wwPDB EM Validation Summary Report ⓘ

Dec 11, 2022 – 05:28 pm GMT

PDB ID	:	5AJ0
EMDB ID	:	EMD-2875
Title	:	Cryo electron microscopy of actively translating human polysomes (POST state).
Authors	:	Behrmann, E.; Loerke, J.; Budkevich, T.V.; Yamamoto, K.; Schmidt, A.; Penczek, P.A.; Vos, M.R.; Burger, J.; Mielke, T.; Scheerer, P.; Spahn, C.M.T.
Deposited on	:	2015-02-19
Resolution	:	3.50 Å(reported)
Based on initial model	:	4UJE

The following versions of software and data (see references ⓘ) were used in the production of this report:

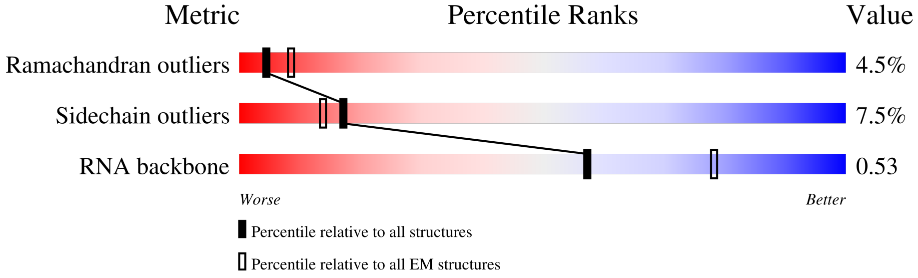
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance ⓘ

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

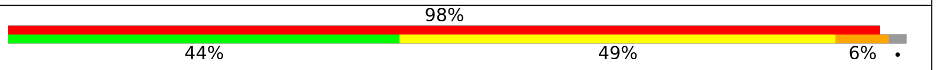
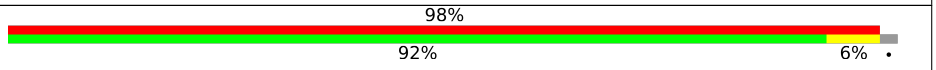
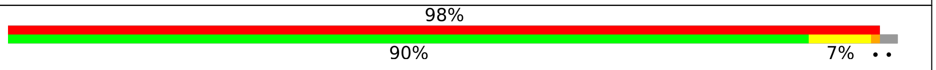
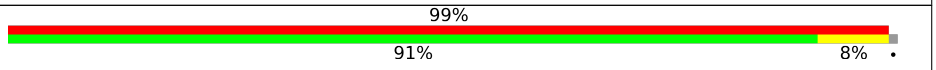
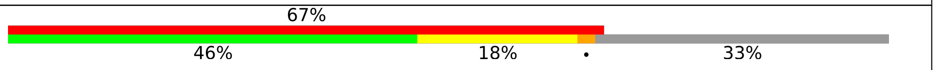
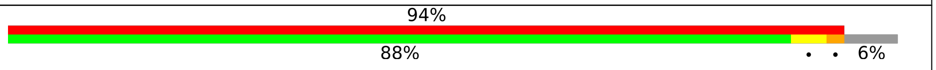
The reported resolution of this entry is 3.50 Å.

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



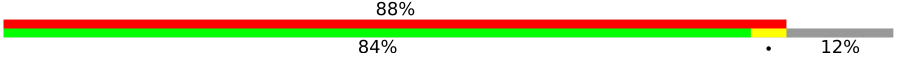
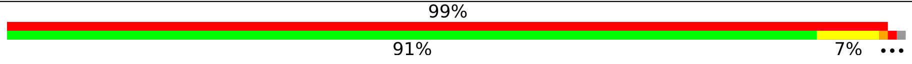
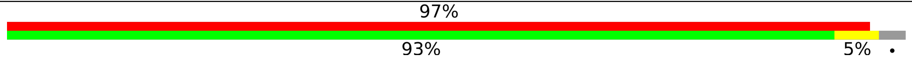
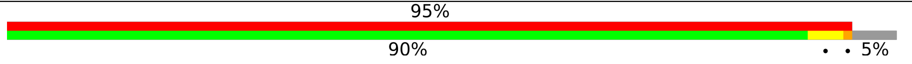
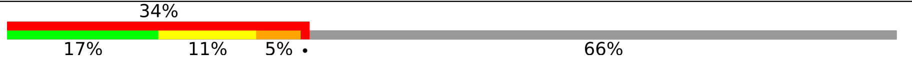
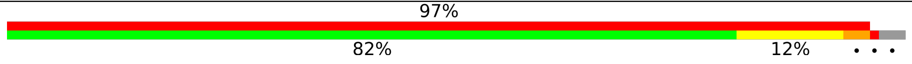
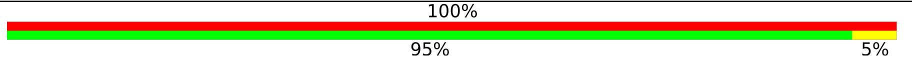
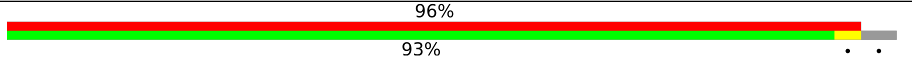
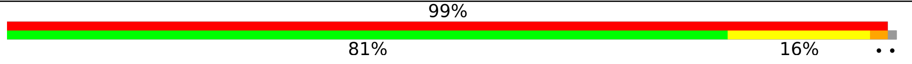
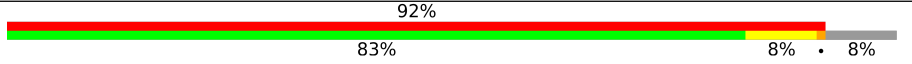
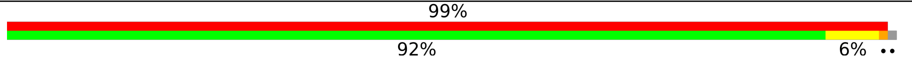
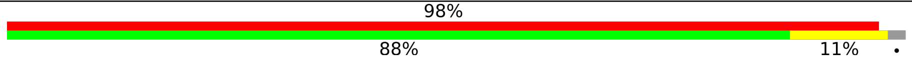
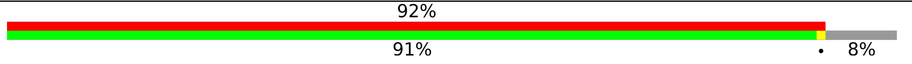
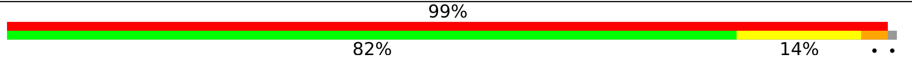
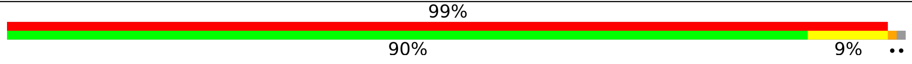
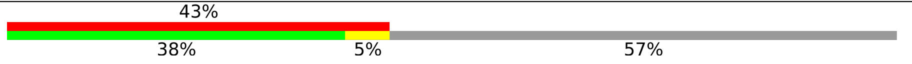
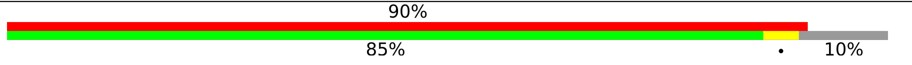
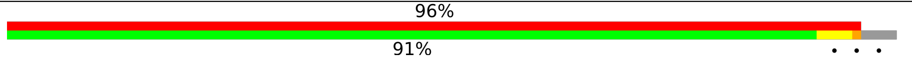
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A3	194	
2	A4	121	
3	AA	257	
4	AB	403	
5	AC	427	
6	AD	297	
7	AE	288	
8	AF	248	

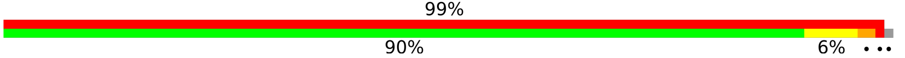
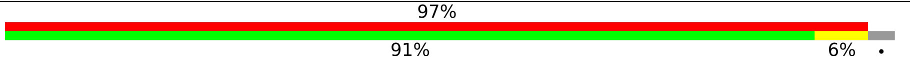
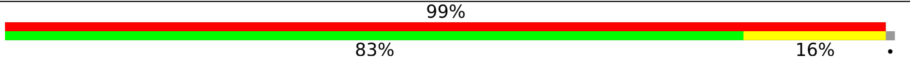
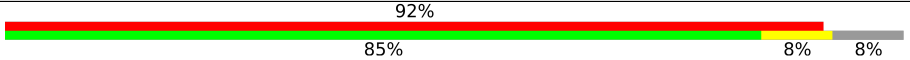
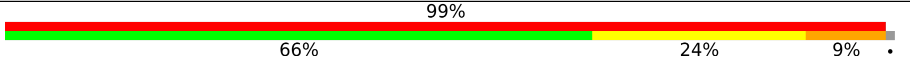
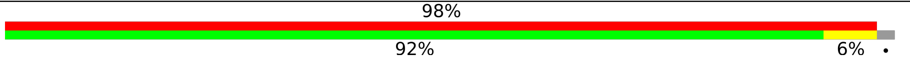
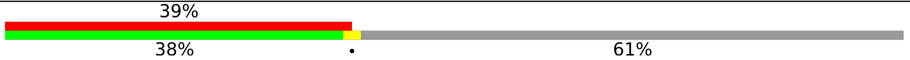
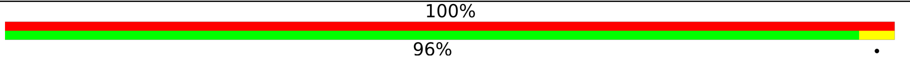
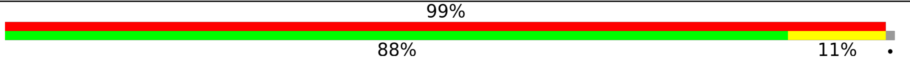
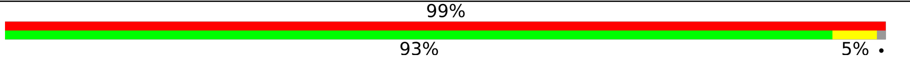
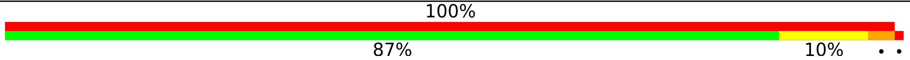
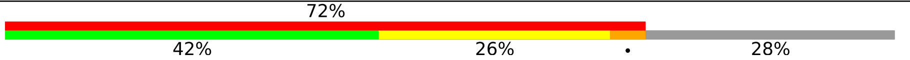
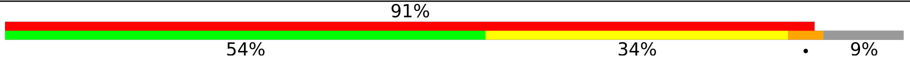
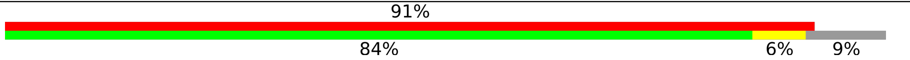
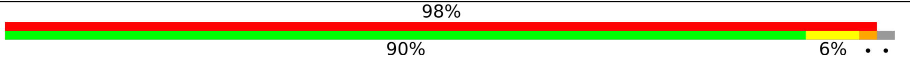
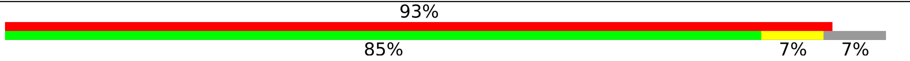
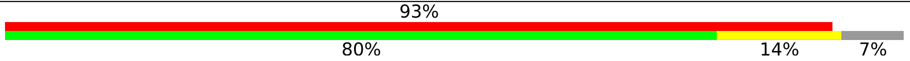
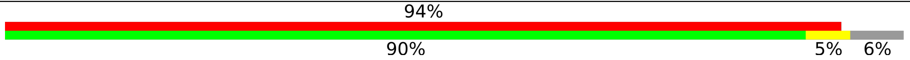
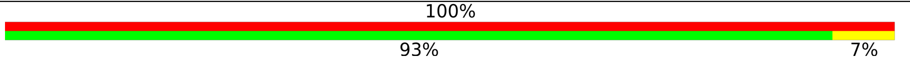
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	AG	266	
10	AH	192	
11	AI	214	
12	AJ	178	
13	AK	317	
14	AL	211	
15	AM	215	
16	AN	204	
17	AO	203	
18	AP	184	
19	AQ	188	
20	AR	196	
21	AS	176	
22	AT	160	
23	AU	128	
24	AV	140	
25	AW	157	
26	AX	156	
27	AY	145	
28	AZ	136	
29	Aa	148	
30	Ab	159	
31	Ac	115	
32	Ad	125	
33	Ae	135	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	Af	110	99% 90% 6% • ••
35	Ag	117	97% 91% 6% •
36	Ah	123	99% 83% 16% •
37	Ai	105	92% 85% 8% 8%
38	Aj	97	87% 72% 12% • 13%
39	Ak	70	99% 66% 24% 9% •
40	Al	51	98% 92% 6% •
41	Am	128	39% 38% • 61%
42	An	25	100% 96% •
43	Ao	106	99% 88% 11% •
44	Ap	92	99% 93% 5% •
45	Aq	165	84% 41% 30% 11% • 16%
46	At	137	89% 74% 15% 11%
47	Au	217	100% 87% 10% • •
48	A2	5029	72% 42% 26% • 28%
49	B1	1869	91% 54% 34% • 9%
50	BA	295	73% 66% 6% • 27%
51	BB	264	80% 68% 12% 20%
52	BC	293	76% 69% 7% 24%
53	BD	243	91% 84% 6% 9%
54	BE	263	98% 90% 6% • •
55	BF	204	93% 85% 7% 7%
56	BG	249	93% 80% 14% 7%
57	BH	194	94% 90% 5% 6%
58	BI	208	100% 93% 7%

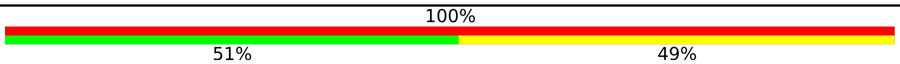
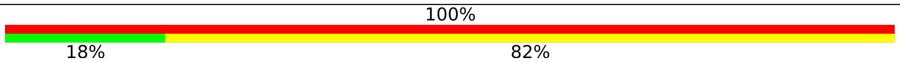
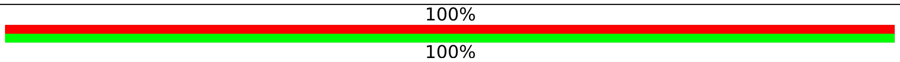
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	BJ	194	92% 81% 10% • 8%
60	BK	165	59% 54% • • 41%
61	BL	158	97% 89% 8% • •
62	BM	132	91% 87% • 9%
63	BN	151	99% 86% 12% ••
64	BO	151	90% 79% 10% • 10%
65	BP	145	83% 65% 12% • • 17%
66	BQ	146	95% 79% 14% •• 5%
67	BR	135	93% 74% 15% • 7%
68	BS	152	91% 77% 14% 9%
69	BT	145	99% 88% 10% •
70	BU	119	82% 75% 7% 18%
71	BV	83	98% 89% 8% •
72	BW	130	99% 92% 5% • •
73	BX	143	97% 86% 10% • •
74	BY	133	94% 90% • 6%
75	BZ	125	69% 52% 17% 31%
76	Ba	115	84% 76% 8% • 16%
77	Bb	84	95% 93% • 5%
78	Bc	69	90% 84% • • 10%
79	Bd	56	91% 71% 18% • 9%
80	Be	59	93% 80% 14% 7%
81	Bf	156	47% 46% • 53%
82	Bg	317	99% 96% • •
83	Bv	76	100% 46% 51% •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
83	Bw	76	
84	Bx	28	
85	By	24	

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 218559 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 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A3	157	3337	1489	587	1104	157	0	0

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A4	119	2541	1132	454	836	119	0	0

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AA	252	1930	1209	395	320	6	0	0

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AB	394	3178	2024	596	544	14	0	0

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AC	363	2888	1817	577	480	14	0	0

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AD	294	2392	1510	436	432	14	0	0

- Molecule 7 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AE	194	Total	C	N	O	S	0	0
			1571	1013	294	263	1		

- Molecule 8 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AF	234	Total	C	N	O	S	0	0
			1950	1252	376	313	9		

- Molecule 9 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AG	234	Total	C	N	O	S	0	0
			1880	1197	362	317	4		

- Molecule 10 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AH	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 11 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AI	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AJ	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 13 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AK	109	Total	C	N	O	S	0	0
			872	554	159	151	8		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL	205	Total	C	N	O	S	0	0
			1657	1036	344	273	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	195	Total	C	N	O	S	0	0
			1606	1034	315	252	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AR	181	Total	C	N	O	S	0	0
			1517	938	329	241	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	AS	175	1449	921	283	234	11	0	0

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	AT	157	1284	815	250	214	5	0	0

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	AU	99	808	518	141	147	2	0	0

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	AV	129	969	613	182	169	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	AW	121	989	617	202	167	3	0	0

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	AX	117	958	612	180	165	1	0	0

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	AY	127	1064	668	216	177	3	0	0

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AZ	134	Total 1103	C 712	N 207	O 181	S 3	0	0

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Aa	147	Total 1162	C 736	N 237	O 186	S 3	0	0

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ab	68	Total 559	C 344	N 122	O 90	S 3	0	0

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ac	103	Total 801	C 508	N 141	O 145	S 7	0	0

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ad	106	Total 879	C 555	N 170	O 152	S 2	0	0

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ae	129	Total 1064	C 673	N 220	O 166	S 5	0	0

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Af	109	Total 876	C 555	N 174	O 144	S 3	0	0

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Ag	114	906	566	187	147	6	0	0

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Ah	122	1015	641	205	168	1	0	0

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	Ai	97	794	497	168	124	5	0	0

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Aj	84	689	423	152	109	5	0	0

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Ak	69	569	366	103	99	1	0	0

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Al	50	444	281	98	64	1	0	0

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	Am	50	411	254	87	64	6	0	0

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	An	25	Total 240	C 145	N 64	O 28	S 3	0	0

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ao	105	Total 863	C 542	N 175	O 140	S 6	0	0

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ap	91	Total 708	C 445	N 136	O 120	S 7	0	0

- Molecule 45 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Aq	138	Total 1046	C 654	N 196	O 193	S 3	0	0

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	At	122	Total 980	C 607	N 204	O 165	S 4	0	0

- Molecule 47 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Au	217	Total 1744	C 1114	N 314	O 307	S 9	0	0

- Molecule 48 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	A2	3612	Total 77427	C 34482	N 14158	O 25175	P 3612	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A2	245	C	-	insertion	GB 337381
A2	246	C	-	insertion	GB 337381
A2	247	C	-	insertion	GB 337381
A2	4684	G	-	insertion	GB 337381

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	B1	1708	36456	16274	6546	11928	1708	0	0

- Molecule 50 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	BA	215	1704	1083	298	315	8	0	0

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	BB	212	1722	1093	308	307	14	0	0

- Molecule 52 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	BC	222	1724	1114	296	304	10	0	0

- Molecule 53 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	BD	220	1709	1090	308	304	7	0	0

- Molecule 54 is a protein called 40S ribosomal protein S4, Y isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	BE	257	2031	1298	381	344	8	0	0

- Molecule 55 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BF	190	Total	C	N	O	S	0	0
			1502	939	285	271	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BG	232	Total	C	N	O	S	0	0
			1884	1176	379	322	7		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BH	183	Total	C	N	O	S	0	0
			1479	941	272	265	1		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BI	207	Total	C	N	O	S	0	0
			1696	1064	334	293	5		

- Molecule 59 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BJ	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BL	153	Total	C	N	O	S	0	0
			1258	804	235	213	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	BM	120	931	584	164	174	9	0	0

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	BN	149	1202	770	228	203	1	0	0

- Molecule 64 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	BO	136	1016	621	199	190	6	0	0

- Molecule 65 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	BP	120	999	636	188	168	7	0	0

- Molecule 66 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	BQ	139	1109	704	210	192	3	0	0

- Molecule 67 is a protein called 40S ribosomal protein S17-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	BR	125	1011	634	187	186	4	0	0

- Molecule 68 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	BS	139	1154	725	233	195	1	0	0

- Molecule 69 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	BT	143	1112	697	214	198	3	0	0

- Molecule 70 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	BU	97	769	483	144	138	4	0	0

- Molecule 71 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	BV	81	617	380	114	118	5	0	0

- Molecule 72 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	BW	129	1034	659	193	176	6	0	0

- Molecule 73 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	BX	139	1080	682	214	181	3	0	0

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	BY	125	1015	642	199	169	5	0	0

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	BZ	86	688	442	129	116	1	0	0

- Molecule 76 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	Ba	97	774	481	160	128	5	0	0

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	Bb	80	625	391	116	111	7	0	0

- Molecule 78 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	Bc	62	488	297	97	92	2	0	0

- Molecule 79 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	Bd	51	427	269	87	66	5	0	0

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	Be	55	437	272	96	68	1	0	0

- Molecule 81 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	Bf	73	601	379	115	100	7	0	0

- Molecule 82 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
82	Bg	314	2440	1537	425	466	12	0	0

- Molecule 83 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
83	Bv	76	Total C N O P 1623 723 290 534 76	0	0
83	Bw	76	Total C N O P 1623 723 290 534 76	0	0

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
84	Bx	28	Total C N O P 561 252 56 225 28	0	0

- Molecule 85 is a protein called Nascent protein chain.

Mol	Chain	Residues	Atoms	AltConf	Trace
85	By	24	Total C N O 120 72 24 24	0	0

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
86	A3	8	Total Mg 8 8	0
86	A4	9	Total Mg 9 9	0
86	AA	1	Total Mg 1 1	0
86	AB	2	Total Mg 2 2	0
86	AN	2	Total Mg 2 2	0
86	AY	1	Total Mg 1 1	0
86	Aa	3	Total Mg 3 3	0
86	Ae	2	Total Mg 2 2	0
86	An	1	Total Mg 1 1	0
86	A2	220	Total Mg 220 220	0
86	B1	72	Total Mg 72 72	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf
86	BD	1	Total Mg 1 1	0
86	BX	1	Total Mg 1 1	0
86	Bv	2	Total Mg 2 2	0
86	Bx	1	Total Mg 1 1	0

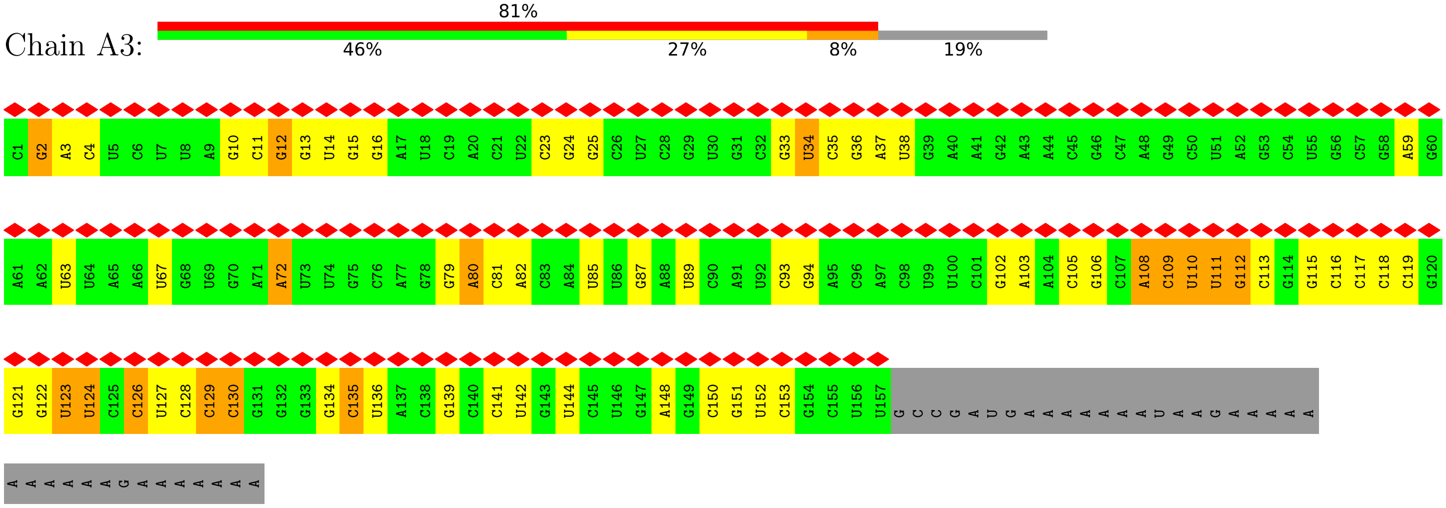
- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
87	Aj	1	Total Zn 1 1	0
87	Ao	1	Total Zn 1 1	0
87	Ap	1	Total Zn 1 1	0
87	Ba	1	Total Zn 1 1	0
87	Bd	1	Total Zn 1 1	0

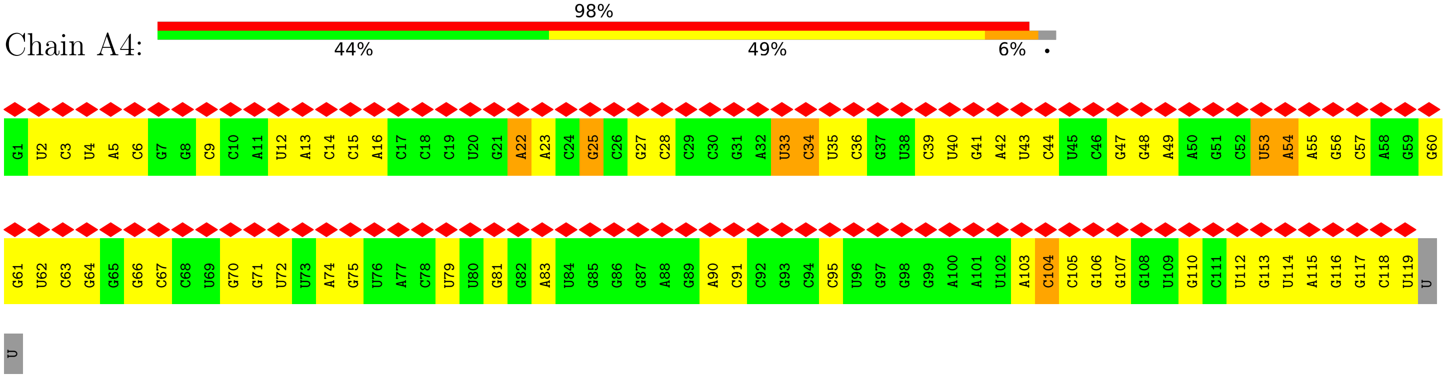
3 Residue-property plots ⓘ

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.

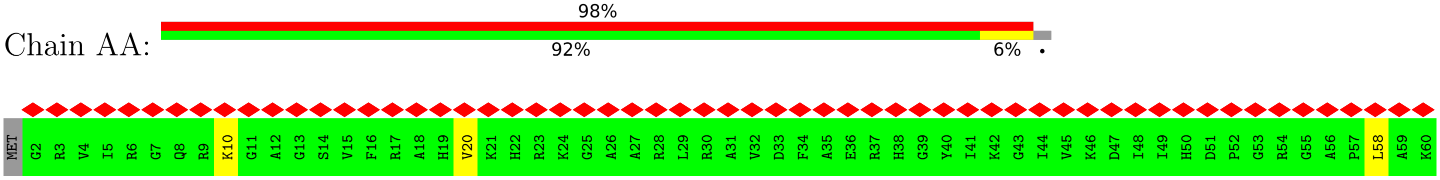
- Molecule 1: 5.8S ribosomal RNA

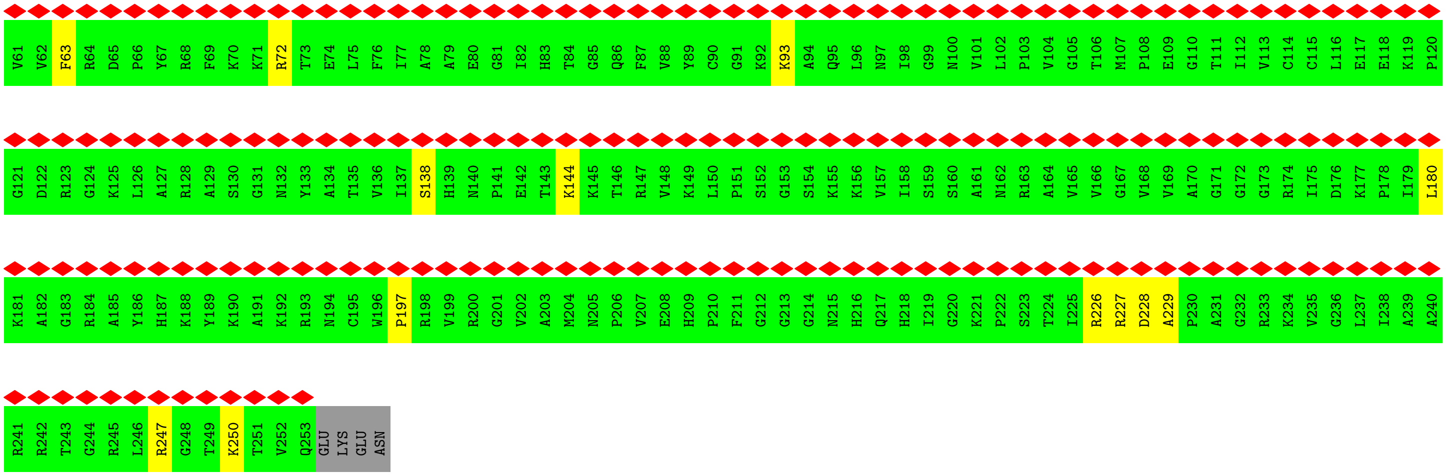


- Molecule 2: 5S ribosomal RNA



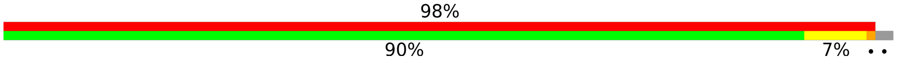
- Molecule 3: 60S ribosomal protein L8

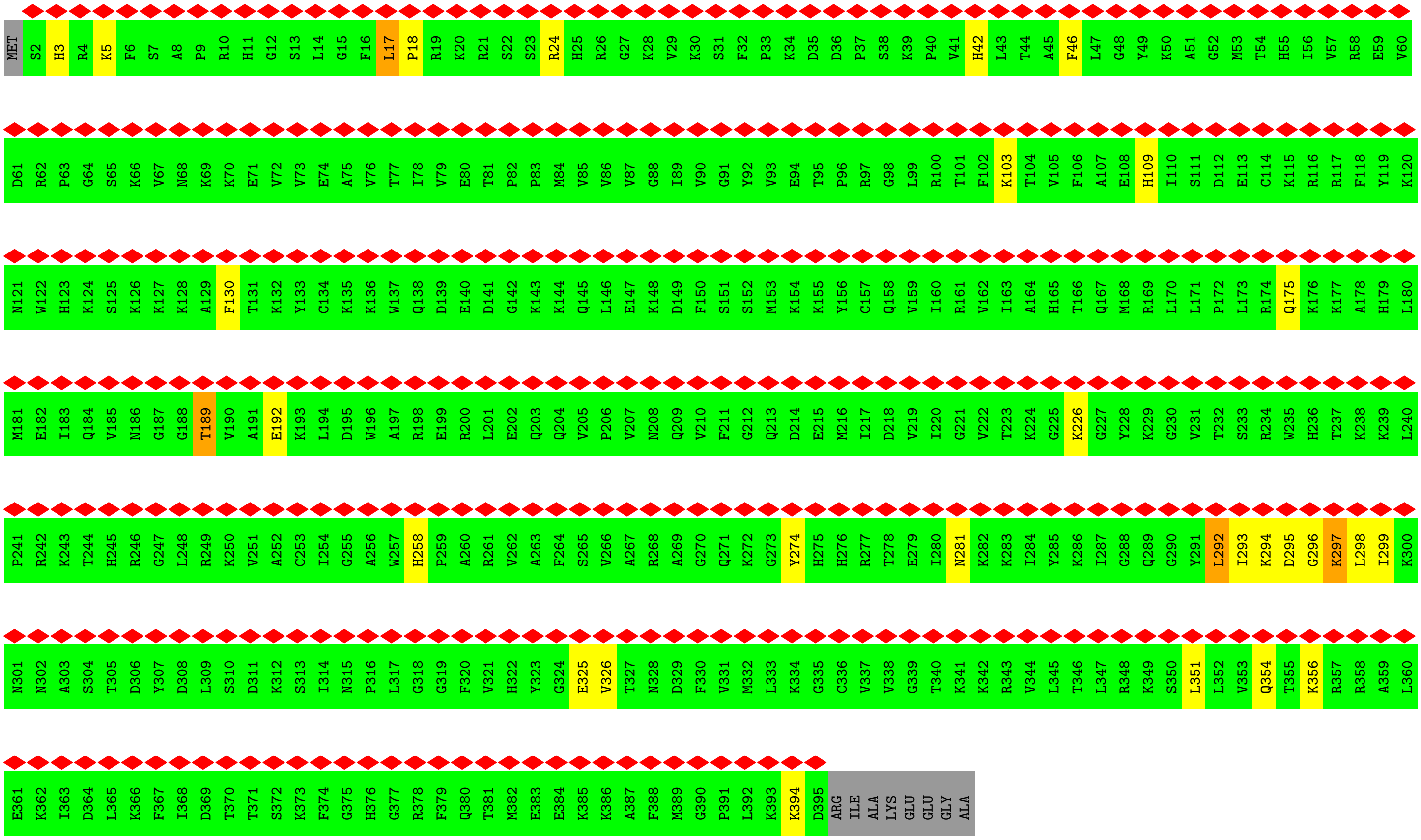




- Molecule 4: 60S ribosomal protein L3

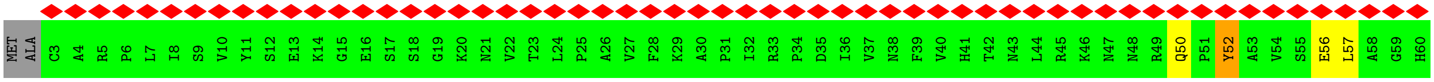
Chain AB:

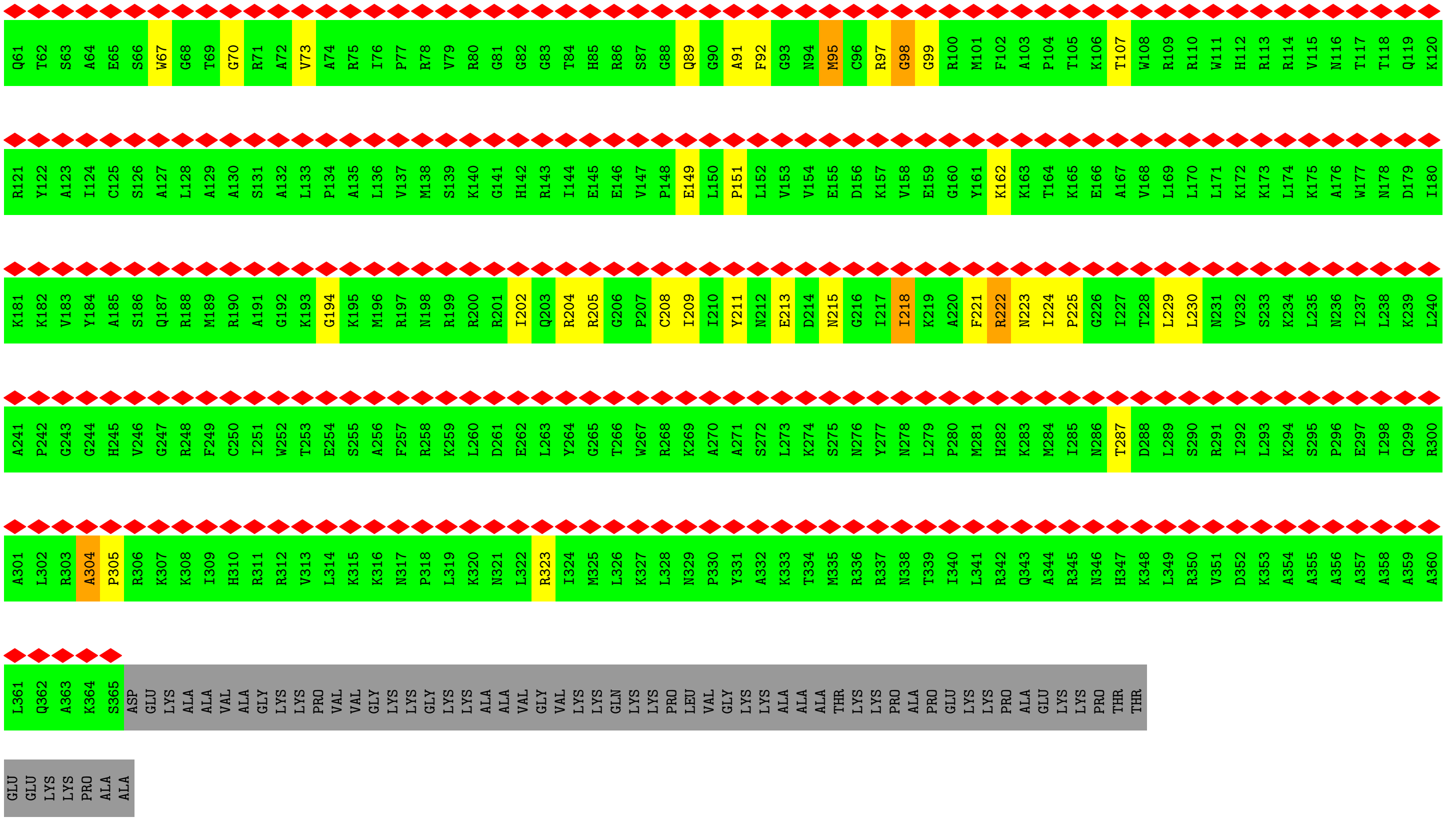




- Molecule 5: 60S ribosomal protein L4

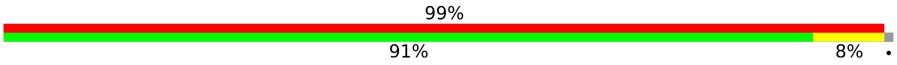
Chain AC:

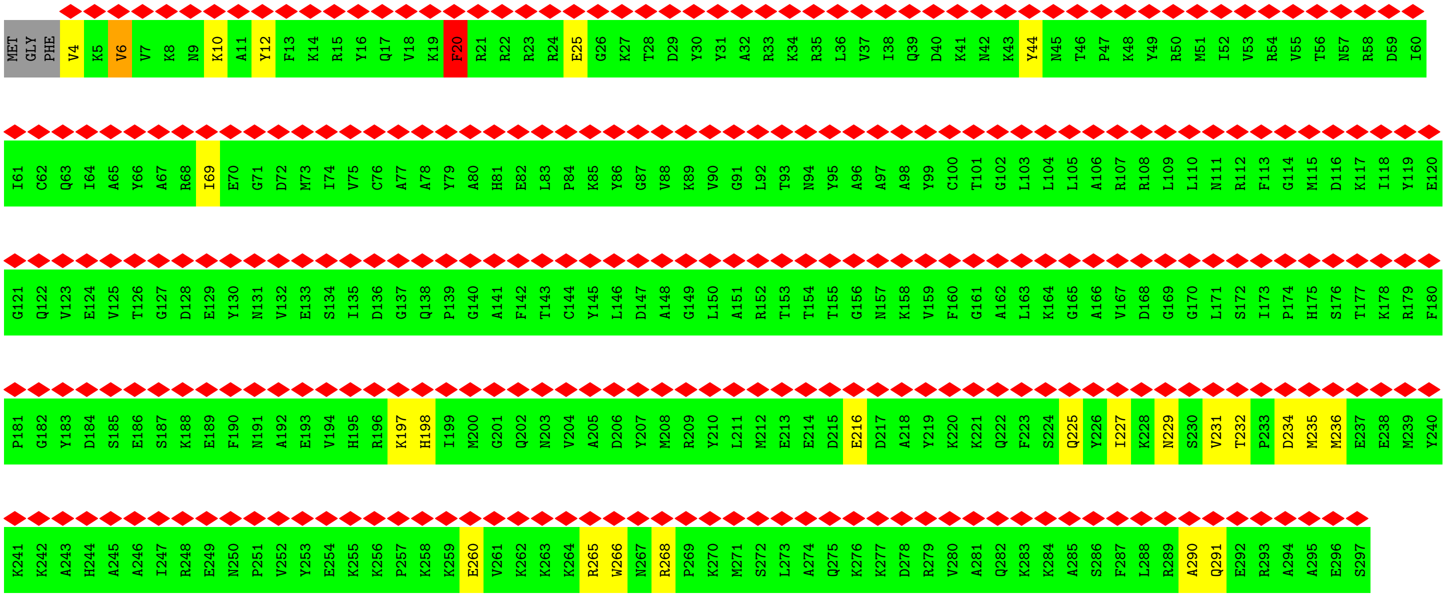




- Molecule 6: 60S ribosomal protein L5

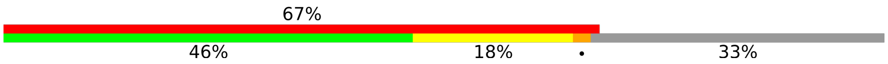
Chain AD:

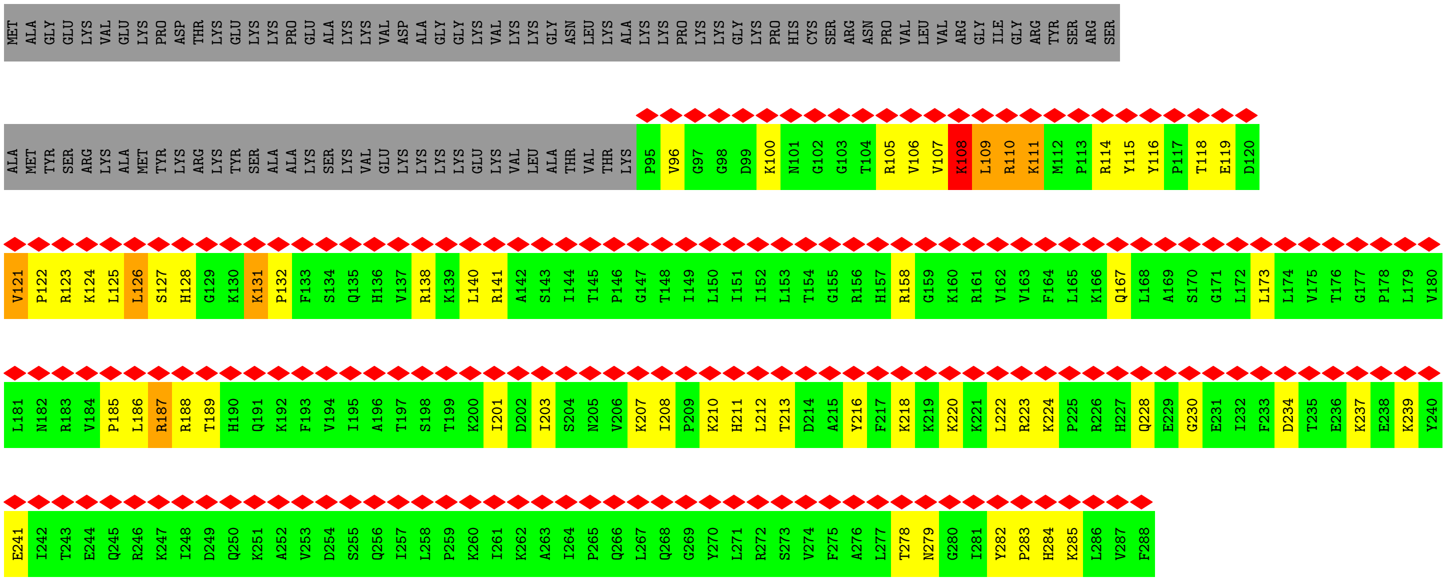




- Molecule 7: 60S ribosomal protein L6

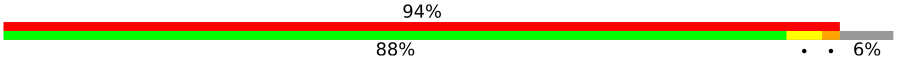
Chain AE:

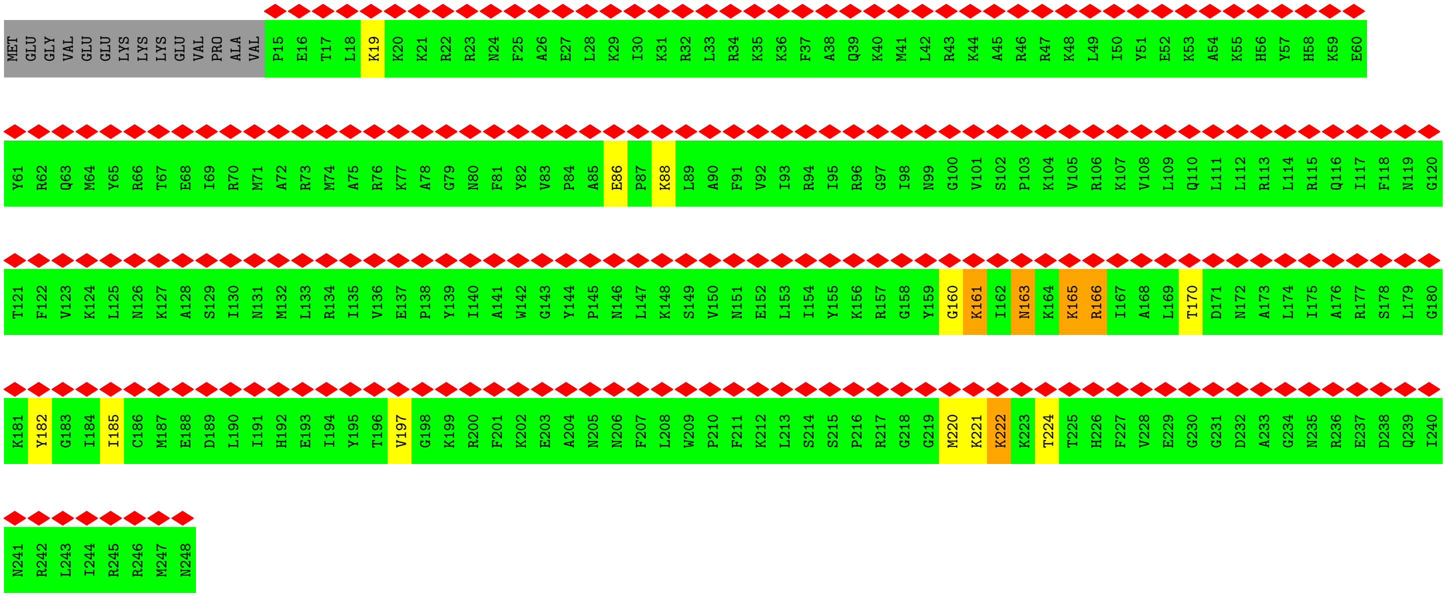




- Molecule 8: 60S ribosomal protein L7

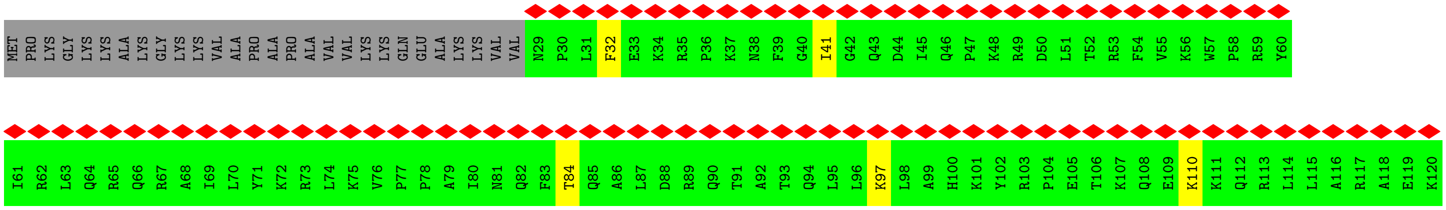
Chain AF:

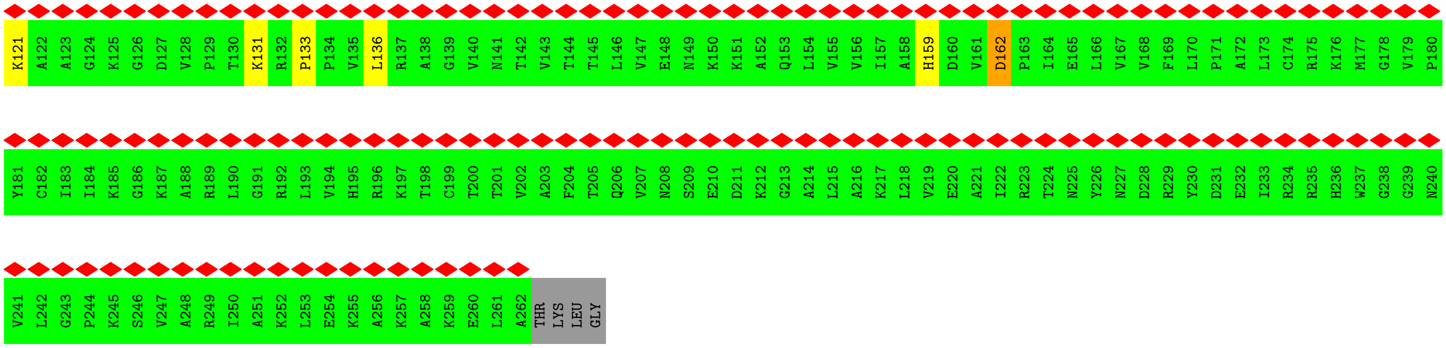




- Molecule 9: 60S ribosomal protein L7a

Chain AG:





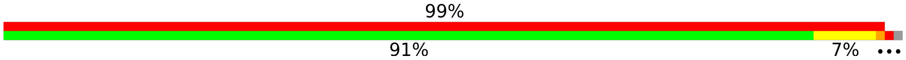
K121 A122 A123 G124 K125 G126 D127 V128 P129 T130 K131 R132 P133 P134 V135 L136 R137 A138 G139 V140 N141 T142 V143 T144 T145 L146 V147 E148 N149 K150 K151 A152 Q153 L154 V155 V156 I157 A158 H159 D160 V161 D162 P163 I164 E165 L166 V167 V168 F169 L170 P171 A172 L173 C174 R175 K176 M177 G178 V179 P180

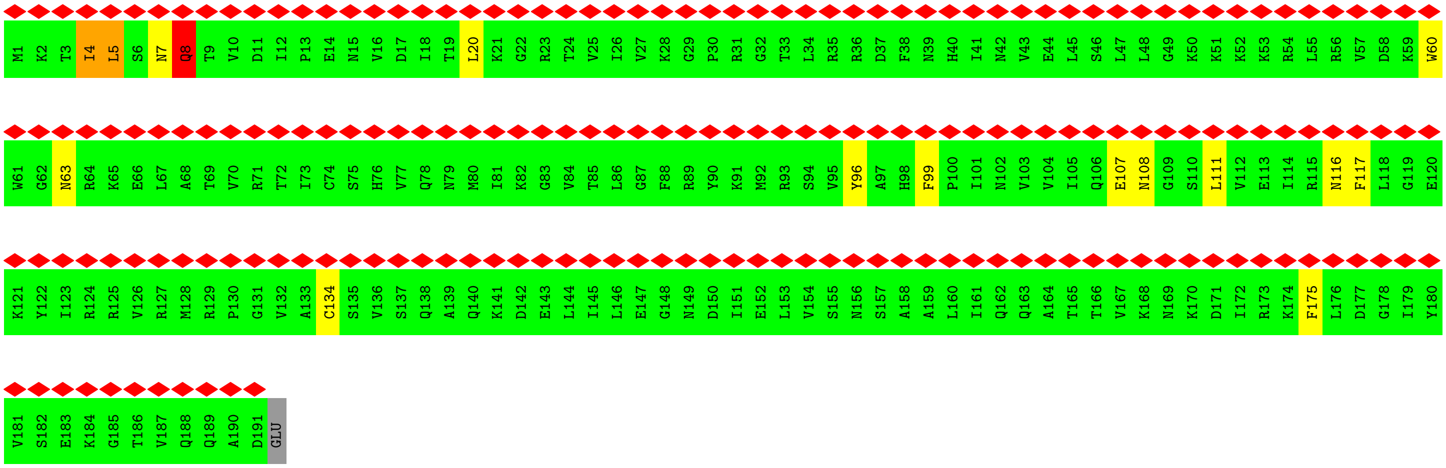
Y181 C182 I183 I184 K185 G186 K187 A188 R189 L190 G191 R192 L193 V194 H195 R196 K197 T198 C199 T200 T201 V202 A203 F204 T205 Q206 V207 N208 S209 E210 D211 K212 G213 A214 L215 A216 K217 L218 V219 E220 A221 I222 R223 T224 N225 Y226 N227 D228 R229 Y230 D231 E232 I233 R234 R235 H236 W237 G238 G239 N240

V241 L242 G243 P244 K245 S246 V247 A248 R249 I250 A251 K252 L253 E254 K255 A256 K257 A258 K259 E260 L261 A262 THR LYS LEU GLY

- Molecule 10: 60S ribosomal protein L9

Chain AH:





M1 K2 T3 I4 L5 S6 N7 Q8 T9 V10 D11 I12 P13 E14 N15 V16 D17 I18 T19 L20 K21 G22 R23 T24 V25 I26 V27 K28 G29 P30 R31 G32 T33 L34 R35 R36 D37 F38 N39 H40 I41 N42 V43 E44 L45 S46 L47 L48 G49 K50 K51 K52 K53 R54 L55 R56 V57 D58 K59 W60

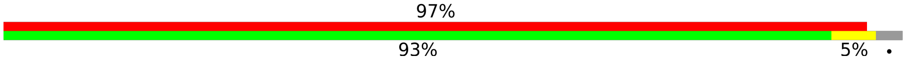
W61 G62 N63 R64 K65 E66 L67 A68 T69 V70 R71 T72 I73 C74 S75 H76 V77 Q78 N79 M80 I81 K82 G83 V84 T85 L86 G87 F88 R89 Y90 K91 M92 R93 S94 V95 Y96 A97 H98 F99 P100 I101 N102 V103 V104 I105 Q106 E107 N108 G109 S110 L111 V112 E113 I114 R115 N116 F117 L118 G119 E120

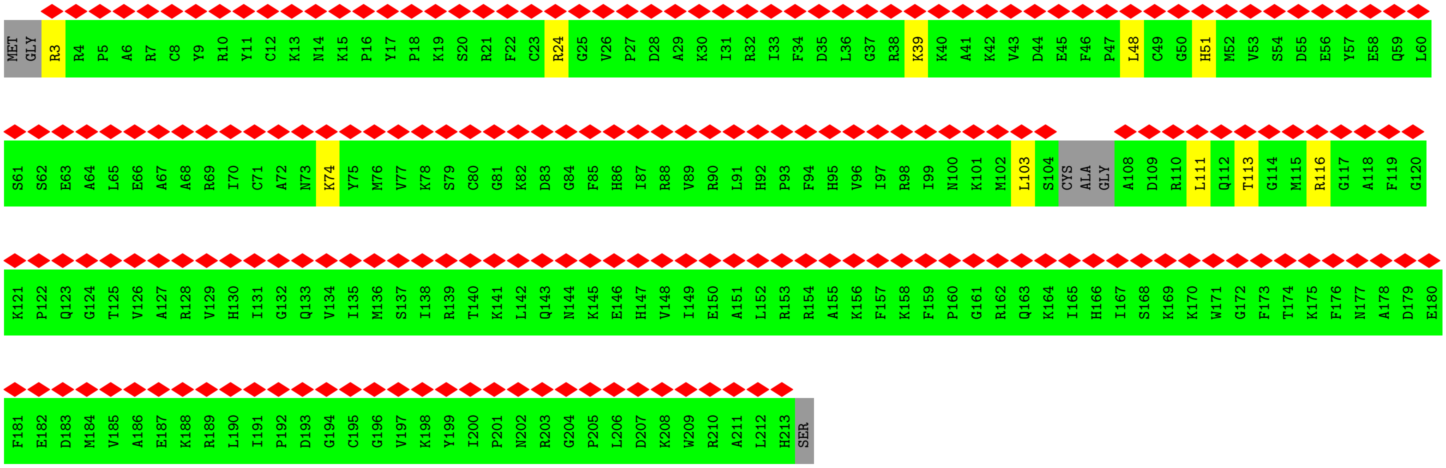
K121 Y122 I123 R124 R125 V126 R127 M128 R129 P130 G131 V132 A133 C134 S135 V136 S137 Q138 A139 Q140 K141 D142 E143 L144 I145 L146 E147 G148 N149 D150 I151 E152 L153 V154 S155 N156 S157 A158 A159 L160 I161 Q162 Q163 A164 T165 T166 V167 K168 N169 K170 D171 I172 R173 K174 F175 L176 D177 G178 I179 Y180

V181 S182 E183 K184 G185 T186 V187 Q188 Q189 A190 D191 GLU

- Molecule 11: 60S ribosomal protein L10

Chain AI:





MET GLY R3 R4 P5 A6 R7 C8 Y9 R10 Y11 C12 K13 N14 K15 P16 Y17 P18 K19 S20 R21 F22 C23 R24 G25 V26 P27 D28 A29 K30 I31 R32 I33 F34 D35 L36 G37 R38 K39 K40 A41 K42 V43 D44 E45 F46 P47 L48 C49 G50 H51 M52 V53 S54 D55 E56 Y57 E58 Q59 L60

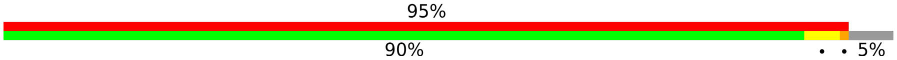
S61 S62 E63 A64 L65 E66 A67 A68 R69 I70 C71 A72 N73 K74 Y75 M76 V77 K78 S79 C80 G81 K82 D83 G84 F85 H86 I87 R88 V89 R90 L91 H92 P93 F94 H95 V96 I97 R98 I99 N100 K101 M102 L103 S104 CYS ALA GLY A108 D109 R110 L111 Q112 T113 G114 M115 R116 G117 A118 F119 G120

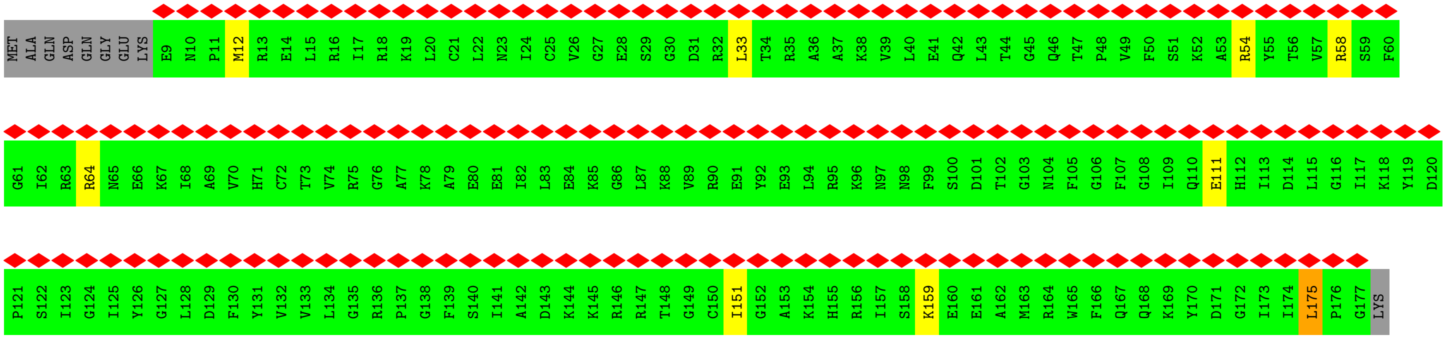
K121 P122 Q123 G124 T125 V126 A127 R128 V129 H130 I131 G132 Q133 V134 I135 M136 S137 I138 R139 T140 K141 L142 Q143 N144 K145 E146 H147 V148 I149 E150 A151 L152 R153 R154 A155 K156 F157 K158 F159 P160 G161 R162 Q163 K164 I165 H166 I167 S168 K169 K170 W171 G172 F173 T174 K175 F176 N177 A178 D179 E180

F181 E182 D183 M184 V185 A186 E187 K188 R189 L190 I191 P192 D193 G194 C195 G196 V197 K198 Y199 I200 P201 N202 R203 G204 P205 L206 D207 K208 W209 R210 A211 L212 H213 SER

- Molecule 12: 60S ribosomal protein L11

Chain AJ:



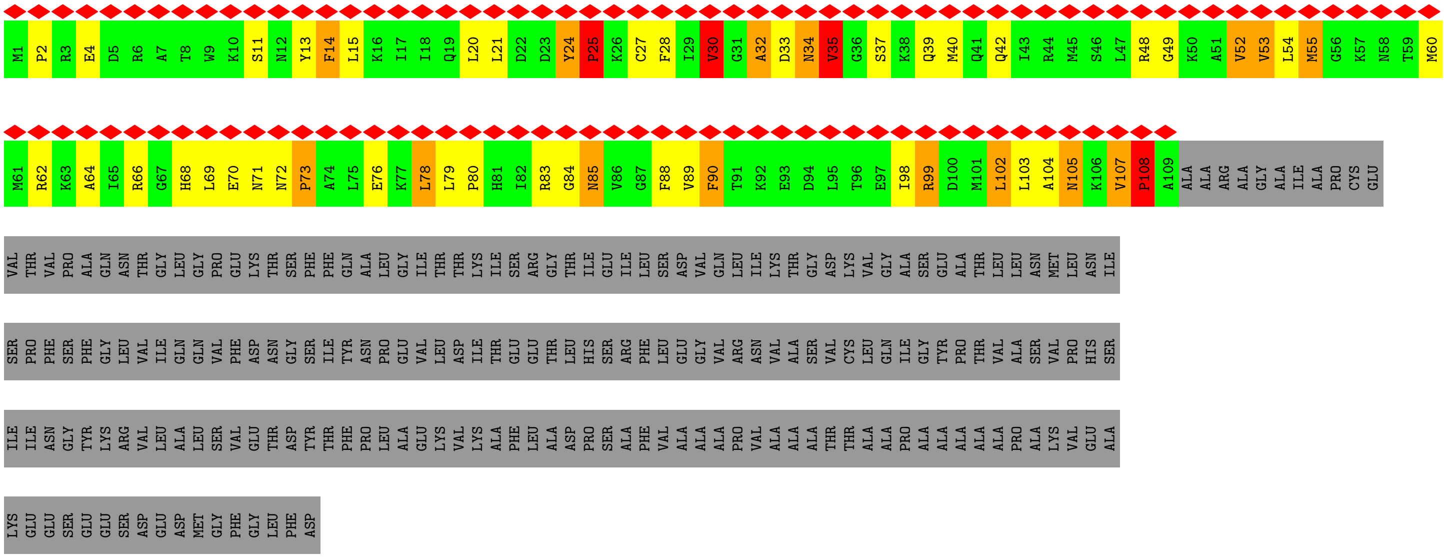

MET ALA GLN ASP GLN GLY GLU LYS E9 N10 P11 M12 R13 E14 L15 R16 I17 R18 K19 L20 C21 L22 N23 I24 C25 V26 G27 E28 S29 G30 D31 R32 L33 T34 R35 A36 A37 K38 V39 L40 E41 Q42 L43 T44 G45 Q46 T47 P48 V49 F50 S51 K52 A53 R54 Y55 T56 V57 R58 S59 F60

G61 I62 R63 R64 N65 E66 K67 I68 A69 V70 H71 C72 T73 V74 R75 G76 A77 K78 A79 E80 E81 I82 L83 E84 K85 G86 L87 K88 V89 R90 E91 Y92 E93 L94 R95 K96 N97 N98 F99 S100 D101 T102 G103 N104 F105 G106 F107 G108 I109 Q110 E111 H112 I113 D114 L115 G116 I117 K118 Y119 D120

P121 S122 I123 G124 I125 Y126 G127 L128 D129 F130 Y131 V132 V133 L134 G135 R136 P137 G138 F139 S140 I141 A142 D143 K144 K145 R146 R147 T148 G149 C150 I151 G152 A153 K154 H155 R156 I157 S158 K159 E160 E161 A162 M163 R164 W165 F166 Q167 Q168 K169 Y170 D171 G172 I173 I174 L175 P176 G177 LYS

- Molecule 13: 60S acidic ribosomal protein P0

Chain AK:


M1 P2 R3 E4 D5 R6 A7 T8 W9 K10 S11 N12 Y13 F14 L15 K16 I17 I18 Q19 L20 L21 D22 D23 Y24 P25 K26 C27 F28 I29 V30 G31 A32 D33 N34 V35 G36 S37 K38 Q39 M40 Q41 Q42 I43 R44 M45 S46 L47 R48 G49 K50 A51 V52 V53 L54 M55 G56 K57 N58 T59 M60

M61 R62 K63 A64 I65 R66 G67 H68 L69 E70 N71 N72 P73 A74 L75 E76 K77 L78 L79 P80 H81 I82 R83 G84 N85 V86 G87 F88 V89 F90 T91 K92 E93 D94 L95 T96 E97 I98 R99 D100 M101 L102 L103 A104 N105 K106 V107 P108 A109 ALA ALA ARG ALA GLY ALA ILE ALA PRO CYS GLU

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

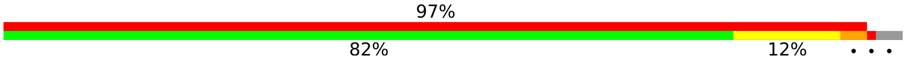
SER PRO PHE SER PHE GLY LEU VAL ILE GLN GLN VAL PHE ASP ASN GLY SER ILE TYR ASN PRO GLU VAL LEU ASP ILE THR GLU GLU THR LEU HIS SER ARG PHE LEU GLU GLY VAL ARG ASN VAL ALA SER VAL CYS LEU GLN ILE GLY TYR PRO THR VAL ALA SER VAL PRO HIS SER

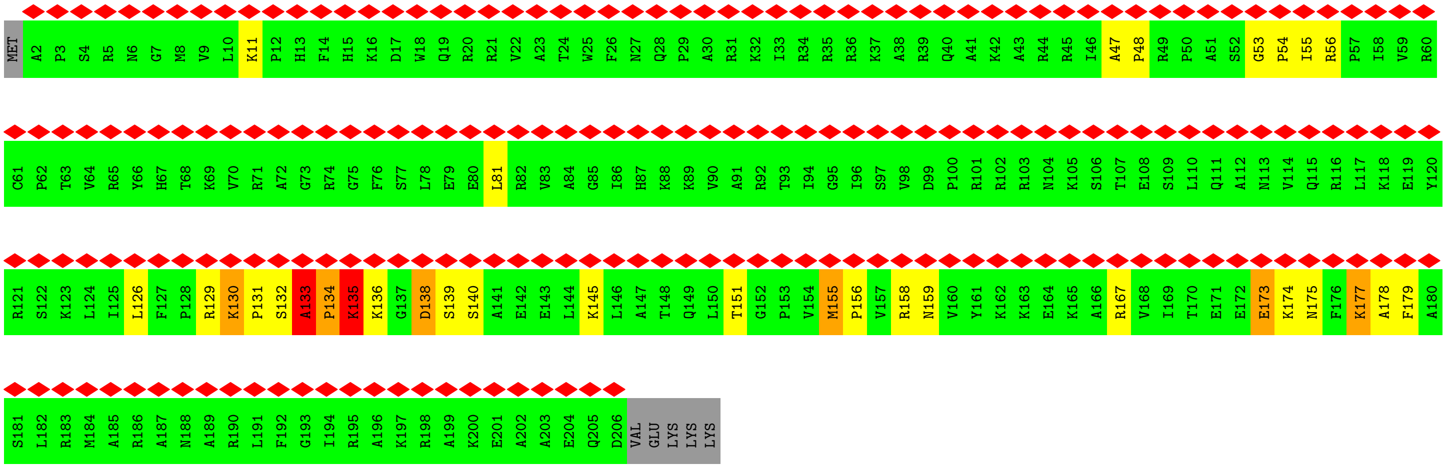
ILE ILE ASN GLY TYR LYS ARG VAL LEU ALA LEU SER VAL GLU THR ASP TYR THR PHE PRO LEU ALA GLU LYS VAL LYS ALA PHE LEU ALA ASP PRO SER ALA PHE VAL ALA ALA ALA ALA PRO VAL ALA ALA ALA THR THR ALA ALA PRO ALA ALA ALA ALA ALA PRO ALA LYS VAL GLU ALA

LYS GLU GLU SER GLU GLU SER ASP GLU ASP MET GLY PHE GLY LEU PHE ASP

- Molecule 14: 60S ribosomal protein L13

Chain AL:




MET A2 P3 S4 R5 N6 G7 M8 V9 L10 K11 P12 H13 F14 H15 K16 D17 W18 Q19 R20 R21 V22 A23 T24 W25 F26 N27 Q28 P29 A30 R31 K32 I33 R34 R35 R36 K37 A38 R39 Q40 A41 K42 A43 R44 R45 I46 A47 P48 R49 P50 A51 S52 G53 P54 I55 R56 P57 I58 V59 R60

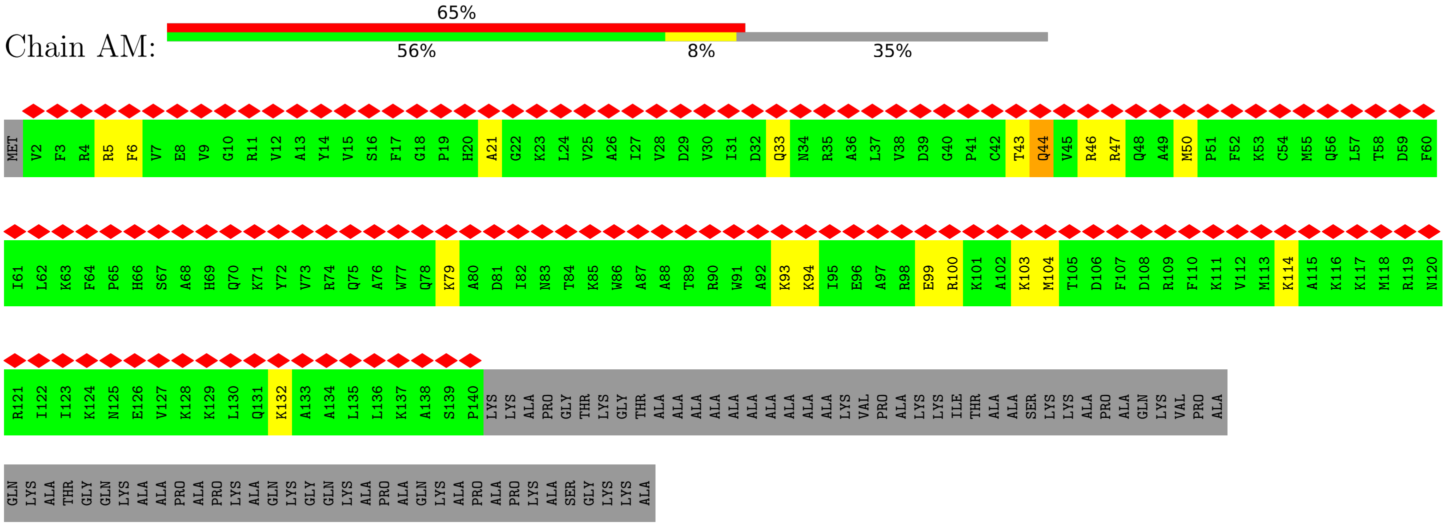
C61 P62 T63 V64 R65 Y66 H67 T68 K69 V70 R71 A72 G73 R74 G75 F76 S77 L78 E79 E80 L81 R82 V83 A84 G85 I86 H87 K88 K89 V90 A91 R92 T93 I94 G95 I96 S97 V98 D99 P100 R101 R102 R103 N104 K105 S106 T107 E108 S109 L110 Q111 A112 N113 V114 Q115 R116 L117 K118 E119 Y120

R121 S122 K123 L124 I125 L126 F127 P128 R129 K130 P131 S132 A133 P134 K135 K136 G137 D138 S139 S140 A141 E142 E143 L144 K145 L146 A147 T148 Q149 L150 T151 G152 P153 V154 M155 P156 V157 R158 N159 V160 Y161 K162 K163 E164 K165 A166 R167 V168 I169 T170 E171 E172 E173 K174 N175 F176 K177 A178 F179 A180

S181 L182 R183 M184 A185 R186 A187 N188 A189 R190 L191 F192 G193 I194 R195 A196 K197 R198 A199 K200 E201 A202 A203 E204 Q205 D206 VAL GLU LYS LYS LYS

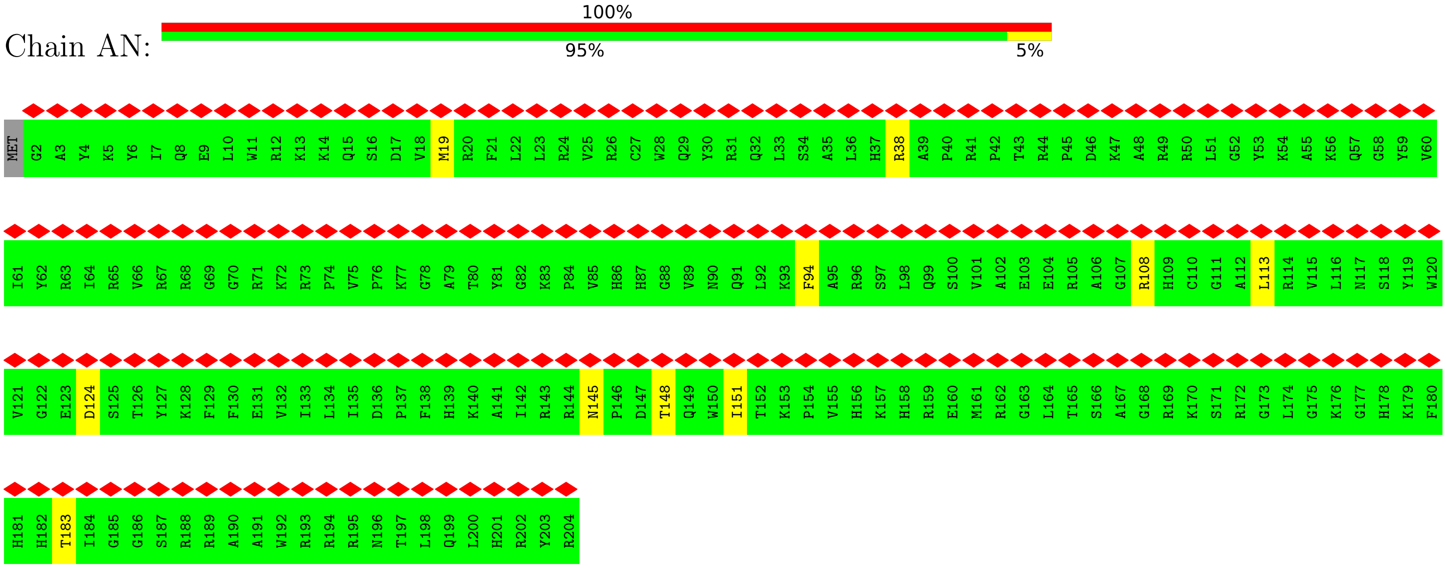
- Molecule 15: 60S ribosomal protein L14

Chain AM:



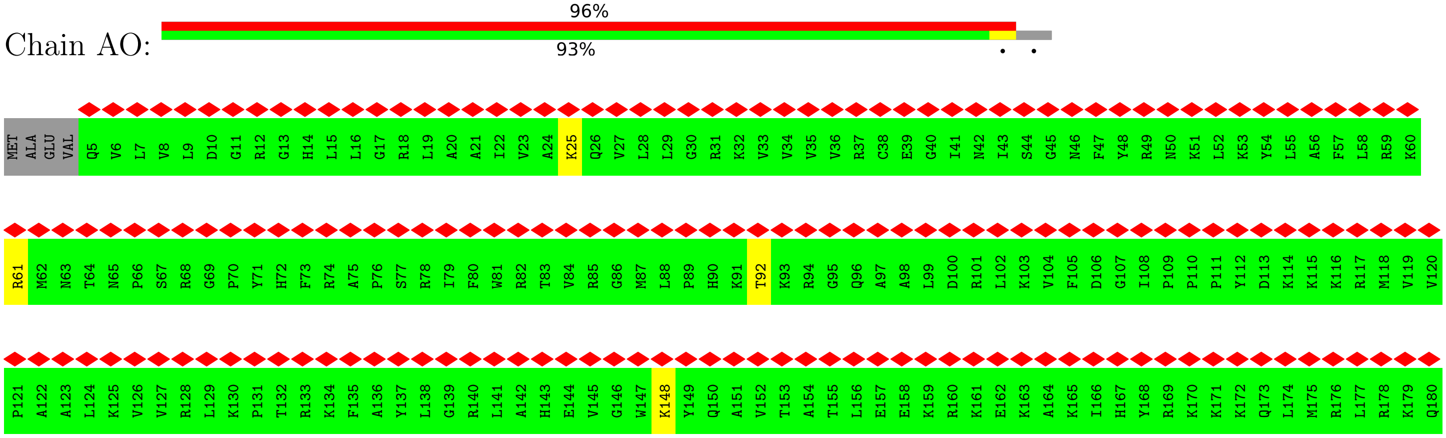
- Molecule 16: 60S ribosomal protein L15

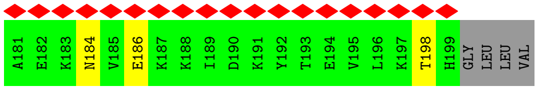
Chain AN:



- Molecule 17: 60S ribosomal protein L13a

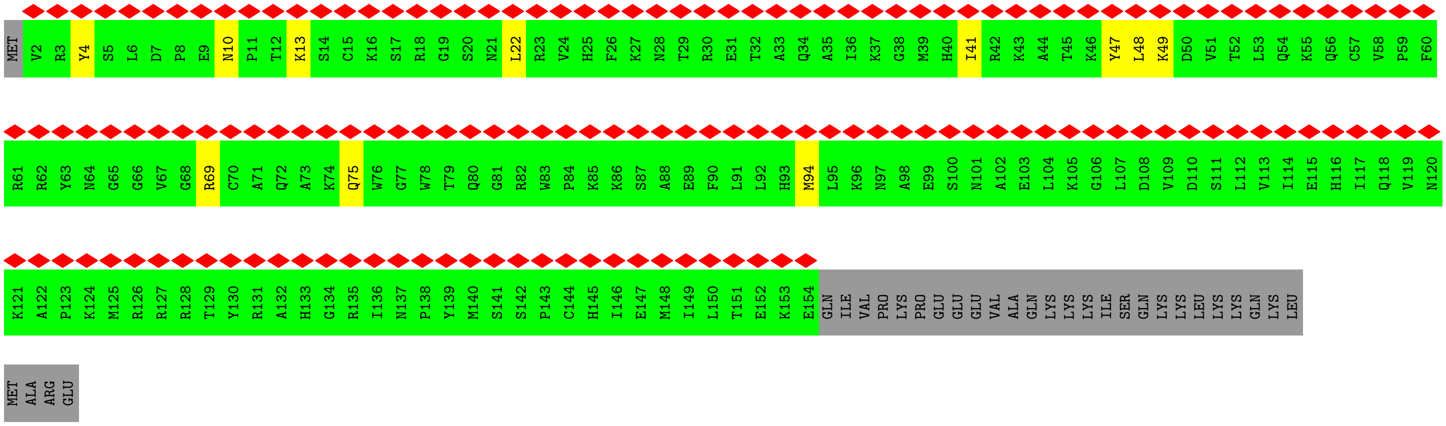
Chain AO:





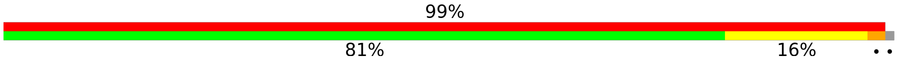
- Molecule 18: 60S ribosomal protein L17

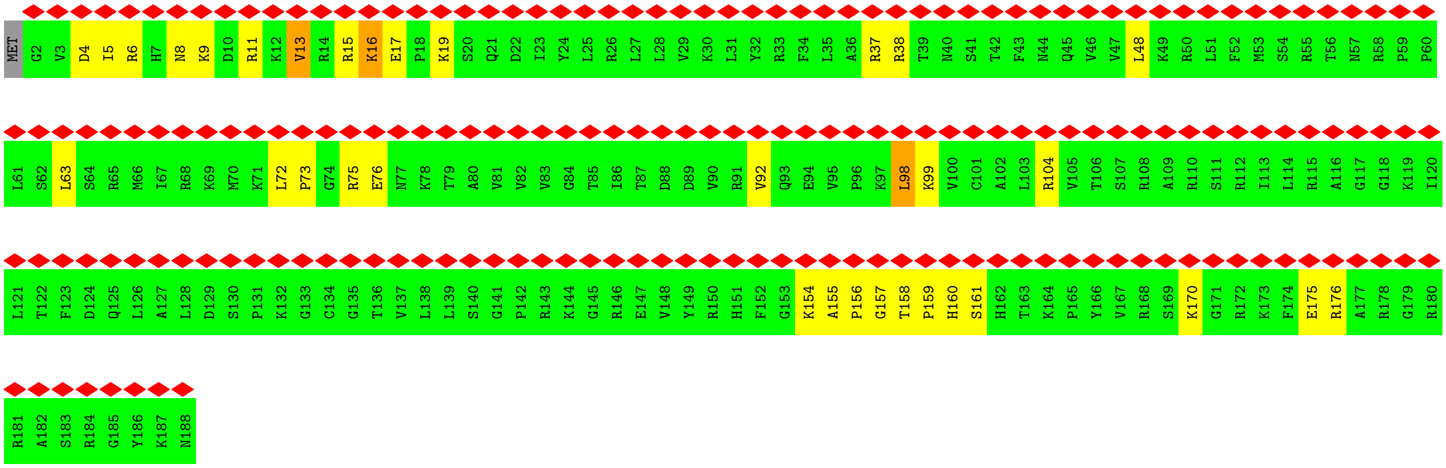
Chain AP:



- Molecule 19: 60S ribosomal protein L18

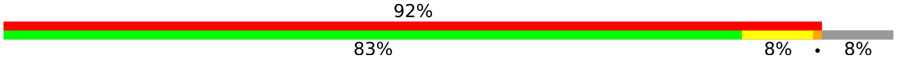
Chain AQ:

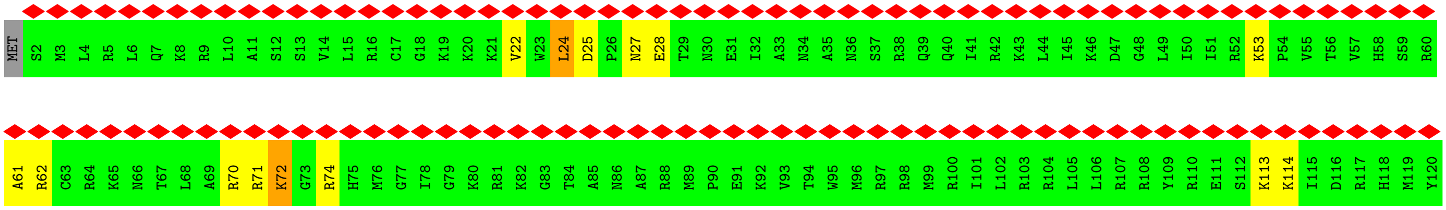




- Molecule 20: 60S ribosomal protein L19

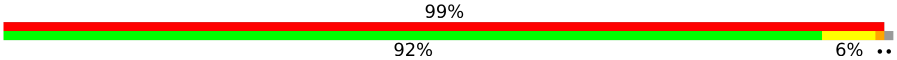
Chain AR:

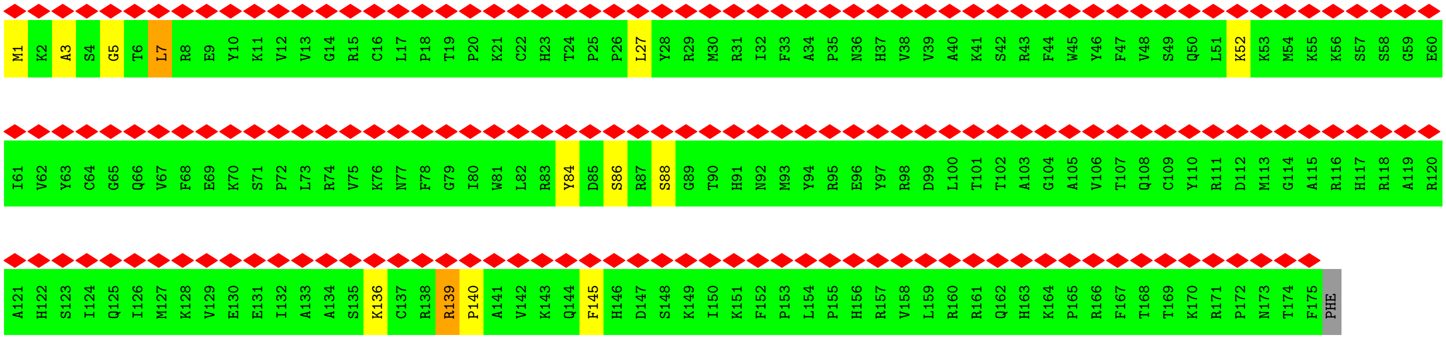




- Molecule 21: 60S ribosomal protein L18a

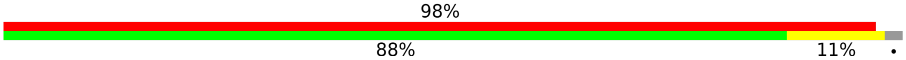
Chain AS:

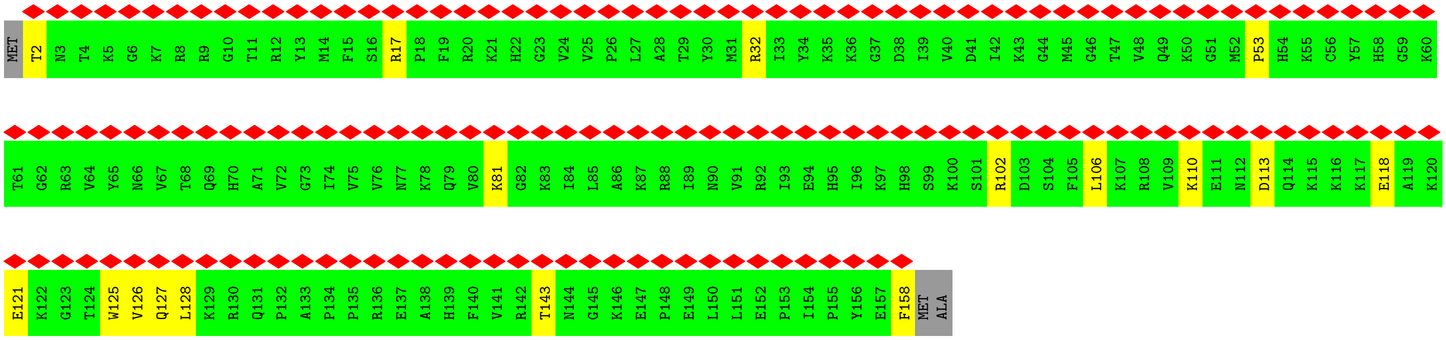




- Molecule 22: 60S ribosomal protein L21

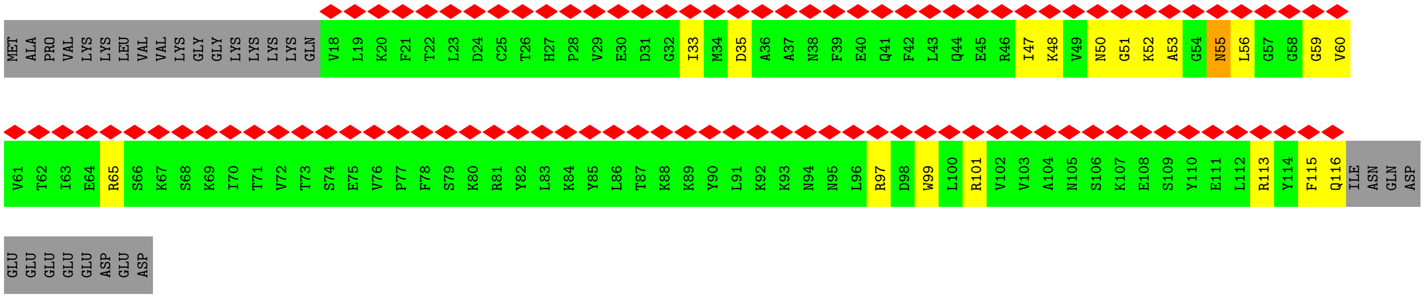
Chain AT:





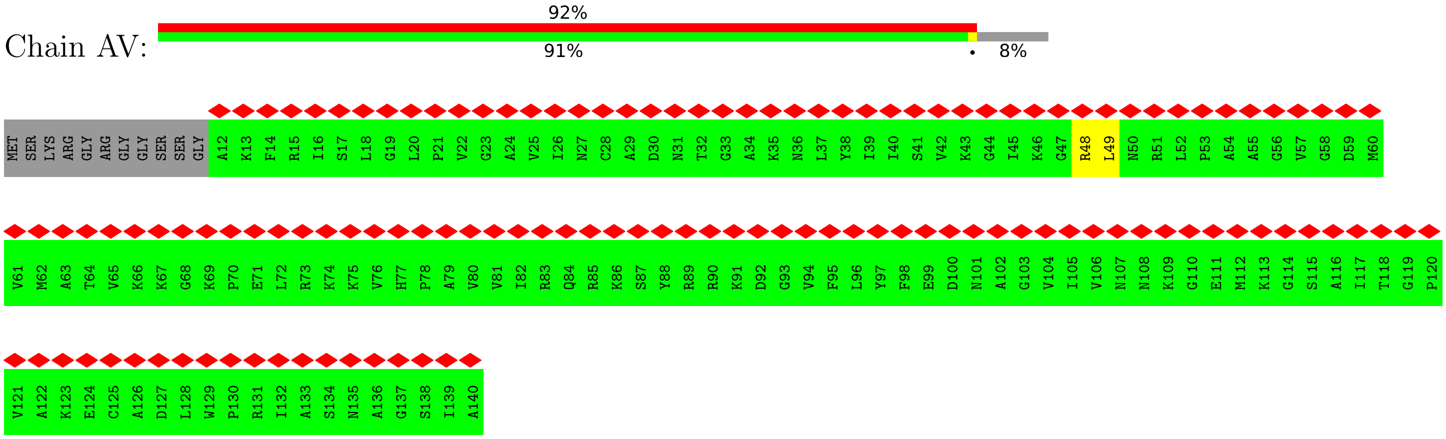
- Molecule 23: 60S ribosomal protein L22

Chain AU:



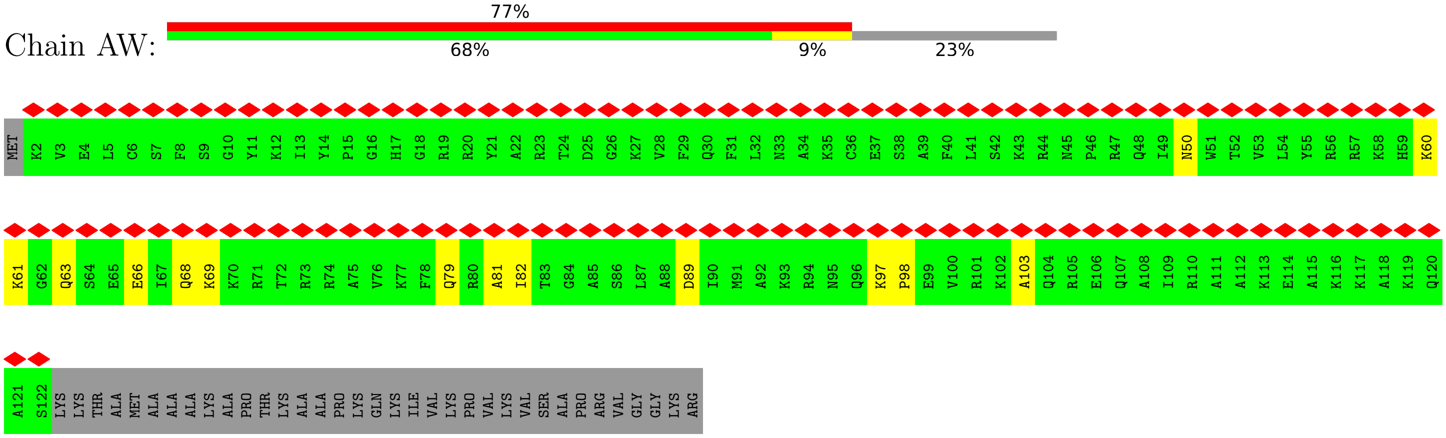
- Molecule 24: 60S ribosomal protein L23

Chain AV:



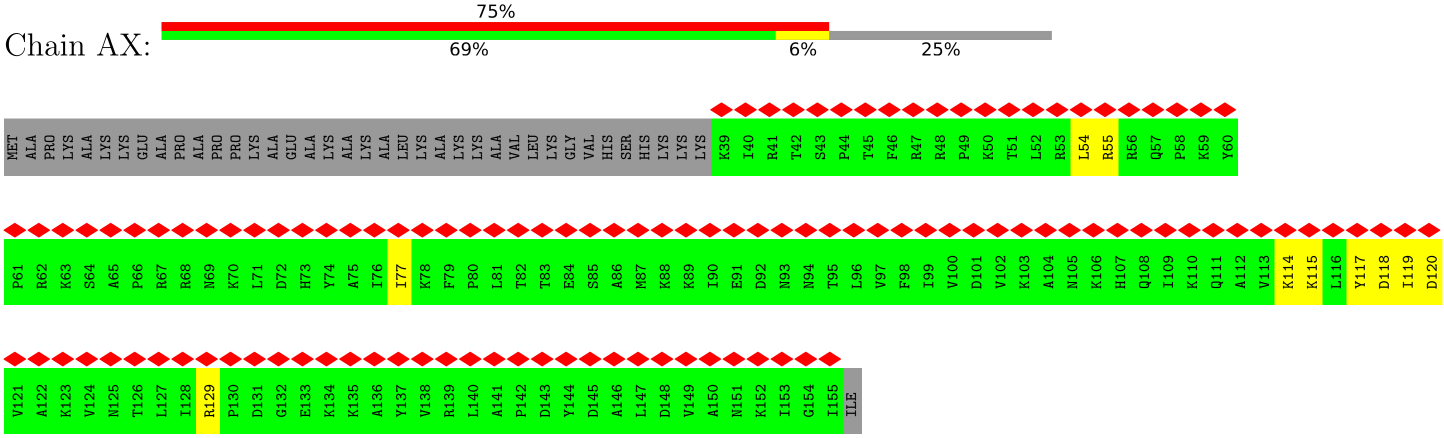
- Molecule 25: 60S ribosomal protein L24

Chain AW:



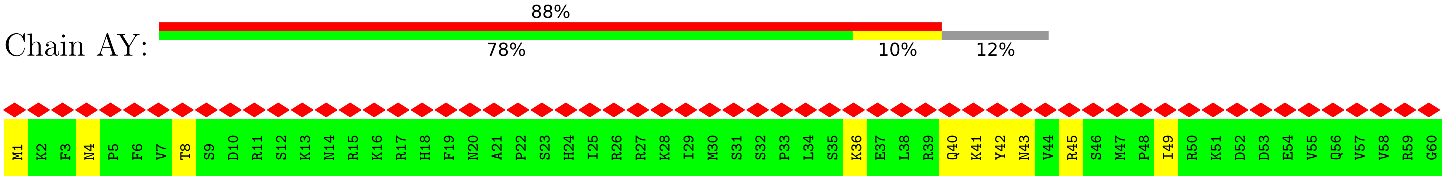
- Molecule 26: 60S ribosomal protein L23a

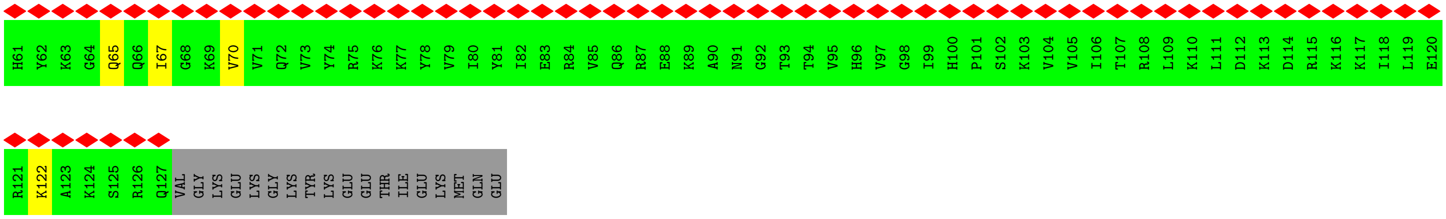
Chain AX:



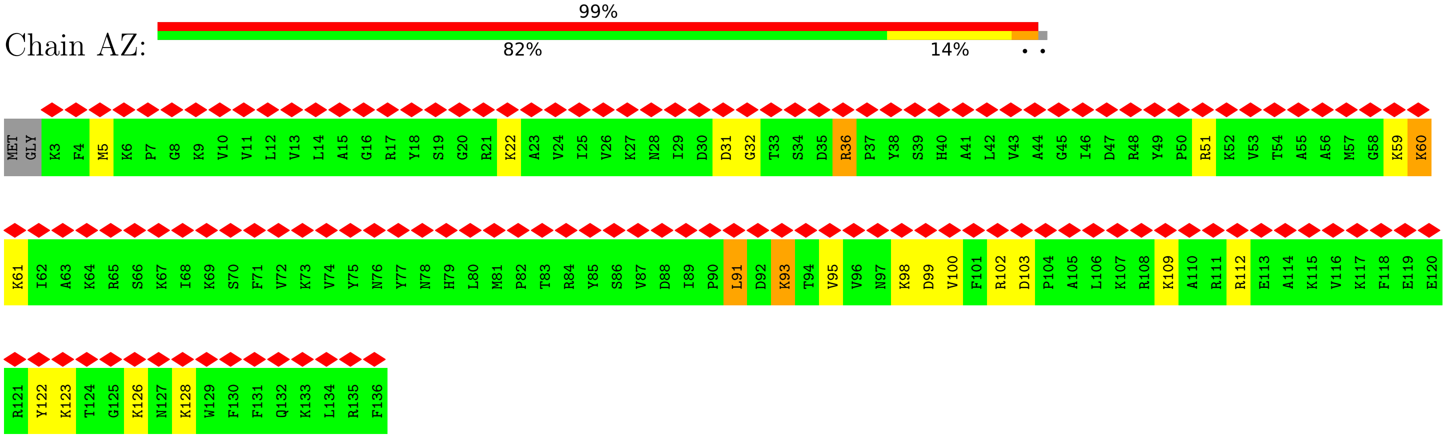
- Molecule 27: 60S ribosomal protein L26

Chain AY:

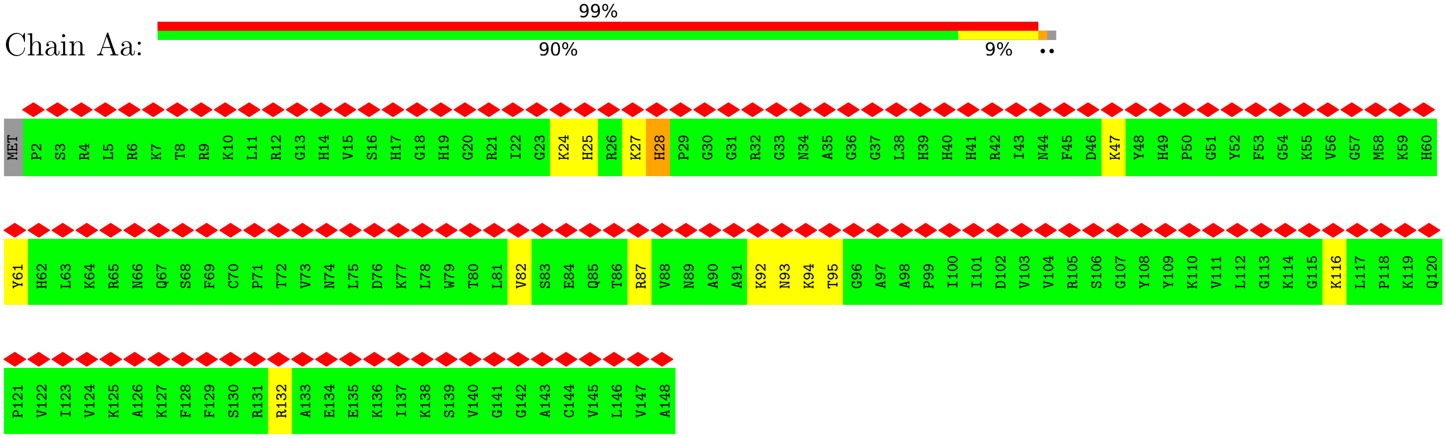




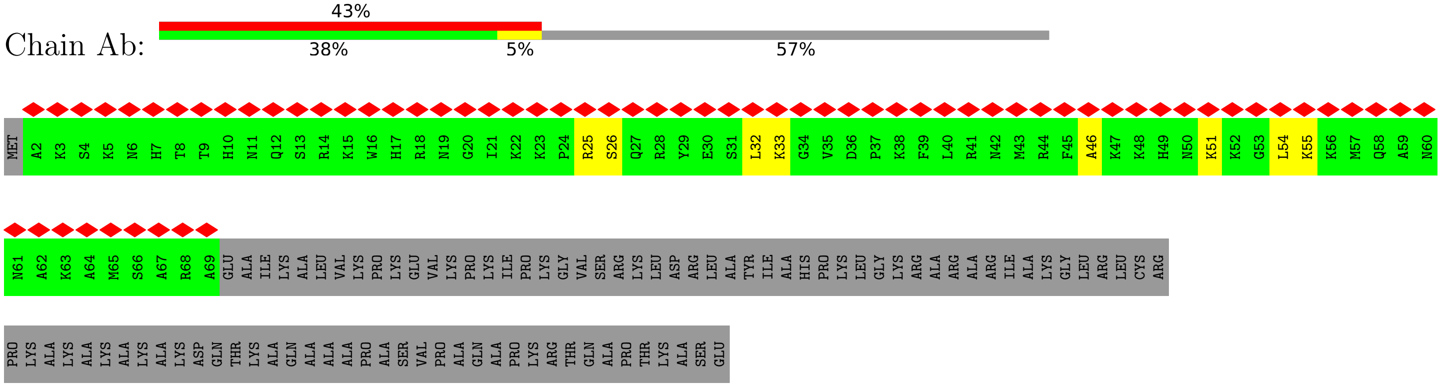
- Molecule 28: 60S ribosomal protein L27



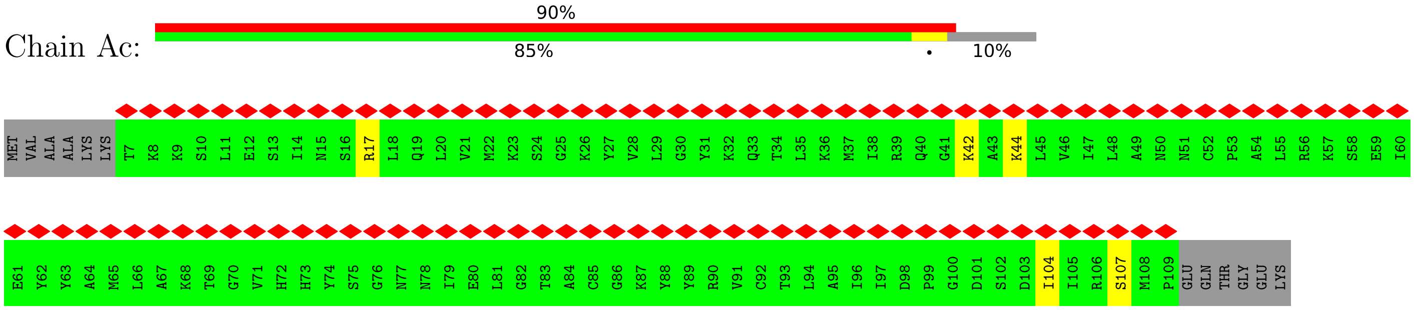
- Molecule 29: 60S ribosomal protein L27a



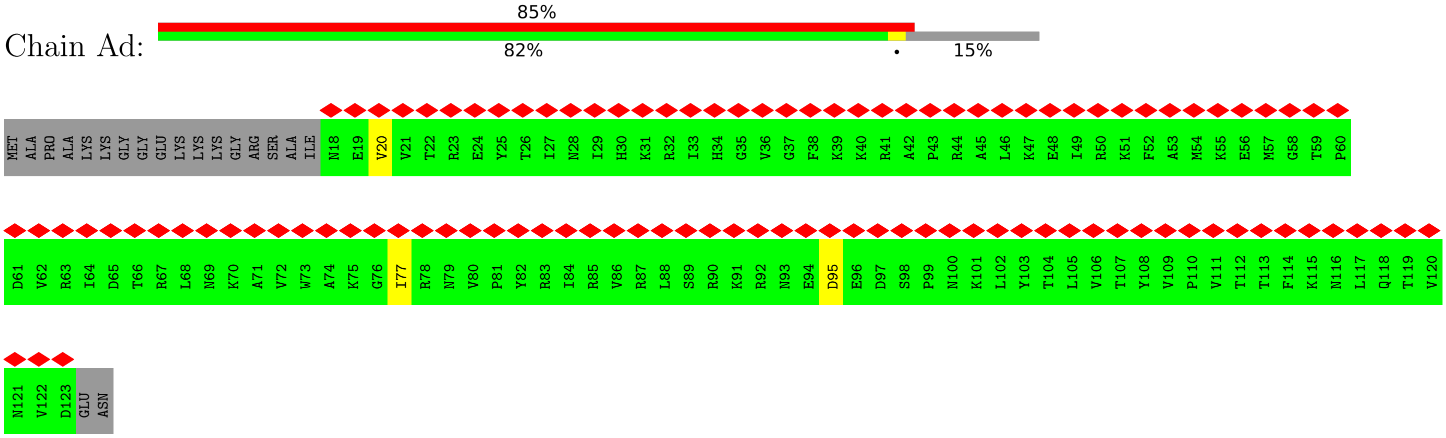
- Molecule 30: 60S ribosomal protein L29



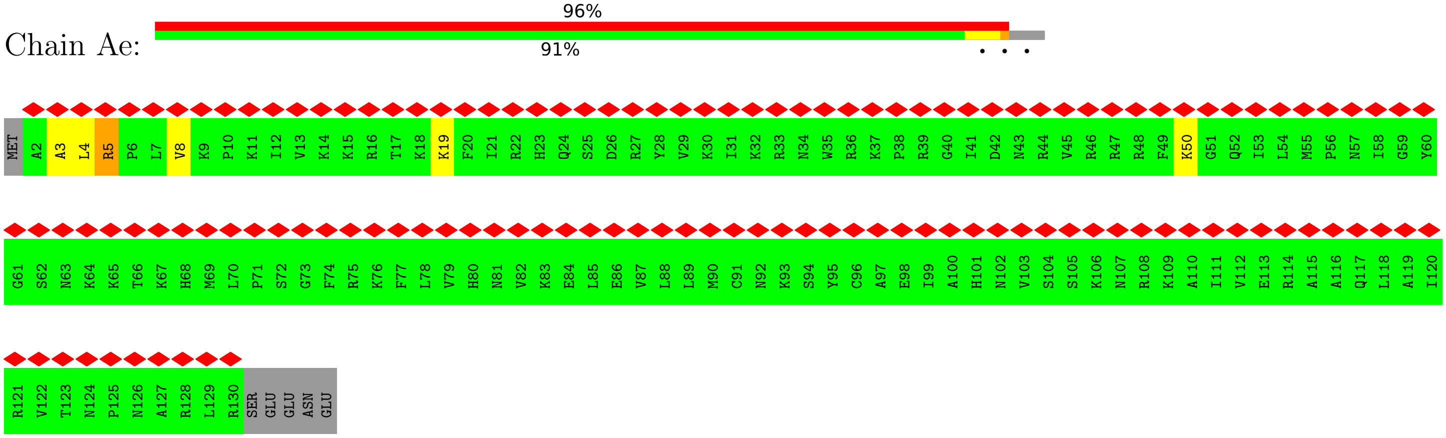
- Molecule 31: 60S ribosomal protein L30



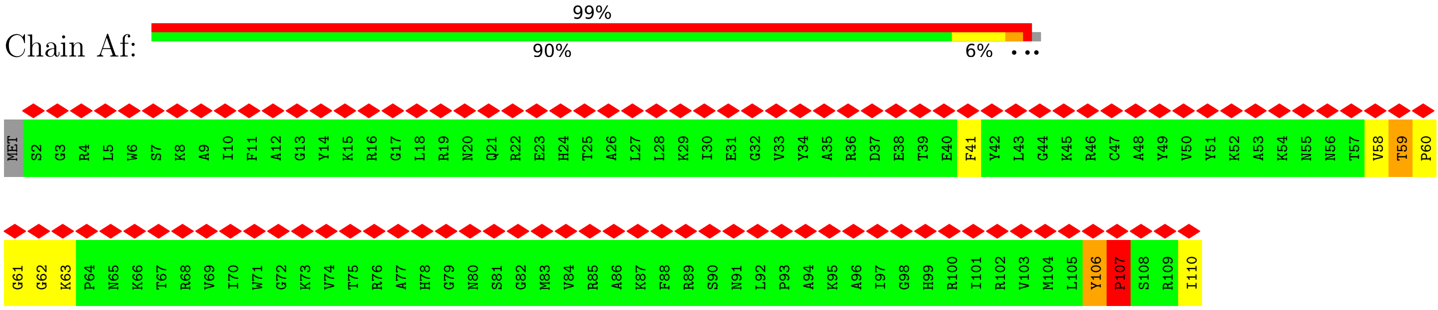
- Molecule 32: 60S ribosomal protein L31



- Molecule 33: 60S ribosomal protein L32

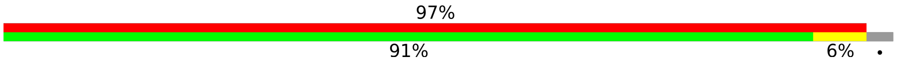


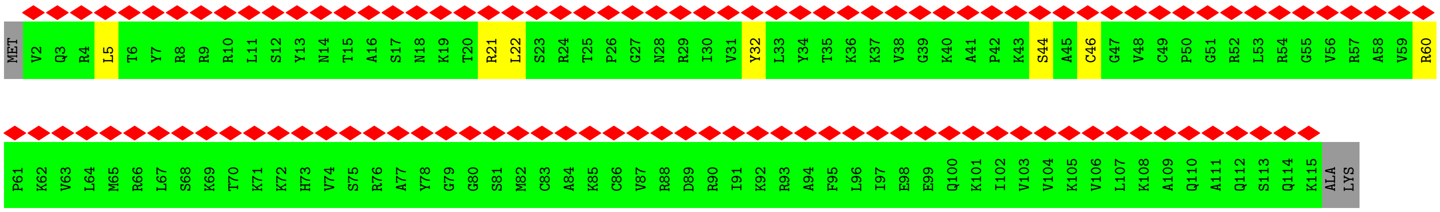
- Molecule 34: 60S ribosomal protein L35a



- Molecule 35: 60S ribosomal protein L34

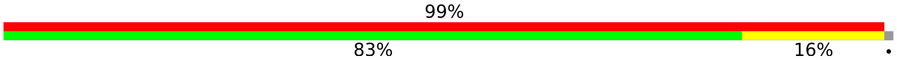
Chain Ag:

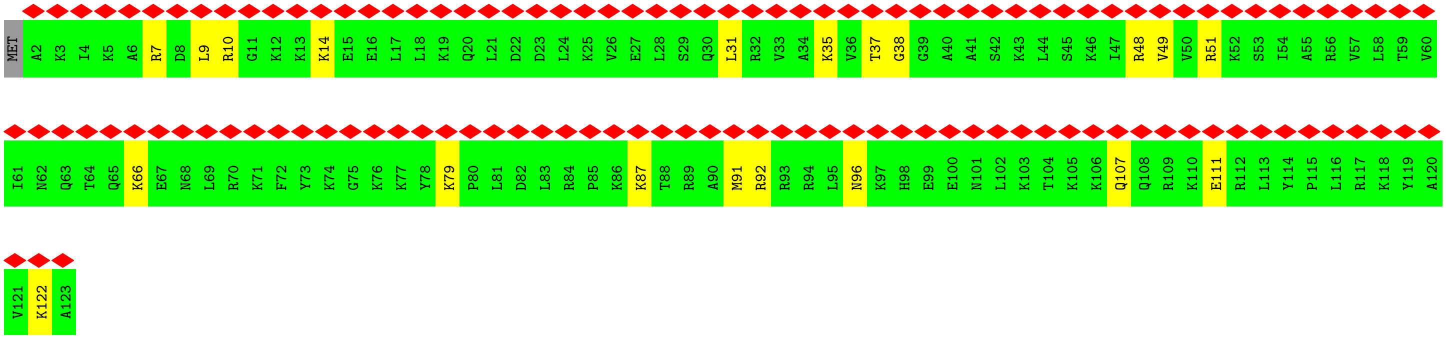




- Molecule 36: 60S ribosomal protein L35

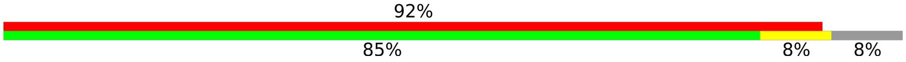
Chain Ah:

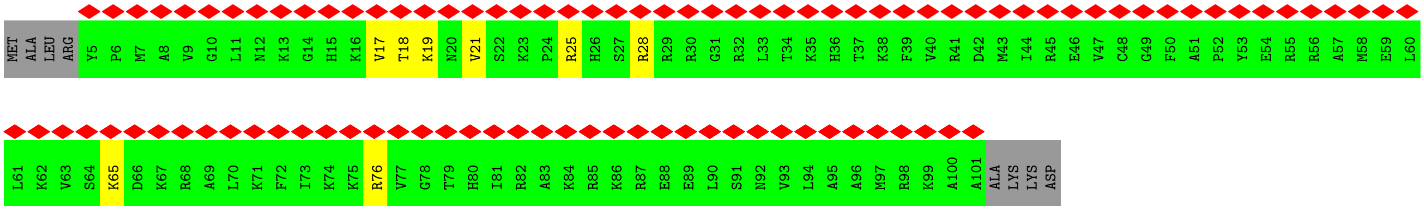




- Molecule 37: 60S ribosomal protein L36

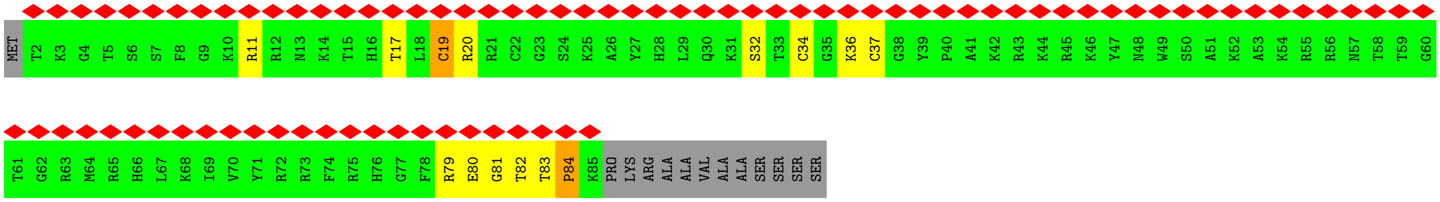
Chain Ai:





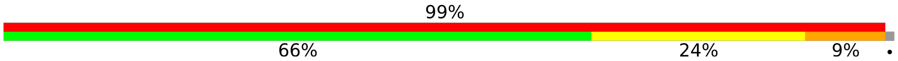
- Molecule 38: 60S ribosomal protein L37

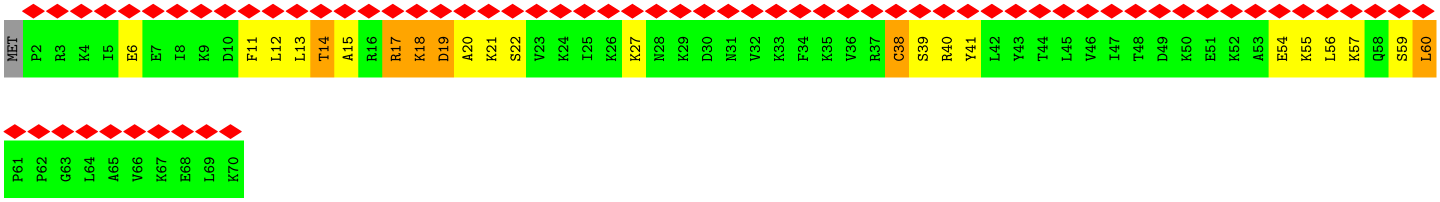
Chain Aj:



- Molecule 39: 60S ribosomal protein L38

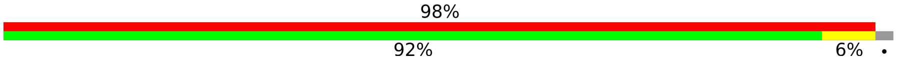
Chain Ak:

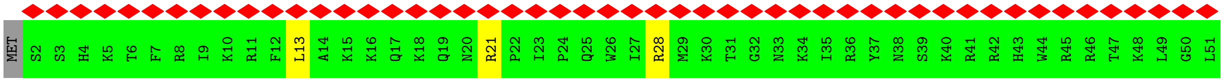




- Molecule 40: 60S ribosomal protein L39

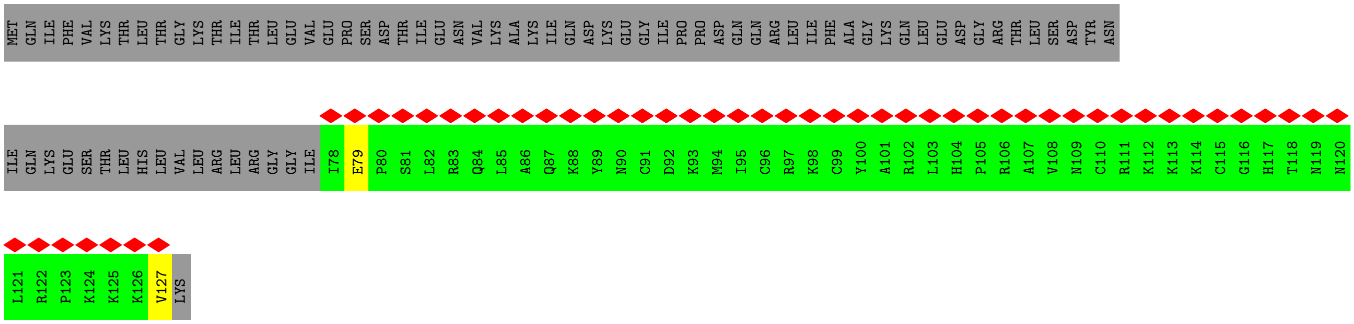
Chain Al:





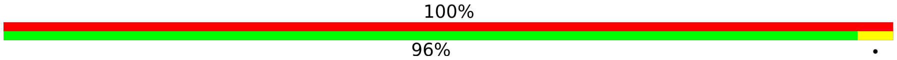
- Molecule 41: Ubiquitin-60S ribosomal protein L40

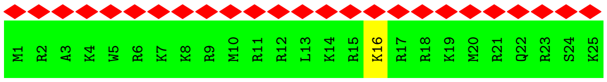
Chain Am:



- Molecule 42: 60S ribosomal protein L41

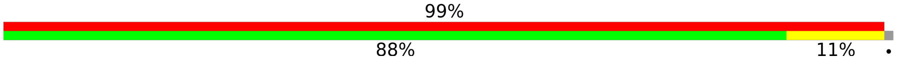
Chain An:

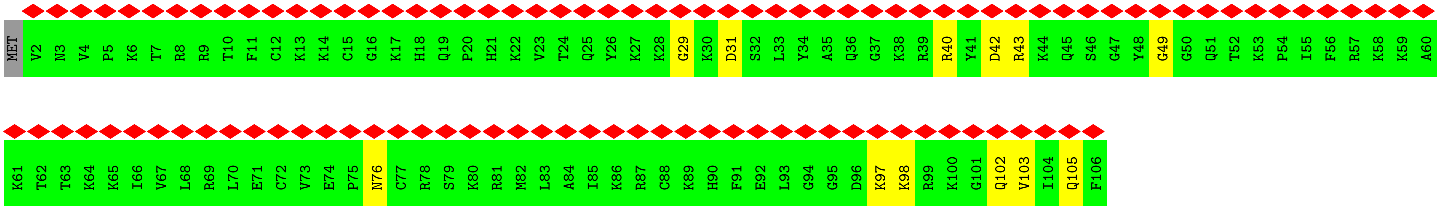




- Molecule 43: 60S ribosomal protein L36a

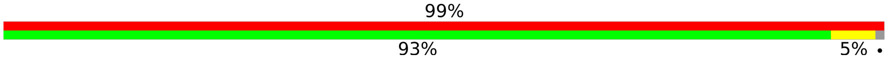
Chain Ao:

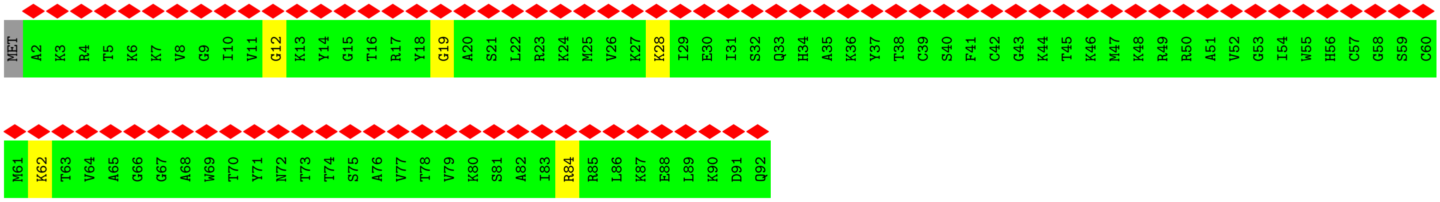




- Molecule 44: 60S ribosomal protein L37a

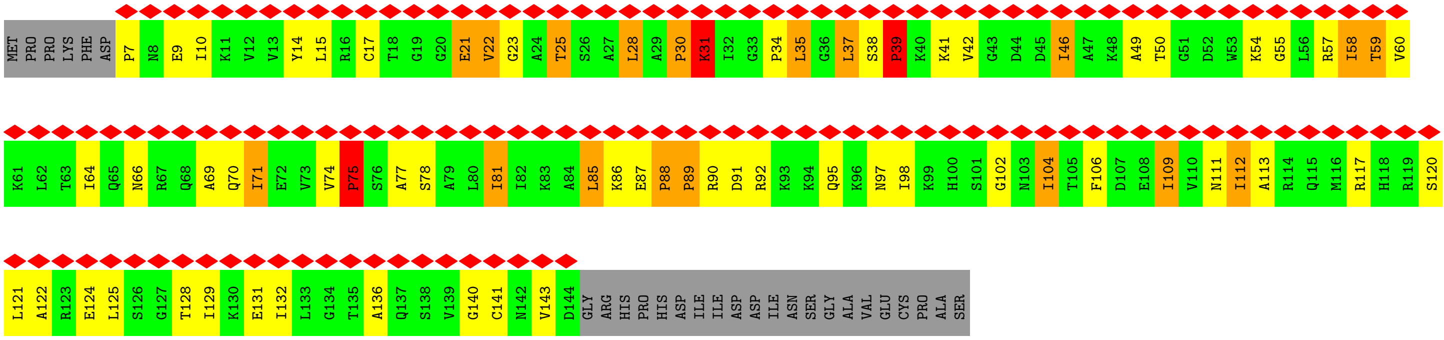
Chain Ap:





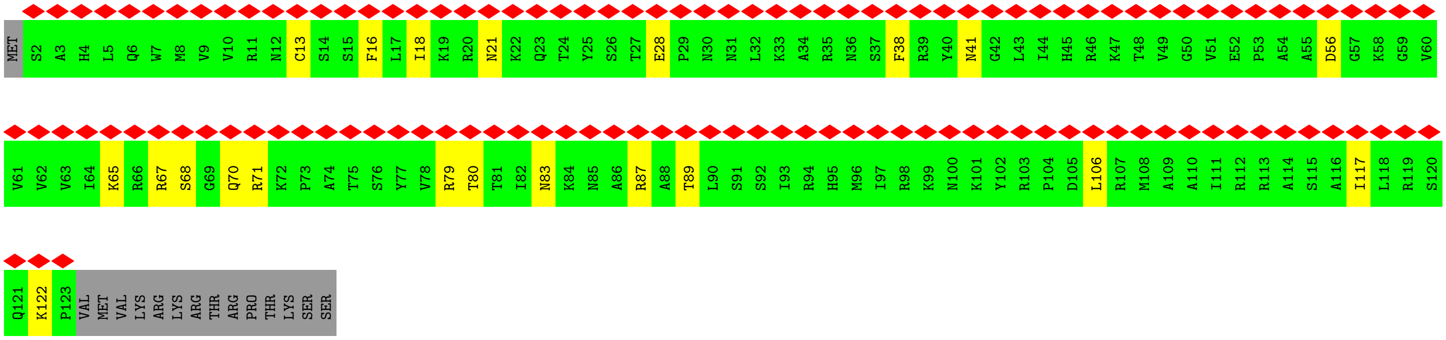
- Molecule 45: 60S ribosomal protein L12

Chain Aq:



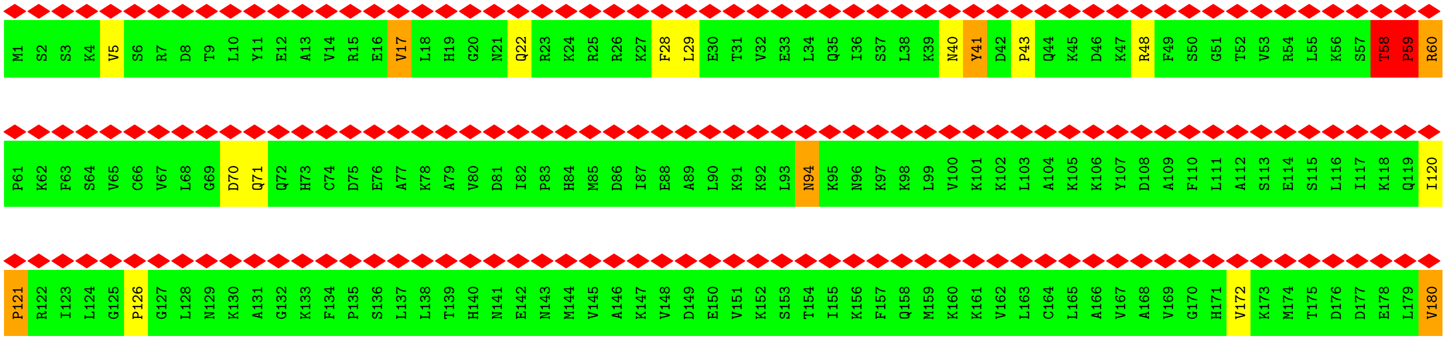
- Molecule 46: 60S ribosomal protein L28

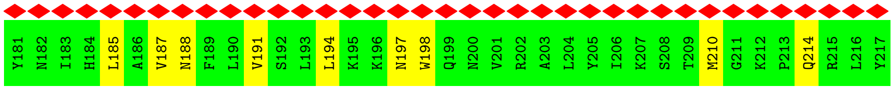
Chain At:



- Molecule 47: 60S ribosomal protein L10a

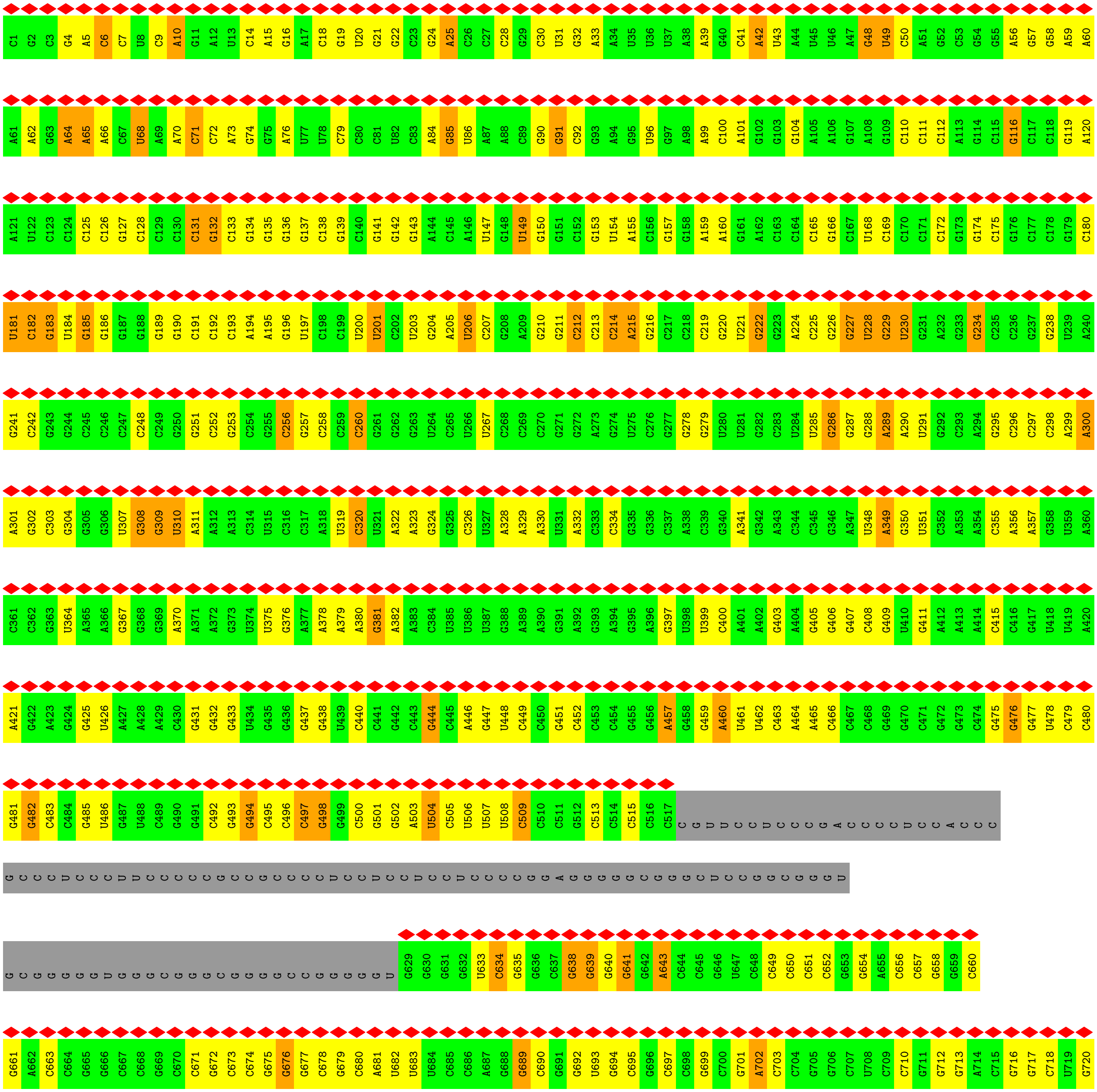
Chain Au:

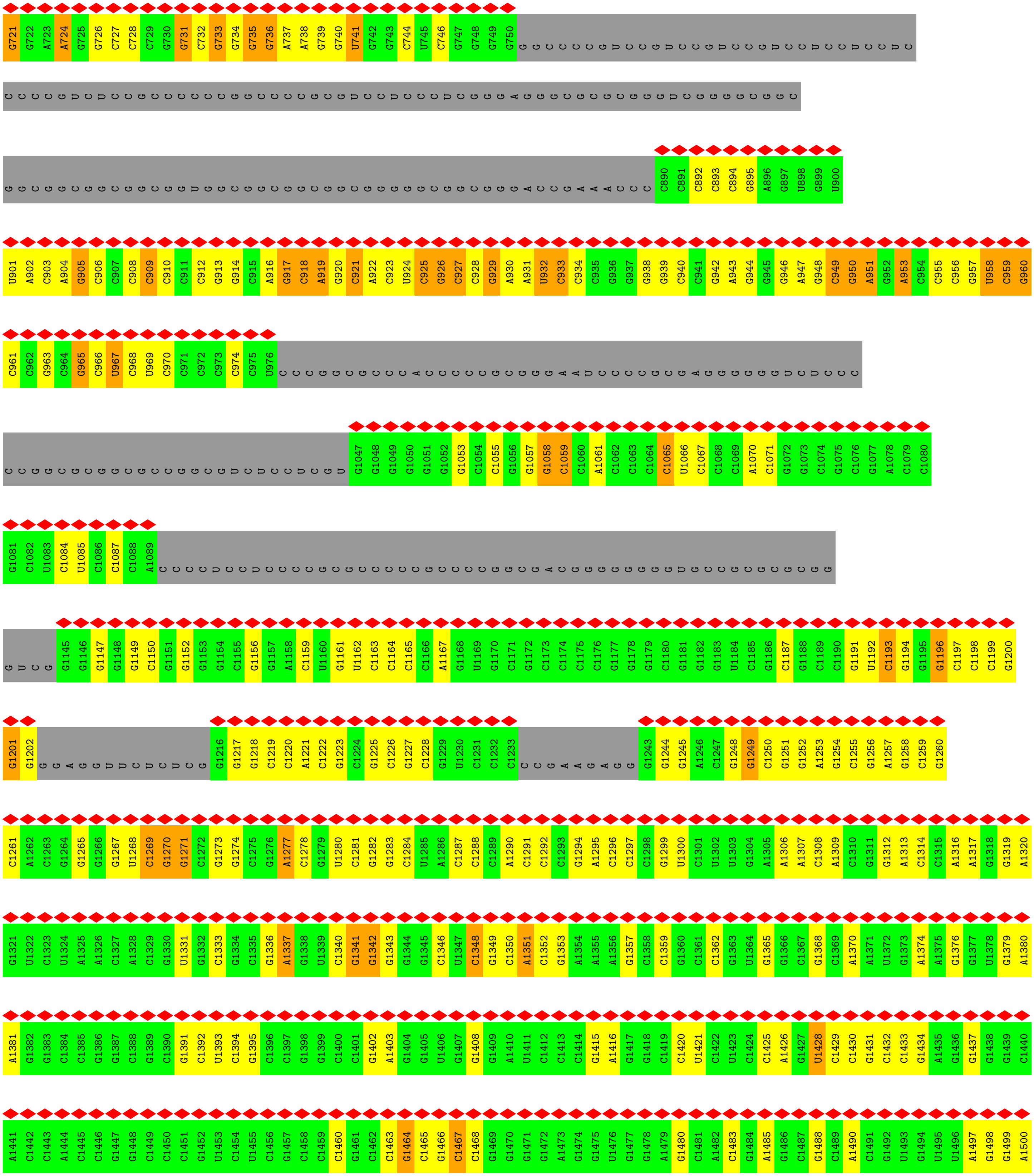


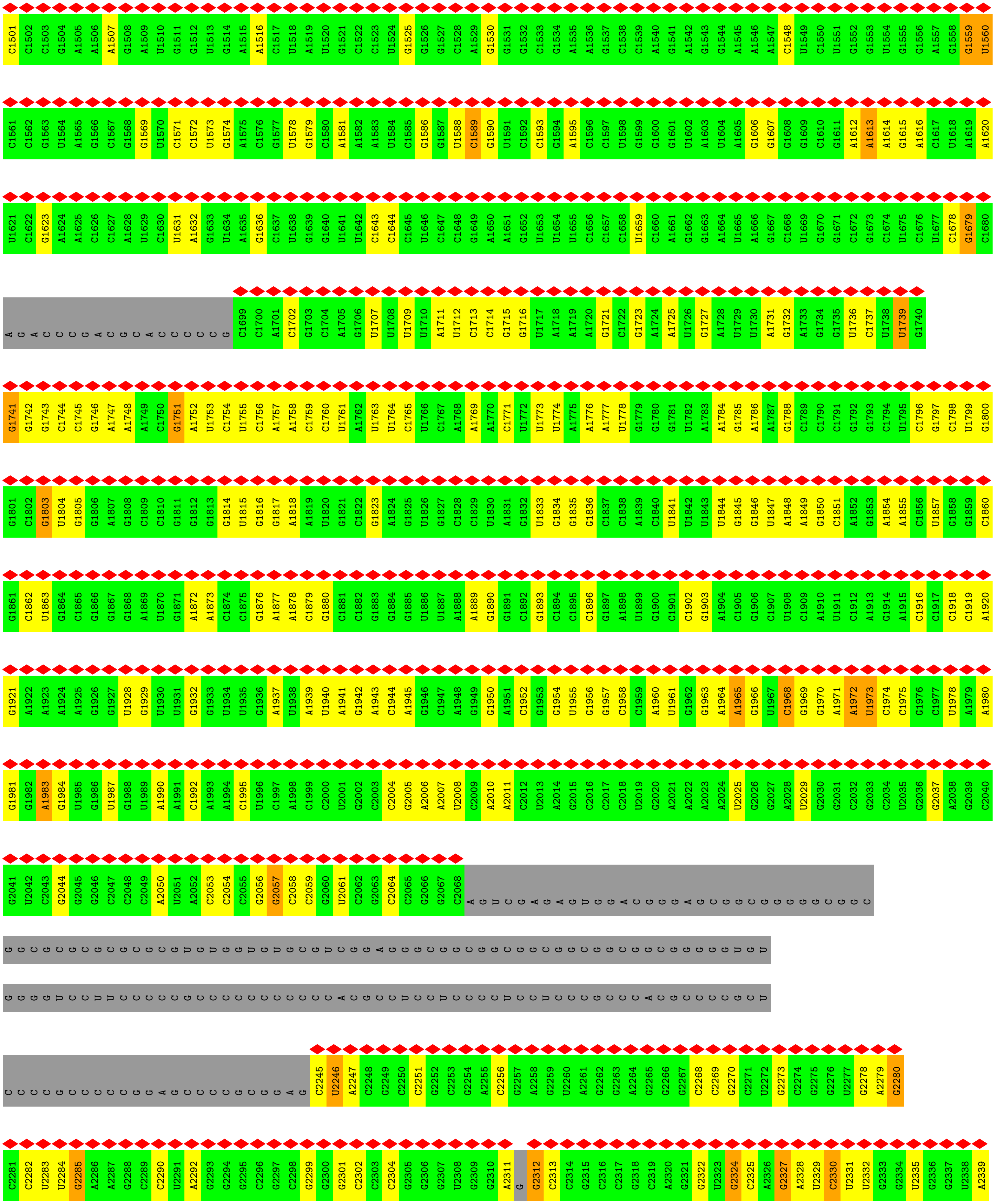


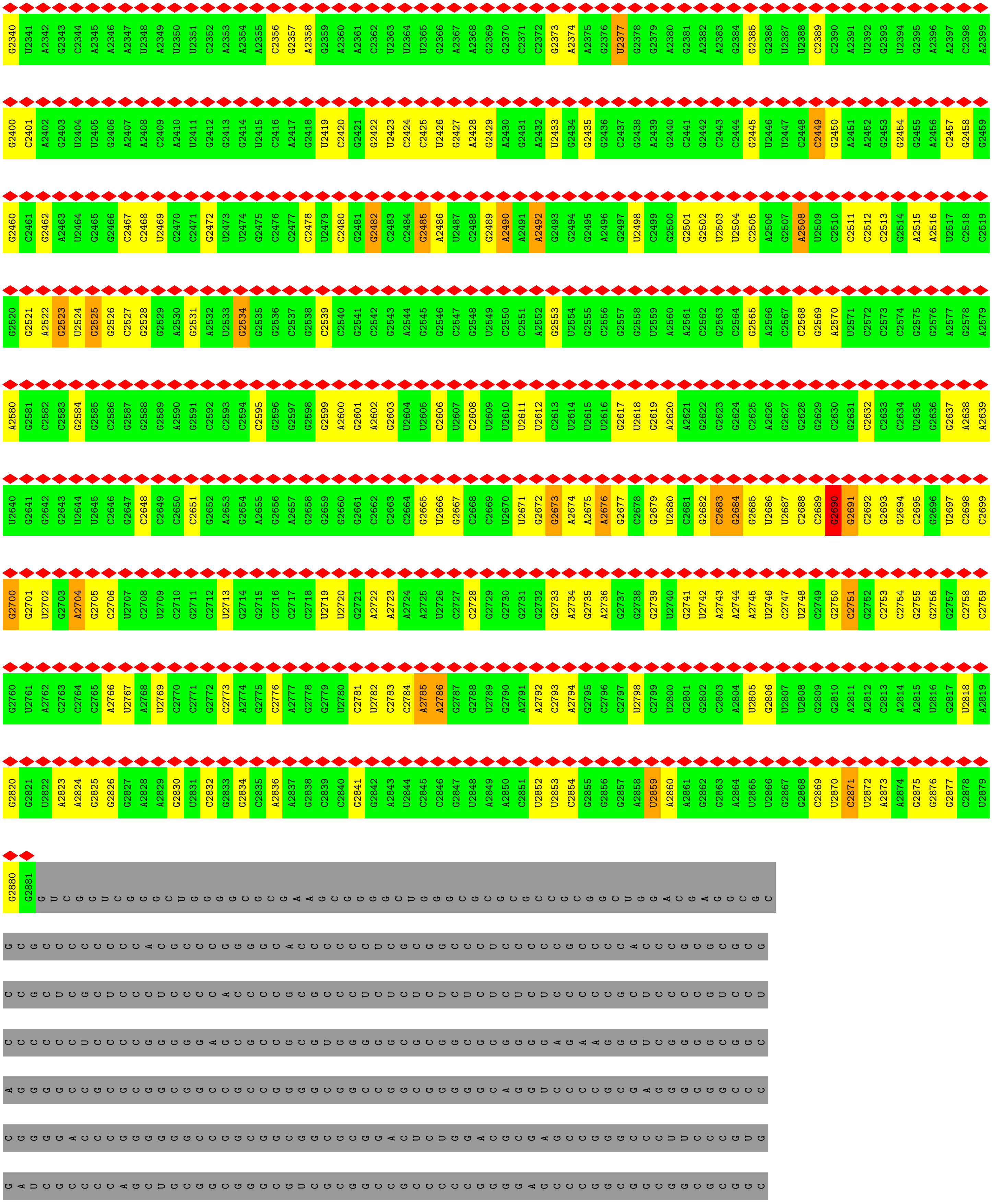
- Molecule 48: 28S ribosomal RNA

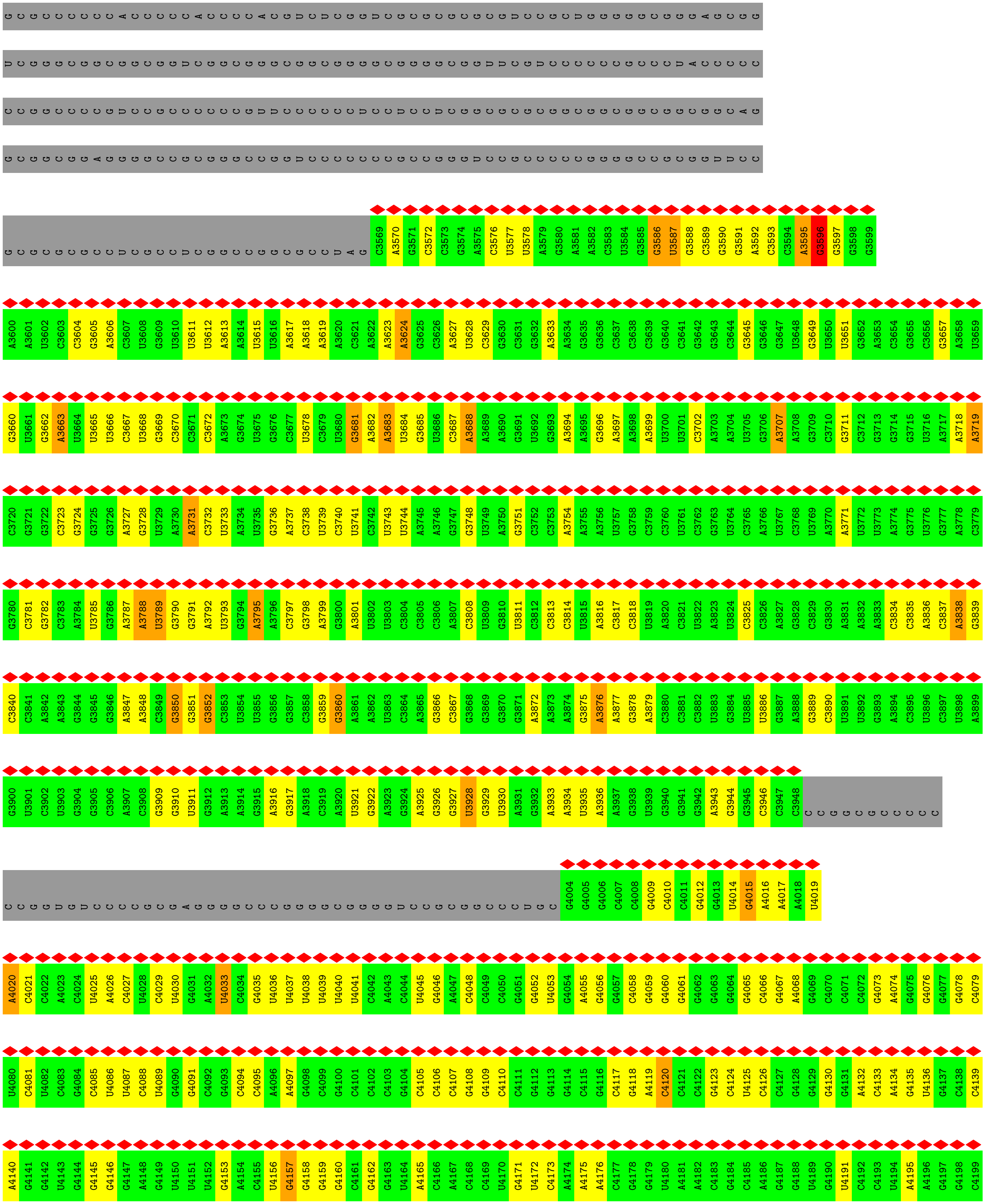
Chain A2:




G721 G722 A723 A724 G725 G726 C727 C728 C729 G730 G731 C732 G733 G734 G735 G736 A737 A738 G739 G740 U741 G742 G743 C744 U745 C746 G747 G748 G749 G750 G G C C C C G U C C G U C C G U C C G U C C U C C U C C U C
C C C C G U C U C C G C C C C C C G G C C C C G C G U C C U C C C U C G G G A G G G C G C G C G G G U C G G G G C G G C
G G C G G C G G C G G C G G U G G C G G C G G C G G C G G G G C G G C G G G A C C G A A A C C C C890 C891 C892 C893 C894 G895 A896 G897 U898 G899 U900
U901 A902 C903 A904 G905 C906 C907 C908 C909 C910 C911 C912 G913 G914 C915 A916 G917 C918 A919 G920 C921 A922 C923 U924 C925 G926 C927 C928 G929 A930 A931 U932 C933 C934 C935 G936 G937 G938 G939 C940 C941 G942 A943 G944 G945 G946 A947 G948 C949 G950 A951 G952 A953 C954 C955 C956 G957 U958 C959 G960
C961 C962 G963 C964 G965 C966 U967 C968 U969 C970 C971 C972 C973 C974 C975 U976 C C C G G C G C C C A C C C C C G C G G G A A U C C C C G C G A G G G G G G U C U C C C
C C G G C G C G G C G C C G G C G U C U C C U C G U G1047 G1048 G1049 G1050 G1051 G1052 G1053 C1054 C1055 G1056 G1057 G1058 C1059 C1060 A1061 C1062 C1063 C1064 C1065 U1066 C1067 C1068 G1069 A1070 C1071 G1072 G1073 C1074 G1075 C1076 G1077 A1078 C1079 C1080
G1081 C1082 U1083 C1084 U1085 C1086 C1087 C1088 A1089 C C C C U C C U C C C C G C G C C C C C G C C C C G G C G A C G G G G G G G G U G C C G C G C G C G G
G U C G G1145 G1146 G1147 G1148 G1149 C1150 G1151 G1152 G1153 G1154 C1155 G1156 G1157 A1158 C1159 U1160 C1161 U1162 C1163 C1164 C1165 C1166 A1167 G1168 U1169 G1170 C1171 G1172 C1173 C1174 C1175 C1176 G1177 G1178 G1179 C1180 G1181 G1182 G1183 U1184 C1185 G1186 C1187 G1188 C1189 C1190 G1191 U1192 C1193 G1194 G1195 G1196 C1197 C1198 C1199 G1200
G1201 G1202 G G A G G U U C U C U C G G1216 G1217 G1218 C1219 C1220 A1221 C1222 G1223 C1224 G1225 C1226 G1227 C1228 G1229 U1230 C1231 C1232 C1233 C C G A A G A G G G1243 G1244 G1245 A1246 C1247 G1248 G1249 C1250 G1251 G1252 A1253 G1254 C1255 G1256 A1257 G1258 C1259 G1260
C1261 A1262 C1263 G1264 G1265 G1266 G1267 U1268 C1269 G1270 G1271 C1272 G1273 G1274 C1275 G1276 A1277 C1278 G1279 U1280 C1281 G1282 G1283 C1284 U1285 A1286 C1287 C1288 C1289 A1290 C1291 C1292 C1293 G1294 A1295 C1296 C1297 C1298 G1299 U1300 C1301 U1302 U1303 G1304 A1305 A1306 A1307 C1308 A1309 C1310 G1311 G1312 A1313 C1314 C1315 A1316 A1317 G1318 G1319 A1320
G1321 U1322 C1323 U1324 A1325 A1326 C1327 A1328 C1329 C1330 U1331 G1332 C1333 G1334 C1335 G1336 A1337 G1338 U1339 C1340 G1341 G1342 G1343 G1344 G1345 C1346 U1347 C1348 G1349 C1350 A1351 C1352 G1353 A1354 A1355 A1356 G1357 C1358 C1359 G1360 C1361 C1362 G1363 U1364 G1365 G1366 C1367 G1368 C1369 A1370 A1371 U1372 G1373 A1374 A1375 G1376 G1377 U1378 G1379 A1380
A1381 G1382 G1383 C1384 C1385 G1386 G1387 C1388 G1389 C1390 G1391 C1392 U1393 C1394 G1395 C1396 C1397 G1398 G1399 C1400 C1401 G1402 A1403 G1404 G1405 U1406 G1407 G1408 G1409 A1410 U1411 C1412 C1413 C1414 G1415 A1416 G1417 G1418 C1419 C1420 U1421 C1422 U1423 C1424 C1425 A1426 G1427 U1428 C1429 C1430 G1431 C1432 C1433 C1434 A1435 G1436 G1437 G1438 G1439 C1440
A1441 C1442 C1443 A1444 C1445 C1446 G1447 G1448 C1449 C1450 C1451 G1452 U1453 C1454 U1455 C1456 G1457 C1458 C1459 C1460 G1461 C1462 C1463 G1464 C1465 G1466 C1467 C1468 G1469 G1470 G1471 G1472 A1473 G1474 G1475 U1476 G1477 G1478 A1479 G1480 C1481 A1482 C1483 G1484 A1485 G1486 C1487 G1488 C1489 A1490 C1491 G1492 U1493 G1494 U1495 U1496 A1497 G1498 G1499 A1500


C1501 G1502 C1503 G1504 A1505 A1506 A1507 G1508 A1509 U1510 G1511 G1512 U1513 G1514 A1515 A1516 C1517 U1518 A1519 U1520 G1521 C1522 C1523 U1524 G1525 G1526 G1527 C1528 A1529 G1530 G1531 C1532 C1533 G1534 A1535 A1536 G1537 C1538 G1539 A1540 C1541 A1542 G1543 G1544 A1545 A1546 A1547 C1548 U1549 C1550 U1551 G1552 G1553 U1554 G1555 G1556 A1557 G1558 G1559 U1560
C1561 C1562 G1563 U1564 A1565 G1566 C1567 G1568 G1569 U1570 C1571 C1572 U1573 G1574 A1575 C1576 G1577 U1578 G1579 C1580 A1581 A1582 A1583 U1584 C1585 G1586 G1587 U1588 C1589 G1590 U1591 C1592 C1593 G1594 A1595 C1596 C1597 U1598 G1599 G1600 G1601 U1602 A1603 U1604 A1605 G1606 G1607 G1608 G1609 C1610 G1611 A1612 A1613 A1614 G1615 A1616 C1617 U1618 A1619 A1620
U1621 C1622 G1623 A1624 A1625 C1626 C1627 A1628 U1629 C1630 U1631 A1632 G1633 U1634 A1635 G1636 C1637 U1638 G1639 G1640 U1641 U1642 C1643 C1644 C1645 U1646 C1647 C1648 G1649 A1650 A1651 G1652 U1653 U1654 U1655 C1656 C1657 C1658 U1659 C1660 A1661 G1662 G1663 A1664 U1665 A1666 G1667 C1668 U1669 G1670 G1671 G1672 G1673 C1674 U1675 C1676 U1677 C1678 G1679 C1680
A G A C C C G A C G C A C C C C C G C1699 C1700 A1701 C1702 G1703 C1704 A1705 G1706 U1707 U1708 U1709 U1710 A1711 U1712 C1713 C1714 G1715 G1716 U1717 A1718 A1719 A1720 G1721 C1722 G1723 A1724 A1725 U1726 G1727 A1728 U1729 U1730 A1731 G1732 A1733 G1734 G1735 U1736 C1737 U1738 U1739 G1740
G1741 G1742 G1743 C1744 C1745 G1746 A1747 A1748 A1749 C1750 G1751 A1752 U1753 C1754 U1755 C1756 A1757 A1758 C1759 C1760 U1761 A1762 U1763 U1764 C1765 U1766 C1767 A1768 A1769 A1770 C1771 U1772 U1773 U1774 A1775 A1776 A1777 U1778 G1779 G1780 G1781 U1782 A1783 A1784 G1785 A1786 A1787 G1788 C1789 C1790 G1791 G1792 G1793 C1794 U1795 C1796 G1797 C1798 U1799 G1800
G1801 C1802 G1803 U1804 G1805 G1806 A1807 G1808 C1809 C1810 G1811 G1812 G1813 G1814 U1815 G1816 G1817 A1818 A1819 U1820 G1821 C1822 G1823 A1824 G1825 U1826 G1827 C1828 C1829 U1830 A1831 G1832 U1833 G1834 G1835 G1836 C1837 C1838 A1839 C1840 U1841 U1842 U1843 U1844 G1845 G1846 U1847 A1848 A1849 G1850 C1851 A1852 G1853 A1854 A1855 C1856 U1857 G1858 G1859 C1860
G1861 C1862 U1863 G1864 C1865 G1866 G1867 G1868 A1869 U1870 G1871 A1872 A1873 C1874 C1875 G1876 A1877 A1878 C1879 G1880 C1881 C1882 G1883 G1884 G1885 U1886 U1887 A1888 A1889 G1890 G1891 C1892 G1893 C1894 C1895 C1896 G1897 A1898 U1899 G1900 C1901 C1902 G1903 A1904 G1905 G1906 C1907 U1908 C1909 A1910 U1911 C1912 A1913 G1914 A1915 C1916 C1917 C1918 C1919 A1920
G1921 A1922 A1923 A1924 A1925 G1926 G1927 U1928 G1929 U1930 U1931 G1932 G1933 U1934 U1935 G1936 A1937 U1938 A1939 U1940 A1941 G1942 A1943 C1944 A1945 G1946 C1947 A1948 G1949 G1950 A1951 C1952 G1953 G1954 U1955 G1956 G1957 C1958 C1959 A1960 U1961 G1962 G1963 A1964 A1965 G1966 U1967 C1968 G1969 G1970 A1971 A1972 U1973 C1974 C1975 G1976 C1977 U1978 A1979 A1980
G1981 G1982 A1983 G1984 U1985 G1986 U1987 G1988 U1989 A1990 A1991 C1992 A1993 A1994 C1995 U1996 C1997 A1998 C1999 C2000 U2001 G2002 C2003 C2004 G2005 A2006 A2007 U2008 C2009 A2010 A2011 C2012 U2013 A2014 G2015 C2016 C2017 C2018 U2019 G2020 A2021 A2022 A2023 A2024 U2025 G2026 G2027 A2028 U2029 G2030 G2031 C2032 G2033 C2034 U2035 G2036 G2037 A2038 G2039 C2040
G2041 U2042 C2043 G2044 G2045 G2046 C2047 G2048 C2049 A2050 U2051 A2052 C2053 C2054 C2055 G2056 G2057 C2058 C2059 G2060 U2061 C2062 G2063 C2064 C2065 G2066 G2067 C2068 A G U C G A G A G U G G A C G G G A G C G G C G G G G G C G G C
G G C G C G C G C G C G C G U G U G G U G U G C G U C G G A G G G C G G C G G C G G C G G C G G C G G C G G G G G U G U
G G G G U C C U U C C C C C G C C C C C C C C C C C A C G C C U C C U C C C C U C C U C C C G C C C A C G C C C C G C U
C C C C G C C C C C G G A G C C C C G C G G A G C2245 U2246 A2247 C2248 G2249 C2250 C2251 G2252 C2253 G2254 A2255 C2256 G2257 A2258 G2259 U2260 A2261 G2262 G2263 A2264 G2265 G2266 C2267 C2268 C2269 G2270 C2271 U2272 G2273 C2274 G2275 C2276 U2277 G2278 A2279 G2280
C2281 C2282 U2283 U2284 G2285 A2286 A2287 G2288 C2289 C2290 U2291 A2292 G2293 G2294 G2295 C2296 G2297 C2298 G2299 G2300 G2301 C2302 C2303 C2304 G2305 G2306 G2307 U2308 G2309 G2310 A2311 G G2312 C2313 C2314 G2315 C2316 C2317 G2318 C2319 A2320 G2321 G2322 U2323 G2324 C2325 A2326 G2327 A2328 U2329 C2330 U2331 U2332 G2333 G2334 U2335 G2336 G2337 U2338 A2339


G2340 U2341 A2342 G2343 C2344 A2345 A2346 A2347 U2348 A2349 U2350 U2351 C2352 A2353 A2354 A2355 C2356 G2357 A2358 G2359 A2360 A2361 C2362 U2363 U2364 U2365 G2366 A2367 A2368 G2369 G2370 C2371 C2372 G2373 A2374 A2375 G2376 U2377 G2378 G2379 A2380 G2381 A2382 A2383 G2384 G2385 G2386 U2387 U2388 C2389 G2390 A2391 U2392 G2393 U2394 G2395 A2396 A2397 C2398 A2399
G2400 C2401 A2402 G2403 U2404 U2405 G2406 A2407 A2408 C2409 A2410 U2411 G2412 G2413 A2414 U2415 C2416 A2417 G2418 U2419 C2420 G2421 G2422 U2423 C2424 C2425 U2426 G2427 A2428 G2429 A2430 G2431 A2432 U2433 G2434 G2435 G2436 C2437 G2438 A2439 G2440 C2441 G2442 C2443 G2444 G2445 U2446 U2447 C2448 C2449 G2450 A2451 A2452 G2453 G2454 U2455 A2456 C2457 G2458 G2459
G2460 C2461 G2462 A2463 U2464 G2465 G2466 C2467 C2468 U2469 C2470 C2471 G2472 U2473 U2474 G2475 C2476 C2477 C2478 U2479 C2480 G2481 G2482 C2483 C2484 G2485 A2486 U2487 C2488 G2489 A2490 A2491 A2492 G2493 G2494 G2495 A2496 G2497 U2498 C2499 G2500 G2501 G2502 U2503 U2504 C2505 A2506 G2507 A2508 U2509 C2510 C2511 G2512 C2513 G2514 A2515 A2516 U2517 C2518 C2519
G2520 G2521 A2522 G2523 U2524 G2525 G2526 C2527 G2528 G2529 A2530 G2531 A2532 U2533 G2534 G2535 G2536 C2537 G2538 C2539 C2540 G2541 C2542 G2543 A2544 G2545 G2546 C2547 G2548 U2549 C2550 C2551 A2552 G2553 U2554 G2555 C2556 G2557 G2558 U2559 A2560 A2561 C2562 G2563 G2564 G2565 A2566 C2567 C2568 G2569 A2570 U2571 C2572 G2573 C2574 G2575 G2576 A2577 G2578 A2579
A2580 G2581 C2582 C2583 G2584 G2585 C2586 G2587 G2588 G2589 A2590 G2591 C2592 C2593 C2594 C2595 G2596 G2597 G2598 G2599 A2600 G2601 A2602 G2603 U2604 U2605 C2606 U2607 C2608 U2609 U2610 U2611 U2612 C2613 U2614 U2615 U2616 G2617 U2618 G2619 A2620 A2621 G2622 G2623 G2624 C2625 A2626 G2627 G2628 G2629 C2630 G2631 C2632 C2633 C2634 U2635 G2636 G2637 A2638 A2639
U2640 G2641 G2642 G2643 U2644 U2645 C2646 G2647 C2648 C2649 C2650 C2651 G2652 A2653 G2654 A2655 G2656 A2657 G2658 G2659 G2660 G2661 C2662 C2663 C2664 G2665 U2666 G2667 C2668 C2669 U2670 U2671 G2672 G2673 A2674 A2675 A2676 G2677 C2678 G2679 U2680 C2681 G2682 C2683 G2684 G2685 U2686 U2687 C2688 C2689 G2690 G2691 C2692 G2693 G2694 C2695 G2696 U2697 C2698 C2699
G2700 G2701 U2702 G2703 A2704 G2705 C2706 U2707 C2708 U2709 C2710 G2711 C2712 U2713 G2714 G2715 C2716 C2717 C2718 U2719 U2720 G2721 A2722 A2723 A2724 A2725 U2726 C2727 C2728 G2729 G2730 G2731 G2732 G2733 A2734 G2735 A2736 G2737 G2738 G2739 U2740 G2741 U2742 A2743 A2744 A2745 U2746 C2747 U2748 C2749 G2750 C2751 G2752 C2753 C2754 G2755 G2756 G2757 C2758 C2759
G2760 U2761 A2762 C2763 C2764 C2765 A2766 U2767 A2768 U2769 C2770 C2771 G2772 C2773 A2774 G2775 C2776 A2777 G2778 G2779 U2780 C2781 U2782 C2783 C2784 A2785 A2786 G2787 G2788 U2789 G2790 A2791 A2792 C2793 A2794 G2795 C2796 C2797 U2798 C2799 U2800 G2801 G2802 C2803 A2804 U2805 G2806 U2807 U2808 G2809 G2810 A2811 A2812 C2813 A2814 A2815 U2816 G2817 U2818 A2819
G2820 G2821 U2822 A2823 A2824 G2825 G2826 G2827 A2828 A2829 G2830 U2831 C2832 G2833 G2834 C2835 A2836 A2837 G2838 G2839 C2840 G2841 G2842 A2843 U2844 C2845 C2846 G2847 U2848 A2849 A2850 C2851 U2852 U2853 C2854 G2855 G2856 G2857 A2858 U2859 A2860 A2861 G2862 G2863 A2864 U2865 U2866 G2867 G2868 C2869 U2870 C2871 U2872 A2873 A2874 G2875 G2876 G2877 C2878 U2879
G2880 G2881 G U C G G U C G G G C U G G G G C G C G A A G C G G G G C U G G G C G C G C G C C G C G G C U G G A C G A G G C G C
G C G C C C C C C C C A C G C C C G G G G C A C C C C C U C G C G G C C C U C C C C C G C C C C A C C C G C G C G C G
C C G C U C G C U C C C U C C C C A C C C C G C G C C C U C U C U C U C U C U C U C U C C C C C G C U C C C C G U C C U
C C C C C C U C C C C G G G G G A G C G C C G C G U G G G G G C G C G G C G G G G G A G A A G G G U C G G G G C G G C
A G G G G C C G C G C G G C G G C C G C C G G G G C G G C C G G C G G G G G C A G G U C C C C G C G A G G G G G G C C C
C G G G G A C C C G G G G G G C C G G C G G C G G C G C G G A C U C U G G A C G C G A G C C G G G C C C U U C C C G U G
G A U C G C C C C A G C U G C G G C G G G C G U C G C G G C C G C C C C C G G G G A G C C C G G C G G C G G C G C G G C



G C G C C C C C C A C C C C C A C C C C A C G U C U C G G U C G C G C G C G C G U C C G C U G G G G G C G G G A G C G G

U C G G G C G G C G G C G G U C G G C G G G C G G C G G G G C G G G G C G G U U C G U C C C C C C G C C C U A C C C C C

C C G G C C C C G U C C G C C C C C C G U U C C C C C C U C C U C C U C G G C G C G C G G C G G C G G C G G C G G C A G

G C G G C G G A G G G G C C G C G G G C C G G U C C C C C C C G C C G G G U C C G C C C C C G G G G C C G C G G U U C C

G C G C G C G C C U C G C C U C G G C C G G C G C C U A G C3569 A3570 G3571 C3572 C3573 G3574 A3575 C3576 U3577 U3578 A3579 G3580 A3581 A3582 C3583 U3584 G3585 G3586 U3587 G3588 C3589 G3590 G3591 A3592 C3593 C3594 A3595 G3596 G3597 G3598 G3599

A3600 A3601 U3602 C3603 C3604 G3605 A3606 C3607 U3608 G3609 U3610 U3611 U3612 A3613 A3614 U3615 U3616 A3617 A3618 A3619 A3620 C3621 A3622 A3623 A3624 G3625 C3626 A3627 U3628 C3629 G3630 C3631 G3632 A3633 A3634 G3635 G3636 C3637 C3638 C3639 G3640 C3641 G3642 G3643 C3644 G3645 G3646 G3647 U3648 G3649 U3650 U3651 G3652 A3653 C3654 G3655 C3656 G3657 A3658 U3659

G3660 U3661 G3662 A3663 U3664 U3665 U3666 C3667 U3668 G3669 C3670 C3671 C3672 A3673 G3674 U3675 G3676 C3677 U3678 G3679 U3680 G3681 A3682 A3683 U3684 G3685 U3686 C3687 A3688 A3689 A3690 G3691 U3692 G3693 A3694 G3695 G3696 A3697 A3698 A3699 U3700 U3701 C3702 A3703 A3704 U3705 G3706 A3707 A3708 G3709 C3710 G3711 C3712 G3713 G3714 G3715 U3716 A3717 A3718 A3719

C3720 G3721 G3722 C3723 G3724 G3725 G3726 A3727 G3728 U3729 A3730 A3731 C3732 U3733 A3734 U3735 G3736 A3737 G3738 U3739 C3740 U3741 G3742 U3743 U3744 A3745 A3746 G3747 G3748 U3749 A3750 G3751 C3752 G3753 A3754 A3755 A3756 U3757 G3758 C3759 C3760 U3761 C3762 G3763 U3764 C3765 A3766 U3767 C3768 U3769 A3770 A3771 U3772 U3773 A3774 G3775 U3776 G3777 A3778 C3779

G3780 C3781 G3782 C3783 A3784 U3785 G3786 A3787 A3788 U3789 G3790 G3791 A3792 U3793 G3794 A3795 A3796 C3797 G3798 A3799 G3800 A3801 U3802 U3803 C3804 C3805 C3806 A3807 C3808 U3809 G3810 U3811 C3812 C3813 C3814 U3815 A3816 C3817 C3818 U3819 A3820 C3821 U3822 A3823 U3824 C3825 C3826 A3827 G3828 C3829 G3830 A3831 A3832 A3833 C3834 C3835 A3836 C3837 A3838 G3839

C3840 C3841 A3842 A3843 G3844 G3845 G3846 A3847 A3848 C3849 G3850 G3851 G3852 C3853 U3854 U3855 G3856 G3857 C3858 G3859 G3860 A3861 A3862 U3863 C3864 A3865 G3866 C3867 G3868 G3869 G3870 G3871 A3872 A3873 A3874 G3875 A3876 A3877 G3878 A3879 C3880 C3881 C3882 U3883 G3884 U3885 U3886 G3887 A3888 G3889 C3890 U3891 U3892 G3893 A3894 C3895 U3896 C3897 U3898 A3899

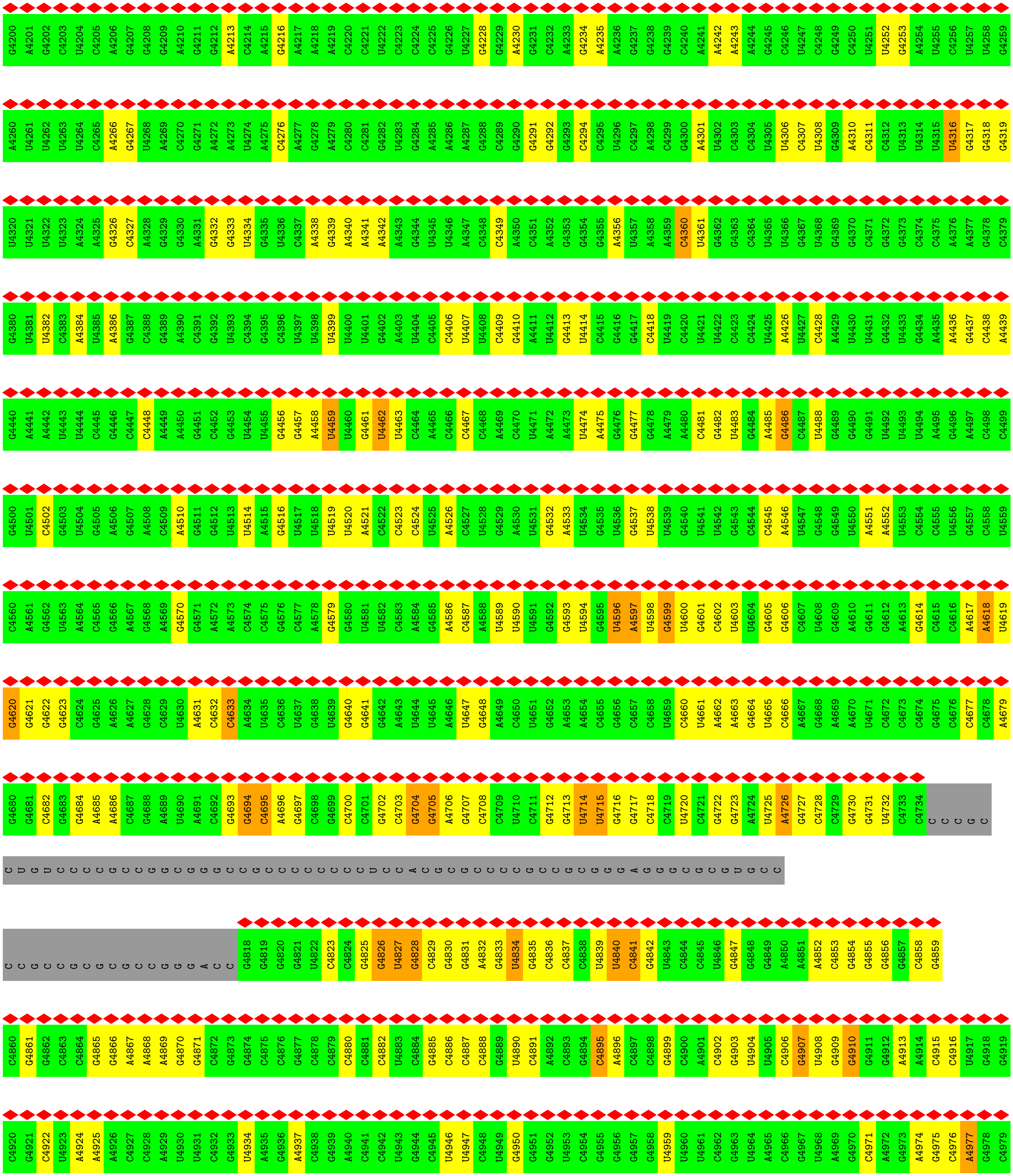
G3900 U3901 C3902 U3903 G3904 G3905 C3906 A3907 C3908 G3909 G3910 U3911 G3912 A3913 A3914 G3915 A3916 G3917 A3918 C3919 A3920 U3921 G3922 A3923 G3924 A3925 G3926 G3927 U3928 G3929 U3930 A3931 G3932 A3933 A3934 U3935 A3936 A3937 G3938 U3939 G3940 G3941 G3942 A3943 G3944 G3945 C3946 C3947 C3948 C C G G C G C C C C C

C C G G U G U C C C C G C G A G G G G C C C G G G G C G G G G U C C G C G G C C C U G C G4004 G4005 G4006 C4007 C4008 G4009 C4010 C4011 G4012 G4013 U4014 G4015 A4016 A4017 A4018 U4019

A4020 C4021 C4022 A4023 C4024 U4025 A4026 C4027 U4028 C4029 U4030 G4031 A4032 U4033 C4034 G4035 U4036 U4037 U4038 G4039 U4040 U4041 C4042 A4043 C4044 U4045 G4046 A4047 C4048 C4049 C4050 G4051 G4052 U4053 G4054 A4055 G4056 G4057 C4058 G4059 G4060 C4061 G4062 G4063 G4064 G4065 C4066 G4067 A4068 G4069 C4070 C4071 C4072 G4073 A4074 G4075 G4076 G4077 G4078 C4079

U4080 C4081 U4082 C4083 G4084 C4085 U4086 U4087 C4088 U4089 G4090 G4091 C4092 G4093 C4094 C4095 A4096 A4097 G4098 C4099 G4100 C4101 G4102 C4103 G4104 C4105 C4106 C4107 G4108 G4109 C4110 C4111 G4112 G4113 G4114 C4115 G4116 C4117 G4118 A4119 C4120 C4121 C4122 G4123 C4124 U4125 C4126 C4127 G4128 G4129 G4130 G4131 A4132 C4133 A4134 G4135 U4136 G4137 C4138 C4139

A4140 G4141 G4142 U4143 G4144 G4145 G4146 G4147 A4148 G4149 U4150 U4151 U4152 G4153 A4154 C4155 U4156 G4157 G4158 G4159 G4160 C4161 G4162 G4163 U4164 A4165 C4166 A4167 C4168 C4169 U4170 G4171 U4172 C4173 A4174 A4175 A4176 C4177 G4178 G4179 U4180 A4181 A4182 C4183 G4184 C4185 A4186 G4187 G4188 U4189 G4190 U4191 C4192 G4193 U4194 A4195 A4196 G4197 G4198 C4199



G4200 A4201 G4202 C4203 U4204 C4205 A4206 G4207 G4208 G4209 A4210 G4211 G4212 A4213 C4214 A4215 G4216 A4217 A4218 A4219 C4220 C4221 U4222 C4223 A4224 C4225 C4226 U4227 G4228 G4229 A4230 G4231 C4232 A4233 G4234 A4235 G4236 G4237 G4238 G4239 C4240 A4241 A4242 A4243 A4244 G4245 C4246 U4247 C4248 G4249 C4250 U4251 U4252 G4253 A4254 U4255 C4256 U4257 U4258 G4259

A4260 U4261 U4262 U4263 U4264 C4265 A4266 G4267 U4268 A4269 C4270 G4271 A4272 A4273 U4274 A4275 C4276 A4277 G4278 A4279 C4280 C4281 G4282 U4283 G4284 A4285 A4286 A4287 G4288 C4289 G4290 G4291 G4292 G4293 C4294 C4295 U4296 C4297 A4298 C4299 G4300 A4301 U4302 C4303 C4304 U4305 U4306 C4307 U4308 G4309 A4310 C4311 C4312 U4313 U4314 U4315 U4316 G4317 G4318 G4319

U4320 U4321 U4322 U4323 A4324 A4325 G4326 C4327 A4328 G4329 G4330 A4331 G4332 G4333 U4334 G4335 U4336 C4337 A4338 G4339 A4340 A4341 A4342 A4343 G4344 U4345 U4346 A4347 C4348 C4349 A4350 C4351 A4352 G4353 G4354 G4355 A4356 U4357 A4358 A4359 C4360 U4361 G4362 G4363 C4364 U4365 U4366 G4367 U4368 G4369 C4370 C4371 G4372 G4373 C4374 C4375 A4376 A4377 G4378 C4379

G4380 U4381 U4382 C4383 A4384 U4385 A4386 G4387 C4388 G4389 A4390 C4391 G4392 U4393 C4394 G4395 C4396 U4397 U4398 U4399 U4400 U4401 G4402 A4403 U4404 C4405 C4406 U4407 U4408 C4409 G4410 A4411 U4412 G4413 U4414 C4415 G4416 G4417 C4418 U4419 C4420 U4421 U4422 C4423 C4424 U4425 A4426 U4427 C4428 A4429 U4430 U4431 G4432 U4433 G4434 A4435 A4436 G4437 C4438 A4439

G4440 A4441 A4442 U4443 U4444 C4445 G4446 C4447 C4448 A4449 A4450 G4451 C4452 G4453 U4454 U4455 G4456 G4457 A4458 U4459 U4460 G4461 U4462 U4463 C4464 A4465 C4466 C4467 G4468 A4469 C4470 U4471 A4472 A4473 U4474 A4475 G4476 G4477 G4478 A4479 A4480 C4481 G4482 U4483 G4484 A4485 G4486 C4487 U4488 G4489 G4490 G4491 G4492 U4493 U4494 A4495 G4496 A4497 C4498 C4499

G4500 U4501 C4502 G4503 U4504 G4505 A4506 G4507 A4508 C4509 A4510 G4511 G4512 U4513 U4514 A4515 G4516 U4517 U4518 U4519 U4520 A4521 C4522 C4523 C4524 U4525 A4526 C4527 U4528 G4529 A4530 U4531 G4532 A4533 U4534 G4535 U4536 G4537 U4538 U4539 G4540 U4541 U4542 G4543 C4544 C4545 A4546 U4547 G4548 G4549 U4550 A4551 A4552 U4553 C4554 C4555 U4556 G4557 C4558 U4559

C4560 A4561 G4562 U4563 A4564 C4565 G4566 A4567 G4568 A4569 G4570 G4571 A4572 A4573 C4574 C4575 G4576 C4577 A4578 G4579 G4580 U4581 U4582 C4583 A4584 G4585 A4586 C4587 A4588 U4589 U4590 U4591 G4592 G4593 U4594 G4595 U4596 A4597 U4598 G4599 U4600 G4601 C4602 U4603 U4604 G4605 G4606 C4607 U4608 G4609 A4610 G4611 G4612 A4613 G4614 C4615 C4616 A4617 A4618 U4619

G4620 G4621 G4622 G4623 C4624 G4625 A4626 A4627 G4628 G4629 U4630 A4631 C4632 C4633 A4634 U4635 C4636 U4637 G4638 U4639 G4640 G4641 G4642 A4643 U4644 U4645 A4646 U4647 G4648 A4649 C4650 U4651 G4652 A4653 A4654 C4655 G4656 C4657 G4658 U4659 C4660 U4661 A4662 G4663 G4664 U4665 C4666 A4667 G4668 A4669 A4670 U4671 C4672 G4673 C4674 G4675 C4676 C4677 G4678 A4679

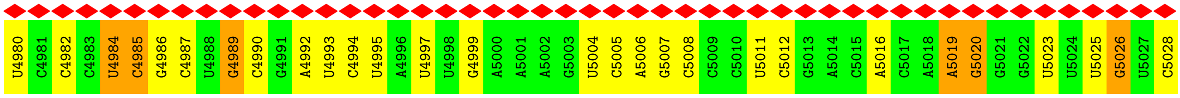
G4680 G4681 C4682 G4683 G4684 A4685 A4686 C4687 G4688 A4689 U4690 A4691 C4692 G4693 G4694 C4695 A4696 G4697 G4698 G4699 C4700 C4701 G4702 C4703 G4704 G4705 A4706 G4707 C4708 C4709 U4710 C4711 G4712 G4713 U4714 U4715 G4716 G4717 C4718 C4719 U4720 C4721 G4722 G4723 A4724 U4725 A4726 G4727 C4728 C4729 G4730 G4731 U4732 C4733 C4734 C C C G C

C U G U C C C C G C C G G C G G G G C C G C C C C C C C U C C A C G C G C C C C G C C G C G G G A G G C G C G U G C C

C C G C C G C G C G C C G G A C C G4818 G4819 G4820 G4821 U4822 C4823 C4824 G4825 G4826 U4827 G4828 C4829 G4830 C4831 A4832 G4833 U4834 G4835 C4836 C4837 C4838 U4839 U4840 C4841 G4842 U4843 C4844 C4845 U4846 G4847 G4848 G4849 A4850 A4851 A4852 C4853 G4854 G4855 G4856 G4857 C4858 G4859

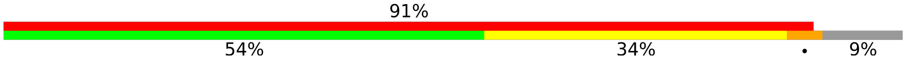
C4860 G4861 G4862 C4863 C4864 G4865 G4866 A4867 A4868 A4869 G4870 G4871 C4872 G4873 G4874 C4875 C4876 G4877 C4878 C4879 C4880 C4881 C4882 U4883 C4884 G4885 C4886 C4887 G4888 G4889 U4890 C4891 A4892 C4893 G4894 C4895 A4896 C4897 G4898 G4899 C4900 A4901 C4902 G4903 U4904 U4905 C4906 G4907 U4908 G4909 G4910 G4911 G4912 A4913 A4914 C4915 C4916 U4917 G4918 G4919

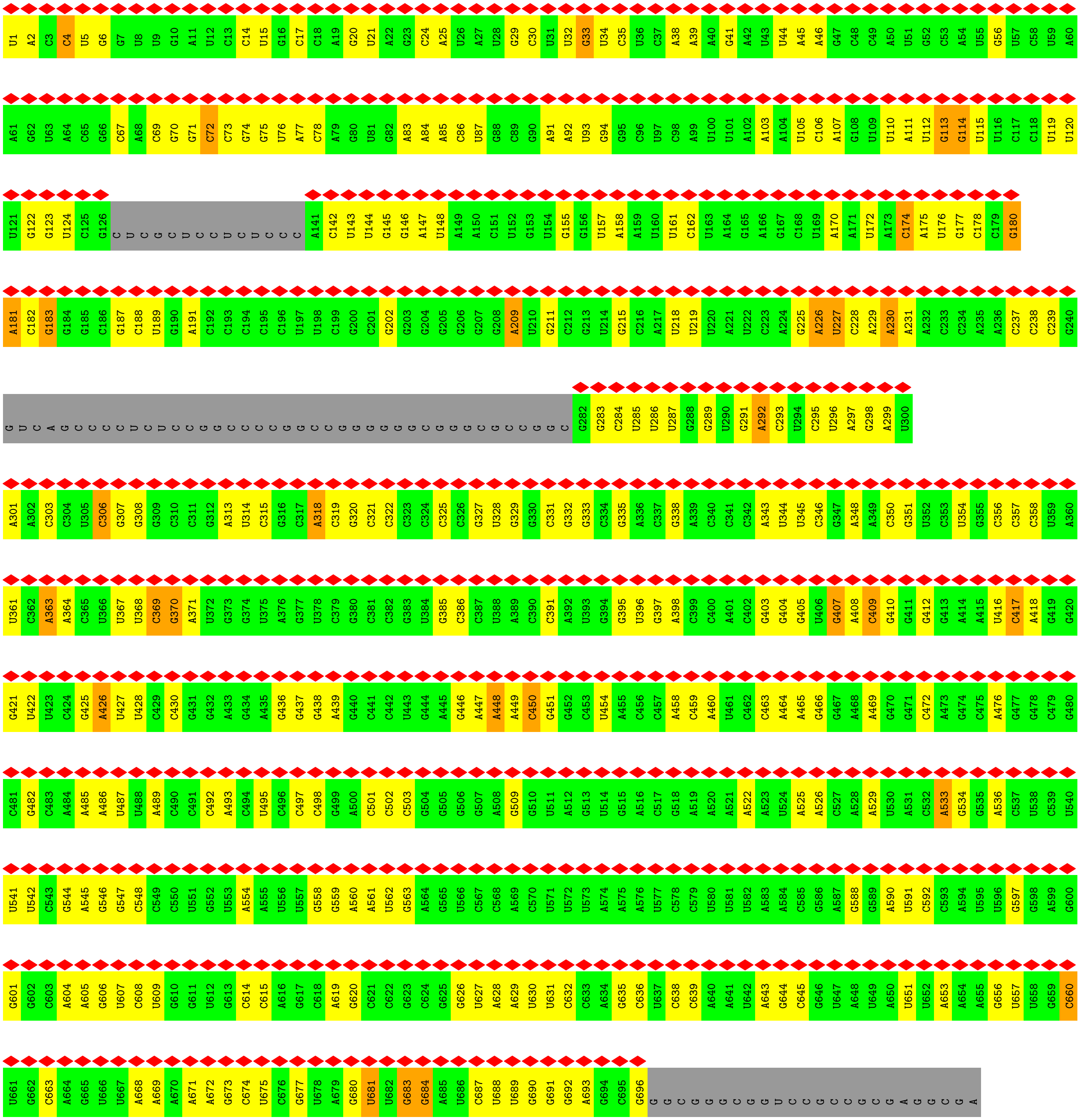
C4920 G4921 C4922 U4923 A4924 A4925 A4926 C4927 C4928 A4929 G4930 U4931 C4932 G4933 U4934 A4935 G4936 A4937 C4938 G4939 A4940 C4941 C4942 U4943 G4944 C4945 U4946 U4947 C4948 U4949 G4950 G4951 G4952 U4953 C4954 G4955 G4956 G4957 G4958 U4959 U4960 U4961 C4962 G4963 U4964 A4965 C4966 G4967 U4968 A4969 G4970 C4971 A4972 G4973 A4974 G4975 C4976 A4977 G4978 C4979

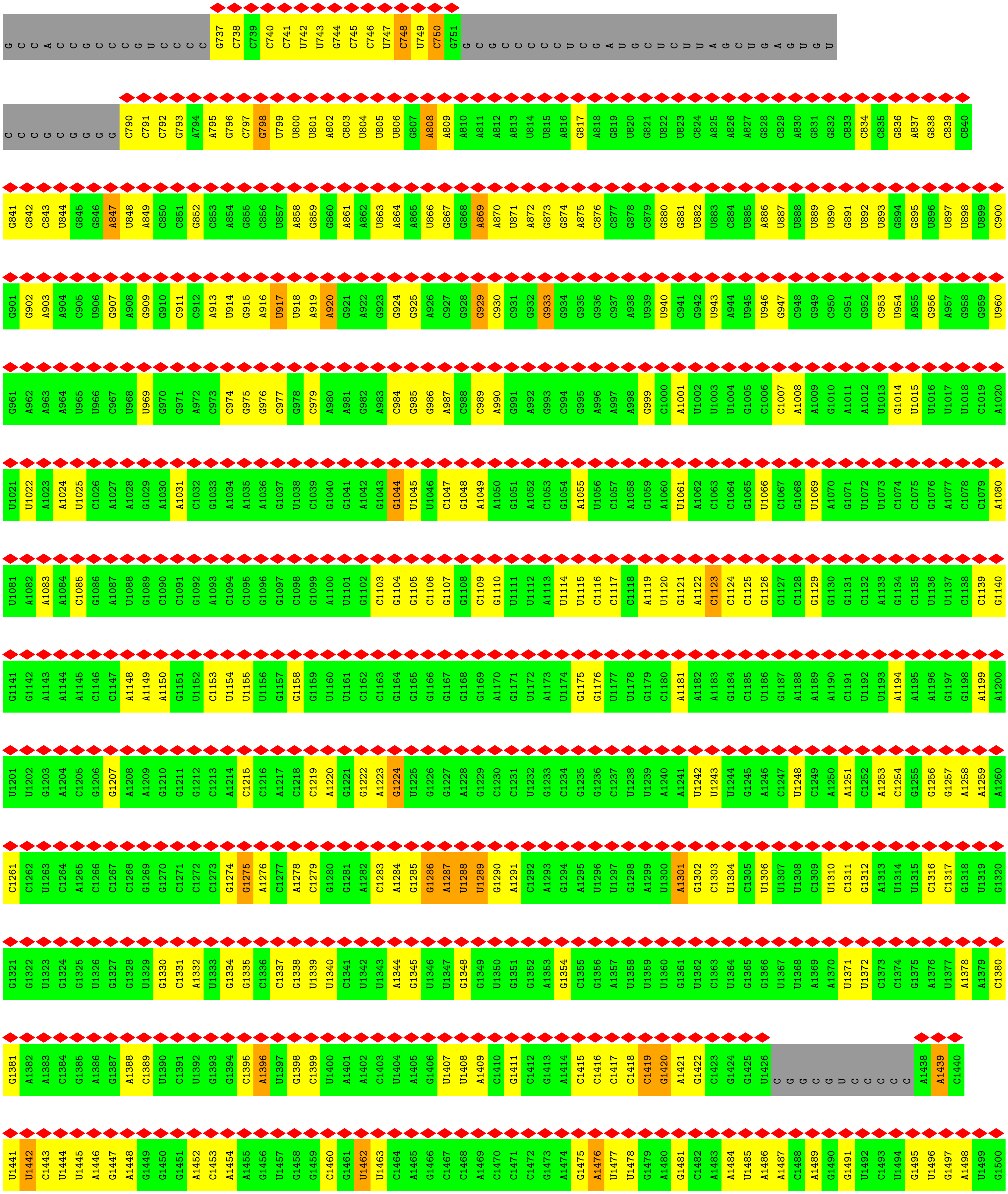


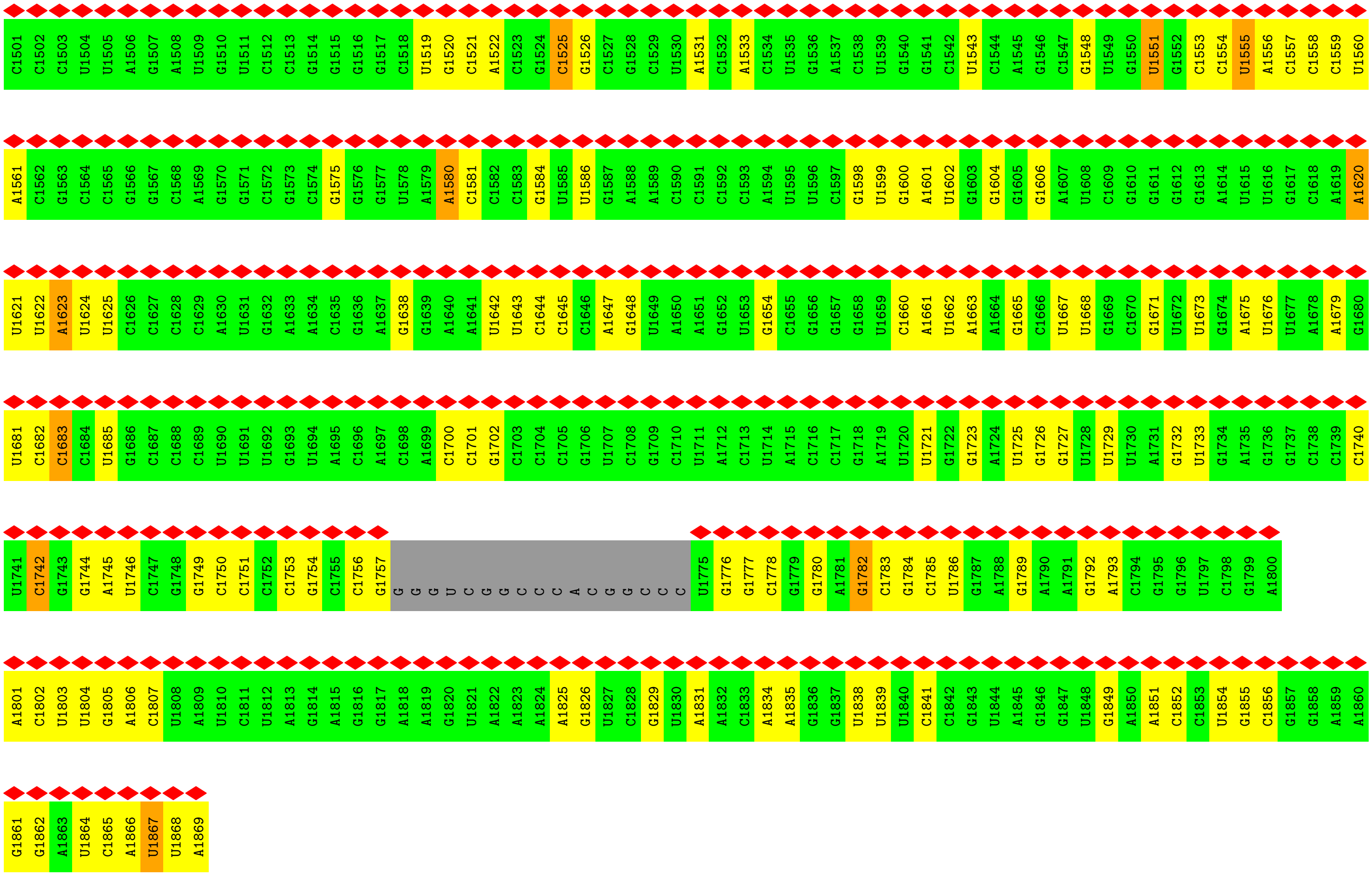
- Molecule 49: 18S ribosomal RNA

Chain B1:






G C C A C C G C C C G U C C C C G737 C738 C739 C740 C741 U742 U743 G744 C745 C746 U747 C748 U749 C750 G751 G C G C C C C C U C G A U G C U C U U A G C U G A G U G U
C C C G C G G G G C790 C791 C792 G793 A794 A795 G796 C797 G798 U799 U800 U801 A802 C803 U804 U805 U806 G807 A808 A809 A810 A811 A812 A813 U814 U815 A816 G817 A818 G819 U820 G821 U822 U823 C824 A825 A826 A827 G828 C829 A830 G831 G832 C833 C834 C835 G836 A837 G838 C839 C840
G841 C842 C843 U844 G845 G846 A847 U848 A849 C850 C851 G852 C853 A854 G855 C856 U857 A858 G859 G860 A861 A862 U863 A864 A865 U866 G867 G868 A869 A870 U871 A872 G873 G874 A875 C876 C877 G878 C879 G880 G881 U882 U883 C884 U885 A886 U887 U888 U889 U890 G891 U892 U893 G894 G895 U896 U897 U898 U899 C900
G901 G902 A903 A904 C905 U906 G907 A908 G909 G910 C911 C912 A913 U914 G915 A916 U917 U918 A919 A920 G921 A922 G923 G924 G925 A926 C927 G928 G929 C930 C931 G932 G933 G934 G935 G936 C937 A938 U939 U940 C941 G942 U943 A944 U945 U946 G947 C948 G949 C950 C951 G952 C953 U954 A955 G956 A957 G958 G959 U960
G961 A962 A963 A964 U965 U966 C967 U968 U969 G970 G971 A972 C973 C974 G975 G976 C977 G978 C979 A980 A981 G982 A983 C984 G985 G986 A987 C988 C989 A990 G991 A992 G993 C994 G995 A996 A997 A998 G999 C1000 A1001 U1002 U1003 U1004 G1005 C1006 C1007 A1008 A1009 G1010 A1011 A1012 U1013 G1014 U1015 U1016 U1017 U1018 C1019 A1020
U1021 U1022 A1023 A1024 U1025 C1026 A1027 A1028 G1029 A1030 A1031 C1032 G1033 A1034 A1035 A1036 G1037 U1038 C1039 G1040 G1041 A1042 G1043 G1044 U1045 U1046 C1047 G1048 A1049 A1050 G1051 A1052 C1053 G1054 A1055 U1056 C1057 A1058 G1059 A1060 U1061 A1062 C1063 C1064 G1065 U1066 C1067 G1068 U1069 A1070 G1071 U1072 U1073 C1074 C1075 G1076 A1077 C1078 C1079 A1080
U1081 A1082 A1083 A1084 C1085 G1086 A1087 U1088 G1089 C1090 C1091 G1092 A1093 C1094 C1095 G1096 G1097 C1098 G1099 A1100 U1101 G1102 C1103 G1104 G1105 C1106 G1107 G1108 C1109 G1110 U1111 U1112 A1113 U1114 U1115 C1116 C1117 C1118 A1119 U1120 G1121 A1122 C1123 C1124 C1125 G1126 C1127 C1128 G1129 G1130 G1131 C1132 A1133 G1134 C1135 U1136 U1137 G1138 C1139 G1140
G1141 G1142 A1143 A1144 A1145 C1146 C1147 A1148 A1149 A1150 G1151 U1152 C1153 U1154 U1155 U1156 G1157 G1158 G1159 U1160 U1161 C1162 C1163 G1164 G1165 G1166 G1167 G1168 G1169 A1170 G1171 U1172 A1173 U1174 G1175 G1176 U1177 U1178 G1179 C1180 A1181 A1182 A1183 G1184 C1185 U1186 G1187 A1188 A1189 A1190 C1191 U1192 U1193 A1194 A1195 A1196 G1197 G1198 A1199 A1200
U1201 U1202 G1203 A1204 C1205 G1206 G1207 A1208 A1209 G1210 G1211 G1212 C1213 A1214 C1215 C1216 A1217 C1218 C1219 A1220 G1221 G1222 A1223 G1224 U1225 G1226 G1227 A1228 G1229 C1230 C1231 U1232 G1233 C1234 G1235 G1236 C1237 U1238 U1239 A1240 A1241 U1242 U1243 U1244 G1245 A1246 C1247 U1248 C1249 A1250 A1251 C1252 A1253 C1254 G1255 G1256 G1257 A1258 A1259 A1260
C1261 C1262 U1263 C1264 A1265 C1266 C1267 C1268 G1269 G1270 C1271 C1272 C1273 G1274 G1275 A1276 C1277 A1278 C1279 G1280 G1281 A1282 C1283 A1284 G1285 G1286 A1287 U1288 U1289 G1290 A1291 C1292 A1293 G1294 A1295 U1296 U1297 G1298 A1299 U1300 A1301 G1302 C1303 U1304 C1305 U1306 U1307 U1308 C1309 U1310 C1311 G1312 A1313 U1314 U1315 C1316 C1317 G1318 U1319 G1320
G1321 G1322 U1323 G1324 G1325 U1326 G1327 G1328 U1329 G1330 C1331 A1332 U1333 G1334 G1335 C1336 C1337 G1338 U1339 C1340 C1341 U1342 U1343 A1344 G1345 U1346 U1347 C1348 G1349 U1350 G1351 G1352 A1353 G1354 C1355 G1356 A1357 U1358 U1359 C1360 G1361 U1362 C1363 U1364 G1365 G1366 U1367 U1368 A1369 A1370 U1371 U1372 C1373 C1374 G1375 A1376 U1377 A1378 A1379 C1380
G1381 A1382 A1383 C1384 G1385 A1386 G1387 A1388 C1389 U1390 C1391 U1392 G1393 G1394 C1395 A1396 U1397 G1398 C1399 U1400 A1401 A1402 C1403 U1404 A1405 G1406 U1407 U1408 A1409 C1410 G1411 C1412 G1413 A1414 C1415 C1416 C1417 C1418 C1419 G1420 A1421 G1422 C1423 G1424 G1425 U1426 C G G C G U C C C C C A1438 A1439 C1440
U1441 U1442 C1443 U1444 U1445 A1446 G1447 A1448 G1449 G1450 G1451 A1452 C1453 A1454 A1455 G1456 U1457 G1458 G1459 C1460 G1461 U1462 U1463 C1464 A1465 G1466 C1467 C1468 A1469 C1470 C1471 G1472 G1473 A1474 G1475 A1476 U1477 U1478 G1479 A1480 G1481 C1482 A1483 A1484 U1485 A1486 A1487 C1488 A1489 G1490 G1491 U1492 C1493 U1494 G1495 U1496 G1497 A1498 U1499 G1500



C1501 C1502 C1503 U1504 U1505 A1506 G1507 A1508 U1509 G1510 U1511 C1512 C1513 G1514 G1515 G1516 G1517 C1518 U1519 G1520 C1521 A1522 C1523 G1524 C1525 G1526 C1527 C1528 G1529 U1530 A1531 C1532 A1533 C1534 U1535 G1536 A1537 C1538 U1539 G1540 C1541 C1542 U1543 C1544 A1545 G1546 C1547 G1548 U1549 G1550 U1551 G1552 C1553 C1554 U1555 A1556 C1557 C1558 C1559 U1560

A1561 C1562 G1563 C1564 C1565 G1566 G1567 C1568 A1569 G1570 G1571 C1572 G1573 C1574 G1575 C1576 G1577 U1578 A1579 A1580 C1581 C1582 C1583 G1584 U1585 U1586 G1587 A1588 A1589 C1590 C1591 C1592 C1593 A1594 U1595 U1596 C1597 G1598 U1599 G1600 A1601 U1602 G1603 G1604 G1605 G1606 A1607 U1608 C1609 G1610 G1611 G1612 G1613 A1614 U1615 U1616 G1617 C1618 A1619 A1620

U1621 U1622 A1623 U1624 U1625 C1626 C1627 C1628 C1629 A1630 U1631 G1632 A1633 A1634 C1635 G1636 A1637 G1638 G1639 A1640 A1641 U1642 U1643 C1644 C1645 C1646 A1647 G1648 U1649 A1650 A1651 G1652 U1653 G1654 C1655 G1656 G1657 G1658 U1659 C1660 A1661 U1662 A1663 A1664 G1665 C1666 U1667 U1668 G1669 C1670 G1671 U1672 U1673 G1674 A1675 U1676 U1677 A1678 A1679 G1680

U1681 C1682 C1683 C1684 U1685 G1686 C1687 C1688 C1689 U1690 U1691 U1692 G1693 U1694 A1695 C1696 A1697 C1698 A1699 C1700 C1701 G1702 C1703 C1704 C1705 G1706 U1707 C1708 G1709 C1710 U1711 A1712 C1713 U1714 A1715 C1716 C1717 G1718 A1719 U1720 U1721 G1722 G1723 A1724 U1725 G1726 G1727 U1728 U1729 U1730 A1731 G1732 U1733 G1734 A1735 G1736 G1737 C1738 C1739 C1740

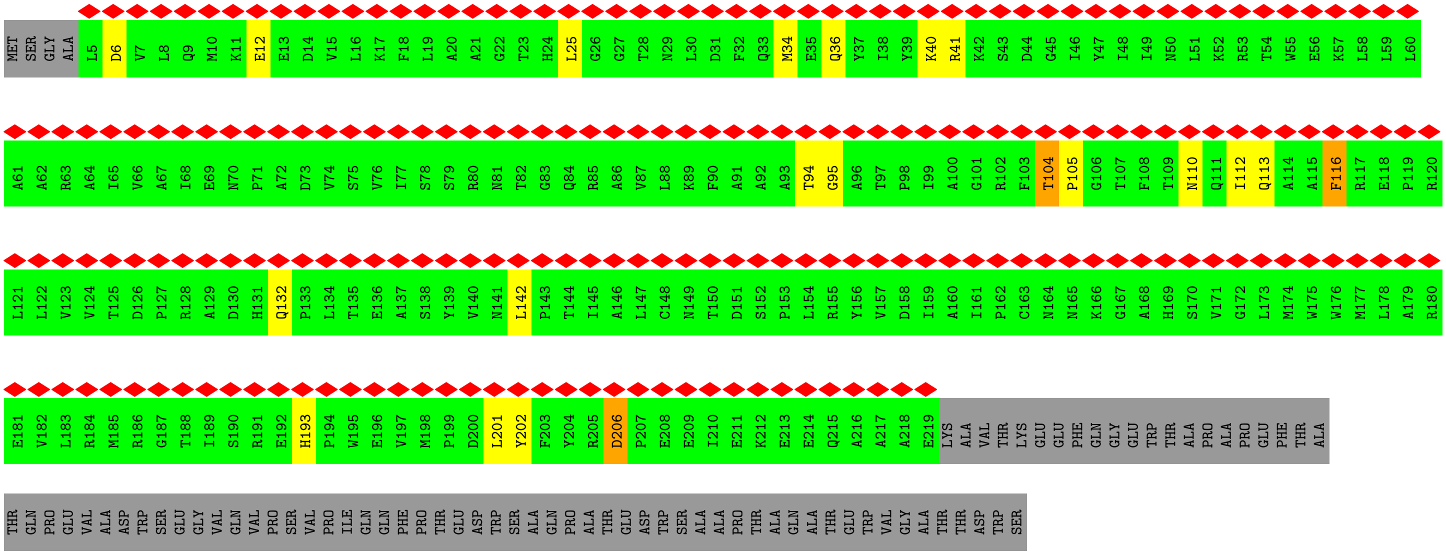
U1741 C1742 G1743 G1744 A1745 U1746 C1747 G1748 G1749 C1750 C1751 C1752 C1753 G1754 C1755 C1756 G1757 G G G U C G G C C C A C G G C C C U1775 G1776 G1777 C1778 G1779 C1780 A1781 G1782 C1783 G1784 C1785 U1786 G1787 A1788 G1789 A1790 A1791 G1792 A1793 C1794 G1795 G1796 U1797 C1798 G1799 A1800

A1801 C1802 U1803 U1804 G1805 A1806 C1807 U1808 A1809 U1810 C1811 U1812 A1813 G1814 A1815 G1816 G1817 A1818 A1819 G1820 U1821 A1822 A1823 A1824 A1825 G1826 U1827 C1828 G1829 U1830 A1831 A1832 C1833 A1834 A1835 G1836 G1837 U1838 U1839 U1840 C1841 C1842 G1843 U1844 A1845 G1846 G1847 U1848 G1849 A1850 A1851 C1852 C1853 U1854 G1855 C1856 G1857 G1858 A1859 A1860

G1861 G1862 A1863 U1864 C1865 A1866 U1867 U1868 A1869

- Molecule 50: 40S ribosomal protein SA

Chain BA:



MET SER GLY ALA L5 D6 V7 L8 Q9 M10 K11 E12 E13 D14 V15 L16 K17 F18 L19 A20 A21 G22 T23 H24 L25 G26 G27 T28 N29 L30 D31 F32 Q33 M34 E35 Q36 Y37 I38 Y39 K40 R41 K42 S43 D44 G45 I46 Y47 I48 I49 N50 L51 K52 R53 T54 W55 E56 K57 L58 L59 L60

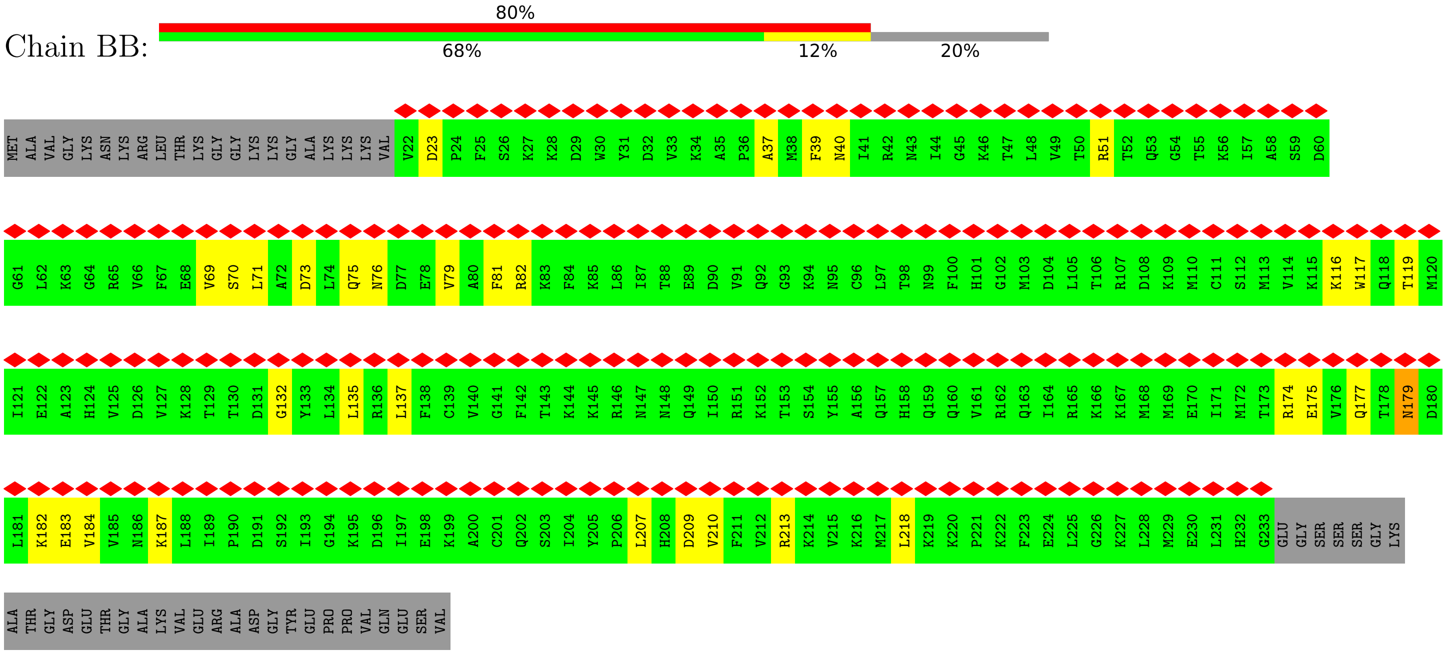
A61 A62 R63 A64 I65 V66 A67 I68 E69 N70 P71 A72 D73 V74 S75 V76 I77 S78 S79 R80 N81 T82 G83 Q84 R85 A86 V87 L88 K89 F90 A91 A92 A93 T94 G95 A96 T97 P98 I99 A100 G101 R102 F103 T104 P105 G106 T107 F108 T109 N110 Q111 I112 Q113 A114 A115 F116 R117 E118 P119 R120

L121 L122 V123 V124 T125 D126 P127 R128 A129 D130 H131 Q132 P133 L134 T135 E136 A137 S138 Y139 V140 N141 L142 P143 T144 I145 A146 L147 C148 N149 T150 D151 S152 P153 L154 R155 Y156 V157 D158 I159 A160 I161 P162 C163 N164 N165 K166 G167 A168 H169 S170 V171 G172 L173 M174 W175 W176 M177 L178 A179 R180

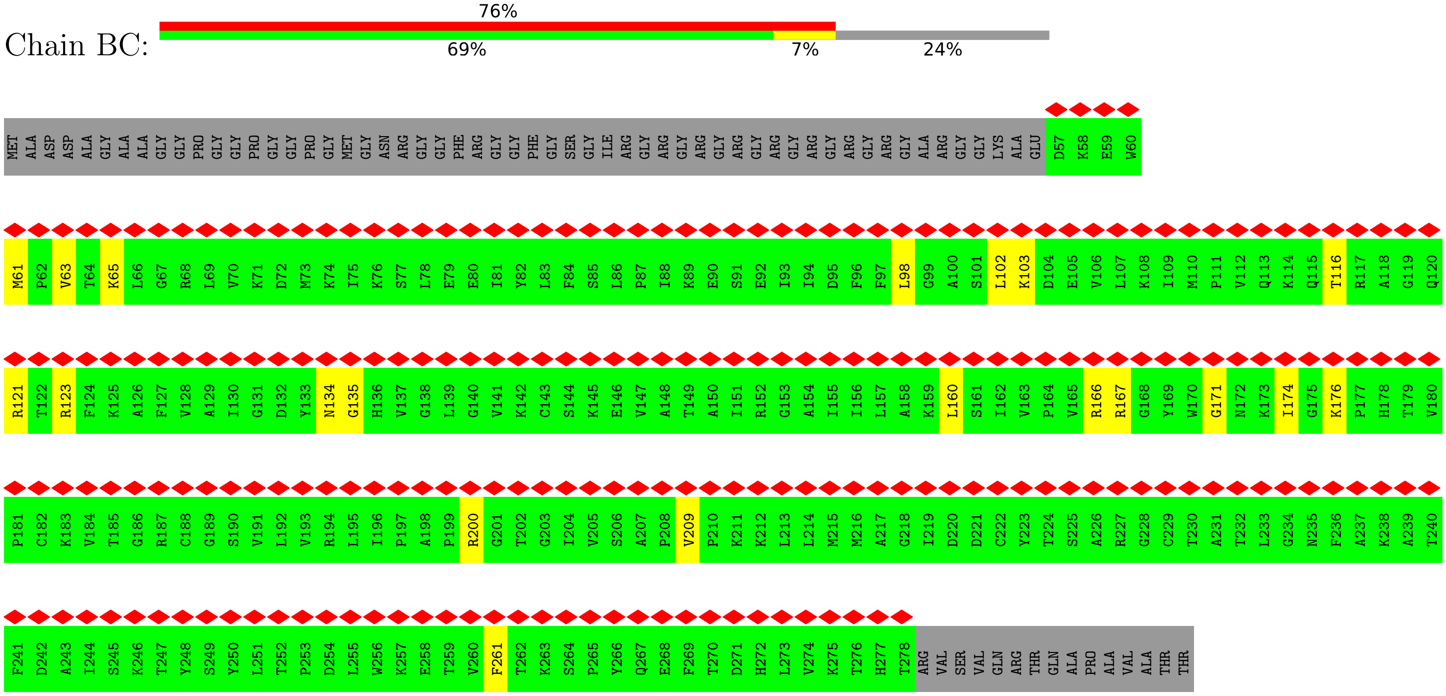
E181 V182 L183 R184 M185 R186 G187 T188 I189 S190 R191 E192 H193 P194 W195 E196 V197 M198 P199 D200 L201 Y202 F203 Y204 R205 D206 P207 E208 E209 I210 E211 K212 E213 E214 Q215 A216 A217 A218 E219 LYS ALA VAL THR LYS GLU GLU PHE GLN GLY GLU TRP THR ALA PRO ALA PRO GLU PHE THR ALA

THR GLN PRO GLU VAL ALA ASP TRP SER GLU GLY VAL GLN VAL PRO SER VAL PRO ILE GLN GLN PHE PRO THR GLU ASP TRP SER ALA GLN PRO ALA THR GLU ASP TRP SER ALA ALA PRO THR ALA GLN ALA THR GLU TRP VAL GLY ALA THR THR ASP TRP SER

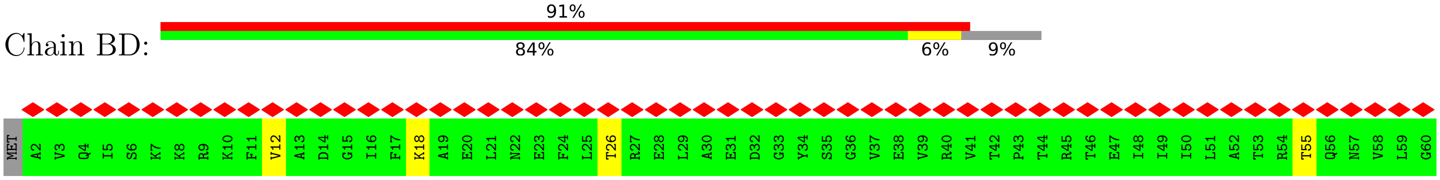
- Molecule 51: 40S ribosomal protein S3a

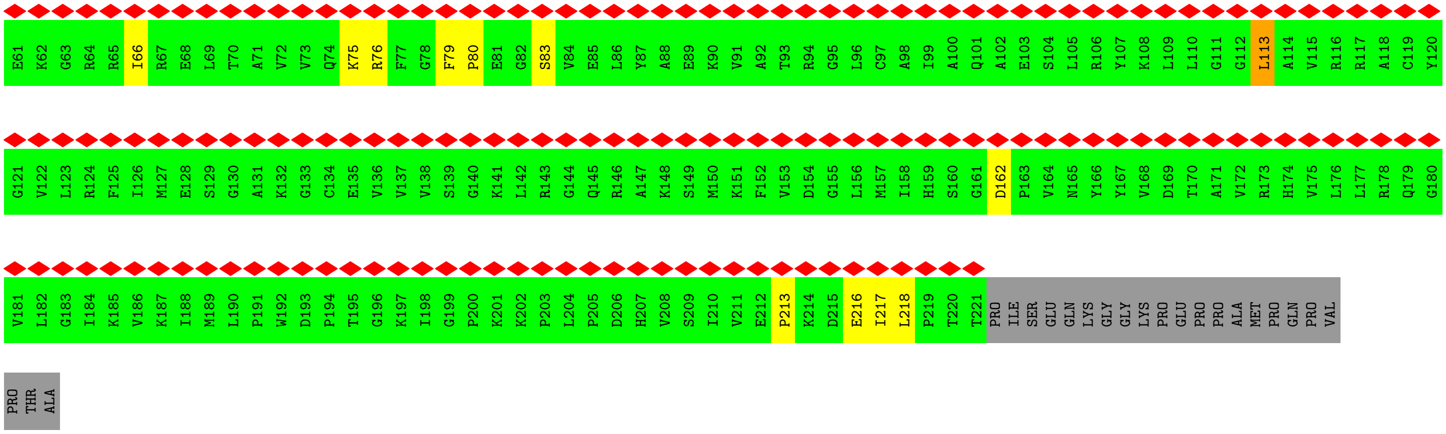


- Molecule 52: 40S ribosomal protein S2



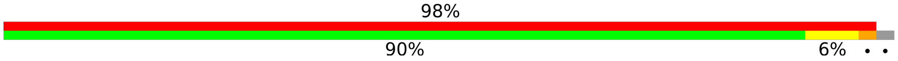
- Molecule 53: 40S ribosomal protein S3

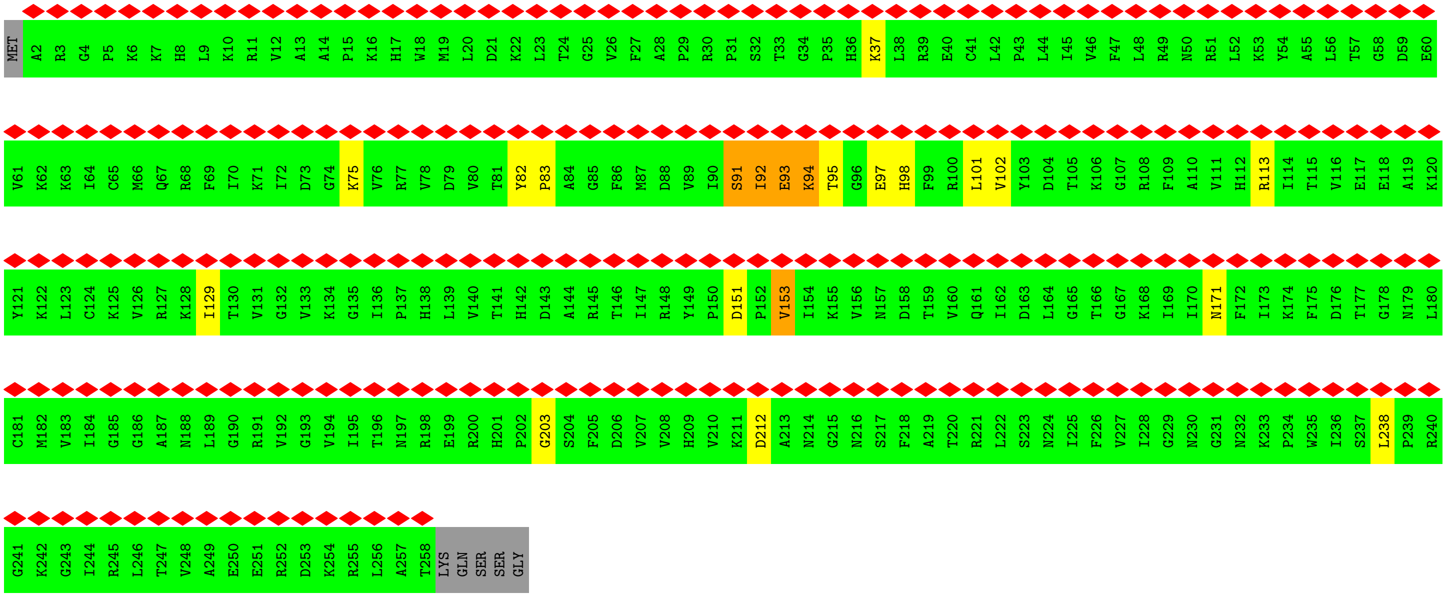




- Molecule 54: 40S ribosomal protein S4, Y isoform 1

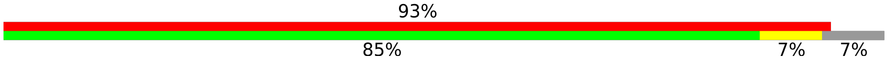
Chain BE:

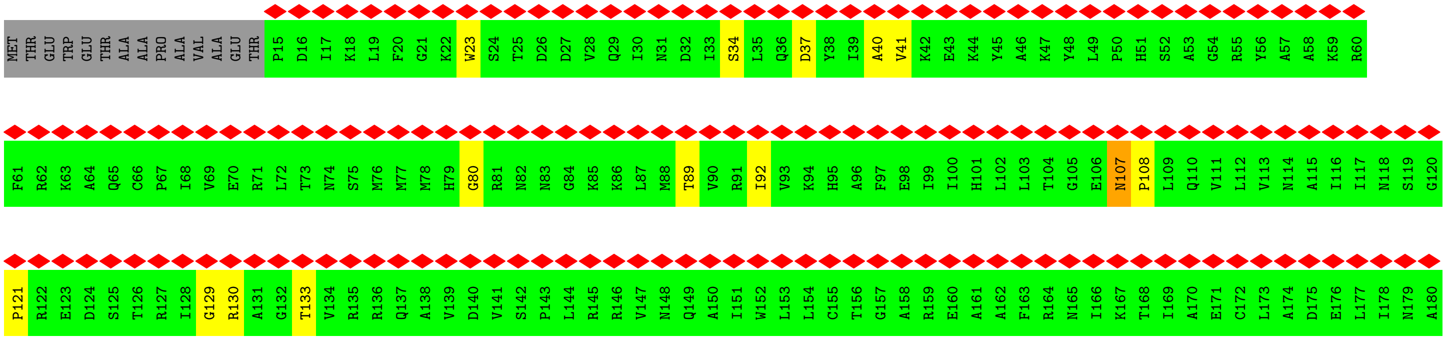


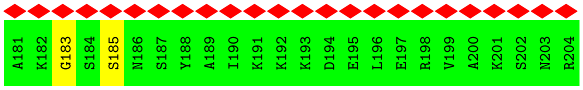


- Molecule 55: 40S ribosomal protein S5

Chain BF:

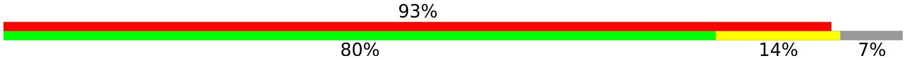


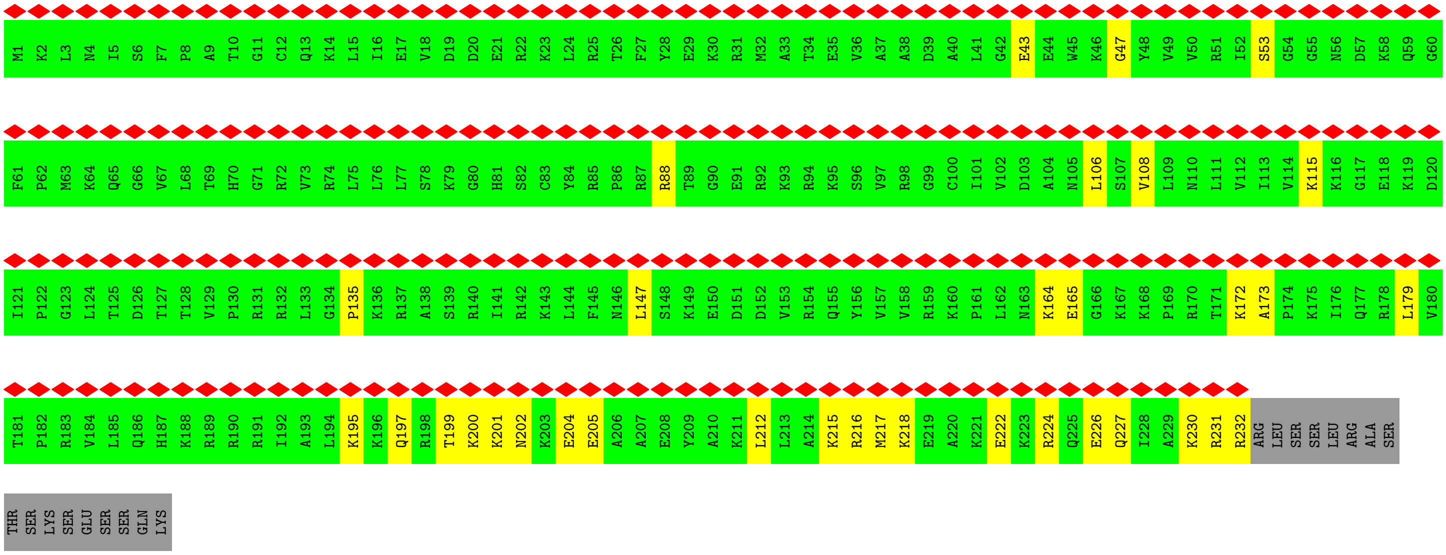




- Molecule 56: 40S ribosomal protein S6

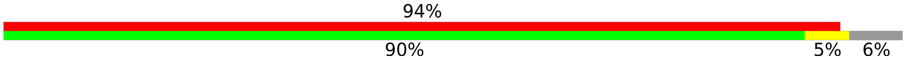
Chain BG:

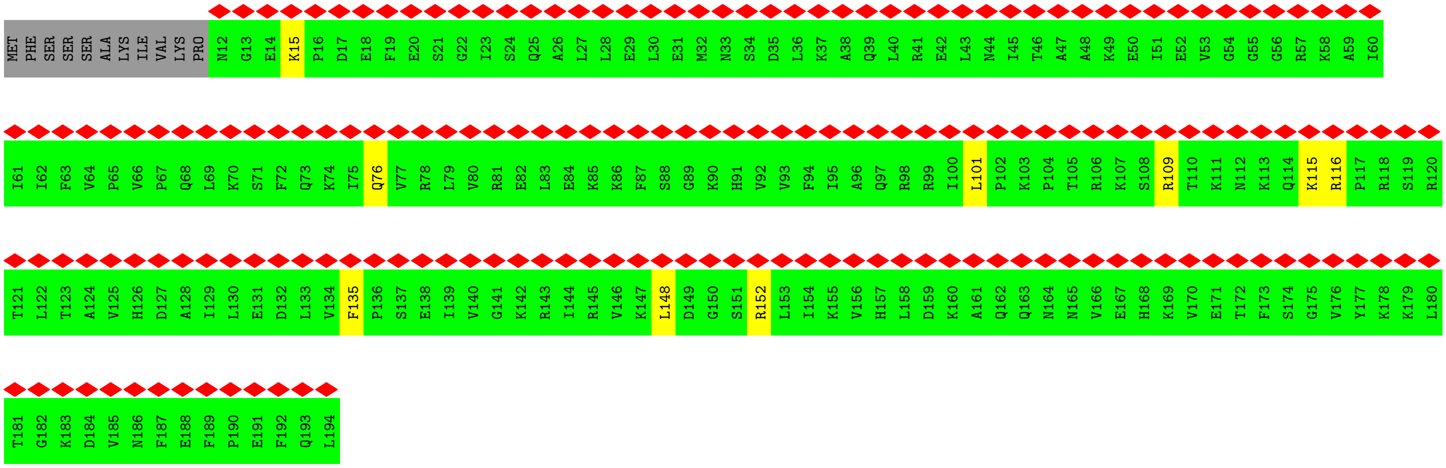




- Molecule 57: 40S ribosomal protein S7

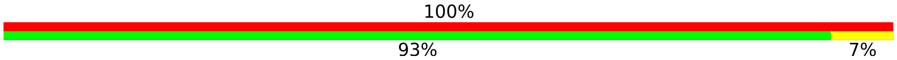
Chain BH:

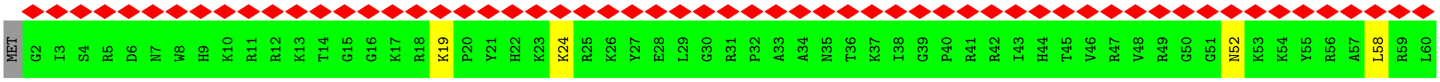


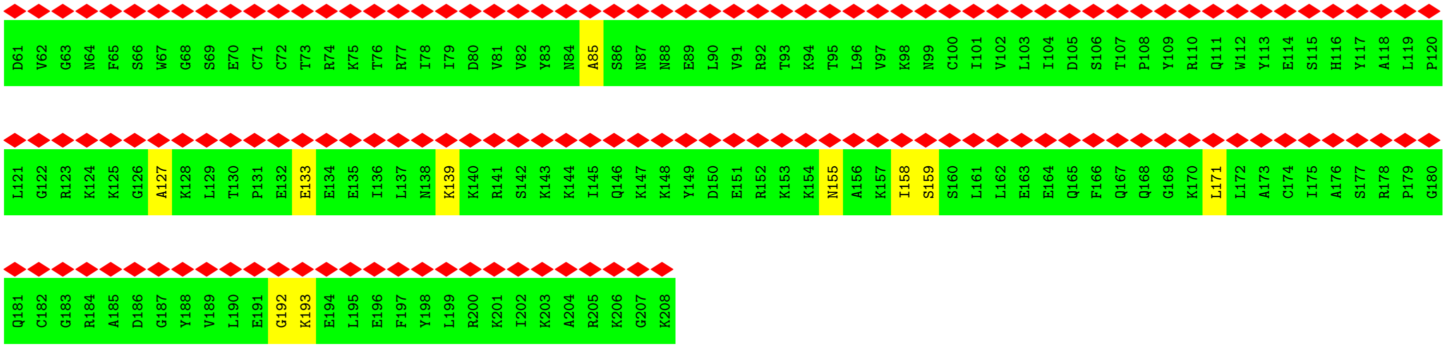


- Molecule 58: 40S ribosomal protein S8

Chain BI:

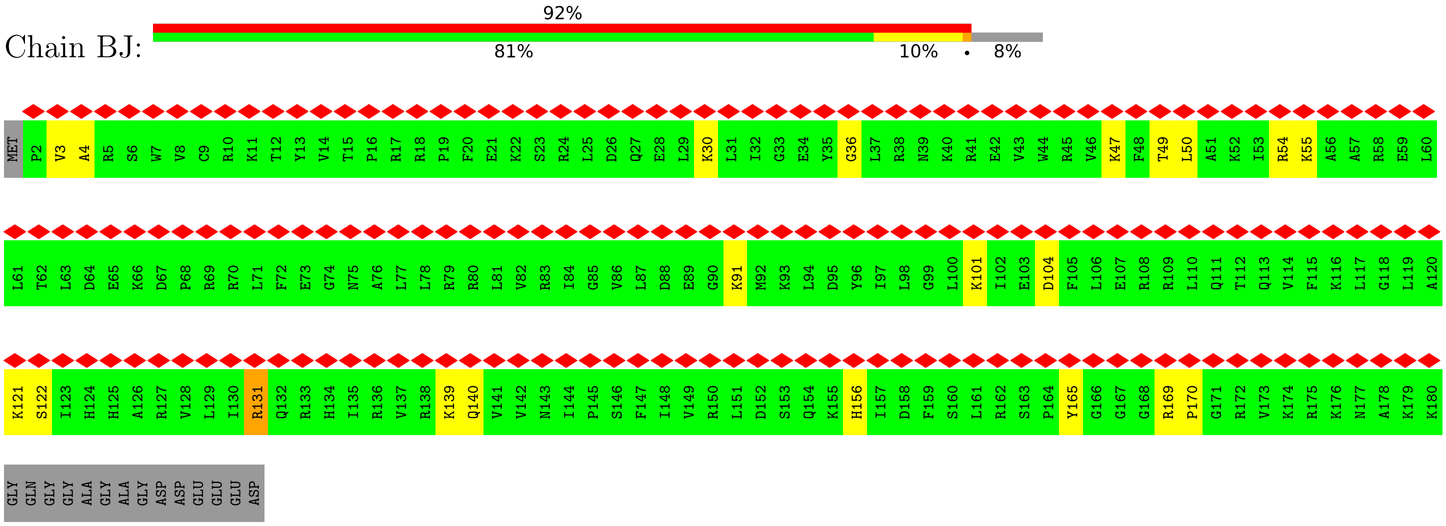






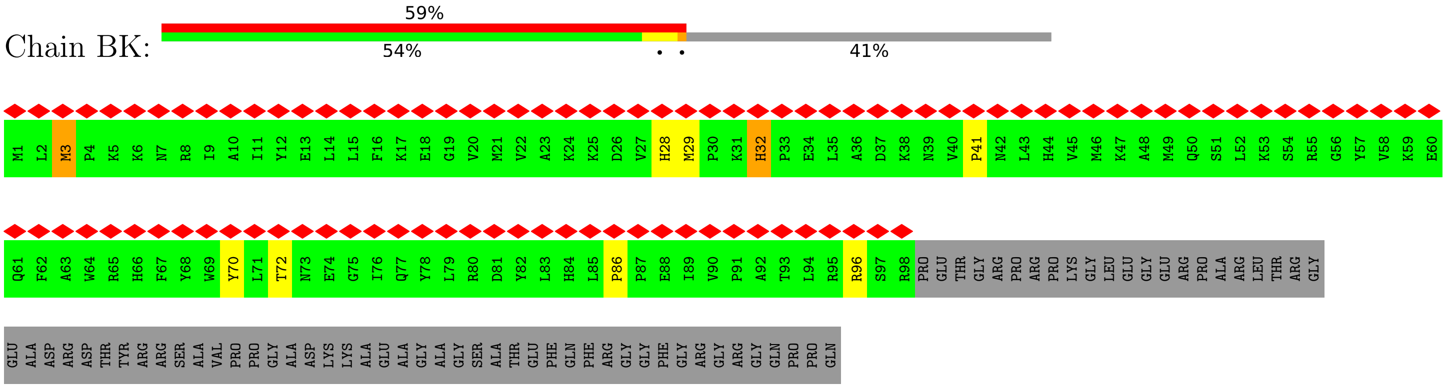
- Molecule 59: 40S ribosomal protein S9

Chain BJ:



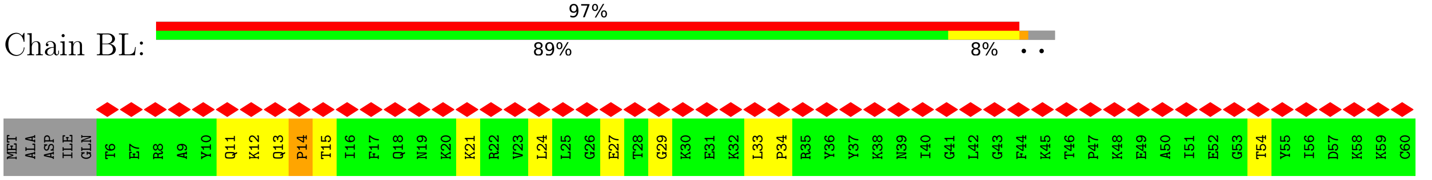
- Molecule 60: 40S ribosomal protein S10

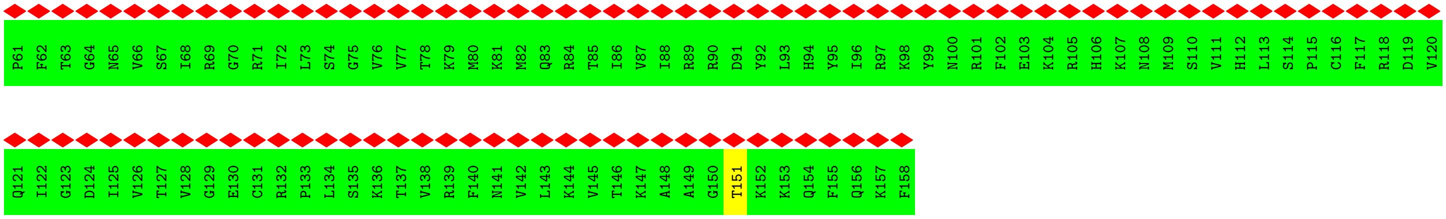
Chain BK:



- Molecule 61: 40S ribosomal protein S11

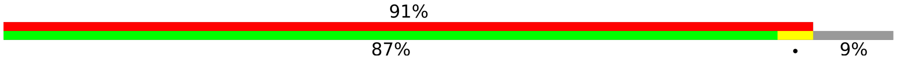
Chain BL:

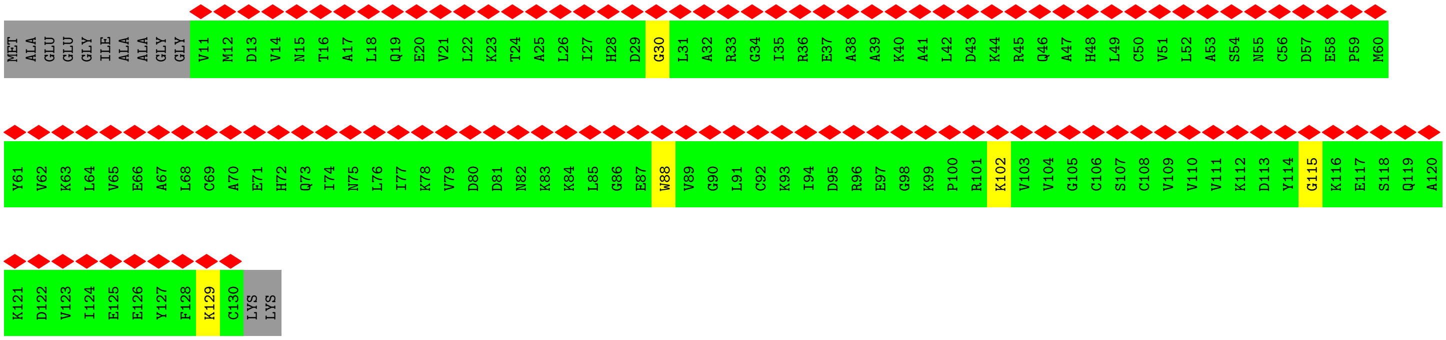




- Molecule 62: 40S ribosomal protein S12

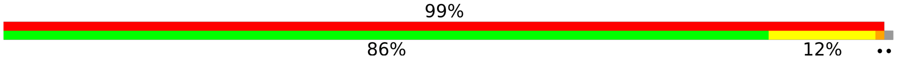
Chain BM:

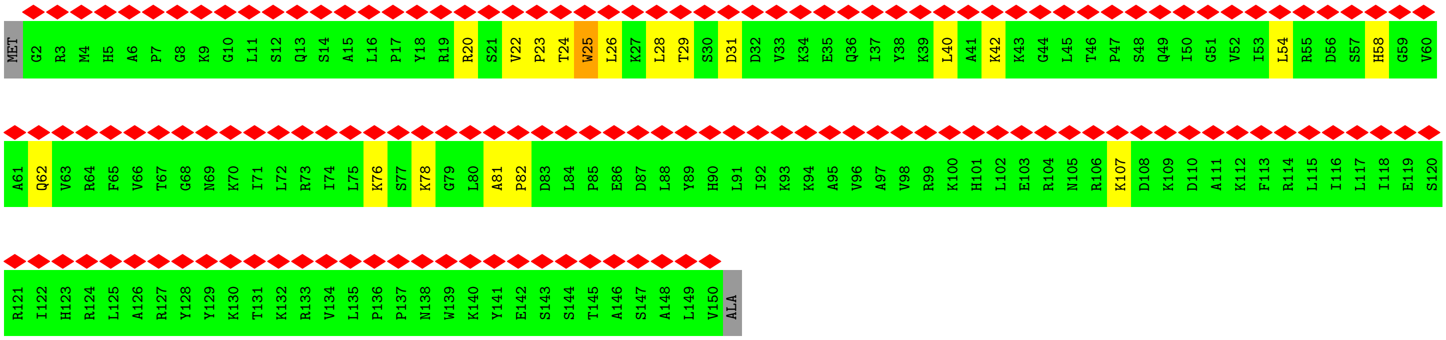




- Molecule 63: 40S ribosomal protein S13

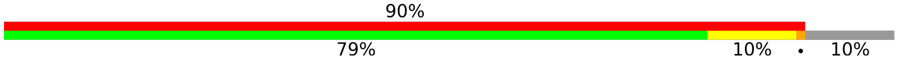
Chain BN:

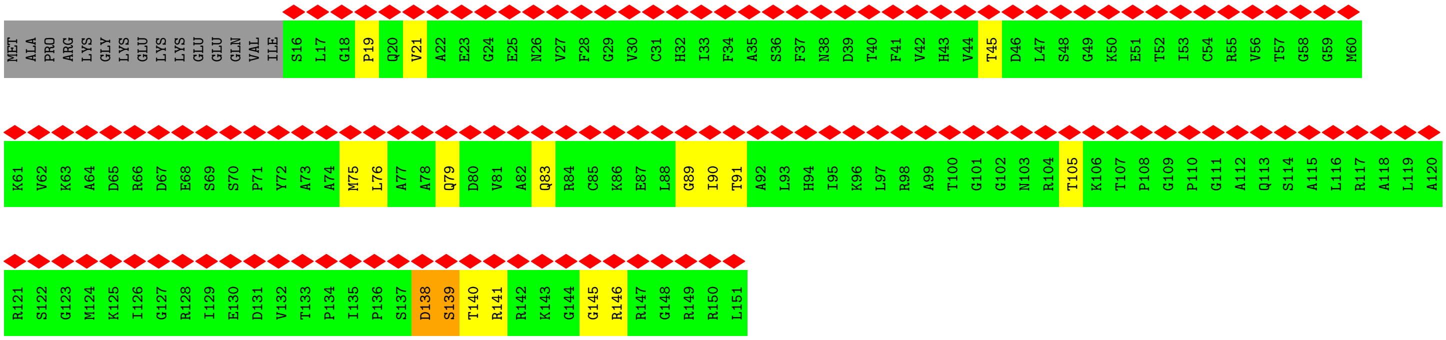




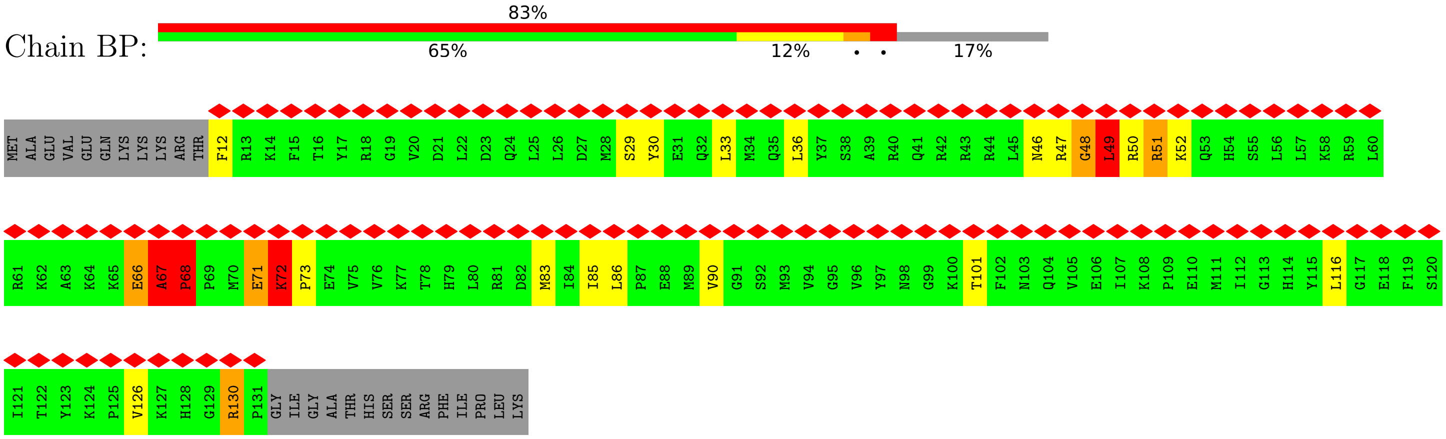
- Molecule 64: 40S ribosomal protein S14

Chain BO:

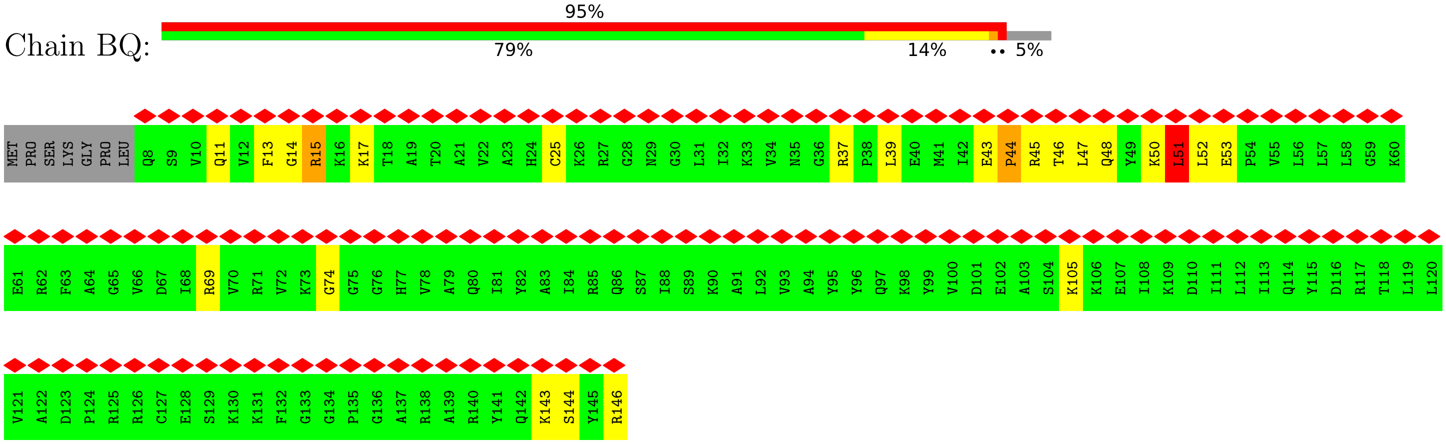




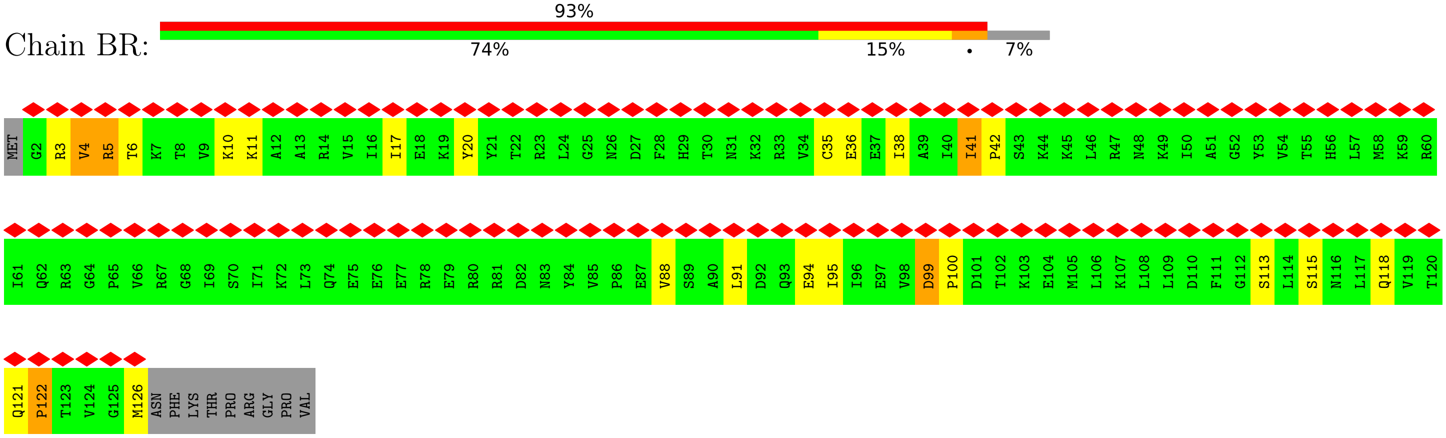
- Molecule 65: 40S ribosomal protein S15



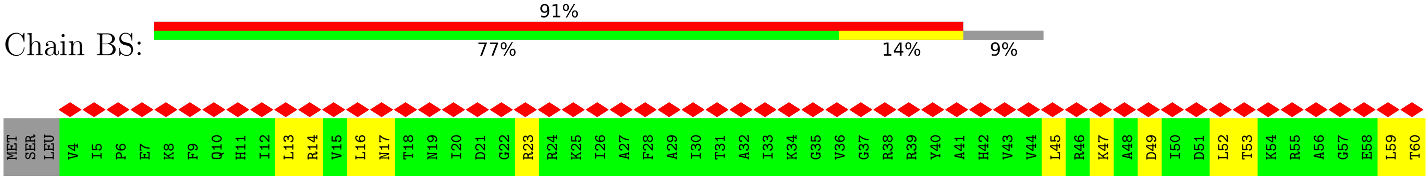
- Molecule 66: 40S ribosomal protein S16

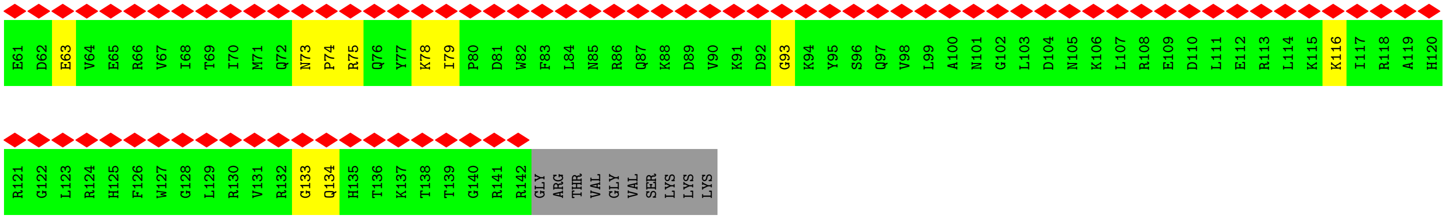


- Molecule 67: 40S ribosomal protein S17-like

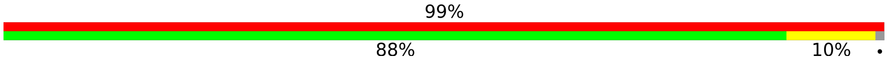


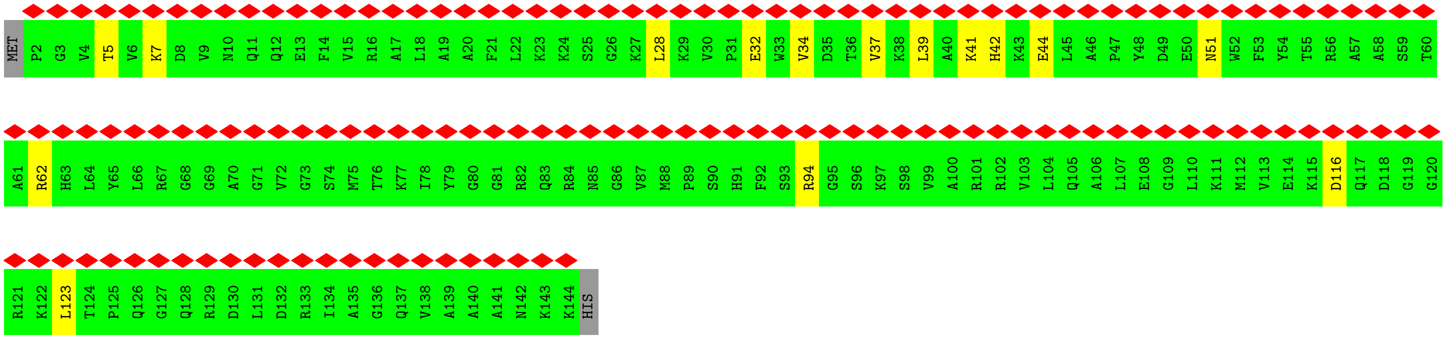
- Molecule 68: 40S ribosomal protein S18





- Molecule 69: 40S ribosomal protein S19

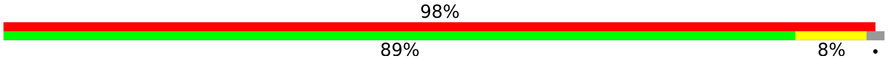
Chain BT:


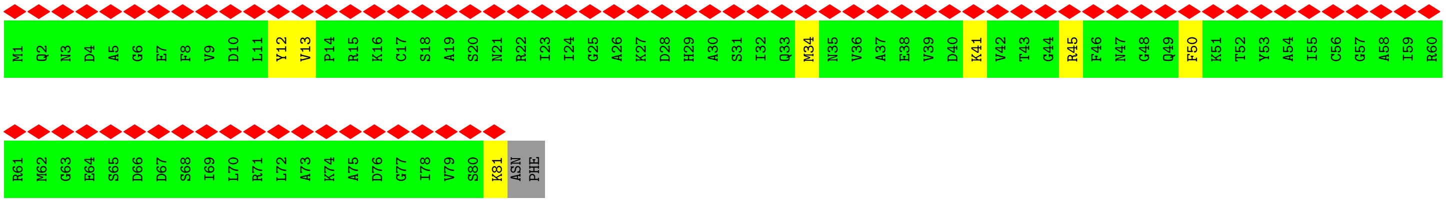


- Molecule 70: 40S ribosomal protein S20

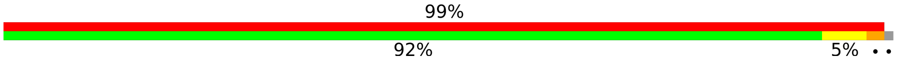
Chain BU:

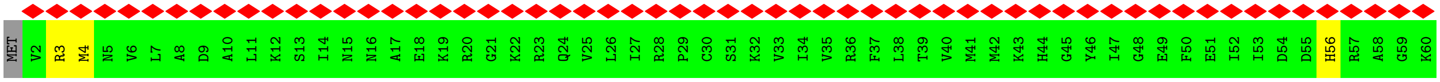

- Molecule 71: 40S ribosomal protein S21

Chain BV:




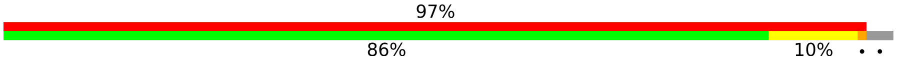
- Molecule 72: 40S ribosomal protein S15a

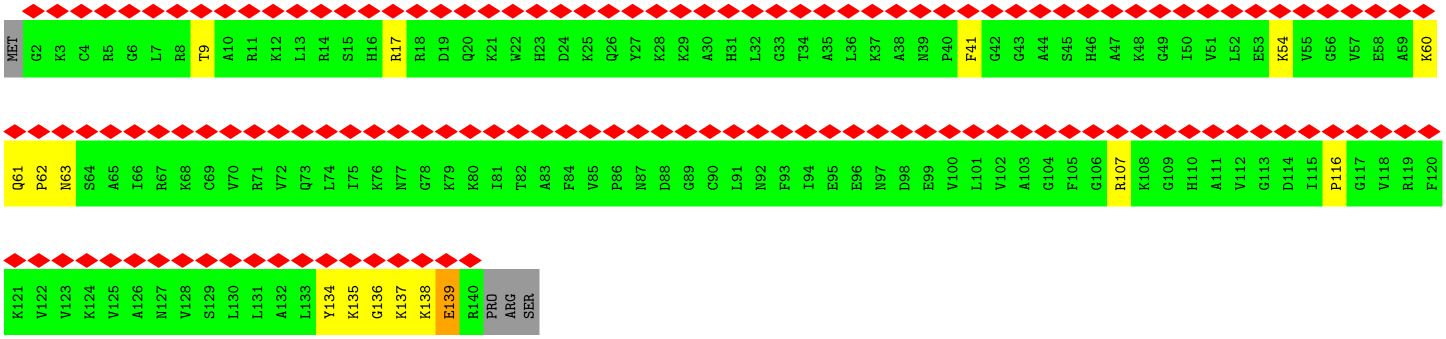
Chain BW:




- Molecule 73: 40S ribosomal protein S23

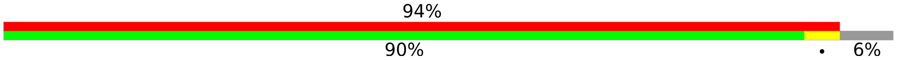
Chain BX:

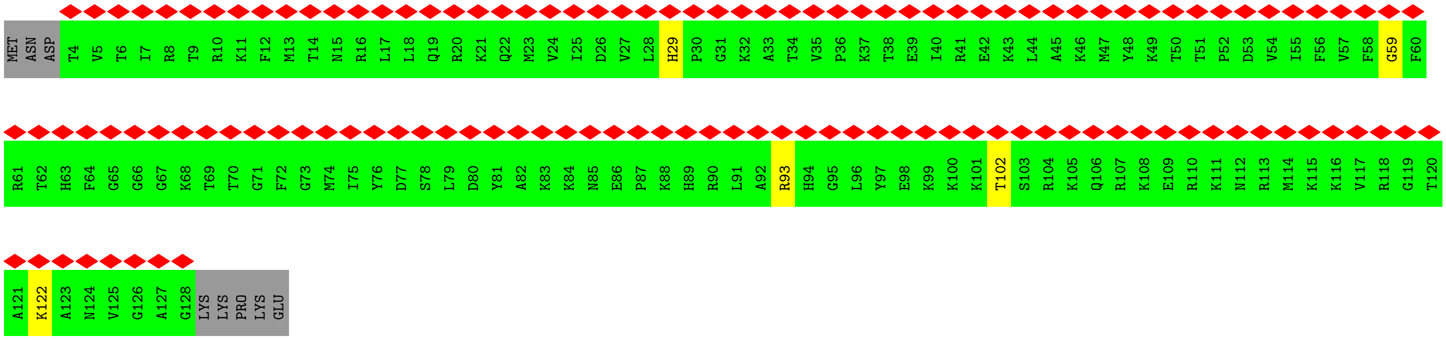




- Molecule 74: 40S ribosomal protein S24

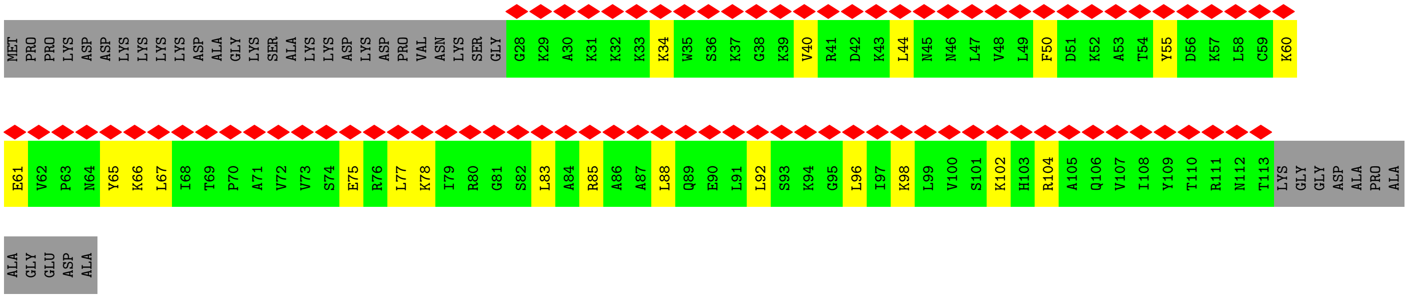
Chain BY:



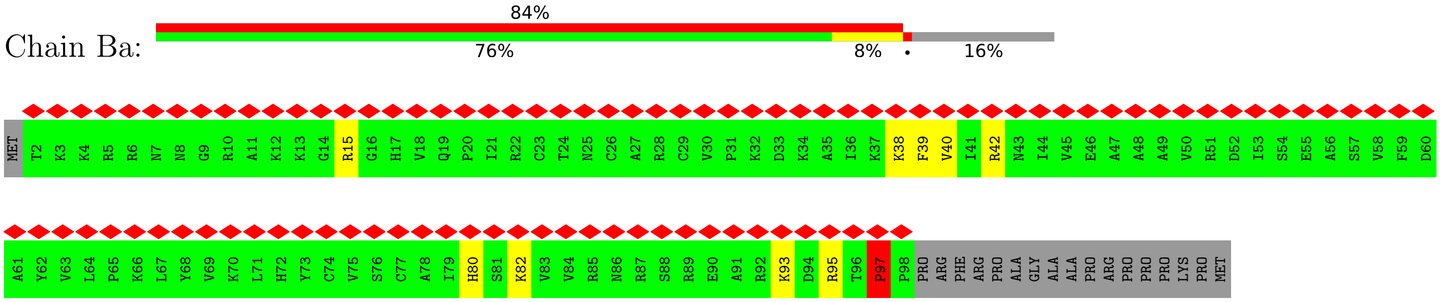


- Molecule 75: 40S ribosomal protein S25

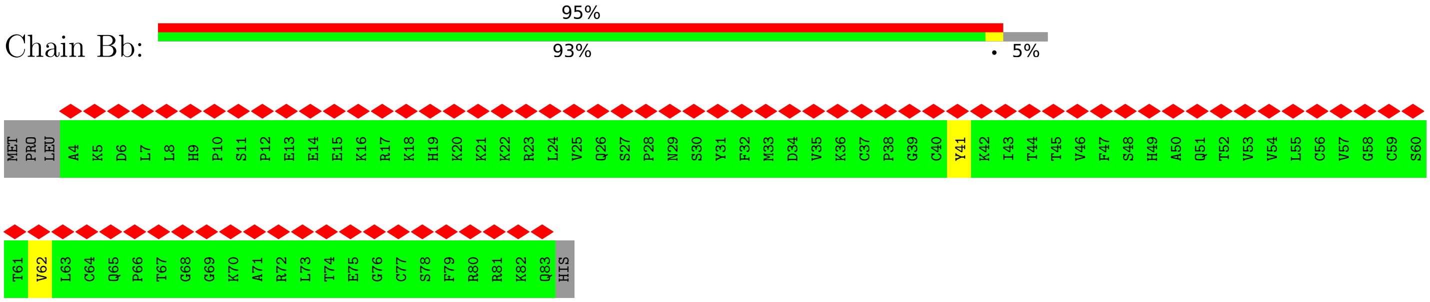
Chain BZ:



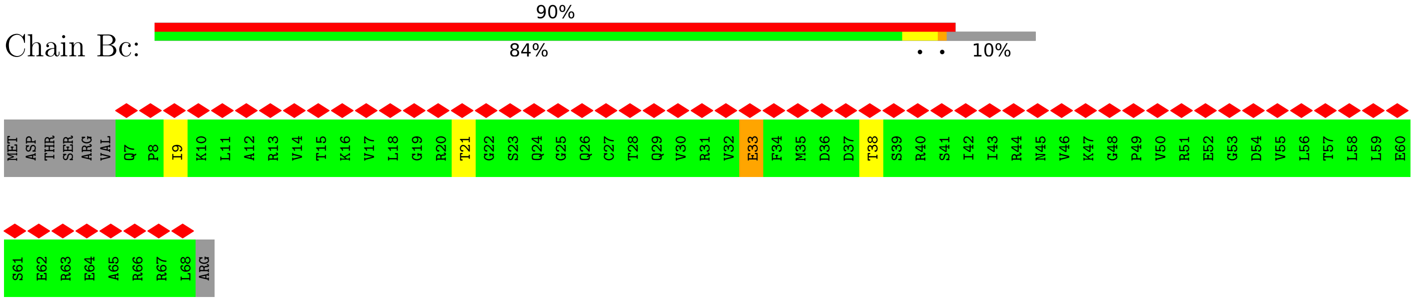
- Molecule 76: 40S ribosomal protein S26



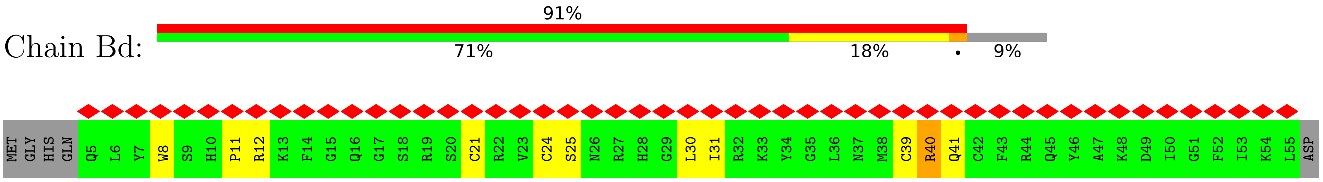
- Molecule 77: 40S ribosomal protein S27



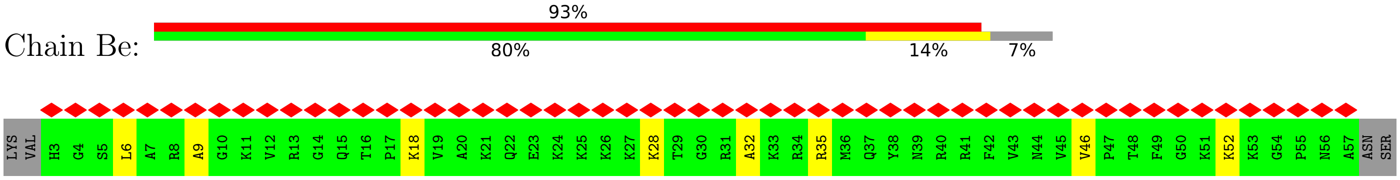
- Molecule 78: 40S ribosomal protein S28



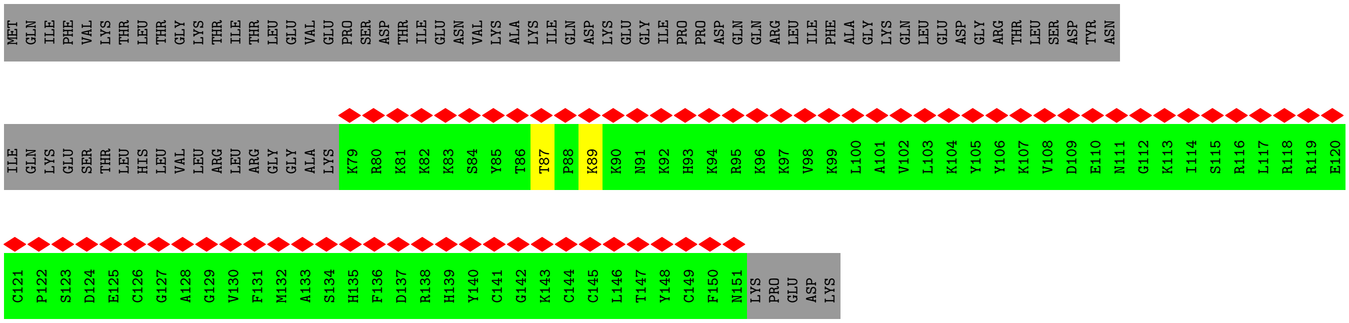
- Molecule 79: 40S ribosomal protein S29



- Molecule 80: 40S ribosomal protein S30

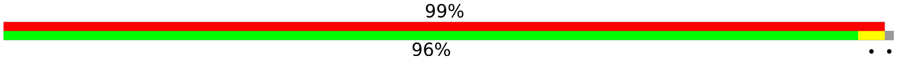


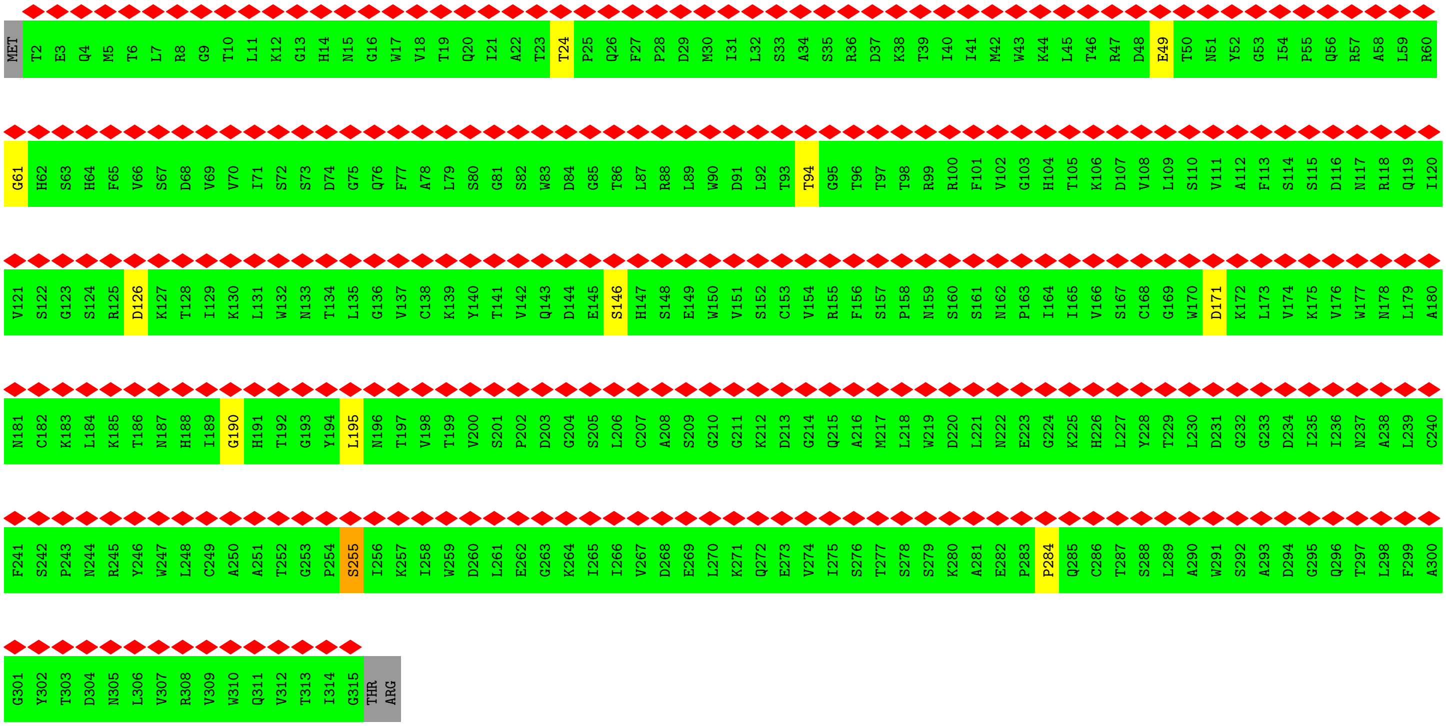
- Molecule 81: Ubiquitin-40S ribosomal protein S27a



• Molecule 82: Guanine nucleotide-binding protein subunit beta-2-like 1

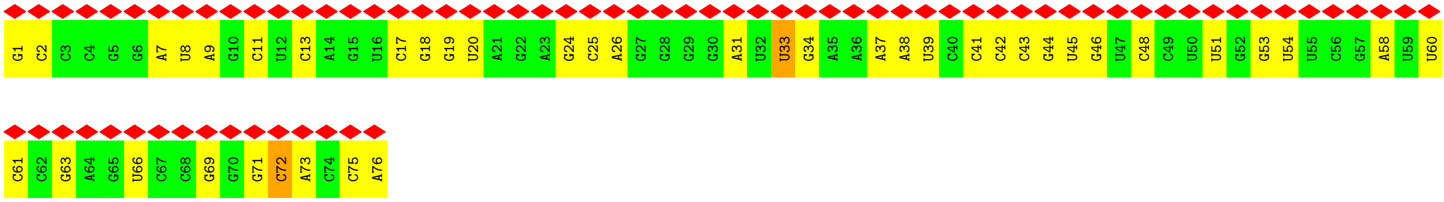
Chain Bg:





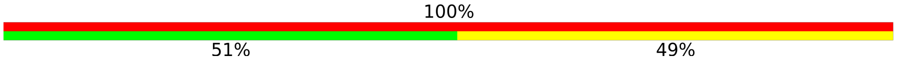
• Molecule 83: tRNA

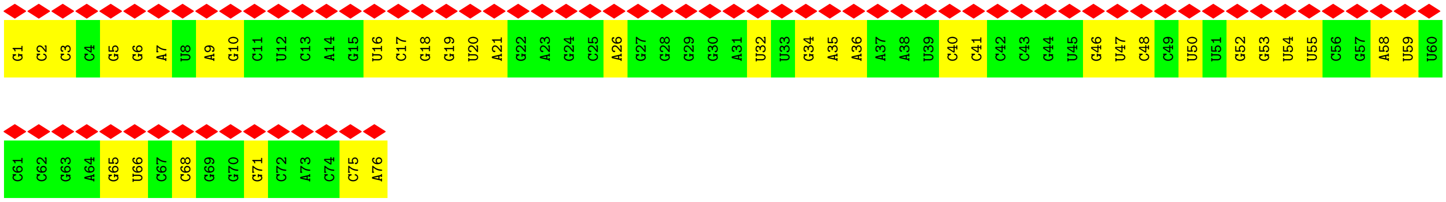
Chain Bv:



• Molecule 83: tRNA

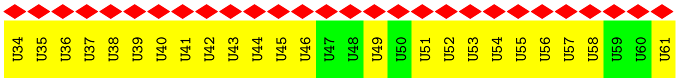
Chain Bw:





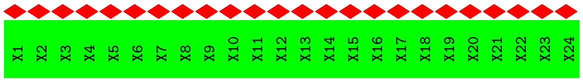
- Molecule 84: mRNA

Chain Bx:



- Molecule 85: Nascent protein chain

Chain By:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	313321	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\mathring{A}^2)$	20.00	Depositor
Minimum defocus (nm)	2000.00	Depositor
Maximum defocus (nm)	4500.00	Depositor
Magnification	205000	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor
Maximum map value	15.028	Depositor
Minimum map value	-7.978	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.0	Depositor
Map size (Å)	378.0, 378.0, 378.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.945, 0.945, 0.945	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A3	1.12	40/3726 (1.1%)	1.17	52/5804 (0.9%)
2	A4	1.10	32/2839 (1.1%)	1.13	40/4425 (0.9%)
3	AA	0.44	0/1968	0.65	1/2639 (0.0%)
4	AB	0.39	0/3246	0.64	0/4345
5	AC	0.41	1/2942 (0.0%)	0.62	3/3951 (0.1%)
6	AD	0.42	0/2437	0.65	2/3262 (0.1%)
7	AE	0.50	0/1603	0.80	4/2153 (0.2%)
8	AF	0.37	0/1986	0.57	0/2644
9	AG	0.38	0/1913	0.57	0/2576
10	AH	0.38	0/1545	0.54	1/2077 (0.0%)
11	AI	0.41	0/1730	0.61	1/2311 (0.0%)
12	AJ	0.39	0/1376	0.59	0/1841
13	AK	0.85	3/886 (0.3%)	1.53	23/1188 (1.9%)
14	AL	0.48	3/1688 (0.2%)	0.73	5/2260 (0.2%)
15	AM	0.39	0/1161	0.64	0/1554
16	AN	0.39	0/1746	0.57	0/2338
17	AO	0.37	0/1638	0.60	0/2191
18	AP	0.42	0/1268	0.70	0/1701
19	AQ	0.47	2/1537 (0.1%)	0.63	3/2052 (0.1%)
20	AR	0.38	0/1533	0.63	1/2025 (0.0%)
21	AS	0.38	1/1488 (0.1%)	0.60	1/1997 (0.1%)
22	AT	0.38	0/1312	0.60	0/1753
23	AU	0.35	0/822	0.58	0/1103
24	AV	0.37	0/983	0.55	0/1319
25	AW	0.42	1/1004 (0.1%)	0.74	3/1332 (0.2%)
26	AX	0.34	0/975	0.51	0/1312
27	AY	0.35	0/1081	0.56	0/1439
28	AZ	0.42	0/1126	0.69	2/1502 (0.1%)
29	Aa	0.50	0/1191	0.70	1/1591 (0.1%)
30	Ab	0.36	0/569	0.58	0/750
31	Ac	0.38	0/812	0.60	0/1089
32	Ad	0.38	0/894	0.58	0/1204

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Ae	0.42	0/1082	0.58	1/1443 (0.1%)
34	Af	0.47	0/895	0.73	2/1198 (0.2%)
35	Ag	0.39	0/916	0.58	0/1220
36	Ah	0.37	0/1023	0.63	1/1351 (0.1%)
37	Ai	0.35	0/805	0.58	0/1065
38	Aj	0.47	1/703 (0.1%)	0.92	3/929 (0.3%)
39	Ak	0.51	0/575	0.74	0/761
40	Al	0.37	0/454	0.54	0/599
41	Am	0.42	0/417	0.59	0/553
42	An	0.36	0/241	0.60	0/305
43	Ao	0.39	0/877	0.66	0/1156
44	Ap	0.39	0/718	0.60	0/953
45	Aq	0.89	3/1058 (0.3%)	1.93	34/1424 (2.4%)
46	At	0.41	0/995	0.69	0/1334
47	Au	0.73	1/1772 (0.1%)	1.28	17/2375 (0.7%)
48	A2	0.98	666/86613 (0.8%)	1.13	1094/135108 (0.8%)
49	B1	0.96	275/40767 (0.7%)	1.13	515/63536 (0.8%)
50	BA	0.52	1/1741 (0.1%)	0.72	5/2366 (0.2%)
51	BB	0.42	0/1749	0.62	0/2340
52	BC	0.37	0/1761	0.58	0/2379
53	BD	0.44	1/1736 (0.1%)	0.63	1/2338 (0.0%)
54	BE	0.41	1/2072 (0.0%)	0.59	1/2793 (0.0%)
55	BF	0.40	1/1524 (0.1%)	0.62	1/2048 (0.0%)
56	BG	0.41	0/1907	0.62	1/2538 (0.0%)
57	BH	0.43	0/1501	0.64	1/2009 (0.0%)
58	BI	0.41	0/1725	0.59	0/2298
59	BJ	0.36	0/1520	0.55	1/2030 (0.0%)
60	BK	0.43	0/851	0.68	0/1147
61	BL	0.44	1/1281 (0.1%)	0.65	2/1710 (0.1%)
62	BM	0.39	0/941	0.63	0/1264
63	BN	0.40	1/1226 (0.1%)	0.57	1/1649 (0.1%)
64	BO	0.43	0/1029	0.64	0/1380
65	BP	0.50	1/1019 (0.1%)	0.74	3/1361 (0.2%)
66	BQ	0.38	0/1126	0.58	2/1506 (0.1%)
67	BR	0.49	3/1023 (0.3%)	0.68	3/1373 (0.2%)
68	BS	0.42	1/1172 (0.1%)	0.63	1/1570 (0.1%)
69	BT	0.36	0/1131	0.60	0/1515
70	BU	0.45	0/778	0.65	1/1045 (0.1%)
71	BV	0.41	0/623	0.60	1/833 (0.1%)
72	BW	0.37	0/1051	0.55	0/1406
73	BX	0.44	1/1097 (0.1%)	0.61	1/1464 (0.1%)
74	BY	0.40	0/1032	0.64	0/1371
75	BZ	0.43	0/696	0.62	0/929

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	Ba	0.49	0/786	0.75	2/1053 (0.2%)
77	Bb	0.42	0/637	0.59	0/854
78	Bc	0.40	0/490	0.66	0/656
79	Bd	0.54	0/437	0.89	3/580 (0.5%)
80	Be	0.37	0/443	0.60	0/583
81	Bf	0.44	0/613	0.62	0/811
82	Bg	0.40	0/2497	0.60	0/3399
83	Bv	0.58	4/1813 (0.2%)	0.84	5/2823 (0.2%)
83	Bw	0.43	2/1813 (0.1%)	0.90	4/2823 (0.1%)
84	Bx	0.60	2/616 (0.3%)	1.20	11/948 (1.2%)
All	All	0.80	1049/234393 (0.4%)	0.98	1861/344230 (0.5%)

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	AB	0	3
5	AC	0	2
7	AE	0	1
8	AF	0	2
10	AH	0	3
13	AK	0	3
14	AL	0	6
39	Ak	0	1
48	A2	2	3
49	B1	1	0
54	BE	0	6
63	BN	0	2
64	BO	0	2
65	BP	0	11
66	BQ	0	6
72	BW	0	3
76	Ba	0	1
79	Bd	0	1
All	All	3	56

The worst 5 of 1049 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	A2	3612	U	O3'-P	-21.32	1.35	1.61

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	B1	842	C	O3'-P	20.18	1.85	1.61
48	A2	2689	C	O3'-P	-19.59	1.37	1.61
49	B1	558	G	O3'-P	19.39	1.84	1.61
49	B1	497	C	O3'-P	18.59	1.83	1.61

The worst 5 of 1861 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	Aq	75	PRO	CA-N-CD	-36.28	60.70	111.50
48	A2	1225	G	O5'-P-OP1	-28.99	75.91	110.70
48	A2	131	C	C4'-C3'-O3'	28.78	170.56	113.00
49	B1	558	G	P-O3'-C3'	-28.42	85.60	119.70
48	A2	137	G	C4'-C3'-O3'	26.49	165.98	113.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
48	A2	131	C	C3'
48	A2	137	G	C3'
49	B1	1289	U	C4'

5 of 56 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AB	295	ASP	Peptide
4	AB	296	GLY	Peptide
4	AB	297	LYS	Peptide
5	AC	98	GLY	Peptide
5	AC	99	GLY	Peptide

5.2 Too-close contacts ⓘ

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AA	250/257 (97%)	237 (95%)	7 (3%)	6 (2%)	6	35
4	AB	392/403 (97%)	370 (94%)	10 (3%)	12 (3%)	4	30
5	AC	361/427 (84%)	333 (92%)	13 (4%)	15 (4%)	3	23
6	AD	292/297 (98%)	270 (92%)	14 (5%)	8 (3%)	5	33
7	AE	192/288 (67%)	161 (84%)	12 (6%)	19 (10%)	0	7
8	AF	232/248 (94%)	213 (92%)	10 (4%)	9 (4%)	3	25
9	AG	232/266 (87%)	217 (94%)	10 (4%)	5 (2%)	6	37
10	AH	189/192 (98%)	175 (93%)	8 (4%)	6 (3%)	4	29
11	AI	204/214 (95%)	192 (94%)	7 (3%)	5 (2%)	5	34
12	AJ	167/178 (94%)	154 (92%)	7 (4%)	6 (4%)	3	26
13	AK	107/317 (34%)	34 (32%)	37 (35%)	36 (34%)	0	0
14	AL	203/211 (96%)	175 (86%)	14 (7%)	14 (7%)	1	12
15	AM	137/215 (64%)	127 (93%)	5 (4%)	5 (4%)	3	26
16	AN	201/204 (98%)	193 (96%)	6 (3%)	2 (1%)	15	54
17	AO	193/203 (95%)	187 (97%)	3 (2%)	3 (2%)	9	43
18	AP	151/184 (82%)	147 (97%)	4 (3%)	0	100	100
19	AQ	185/188 (98%)	163 (88%)	10 (5%)	12 (6%)	1	14
20	AR	179/196 (91%)	171 (96%)	4 (2%)	4 (2%)	6	37
21	AS	173/176 (98%)	156 (90%)	11 (6%)	6 (4%)	3	27
22	AT	155/160 (97%)	144 (93%)	6 (4%)	5 (3%)	4	29
23	AU	97/128 (76%)	81 (84%)	7 (7%)	9 (9%)	0	8
24	AV	127/140 (91%)	125 (98%)	2 (2%)	0	100	100
25	AW	119/157 (76%)	96 (81%)	18 (15%)	5 (4%)	3	23
26	AX	115/156 (74%)	113 (98%)	2 (2%)	0	100	100
27	AY	125/145 (86%)	119 (95%)	2 (2%)	4 (3%)	4	29
28	AZ	132/136 (97%)	118 (89%)	6 (4%)	8 (6%)	1	15
29	Aa	145/148 (98%)	135 (93%)	6 (4%)	4 (3%)	5	32
30	Ab	66/159 (42%)	57 (86%)	5 (8%)	4 (6%)	1	15
31	Ac	101/115 (88%)	97 (96%)	2 (2%)	2 (2%)	7	39
32	Ad	104/125 (83%)	99 (95%)	3 (3%)	2 (2%)	8	40

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	Ae	127/135 (94%)	116 (91%)	6 (5%)	5 (4%)	3	25
34	Af	107/110 (97%)	93 (87%)	5 (5%)	9 (8%)	1	9
35	Ag	112/117 (96%)	107 (96%)	3 (3%)	2 (2%)	8	41
36	Ah	120/123 (98%)	112 (93%)	2 (2%)	6 (5%)	2	19
37	Ai	95/105 (90%)	83 (87%)	7 (7%)	5 (5%)	2	17
38	Aj	82/97 (84%)	69 (84%)	7 (8%)	6 (7%)	1	11
39	Ak	67/70 (96%)	50 (75%)	7 (10%)	10 (15%)	0	3
40	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	Am	48/128 (38%)	44 (92%)	3 (6%)	1 (2%)	7	38
42	An	23/25 (92%)	23 (100%)	0	0	100	100
43	Ao	103/106 (97%)	94 (91%)	5 (5%)	4 (4%)	3	25
44	Ap	89/92 (97%)	84 (94%)	3 (3%)	2 (2%)	6	37
45	Aq	136/165 (82%)	40 (29%)	47 (35%)	49 (36%)	0	0
46	At	120/137 (88%)	107 (89%)	10 (8%)	3 (2%)	5	34
47	Au	215/217 (99%)	185 (86%)	20 (9%)	10 (5%)	2	20
50	BA	213/295 (72%)	197 (92%)	12 (6%)	4 (2%)	8	40
51	BB	210/264 (80%)	180 (86%)	12 (6%)	18 (9%)	1	9
52	BC	220/293 (75%)	204 (93%)	7 (3%)	9 (4%)	3	23
53	BD	218/243 (90%)	201 (92%)	10 (5%)	7 (3%)	4	29
54	BE	255/263 (97%)	230 (90%)	14 (6%)	11 (4%)	2	22
55	BF	188/204 (92%)	163 (87%)	15 (8%)	10 (5%)	2	17
56	BG	230/249 (92%)	211 (92%)	11 (5%)	8 (4%)	3	27
57	BH	181/194 (93%)	169 (93%)	8 (4%)	4 (2%)	6	37
58	BI	205/208 (99%)	175 (85%)	20 (10%)	10 (5%)	2	19
59	BJ	177/194 (91%)	137 (77%)	28 (16%)	12 (7%)	1	13
60	BK	96/165 (58%)	84 (88%)	7 (7%)	5 (5%)	2	18
61	BL	151/158 (96%)	133 (88%)	11 (7%)	7 (5%)	2	21
62	BM	118/132 (89%)	113 (96%)	1 (1%)	4 (3%)	3	28
63	BN	147/151 (97%)	126 (86%)	13 (9%)	8 (5%)	2	17
64	BO	134/151 (89%)	113 (84%)	11 (8%)	10 (8%)	1	11
65	BP	118/145 (81%)	100 (85%)	9 (8%)	9 (8%)	1	10

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	BQ	137/146 (94%)	120 (88%)	10 (7%)	7 (5%)	2	19
67	BR	123/135 (91%)	106 (86%)	9 (7%)	8 (6%)	1	14
68	BS	137/152 (90%)	125 (91%)	7 (5%)	5 (4%)	3	26
69	BT	141/145 (97%)	131 (93%)	6 (4%)	4 (3%)	5	32
70	BU	95/119 (80%)	91 (96%)	2 (2%)	2 (2%)	7	38
71	BV	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
72	BW	127/130 (98%)	120 (94%)	3 (2%)	4 (3%)	4	30
73	BX	137/143 (96%)	124 (90%)	8 (6%)	5 (4%)	3	26
74	BY	123/133 (92%)	116 (94%)	6 (5%)	1 (1%)	19	58
75	BZ	84/125 (67%)	80 (95%)	1 (1%)	3 (4%)	3	26
76	Ba	95/115 (83%)	87 (92%)	7 (7%)	1 (1%)	14	52
77	Bb	78/84 (93%)	72 (92%)	4 (5%)	2 (3%)	5	33
78	Bc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	4	28
79	Bd	49/56 (88%)	42 (86%)	4 (8%)	3 (6%)	1	15
80	Be	53/59 (90%)	49 (92%)	2 (4%)	2 (4%)	3	25
81	Bf	71/156 (46%)	63 (89%)	7 (10%)	1 (1%)	11	46
82	Bg	312/317 (98%)	292 (94%)	12 (4%)	8 (3%)	5	33
All	All	11580/13387 (86%)	10401 (90%)	657 (6%)	522 (4%)	4	21

5 of 522 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AA	138	SER
3	AA	144	LYS
3	AA	197	PRO
4	AB	189	THR
4	AB	356	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AA	194/199 (98%)	185 (95%)	9 (5%)	27	61
4	AB	343/349 (98%)	323 (94%)	20 (6%)	20	53
5	AC	302/348 (87%)	278 (92%)	24 (8%)	12	41
6	AD	248/250 (99%)	229 (92%)	19 (8%)	13	42
7	AE	174/252 (69%)	127 (73%)	47 (27%)	0	3
8	AF	203/215 (94%)	193 (95%)	10 (5%)	25	59
9	AG	199/223 (89%)	192 (96%)	7 (4%)	36	67
10	AH	170/171 (99%)	160 (94%)	10 (6%)	19	53
11	AI	178/181 (98%)	174 (98%)	4 (2%)	52	78
12	AJ	142/149 (95%)	138 (97%)	4 (3%)	43	72
13	AK	95/258 (37%)	70 (74%)	25 (26%)	0	3
14	AL	171/177 (97%)	156 (91%)	15 (9%)	10	38
15	AM	118/161 (73%)	104 (88%)	14 (12%)	5	25
16	AN	171/172 (99%)	163 (95%)	8 (5%)	26	60
17	AO	168/174 (97%)	164 (98%)	4 (2%)	49	76
18	AP	134/163 (82%)	123 (92%)	11 (8%)	11	40
19	AQ	164/165 (99%)	144 (88%)	20 (12%)	5	23
20	AR	160/175 (91%)	145 (91%)	15 (9%)	8	35
21	AS	156/157 (99%)	149 (96%)	7 (4%)	27	61
22	AT	138/140 (99%)	126 (91%)	12 (9%)	10	38
23	AU	89/115 (77%)	78 (88%)	11 (12%)	4	23
24	AV	100/107 (94%)	98 (98%)	2 (2%)	55	79
25	AW	100/126 (79%)	94 (94%)	6 (6%)	19	52
26	AX	105/133 (79%)	95 (90%)	10 (10%)	8	34
27	AY	119/135 (88%)	109 (92%)	10 (8%)	11	40
28	AZ	117/118 (99%)	100 (86%)	17 (14%)	3	18
29	Aa	120/121 (99%)	110 (92%)	10 (8%)	11	40
30	Ab	58/126 (46%)	54 (93%)	4 (7%)	15	47
31	Ac	88/97 (91%)	85 (97%)	3 (3%)	37	68
32	Ad	97/110 (88%)	96 (99%)	1 (1%)	76	88
33	Ae	115/121 (95%)	114 (99%)	1 (1%)	78	90
34	Af	88/89 (99%)	85 (97%)	3 (3%)	37	68

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	Ag	98/100 (98%)	93 (95%)	5 (5%)	24	57
36	Ah	109/110 (99%)	96 (88%)	13 (12%)	5	25
37	Ai	83/89 (93%)	80 (96%)	3 (4%)	35	66
38	Aj	71/80 (89%)	65 (92%)	6 (8%)	10	39
39	Ak	64/65 (98%)	46 (72%)	18 (28%)	0	3
40	Al	47/48 (98%)	44 (94%)	3 (6%)	17	50
41	Am	46/116 (40%)	45 (98%)	1 (2%)	52	78
42	An	24/24 (100%)	23 (96%)	1 (4%)	30	63
43	Ao	93/94 (99%)	85 (91%)	8 (9%)	10	38
44	Ap	74/75 (99%)	71 (96%)	3 (4%)	30	63
45	Aq	114/137 (83%)	90 (79%)	24 (21%)	1	5
46	At	106/121 (88%)	88 (83%)	18 (17%)	2	12
47	Au	196/196 (100%)	180 (92%)	16 (8%)	11	40
50	BA	180/243 (74%)	165 (92%)	15 (8%)	11	40
51	BB	193/231 (84%)	177 (92%)	16 (8%)	11	40
52	BC	188/225 (84%)	177 (94%)	11 (6%)	19	53
53	BD	183/202 (91%)	175 (96%)	8 (4%)	28	62
54	BE	220/225 (98%)	213 (97%)	7 (3%)	39	69
55	BF	160/170 (94%)	155 (97%)	5 (3%)	40	70
56	BG	202/218 (93%)	177 (88%)	25 (12%)	4	23
57	BH	164/174 (94%)	160 (98%)	4 (2%)	49	76
58	BI	179/180 (99%)	175 (98%)	4 (2%)	52	78
59	BJ	160/168 (95%)	151 (94%)	9 (6%)	21	54
60	BK	89/136 (65%)	83 (93%)	6 (7%)	16	48
61	BL	138/142 (97%)	134 (97%)	4 (3%)	42	71
62	BM	102/108 (94%)	101 (99%)	1 (1%)	76	88
63	BN	130/131 (99%)	122 (94%)	8 (6%)	18	51
64	BO	106/119 (89%)	99 (93%)	7 (7%)	16	49
65	BP	109/130 (84%)	93 (85%)	16 (15%)	3	18
66	BQ	115/121 (95%)	102 (89%)	13 (11%)	6	27
67	BR	113/122 (93%)	97 (86%)	16 (14%)	3	19

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	BS	121/132 (92%)	106 (88%)	15 (12%)	4	23
69	BT	113/115 (98%)	102 (90%)	11 (10%)	8	33
70	BU	90/107 (84%)	85 (94%)	5 (6%)	21	54
71	BV	65/67 (97%)	59 (91%)	6 (9%)	9	36
72	BW	112/113 (99%)	108 (96%)	4 (4%)	35	66
73	BX	111/115 (96%)	101 (91%)	10 (9%)	9	37
74	BY	107/115 (93%)	103 (96%)	4 (4%)	34	65
75	BZ	75/103 (73%)	57 (76%)	18 (24%)	0	4
76	Ba	84/98 (86%)	75 (89%)	9 (11%)	6	30
77	Bb	72/76 (95%)	72 (100%)	0	100	100
78	Bc	55/62 (89%)	52 (94%)	3 (6%)	21	54
79	Bd	45/49 (92%)	40 (89%)	5 (11%)	6	28
80	Be	44/48 (92%)	38 (86%)	6 (14%)	3	20
81	Bf	66/140 (47%)	65 (98%)	1 (2%)	65	84
82	Bg	272/275 (99%)	268 (98%)	4 (2%)	65	84
All	All	10112/11392 (89%)	9354 (92%)	758 (8%)	17	43

5 of 758 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	At	89	THR
58	BI	19	LYS
47	Au	185	LEU
46	At	87	ARG
52	BC	166	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 196 such sidechains are listed below:

Mol	Chain	Res	Type
46	At	70	GLN
57	BH	114	GLN
47	Au	143	ASN
52	BC	235	ASN
61	BL	13	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A3	156/194 (80%)	28 (17%)	4 (2%)
2	A4	118/121 (97%)	23 (19%)	1 (0%)
48	A2	3600/5029 (71%)	695 (19%)	48 (1%)
49	B1	1701/1869 (91%)	290 (17%)	19 (1%)
83	Bv	75/76 (98%)	38 (50%)	0
83	Bw	75/76 (98%)	34 (45%)	0
84	Bx	27/28 (96%)	18 (66%)	0
All	All	5752/7393 (77%)	1126 (19%)	72 (1%)

5 of 1126 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A3	2	G
1	A3	12	G
1	A3	16	G
1	A3	35	C
1	A3	59	A

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	B1	283	G
49	B1	1756	C
49	B1	369	C
49	B1	797	C
48	A2	1402	G

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 331 ligands modelled in this entry, 331 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
49	B1	8
48	A2	5

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B1	842:C	O3’	843:C	P	1.85
1	B1	558:G	O3’	559:G	P	1.84
1	B1	497:C	O3’	498:C	P	1.83
1	B1	72:C	O3’	73:C	P	1.82
1	B1	1253:A	O3’	1254:C	P	1.82

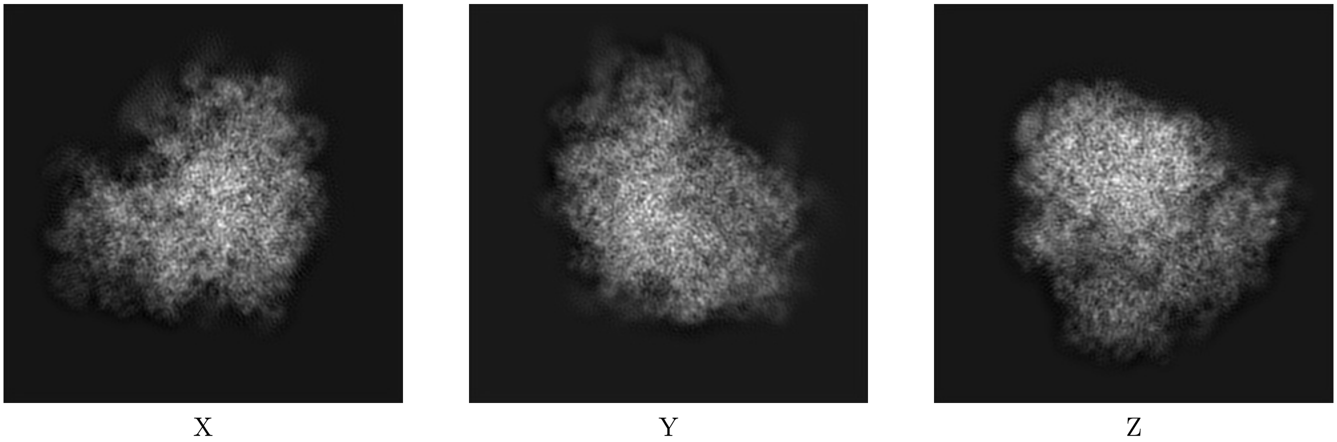
6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-2875. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections ⓘ

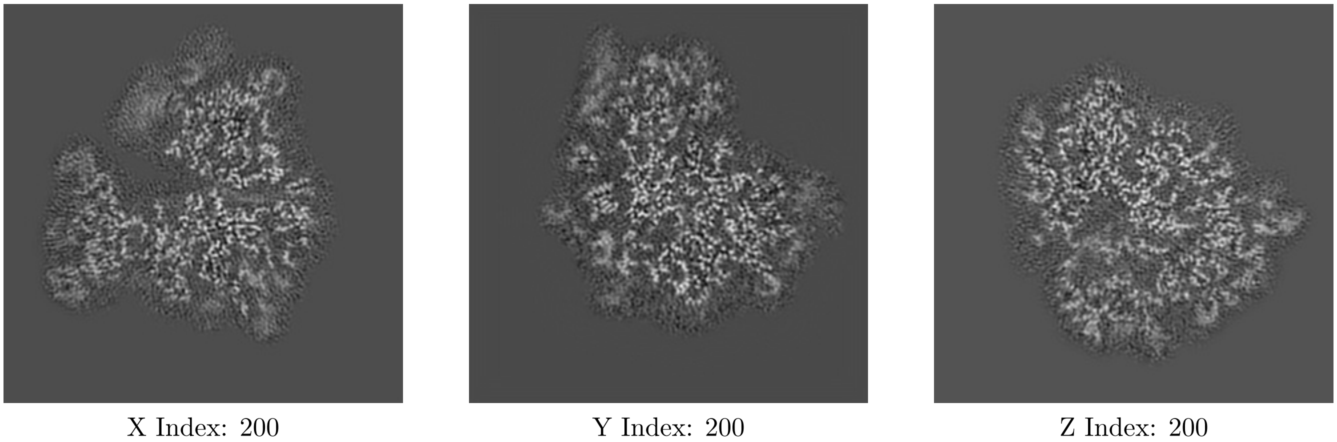
6.1.1 Primary map



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

6.2 Central slices ⓘ

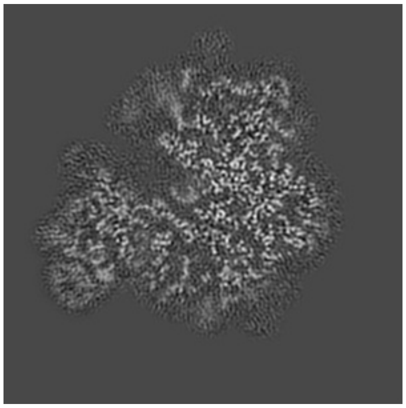
6.2.1 Primary map



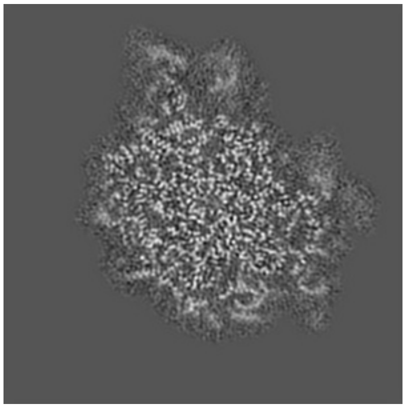
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices ⓘ

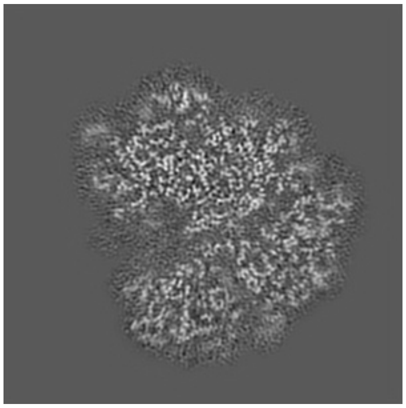
6.3.1 Primary map



X Index: 186



Y Index: 220

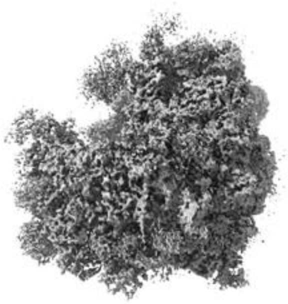


Z Index: 184

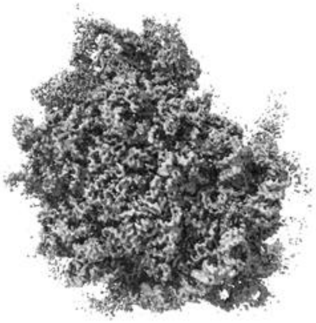
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views ⓘ

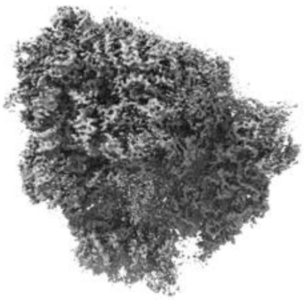
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

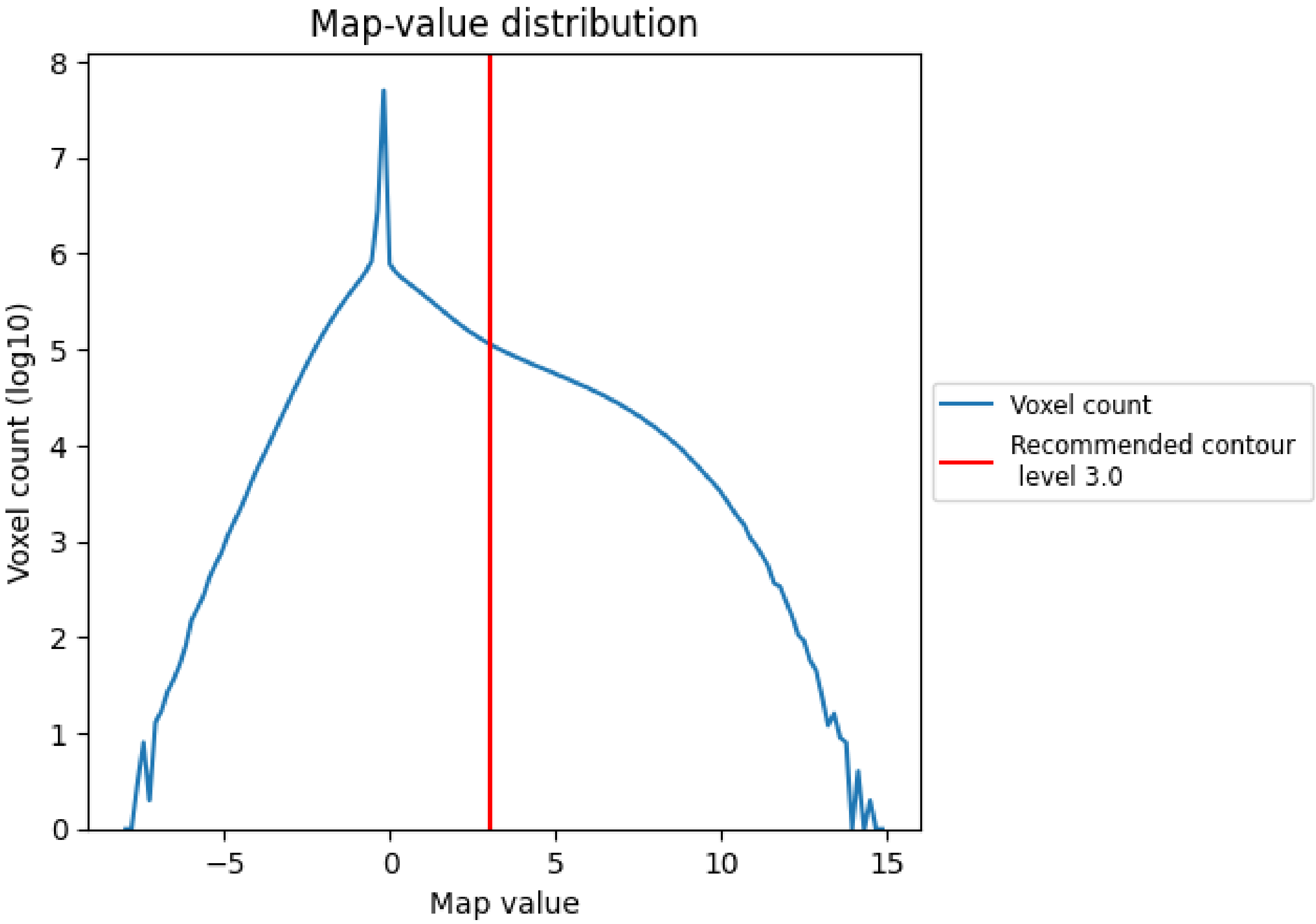
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

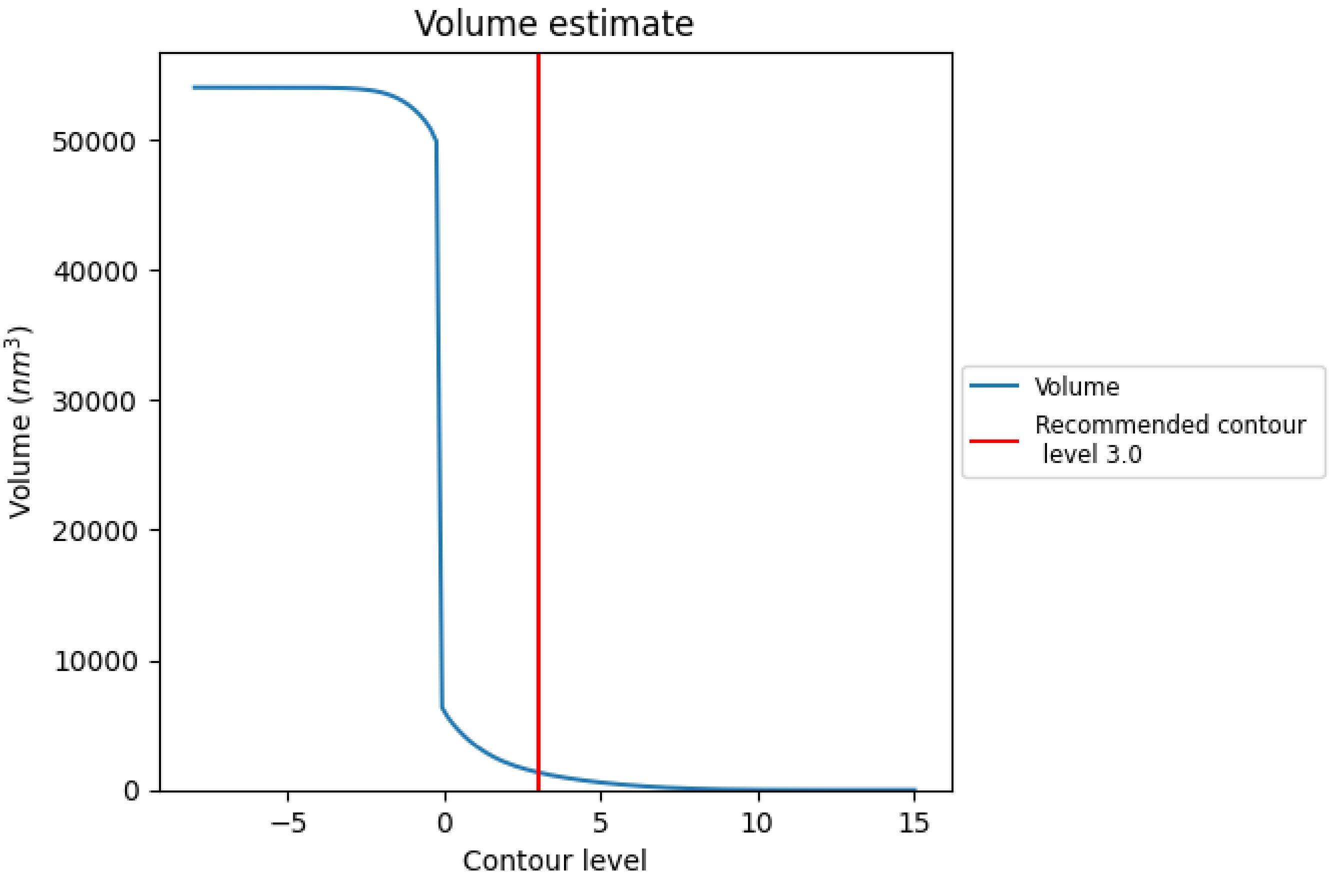
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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

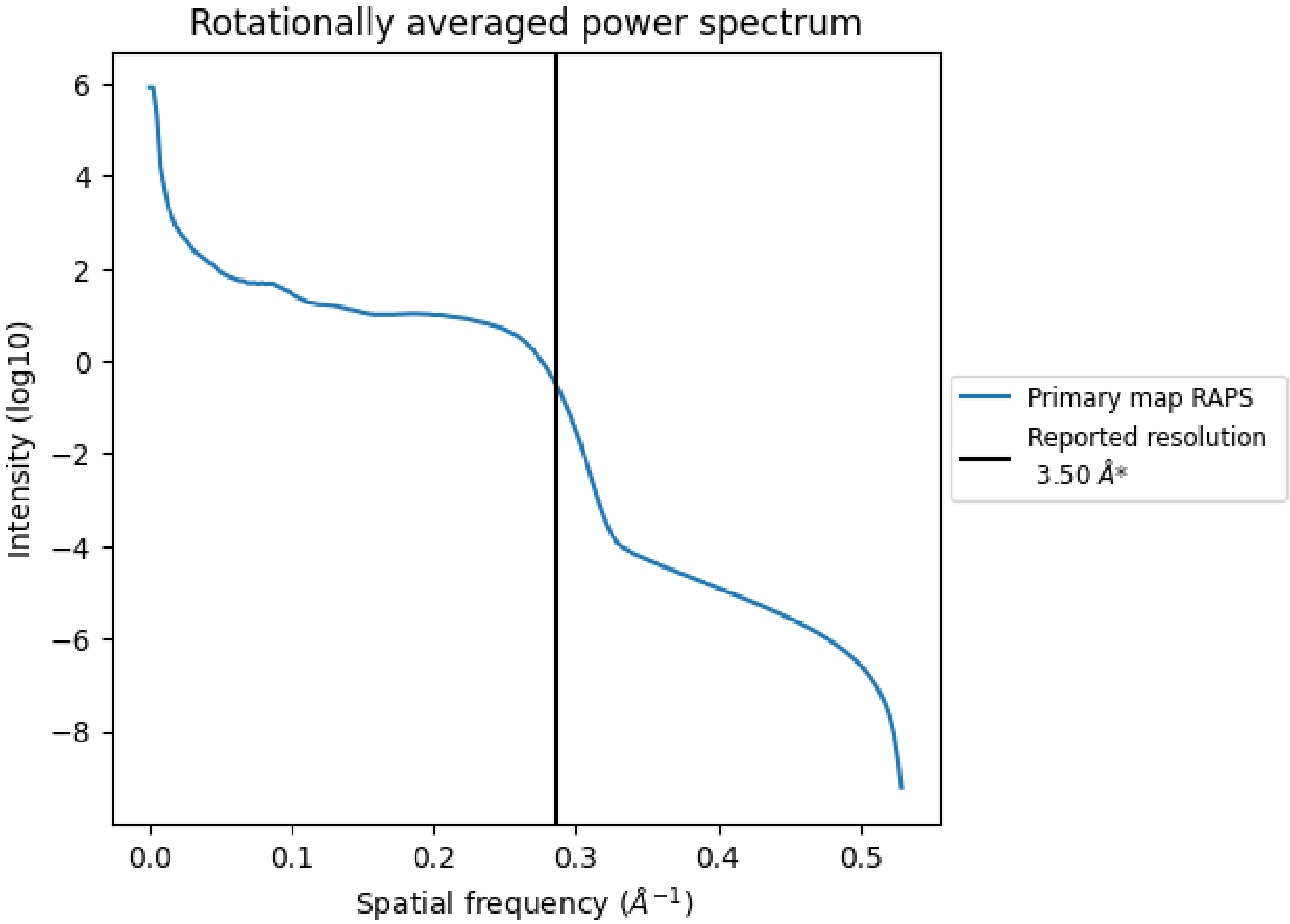
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1346 nm^3; this corresponds to an approximate mass of 1216 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.286 $Å^{-1}$

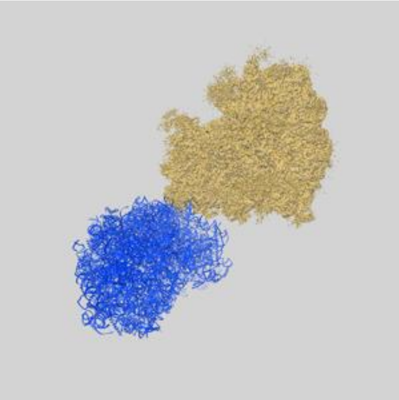
8 Fourier-Shell correlation

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

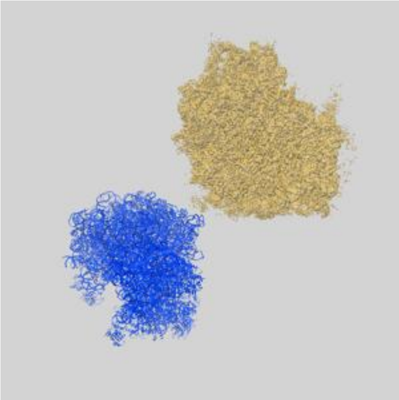
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-2875 and PDB model 5AJ0. Per-residue inclusion information can be found in section 3 on page 21.

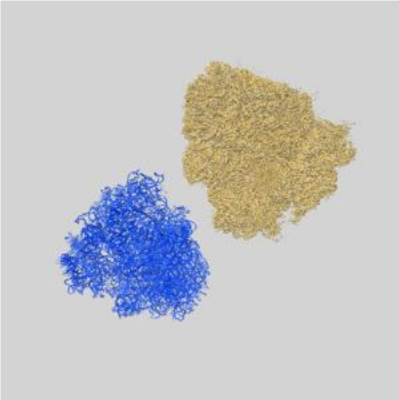
9.1 Map-model overlay



X



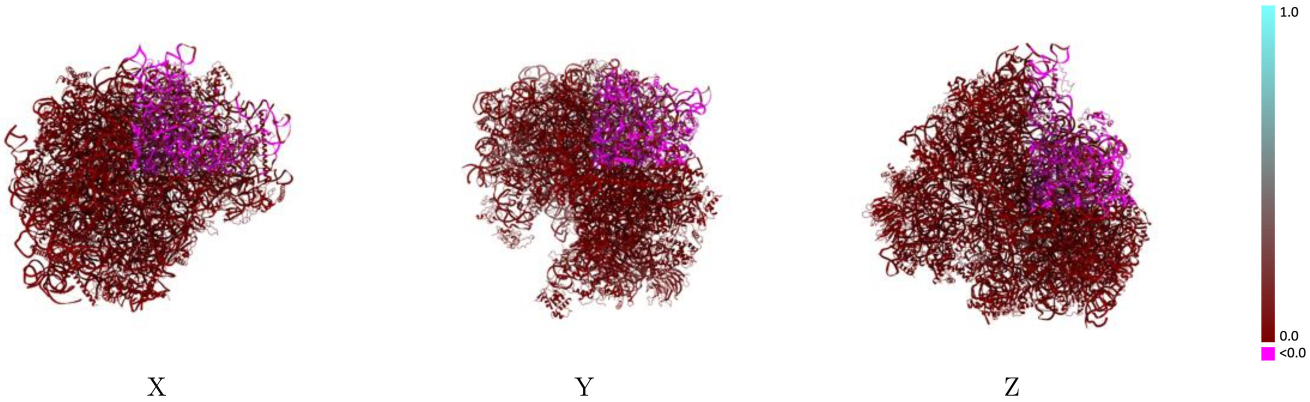
Y



Z

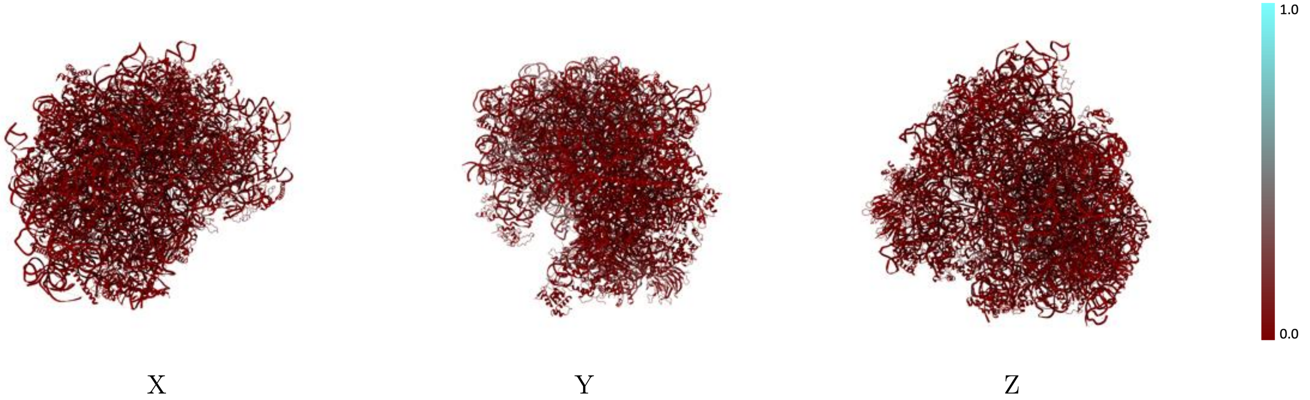
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model ⓘ



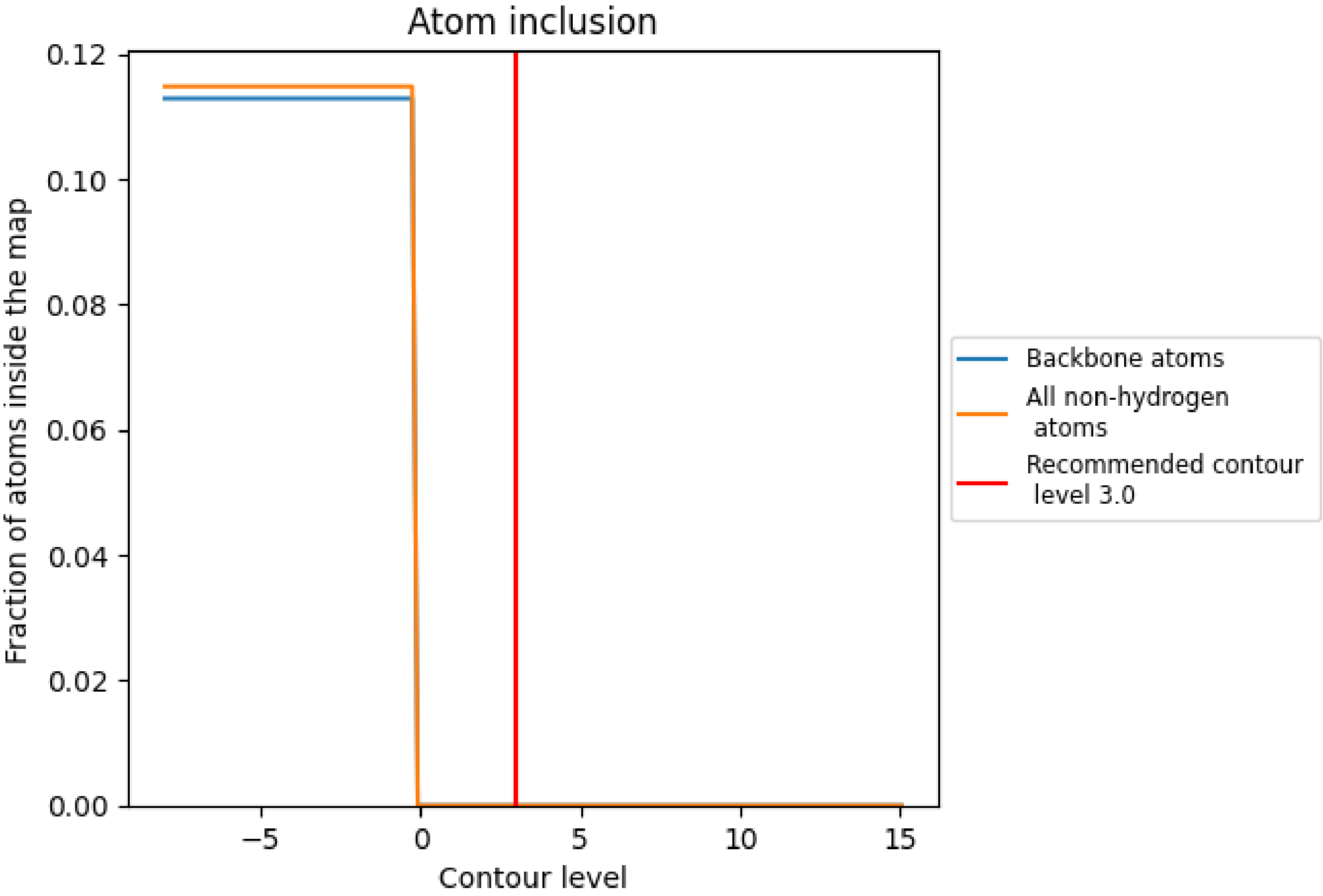
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 ⓘ



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.0).

9.4 Atom inclusion ⓘ



At the recommended contour level, 0% of all backbone atoms, 0% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	🟥 0.0000	🟥 0.0000
A2	🟥 0.0000	🟥 0.0000
A3	🟥 0.0000	🟥 0.0030
A4	🟥 0.0000	🟥 0.0000
AA	🟥 0.0000	🟥 0.0010
AB	🟥 0.0000	🟥 0.0000
AC	🟥 0.0000	🟥 0.0000
AD	🟥 0.0000	🟥 0.0000
AE	🟥 0.0000	🟥 0.0000
AF	🟥 0.0000	🟥 0.0000
AG	🟥 0.0000	🟪 -0.0010
AH	🟥 0.0000	🟥 0.0000
AI	🟥 0.0000	🟥 0.0000
AJ	🟥 0.0000	🟥 0.0000
AK	🟥 0.0000	🟥 0.0000
AL	🟥 0.0000	🟥 0.0000
AM	🟥 0.0000	🟥 0.0000
AN	🟥 0.0000	🟥 0.0000
AO	🟥 0.0000	🟥 0.0000
AP	🟥 0.0000	🟥 0.0010
AQ	🟥 0.0000	🟥 0.0000
AR	🟥 0.0000	🟥 0.0150
AS	🟥 0.0000	🟥 0.0000
AT	🟥 0.0000	🟥 0.0000
AU	🟥 0.0000	🟪 -0.0210
AV	🟥 0.0000	🟥 0.0000
AW	🟥 0.0000	🟥 0.0000
AX	🟥 0.0000	🟥 0.0020
AY	🟥 0.0000	🟥 0.0000
AZ	🟥 0.0000	🟥 0.0050
Aa	🟥 0.0000	🟥 0.0000
Ab	🟥 0.0000	🟥 0.0000
Ac	🟥 0.0000	🟪 -0.0080
Ad	🟥 0.0000	🟥 0.0000
Ae	🟥 0.0000	🟥 0.0000

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Af	🟥 0.0000	🟥 0.0000
Ag	🟥 0.0000	🟥 0.0190
Ah	🟥 0.0000	🟥 0.0000
Ai	🟥 0.0000	🟥 0.0000
Aj	🟥 0.0000	🟪 -0.0050
Ak	🟥 0.0000	🟥 0.0040
Al	🟥 0.0000	🟥 0.0220
Am	🟥 0.0000	🟥 0.0000
An	🟥 0.0000	🟥 0.0000
Ao	🟥 0.0000	🟥 0.0000
Ap	🟥 0.0000	🟪 -0.0110
Aq	🟥 0.0000	🟥 0.0000
At	🟥 0.0000	🟥 0.0000
Au	🟥 0.0000	🟥 0.0000
B1	🟥 0.0000	🟥 0.0000
BA	🟥 0.0000	🟥 0.0000
BB	🟥 0.0000	🟥 0.0000
BC	🟥 0.0000	🟥 0.0000
BD	🟥 0.0000	🟥 0.0000
BE	🟥 0.0000	🟥 0.0000
BF	🟥 0.0000	🟥 0.0000
BG	🟥 0.0000	🟥 0.0000
BH	🟥 0.0000	🟥 0.0000
BI	🟥 0.0000	🟥 0.0150
BJ	🟥 0.0000	🟥 0.0000
BK	🟥 0.0000	🟥 0.0000
BL	🟥 0.0000	🟥 0.0040
BM	🟥 0.0000	🟥 0.0000
BN	🟥 0.0000	🟥 0.0010
BO	🟥 0.0000	🟥 0.0000
BP	🟥 0.0000	🟥 0.0000
BQ	🟥 0.0000	🟥 0.0000
BR	🟥 0.0000	🟥 0.0000
BS	🟥 0.0000	🟥 0.0000
BT	🟥 0.0000	🟥 0.0000
BU	🟥 0.0000	🟥 0.0000
BV	🟥 0.0000	🟥 0.0000
BW	🟥 0.0000	🟥 0.0000
BX	🟥 0.0000	🟥 0.0000
BY	🟥 0.0000	🟥 0.0000
BZ	🟥 0.0000	🟥 0.0000
Ba	🟥 0.0000	🟥 0.0000

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bb	0.0000	0.0000
Bc	0.0000	0.0000
Bd	0.0000	0.0000
Be	0.0000	0.0000
Bf	0.0000	0.0000
Bg	0.0000	0.0000
Bv	0.0000	0.0000
Bw	0.0000	0.0000
Bx	0.0000	0.0000
By	0.0000	0.0220