wwPDB EM Validation Summary Report (i)

Feb 22, 2024 – 05:58 PM EST

PDB ID	:	4V6I
EMDB ID	:	EMD-1669
Title	:	Localization of the small subunit ribosomal proteins into a 6.1 A cryo-EM map of Saccharomyces cerevisiae translating 80S ribosome
Authors	:	Armache, J.-P.; Jarasch, A.; Anger, A.M.; Villa, E.; Becker, T.; Bhushan, S.; Jossinet, F.; Habeck, M.; Dindar, G.; Franckenberg, S.; Marquez, V.; Mielke, T.; Thomm, M.; Berninghausen, O.; Beatrix, B.; Soeding, J.; Westhof, E.; Wilson, D.N.; Beckmann, R.
Deposited on	:	2010-10-12
Resolution	:	8.80 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:

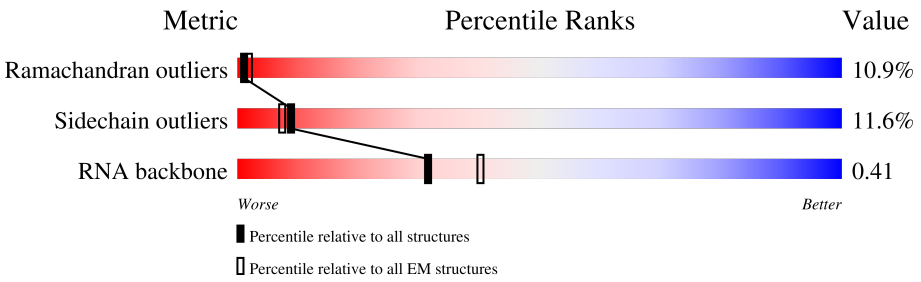
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 8.80 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	Aa	319	47%; 72%, 19%, 8%, •
2	AA	252	27%; 65%, 25%, 6%, 5%
3	AB	240	41%; 49%, 23%, 10%, •, 15%
4	AD	261	24%; 43%, 21%, 11%, •, 23%
5	AC	197	35%; 49%, 31%, 14%, 6%
6	AE	254	33%; 64%, 19%, 13%, •
7	AG	144	31%; 78%, 21%, •
8	AF	225	38%; 61%, 19%, 7%, •, 12%

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Mol	Chain	Length	Quality of chain
9	AH	130	38% 61% 24% 10% 5%
10	AI	143	32% 50% 21% 15% • 12%
11	AJ	121	38% 62% 21% 9% • 7%
12	AK	137	30% 48% 28% 7% • 13%
13	AL	145	31% 57% 32% 6% 5%
14	AM	146	66% 53% 32% 10% • •
15	AN	56	50% 36% 23% 25% • 14%
16	AO	151	38% 48% 19% 11% • 20%
17	AQ	136	67% 51% 31% 12% 6%
18	AP	156	30% 31% 12% 9% • 46%
19	AR	142	39% 37% 17% 8% 38%
20	AS	144	42% 55% 32% 8% 6%
21	AT	87	55% 62% 18% 16% •
22	AV	108	44% 44% 24% 6% • 21%
23	AW	93	23% 78% 20% •
24	AX	82	28% 32% 23% • • 39%
25	AY	67	58% 58% 27% • 10%
26	AZ	63	43% 51% 21% 17% 11%
27	Ab	37	5% 89% 8% •
28	Ac	26	35% 92% • •
29	AU	135	30% 38% 18% 14% • 29%
30	BA	217	73% 76% 20% •
31	BB	254	47% 67% 17% 13% •
32	BC	388	30% 56% 28% 12% •
33	BD	362	30% 55% 23% 7% 6% 9%

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Mol	Chain	Length	Quality of chain
34	BE	174	33% 60% 20% 11% 6%
35	BG	176	28% 36% 28% 22% 14%
36	BF	191	37% 79% 16%
37	BH	256	21% 46% 19% 7% 23%
38	Bs	312	57% 60% 16% 5% 18%
39	BJ	165	48% 53% 17% 5% 23%
40	BK	199	33% 63% 21% 13%
41	BN	138	27% 55% 33% 11%
42	BM	137	67% 60% 26% 9%
43	BP	204	30% 50% 25% 16% 5%
44	BO	149	42% 54% 26% 15% 5%
45	BR	186	30% 49% 20% 12% 5% 13%
46	BT	189	42% 67% 23% 8%
47	BU	160	25% 64% 27% 6%
48	BW	121	31% 50% 24% 10% 13%
49	BV	170	40% 71% 16% 11%
50	BX	142	34% 53% 23% 9% 14%
51	BZ	155	25% 25% 11% 7% 53%
52	BY	123	15% 67% 25% 5%
53	Ba	136	30% 32% 18% 14% 6% 30%
54	Bd	59	12% 25% 10% 63%
55	Bc	120	8% 62% 21% 10% 6%
56	Bf	105	40% 76% 17% 6%
57	Be	244	29% 70% 19% 7%
58	Bg	113	35% 62% 20% 12%

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Mol	Chain	Length	Quality of chain
59	Bh	130	43% 65% 24% 7% •
60	Bi	118	49% 53% 25% 14% 8%
61	Bj	107	46% 46% 27% 15% 6% 7%
62	Bk	100	12% 46% 15% 13% • 23%
63	Bm	92	51% 72% 22% • •
64	Bl	88	28% 64% 20% 14% •
65	Bn	78	33% 59% 21% 12% 9%
66	Bo	51	43% 45% 29% 18% 8%
67	Bp	52	38% 46% 17% 12% • 23%
68	Bq	25	48% 44% 40% 16%
69	Br	106	46% 53% 25% 14% 8%
70	Bx	21	19% 76% 19% 5%
70	By	21	5% 95% 5%
71	Bz	15	33% 87% 7% 7%
72	Bt	106	33% 43% 9% •• 45%
72	Bu	106	55% 41% 12% •• 45%
73	Bv	106	40% 49% 5% • 45%
73	Bw	106	52% 49% 5% • 45%
74	BQ	297	16% 60% 21% 13% 6%
75	BL	170	19% 96% • •
76	BS	167	41% 43% 31% 14% 13%
77	BI	221	20% 57% 15% 7% • 18%
78	CA	1800	11% 11% 52% 32% • •
79	CB	75	95% • 56% 41%
80	CC	11	91% 9% 27% 64%

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Mol	Chain	Length	Quality of chain
81	DA	3396	10% 7% 49% 43%
82	DB	158	9% 9% 42% 49%
83	DC	118	44% 56%

2 Entry composition (i)

There are 83 unique types of molecules in this entry. The entry contains 191627 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 protein called 40S ribosomal protein RACK1 (RACK1).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	Aa	319	2442	1544	420	469	9	0	0

- Molecule 2 is a protein called 40S ribosomal protein rpS0 (S2p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AA	252	1922	1204	336	380	2	0	0

- Molecule 3 is a protein called 40S ribosomal protein rpS3 (S3p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AB	204	1511	945	282	278	6	0	0

- Molecule 4 is a protein called 40S ribosomal protein rpS4 (S4e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AD	200	1591	1018	288	283	2	0	0

- Molecule 5 is a protein called 40S ribosomal protein rpS9 (S4p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AC	197	1521	951	298	270	2	0	0

- Molecule 6 is a protein called 40S ribosomal protein rpS2 (S5p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AE	254	1936	1224	360	349	3	0	0

- Molecule 7 is a protein called 40S ribosomal protein rpS7 (S7e).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	AG	143	716	429	143	144	0	0

- Molecule 8 is a protein called 40S ribosomal protein rpS5 (S7p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AF	199	1543	958	293	289	3	0	0

- Molecule 9 is a protein called 40S ribosomal protein rpS22 (S8p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AH	130	1030	655	189	182	4	0	0

- Molecule 10 is a protein called 40S ribosomal protein rpS16 (S9p).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	AI	126	998	639	184	175	0	0

- Molecule 11 is a protein called 40S ribosomal protein rpS20 (S10p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AJ	113	849	528	158	162	1	0	0

- Molecule 12 is a protein called 40S ribosomal protein rpS14 (S11p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AK	119	833	508	157	165	3	0	0

- Molecule 13 is a protein called 40S ribosomal protein rpS23 (S12p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AL	145	978	588	203	184	3	0	0

- Molecule 14 is a protein called 40S ribosomal protein rpS18 (S13p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	AM	140	1156	719	231	204	2	0	0

- Molecule 15 is a protein called 40S ribosomal protein rpS29 (S14p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	AN	48	353	209	79	61	4	0	0

- Molecule 16 is a protein called 40S ribosomal protein rpS13 (S15p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	AO	121	978	624	183	170	1	0	0

- Molecule 17 is a protein called 40S ribosomal protein rpS17 (S17e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	AQ	136	1098	682	213	201	2	0	0

- Molecule 18 is a protein called 40S ribosomal protein rpS11 (S17p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	AP	85	631	402	124	104	1	0	0

- Molecule 19 is a protein called 40S ribosomal protein rpS15 (S19p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	AR	88	676	429	123	118	6	0	0

- Molecule 20 is a protein called 40S ribosomal protein rpS19 (S19e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	AS	144	1120	699	209	209	3	0	0

- Molecule 21 is a protein called 40S ribosomal protein rpS21 (S21e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	AT	87	685	420	125	138	2	0	0

- Molecule 22 is a protein called 40S ribosomal protein rpS25 (S25e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	AV	85	688	437	128	122	1	0	0

- Molecule 23 is a protein called 40S ribosomal protein rpS26 (S26e).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	AW	92	461	276	92	93	0	0

- Molecule 24 is a protein called 40S ribosomal protein rpS27 (S27e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	AX	50	366	229	60	72	5	0	0

- Molecule 25 is a protein called 40S ribosomal protein rpS28 (S28e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	AY	60	445	276	80	87	2	0	0

- Molecule 26 is a protein called 40S ribosomal protein rpS30 (S30e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	AZ	63	492	307	102	81	2	0	0

- Molecule 27 is a protein called Unknown 40S ribosomal protein XS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	Ab	36	181	108	36	37	0	0

- Molecule 28 is a protein called Unknown 40S ribosomal protein XS2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	Ac	25	126	75	25	26	0	0

- Molecule 29 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	AU	96	714	450	134	129	1	0	0

- Molecule 30 is a protein called 60S ribosomal protein rpL1 (L1p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	BA	217	1718	1097	299	312	10	0	0

- Molecule 31 is a protein called 60S ribosomal protein rpL2 (L2p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	BB	254	1904	1183	385	334	2	0	0

- Molecule 32 is a protein called 60S ribosomal protein rpL3 (L3p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	BC	388	3055	1933	579	534	9	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BC	388	GLY	-	expression tag	UNP P14126

- Molecule 33 is a protein called 60S ribosomal protein rpL4 (L4p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	BD	329	2486	1564	480	438	4	0	0

- Molecule 34 is a protein called 60S ribosomal protein rpL11 (L5p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	BE	168	1341	839	252	245	5	0	0

- Molecule 35 is a protein called 60S ribosomal protein rpL6 (L6e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	BG	176	1409	907	252	248	2	0	0

- Molecule 36 is a protein called 60S ribosomal protein rpL9 (L6p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	BF	191	1516	961	274	277	4	0	0

- Molecule 37 is a protein called 60S ribosomal protein rpL8 (L7ae).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	BH	197	1505	959	269	274	3	0	0

- Molecule 38 is a protein called 60S acidic ribosomal protein rpP0 (L10P).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Bs	257	1976	1269	334	368	5	0	0

- Molecule 39 is a protein called 60S ribosomal protein rpL12 (L11p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	BJ	127	954	601	174	178	1	0	0

- Molecule 40 is a protein called 60S ribosomal protein rpL16 (L13p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	BK	199	1570	1011	291	266	2	0	0

- Molecule 41 is a protein called 60S ribosomal protein rpL14 (L14e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	BN	138	1068	683	201	181	3	0	0

- Molecule 42 is a protein called 60S ribosomal protein rpL23 (L14p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	BM	131	972	611	182	172	7	0	0

- Molecule 43 is a protein called 60S ribosomal protein rpL15 (L15e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	BP	193	1625	1016	341	266	2	0	0

- Molecule 44 is a protein called 60S ribosomal protein rpL28 (L15p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	BO	149	1182	754	232	192	4	0	0

- Molecule 45 is a protein called 60S ribosomal protein rpL18 (L18e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	BR	161	1243	786	242	212	3	0	0

- Molecule 46 is a protein called 60S ribosomal protein rpL19 (L19e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	BT	189	1530	940	327	262	1	0	0

- Molecule 47 is a protein called 60S ribosomal protein rpL21 (L21e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	BU	160	1261	793	242	222	4	0	0

- Molecule 48 is a protein called 60S ribosomal protein rpL22 (L22e).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
48	BW	105	830	535	140	155	0	0

- Molecule 49 is a protein called 60S ribosomal protein rpL17 (L22p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	BV	170	1312	814	254	243	1	0	0

- Molecule 50 is a protein called 60S ribosomal protein rpL25 (L23p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	BX	122	978	629	172	175	2	0	0

- Molecule 51 is a protein called 60S ribosomal protein rpL24 (L24e).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
51	BZ	73	579	366	115	98	0	0

- Molecule 52 is a protein called 60S ribosomal protein rpL26 (L24p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	BY	123	972	611	188	172	1	0	0

- Molecule 53 is a protein called 60S ribosomal protein rpL27 (L27e).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
53	Ba	95	708	455	134	119	0	0

- Molecule 54 is a protein called 60S ribosomal protein rpL29 (L29e).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
54	Bd	22	174	109	40	25	0	0

- Molecule 55 is a protein called 60S ribosomal protein rpL35 (L29p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	Bc	118	965	612	185	167	1	0	0

- Molecule 56 is a protein called 60S ribosomal protein rpL30 (L30e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	Bf	105	785	501	133	150	1	0	0

- Molecule 57 is a protein called 60S ribosomal protein rpL7 (L30p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	Be	239	1919	1235	348	335	1	0	0

- Molecule 58 is a protein called 60S ribosomal protein rpL31 (L31e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	Bg	110	873	552	169	150	2	0	0

- Molecule 59 is a protein called 60S ribosomal protein pL32 (L32e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	Bh	130	1043	660	208	173	2	0	0

- Molecule 60 is a protein called 60S ribosomal protein rpL34 (L34e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	Bi	118	926	572	188	161	5	0	0

- Molecule 61 is a protein called 60S ribosomal protein rpL33 (L35ae).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	Bj	100	738	461	147	128	2	0	0

- Molecule 62 is a protein called 60S ribosomal protein rpL36 (L36e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	Bk	77	619	384	129	105	1	0	0

- Molecule 63 is a protein called 60S ribosomal protein rpL43 (L37ae).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	Bm	92	703	434	139	123	7	0	0

- Molecule 64 is a protein called 60S ribosomal protein rpL37 (L37e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	Bl	88	678	410	148	114	6	0	0

- Molecule 65 is a protein called 60S ribosomal protein rpL38 (L38e).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
65	Bn	78	604	385	113	106	0	0

- Molecule 66 is a protein called 60S ribosomal protein rpL39 (L39e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	Bo	51	445	277	98	67	3	0	0

- Molecule 67 is a protein called 60S ribosomal protein rpL40 (L40e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Bp	40	330	201	72	52	5	0	0

- Molecule 68 is a protein called 60S ribosomal protein rpL41 (L41e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	Bq	25	234	142	63	28	1	0	0

- Molecule 69 is a protein called 60S ribosomal protein rpL42 (L44e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Br	106	834	521	169	138	6	0	0

- Molecule 70 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
70	Bx	20	100	60	20	20	0	0
70	By	20	100	60	20	20	0	0

- Molecule 71 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
71	Bz	14	70	42	14	14	0	0

- Molecule 72 is a protein called 60S acidic ribosomal protein rpP11 (P1).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
72	Bt	58	440	281	68	91	0	0
72	Bu	58	440	281	68	91	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bt	37	ASP	VAL	conflict	UNP P05318
Bu	37	ASP	VAL	conflict	UNP P05318

- Molecule 73 is a protein called 60S acidic ribosomal protein (P2).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	Bv	58	429	271	66	91	1	0	0
73	Bw	58	429	271	66	91	1	0	0

- Molecule 74 is a protein called 60S ribosomal protein rpL5 (L18p).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	BQ	297	2356	1485	414	454	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BQ	112	ARG	LYS	conflict	UNP P26321

- Molecule 75 is a protein called 60S ribosomal protein rpL13 (L13e).

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
75	BL	169	845	507	169	169	0	0

- Molecule 76 is a protein called 60S ribosomal protein rpL20 (L18ae).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	BS	167	1420	916	263	234	7	0	0

- Molecule 77 is a protein called 60S ribosomal protein rpL10 (L10e).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	BI	181	1444	907	281	248	8	0	0

- Molecule 78 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
78	CA	1721	33643	14904	5670	11348	1721	0	10

- Molecule 79 is a RNA chain called P-SITE TRNA ASP.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
79	CB	75	1599	712	280	532	75	0	0

- Molecule 80 is a RNA chain called MRNA, RNA (5'-R(P*AP*AP*AP*AP*GP*AP*CP*UP*UP*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
80	CC	11	236	106	45	74	11	0	0

- Molecule 81 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
81	DA	3354	68830	30640	12220	22616	3354	0	75

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
82	DB	157	3129	1391	523	1058	157	0	0

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

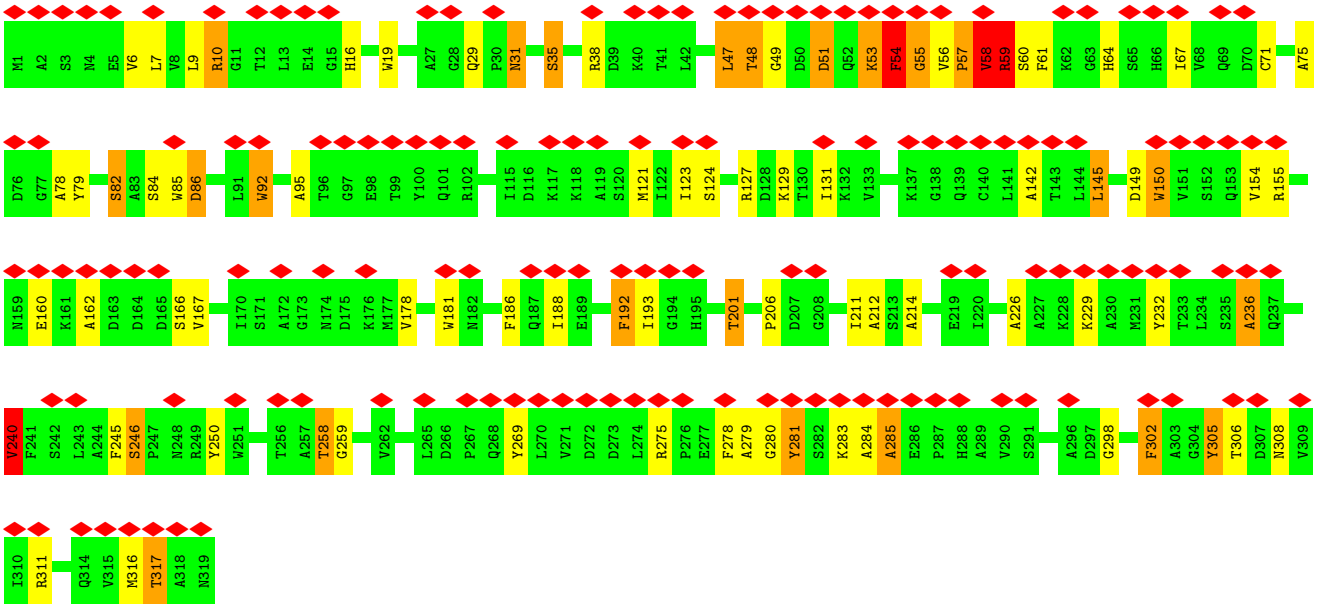
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
83	DC	118	2513	1122	446	827	118	0	0

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.

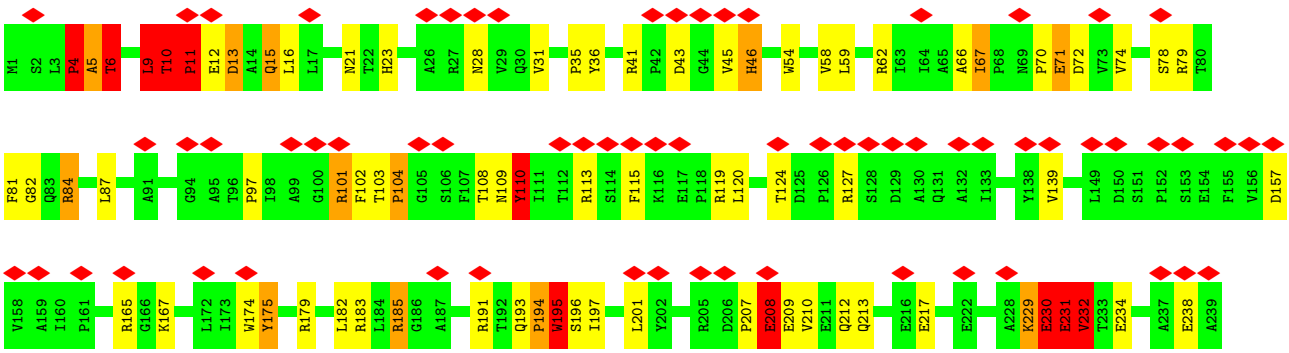
- Molecule 1: 40S ribosomal protein RACK1 (RACK1)

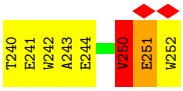
Chain Aa: 47% 72% 19% 8%



- Molecule 2: 40S ribosomal protein rpS0 (S2p)

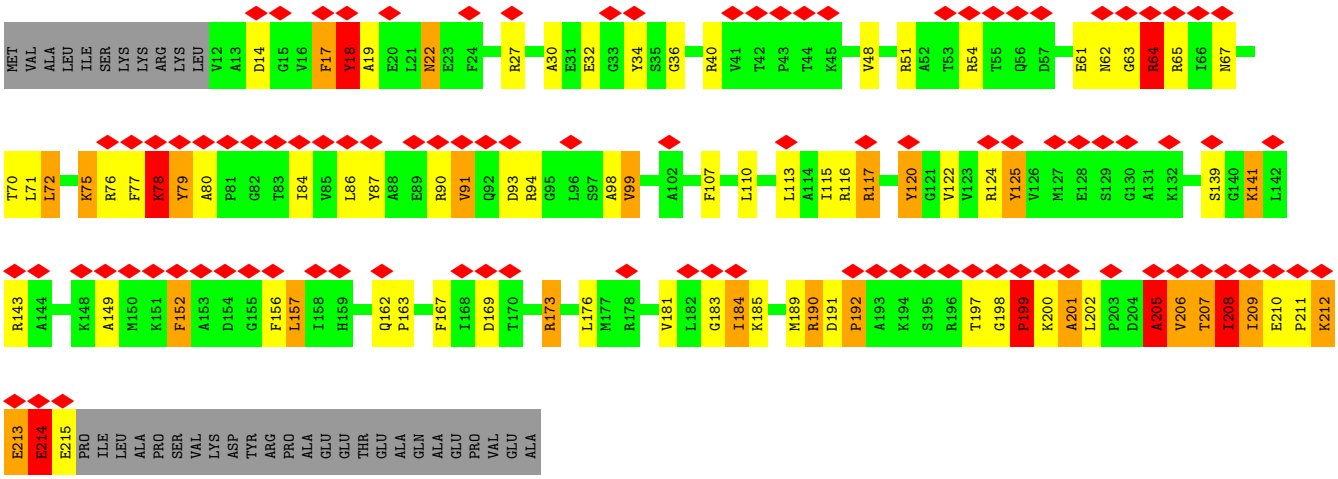
Chain AA: 27% 65% 25% 6% 5%





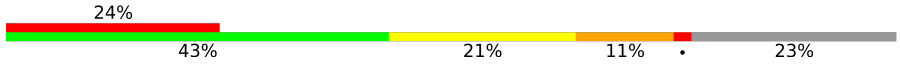
- Molecule 3: 40S ribosomal protein rpS3 (S3p)

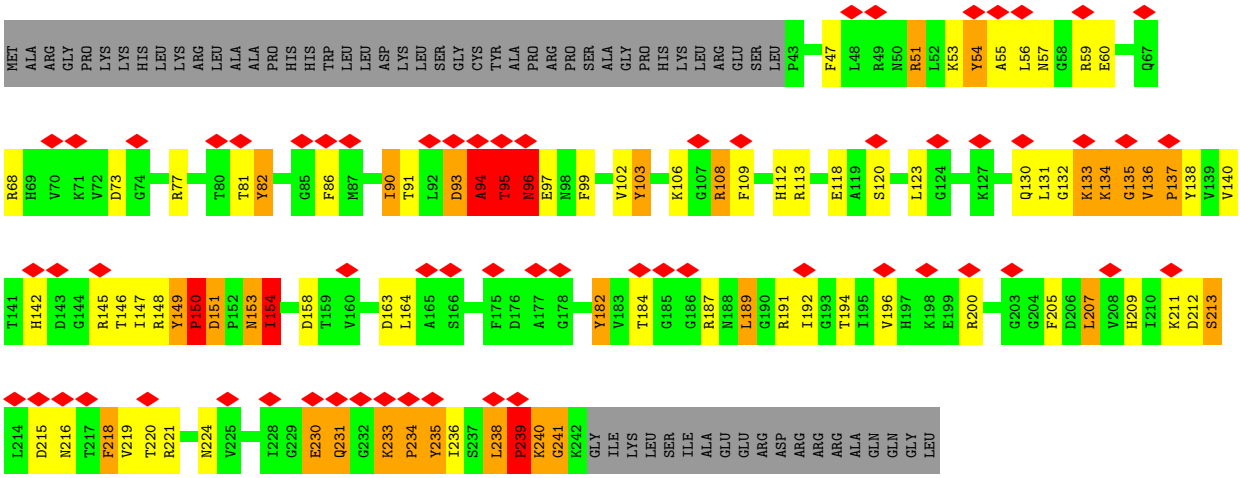
Chain AB:



- Molecule 4: 40S ribosomal protein rpS4 (S4e)

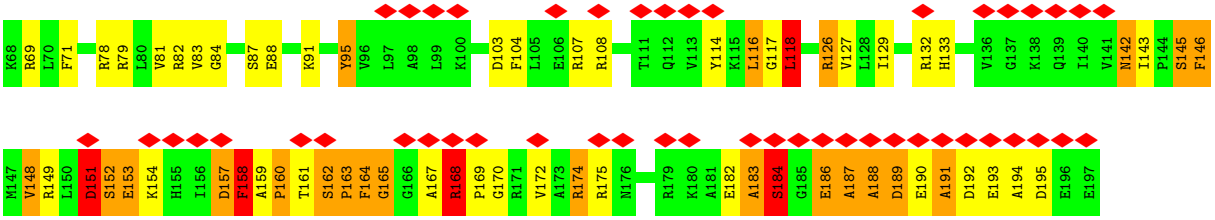
Chain AD:





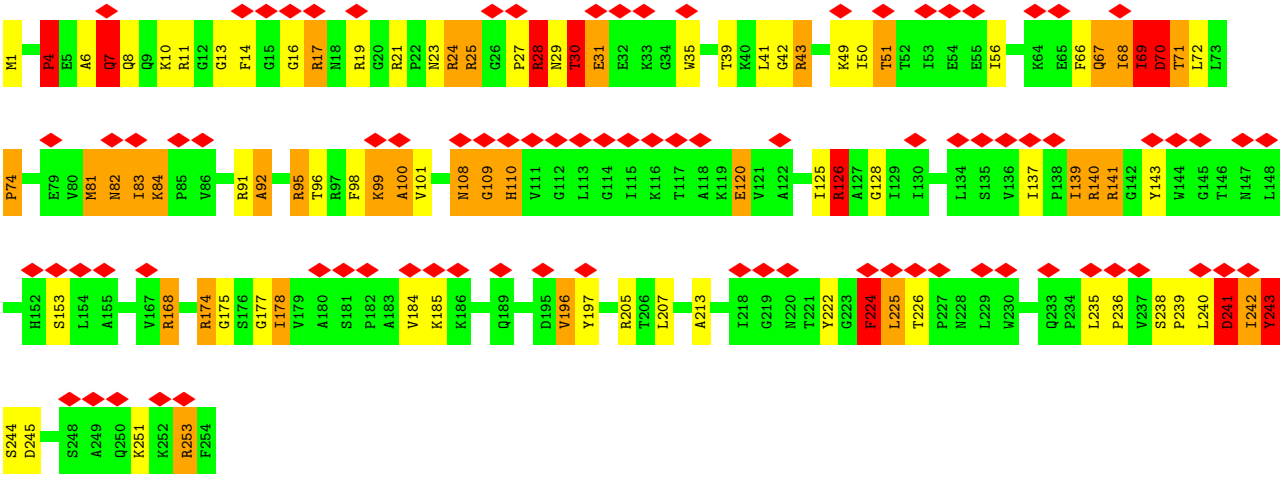
- Molecule 5: 40S ribosomal protein rpS9 (S4p)

Chain AC:



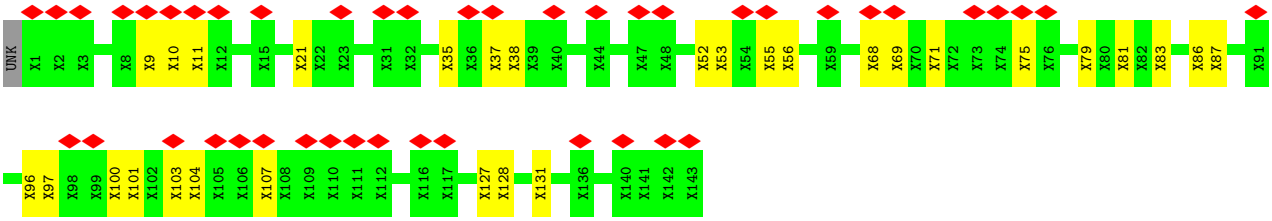
• Molecule 6: 40S ribosomal protein rpS2 (S5p)

Chain AE:



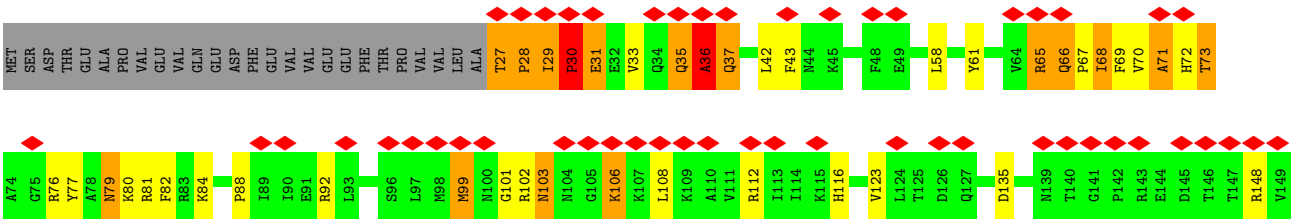
• Molecule 7: 40S ribosomal protein rpS7 (S7e)

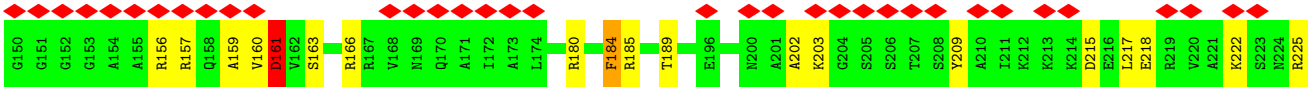
Chain AG:



• Molecule 8: 40S ribosomal protein rpS5 (S7p)

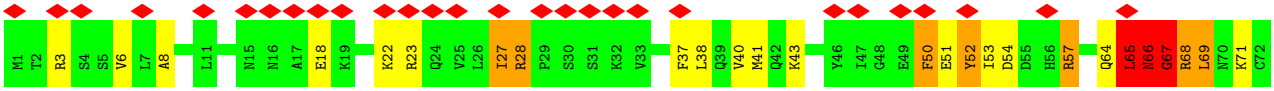
Chain AF:

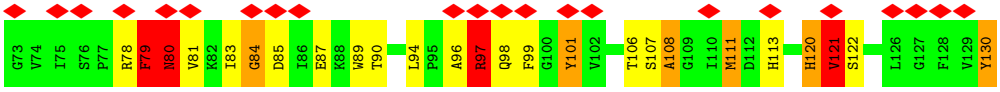




- Molecule 9: 40S ribosomal protein rpS22 (S8p)

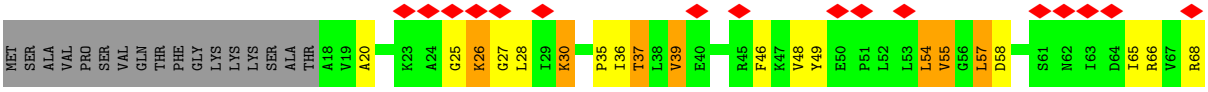
Chain AH:

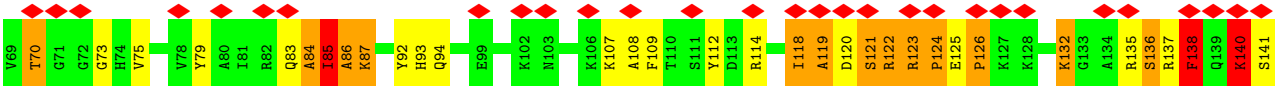




- Molecule 10: 40S ribosomal protein rpS16 (S9p)

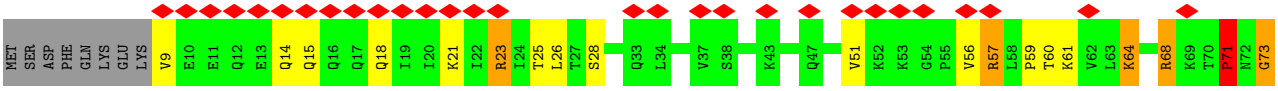
Chain AI:

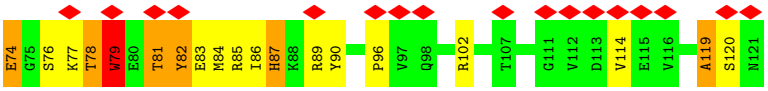




- Molecule 11: 40S ribosomal protein rpS20 (S10p)

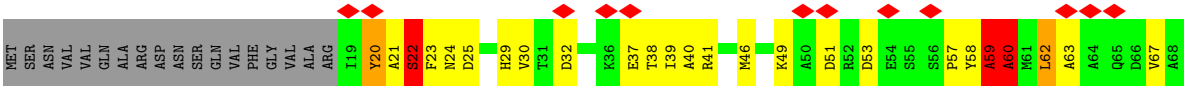
Chain AJ:

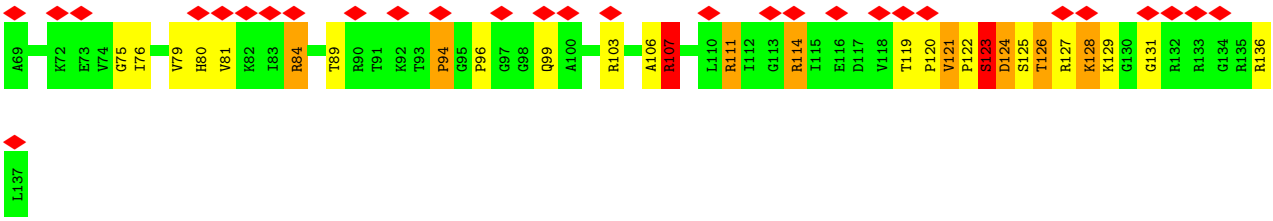




- Molecule 12: 40S ribosomal protein rpS14 (S11p)

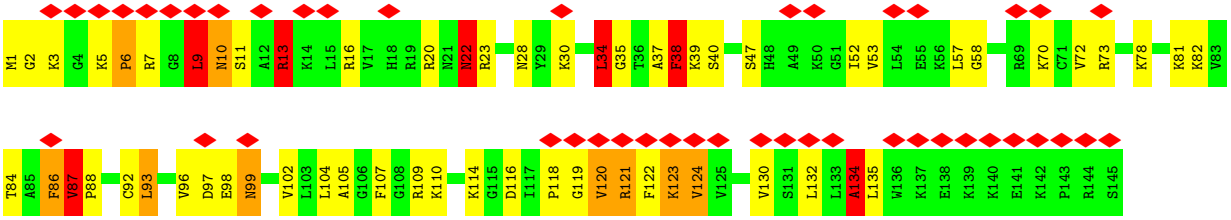
Chain AK:





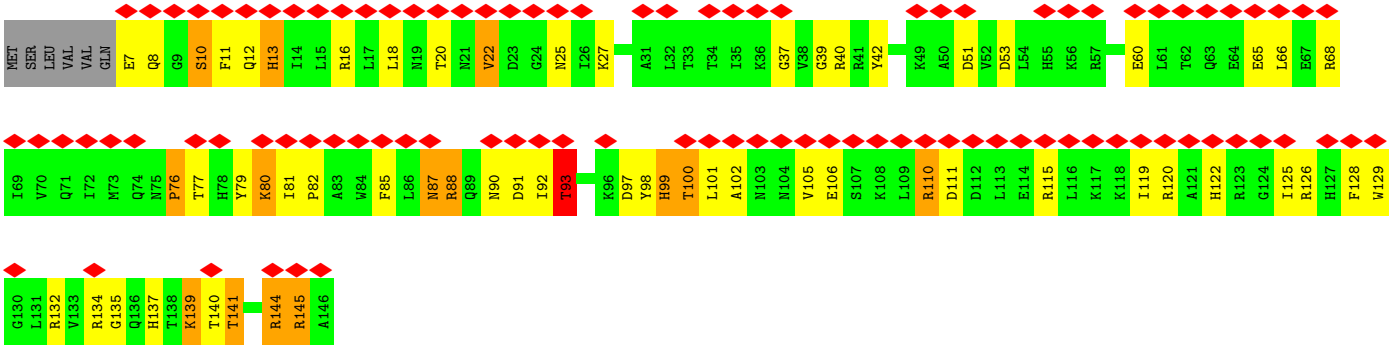
• Molecule 13: 40S ribosomal protein rpS23 (S12p)

Chain AL:



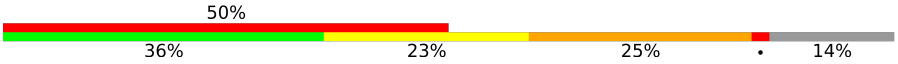
• Molecule 14: 40S ribosomal protein rpS18 (S13p)

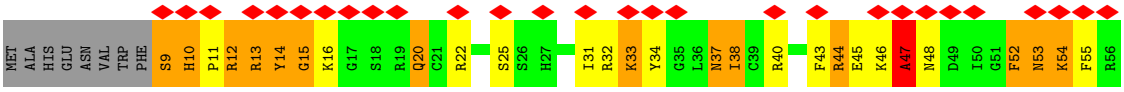
Chain AM:



• Molecule 15: 40S ribosomal protein rpS29 (S14p)

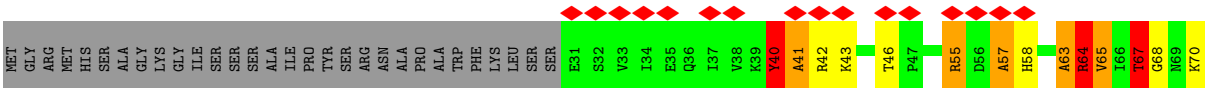
Chain AN:

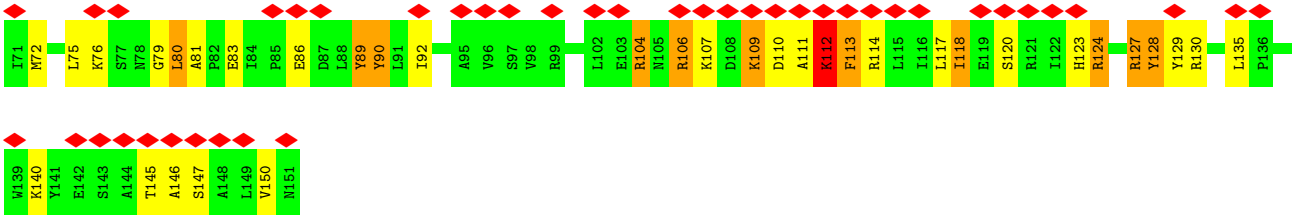




• Molecule 16: 40S ribosomal protein rpS13 (S15p)

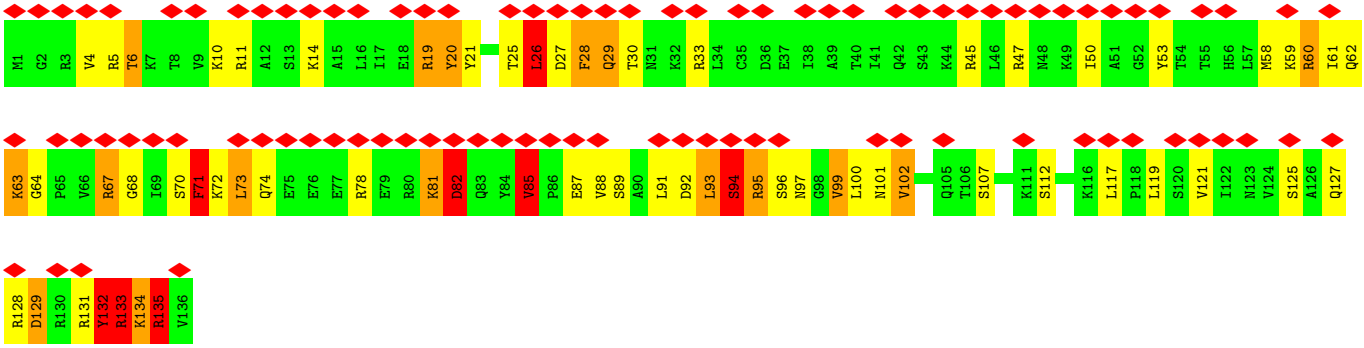
Chain AO:





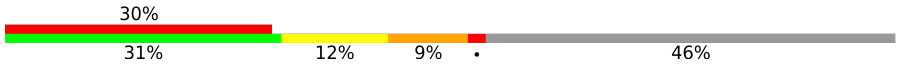
- Molecule 17: 40S ribosomal protein rpS17 (S17e)

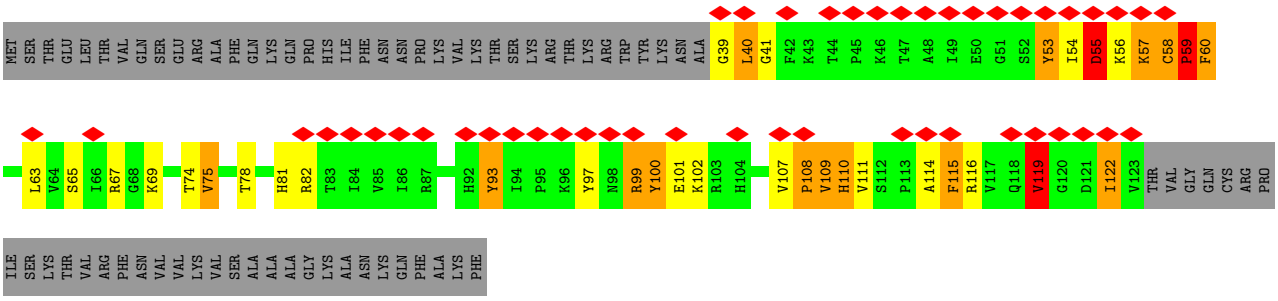
Chain AQ:



- Molecule 18: 40S ribosomal protein rpS11 (S17p)

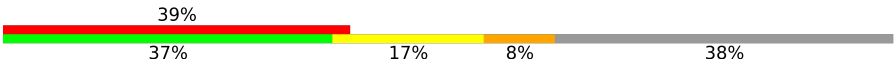
Chain AP:

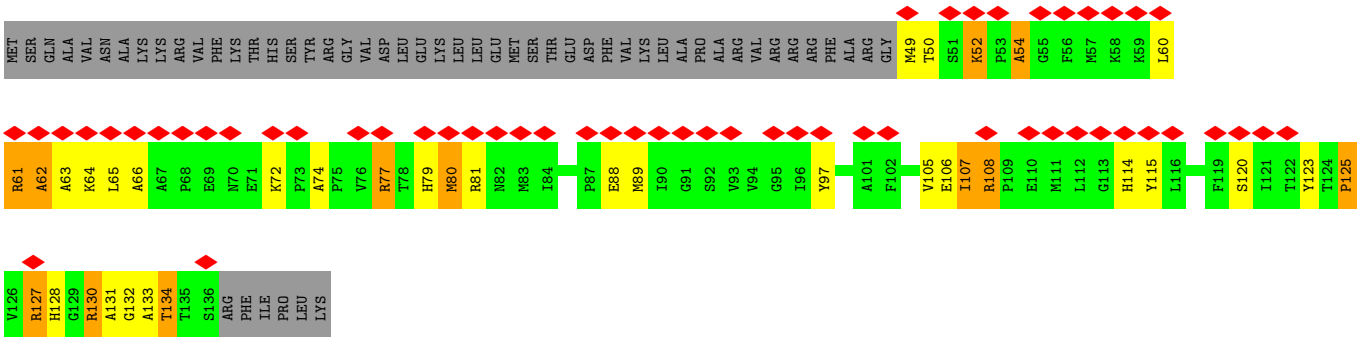




- Molecule 19: 40S ribosomal protein rpS15 (S19p)

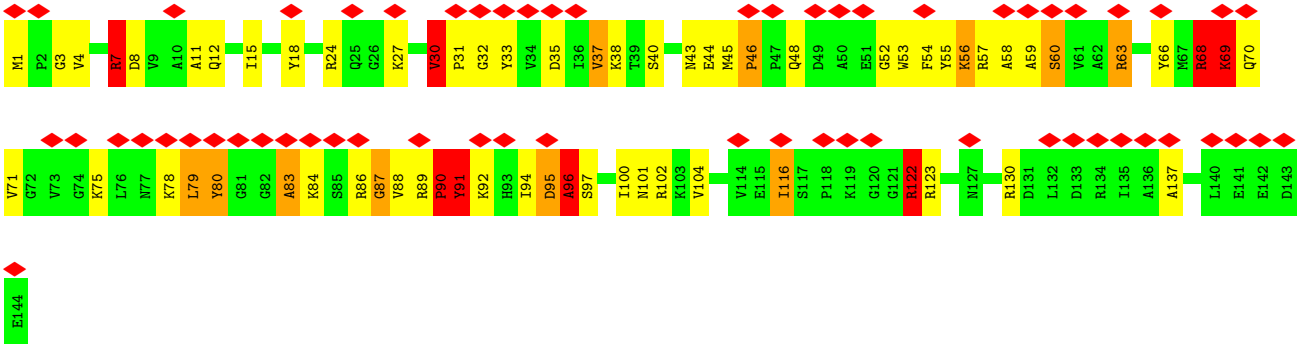
Chain AR:





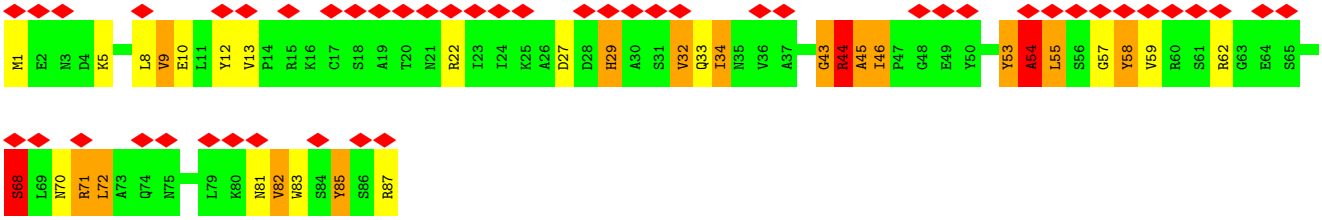
• Molecule 20: 40S ribosomal protein rpS19 (S19e)

Chain AS:



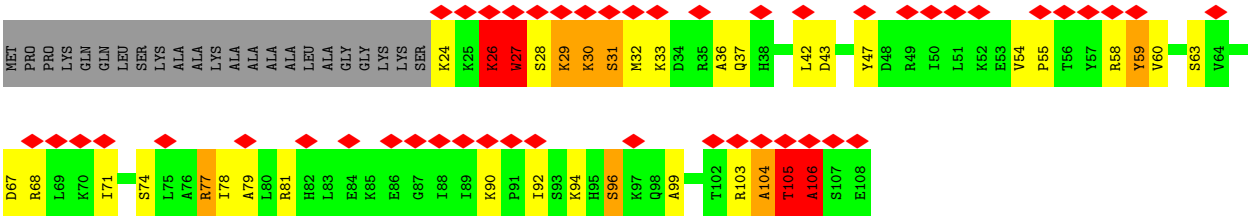
• Molecule 21: 40S ribosomal protein rpS21 (S21e)

Chain AT:



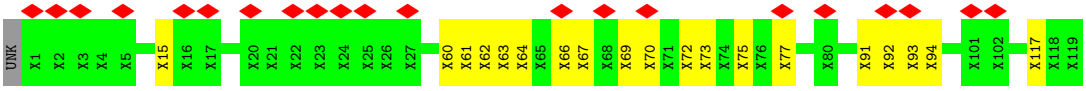
• Molecule 22: 40S ribosomal protein rpS25 (S25e)

Chain AV:



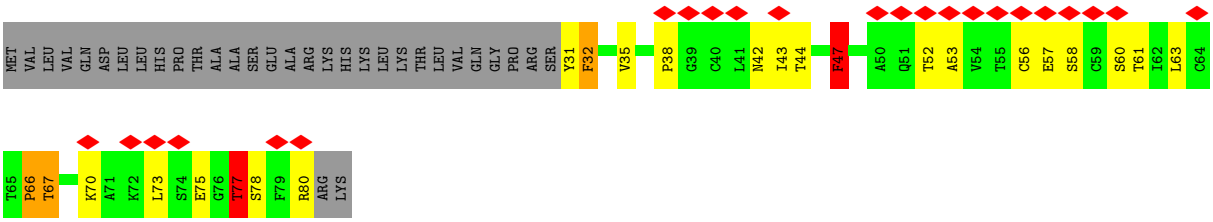
• Molecule 23: 40S ribosomal protein rpS26 (S26e)

Chain AW:



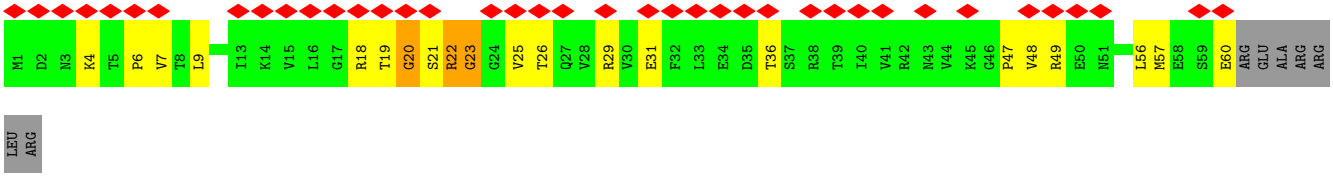
• Molecule 24: 40S ribosomal protein rpS27 (S27e)

Chain AX:



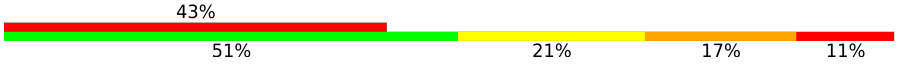
• Molecule 25: 40S ribosomal protein rpS28 (S28e)

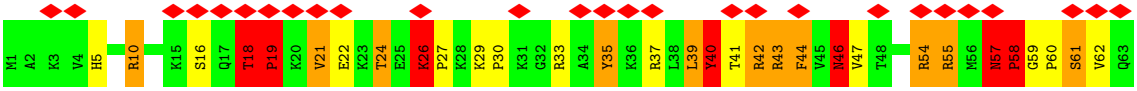
Chain AY:



• Molecule 26: 40S ribosomal protein rpS30 (S30e)

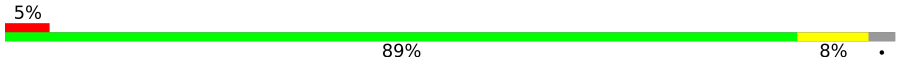
Chain AZ:

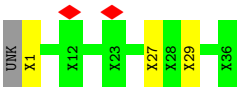




• Molecule 27: Unknown 40S ribosomal protein XS1

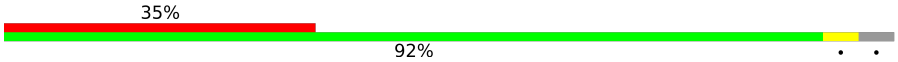
Chain Ab:

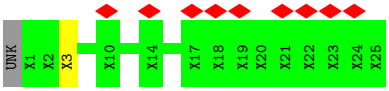




• Molecule 28: Unknown 40S ribosomal protein XS2

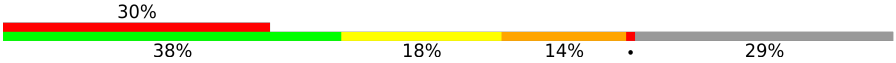
Chain Ac:

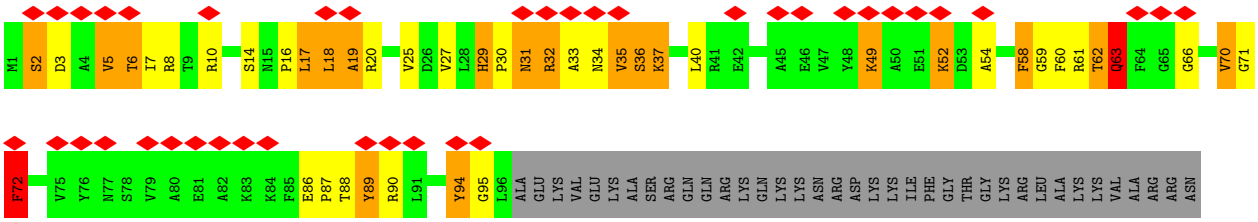




• Molecule 29: 40S ribosomal protein S24

Chain AU:





ALA
ASP

- Molecule 30: 60S ribosomal protein rpL1 (L1p)

Chain BA: 73% 76% 20% •

M1 S6 S7 Q8 E11 H12 V13 K14 E15 L16 L17 K18 Y19 S20 N21 E22 T23 K24 K25 R26 N27 F28 L29 Q35 V36 G37 L38 K39 N40 Y41 D42 P43 Q44 R45 D46 K47 R48 F49 S50 G51 S52 L53 K54 L55 P56 N57 G58 P59 R60 P61 N62 M63 S64 I65 C66 I67 F68

G69 D70 A71 F72 D73 V74 D75 R76 A77 K78 S79 C80 G81 V82 D83 A84 M85 S86 V87 D88 D89 L90 K91 K92 L93 N94 K95 N96 K97 K98 L99 I100 K101 K102 L103 S104 K105 K106 Y107 N108 A109 F110 I111 A112 S113 E114 V115 L116 I117 K118 Q119 V120 P121 R122 L123 L124 G125 P126 Q127 L128

S129 K130 A131 G132 K133 F134 P135 T136 P137 V138 S139 H140 N141 D142 D143 L144 Y145 G146 K147 V148 T149 D150 V151 R152 S153 T154 I155 L159 K160 K161 A168 V169 G170 N171 V172 E173 M174 E175 E176 D177 V178 L179 V180 N181 Q182 I183 S186 V187 N188 F189 F190 V191 S192 L193 L194 K195 K196

N197 W198 Q199 N200 V201 G202 S203 L204 V205 V206 K207 S208 S209 M210 F214 R215 L216 Y217

- Molecule 31: 60S ribosomal protein rpL2 (L2p)

Chain BB: 47% 67% 17% 13% •

M1 G2 R3 V4 I5 R6 N7 Q8 R9 K10 G11 I15 H19 T20 R21 L22 R23 Q24 G25 A26 A27 K28 L29 R30 T31 L32 D33 Y34 A35 E36 R37 H38 G39 Y40 I41 R42 K46 Q47 I48 V49 H50 D51 S52 G53 R54 G55 A56 P57 L58 A59 K60 V61 V62 F63 R64 D65 P66

Y67 K68 Y69 R70 L71 R72 E73 E74 I75 F76 I77 A78 N79 E80 G81 V82 H83 T84 Y89 K93 A94 S95 L96 N97 V98 G99 N100 V101 L102 G105 S106 V107 P108 E109 G110 T111 I112 N115 V116 E117 E118 K119 P120 G121 D122 L126 A127 R128 G131 N132 Y133 V134 G138

H139 N140 P141 D142 E143 N144 K145 T146 R147 S152 G153 A154 K155 K156 V157 I158 D161 A162 R163 G164 V165 I166 G167 V168 G171 G172 G173 R174 V175 D176 K177 P178 L179 L180 G183 R184 A185 F186 L191 K192 R193 N194 S195 W196 P197 K198 T199 R200 A203 G214 N215 H216 Q217

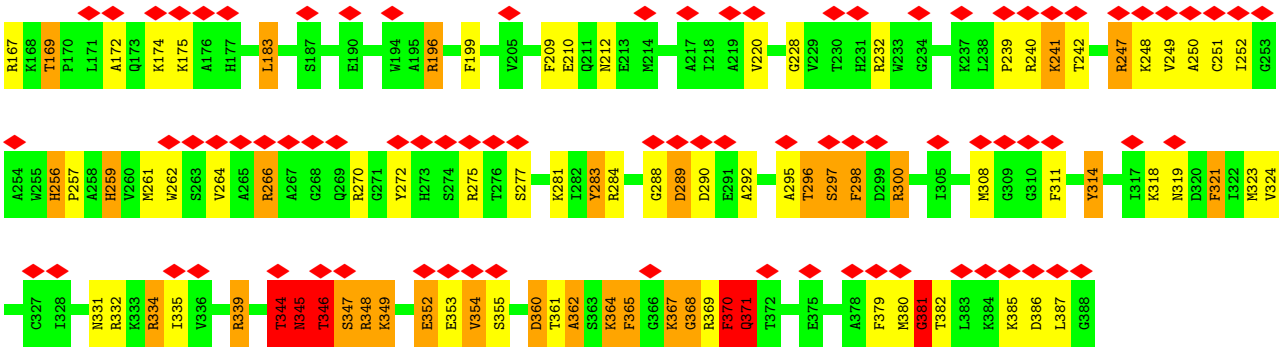
H218 K221 S226 R227 G228 A229 V230 S231 G232 Q233 K234 L237 I238 A239 A240 R241 R242 T243 G244 L245 L246 R247 G248 S249 Q250 K251 T252 Q253 D254

- Molecule 32: 60S ribosomal protein rpL3 (L3p)

Chain BC: 30% 56% 28% 12% •

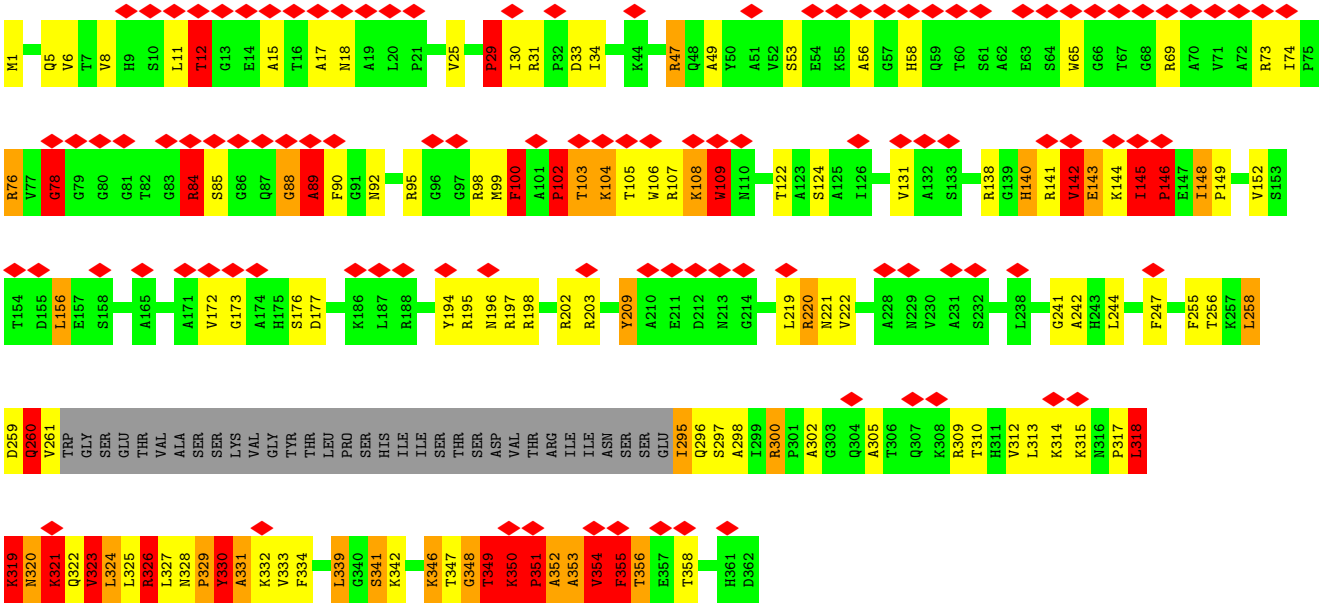
M1 S2 H3 R4 K5 Y6 E7 A8 P9 R10 F16 L17 P18 R19 K20 R21 A22 A23 S24 I25 R26 A27 R28 V29 K30 A31 F32 D35 D36 R37 S38 K39 P40 V41 A42 L43 T44 S45 F46 L47 G48 Y49 K50 A51 G52 T55 D59 L60 D61 R62 S65 K66 F67 H68 K69

R70 E71 V72 V73 E74 V78 V84 Y92 V93 E94 T95 P96 R97 G98 L99 R100 S101 L102 T103 T104 V105 E108 H109 R116 R117 F118 Y119 K120 N121 W122 Y123 K124 S125 K126 K127 K128 A129 F130 T131 K136 Y137 A138 Q139 Y154 A155 S156 V157 V158 V162 H163 T164



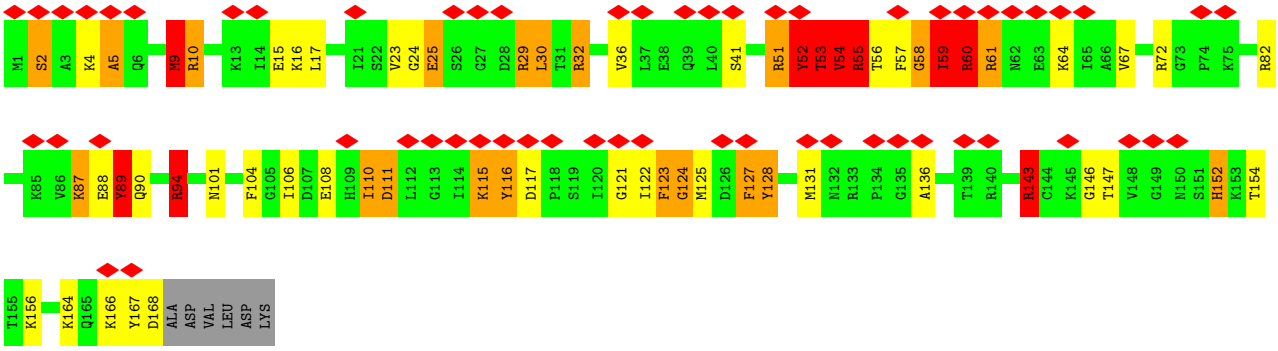
• Molecule 33: 60S ribosomal protein rpL4 (L4p)

Chain BD:



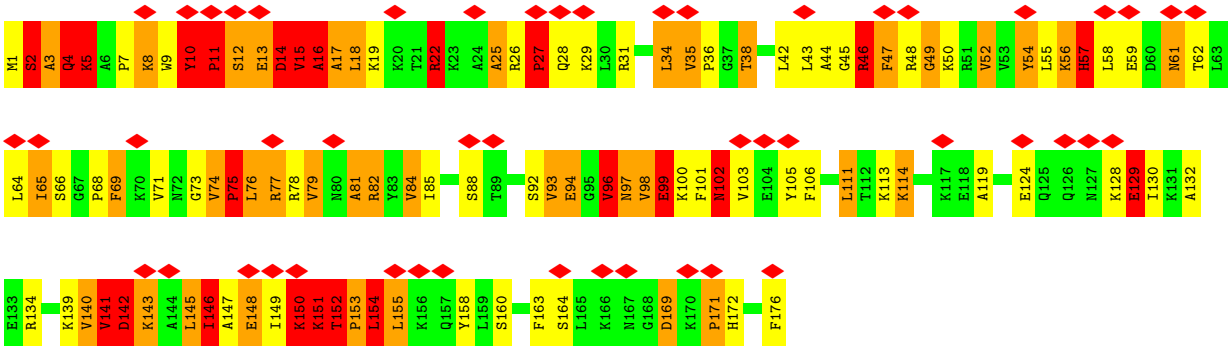
• Molecule 34: 60S ribosomal protein rpL11 (L5p)

Chain BE:



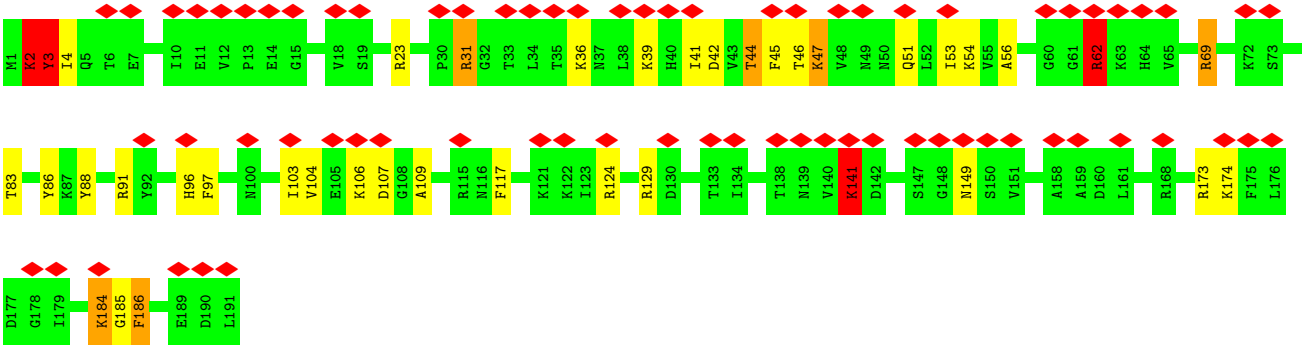
• Molecule 35: 60S ribosomal protein rpL6 (L6e)

Chain BG: 28% 36% 28% 22% 14%



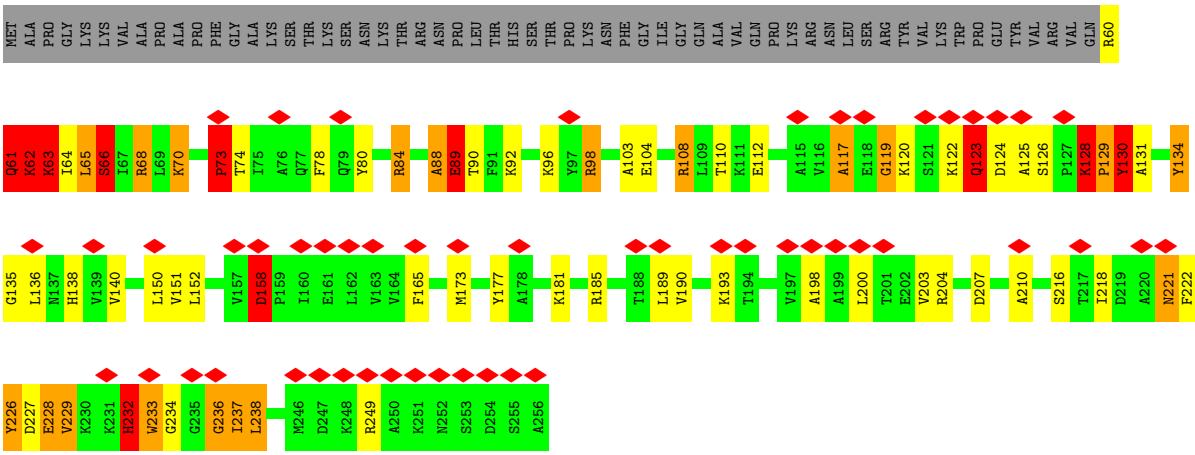
- Molecule 36: 60S ribosomal protein rpL9 (L6p)

Chain BF: 37% 79% 16%



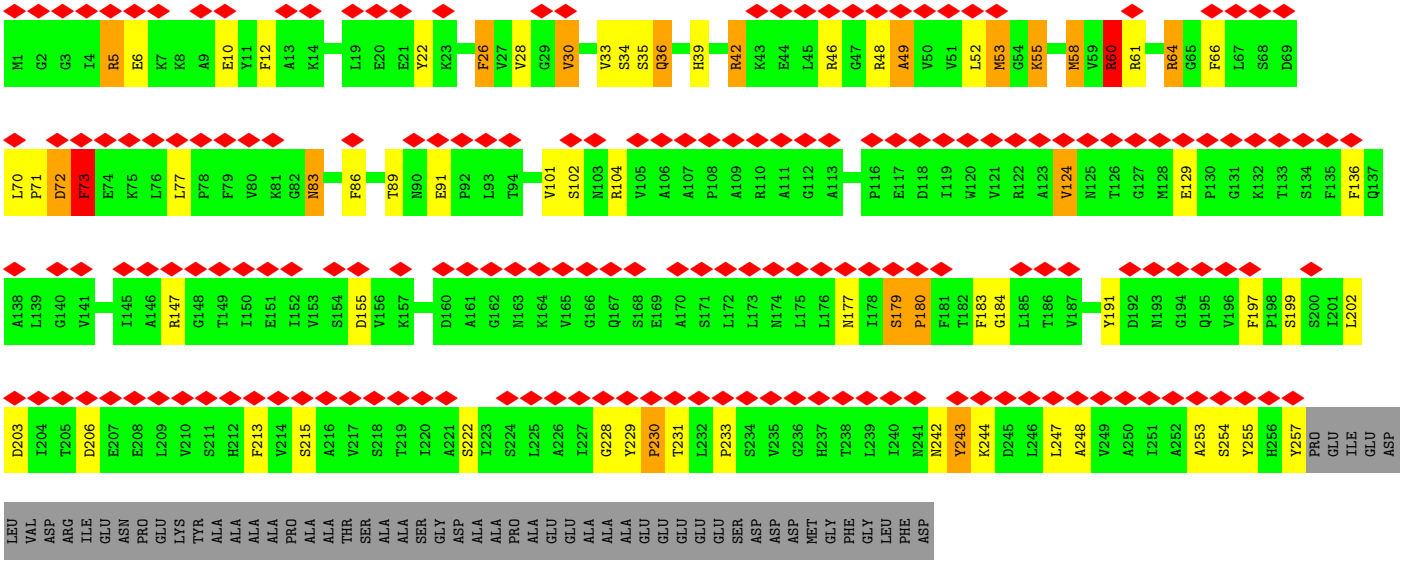
- Molecule 37: 60S ribosomal protein rpL8 (L7ae)

Chain BH: 21% 46% 19% 7% 23%



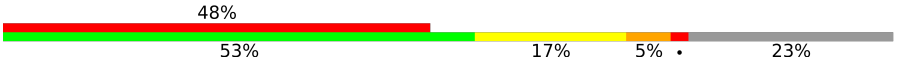
- Molecule 38: 60S acidic ribosomal protein rpP0 (L10P)

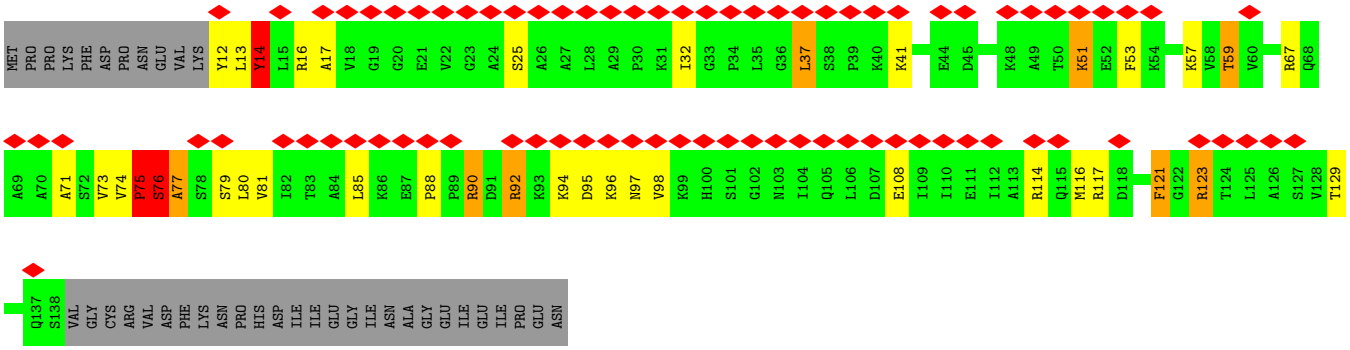
Chain Bs: 57% 60% 16% 5% 18%



- Molecule 39: 60S ribosomal protein rpL12 (L11p)

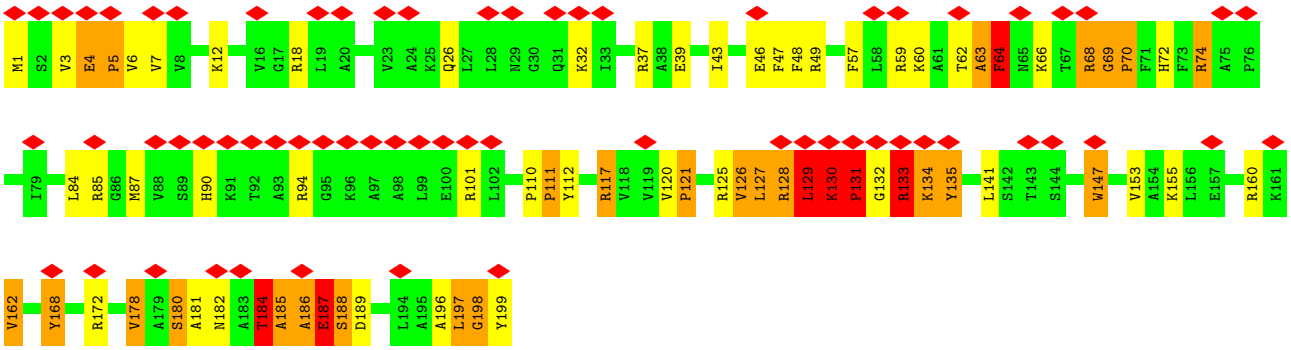
Chain BJ:





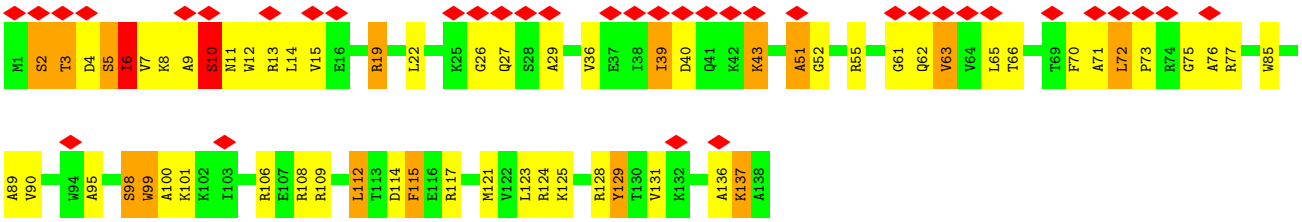
- Molecule 40: 60S ribosomal protein rpL16 (L13p)

Chain BK:



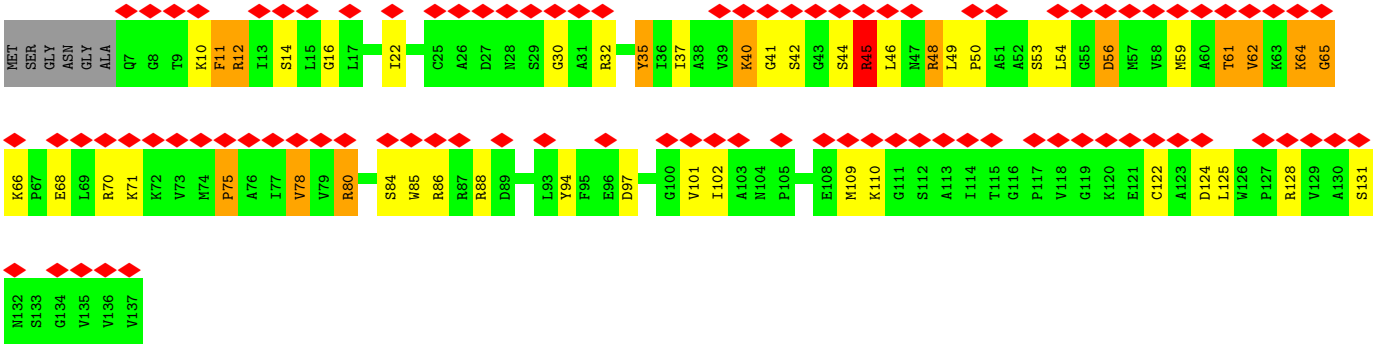
- Molecule 41: 60S ribosomal protein rpL14 (L14e)

Chain BN:



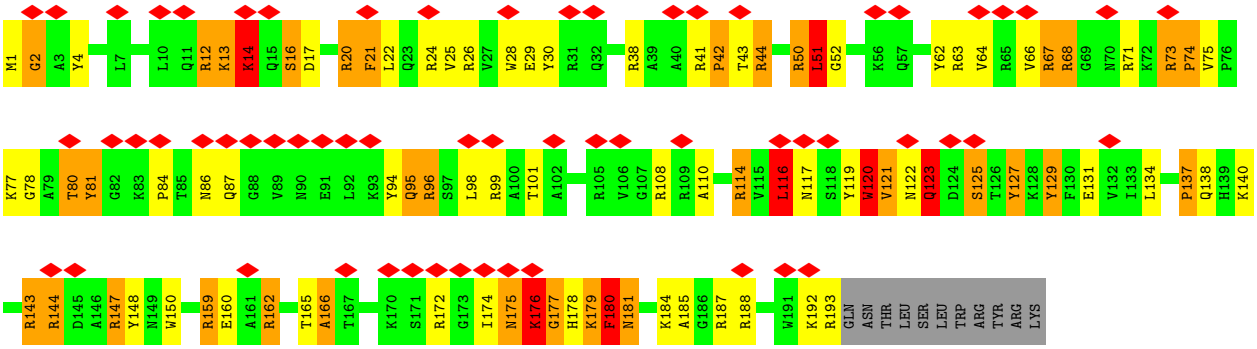
• Molecule 42: 60S ribosomal protein rpL23 (L14p)

Chain BM:



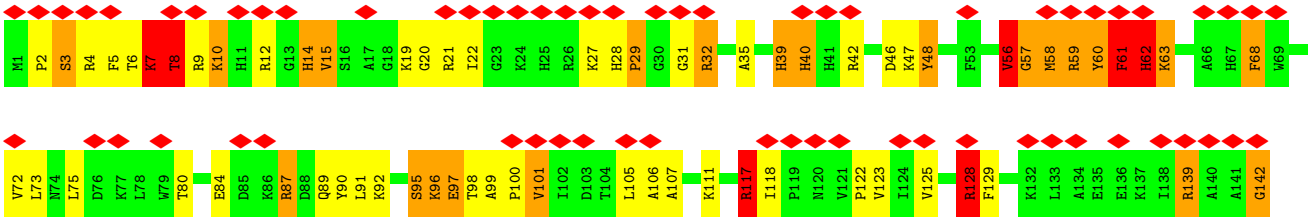
• Molecule 43: 60S ribosomal protein rpL15 (L15e)

Chain BP:



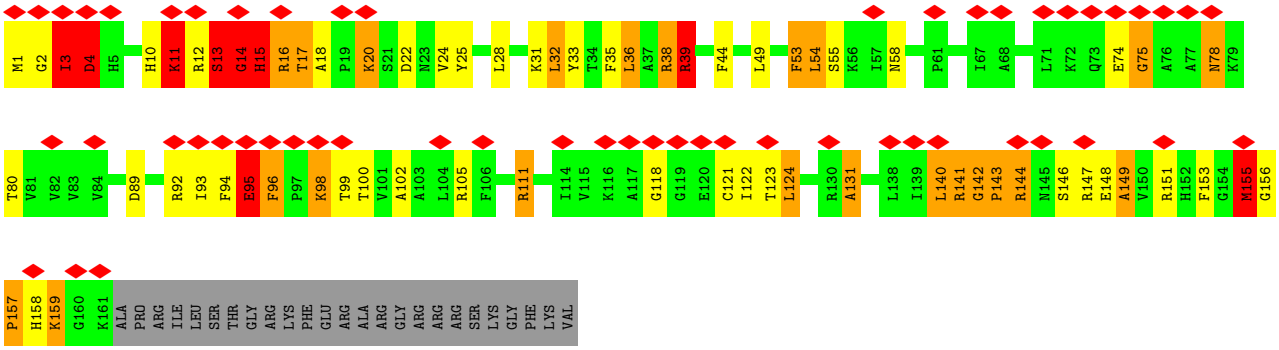
• Molecule 44: 60S ribosomal protein rpL28 (L15p)

Chain BO:



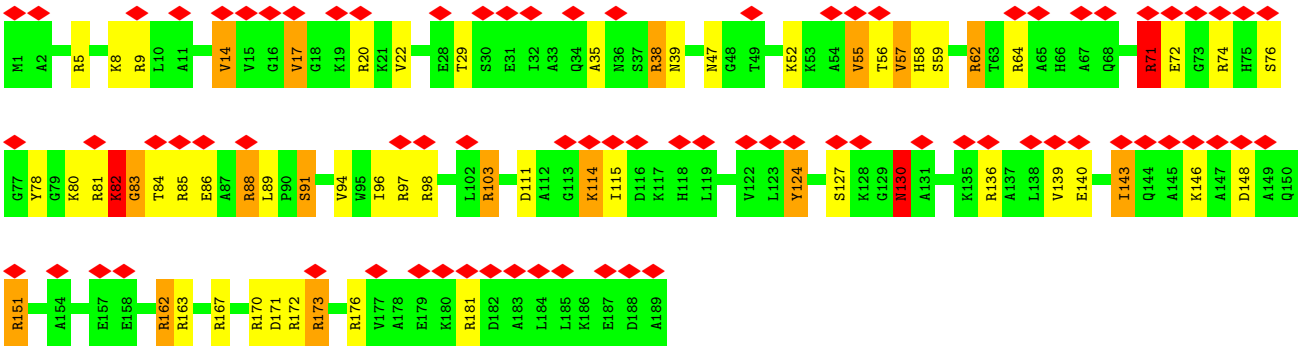
• Molecule 45: 60S ribosomal protein rpL18 (L18e)

Chain BR:



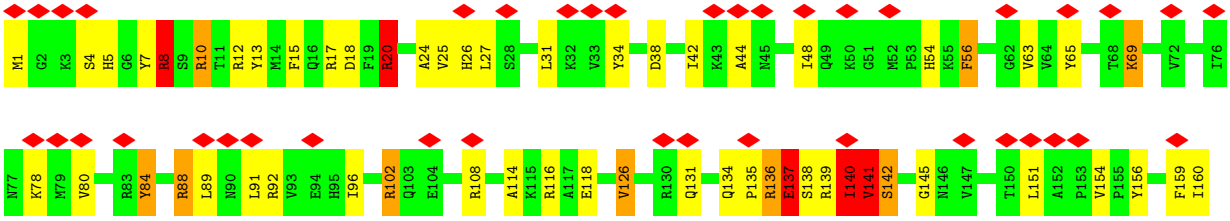
• Molecule 46: 60S ribosomal protein rpL19 (L19e)

Chain BT:



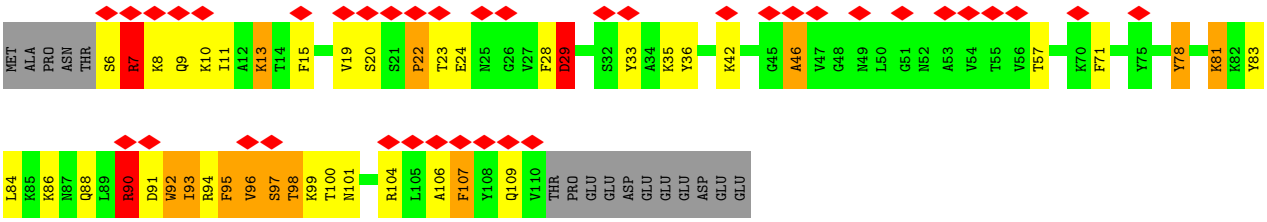
• Molecule 47: 60S ribosomal protein rpL21 (L21e)

Chain BU:



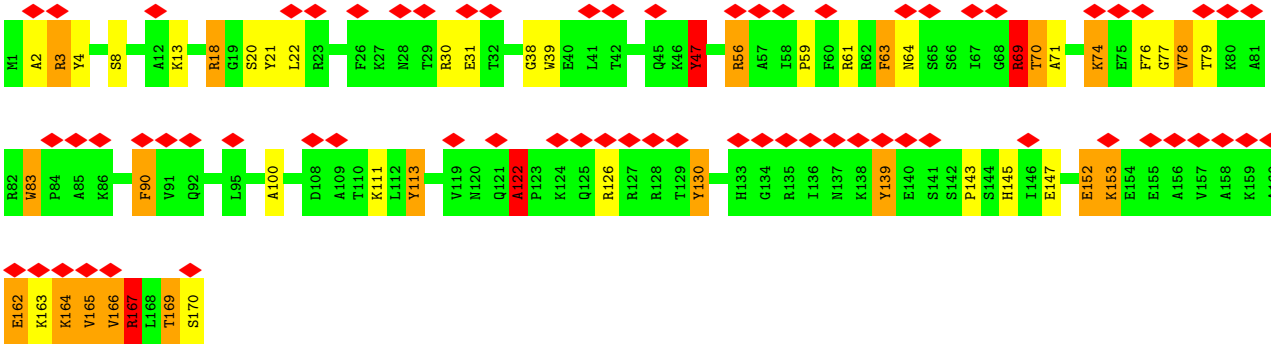
• Molecule 48: 60S ribosomal protein rpL22 (L22e)

Chain BW:



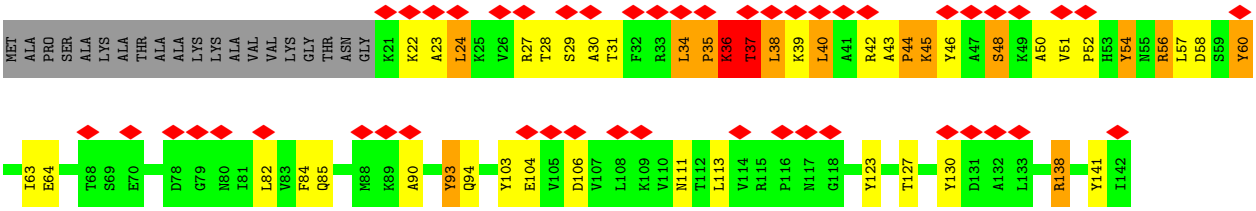
• Molecule 49: 60S ribosomal protein rpL17 (L22p)

Chain BV:



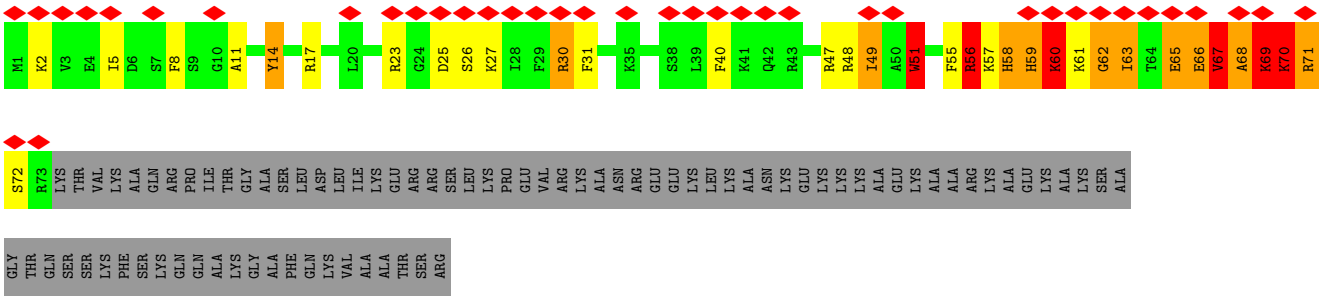
• Molecule 50: 60S ribosomal protein rpL25 (L23p)

Chain BX:



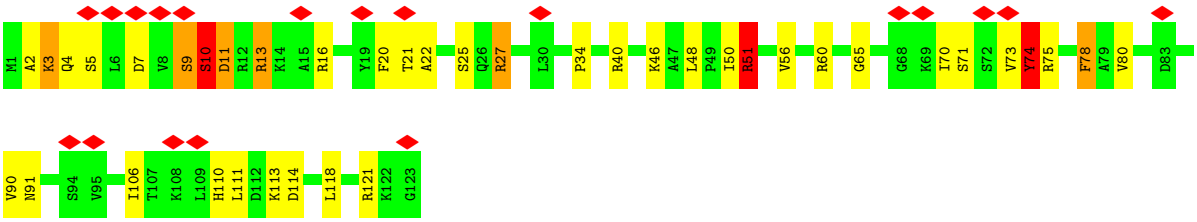
• Molecule 51: 60S ribosomal protein rpL24 (L24e)

Chain BZ:



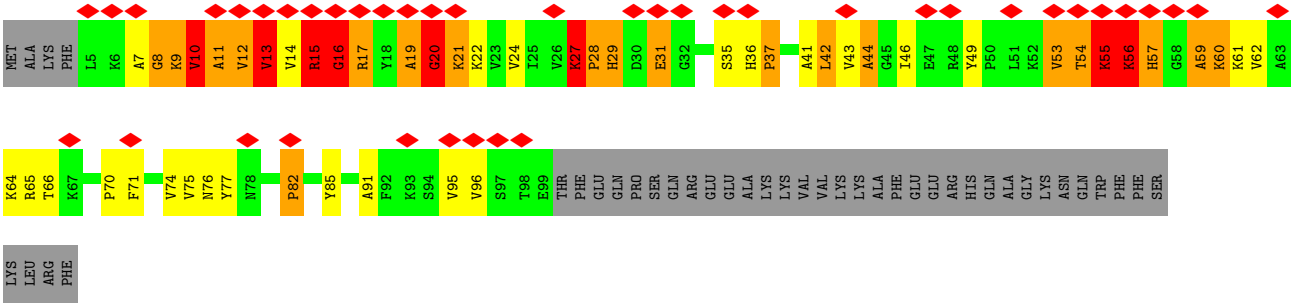
• Molecule 52: 60S ribosomal protein rpL26 (L24p)

Chain BY:



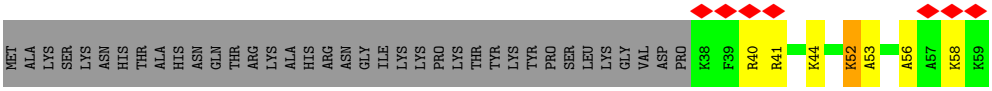
- Molecule 53: 60S ribosomal protein rpL27 (L27e)

Chain Ba:



- Molecule 54: 60S ribosomal protein rpL29 (L29e)

Chain Bd:

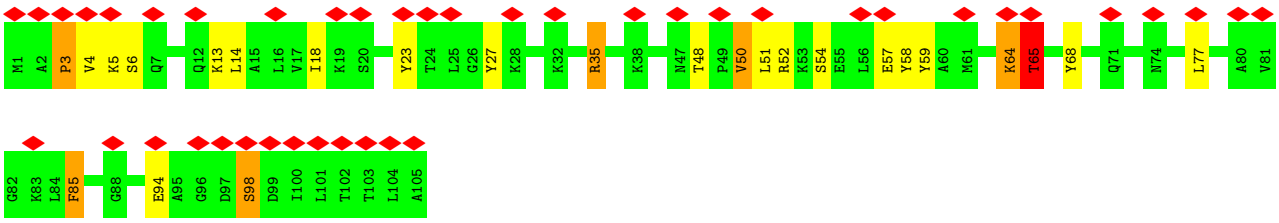


- Molecule 55: 60S ribosomal protein rpL35 (L29p)

Chain Bc:

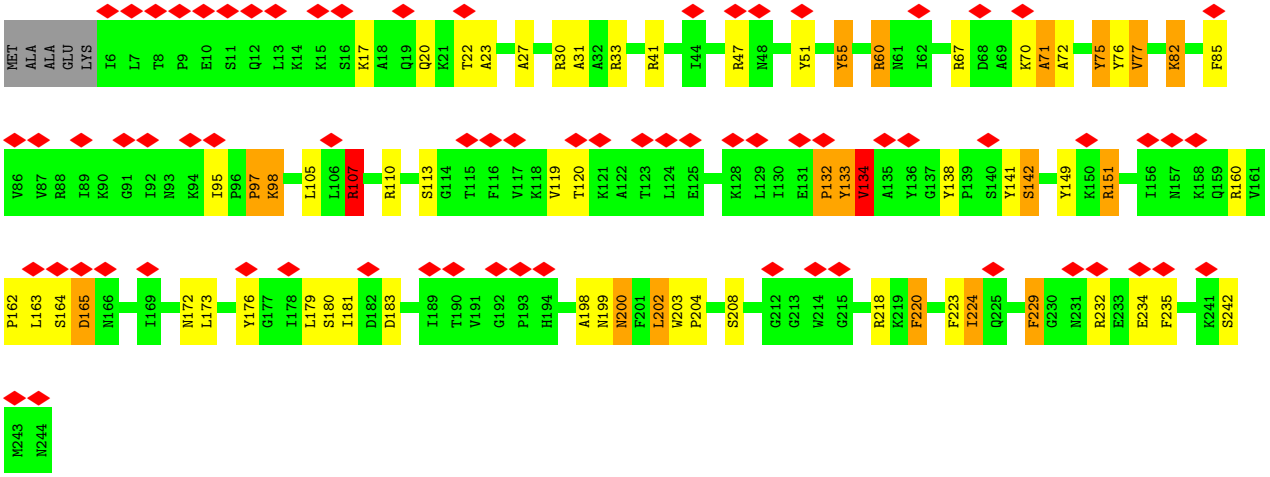
- Molecule 56: 60S ribosomal protein rpL30 (L30e)

Chain Bf:



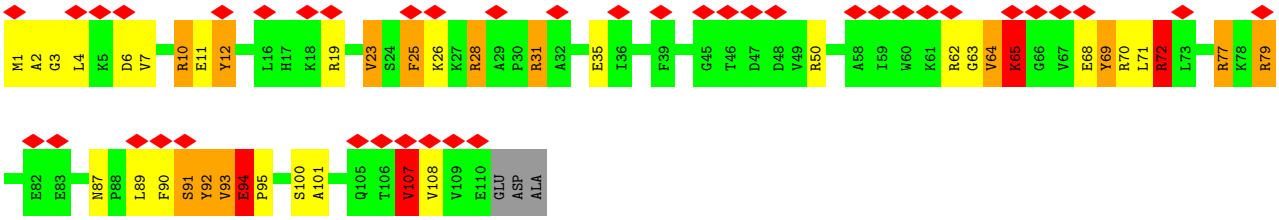
- Molecule 57: 60S ribosomal protein rpL7 (L30p)

Chain Be:



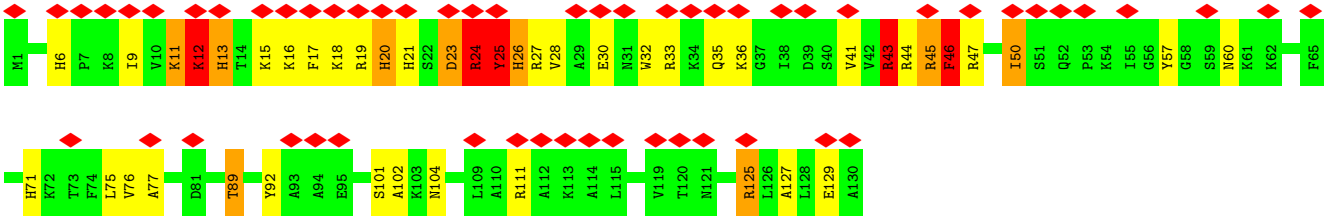
- Molecule 58: 60S ribosomal protein rpL31 (L31e)

Chain Bg:



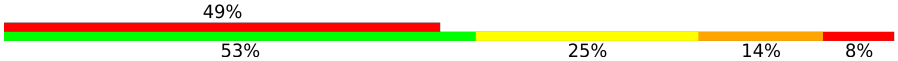
- Molecule 59: 60S ribosomal protein pL32 (L32e)

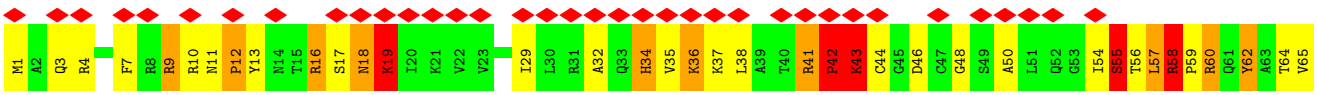
Chain Bh:

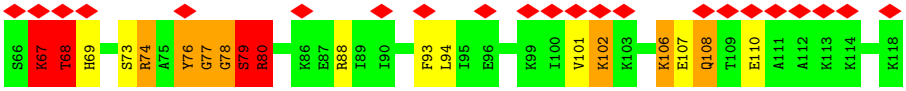


- Molecule 60: 60S ribosomal protein rpL34 (L34e)

Chain Bi:

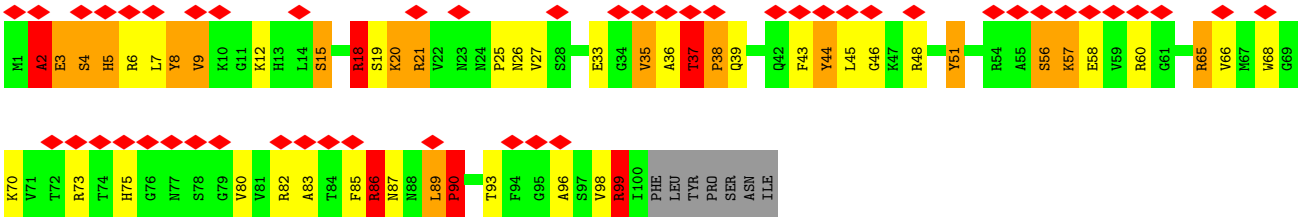






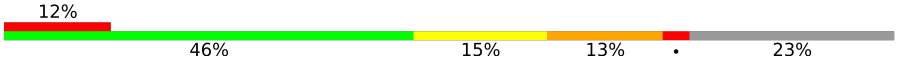
- Molecule 61: 60S ribosomal protein rpL33 (L35ae)

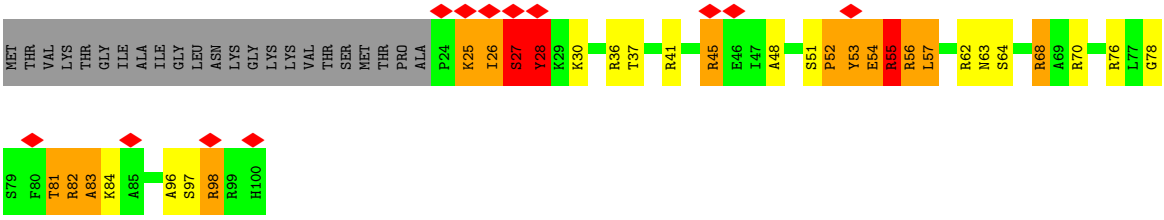
Chain Bj:



- Molecule 62: 60S ribosomal protein rpL36 (L36e)

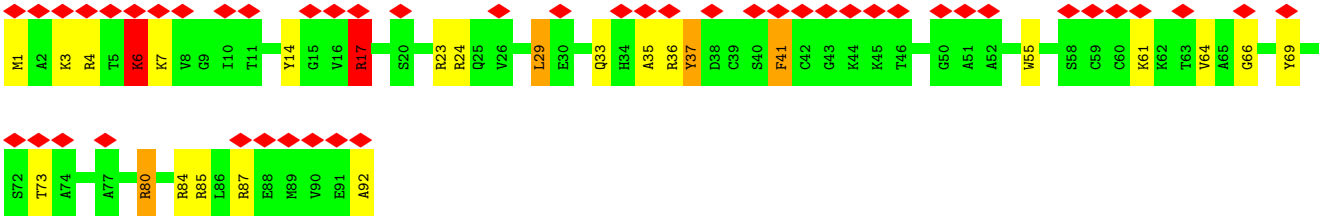
Chain Bk:





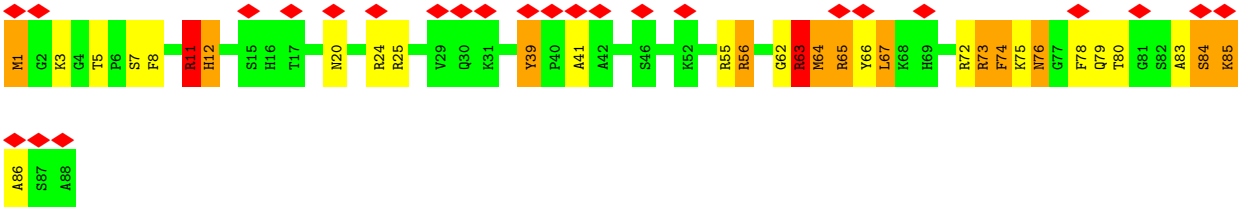
- Molecule 63: 60S ribosomal protein rpL43 (L37ae)

Chain Bm:



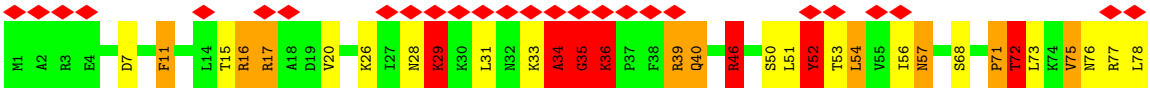
- Molecule 64: 60S ribosomal protein rpL37 (L37e)

Chain Bl:



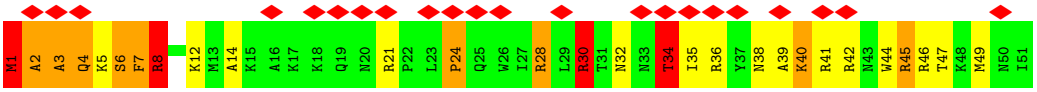
- Molecule 65: 60S ribosomal protein rpL38 (L38e)

Chain Bn: 33% 59% 21% 12% 9%



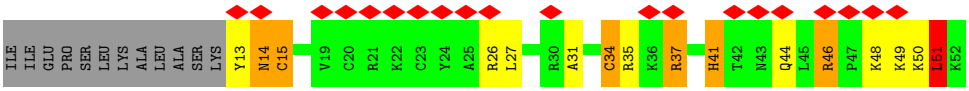
- Molecule 66: 60S ribosomal protein rpL39 (L39e)

Chain Bo: 43% 45% 29% 18% 8%



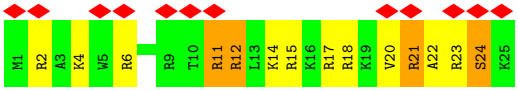
- Molecule 67: 60S ribosomal protein rpL40 (L40e)

Chain Bp: 38% 46% 17% 12% • 23%



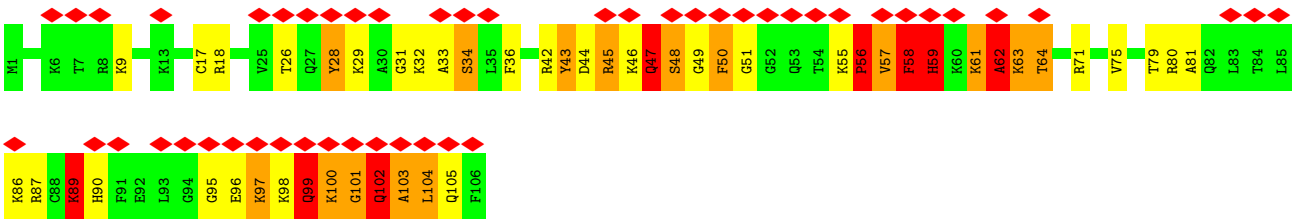
- Molecule 68: 60S ribosomal protein rpL41 (L41e)

Chain Bq: 48% 44% 40% 16%



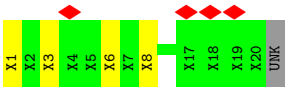
- Molecule 69: 60S ribosomal protein rpL42 (L44e)

Chain Br: 46% 53% 25% 14% 8%



- Molecule 70: Unknown protein

Chain Bx: 19% 76% 19% 5%

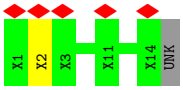


- Molecule 70: Unknown protein

Chain By: 5% 95% 5%

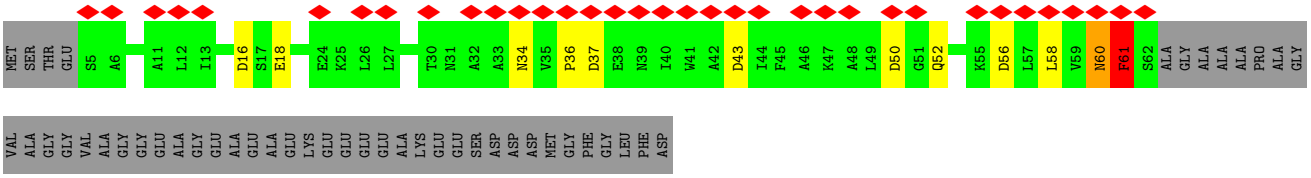
• Molecule 71: Unknown protein

Chain Bz: 33% 87% 7% 7%



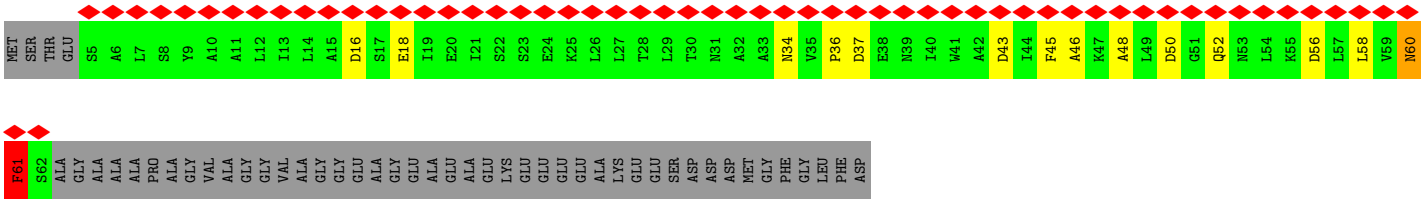
• Molecule 72: 60S acidic ribosomal protein rpP11 (P1)

Chain Bt: 33% 43% 9% •• 45%



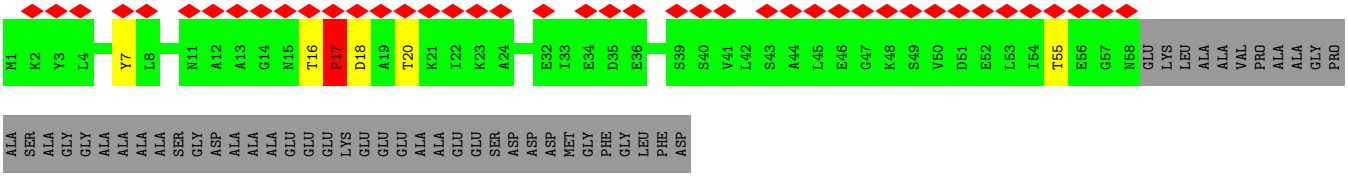
• Molecule 72: 60S acidic ribosomal protein rpP11 (P1)

Chain Bu: 55% 41% 12% •• 45%



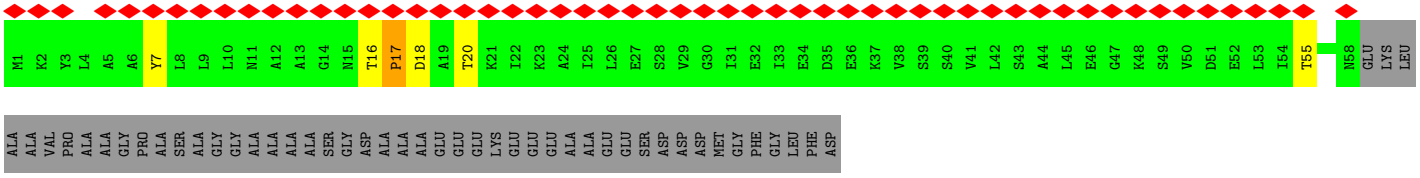
• Molecule 73: 60S acidic ribosomal protein (P2)

Chain Bv: 40% 49% 5% • 45%



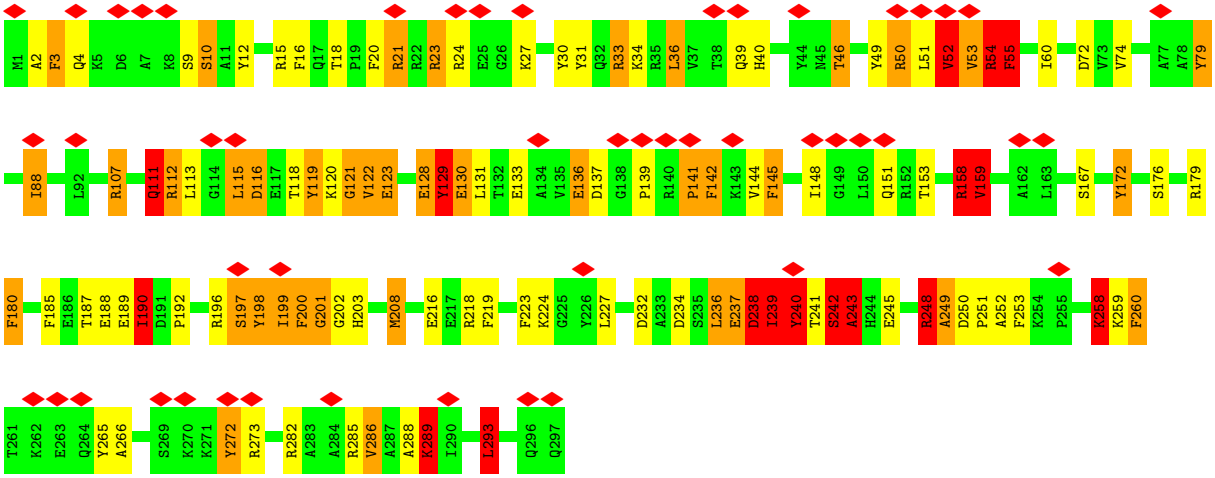
• Molecule 73: 60S acidic ribosomal protein (P2)

Chain Bw: 52% 49% 5% • 45%



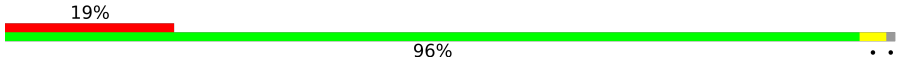
• Molecule 74: 60S ribosomal protein rpL5 (L18p)

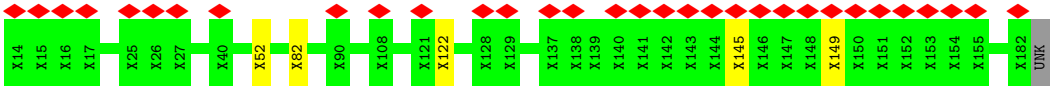
Chain BQ:



• Molecule 75: 60S ribosomal protein rpL13 (L13e)

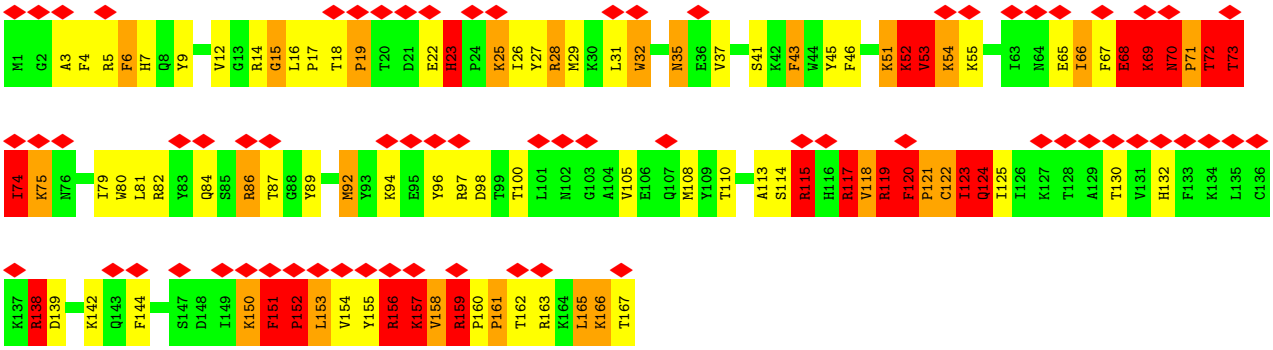
Chain BL:





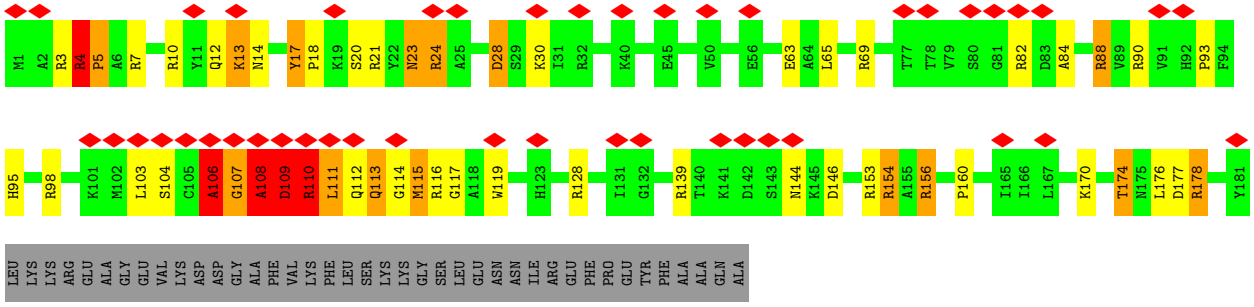
• Molecule 76: 60S ribosomal protein rpL20 (L18ae)

Chain BS:



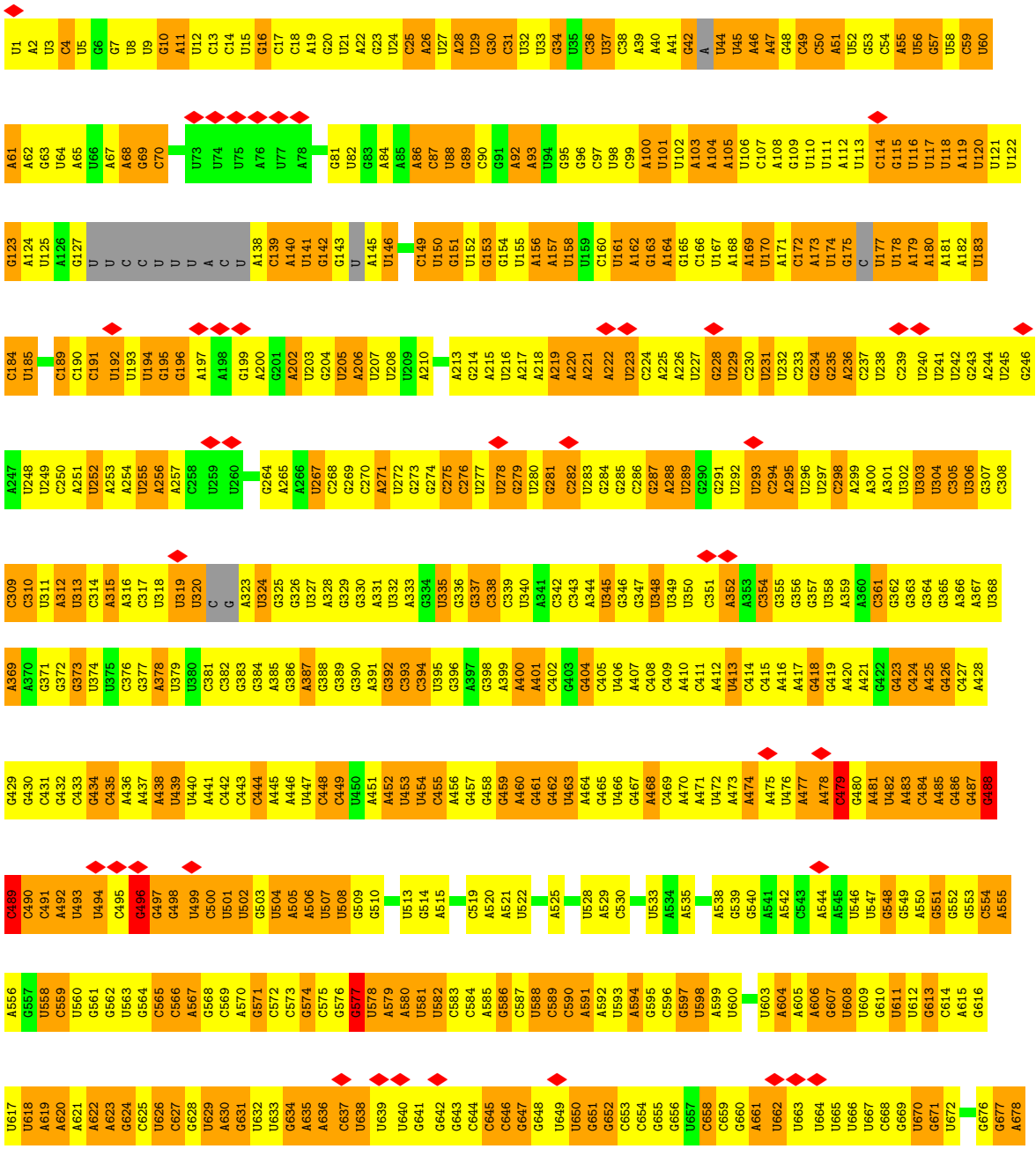
• Molecule 77: 60S ribosomal protein rpL10 (L10e)

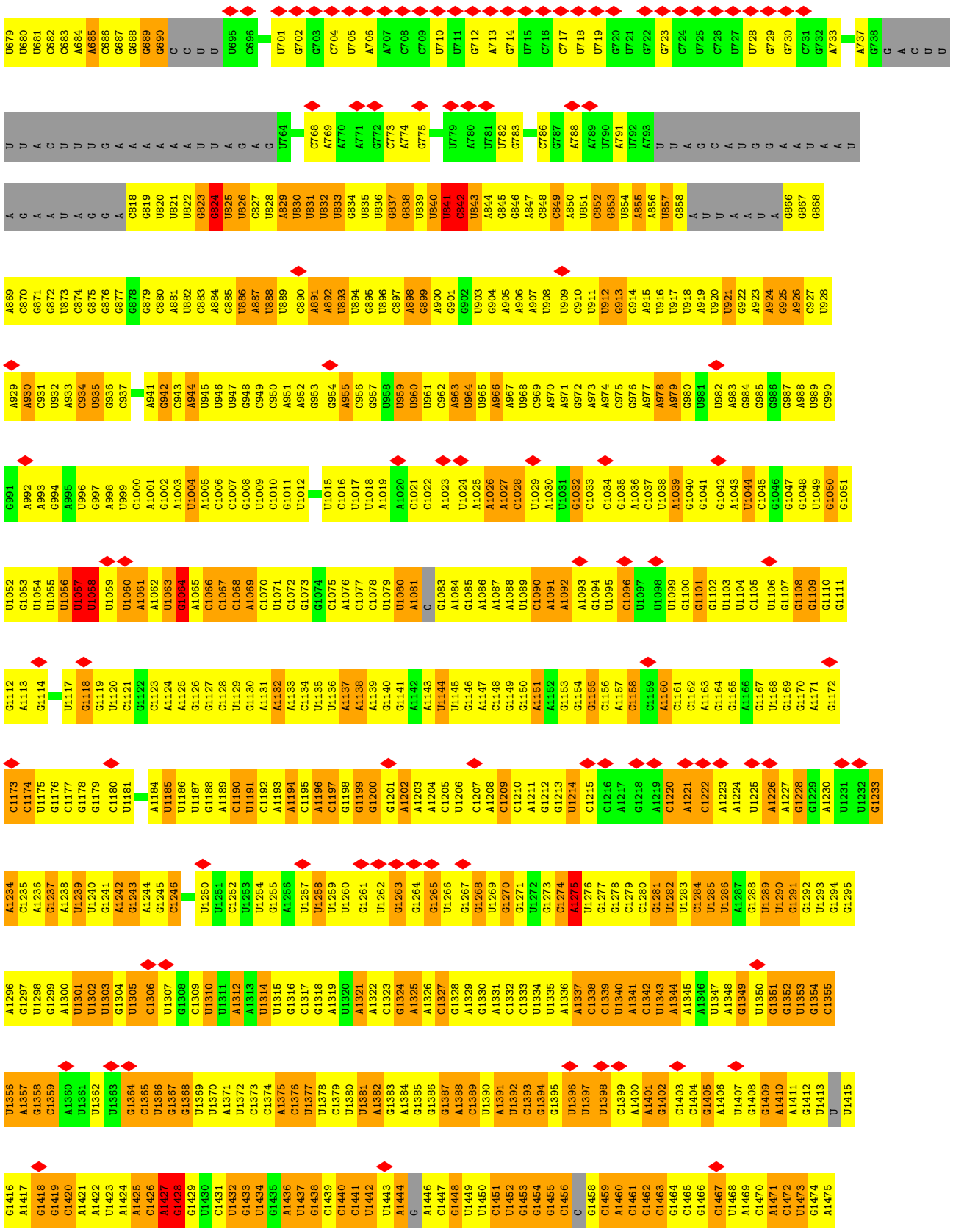
Chain BI:



- Molecule 78: 18S rRNA

Chain CA:

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U U A C U U U G A A A A A U U A G A G U764 C768 A769 A770 A771 G772 C773 A774 G775 U779 A780 U781 U782 G783 C786 G787 A788 A789 U790 A791 U792 A793 U U A G C A U G G A A U A U
A G A A U A G G A C818 G819 U820 U821 U822 G823 G824 U825 U826 C827 U828 A829 U830 U831 U832 U833 G834 U835 U836 G837 G838 U839 U840 U841 C842 U843 A844 G845 G846 A847 C848 C849 A850 U851 C852 G853 U854 A855 A856 U857 G858 A U U A A U A G866 G867 G868
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A929 A930 C931 U932 A933 C934 U935 G936 C937 A941 G942 C943 A944 U945 U946 U947 G948 C949 C950 A951 A952 G953 G954 A955 C956 G957 U958 U959 U960 U961 C962 A963 U964 U965 A966 A967 U968 C969 A970 A971 G972 A973 A974 C975 G976 A977 A978 A979 G980 U981 U982 A983 G984 G985 G986 G987 A988 U989 C990
G991 A992 A993 G994 A995 U996 G997 A998 U999 C1000 A1001 G1002 A1003 U1004 A1005 C1006 C1007 G1008 U1009 C1010 G1011 U1012 U1015 C1016 U1017 U1018 A1019 A1020 C1021 C1022 A1023 U1024 A1025 A1026 A1027 C1028 U1029 A1030 U1031 G1032 C1033 C1034 G1035 A1036 C1037 U1038 A1039 G1040 G1041 G1042 A1043 U1044 C1045 G1046 G1047 G1048 U1049 G1050 G1051
U1052 G1053 U1054 U1055 U1056 U1057 U1058 U1059 U1060 A1061 A1062 U1063 G1064 A1065 C1066 C1067 C1068 A1069 C1070 U1071 C1072 G1073 G1074 C1075 A1076 C1077 C1078 U1079 U1080 A1081 C G1083 A1084 G1085 A1086 A1087 A1088 U1089 C1090 A1091 A1092 A1093 G1094 U1095 C1096 U1097 U1098 U1099 G1100 G1101 G1102 U1103 U1104 C1105 U1106 G1107 G1108 G1109 G1110 G1111
G1112 A1113 G1114 U1117 G1118 G1119 U1120 C1121 G1122 C1123 A1124 A1125 G1126 G1127 C1128 U1129 G1130 A1131 A1132 A1133 C1134 U1135 U1136 A1137 A1138 A1139 G1140 G1141 A1142 A1143 U1144 U1145 G1146 A1147 C1148 G1149 G1150 A1151 A1152 G1153 G1154 G1155 C1156 A1157 C1158 C1159 A1160 C1161 C1162 A1163 G1164 G1165 A1166 G1167 U1168 G1169 G1170 A1171 G1172
C1173 C1174 U1175 G1176 C1177 G1178 G1179 C1180 U1181 A1184 U1185 U1186 U1187 G1188 A1189 C1190 U1191 C1192 A1193 A1194 C1195 A1196 C1197 G1198 G1199 G1200 G1201 A1202 A1203 A1204 C1205 U1206 C1207 A1208 C1209 C1210 A1211 G1212 G1213 U1214 C1215 C1216 A1217 G1218 A1219 C1220 A1221 C1222 A1223 A1224 U1225 A1226 A1227 G1228 G1229 A1230 U1231 U1232 G1233
A1234 C1235 A1236 G1237 A1238 U1239 U1240 G1241 A1242 G1243 A1244 G1245 C1246 U1250 U1251 C1252 U1253 U1254 G1255 A1256 U1257 U1258 U1259 U1260 G1261 U1262 G1263 G1264 G1265 U1266 G1267 G1268 U1269 G1270 C1271 U1272 G1273 C1274 A1275 U1276 G1277 G1278 C1279 C1280 G1281 U1282 U1283 C1284 U1285 U1286 A1287 G1288 U1289 U1290 G1291 U1292 U1293 G1294 G1295
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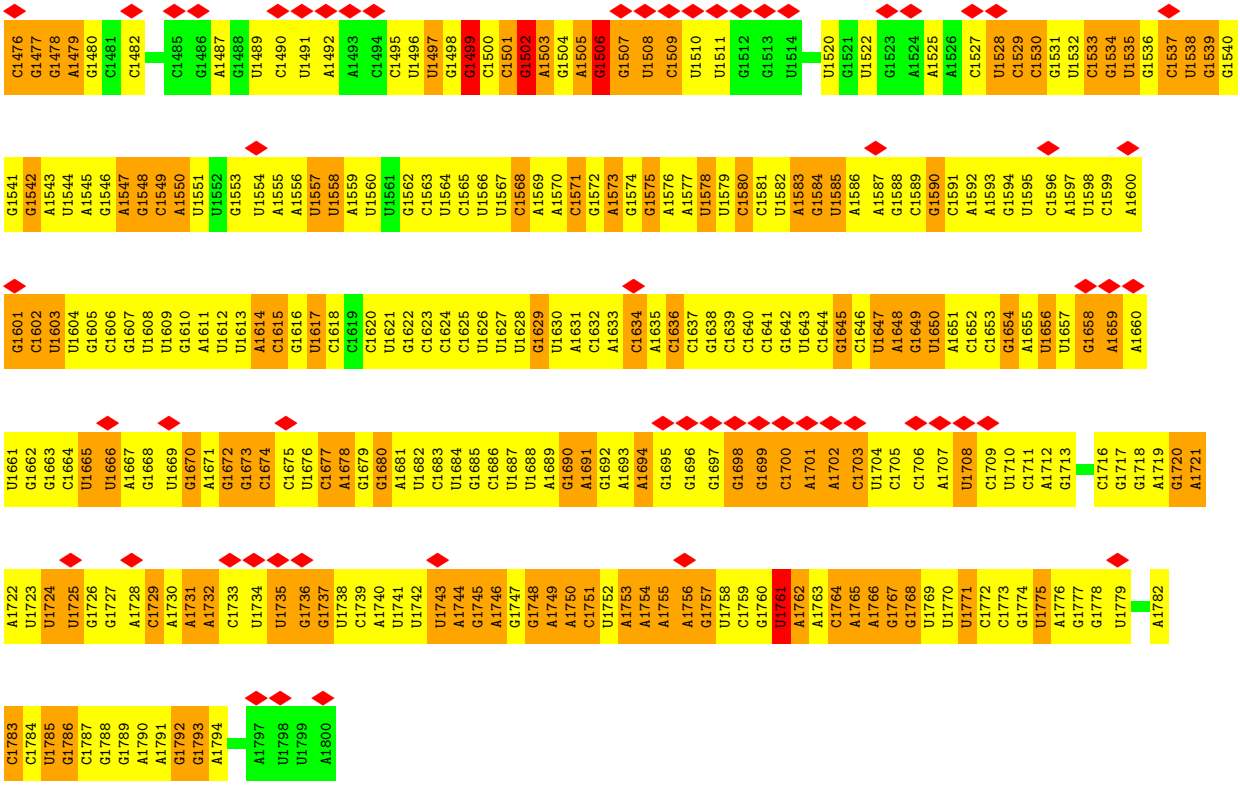
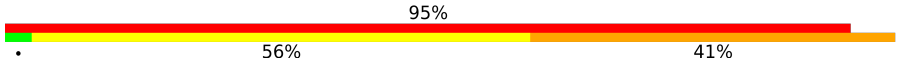
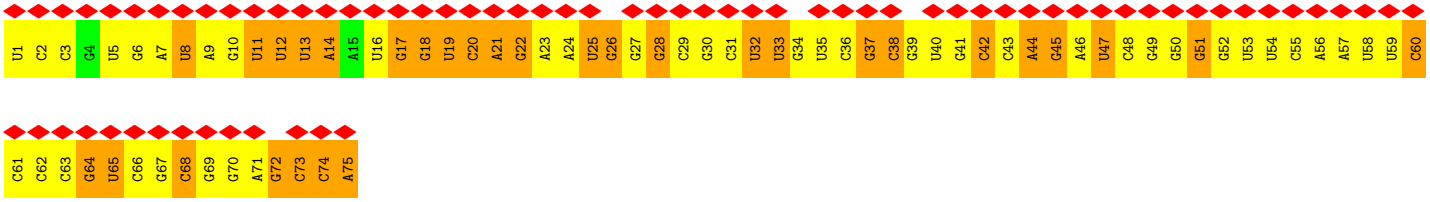


- Molecule 79: P-SITE TRNA ASP

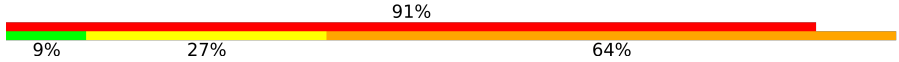
Chain CB:

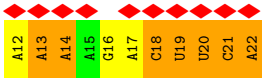




- Molecule 80: MRNA, RNA (5'-R(P*AP*AP*AP*AP*GP*AP*CP*UP*UP*CP*A)-3')

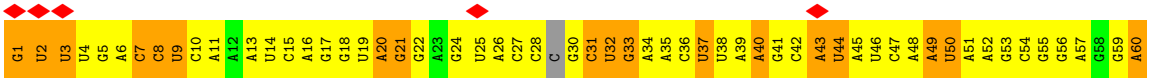
Chain CC:

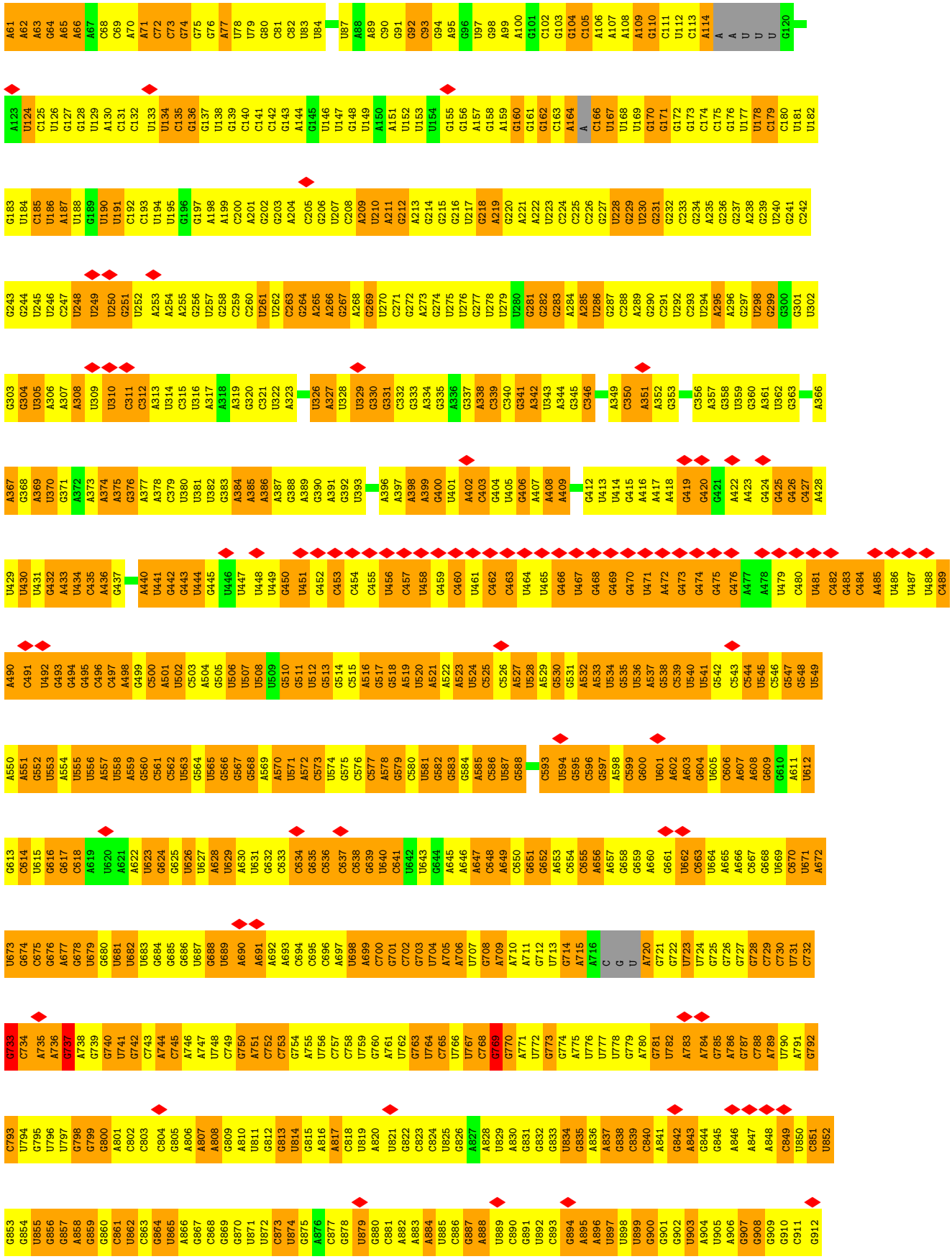




- Molecule 81: 25S rRNA

Chain DA:

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A123 U124 C125 U126 G127 G128 U129 A130 C131 C132 U133 U134 C135 G136 G137 U138 G139 C140 C141 C142 G143 A144 G145 U146 U147 G148 U149 A150 A151 U152 U153 U154 G155 G156 A157 G158 A159 G160 G161 G162 C163 A164 A C166 U167 U168 U169 G170 G171 G172 G173 C174 C175 G176 U177 U178 C179 C180 U181 U182
G183 U184 C185 U186 A187 U188 G189 U190 U191 C192 C193 U194 U195 G196 G197 A198 A199 C200 A201 G202 G203 A204 C205 G206 U207 C208 A209 U210 A211 G212 A213 G214 G215 G216 U217 G218 A219 G220 A221 A222 U223 C224 C225 C226 G227 U228 G229 U230 G231 C232 C233 G234 A235 G236 G237 A238 G239 U240 G241 C242
G243 G244 U245 U246 C247 U248 U249 U250 G251 U252 A253 A254 A255 G256 U257 G258 C259 C260 U261 U262 C263 G264 A265 A266 G267 A268 G269 U270 C271 G272 A273 G274 U275 U276 G277 U278 U279 U280 G281 G282 G283 A284 A285 U286 G287 C288 A289 G290 C291 U292 C293 U294 A295 A296 G297 U298 G299 G300 G301 U302
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A367 G368 A369 U370 G371 A372 A373 A374 A375 G376 A377 A378 C379 U380 U381 U382 G383 A384 A385 A386 A387 G388 A389 G390 A391 G392 U393 A396 A397 A398 A399 G400 U401 A402 C403 G404 U405 G406 A407 A408 A409 G412 U413 U414 G415 A416 A417 A418 G419 G420 G421 A422 A423 G424 G425 G426 C427 A428
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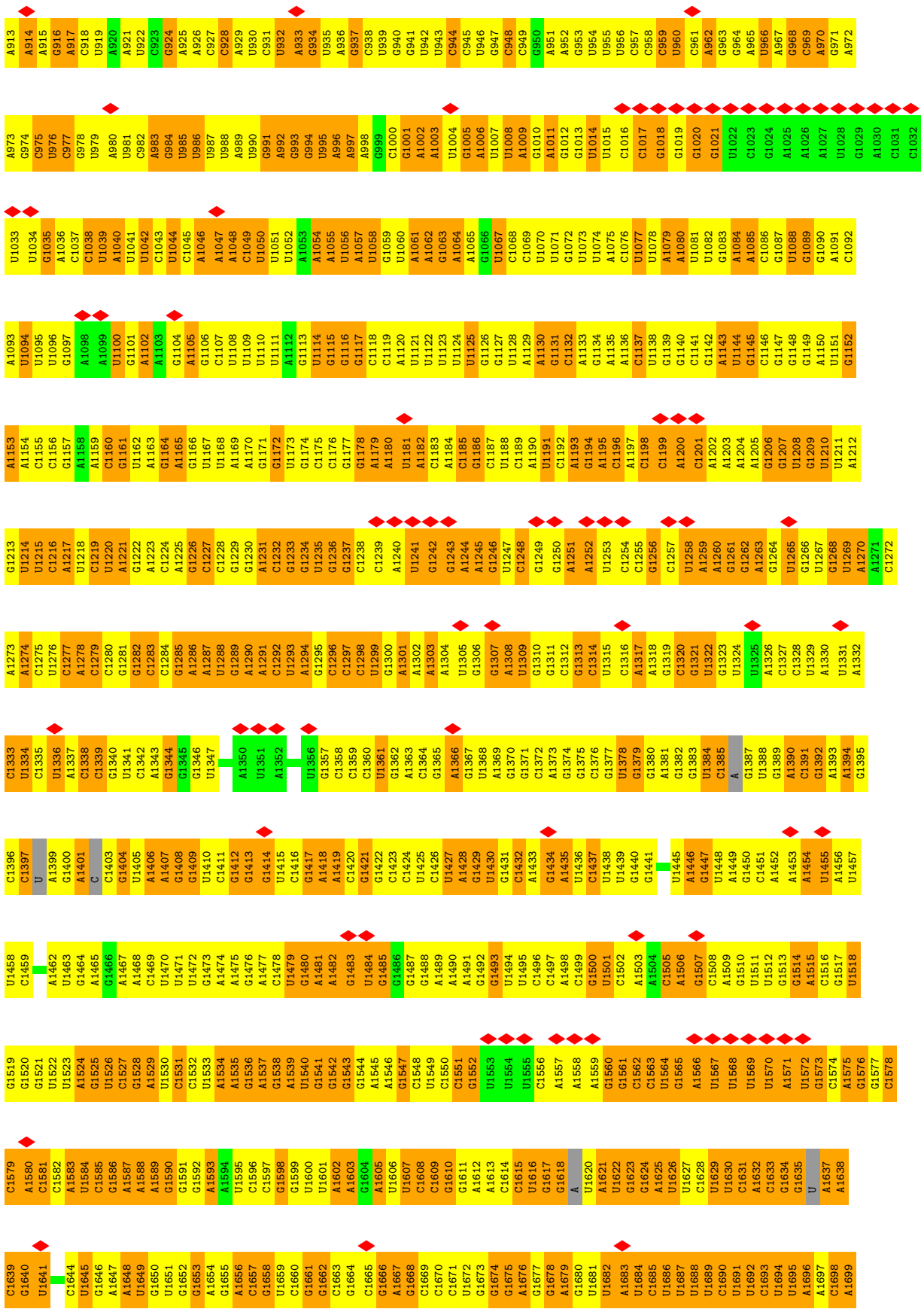
C793 U794 G795 U796 U797 G798 G799 G800 A801 C802 C803 C804 G805 A806 A807 A808 G809 A810 U811 C812 G813 U814 G815 A816 A817 C818 U819 A820 U821 C822 C823 C824 U825 G826 A827 A828 U829 A830 G831 G832 G833 U834 G835 A836 A837 G838 C839 C840 A841 G842 A843 G844 G845 A846 A847 A848 C849 U850 C851 U852
G853 C854 U855 G856 G857 A858 G859 G860 C861 U862 C863 C864 U865 A866 G867 C868 G869 G870 U871 U872 C873 U874 G875 A876 C877 G878 U879 G880 C881 A882 A883 A884 U885 C886 G887 A888 U889 C890 G891 U892 C893 G894 A895 A896 U897 U898 U899 G900 G901 G902 U903 A904 U905 A906 G907 G908 G909 G910 C911 G912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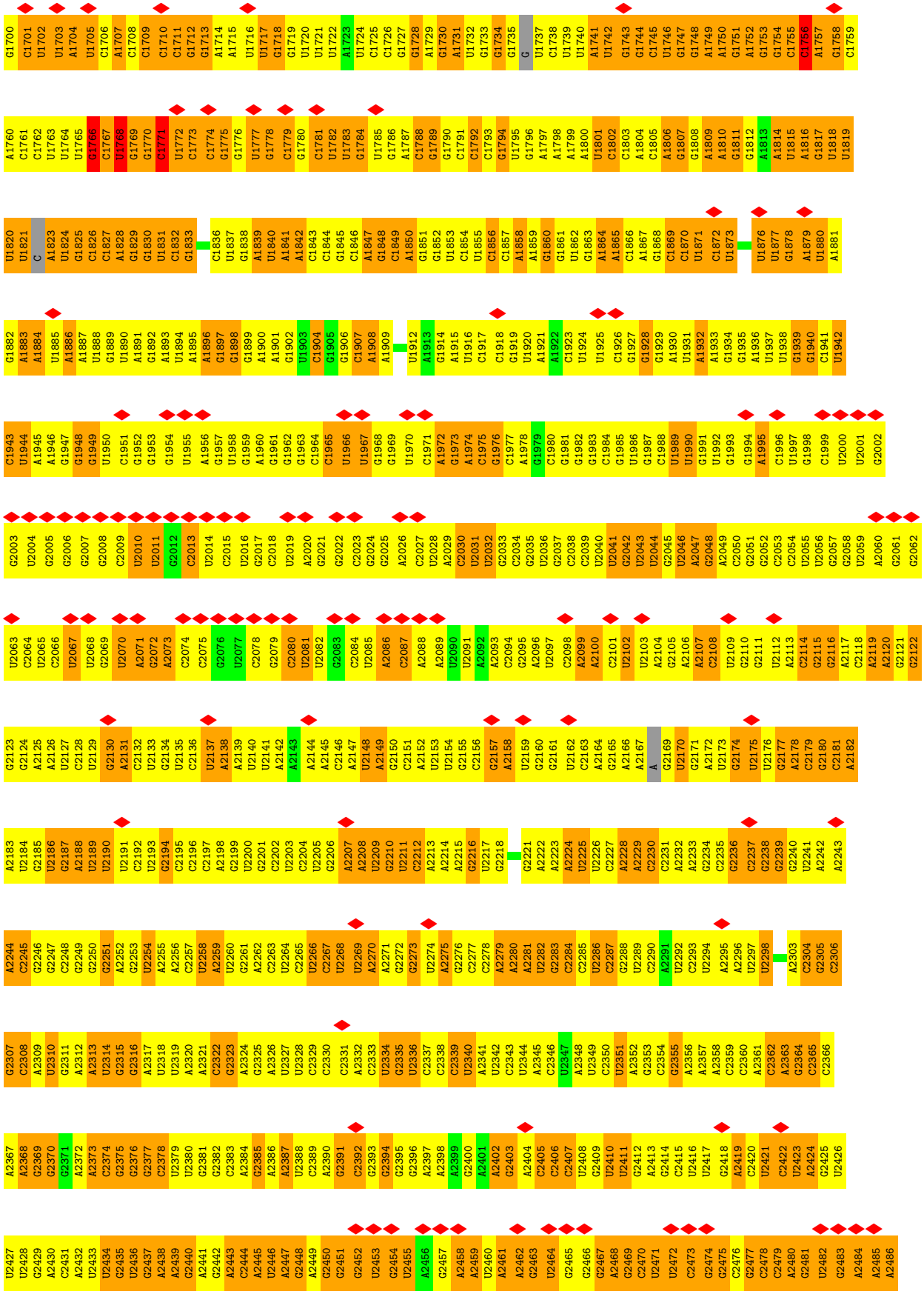
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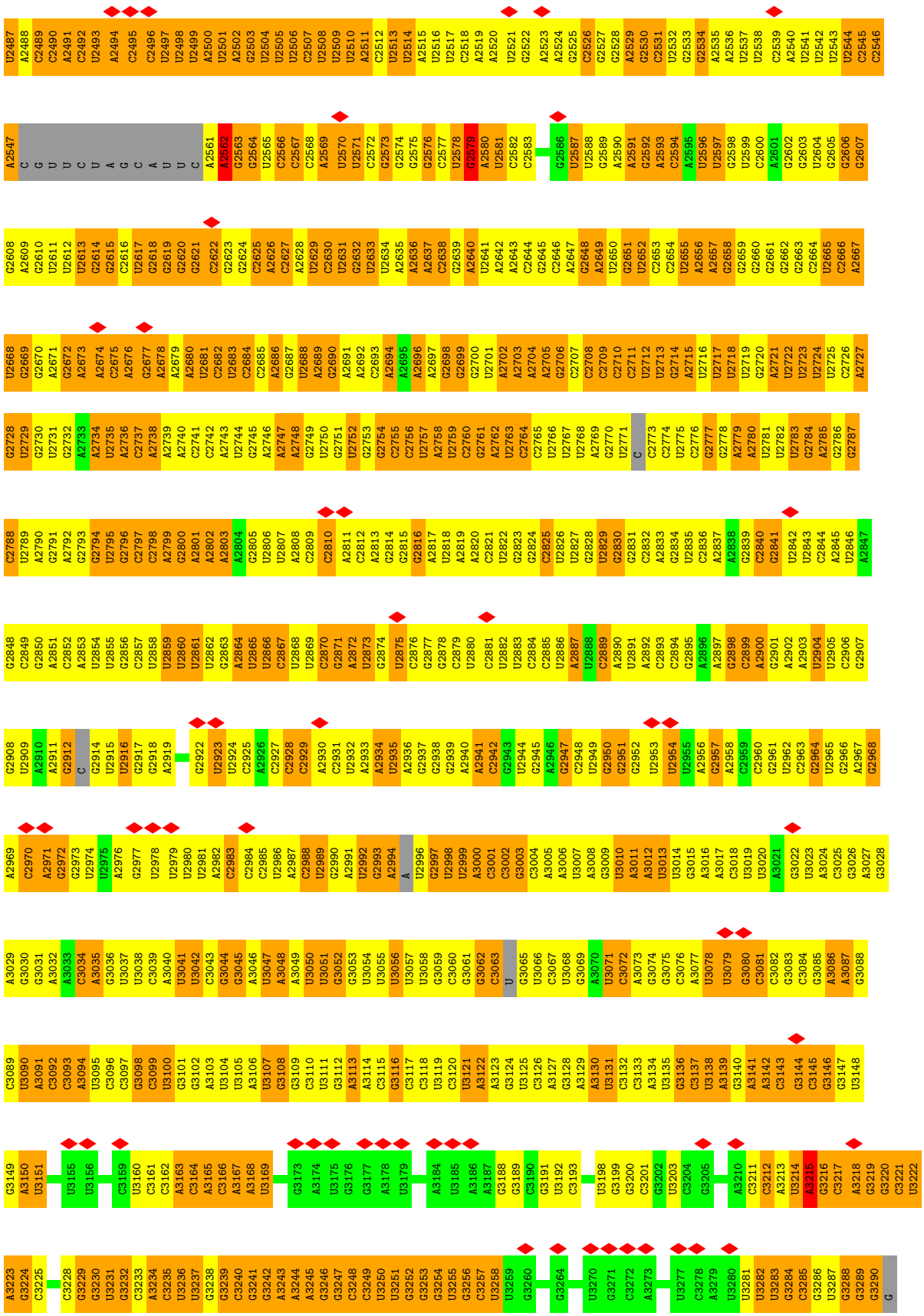
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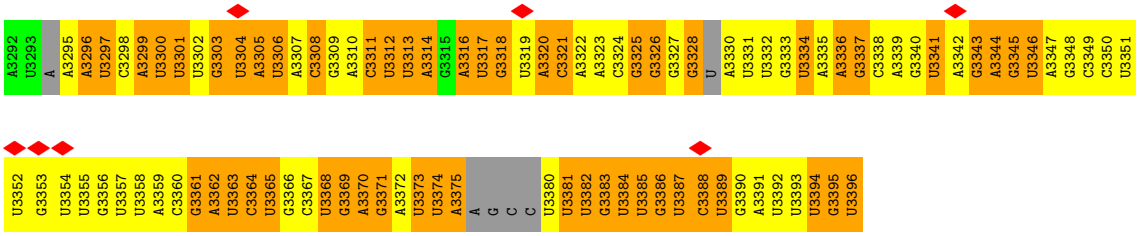

- Molecule 82: 5.8S rRNA

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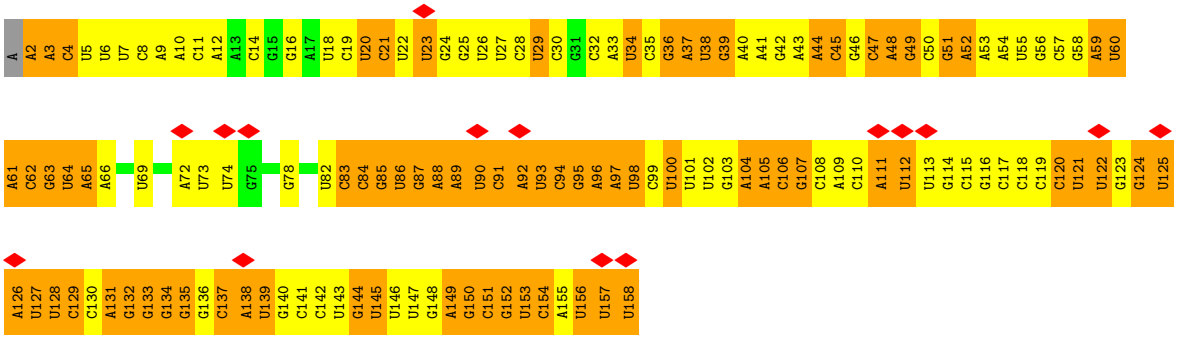

- Molecule 83: 5S rRNA

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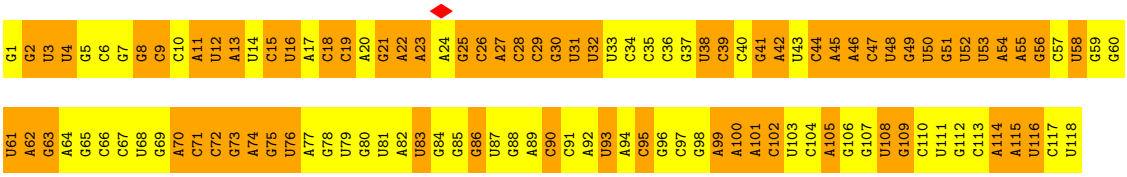

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	20400	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	7.747	Depositor
Minimum map value	-3.672	Depositor
Average map value	0.049	Depositor
Map value standard deviation	0.609	Depositor
Recommended contour level	1.75	Depositor
Map size (Å)	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2375, 1.2375, 1.2375	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	Aa	1.65	23/2495 (0.9%)	2.01	81/3391 (2.4%)
2	AA	1.99	33/1962 (1.7%)	2.62	83/2674 (3.1%)
3	AB	1.87	20/1530 (1.3%)	2.48	72/2049 (3.5%)
4	AD	1.95	29/1620 (1.8%)	2.88	94/2182 (4.3%)
5	AC	2.12	34/1544 (2.2%)	3.02	112/2059 (5.4%)
6	AE	1.82	21/1971 (1.1%)	2.46	79/2664 (3.0%)
8	AF	1.70	13/1561 (0.8%)	1.94	47/2103 (2.2%)
9	AH	1.85	10/1047 (1.0%)	2.39	47/1405 (3.3%)
10	AI	1.94	15/1016 (1.5%)	2.50	48/1362 (3.5%)
11	AJ	1.93	13/857 (1.5%)	2.90	38/1148 (3.3%)
12	AK	1.98	14/843 (1.7%)	2.28	38/1134 (3.4%)
13	AL	2.41	23/990 (2.3%)	3.21	80/1304 (6.1%)
14	AM	1.85	23/1175 (2.0%)	2.38	47/1577 (3.0%)
15	AN	1.78	5/358 (1.4%)	2.77	29/469 (6.2%)
16	AO	1.85	10/994 (1.0%)	2.70	58/1339 (4.3%)
17	AQ	2.16	24/1109 (2.2%)	3.08	59/1483 (4.0%)
18	AP	2.29	17/646 (2.6%)	3.39	49/867 (5.7%)
19	AR	1.65	5/691 (0.7%)	2.07	20/931 (2.1%)
20	AS	1.83	17/1138 (1.5%)	2.73	74/1527 (4.8%)
21	AT	2.06	13/694 (1.9%)	2.67	32/935 (3.4%)
22	AV	1.91	14/698 (2.0%)	2.68	44/932 (4.7%)
24	AX	1.77	5/372 (1.3%)	2.15	13/504 (2.6%)
25	AY	1.80	3/447 (0.7%)	2.08	19/601 (3.2%)
26	AZ	2.63	17/499 (3.4%)	3.77	31/660 (4.7%)
29	AU	1.93	8/725 (1.1%)	2.49	45/969 (4.6%)
30	BA	1.42	4/1745 (0.2%)	1.78	32/2342 (1.4%)
31	BB	2.07	31/1938 (1.6%)	2.90	100/2600 (3.8%)
32	BC	2.25	65/3124 (2.1%)	3.27	171/4196 (4.1%)
33	BD	2.15	53/2531 (2.1%)	2.93	146/3414 (4.3%)
34	BE	2.08	25/1362 (1.8%)	3.17	79/1824 (4.3%)
35	BG	2.50	42/1433 (2.9%)	3.60	142/1922 (7.4%)
36	BF	1.65	9/1537 (0.6%)	2.05	27/2068 (1.3%)
37	BH	2.09	26/1527 (1.7%)	2.60	82/2052 (4.0%)
38	Bs	1.71	18/2013 (0.9%)	2.32	75/2731 (2.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
39	BJ	1.89	16/964 (1.7%)	2.63	44/1295 (3.4%)
40	BK	1.93	21/1600 (1.3%)	2.78	76/2146 (3.5%)
41	BN	1.88	15/1083 (1.4%)	2.30	56/1456 (3.8%)
42	BM	1.73	12/987 (1.2%)	2.20	45/1326 (3.4%)
43	BP	2.03	23/1659 (1.4%)	2.68	113/2221 (5.1%)
44	BO	2.47	29/1213 (2.4%)	3.20	74/1623 (4.6%)
45	BR	2.41	29/1264 (2.3%)	3.18	68/1701 (4.0%)
46	BT	1.82	26/1547 (1.7%)	2.27	54/2060 (2.6%)
47	BU	1.78	21/1285 (1.6%)	2.44	54/1720 (3.1%)
48	BW	2.02	13/846 (1.5%)	2.75	47/1142 (4.1%)
49	BV	1.71	14/1335 (1.0%)	2.03	40/1794 (2.2%)
50	BX	1.58	5/993 (0.5%)	2.19	41/1336 (3.1%)
51	BZ	2.29	14/590 (2.4%)	2.74	40/783 (5.1%)
52	BY	1.61	10/983 (1.0%)	1.95	25/1312 (1.9%)
53	Ba	2.24	20/722 (2.8%)	3.30	75/967 (7.8%)
54	Bd	1.63	2/177 (1.1%)	1.91	5/231 (2.2%)
55	Bc	2.06	14/974 (1.4%)	2.76	53/1294 (4.1%)
56	Bf	1.59	7/793 (0.9%)	1.92	17/1062 (1.6%)
57	Be	1.85	25/1957 (1.3%)	2.29	69/2631 (2.6%)
58	Bg	1.83	16/887 (1.8%)	2.38	32/1185 (2.7%)
59	Bh	1.80	11/1064 (1.0%)	2.30	47/1423 (3.3%)
60	Bi	2.51	24/935 (2.6%)	3.64	59/1242 (4.8%)
61	Bj	2.79	19/751 (2.5%)	3.05	68/1004 (6.8%)
62	Bk	2.48	19/625 (3.0%)	3.48	45/826 (5.4%)
63	Bm	1.73	9/710 (1.3%)	2.09	24/944 (2.5%)
64	Bl	2.03	9/693 (1.3%)	2.42	34/915 (3.7%)
65	Bn	2.32	13/610 (2.1%)	3.37	37/813 (4.6%)
66	Bo	1.80	4/452 (0.9%)	2.23	17/598 (2.8%)
67	Bp	1.57	2/335 (0.6%)	2.25	18/442 (4.1%)
68	Bq	1.98	3/235 (1.3%)	2.32	14/300 (4.7%)
69	Br	2.01	14/846 (1.7%)	2.74	44/1113 (4.0%)
72	Bt	0.69	1/445 (0.2%)	1.49	16/606 (2.6%)
72	Bu	0.92	1/445 (0.2%)	1.63	18/606 (3.0%)
73	Bv	0.97	0/431	1.29	4/582 (0.7%)
73	Bw	0.96	0/431	1.28	4/582 (0.7%)
74	BQ	2.23	50/2404 (2.1%)	3.27	146/3236 (4.5%)
76	BS	1.92	23/1458 (1.6%)	2.70	109/1957 (5.6%)
77	BI	0.95	1/1473 (0.1%)	1.60	29/1976 (1.5%)
78	CA	2.64	1783/37406 (4.8%)	2.65	3176/57948 (5.5%)
79	CB	2.75	77/1785 (4.3%)	2.58	142/2779 (5.1%)
80	CC	3.40	11/264 (4.2%)	3.22	29/407 (7.1%)
81	DA	2.74	3996/76832 (5.2%)	2.77	7042/119578 (5.9%)
82	DB	2.68	166/3480 (4.8%)	2.64	305/5395 (5.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
83	DC	2.90	156/2808 (5.6%)	3.09	331/4372 (7.6%)
All	All	2.44	7406/202969 (3.6%)	2.70	14979/298347 (5.0%)

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
1	Aa	0	18
2	AA	1	30
3	AB	0	29
4	AD	0	36
5	AC	2	40
6	AE	3	29
7	AG	0	52
8	AF	0	14
9	AH	0	15
10	AI	0	14
11	AJ	0	17
12	AK	1	15
13	AL	0	14
14	AM	0	12
15	AN	0	12
16	AO	2	15
17	AQ	0	29
18	AP	0	15
19	AR	0	8
20	AS	0	19
21	AT	0	15
22	AV	0	12
23	AW	0	20
24	AX	0	2
25	AY	0	4
26	AZ	0	25
27	Ab	0	3
28	Ac	0	1
29	AU	2	12
30	BA	0	8
31	BB	2	45
32	BC	2	56
33	BD	2	53

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	BE	2	25
35	BG	2	57
36	BF	0	10
37	BH	0	36
38	Bs	0	18
39	BJ	1	10
40	BK	0	29
41	BN	1	13
42	BM	0	11
43	BP	4	44
44	BO	1	28
45	BR	0	31
46	BT	0	17
47	BU	1	16
48	BW	0	12
49	BV	0	20
50	BX	0	13
51	BZ	0	18
52	BY	0	8
53	Ba	0	25
54	Bd	0	1
55	Bc	0	16
56	Bf	0	6
57	Be	1	14
58	Bg	0	13
59	Bh	0	14
60	Bi	0	25
61	Bj	1	26
62	Bk	1	15
63	Bm	1	5
64	Bl	0	13
65	Bn	0	15
66	Bo	0	15
67	Bp	0	8
68	Bq	0	4
69	Br	0	23
70	Bx	0	7
71	Bz	0	1
72	Bt	0	3
72	Bu	0	3
73	Bv	0	1
73	Bw	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
74	BQ	0	48
75	BL	0	5
76	BS	1	41
77	BI	2	24
78	CA	10	22
79	CB	1	0
80	CC	1	0
81	DA	32	15
82	DB	5	0
All	All	85	1514

The worst 5 of 7406 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	DA	1261	G	C2'-C1'	59.16	2.18	1.53
79	CB	55	C	C2'-C1'	-55.11	0.92	1.53
78	CA	636	A	C2'-C1'	54.35	2.13	1.53
81	DA	3215	A	C2'-C1'	-49.15	0.99	1.53
78	CA	1190	C	O5'-C5'	-48.72	0.65	1.42

The worst 5 of 14979 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	BC	266	ARG	NE-CZ-NH1	-73.84	83.38	120.30
81	DA	3305	A	P-O3'-C3'	50.10	179.82	119.70
81	DA	3047	U	P-O3'-C3'	47.61	176.83	119.70
81	DA	2046	U	P-O3'-C3'	47.25	176.40	119.70
81	DA	2071	A	P-O3'-C3'	46.20	175.13	119.70

5 of 85 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	AA	241	GLU	CA
5	AC	129	ILE	CA
5	AC	162	SER	CA
6	AE	28	ARG	CA
6	AE	30	THR	CA

5 of 1514 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Aa	10	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	Aa	48	THR	Peptide
1	Aa	49	GLY	Peptide
1	Aa	53	LYS	Peptide,Mainchain
1	Aa	54	PHE	Mainchain

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
1	Aa	317/319 (99%)	274 (86%)	23 (7%)	20 (6%)	1 17
2	AA	250/252 (99%)	199 (80%)	21 (8%)	30 (12%)	0 6
3	AB	202/240 (84%)	137 (68%)	30 (15%)	35 (17%)	0 3
4	AD	198/261 (76%)	160 (81%)	17 (9%)	21 (11%)	0 8
5	AC	192/197 (98%)	136 (71%)	28 (15%)	28 (15%)	0 4
6	AE	252/254 (99%)	176 (70%)	36 (14%)	40 (16%)	0 3
8	AF	197/225 (88%)	170 (86%)	9 (5%)	18 (9%)	1 11
9	AH	128/130 (98%)	95 (74%)	17 (13%)	16 (12%)	0 5
10	AI	124/143 (87%)	84 (68%)	16 (13%)	24 (19%)	0 2
11	AJ	108/121 (89%)	92 (85%)	8 (7%)	8 (7%)	1 14
12	AK	117/137 (85%)	81 (69%)	9 (8%)	27 (23%)	0 1
13	AL	143/145 (99%)	100 (70%)	22 (15%)	21 (15%)	0 4
14	AM	138/146 (94%)	107 (78%)	21 (15%)	10 (7%)	1 14
15	AN	46/56 (82%)	31 (67%)	2 (4%)	13 (28%)	0 0
16	AO	119/151 (79%)	95 (80%)	12 (10%)	12 (10%)	0 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	AQ	134/136 (98%)	90 (67%)	22 (16%)	22 (16%)	0	3
18	AP	83/156 (53%)	65 (78%)	12 (14%)	6 (7%)	1	14
19	AR	86/142 (61%)	64 (74%)	10 (12%)	12 (14%)	0	4
20	AS	142/144 (99%)	118 (83%)	8 (6%)	16 (11%)	0	7
21	AT	85/87 (98%)	66 (78%)	10 (12%)	9 (11%)	0	8
22	AV	83/108 (77%)	66 (80%)	7 (8%)	10 (12%)	0	6
24	AX	48/82 (58%)	37 (77%)	7 (15%)	4 (8%)	1	12
25	AY	58/67 (87%)	46 (79%)	7 (12%)	5 (9%)	1	12
26	AZ	61/63 (97%)	41 (67%)	6 (10%)	14 (23%)	0	1
29	AU	94/135 (70%)	62 (66%)	14 (15%)	18 (19%)	0	2
30	BA	215/217 (99%)	194 (90%)	11 (5%)	10 (5%)	2	21
31	BB	252/254 (99%)	208 (82%)	18 (7%)	26 (10%)	0	8
32	BC	386/388 (100%)	316 (82%)	33 (8%)	37 (10%)	0	10
33	BD	325/362 (90%)	250 (77%)	34 (10%)	41 (13%)	0	5
34	BE	166/174 (95%)	136 (82%)	11 (7%)	19 (11%)	0	7
35	BG	174/176 (99%)	108 (62%)	15 (9%)	51 (29%)	0	0
36	BF	189/191 (99%)	173 (92%)	13 (7%)	3 (2%)	9	44
37	BH	195/256 (76%)	156 (80%)	18 (9%)	21 (11%)	0	8
38	Bs	255/312 (82%)	224 (88%)	16 (6%)	15 (6%)	1	17
39	BJ	125/165 (76%)	107 (86%)	11 (9%)	7 (6%)	2	19
40	BK	197/199 (99%)	161 (82%)	15 (8%)	21 (11%)	0	8
41	BN	136/138 (99%)	104 (76%)	14 (10%)	18 (13%)	0	5
42	BM	129/137 (94%)	124 (96%)	5 (4%)	0	100	100
43	BP	191/204 (94%)	168 (88%)	14 (7%)	9 (5%)	2	21
44	BO	147/149 (99%)	100 (68%)	24 (16%)	23 (16%)	0	3
45	BR	159/186 (86%)	116 (73%)	22 (14%)	21 (13%)	0	5
46	BT	187/189 (99%)	163 (87%)	14 (8%)	10 (5%)	2	19
47	BU	158/160 (99%)	144 (91%)	7 (4%)	7 (4%)	2	22
48	BW	103/121 (85%)	79 (77%)	15 (15%)	9 (9%)	1	11
49	BV	168/170 (99%)	135 (80%)	20 (12%)	13 (8%)	1	13
50	BX	120/142 (84%)	95 (79%)	11 (9%)	14 (12%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	BZ	71/155 (46%)	48 (68%)	13 (18%)	10 (14%)	0	4
52	BY	121/123 (98%)	115 (95%)	2 (2%)	4 (3%)	4	26
53	Ba	93/136 (68%)	62 (67%)	15 (16%)	16 (17%)	0	3
54	Bd	20/59 (34%)	19 (95%)	1 (5%)	0	100	100
55	Bc	116/120 (97%)	92 (79%)	11 (10%)	13 (11%)	0	7
56	Bf	103/105 (98%)	91 (88%)	7 (7%)	5 (5%)	2	20
57	Be	237/244 (97%)	213 (90%)	14 (6%)	10 (4%)	3	22
58	Bg	108/113 (96%)	95 (88%)	4 (4%)	9 (8%)	1	12
59	Bh	128/130 (98%)	115 (90%)	7 (6%)	6 (5%)	2	21
60	Bi	116/118 (98%)	76 (66%)	13 (11%)	27 (23%)	0	1
61	Bj	98/107 (92%)	66 (67%)	15 (15%)	17 (17%)	0	3
62	Bk	75/100 (75%)	61 (81%)	6 (8%)	8 (11%)	0	8
63	Bm	90/92 (98%)	78 (87%)	10 (11%)	2 (2%)	6	35
64	Bl	86/88 (98%)	65 (76%)	14 (16%)	7 (8%)	1	12
65	Bn	76/78 (97%)	56 (74%)	10 (13%)	10 (13%)	0	5
66	Bo	49/51 (96%)	38 (78%)	3 (6%)	8 (16%)	0	3
67	Bp	38/52 (73%)	28 (74%)	7 (18%)	3 (8%)	1	13
68	Bq	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2	22
69	Br	104/106 (98%)	71 (68%)	14 (14%)	19 (18%)	0	3
72	Bt	56/106 (53%)	53 (95%)	0	3 (5%)	2	19
72	Bu	56/106 (53%)	53 (95%)	0	3 (5%)	2	19
73	Bv	56/106 (53%)	53 (95%)	1 (2%)	2 (4%)	3	25
73	Bw	56/106 (53%)	53 (95%)	1 (2%)	2 (4%)	3	25
74	BQ	295/297 (99%)	232 (79%)	27 (9%)	36 (12%)	0	6
76	BS	165/167 (99%)	116 (70%)	15 (9%)	34 (21%)	0	2
77	BI	179/221 (81%)	135 (75%)	23 (13%)	21 (12%)	0	6
All	All	9997/11298 (88%)	7958 (80%)	949 (10%)	1090 (11%)	1	8

5 of 1090 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Aa	29	GLN
1	Aa	51	ASP

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Mol	Chain	Res	Type
1	Aa	55	GLY
1	Aa	57	PRO
1	Aa	84	SER

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	
1	Aa	259/262 (99%)	238 (92%)	21 (8%)	11	35
2	AA	198/210 (94%)	180 (91%)	18 (9%)	9	29
3	AB	148/195 (76%)	136 (92%)	12 (8%)	11	35
4	AD	173/222 (78%)	158 (91%)	15 (9%)	10	31
5	AC	153/166 (92%)	132 (86%)	21 (14%)	3	17
6	AE	205/205 (100%)	188 (92%)	17 (8%)	11	34
8	AF	163/191 (85%)	144 (88%)	19 (12%)	5	21
9	AH	111/111 (100%)	98 (88%)	13 (12%)	5	21
10	AI	105/119 (88%)	93 (89%)	12 (11%)	5	21
11	AJ	93/114 (82%)	88 (95%)	5 (5%)	22	47
12	AK	82/105 (78%)	77 (94%)	5 (6%)	18	44
13	AL	87/120 (72%)	75 (86%)	12 (14%)	3	17
14	AM	123/129 (95%)	104 (85%)	19 (15%)	2	14
15	AN	34/49 (69%)	30 (88%)	4 (12%)	5	20
16	AO	105/128 (82%)	91 (87%)	14 (13%)	4	18
17	AQ	122/124 (98%)	109 (89%)	13 (11%)	6	23
18	AP	63/137 (46%)	56 (89%)	7 (11%)	6	22
19	AR	71/118 (60%)	62 (87%)	9 (13%)	4	18
20	AS	115/116 (99%)	100 (87%)	15 (13%)	4	18
21	AT	74/74 (100%)	67 (90%)	7 (10%)	8	27
22	AV	74/89 (83%)	67 (90%)	7 (10%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	AX	43/71 (61%)	33 (77%)	10 (23%)	1	4
25	AY	50/60 (83%)	47 (94%)	3 (6%)	19	44
26	AZ	51/54 (94%)	47 (92%)	4 (8%)	12	36
29	AU	72/113 (64%)	62 (86%)	10 (14%)	3	17
30	BA	198/198 (100%)	184 (93%)	14 (7%)	14	39
31	BB	189/196 (96%)	177 (94%)	12 (6%)	18	43
32	BC	315/323 (98%)	265 (84%)	50 (16%)	2	13
33	BD	253/289 (88%)	222 (88%)	31 (12%)	4	19
34	BE	145/150 (97%)	118 (81%)	27 (19%)	1	9
35	BG	153/153 (100%)	124 (81%)	29 (19%)	1	8
36	BF	170/171 (99%)	152 (89%)	18 (11%)	6	24
37	BH	154/208 (74%)	136 (88%)	18 (12%)	5	21
38	Bs	216/254 (85%)	209 (97%)	7 (3%)	39	61
39	BJ	102/136 (75%)	94 (92%)	8 (8%)	12	36
40	BK	162/162 (100%)	143 (88%)	19 (12%)	5	21
41	BN	109/109 (100%)	96 (88%)	13 (12%)	5	20
42	BM	101/105 (96%)	85 (84%)	16 (16%)	2	13
43	BP	165/176 (94%)	141 (86%)	24 (14%)	3	15
44	BO	119/119 (100%)	100 (84%)	19 (16%)	2	13
45	BR	131/151 (87%)	106 (81%)	25 (19%)	1	8
46	BT	154/154 (100%)	144 (94%)	10 (6%)	17	42
47	BU	132/137 (96%)	113 (86%)	19 (14%)	3	16
48	BW	90/107 (84%)	77 (86%)	13 (14%)	3	16
49	BV	131/137 (96%)	117 (89%)	14 (11%)	6	23
50	BX	106/118 (90%)	99 (93%)	7 (7%)	16	41
51	BZ	59/129 (46%)	51 (86%)	8 (14%)	3	17
52	BY	107/107 (100%)	93 (87%)	14 (13%)	4	18
53	Ba	73/116 (63%)	63 (86%)	10 (14%)	3	17
54	Bd	15/47 (32%)	13 (87%)	2 (13%)	4	18
55	Bc	104/105 (99%)	88 (85%)	16 (15%)	2	14
56	Bf	83/88 (94%)	75 (90%)	8 (10%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	Be	202/205 (98%)	182 (90%)	20 (10%)	8	26
58	Bg	90/97 (93%)	79 (88%)	11 (12%)	5	20
59	Bh	111/111 (100%)	95 (86%)	16 (14%)	3	16
60	Bi	99/101 (98%)	87 (88%)	12 (12%)	5	20
61	Bj	71/91 (78%)	63 (89%)	8 (11%)	6	21
62	Bk	64/82 (78%)	58 (91%)	6 (9%)	8	28
63	Bm	72/72 (100%)	67 (93%)	5 (7%)	15	40
64	Bl	68/71 (96%)	61 (90%)	7 (10%)	7	25
65	Bn	66/69 (96%)	53 (80%)	13 (20%)	1	8
66	Bo	46/46 (100%)	38 (83%)	8 (17%)	2	11
67	Bp	37/47 (79%)	35 (95%)	2 (5%)	22	47
68	Bq	23/23 (100%)	21 (91%)	2 (9%)	10	31
69	Br	87/91 (96%)	76 (87%)	11 (13%)	4	19
72	Bt	48/76 (63%)	48 (100%)	0	100	100
72	Bu	48/76 (63%)	48 (100%)	0	100	100
73	Bv	47/74 (64%)	45 (96%)	2 (4%)	29	53
73	Bw	47/74 (64%)	46 (98%)	1 (2%)	53	72
74	BQ	238/245 (97%)	196 (82%)	42 (18%)	2	11
76	BS	153/153 (100%)	116 (76%)	37 (24%)	0	4
77	BI	151/187 (81%)	133 (88%)	18 (12%)	5	20
All	All	8278/9418 (88%)	7314 (88%)	964 (12%)	9	21

5 of 964 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	BF	47	LYS
74	BQ	131	LEU
43	BP	174	ILE
74	BQ	53	VAL
77	BI	4	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
60	Bi	52	GLN
61	Bj	13	HIS
76	BS	124	GLN
31	BB	216	HIS
31	BB	205	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
78	CA	1485/1800 (82%)	521 (35%)	209 (14%)
79	CB	74/75 (98%)	26 (35%)	10 (13%)
80	CC	10/11 (90%)	7 (70%)	1 (10%)
81	DA	3156/3396 (92%)	1246 (39%)	607 (19%)
82	DB	142/158 (89%)	65 (45%)	36 (25%)
83	DC	117/118 (99%)	60 (51%)	26 (22%)
All	All	4984/5558 (89%)	1925 (38%)	889 (17%)

5 of 1925 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
78	CA	3	U
78	CA	4	C
78	CA	5	U
78	CA	10	G
78	CA	11	A

5 of 889 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
81	DA	1526	U
83	DC	75	G
81	DA	2031	U
83	DC	32	U
81	DA	3258	U

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

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

5.5 Carbohydrates (i)

There are no 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
78	CA	4
44	BO	3
23	AW	1
80	CC	1
74	BQ	1
76	BS	1
20	AS	1
7	AG	1
14	AM	1
34	BE	1
32	BC	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	31:UNK	C	59:UNK	N	10.96
1	CC	18:C	O3'	19:U	P	2.07
1	CA	1255:G	O3'	1256:A	P	1.94
1	BQ	39:GLN	C	40:HIS	N	1.90
1	CA	1254:U	O3'	1255:G	P	1.83

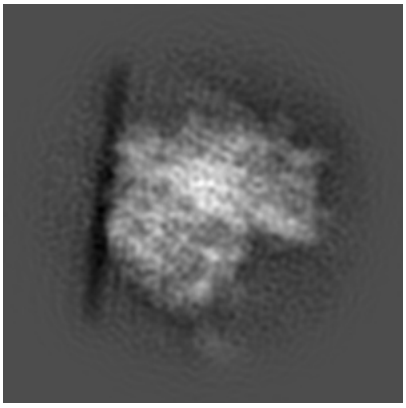
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-1669. These allow visual inspection of the internal detail of the map and identification of artifacts.

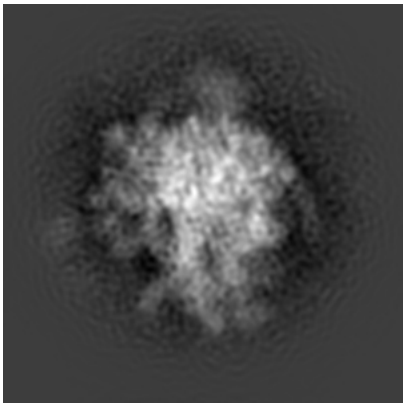
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

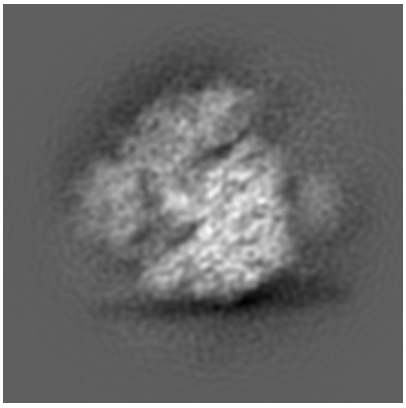
6.1.1 Primary map



X



Y

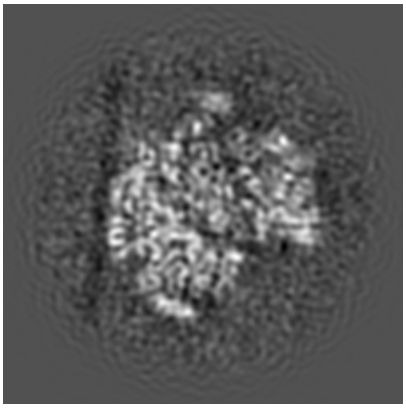


Z

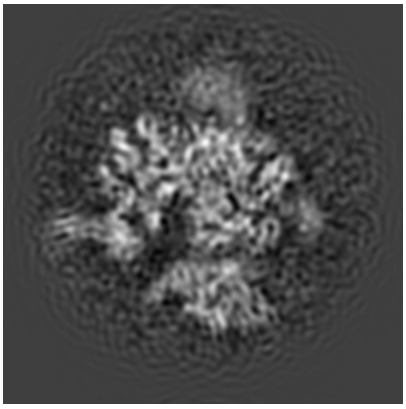
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

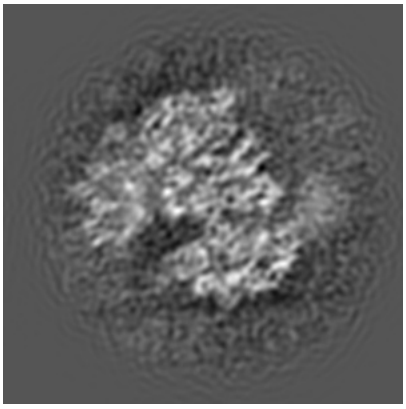
6.2.1 Primary map



X Index: 184



Y Index: 184

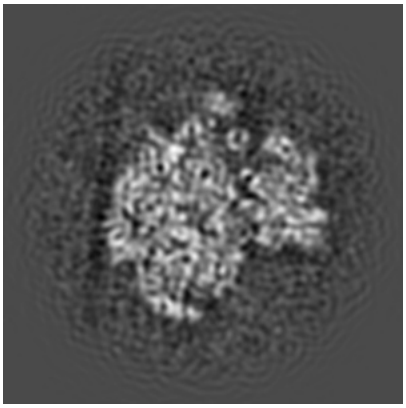


Z Index: 184

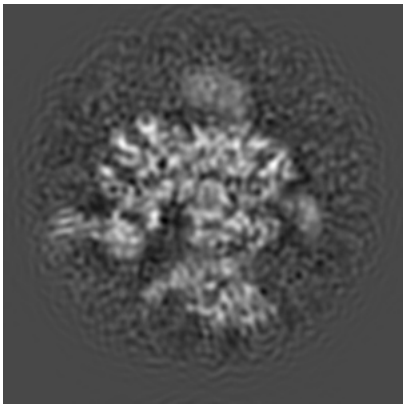
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

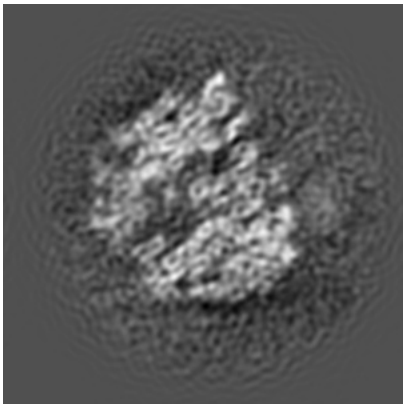
6.3.1 Primary map



X Index: 188



Y Index: 187

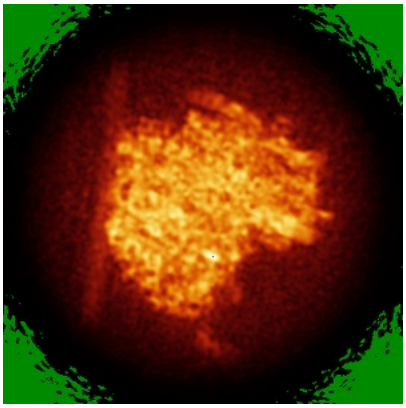


Z Index: 172

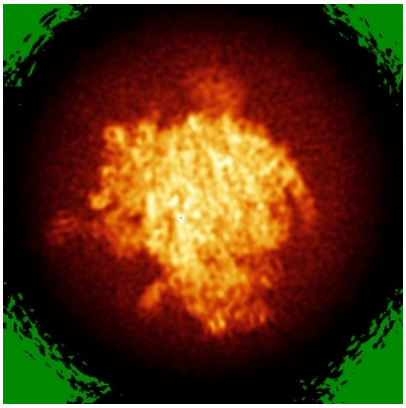
The images above show the largest variance slices of the map in three orthogonal directions.

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

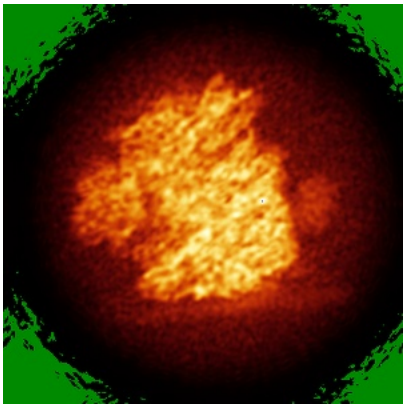
6.4.1 Primary map



X



Y

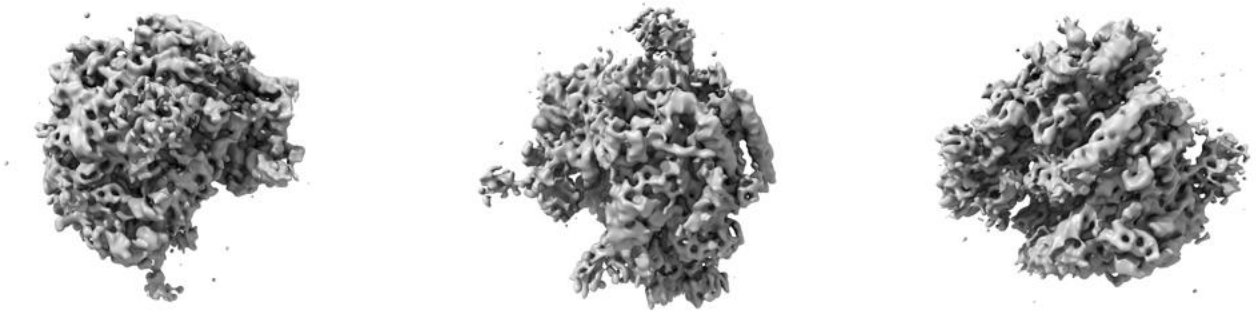


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 1.75. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

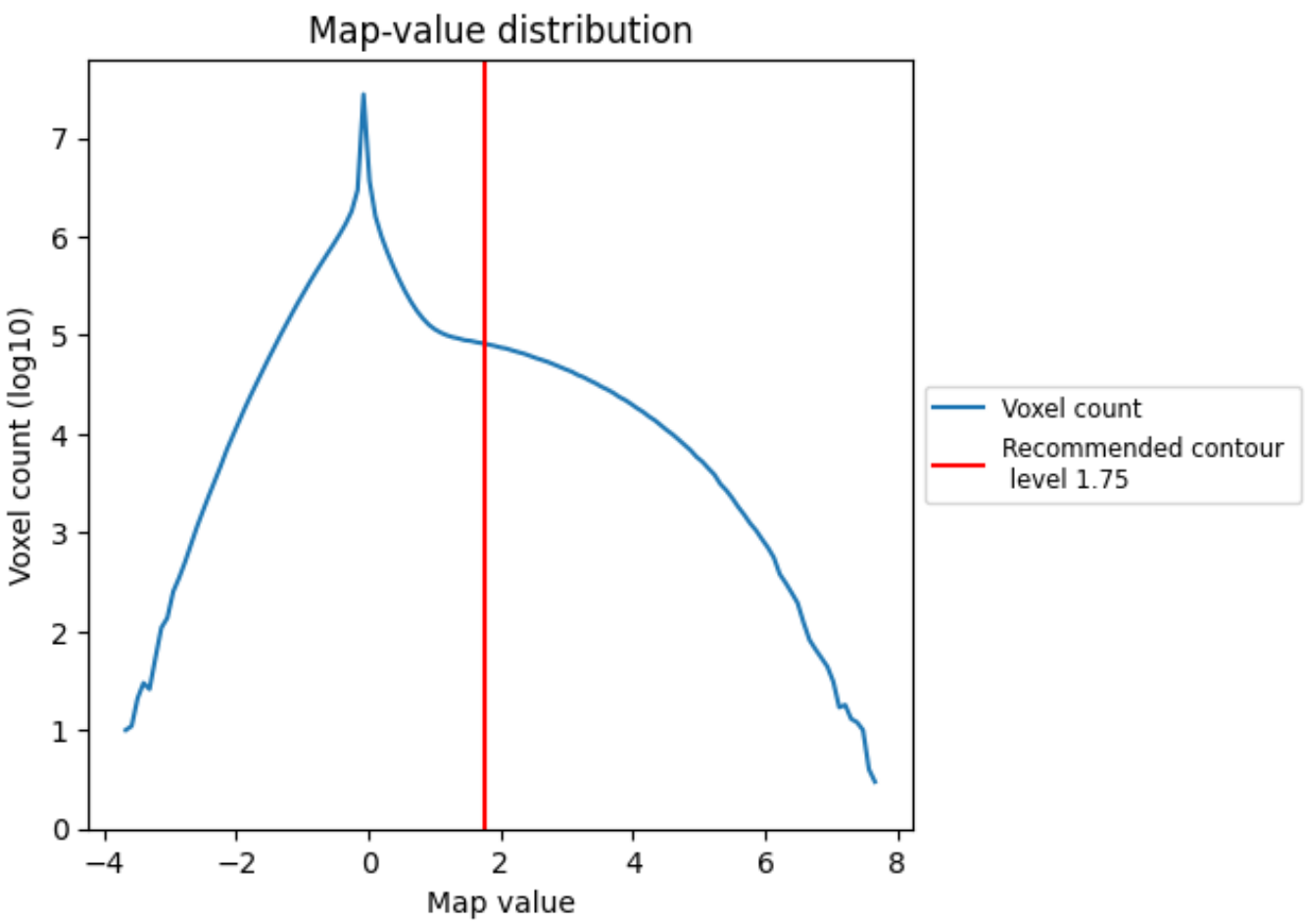
6.6 Mask visualisation (i)

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

7 Map analysis (i)

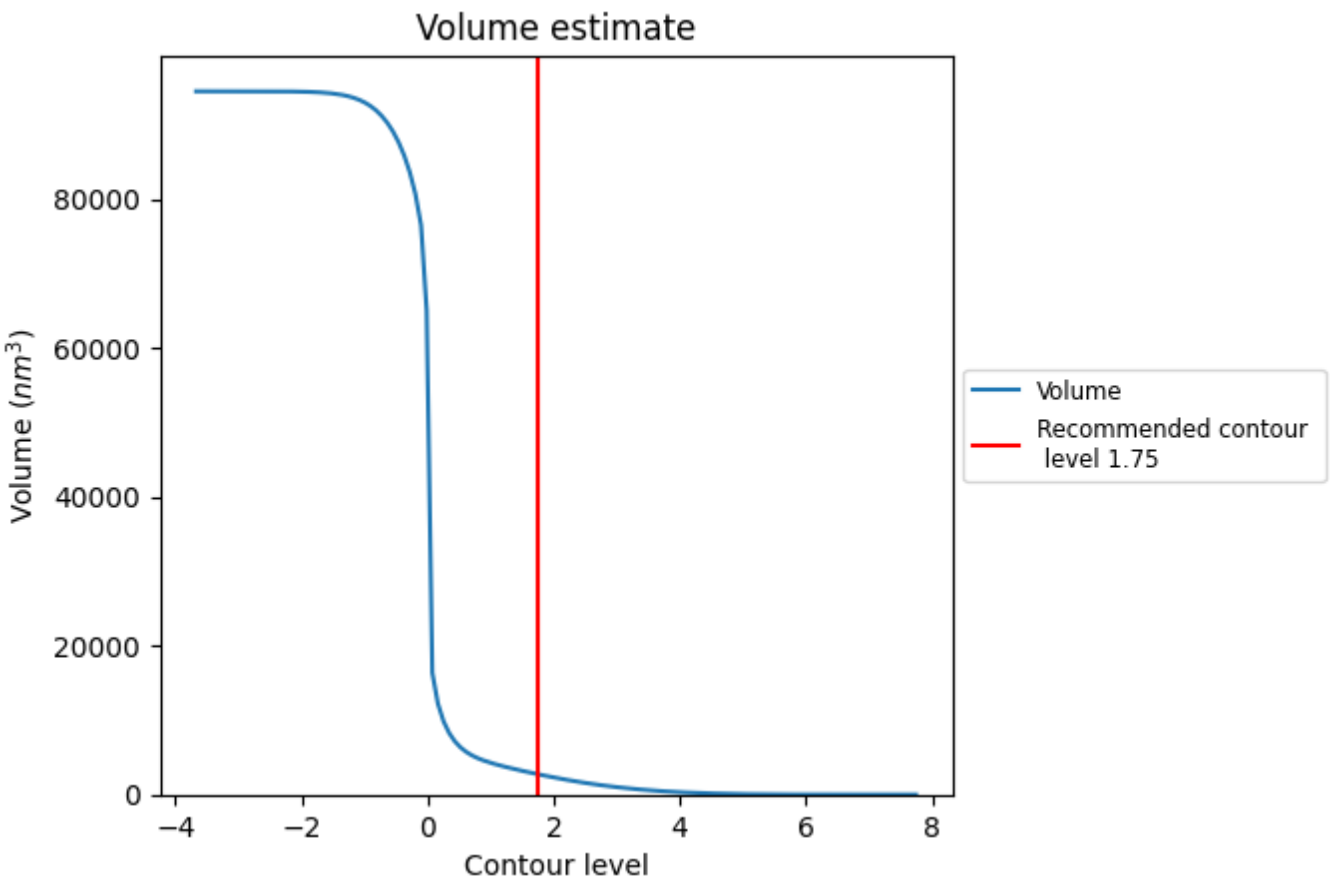
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

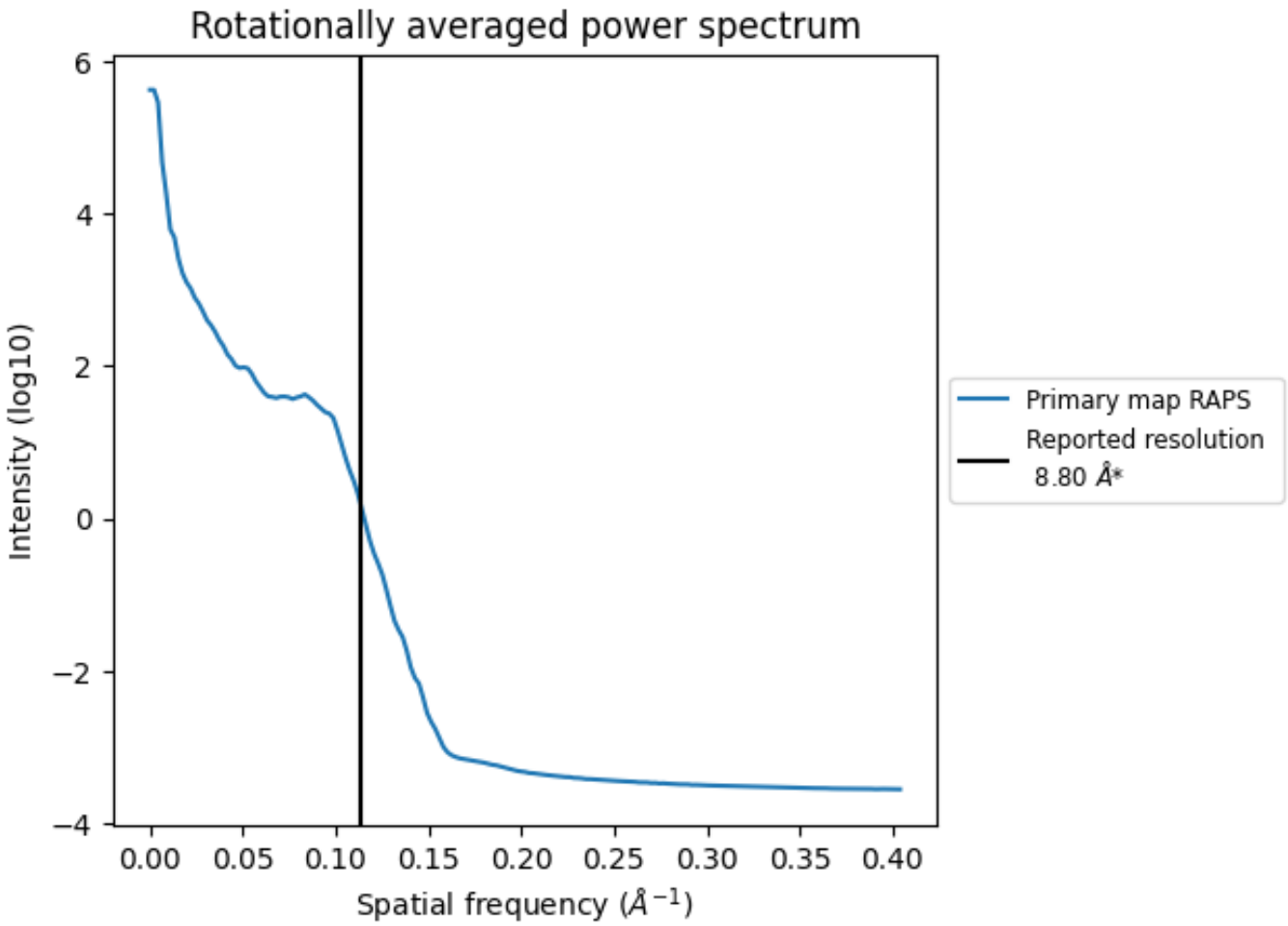
7.2 Volume estimate (i)



The volume at the recommended contour level is 2728 nm^3; this corresponds to an approximate mass of 2464 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 0.114 Å^{-1}

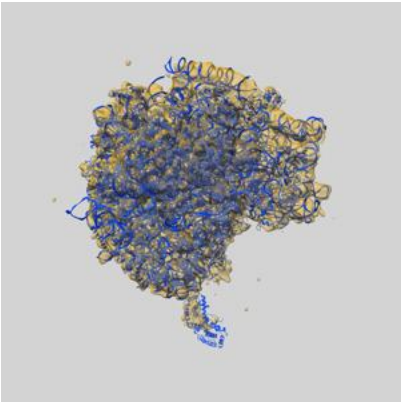
8 Fourier-Shell correlation (i)

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

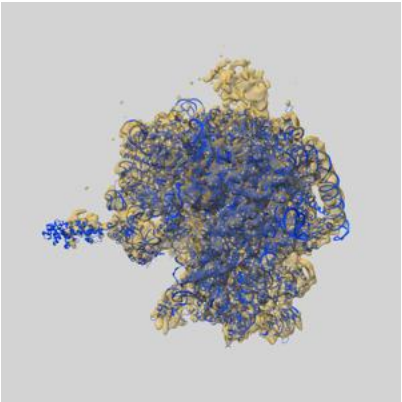
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-1669 and PDB model 4V6I. Per-residue inclusion information can be found in section 3 on page 20.

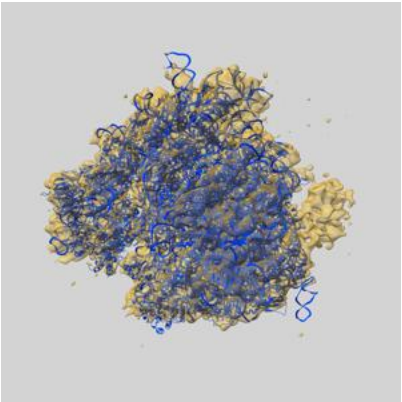
9.1 Map-model overlay (i)



X



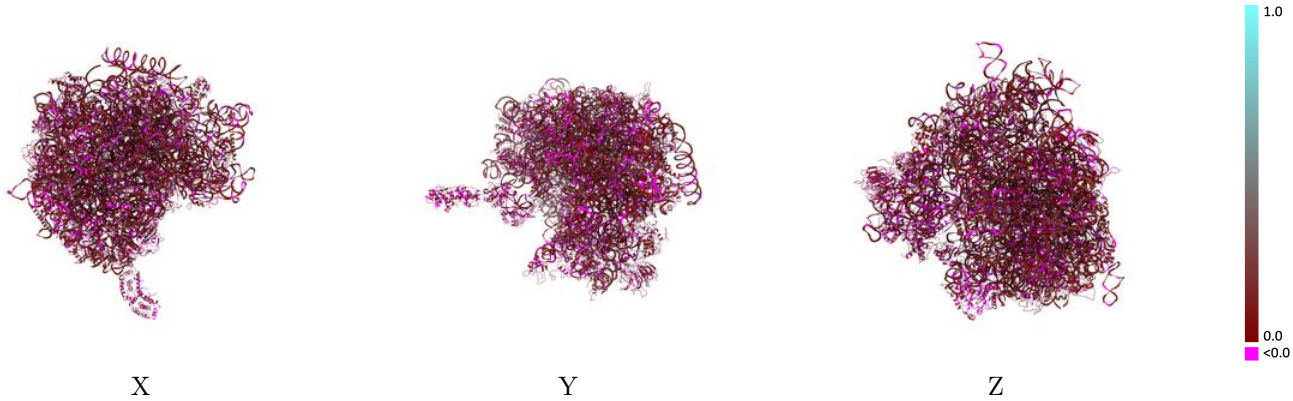
Y



Z

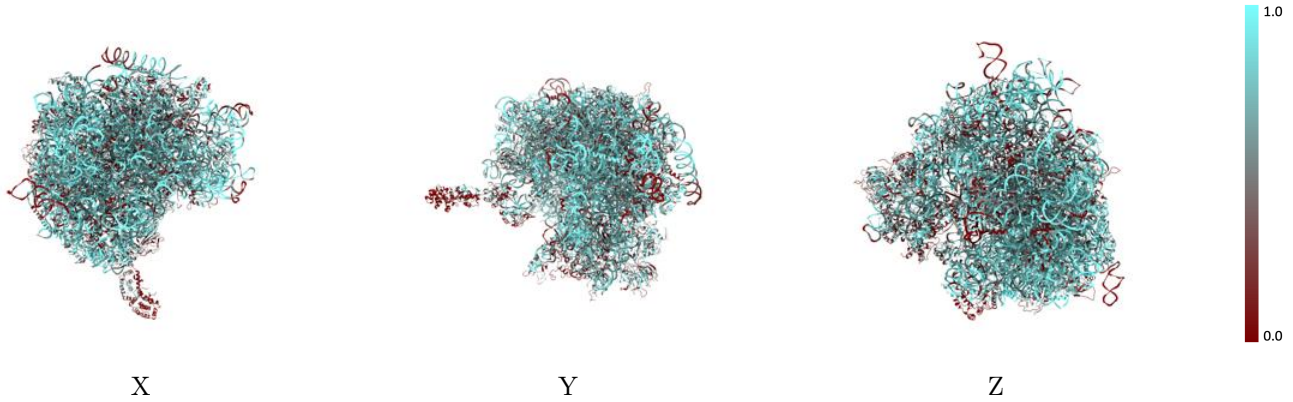
The images above show the 3D surface view of the map at the recommended contour level 1.75 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



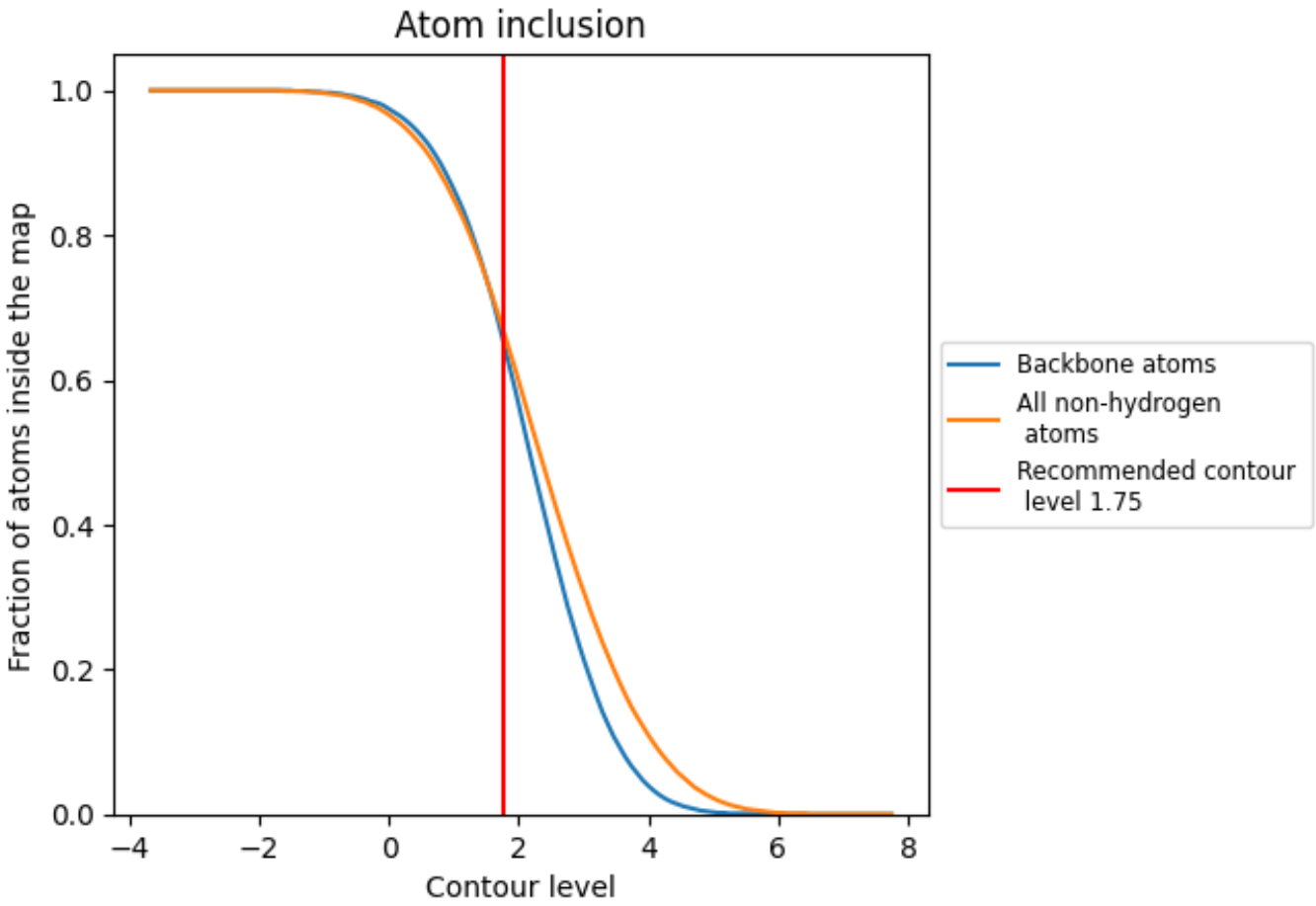
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.75).

9.4 Atom inclusion (i)



At the recommended contour level, 66% of all backbone atoms, 67% 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 (1.75) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6720	0.0940
AA	0.6070	0.1010
AB	0.4530	0.0770
AC	0.5850	0.0770
AD	0.5780	0.0860
AE	0.5530	0.0920
AF	0.5030	0.0710
AG	0.6840	0.1610
AH	0.5130	0.0870
AI	0.5430	0.0530
AJ	0.5000	0.0680
AK	0.5770	0.0700
AL	0.6540	0.0570
AM	0.2950	0.0500
AN	0.3770	0.0420
AO	0.4520	0.0830
AP	0.4140	0.0750
AQ	0.3000	0.0670
AR	0.3300	0.0730
AS	0.5260	0.0540
AT	0.4160	0.1050
AU	0.5370	0.0730
AV	0.3770	0.0800
AW	0.7200	0.1670
AX	0.4820	0.0650
AY	0.3320	0.0120
AZ	0.4960	0.0540
Aa	0.4650	0.0690
Ab	0.8670	0.2310
Ac	0.6350	0.2370
BA	0.2180	0.0010
BB	0.4620	0.0460
BC	0.5830	0.0580
BD	0.5840	0.0660
BE	0.5590	0.0870

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Chain	Atom inclusion	Q-score
BF	0.5300	0.0860
BG	0.5860	0.0780
BH	0.6210	0.0830
BI	0.6600	0.0620
BJ	0.3380	0.0300
BK	0.5740	0.0870
BL	0.7800	0.1700
BM	0.2620	0.0860
BN	0.6400	0.0980
BO	0.4910	0.0400
BP	0.5560	0.0370
BQ	0.7450	0.0620
BR	0.5520	0.1000
BS	0.5020	0.0650
BT	0.4790	0.0960
BU	0.6290	0.0650
BV	0.5070	0.0570
BW	0.6070	0.0800
BX	0.5130	0.0770
BY	0.6950	0.0860
BZ	0.3940	0.0600
Ba	0.4830	0.0350
Bc	0.7380	0.1170
Bd	0.6180	0.0590
Be	0.5650	0.0900
Bf	0.4790	0.1190
Bg	0.5580	0.0760
Bh	0.4620	0.0730
Bi	0.4370	0.0580
Bj	0.4450	0.0490
Bk	0.6900	0.0950
Bl	0.6730	0.0500
Bm	0.3920	0.0810
Bn	0.5630	0.0860
Bo	0.4720	0.0500
Bp	0.4370	-0.0300
Bq	0.4880	0.1170
Br	0.4650	0.0650
Bs	0.2770	0.0350
Bt	0.3560	0.0260
Bu	0.0000	0.0530
Bv	0.2740	0.0480

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Chain	Atom inclusion	Q-score
Bw	0.0370	0.0100
Bx	0.7900	0.1580
By	0.9100	0.2380
Bz	0.6140	0.2150
CA	0.7890	0.1050
CB	0.0690	0.0440
CC	0.1440	-0.0370
DA	0.7960	0.1160
DB	0.8120	0.1140
DC	0.9130	0.1250