wwPDB EM Validation Summary Report (i)

Mar 8, 2026 – 10:42 AM UTC

PDB ID	:	6LQQ / pdb_00006lqq
EMDB ID	:	EMD-0950
Title	:	Cryo-EM structure of 90S small subunit preribosomes in transition states (State B)
Authors	:	Du, Y.; Ye, K.
Deposited on	:	2020-01-14
Resolution	:	4.10 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 (1)) were used in the production of this report:

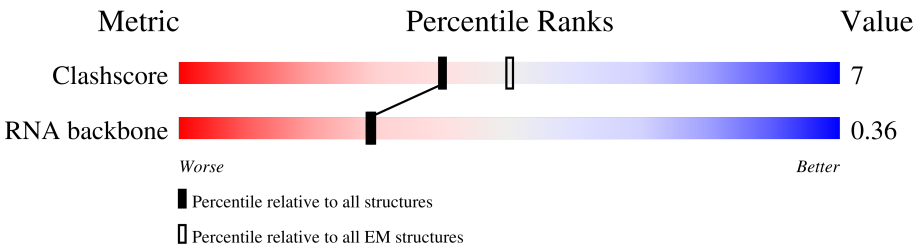
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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

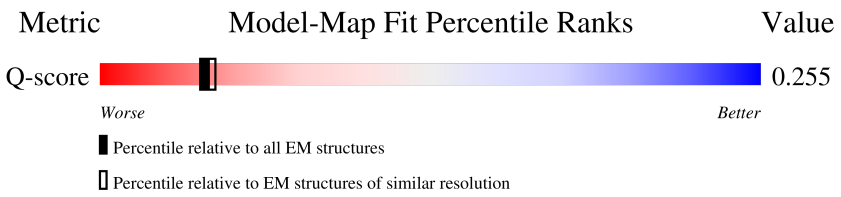
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.10 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

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	11%; 34%, 17%, •, 47%
2	5A	700	41%; 33%, 18%, •, 46%
3	SA	1808	27%; 36%, 31%, 6%, 27%
4	SC	255	23%; 71%, 19%, 10%
5	SF	261	26%; 64%, 24%, 12%

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Mol	Chain	Length	Quality of chain
6	SG	225	9% 81% 13% 5%
7	SH	236	36% 55% 16% 29%
8	SI	190	30% 68% 17% • 13%
9	SJ	200	42% 56% 28% 17%
10	SK	197	8% 75% 12% 13%
11	SM	156	58% 53% 26% 21%
12	SO	151	9% 77% 11% • 11%
13	SP	137	18% 70% 16% 14%
14	SR	143	6% 73% 15% 13%
15	SX	130	11% 82% 15% •
16	SY	145	8% 63% 8% 29%
17	SZ	135	15% 59% 16% • 24%
18	Sc	82	11% 83% 13% • •
19	Sd	67	16% 88% 6% 6%
20	3B	327	7% 61% 13% 27%
20	3C	327	64% 53% 16% 31%
21	3D	504	12% 60% 13% 27%
22	3E	511	40% 66% 18% 16%
23	3F	573	14% 61% 18% 21%
24	3G	126	22% 81% 15% •
24	3H	126	8% 75% 21% •
25	A4	776	61% 66% 19% 15%
26	A5	643	37% 66% 14% 20%
27	A8	713	77% 69% 8% 23%
28	A9	575	22% 18% • 78%

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Mol	Chain	Length	Quality of chain
29	AE	1769	65% 77% 9% 13%
30	AF	513	80% 76% 20%
31	AG	896	70% 71% 21% 8%
32	B1	923	7% 75% 15% 10%
33	B2	943	17% 69% 21% 10%
34	B3	817	34% 68% 24% 7%
35	B8	594	14% 67% 13% 20%
36	BE	939	9% 78% 14% 8%
37	B6	440	25% 75% 10% 15%
38	5B	214	28% 21% 7% 72%
39	5C	554	20% 77% 20%
40	5D	250	42% 58% 8% 33%
41	5E	593	9% 28% 6% 66%
42	5F	183	80% 19%
43	5G	290	19% 78% 19%
44	5H	610	11% 88%
45	5I	489	72% 22% 6%
46	5J	217	35% 57% 12% 30%
47	5K	189	11% 78% 14% 7%
48	RA	707	24% 35% 12% 52%
49	RB	357	15% 27% 10% 62%
50	RC	316	45% 76% 12% 12%
51	RD	1729	18% 15% 82%
52	RE	1237	51% 64% 23% 13%
53	RF	297	53% 61% 20% 19%

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Mol	Chain	Length	Quality of chain
54	RG	252	85% 63% 23% 14%
54	RH	252	90% 73% 18% 9%
55	RJ	1183	10% 54% 13% 33%
56	RK	367	9% 77% 21%
57	RL	1056	42% 71% 5% 24%
57	RM	1056	62% 71% 27%
58	RN	810	68% 62% 13% 25%
59	RO	552	95% 82% 13% 5%
60	RP	2493	65% 79% 5% 15%
61	RQ	899	11% 22% 75%
62	RS	483	52% 36% 16% 48%
63	RT	326	44% 45% 8% 48%
64	RV	346	32% 49% 5% 45%
65	RY	534	5% 6% 93%
66	X1	347	20% 21% 78%

2 Entry composition (i)

There are 69 unique types of molecules in this entry. The entry contains 226161 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	375	8009	3578	1426	2630	375	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	1323	28210	12608	5022	9257	1323	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	548	3307	2054	608	642	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	834	6635	4223	1140	1253	19	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	851	6723	4294	1133	1269	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	865	6810	4322	1175	1292	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	535	4237	2656	762	807	12	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	204	1647	1021	294	328	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	282	2296	1441	430	418	7	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 KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	RC	278	2207	1408	391	395	13	0	0

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

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

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

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

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

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

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

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

- Molecule 55 is a protein called Ribosome biogenesis protein BMS1.

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

- Molecule 56 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 57 is a protein called RNA cytidine acetyltransferase.

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

- Molecule 58 is a protein called Nucleolar complex protein 14.

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

- Molecule 59 is a protein called Nucleolar complex protein 4.

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

- Molecule 60 is a protein called U3 small nucleolar RNA-associated protein 20.

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

- Molecule 61 is a protein called U3 small nucleolar RNA-associated protein 14.

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

- Molecule 62 is a protein called Essential nuclear protein 1.

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

- Molecule 63 is a protein called Pno1.

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

- Molecule 64 is a protein called Protein FAF1.

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

- Molecule 65 is a protein called Protein BFR2.

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

- Molecule 66 is a protein called Unassigned helices.

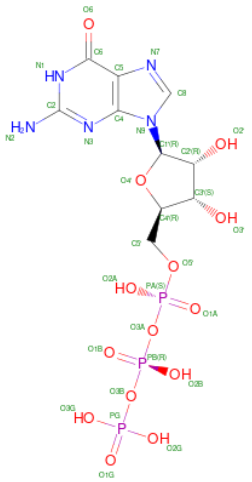
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
66	X1	75	375	225	75	75	0	0

- Molecule 67 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
67	Sc	1	1	1	0
67	5K	1	1	1	0

- Molecule 68 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

GTP



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

- Molecule 69 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

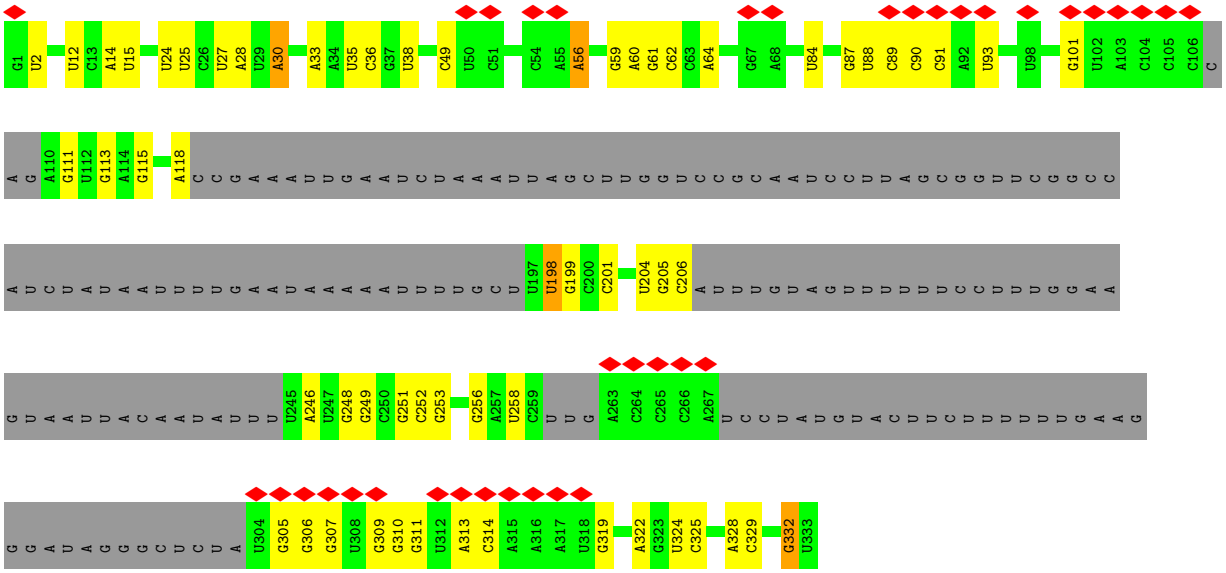
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
69	RJ	1	1	1	0

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.

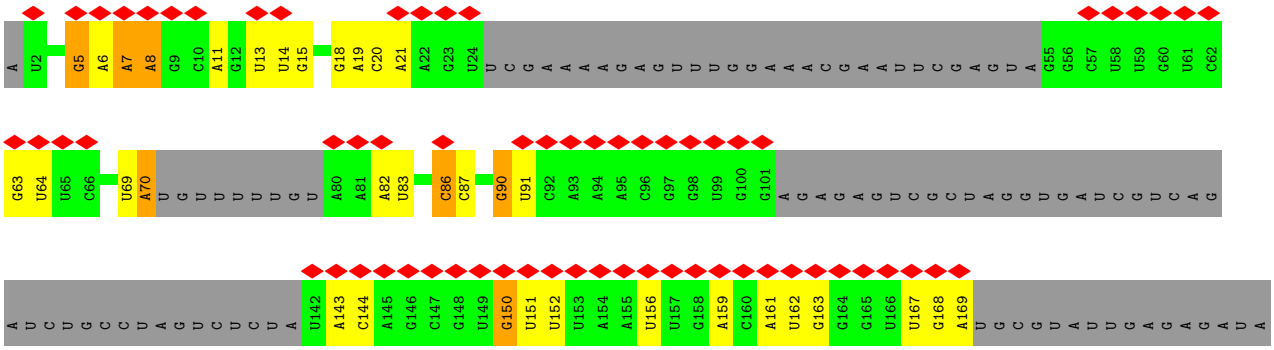
- Molecule 1: U3 snoRNA

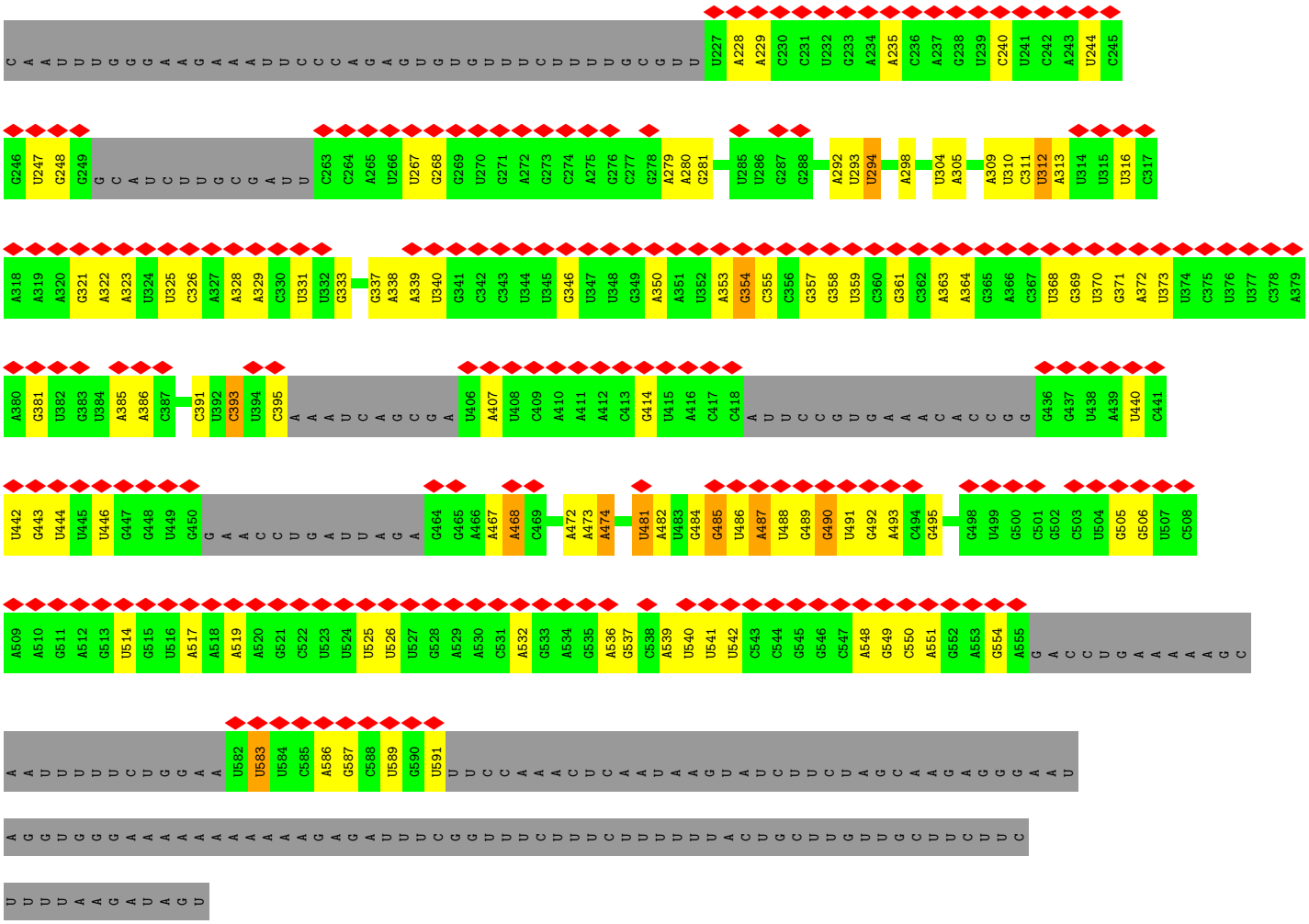
Chain 3A:



- Molecule 2: 5' ETS

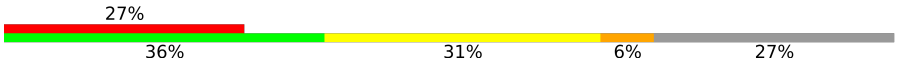
Chain 5A:

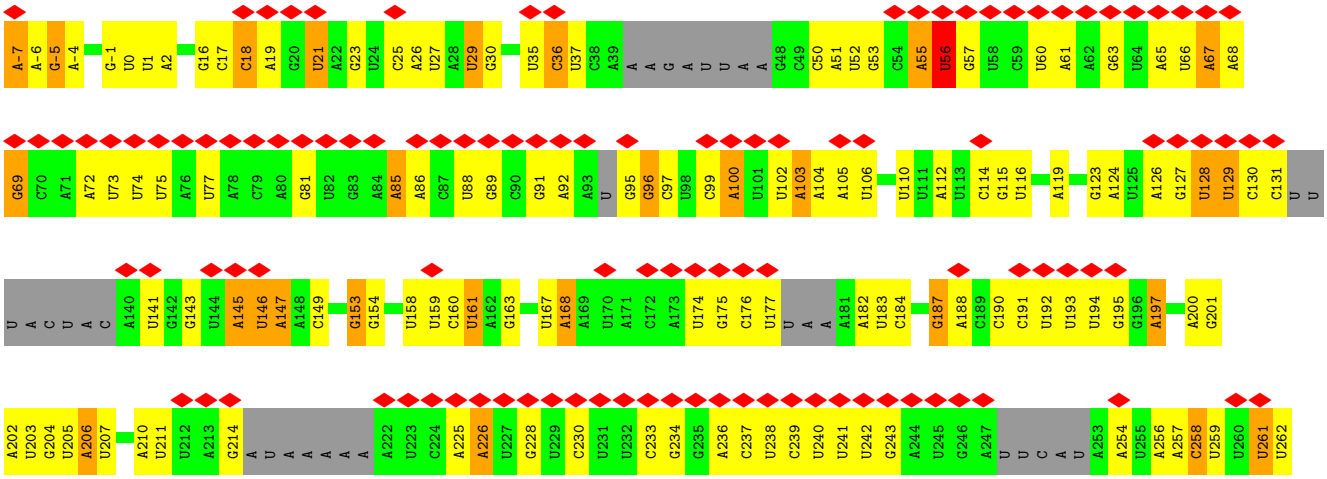


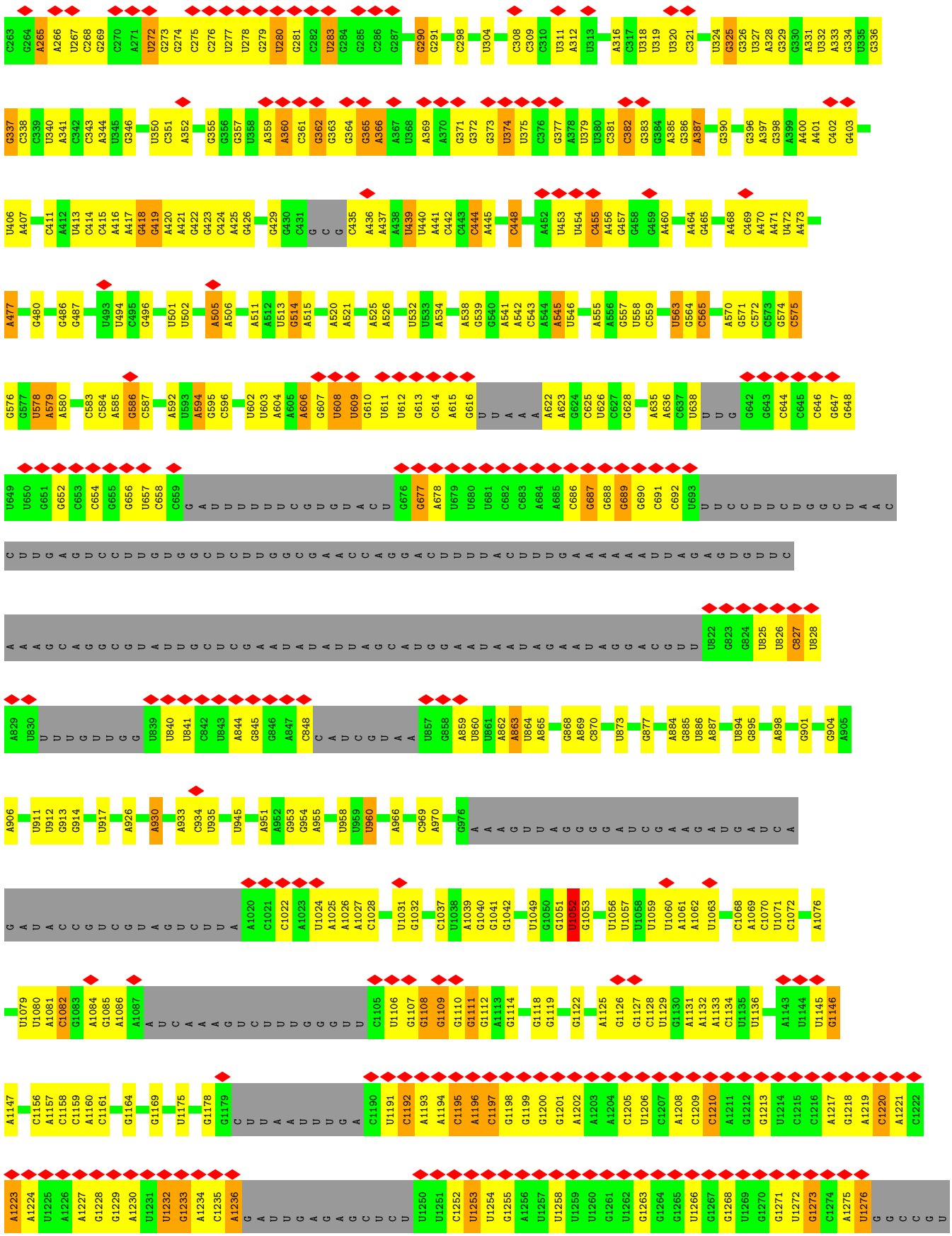


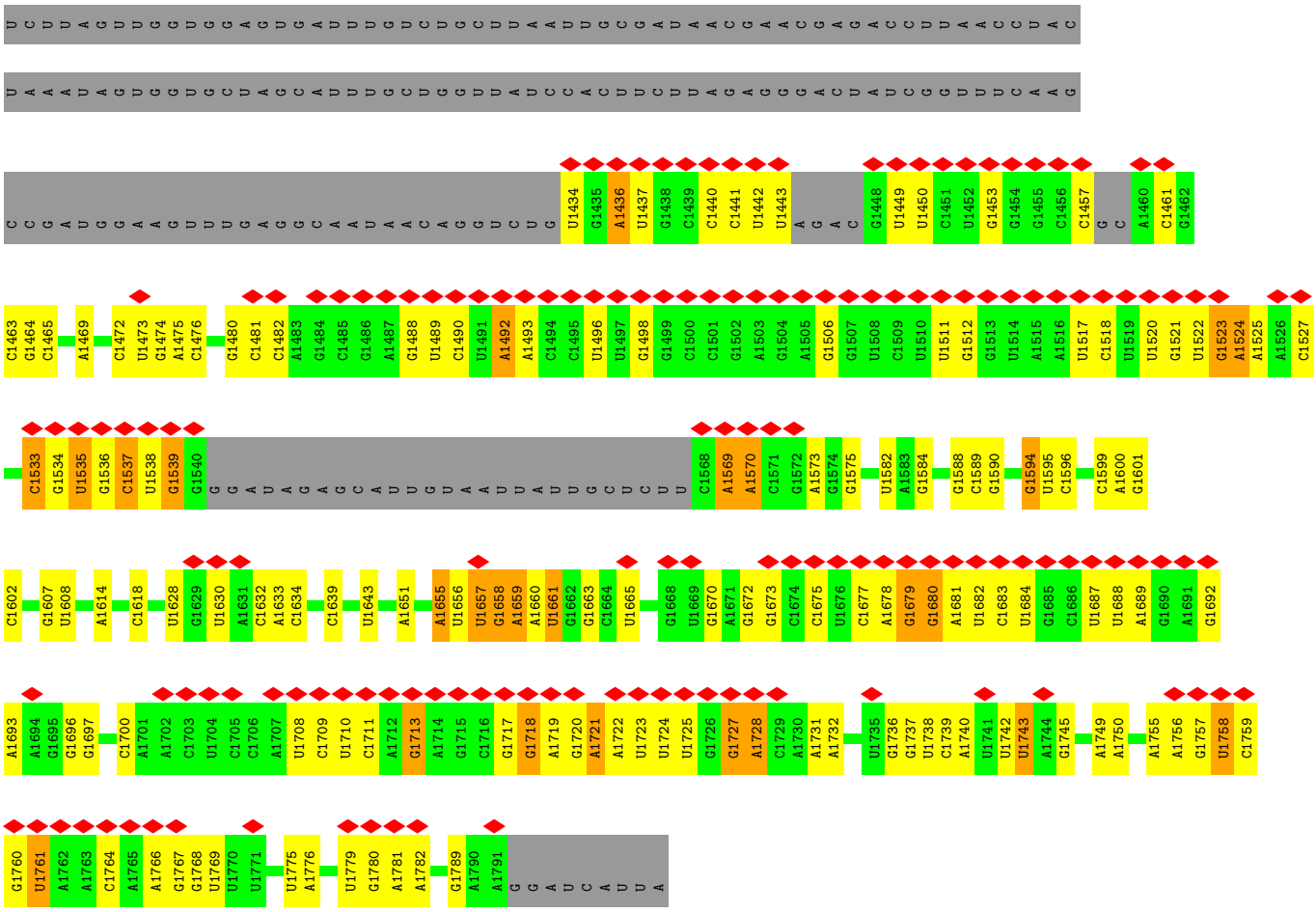
- Molecule 3: 18S pre-rRNA

Chain SA:



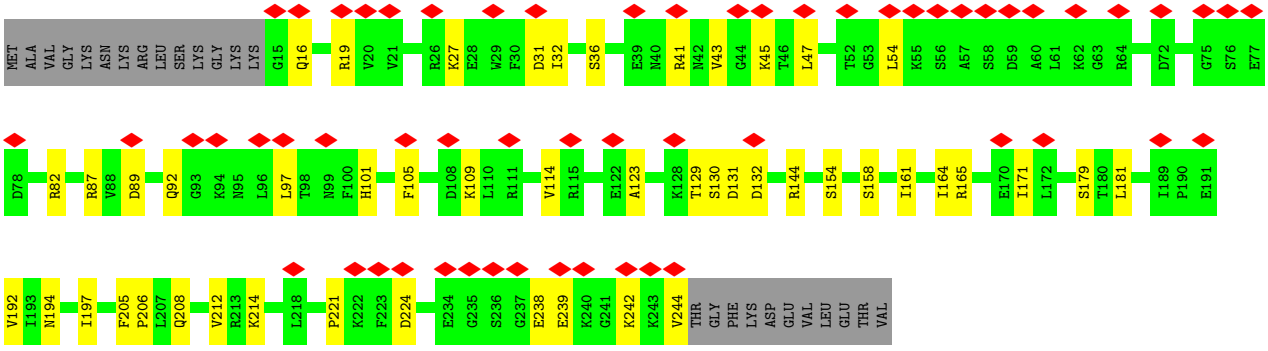






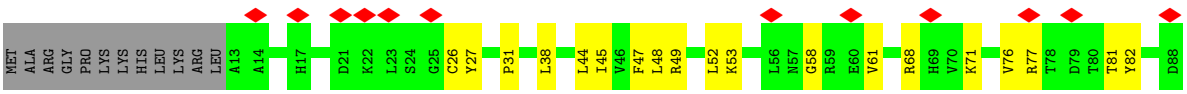
• Molecule 4: 40S ribosomal protein S1-A

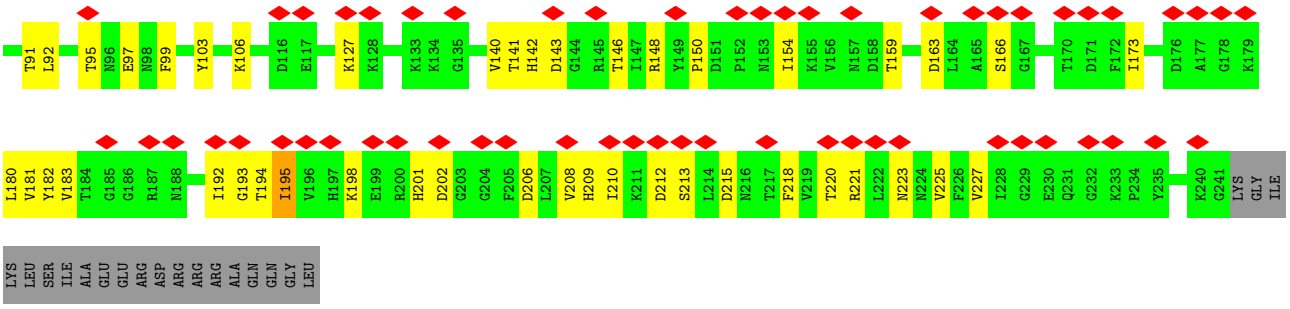
Chain SC:



• Molecule 5: 40S ribosomal protein S4-A

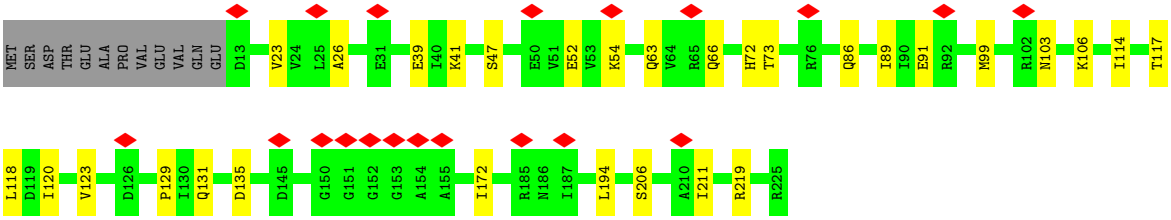
Chain SF:





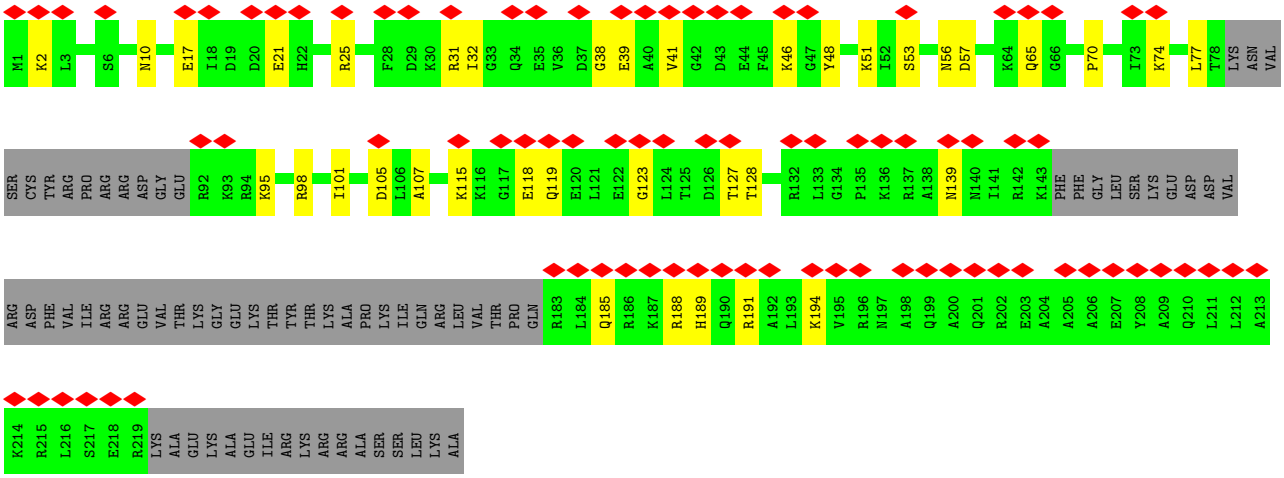
- Molecule 6: 40S ribosomal protein S5

Chain SG:



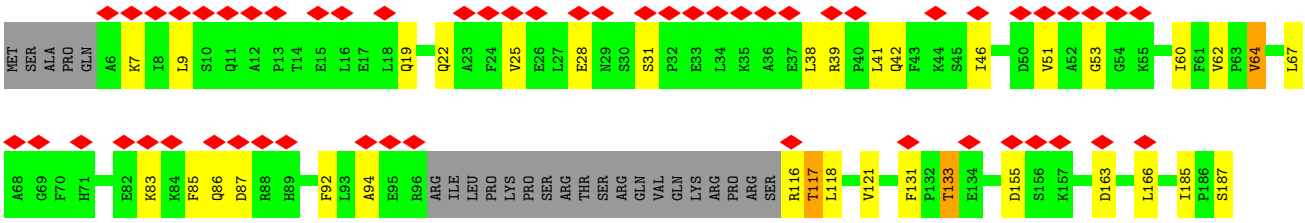
- Molecule 7: 40S ribosomal protein S6-A

Chain SH:



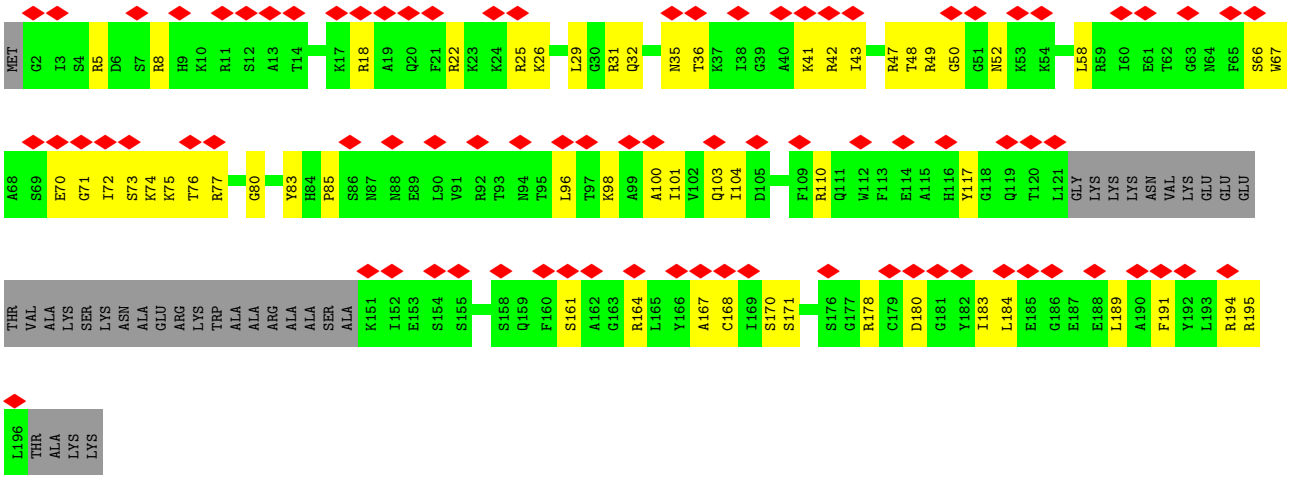
- Molecule 8: 40S ribosomal protein S7-A

Chain SI:



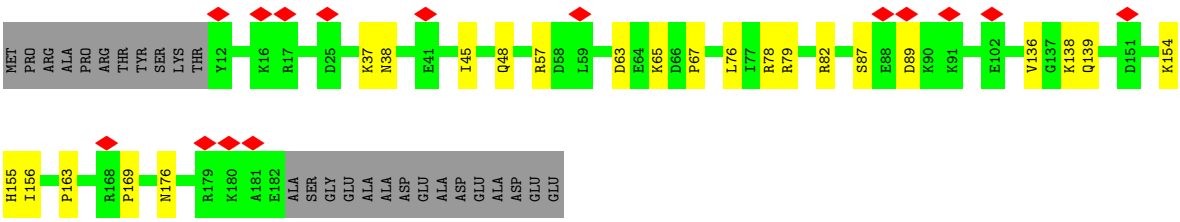
• Molecule 9: 40S ribosomal protein S8-A

Chain SJ:



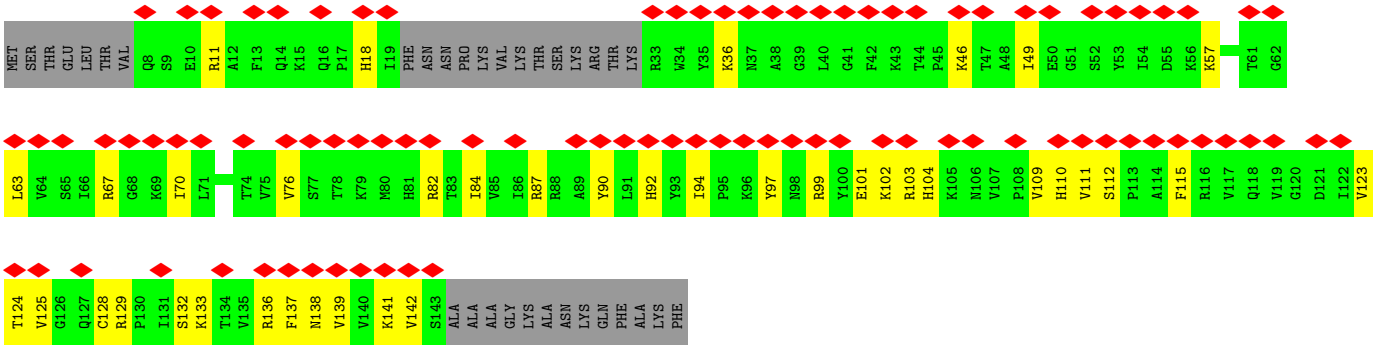
• Molecule 10: 40S ribosomal protein S9-A

Chain SK:



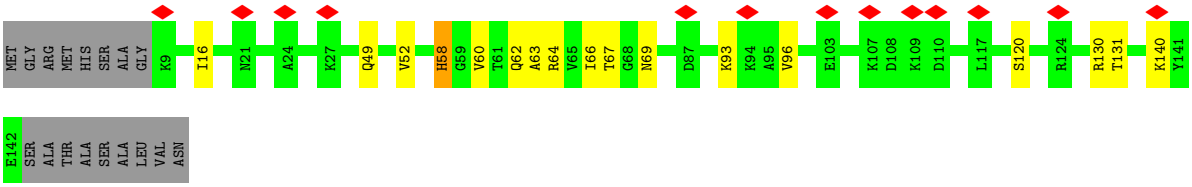
• Molecule 11: 40S ribosomal protein S11-A

Chain SM:



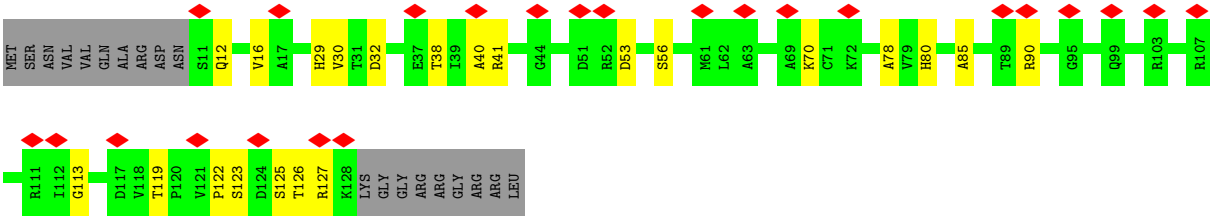
• Molecule 12: 40S ribosomal protein S13

Chain SO:



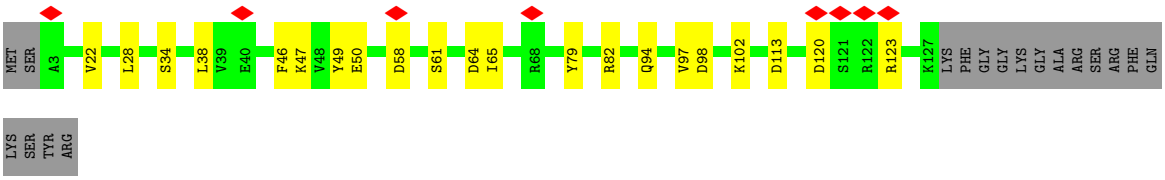
- Molecule 13: 40S ribosomal protein S14-A

Chain SP:



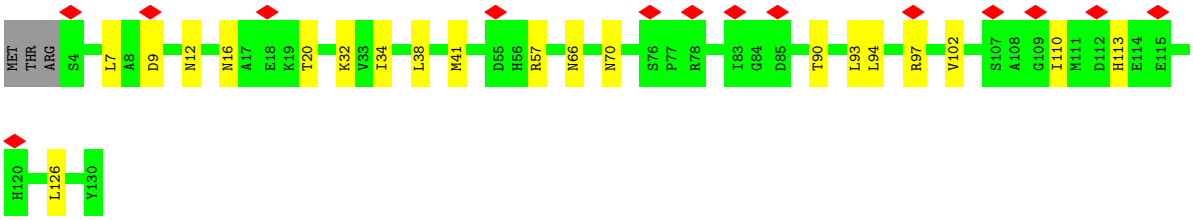
- Molecule 14: 40S ribosomal protein S16-A

Chain SR:



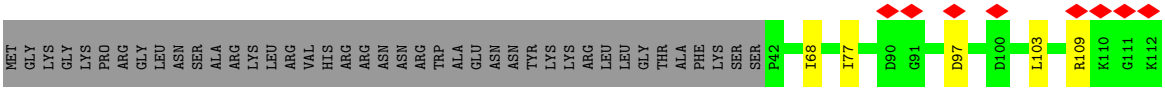
- Molecule 15: 40S ribosomal protein S22-B

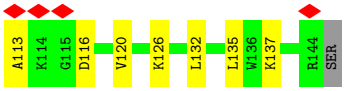
Chain SX:



- Molecule 16: 40S ribosomal protein S23-A

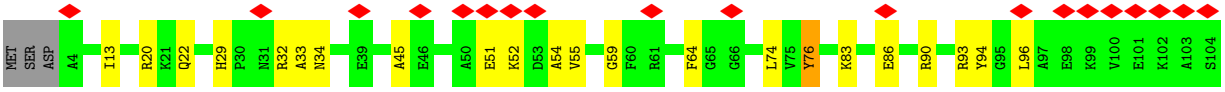
Chain SY:

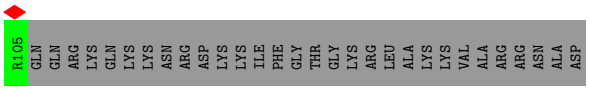




- Molecule 17: 40S ribosomal protein S24-A

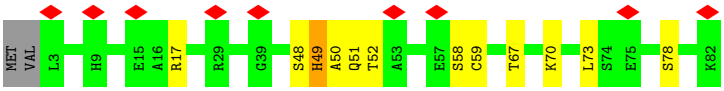
Chain SZ:





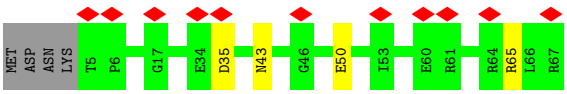
- Molecule 18: 40S ribosomal protein S27-A

Chain Sc:



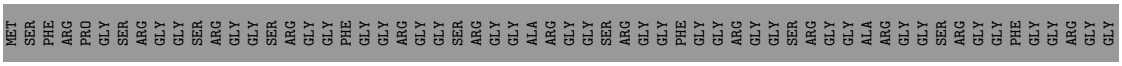
- Molecule 19: 40S ribosomal protein S28-A

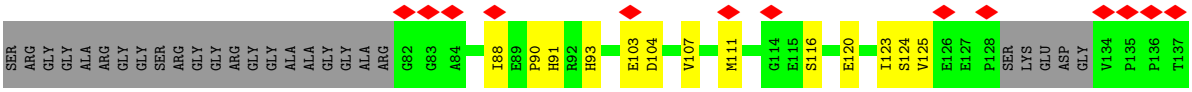
Chain Sd:

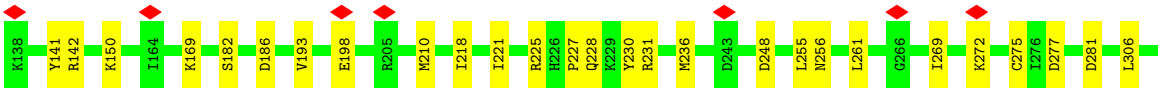


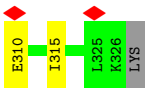
- Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

Chain 3B:



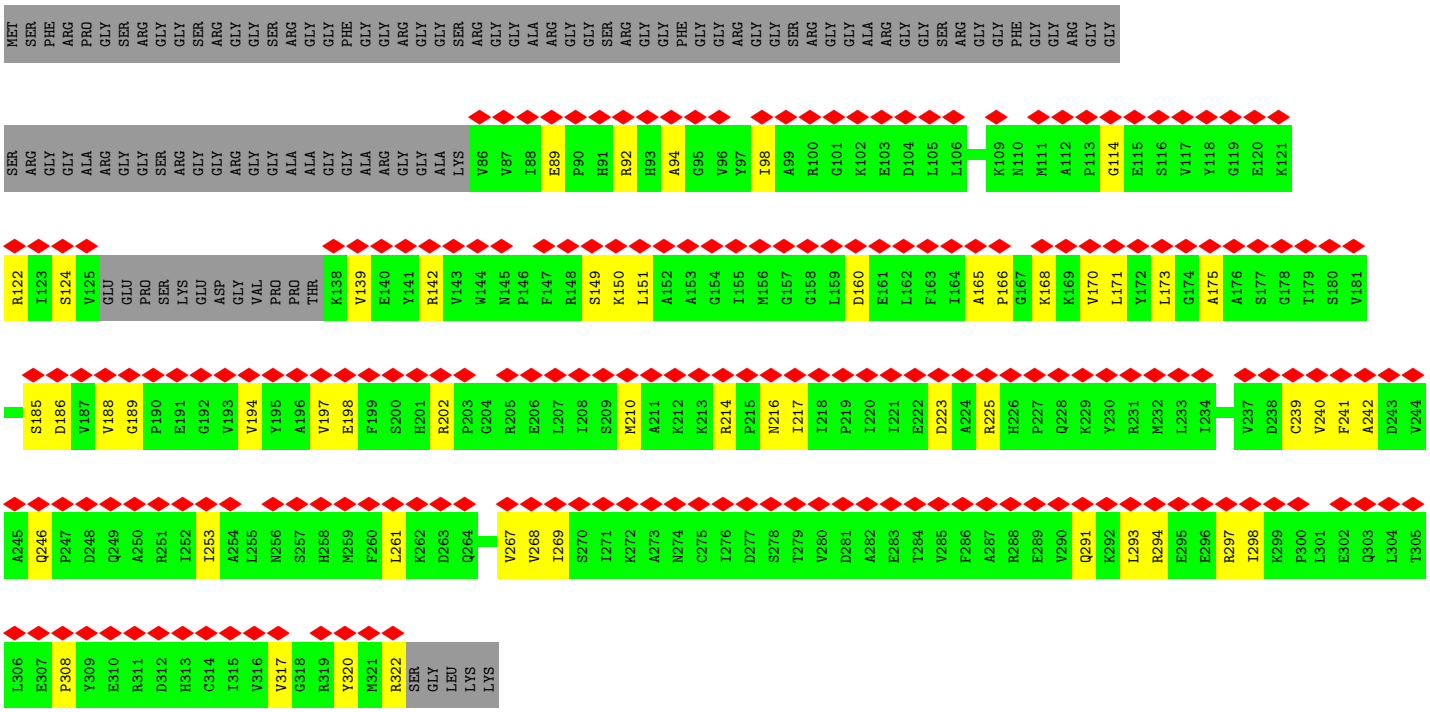






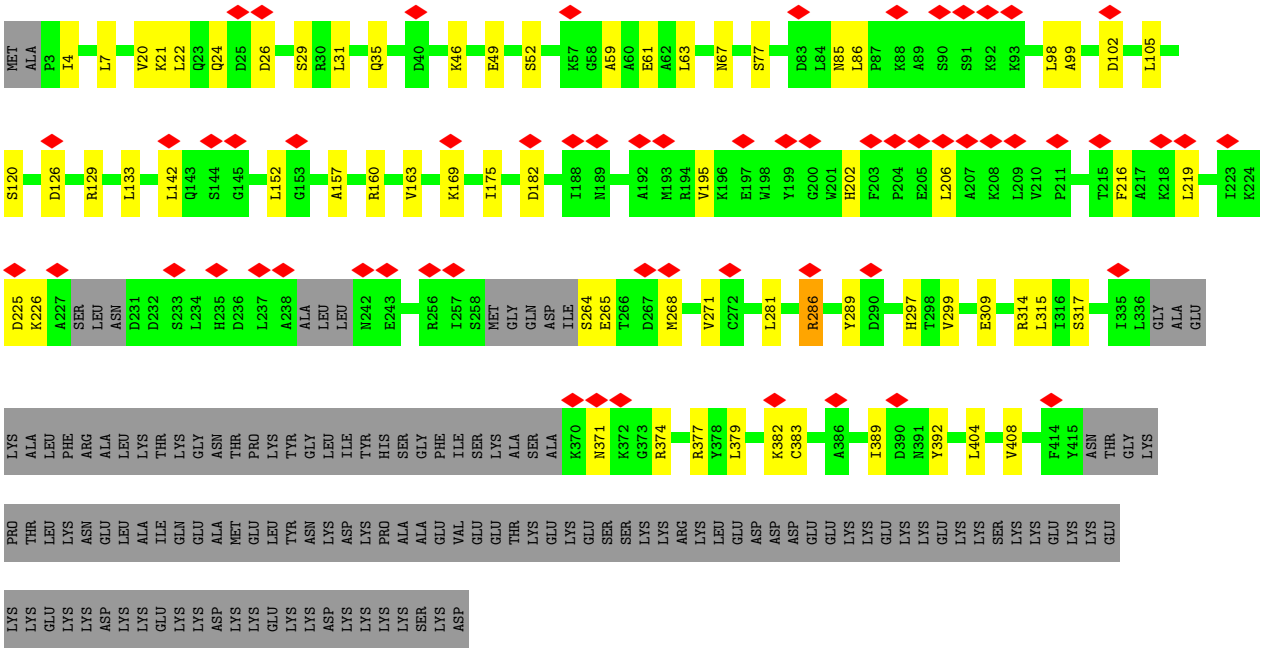
- Molecule 20: rRNA 2'-O-methyltransferase fibrillarin

Chain 3C:



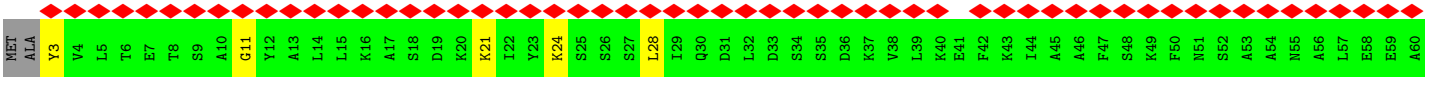
• Molecule 21: Nucleolar protein 56

Chain 3D:



• Molecule 22: Nucleolar protein 58

Chain 3E:



N61 S62 I63 I64 E65 G66 K67 V68 S69 S70 Q71 L72 E73 K74 L75 L76 E77 E78 I79 K80 K81 D82 K83 K84 S85 T86 L87 I88 V89 S90 E91 T92 K93 L94 A95 N96 A97 I98 N99 K100 L101 G102 L103 N104 F105 N106 V107 V108 S109 D110 A111 V112 T113 L114 D115 I116 Y117 R118 A119 I120

K121 E122 Y123 L124 P125 E126 L127 L128 P129 G130 M131 S132 D133 N134 D135 L136 S137 K138 M139 S140 L141 G142 L143 A144 H145 S146 I147 G148 R149 H150 K151 L152 K153 F154 SER ALA ASP LYS V159 D160 V161 M162 I163 I164 Q165 D171 D172 L173 E176 T179 H191 F192 L195 A196

D201 A204 Y205 A206 R207 L210 I214 R215 A218 T221 D222 E225 I226 L227 P228 E229 E230 I231 K236 A239 E240 V241 S242 M243 G244 T245 E246 I247 T248 D251 L252 N256 Q261 I262 F265 L276 R279 M280 I283 L287 T288 Q289 L290 V291

G292 L299 I300 A301 H302 S305 L306 I307 S308 K311 I319 L320 L326 L330 K331 T332 K333 H334 D335 Y339 Y343 G349 N355 K358 I359 A360 R361 V362 A367 A368 L371 R372 A375 L376 A377 E378 D379 R380 D381 D382 S383 G384 D385 I386 G387 L388

A392 N396 R397 L398 S399 Q400 L401 R404 D405 L406 R407 R414 E415 A416 K417 K418 V419 E420 E423 A426 D430 A431 K435 A436 A437 SER ASP SER GLU SER ASP SER ASP ASP GLU GLU GLU GLU LYS LYS GLU LYS LYS GLU LYS LYS ARG LYS ARG ASP ASP ASP

GLU ASP SER LYS ASP SER LYS LYS ALA LYS LYS GLU LYS LYS ASP LYS LYS GLU LYS LYS GLU LYS LYS GLU LYS LYS GLU LYS LYS GLU LYS LYS GLU LYS LYS GLU LYS LYS GLU LYS LYS GLU LYS LYS SER LYS LYS GLU LYS LYS GLU LYS LYS

- Molecule 23: Ribosomal RNA-processing protein 9

Chain 3F:

MET SER ASP VAL THR GLN GLN LYS LYS ARG LYS ARG SER LYS GLY GLU VAL ASN PRO SER LYS PRO THR VAL ASP GLU GLU ILE THR ASP PRO SER SER ASN GLU GLU ASP GLU GLN LEU GLU VAL SER ASP GLU GLU ASP ALA LEU GLU GLU SER GLU GLU GLU PHE GLU GLY GLU N58 P59

R63 L66 A67 K68 Q69 Y70 L74 E77 ALA ASN ASP ILE LEU THR ASP ASN ARG ASN ALA GLU GLU LYS ASP LEU ASN ASN LEU LYS GLU ARG THR ILE D102 E103 Y104 N105 N106 F107 D108 A109 G110 D111 K114 R120 L121 K122 E123 D124 V125 A126 E127 Q128 Q129 V132

F136 G137 D138 L141 I142 S143 E144 A145 K146 F149 T150 R151 E154 N155 N156 L157 T158 C159 I160 S161 C162 F163 Q164 P165 V166 LEU ASN LYS TYR THR PHE GLU GLU SER SER ASN GLY ASP LYS ASN LYS GLY R184 L185 F186 A187 K192 I201 T202 S205 K206 R207 P208

K209 K212 A218 S224 K225 H226 E227 D237 E238 T241 L260 W263 E266 S267 L268 S269 R279 R280 G281 E282 V283 L284 S285 R289 K290 N291 S292 D293 D301 F302 K303 I304 R305 L315 E316 I317 L318 Y319 G320 H321 H322 D323 E326 D327 I328 A332

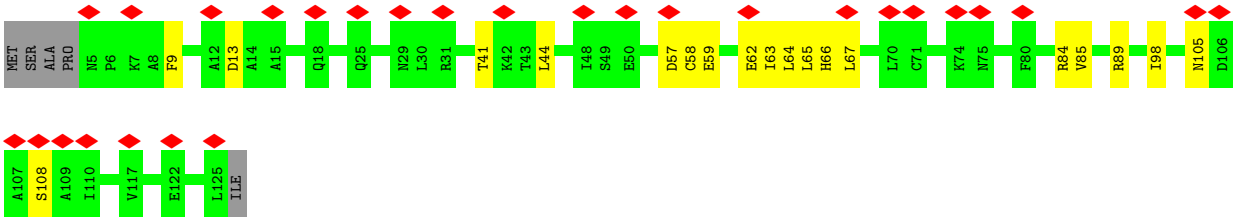
V337 T338 V339 G340 D343 D353 R356 L357 G362 D363 E364 P365 L368 L369 R370 M373 K374 E375 ASN ALA LYS GLU GLY GLU ASP GLY GLU VAL LYS TYR PRO ASP GLU SER GLU ALA P394 L395 F396 F397 C398 E399 D403 V404 V405 S406 M407 I414 T415 G416 S417

D418 N419 G420 N421 W425 K431 R437 I442 L443 F448 N449 D450 I451 S452 E457 R460 K461 Q465 G466 K467 P472 T476 S477 L478 Y479 A480 I481 S484 N485 V486 F487 I488 S491 W492 S502 D503 N504 L505 R506 L510 E513 V521 T522 K523

I524 Q525 V526 V527 H532 G533 K534 E535 R538 I539 L540 A541 S542 K545 E546 H547 R548 W552 I553 A554 N555 V556 S557 R560 N561 A566 V567 I568 D569 Q570 THR GLY PHE

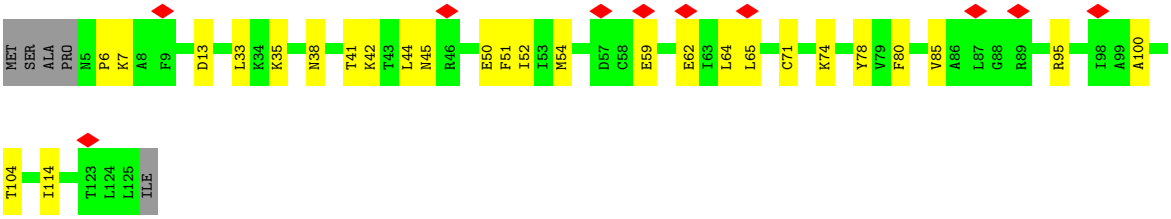
- Molecule 24: 13 kDa ribonucleoprotein-associated protein

Chain 3G:



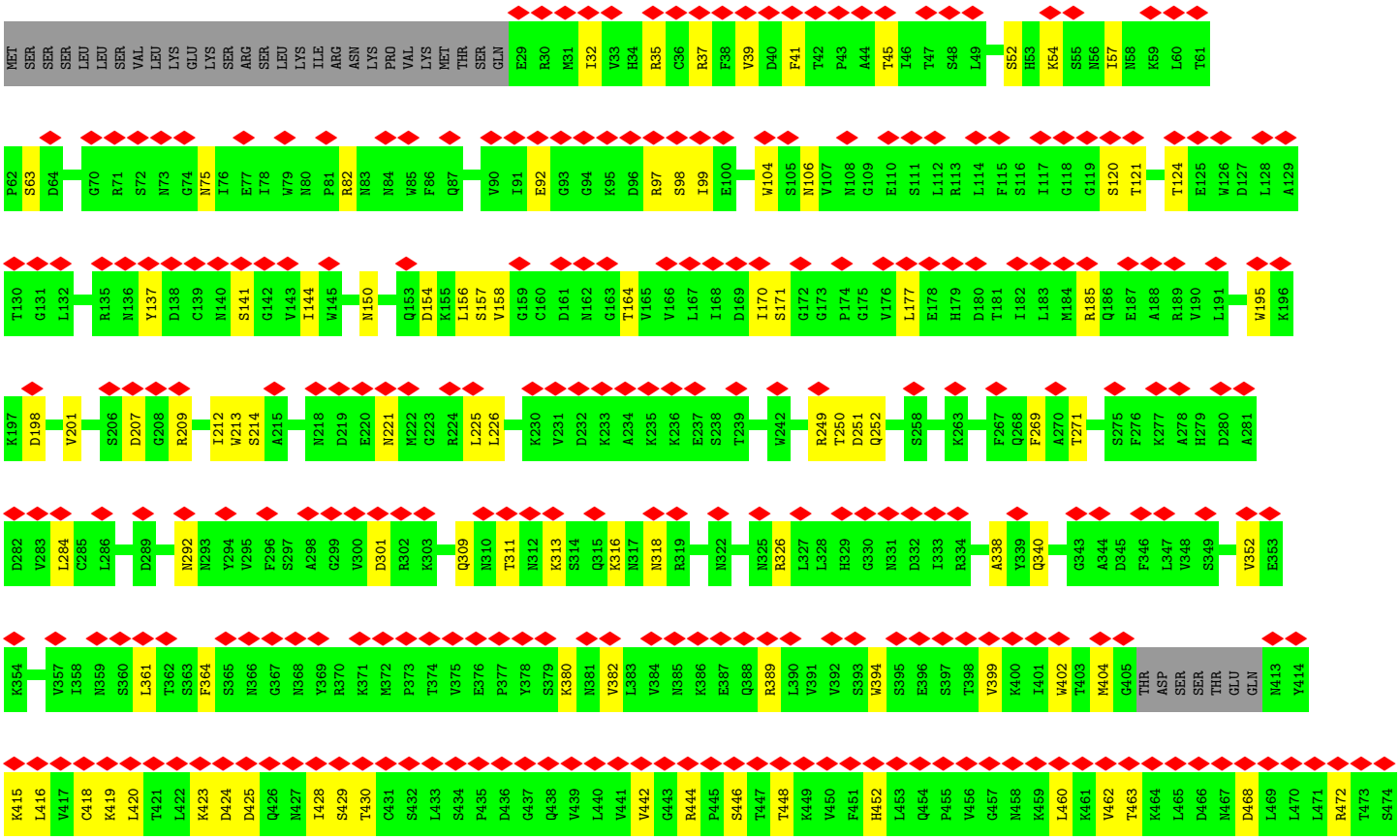
- Molecule 24: 13 kDa ribonucleoprotein-associated protein

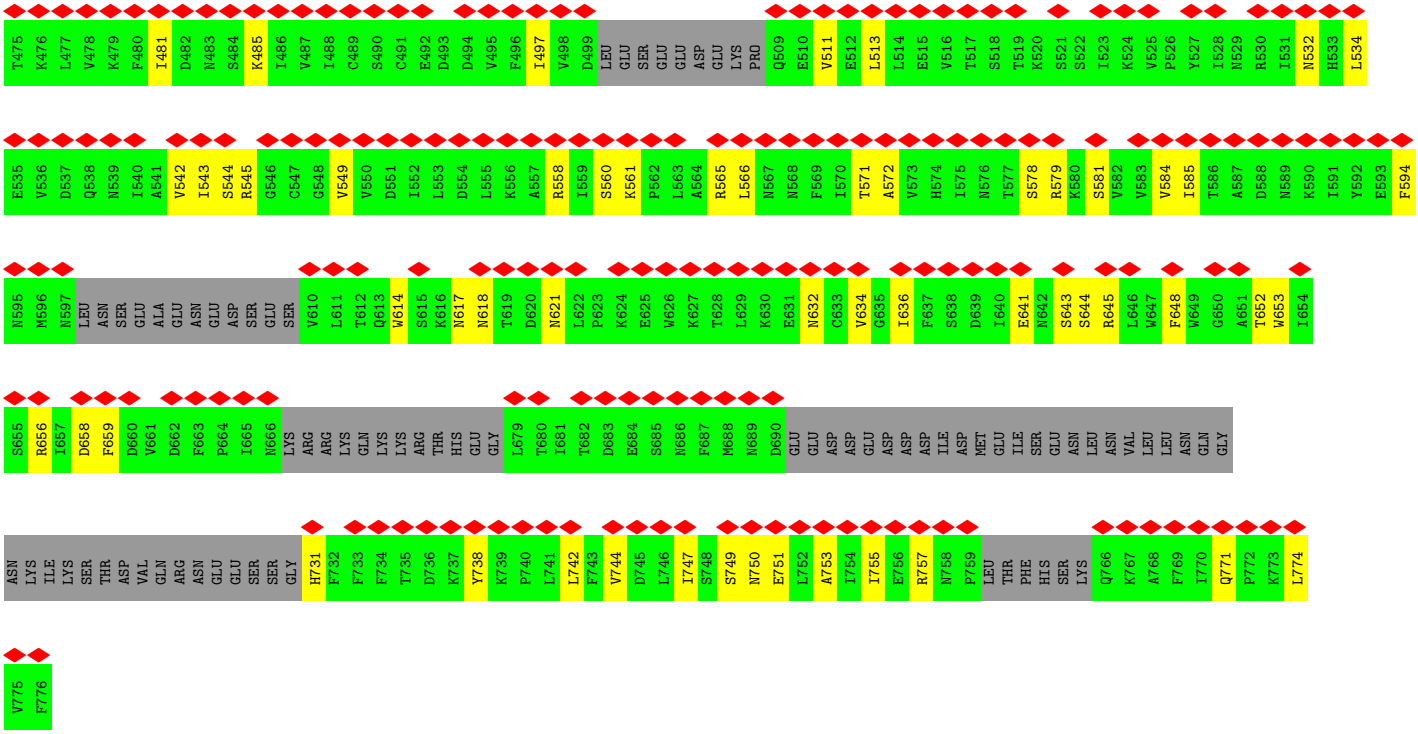
Chain 3H:



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

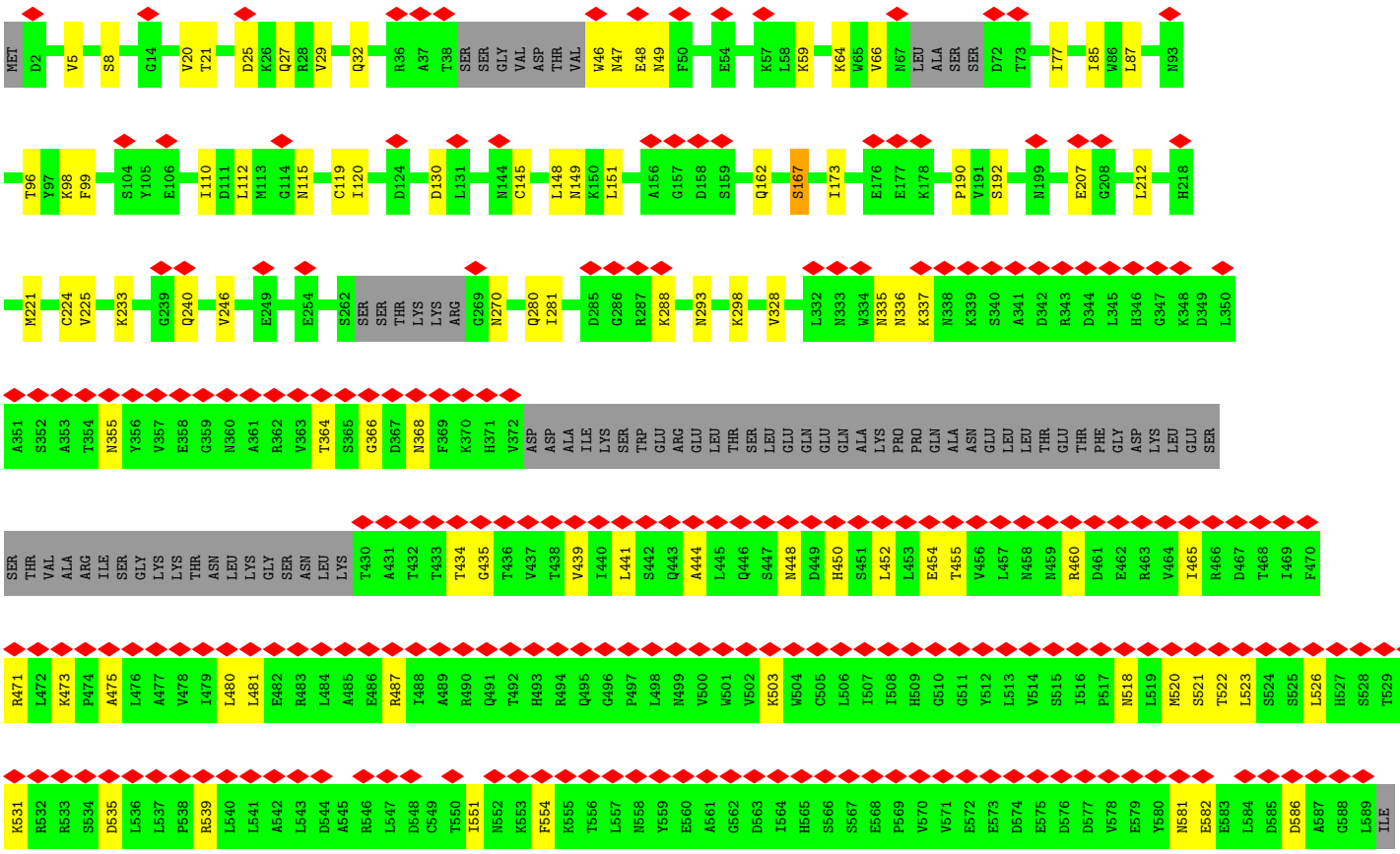
Chain A4:





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

Chain A5:



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

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

Chain A8:

MET PRO SER LEU SER GLN PRO PHE ARG LEU ALA THR LEU PRO LYS ILE ALA SER LEU SER ASN PHE SER LEU GLN ALA D27 Y28 V29 Q30 V31 A32 D33 G34 THR PHE ASN GLU SER THR ASN ASN ILE THR LEU GLY ILE SER GLY SER SER ILE SER GLN TYR ILE ILE ASN PRO THR

PRO LYS LEU THR PHE ASP TYR PRO ILE PRO SER THR ASN ILE ILE THR ALA CYS ASN ALA GLU LYS GLY GLN ALA ASN ILE ASP GLY ASN ILE GLU ALA SER THR ASP ASP GLU ALA ASN ASN GLU LYS THR ILE ASN THR GLN LYS LYS ARG ASN VAL GLU ILE TRP ALA PHE GLY L120

M121 V122 N123 K124 G125 N126 Y127 T128 L129 N130 V131 I132 T133 K134 A135 L136 E137 D138 T139 T140 D141 T142 S143 N144 D145 H146 L147 SER GLU SER ASP ILE D153 N154 K155 A156 Y157 T158 G159 S160 D161 E162 F163 L164 S165 Q166 Y167 K168 I169 K170 A171 K172 A173 K174 V175 M176 S177 I178 K179 I180

D181 T182 K183 N184 S185 L186 V187 I188 A189 I190 L191 Q192 N193 G194 L195 I196 E197 I198 F199 D200 F201 K202 L203 T204 L205 L206 H207 S208 F209 D210 I211 S212 Y213 D214 N215 L216 K217 Y218 A219 K220 W221 F222 T223 E224 N225 G226 T227 E228 Y229 V230 F231 V232 L233 C234 P235 L236 Q237 D238 D239 K240

V241 C242 Y243 K244 L245 L246 E247 L248 T249 D250 C251 G252 S253 G254 E255 S256 S257 P258 I259 K260 E261 L262 S263 S264 T265 I266 I267 E268 G269 F270 S271 F272 E273 N274 S275 K276 L277 C278 Y279 Q280 F281 G282 K283 L284 Y285 K286 L287 N288 Q289 G290 K291 I292 Y293 I294 Y295 S296 L297 P298 H299 C300

Q301 L302 Q303 Q304 V305 I306 E307 F308 P309 M310 V311 D312 K313 L314 S315 P316 G317 D318 D319 L320 I321 S322 F323 Q324 P325 V326 S327 V328 N329 R330 V331 L332 L333 T334 V335 N336 N337 V338 I339 Y340 L341 L342 D343 L344 L345 H346 C347 S348 T349 L350 S351 Q352 R353 E354 L355 T356 H357 V358 LYS THR

PHE GLN LEU LEU LYS SER ALA V368 I369 N370 S371 E372 K373 S374 H375 N376 S377 K378 T379 D380 I381 A382 G383 I384 S385 T386 K387 N388 G389 P390 N391 P392 T393 S394 S395 L396 E397 I398 I399 N400 I401 D402 V403 G404 T405 N406 T407 L408 K409 D410 S411 L412 G413 K414 S415 F416 Q417 V418 G419 N420

N421 D422 S423 S424 V425 I426 L427 K428 P429 L430 F431 D432 D433 K434 D435 I436 N437 D438 K439 R440 V441 K442 C443 N444 D445 V446 S447 G448 D449 S450 S451 V452 P453 V454 L455 H456 C457 N458 E459 V460 I461 E462 K463 L464 S465 A466 L467 Q468 D469 N470 D471 I472 T473 S474 F475 D476 D477 I478 F479 F480

K481 E482 L483 K484 I485 K486 E487 E488 H489 Y490 T491 E492 K493 D494 R495 Y496 I497 S498 D499 P500 G501 F502 L503 N504 K505 V506 L507 D508 L509 I510 F511 G512 K513 F514 SER GLY ASN ASP TYR P520 K521 T522 L523 T524 F525 L526 L527 T528 H529 P530 L531 F532 P533 L534 S535 R536 T537 R538 N539 L540

L541 S542 L543 L544 R545 D546 Q547 P548 R549 L550 F551 K552 Q553 A554 I555 V556 T557 C558 P559 N560 L561 P562 L563 N564 E565 L566 L567 E568 E569 L570 F571 S572 I573 R574 N575 R576 E577 L578 L579 L580 D581 I582 S583 F584 R585 I586 L587 Q588 D589 F590 T591 R592 D593 S594 I595 K596 Q597 E598 M599 K600

K601 L602 S603 K604 L605 D606 V607 Q608 N609 F610 I611 E612 F613 I614 T615 S616 G617 GLY GLU ASP SER SER PRO GLU CYS PHE ASN PRO SER GLN S631 T632 Q633 L634 F635 Q636 L637 L638 S639 L640 V641 L642 D643 S644 I645 G646 L647 F648 S649 L650 E651 G652 A653 L654 L655 E656 M657 L658 T659 L660

Y661 I662 D663 K664 Q665 V666 E667 I668 A669 E670 R671 N672 T673 E674 L675 W676 N677 L678 I679 ASP THR LYS GLY PHE GLN HIS GLY PHE ALA SER SER THR PHE ASP ASN GLY THR SER GLN LYS ARG A702 L703 P704 T705 Y706 T707 M708 E709 Y710 L711 D712 I713

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

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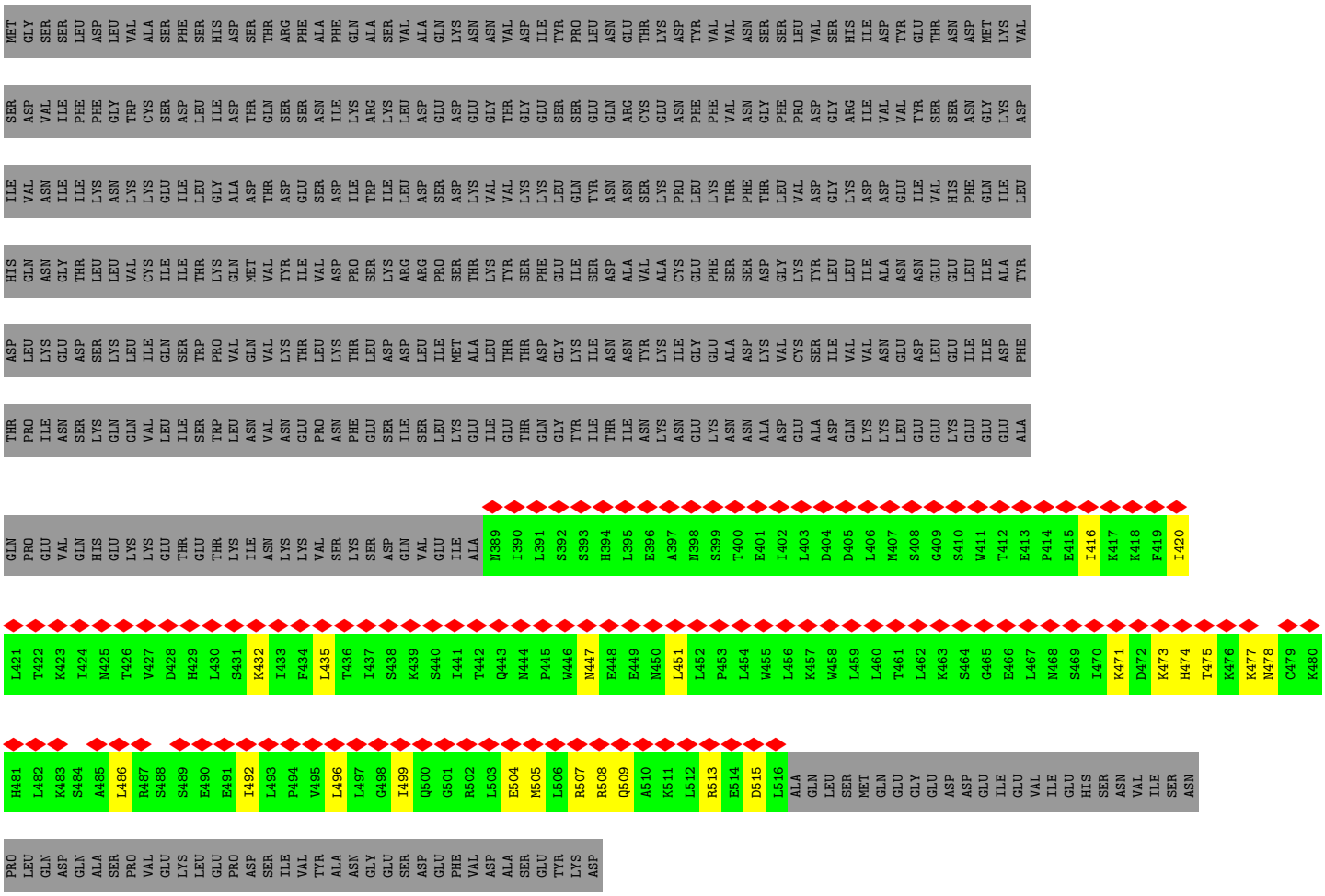
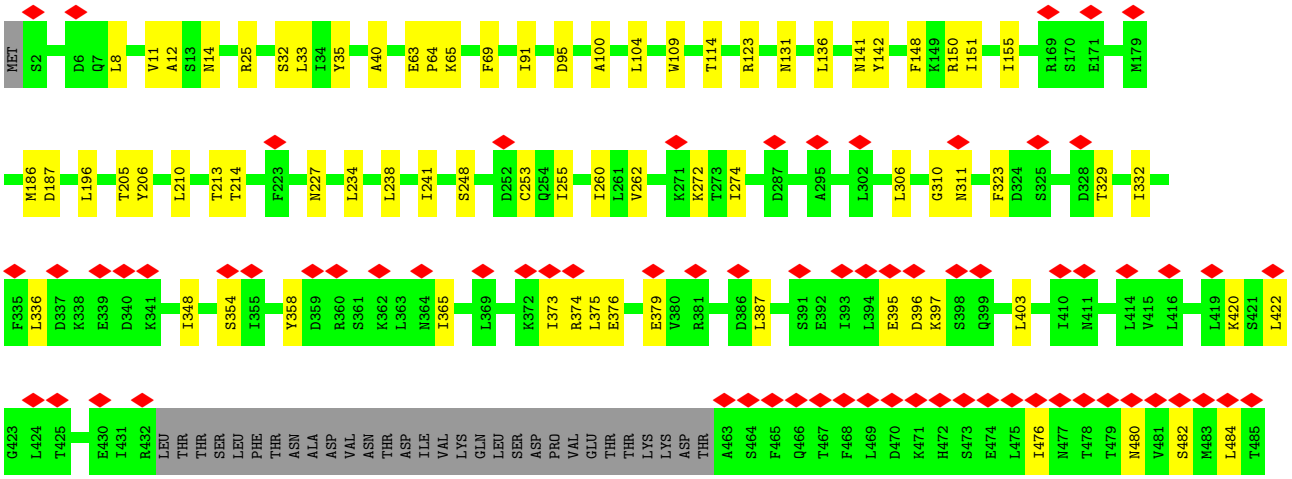
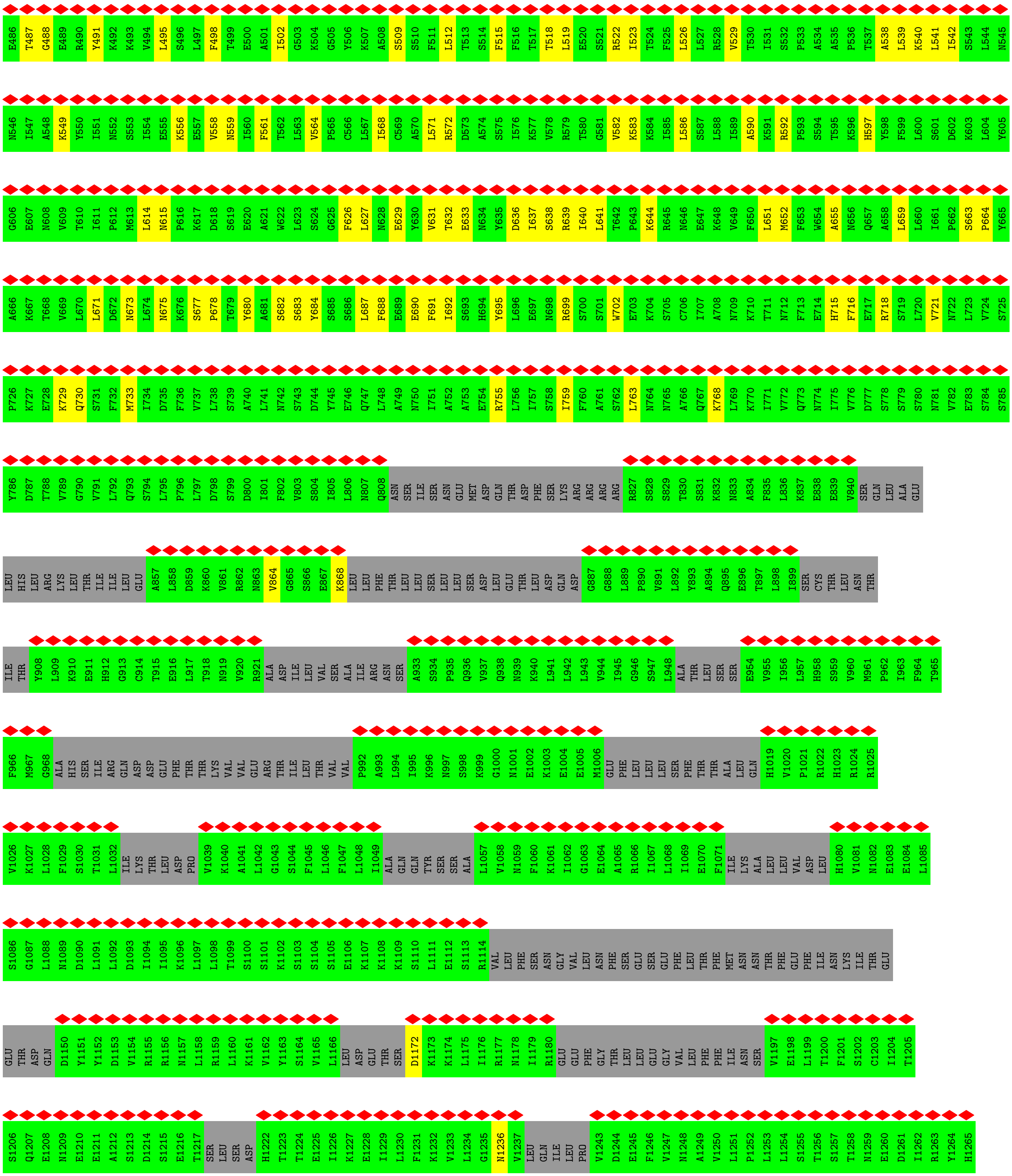


- Molecule 29: U3 small nucleolar RNA-associated protein 10

Chain AE:

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N546 I547 A548 K549 Y550 I551 N552 S553 I554 E555 K556 E557 V558 N559 I560 F561 T562 L563 V564 P565 C566 L567 I568 C569 A570 L571 R572 D573 A574 S575 I576 K577 V578 R579 T580 G581 V582 K583 K584 I585 L586 S587 L588 I589 A590 K591 R592 P593 S594 T595 K596 H597 Y598 F599 L600 S601 D602 K603 L604 Y605
G606 E607 N608 V609 T610 I611 P612 M613 L614 N615 P616 K617 D618 S619 E620 A621 W622 L623 S624 G625 F626 L627 N628 E629 Y630 V631 T632 E633 N634 Y635 D636 I637 S638 R639 I640 L641 T642 P643 K644 R645 N646 E647 K648 V649 F650 L651 M652 F653 W654 A655 N656 Q657 A658 L659 L660 I661 P662 S663 P664 Y665
A666 K667 T668 V669 L670 L671 D672 N673 L674 N675 K676 S677 P678 T679 Y680 A681 S682 S683 Y684 S685 S686 L687 F688 E689 E690 F691 I692 S693 H694 Y695 L696 E697 N698 R699 S700 S701 W702 E703 K704 S705 C706 I707 A708 N709 K710 T711 N712 F713 E714 H715 F716 E717 R718 S719 L720 V721 N722 L723 V724 S725
P726 K727 E728 K729 Q730 S731 F732 M733 I734 D735 F736 V737 L738 S739 A740 L741 N742 S743 D744 Y745 E746 Q747 L748 A749 N750 I751 A752 A753 E754 R755 L756 I757 S758 I759 F760 A761 S762 L763 N764 N765 A766 Q767 K768 L769 K770 I771 V772 Q773 N774 I775 V776 D777 S778 S779 S780 N781 V782 E783 S784 S785
Y786 D787 T788 V789 G790 V791 L792 Q793 S794 L795 P796 L797 D798 S799 D800 I801 F802 V803 S804 I805 L806 N807 Q808 ASN SER ILE SER ASN GLU MET ASP GLN THR ASP PHE SER LYS ARG ARG ARG ARG R827 S828 S829 T830 S831 K832 N833 A834 F835 L836 K837 E838 E839 V840 SER GLN LEU ALA GLU
LEU HIS LEU ARG LYS LEU THR ILE ILE LEU GLU A857 L858 D859 K860 V861 R862 N863 V864 G865 S866 E867 K868 LEU LEU PHE THR LEU LEU SER LEU LEU SER ASP LEU GLU THR LEU ASP GLN ASP G887 G888 L889 P890 V891 L892 Y893 A894 Q895 E896 T897 L898 I899 SER CYS THR LEU ASN THR
ILE THR Y908 L909 K910 E911 H912 G913 C914 T915 E916 L917 T918 N919 V920 R921 ALA ASP ILE LEU VAL SER ALA ILE ARG ASN SER A933 S934 P935 Q936 V937 Q938 N939 K940 L941 L942 L943 V944 I945 G946 S947 L948 ALA THR LEU SER SER E954 V955 I956 L957 H958 S959 V960 M961 P962 I963 F964 T965
F966 M967 G968 ALA HIS SER ILE ARG GLN ASP ASP GLU PHE THR THR LYS VAL VAL GLU ARG THR ILE LEU THR VAL VAL P992 A993 L994 I995 K996 N997 S998 K999 G1000 N1001 E1002 K1003 E1004 E1005 M1006 GLU PHE LEU LEU LEU SER PHE THR THR ALA LEU GLN H1019 V1020 P1021 R1022 H1023 R1024 R1025
V1026 K1027 L1028 F1029 S1030 T1031 L1032 ILE LYS THR LEU ASP PRO V1039 K1040 A1041 L1042 G1043 S1044 F1045 L1046 F1047 L1048 I1049 ALA GLN GLN TYR SER SER ALA L1057 V1058 N1059 F1060 K1061 I1062 G1063 E1064 A1065 R1066 I1067 L1068 I1069 E1070 F1071 ILE LYS ALA LEU LEU VAL ASP LEU H1080 V1081 N1082 E1083 E1084 L1085
S1086 G1087 L1088 N1089 D1090 L1091 L1092 D1093 I1094 I1095 K1096 L1097 L1098 T1099 S1100 S1101 K1102 S1103 S1104 S1105 E1106 K1107 K1108 K1109 S1110 L1111 E1112 S1113 R1114 VAL LEU PHE SER ASN GLY VAL LEU ASN PHE SER GLU SER GLU PHE LEU THR PHE MET ASN ASN THR PHE GLU PHE ILE ASN LYS ILE THR GLU
GLU THR ASP GLN D1150 Y1151 Y1152 D1153 V1154 R1155 R1156 N1157 L1158 R1159 L1160 K1161 V1162 Y1163 S1164 V1165 L1166 LEU ASP GLU THR SER D1172 K1173 K1174 L1175 I1176 R1177 N1178 I1179 R1180 GLU GLU PHE GLY THR LEU LEU GLU GLY VAL LEU PHE PHE ILE ASN SER V1197 E1198 L1199 T1200 F1201 S1202 C1203 I1204 T1205
S1206 Q1207 E1208 N1209 E1210 E1211 A1212 S1213 D1214 S1215 E1216 T1217 SER LEU SER ASP H1222 T1223 T1224 E1225 I1226 K1227 E1228 I1229 L1230 F1231 K1232 V1233 L1234 G1235 N1236 V1237 LEU GLN ILE LEU PRO V1243 D1244 E1245 F1246 V1247 N1248 A1249 V1250 L1251 P1252 L1253 L1254 S1255 T1256 S1257 T1258 N1259 E1260 D1261 I1262 R1263 Y1264 H1265

L1266 T1267 L1268 V1269 I1270 G1271 S1272 K1273 F1274 E1275 L1276 E1277 G1278 S1279 E1280 A1281 I1282 P1283 I1284 V1285 N1286 N1287 V1288 M1289 K1290 V1291 L1292 L1293 D1294 R1295 M1296 P1297 L1298 E1299 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 I1408 K1409 R1410 I1411 P1412 S1413 F1414 L1415 M1416 S1417 N1418 I1419 L1420 D1421 V1422 L1423 H1424 V1425 I1426 Y1427 F1428 S1429 R1430 E1431 V1432 D1433 S1434 S1435 I1436 R1437 L1438 S1439 V1440 I1441 S1442 L1443 I1444 I1445

E1446 N1447 I1448 D1449 L1450 K1451 E1452 V1453 L1454 K1455 V1456 L1457 F1458 R1459 I1460 W1461 S1462 T1463 E1464 I1465 A1466 T1467 S1468 N1469 D1470 T1471 V1472 A1473 V1474 S1475 L1476 F1477 L1478 S1479 T1480 L1481 E1482 S1483 T1484 V1485 E1486 N1487 I1488 D1489 K1490 K1491 S1492 A1493 T1494 S1495 Q1496 S1497 P1498 I1499 F1500 F1501 K1502 L1503 L1504 L1505

S1506 L1507 F1508 E1509 F1510 R1511 S1512 I1513 S1514 S1515 F1516 D1517 N1518 N1519 T1520 I1521 S1522 R1523 I1524 E1525 A1526 S1527 V1528 H1529 E1530 I1531 S1532 N1533 S1534 Y1535 V1536 L1537 K1538 M1539 N1540 D1541 K1542 V1543 F1544 R1545 P1546 L1547 F1548 V1549 I1550 L1551 V1552 R1553 W1554 A1555 F1556 D1557 G1558 E1559 G1560 V1561 T1562 N1563 A1564 G1565

I1566 T1567 E1568 T1569 E1570 R1571 L1572 L1573 A1574 F1575 F1576 K1577 F1578 F1579 N1580 K1581 L1582 Q1583 E1584 N1585 L1586 R1587 G1588 I1589 I1590 T1591 S1592 Y1593 F1594 T1595 Y1596 L1597 L1598 E1599 P1600 V1601 D1602 M1603 L1604 L1605 K1606 R1607 F1608 I1609 S1610 K1611 D1612 M1613 E1614 N1615 V1616 N1617 L1618 R1619 R1620 L1621 V1622 I1623 N1624 S1625

L1626 T1627 S1628 S1629 L1630 K1631 F1632 D1633 R1634 D1635 E1636 Y1637 W1638 K1639 S1640 T1641 S1642 R1643 F1644 E1645 L1646 I1647 S1648 V1649 S1650 L1651 V1652 N1653 Q1654 L1655 S1656 N1657 I1658 E1659 N1660 S1661 I1662 G1663 K1664 Y1665 L1666 V1667 K1668 A1669 I1670 G1671 A1672 L1673 A1674 S1675 N1676 N1677 S1678 G1679 V1680 D1681 E1682 H1683 N1684 Q1685

I1686 L1687 N1688 K1689 L1690 I1691 V1692 E1693 H1694 M1695 K1696 A1697 S1698 C1699 S1700 S1701 N1702 E1703 K1704 L1705 W1706 A1707 I1708 R1709 A1710 M1711 K1712 L1713 I1714 Y1715 S1716 K1717 I1718 G1719 E1720 S1721 W1722 L1723 V1724 L1725 L1726 P1727 Q1728 L1729 V1730 P1731 V1732 I1733 A1734 E1735 L1736 L1737 E1738 D1739 D1740 D1741 E1742 E1743 I1744 E1745

R1746 E1747 V1748 R1749 T1750 G1751 L1752 V1753 K1754 V1755 V1756 E1757 N1758 V1759 L1760 G1761 E1762 P1763 F1764 D1765 R1766 Y1767 LEU ASP

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

Chain AF: 80% 76% 20%

MET S2 T3 A4 R5 P6 R7 I8 I9 T10 S11 K12 A13 P14 L15 L16 P17 Q18 Q19 T20 T21 P22 E23 Q24 R25 Y26 W27 R28 Q29 Y30 T31 S32 A33 Q34 L35 V36 K37 E38 H39 N40 S41 V42 T43 H44 I45 S46 F47 N48 P49 Q50 H51 P52 H53 D54 F55 A56 V57 T58 S59 S60

T61 R62 S67 S68 R69 T70 R71 Q72 V73 I74 K75 T76 F77 S78 R79 F80 K81 D82 Y85 S86 A87 R90 S91 D92 G93 L96 C97 A98 G99 D100 A101 T102 G103 L104 V105 S106 D109 S110 Y111 N112 P113 R114 T115 I116 L117 L118 S119 I120 N121 A122 S123 T124 H128 V129

T130 K131 F132 H133 T134 Q135 D136 N137 K138 I139 L140 A141 T142 A143 S144 D145 D146 R147 V148 T149 R150 D153 N156 A157 Y158 E159 P160 Q161 L162 E163 L164 T165 G166 A167 T168 D169 Y170 V171 R172 T173 L174 S175 F176 I177 P178 A179 A180 P181 H182 L183 V184 A185 T186 G187 S188 Y189 D190 G191

L192 I193 R194 L195 Y196 D197 T198 R199 S200 S201 G202 S203 T204 P205 I206 Y207 S208 L209 N210 H211 D212 Q213 P214 V215 E216 N217 V218 I219 A220 V221 S222 P223 T224 Q225 I226 V227 S228 C229 G230 G231 N232 N233 F234 K235 V236 W237 D238 L239 T240 S241 N242 K243 K244 L245 Y246 E247 R248 G249 N250 F251

N252 K253 A254 V255 T256 C257 L258 D259 Y260 V261 E262 N263 F264 D265 S266 P267 M268 Q269 S270 A271 L272 I273 A274 S275 S276 L277 D278 G279 H280 V281 K282 V283 F284 D285 P286 L287 D288 N289 F290 Q291 V292 K293 F294 G295 W296 K297 F298 S299 G300 P301 V302 L303 S304 C305 A306 V307 S308 P309 S310 T311

A312 Q313 G314 N315 R316 H317 L318 V319 A320 G321 L322 S323 S324 G325 L326 L327 A328 I329 K332 K333 K334 GLU LYS ARG SER SER ASP LYS GLU ASN ALA PRO ALA SER PHE ASN LYS ASN ALA K353 S354 N355 N356 F357 Q358 R359 M360 M361 R362 G363 S364 E365 Y366 Q367 G368 D369 Q370 E371

H375 N376 D377 K378 V379 R380 S381 Q382 R383 R384 M385 R386 A387 F388 E389 R390 N391 I392 N393 Q394 F395 K396 W397 S398 E399 A400 L401 D402 N403 A404 F405 V406 P407 G408 M409 A410 K411 E412 L413 T414 L415 T416 V417 L418 Q419 E420 K423 R424 G425 K426 V427 R428 V429 A430 L431 Y432 G433 R434 D435

E436 S437 T438 L439 E440 P441 L442 L443 N444 W445 C446 L447 K448 G449 I450 E451 D452 V453 R454 S455 A456 S457 I458 V459 A460 D461 W462 V463 A464 V465 V466 L467 E468 L469 Y470 G471 N472 T473 L474 E475 S476 S477 P478 V479 L480 Q481 E482 L483 M484 I485 D486 L487 K488 T489 K490 V491 R492 H493 E494 I495

H496 K497 S498 K499 E500 A501 Q502 R503 I504 E505 G506 M507 L508 Q509 L510 L511 T512 SER

- Molecule 31: NET1-associated nuclear protein 1

Chain AG: 70% 71% 21% 8%

MET THR GLN SER LEU GLY ILE GLU Q9 Y10 K11 L12 S13 V14 V15 S16 G17 G18 K19 L22 N23 N24 L25 S26 S27 V28 T29 G30 N31 K32 N33 T34 A35 R36 L37 S38 Q39 D40 Q41 R42 N43 Y44 I45 I46 P47 F48 N49 N50 Q51 I52 K53 E58 T59 R60 Q61 G62 V63 K64

T65 L66 K67 F68 A69 N70 N71 S72 S75 G76 I77 F78 L79 Q80 E81 E82 E83 N84 N85 E86 S87 I88 V89 K90 I91 L92 L93 G94 D95 I96 T97 V98 P99 Q100 Q101 GLU ASP A104 H105 L106 I107 T108 V109 F110 T111 N112 N113 V116 I117 V118 L119 N120 Y121 K122 G123 K124 L125 V126

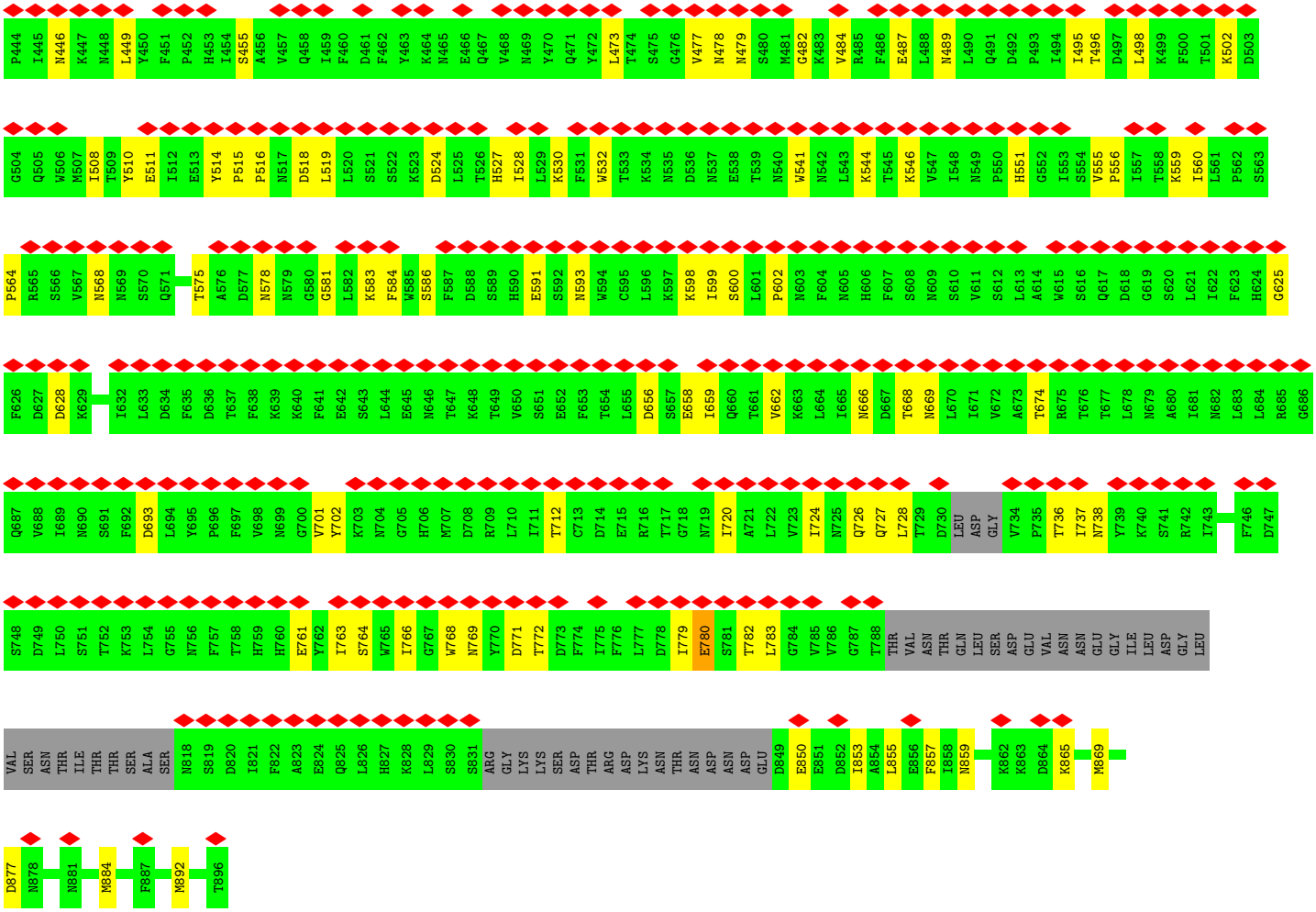
E127 S128 P129 K130 H131 S135 L136 A137 D138 E139 K140 L141 A142 N143 V144 F145 H146 S147 E148 G149 N150 Y151 R152 I153 L154 T155 T156 F157 K158 ASP PRO SER GLN LYS ALA H165 N166 S167 L168 Q169 S170 Y171 Y174 A175 L176 T177 F178 D179 D180 A181 K182 K183 Q184 F185 E186 V187 A188 H189

Q190 W193 H194 N195 V196 I197 L198 S199 N200 I201 S202 S203 N204 L207 L208 A209 H210 M211 C212 K213 D214 V215 SER THR LYS ASP HIS E221 H222 K223 S224 I225 S226 V227 V228 S229 L230 F231 D232 D233 S234 V235 N236 L237 S238 F239 P240 L241 I244 L245 S246 S247 Q248 T249 Q250 S251 L252

S253 Y254 N255 T256 R257 Y258 V259 S260 S261 M262 A263 I264 D265 N266 M267 G268 Q269 Q270 L271 A272 V273 G274 F275 A276 S277 I282 V283 S284 L285 A286 D287 L288 Q289 I290 R291 L292 L293 H296 I297 D298 S299 V300 L301 S302 L303 S304 F305 S306 H307 D308 Y311 L312 L313 S314 G315 G316 W317

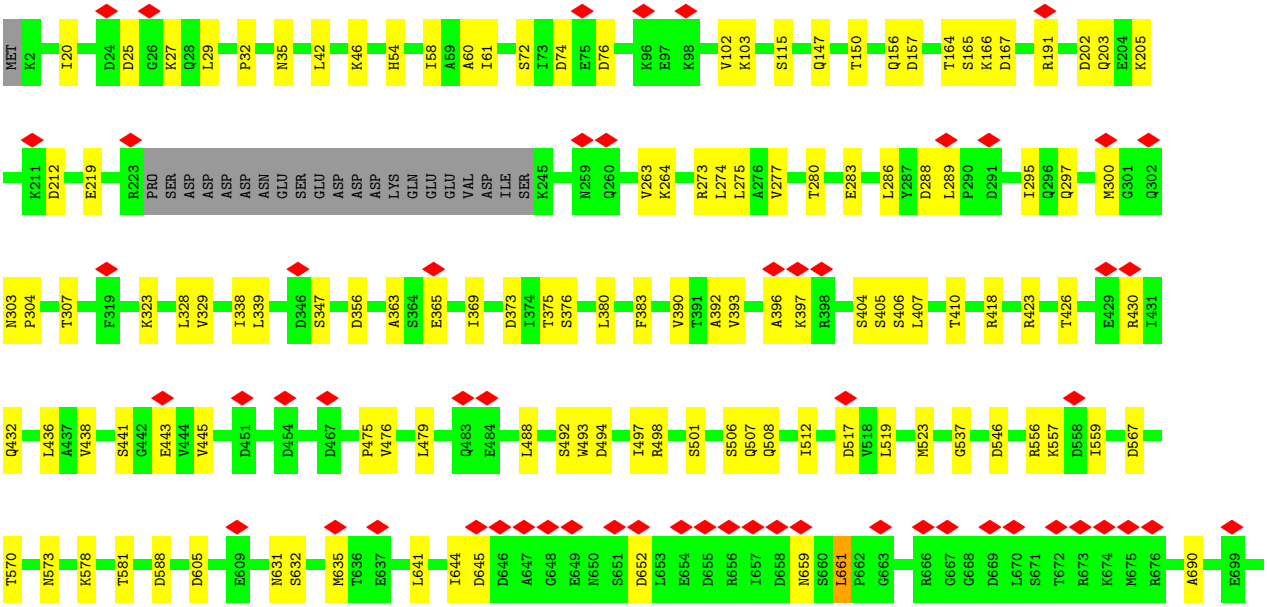
E318 K319 L323 W324 Q325 L326 E327 T328 N329 S330 Q331 Q332 F333 L334 P335 R336 L337 N338 G339 I340 I341 I342 D343 C344 Q345 V346 L347 G348 P349 Q350 G351 M352 S355 L356 I357 L358 Q359 M360 T361 E362 N363 N364 S365 N366 S367 D368 Y369 Q370 F371 L372 N375 A376 S377 D378 L379 T380 S381

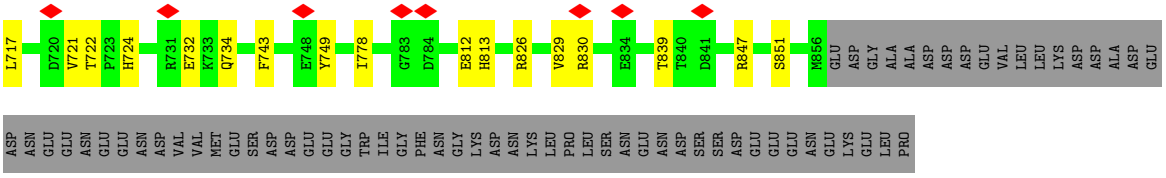
K382 L383 S384 I385 N386 G387 P388 L389 P390 V391 F392 N393 S394 T395 I396 K397 H398 I399 Q400 Q401 P402 I403 S404 A405 M406 N407 T408 K409 N410 S411 N412 S413 I414 T415 S416 L417 N418 H419 S420 K421 K422 K423 Q424 S425 R426 K427 L428 I429 R432 R433 Q434 D435 F436 T437 T438 N439 V440 N443



- Molecule 32: Periodic tryptophan protein 2

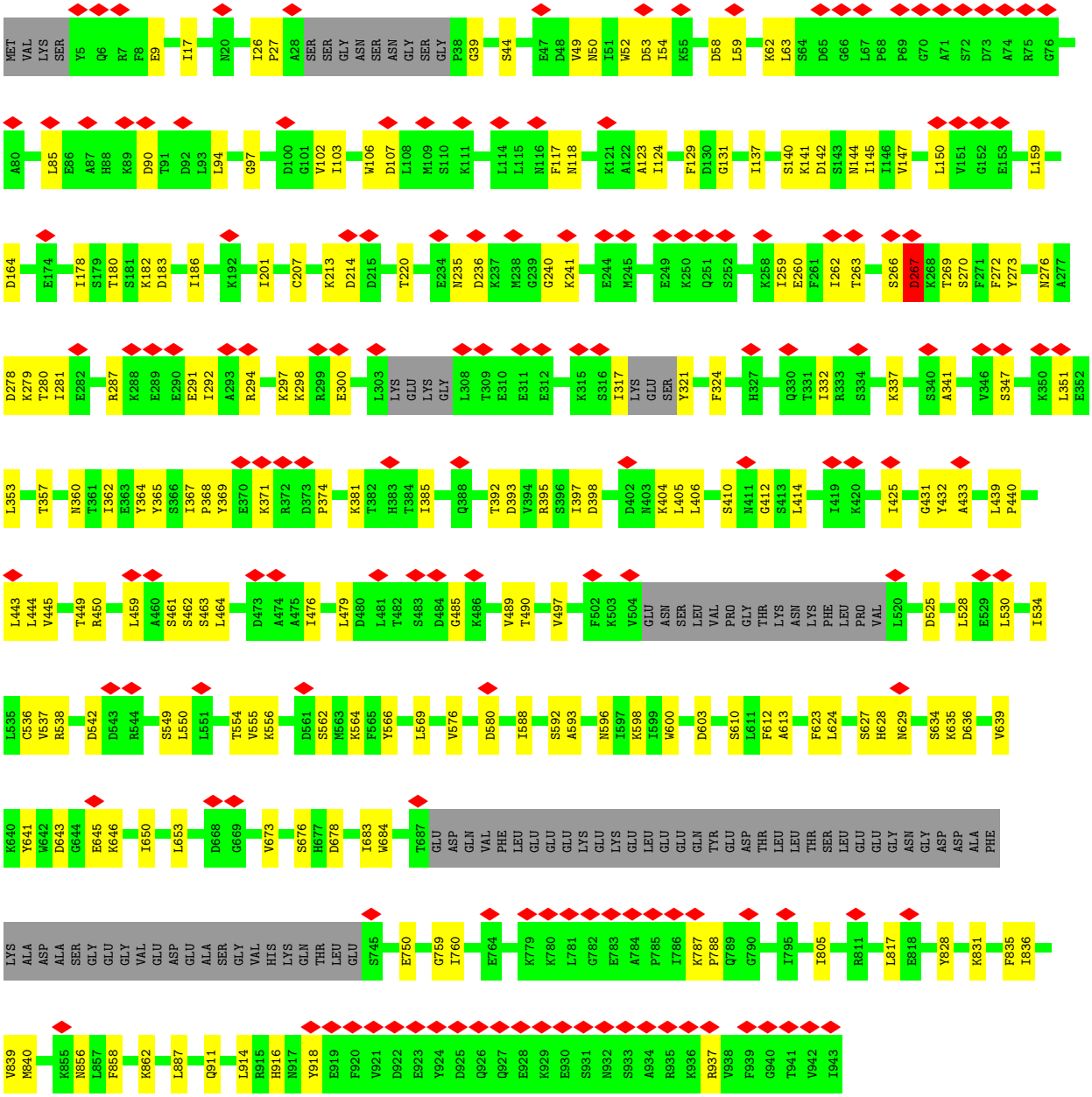
Chain B1:





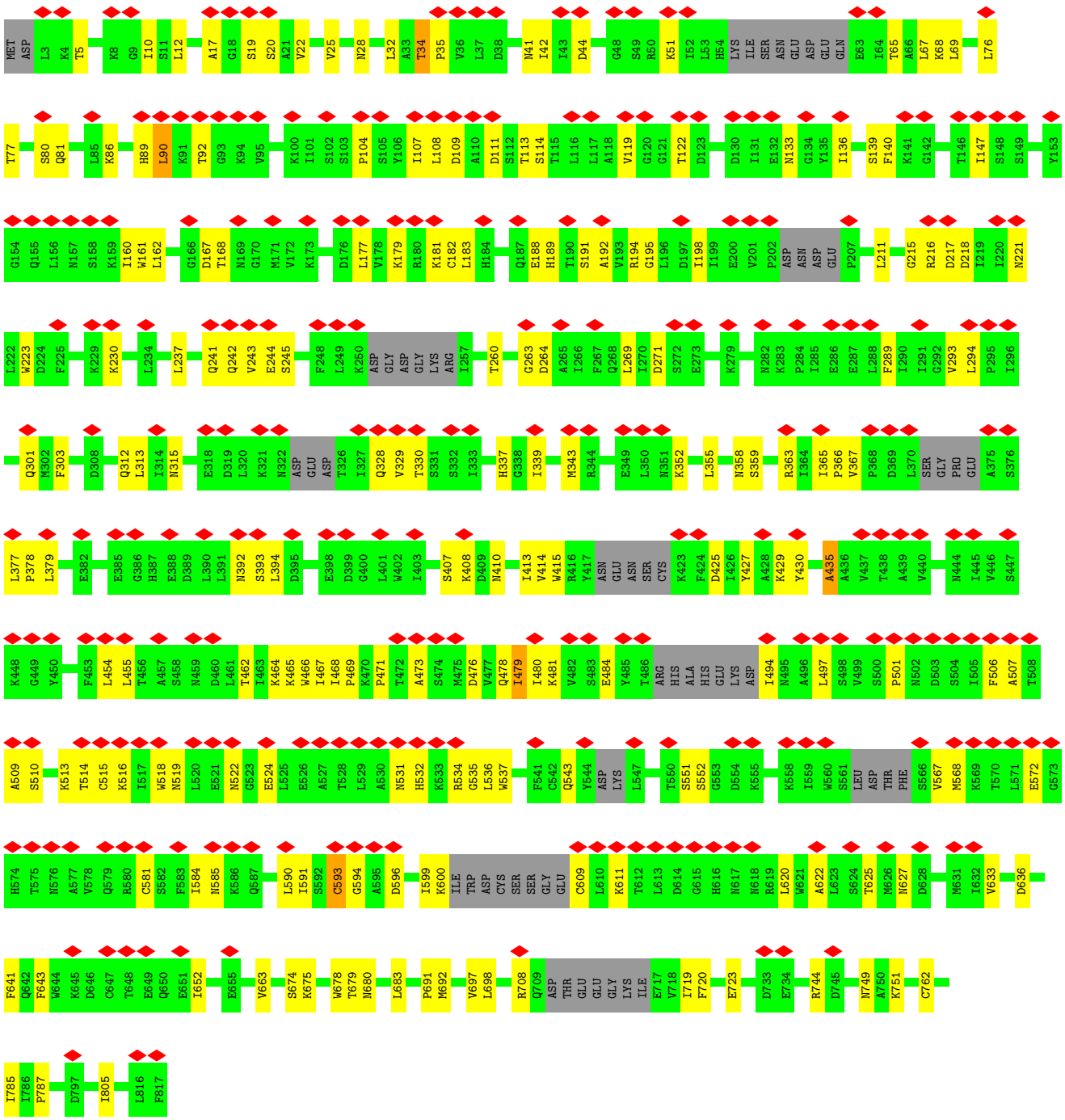
- Molecule 33: U3 small nucleolar RNA-associated protein 12

Chain B2:



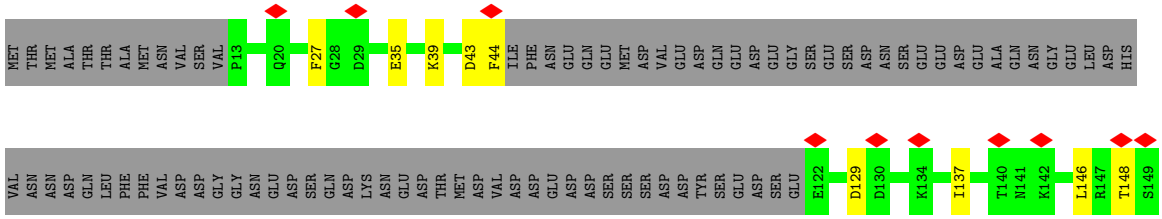
- Molecule 34: U3 small nucleolar RNA-associated protein 13

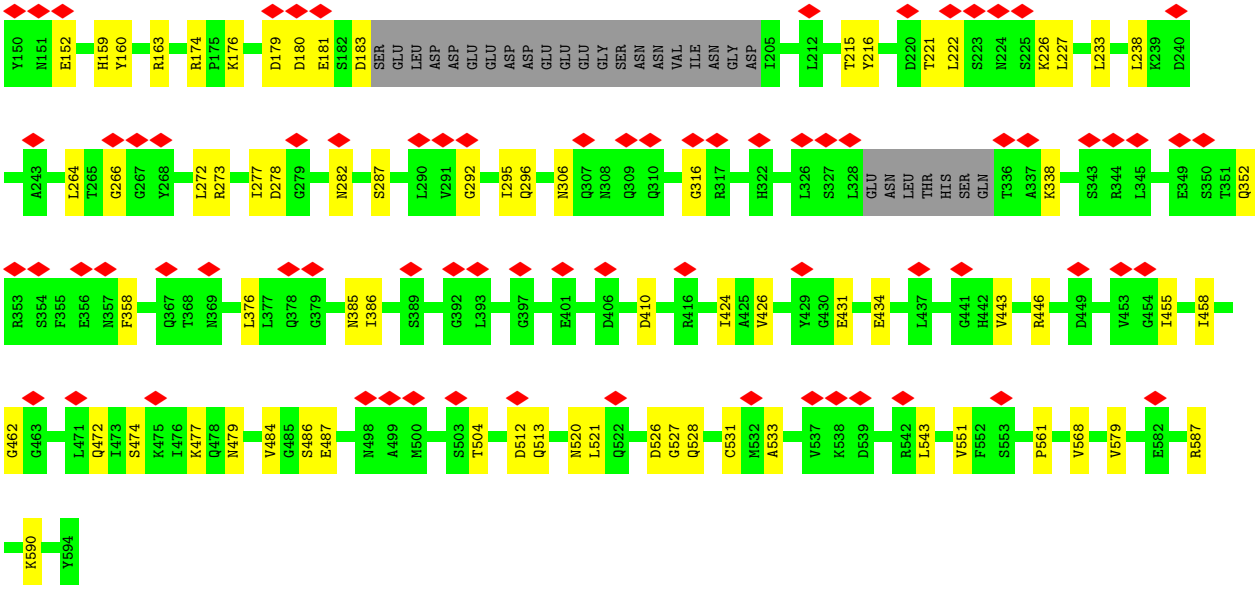
Chain B3:



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

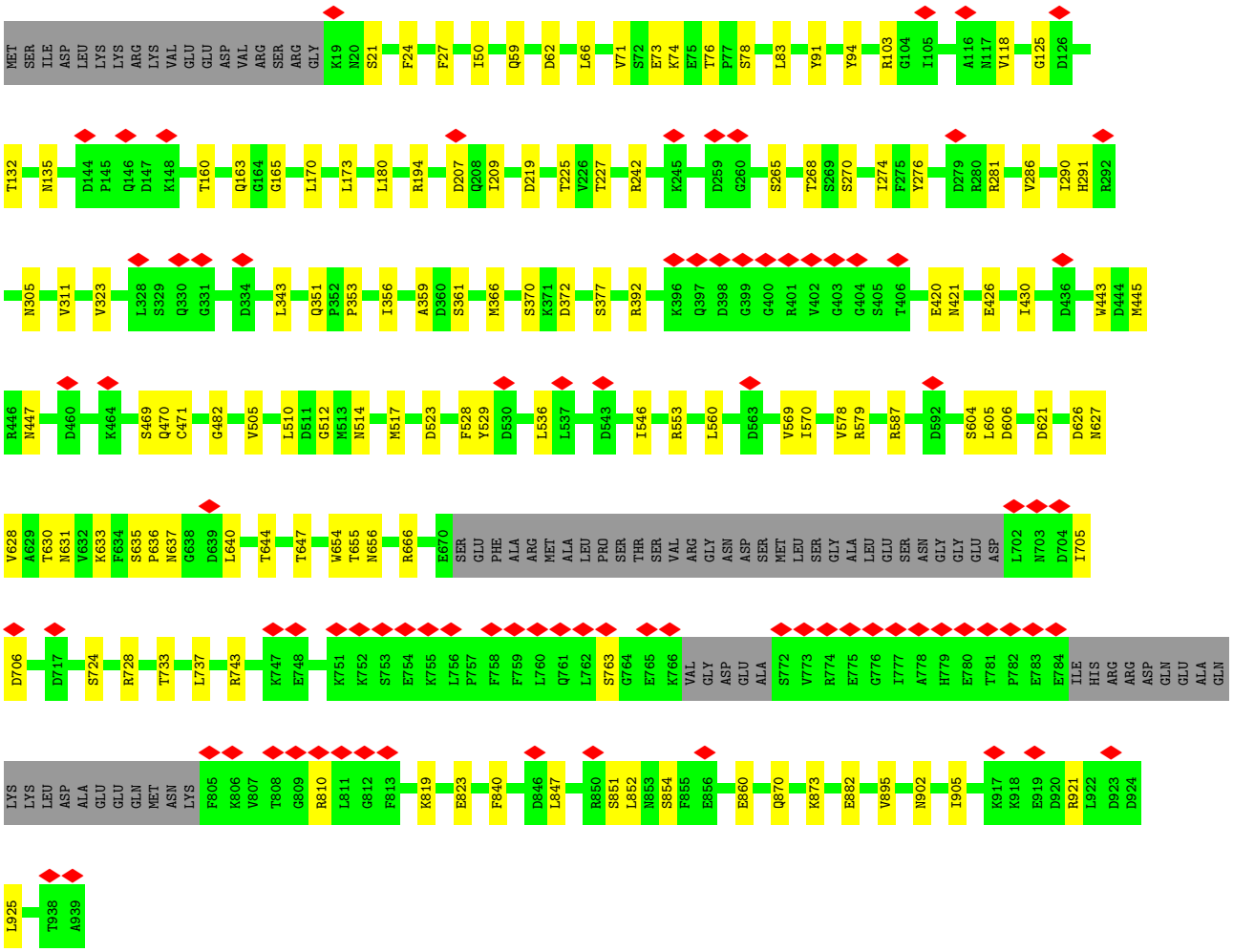
Chain B8:





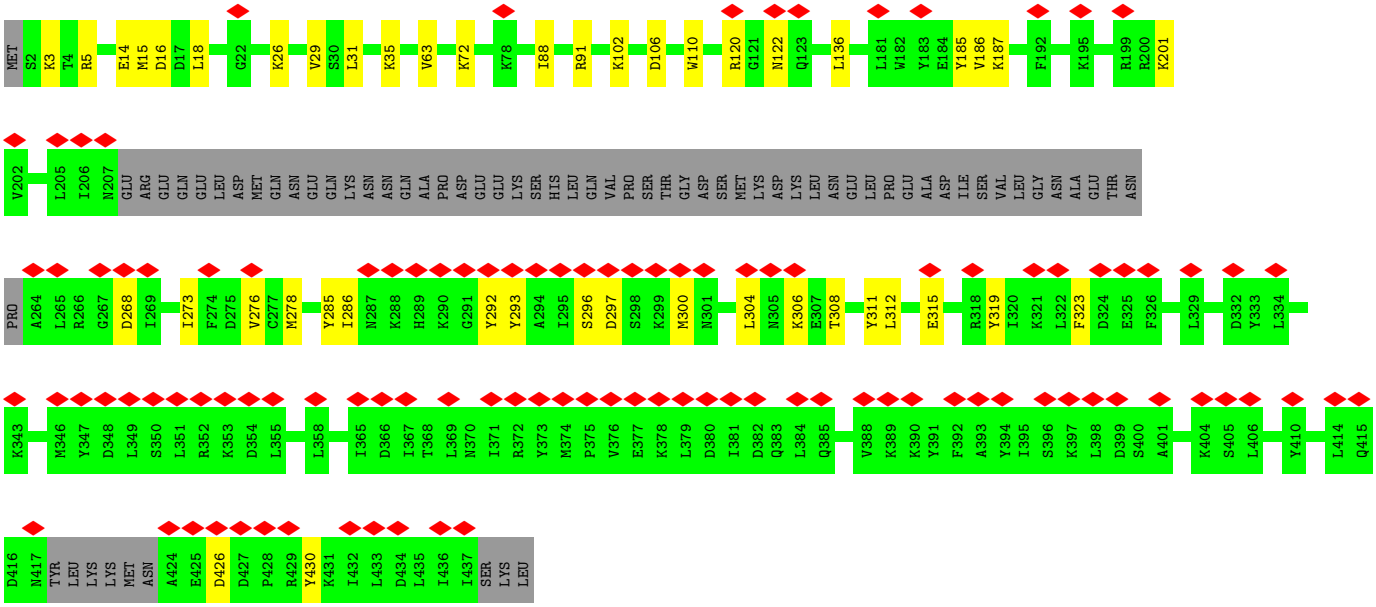
• Molecule 36: U3 small nucleolar RNA-associated protein 21

Chain BE:



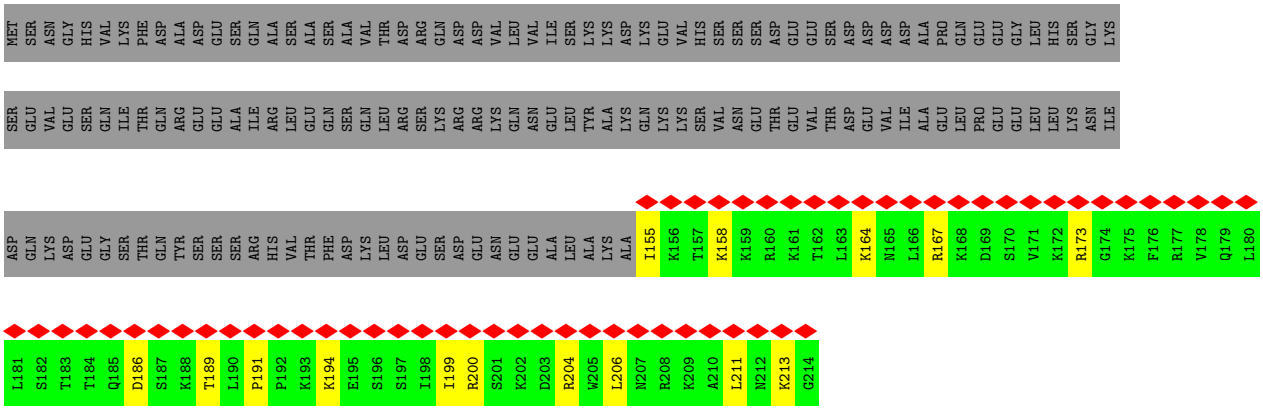
• Molecule 37: U3 small nucleolar RNA-associated protein 6

Chain B6:



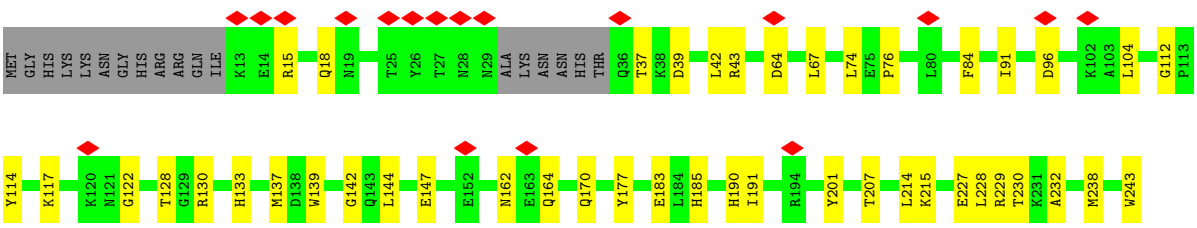
• Molecule 38: Bud site selection protein 21

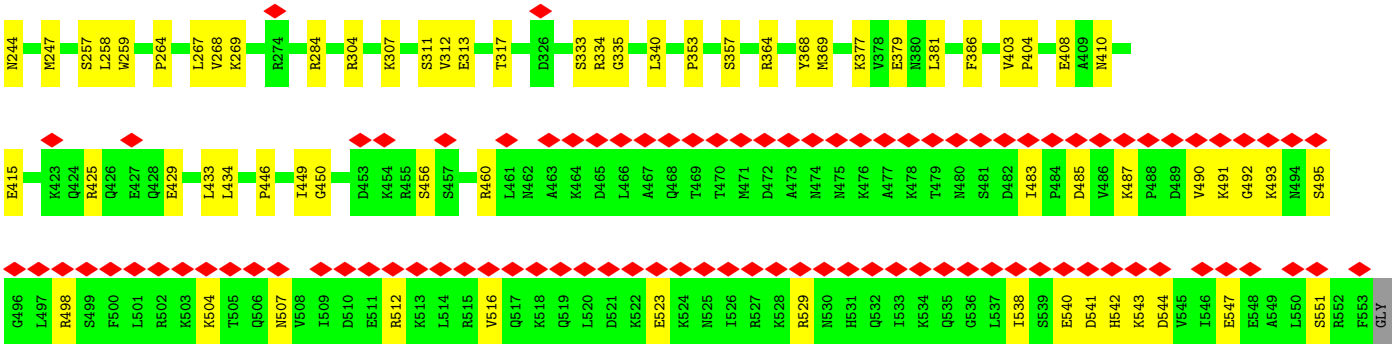
Chain 5B:



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

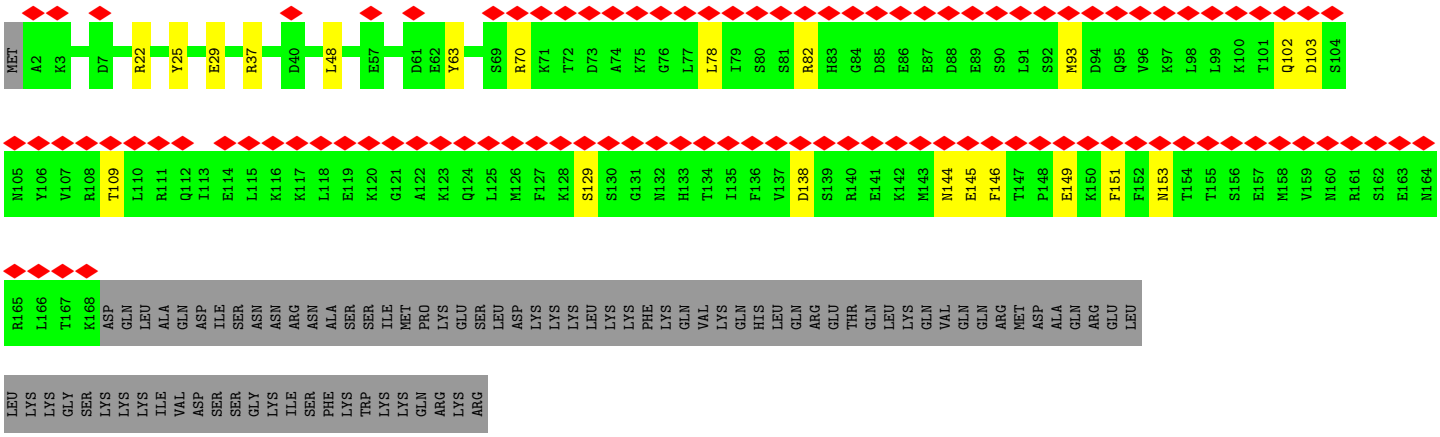
Chain 5C:





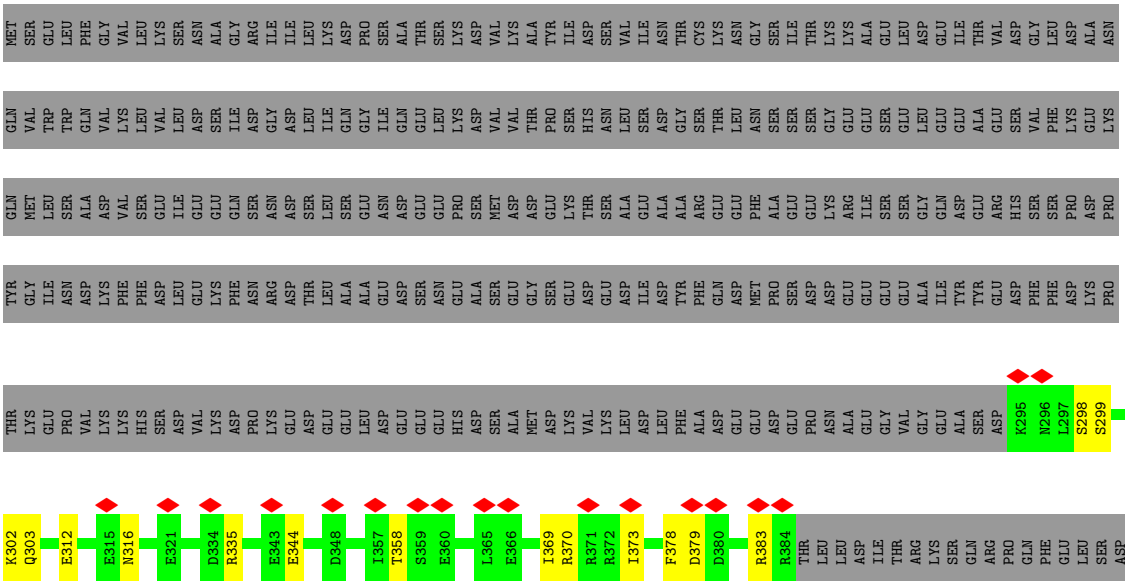
• Molecule 40: U3 small nucleolar RNA-associated protein 11

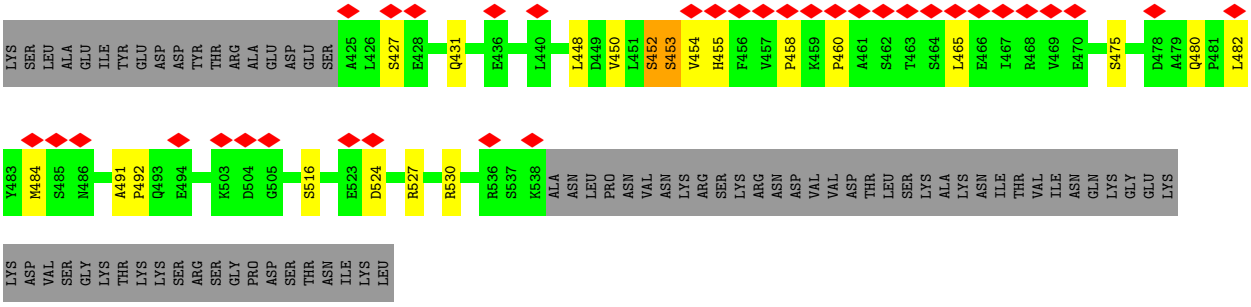
Chain 5D:



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

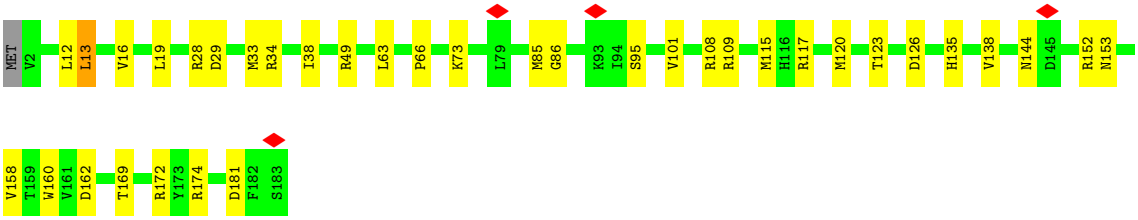
Chain 5E:





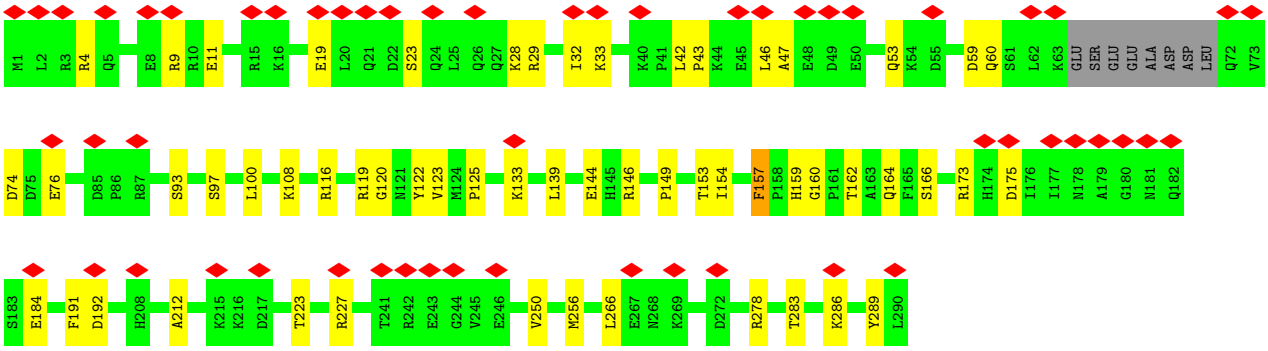
• Molecule 42: U3 small nucleolar ribonucleoprotein protein IMP3

Chain 5F:



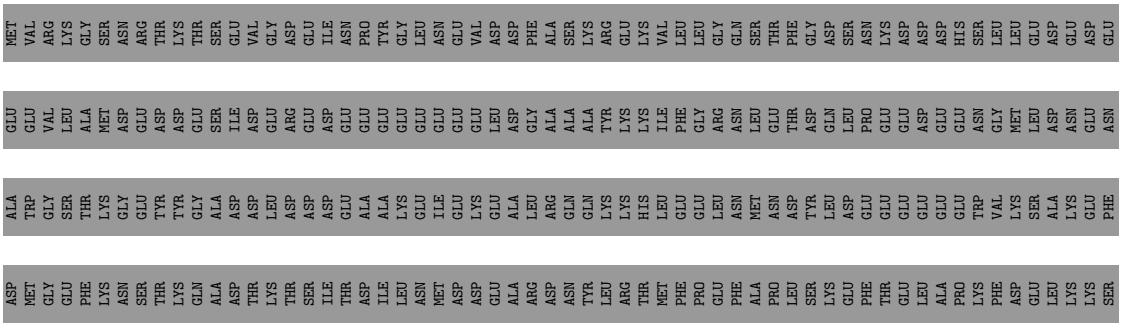
• Molecule 43: U3 small nucleolar ribonucleoprotein protein IMP4

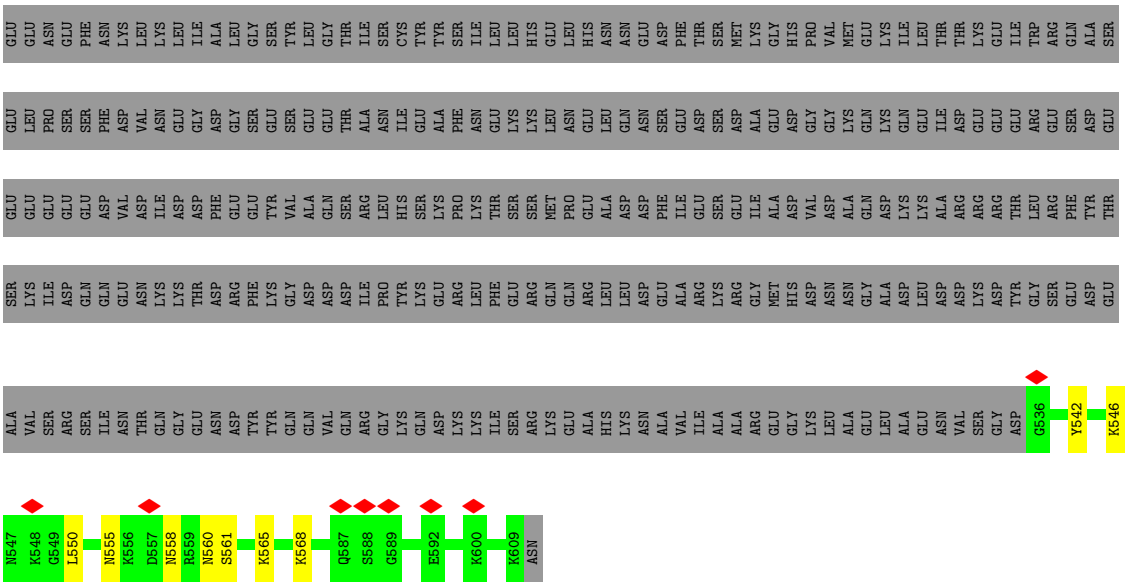
Chain 5G:



• Molecule 44: Something about silencing protein 10

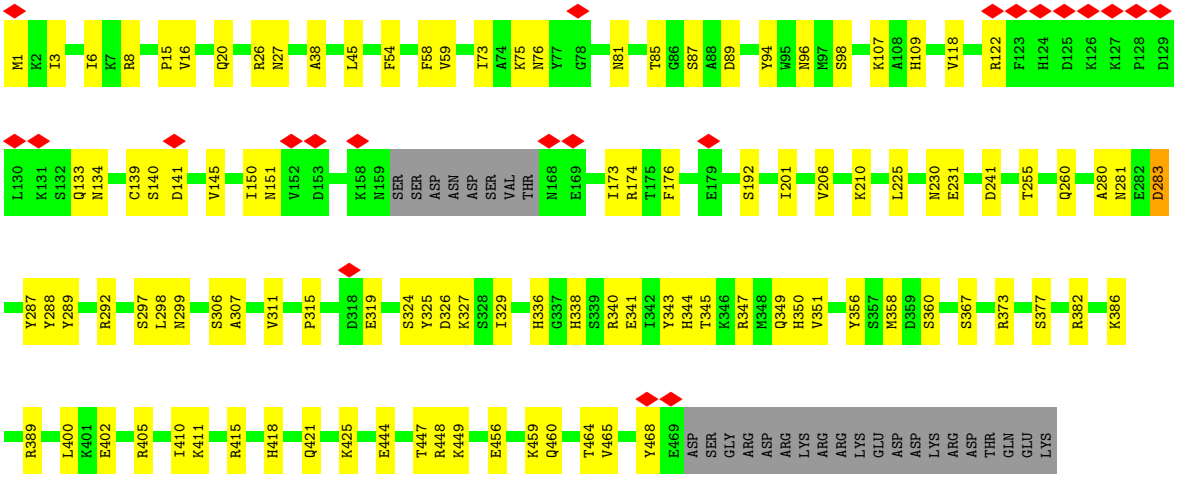
Chain 5H:





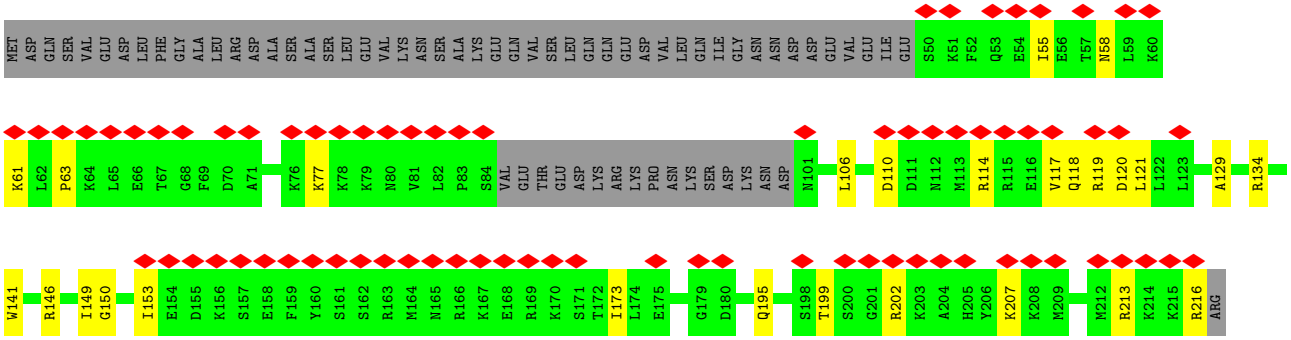
- Molecule 45: Protein SOF1

Chain 5I:



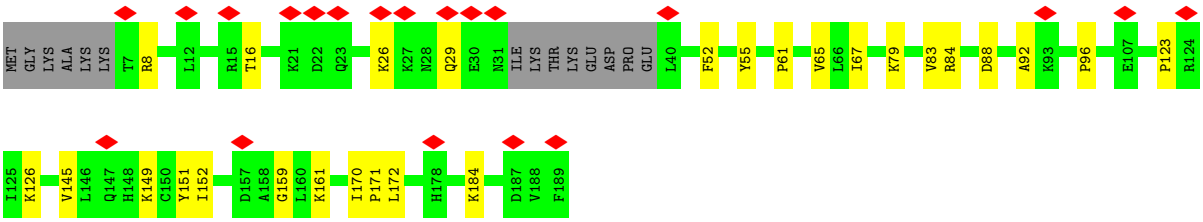
- Molecule 46: rRNA-processing protein FCF2

Chain 5J:



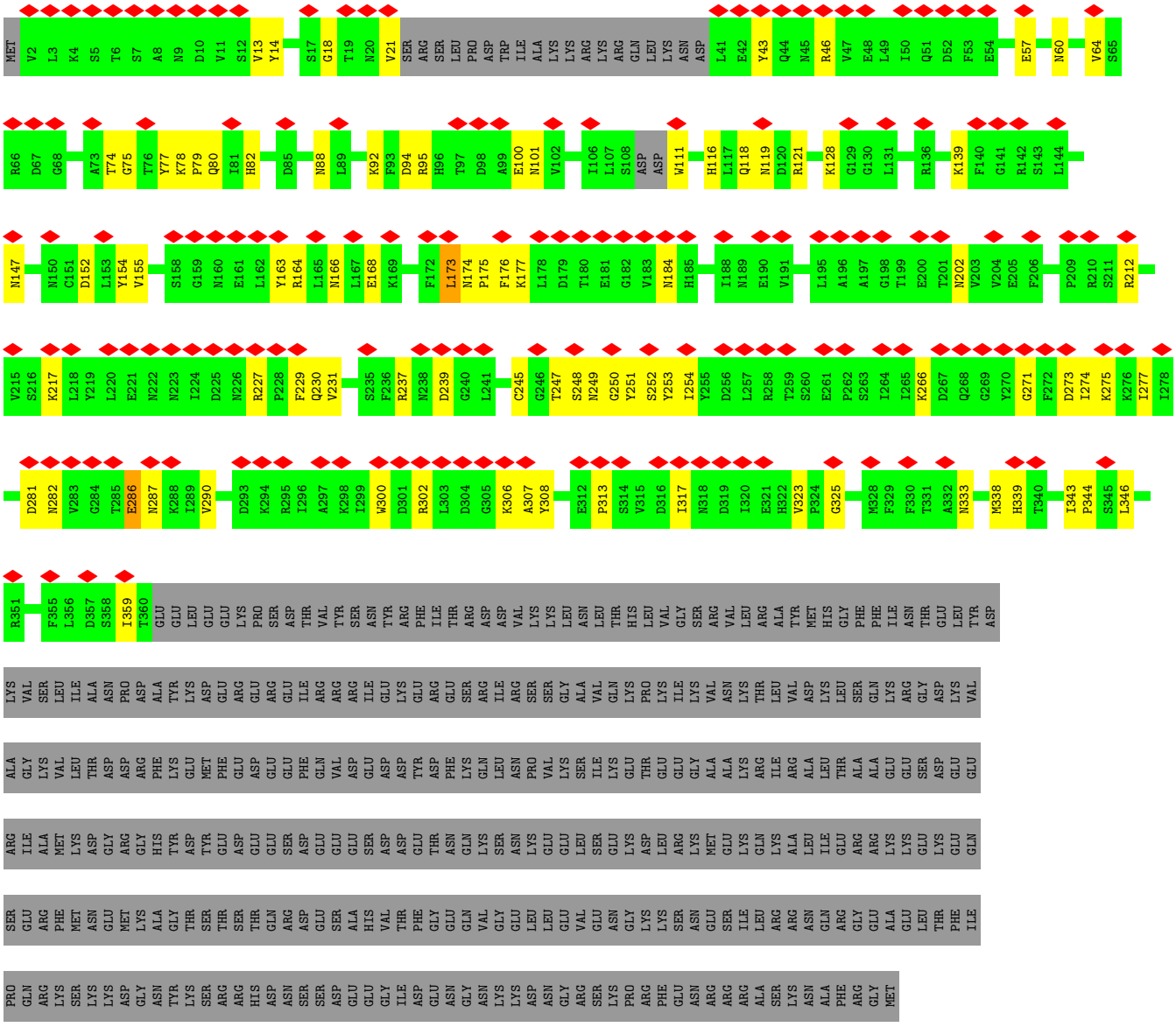
• Molecule 47: rRNA-processing protein FCF1

Chain 5K:



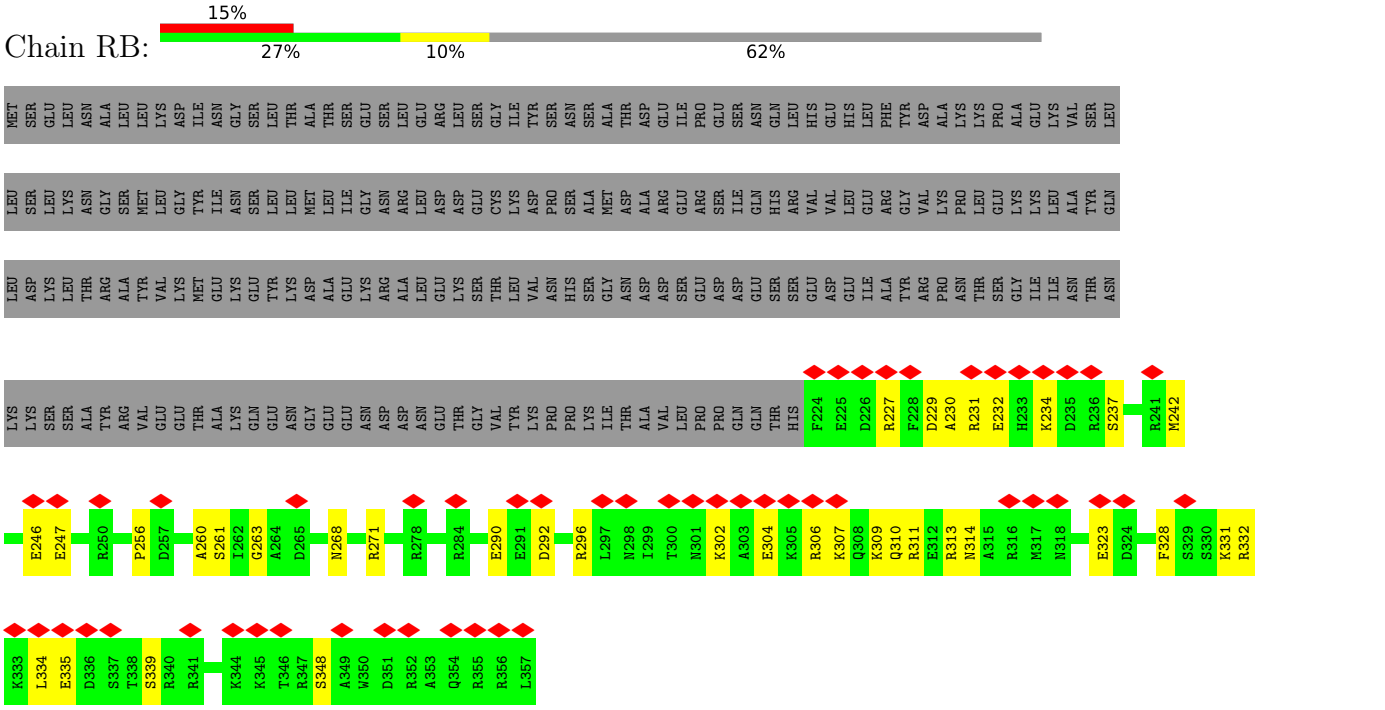
• Molecule 48: Ribosome biogenesis protein ENP2

Chain RA:



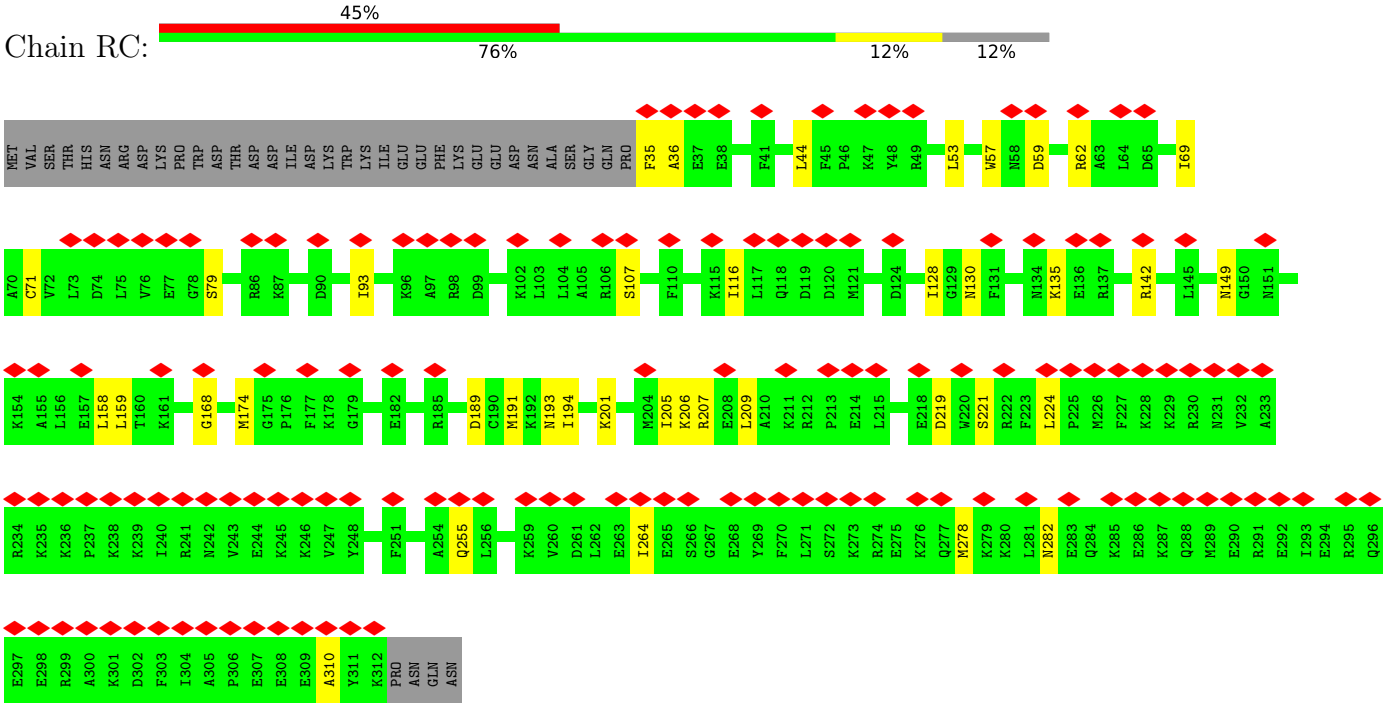
• Molecule 49: U3 small nucleolar ribonucleoprotein protein LCP5

Chain RB:



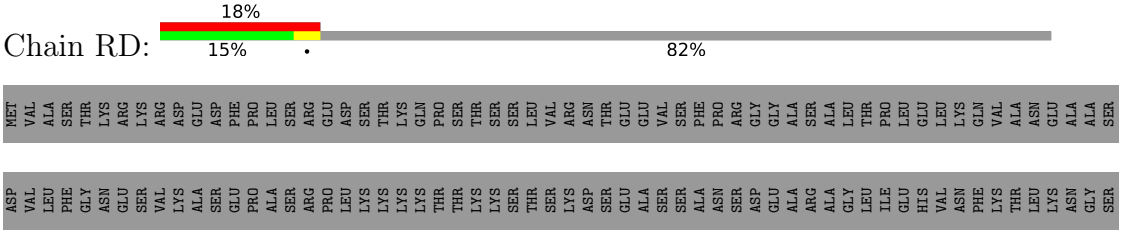
• Molecule 50: KRR1 small subunit processome component

Chain RC:



• Molecule 51: rRNA biogenesis protein RRP5

Chain RD:



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

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

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

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

ARG LYS GLU ASN VAL VAL GLN ASP LYS THR ILE ASP ILE ASN THR ARG A1457 P1458 E1459 S1460 V1461 A1462 D1463 F1464 E1465 R1466 L1467 L1468 I1469 G1470 N1471 P1472 N1473 S1474 S1475 V1476 V1477 W1478 M1479 N1480 Y1481 M1482 A1483 F1484 Q1485 L1486 Q1487 L1488 S1489 E1490 I1491 E1492 K1493 A1494 R1495 E1496 L1497 A1498 E1499 R1500

A1501 L1502 K1503 T1504 I1505 N1506 F1507 R1508 E1509 E1510 A1511 E1512 K1513 L1514 N1515 I1516 W1517 I1518 A1519 M1520 L1521 N1522 L1523 E1524 N1525 T1526 F1527 G1528 T1529 E1530 E1531 T1532 L1533 E1534 E1535 V1536 F1537 S1538 R1539 A1540 C1541 Q1542 Y1543 M1544 D1545 S1546 Y1547 T1548 I1549 H1550 T1551 K1552 L1553 L1554 G1555 I1556 Y1557 E1558 I1559 S1560

E1561 K1562 F1563 D1564 K1565 A1566 A1567 E1568 L1569 F1570 K1571 A1572 T1573 A1574 K1575 K1576 F1577 G1578 G1579 E1580 K1581 V1582 S1583 I1584 W1585 V1586 S1587 W1588 G1589 D1590 F1591 L1592 I1593 S1594 H1595 N1596 E1597 E1598 Q1599 E1600 A1601 R1602 T1603 I1604 L1605 G1606 N1607 A1608 L1609 K1610 A1611 L1612 P1613 K1614 R1615 N1616 H1617 I1618 E1619 V1620

V1621 R1622 K1623 F1624 A1625 Q1626 L1627 E1628 F1629 A1630 K1631 G1632 D1633 P1634 E1635 R1636 G1637 R1638 S1639 L1640 F1641 E1642 G1643 L1644 V1645 A1646 D1647 A1648 P1649 K1650 R1651 I1652 D1653 L1654 W1655 N1656 V1657 Y1658 V1659 D1660 Q1661 E1662 V1663 K1664 A1665 K1666 D1667 K1668 K1669 K1670 V1671 E1672 D1673 L1674 F1675 E1676 R1677 I1678 I1679 T1680

K1681 K1682 I1683 T1684 R1685 K1686 Q1687 A1688 K1689 F1690 F1691 F1692 N1693 K1694 W1695 L1696 Q1697 F1698 E1699 E1700 S1701 GLU GLY ASP GLU K1706 T1707 I1708 E1709 Y1710 V1711 K1712 A1713 K1714 A1715 T1716 E1717 Y1718 V1719 A1720 S1721 HIS GLU SER GLN LYS ALA ASP GLU

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

Chain RE: 51% 64% 23% 13%

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

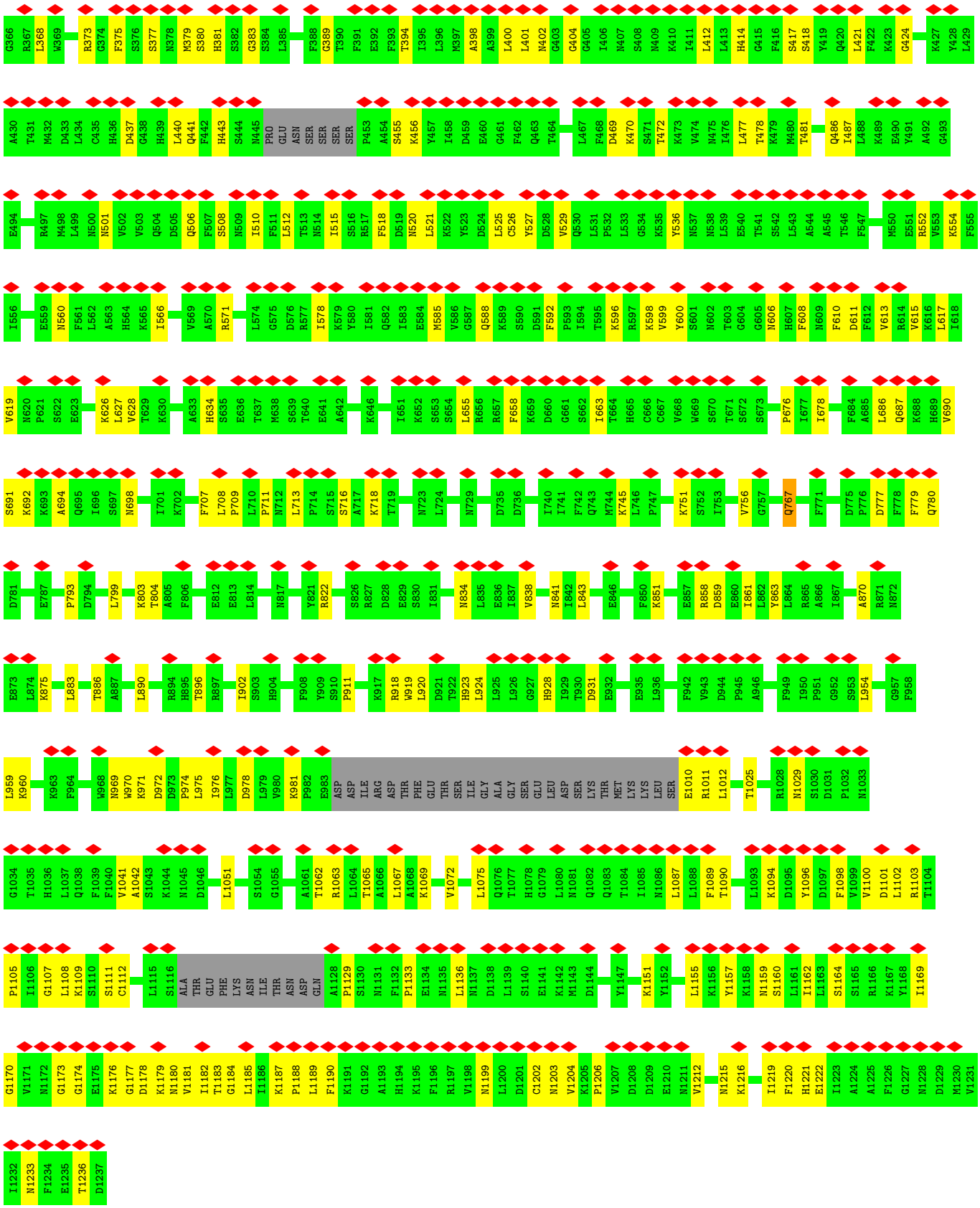
SER PRO GLU SER ASN GLU VAL ALA THR ASN THR ALA ALA THR ARG HIS ASN GLY LYS VAL THR ALA THR GLU SER TYR ASP ILE HIS ILE ALA ARG GLU THR ALA GLU LEU PHE LYS S100 N101 I102 F103 K104 L105 Q106 I107 D108 E109 L110 L111 E112 Q113 V114 K115 L116 K117 Q118 K119 H120

V121 L122 K123 V124 E125 K126 F127 L128 H129 K130 L131 Y132 D133 I134 L135 Q136 E137 I138 P139 D140 W141 E142 E143 L146 A147 E148 V149 D150 S151 F152 F153 K154 N155 K156 I157 V158 S159 V160 P161 F162 V163 D164 P165 K166 P167 I168 P169 Q170 N171 T172 N173 Y174 K175 F176 N177 Y178 K179 K180 P181

D182 I183 S184 L185 I186 G187 S188 F189 A190 L191 K192 A193 G194 I195 Y196 N199 G200 S201 S202 I203 D204 T205 L206 L207 T208 M209 P210 K211 E212 L213 F214 E215 K216 K217 D218 F219 F222 R223 C224 L225 H226 K227 R228 S229 V230 Y231 L232 A233 Y234 L235 H238 L239 L240 I241 K244 K245

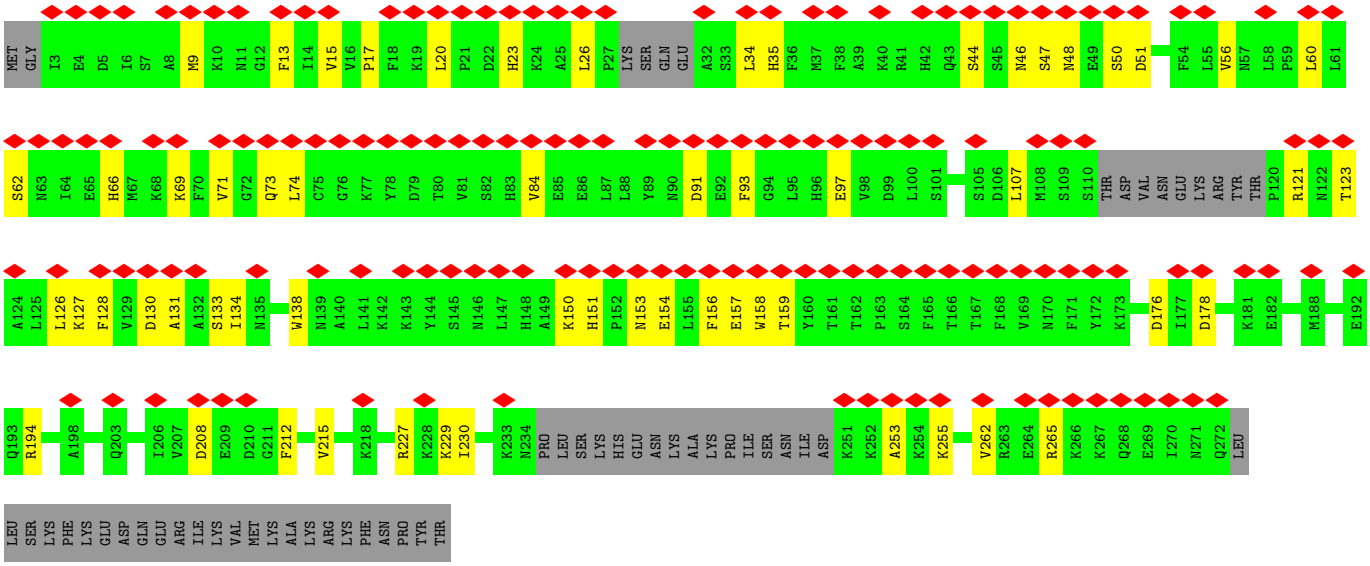
D246 K247 L248 D249 S250 F251 L252 Q253 L254 E255 Y256 S257 Y258 F259 D260 N261 D262 P263 L264 L265 P266 I267 L268 R269 I270 S271 C272 S273 K274 PRO THR GLY ASP SER LEU SER D282 Y283 N284 F285 Y286 R223 K287 T288 R289 F290 S291 I292 N293 L294 L295 I296 G297 F298 P299 Y300 K301 V302 F303 E304 P305

K306 K307 L308 L309 P310 N311 R312 N313 C314 I315 R316 I317 ALA GLN GLU SER LYS GLU GLN SER L326 P327 A328 T329 P330 L331 Y332 N333 F334 S335 V336 L337 S338 S339 S340 T341 H342 E343 N344 Y345 L346 K347 Y348 L349 Y350 K351 T352 K353 K354 Q355 T356 E357 S358 F359 V360 E361 A362 T363 V364 L365



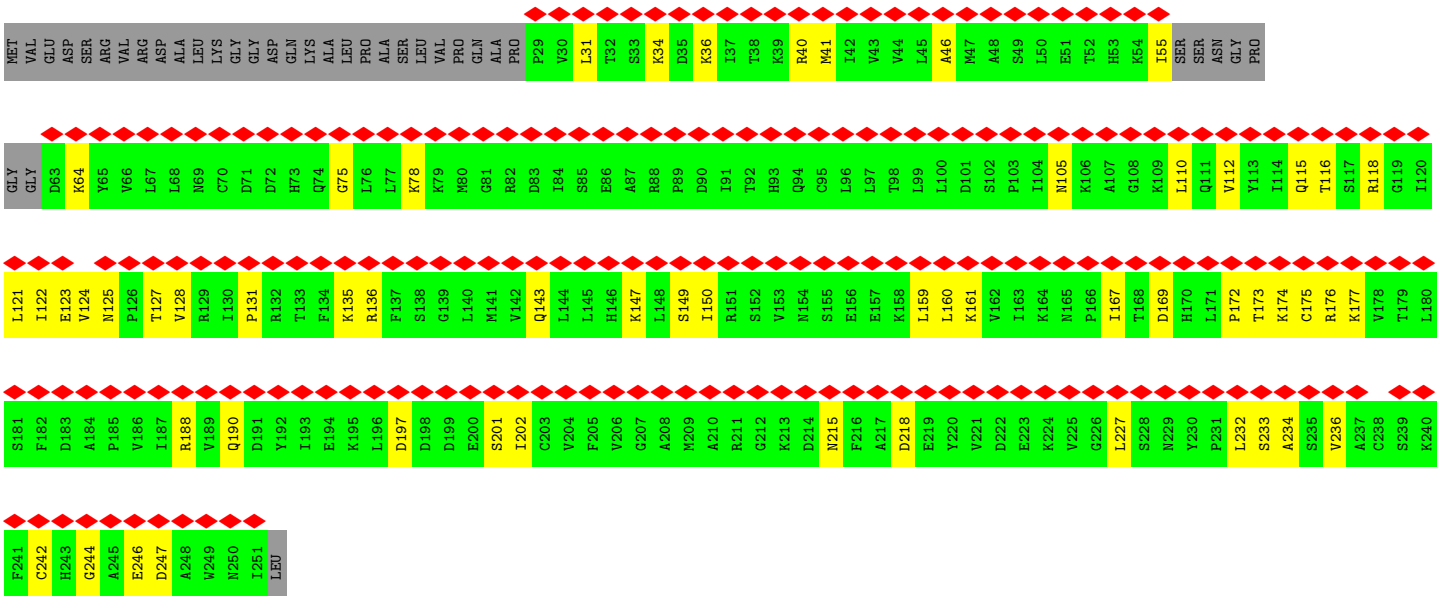
- Molecule 53: Ribosomal RNA-processing protein 7

Chain RF:



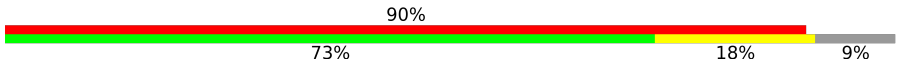
- Molecule 54: Ribosomal RNA small subunit methyltransferase NEP1

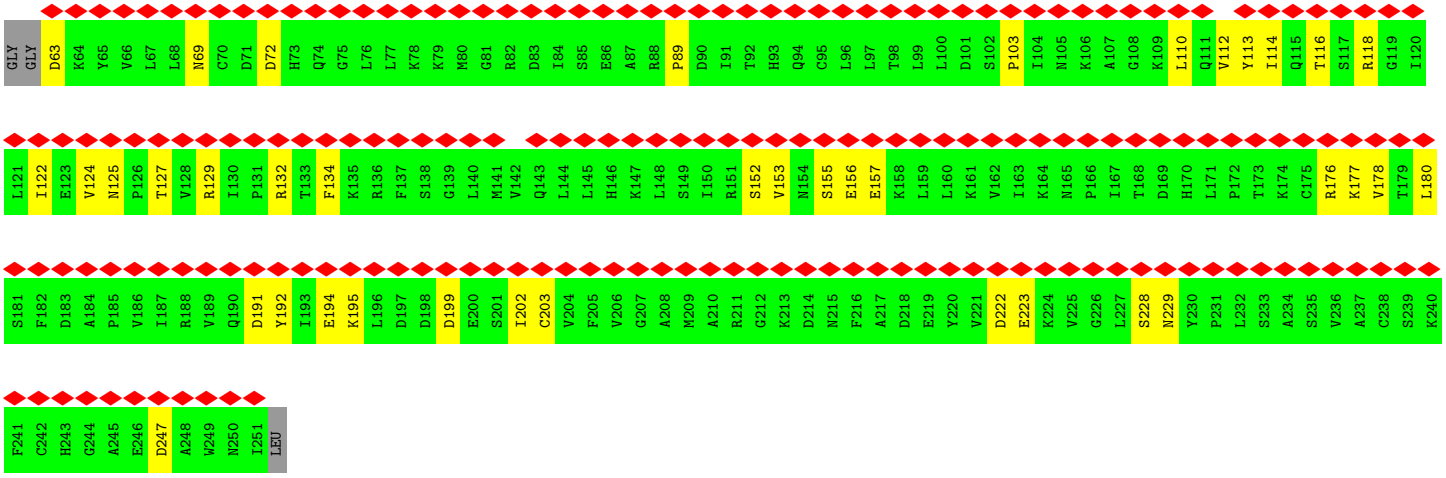
Chain RG:



- Molecule 54: Ribosomal RNA small subunit methyltransferase NEP1

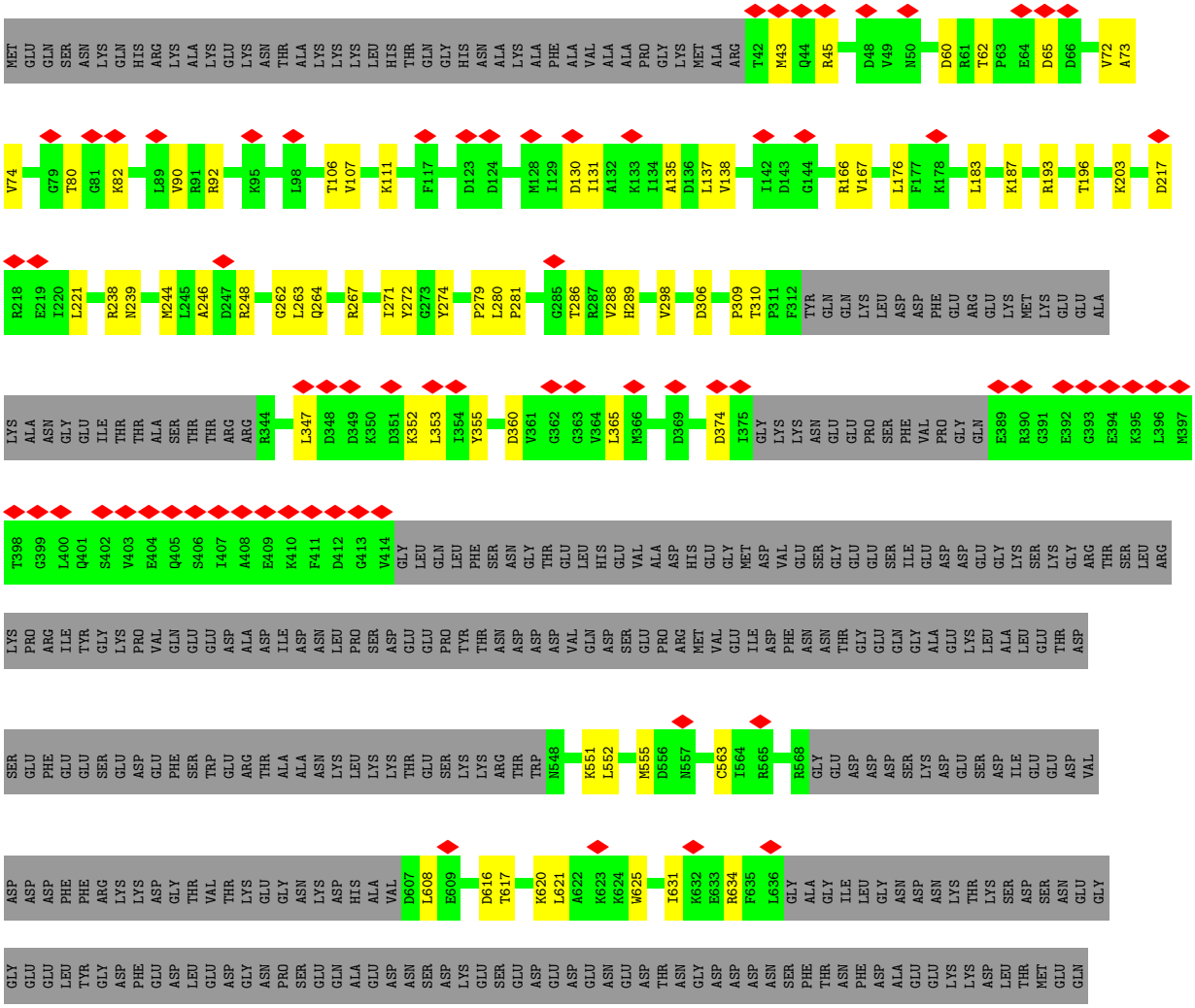
Chain RH:

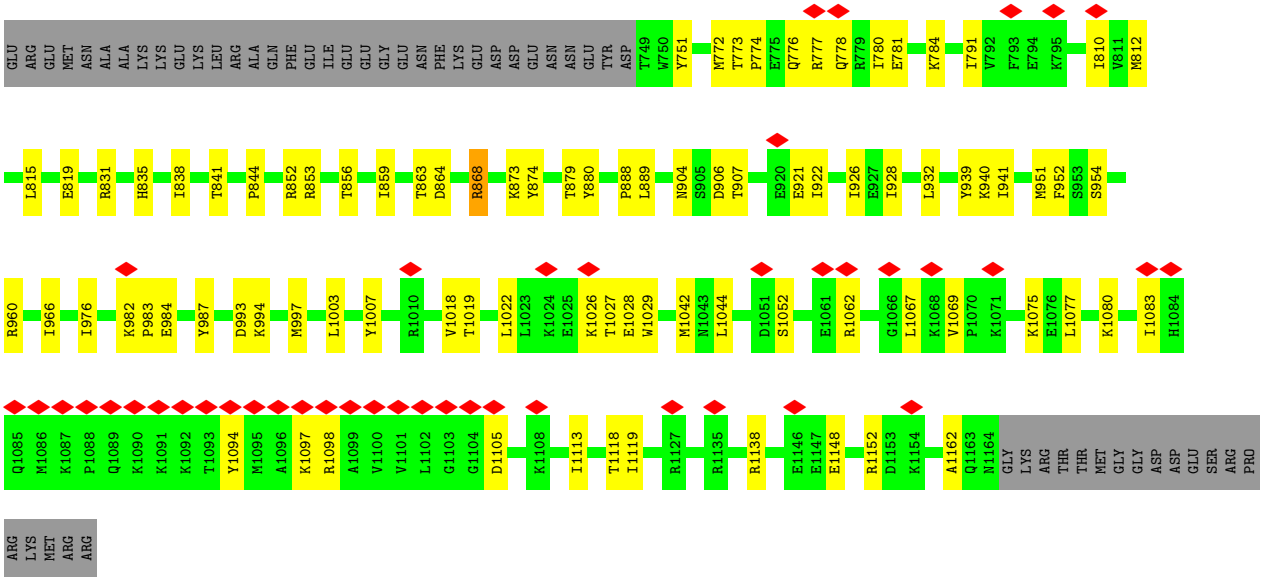




- Molecule 55: Ribosome biogenesis protein BMS1

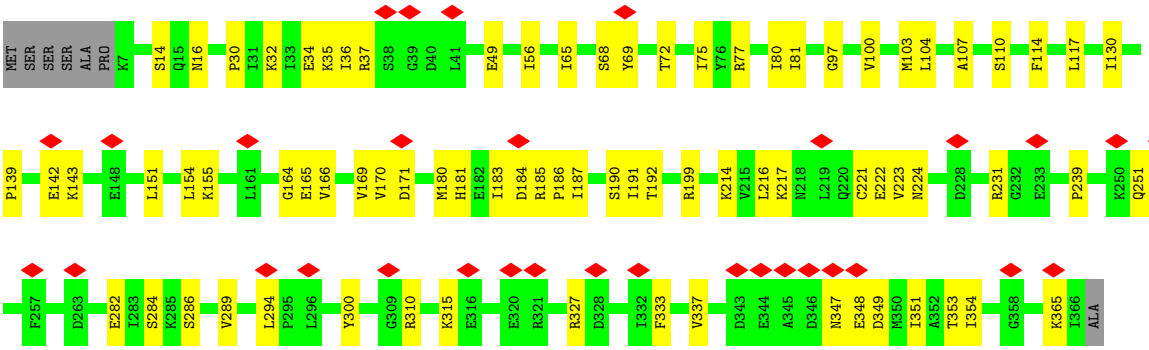
Chain RJ:





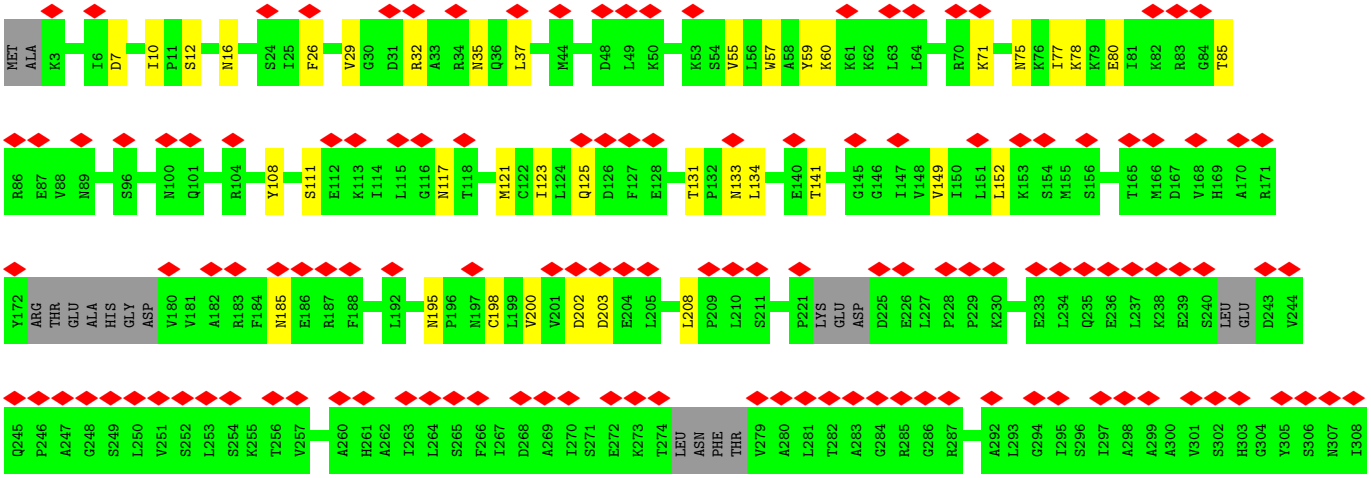
- Molecule 56: RNA 3'-terminal phosphate cyclase-like protein

Chain RK:



- Molecule 57: RNA cytidine acetyltransferase

Chain RL:



F309 V310 P313 S314 P315 E316 N317 L318 K319 T320 L321 F322 E323 F324 I325 G328 F329 D330 A331 L332 G333 Y334 Q335 E336 H337 ILE ASP TYR ASP ILE ILE GLN SER THR ASN PRO ASP F350 N351 K352 A353 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 N399 L400 L401 G402 P403 Y404 L405 V406 S410 T411 I412 N413 G414 Y415 E416 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 Q464 L465 R466 E467 I468 S469 L470 D471 E472 P473 P478 L492 D493 V494 T495 L496 I497 K498 N499 P500 R501 F502 A503 T504 R505 G506 T507 P508

H509 P510 S511 Q512 C513 N514 V517 V518 L523 Y526 H527 P528 E531 N532 E535 M538 A539 L540 Y541 V542 S543 Y546 K547 N548 S549 P550 N551 D552 L555 M556 S557 D558 A561 H562 K563 L564 L568 P569 P570 I571 D572 P573 K574 D575 G576 G577 R578 I579 P580 D581

C584 V585 I586 Q587 I588 A589 L590 E591 G592 E593 I594 S598 L603 S604 R605 G606 Q607 R608 A609 G610 G611 I614 Q620 Q621 F622 Q623 D624 E625 S629 L630 A633 R634 I635 V636 R637 I638 A639 T640 N641 P642 E643 Y644 A645 S646 A653 L657 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 Y727

G728 L729 S732 L733 V743 P744 V745 Y746 L747 R748 Q749 D753 L754 T755 G756 E757 H758 T759 M762 L763 N764 V765 L766 R769 E770 W773 A778 F781 L786 L789 K795 V799 Q800 A801 L802 S803 V804 S808 K809 K810 A811 Q812 D813 L814 S815 D816 D817

E818 K819 H820 D821 N822 K823 E824 L825 T826 R827 T828 H829 L830 D831 D832 I833 F834 S835 P836 F837 D838 L839 K840 R841 L842 D843 S844 Y845 S846 N847 N848 L849 L850 D851 Y852 H853 V854 I855 G856 D857 M858 I859 P860 A863 L864 L865 D869 K870 M871 GLY ASP SER VAL LYS LEU S878 S879 V880

Q881 S882 A883 I884 L885 L886 A887 I888 G889 L890 Q891 N894 I895 D896 T897 I898 A899 K900 E901 L902 N903 L904 P905 S906 N907 Q908 T909 I910 A911 A914 R918 F924 S929 Q930 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: RNA cytidine acetyltransferase

Chain RM: 62% 71% • 27%

MET ALA K3 K4 A5 I6 D7 S8 R9 I10 P11 S12 L13 I14 R15 N16 G17 V18 Q19 T20 K21 Q22 R23 S24 I25 F26 V27 I28 V29 G30 D31 R32 A33 R34 N35 Q36 L37 P38 N39 L40 H41 Y42 L43 M44 M45 S46 A47 D48 L49 K50 M51 N52 K53 S54 V55 L56 W57 A58 Y59 K60

K61 K62 L63 L64 G65 F66 THR SER HIS ARG LYS LYS ARG GLU ASN LYS ILE LYS LYS GLU ILE LYS ARG GLY THR ARG GLU VAL ASN GLU MET D92 P93 F94 E95 S96 F97 I98 S99 N100 Q101 N102 I103 R104 Y105 V106 Y107 Y108 K109 E110 S111 E112 K113 I114 L115 G116 N117 T118 Y119 G120

M121 C122 I123 L124 Q125 D126 F127 E128 A129 L130 T131 P132 N133 L134 L135 A136 R137 T138 I139 E140 T141 V142 E143 G144 G145 G146 I147 V148 V149 I150 L151 L152 K153 S154 M155 S156 S157 L158 K159 Q160 L161 Y162 T163 M164 T165 M166 D167 V168 H169 A170 R171 Y172 ARG THR GLU ALA HIS GLY ASP V180

V181 A182 R183 F184 N185 E186 R187 F188 I189 L190 S191 L192 G193 S194 N195 P196 N197 C198 I199 V200 V201 D202 D203 E204 L205 N206 V207 L208 P209 L210 S211 G212 A213 K214 N215 V216 K217 P218 LEU PRO PRO LYS GLU D224 D225 E226 L227 P228 P229 K230 Q231 L232 E233 L234 Q235 E236 L237 K238 E239 SER

LEU GLU D243 V244 Q245 P246 A247 G248 S249 L250 V251 S252 L253 S254 K255 T256 V257 N258 Q259 A260 H261 A262 I263 L264 S265 F266 I267 D268 A269 I270 S271 E272 K273 T274 LEU ASN PHE THR V279 A280 L281 T282 A283 G284 R285 G286 R287 G288 K289 S290 A291 A292 L293 G294 I295 S296 I297 A298 A299 A300

V301 S302 H303 G304 Y305 S306 N307 I308 F309 V310 T311 S312 P313 S314 P315 E316 N317 L318 K319 T320 L321 F322 E323 F324 I325 F326 K327 G328 F329 D330 A331 L332 G333 Y334 Q335 E336 H337 ILE ASP TYR ASP ILE ILE GLN SER THR ASN PRO ASP PHE ASN LYS ALA I354 V355 R356 V357 D358 I359 K360

ARG ASP HIS ARG GLN THR ILE Q368 Y369 I370 V371 P372 Q373 D374 H375 Q376 V377 L378 G379 Q380 A381 E382 L383 V384 V385 I386 D387 E388 A389 A390 A391 I392 PRO LEU PRO I396 V397 K398 N399 L400 L401 G402 P403 Y404 L405 V406 F407 M408 A409 S410 T411 I412 N413 G414 TYR GLU GLY THR GLY ARG

SER L422 S423 L424 K425 L426 I427 Q428 Q429 L430 R431 N432 Q433 ASN ASN THR SER GLY ARG GLU SER THR GLN THR ALA VAL VAL SER ARG ASP ASN LYS GLU LYS ASP SER HIS LEU HIS SER GLN SER ARG GLN LEU ARG E467 I468 S469 L470 D471 E472 P473 I474 R475 Y476 A477 P478 G479 D480

P481 I482 E483 K484 W485 L486 N487 K488 L489 L490 C491 L492 D493 V494 T495 L496 I497 K498 N499 P500 R501 F502 A503 T504 R505 G506 T507 P508 H509 P510 S511 Q512 C513 N514 L515 F516 V517 V518 N519 R520 D521 F524 S525 Y526 H527 P528 V529 S530 E531 N532 F533 L534 E535 K536 M537 M538 A539 L540 Y541

V542 S543 S544 H545 Y546 K547 N548 S549 P550 N551 D552 L553 Q554 L555 M556 S557 D558 A559 P560 A561 H562 K563 L564 F565 V566 P569 P570 I571 D572 P573 K574 D575 G576 G577 R578 I579 P580 D581 P582 L583 C584 V585 I586 Q587 I588 A589 LEU GLU G592 E593 I594 S595 K596 E597 S598 V599 R600 N601 S602

L603 S604 R605 G606 Q607 R608 A609 G610 G611 D612 L613 I614 P615 W616 L617 I618 S619 Q620 Q621 F622 Q623 D624 E625 E626 F627 A628 S629 L630 S631 G632 A633 R634 I635 V636 R637 I638 A639 T640 N641 P642 E643 Y644 A645 S646 M647 G648 Y649 G650 S651 R652 A653 I654 E655 L656 L657 R658 D659 Y660 F661 GLU

GLY LYS PHE THR ASP MET SER GLU ASP VAL ARG PRO LYS ASP TYR SER ILE LYS ARG VAL SER ASP LYS GLU LEU ALA LYS THR ASN LEU LEU LYS ASP ASP VAL LYS LEU ARG ASP ALA LYS THR LEU PRO PRO L708 L709 L710 K711 E714 Q715 P716 P717 H718 Y719 L720 H721 Y722 L723

G724 V725 S726 Y727 G728 L729 T730 Q731 S732 V743 P744 V745 Y746 L747 R748 Q749 T750 A751 N752 D753 L754 T755 G756 E757 H758 T759 C760 V761 V765 L766 E767 G768 R769 E770 S771 N772 W773 L774 V775 K779 D780 K783 L789 S790 H794 K795 F796 T797 A798 V799 Q800 A801 L802 S803

E806 S807 S808 K809 K810 A811 Q812 D813 L814 S815 D816 D817 E818 K819 H820 D821 N822 K823 E824 L825 T826 R827 T828 H829 L830 D831 D832 I833 F834 S835 L839 K840 R841 L842 D843 D851 Y852 I855 M858 I859 A863 L864 L865 Y866 K870 M871 GLY ASP SER VAL LYS LEU S878

S879 V880 Q881 S882 A883 I884 L885 L886 A887 Q891 N894 I895 D896 T897 I898 E901 L902 N903 L904 P905 T909 R918 S921 S929 Q930 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 58: Nucleolar complex protein 14

Chain RN: 68% 62% 13% 25%

MET A2 G3 S4 Q5 L6 K7 N8 L9 K10 A11 A12 L13 K14 A15 R16 G17 LEU THR GLY GLN THR ASN VAL LYS SER LYS ASN LYS LYS ASN SER LYS ARG GLN ALA LYS GLU Y39 D40 R41 E42 E43 K44 K45 K46 A47 I48 A49 E50 I51 R52 E53 E54 F55 N56 P57 F58 E59 I60

K61 A62 A63 R64 N65 K66 R67 ARG ASP GLY LEU PRO SER LYS THR ALA ASP ARG I79 A80 V81 G82 K83 P84 G85 I86 S87 K88 Q89 I90 G91 E92 E93 Q94 R95 K96 R97 A98 F99 E100 A101 R102 K103 M104 M105 K106 N107 K108 R109 G110 G111 V112 I113 D114 K115 R116 PHE GLY GLU ARG

ASP LYS LEU LEU THR GLU GLU GLU LYS MET LEU GLU ARG PHE THR ARG GLU ARG GLN SER GLN SER LYS ARG ASN ALA ASN LEU PHE ASN LEU GLU ASP ASP GLU ASP ASP GLY ASP MET PHE GLY ASP GLY LEU THR HIS LEU GLY GLN SER LEU SER LEU GLU ASP GLU LEU ALA ASN

ASP GLU GLU ASP PHE LEU ALA SER LYS ARG PHE ASN GLU ASP ASP ALA GLU LEU GLN GLN P201 Q202 R203 K204 K205 T206 K207 A208 E209 V210 M211 K212 E213 V214 I215 A216 K217 S218 K219 F220 Y221 K222 Q223 E224 R225 Q226 K227 A228 Q229 G230 I231 M232 E233 D234 Q235 I236 D237 N238 L239 D240

D241 N242 F243 E244 D245 V246 M247 S248 E249 L250 M251 M252 THR GLN PRO LYS LYS ASN PRO MET GLU PRO LYS T264 D265 L266 D267 K268 E269 Y270 D271 I272 K273 V274 K275 E276 L277 Q278 L279 D280 K281 R282 A283 A284 P285 S286 D287 R288 T289 K290 T291 E292 E293 E294 K295 N296 A297 E298 A299 E300

E301 K302 K303 R304 E305 L306 E307 Q308 Q309 R310 L311 D312 R313 M314 N315 G316 MET ILE GLU LEU GLU GLU GLY GLU GLU ARG GLY VAL GLU ASP LEU ASP ASP GLY PHE TRP GLU ASN GLU GLU ASP TYR GLU ASP ASP ASN ASP GLY ILE ALA ASP SER ASP ASP ASP ILE LYS PHE GLU ASP

GLN GLY ARG ASP GLU GLY PHE SER GLN ILE LEU LYS LYS LYS ASN ILE SER ILE SER CYS PRO R382 T383 H384 D385 A386 L387 L388 D389 Q390 V391 K392 K393 L394 D395 L396 D397 D398 H399 P400 K401 I402 V403 K404 N405 I406 I407 K408 A409 Y410 Q411 P412 K413 L414 A415 E416 G417 N418 K419 E420

K421 L422 G423 K424 F425 T426 A427 V428 L429 L430 R431 H432 I433 I434 F435 L436 S437 N438 Q439 N440 Y441 L442 K443 N444 V445 Q446 S447 F448 K449 R450 T451 Q452 N453 A454 L455 I456 S457 I458 L459 K460 S461 L462 S463 E464 K465 Y466 N467 R468 E469 L470 S471 E472 E473 C474 R475 D476 Y477 I478 N479 E480

M481 Q482 A483 R484 Y485 K486 K487 N488 H489 F490 D491 A492 L493 S494 N495 G496 D497 L498 V499 F500 F501 S502 I503 I504 G505 I506 L507 F508 S509 T510 S511 D512 Q513 Y514 H515 L516 V517 I518 T519 P520 A521 L522 I523 L524 M525 S526 Q527 F528 L529 E530 Q531 I532 K533 F534 N535 S536 L537 K538 R539 I540

A541 F542 G543 A544 V545 L546 V547 R548 I549 V550 S551 Q552 Y553 Q554 R555 I556 S557 K558 R559 Y560 I561 P562 E563 V564 V565 Y566 F567 F568 Q569 K570 T571 L572 L573 T574 F575 I576 V577 E578 LYS GLU ASN GLN GLU LYS P585 L586 D587 F588 E589 N590 T591 R592 L593 D594 S595 Y596 E597 L598 G599 L600

P601 L602 D603 V604 D605 F606 T607 K608 K609 R610 S611 T612 I613 I614 P615 L616 H617 T618 L619 S620 T621 M622 D623 T624 E625 A626 H627 P628 V629 D630 Q631 C632 V633 S634 V635 L636 L637 N638 V639 M640 E641 S642 L643 D644 A645 T646 I647 S648 T649 V650 W651 K652 S653 L654 P655 A656 F657 N658 E659 I660

I661 L662 P663 I664 Q665 Q666 L667 L668 S669 A670 Y671 T672 S673 K674 Y675 S676 D677 F678 E679 K680 P681 R682 N683 I684 L685 N686 K687 V688 E689 K690 L691 T692 K693 F694 T695 E696 H697 I698 P699 L700 A701 L702 Q703 N704 H705 K706 P707 V708 S709 I710 P711 T712 H713 A714 P715 K716 Y717 E718 E719 N720

F721 N722 P723 D724 K725 K726 S727 Y728 D729 P730 D731 R732 T733 R734 S735 E736 I737 N738 K739 M740 K741 A742 K745 R748 K749 M752 I755 R756 K757 K760 F761 K770 K780 M781 I784 V785 N786 T787 I788 N789 T790 E791 K796 R801 E802 R803 K804 L805 R806 GLY

GLY LYS LYS

• Molecule 59: Nucleolar complex protein 4

Chain RO: 95% 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 K408 H409 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 60: U3 small nucleolar RNA-associated protein 20

Chain RP: 65% 79% 5% 15%

MET ALA LYS GLN ARG GLN THR THR LYS SER SER LYS ARG TYR ARG TYR SER S18 F19 K20 A21 R22 I23 D24 D25 L26 K27 I28 E29 P30 A31 ARG ASN LEU GLU LYS ARG VAL HIS ASP TYR VAL GLU SER S45 H46 F47 L48 A49 S50 F51 D52 Q53 W54 K55 E56 I57 N58 L59 S60

A61 K62 F63 T64 E65 F66 A67 A68 E69 I70 E71 H72 D73 V74 Q75 T76 L77 P78 Q79 I80 L81 Y82 H83 D84 K85 K86 I87 F88 N89 S90 L91 V92 S93 F94 I95 N96 F97 H98 D99 E100 F101 S102 L103 Q104 P105 L106 L107 D108 L109 L110 A111 Q112 F113 C114 H115 D116 L117 G118 P119 D120

F121 L122 K123 F124 Y125 E126 E127 A128 I129 K130 T131 L132 I133 N134 L135 L136 D137 A138 A139 I140 E141 F142 E143 S144 S145 N146 V147 F148 E149 W150 G151 F152 L155 A156 Y157 I158 F159 K160 Y161 L162 S163 K164 F165 L166 V167 K168 K169 L170 V171 L172 T173 C174 D175 L176 L177 I178 P179 L180 L181

S182 H183 S184 K185 E186 Y187 L188 S189 R190 F191 S192 A193 E194 A195 L196 S197 F198 L199 V200 R201 K202 C203 P204 V205 S206 N207 L208 R209 E210 R213 S214 V215 F216 E217 K218 L219 E220 GLY ASP ASP GLU GLN THR ASN L228 Y229 E230 G231 L232 L233 I234 T237 E238 S239 M240 T241 E245

T246 L247 H248 S249 K250 A251 K252 A253 I254 M255 S256 V257 L258 L259 H260 E261 A262 L263 T264 K265 S266 S267 P268 E269 R270 S271 V272 S273 L274 D277 I278 W279 M280 N281 I282 S283 K284 Y285 A286 S287 I288 E289 S290 L291 L292 P293 V294 Y295 E296 V297 M298 Y299 Q300 D301 F302 N303 D304 S305 LEU

ASP ALA THR ASN ILE ASP R313 I314 L315 K316 V317 L318 T319 T320 I321 V322 F323 S324 E325 SER GLY ARG LYS I330 P331 D332 W333 N334 K335 I336 T337 I338 L339 I340 E341 R342 I343 M344 SER GLN SER GLU ASN CYS ALA SER L353 S354 Q355 D356 K357 V358 A359 F360 L361 F362 A363 L364 F365 I366

R367 N368 S369 D370 V371 K372 T373 L374 T375 L376 F377 H378 Q379 K380 L381 F382 N383 Y384 A385 L386 T387 N388 I389 S390 D391 C392 F393 L394 E395 F396 F397 Q398 F399 A400 L401 R402 L403 S404 Y405 E406 R407 V408 F409 S410 F411 ASN GLY LEU LYS PHE LEU GLN L419 F420 L421 K422 K423 N424 W425 Q426

S427 Q428 G429 K430 K431 I432 A433 L434 F435 F436 L437 E438 V439 D440 D441 K442 P443 E444 L445 Q446 K447 V448 R449 E450 V451 N452 F453 P454 E455 E456 F457 I458 L459 S460 I461 R462 D463 F464 F465 V466 T467 A468 E469 I470 N471 D472 S473 N474 D475 L476 F477 E478 I479 TYR TRP ARG ALA ILE I485 F486

K487 Y488 S489 K490 L491 Q492 N493 T494 E495 I496 I497 ILE PRO LEU LEU E502 R503 I504 T507 F508 A509 S510 P511 D512 N513 F514 T515 K516 ASP MET VAL G520 T521 L522 L523 K524 R527 K528 E529 D530 D531 A532 S533 GLY ASN ASN LEU L538 K539 T540 I541 L542 D543 N544 Y545 E546 N547 Y548

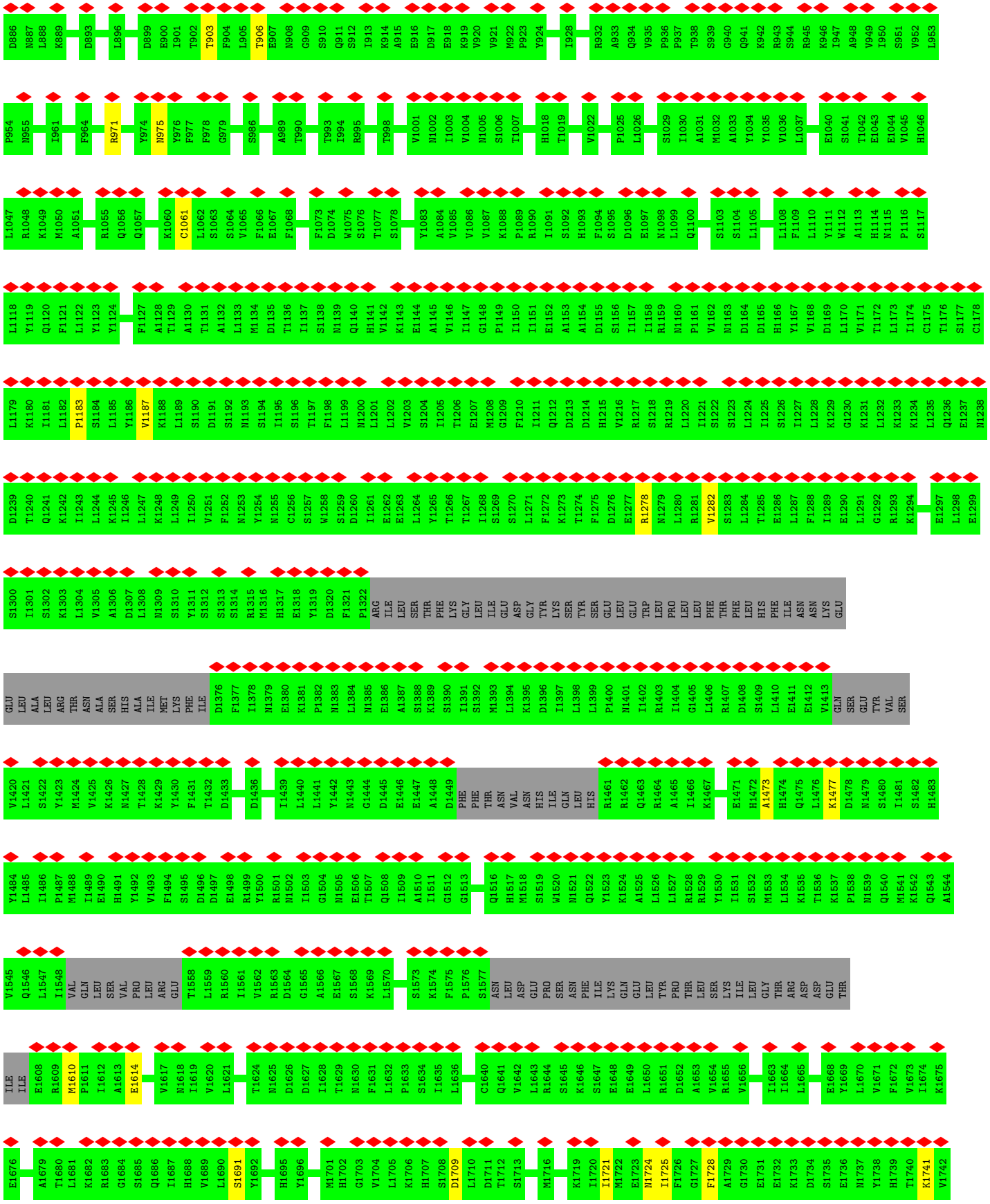
K549 E550 S551 L552 ASN PHE LEU ARG G557 W558 N559 K560 L561 V562 S563 N564 L565 H566 P567 S568 E569 S570 L571 K572 G573 L574 M575 S576 H577 Y578 P579 S580 L581 L582 L583 S584 L585 T586 D587 N588 F589 M590 L591 P592 D593 G594 K595 I596 R597 Y598 GLU THR LEU GLU LEU MET K605 T606 L607 M608

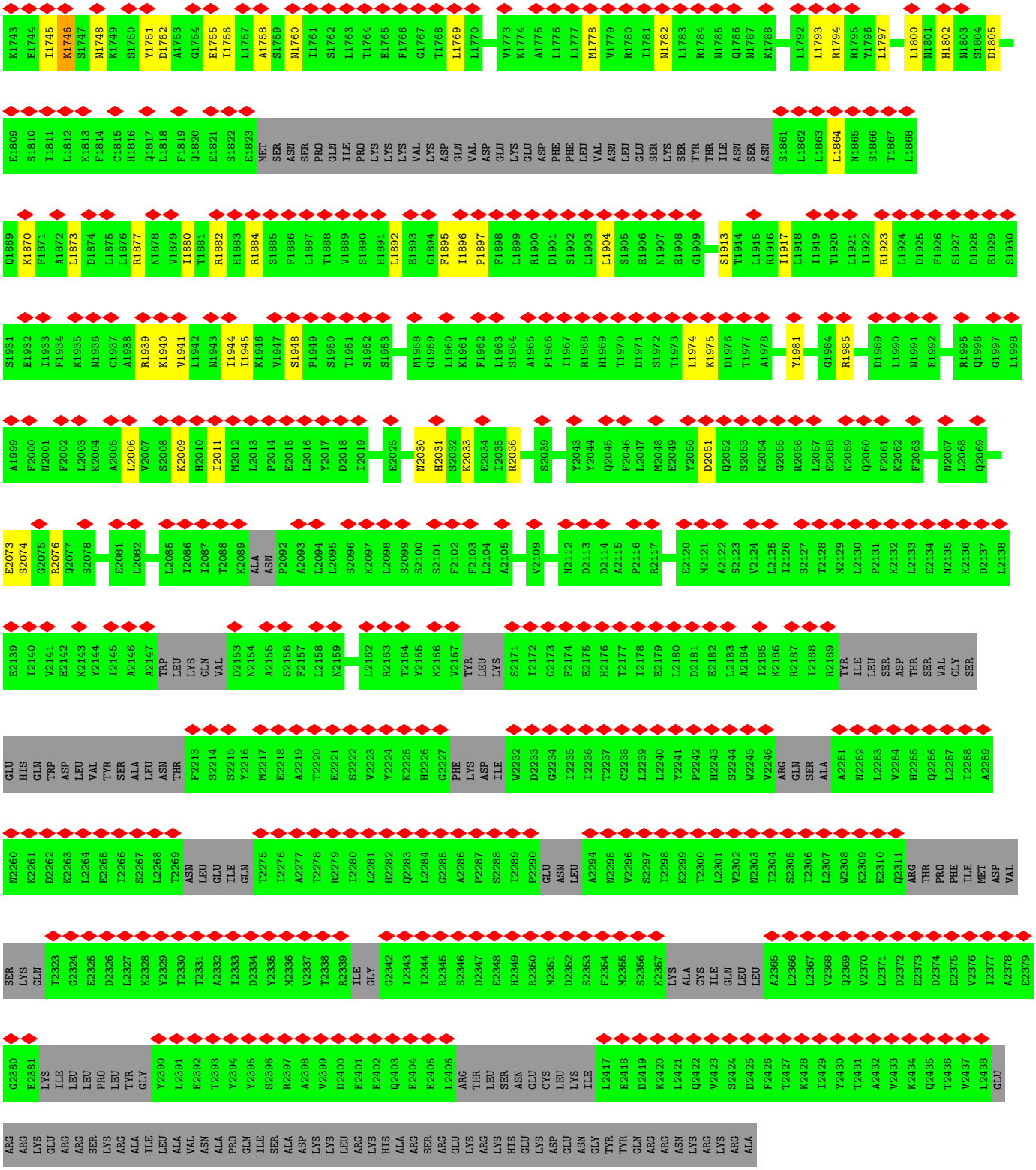
I609 L610 Q611 G612 M613 Q614 V615 P616 D617 L618 L619 S620 S621 C622 M623 V624 I625 E626 E627 Q633 N634 A635 T639 I640 R641 I642 K643 ASN VAL GLY ALA GLU PHE GLY LYS T652 K653 T654 S659 F662 L663 K664 Y665 L666 F667 G668 L669 L670 T671 V672 R673 P676 V677 W678 T679

G680 T684 L685 P686 N687 V688 Y689 T690 K691 D692 L695 V696 V700 L701 S702 F703 I704 K705 L706 P707 D708 E709 N710 Q711 N712 L713 D714 Y715 Y716 Q717 P718 L719 L720 E721 D722 G723 A724 N725 K726 V727 L728 W729 D730 S731 S732 V733 V734 R735 L736 R737 D738 T739 I740 F743 S744 H745

I746 W747 S748 K749 Y750 S751 T752 Q753 N754 T755 S756 I757 I758 S759 T760 T761 I762 E763 R764 R765 G766 N767 T768 T769 Y770 P771 I772 L773 I774 R775 N776 Q777 A778 L779 K780 V781 M782 I785 P786 A789 E790 N791 H792 F793 V794 A797 P798 F799 V800 Y801 N802 D803 K808 E811 D812

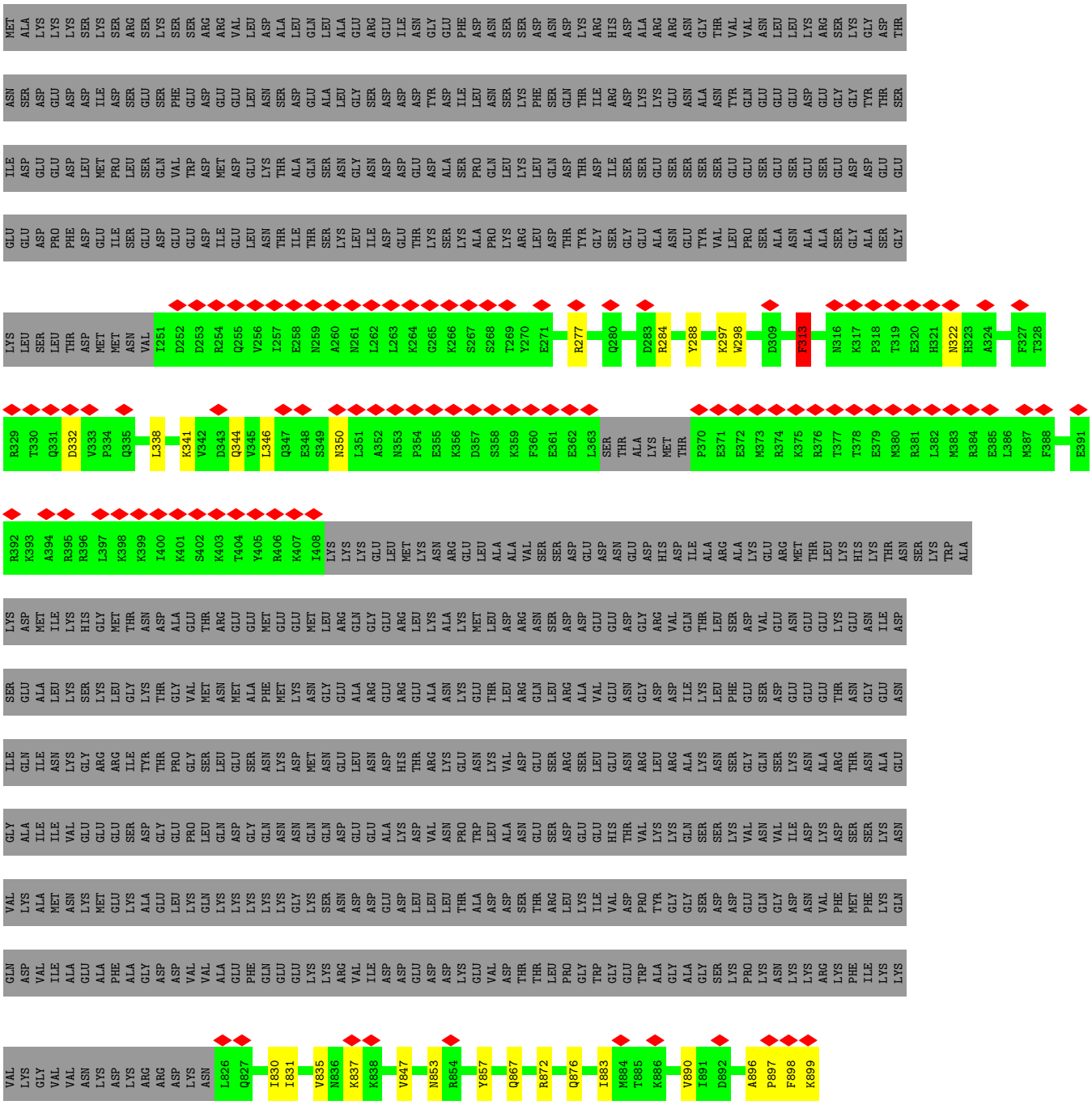
M813 E814 N815 E816 I819 T820 G821 S822 L832 K833 T834 L835 S836 K837 F838 I841 V844 Y845 S846 A847 T848 E849 L850 H851 D852 H853 L854 L857 L858 R861 N862 T863 D864 V865 Q866 K867 L868 A869 L870 D871 A872 L873 L874 A875 Y876 K877 N878 P879 T880 L881 N882 K883 Y884 R885


D886 N887 L888 K889 D893 L896 D899 E900 I901 T902 T903 F904 L905 T906 E907 N908 G909 S910 Q911 S912 I913 K914 A915 E916 D917 E918 K919 V920 V921 M922 P923 Y924 I928 R932 A933 Q934 V935 P936 P937 T938 S939 G940 Q941 K942 R943 S944 R945 K946 I947 A948 V949 I950 S951 V952 L953
P954 N955 I961 F964 R971 Y974 N975 Y976 F977 F978 G979 S986 A989 T990 T993 I994 R995 T998 V1001 N1002 I1003 V1004 N1005 S1006 T1007 H1018 T1019 V1022 P1025 L1026 S1029 I1030 A1031 M1032 A1033 Y1034 Y1035 V1036 L1037 E1040 S1041 T1042 E1043 E1044 V1045 H1046
L1047 R1048 K1049 M1050 A1051 R1055 Q1056 Q1057 K1060 C1061 L1062 S1063 S1064 V1065 F1066 E1067 F1068 F1073 D1074 W1075 S1076 T1077 S1078 Y1083 A1084 V1085 V1086 V1087 K1088 P1089 R1090 I1091 S1092 H1093 F1094 S1095 D1096 E1097 N1098 L1099 Q1100 S1103 S1104 L1105 L1108 F1109 L1110 Y1111 W1112 A1113 H1114 N1115 P1116 S1117
L1118 Y1119 Q1120 F1121 L1122 Y1123 Y1124 F1127 A1128 T1129 A1130 T1131 A1132 L1133 M1134 D1135 T1136 I1137 S1138 N1139 Q1140 H1141 V1142 K1143 E1144 A1145 V1146 I1147 G1148 P1149 I1150 I1151 E1152 A1153 A1154 D1155 S1156 I1157 I1158 R1159 N1160 P1161 V1162 N1163 D1164 D1165 H1166 Y1167 V1168 D1169 L1170 V1171 T1172 L1173 I1174 C1175 T1176 S1177 C1178
L1179 K1180 I1181 L1182 P1183 S1184 L1185 Y1186 V1187 K1188 L1189 S1190 D1191 S1192 N1193 S1194 I1195 S1196 T1197 F1198 L1199 N1200 L1201 L1202 V1203 S1204 I1205 T1206 E1207 M1208 G1209 F1210 I1211 Q1212 D1213 D1214 H1215 V1216 R1217 S1218 R1219 L1220 I1221 S1222 S1223 L1224 I1225 S1226 L1227 L1228 K1229 G1230 K1231 L1232 K1233 K1234 L1235 Q1236 E1237 N1238
D1239 T1240 Q1241 K1242 I1243 L1244 K1245 I1246 L1247 K1248 L1249 I1250 V1251 F1252 N1253 Y1254 N1255 C1256 S1257 W1258 S1259 D1260 I1261 E1262 E1263 L1264 Y1265 T1266 T1267 I1268 S1269 S1270 L1271 F1272 K1273 T1274 F1275 D1276 E1277 R1278 N1279 L1280 R1281 V1282 S1283 L1284 T1285 E1286 L1287 F1288 I1289 E1290 L1291 G1292 R1293 K1294 E1297 L1298 E1299
S1300 I1301 S1302 K1303 L1304 V1305 A1306 D1307 L1308 N1309 S1310 Y1311 S1312 S1313 S1314 R1315 M1316 H1317 E1318 Y1319 D1320 F1321 P1322 ARG ILE LEU SER THR PHE LYS GLY LEU ILE GLU ASP GLY TYR LYS SER TYR SER GLU LEU GLU TRP LEU PRO LEU LEU PHE THR PHE LEU HIS PHE ILE ASN ASN LYS GLU
GLU LEU ALA LEU ARG THR ASN ALA SER HIS ALA ILE MET LYS PHE ILE D1376 F1377 I1378 N1379 E1380 K1381 P1382 N1383 L1384 N1385 E1386 A1387 S1388 K1389 S1390 I1391 S1392 M1393 L1394 K1395 D1396 I1397 L1398 L1399 P1400 N1401 I1402 R1403 I1404 G1405 L1406 R1407 D1408 S1409 L1410 E1411 E1412 V1413 GLN SER GLU TYR VAL SER
V1420 L1421 S1422 Y1423 M1424 V1425 K1426 N1427 T1428 K1429 Y1430 F1431 T1432 D1433 D1436 I1439 L1440 L1441 Y1442 N1443 G1444 D1445 E1446 E1447 A1448 D1449 PHE PHE THR ASN VAL ASN HIS ILE GLN LEU HIS R1461 R1462 Q1463 R1464 A1465 I1466 K1467 E1471 H1472 A1473 H1474 Q1475 L1476 K1477 D1478 N1479 S1480 I1481 S1482 H1483
Y1484 L1485 I1486 P1487 M1488 I1489 E1490 H1491 Y1492 Y1493 F1494 S1495 D1496 D1497 E1498 R1499 Y1500 R1501 N1502 I1503 G1504 N1505 E1506 T1507 Q1508 I1509 A1510 I1511 G1512 G1513 Q1516 H1517 M1518 S1519 W1520 N1521 Q1522 Y1523 K1524 A1525 L1526 L1527 R1528 R1529 Y1530 I1531 S1532 M1533 L1534 K1535 T1536 K1537 P1538 N1539 Q1540 M1541 K1542 Q1543 A1544
V1545 Q1546 L1547 I1548 VAL GLN LEU SER VAL PRO LEU ARG GLU T1558 L1559 R1560 I1561 V1562 R1563 D1564 G1565 A1566 E1567 S1568 K1569 L1570 S1573 K1574 F1575 P1576 S1577 ASN LEU ASP GLU PRO SER ASN PHE ILE LYS GLN GLU LEU TYR PRO THR LEU SER LYS ILE LEU GLY THR ARG ASP ASP GLU THR
ILE ILE E1608 R1609 M1610 P1611 I1612 A1613 E1614 V1617 N1618 I1619 V1620 L1621 T1624 N1625 D1626 D1627 I1628 T1629 N1630 F1631 L1632 P1633 S1634 I1635 L1636 C1640 Q1641 V1642 L1643 R1644 S1645 K1646 S1647 E1648 E1649 L1650 R1651 D1652 A1653 V1654 R1655 V1656 I1663 I1664 L1665 E1668 Y1669 L1670 V1671 F1672 V1673 I1674 K1675
E1676 A1679 T1680 L1681 K1682 R1683 G1684 S1685 Q1686 I1687 H1688 V1689 L1690 S1691 Y1692 H1695 Y1696 M1701 H1702 G1703 V1704 L1705 K1706 H1707 S1708 D1709 L1710 D1711 T1712 S1713 M1716 K1719 I1720 I1721 M1722 E1723 N1724 I1725 F1726 G1727 F1728 A1729 G1730 E1731 E1732 K1733 D1734 S1735 E1736 N1737 Y1738 H1739 T1740 K1741 V1742



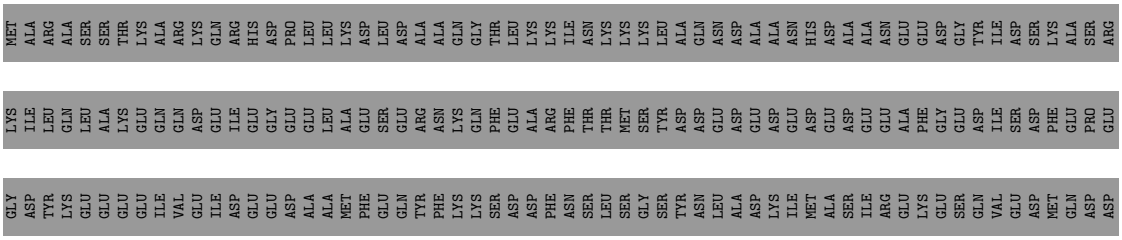
- Molecule 61: U3 small nucleolar RNA-associated protein 14

Chain RQ:



- Molecule 62: Essential nuclear protein 1

Chain RS:



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 V332 R333 E334 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 63: Pno1

Chain RT: 44% 45% 8% 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 S96 R97 K98 I99 M100 V101 P102 P103 H104 R105 M106 T107 P108 L109 R110 N111 S112 W113 T114 K115 I116 Y117 P118 P119 L120

V121 E122 H123 L124 K125 L126 Q127 V128 R129 M130 N131 L132 K133 T134 K135 S136 V137 E138 L139 R140 T141 N142 P143 K144 PHE THR THR ASP PRO G150 A151 L152 Q153 K154 G155 A156 D157 F158 I159 K160 A161 F162 T163 L164 G165 F166 D167 L168 D169 D170 S171 I172 A173 L174 L175 R176 L177 D178 D179 L180

Y181 I182 E183 T184 F185 E186 V187 K188 D189 VAL LYS THR LEU T194 G195 D196 H197 L198 S199 R200 A201 I202 G203 R204 I205 A206 G207 K208 D209 G210 K211 T212 K213 F214 A215 I216 E217 N218 A219 T220 R221 T222 R223 I224 V225 L226 A227 D228 S229 K230 I231 H232 I233 L234 G235 T238 H239 I240 R241

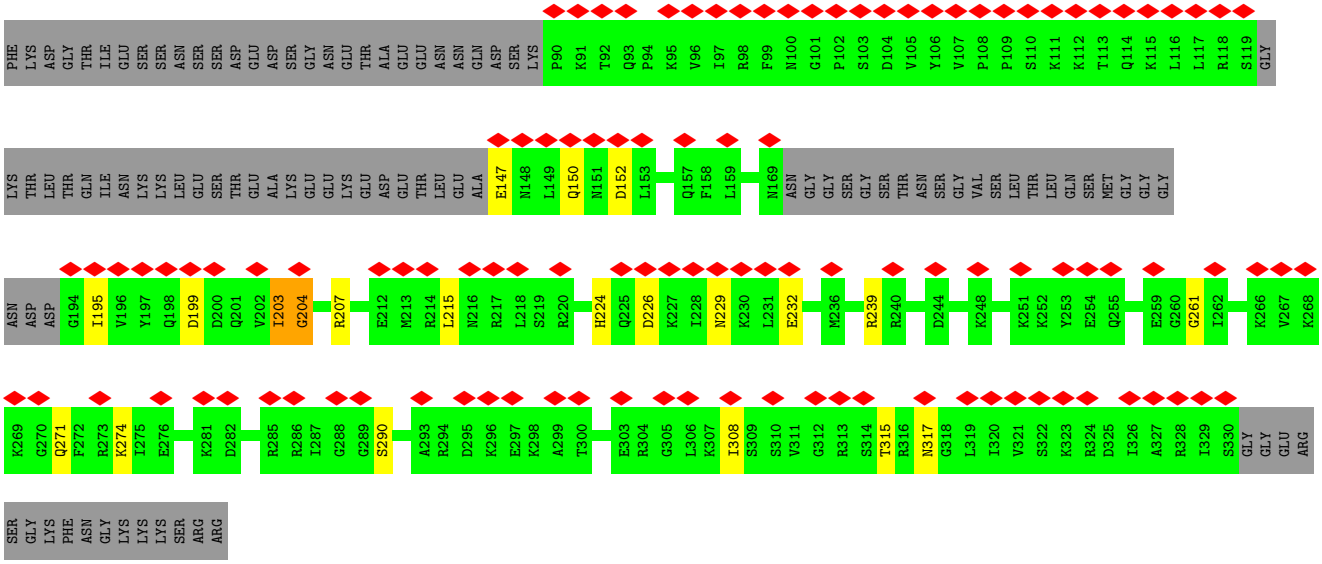
M242 A243 R244 E245 S246 V247 V248 S249 L250 I251 L252 G253 S254 K258 V259 Y260 G261 N262 L263 R264 T265 V266 A267 S268 R269 L270 K271 E272 R273 Y274 GLY ARG ARG ILE PRO GLY LEU ILE ASN PRO TRP LYS ARG ARG TRP LYS LYS ASN PHE ILE ALA VAL SER ALA ALA ASN ARG PHE LYS

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

- Molecule 64: Protein FAF1

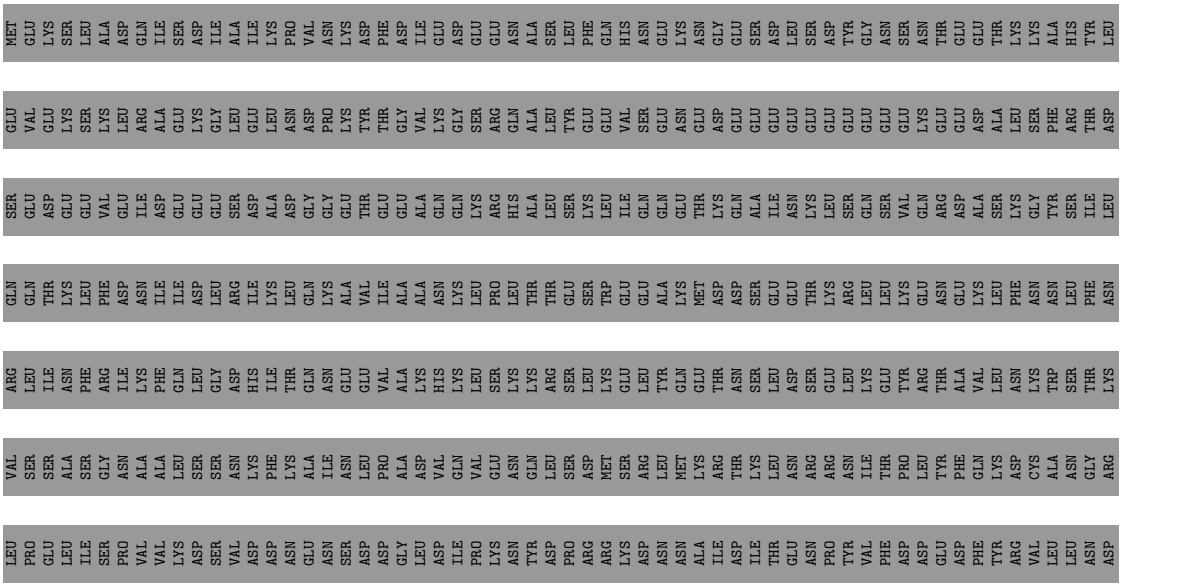
Chain RV: 32% 49% 5% • 45%

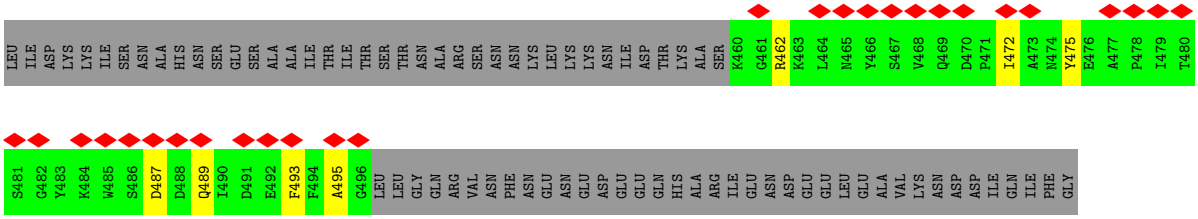
MET THR LEU ASP ASP ASP ASP TYR ILE LYS GLN MET GLU LEU GLN ARG LYS ALA PHE GLU SER GLN PHE GLY SER LEU GLU SER MET GLY PHE GLU ASP LYS THR LYS ASN ILE ARG THR GLU VAL ASP THR ARG ASP SER SER GLY ASP GLU ILE ASP ASN SER ASP SER GLY ASP ASP ASN ARG PHE LYS



- Molecule 65: Protein BFR2

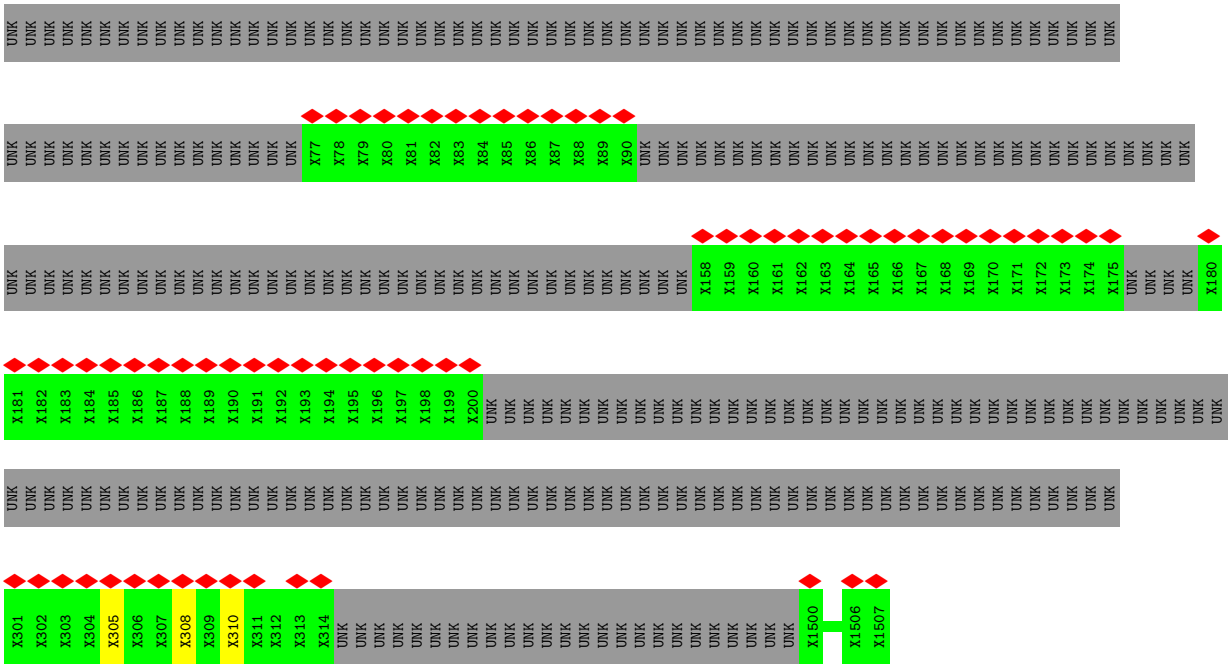
Chain RY:





- Molecule 66: Unassigned helices

Chain X1:


UNK
X77
X78
X79
X80
X81
X82
X83
X84
X85
X86
X87
X88
X89
X90
X158
X159
X160
X161
X162
X163
X164
X165
X166
X167
X168
X169
X170
X171
X172
X173
X174
X175
X180
X181
X182
X183
X184
X185
X186
X187
X188
X189
X190
X191
X192
X193
X194
X195
X196
X197
X198
X199
X200
X301
X302
X303
X304
X305
X306
X307
X308
X309
X310
X311
X312
X313
X314
X1500
X1506
X1507

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	17924	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	0.126	Depositor
Minimum map value	-0.059	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.03	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: MG, ZN, GTP

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	0.45	0/4141	0.48	0/6433
2	5A	0.44	0/8952	0.47	1/13931 (0.0%)
3	SA	0.35	0/31535	0.47	5/49095 (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	0.46	0/879	0.79	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	0.66	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	0.23	0/3328	0.62	0/4565
28	A9	0.28	0/951	0.60	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	0.58	0/6780	0.69	0/9175
33	B2	0.39	0/6853	0.68	2/9256 (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	0.53	0/6948	0.64	2/9391 (0.0%)
37	B6	0.37	0/2849	0.60	0/3853
38	5B	0.31	0/499	0.62	0/659
39	5C	0.55	0/4321	0.66	2/5832 (0.0%)
40	5D	0.47	0/1417	0.73	0/1885
41	5E	0.44	0/1665	0.66	2/2233 (0.1%)
42	5F	0.64	0/1559	0.72	1/2097 (0.0%)
43	5G	0.52	0/2337	0.67	2/3148 (0.1%)
44	5H	0.47	0/601	0.59	0/789
45	5I	0.56	0/3844	0.68	0/5174
46	5J	0.36	0/1302	0.58	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	RC	0.40	0/2245	0.60	0/3021
51	RD	0.26	0/2453	0.67	2/3308 (0.1%)
52	RE	0.33	0/8924	0.64	4/12070 (0.0%)
53	RF	0.28	0/2004	0.66	1/2697 (0.0%)
54	RG	0.32	0/1727	0.70	0/2329
54	RH	0.37	0/1828	0.59	0/2470
55	RJ	0.44	0/6514	0.61	0/8768
56	RK	0.39	0/2832	0.64	0/3825
57	RL	0.21	0/4549	0.51	1/6241 (0.0%)
57	RM	0.15	0/3765	0.44	1/5218 (0.0%)
58	RN	0.30	0/4591	0.63	1/6187 (0.0%)
59	RO	0.32	0/3849	0.63	0/5261
60	RP	0.21	0/12225	0.54	4/16812 (0.0%)
61	RQ	0.41	0/1678	0.63	1/2282 (0.0%)
62	RS	0.30	0/2104	0.70	0/2854
63	RT	0.38	0/1379	0.68	0/1853
64	RV	0.43	0/1456	0.60	1/1937 (0.1%)
65	RY	0.23	0/307	0.53	0/415
All	All	0.40	1/233403 (0.0%)	0.60	56/325072 (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	4
31	AG	0	2
32	B1	0	3
33	B2	0	9
34	B3	0	11
36	BE	0	1
39	5C	0	2
40	5D	0	1
41	5E	0	1
42	5F	0	1
43	5G	0	1
45	5I	0	2
48	RA	0	2
49	RB	0	1
52	RE	0	1
53	RF	0	1
55	RJ	0	2
56	RK	0	1
57	RL	0	1
57	RM	0	1
58	RN	0	1
59	RO	0	1
60	RP	0	3
61	RQ	0	1
64	RV	0	2
All	All	0	78

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 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
51	RD	1223	PRO	N-CA-CB	8.04	111.69	103.25
52	RE	1105	PRO	O-C-N	-7.87	112.02	122.64
51	RD	1205	PRO	N-CA-CB	7.68	110.60	103.15
33	B2	267	ASP	CA-C-N	6.86	134.65	121.54
33	B2	267	ASP	C-N-CA	6.86	134.65	121.54

There are no chirality outliers.

5 of 78 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	21	0
2	5A	8009	0	4030	52	0
3	SA	28210	0	14226	240	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	13	0
13	SP	868	0	894	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	SR	973	0	1029	14	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	34	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	56	0
27	A8	3307	0	2316	39	0
28	A9	939	0	898	19	0
29	AE	9955	0	7968	103	0
30	AF	3911	0	3906	71	0
31	AG	6570	0	6473	127	0
32	B1	6635	0	6525	103	0
33	B2	6723	0	6698	121	0
34	B3	5919	0	6007	127	0
35	B8	3764	0	3757	58	0
36	BE	6810	0	6787	86	0
37	B6	2800	0	2517	35	0
38	5B	495	0	561	13	0
39	5C	4237	0	4239	85	0
40	5D	1396	0	1407	20	0
41	5E	1647	0	1678	30	0
42	5F	1530	0	1572	30	0
43	5G	2296	0	2325	41	0
44	5H	596	0	661	8	0
45	5I	3765	0	3714	73	0
46	5J	1280	0	1331	23	0
47	5K	1403	0	1484	19	0
48	RA	2709	0	2622	66	0
49	RB	1108	0	1087	27	0
50	RC	2207	0	2229	29	0
51	RD	2412	0	2263	40	0
52	RE	8716	0	8828	240	0
53	RF	1963	0	1942	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	RG	1701	0	1767	40	0
54	RH	1799	0	1872	29	0
55	RJ	6379	0	6506	110	0
56	RK	2781	0	2878	51	0
57	RL	4539	0	2874	29	0
57	RM	3779	0	1650	8	0
58	RN	4529	0	4262	69	0
59	RO	3766	0	3269	47	0
60	RP	12171	0	7749	76	0
61	RQ	1651	0	1450	28	0
62	RS	2051	0	2096	53	0
63	RT	1357	0	1426	15	0
64	RV	1448	0	1435	16	0
65	RY	299	0	275	6	0
66	X1	375	0	92	4	0
67	5K	1	0	0	0	0
67	Sc	1	0	0	0	0
68	RJ	32	0	12	2	0
69	RJ	1	0	0	0	0
All	All	226161	0	194704	2951	0

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

The worst 5 of 2951 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)
52:RE:1203:ASN:HD22	52:RE:1219:ILE:CG2	1.50	1.22
52:RE:1102:LEU:HD23	52:RE:1180:ASN:O	1.40	1.20
52:RE:1216:LYS:NZ	52:RE:1236:THR:HG23	1.65	1.11
52:RE:518:PHE:CZ	52:RE:1075:LEU:HG	1.92	1.05
52:RE:1203:ASN:HD22	52:RE:1219:ILE:HG21	1.18	1.04

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	365/700 (52%)	104 (28%)	7 (1%)
3	SA	1303/1808 (72%)	494 (37%)	19 (1%)
All	All	1837/2841 (64%)	642 (34%)	28 (1%)

5 of 642 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 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	372	G
3	SA	1632	C
3	SA	538	A
3	SA	1197	C
3	SA	417	A

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

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

5.5 Carbohydrates (i)

There are no 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	$\#\|Z\| > 2$
68	GTP	RJ	1201	69	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
68	GTP	RJ	1201	69	-	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})
68	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
68	RJ	1201	GTP	O4'-C4'-C5'-O5'
68	RJ	1201	GTP	C3'-C4'-C5'-O5'
68	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

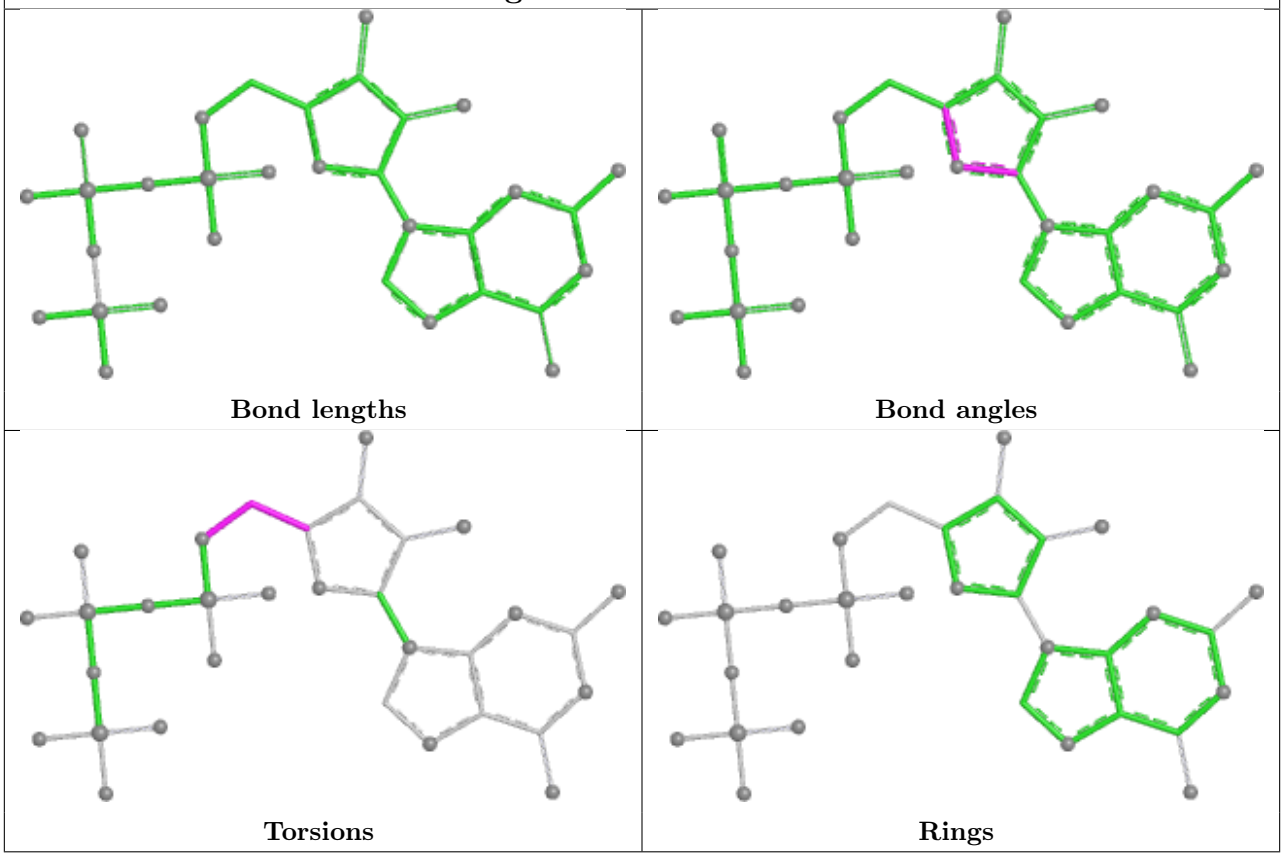
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
68	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.

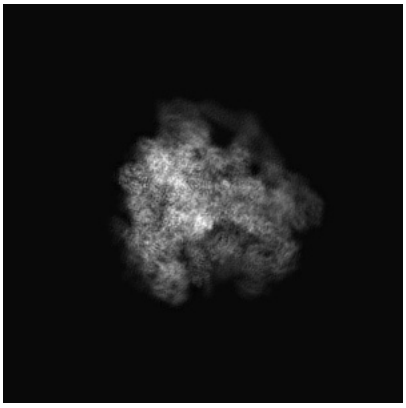
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-0950. These allow visual inspection of the internal detail of the map and identification of artifacts.

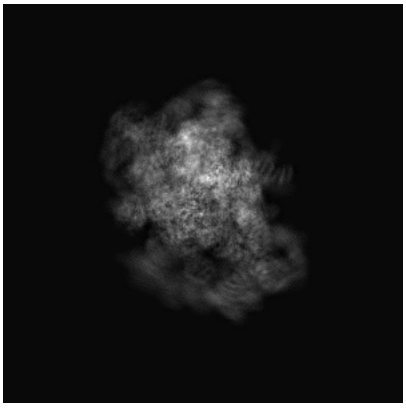
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

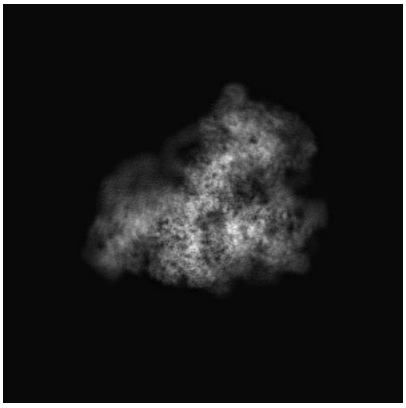
6.1.1 Primary map



X



Y

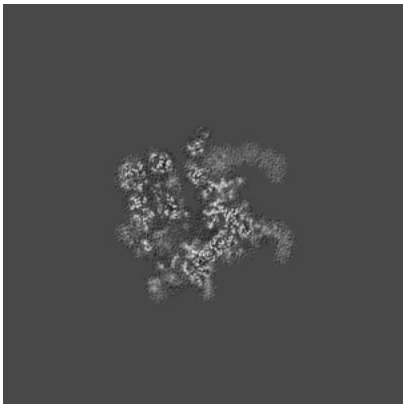


Z

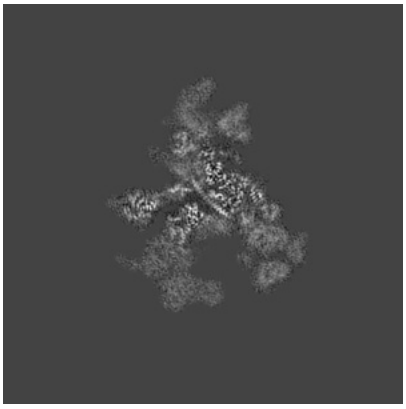
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

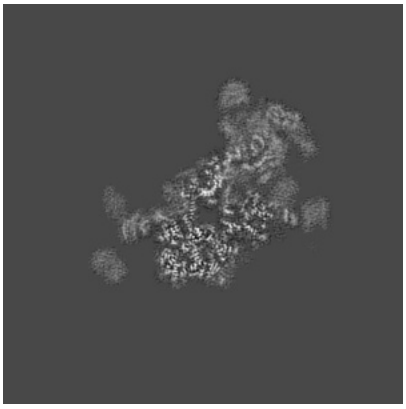
6.2.1 Primary map



X Index: 224



Y Index: 224

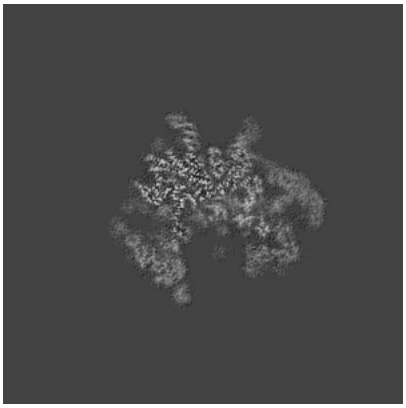


Z Index: 224

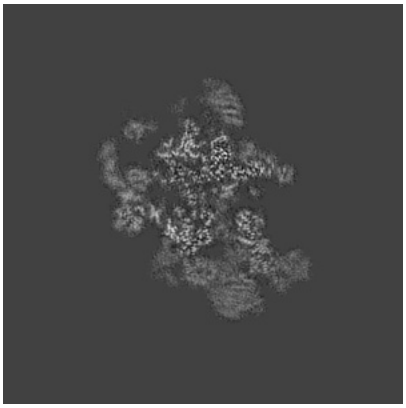
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

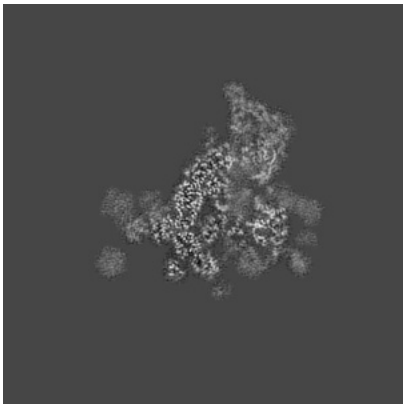
6.3.1 Primary map



X Index: 253



Y Index: 197

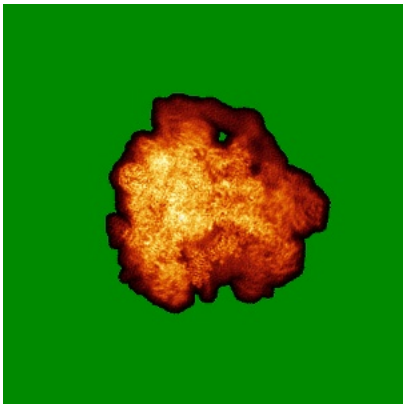


Z Index: 208

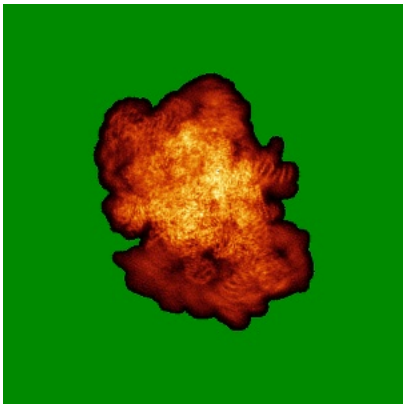
The images above show the largest variance slices of the map in three orthogonal directions.

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

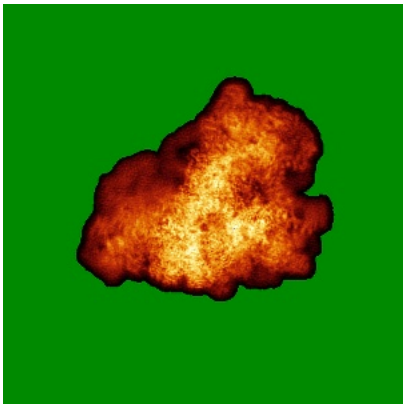
6.4.1 Primary map



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

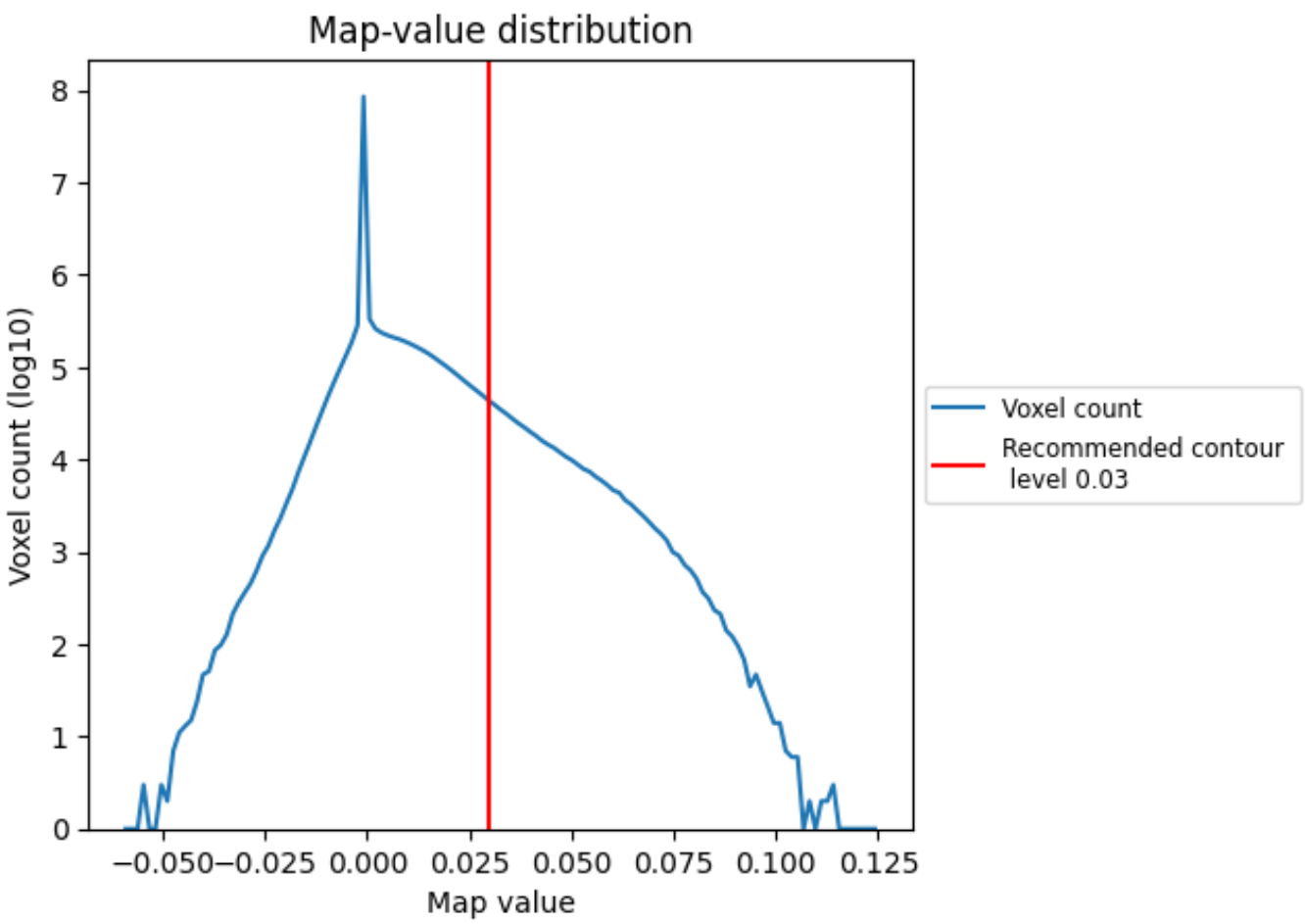
6.6 Mask visualisation (i)

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

7 Map analysis (i)

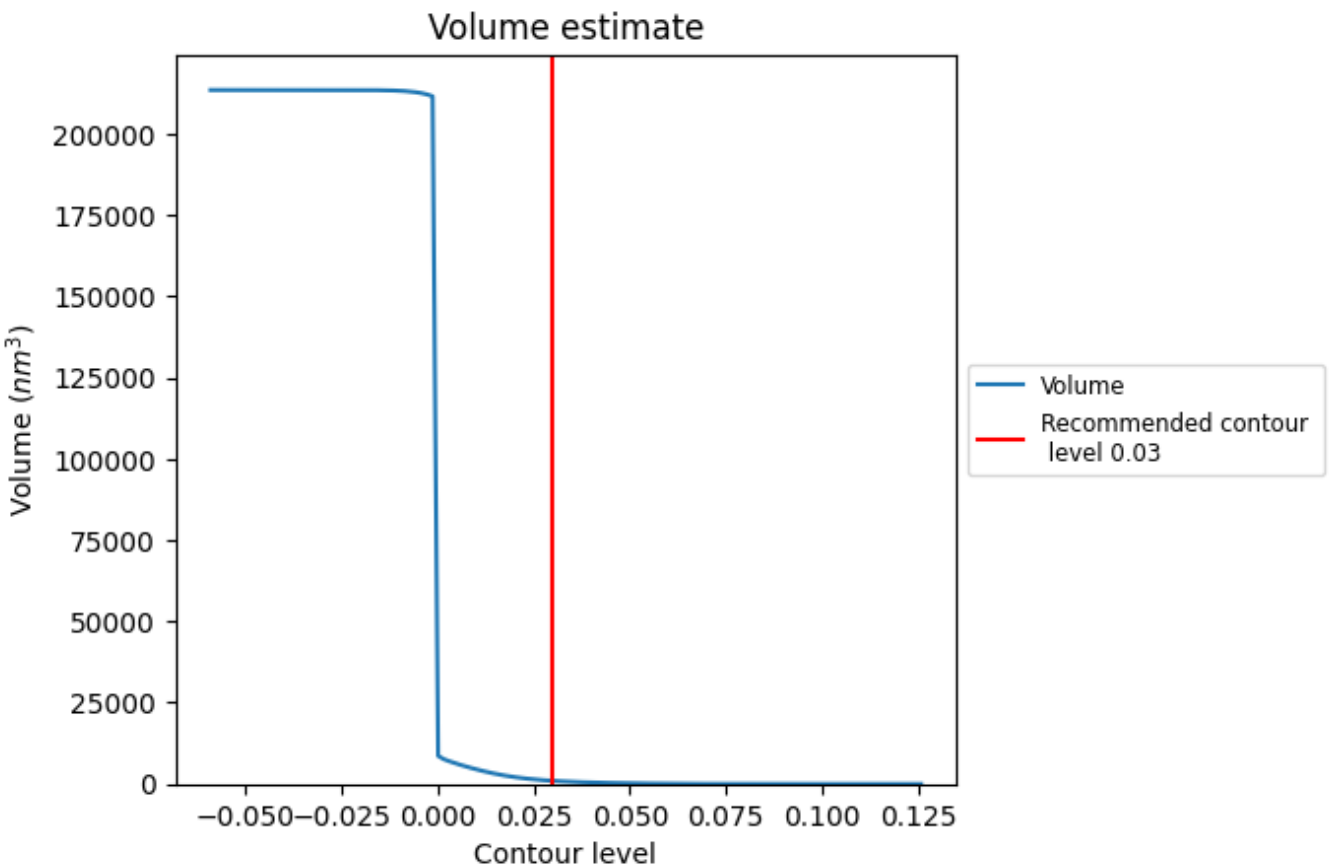
This section contains the results of statistical analysis of the map.

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.

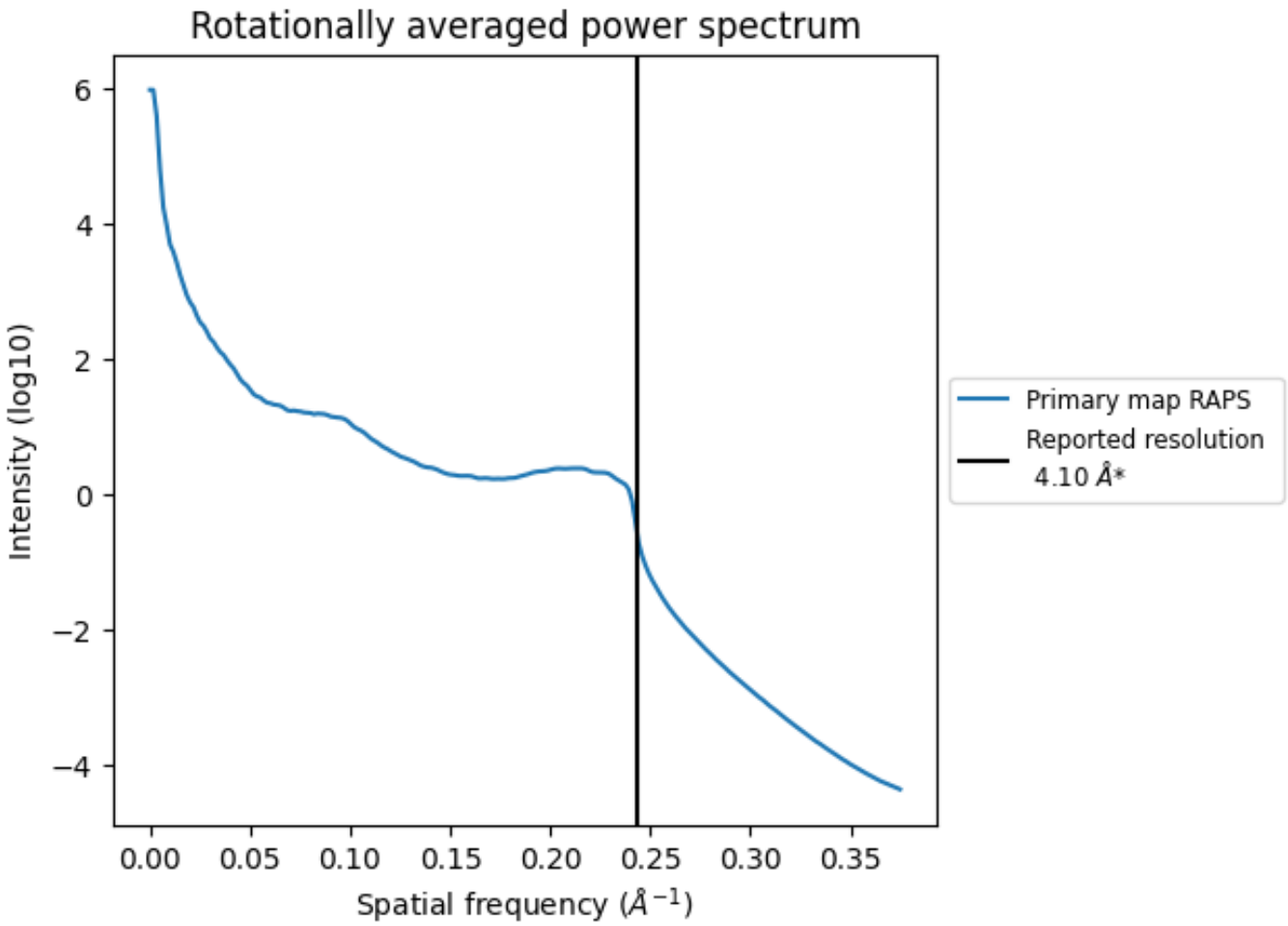
7.2 Volume estimate (i)



The volume at the recommended contour level is 963 nm^3; this corresponds to an approximate mass of 870 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 0.244 Å^{-1}

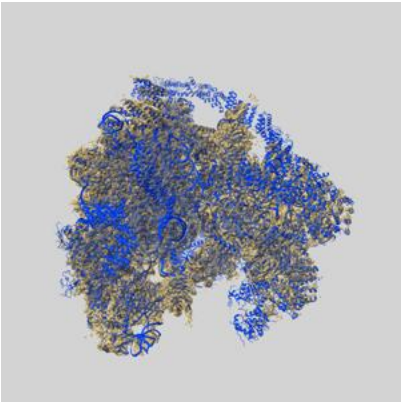
8 Fourier-Shell correlation (i)

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

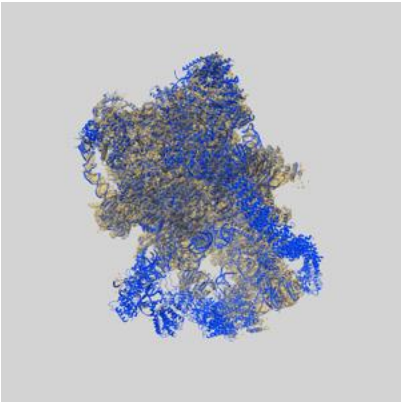
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-0950 and PDB model 6LQQ. Per-residue inclusion information can be found in section 3 on page 17.

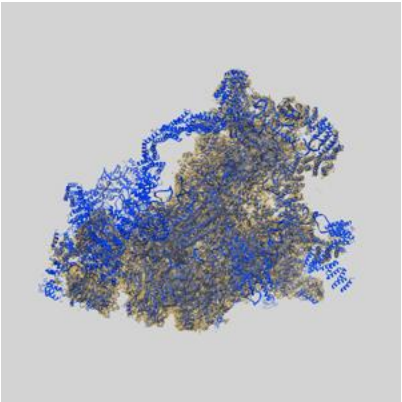
9.1 Map-model overlay (i)



X



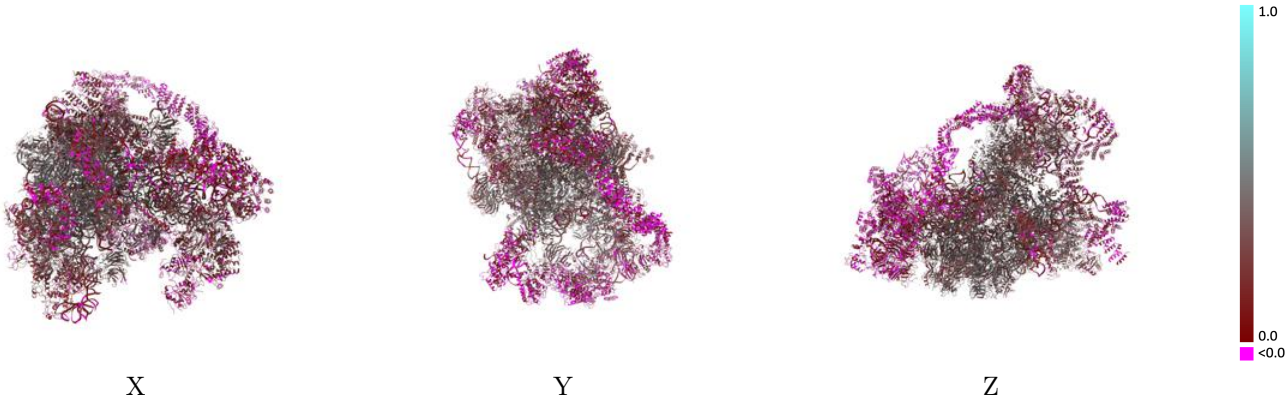
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)

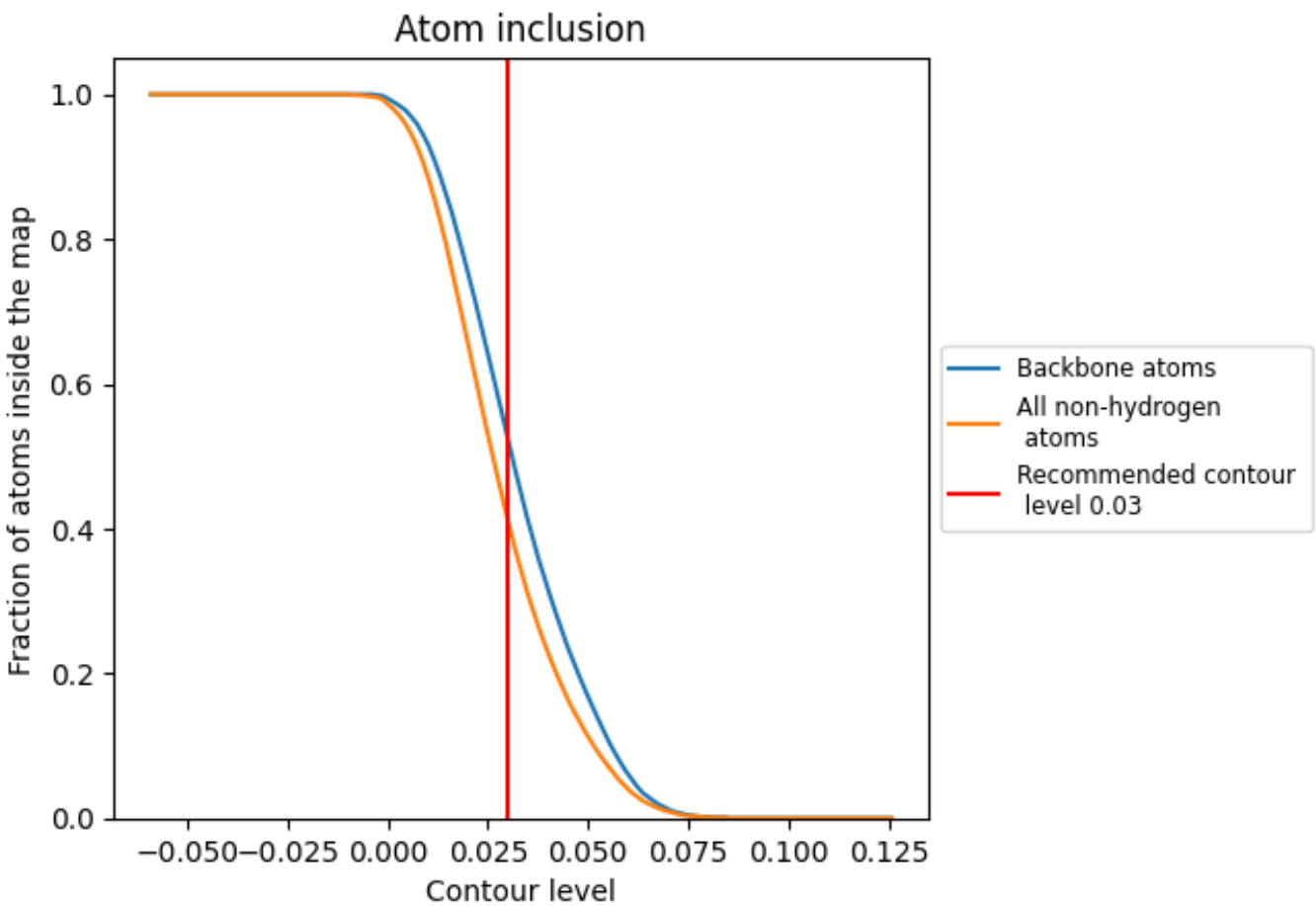


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)

This section was not generated.

9.4 Atom inclusion (i)



At the recommended contour level, 52% of all backbone atoms, 41% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4110	0.2550
3A	0.6470	0.2880
3B	0.6400	0.3850
3C	0.1330	0.1640
3D	0.5950	0.3190
3E	0.4170	0.2480
3F	0.5760	0.3330
3G	0.5180	0.2880
3H	0.6120	0.3680
5A	0.2360	0.2060
5B	0.0290	0.1290
5C	0.5690	0.3810
5D	0.2920	0.2640
5E	0.5310	0.3520
5F	0.6520	0.3990
5G	0.5730	0.3840
5H	0.6500	0.3910
5I	0.6900	0.4090
5J	0.3860	0.2600
5K	0.6320	0.4030
A4	0.2650	0.1750
A5	0.4090	0.2640
A8	0.0170	0.0350
A9	0.0500	0.0530
AE	0.2040	0.1300
AF	0.1830	0.1930
AG	0.2310	0.1370
B1	0.6490	0.4020
B2	0.5870	0.3260
B3	0.4860	0.2820
B6	0.5520	0.2760
B8	0.5770	0.3310
BE	0.6500	0.3950
RA	0.4000	0.2630
RB	0.4710	0.2910

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Chain	Atom inclusion	Q-score
RC	0.3940	0.3180
RD	0.0020	0.0240
RE	0.3440	0.2480
RF	0.2870	0.2400
RG	0.0150	0.1160
RH	0.0410	0.1740
RJ	0.5980	0.3620
RK	0.6270	0.3690
RL	0.4210	0.2740
RM	0.1620	0.1440
RN	0.0760	0.1140
RO	0.0000	0.0830
RP	0.2500	0.1580
RQ	0.4550	0.3130
RS	0.0020	0.0210
RT	0.2210	0.3060
RV	0.3570	0.3440
RY	0.3040	0.2060
SA	0.5390	0.2470
SC	0.5380	0.3630
SF	0.4940	0.2910
SG	0.6060	0.3600
SH	0.3660	0.2430
SI	0.4620	0.2910
SJ	0.3960	0.2340
SK	0.6400	0.3810
SM	0.2530	0.1500
SO	0.5920	0.3670
SP	0.5510	0.3690
SR	0.6340	0.3890
SX	0.5970	0.3850
SY	0.6040	0.4080
SZ	0.5550	0.3210
Sc	0.5900	0.3860
Sd	0.5950	0.3980
X1	0.0830	0.1700