wwPDB EM Validation Summary Report (i)

Mar 26, 2026 – 06:01 AM UTC

PDB ID	:	6LQR / pdb_00006lqr
EMDB ID	:	EMD-0951
Title	:	Cryo-EM structure of 90S small subunit preribosomes in transition states (State C)
Authors	:	Du, Y.; Ye, K.
Deposited on	:	2020-01-14
Resolution	:	8.60 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:

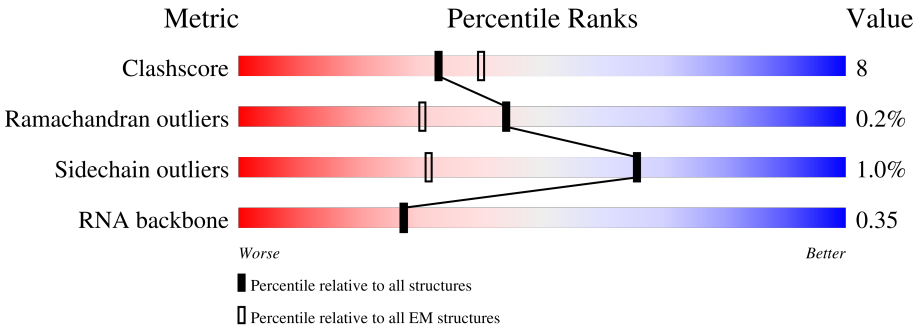
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

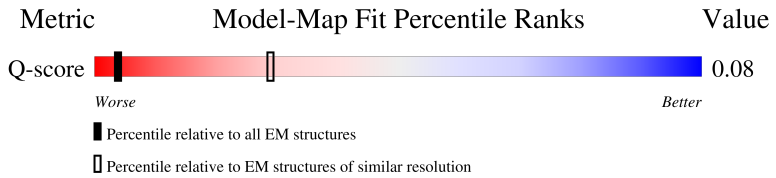
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 8.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	292 (8.10 - 9.10)

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	• 29% 17% 5% • 47%
2	5A	700	9% 16% 9% • 73%
3	SA	1809	15% 34% 30% 6% 29%

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Mol	Chain	Length	Quality of chain
4	SC	255	36% 71% 19% 10%
5	SF	261	11% 64% 22% • 12%
6	SG	225	7% 81% 14% 5%
7	SH	236	24% 54% 17% 29%
8	SI	190	16% 66% 19% • 13%
9	SJ	200	20% 55% 28% 17%
10	SK	197	5% 75% 12% 13%
11	SM	156	8% 52% 27% 21%
12	SO	151	17% 79% 9% • 11%
13	SP	137	26% 68% 17% • 14%
14	SR	143	6% 71% 16% 13%
15	SX	130	25% 82% 15% • •
16	SY	145	13% 63% 7% • 29%
17	SZ	135	10% 59% 15% • 24%
18	Sc	82	34% 83% 13% • •
19	Sd	67	7% 88% 6% 6%
20	3B	327	• 61% 13% 27%
20	3C	327	17% 52% 17% 31%
21	3D	504	• 60% 13% 27%
22	3E	511	21% 66% 18% 16%
23	3F	573	5% 61% 18% 21%
24	3G	126	11% 80% 16% •
24	3H	126	6% 75% 21% •
25	A4	776	20% 65% 20% 15%
26	A5	643	28% 65% 15% 20%

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Mol	Chain	Length	Quality of chain
27	A8	713	33% 62% 11% • 25%
28	A9	575	11% 17% 5% 78%
29	AE	1769	54% 77% 9% 13%
30	AF	513	43% 75% 20% •
31	AG	896	24% 71% 21% 8%
32	B1	923	• 70% 16% • 14%
33	B2	943	9% 66% 21% • 13%
34	B3	817	12% 66% 25% • 7%
35	B8	594	8% 66% 14% 20%
36	BE	939	5% 73% 14% 13%
37	B6	440	8% 75% 10% 15%
38	5B	214	24% 21% 7% 72%
39	5C	554	9% 66% 17% 17%
40	5D	250	34% 56% 11% 33%
41	5E	593	• 19% 11% • 67%
42	5F	183	8% 63% 36% ••
43	5G	290	14% 58% 17% • 24%
44	5H	610	• 11% • 88%
45	5I	489	5% 72% 22% • 6%
46	5J	217	23% 57% 13% 30%
47	5K	189	9% 79% 14% 7%
48	RA	707	15% 35% 12% • 52%
49	RB	357	• 27% 11% 62%
50	RD	1729	17% 15% • 82%
51	RE	1237	33% 64% 23% 13%

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Mol	Chain	Length	Quality of chain
52	RF	297	47% 61% 20% 19%
53	RG	252	74% 62% 23% 14%
53	RH	252	76% 73% 18% 9%
54	RJ	1183	11% 54% 13% 33%
55	RK	367	10% 76% 22%
56	RL	1056	52% 71% 5% 24%
56	RM	1056	62% 71% 27%
57	RN	810	66% 61% 14% 25%
58	RO	552	94% 82% 13% 5%
59	RP	2493	31% 79% 5% 15%
60	RQ	899	10% 22% 75%
61	RS	483	49% 36% 16% 48%
62	RT	326	22% 40% 10% 48%
63	RY	534	6% 93%
64	X1	347	5% 94%

2 Entry composition (i)

There are 67 unique types of molecules in this entry. The entry contains 215267 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called U3 snoRNA.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	SA	1283	27362	12228	4872	8979	1283	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 21 is a protein called Nucleolar protein 56.

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

- Molecule 22 is a protein called Nucleolar protein 58.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 45 is a protein called Protein SOF1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	5J	151	1280	807	240	228	5	0	0

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

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

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

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

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

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

- Molecule 50 is a protein called rRNA biogenesis protein RRP5.

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

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 52 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 53 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 54 is a protein called Ribosome biogenesis protein BMS1.

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

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

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

- Molecule 56 is a protein called RNA cytidine acetyltransferase.

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

- Molecule 57 is a protein called Nucleolar complex protein 14.

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

- Molecule 58 is a protein called Nucleolar complex protein 4.

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

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 20.

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

- Molecule 60 is a protein called U3 small nucleolar RNA-associated protein 14.

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

- Molecule 61 is a protein called Essential nuclear protein 1.

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

- Molecule 62 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	RT	169	1334	849	244	237	4	0	0

- Molecule 63 is a protein called Protein BFR2.

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

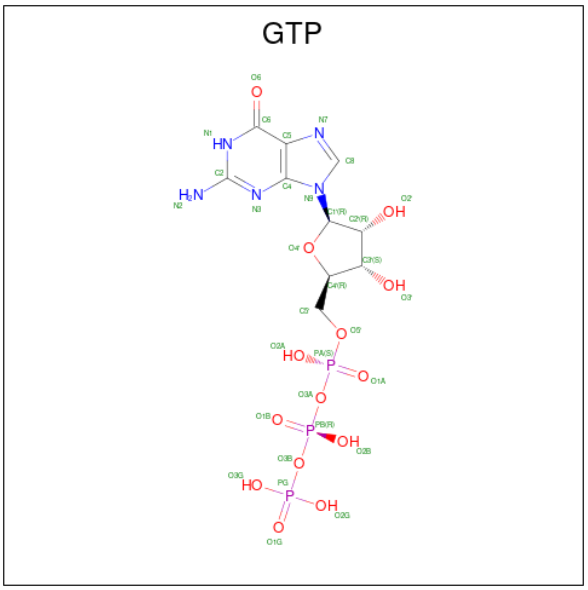
- Molecule 64 is a protein called Unassigned helices.

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

- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
65	Sc	1	1	1	0
			Total	Zn	
65	5K	1	1	1	0

- Molecule 66 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

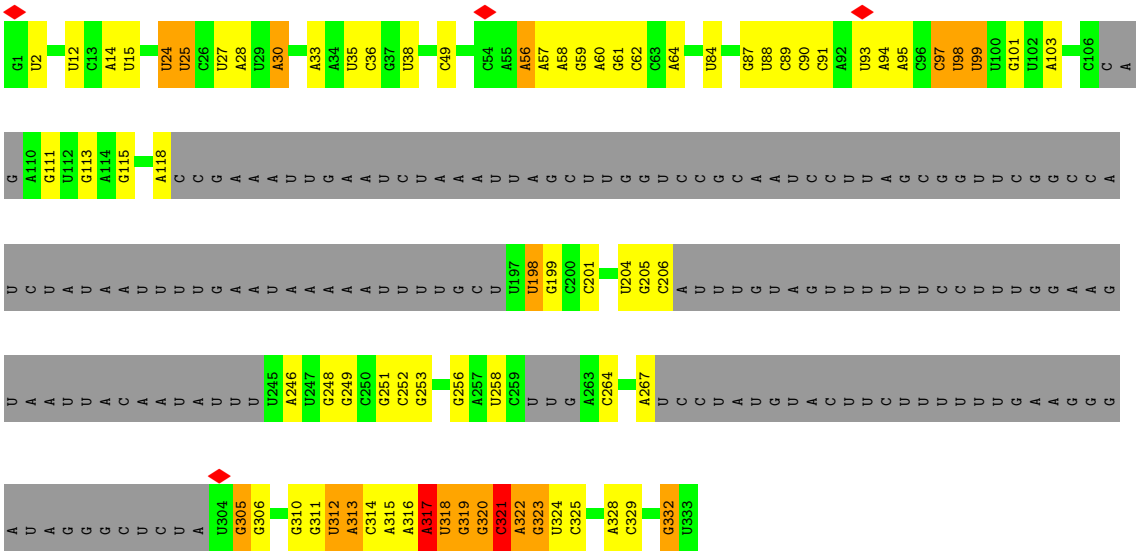
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
67	RJ	1	1	1	0

3 Residue-property plots (i)

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

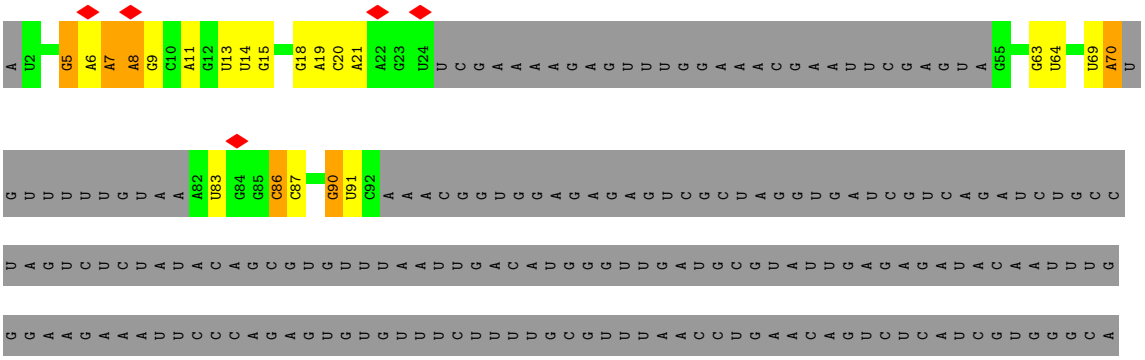
- Molecule 1: U3 snoRNA

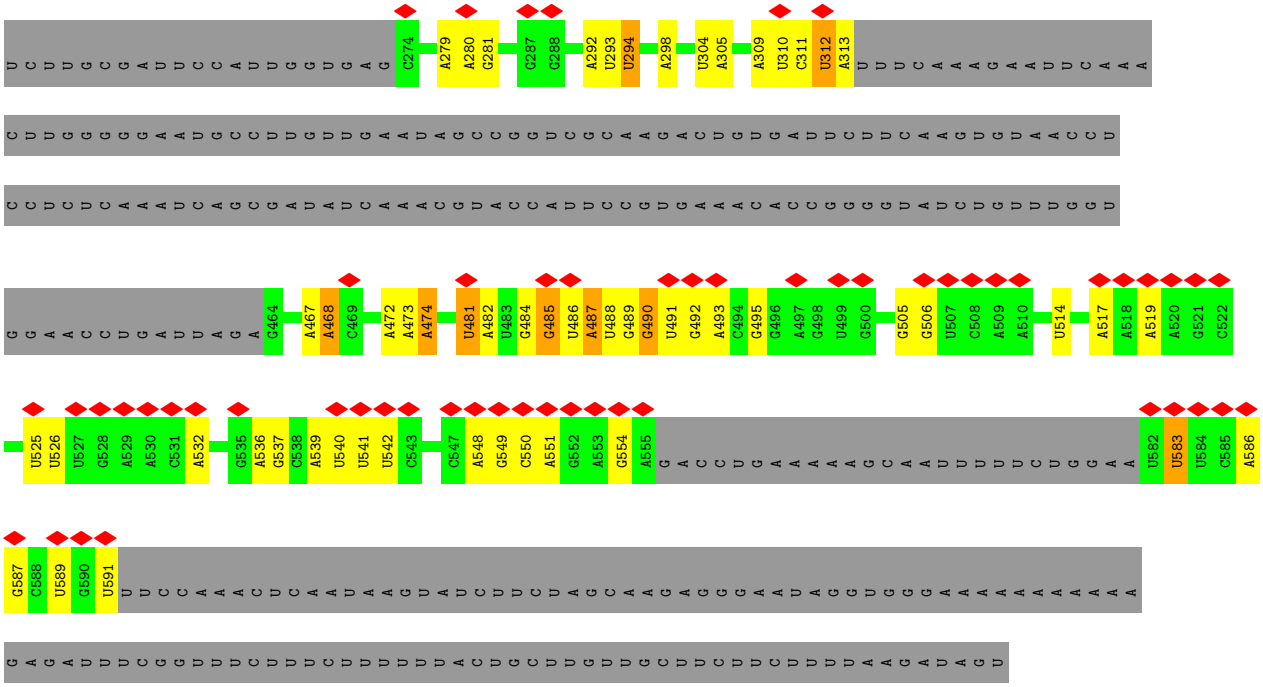
Chain 3A: 29% 17% 5% 47%



- Molecule 2: 5' ETS

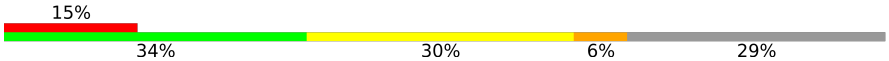
Chain 5A: 9% 16% 9% 73%

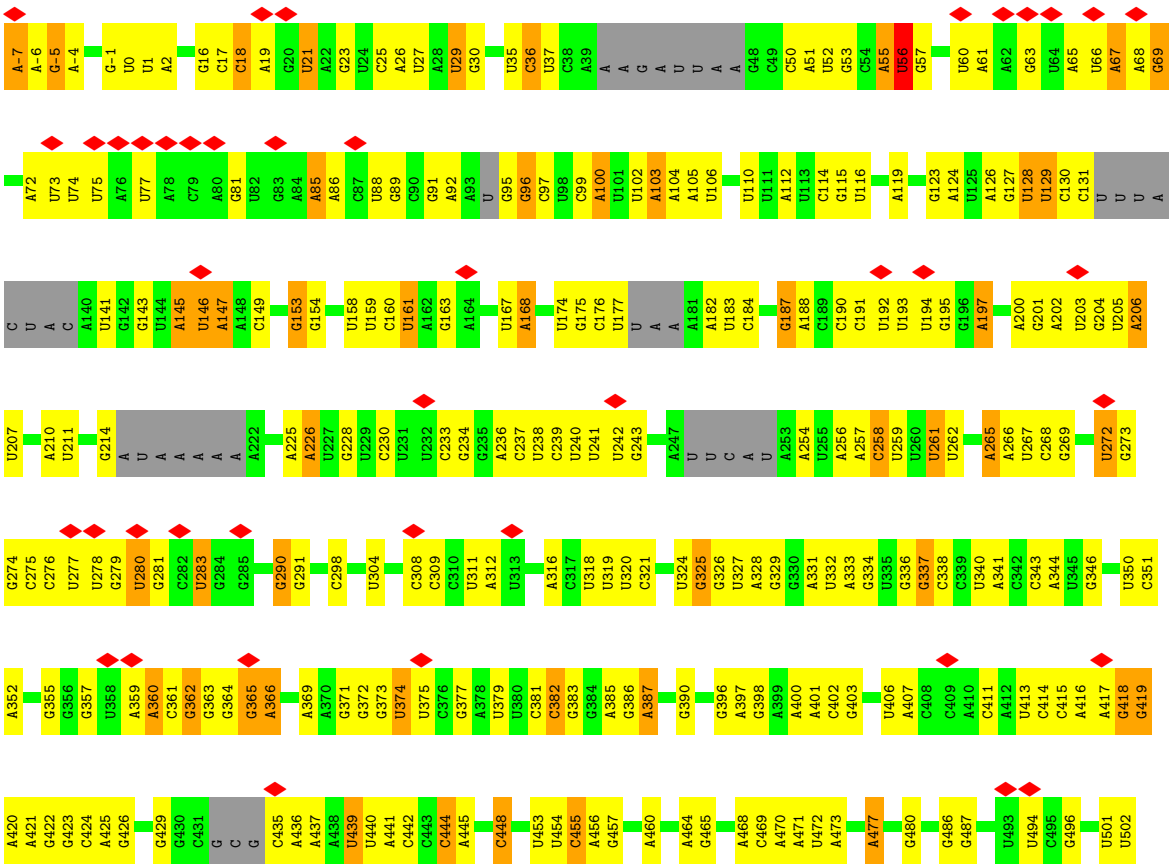


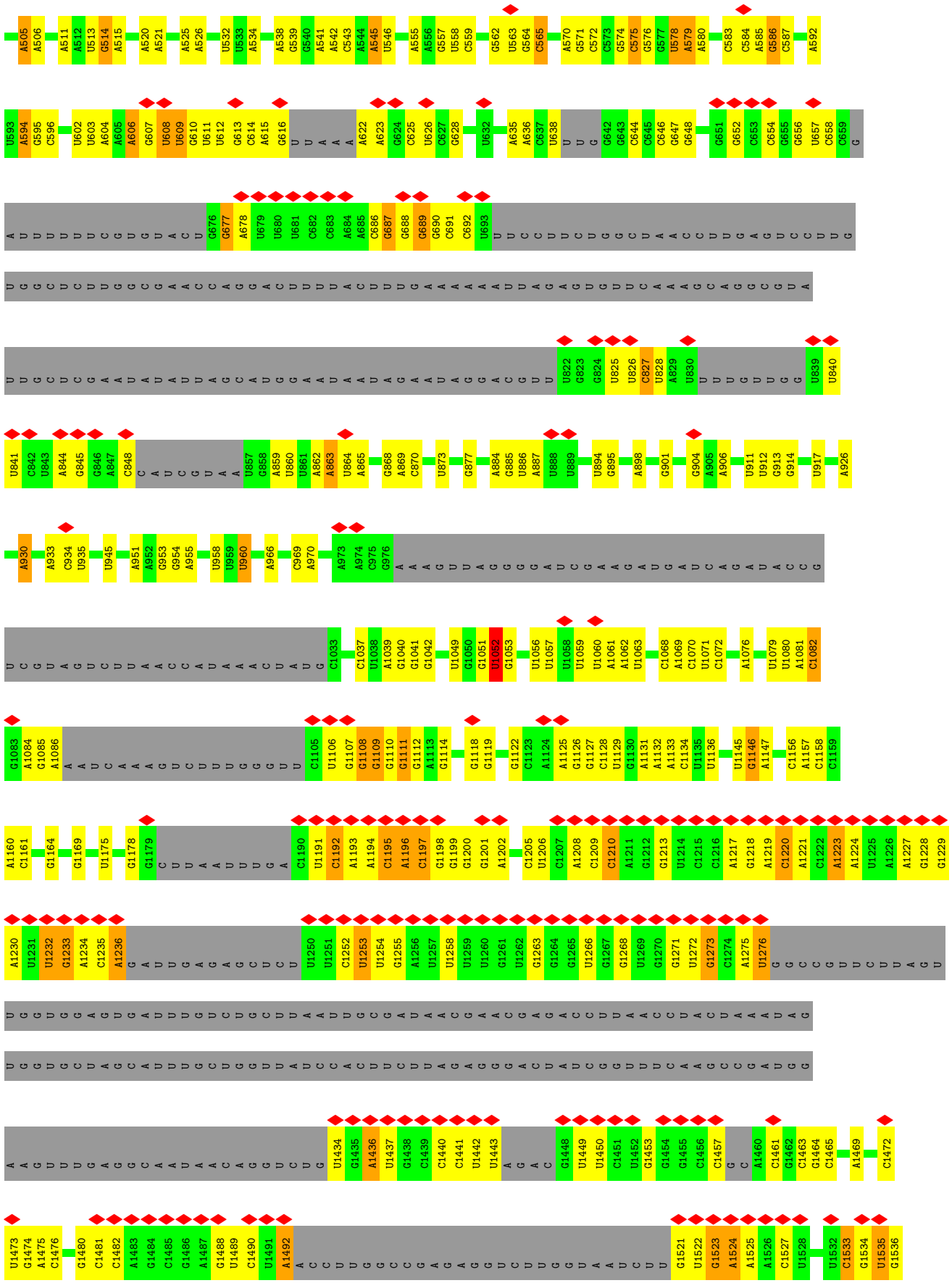


- Molecule 3: 18S pre-rRNA

Chain SA:



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U593 A594 G595 C596 U602 U603 A604 A605 A606 G607 U608 U609 G610 U611 U612 G613 C614 A615 G616 U U A A A622 A623 G624 C625 U626 C627 G628 U632 A635 A636 C637 U638 U U G G642 G643 C644 C645 C646 G647 G648 G651 G652 C653 C654 G655 G656 U657 C658 C659 G
A U U U U U C C G U G U A C U G676 G677 A678 U679 U680 U681 C682 C683 A684 A685 C686 G687 G688 G689 G690 C691 C692 U693 U U C C U U C U G G C A A C C U U G A G A U G G C U C C U U G
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U U G C U U C G A A U A U A U U A G C A U U G G U U A A A U A G A A U A G G A C G U U A G G A U A G U U G G
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G1083 A1084 G1085 A1086 A A U C A A A A G U C U U U G G G G U U C1105 U1106 G1107 G1108 G1109 G1110 G1111 G1112 A1113 G1114 G1118 G1119 G1122 C1123 A1124 A1125 G1126 G1127 C1128 U1129 G1130 A1131 A1132 A1133 C1134 U1135 U1136 U1145 G1146 A1147 C1156 A1157 C1158 C1159
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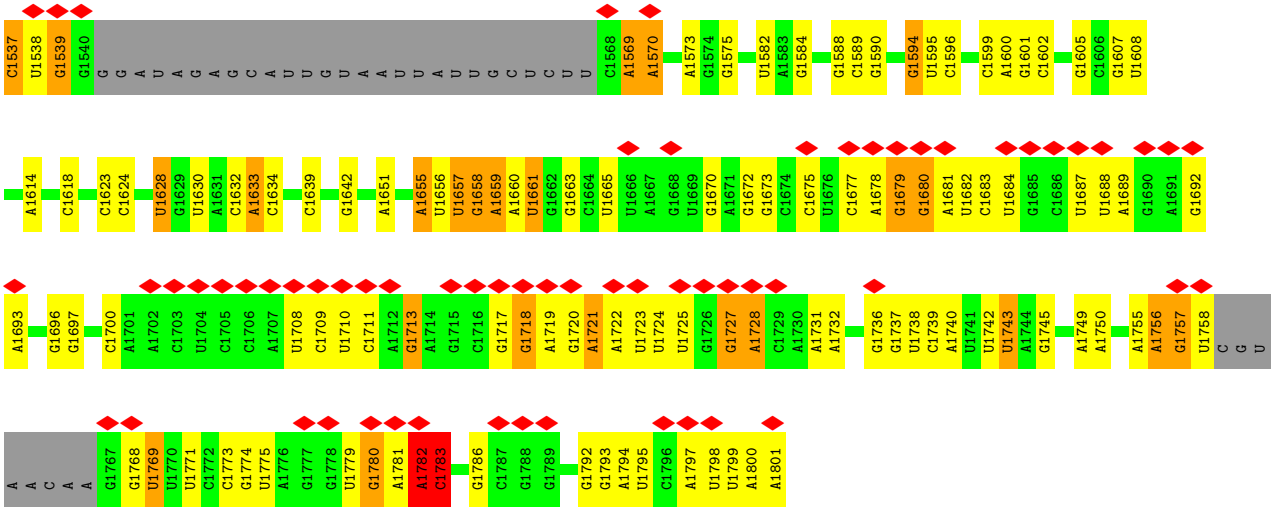
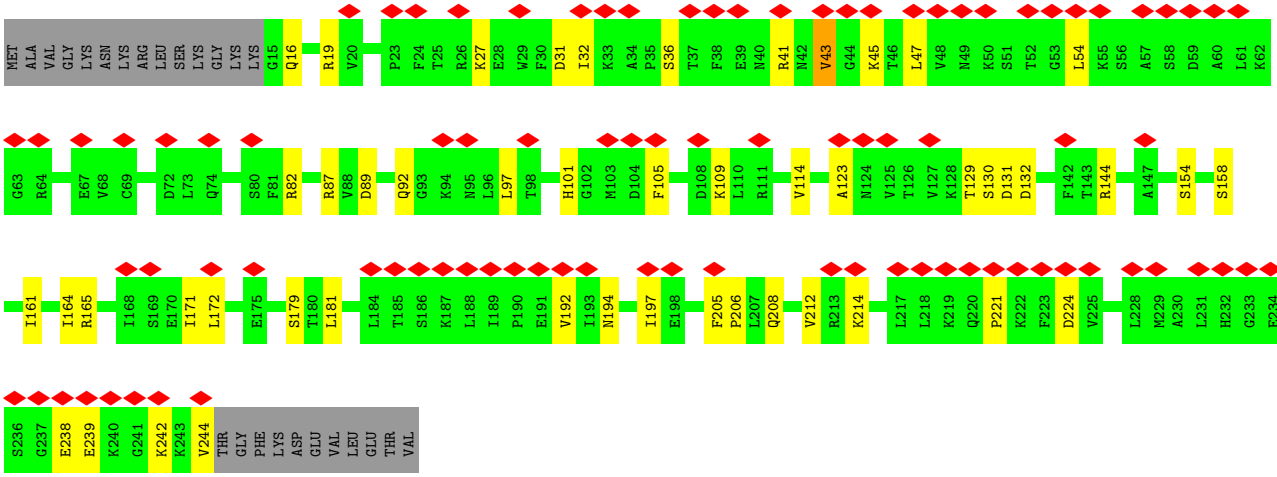
U G G G U G C U A G C A U U G C U A A U C C A C U U A A G G A G G G A C U A U C G G U U C A A G C C G A U G G
A A G U U U G A G U A A C U U G A G A C U U C U U A A G G G U C U U G G U A A U C U U G1434 G1435 A1436 U1437 G1438 C1439 C1440 C1441 U1442 U1443 A G A C G1448 U1449 U1450 C1451 U1452 G1453 G1454 G1455 C1456 C1457 G C A1460 C1461 G1462 C1463 G1464 C1465 A1469 C1472
U1473 G1474 A1475 C1476 G1480 C1481 C1482 A1483 G1484 C1485 G1486 A1487 G1488 U1489 C1490 U1491 A1492 A C U U G G C C G A G A G U C U U G G U A A U C U U G1521 U1522 G1523 A1524 A1525 A1526 C1527 U1528 U1532 C1533 G1534 U1535 G1536



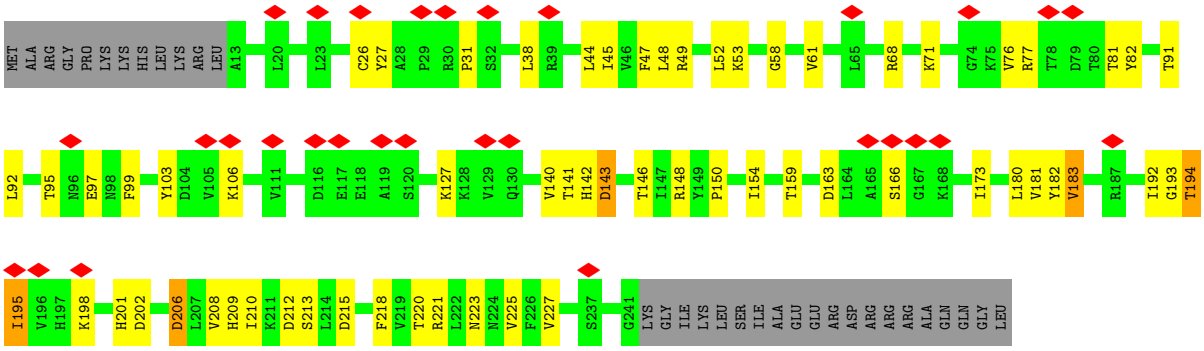
- Molecule 4: 40S ribosomal protein S1-A

Chain SC:



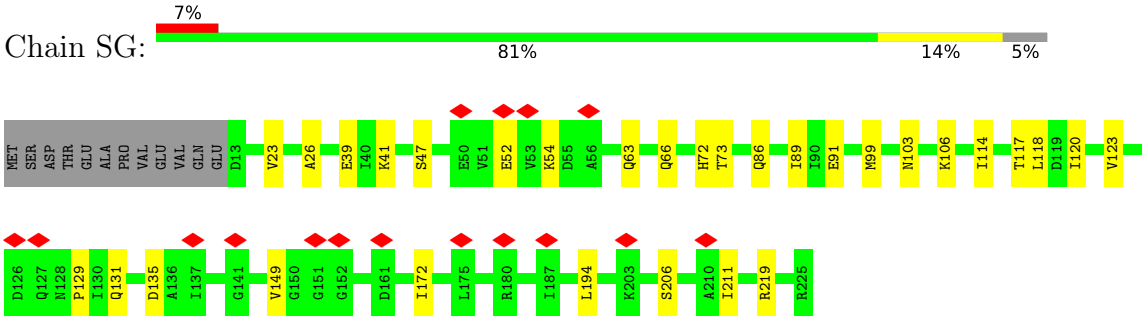
- Molecule 5: 40S ribosomal protein S4-A

Chain SF:



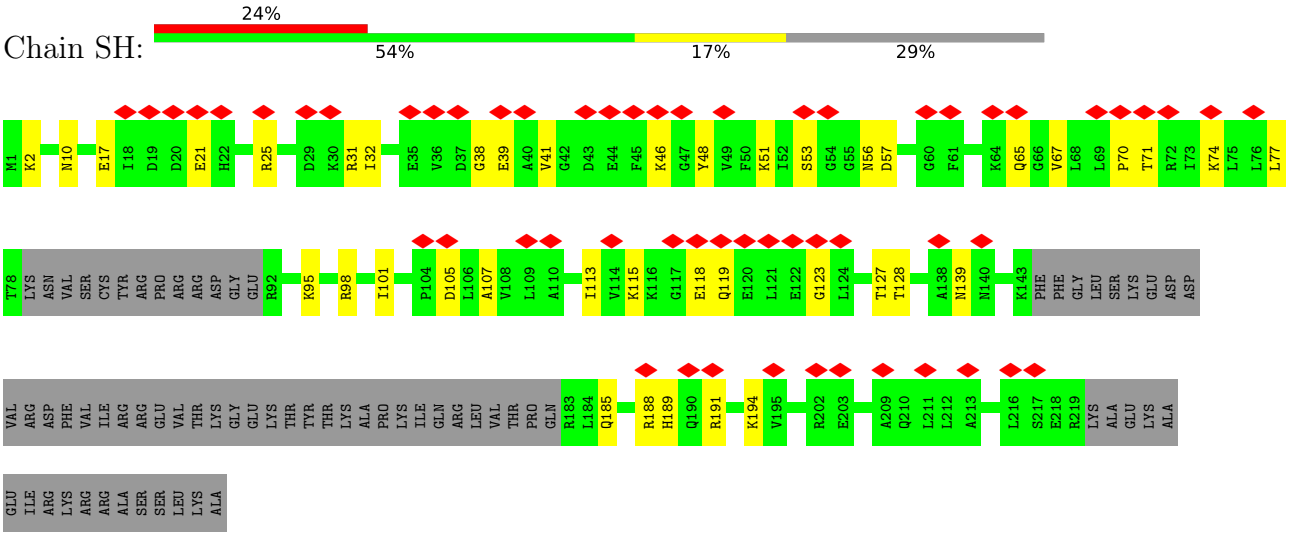
- Molecule 6: 40S ribosomal protein S5

Chain SG:



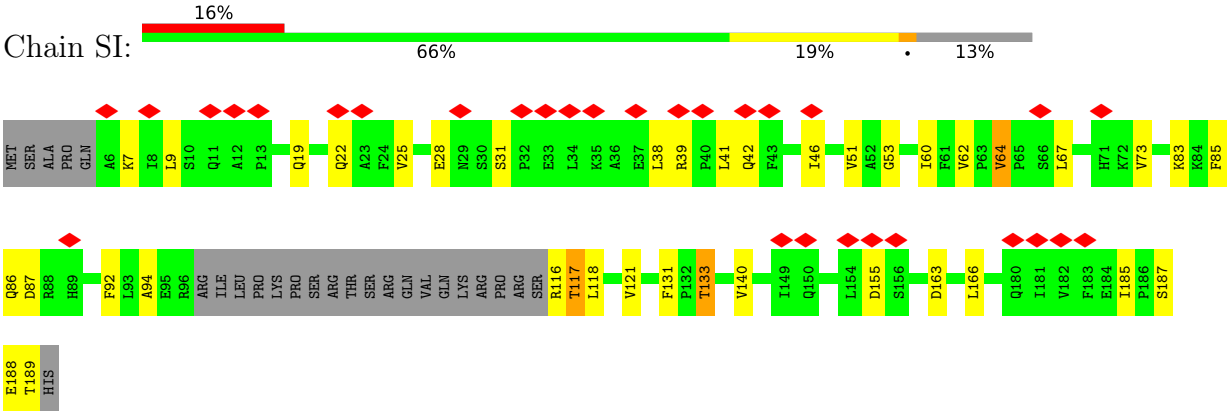
- Molecule 7: 40S ribosomal protein S6-A

Chain SH:



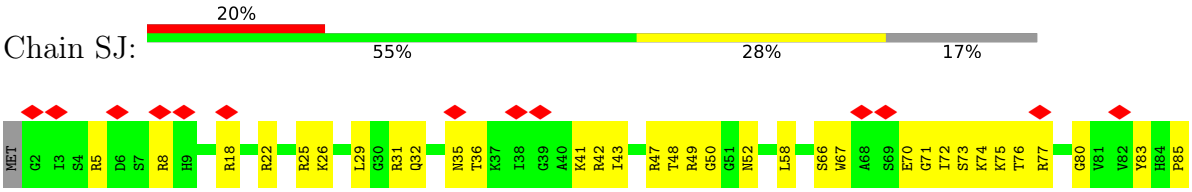
- Molecule 8: 40S ribosomal protein S7-A

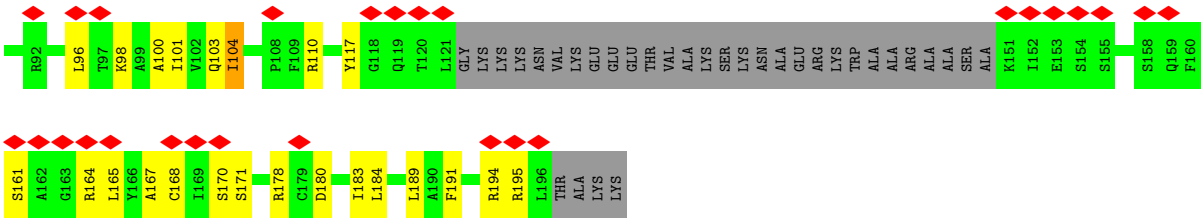
Chain SI:



- Molecule 9: 40S ribosomal protein S8-A

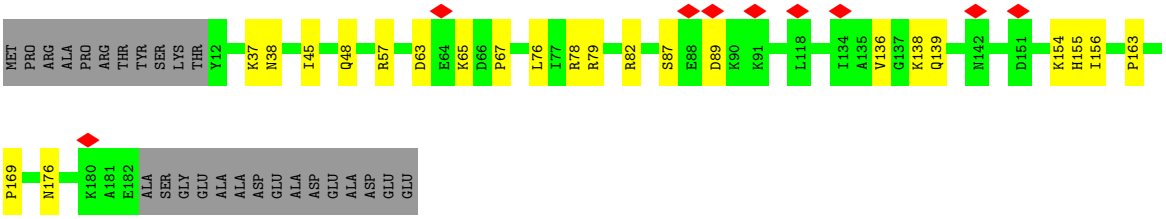
Chain SJ:





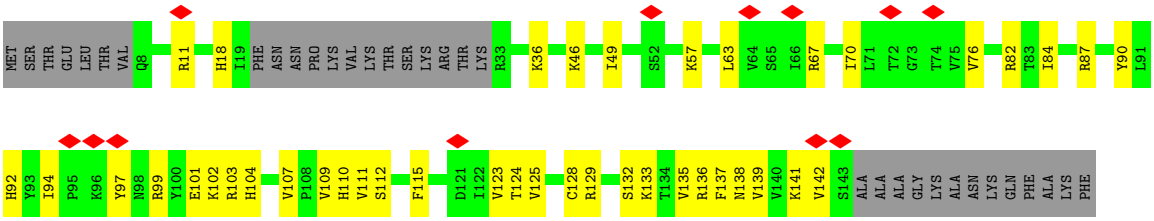
• Molecule 10: 40S ribosomal protein S9-A

Chain SK:



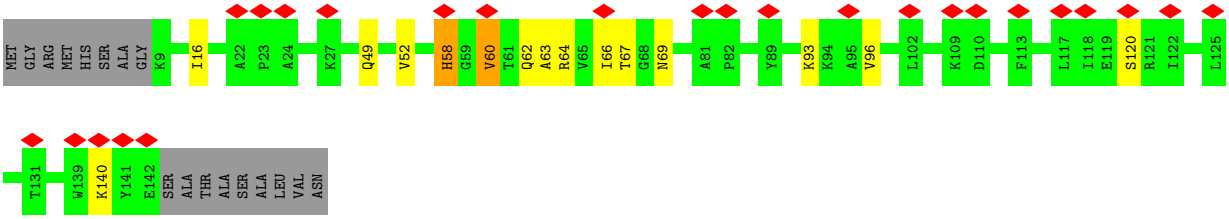
• Molecule 11: 40S ribosomal protein S11-A

Chain SM:



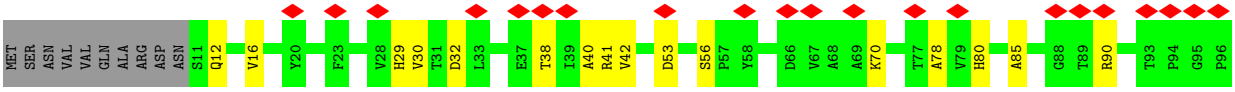
• Molecule 12: 40S ribosomal protein S13

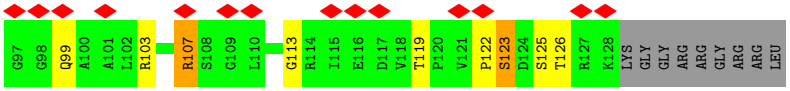
Chain SO:



• Molecule 13: 40S ribosomal protein S14-A

Chain SP:



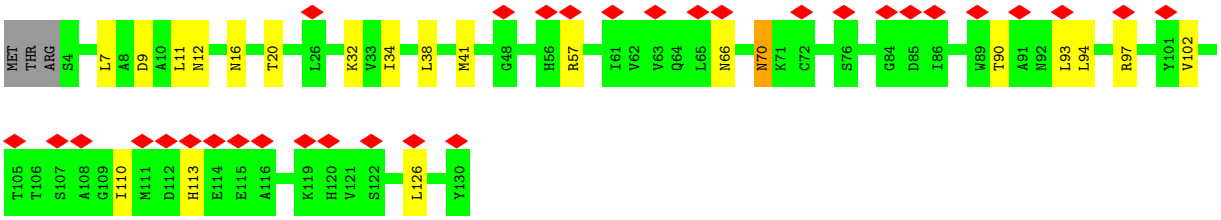


- Molecule 14: 40S ribosomal protein S16-A

Chain SR:

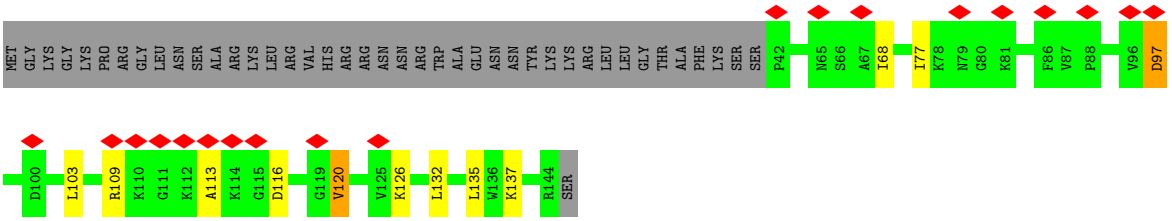
- Molecule 15: 40S ribosomal protein S22-B

Chain SX:



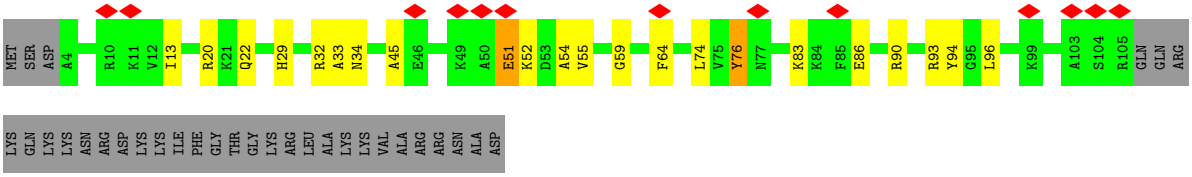
- Molecule 16: 40S ribosomal protein S23-A

Chain SY:



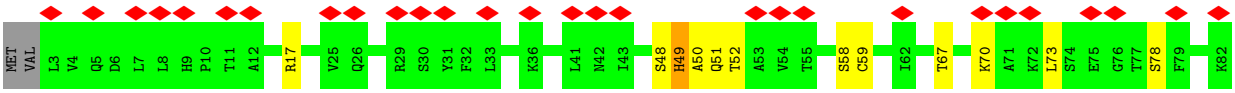
- Molecule 17: 40S ribosomal protein S24-A

Chain SZ:



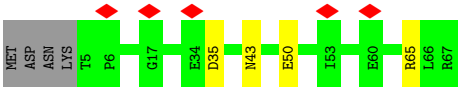
- Molecule 18: 40S ribosomal protein S27-A

Chain Sc:



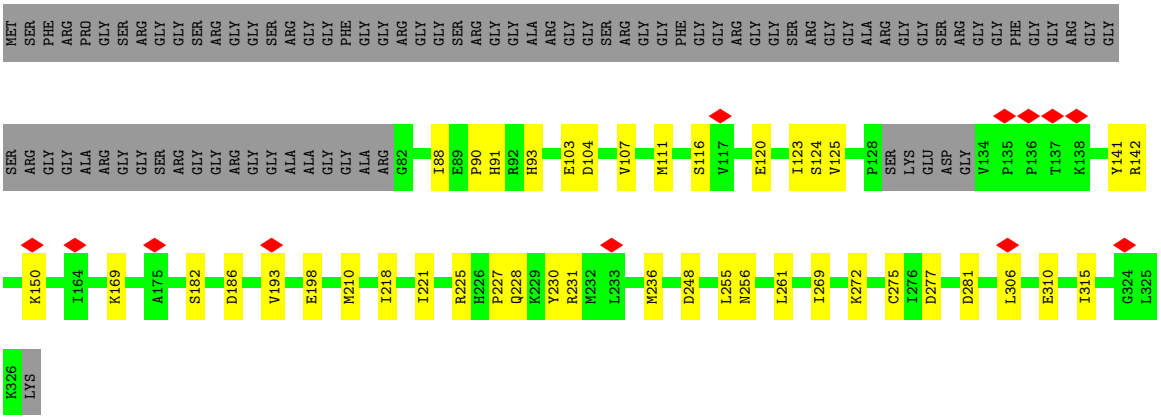
• Molecule 19: 40S ribosomal protein S28-A

Chain Sd:



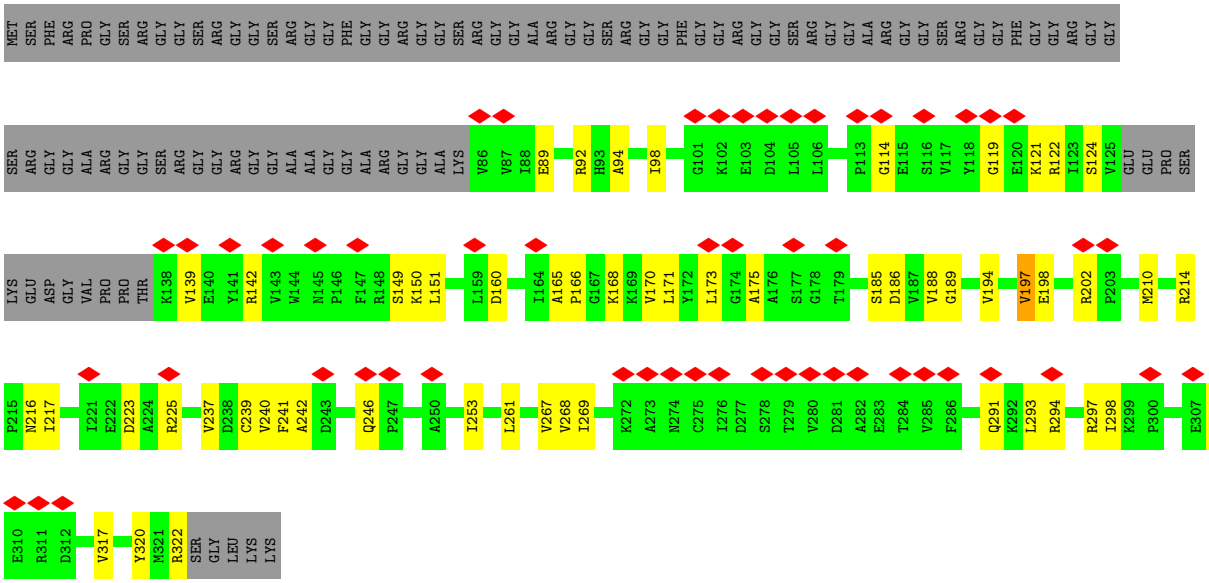
• Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

Chain 3B:

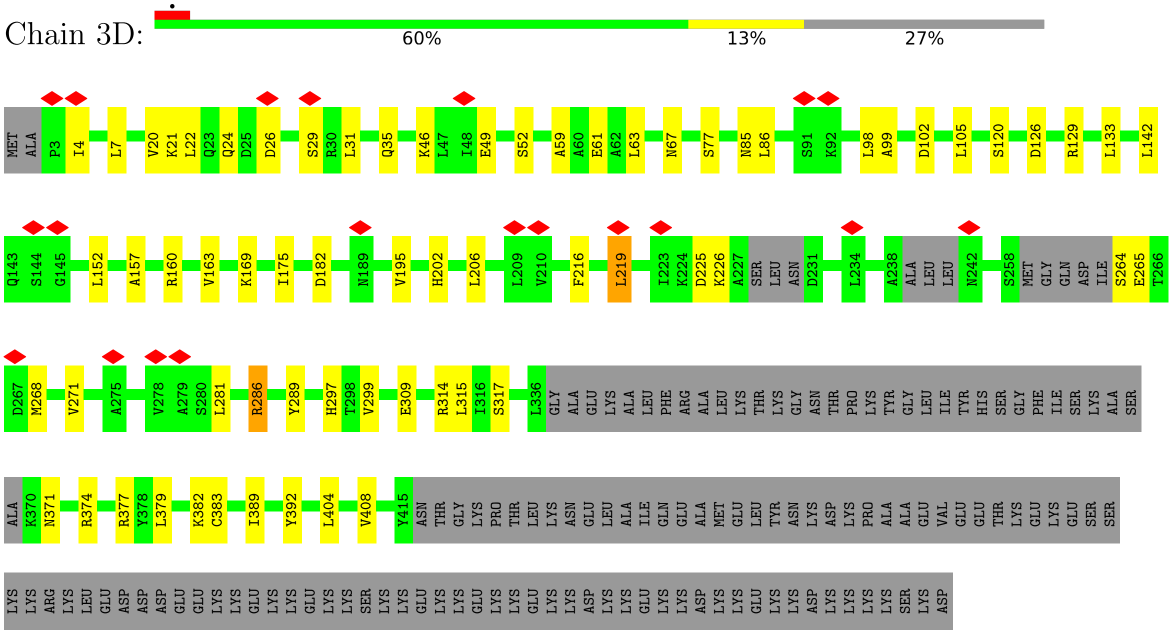


• Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

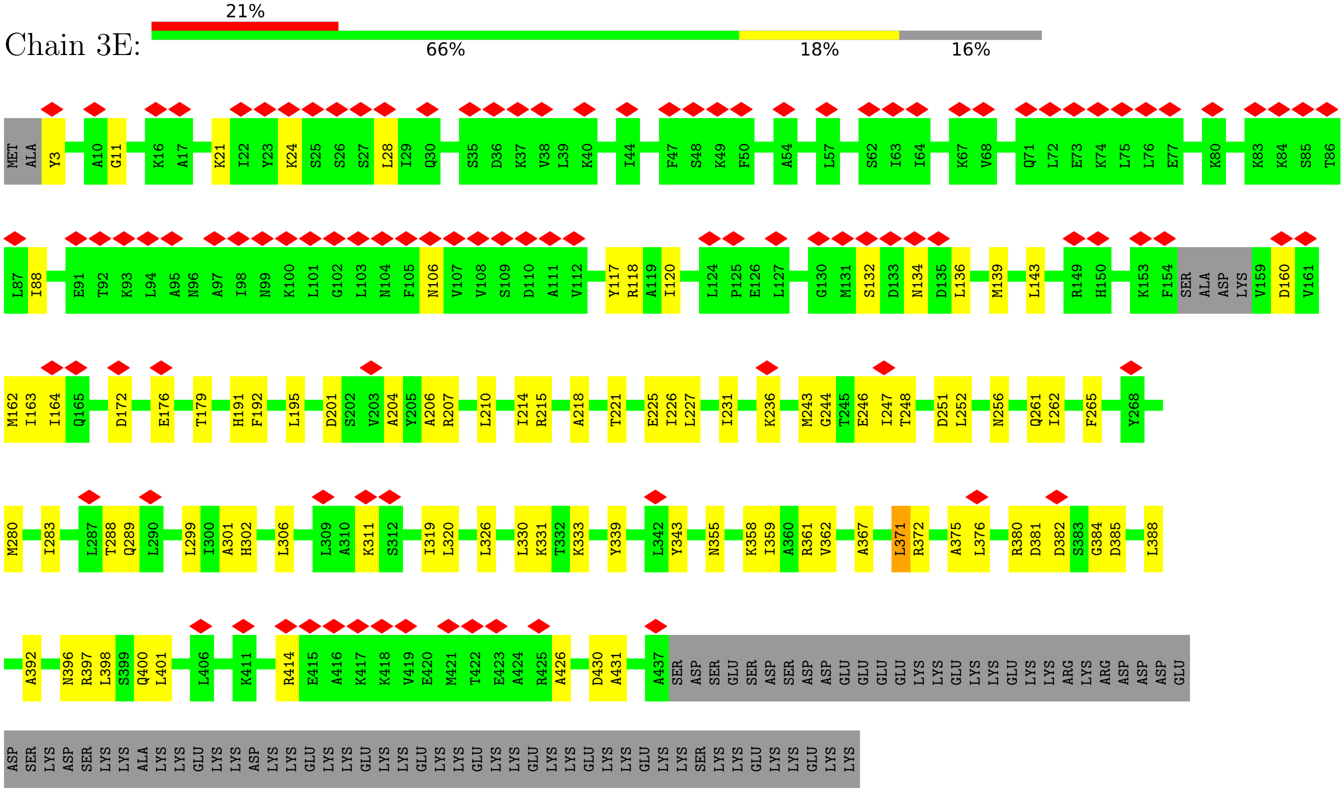
Chain 3C:



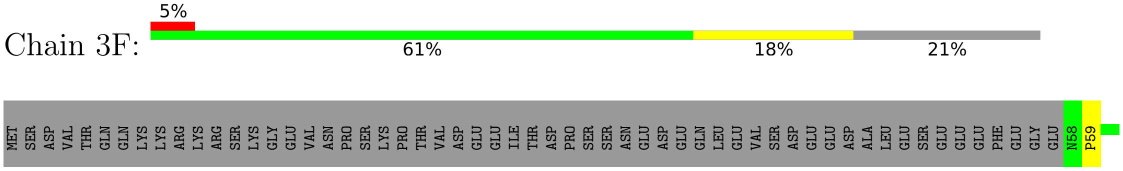
• Molecule 21: Nucleolar protein 56

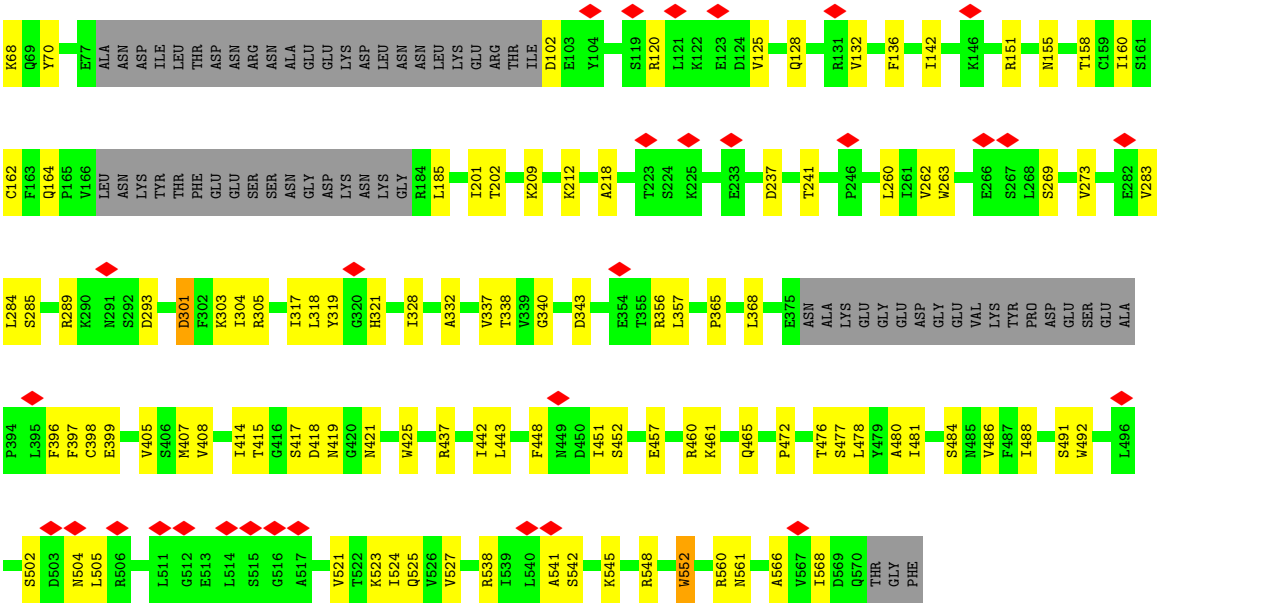


• Molecule 22: Nucleolar protein 58



• Molecule 23: Ribosomal RNA-processing protein 9



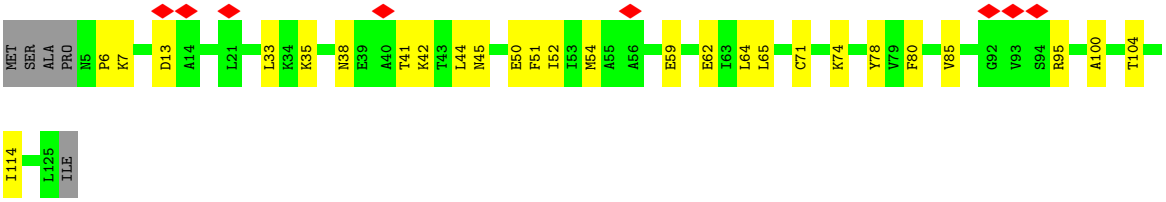


- Molecule 24: 13 kDa ribonucleoprotein-associated protein

Chain 3G:

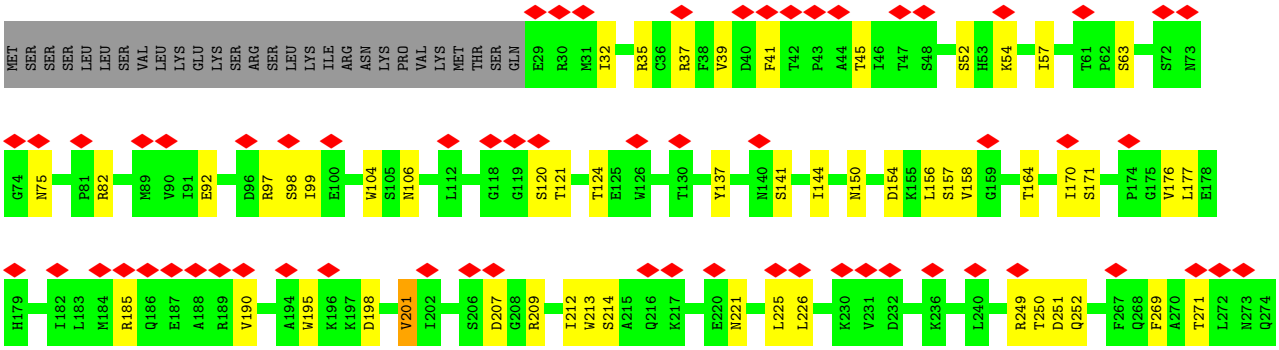
- Molecule 24: 13 kDa ribonucleoprotein-associated protein

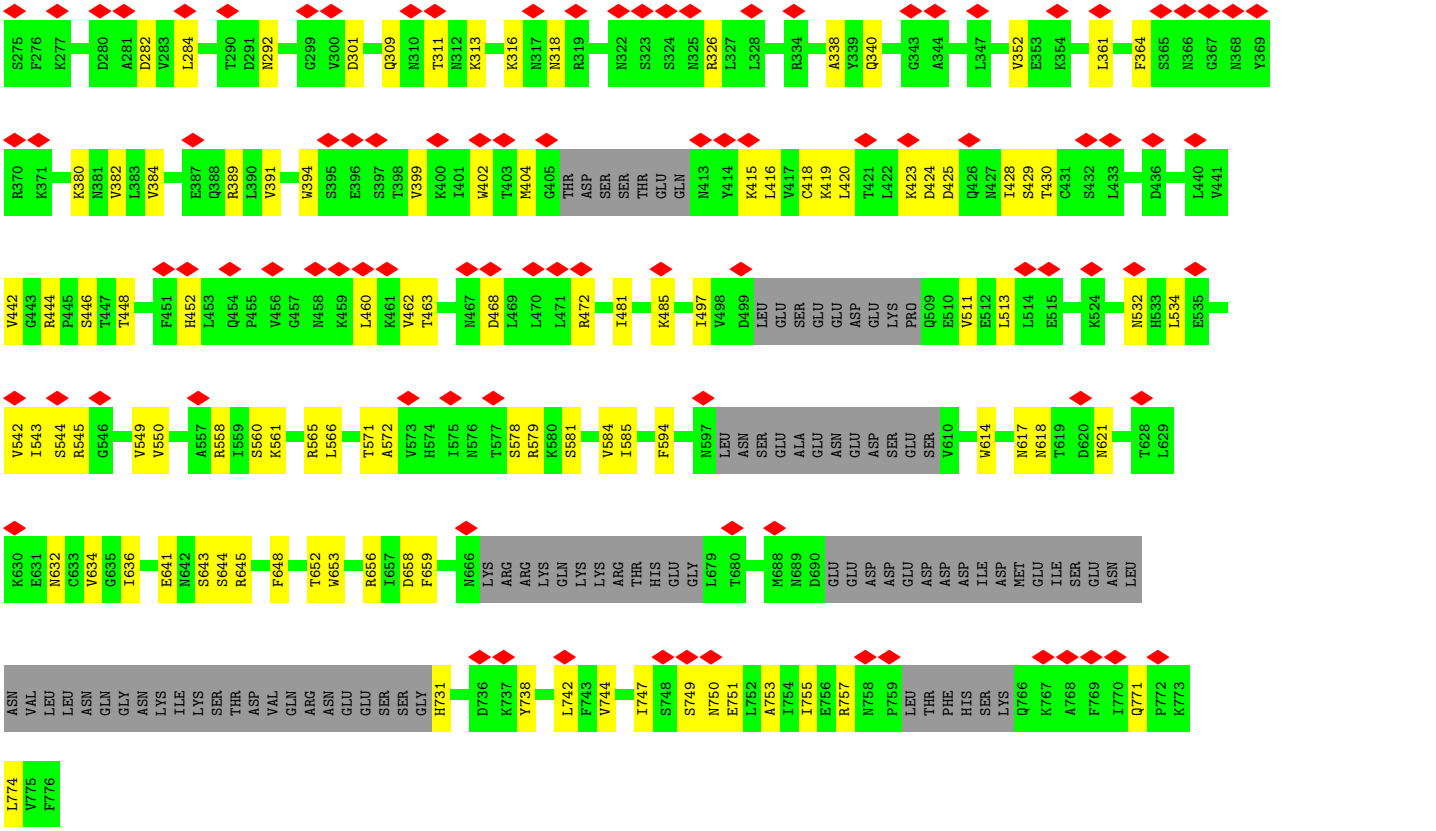
Chain 3H:



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

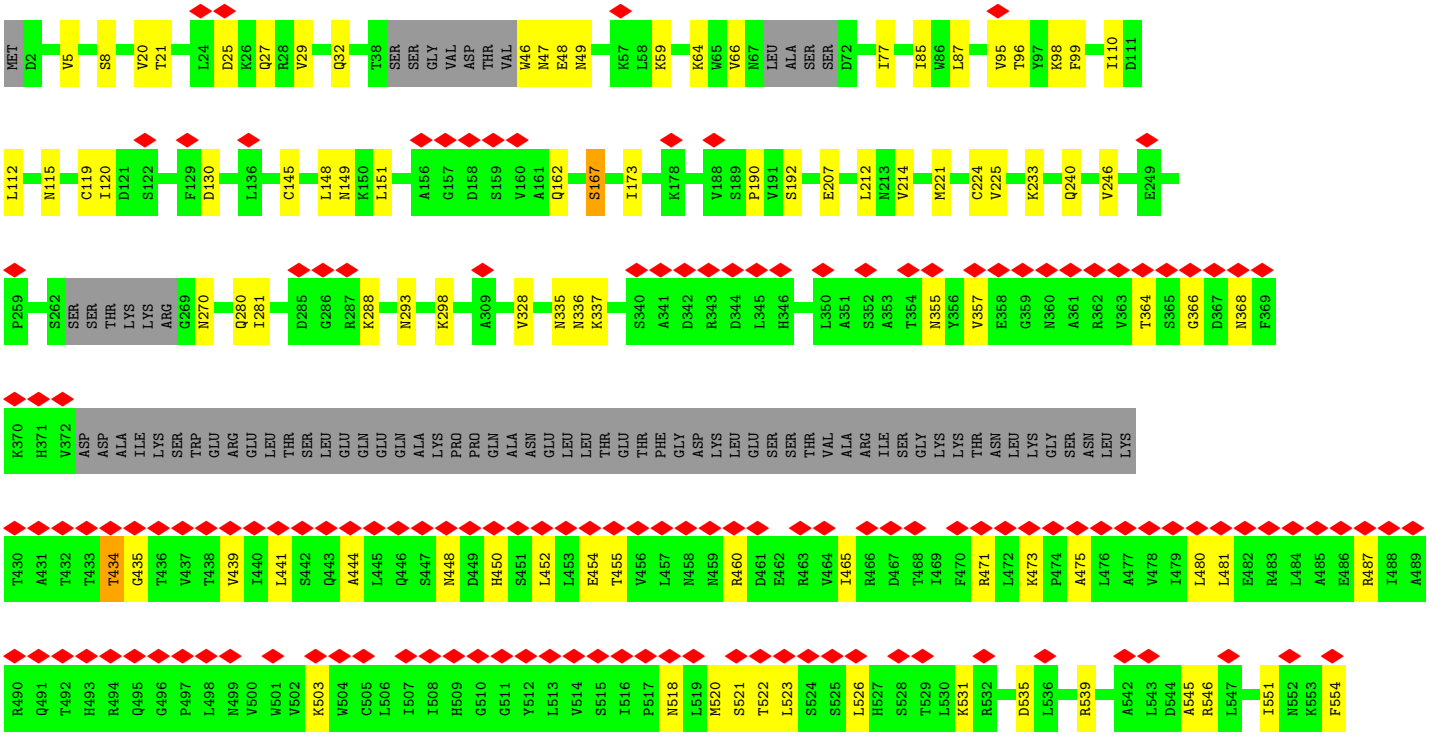
Chain A4:

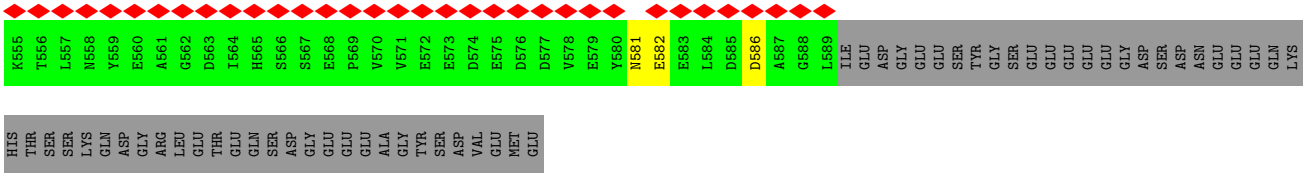




- Molecule 26: U3 small nucleolar RNA-associated protein 5

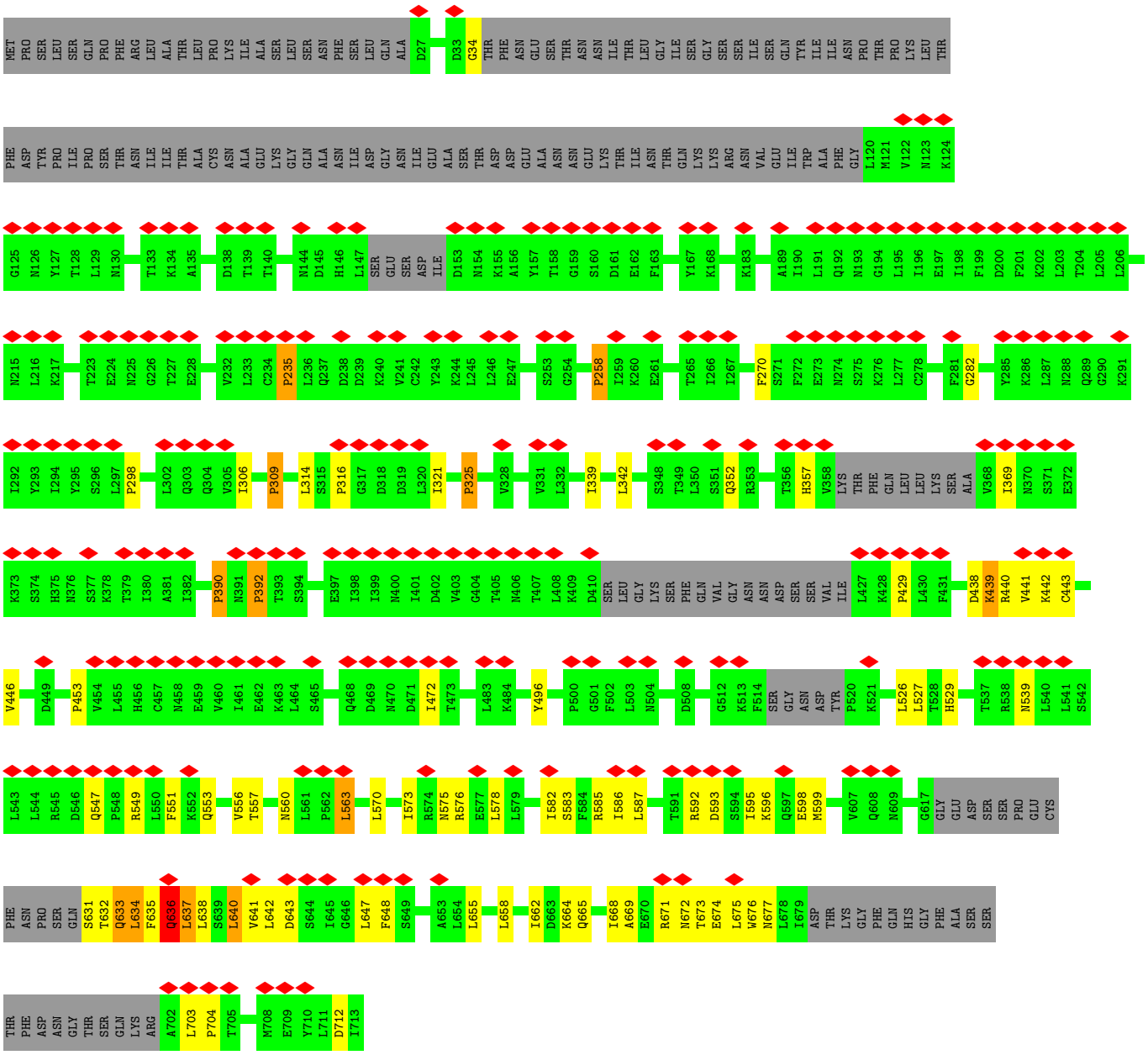
Chain A5:





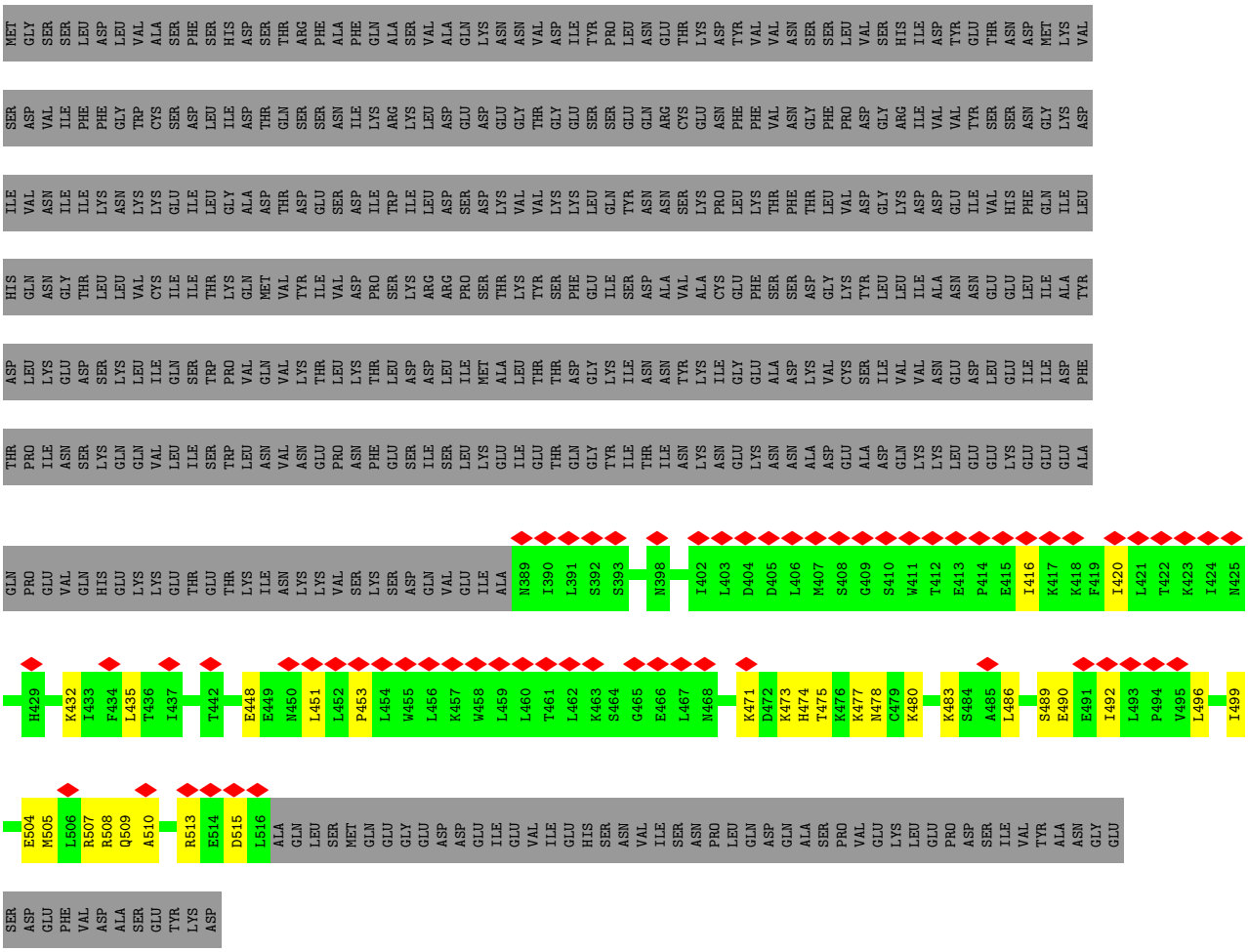
• Molecule 27: U3 small nucleolar RNA-associated protein 8

Chain A8:



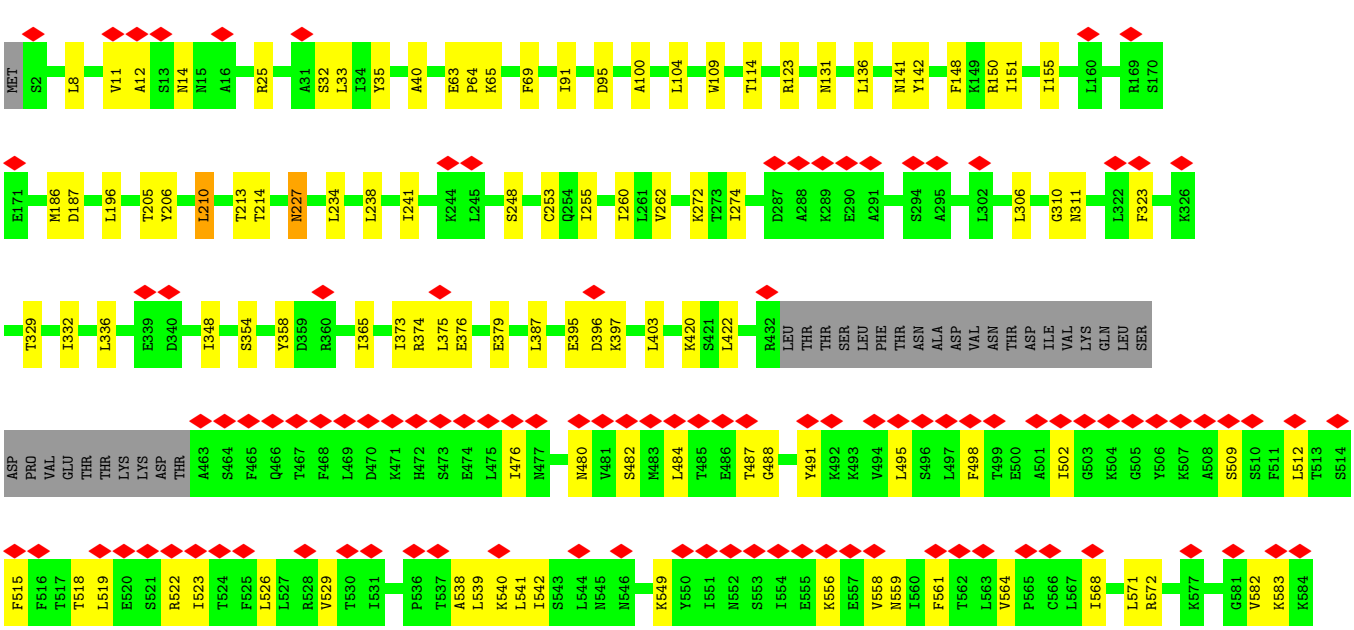
• Molecule 28: U3 small nucleolar RNA-associated protein 9

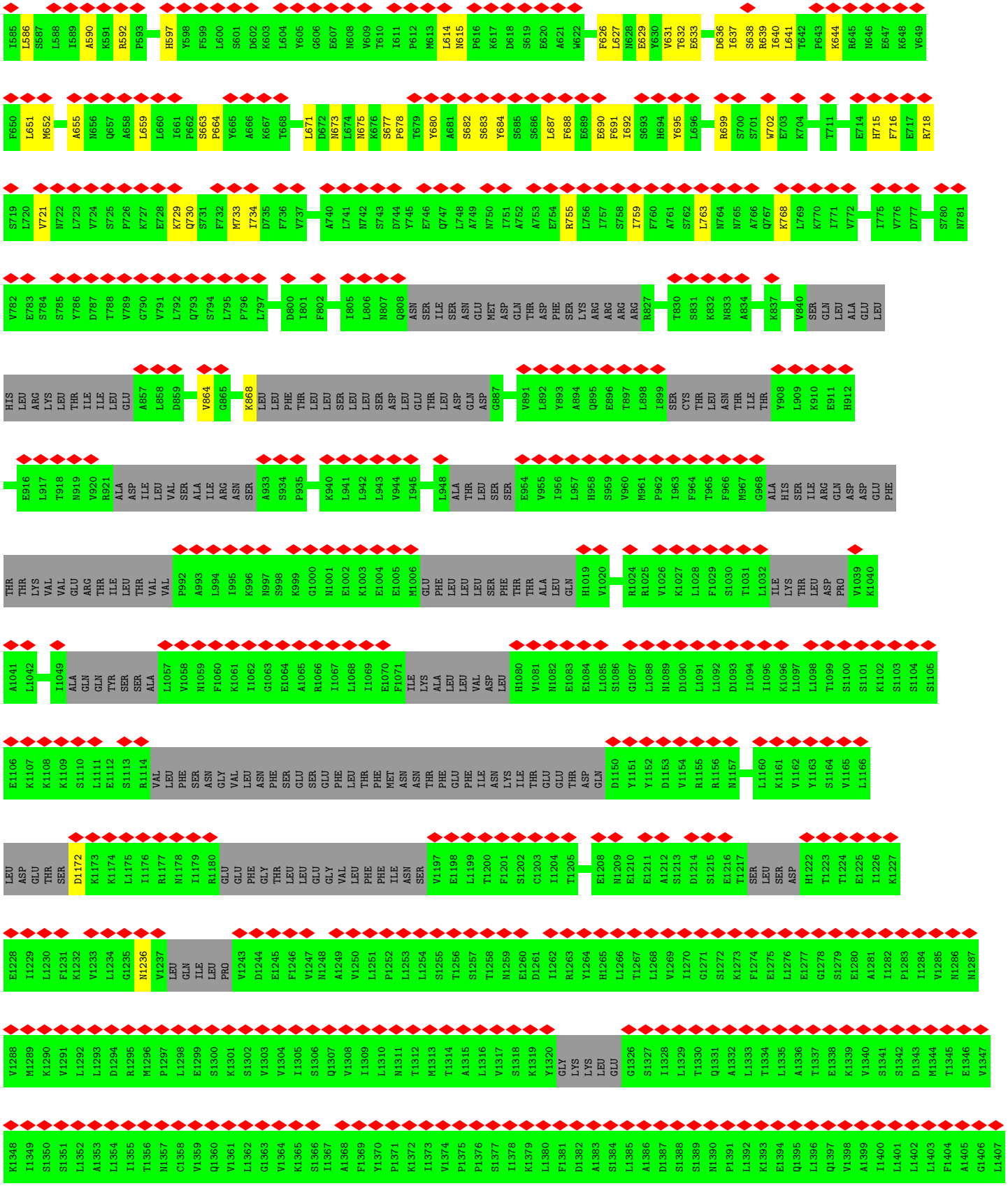
Chain A9:



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

Chain AE:

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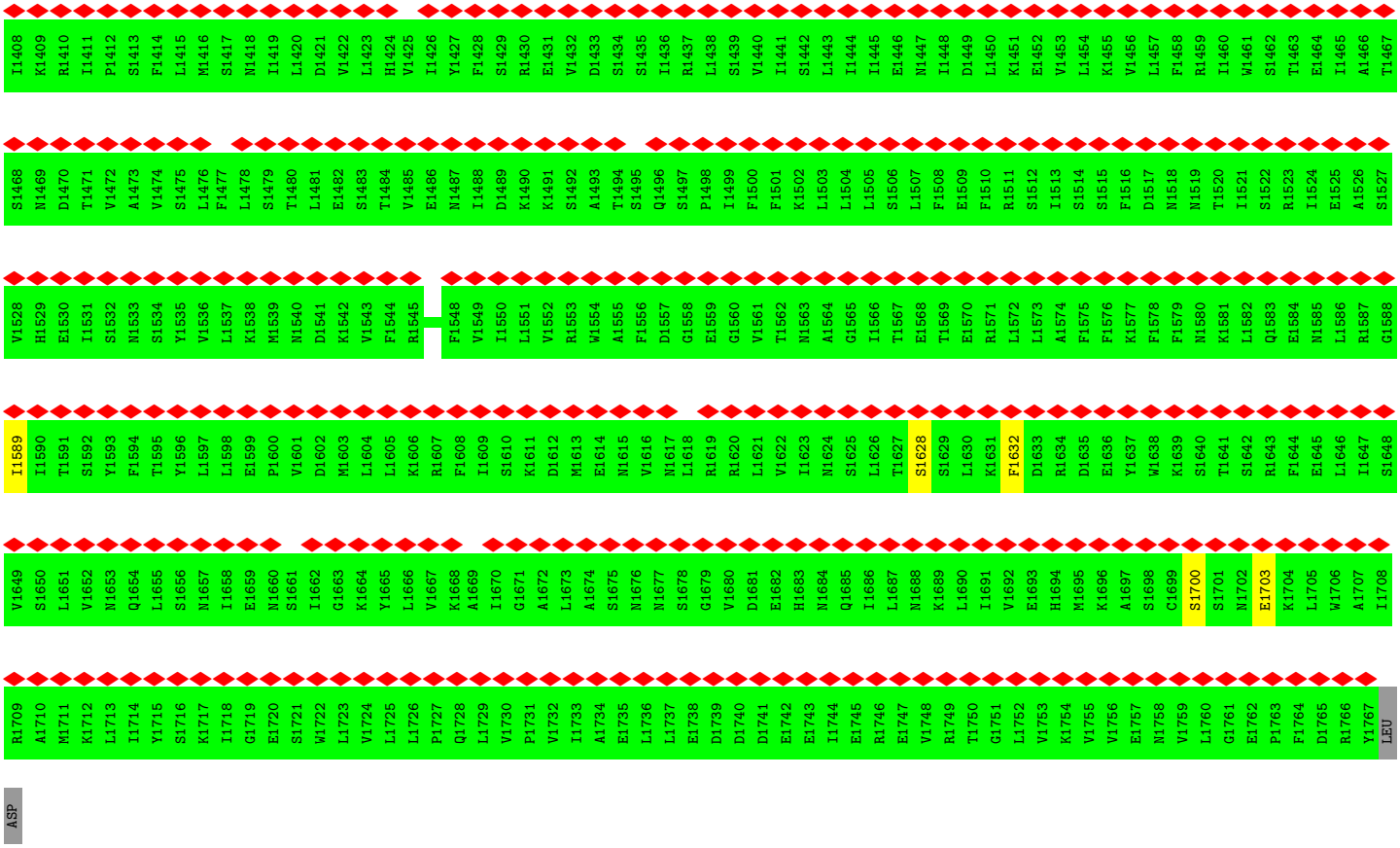
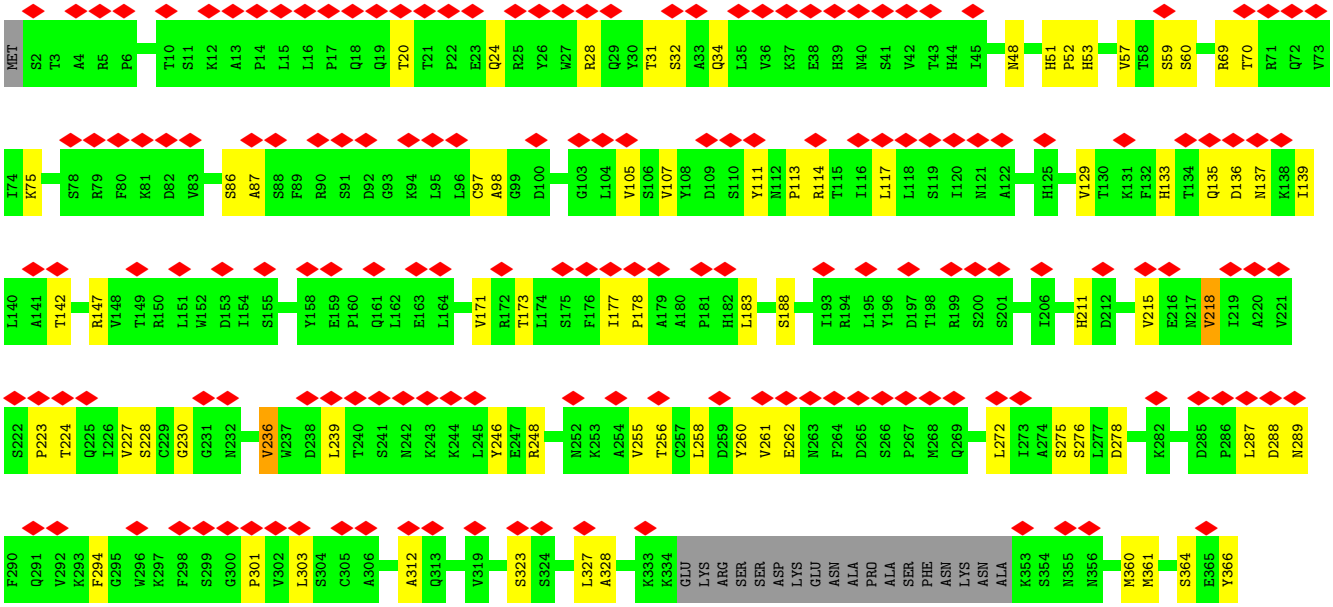
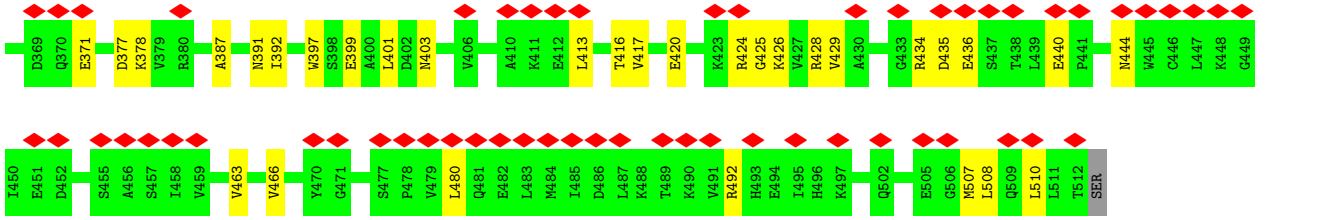
V782 E783 S784 S785 Y786 D787 T788 V789 G790 V791 L792 Q793 S794 L795 P796 L797 D800 I801 F802 I805 L806 N807 Q808 ASN SER ILE SER ASN GLU MET ASP GLN THR ASP PHE SER LYS ARG ARG ARG ARG R827 T830 S831 K832 N833 A834 K837 V840 SER GLN LEU ALA GLU LEU
HIS LEU ARG LYS LEU THR ILE ILE LEU GLU A857 L858 D859 V864 G865 K868 LEU LEU PHE THR LEU LEU LEU SER LEU LEU SER ASP LEU GLU THR LEU ASP GLN ASP G887 V891 L892 Y893 A894 Q895 E896 T897 L898 I899 SER CYS THR LEU ASN THR ILE THR Y908 L909 K910 E911 H912
E916 L917 T918 N919 V920 R921 ALA ASP ILE LEU VAL SER ALA ILE ARG ASN SER A933 S934 P935 K940 L941 L942 L943 V944 I945 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 R1024 R1025 V1026 K1027 L1028 F1029 S1030 T1031 L1032 ILE LYS THR LEU ASP PRO V1039 K1040
A1041 L1042 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 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 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 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 S1300 K1301 S1302 V1303 V1304 I1305 S1306 Q1307 V1308 I1309 L1310 N1311 T1312 M1313 T1314 A1315 L1316 V1317 S1318 K1319 Y1320 GLY LYS LYS LEU GLU G1326 S1327 I1328 L1329 T1330 Q1331 A1332 L1333 T1334 L1335 A1336 T1337 E1338 K1339 V1340 S1341 S1342 D1343 M1344 T1345 E1346 V1347
K1348 I1349 S1350 S1351 L1352 A1353 L1354 I1355 T1356 N1357 C1358 V1359 Q1360 V1361 L1362 G1363 V1364 K1365 S1366 I1367 A1368 F1369 Y1370 P1371 K1372 I1373 V1374 P1375 P1376 S1377 I1378 K1379 L1380 F1381 D1382 A1383 S1384 L1385 A1386 D1387 S1388 S1389 N1390 P1391 L1392 K1393 E1394 Q1395 L1396 Q1397 V1398 A1399 I1400 L1401 L1402 L1403 F1404 A1405 G1406 L1407



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

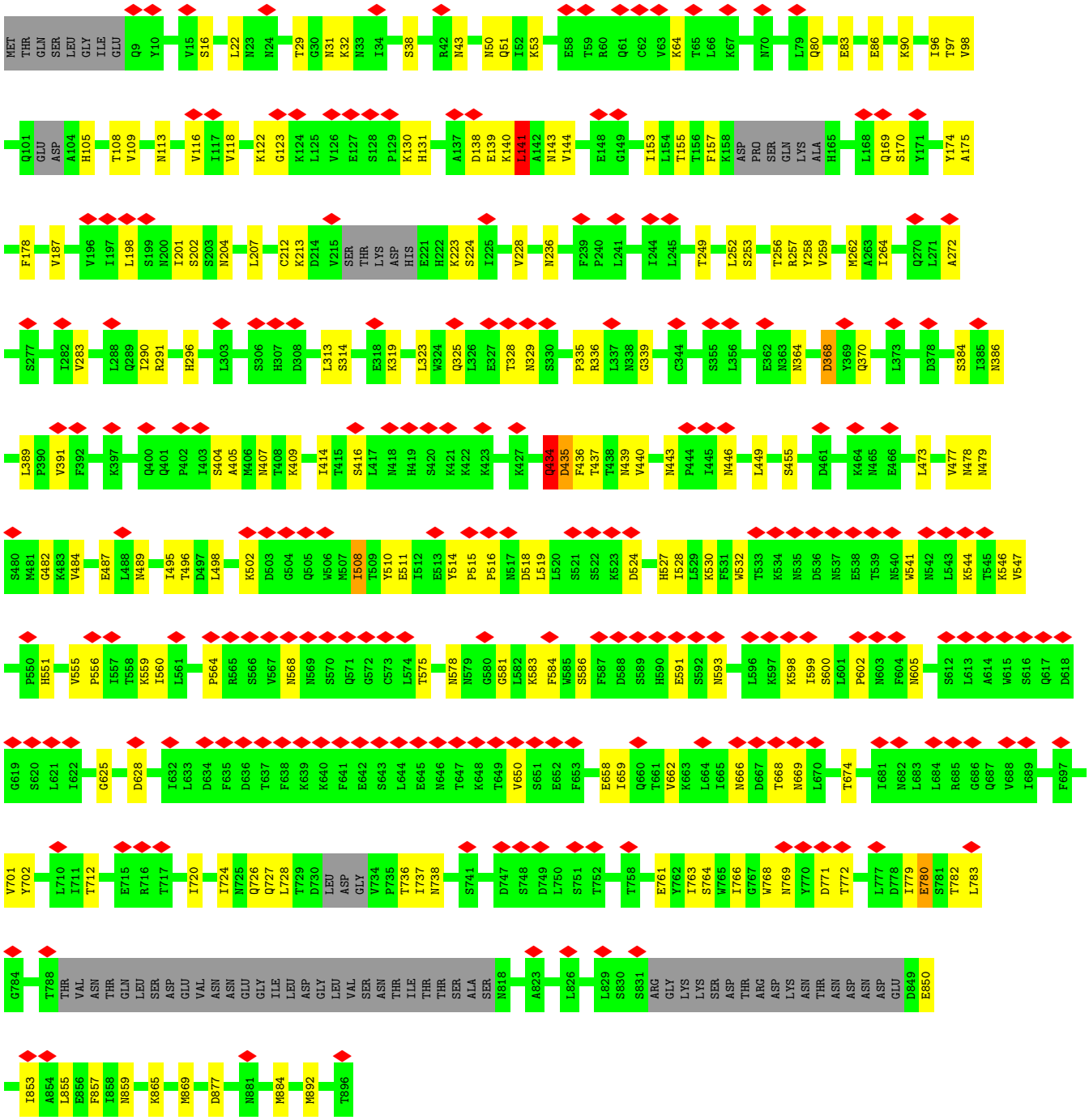
Chain AF:





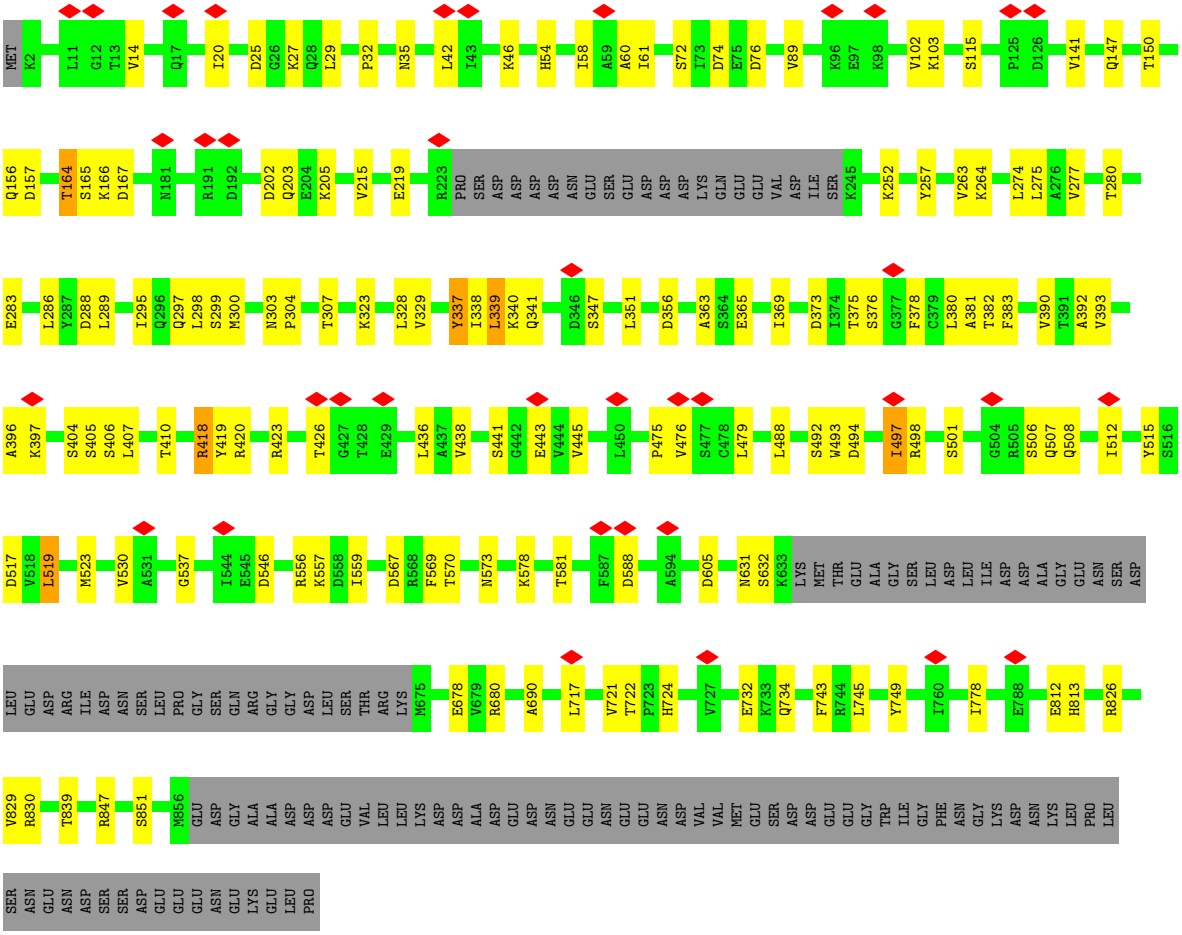
- Molecule 31: NET1-associated nuclear protein 1

Chain AG:



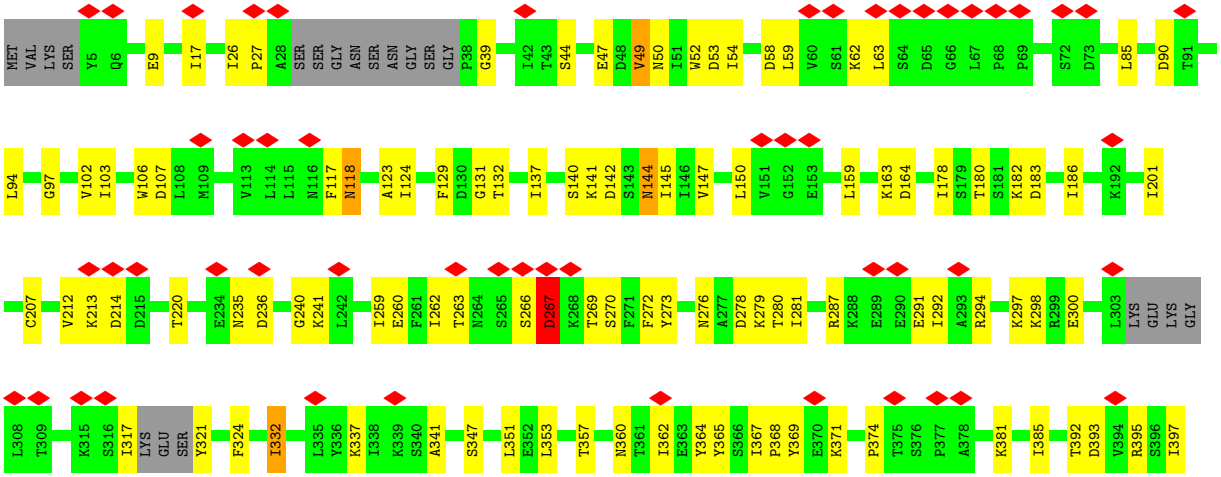
• Molecule 32: Periodic tryptophan protein 2

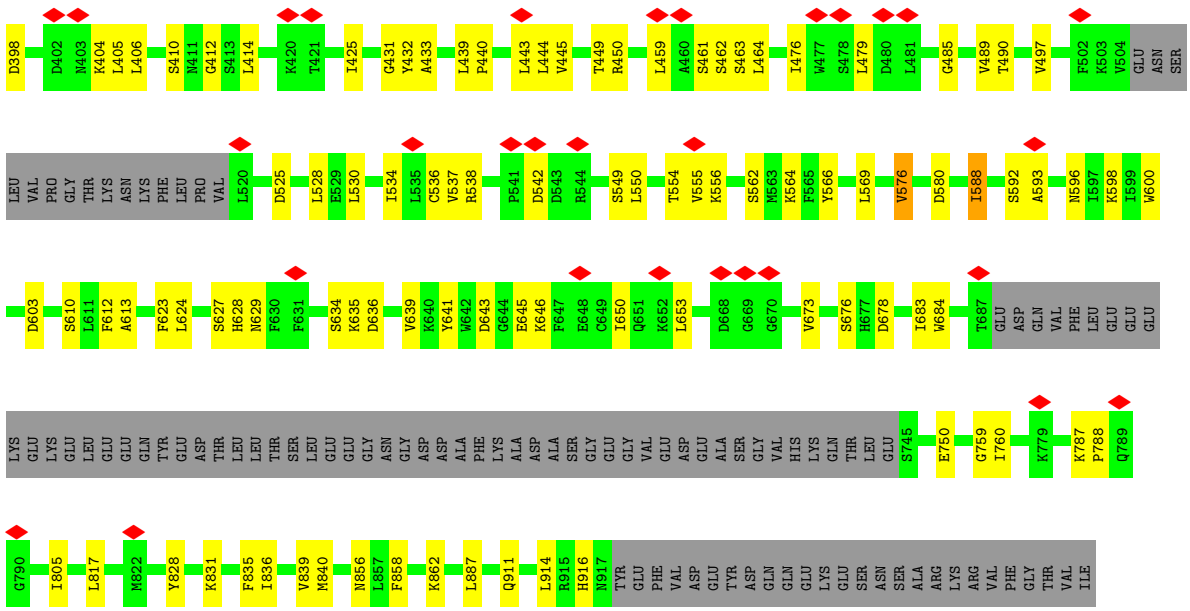
Chain B1: 70% 16% • 14%



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

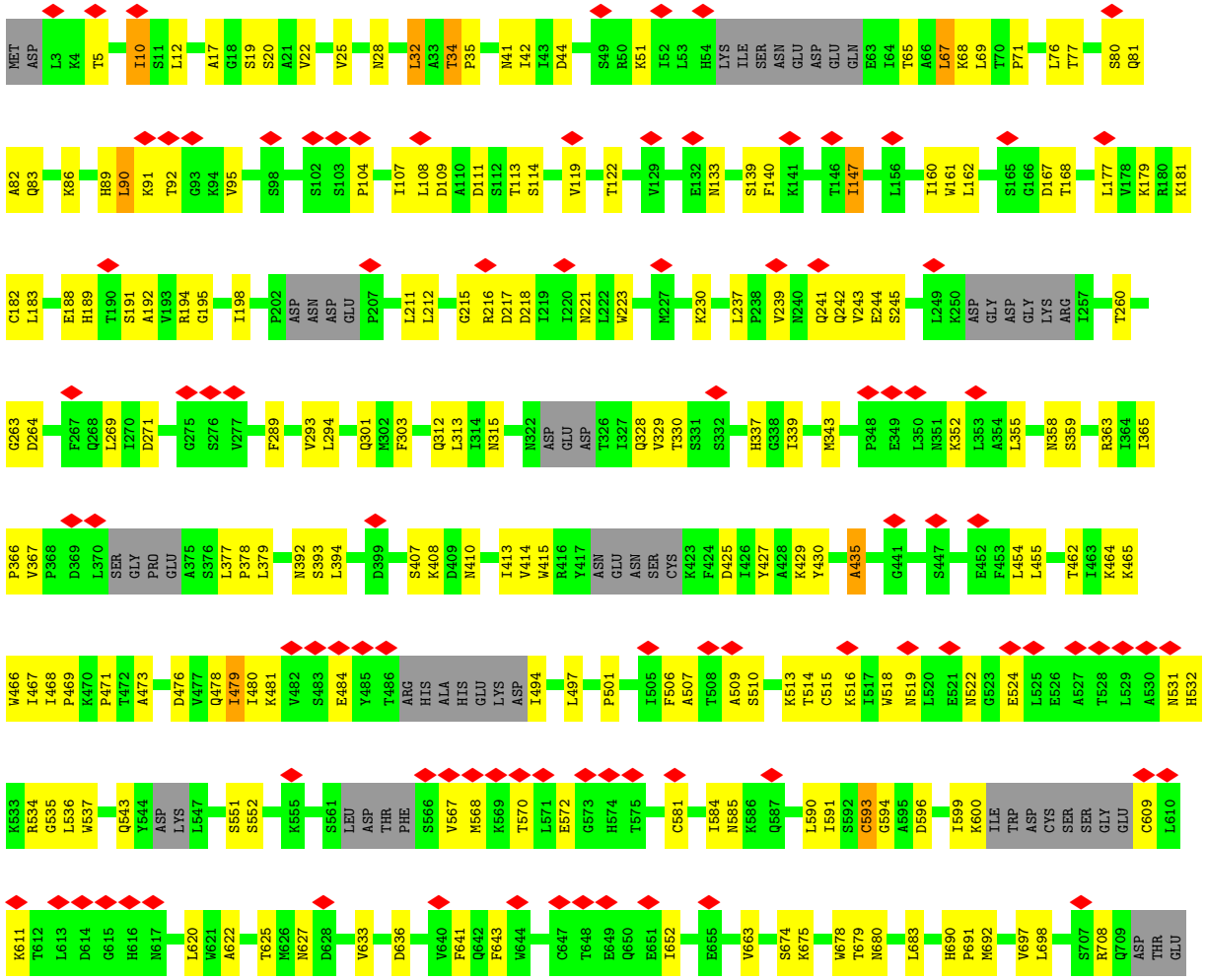
Chain B2: 9% 66% 21% • 13%

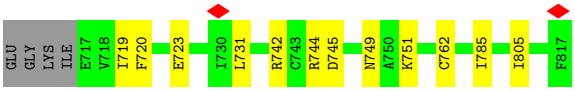




- Molecule 34: U3 small nucleolar RNA-associated protein 13

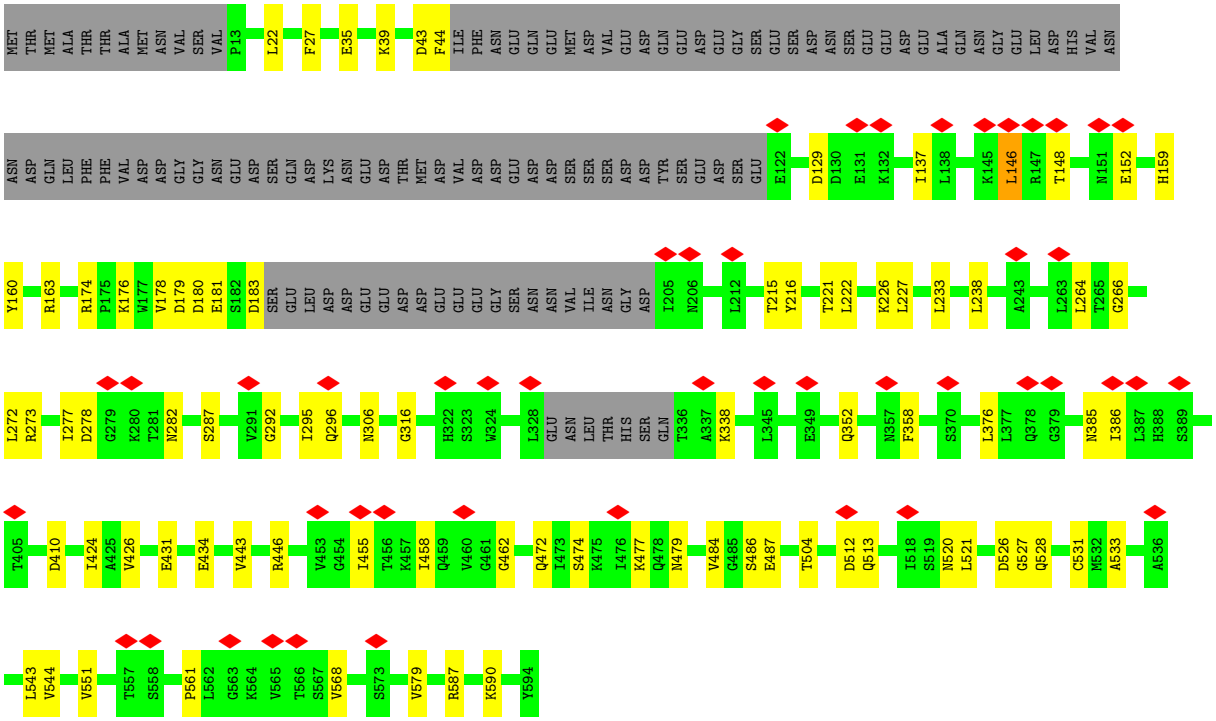
Chain B3:





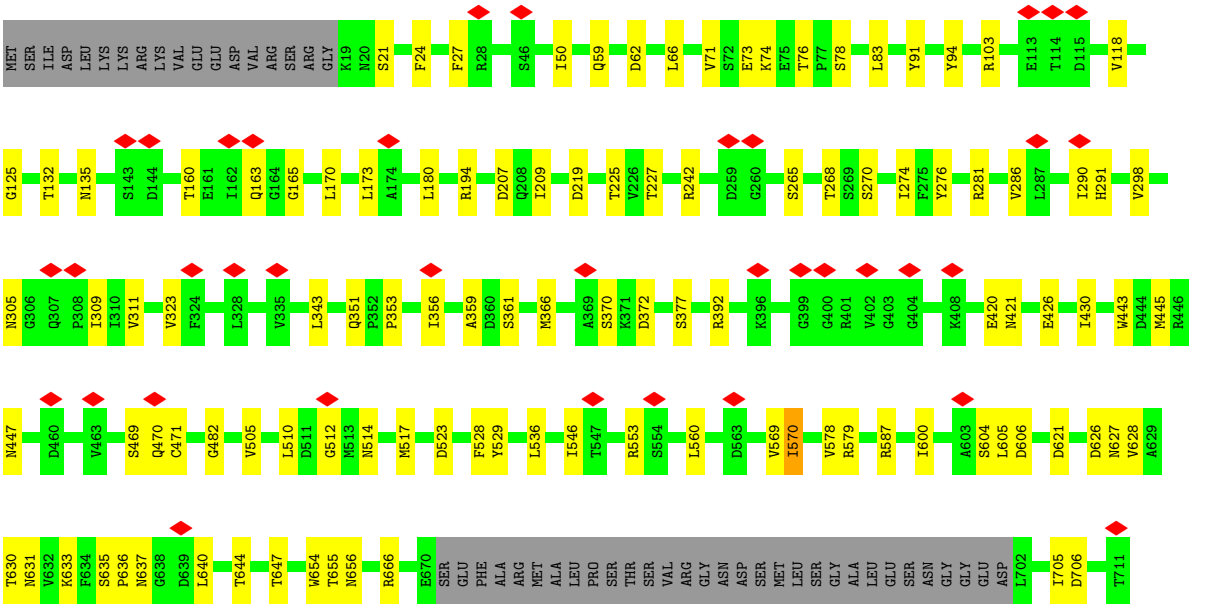
• Molecule 35: U3 small nucleolar RNA-associated protein 18

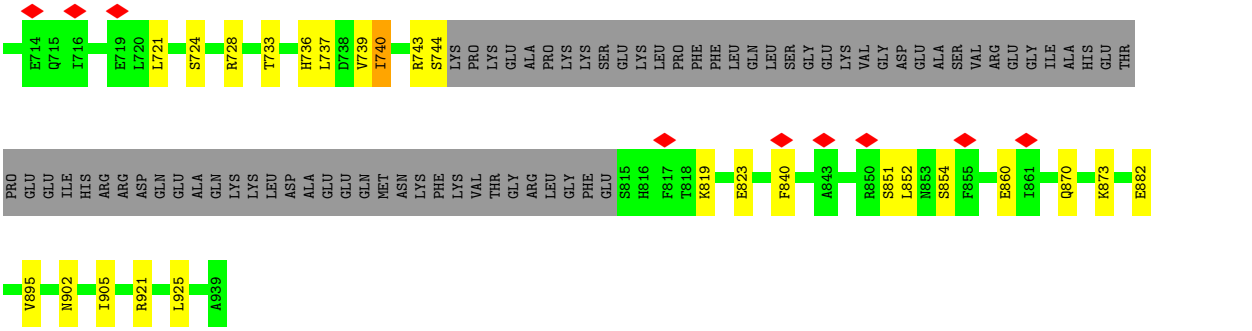
Chain B8:



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

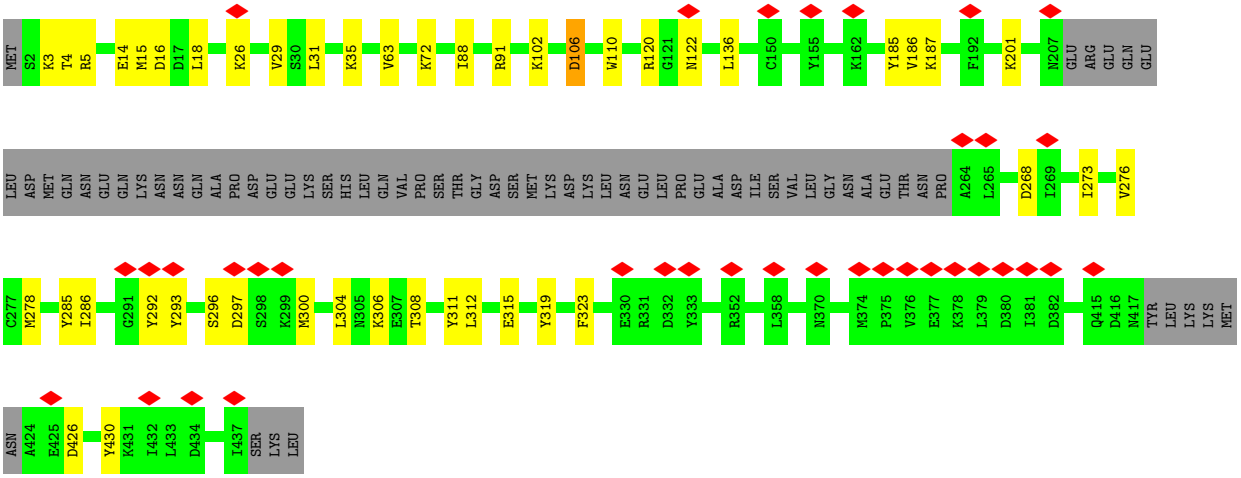
Chain BE:





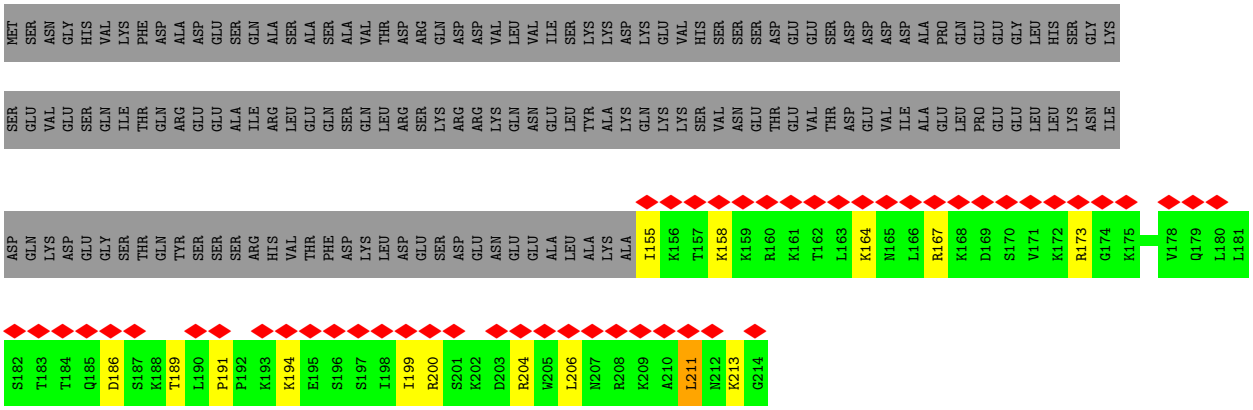
• Molecule 37: U3 small nucleolar RNA-associated protein 6

Chain B6:



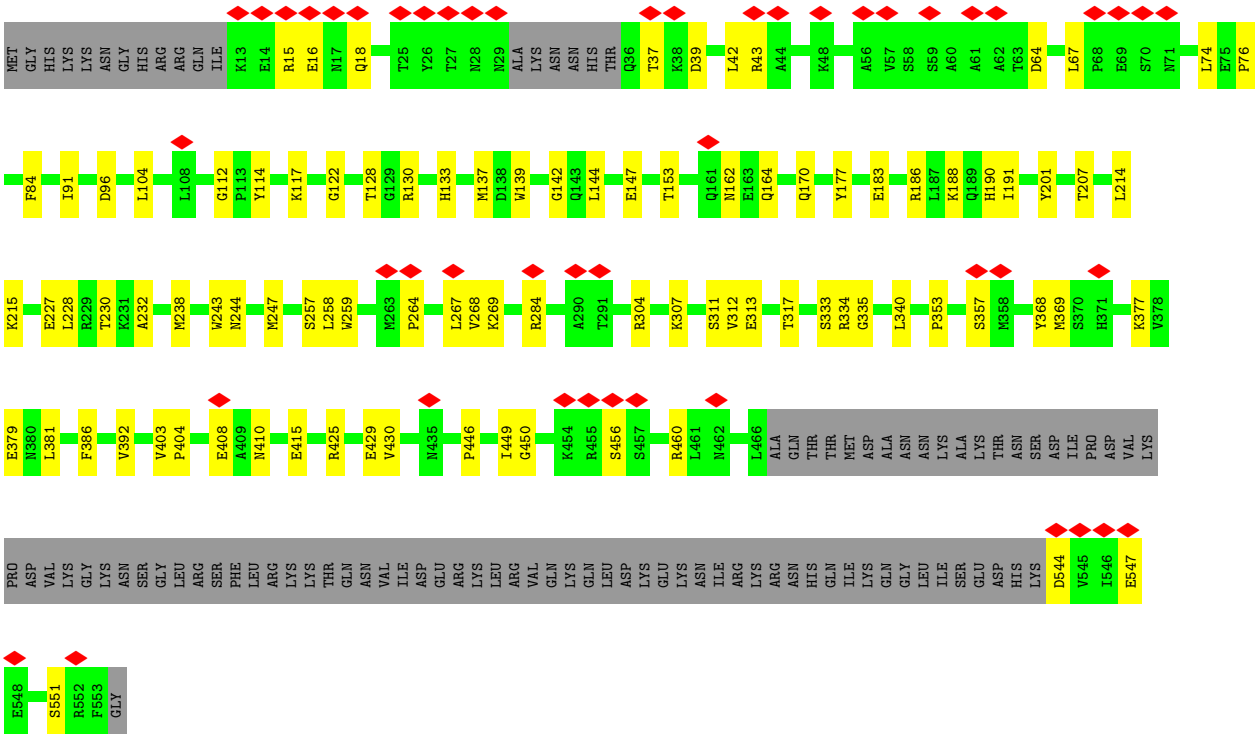
• Molecule 38: Bud site selection protein 21

Chain 5B:



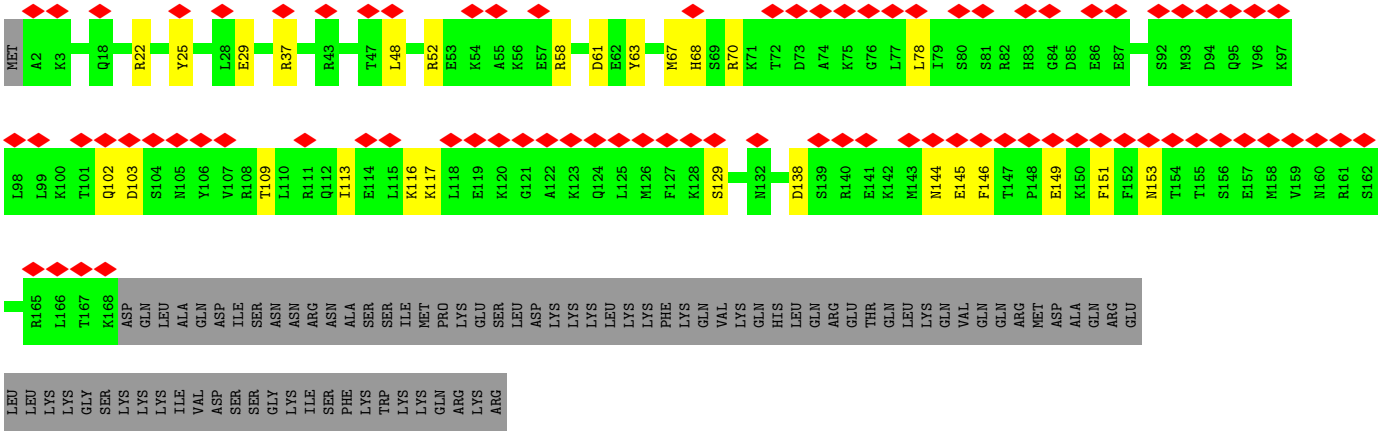
• Molecule 39: U3 small nucleolar RNA-associated protein 7

Chain 5C:



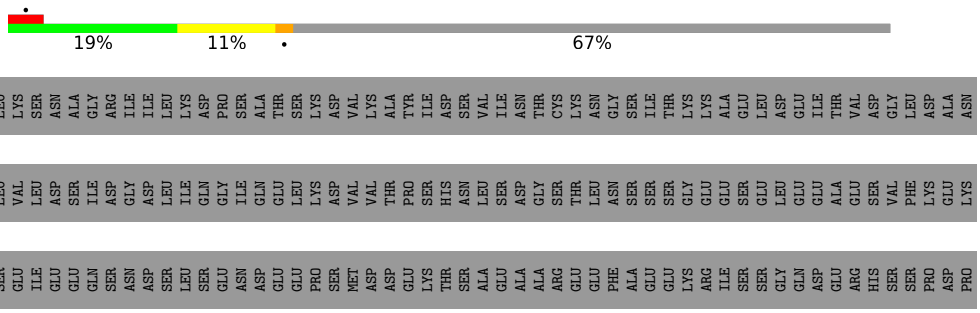
- Molecule 40: U3 small nucleolar RNA-associated protein 11

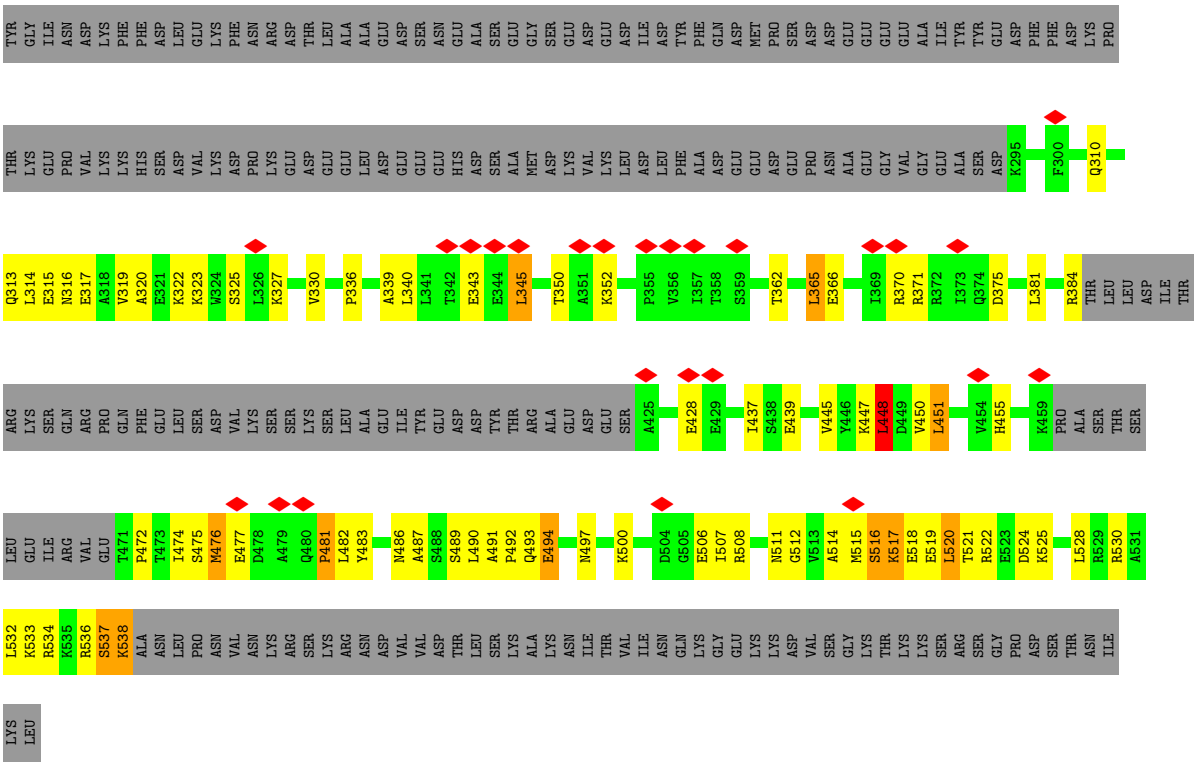
Chain 5D:



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

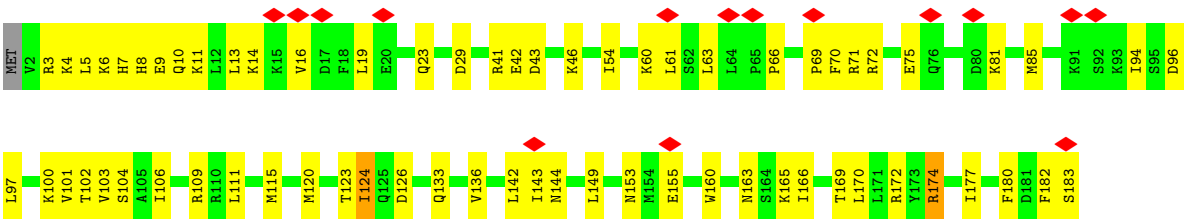
Chain 5E:





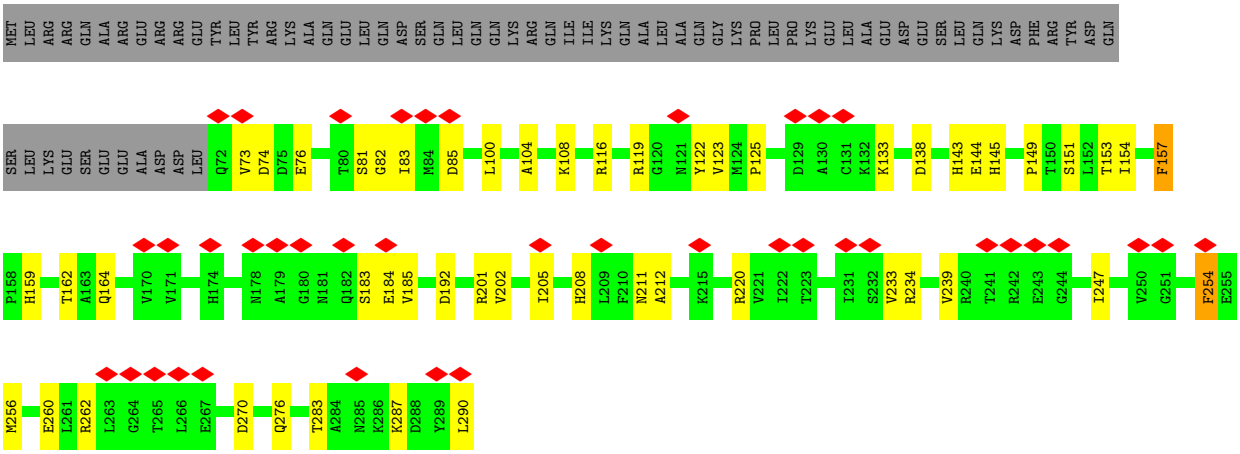
• Molecule 42: U3 small nucleolar ribonucleoprotein protein IMP3

Chain 5F:



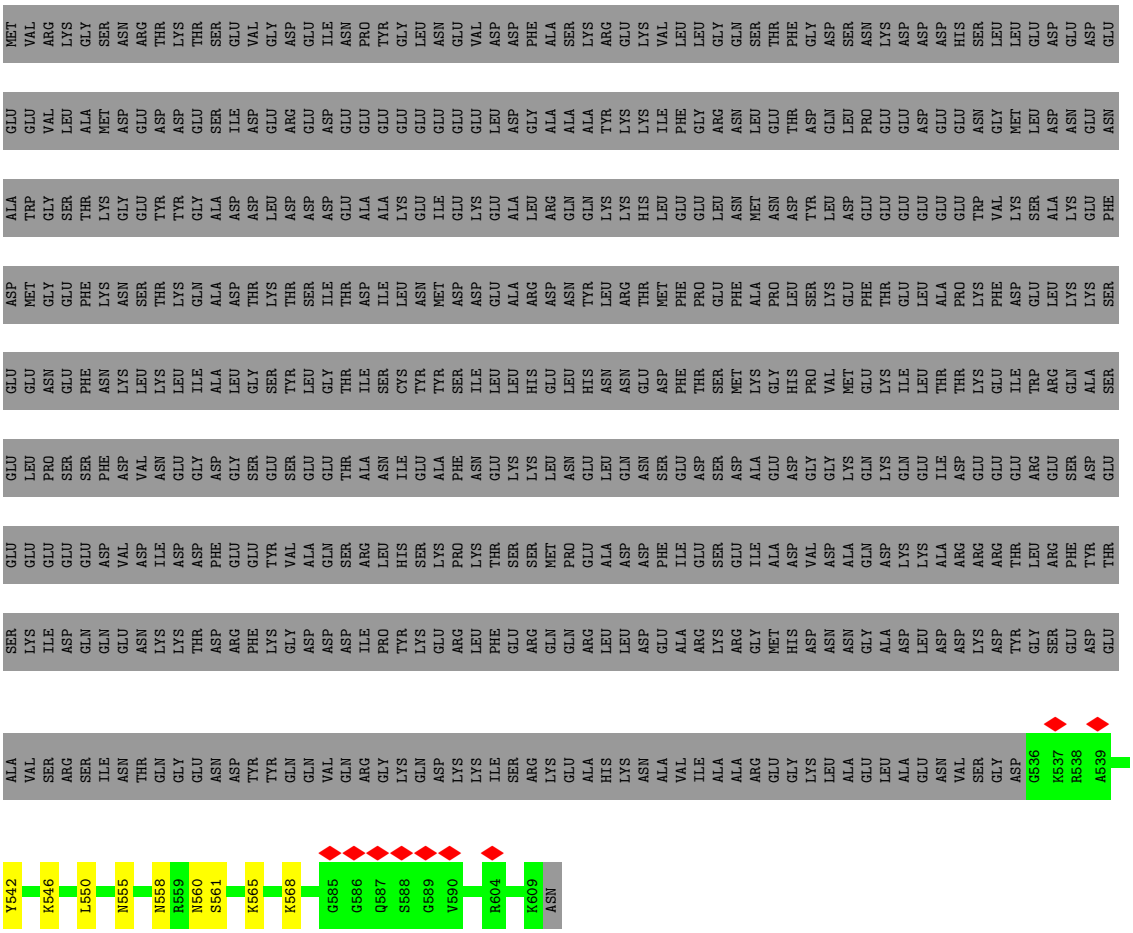
• Molecule 43: U3 small nucleolar ribonucleoprotein protein IMP4

Chain 5G:



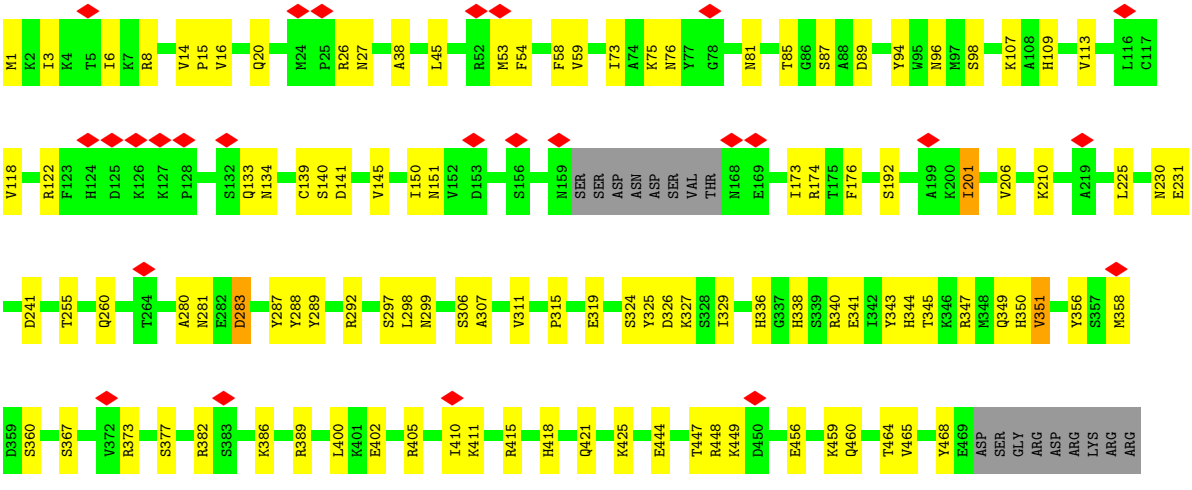
- Molecule 44: Something about silencing protein 10

Chain 5H:

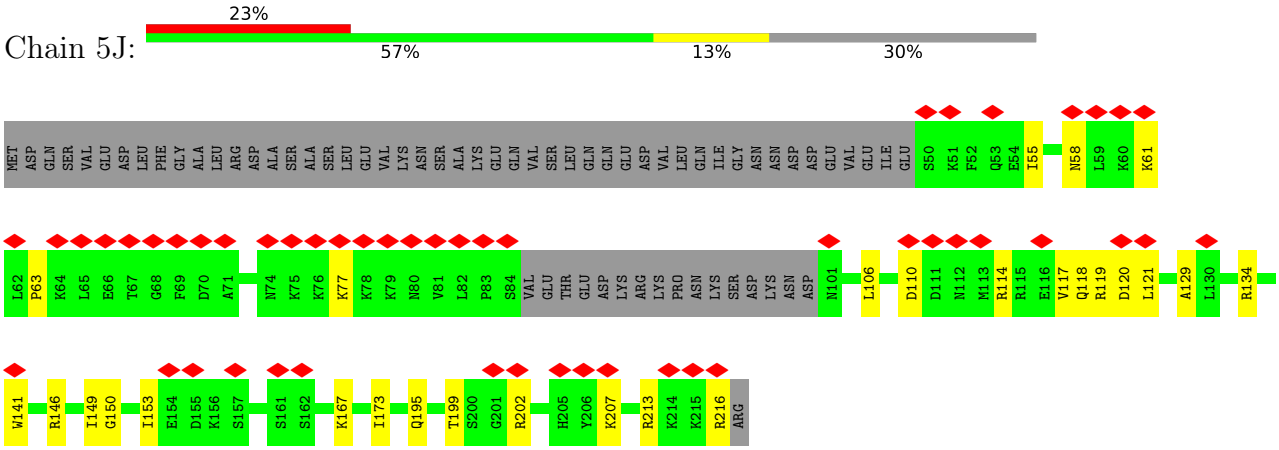


- Molecule 45: Protein SOF1

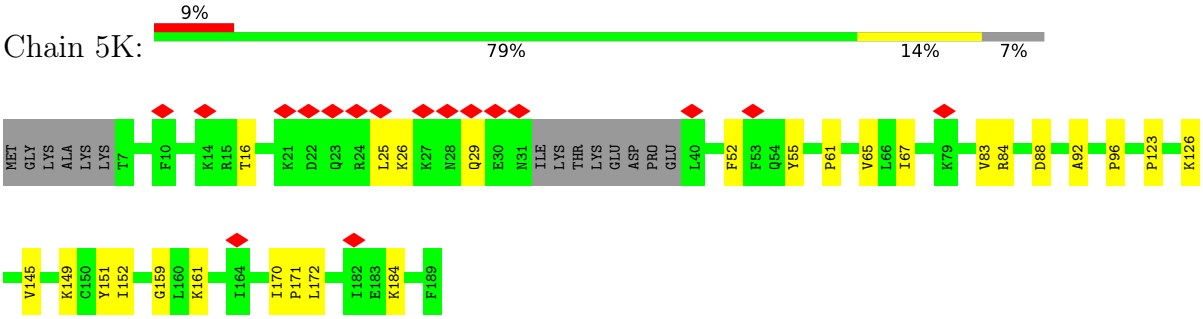
Chain 5I:



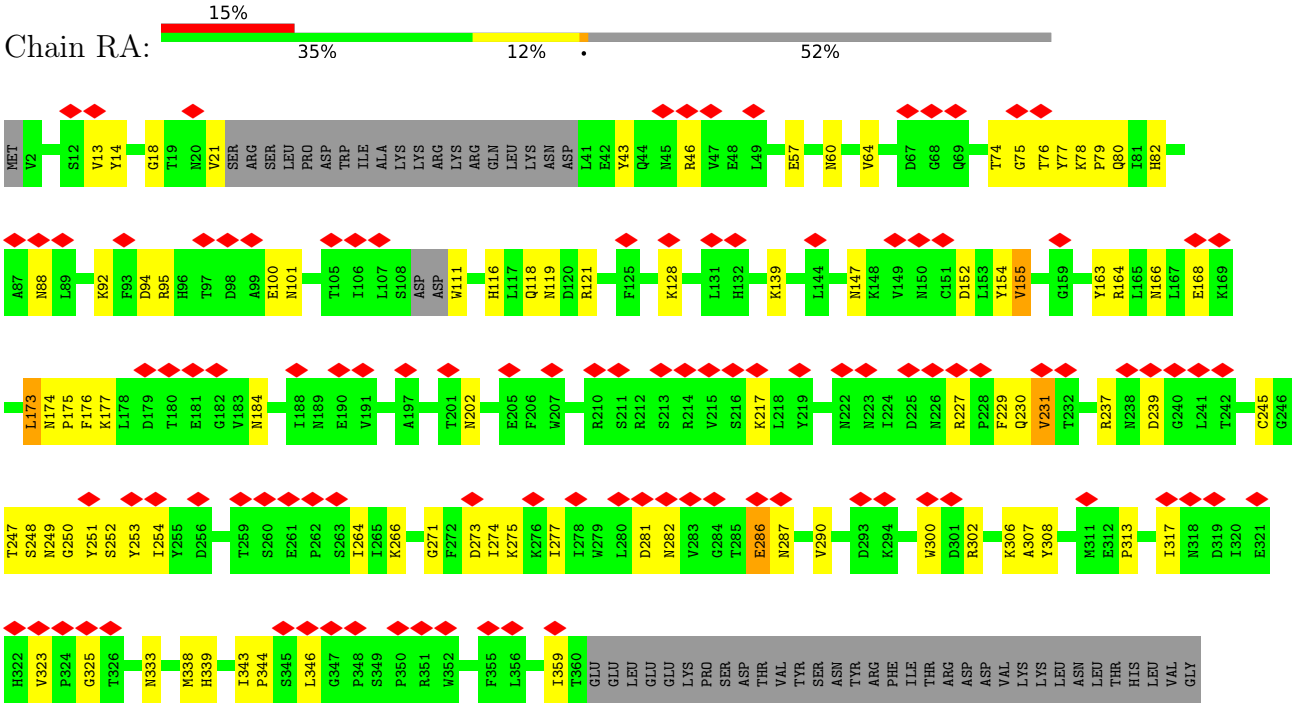
- Molecule 46: rRNA-processing protein FCF2

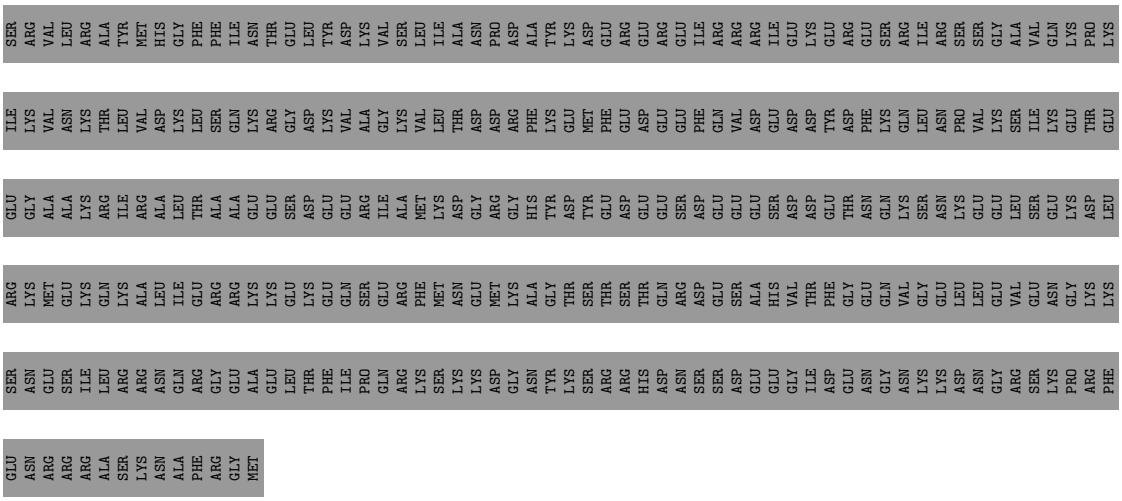


- Molecule 47: rRNA-processing protein FCF1



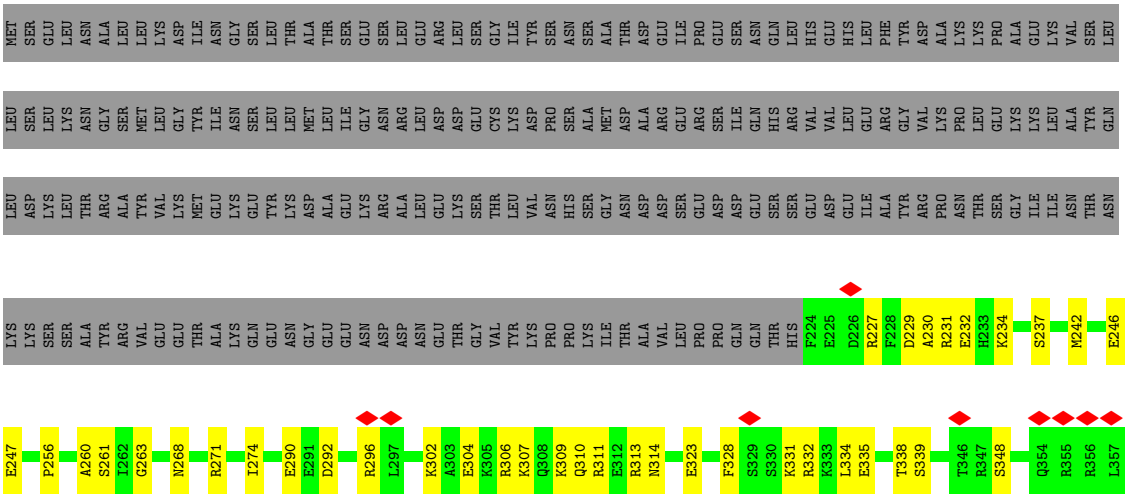
- Molecule 48: Ribosome biogenesis protein ENP2





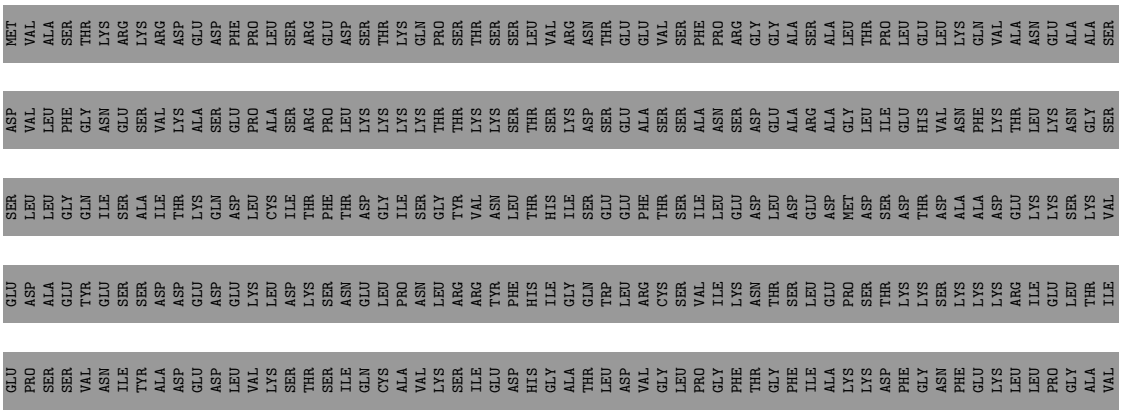
- Molecule 49: U3 small nucleolar ribonucleoprotein protein LCP5

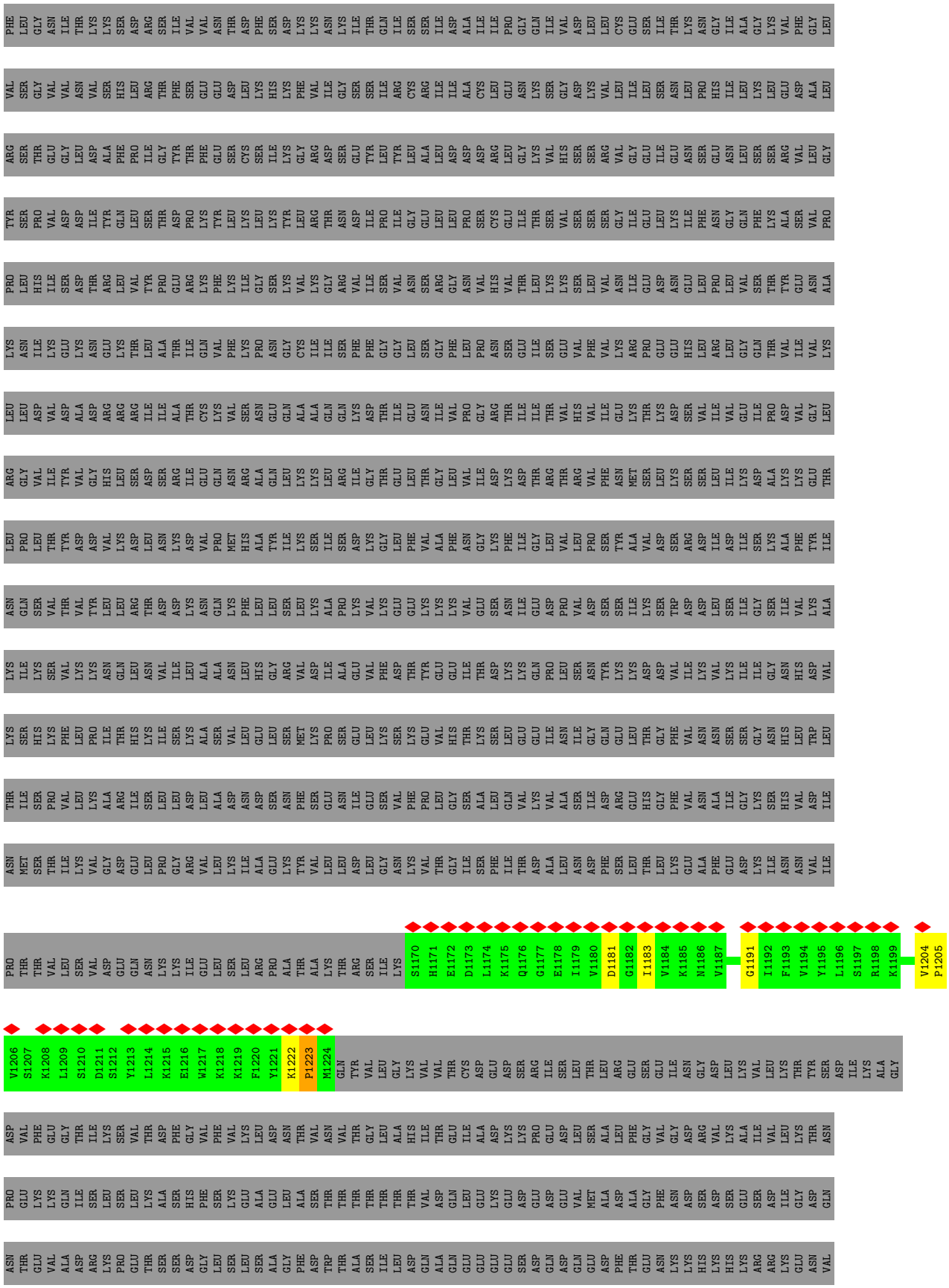
Chain RB:



- Molecule 50: rRNA biogenesis protein RRP5

Chain RD:

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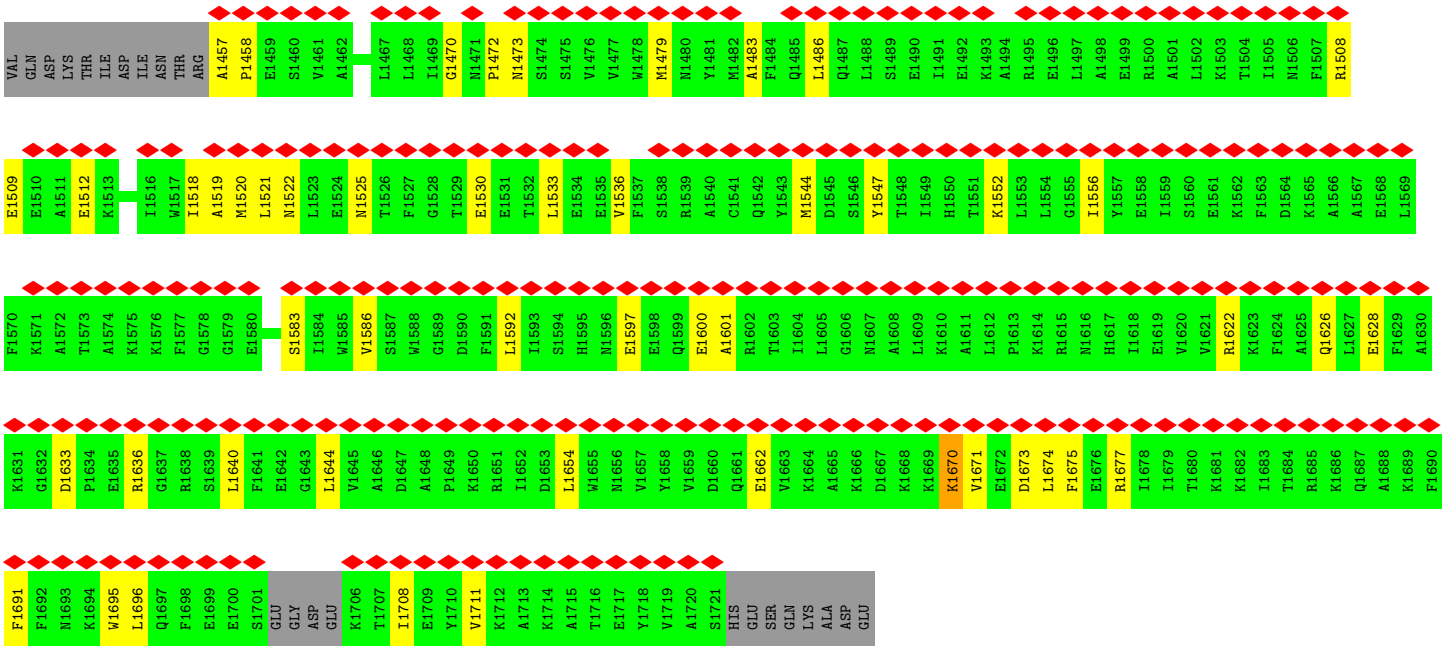
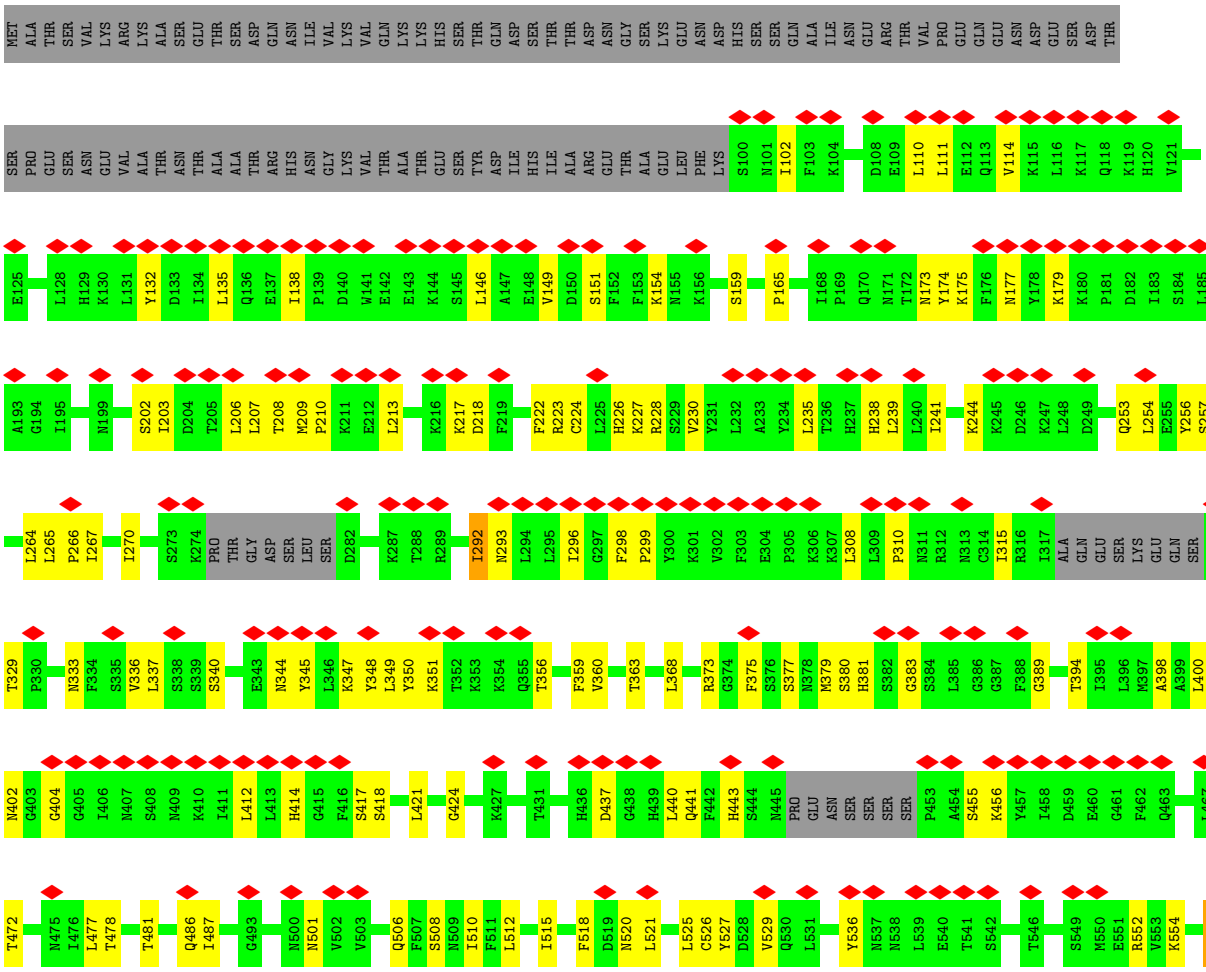
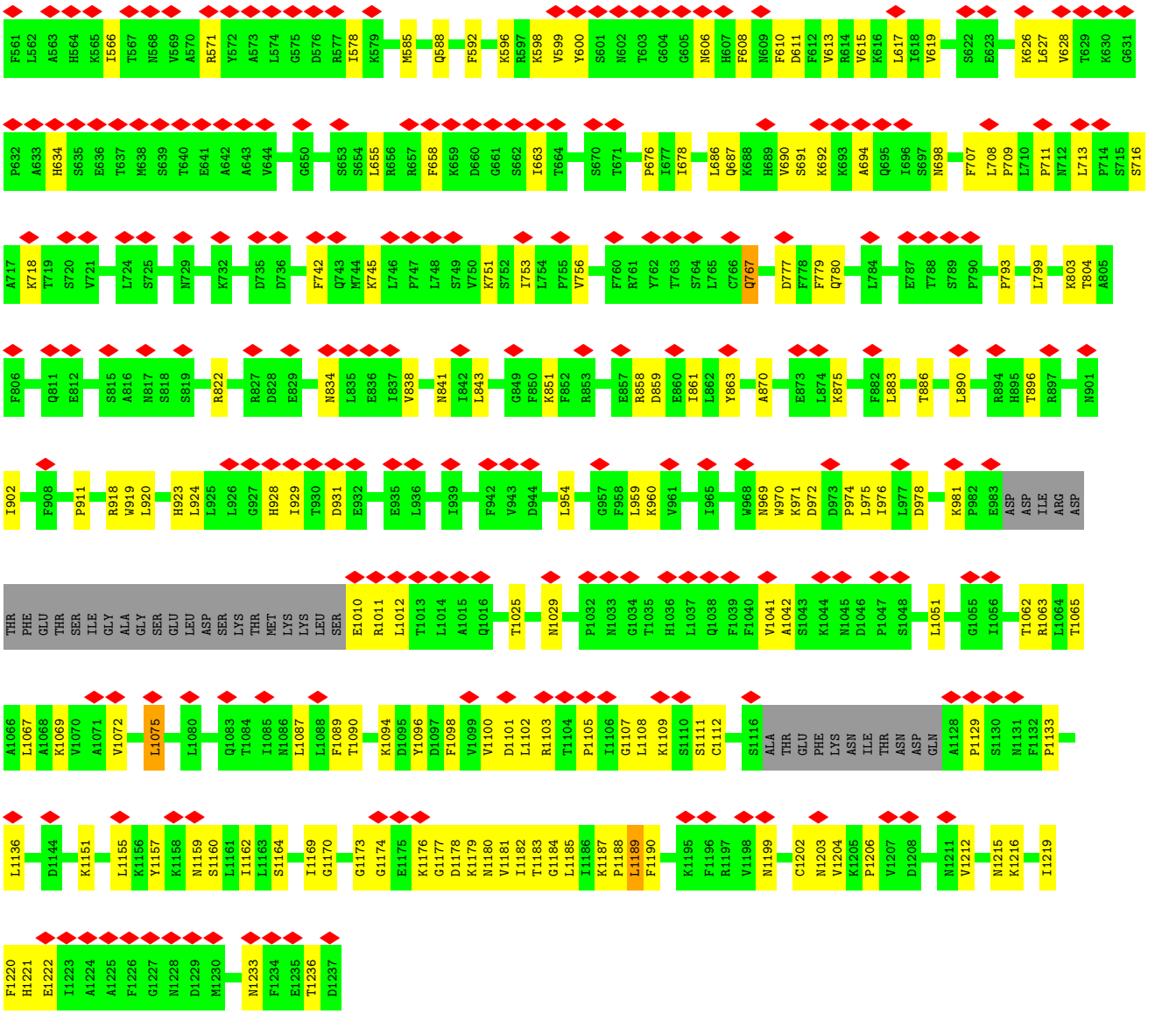
THR ILE SER PRO VAL LEU LYS ALA ARG ILE SER LEU LEU ASP LEU ALA ASP ASN ASP ASP ASN ASP ILE ALA LEU ASP ILE ASP ARG GLU HIS GLY PHE VAL ALA SER LEU GLN VAL LYS VAL ALA SER ILE ASP ARG GLU HIS LEU ALA ILE GLY LYS SER HIS VAL ASP ILE
ASN MET SER THR ILE LYS VAL GLY ASP GLU GLU LEU PRO LEU ALA LEU LYS ILE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



- Molecule 51: U3 small nucleolar RNA-associated protein 22

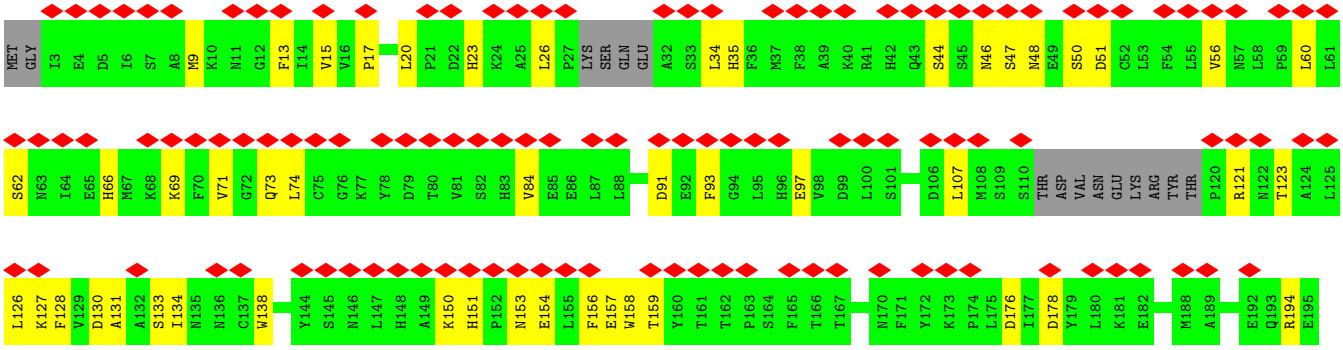
Chain RE:

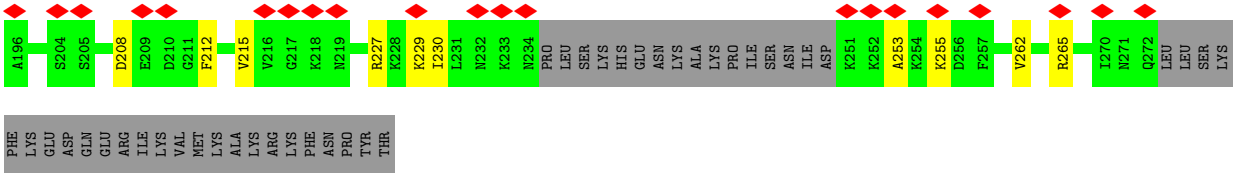




- Molecule 52: Ribosomal RNA-processing protein 7

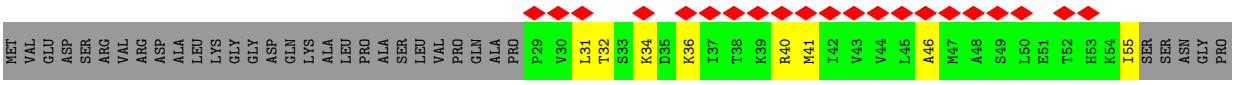
Chain RF:

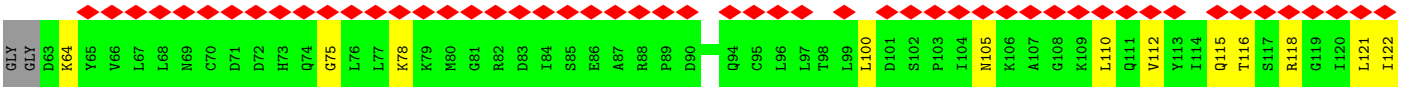


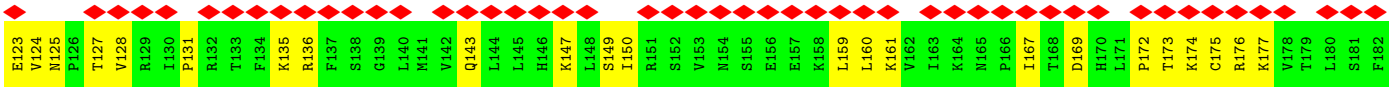


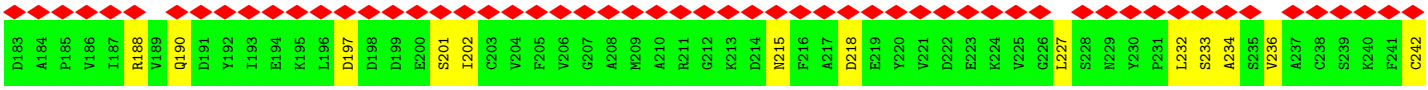
• Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

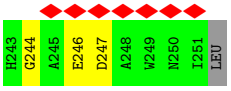
Chain RG:





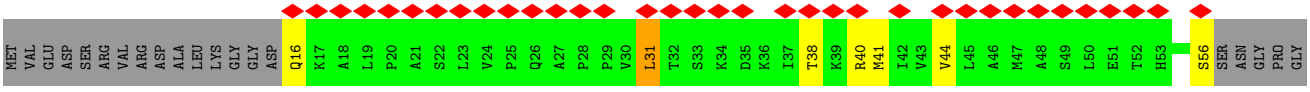


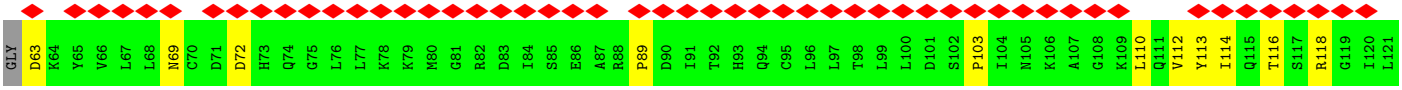


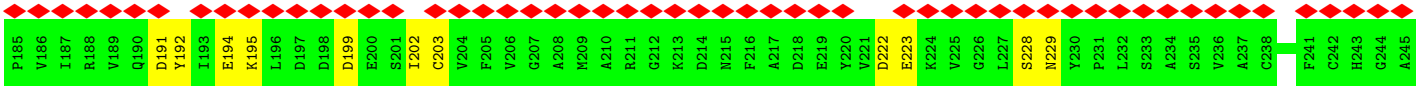


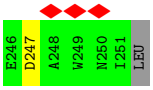
• Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

Chain RH:



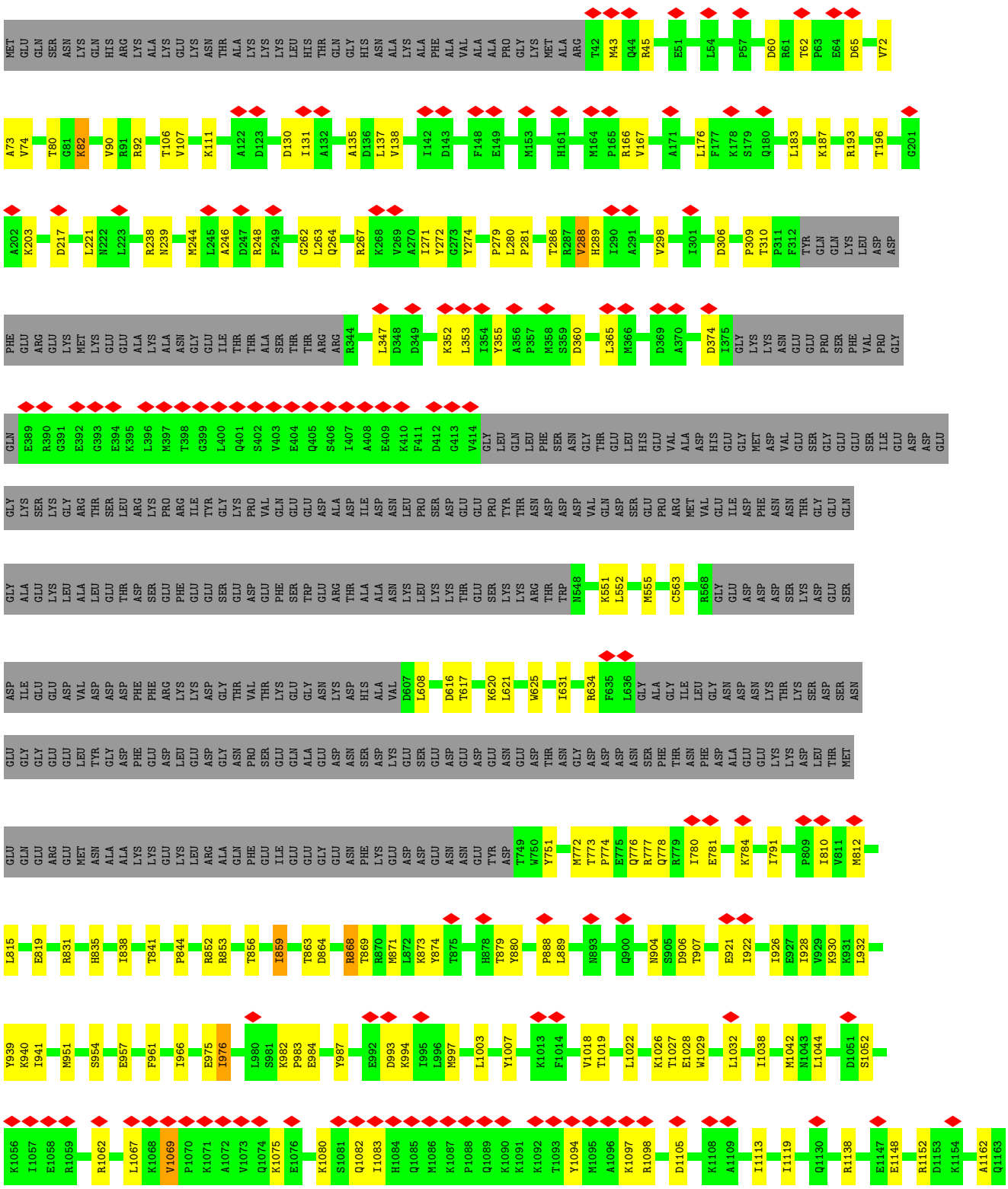






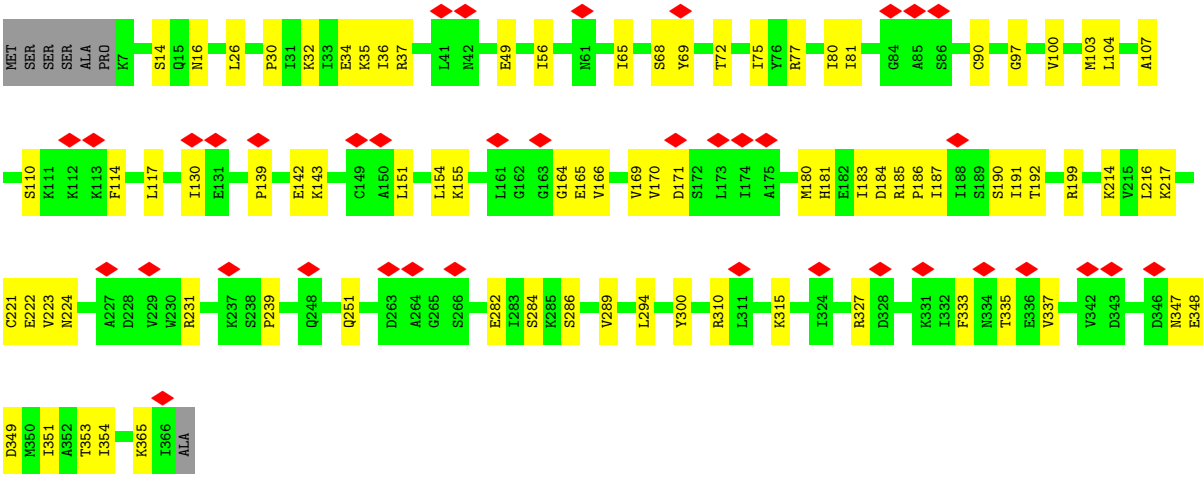
- Molecule 54: Ribosome biogenesis protein BMS1

Chain RJ: 11% 54% 13% • 33%



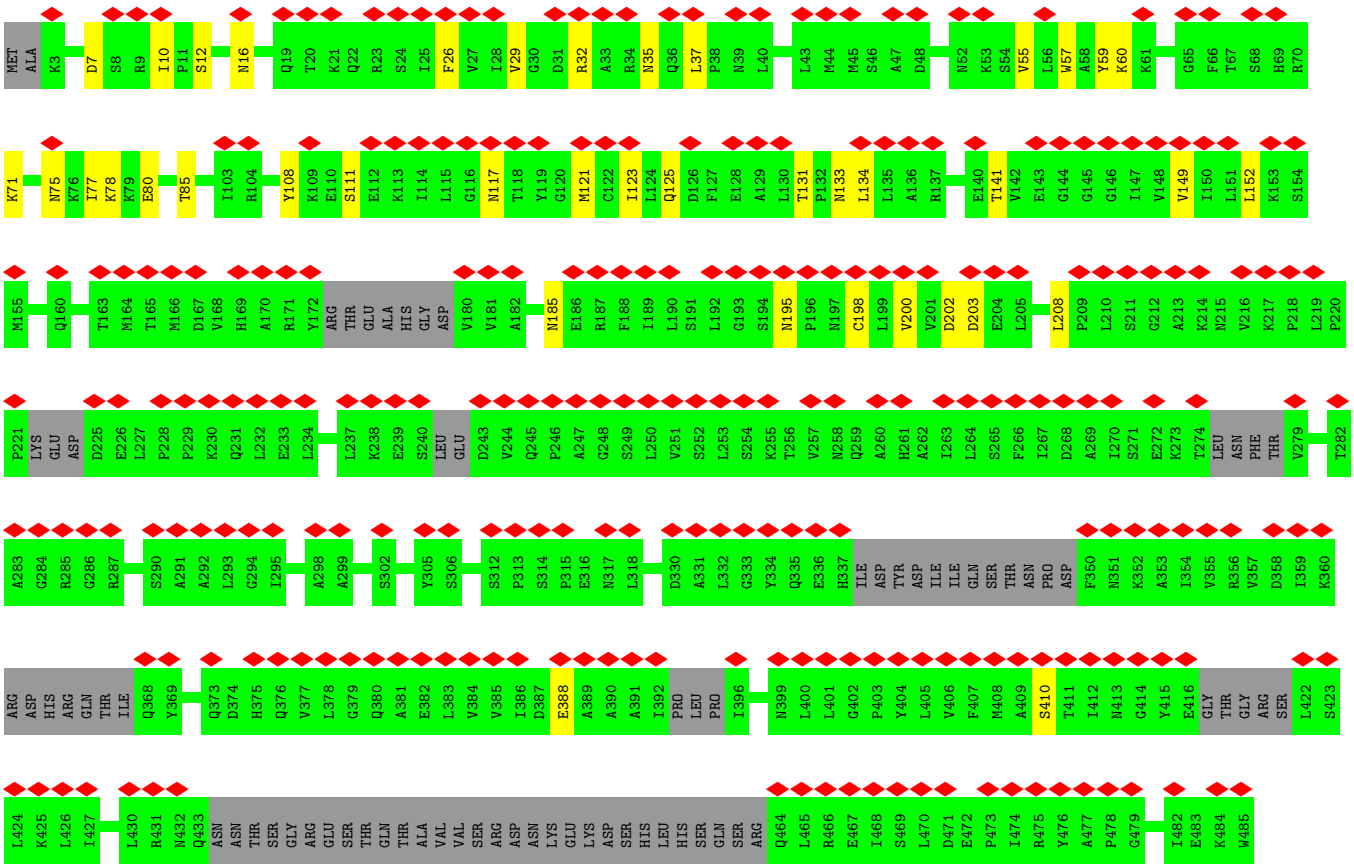
• Molecule 55: RNA 3'-terminal phosphate cyclase-like protein

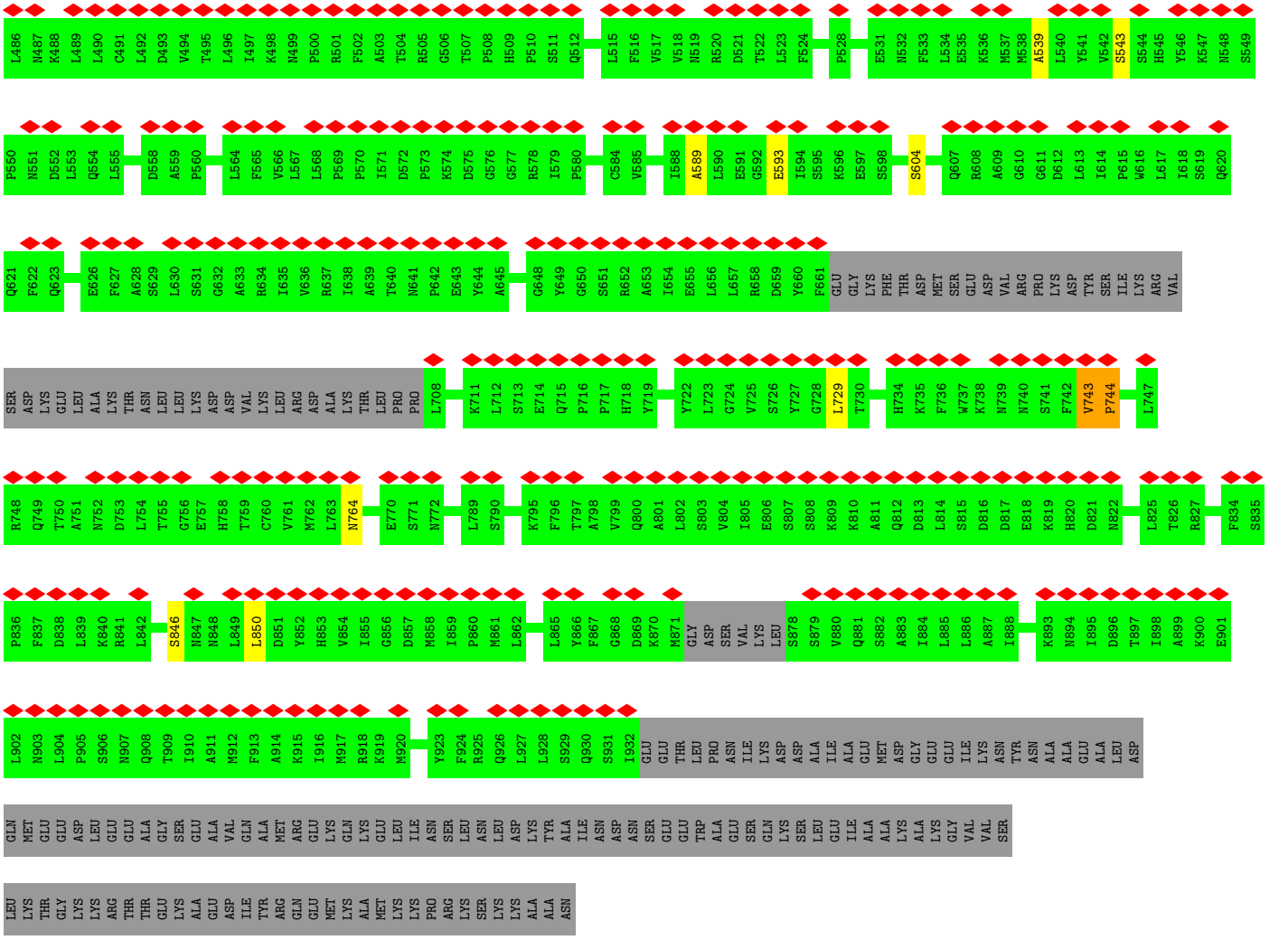
Chain RK:



• Molecule 56: RNA cytidine acetyltransferase

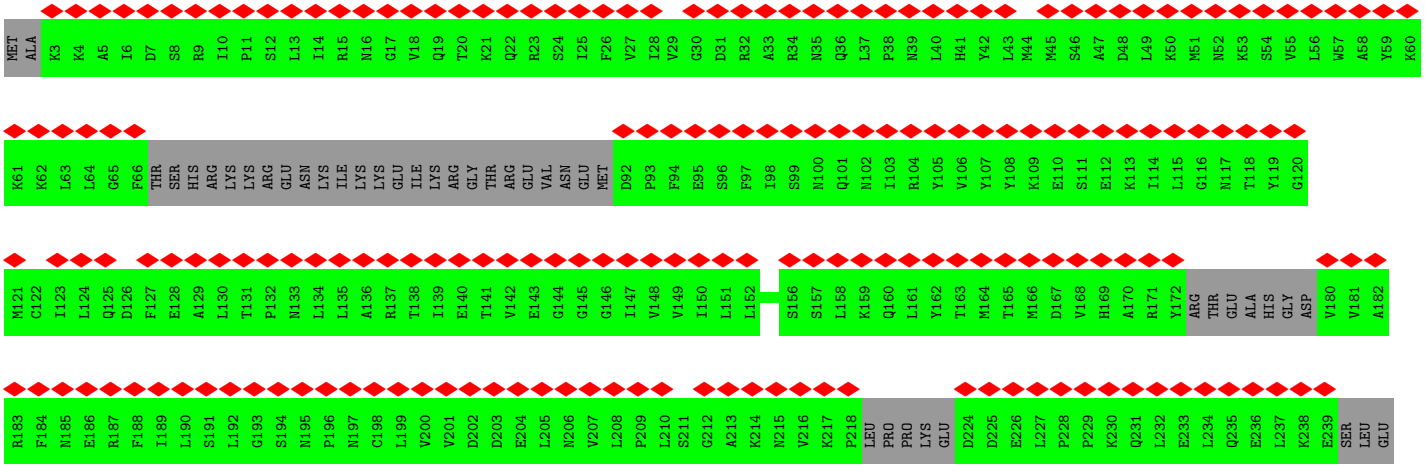
Chain RL:





- Molecule 56: RNA cytidine acetyltransferase

Chain RM:



D243 V244 Q245 P246 A247 G248 S249 L250 V251 S252 L253 S254 K255 T256 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 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 M413 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 Q512 C513 N514 L515 F516 V517 V518 N519 T522 L523 F524 S525 Y526 H527 P528 V529 S530 E531 N532 F533 L534 E535 K536 M537 M538 A539 L540 Y541 V542 S543 S544 H545 N548

N551 D552 L553 Q554 L555 N556 S557 D558 A559 P560 A561 H562 K563 L564 F565 L568 P569 P570 I571 D572 P573 K574 G577 R578 I579 P580 D581 P582 L583 C584 V585 I586 Q587 I588 A589 LEU GLU G592 E593 I594 S595 K596 E597 S602 L603 S604 R605 G606 Q607 R608 A609 G610 G611 D612 L613 I614

P615 W616 L617 I618 S619 Q620 Q621 F622 E625 E626 F627 S631 G632 A633 R634 I635 V636 R637 I638 A639 T640 Y644 A645 S646 M647 G648 R652 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 S726 Y727 G728 L729 T730 Q731 S732 L733 H734 K735 F736 W737 N740 S741 F742 V743 P744 V745

Y746 Q749 L754 T755 G756 E757 H758 T759 C760 V761 M762 L763 N764 V765 L766 E767 G768 R769 E770 S771 V775 E776 F777 A778 K779 D780 K783 R784 F785 L786 S787 L788 L789 S790 Y791 K795 F796 T797 A798 V799 Q800 A801 L802 S803 V804 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 D843 S844 N847 N848 L849 L850 D851 Y852 H853 V854 I855 G856 D857 M858 I859 P860 A863 L864 L865 Y866 F867 G868 D869 K870 M871 GLY ASP SER VAL LYS LEU S878 S879

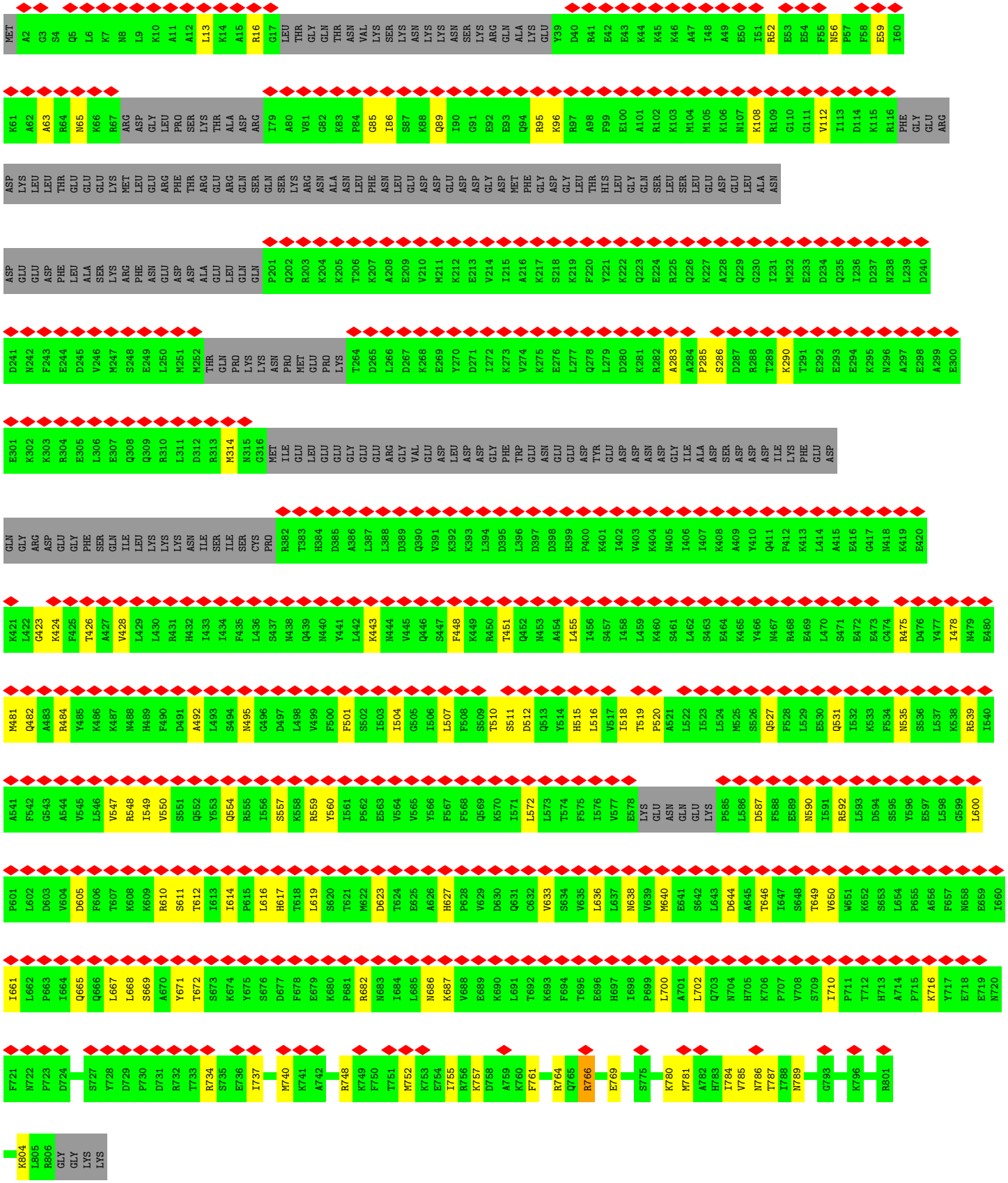
V880 Q881 S882 A883 I884 L885 L886 A887 I888 G889 L890 Q891 R892 K893 N894 I895 L902 N903 L904 P905 S906 N907 Q908 T909 I910 A911 M912 F913 A914 K915 I916 M917 R925 S931 I932 GLU GLU THR LEU PRO ASN ILE LYS ASP ASP ALA ILE ALA GLU MET ASP GLY GLU GLU ILE LYS ASN

TYR ASN ALA ALA GLU ALA LEU ASP GLN MET GLU GLU ASP LEU GLU GLU ALA GLY SER GLU ALA VAL GLN ALA MET ARG GLU LYS GLN LYS GLU LEU ILE ASN SER LEU ASN LEU ASP LYS TYR ALA ILE ASN ASP ASN SER GLU GLU TRP ALA GLU SER GLN LYS SER LEU GLU ILE ALA

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

- Molecule 57: Nucleolar complex protein 14

Chain RN:



- Molecule 58: Nucleolar complex protein 4

Chain RO: 94% 82% 13% 5%

MET VAL LEU LEU ILE SER GLU ILE LYS D10 I11 A12 K13 R14 L15 T16 A17 A18 G19 D20 R21 K22 Q23 Y24 N25 S26 I27 I28 K29 L30 I31 N32 E33 L34 V35 I36 P37 E38 N39 V40 T41 Q42 L43 E44 E45 D46 E47 T48 E49 K50 N51 L52 R53 F54 L55 V56 M57 S58 L59 F60

Q61 I62 F63 R64 K65 L66 F67 S68 R69 G70 D71 L72 T73 L74 P75 S76 S77 K78 K79 S80 T81 L82 E83 K84 E85 Q86 F87 V88 N89 W90 C91 R92 K93 V94 Y95 E96 A97 F98 K99 T100 K101 L102 L103 A104 I105 I106 S107 D108 I109 P110 F111 E112 T113 S114 L115 G116 L117 D118 S119 L120

D121 V122 Y123 L124 Q125 L126 A127 E128 L129 E130 S131 T132 H133 F134 A135 S136 E137 K138 G139 A140 P141 F142 F143 P144 N145 K146 T147 F148 R149 K150 L151 L152 I153 A154 L155 W156 S157 S158 N159 M160 G161 E162 I163 E164 D165 V166 K167 S168 S169 G170 A171 S172 E173 N174 L175 I176 I177 V178 E179 F180

T181 E182 K183 Y184 Y185 T186 K187 F188 A189 D190 I191 Q192 Y193 Y194 F195 Q196 S197 E198 F199 N200 Q201 L202 L203 E204 D205 P206 A207 Y208 Q209 D210 L211 L212 L213 K214 N215 V216 G217 K218 W219 L220 A221 L222 V223 N224 H225 D226 K227 H228 C229 S230 S231 V232 D233 A234 D235 L236 E237 I238 F239 V240

P241 N242 P243 P244 Q245 A246 I247 E248 N249 E250 S251 K252 F253 K254 S255 N256 F257 E258 K259 N260 W261 L262 S263 L264 L265 N266 G267 Q268 L269 S270 L271 Q272 Q273 Y274 K275 S276 I277 L278 L279 I280 L281 H282 K283 R284 I285 I286 P287 H288 F289 H290 T291 P292 T293 K294 L295 M296 D297 F298 L299 T300

D301 S302 Y303 N304 L305 Q306 S307 S308 N309 K310 N311 A312 G313 V314 V315 P316 I317 L318 A319 L320 N321 G322 L323 F324 E325 L326 M327 K328 R329 F330 N331 L332 E333 Y334 P335 N336 F337 Y338 M339 K340 L341 Y342 Q343 I344 I345 N346 P347 D348 L349 M350 H351 V352 K353 Y354 R355 A356 R357 F358 F359 R360

L361 M362 D363 V364 F365 L366 S367 S368 T369 H370 L371 S372 A373 H374 L375 V376 A377 S378 F379 I380 K381 K382 L383 A384 R385 L386 T387 L388 E389 S390 P391 P392 S393 A394 I395 V396 T397 V398 I399 P400 F401 I402 Y403 N404 L405 I406 R407 P410 N411 C412 M413 I414 M415 L416 H417 N418 P419 A420 F421

I422 S423 N424 P425 F426 Q427 T428 P429 D430 Q431 V432 A433 N434 L435 K436 T437 L438 K439 E440 N441 Y442 V443 D444 P445 F446 D447 V448 H449 E450 S451 D452 P453 E454 L455 T456 H457 A458 L459 D460 S461 S462 L463 W464 E465 L466 A467 S468 L469 M470 E471 H472 Y473 H474 P475 N476 V477 A478 T479 L480 A481

K482 I483 F484 A485 Q486 P487 F488 K489 K490 L491 S492 Y493 N494 M495 E496 D497 F498 L499 D500 W501 N502 Y503 D504 S505 L506 L507 N508 A509 E510 S511 S512 R513 K514 L515 K516 T517 L518 P519 T520 L521 E522 F523 E524 A525 F526 T527 N528 V529 F530 D531 N532 E533 D534 GLY ASP SER GLU ALA SER SER

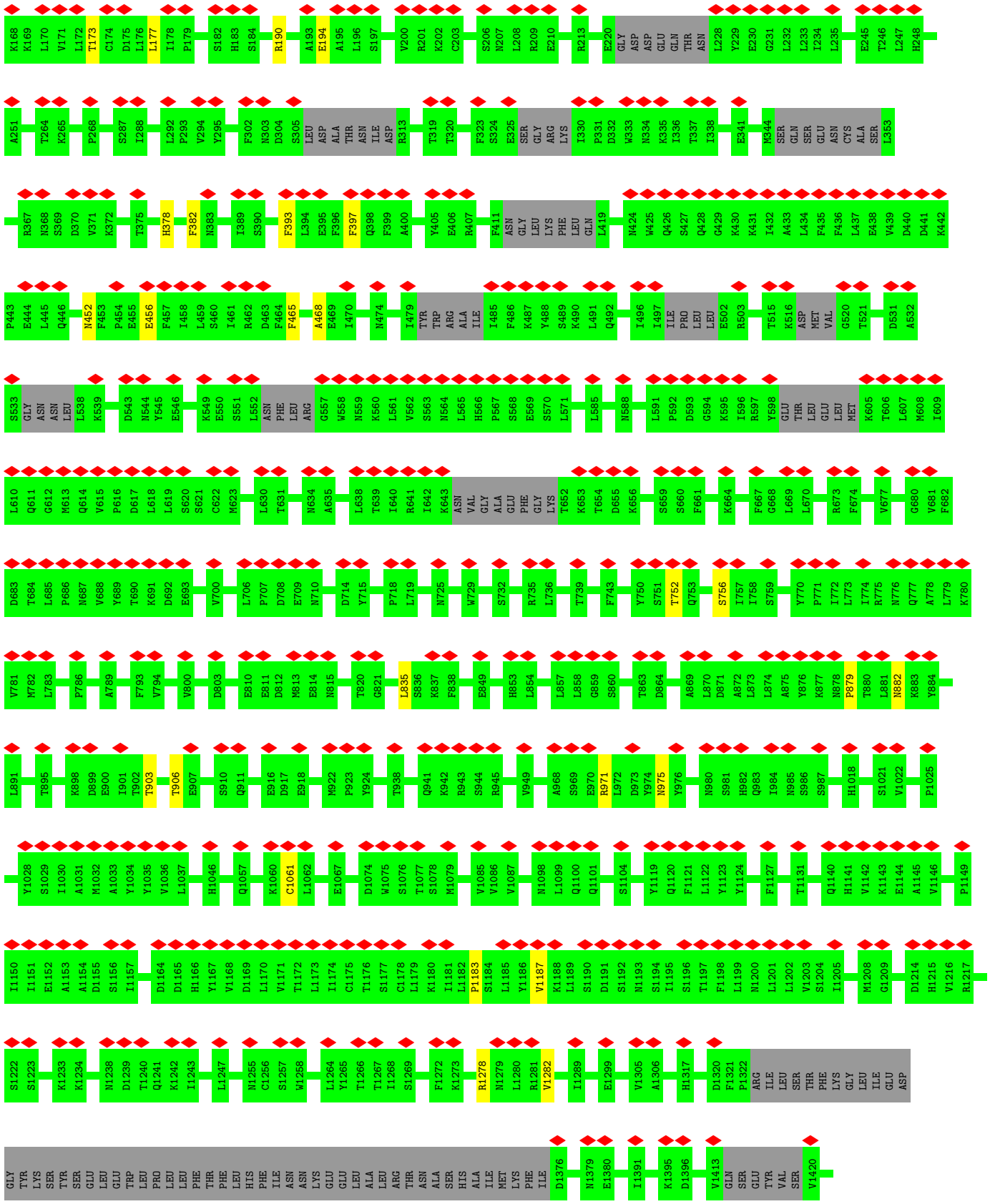
GLN GLY ASN VAL TYR LEU PRO GLY VAL ALA TRP

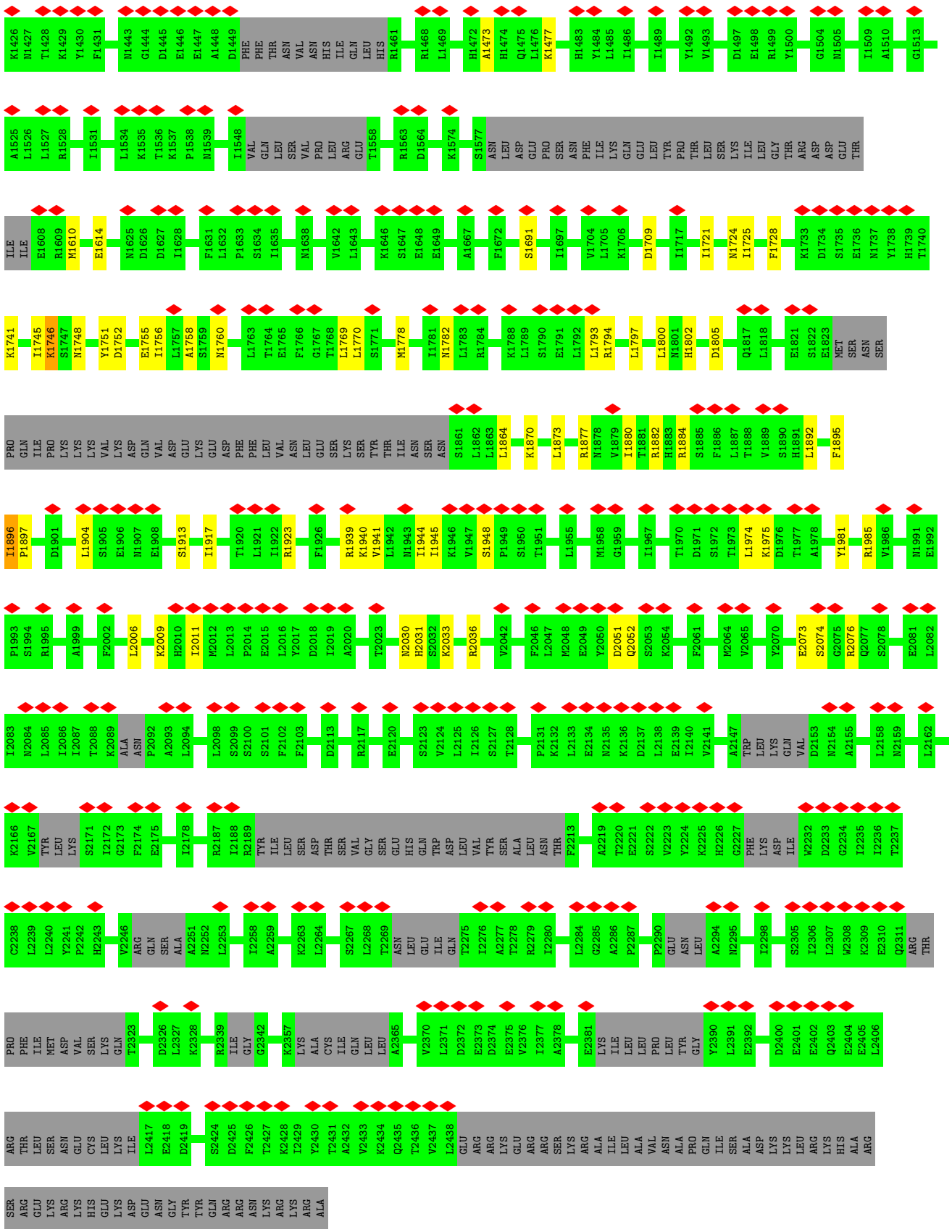
- Molecule 59: U3 small nucleolar RNA-associated protein 20

Chain RP: 31% 79% 5% 15%

MET ALA LYS GLN ARG GLN THR THR LYS SER SER LYS ARG TYR ARG TYR SER S18 F19 R22 E29 P30 A31 ARG ASN LEU GLU LYS ARG VAL HIS ASP TYR VAL GLU SER S45 L48 A49 W54 I57 N58 L59 S60 A61 K62 F63 T64 E65 F66 A67 A68 E69 I70 E71

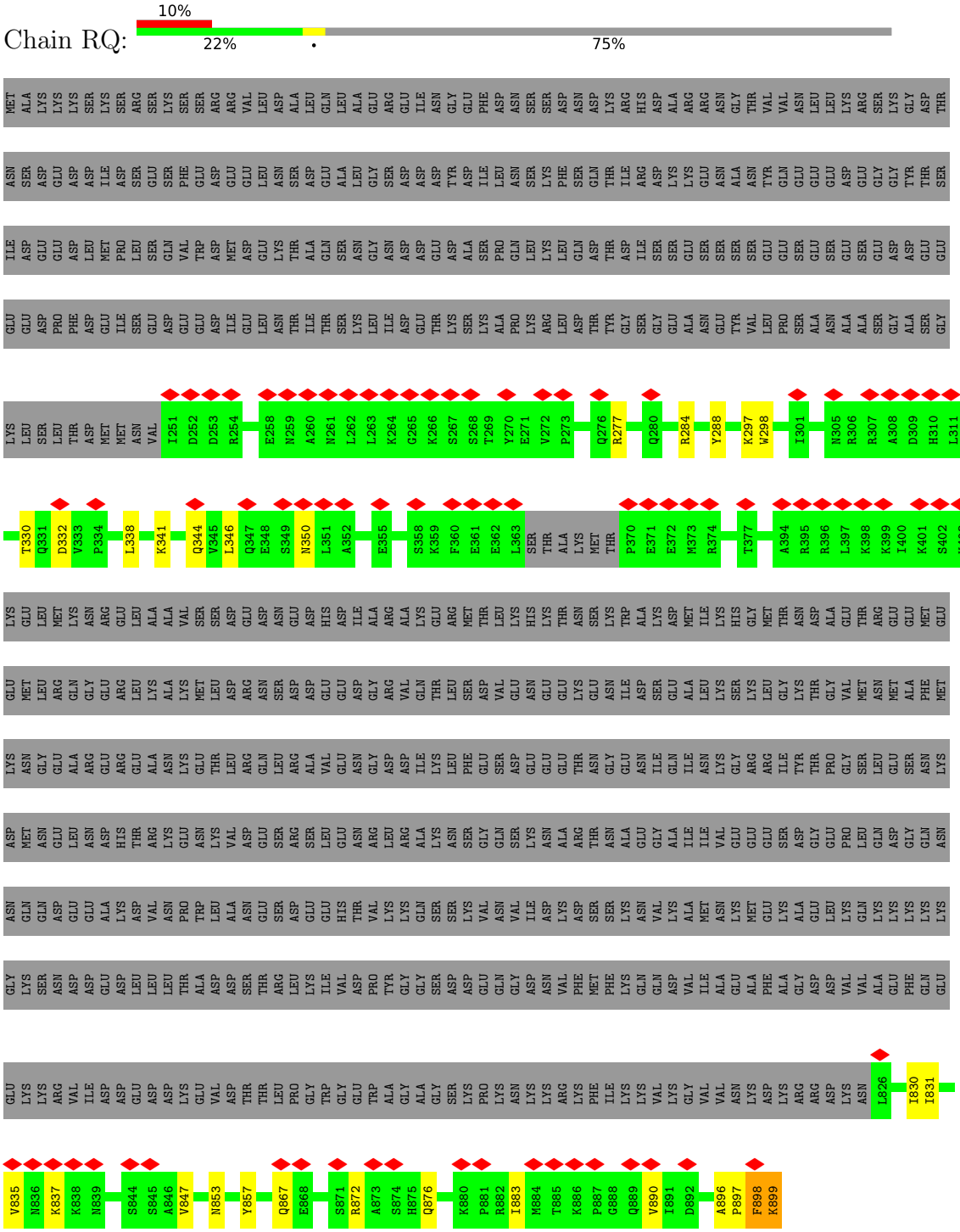
H72 D73 V74 Q75 T76 Q79 H83 D84 K85 K86 I87 F88 N89 S90 L91 E100 F101 S102 L103 Q104 P105 L106 L107 L110 A111 Q112 D116 L122 K123 E126 E127 A128 I129 K130 T131 L132 I133 A138 E141 F142 E143 S144 S145 N146 V147 F148 E149 W150 G151 F152


K168 K169 L170 V171 L172 T173 C174 D175 L176 L177 I178 P179 S182 H183 S184 R190 A193 E194 A195 L196 S197 V200 R201 K202 C203 S206 N207 L208 R209 E210 R213 E220 GLY ASP ASP GLU GLN THR ASN L228 Y229 E230 G231 L232 L233 I234 L235 E245 T246 L247 H248
A251 T264 K265 P268 S287 I288 L292 P293 V294 Y295 F302 N303 D304 S305 LEU ASP ALA THR ASN ILE ASP R313 T319 T320 F323 S324 E325 SER GLY ARG LYS I330 P331 D332 W333 N334 K335 I336 T337 I338 E341 M344 SER GLN SER GLU ASN CYS ALA SER L353
R367 N368 S369 D370 V371 K372 T375 H378 F382 N383 I389 S390 F393 L394 E395 F396 F397 Q398 F399 A400 Y405 E406 R407 F411 ASN GLY LEU LYS PHE LEU GLN L419 N424 W425 Q426 Q427 Q428 G429 K430 K431 I432 A433 L434 F435 F436 L437 E438 V439 D440 D441 K442
P443 E444 L445 Q446 N452 F453 P454 E455 E456 F457 I458 L459 S460 I461 R462 D463 F464 F465 A468 E469 I470 N474 I479 TYR TRP ARG ALA ILE I485 F486 K487 Y488 S489 K490 L491 Q492 I496 I497 ILE PRO LEU LEU E502 R503 T515 K516 ASP MET VAL G520 T521 D531 A532
S533 GLY ASN ASN LEU L538 K539 D543 N544 Y545 E546 K549 E550 S551 L552 ASN PHE LEU ARG G557 W558 N559 K560 L561 V562 S563 N564 L565 H566 P567 S568 E569 S570 L571 L585 N588 L591 P592 D593 G594 K595 I596 R597 Y598 GLU THR LEU GLU LEU MET K605 T606 L607 M608 I609
L610 Q611 G612 M613 Q614 V615 P616 D617 L618 L619 S620 S621 C622 M623 L630 T631 N634 A635 L638 T639 I640 R641 I642 K643 ASN VAL GLY ALA GLU PHE GLY LYS T652 K653 T654 D655 K656 S659 S660 F661 K664 F667 G668 L669 L670 R673 F674 V677 G680 V681 F682
D683 T684 L685 P686 N687 V688 Y689 T690 K691 D692 E693 V700 L706 P707 D708 E709 N710 D714 Y715 P718 L719 N725 W729 S732 R735 L736 T739 F743 Y750 S751 T752 Q753 S756 I757 I758 S759 Y770 P771 I772 L773 I774 R775 N776 Q777 A778 L779 K780
V781 M782 L783 P786 A789 F793 V794 V800 D803 E810 E811 D812 M813 E814 N815 T820 G821 L835 S836 K837 F838 E849 H853 L854 L857 L858 G859 S860 T863 D864 A869 L870 D871 A872 L873 L874 A875 Y876 K877 N878 P879 T880 L881 N882 K883 Y884
L891 T895 K898 D899 E900 I901 T902 T903 T906 E907 S910 Q911 E916 D917 E918 M922 P923 Y924 T938 Q941 K942 R943 S944 R945 V949 A968 S969 E970 R971 L972 D973 Y974 N975 Y976 N980 S981 H982 Q983 I984 N985 S986 S987 H1018 S1021 V1022 P1025
Y1028 S1029 I1030 A1031 M1032 A1033 Y1034 Y1035 V1036 L1037 H1046 Q1057 K1060 C1061 L1062 E1067 D1074 W1075 S1076 T1077 S1078 M1079 V1085 V1086 V1087 N1098 L1099 Q1100 Q1101 S1104 Y1119 Q1120 F1121 L1122 Y1123 Y1124 F1127 T1131 Q1140 H1141 V1142 K1143 E1144 A1145 V1146 P1149
I1150 I1151 E1152 A1153 A1154 D1155 S1156 I1157 D1164 D1165 H1166 Y1167 V1168 D1169 L1170 V1171 T1172 L1173 I1174 C1175 T1176 S1177 C1178 L1179 K1180 I1181 L1182 P1183 S1184 L1185 Y1186 V1187 K1188 L1189 S1190 D1191 S1192 N1193 S1194 I1195 S1196 T1197 F1198 L1199 N1200 L1201 L1202 V1203 S1204 I1205 M1208 G1209 D1214 H1215 V1216 R1217
S1222 S1223 K1233 K1234 N1238 D1239 T1240 Q1241 K1242 I1243 L1247 N1255 C1256 S1257 W1258 L1264 Y1265 T1266 T1267 I1268 S1269 F1272 K1273 R1278 N1279 L1280 R1281 V1282 I1289 E1299 V1305 A1306 H1317 D1320 F1321 P1322 ARG ILE LEU SER THR PHE LYS GLY LEU ILE GLU ASP
GLY TYR LYS SER TYR SER GLU LEU GLU TRP LEU PRO LEU LEU PHE THR PHE LEU HIS PHE ILE ASN ASN LYS GLU GLU LEU ALA LEU ARG THR ASN ALA SER HIS ALA ILE MET LYS PHE ILE D1376 N1379 E1380 I1391 K1395 D1396 V1413 GLN SER GLU TYR VAL SER V1420



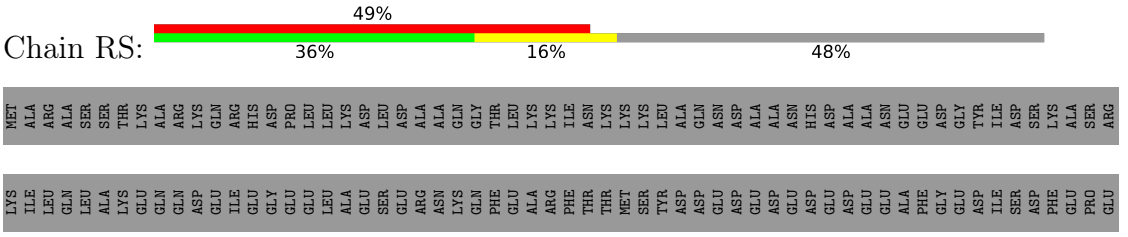
- Molecule 60: U3 small nucleolar RNA-associated protein 14

Chain RQ:



- Molecule 61: Essential nuclear protein 1

Chain RS:



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

GLU PRO LEU ALA ASN GLU GLN ASN THR SER ARG GLY ASN ILE SER SER GLY LEU LYS SER GLY GLU GLY VAL ALA LEU PRO GLU K209 V210 I211 K212 A213 Y214 T215 T216 V217 G218 S219 I220 L221 K222 T223 W224 T225 H226 G227 K228 L229 P230 K231 L232 F233 K234 V235 I236 P237 S238 L239 R240

N241 W242 Q243 D244 V245 I246 Y247 V248 T249 N250 P251 E252 E253 W254 S255 P256 H257 V258 V259 Y260 E261 A262 T263 K264 L265 F266 V267 S268 N269 L270 T271 A272 K273 E274 S275 Q276 K277 F278 I279 N280 L281 I282 L283 L284 E285 R286 F287 R288 D289 N290 I291 E292 T293 S294 E295 D296 H297 S298 L299 N300

Y301 H302 I303 Y304 R305 A306 V307 K308 K309 S310 L311 Y312 K313 P314 S315 A316 F317 F318 K319 G320 F321 L322 F323 P324 L325 V326 E327 T328 G329 C330 N331 A335 T336 I337 A338 G339 S340 V341 L342 A343 K344 V345 S346 V347 P348 A349 L350 H351 S352 S353 A354 A355 L356 S357 Y358 L359 L360 R361 L362

P363 F364 S365 P366 P367 T368 T369 V370 F371 I372 K373 I374 L375 L376 D377 K378 K379 Y380 A381 L382 P383 Y384 Q385 T386 V387 D388 D389 C390 V391 Y392 Y393 F394 M395 R396 F397 R398 I399 LEU ASP ASP GLY SER ASN G406 E407 D408 A409 T410 R411 V412 L413 P414 V415 I416 W417 H418 K419 A420 F421 L422

T423 F424 A425 Q426 R427 Y428 K429 N430 D431 I432 T433 Q434 D435 Q436 R437 D438 F439 L440 L441 E442 T443 V444 R445 Q446 R447 G448 H449 K450 D451 I452 G453 P454 E455 I456 R457 R458 E459 L460 L461 A462 G463 A464 S465 ARG GLU PHE VAL ASP PRO GLN GLU ALA ASN ASP ASP LEU MET ILE ASP VAL

ASN

- Molecule 62: Pno1

Chain RT: 22% 40% 10% 48%

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

GLY SER ARG LYS THR HIS GLU SER LYS THR VAL VAL VAL ASP ASP GLN GLY LYS PRO ARG PHE THR SER ALA SER LYS THR GLN GLY ASN LYS ILE LYS PHE E95 K98 I99 L109 R110 N111 S112 W113 T114 K115 I116 Y117 P118 P119 H123 L124 V128 R129 M130 N131 L132

E138 K144 PHE THR THR ASP PRO G150 K154 D157 F158 I159 K160 A161 L168 D169 D170 S171 I172 A173 L174 L175 R176 L177 D178 D179 L180 Y181 I182 E186 V187 K188 D189 VAL LYS THR LEU T194 G195 S199 R200 R204 K208 D209 G210 K211 T212 K213 F214 A215 I216 E217

N218 A219 T220 R221 T222 R223 I224 V225 L226 A227 D228 I233 L234 G235 G236 F237 T238 H239 I240 R241 M242 A243 R244 V247 L250 I251 S254 P255 P256 G257 K258 V259 Y260 G261 N262 L263 R264 T265 V266 A267 S268 R269 L270 K271 E272 ARG TYR GLY ARG ARG ILE PRO GLY LEU ILE ASN

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

- Molecule 63: Protein BFR2

Chain RY: 6% 93%

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

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

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

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

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

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

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

LEU ILE ASP LYS LYS ILE SER ASN ALA HIS ASN SER GLU SER ALA ALA ILE THR ILE THR SER THR ASN ALA ARG SER ASN ASN LYS LEU LYS LYS ASN ILE ASP THR LYS ALA SER K460 G461 R462 V468 Q469 D470 P471 I472 A473 N474 Y475 E476 A477 P478 I479 T480 S481 G482 Y483 K484

W485 S486 D487 D488 Q489 I490 D491 E492 F493 F494 A495 G496 LEU LEU GLY GLN ARG VAL ASN PHE ASN GLU ASN GLU ASP GLU GLU GLN HIS ALA ARG ILE GLU ASN ASP GLU GLU LEU GLU ALA VAL LYS ASN ASP ASP ILE GLN ILE PHE GLY

- Molecule 64: Unassigned helices

Chain X1: 5% 94%

UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK

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X301 X305 X306 X307 X308 X309 X310 X311 X312 X313 X314 UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK UNK X1500 X1503 X1506 X1507

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3050	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	0.062	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	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 (i)

5.1 Standard geometry (i)

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

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	0.46	0/4141	0.62	3/6433 (0.0%)
2	5A	0.40	0/4605	0.46	1/7168 (0.0%)
3	SA	0.35	0/30585	0.47	8/47611 (0.0%)
4	SC	0.44	0/1856	0.77	3/2490 (0.1%)
5	SF	0.29	0/1854	0.66	0/2504
6	SG	0.49	0/1690	0.67	2/2285 (0.1%)
7	SH	0.24	0/1341	0.61	1/1789 (0.1%)
8	SI	0.32	0/1341	0.69	2/1806 (0.1%)
9	SJ	0.26	0/1347	0.60	0/1801
10	SK	0.44	0/1410	0.63	0/1888
11	SM	0.26	0/1020	0.64	0/1374
12	SO	0.39	0/1109	0.63	0/1495
13	SP	0.47	0/879	0.80	0/1186
14	SR	0.52	0/990	0.77	3/1335 (0.2%)
15	SX	0.46	0/1020	0.63	0/1371
16	SY	0.48	0/798	0.65	0/1065
17	SZ	0.36	0/822	0.73	0/1103
18	Sc	0.40	0/613	0.63	0/828
19	Sd	0.50	0/499	0.72	2/670 (0.3%)
20	3B	0.51	0/1901	0.66	1/2567 (0.0%)
20	3C	0.37	0/1796	0.67	0/2424
21	3D	0.40	0/2891	0.62	0/3895
22	3E	0.38	0/3059	0.62	0/4153
23	3F	0.36	0/3715	0.64	0/5001
24	3G	0.51	0/928	0.72	1/1262 (0.1%)
24	3H	0.45	0/928	0.70	0/1262
25	A4	0.43	0/5321	0.66	0/7207
26	A5	0.44	0/4044	0.65	0/5493
27	A8	0.38	0/3249	0.86	12/4454 (0.3%)
28	A9	0.29	0/951	0.61	0/1287
29	AE	0.32	1/10049 (0.0%)	0.56	1/13737 (0.0%)
30	AF	0.48	0/3993	0.68	0/5413

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
31	AG	0.42	0/6699	0.64	3/9077 (0.0%)
32	B1	0.59	0/6474	0.70	3/8763 (0.0%)
33	B2	0.39	0/6628	0.69	2/8954 (0.0%)
34	B3	0.35	0/6014	0.70	2/8137 (0.0%)
35	B8	0.55	0/3848	0.63	0/5218
36	BE	0.54	0/6580	0.65	2/8901 (0.0%)
37	B6	0.37	0/2849	0.60	0/3853
38	5B	0.31	0/499	0.62	0/659
39	5C	0.58	0/3690	0.67	2/4991 (0.0%)
40	5D	0.47	0/1417	0.74	0/1885
41	5E	0.42	0/1580	0.87	1/2115 (0.0%)
42	5F	0.37	0/1559	0.81	2/2097 (0.1%)
43	5G	0.34	0/1792	0.76	3/2425 (0.1%)
44	5H	0.47	0/601	0.59	0/789
45	5I	0.56	0/3844	0.68	0/5174
46	5J	0.37	0/1302	0.59	0/1728
47	5K	0.51	0/1426	0.66	0/1917
48	RA	0.27	0/2769	0.66	2/3753 (0.1%)
49	RB	0.37	0/1121	0.79	0/1487
50	RD	0.26	0/2453	0.67	2/3308 (0.1%)
51	RE	0.33	0/8924	0.64	4/12070 (0.0%)
52	RF	0.28	0/2004	0.66	1/2697 (0.0%)
53	RG	0.32	0/1727	0.70	0/2329
53	RH	0.37	0/1828	0.59	0/2470
54	RJ	0.44	0/6514	0.62	0/8768
55	RK	0.39	0/2832	0.64	0/3825
56	RL	0.21	0/4549	0.51	1/6241 (0.0%)
56	RM	0.15	0/3765	0.44	1/5218 (0.0%)
57	RN	0.31	0/4591	0.63	1/6187 (0.0%)
58	RO	0.32	0/3849	0.63	0/5261
59	RP	0.21	0/12225	0.54	4/16812 (0.0%)
60	RQ	0.41	0/1678	0.63	1/2282 (0.0%)
61	RS	0.30	0/2104	0.70	0/2854
62	RT	0.37	0/1355	0.74	0/1821
63	RY	0.23	0/307	0.53	0/415
All	All	0.39	1/222142 (0.0%)	0.62	77/308838 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
12	SO	0	1
13	SP	0	1
17	SZ	0	1
18	Sc	0	1
21	3D	0	3
22	3E	0	1
23	3F	0	1
24	3G	0	2
24	3H	0	1
25	A4	0	1
26	A5	0	1
27	A8	0	2
31	AG	0	2
32	B1	0	2
33	B2	0	8
34	B3	0	11
36	BE	0	1
39	5C	0	1
40	5D	0	1
43	5G	0	2
45	5I	0	2
48	RA	0	2
49	RB	0	1
51	RE	0	1
52	RF	0	1
54	RJ	0	2
55	RK	0	1
56	RL	0	1
56	RM	0	1
57	RN	0	1
58	RO	0	1
59	RP	0	3
60	RQ	0	1
62	RT	0	1
All	All	0	71

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	AE	564	VAL	C-N	5.39	1.40	1.34

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	SA	1783	C	C4'-C3'-O3'	10.71	129.07	113.00
27	A8	316	PRO	N-CA-CB	10.46	109.82	102.81
1	3A	99	U	C4'-C3'-O3'	8.84	126.25	113.00
1	3A	317	A	C4'-C3'-O3'	8.46	125.68	113.00
27	A8	258	PRO	N-CA-CB	8.38	112.05	103.25

There are no chirality outliers.

5 of 71 planarity outliers are listed below:

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

5.2 Too-close contacts (i)

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	58	0
2	5A	4117	0	2068	38	0
3	SA	27362	0	13798	266	0
4	SC	1830	0	1914	33	0
5	SF	1815	0	1870	45	0
6	SG	1669	0	1724	18	0
7	SH	1327	0	1403	30	0
8	SI	1321	0	1387	23	0
9	SJ	1324	0	1344	48	0
10	SK	1388	0	1467	32	0
11	SM	997	0	1048	34	0
12	SO	1087	0	1152	10	0
13	SP	868	0	894	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	SR	973	0	1029	19	0
15	SX	1003	0	1040	16	0
16	SY	786	0	843	8	0
17	SZ	809	0	842	15	0
18	Sc	603	0	623	9	0
19	Sd	497	0	535	3	0
20	3B	1865	0	1910	30	0
20	3C	1763	0	1805	43	0
21	3D	2848	0	2815	46	0
22	3E	3028	0	2813	62	0
23	3F	3643	0	3654	79	0
24	3G	916	0	964	11	0
24	3H	916	0	964	26	0
25	A4	5226	0	5199	96	0
26	A5	3976	0	3919	60	0
27	A8	3229	0	2281	133	0
28	A9	939	0	898	47	0
29	AE	9955	0	7968	103	0
30	AF	3911	0	3906	75	0
31	AG	6570	0	6473	143	0
32	B1	6331	0	6236	151	0
33	B2	6502	0	6493	122	0
34	B3	5919	0	6007	139	0
35	B8	3764	0	3757	58	0
36	BE	6450	0	6420	97	0
37	B6	2800	0	2517	35	0
38	5B	495	0	561	13	0
39	5C	3612	0	3578	65	0
40	5D	1396	0	1407	46	0
41	5E	1564	0	1592	165	0
42	5F	1530	0	1572	82	0
43	5G	1756	0	1765	57	0
44	5H	596	0	661	8	0
45	5I	3765	0	3714	76	0
46	5J	1280	0	1331	24	0
47	5K	1403	0	1484	17	0
48	RA	2709	0	2622	64	0
49	RB	1108	0	1087	27	0
50	RD	2412	0	2263	40	0
51	RE	8716	0	8828	239	0
52	RF	1963	0	1942	45	0
53	RG	1701	0	1767	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	RH	1799	0	1872	29	0
54	RJ	6379	0	6506	147	0
55	RK	2781	0	2878	51	0
56	RL	4539	0	2874	29	0
56	RM	3779	0	1650	8	0
57	RN	4529	0	4262	86	0
58	RO	3766	0	3269	47	0
59	RP	12171	0	7749	76	0
60	RQ	1651	0	1450	28	0
61	RS	2051	0	2096	53	0
62	RT	1334	0	1404	58	0
63	RY	299	0	275	6	0
64	X1	110	0	29	4	0
65	5K	1	0	0	0	0
65	Sc	1	0	0	0	0
66	RJ	32	0	12	2	0
67	RJ	1	0	0	0	0
All	All	215267	0	186362	3316	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 8.

The worst 5 of 3316 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)
27:A8:596:LYS:HE3	27:A8:637:LEU:CD2	1.25	1.58
51:RE:1203:ASN:HD22	51:RE:1219:ILE:CG2	1.50	1.22
32:B1:382:THR:O	41:5E:481:PRO:HB3	1.40	1.22
62:RT:174:LEU:CG	62:RT:180:LEU:HD21	1.69	1.22
27:A8:596:LYS:HE3	27:A8:637:LEU:HD23	1.23	1.21

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	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100	100
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	30	67
6	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
7	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
8	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
9	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/156 (76%)	103 (87%)	16 (13%)	0	100	100
12	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
13	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	14	51
14	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
15	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
16	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
17	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	12	49
18	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100
19	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
20	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
20	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
21	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
22	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
23	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	43	78
24	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	16	54
24	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
25	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
26	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
27	A8	516/713 (72%)	397 (77%)	107 (21%)	12 (2%)	5	28
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%)	48	83

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	B1	787/923 (85%)	732 (93%)	55 (7%)	0	100	100
33	B2	813/943 (86%)	724 (89%)	87 (11%)	2 (0%)	43	78
34	B3	733/817 (90%)	606 (83%)	125 (17%)	2 (0%)	36	72
35	B8	469/594 (79%)	439 (94%)	30 (6%)	0	100	100
36	BE	814/939 (87%)	765 (94%)	49 (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	452/554 (82%)	419 (93%)	32 (7%)	1 (0%)	43	78
40	5D	165/250 (66%)	145 (88%)	20 (12%)	0	100	100
41	5E	187/593 (32%)	175 (94%)	10 (5%)	2 (1%)	11	46
42	5F	180/183 (98%)	164 (91%)	16 (9%)	0	100	100
43	5G	217/290 (75%)	203 (94%)	14 (6%)	0	100	100
44	5H	72/610 (12%)	65 (90%)	7 (10%)	0	100	100
45	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
46	5J	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%)	16	54
50	RD	310/1729 (18%)	284 (92%)	23 (7%)	3 (1%)	12	49
51	RE	1067/1237 (86%)	999 (94%)	68 (6%)	0	100	100
52	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
53	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
53	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
54	RJ	784/1183 (66%)	721 (92%)	62 (8%)	1 (0%)	48	83
55	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
56	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	36	72
56	RM	738/1056 (70%)	625 (85%)	109 (15%)	4 (0%)	24	63
57	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	43	78
58	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
59	RP	2042/2493 (82%)	1815 (89%)	226 (11%)	1 (0%)	100	100
60	RQ	220/899 (24%)	199 (90%)	21 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
62	RT	163/326 (50%)	147 (90%)	16 (10%)	0	100	100
63	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
All	All	23878/33924 (70%)	21529 (90%)	2311 (10%)	38 (0%)	44	78

5 of 38 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	SC	203/224 (91%)	201 (99%)	2 (1%)	68	78
5	SF	196/222 (88%)	193 (98%)	3 (2%)	57	72
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	83
7	SH	139/201 (69%)	136 (98%)	3 (2%)	45	64
8	SI	146/170 (86%)	143 (98%)	3 (2%)	47	65
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	57	72
10	SK	147/166 (89%)	147 (100%)	0	100	100
11	SM	110/137 (80%)	108 (98%)	2 (2%)	51	68
12	SO	117/128 (91%)	116 (99%)	1 (1%)	70	79
13	SP	90/105 (86%)	88 (98%)	2 (2%)	45	64
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	106 (98%)	2 (2%)	50	67
16	SY	85/120 (71%)	83 (98%)	2 (2%)	43	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	SZ	85/113 (75%)	85 (100%)	0	100	100
18	Sc	69/71 (97%)	69 (100%)	0	100	100
19	Sd	56/60 (93%)	56 (100%)	0	100	100
20	3B	201/240 (84%)	201 (100%)	0	100	100
20	3C	190/240 (79%)	188 (99%)	2 (1%)	65	76
21	3D	296/435 (68%)	295 (100%)	1 (0%)	86	86
22	3E	262/433 (60%)	261 (100%)	1 (0%)	84	84
23	3F	396/503 (79%)	392 (99%)	4 (1%)	68	78
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%)	63	75
26	A5	433/574 (75%)	429 (99%)	4 (1%)	70	79
27	A8	174/657 (26%)	168 (97%)	6 (3%)	32	54
28	A9	89/533 (17%)	89 (100%)	0	100	100
29	AE	708/1633 (43%)	705 (100%)	3 (0%)	84	84
30	AF	437/454 (96%)	431 (99%)	6 (1%)	59	72
31	AG	750/826 (91%)	739 (98%)	11 (2%)	57	72
32	B1	696/812 (86%)	685 (98%)	11 (2%)	55	70
33	B2	712/832 (86%)	705 (99%)	7 (1%)	68	78
34	B3	665/719 (92%)	656 (99%)	9 (1%)	59	72
35	B8	421/529 (80%)	417 (99%)	4 (1%)	68	78
36	BE	718/819 (88%)	712 (99%)	6 (1%)	73	80
37	B6	251/414 (61%)	249 (99%)	2 (1%)	73	80
38	5B	57/196 (29%)	56 (98%)	1 (2%)	51	68
39	5C	394/480 (82%)	392 (100%)	2 (0%)	81	83
40	5D	156/234 (67%)	156 (100%)	0	100	100
41	5E	175/535 (33%)	162 (93%)	13 (7%)	13	33
42	5F	171/172 (99%)	169 (99%)	2 (1%)	63	75
43	5G	194/258 (75%)	194 (100%)	0	100	100
44	5H	63/538 (12%)	63 (100%)	0	100	100
45	5I	416/443 (94%)	412 (99%)	4 (1%)	68	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	299 (99%)	4 (1%)	61	74
49	RB	117/315 (37%)	116 (99%)	1 (1%)	70	79
50	RD	226/1544 (15%)	224 (99%)	2 (1%)	70	79
51	RE	984/1125 (88%)	976 (99%)	8 (1%)	73	80
52	RF	221/274 (81%)	221 (100%)	0	100	100
53	RG	195/222 (88%)	193 (99%)	2 (1%)	68	78
53	RH	206/222 (93%)	205 (100%)	1 (0%)	81	83
54	RJ	683/1039 (66%)	678 (99%)	5 (1%)	76	81
55	RK	307/312 (98%)	304 (99%)	3 (1%)	68	78
56	RL	164/934 (18%)	164 (100%)	0	100	100
57	RN	422/732 (58%)	421 (100%)	1 (0%)	87	87
58	RO	329/506 (65%)	326 (99%)	3 (1%)	70	79
59	RP	499/2307 (22%)	496 (99%)	3 (1%)	78	83
60	RQ	148/808 (18%)	145 (98%)	3 (2%)	48	66
61	RS	225/424 (53%)	224 (100%)	1 (0%)	84	84
62	RT	146/282 (52%)	143 (98%)	3 (2%)	47	65
63	RY	31/482 (6%)	31 (100%)	0	100	100
All	All	17291/29262 (59%)	17122 (99%)	169 (1%)	65	78

5 of 169 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	5E	451	LEU
51	RE	1189	LEU
41	5E	517	LYS
48	RA	155	VAL
54	RJ	976	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 417 such sidechains are listed below:

Mol	Chain	Res	Type
36	BE	736	HIS

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Mol	Chain	Res	Type
45	5I	371	ASN
59	RP	58	ASN
37	B6	115	ASN
41	5E	303	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	55 (32%)	8 (4%)
2	5A	186/700 (26%)	54 (29%)	4 (2%)
3	SA	1262/1809 (69%)	483 (38%)	19 (1%)
All	All	1617/2842 (56%)	592 (36%)	31 (1%)

5 of 592 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 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	56	U
3	SA	1521	G
3	SA	372	G
3	SA	1632	C
3	SA	1052	U

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 3 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	$\#\|Z\| > 2$
66	GTP	RJ	1201	67	33,34,34	0.56	0	50,54,54	0.72	1 (2%)

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
66	GTP	RJ	1201	67	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
66	RJ	1201	GTP	C4'-O4'-C1'	-2.15	104.72	109.47

There are no chirality outliers.

All (3) torsion outliers are listed below:

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

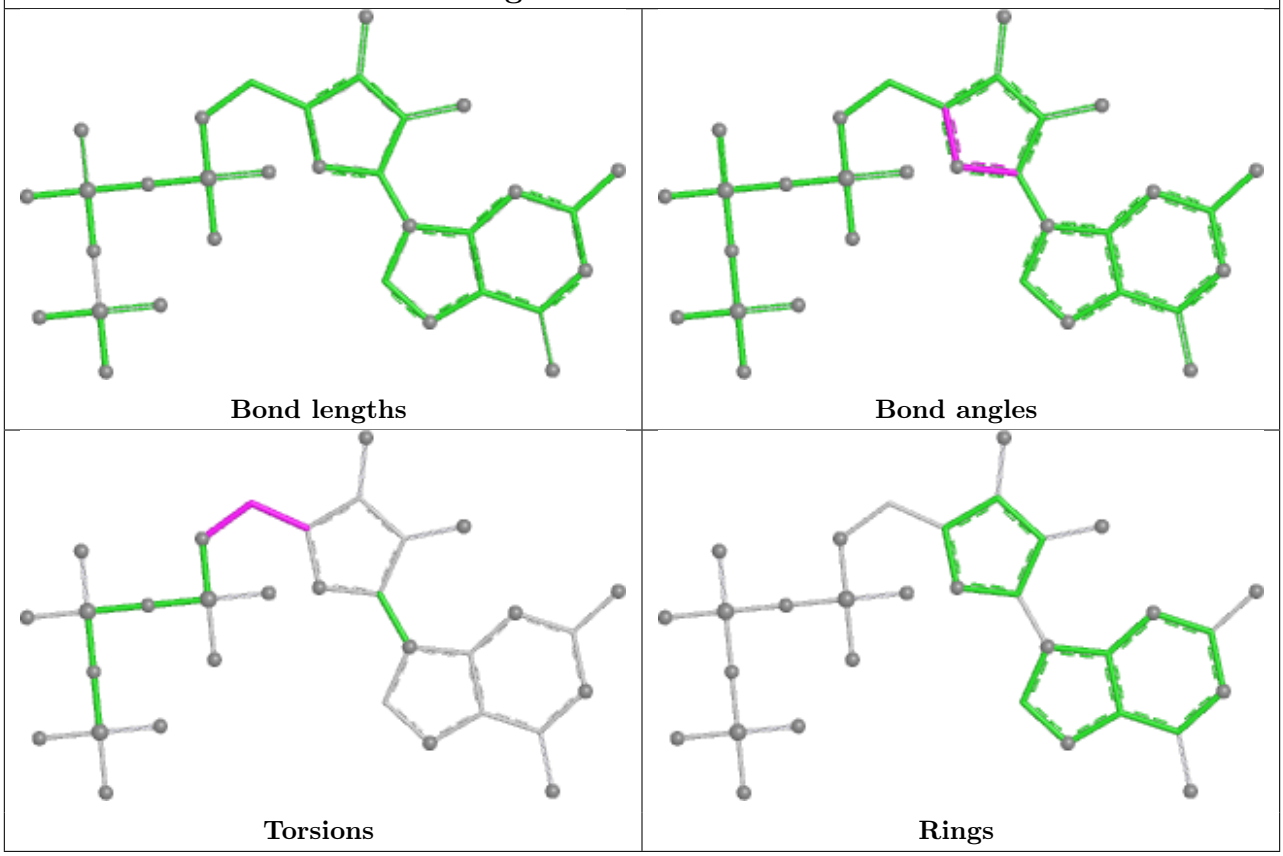
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	RJ	1201	GTP	2	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.

Ligand GTP RJ 1201



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

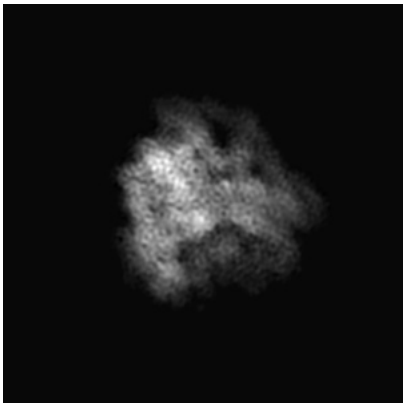
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-0951. These allow visual inspection of the internal detail of the map and identification of artifacts.

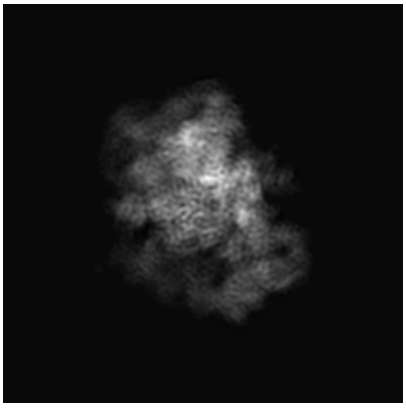
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

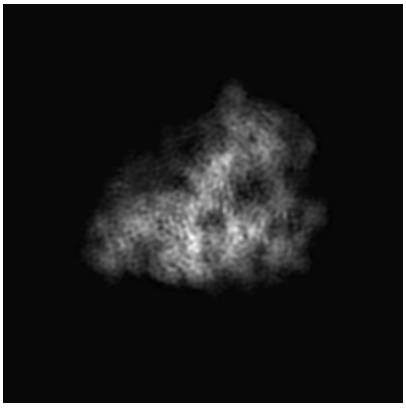
6.1.1 Primary map



X



Y

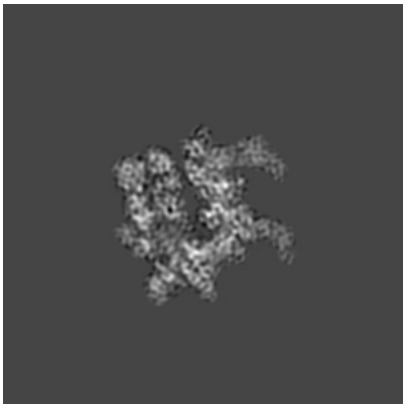


Z

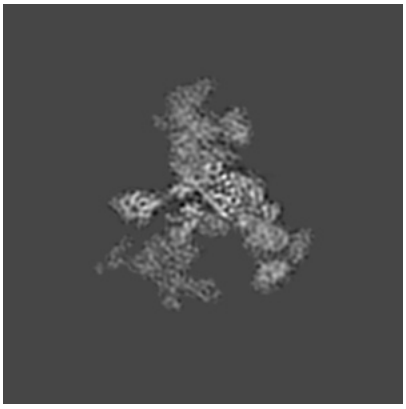
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

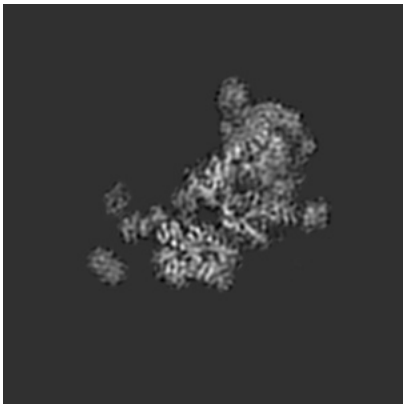
6.2.1 Primary map



X Index: 224



Y Index: 224

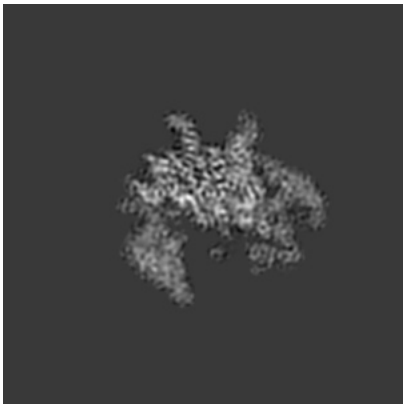


Z Index: 224

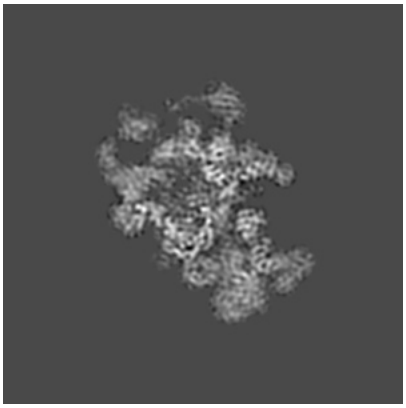
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

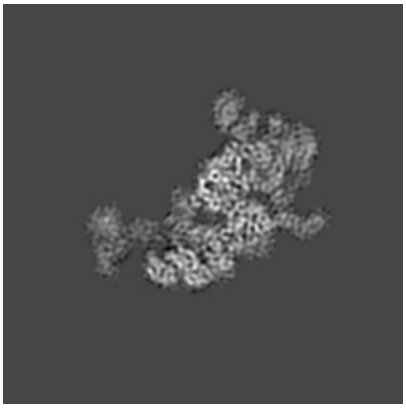
6.3.1 Primary map



X Index: 252



Y Index: 194

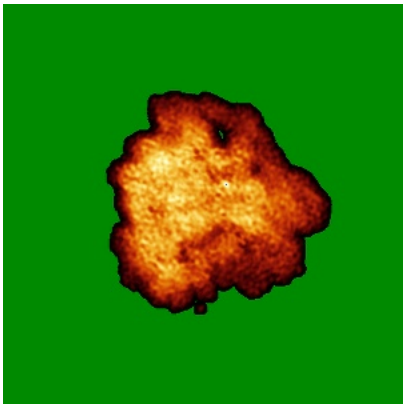


Z Index: 243

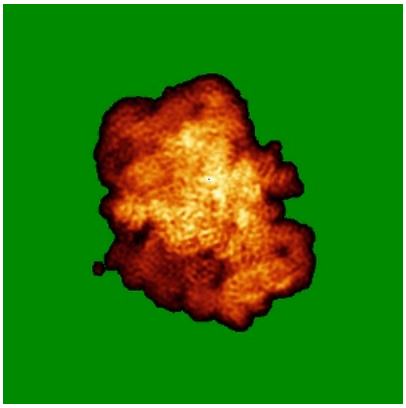
The images above show the largest variance slices of the map in three orthogonal directions.

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

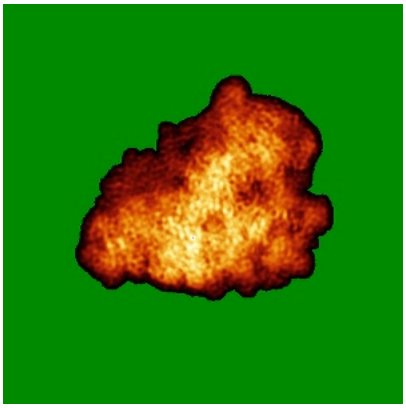
6.4.1 Primary map



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

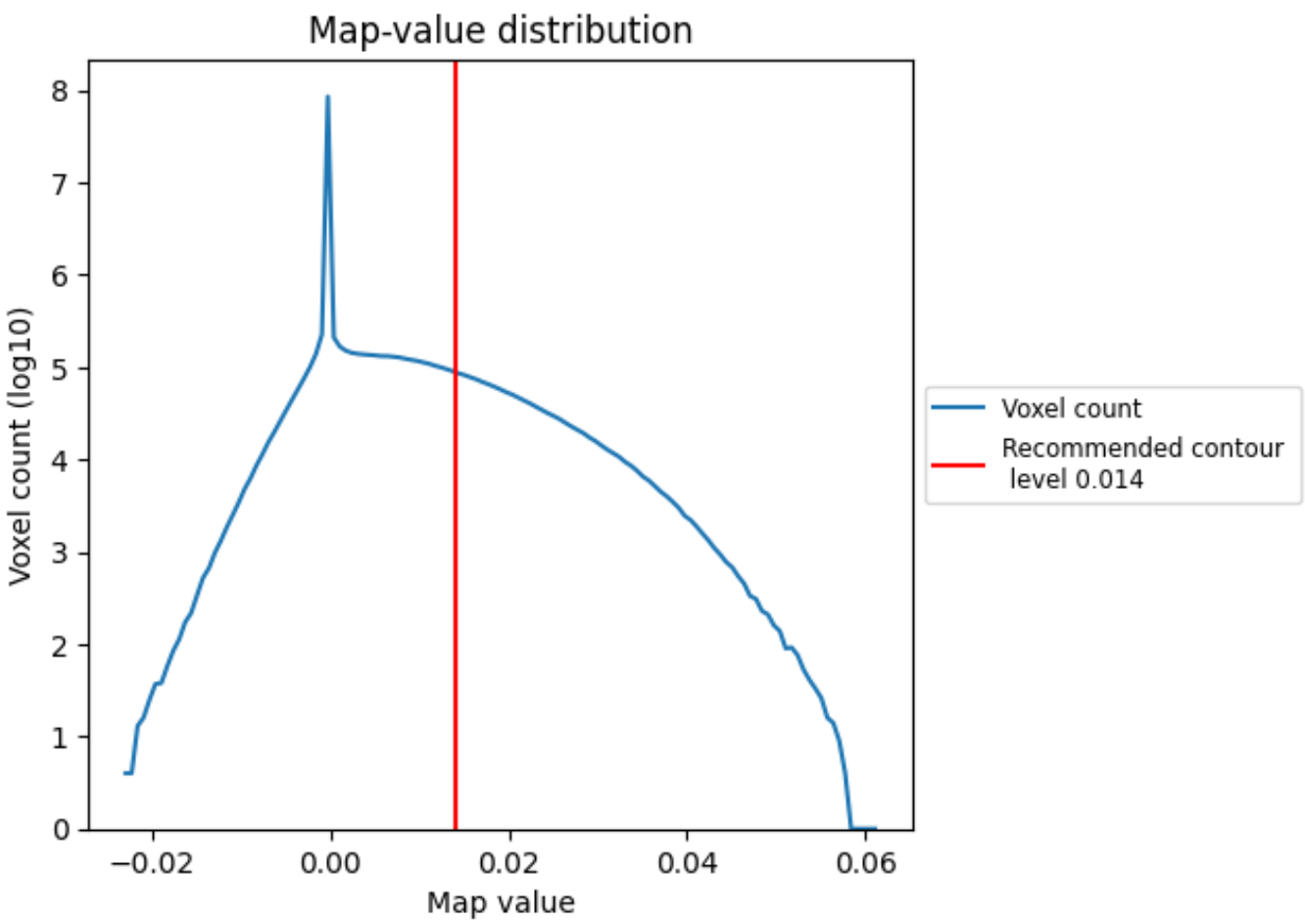
6.6 Mask visualisation (i)

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

7 Map analysis (i)

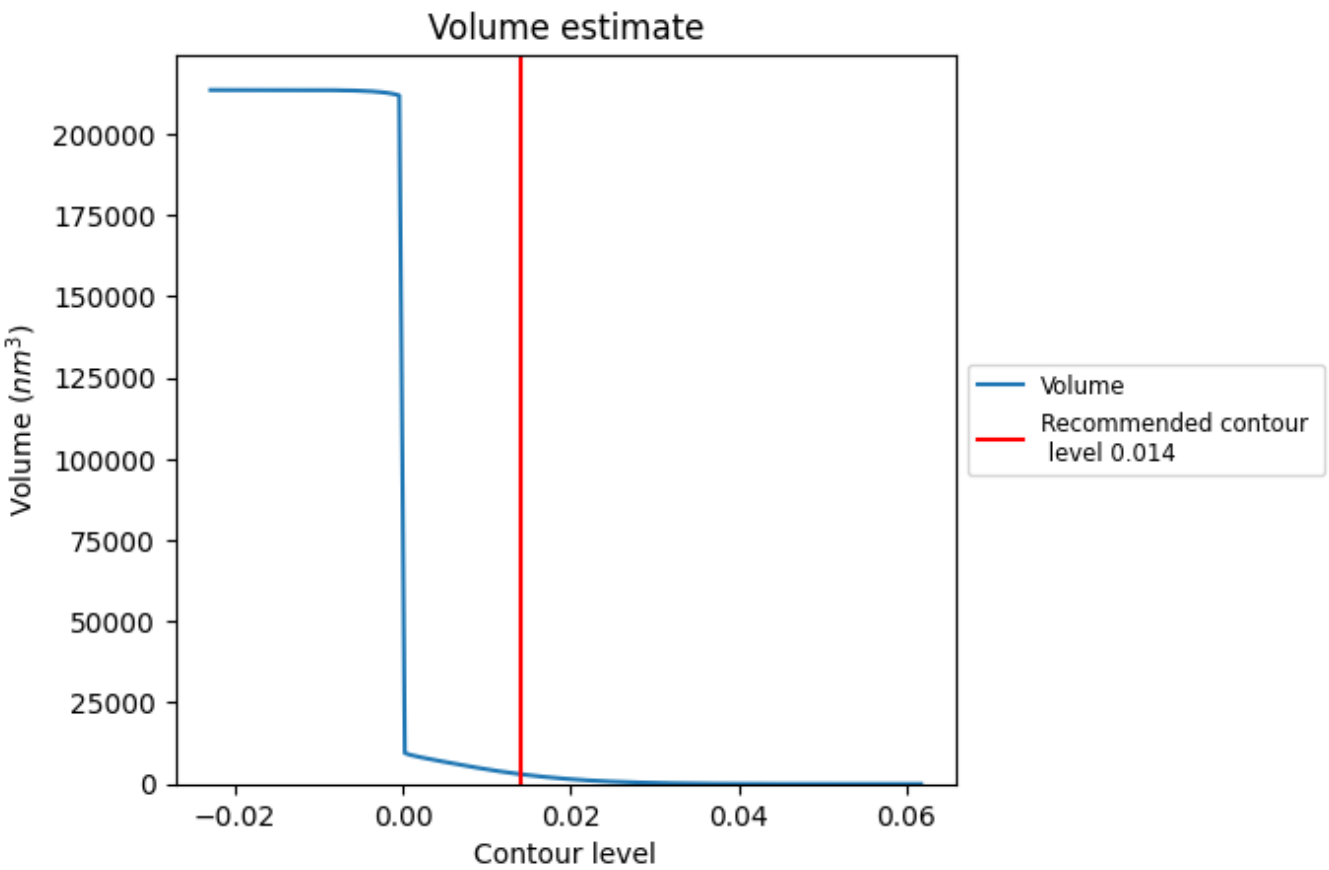
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

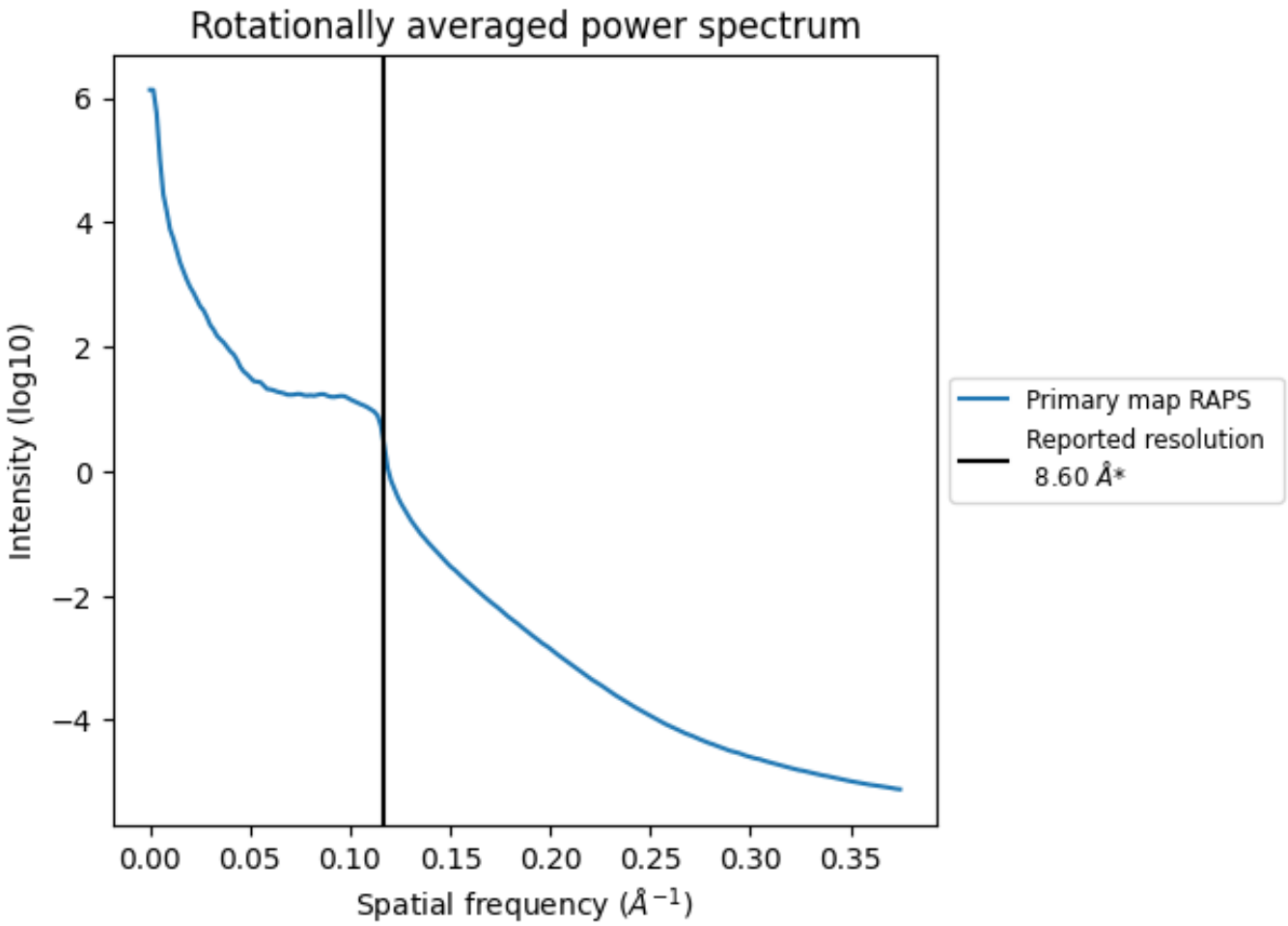
7.2 Volume estimate (i)



The volume at the recommended contour level is 3008 nm^3; this corresponds to an approximate mass of 2717 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 0.116 Å^{-1}

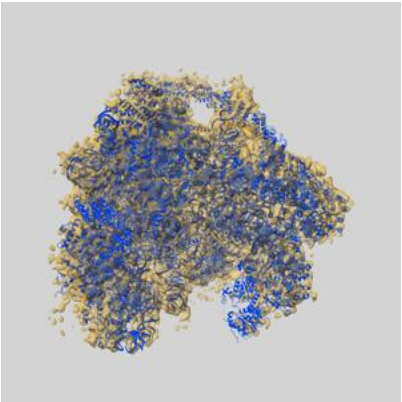
8 Fourier-Shell correlation (i)

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

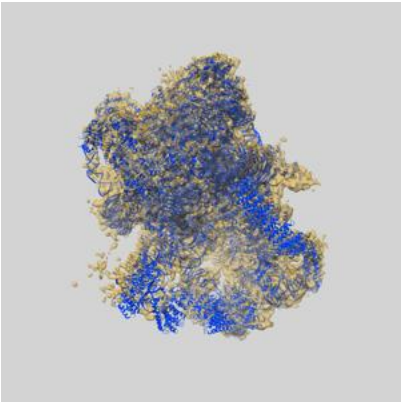
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-0951 and PDB model 6LQR. Per-residue inclusion information can be found in section 3 on page 17.

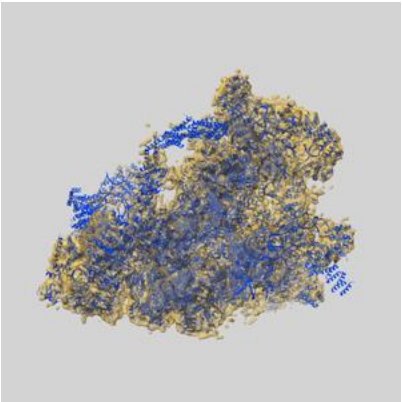
9.1 Map-model overlay (i)



X



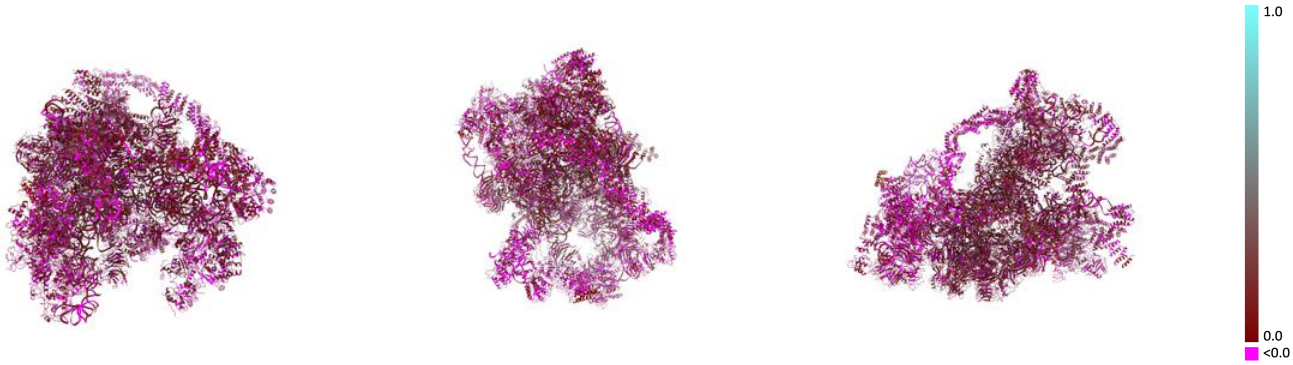
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

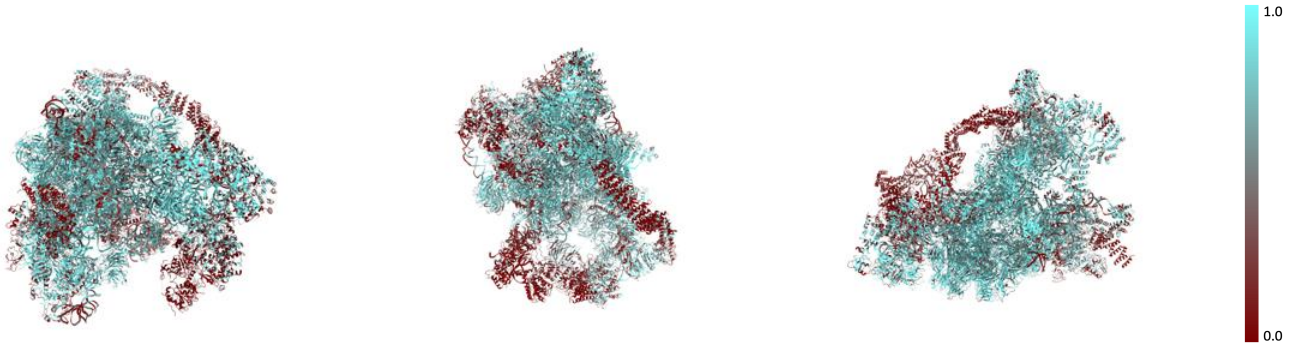
9.2 Q-score mapped to coordinate model (i)



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.

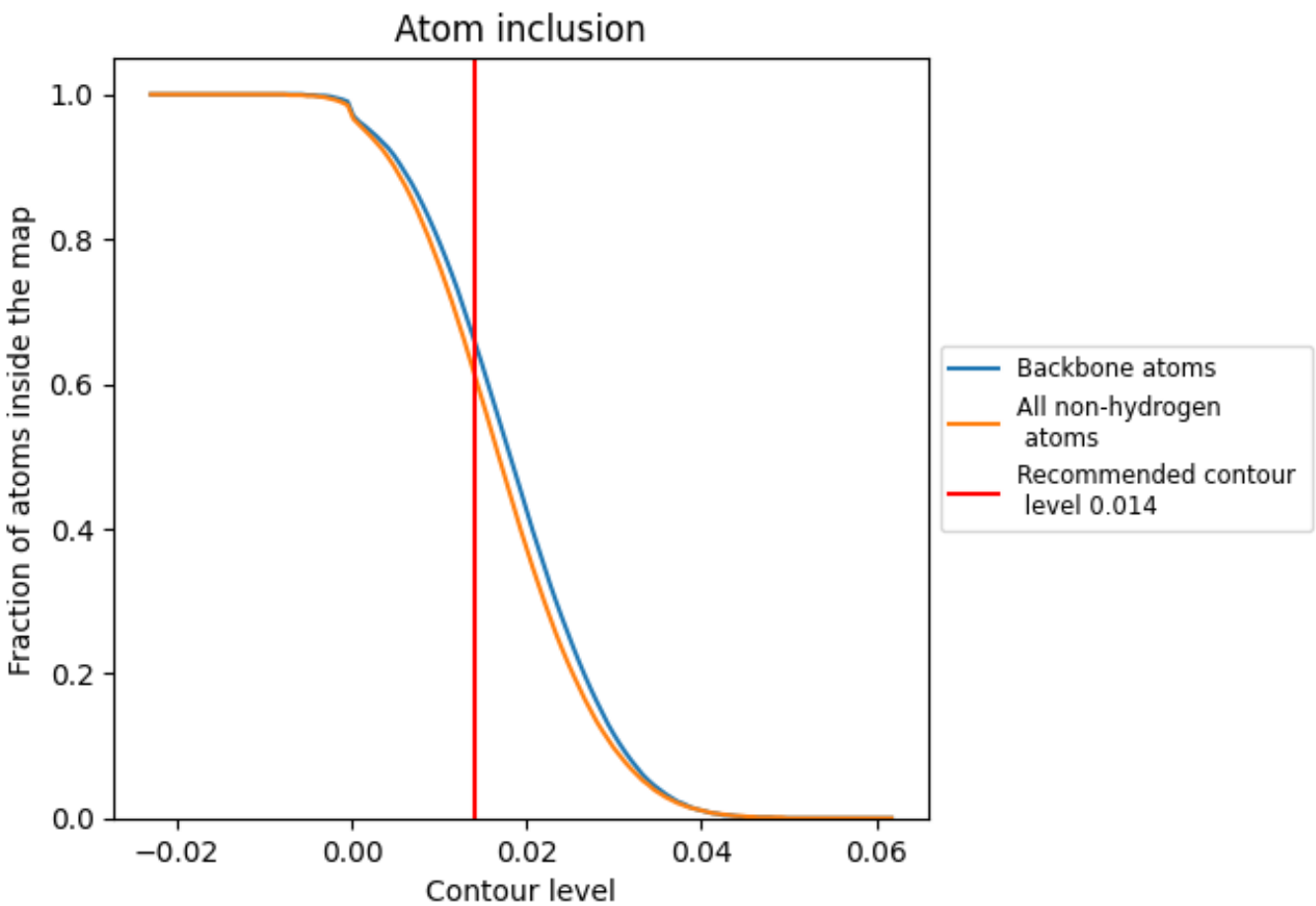
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.014).

9.4 Atom inclusion (i)



At the recommended contour level, 66% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6160	0.0800
3A	0.9100	0.1510
3B	0.7970	0.1140
3C	0.6800	0.0660
3D	0.8060	0.1300
3E	0.6940	0.0930
3F	0.8070	0.1120
3G	0.7630	0.1090
3H	0.7880	0.1290
5A	0.5880	0.0630
5B	0.1210	0.0310
5C	0.7700	0.1040
5D	0.4060	0.0490
5E	0.7420	0.1350
5F	0.7360	0.1260
5G	0.6730	0.0950
5H	0.7540	0.1070
5I	0.8410	0.1040
5J	0.5670	0.0960
5K	0.7420	0.1100
A4	0.6850	0.0470
A5	0.6060	0.0740
A8	0.5480	0.0590
A9	0.4820	0.0400
AE	0.3840	0.0540
AF	0.4860	0.0490
AG	0.6670	0.0340
B1	0.8250	0.1060
B2	0.7950	0.0960
B3	0.7850	0.0710
B6	0.7680	0.1260
B8	0.7800	0.0970
BE	0.8310	0.1070
RA	0.5970	0.0600
RB	0.7440	0.1240

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Chain	Atom inclusion	Q-score
RD	0.0800	0.0120
RE	0.5560	0.0610
RF	0.3930	0.0800
RG	0.1280	0.0160
RH	0.1390	0.0120
RJ	0.7030	0.1020
RK	0.7460	0.1140
RL	0.3280	0.0860
RM	0.1560	0.0450
RN	0.1110	0.0080
RO	0.0220	-0.0030
RP	0.6090	0.0830
RQ	0.5520	0.0900
RS	0.0450	-0.0100
RT	0.4820	0.0510
RY	0.3750	0.0560
SA	0.7140	0.1010
SC	0.5150	0.0690
SF	0.7690	0.0950
SG	0.7890	0.1220
SH	0.5730	0.0710
SI	0.6500	0.1140
SJ	0.7190	0.0430
SK	0.7950	0.1150
SM	0.8200	0.0610
SO	0.6930	0.0860
SP	0.6230	0.0520
SR	0.7910	0.1080
SX	0.5930	0.1030
SY	0.6430	0.0990
SZ	0.7610	0.1050
Sc	0.5460	0.0810
Sd	0.7760	0.1250
X1	0.5360	0.0930