



wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 06:34 PM JST

PDB ID : 7D63
EMDB ID : EMD-30588
Title : Cryo-EM structure of 90S preribosome with inactive Utp24 (state C)
Authors : Du, Y.; Zhang, J.; An, W.; Ye, K.
Deposited on : 2020-09-29
Resolution : 12.30 Å (reported)
Based on initial model : 6LQR

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:

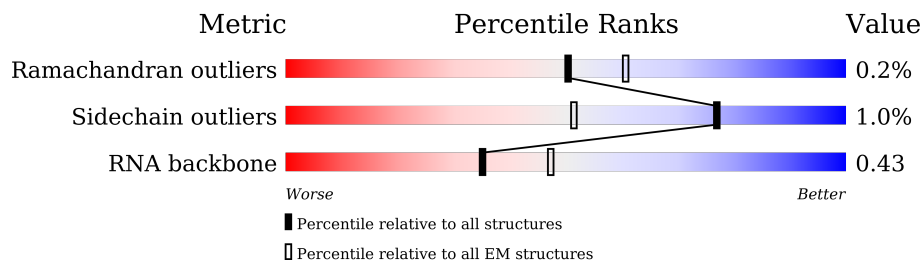
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 12.30 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	3A	333	
2	5A	700	
3	SA	1812	
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	

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Mol	Chain	Length	Quality of chain
9	SJ	200	28% 81% 17%
10	SK	197	30% 86% 13%
11	SM	155	28% 77% 21%
12	SO	151	72% 87% 11%
13	SP	137	68% 84% 14%
14	SR	143	26% 87% 13%
15	SX	130	83% 96%
16	SY	145	26% 70% 29%
17	SZ	135	27% 74% 24%
18	Sc	82	83% 96%
19	Sd	67	24% 94% 6%
20	3B	327	30% 73% 27%
20	3C	327	28% 68% 31%
21	3D	504	18% 72% 27%
22	3E	511	35% 83% 16%
23	3F	573	18% 78% 21%
24	3G	126	16% 93%
24	3H	126	32% 94%
25	A4	776	19% 84% 15%
26	A5	643	25% 79% 20%
27	A8	713	32% 71% 25%
28	A9	575	6% 22% 78%
29	AE	1769	62% 86% 13%
30	AF	513	26% 95%
31	AG	896	21% 91% 8%

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Mol	Chain	Length	Quality of chain
32	B1	900	26% 87% 12%
33	B2	943	19% 86% 13%
34	B3	817	38% 89% 7%
35	B8	594	26% 80% 20%
36	BE	939	19% 86% 13%
37	B6	440	43% 84% 15%
38	5B	214	24% 27% 72%
39	5C	554	32% 81% 17%
40	5D	250	40% 65% 33%
41	5E	593	13% 30% 67%
42	5F	183	43% 98% ..
43	5G	290	31% 73% 24%
44	5H	610	12% 88%
45	5I	489	27% 93% 6%
46	5J	217	33% 62% 38%
47	5K	189	50% 92% 7%
48	RA	707	27% 47% 52%
49	RB	357	23% 36% 62%
50	RE	1237	83% 86% 13%
51	RF	297	78% 79% 19%
52	RG	252	25% 84% 14%
52	RH	252	41% 90% 9%
53	RJ	1183	20% 66% 33%
54	RK	367	24% 96% ..
55	RL	1056	60% 76% 24%

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Mol	Chain	Length	Quality of chain
55	RM	1056	
56	RN	810	
57	RO	552	
58	RP	2493	
59	RQ	899	
60	RS	480	
61	RY	534	
62	X1	611	
63	RT	326	
64	ST	146	
65	SU	144	
66	RD	1729	
67	RZ	1267	

2 Entry composition

There are 71 unique types of molecules in this entry. The entry contains 225233 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 U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	3A	175	3711	1661	648	1227	175	0	0

- Molecule 2 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	5A	192	4117	1838	746	1341	192	0	0

- Molecule 3 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	SA	1331	28383	12684	5049	9319	1331	0	0

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SC	230	1830	1156	335	335	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SF	229	1815	1161	331	320	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SG	213	1669	1045	307	314	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	SH	167	1327	834	256	235	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	SI	165	1321	853	226	242		0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	SJ	166	1324	824	262	236	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	SK	171	1388	879	268	240	1	0	0

- Molecule 11 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	SM	123	997	641	189	164	3	0	0

- Molecule 12 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	SO	134	1087	698	202	186	1	0	0

- Molecule 13 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	SP	118	868	536	164	165	3	0	0

- Molecule 14 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	SR	125	Total	C	N	O	0	0
			973	625	174	174		

- Molecule 15 is a protein called 40S ribosomal protein S22-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SX	127	Total	C	N	O	S	0	0
			1003	640	183	177	3		

- Molecule 16 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SY	103	Total	C	N	O	S	0	0
			786	503	144	137	2		

- Molecule 17 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	SZ	102	Total	C	N	O	0	0
			809	517	148	144		

- Molecule 18 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Sc	80	Total	C	N	O	S	0	0
			603	377	109	112	5		

- Molecule 19 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Sd	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 20 is a protein called rRNA 2'-O-methyltransferase fibrillar.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
20	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 21 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	3D	369	2848	1811	489	540	8	0	0

- Molecule 22 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	3E	431	3028	1888	543	588	9	0	0

- Molecule 23 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	3F	454	3643	2315	638	680	10	0	0

- Molecule 24 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	3G	121	916	583	158	171	4	0	0
24	3H	121	916	583	158	171	4	0	0

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	A4	662	5226	3309	910	986	21	0	0

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	A5	514	3976	2520	688	755	13	0	0

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	A8	532	3229	2008	592	626	3	0	0

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	A9	128	939	594	173	170	2	0	0

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	AE	1534	9955	6242	1771	1923	19	0	0

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	AF	493	3911	2462	702	735	12	0	0

- Molecule 31 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	AG	826	6570	4181	1111	1259	19	0	0

- Molecule 32 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	B1	793	6331	4046	1085	1182	18	0	0

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	B2	825	6502	4156	1096	1223	27	0	0

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	B3	757	5919	3769	993	1130	27	0	0

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	B8	477	3764	2387	662	705	10	0	0

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	BE	820	6450	4090	1114	1225	21	0	0

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	B6	374	2800	1782	501	505	12	0	0

- Molecule 38 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
38	5B	60	495	310	101	84	0	0

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	5C	458	3612	2276	636	689	11	0	0

- Molecule 40 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	5D	167	1396	862	266	263	5	0	0

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	5E	193	1564	970	280	310	4	0	0

- Molecule 42 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 43 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5G	219	Total	C	N	O	S	0	0
			1756	1107	325	318	6		

- Molecule 44 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	5H	74	Total	C	N	O	0	0
			596	373	122	101		

- Molecule 45 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 46 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5J	134	Total	C	N	O	S	0	0
			1131	715	206	207	3		

- Molecule 47 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 48 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	RA	338	Total	C	N	O	S	0	0
			2709	1713	463	524	9		

- Molecule 49 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	RB	134	Total	C	N	O	S	0	0
			1108	664	227	214	3		

- Molecule 50 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RE	1079	Total	C	N	O	S	0	0
			8716	5666	1437	1589	24		

- Molecule 51 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RF	241	Total	C	N	O	S	0	0
			1963	1253	335	367	8		

- Molecule 52 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RG	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
52	RH	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 53 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RJ	796	Total	C	N	O	S	0	0
			6379	4086	1136	1128	29		

- Molecule 54 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RK	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 55 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RL	805	Total	C	N	O	S	0	0
			4539	2760	885	887	7		
55	RM	766	Total	C	N	O		0	0
			3779	2247	766	766			

- Molecule 56 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	RN	607	4529	2861	820	837	11	0	0

- Molecule 57 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	RO	525	3766	2412	646	696	12	0	0

- Molecule 58 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	RP	2108	12171	7483	2291	2381	16	0	0

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	RQ	275	1853	1139	356	356	2	0	0

- Molecule 60 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	RS	251	2051	1340	349	359	3	0	0

- Molecule 61 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
61	RY	37	299	191	48	60	0	0

- Molecule 62 is a protein called Unassigned peptides 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
62	X1	22	110	66	22	22	0	0

- Molecule 63 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	RT	212	1587	1010	290	283	4	0	0

- Molecule 64 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	ST	110	896	565	170	159	2	0	0

- Molecule 65 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	SU	143	1112	694	208	208	2	0	0

- Molecule 66 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	RD	316	2412	1541	414	452	5	0	0

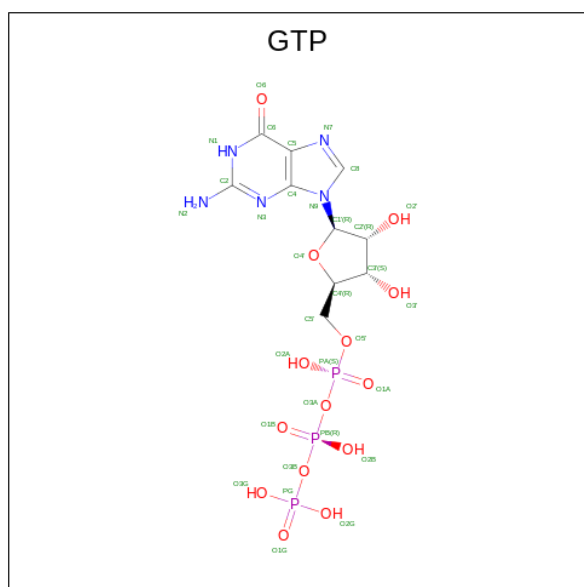
- Molecule 67 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	RZ	839	6604	4215	1146	1208	35	1	0

- Molecule 68 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
68	Sc	1	1	1	0
68	5K	1	1	1	0

- Molecule 69 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

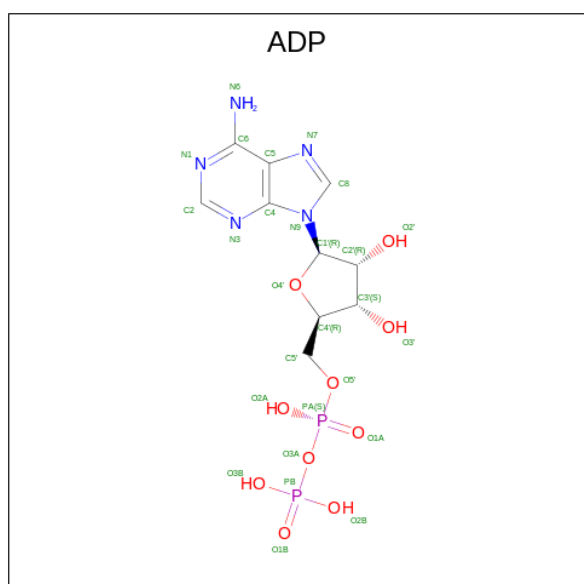


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
69	RJ	1	32	10	5	14	3	0

- Molecule 70 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
70	RJ	1	1	1	0

- Molecule 71 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

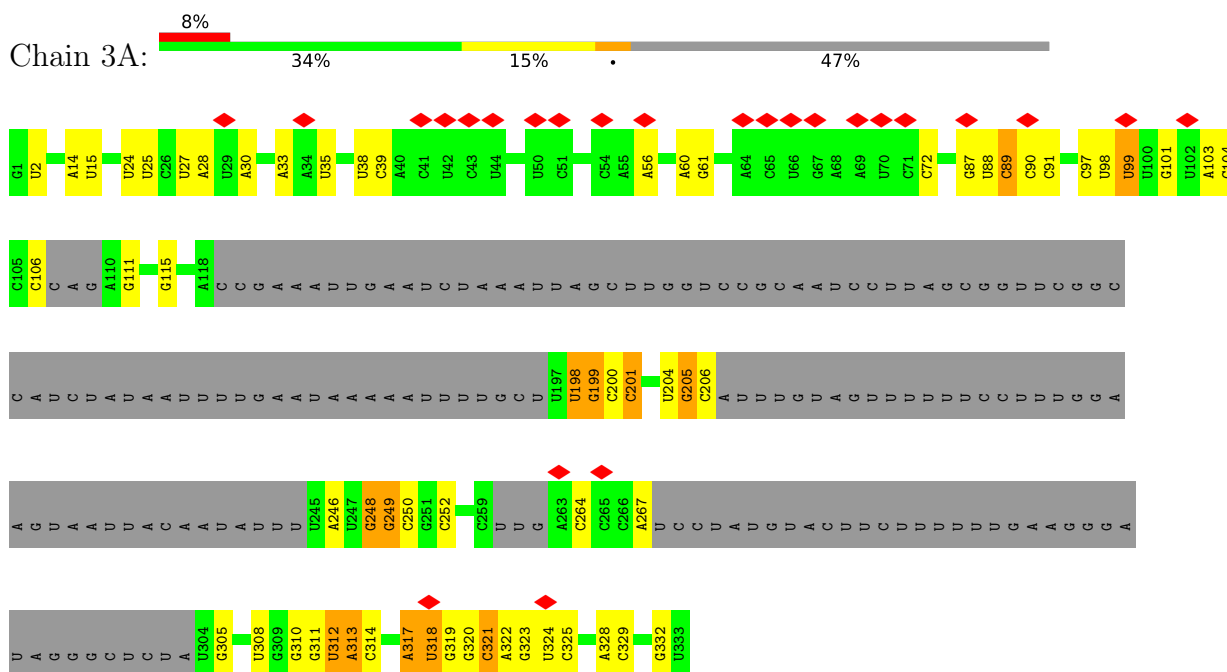


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
71	RZ	1	27	10	5	10	2	0

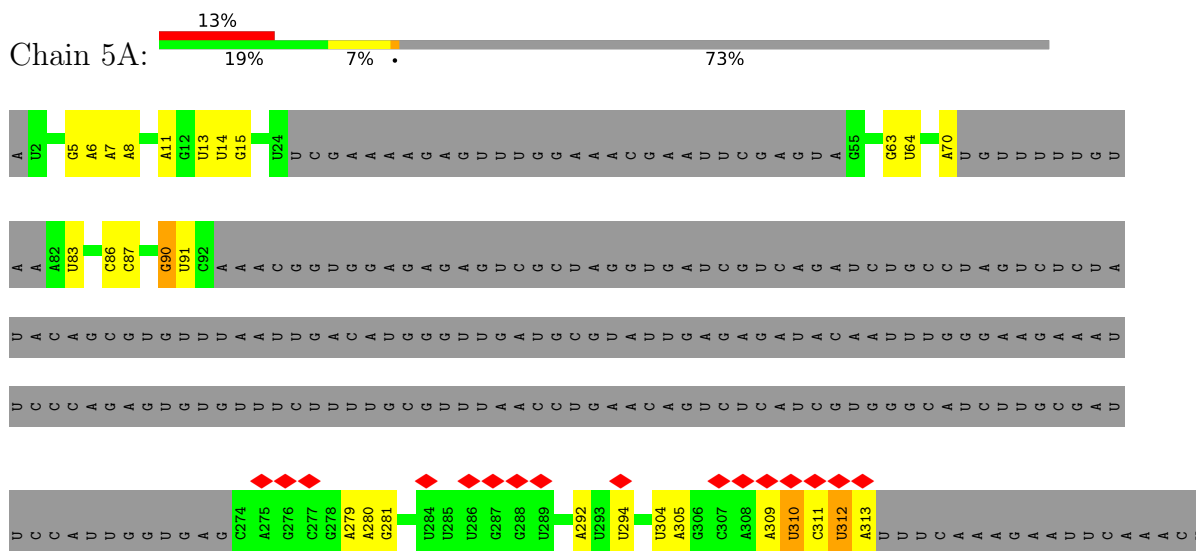
3 Residue-property plots [i](#)

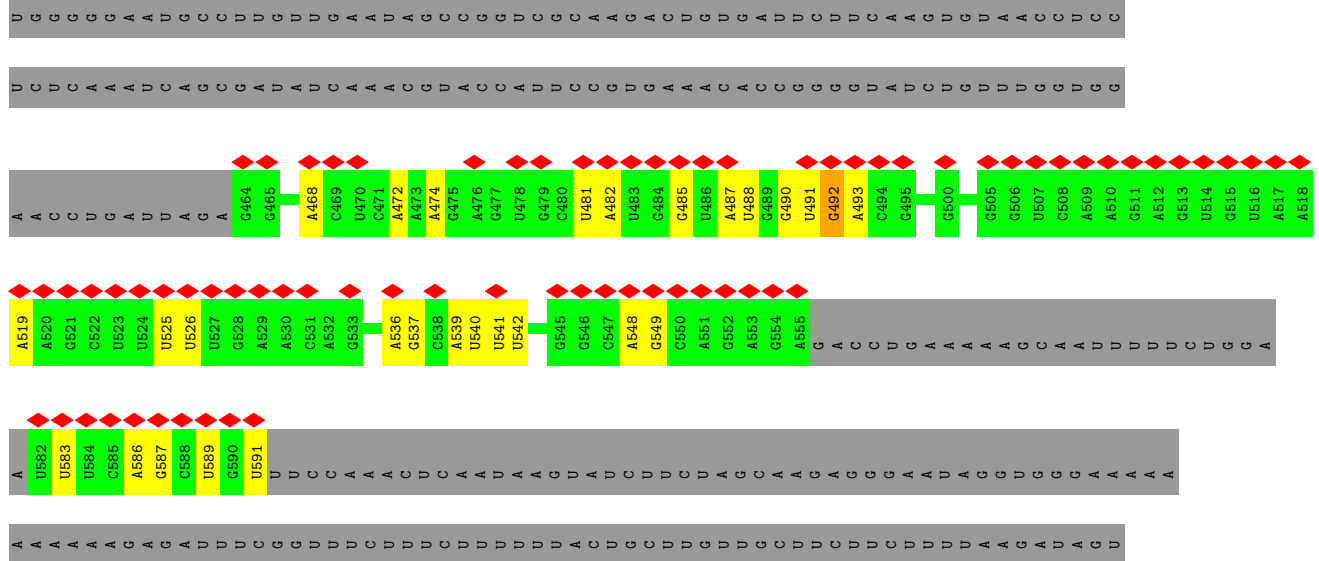
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: U3 snoRNA

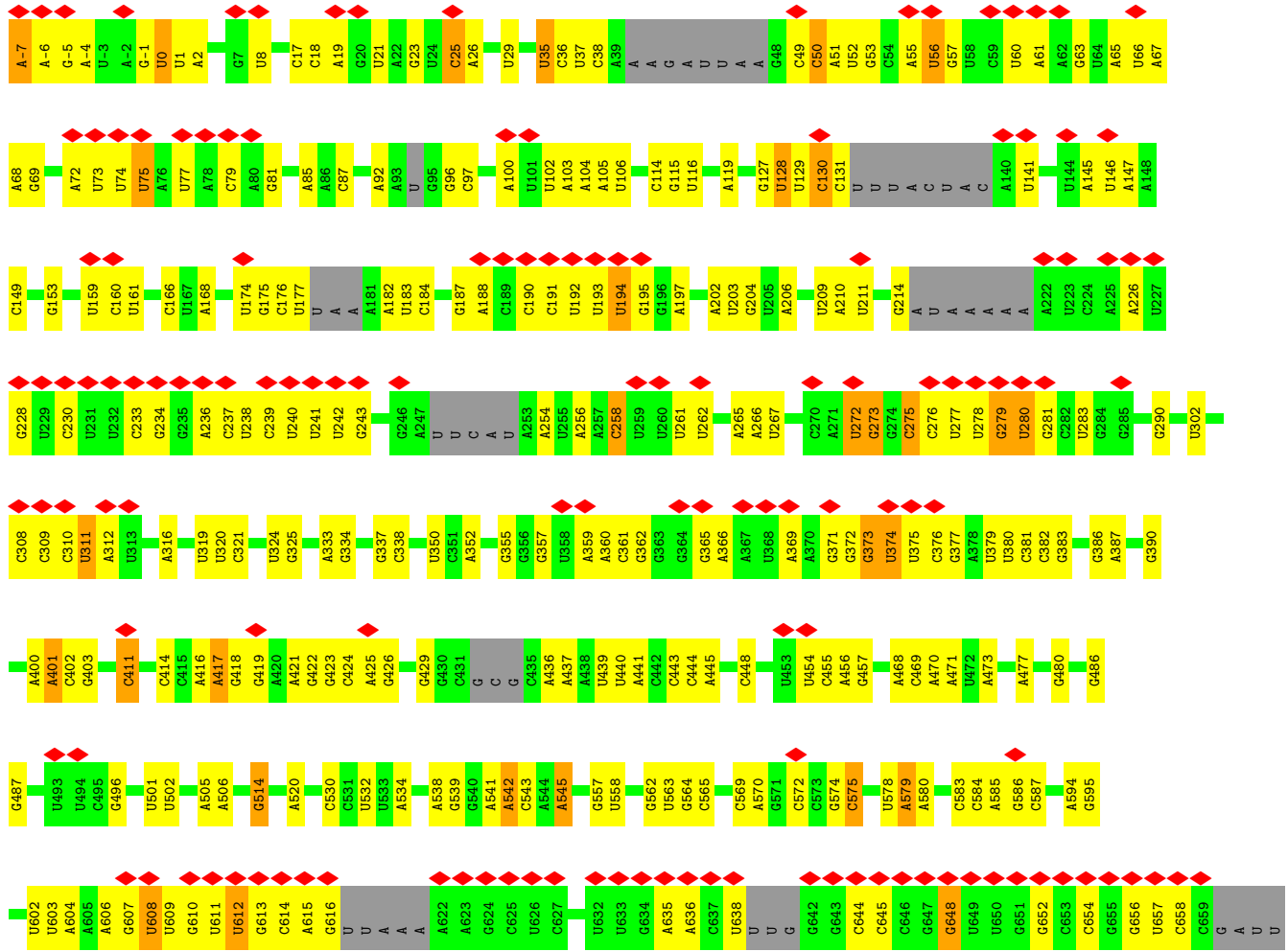


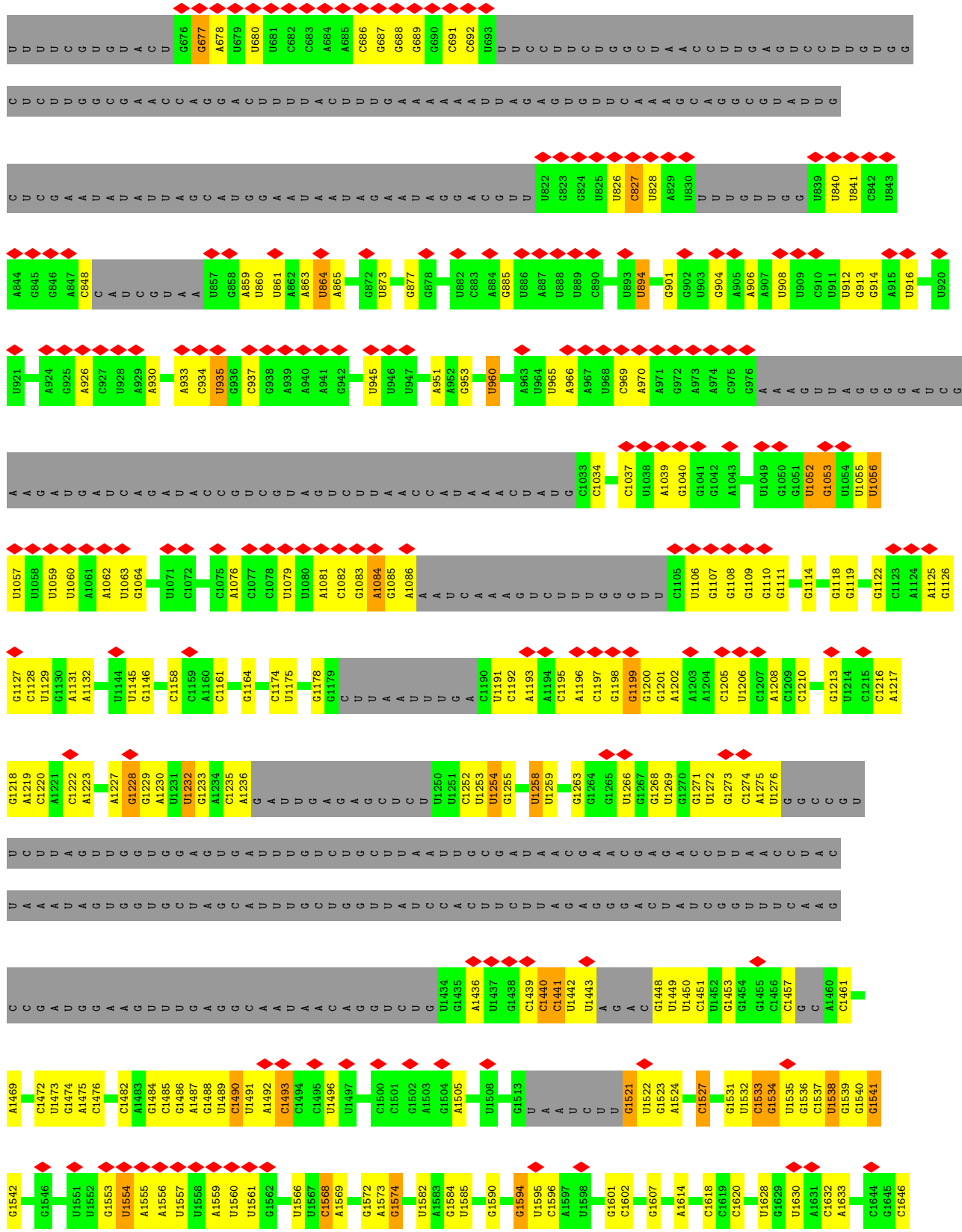
- Molecule 2: 5' ETS

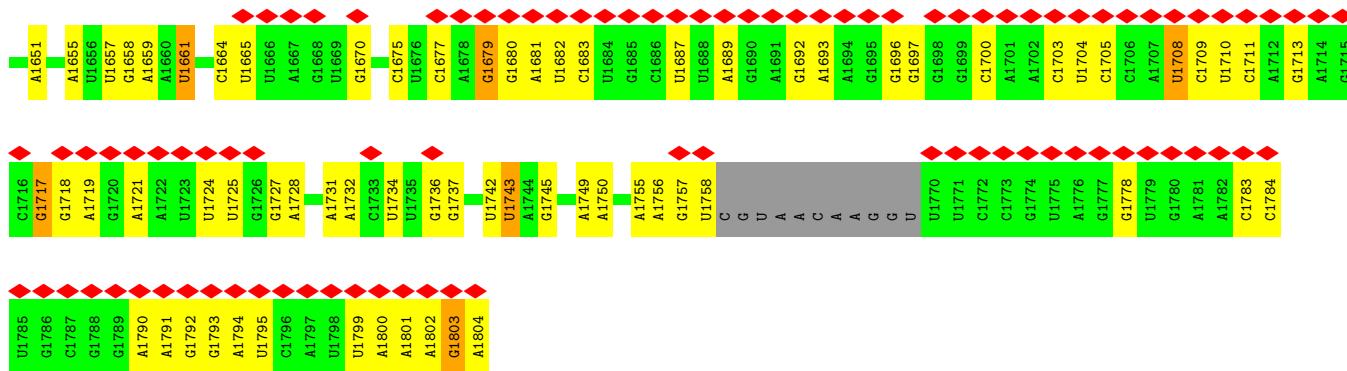




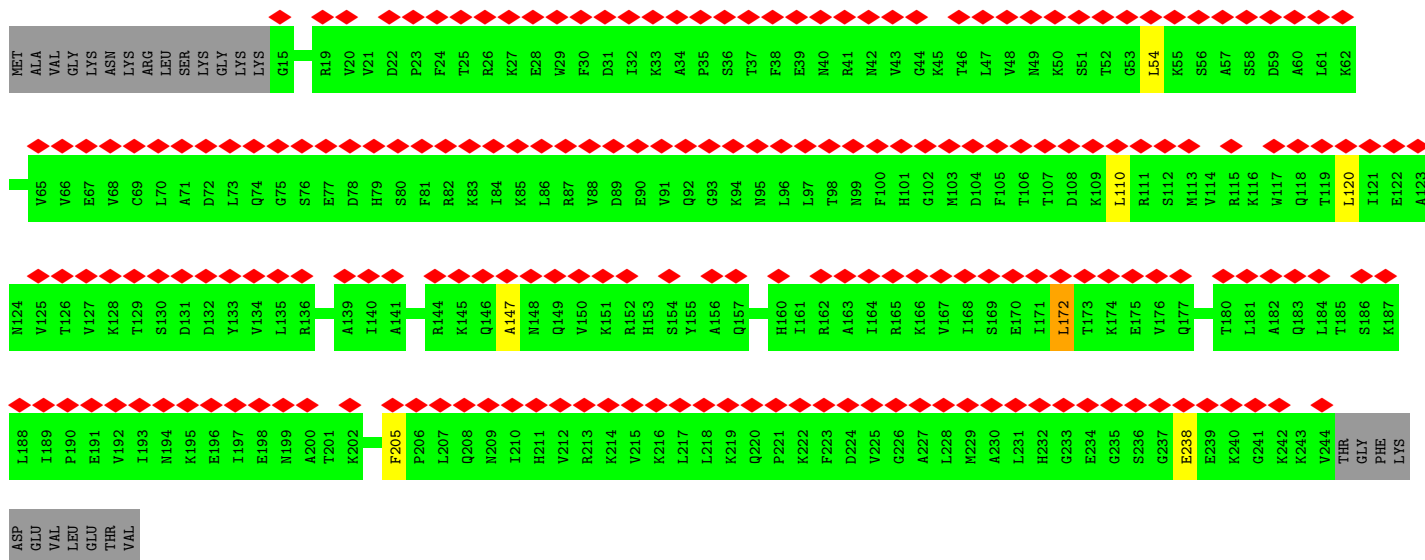
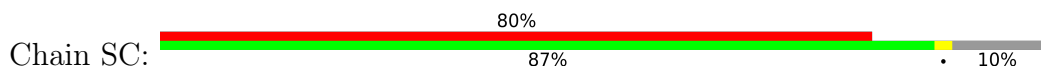
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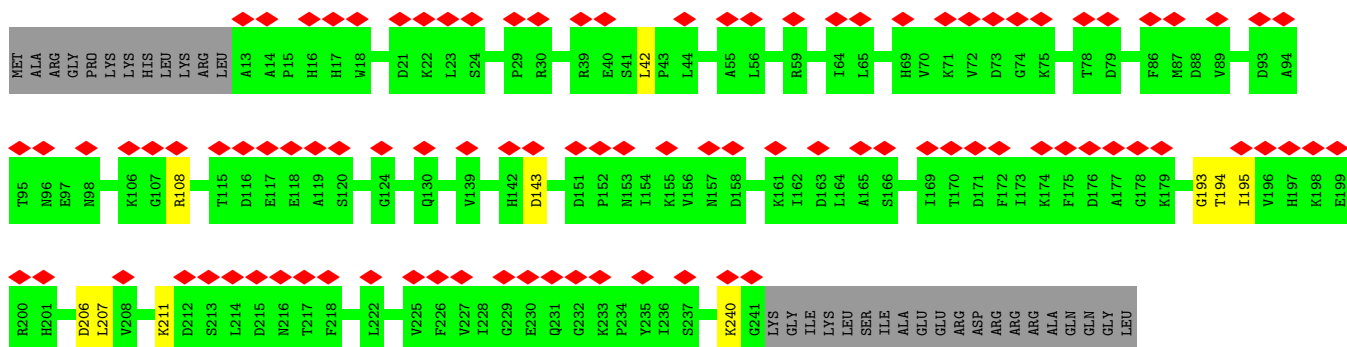
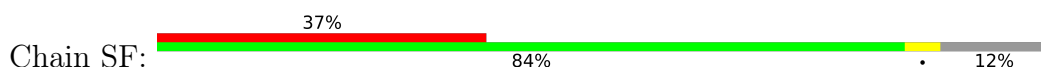




• Molecule 4: 40S ribosomal protein S1-A

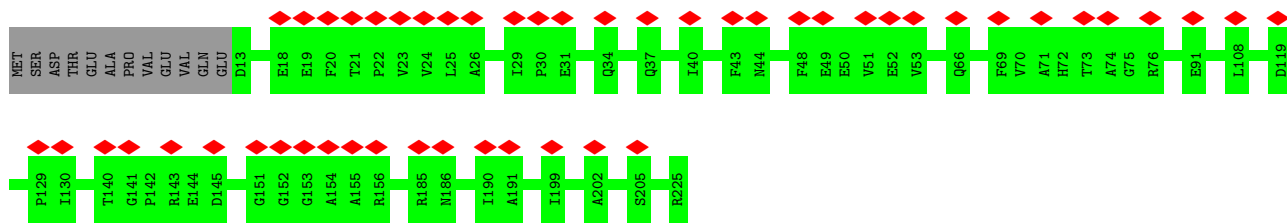


• Molecule 5: 40S ribosomal protein S4-A

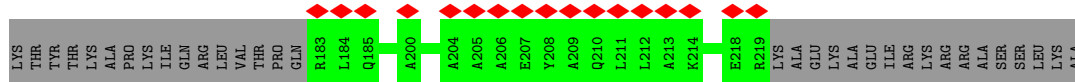
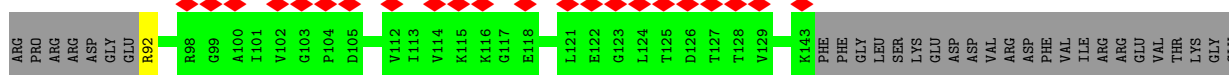
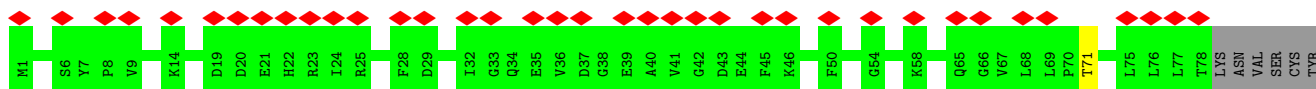


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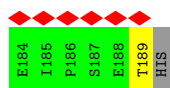
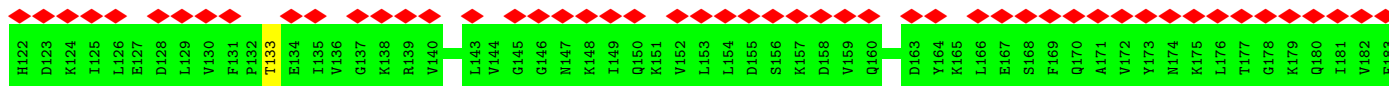
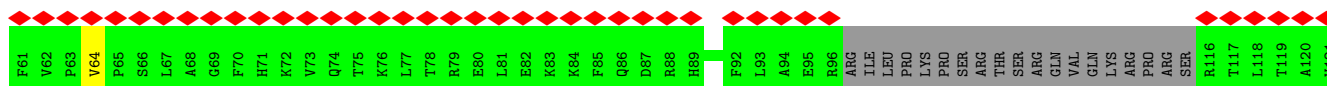
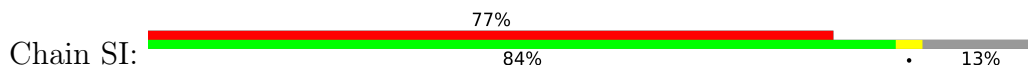




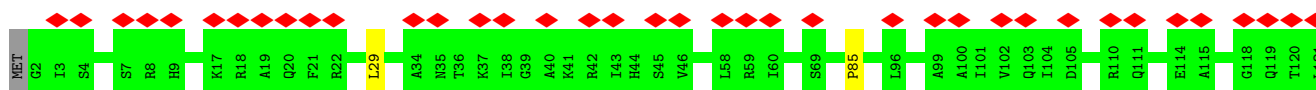
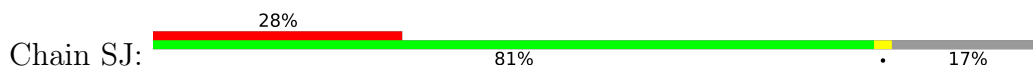
• Molecule 7: 40S ribosomal protein S6-A

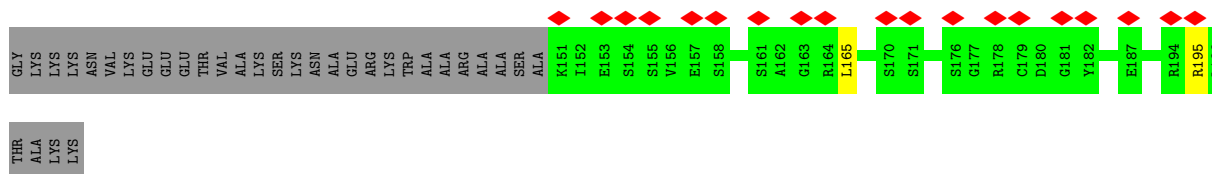


• Molecule 8: 40S ribosomal protein S7-A

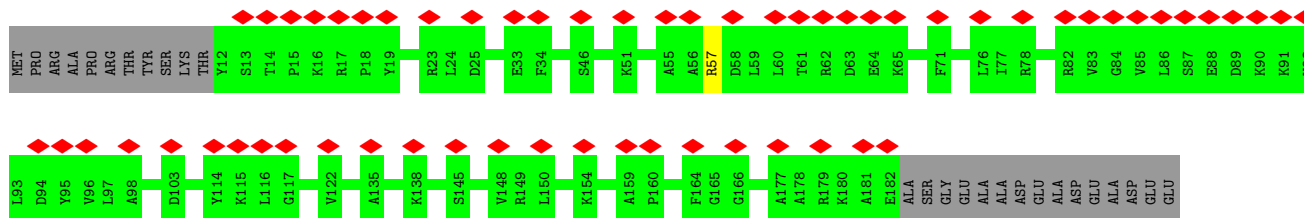
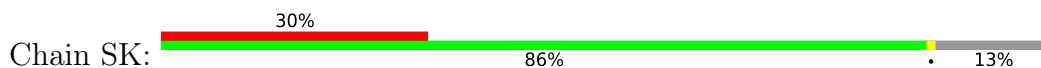


• Molecule 9: 40S ribosomal protein S8-A

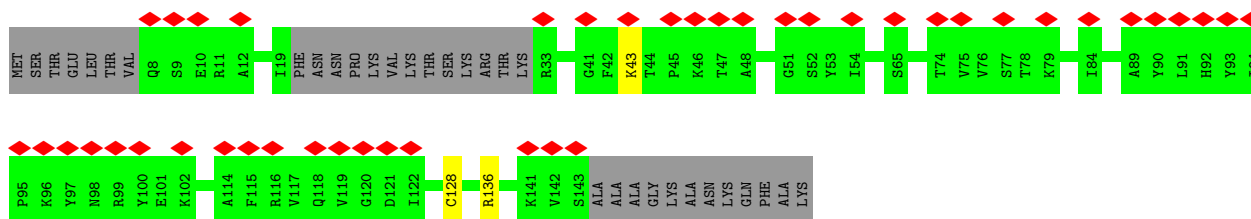
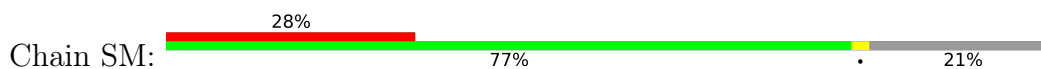




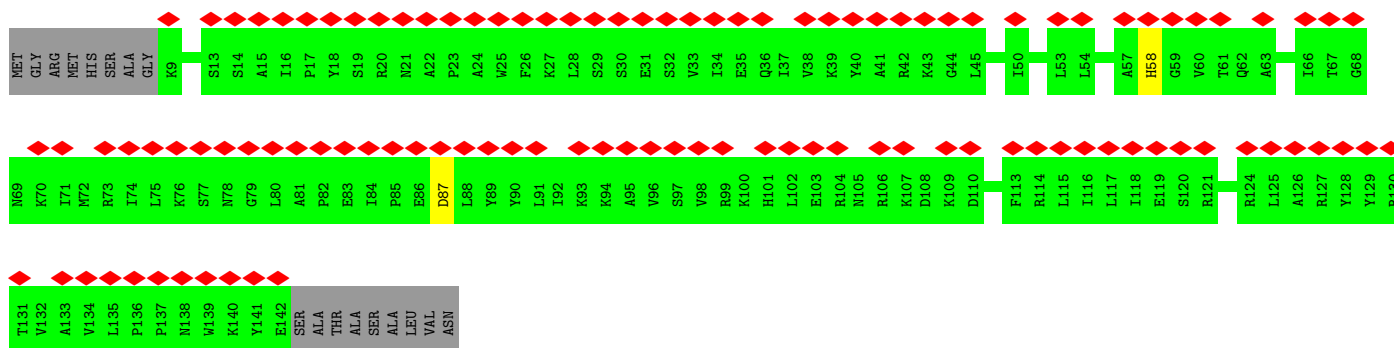
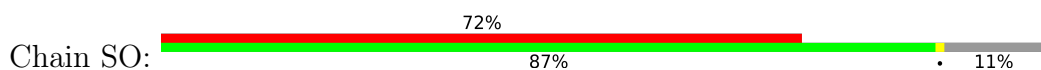
• Molecule 10: 40S ribosomal protein S9-A



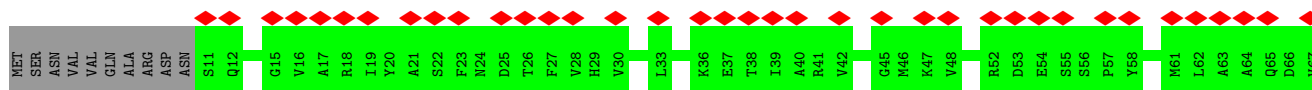
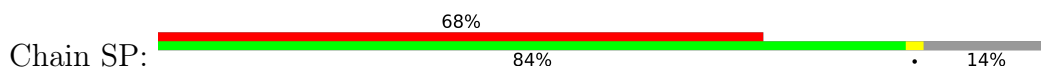
• Molecule 11: 40S ribosomal protein S11-A

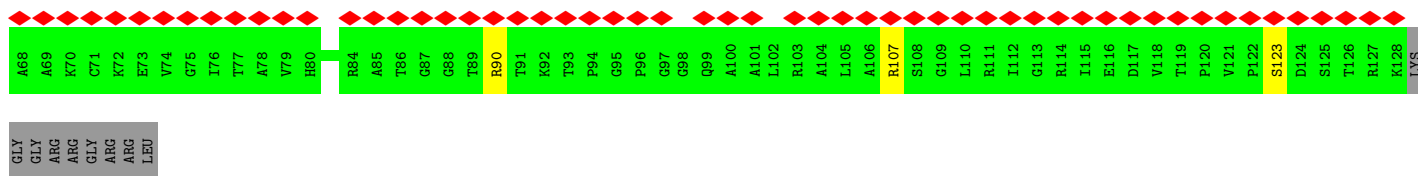


• Molecule 12: 40S ribosomal protein S13

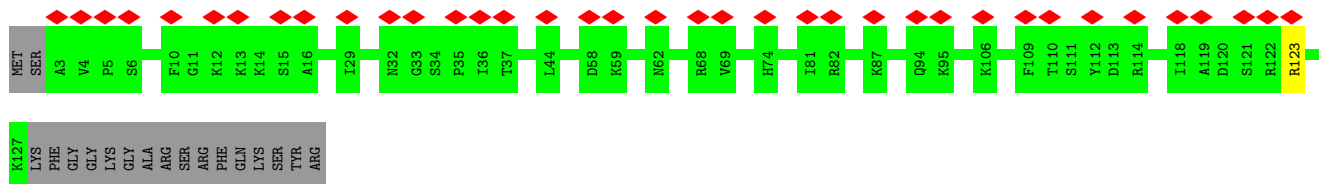
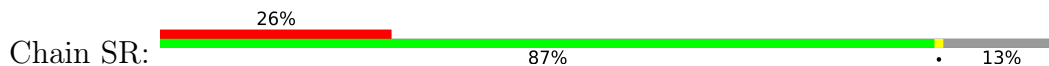


• Molecule 13: 40S ribosomal protein S14-A

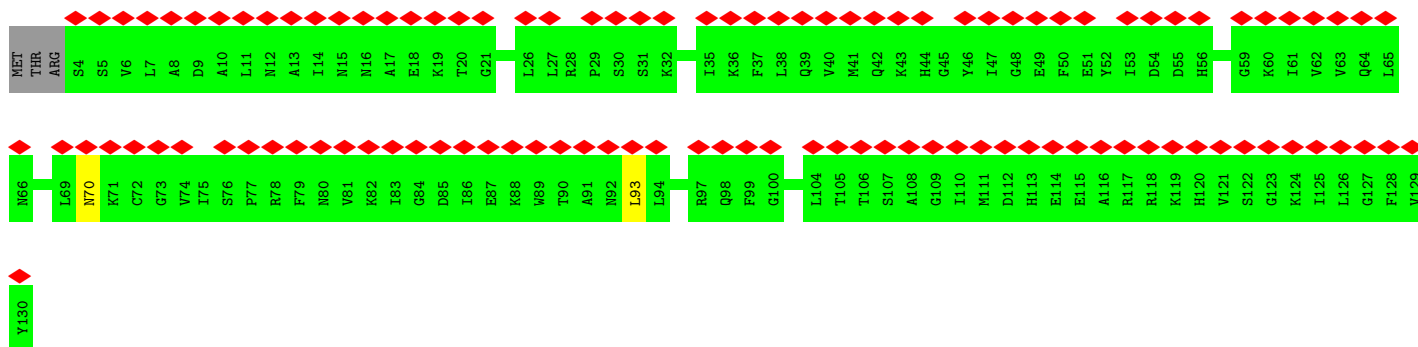
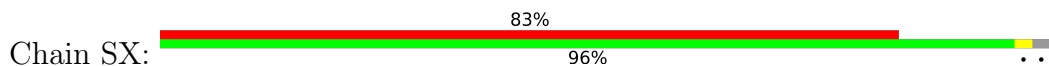




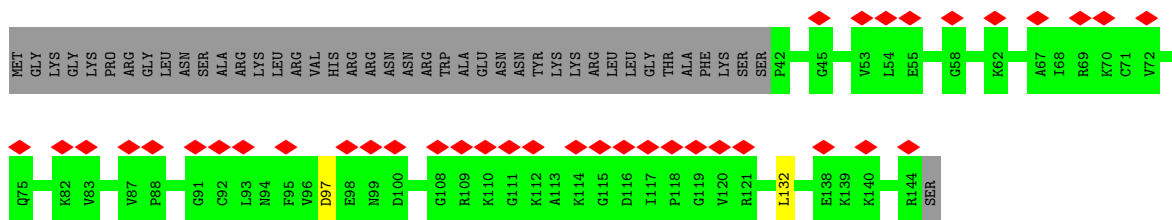
• Molecule 14: 40S ribosomal protein S16-A



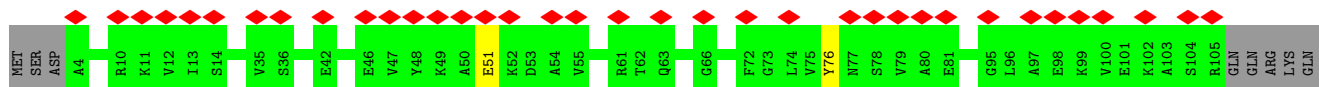
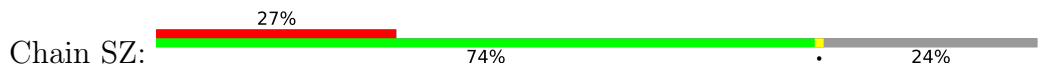
• Molecule 15: 40S ribosomal protein S22-B



• Molecule 16: 40S ribosomal protein S23-A

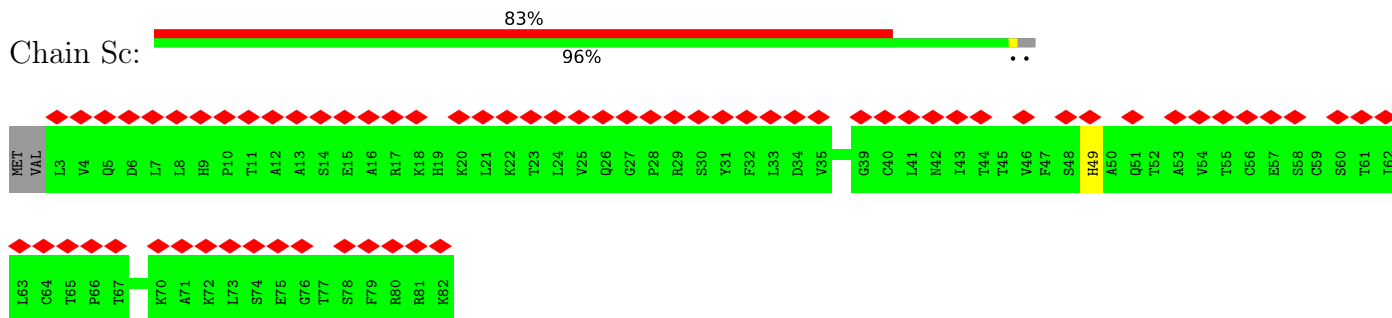


• Molecule 17: 40S ribosomal protein S24-A

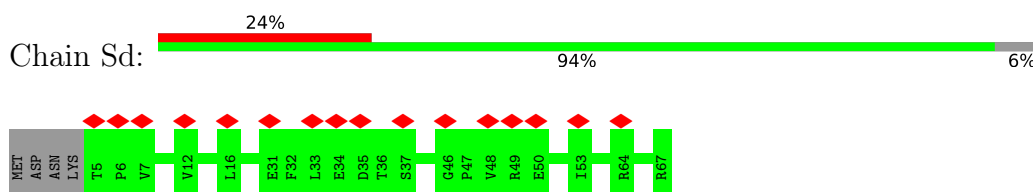


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LYS
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ASN
ARG
ASP
ASP
LYS
LYS
LLE
PHE
THR
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GLY
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ARG
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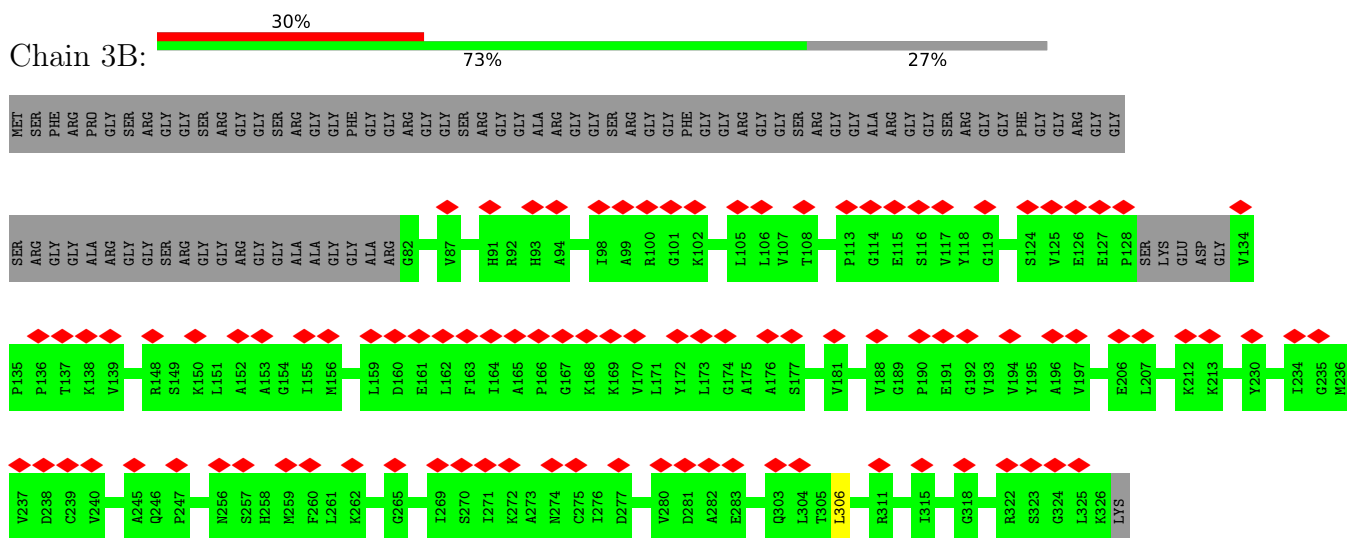
• Molecule 18: 40S ribosomal protein S27-A



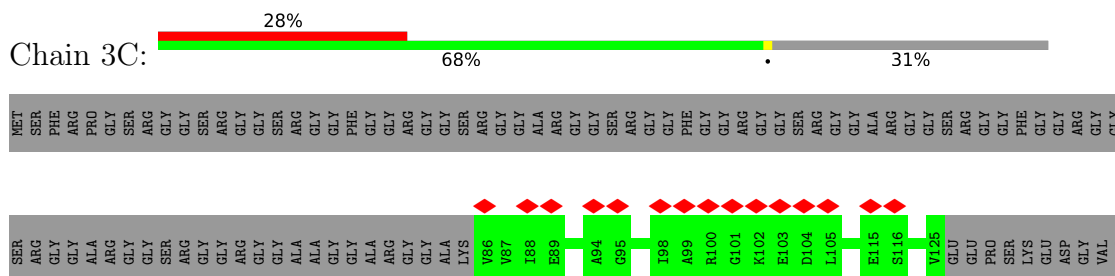
• Molecule 19: 40S ribosomal protein S28-A

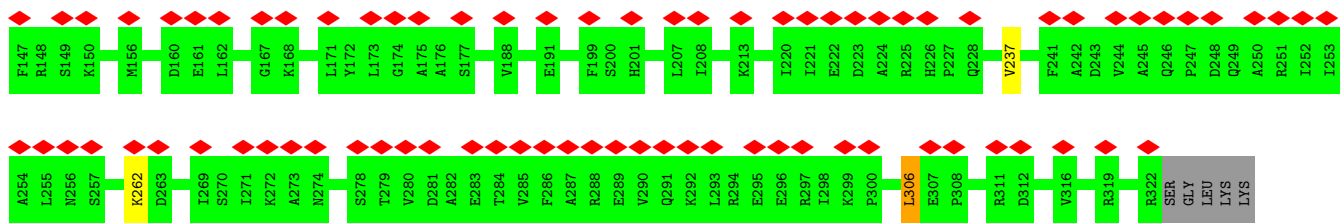


• Molecule 20: rRNA 2'-O-methyltransferase fibrillar

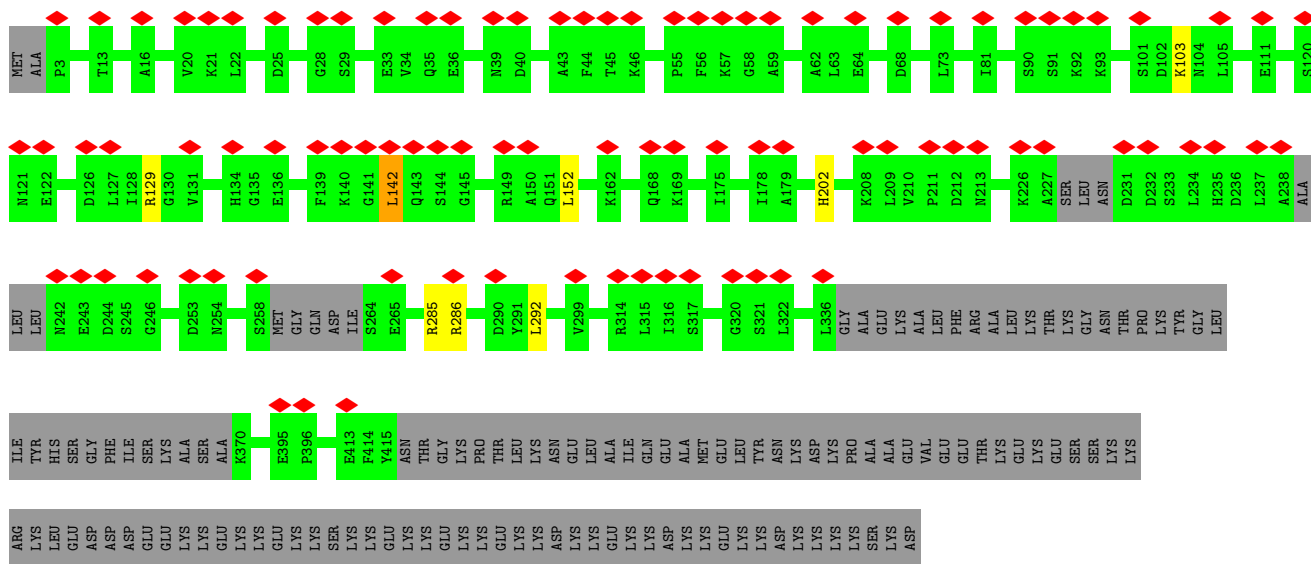
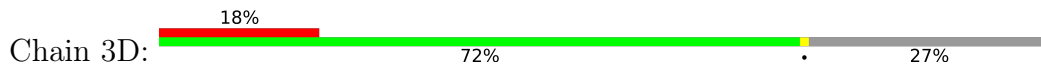


• Molecule 20: rRNA 2'-O-methyltransferase fibrillar

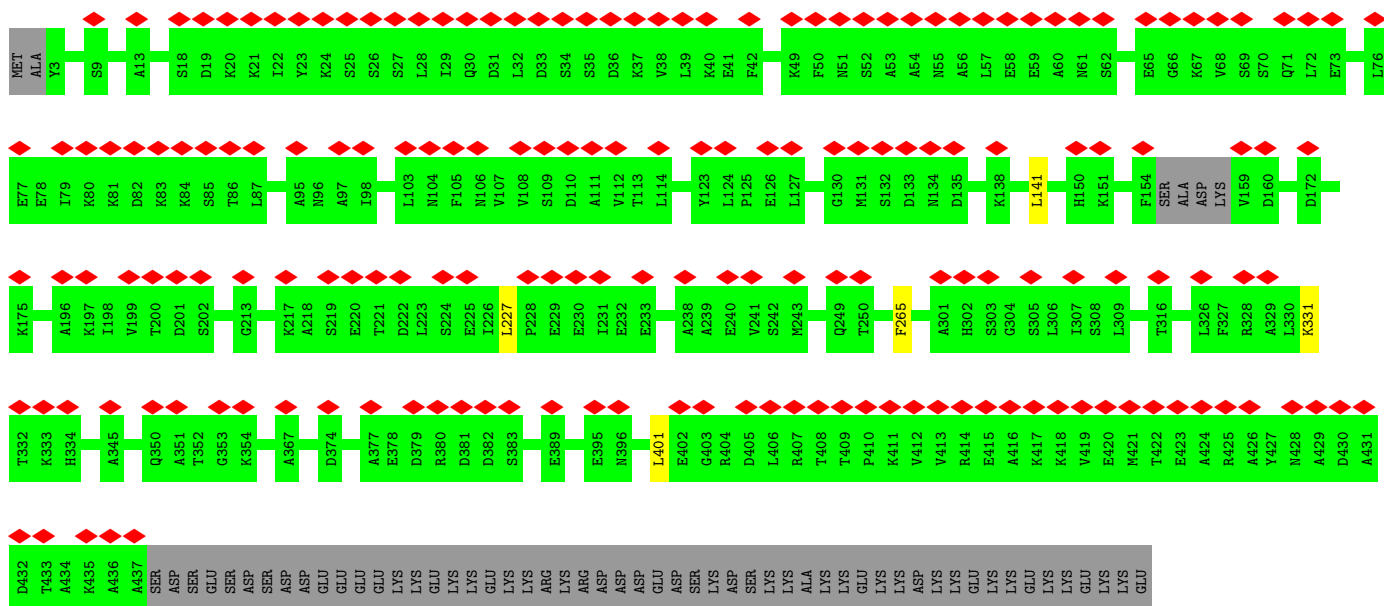
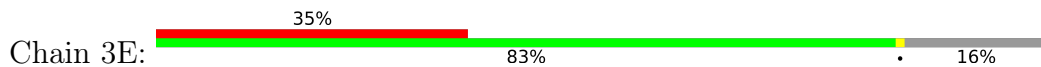




• Molecule 21: Nucleolar protein 56



• Molecule 22: Nucleolar protein 58

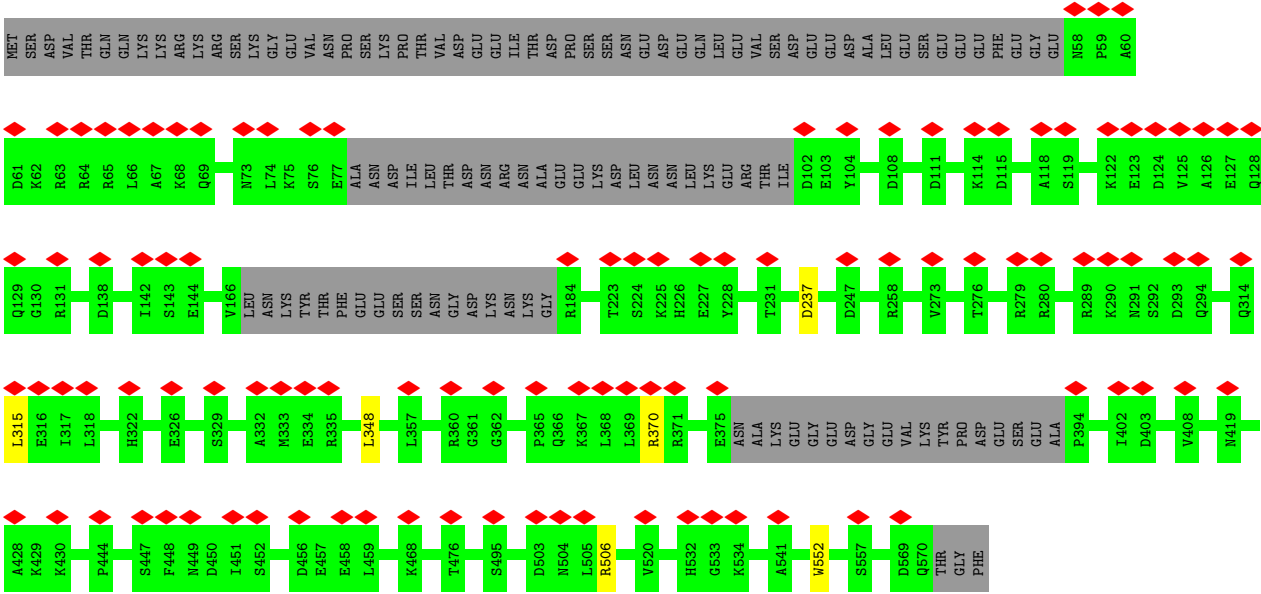
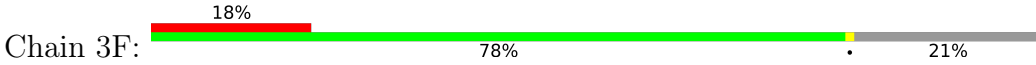


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LYS
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LYS
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GLU
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LYS

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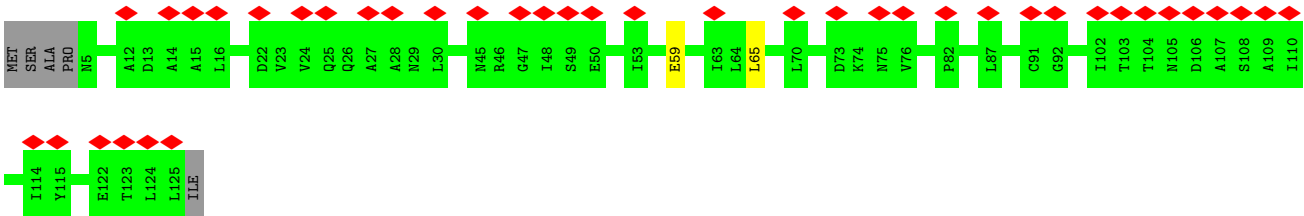
Molecule 23: Ribosomal RNA-processing protein 9



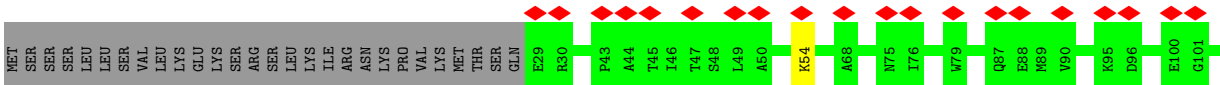
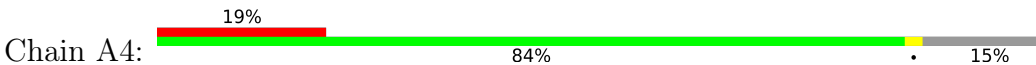
Molecule 24: 13 kDa ribonucleoprotein-associated protein

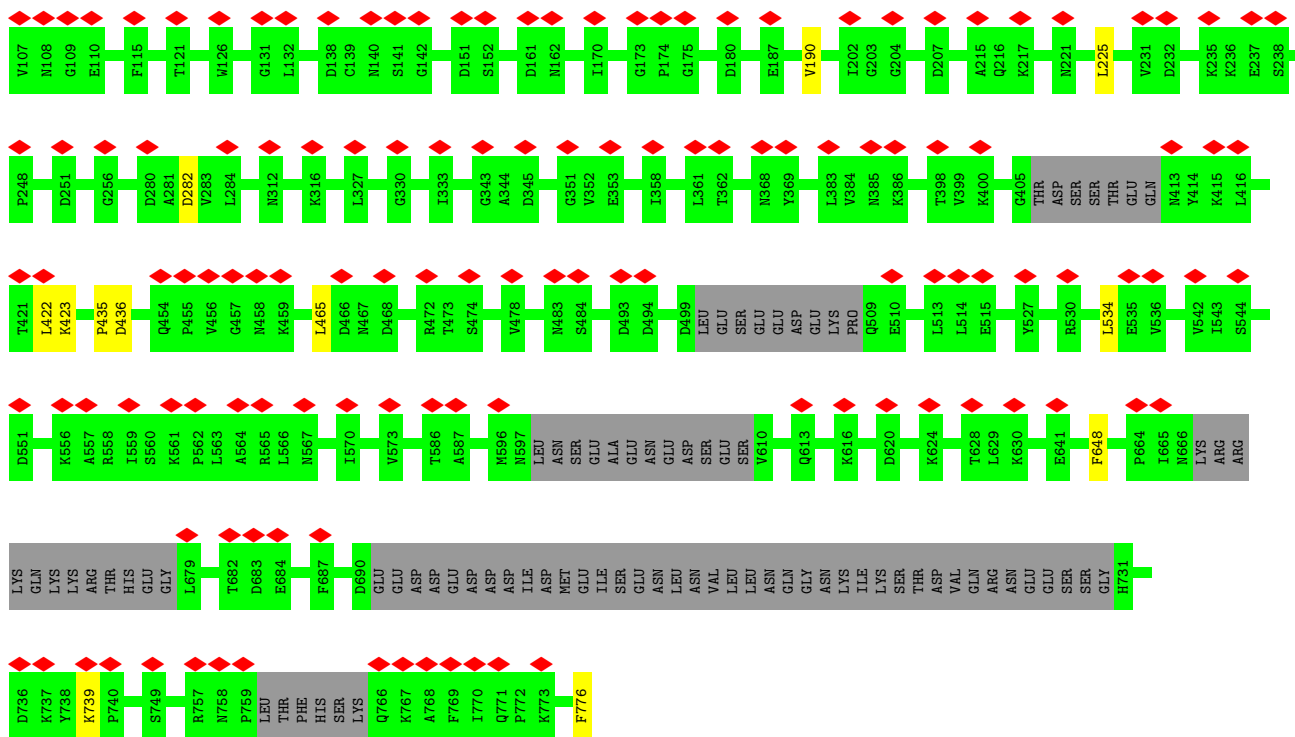


Molecule 24: 13 kDa ribonucleoprotein-associated protein

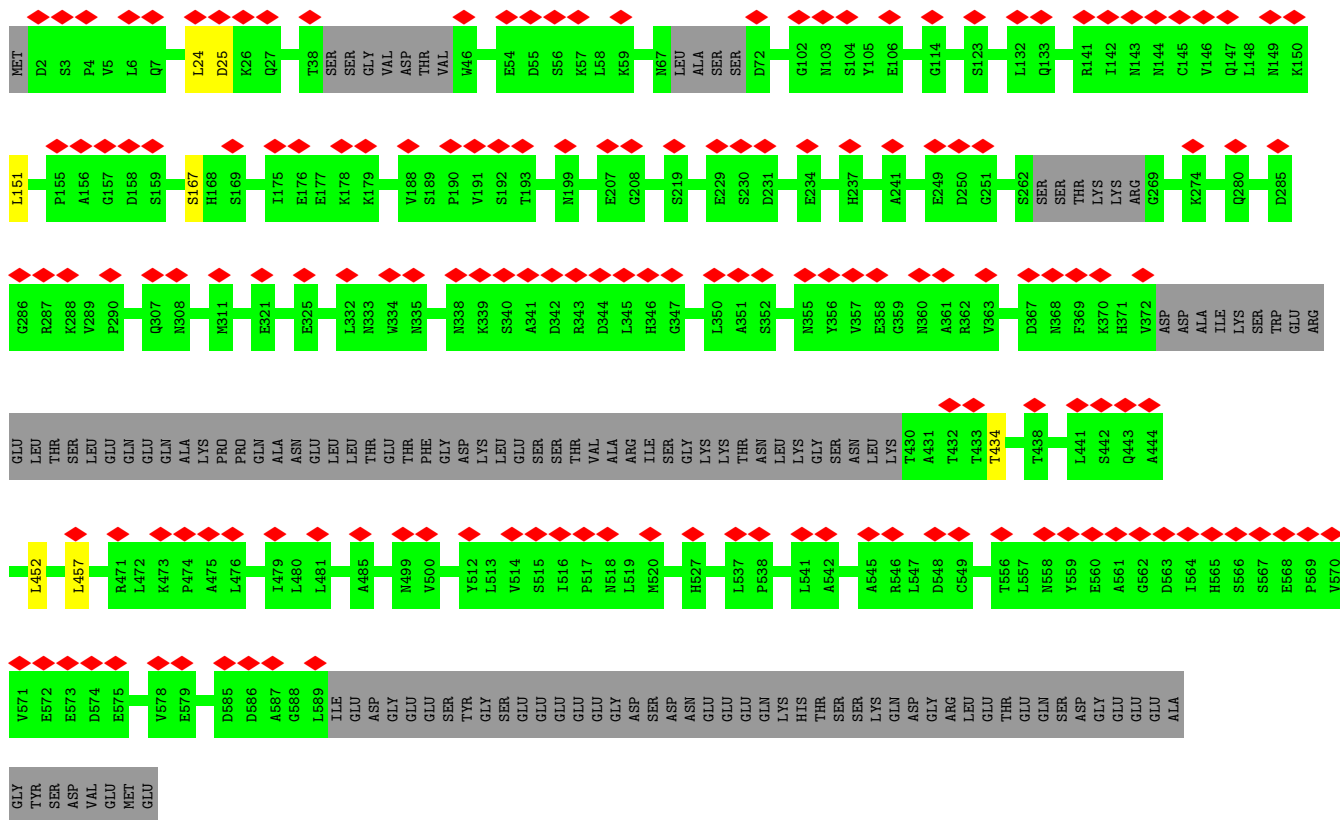
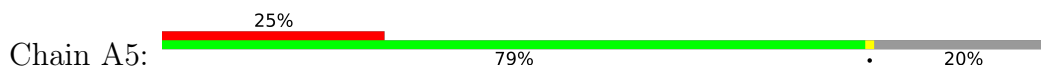


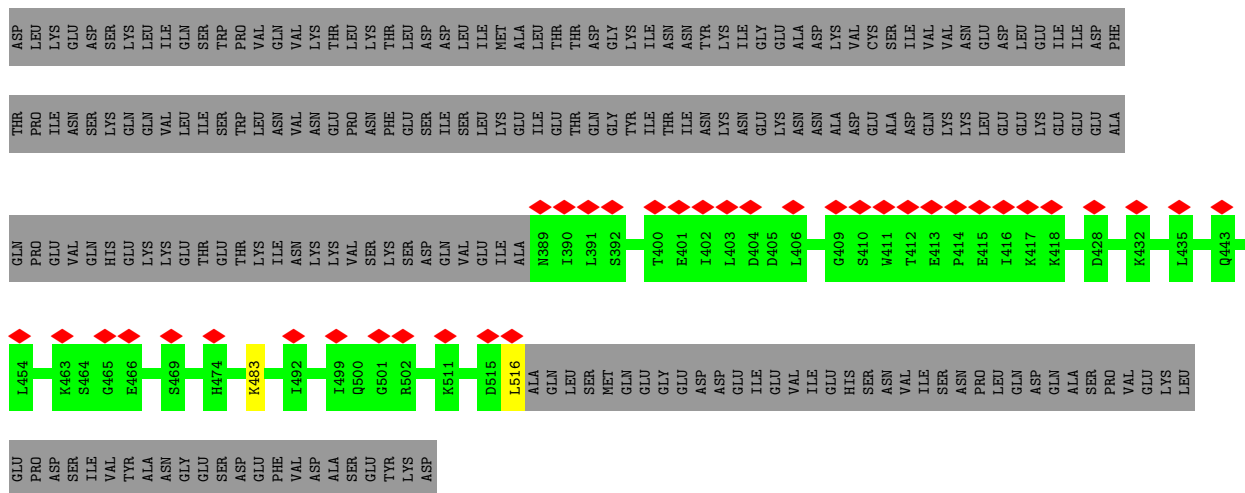
Molecule 25: U3 small nucleolar RNA-associated protein 4



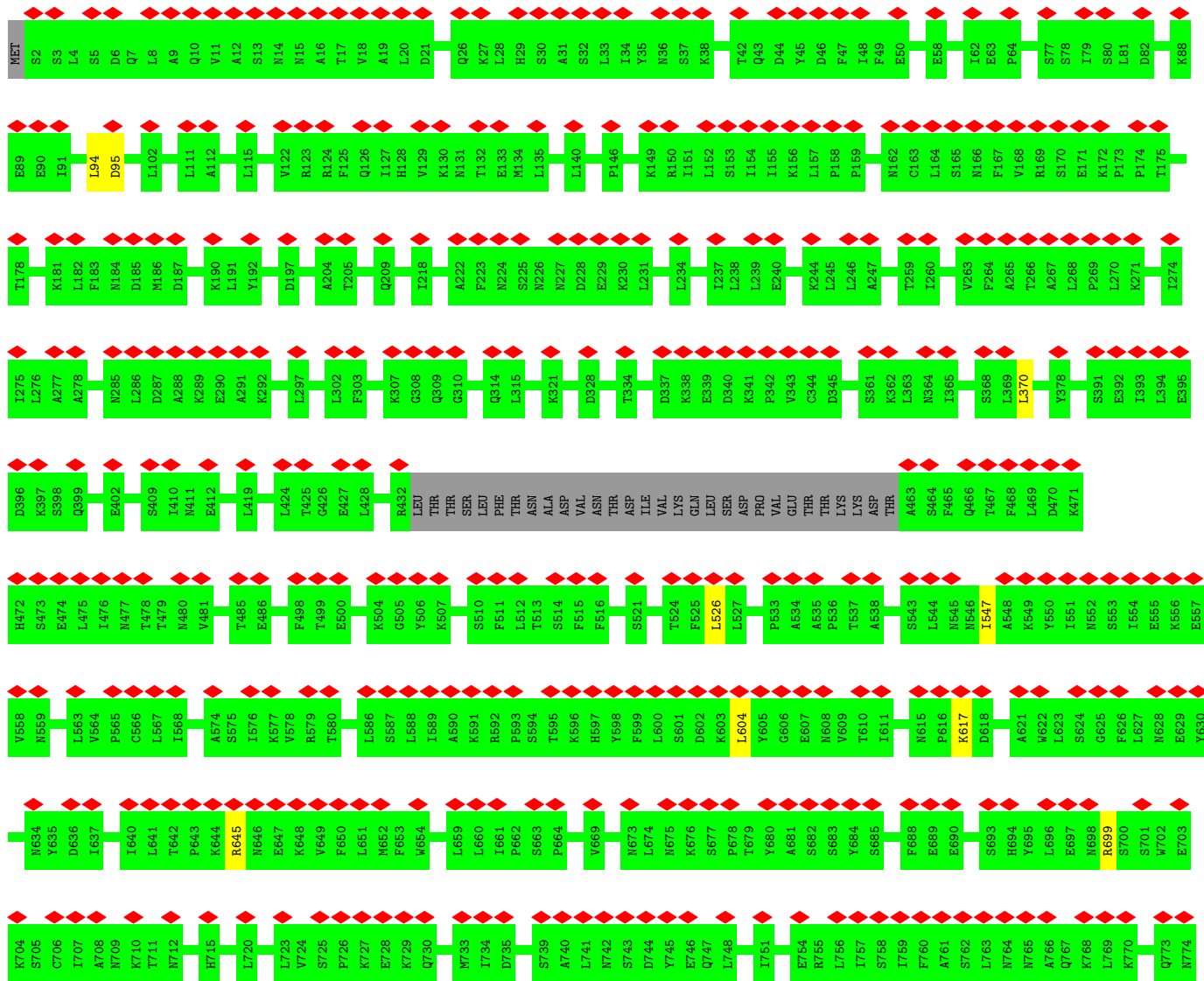
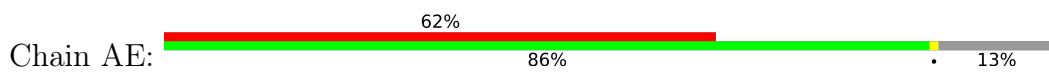


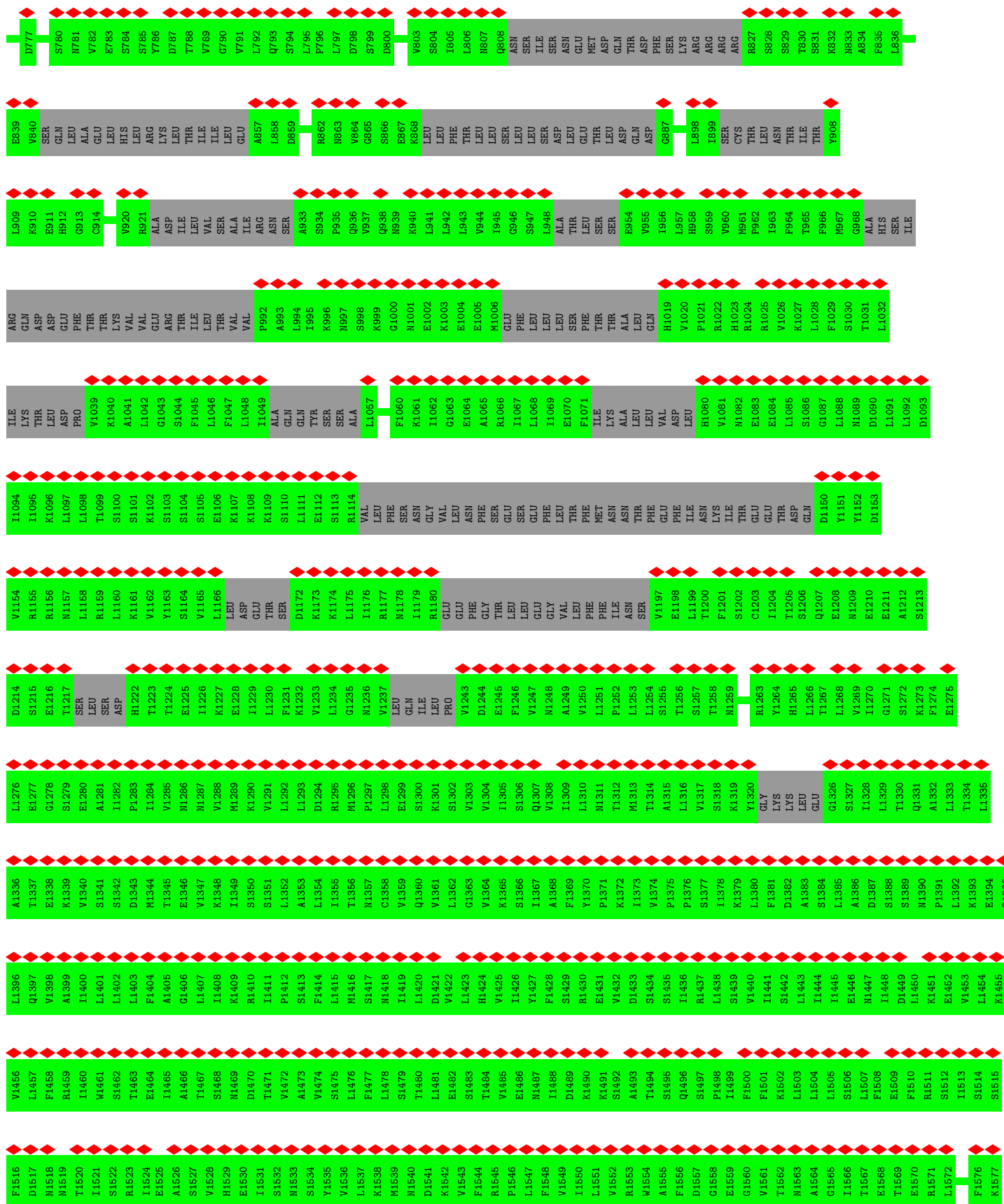
• Molecule 26: U3 small nucleolar RNA-associated protein 5

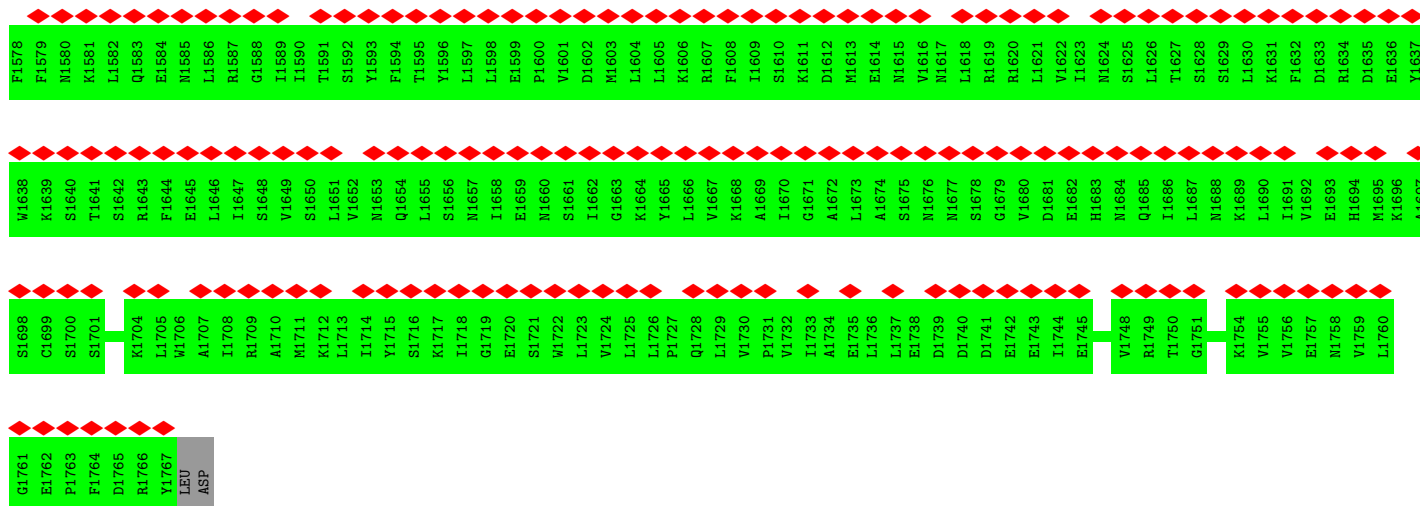




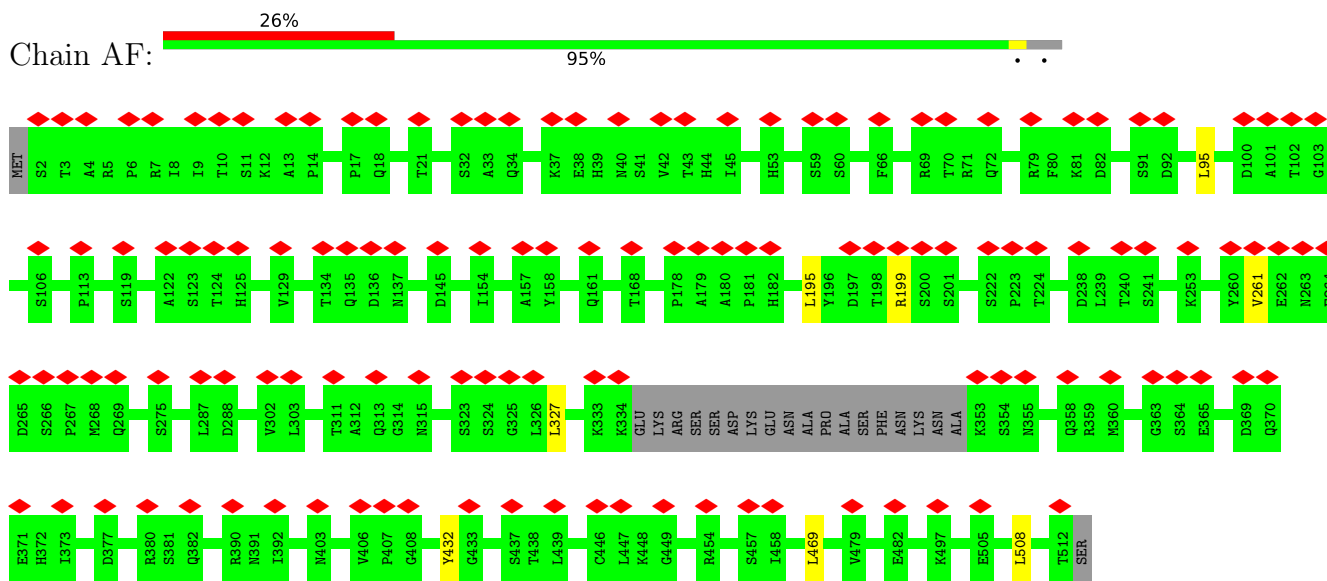
• Molecule 29: U3 small nucleolar RNA-associated protein 10



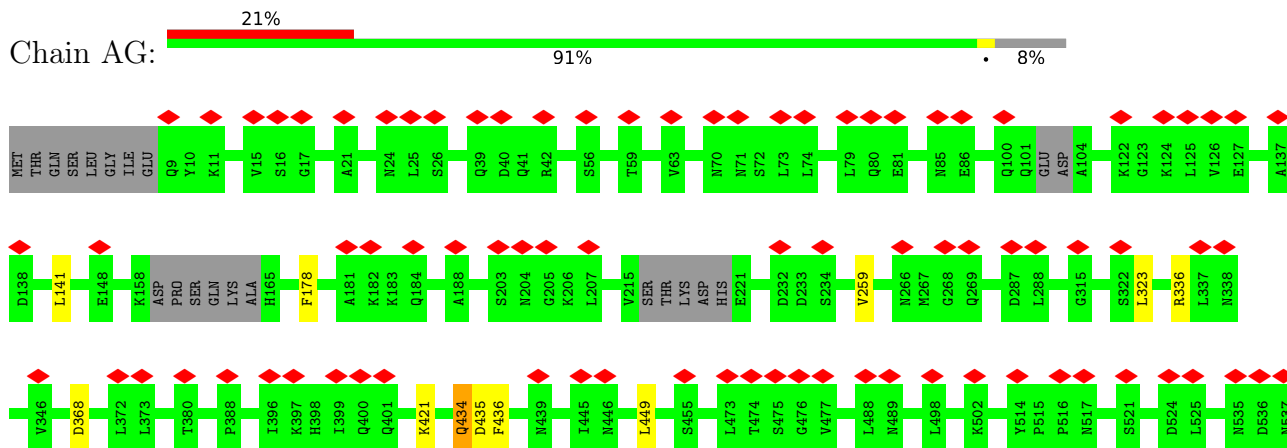


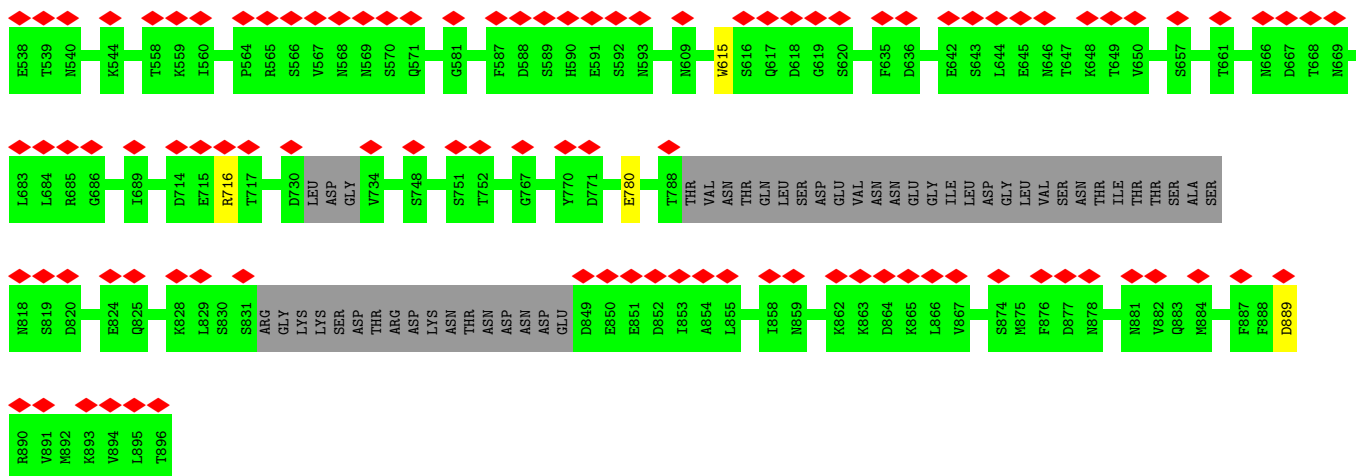


• Molecule 30: U3 small nucleolar RNA-associated protein 15

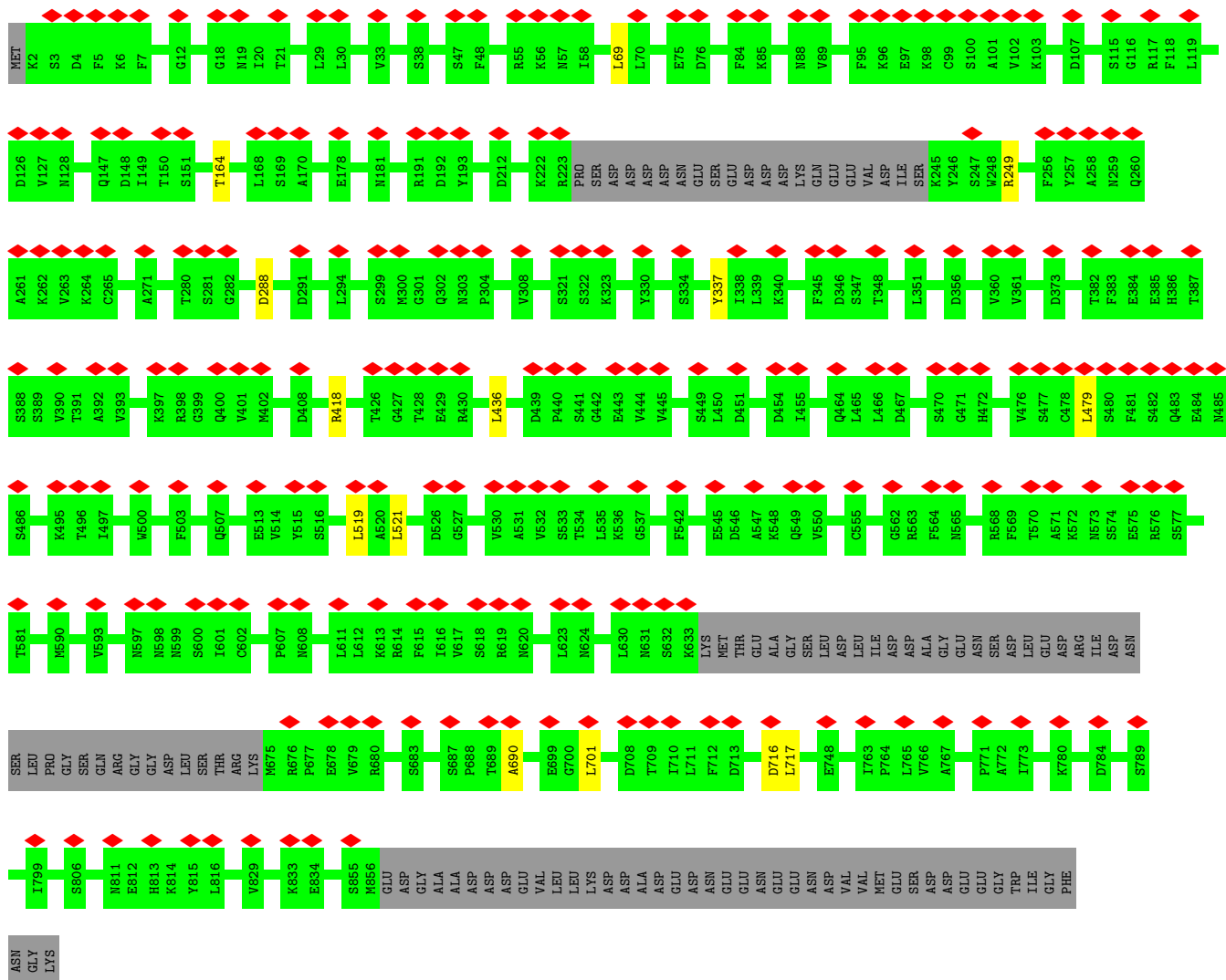
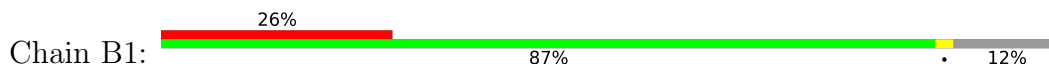


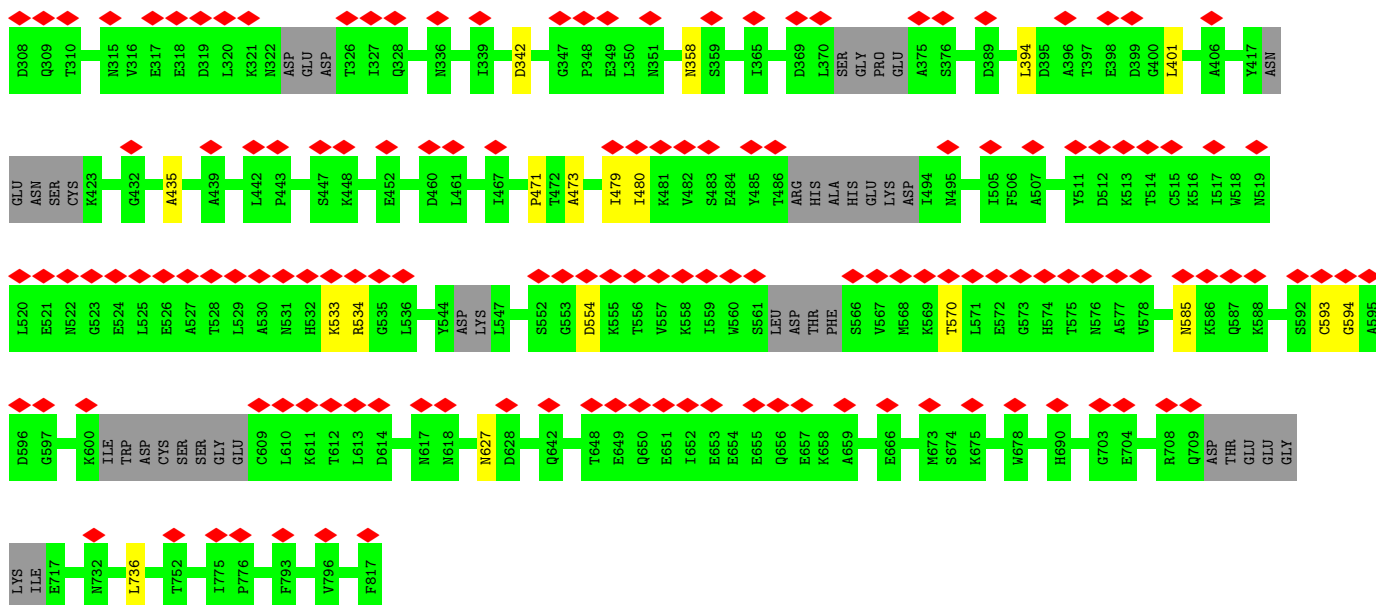
• Molecule 31: NET1-associated nuclear protein 1



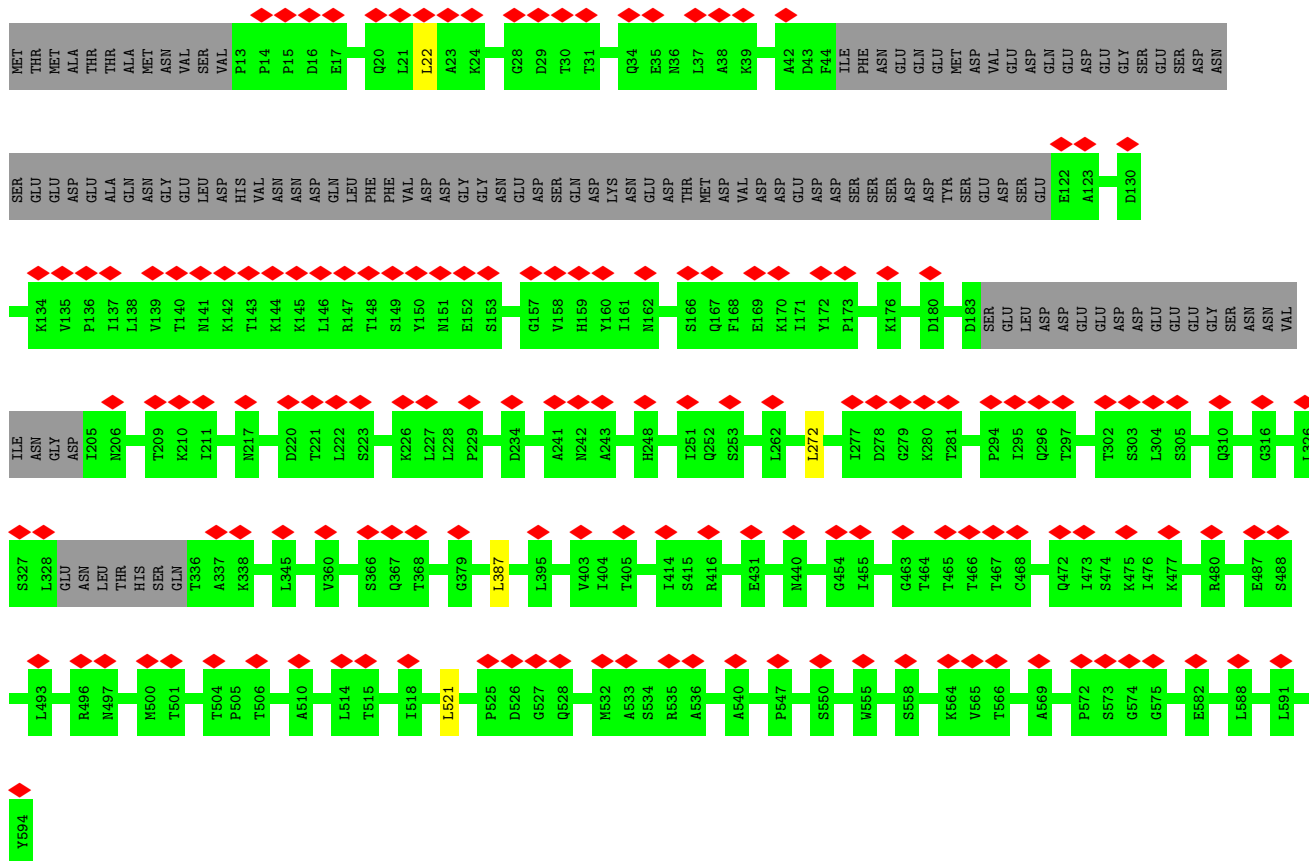
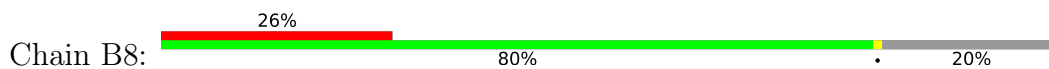


• Molecule 32: Periodic tryptophan protein 2

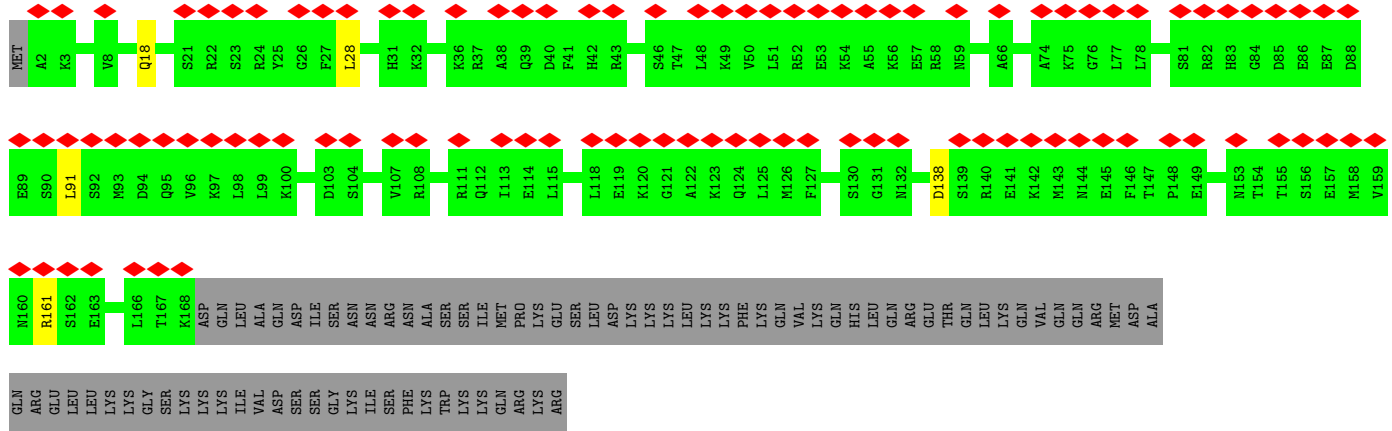




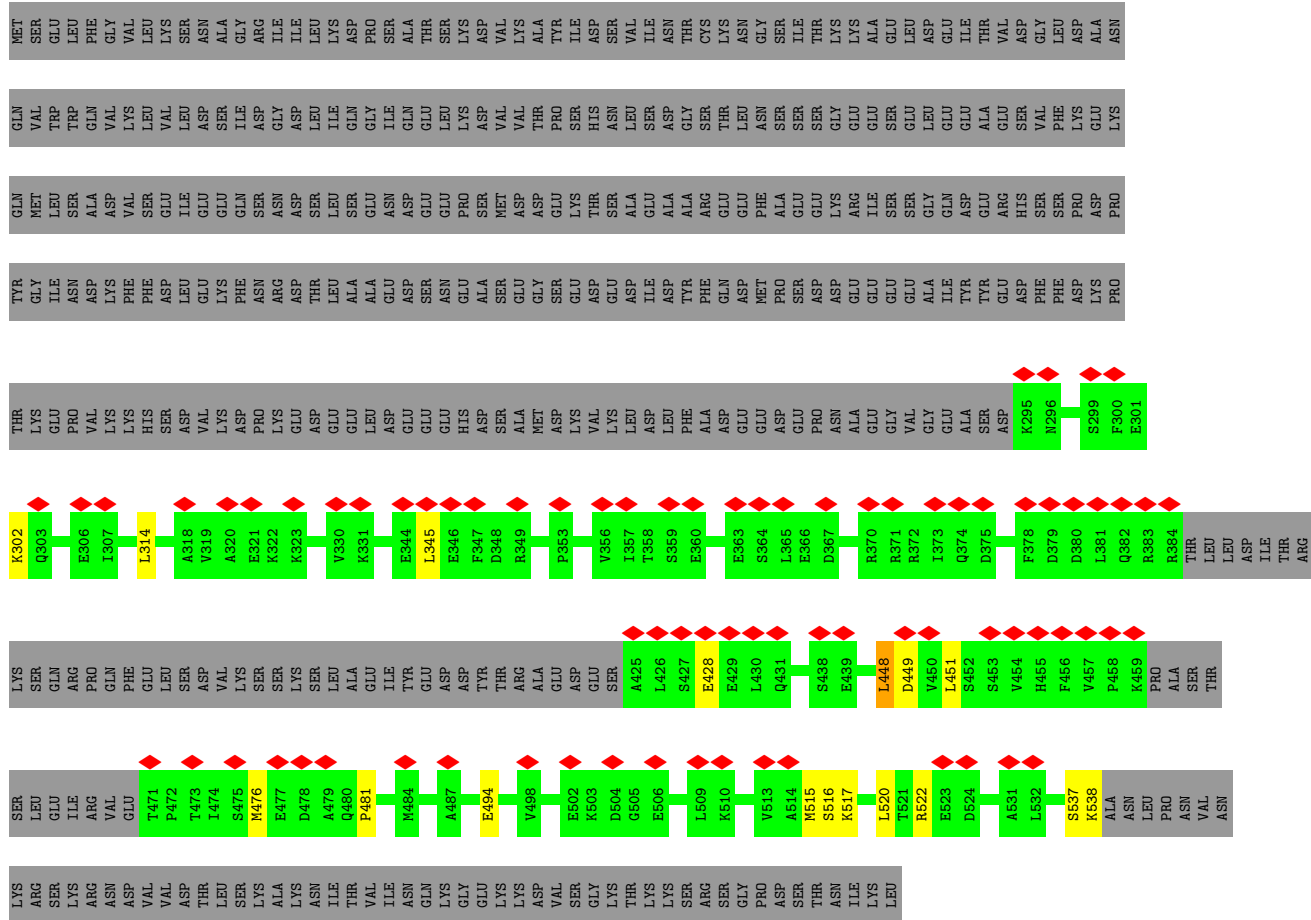
• Molecule 35: U3 small nucleolar RNA-associated protein 18



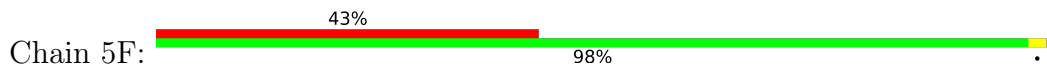
• Molecule 36: U3 small nucleolar RNA-associated protein 21

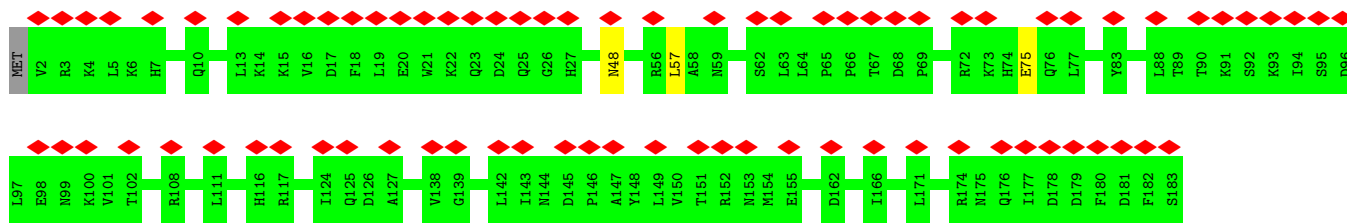


• Molecule 41: U3 small nucleolar RNA-associated protein MPP10

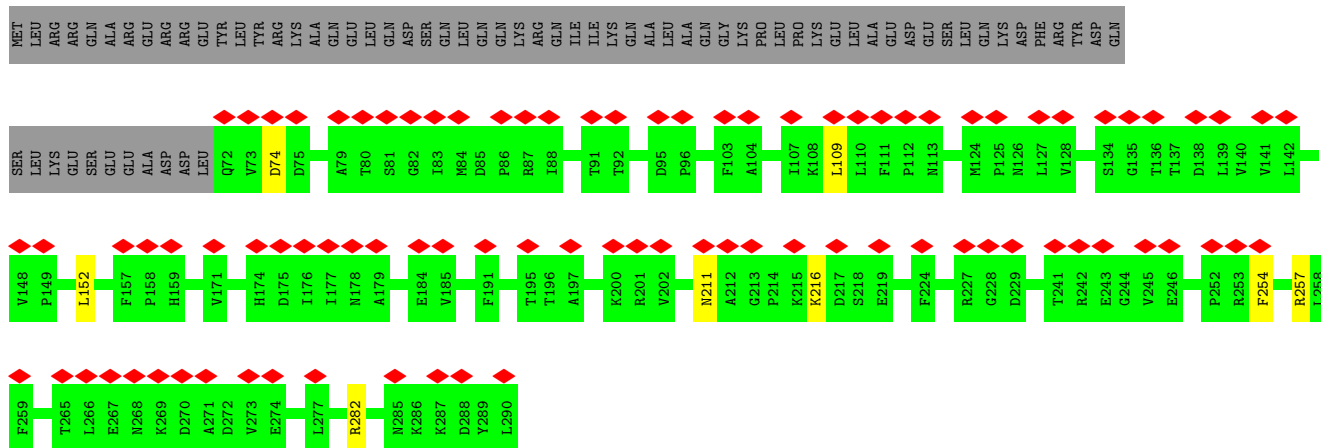
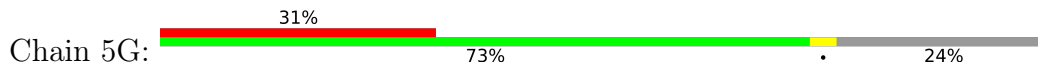


• Molecule 42: U3 small nucleolar ribonucleoprotein protein IMP3

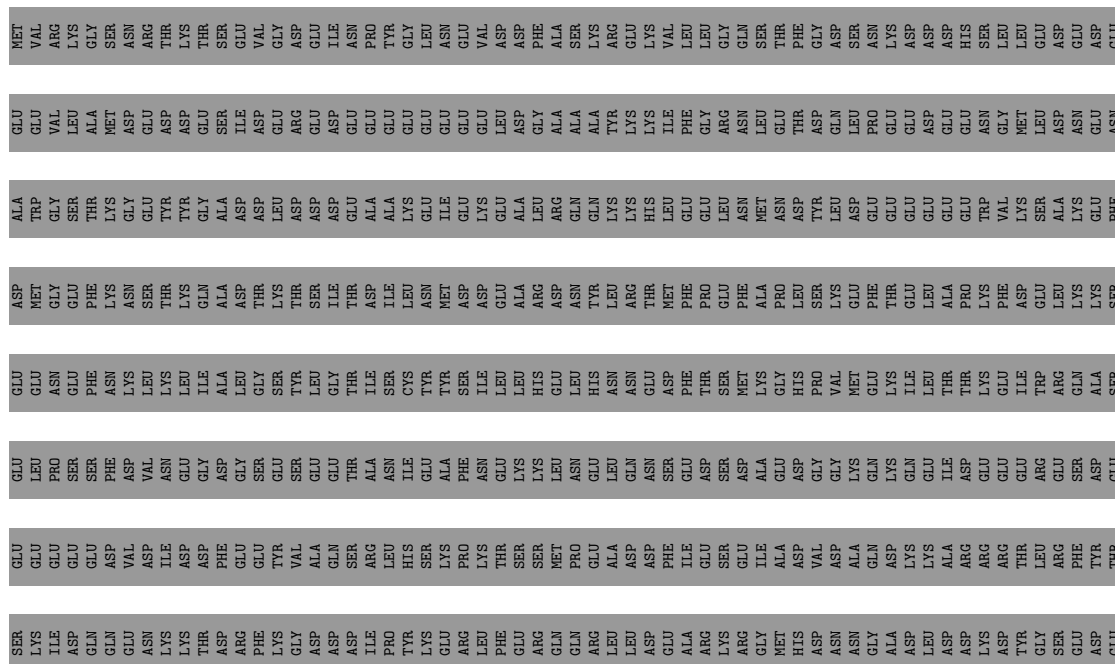


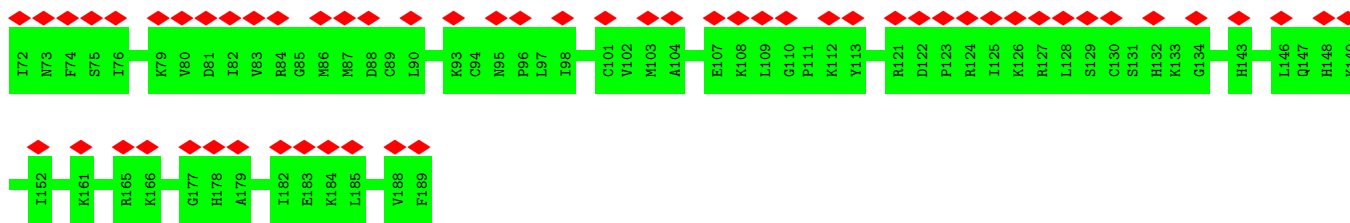


• Molecule 43: U3 small nucleolar ribonucleoprotein protein IMP4

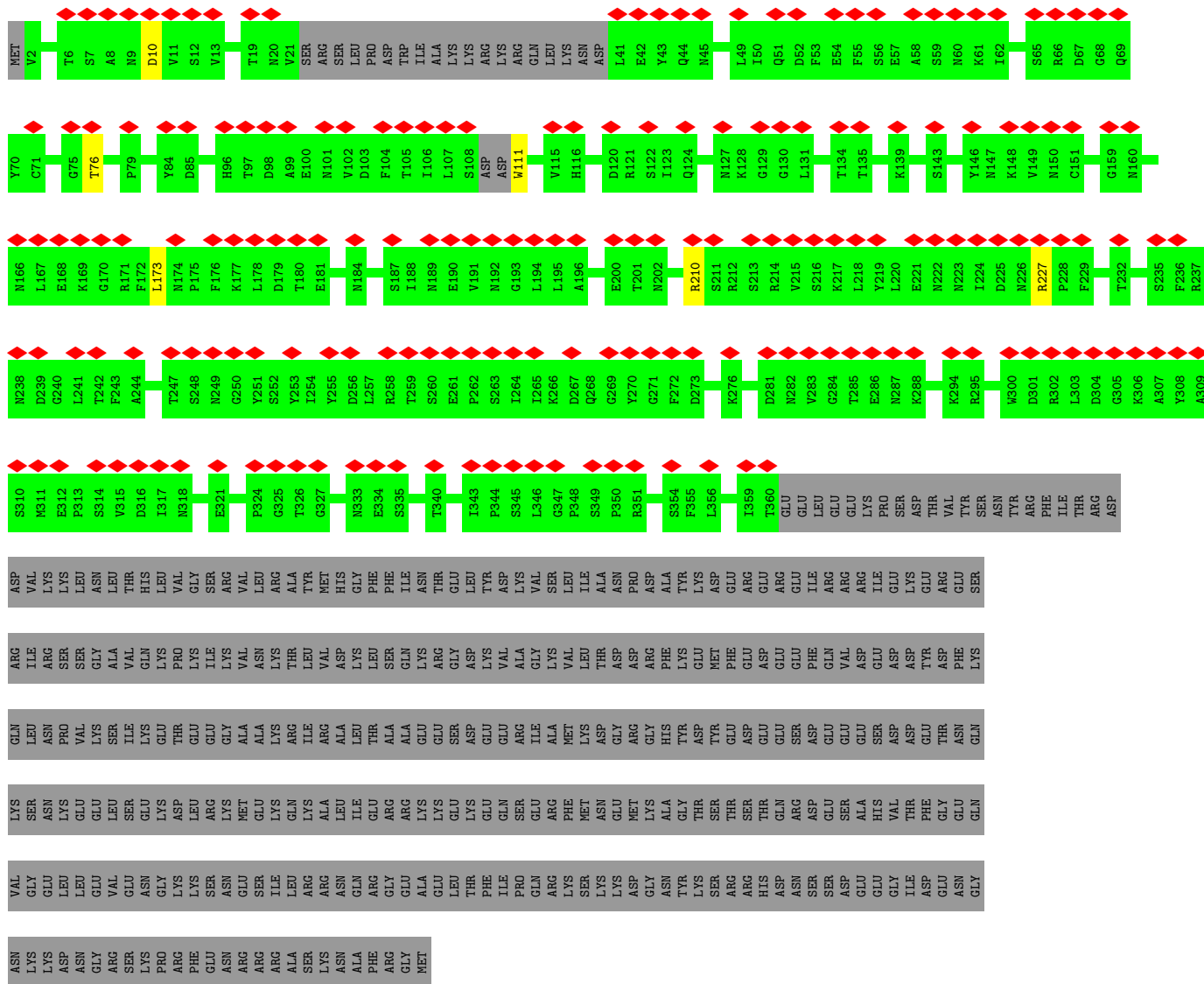


• Molecule 44: Something about silencing protein 10

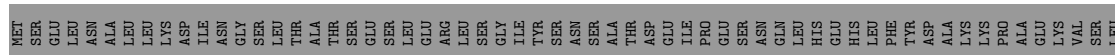


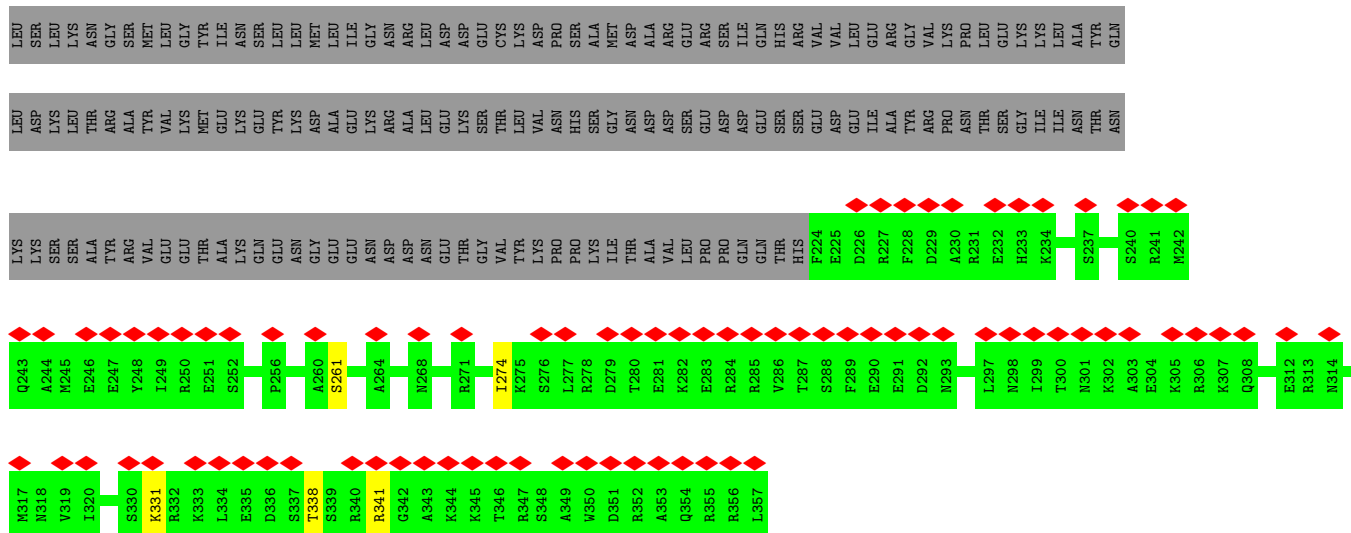


• Molecule 48: Ribosome biogenesis protein ENP2

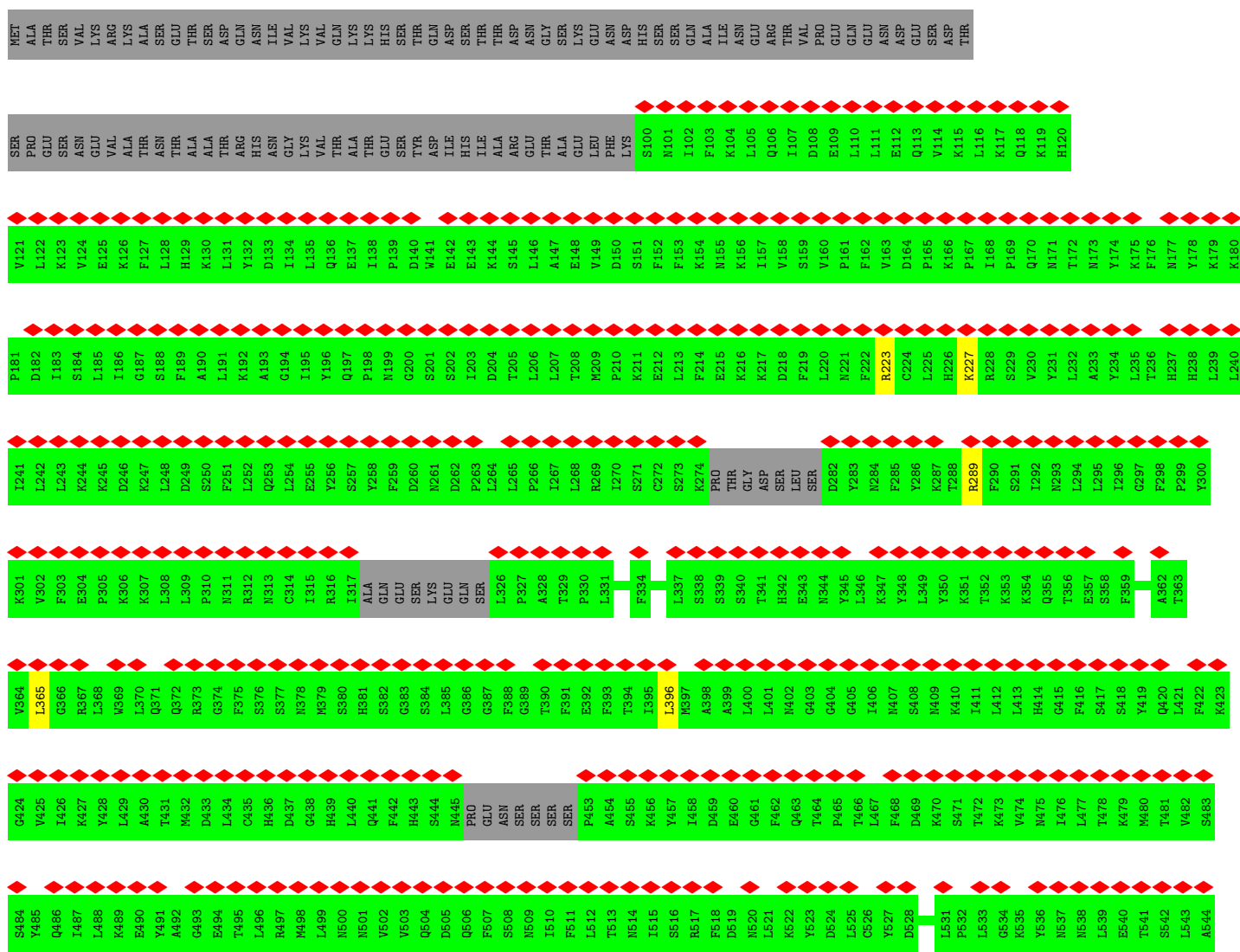
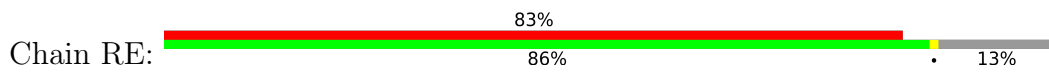


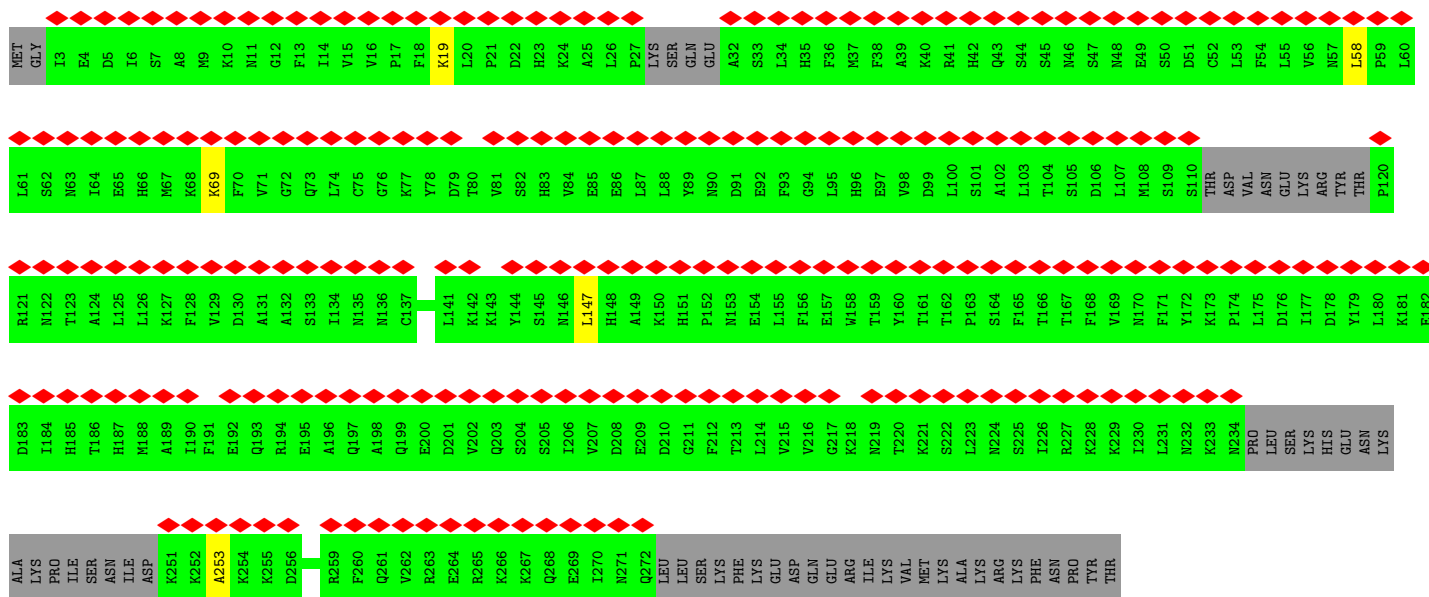
• Molecule 49: U3 small nucleolar ribonucleoprotein protein LCP5



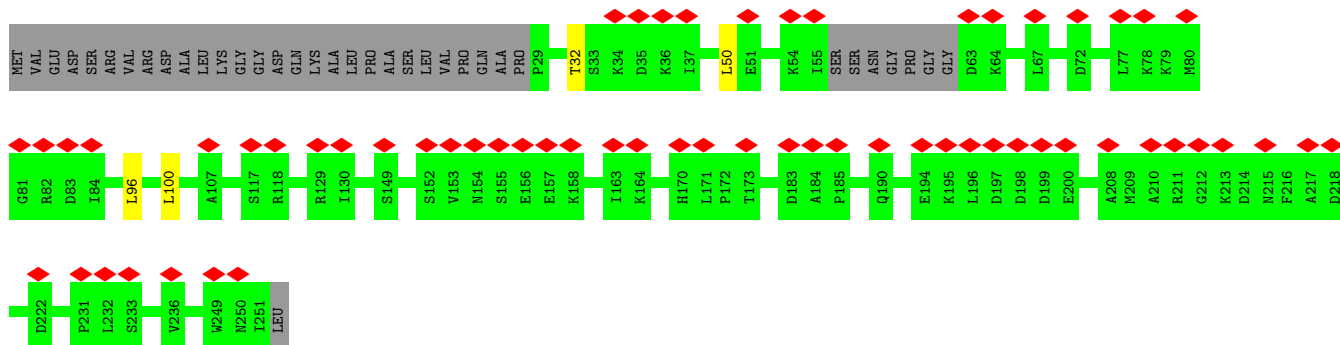
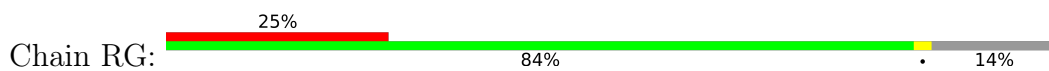


• Molecule 50: U3 small nucleolar RNA-associated protein 22

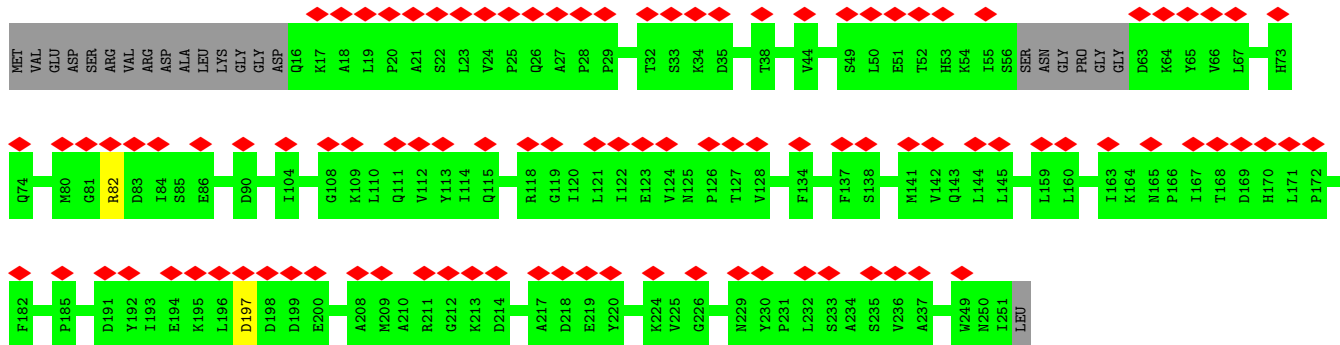
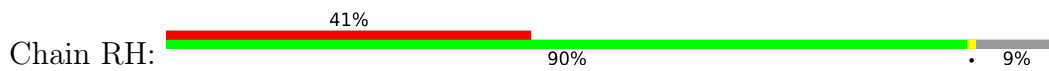




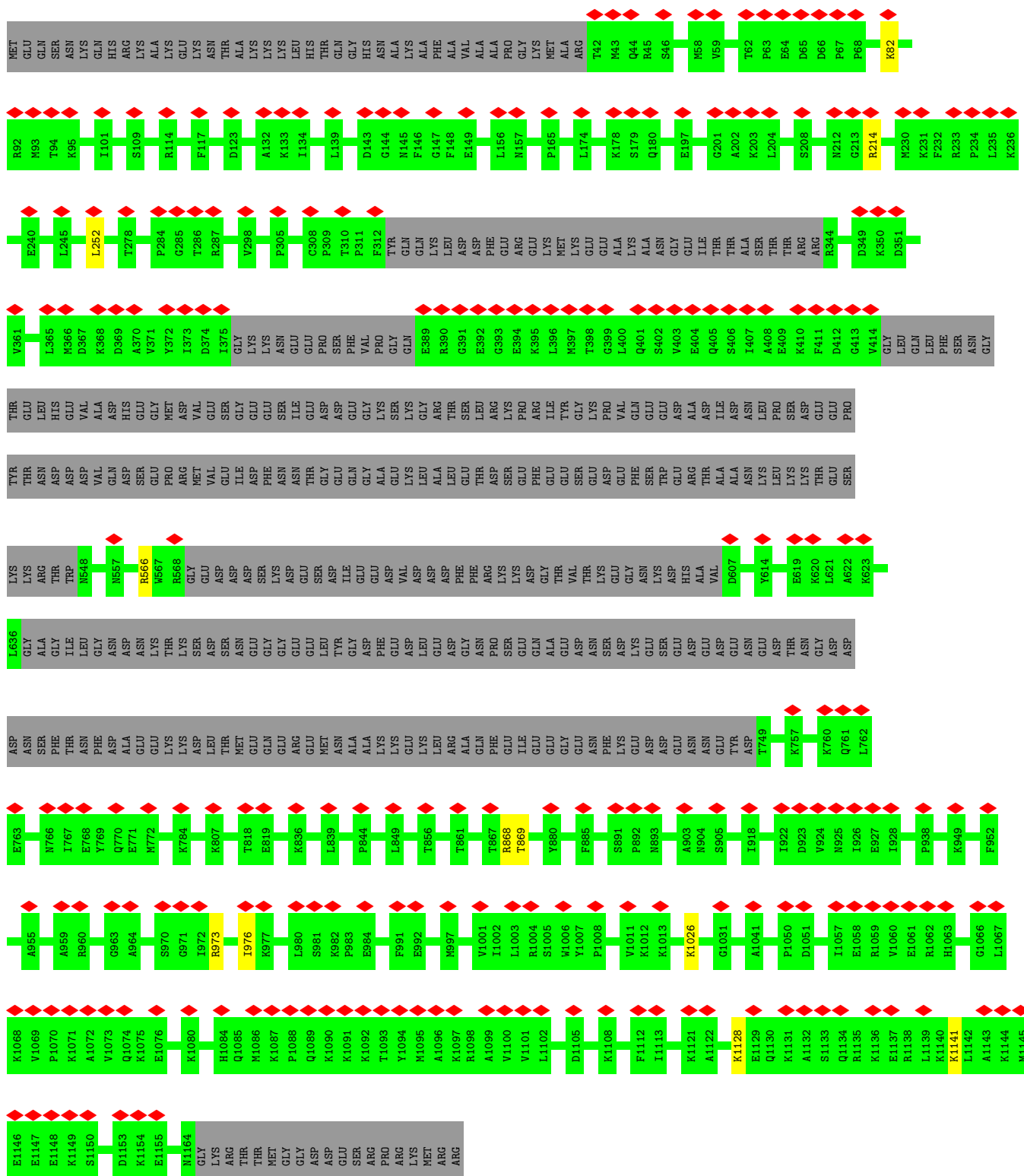
• Molecule 52: Ribosomal RNA small subunit methyltransferase NEP1



• Molecule 52: Ribosomal RNA small subunit methyltransferase NEP1

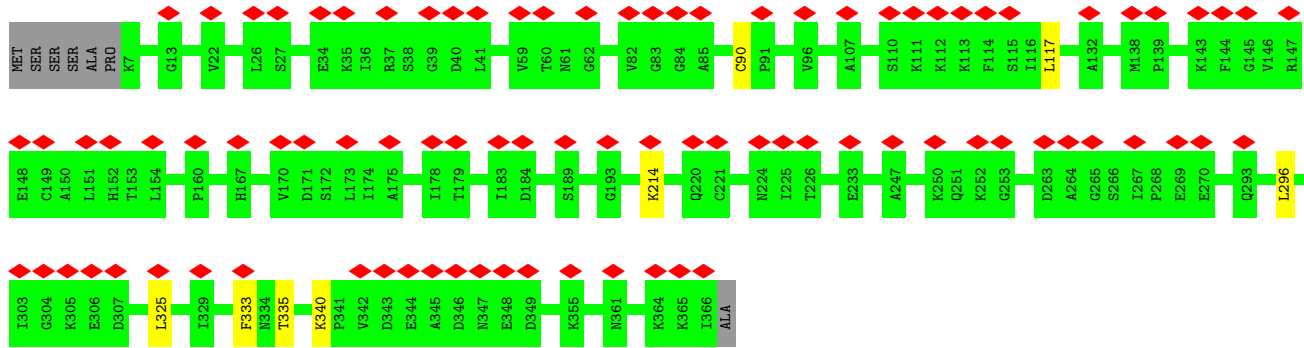


• Molecule 53: Ribosome biogenesis protein BMS1

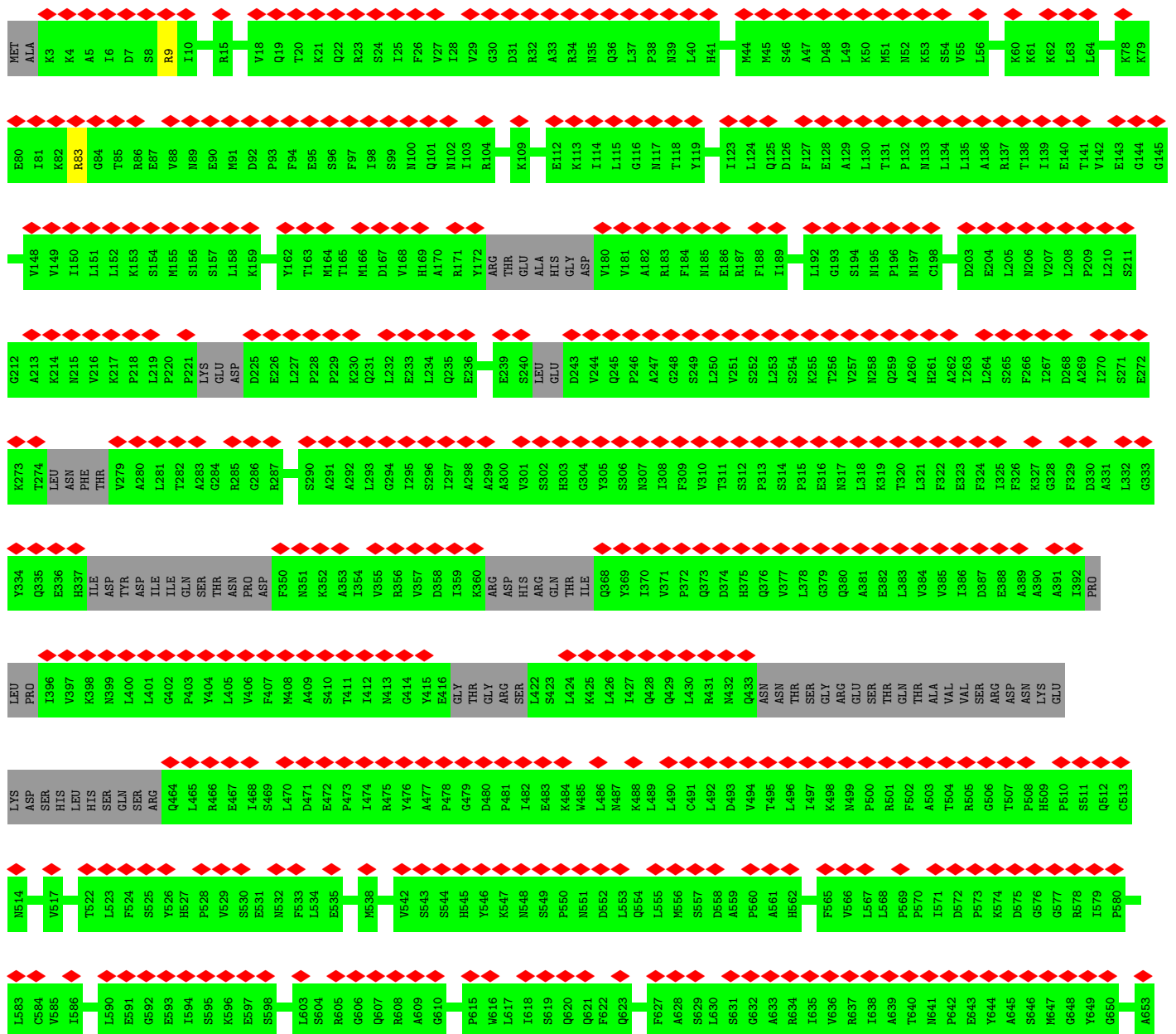
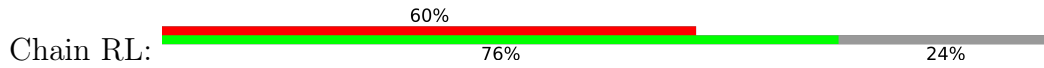


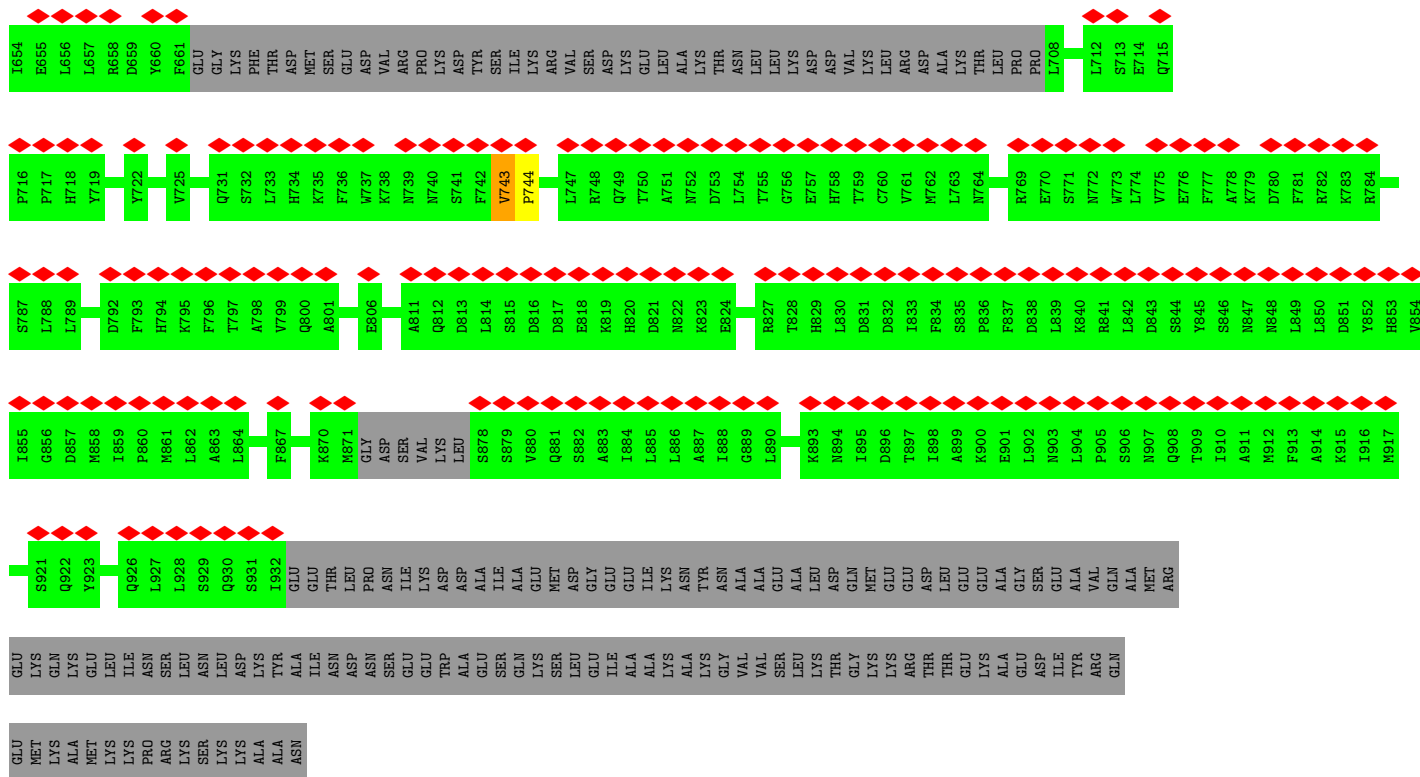
• Molecule 54: RNA 3'-terminal phosphate cyclase-like protein



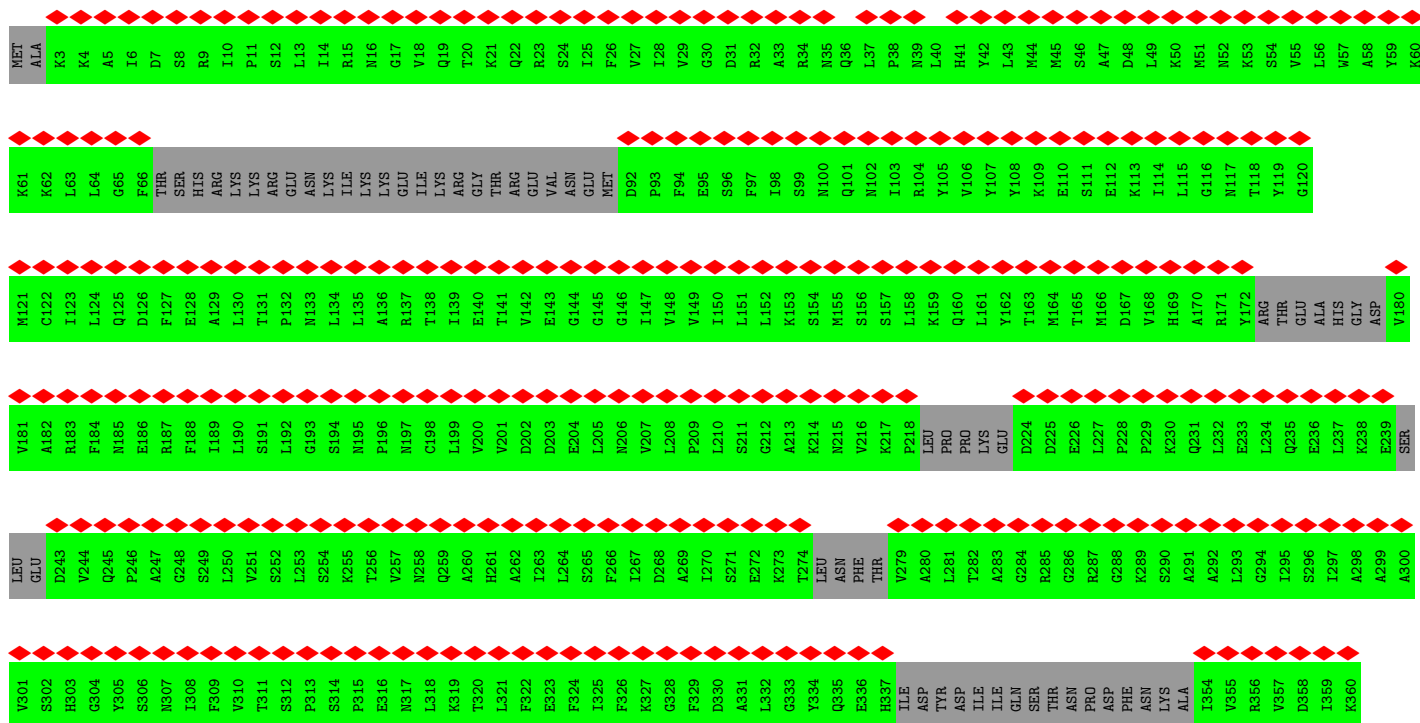
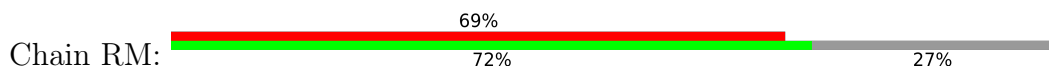


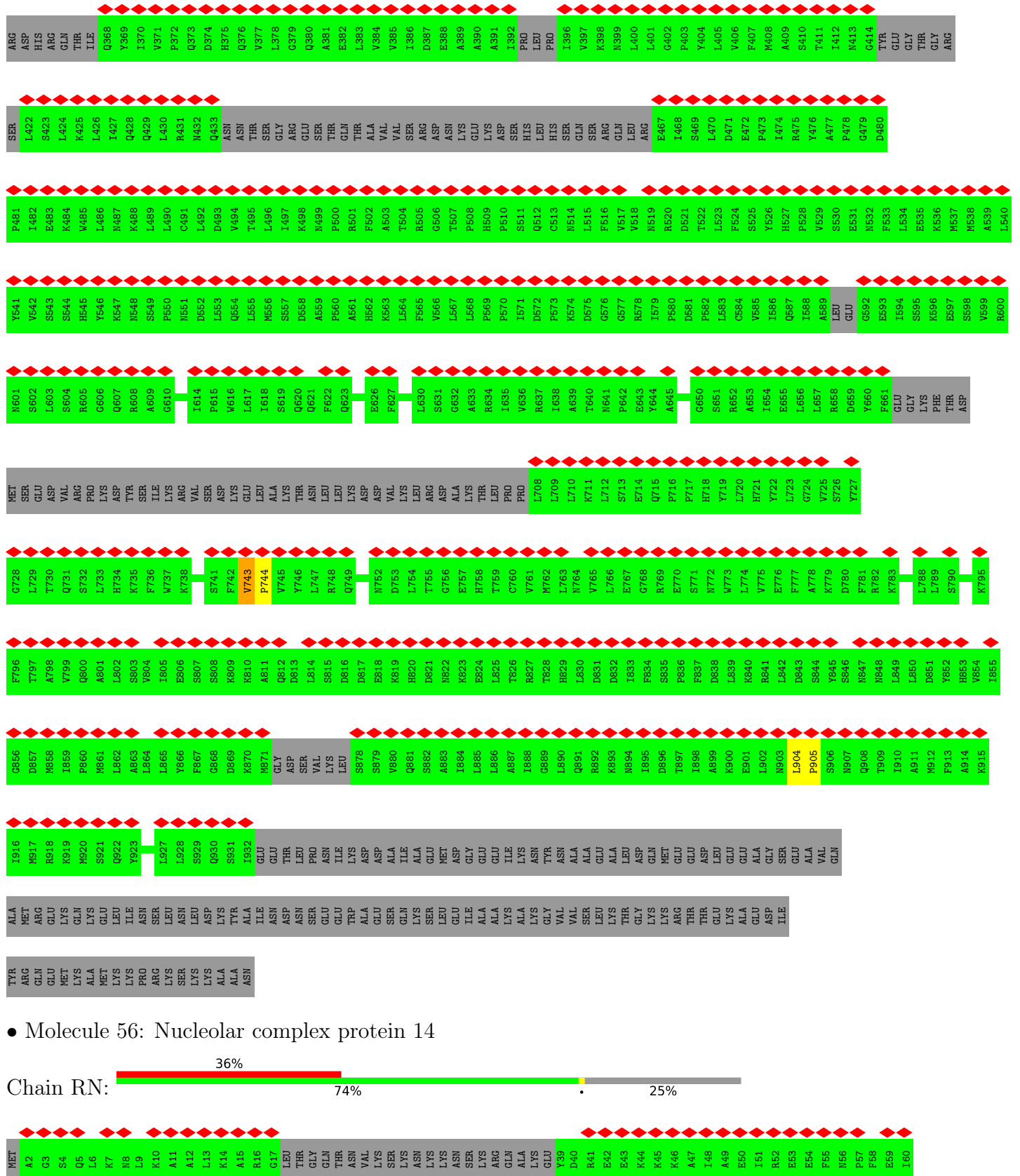
• Molecule 55: RNA cytidine acetyltransferase

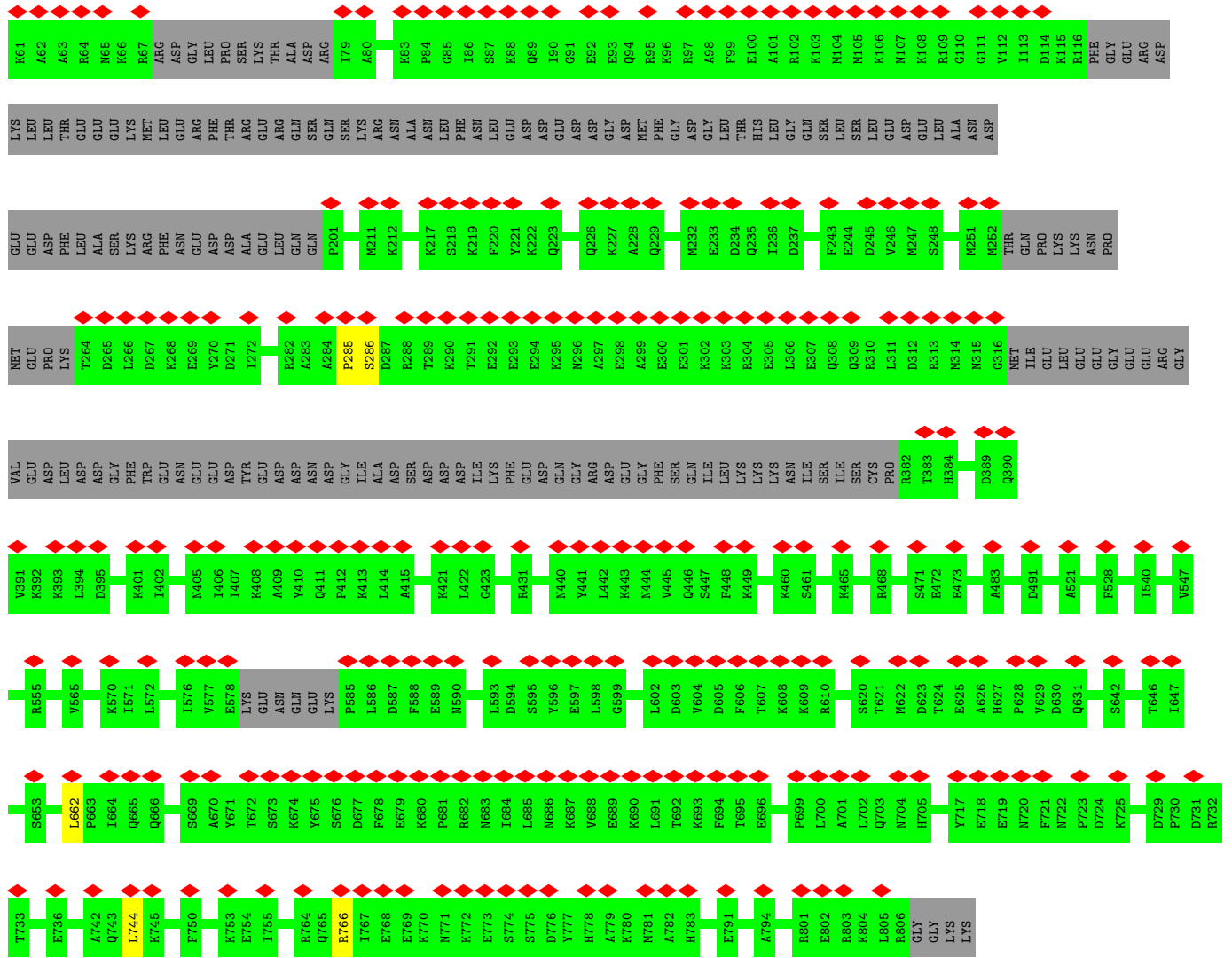




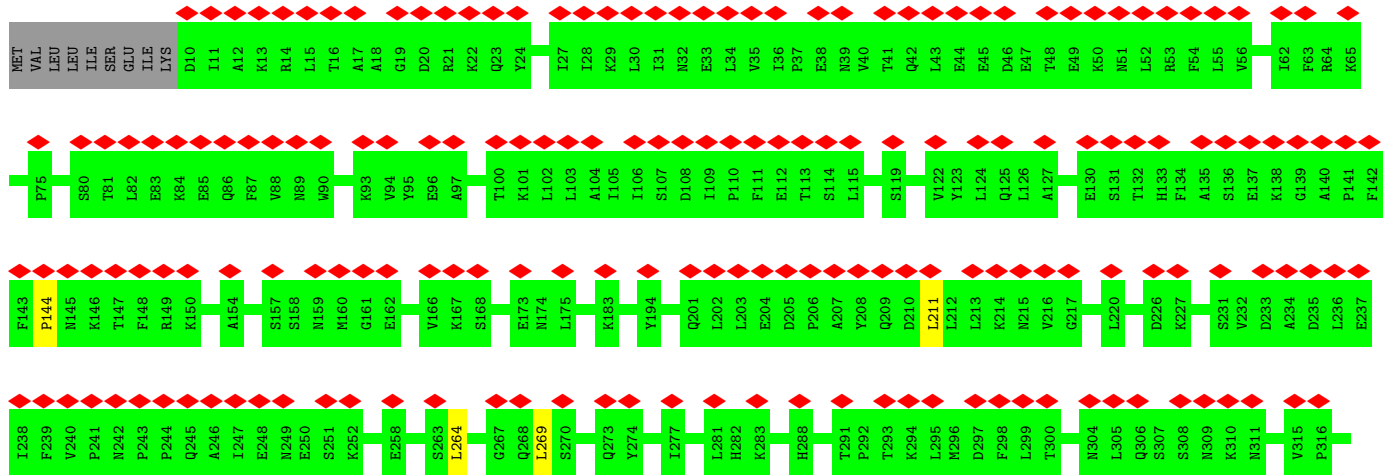
- Molecule 55: RNA cytidine acetyltransferase

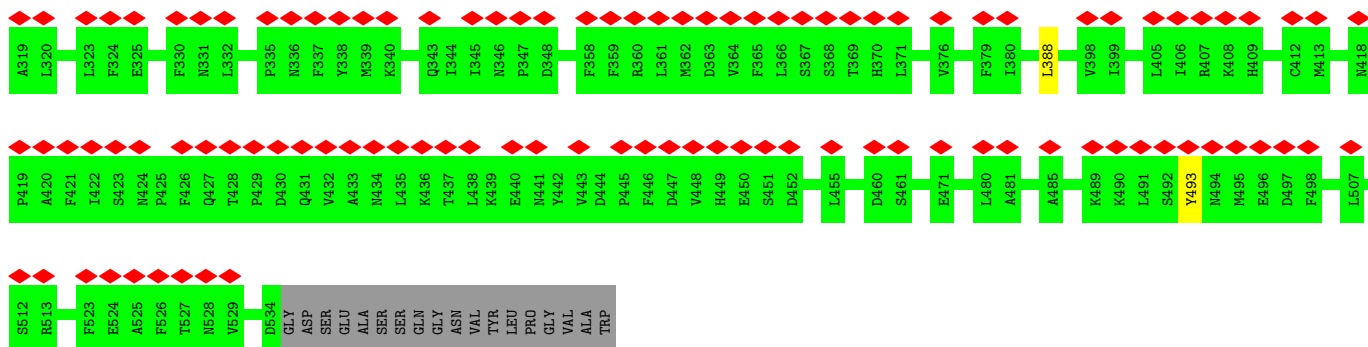




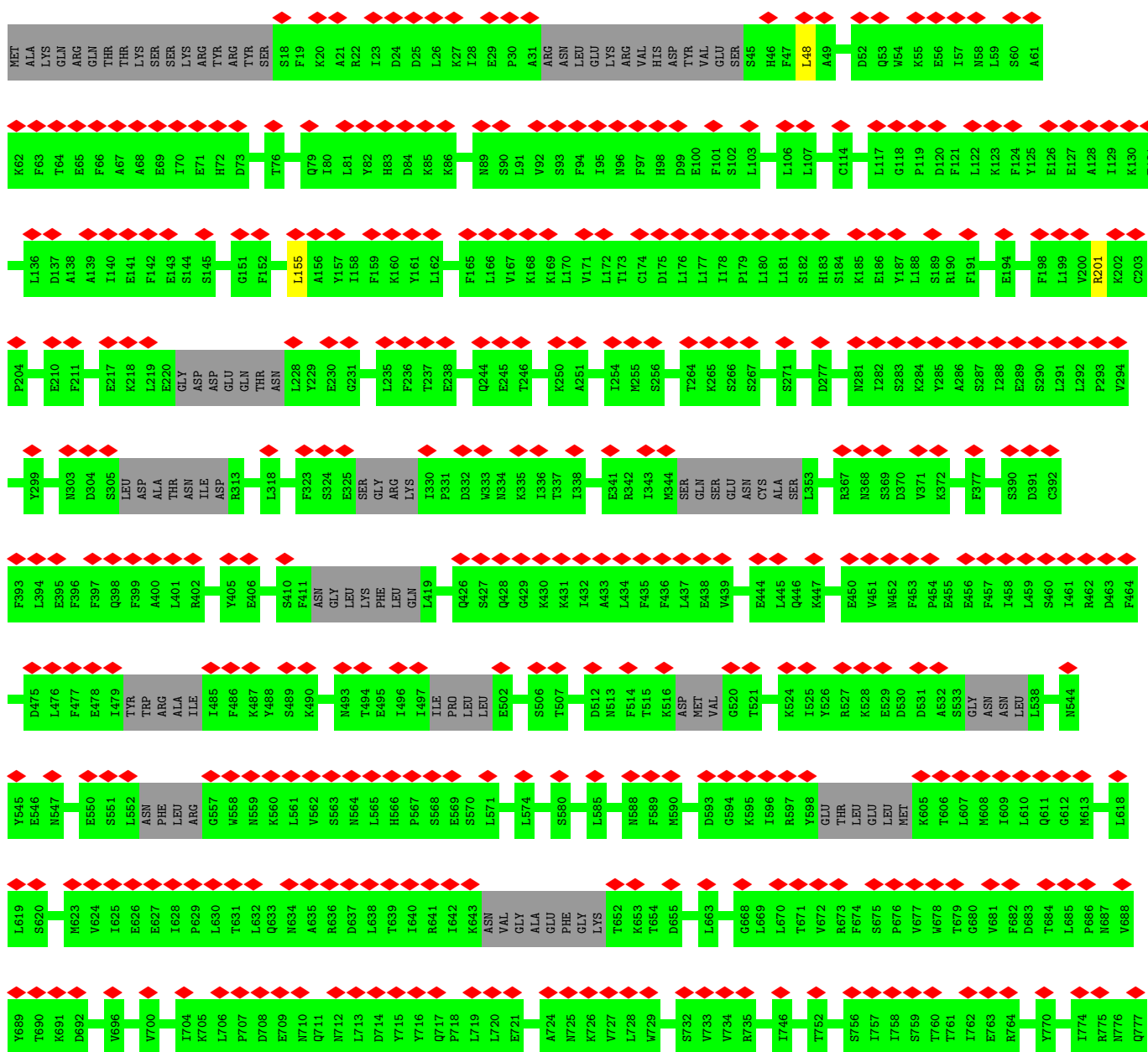
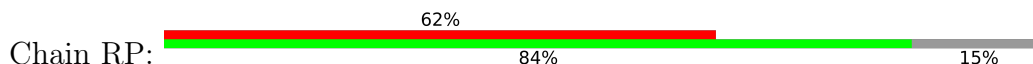


• Molecule 57: Nucleolar complex protein 4





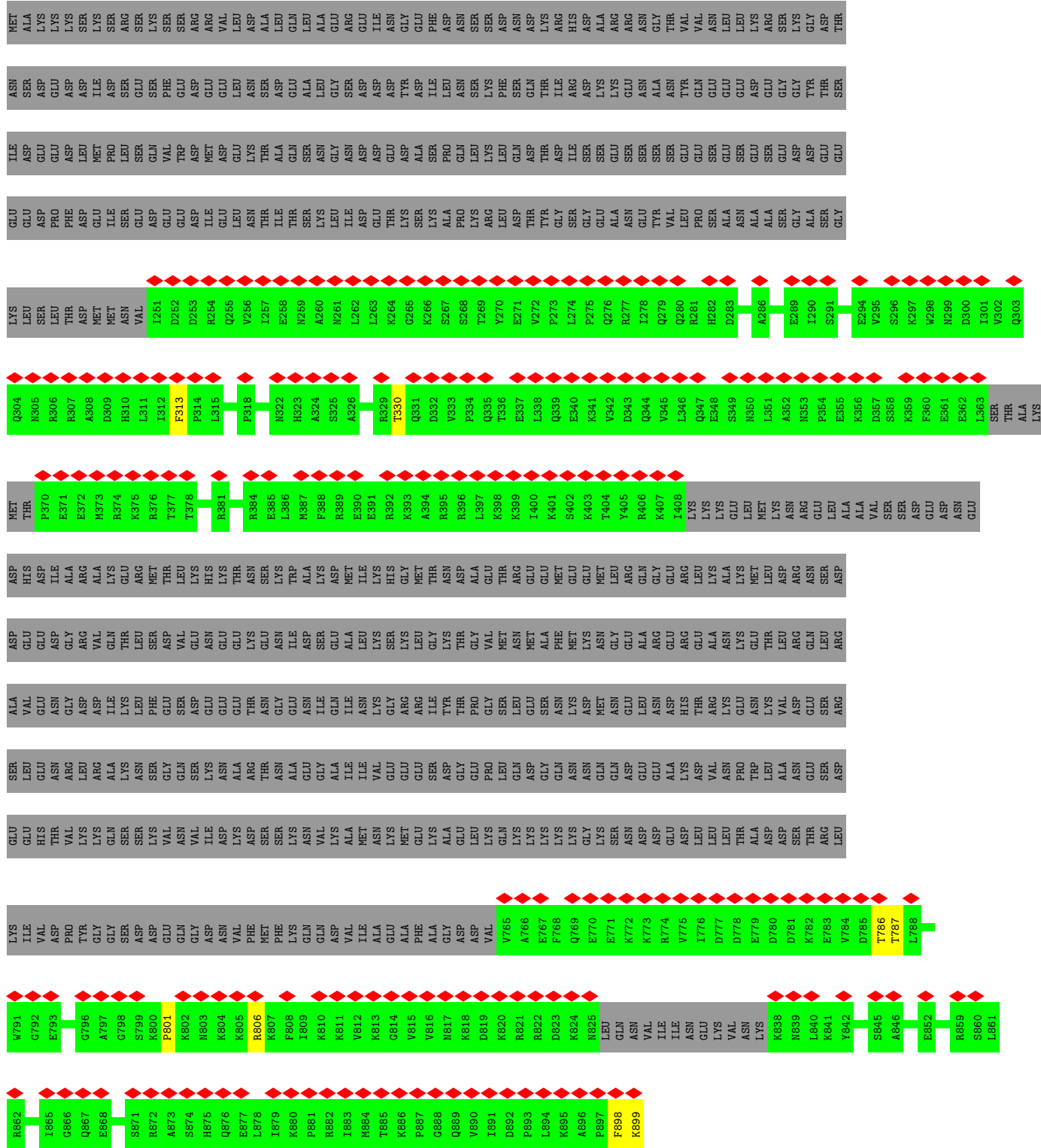
• Molecule 58: U3 small nucleolar RNA-associated protein 20



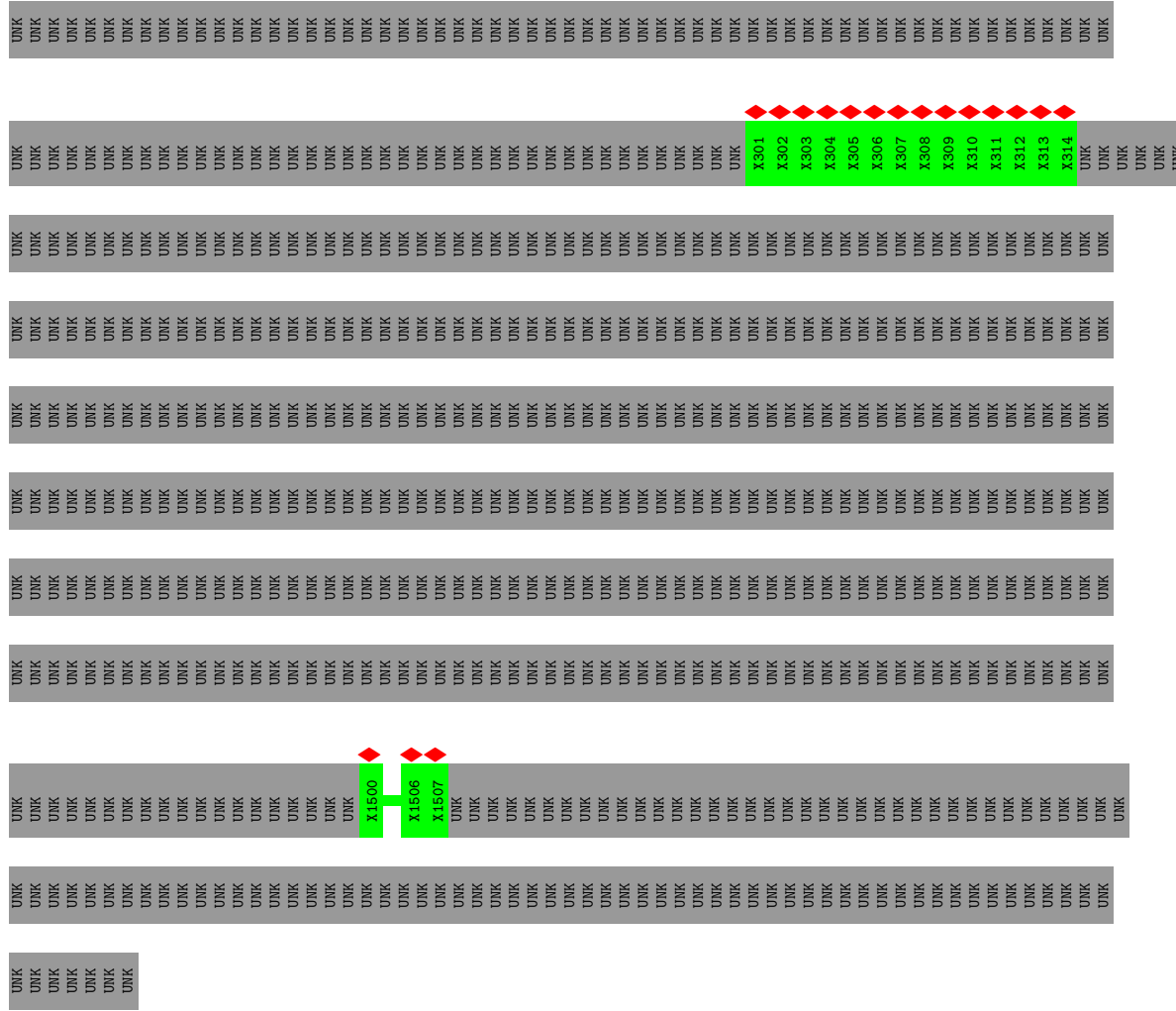
ILE	E1608	R1609	II612	A1613	E1614	A1615	L1616	V1617	L1658	L1659	R1660	V1661	I1662	G1622	L1623	T1624	N1625	D1626	E1667	S1668	L1669	L1670	T1671	L1672	S1673	K1674	F1675	P1676	S1677	ASN	L1638	ASP	GLU	PRO	SER	L1643	R1644	S1645	K1646	S1647	E1648	E1649	L1650	R1651	D1652	A1653	V1654	R1655	V1656	T1657	L1658	G1659	K1660	I1661	I1663	I1664	L1665	G1666	A1667	E1668	
L1547	I1548	VAL	GLN	LEU	SER	VAL	PRO	LEU	LEU	ARG	GLU	T1558	L1559	R1560	V1561	I1562	R1563	D1564	G1565	A1566	E1567	S1568	L1569	L1570	T1571	L1572	S1573	K1574	F1575	P1576	S1577	ASN	L1510	ASP	GLU	PRO	SER	L1461	R1462	Q1463	R1464	A1465	L1466	L1467	R1468	L1469	G1470	E1471	H1472	A1473	H1474	Q1475	L1476	K1477	D1478	S1480	I1481	S1482	Y1484	L1485	Q1546
II486	P1487	M1488	I1489	E1490	H1491	Y1492	V1493	F1494	S1495	D1496	D1497	E1498	R1499	Y1500	R1501	M1502	M1505	E1506	T1507	Q1508	I1509	A1510	I1511	G1512	G1513	L1514	A1515	Q1516	H1517	M1518	L1519	M1520	N1521	P1522	Y1523	K1524	A1525	L1526	L1527	R1528	L1529	Y1530	I1531	S1532	M1533	L1534	K1535	L1536	T1537	P1538	M1539	Q1540	M1541	L1542	Q1543	A1544	Q1545	V1546			
L1304	V1305	A1306	D1307	L1308	M1309	S1310	Y1311	S1312	S1313	S1314	R1315	M1316	H1317	E1318	Y1319	D1320	F1321	P1322	ARG	ILE	LEU	THR	PHE	LYS	GLY	LEU	GLU	ASP	GLY	TYR	SER	TYR	SER	GLU	LEU	LEU	TRP	LEU	PRO	LEU	LEU	PHE	THR	PHE	LEU	HIS	PHE	ASN	ASN	GLY	GLU	VAL	SER	V1420	L1421	S1422	Y1423	M1424	V1425		
Q1236	E1237	N1238	D1239	L1240	Q1241	K1242	I1243	I1246	L1247	K1248	L1249	I1250	V1251	F1252	N1253	Y1254	M1255	C1256	S1257	E1262	E1263	L1264	Y1265	T1266	T1267	I1268	S1269	L1270	E1271	F1272	K1273	G1209	F1210	I1211	Q1212	D1213	D1214	H1215	V1216	R1217	S1218	R1219	I1221	S1222	S1223	L1224	I1225	S1226	I1227	L1228	K1229	K1231	L1232	K1233	L1234	K1303					
L1176	S1177	C1178	L1179	L1180	Y1181	L1182	P1183	S1184	L1185	Y1186	V1187	L1188	L1189	S1190	D1191	S1192	N1193	S1194	I1195	S1196	T1197	F1198	L1199	M1200	L1201	L1202	V1203	S1204	I1205	T1206	E1207	I1147	K1148	P1149	I1150	I1151	E1152	A1153	A1154	D1155	S1156	I1157	I1158	P1161	V1162	M1163	D1164	L1165	H1166	Y1167	V1168	D1169	L1170	V1171	T1172	L1173	I1174	C1175			
M1115	P1116	S1117	L1118	Y1119	Q1120	F1121	L1122	Y1123	Y1124	D1125	E1126	F1127	A1128	T1131	A1132	L1133	M1134	D1135	T1136	I1137	S1138	M1139	Q1140	H1141	V1142	K1143	E1144	A1145	V1146	I1147	K1148	P1149	I1150	I1151	E1152	A1153	A1154	D1155	S1156	I1157	I1158	P1161	V1162	M1163	D1164	L1165	H1166	Y1167	V1168	D1169	L1170	V1171	T1172	L1173	I1174	C1175					
D1038	T1039	E1040	S1041	T1042	E1043	E1044	V1045	H1046	L1047	R1048	K1049	M1050	A1051	S1052	N1053	L1054	G1058	L1059	K1060	A968	S969	E970	R971	L972	D973	F977	F978	G979	N980	G983	T993	T998	G999	F1000	V1001	M1002	I1003	V1004	M1005	S1006	T1007	L1008	S1009	V1010	Y1028	S1029	I1030	F229	M1032	A1033	V1036	L1037	F1109	L1110							
S860	R861	M862	T863	D864	V865	Q866	L873	L874	A875	Y876	K877	N878	P879	T880	L881	N882	K883	Y884	R885	D886	N887	L888	K889	M890	E900	I901	F904	L905	T906	E907	N908	G909	I913	K914	A915	E918	K919	V920	V921	M922	P923	Y924	V925	L926	R927	I928	F229	F930	G931	R932	A933	Q934	V935								
A778	L779	K780	V781	M782	L783	S784	Q787	V788	F793	I796	A797	P798	F799	D803	F804	K805	T806	Y807	M813	E814	M815	E816	R817	V818	I819	T820	G821	S822	M823	T824	M829	V830	F831	L832	L835	F838	K839	M840	I841	V844	Y845	T848	D852	H853	L854	M855	V856	L857													

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

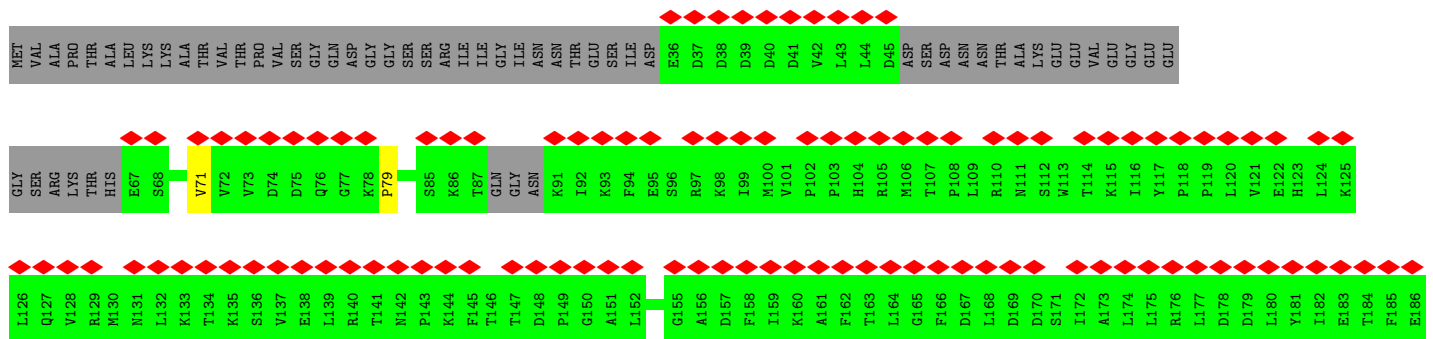
● Molecule 59: U3 small nucleolar RNA-associated protein 14

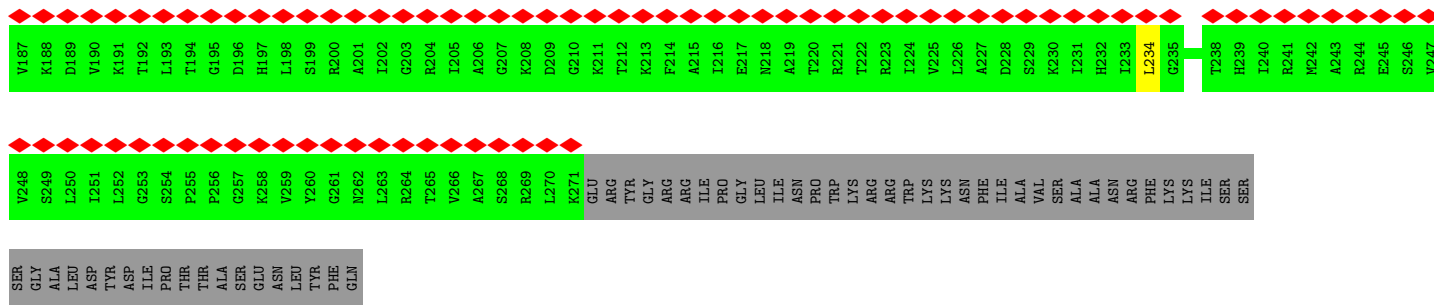


• Molecule 62: Unassigned peptides 1

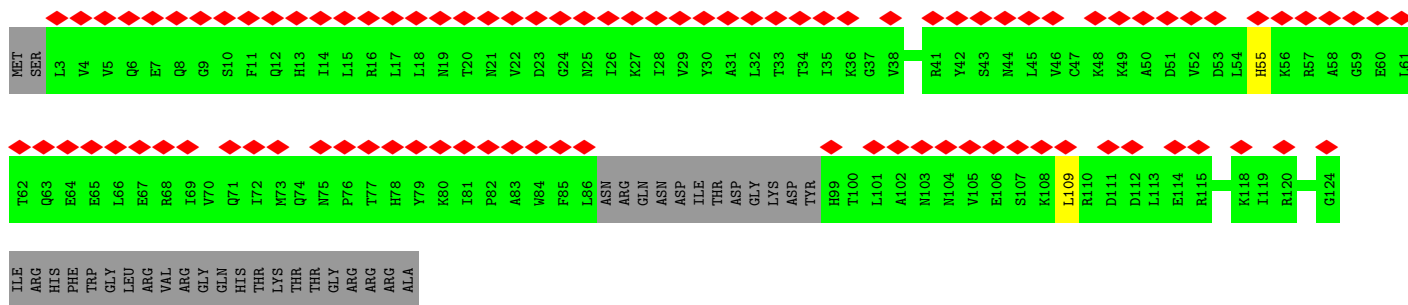
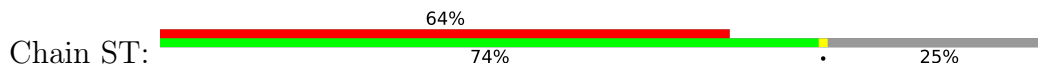


• Molecule 63: Pno1

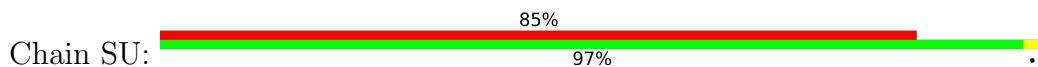




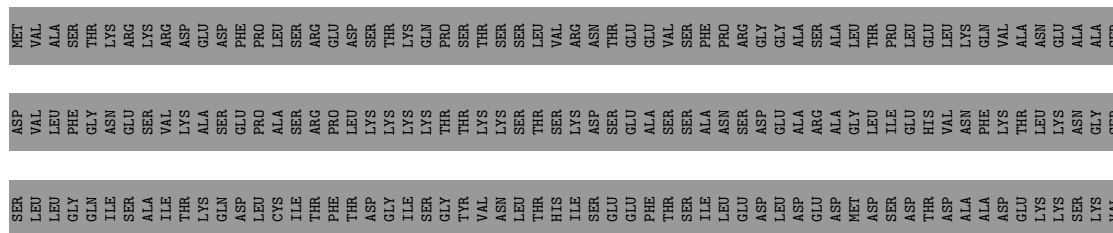
• Molecule 64: 40S ribosomal protein S18-A



• Molecule 65: 40S ribosomal protein S19-A



• Molecule 66: rRNA biogenesis protein RRP5



Y1210	Y1154	E1146	I1084	E1022	K901	E842	R781	E721	K661	M601	K541	S481
C1211	Y1155	M1147	C1086	I1023	M902	I842	S782	G722	M662	Y602	L642	T482
Y1212	Y1156	P1148	A1086	F1024	S903	L843	K783	Q723	G663	T603	H643	A483
V1213	F1088	P1149	G1087	M1025	L904	R844	E784	T724	I664	D604	K644	K484
R1214	V1089	Y1154	F1088	K1026	F905	M845	R785	A725	M665	E605	E845	E485
R1216	D1090	Y1155	D1090	K1027	P906	P846	K786	N726	S666	A606	M646	D486
F1217	H1091	S1156	H1091	M1028	S908	E848	N788	P728	T668	R608	I648	K488
G1218	V1092	L1157	V1092	F1029	P909	S849	E789	L729	T669	K609	E849	V489
S1219	A1093	H1158	A1093	L1030	R910	R850	S790	V730	D670	T610	H650	K490
V1220	V1094	L1159	V1094	G1032	F911	M851	N791	V731	L671	C611	K551	F491
V1221	R1095	G1160	R1095	S912	S912	L852	G792	L732	E672	K612	K652	M492
D1222	A1096	G1161	A1096	K913	K913	Q853	V793	F733	A673	I613	L653	T493
N1223	D1097	M1162	D1097	M1035	M914	Q854	Q794	L734	A674	H614	K654	D494
D1224	L1098	M1163	L1098	E1036	L915	K855	S795	Y735	D875	Q615	L655	G495
L1225	L1099	K1164	L1099	E1037	L916	S856	F796	S736	I676	K616	I656	V496
K1226	F1100	T1165	F1100	I1038	Y917	M857	E797	L737	D677	L617	I657	L497
I1227	P1101	R1166	P1101	I1039	S918	A858	V798	L738	F678	P618	M658	L498
G1228	D1102	M1167	D1102	K1040	D919	I859	G799	P739	S679	P619	S659	R499
P1233	A1104	M1168	A1104	R1041	E920	H860	S799	T740	V880	G620	A660	E500
I1234	K1105	T1169	K1105	K1043	K921	M861	V801	K741	Q881	A621	T661	M501
H1237	I1106	D1172	I1106	Q923	A922	I862	S802	E742	V682	I622	L662	M502
Q1238	T1107	I1173	T1107	C923	C923	I863	K303	Q743	I683	L623	R663	H503
K1239	M1108	A1174	M1108	L924	L924	M864	A804	R744	D884	V624	V664	D504
K1240	R1109	S1175	R1109	P925	P925	F865	S805	M745	Q885	F625	S665	F505
Q1241	I1110	T1176	I1110	Y926	Y926	P866	A806	V746	D886	L626	D666	K506
K1242	S1111	L1177	S1111	I927	I927	F867	N807	F747	K887	T627	F667	L507
W1245	I1112	L1178	I1112	V928	V928	P868	Q808	Q748	F888	G628	S668	T508
T1246	I1113	A1179	I1113	A929	A929	R869	R809	K749	K889	Q629	E669	K509
V1247	I1114	M1180	V1247	R930	R930	P870	S810	P750	S690	Q630	N670	Y510
I1248	Y1117	I1181	Y1117	Y931	Y931	P871	G811	P751	A691	E631	K571	S511
K1249	V1120	A1182	V1120	S932	S932	D872	R812	Q752	I692	I632	T672	S512
F1250	L1121	K1183	L1121	A933	A933	R873	A813	G753	R693	T633	L673	I513
I1251	L1122	K1184	L1122	L934	L934	V874	G814	S754	R694	H634	F574	I514
I1252	F1126	G1185	F1126	S935	S935	A875	R815	R755	E895	M635	P675	I515
R1253	E1129	L1186	E1129	V936	V936	L876	T816	L756	E996	V636	I676	D516
LYS	R1253	L1187	LYS	G937	G937	S877	G817	C757	ASP	K637	A677	E517
GLY	T1189	L1188	GLY	D938	D938	K878	P818	I758	GLU	R638	P678	A518
PHE	P1126	T1189	PHE	P939	P939	A879	G819	V759	GLY	L639	P679	H519
GLN	P1126	T1125	GLN	F940	F940	R880	R820	A760	ASN	R640	P680	E520
THR	S1191	P1126	THR	R1005	R1005	Q881	C821	T761	GLY	K641	L681	R521
ILE	K1192	I1128	ILE	L1006	L1006	L882	Y822	M762	ASN	E642	Q882	R522
THR	P1193	E1129	THR	N942	N942	L883	R823	V763	GLY	F643	V683	I523
GLY	D1194	L1067	GLY	E943	E943	Q884	L824	A764	GLU	P644	N684	N524
GLU	C1131	K1068	GLU	F944	F944	Y885	Y825	E765	GLU	F645	A685	T525
LYS	F1132	S1069	LYS	V1009	V1009	L886	S826	T766	ASP	K646	R686	T526
GLY	D1070	D1012	GLY	G947	G947	Q887	S827	S767	GLU	K647	Q687	I527
LYS	V1133	M1013	LYS	I1071	I1071	A888	A828	L768	ASP	F688	R688	L528
LYS	V1134	D1014	LYS	D1014	D1014	L889	V829	T769	GLU	S649	P689	L529
LYS	I1135	P1072	LYS	I1015	I1015	D890	F830	I770	ILE	K650	V689	G530
LYS	H1136	S1073	LYS	V1016	V1016	M891	E831	P771	ARG	G651	S691	M531
LYS	H1136	V1074	LYS	I1075	I1075	K892	H832	G772	THR	I652	I692	L532
LYS	P1137	Q1076	LYS	Q1076	Q1076	K1018	D833	V773	PRO	K653	H693	S533
LYS	T1138	I1077	LYS	K1018	K1018	M894	F834	R774	ASN	D654	F694	R534
LYS	S1139	I1077	LYS	E1019	E1019	I895	E835	V775	THR	L655	N695	C535
LYS	M1203	I1140	LYS	Q1020	Q1020	T896	Q836	V776	GLY	V656	R696	V536
LYS	L1204	L1141	LYS	K1021	K1021	E897	F837	V777	ASN	T657	R697	R537
LYS	L1142	L1141	LYS	M1021	M1021	D898	S838	D778	ASP	P658	T698	L538
LYS	S1205	L1144	LYS	Q1082	Q1082	G899	S839	G780	GLU	V659	A699	R539
LYS	T1207	L1144	LYS	M1083	M1083				ASP	F600		A540

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3841	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	531.19995, 531.19995, 531.19995	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3279998, 1.3279998, 1.3279998	Depositor

5 Model quality i

5.1 Standard geometry i

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

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	3A	0.91	0/4141	1.25	39/6433 (0.6%)
2	5A	0.80	0/4605	1.08	13/7168 (0.2%)
3	SA	0.70	3/31727 (0.0%)	1.17	255/49393 (0.5%)
4	SC	0.47	0/1856	0.73	5/2490 (0.2%)
5	SF	0.35	0/1854	0.66	1/2504 (0.0%)
6	SG	0.53	0/1690	0.64	0/2285
7	SH	0.31	0/1341	0.60	0/1789
8	SI	0.38	0/1341	0.67	1/1806 (0.1%)
9	SJ	0.31	0/1347	0.59	1/1801 (0.1%)
10	SK	0.47	0/1410	0.60	0/1888
11	SM	0.31	0/1020	0.58	0/1374
12	SO	0.45	0/1109	0.62	0/1495
13	SP	0.49	0/879	0.69	0/1186
14	SR	0.58	0/990	0.73	1/1335 (0.1%)
15	SX	0.51	0/1020	0.65	1/1371 (0.1%)
16	SY	0.55	0/798	0.67	1/1065 (0.1%)
17	SZ	0.43	0/822	0.64	0/1103
18	Sc	0.44	0/613	0.65	0/828
19	Sd	0.54	0/499	0.66	0/670
20	3B	0.59	0/1901	0.66	1/2567 (0.0%)
20	3C	0.44	0/1796	0.62	1/2424 (0.0%)
21	3D	0.44	0/2891	0.63	3/3895 (0.1%)
22	3E	0.41	0/3059	0.62	3/4153 (0.1%)
23	3F	0.42	0/3715	0.64	2/5001 (0.0%)
24	3G	0.52	0/928	0.76	1/1262 (0.1%)
24	3H	0.47	0/928	0.69	2/1262 (0.2%)
25	A4	0.47	0/5321	0.66	5/7207 (0.1%)
26	A5	0.48	0/4044	0.68	5/5493 (0.1%)
27	A8	0.34	0/3249	0.71	10/4454 (0.2%)
28	A9	0.31	0/951	0.58	1/1287 (0.1%)
29	AE	0.37	0/10049	0.56	6/13737 (0.0%)
30	AF	0.53	0/3993	0.67	4/5413 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AG	0.47	0/6699	0.65	3/9077 (0.0%)
32	B1	0.64	0/6474	0.68	7/8763 (0.1%)
33	B2	0.43	0/6628	0.67	3/8954 (0.0%)
34	B3	0.39	0/6014	0.69	7/8137 (0.1%)
35	B8	0.58	0/3848	0.66	4/5218 (0.1%)
36	BE	0.58	0/6580	0.66	7/8901 (0.1%)
37	B6	0.45	0/2849	0.58	1/3853 (0.0%)
38	5B	0.34	0/499	0.62	0/659
39	5C	0.61	0/3690	0.69	5/4991 (0.1%)
40	5D	0.51	0/1417	0.67	2/1885 (0.1%)
41	5E	0.38	0/1580	0.74	3/2115 (0.1%)
42	5F	0.38	0/1559	0.69	1/2097 (0.0%)
43	5G	0.39	0/1792	0.72	2/2425 (0.1%)
44	5H	0.52	0/601	0.57	0/789
45	5I	0.61	0/3844	0.66	2/5174 (0.0%)
46	5J	0.41	0/1151	0.54	0/1535
47	5K	0.57	0/1426	0.67	1/1917 (0.1%)
48	RA	0.34	0/2769	0.67	1/3753 (0.0%)
49	RB	0.38	0/1121	0.62	0/1487
50	RE	0.38	0/8924	0.63	8/12070 (0.1%)
51	RF	0.34	0/2004	0.63	2/2697 (0.1%)
52	RG	0.39	0/1727	0.68	2/2329 (0.1%)
52	RH	0.42	0/1828	0.61	0/2470
53	RJ	0.50	0/6514	0.61	1/8768 (0.0%)
54	RK	0.44	0/2832	0.65	3/3825 (0.1%)
55	RL	0.29	0/4549	0.50	0/6241
55	RM	0.25	0/3765	0.47	0/5218
56	RN	0.36	0/4591	0.58	2/6187 (0.0%)
57	RO	0.38	0/3849	0.62	4/5261 (0.1%)
58	RP	0.28	0/12225	0.51	5/16812 (0.0%)
59	RQ	0.46	0/1879	0.62	1/2564 (0.0%)
60	RS	0.33	0/2104	0.67	2/2854 (0.1%)
61	RY	0.29	0/307	0.51	0/415
63	RT	0.42	0/1611	0.69	1/2174 (0.0%)
64	ST	0.37	0/908	0.67	1/1221 (0.1%)
65	SU	0.49	1/1130 (0.1%)	0.65	0/1517
66	RD	0.31	0/2453	0.63	3/3308 (0.1%)
67	RZ	0.32	0/6737	0.58	1/9099 (0.0%)
All	All	0.50	4/232365 (0.0%)	0.77	447/322899 (0.1%)

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

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
12	SO	0	1
13	SP	0	1
17	SZ	0	1
18	Sc	0	1
21	3D	0	3
22	3E	0	1
23	3F	0	1
24	3G	0	2
24	3H	0	1
25	A4	0	1
26	A5	0	1
27	A8	0	2
31	AG	0	2
32	B1	0	2
33	B2	0	8
34	B3	0	11
36	BE	0	1
39	5C	0	1
40	5D	0	1
43	5G	0	2
45	5I	0	2
48	RA	0	2
49	RB	0	1
50	RE	0	1
51	RF	0	1
53	RJ	0	2
54	RK	0	1
55	RL	0	1
55	RM	0	1
56	RN	0	1
57	RO	0	1
58	RP	0	3
59	RQ	0	4
67	RZ	0	2
All	All	0	75

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	SU	46	PRO	C-N	8.58	1.50	1.34
3	SA	1572	G	O3'-P	-6.56	1.53	1.61
3	SA	1538	U	O3'-P	-5.78	1.54	1.61
3	SA	1541	G	O3'-P	5.54	1.67	1.61

The worst 5 of 447 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3A	321	C	N1-C1'-C2'	-10.83	99.92	114.00
3	SA	861	U	C2-N1-C1'	10.61	130.44	117.70
3	SA	376	C	N1-C2-O2	10.38	125.13	118.90
3	SA	1174	C	N1-C2-O2	10.36	125.12	118.90
3	SA	1034	C	C5-C6-N1	10.05	126.02	121.00

There are no chirality outliers.

5 of 75 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	238	GLU	Peptide
5	SF	193	GLY	Peptide
5	SF	195	ILE	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	34	72
6	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
7	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
8	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
9	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/155 (77%)	103 (87%)	16 (13%)	0	100	100
12	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
13	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	17	57
14	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
15	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
16	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
17	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	15	55
18	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100
19	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
20	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
20	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
21	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
22	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
23	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	47	81
24	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	19	60
24	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
25	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
26	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
27	A8	516/713 (72%)	397 (77%)	107 (21%)	12 (2%)	6	34
28	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
29	AE	1496/1769 (85%)	1367 (91%)	129 (9%)	0	100	100
30	AF	489/513 (95%)	443 (91%)	46 (9%)	0	100	100
31	AG	812/896 (91%)	732 (90%)	79 (10%)	1 (0%)	51	86
32	B1	787/900 (87%)	732 (93%)	55 (7%)	0	100	100
33	B2	813/943 (86%)	723 (89%)	88 (11%)	2 (0%)	47	81

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	B3	733/817 (90%)	605 (82%)	126 (17%)	2 (0%)	41	77
35	B8	469/594 (79%)	440 (94%)	29 (6%)	0	100	100
36	BE	814/939 (87%)	764 (94%)	50 (6%)	0	100	100
37	B6	368/440 (84%)	342 (93%)	26 (7%)	0	100	100
38	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
39	5C	452/554 (82%)	419 (93%)	32 (7%)	1 (0%)	47	81
40	5D	165/250 (66%)	146 (88%)	19 (12%)	0	100	100
41	5E	187/593 (32%)	175 (94%)	10 (5%)	2 (1%)	14	52
42	5F	180/183 (98%)	164 (91%)	16 (9%)	0	100	100
43	5G	217/290 (75%)	203 (94%)	14 (6%)	0	100	100
44	5H	72/610 (12%)	65 (90%)	7 (10%)	0	100	100
45	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
46	5J	130/217 (60%)	121 (93%)	9 (7%)	0	100	100
47	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
48	RA	332/707 (47%)	276 (83%)	56 (17%)	0	100	100
49	RB	132/357 (37%)	117 (89%)	14 (11%)	1 (1%)	19	60
50	RE	1067/1237 (86%)	998 (94%)	69 (6%)	0	100	100
51	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
52	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
52	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
53	RJ	784/1183 (66%)	722 (92%)	61 (8%)	1 (0%)	51	86
54	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
55	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	41	77
55	RM	738/1056 (70%)	626 (85%)	108 (15%)	4 (0%)	29	69
56	RN	593/810 (73%)	546 (92%)	46 (8%)	1 (0%)	47	81
57	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
58	RP	2042/2493 (82%)	1816 (89%)	226 (11%)	0	100	100
59	RQ	267/899 (30%)	227 (85%)	40 (15%)	0	100	100
60	RS	247/480 (52%)	225 (91%)	22 (9%)	0	100	100
61	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
63	RT	206/326 (63%)	178 (86%)	27 (13%)	1 (0%)	29	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	ST	106/146 (73%)	89 (84%)	17 (16%)	0	100	100
65	SU	141/144 (98%)	124 (88%)	16 (11%)	1 (1%)	22	63
66	RD	310/1729 (18%)	284 (92%)	23 (7%)	3 (1%)	15	55
67	RZ	834/1267 (66%)	739 (89%)	91 (11%)	4 (0%)	29	69
All	All	25032/35454 (71%)	22530 (90%)	2459 (10%)	43 (0%)	50	81

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	A8	258	PRO
27	A8	309	PRO
27	A8	325	PRO
27	A8	390	PRO
27	A8	392	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	SC	203/224 (91%)	201 (99%)	2 (1%)	76	86
5	SF	196/222 (88%)	190 (97%)	6 (3%)	40	62
6	SG	180/191 (94%)	180 (100%)	0	100	100
7	SH	139/201 (69%)	137 (99%)	2 (1%)	67	80
8	SI	146/170 (86%)	145 (99%)	1 (1%)	84	90
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	65	80
10	SK	147/166 (89%)	146 (99%)	1 (1%)	84	90
11	SM	110/136 (81%)	108 (98%)	2 (2%)	59	77
12	SO	117/128 (91%)	116 (99%)	1 (1%)	78	87
13	SP	90/105 (86%)	89 (99%)	1 (1%)	73	84
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	107 (99%)	1 (1%)	78	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	SY	85/120 (71%)	84 (99%)	1 (1%)	71	83
17	SZ	85/113 (75%)	85 (100%)	0	100	100
18	Sc	69/71 (97%)	69 (100%)	0	100	100
19	Sd	56/60 (93%)	56 (100%)	0	100	100
20	3B	201/240 (84%)	201 (100%)	0	100	100
20	3C	190/240 (79%)	187 (98%)	3 (2%)	62	79
21	3D	296/435 (68%)	293 (99%)	3 (1%)	76	86
22	3E	262/433 (60%)	261 (100%)	1 (0%)	91	94
23	3F	396/503 (79%)	394 (100%)	2 (0%)	88	93
24	3G	100/104 (96%)	100 (100%)	0	100	100
24	3H	100/104 (96%)	100 (100%)	0	100	100
25	A4	591/713 (83%)	584 (99%)	7 (1%)	71	83
26	A5	433/574 (75%)	432 (100%)	1 (0%)	93	96
27	A8	174/657 (26%)	164 (94%)	10 (6%)	20	45
28	A9	89/533 (17%)	88 (99%)	1 (1%)	73	84
29	AE	708/1633 (43%)	705 (100%)	3 (0%)	91	94
30	AF	437/454 (96%)	433 (99%)	4 (1%)	78	87
31	AG	750/826 (91%)	740 (99%)	10 (1%)	69	81
32	B1	696/789 (88%)	691 (99%)	5 (1%)	84	90
33	B2	712/832 (86%)	707 (99%)	5 (1%)	84	90
34	B3	665/719 (92%)	655 (98%)	10 (2%)	65	80
35	B8	421/529 (80%)	420 (100%)	1 (0%)	93	96
36	BE	718/819 (88%)	714 (99%)	4 (1%)	86	92
37	B6	251/414 (61%)	247 (98%)	4 (2%)	62	79
38	5B	57/196 (29%)	55 (96%)	2 (4%)	36	59
39	5C	394/480 (82%)	392 (100%)	2 (0%)	88	93
40	5D	156/234 (67%)	154 (99%)	2 (1%)	69	81
41	5E	175/535 (33%)	162 (93%)	13 (7%)	13	38
42	5F	171/172 (99%)	169 (99%)	2 (1%)	71	83
43	5G	194/258 (75%)	190 (98%)	4 (2%)	53	72
44	5H	63/538 (12%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	5I	416/443 (94%)	414 (100%)	2 (0%)	88	93
46	5J	125/200 (62%)	125 (100%)	0	100	100
47	5K	157/169 (93%)	157 (100%)	0	100	100
48	RA	303/636 (48%)	300 (99%)	3 (1%)	76	86
49	RB	117/315 (37%)	114 (97%)	3 (3%)	46	66
50	RE	984/1125 (88%)	975 (99%)	9 (1%)	78	87
51	RF	221/274 (81%)	219 (99%)	2 (1%)	78	87
52	RG	195/222 (88%)	193 (99%)	2 (1%)	76	86
52	RH	206/222 (93%)	204 (99%)	2 (1%)	76	86
53	RJ	683/1039 (66%)	676 (99%)	7 (1%)	76	86
54	RK	307/312 (98%)	303 (99%)	4 (1%)	69	81
55	RL	164/934 (18%)	162 (99%)	2 (1%)	71	83
56	RN	422/732 (58%)	421 (100%)	1 (0%)	93	96
57	RO	329/506 (65%)	328 (100%)	1 (0%)	92	95
58	RP	499/2307 (22%)	493 (99%)	6 (1%)	71	83
59	RQ	136/808 (17%)	133 (98%)	3 (2%)	52	71
60	RS	225/421 (53%)	225 (100%)	0	100	100
61	RY	31/482 (6%)	30 (97%)	1 (3%)	39	61
63	RT	158/282 (56%)	157 (99%)	1 (1%)	86	92
64	ST	98/129 (76%)	97 (99%)	1 (1%)	76	86
65	SU	115/116 (99%)	114 (99%)	1 (1%)	78	87
66	RD	226/1544 (15%)	220 (97%)	6 (3%)	44	65
67	RZ	718/1140 (63%)	713 (99%)	5 (1%)	84	90
All	All	18207/30620 (60%)	18026 (99%)	181 (1%)	77	86

5 of 181 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	5G	211	ASN
53	RJ	566	ARG
45	5I	250	ARG
50	RE	742	PHE
54	RK	214	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 305 such sidechains are listed below:

Mol	Chain	Res	Type
50	RE	872	ASN
58	RP	1802	HIS
50	RE	1194	HIS
54	RK	334	ASN
67	RZ	385	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	55 (32%)	8 (4%)
2	5A	186/700 (26%)	54 (29%)	4 (2%)
3	SA	1310/1812 (72%)	499 (38%)	32 (2%)
All	All	1665/2845 (58%)	608 (36%)	44 (2%)

5 of 608 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	14	A
1	3A	15	U
1	3A	24	U
1	3A	25	U

5 of 44 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	1475	A
3	SA	1533	C
3	SA	1486	G
3	SA	1521	G
3	SA	1540	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
69	GTP	RJ	1201	70	26,34,34	0.94	2 (7%)	32,54,54	0.92	0
71	ADP	RZ	1301	-	24,29,29	0.95	1 (4%)	29,45,45	1.37	4 (13%)

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
69	GTP	RJ	1201	70	-	3/18/38/38	0/3/3/3
71	ADP	RZ	1301	-	-	4/12/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
69	RJ	1201	GTP	C5-C6	-2.50	1.42	1.47
71	RZ	1301	ADP	C5-C4	2.43	1.47	1.40
69	RJ	1201	GTP	C8-N7	-2.03	1.31	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
71	RZ	1301	ADP	N3-C2-N1	-3.42	123.33	128.68
71	RZ	1301	ADP	C3'-C2'-C1'	3.02	105.53	100.98
71	RZ	1301	ADP	C4-C5-N7	-2.90	106.37	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
71	RZ	1301	ADP	PA-O3A-PB	-2.26	125.09	132.83

There are no chirality outliers.

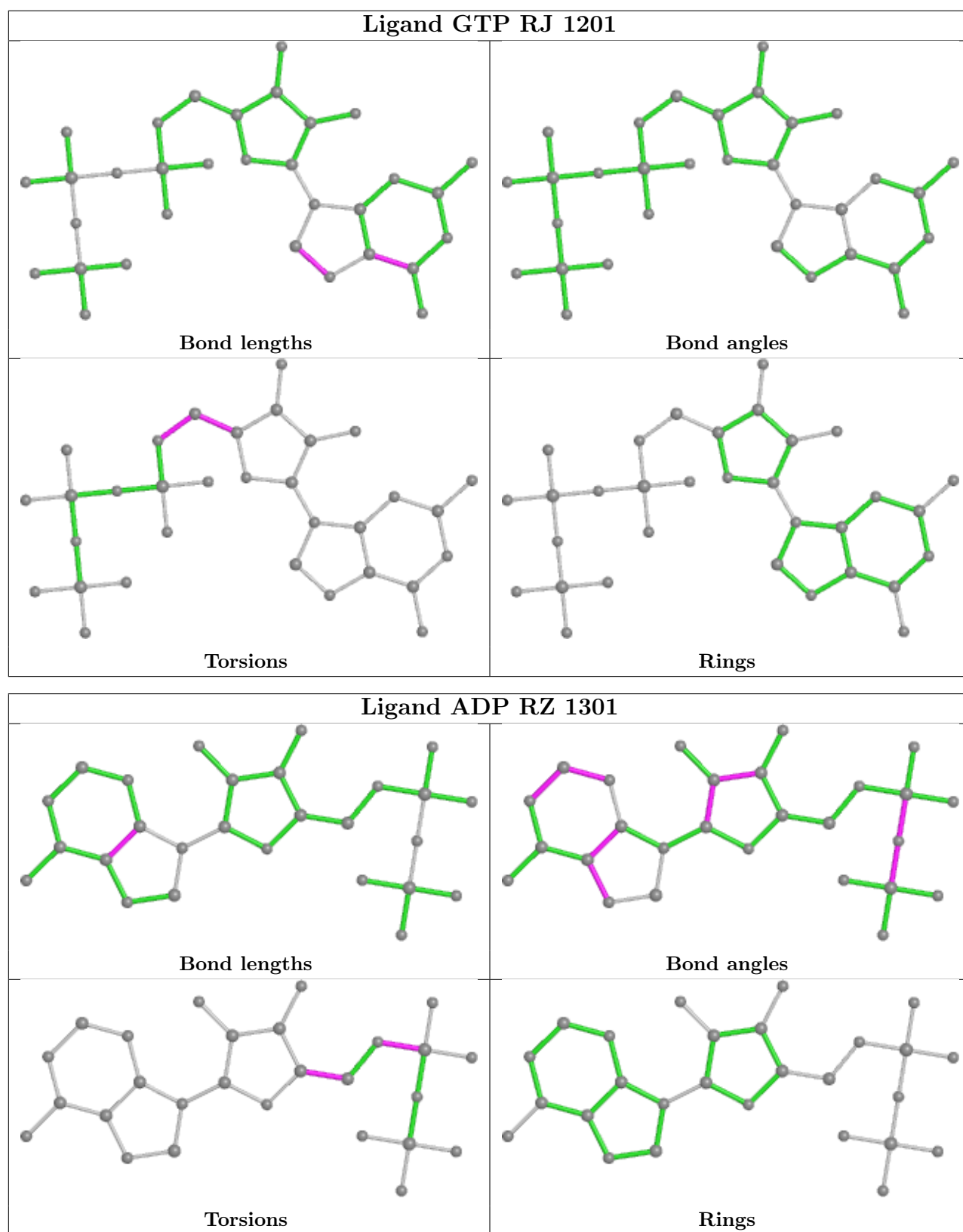
5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
71	RZ	1301	ADP	C5'-O5'-PA-O2A
71	RZ	1301	ADP	C5'-O5'-PA-O3A
69	RJ	1201	GTP	O4'-C4'-C5'-O5'
69	RJ	1201	GTP	C3'-C4'-C5'-O5'
69	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

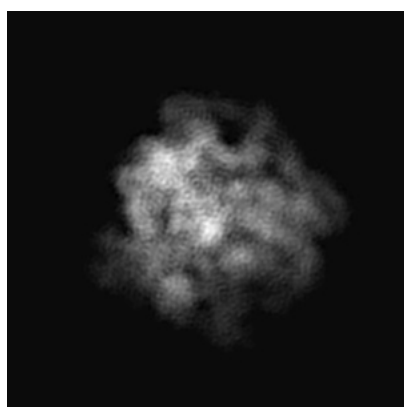
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30588. These allow visual inspection of the internal detail of the map and identification of artifacts.

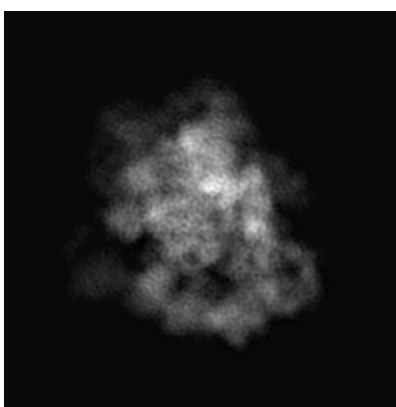
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

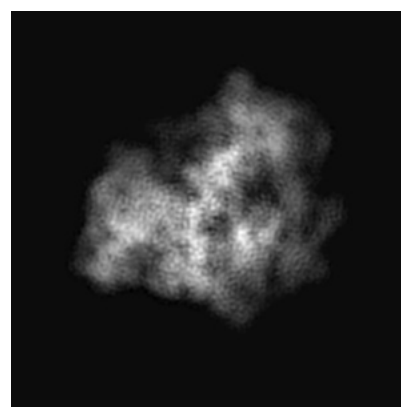
6.1.1 Primary map



X



Y

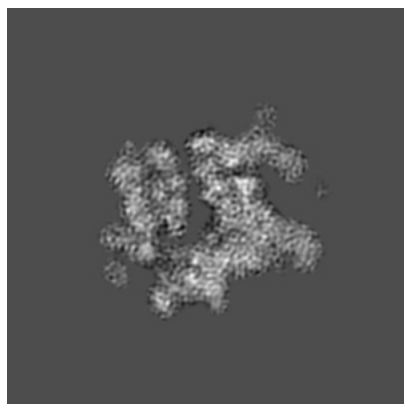


Z

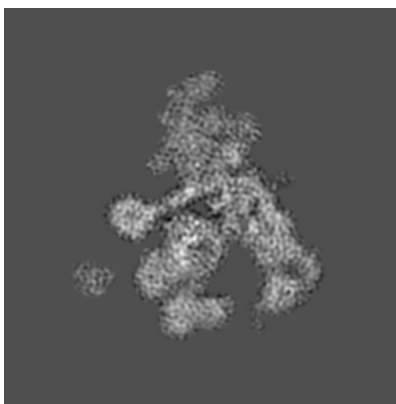
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

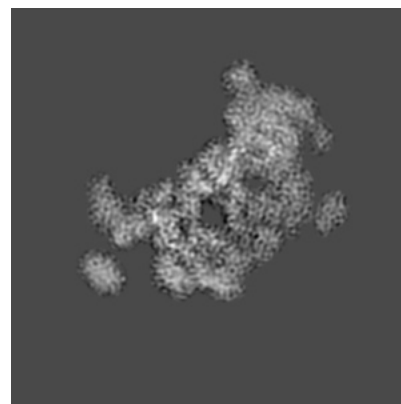
6.2.1 Primary map



X Index: 200



Y Index: 200

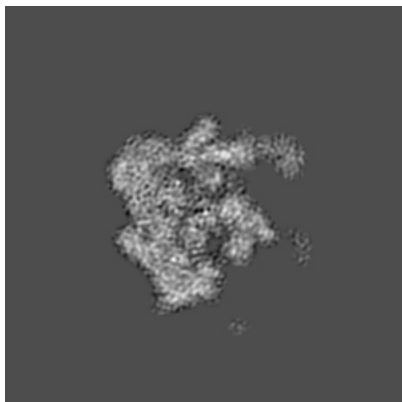


Z Index: 200

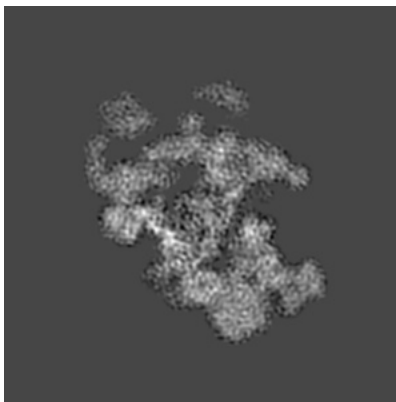
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

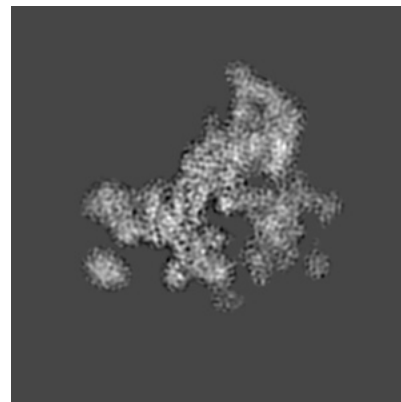
6.3.1 Primary map



X Index: 185



Y Index: 174



Z Index: 185

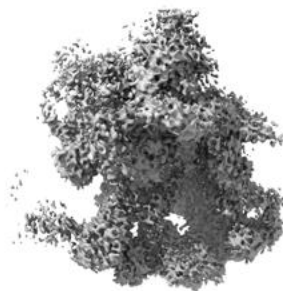
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

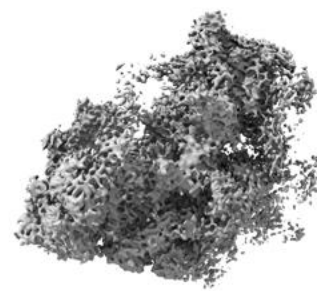
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

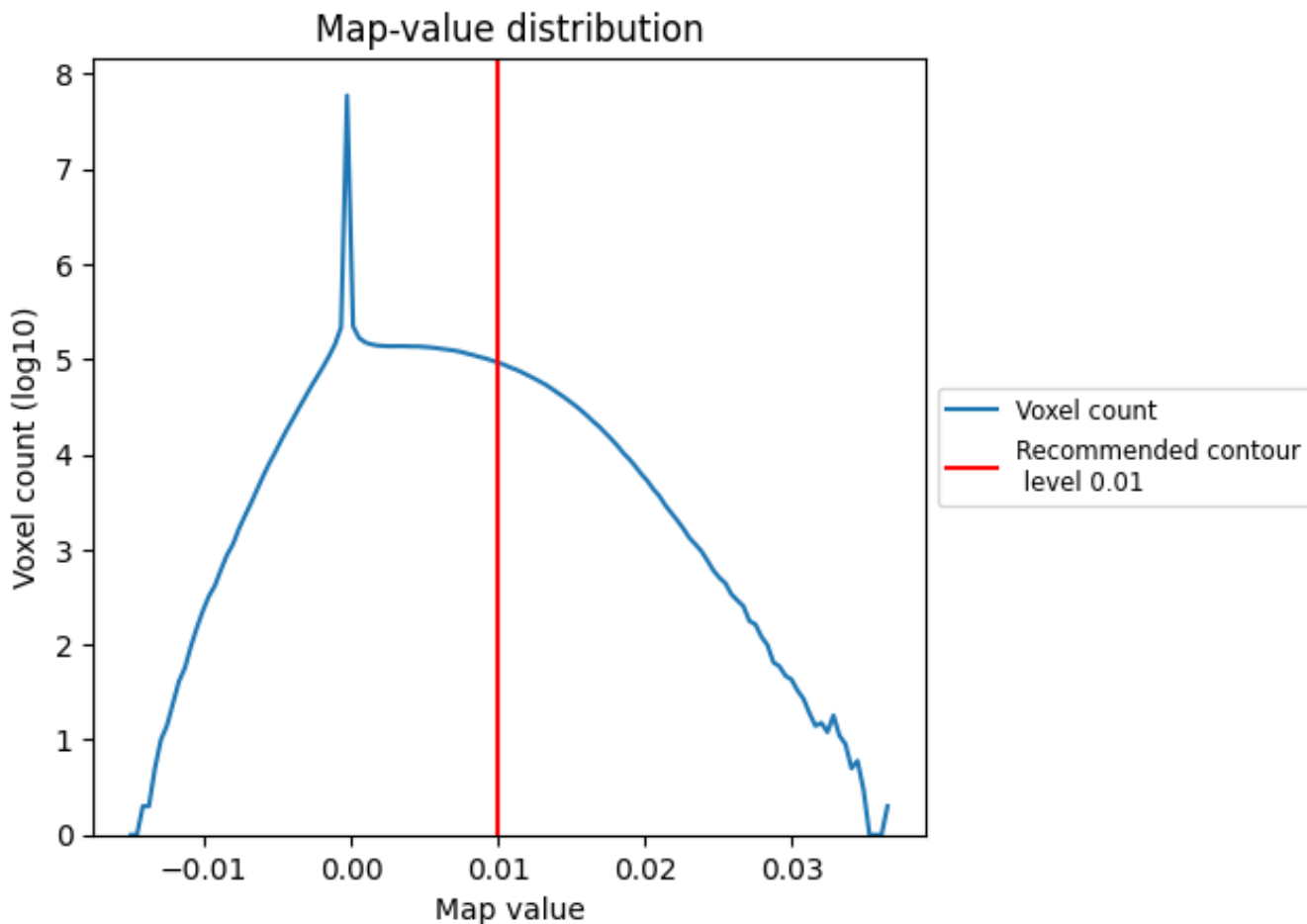
6.5 Mask visualisation

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

7 Map analysis [i](#)

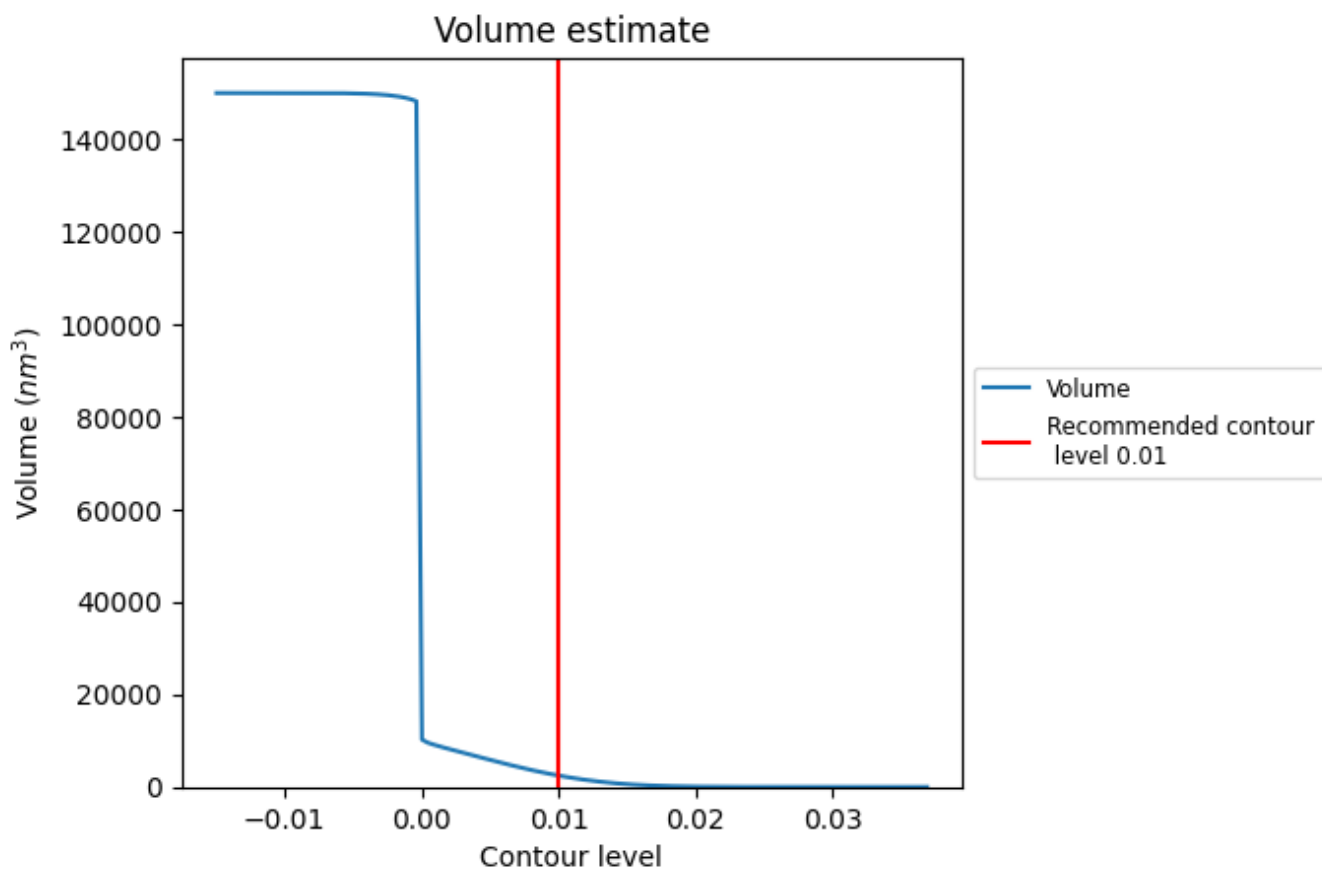
This section contains the results of statistical analysis of the map.

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.

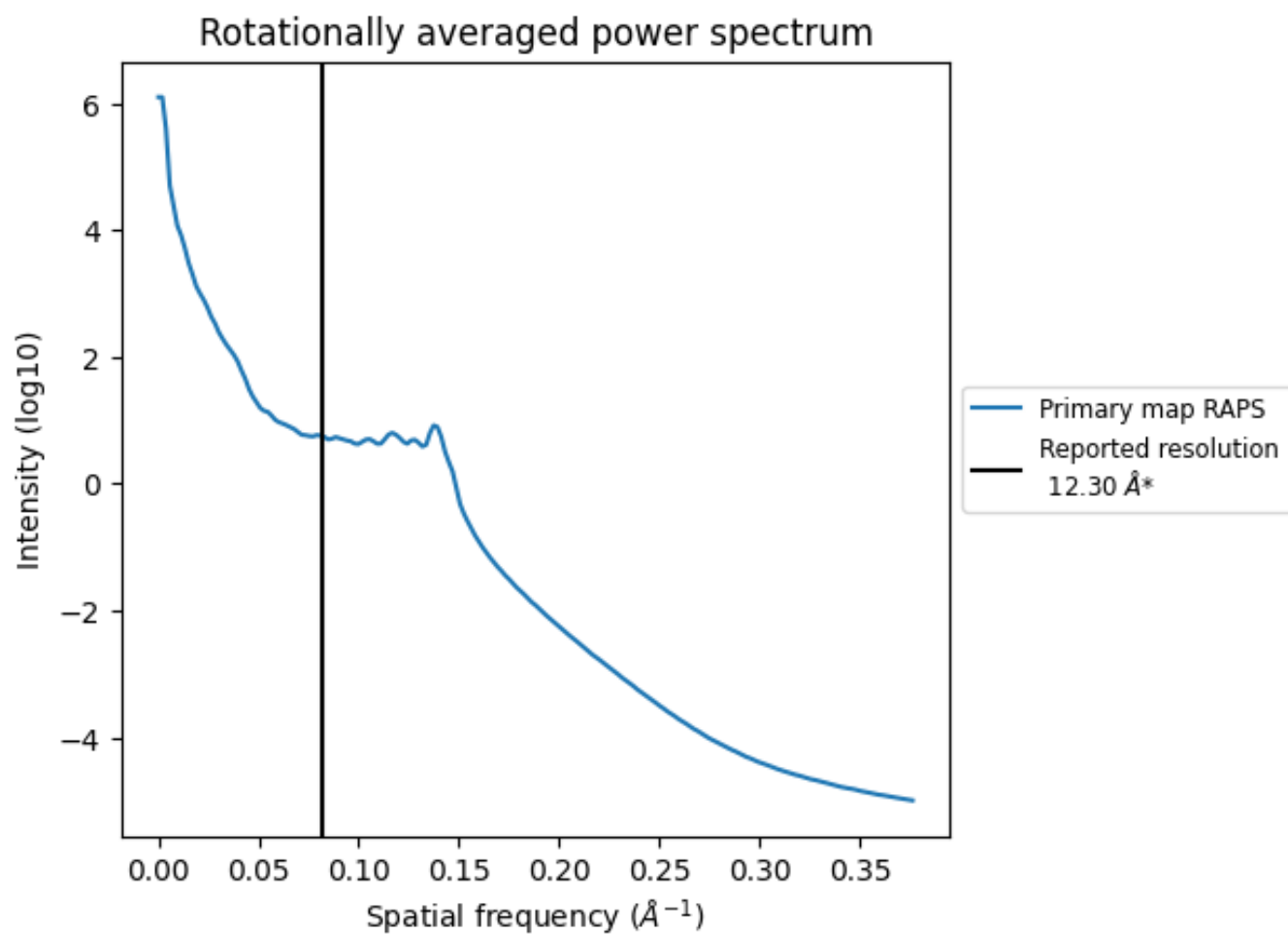
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2465 nm³; this corresponds to an approximate mass of 2227 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.081 Å⁻¹

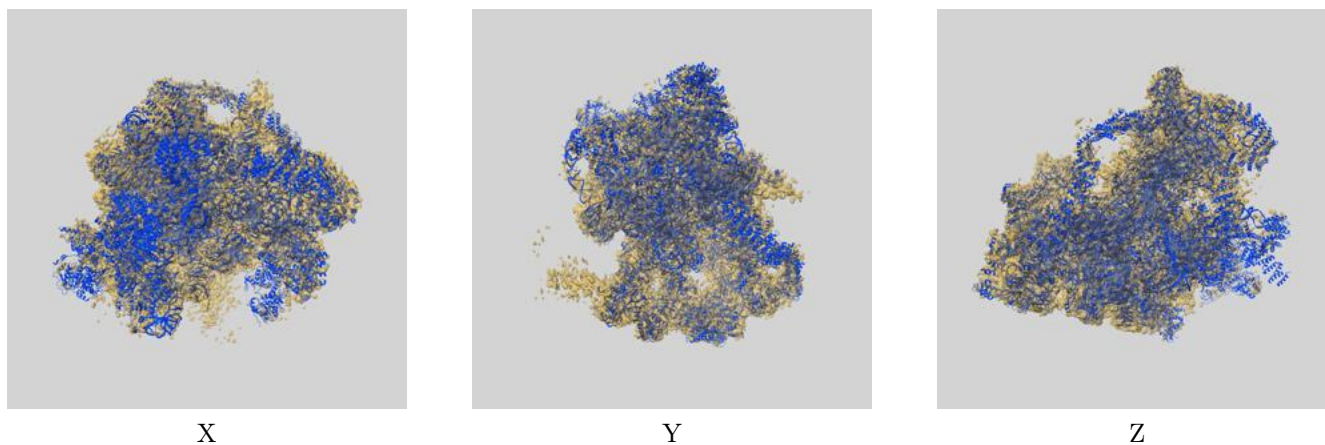
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

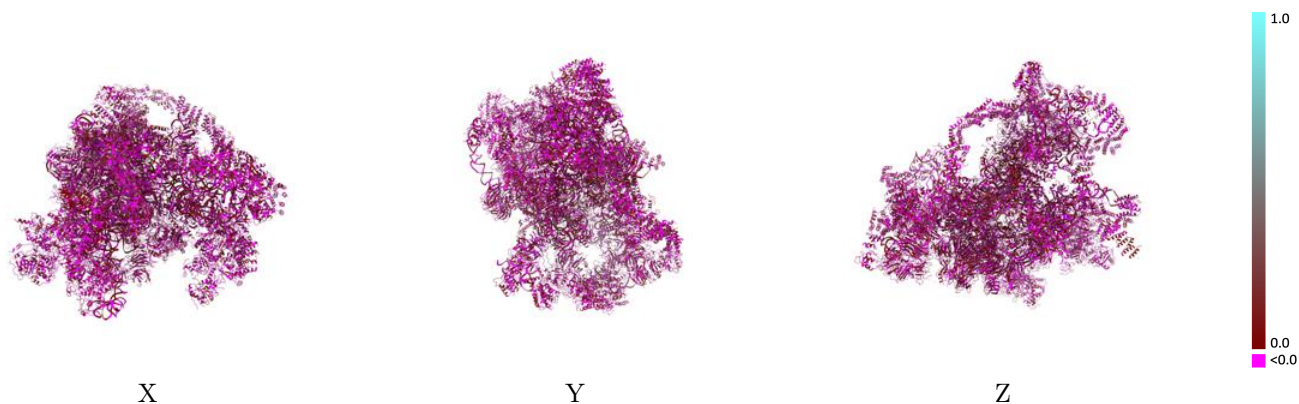
This section contains information regarding the fit between EMDB map EMD-30588 and PDB model 7D63. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



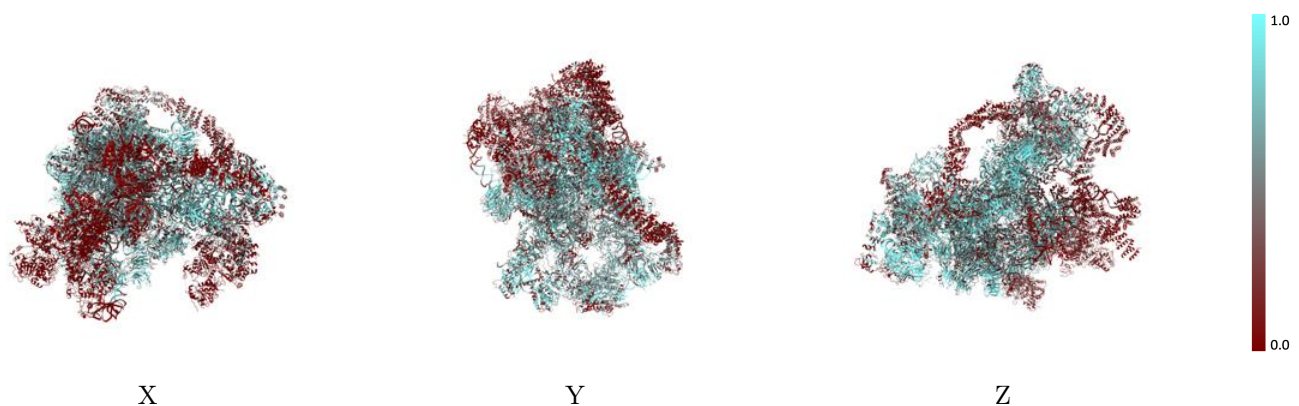
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



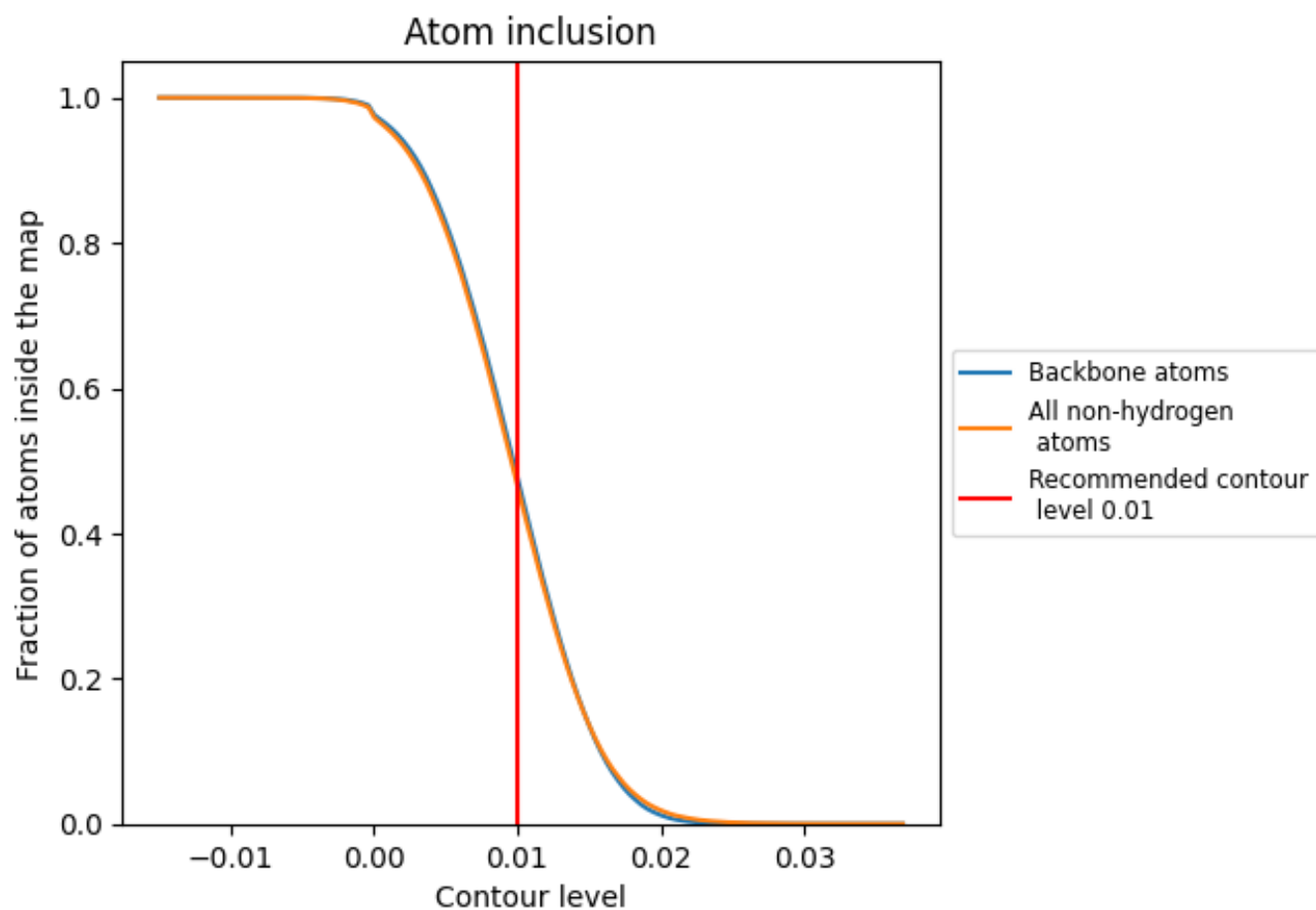
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 47% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary











































































The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4663	 0.0430
3A	 0.7300	 0.0750
3B	 0.4846	 0.0720
3C	 0.5047	 0.0300
3D	 0.6483	 0.0740
3E	 0.5398	 0.0530
3F	 0.6800	 0.0520
3G	 0.7002	 0.0700
3H	 0.5476	 0.0570
5A	 0.4617	 0.0410
5B	 0.1729	 0.0220
5C	 0.5190	 0.0420
5D	 0.3622	 0.0510
5E	 0.4859	 0.0690
5F	 0.4842	 0.0750
5G	 0.4939	 0.0710
5H	 0.5398	 0.0360
5I	 0.6095	 0.0490
5J	 0.3962	 0.0810
5K	 0.3806	 0.0530
A4	 0.6796	 0.0470
A5	 0.6300	 0.0460
A8	 0.5599	 0.0260
A9	 0.6911	 0.0700
AE	 0.3060	 0.0360
AF	 0.6458	 0.0650
AG	 0.7177	 0.0530
B1	 0.6051	 0.0590
B2	 0.7074	 0.0560
B3	 0.5319	 0.0300
B6	 0.4546	 0.0650
B8	 0.5905	 0.0510
BE	 0.6955	 0.0560
RA	 0.3732	 0.0180
RB	 0.3330	 0.0360



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Chain	Atom inclusion	Q-score
RD	 0.0004	 -0.0180
RE	 0.0598	 0.0080
RF	 0.0433	 0.0160
RG	 0.6276	 0.0530
RH	 0.4675	 0.0300
RJ	 0.5959	 0.0590
RK	 0.6341	 0.0620
RL	 0.2219	 0.0320
RM	 0.0712	 0.0130
RN	 0.4697	 0.0370
RO	 0.4465	 0.0330
RP	 0.2622	 0.0280
RQ	 0.2178	 0.0110
RS	 0.6409	 0.0240
RT	 0.0868	 -0.0040
RY	 0.1741	 -0.0020
RZ	 0.0696	 0.0220
SA	 0.5941	 0.0540
SC	 0.1118	 0.0220
SF	 0.5138	 0.0200
SG	 0.6419	 0.0910
SH	 0.4744	 0.0360
SI	 0.1106	 0.0190
SJ	 0.5737	 0.0260
SK	 0.5503	 0.0880
SM	 0.5310	 -0.0050
SO	 0.1892	 0.0210
SP	 0.1962	 0.0140
SR	 0.5556	 0.0800
ST	 0.1510	 0.0370
SU	 0.1314	 0.0350
SX	 0.1589	 0.0140
SY	 0.5432	 0.0730
SZ	 0.5909	 0.0530
Sc	 0.1361	 0.0130
Sd	 0.6436	 0.0760
X1	 0.2727	 0.0560