



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 07:24 PM UTC

PDB ID : 9N73 / pdb_00009n73
EMDB ID : EMD-49083
Title : SSU processome maturation and disassembly, State G
Authors : Buzovetsky, O.; Klinge, S.
Deposited on : 2025-02-05
Resolution : 5.96 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
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

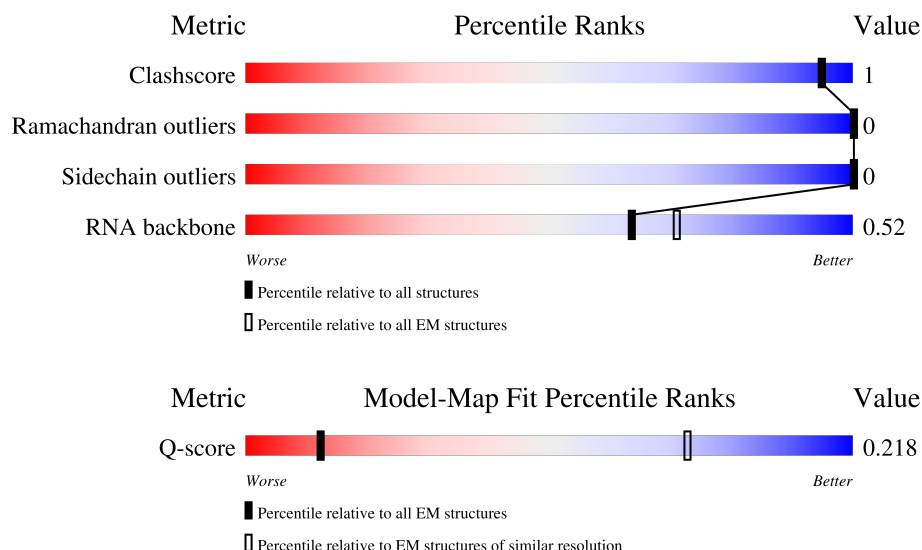
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.96 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.



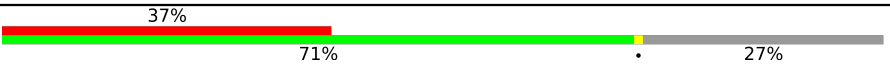
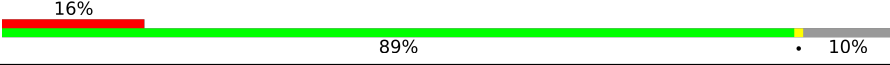
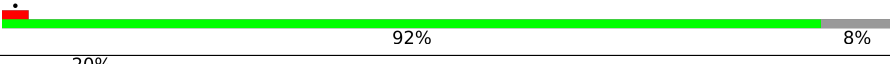
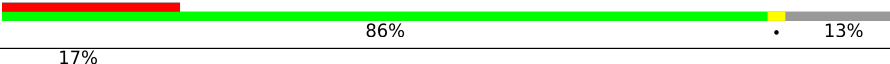
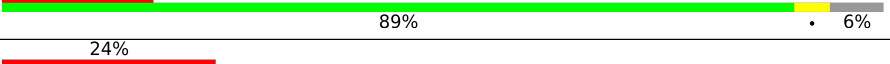
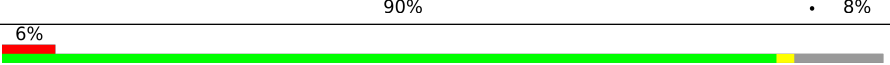
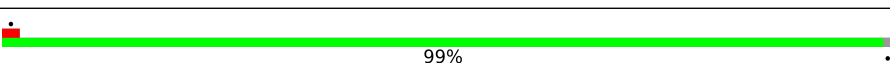
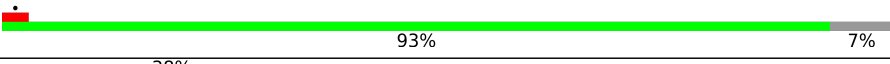
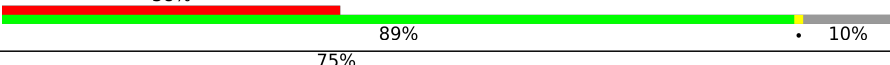
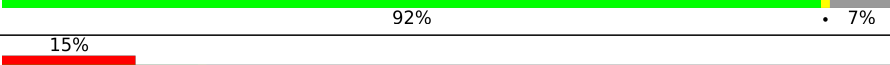
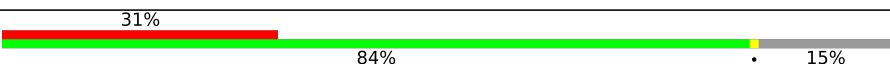
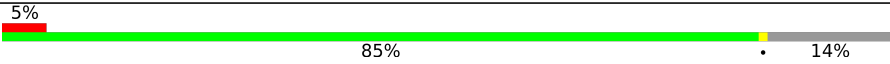
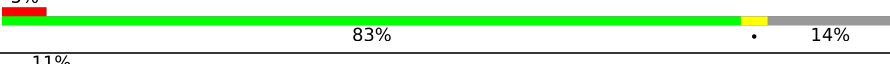
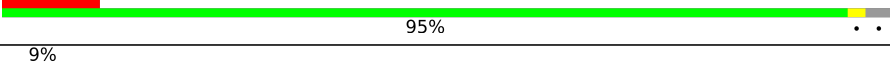
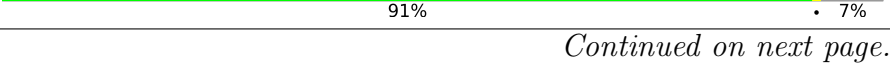
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	474 (5.47 - 6.46)

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	7% 91%
2	L1	1810	10% 54% 14% 30%
3	L2	333	8% 34% 8% 57%

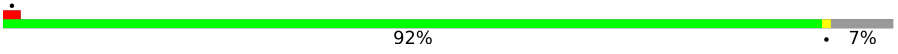
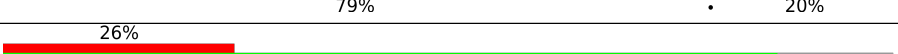
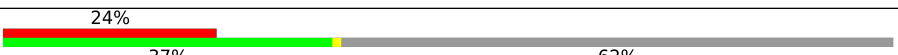
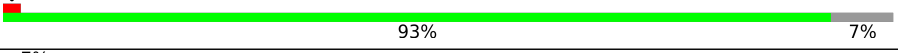
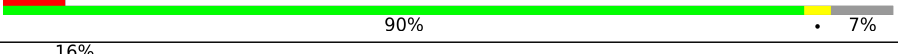
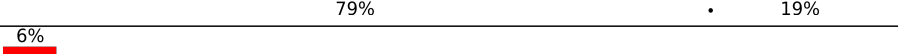
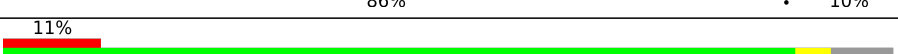
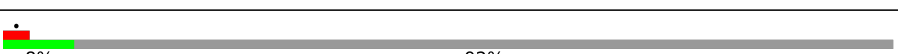
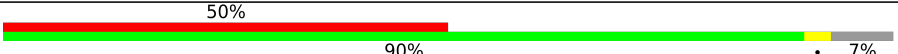
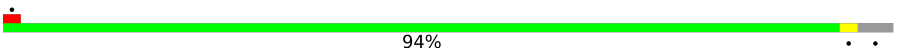
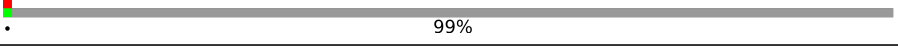
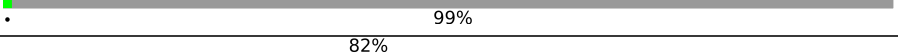
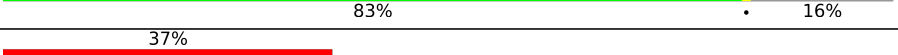
Continued on next page...

Continued from previous page...

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	

Continued on next page...

Continued from previous page...

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	NL	318	
43	NM	255	
44	NN	534	
45	NP	144	
46	NQ	82	
47	NS	1267	
48	NV	733	
49	OA	1729	
50	OH	143	
51	OU	152	
52	SA	504	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
53	SB	511	
54	SC	327	
54	SD	327	
55	SE	126	
55	SF	126	
56	SG	573	
57	SH	367	
58	SI	1183	
59	SJ	252	
59	SK	252	
60	SL	189	
61	SM	290	
62	SP	2493	
63	SQ	217	
64	SR	145	
65	SS	899	
66	ST	810	
67	SU	552	
68	SW	274	
69	SY	250	
70	SZ	483	

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 163806 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	1266	Total	C	N	O	P	0	0
			27015	12076	4829	8844	1266		

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	144	Total	C	N	O	P	0	0
			3064	1369	540	1011	144		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	L3	106	Total	C	N	O	0	0
			529	317	106	106		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
5	L4	234	Total	C	N	O	0	0
			1172	704	234	234		

- 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	171	Total	C	N	O	0	0
			848	506	171	171		

- 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	97	Total	C	N	O	0	0
			484	290	97	97		

- 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	806	Total	C	N	O	0	0
			4034	2422	806	806		

- 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	815	Total	C	N	O	0	0
			4063	2433	815	815		

- 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	357	Total	C	N	O	0	0
			1791	1077	357	357		

- 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	852	Total	C	N	O	0	0
			4302	2598	852	852		
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	329	Total	C	N	O	0	0
			1654	996	329	329		

- 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	135	Total	C	N	O	0	0
			669	399	135	135		

- 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 Dimethyladenosine transferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	NL	285	Total	C	N	O	0	0
			1446	876	285	285		

- Molecule 43 is a protein called Small ribosomal subunit protein eS1A.

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

- Molecule 44 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	NN	43	Total	C	N	O	0	0
			215	129	43	43		

- Molecule 45 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	NP	134	Total	C	N	O	0	0
			666	398	134	134		

- Molecule 46 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 47 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	NS	891	Total	C	N	O	0	0
			4500	2718	891	891		

- Molecule 48 is a protein called Exosome complex exonuclease RRP6.

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

- Molecule 49 is a protein called rRNA biogenesis protein RRP5.

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

- Molecule 50 is a protein called 40S ribosomal protein S12.

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

- Molecule 51 is a protein called Ubiquitin-40S ribosomal protein S31.

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

- Molecule 52 is a protein called Nucleolar protein 56.

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

- Molecule 53 is a protein called Nucleolar protein 58.

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

- Molecule 54 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

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

- Molecule 55 is a protein called 13 kDa ribonucleoprotein-associated protein.

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

- Molecule 56 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	SG	453	Total	C	N	O	0	0
			2260	1354	453	453		

- Molecule 57 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 58 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	SI	780	Total	C	N	O	0	0
			3939	2379	780	780		

- Molecule 59 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 60 is a protein called rRNA-processing protein FCF1.

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

- Molecule 61 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

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

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	SP	2156	Total	C	N	O	0	0
			10847	6535	2156	2156		

- Molecule 63 is a protein called rRNA-processing protein FCF2.

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

- Molecule 64 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 65 is a protein called U3 small nucleolar RNA-associated protein 14.

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

- Molecule 66 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	ST	597	Total	C	N	O	0	0
			3010	1816	597	597		

- Molecule 67 is a protein called Nucleolar complex protein 4.

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

- Molecule 68 is a protein called Pre-rRNA-processing protein PNO1.

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

- Molecule 69 is a protein called U3 small nucleolar RNA-associated protein 11.

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

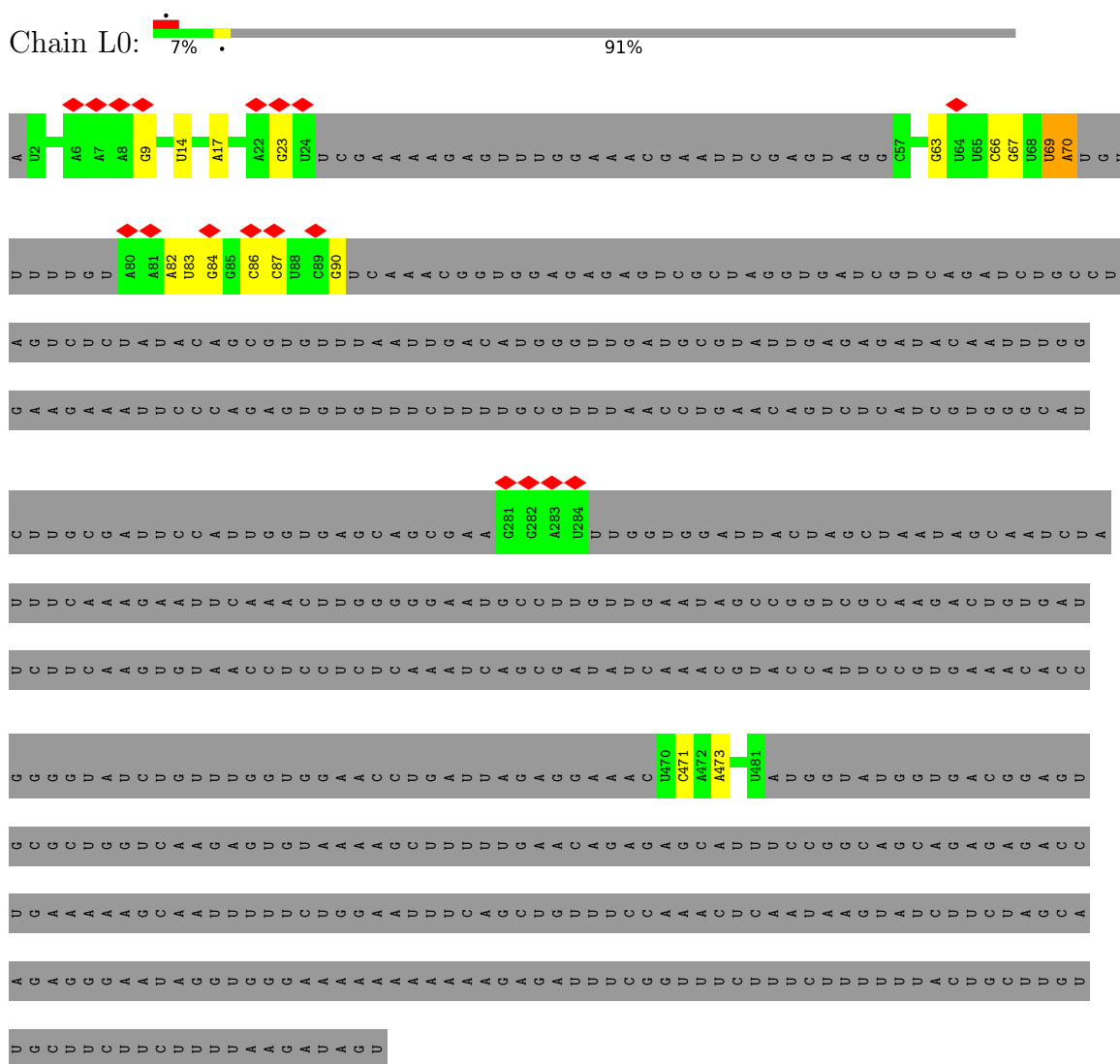
- Molecule 70 is a protein called Essential nuclear protein 1.

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

3 Residue-property plots [i](#)

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

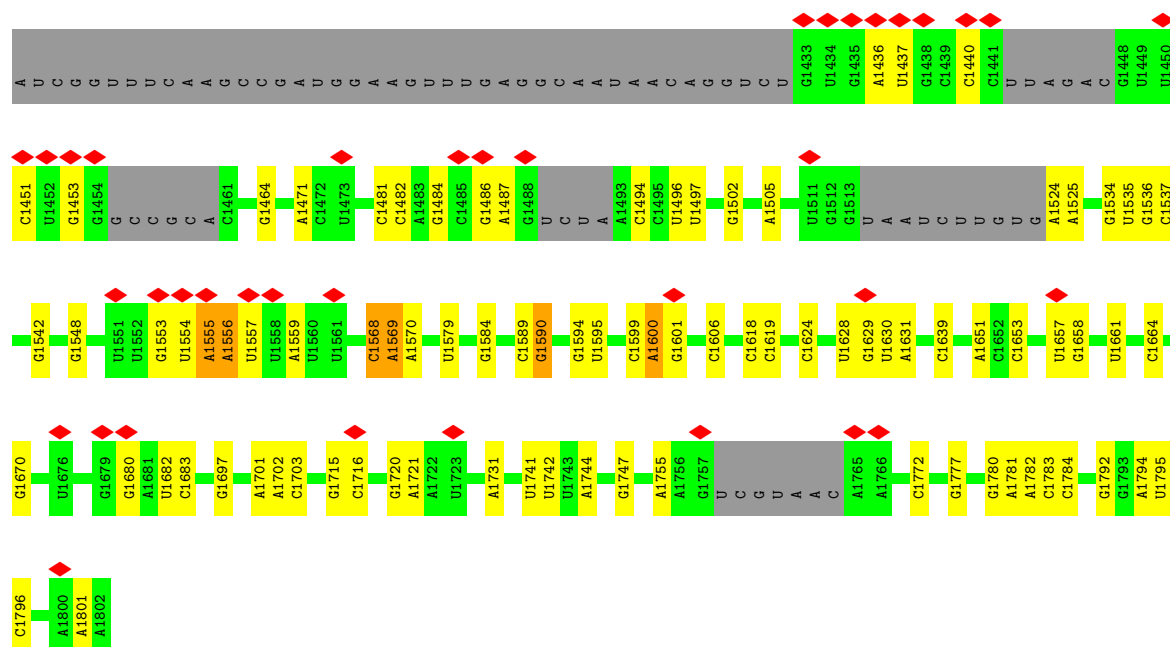
• Molecule 1: 5'ETS rRNA



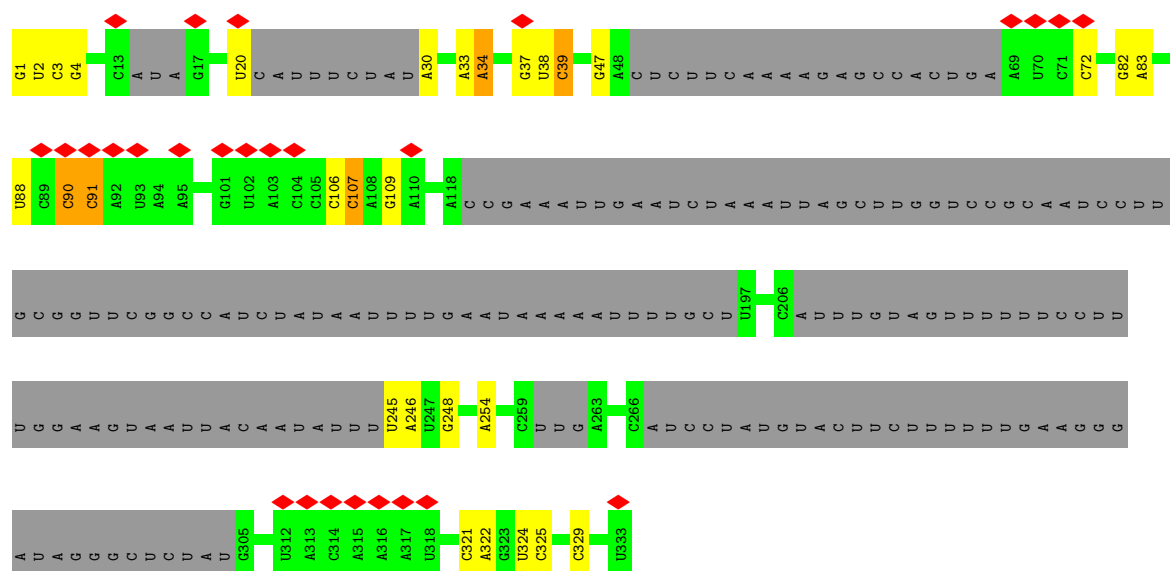
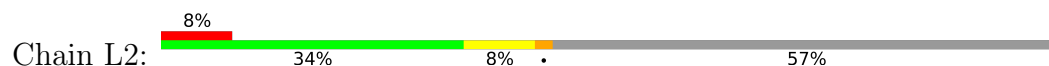
• Molecule 2: 18S rRNA



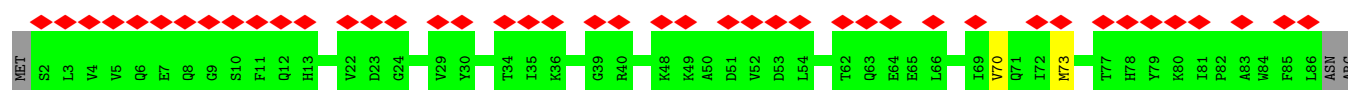
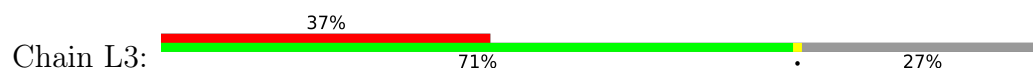


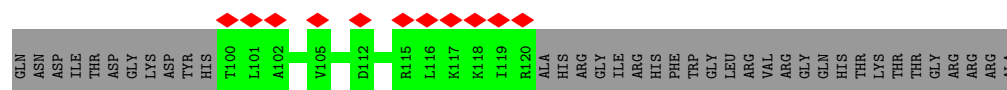


- Molecule 3: U3 snoRNA

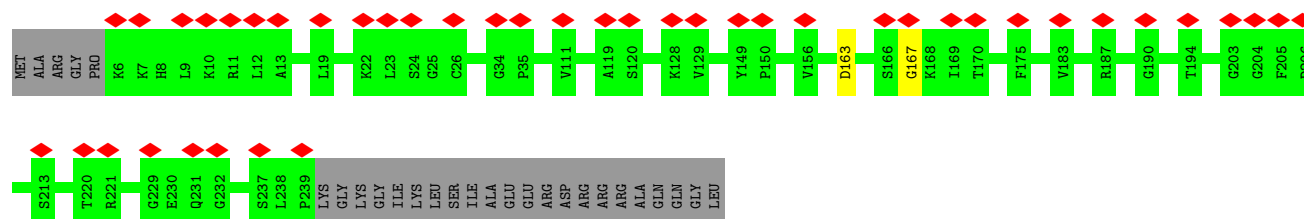
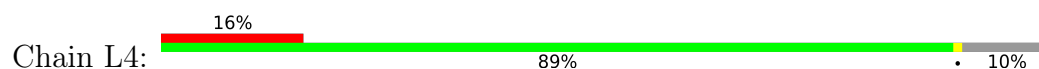


- Molecule 4: 40S ribosomal protein S18-A

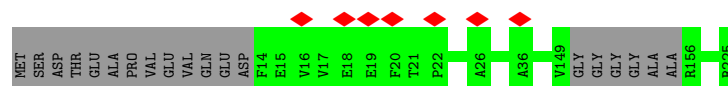




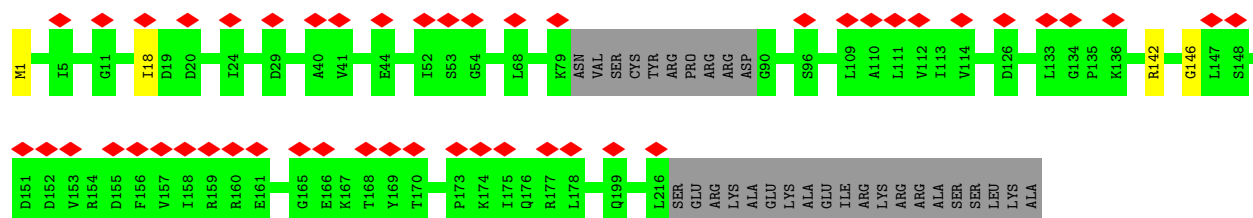
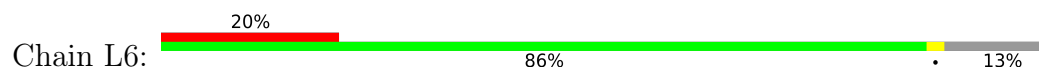
- Molecule 5: 40S ribosomal protein S4-A



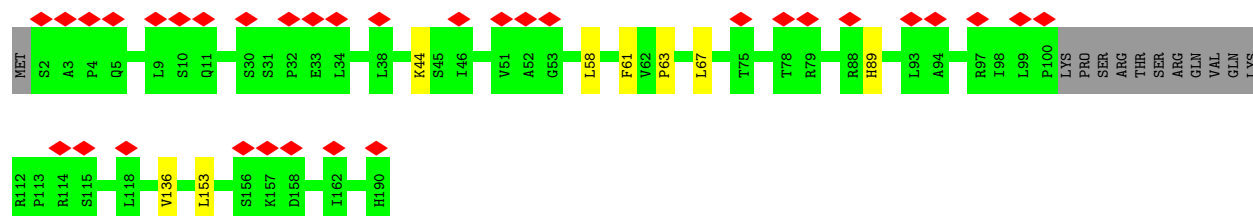
- Molecule 6: 40S ribosomal protein S5



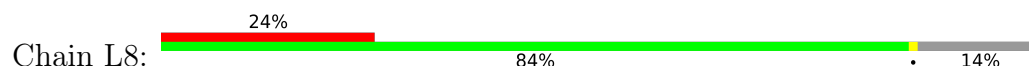
- Molecule 7: 40S ribosomal protein S6-A

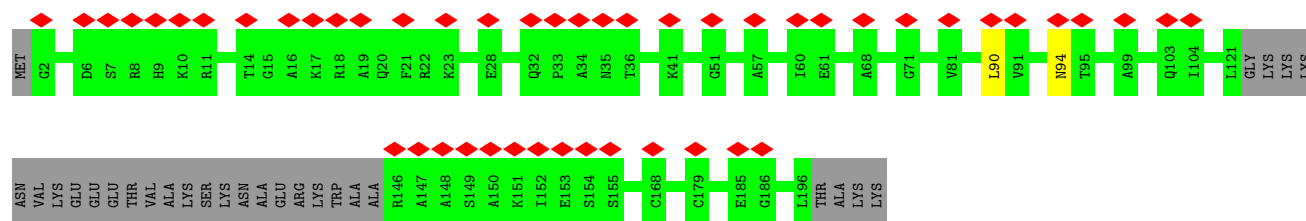


- Molecule 8: 40S ribosomal protein S7-A

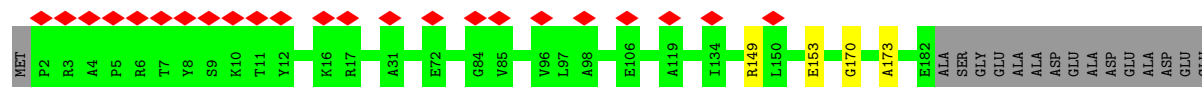


- Molecule 9: 40S ribosomal protein S8-A

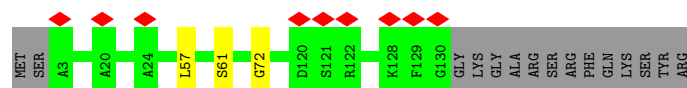
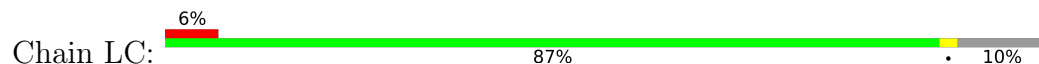




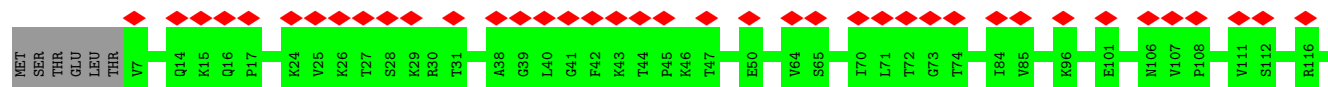
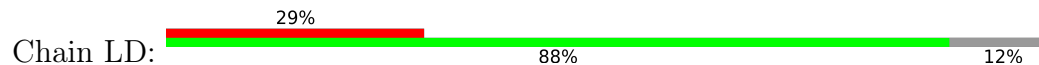
- Molecule 10: 40S ribosomal protein S9-A



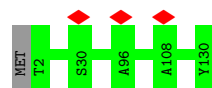
- Molecule 11: 40S ribosomal protein S16-A



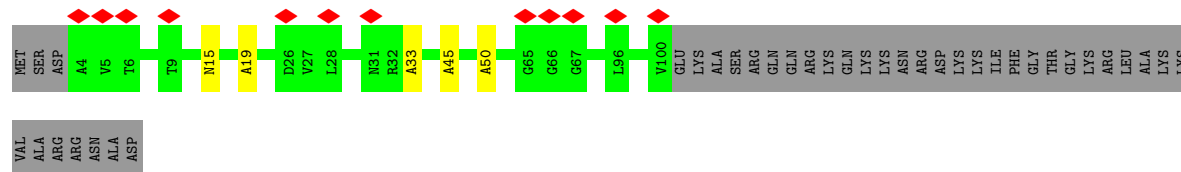
- Molecule 12: 40S ribosomal protein S11-A



- Molecule 13: 40S ribosomal protein S22-A

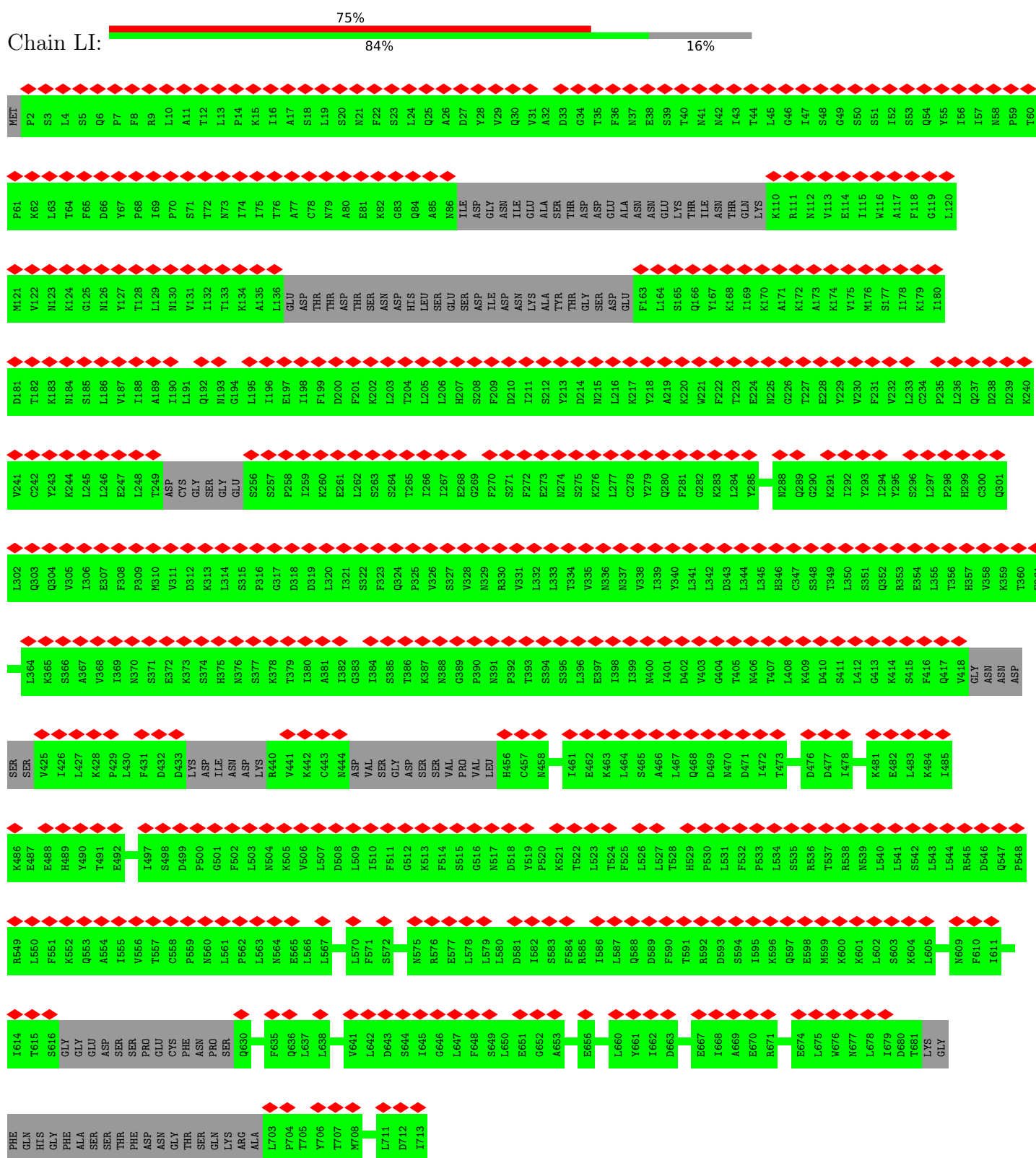


- Molecule 14: 40S ribosomal protein S24-A



-
- | Amino Acid | Percentage (%) | Category |
|------------|----------------|-------------------|
| D820 | ~1.5 | Aromatic |
| A823 | ~1.5 | Aromatic |
| H827 | ~1.5 | Aromatic |
| K828 | ~1.5 | Aromatic |
| L829 | ~1.5 | Aromatic |
| S829 | ~1.5 | Sulfur-containing |
| SER | ~1.5 | Aliphatic |
| ARG | ~1.5 | Aliphatic |
| GLY | ~1.5 | Aliphatic |
| LYS | ~1.5 | Aliphatic |
| LYS | ~1.5 | Aliphatic |
| SER | ~1.5 | Aliphatic |
| ASP | ~1.5 | Aliphatic |
| THR | ~1.5 | Aliphatic |
| THR | ~1.5 | Aliphatic |
| ARG | ~1.5 | Aliphatic |
| ASP | ~1.5 | Aliphatic |
| LYS | ~1.5 | Aliphatic |
| ASN | ~1.5 | Aliphatic |
| ASN | ~1.5 | Aliphatic |
| THR | ~1.5 | Aliphatic |
| ASN | ~1.5 | Aliphatic |
| ASP | ~1.5 | Aliphatic |
| E848 | ~1.5 | Blue |
| G860 | ~1.5 | Basic |
| E861 | ~1.5 | Basic |
| K862 | ~1.5 | Basic |
| M822 | ~1.5 | Other |
| T896 | ~1.5 | Other |

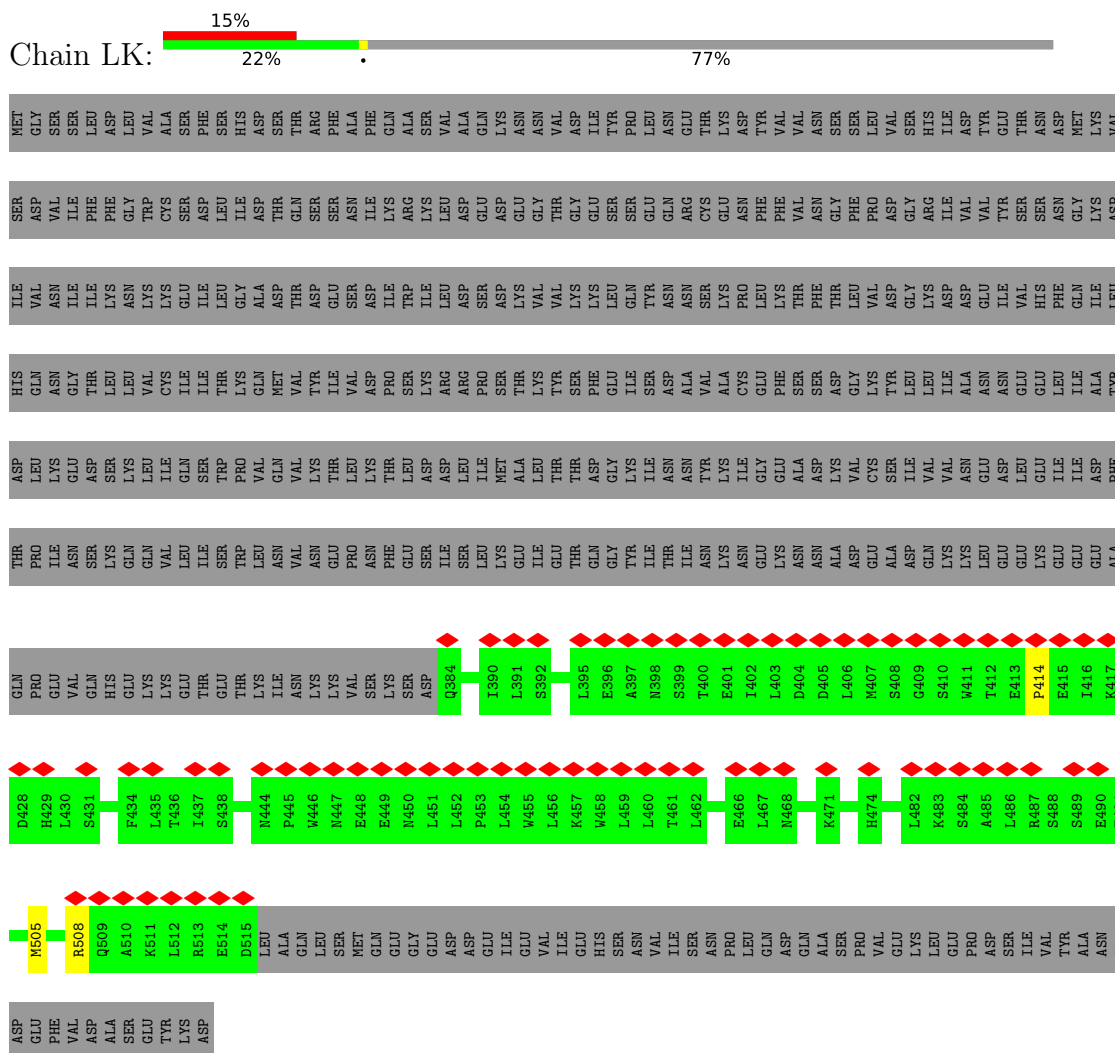
- Molecule 17: U3 small nucleolar RNA-associated protein 8



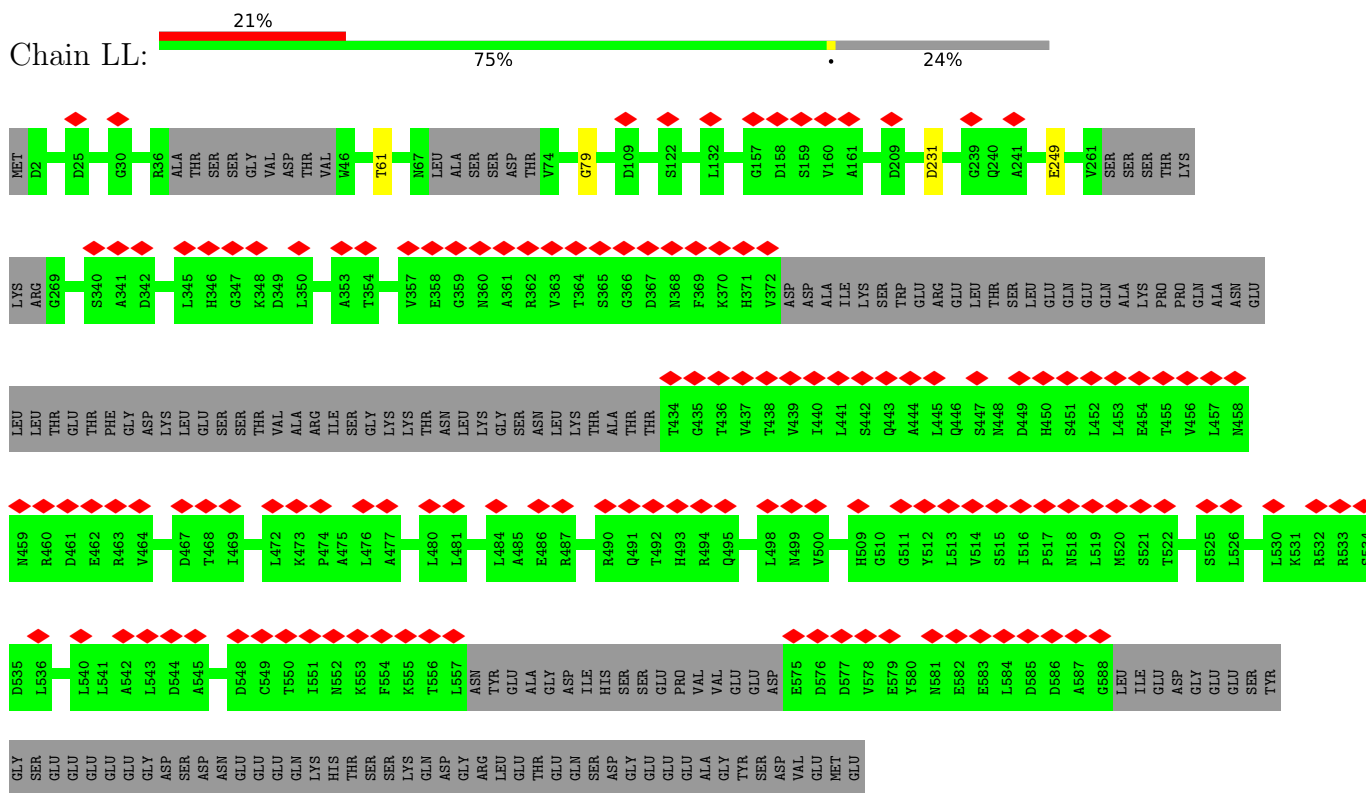
- Molecule 18: U3 small nucleolar RNA-associated protein 15



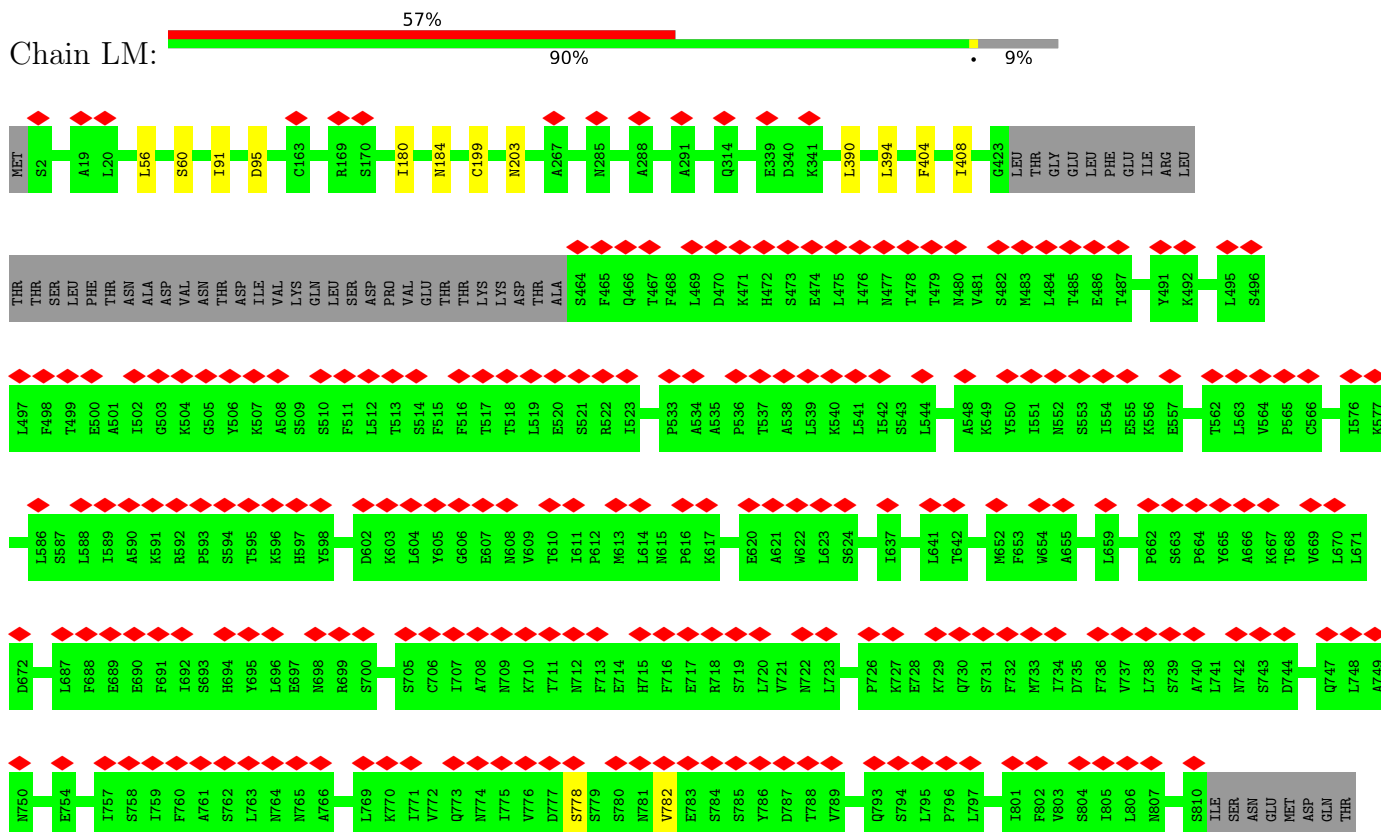
- Molecule 19: U3 small nucleolar RNA-associated protein 9



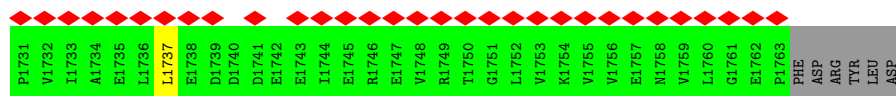
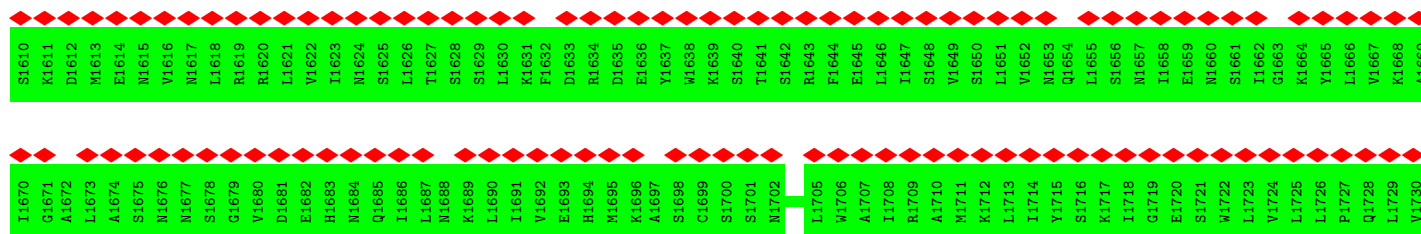
Chain LL:



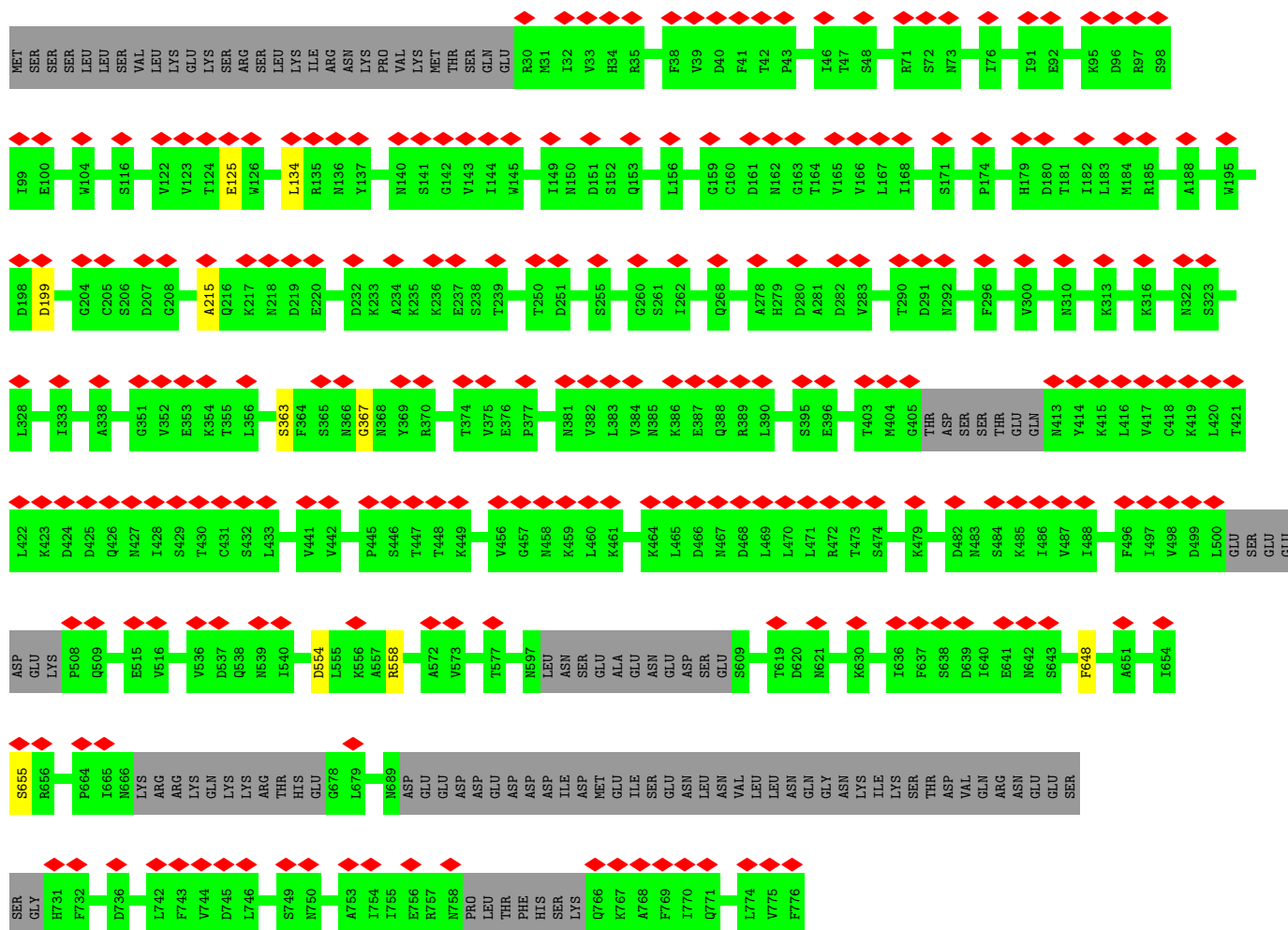
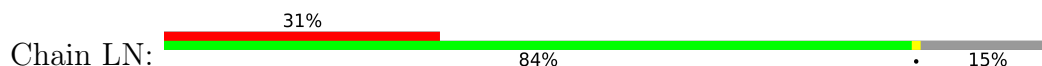
Chain LM:



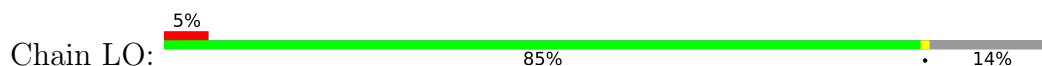


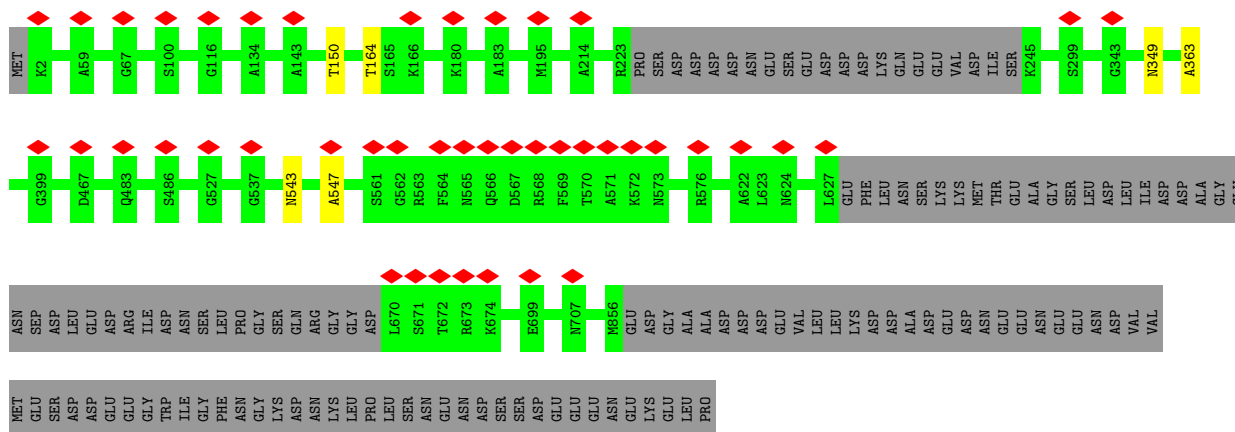


• Molecule 22: U3 small nucleolar RNA-associated protein 4

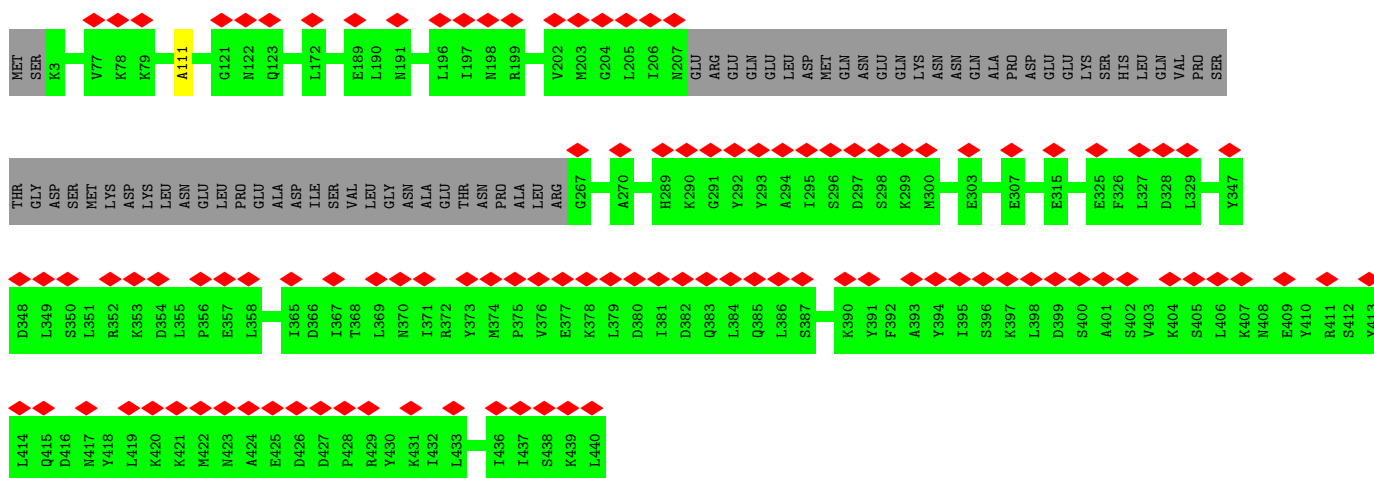
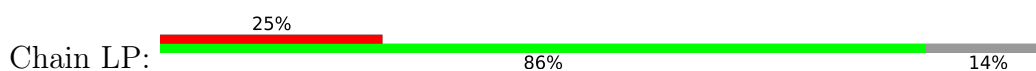


• Molecule 23: Periodic tryptophan protein 2

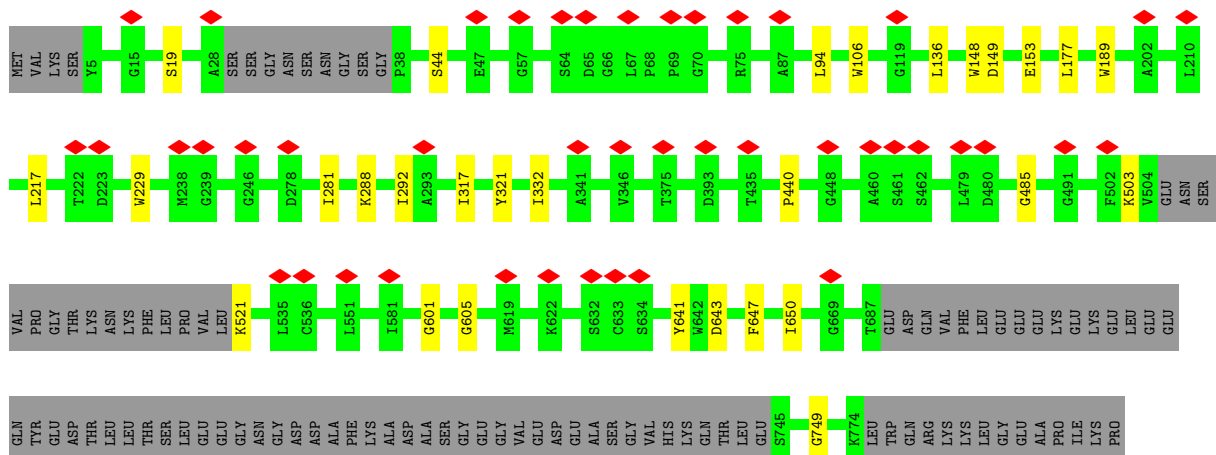
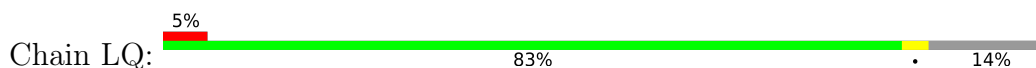


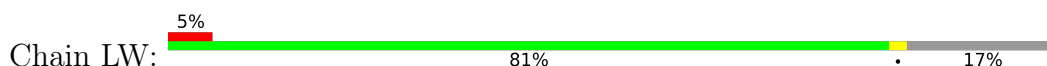


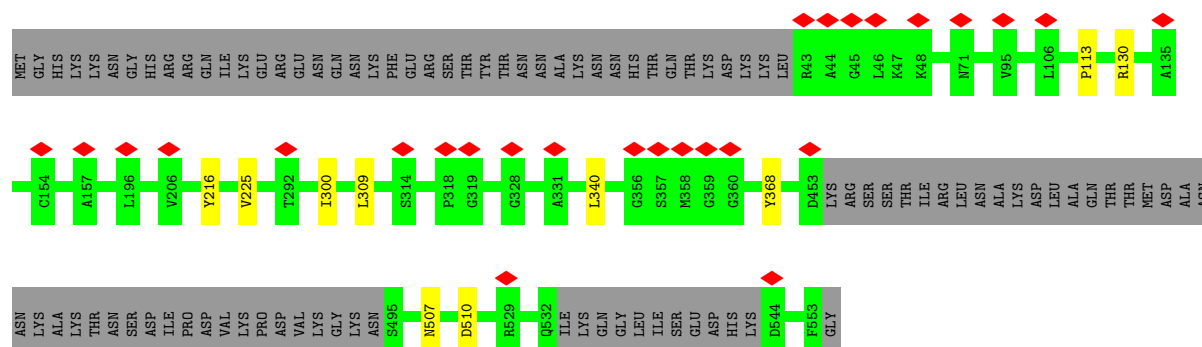
• Molecule 24: U3 small nucleolar RNA-associated protein 6



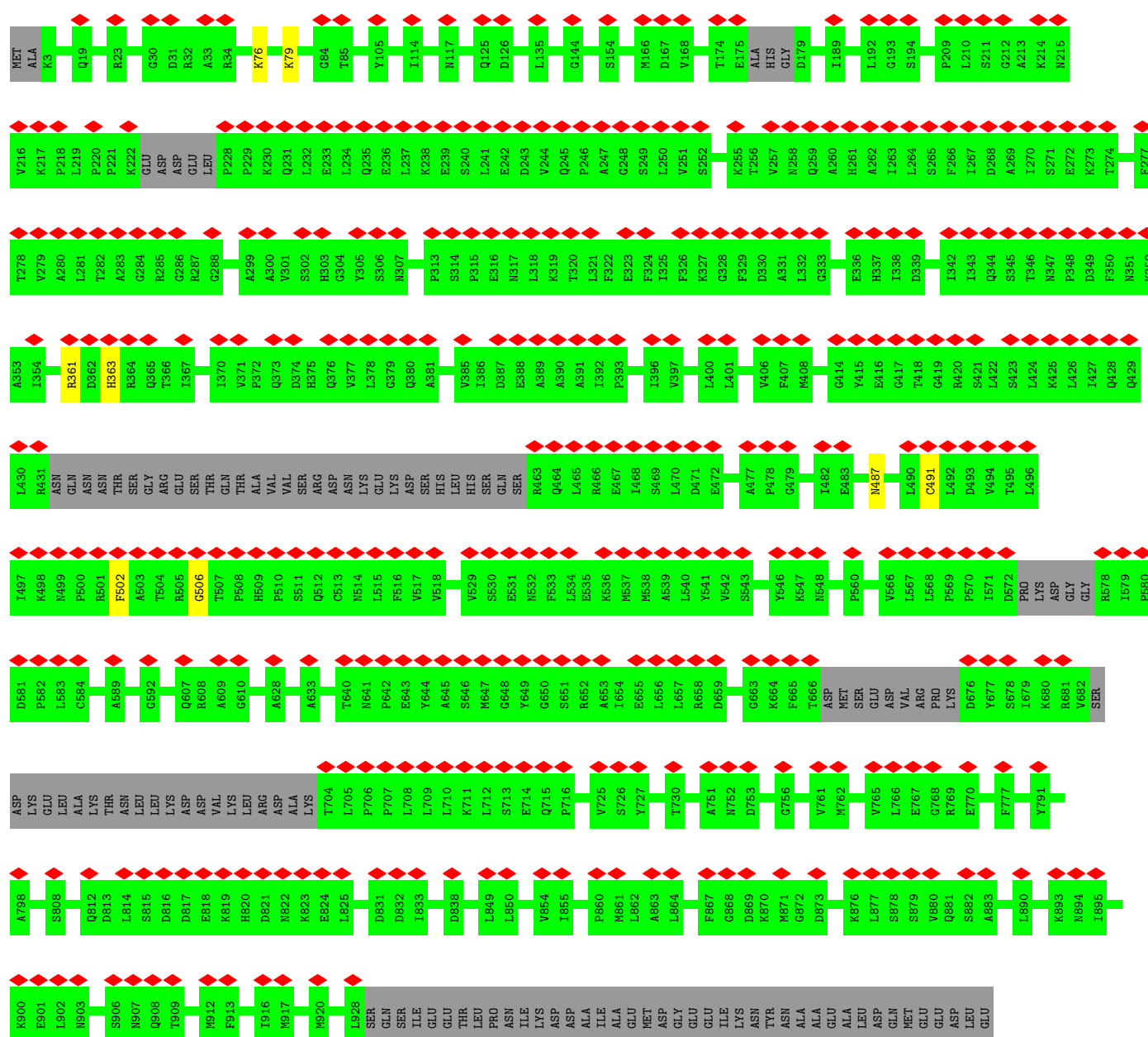
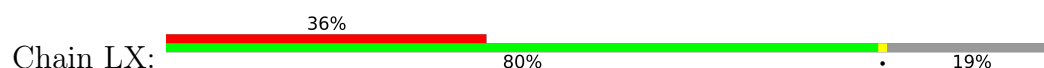
• Molecule 25: U3 small nucleolar RNA-associated protein 12

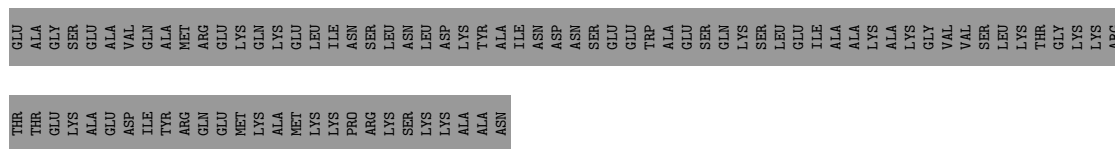




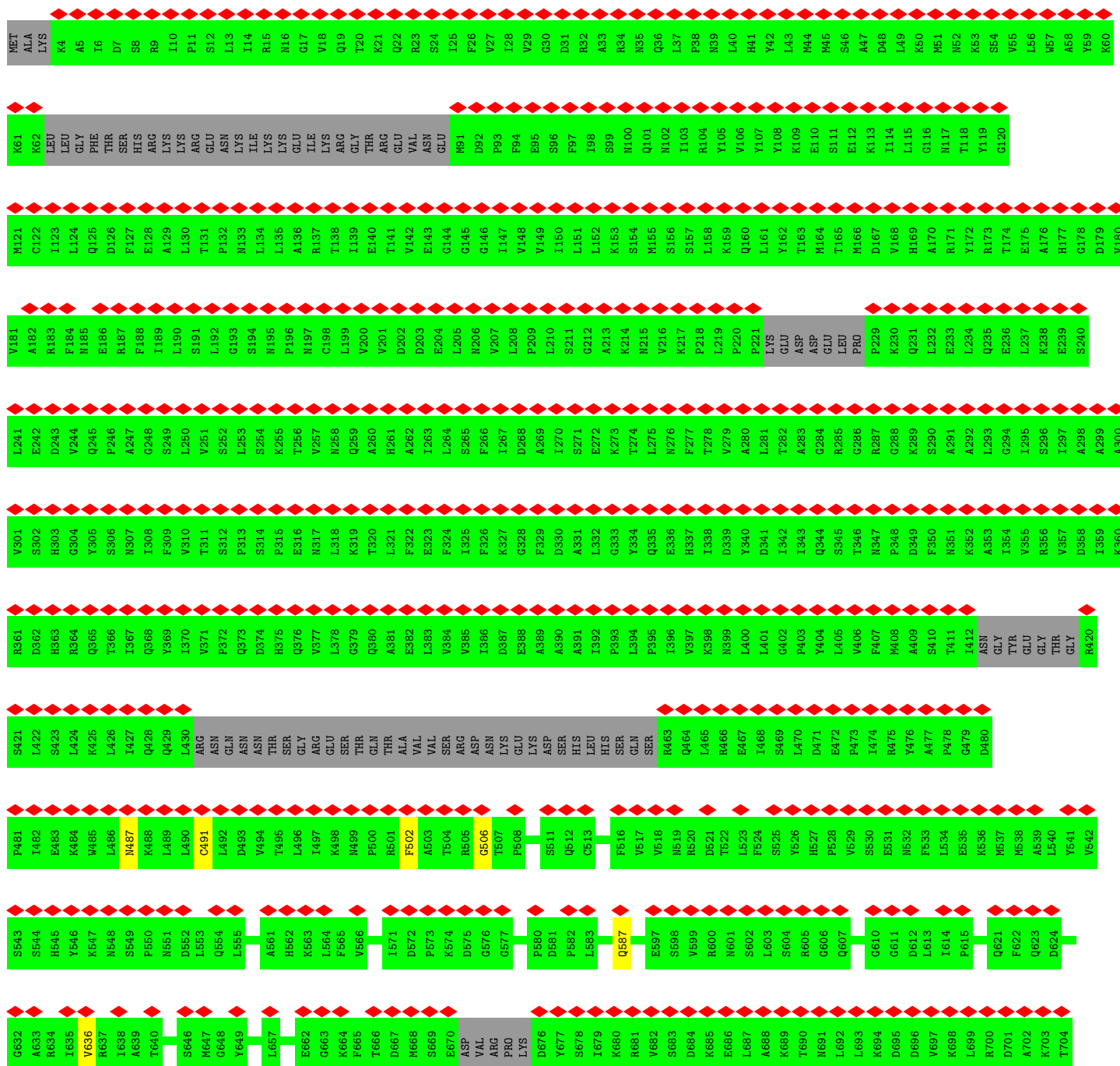
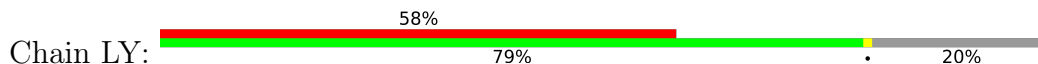


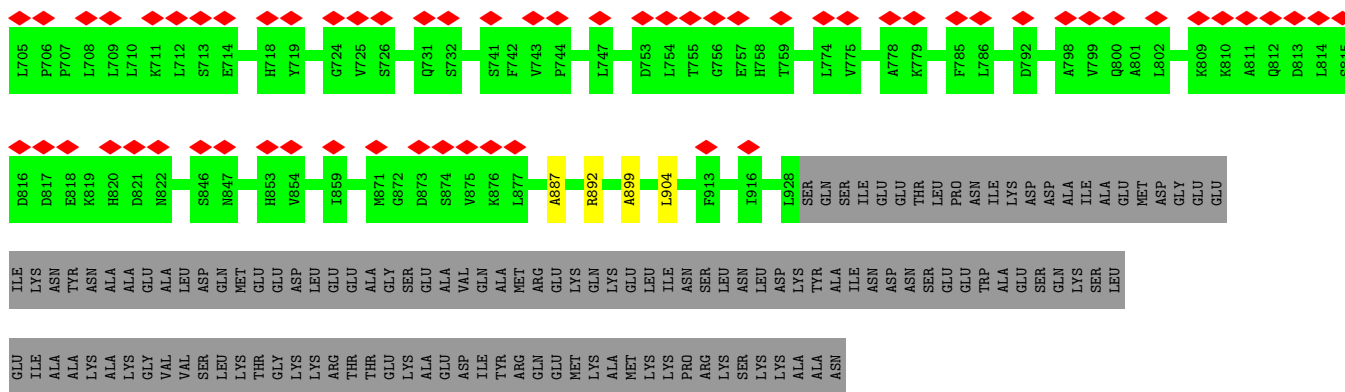
• Molecule 32: RNA cytidine acetyltransferase



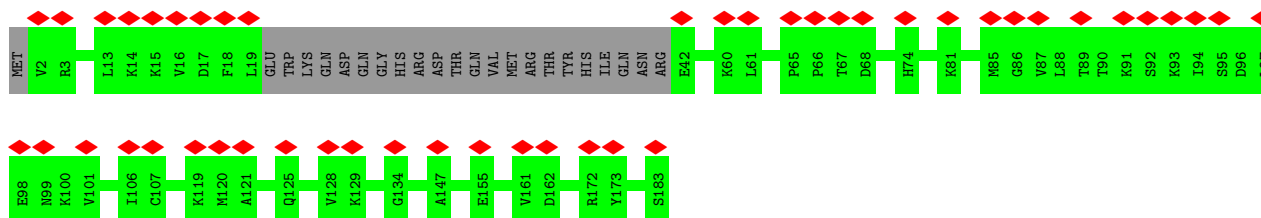
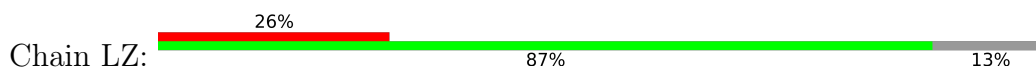


- Molecule 32: RNA cytidine acetyltransferase

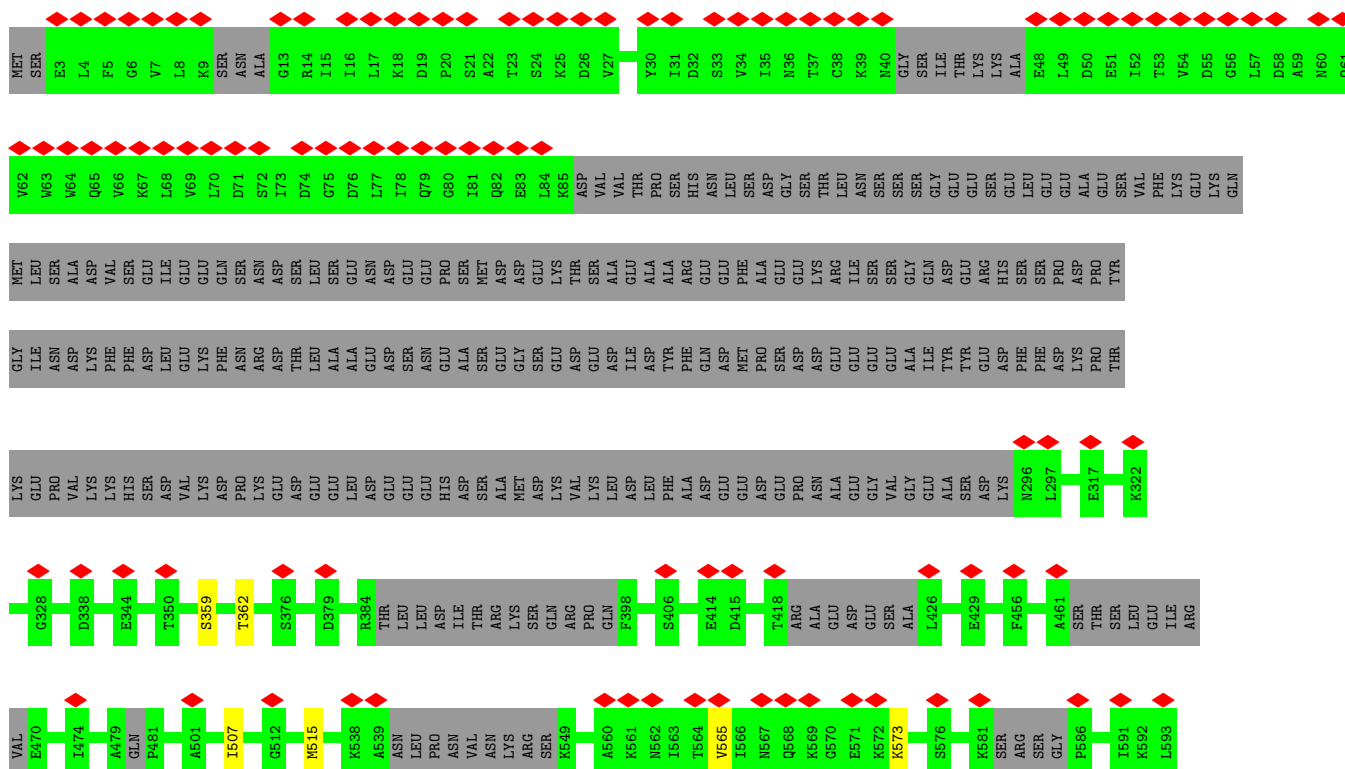




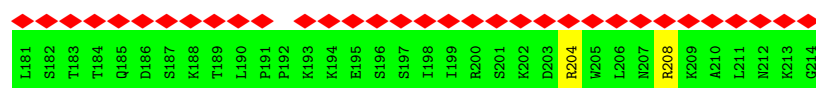
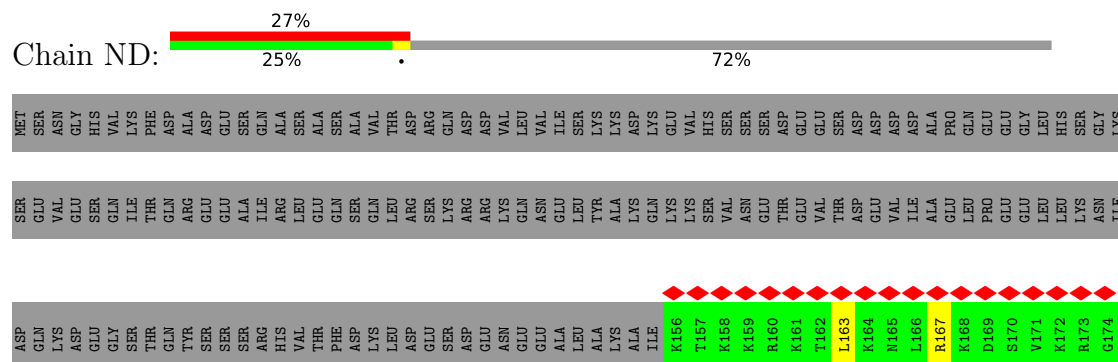
- Molecule 33: U3 small nucleolar ribonucleoprotein protein IMP3



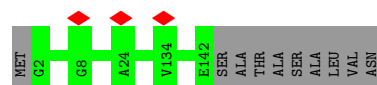
- Molecule 34: U3 small nucleolar RNA-associated protein MPP10



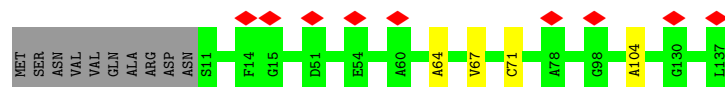
- Molecule 37: Bud site selection protein 21



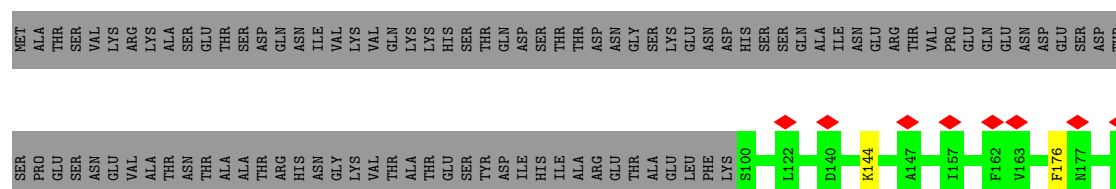
- Molecule 38: 40S ribosomal protein S13

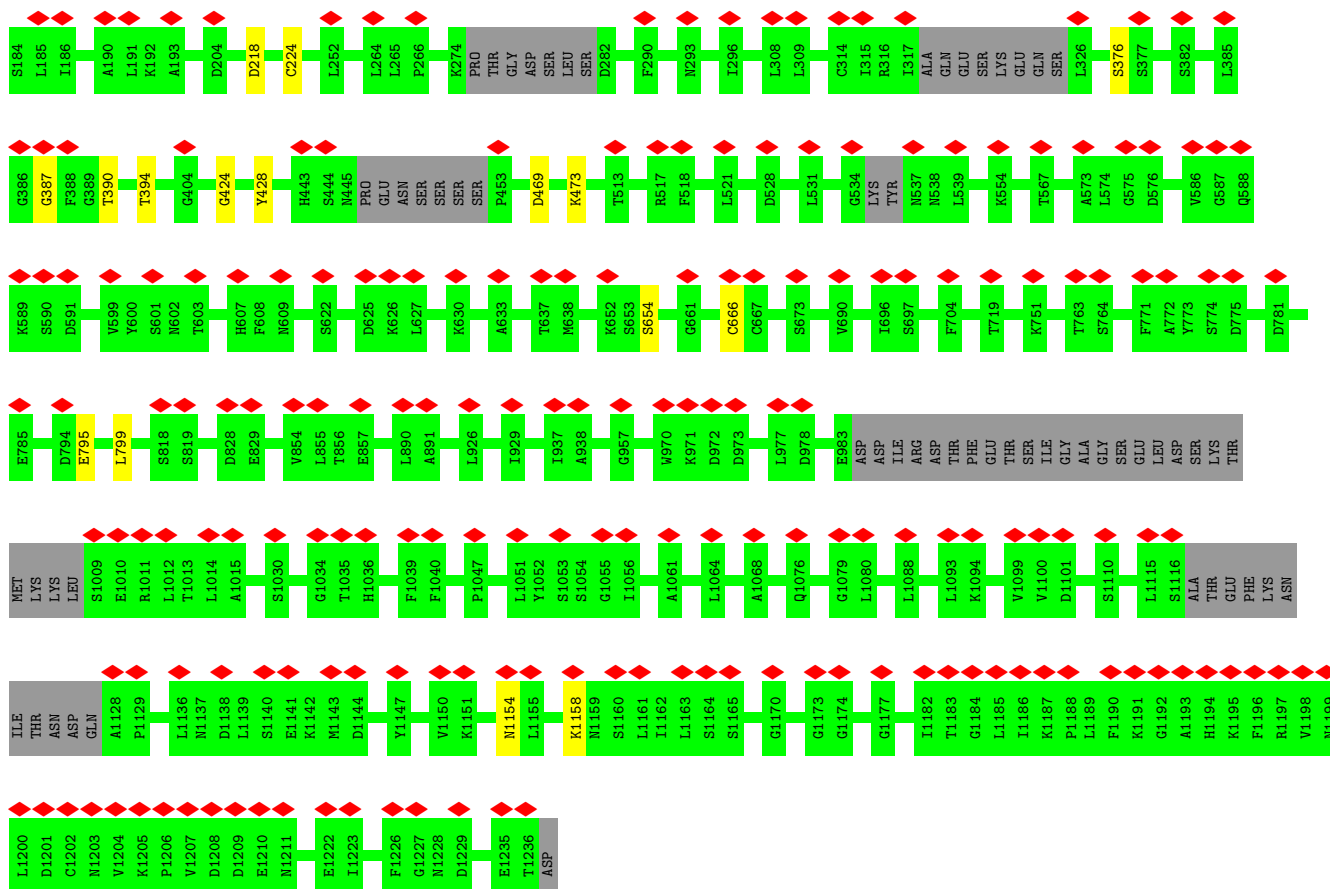


- Molecule 39: 40S ribosomal protein S14-A

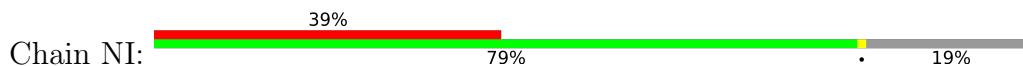


- Molecule 40: U3 small nucleolar RNA-associated protein 22

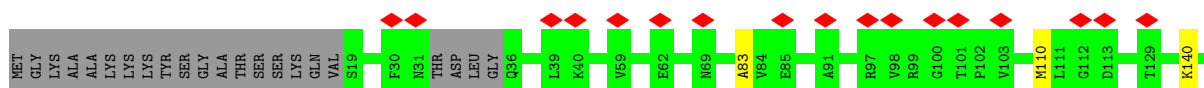
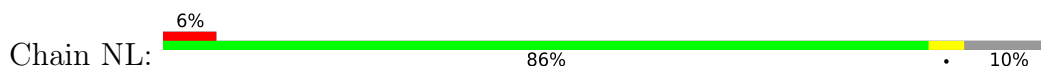


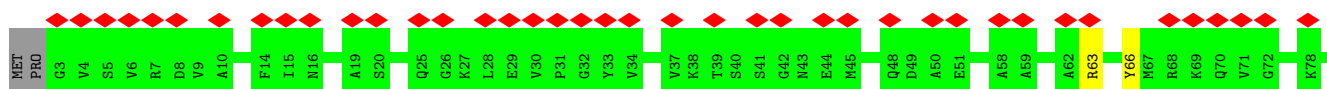


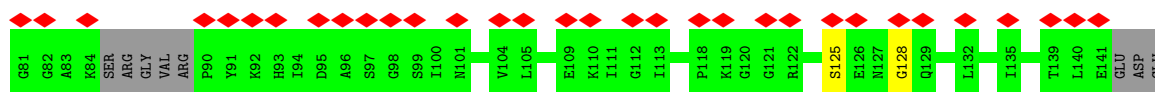
• Molecule 41: Ribosomal RNA-processing protein 7



• Molecule 42: Dimethyladenosine transferase

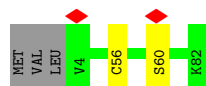






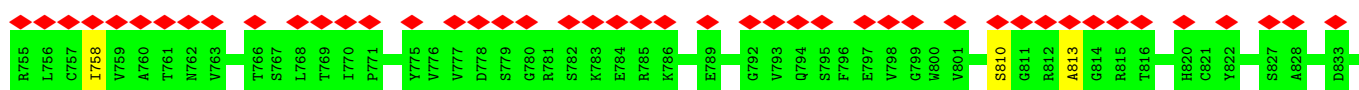
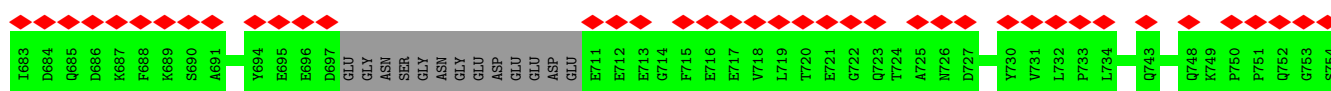
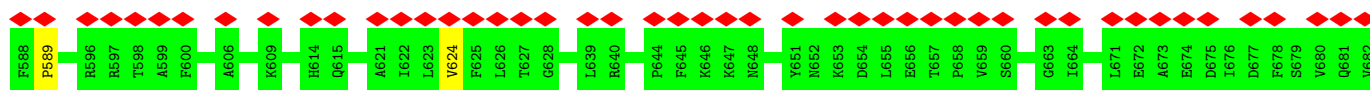
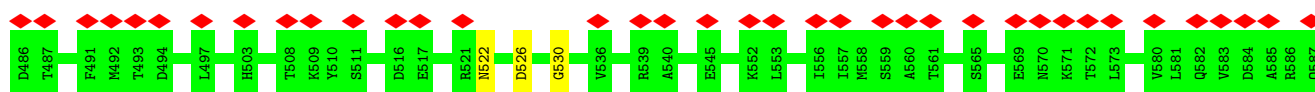
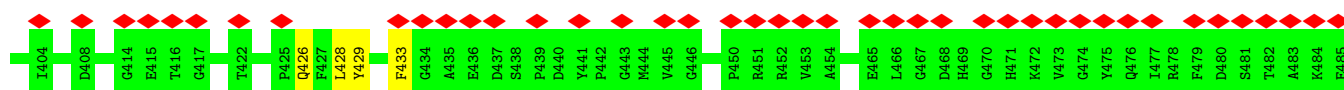
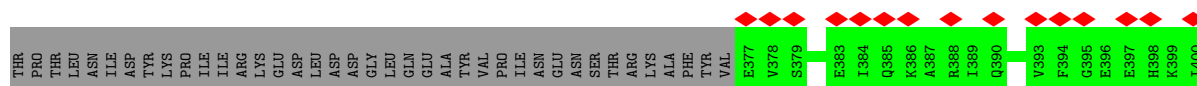
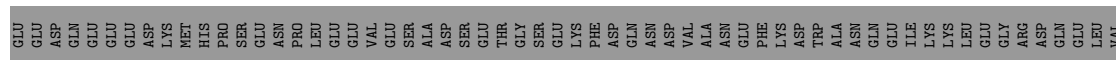
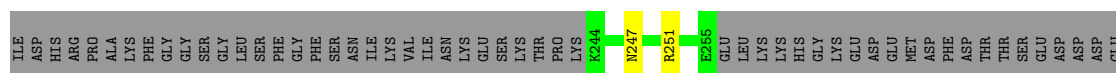
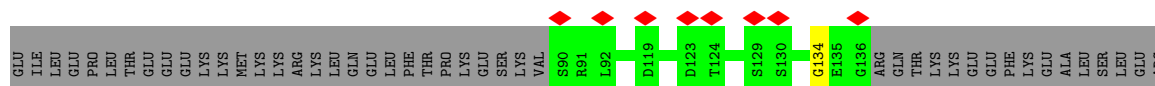
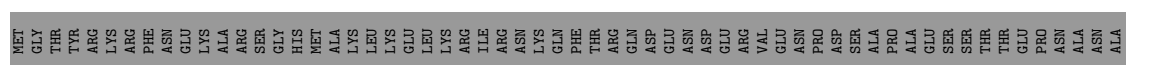
- Molecule 46: 40S ribosomal protein S27-A

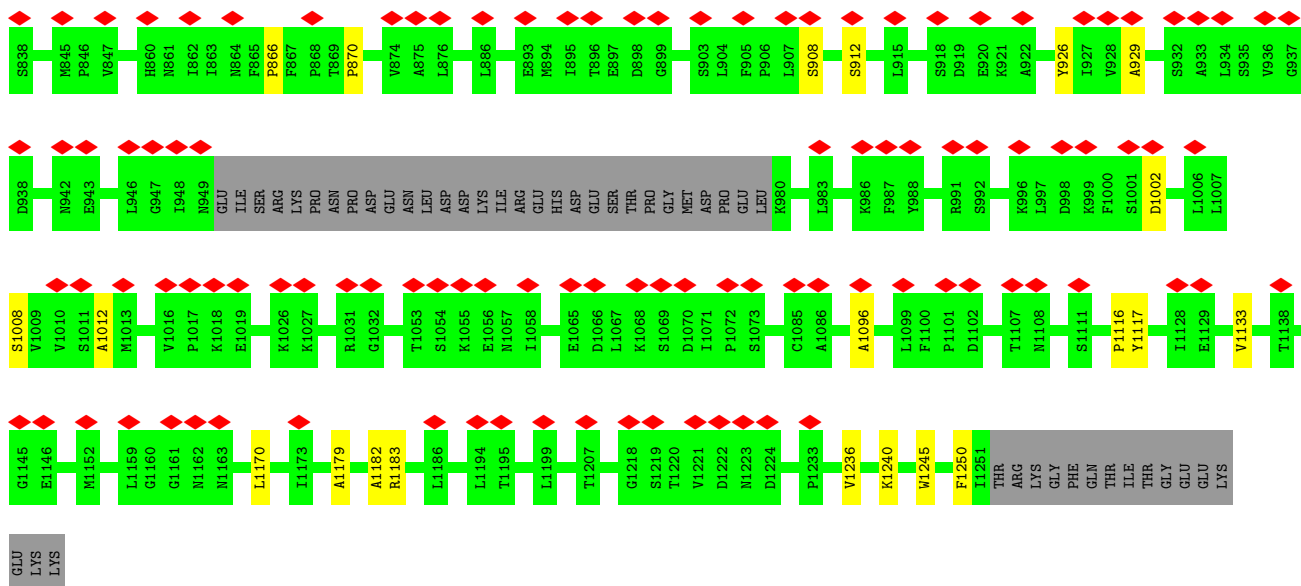
Chain NQ: 94%



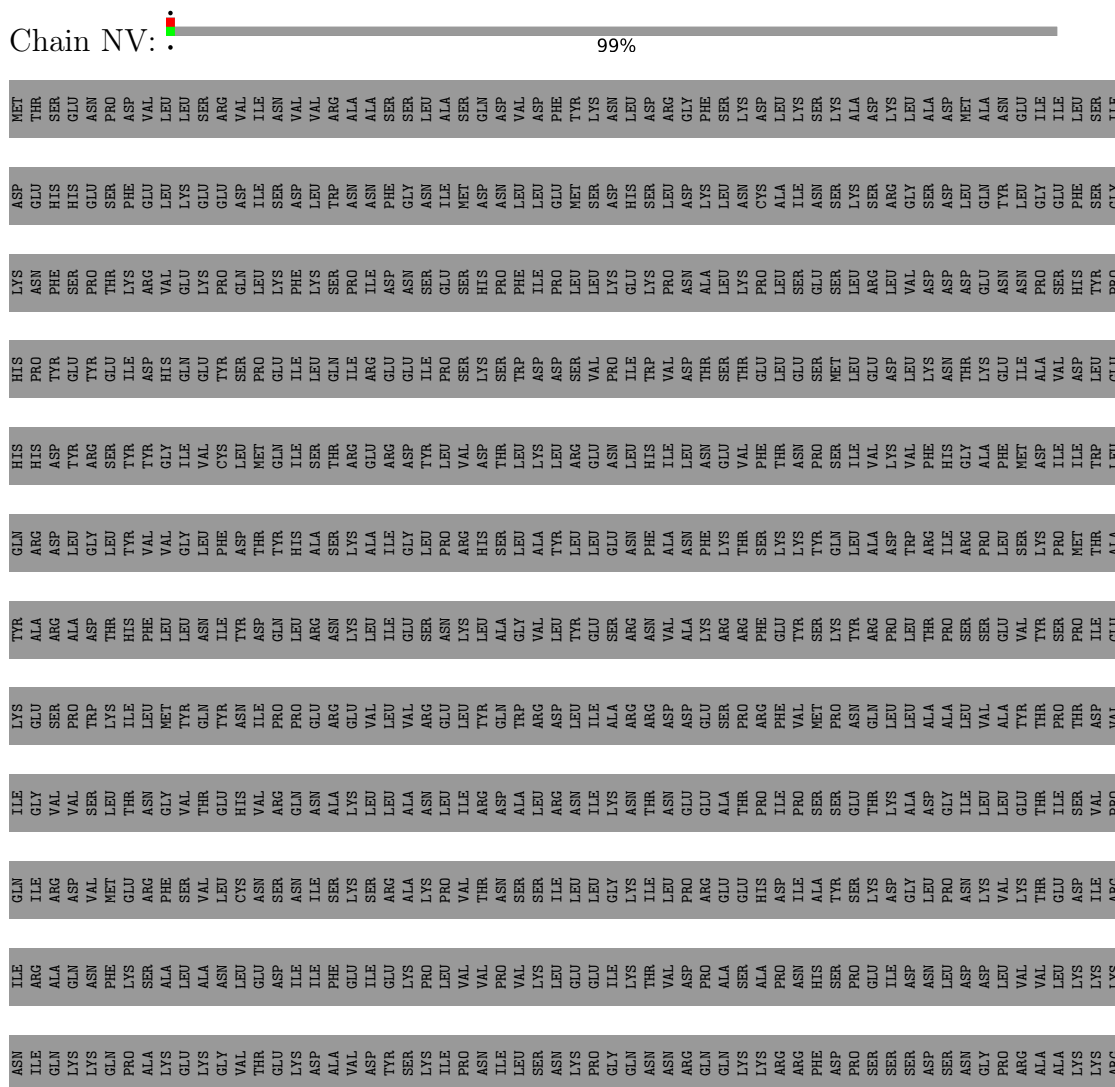
- Molecule 47: Probable ATP-dependent RNA helicase DHR1

Chain NS: 27% 67% 30%

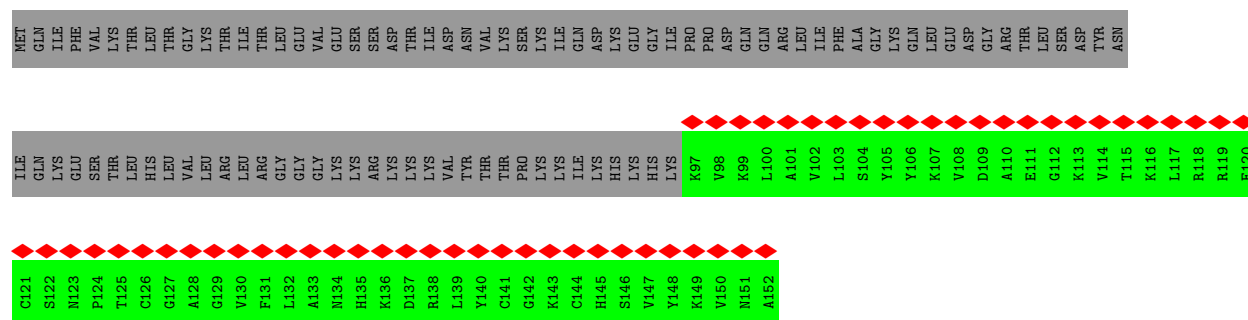




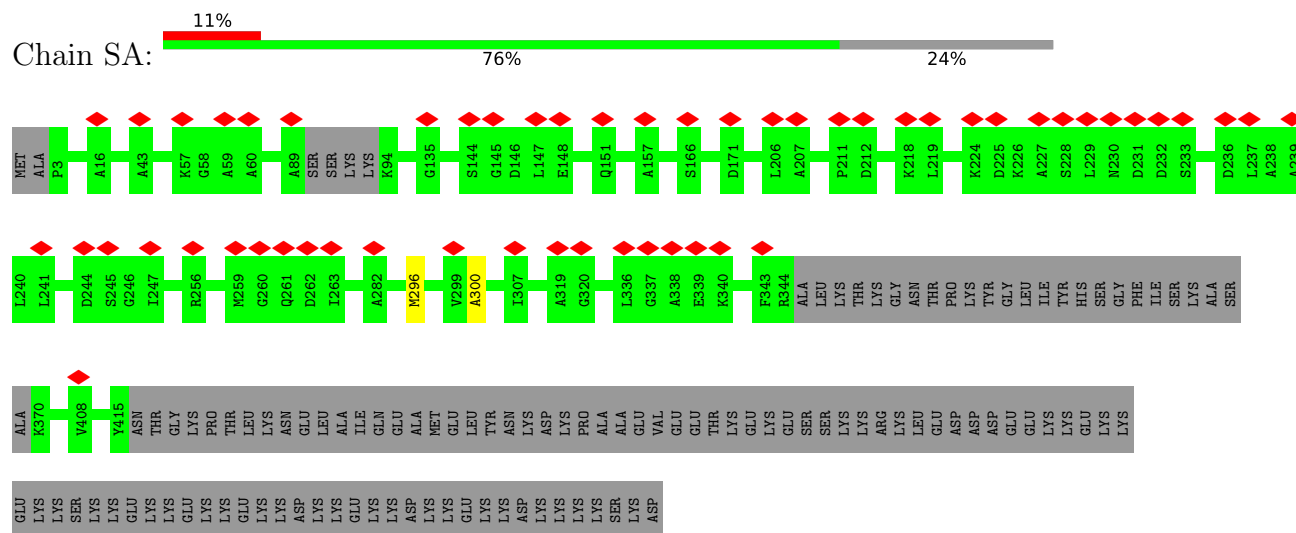
● Molecule 48: Exosome complex exonuclease RRP6



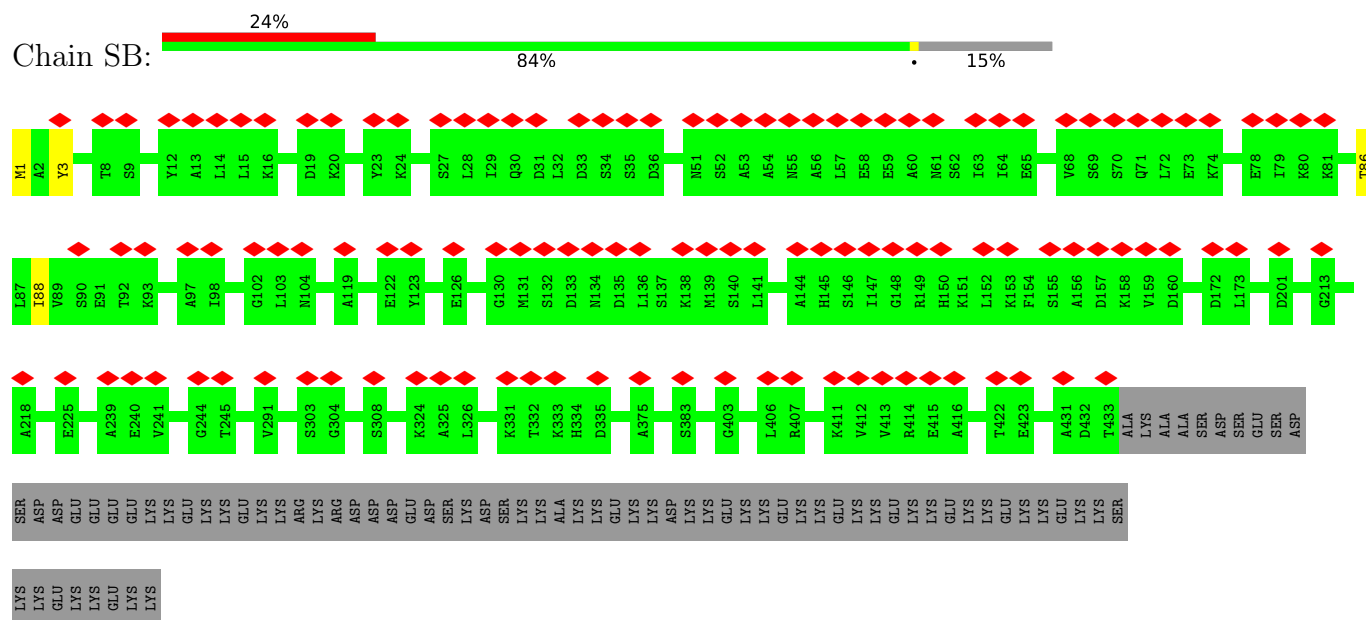
[illegible]



• Molecule 52: Nucleolar protein 56



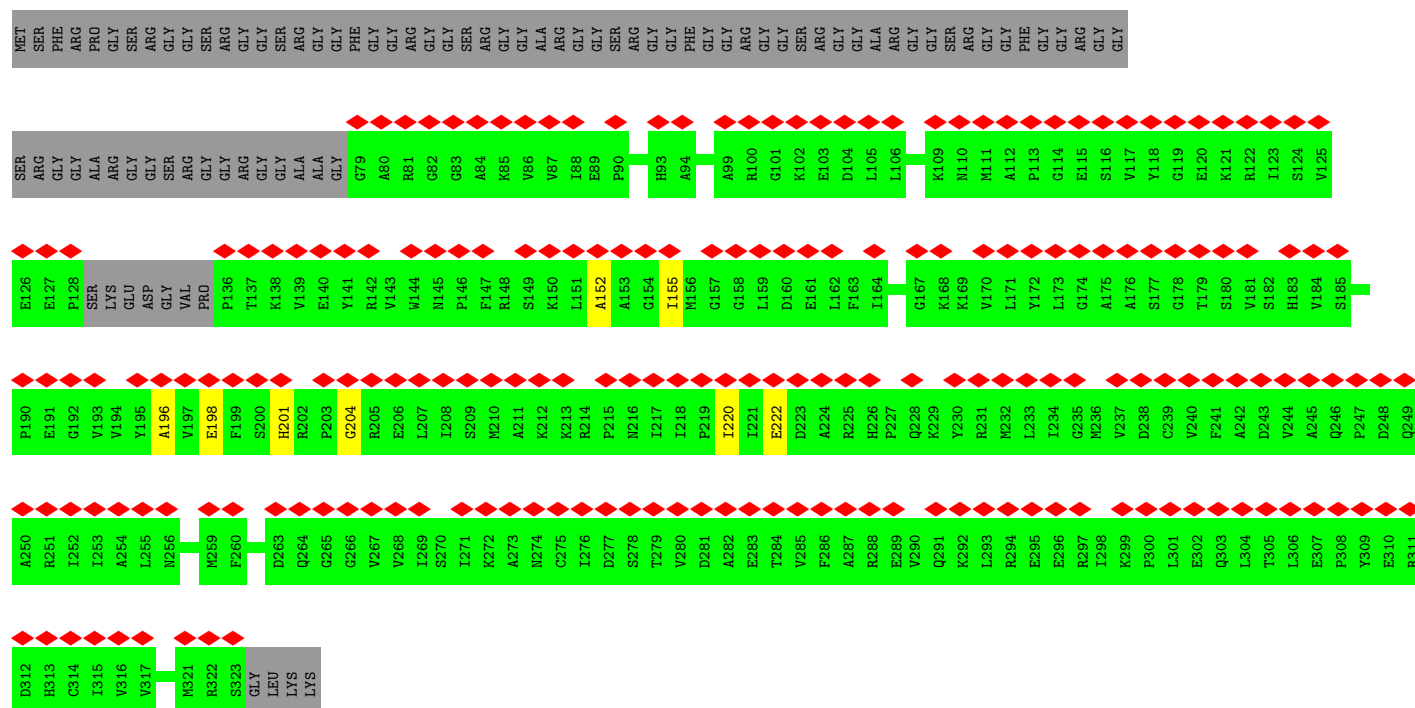
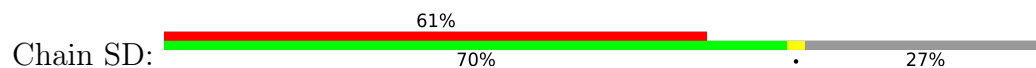
• Molecule 53: Nucleolar protein 58



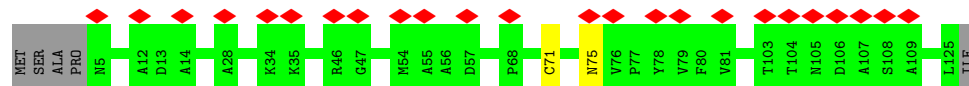
• Molecule 54: rRNA 2'-O-methyltransferase fibrillar



- Molecule 54: rRNA 2'-O-methyltransferase fibrillar



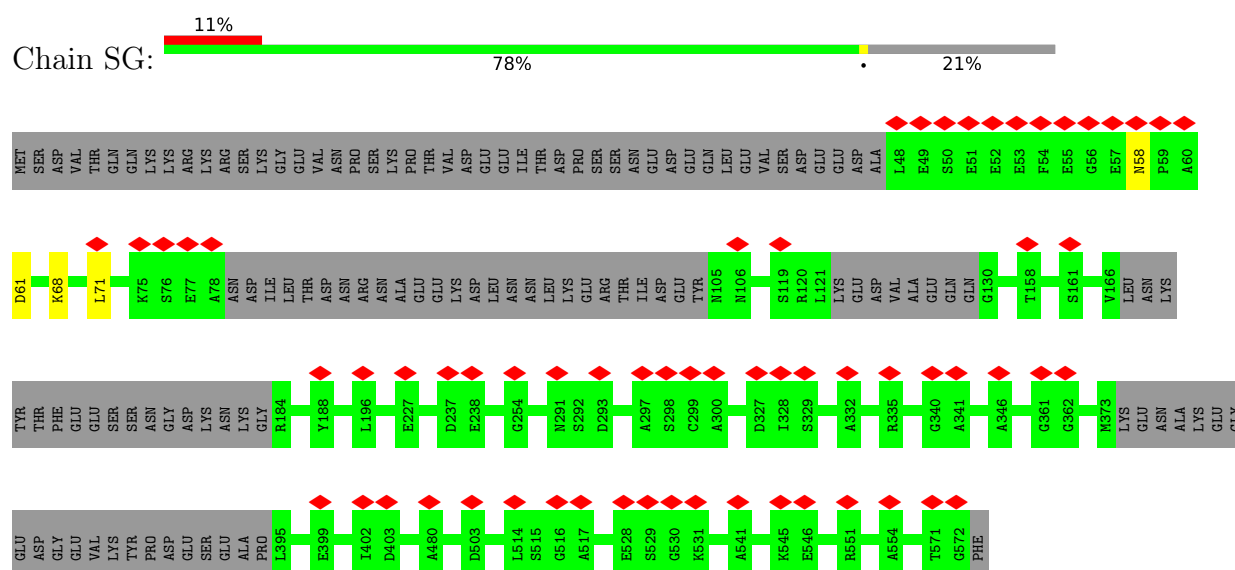
- Molecule 55: 13 kDa ribonucleoprotein-associated protein



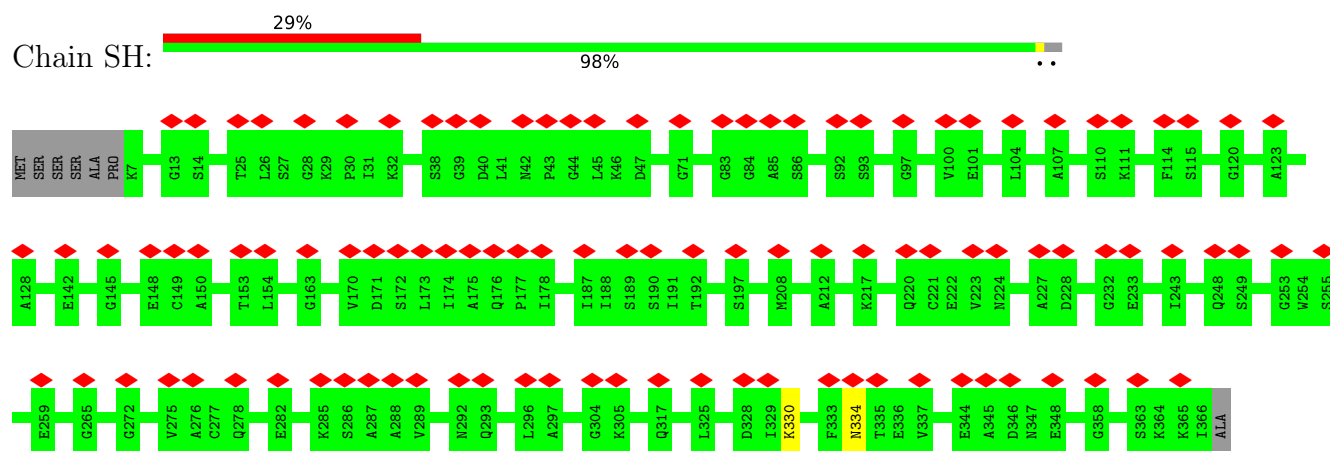
- Molecule 55: 13 kDa ribonucleoprotein-associated protein



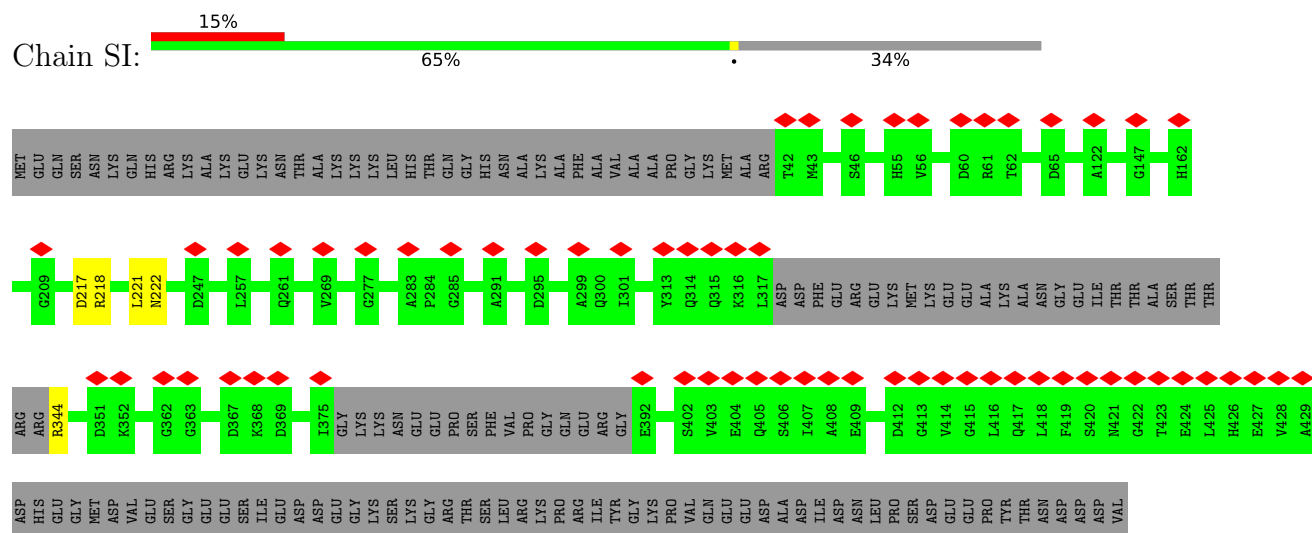
- Molecule 56: Ribosomal RNA-processing protein 9

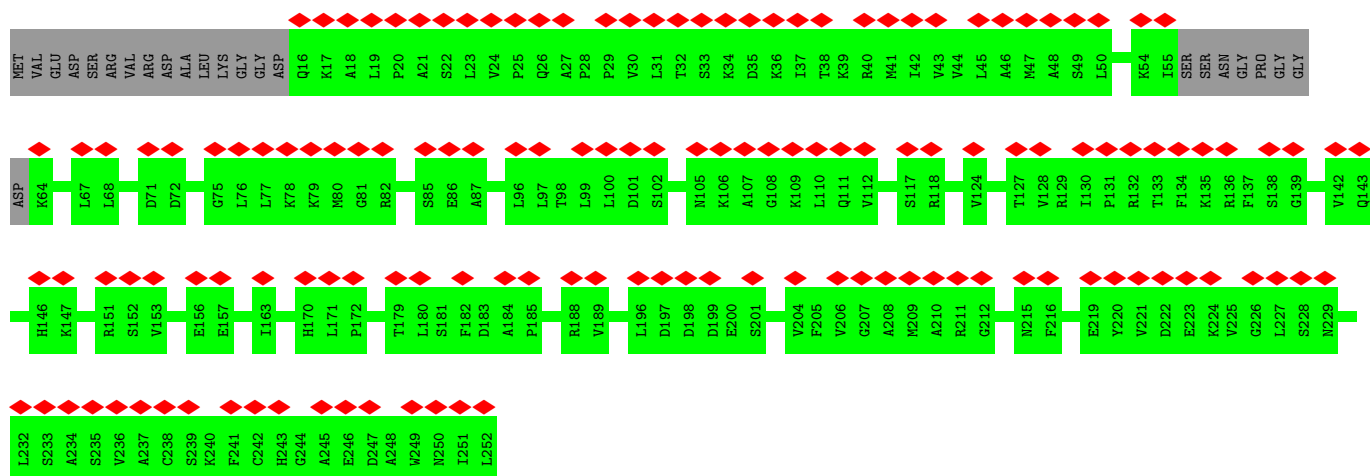


- Molecule 57: RNA 3'-terminal phosphate cyclase-like protein.



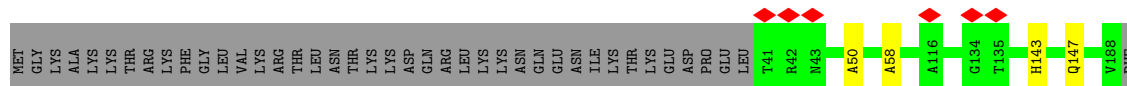
- Molecule 58: Ribosome biogenesis protein BMS1





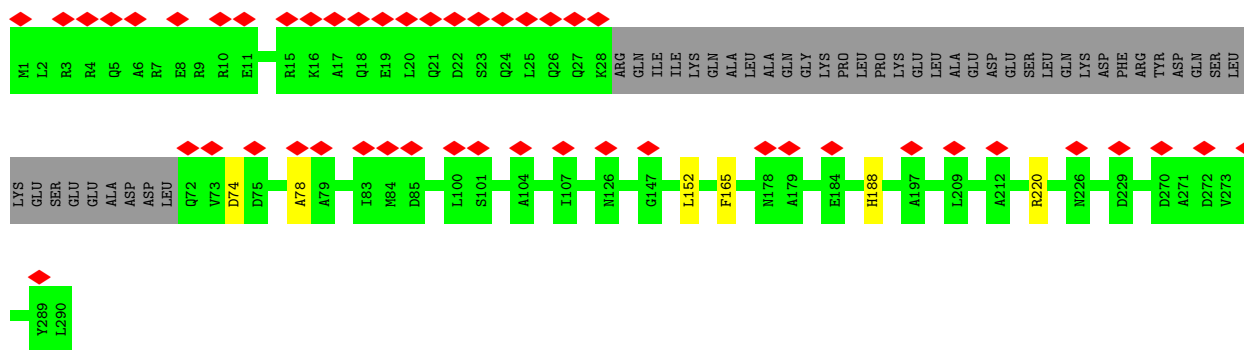
- Molecule 60: rRNA-processing protein FCF1

Chain SL: 76% 22%



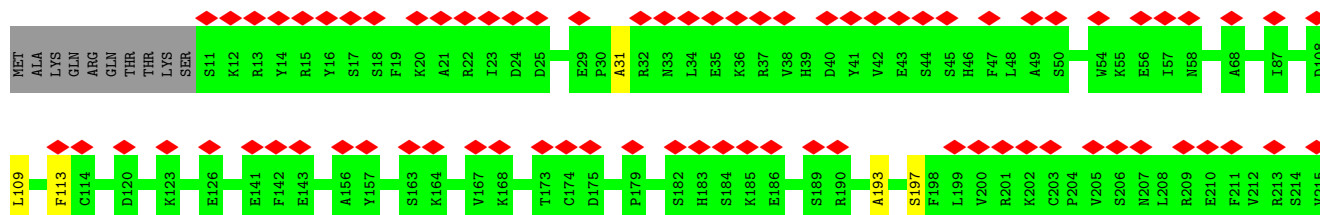
- Molecule 61: U3 small nucleolar ribonucleoprotein protein IMP4

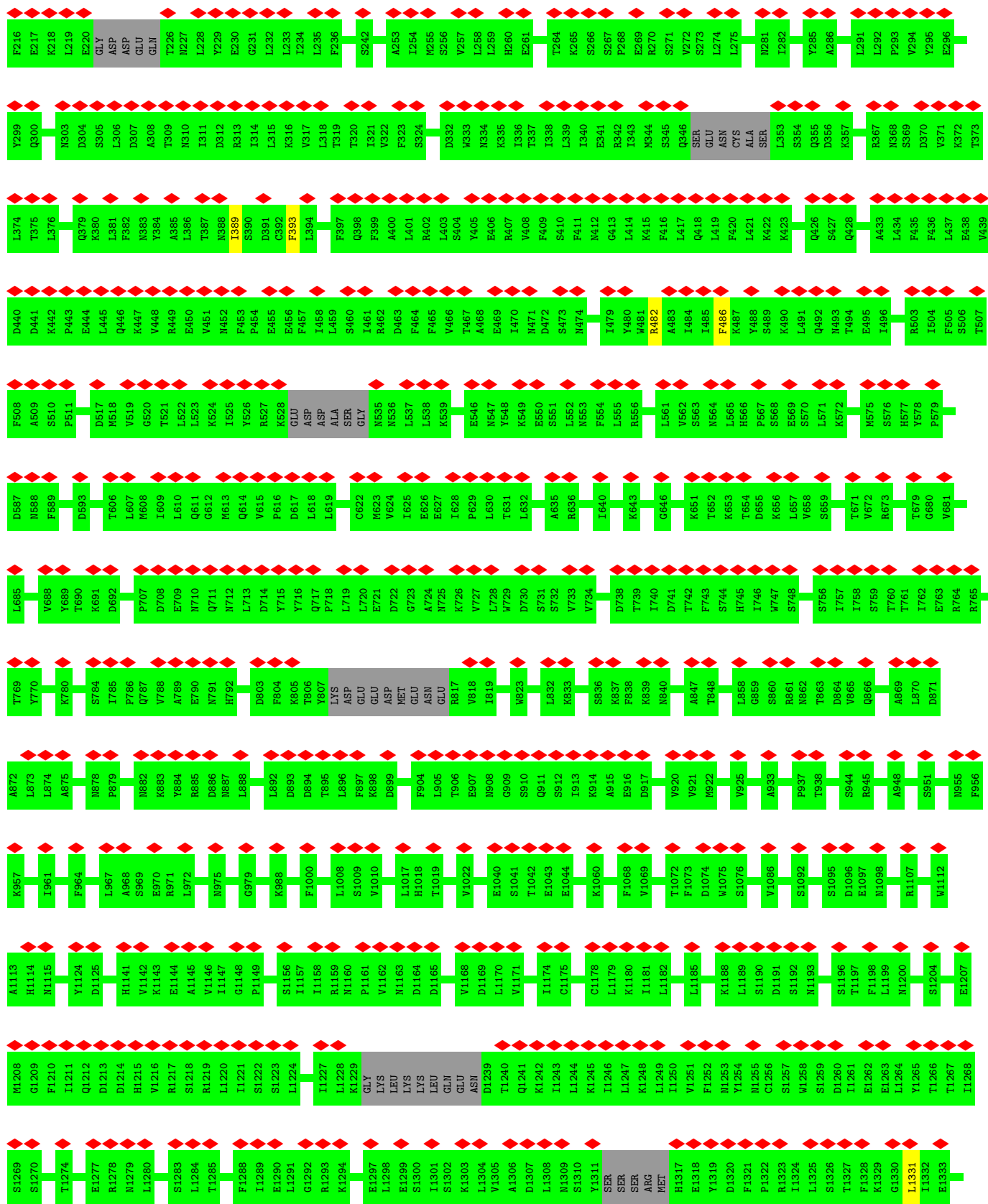
Chain SM: 17% 83% 15%



- Molecule 62: U3 small nucleolar RNA-associated protein 20

Chain SP: 42% 86% 14%

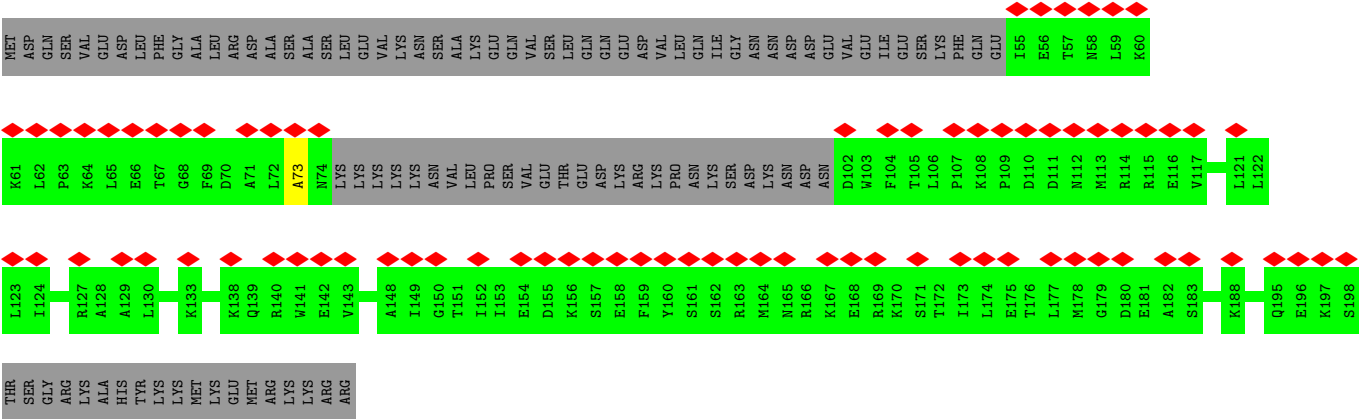




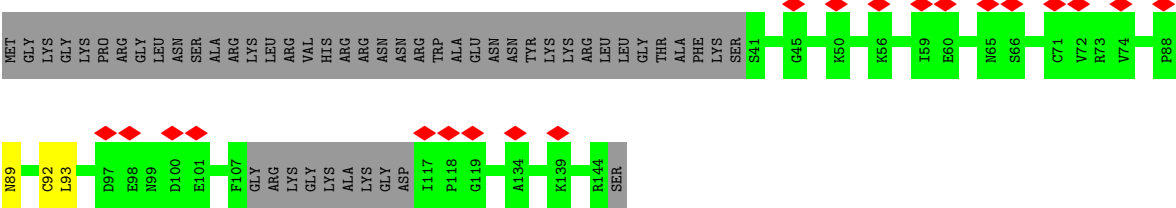
[illegible]

ARG
SER
GLN
ARG
GLY
LYS
LYS
LYS
HIS
GLU
LYS
LYS
ASP
GLU
ARG
ASN
GLY
TYR
SER
GLN
ARG
ARG
ASN
LYS
LYS
ARG
LYS
ALA

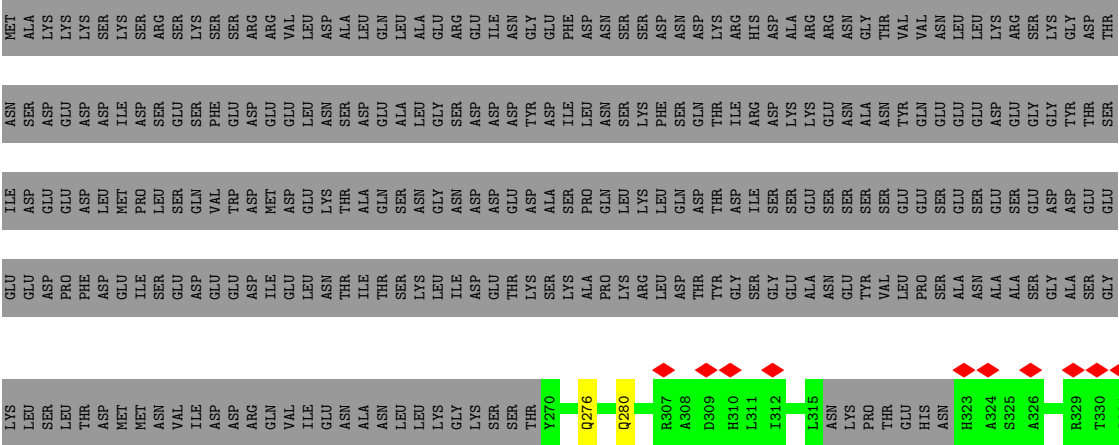
• Molecule 63: rRNA-processing protein FCF2

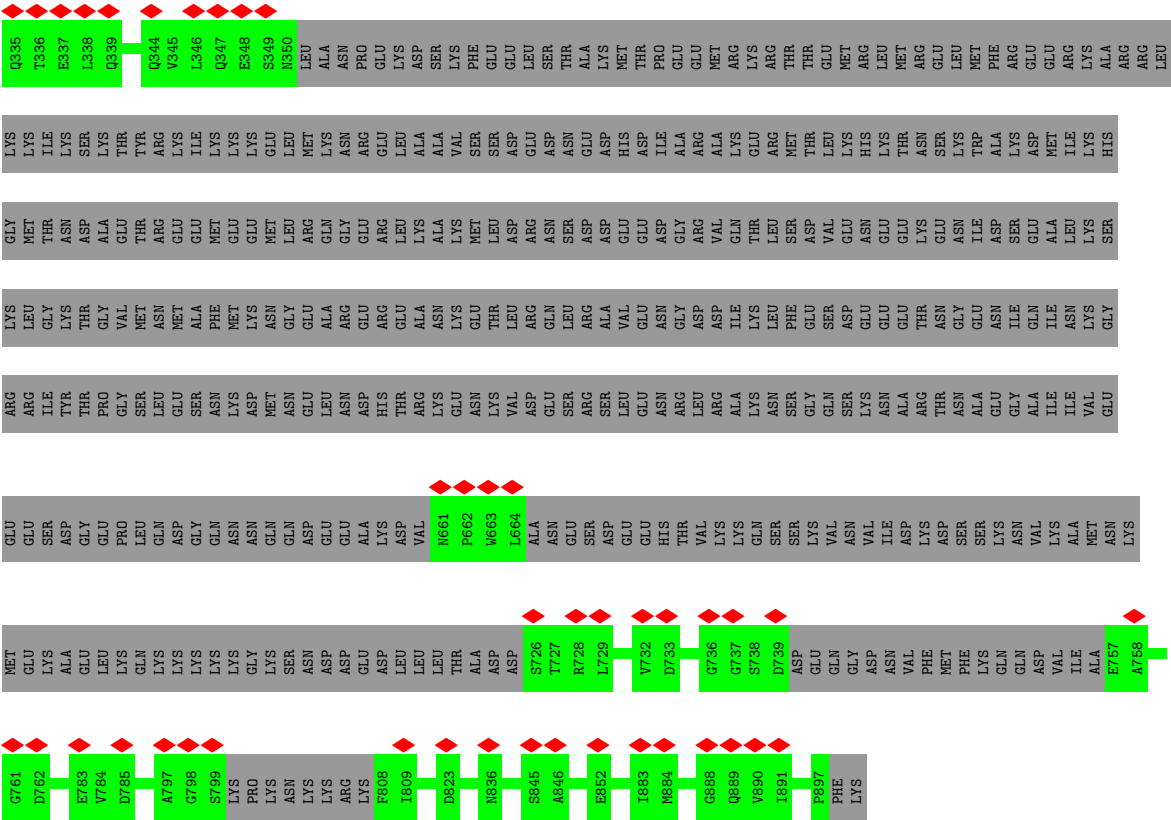


• Molecule 64: 40S ribosomal protein S23-A

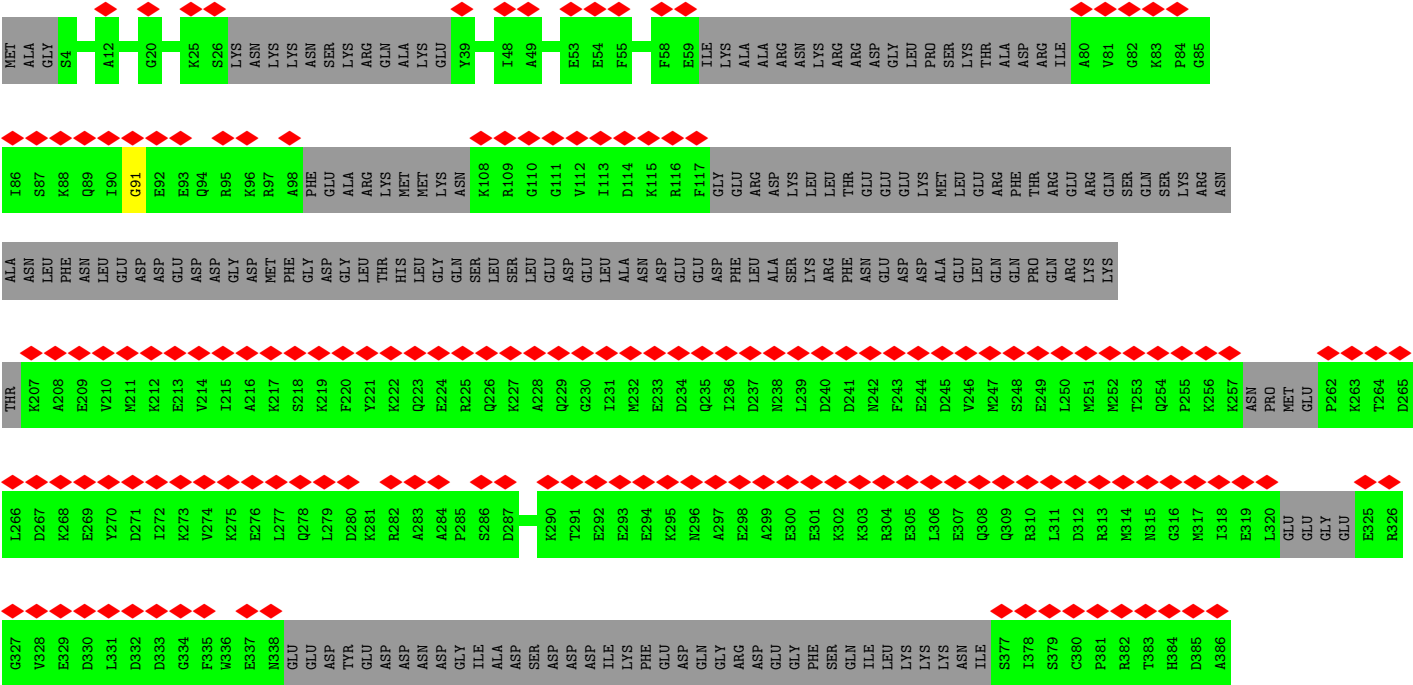
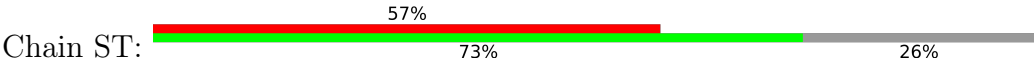


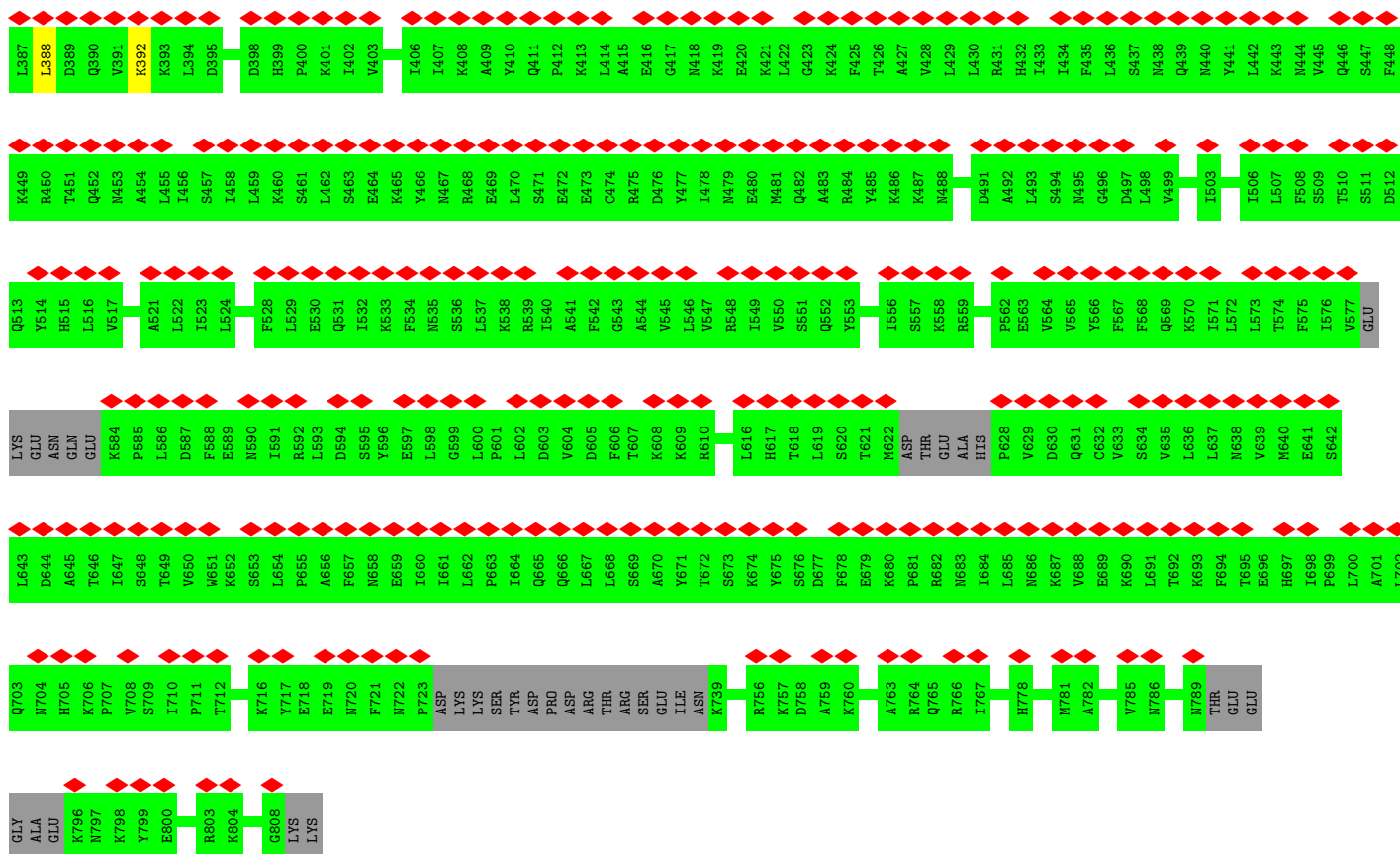
• Molecule 65: U3 small nucleolar RNA-associated protein 14



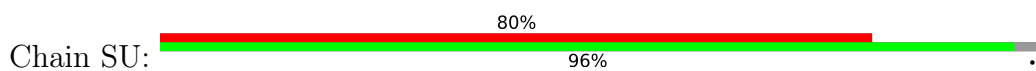


• Molecule 66: Nucleolar complex protein 14





• Molecule 67: Nucleolar complex protein 4



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4987	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	4.783	Depositor
Minimum map value	0.000	Depositor
Average map value	0.116	Depositor
Map value standard deviation	0.209	Depositor
Recommended contour level	1	Depositor
Map size (Å)	535.75195, 535.75195, 535.75195	wwPDB
Map dimensions	504, 504, 504	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.11	0/1529	0.29	0/2372
2	L1	0.09	0/30206	0.26	0/47024
3	L2	0.09	0/3417	0.26	0/5305
4	L3	0.16	0/529	0.39	0/736
5	L4	0.15	0/1182	0.39	0/1650
6	L5	0.17	0/1046	0.42	0/1464
7	L6	0.17	0/1035	0.36	0/1442
8	L7	0.22	0/911	0.55	0/1276
9	L8	0.17	0/850	0.39	0/1181
10	L9	0.19	0/922	0.54	0/1290
11	LC	0.18	0/647	0.47	0/903
12	LD	0.15	0/700	0.36	0/980
13	LE	0.22	0/642	0.58	0/893
14	LF	0.20	0/486	0.54	0/677
15	LG	0.15	0/310	0.39	0/430
16	LH	0.19	1/4046 (0.0%)	0.41	2/5644 (0.0%)
17	LI	0.15	0/3042	0.38	0/4250
18	LJ	0.14	0/2410	0.37	0/3370
19	LK	0.59	2/667 (0.3%)	0.84	5/933 (0.5%)
20	LL	0.14	0/2448	0.36	0/3415
21	LM	0.12	0/8150	0.30	0/11410
22	LN	0.14	0/3326	0.36	0/4637
23	LO	0.14	0/3976	0.35	0/5552
24	LP	0.12	0/1907	0.34	0/2667
25	LQ	0.17	0/4075	0.43	0/5682
26	LR	0.14	0/3980	0.36	0/5555
27	LS	0.18	0/2288	0.38	0/3188
28	LT	0.13	0/4367	0.34	0/6091
29	LU	0.15	0/2284	0.42	0/3190
30	LV	0.15	0/1804	0.41	0/2522
31	LW	0.17	0/2322	0.42	0/3243
32	LX	0.14	0/4337	0.36	0/6068

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LY	0.12	0/4310	0.32	0/6033
33	LZ	0.17	0/812	0.41	0/1136
34	NA	0.13	0/1654	0.34	0/2299
35	NB	0.14	0/1162	0.37	0/1618
36	NC	0.18	0/669	0.49	0/931
37	ND	0.13	0/298	0.37	0/416
38	NF	0.16	0/717	0.40	0/1003
39	NG	0.16	0/634	0.40	0/881
40	NH	0.13	0/5489	0.34	0/7686
41	NI	0.13	0/1214	0.34	0/1695
42	NL	0.19	0/1460	0.45	0/2045
43	NM	0.13	0/1185	0.34	0/1651
44	NN	0.12	0/216	0.35	0/300
45	NP	0.15	0/669	0.39	0/928
46	NQ	0.15	0/401	0.38	0/560
47	NS	0.18	0/4540	0.43	1/6357 (0.0%)
48	NV	0.21	0/38	0.48	0/51
49	OA	0.11	0/68	0.35	0/93
50	OH	0.09	0/595	0.25	0/827
51	OU	0.10	0/278	0.30	0/386
52	SA	0.13	0/1931	0.34	0/2693
53	SB	0.13	0/2168	0.35	0/3028
54	SC	0.17	0/1210	0.46	0/1689
54	SD	0.15	0/1210	0.42	0/1689
55	SE	0.18	0/621	0.43	0/871
55	SF	0.19	0/621	0.43	0/871
56	SG	0.14	0/2263	0.37	0/3150
57	SH	0.16	0/1817	0.42	0/2536
58	SI	0.16	0/3975	0.39	0/5560
59	SJ	0.13	0/1080	0.32	0/1508
59	SK	0.13	0/1170	0.31	0/1639
60	SL	0.17	0/759	0.41	0/1064
61	SM	0.16	0/1251	0.42	0/1749
62	SP	0.14	0/10900	0.35	0/15259
63	SQ	0.17	0/595	0.43	0/832
64	SR	0.18	0/479	0.45	0/666
65	SS	0.18	0/1150	0.42	0/1604
66	ST	0.12	0/3020	0.30	0/4213
67	SU	0.12	0/2726	0.33	0/3825
68	SW	0.17	0/1111	0.45	0/1550
69	SY	0.16	0/609	0.46	0/846
70	SZ	0.11	0/1326	0.30	0/1859
All	All	0.14	3/168242 (0.0%)	0.36	8/240637 (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
36	NC	0	1
47	NS	0	1
58	SI	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	LK	414	PRO	CG-CD	-11.24	1.12	1.50
16	LH	549	ASN	C-O	7.61	1.27	1.23
19	LK	494	PRO	CG-CD	-7.40	1.25	1.50

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	LK	414	PRO	N-CD-CG	-13.45	83.02	103.20
19	LK	414	PRO	CA-N-CD	-9.27	99.03	112.00
19	LK	494	PRO	CA-N-CD	-9.16	99.17	112.00
19	LK	494	PRO	N-CD-CG	-8.99	89.72	103.20
19	LK	414	PRO	CA-CB-CG	-6.99	91.22	104.50

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	NC	242	MET	Peptide
47	NS	870	PRO	Peptide
58	SI	866	ARG	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	1	0
2	L1	27015	0	13616	51	0
3	L2	3064	0	1554	8	0
4	L3	529	0	240	1	0
5	L4	1172	0	578	1	0
6	L5	1040	0	519	0	0
7	L6	1029	0	512	2	0
8	L7	903	0	450	4	0
9	L8	848	0	429	1	0
10	L9	914	0	464	4	0
11	LC	642	0	328	2	0
12	LD	693	0	336	0	0
13	LE	640	0	307	0	0
14	LF	484	0	242	3	0
15	LG	309	0	145	0	0
16	LH	4034	0	1821	5	0
17	LI	3027	0	1390	0	0
18	LJ	2394	0	1161	3	0
19	LK	664	0	299	2	0
20	LL	2440	0	1139	2	0
21	LM	8115	0	3739	9	0
22	LN	3315	0	1518	5	0
23	LO	3958	0	1889	3	0
24	LP	1901	0	836	1	0
25	LQ	4063	0	1898	17	0
26	LR	3962	0	1883	7	0
27	LS	2279	0	1110	3	0
28	LT	4347	0	2073	7	0
29	LU	2274	0	1064	3	0
30	LV	1791	0	844	3	0
31	LW	2304	0	1146	5	0
32	LX	4302	0	2100	4	0
32	LY	4274	0	2096	5	0
33	LZ	808	0	370	0	0
34	NA	1654	0	771	3	0
35	NB	1159	0	548	4	0
36	NC	669	0	309	6	0
37	ND	297	0	132	3	0
38	NF	711	0	360	0	0
39	NG	630	0	341	2	0
40	NH	5443	0	2602	9	0
41	NI	1210	0	565	2	0
42	NL	1446	0	710	6	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	NM	1183	0	553	5	0
44	NN	215	0	111	0	0
45	NP	666	0	345	2	0
46	NQ	398	0	200	1	0
47	NS	4500	0	2179	19	0
48	NV	39	0	16	0	0
49	OA	69	0	34	0	0
50	OH	594	0	298	1	0
51	OU	278	0	135	0	0
52	SA	1924	0	946	1	0
53	SB	2161	0	1090	2	0
54	SC	1198	0	625	3	0
54	SD	1198	0	625	4	0
55	SE	615	0	331	1	0
55	SF	615	0	331	1	0
56	SG	2260	0	1085	2	0
57	SH	1801	0	897	1	0
58	SI	3939	0	1944	6	0
59	SJ	1074	0	514	2	0
59	SK	1160	0	570	0	0
60	SL	751	0	377	2	0
61	SM	1243	0	602	3	0
62	SP	10847	0	4961	8	0
63	SQ	592	0	278	1	0
64	SR	476	0	237	2	0
65	SS	1145	0	565	1	0
66	ST	3010	0	1415	2	0
67	SU	2703	0	1302	0	0
68	SW	1104	0	544	1	0
69	SY	611	0	265	3	0
70	SZ	1314	0	649	0	0
All	All	163806	0	79150	253	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 253 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)
2:L1:1108:G:OP2	2:L1:1108:G:N2	2.12	0.81
24:LP:111:ALA:HB1	63:SQ:73:ALA:HB2	1.62	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L2:39:C:O2'	29:LU:18:SER:O	1.98	0.80
16:LH:892:MET:O	16:LH:896:THR:N	2.15	0.79
2:L1:562:G:N2	2:L1:564:G:OP1	2.16	0.78

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	102/146 (70%)	100 (98%)	2 (2%)	0	100	100
5	L4	232/261 (89%)	230 (99%)	2 (1%)	0	100	100
6	L5	202/225 (90%)	199 (98%)	3 (2%)	0	100	100
7	L6	202/236 (86%)	199 (98%)	3 (2%)	0	100	100
8	L7	174/190 (92%)	170 (98%)	4 (2%)	0	100	100
9	L8	167/200 (84%)	164 (98%)	3 (2%)	0	100	100
10	L9	179/197 (91%)	175 (98%)	4 (2%)	0	100	100
11	LC	126/143 (88%)	122 (97%)	4 (3%)	0	100	100
12	LD	135/156 (86%)	131 (97%)	4 (3%)	0	100	100
13	LE	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
14	LF	95/135 (70%)	90 (95%)	5 (5%)	0	100	100
15	LG	60/67 (90%)	60 (100%)	0	0	100	100
16	LH	788/896 (88%)	766 (97%)	22 (3%)	0	100	100
17	LI	582/713 (82%)	574 (99%)	8 (1%)	0	100	100
18	LJ	470/513 (92%)	458 (97%)	12 (3%)	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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	LM	1597/1769 (90%)	1575 (99%)	22 (1%)	0	100	100
22	LN	649/776 (84%)	637 (98%)	12 (2%)	0	100	100
23	LO	786/923 (85%)	769 (98%)	17 (2%)	0	100	100
24	LP	375/440 (85%)	373 (100%)	2 (0%)	0	100	100
25	LQ	805/943 (85%)	791 (98%)	14 (2%)	0	100	100
26	LR	785/817 (96%)	768 (98%)	17 (2%)	0	100	100
27	LS	441/594 (74%)	431 (98%)	10 (2%)	0	100	100
28	LT	861/939 (92%)	841 (98%)	20 (2%)	0	100	100
29	LU	448/489 (92%)	441 (98%)	7 (2%)	0	100	100
30	LV	355/707 (50%)	345 (97%)	10 (3%)	0	100	100
31	LW	453/554 (82%)	439 (97%)	14 (3%)	0	100	100
32	LX	838/1056 (79%)	821 (98%)	17 (2%)	0	100	100
32	LY	834/1056 (79%)	824 (99%)	10 (1%)	0	100	100
33	LZ	156/183 (85%)	155 (99%)	1 (1%)	0	100	100
34	NA	309/593 (52%)	305 (99%)	4 (1%)	0	100	100
35	NB	221/610 (36%)	218 (99%)	3 (1%)	0	100	100
36	NC	133/357 (37%)	125 (94%)	8 (6%)	0	100	100
37	ND	57/214 (27%)	57 (100%)	0	0	100	100
38	NF	139/151 (92%)	138 (99%)	1 (1%)	0	100	100
39	NG	125/137 (91%)	122 (98%)	3 (2%)	0	100	100
40	NH	1063/1237 (86%)	1056 (99%)	7 (1%)	0	100	100
41	NI	232/297 (78%)	225 (97%)	7 (3%)	0	100	100
42	NL	279/318 (88%)	276 (99%)	3 (1%)	0	100	100
43	NM	231/255 (91%)	228 (99%)	3 (1%)	0	100	100
44	NN	41/534 (8%)	41 (100%)	0	0	100	100
45	NP	130/144 (90%)	128 (98%)	2 (2%)	0	100	100
46	NQ	77/82 (94%)	75 (97%)	2 (3%)	0	100	100
47	NS	881/1267 (70%)	862 (98%)	19 (2%)	0	100	100
48	NV	6/733 (1%)	6 (100%)	0	0	100	100
49	OA	12/1729 (1%)	12 (100%)	0	0	100	100
50	OH	118/143 (82%)	118 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	OU	54/152 (36%)	54 (100%)	0	0	100	100
52	SA	379/504 (75%)	372 (98%)	7 (2%)	0	100	100
53	SB	431/511 (84%)	424 (98%)	7 (2%)	0	100	100
54	SC	234/327 (72%)	227 (97%)	7 (3%)	0	100	100
54	SD	234/327 (72%)	228 (97%)	6 (3%)	0	100	100
55	SE	119/126 (94%)	116 (98%)	3 (2%)	0	100	100
55	SF	119/126 (94%)	115 (97%)	4 (3%)	0	100	100
56	SG	442/573 (77%)	434 (98%)	8 (2%)	0	100	100
57	SH	358/367 (98%)	349 (98%)	9 (2%)	0	100	100
58	SI	766/1183 (65%)	748 (98%)	18 (2%)	0	100	100
59	SJ	207/252 (82%)	206 (100%)	1 (0%)	0	100	100
59	SK	225/252 (89%)	224 (100%)	1 (0%)	0	100	100
60	SL	146/189 (77%)	139 (95%)	7 (5%)	0	100	100
61	SM	243/290 (84%)	237 (98%)	6 (2%)	0	100	100
62	SP	2136/2493 (86%)	2102 (98%)	34 (2%)	0	100	100
63	SQ	113/217 (52%)	112 (99%)	1 (1%)	0	100	100
64	SR	91/145 (63%)	89 (98%)	2 (2%)	0	100	100
65	SS	213/899 (24%)	210 (99%)	3 (1%)	0	100	100
66	ST	573/810 (71%)	561 (98%)	12 (2%)	0	100	100
67	SU	524/552 (95%)	518 (99%)	6 (1%)	0	100	100
68	SW	211/274 (77%)	204 (97%)	7 (3%)	0	100	100
69	SY	114/250 (46%)	111 (97%)	3 (3%)	0	100	100
70	SZ	255/483 (53%)	249 (98%)	6 (2%)	0	100	100
All	All	25870/36775 (70%)	25385 (98%)	485 (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	11/222 (5%)	11 (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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	NB	8/538 (2%)	8 (100%)	0	100	100
36	NC	1/315 (0%)	1 (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	NL	17/283 (6%)	17 (100%)	0	100	100
43	NM	5/224 (2%)	5 (100%)	0	100	100
44	NN	2/482 (0%)	2 (100%)	0	100	100
45	NP	5/116 (4%)	5 (100%)	0	100	100
46	NQ	4/71 (6%)	4 (100%)	0	100	100
47	NS	45/1140 (4%)	45 (100%)	0	100	100
50	OH	2/119 (2%)	2 (100%)	0	100	100
51	OU	1/135 (1%)	1 (100%)	0	100	100
52	SA	10/435 (2%)	10 (100%)	0	100	100
53	SB	8/433 (2%)	8 (100%)	0	100	100
54	SC	14/240 (6%)	14 (100%)	0	100	100
54	SD	14/240 (6%)	14 (100%)	0	100	100
55	SE	7/104 (7%)	7 (100%)	0	100	100
55	SF	7/104 (7%)	7 (100%)	0	100	100
56	SG	14/502 (3%)	14 (100%)	0	100	100
57	SH	17/312 (5%)	17 (100%)	0	100	100
58	SI	43/1039 (4%)	43 (100%)	0	100	100
59	SJ	9/222 (4%)	9 (100%)	0	100	100
59	SK	12/222 (5%)	12 (100%)	0	100	100
60	SL	9/169 (5%)	9 (100%)	0	100	100
61	SM	10/258 (4%)	10 (100%)	0	100	100
62	SP	63/2307 (3%)	63 (100%)	0	100	100
63	SQ	5/200 (2%)	5 (100%)	0	100	100
64	SR	5/120 (4%)	5 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	SS	14/807 (2%)	14 (100%)	0	100	100
66	ST	22/732 (3%)	22 (100%)	0	100	100
67	SU	27/506 (5%)	27 (100%)	0	100	100
68	SW	11/238 (5%)	11 (100%)	0	100	100
69	SY	2/234 (1%)	2 (100%)	0	100	100
70	SZ	14/424 (3%)	14 (100%)	0	100	100
All	All	981/30526 (3%)	981 (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%)	17 (28%)	1 (1%)
2	L1	1243/1810 (68%)	228 (18%)	4 (0%)
3	L2	137/333 (41%)	20 (14%)	1 (0%)
All	All	1439/2843 (50%)	265 (18%)	6 (0%)

5 of 265 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	9	G
1	L0	14	U
1	L0	17	A
1	L0	23	G
1	L0	63	G

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L1	1555	A
2	L1	1568	C
3	L2	1	G
2	L1	320	U
1	L0	69	U

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

3 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	$\# Z > 2$
65	SEP	SS	738	65	3,4,10	0.71	0	2,4,14	0.74	0
56	SEP	SG	50	56	3,4,10	0.62	0	2,4,14	0.90	0
27	SEP	LS	128	27	3,4,10	0.69	0	2,4,14	0.77	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
65	SEP	SS	738	65	-	0/1/2/10	-
56	SEP	SG	50	56	-	0/1/2/10	-
27	SEP	LS	128	27	-	1/1/2/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
27	LS	128	SEP	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

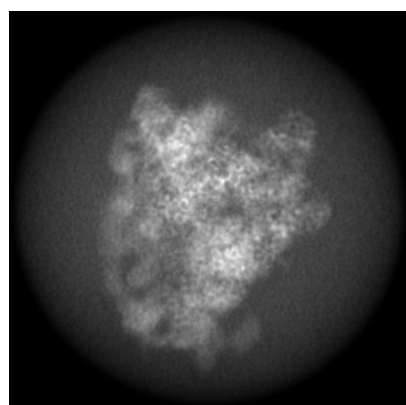
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49083. These allow visual inspection of the internal detail of the map and identification of artifacts.

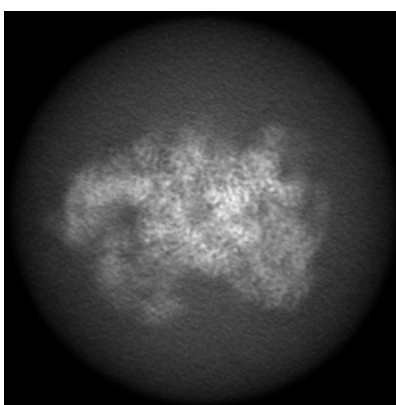
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

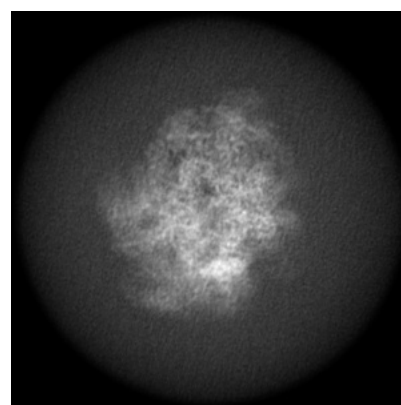
6.1.1 Primary map



X



Y

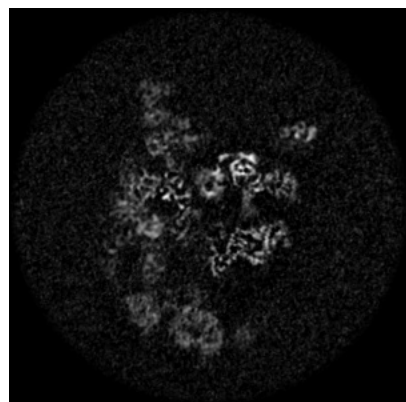


Z

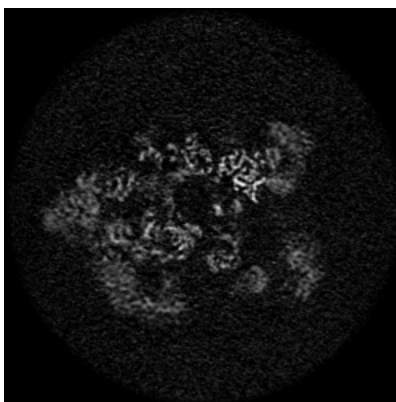
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

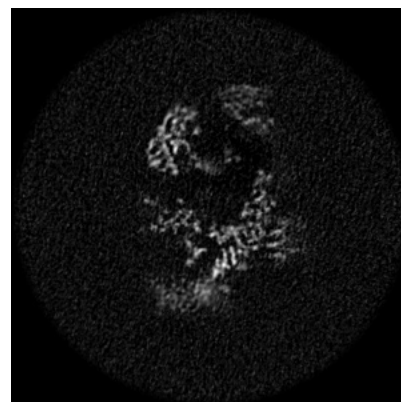
6.2.1 Primary map



X Index: 252



Y Index: 252

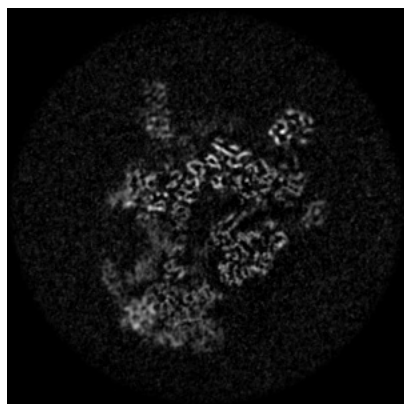


Z Index: 252

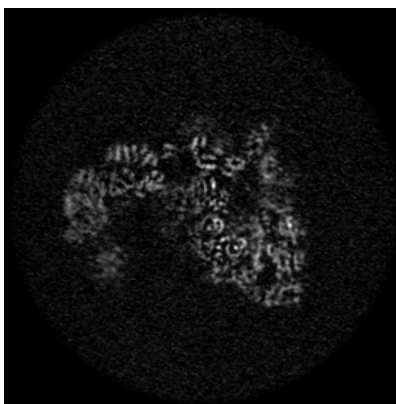
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

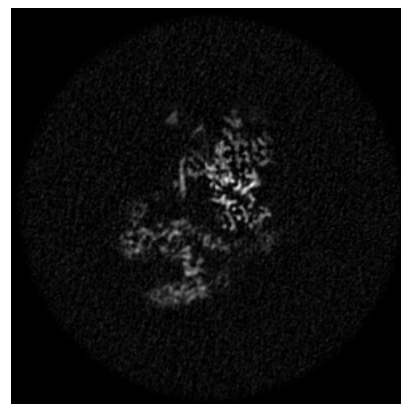
6.3.1 Primary map



X Index: 269



Y Index: 222

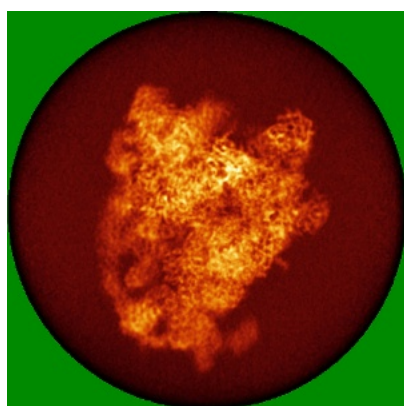


Z Index: 304

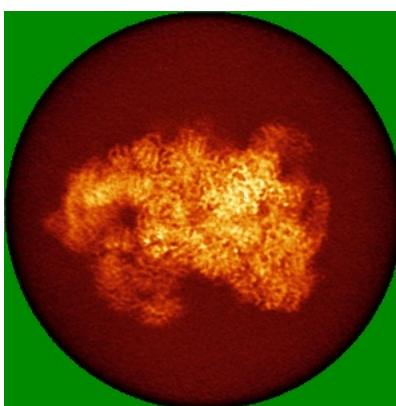
The images above show the largest variance slices of the map in three orthogonal directions.

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

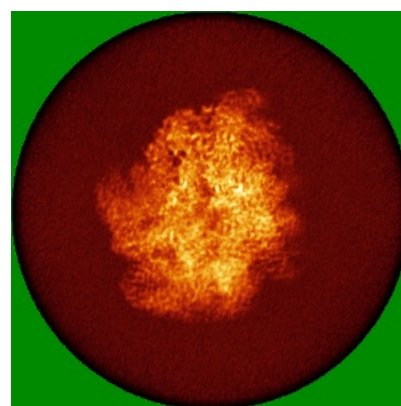
6.4.1 Primary map



X



Y



Z

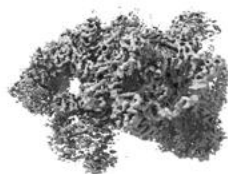
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

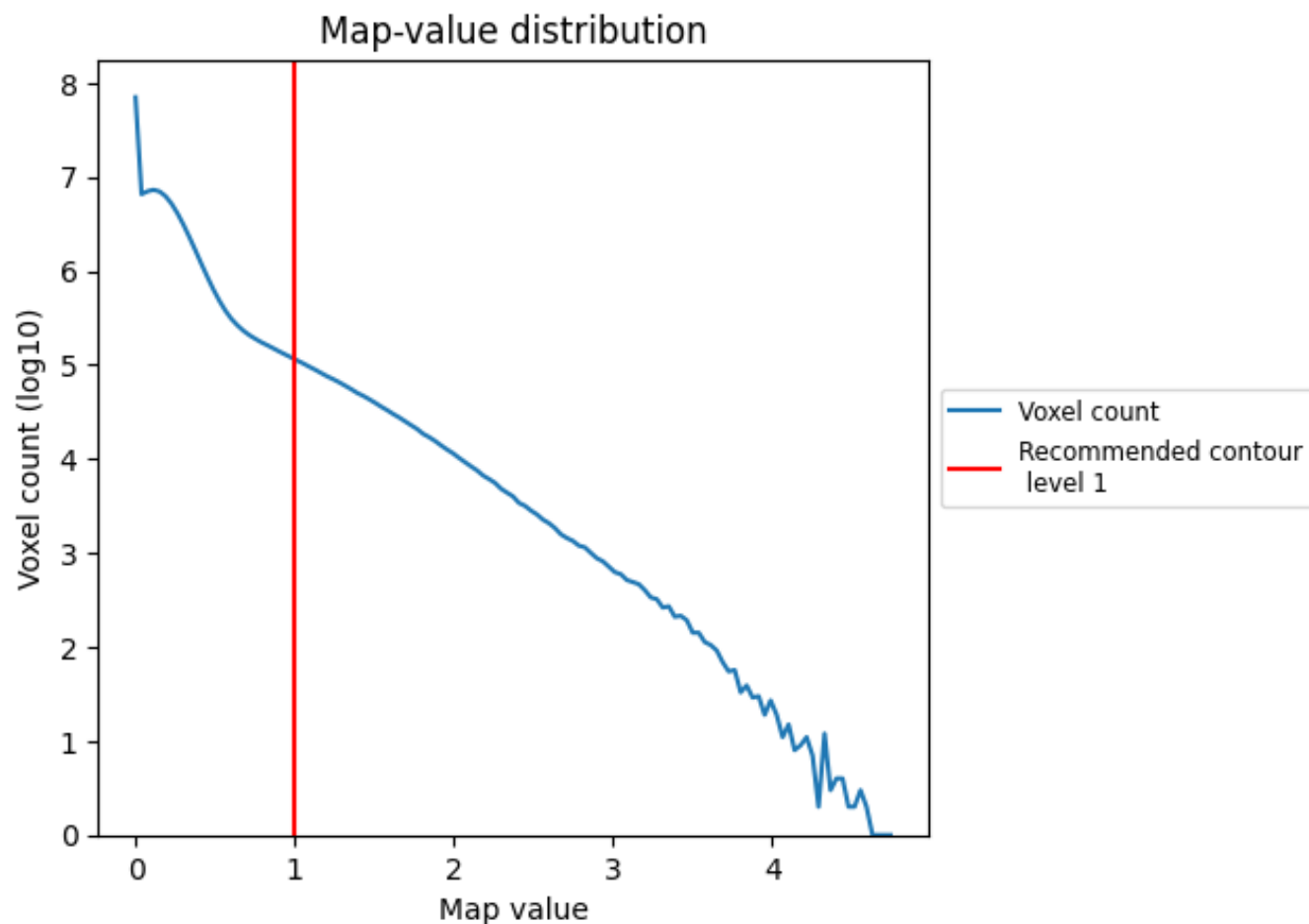
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

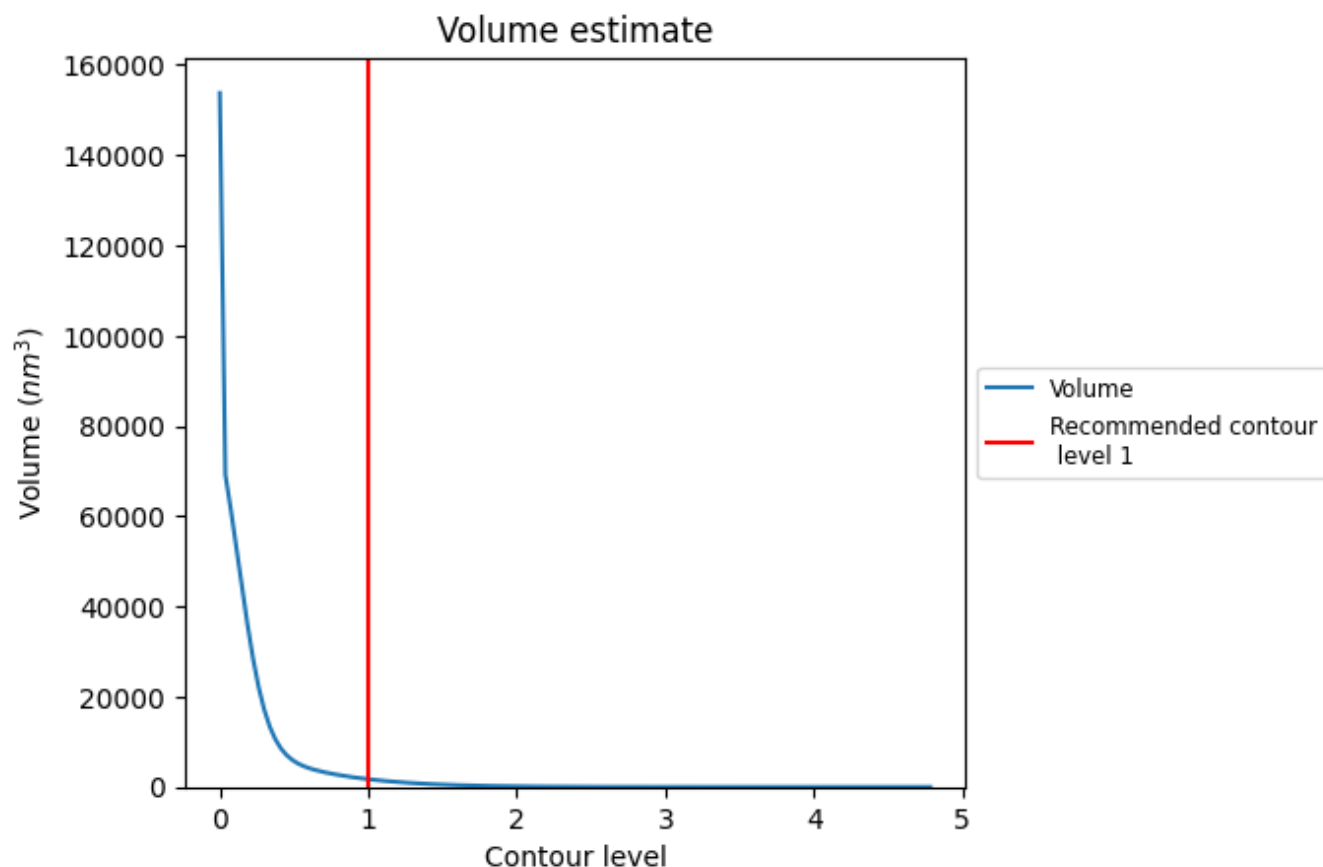
This section contains the results of statistical analysis of the map.

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.

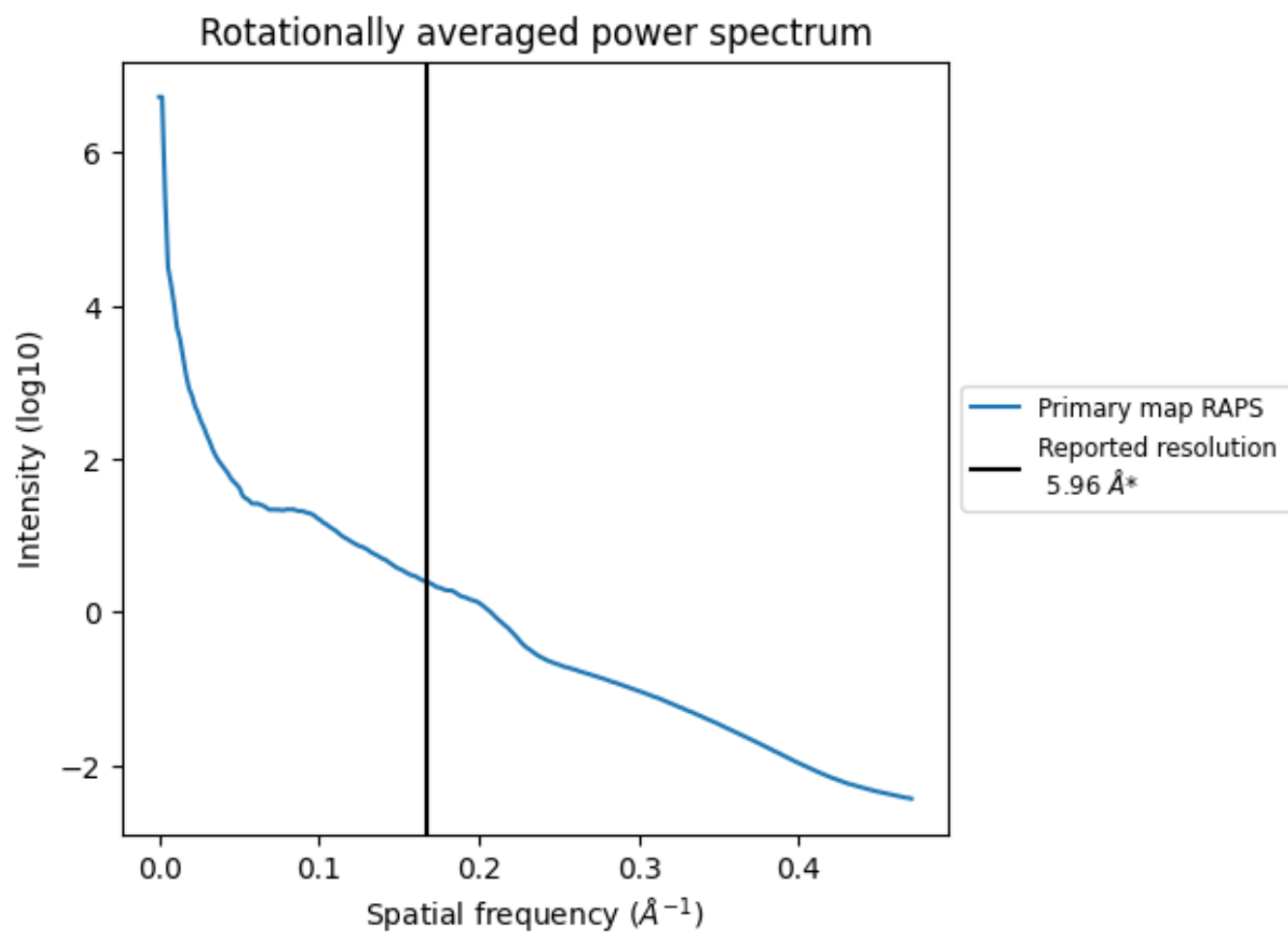
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1717 nm^3 ; this corresponds to an approximate mass of 1551 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 0.168 Å⁻¹

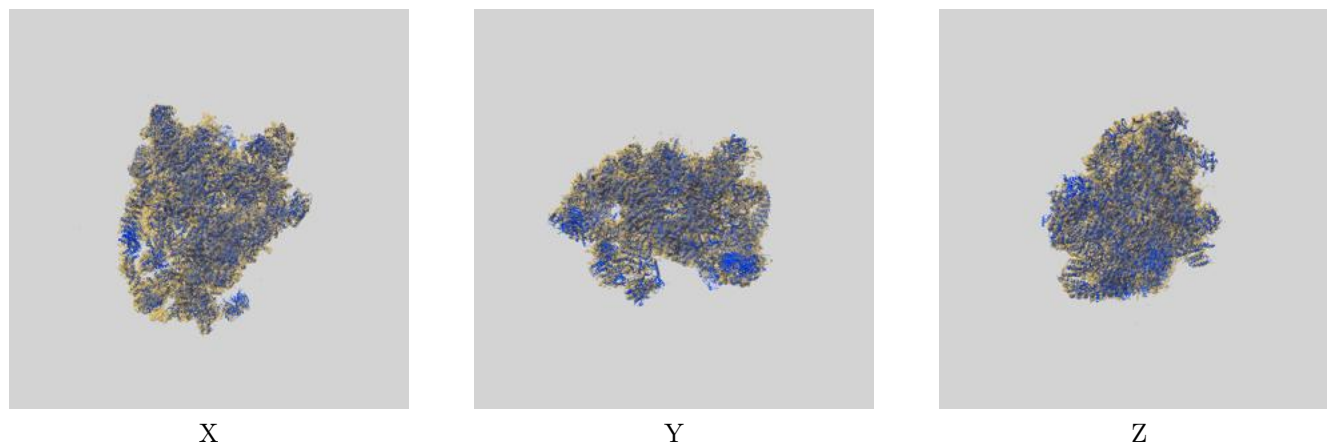
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

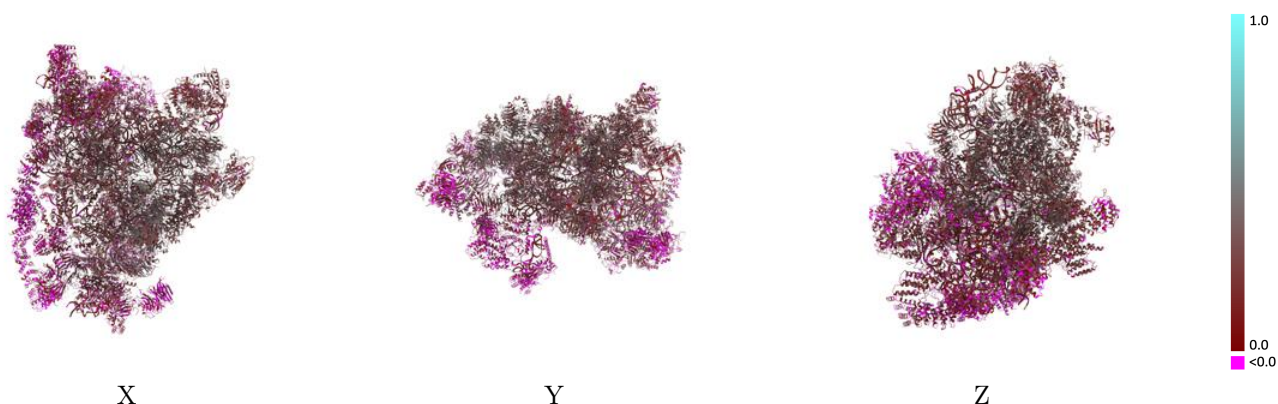
This section contains information regarding the fit between EMDB map EMD-49083 and PDB model 9N73. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 1.0 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](#)

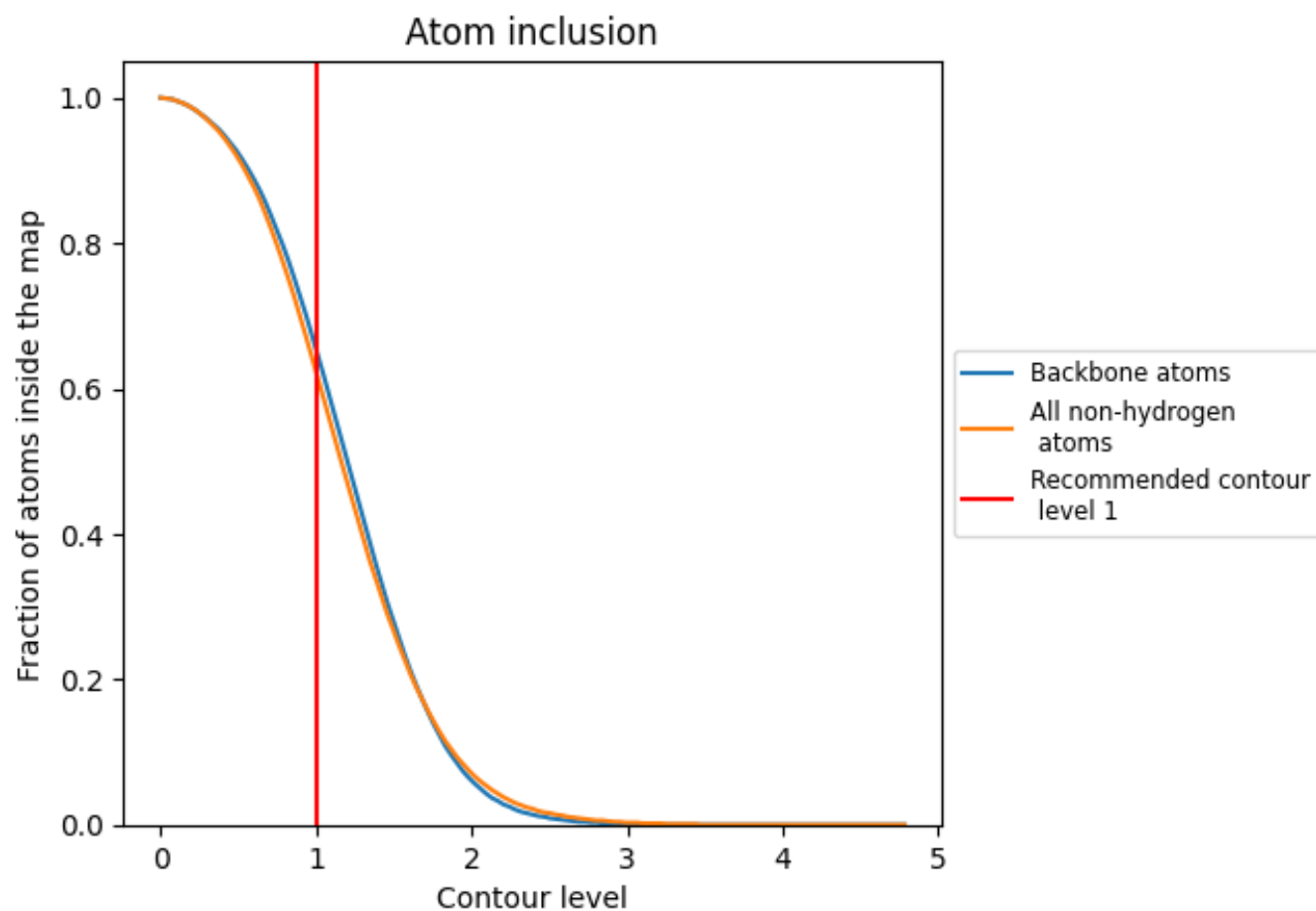


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 62% 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) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6230	 0.2180
L0	 0.5670	 0.1330
L1	 0.7520	 0.2040
L2	 0.7080	 0.1850
L3	 0.4900	 0.2050
L4	 0.7510	 0.2000
L5	 0.8860	 0.3320
L6	 0.7150	 0.1840
L7	 0.7520	 0.2450
L8	 0.6890	 0.1740
L9	 0.7670	 0.2580
LC	 0.8260	 0.3350
LD	 0.6090	 0.1530
LE	 0.8870	 0.3140
LF	 0.8450	 0.2340
LG	 0.8670	 0.3760
LH	 0.5320	 0.2020
LI	 0.1290	 0.0540
LJ	 0.6410	 0.2070
LK	 0.3300	 0.1660
LL	 0.6750	 0.2850
LM	 0.3650	 0.0900
LN	 0.6110	 0.1710
LO	 0.8590	 0.3770
LP	 0.6520	 0.2460
LQ	 0.8730	 0.2880
LR	 0.7970	 0.3290
LS	 0.7810	 0.3450
LT	 0.8660	 0.3590
LU	 0.8940	 0.3320
LV	 0.6520	 0.1720
LW	 0.8330	 0.3660
LX	 0.5210	 0.1760
LY	 0.2610	 0.0770
LZ	 0.6440	 0.2790



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
NA	 0.6240	 0.2480
NB	 0.3300	 0.1320
NC	 0.5850	 0.2320
ND	 0.0370	 0.1550
NF	 0.9040	 0.2930
NG	 0.7940	 0.3670
NH	 0.7220	 0.2770
NI	 0.4840	 0.2510
NL	 0.7780	 0.3300
NM	 0.8040	 0.3560
NN	 0.5720	 0.1700
NP	 0.4640	 0.2650
NQ	 0.8790	 0.2940
NS	 0.5570	 0.2790
NV	 0.0000	 -0.1640
OA	 0.0000	 0.0600
OH	 0.0180	 -0.0470
OU	 0.0000	 -0.0180
SA	 0.7750	 0.2810
SB	 0.6660	 0.2320
SC	 0.7520	 0.3030
SD	 0.2070	 0.0690
SE	 0.7040	 0.2590
SF	 0.8420	 0.2790
SG	 0.7900	 0.2400
SH	 0.6450	 0.2660
SI	 0.6820	 0.2860
SJ	 0.2720	 0.0980
SK	 0.3840	 0.1110
SL	 0.8630	 0.3200
SM	 0.7000	 0.3150
SP	 0.5010	 0.1450
SQ	 0.3350	 0.2640
SR	 0.7120	 0.2860
SS	 0.6600	 0.3130
ST	 0.2300	 0.0910
SU	 0.1910	 0.0770
SW	 0.7460	 0.3600
SY	 0.2900	 0.1990
SZ	 0.2040	 0.0580