wwPDB EM Validation Summary Report

May 20, 2024 – 02:08 AM 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:

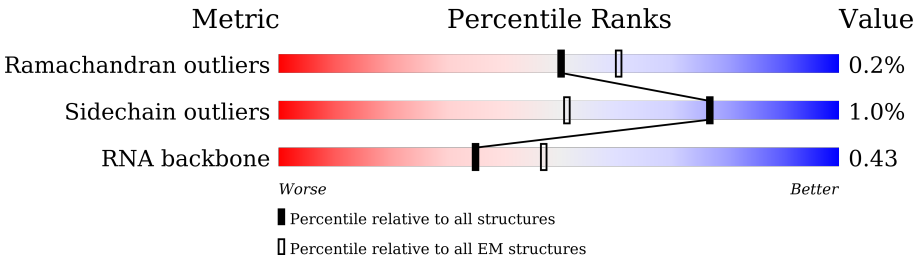
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 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 <=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	8% 34% 15% • 47%
2	5A	700	13% 19% 7% • 73%
3	SA	1812	23% 42% 28% • 27%
4	SC	255	80% 87% • 10%
5	SF	261	37% 84% • 12%
6	SG	225	22% 95% 5%
7	SH	236	32% 70% • 29%
8	SI	190	77% 84% • 13%

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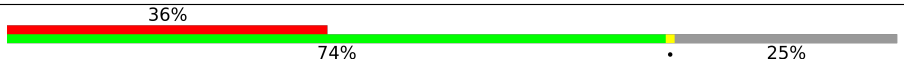
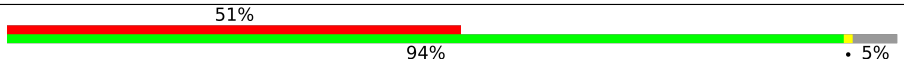
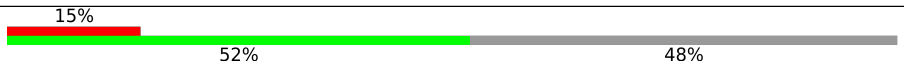
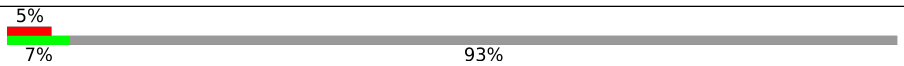
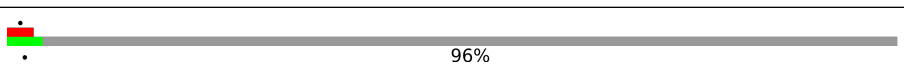
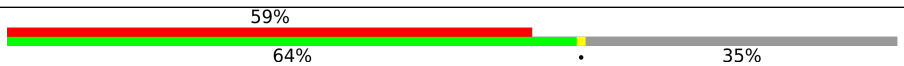
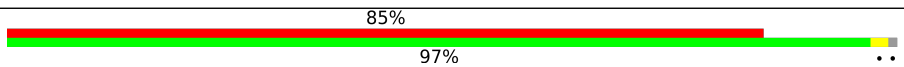
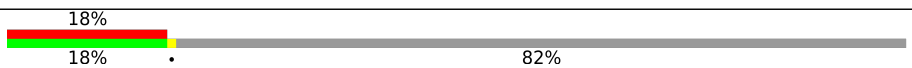
Mol	Chain	Length	Quality of chain
55	RM	1056	
56	RN	810	
57	RO	552	
58	RP	2493	
59	RQ	899	
60	RS	480	
61	RY	534	
62	X1	611	
63	RT	326	
64	ST	146	
65	SU	144	
66	RD	1729	
67	RZ	1267	

2 Entry composition (i)

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
7	SH	167	Total	C	N	O	S	0	0
			1327	834	256	235	2		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 21 is a protein called Nucleolar protein 56.

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

- Molecule 22 is a protein called Nucleolar protein 58.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
56	RN	607	Total	C	N	O	S	0	0
			4529	2861	820	837	11		

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

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

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

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

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

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

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

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

- Molecule 61 is a protein called Protein BFR2.

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

- Molecule 62 is a protein called Unassigned peptides 1.

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

- Molecule 63 is a protein called Pno1.

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

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

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

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

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

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

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

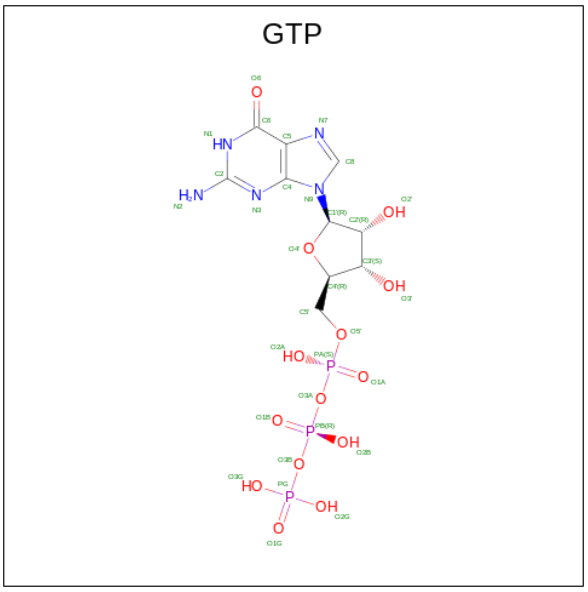
- Molecule 67 is a protein called Probable ATP-dependent RNA helicase DHR1.

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

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

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

- Molecule 69 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

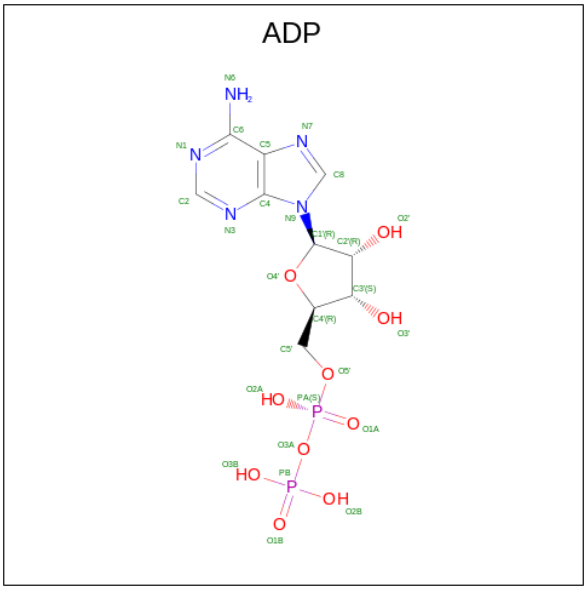


Mol	Chain	Residues	Atoms					AltConf
69	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

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

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

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



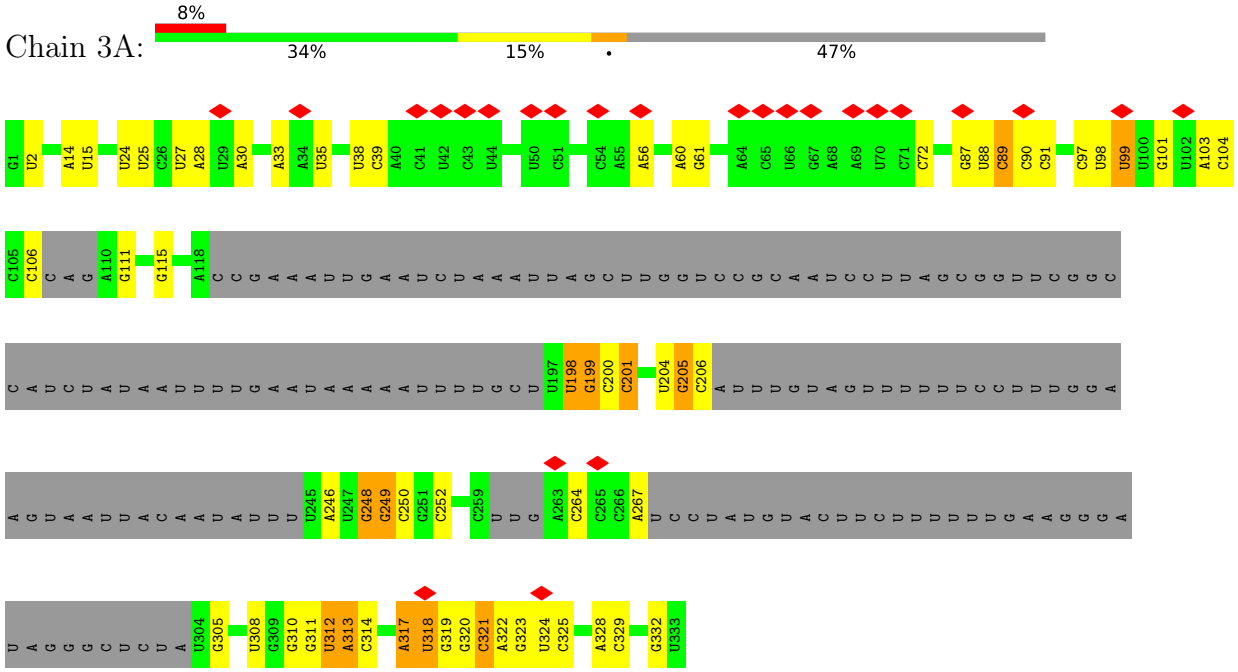
Mol	Chain	Residues	Atoms					AltConf
71	RZ	1	Total	C	N	O	P	0
			27	10	5	10	2	

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.

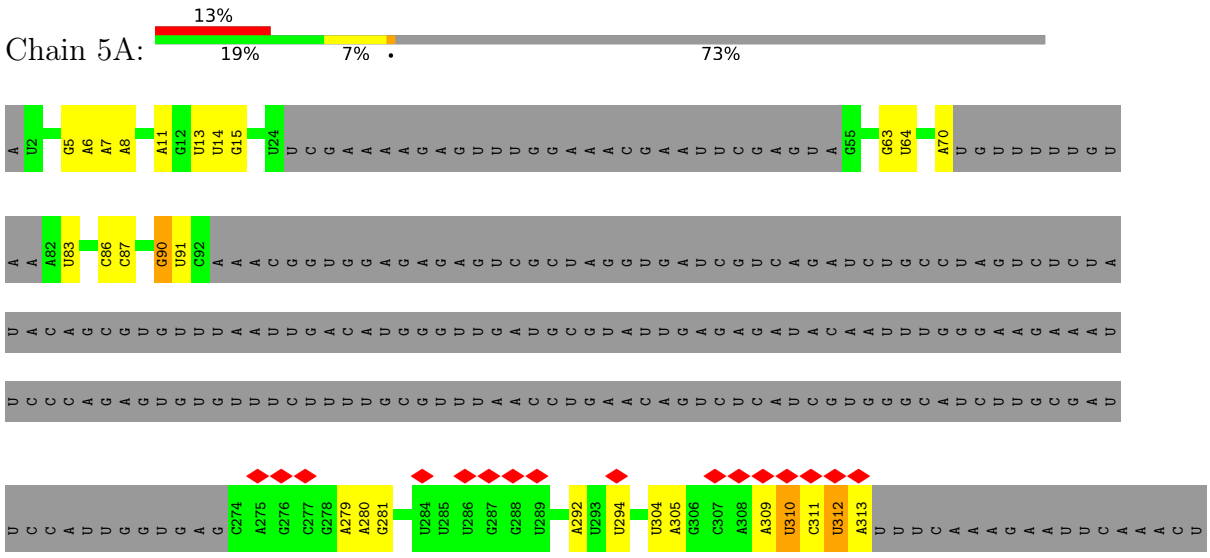
• Molecule 1: U3 snoRNA

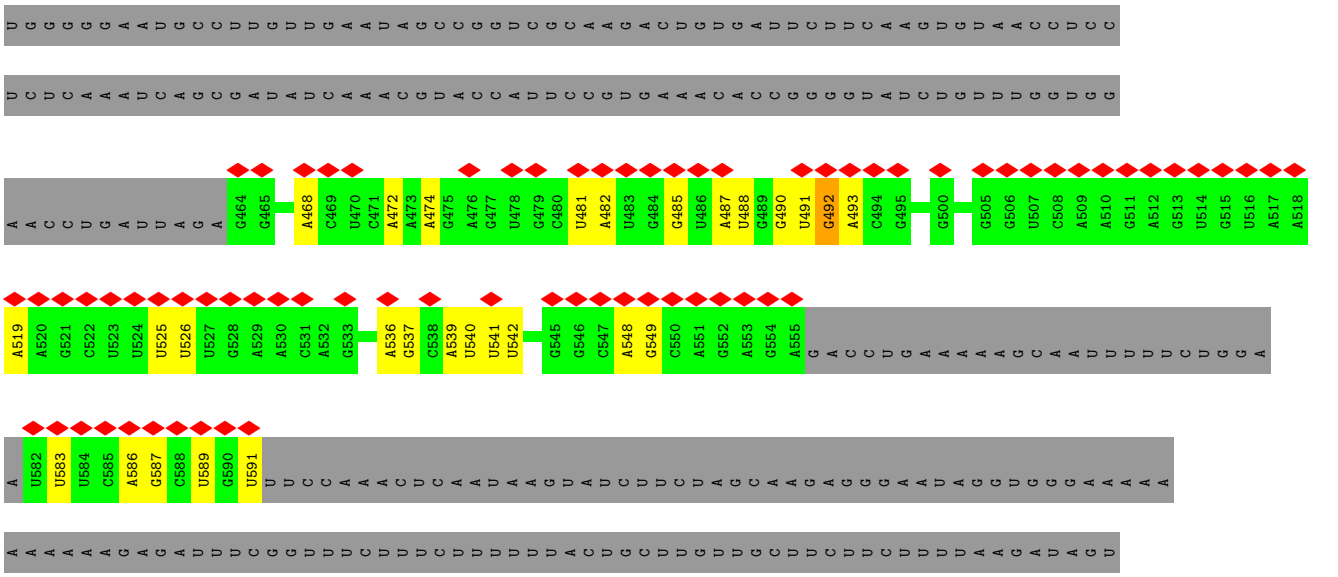
Chain 3A:



• Molecule 2: 5' ETS

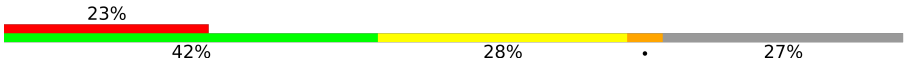
Chain 5A:

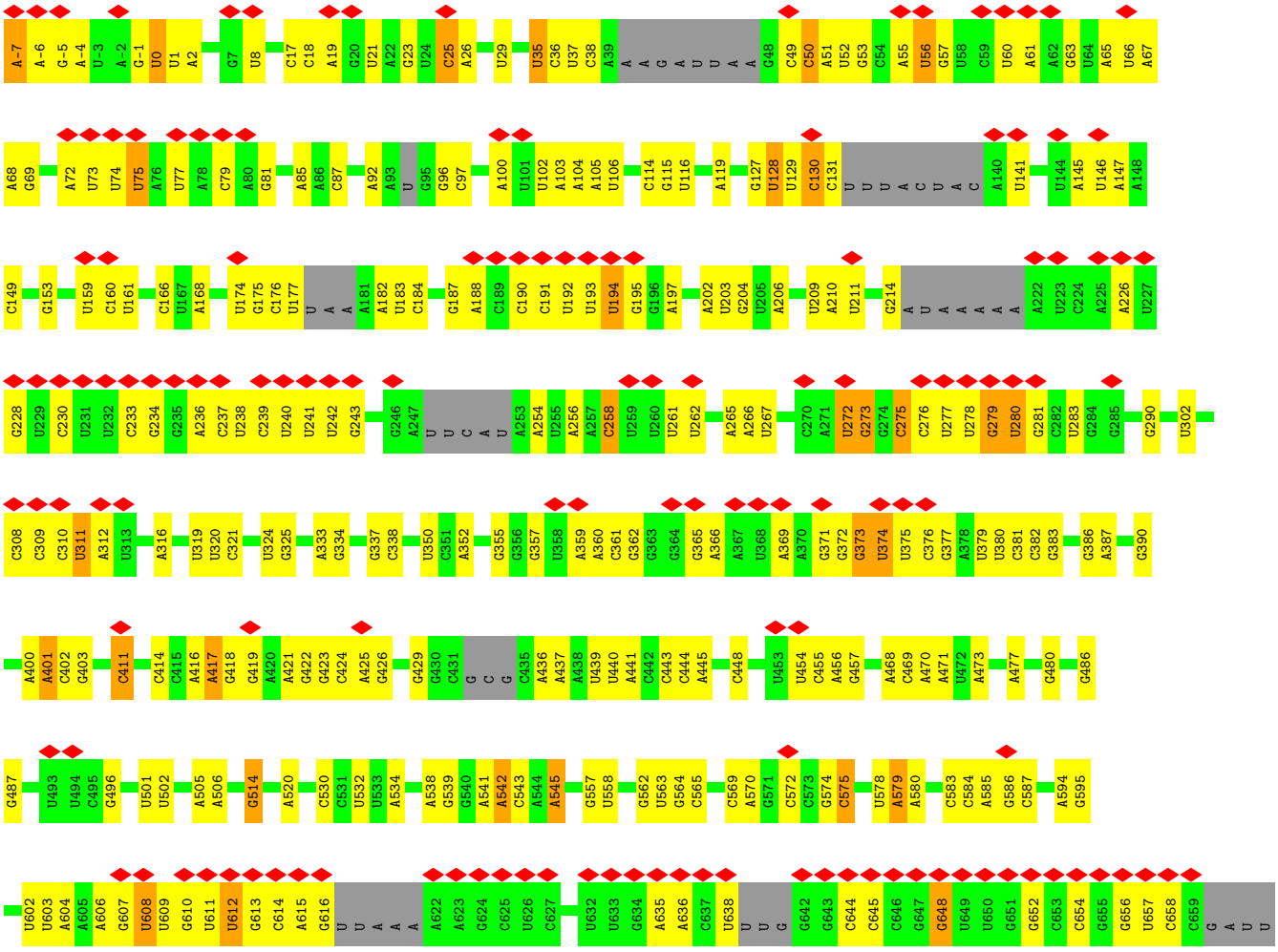


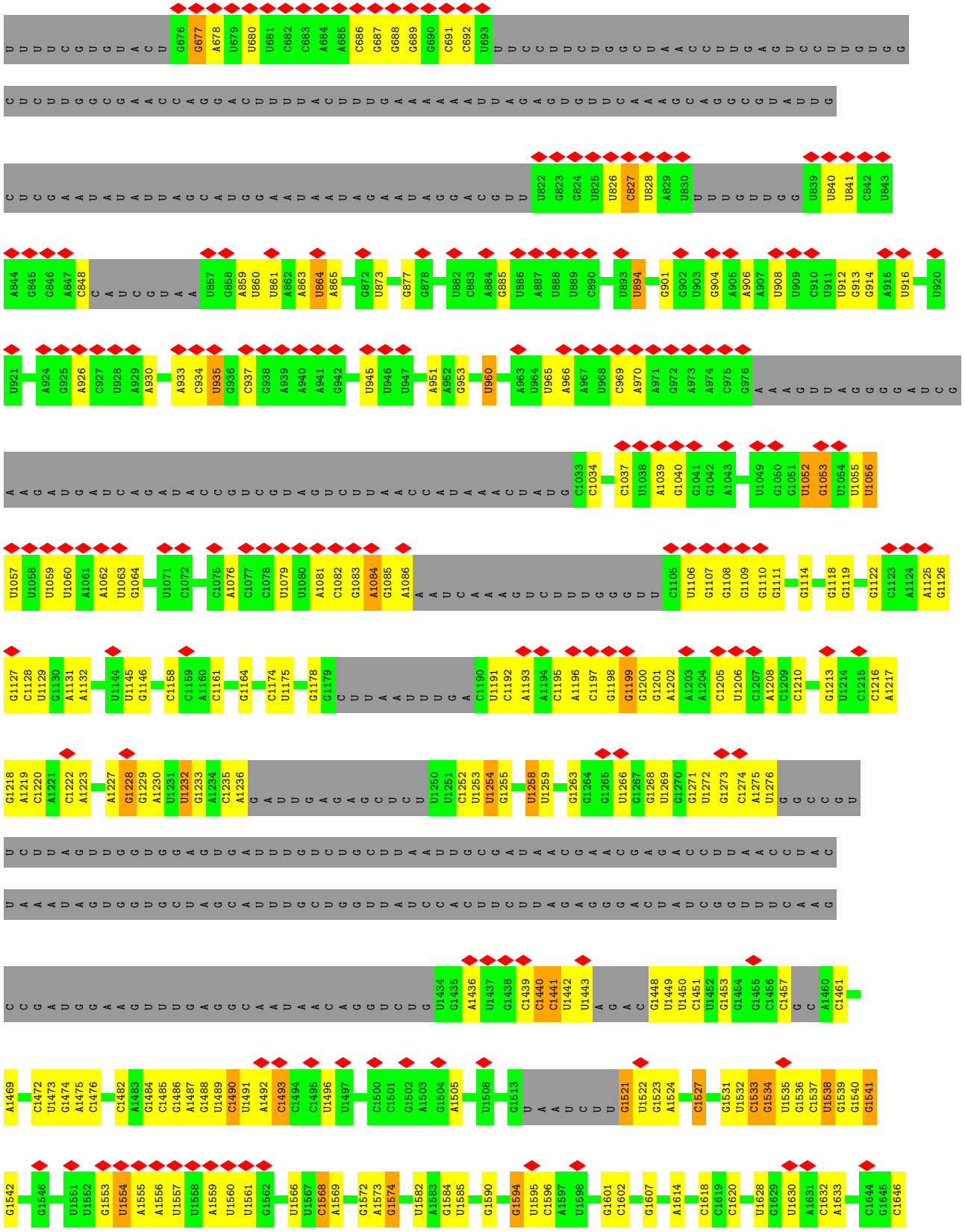


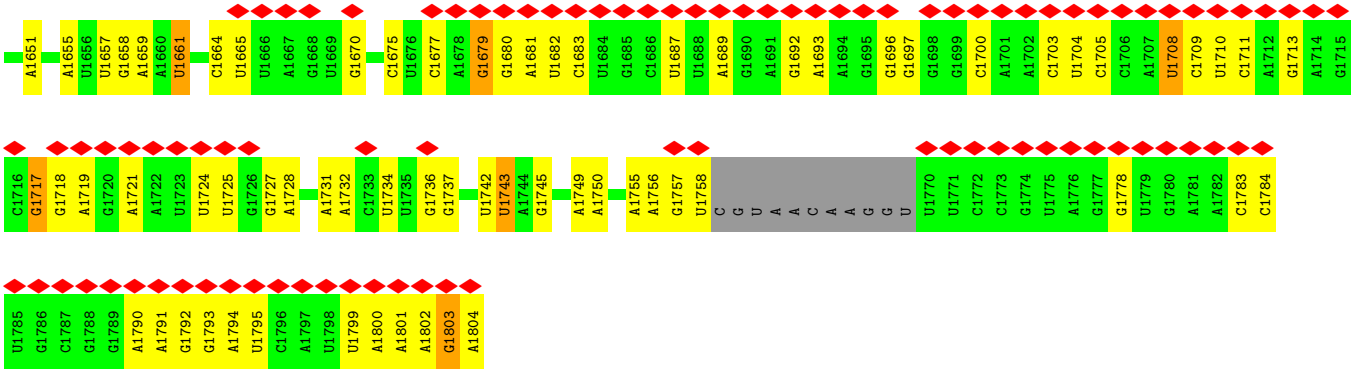
• Molecule 3: 18S rRNA

Chain SA:



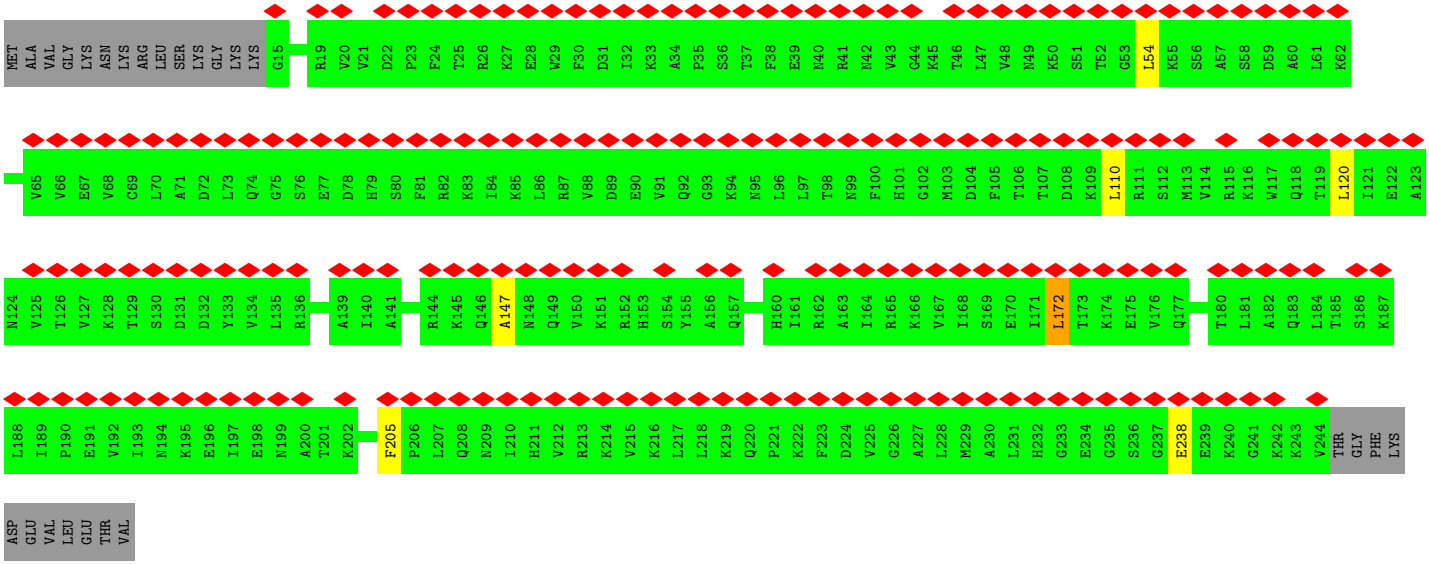






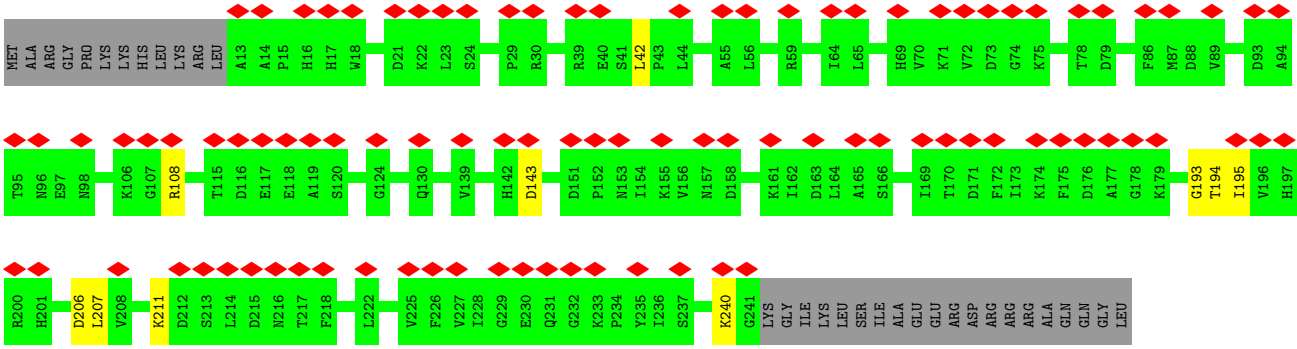
• Molecule 4: 40S ribosomal protein S1-A

Chain SC:



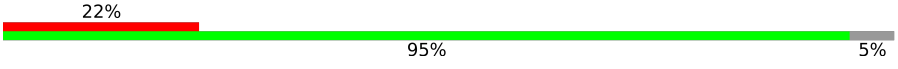
• Molecule 5: 40S ribosomal protein S4-A

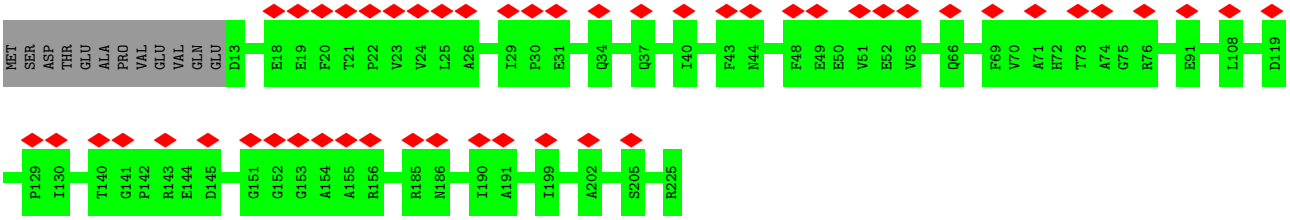
Chain SF:



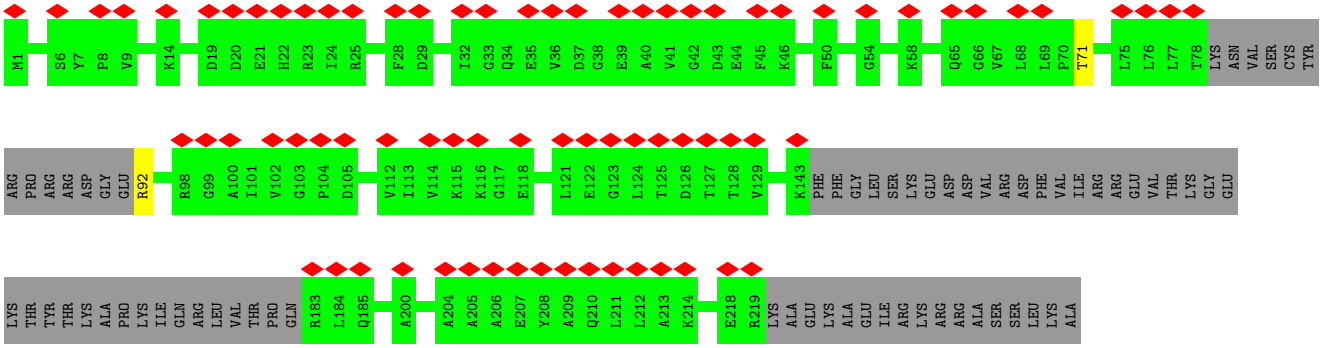
• Molecule 6: 40S ribosomal protein S5

Chain SG:

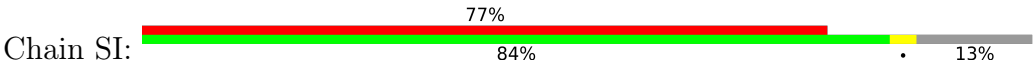


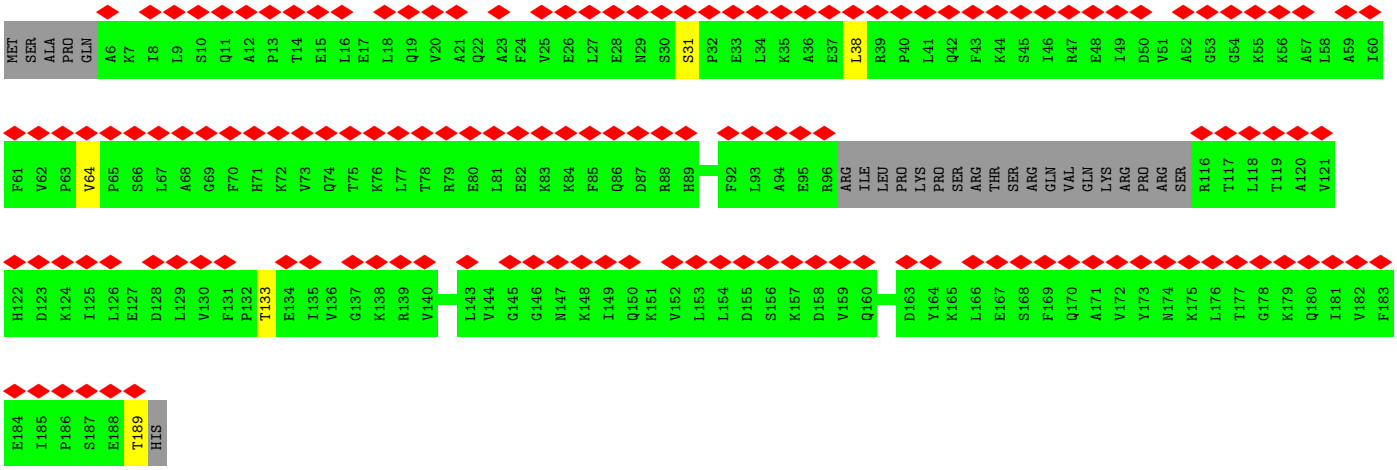


• Molecule 7: 40S ribosomal protein S6-A

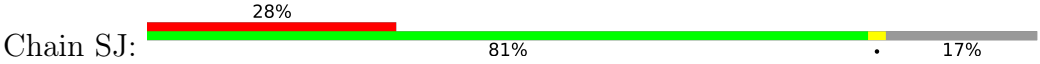


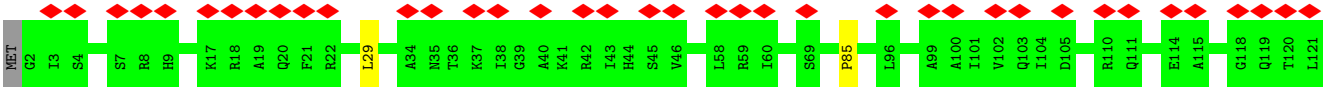
• Molecule 8: 40S ribosomal protein S7-A

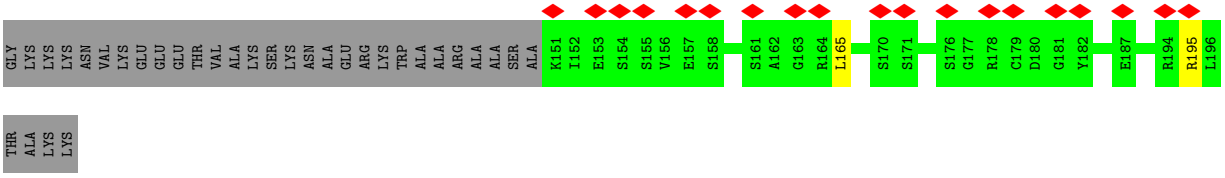




• Molecule 9: 40S ribosomal protein S8-A

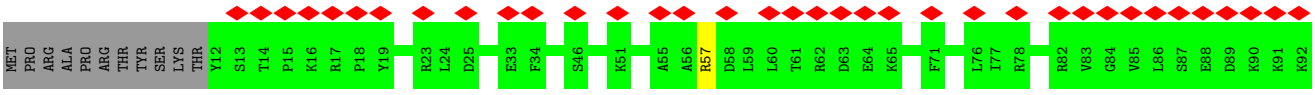


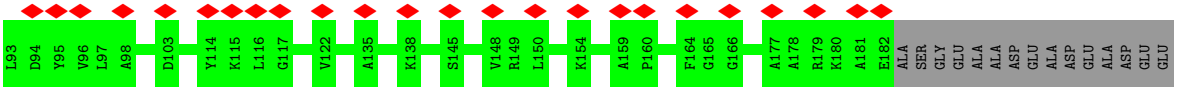




• Molecule 10: 40S ribosomal protein S9-A

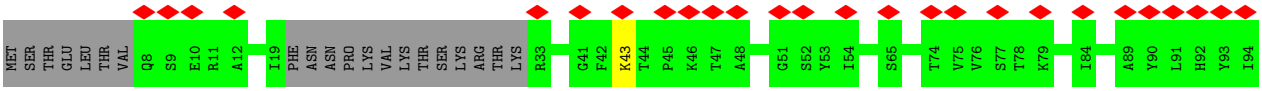
Chain SK:

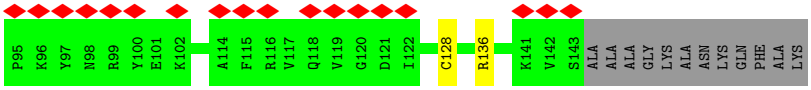




• Molecule 11: 40S ribosomal protein S11-A

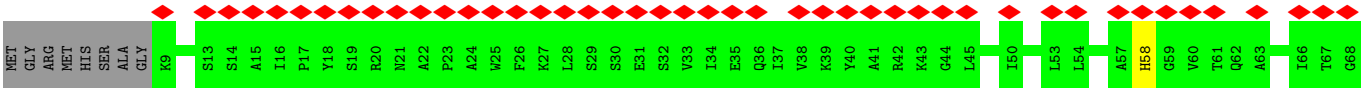
Chain SM:

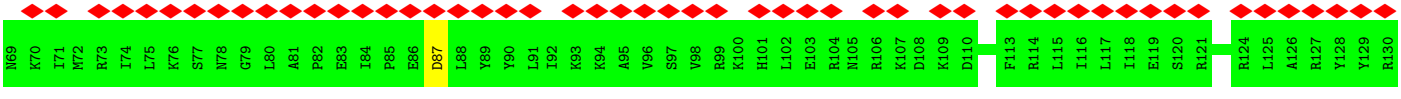


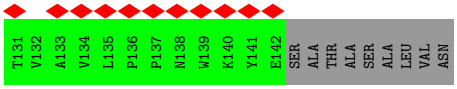


• Molecule 12: 40S ribosomal protein S13

Chain SO:

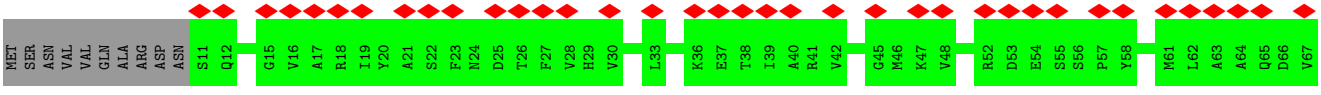


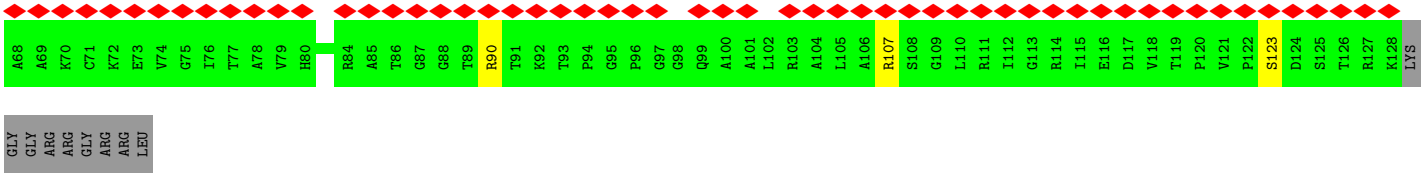




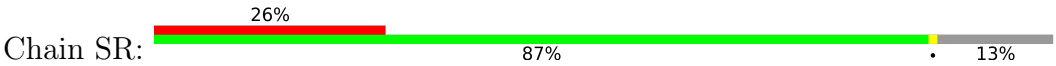
• Molecule 13: 40S ribosomal protein S14-A

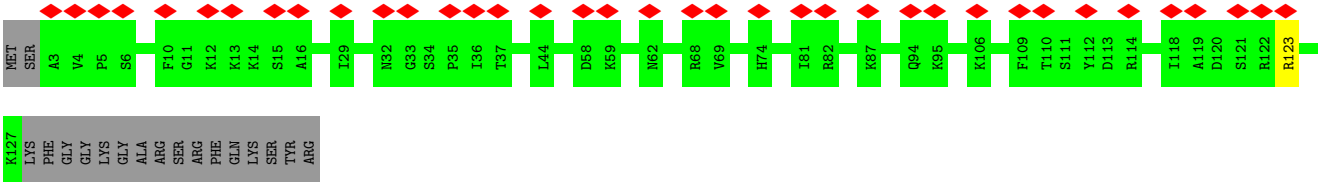
Chain SP:



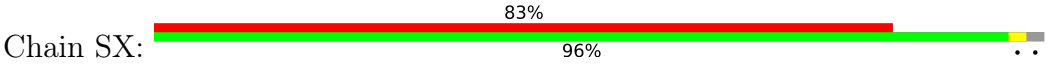


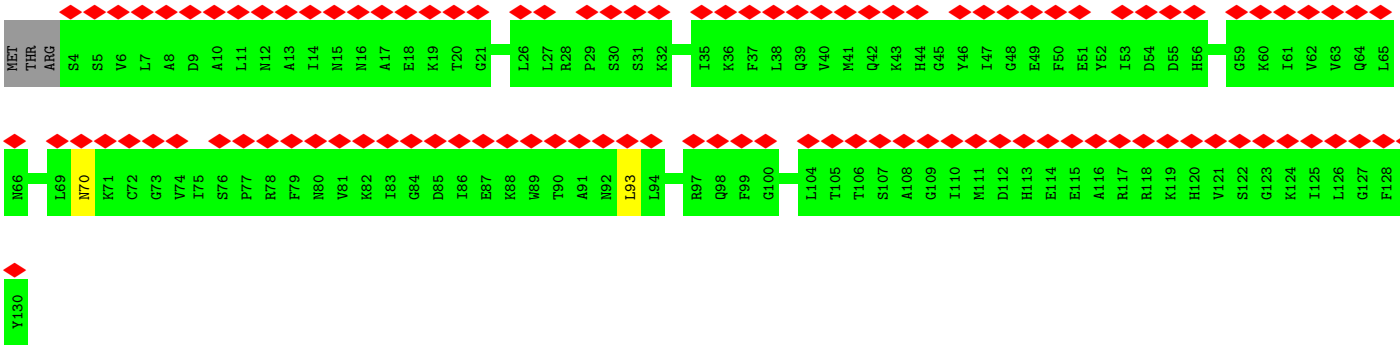
• Molecule 14: 40S ribosomal protein S16-A



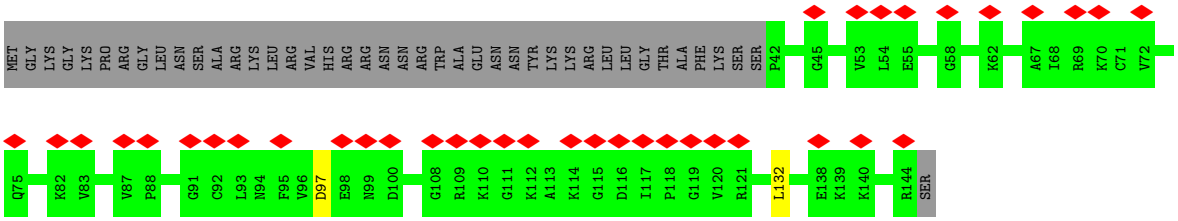


• Molecule 15: 40S ribosomal protein S22-B

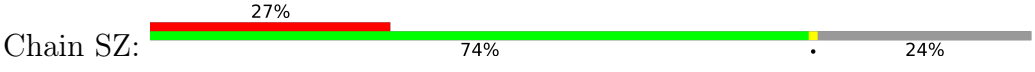


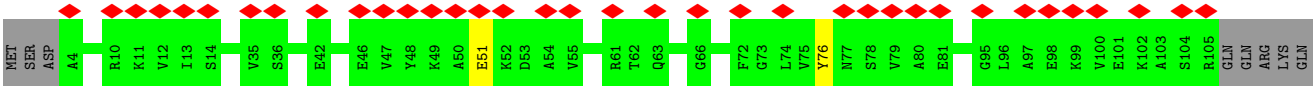


• Molecule 16: 40S ribosomal protein S23-A



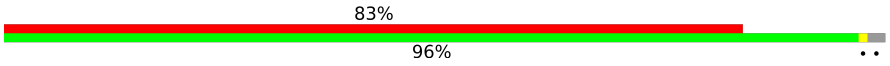
• Molecule 17: 40S ribosomal protein S24-A

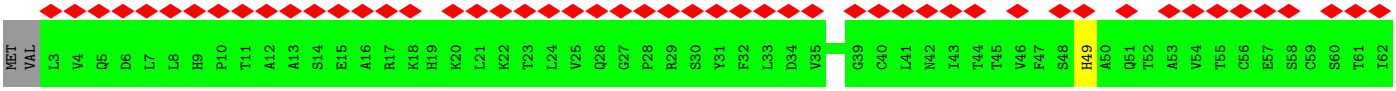


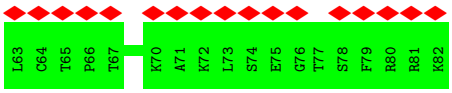


• Molecule 18: 40S ribosomal protein S27-A

Chain Sc:

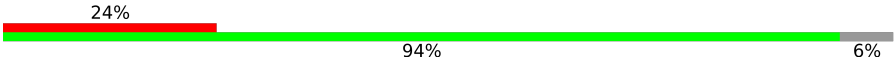


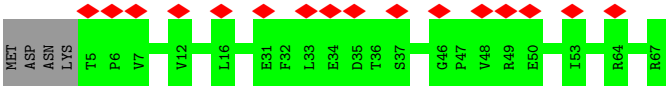




• Molecule 19: 40S ribosomal protein S28-A

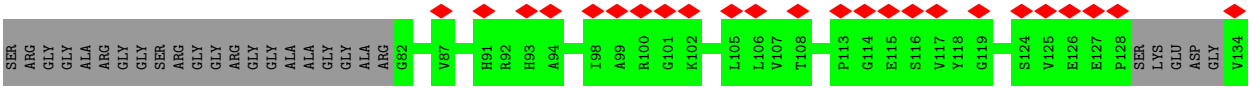
Chain Sd:

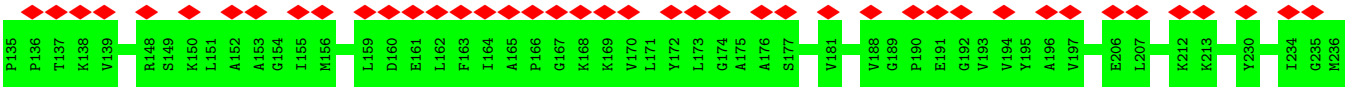


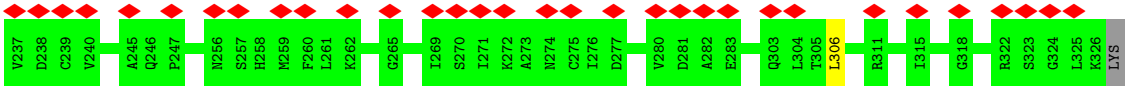


• Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

Chain 3B:

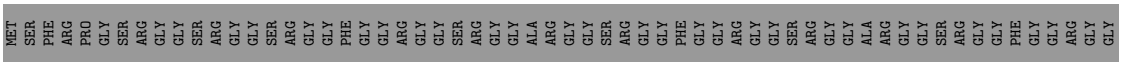


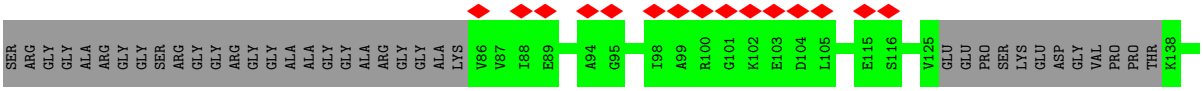


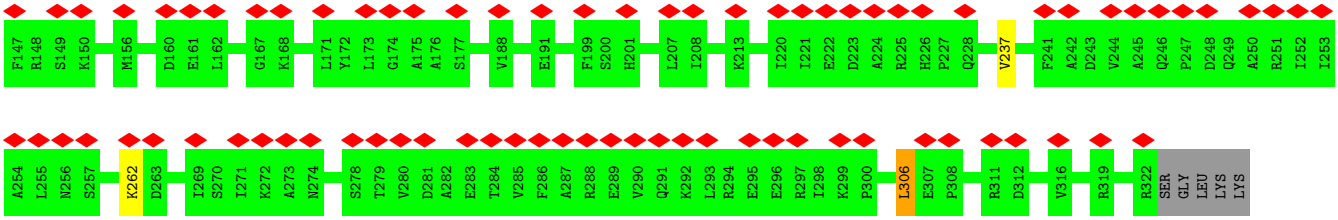


• Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

Chain 3C:

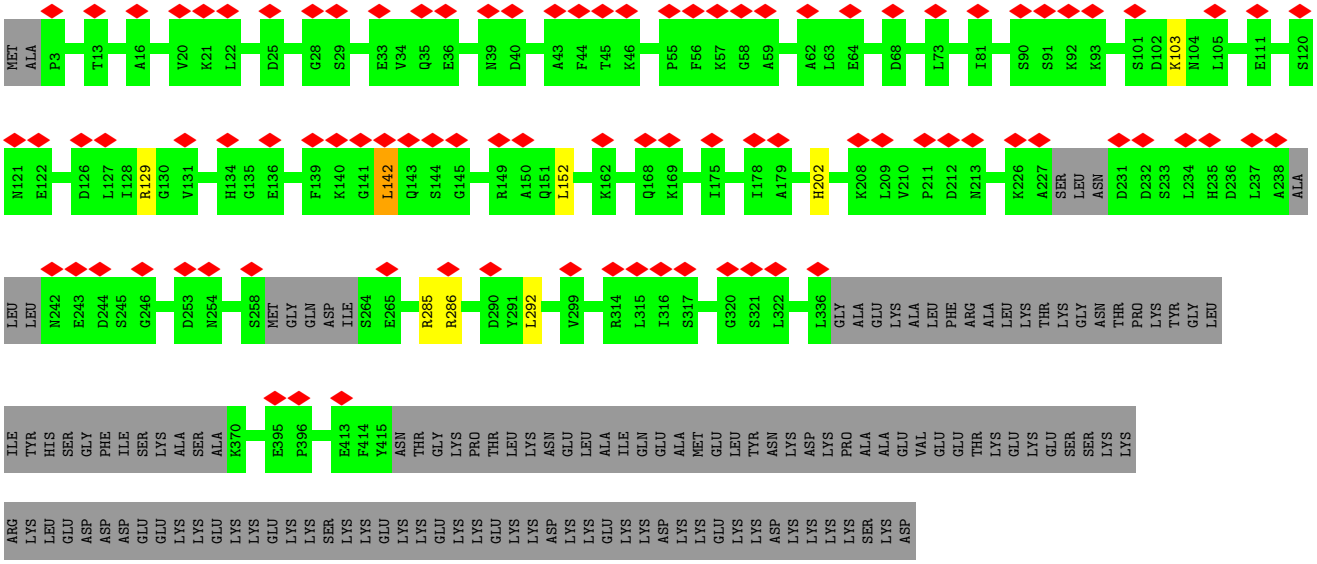






• Molecule 21: Nucleolar protein 56

Chain 3D: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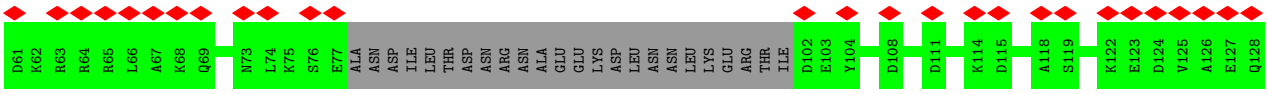
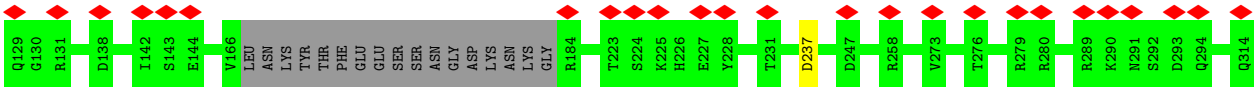
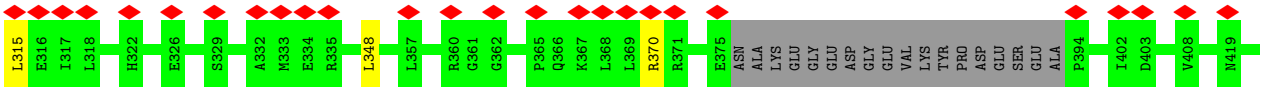
N121 E122 D126 L127 I128 R129 G130 V131 H134 G135 E136 F139 K140 G141 L142 Q143 S144 G145 R149 A150 Q151 L152 K162 Q168 K169 I175 I178 A179 H202 K208 L209 V210 P211 D212 N213 K226 A227 SER LEU ASN D231 D232 S233 L234 H235 D236 L237 A238 ALA
LEU LEU N242 E243 D244 S245 G246 D253 N254 S258 MET GLY GLN ASP ILE S264 E265 R285 R286 D290 Y291 L292 V299 R314 L315 I316 S317 G320 S321 L322 L336 GLY ALA GLU LYS ALA LEU PHE ARG ALA LEU LYS THR LYS GLY ASN THR PRO LYS TYR GLY LEU
ILE TYR HIS SER GLY PHE ILE SER LYS ALA SER ALA K370 E395 P396 E413 F414 Y415 ASN THR GLY LYS PRO THR LEU LYS ASN GLU LEU ALA ILE GLN GLU ALA MET GLU LEU TYR ASN LYS ASP LYS PRO ALA ALA GLU VAL GLU GLU THR LYS GLU LYS GLU SER SER LYS LYS
ARG LYS LEU GLU ASP ASP ASP GLU GLU LYS LYS GLU LYS LYS GLU LYS LYS SER LYS LYS GLU LYS LYS GLU LYS LYS GLU

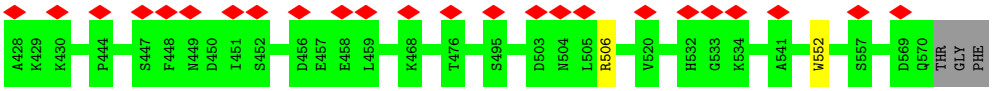
• Molecule 23: Ribosomal RNA-processing protein 9

Chain 3F:



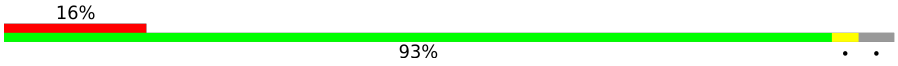


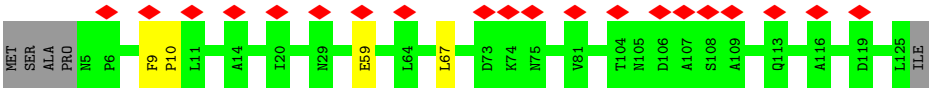




• Molecule 24: 13 kDa ribonucleoprotein-associated protein

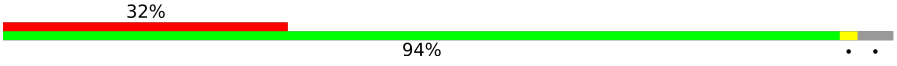
Chain 3G:

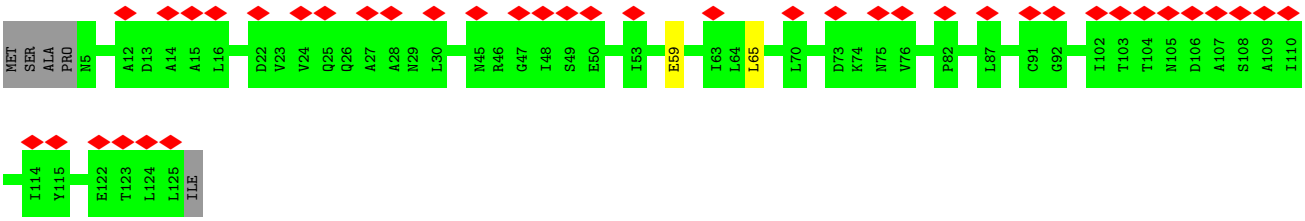




• Molecule 24: 13 kDa ribonucleoprotein-associated protein

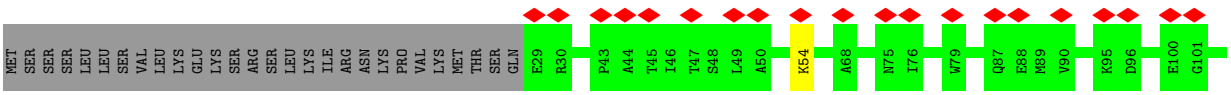
Chain 3H:

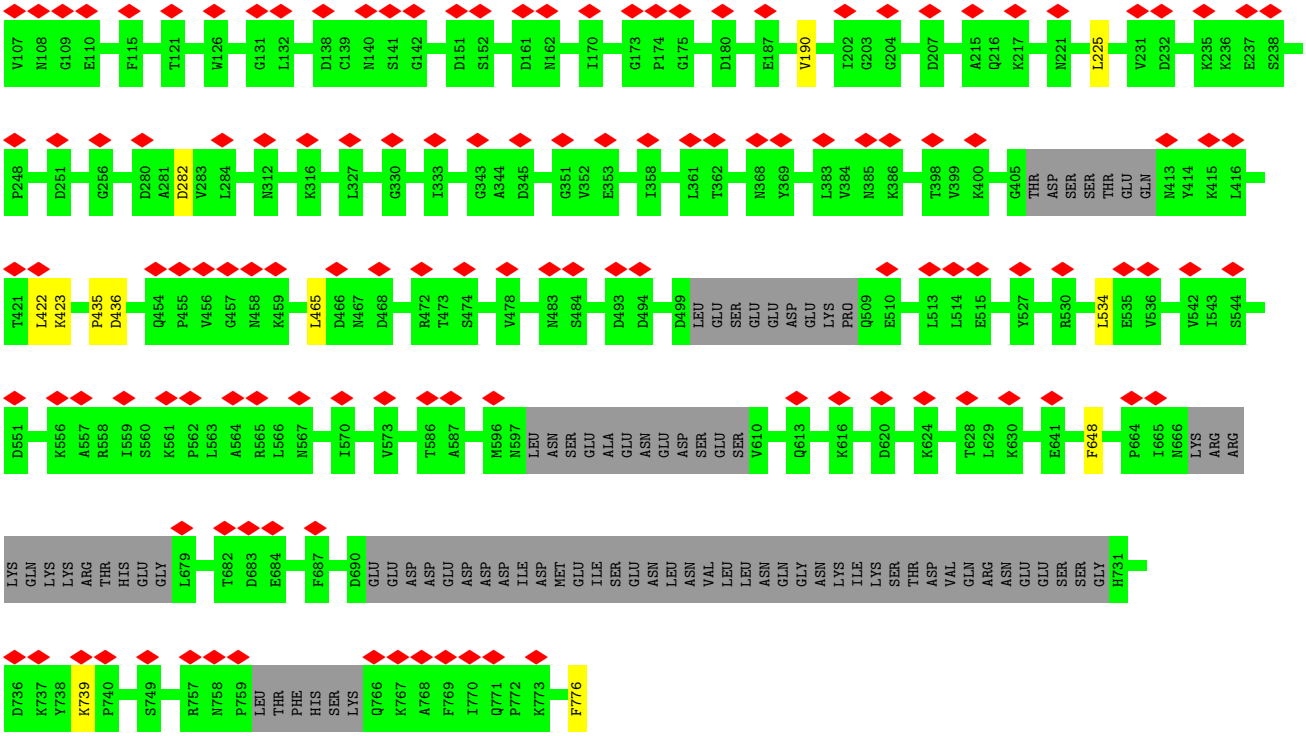




• Molecule 25: U3 small nucleolar RNA-associated protein 4

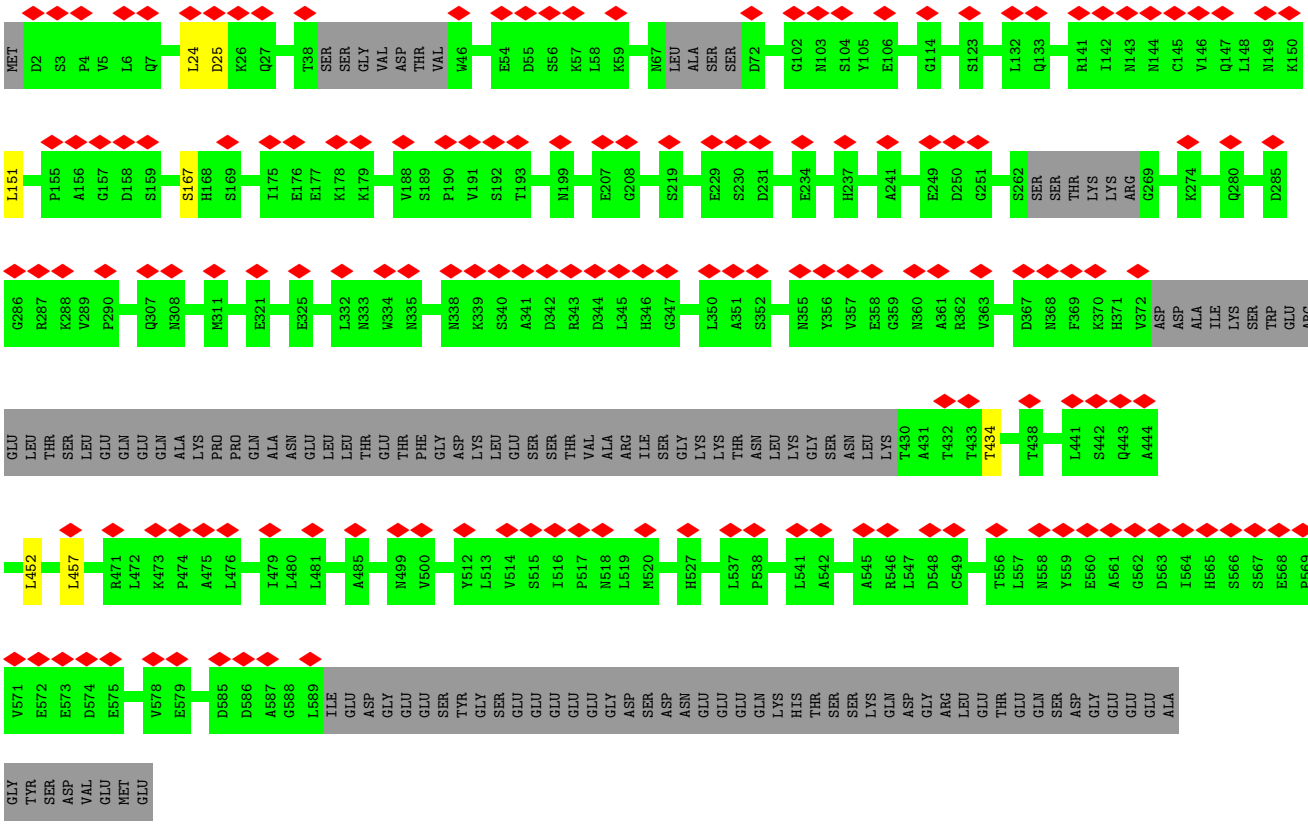
Chain A4:





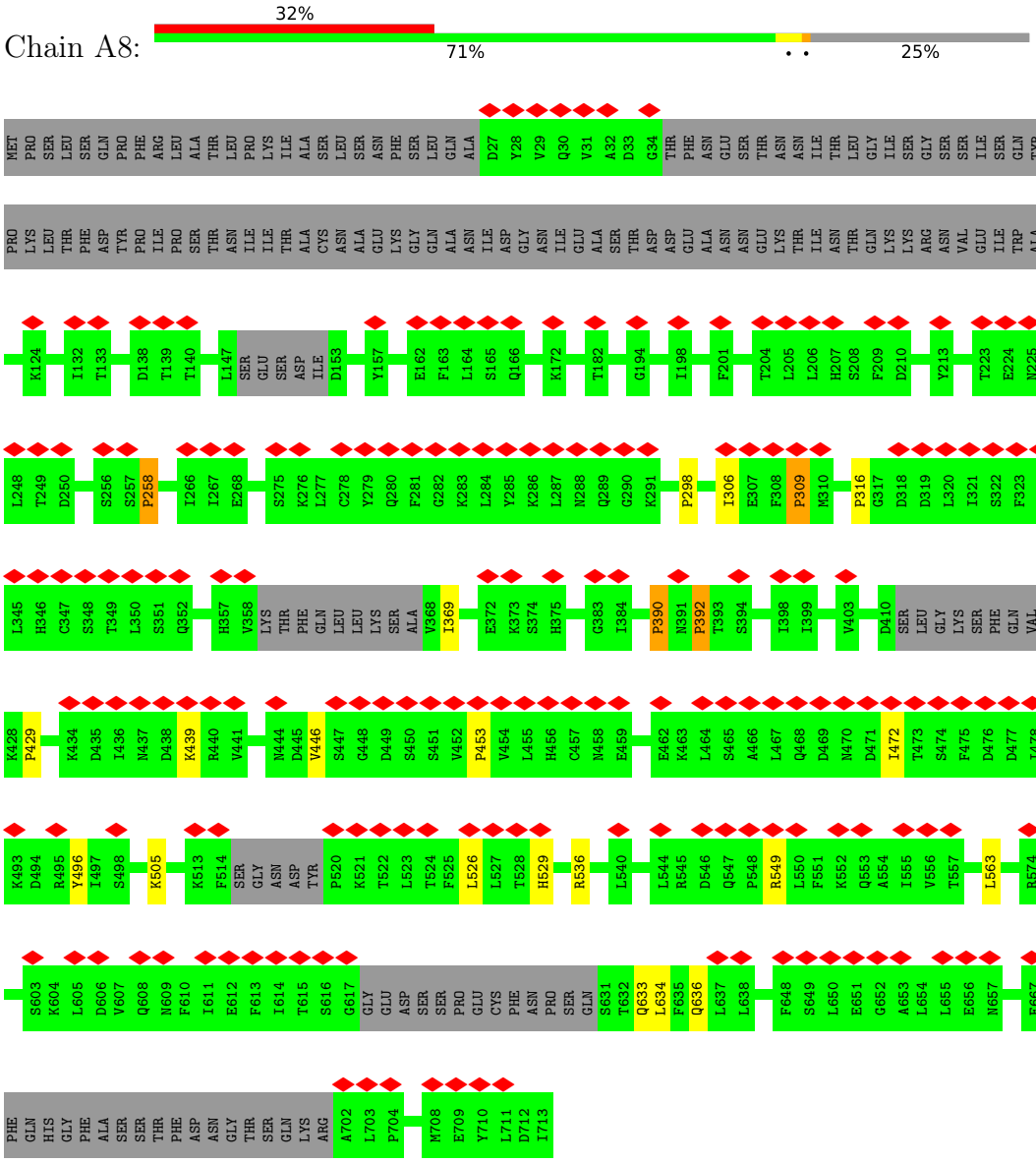
• Molecule 26: U3 small nucleolar RNA-associated protein 5

Chain A5:



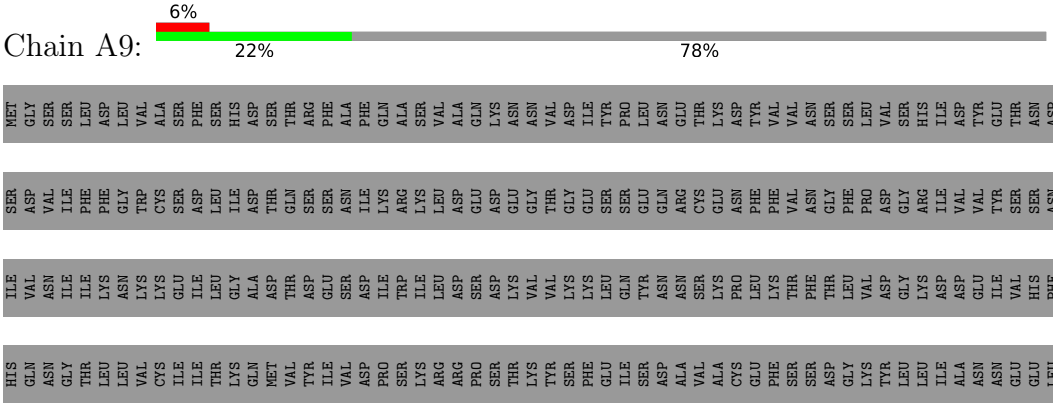
• Molecule 27: U3 small nucleolar RNA-associated protein 8

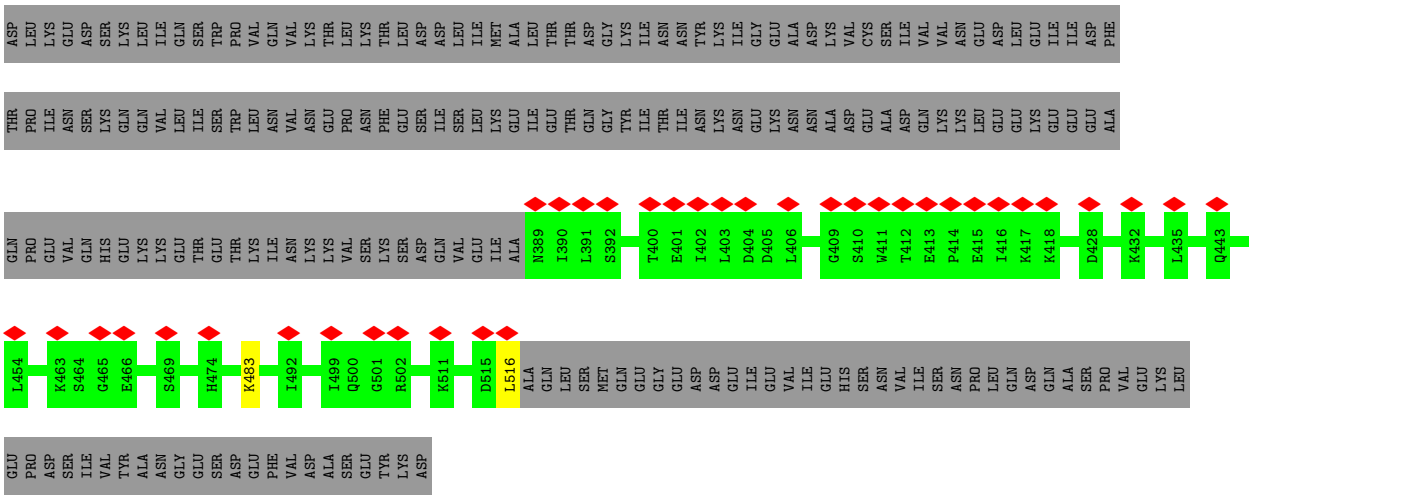
Chain A8:



• Molecule 28: U3 small nucleolar RNA-associated protein 9

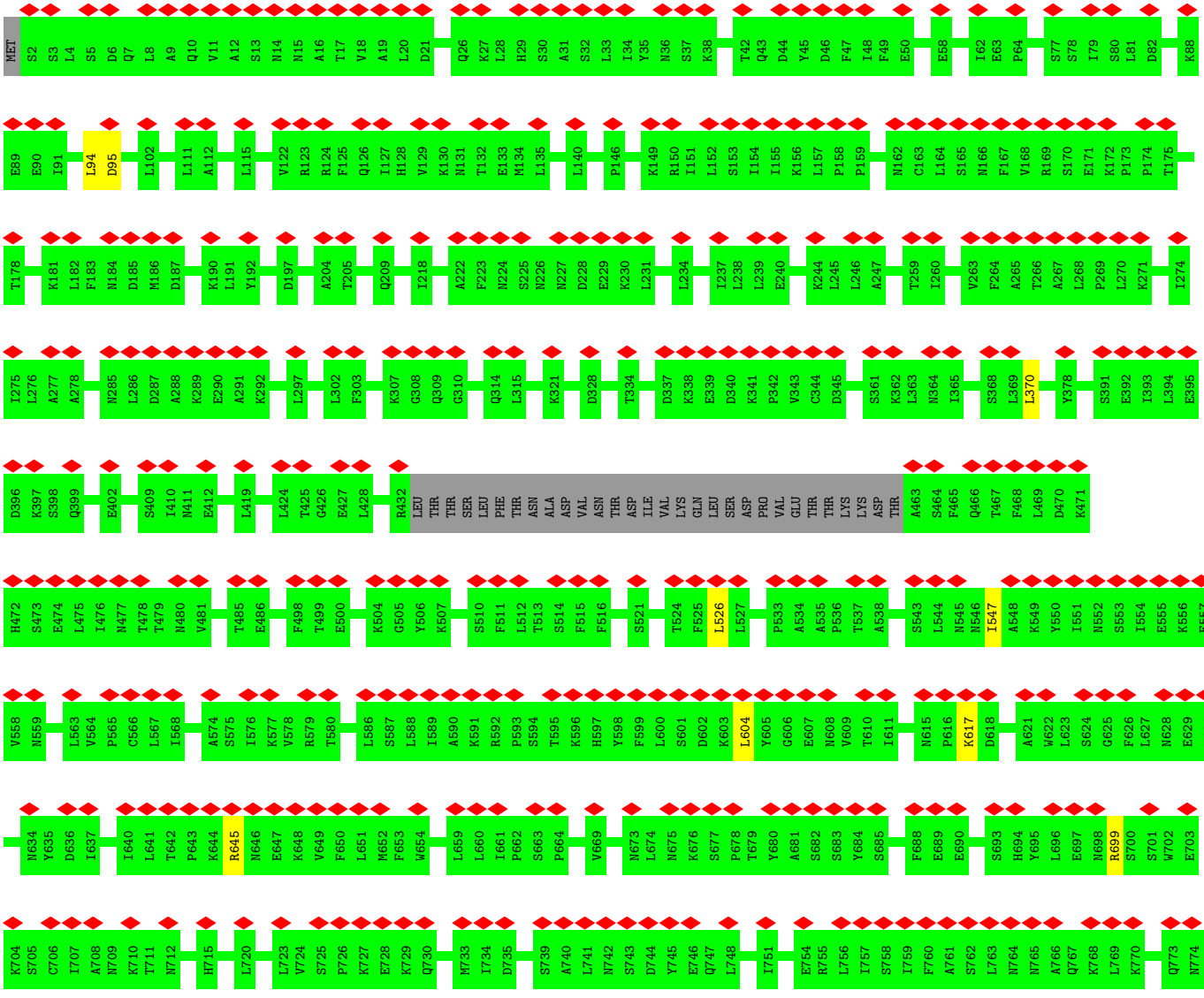
Chain A9:

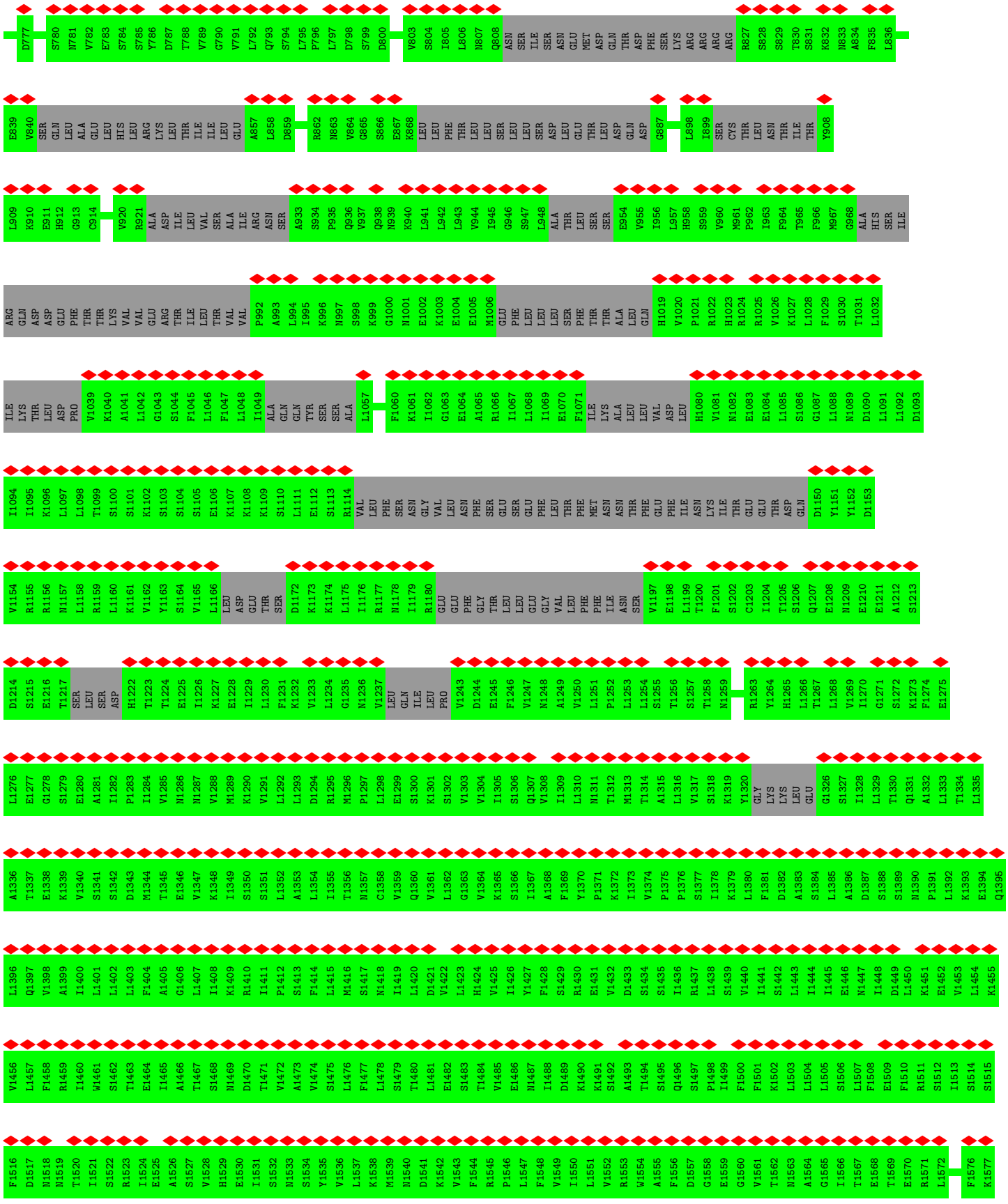




• Molecule 29: U3 small nucleolar RNA-associated protein 10

Chain AE:




D777 S780 N781 V782 E783 S784 S785 Y786 D787 T788 V789 G790 V791 L792 Q793 S794 L795 P796 L797 D798 S799 D800 V803 S804 I805 L806 N807 Q808 ASN SER ILE SER ASN GLU MET ASP GLN THR ASP PHE SER LYS ARG ARG ARG R827 S828 S829 T830 S831 K832 N833 A834 F835 L836
E839 V840 SER GLN LEU ALA GLU LEU HIS LEU ARG LYS LEU THR ILE ILE LEU GLU A857 L858 D859 R862 N863 V864 G865 S866 E867 K868 LEU LEU PHE THR LEU LEU SER LEU LEU SER ASP LEU GLU THR LEU ASP GLN ASP G887 L898 I899 SER CYS THR LEU ASN THR ILE THR Y908
L909 K910 E911 H912 G913 C914 V920 R921 ALA ASP ILE LEU VAL SER ALA ILE ARG ASN SER A933 S934 P935 Q936 V937 Q938 N939 K940 L941 L942 L943 V944 I945 G946 S947 L948 ALA THR LEU SER SER E954 V955 I956 L957 H958 S959 V960 M961 P962 I963 F964 T965 F966 M967 G968 ALA HIS SER ILE
ARG GLN ASP ASP GLU PHE THR THR LYS VAL VAL GLU ARG THR ILE LEU THR VAL VAL P992 A993 L994 I995 K996 N997 S998 K999 G1000 N1001 E1002 K1003 E1004 E1005 M1006 GLU PHE LEU LEU LEU SER PHE THR THR ALA LEU GLN H1019 V1020 P1021 R1022 H1023 R1024 R1025 V1026 K1027 L1028 F1029 S1030 T1031 L1032
ILE LYS THR LEU ASP PRO V1039 K1040 A1041 L1042 G1043 S1044 F1045 L1046 F1047 L1048 I1049 ALA GLN GLN TYR SER SER ALA L1057 F1060 K1061 I1062 G1063 E1064 A1065 R1066 I1067 L1068 I1069 E1070 F1071 ILE LYS ALA LEU LEU VAL ASP LEU H1080 V1081 N1082 E1083 E1084 L1085 S1086 G1087 L1088 N1089 D1090 L1091 L1092 D1093
I1094 I1095 K1096 L1097 L1098 T1099 S1100 S1101 K1102 S1103 S1104 S1105 E1106 K1107 K1108 K1109 S1110 L1111 E1112 S1113 R1114 VAL LEU PHE SER ASN GLY VAL LEU ASN PHE SER GLU SER GLU PHE LEU THR PHE MET ASN ASN THR PHE GLU PHE ILE ASN LYS ILE THR GLU GLU THR ASP GLN D1150 Y1151 Y1152 D1153
V1154 R1155 R1156 N1157 L1158 R1159 L1160 K1161 V1162 Y1163 S1164 V1165 L1166 LEU ASP GLU THR SER D1172 K1173 K1174 L1175 I1176 R1177 N1178 I1179 R1180 GLU GLU PHE GLY THR LEU LEU GLU GLY VAL LEU PHE PHE ILE ASN SER V1197 E1198 L1199 T1200 F1201 S1202 C1203 I1204 T1205 S1206 Q1207 E1208 N1209 E1210 E1211 A1212 S1213
D1214 S1215 E1216 T1217 SER LEU SER ASP H1222 T1223 T1224 E1225 I1226 K1227 E1228 I1229 L1230 F1231 K1232 V1233 L1234 G1235 N1236 V1237 LEU GLN ILE LEU PRO V1243 D1244 E1245 F1246 V1247 N1248 A1249 V1250 L1251 P1252 L1253 L1254 S1255 T1256 S1257 T1258 N1259 R1263 Y1264 H1265 L1266 T1267 L1268 V1269 I1270 G1271 S1272 K1273 F1274 E1275
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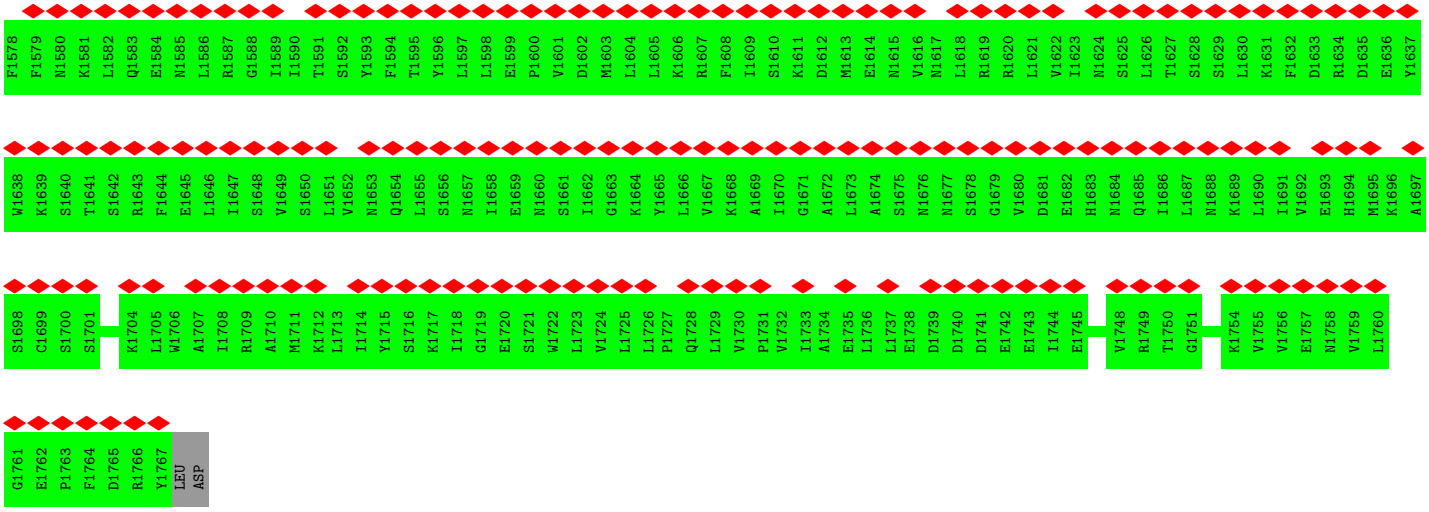
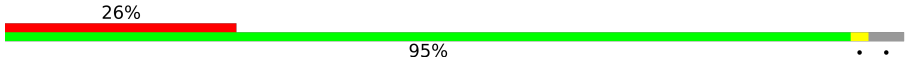
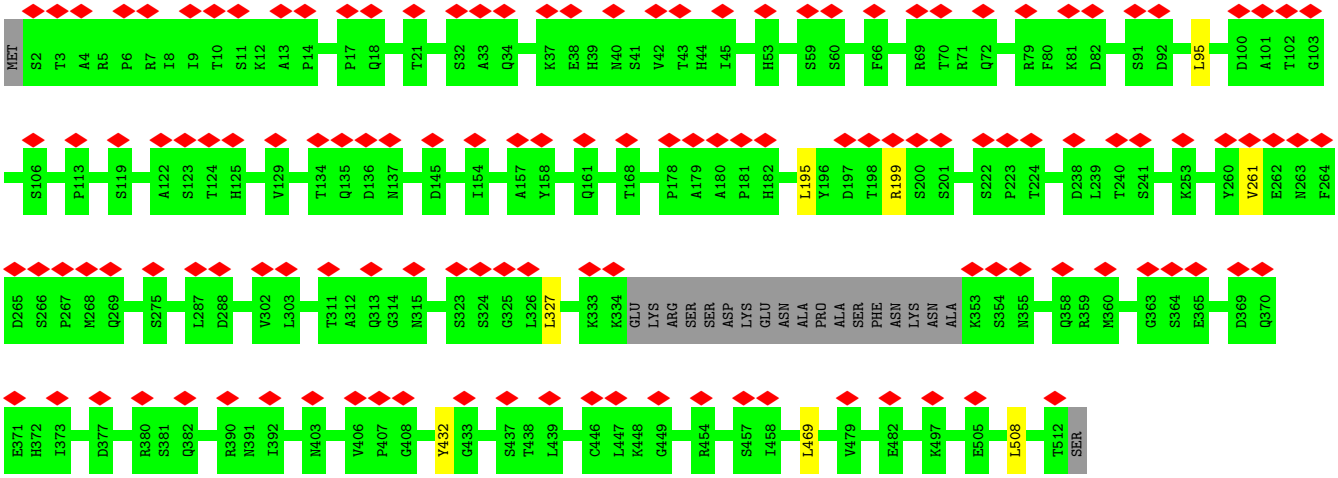
A1336 T1337 E1338 K1339 V1340 S1341 S1342 D1343 M1344 T1345 E1346 V1347 K1348 I1349 S1350 S1351 L1352 A1353 I1354 I1355 T1356 N1357 C1358 V1359 Q1360 V1361 L1362 G1363 V1364 K1365 S1366 I1367 A1368 F1369 Y1370 P1371 K1372 I1373 V1374 P1375 P1376 S1377 I1378 K1379 L1380 F1381 D1382 A1383 S1384 L1385 A1386 D1387 I1388 S1389 N1390 P1391 L1392 K1393 E1394 Q1395
L1396 Q1397 V1398 A1399 I1400 L1401 L1402 L1403 F1404 A1405 G1406 L1407 I1408 K1409 R1410 I1411 P1412 S1413 F1414 L1415 M1416 S1417 N1418 I1419 L1420 D1421 V1422 L1423 H1424 V1425 I1426 Y1427 F1428 S1429 R1430 E1431 V1432 D1433 S1434 S1435 I1436 R1437 L1438 S1439 V1440 I1441 S1442 L1443 I1444 I1445 E1446 N1447 I1448 D1449 L1450 K1451 E1452 V1453 L1454 K1455
V1456 L1457 F1458 R1459 I1460 W1461 S1462 T1463 E1464 I1465 A1466 T1467 S1468 N1469 D1470 T1471 V1472 A1473 V1474 S1475 L1476 F1477 L1478 S1479 T1480 L1481 E1482 S1483 T1484 V1485 E1486 N1487 I1488 D1489 K1490 K1491 S1492 A1493 T1494 S1495 Q1496 S1497 P1498 I1499 F1500 F1501 K1502 L1503 L1504 L1505 S1506 L1507 F1508 E1509 F1510 R1511 S1512 I1513 S1514 S1515
F1516 D1517 N1518 N1519 T1520 I1521 S1522 R1523 I1524 E1525 A1526 S1527 V1528 H1529 E1530 I1531 S1532 N1533 S1534 Y1535 V1536 L1537 K1538 M1539 N1540 D1541 K1542 V1543 F1544 R1545 P1546 L1547 F1548 V1549 I1550 L1551 V1552 R1553 W1554 A1555 F1556 D1557 G1558 E1559 G1560 V1561 T1562 N1563 A1564 G1565 I1566 T1567 E1568 T1569 E1570 R1571 L1572 F1576 K1577



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

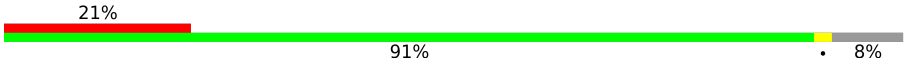
Chain AF:

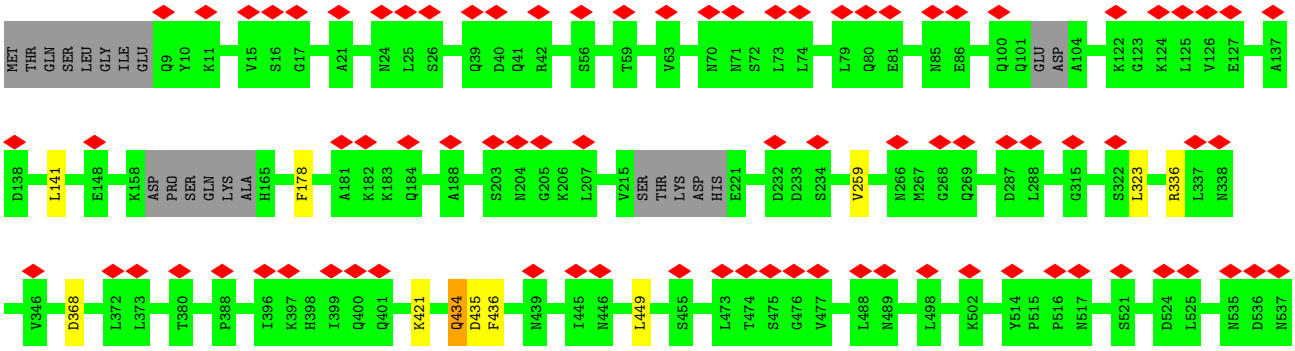


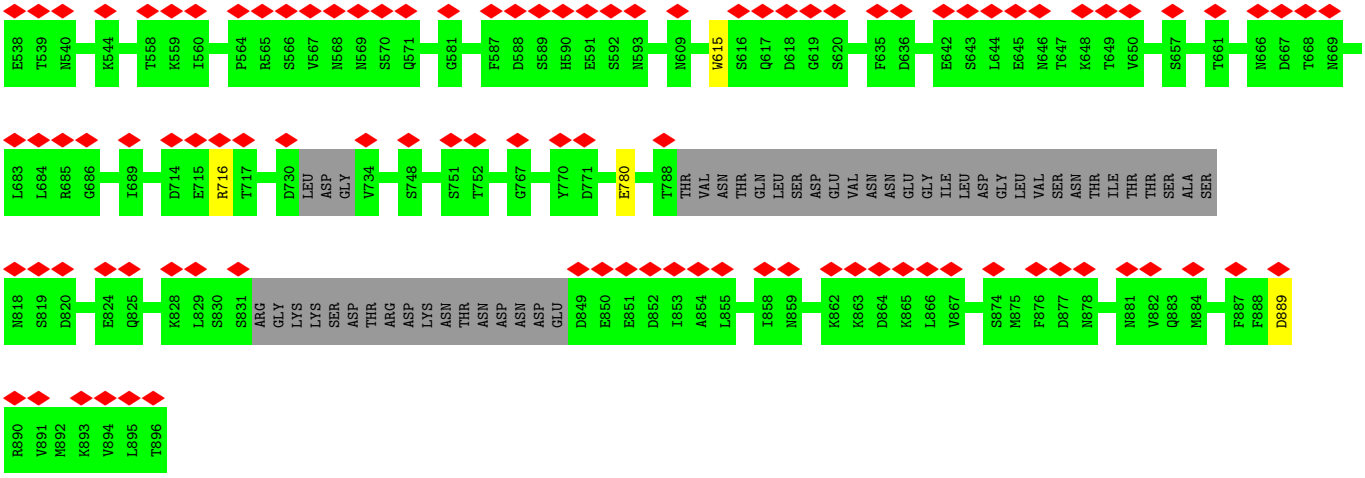


• Molecule 31: NET1-associated nuclear protein 1

Chain AG:

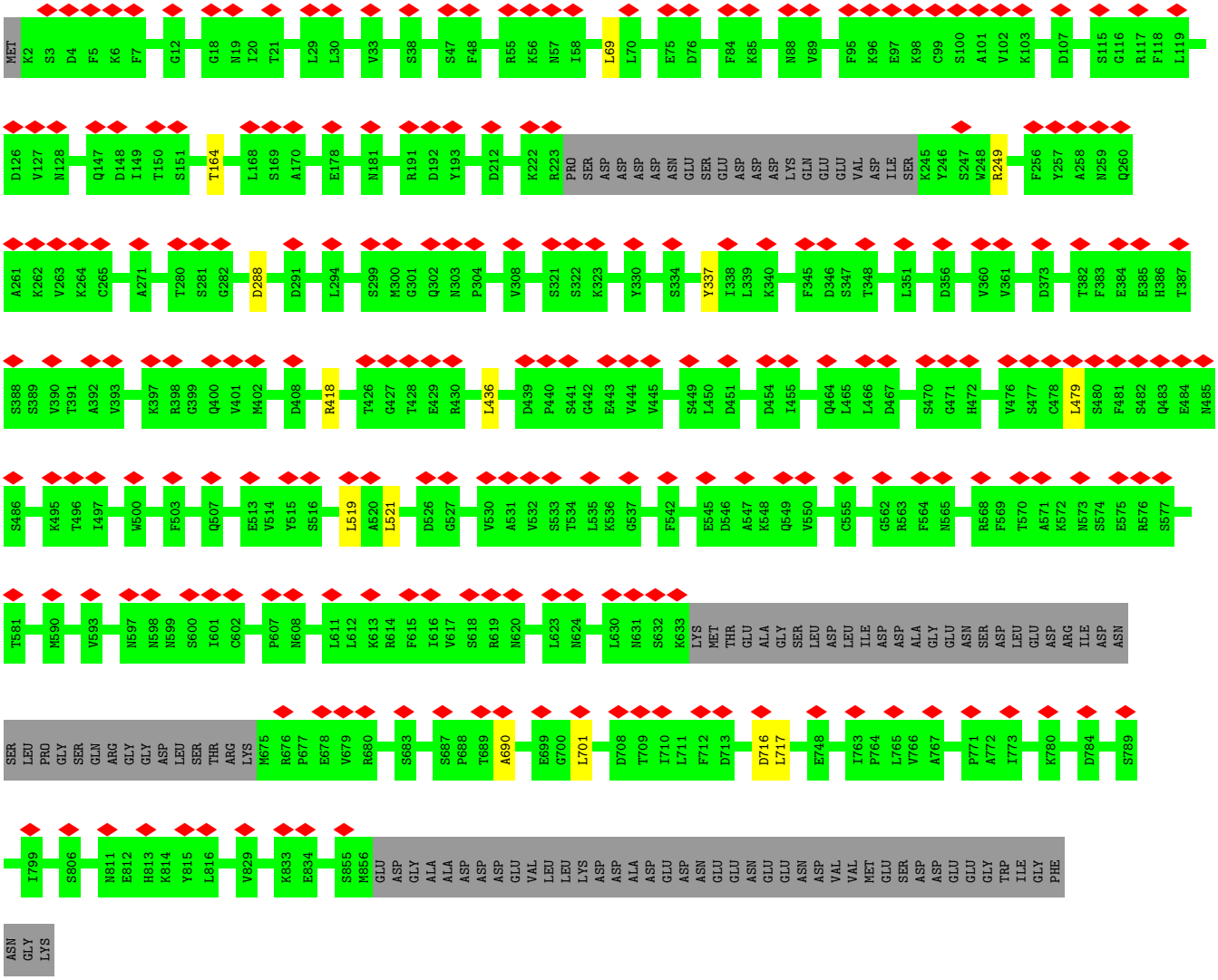






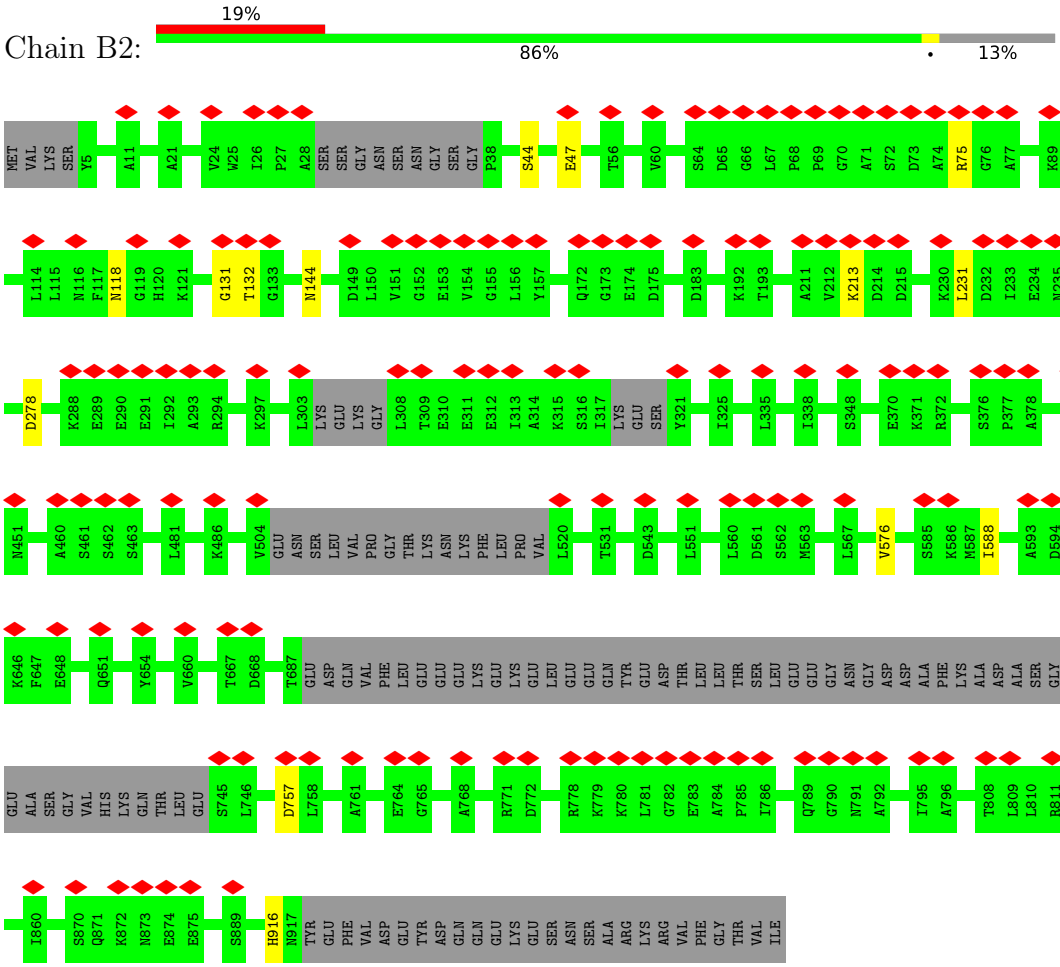
• Molecule 32: Periodic tryptophan protein 2

Chain B1:



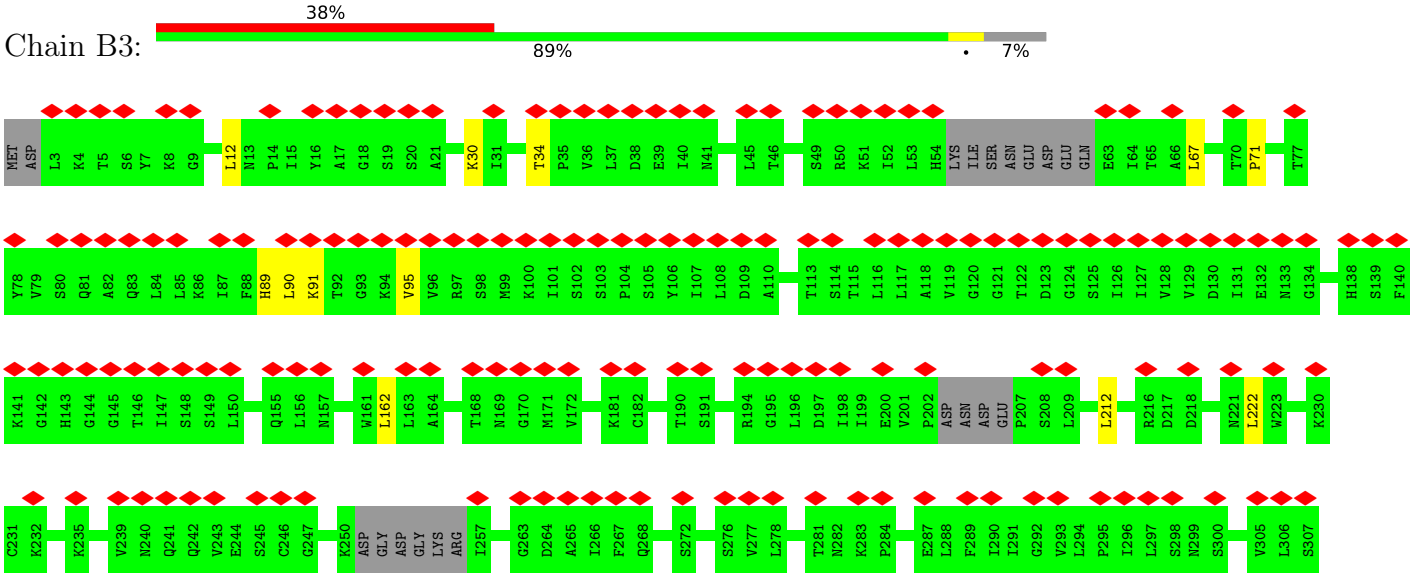
• Molecule 33: U3 small nucleolar RNA-associated protein 12

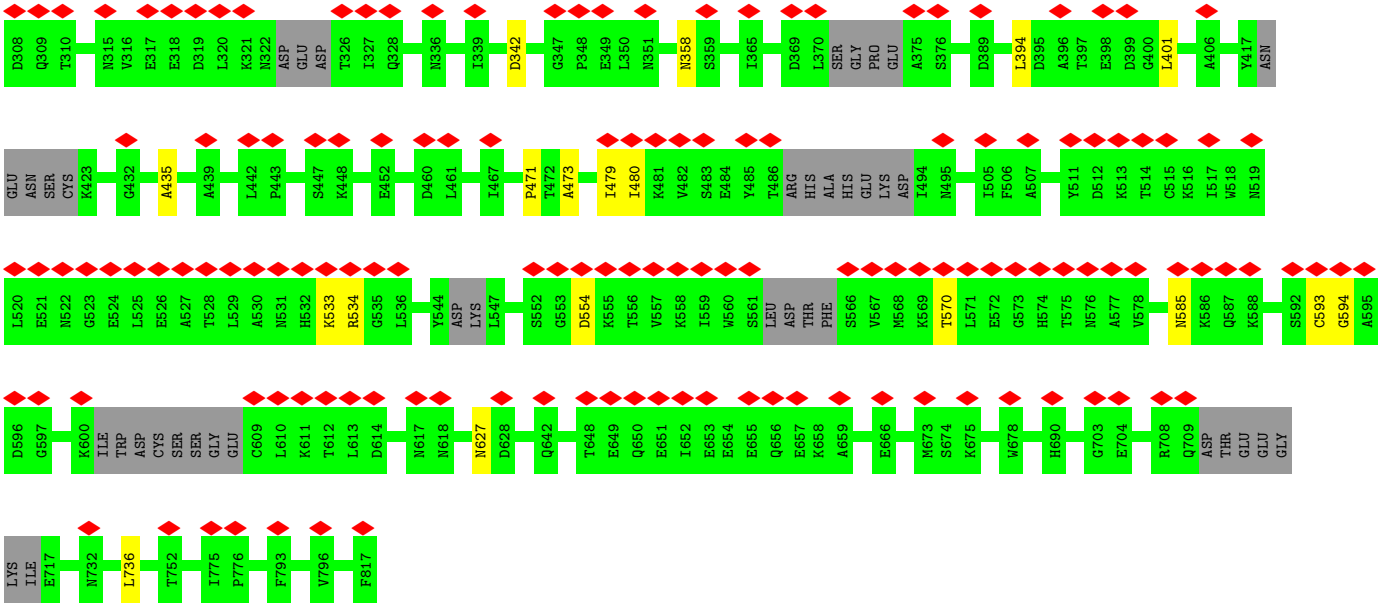
Chain B2:



• Molecule 34: U3 small nucleolar RNA-associated protein 13

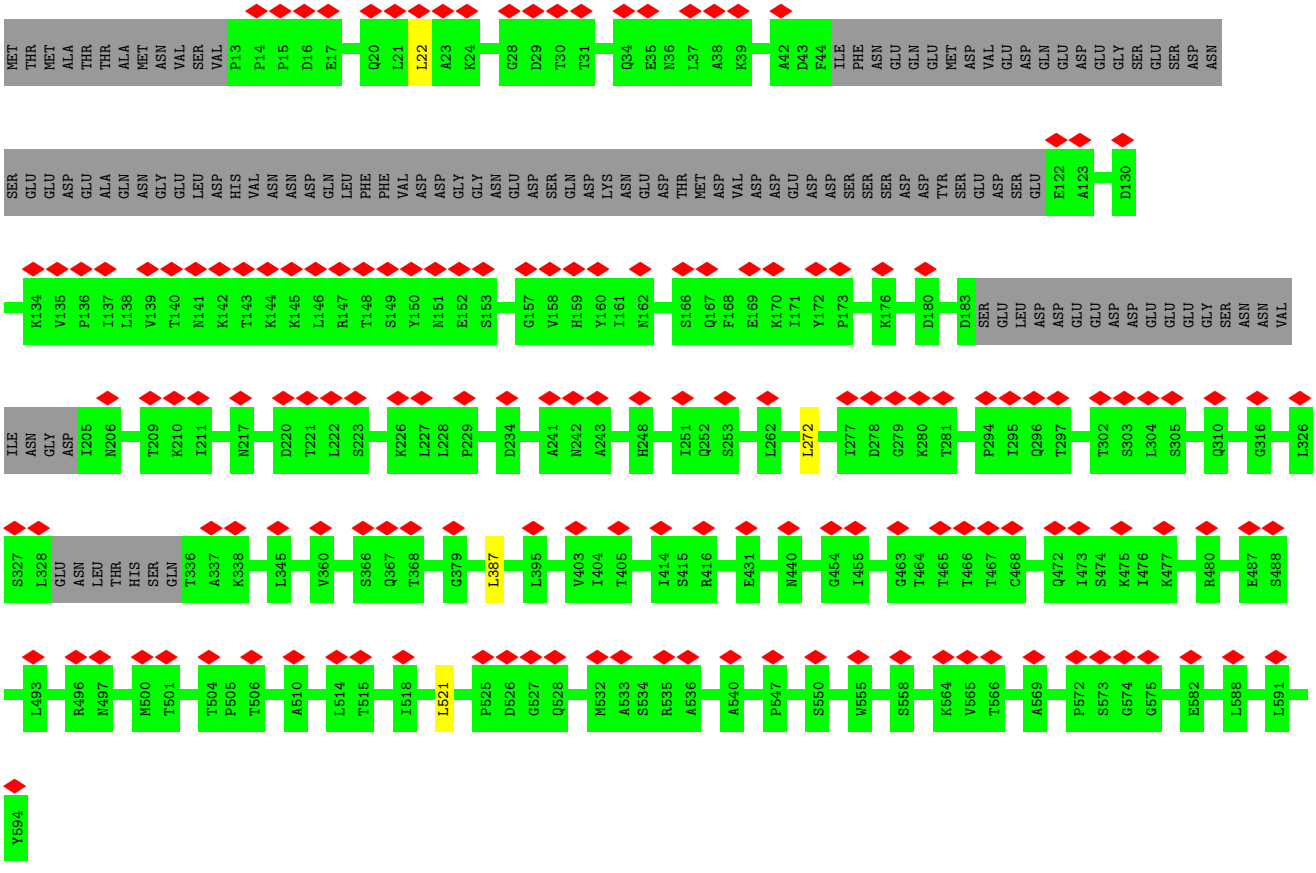
Chain B3:





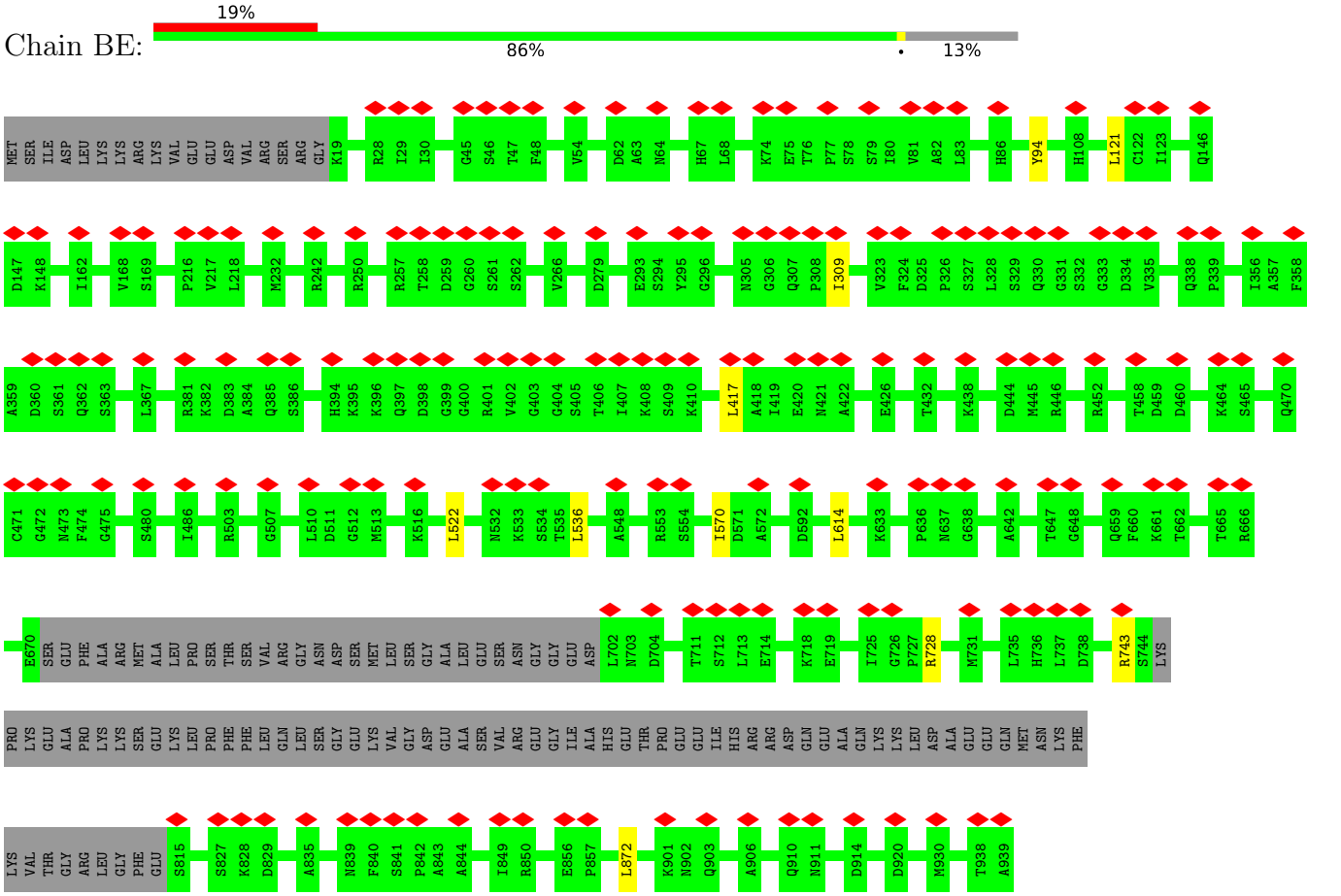
• Molecule 35: U3 small nucleolar RNA-associated protein 18

Chain B8:



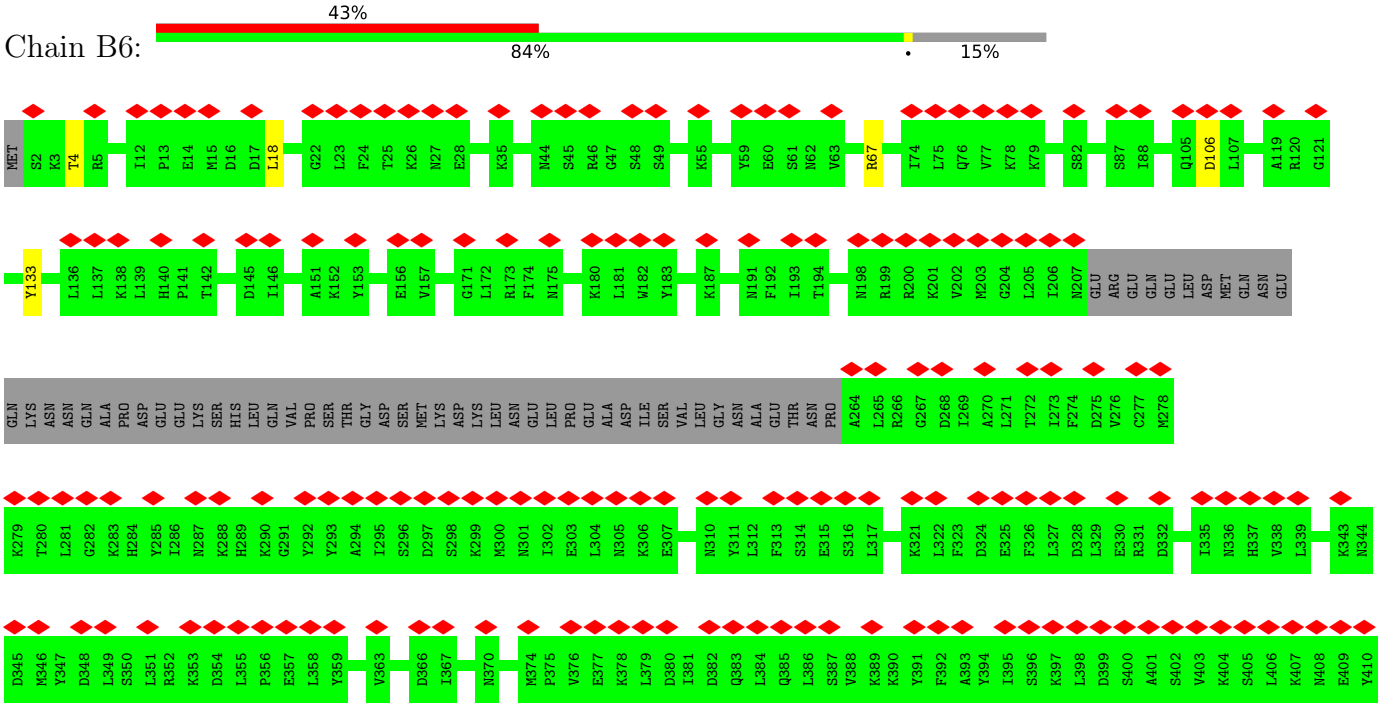
• Molecule 36: U3 small nucleolar RNA-associated protein 21

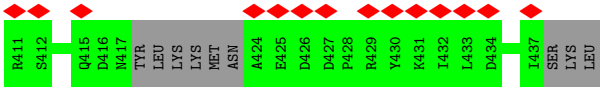
Chain BE:



• Molecule 37: U3 small nucleolar RNA-associated protein 6

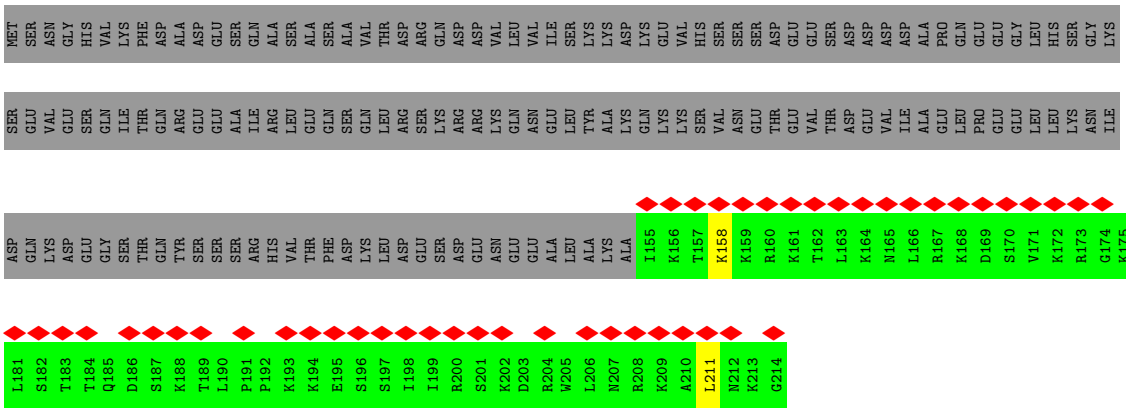
Chain B6:





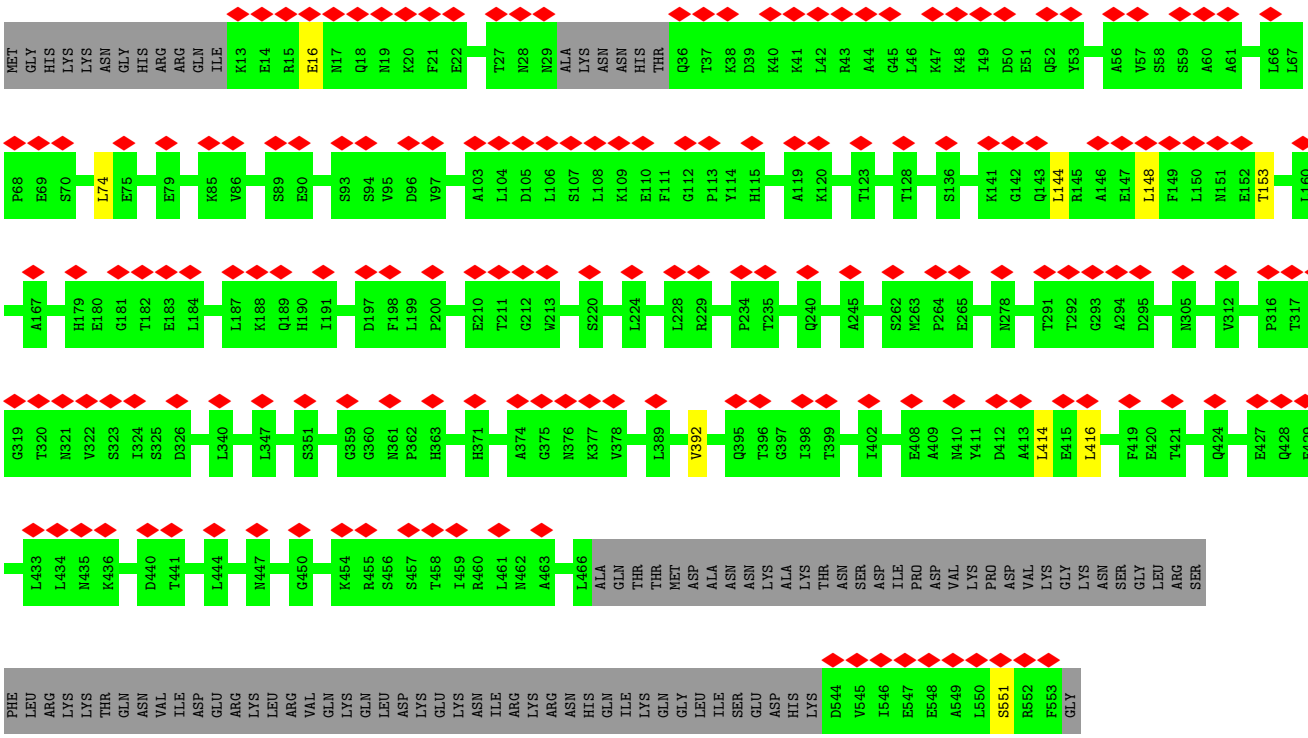
• Molecule 38: Bud site selection protein 21

Chain 5B:



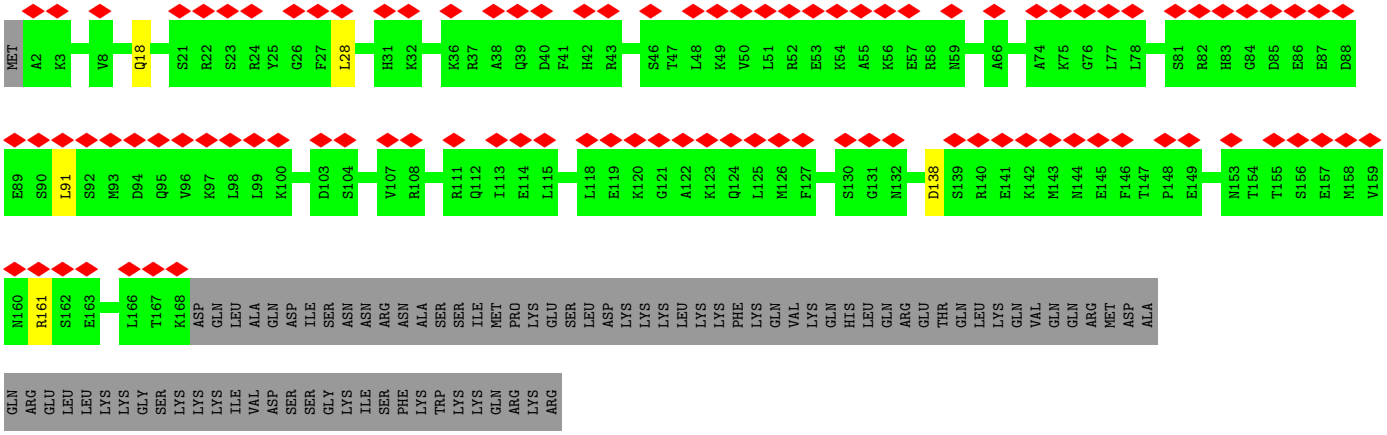
• Molecule 39: U3 small nucleolar RNA-associated protein 7

Chain 5C:



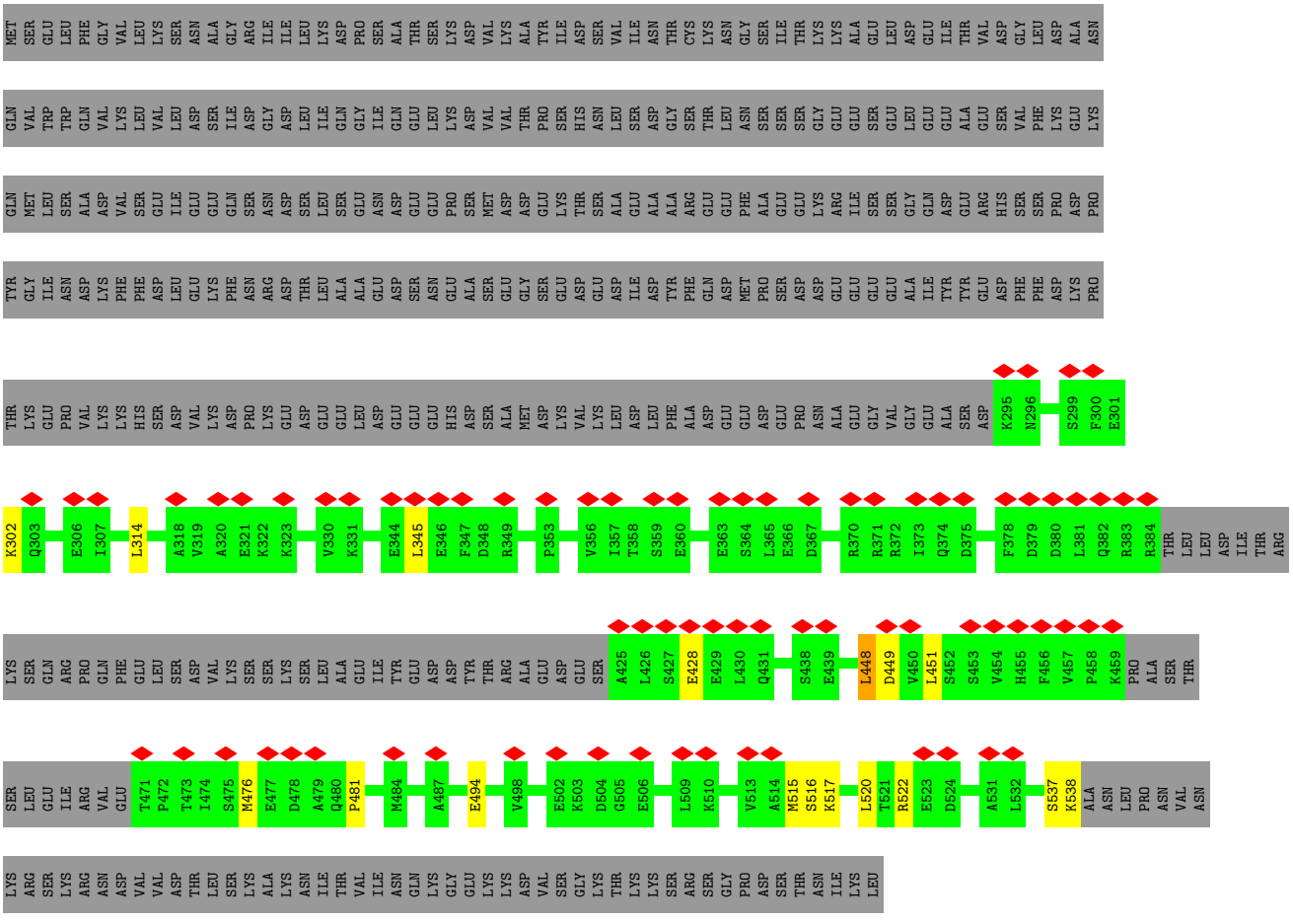
• Molecule 40: U3 small nucleolar RNA-associated protein 11

Chain 5D:



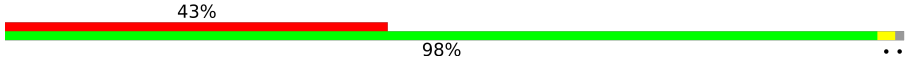
• Molecule 41: U3 small nucleolar RNA-associated protein MPP10

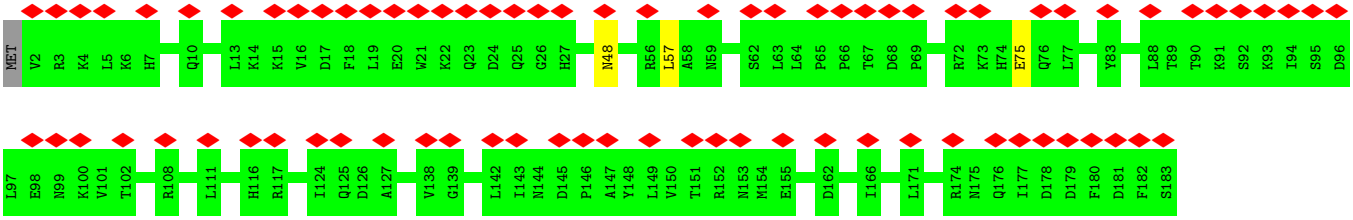
Chain 5E:



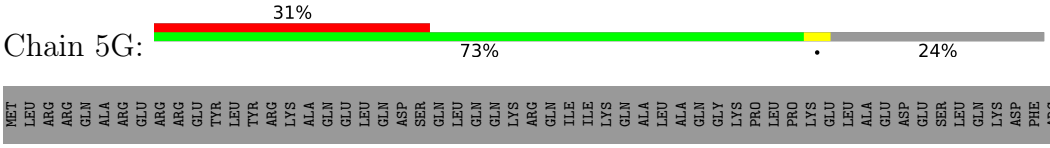
• Molecule 42: U3 small nucleolar ribonucleoprotein protein IMP3

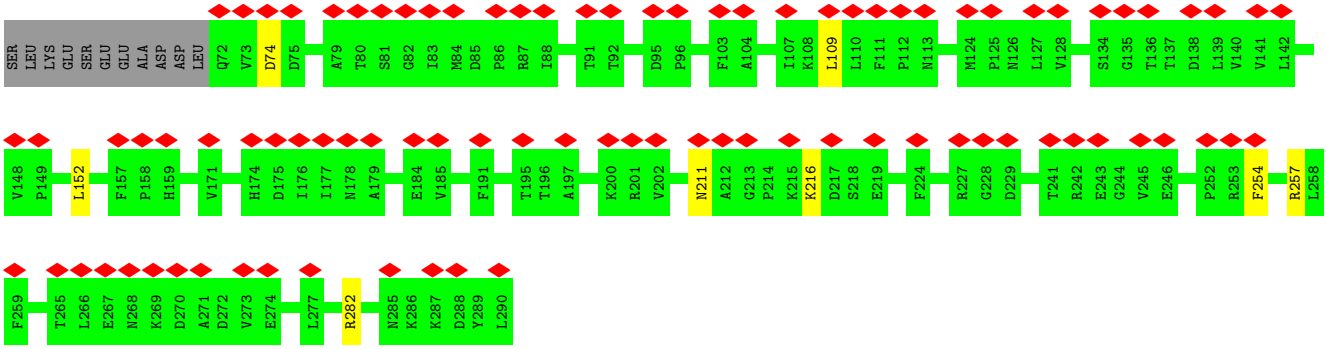
Chain 5F:



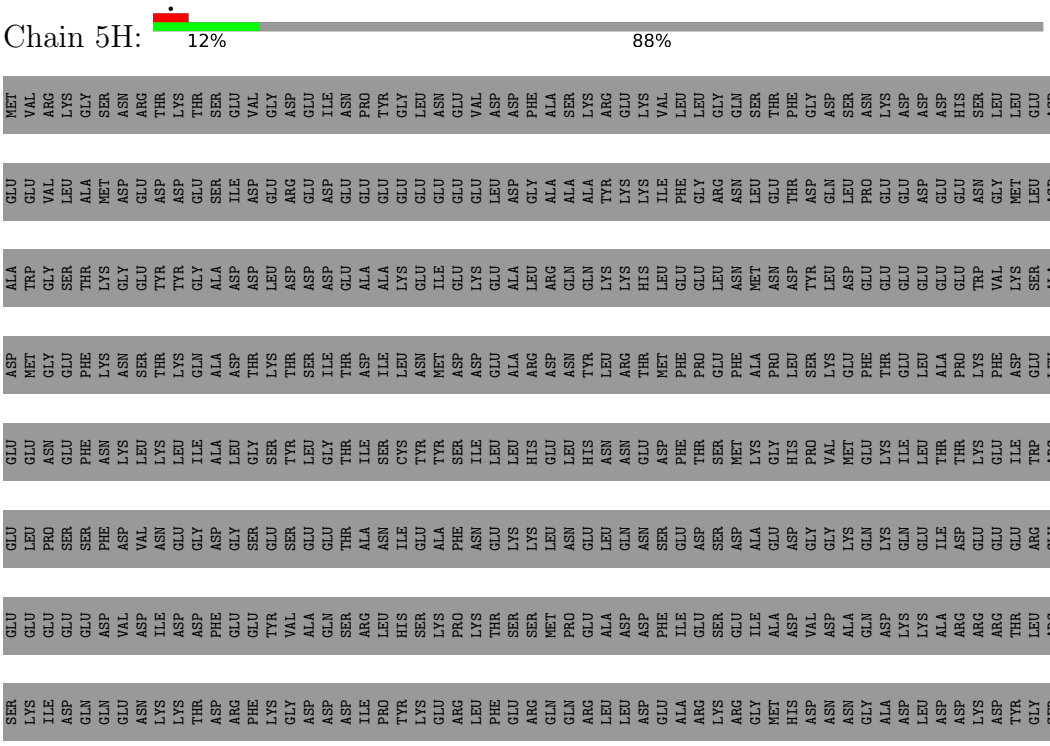


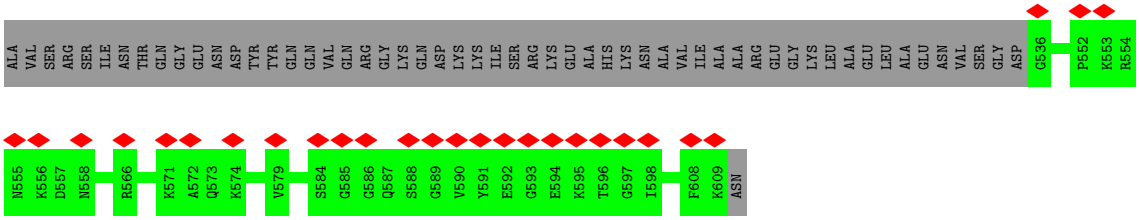
• Molecule 43: U3 small nucleolar ribonucleoprotein protein IMP4



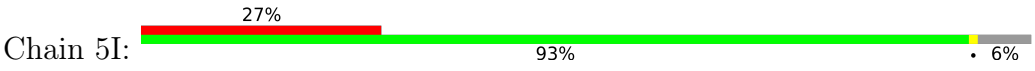


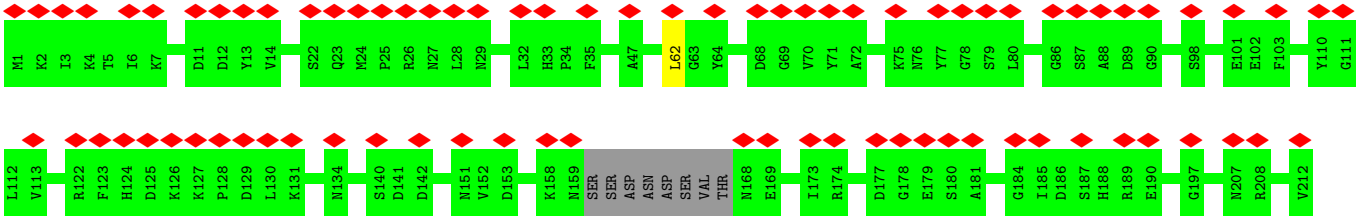
• Molecule 44: Something about silencing protein 10



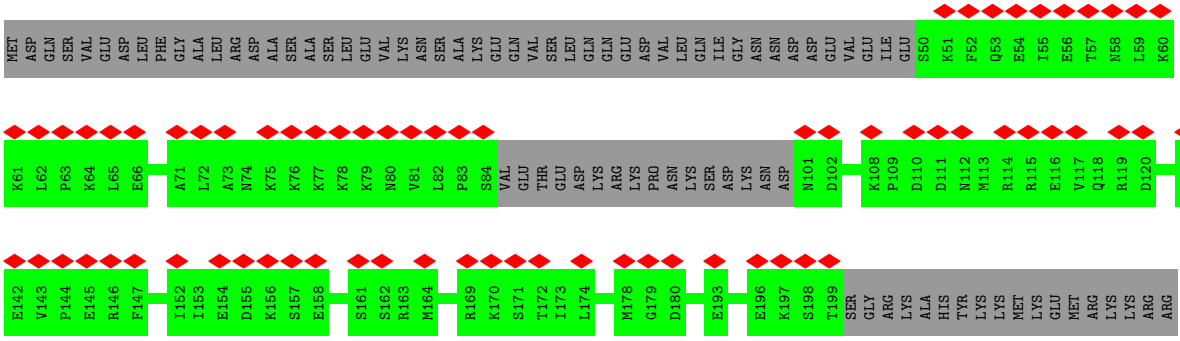


• Molecule 45: Protein SOF1

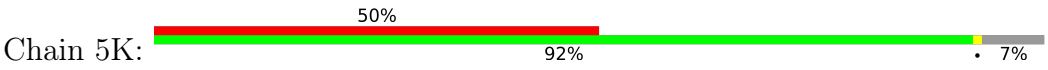


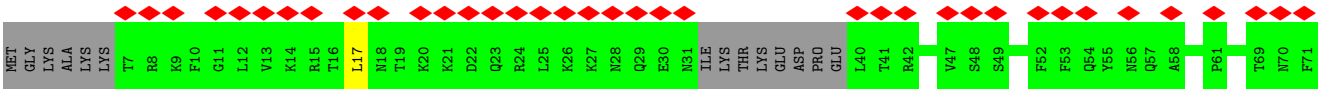


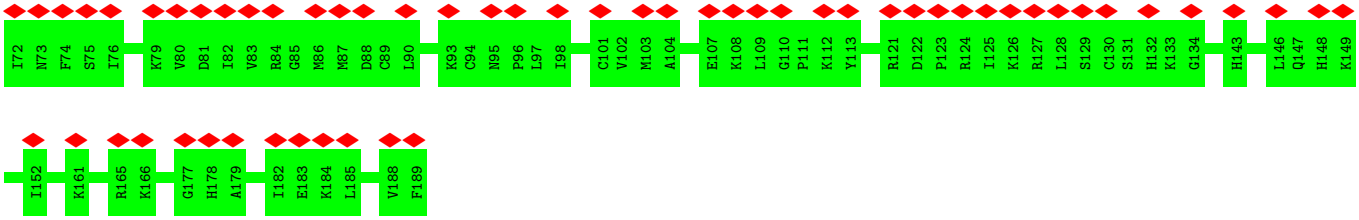
• Molecule 46: rRNA-processing protein FCF2



• Molecule 47: rRNA-processing protein FCF1

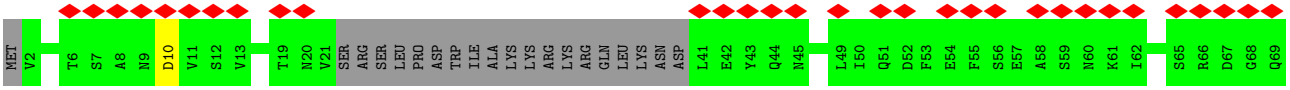


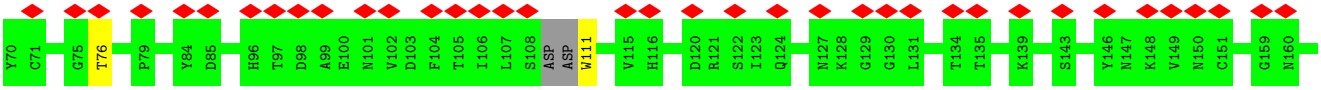


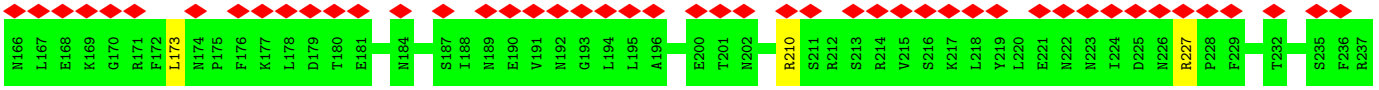


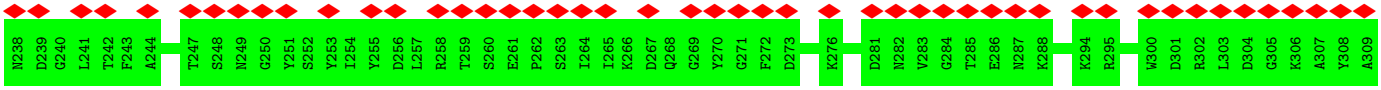
• Molecule 48: Ribosome biogenesis protein ENP2

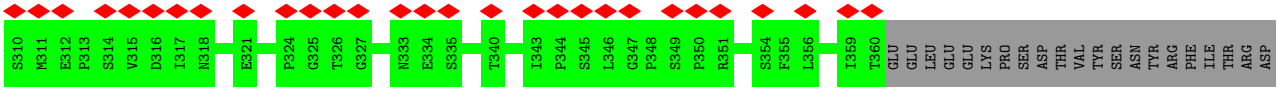
Chain RA:





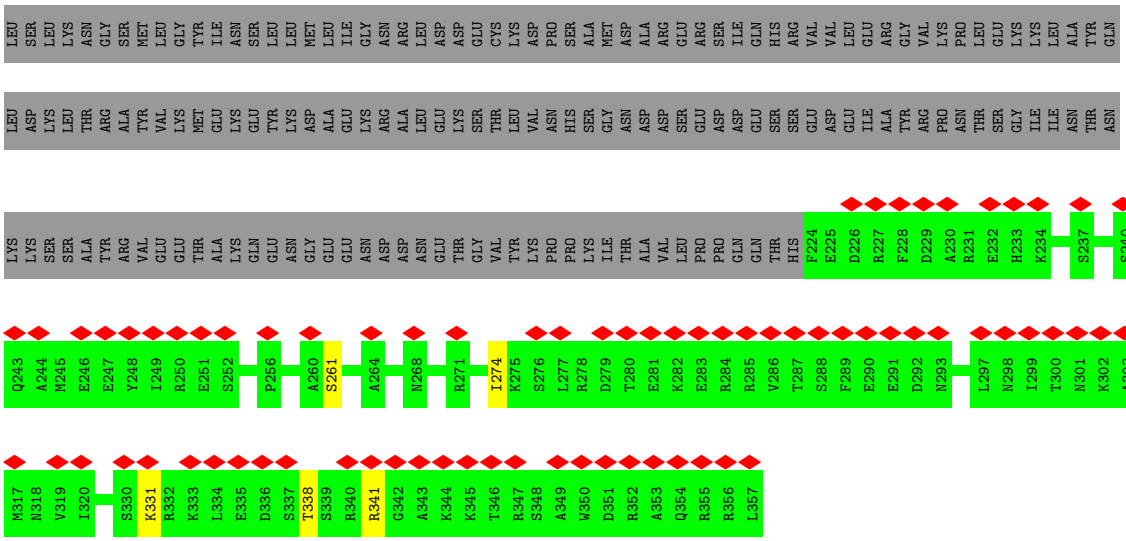






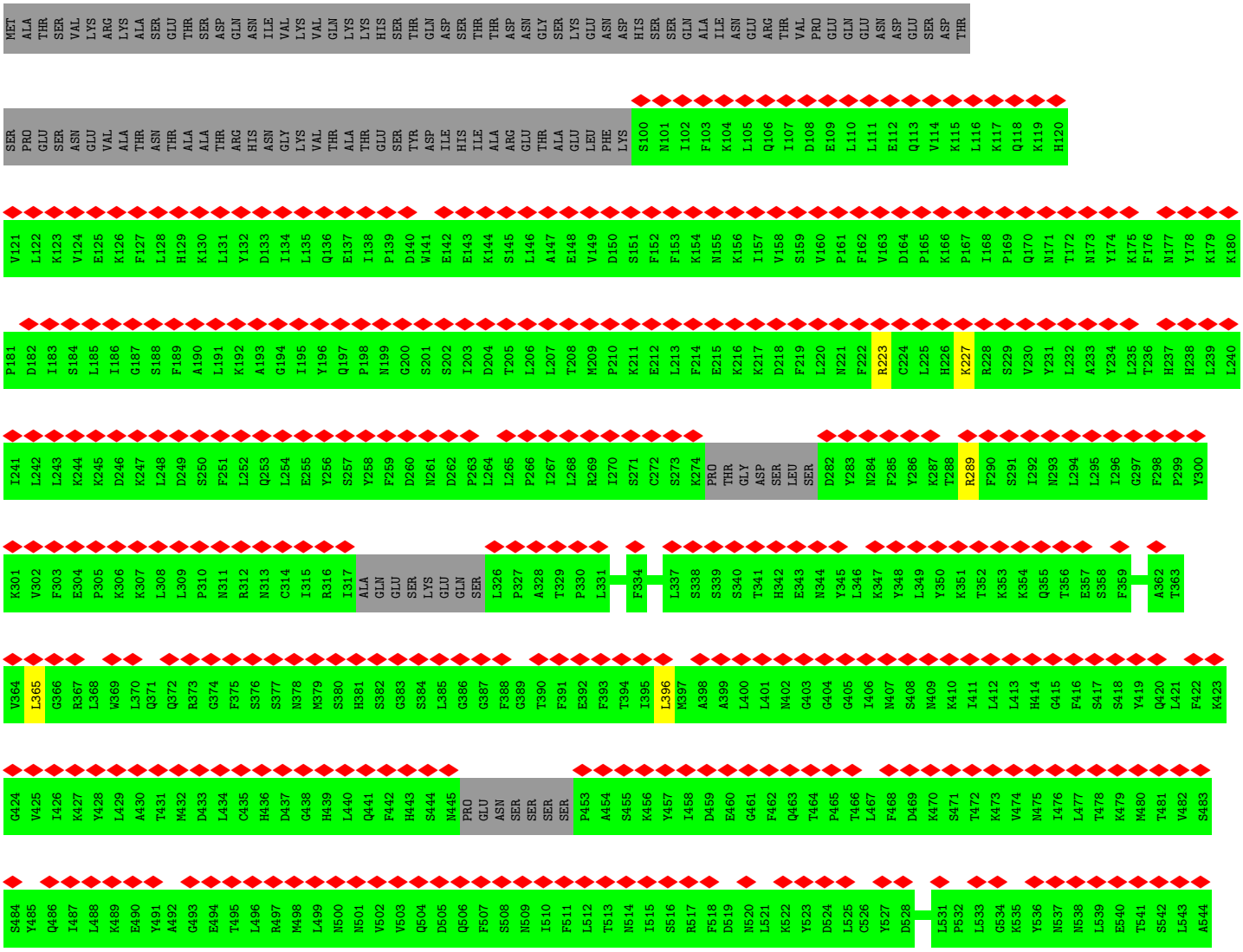
• Molecule 49: U3 small nucleolar ribonucleoprotein protein LCP5

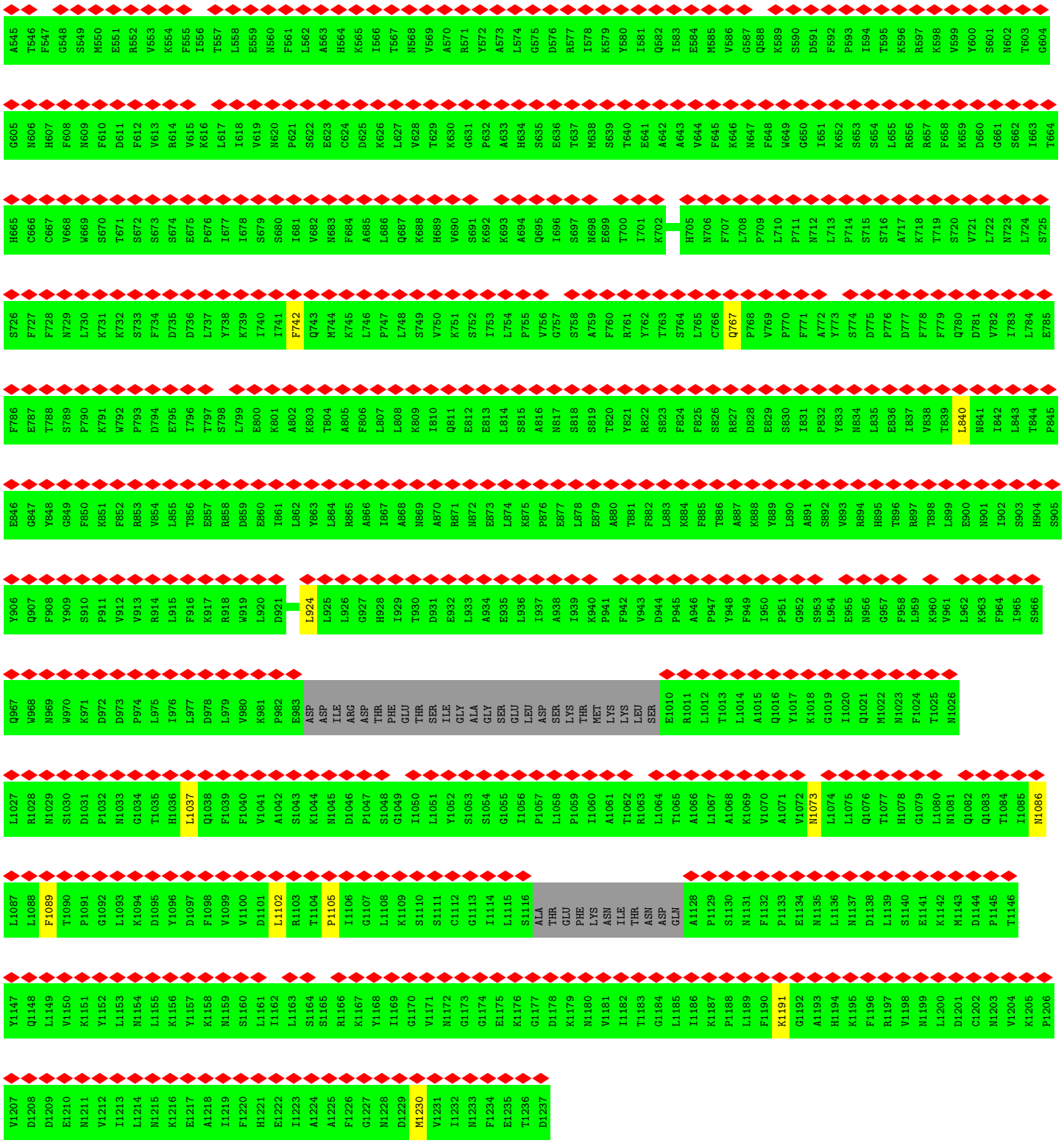
Chain RB:



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

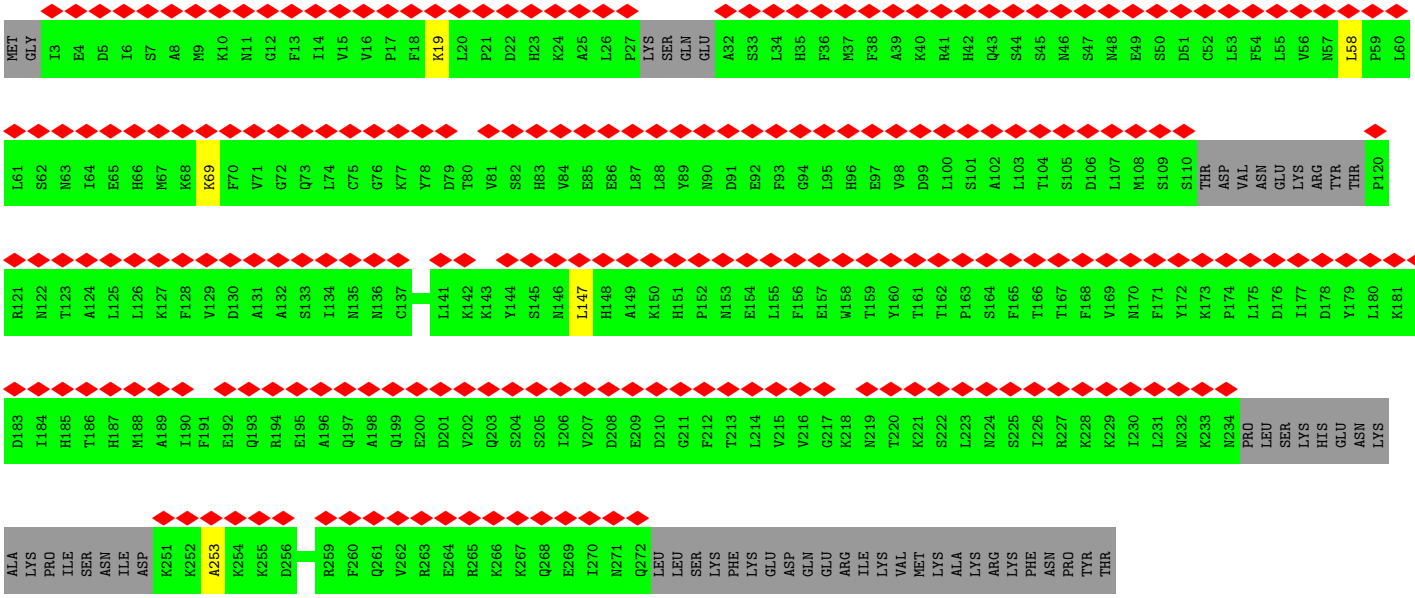
Chain RE:



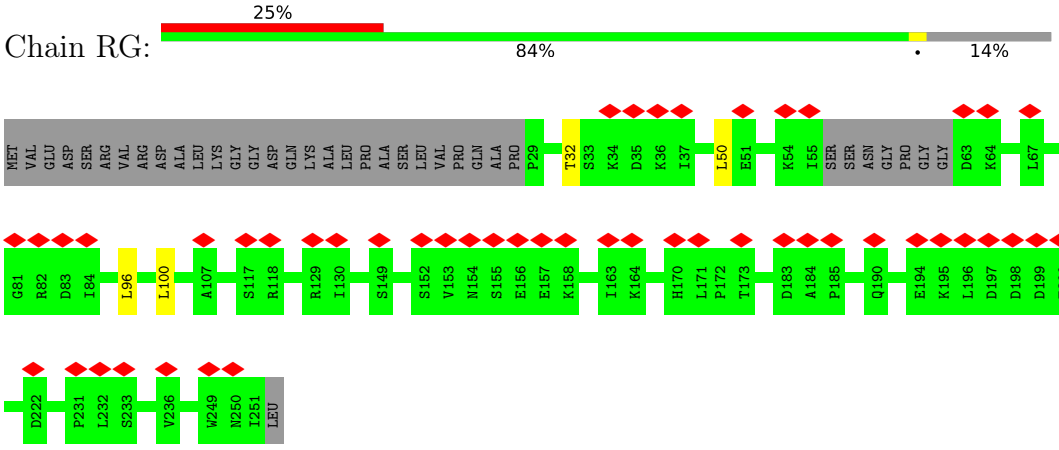


• Molecule 51: Ribosomal RNA-processing protein 7

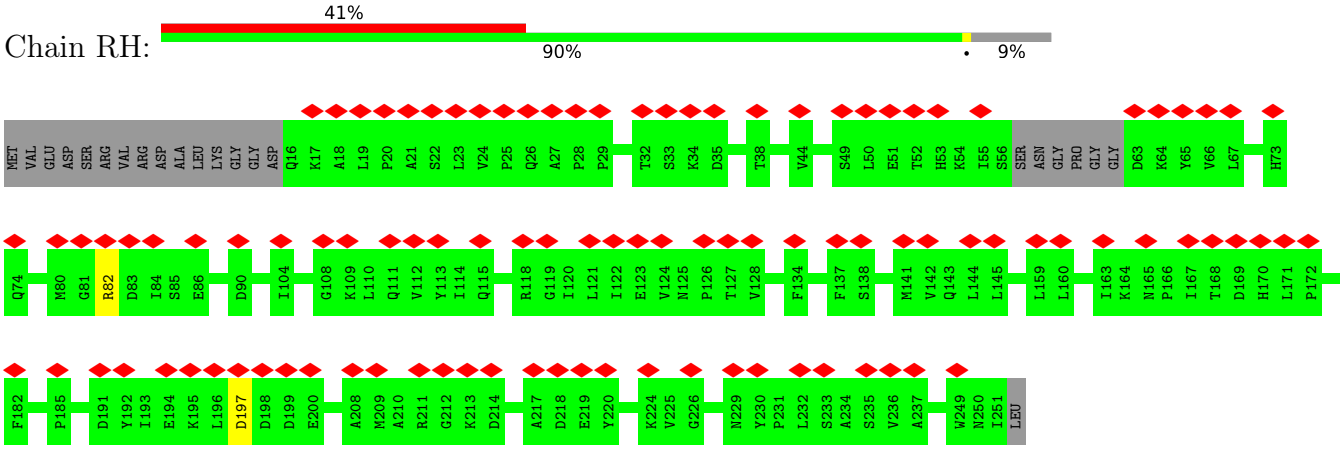
Chain RF:



• Molecule 52: Ribosomal RNA small subunit methyltransferase NEP1

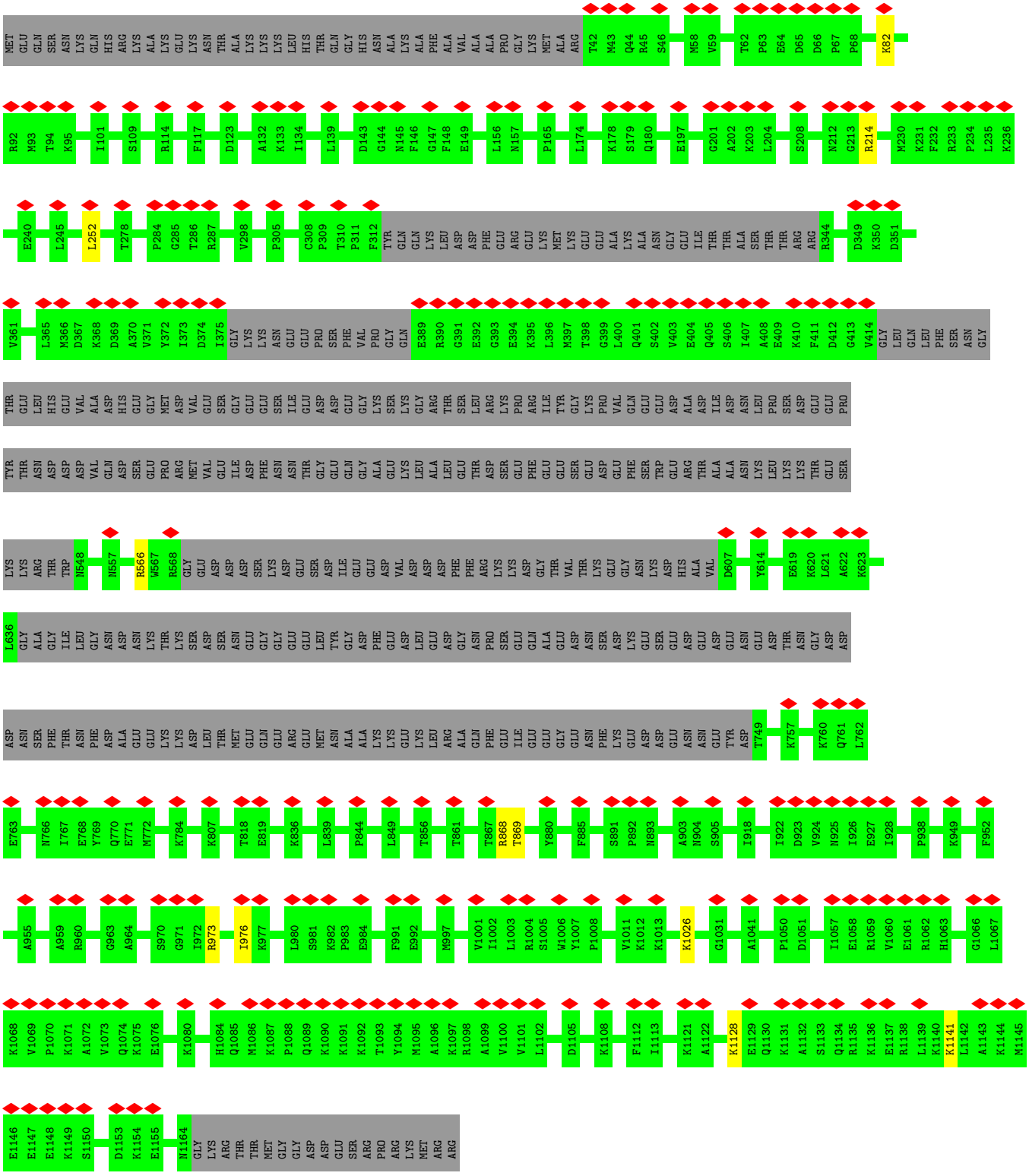


• Molecule 52: Ribosomal RNA small subunit methyltransferase NEP1



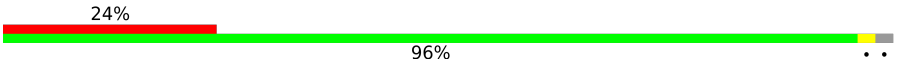
• Molecule 53: Ribosome biogenesis protein BMS1

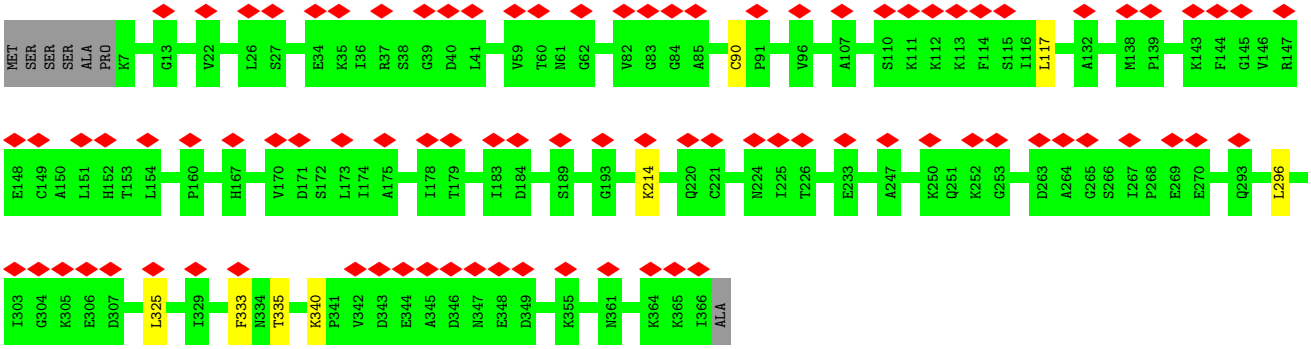
Chain RJ:



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

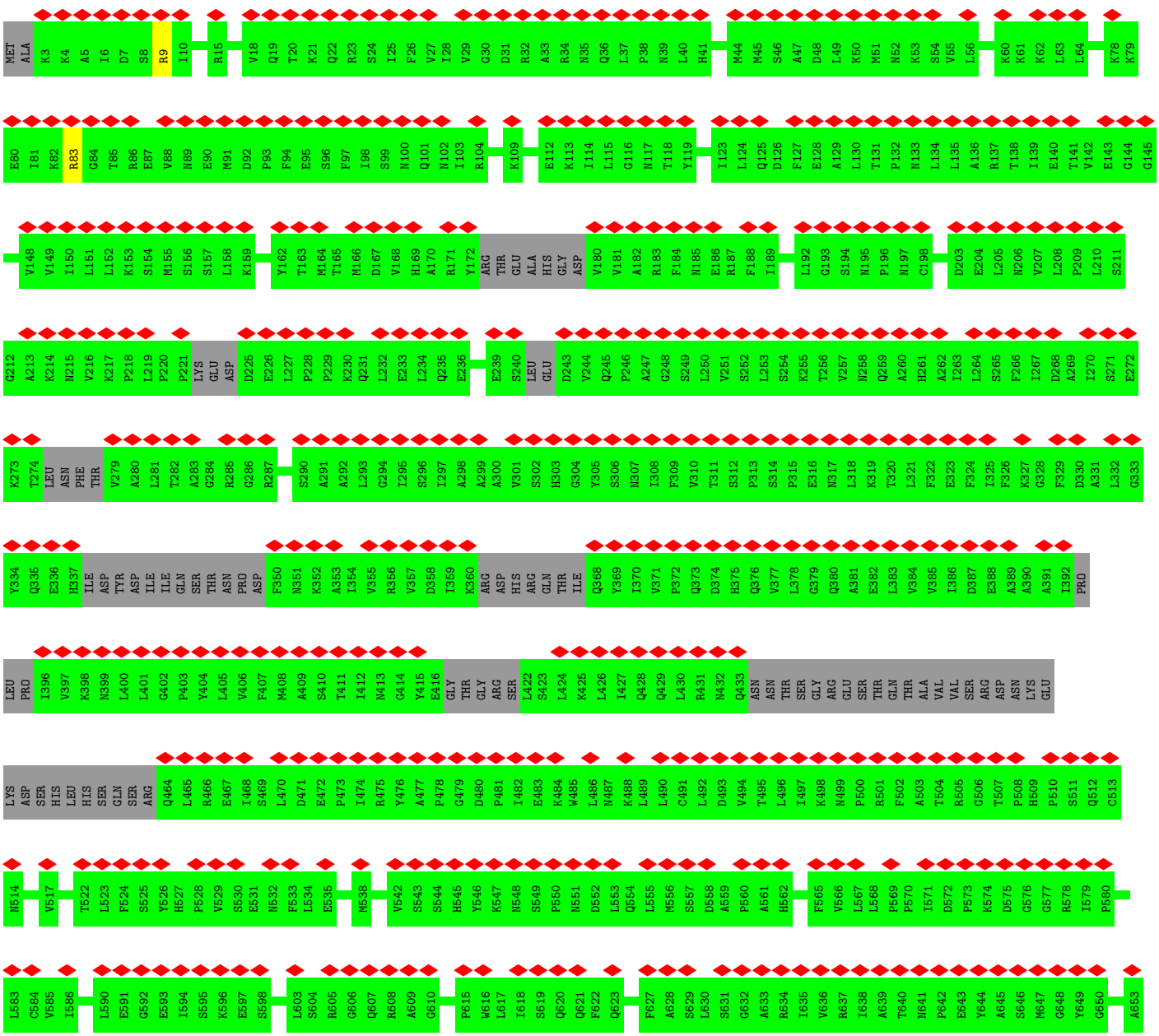
Chain RK:

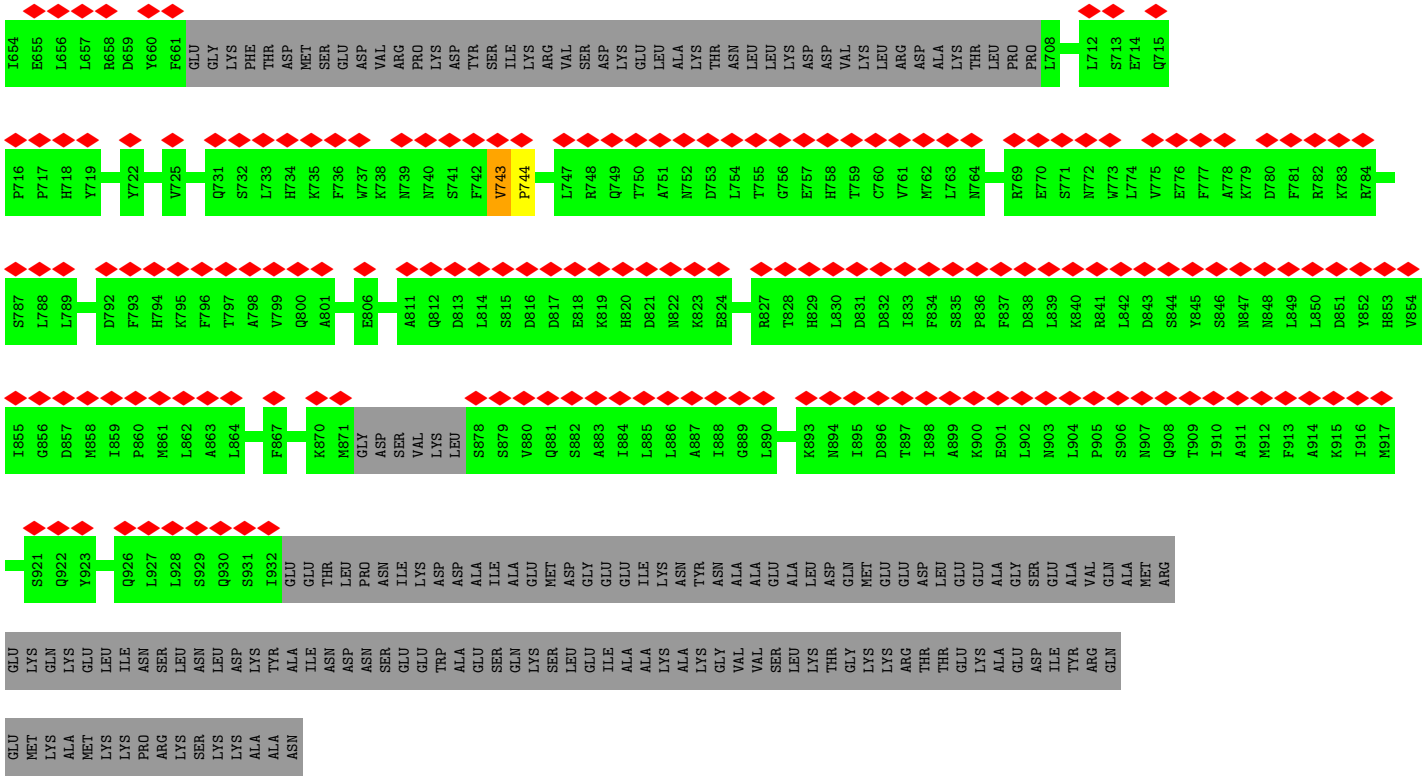




• Molecule 55: RNA cytidine acetyltransferase

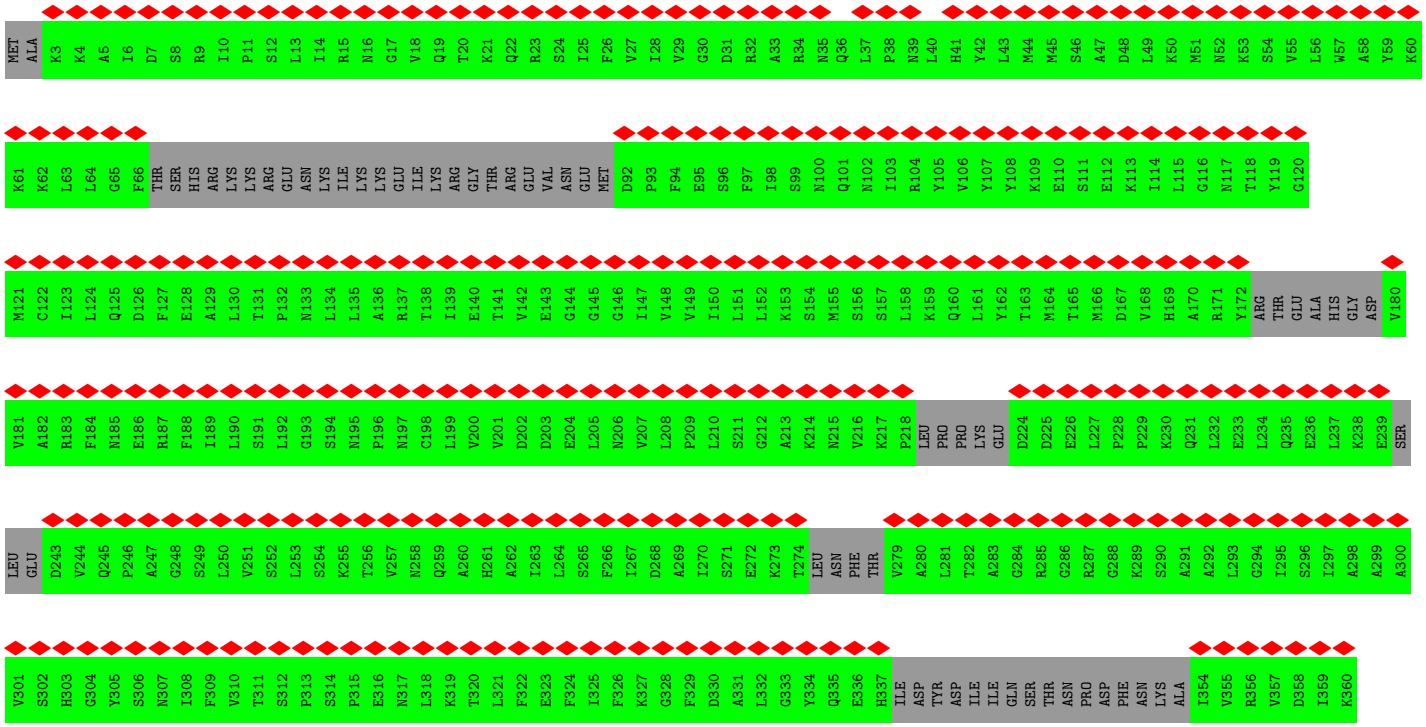
Chain RL:

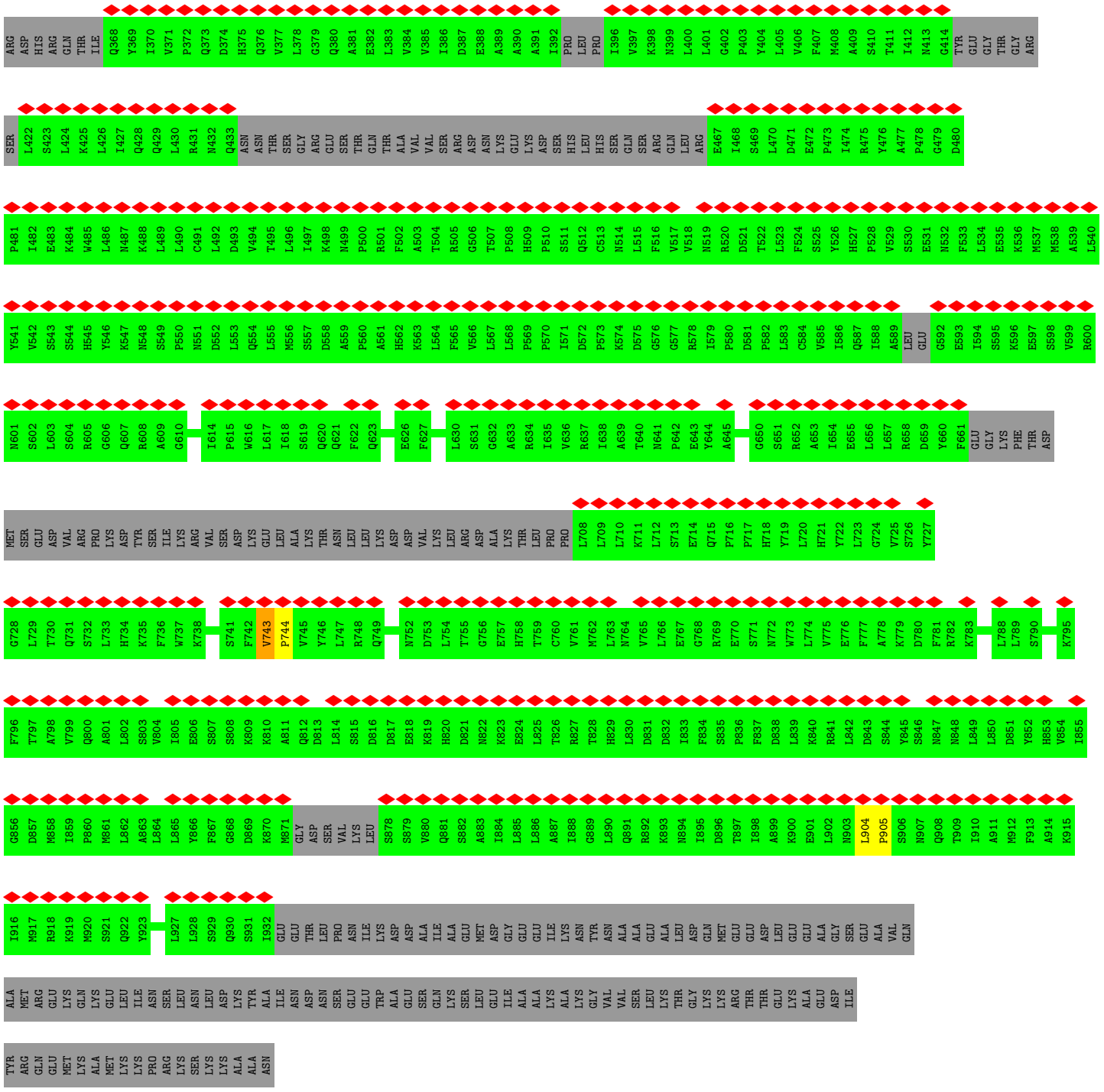




• Molecule 55: RNA cytidine acetyltransferase

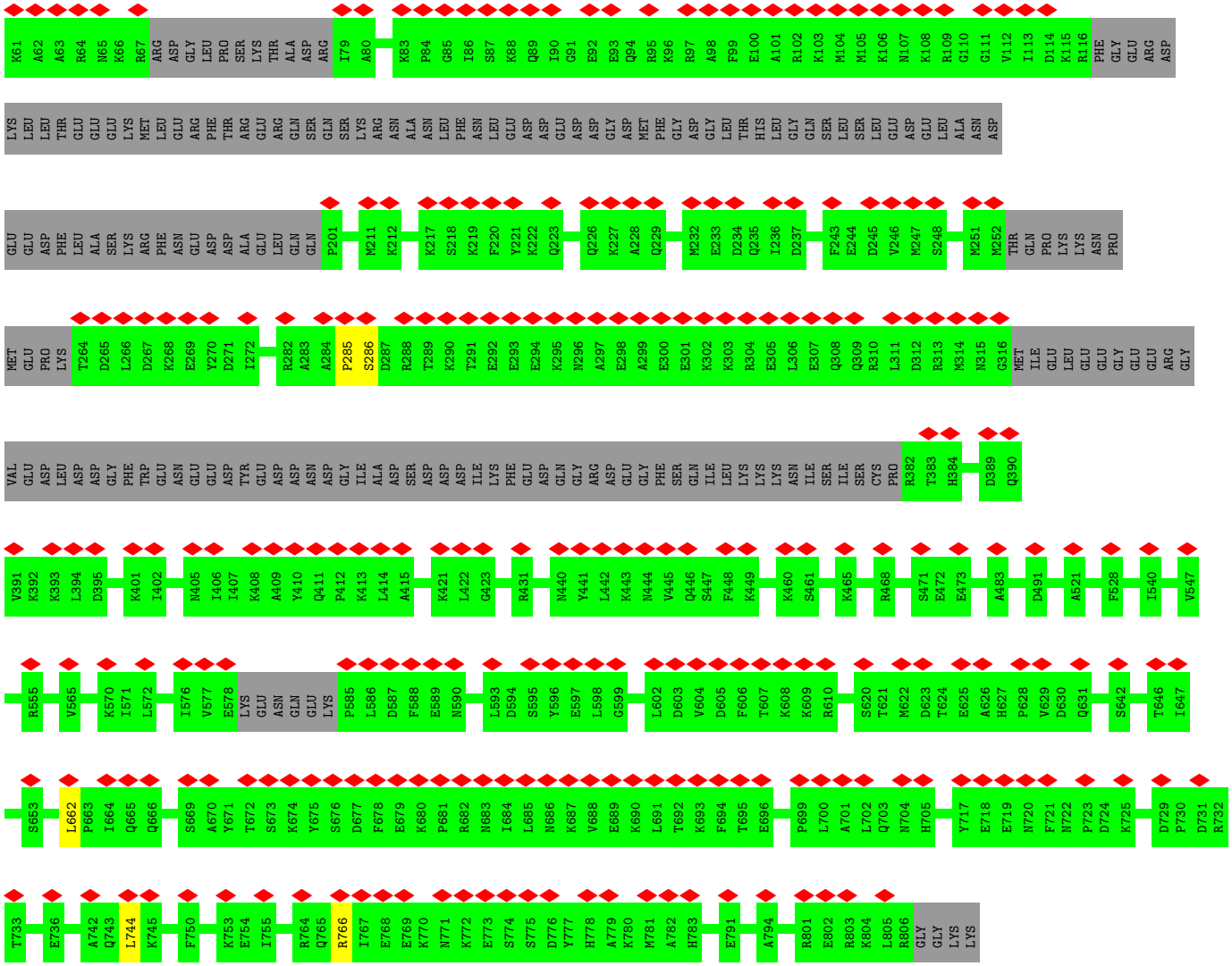
Chain RM:





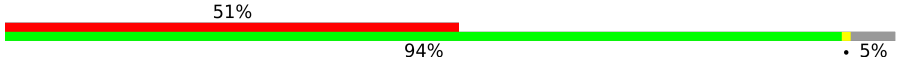
• Molecule 56: Nucleolar complex protein 14

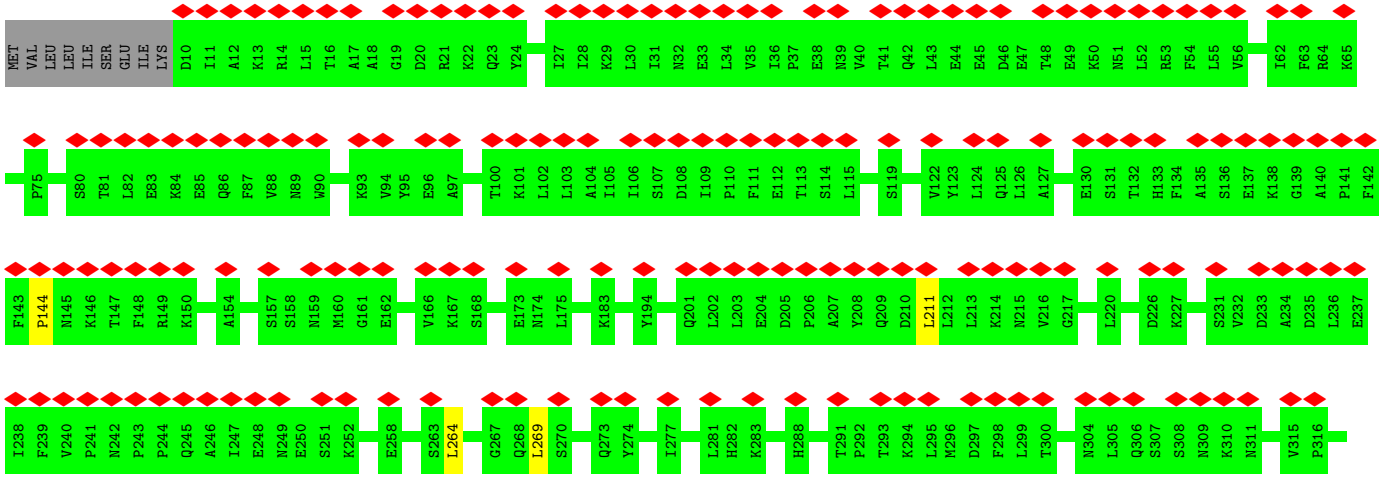
Chain RN:

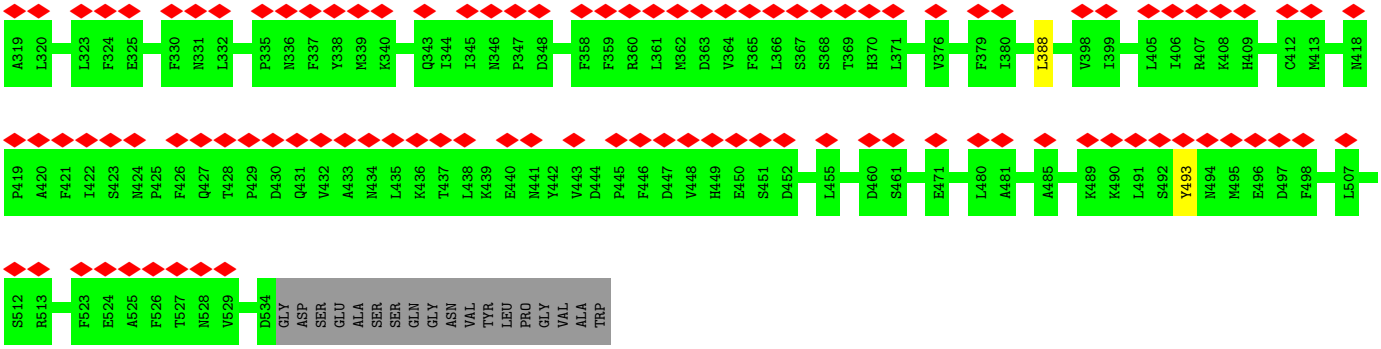


• Molecule 57: Nucleolar complex protein 4

Chain RO:

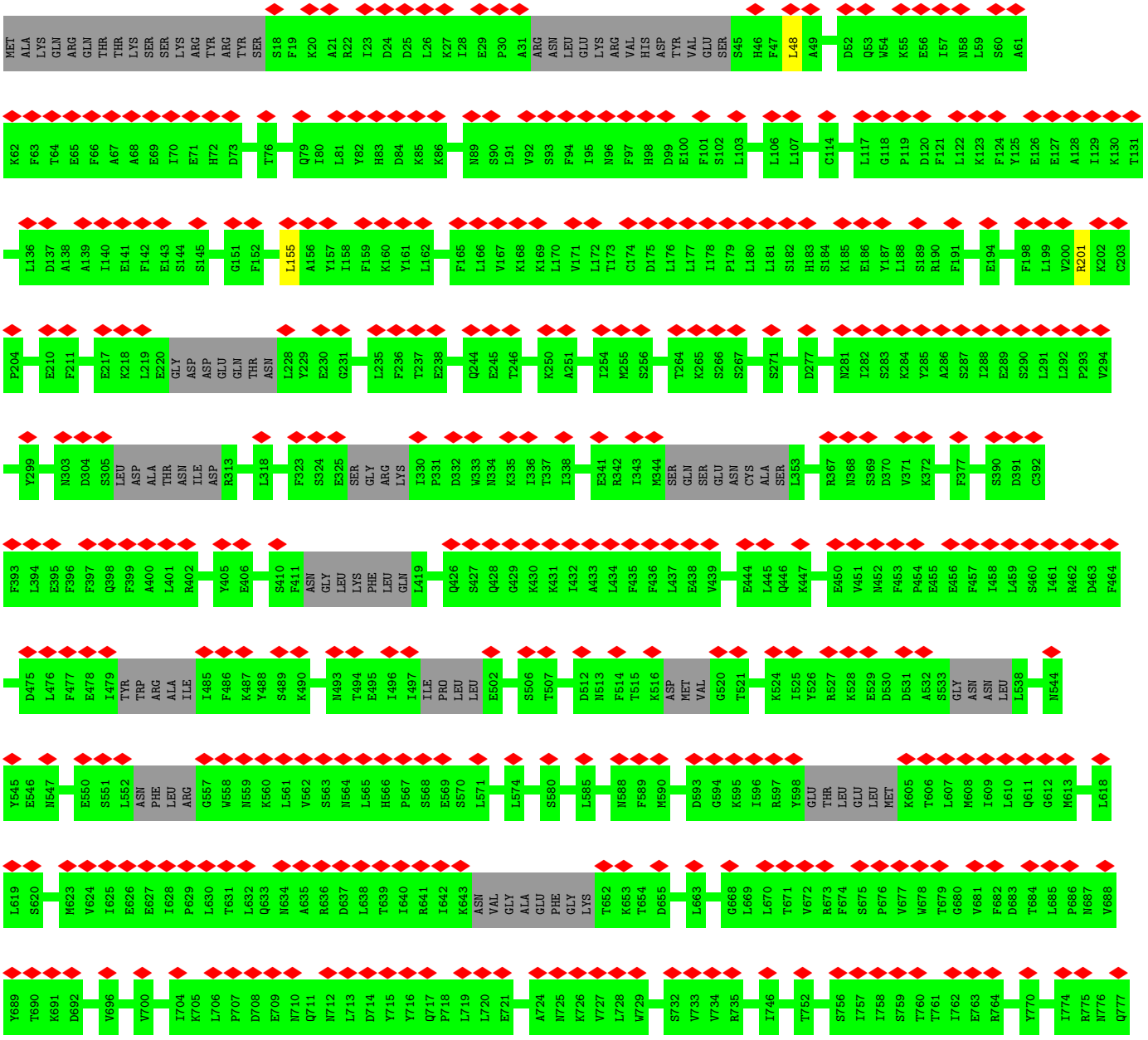


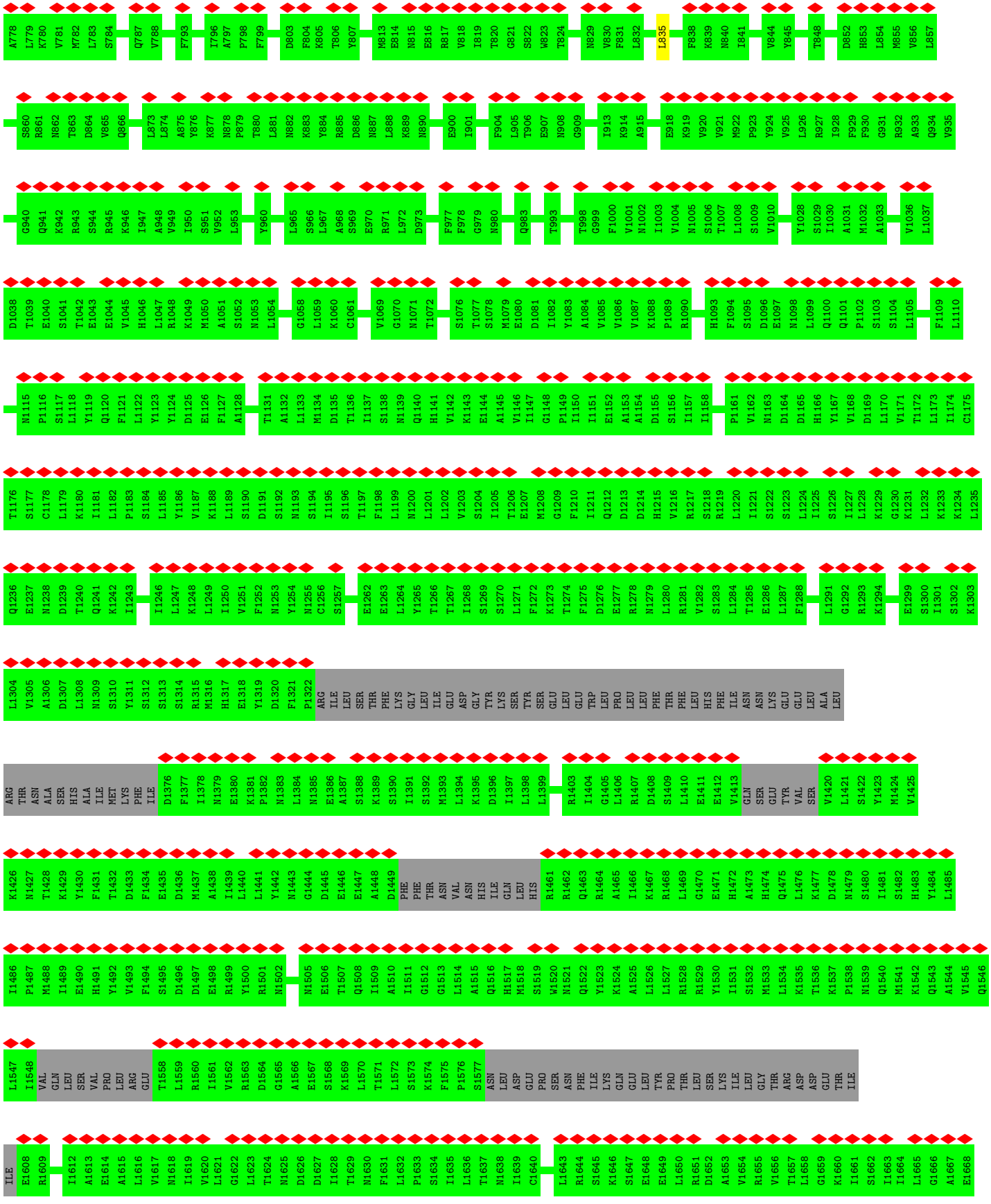




• Molecule 58: U3 small nucleolar RNA-associated protein 20

Chain RP:

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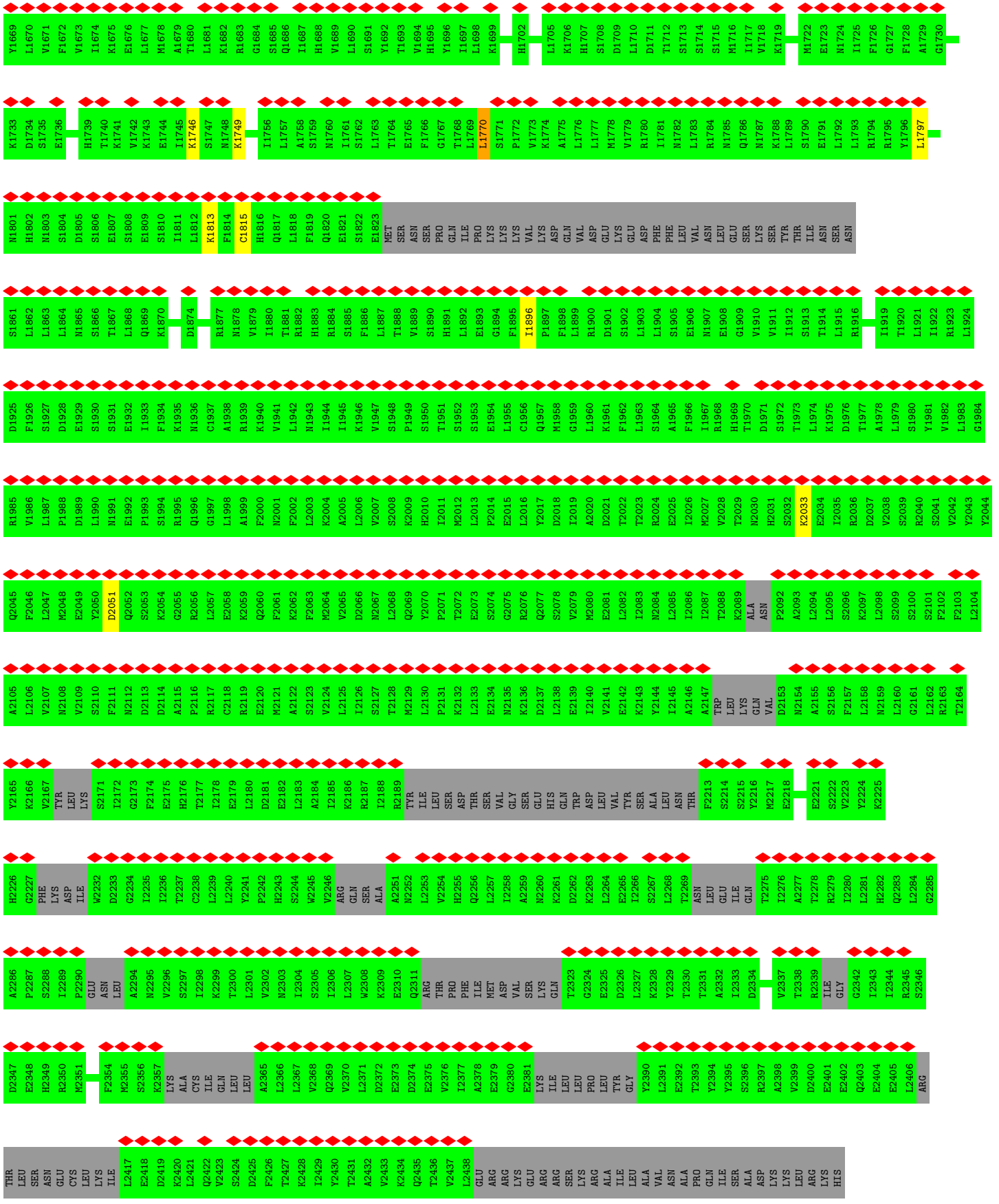
Q787 V788
F793
I796 A797 P798 F799
D803 F804 K805 T806 Y807
M813 E814 N815 E816 R817 V818 I819 T820 G821 S822 W823 T824
N829 V830 F831 L832
L835
F838 K839 N840 I841
V844 Y845
T848
D852 H853 L854 M855 V856 L857
S860 R861 N862 T863 D864 V865 Q866
L873 L874 A875 Y876 K877 N878 P879 T880 L881 N882 K883 Y884 R885 D886 N887 L888 K889 N890
E900 I901
F904 L905 T906 E907 N908 G909
I913 K914 A915
E918 K919 V920 V921 M922 P923 Y924 V925 L926 R927 I928 F929 F930 G931 R932 A933 Q934 V935
G940 Q941 K942 R943 S944 R945 K946 I947 A948 V949 I950 S951 V952 L953
Y960
L965 S966 L967 A968 S969 E970 R971 L972 D973
F977 F978 G979 N980
Q983
T993
T998 G999 F1000 V1001 N1002 I1003 V1004 N1005 S1006 T1007 L1008 S1009 V1010
Y1028 S1029 I1030 A1031 M1032 A1033
V1036 L1037
D1038 T1039 E1040 S1041 T1042 E1043 E1044 V1045 H1046 L1047 R1048 K1049 M1050 A1051 S1052 N1053 L1054
G1058 L1059 K1060 C1061
V1069 G1070 N1071 T1072
S1076 T1077 S1078 M1079 E1080 D1081 I1082 Y1083 A1084 V1085 V1086 V1087 K1088 P1089 R1090
H1093 F1094 S1095 D1096 E1097 N1098 L1099 Q1100 Q1101 P1102 S1103 S1104 L1105
F1109 L1110
N1115 P1116 S1117 L1118 Y1119 Q1120 F1121 L1122 Y1123 Y1124 D1125 E1126 F1127 A1128
T1131 A1132 L1133 M1134 D1135 T1136 I1137 S1138 N1139 Q1140 H1141 V1142 K1143 E1144 A1145 V1146 I1147 G1148 P1149 I1150 I1151 E1152 A1153 A1154 D1155 S1156 I1157 I1158
P1161 V1162 N1163 D1164 D1165 H1166 Y1167 V1168 D1169 L1170 V1171 T1172 L1173 I1174 C1175
T1176 S1177 C1178 L1179 K1180 I1181 L1182 P1183 S1184 L1185 Y1186 V1187 K1188 L1189 S1190 D1191 S1192 N1193 S1194 I1195 S1196 T1197 F1198 L1199 N1200 L1201 L1202 V1203 S1204 I1205 T1206 E1207 M1208 G1209 F1210 I1211 Q1212 D1213 D1214 H1215 V1216 R1217 S1218 R1219 L1220 I1221 S1222 S1223 L1224 I1225 S1226 I1227 L1228 K1229 G1230 K1231 L1232 K1233 K1234 L1235
Q1236 E1237 N1238 D1239 T1240 Q1241 K1242 I1243
I1246 L1247 K1248 L1249 I1250 V1251 F1252 N1253 Y1254 N1255 C1256 S1257
E1262 E1263 L1264 Y1265 T1266 T1267 I1268 S1269 S1270 L1271 F1272 K1273 T1274 F1275 D1276 E1277 R1278 N1279 L1280 R1281 V1282 S1283 L1284 T1285 E1286 L1287 F1288
L1291 G1292 R1293 K1294
E1299 S1300 I1301 S1302 K1303
L1304 V1305 A1306 D1307 L1308 N1309 S1310 Y1311 S1312 S1313 S1314 R1315 M1316 H1317 E1318 Y1319 D1320 F1321 P1322
ARG ILE LEU SER THR PHE LYS GLY LEU ILE GLU ASP GLY TYR LYS SER TYR SER GLU LEU GLU TRP LEU PRO LEU LEU PHE THR PHE LEU HIS PHE ILE ASN ASN LYS GLU GLU LEU ALA LEU
ARG THR ASN ALA SER HIS ALA ILE MET LYS PHE ILE
D1376 F1377 I1378 N1379 E1380 K1381 P1382 N1383 L1384 N1385 E1386 A1387 S1388 K1389 S1390 I1391 S1392 M1393 L1394 K1395 D1396 I1397 L1398 L1399
R1403 I1404 G1405 L1406 R1407 D1408 S1409 L1410 E1411 E1412 V1413
GLN SER GLU TYR VAL SER
V1420 L1421 S1422 Y1423 M1424 V1425
K1426 N1427 T1428 K1429 Y1430 F1431 T1432 D1433 F1434 E1435 D1436 M1437 A1438 I1439 L1440 L1441 Y1442 N1443 G1444 D1445 E1446 E1447 A1448 D1449
PHE PHE THR ASN VAL ASN HIS ILE GLN LEU HIS
R1461 R1462 Q1463 R1464 A1465 I1466 K1467 R1468 L1469 G1470 E1471 H1472 A1473 H1474 Q1475 L1476 K1477 D1478 N1479 S1480 I1481 S1482 H1483 Y1484 L1485
I1486 P1487 M1488 I1489 E1490 H1491 Y1492 V1493 F1494 S1495 D1496 D1497 E1498 R1499 Y1500 R1501 N1502
N1505 E1506 T1507 Q1508 I1509 A1510 I1511 G1512 G1513 L1514 A1515 Q1516 H1517 M1518 S1519 W1520 N1521 Q1522 Y1523 K1524 A1525 L1526 L1527 R1528 R1529 Y1530 I1531 S1532 M1533 L1534 K1535 T1536 K1537 P1538 N1539 Q1540 M1541 K1542 Q1543 A1544 V1545 Q1546
L1547 I1548
VAL GLN LEU SER VAL PRO LEU ARG GLU
T1558 L1559 R1560 I1561 V1562 R1563 D1564 G1565 A1566 E1567 S1568 K1569 L1570 T1571 L1572 S1573 K1574 F1575 P1576 S1577
ASN LEU ASP GLU PRO SER ASN PHE ILE LYS GLN GLU LEU TYR PRO THR LEU SER LYS ILE LEU GLY THR ARG ASP ASP GLU THR ILE
ILE E1608 R1609
I1612 A1613 E1614 A1615 L1616 V1617 N1618 I1619 V1620 L1621 G1622 L1623 T1624 N1625 D1626 D1627 I1628 T1629 N1630 F1631 L1632 P1633 S1634 L1635 L1636 T1637 N1638 I1639 C1640
L1643 R1644 S1645 K1646 S1647 E1648 E1649 L1650 R1651 D1652 A1653 V1654 R1655 V1656 T1657 L1658 G1659 K1660 I1661 S1662 I1663 I1664 L1665 G1666 A1667 E1668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N1801 H1802 N1803 S1804 D1805 S1806 E1807 S1808 E1809 S1810 I1811 L1812 K1813 F1814 C1815 H1816 Q1817 L1818 F1819 Q1820 E1821 S1822 E1823 MET SER ASN SER PRO GLN ILE PRO LYS LYS LYS VAL LYS ASP GLN VAL ASP GLU LYS GLU ASP PHE PHE LEU VAL ASN LEU GLU SER LYS SER TYR THR ILE ASN SER ASN
S1861 L1862 L1863 L1864 N1865 S1866 T1867 L1868 Q1869 K1870 D1874 R1877 N1878 V1879 I1880 T1881 R1882 H1883 R1884 S1885 F1886 L1887 T1888 V1889 S1890 H1891 L1892 E1893 G1894 F1895 I1896 P1897 F1898 L1899 R1900 D1901 S1902 L1903 L1904 S1905 E1906 N1907 E1908 G1909 V1910 V1911 I1912 S1913 T1914 L1915 R1916 I1919 T1920 L1921 I1922 R1923 L1924
D1925 F1926 S1927 D1928 E1929 S1930 S1931 E1932 I1933 F1934 K1935 N1936 C1937 A1938 R1939 K1940 V1941 L1942 N1943 I1944 I1945 K1946 V1947 S1948 P1949 S1950 T1951 S1952 S1953 E1954 L1955 C1956 Q1957 M1958 G1959 L1960 K1961 F1962 L1963 S1964 A1965 F1966 I1967 R1968 H1969 T1970 D1971 S1972 T1973 L1974 K1975 D1976 T1977 A1978 L1979 S1980 Y1981 V1982 L1983 G1984
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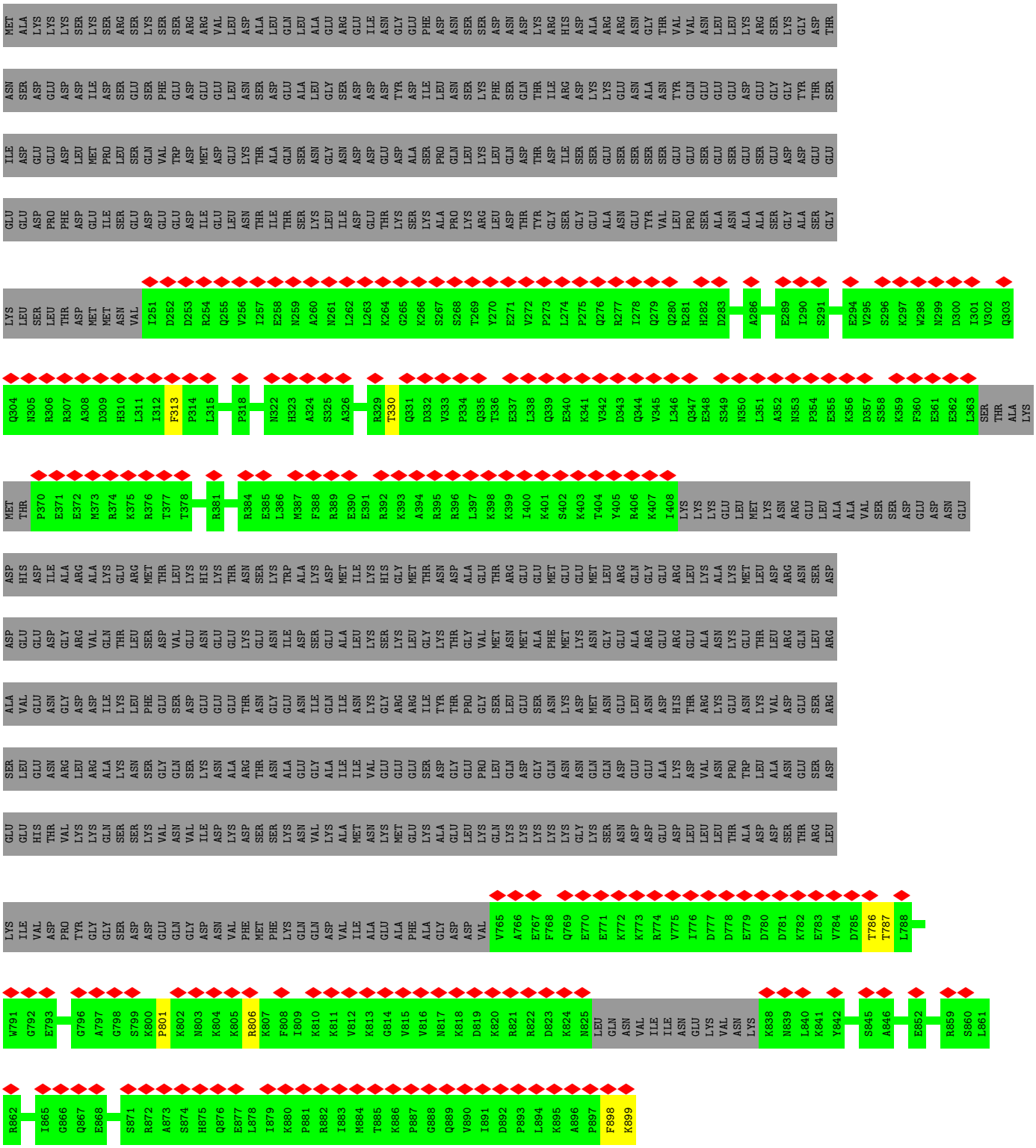
Q2045 F2046 L2047 M2048 E2049 Y2050 D2051 Q2052 S2053 K2054 G2055 R2056 L2057 E2058 K2059 Q2060 F2061 K2062 F2063 M2064 V2065 D2066 N2067 L2068 Q2069 Y2070 P2071 T2072 E2073 S2074 G2075 R2076 Q2077 S2078 V2079 M2080 E2081 L2082 I2083 N2084 L2085 I2086 I2087 T2088 K2089 ALA ASN P2092 A2093 L2094 L2095 S2096 K2097 L2098 S2099 S2100 S2101 F2102 F2103 L2104
A2105 L2106 V2107 N2108 V2109 S2110 F2111 N2112 D2113 D2114 A2115 P2116 R2117 C2118 R2119 E2120 M2121 A2122 S2123 V2124 L2125 I2126 S2127 T2128 M2129 L2130 P2131 K2132 L2133 E2134 N2135 K2136 D2137 L2138 E2139 I2140 V2141 E2142 K2143 Y2144 I2145 A2146 A2147 TRP LEU LYS GLN VAL D2153 N2154 A2155 S2156 F2157 L2158 N2159 L2160 G2161 L2162 R2163 T2164
Y2165 K2166 V2167 TYR LEU LYS S2171 I2172 G2173 F2174 E2175 H2176 T2177 I2178 E2179 L2180 D2181 E2182 L2183 A2184 I2185 K2186 R2187 I2188 R2189 TYR ILE LEU SER ASP THR SER VAL GLY SER GLU HIS GLN TRP ASP LEU VAL TYR SER ALA LEU ASN THR F2213 S2214 S2215 Y2216 M2217 E2218 E2221 S2222 V2223 Y2224 K2225
H2226 G2227 PHE LYS ASP ILE W2232 D2233 G2234 I2235 I2236 T2237 C2238 L2239 L2240 Y2241 P2242 H2243 S2244 W2245 V2246 ARG GLN SER ALA A2251 N2252 L2253 V2254 H2255 Q2256 L2257 I2258 A2259 N2260 K2261 D2262 K2263 L2264 E2265 I2266 S2267 L2268 T2269 ASN LEU GLU ILE GLN T2275 I2276 A2277 T2278 R2279 I2280 L2281 H2282 Q2283 L2284 G2285
A2286 P2287 S2288 I2289 P2290 GLU ASN LEU A2294 N2295 V2296 S2297 I2298 K2299 T2300 L2301 V2302 N2303 I2304 S2305 I2306 L2307 W2308 K2309 E2310 Q2311 ARG THR PRO PHE ILE MET ASP VAL SER LYS GLN T2323 G2324 E2325 D2326 L2327 K2328 Y2329 T2330 T2331 A2332 I2333 D2334 V2337 T2338 R2339 ILE GLY G2342 I2343 I2344 R2345 S2346
D2347 E2348 H2349 R2350 M2351 F2354 M2355 S2356 K2357 LYS ALA CYS ILE GLN LEU LEU A2365 L2366 L2367 V2368 Q2369 V2370 L2371 D2372 E2373 D2374 E2375 V2376 I2377 A2378 E2379 G2380 E2381 LYS ILE LEU LEU PRO LEU TYR GLY Y2390 L2391 E2392 T2393 Y2394 Y2395 S2396 R2397 A2398 V2399 D2400 E2401 E2402 Q2403 E2404 E2405 L2406 ARG
THR LEU SER ASN GLU CYS LEU LYS ILE L2417 E2418 D2419 K2420 L2421 Q2422 V2423 S2424 D2425 F2426 T2427 K2428 I2429 Y2430 T2431 A2432 V2433 K2434 Q2435 T2436 V2437 L2438 GLU ARG ARG LYS GLU ARG ARG SER LYS ARG ALA ILE LEU ALA VAL ASN ALA PRO GLN ILE SER ALA ASP LYS LYS LEU ARG LYS HIS

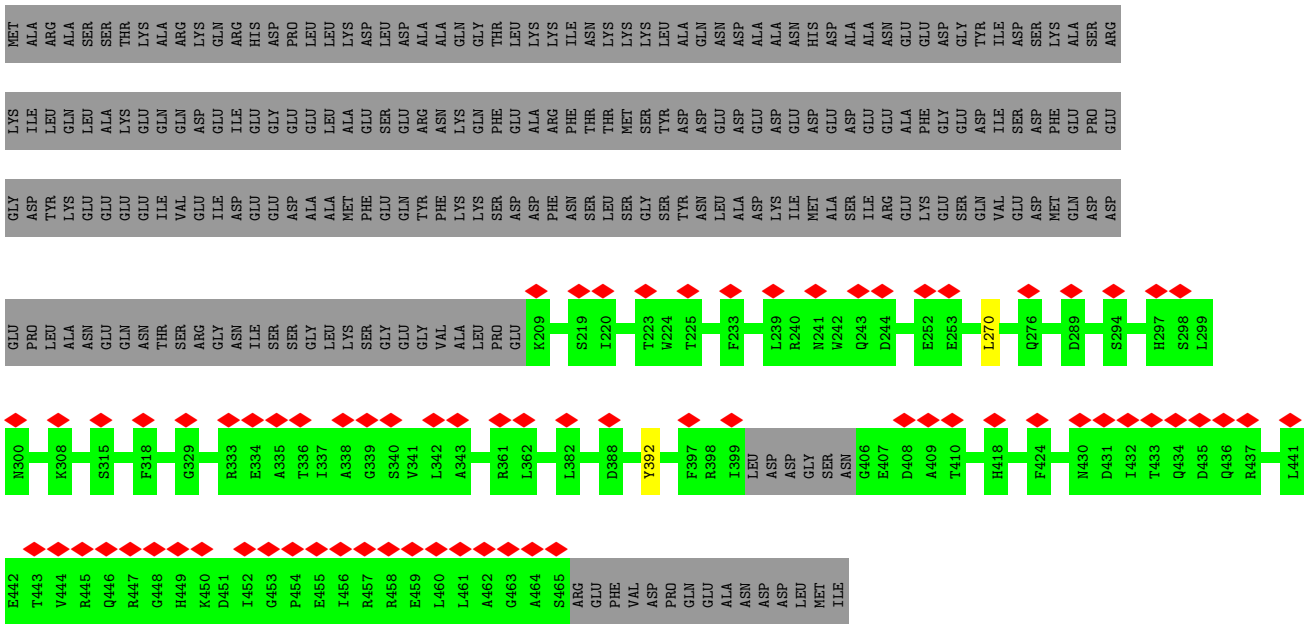
• Molecule 59: U3 small nucleolar RNA-associated protein 14

Chain RQ:



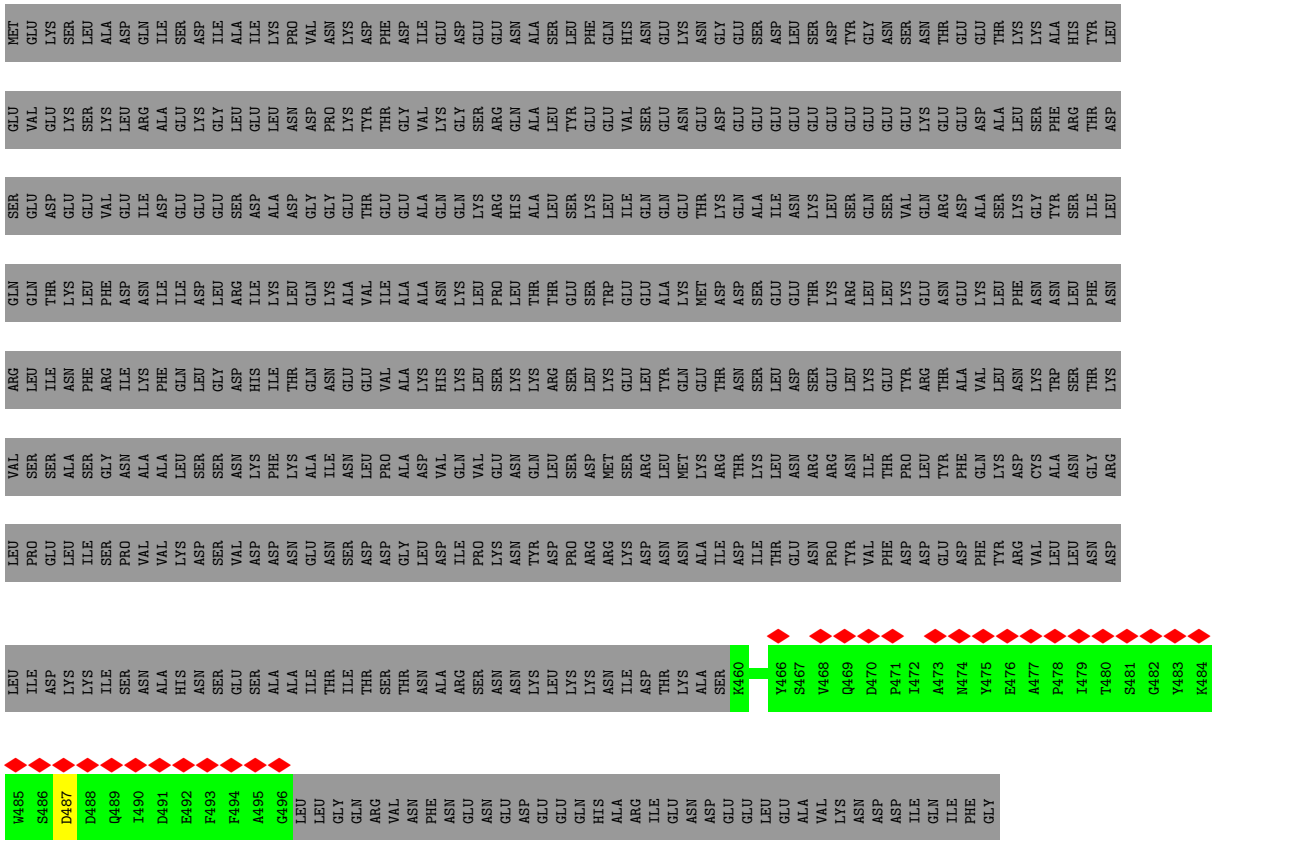
• Molecule 60: Essential nuclear protein 1

Chain RS:



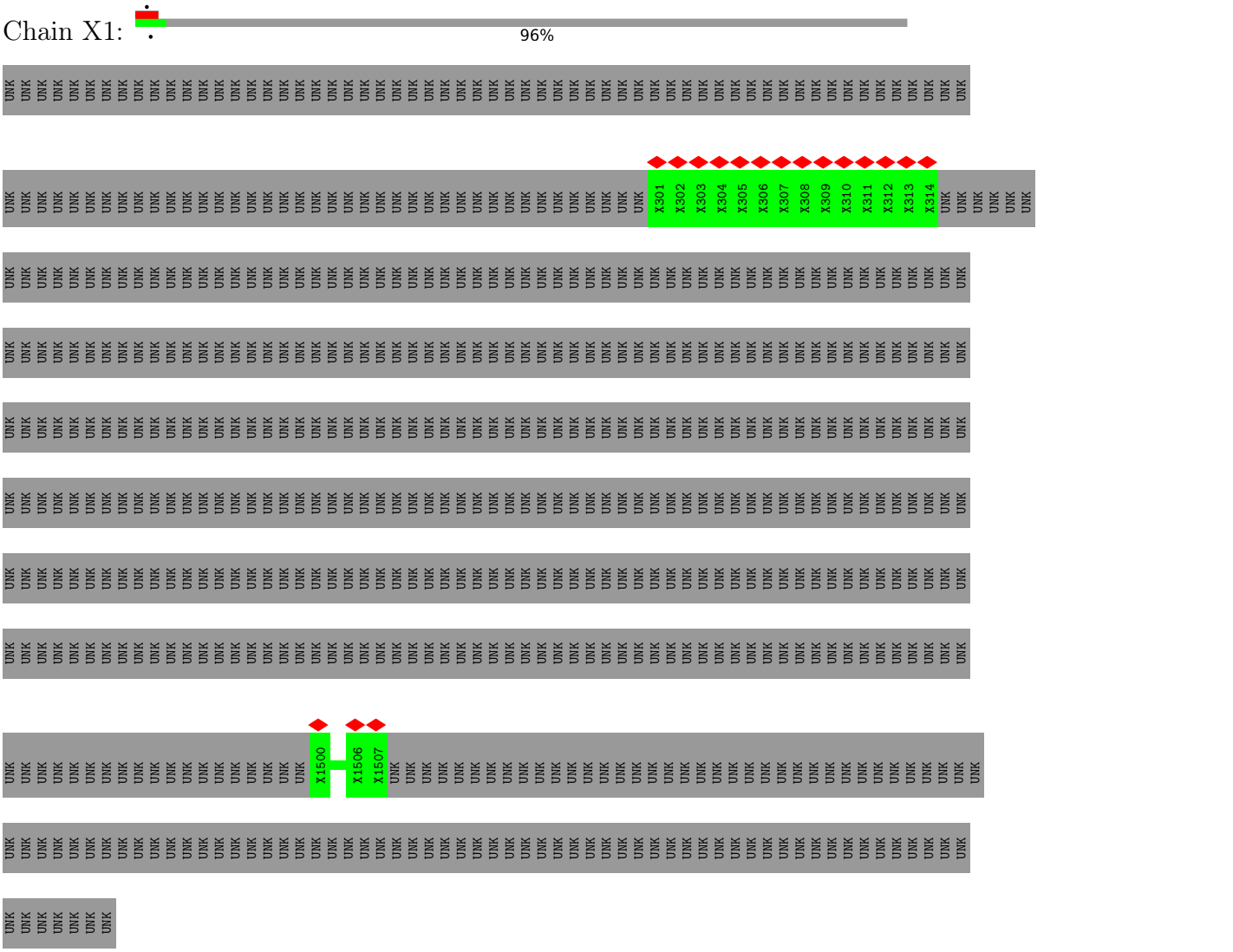
• Molecule 61: Protein BFR2

Chain RY:



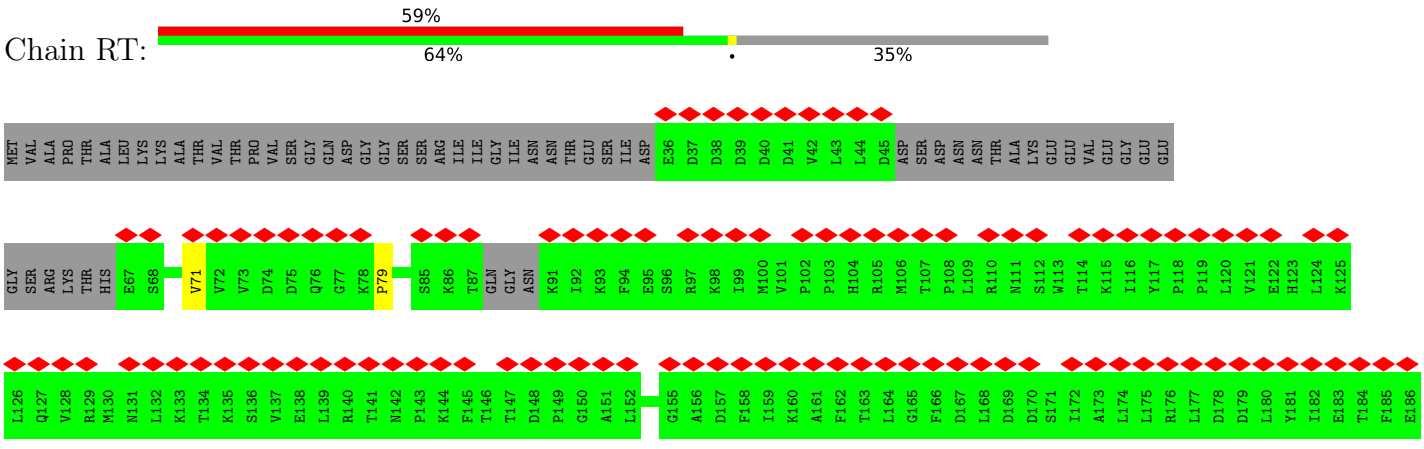
• Molecule 62: Unassigned peptides 1

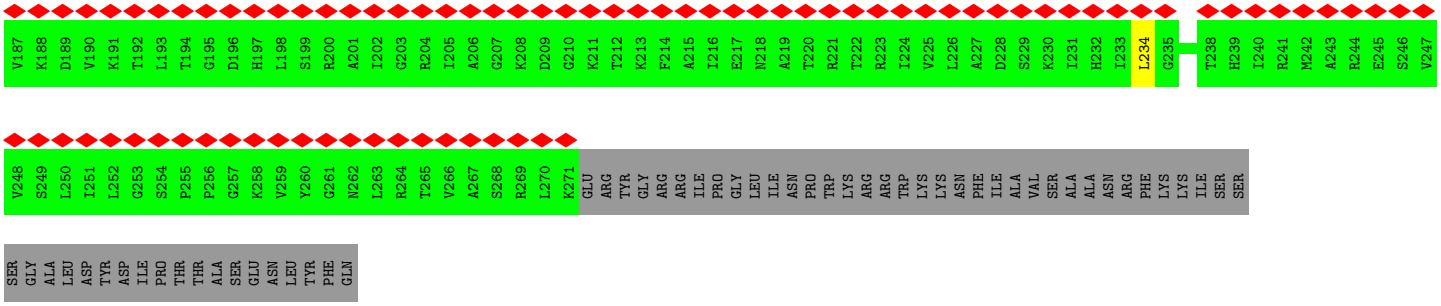
Chain X1:



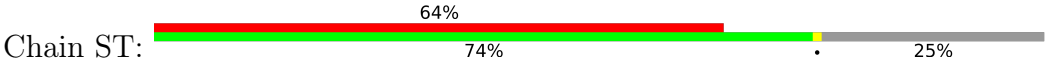
• Molecule 63: Pno1

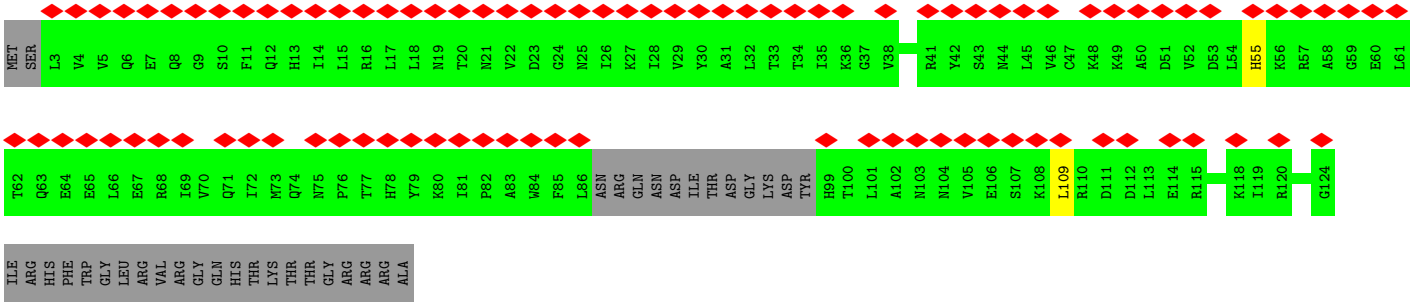
Chain RT:



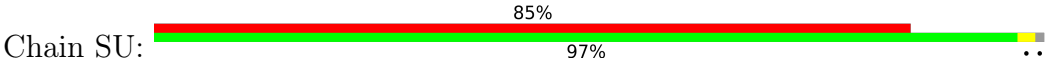


• Molecule 64: 40S ribosomal protein S18-A

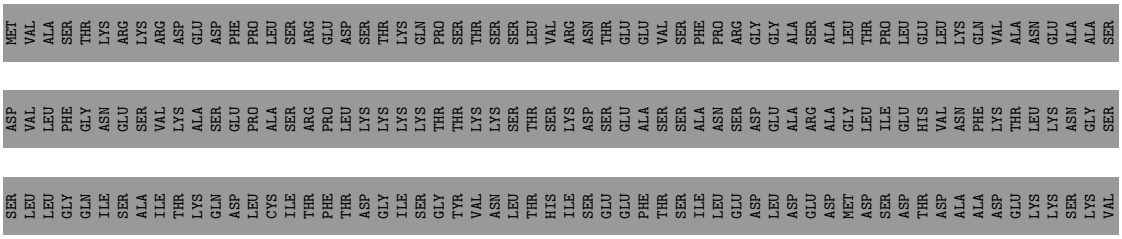


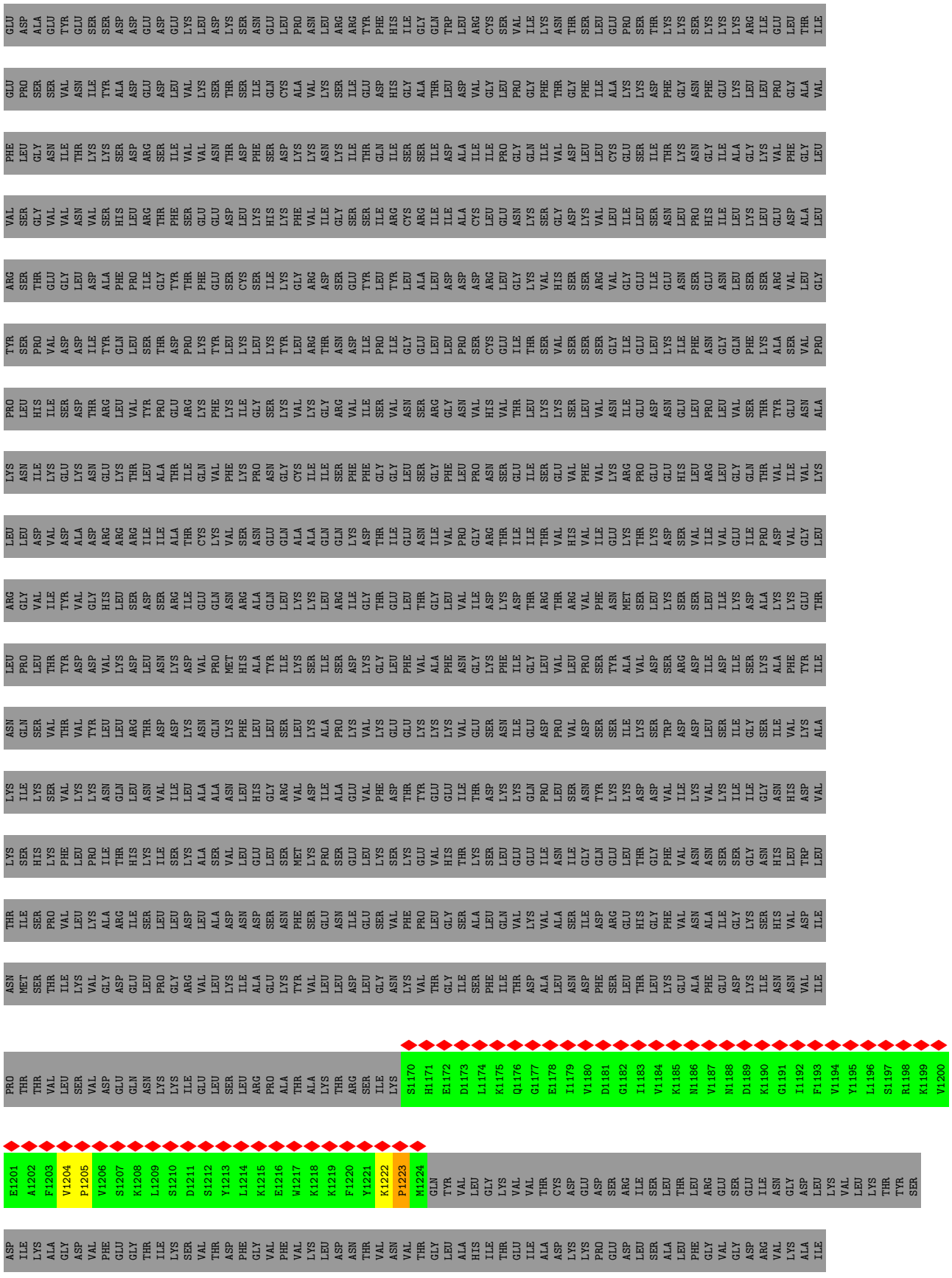


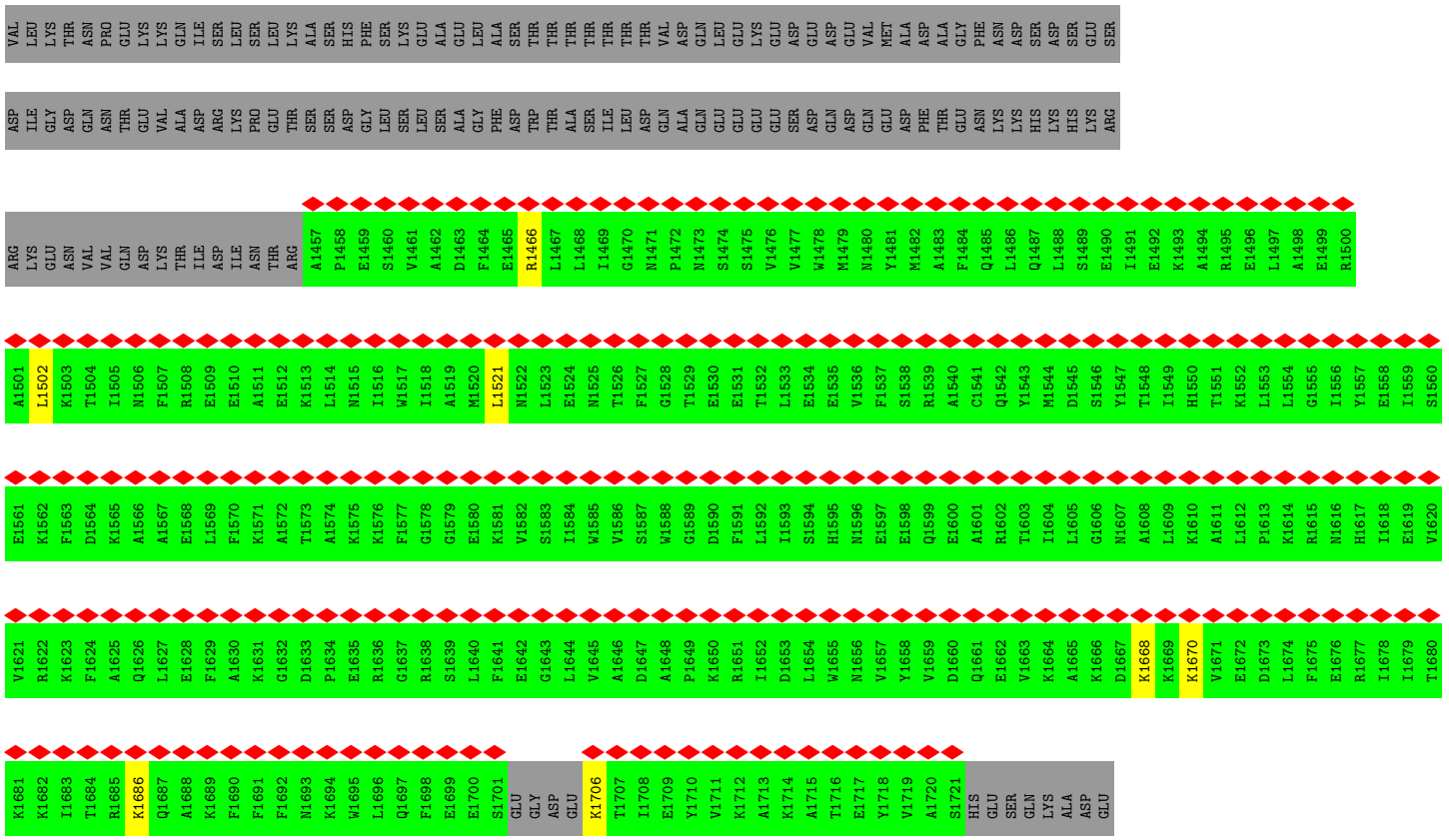
• Molecule 65: 40S ribosomal protein S19-A



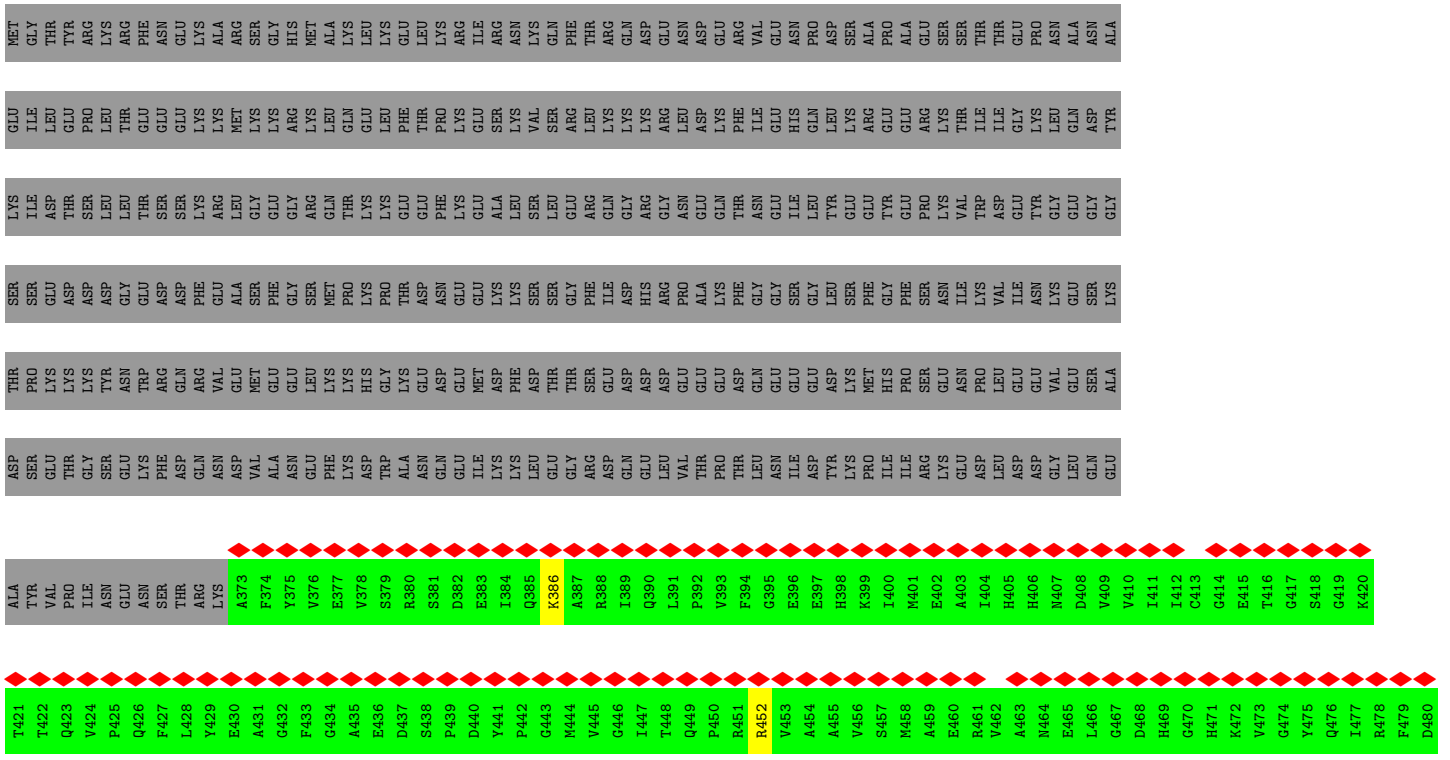
• Molecule 66: rRNA biogenesis protein RRP5

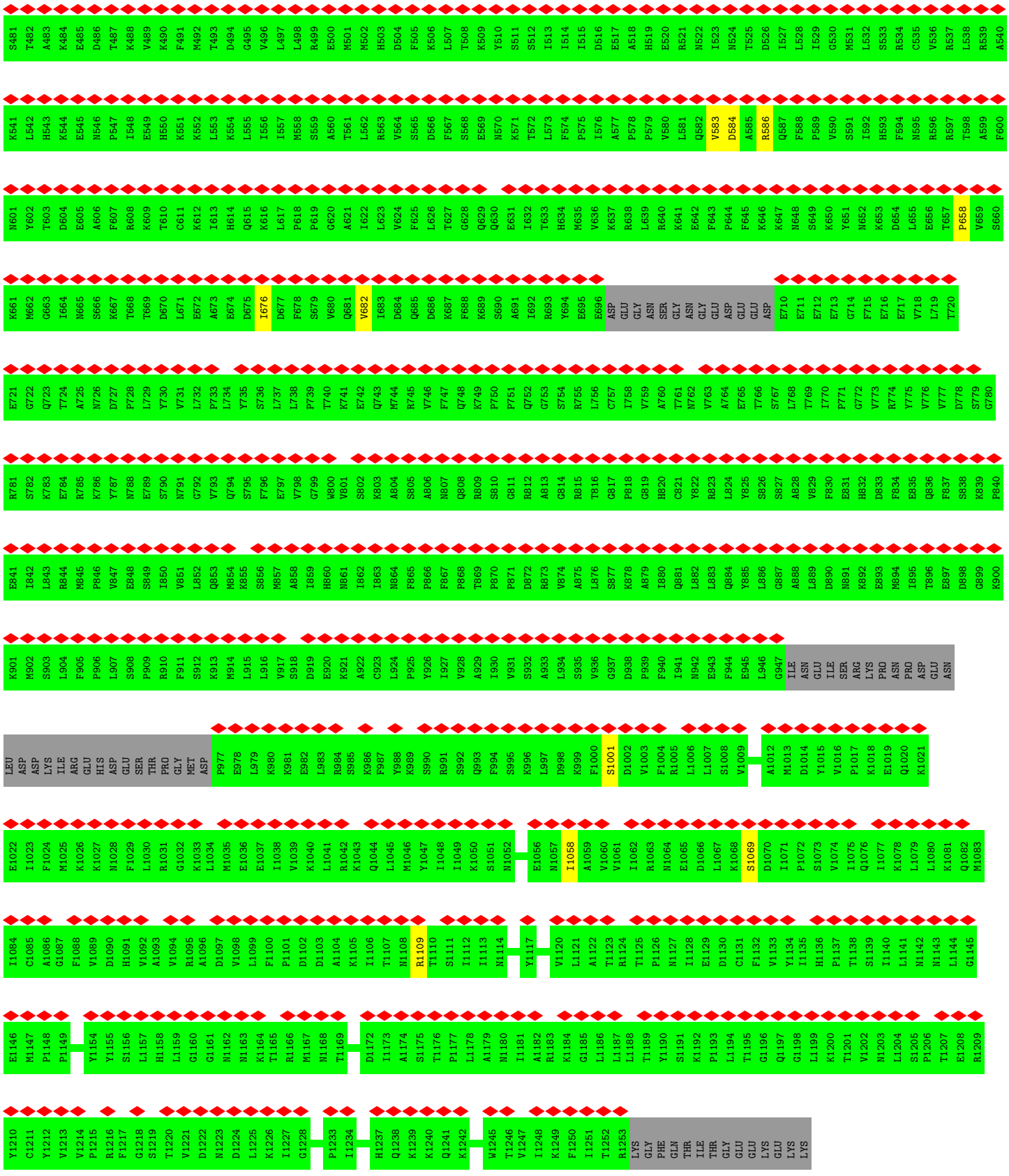



GLU ASP ALA GLU TYR GLU SER SER ASP ASP GLU ASP GLU LYS LEU ASP LYS SER ASN GLU LEU PRO ASN LEU ARG ARG TYR PHE HIS ILE GLY GLN TRP LEU ARG CYS SER VAL ILE LYS ASN THR SER LEU GLU PRO SER THR LYS LYS SER LYS LYS LYS ARG ILE GLU LEU THR ILE
GLU PRO SER SER VAL ASN ILE TYR ALA ASP GLU ASP GLU LEU VAL LYS SER THR SER ILE GLN CYS ALA VAL LYS SER ILE GLU ASP HIS GLY ALA THR LEU ASP VAL GLY LEU PRO GLY PHE THR GLY PHE ILE ALA LYS LYS ASP PHE GLY ASN PHE GLU LYS LEU LEU PRO GLY ALA VAL
PHE LEU GLY ASN ILE THR LYS LYS SER ASP ARG SER ILE VAL VAL ASN THR ASP PHE SER ASP LYS LYS ASN LYS ILE THR GLN ILE SER SER ILE THR LYS ASN LEU ILE GLY GLN ILE VAL ASP LEU LEU CYS GLU SER ILE THR LYS ASN PRO GLY ILE ILE LEU ALA ALA ILE ILE PRO GLY GLN ILE VAL ASP LEU LEU SER ASN LEU ILE LEU LYS LEU LEU GLY LYS VAL PHE GLY LEU
VAL SER GLY VAL VAL ASN VAL SER HIS LEU ARG THR PHE SER GLU GLU ASP LEU LYS HIS LYS PHE VAL ILE GLY ASP LYS VAL LEU ASP LEU ASP ASP ARG LEU GLY GLY LYS VAL SER GLY ASP LYS SER GLY VAL HIS SER SER ARG VAL LEU ILE GLU SER GLU ASN LEU SER SER ARG VAL LEU GLU ASP ALA LEU
ARG SER THR GLU GLY LEU ASP ALA PHE PRO ILE GLY TYR THR PHE GLU SER CYS SER ILE LYS GLY ARG ASP SER GLU TYR LEU TYR LEU ALA LEU ASP ASP ARG CYS ARG ILE LEU ASP ASP ARG LEU GLY LYS VAL HIS SER SER ARG VAL LEU GLY ILE LEU GLU ASN SER GLU SER ASN LEU SER SER ARG VAL LEU GLY
TYR SER PRO VAL ASP ASP ILE TYR GLN LEU SER THR ASP PRO LYS TYR LEU LYS LEU LYS ILE GLY SER LYS VAL ARG ASN THR ASP ILE PRO ILE GLY GLU LEU GLU ASP ILE THR SER VAL SER SER SER GLY ILE GLU GLU LEU LYS ILE PHE ASN GLY GLN PHE LYS ILE ALA SER VAL PRO
PRO LEU HIS ILE SER ASP THR ARG LEU VAL TYR PRO GLU ARG LYS PHE LYS ILE GLY ARG VAL ILE SER VAL ASN SER ARG GLY ASN VAL PHE SER LYS VAL LYS GLY ARG VAL ILE SER PHE PHE GLY GLY LEU SER GLY PHE SER VAL PRO GLU LEU VAL LYS LYS SER LEU VAL ASN ILE GLU ASP ASN GLU LEU PRO ASN SER VAL LEU GLU ASN ALA
LYS ASN ILE LYS GLU LYS THR LEU ALA THR ILE GLN VAL PHE LYS PRO ASN GLY CYS ILE ILE SER PHE PHE GLY GLY LEU SER GLY PHE SER ILE GLU GLU ASP ASN GLU LEU VAL PHE VAL LYS ARG PRO GLU GLU HIS LEU GLU LEU ARG LEU ASP ASN GLU LYS
LEU LEU ASP VAL ALA ASP ARG ARG ILE ILE ILE ALA THR CYS LYS VAL SER ASN GLU GLN ALA ALA GLN GLN LYS ASP THR ILE GLU ASN ILE VAL PRO GLY ARG THR ILE ILE ILE THR VAL HIS VAL ILE ILE GLU LYS THR LYS ASP SER VAL ILE GLU VAL LEU GLY GLN THR VAL ILE PRO ASP VAL GLY LEU
ARG GLY VAL ILE TYR VAL GLY HIS LEU SER ASP SER ARG ILE GLN GLN ASN ARG ALA GLN LEU LYS LYS LEU ARG ILE GLY THR GLU LEU THR GLY LEU VAL ILE ASP LYS ASP THR ARG THR ARG VAL PHE ASN MET SER LEU LYS LEU GLY LEU LYS SER SER LEU ILE LYS ASP SER ALA LYS LYS GLU THR
LEU PRO LEU THR TYR ASP ASP VAL LYS ASP LEU ASN LYS ASP VAL ASP PRO MET HIS ALA TYR ILE LYS SER ILE SER ASP LYS GLY LEU PHE VAL ALA PHE ASN GLY LYS PHE ILE GLY LEU VAL LEU PRO SER TYR ALA VAL ASP SER ARG ASP ILE ASP ILE SER LYS ALA PHE TYR ILE
ASN GLN SER VAL THR VAL TYR LEU LEU LEU ARG THR ASP ASP LYS ASN GLN LYS PHE LEU LEU LEU SER LEU LYS ALA PRO LYS VAL LYS GLU GLU LEU LYS LYS LEU ARG ILE GLU LYS LEU ASP LYS ASP PRO VAL ASP SER SER ILE LYS SER TRP ASP ARG ASP ILE ALA VAL ASP SER ILE LYS ASP
LYS ILE LYS SER VAL LYS LYS ASN GLN LEU ASN VAL ILE LEU ALA ALA ASN LEU HIS GLY ARG VAL ASP ILE ALA GLU VAL LYS LYS LYS VAL GLU GLU ILE THR ASP LYS LYS GLU GLU ILE THR ASP LYS LYS GLN PRO LEU SER ASN TYR LYS LYS ASP VAL LEU ASP
LYS SER HIS LYS PHE LEU PRO ILE THR HIS LYS ILE SER LYS ALA SER VAL LEU GLU LEU LYS SER LYS GLU VAL HIS THR LYS SER LEU GLU GLU ILE ASN ILE GLY GLN GLU LEU THR GLY PHE VAL ASN ASN SER SER ILE LEU GLY ASN HIS LEU VAL LYS
THR ILE SER PRO VAL LEU ASP ILE SER LEU ASP ALA ASP SER ASN PHE SER GLU ASN ILE GLU GLU SER VAL PHE PRO LEU GLY SER ALA LEU GLN VAL LYS VAL ALA ALA SER ILE ASP ARG GLU HIS GLY PHE VAL ASN ALA ILE GLY GLY LYS SER HIS VAL ASP ILE
ASN MET SER THR ILE LYS VAL GLY ASP GLU LEU ASP LEU ARG PRO ALA THR ALA LYS THR ARG ASN SER VAL ASN LYS VAL THR GLY ILE ASP THR ASP ALA LEU ASN ASP PHE SER LEU LYS GLU ALA ASP PHE ILE ASN ILE LEU ILE ASN VAL ILE
PRO THR THR VAL LEU SER VAL ASP GLU GLN LYS LYS ILE LEU GLU LEU SER LEU ARG PRO ALA THR ALA LYS THR ARG SER ILE LYS S1170 H1171 E1172 D1173 L1174 K1175 Q1176 G1177 E1178 I1179 V1180 D1181 G1182 I1183 V1184 K1185 N1186 V1187 N1188 D1189 K1190 G1191 I1192 F1193 V1194 Y1195 L1196 S1197 R1198 K1199 V1200
E1201 A1202 F1203 V1204 P1205 V1206 S1207 K1208 L1209 S1210 D1211 S1212 Y1213 L1214 K1215 E1216 W1217 K1218 K1219 F1220 Y1221 K1222 P1223 M1224 GLN TYR VAL LEU GLY LYS VAL VAL THR CYS ASP GLU ASP SER ARG ILE SER LEU THR LEU ARG GLU SER GLU ILE ASN GLY VAL LEU LYS THR TYR SER
ASP ILE LYS ALA GLY ASP VAL PHE GLU GLY THR ILE LYS SER VAL THR ASP PHE GLY VAL PHE VAL LYS LEU ASP ASN THR VAL ASN VAL THR GLY LEU ALA HIS ILE THR GLU ILE ALA ASP LYS LYS PRO GLU ASP LEU SER ALA LEU PHE GLY VAL GLY ASP ARG VAL LYS ALA ILE



• Molecule 67: Probable ATP-dependent RNA helicase DHR1




S481 T482 A483 K484 E485 D486 T487 K488 V489 K490 F491 M492 T493 D494 G495 V496 L497 L498 R499 E500 M501 M502 H503 D504 F505 K506 L507 T508 K509 Y510 S511 S512 I513 I514 I515 D516 E517 A518 H519 E520 R521 N522 I523 N524 T525 D526 I527 L528 I529 G530 M531 L532 S533 R534 C535 V536 R537 L538 R539 A540
K541 L542 H543 K544 E545 N546 P547 I548 E549 H550 K551 K552 L553 K554 L555 I556 I557 M558 S559 A560 T561 L562 R563 V564 S565 D566 F567 S568 E569 N570 K571 T572 L573 F574 P575 I576 A577 P578 P579 V580 L581 Q582 V583 D584 A585 R586 Q587 F588 P589 V590 S591 I592 H593 F594 N595 R596 R597 T598 A599 F600
N601 Y602 T603 D604 E605 A606 F607 R608 K609 T610 C611 K612 I613 H614 Q615 K616 L617 P618 P619 G620 A621 I622 L623 V624 F625 L626 T627 G628 Q629 Q630 E631 I632 T633 H634 M635 V636 K637 R638 L639 R640 K641 E642 F643 P644 F645 K646 K647 N648 S649 K650 Y651 N652 K653 D654 L655 E656 T657 P658 V659 S660
K661 M662 G663 I664 N665 S666 K667 T668 T669 D670 L671 E672 A673 E674 D675 I676 D677 F678 S679 V680 Q681 V682 I683 D684 Q685 D686 K687 F688 K689 S690 A691 I692 R693 Y694 E695 E696 ASP GLU GLY ASN SER GLY ASN GLY GLU ASP GLU GLU ASP E710 E711 E712 E713 G714 F715 E716 E717 V718 L719 T720
E721 G722 Q723 T724 A725 N726 D727 P728 L729 Y730 V731 L732 P733 L734 Y735 S736 L737 L738 P739 T740 K741 E742 Q743 M744 R745 V746 F747 Q748 K749 P750 P751 Q752 G753 S754 R755 L756 C757 I758 V759 A760 T761 N762 V763 A764 E765 T766 S767 L768 T769 I770 P771 G772 V773 R774 Y775 V776 V777 D778 S779 G780
R781 S782 K783 E784 R785 K786 Y787 N788 E789 S790 N791 G792 V793 Q794 S795 F796 E797 V798 G799 W800 V801 S802 K803 A804 S805 A806 N807 Q808 R809 S810 G811 R812 A813 G814 R815 T816 G817 P818 G819 H820 C821 Y822 R823 L824 Y825 S826 S827 A828 V829 F830 E831 H832 D833 F834 E835 Q836 F837 S838 K839 P840
E841 I842 L843 R844 M845 P846 V847 E848 S849 I850 V851 L852 Q853 M854 K855 S856 M857 A858 I859 H860 N861 I862 I863 N864 F865 P866 F867 P868 T869 P870 P871 D872 R873 V874 A875 L876 S877 K878 A879 I880 Q881 L882 L883 Q884 Y885 L886 G887 A888 L889 D890 N891 K892 E893 M894 I895 T896 E897 D898 G899 K900
K901 M902 S903 L904 F905 P906 L907 S908 P909 R910 F911 S912 K913 M914 L915 L916 V917 S918 D919 E920 K921 A922 C923 L924 P925 Y926 I927 V928 A929 I930 V931 S932 A933 L934 S935 V936 G937 D938 P939 F940 I941 N942 E943 F944 E945 L946 G947 ILE ASN GLU ILE SER ARG LYS PRO ASN PRO ASP GLU ASN
LEU ASP ASP LYS ILE ARG GLU HIS ASP GLU SER THR PRO GLY MET ASP P977 E978 L979 K980 K981 E982 L983 R984 S985 K986 F987 Y988 K989 S990 R991 S992 Q993 F994 S995 K996 L997 D998 K999 F1000 S1001 D1002 V1003 F1004 R1005 L1006 L1007 S1008 V1009 A1012 M1013 D1014 Y1015 V1016 P1017 K1018 E1019 Q1020 K1021
E1022 I1023 F1024 M1025 K1026 K1027 N1028 F1029 L1030 R1031 G1032 K1033 L1034 M1035 E1036 E1037 I1038 V1039 K1040 L1041 R1042 K1043 Q1044 L1045 M1046 Y1047 I1048 I1049 K1050 S1051 N1052 E1056 N1057 I1058 A1059 V1060 V1061 I1062 R1063 N1064 E1065 D1066 L1067 K1068 S1069 D1070 I1071 P1072 S1073 V1074 I1075 Q1076 I1077 K1078 L1079 L1080 K1081 Q1082 M1083
I1084 C1085 A1086 G1087 F1088 V1089 D1090 H1091 V1092 A1093 V1094 R1095 A1096 D1097 V1098 L1099 F1100 P1101 D1102 D1103 A1104 K1105 I1106 T1107 N1108 R1109 T1110 S1111 I1112 I1113 N1114 Y1117 V1120 L1121 A1122 T1123 R1124 T1125 P1126 N1127 I1128 E1129 D1130 C1131 F1132 V1133 Y1134 I1135 H1136 P1137 T1138 S1139 I1140 L1141 N1142 N1143 L1144 G1145
E1146 M1147 P1148 P1149 Y1154 Y1155 S1156 L1157 H1158 L1159 G1160 G1161 N1162 N1163 K1164 T1165 R1166 M1167 N1168 T1169 D1172 I1173 A1174 S1175 T1176 P1177 L1178 A1179 N1180 I1181 A1182 R1183 K1184 G1185 L1186 L1187 L1188 T1189 Y1190 S1191 K1192 P1193 L1194 T1195 G1196 Q1197 G1198 L1199 K1200 T1201 V1202 N1203 L1204 S1205 P1206 T1207 E1208 R1209
Y1210 C1211 Y1212 V1213 V1214 P1215 R1216 F1217 G1218 S1219 T1220 V1221 D1222 N1223 D1224 L1225 K1226 I1227 G1228 P1233 I1234 H1237 Q1238 K1239 K1240 Q1241 K1242 W1245 T1246 V1247 I1248 K1249 F1250 I1251 T1252 R1253 LYS GLY PHE GLN THR ILE THR GLY GLU GLU LYS GLU LYS LYS

4 Experimental information (i)

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 ($e^-/Å^2$)	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, GTP, ZN, 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(^{o})	Ideal(^{o})
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	$\#\|Z\| > 2$
71	ADP	RZ	1301	-	24,29,29	0.95	1 (4%)	29,45,45	1.37	4 (13%)
69	GTP	RJ	1201	70	26,34,34	0.94	2 (7%)	32,54,54	0.92	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
71	ADP	RZ	1301	-	-	4/12/32/32	0/3/3/3
69	GTP	RJ	1201	70	-	3/18/38/38	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(^{o})	Ideal(^{o})
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(^{o})	Ideal(^{o})
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:

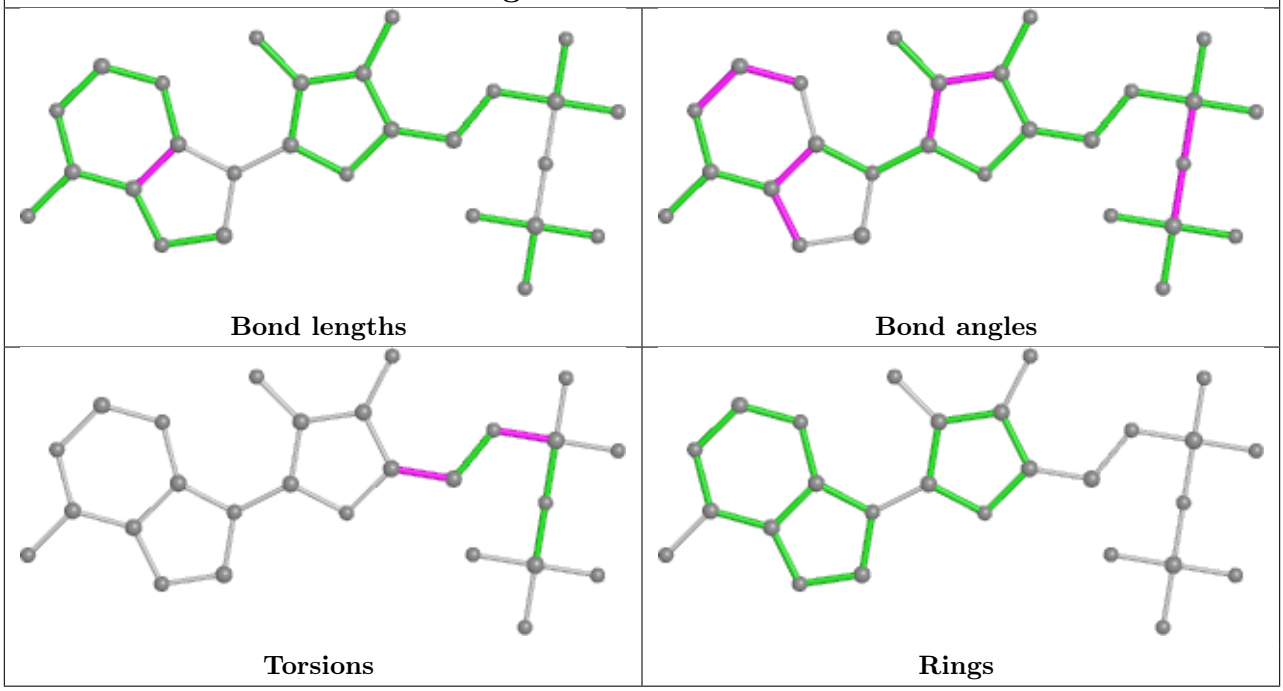
Mol	Chain	Res	Type	Atoms
71	RZ	1301	ADP	C5'-O5'-PA-O2A
71	RZ	1301	ADP	C5'-O5'-PA-O3A
69	RJ	1201	GTP	O4'-C4'-C5'-O5'
69	RJ	1201	GTP	C3'-C4'-C5'-O5'
69	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

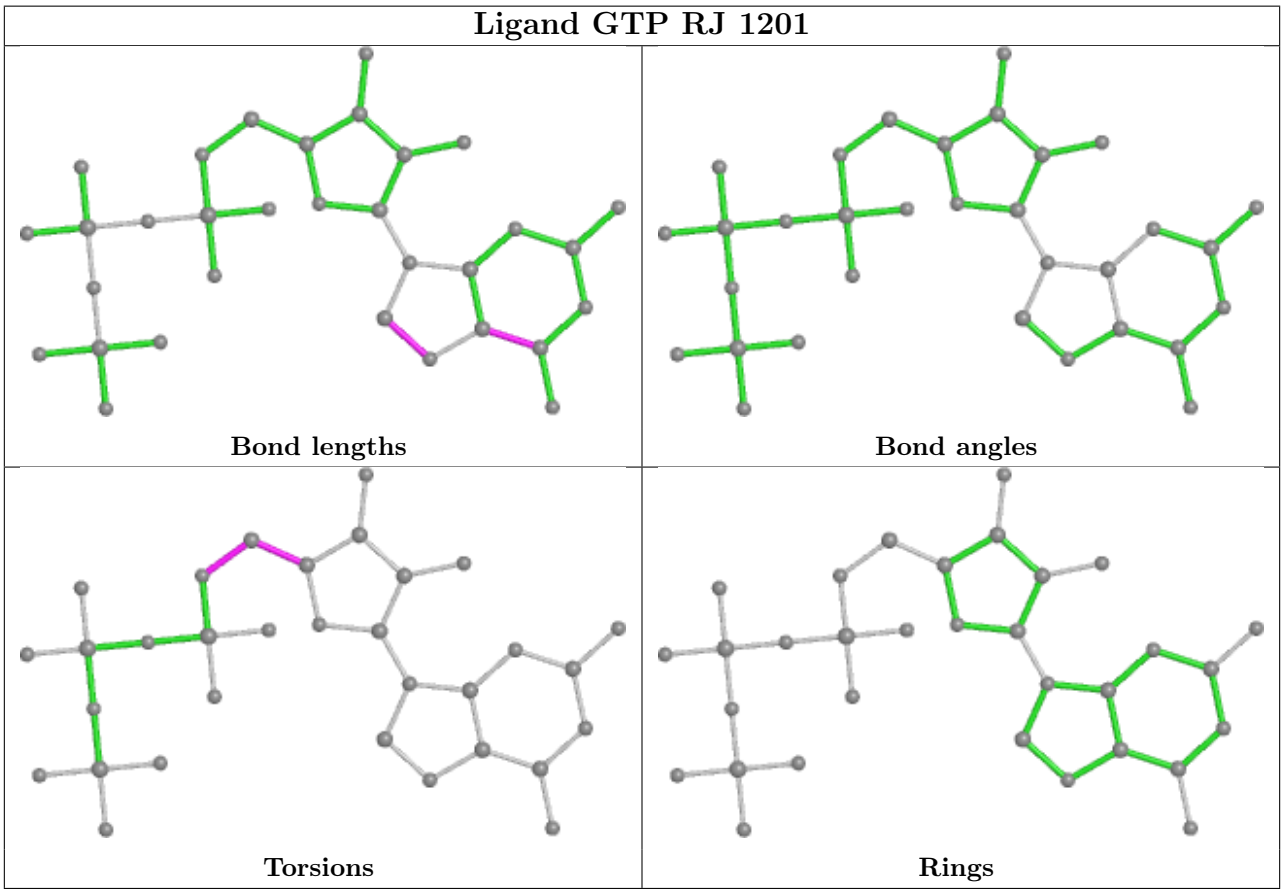
No monomer is involved in short contacts.

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 then 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.

Ligand ADP RZ 1301



Ligand GTP RJ 1201



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.

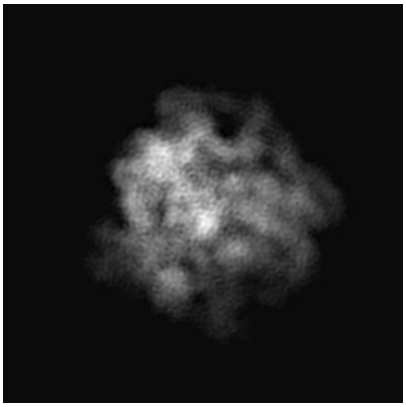
6 Map visualisation

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.

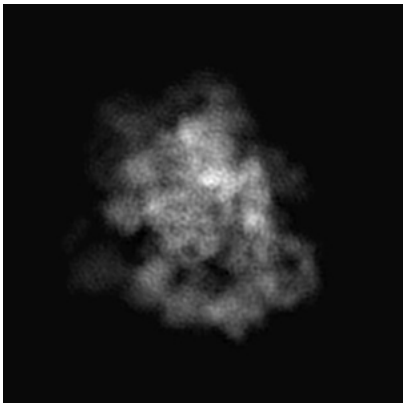
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

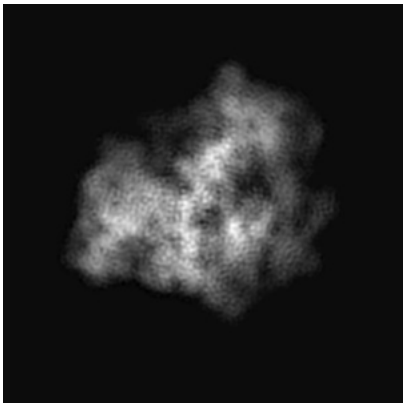
6.1.1 Primary map



X



Y

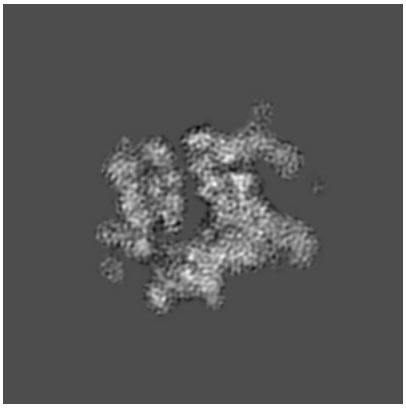


Z

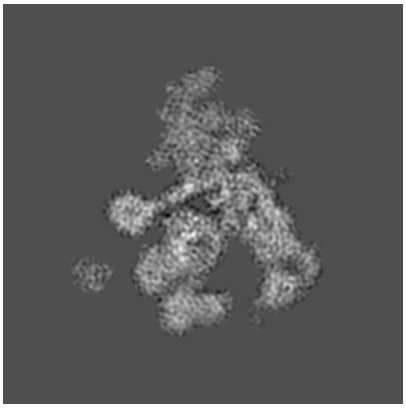
The images above show the map projected in three orthogonal directions.

6.2 Central slices

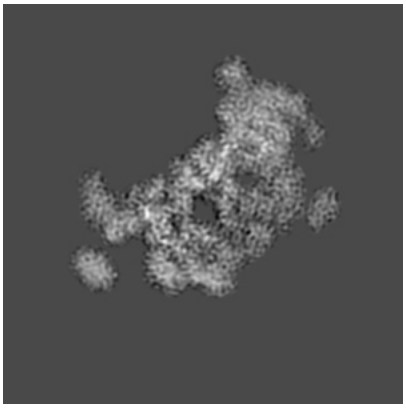
6.2.1 Primary map



X Index: 200



Y Index: 200

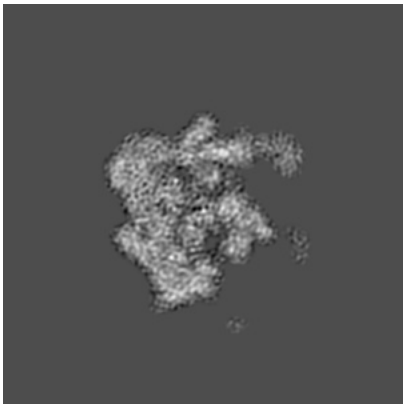


Z Index: 200

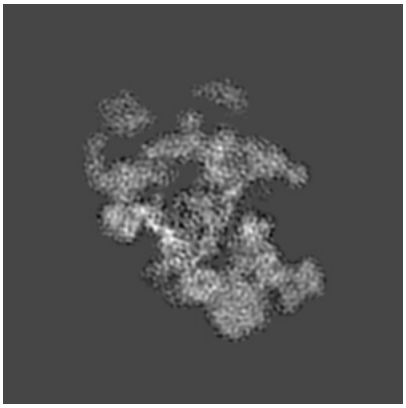
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

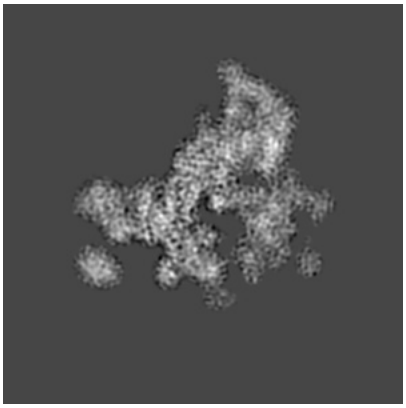
6.3.1 Primary map



X Index: 185



Y Index: 174

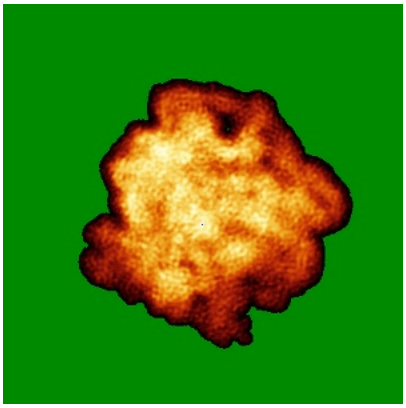


Z Index: 185

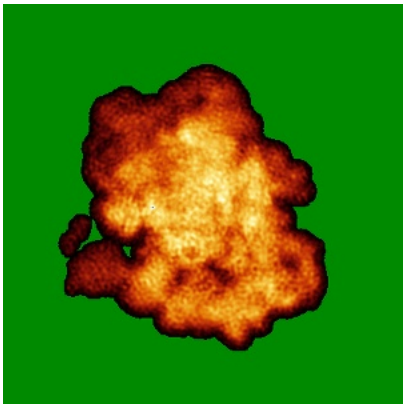
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

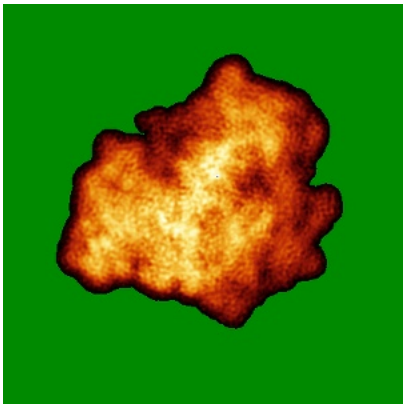
6.4.1 Primary map



X



Y

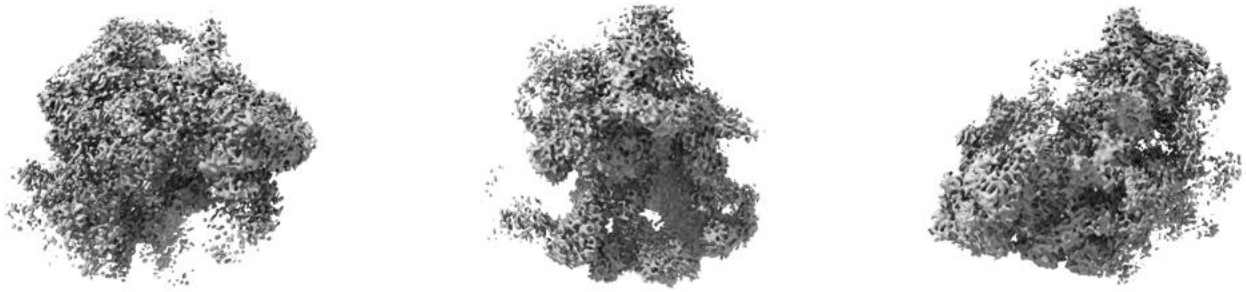


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

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

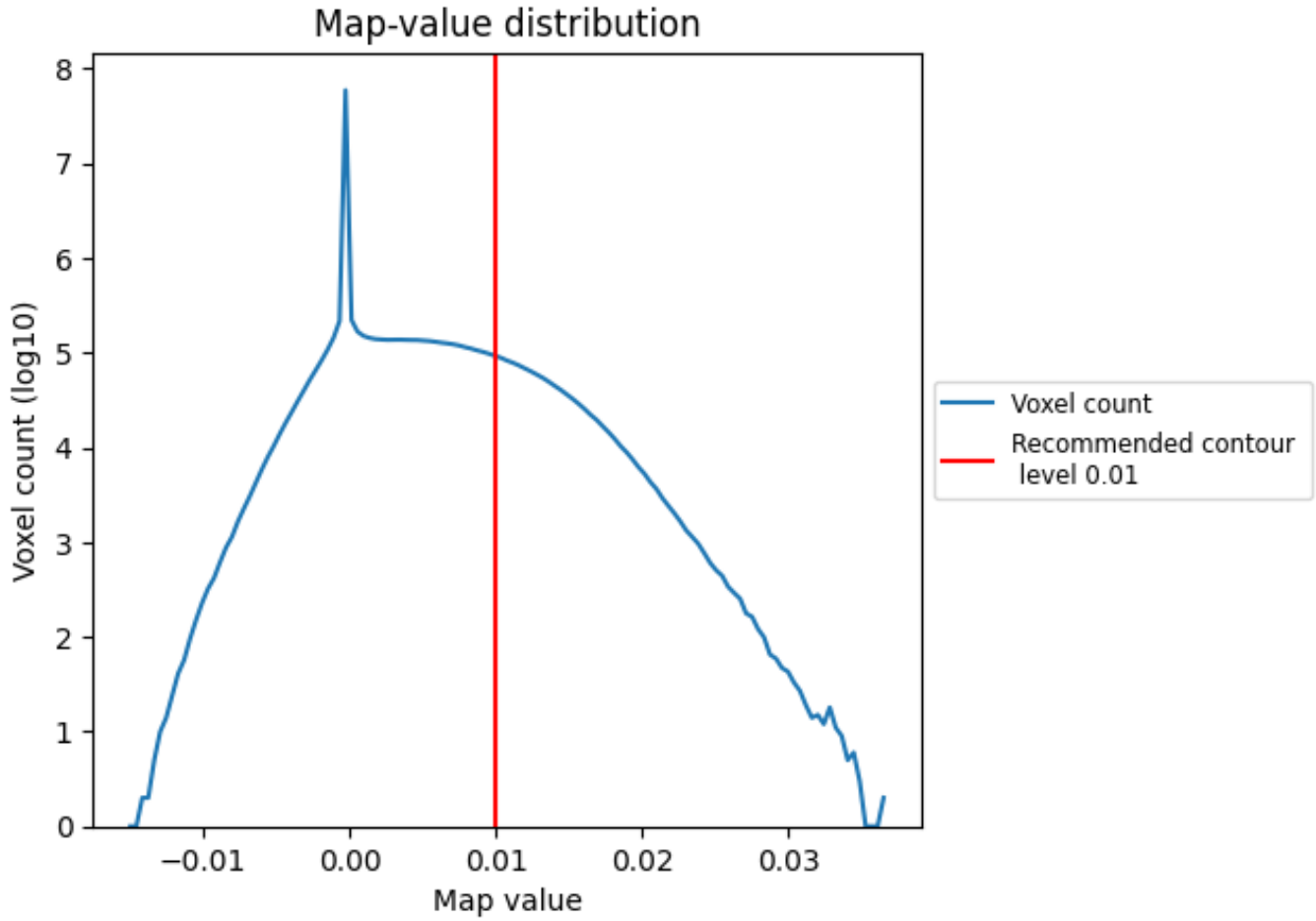
6.6 Mask visualisation (i)

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

7 Map analysis

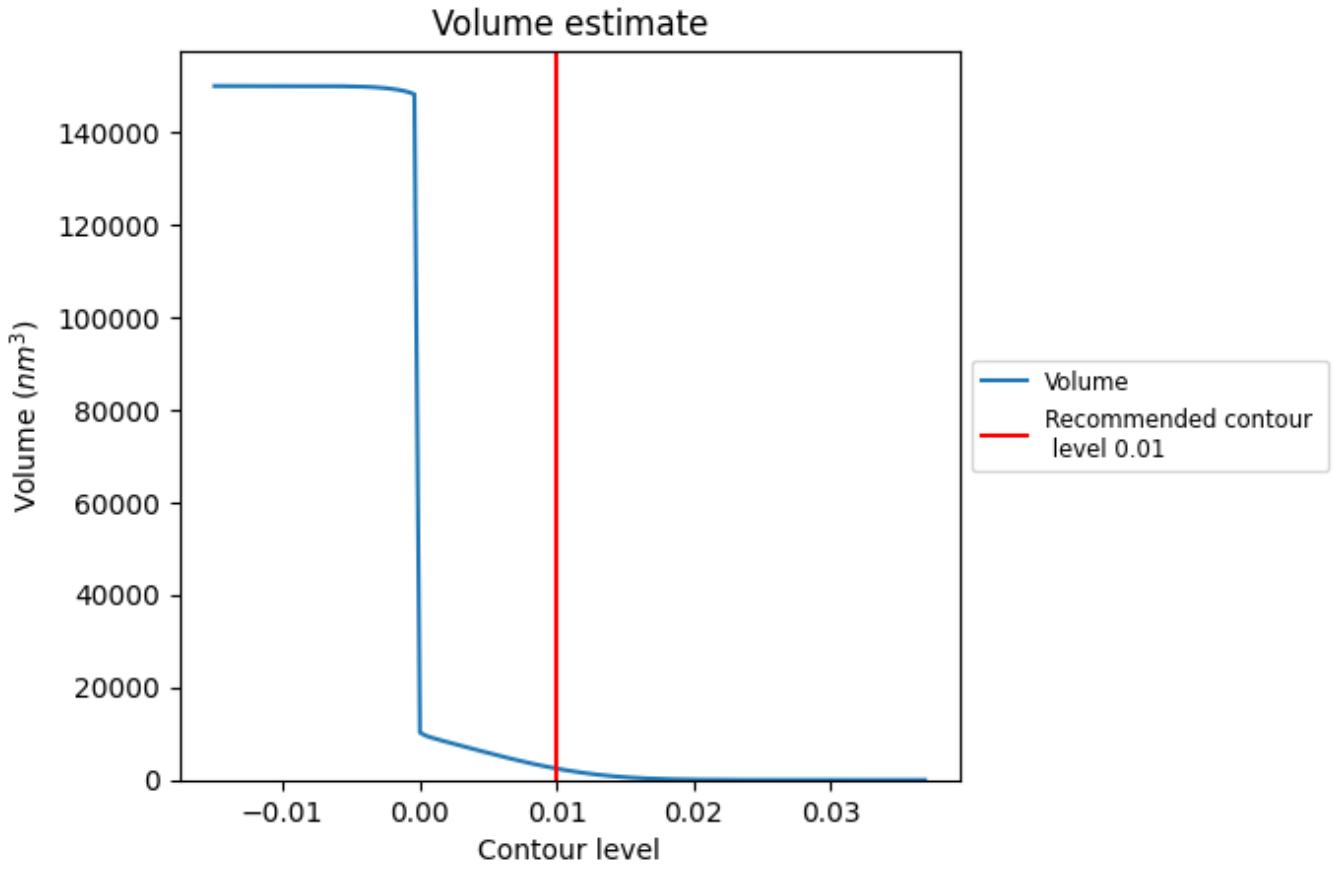
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

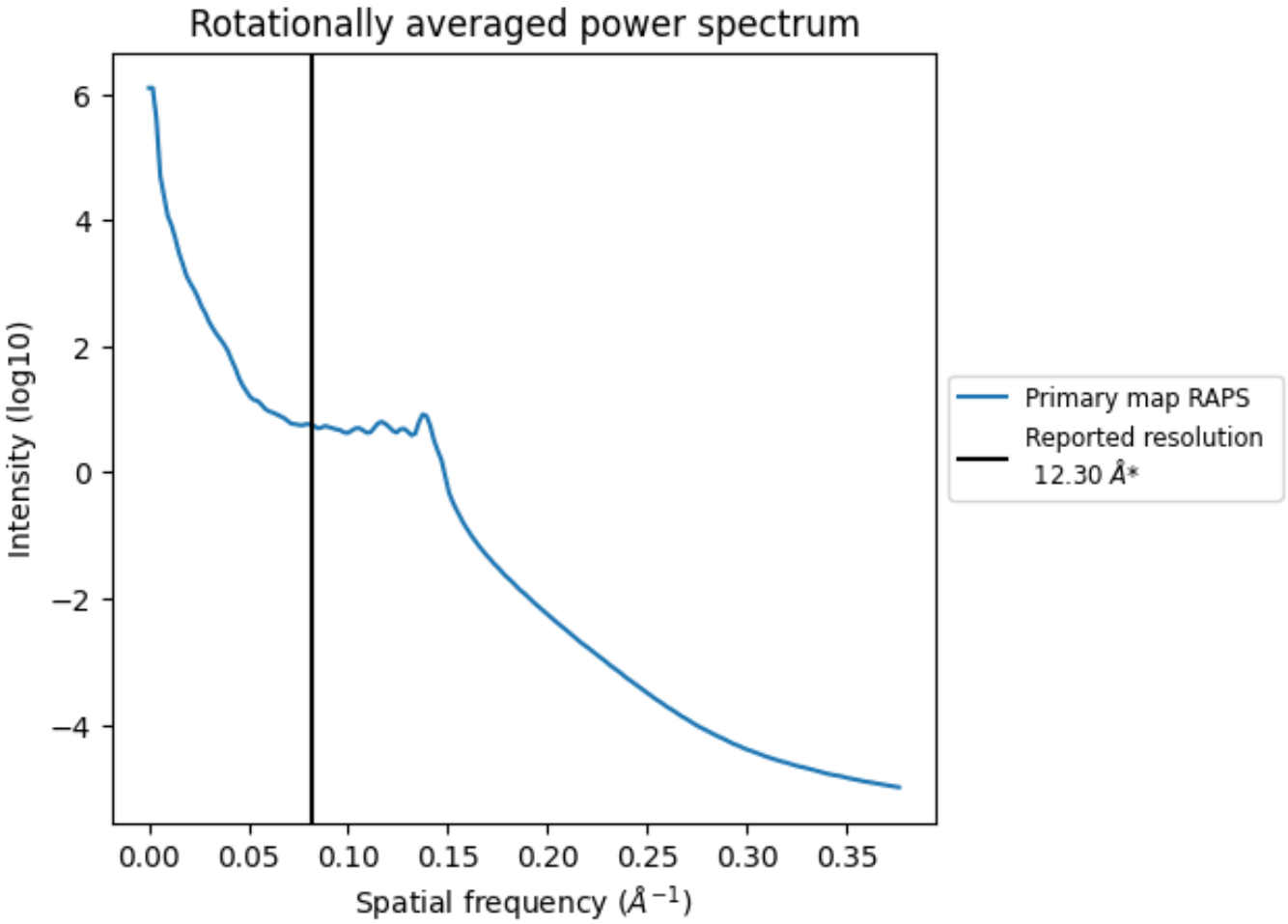
7.2 Volume estimate (i)



The volume at the recommended contour level is 2465 nm^3; 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}

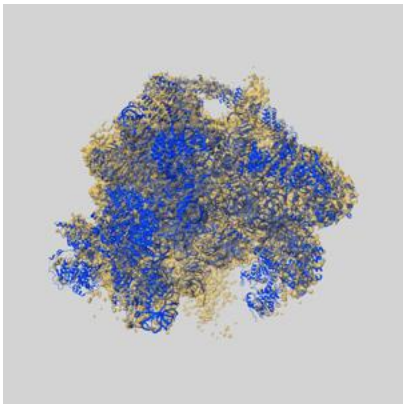
8 Fourier-Shell correlation (i)

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

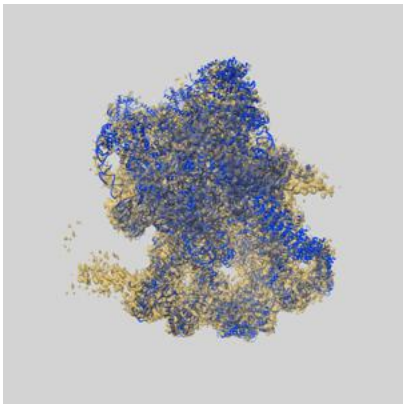
9 Map-model fit

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.

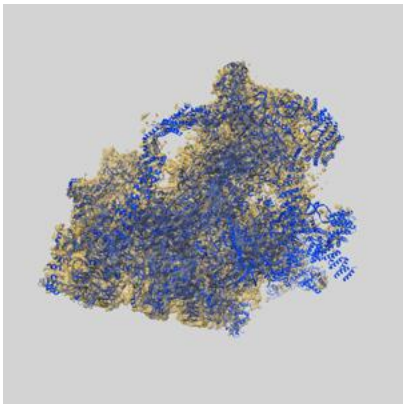
9.1 Map-model overlay



X



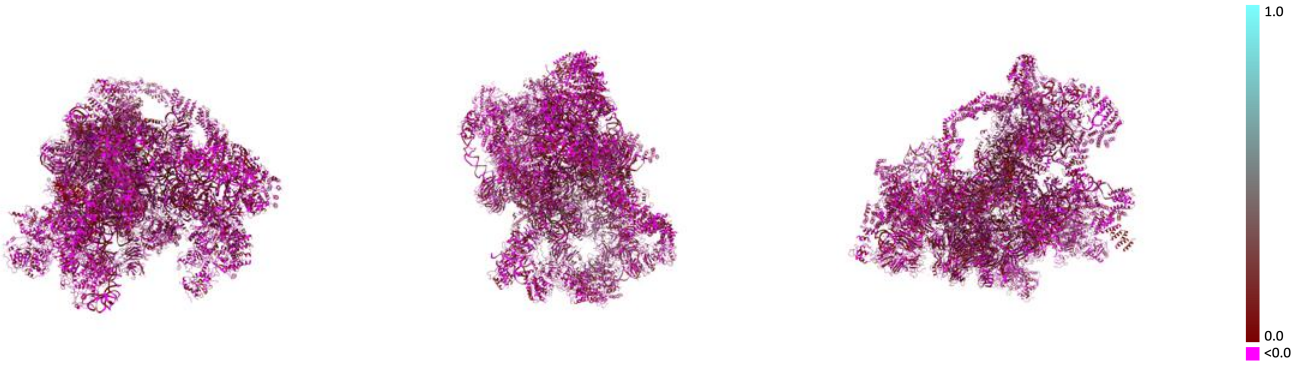
Y



Z

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.

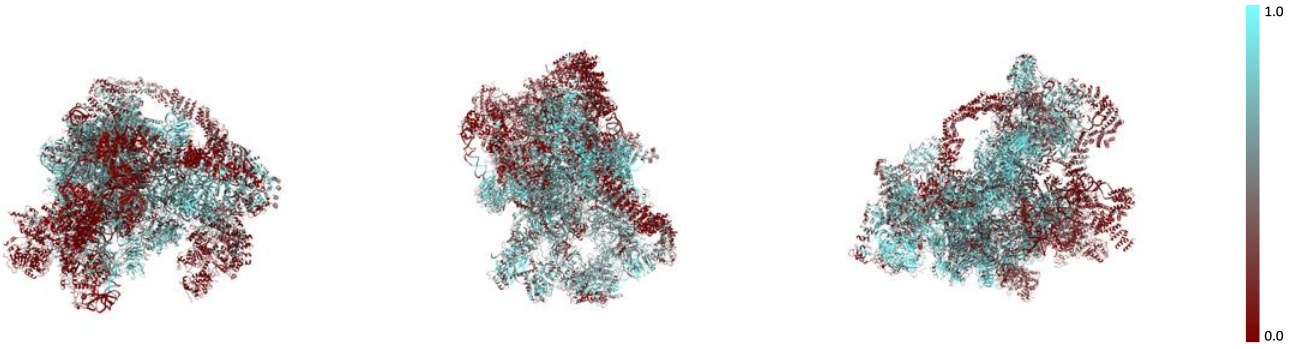
9.2 Q-score mapped to coordinate model



X Y Z

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

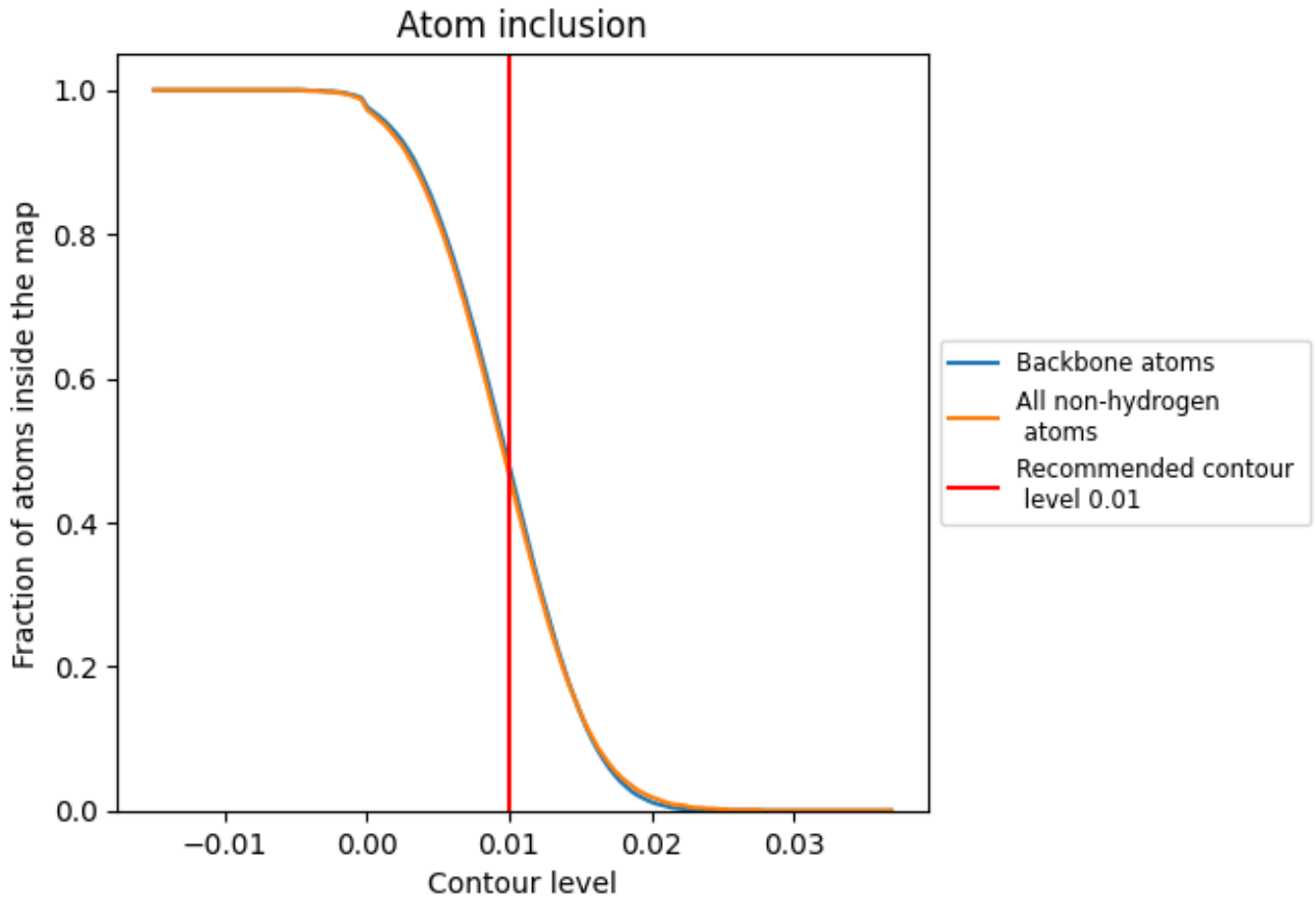
9.3 Atom inclusion mapped to coordinate model



X Y Z

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	0.4660	0.0430
3A	0.7300	0.0750
3B	0.4850	0.0720
3C	0.5050	0.0300
3D	0.6480	0.0740
3E	0.5400	0.0530
3F	0.6800	0.0520
3G	0.7000	0.0700
3H	0.5480	0.0570
5A	0.4620	0.0410
5B	0.1730	0.0220
5C	0.5190	0.0420
5D	0.3620	0.0510
5E	0.4860	0.0690
5F	0.4840	0.0750
5G	0.4940	0.0710
5H	0.5400	0.0360
5I	0.6100	0.0490
5J	0.3960	0.0810
5K	0.3810	0.0530
A4	0.6800	0.0470
A5	0.6300	0.0460
A8	0.5600	0.0260
A9	0.6910	0.0700
AE	0.3060	0.0360
AF	0.6460	0.0650
AG	0.7180	0.0530
B1	0.6050	0.0590
B2	0.7070	0.0560
B3	0.5320	0.0300
B6	0.4550	0.0650
B8	0.5910	0.0510
BE	0.6960	0.0560
RA	0.3730	0.0180
RB	0.3330	0.0360

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Continued from previous page...

Chain	Atom inclusion	Q-score
RD	0.0000	-0.0170
RE	0.0600	0.0080
RF	0.0430	0.0160
RG	0.6280	0.0530
RH	0.4680	0.0300
RJ	0.5960	0.0590
RK	0.6340	0.0620
RL	0.2220	0.0320
RM	0.0710	0.0130
RN	0.4700	0.0370
RO	0.4470	0.0330
RP	0.2620	0.0280
RQ	0.2180	0.0110
RS	0.6410	0.0240
RT	0.0870	-0.0040
RY	0.1740	-0.0020
RZ	0.0700	0.0220
SA	0.5940	0.0540
SC	0.1120	0.0220
SF	0.5140	0.0200
SG	0.6420	0.0910
SH	0.4740	0.0360
SI	0.1110	0.0190
SJ	0.5740	0.0260
SK	0.5500	0.0880
SM	0.5310	-0.0050
SO	0.1890	0.0210
SP	0.1960	0.0140
SR	0.5560	0.0800
ST	0.1510	0.0370
SU	0.1310	0.0350
SX	0.1590	0.0140
SY	0.5430	0.0730
SZ	0.5910	0.0530
Sc	0.1360	0.0130
Sd	0.6440	0.0760
X1	0.2730	0.0560