wwPDB EM Validation Summary Report (i)

Mar 20, 2024 – 10:34 AM JST

PDB ID	:	6LQU
EMDB ID	:	EMD-0954
Title	:	Cryo-EM structure of 90S small subunit preribosomes in transition states (State A1)
Authors	:	Du, Y.; Ye, K.
Deposited on	:	2020-01-14
Resolution	:	3.70 Å(reported)
Based on initial model	:	6LQP

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 (i) 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 (i)) were used in the production of this report:

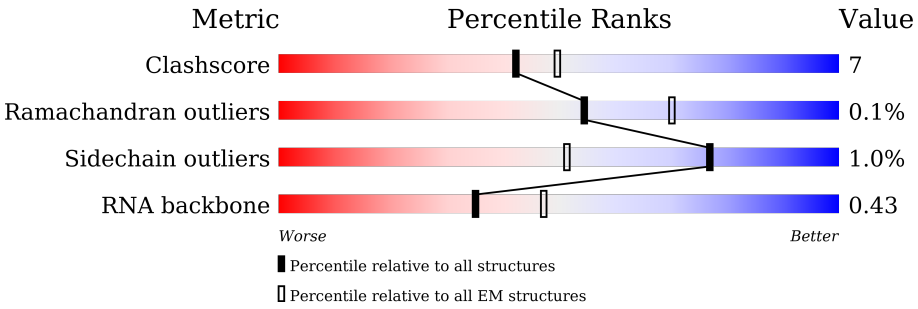
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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)
Clashscore	158937	4297
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	33% 17% • 47%
2	5A	700	• 42% 25% 7% 25%
3	SA	1808	27% 31% 29% 9% • 31%
4	SF	261	47% 62% 25% • 12%
5	SG	225	• 82% 13% 5%
6	SH	236	61% 56% 15% 29%
7	SI	190	81% 67% 18% • 13%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	SJ	200	66% 55% 27% 17%
9	SK	197	76% 11% 13%
10	SM	156	54% 53% 26% 21%
11	SN	143	76% 66% 17% 17%
12	SO	151	88% 75% 13% 11%
13	SP	137	75% 62% 23% 14%
14	SR	143	73% 15% 13%
15	ST	146	64% 16% 20%
16	SX	130	58% 84% 12%
17	SY	145	63% 7% 29%
18	SZ	135	24% 59% 15% 24%
19	Sd	67	94% 6%
20	3B	327	61% 13% 27%
20	3C	327	52% 17% 31%
21	3D	504	60% 13% 27%
22	3E	511	67% 17% 16%
23	3F	573	5% 61% 18% 21%
24	3G	126	80% 16%
24	3H	126	76% 19%
25	A4	776	65% 19% 15%
26	A5	643	65% 14% 20%
27	A8	713	10% 68% 8% 23%
28	A9	575	18% 78%
29	AE	1769	54% 77% 9% 13%
30	AF	513	75% 21%

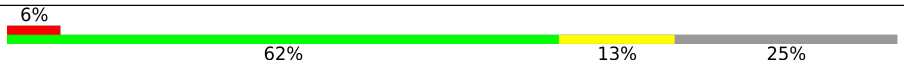
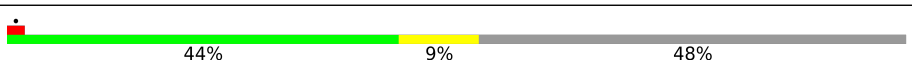
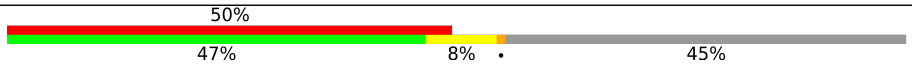
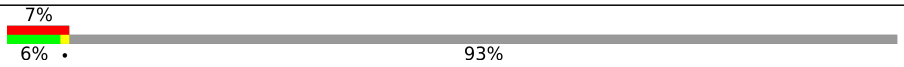
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
31	AG	896	71% 20% 8%
32	B1	923	75% 15% 10%
33	B2	943	69% 21% 10%
34	B3	817	43% 66% 24% 8%
35	B8	594	66% 14% 20%
36	BE	939	78% 14% 8%
37	B6	440	7% 74% 10% 15%
38	5B	214	21% 7% 72%
39	5C	554	8% 74% 19% 7%
40	5D	250	81% 12% 6%
41	5E	593	28% 6% 66%
42	5F	183	79% 20%
43	5G	290	78% 20%
44	5H	610	20% 78%
45	5I	489	72% 22% 6%
46	5J	217	6% 58% 12% 30%
47	5K	189	78% 15% 7%
48	RA	707	44% 35% 12% 52%
49	RB	357	12% 27% 10% 62%
50	RC	316	48% 42% 13% 45%
51	RD	1729	14% 15% 85%
52	RE	1237	87% 66% 20% 13%
53	RF	297	59% 44% 13% 41%
54	RG	252	62% 24% 14%
54	RH	252	72% 19% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
55	RI	274	
56	RJ	1183	
57	RK	367	
58	RL	1056	
58	RM	1056	
59	RN	810	
60	RO	552	
61	RP	2493	
62	RQ	899	
63	RS	483	
64	RT	326	
65	RV	346	
66	RW	206	
67	RY	534	
68	X1	347	

2 Entry composition (i)

There are 71 unique types of molecules in this entry. The entry contains 227765 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	523	11163	4988	1984	3668	523	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	SA	1242	26503	11846	4736	8679	1242	0	0

- Molecule 4 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 5 is a protein called 40S ribosomal protein S5.

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

- Molecule 6 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 7 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 10 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SN	119	Total	C	N	O	S	0	0
			865	545	151	167	2		

- 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 S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	ST	117	Total 964	C 610	N 184	O 168	S 2	0	0

- Molecule 16 is a protein called 40S ribosomal protein S22-B.

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

- Molecule 17 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	SZ	102	Total 809	C 517	N 148	O 144	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	548	Total	C	N	O	S	0	0
			3307	2054	608	642	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	834	Total	C	N	O	S	0	0
			6635	4223	1140	1253	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B2	851	Total	C	N	O	S	0	0
			6723	4294	1133	1269	27		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B3	752	Total	C	N	O	S	0	0
			5882	3746	987	1122	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	865	Total	C	N	O	S	0	0
			6810	4322	1175	1292	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	516	Total	C	N	O	S	0	0
			4084	2561	736	775	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5D	235	Total	C	N	O	S	0	0
			1972	1226	380	359	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	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	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
44	5H	136	Total	C	N	O	0	0
			1065	658	211	196		

- 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	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- 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 KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RC	175	Total	C	N	O	S	0	0
			1410	903	252	245	10		

- Molecule 51 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	RD	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 52 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 53 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RF	174	Total	C	N	O	S	0	0
			1404	905	230	261	8		

- Molecule 54 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 55 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RI	252	Total	C	N	O	S	0	0
			2045	1309	362	366	8		

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

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

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

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

- Molecule 58 is a protein called RNA cytidine acetyltransferase.

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

- Molecule 59 is a protein called Nucleolar complex protein 14.

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

- Molecule 60 is a protein called Nucleolar complex protein 4.

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

- Molecule 61 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	RP	2109	Total	C	N	O	S	0	0
			12176	7486	2292	2382	16		

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RQ	226	Total	C	N	O	S	0	0
			1651	1023	313	313	2		

- Molecule 63 is a protein called Essential nuclear protein 1.

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

- Molecule 64 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	RT	171	Total	C	N	O	S	0	0
			1357	864	249	240	4		

- Molecule 65 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	RV	190	Total	C	N	O	S	0	0
			1448	891	290	264	3		

- Molecule 66 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	RW	63	Total	C	N	O	0	0
			381	234	69	78		

- Molecule 67 is a protein called Protein BFR2.

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

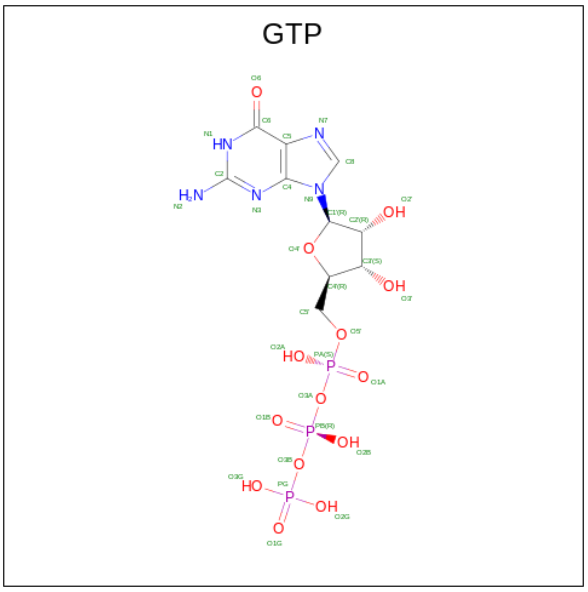
- Molecule 68 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	X1	61	Total	C	N	O	0	0
			305	183	61	61		

- Molecule 69 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
69	5K	1	Total	Zn	0
			1	1	

- Molecule 70 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 71 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

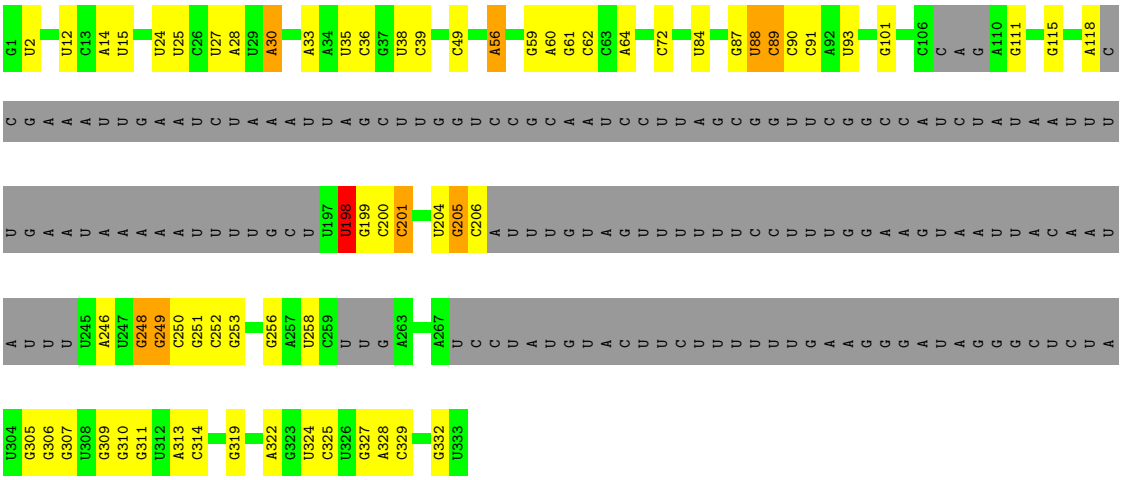
Mol	Chain	Residues	Atoms		AltConf
71	RJ	1	Total	Mg	0
			1	1	

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.

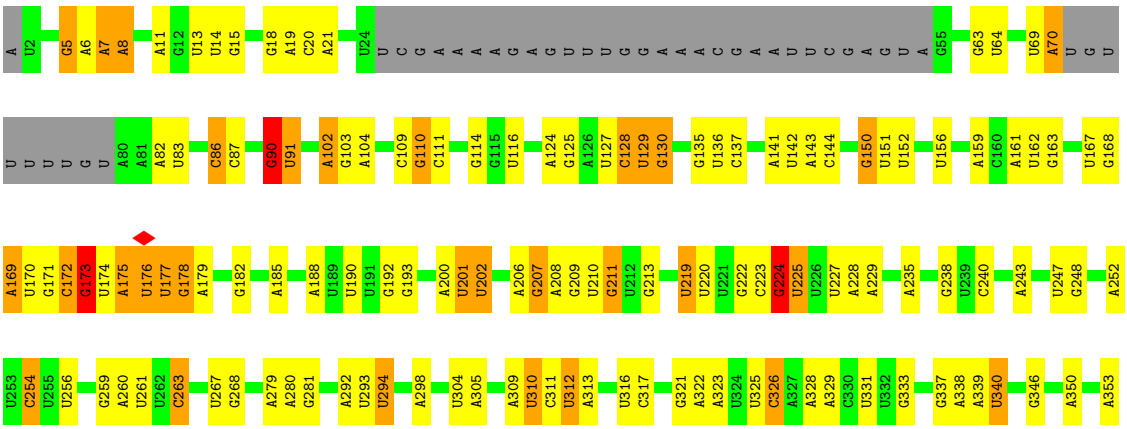
- Molecule 1: U3 snoRNA

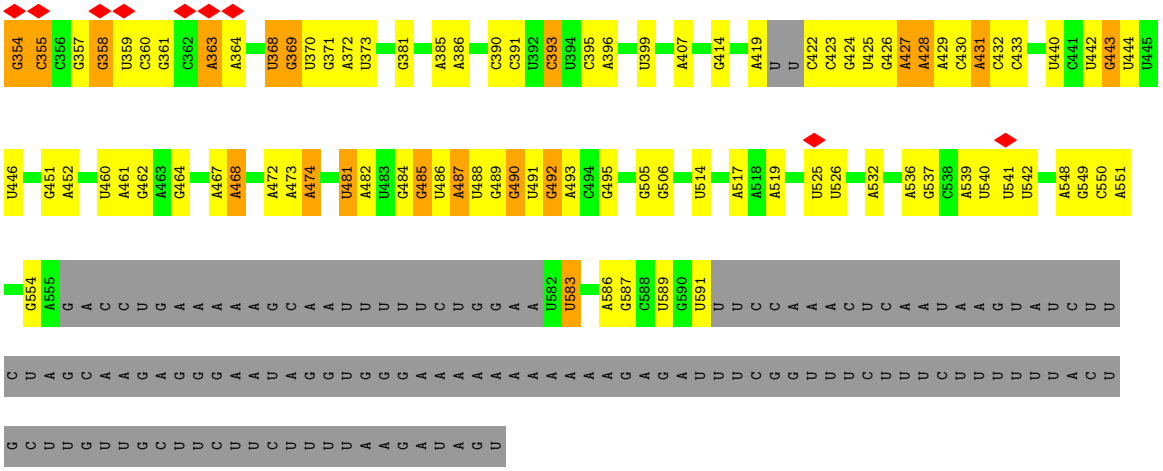
Chain 3A:



- Molecule 2: 5’ ETS

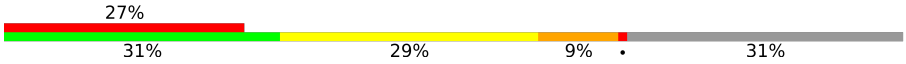
Chain 5A:

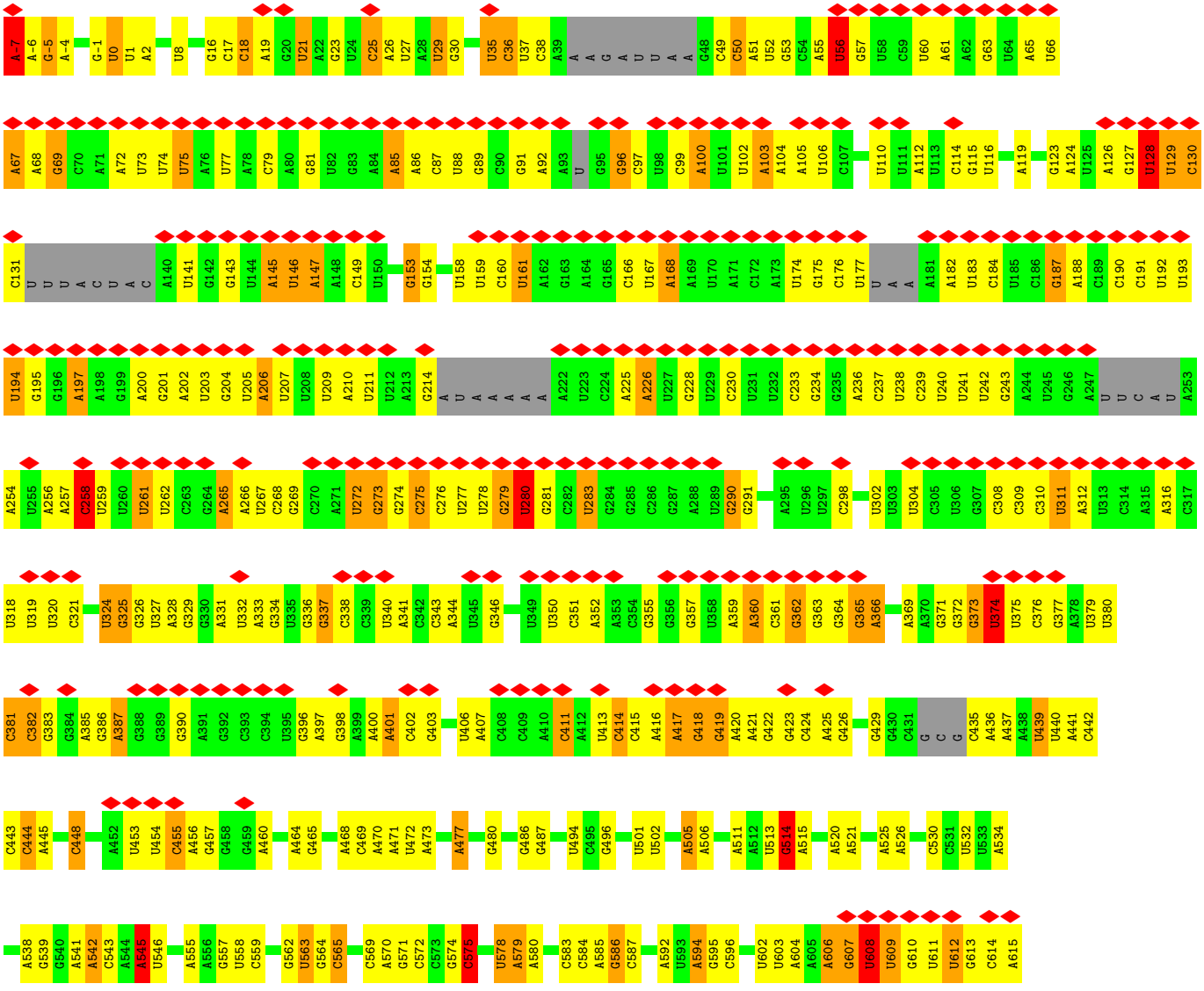


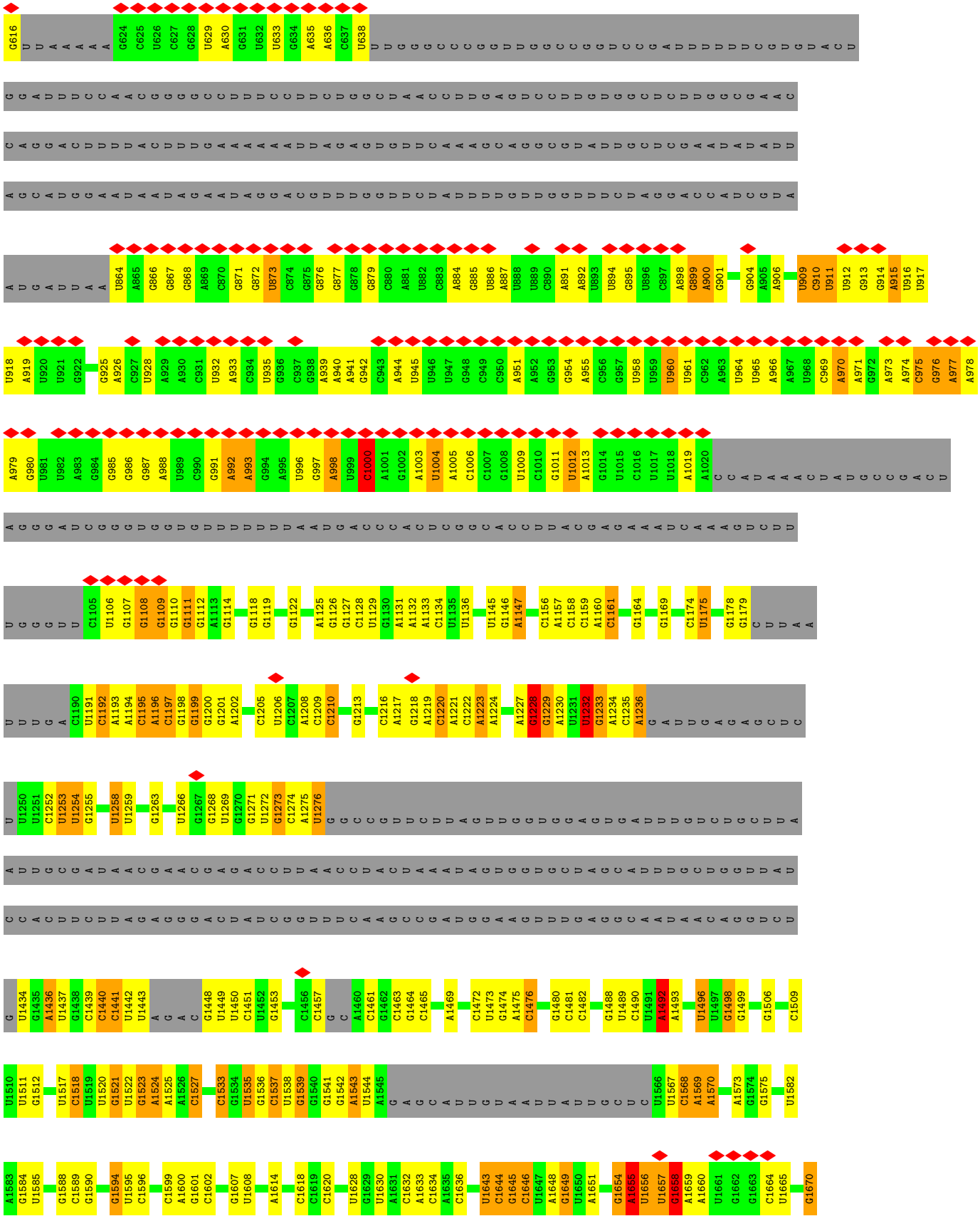


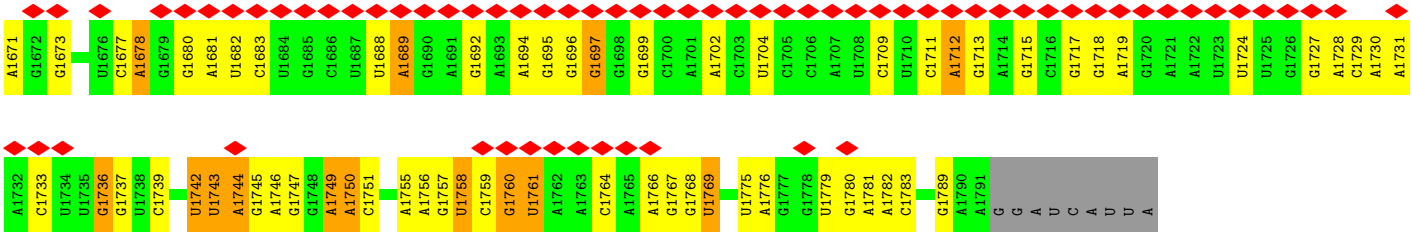
• Molecule 3: 18S pre-rRNA

Chain SA:



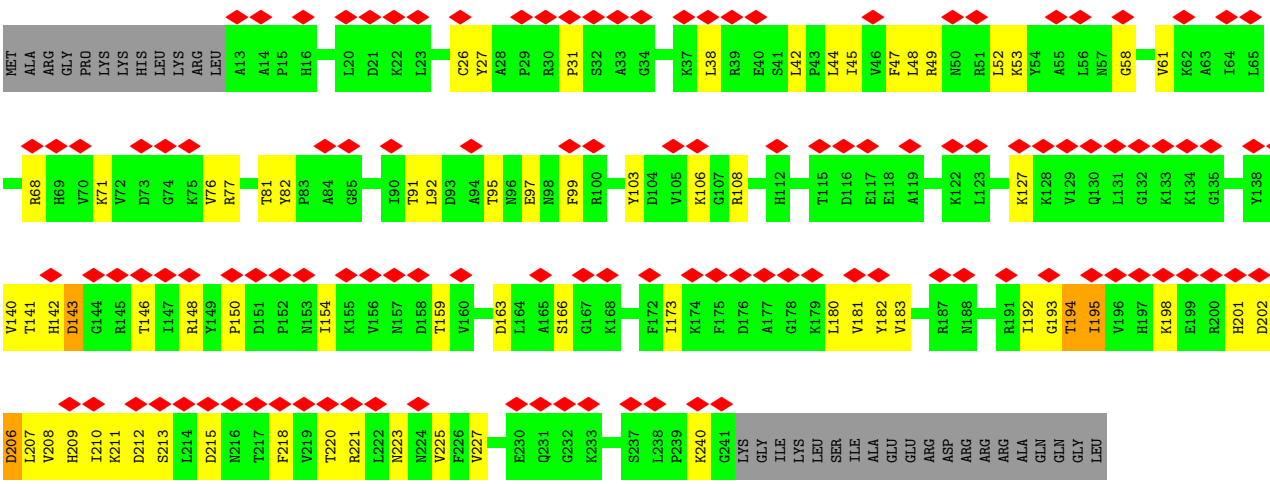






• Molecule 4: 40S ribosomal protein S4-A

Chain SF:

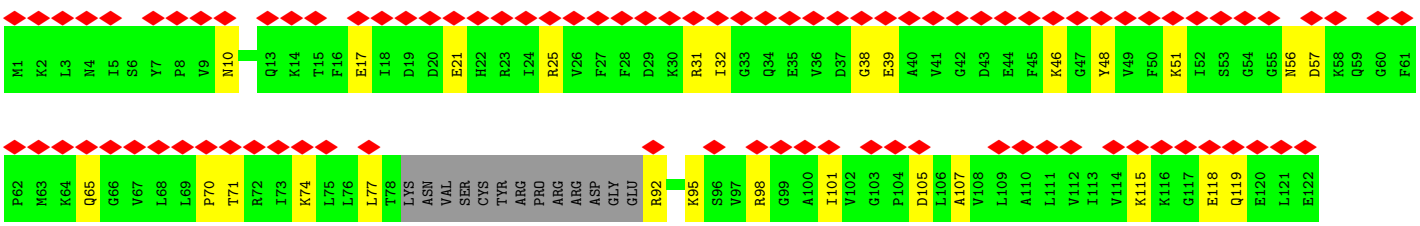


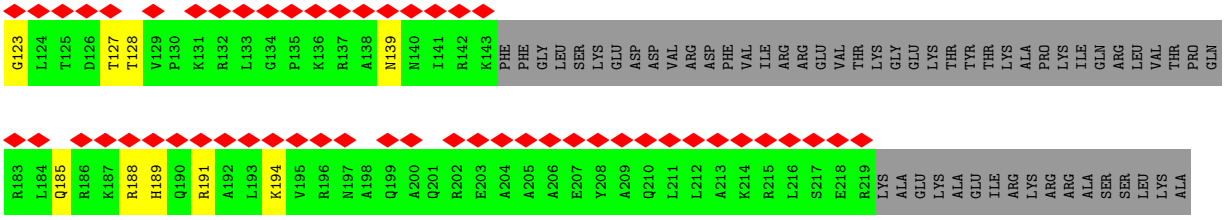
• Molecule 5: 40S ribosomal protein S5

Chain SG:

• Molecule 6: 40S ribosomal protein S6-A

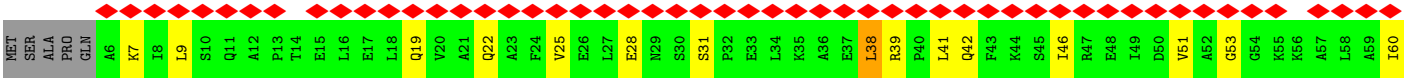
Chain SH:

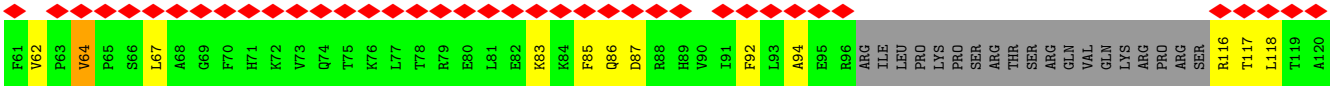


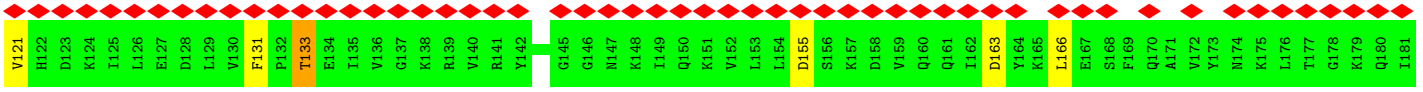


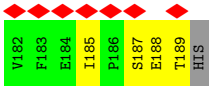
• Molecule 7: 40S ribosomal protein S7-A

Chain SI:



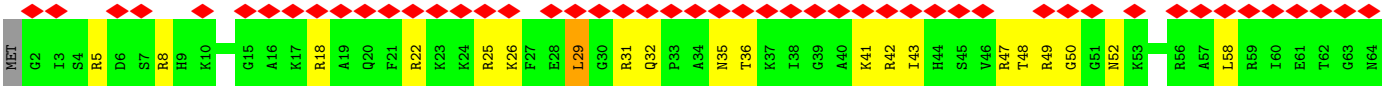


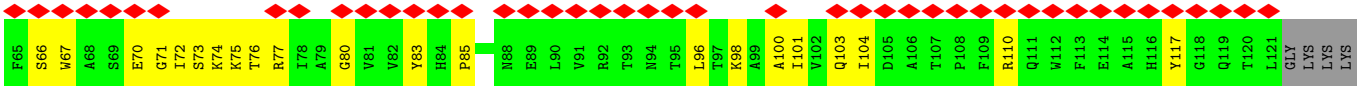


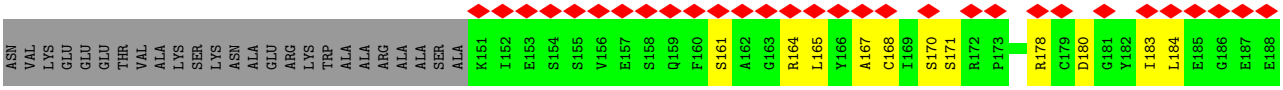


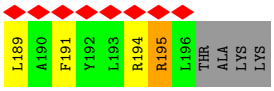
• Molecule 8: 40S ribosomal protein S8-A

Chain SJ:



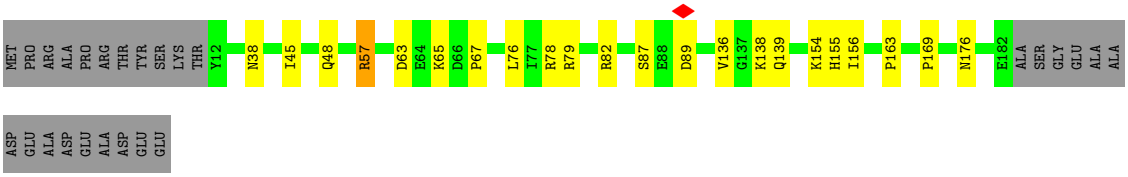






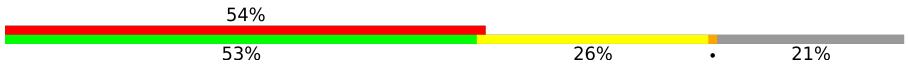
• Molecule 9: 40S ribosomal protein S9-A

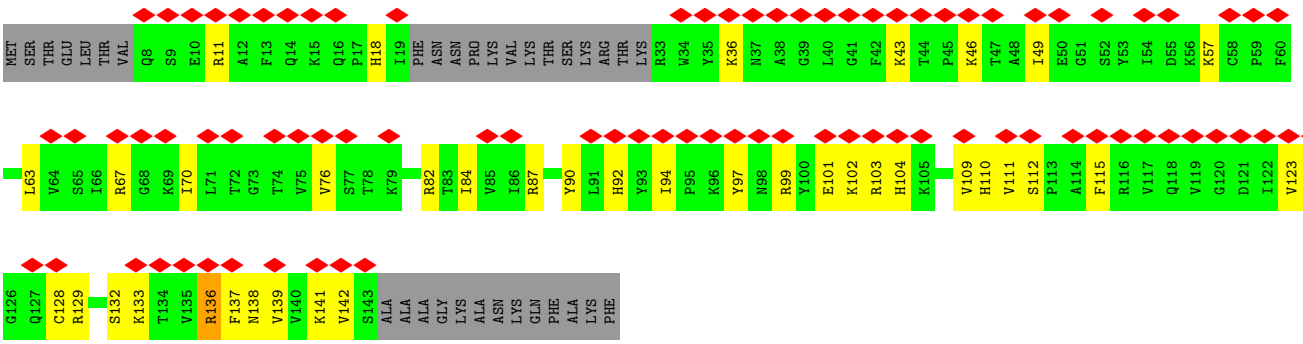
Chain SK:



• Molecule 10: 40S ribosomal protein S11-A

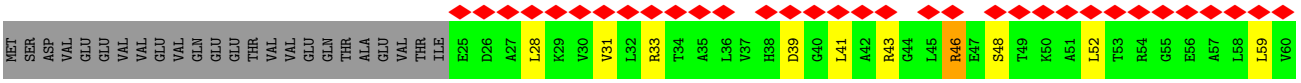
Chain SM:

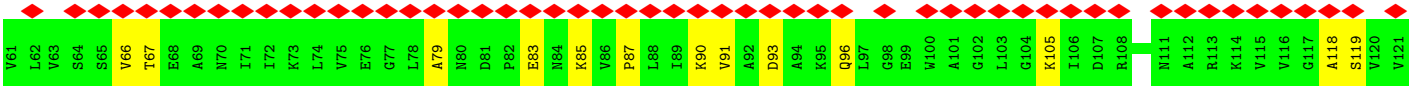


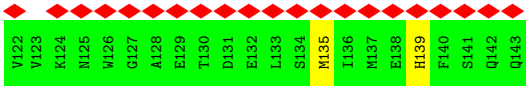


• Molecule 11: 40S ribosomal protein S12

Chain SN:

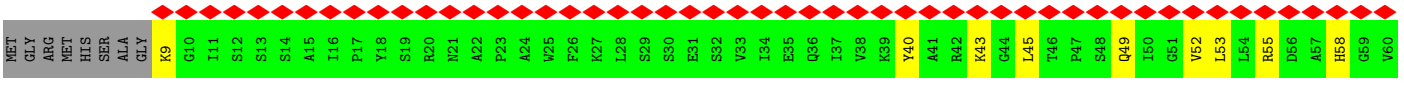


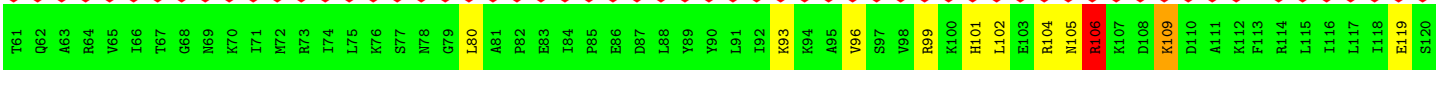


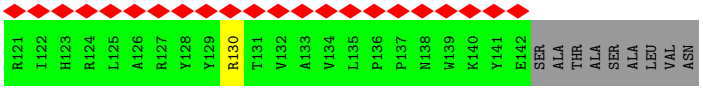


• Molecule 12: 40S ribosomal protein S13

Chain SO:

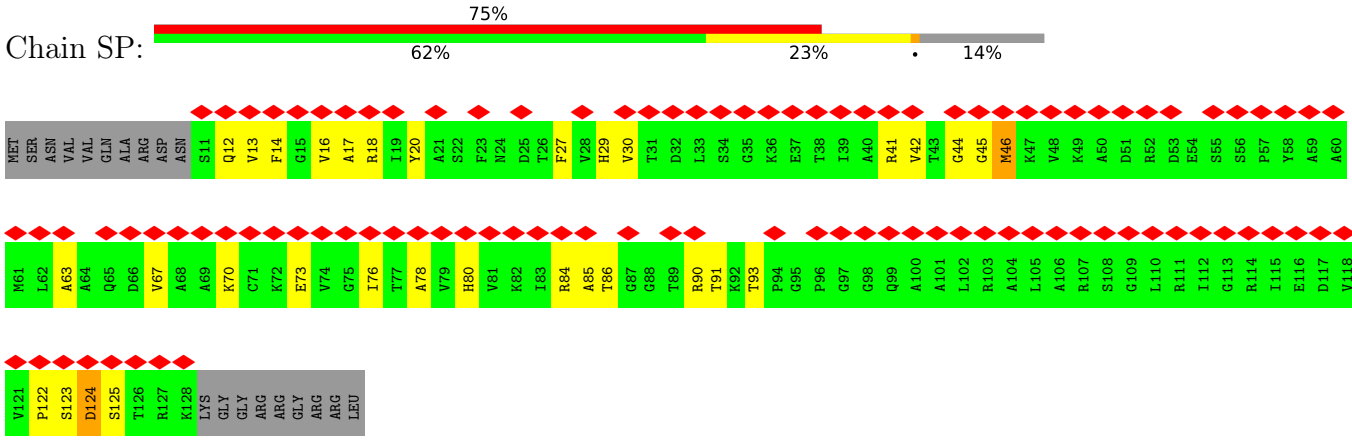






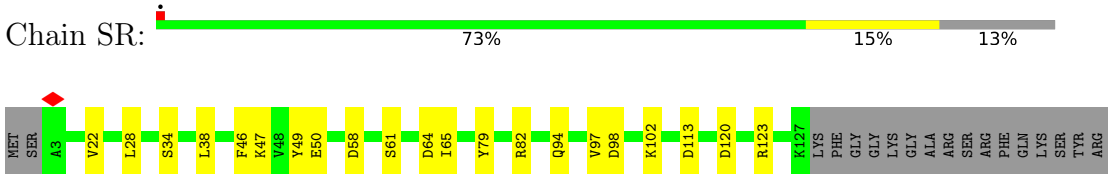
• Molecule 13: 40S ribosomal protein S14-A

Chain SP:



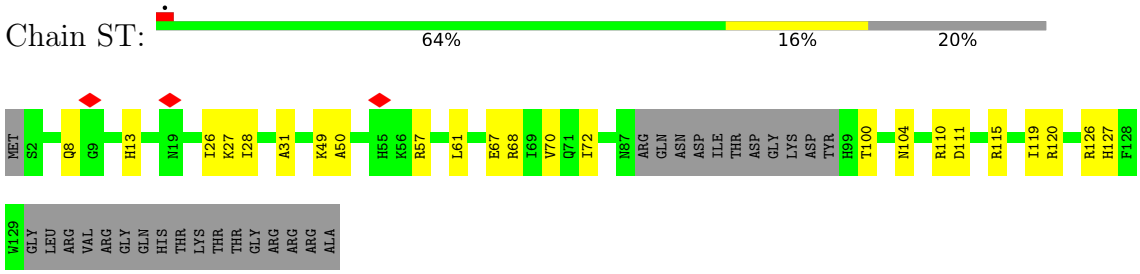
• Molecule 14: 40S ribosomal protein S16-A

Chain SR:



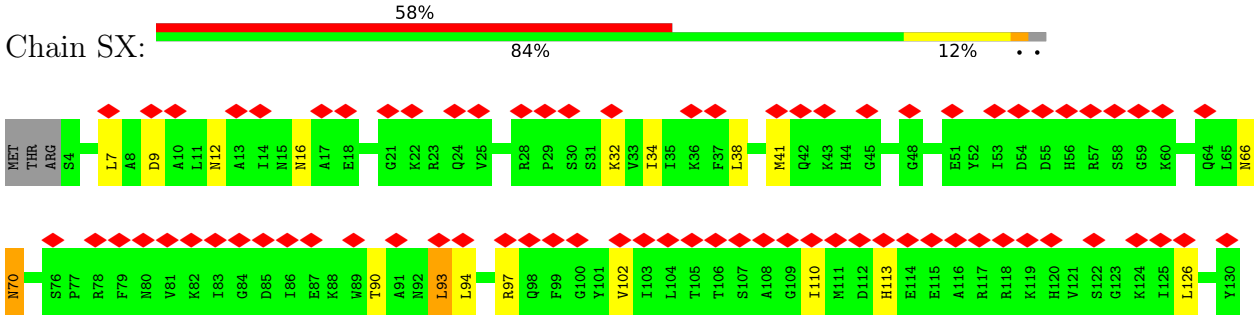
• Molecule 15: 40S ribosomal protein S18-A

Chain ST:



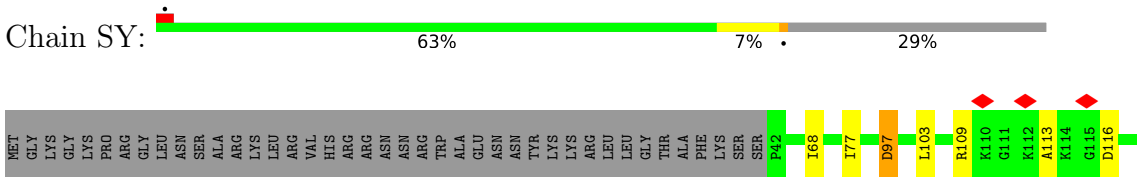
• Molecule 16: 40S ribosomal protein S22-B

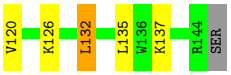
Chain SX:



• Molecule 17: 40S ribosomal protein S23-A

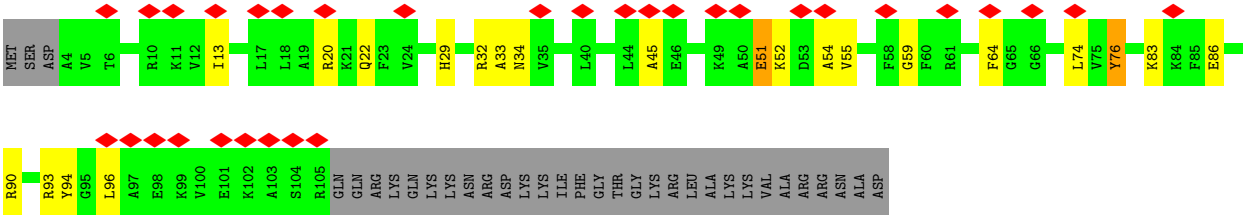
Chain SY:





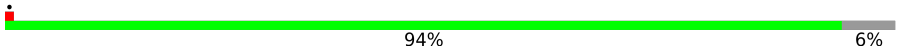
• Molecule 18: 40S ribosomal protein S24-A

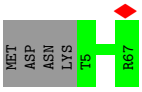
Chain SZ:



• Molecule 19: 40S ribosomal protein S28-A

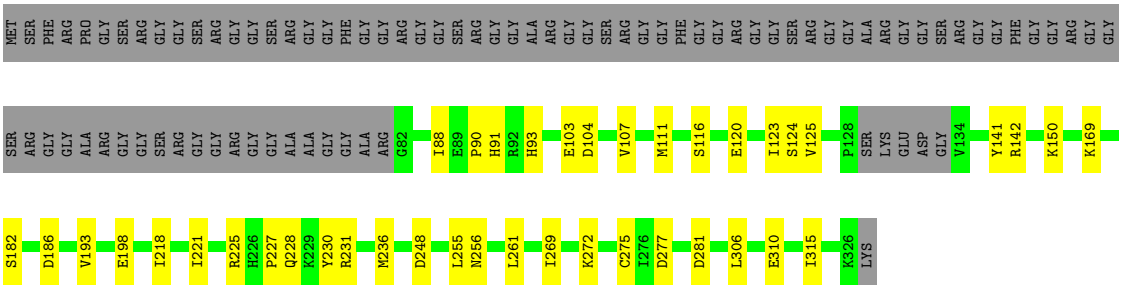
Chain Sd:





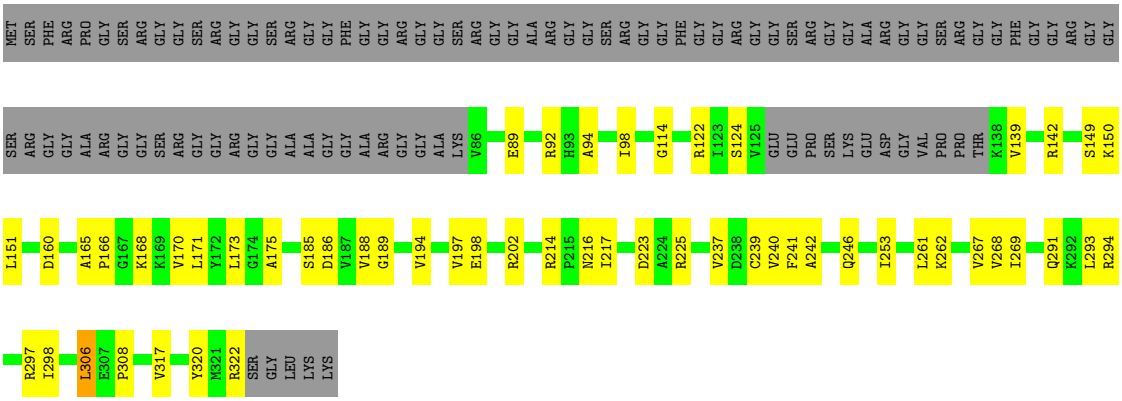
• Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

Chain 3B:



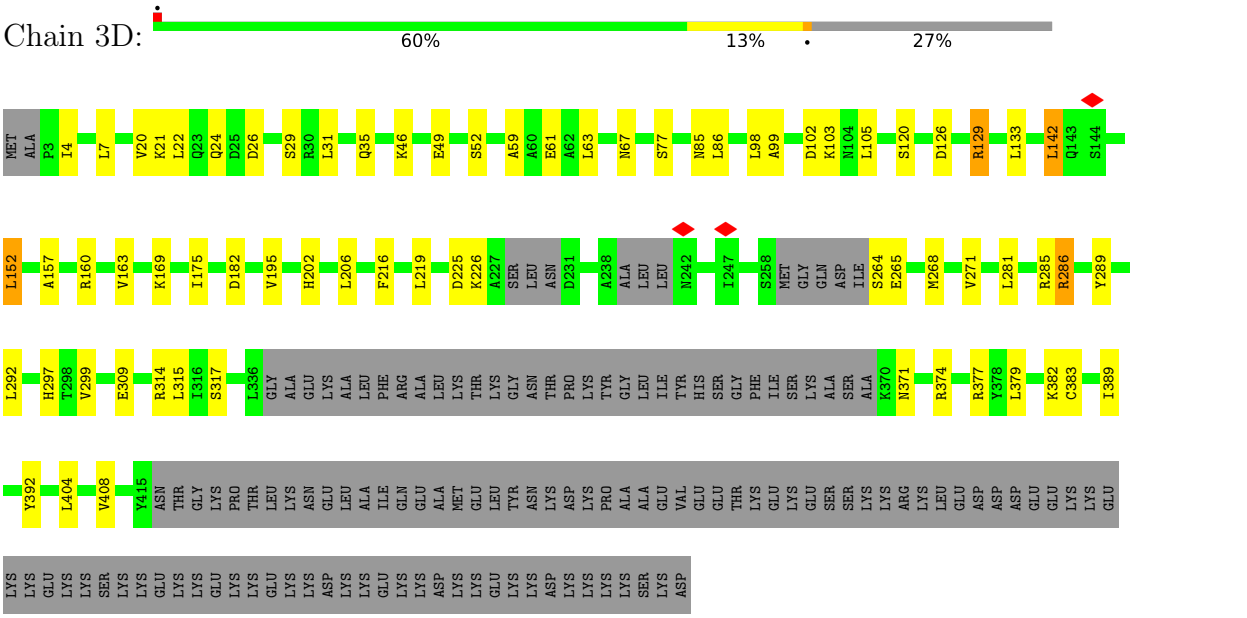
• Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

Chain 3C:



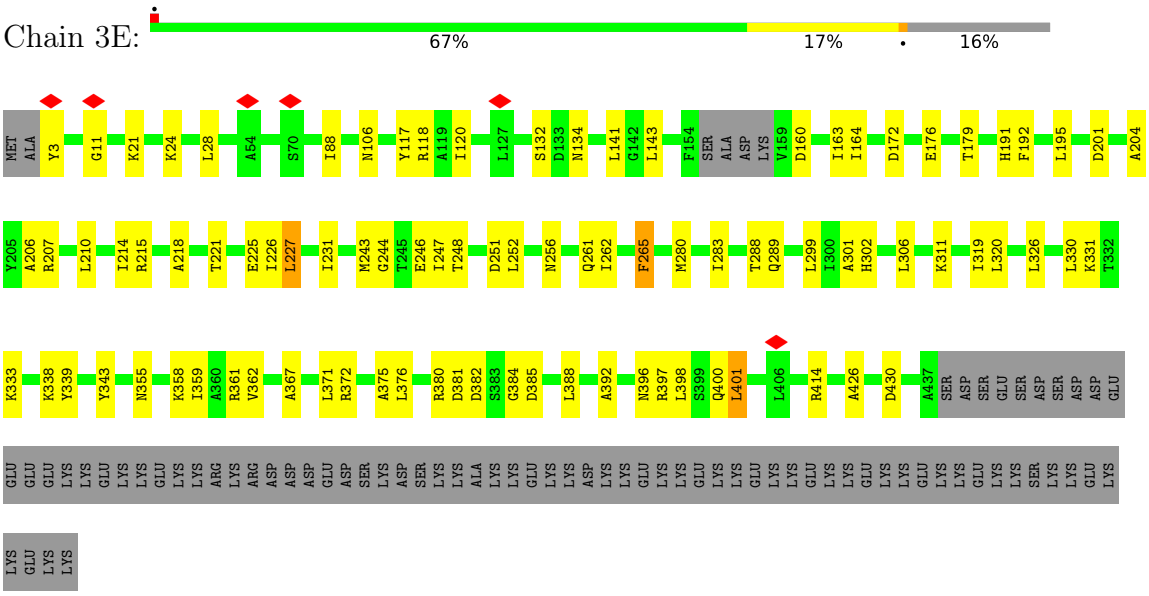
• Molecule 21: Nucleolar protein 56

Chain 3D:



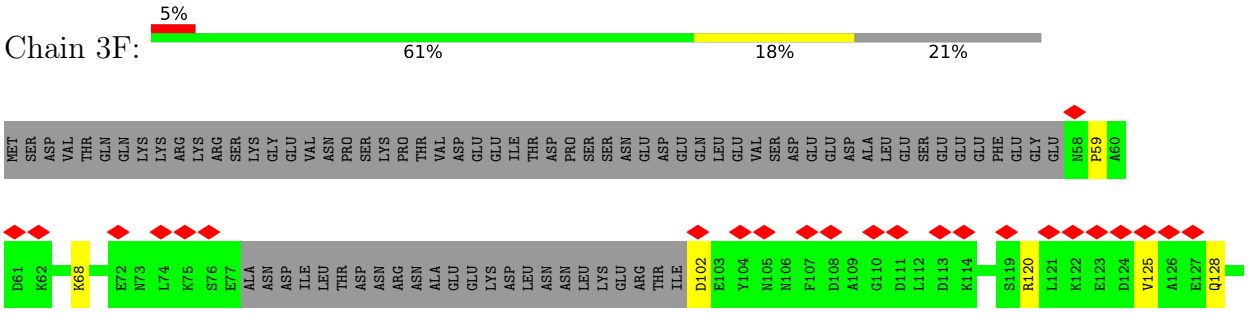
• Molecule 22: Nucleolar protein 58

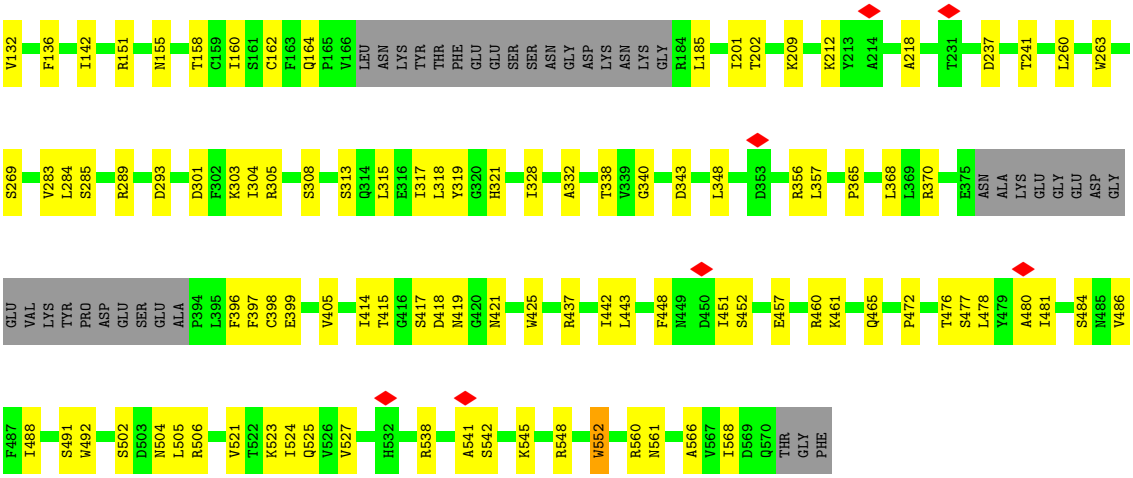
Chain 3E:



• Molecule 23: Ribosomal RNA-processing protein 9

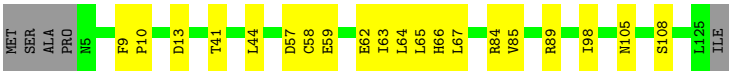
Chain 3F:





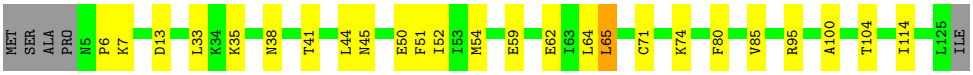
• Molecule 24: 13 kDa ribonucleoprotein-associated protein

Chain 3G:



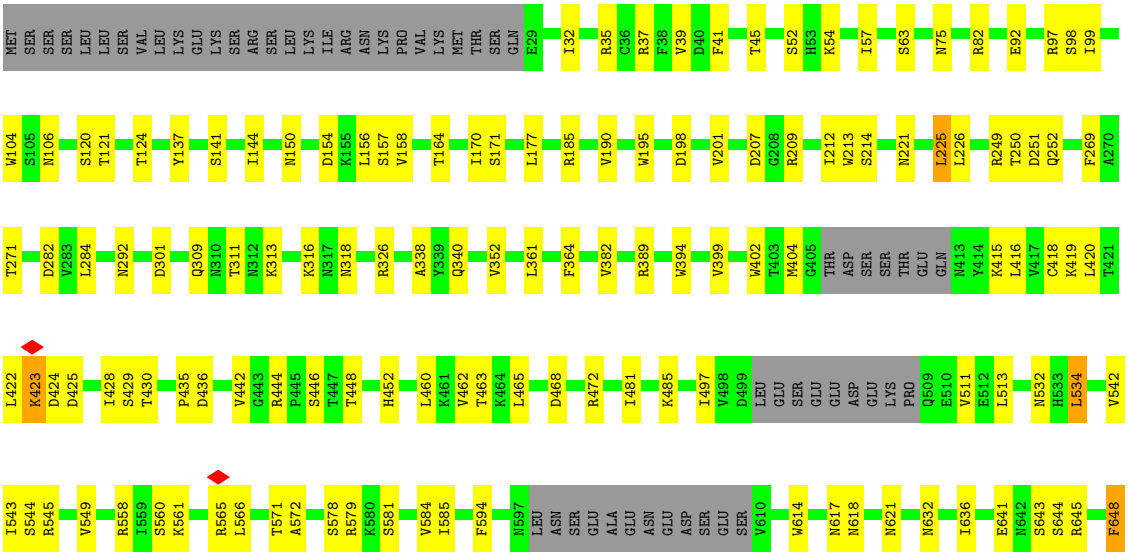
• Molecule 24: 13 kDa ribonucleoprotein-associated protein

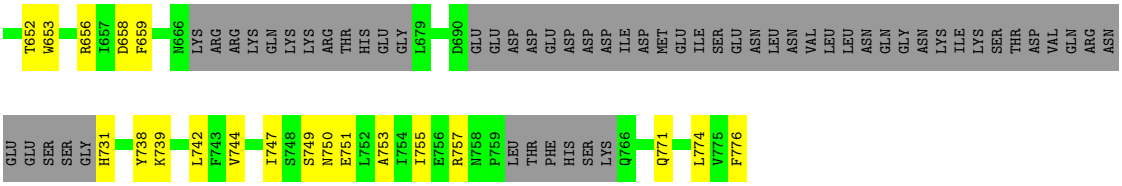
Chain 3H:



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

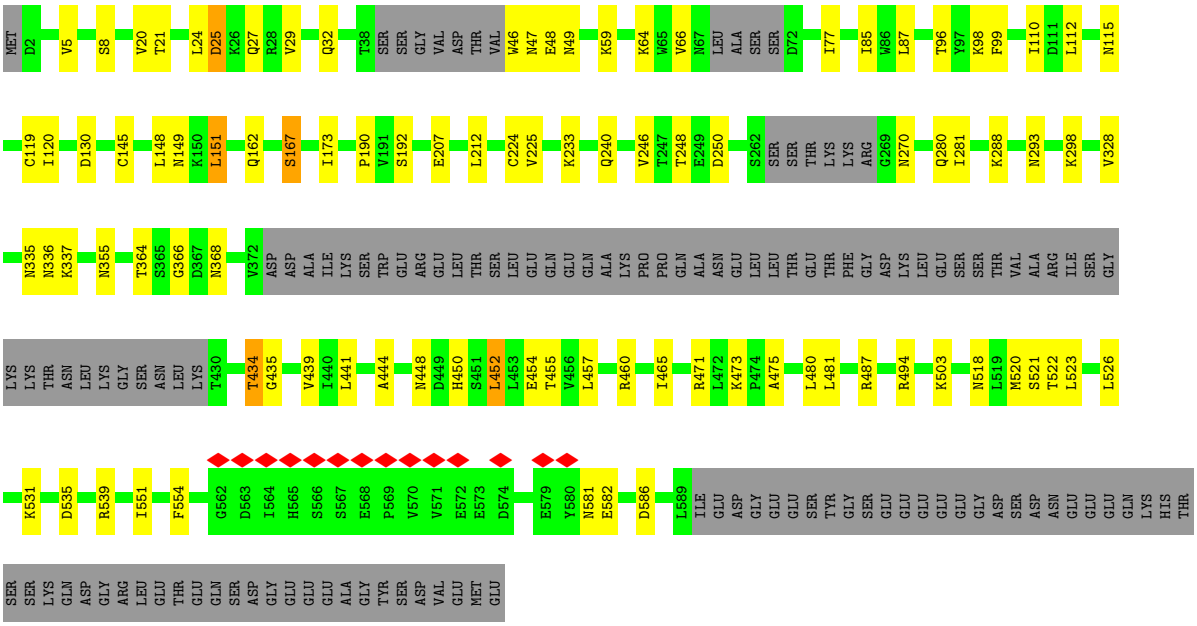
Chain A4:





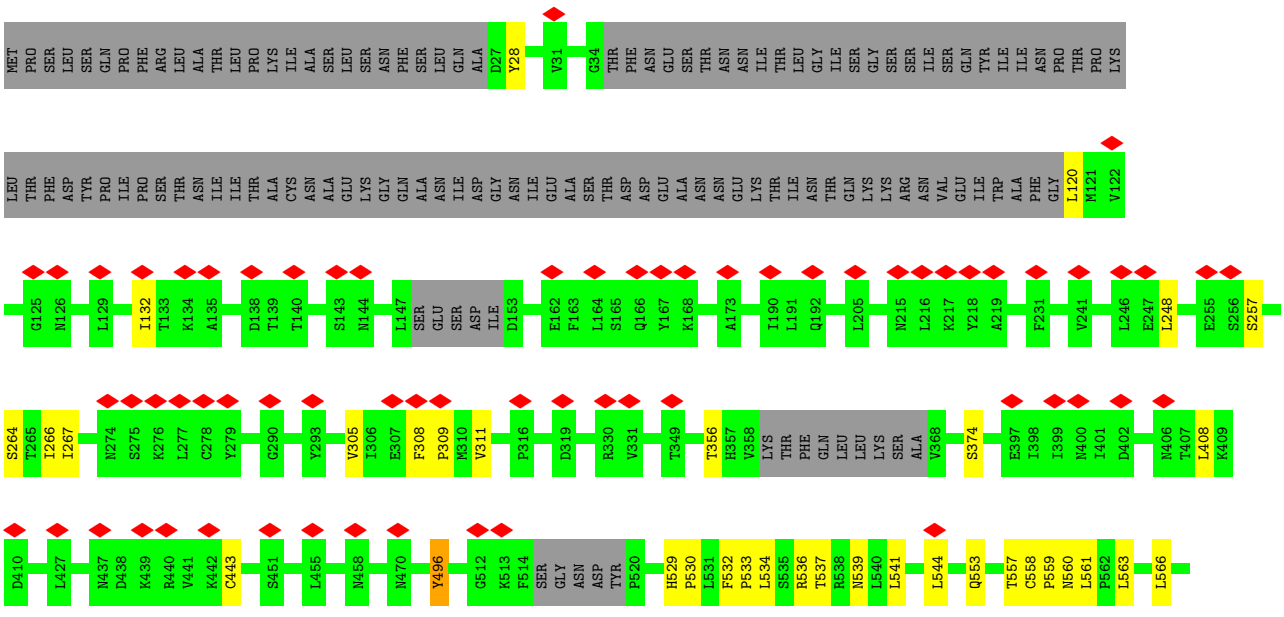
• Molecule 26: U3 small nucleolar RNA-associated protein 5

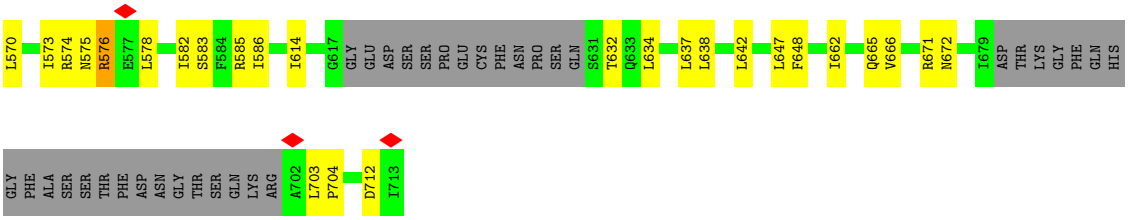
Chain A5:



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

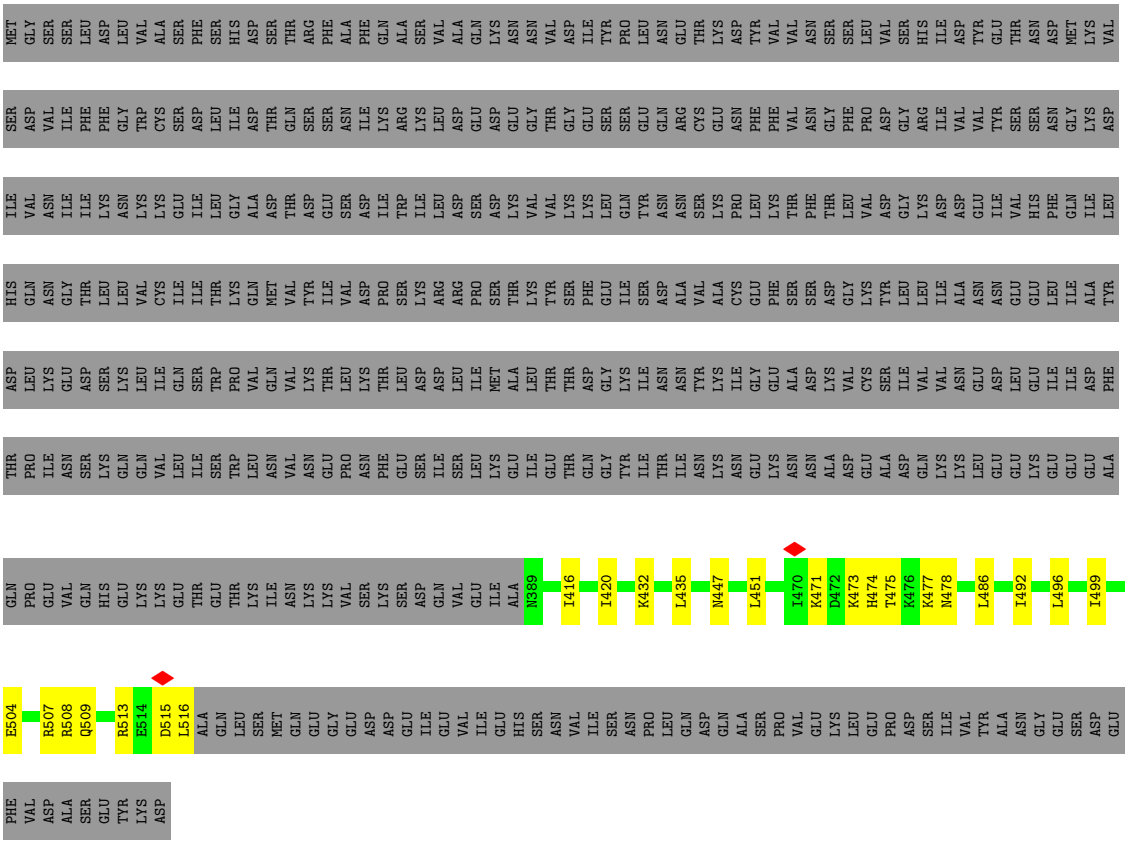
Chain A8:





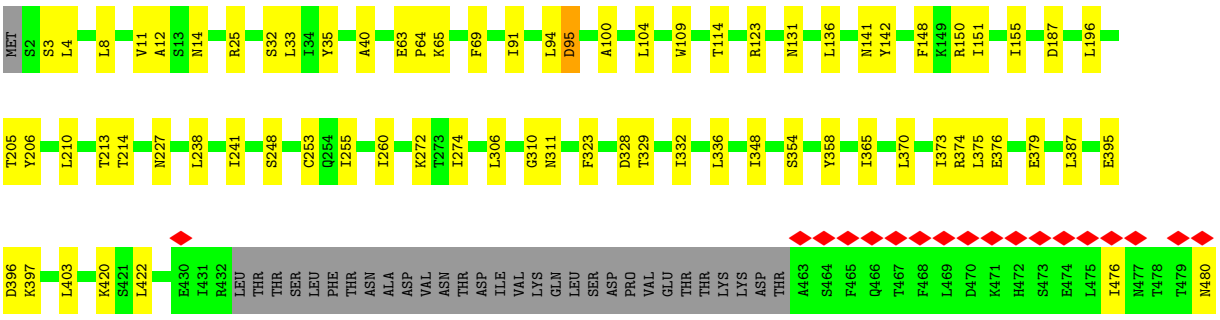
• Molecule 28: U3 small nucleolar RNA-associated protein 9

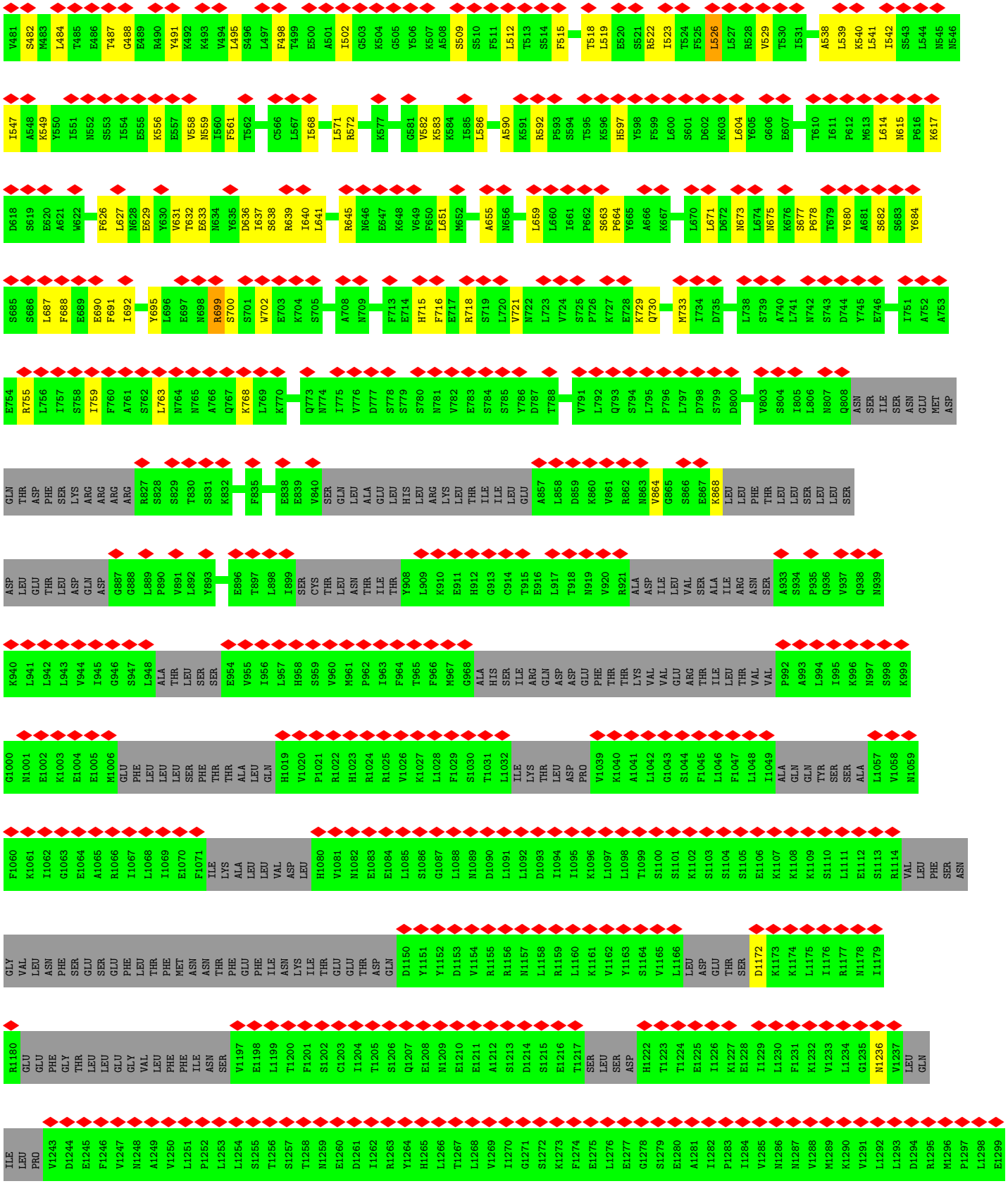
Chain A9:



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

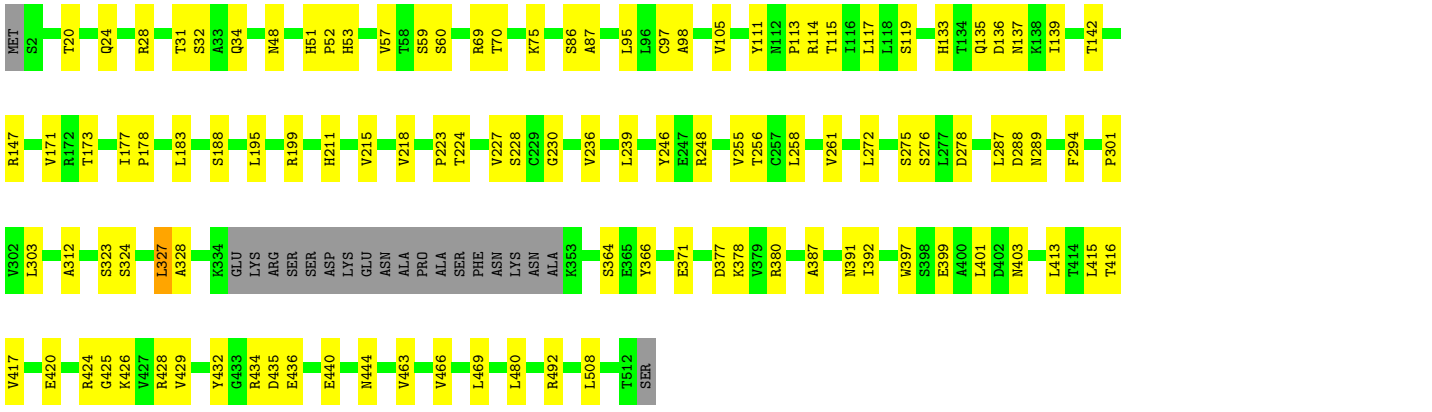
Chain AE:




V481 S482 M483 L484 T485 E486 T487 G488 E489 R490 Y491 K492 K493 V494 L495 S496 L497 F498 T499 E500 A501 I502 G503 K504 G505 Y506 K507 A508 S509 S510 F511 L512 T513 S514 F515 T518 L519 E520 S521 R522 I523 T524 F525 L526 L527 R528 V529 T530 I531 A538 L539 K540 L541 I542 S543 L544 N545 N546
I547 A548 K549 Y550 I551 N552 S553 I554 E555 K556 E557 V558 N559 I560 F561 T562 C566 L567 I568 L571 R572 K577 G581 V582 K583 K584 I585 L586 A590 K591 R592 P593 S594 T595 K596 H597 Y598 F599 L600 S601 D602 K603 L604 Y605 G606 E607 T610 I611 P612 M613 L614 N615 P616 K617
D618 S619 E620 A621 W622 F626 L627 M628 E629 Y630 V631 T632 E633 M634 Y635 D636 I637 S638 R639 I640 L641 R645 N646 E647 K648 V649 F650 L651 M652 A655 N656 L659 L660 I661 P662 S663 P664 Y665 A666 K667 L670 L671 D672 N673 L674 N675 K676 S677 P678 T679 Y680 A681 S682 S683 Y684
S685 S686 L687 F688 E689 E690 F691 I692 Y695 L696 E697 N698 R699 S700 S701 W702 E703 K704 S705 A708 N709 F713 E714 H715 F716 E717 R718 S719 L720 V721 N722 L723 V724 S725 P726 K727 E728 K729 Q730 M733 I734 D735 L738 S739 A740 L741 N742 S743 D744 Y745 E746 I751 A752 A753
E754 R755 L756 I757 S758 I759 F760 A761 S762 L763 N764 N765 A766 Q767 K768 L769 K770 Q773 N774 I775 V776 D777 S778 S779 S780 N781 V782 E783 S784 S785 Y786 D787 T788 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 ARG R827 S828 S829 T830 S831 K832 F835 E838 E839 V840 SER GLN LEU ALA GLU LEU HIS LEU ARG LYS LEU THR ILE ILE LEU GLU A857 L858 D859 K860 V861 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 G888 L889 P890 V891 L892 Y893 E896 T897 L898 I899 SER CYS THR LEU ASN THR ILE THR Y908 L909 K910 E911 H912 G913 C914 T915 E916 L917 T918 N919 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 V1058 N1059
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 E1260 D1261 I1262 R1263 Y1264 H1265 L1266 T1267 L1268 V1269 I1270 G1271 S1272 K1273 F1274 E1275 L1276 E1277 G1278 S1279 E1280 A1281 I1282 P1283 I1284 V1285 N1286 N1287 V1288 M1289 K1290 V1291 L1292 L1293 D1294 R1295 M1296 P1297 L1298 E1299

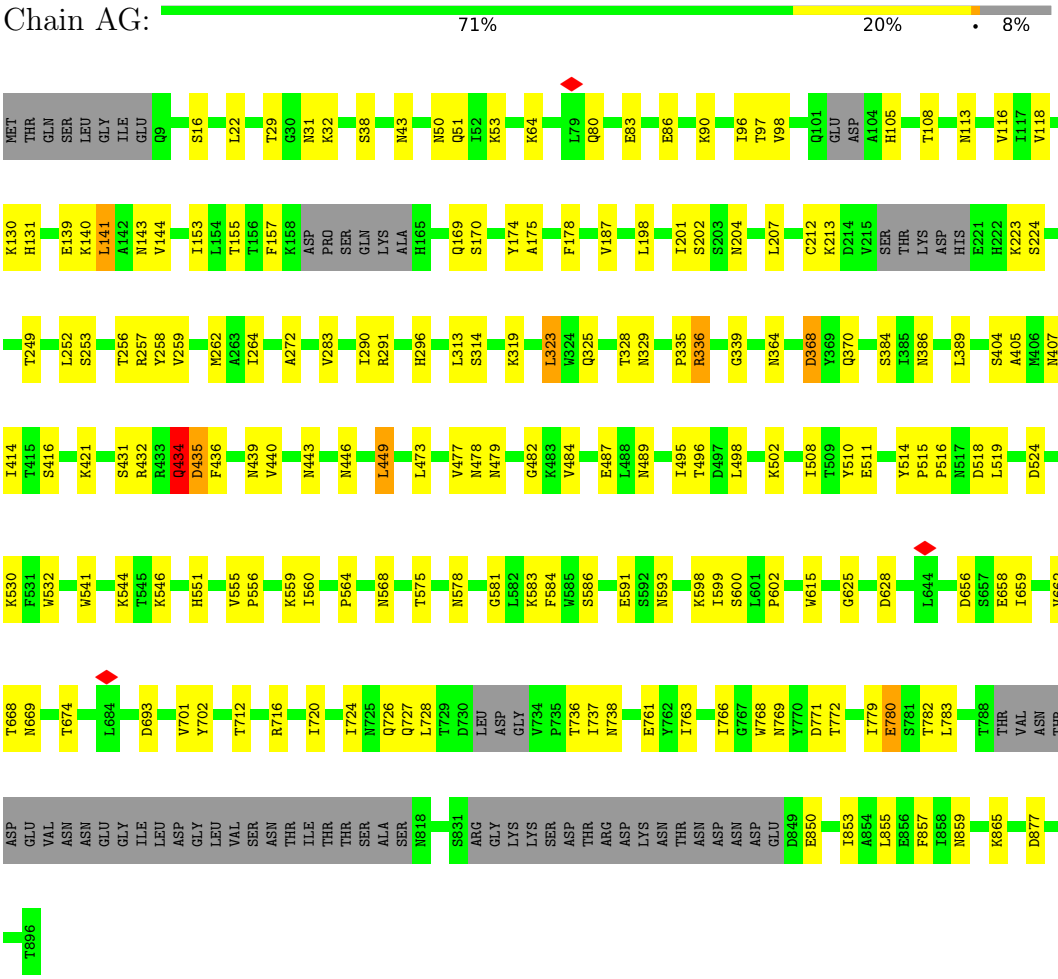
• Molecule 30: U3 small nucleolar RNA-associated protein 15

Chain AF:



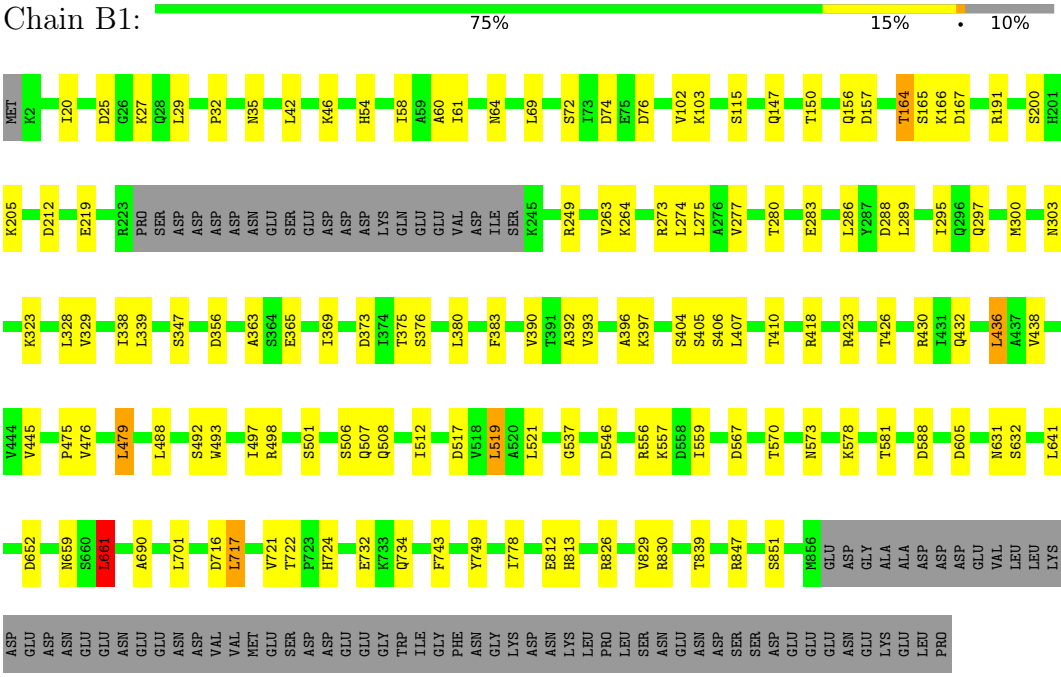
• Molecule 31: NET1-associated nuclear protein 1

Chain AG:



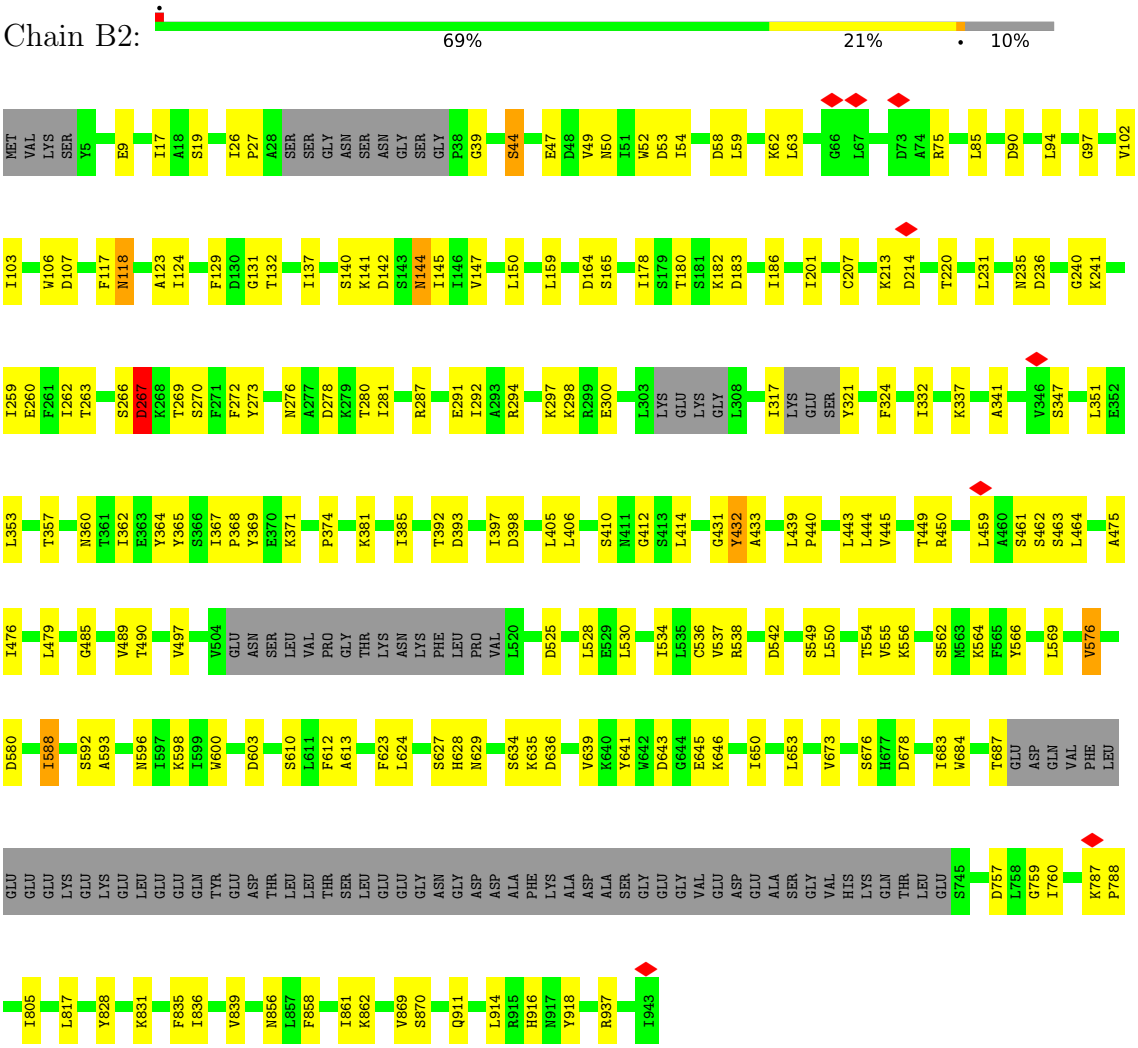
• Molecule 32: Periodic tryptophan protein 2

Chain B1:



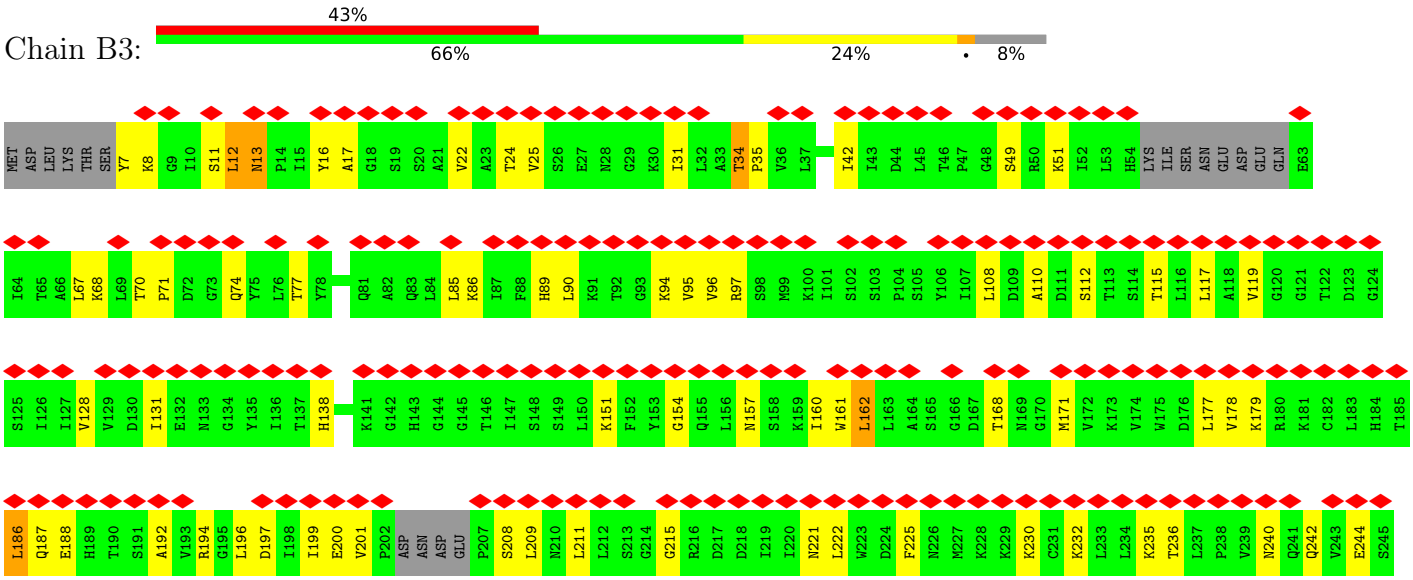
• Molecule 33: U3 small nucleolar RNA-associated protein 12

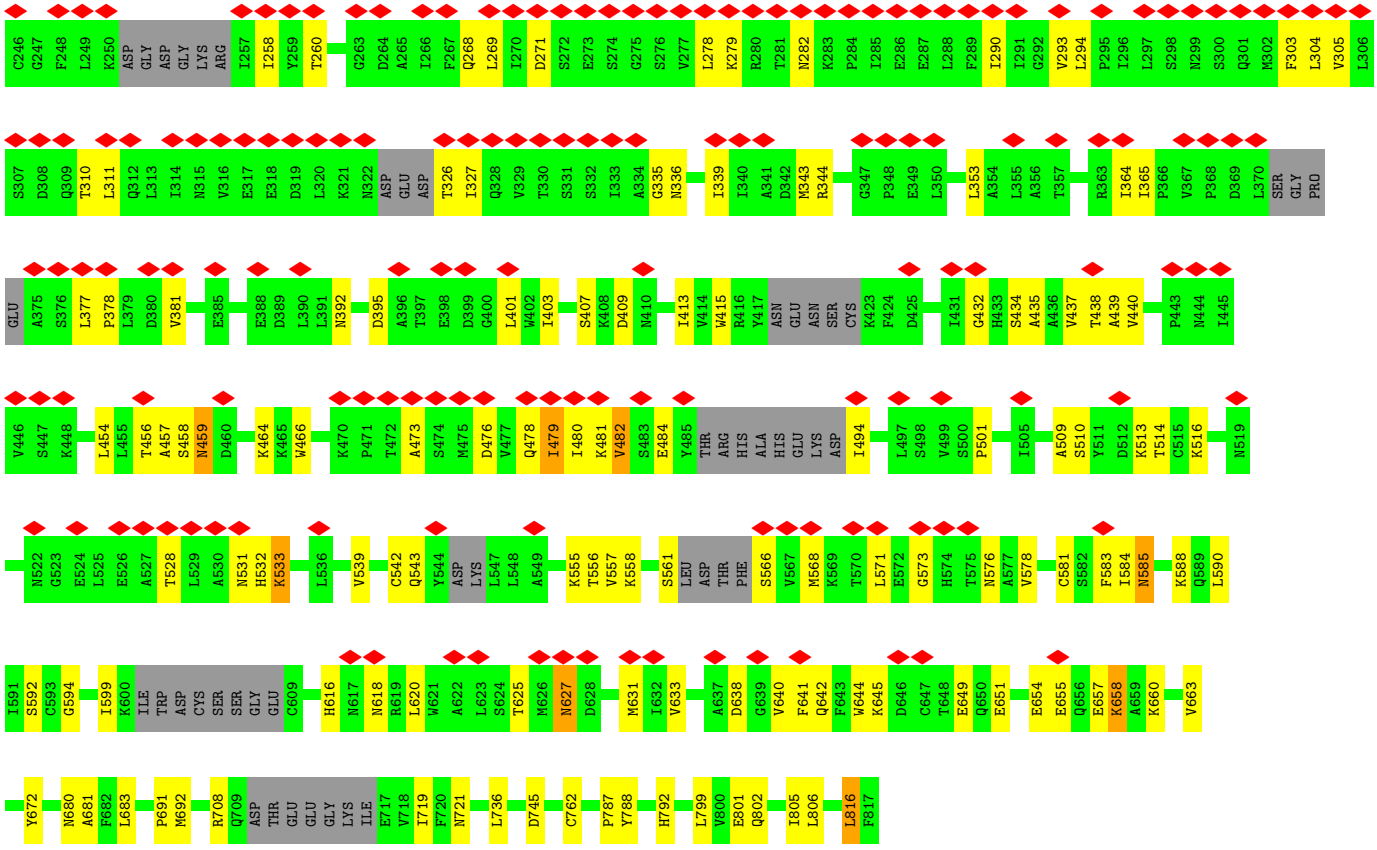
Chain B2:



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

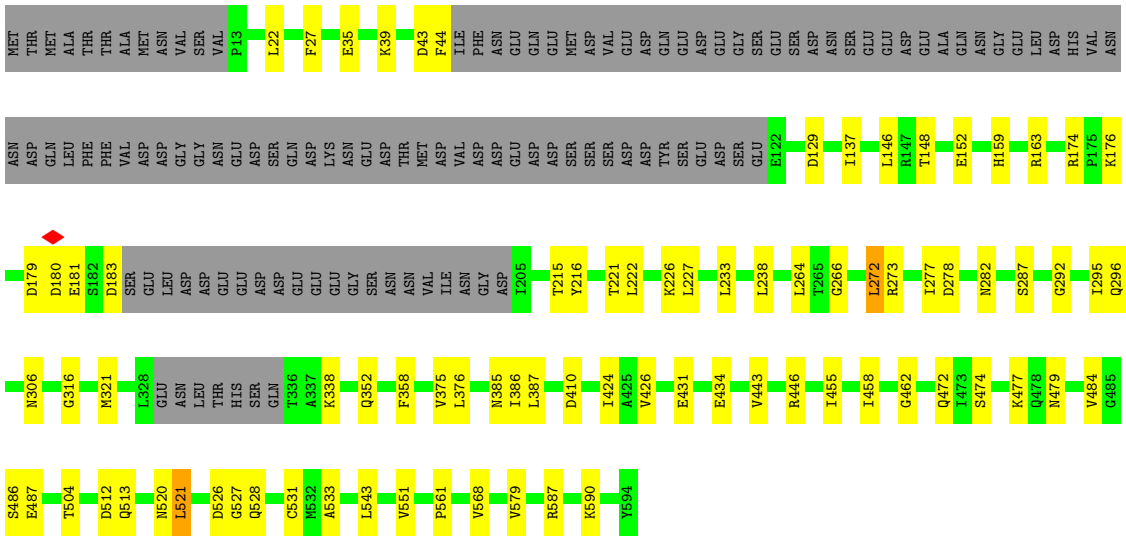
Chain B3:





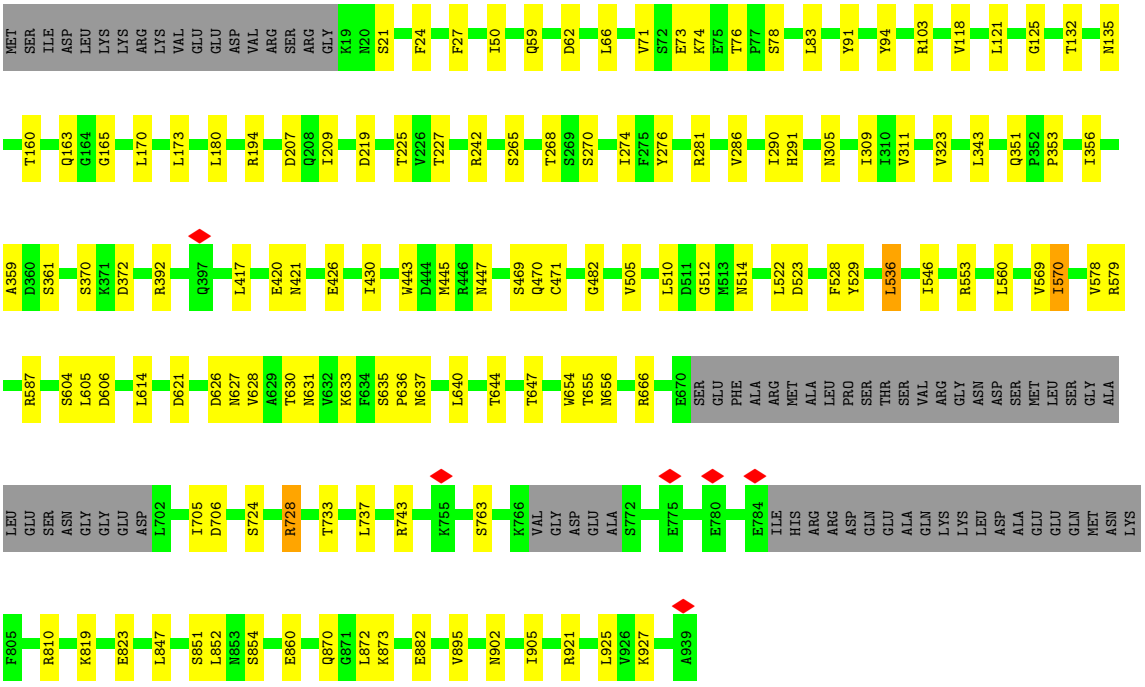
• Molecule 35: U3 small nucleolar RNA-associated protein 18

Chain B8:



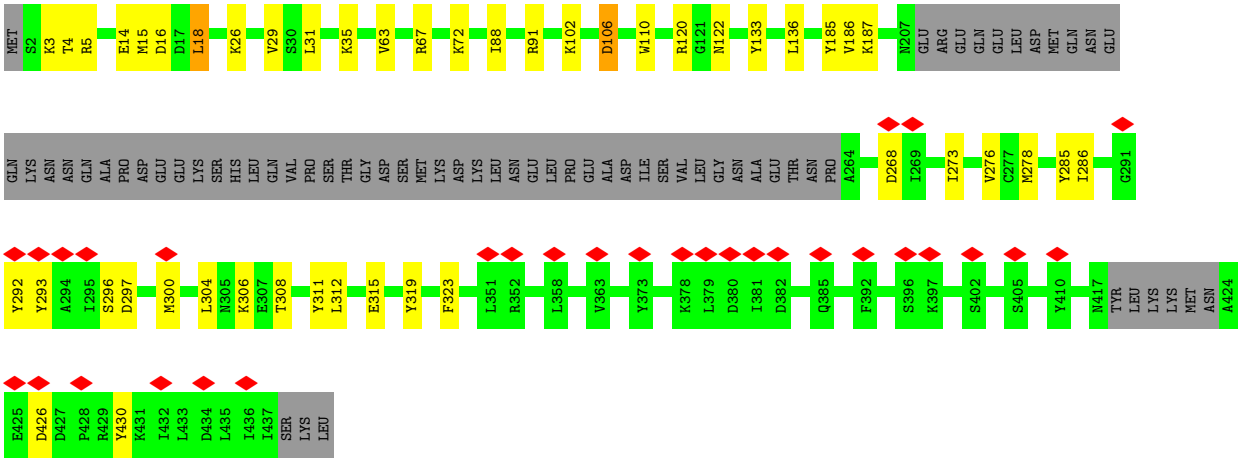
• Molecule 36: U3 small nucleolar RNA-associated protein 21

Chain BE:



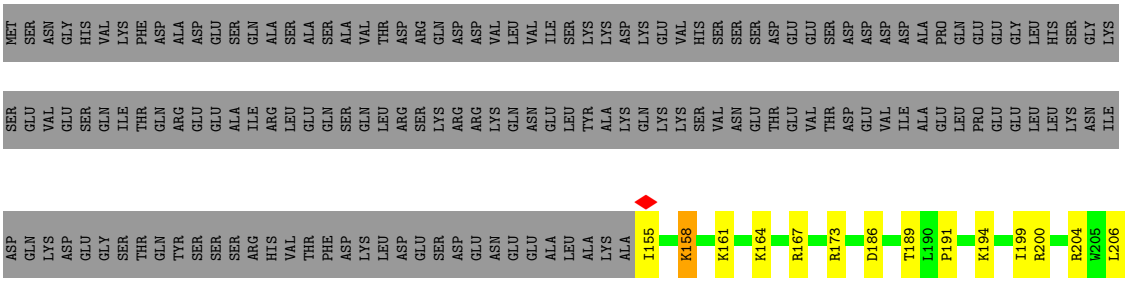
• Molecule 37: U3 small nucleolar RNA-associated protein 6

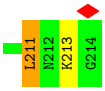
Chain B6:



• Molecule 38: Bud site selection protein 21

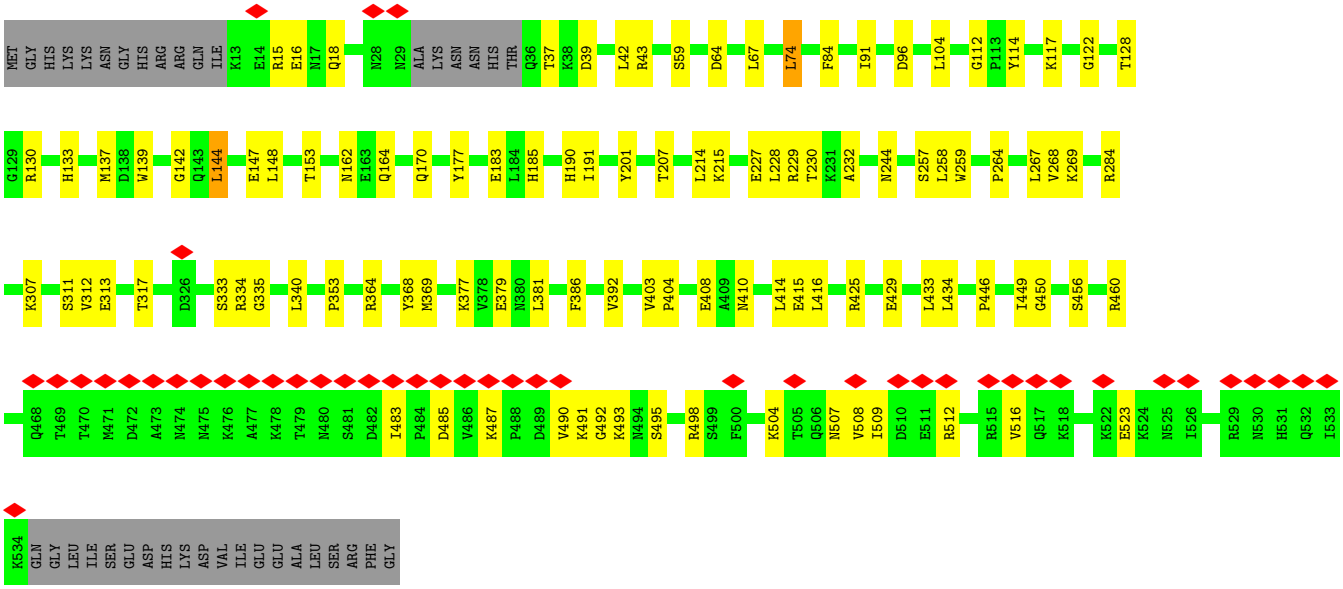
Chain 5B:





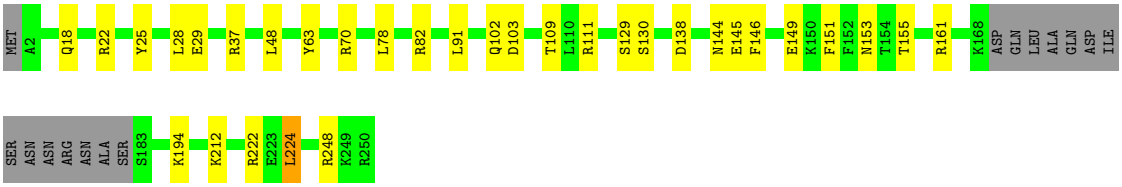
• Molecule 39: U3 small nucleolar RNA-associated protein 7

Chain 5C:



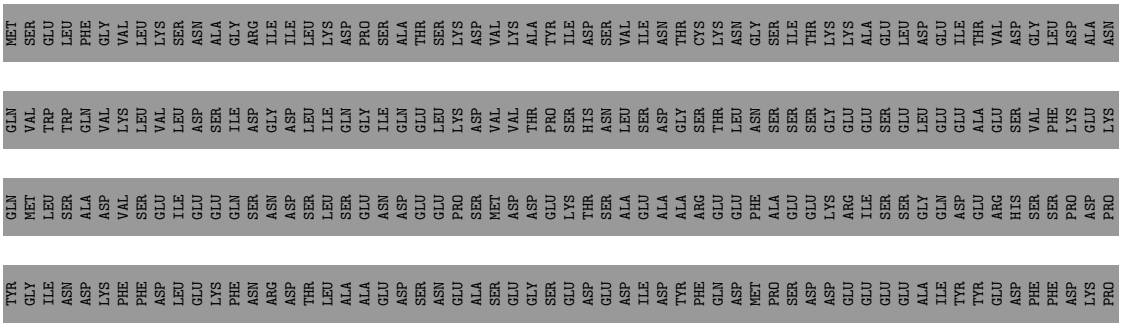
• Molecule 40: U3 small nucleolar RNA-associated protein 11

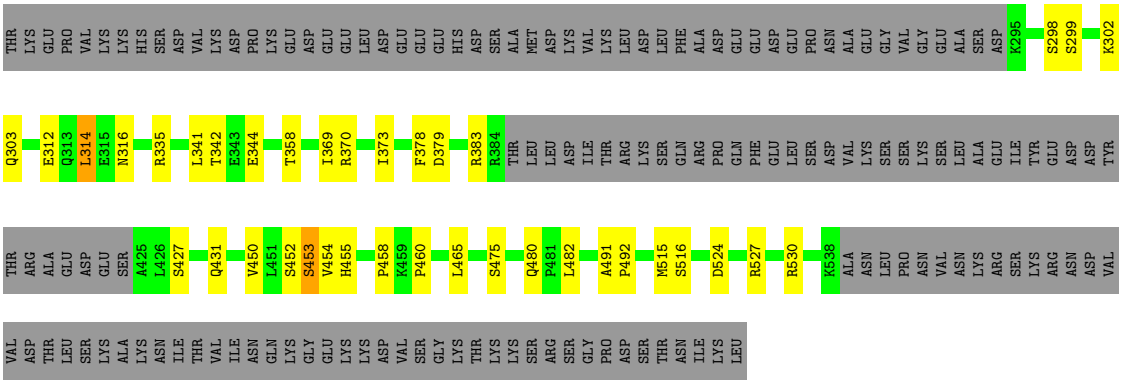
Chain 5D:



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

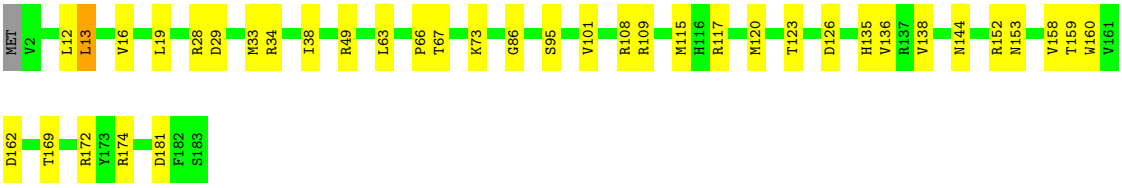
Chain 5E:





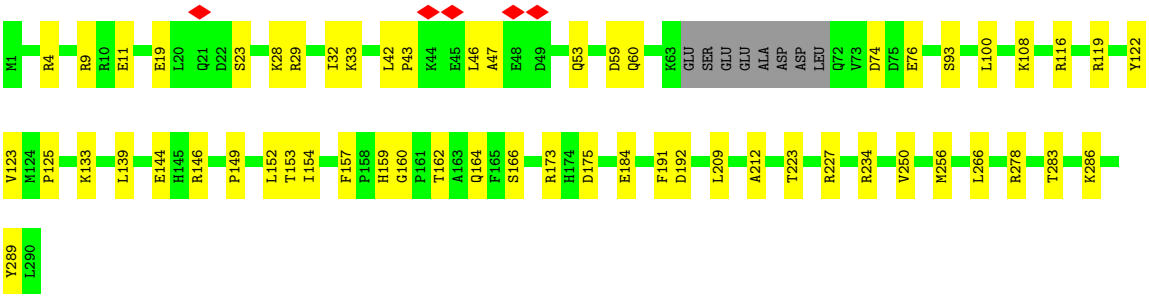
• Molecule 42: U3 small nucleolar ribonucleoprotein protein IMP3

Chain 5F:



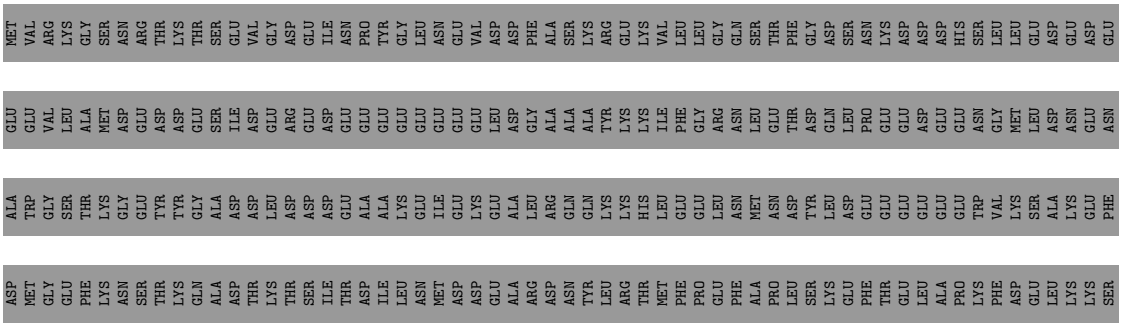
• Molecule 43: U3 small nucleolar ribonucleoprotein protein IMP4

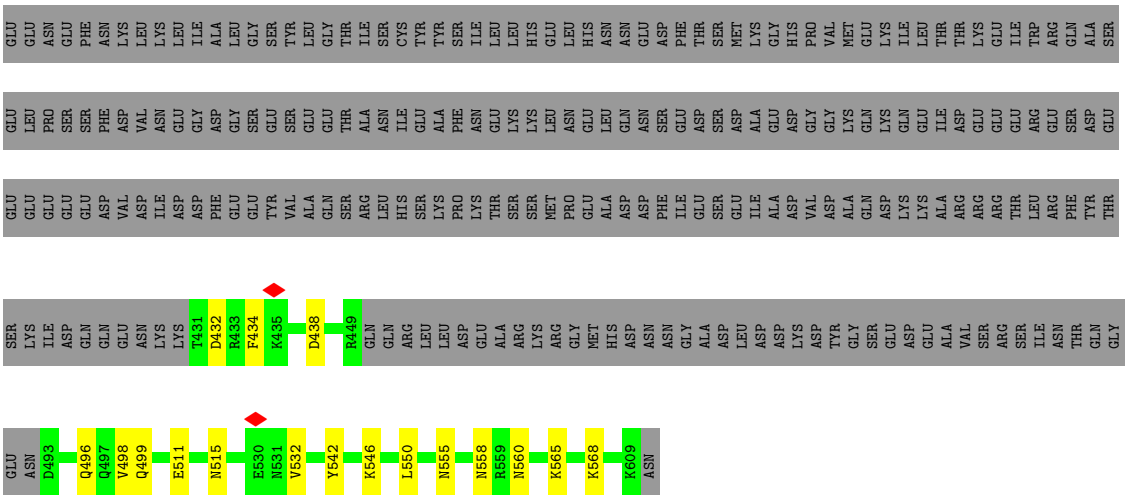
Chain 5G:



• Molecule 44: Something about silencing protein 10

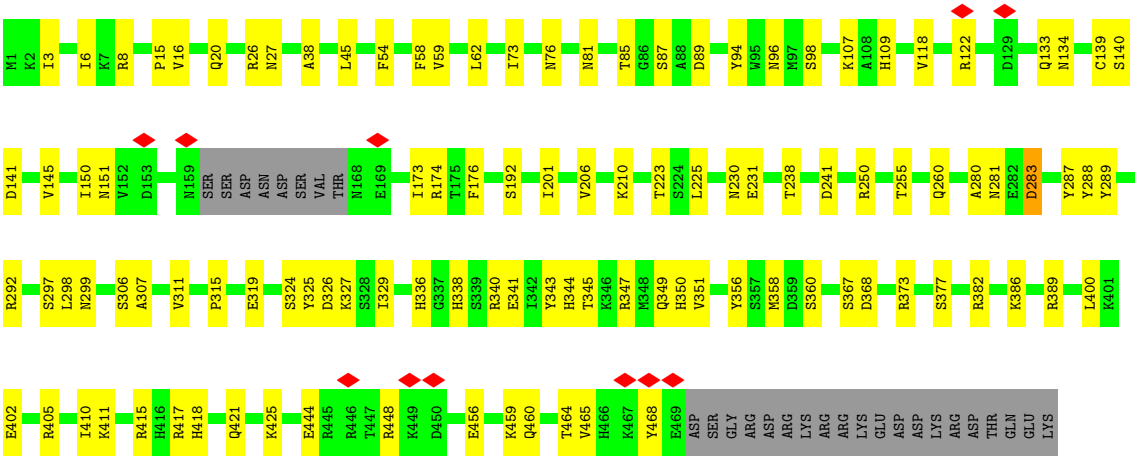
Chain 5H:





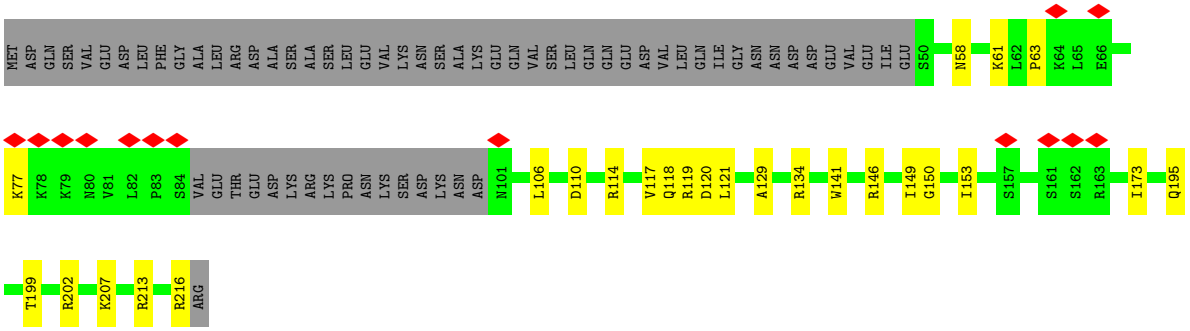
• Molecule 45: Protein SOF1

Chain 5I:



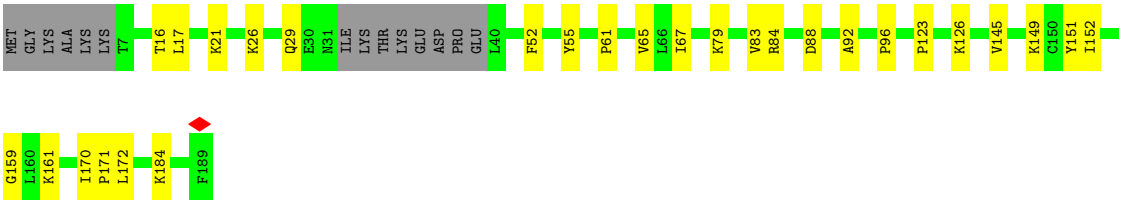
• Molecule 46: rRNA-processing protein FCF2

Chain 5J:



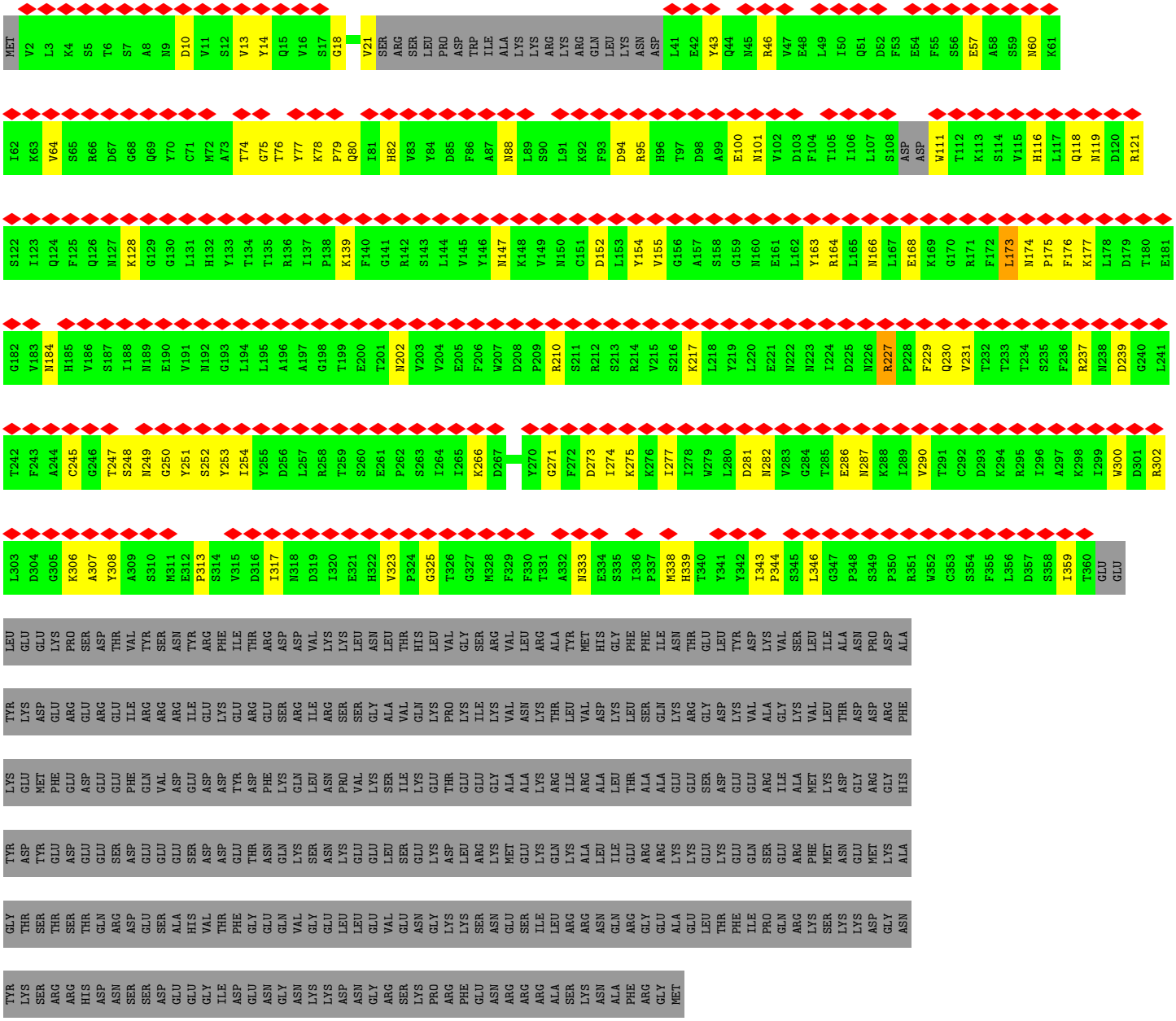
• Molecule 47: rRNA-processing protein FCF1

Chain 5K:



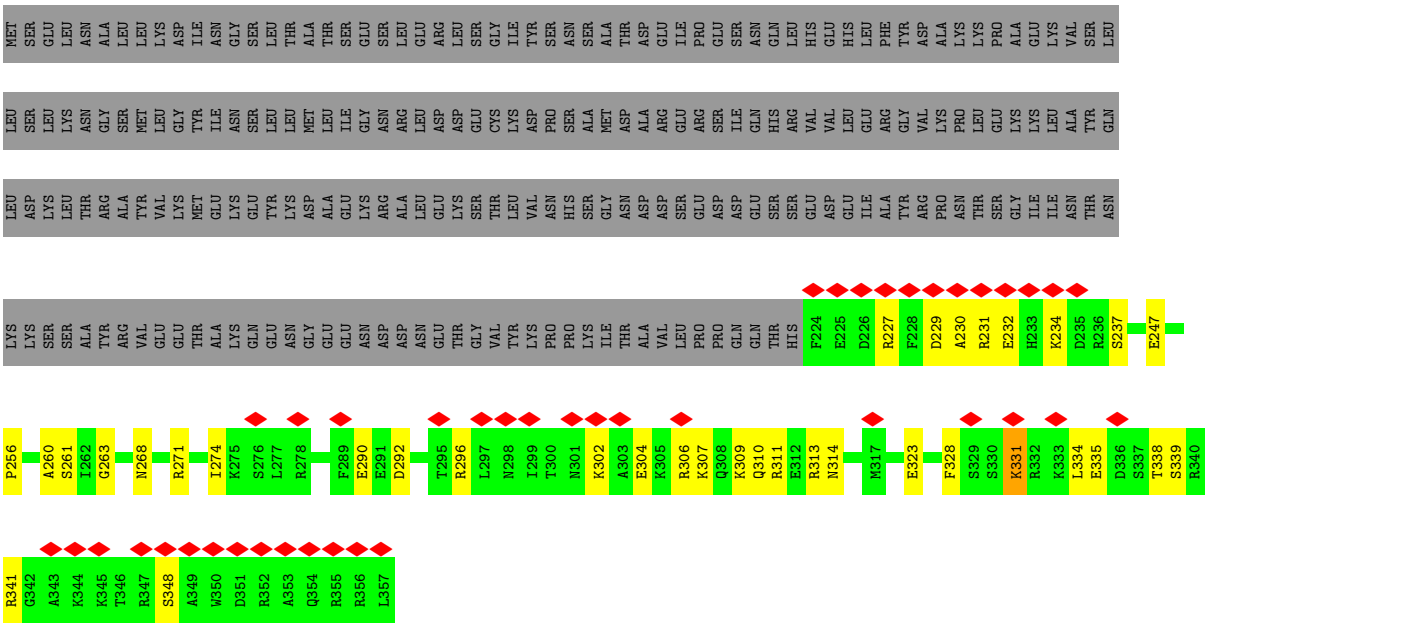
• Molecule 48: Ribosome biogenesis protein ENP2

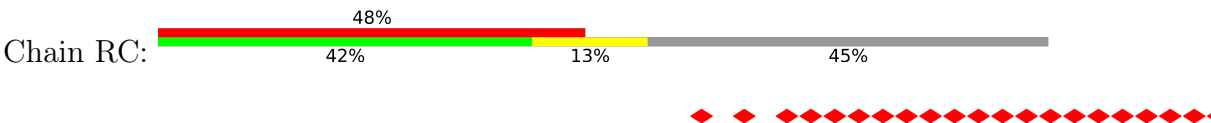
Chain RA:

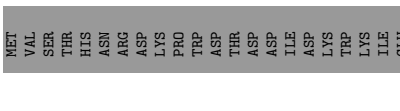


• Molecule 49: U3 small nucleolar ribonucleoprotein protein LCP5

Chain RB:

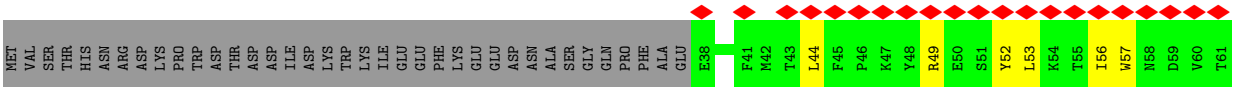


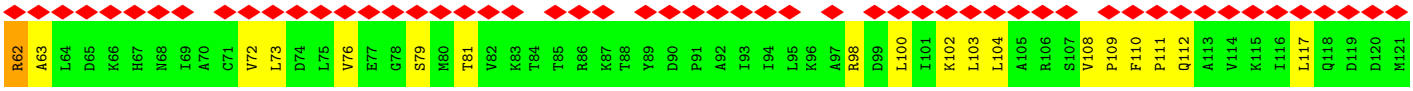


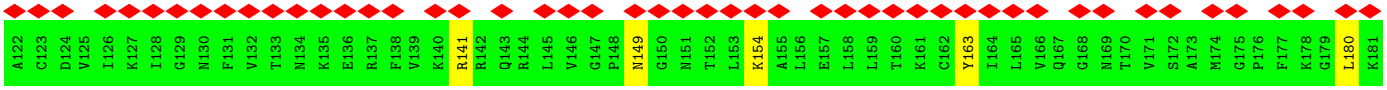


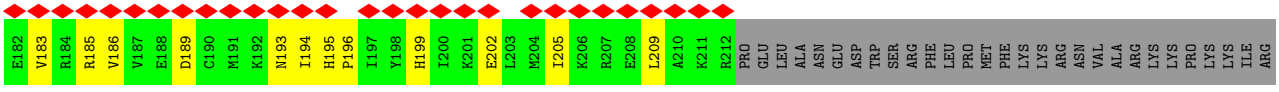
• Molecule 50: KRR1 small subunit processome component

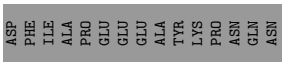
Chain RC:











• Molecule 51: rRNA biogenesis protein RRP5

Chain RD:

SER LEU LEU GLY GLN ILE SER ALA ILE THR LYS GLN ASP LEU CYS ILE THR PHE THR ASP GLY ILE SER GLY TYR VAL ASN LEU THR HIS ILE SER GLU GLU PHE THR SER ILE LEU GLU ASP LEU ASP GLU ASP MET ASP SER ASP THR ASP ALA ALA ASP GLU LYS LYS SER LYS VAL

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 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 ASP ALA ILE ILE PRO GLY GLN ILE VAL ASP LEU LEU CYS GLU SER ILE THR LYS ASN GLY ILE ALA 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 SER SER ILE ARG CYS ARG ILE ILE ALA CYS LEU GLU ASN LYS SER GLY ASP LYS VAL LEU ILE LEU SER ASN LEU PRO HIS ILE LEU LYS 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 ASP ARG LEU GLY LYS VAL HIS SER SER ARG VAL GLY GLU ILE GLU ASN SER GLU 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 TYR LEU ARG THR ASN ASP ILE PRO ILE GLY GLU LEU LEU PRO SER CYS GLU ILE THR SER VAL SER SER SER GLY ILE GLU LEU LYS ILE PHE ASN GLY GLN PHE LYS ALA SER VAL PRO

PRO LEU HIS ILE SER ASP THR ARG LEU VAL TYR PRO GLU ARG LYS PHE LYS ILE GLY SER LYS VAL LYS GLY ARG VAL ILE SER VAL ASN SER ARG GLY ASN VAL HIS VAL THR LEU LYS LYS SER LEU VAL ASN ILE GLU ASP ASN GLU LEU PRO LEU VAL SER THR TYR GLU ASN ALA

LYS ASN ILE LYS GLU LYS ASN 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 LEU PRO ASN SER GLU ILE SER GLU VAL PHE VAL LYS ARG PRO GLU GLU HIS LEU ARG LEU GLY GLN THR VAL ILE VAL LYS

LEU LEU ASP VAL ASP ALA ASP ARG ARG ARG 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 THR VAL HIS VAL ILE GLU LYS THR LYS ASP SER VAL ILE VAL GLU ILE PRO ASP VAL GLY LEU

ARG GLY VAL ILE TYR VAL GLY HIS LEU SER ASP SER ARG ILE GLU 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 SER SER LEU ILE LYS ASP ALA LYS LYS GLU THR

LEU PRO LEU THR TYR ASP ASP VAL LYS ASP LEU ASN LYS ASP VAL 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 ARG THR ASP ASP LYS ASN GLN LYS PHE LEU LEU SER LEU LYS ALA PRO LYS VAL LYS GLU GLU LYS LYS VAL GLU SER ASN ILE GLU ASP PRO VAL ASP SER SER ILE LYS SER TRP ASP ASP LEU SER ILE GLY SER ILE VAL LYS ALA

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 PHE ASP THR TYR GLU GLU ILE THR ASP LYS LYS GLN PRO LEU SER ASN TYR LYS LYS ASP ASP VAL ILE LYS VAL LYS ILE ILE GLY ASN HIS ASP VAL

LYS SER HIS LYS PHE LEU PRO ILE THR HIS LYS ILE SER LYS ALA SER VAL LEU GLU LEU SER MET LYS PRO SER 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 GLY ASN HIS LEU TRP LEU

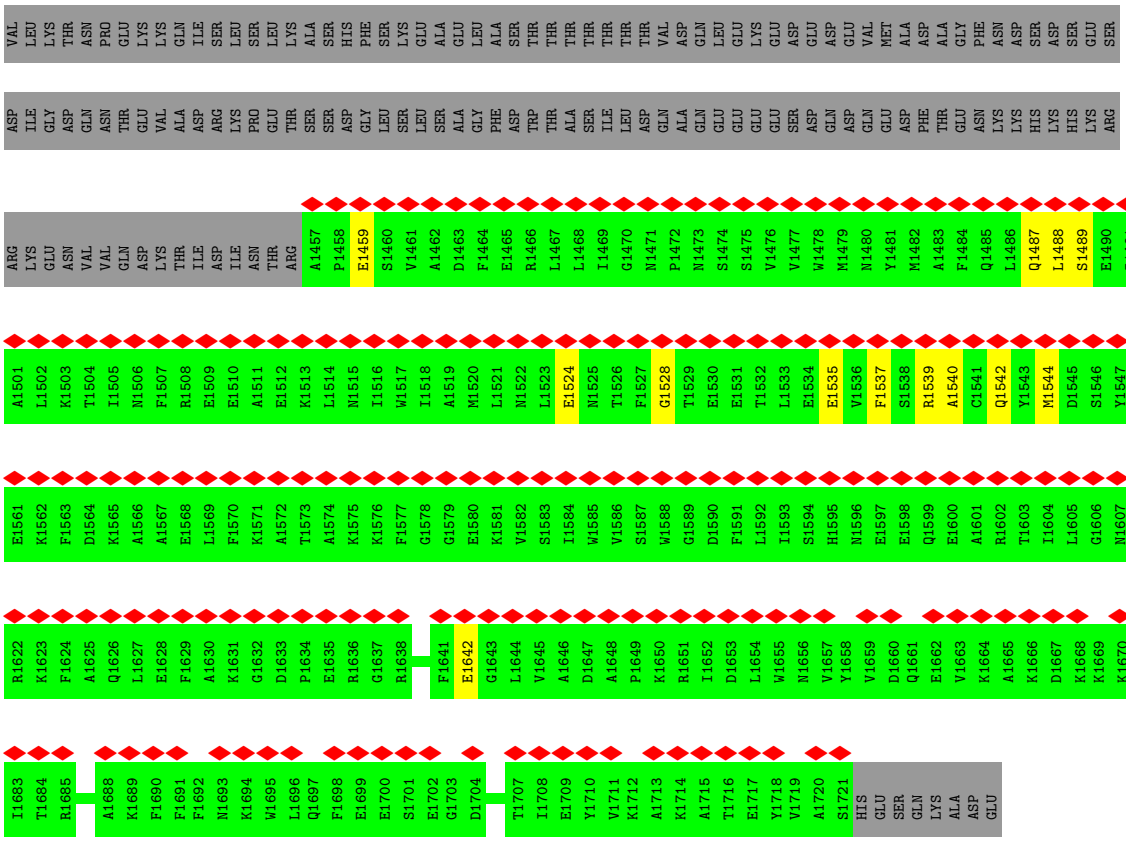
THR ILE SER PRO VAL LEU LYS ALA ARG ILE SER LEU LEU ASP LEU ALA ASP ASN ASP SER ASN PHE SER GLU ASN ILE GLU SER VAL PHE PRO LEU GLY SER ALA LEU GLN VAL LYS VAL ALA SER ILE ASP ARG GLU HIS GLY PHE VAL ASN ALA ILE GLY LYS SER HIS VAL ASP ILE

ASN MET SER THR ILE LYS VAL GLY ASP GLU LEU PRO GLY ARG VAL LEU LYS ILE ALA GLU LYS TYR VAL LEU LEU ASP LEU GLY ASN LYS VAL THR GLY ILE SER PHE ILE THR ASP ALA LEU ASN ASP PHE SER LEU THR LEU LYS GLU ALA PHE GLU ASP LYS ILE ASN ASN VAL ILE

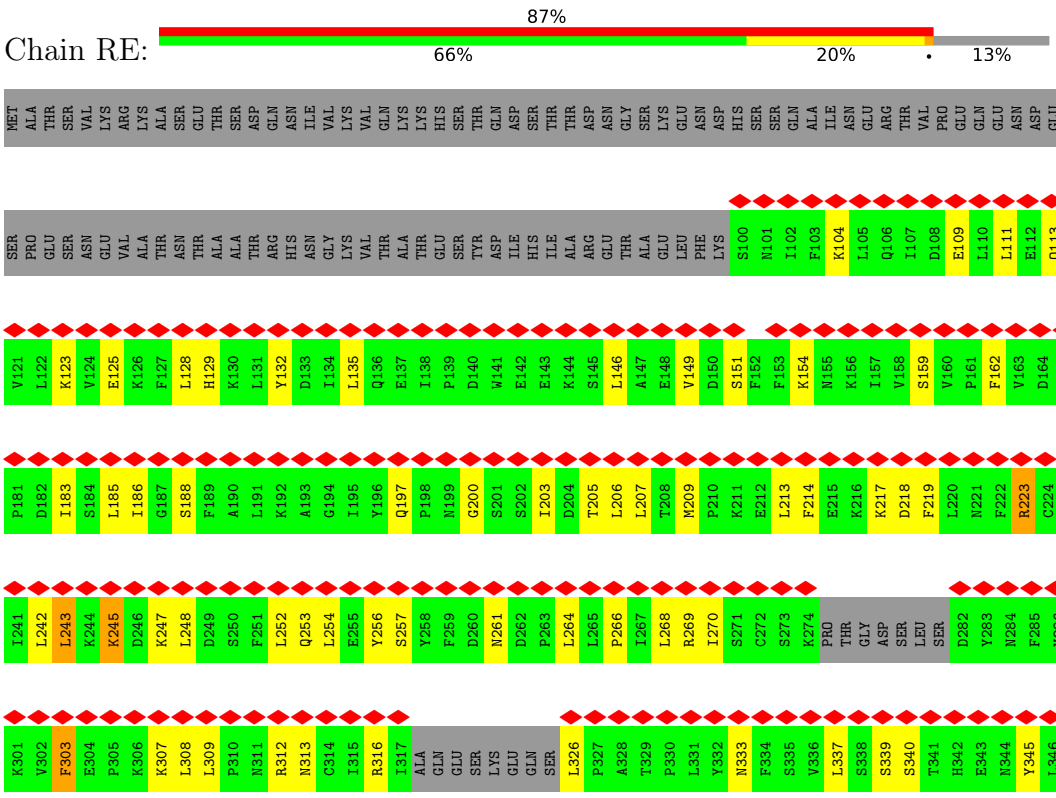
PRO THR THR VAL LEU SER VAL ASP GLU GLN ASN LYS LYS ILE GLU LEU SER LEU ARG PRO ALA THR ALA LYS THR ARG SER ILE LYS SER HIS GLU ASP LEU LYS GLN GLY GLU ILE VAL ASP GLY ILE VAL LYS ASN VAL ASN ASP LYS GLY ILE PHE VAL TYR LEU SER ARG LYS VAL

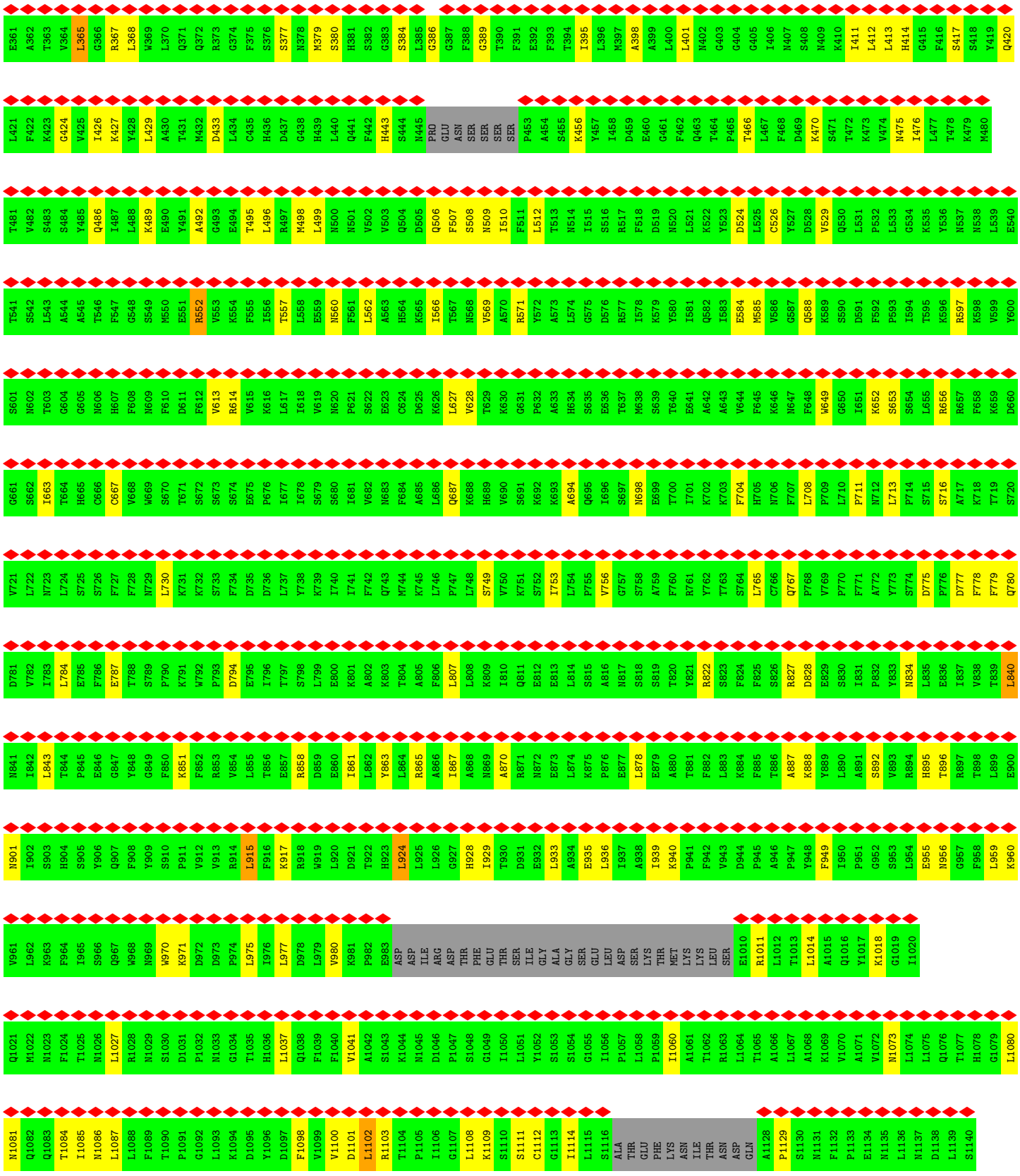
GLU ALA PHE VAL PRO VAL SER LYS LEU SER ASP SER TYR LEU LYS GLU TRP LYS LYS PHE TYR LYS PRO MET GLN TYR VAL LEU GLY LYS VAL VAL THR CYS ASP GLU ASP SER ARG ILE SER LEU THR LEU ARG GLU SER GLU ILE ASN GLY ASP LEU LYS VAL LEU LYS THR TYR SER

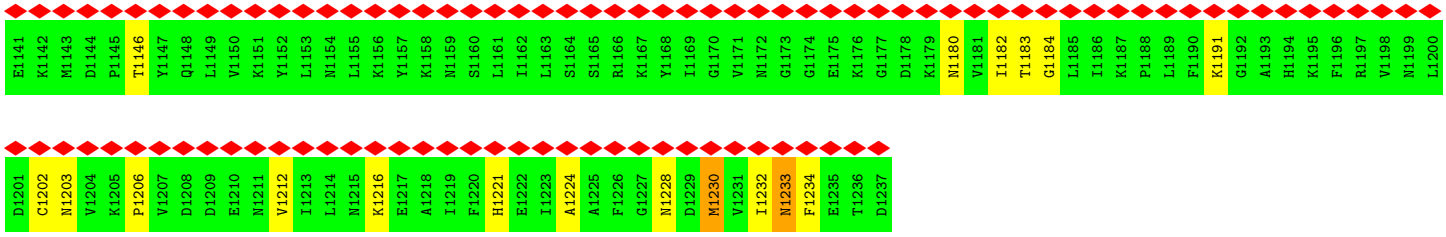
ASP ILE LYS ALA GLY ASP VAL PHE GLU GLY THR ILE LYS SER VAL THR ASP PHE GLY VAL PHE VAL LYS LEU ASP ASN THR VAL ASN VAL THR GLY LEU ALA HIS ILE THR GLU ILE ALA ASP LYS LYS PRO GLU ASP LEU SER ALA LEU PHE GLY VAL GLY ASP ARG VAL LYS ALA ILE



• Molecule 52: U3 small nucleolar RNA-associated protein 22

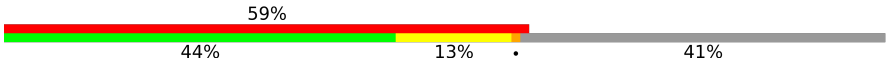


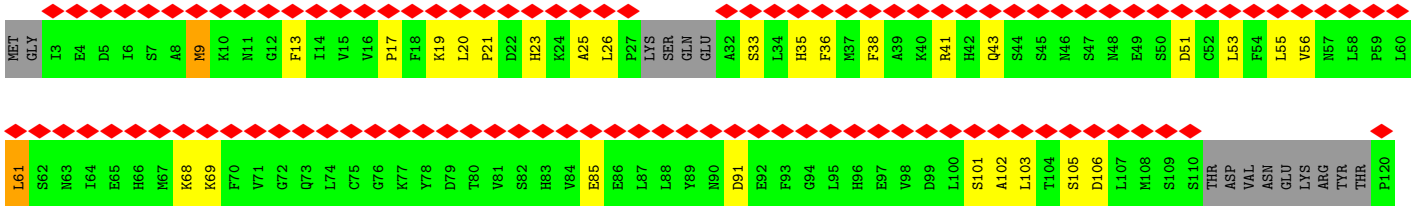

E361 A362 T363 V364 L365 G366 R367 L368 W369 L370 Q371 Q372 R373 G374 F375 S376 S377 N378 M379 S380 H381 S382 G383 S384 L385 G386 G387 F388 G389 T390 F391 E392 F393 T394 I395 L396 M397 A398 A399 L400 L401 N402 G403 G404 G405 I406 N407 S408 N409 K410 I411 L412 L413 H414 G415 F416 S417 S418 Y419 Q420
L421 F422 K423 G424 V425 I426 K427 Y428 L429 A430 T431 M432 D433 L434 C435 H436 D437 G438 H439 L440 Q441 F442 H443 S444 N445 PRO GLU ASN SER SER SER SER P453 A454 S455 K456 Y457 I458 D459 E460 G461 F462 Q463 T464 P465 T466 L467 F468 D469 K470 S471 T472 K473 V474 N475 I476 L477 T478 K479 M480
T481 V482 S483 S484 Y485 Q486 I487 L488 K489 E490 Y491 A492 G493 E494 T495 L496 R497 M498 L499 N500 N501 V502 V503 Q504 D505 Q506 F507 S508 N509 I510 F511 L512 T513 N514 I515 S516 R517 F518 D519 N520 L521 K522 Y523 D524 L525 C526 Y527 D528 V529 Q530 L531 P532 L533 G534 K535 Y536 N537 N538 L539 E540
T541 S542 L543 A544 A545 T546 F547 G548 S549 M550 E551 R552 V553 K554 F555 I556 T557 L558 E559 N560 F561 L562 A563 H564 K565 I566 T567 N568 V569 A570 R571 Y572 A573 L574 G575 D576 R577 I578 K579 Y580 I581 Q582 I583 E584 M585 V586 G587 Q588 K589 S590 D591 F592 P593 I594 T595 K596 R597 K598 V599 Y600
S601 N602 T603 G604 G605 N606 H607 F608 N609 F610 D611 F612 V613 R614 V615 K616 L617 I618 V619 N620 P621 S622 E623 C624 D625 K626 L627 V628 T629 K630 G631 P632 A633 H634 S635 E636 T637 M638 S639 T640 E641 A642 A643 V644 F645 K646 N647 F648 W649 G650 I651 K652 S653 S654 L655 R656 R657 F658 K659 D660
G661 S662 I663 T664 H665 C666 C667 V668 W669 S670 T671 S672 S673 S674 E675 P676 I677 I678 S679 S680 I681 V682 N683 F684 A685 L686 Q687 K688 H689 V690 S691 K692 K693 A694 Q695 I696 S697 N698 E699 T700 I701 K702 K703 F704 H705 N706 F707 L708 P709 L710 P711 N712 L713 P714 S715 S716 A717 K718 T719 S720
V721 L722 N723 L724 S725 S726 F727 F728 N729 L730 K731 K732 S733 F734 D735 D736 L737 Y738 K739 T740 I741 F742 Q743 M744 K745 L746 P747 L748 S749 V750 K751 S752 I753 L754 P755 V756 G757 S758 A759 F760 R761 Y762 T763 S764 L765 C766 Q767 F768 V769 P770 F771 A772 Y773 S774 D775 P776 D777 F778 F779 Q780
D781 V782 I783 L784 E785 F786 E787 T788 S789 P790 K791 W792 P793 D794 E795 I796 T797 S798 L799 E800 K801 A802 K803 T804 A805 F806 L807 L808 K809 I810 Q811 E812 E813 L814 S815 A816 N817 S818 S819 T820 Y821 R822 S823 F824 F825 S826 R827 D828 E829 S830 I831 P832 Y833 N834 L835 E836 I837 V838 T839 L840
N841 I842 L843 T844 P845 E846 G847 Y848 G849 F850 K851 F852 R853 V854 L855 T856 E857 R858 D859 E860 I861 L862 Y863 L864 R865 A866 I867 A868 N869 A870 R871 N872 E873 L874 K875 P876 E877 L878 E879 A880 T881 F882 L883 K884 F885 T886 A887 K888 Y889 L890 A891 S892 V893 R894 H895 T896 R897 T898 L899 E900
N901 I902 S903 H904 S905 Y906 Q907 F908 Y909 S910 P911 V912 V913 R914 L915 F916 K917 R918 W919 L920 D921 T922 H923 L924 L925 L926 G927 H928 I929 T930 D931 E932 L933 A934 E935 L936 I937 A938 I939 K940 P941 F942 V943 D944 P945 A946 P947 Y948 F949 I950 P951 G952 S953 L954 E955 N956 G957 F958 L959 K960
V961 L962 K963 F964 I965 S966 Q967 W968 N969 W970 K971 D972 D973 P974 L975 I976 L977 D978 L979 V980 K981 P982 E983 ASP ASP ILE ARG ASP THR PHE GLU THR SER ILE GLY ALA GLY SER GLU LEU ASP SER LYS THR MET LYS LYS LEU SER E1010 R1011 L1012 T1013 L1014 A1015 Q1016 Y1017 K1018 G1019 I1020
Q1021 M1022 N1023 F1024 T1025 N1026 L1027 R1028 N1029 S1030 D1031 P1032 N1033 G1034 T1035 H1036 L1037 Q1038 F1039 F1040 V1041 A1042 S1043 K1044 N1045 D1046 P1047 S1048 G1049 I1050 L1051 Y1052 S1053 S1054 G1055 I1056 P1057 L1058 P1059 I1060 A1061 T1062 R1063 L1064 T1065 A1066 L1067 A1068 K1069 V1070 A1071 V1072 N1073 L1074 L1075 Q1076 T1077 H1078 G1079 L1080
N1081 Q1082 Q1083 T1084 I1085 N1086 L1087 L1088 F1089 T1090 P1091 G1092 L1093 K1094 D1095 Y1096 D1097 F1098 V1099 V1100 D1101 L1102 R1103 T1104 P1105 I1106 G1107 L1108 K1109 S1110 S1111 C1112 G1113 I1114 L1115 S1116 ALA THR GLU PHE LYS ASN ILE THR ASN ASP GLN A1128 P1129 S1130 N1131 F1132 P1133 E1134 N1135 L1136 N1137 D1138 L1139 S1140



• Molecule 53: Ribosomal RNA-processing protein 7

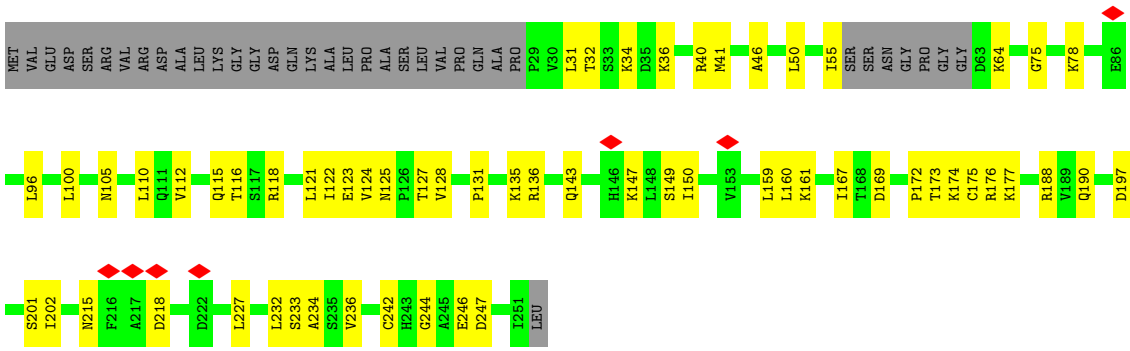
Chain RF:





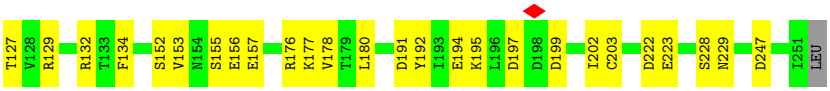
• Molecule 54: Ribosomal RNA small subunit methyltransferase NEP1

Chain RG:



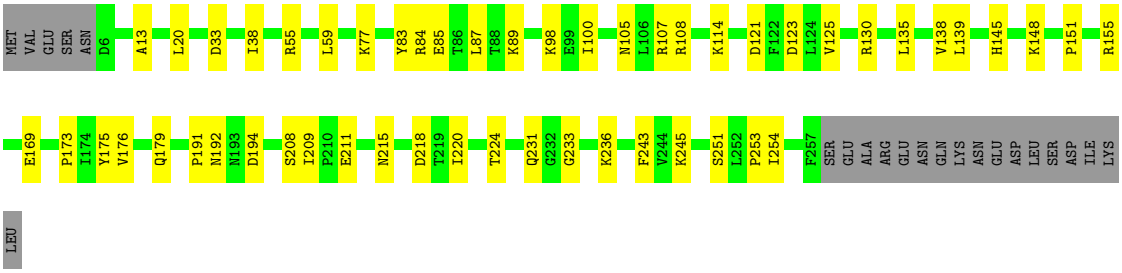
• Molecule 54: Ribosomal RNA small subunit methyltransferase NEP1

Chain RH:



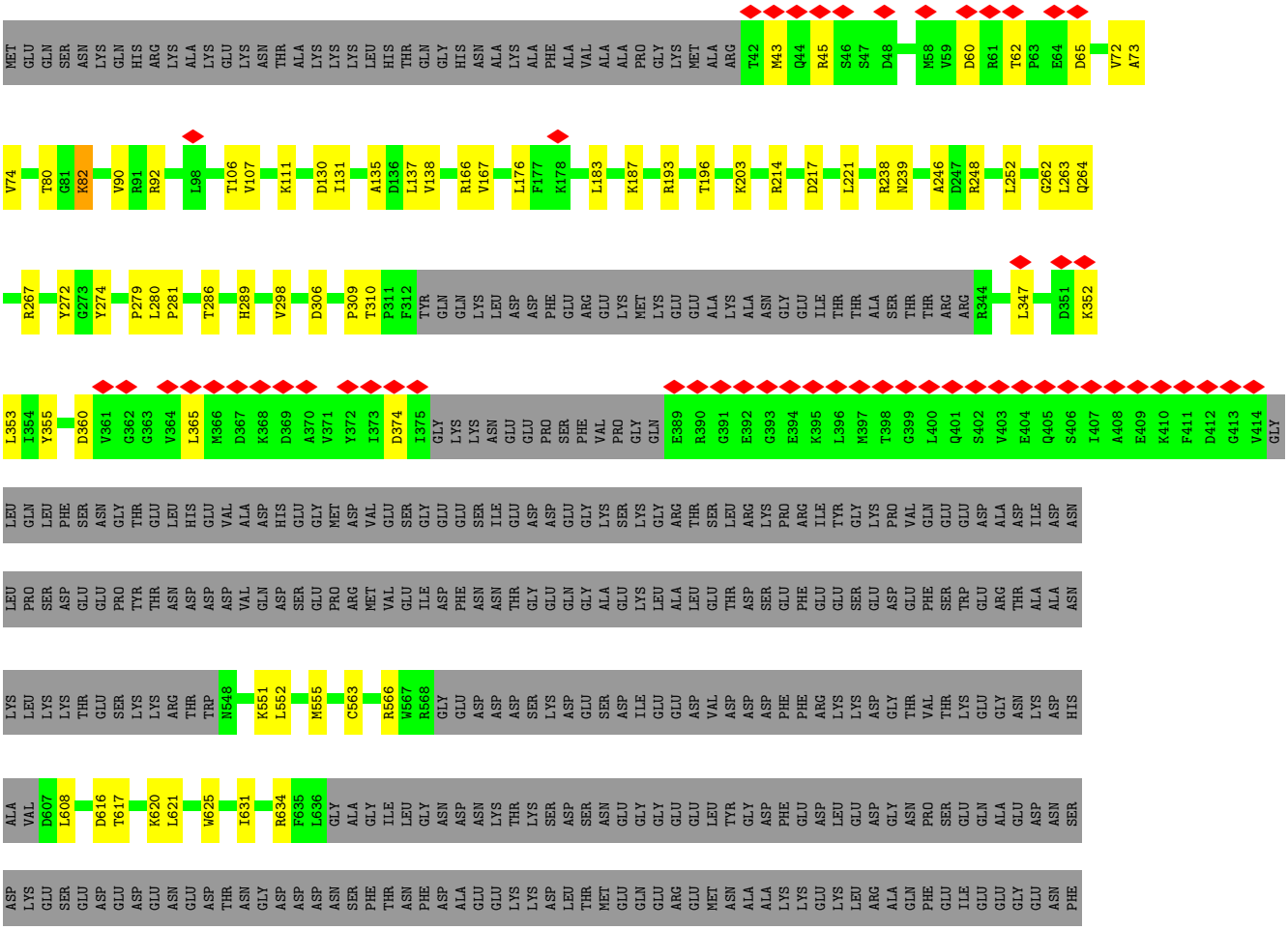
• Molecule 55: Ribosome biogenesis protein UTP30

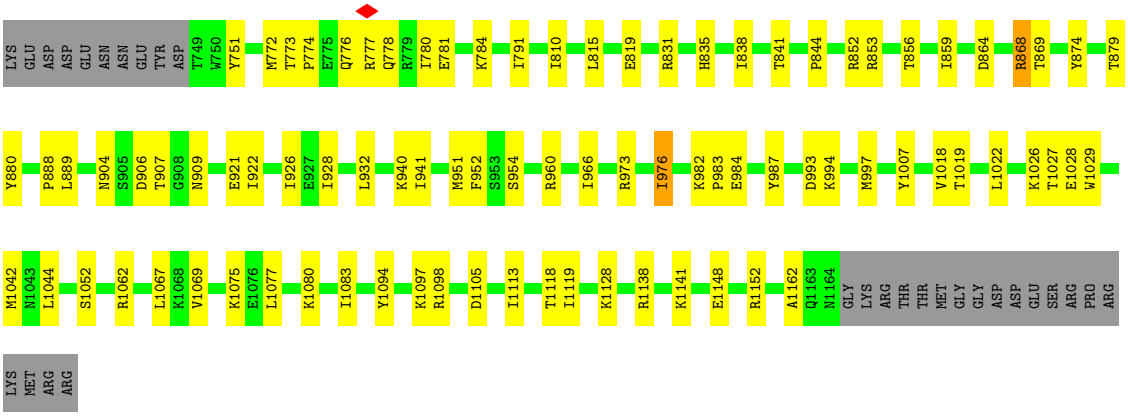
Chain RI:



• Molecule 56: Ribosome biogenesis protein BMS1

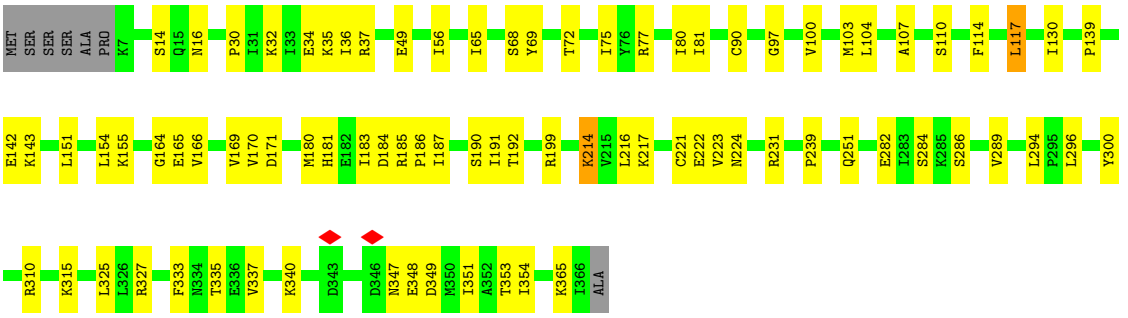
Chain RJ:





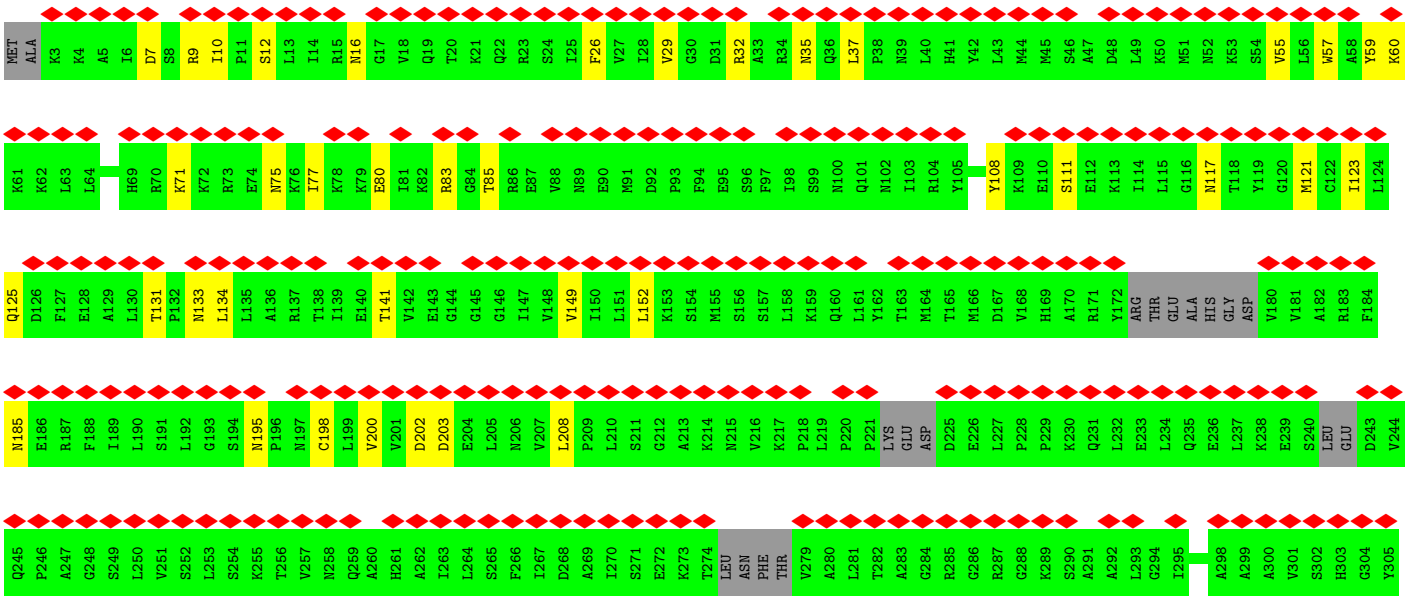
• Molecule 57: RNA 3'-terminal phosphate cyclase-like protein

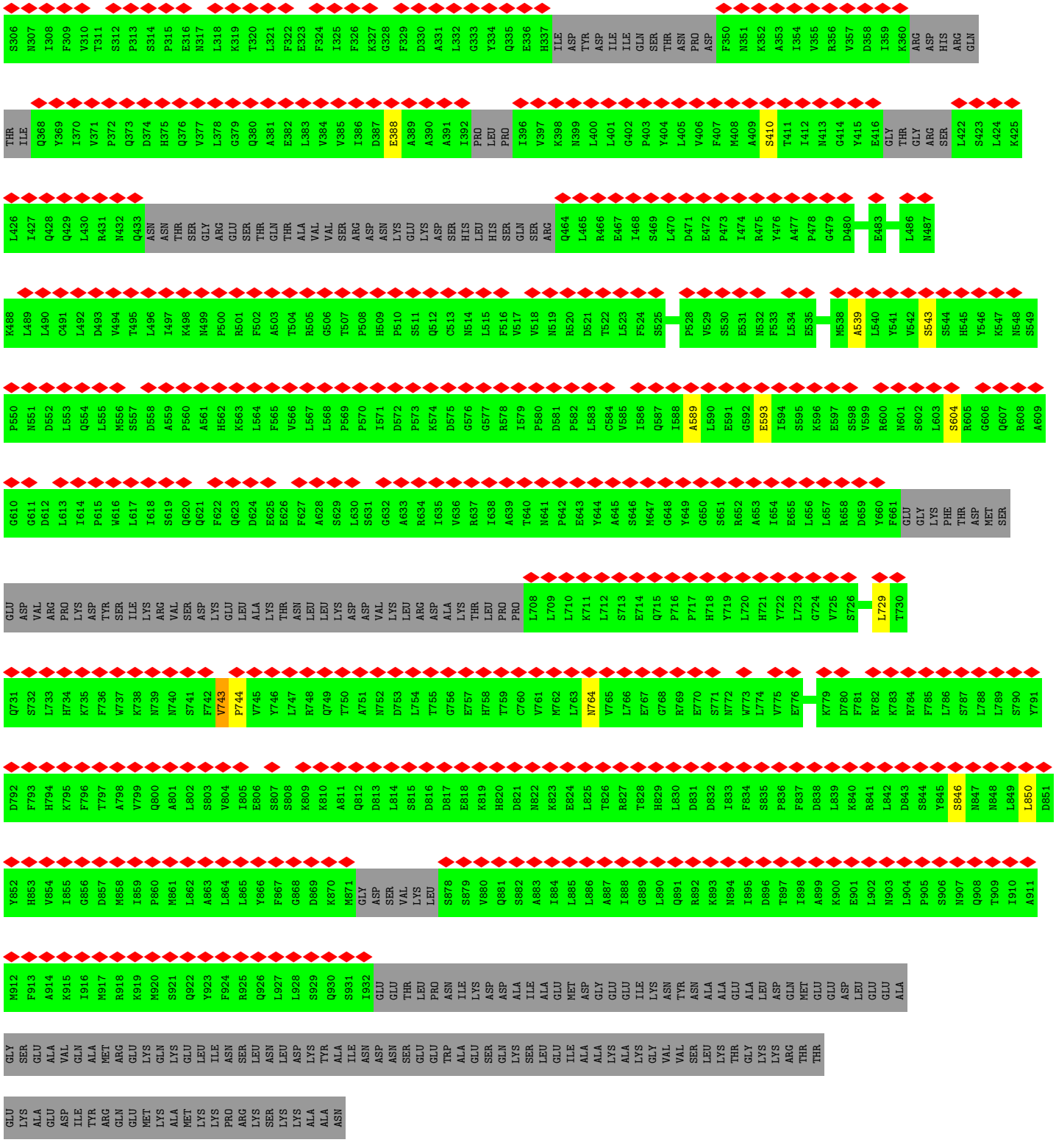
Chain RK:



• Molecule 58: RNA cytidine acetyltransferase

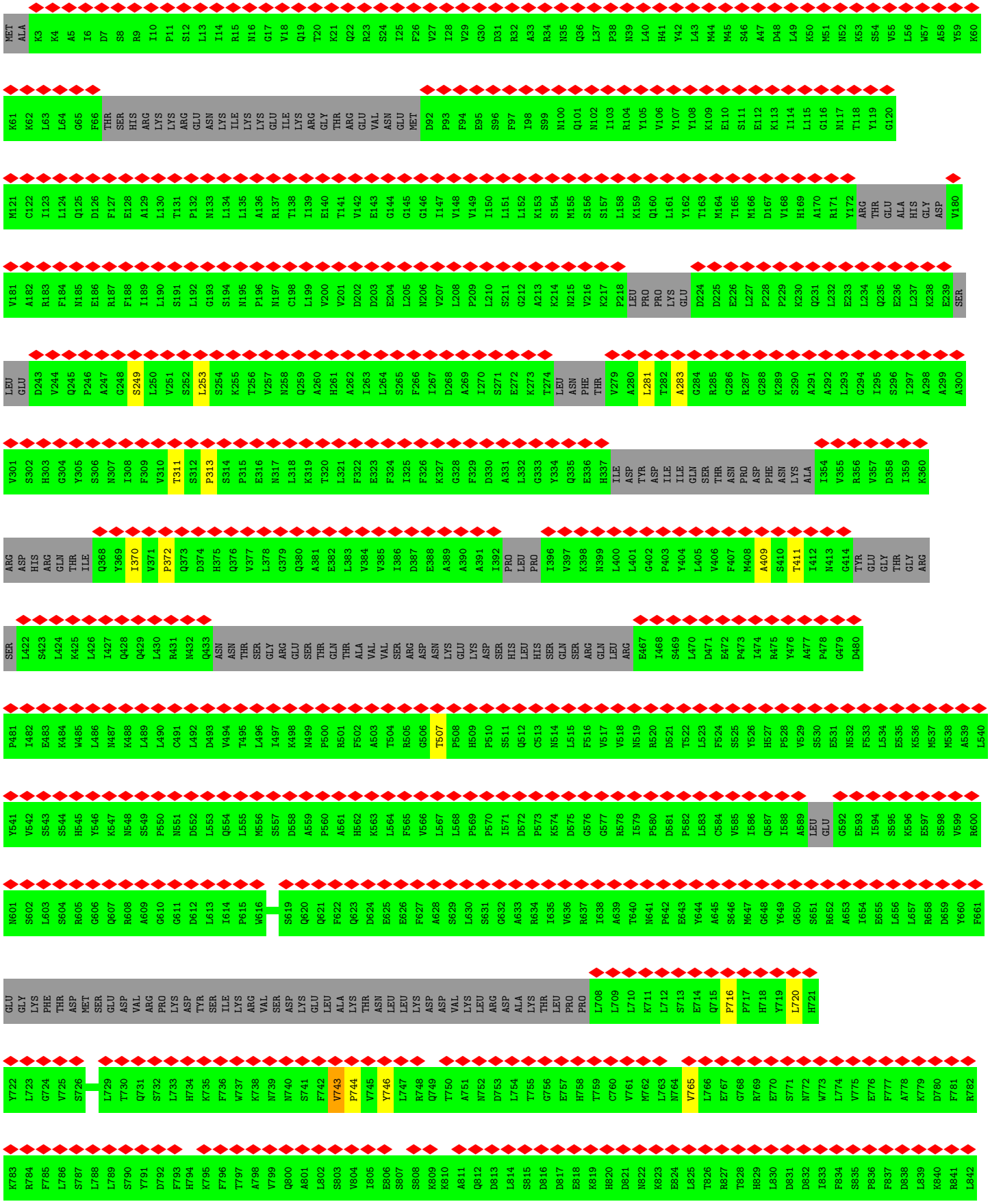
Chain RL:

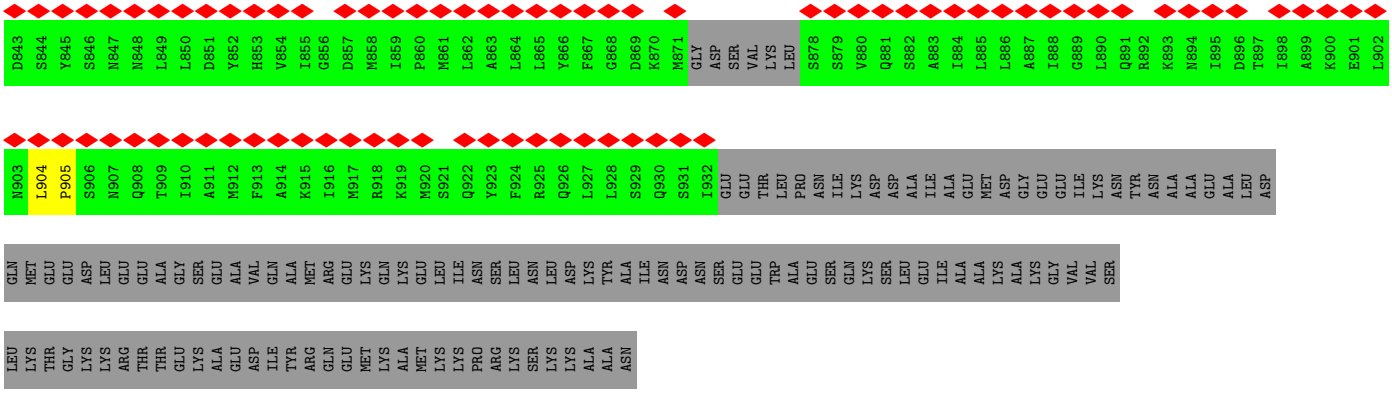




• Molecule 58: RNA cytidine acetyltransferase

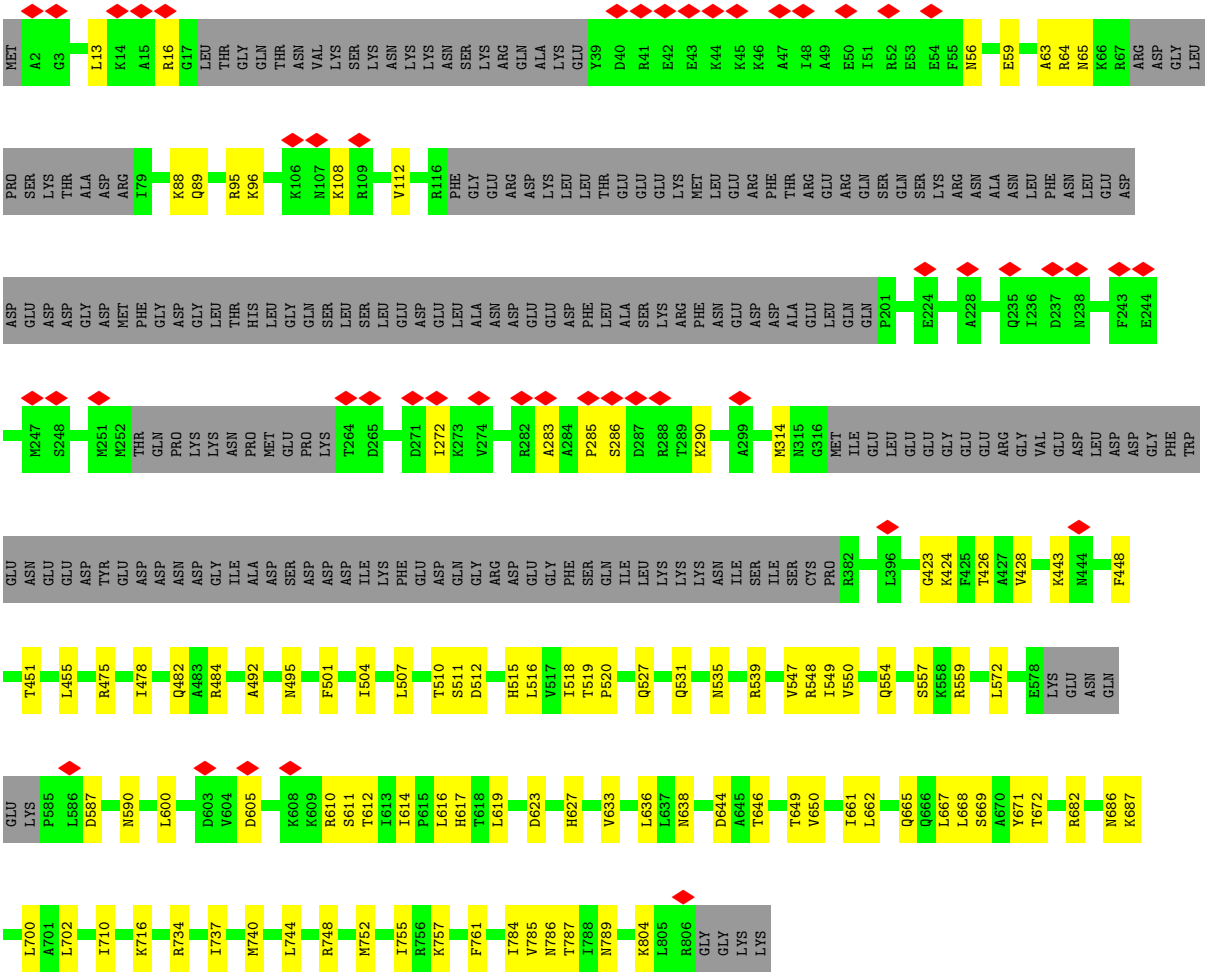
Chain RM:


MET ALA K3 K4 A5 I6 D7 S8 R9 I10 P11 S12 L13 I14 R15 N16 G17 V18 Q19 T20 K21 Q22 R23 S24 I25 F26 V27 I28 Y29 G30 D31 R32 A33 R34 N35 Q36 L37 P38 N39 L40 H41 Y42 L43 M44 M45 S46 A47 D48 L49 K50 M51 N52 K53 S54 V55 L56 W57 A58 Y59 K60
K61 K62 L63 L64 G65 F66 THR SER HIS ARG LYS LYS ARG GLU ASN LYS ILE LYS LYS GLU ILE LYS ARG GLY THR ARG GLU VAL ASN GLU MET D92 P93 F94 E95 S96 F97 I98 S99 N100 Q101 N102 I103 R104 Y105 V106 Y107 Y108 K109 E110 S111 E112 K113 I114 L115 G116 N117 T118 Y119 G120
M121 C122 I123 L124 Q125 D126 F127 E128 A129 L130 T131 P132 N133 L134 L135 A136 R137 T138 I139 E140 T141 V142 E143 G144 G145 G146 I147 V148 V149 I150 L151 L152 K153 S154 M155 S156 S157 L158 K159 Q160 L161 Y162 T163 M164 T165 M166 D167 V168 H169 A170 R171 Y172 ARG THR GLU ALA HIS GLY ASP V180
V181 A182 R183 F184 N185 E186 R187 F188 I189 L190 S191 L192 G193 S194 N195 P196 N197 C198 L199 V200 V201 D202 D203 E204 L205 N206 V207 L208 P209 L210 S211 G212 A213 K214 N215 V216 K217 P218 LEU PRO PRO LYS GLU D224 D225 E226 L227 P228 P229 K230 Q231 L232 E233 L234 Q235 E236 L237 K238 E239 SER
LEU GLU D243 V244 Q245 P246 A247 G248 S249 L250 V251 S252 L253 S254 K255 T256 V257 N258 Q259 A260 H261 A262 I263 L264 S265 F266 I267 D268 A269 I270 S271 E272 K273 T274 LEU ASN PHE THR V279 A280 L281 T282 A283 G284 R285 G286 R287 G288 K289 S290 A291 A292 L293 G294 I295 S296 I297 A298 A299 A300
V301 S302 H303 G304 Y305 S306 N307 I308 F309 V310 T311 S312 P313 S314 P315 E316 N317 L318 K319 T320 L321 F322 E323 F324 I325 F326 K327 G328 F329 D330 A331 L332 G333 Y334 Q335 E336 H337 ILE ASP TYR ASP ILE ILE GLN SER THR ASN PRO ASP PHE ASN LYS ALA I354 V355 R356 V357 D358 I359 K360
ARG ASP HIS ARG GLN THR ILE Q368 Y369 I370 V371 P372 Q373 D374 H375 Q376 V377 L378 G379 Q380 A381 E382 L383 V384 V385 I386 D387 E388 A389 A390 A391 I392 PRO LEU PRO I396 V397 K398 N399 L400 L401 G402 P403 Y404 L405 V406 F407 M408 A409 S410 T411 I412 N413 G414 TYR GLU GLY THR GLY ARG
SER L422 S423 L424 K425 L426 I427 Q428 Q429 L430 R431 N432 Q433 ASN ASN THR SER GLY ARG GLU SER THR GLN THR ALA VAL VAL SER ARG ASP ASN LYS GLU LYS ASP SER HIS LEU HIS SER GLN SER ARG GLN LEU ARG E467 I468 S469 L470 D471 E472 P473 I474 R475 Y476 A477 P478 G479 D480
P481 I482 E483 K484 W485 L486 N487 K488 L489 L490 C491 L492 D493 V494 T495 L496 I497 K498 N499 P500 R501 F502 A503 T504 R505 G506 T507 P508 H509 P510 S511 Q512 C513 N514 L515 F516 V517 V518 N519 R520 D521 T522 L523 F524 S525 Y526 H527 P528 V529 S530 E531 N532 F533 L534 E535 K536 M537 M538 A539 L540
Y541 V542 S543 S544 H545 Y546 K547 N548 S549 P550 N551 D552 L553 Q554 L555 M556 S557 D558 A559 P560 A561 H562 K563 L564 F565 V566 L567 L568 P569 P570 I571 D572 P573 K574 D575 G576 G577 R578 I579 P580 D581 P582 L583 C584 V585 I586 Q587 I588 A589 LEU GLU G592 E593 I594 S595 K596 E597 S598 V599 R600
N601 S602 L603 S604 R605 G606 Q607 R608 A609 G610 G611 D612 L613 I614 P615 W616 S619 Q620 Q621 F622 Q623 D624 E625 E626 F627 A628 S629 L630 S631 G632 A633 R634 I635 V636 R637 I638 A639 T640 N641 P642 E643 Y644 A645 S646 M647 G648 Y649 G650 S651 R652 A653 I654 E655 L656 L657 R658 D659 Y660 F661
GLU GLY LYS PHE THR ASP MET SER GLU ASP VAL ARG PRO LYS ASP TYR SER ILE LYS ARG VAL SER ASP LYS GLU LEU ALA LYS THR ASN LEU LEU LYS ASP ASP VAL LYS LEU ARG ASP ALA LYS THR LEU PRO PRO L708 L709 L710 K711 L712 S713 E714 Q715 P716 P717 H718 Y719 L720 H721
Y722 L723 G724 V725 S726 L729 T730 Q731 S732 L733 H734 K735 F736 W737 K738 N739 N740 S741 F742 V743 P744 V745 Y746 L747 R748 Q749 T750 A751 N752 D753 L754 T755 G756 E757 H758 T759 C760 V761 M762 L763 N764 V765 L766 E767 G768 R769 E770 S771 N772 W773 L774 V775 E776 F777 A778 K779 D780 F781 R782
K783 R784 F785 L786 S787 L788 L789 S790 Y791 D792 F793 H794 K795 F796 T797 A798 V799 Q800 A801 L802 S803 V804 I805 E806 S807 S808 K809 K810 A811 Q812 D813 L814 S815 D816 D817 E818 K819 H820 D821 N822 K823 E824 L825 T826 R827 T828 H829 L830 D831 D832 I833 F834 S835 P836 F837 D838 L839 K840 R841 L842



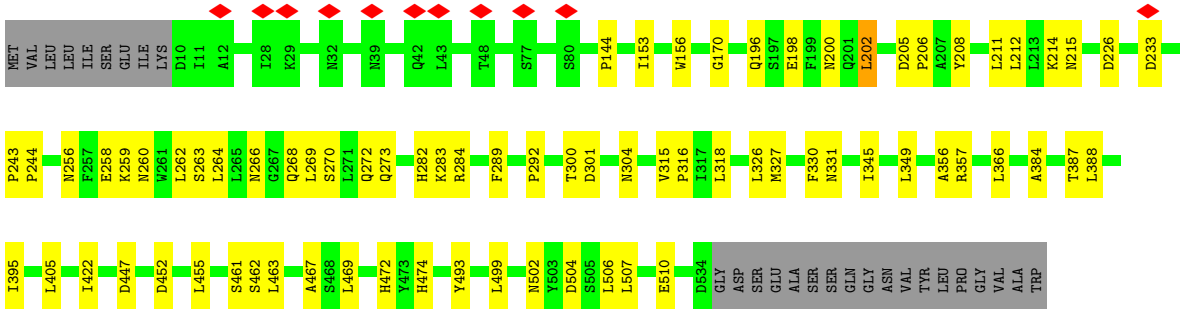
• Molecule 59: Nucleolar complex protein 14

Chain RN:



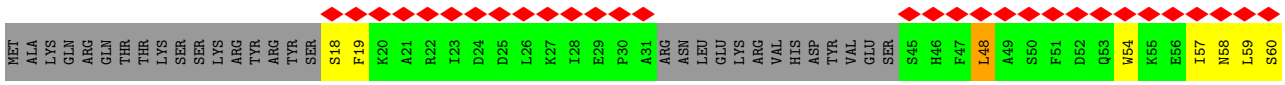
• Molecule 60: Nucleolar complex protein 4

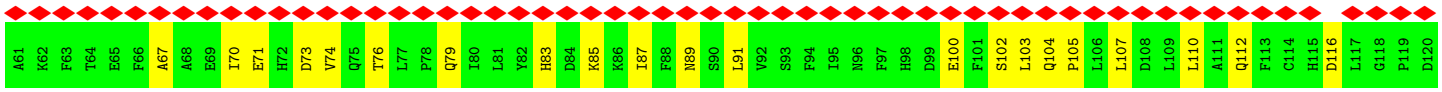
Chain RO:

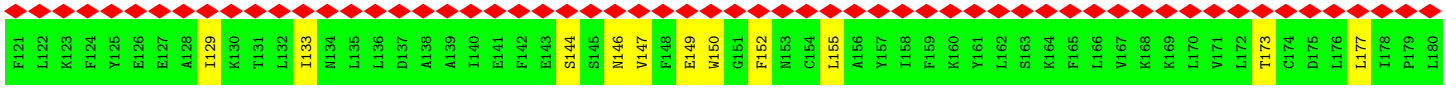


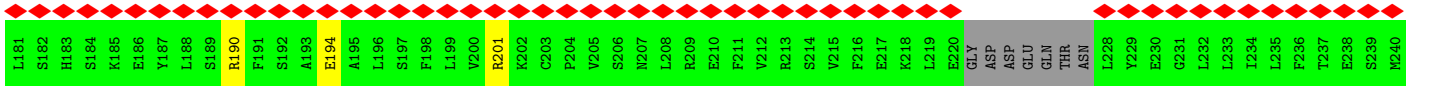
• Molecule 61: U3 small nucleolar RNA-associated protein 20

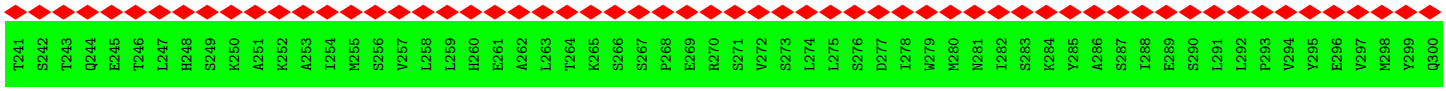
Chain RP:

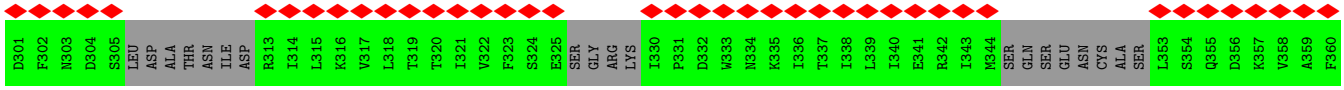


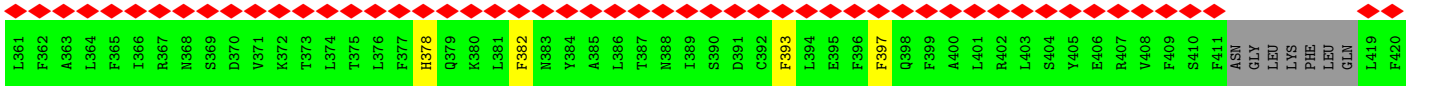


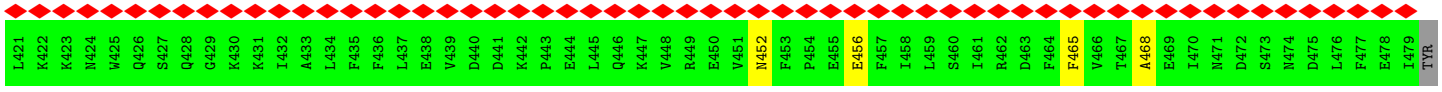


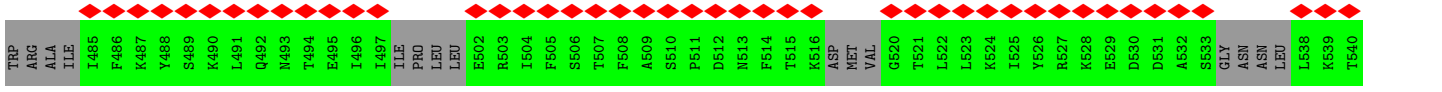


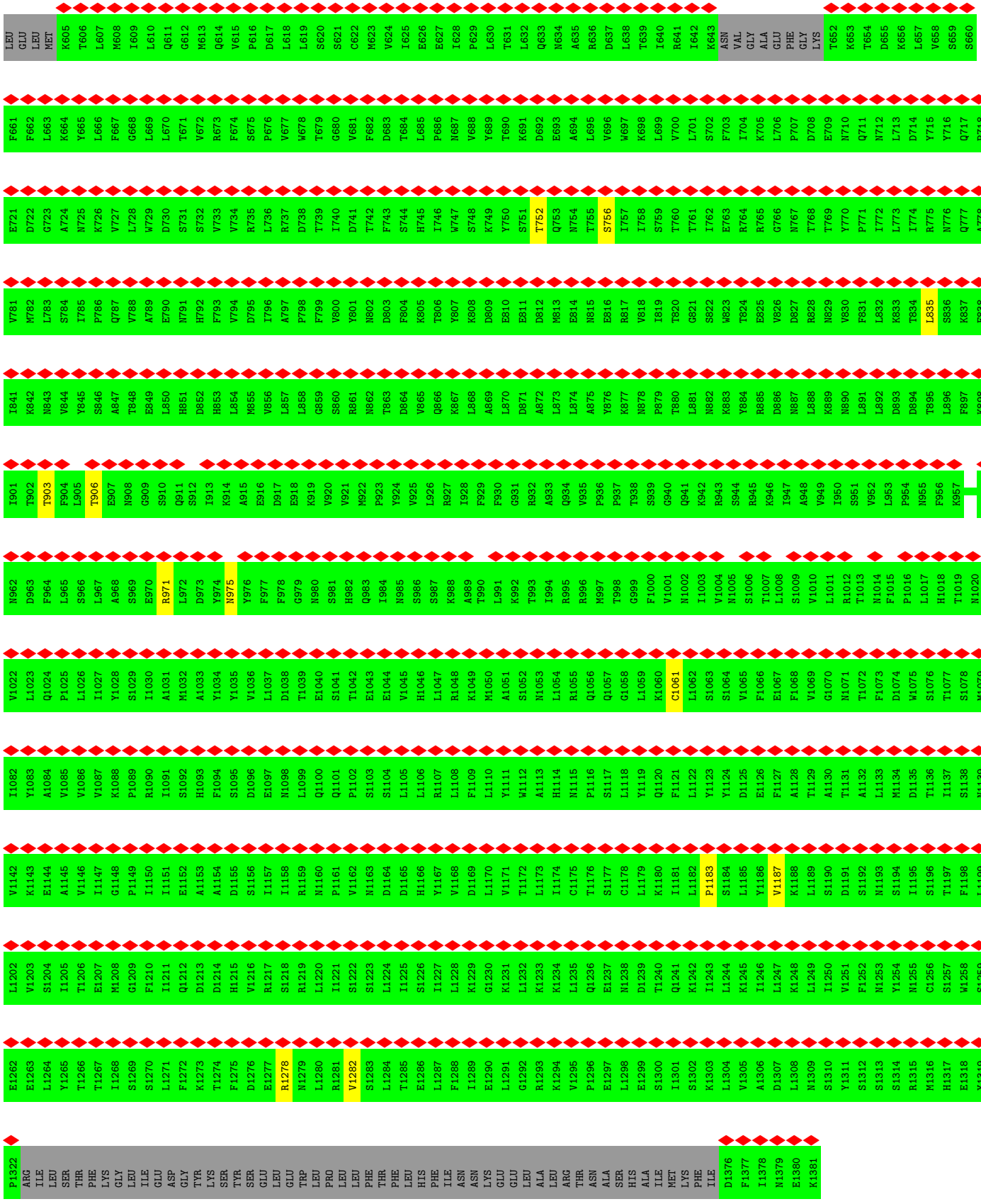


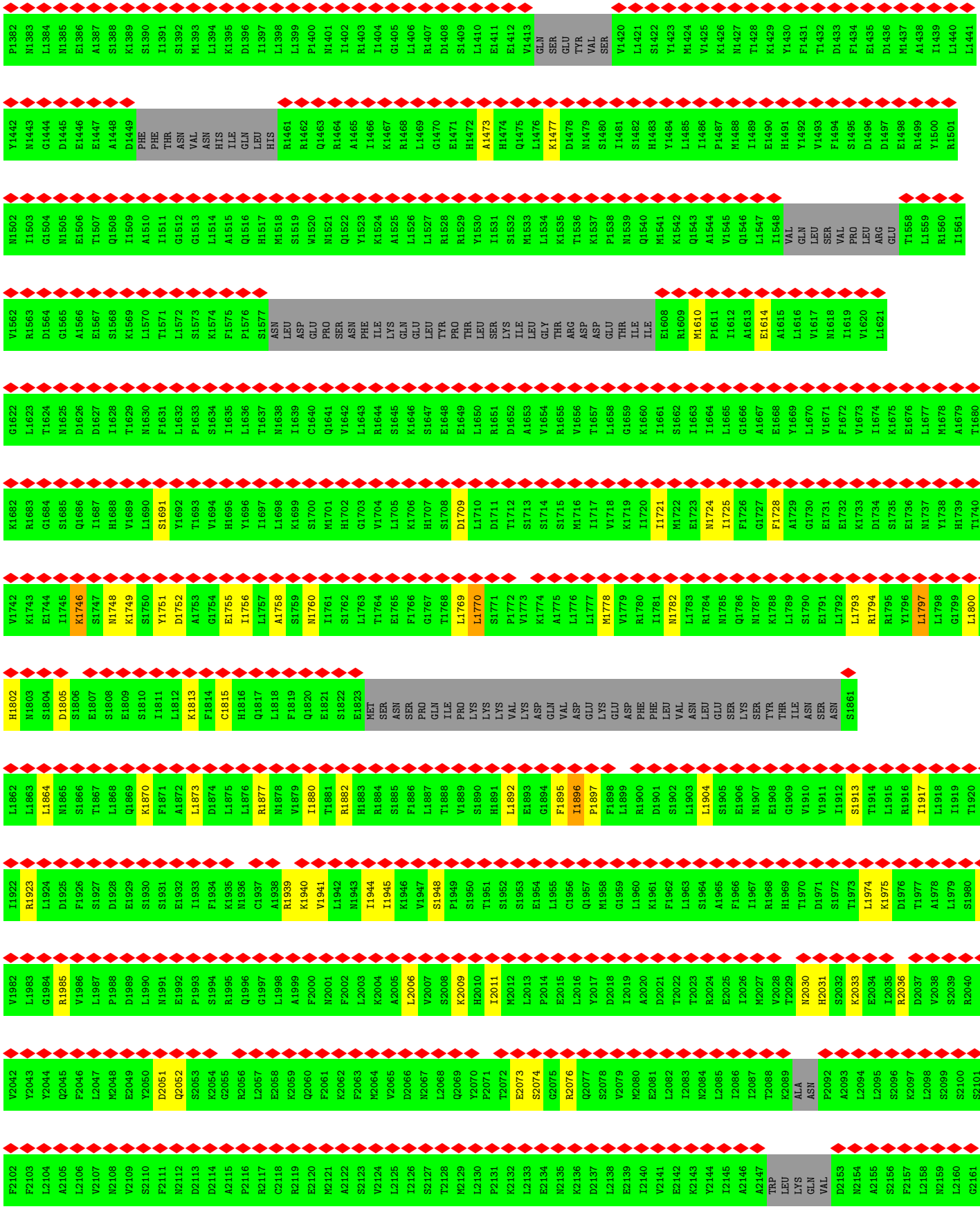


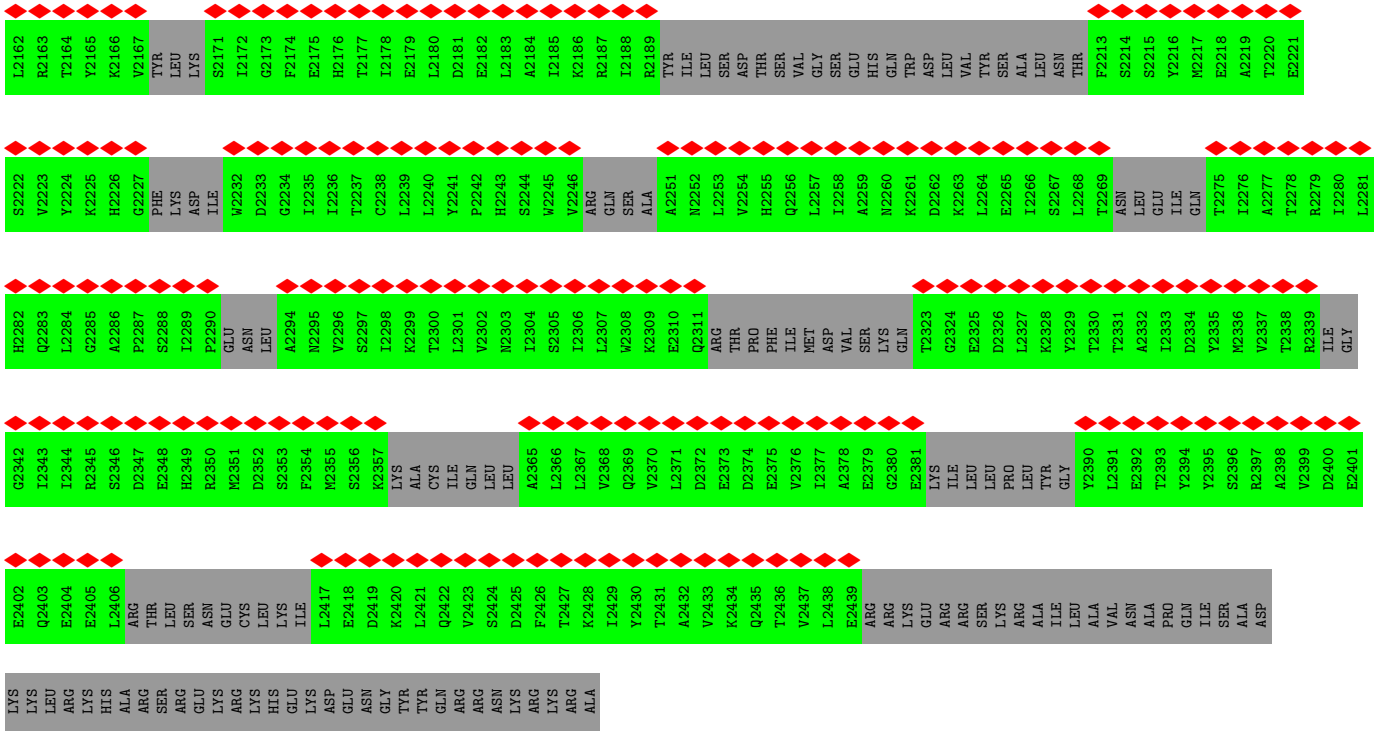


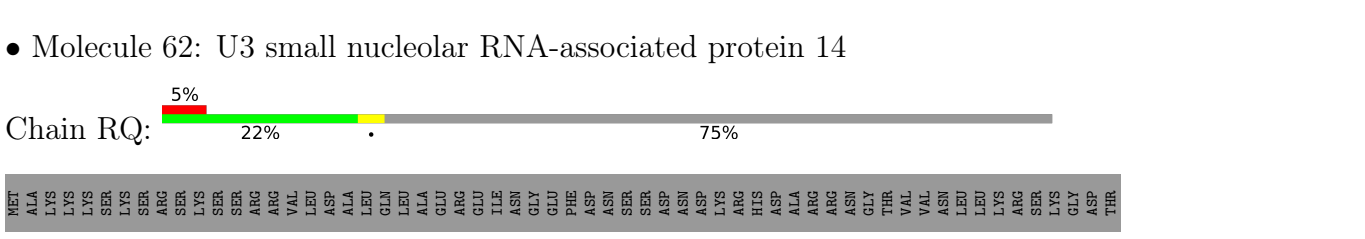


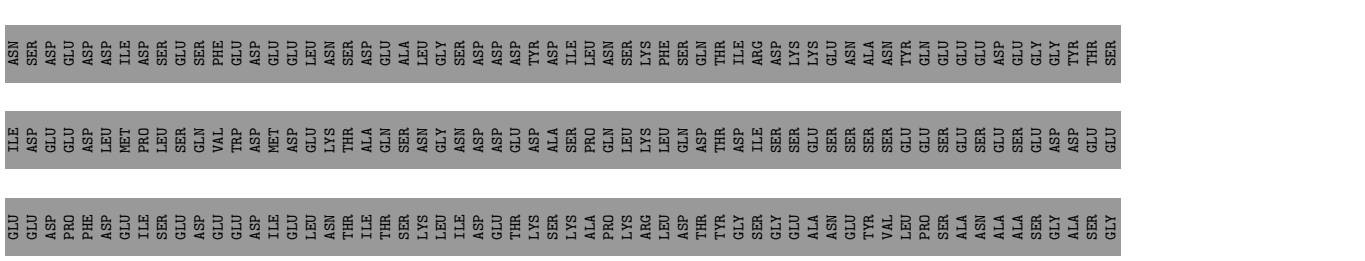


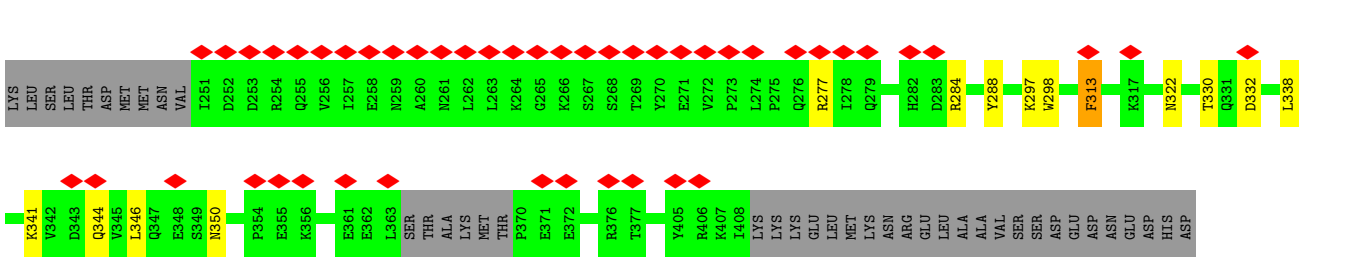

LEU GLU LEU MET K605 T606 L607 M608 I609 L610 Q611 G612 M613 Q614 V615 P616 D617 L618 L619 S620 S621 C622 M623 V624 I625 E626 E627 I628 P629 L630 T631 L632 Q633 N634 A635 R636 D637 L638 T639 I640 R641 I642 K643 ASN VAL GLY ALA GLU PHE GLY LYS T652 K653 T654 D655 K656 L657 V658 S659 S660
F661 F662 L663 K664 Y665 L666 F667 G668 L669 L670 T671 V672 R673 F674 S675 P676 V677 W678 T679 G680 V681 F682 D683 T684 L685 P686 N687 V688 Y689 T690 K691 D692 E693 A694 L695 V696 W697 K698 L699 V700 L701 S702 F703 I704 K705 L706 P707 D708 E709 N710 Q711 N712 L713 D714 Y715 Y716 Q717 P718 L719 L720
E721 D722 G723 A724 N725 K726 V727 L728 W729 D730 S731 S732 V733 V734 R735 L736 R737 D738 T739 I740 D741 T742 F743 S744 H745 I746 W747 S748 K749 Y750 S751 T752 Q753 N754 T755 S756 I757 I758 S759 T760 T761 I762 E763 R764 R765 G766 N767 T768 T769 Y770 P771 I772 L773 D774 R775 N776 Q777 A778 L779 K780
V781 M782 L783 S784 I785 P786 Q787 V788 A789 E790 N791 H792 F793 V794 D795 I796 A797 P798 F799 V800 Y801 N802 D803 F804 K805 T806 Y807 K808 D809 E810 E811 D812 M813 E814 N815 E816 R817 V818 I819 T820 G821 S822 W823 T824 E825 V826 D827 R828 N829 V830 P831 L832 K833 T834 L835 S836 K837 F838 K839 N840
I841 K842 N843 V844 Y845 S846 A847 T848 E849 L850 H851 D852 H853 L854 M855 V856 L857 L858 G859 S860 R861 N862 T863 D864 V865 Q866 K867 L868 A869 L870 D871 A872 L873 L874 A875 Y876 K877 N878 P879 T880 L881 N882 K883 Y884 R885 D886 N887 L888 K889 N890 L891 L892 D893 D894 T895 L896 F897 K898 D899 E900
I901 T902 T903 F904 L905 T906 E907 N908 G909 S910 Q911 S912 I913 K914 A915 E916 D917 E918 K919 V920 V921 M922 P923 Y924 V925 L926 R927 I928 F929 F930 G931 R932 A933 Q934 V935 P936 P937 T938 S939 G940 Q941 K942 R943 S944 R945 K946 I947 A948 V949 I950 S951 V952 L953 P954 N955 F956 K957 Y960 I961
N962 D963 F964 L965 S966 L967 A968 S969 E970 R971 L972 D973 Y974 N975 Y976 F977 F978 G979 N980 S981 H982 Q983 I984 N985 S986 S987 K988 A989 T990 L991 K992 T993 I994 R995 R996 M997 T998 G999 F1000 V1001 N1002 I1003 V1004 N1005 S1006 T1007 L1008 S1009 V1010 L1011 R1012 T1013 N1014 F1015 P1016 L1017 H1018 T1019 N1020 S1021
V1022 L1023 Q1024 P1025 L1026 I1027 Y1028 S1029 I1030 A1031 M1032 A1033 Y1034 Y1035 V1036 L1037 D1038 T1039 E1040 S1041 T1042 E1043 E1044 V1045 H1046 L1047 R1048 K1049 M1050 A1051 S1052 N1053 L1054 R1055 Q1056 Q1057 G1058 L1059 K1060 C1061 L1062 S1063 S1064 V1065 F1066 E1067 F1068 V1069 G1070 N1071 T1072 F1073 D1074 W1075 S1076 T1077 S1078 M1079 E1080 D1081
I1082 Y1083 A1084 V1085 V1086 V1087 K1088 P1089 R1090 I1091 S1092 H1093 F1094 S1095 D1096 E1097 N1098 L1099 Q1100 Q1101 P1102 S1103 S1104 L1105 L1106 R1107 L1108 F1109 L1110 Y1111 W1112 A1113 H1114 N1115 P1116 S1117 L1118 Y1119 Q1120 F1121 L1122 Y1123 Y1124 D1125 E1126 F1127 A1128 T1129 A1130 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 R1159 N1160 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 I1196 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 L1244 K1245 I1246 L1247 K1248 L1249 I1250 V1251 F1252 N1253 Y1254 N1255 C1256 S1257 W1258 S1259 D1260 I1261
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 I1289 E1290 L1291 G1292 R1293 K1294 V1295 P1296 E1297 L1298 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 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

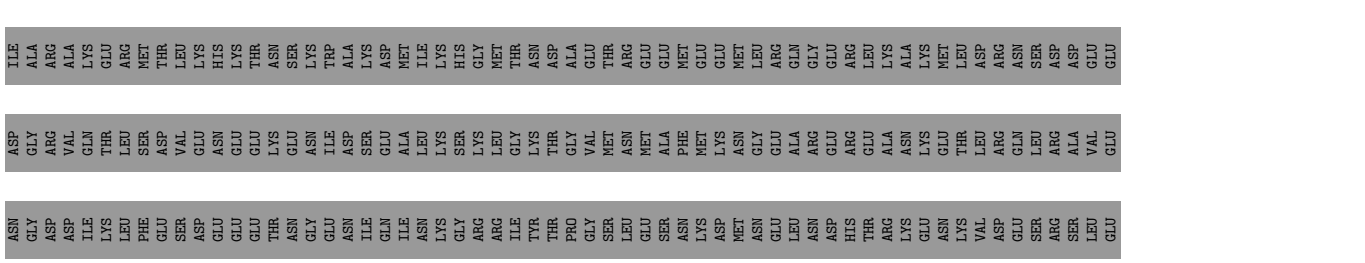

P1382 N1383 L1384 N1385 E1386 A1387 S1388 K1389 S1390 I1391 S1392 M1393 L1394 K1395 D1396 I1397 L1398 L1399 P1400 N1401 I1402 R1403 I1404 G1405 L1406 R1407 D1408 S1409 L1410 E1411 E1412 V1413 GLN SER GLU TYR VAL SER V1420 L1421 S1422 Y1423 M1424 V1425 K1426 N1427 T1428 K1429 Y1430 F1431 T1432 D1433 F1434 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 I1503 G1504 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 M1610 P1611 I1612 A1613 E1614 A1615 L1616 V1617 N1618 I1619 V1620 L1621
G1622 L1623 T1624 N1625 D1626 D1627 I1628 T1629 N1630 F1631 L1632 P1633 S1634 I1635 L1636 T1637 N1638 I1639 C1640 Q1641 V1642 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 Y1669 L1670 V1671 F1672 V1673 I1674 K1675 E1676 L1677 M1678 A1679 T1680 L1681
K1682 R1683 G1684 S1685 Q1686 I1687 H1688 V1689 L1690 S1691 Y1692 T1693 V1694 H1695 Y1696 I1697 L1698 K1699 S1700 M1701 H1702 G1703 V1704 L1705 K1706 H1707 S1708 D1709 L1710 D1711 T1712 S1713 S1714 S1715 M1716 I1717 V1718 K1719 I1720 I1721 M1722 E1723 N1724 I1725 F1726 G1727 F1728 A1729 G1730 E1731 E1732 K1733 D1734 S1735 E1736 N1737 Y1738 H1739 T1740 K1741
V1742 K1743 E1744 I1745 K1746 S1747 N1748 K1749 S1750 Y1751 D1752 A1753 G1754 E1755 I1756 L1757 A1758 S1759 N1760 I1761 S1762 L1763 T1764 E1765 F1766 G1767 T1768 L1769 L1770 S1771 P1772 V1773 K1774 A1775 L1776 L1777 M1778 V1779 R1780 I1781 N1782 L1783 R1784 N1785 Q1786 N1787 K1788 L1789 S1790 E1791 L1792 L1793 R1794 R1795 Y1796 L1797 L1798 G1799 L1800 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 F1871 A1872 L1873 D1874 L1875 L1876 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 I1917 L1918 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 R1985 V1986 L1987 P1988 D1989 L1990 N1991 E1992 P1993 S1994 R1995 Q1996 G1997 L1998 A1999 F2000 N2001 F2002 L2003 K2004 A2005 L2006 V2007 S2008 K2009 H2010 I2011 M2012 L2013 P2014 E2015 L2016 Y2017 D2018 I2019 A2020 D2021 T2022 T2023 R2024 E2025 I2026 M2027 V2028 T2029 N2030 H2031 S2032 K2033 E2034 I2035 R2036 D2037 V2038 S2039 R2040 S2041
V2042 Y2043 Y2044 Q2045 F2046 L2047 M2048 E2049 Y2050 D2051 Q2052 S2063 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



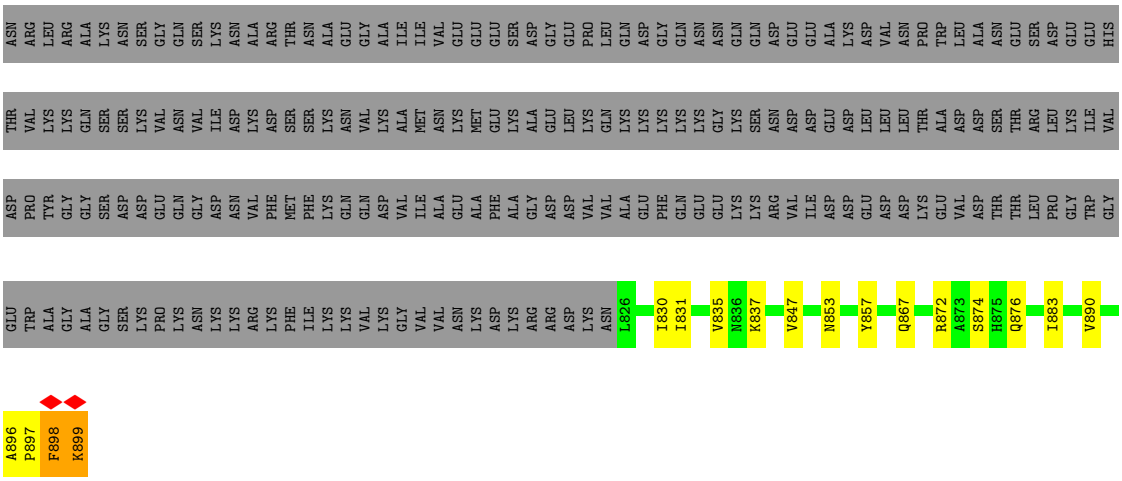






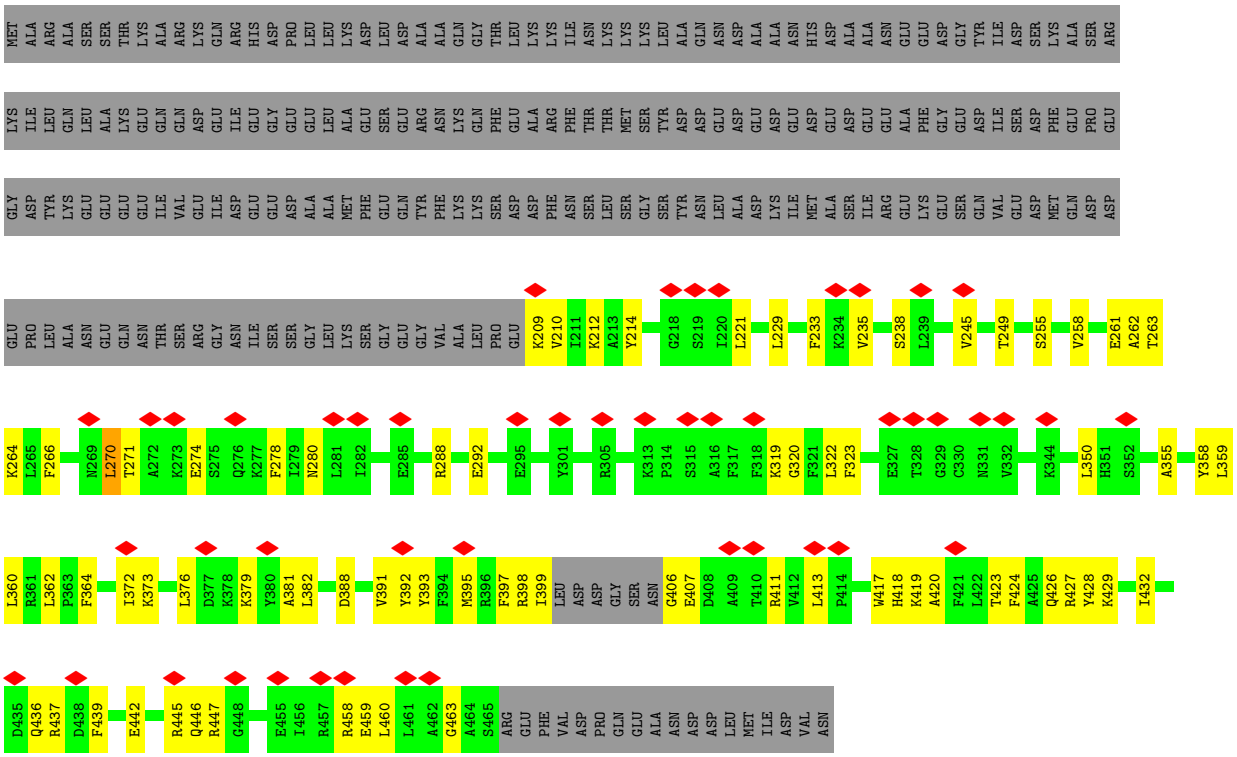


• Molecule 62: U3 small nucleolar RNA-associated protein 14



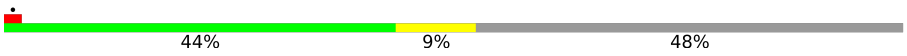
• Molecule 63: Essential nuclear protein 1

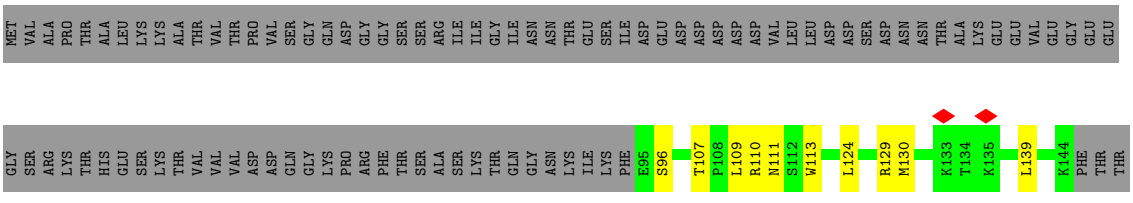
Chain RS:

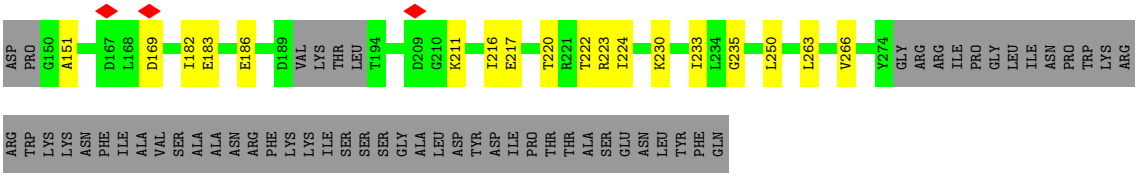


• Molecule 64: Pno1

Chain RT:

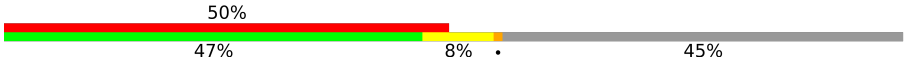


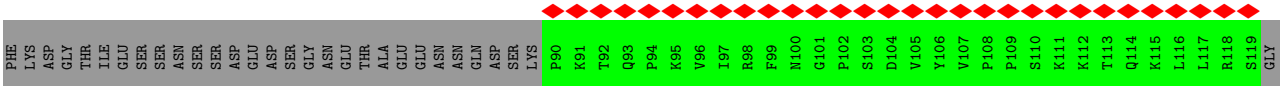


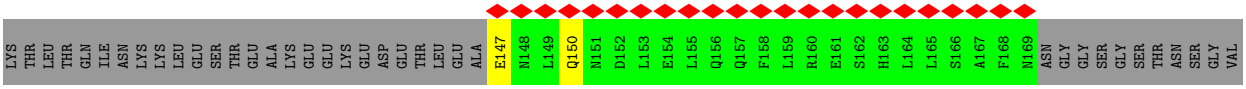


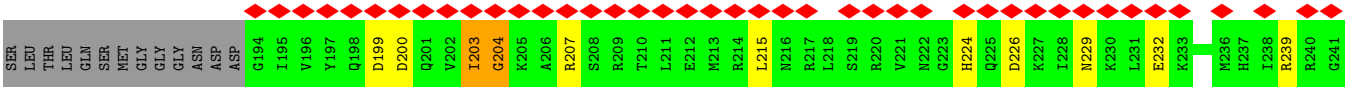
• Molecule 65: Protein FAF1

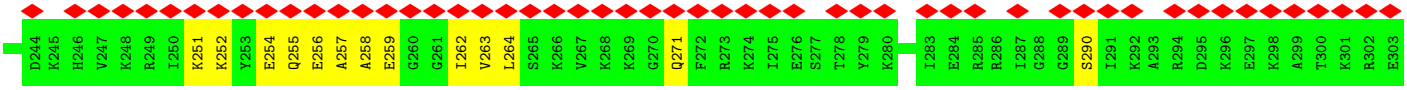
Chain RV:

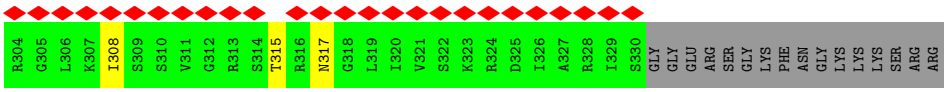






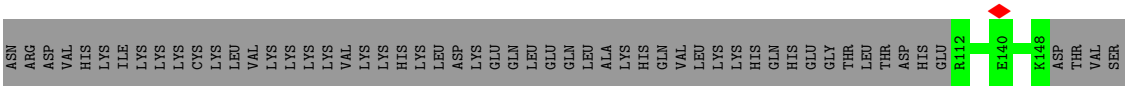


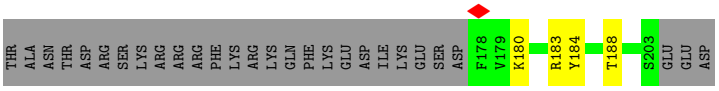




• Molecule 66: Regulator of rDNA transcription protein 14

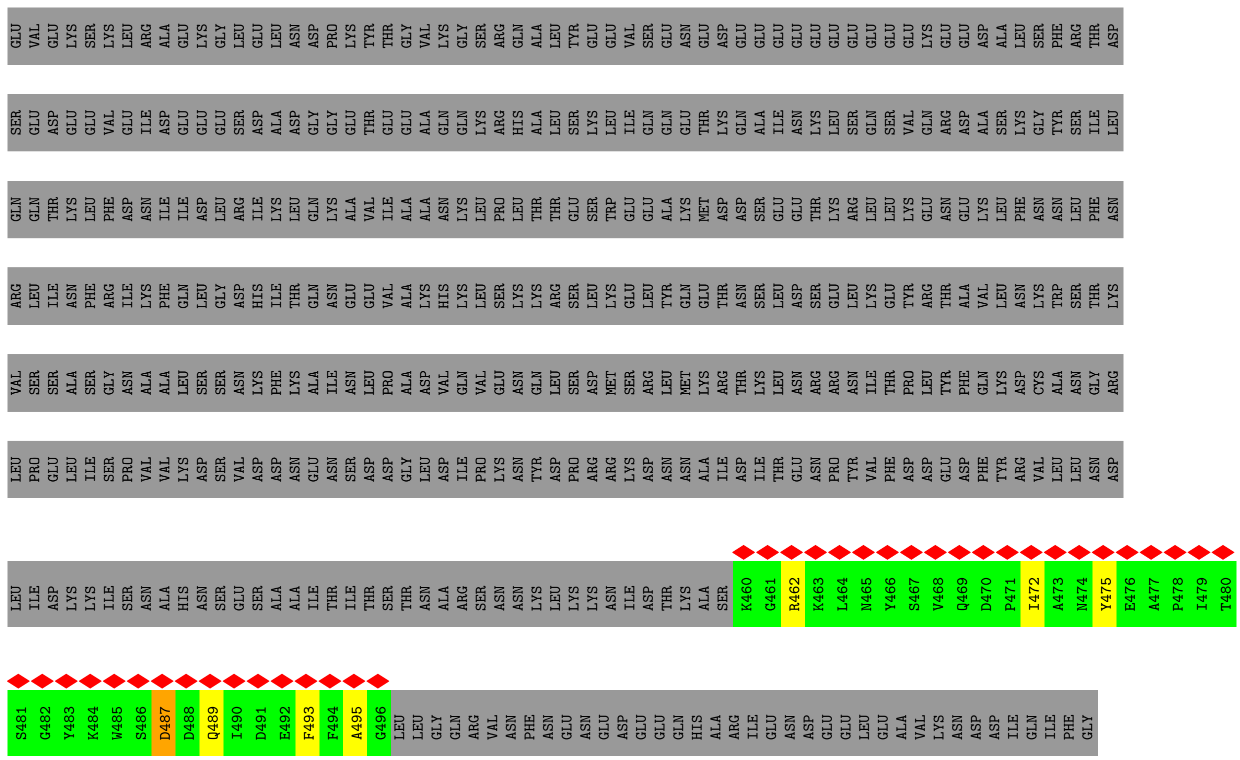
Chain RW:





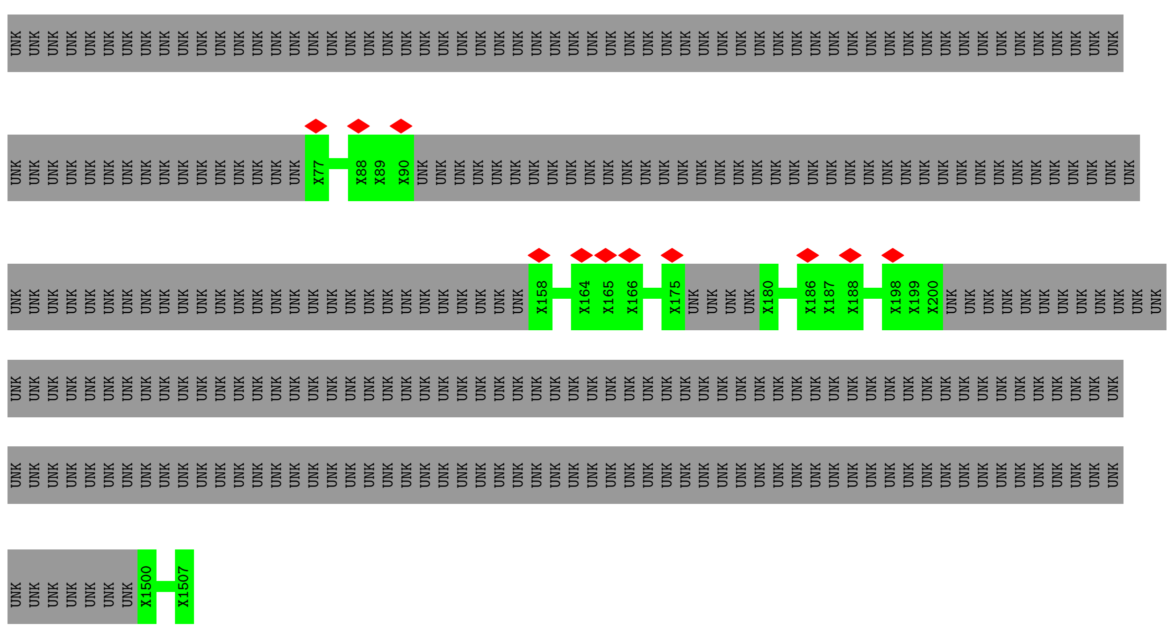
• Molecule 67: Protein BFR2

Chain RY:



• Molecule 68: Unassigned helices

Chain X1:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26582	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	0.169	Depositor
Minimum map value	-0.082	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	597.632, 597.632, 597.632	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.92	0/4141	1.17	24/6433 (0.4%)
2	5A	0.84	0/12485	1.11	48/19449 (0.2%)
3	SA	0.64	0/29638	1.14	201/46154 (0.4%)
4	SF	0.35	0/1854	0.66	1/2504 (0.0%)
5	SG	0.53	0/1690	0.64	0/2285
6	SH	0.31	0/1341	0.60	0/1789
7	SI	0.38	0/1341	0.67	1/1806 (0.1%)
8	SJ	0.31	0/1347	0.59	1/1801 (0.1%)
9	SK	0.47	0/1410	0.60	0/1888
10	SM	0.31	0/1020	0.58	0/1374
11	SN	0.32	0/873	0.73	1/1185 (0.1%)
12	SO	0.35	0/1109	0.66	1/1495 (0.1%)
13	SP	0.36	0/879	0.75	1/1186 (0.1%)
14	SR	0.58	0/990	0.73	1/1335 (0.1%)
15	ST	0.38	0/980	0.63	0/1319
16	SX	0.51	0/1020	0.66	1/1371 (0.1%)
17	SY	0.54	0/798	0.67	1/1065 (0.1%)
18	SZ	0.43	0/822	0.64	0/1103
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	0.30	0/3328	0.61	0/4565
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	0/6780	0.68	7/9175 (0.1%)
33	B2	0.43	0/6853	0.67	3/9256 (0.0%)
34	B3	0.34	0/5977	0.73	7/8087 (0.1%)
35	B8	0.58	0/3848	0.66	4/5218 (0.1%)
36	BE	0.57	0/6948	0.66	7/9391 (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	0.59	0/4166	0.68	5/5624 (0.1%)
40	5D	0.50	0/1998	0.66	3/2644 (0.1%)
41	5E	0.47	0/1665	0.64	1/2233 (0.0%)
42	5F	0.66	0/1559	0.73	2/2097 (0.1%)
43	5G	0.56	0/2337	0.66	1/3148 (0.0%)
44	5H	0.45	0/1074	0.56	0/1422
45	5I	0.61	0/3844	0.66	2/5174 (0.0%)
46	5J	0.42	0/1302	0.54	0/1728
47	5K	0.56	0/1426	0.66	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	RC	0.36	0/1432	0.64	0/1926
51	RD	0.27	0/1313	0.41	0/1830
52	RE	0.32	0/8924	0.67	9/12070 (0.1%)
53	RF	0.32	0/1441	0.69	2/1951 (0.1%)
54	RG	0.39	0/1727	0.68	2/2329 (0.1%)
54	RH	0.42	0/1828	0.61	0/2470
55	RI	0.46	0/2080	0.65	0/2797
56	RJ	0.50	0/6514	0.60	1/8768 (0.0%)
57	RK	0.44	0/2832	0.65	3/3825 (0.1%)
58	RL	0.29	0/4549	0.50	0/6241
58	RM	0.25	0/3765	0.47	0/5218
59	RN	0.36	0/4591	0.58	2/6187 (0.0%)
60	RO	0.38	0/3849	0.62	5/5261 (0.1%)
61	RP	0.28	0/12230	0.51	5/16819 (0.0%)
62	RQ	0.46	0/1678	0.58	0/2282
63	RS	0.33	0/2104	0.67	1/2854 (0.0%)
64	RT	0.42	0/1379	0.63	1/1853 (0.1%)
65	RV	0.48	0/1456	0.64	2/1937 (0.1%)
66	RW	0.34	0/385	0.50	0/529
67	RY	0.29	0/307	0.51	0/415
All	All	0.51	0/235239	0.77	397/327983 (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	SF	0	2
7	SI	0	3
8	SJ	0	1
10	SM	0	1
12	SO	0	1
15	ST	0	1
18	SZ	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	4
31	AG	0	2
32	B1	0	3
33	B2	0	9
34	B3	0	7
36	BE	0	1
40	5D	0	1
41	5E	0	1
42	5F	0	1
43	5G	0	1
45	5I	0	2
48	RA	0	2
49	RB	0	1
52	RE	0	2
56	RJ	0	2
57	RK	0	1
58	RL	0	1
58	RM	0	1
59	RN	0	1
60	RO	0	1
61	RP	0	3
62	RQ	0	1
65	RV	0	1
All	All	0	69

There are no bond length outliers.

The worst 5 of 397 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	SA	376	C	N1-C2-O2	10.43	125.16	118.90
3	SA	1174	C	N1-C2-O2	10.35	125.11	118.90
42	5F	13	LEU	CA-CB-CG	10.29	138.96	115.30
26	A5	25	ASP	CB-CG-OD1	9.52	126.87	118.30
3	SA	1000	C	N1-C2-O2	9.36	124.52	118.90

There are no chirality outliers.

5 of 69 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SF	193	GLY	Peptide
4	SF	195	ILE	Peptide
7	SI	133	THR	Peptide
7	SI	31	SER	Peptide
7	SI	64	VAL	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	3711	0	1882	21	0
2	5A	11163	0	5611	84	0
3	SA	26503	0	13353	301	0
4	SF	1815	0	1870	45	0
5	SG	1669	0	1724	18	0
6	SH	1327	0	1403	28	0
7	SI	1321	0	1387	23	0
8	SJ	1324	0	1344	48	0
9	SK	1388	0	1467	31	0
10	SM	997	0	1048	35	0
11	SN	865	0	874	16	0
12	SO	1087	0	1152	22	0
13	SP	868	0	894	26	0
14	SR	973	0	1029	14	0
15	ST	964	0	991	16	0
16	SX	1003	0	1040	13	0
17	SY	786	0	843	8	0
18	SZ	809	0	842	15	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	Sd	497	0	535	0	0
20	3B	1865	0	1910	29	0
20	3C	1763	0	1805	33	0
21	3D	2848	0	2815	46	0
22	3E	3028	0	2813	59	0
23	3F	3643	0	3654	79	0
24	3G	916	0	964	11	0
24	3H	916	0	964	24	0
25	A4	5226	0	5199	95	0
26	A5	3976	0	3919	58	0
27	A8	3307	0	2316	39	0
28	A9	939	0	898	18	0
29	AE	9955	0	7968	102	0
30	AF	3911	0	3906	72	0
31	AG	6570	0	6473	124	0
32	B1	6635	0	6525	99	0
33	B2	6723	0	6698	130	0
34	B3	5882	0	5964	141	0
35	B8	3764	0	3757	59	0
36	BE	6810	0	6787	85	0
37	B6	2800	0	2517	33	0
38	5B	495	0	561	13	0
39	5C	4084	0	4092	77	0
40	5D	1972	0	2054	27	0
41	5E	1647	0	1678	32	0
42	5F	1530	0	1572	29	0
43	5G	2296	0	2325	41	0
44	5H	1065	0	1097	16	0
45	5I	3765	0	3714	69	0
46	5J	1280	0	1331	22	0
47	5K	1403	0	1484	19	0
48	RA	2709	0	2622	63	0
49	RB	1108	0	1087	25	0
50	RC	1410	0	1503	70	0
51	RD	1314	0	610	21	0
52	RE	8716	0	8828	159	0
53	RF	1404	0	1364	25	0
54	RG	1701	0	1767	40	0
54	RH	1799	0	1872	32	0
55	RI	2045	0	2162	37	0
56	RJ	6379	0	6506	102	0
57	RK	2781	0	2878	49	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	RL	4539	0	2874	28	0
58	RM	3779	0	1650	8	0
59	RN	4529	0	4262	67	0
60	RO	3766	0	3269	47	0
61	RP	12176	0	7751	74	0
62	RQ	1651	0	1450	29	0
63	RS	2051	0	2096	54	0
64	RT	1357	0	1426	15	0
65	RV	1448	0	1435	51	0
66	RW	381	0	255	4	0
67	RY	299	0	275	6	0
68	X1	305	0	73	0	0
69	5K	1	0	0	0	0
70	RJ	32	0	12	1	0
71	RJ	1	0	0	0	0
All	All	227765	0	195076	2992	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 2992 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RC:163:TYR:CE2	65:RV:262:ILE:HG22	1.49	1.46
50:RC:112:GLN:CB	65:RV:262:ILE:HG21	1.69	1.22
51:RD:1487:GLN:O	52:RE:411:ILE:HG23	1.40	1.19
34:B3:12:LEU:HD23	34:B3:377:LEU:HB2	1.23	1.18
13:SP:42:VAL:HG12	13:SP:67:VAL:HG23	1.31	1.13

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	34	69
5	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
6	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
7	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
8	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
9	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
10	SM	119/156 (76%)	103 (87%)	16 (13%)	0	100	100
11	SN	117/143 (82%)	89 (76%)	28 (24%)	0	100	100
12	SO	132/151 (87%)	121 (92%)	10 (8%)	1 (1%)	19	56
13	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	17	54
14	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
15	ST	113/146 (77%)	103 (91%)	10 (9%)	0	100	100
16	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
17	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
18	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	15	51
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	78
24	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	19	56
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	534/713 (75%)	398 (74%)	134 (25%)	2 (0%)	34	69
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%)	442 (90%)	47 (10%)	0	100	100
31	AG	812/896 (91%)	731 (90%)	80 (10%)	1 (0%)	51	83
32	B1	830/923 (90%)	767 (92%)	63 (8%)	0	100	100
33	B2	839/943 (89%)	748 (89%)	89 (11%)	2 (0%)	47	78

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
34	B3	728/817 (89%)	595 (82%)	131 (18%)	2 (0%)	41 74
35	B8	469/594 (79%)	439 (94%)	30 (6%)	0	100 100
36	BE	857/939 (91%)	803 (94%)	54 (6%)	0	100 100
37	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100 100
38	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100 100
39	5C	512/554 (92%)	474 (93%)	37 (7%)	1 (0%)	47 78
40	5D	231/250 (92%)	204 (88%)	27 (12%)	0	100 100
41	5E	200/593 (34%)	183 (92%)	16 (8%)	1 (0%)	29 66
42	5F	180/183 (98%)	172 (96%)	8 (4%)	0	100 100
43	5G	278/290 (96%)	256 (92%)	22 (8%)	0	100 100
44	5H	132/610 (22%)	123 (93%)	9 (7%)	0	100 100
45	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100 100
46	5J	147/217 (68%)	136 (92%)	11 (8%)	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 56
50	RC	173/316 (55%)	169 (98%)	4 (2%)	0	100 100
51	RD	263/1729 (15%)	254 (97%)	9 (3%)	0	100 100
52	RE	1067/1237 (86%)	998 (94%)	69 (6%)	0	100 100
53	RF	168/297 (57%)	145 (86%)	23 (14%)	0	100 100
54	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100 100
54	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100 100
55	RI	250/274 (91%)	233 (93%)	17 (7%)	0	100 100
56	RJ	784/1183 (66%)	721 (92%)	62 (8%)	1 (0%)	51 83
57	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100 100
58	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	41 74
58	RM	738/1056 (70%)	625 (85%)	109 (15%)	4 (0%)	29 66
59	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	47 78
60	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100 100
61	RP	2043/2493 (82%)	1815 (89%)	227 (11%)	1 (0%)	100 100
62	RQ	220/899 (24%)	199 (90%)	21 (10%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
64	RT	165/326 (51%)	150 (91%)	15 (9%)	0	100	100
65	RV	184/346 (53%)	164 (89%)	20 (11%)	0	100	100
66	RW	59/206 (29%)	54 (92%)	5 (8%)	0	100	100
67	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
All	All	24744/35018 (71%)	22316 (90%)	2403 (10%)	25 (0%)	54	83

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
41	5E	454	VAL
58	RL	744	PRO
58	RM	744	PRO
58	RM	905	PRO
12	SO	106	ARG

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	SF	196/222 (88%)	190 (97%)	6 (3%)	40	65
5	SG	180/191 (94%)	180 (100%)	0	100	100
6	SH	139/201 (69%)	137 (99%)	2 (1%)	67	82
7	SI	146/170 (86%)	145 (99%)	1 (1%)	84	91
8	SJ	136/161 (84%)	134 (98%)	2 (2%)	65	81
9	SK	147/166 (89%)	146 (99%)	1 (1%)	84	91
10	SM	110/137 (80%)	108 (98%)	2 (2%)	59	77
11	SN	88/119 (74%)	86 (98%)	2 (2%)	50	71
12	SO	117/128 (91%)	114 (97%)	3 (3%)	46	69
13	SP	90/105 (86%)	89 (99%)	1 (1%)	73	85
14	SR	105/119 (88%)	105 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
15	ST	105/129 (81%)	104 (99%)	1 (1%)	76 86
16	SX	108/111 (97%)	107 (99%)	1 (1%)	78 88
17	SY	85/120 (71%)	84 (99%)	1 (1%)	71 84
18	SZ	85/113 (75%)	85 (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 80
21	3D	296/435 (68%)	293 (99%)	3 (1%)	76 86
22	3E	262/433 (60%)	261 (100%)	1 (0%)	91 95
23	3F	396/503 (79%)	394 (100%)	2 (0%)	88 94
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 84
26	A5	433/574 (75%)	432 (100%)	1 (0%)	93 97
27	A8	174/657 (26%)	173 (99%)	1 (1%)	86 93
28	A9	89/533 (17%)	89 (100%)	0	100 100
29	AE	708/1633 (43%)	705 (100%)	3 (0%)	91 95
30	AF	437/454 (96%)	433 (99%)	4 (1%)	78 88
31	AG	750/826 (91%)	740 (99%)	10 (1%)	69 83
32	B1	730/812 (90%)	726 (100%)	4 (0%)	88 94
33	B2	736/832 (88%)	730 (99%)	6 (1%)	81 89
34	B3	660/719 (92%)	640 (97%)	20 (3%)	41 66
35	B8	421/529 (80%)	420 (100%)	1 (0%)	93 97
36	BE	757/819 (92%)	754 (100%)	3 (0%)	91 95
37	B6	251/414 (61%)	247 (98%)	4 (2%)	62 80
38	5B	57/196 (29%)	55 (96%)	2 (4%)	36 63
39	5C	448/480 (93%)	445 (99%)	3 (1%)	84 91
40	5D	221/234 (94%)	219 (99%)	2 (1%)	78 88
41	5E	185/535 (35%)	184 (100%)	1 (0%)	88 94
42	5F	171/172 (99%)	170 (99%)	1 (1%)	86 93
43	5G	251/258 (97%)	249 (99%)	2 (1%)	81 89

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	5H	107/538 (20%)	107 (100%)	0	100	100
45	5I	416/443 (94%)	414 (100%)	2 (0%)	88	94
46	5J	140/200 (70%)	140 (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	69
50	RC	158/289 (55%)	156 (99%)	2 (1%)	69	83
52	RE	984/1125 (88%)	960 (98%)	24 (2%)	49	71
53	RF	159/274 (58%)	153 (96%)	6 (4%)	33	61
54	RG	195/222 (88%)	193 (99%)	2 (1%)	76	86
54	RH	206/222 (93%)	204 (99%)	2 (1%)	76	86
55	RI	235/256 (92%)	235 (100%)	0	100	100
56	RJ	683/1039 (66%)	676 (99%)	7 (1%)	76	86
57	RK	307/312 (98%)	303 (99%)	4 (1%)	69	83
58	RL	164/934 (18%)	162 (99%)	2 (1%)	71	84
59	RN	422/732 (58%)	422 (100%)	0	100	100
60	RO	329/506 (65%)	328 (100%)	1 (0%)	92	96
61	RP	499/2307 (22%)	493 (99%)	6 (1%)	71	84
62	RQ	148/808 (18%)	145 (98%)	3 (2%)	55	74
63	RS	225/424 (53%)	225 (100%)	0	100	100
64	RT	148/282 (52%)	146 (99%)	2 (1%)	67	82
65	RV	141/304 (46%)	141 (100%)	0	100	100
66	RW	22/192 (12%)	22 (100%)	0	100	100
67	RY	31/482 (6%)	30 (97%)	1 (3%)	39	65
All	All	17804/28712 (62%)	17627 (99%)	177 (1%)	77	86

5 of 177 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	RC	62	ARG
53	RF	69	LYS
52	RE	223	ARG
52	RE	552	ARG
54	RH	197	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 300 such sidechains are listed below:

Mol	Chain	Res	Type
52	RE	834	ASN
61	RP	1787	ASN
52	RE	1233	ASN
57	RK	334	ASN
31	AG	410	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	518/700 (74%)	161 (31%)	11 (2%)
3	SA	1226/1808 (67%)	464 (37%)	26 (2%)
All	All	1913/2841 (67%)	669 (34%)	39 (2%)

5 of 669 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 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	970	A
3	SA	1654	G
3	SA	971	A
3	SA	1521	G
3	SA	1744	A

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
70	GTP	RJ	1201	71	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
70	GTP	RJ	1201	71	-	3/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
70	RJ	1201	GTP	C5-C6	-2.47	1.42	1.47
70	RJ	1201	GTP	C8-N7	-2.05	1.31	1.35

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

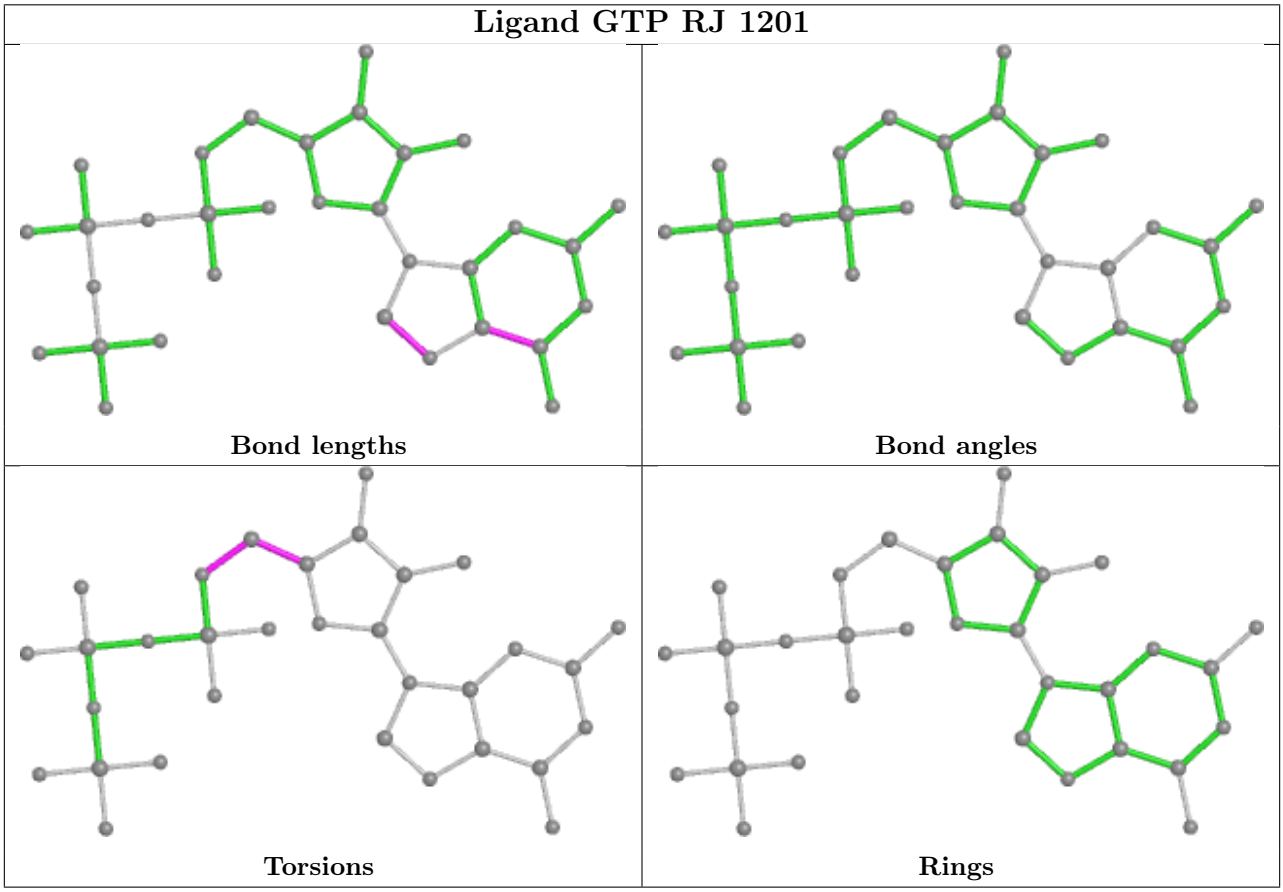
Mol	Chain	Res	Type	Atoms
70	RJ	1201	GTP	O4'-C4'-C5'-O5'
70	RJ	1201	GTP	C3'-C4'-C5'-O5'
70	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
70	RJ	1201	GTP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

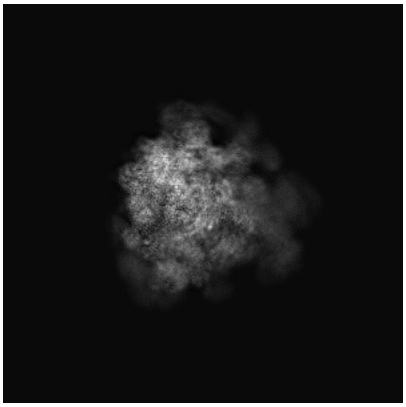
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-0954. These allow visual inspection of the internal detail of the map and identification of artifacts.

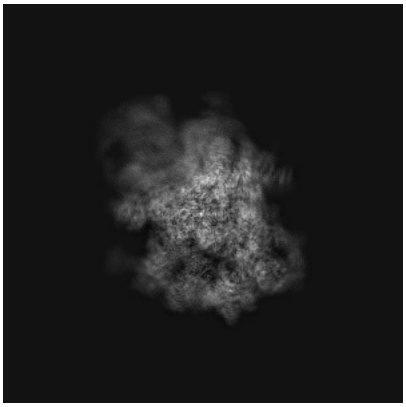
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

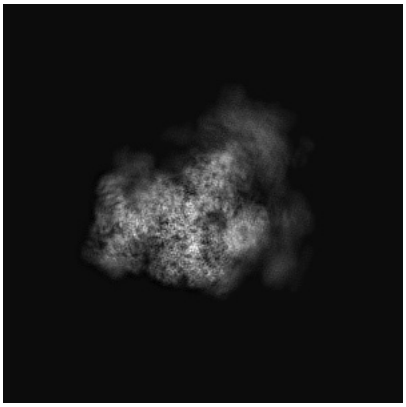
6.1.1 Primary map



X



Y

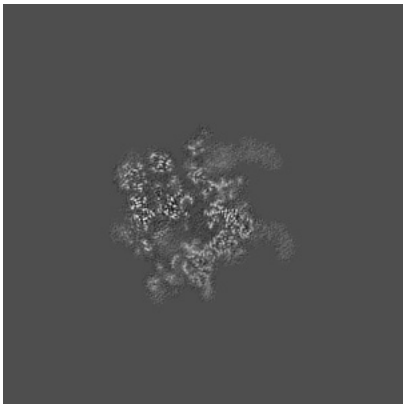


Z

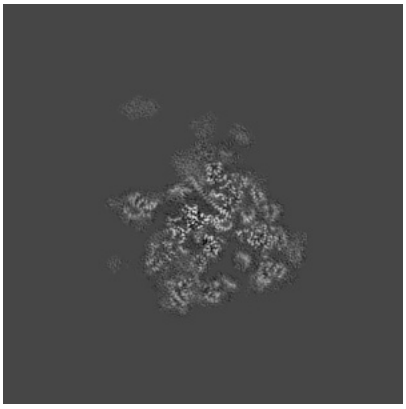
The images above show the map projected in three orthogonal directions.

6.2 Central slices

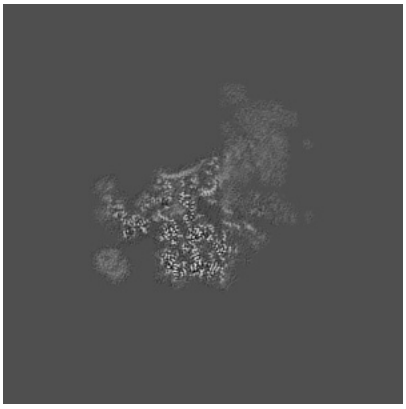
6.2.1 Primary map



X Index: 224



Y Index: 224

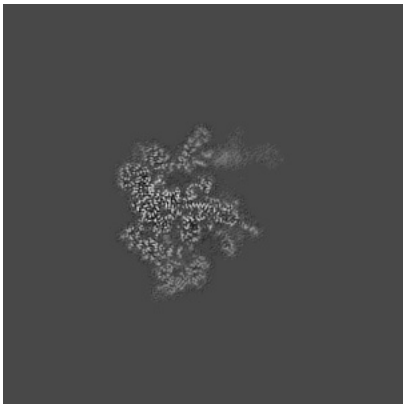


Z Index: 224

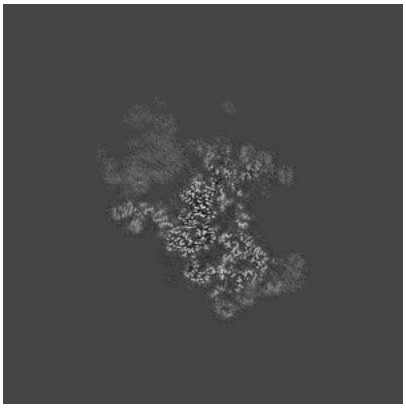
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

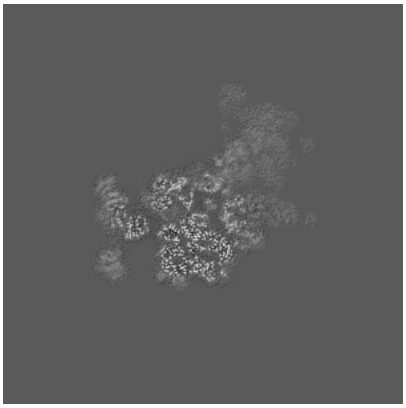
6.3.1 Primary map



X Index: 212



Y Index: 189

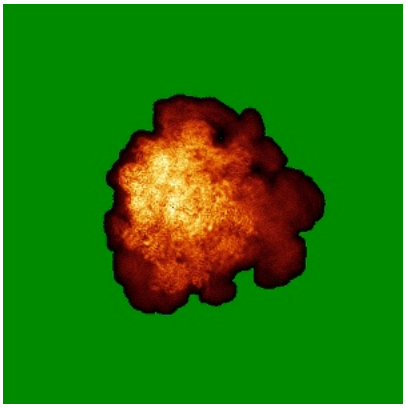


Z Index: 229

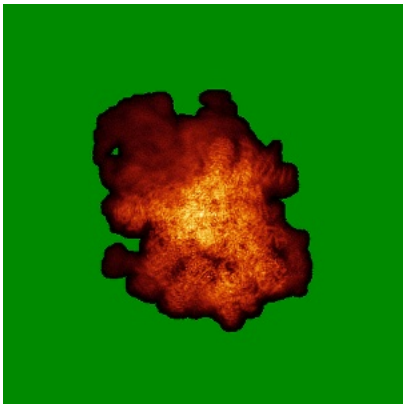
The images above show the largest variance slices of the map in three orthogonal directions.

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

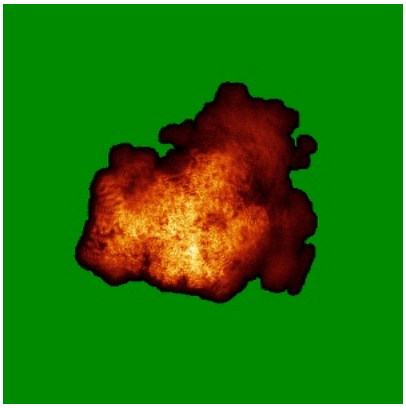
6.4.1 Primary map



X



Y

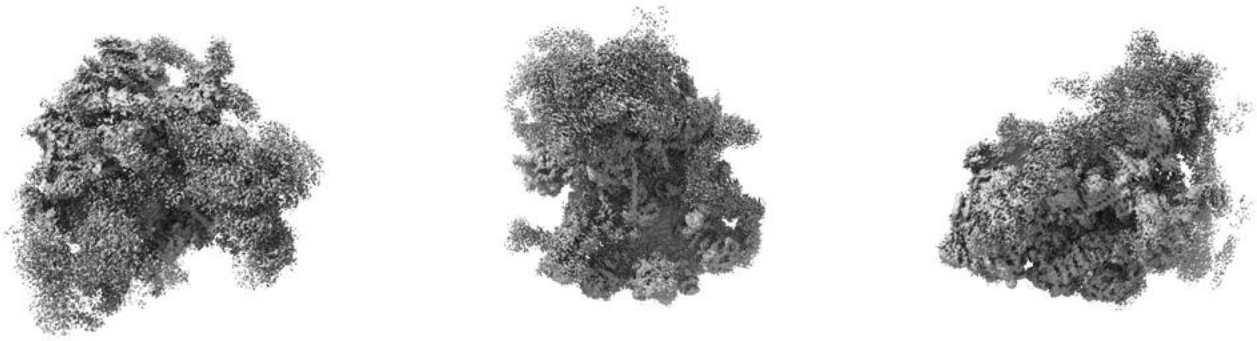


Z

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

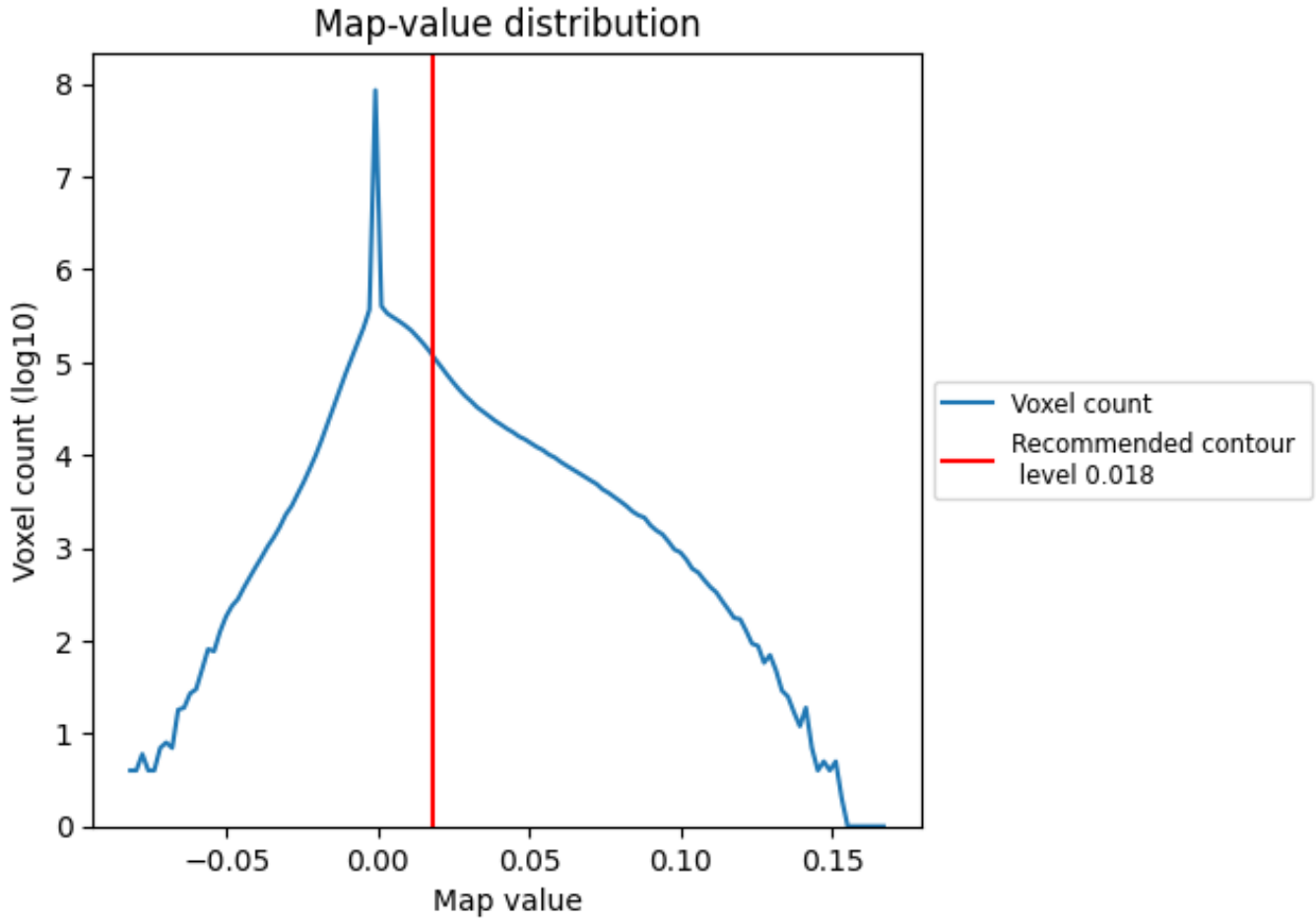
6.6 Mask visualisation (i)

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

7 Map analysis

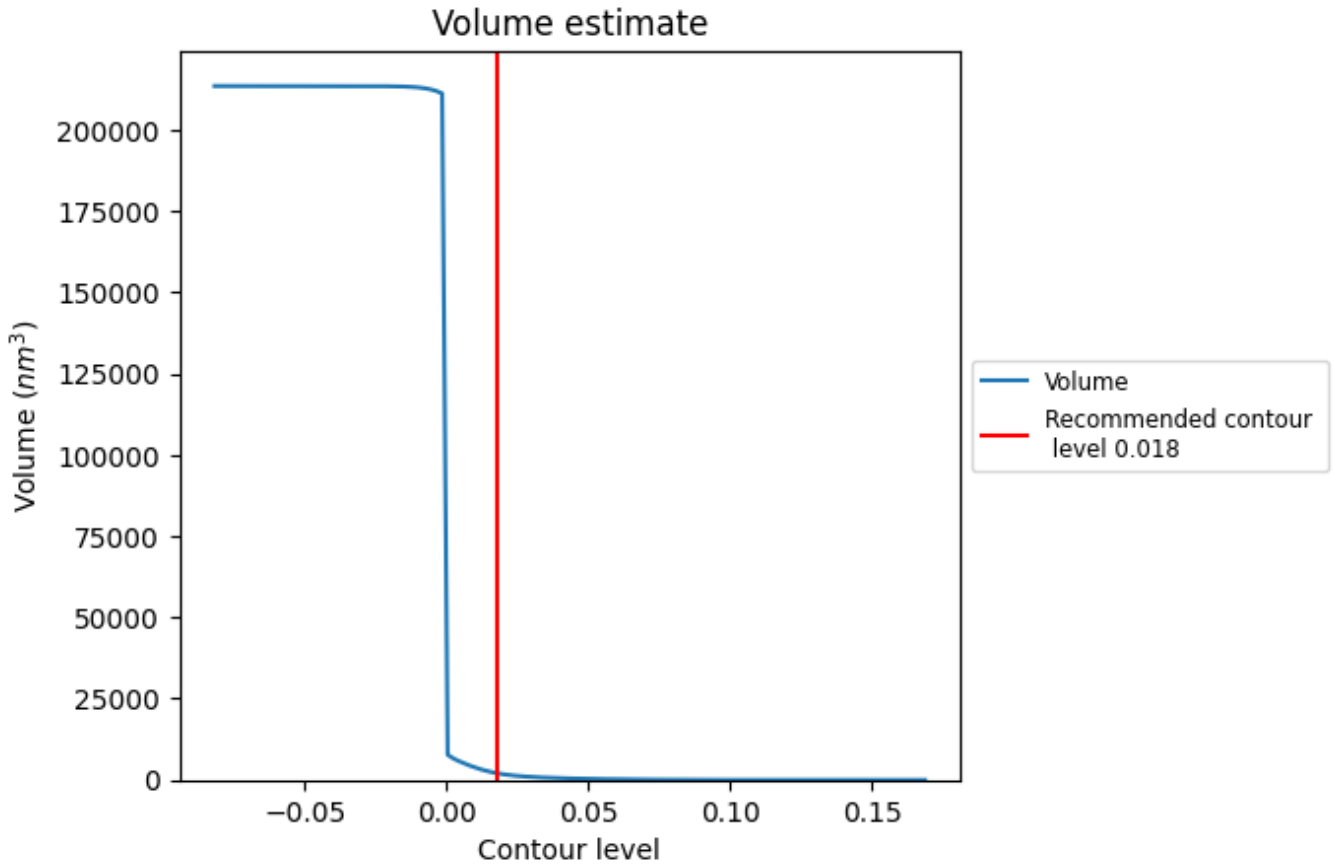
This section contains the results of statistical analysis of the map.

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.

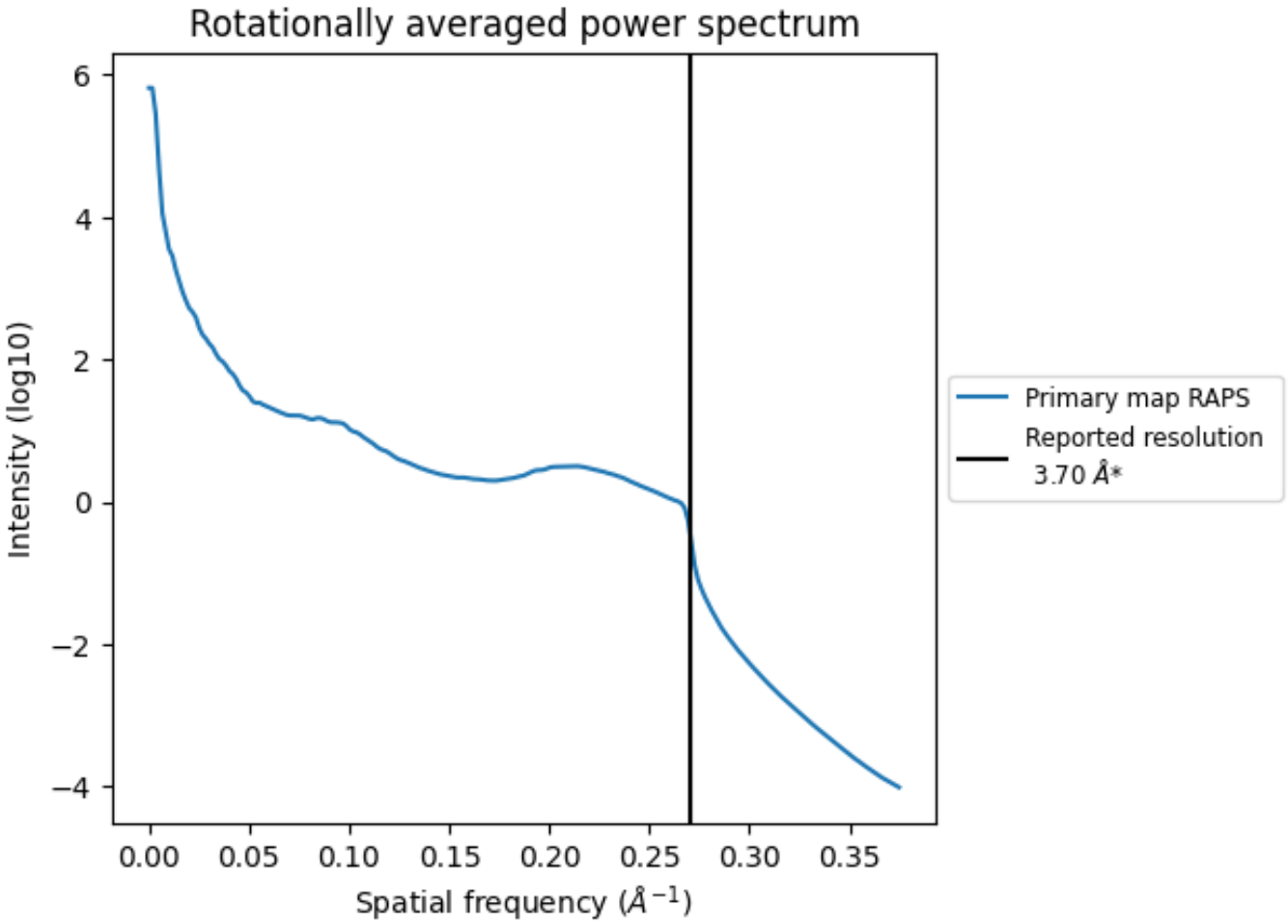
7.2 Volume estimate (i)



The volume at the recommended contour level is 2043 nm^3; this corresponds to an approximate mass of 1845 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 0.270 Å^{-1}

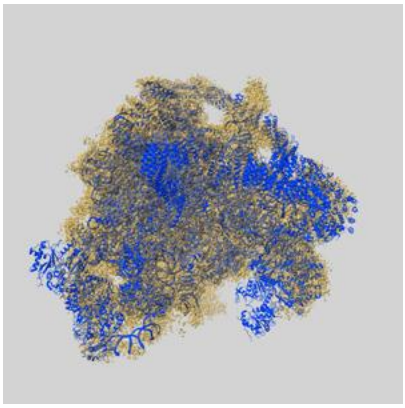
8 Fourier-Shell correlation (i)

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

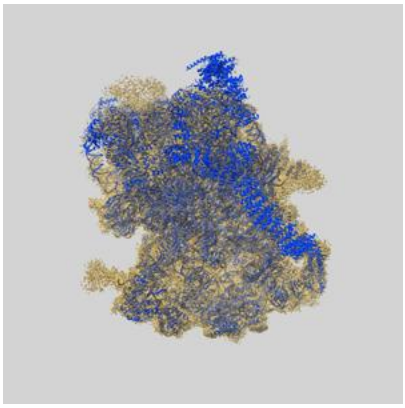
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-0954 and PDB model 6LQU. Per-residue inclusion information can be found in section 3 on page 17.

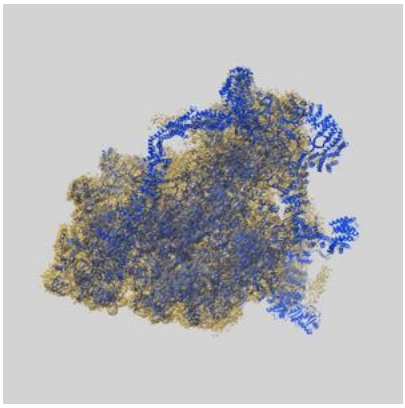
9.1 Map-model overlay



X



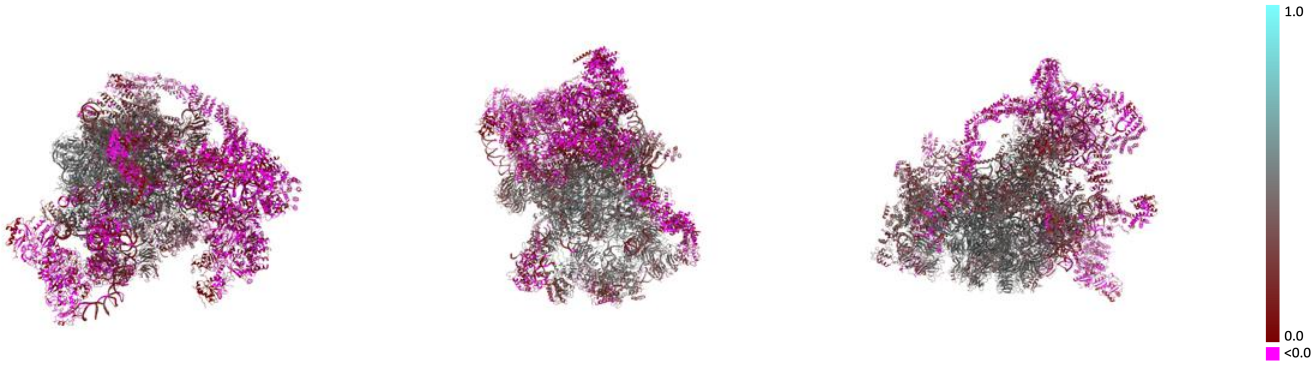
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.018 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.

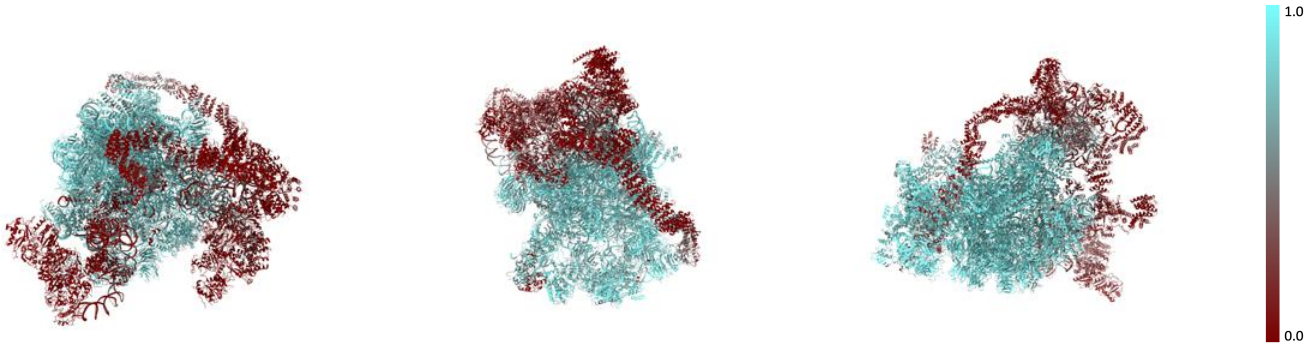
9.2 Q-score mapped to coordinate model



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.

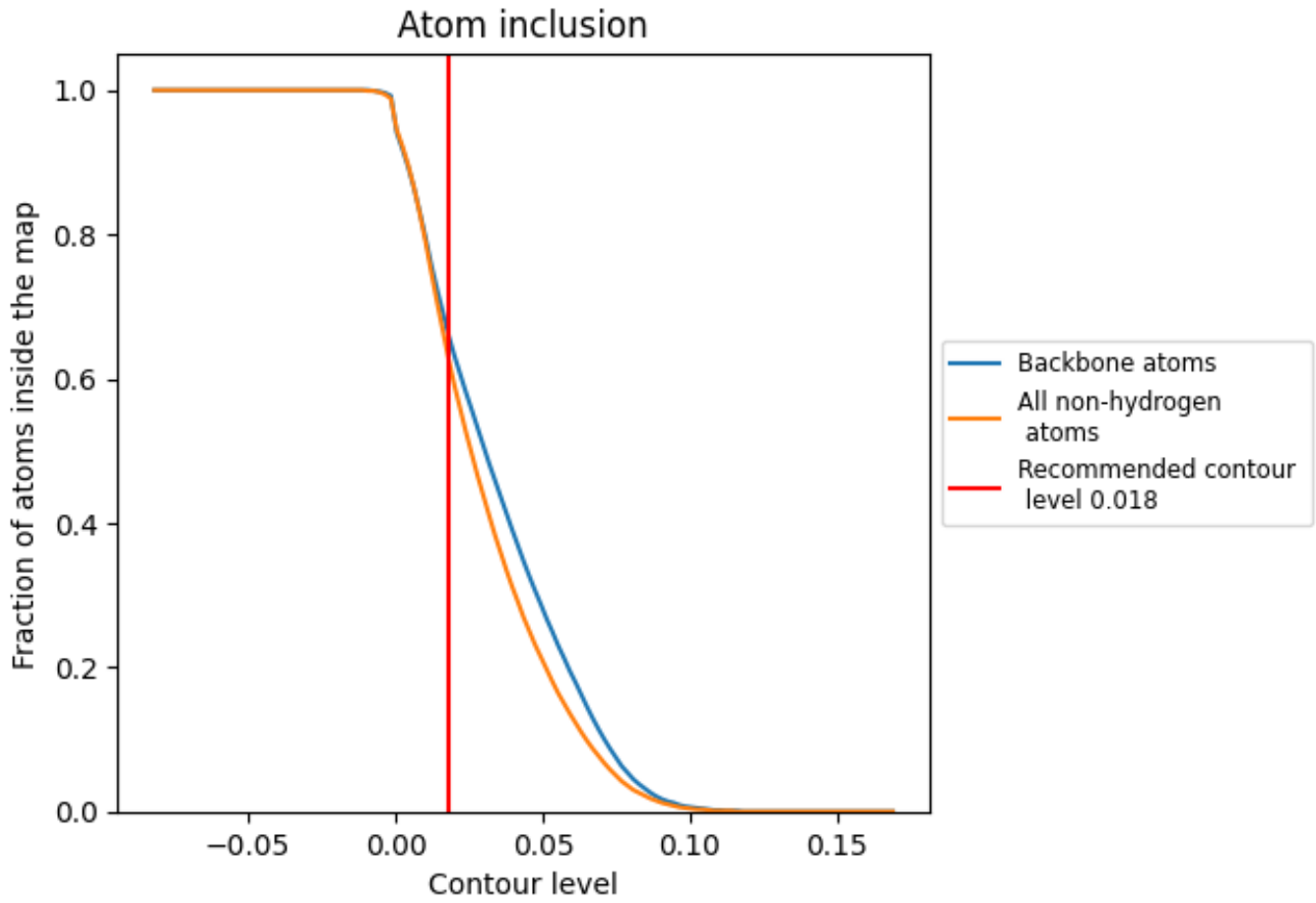
9.3 Atom inclusion mapped to coordinate model



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 (0.018).

9.4 Atom inclusion (i)



At the recommended contour level, 66% of all backbone atoms, 63% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6280	0.2690
3A	0.9450	0.3580
3B	0.8700	0.4390
3C	0.8510	0.3850
3D	0.8320	0.3650
3E	0.8690	0.3710
3F	0.7670	0.2850
3G	0.8900	0.4580
3H	0.8100	0.3790
5A	0.9200	0.3530
5B	0.8100	0.3420
5C	0.8110	0.4140
5D	0.8680	0.4210
5E	0.8260	0.4090
5F	0.8930	0.4730
5G	0.8470	0.4460
5H	0.8480	0.3810
5I	0.8650	0.4100
5J	0.7470	0.3500
5K	0.8390	0.4160
A4	0.8900	0.4110
A5	0.8900	0.4370
A8	0.7920	0.2170
A9	0.8720	0.3140
AE	0.4050	0.1610
AF	0.9130	0.4650
AG	0.8930	0.4240
B1	0.9070	0.4800
B2	0.8400	0.3490
B3	0.4800	0.1390
B6	0.7930	0.3160
B8	0.9110	0.4700
BE	0.9070	0.4710
RA	0.1100	-0.0100
RB	0.5240	0.2010

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
RC	0.1760	-0.0000
RD	0.1130	0.1140
RE	0.0280	-0.0040
RF	0.0010	-0.0160
RG	0.8060	0.3430
RH	0.8550	0.4220
RI	0.8890	0.4180
RJ	0.8160	0.3800
RK	0.8360	0.3870
RL	0.1390	0.0650
RM	0.0430	0.0070
RN	0.7750	0.3080
RO	0.8690	0.3620
RP	0.0370	0.0250
RQ	0.6370	0.3100
RS	0.6340	0.1090
RT	0.7450	0.3090
RV	0.1170	0.1620
RW	0.8150	0.3760
RY	0.0210	-0.0030
SA	0.5710	0.1800
SF	0.3800	0.1180
SG	0.8880	0.4590
SH	0.1570	0.0180
SI	0.1280	0.1320
SJ	0.2300	0.0170
SK	0.8150	0.3670
SM	0.2660	-0.0210
SN	0.1370	0.0140
SO	0.0360	-0.0160
SP	0.1510	0.0180
SR	0.9140	0.4870
ST	0.7880	0.3280
SX	0.3450	0.2490
SY	0.8130	0.3940
SZ	0.5510	0.2020
Sd	0.8870	0.4620
X1	0.7640	0.2960