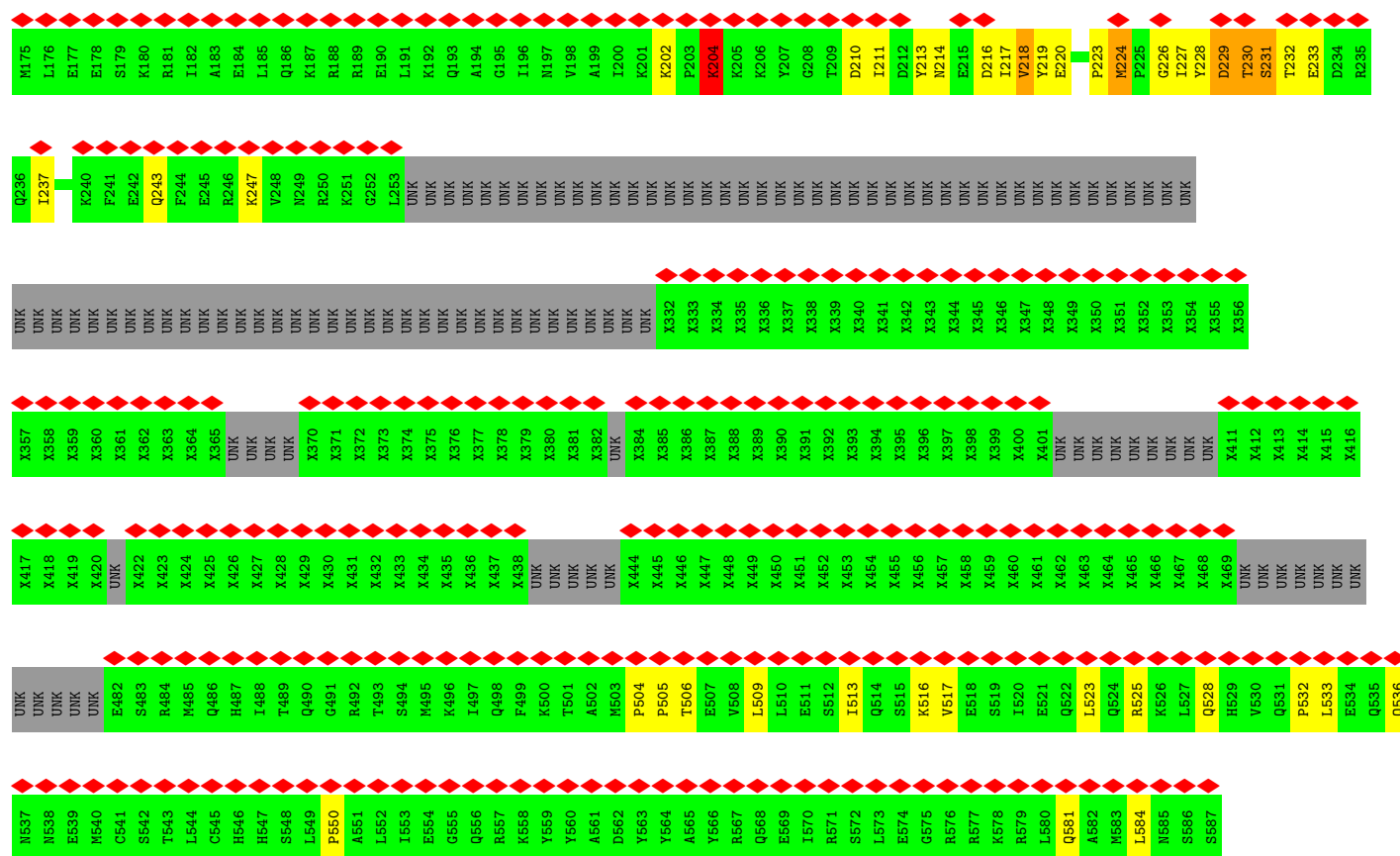
• Molecule 23: Pre-mRNA-splicing factor ATP-dependent RNA helicase-like protein PRP2



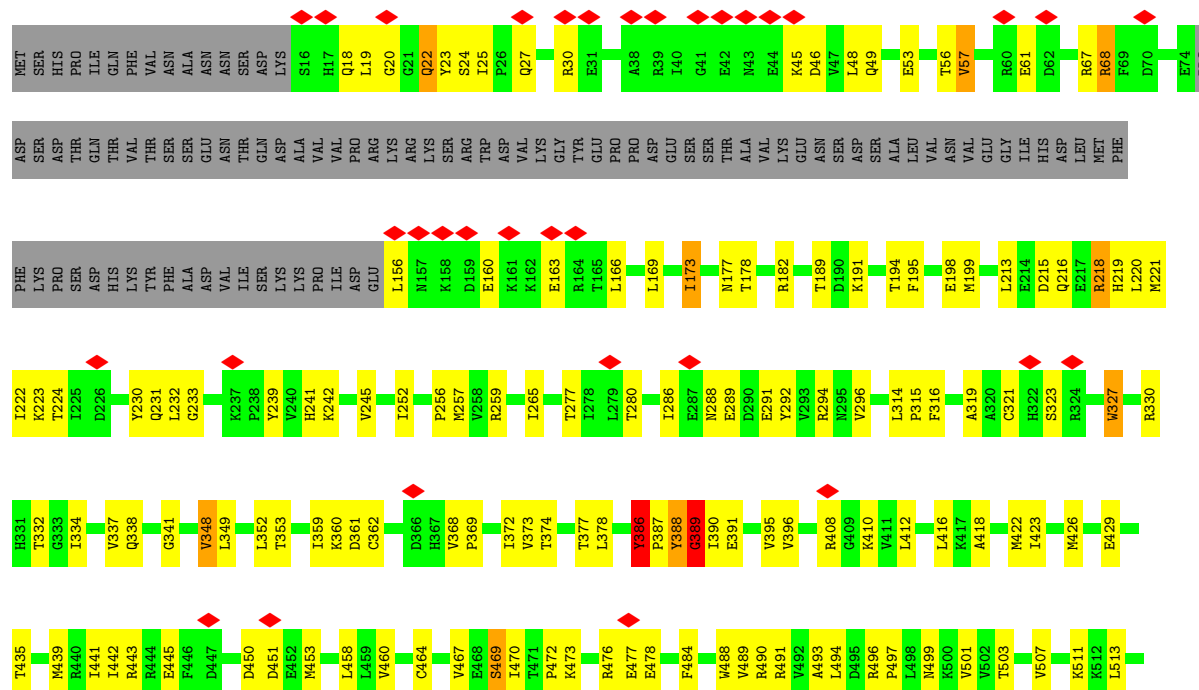


• Molecule 24: Pre-mRNA-splicing factor CWC22

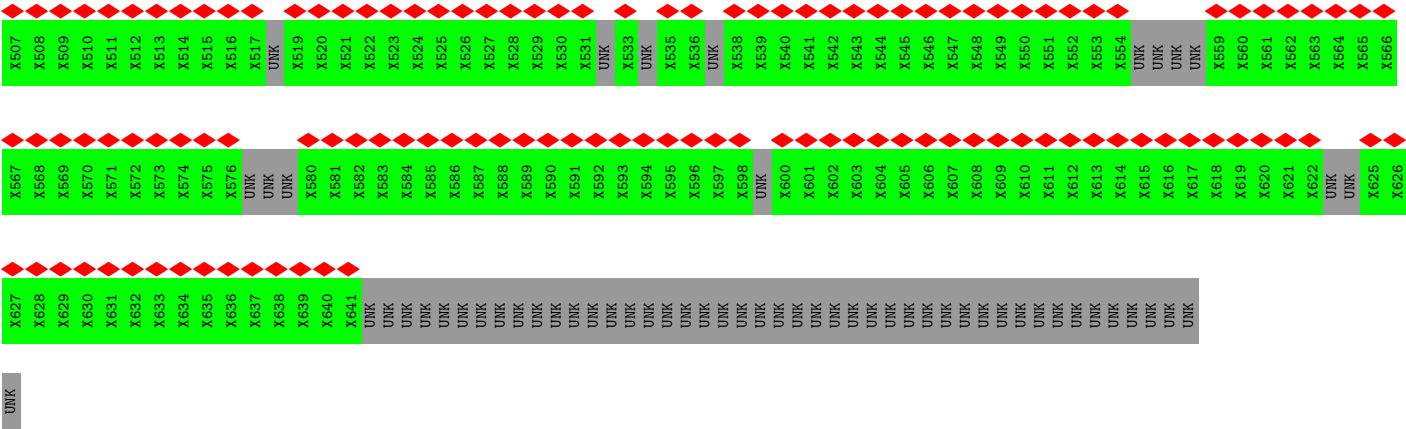




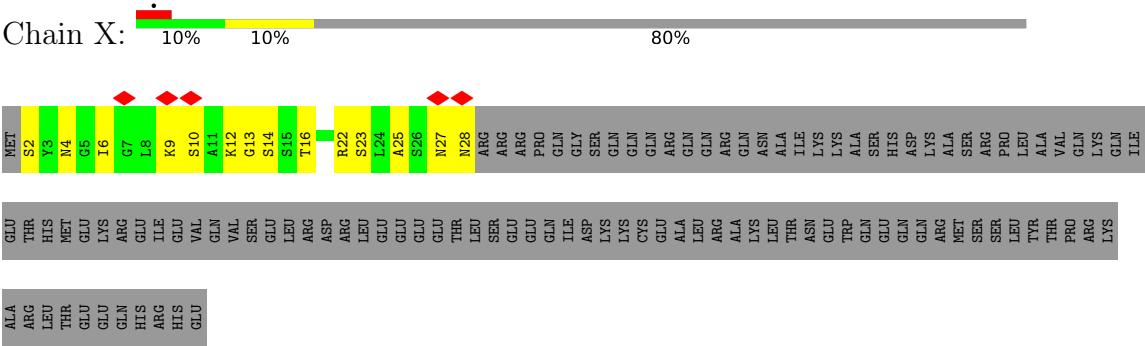
• Molecule 28: U2 snRNP component HSH155



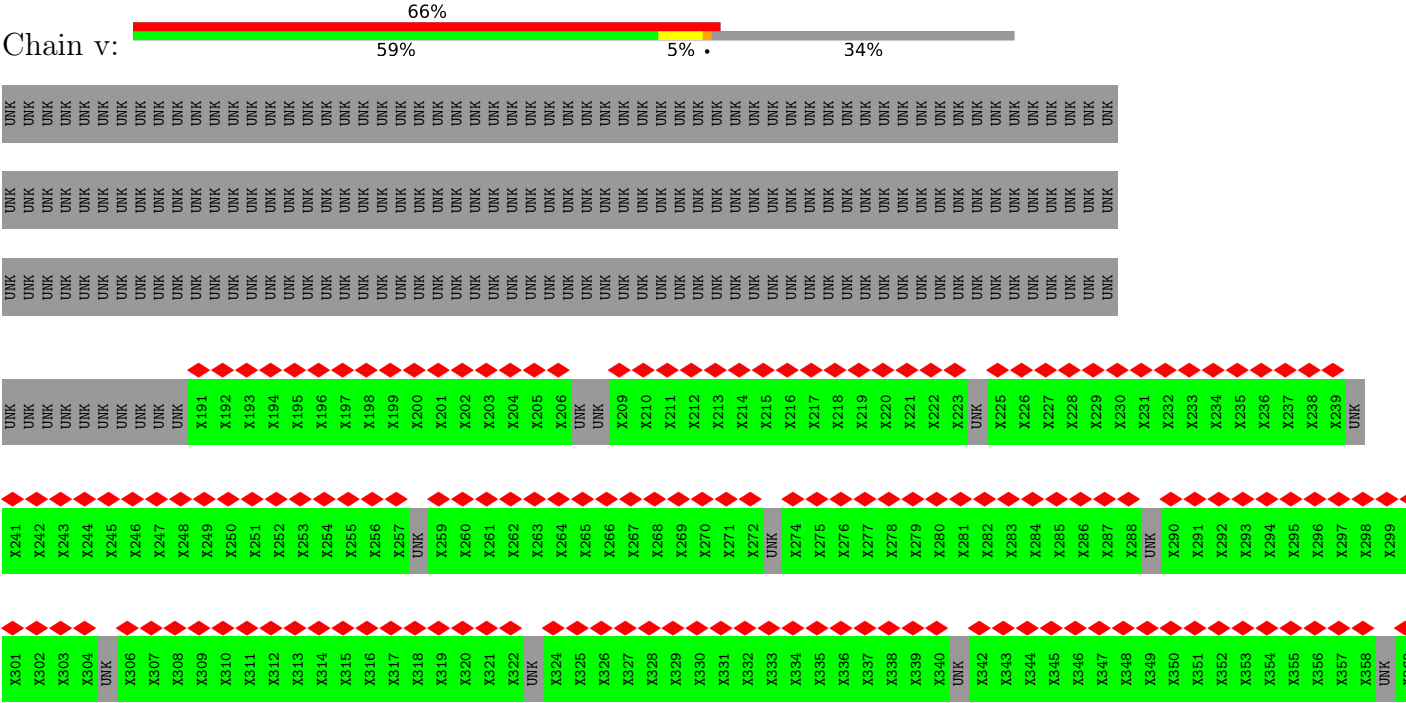


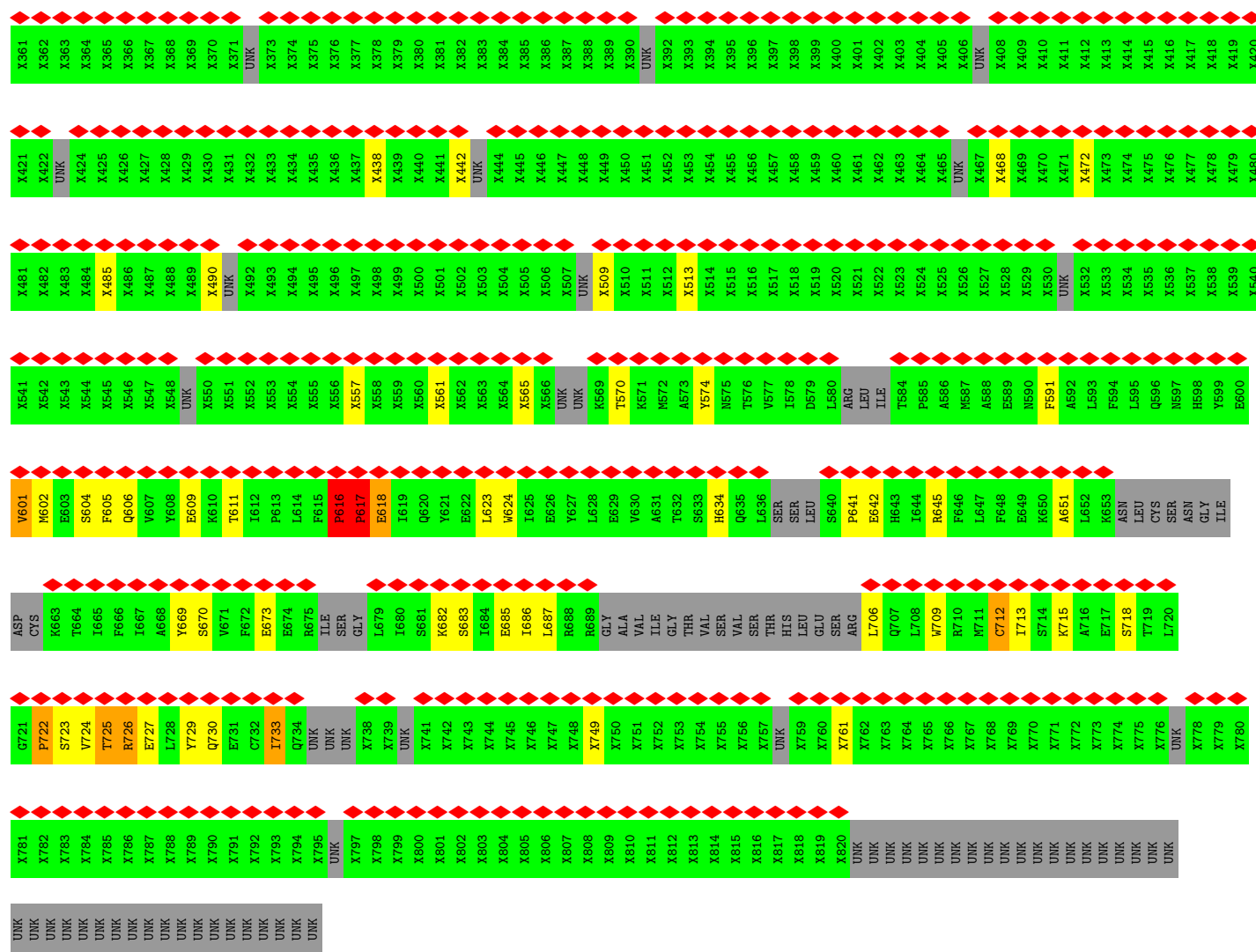


• Molecule 30: Pre-mRNA-splicing factor CWC21

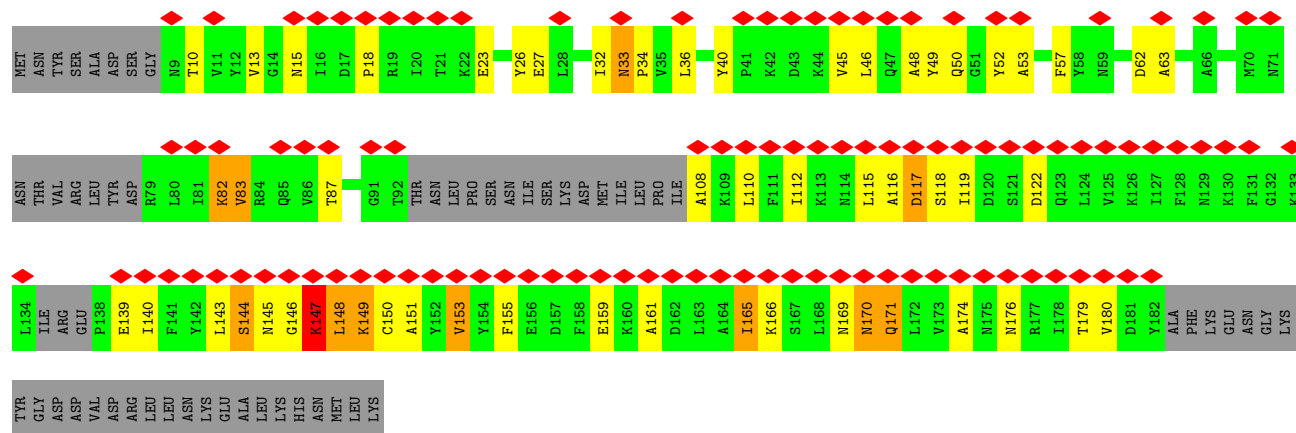


• Molecule 31: Pre-mRNA-splicing factor SYF1

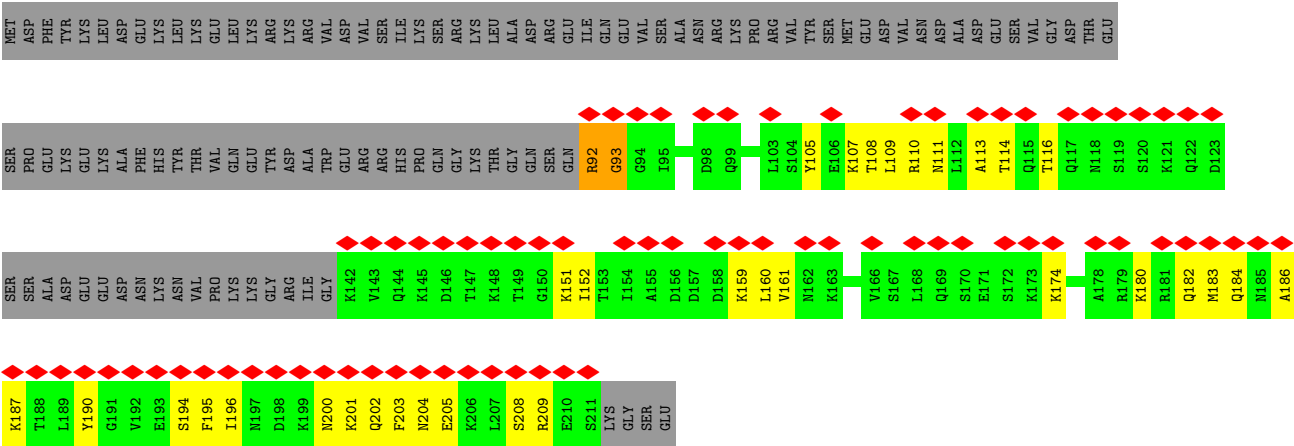
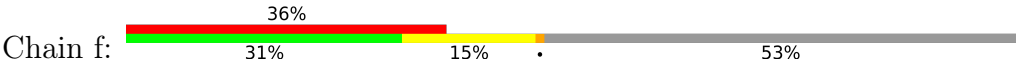




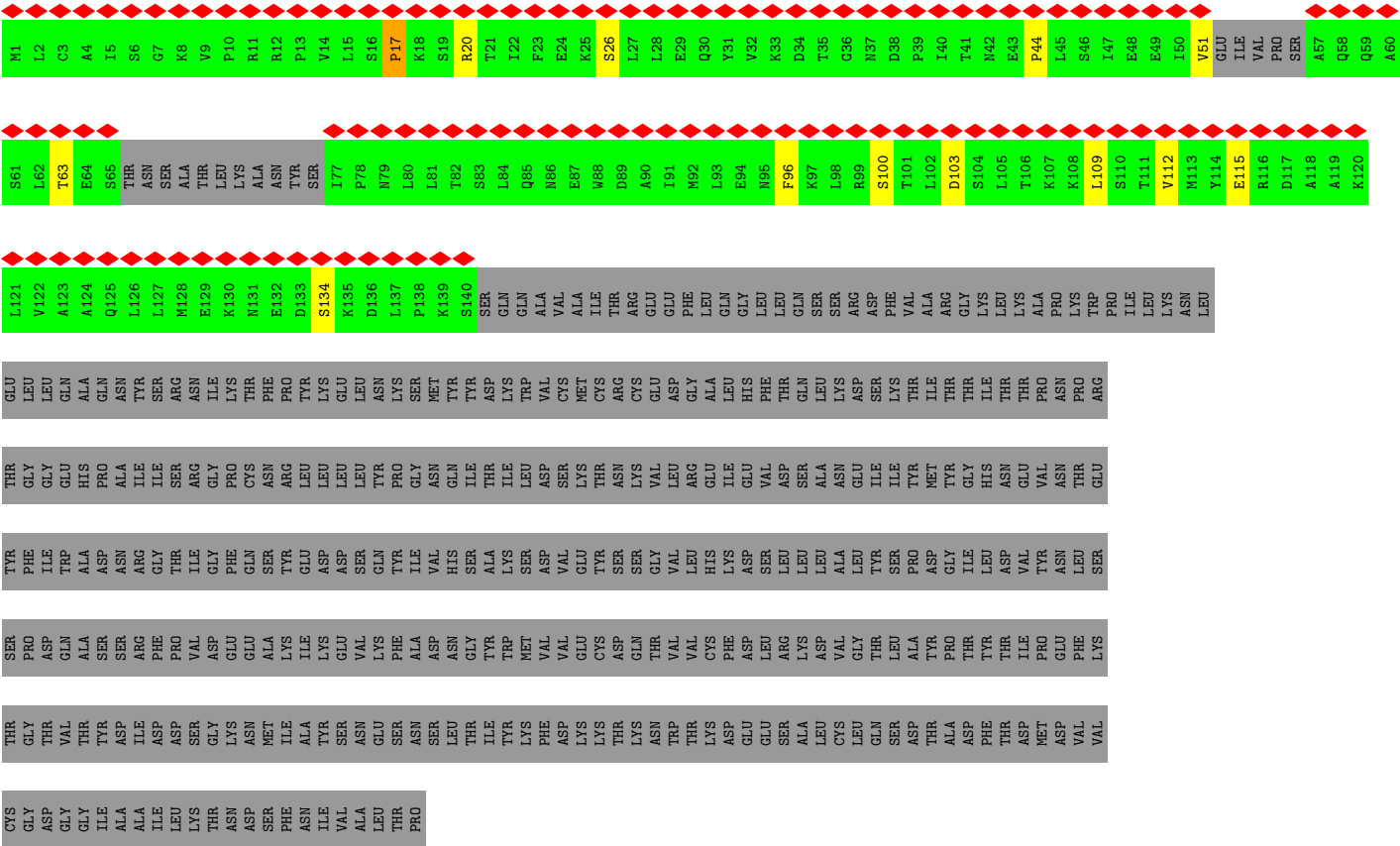
• Molecule 32: Protein HSH49



• Molecule 33: Pre-mRNA-splicing factor SYF2

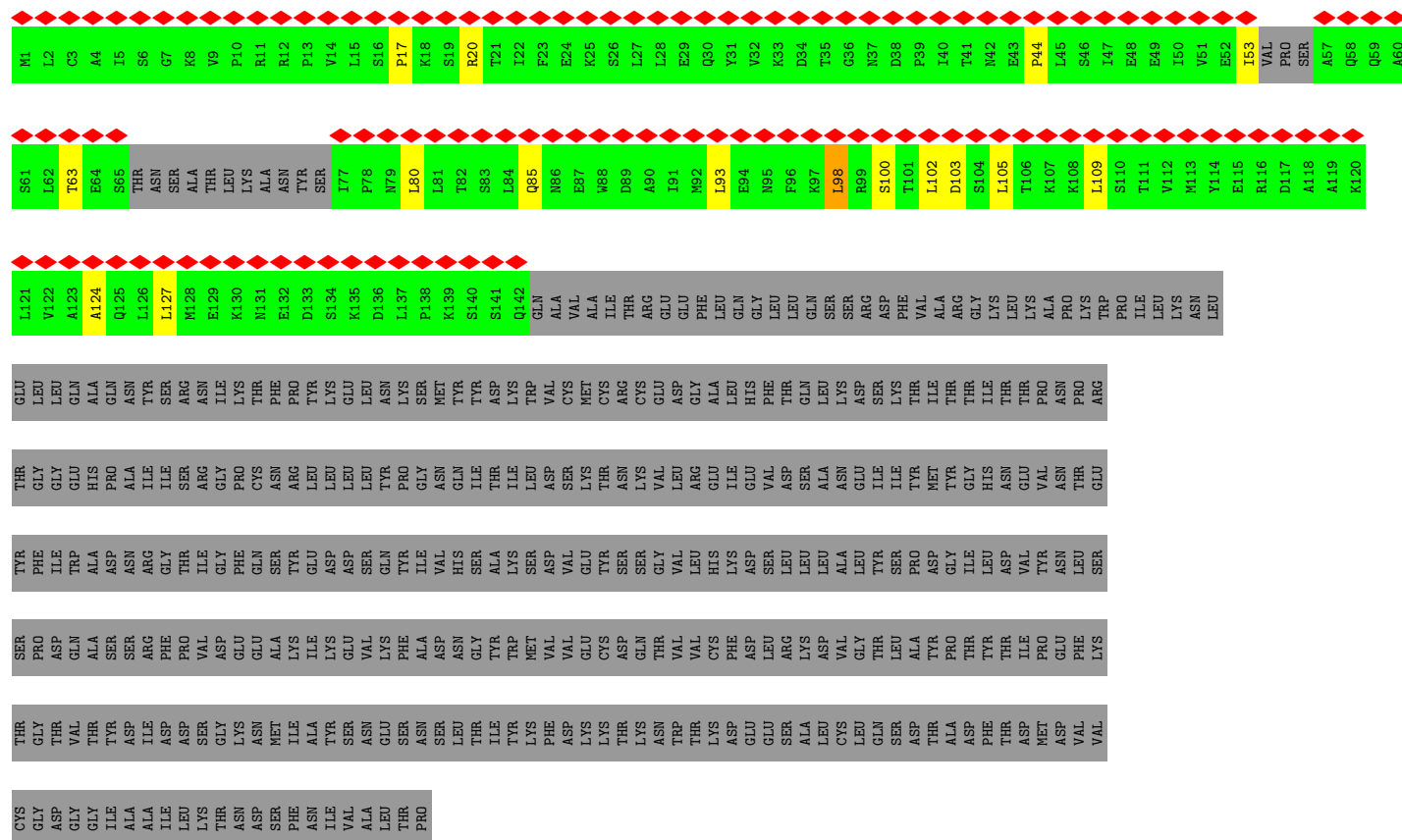


• Molecule 34: Pre-mRNA-processing factor 19

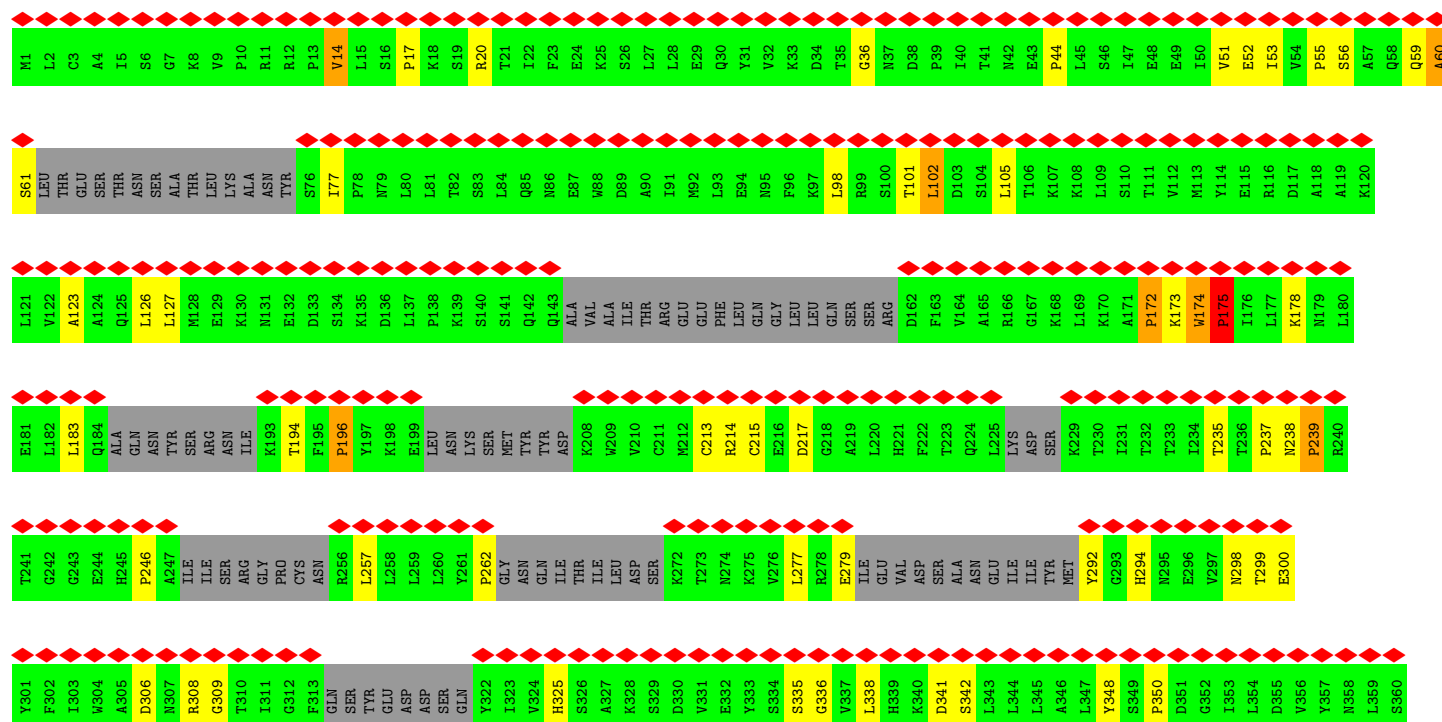
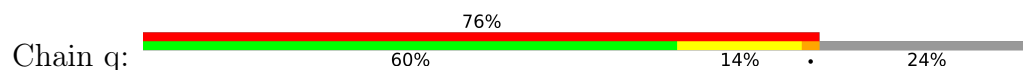


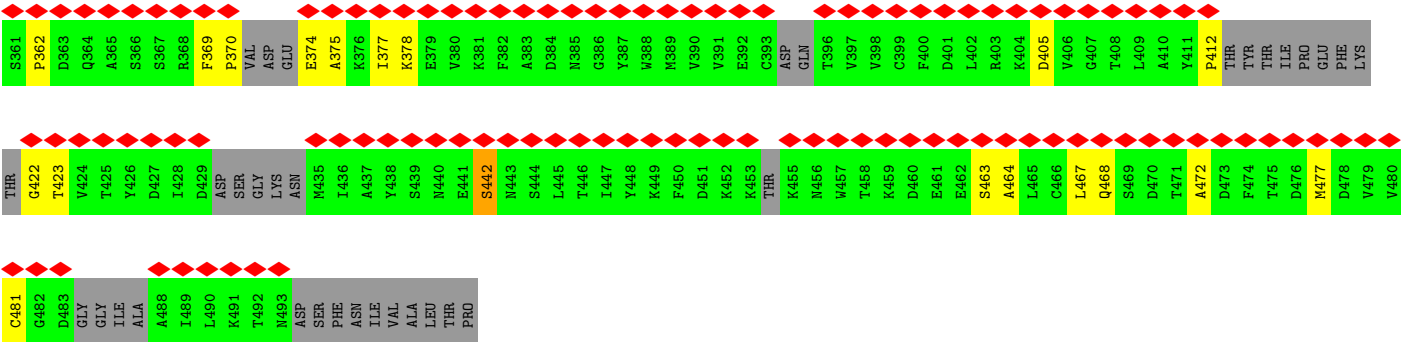
• Molecule 34: Pre-mRNA-processing factor 19



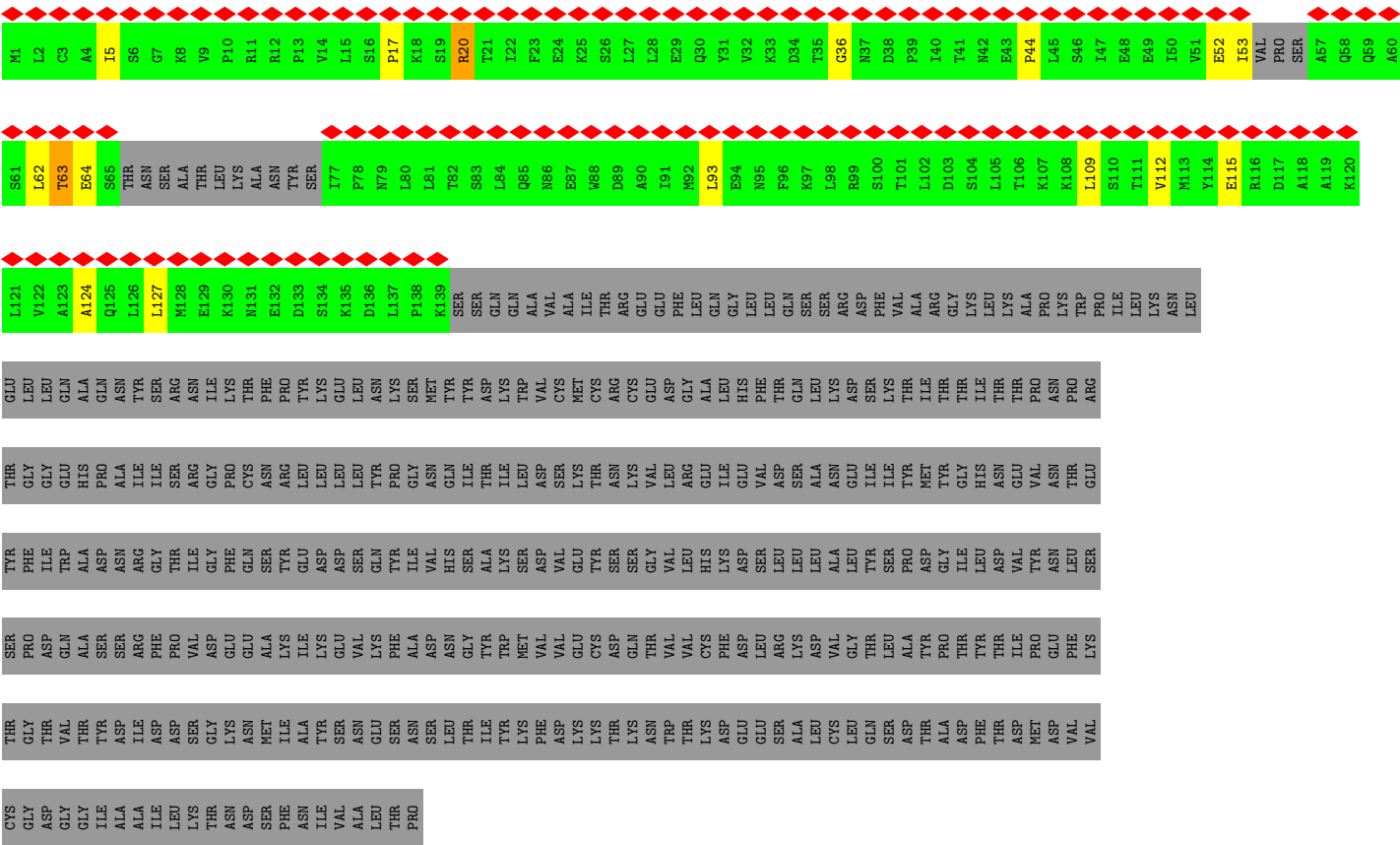


• Molecule 34: Pre-mRNA-processing factor 19

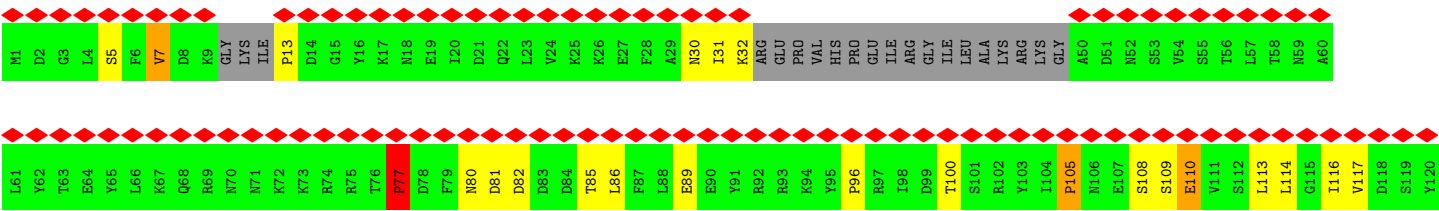
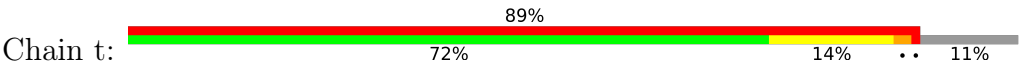


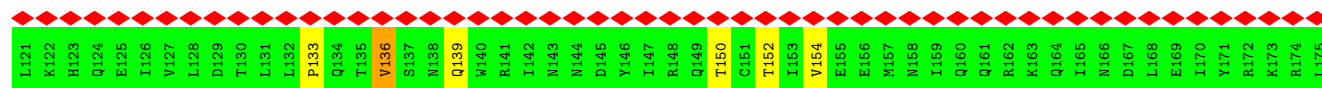


• Molecule 34: Pre-mRNA-processing factor 19



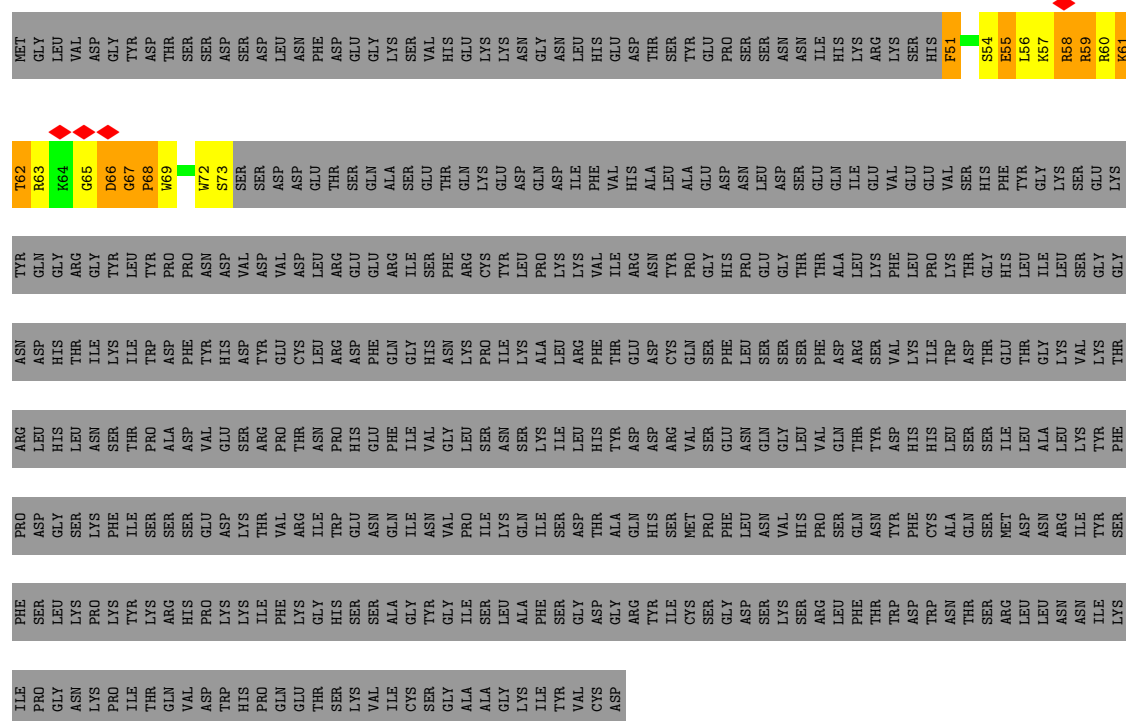
• Molecule 35: Pre-mRNA-splicing factor SNT309





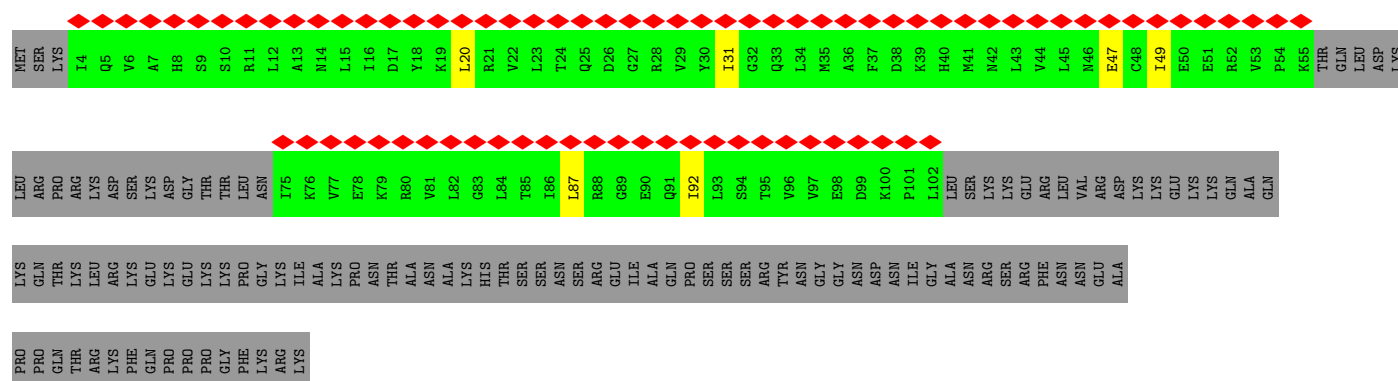
• Molecule 36: Pre-mRNA-processing factor 17

Chain n: 95%



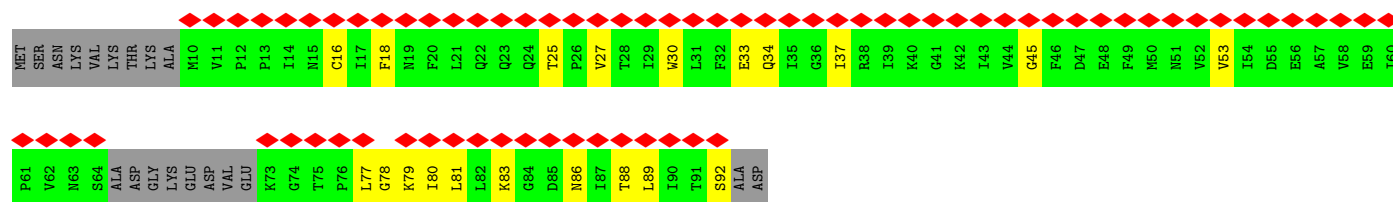
• Molecule 37: Small nuclear ribonucleoprotein-associated protein B

Chain k: 41%
38% 59%

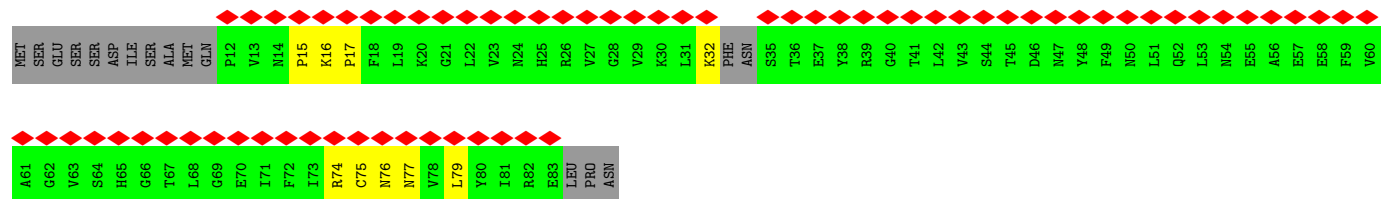
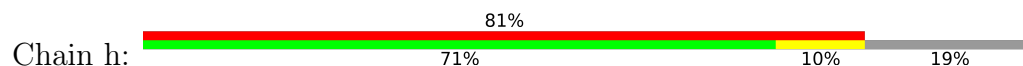


• Molecule 38: Small nuclear ribonucleoprotein E

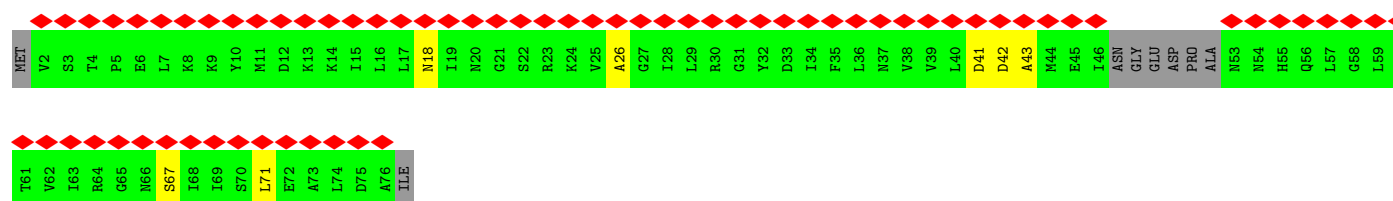
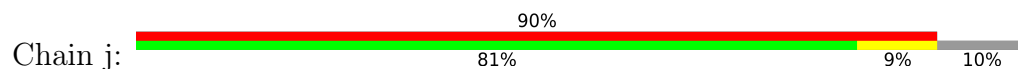
Chain i: 79%
59% 21% 20%



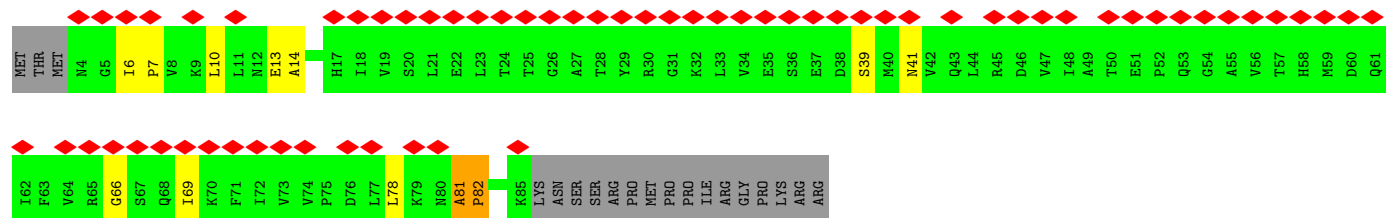
• Molecule 39: Small nuclear ribonucleoprotein F



• Molecule 40: Small nuclear ribonucleoprotein G



• Molecule 41: Small nuclear ribonucleoprotein Sm D3

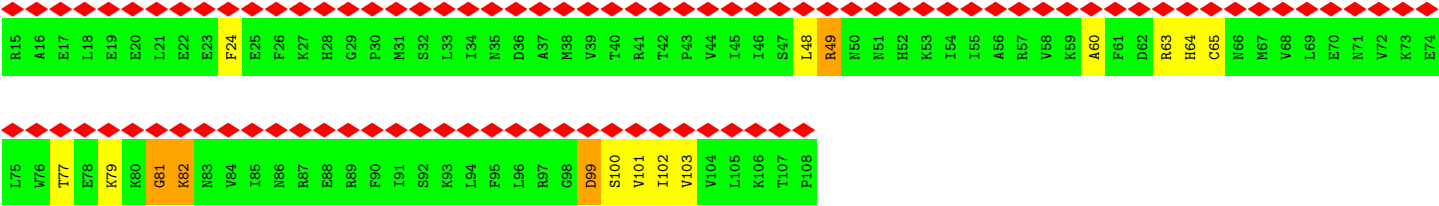
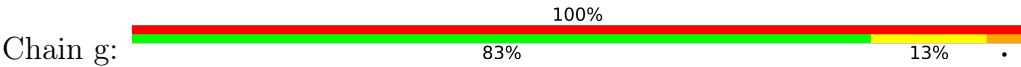


• Molecule 42: Small nuclear ribonucleoprotein Sm D1



GLN
ILE
ALA
ASN
ASP
PRO
SER
LYS
LYS
ARG
ARG
ARG
ASP
PHE
GLY
ALA
PRO
ALA
ALA
ASN
LYS
ARG
PRO
ARG
ARG
GLY
LEU

● Molecule 43: Small nuclear ribonucleoprotein Sm D2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	77312	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	4.7	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.285	Depositor
Minimum map value	-0.174	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0405	Depositor
Map size ($\text{\AA}$)	522.4, 522.4, 522.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3060001, 1.3060001, 1.3060001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, ADP, MG, GTP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.94	9/18560 (0.0%)	0.89	19/25158 (0.1%)
2	B	0.45	0/14812	0.57	0/20077
3	C	0.65	1/7162 (0.0%)	0.74	6/9698 (0.1%)
4	D	0.51	0/2747	0.67	0/4267
5	E	0.52	0/2452	0.65	0/3817
6	F	0.99	11/9564 (0.1%)	0.97	7/12963 (0.1%)
7	H	0.92	2/1281 (0.2%)	1.09	6/1727 (0.3%)
8	I	0.97	1/812 (0.1%)	0.95	3/1081 (0.3%)
9	J	1.04	0/827	0.98	1/1105 (0.1%)
10	K	1.09	2/702 (0.3%)	1.00	1/939 (0.1%)
11	L	0.50	0/1547	0.67	0/2404
12	N	0.47	0/579	0.65	0/897
13	M	0.50	1/1183 (0.1%)	0.94	9/1833 (0.5%)
14	O	0.92	0/2704	0.86	3/3676 (0.1%)
15	P	0.64	0/2008	0.84	5/2703 (0.2%)
16	Q	0.56	1/1496 (0.1%)	0.80	4/2014 (0.2%)
17	R	0.63	0/2135	0.83	3/2871 (0.1%)
18	S	0.57	0/592	0.72	0/790
19	T	0.79	1/1315 (0.1%)	0.84	0/1759
20	U	0.40	0/1424	0.63	0/1922
21	V	0.84	0/1071	0.87	2/1445 (0.1%)
22	W	0.76	1/856 (0.1%)	1.01	2/1149 (0.2%)
23	Y	0.49	0/4085	0.67	3/5499 (0.1%)
24	Z	0.79	2/3712 (0.1%)	1.02	5/5004 (0.1%)
25	a	0.76	0/1010	0.83	0/1351
26	b	0.48	0/1252	0.58	0/1692
27	c	0.70	0/2237	0.84	1/2995 (0.0%)
28	G	0.95	1/7104 (0.0%)	0.92	11/9632 (0.1%)
29	d	0.51	0/2075	0.65	2/2808 (0.1%)
30	X	0.77	0/191	1.01	0/254
31	v	0.56	0/899	0.99	0/1206
32	e	0.62	0/954	1.07	5/1285 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.52	0/826	0.68	1/1097 (0.1%)
34	o	0.54	0/824	0.85	0/1111
34	p	0.54	0/848	0.91	0/1143
34	q	0.63	0/2312	0.93	2/3097 (0.1%)
34	r	0.53	0/828	0.86	0/1117
35	t	0.57	0/919	1.06	2/1237 (0.2%)
36	n	0.65	0/200	1.10	1/264 (0.4%)
37	k	0.55	0/636	0.76	0/856
38	i	0.63	0/585	0.86	0/795
39	h	0.60	0/564	0.87	0/761
40	j	0.53	0/532	0.82	1/715 (0.1%)
41	l	0.55	0/634	0.96	2/859 (0.2%)
42	m	0.58	0/649	0.81	0/880
43	g	0.65	0/753	0.96	2/1013 (0.2%)
All	All	0.75	33/110458 (0.0%)	0.83	109/150966 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
2	B	0	2
3	C	0	5
6	F	0	13
7	H	0	6
8	I	0	3
14	O	0	6
15	P	0	1
16	Q	0	2
19	T	0	2
20	U	0	2
24	Z	0	4
28	G	0	3
29	d	0	1
33	f	0	1
36	n	0	2
40	j	0	1
41	l	0	2
43	g	0	2
All	All	0	64

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	1226	GLY	CA-C	-7.91	1.43	1.51
19	T	121	ILE	C-O	-6.59	1.16	1.24
1	A	1384	PRO	C-O	-6.51	1.19	1.24
13	M	468	A	C3'-O3'	6.38	1.51	1.42
24	Z	299	LEU	C-O	-6.12	1.16	1.24

The worst 5 of 109 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	M	468	A	C4'-C3'-O3'	-15.40	89.89	113.00
24	Z	397	LEU	CA-C-N	13.82	137.12	119.84
24	Z	397	LEU	C-N-CA	13.82	137.12	119.84
28	G	680	PRO	CA-C-N	13.19	136.32	119.84
28	G	680	PRO	C-N-CA	13.19	136.32	119.84

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1418	THR	Peptide
1	A	239	PHE	Mainchain,Peptide
1	A	539	PRO	Peptide
1	A	772	GLU	Peptide

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	18101	0	18027	790	0
2	B	14504	0	14508	420	0
3	C	7014	0	7189	289	0
4	D	2465	0	1251	61	0
5	E	2192	0	1106	58	0
6	F	9380	0	9482	466	0
7	H	1248	0	1263	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	I	800	0	802	48	0
9	J	814	0	809	54	0
10	K	693	0	705	45	0
11	L	1388	0	701	39	0
12	N	521	0	260	24	0
13	M	1057	0	537	53	0
14	O	2646	0	2639	98	0
15	P	1978	0	1981	130	0
16	Q	1472	0	1485	179	0
17	R	2089	0	2053	171	0
18	S	578	0	565	35	0
19	T	1291	0	1312	44	0
20	U	1401	0	1362	78	0
21	V	1051	0	1015	77	0
22	W	842	0	818	106	0
23	Y	4047	0	3394	125	0
24	Z	3651	0	3707	153	0
25	a	988	0	954	93	0
26	b	1224	0	1217	47	0
27	c	2803	0	2169	74	0
28	G	6970	0	7181	308	0
29	d	3558	0	2329	131	0
30	X	190	0	186	16	0
31	v	3047	0	1177	55	0
32	e	947	0	703	58	0
33	f	822	0	845	66	0
34	o	819	0	657	10	0
34	p	843	0	672	13	0
34	q	2315	0	1626	46	0
34	r	823	0	654	7	0
35	t	921	0	605	14	0
36	n	195	0	198	40	0
37	k	631	0	670	3	0
38	i	575	0	597	21	0
39	h	554	0	556	18	0
40	j	529	0	557	2	0
41	l	625	0	647	6	0
42	m	644	0	686	14	0
43	g	741	0	778	17	0
44	C	32	0	12	4	0
45	E	4	0	0	0	0
45	Y	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	I	1	0	0	0	0
46	J	3	0	0	0	0
46	Q	2	0	0	0	0
46	R	1	0	0	0	0
46	T	3	0	0	0	0
46	a	3	0	0	0	0
47	Y	27	0	12	2	0
All	All	112064	0	102659	4093	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 19.

The worst 5 of 4093 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:769:MET:HE1	1:A:811:ILE:CD1	1.28	1.56
7:H:262:HIS:CD2	7:H:283:LYS:HZ1	1.31	1.46
29:d:115:ILE:HD11	29:d:119:ARG:NH2	1.35	1.42
23:Y:699:GLU:HB3	23:Y:702:SER:CB	1.49	1.41
22:W:207:THR:O	22:W:214:LEU:CD1	1.68	1.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2192/2287 (96%)	2037 (93%)	134 (6%)	21 (1%)	12	44
2	B	1803/2163 (83%)	1687 (94%)	112 (6%)	4 (0%)	43	74
3	C	872/1008 (86%)	800 (92%)	62 (7%)	10 (1%)	11	43
6	F	1164/1361 (86%)	1042 (90%)	110 (10%)	12 (1%)	12	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	H	147/436 (34%)	139 (95%)	6 (4%)	2 (1%)	9	38
8	I	98/266 (37%)	87 (89%)	9 (9%)	2 (2%)	6	32
9	J	101/107 (94%)	87 (86%)	14 (14%)	0	100	100
10	K	82/85 (96%)	78 (95%)	3 (4%)	1 (1%)	10	41
14	O	335/451 (74%)	302 (90%)	26 (8%)	7 (2%)	5	31
15	P	236/379 (62%)	209 (89%)	23 (10%)	4 (2%)	7	35
16	Q	177/364 (49%)	157 (89%)	16 (9%)	4 (2%)	5	30
17	R	259/339 (76%)	238 (92%)	18 (7%)	3 (1%)	10	41
18	S	65/175 (37%)	53 (82%)	9 (14%)	3 (5%)	2	17
19	T	155/157 (99%)	139 (90%)	13 (8%)	3 (2%)	6	33
20	U	172/207 (83%)	162 (94%)	9 (5%)	1 (1%)	21	54
21	V	126/148 (85%)	118 (94%)	6 (5%)	2 (2%)	7	36
22	W	98/266 (37%)	89 (91%)	6 (6%)	3 (3%)	3	25
23	Y	570/876 (65%)	548 (96%)	21 (4%)	1 (0%)	43	74
24	Z	443/577 (77%)	399 (90%)	32 (7%)	12 (3%)	4	27
25	a	119/259 (46%)	104 (87%)	13 (11%)	2 (2%)	7	35
26	b	146/301 (48%)	134 (92%)	9 (6%)	3 (2%)	5	31
27	c	291/587 (50%)	276 (95%)	9 (3%)	6 (2%)	5	31
28	G	871/971 (90%)	820 (94%)	41 (5%)	10 (1%)	11	43
29	d	234/687 (34%)	214 (92%)	19 (8%)	1 (0%)	30	62
30	X	25/135 (18%)	20 (80%)	5 (20%)	0	100	100
31	v	120/859 (14%)	110 (92%)	5 (4%)	5 (4%)	2	19
32	e	141/213 (66%)	114 (81%)	16 (11%)	11 (8%)	1	8
33	f	98/215 (46%)	95 (97%)	3 (3%)	0	100	100
34	o	118/503 (24%)	113 (96%)	4 (3%)	1 (1%)	16	49
34	p	122/503 (24%)	116 (95%)	6 (5%)	0	100	100
34	q	349/503 (69%)	321 (92%)	16 (5%)	12 (3%)	3	23
34	r	119/503 (24%)	111 (93%)	5 (4%)	3 (2%)	4	28
35	t	149/175 (85%)	133 (89%)	13 (9%)	3 (2%)	6	32
36	n	21/455 (5%)	19 (90%)	1 (5%)	1 (5%)	2	16
37	k	76/196 (39%)	69 (91%)	7 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
39	h	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	37
40	j	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
41	l	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	39
42	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
43	g	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	11	43
All	All	12546/19315 (65%)	11559 (92%)	831 (7%)	156 (1%)	13	41

5 of 156 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	265	ASN
1	A	1376	ASN
1	A	1405	ILE
1	A	1829	SER
1	A	1830	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1994/2066 (96%)	1912 (96%)	82 (4%)	27	53
2	B	1632/1955 (84%)	1632 (100%)	0	100	100
3	C	791/910 (87%)	774 (98%)	17 (2%)	47	66
6	F	1088/1244 (88%)	1063 (98%)	25 (2%)	44	64
7	H	139/392 (36%)	127 (91%)	12 (9%)	10	33
8	I	89/236 (38%)	84 (94%)	5 (6%)	19	46
9	J	93/97 (96%)	88 (95%)	5 (5%)	20	46
10	K	76/77 (99%)	68 (90%)	8 (10%)	6	27
14	O	295/397 (74%)	293 (99%)	2 (1%)	76	78
15	P	218/328 (66%)	202 (93%)	16 (7%)	13	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	Q	171/332 (52%)	161 (94%)	10 (6%)	18	44
17	R	224/296 (76%)	208 (93%)	16 (7%)	13	38
18	S	58/151 (38%)	58 (100%)	0	100	100
19	T	141/141 (100%)	137 (97%)	4 (3%)	38	61
20	U	157/189 (83%)	152 (97%)	5 (3%)	34	59
21	V	114/132 (86%)	111 (97%)	3 (3%)	40	62
22	W	91/240 (38%)	73 (80%)	18 (20%)	1	7
23	Y	299/789 (38%)	291 (97%)	8 (3%)	39	62
24	Z	417/538 (78%)	384 (92%)	33 (8%)	11	36
25	a	112/237 (47%)	104 (93%)	8 (7%)	13	38
26	b	134/273 (49%)	133 (99%)	1 (1%)	76	78
27	c	196/316 (62%)	188 (96%)	8 (4%)	27	53
28	G	778/867 (90%)	766 (98%)	12 (2%)	57	71
29	d	215/249 (86%)	213 (99%)	2 (1%)	70	76
30	X	21/121 (17%)	21 (100%)	0	100	100
31	v	59/152 (39%)	49 (83%)	10 (17%)	2	13
32	e	48/189 (25%)	42 (88%)	6 (12%)	4	22
33	f	92/193 (48%)	92 (100%)	0	100	100
34	o	61/451 (14%)	55 (90%)	6 (10%)	7	30
34	p	62/451 (14%)	54 (87%)	8 (13%)	4	21
34	q	121/451 (27%)	104 (86%)	17 (14%)	3	19
34	r	59/451 (13%)	54 (92%)	5 (8%)	10	34
35	t	39/165 (24%)	27 (69%)	12 (31%)	0	2
36	n	20/413 (5%)	13 (65%)	7 (35%)	0	1
37	k	70/176 (40%)	69 (99%)	1 (1%)	59	71
38	i	65/83 (78%)	60 (92%)	5 (8%)	12	37
39	h	61/77 (79%)	60 (98%)	1 (2%)	55	70
40	j	58/66 (88%)	56 (97%)	2 (3%)	32	57
41	l	69/89 (78%)	68 (99%)	1 (1%)	59	71
42	m	77/129 (60%)	74 (96%)	3 (4%)	28	54
43	g	79/87 (91%)	73 (92%)	6 (8%)	12	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	10583/16196 (65%)	10193 (96%)	390 (4%)	31 56

5 of 390 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	Y	578	PRO
28	G	22	GLN
24	Z	34	MET
24	Z	195	GLU
31	v	616	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 238 such sidechains are listed below:

Mol	Chain	Res	Type
6	F	1222	GLN
29	d	252	HIS
14	O	382	HIS
29	d	179	GLN
42	m	30	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	L	65/1175 (5%)	12 (18%)	0
12	N	24/25 (96%)	9 (37%)	0
13	M	47/61 (77%)	23 (48%)	5 (10%)
4	D	114/214 (53%)	24 (21%)	2 (1%)
5	E	102/112 (91%)	17 (16%)	0
All	All	352/1587 (22%)	85 (24%)	7 (1%)

5 of 85 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	29	G
4	D	31	G
4	D	42	A
4	D	43	G
4	D	45	A

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
13	M	480	A
13	M	500	A
13	M	515	U
13	M	514	U
13	M	472	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 18 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
47	ADP	Y	902	45	28,29,29	1.49	5 (17%)	43,45,45	1.93	10 (23%)
44	GTP	C	1500	-	33,34,34	1.27	4 (12%)	50,54,54	1.92	7 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	ADP	Y	902	45	-	4/16/32/32	0/3/3/3
44	GTP	C	1500	-	-	8/22/38/38	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	Y	902	ADP	C5-C4	4.87	1.47	1.39
44	C	1500	GTP	C5-N7	-3.12	1.32	1.39
44	C	1500	GTP	C6-N1	-3.07	1.33	1.38
47	Y	902	ADP	C5-C6	2.93	1.49	1.41
44	C	1500	GTP	PA-O3A	2.79	1.62	1.59

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	C	1500	GTP	C5-C4-N3	-6.51	118.04	128.39
47	Y	902	ADP	C5-C4-N3	-6.15	118.25	126.72
44	C	1500	GTP	C2-N3-C4	5.59	121.93	112.30
44	C	1500	GTP	N9-C4-N3	5.47	136.88	125.95
47	Y	902	ADP	N3-C4-N9	4.91	135.52	127.17

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
44	C	1500	GTP	C5'-O5'-PA-O3A
44	C	1500	GTP	C5'-O5'-PA-O1A
44	C	1500	GTP	C5'-O5'-PA-O2A
44	C	1500	GTP	O4'-C4'-C5'-O5'
44	C	1500	GTP	C3'-C4'-C5'-O5'

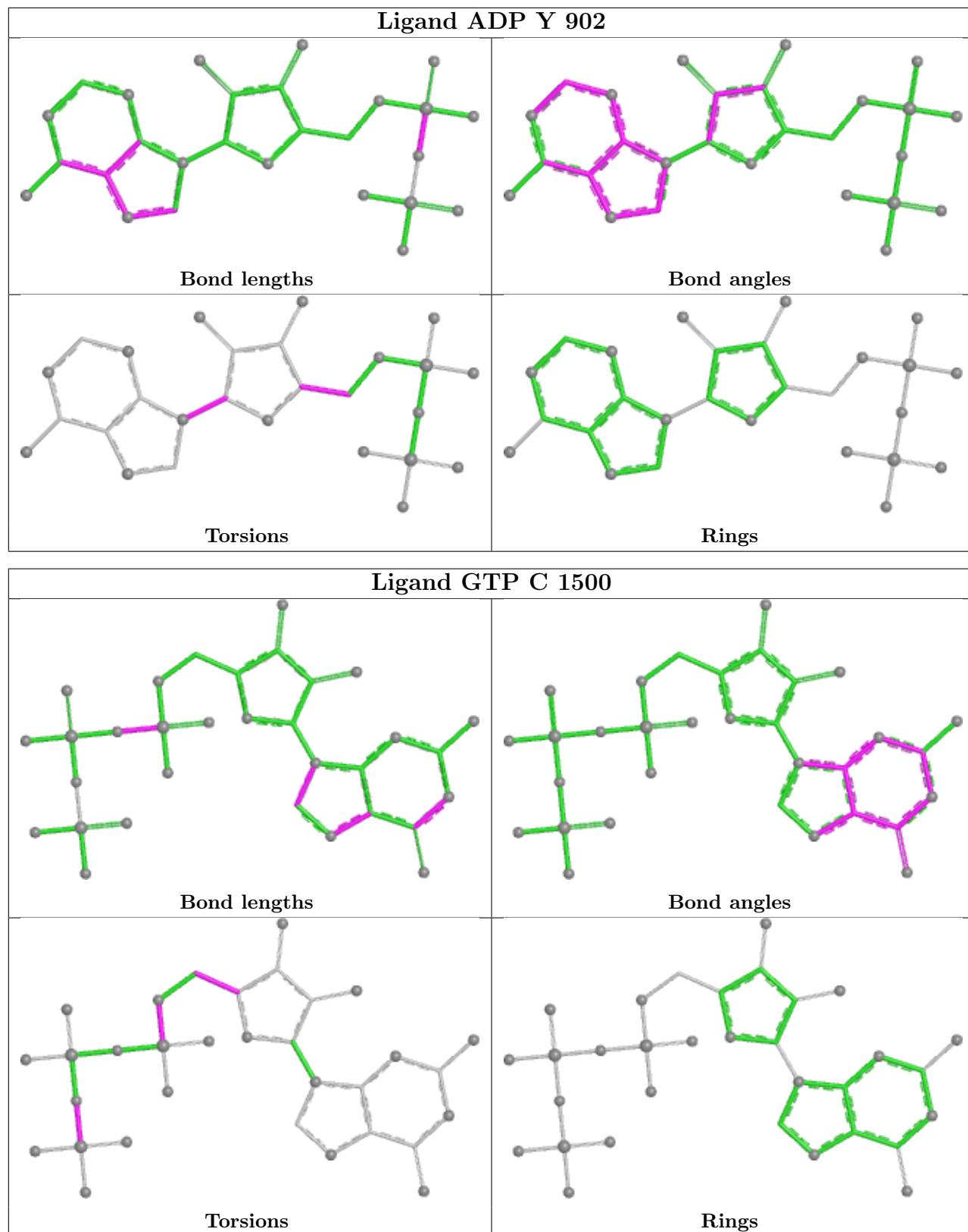
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
47	Y	902	ADP	2	0
44	C	1500	GTP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

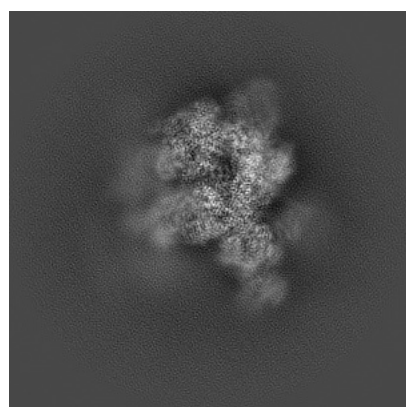
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9524. These allow visual inspection of the internal detail of the map and identification of artifacts.

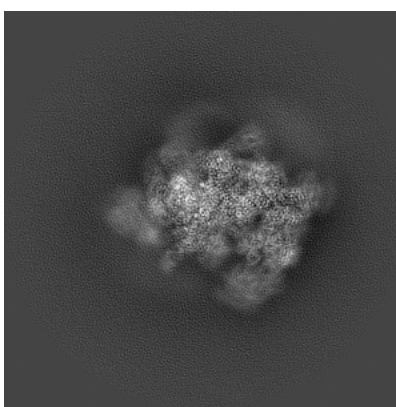
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

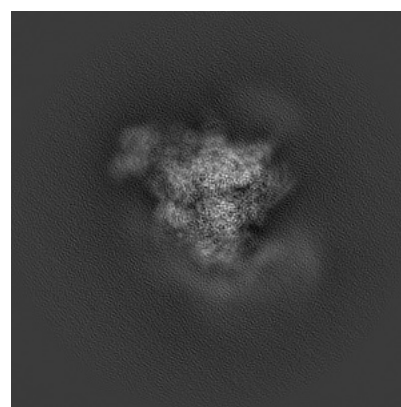
6.1.1 Primary map



X



Y

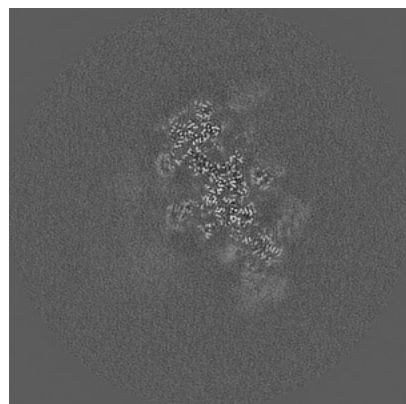


Z

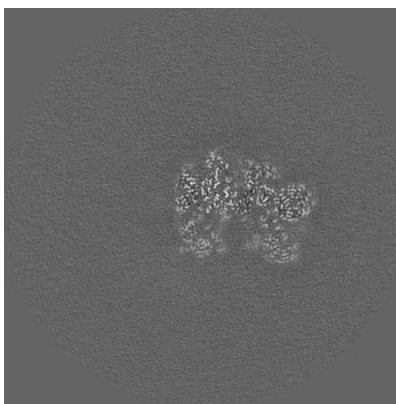
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

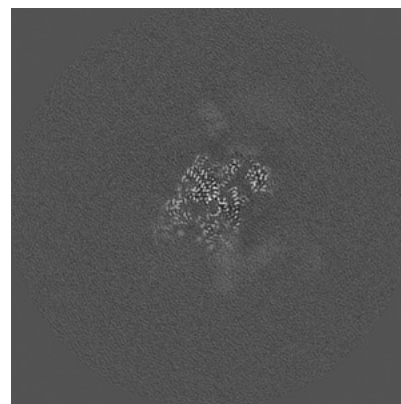
6.2.1 Primary map



X Index: 200



Y Index: 200

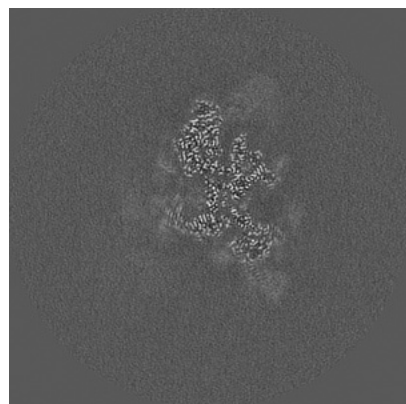


Z Index: 200

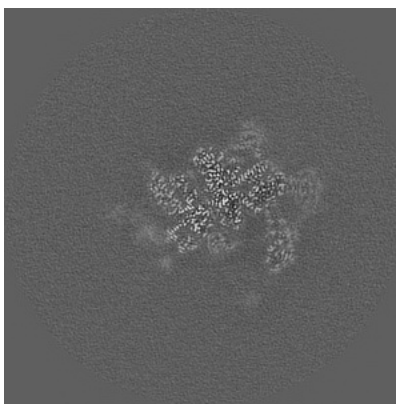
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

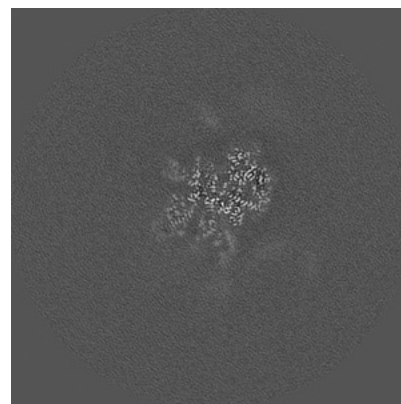
6.3.1 Primary map



X Index: 210



Y Index: 230

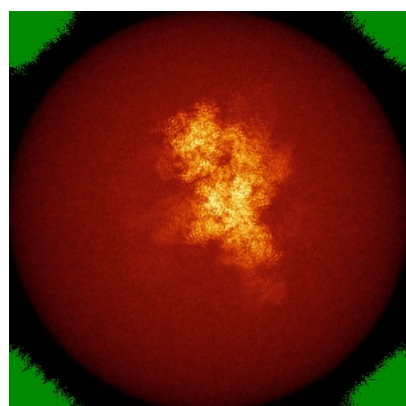


Z Index: 205

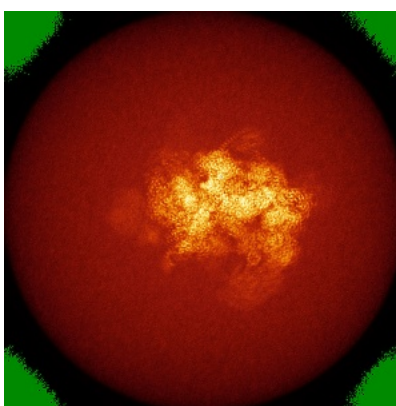
The images above show the largest variance slices of the map in three orthogonal directions.

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

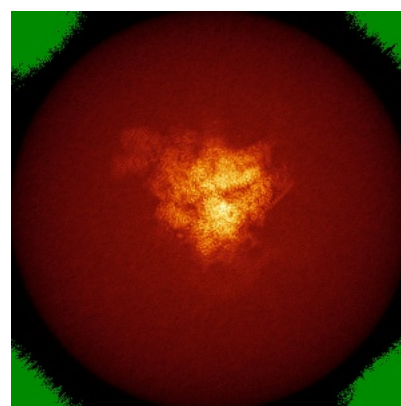
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0405. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

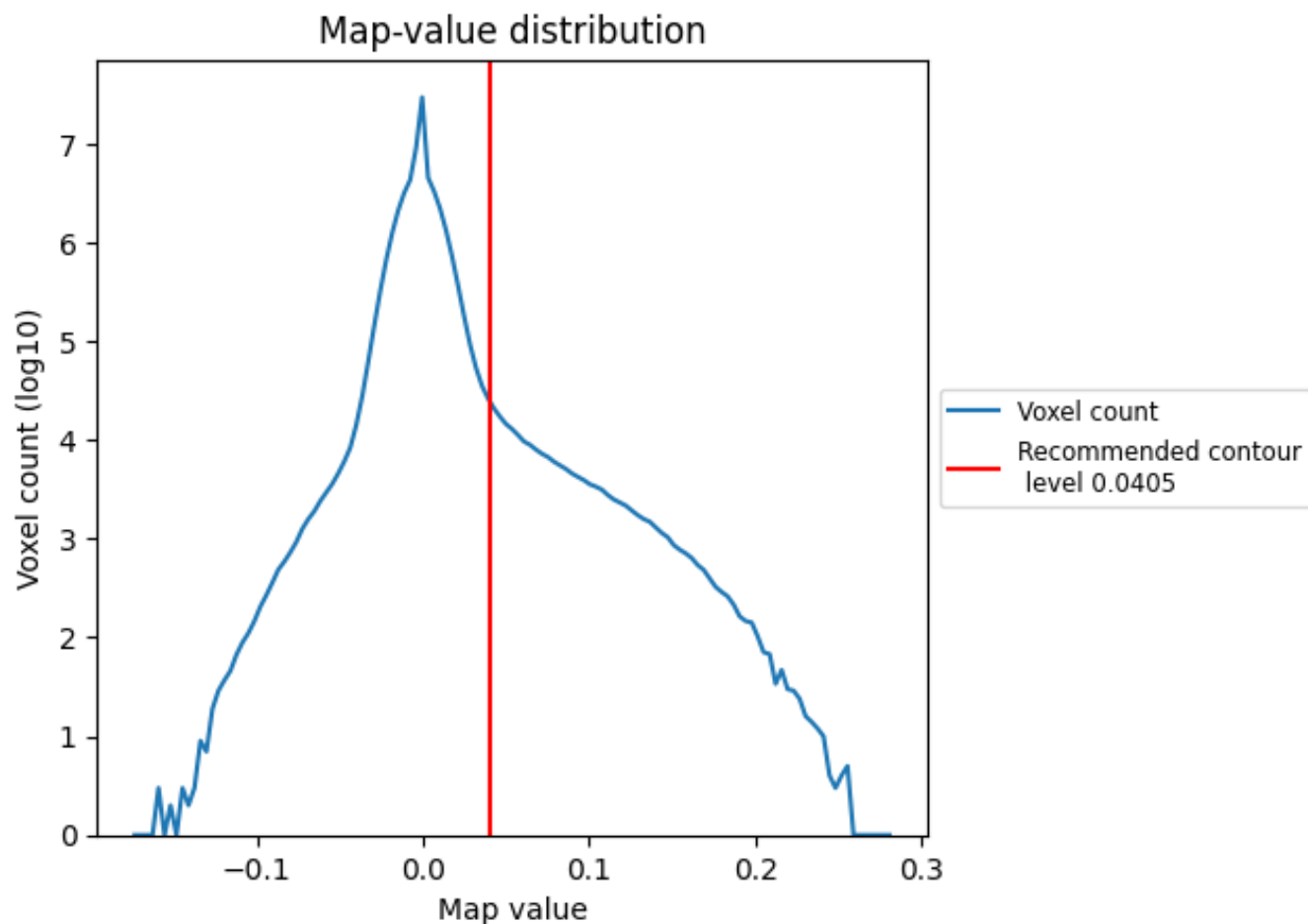
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

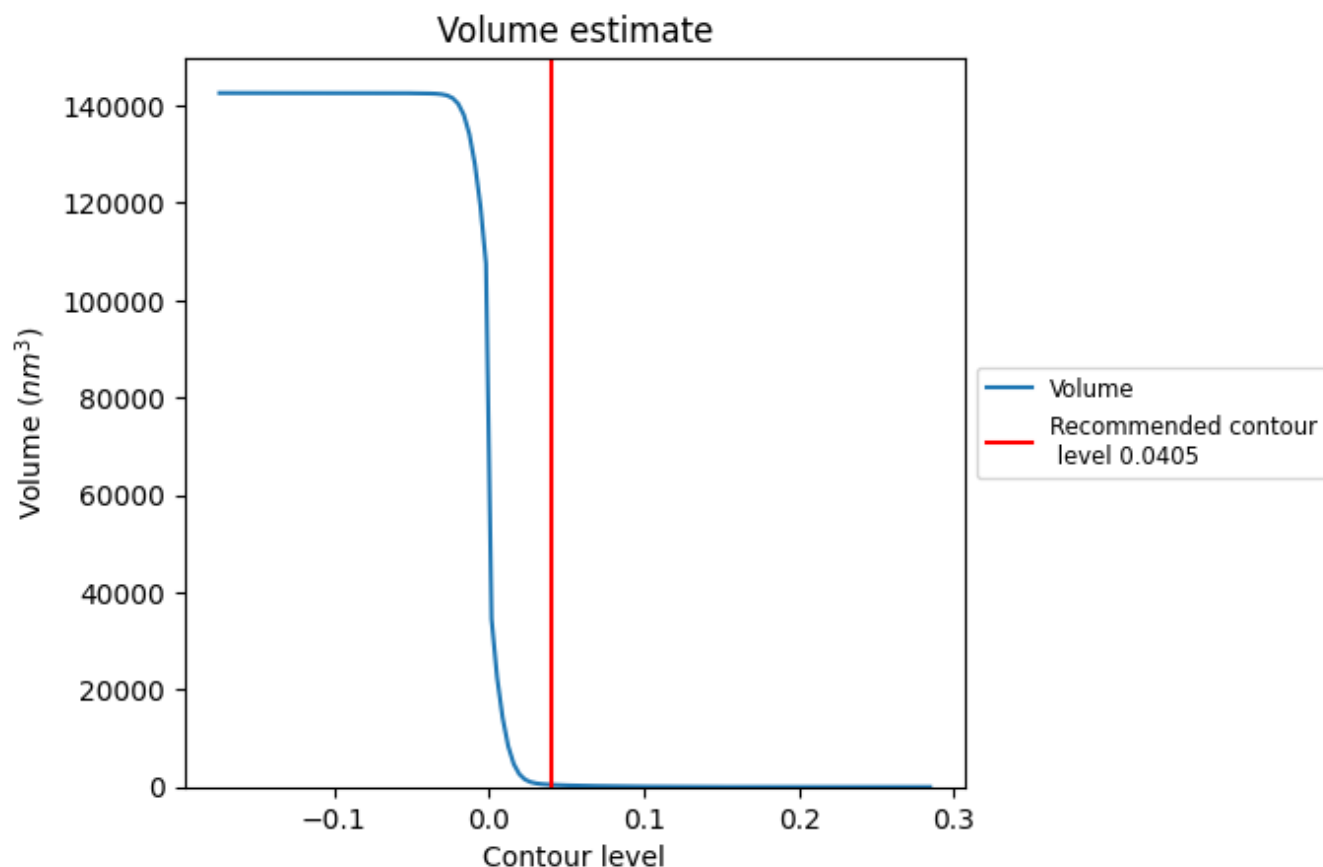
This section contains the results of statistical analysis of the map.

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.

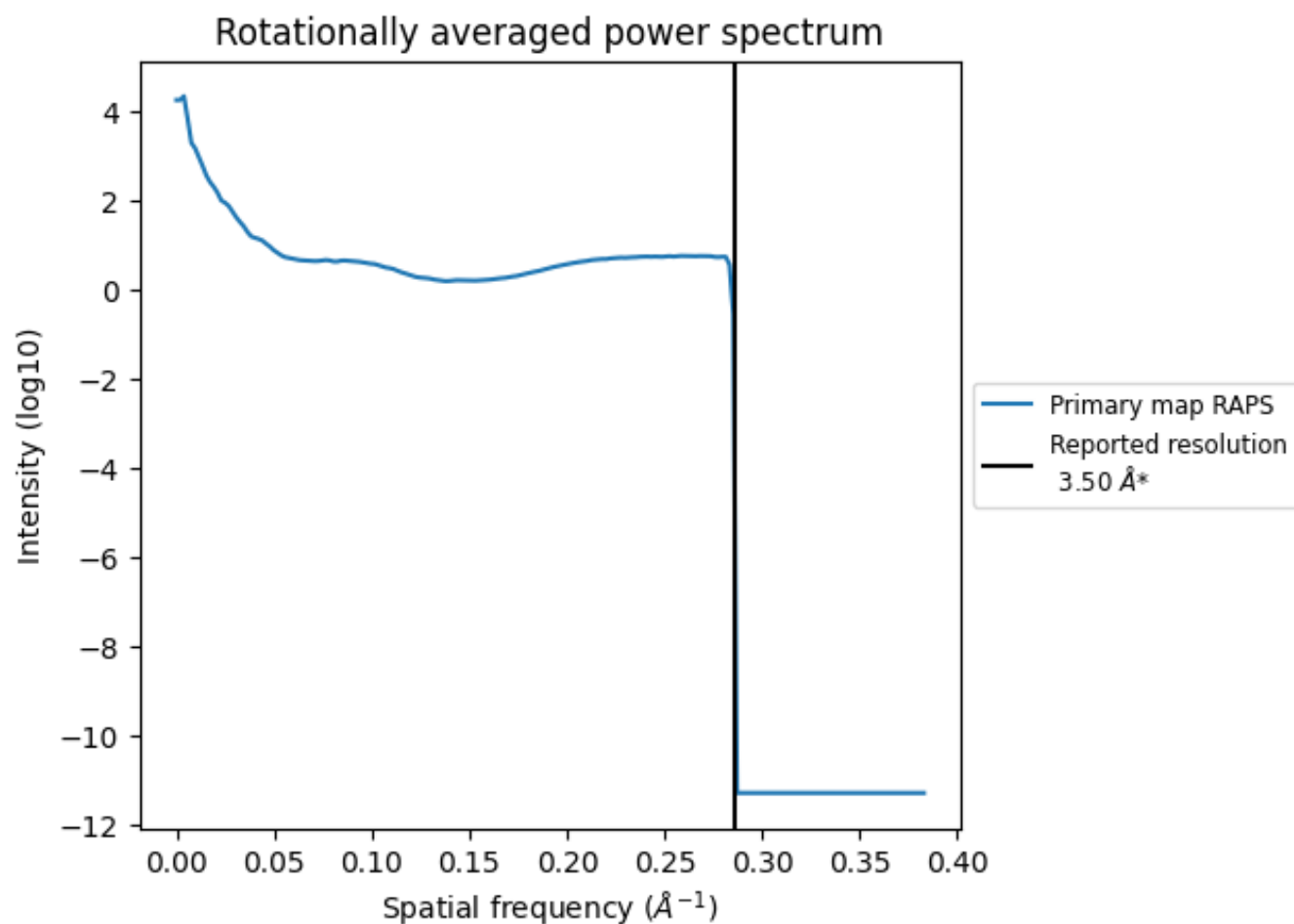
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 444 nm³; this corresponds to an approximate mass of 401 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

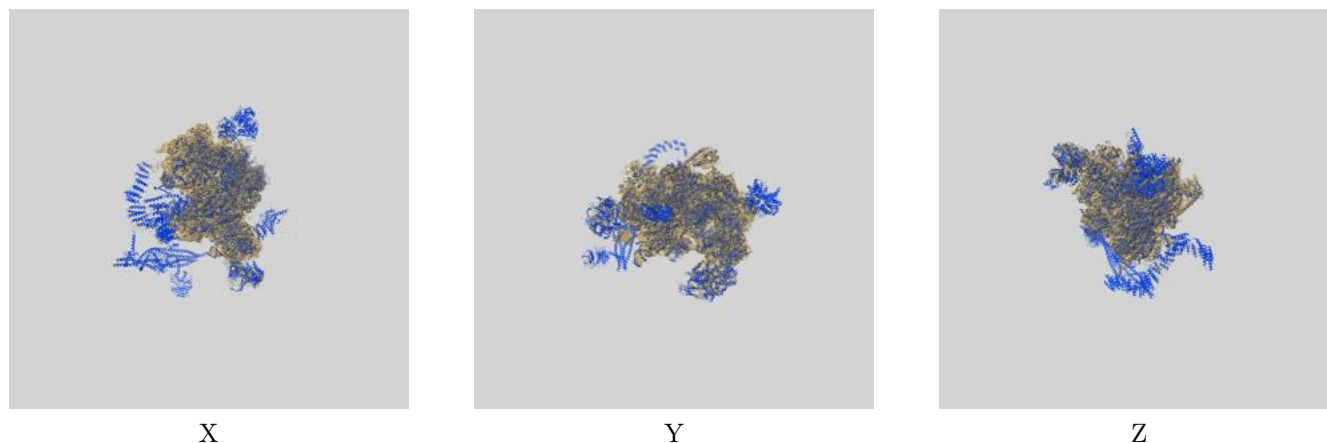
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

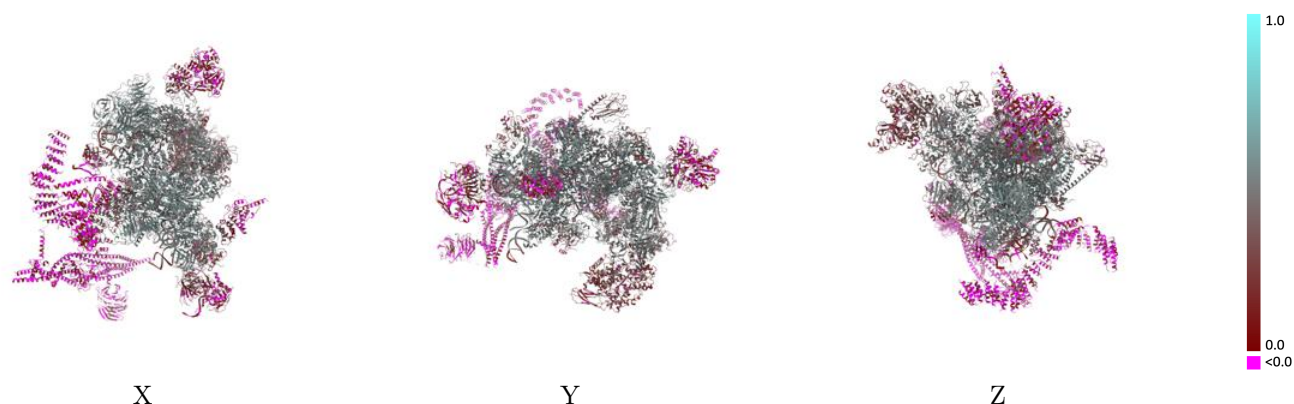
This section contains information regarding the fit between EMDB map EMD-9524 and PDB model 5GM6. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



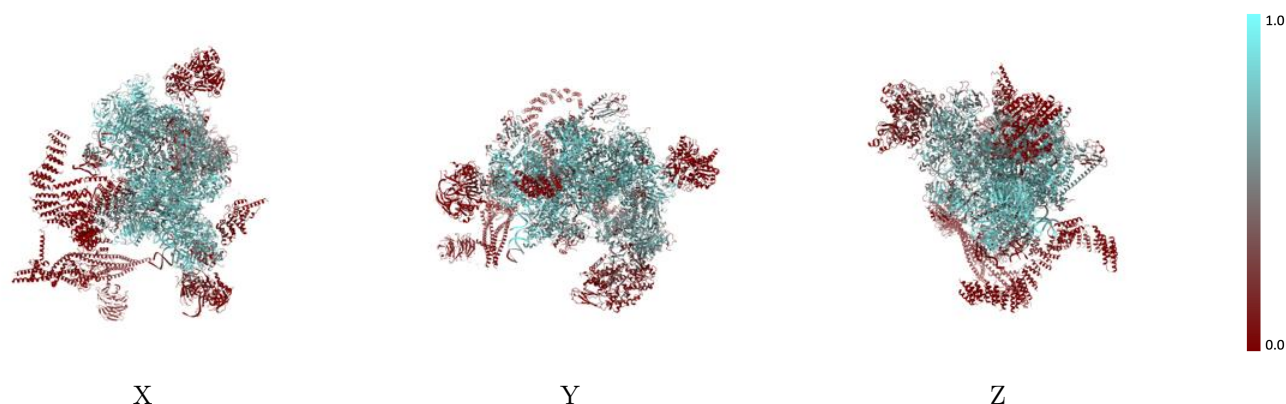
The images above show the 3D surface view of the map at the recommended contour level 0.0405 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



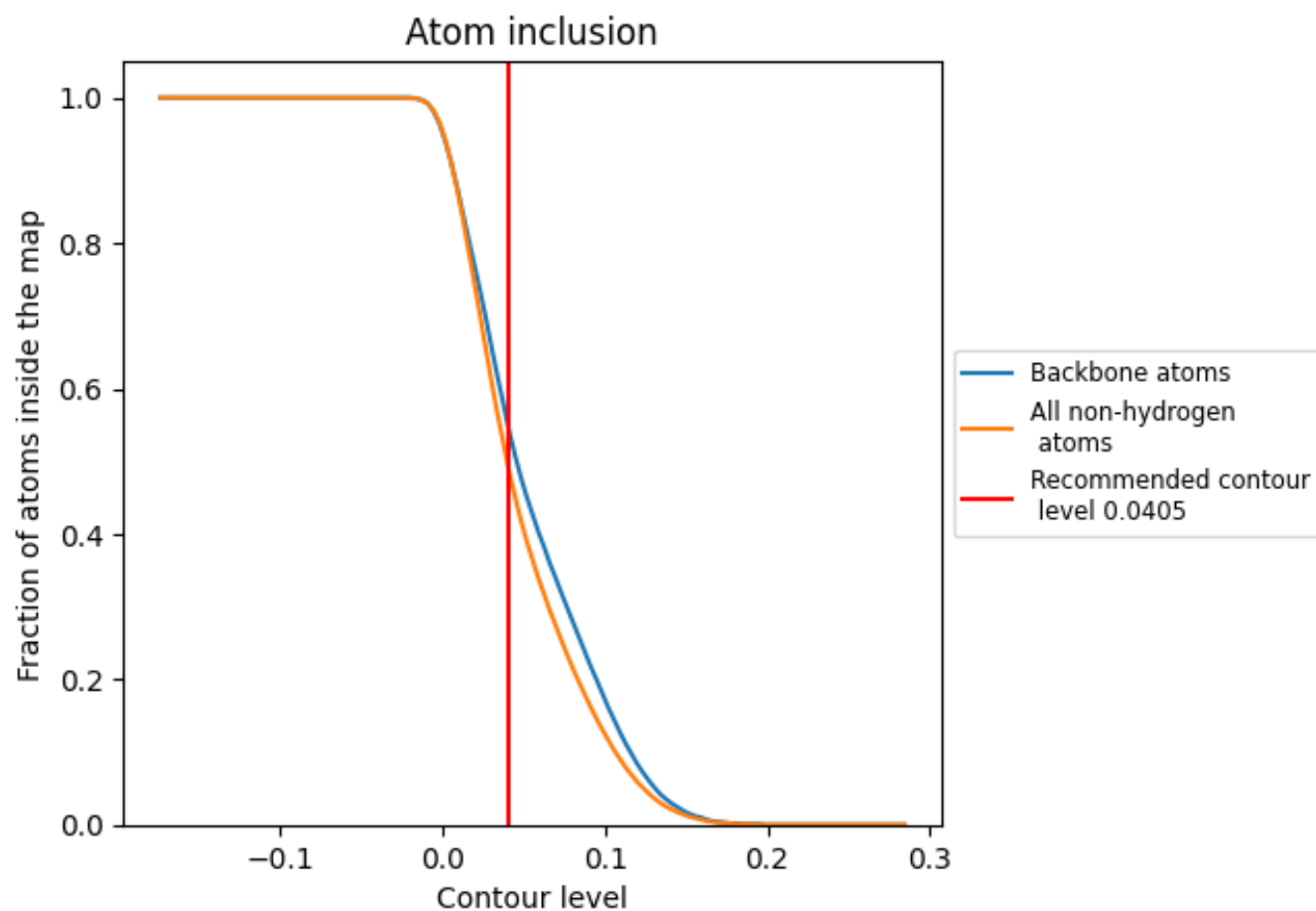
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0405).

9.4 Atom inclusion [i](#)



At the recommended contour level, 55% of all backbone atoms, 49% 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 (0.0405) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4900	 0.3770
A	 0.7180	 0.5060
B	 0.3690	 0.3670
C	 0.6530	 0.4590
D	 0.6510	 0.4110
E	 0.7100	 0.4250
F	 0.7260	 0.4990
G	 0.7370	 0.5160
H	 0.7320	 0.5150
I	 0.7080	 0.5150
J	 0.7820	 0.5380
K	 0.7560	 0.5180
L	 0.5520	 0.3720
M	 0.4310	 0.2930
N	 0.6830	 0.4730
O	 0.7490	 0.5090
P	 0.5780	 0.4550
Q	 0.4370	 0.3720
R	 0.6050	 0.4360
S	 0.3680	 0.4690
T	 0.7270	 0.5000
U	 0.3670	 0.3550
V	 0.7040	 0.4770
W	 0.5710	 0.4320
X	 0.6150	 0.5320
Y	 0.0380	 0.1520
Z	 0.3500	 0.2870
a	 0.4190	 0.4020
b	 0.3770	 0.4070
c	 0.2530	 0.2320
d	 0.2480	 0.2260
e	 0.2340	 0.1550
f	 0.2130	 0.1990
g	 0.0370	 0.0960
h	 0.0310	 0.0760



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Chain	Atom inclusion	Q-score
i	 0.0230	 0.1060
j	 0.0540	 0.1780
k	 0.0870	 0.2060
l	 0.2220	 0.3230
m	 0.0280	 0.1040
n	 0.6810	 0.4770
o	 0.0000	 0.0280
p	 0.0000	 0.0060
q	 0.0000	 0.0160
r	 0.0000	 0.0140
t	 0.0000	 0.0420
v	 0.0000	 0.0180