



wwPDB EM Validation Summary Report ⓘ

Nov 4, 2025 – 12:57 PM EST

PDB ID : 9N70 / pdb_00009n70
EMDB ID : EMD-49080
Title : SSU processome maturation and disassembly, State E
Authors : Buzovetsky, O.; Klinge, S.
Deposited on : 2025-02-05
Resolution : 5.17 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:

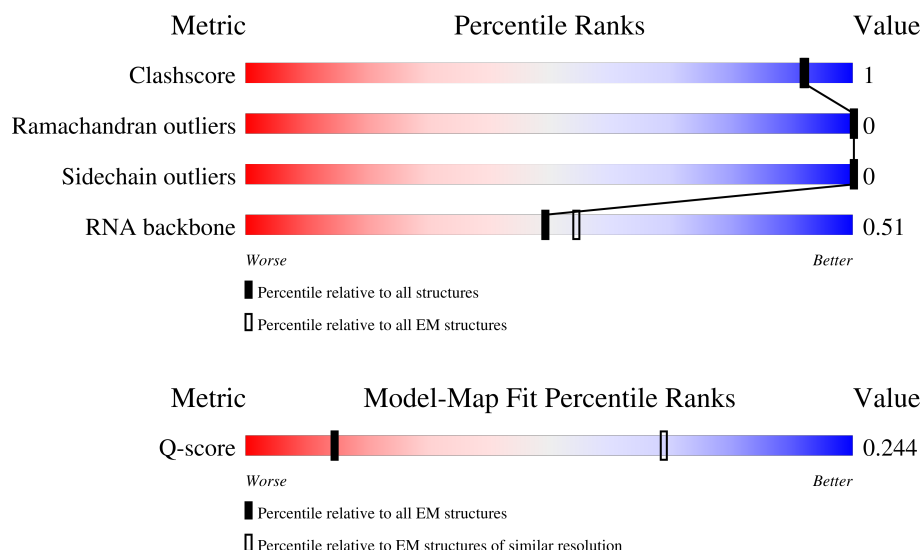
EMDB validation analysis	:	0.0.1.dev129
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.46

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 5.17 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	687 (4.67 - 5.67)

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	L0	700	
2	L1	1810	
3	L2	333	








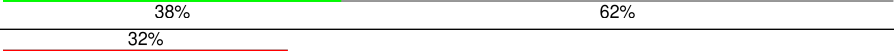
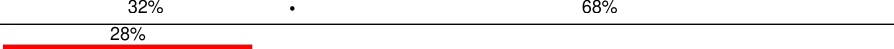
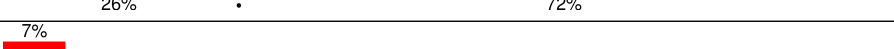
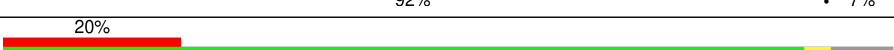

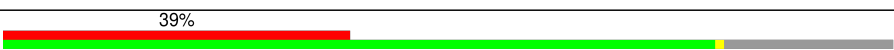

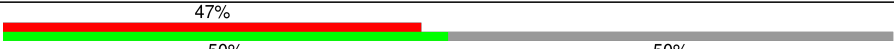
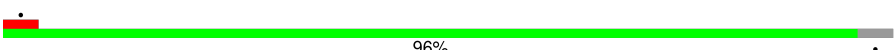

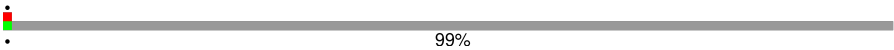
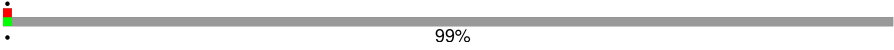


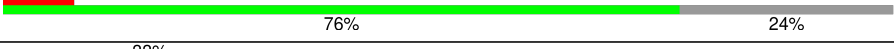



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Mol	Chain	Length	Quality of chain
4	L3	146	
5	L4	261	
6	L5	225	
7	L6	236	
8	L7	190	
9	L8	200	
10	L9	197	
11	LC	143	
12	LD	156	
13	LE	130	
14	LF	135	
15	LG	67	
16	LH	896	
17	LI	713	
18	LJ	513	
19	LK	575	
20	LL	643	
21	LM	1769	
22	LN	776	
23	LO	923	
24	LP	440	
25	LQ	943	
26	LR	817	
27	LS	594	
28	LT	939	

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Mol	Chain	Length	Quality of chain
29	LU	489	
30	LV	707	
31	LW	554	
32	LX	1056	
32	LY	1056	
33	LZ	183	
34	NA	593	
35	NB	610	
36	NC	357	
37	ND	214	
38	NF	151	
39	NG	137	
40	NH	1237	
41	NI	297	
42	NM	255	
43	NN	534	
44	NQ	82	
45	NS	1267	
46	NV	733	
47	OA	1729	
48	OH	143	
49	OU	152	
50	SA	504	
51	SB	511	
52	SC	327	

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Mol	Chain	Length	Quality of chain
52	SD	327	
53	SE	126	
53	SF	126	
54	SG	573	
55	SH	367	
56	SI	1183	
57	SJ	252	
57	SK	252	
58	SL	189	
59	SM	290	
60	SP	2493	
61	SQ	217	
62	SR	145	
63	SS	899	
64	ST	810	
65	SU	552	
66	SW	274	
67	SY	250	
68	SZ	483	

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 162545 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 5'ETS rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L0	64	Total	C	N	O	P	0	0
			1370	612	247	447	64		

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1252	Total	C	N	O	P	0	0
			26727	11947	4790	8738	1252		

- Molecule 3 is a RNA chain called Saccharomyces cerevisiae U3a gene for small nucleolar RNA U3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	155	Total	C	N	O	P	0	0
			3289	1471	573	1090	155		

- Molecule 4 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	L3	97	Total	C	N	O	0	0
			485	291	97	97		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	L4	244	Total	C	N	O	0	0
			1221	733	244	244		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	L5	206	Total	C	N	O	0	0
			1040	628	206	206		

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	L6	206	Total	C	N	O	0	0
			1029	617	206	206		

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	L7	178	Total	C	N	O	0	0
			903	547	178	178		

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	L8	170	Total	C	N	O	0	0
			843	503	170	170		

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	L9	181	Total	C	N	O	0	0
			914	552	181	181		

- Molecule 11 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	LC	128	Total	C	N	O	0	0
			642	386	128	128		

- Molecule 12 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	LD	137	Total	C	N	O	0	0
			693	419	137	137		

- Molecule 13 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	LE	129	Total	C	N	O	0	0
			640	382	129	129		

- Molecule 14 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	LF	130	Total	C	N	O	0	0
			647	387	130	130		

- Molecule 15 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	LG	62	Total	C	N	O	0	0
			309	185	62	62		

- Molecule 16 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	LH	802	Total	C	N	O	0	0
			4014	2410	802	802		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	LI	600	Total	C	N	O	0	0
			3027	1827	600	600		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	LJ	476	Total	C	N	O	0	0
			2394	1442	476	476		

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	LK	132	Total	C	N	O	0	0
			664	400	132	132		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	LL	487	Total	C	N	O	0	0
			2440	1466	487	487		

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	LM	1613	Total	C	N	O	0	0
			8115	4889	1613	1613		

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	LN	663	Total	C	N	O	0	0
			3315	1989	663	663		

- Molecule 23 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	LO	792	Total	C	N	O	0	0
			3958	2374	792	792		

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	LP	379	Total	C	N	O	0	0
			1901	1143	379	379		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	LQ	816	Total	C	N	O	0	0
			4068	2436	816	816		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	LR	793	Total	C	N	O	0	0
			3962	2376	793	793		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	LS	454	Total	C	N	O	0	0
			2279	1371	454	454		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	LT	871	Total	C	N	O	0	0
			4347	2605	871	871		

- Molecule 29 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	LU	454	Total	C	N	O	0	0
			2274	1366	454	454		

- Molecule 30 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	LV	405	Total	C	N	O	0	0
			2029	1219	405	405		

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	LW	459	Total	C	N	O	0	0
			2304	1386	459	459		

- Molecule 32 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	LX	842	Total	C	N	O	0	0
			4253	2569	842	842		
32	LY	846	Total	C	N	O	0	0
			4274	2582	846	846		

- Molecule 33 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	LZ	160	Total	C	N	O	0	0
			808	488	160	160		

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	NA	296	Total	C	N	O	0	0
			1491	899	296	296		

- Molecule 35 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	NB	231	Total	C	N	O	0	0
			1159	697	231	231		

- Molecule 36 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	NC	115	Total	C	N	O	0	0
			575	345	115	115		

- Molecule 37 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	ND	59	Total	C	N	O	0	0
			297	179	59	59		

- Molecule 38 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	NF	141	Total	C	N	O	0	0
			711	429	141	141		

- Molecule 39 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	NG	127	Total	C	N	O	0	0
			630	376	127	127		

- Molecule 40 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	NH	1077	Total	C	N	O	0	0
			5443	3289	1077	1077		

- Molecule 41 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	NI	240	Total	C	N	O	0	0
			1210	730	240	240		

- Molecule 42 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	NM	237	Total	C	N	O	0	0
			1183	709	237	237		

- Molecule 43 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	NN	267	Total	C	N	O	0	0
			1341	807	267	267		

- Molecule 44 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	NQ	79	Total	C	N	O	0	0
			398	240	79	79		

- Molecule 45 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	NS	844	Total	C	N	O	0	0
			4268	2580	844	844		

- Molecule 46 is a protein called Exosome complex exonuclease RRP6.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	NV	8	Total	C	N	O	0	0
			39	23	8	8		

- Molecule 47 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	OA	14	Total	C	N	O	0	0
			69	41	14	14		

- Molecule 48 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	OH	120	Total	C	N	O	0	0
			594	354	120	120		

- Molecule 49 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	OU	56	Total	C	N	O	0	0
			278	166	56	56		

- Molecule 50 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	SA	384	Total	C	N	O	1	0
			1924	1154	385	385		

- Molecule 51 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	SB	433	Total	C	N	O	0	0
			2161	1295	433	433		

- Molecule 52 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	SC	238	Total	C	N	O	0	0
			1198	722	238	238		
52	SD	238	Total	C	N	O	0	0
			1198	722	238	238		

- Molecule 53 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	SE	121	Total	C	N	O	0	0
			615	373	121	121		
53	SF	121	Total	C	N	O	0	0
			615	373	121	121		

- Molecule 54 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	SG	459	Total	C	N	O	0	0
			2290	1372	459	459		

- Molecule 55 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	SH	360	Total	C	N	O	0	0
			1801	1081	360	360		

- Molecule 56 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	SI	790	Total	C	N	O	0	0
			3990	2410	790	790		

- Molecule 57 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	SJ	213	Total	C	N	O	0	0
			1074	648	213	213		
57	SK	229	Total	C	N	O	0	0
			1160	702	229	229		

- Molecule 58 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	SL	148	Total	C	N	O	0	0
			751	455	148	148		

- Molecule 59 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	SM	247	Total	C	N	O	0	0
			1243	749	247	247		

- Molecule 60 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	SP	2185	Total	C	N	O	0	0
			10989	6619	2185	2185		

- Molecule 61 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	SQ	117	Total	C	N	O	0	0
			592	358	117	117		

- Molecule 62 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	SR	95	Total	C	N	O	0	0
			476	286	95	95		

- Molecule 63 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	SS	225	Total	C	N	O	1	0
			1145	695	225	225		

- Molecule 64 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	ST	540	Total	C	N	O	0	0
			2727	1647	540	540		

- Molecule 65 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	SU	532	Total	C	N	O	0	0
			2703	1639	532	532		

- Molecule 66 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	SW	219	Total	C	N	O	0	0
			1104	666	219	219		

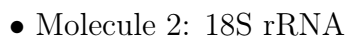
- Molecule 67 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	SY	122	Total	C	N	O	0	0
			611	367	122	122		

- Molecule 68 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	SZ	259	Total	C	N	O	0	0
			1314	796	259	259		

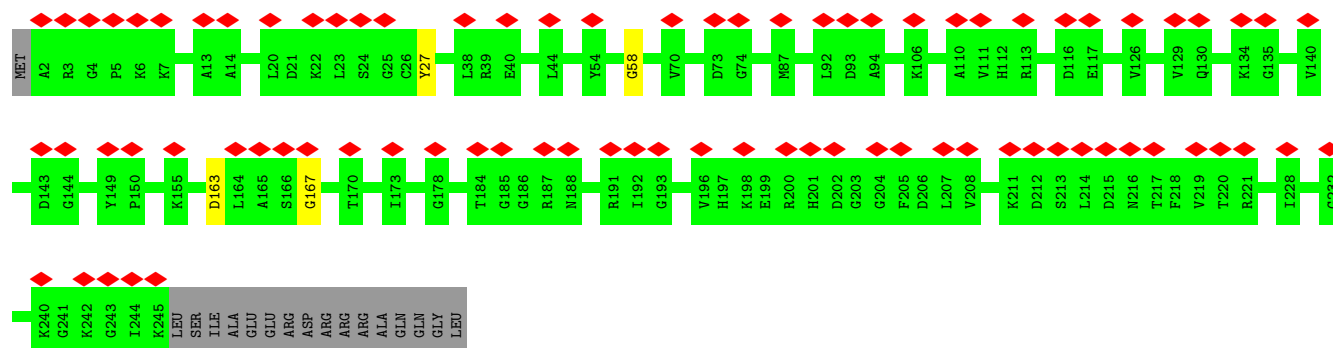
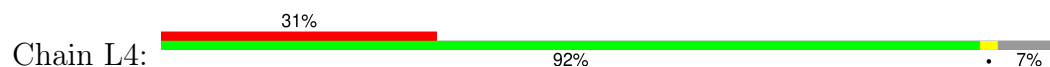
- Molecule 1: 5'ETS rRNA



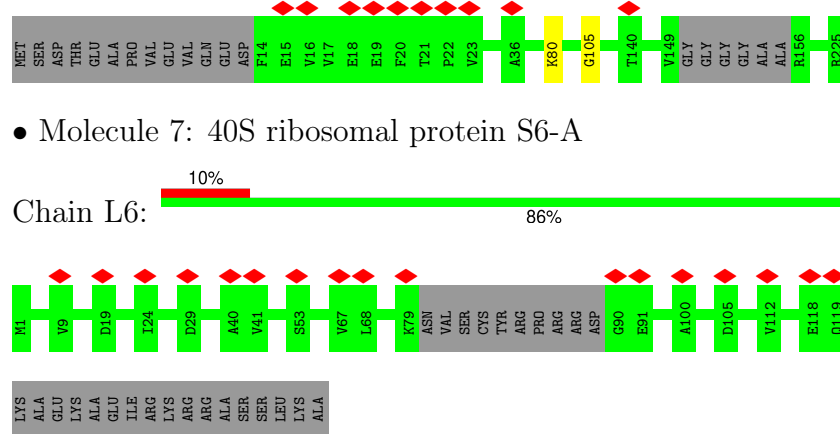




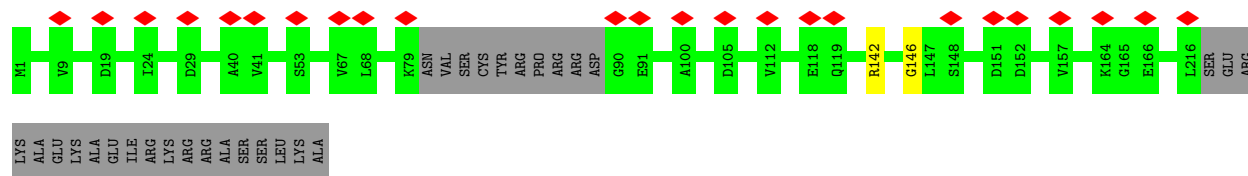
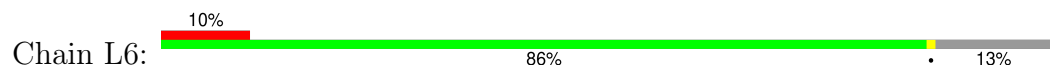
- Molecule 5: 40S ribosomal protein S4-A



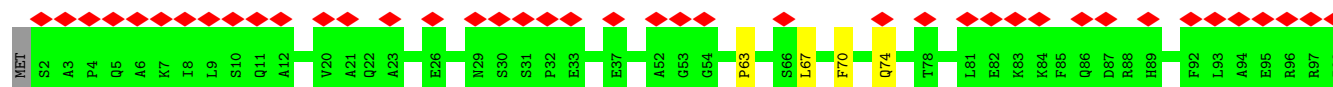
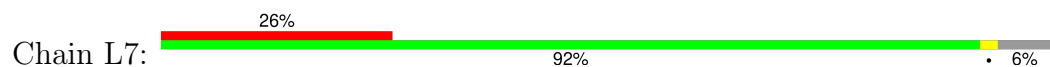
- Molecule 6: 40S ribosomal protein S5

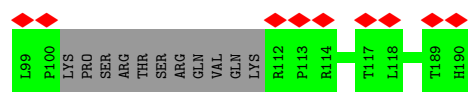


- Molecule 7: 40S ribosomal protein S6-A

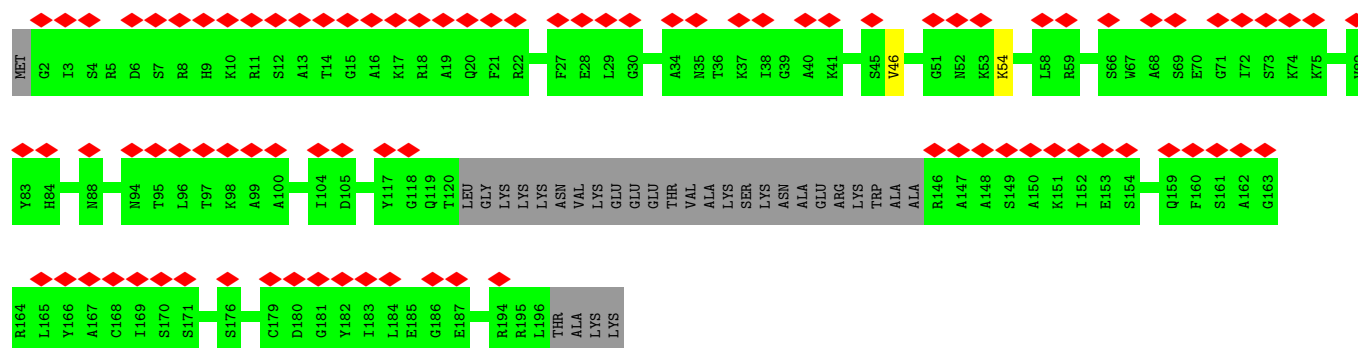
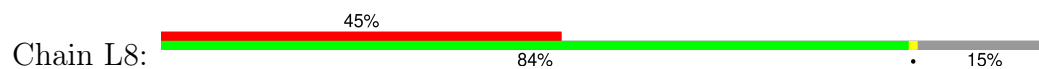


- Molecule 8: 40S ribosomal protein S7-A

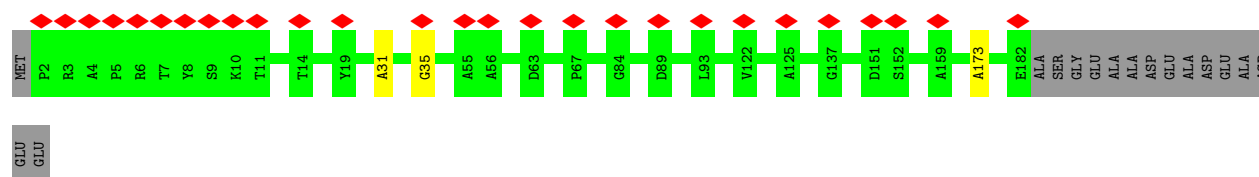
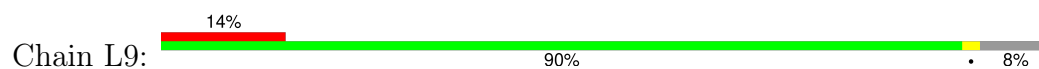




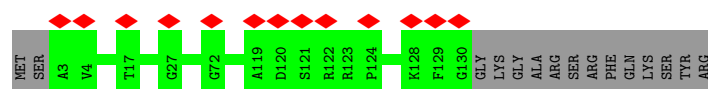
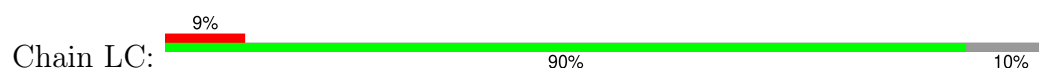
• Molecule 9: 40S ribosomal protein S8-A



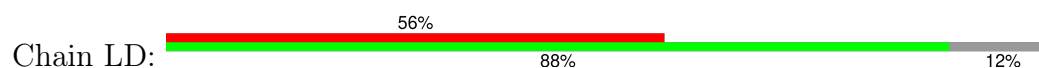
• Molecule 10: 40S ribosomal protein S9-A



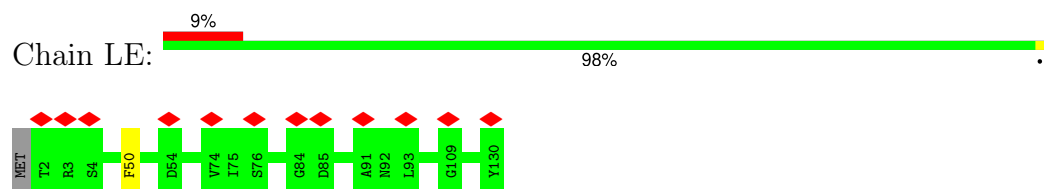
• Molecule 11: 40S ribosomal protein S16-A



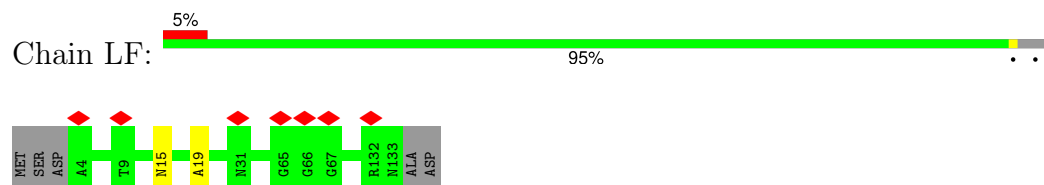
• Molecule 12: 40S ribosomal protein S11-A



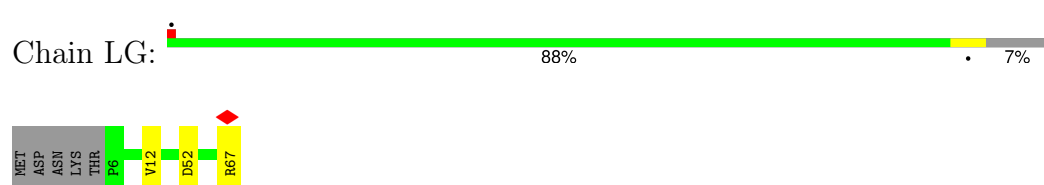
- Molecule 13: 40S ribosomal protein S22-A



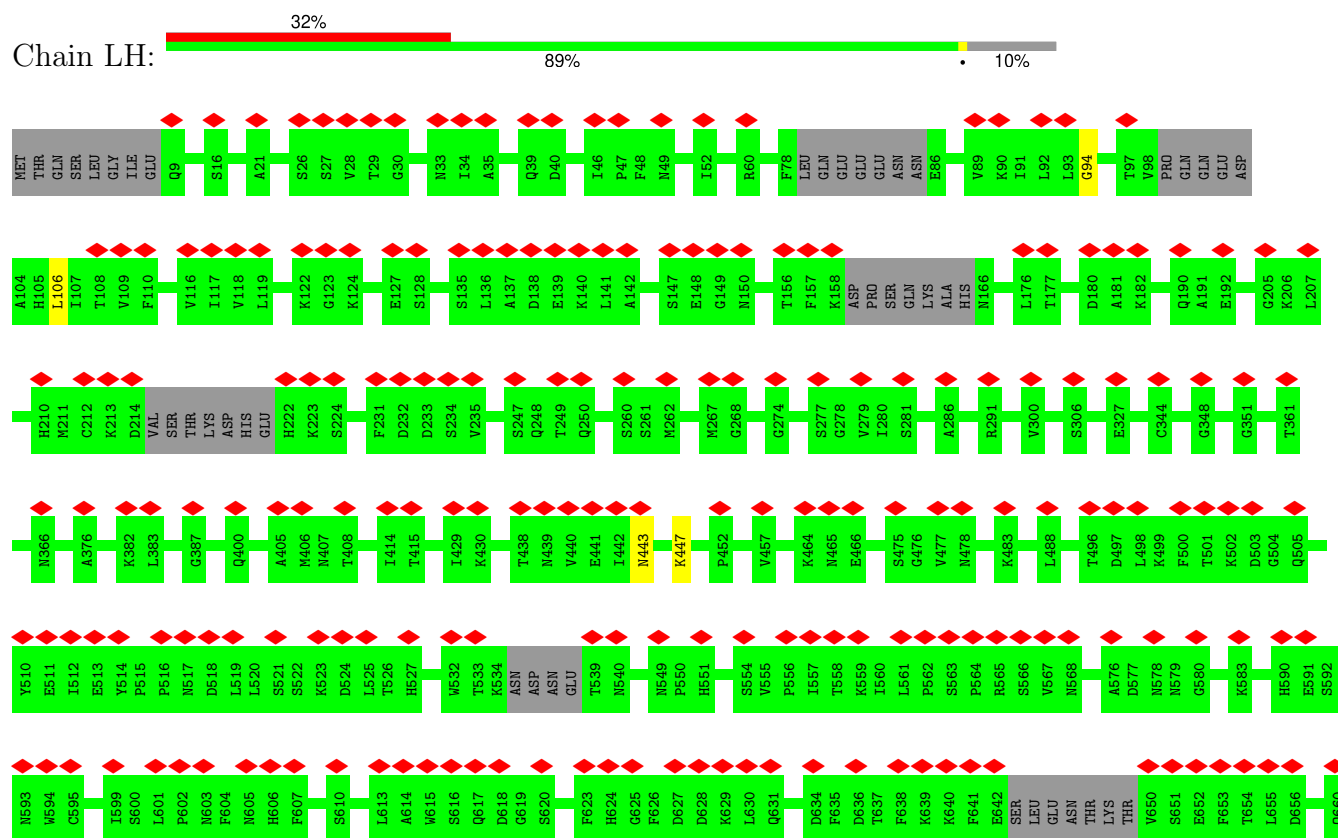
- Molecule 14: 40S ribosomal protein S24-A

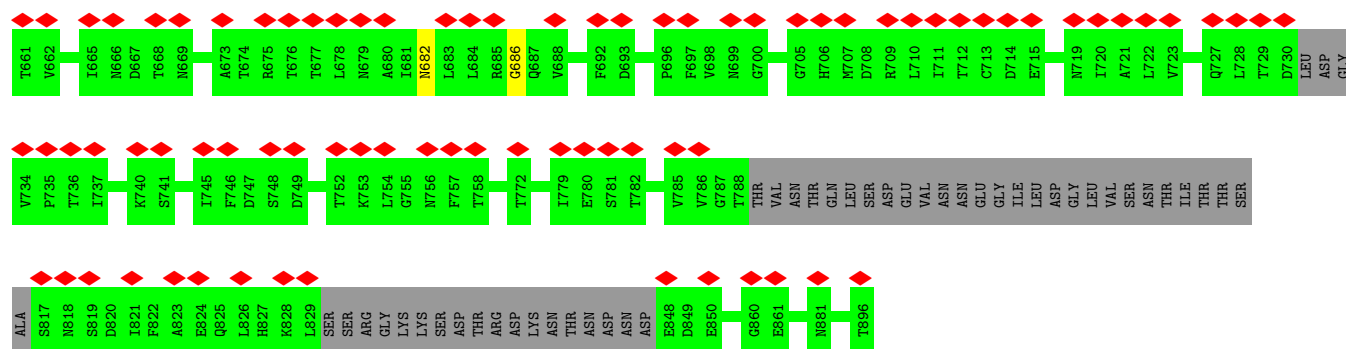


- Molecule 15: 40S ribosomal protein S28-A

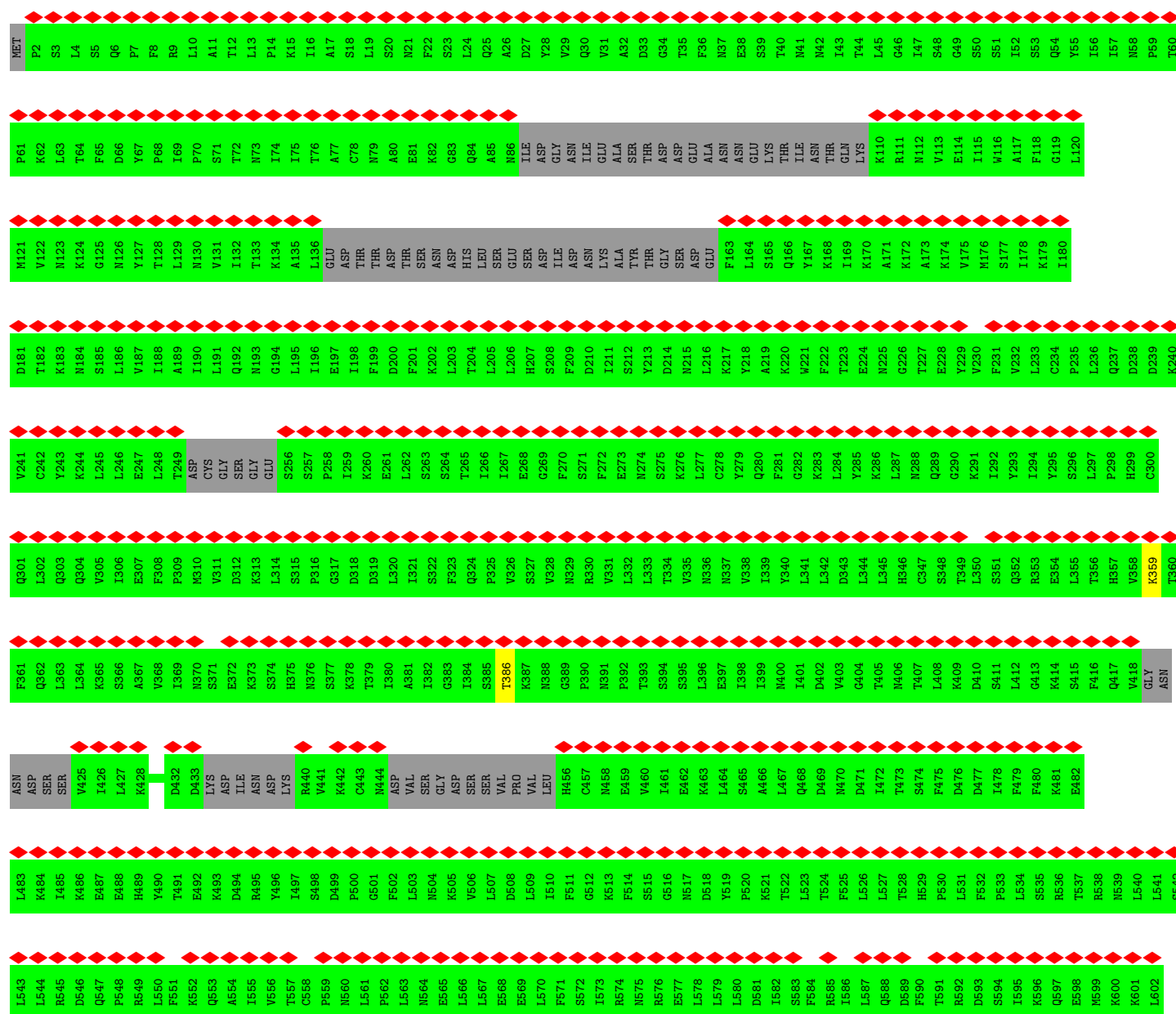
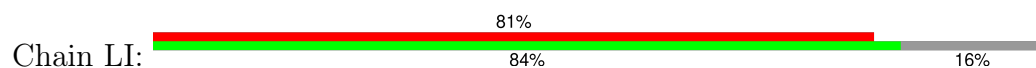


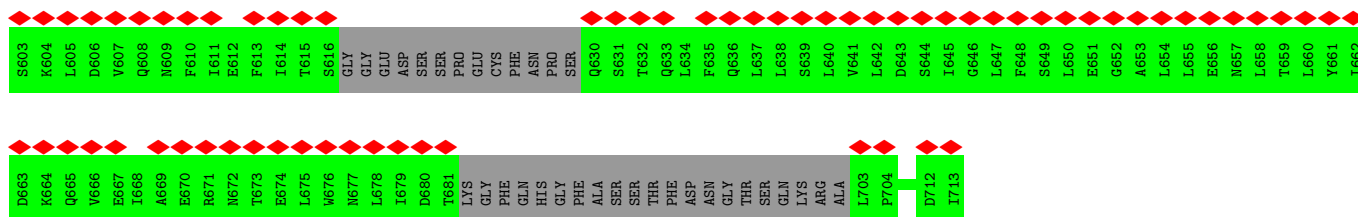
- Molecule 16: NET1-associated nuclear protein 1



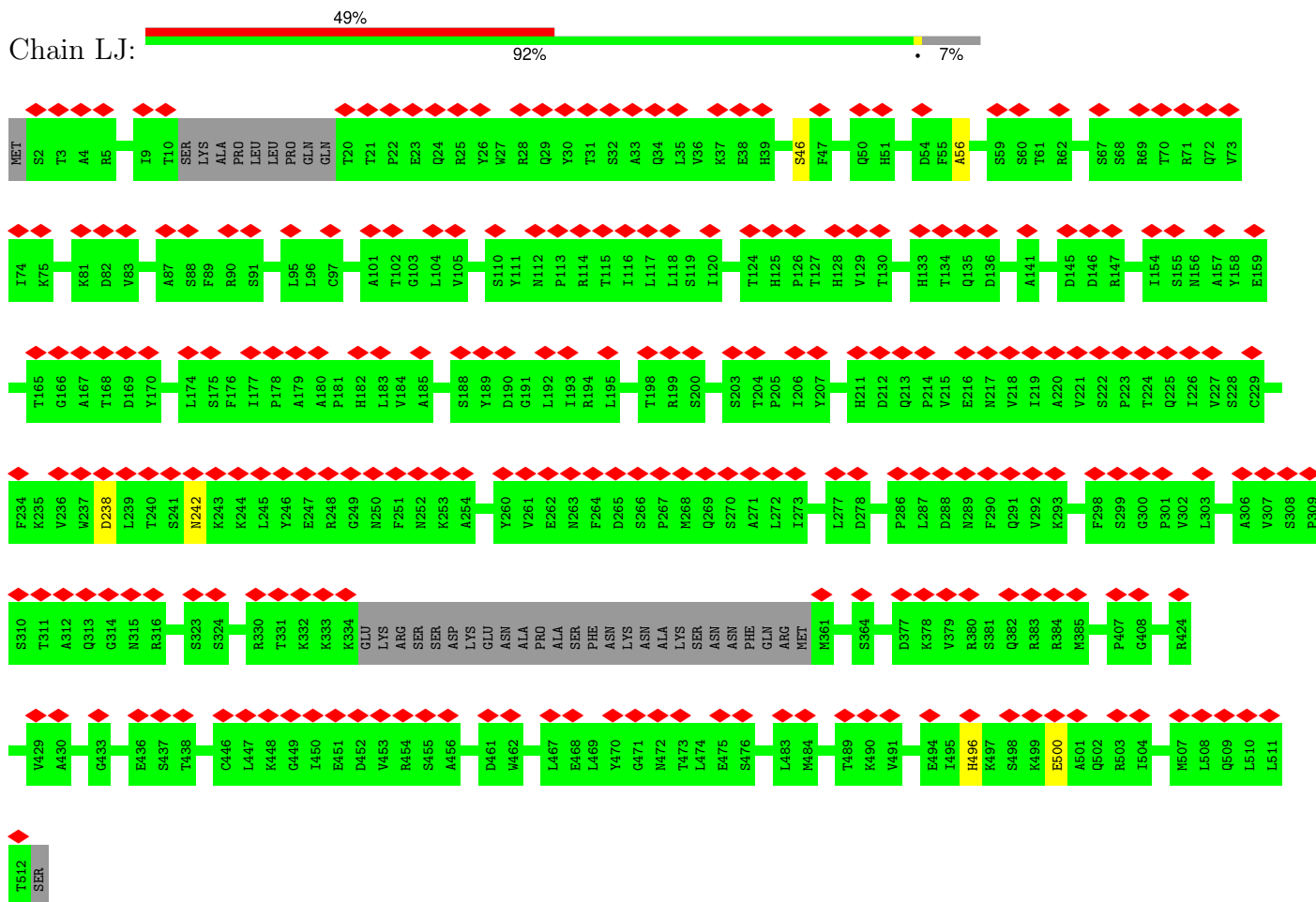


• Molecule 17: U3 small nucleolar RNA-associated protein 8

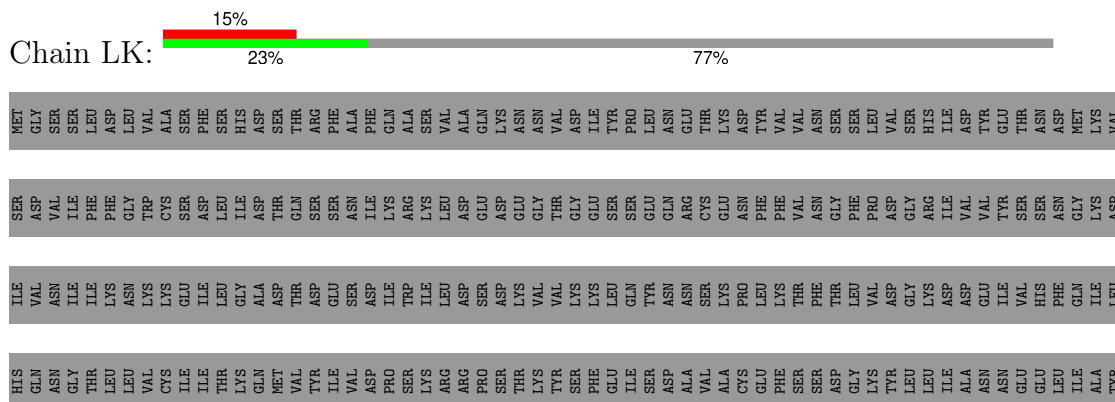




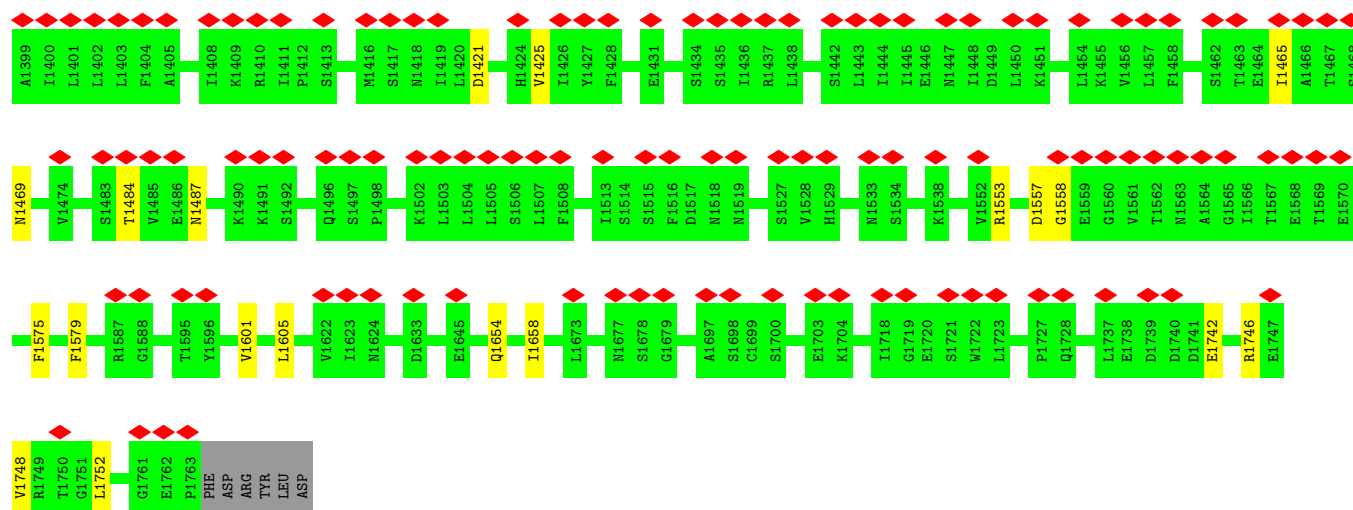
• Molecule 18: U3 small nucleolar RNA-associated protein 15



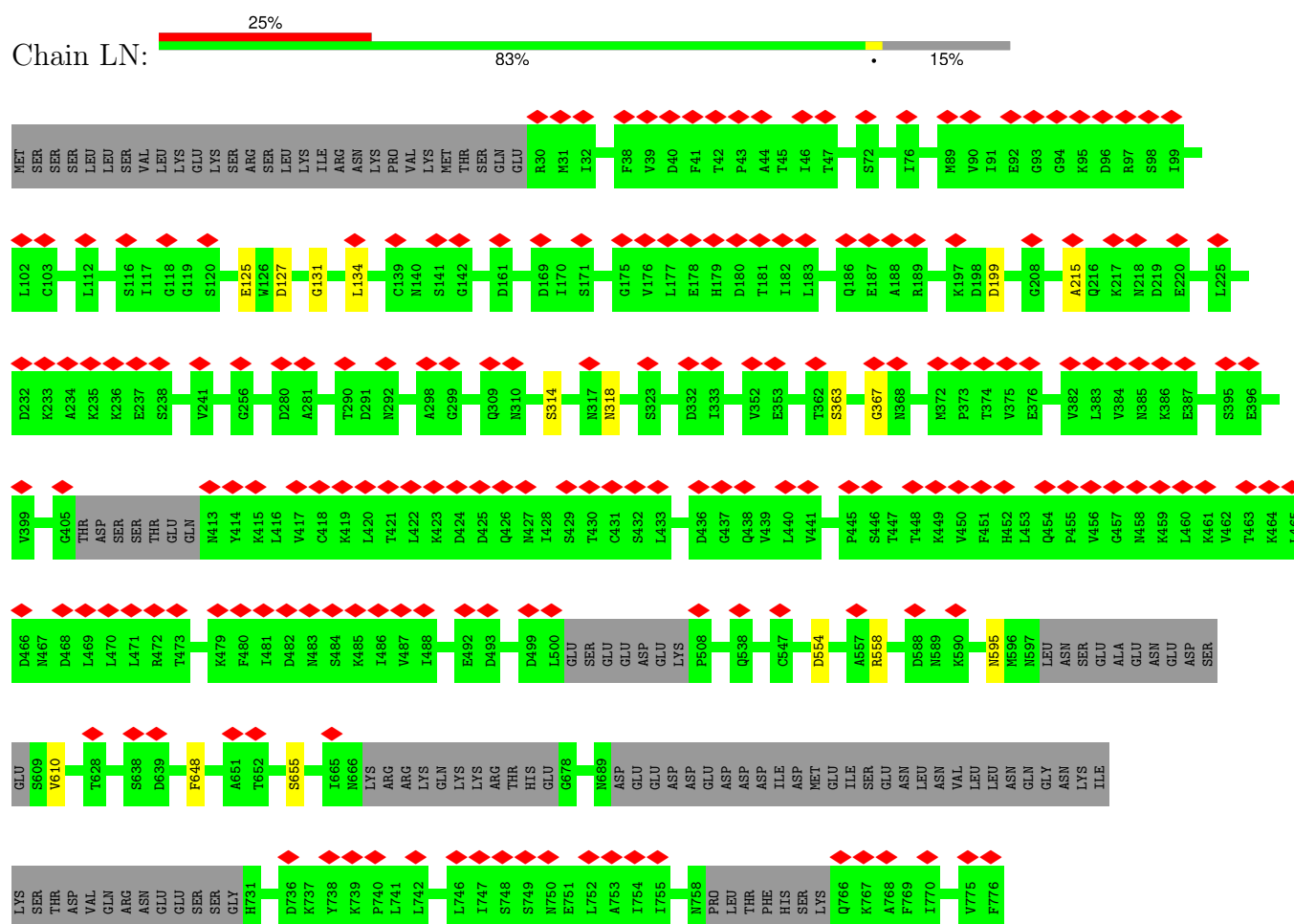
• Molecule 19: U3 small nucleolar RNA-associated protein 9



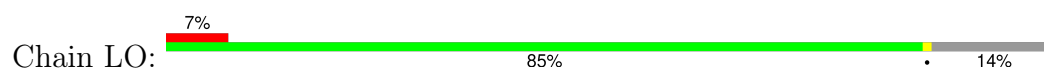


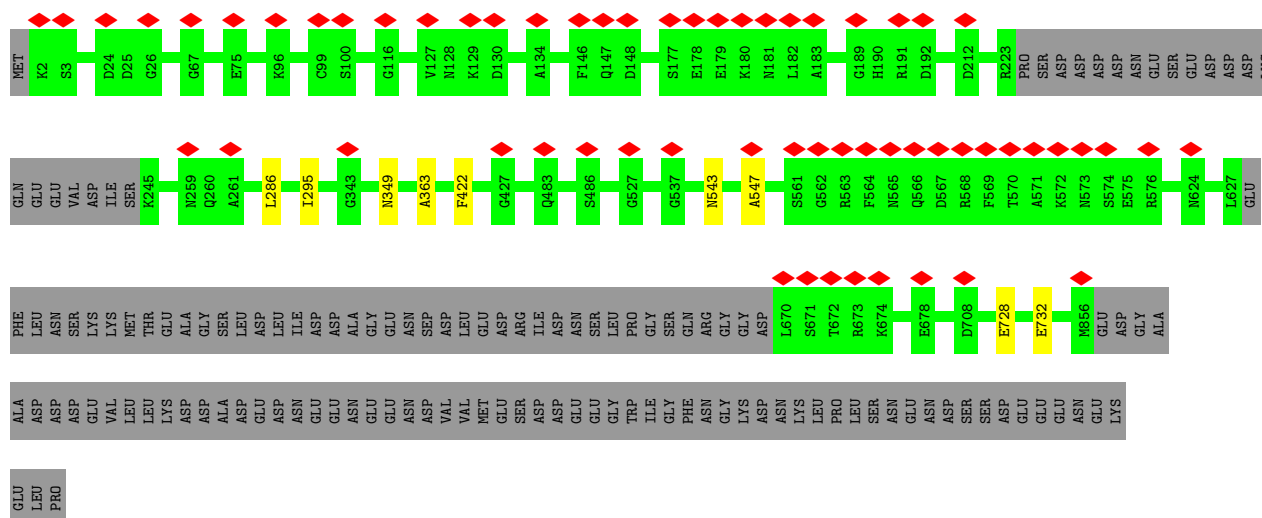


- Molecule 22: U3 small nucleolar RNA-associated protein 4

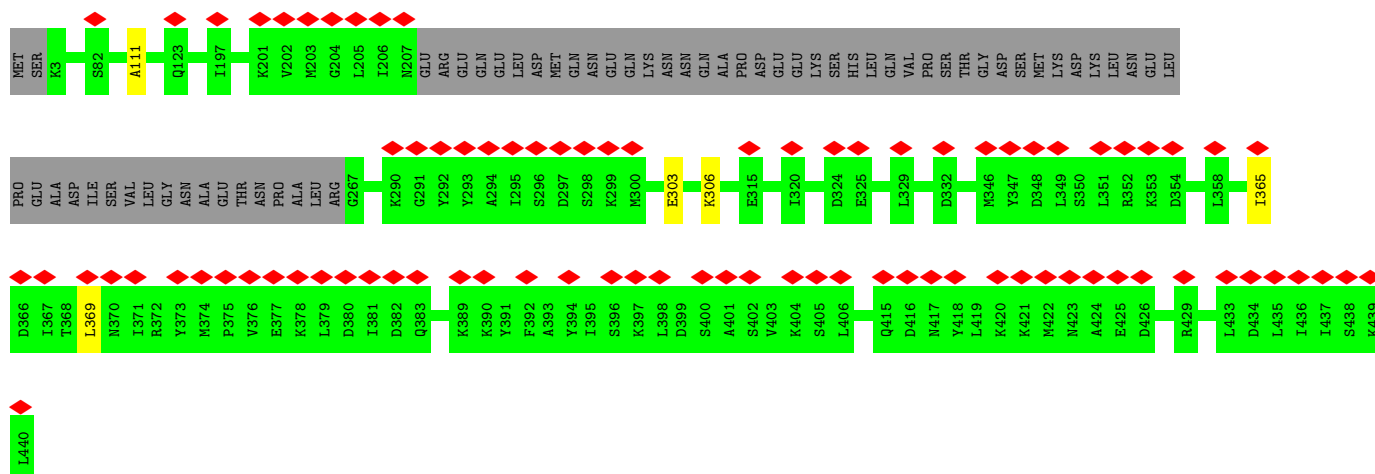
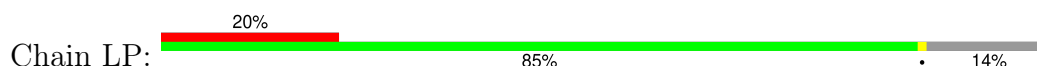


- Molecule 23: Periodic tryptophan protein 2

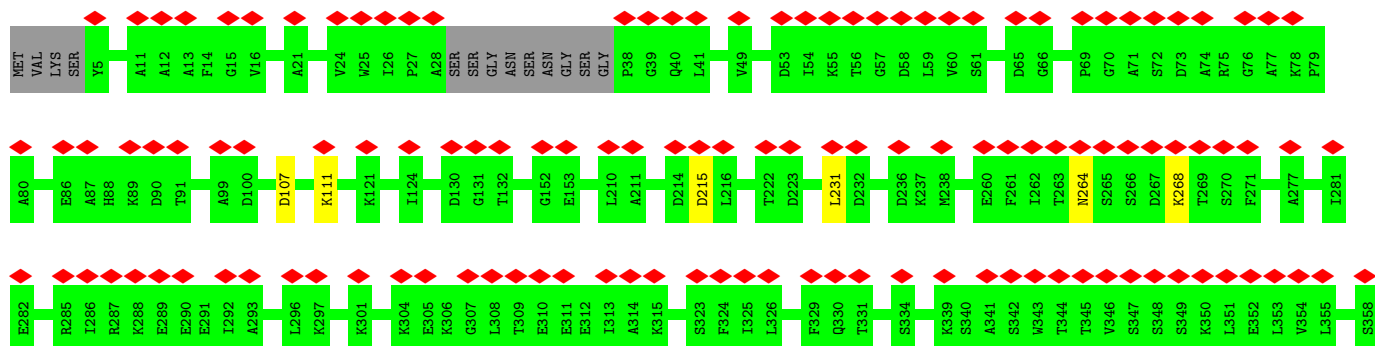
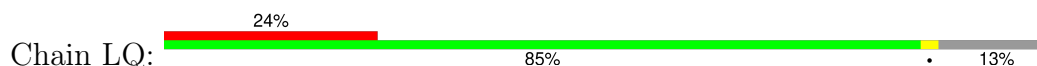




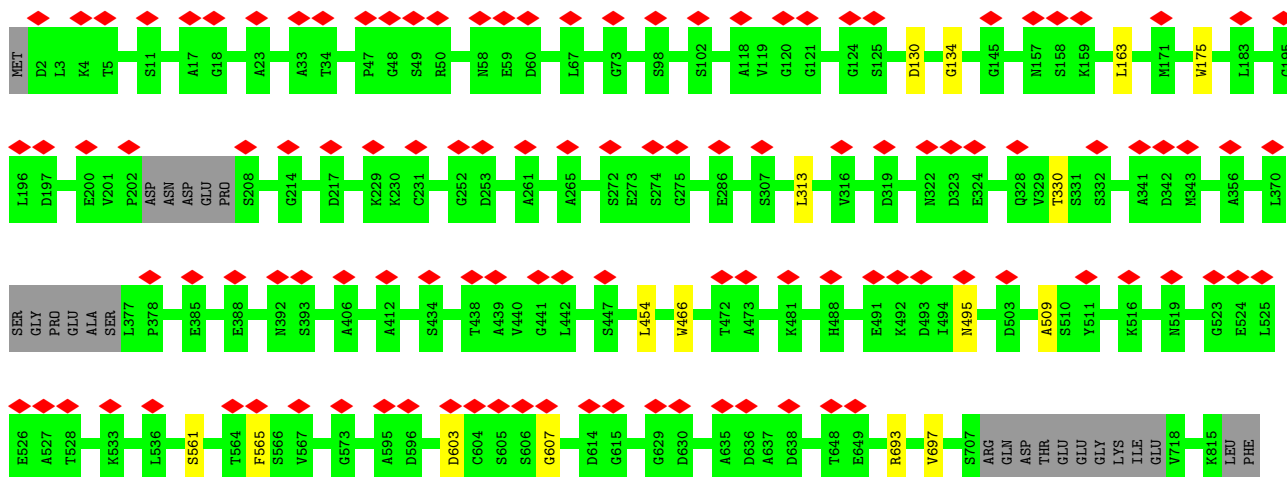
• Molecule 24: U3 small nucleolar RNA-associated protein 6



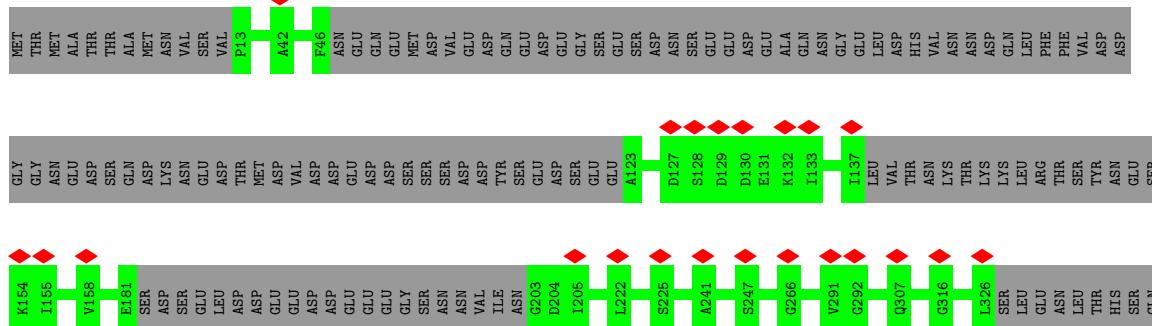
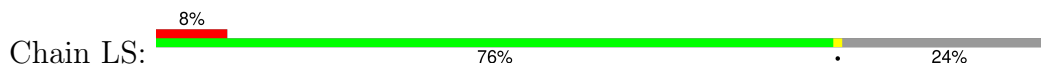
• Molecule 25: U3 small nucleolar RNA-associated protein 12

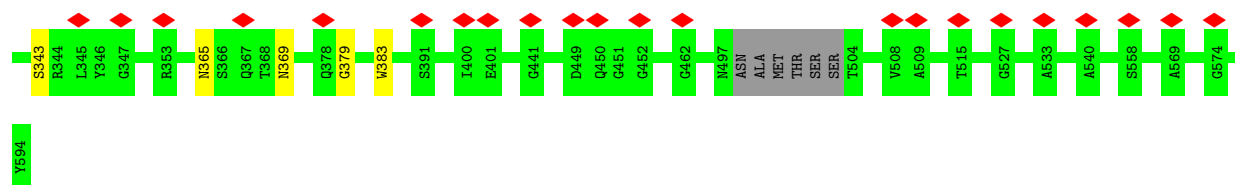


- Molecule 26: U3 small nucleolar RNA-associated protein 13



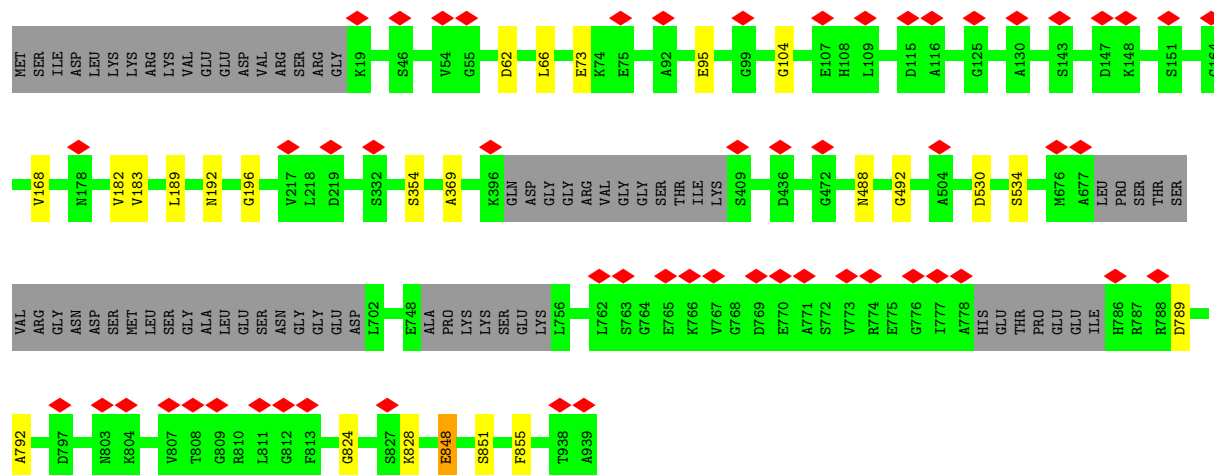
- Molecule 27: U3 small nucleolar RNA-associated protein 18





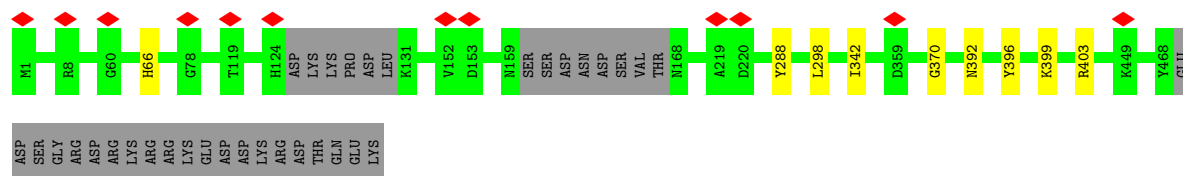
- Molecule 28: U3 small nucleolar RNA-associated protein 21

Chain LT: 6% 90% 7%



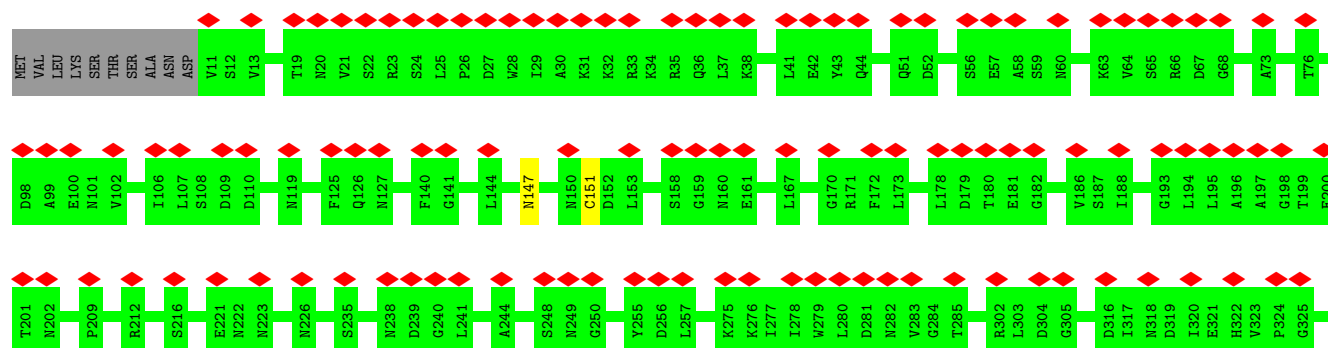
- Molecule 29: Protein SOF1

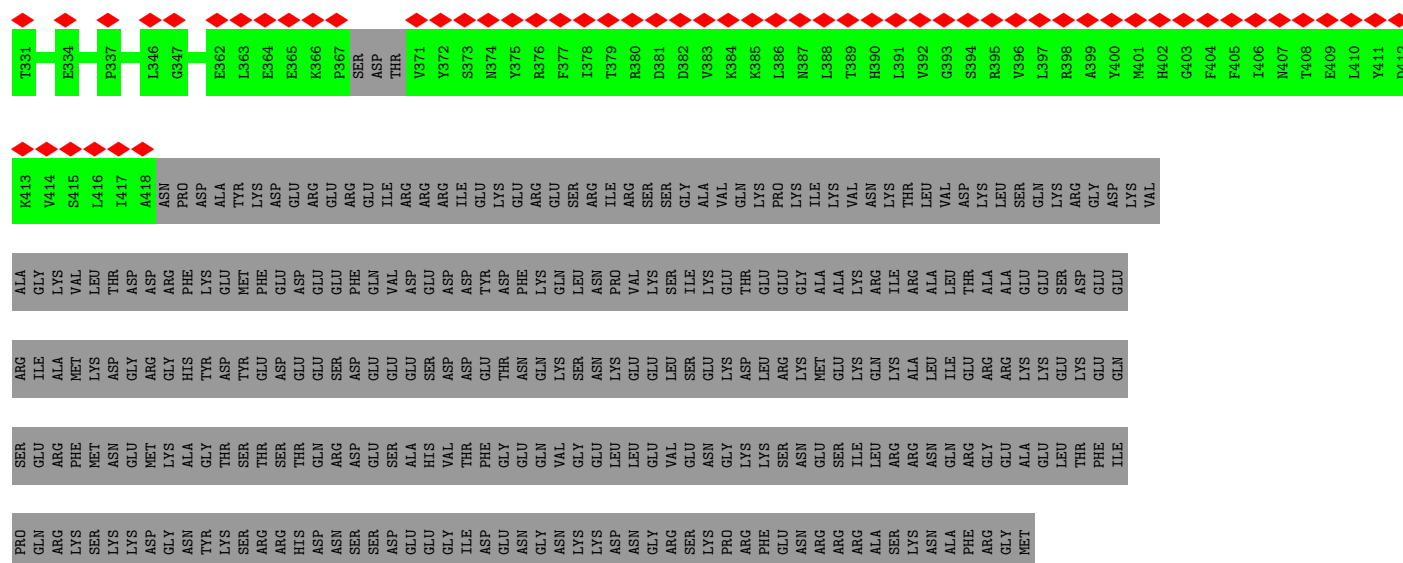
Chain LU: 91% 7%



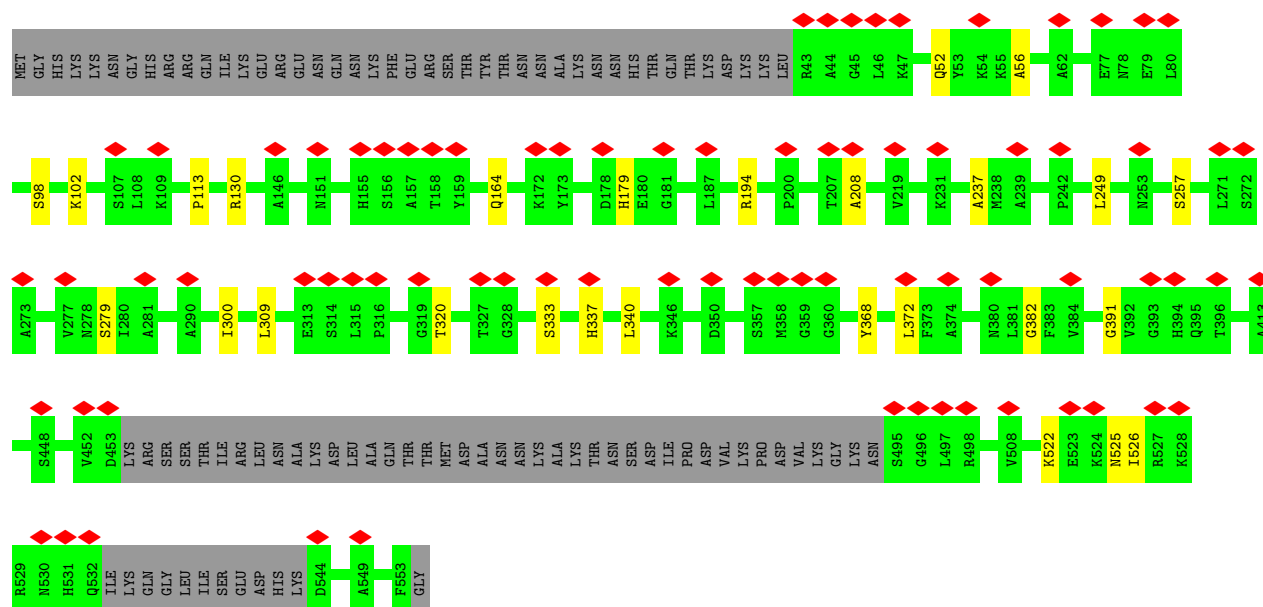
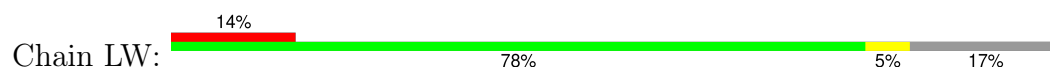
- Molecule 30: Ribosome biogenesis protein ENP2

Chain LV: 25% 57% 43%

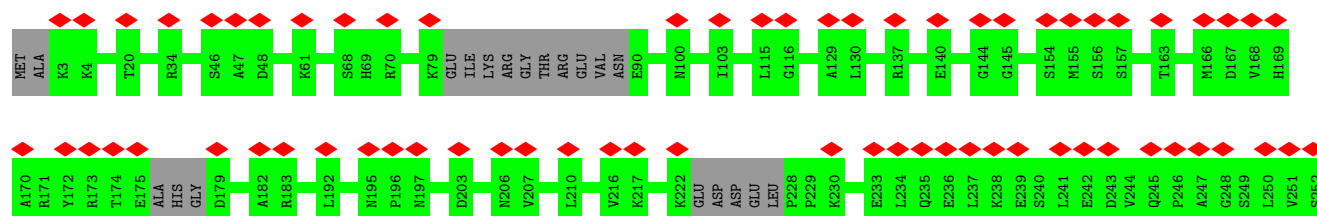
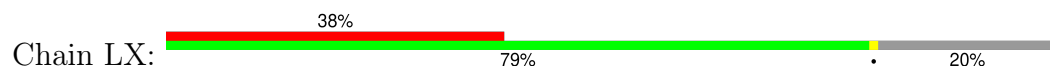


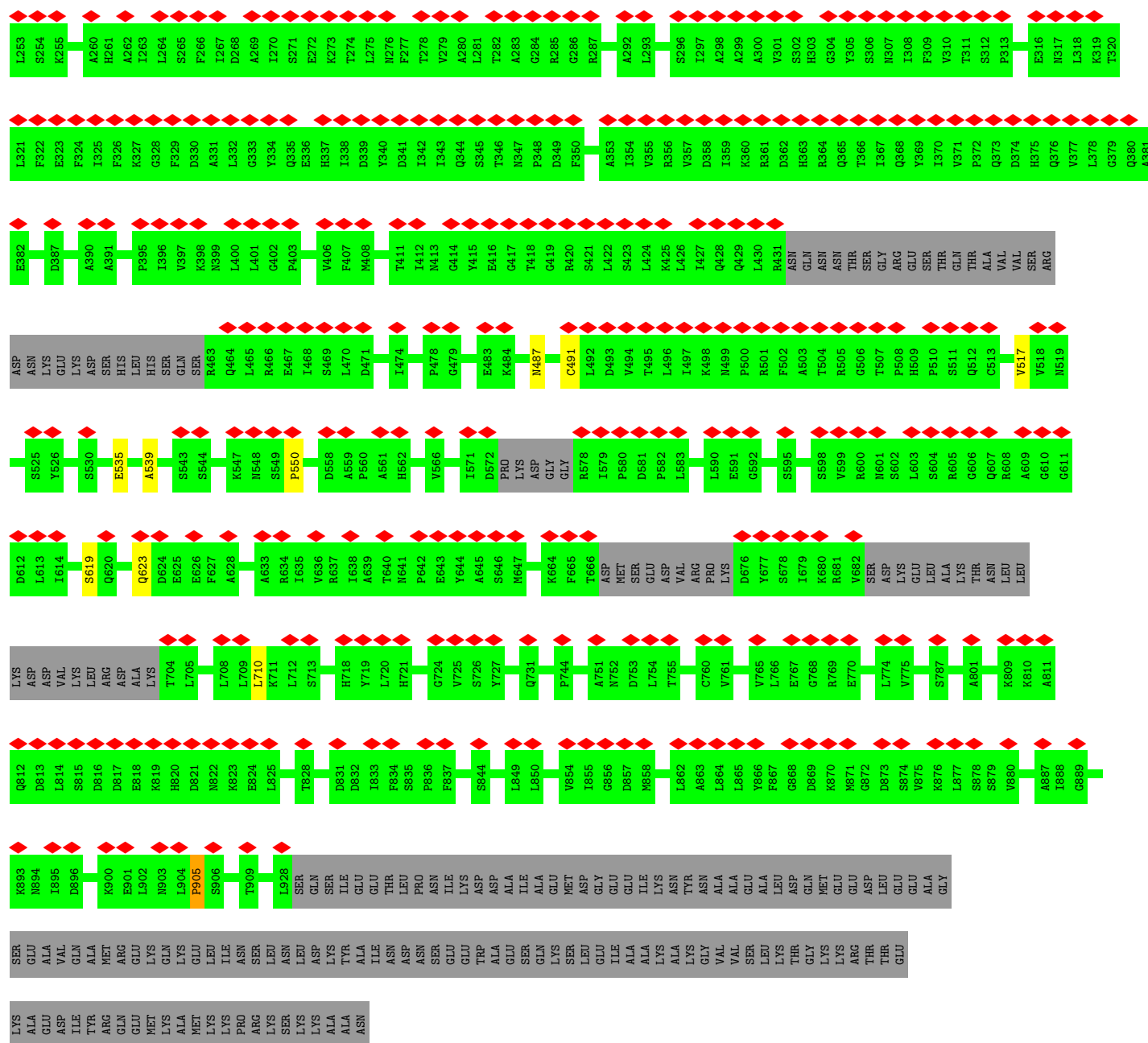


• Molecule 31: U3 small nucleolar RNA-associated protein 7

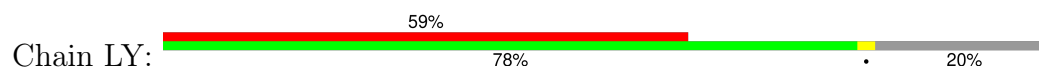


• Molecule 32: RNA cytidine acetyltransferase



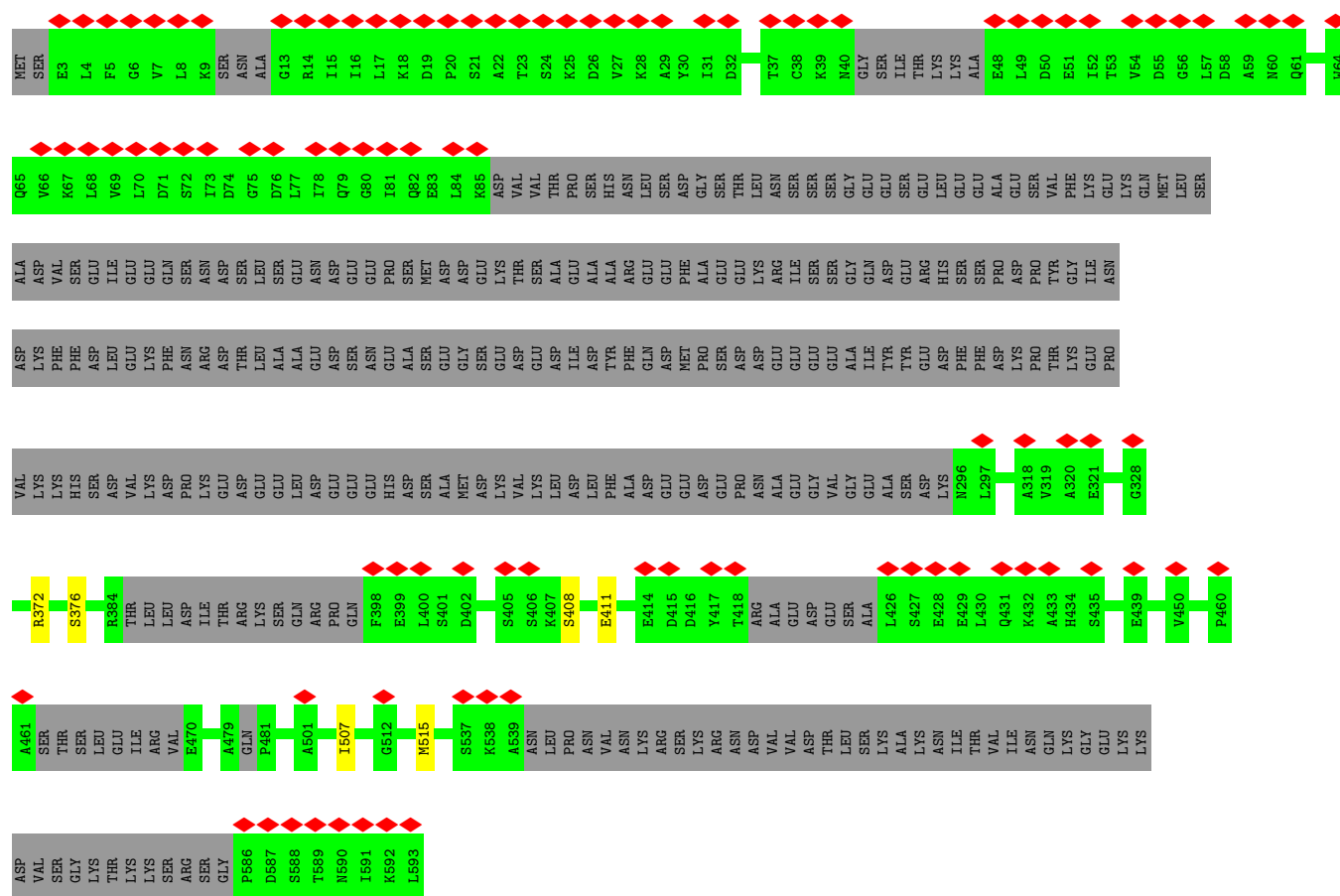


• Molecule 32: RNA cytidine acetyltransferase

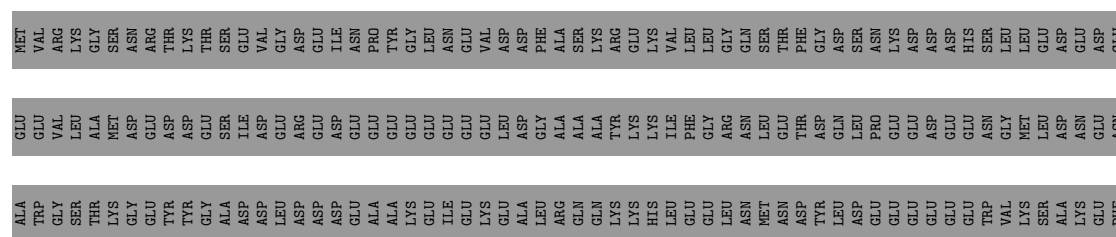


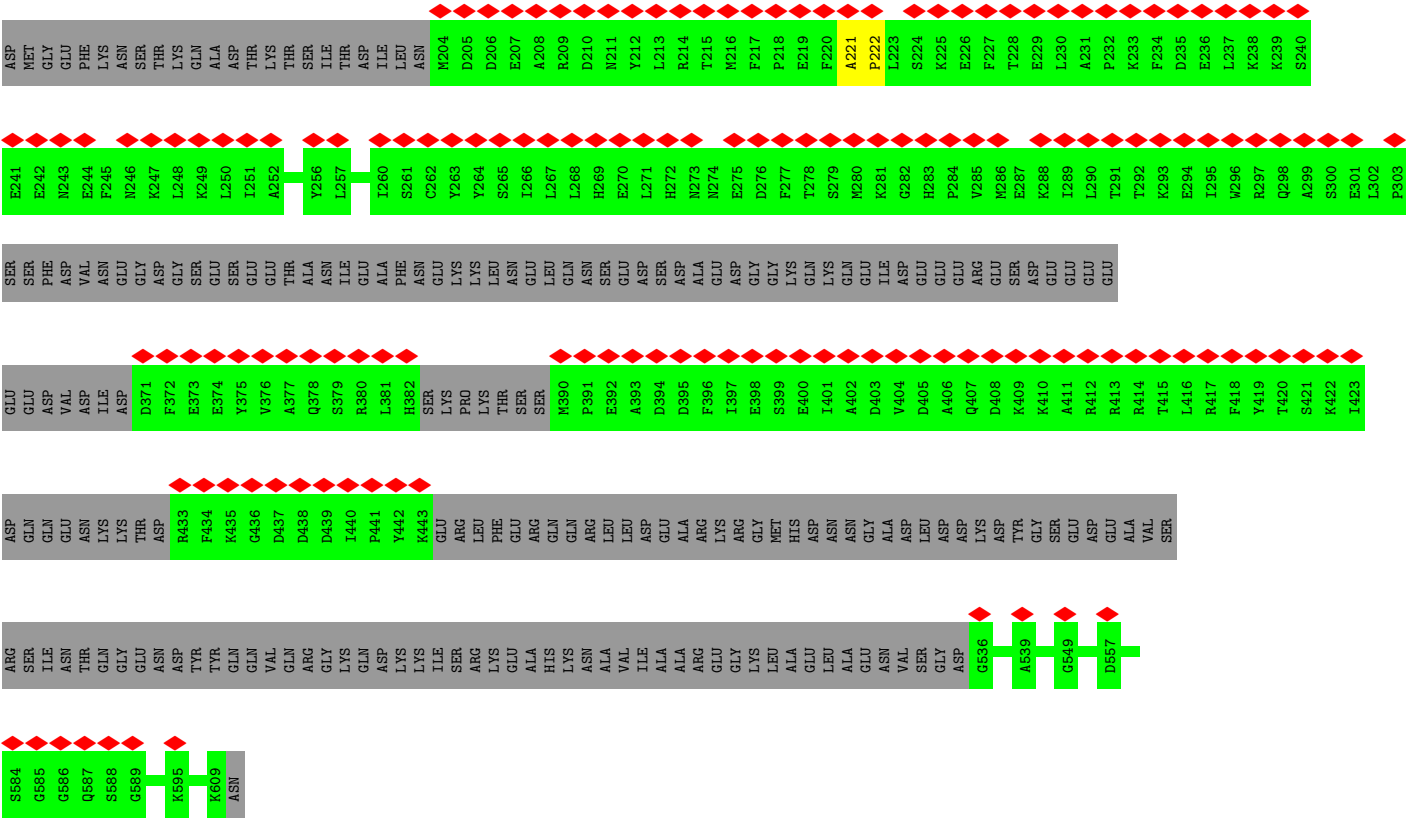


- Molecule 34: U3 small nucleolar RNA-associated protein MPP10

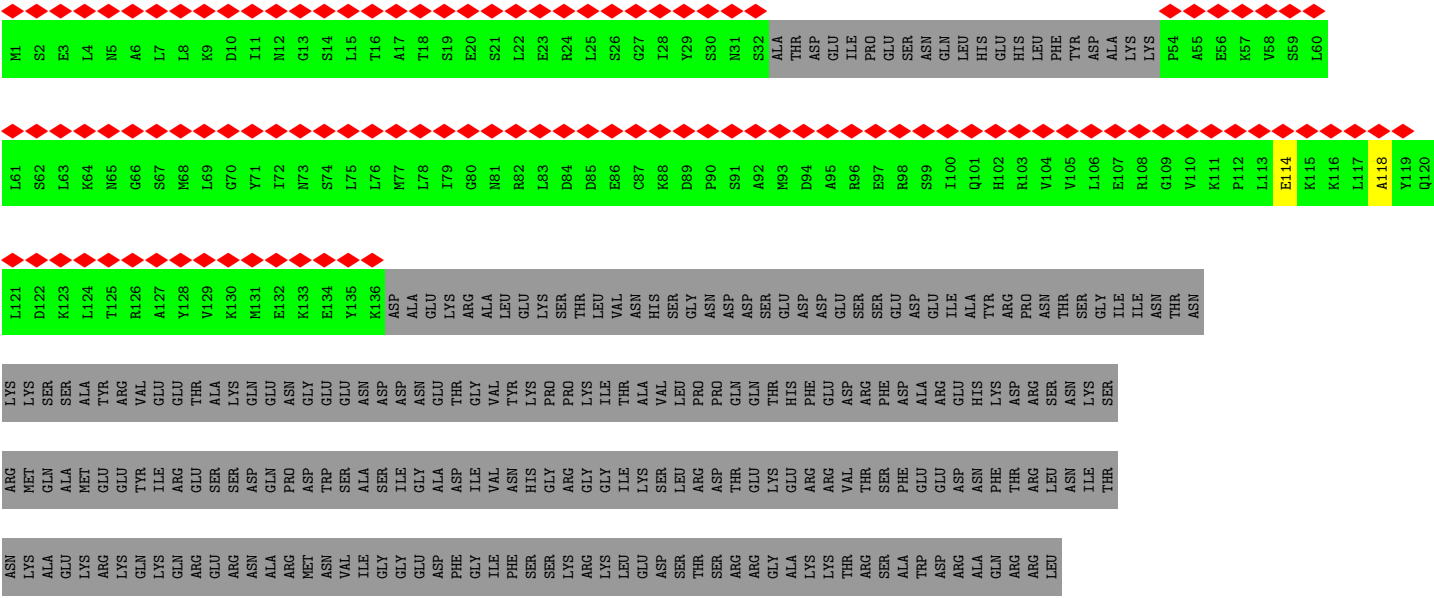


- Molecule 35: Something about silencing protein 10



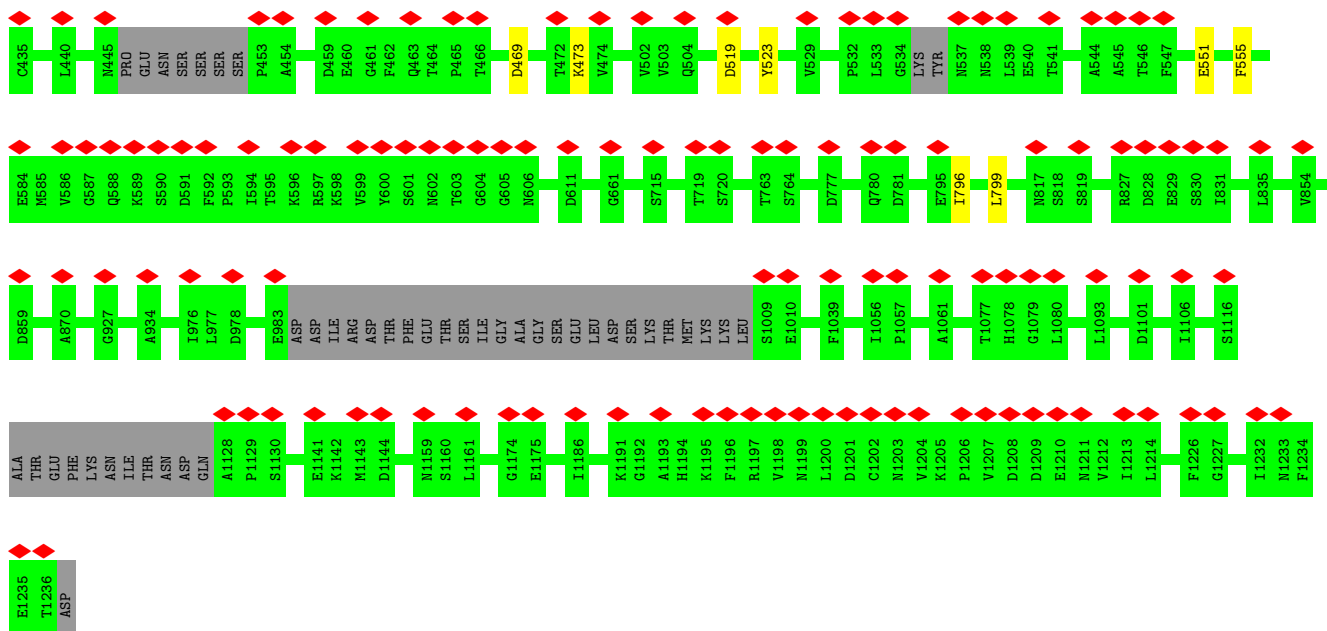


● Molecule 36: U3 small nucleolar ribonucleoprotein protein LCP5

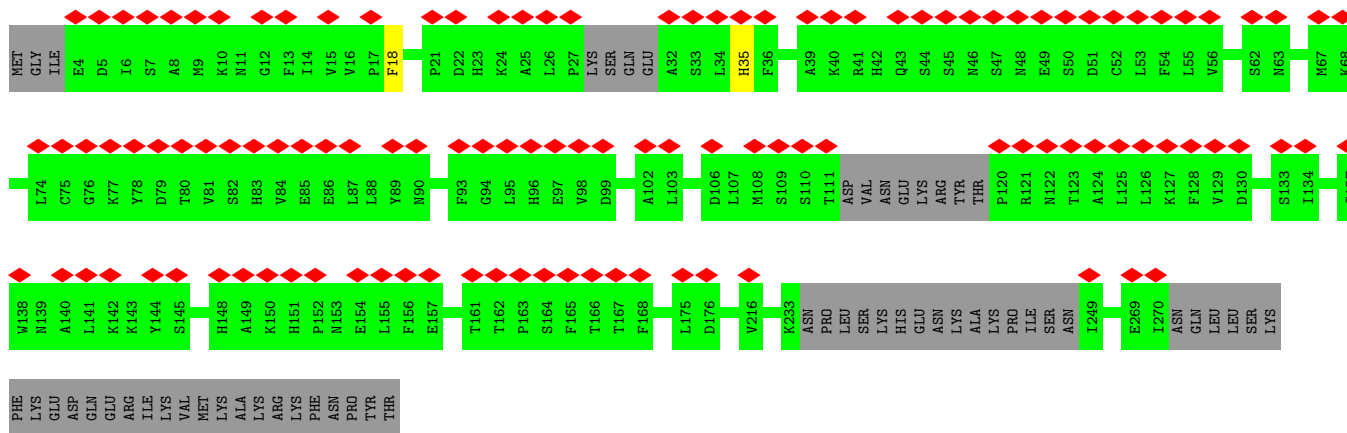
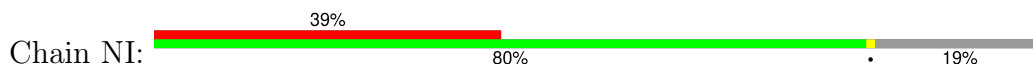


● Molecule 37: Bud site selection protein 21

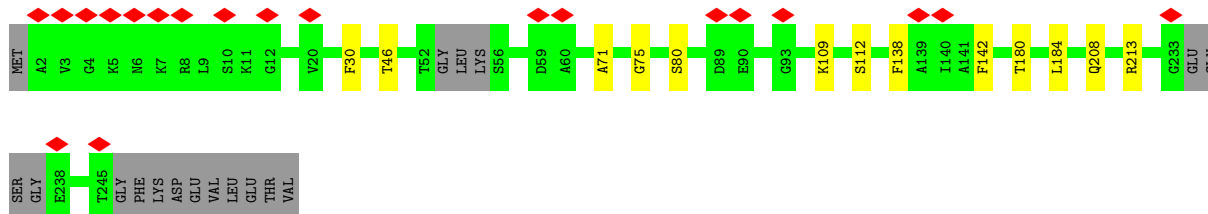
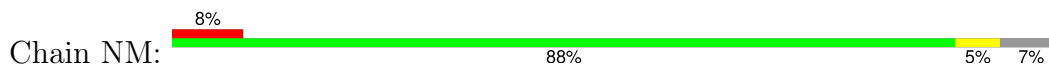




• Molecule 41: Ribosomal RNA-processing protein 7







































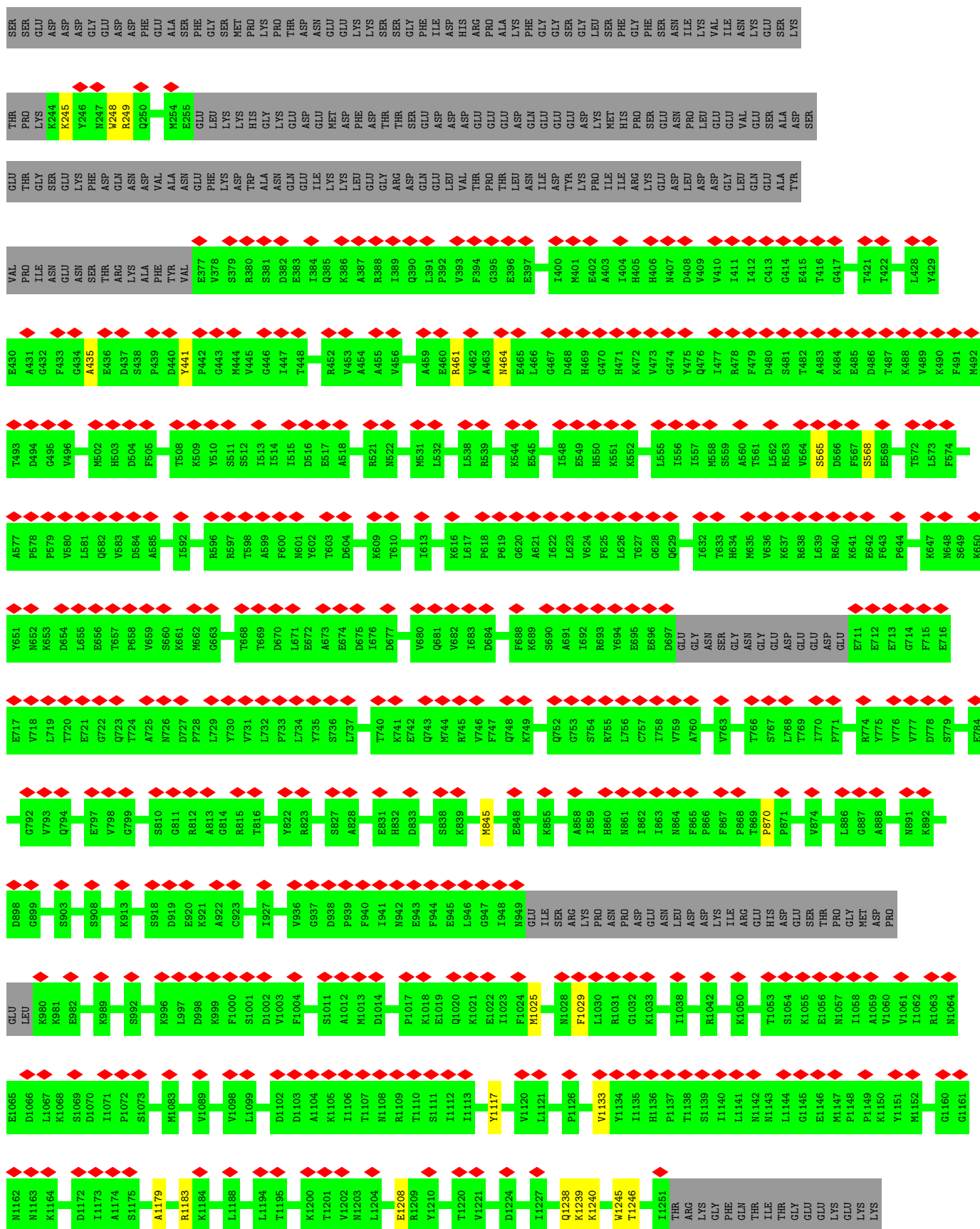
• Molecule 42: Small ribosomal subunit protein eS1A



• Molecule 43: Protein BFR2





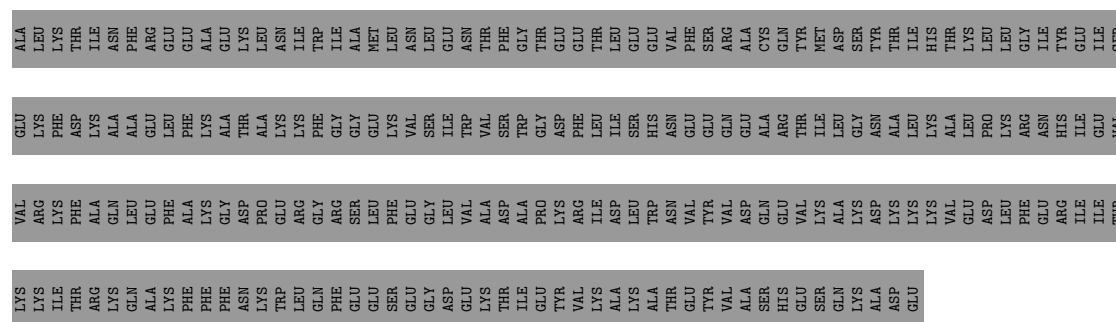
- Molecule 46: Exosome complex exonuclease RRP6

[illegible]

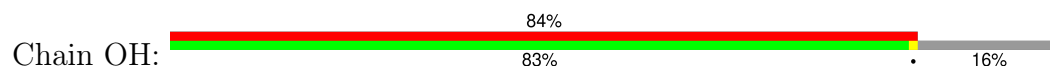
- Chain OA:  99%

[illegible]

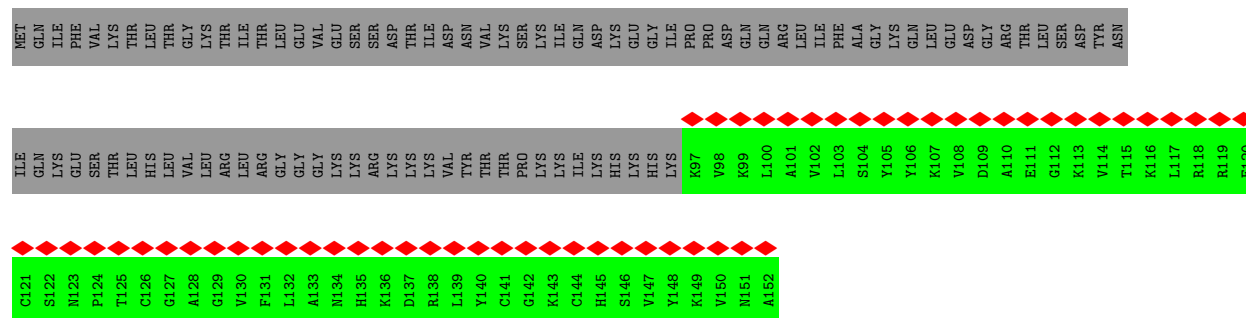




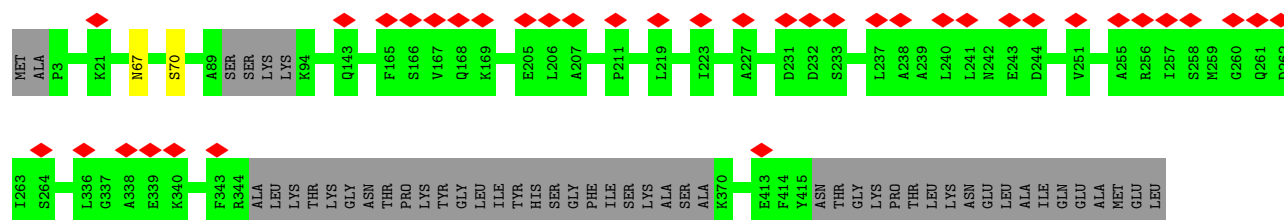
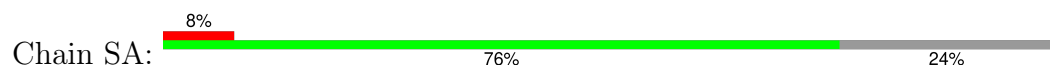
- Molecule 48: 40S ribosomal protein S12



- Molecule 49: Ubiquitin-40S ribosomal protein S31

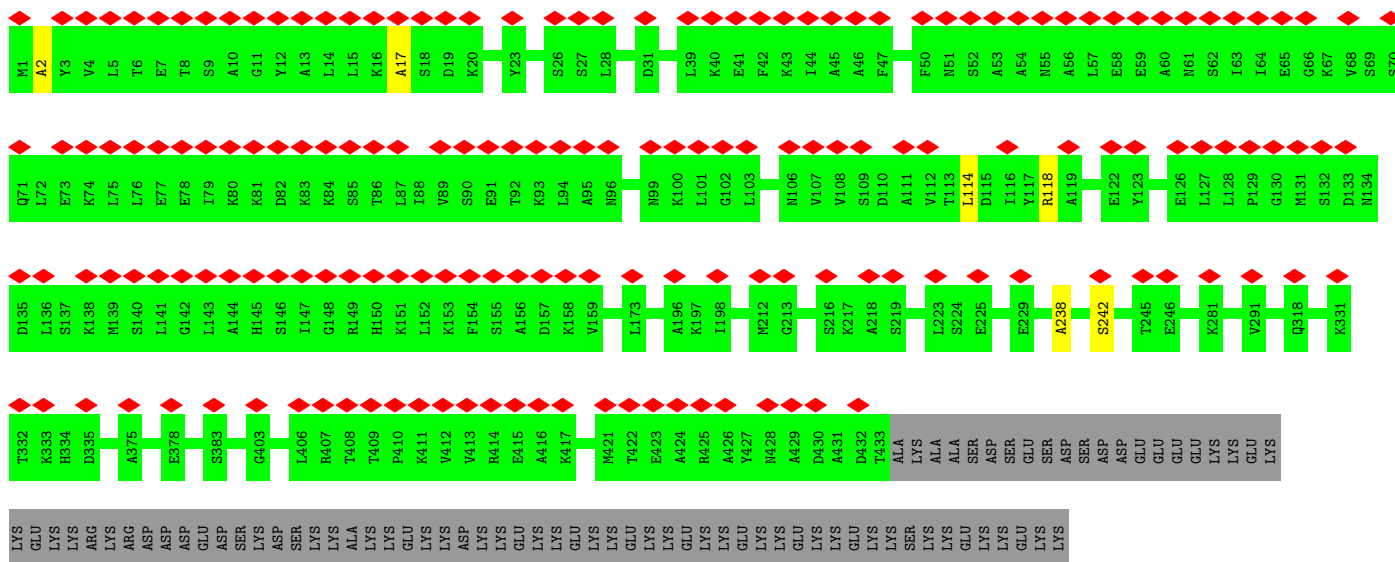
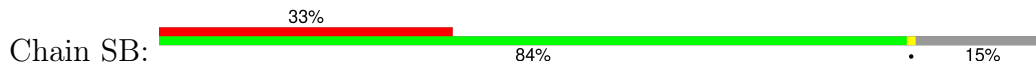


- Molecule 50: Nucleolar protein 56

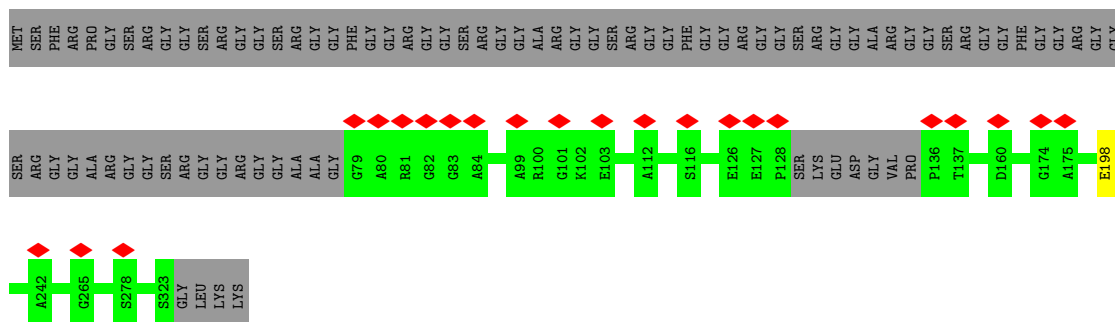
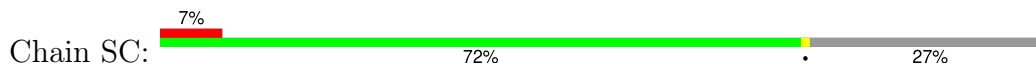


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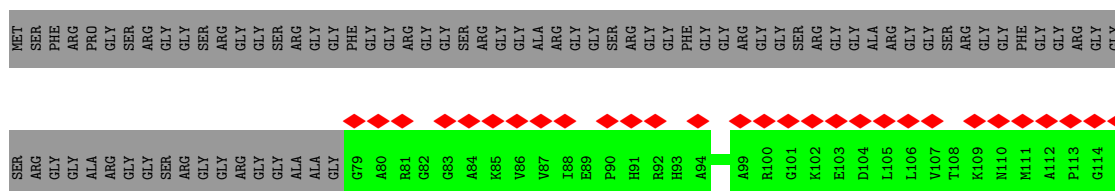
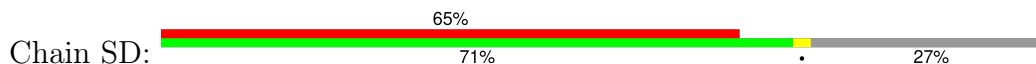
- Molecule 51: Nucleolar protein 58

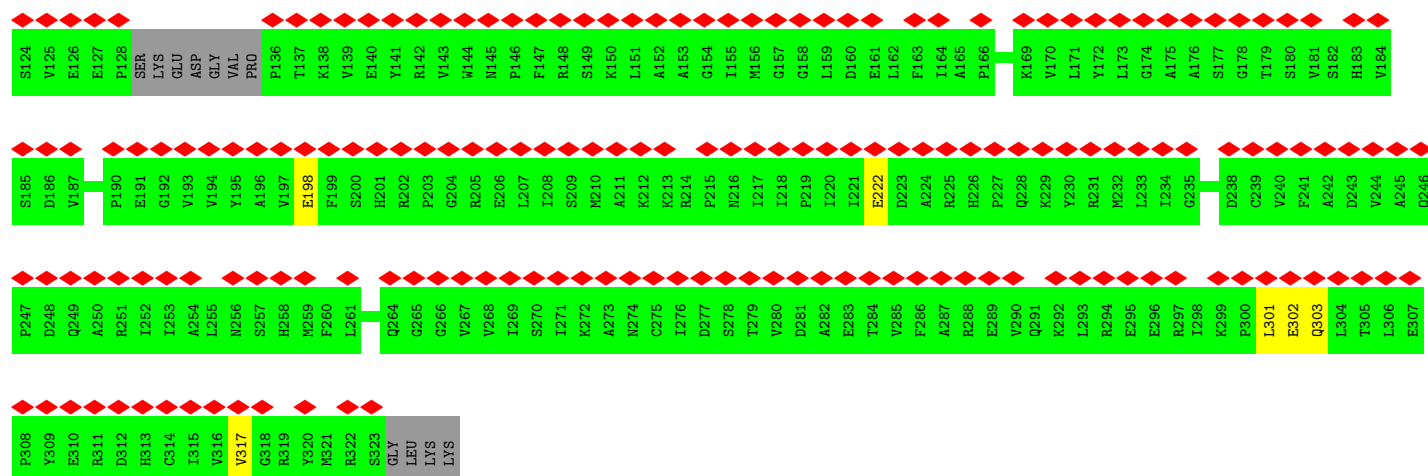


- Molecule 52: rRNA 2'-O-methyltransferase fibrillar

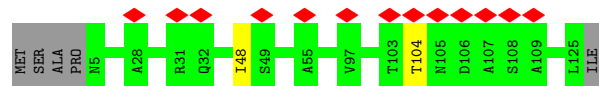


- Molecule 52: rRNA 2'-O-methyltransferase fibrillar

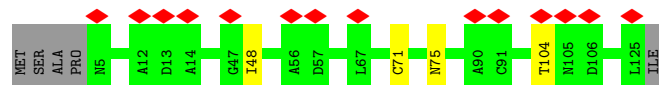




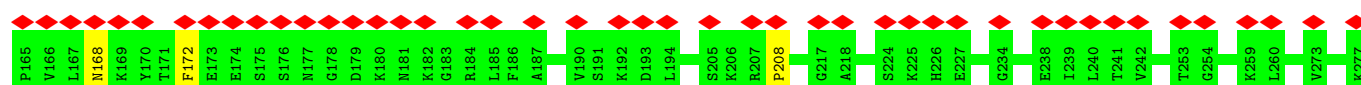
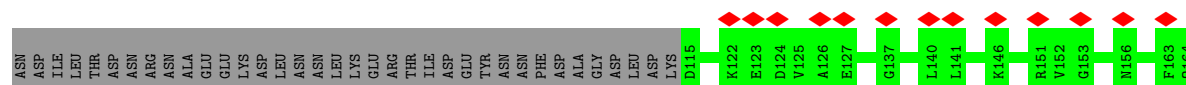
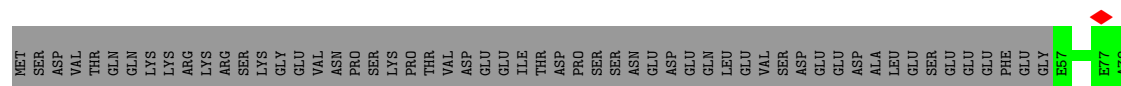
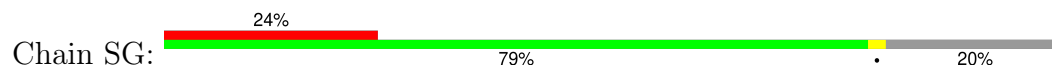
- Molecule 53: 13 kDa ribonucleoprotein-associated protein

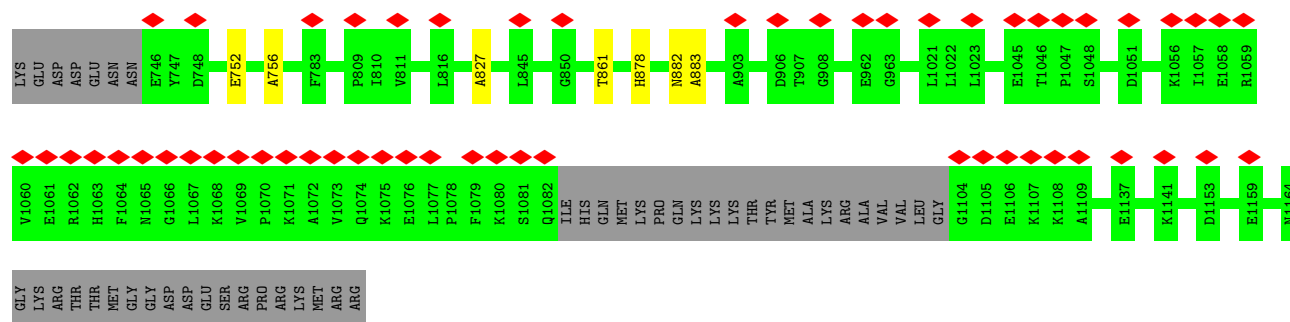


- Molecule 53: 13 kDa ribonucleoprotein-associated protein

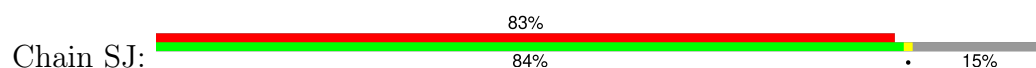


- Molecule 54: Ribosomal RNA-processing protein 9

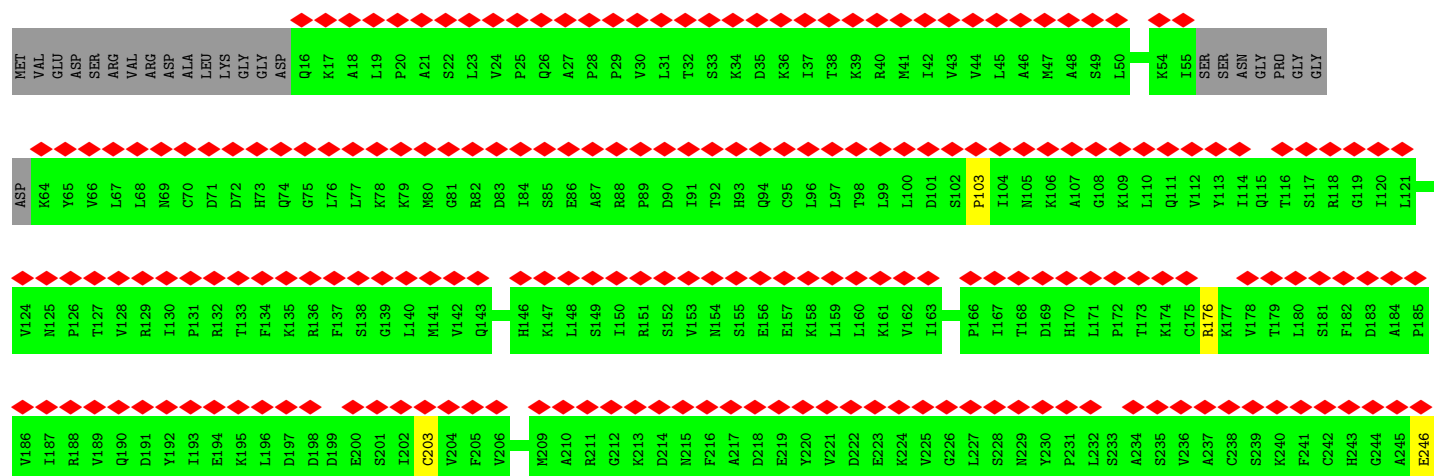
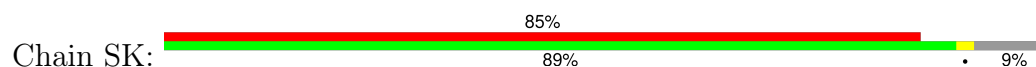


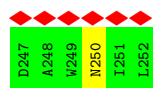


• Molecule 57: Ribosomal RNA small subunit methyltransferase NEP1

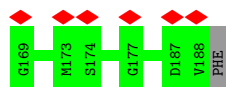
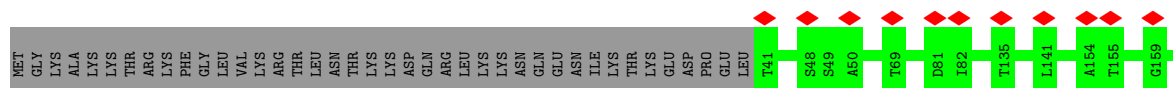
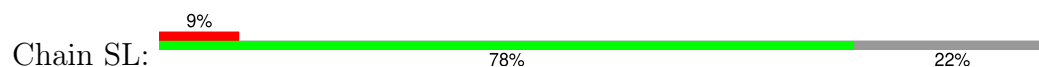


• Molecule 57: Ribosomal RNA small subunit methyltransferase NEP1

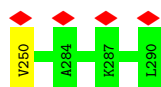
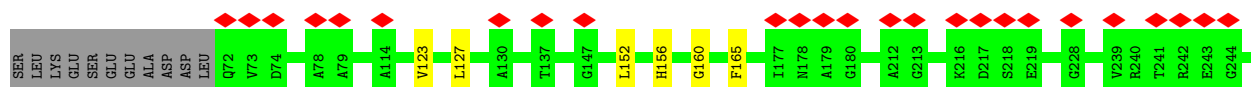
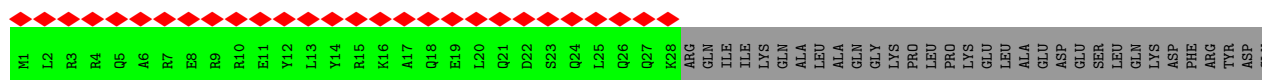
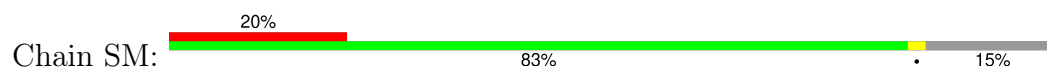




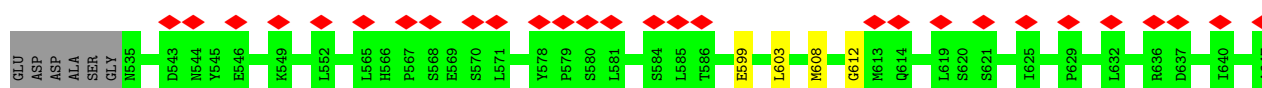
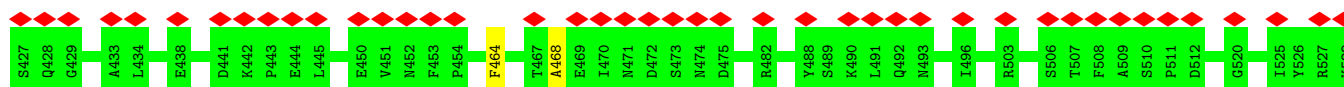
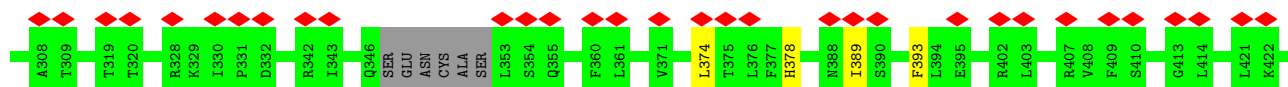
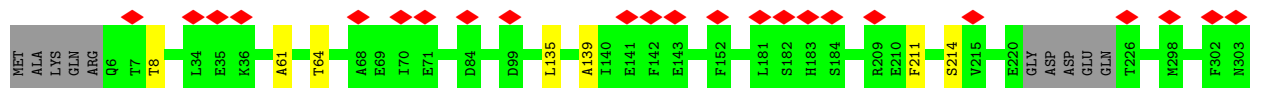
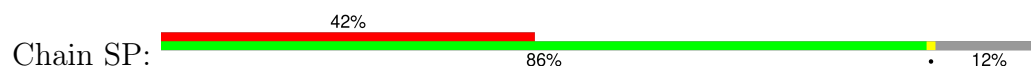
- Molecule 58: rRNA-processing protein FCF1



- Molecule 59: U3 small nucleolar ribonucleoprotein protein IMP4



- Molecule 60: U3 small nucleolar RNA-associated protein 20



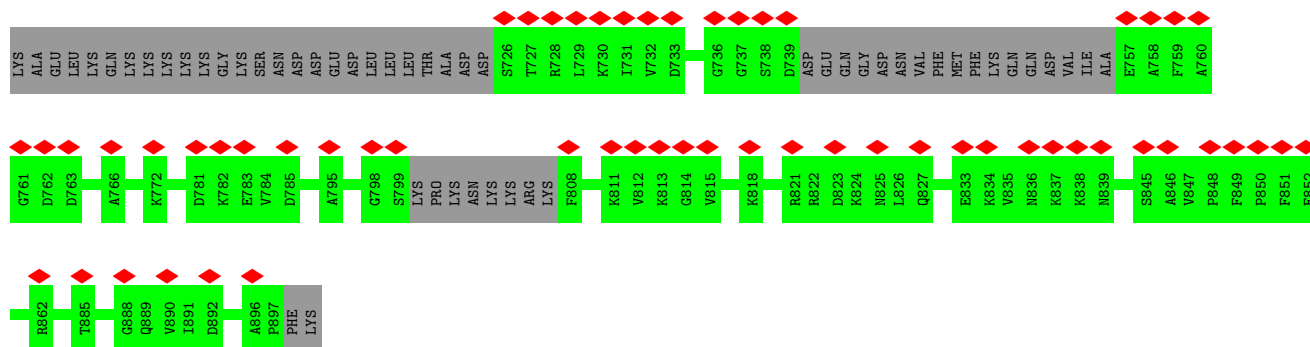


THR	VAL	ILE	THR	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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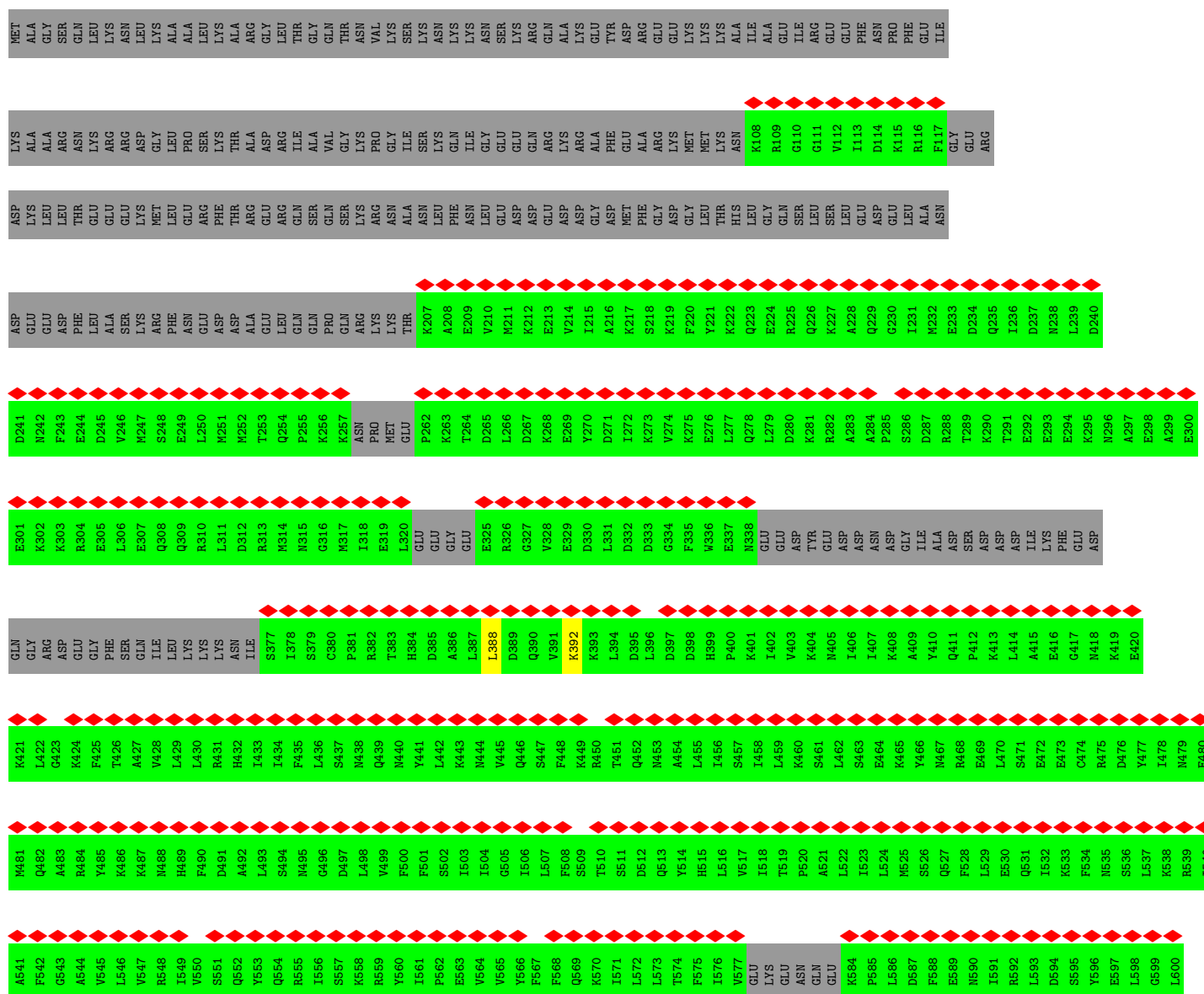
• Molecule 61: rRNA-processing protein FCF2

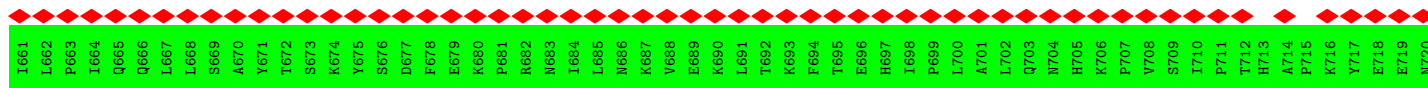


MET	ASP	GLN	SER	VAL	GLU	ASP	LEU	PHE	GLY	ALA	ARG	ASP	ALA	LYS	SER	SER	LEU	GLU	VAL	ASN	LYS	PRO	LEU	GLN	GLU	VAL	ASN	GLY	ASN	ASP	ASN	ASP	GLU	VAL	ILE	ILE	GLU	LYS	PHE	GLN	GLU	155	E56	757	N58	L59	K60
K61	L62	P63	K64	L65	E66	T67	A71	L72	A73	N74	LYS	LYS	LYS	LYS	LYS	ASN	VAL	VAL	LEU	PRO	SER	VAL	VAL	GLU	THR	GLU	ASP	LYS	GLN	GLU	VAL	ASP	ASN	D102	L106	D110	D111	N112	R115	E116	D120	L121	A128	A129	L130	A148	D155

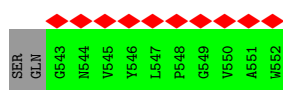
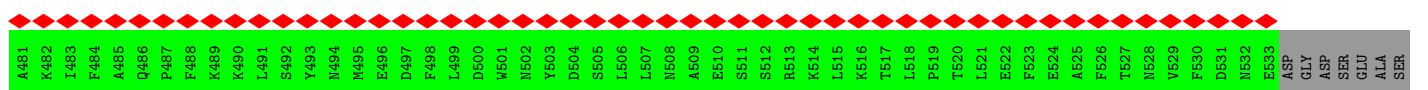
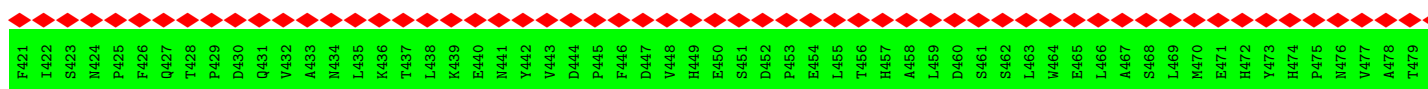
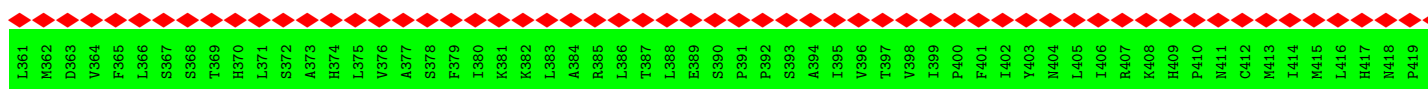
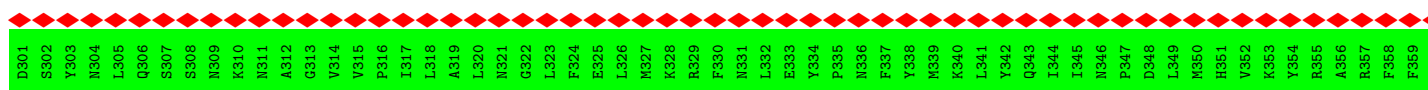
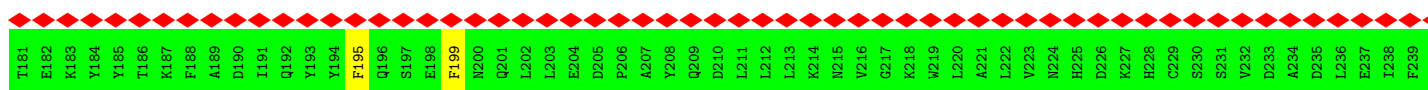
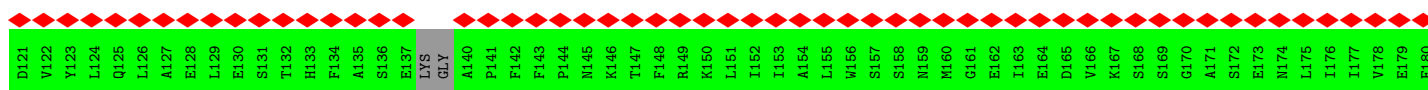
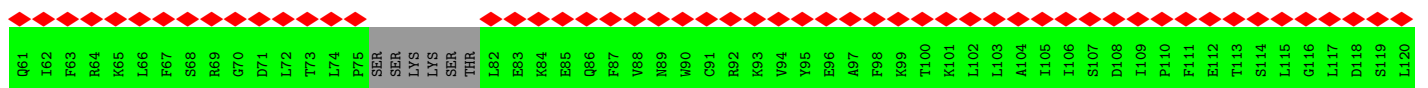
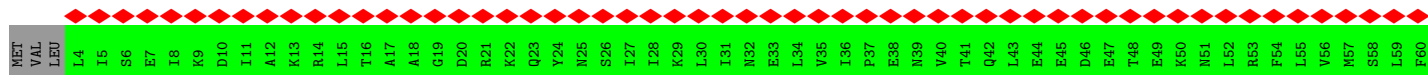


• Molecule 64: Nucleolar complex protein 14





- Molecule 65: Nucleolar complex protein 4



ASP VAL ASN	F421	R361	Y301	N241
	L422	L362	H302	W242
	T423	P363	I303	Q243
	F424	F364	Y304	D244
A425	S365	R305	V245	
Q426	P366	A306	I246	
R427	P367	V307	Y247	
Y428	T368	K308	V248	
K429	T369	K309	T249	
N430	V370	S310	N250	
D431	F371	L311	P251	
I432	I372	Y312	E252	
T433	K373	K313	E253	
Q434	I374	P314	W254	
D435	L375	S315	S255	
Q436	L376	A316	P256	
R437	D377	F317	H257	
D438	K378	F318	V258	
F439	K379	K319	V259	
L440	Y380	G320	Y260	
L441	A381	F321	E261	
E442	L382	L322	A262	
T443	P383	F323	T263	
V444	Y384	P324	K264	
R445	Q385	L325	L265	
Q446	T386	V326	F266	
R447	V387	E327	V267	
G448	D388	T328	S268	
H449	D389	G329	N269	
K450	C390	C330	L270	
D451	V391	N331	T271	
I452	Y392	V332	A272	
G453	Y393	R333	K273	
P454	F394	E334	E274	
E455	K395	A335	S275	
I456	R396	T336	Q276	
R457	F397	I337	K277	
R458	R398	A338	F278	
E459	I399	G339	I279	
L460	L400	S340	N280	
L461	ASP	V341	L281	
A462	ASP	L342	I282	
G463	GLY	A343	L283	
A464	S404	K344	L284	
S465	N405	V345	E285	
R466	G406	S346	R286	
	E407	V347	F287	
GLU	D408	P348	R288	
PHE	A409	A349	D289	
VAL	T410			
ASP				
PRO	GLN			
GLN	R411	L350	N290	
GLU	V412	H351	I291	
ALA	L413	S352	E292	
ASN	P414	S353	T293	
ASP	ASP	A354	S294	
ASP	V415	A355	E295	
LEU	I416	L356	D296	
MET	W417	S357	H297	
ILE	H418	Y358	S298	
	K419	L359	L299	
	A420	L360	N300	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9125	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.999	Depositor
Minimum map value	0.000	Depositor
Average map value	0.117	Depositor
Map value standard deviation	0.204	Depositor
Recommended contour level	1.1	Depositor
Map size (\AA)	535.75195, 535.75195, 535.75195	wwPDB
Map dimensions	504, 504, 504	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.063, 1.063, 1.063	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SEP

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	L0	0.10	0/1529	0.26	0/2372
2	L1	0.11	0/29890	0.27	0/46541
3	L2	0.11	0/3669	0.25	0/5700
4	L3	0.13	0/484	0.32	0/672
5	L4	0.15	0/1232	0.39	0/1719
6	L5	0.20	0/1046	0.45	0/1464
7	L6	0.15	0/1035	0.35	0/1442
8	L7	0.18	0/911	0.47	0/1276
9	L8	0.13	0/845	0.34	0/1174
10	L9	0.18	0/922	0.47	0/1290
11	LC	0.19	0/647	0.44	0/903
12	LD	0.14	0/700	0.37	0/980
13	LE	0.20	0/642	0.50	0/893
14	LF	0.16	0/649	0.40	0/904
15	LG	0.18	0/310	0.46	0/430
16	LH	0.16	0/4025	0.44	0/5613
17	LI	0.15	0/3042	0.39	0/4250
18	LJ	0.13	0/2410	0.35	0/3370
19	LK	0.13	0/667	0.35	0/933
20	LL	0.12	0/2448	0.33	0/3415
21	LM	0.35	2/8150 (0.0%)	0.52	7/11410 (0.1%)
22	LN	0.13	0/3326	0.37	0/4637
23	LO	0.13	0/3976	0.34	0/5552
24	LP	0.14	0/1907	0.35	0/2667
25	LQ	0.13	0/4080	0.33	0/5689
26	LR	0.13	0/3980	0.33	0/5555
27	LS	0.14	0/2288	0.34	0/3188
28	LT	0.15	0/4367	0.36	1/6091 (0.0%)
29	LU	0.15	0/2284	0.42	0/3190
30	LV	0.15	0/2041	0.38	0/2851
31	LW	0.16	0/2322	0.42	0/3243
32	LX	0.24	2/4287 (0.0%)	0.46	6/5997 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LY	0.24	1/4310 (0.0%)	0.42	3/6033 (0.0%)
33	LZ	0.15	0/812	0.41	0/1136
34	NA	0.12	0/1492	0.30	0/2075
35	NB	0.12	0/1162	0.34	0/1618
36	NC	0.11	0/576	0.26	0/801
37	ND	0.20	0/298	0.39	0/416
38	NF	0.14	0/717	0.34	0/1003
39	NG	0.13	0/634	0.31	0/881
40	NH	0.12	0/5489	0.31	0/7686
41	NI	0.12	0/1214	0.35	0/1695
42	NM	0.15	0/1185	0.37	0/1651
43	NN	0.09	0/1343	0.26	0/1873
44	NQ	0.15	0/401	0.42	0/560
45	NS	0.18	0/4309	0.43	0/6037
46	NV	0.16	0/38	0.34	0/51
47	OA	0.10	0/68	0.36	0/93
48	OH	0.11	0/595	0.31	0/827
49	OU	0.09	0/278	0.26	0/386
50	SA	0.12	0/1931	0.31	0/2693
51	SB	0.13	0/2168	0.32	0/3028
52	SC	0.16	0/1210	0.39	0/1689
52	SD	0.13	0/1210	0.36	0/1689
53	SE	0.15	0/621	0.33	0/871
53	SF	0.18	0/621	0.42	0/871
54	SG	0.15	0/2301	0.41	1/3208 (0.0%)
55	SH	0.15	0/1817	0.38	0/2536
56	SI	0.14	0/4026	0.37	0/5632
57	SJ	0.12	0/1080	0.34	0/1508
57	SK	0.18	0/1170	0.46	1/1639 (0.1%)
58	SL	0.22	0/759	0.44	0/1064
59	SM	0.16	0/1251	0.40	1/1749 (0.1%)
60	SP	0.13	0/11042	0.34	0/15458
61	SQ	0.14	0/595	0.40	0/832
62	SR	0.20	0/479	0.48	0/666
63	SS	0.15	0/1150	0.42	0/1604
64	ST	0.13	0/2739	0.32	0/3828
65	SU	0.27	1/2726 (0.0%)	0.43	3/3825 (0.1%)
66	SW	0.13	0/1111	0.34	0/1550
67	SY	0.20	0/609	0.49	0/846
68	SZ	0.13	0/1326	0.33	0/1859
All	All	0.16	6/166974 (0.0%)	0.36	23/238878 (0.0%)

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
13	LE	0	1
28	LT	0	2
45	NS	0	3
56	SI	0	1
All	All	0	7

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	LM	939	ASN	C-N	20.51	1.59	1.33
21	LM	940	LYS	N-CA	18.32	1.68	1.46
32	LY	218	PRO	CG-CD	-12.24	1.09	1.50
65	SU	292	PRO	CG-CD	-11.90	1.10	1.50
32	LX	550	PRO	CG-CD	-8.50	1.21	1.50

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	LM	939	ASN	CA-C-N	17.09	153.09	121.81
21	LM	939	ASN	C-N-CA	17.09	153.09	121.81
32	LY	218	PRO	N-CD-CG	-15.60	79.80	103.20
65	SU	292	PRO	N-CD-CG	-15.33	80.21	103.20
32	LX	550	PRO	N-CD-CG	-10.88	86.88	103.20

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	LE	50	PHE	Peptide
28	LT	848	GLU	Peptide
28	LT	855	PHE	Peptide
45	NS	249	ARG	Peptide
45	NS	845	MET	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L0	1370	0	692	3	0
2	L1	26727	0	13468	66	0
3	L2	3289	0	1667	13	0
4	L3	485	0	220	0	0
5	L4	1221	0	609	3	0
6	L5	1040	0	519	2	0
7	L6	1029	0	512	1	0
8	L7	903	0	450	2	0
9	L8	843	0	427	1	0
10	L9	914	0	464	3	0
11	LC	642	0	328	0	0
12	LD	693	0	336	0	0
13	LE	640	0	307	0	0
14	LF	647	0	319	1	0
15	LG	309	0	145	2	0
16	LH	4014	0	1812	3	0
17	LI	3027	0	1390	1	0
18	LJ	2394	0	1161	3	0
19	LK	664	0	299	0	0
20	LL	2440	0	1139	1	0
21	LM	8115	0	3739	45	0
22	LN	3315	0	1518	8	0
23	LO	3958	0	1889	5	0
24	LP	1901	0	836	3	0
25	LQ	4068	0	1900	8	0
26	LR	3962	0	1883	8	0
27	LS	2279	0	1110	3	0
28	LT	4347	0	2073	12	0
29	LU	2274	0	1064	5	0
30	LV	2029	0	947	1	0
31	LW	2304	0	1146	14	0
32	LX	4253	0	2078	5	0
32	LY	4274	0	2096	11	0
33	LZ	808	0	370	1	0
34	NA	1491	0	701	3	0
35	NB	1159	0	548	1	0
36	NC	575	0	274	1	0
37	ND	297	0	132	2	0
38	NF	711	0	360	1	0
39	NG	630	0	341	2	0
40	NH	5443	0	2602	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	NI	1210	0	565	1	0
42	NM	1183	0	553	7	0
43	NN	1341	0	623	1	0
44	NQ	398	0	200	0	0
45	NS	4268	0	2083	11	0
46	NV	39	0	16	0	0
47	OA	69	0	34	0	0
48	OH	594	0	298	1	0
49	OU	278	0	135	0	0
50	SA	1924	0	946	1	0
51	SB	2161	0	1090	3	0
52	SC	1198	0	625	1	0
52	SD	1198	0	625	4	0
53	SE	615	0	331	1	0
53	SF	615	0	331	2	0
54	SG	2290	0	1099	4	0
55	SH	1801	0	897	1	0
56	SI	3990	0	1966	5	0
57	SJ	1074	0	514	1	0
57	SK	1160	0	570	2	0
58	SL	751	0	377	0	0
59	SM	1243	0	602	3	0
60	SP	10989	0	5019	15	0
61	SQ	592	0	278	1	0
62	SR	476	0	237	2	0
63	SS	1145	0	565	0	0
64	ST	2727	0	1271	1	0
65	SU	2703	0	1302	1	0
66	SW	1104	0	544	1	0
67	SY	611	0	265	3	0
68	SZ	1314	0	649	1	0
All	All	162545	0	78481	306	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 1.

The worst 5 of 306 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)
21:LM:940:LYS:N	21:LM:940:LYS:CA	1.68	1.56
2:L1:1524:A:N3	2:L1:1590:G:O2'	2.12	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L1:443:C:O2	2:L1:445:A:N6	2.14	0.80
52:SD:198:GLU:O	52:SD:222:GLU:N	2.15	0.80
2:L1:1108:G:OP2	2:L1:1108:G:N2	2.13	0.79

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	
4	L3	91/146 (62%)	91 (100%)	0	0	100	100
5	L4	242/261 (93%)	238 (98%)	4 (2%)	0	100	100
6	L5	202/225 (90%)	198 (98%)	4 (2%)	0	100	100
7	L6	202/236 (86%)	198 (98%)	4 (2%)	0	100	100
8	L7	174/190 (92%)	170 (98%)	4 (2%)	0	100	100
9	L8	166/200 (83%)	163 (98%)	3 (2%)	0	100	100
10	L9	179/197 (91%)	176 (98%)	3 (2%)	0	100	100
11	LC	126/143 (88%)	121 (96%)	5 (4%)	0	100	100
12	LD	135/156 (86%)	132 (98%)	3 (2%)	0	100	100
13	LE	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
14	LF	128/135 (95%)	124 (97%)	4 (3%)	0	100	100
15	LG	60/67 (90%)	58 (97%)	2 (3%)	0	100	100
16	LH	782/896 (87%)	761 (97%)	21 (3%)	0	100	100
17	LI	582/713 (82%)	572 (98%)	10 (2%)	0	100	100
18	LJ	470/513 (92%)	462 (98%)	8 (2%)	0	100	100
19	LK	130/575 (23%)	130 (100%)	0	0	100	100
20	LL	475/643 (74%)	463 (98%)	12 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	LM	1597/1769 (90%)	1552 (97%)	45 (3%)	0	100	100
22	LN	649/776 (84%)	635 (98%)	14 (2%)	0	100	100
23	LO	786/923 (85%)	769 (98%)	17 (2%)	0	100	100
24	LP	375/440 (85%)	372 (99%)	3 (1%)	0	100	100
25	LQ	806/943 (86%)	791 (98%)	15 (2%)	0	100	100
26	LR	785/817 (96%)	768 (98%)	17 (2%)	0	100	100
27	LS	441/594 (74%)	437 (99%)	4 (1%)	0	100	100
28	LT	861/939 (92%)	849 (99%)	12 (1%)	0	100	100
29	LU	448/489 (92%)	442 (99%)	6 (1%)	0	100	100
30	LV	401/707 (57%)	389 (97%)	12 (3%)	0	100	100
31	LW	453/554 (82%)	445 (98%)	8 (2%)	0	100	100
32	LX	826/1056 (78%)	813 (98%)	13 (2%)	0	100	100
32	LY	834/1056 (79%)	821 (98%)	13 (2%)	0	100	100
33	LZ	156/183 (85%)	155 (99%)	1 (1%)	0	100	100
34	NA	278/593 (47%)	276 (99%)	2 (1%)	0	100	100
35	NB	221/610 (36%)	219 (99%)	2 (1%)	0	100	100
36	NC	111/357 (31%)	111 (100%)	0	0	100	100
37	ND	57/214 (27%)	56 (98%)	1 (2%)	0	100	100
38	NF	139/151 (92%)	137 (99%)	2 (1%)	0	100	100
39	NG	125/137 (91%)	120 (96%)	5 (4%)	0	100	100
40	NH	1063/1237 (86%)	1052 (99%)	11 (1%)	0	100	100
41	NI	232/297 (78%)	225 (97%)	7 (3%)	0	100	100
42	NM	231/255 (91%)	228 (99%)	3 (1%)	0	100	100
43	NN	257/534 (48%)	256 (100%)	1 (0%)	0	100	100
44	NQ	77/82 (94%)	76 (99%)	1 (1%)	0	100	100
45	NS	836/1267 (66%)	826 (99%)	10 (1%)	0	100	100
46	NV	6/733 (1%)	6 (100%)	0	0	100	100
47	OA	12/1729 (1%)	12 (100%)	0	0	100	100
48	OH	118/143 (82%)	118 (100%)	0	0	100	100
49	OU	54/152 (36%)	54 (100%)	0	0	100	100
50	SA	379/504 (75%)	372 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	SB	431/511 (84%)	422 (98%)	9 (2%)	0	100	100
52	SC	234/327 (72%)	230 (98%)	4 (2%)	0	100	100
52	SD	234/327 (72%)	229 (98%)	5 (2%)	0	100	100
53	SE	119/126 (94%)	117 (98%)	2 (2%)	0	100	100
53	SF	119/126 (94%)	116 (98%)	3 (2%)	0	100	100
54	SG	453/573 (79%)	445 (98%)	8 (2%)	0	100	100
55	SH	358/367 (98%)	345 (96%)	13 (4%)	0	100	100
56	SI	776/1183 (66%)	763 (98%)	13 (2%)	0	100	100
57	SJ	207/252 (82%)	204 (99%)	3 (1%)	0	100	100
57	SK	225/252 (89%)	221 (98%)	4 (2%)	0	100	100
58	SL	146/189 (77%)	139 (95%)	7 (5%)	0	100	100
59	SM	243/290 (84%)	241 (99%)	2 (1%)	0	100	100
60	SP	2167/2493 (87%)	2138 (99%)	29 (1%)	0	100	100
61	SQ	113/217 (52%)	112 (99%)	1 (1%)	0	100	100
62	SR	91/145 (63%)	89 (98%)	2 (2%)	0	100	100
63	SS	213/899 (24%)	208 (98%)	5 (2%)	0	100	100
64	ST	524/810 (65%)	513 (98%)	11 (2%)	0	100	100
65	SU	524/552 (95%)	519 (99%)	5 (1%)	0	100	100
66	SW	211/274 (77%)	205 (97%)	6 (3%)	0	100	100
67	SY	114/250 (46%)	108 (95%)	6 (5%)	0	100	100
68	SZ	255/483 (53%)	250 (98%)	5 (2%)	0	100	100
All	All	25642/36313 (71%)	25179 (98%)	463 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	L3	2/129 (2%)	2 (100%)	0	100	100
5	L4	12/222 (5%)	12 (100%)	0	100	100
6	L5	8/191 (4%)	8 (100%)	0	100	100
7	L6	8/201 (4%)	8 (100%)	0	100	100
8	L7	10/170 (6%)	10 (100%)	0	100	100
9	L8	4/161 (2%)	4 (100%)	0	100	100
10	L9	9/166 (5%)	9 (100%)	0	100	100
11	LC	6/119 (5%)	6 (100%)	0	100	100
12	LD	8/137 (6%)	8 (100%)	0	100	100
13	LE	3/111 (3%)	3 (100%)	0	100	100
14	LF	3/113 (3%)	3 (100%)	0	100	100
15	LG	2/60 (3%)	2 (100%)	0	100	100
16	LH	21/826 (2%)	21 (100%)	0	100	100
17	LI	24/657 (4%)	24 (100%)	0	100	100
18	LJ	19/454 (4%)	19 (100%)	0	100	100
19	LK	4/533 (1%)	4 (100%)	0	100	100
20	LL	14/574 (2%)	14 (100%)	0	100	100
21	LM	43/1633 (3%)	43 (100%)	0	100	100
22	LN	18/713 (2%)	18 (100%)	0	100	100
23	LO	21/811 (3%)	21 (100%)	0	100	100
24	LP	8/414 (2%)	8 (100%)	0	100	100
25	LQ	17/832 (2%)	17 (100%)	0	100	100
26	LR	22/719 (3%)	22 (100%)	0	100	100
27	LS	21/528 (4%)	21 (100%)	0	100	100
28	LT	25/819 (3%)	25 (100%)	0	100	100
29	LU	13/443 (3%)	13 (100%)	0	100	100
30	LV	14/636 (2%)	14 (100%)	0	100	100
31	LW	21/480 (4%)	21 (100%)	0	100	100
32	LX	42/934 (4%)	42 (100%)	0	100	100
32	LY	42/934 (4%)	42 (100%)	0	100	100
33	LZ	6/172 (4%)	6 (100%)	0	100	100
34	NA	10/535 (2%)	10 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	NB	8/538 (2%)	8 (100%)	0	100	100
36	NC	3/315 (1%)	3 (100%)	0	100	100
37	ND	2/196 (1%)	2 (100%)	0	100	100
38	NF	7/128 (6%)	7 (100%)	0	100	100
39	NG	5/105 (5%)	5 (100%)	0	100	100
40	NH	53/1125 (5%)	53 (100%)	0	100	100
41	NI	8/274 (3%)	8 (100%)	0	100	100
42	NM	5/224 (2%)	5 (100%)	0	100	100
43	NN	7/482 (2%)	7 (100%)	0	100	100
44	NQ	4/71 (6%)	4 (100%)	0	100	100
45	NS	45/1140 (4%)	45 (100%)	0	100	100
48	OH	2/119 (2%)	2 (100%)	0	100	100
49	OU	1/135 (1%)	1 (100%)	0	100	100
50	SA	10/435 (2%)	10 (100%)	0	100	100
51	SB	8/433 (2%)	8 (100%)	0	100	100
52	SC	14/240 (6%)	14 (100%)	0	100	100
52	SD	14/240 (6%)	14 (100%)	0	100	100
53	SE	7/104 (7%)	7 (100%)	0	100	100
53	SF	7/104 (7%)	7 (100%)	0	100	100
54	SG	14/503 (3%)	14 (100%)	0	100	100
55	SH	17/312 (5%)	17 (100%)	0	100	100
56	SI	43/1039 (4%)	43 (100%)	0	100	100
57	SJ	9/222 (4%)	9 (100%)	0	100	100
57	SK	12/222 (5%)	12 (100%)	0	100	100
58	SL	9/169 (5%)	9 (100%)	0	100	100
59	SM	10/258 (4%)	10 (100%)	0	100	100
60	SP	62/2307 (3%)	62 (100%)	0	100	100
61	SQ	5/200 (2%)	5 (100%)	0	100	100
62	SR	5/120 (4%)	5 (100%)	0	100	100
63	SS	14/807 (2%)	14 (100%)	0	100	100
64	ST	20/732 (3%)	20 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	SU	27/506 (5%)	27 (100%)	0	100	100
66	SW	11/238 (5%)	11 (100%)	0	100	100
67	SY	2/234 (1%)	2 (100%)	0	100	100
68	SZ	14/424 (3%)	14 (100%)	0	100	100
All	All	964/30128 (3%)	964 (100%)	0	100	100

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

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

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	59/700 (8%)	16 (27%)	0
2	L1	1232/1810 (68%)	232 (18%)	4 (0%)
3	L2	149/333 (44%)	22 (14%)	0
All	All	1440/2843 (50%)	270 (18%)	4 (0%)

5 of 270 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	9	G
1	L0	14	U
1	L0	16	A
1	L0	17	A
1	L0	23	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L1	248	U
2	L1	345	U
2	L1	1568	C
2	L1	1600	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z > 2$
63	SEP	SS	738	63	3,4,10	0.71	0	2,4,14	0.73	0
27	SEP	LS	128	27	3,4,10	0.70	0	2,4,14	0.79	0

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
63	SEP	SS	738	63	-	0/1/2/10	-
27	SEP	LS	128	27	-	0/1/2/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

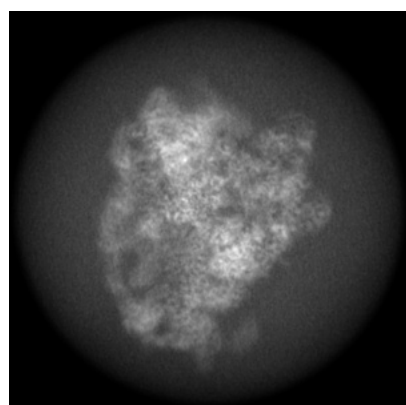
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49080. These allow visual inspection of the internal detail of the map and identification of artifacts.

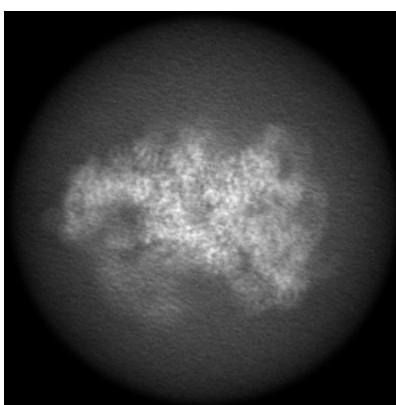
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

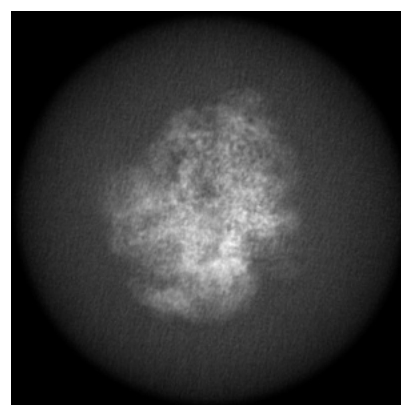
6.1.1 Primary map



X



Y

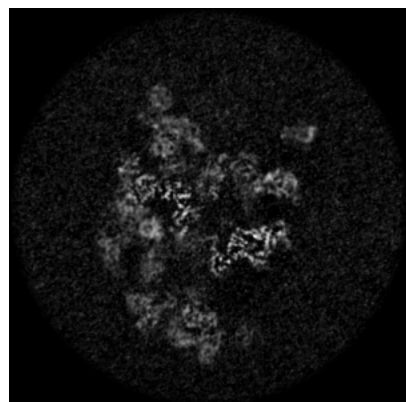


Z

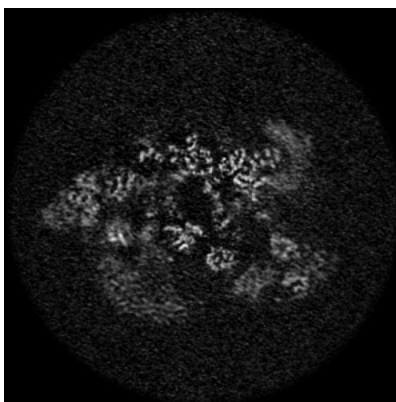
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

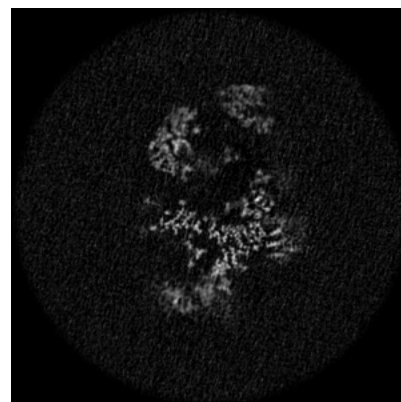
6.2.1 Primary map



X Index: 252



Y Index: 252

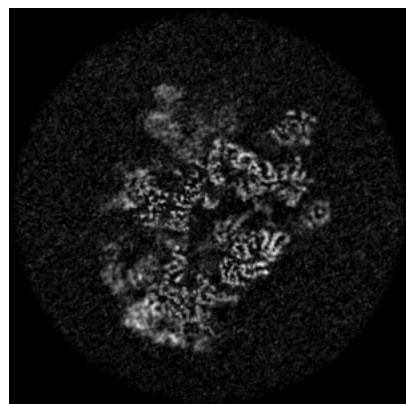


Z Index: 252

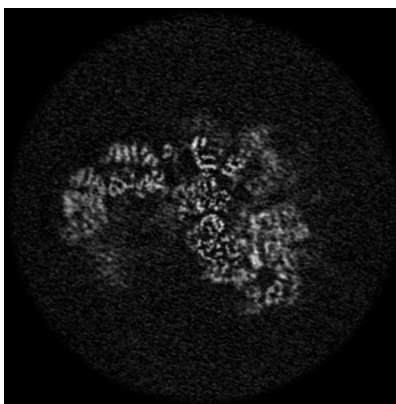
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

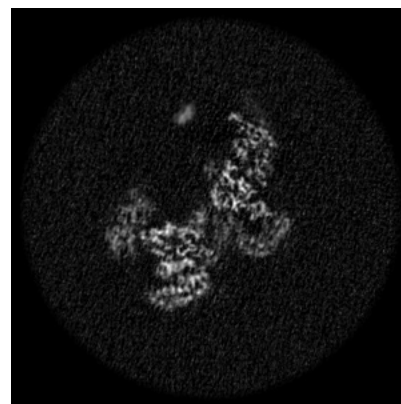
6.3.1 Primary map



X Index: 273



Y Index: 222

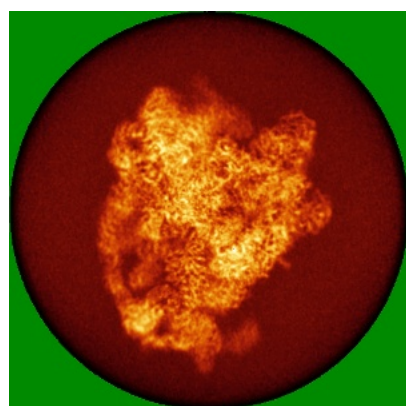


Z Index: 317

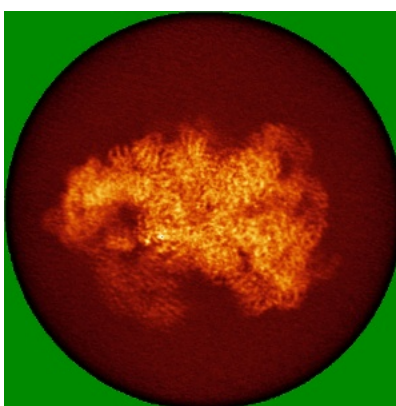
The images above show the largest variance slices of the map in three orthogonal directions.

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

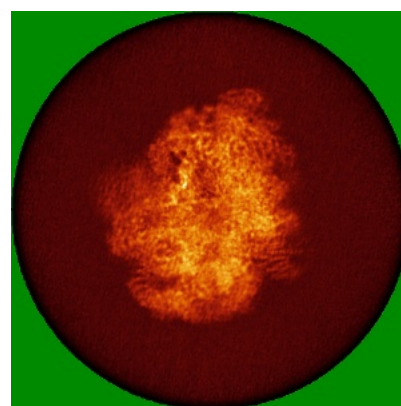
6.4.1 Primary map



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

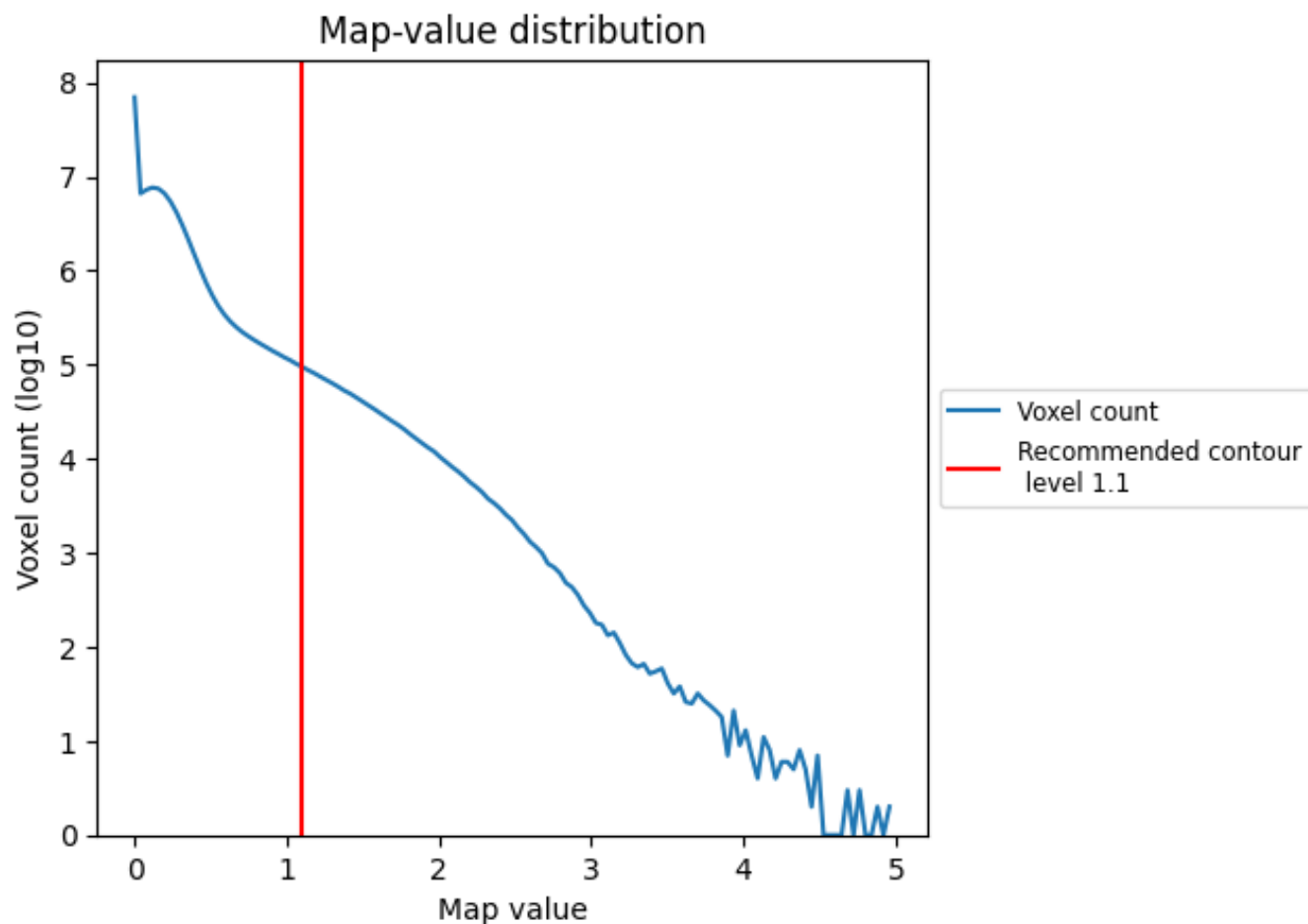
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

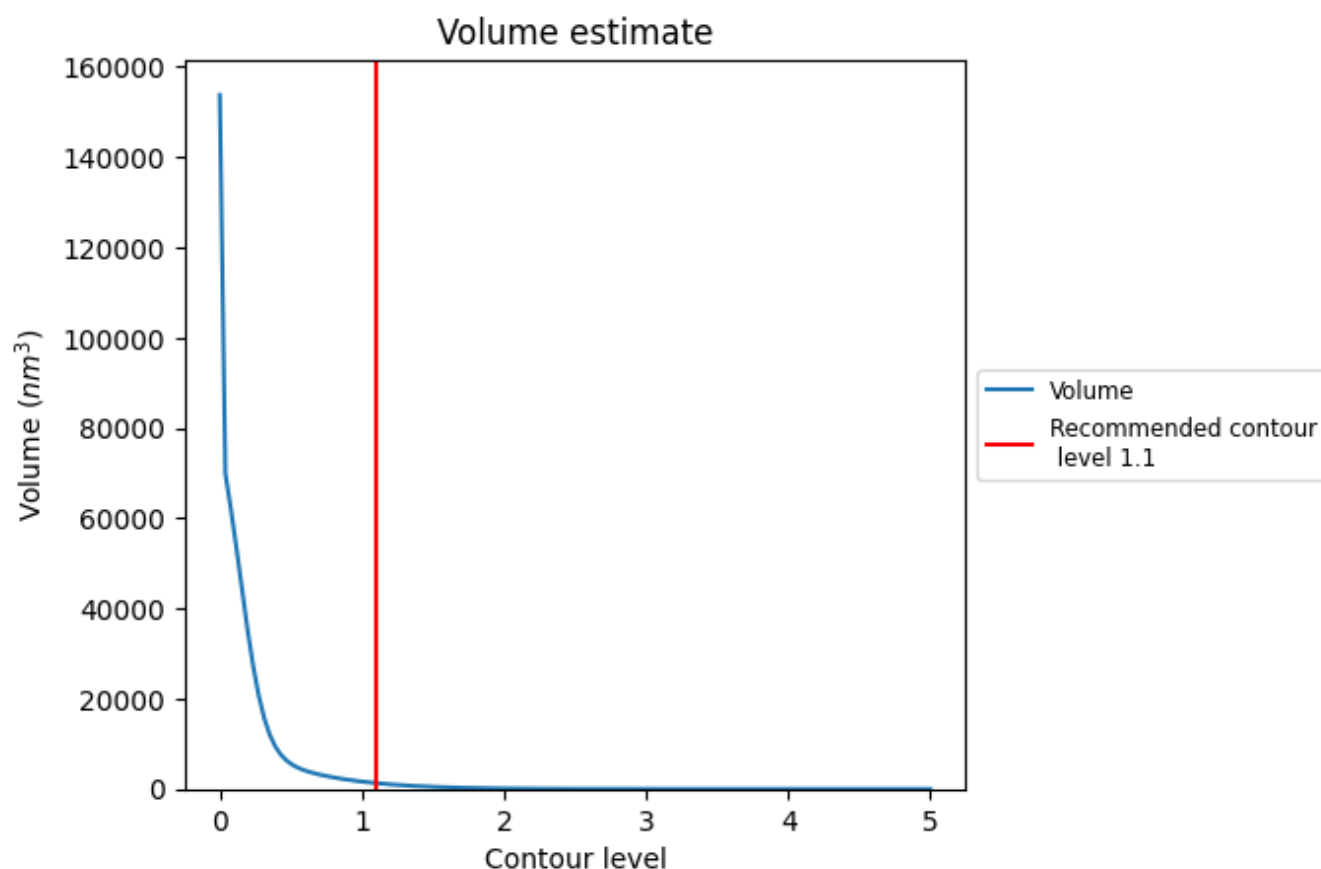
This section contains the results of statistical analysis of the map.

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.

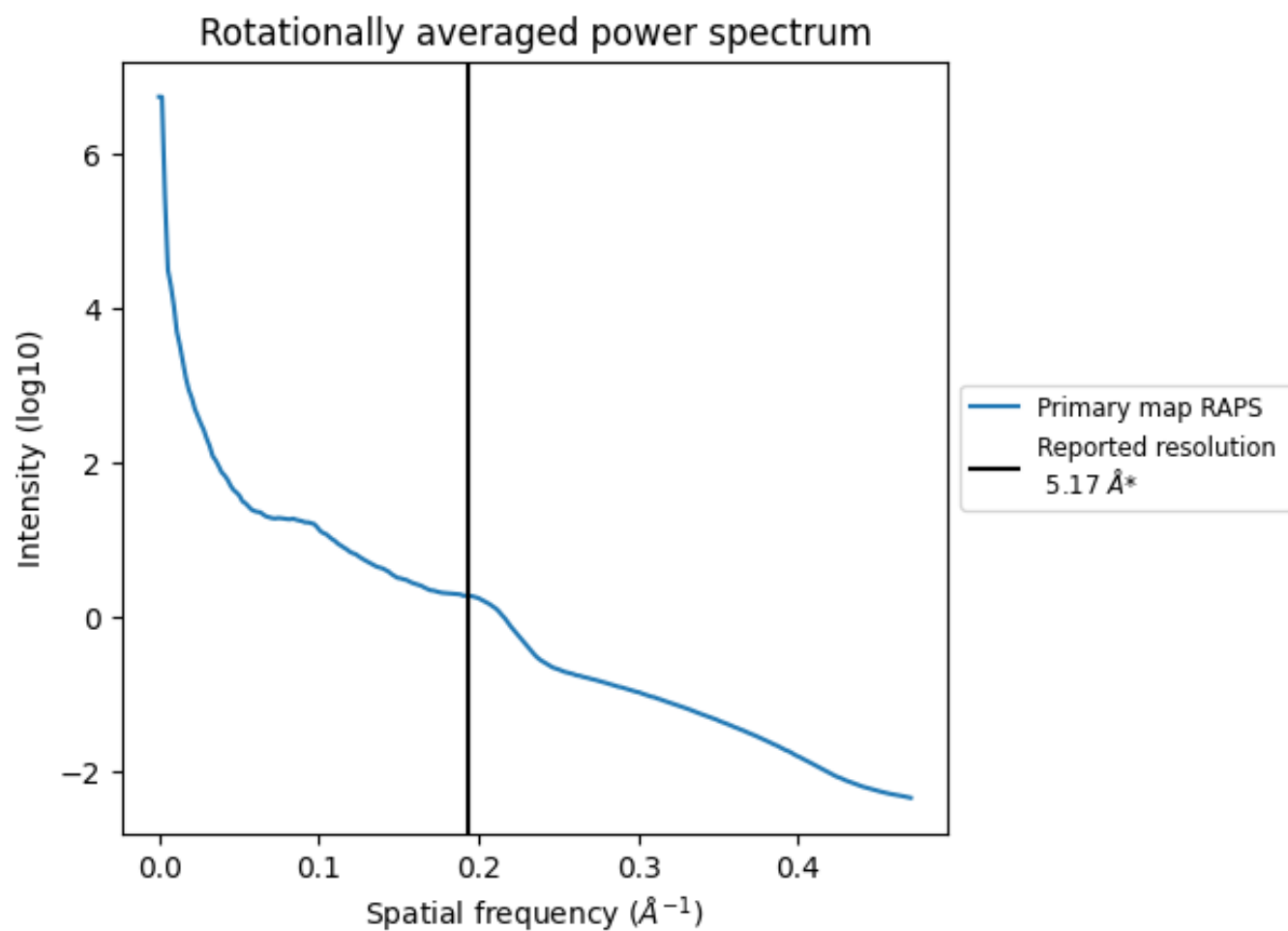
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1298 nm³; this corresponds to an approximate mass of 1172 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 0.193 Å⁻¹

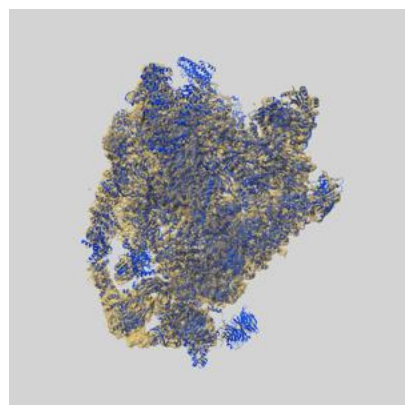
8 Fourier-Shell correlation

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

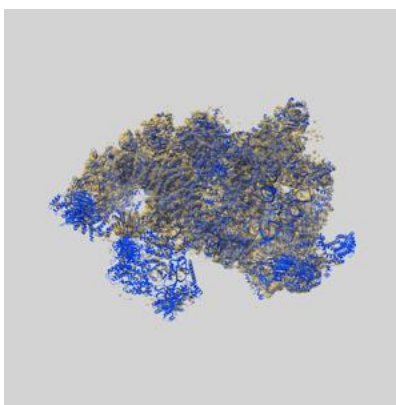
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49080 and PDB model 9N70. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

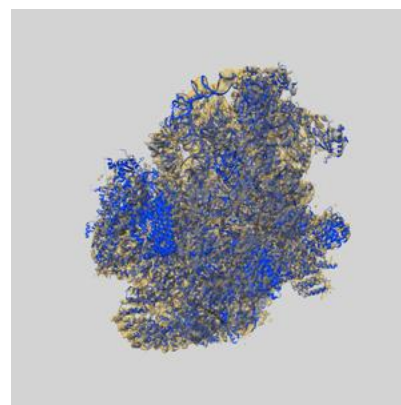
9.1 Map-model overlay [i](#)



X



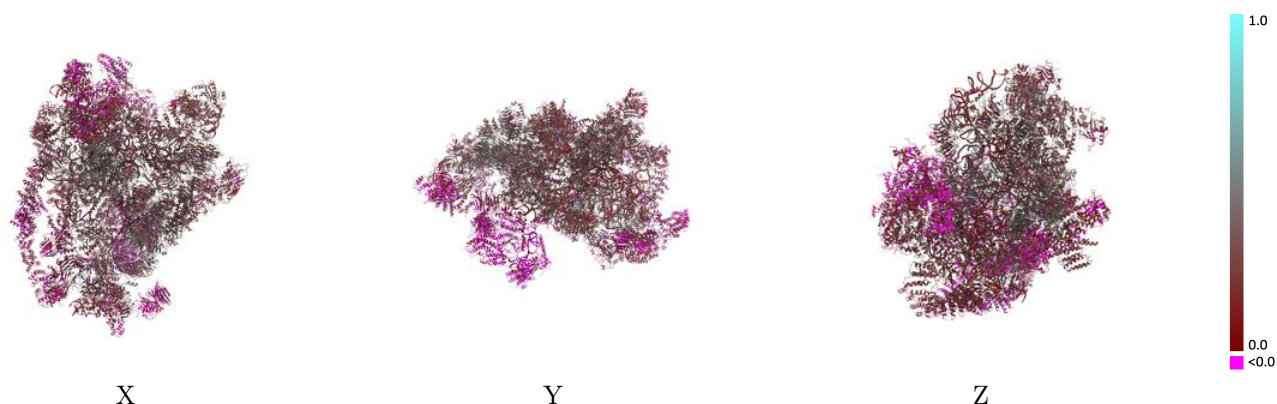
Y



Z

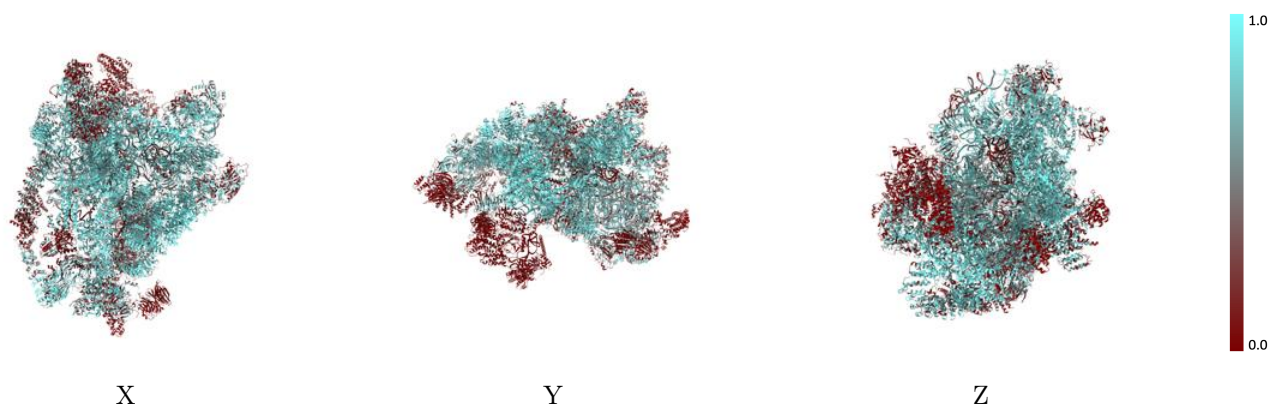
The images above show the 3D surface view of the map at the recommended contour level 1.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



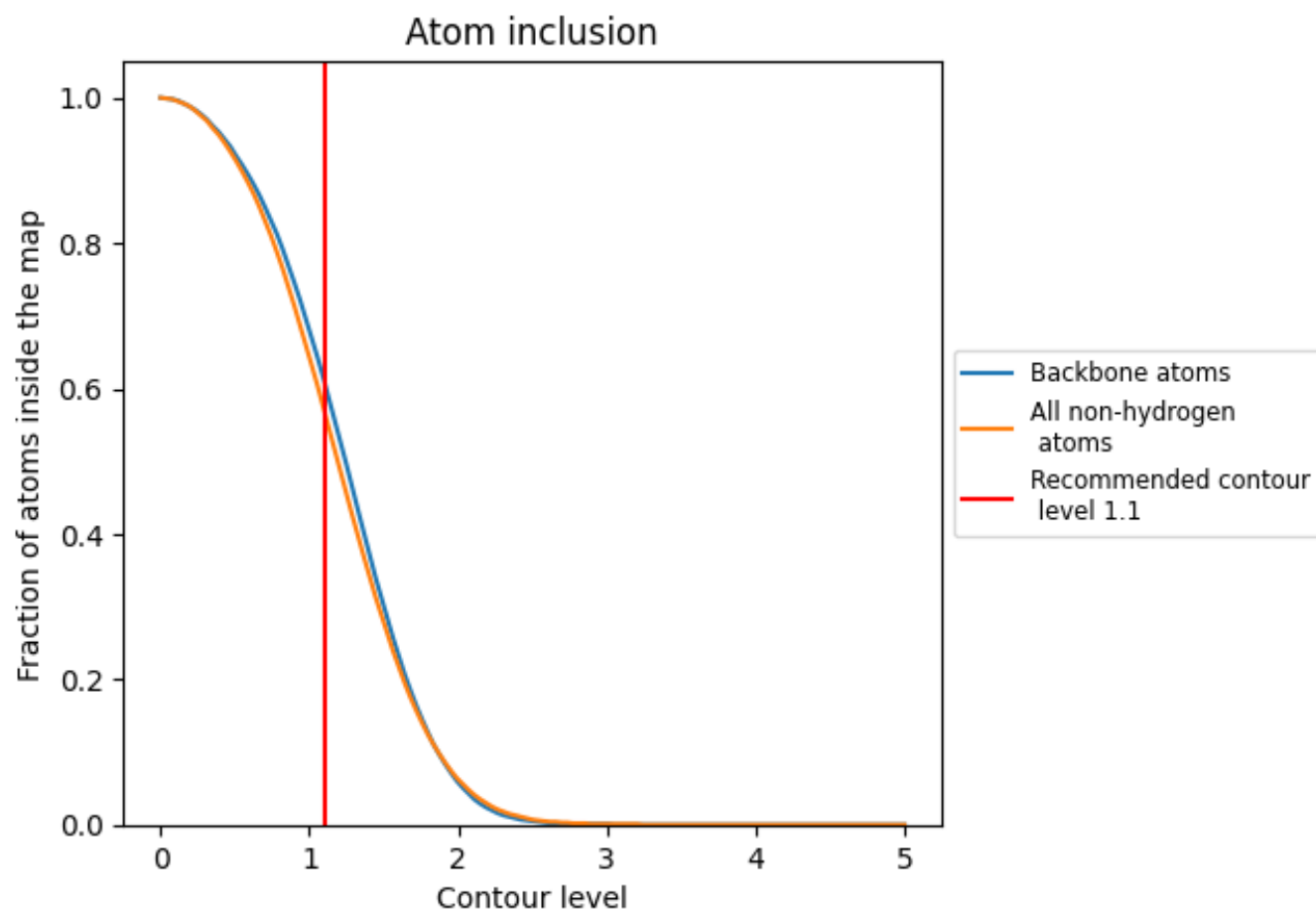
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 57% 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 (1.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5690	 0.2440
L0	 0.7020	 0.2160
L1	 0.6440	 0.2290
L2	 0.6240	 0.2250
L3	 0.0000	 -0.0440
L4	 0.6080	 0.2530
L5	 0.8520	 0.3400
L6	 0.8020	 0.2860
L7	 0.6400	 0.2650
L8	 0.4600	 0.1820
L9	 0.7230	 0.3450
LC	 0.8010	 0.3660
LD	 0.3300	 0.1480
LE	 0.7920	 0.3580
LF	 0.8660	 0.3060
LG	 0.8960	 0.4050
LH	 0.5770	 0.2760
LI	 0.0610	 0.0690
LJ	 0.4470	 0.1410
LK	 0.3000	 0.1920
LL	 0.5690	 0.2930
LM	 0.6080	 0.2000
LN	 0.6660	 0.2280
LO	 0.8310	 0.3850
LP	 0.7150	 0.2870
LQ	 0.6590	 0.2940
LR	 0.7690	 0.3180
LS	 0.7750	 0.3870
LT	 0.8380	 0.3800
LU	 0.8670	 0.3960
LV	 0.5190	 0.2310
LW	 0.7420	 0.3290
LX	 0.4820	 0.2240
LY	 0.2560	 0.1340
LZ	 0.6990	 0.3240



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Chain	Atom inclusion	Q-score
NA	 0.5870	 0.2720
NB	 0.2890	 0.1540
NC	 0.0090	 0.0610
ND	 0.0200	 0.1120
NF	 0.8140	 0.3230
NG	 0.6750	 0.3380
NH	 0.6610	 0.3260
NI	 0.4910	 0.2740
NM	 0.8130	 0.3660
NN	 0.0780	 0.1050
NQ	 0.8420	 0.3550
NS	 0.4570	 0.2580
NV	 0.0000	 -0.0520
OA	 0.0000	 0.2140
OH	 0.0000	 -0.0300
OU	 0.0000	 -0.0690
SA	 0.7820	 0.3270
SB	 0.5620	 0.2510
SC	 0.7730	 0.4030
SD	 0.1310	 0.1200
SE	 0.7710	 0.3340
SF	 0.7400	 0.3830
SG	 0.6410	 0.2880
SH	 0.7250	 0.3580
SI	 0.7170	 0.3560
SJ	 0.0310	 0.0250
SK	 0.0770	 0.0130
SL	 0.7460	 0.4020
SM	 0.6730	 0.3570
SP	 0.4980	 0.1910
SQ	 0.5130	 0.2860
SR	 0.7860	 0.4230
SS	 0.5570	 0.3160
ST	 0.1180	 0.0440
SU	 0.0040	 0.0070
SW	 0.6290	 0.3100
SY	 0.2730	 0.2220
SZ	 0.0150	 0.0060