wwPDB EM Validation Summary Report (i)

Dec 10, 2022 – 12:35 pm GMT

PDB ID	:	4UJE
EMDB ID	:	EMD-2620
Title	:	Regulation of the mammalian elongation cycle by 40S subunit rolling: a eukaryotic-specific ribosome rearrangement
Authors	:	Budkevich, T.V.; Giesebrecht, J.; Behrmann, E.; Loerke, J.; Ramrath, D.J.F.; Mielke, T.; Ismer, J.; Hildebrand, P.; Tung, C.-S.; Nierhaus, K.H.; Sanbonmatsu, K.Y.; Spahn, C.M.T.
Deposited on	:	2014-04-05
Resolution	:	6.90 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

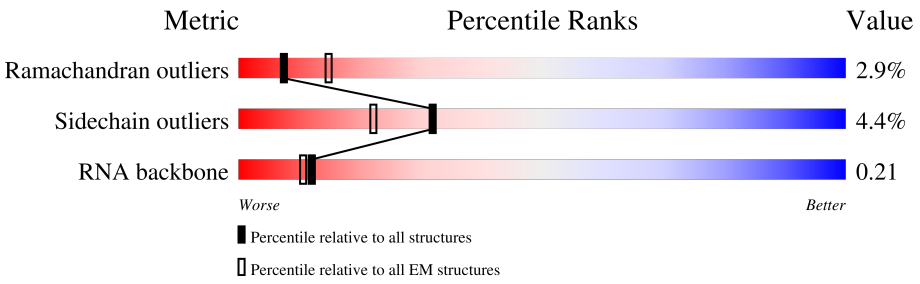
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 6.90 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	AV	76	11% 51% 49%
2	AW	76	13% 54% 46%
3	AX	28	50% 32% 64% •
4	B1	1869	5% 36% 55% • 7%
5	BA	295	29% 72% • 26%
6	BB	264	20% 71% 8% • 19%
7	BC	293	19% 72% • 24%
8	BD	243	14% 81% 6% 13%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	BE	263	10% 92% 6%
10	BF	204	20% 84% 8% 8%
11	BG	249	15% 87% 6% 7%
12	BH	194	52% 94%
13	BI	208	33% 91% 8%
14	BJ	194	9% 86% 7% 8%
15	BK	165	52% 5% 43%
16	BL	158	37% 87% 5% 8%
17	BM	132	58% 83% 7% 9%
18	BN	151	30% 95%
19	BO	151	26% 85% 5% 9%
20	BP	145	8% 75% 6% 19%
21	BQ	146	7% 91% 5%
22	BR	135	24% 76% 5% 19%
23	BS	152	9% 82% 11% 7%
24	BT	145	6% 92% 6%
25	BU	119	15% 81% 15%
26	BV	83	53% 96%
27	BW	130	17% 94% 5%
28	BX	143	37% 85% 8% 6%
29	BY	133	9% 84% 8% 8%
30	BZ	125	11% 55% 6% 39%
31	Ba	115	30% 74% 9% 17%
32	Bb	84	27% 90% 5% 5%
33	Bc	69	29% 83% 7% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	Bd	56	9% 88% 7% 5%
35	Be	59	20% 81% 5% 14%
36	Bf	156	19% 37% 61%
37	Bg	317	28% 93% 5%
38	CA	257	48% 93%
39	CB	403	16% 90% 7%
40	CC	427	21% 78% 6% 15%
41	CD	297	8% 93%
42	CE	288	16% 50% 5% 45%
43	CF	248	26% 90% 6%
44	CG	266	24% 83% 5% 12%
45	CH	192	13% 95% 5%
46	CI	214	28% 86% 6% 8%
47	CJ	178	8% 85% 10%
48	CL	211	30% 84% 9% 5%
49	CM	215	9% 62% 35%
50	CN	204	24% 98%
51	CO	203	13% 94%
52	CP	184	11% 78% 5% 17%
53	CQ	188	30% 92% 6%
54	CR	196	25% 86% 7% 7%
55	CS	176	19% 91% 7%
56	CT	160	26% 95%
57	CU	128	26% 77% 20%
58	CV	140	36% 89% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	CW	157	12% 39% 59%
60	CX	156	19% 75% 24%
61	CY	145	8% 83% 6% 12%
62	CZ	136	24% 93% 7%
63	Ca	148	24% 94% 5%
64	Cb	159	17% 40% 57%
65	Cc	115	32% 88% 10%
66	Cd	125	16% 83% 13%
67	Ce	135	33% 90% 5%
68	Cf	110	24% 86% 10%
69	Cg	117	31% 87% 10%
70	Ch	123	15% 94% 5%
71	Ci	105	20% 83% 8% 8%
72	Cj	97	20% 84% 12%
73	Ck	70	36% 97%
74	Cl	51	35% 94%
75	Cm	128	12% 38% 59%
76	Cn	25	44% 100%
77	Co	106	47% 93% 7%
78	Cp	92	41% 93% 5%
79	Ct	137	36% 86% 7% 5%
80	Cu	210	77% 92% 8%
81	A2	5025	5% 30% 41% 28%
82	A3	194	5% 39% 41% 19%
83	A4	121	40% 56%

2 Entry composition (i)

There are 83 unique types of molecules in this entry. The entry contains 215620 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 TRNA-LYS.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AV	76	1619	723	290	531	75	0	0

- Molecule 2 is a RNA chain called TRNA-PHE.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
2	AW	76	1626	729	290	531	75	1	0	0

- Molecule 3 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	AX	28	560	252	56	224	28	0	0

- Molecule 4 is a RNA chain called 18S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	B1	1742	37159	16589	6665	12164	1741	0	0

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	BA	218	1719	1091	301	319	8	0	0

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN S3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	BB	213	1729	1098	309	308	14	0	0

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN S2.

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

- Molecule 8 is a protein called 40S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	BD	212	1646	1050	299	290	7	0	0

- Molecule 9 is a protein called 40S RIBOSOMAL PROTEIN S4, Y ISOFORM 1.

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

- Molecule 10 is a protein called 40S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	BF	188	1486	930	283	266	7	0	0

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN S6.

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

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	BH	191	1535	978	282	274	1	0	0

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	BI	207	1695	1064	334	292	5	0	0

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN S9.

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

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	BK	94	791	519	138	129	5	0	0

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	BL	146	1199	764	224	205	6	0	0

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S12.

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

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	BN	150	1207	773	229	204	1	0	0

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	BO	137	1023	627	200	190	6	0	0

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	BP	118	981	625	183	166	7	0	0

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	BQ	139	1108	704	210	191	3	0	0

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	BR	109	893	561	170	159	3	0	0

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	BS	142	1172	736	236	199	1	0	0

- Molecule 24 is a protein called 40S RIBOSOMAL PROTEIN S19.

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

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	BU	101	803	502	153	144	4	0	0

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	BV	83	636	393	117	121	5	0	0

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	BW	129	1033	659	193	175	6	0	0

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	BX	134	1046	663	205	176	2	0	0

- Molecule 29 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	BY	122	1002	635	196	166	5	0	0

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	BZ	76	605	387	112	105	1	0	0

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	Ba	96	767	476	159	127	5	0	0

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S27.

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

- Molecule 33 is a protein called 40S RIBOSOMAL PROTEIN S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	Bc	62	490	298	99	91	2	0	0

- Molecule 34 is a protein called 40S RIBOSOMAL PROTEIN S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Bd	53	444	278	90	71	5	0	0

- Molecule 35 is a protein called 40S RIBOSOMAL PROTEIN S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Be	51	412	258	90	63	1	0	0

- Molecule 36 is a protein called UBIQUITIN-40S RIBOSOMAL PROTEIN S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Bf	61	497	312	94	84	7	0	0

- Molecule 37 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1.

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

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	CA	247	1888	1183	388	311	6	0	1

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	CB	396	3190	2030	601	545	14	0	1

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	CC	364	2889	1817	578	480	14	0	1

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	CD	290	2361	1489	431	427	14	0	0

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	CE	158	1286	834	238	214	0	0

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	CF	234	1949	1252	376	312	9	0	0

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	CG	235	1881	1197	363	317	4	0	1

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	CH	192	1535	965	286	278	6	0	0

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	CI	196	1604	1022	308	262	12	0	0

- Molecule 47 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	CJ	170	1362	861	254	241	6	0	0

- Molecule 48 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	CL	200	1617	1013	335	265	4	0	1

- Molecule 49 is a protein called 60S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	CM	140	1139	730	219	183	7	0	1

- Molecule 50 is a protein called 60S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	CN	204	1708	1077	360	266	5	0	0

- Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	CO	196	1607	1034	316	252	5	0	1

- Molecule 52 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	CP	153	1234	771	241	213	9	0	1

- Molecule 53 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	CQ	184	1493	933	311	244	5	0	0

- Molecule 54 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	CR	183	1526	943	331	242	10	0	1

- Molecule 55 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	CS	173	1438	916	280	232	10	0	0

- Molecule 56 is a protein called 60S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	CT	159	1297	823	252	216	6	0	0

- Molecule 57 is a protein called 60S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	CU	102	827	529	146	150	2	0	1

- Molecule 58 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	CV	128	963	610	181	167	5	0	0

- Molecule 59 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	CW	64	529	337	104	85	3	0	1

- Molecule 60 is a protein called 60S RIBOSOMAL PROTEIN L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	CX	119	975	624	183	167	1	0	0

- Molecule 61 is a protein called 60S RIBOSOMAL PROTEIN L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	CY	128	1065	668	217	177	3	0	1

- Molecule 62 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	CZ	136	1114	719	209	182	4	0	0

- Molecule 63 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	Ca	147	1161	736	237	185	3	0	0

- Molecule 64 is a protein called 60S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	Cb	69	560	344	123	90	3	0	1

- Molecule 65 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	Cc	104	802	508	142	145	7	0	1

- Molecule 66 is a protein called 60S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	Cd	109	904	570	174	158	2	0	0

- Molecule 67 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Ce	128	1053	664	219	165	5	0	1

- Molecule 68 is a protein called 60S RIBOSOMAL PROTEIN L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	Cf	107	865	550	172	140	3	0	0

- Molecule 69 is a protein called 60S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Cg	115	907	566	188	147	6	0	1

- Molecule 70 is a protein called 60S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	Ch	122	1014	641	205	167	1	0	0

- Molecule 71 is a protein called 60S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	Ci	97	783	488	168	122	5	0	1

- Molecule 72 is a protein called 60S RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	Cj	85	690	423	153	109	5	0	1

- Molecule 73 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	Ck	69	568	366	103	98	1	0	0

- Molecule 74 is a protein called 60S RIBOSOMAL PROTEIN L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	Cl	50	443	281	98	63	1	0	0

- Molecule 75 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	Cm	52	428	266	90	66	6	0	0

- Molecule 76 is a protein called 60S RIBOSOMAL PROTEIN L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	Cn	25	239	145	64	27	3	0	0

- Molecule 77 is a protein called 60S RIBOSOMAL PROTEIN L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	Co	106	870	547	176	140	7	0	0

- Molecule 78 is a protein called 60S RIBOSOMAL PROTEIN L37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	Cp	91	707	445	136	119	7	0	0

- Molecule 79 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	Ct	130	1043	646	220	172	5	0	1

- Molecule 80 is a protein called 60S RIBOSOMAL PROTEIN L10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	Cu	210	1621	990	278	347	6	0	0

- Molecule 81 is a RNA chain called 28S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
81	A2	3616	77488	34508	14153	25212	3615	0	0

- Molecule 82 is a RNA chain called 5.8S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
82	A3	157	3334	1489	587	1102	156	0	0

- Molecule 83 is a RNA chain called 5S Ribosomal RNA.

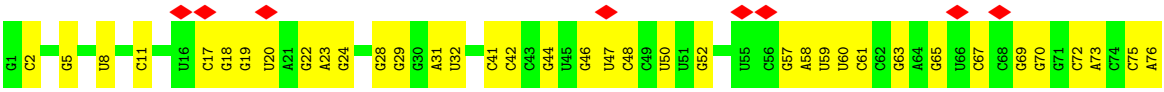
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
83	A4	119	2538	1132	454	834	118	0	0

3 Residue-property plots (i)

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

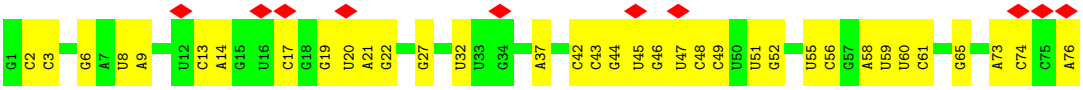
- Molecule 1: TRNA-LYS

Chain AV:



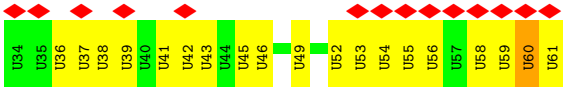
- Molecule 2: TRNA-PHE

Chain AW:



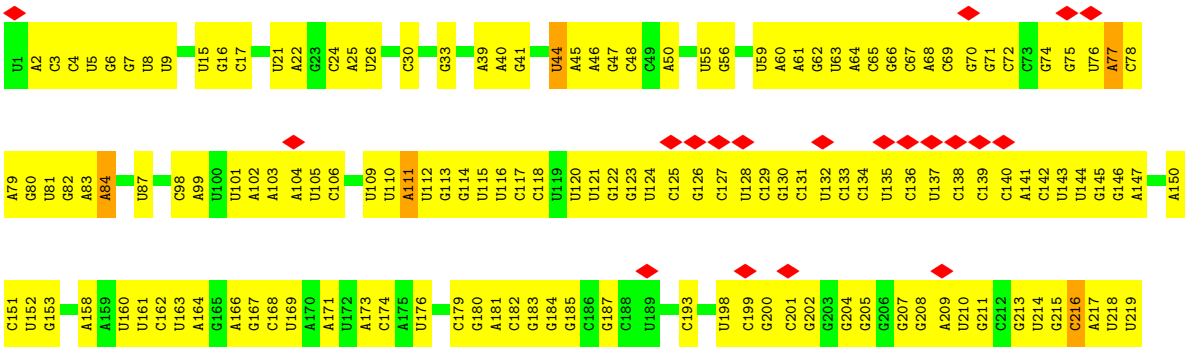
- Molecule 3: Messenger RNA

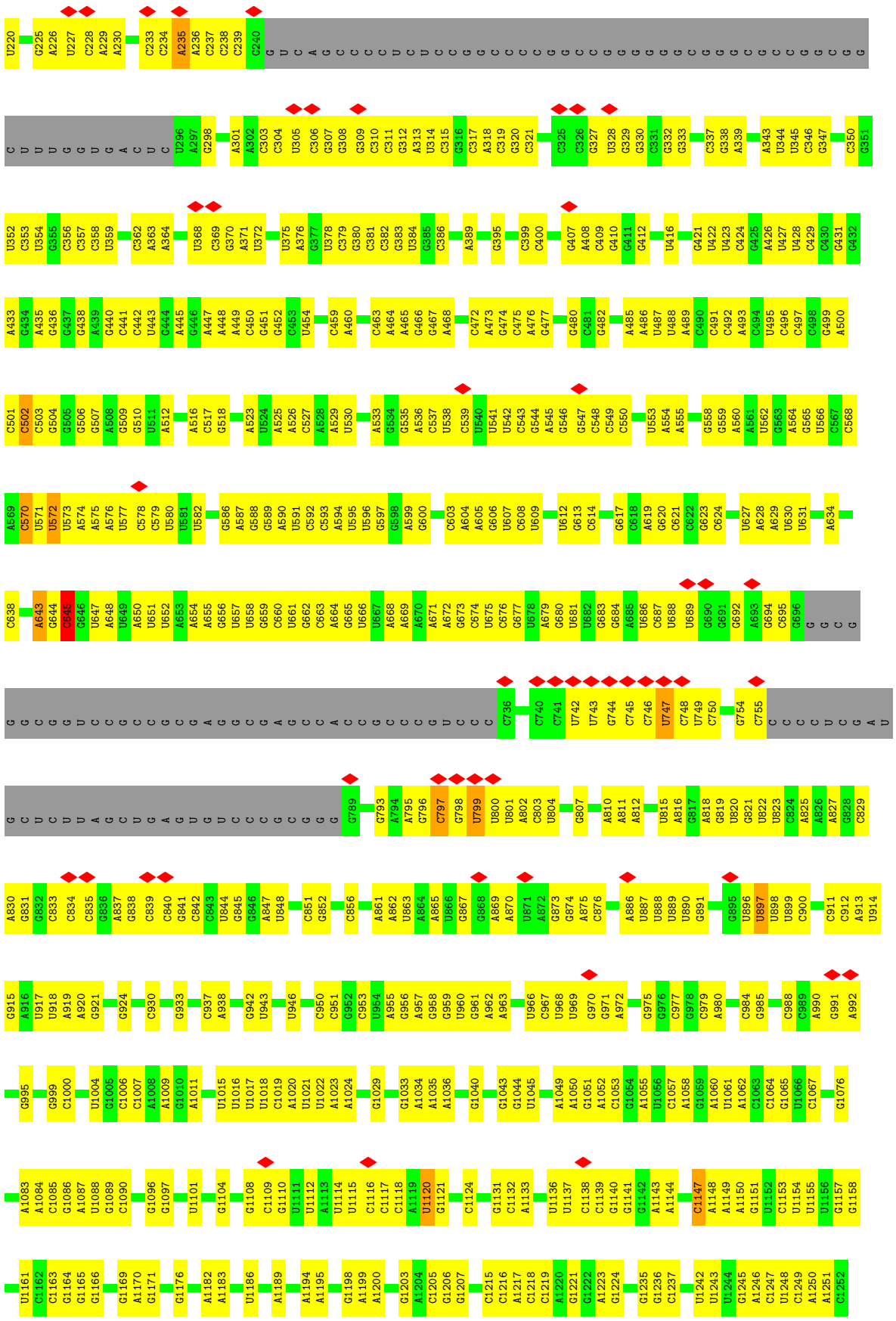
Chain AX:

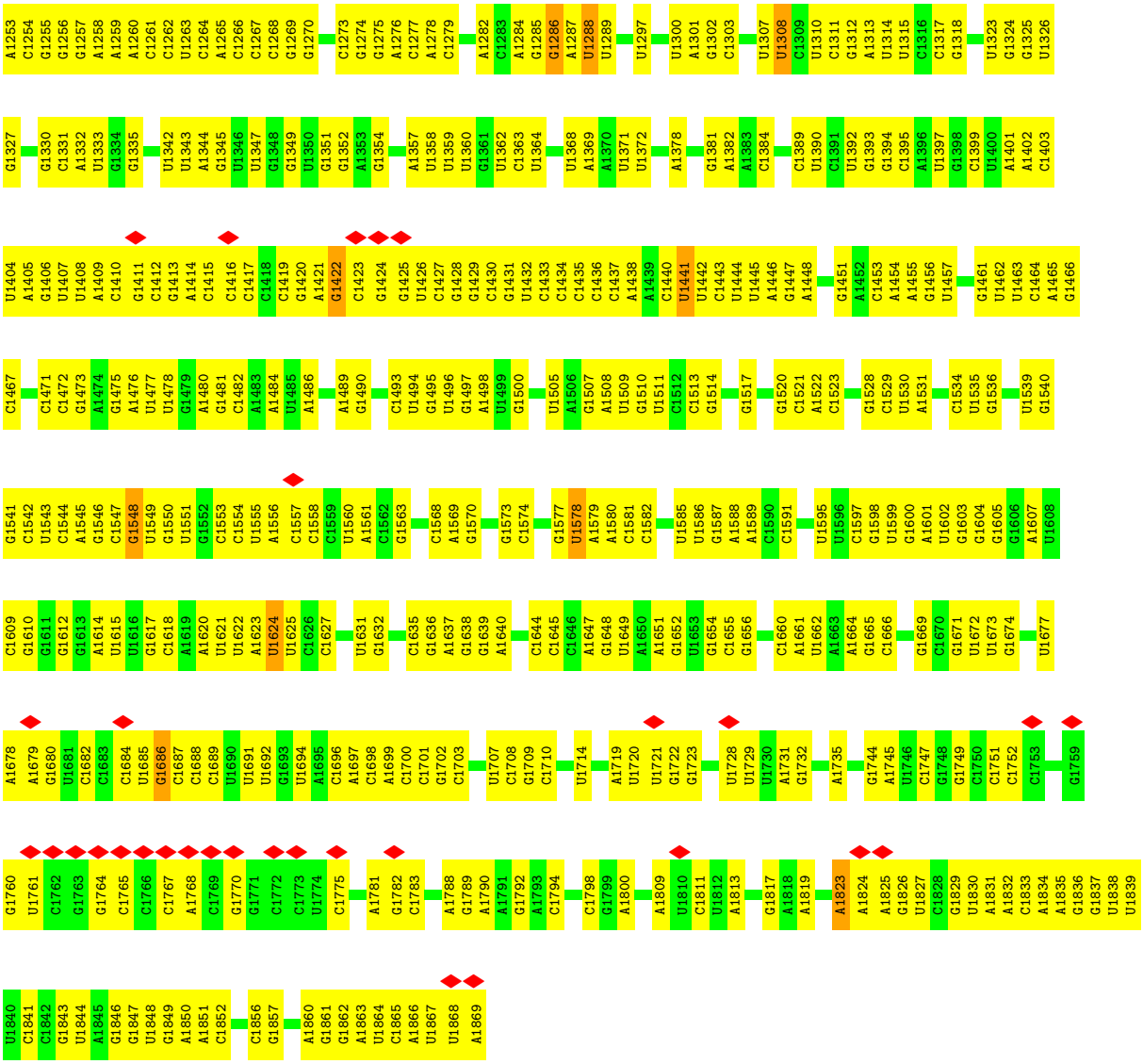


- Molecule 4: 18S Ribosomal RNA

Chain B1:

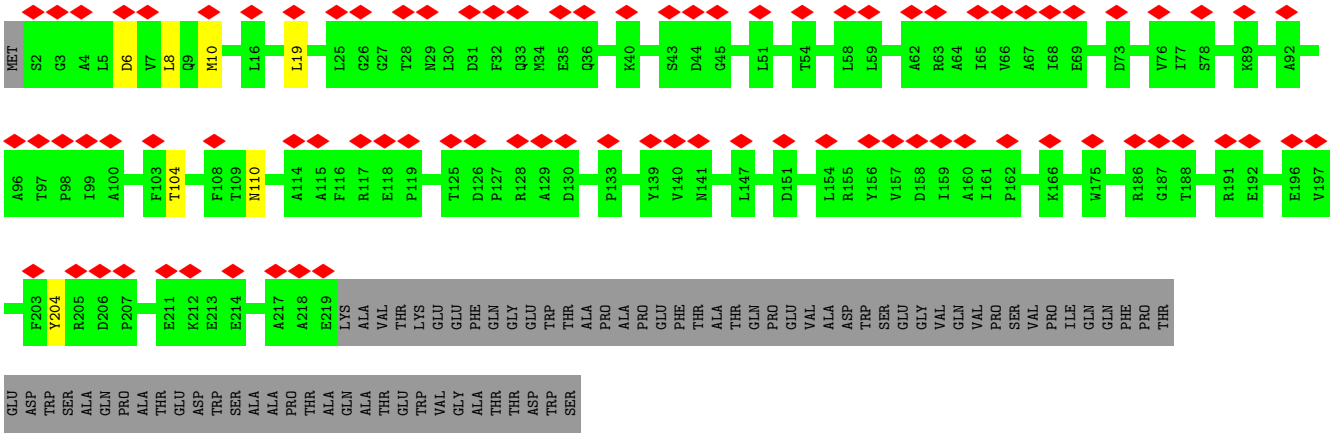



U220 G225 A226 U227 C228 A229 A230 C233 C234 A235 A236 A237 C238 C239 G240
C U U U G G U G A C U C U296 A297 C298 A301 A302 C303 C304 U305 C306 G307 C308 G309 C310 C311 G312 A313 U314 C315 G316 C317 A318 C319 G320 C321 C325 C326 G327 U328 G329 G330 C331 G332 G333 C337 G338 A339 A343 U344 U345 C346 G347 C350 G351
U352 C353 U354 G355 C356 C357 C358 U359 C362 A363 A364 U368 C369 G370 A371 U372 U375 A376 G377 U378 C379 G380 C381 C382 G383 U384 G385 C386 A389 G395 C399 C400 G407 A408 C409 G410 G411 G412 U416 G421 U422 U423 C424 G425 A426 U427 U428 C429 C430 G431 G432
A433 G434 A435 G436 G437 G438 A439 G440 C441 C442 U443 G444 A445 G446 A447 A448 A449 C450 G451 G452 C453 U454 C459 A460 C463 A464 A465 G466 G467 A468 C472 A473 G474 C475 A476 G477 G480 C481 G482 A485 A486 U487 U488 A489 C490 C491 C492 A493 C494 U495 C496 C497 C498 G499 A500
C501 C502 C503 G504 G505 G506 G507 A508 G509 G510 U511 A512 A516 C517 G518 A523 U524 A525 A526 C527 A528 A529 U530 A533 G534 G535 A536 C537 U538 C539 U540 U541 U542 C543 G544 A545 G546 G547 C548 C549 C550 U553 A554 A555 G558 G559 A560 A561 U562 G563 A564 G565 U566 C567 C568
A569 C570 U571 U572 U573 A574 A575 A576 U577 C578 C579 U580 U581 U582 G586 A587 G588 G589 A590 U591 C592 C593 A594 U595 U596 G597 G598 A599 G600 C603 A604 A605 G606 U607 C608 U609 U612 G613 C614 G617 C618 A619 G620 C621 C622 G623 C624 U627 A628 A629 U630 U631 A634
C638 A643 G644 C645 G646 U647 A648 U649 A650 U651 U652 A653 A654 A655 G656 U657 U658 G659 C660 U661 G662 C663 A664 G665 U666 U667 A668 A669 A670 A671 A672 G673 C674 U675 C676 G677 U678 A679 G680 U681 U682 G683 G684 A685 U686 C687 U688 U689 G690 G691 G692 A693 G694 C695 G696 G G C G
G G C G G U C C G C C G G C G A G G C C G A C C C G C G C C G U C C G C U U C G A U C736 C740 C741 U742 U743 G744 C745 C746 U747 C748 U749 C750 G754 C755 C C C C U C G A U
G C U C U U A G C U C G A G U G U C C C C G C G G G G789 G793 A794 A795 G796 C797 G798 U799 U800 U801 A802 C803 U804 G807 A810 A811 A812 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 C851 G852 C856 A861 A862 U863 A864 A865 U866 G867 G868 A869 A870 U871 A872 G873 G874 A875 C876 A886 U887 U888 U889 U890 G891 G895 U896 U897 U898 U899 C900 C911 C912 A913 U914
G915 A916 U917 U918 A919 A920 G921 G924 C930 G933 C937 A938 G942 U943 U946 C950 C951 G952 C953 U954 A955 A956 A957 G958 G959 U960 G961 A962 A963 U966 C967 U968 U969 G970 G971 A972 G975 G976 C977 G978 C979 A980 C984 G985 C988 C989 A990 G991 A992
G995 G999 C1000 U1004 G1005 C1006 C1007 A1008 A1009 G1010 A1011 U1015 U1016 U1017 U1018 C1019 A1020 U1021 U1022 A1023 A1024 G1029 G1033 A1034 A1035 A1036 G1040 G1043 G1044 U1045 A1049 A1050 G1051 A1052 C1053 G1054 A1055 U1056 C1057 A1058 G1059 A1060 U1061 A1062 C1063 C1064 G1065 U1066 C1067 G1076
A1083 A1084 C1085 G1086 A1087 U1088 G1089 C1090 G1096 G1097 U1101 G1104 G1108 C1109 G1110 U1111 U1112 A1113 U1114 U1115 C1116 C1117 C1118 A1119 U1120 G1121 C1124 G1131 C1132 A1133 U1136 U1137 C1138 C1139 G1140 G1141 G1142 A1143 A1144 C1147 A1148 A1149 A1150 G1151 U1152 C1153 U1154 U1155 U1156 G1157 G1158
U1161 C1162 C1163 G1164 G1165 G1166 G1169 A1170 G1171 G1176 A1182 A1183 U1186 A1189 A1194 A1195 G1198 A1199 A1200 G1203 A1204 C1205 G1206 G1207 C1215 C1216 A1217 C1218 C1219 A1220 G1221 G1222 A1223 G1224 G1235 G1236 C1237 U1242 U1243 U1244 G1245 A1246 C1247 U1248 C1249 A1250 A1251 C1252



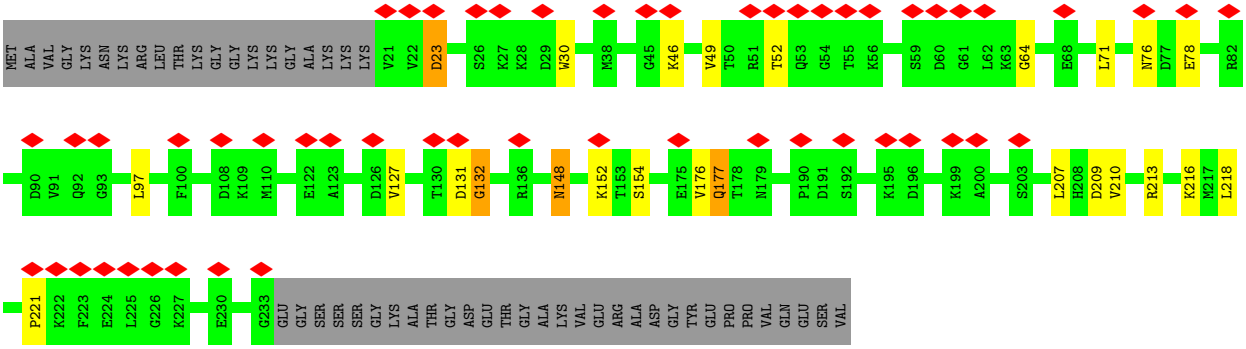
• Molecule 5: 40S RIBOSOMAL PROTEIN SA

Chain BA:



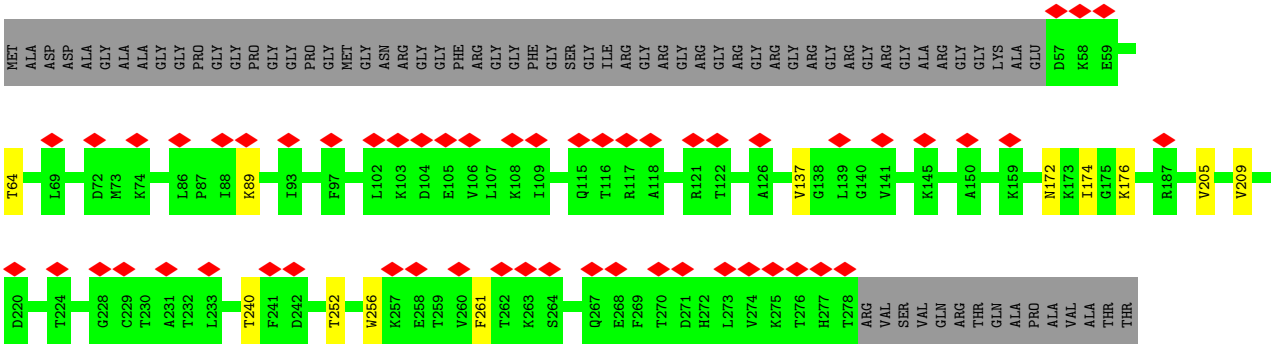
- Molecule 6: 40S RIBOSOMAL PROTEIN S3A

Chain BB:



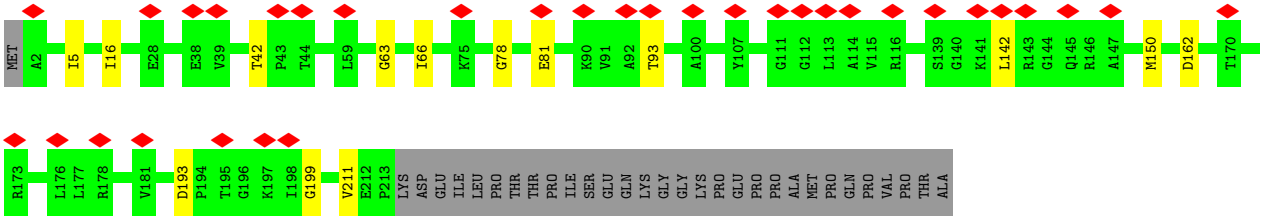
- Molecule 7: 40S RIBOSOMAL PROTEIN S2

Chain BC:



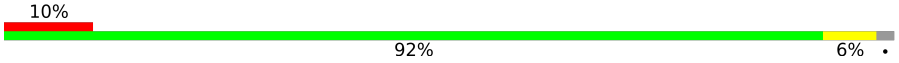
- Molecule 8: 40S RIBOSOMAL PROTEIN S3

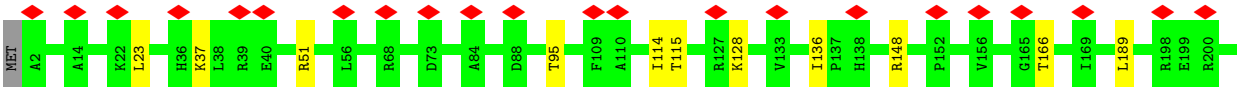
Chain BD:

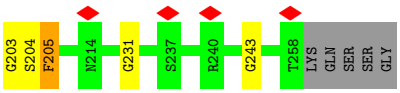


- Molecule 9: 40S RIBOSOMAL PROTEIN S4, Y ISOFORM 1

Chain BE:

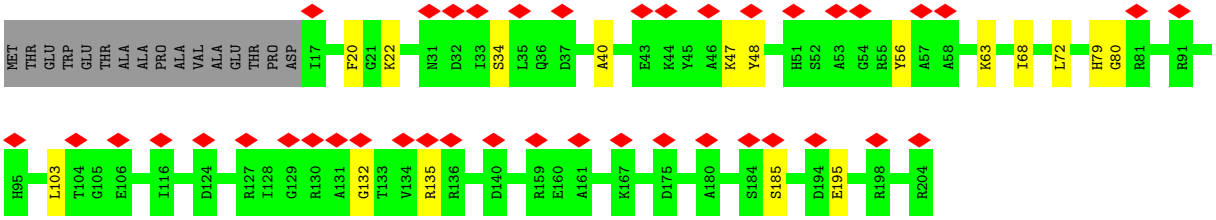






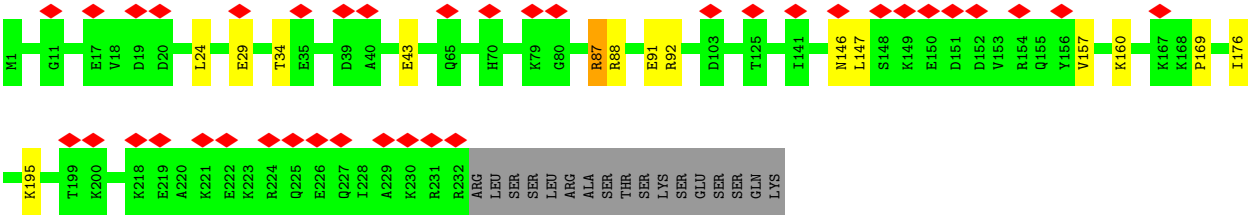
- Molecule 10: 40S RIBOSOMAL PROTEIN S5

Chain BF:



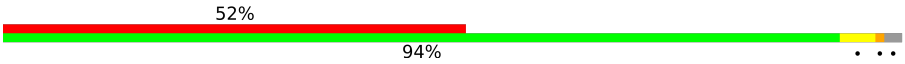
- Molecule 11: 40S RIBOSOMAL PROTEIN S6

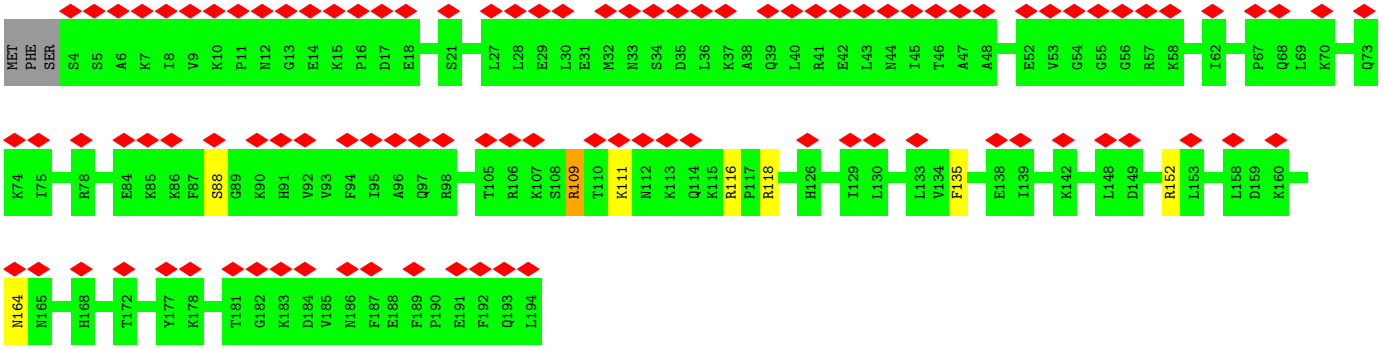
Chain BG:



- Molecule 12: 40S RIBOSOMAL PROTEIN S7

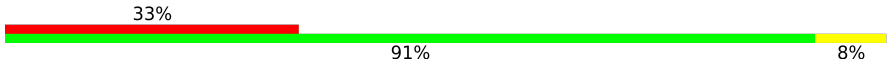
Chain BH:

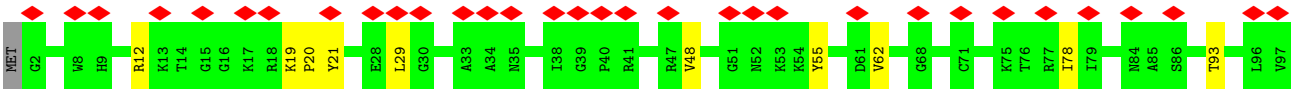


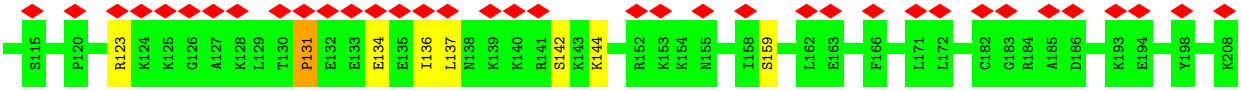


- Molecule 13: 40S RIBOSOMAL PROTEIN S8

Chain BI:

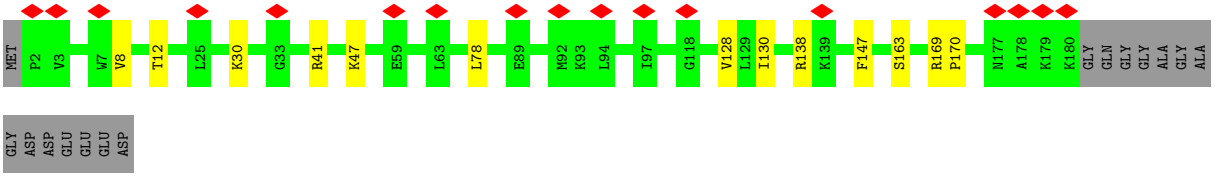






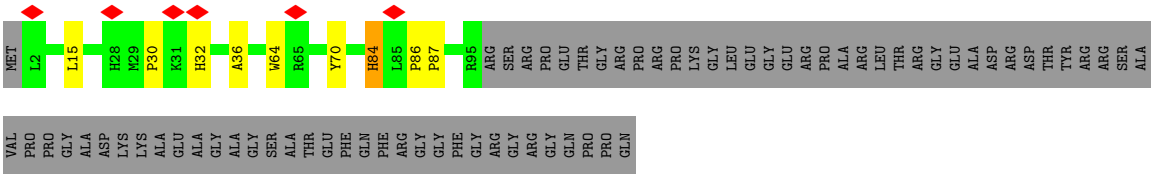
- Molecule 14: 40S RIBOSOMAL PROTEIN S9

Chain BJ:



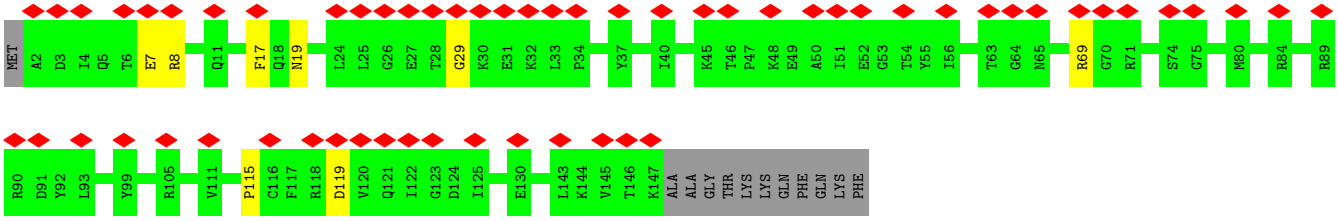
- Molecule 15: 40S RIBOSOMAL PROTEIN S10

Chain BK:



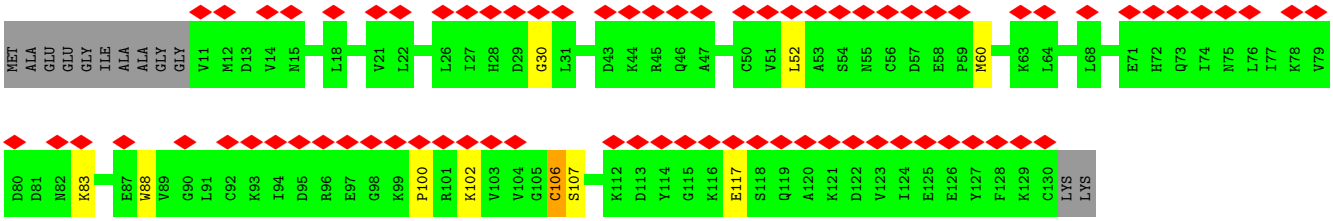
- Molecule 16: 40S RIBOSOMAL PROTEIN S11

Chain BL:



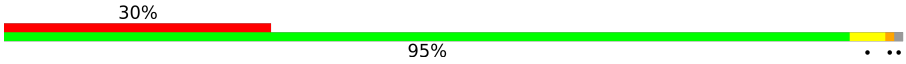
- Molecule 17: 40S RIBOSOMAL PROTEIN S12

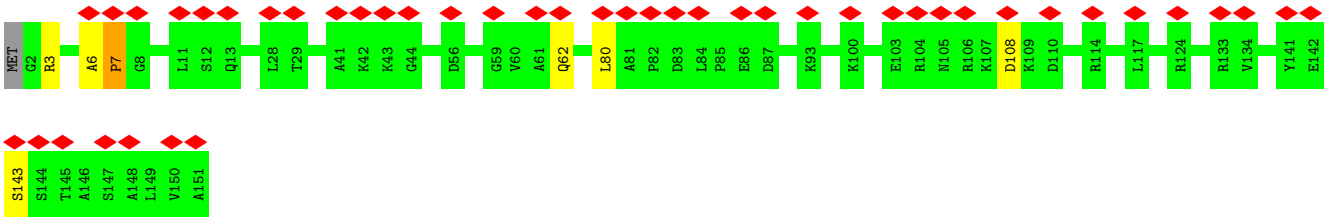
Chain BM:



- Molecule 18: 40S RIBOSOMAL PROTEIN S13

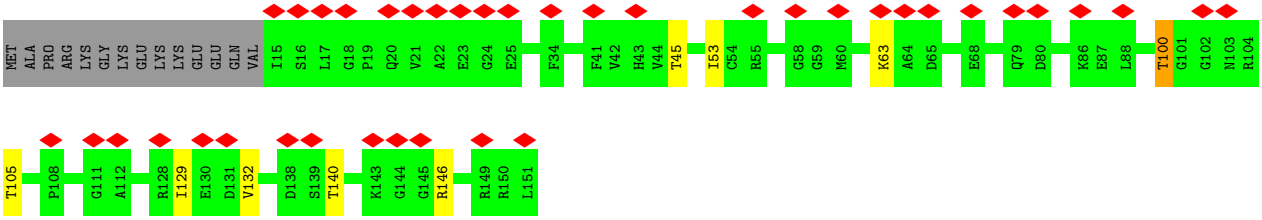
Chain BN:





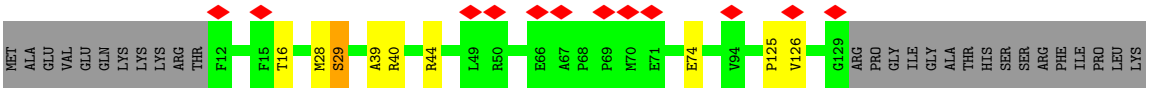
- Molecule 19: 40S RIBOSOMAL PROTEIN S14

Chain BO:



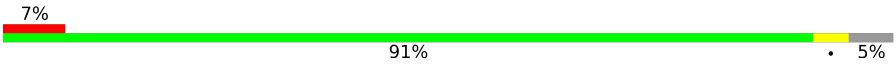
- Molecule 20: 40S RIBOSOMAL PROTEIN S15

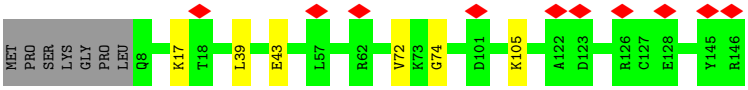
Chain BP:



- Molecule 21: 40S RIBOSOMAL PROTEIN S16

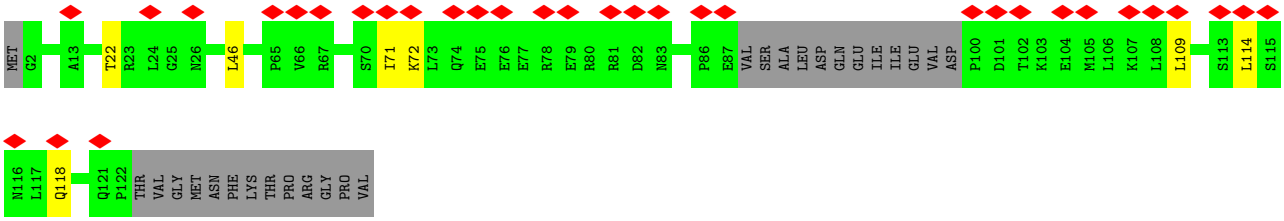
Chain BQ:





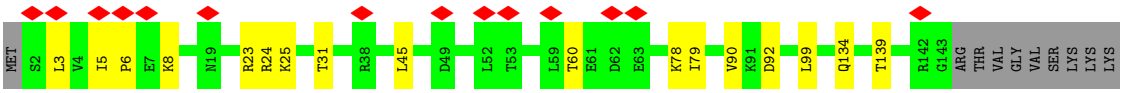
- Molecule 22: 40S RIBOSOMAL PROTEIN S17

Chain BR:



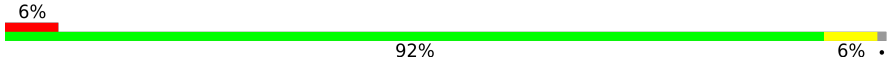
- Molecule 23: 40S RIBOSOMAL PROTEIN S18

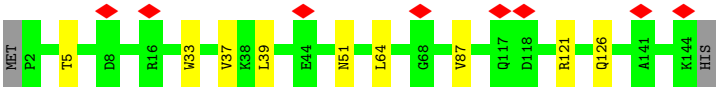
Chain BS:



- Molecule 24: 40S RIBOSOMAL PROTEIN S19

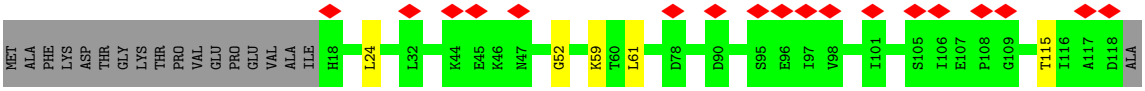
Chain BT:





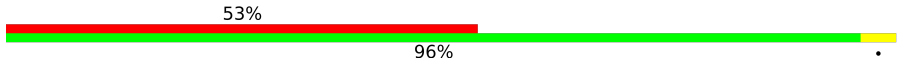
- Molecule 25: 40S RIBOSOMAL PROTEIN S20

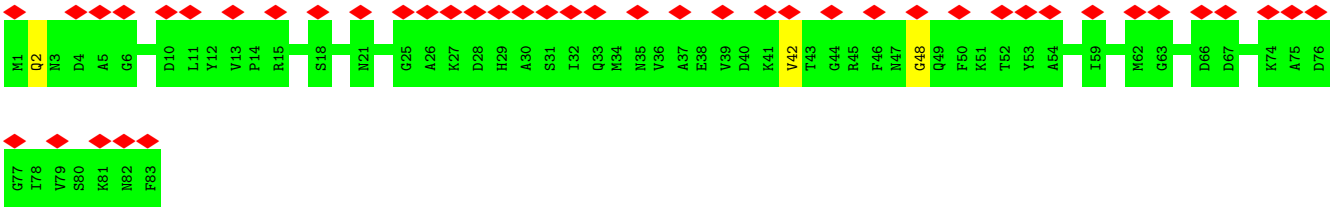
Chain BU:



- Molecule 26: 40S RIBOSOMAL PROTEIN S21

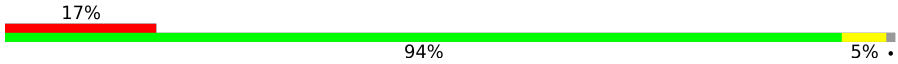
Chain BV:

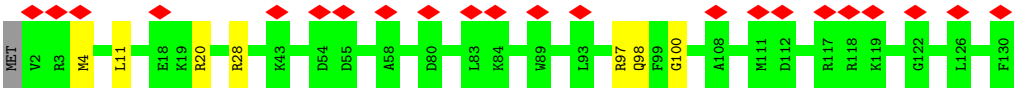




- Molecule 27: 40S RIBOSOMAL PROTEIN S15A

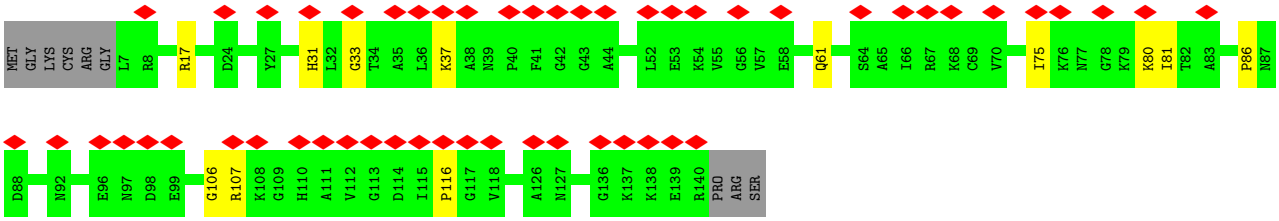
Chain BW:





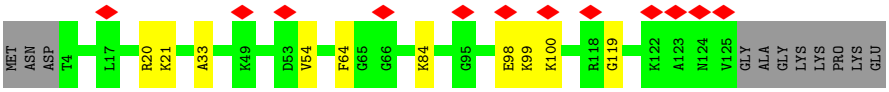
- Molecule 28: 40S RIBOSOMAL PROTEIN S23

Chain BX:



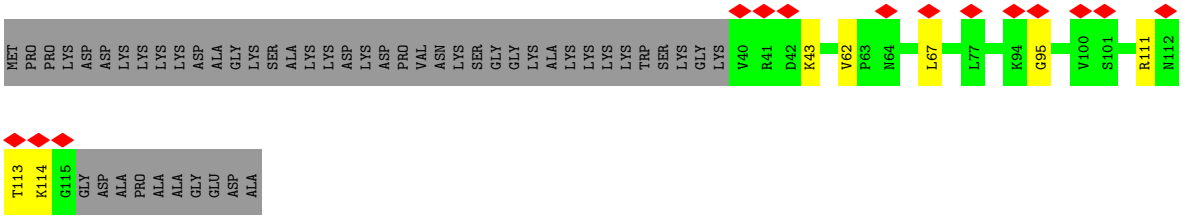
- Molecule 29: 40S RIBOSOMAL PROTEIN S24

Chain BY:



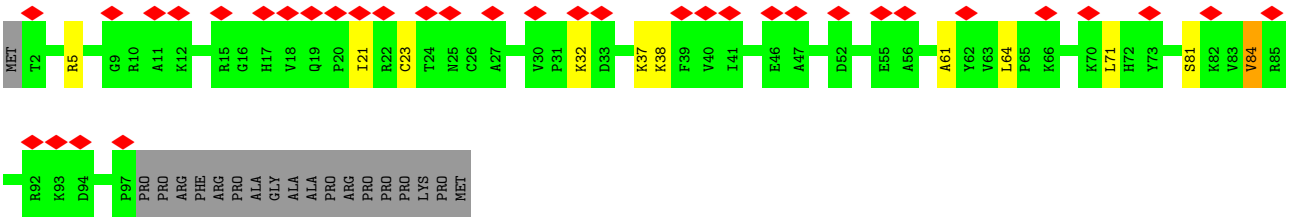
- Molecule 30: 40S RIBOSOMAL PROTEIN S25

Chain BZ:



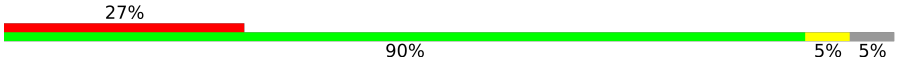
- Molecule 31: 40S RIBOSOMAL PROTEIN S26

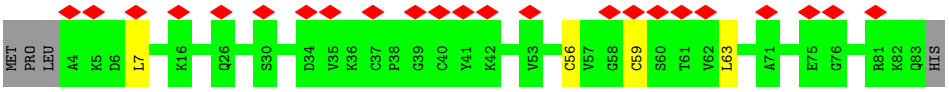
Chain Ba:



- Molecule 32: 40S RIBOSOMAL PROTEIN S27

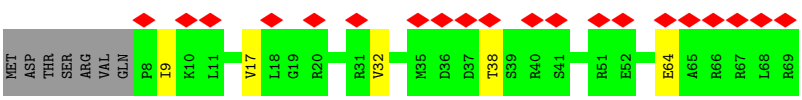
Chain Bb:





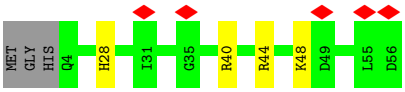
- Molecule 33: 40S RIBOSOMAL PROTEIN S28

Chain Bc:



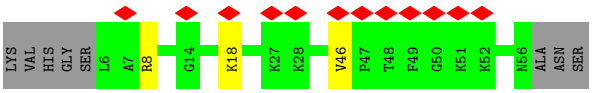
- Molecule 34: 40S RIBOSOMAL PROTEIN S29

Chain Bd:



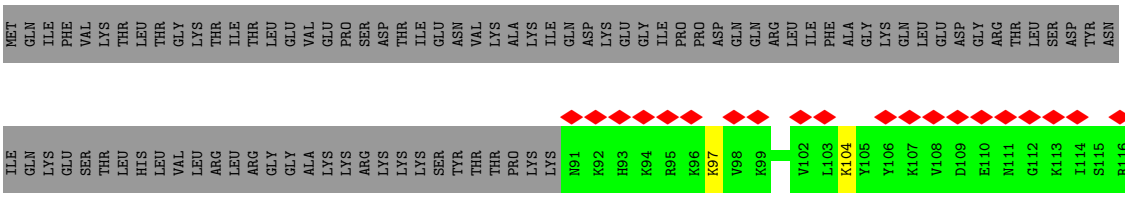
• Molecule 35: 40S RIBOSOMAL PROTEIN S30

Chain Be:



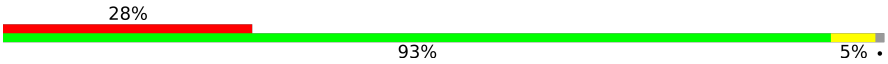
• Molecule 36: UBIQUITIN-40S RIBOSOMAL PROTEIN S27A

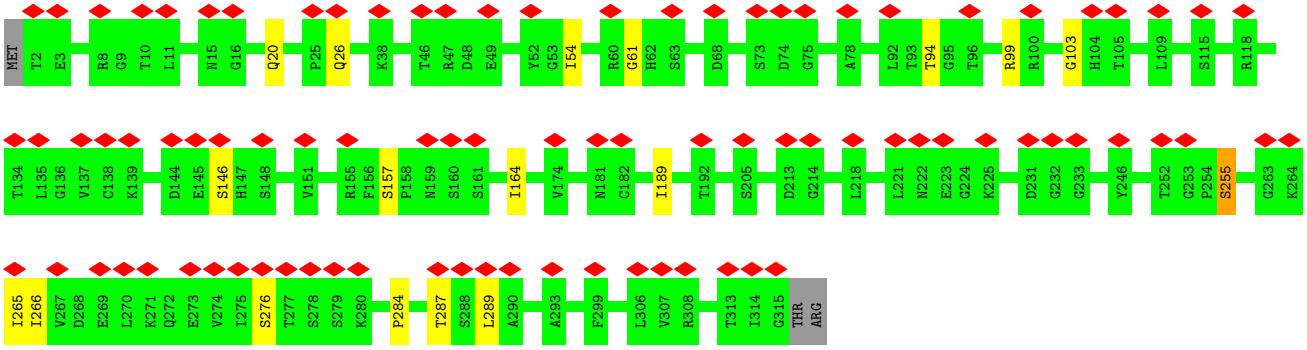
Chain Bf:



• Molecule 37: GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1

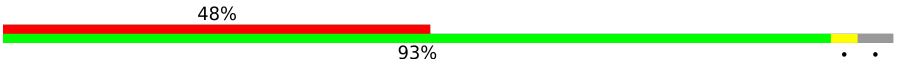
Chain Bg:

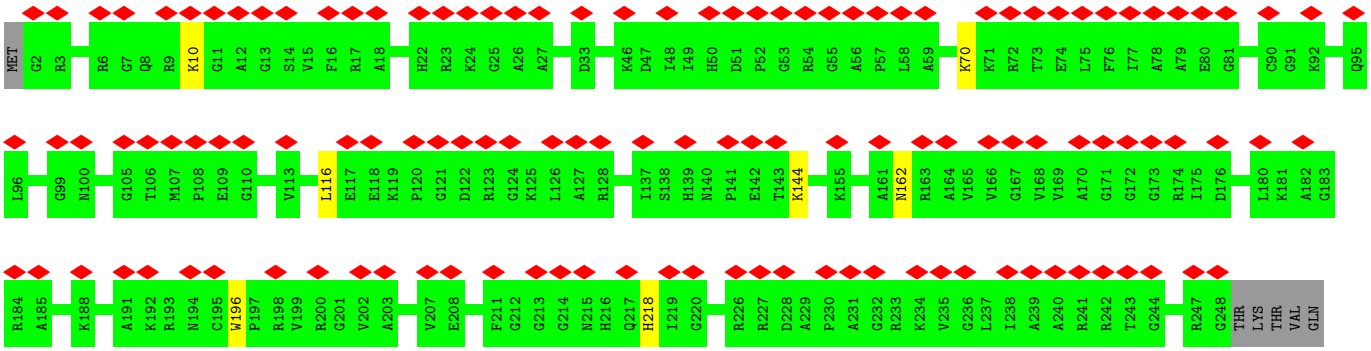




• Molecule 38: 60S RIBOSOMAL PROTEIN L8

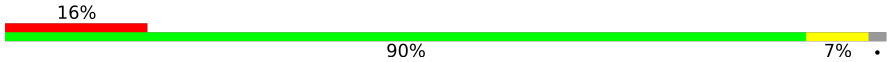
Chain CA:

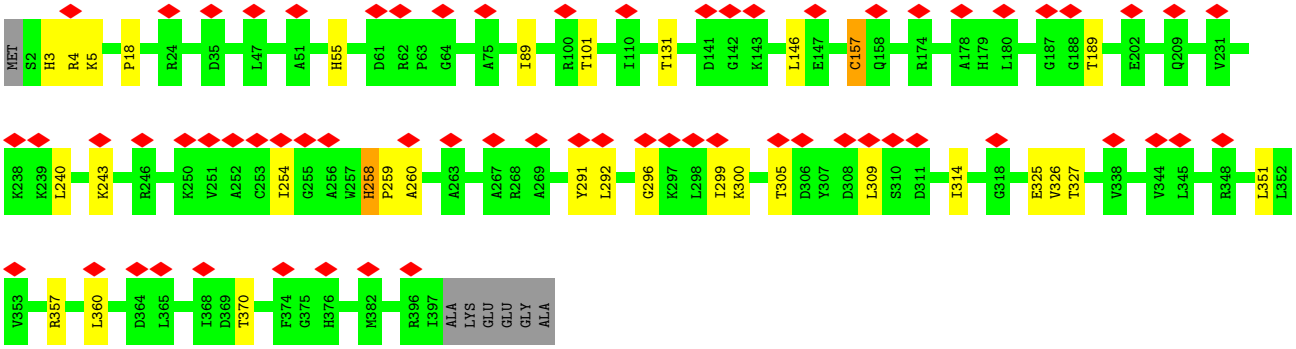




- Molecule 39: 60S RIBOSOMAL PROTEIN L3

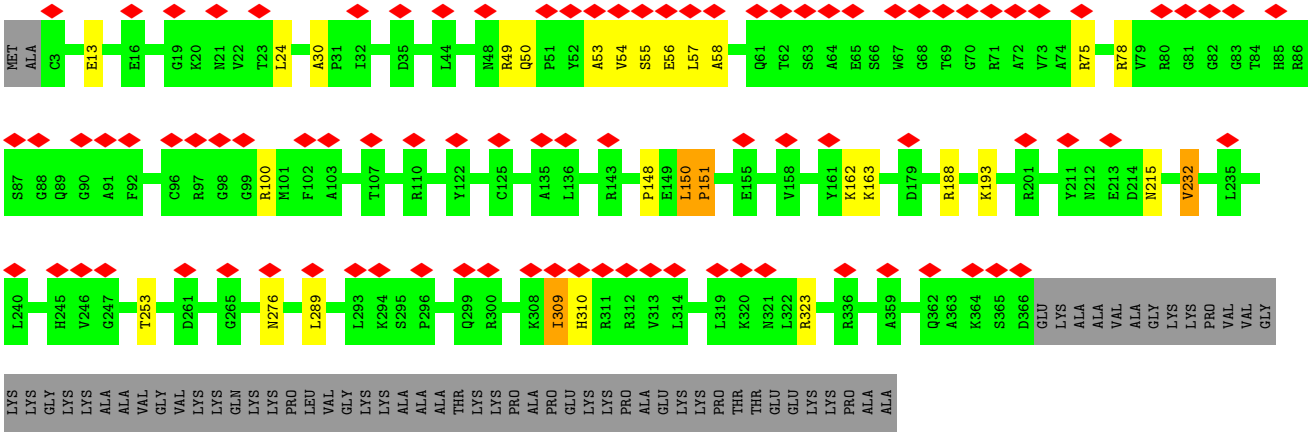
Chain CB:





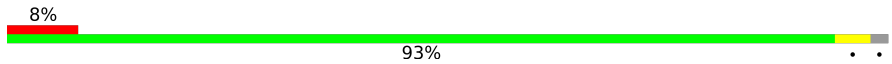
- Molecule 40: 60S RIBOSOMAL PROTEIN L4

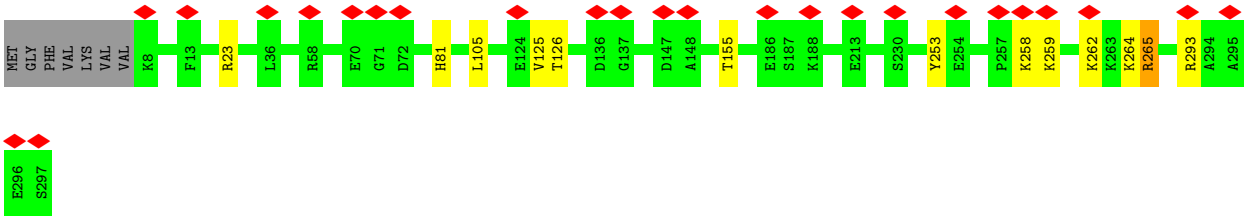
Chain CC:



- Molecule 41: 60S RIBOSOMAL PROTEIN L5

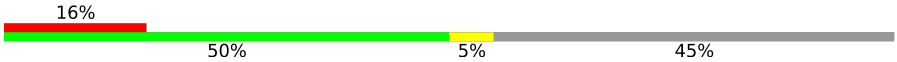
Chain CD:

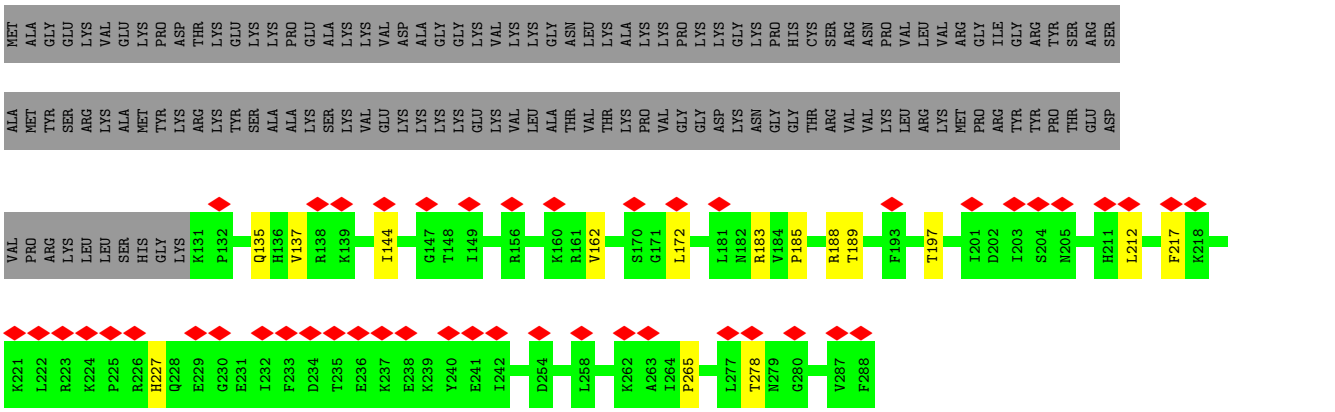




- Molecule 42: 60S RIBOSOMAL PROTEIN L6

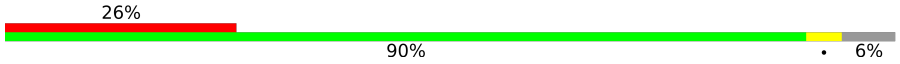
Chain CE:

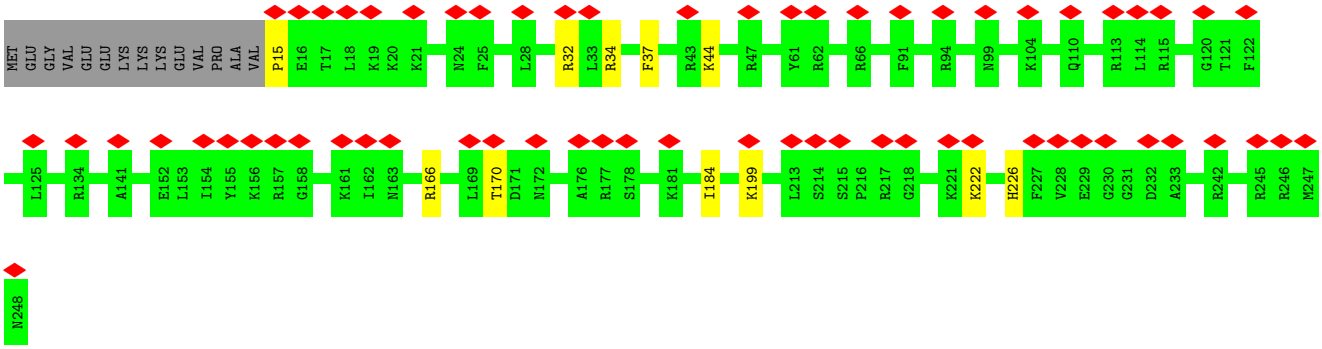




- Molecule 43: 60S RIBOSOMAL PROTEIN L7

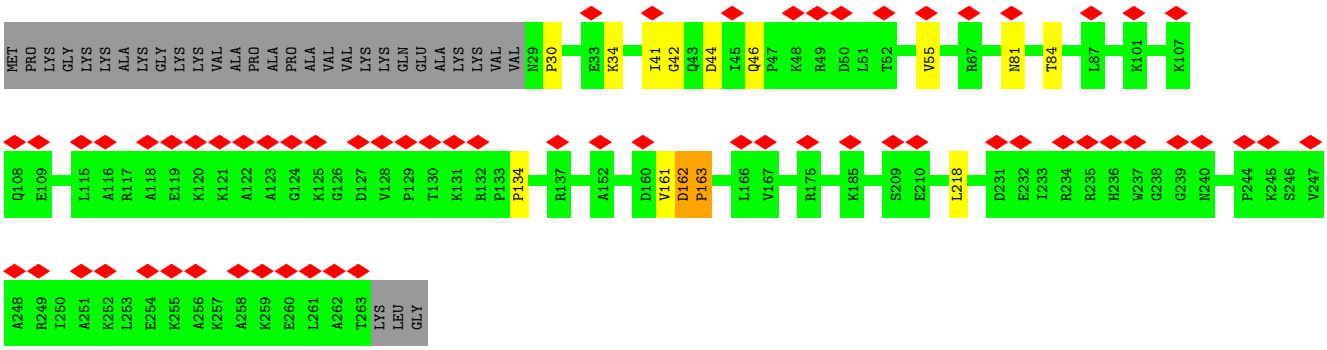
Chain CF:





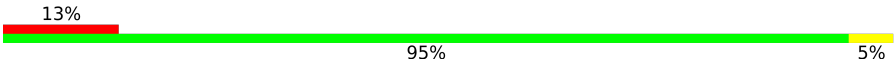
- Molecule 44: 60S RIBOSOMAL PROTEIN L7A

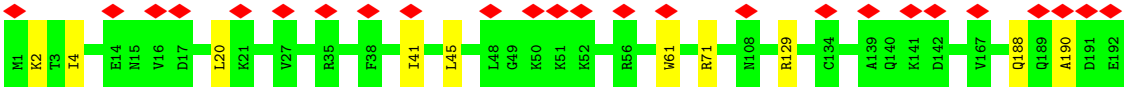
Chain CG:



- Molecule 45: 60S RIBOSOMAL PROTEIN L9

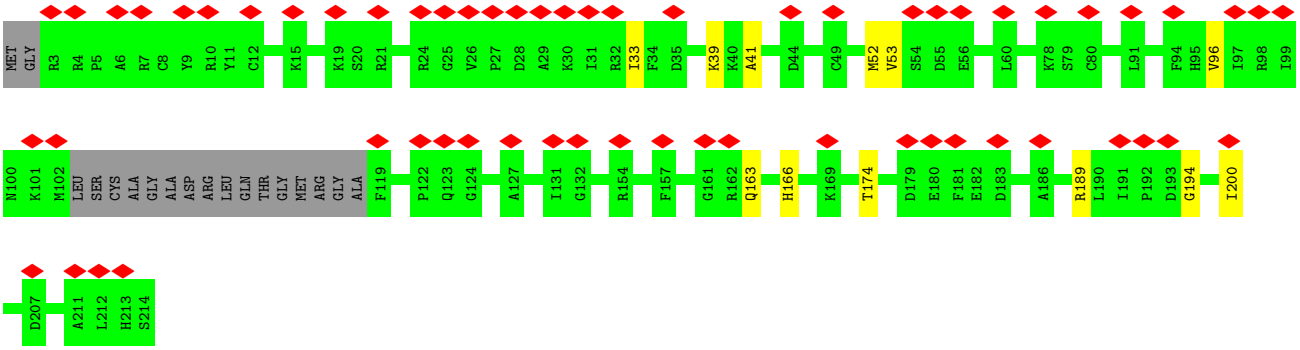
Chain CH:





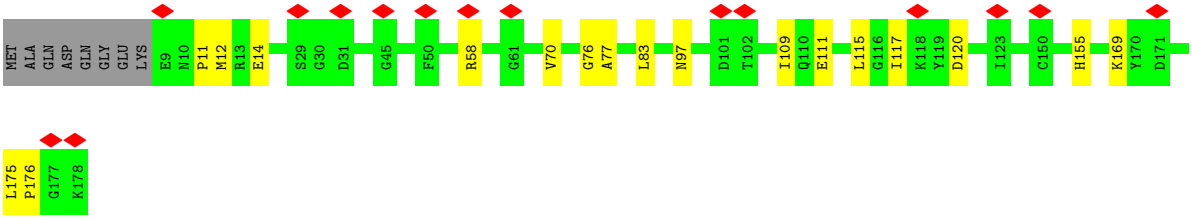
- Molecule 46: 60S RIBOSOMAL PROTEIN L10

Chain CI:



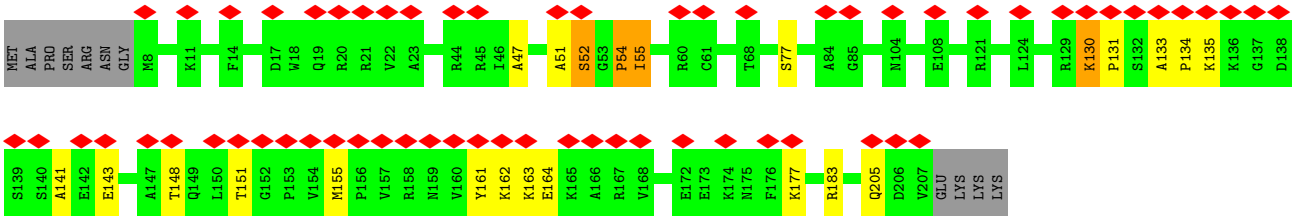
- Molecule 47: 60S RIBOSOMAL PROTEIN L11

Chain CJ:



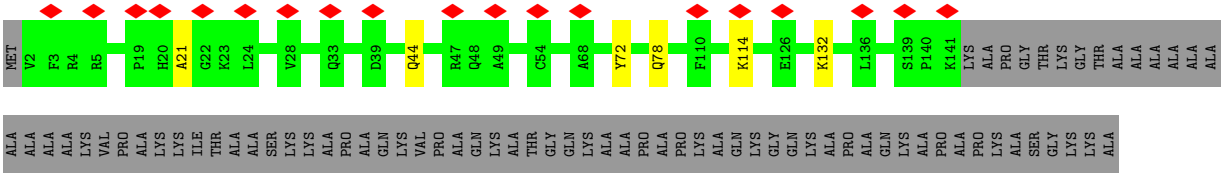
- Molecule 48: 60S RIBOSOMAL PROTEIN L13

Chain CL:



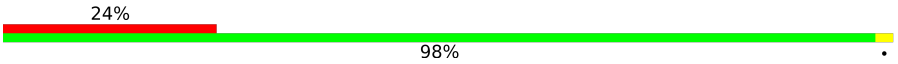
- Molecule 49: 60S RIBOSOMAL PROTEIN L14

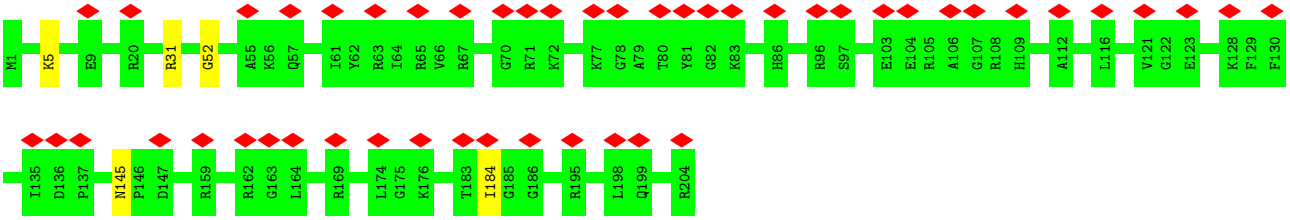
Chain CM:



- Molecule 50: 60S RIBOSOMAL PROTEIN L15

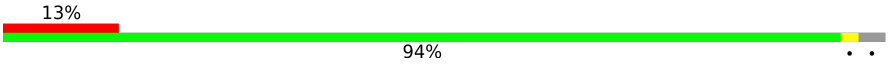
Chain CN:

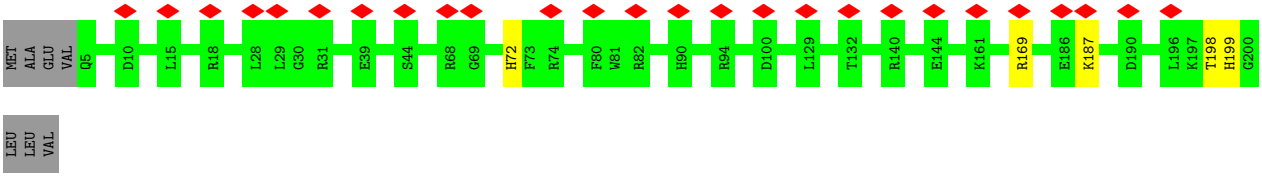




- Molecule 51: 60S RIBOSOMAL PROTEIN L13A

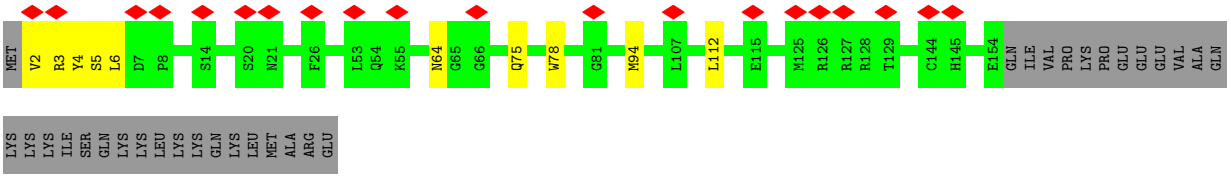
Chain CO:





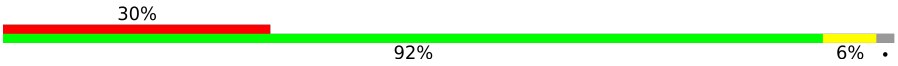
- Molecule 52: 60S RIBOSOMAL PROTEIN L17

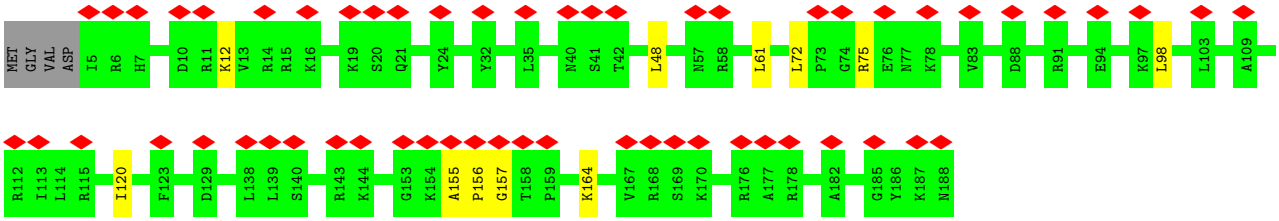
Chain CP:



- Molecule 53: 60S RIBOSOMAL PROTEIN L18

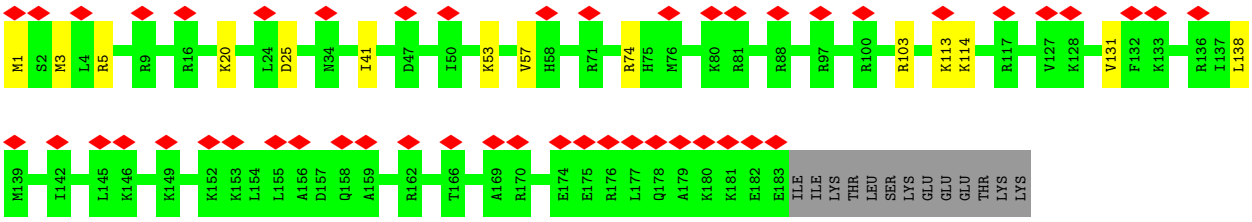
Chain CQ:





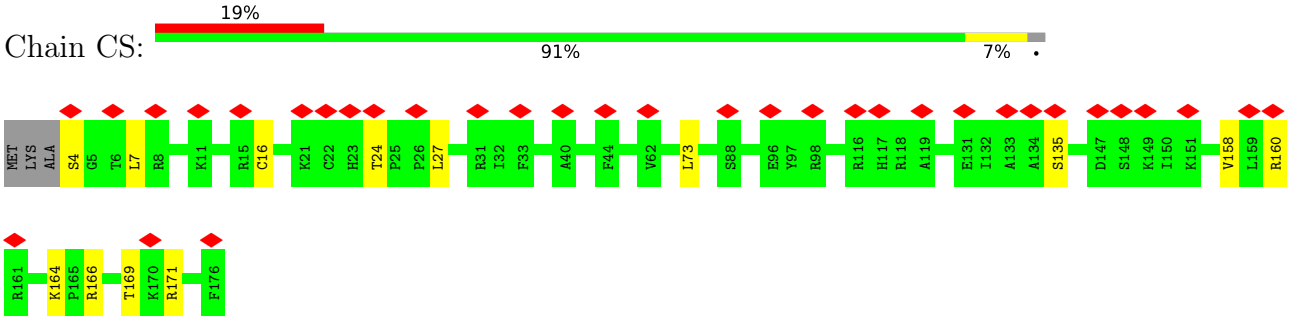
- Molecule 54: 60S RIBOSOMAL PROTEIN L19

Chain CR:



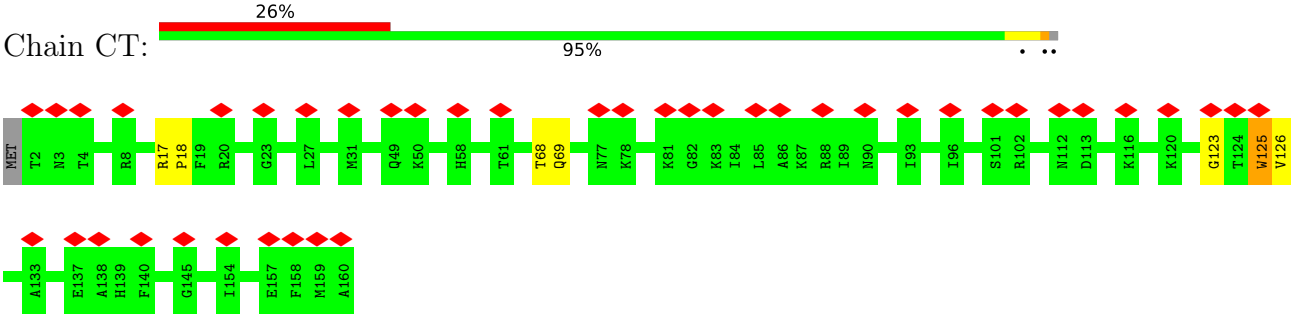
- Molecule 55: 60S RIBOSOMAL PROTEIN L18A

Chain CS:



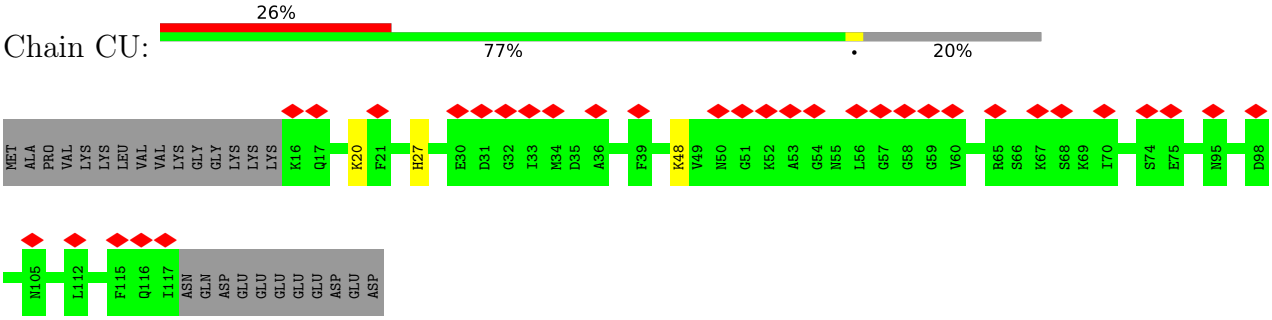
- Molecule 56: 60S RIBOSOMAL PROTEIN L21

Chain CT:



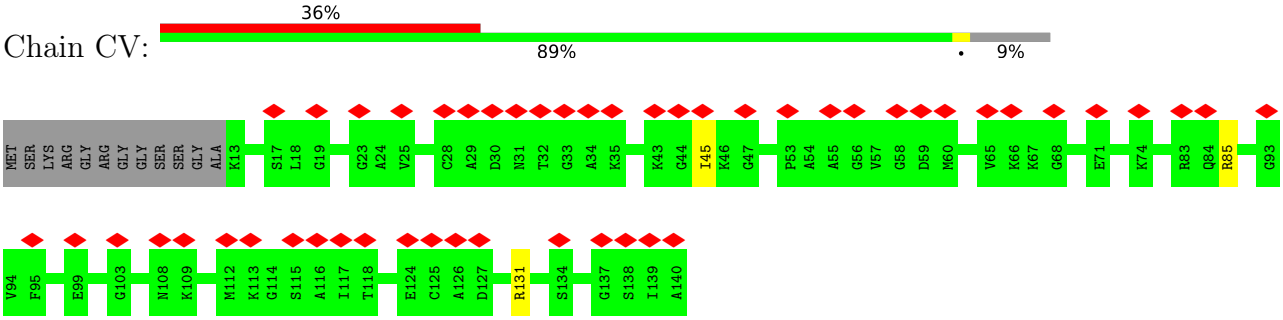
- Molecule 57: 60S RIBOSOMAL PROTEIN L22

Chain CU:



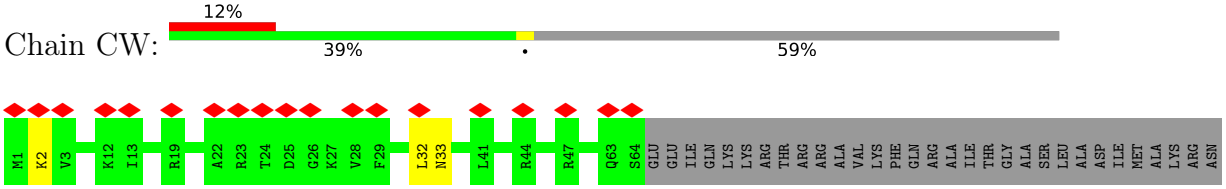
- Molecule 58: 60S RIBOSOMAL PROTEIN L23

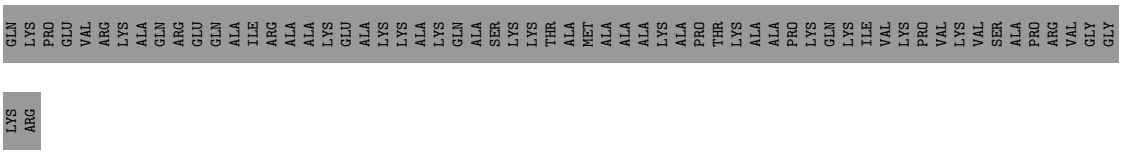
Chain CV:



- Molecule 59: 60S RIBOSOMAL PROTEIN L24

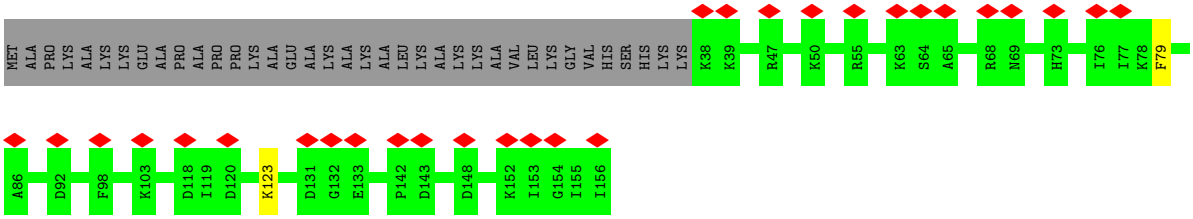
Chain CW:





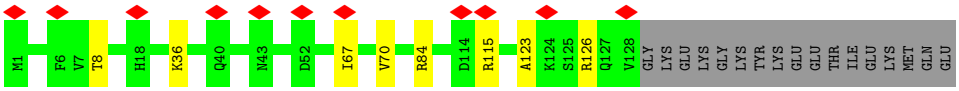
• Molecule 60: 60S RIBOSOMAL PROTEIN L23A

Chain CX:



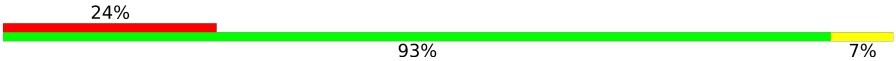
• Molecule 61: 60S RIBOSOMAL PROTEIN L26

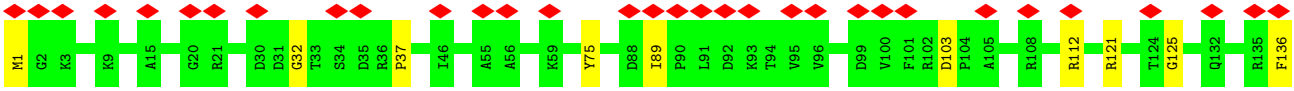
Chain CY:



• Molecule 62: 60S RIBOSOMAL PROTEIN L27

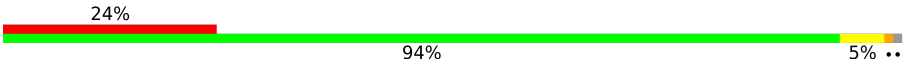
Chain CZ:

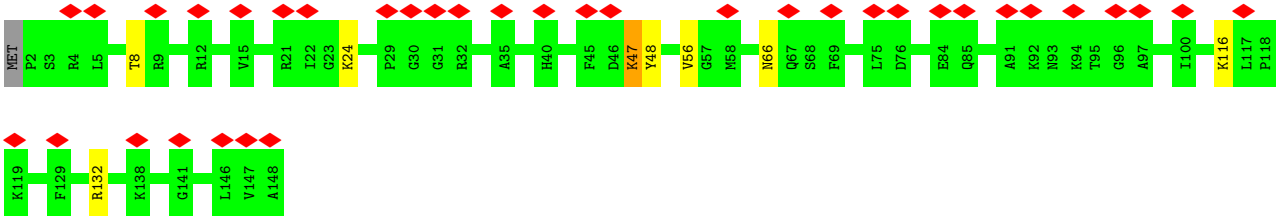




• Molecule 63: 60S RIBOSOMAL PROTEIN L27A

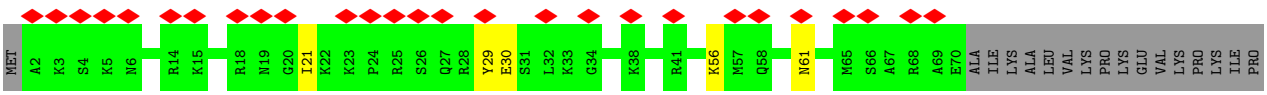
Chain Ca:





• Molecule 64: 60S RIBOSOMAL PROTEIN L29

Chain Cb:



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

ALA PRO LYS ARG THR GLN ALA PRO THR LYS ALA SER GLU

- Molecule 65: 60S RIBOSOMAL PROTEIN L30

Chain Cc: 32% 88% • 10%

MET VAL ALA ALA LYS LYS T7 K8 K9 S10 L11 E12 S13 I14 R17 L20 K23 S24 G25 R39 A43 A49 P53 A54 L55 R56 Y62 Y63 T69 L81 A84 C85 G86 R90 V91 P99 G100 D101 S102 D103 I104 I105 R106 S107 M108 P109 E110

GLN THR GLY GLU LYS

- Molecule 66: 60S RIBOSOMAL PROTEIN L31

Chain Cd: 16% 83% • 13%

MET ALA PRO ALA LYS LYS GLY GLY GLU LYS LYS LYS GLY ARG SER ALA I17 N18 E19 V20 K39 K40 R41 G58 N69 A74 K75 G76 Y82 R92 N93 E94 D95 E96 D97 S98 P99 N100 T112 T113 F114 K115 T119 D123 E124 N125

- Molecule 67: 60S RIBOSOMAL PROTEIN L32

Chain Ce: 33% 90% • 5%

MET ALA ALA ALA LEU R5 P6 L7 V8 K11 I12 V13 K14 K15 R16 K19 F20 I21 S25 D26 I31 K32 R33 R39 G40 I41 D42 N43 R44 R47 R48 F49 K50 G51 Q52 I53 L54 M55 P56 G59 Y60 G61 S62 N63 K64 K65 H68 M69 L70 G73 F74 R75

K76 E84 L85 L88 N92 S105 K109 A110 A116 N124 R130 S131 E132 GLU ASN GLU

- Molecule 68: 60S RIBOSOMAL PROTEIN L35A

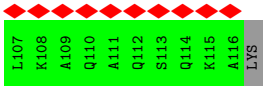
Chain Cf: 24% 86% 10% • •

MET SER GLY R4 F11 A12 L18 T25 A26 E31 E38 Y42 V50 Y51 K52 A53 K54 N55 N56 T57 V58 T59 P60 G61 P64 K73 A77 G82 A86 R89 S90 P93 A94 K95 A96 I97 I101 R102 L105 Y106 P107 I110

- Molecule 69: 60S RIBOSOMAL PROTEIN L34

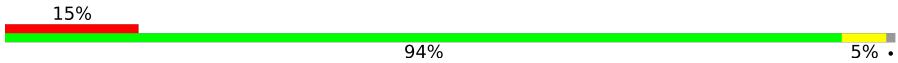
Chain Cg: 31% 87% 10% • •

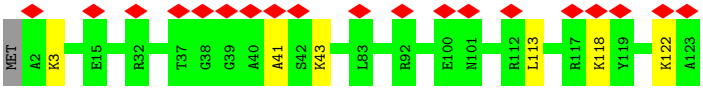
MET V2 Q3 R4 L5 T6 Y7 L11 T20 R21 L22 S23 R24 N28 R29 I30 K36 K40 S44 A45 C46 G47 R52 L53 R54 R57 A58 V59 R60 P61 K62 M65 R66 L67 S68 K69 K72 S75 R76 A77 Y78 G79 G80 S81 A84 A94



- Molecule 70: 60S RIBOSOMAL PROTEIN L35

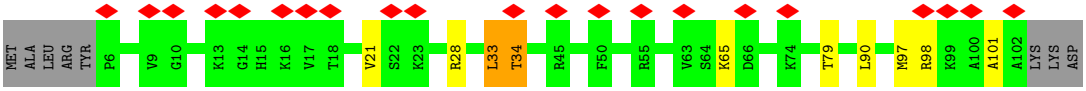
Chain Ch:





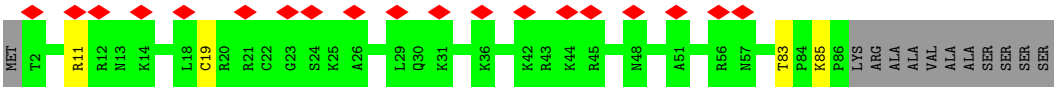
- Molecule 71: 60S RIBOSOMAL PROTEIN L36

Chain Ci:



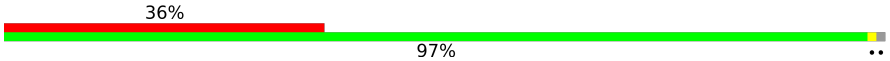
- Molecule 72: 60S RIBOSOMAL PROTEIN L37

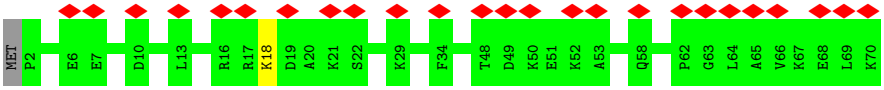
Chain Cj:



- Molecule 73: 60S RIBOSOMAL PROTEIN L38

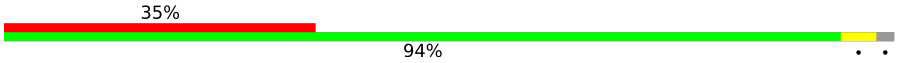
Chain Ck:

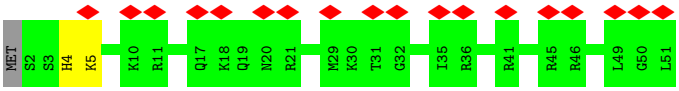




- Molecule 74: 60S RIBOSOMAL PROTEIN L39

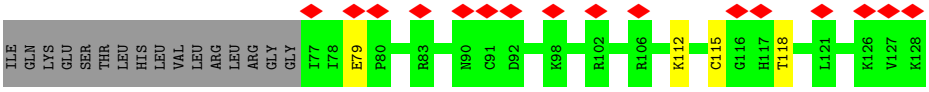
Chain Cl:





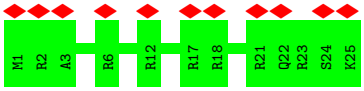
- Molecule 75: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain Cm:



- Molecule 76: 60S RIBOSOMAL PROTEIN L41

Chain Cn: 44% 100%

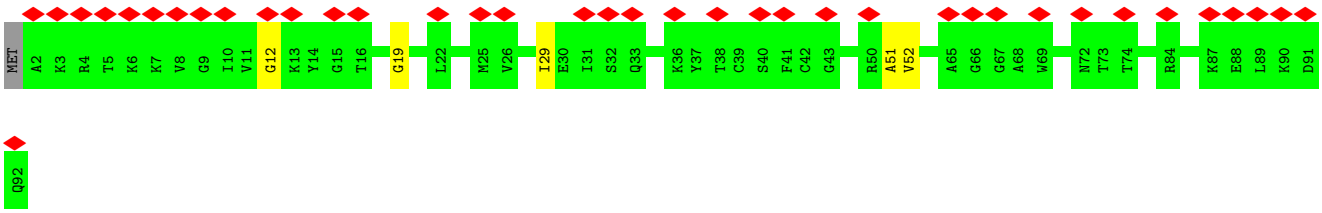


- Molecule 77: 60S RIBOSOMAL PROTEIN L36A

Chain Co: 47% 93% 7%

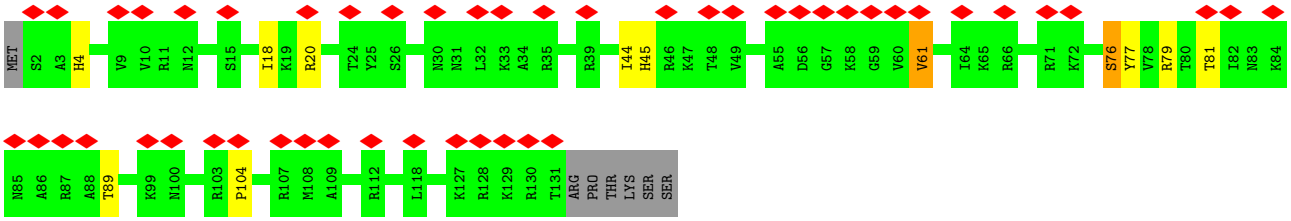
- Molecule 78: 60S RIBOSOMAL PROTEIN L37A

Chain Cp: 41% 93% 5% •



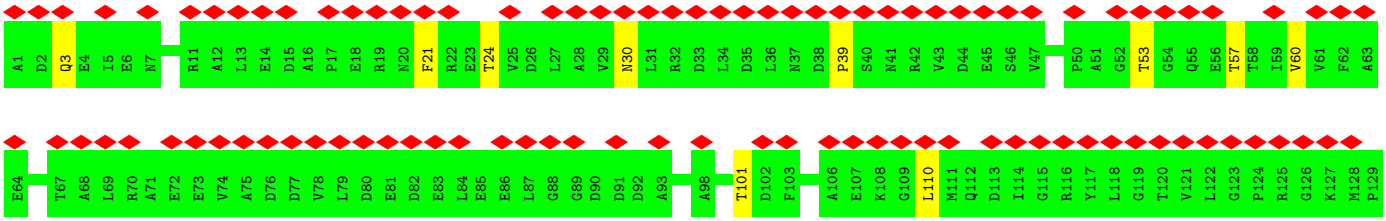
- Molecule 79: 60S RIBOSOMAL PROTEIN L28

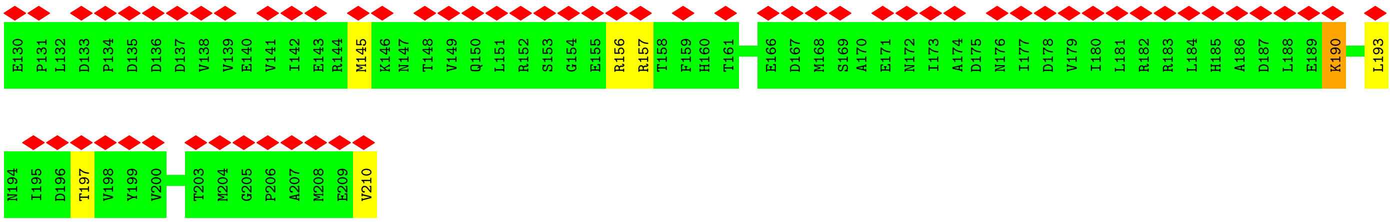
Chain Ct: 36% 86% 7% • 5%



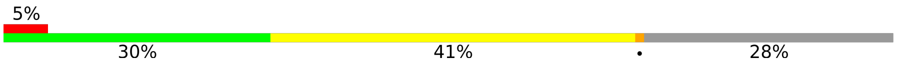
- Molecule 80: 60S RIBOSOMAL PROTEIN L10A

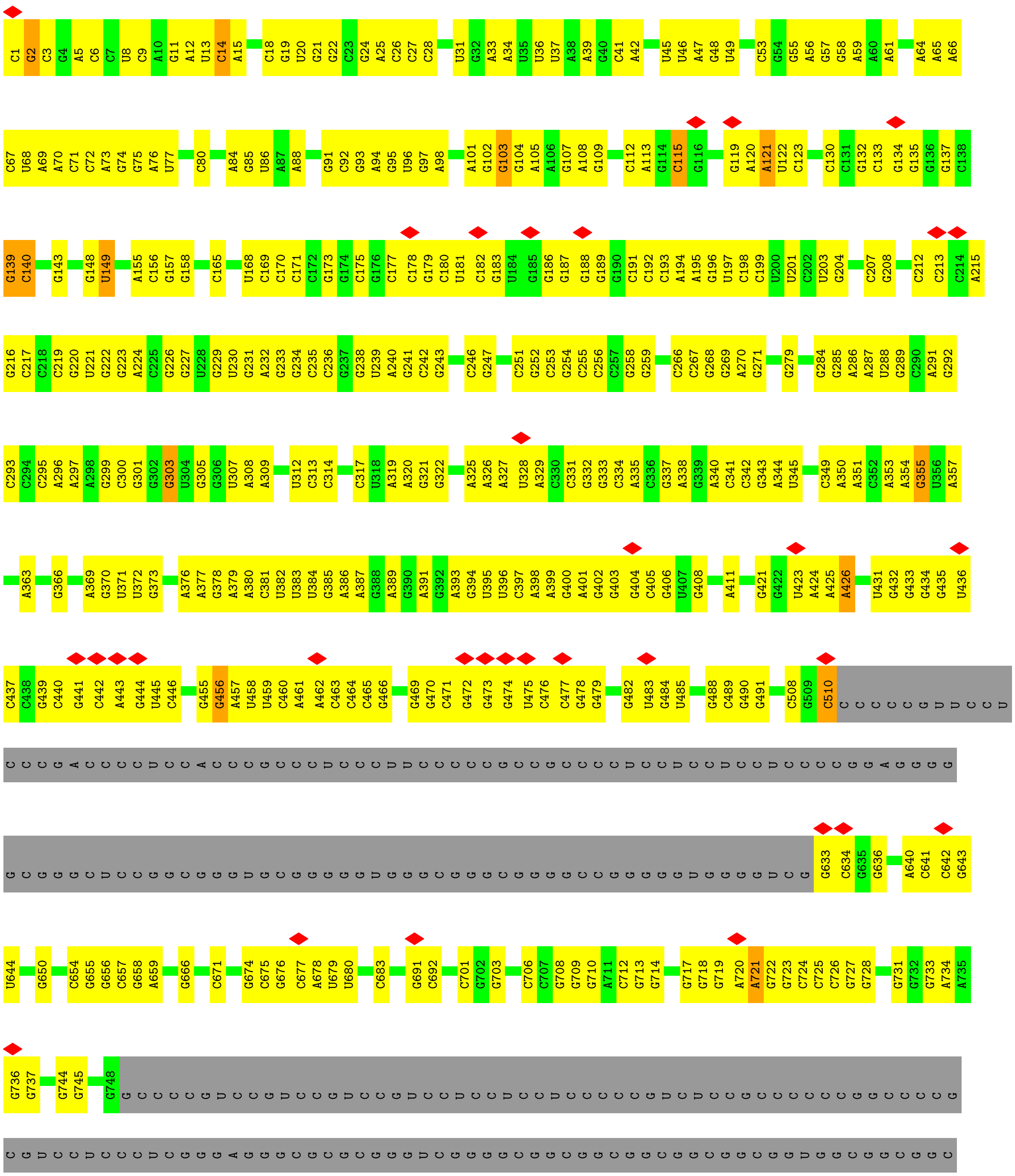
Chain Cu: 77% 92% 8%

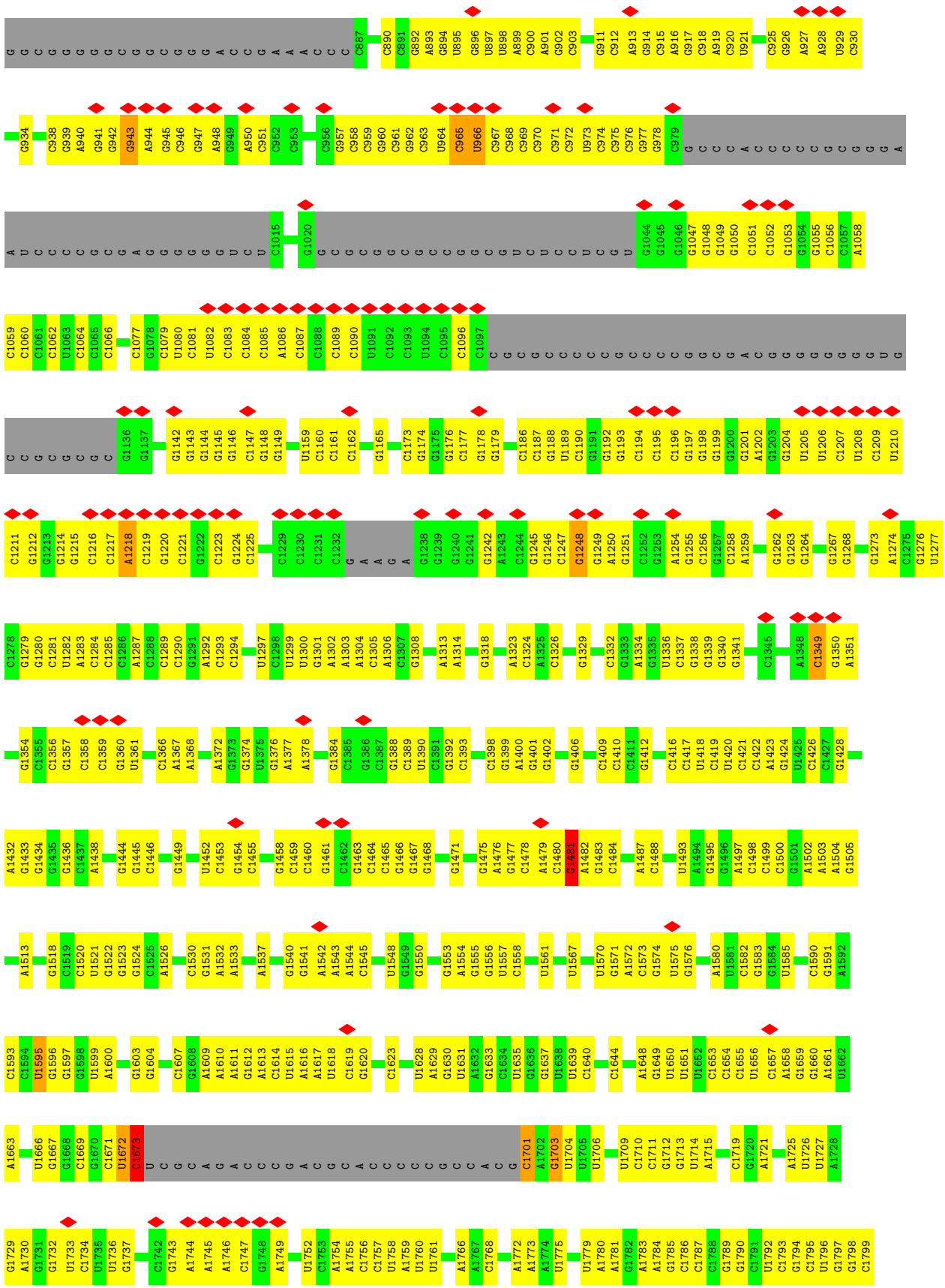


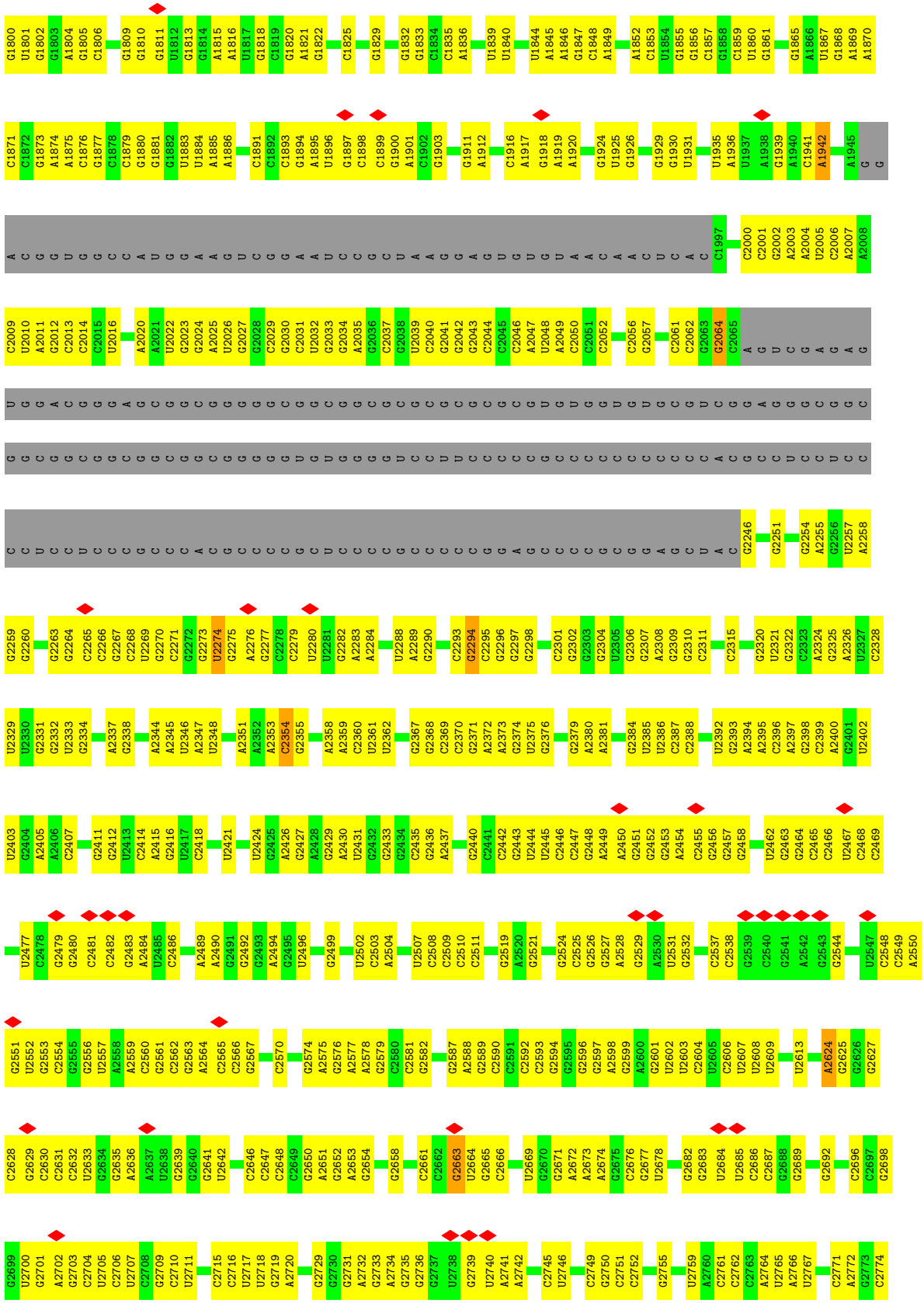


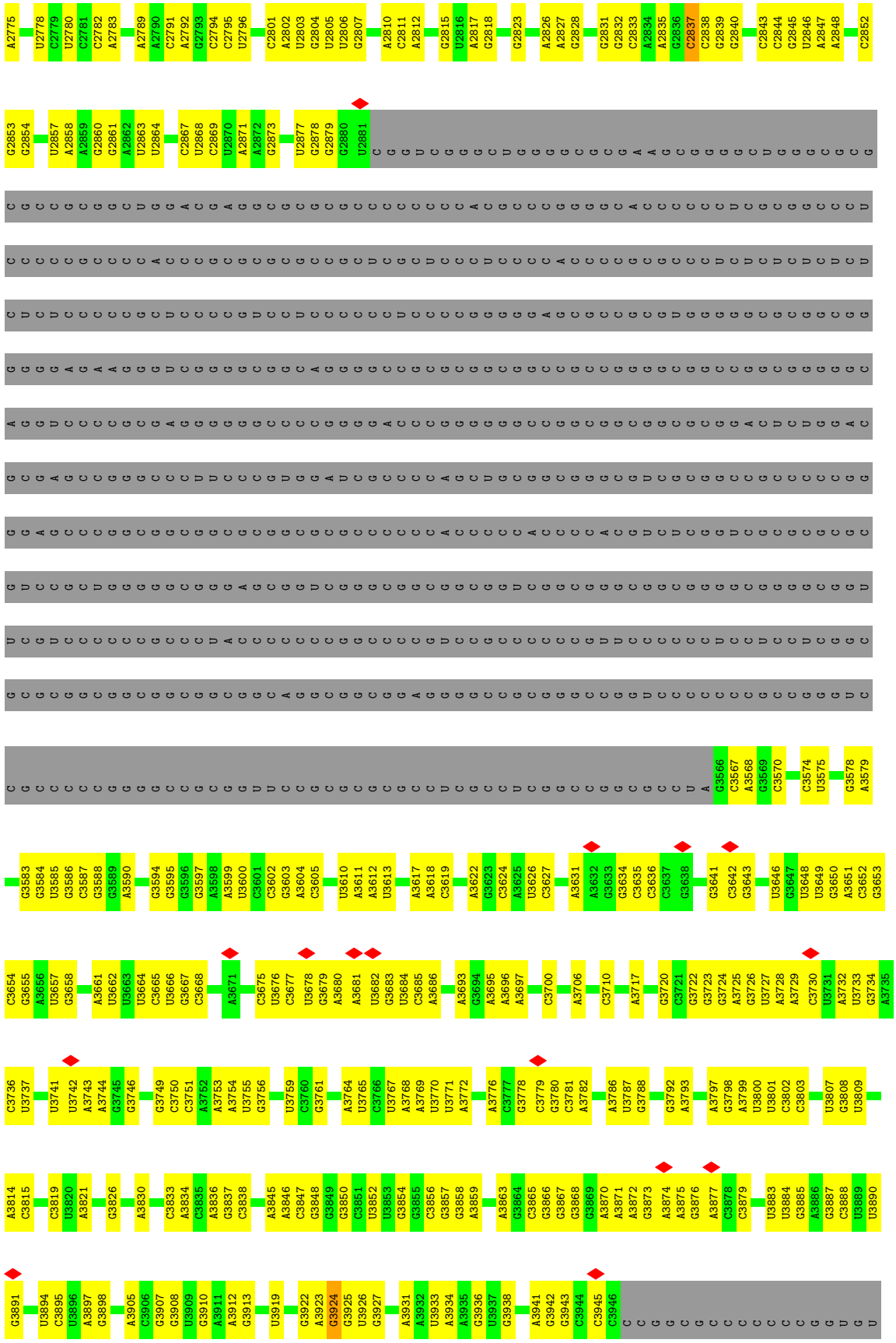
• Molecule 81: 28S Ribosomal RNA

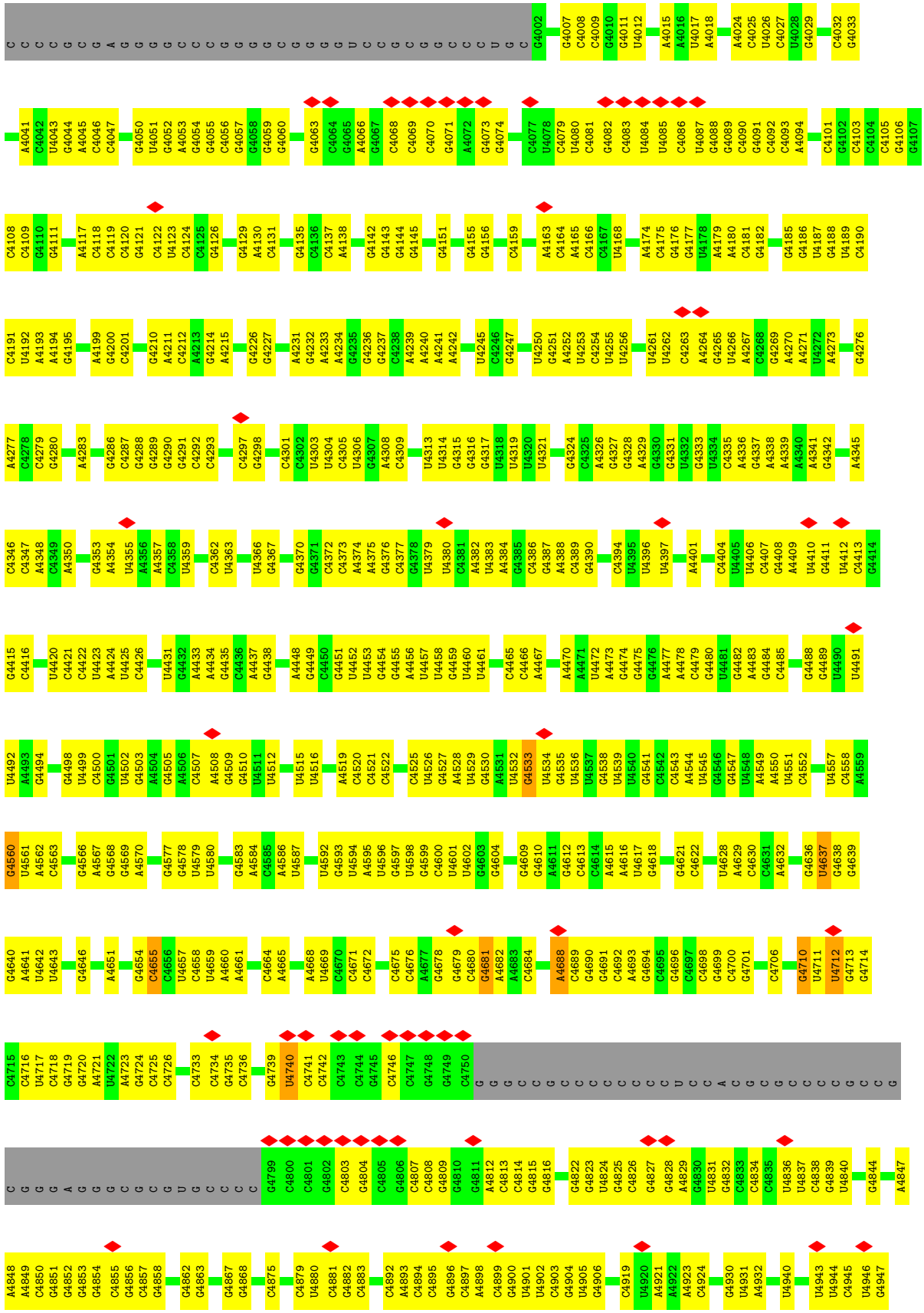
Chain A2:


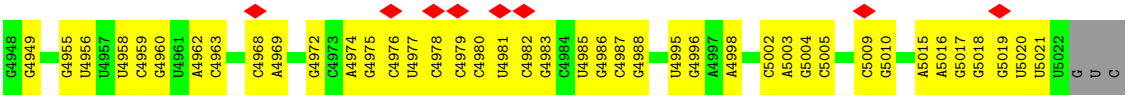



G G C G G G G C G G C G G G A C C G A A A C C C
C387 C890 C891 G892 A893 G894 U895 G896 U897 U898 A899 C900 A901 G902 C903 G911 C912 A913 G914 G915 A916 G917 C918 A919 C920 U921 C925 G926 A927 A928 U929 C930
G934 C938 G939 A940 G941 G942 G943 A944 G945 C946 G947 A948 G949 A950 C951 G952 C953 C956 G957 C958 C959 G960 C961 G962 C963 U964 C965 U966 C967 G968 C969 C970 C971 G972 U973 C974 G975 C976 G977 G978 C979 G C C C A C C C C C G C 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 G C G G G C G C C G C C G U C C U C G U G1044 G1045 G1046 G1047 G1048 G1049 G1050 C1051 C1052 G1053 G1054 G1055 C1056 C1057 A1058
C1059 C1060 C1061 C1062 U1063 C1064 C1065 C1066 C1077 G1078 C1079 U1080 C1081 U1082 C1083 C1084 C1085 A1086 C1087 C1088 C1089 C1090 U1091 C1092 C1093 U1094 C1095 C1096 C1097 C G G C G C C C C C C G C C C C G G G G G G G G G G G G G U G
C C G C G C G C G1136 G1137 G1142 G1143 G1144 G1145 G1146 C1147 G1148 G1149 U1159 C1160 C1161 C1162 G1165 C1173 G1174 G1175 G1176 C1177 G1178 G1179 C1186 C1187 G1188 U1189 C1190 G1191 G1192 G1193 C1194 C1195 C1196 G1197 G1198 G1199 G1200 G1201 A1202 G1203 G1204 U1205 U1206 C1207 U1208 C1209 U1210
C1211 G1212 G1213 G1214 G1215 C1216 C1217 A1218 C1219 G1220 C1221 G1222 C1223 G1224 C1225 C1229 C1230 C1231 C1232 G A A G A G1238 G1239 G1240 G1241 G1242 A1243 C1244 G1245 G1246 C1247 G1248 G1249 A1250 G1251 C1252 G1253 A1254 A1255 C1256 G1257 C1258 A1259 G1262 G1263 G1264 G1267 G1268 G1273 A1274 C1275 G1276 U1277
C1278 G1279 G1280 C1281 U1282 A1283 C1284 C1285 C1286 A1287 C1288 C1289 C1290 G1291 A1292 C1293 C1294 U1297 C1298 U1299 U1300 G1301 A1302 A1303 A1304 C1305 A1306 C1307 G1308 A1313 A1314 G1318 A1323 C1324 A1325 C1326 G1329 C1332 G1333 A1334 G1335 U1336 C1337 G1338 G1339 G1340 G1341 C1345 A1348 C1349 G1350 A1351
G1354 C1355 C1356 G1357 C1358 C1359 G1360 U1361 C1366 A1367 A1368 A1372 G1373 G1374 U1375 G1376 A1377 A1378 G1384 C1385 G1386 C1387 G1388 C1389 U1390 C1391 G1392 C1393 C1398 G1399 A1400 G1401 G1402 G1406 C1409 C1410 C1411 G1412 C1416 C1417 U1418 C1419 U1420 C1421 C1422 A1423 G1424 U1425 C1426 C1427 G1428
A1432 G1433 G1434 G1435 G1436 C1437 A1438 G1444 G1445 C1446 G1449 U1452 C1453 G1454 C1455 G1458 C1459 C1460 G1461 C1462 G1463 C1464 C1465 G1466 G1467 G1468 G1471 G1475 A1476 G1477 C1478 A1479 C1480 G1481 A1482 G1483 C1484 A1487 C1488 U1493 A1494 G1495 G1496 A1497 C1498 C1499 C1500 G1501 A1502 A1503 A1504 G1505
A1513 G1518 C1519 C1520 U1521 G1522 G1523 G1524 C1525 A1526 C1530 G1531 A1532 A1533 A1537 G1540 G1541 A1542 A1543 A1544 C1545 U1548 G1549 G1550 G1553 A1554 G1555 G1556 U1557 C1558 U1561 U1567 U1570 G1571 A1572 C1573 G1574 U1575 G1576 A1580 U1581 C1582 G1583 G1584 U1585 C1590 G1591 A1592
C1593 C1594 U1595 G1596 G1597 G1598 U1599 A1600 G1603 G1604 C1607 G1608 A1609 A1610 A1611 G1612 A1613 C1614 U1615 A1616 A1617 U1618 C1619 G1620 C1623 U1628 A1629 G1630 U1631 A1632 G1633 C1634 U1635 G1636 G1637 U1638 U1639 C1640 C1644 A1648 G1649 U1650 U1651 U1652 C1653 C1654 C1655 U1656 C1657 A1658 G1659 G1660 A1661 U1662
A1663 U1666 G1667 G1668 C1669 G1670 C1671 U1672 C1673 U C G C A G A C C C G A C C C C C G C C A C G C1701 A1702 G1703 U1704 U1705 U1706 U1709 C1710 C1711 G1712 G1713 U1714 A1715 C1719 G1720 A1721 A1725 U1726 U1727 A1728
G1729 A1730 G1731 G1732 U1733 C1734 U1735 U1736 G1737 C1742 G1743 A1744 A1745 A1746 C1747 G1748 A1749 U1752 C1753 A1754 A1755 C1756 C1757 U1758 A1759 U1760 U1761 A1766 A1767 C1768 A1772 A1773 A1774 U1775 U1779 A1780 A1781 G1782 A1783 A1784 G1785 C1786 C1787 C1788 G1789 G1790 C1791 U1792 C1793 C1794 C1795 U1796 G1797 G1798 C1799


G1800 U1801 G1802 G1803 A1804 G1805 C1806 G1809 G1810 G1811 U1812 G1813 G1814 A1815 A1816 U1817 G1818 C1819 G1820 A1821 G1822 C1825 G1829 G1832 G1833 C1834 C1835 A1836 U1839 U1840 U1844 A1845 A1846 G1847 C1848 A1849 A1852 C1853 U1854 G1855 G1856 C1857 G1858 C1859 U1860 G1861 G1865 A1866 U1867 G1868 A1869 A1870
C1871 G1872 G1873 A1874 A1875 C1876 G1877 G1878 C1879 G1880 G1881 G1882 U1883 U1884 A1885 A1886 C1891 C1892 C1893 G1894 A1895 U1896 G1897 C1898 C1899 G1900 A1901 C1902 G1903 G1911 A1912 C1916 A1917 G1918 A1919 A1920 G1924 U1925 G1926 G1929 G1930 U1931 U1935 A1936 U1937 A1938 G1939 A1940 C1941 A1942 A1945 G G
A C G G U G G C C C A U G C G G C U U A A U C G G C A A G G U C G U G U A A C A A C C U C A C C1997 C2000 C2001 G2002 A2003 A2004 U2005 C2006 A2007 A2008
C2009 U2010 A2011 G2012 C2013 C2014 C2015 U2016 A2020 A2021 U2022 G2023 G2024 A2025 U2026 G2027 G2028 C2029 G2030 C2031 U2032 G2033 G2034 A2035 G2036 C2037 G2038 U2039 C2040 G2041 G2042 G2043 C2044 C2045 C2046 A2047 U2048 A2049 C2050 C2051 C2052 C2056 G2057 C2061 C2062 G2063 G2064 C2065 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 G C G G C G G C G C G C G G C G U C G G U G G C G G C G G U G U G G G C G C G C G C G G G C G C G C G G G C G G C G G G C G G C G G C

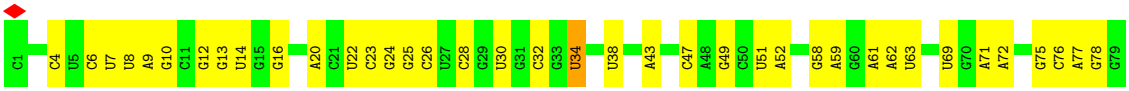

A2775 U2778 C2779 U2780 C2781 C2782 A2783 A2789 A2790 C2791 A2792 G2793 C2794 C2795 U2796 C2801 A2802 U2803 G2804 U2805 U2806 G2807 A2810 C2811 A2812 G2815 U2816 A2817 G2818 G2823 A2826 A2827 G2828 G2831 G2832 C2833 A2834 A2835 G2836 C2837 C2838 G2839 G2840 C2843 C2844 G2845 U2846 A2847 A2848 C2852
G2853 G2854 U2857 A2858 A2859 G2860 G2861 A2862 U2863 U2864 C2867 U2868 C2869 U2870 A2871 A2872 G2873 U2877 G2878 G2879 G2880 U2881
G3566 C3567 A3568 G3569 C3570 C3574 U3575 G3578 A3579
G3583 G3584 U3585 G3586 C3587 G3588 G3589 A3590 G3594 G3595 G3596 G3597 A3598 A3599 U3600 C3601 C3602 G3603 A3604 C3605 U3610 A3611 A3612 U3613 A3617 A3618 C3619 A3622 G3623 C3624 A3625 U3626 C3627 A3631 A3632 G3633 G3634 C3635 C3636 C3637 G3638 G3641 C3642 G3643 U3646 G3647 U3648 U3649 G3650 A3651 C3652 G3653
C3654 G3655 A3656 U3657 G3658 A3661 U3662 U3663 U3664 C3665 U3666 G3667 C3668 A3671 C3675 U3676 C3677 U3678 G3679 A3680 A3681 U3682 G3683 U3684 C3685 A3686 A3693 G3694 A3695 A3696 A3697 C3700 A3706 C3710 A3717 G3720 C3721 G3722 G3723 G3724 A3725 G3726 U3727 A3728 A3729 C3730 U3731 A3732 U3733 G3734 A3735
C3736 U3737 U3741 U3742 A3743 A3744 G3745 G3746 G3749 C3750 C3751 A3752 A3753 A3754 U3755 G3756 U3759 C3760 G3761 A3764 U3765 C3766 U3767 A3768 G3769 U3770 U3771 A3772 A3776 C3777 G3778 C3779 G3780 C3781 A3782 A3786 U3787 G3788 G3792 A3793 A3797 G3798 A3799 U3800 U3801 C3802 C3803 U3807 G3808 U3809
A3814 C3815 C3819 U3820 A3821 G3826 A3830 C3833 A3834 C3835 A3836 G3837 C3838 A3845 A3846 C3847 G3848 G3849 G3850 C3851 U3852 U3853 G3854 G3855 C3856 G3857 G3858 A3859 A3863 G3864 C3865 G3866 G3867 G3868 G3869 A3870 A3871 A3872 G3873 A3874 A3875 G3876 A3877 C3878 C3879 U3883 U3884 G3885 A3886 G3887 C3888 U3889 U3890
G3891 U3894 C3895 U3896 A3897 G3898 A3905 C3906 G3907 G3908 U3909 G3910 A3911 A3912 G3913 U3919 G3922 A3923 G3924 G3925 U3926 G3927 A3931 A3932 U3933 A3934 A3935 G3936 U3937 G3938 A3941 G3942 G3943 C3944 C3945 C3946

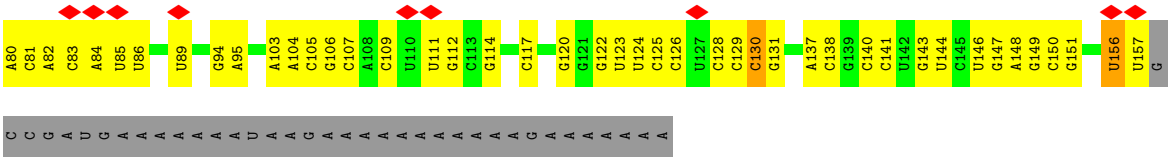

C C C C G C G A G G G G C C C G G G G C G G G U C C G C G G C C U G C
G4002 G4007 C4008 C4009 G4010 G4011 U4012 A4015 A4016 U4017 A4018 A4024 C4025 U4026 C4027 U4028 G4029 C4032 G4033
A4041 C4042 U4043 G4044 A4045 C4046 C4047 G4050 U4051 G4052 A4053 G4054 G4055 C4056 G4057 G4058 G4059 G4060 G4063 C4064 G4065 A4066 G4067 C4068 C4069 C4070 G4071 A4072 G4073 G4074 C4077 U4078 C4079 U4080 C4081 G4082 G4083 U4084 U4085 C4086 U4087 G4088 G4089 C4090 C4091 C4092 C4093 A4094 C4101 G4102 C4103 C4104 C4105 G4106 G4107
C4108 C4109 G4110 G4111 A4117 C4118 C4119 C4120 G4121 C4122 U4123 C4124 C4125 G4126 G4129 A4130 C4131 G4135 C4136 C4137 A4138 G4142 G4143 G4144 G4145 G4151 G4155 G4156 C4159 A4163 C4164 A4165 C4166 C4167 U4168 A4174 C4175 G4176 G4177 U4178 A4179 A4180 C4181 G4182 G4185 G4186 U4187 G4188 U4189 C4190
C4191 U4192 A4193 A4194 G4195 A4199 G4200 C4201 G4210 A4211 C4212 A4213 G4214 A4215 G4226 G4227 A4231 G4232 A4233 A4234 G4235 G4236 G4237 C4238 A4239 A4240 A4241 A4242 U4245 C4246 G4247 U4250 G4251 A4252 U4253 C4254 U4255 U4256 U4261 U4262 C4263 A4264 G4265 U4266 A4267 C4268 G4269 A4270 A4271 U4272 A4273 G4276
A4277 C4278 C4279 G4280 A4283 G4286 C4287 G4288 G4289 G4290 G4291 C4292 C4293 C4297 G4298 C4301 C4302 U4303 U4304 C4305 U4306 G4307 A4308 C4309 U4313 U4314 G4315 G4316 G4317 U4318 U4319 U4320 U4321 G4324 C4325 A4326 G4327 G4328 A4329 G4330 G4331 U4332 G4333 U4334 C4335 A4336 G4337 A4338 A4339 A4340 A4341 G4342 A4345
C4346 C4347 A4348 C4349 A4350 G4353 A4354 U4355 A4356 A4357 C4358 U4359 C4362 U4363 U4366 G4367 G4370 G4371 C4372 C4373 A4374 A4375 G4376 C4377 G4378 U4379 U4380 C4381 A4382 U4383 A4384 G4385 C4386 G4387 A4388 C4389 G4390 C4394 U4395 U4396 U4397 A4401 C4404 U4405 U4406 C4407 G4408 A4409 U4410 G4411 U4412 C4413 G4414
G4415 C4416 U4420 C4421 C4422 U4423 A4424 U4425 C4426 U4431 G4432 A4433 A4434 G4435 C4436 A4437 G4438 A4448 G4449 C4450 G4451 U4452 U4453 G4454 G4455 A4456 U4457 U4458 G4459 U4460 U4461 C4465 C4466 A4467 A4470 A4471 U4472 A4473 G4474 G4475 G4476 A4477 A4478 C4479 G4480 U4481 G4482 A4483 G4484 C4485 G4488 G4489 U4490 U4491
U4492 A4493 G4494 G4498 U4499 C4500 G4501 U4502 G4503 A4504 G4505 A4506 C4507 A4508 G4509 G4510 U4511 U4512 U4515 U4516 A4519 C4520 C4521 C4522 C4525 U4526 G4527 A4528 U4529 G4530 A4531 U4532 G4533 U4534 G4535 U4536 U4537 G4538 U4539 U4540 G4541 C4542 C4543 A4544 U4545 G4546 G4547 U4548 A4549 A4550 U4551 C4552 U4557 C4558 A4559
G4560 U4561 A4562 C4563 G4566 A4567 G4568 G4569 A4570 G4577 G4578 U4579 U4580 G4583 A4584 C4585 A4586 U4587 U4592 G4593 U4594 A4595 U4596 G4597 U4598 G4599 C4600 U4601 U4602 G4603 G4604 G4609 G4610 A4611 G4612 C4613 C4614 A4615 A4616 U4617 G4618 G4621 C4622 U4628 A4629 C4630 C4631 A4632 G4636 U4637 G4638 G4639
G4640 A4641 U4642 U4643 G4646 A4651 G4654 C4655 C4656 U4657 C4658 U4659 A4660 A4661 C4664 A4665 A4668 U4669 C4670 C4671 C4672 C4675 C4676 A4677 G4678 G4679 C4680 G4681 A4682 A4683 C4684 A4688 C4689 G4690 G4691 C4692 A4693 G4694 C4695 G4696 C4697 C4698 G4699 C4700 G4701 C4706 G4710 U4711 U4712 G4713 G4714
C4715 C4716 U4717 C4718 G4719 G4720 A4721 U4722 A4723 G4724 C4725 C4726 C4733 C4734 G4735 C4736 G4739 U4740 C4741 C4742 C4743 C4744 G4745 C4746 C4747 G4748 G4749 C4750 G G G C C G C C C C C C U C C A C G C G C C C C G C G G
C G G G A G G C G C G U G C C C G4799 C4800 C4801 G4802 C4803 G4804 C4805 G4806 C4807 C4808 G4809 G4810 G4811 A4812 C4813 C4814 G4815 G4816 G4822 G4823 U4824 G4825 C4826 G4827 G4828 A4829 G4830 U4831 G4832 C4833 C4834 C4835 U4836 U4837 C4838 G4839 U4840 G4844 A4847
A4848 A4849 C4850 G4851 G4852 G4853 G4854 C4855 G4856 C4857 G4858 G4862 G4863 G4867 G4868 C4875 C4879 U4880 C4881 G4882 C4883 C4892 A4893 C4894 C4895 G4896 C4897 A4898 C4899 G4900 U4901 U4902 C4903 G4904 U4905 G4906 C4919 U4920 A4921 A4922 A4923 C4924 G4930 U4931 A4932 U4940 U4943 U4944 C4945 U4946 G4947



• Molecule 82: 5.8S Ribosomal RNA

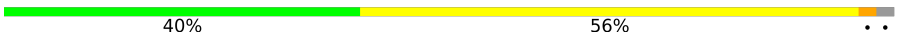
Chain A3:

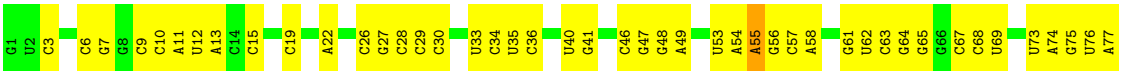


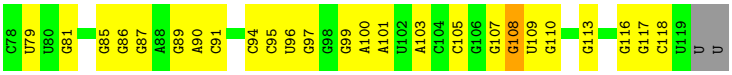


• Molecule 83: 5S Ribosomal RNA

Chain A4:







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	236113	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUP	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	14.352	Depositor
Minimum map value	-4.787	Depositor
Average map value	0.195	Depositor
Map value standard deviation	0.958	Depositor
Recommended contour level	3.5	Depositor
Map size (Å)	453.6, 453.6, 453.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.26, 1.26, 1.26	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	AV	0.29	0/1809	0.75	0/2819
2	AW	0.31	0/1783	0.76	0/2776
3	AX	0.42	1/615 (0.2%)	1.25	11/948 (1.2%)
4	B1	0.37	2/41550 (0.0%)	0.79	6/64763 (0.0%)
5	BA	0.51	0/1756	0.68	0/2386
6	BB	0.51	0/1756	0.75	1/2350 (0.0%)
7	BC	0.42	0/1761	0.65	0/2379
8	BD	0.40	0/1672	0.66	0/2250
9	BE	0.47	0/2072	0.70	0/2793
10	BF	0.43	0/1507	0.74	0/2026
11	BG	0.47	0/1907	0.74	0/2538
12	BH	0.46	0/1558	0.74	1/2087 (0.0%)
13	BI	0.47	0/1724	0.72	0/2298
14	BJ	0.45	0/1520	0.77	0/2030
15	BK	0.48	0/815	0.68	0/1101
16	BL	0.45	0/1220	0.72	0/1633
17	BM	0.48	0/941	0.72	0/1264
18	BN	0.43	0/1231	0.73	1/1656 (0.1%)
19	BO	0.46	0/1036	0.71	0/1391
20	BP	0.43	0/1000	0.67	0/1335
21	BQ	0.43	0/1125	0.66	0/1506
22	BR	0.42	0/904	0.67	0/1208
23	BS	0.42	0/1190	0.68	0/1594
24	BT	0.44	0/1131	0.69	0/1515
25	BU	0.50	0/813	0.70	0/1092
26	BV	0.47	0/643	0.71	0/860
27	BW	0.44	0/1050	0.69	0/1406
28	BX	0.46	0/1063	0.70	0/1421
29	BY	0.45	0/1019	0.70	0/1354
30	BZ	0.46	0/611	0.71	0/820
31	Ba	0.48	0/778	0.75	1/1041 (0.1%)
32	Bb	0.48	0/637	0.68	0/854

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Bc	0.46	0/492	0.74	0/657
34	Bd	0.51	0/454	0.76	0/603
35	Be	0.45	0/417	0.69	0/548
36	Bf	0.53	0/507	0.84	1/673 (0.1%)
37	Bg	0.45	0/2497	0.67	0/3399
38	CA	0.44	0/1926	0.67	0/2583
39	CB	0.45	0/3258	0.73	2/4361 (0.0%)
40	CC	0.47	0/2943	0.73	0/3953
41	CD	0.49	1/2406 (0.0%)	0.70	1/3221 (0.0%)
42	CE	0.52	0/1311	0.73	0/1763
43	CF	0.45	0/1985	0.68	0/2644
44	CG	0.46	0/1914	0.72	0/2578
45	CH	0.43	0/1554	0.69	0/2089
46	CI	0.42	0/1642	0.67	0/2194
47	CJ	0.49	0/1385	0.71	0/1852
48	CL	0.53	2/1647 (0.1%)	0.73	3/2205 (0.1%)
49	CM	0.49	0/1162	0.70	0/1556
50	CN	0.43	0/1753	0.65	0/2348
51	CO	0.44	0/1639	0.69	0/2193
52	CP	0.44	0/1260	0.70	0/1691
53	CQ	0.45	0/1517	0.74	0/2026
54	CR	0.40	0/1542	0.64	0/2037
55	CS	0.44	0/1478	0.73	0/1985
56	CT	0.46	0/1325	0.71	0/1770
57	CU	0.47	0/841	0.71	0/1128
58	CV	0.43	0/977	0.63	0/1312
59	CW	0.43	0/542	0.59	0/722
60	CX	0.41	0/992	0.67	0/1334
61	CY	0.47	0/1082	0.72	1/1441 (0.1%)
62	CZ	0.47	0/1137	0.79	0/1517
63	Ca	0.44	0/1190	0.71	0/1591
64	Cb	0.45	0/570	0.72	0/752
65	Cc	0.46	0/813	0.70	0/1091
66	Cd	0.44	0/919	0.67	0/1238
67	Ce	0.45	0/1071	0.68	0/1428
68	Cf	0.50	0/884	0.81	0/1185
69	Cg	0.48	0/917	0.74	0/1222
70	Ch	0.38	0/1022	0.64	0/1351
71	Ci	0.43	0/793	0.75	0/1048
72	Cj	0.49	0/704	0.76	0/931
73	Ck	0.43	0/574	0.73	0/761
74	Cl	0.41	0/453	0.61	0/599
75	Cm	0.42	0/434	0.70	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	Cn	0.39	0/240	0.50	0/305
77	Co	0.45	0/884	0.74	0/1166
78	Cp	0.40	0/717	0.61	0/953
79	Ct	0.48	0/1058	0.75	0/1416
80	Cu	0.45	0/1638	0.69	1/2222 (0.0%)
81	A2	0.41	23/86672 (0.0%)	0.80	40/135198 (0.0%)
82	A3	0.35	0/3723	0.79	1/5800 (0.0%)
83	A4	0.37	0/2836	0.81	3/4421 (0.1%)
All	All	0.42	29/231894 (0.0%)	0.77	74/341130 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	AX	1	0
4	B1	0	23
81	A2	0	35
82	A3	0	2
All	All	1	60

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	A2	1701	C	C5'-C4'	18.39	1.73	1.51
81	A2	1673	C	C3'-O3'	15.36	1.63	1.42
81	A2	1701	C	O5'-C5'	14.45	1.67	1.44
81	A2	1673	C	O3'-P	14.13	1.78	1.61
81	A2	1701	C	P-O5'	13.52	1.73	1.59

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
81	A2	1701	C	O4'-C4'-C3'	-15.19	88.81	104.00
39	CB	258	HIS	C-N-CD	-13.96	89.88	120.60
3	AX	58	U	P-O5'-C5'	12.68	141.18	120.90
81	A2	1701	C	O4'-C1'-N1	12.30	118.04	108.20
81	A2	1701	C	C4'-C3'-O3'	12.16	137.32	113.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	AX	58	U	C3'

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B1	111	A	Sidechain
4	B1	216	C	Sidechain
4	B1	44	U	Sidechain
4	B1	77	A	Sidechain
4	B1	84	A	Sidechain

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	BA	216/295 (73%)	209 (97%)	5 (2%)	2 (1%)	17	57
6	BB	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1	12
7	BC	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	6	34
8	BD	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	6	33
9	BE	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	7	38
10	BF	186/204 (91%)	163 (88%)	13 (7%)	10 (5%)	2	19
11	BG	230/249 (92%)	216 (94%)	5 (2%)	9 (4%)	3	23
12	BH	189/194 (97%)	178 (94%)	7 (4%)	4 (2%)	7	36
13	BI	205/208 (99%)	184 (90%)	14 (7%)	7 (3%)	3	26
14	BJ	177/194 (91%)	169 (96%)	5 (3%)	3 (2%)	9	42
15	BK	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	13

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	BL	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	3	22
17	BM	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	2	19
18	BN	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	3	26
19	BO	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	6	35
20	BP	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	2	22
21	BQ	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	10	46
22	BR	105/135 (78%)	99 (94%)	4 (4%)	2 (2%)	8	38
23	BS	140/152 (92%)	125 (89%)	7 (5%)	8 (6%)	1	18
24	BT	141/145 (97%)	135 (96%)	4 (3%)	2 (1%)	11	46
25	BU	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	15	54
26	BV	81/83 (98%)	78 (96%)	1 (1%)	2 (2%)	5	32
27	BW	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	9	44
28	BX	132/143 (92%)	120 (91%)	5 (4%)	7 (5%)	2	19
29	BY	120/133 (90%)	114 (95%)	2 (2%)	4 (3%)	4	26
30	BZ	74/125 (59%)	71 (96%)	0	3 (4%)	3	22
31	Ba	94/115 (82%)	85 (90%)	5 (5%)	4 (4%)	2	22
32	Bb	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
33	Bc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	4	26
34	Bd	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
35	Be	49/59 (83%)	43 (88%)	5 (10%)	1 (2%)	7	38
36	Bf	59/156 (38%)	53 (90%)	6 (10%)	0	100	100
37	Bg	312/317 (98%)	291 (93%)	14 (4%)	7 (2%)	6	35
38	CA	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	13	50
39	CB	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	3	25
40	CC	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	3	22
41	CD	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	9	42
42	CE	156/288 (54%)	141 (90%)	8 (5%)	7 (4%)	2	22
43	CF	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	9	42
44	CG	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	3	23
45	CH	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	9	44
46	CI	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	9	44

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	CJ	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	14
48	CL	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	2	18
49	CM	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	11	46
50	CN	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	10	46
51	CO	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	10	46
52	CP	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	7	38
53	CQ	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	4	26
54	CR	181/196 (92%)	175 (97%)	3 (2%)	3 (2%)	9	42
55	CS	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	3	25
56	CT	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	8	38
57	CU	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
58	CV	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	9	44
59	CW	62/157 (40%)	61 (98%)	1 (2%)	0	100	100
60	CX	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
61	CY	126/145 (87%)	119 (94%)	4 (3%)	3 (2%)	6	33
62	CZ	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	4	28
63	Ca	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	3	26
64	Cb	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	1	17
65	Cc	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	7	38
66	Cd	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	17	57
67	Ce	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	6	33
68	Cf	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	2	21
69	Cg	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	3	25
70	Ch	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	5	32
71	Ci	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	1	17
72	Cj	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	6	33
73	Ck	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	10	46
74	Cl	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	7	36
75	Cm	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	7	38
76	Cn	23/25 (92%)	23 (100%)	0	0	100	100
77	Co	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	8	38

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	Cp	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	3	26
79	Ct	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	2	19
80	Cu	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	11	46
All	All	11190/12898 (87%)	10477 (94%)	390 (4%)	323 (3%)	7	29

5 of 323 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	BB	76	ASN
6	BB	132	GLY
6	BB	148	ASN
6	BB	154	SER
6	BB	176	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	BA	181/243 (74%)	176 (97%)	5 (3%)	43	65
6	BB	194/231 (84%)	183 (94%)	11 (6%)	20	45
7	BC	188/225 (84%)	181 (96%)	7 (4%)	34	58
8	BD	175/202 (87%)	166 (95%)	9 (5%)	24	48
9	BE	220/225 (98%)	208 (94%)	12 (6%)	21	47
10	BF	158/170 (93%)	151 (96%)	7 (4%)	28	53
11	BG	202/218 (93%)	195 (96%)	7 (4%)	36	59
12	BH	171/174 (98%)	167 (98%)	4 (2%)	50	70
13	BI	179/180 (99%)	167 (93%)	12 (7%)	16	41
14	BJ	160/168 (95%)	150 (94%)	10 (6%)	18	43
15	BK	85/136 (62%)	82 (96%)	3 (4%)	36	59
16	BL	133/142 (94%)	131 (98%)	2 (2%)	65	80
17	BM	102/108 (94%)	97 (95%)	5 (5%)	25	50

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	BN	130/131 (99%)	128 (98%)	2 (2%)	65	80
19	BO	107/119 (90%)	100 (94%)	7 (6%)	17	42
20	BP	107/130 (82%)	102 (95%)	5 (5%)	26	51
21	BQ	115/121 (95%)	111 (96%)	4 (4%)	36	59
22	BR	99/122 (81%)	94 (95%)	5 (5%)	24	48
23	BS	123/132 (93%)	114 (93%)	9 (7%)	14	39
24	BT	113/115 (98%)	106 (94%)	7 (6%)	18	43
25	BU	93/107 (87%)	89 (96%)	4 (4%)	29	53
26	BV	67/67 (100%)	66 (98%)	1 (2%)	65	80
27	BW	112/113 (99%)	107 (96%)	5 (4%)	27	52
28	BX	108/115 (94%)	103 (95%)	5 (5%)	27	52
29	BY	107/115 (93%)	101 (94%)	6 (6%)	21	46
30	BZ	67/103 (65%)	63 (94%)	4 (6%)	19	44
31	Ba	83/98 (85%)	76 (92%)	7 (8%)	11	33
32	Bb	72/76 (95%)	68 (94%)	4 (6%)	21	46
33	Bc	55/62 (89%)	52 (94%)	3 (6%)	21	47
34	Bd	47/49 (96%)	43 (92%)	4 (8%)	10	33
35	Be	42/48 (88%)	40 (95%)	2 (5%)	25	51
36	Bf	54/140 (39%)	51 (94%)	3 (6%)	21	46
37	Bg	272/275 (99%)	260 (96%)	12 (4%)	28	53
38	CA	189/199 (95%)	185 (98%)	4 (2%)	53	72
39	CB	344/349 (99%)	326 (95%)	18 (5%)	23	48
40	CC	302/348 (87%)	284 (94%)	18 (6%)	19	44
41	CD	244/250 (98%)	237 (97%)	7 (3%)	42	64
42	CE	143/252 (57%)	135 (94%)	8 (6%)	21	46
43	CF	203/215 (94%)	196 (97%)	7 (3%)	37	60
44	CG	199/223 (89%)	192 (96%)	7 (4%)	36	59
45	CH	171/171 (100%)	164 (96%)	7 (4%)	30	55
46	CI	170/181 (94%)	161 (95%)	9 (5%)	22	47
47	CJ	143/149 (96%)	137 (96%)	6 (4%)	30	54
48	CL	167/177 (94%)	156 (93%)	11 (7%)	16	41

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	CM	118/161 (73%)	114 (97%)	4 (3%)	37	60
50	CN	172/172 (100%)	170 (99%)	2 (1%)	71	83
51	CO	168/174 (97%)	166 (99%)	2 (1%)	71	83
52	CP	133/163 (82%)	126 (95%)	7 (5%)	22	47
53	CQ	162/165 (98%)	157 (97%)	5 (3%)	40	62
54	CR	161/175 (92%)	150 (93%)	11 (7%)	16	41
55	CS	155/157 (99%)	148 (96%)	7 (4%)	27	52
56	CT	139/140 (99%)	134 (96%)	5 (4%)	35	59
57	CU	91/115 (79%)	88 (97%)	3 (3%)	38	61
58	CV	100/107 (94%)	99 (99%)	1 (1%)	76	86
59	CW	55/126 (44%)	52 (94%)	3 (6%)	21	47
60	CX	107/133 (80%)	105 (98%)	2 (2%)	57	75
61	CY	119/135 (88%)	115 (97%)	4 (3%)	37	60
62	CZ	118/118 (100%)	112 (95%)	6 (5%)	24	48
63	Ca	120/121 (99%)	116 (97%)	4 (3%)	38	61
64	Cb	58/126 (46%)	57 (98%)	1 (2%)	60	78
65	Cc	88/97 (91%)	87 (99%)	1 (1%)	73	84
66	Cd	100/110 (91%)	96 (96%)	4 (4%)	31	55
67	Ce	115/121 (95%)	112 (97%)	3 (3%)	46	66
68	Cf	87/89 (98%)	79 (91%)	8 (9%)	9	29
69	Cg	98/100 (98%)	88 (90%)	10 (10%)	7	25
70	Ch	109/110 (99%)	106 (97%)	3 (3%)	43	65
71	Ci	82/89 (92%)	76 (93%)	6 (7%)	14	39
72	Cj	71/80 (89%)	69 (97%)	2 (3%)	43	65
73	Ck	64/65 (98%)	64 (100%)	0	100	100
74	Cl	47/48 (98%)	46 (98%)	1 (2%)	53	72
75	Cm	48/116 (41%)	45 (94%)	3 (6%)	18	43
76	Cn	24/24 (100%)	24 (100%)	0	100	100
77	Co	94/94 (100%)	89 (95%)	5 (5%)	22	47
78	Cp	74/75 (99%)	72 (97%)	2 (3%)	44	65
79	Ct	113/121 (93%)	106 (94%)	7 (6%)	18	43

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	Cu	177/177 (100%)	163 (92%)	14 (8%)	12	35
All	All	9763/10978 (89%)	9332 (96%)	431 (4%)	32	53

5 of 431 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	CC	310	HIS
48	CL	55	ILE
74	Cl	5	LYS
41	CD	262	LYS
44	CG	163	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 210 such sidechains are listed below:

Mol	Chain	Res	Type
43	CF	116	GLN
52	CP	54	GLN
75	Cm	87	GLN
44	CG	108	GLN
47	CJ	168	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AV	75/76 (98%)	37 (49%)	2 (2%)
2	AW	74/76 (97%)	33 (44%)	5 (6%)
3	AX	27/28 (96%)	15 (55%)	4 (14%)
4	B1	1738/1869 (92%)	1038 (59%)	152 (8%)
81	A2	3605/5025 (71%)	2042 (56%)	325 (9%)
82	A3	156/194 (80%)	81 (51%)	6 (3%)
83	A4	118/121 (97%)	68 (57%)	9 (7%)
All	All	5793/7389 (78%)	3314 (57%)	503 (8%)

5 of 3314 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AV	2	C
1	AV	5	G
1	AV	8	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AV	11	C
1	AV	17	C

5 of 503 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
81	A2	947	G
81	A2	4596	U
81	A2	1619	C
81	A2	4533	G
81	A2	4848	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	MIA	AW	37	2	24,31,32	2.05	5 (20%)	26,44,47	3.30	8 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MIA	AW	37	2	-	6/11/33/34	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AW	37	MIA	C13-C14	6.16	1.50	1.32
2	AW	37	MIA	C2-S10	4.30	1.79	1.75

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AW	37	MIA	C12-C13	-3.27	1.33	1.48
2	AW	37	MIA	C6-N1	2.71	1.36	1.32
2	AW	37	MIA	C4-N3	-2.46	1.31	1.35

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	AW	37	MIA	C11-S10-C2	11.40	110.78	102.27
2	AW	37	MIA	C2-N3-C4	-6.18	106.80	115.32
2	AW	37	MIA	C12-N6-C6	-6.02	113.64	122.55
2	AW	37	MIA	C5-C6-N1	-5.98	115.84	120.81
2	AW	37	MIA	C12-C13-C14	-3.39	120.54	127.14

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AW	37	MIA	N1-C2-S10-C11
2	AW	37	MIA	N3-C2-S10-C11
2	AW	37	MIA	O4'-C4'-C5'-O5'
2	AW	37	MIA	C3'-C4'-C5'-O5'
2	AW	37	MIA	N6-C12-C13-C14

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

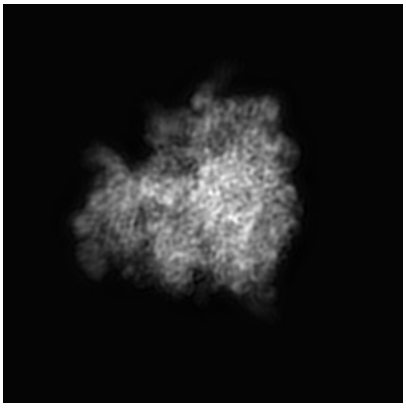
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-2620. These allow visual inspection of the internal detail of the map and identification of artifacts.

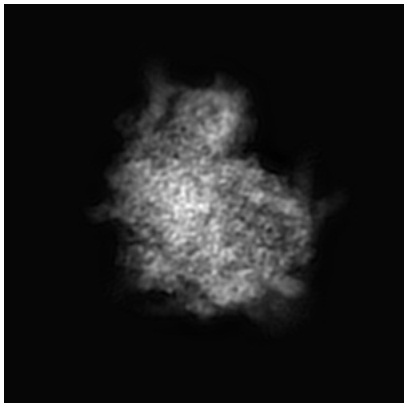
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

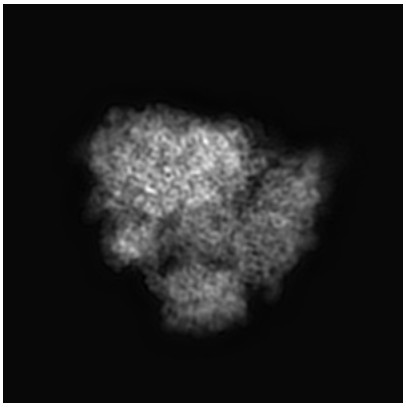
6.1.1 Primary map



X



Y

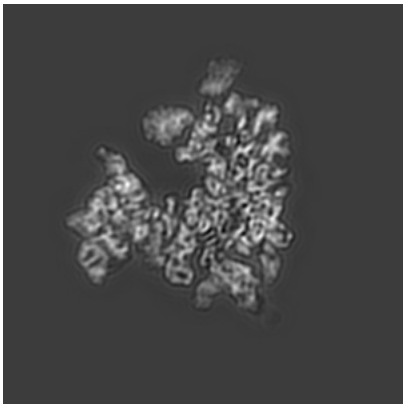


Z

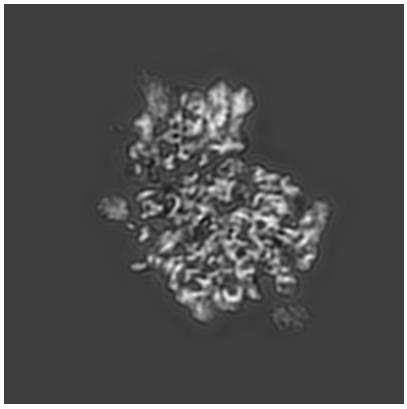
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

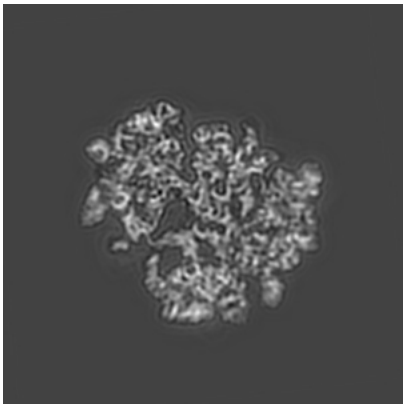
6.2.1 Primary map



X Index: 180



Y Index: 180

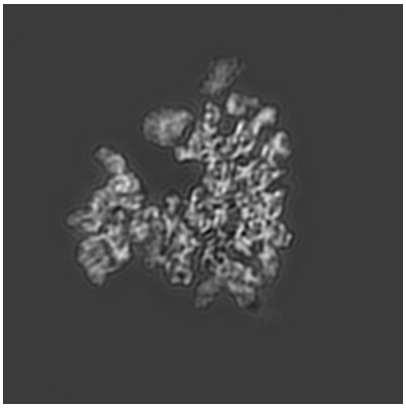


Z Index: 180

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

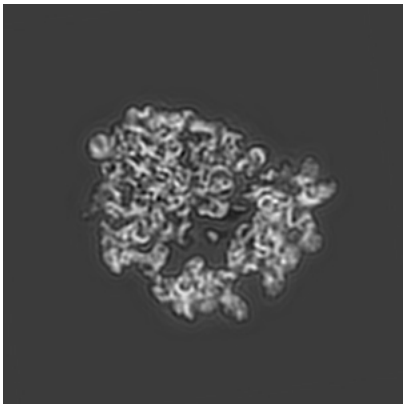
6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 182

Y Index: 217



Z Index: 190

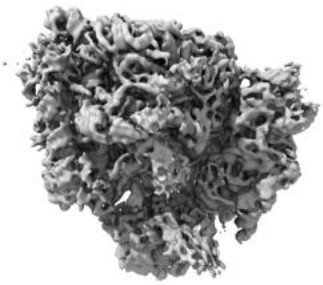
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

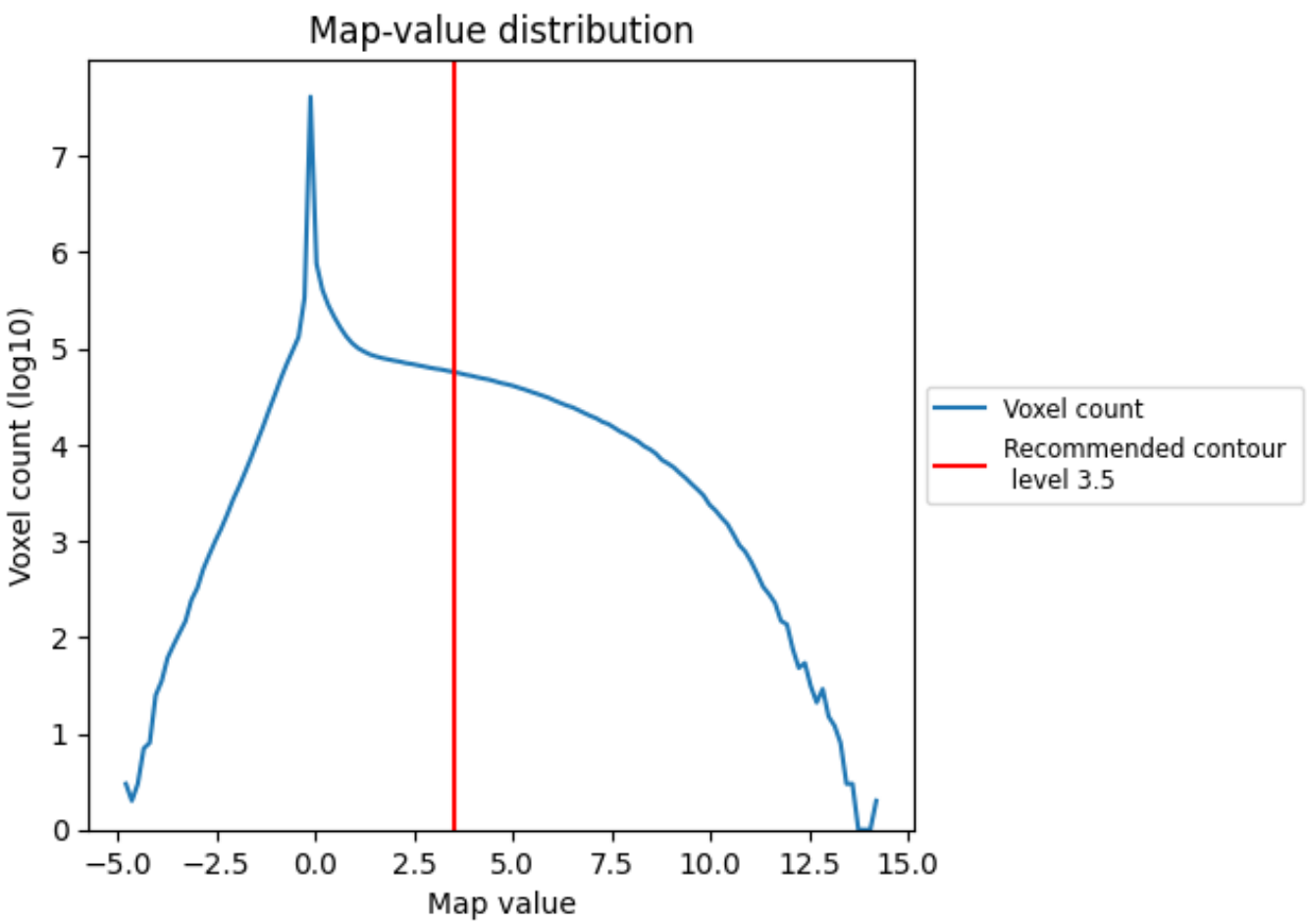
6.5 Mask visualisation (i)

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

7 Map analysis (i)

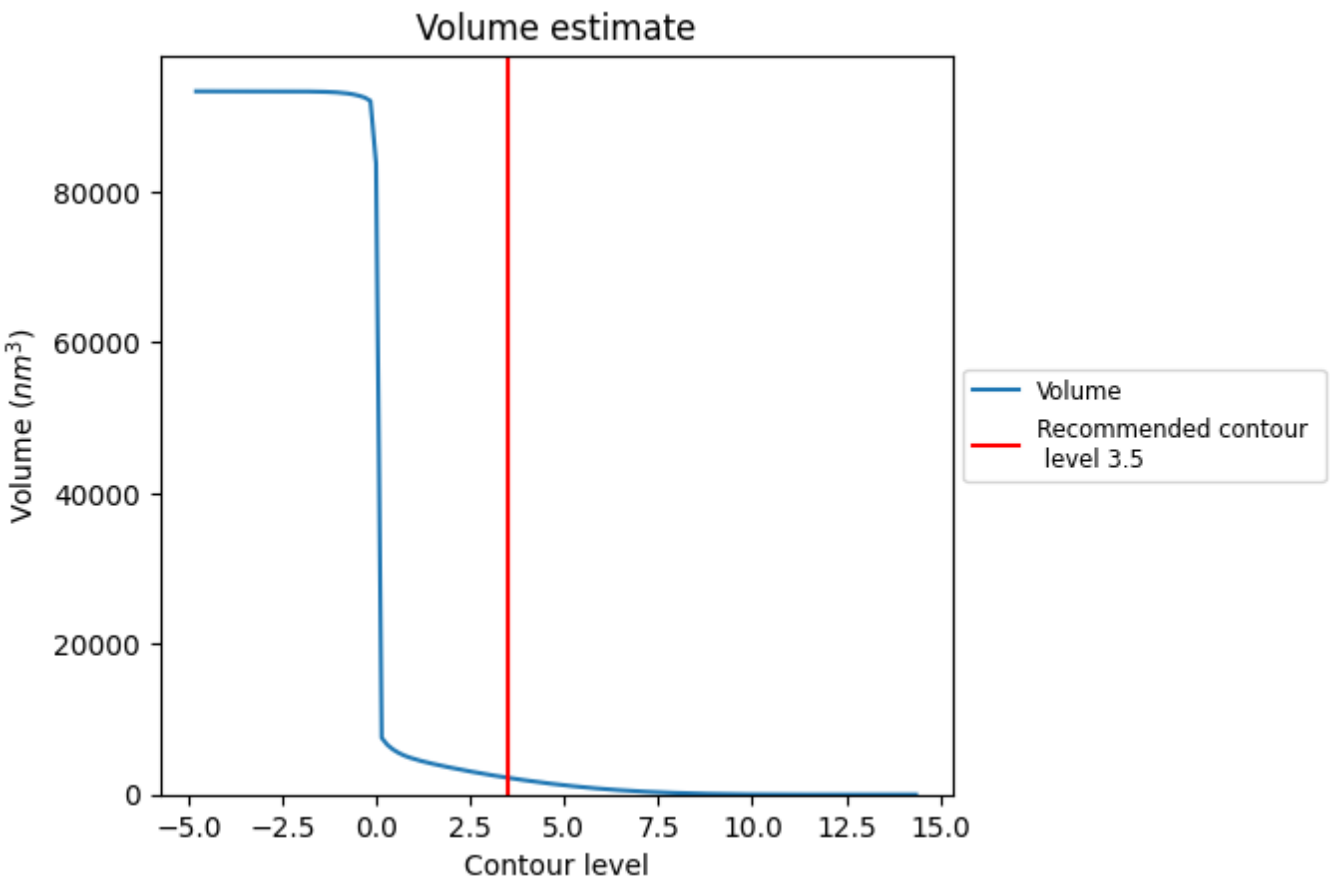
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

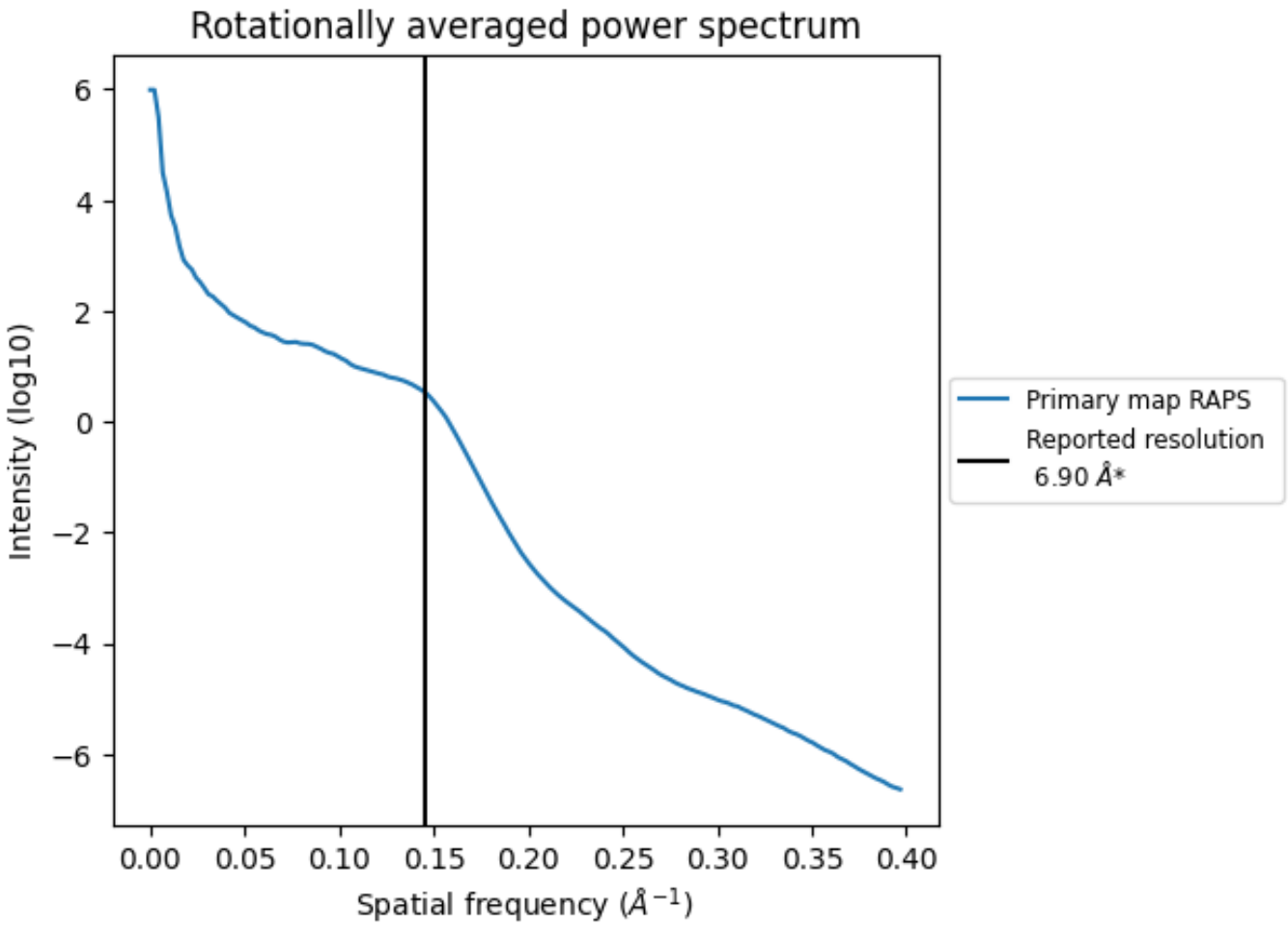
7.2 Volume estimate (i)



The volume at the recommended contour level is 2230 nm^3; this corresponds to an approximate mass of 2014 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.145 Å^{-1}

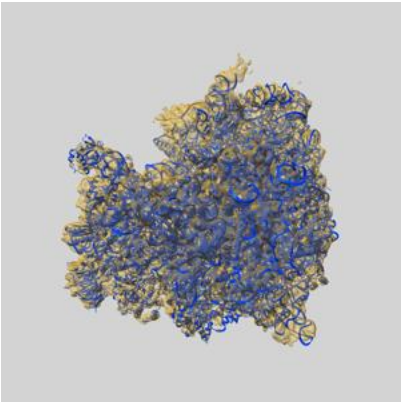
8 Fourier-Shell correlation (i)

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

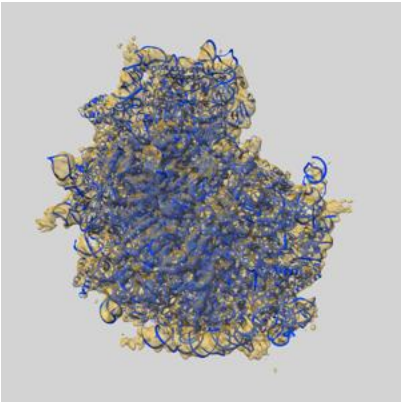
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-2620 and PDB model 4UJE. Per-residue inclusion information can be found in section 3 on page 18.

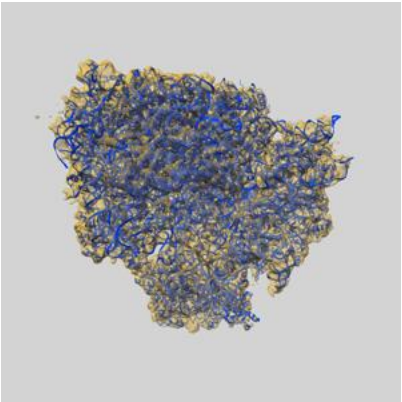
9.1 Map-model overlay (i)



X



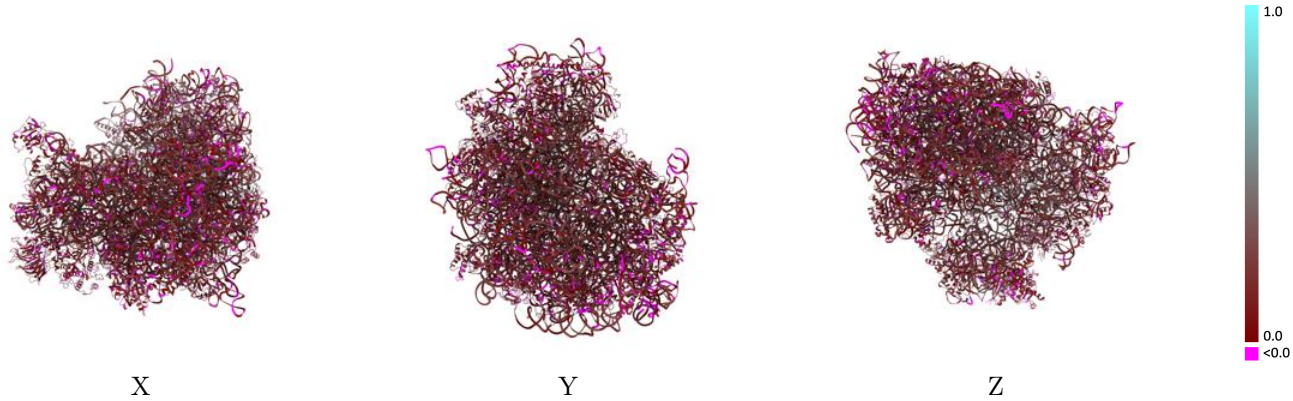
Y



Z

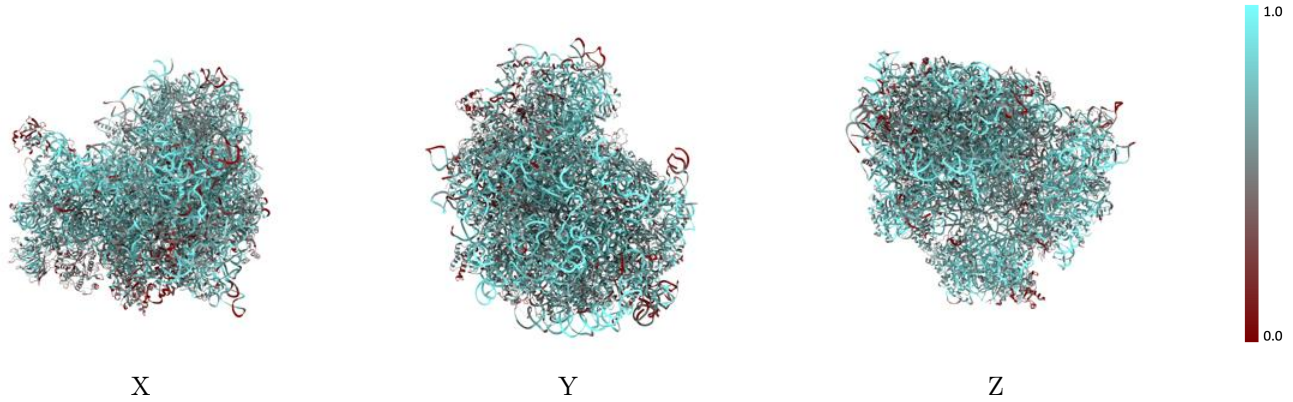
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



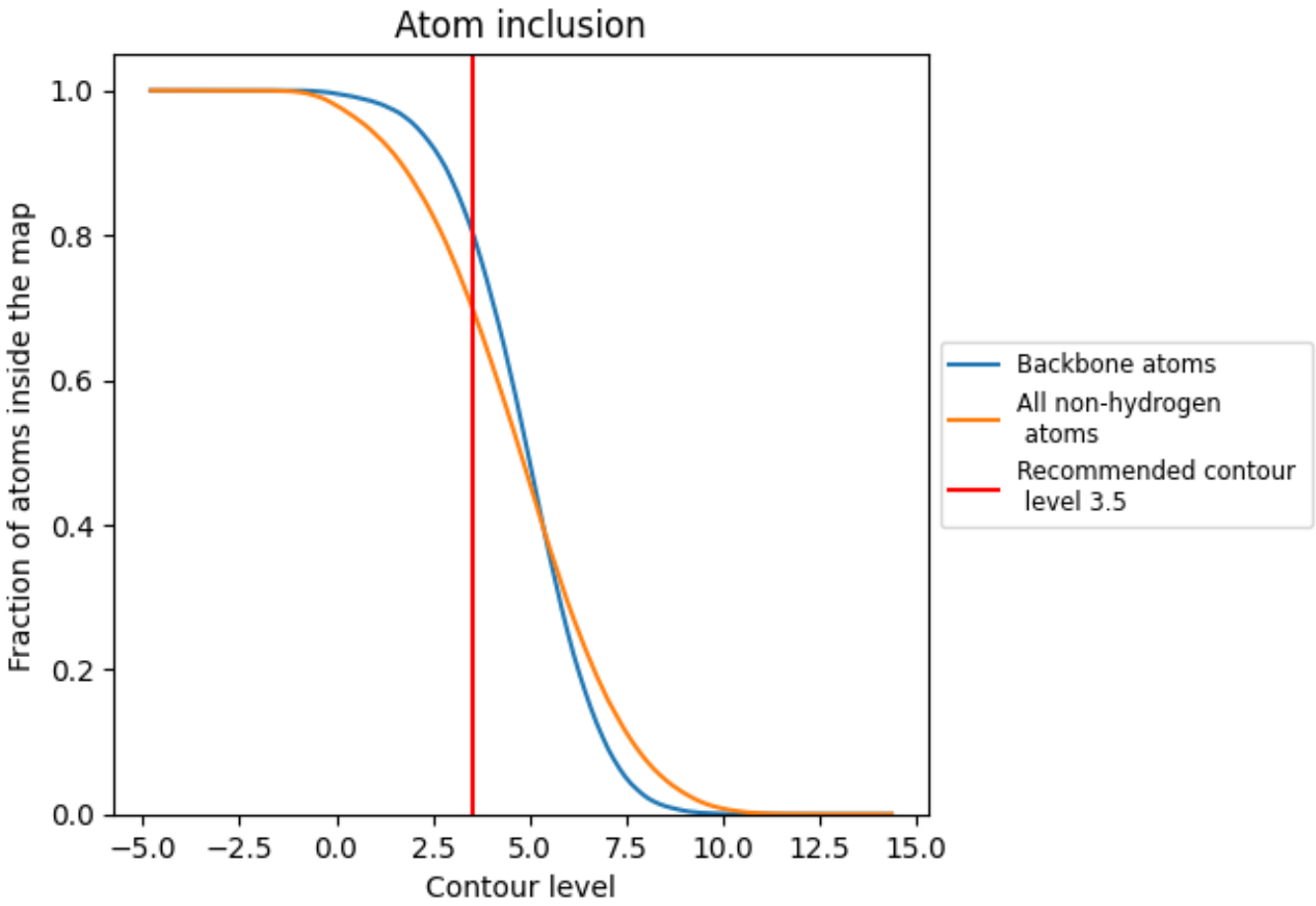
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



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 (3.5).

9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7022	0.1710
A2	0.8020	0.1990
A3	0.8335	0.2060
A4	0.9338	0.2240
AV	0.6980	0.1980
AW	0.6538	0.1800
AX	0.4393	0.1920
B1	0.8421	0.1980
BA	0.4631	0.1340
BB	0.5468	0.1440
BC	0.5272	0.1500
BD	0.6232	0.1450
BE	0.6505	0.1470
BF	0.5931	0.1430
BG	0.6194	0.1270
BH	0.3625	0.1240
BI	0.4994	0.1140
BJ	0.6913	0.1330
BK	0.7038	0.1420
BL	0.4553	0.1310
BM	0.2748	0.0910
BN	0.5081	0.1320
BO	0.5352	0.1440
BP	0.6625	0.1470
BQ	0.6735	0.1220
BR	0.5191	0.1350
BS	0.6767	0.1460
BT	0.7486	0.1450
BU	0.6317	0.1180
BV	0.3923	0.1150
BW	0.5798	0.1400
BX	0.4418	0.1450
BY	0.6821	0.1330
BZ	0.5780	0.1520
Ba	0.4946	0.0950

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bb	0.5024	0.1420
Bc	0.4596	0.1380
Bd	0.7042	0.1140
Be	0.5567	0.1360
Bf	0.4327	0.1020
Bg	0.5612	0.1360
CA	0.4329	0.1330
CB	0.5867	0.1480
CC	0.5340	0.1210
CD	0.6805	0.1550
CE	0.5334	0.1100
CF	0.5175	0.1280
CG	0.5348	0.1330
CH	0.6206	0.1420
CI	0.5103	0.1400
CJ	0.6533	0.1430
CL	0.5206	0.1100
CM	0.6588	0.1560
CN	0.5556	0.1340
CO	0.5860	0.1330
CP	0.5710	0.1350
CQ	0.5112	0.1140
CR	0.5353	0.1250
CS	0.5887	0.1320
CT	0.5357	0.1400
CU	0.4759	0.1410
CV	0.4431	0.1460
CW	0.5118	0.1220
CX	0.5422	0.1390
CY	0.6352	0.1300
CZ	0.5898	0.1460
Ca	0.5492	0.1380
Cb	0.4761	0.1260
Cc	0.4841	0.1410
Cd	0.5750	0.1500
Ce	0.5054	0.1580
Cf	0.5560	0.1140
Cg	0.5161	0.1320
Ch	0.5663	0.1230
Ci	0.5598	0.1380
Cj	0.5556	0.1160
Ck	0.4856	0.1230

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Cl	0.4976	0.1130
Cm	0.5362	0.1320
Cn	0.4358	0.1070
Co	0.4360	0.1130
Cp	0.4440	0.1140
Ct	0.5290	0.0840
Cu	0.2247	0.0560