wwPDB EM Validation Summary Report

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:

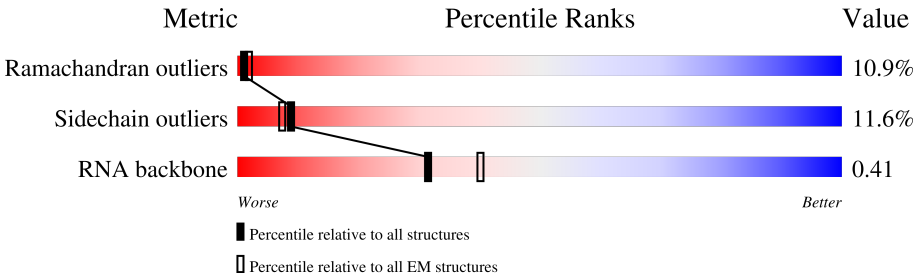
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance

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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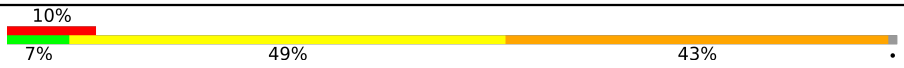
Mol	Chain	Length	Quality of chain
81	DA	3396	
82	DB	158	
83	DC	118	

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
7	AG	143	Total	C	N	O	0	0
			716	429	143	144		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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
33	BD	329	Total	C	N	O	S	0	0
			2486	1564	480	438	4		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 70 is a protein called Unknown protein.

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

- Molecule 71 is a protein called Unknown protein.

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

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

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

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
73	Bv	58	Total	C	N	O	S	0	0
			429	271	66	91	1		
73	Bw	58	Total	C	N	O	S	0	0
			429	271	66	91	1		

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

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

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
75	BL	169	Total	C	N	O	0	0
			845	507	169	169		

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

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

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

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

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

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

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

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

- 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
80	CC	11	Total	C	N	O	P	0	0
			236	106	45	74	11		

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

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

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

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

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

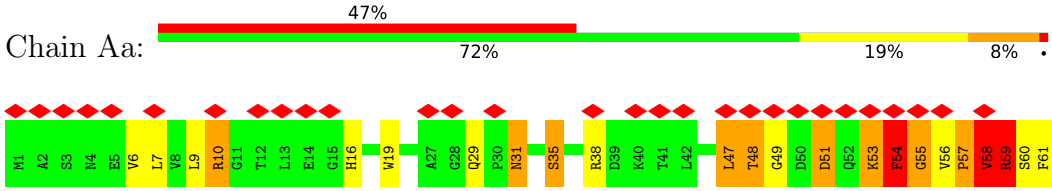
Mol	Chain	Residues	Atoms					AltConf	Trace
83	DC	118	Total	C	N	O	P	0	0
			2513	1122	446	827	118		

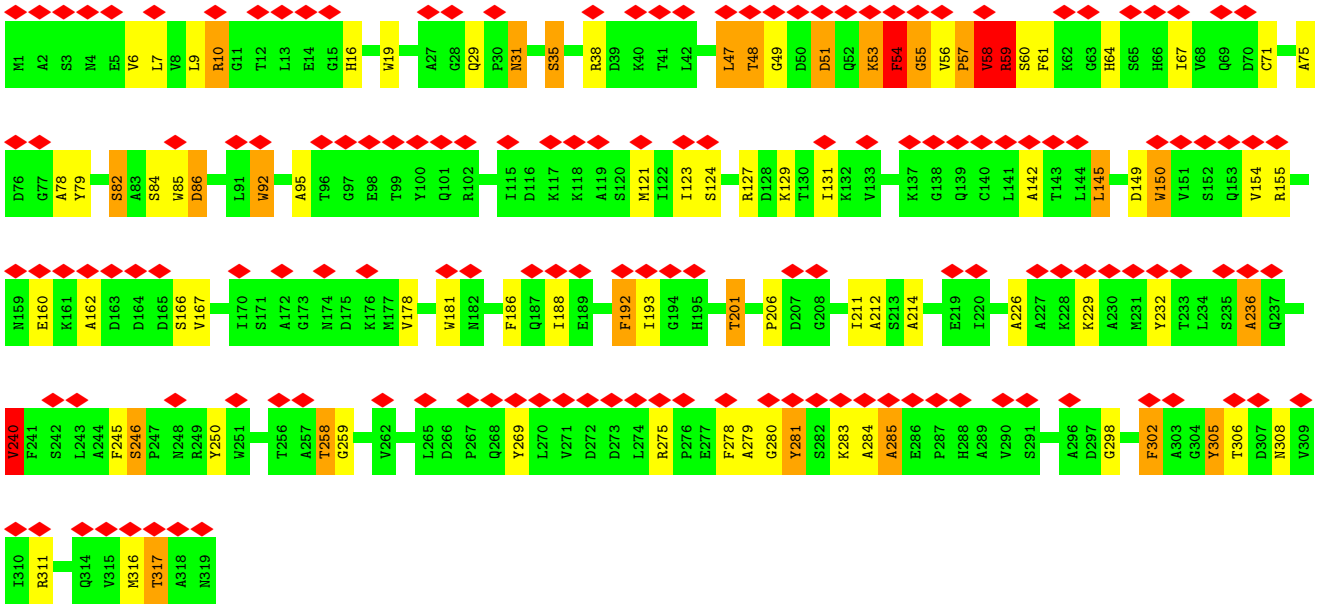
3 Residue-property plots (i)

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)

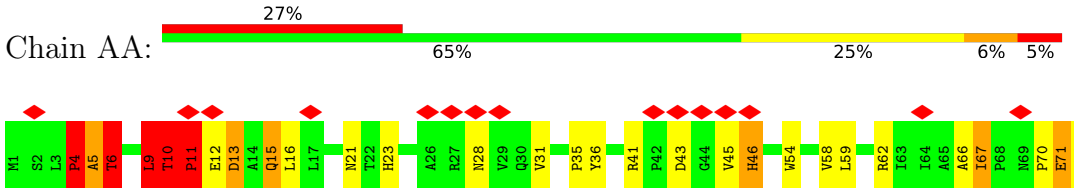
Chain Aa:

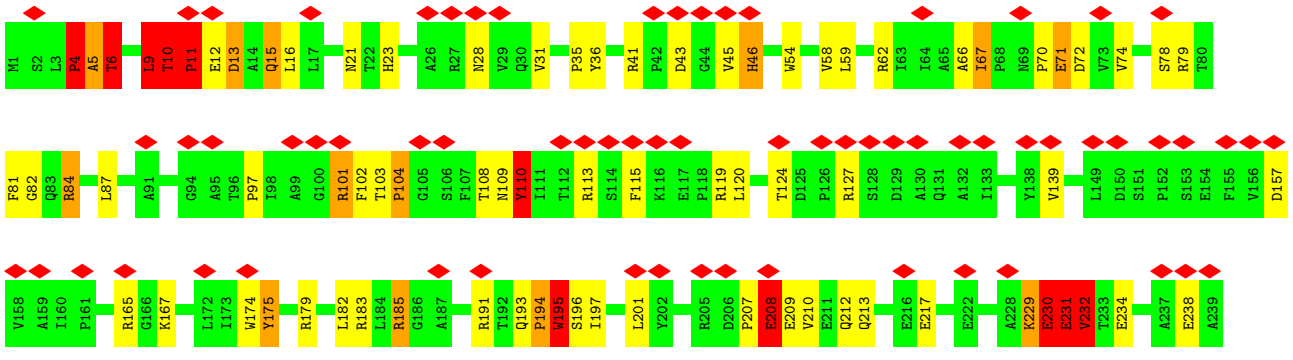


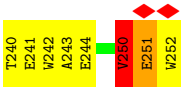


• Molecule 2: 40S ribosomal protein rpS0 (S2p)

Chain AA:

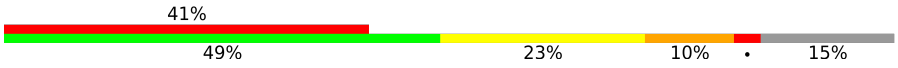


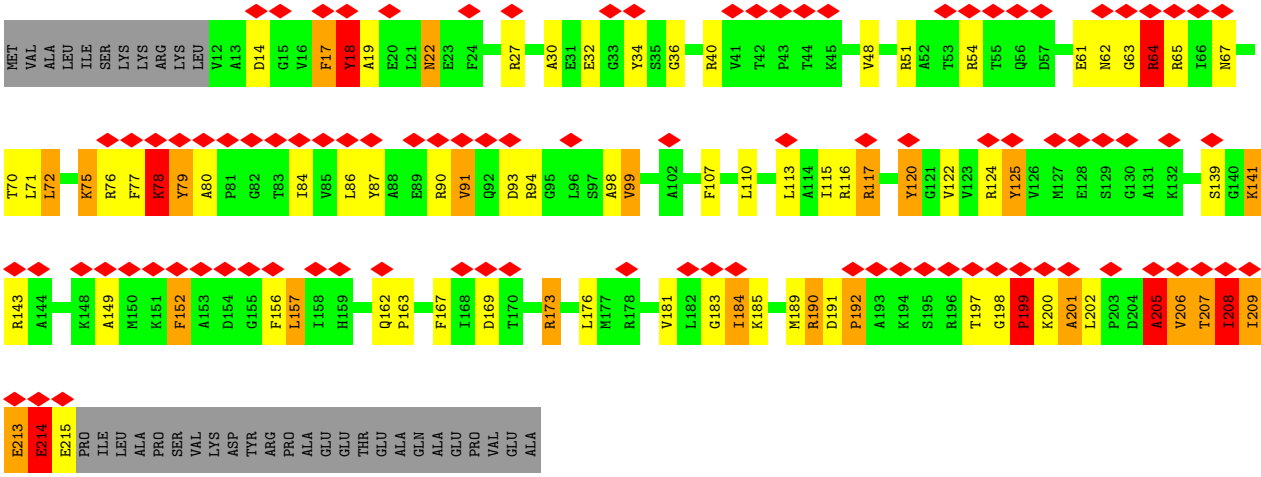




• Molecule 3: 40S ribosomal protein rpS3 (S3p)

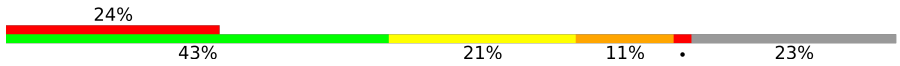
Chain AB:

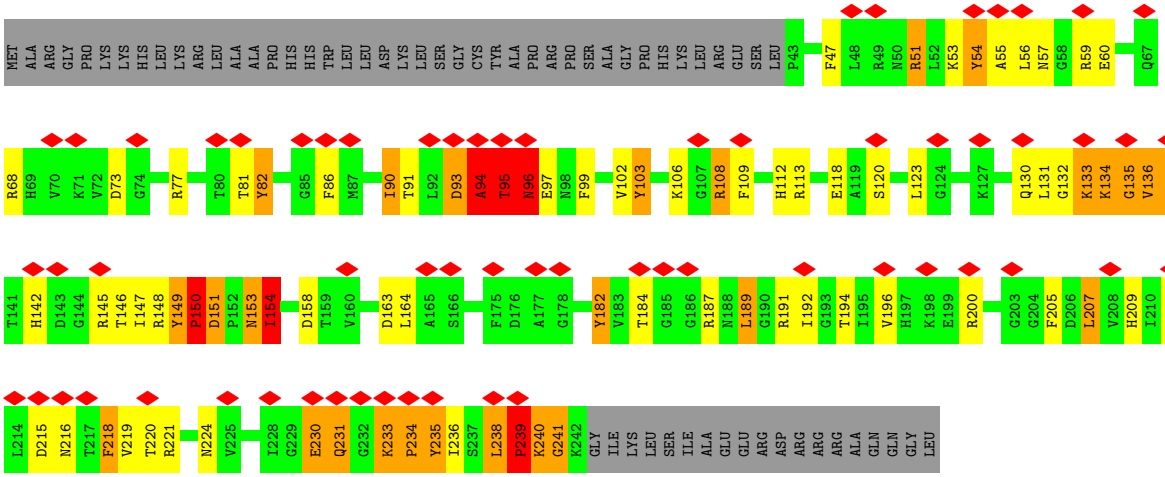




• Molecule 4: 40S ribosomal protein rpS4 (S4e)

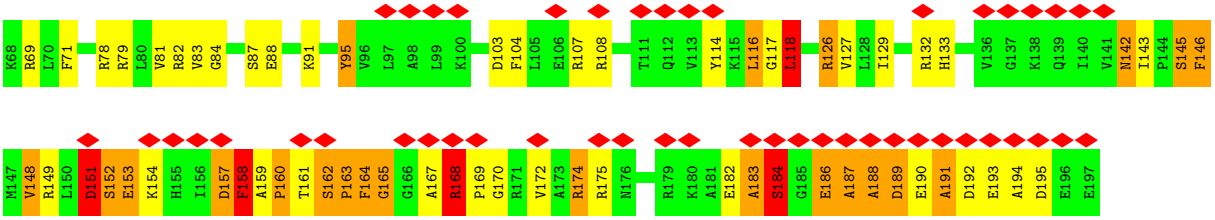
Chain AD:





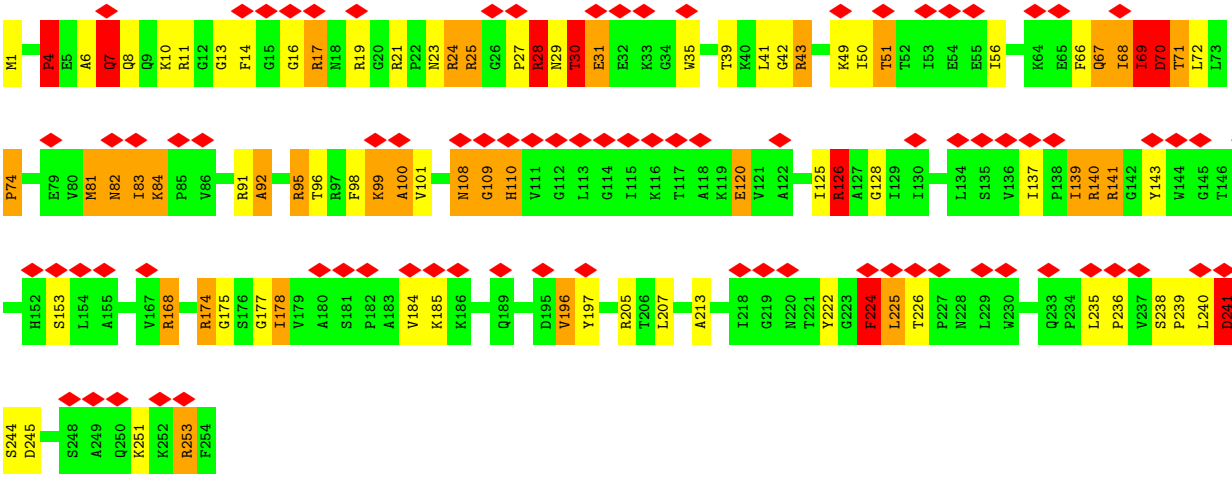
• Molecule 5: 40S ribosomal protein rpS9 (S4p)

Chain AC:



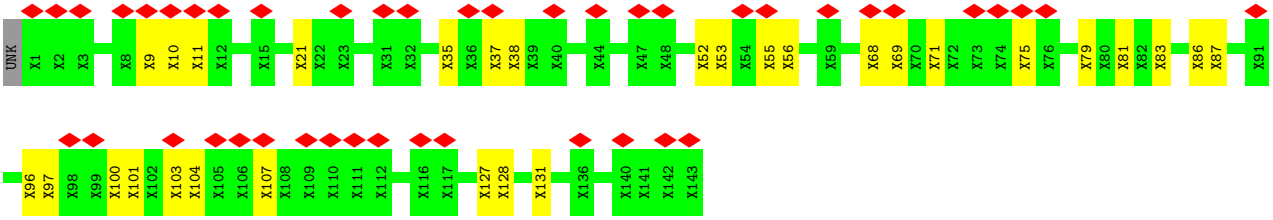
• Molecule 6: 40S ribosomal protein rpS2 (S5p)

Chain AE:



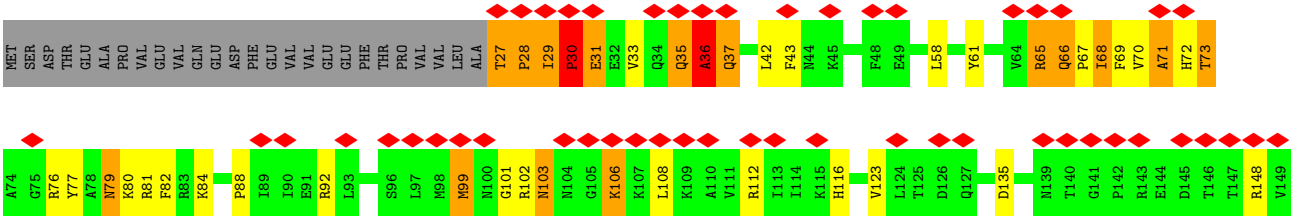
• Molecule 7: 40S ribosomal protein rpS7 (S7e)

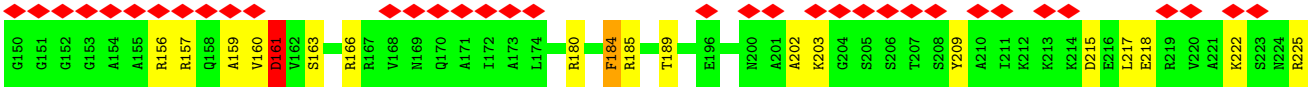
Chain AG:



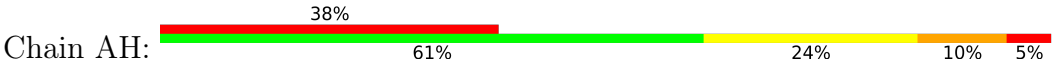
• Molecule 8: 40S ribosomal protein rpS5 (S7p)

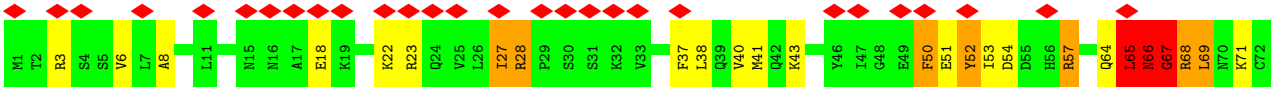
Chain AF:

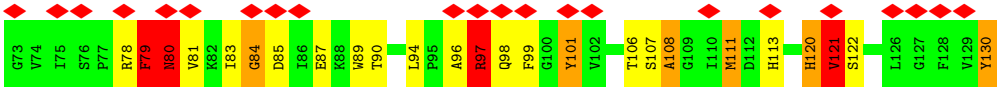




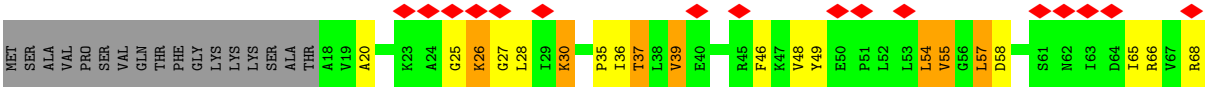
• Molecule 9: 40S ribosomal protein rpS22 (S8p)

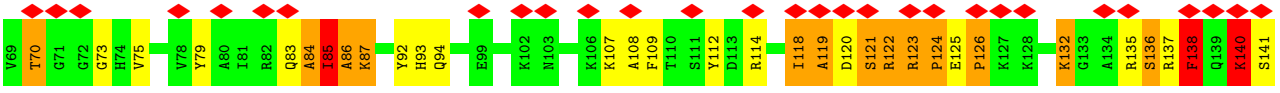




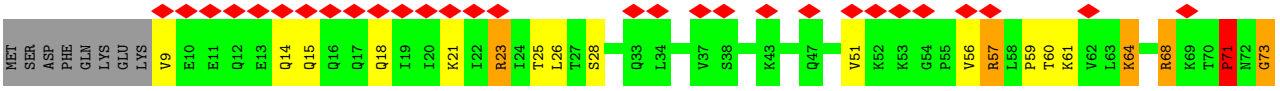


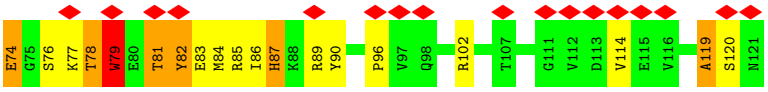
• Molecule 10: 40S ribosomal protein rpS16 (S9p)



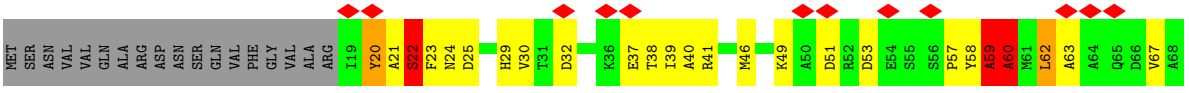


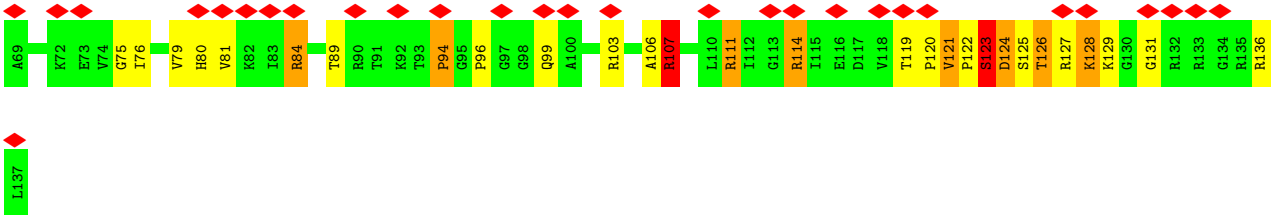
• Molecule 11: 40S ribosomal protein rpS20 (S10p)





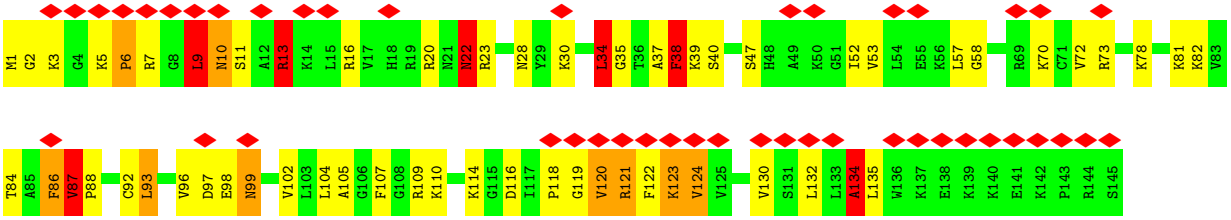
• Molecule 12: 40S ribosomal protein rpS14 (S11p)





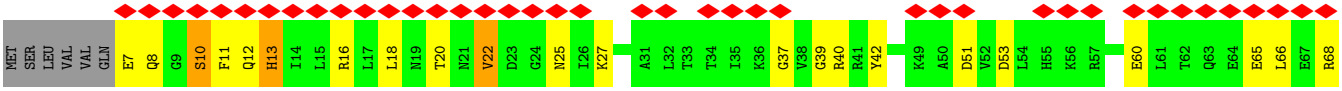
• Molecule 13: 40S ribosomal protein rpS23 (S12p)

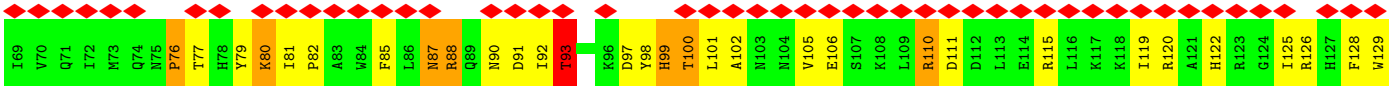
Chain AL:

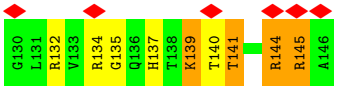


• Molecule 14: 40S ribosomal protein rpS18 (S13p)

Chain AM:

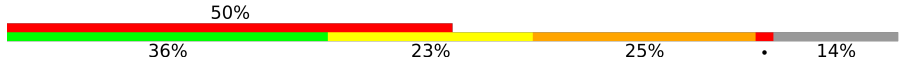


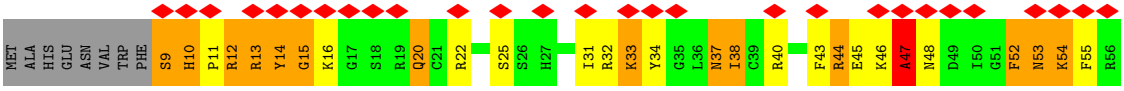




• Molecule 15: 40S ribosomal protein rpS29 (S14p)

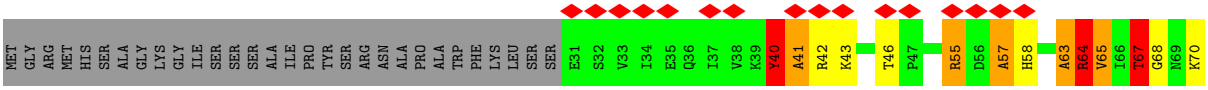
Chain AN:

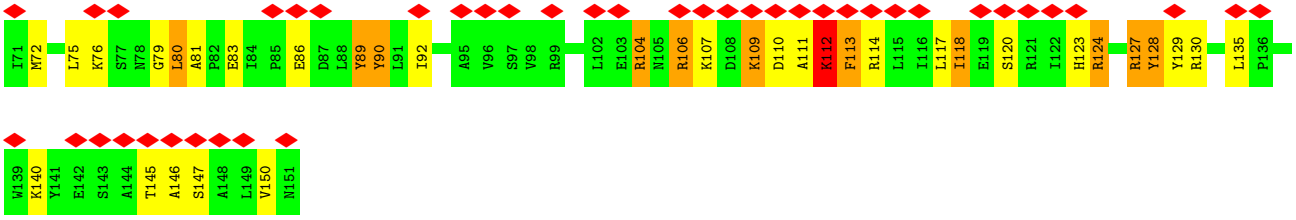




• Molecule 16: 40S ribosomal protein rpS13 (S15p)

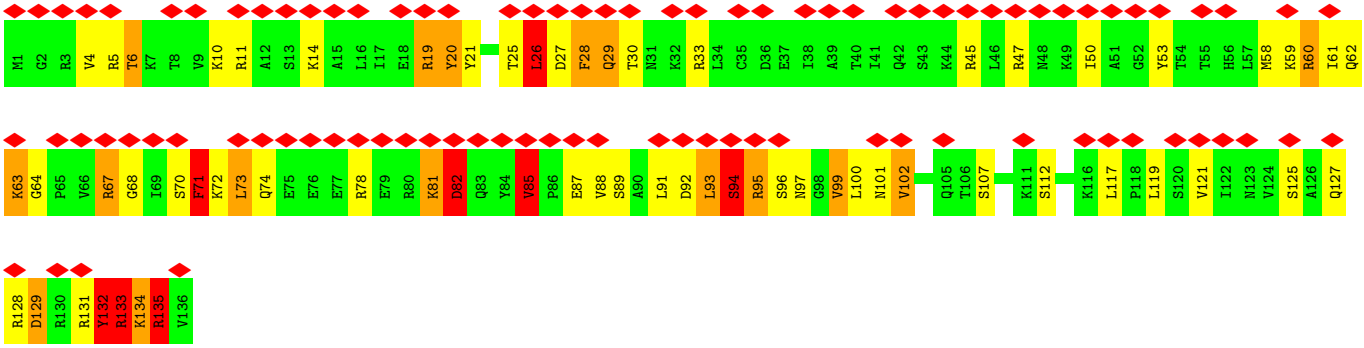
Chain AO:





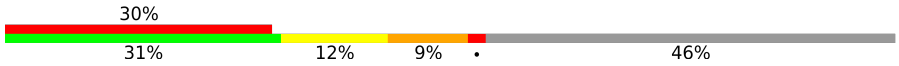
• Molecule 17: 40S ribosomal protein rpS17 (S17e)

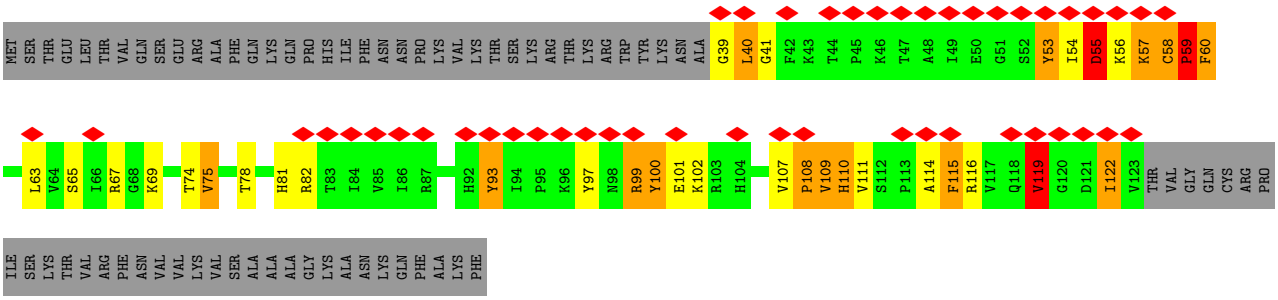
Chain AQ:



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

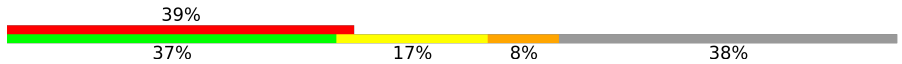
Chain AP:

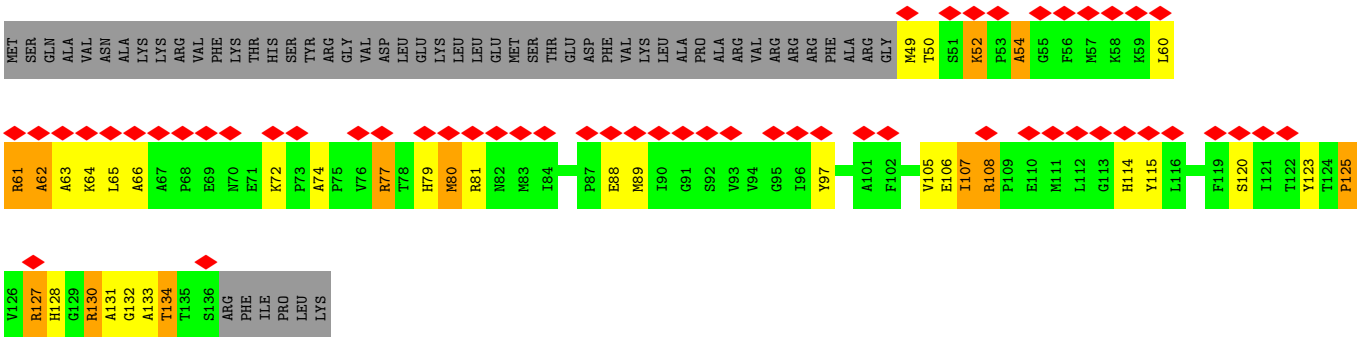




• Molecule 19: 40S ribosomal protein rpS15 (S19p)

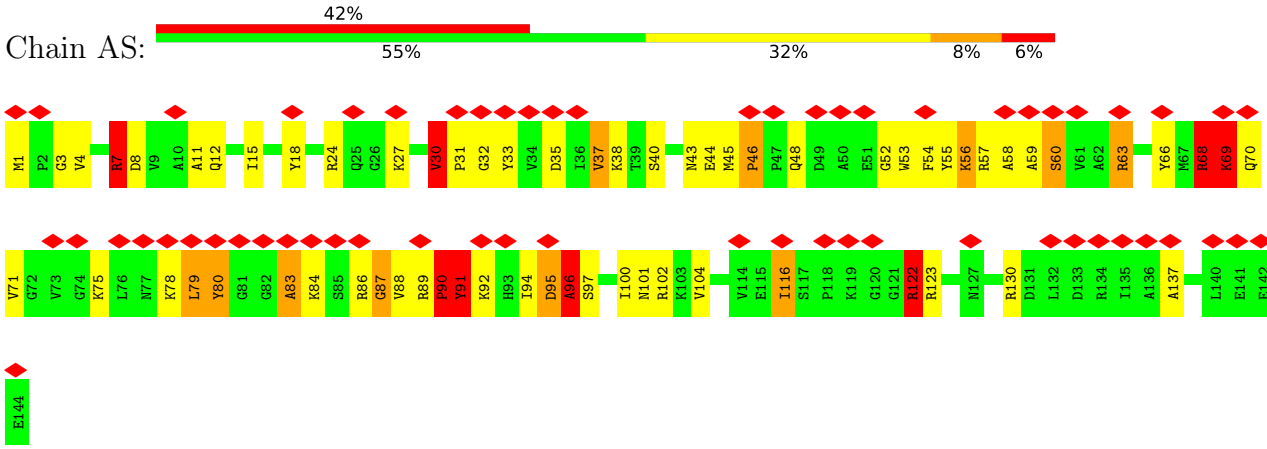
Chain AR:





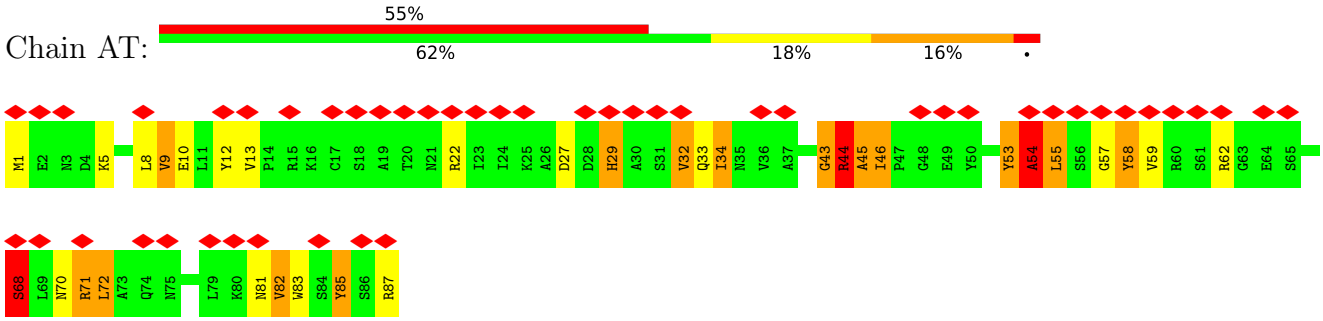
• Molecule 20: 40S ribosomal protein rpS19 (S19e)

Chain AS:



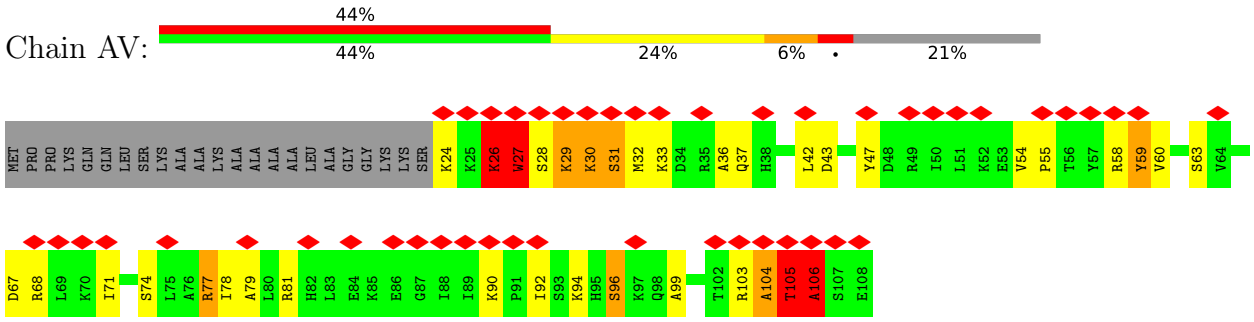
• Molecule 21: 40S ribosomal protein rpS21 (S21e)

Chain AT:



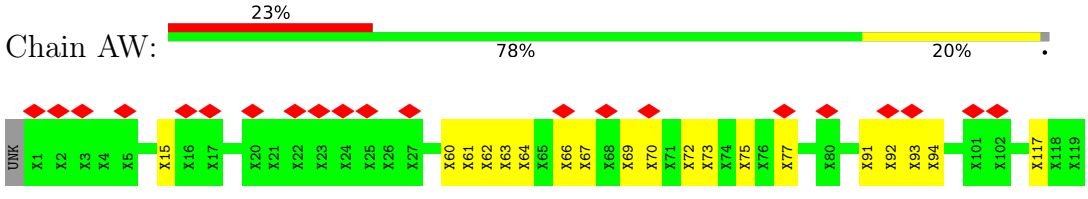
• Molecule 22: 40S ribosomal protein rpS25 (S25e)

Chain AV:



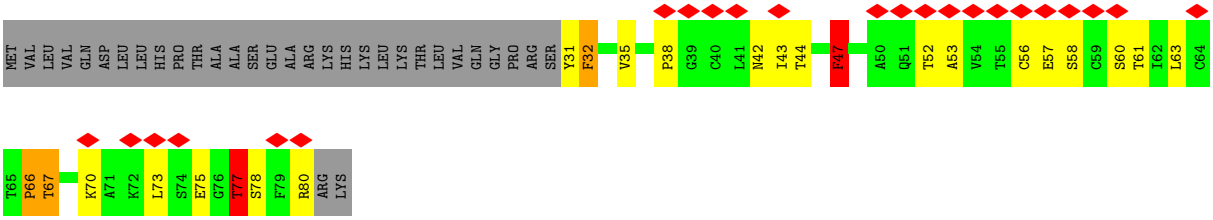
• Molecule 23: 40S ribosomal protein rpS26 (S26e)

Chain AW:



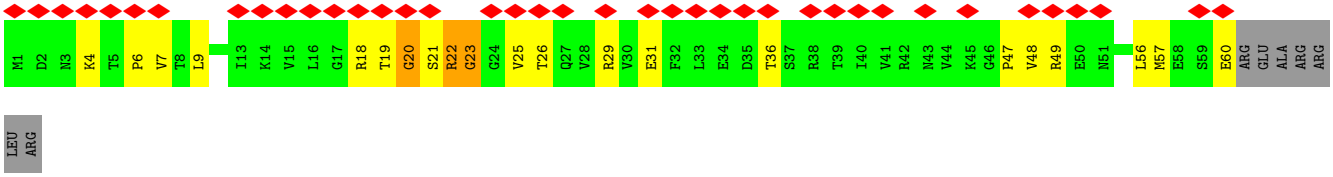
• Molecule 24: 40S ribosomal protein rpS27 (S27e)

Chain AX:



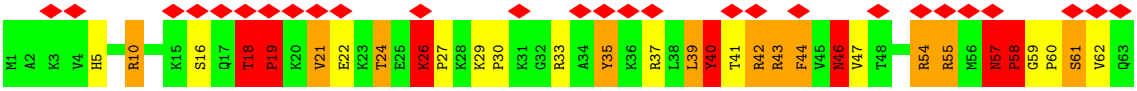
• Molecule 25: 40S ribosomal protein rpS28 (S28e)

Chain AY:



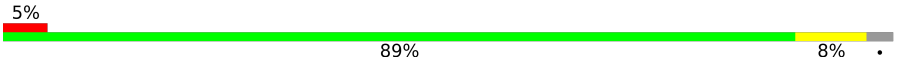
• Molecule 26: 40S ribosomal protein rpS30 (S30e)

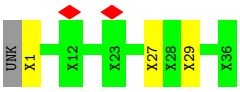
Chain AZ:



• Molecule 27: Unknown 40S ribosomal protein XS1

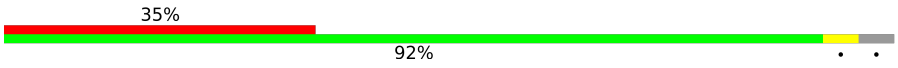
Chain Ab:

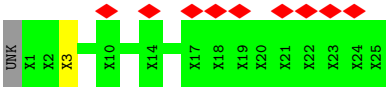




• Molecule 28: Unknown 40S ribosomal protein XS2

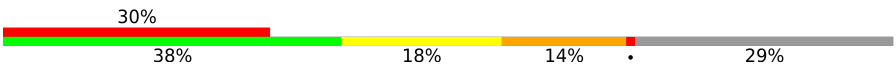
Chain Ac:

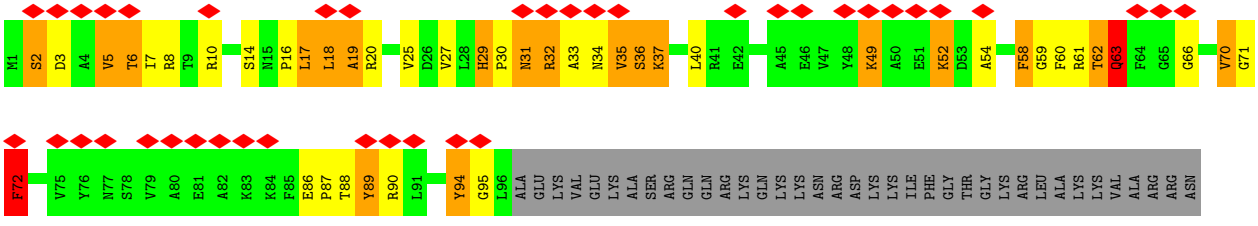




• Molecule 29: 40S ribosomal protein S24

Chain AU:

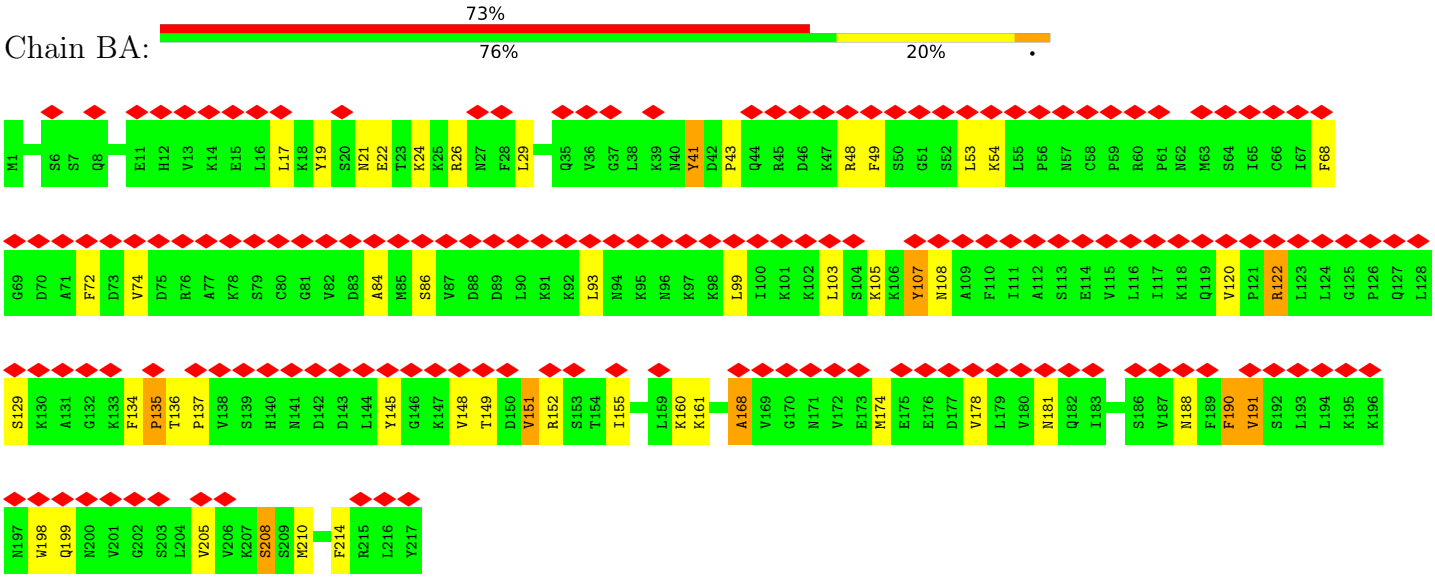




ALA
ASP

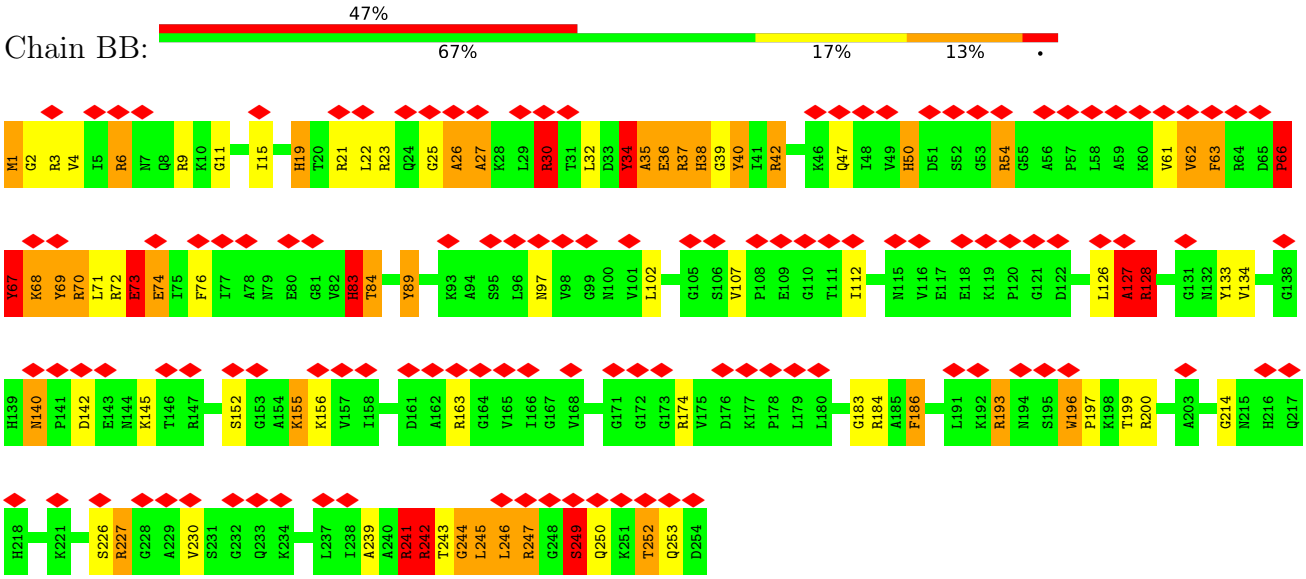
• Molecule 30: 60S ribosomal protein rpL1 (L1p)

Chain BA:



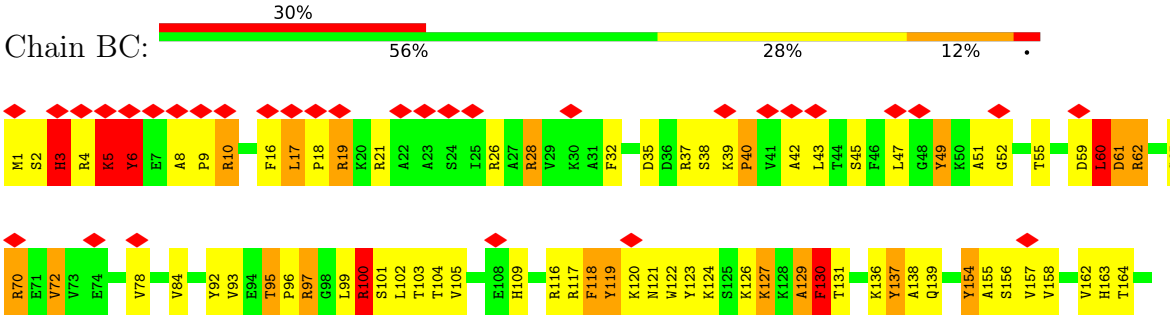
• Molecule 31: 60S ribosomal protein rpL2 (L2p)

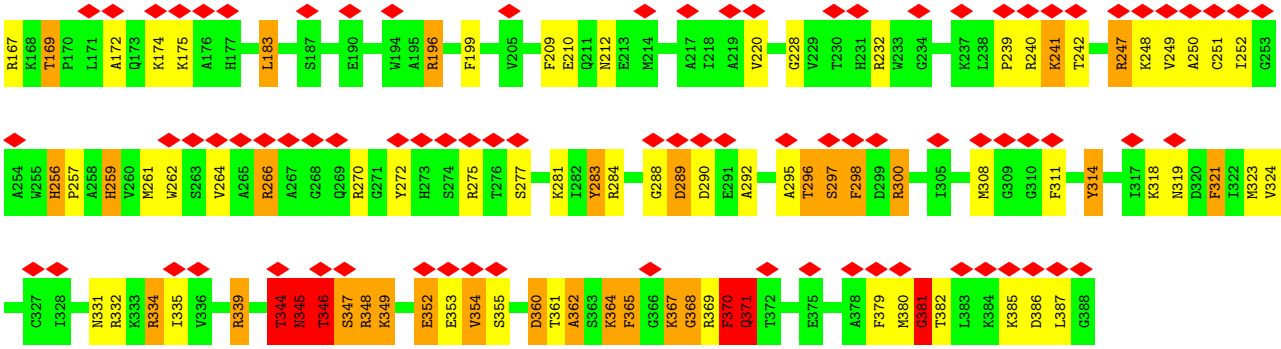
Chain BB:



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

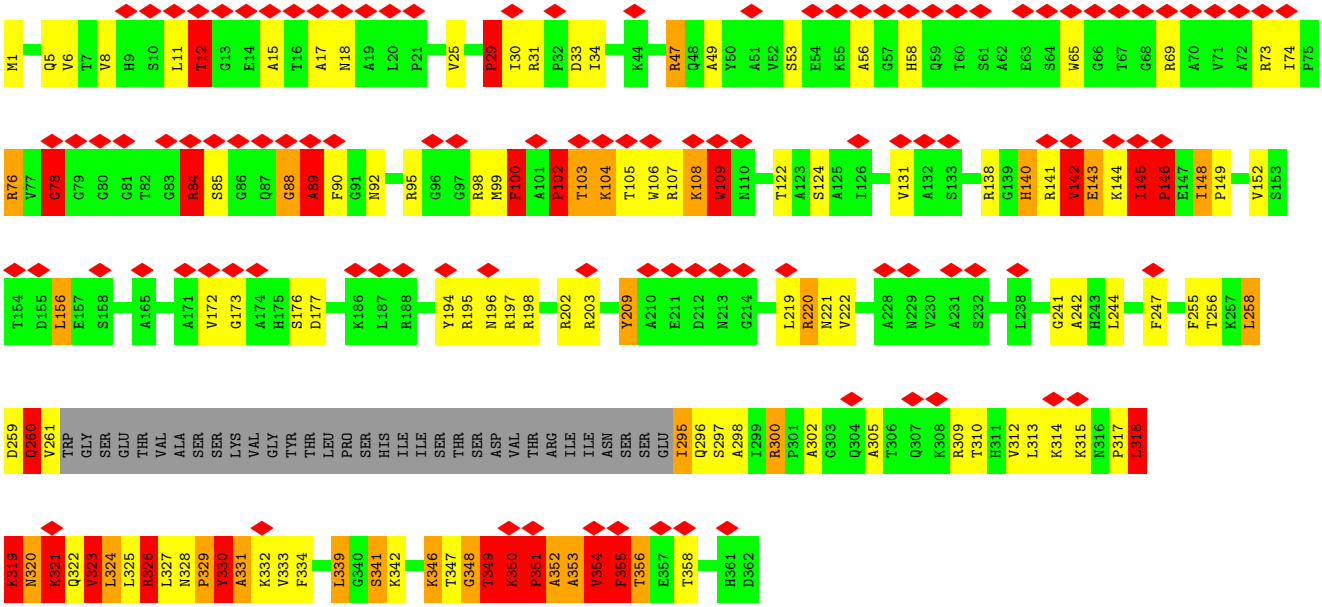
Chain BC:





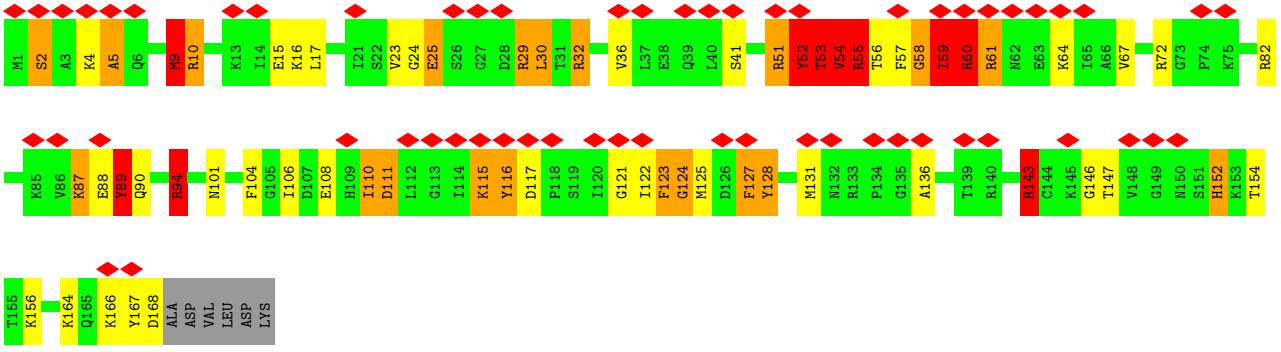
• Molecule 33: 60S ribosomal protein rpL4 (L4p)

Chain BD:



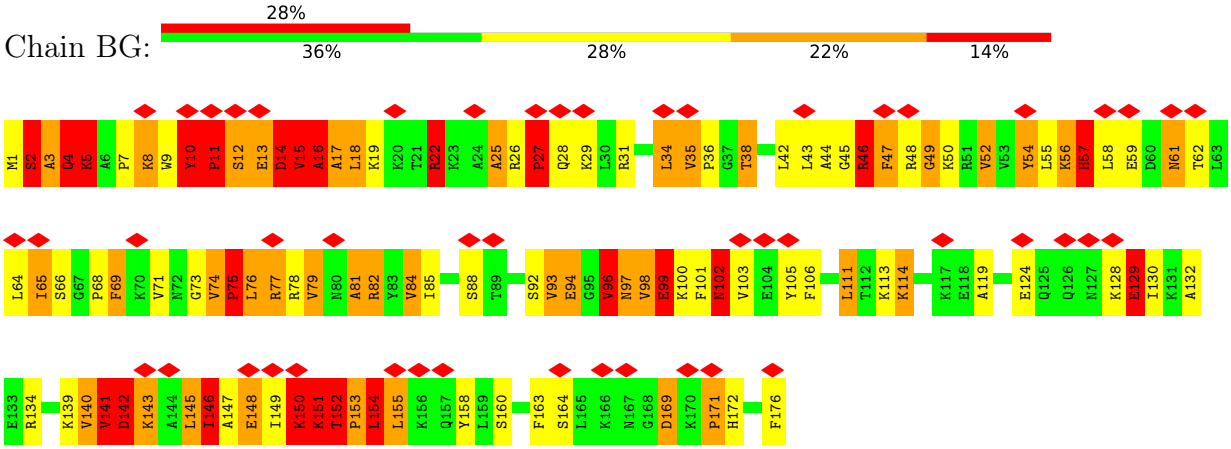
• Molecule 34: 60S ribosomal protein rpL11 (L5p)

Chain BE:



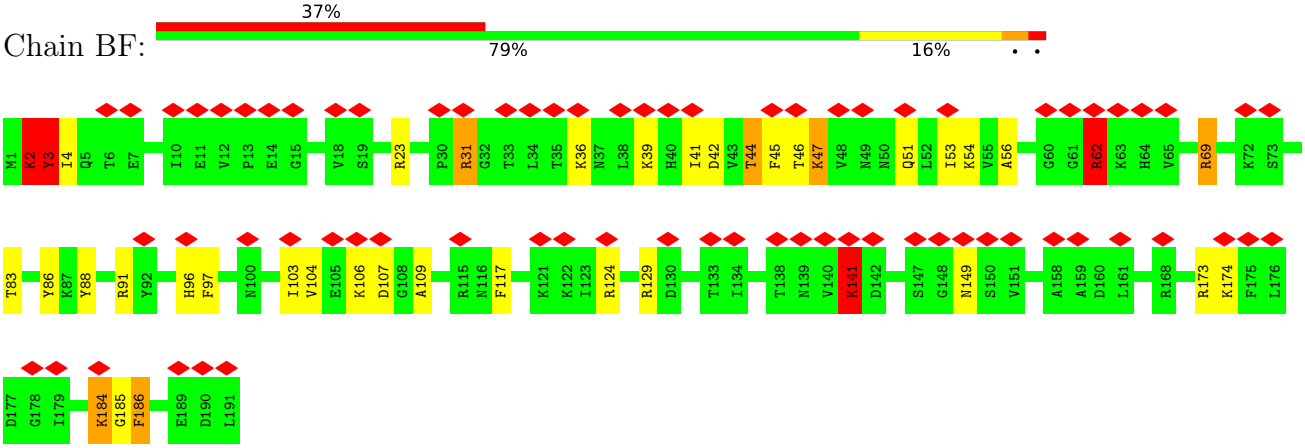
• Molecule 35: 60S ribosomal protein rpL6 (L6e)

Chain BG:



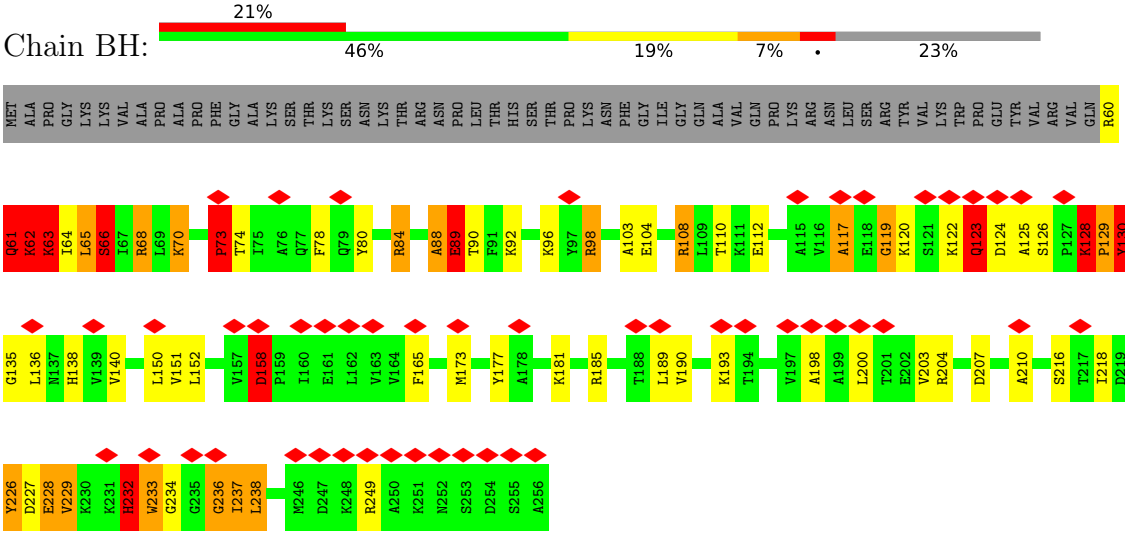
• Molecule 36: 60S ribosomal protein rpL9 (L6p)

Chain BF:



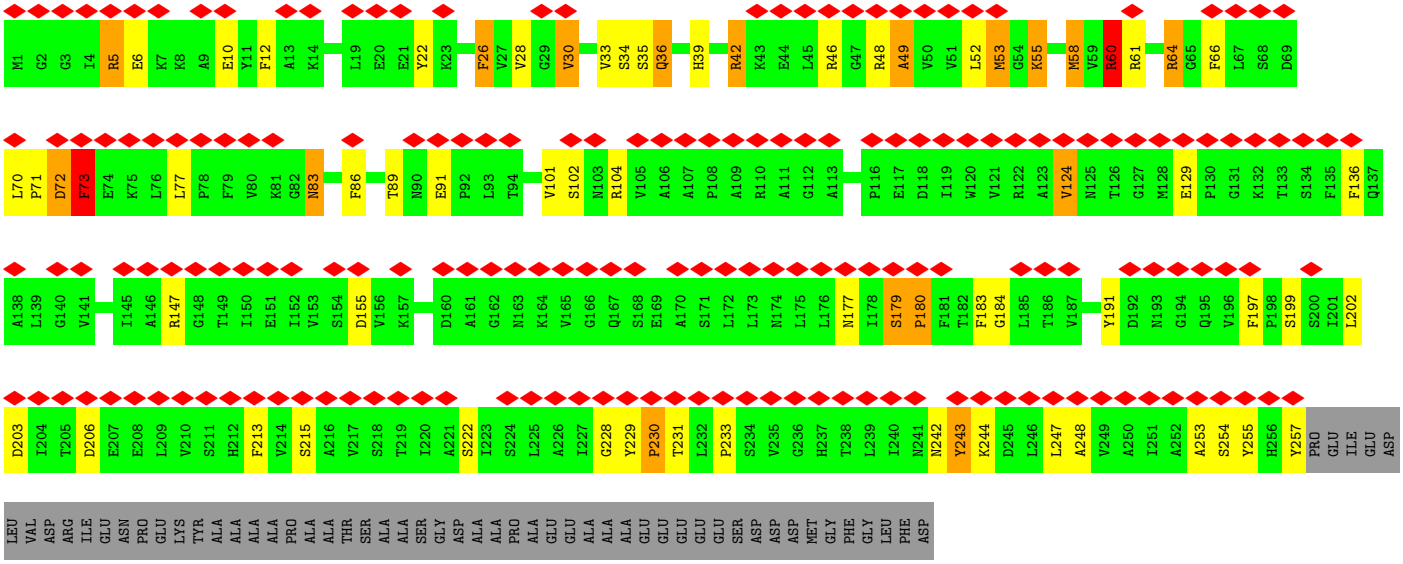
• Molecule 37: 60S ribosomal protein rpL8 (L7ae)

Chain BH:



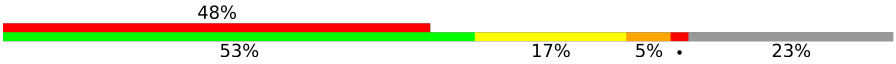
• Molecule 38: 60S acidic ribosomal protein rpP0 (L10P)

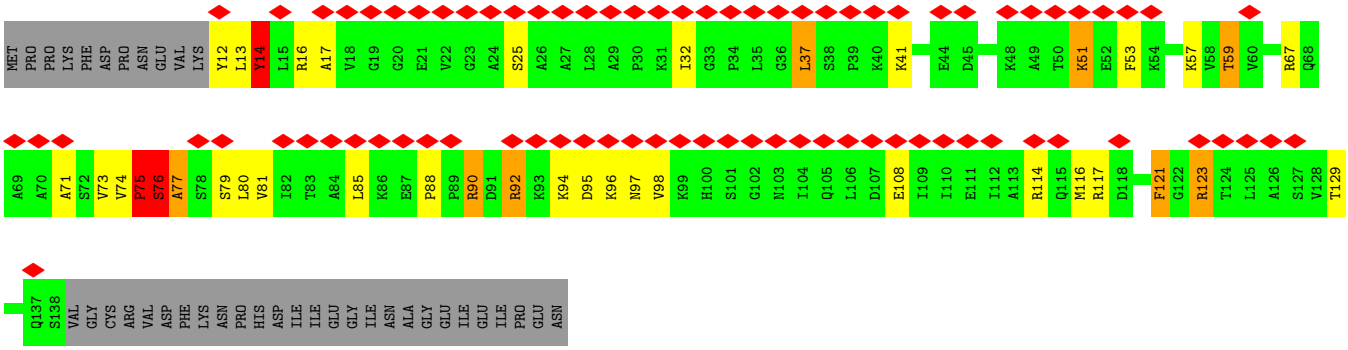
Chain Bs:



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

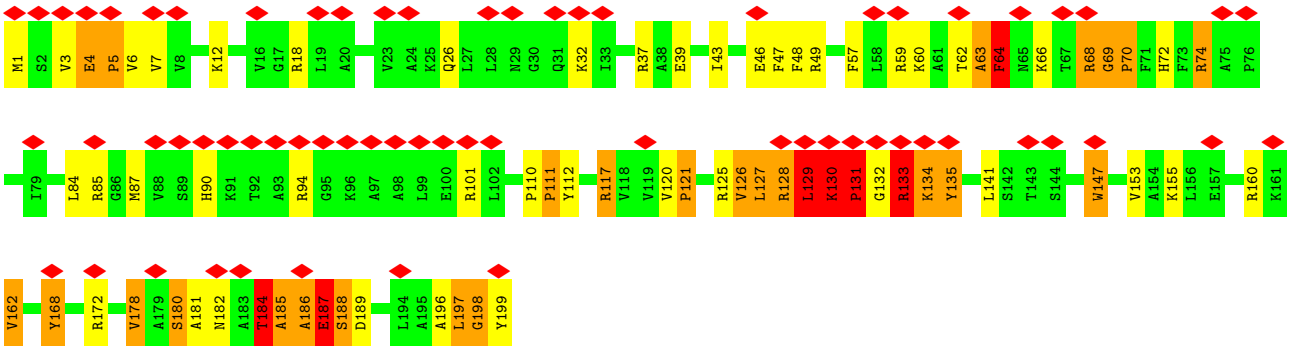
Chain BJ:





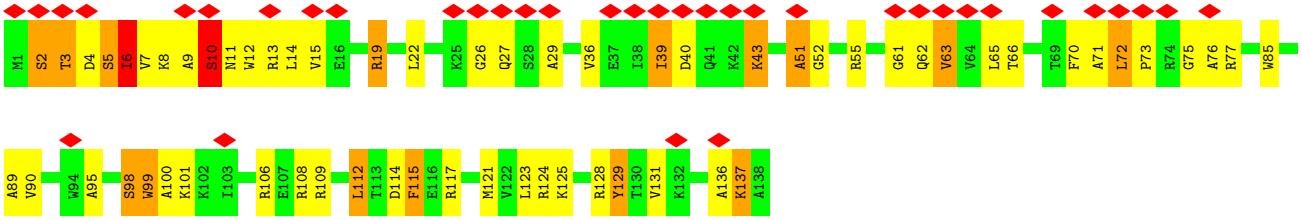
• Molecule 40: 60S ribosomal protein rpL16 (L13p)

Chain BK:



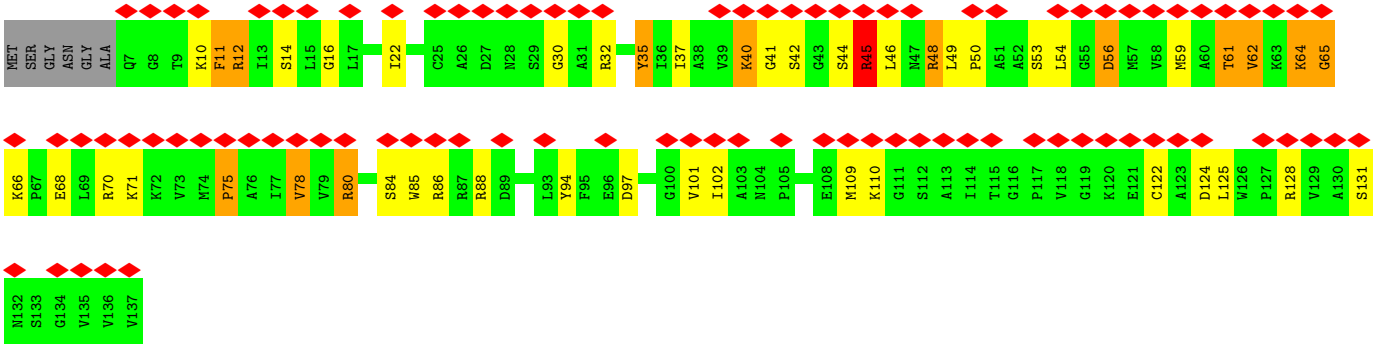
• Molecule 41: 60S ribosomal protein rpL14 (L14e)

Chain BN:



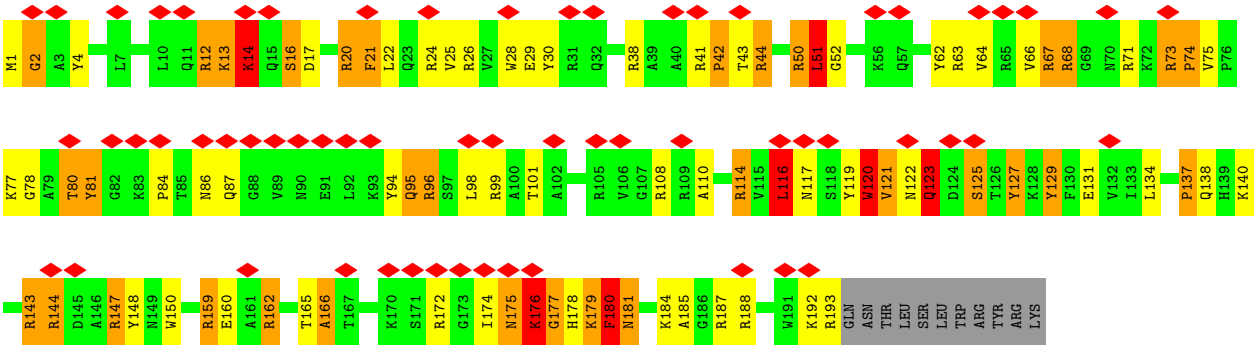
• Molecule 42: 60S ribosomal protein rpL23 (L14p)

Chain BM:



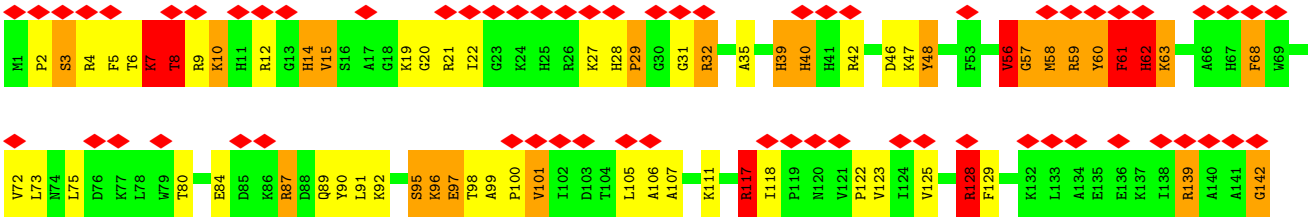
• Molecule 43: 60S ribosomal protein rpL15 (L15e)

Chain BP:



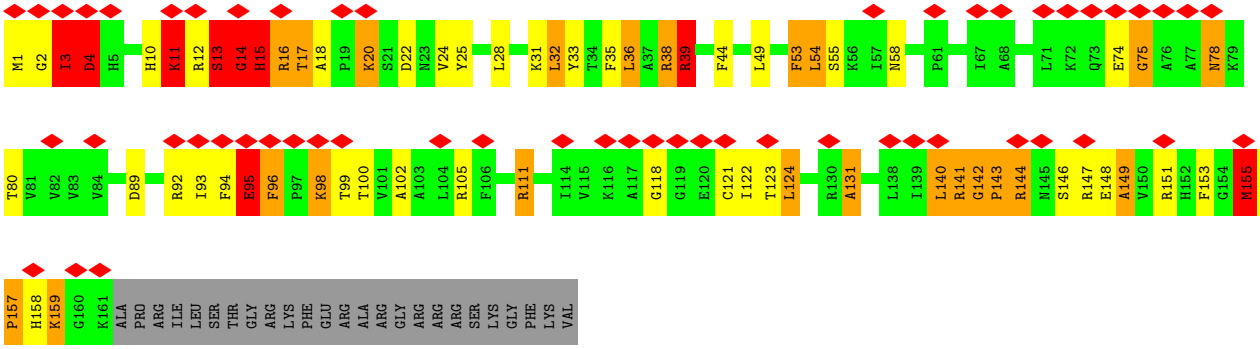
• Molecule 44: 60S ribosomal protein rpL28 (L15p)

Chain BO:



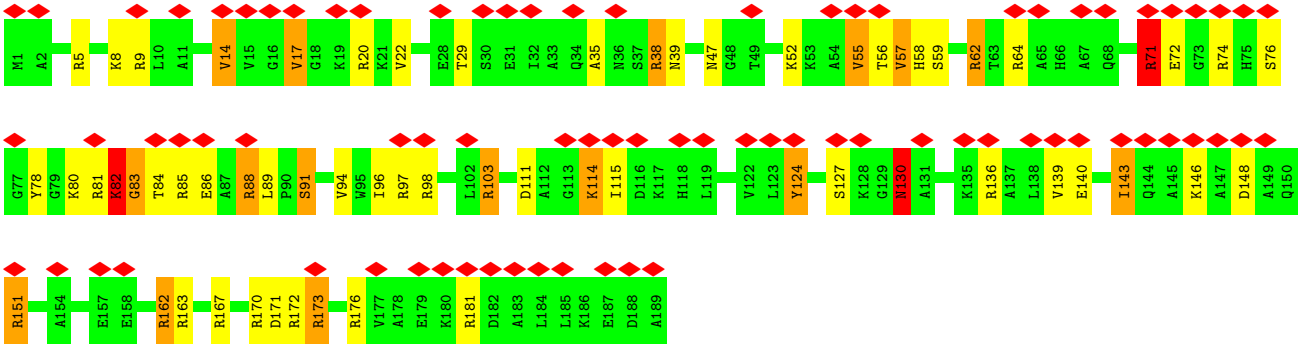
• Molecule 45: 60S ribosomal protein rpL18 (L18e)

Chain BR:



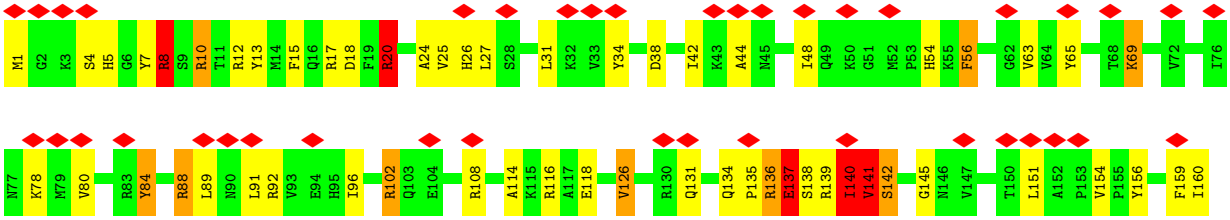
• Molecule 46: 60S ribosomal protein rpL19 (L19e)

Chain BT:



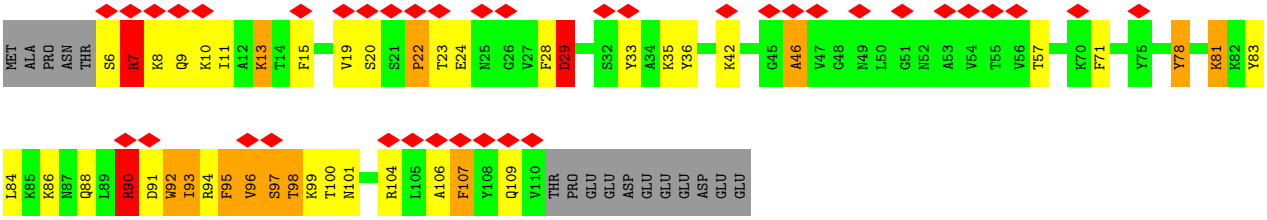
• Molecule 47: 60S ribosomal protein rpL21 (L21e)

Chain BU:



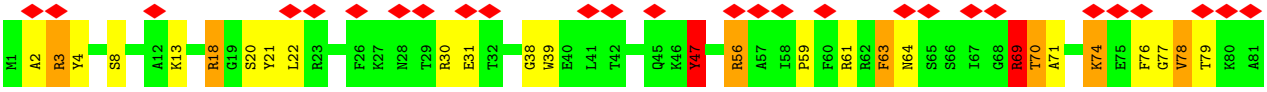
• Molecule 48: 60S ribosomal protein rpL22 (L22e)

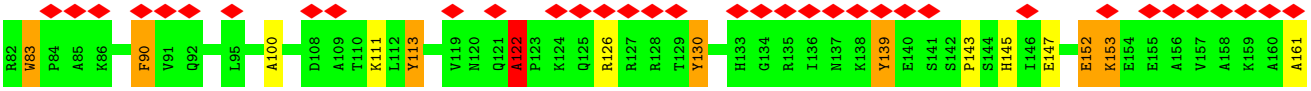
Chain BW:

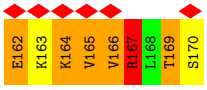


• Molecule 49: 60S ribosomal protein rpL17 (L22p)

Chain BV:

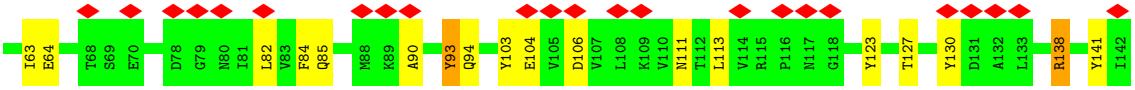






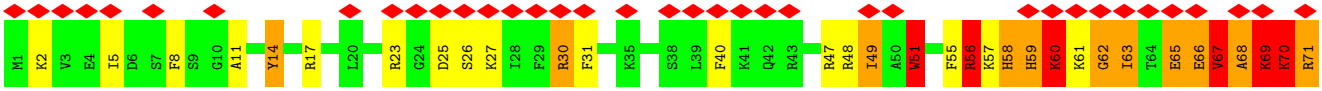
• Molecule 50: 60S ribosomal protein rpL25 (L23p)

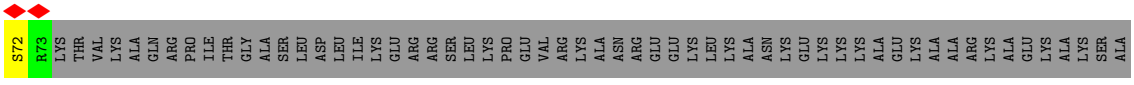
Chain BX:

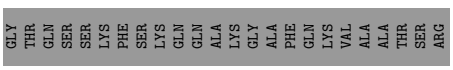


• Molecule 51: 60S ribosomal protein rpL24 (L24e)

Chain BZ:

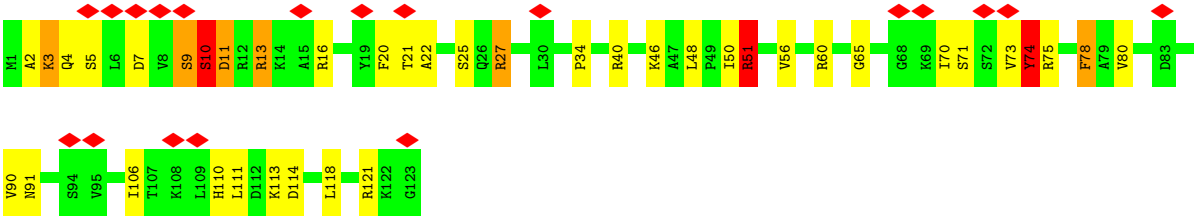






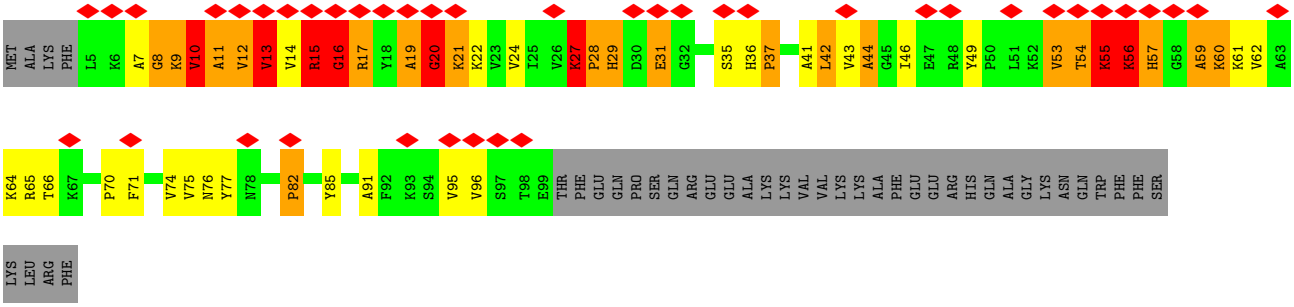
• Molecule 52: 60S ribosomal protein rpL26 (L24p)

Chain BY:



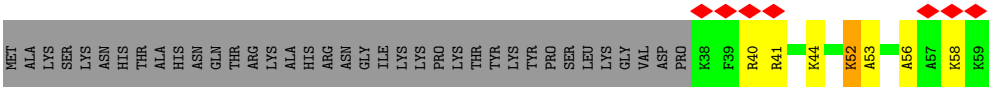
• Molecule 53: 60S ribosomal protein rpL27 (L27e)

Chain Ba:



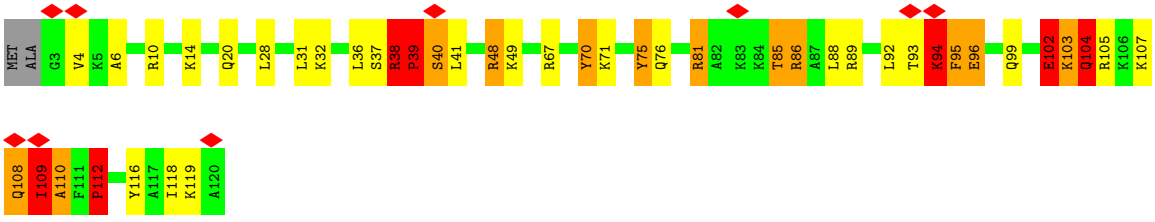
• Molecule 54: 60S ribosomal protein rpL29 (L29e)

Chain Bd:



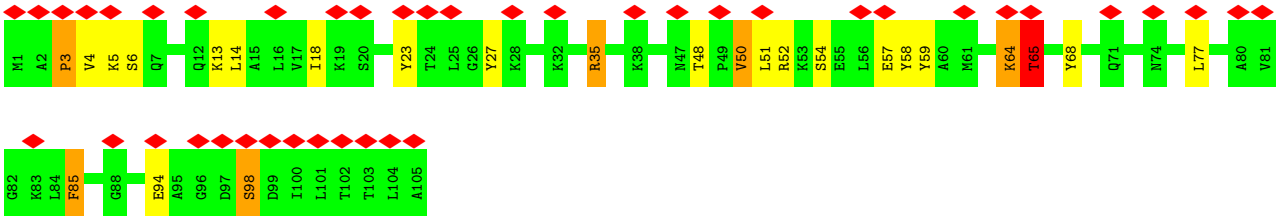
• Molecule 55: 60S ribosomal protein rpL35 (L29p)

Chain Bc:



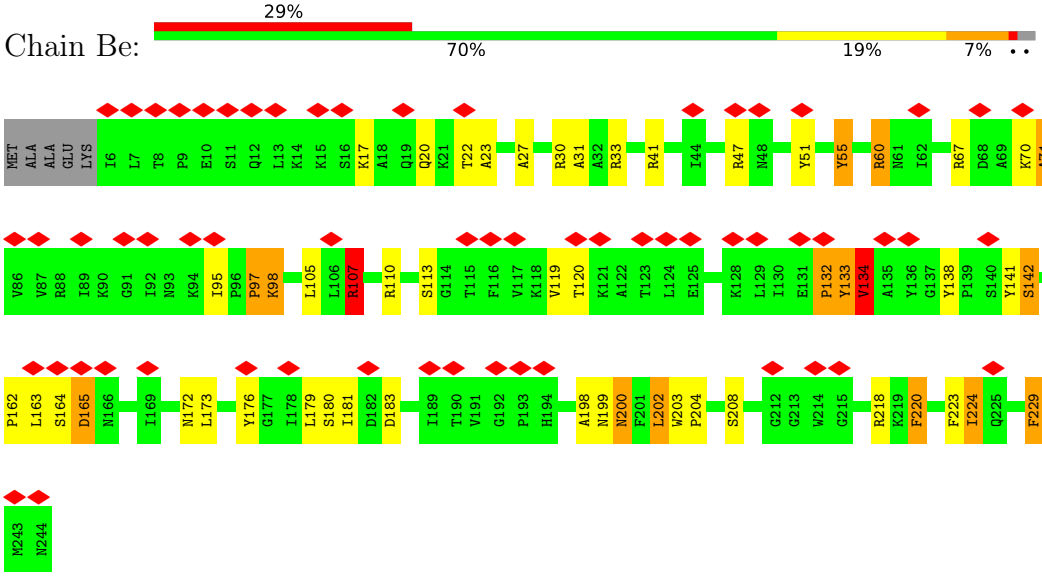
• Molecule 56: 60S ribosomal protein rpL30 (L30e)

Chain Bf:



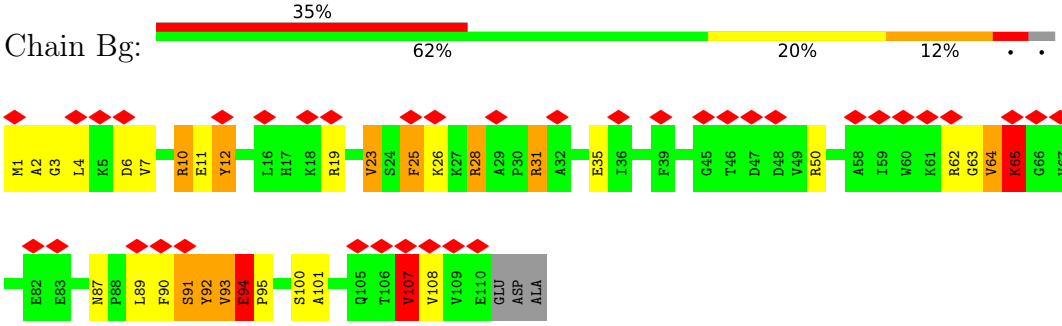
• Molecule 57: 60S ribosomal protein rpL7 (L30p)

Chain Be:



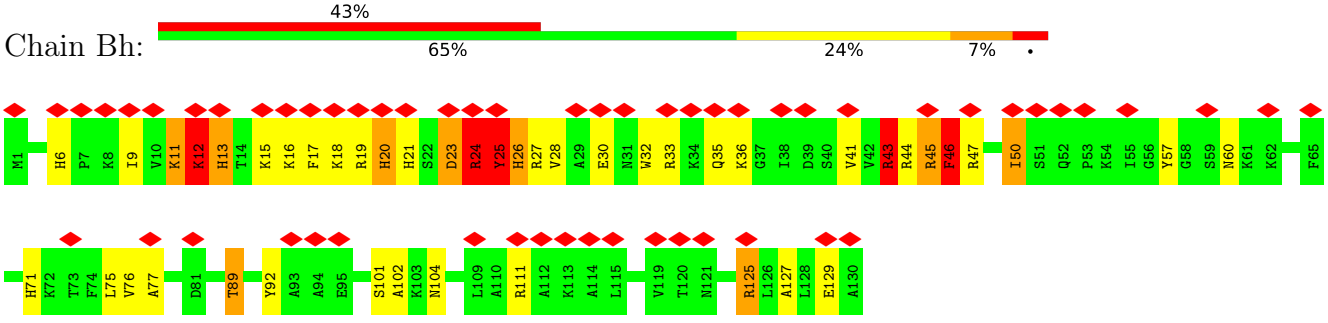
• Molecule 58: 60S ribosomal protein rpL31 (L31e)

Chain Bg:



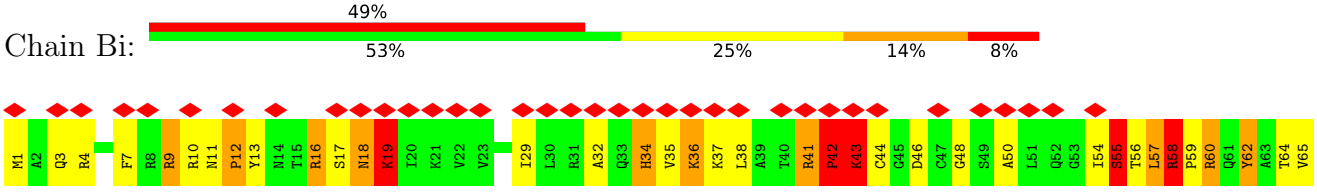
• Molecule 59: 60S ribosomal protein pL32 (L32e)

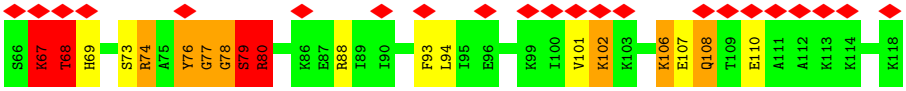
Chain Bh:



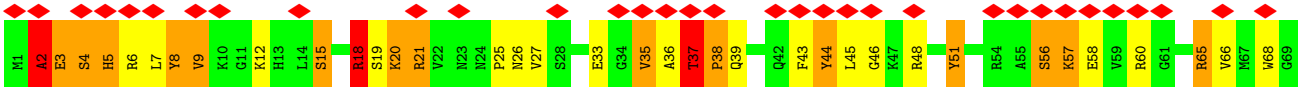
• Molecule 60: 60S ribosomal protein rpL34 (L34e)

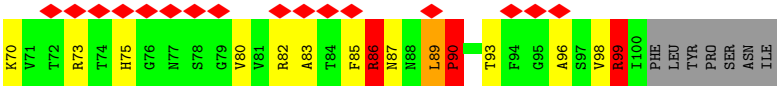
Chain Bi:



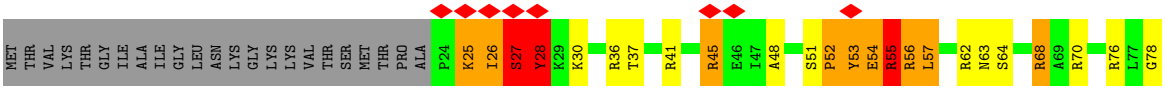


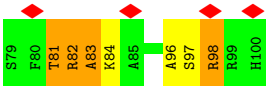
• Molecule 61: 60S ribosomal protein rpL33 (L35ae)



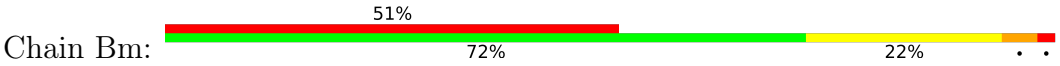


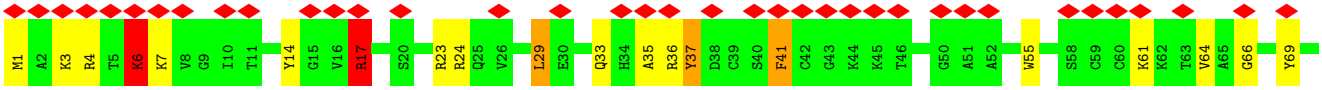
• Molecule 62: 60S ribosomal protein rpL36 (L36e)

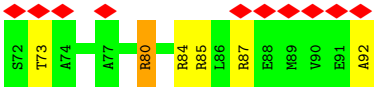




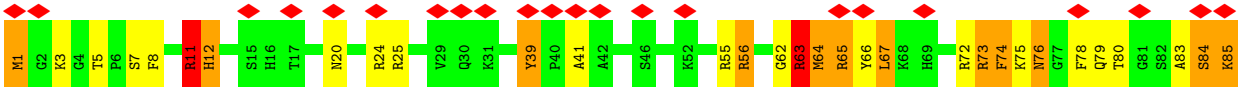
• Molecule 63: 60S ribosomal protein rpL43 (L37ae)





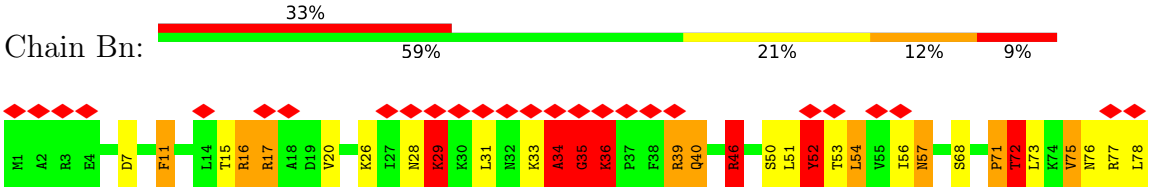


• Molecule 64: 60S ribosomal protein rpL37 (L37e)



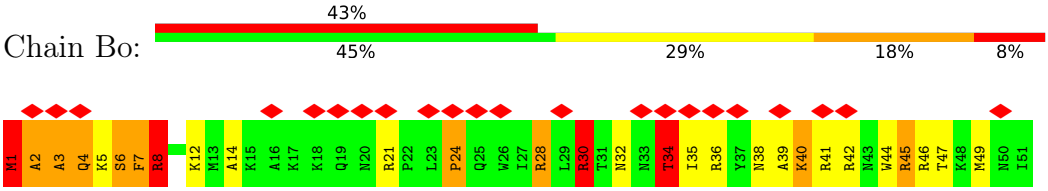
• Molecule 65: 60S ribosomal protein rpL38 (L38e)

Chain Bn:



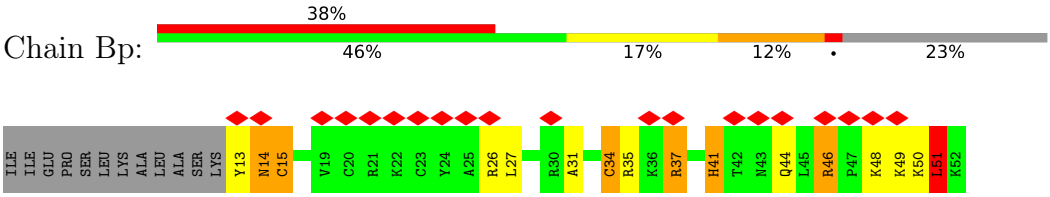
• Molecule 66: 60S ribosomal protein rpL39 (L39e)

Chain Bo:



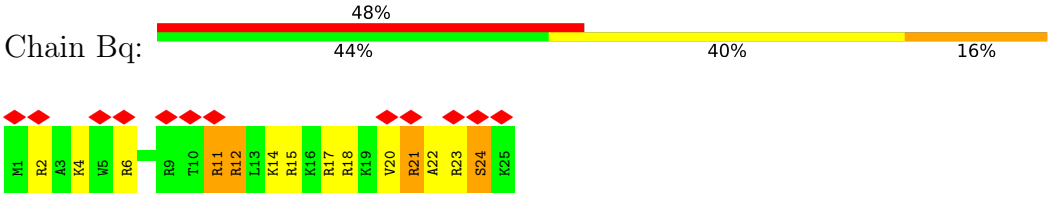
• Molecule 67: 60S ribosomal protein rpL40 (L40e)

Chain Bp:



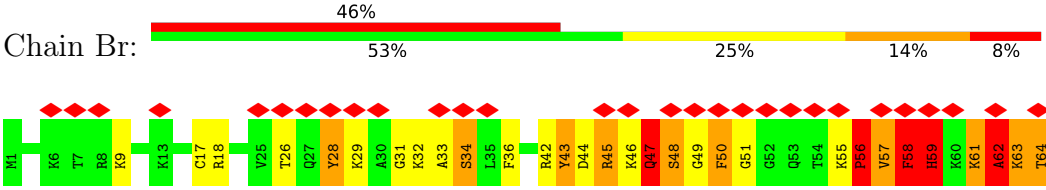
• Molecule 68: 60S ribosomal protein rpL41 (L41e)

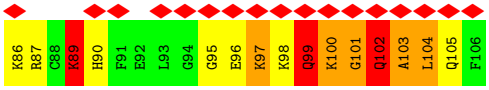
Chain Bq:



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

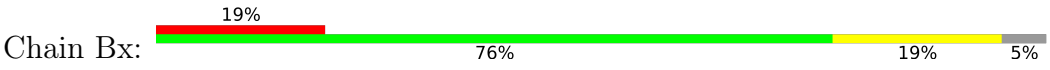
Chain Br:

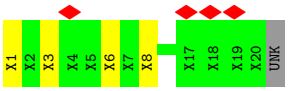




• Molecule 70: Unknown protein

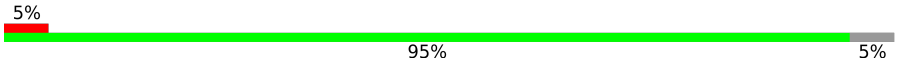
Chain Bx:





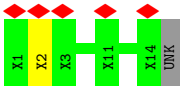
• Molecule 70: Unknown protein

Chain By:



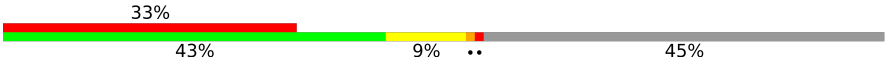
• Molecule 71: Unknown protein

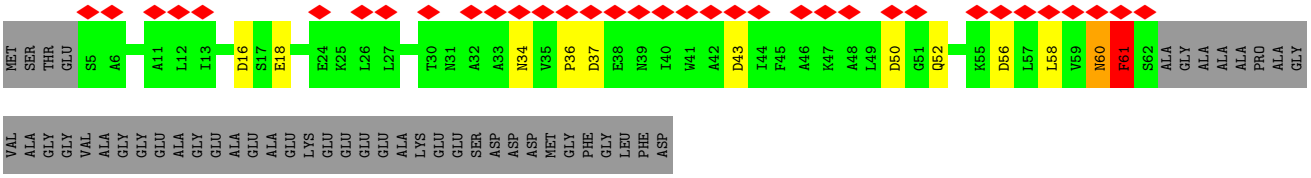
Chain Bz:



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

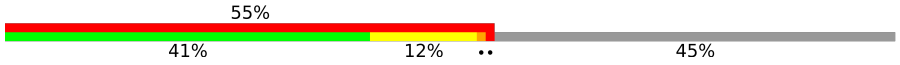
Chain Bt:

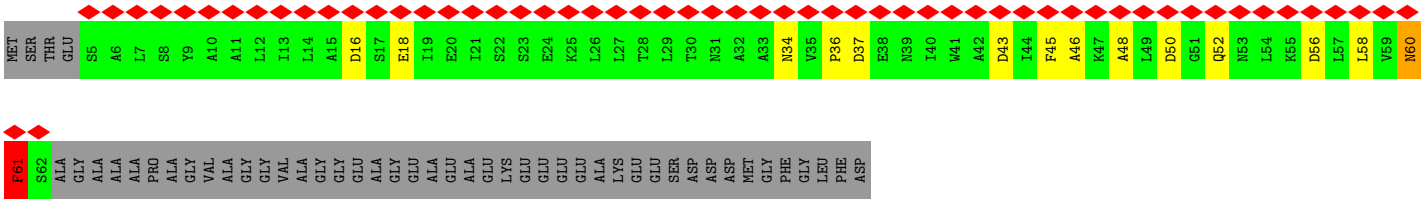




• Molecule 72: 60S acidic ribosomal protein rpP11 (P1)

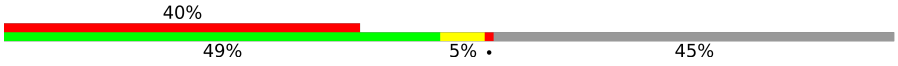
Chain Bu:

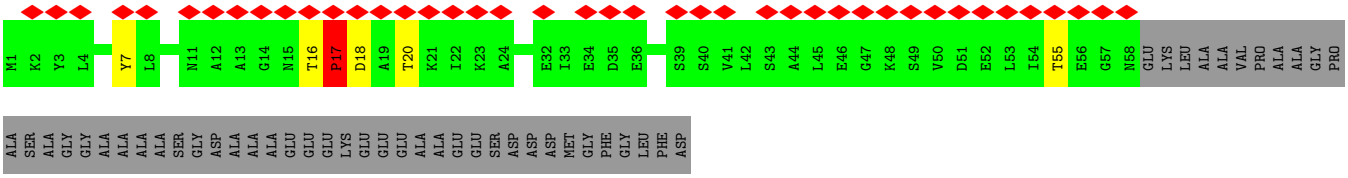




• Molecule 73: 60S acidic ribosomal protein (P2)

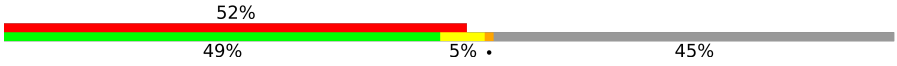
Chain Bv:

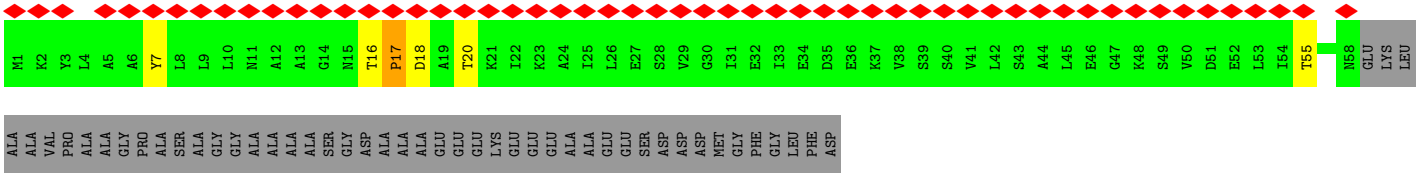




• Molecule 73: 60S acidic ribosomal protein (P2)

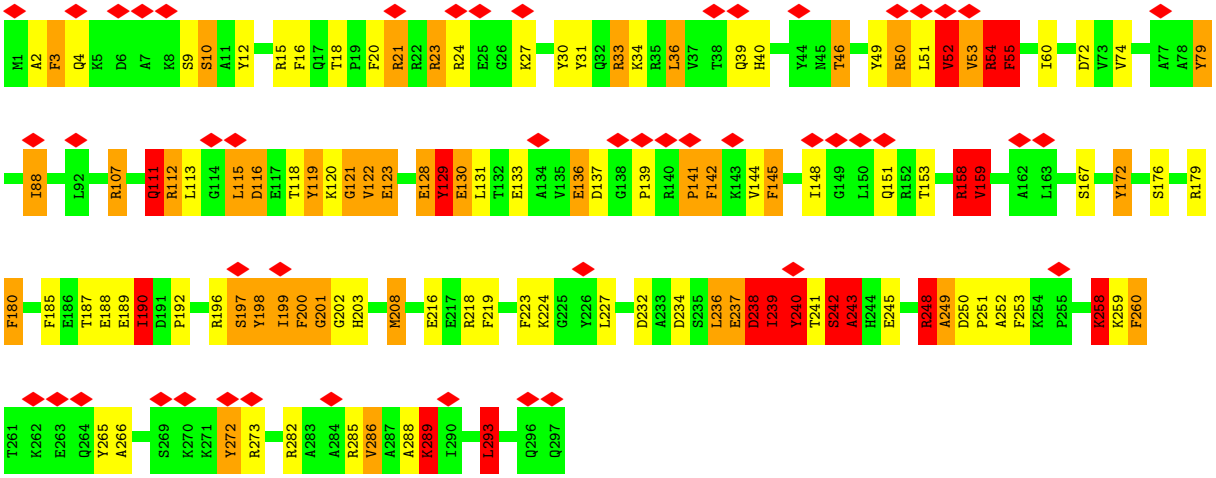
Chain Bw:





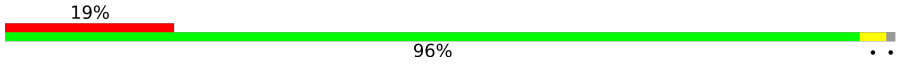
• Molecule 74: 60S ribosomal protein rpL5 (L18p)

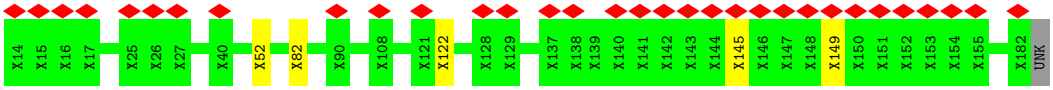
Chain BQ:



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

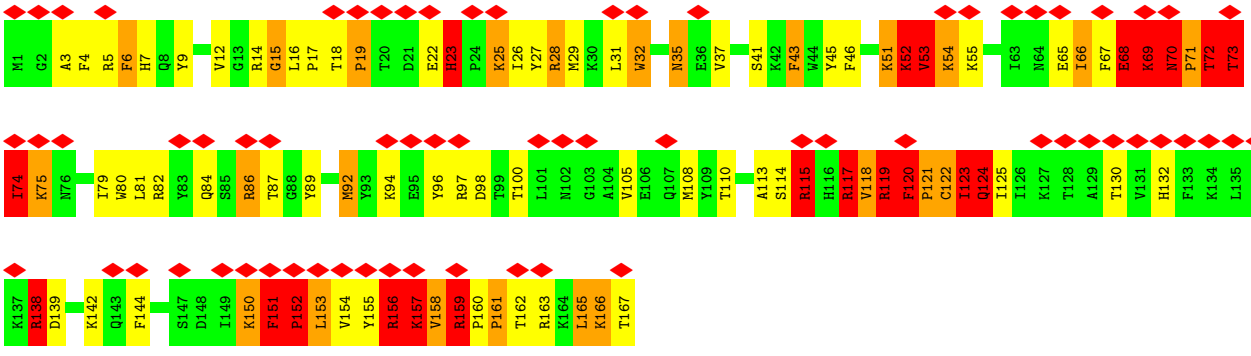
Chain BL:





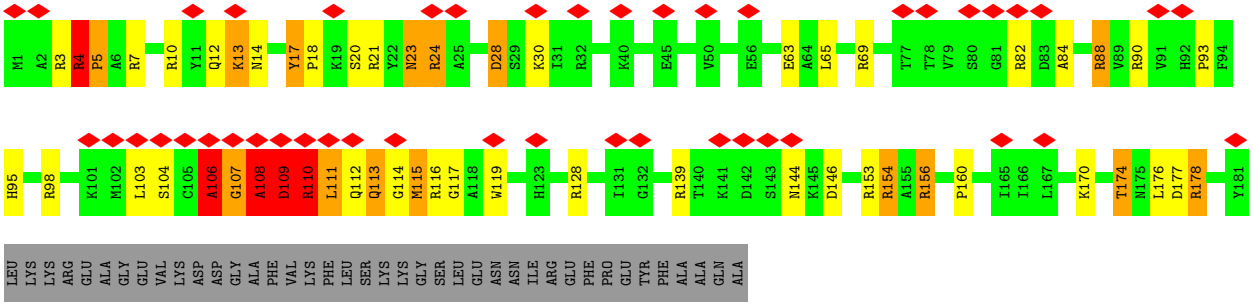
• Molecule 76: 60S ribosomal protein rpL20 (L18ae)

Chain BS:



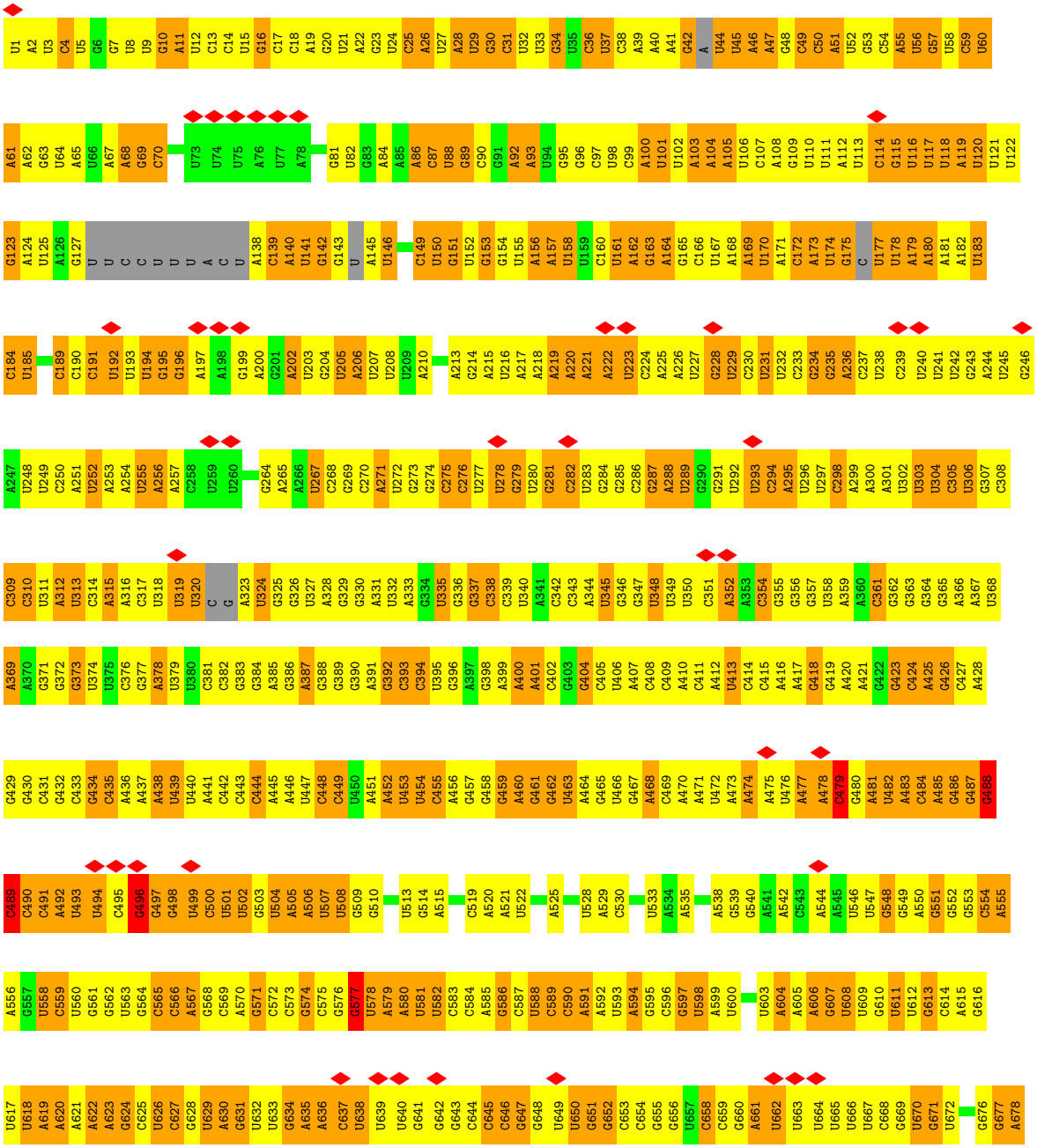
• Molecule 77: 60S ribosomal protein rpL10 (L10e)

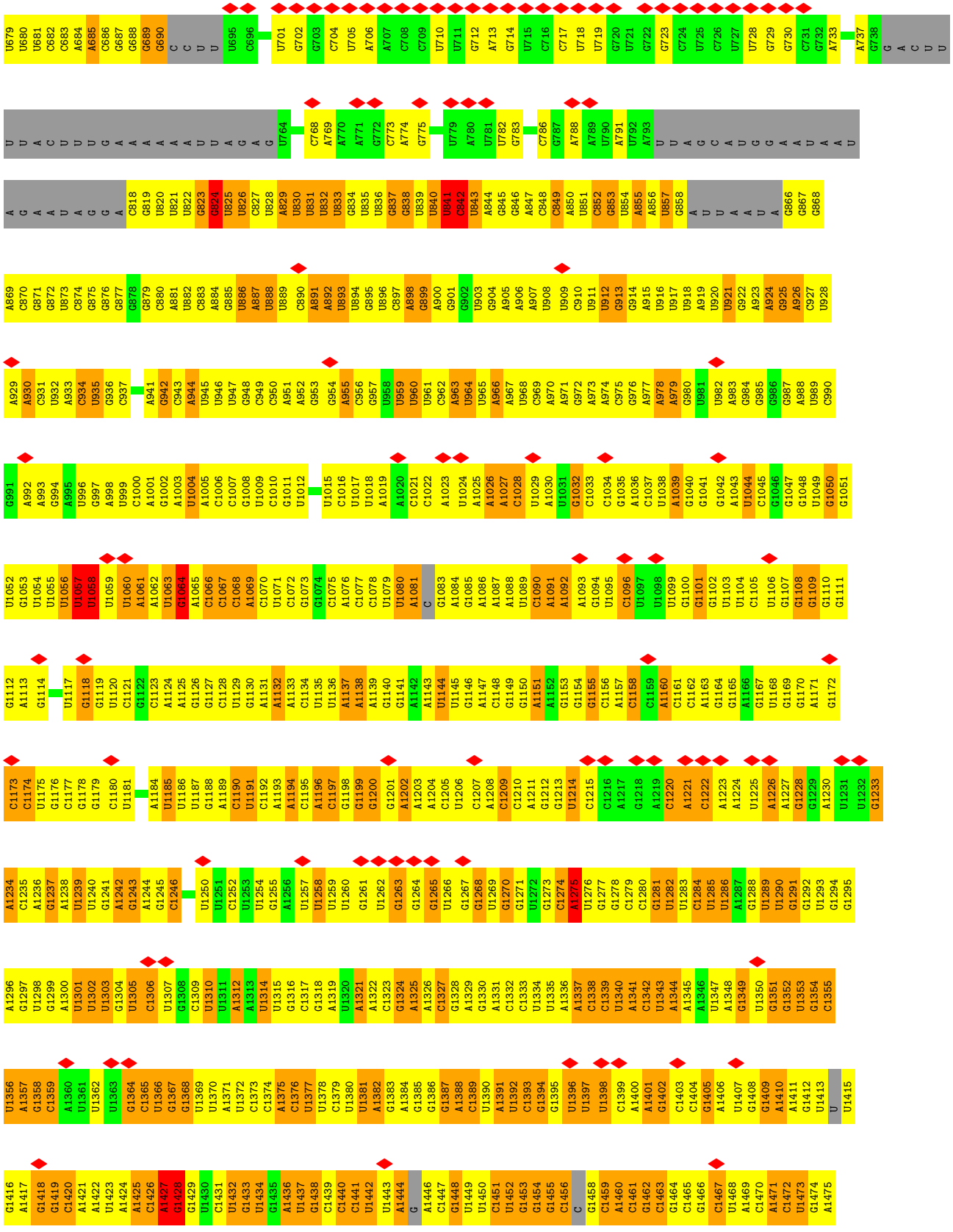
Chain BI:

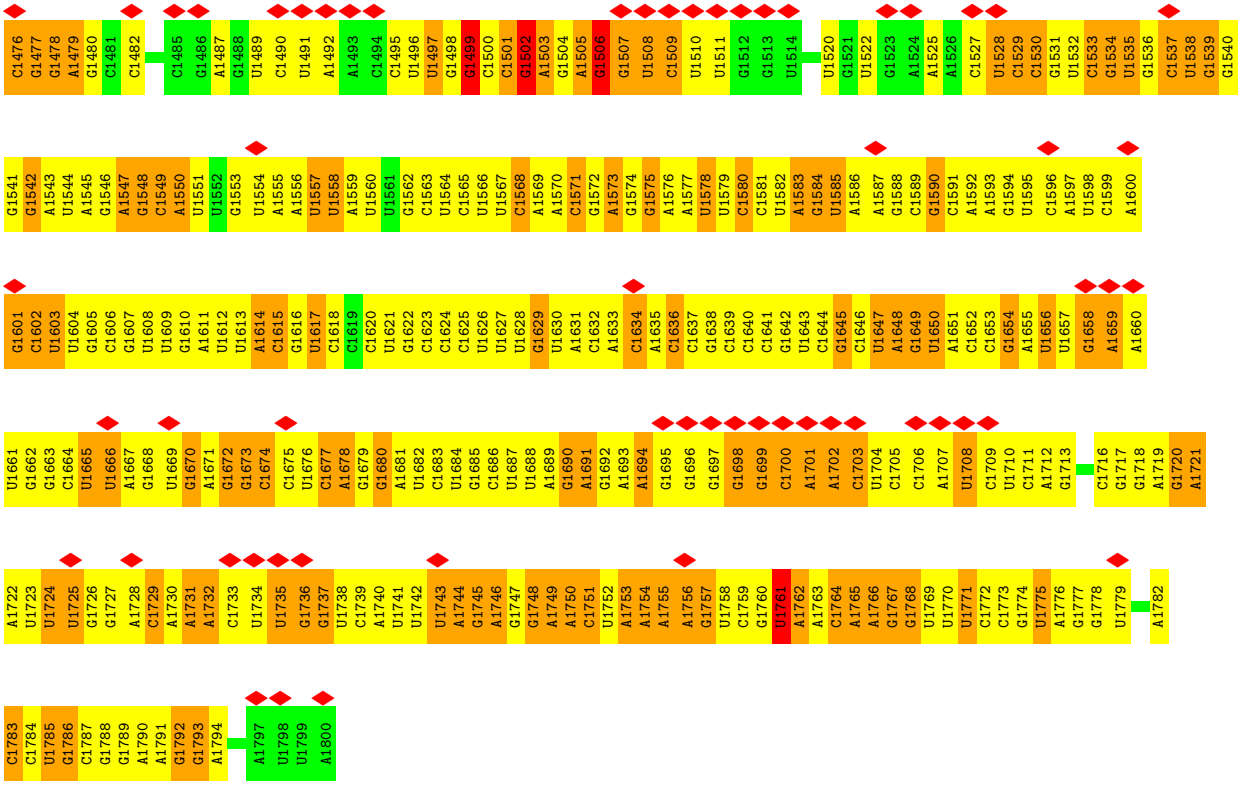


• Molecule 78: 18S rRNA

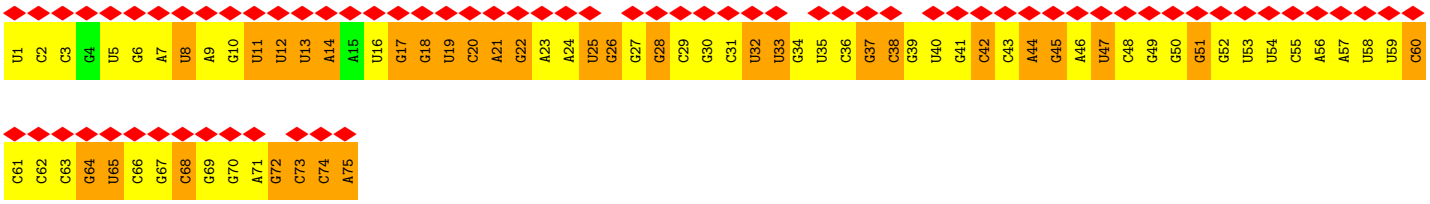
Chain CA:



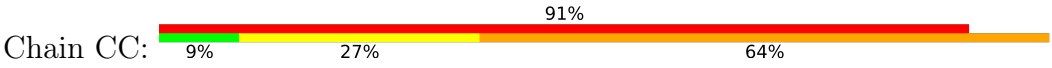


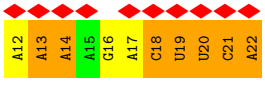


• Molecule 79: P-SITE TRNA ASP

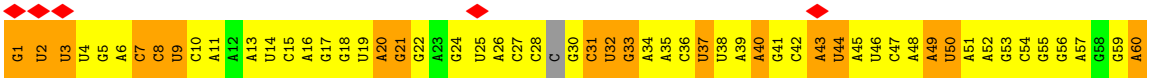


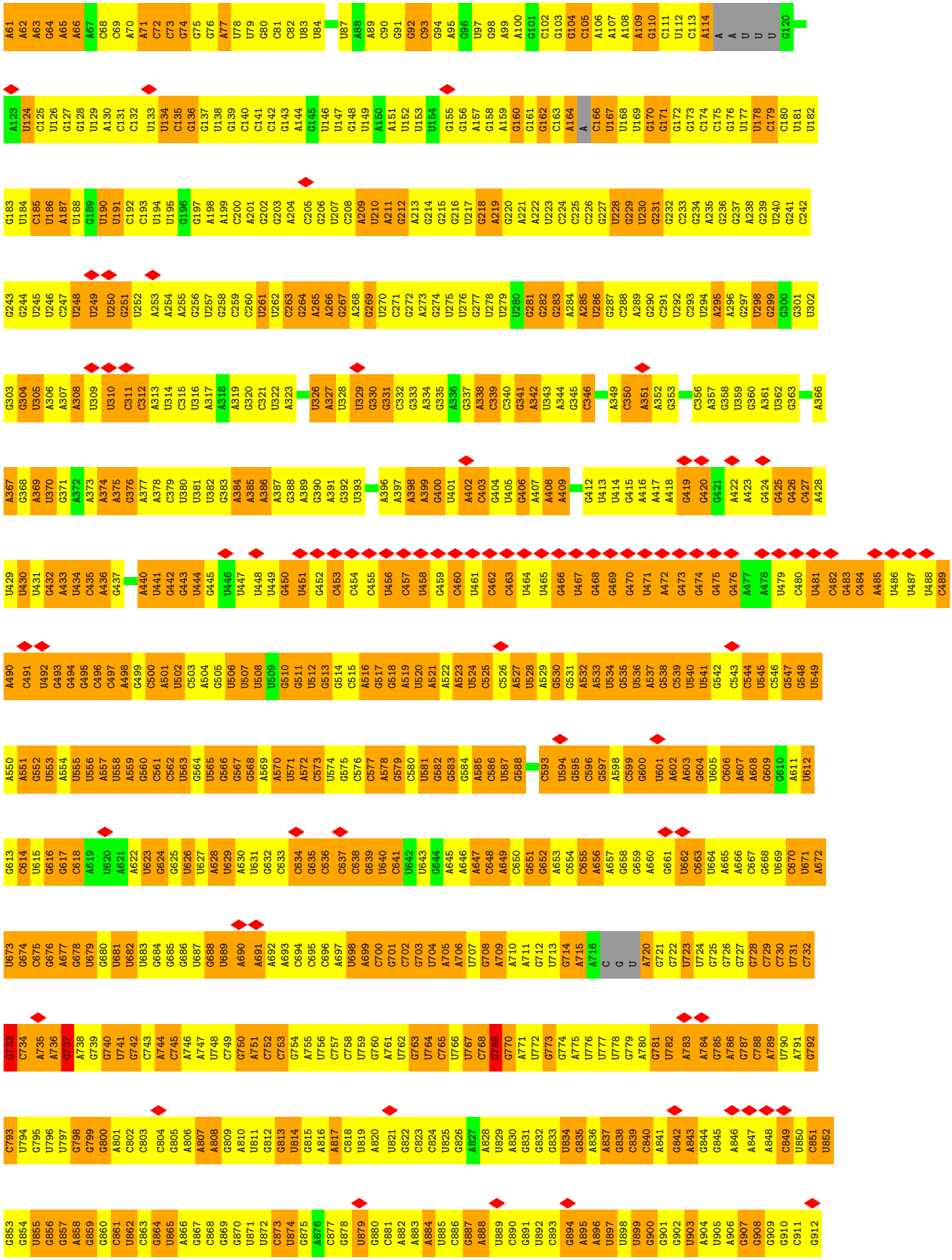
• Molecule 80: MRNA, RNA (5'-R(P*AP*AP*AP*AP*GP*AP*CP*UP*UP*CP*A)-3')

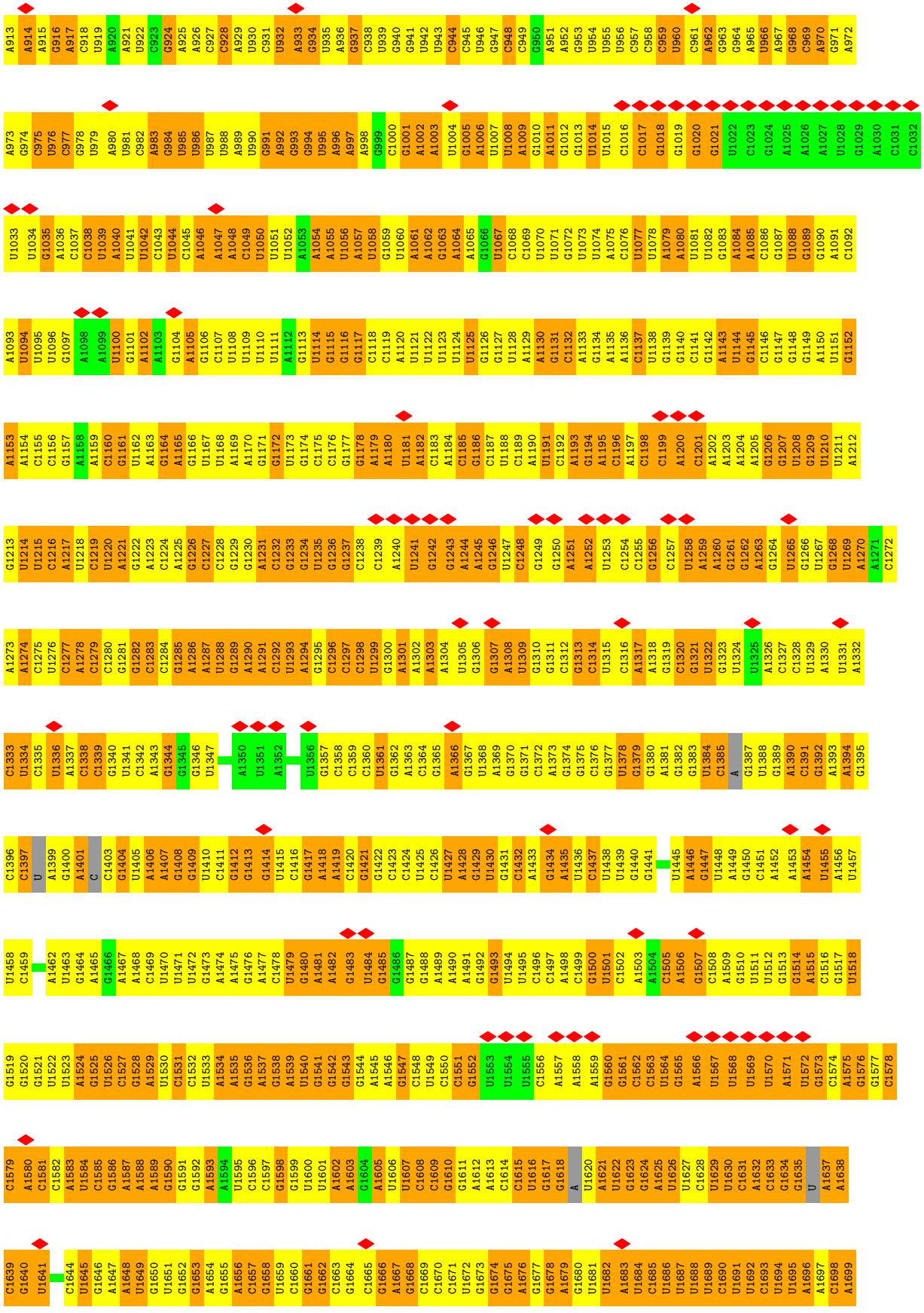


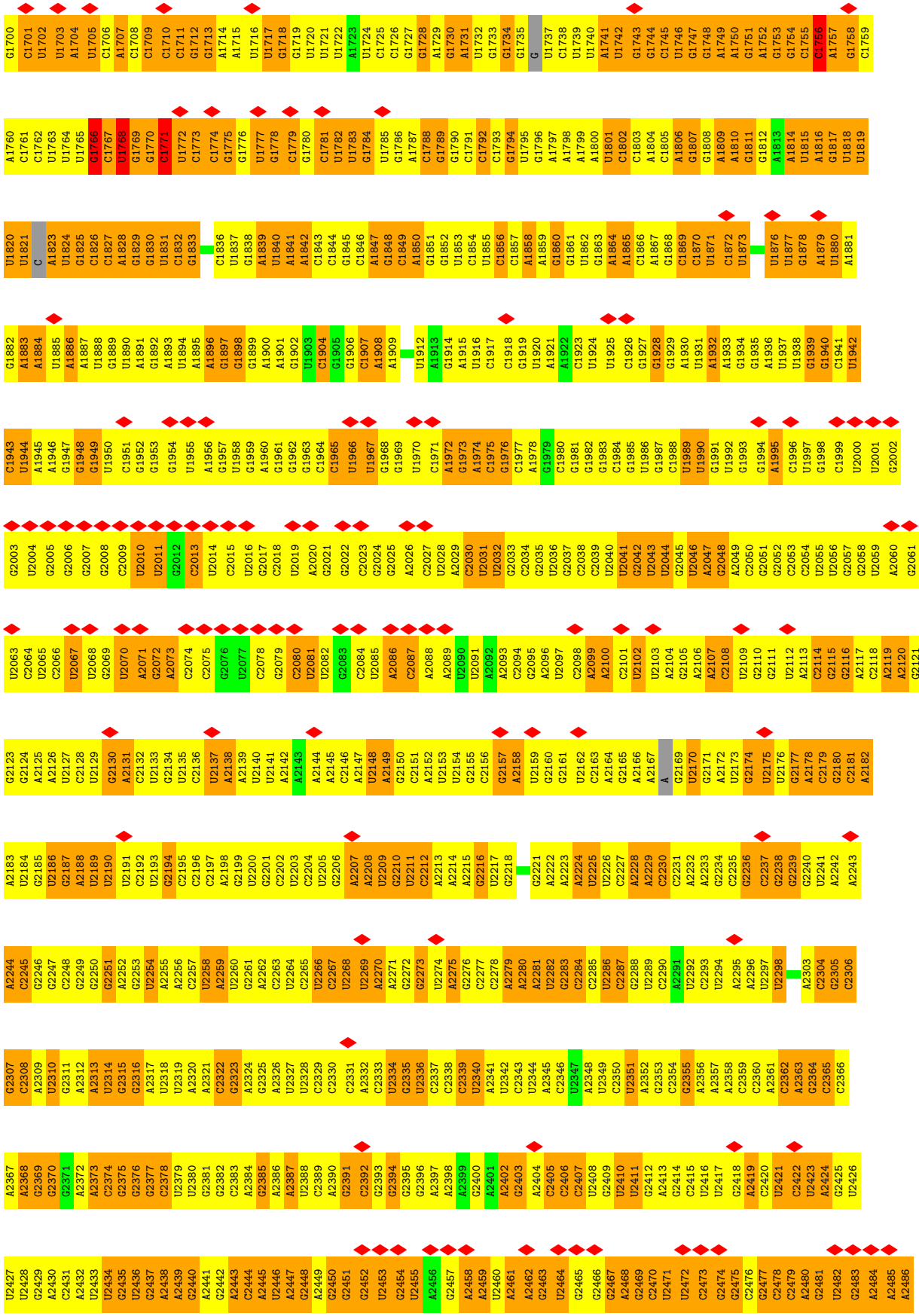


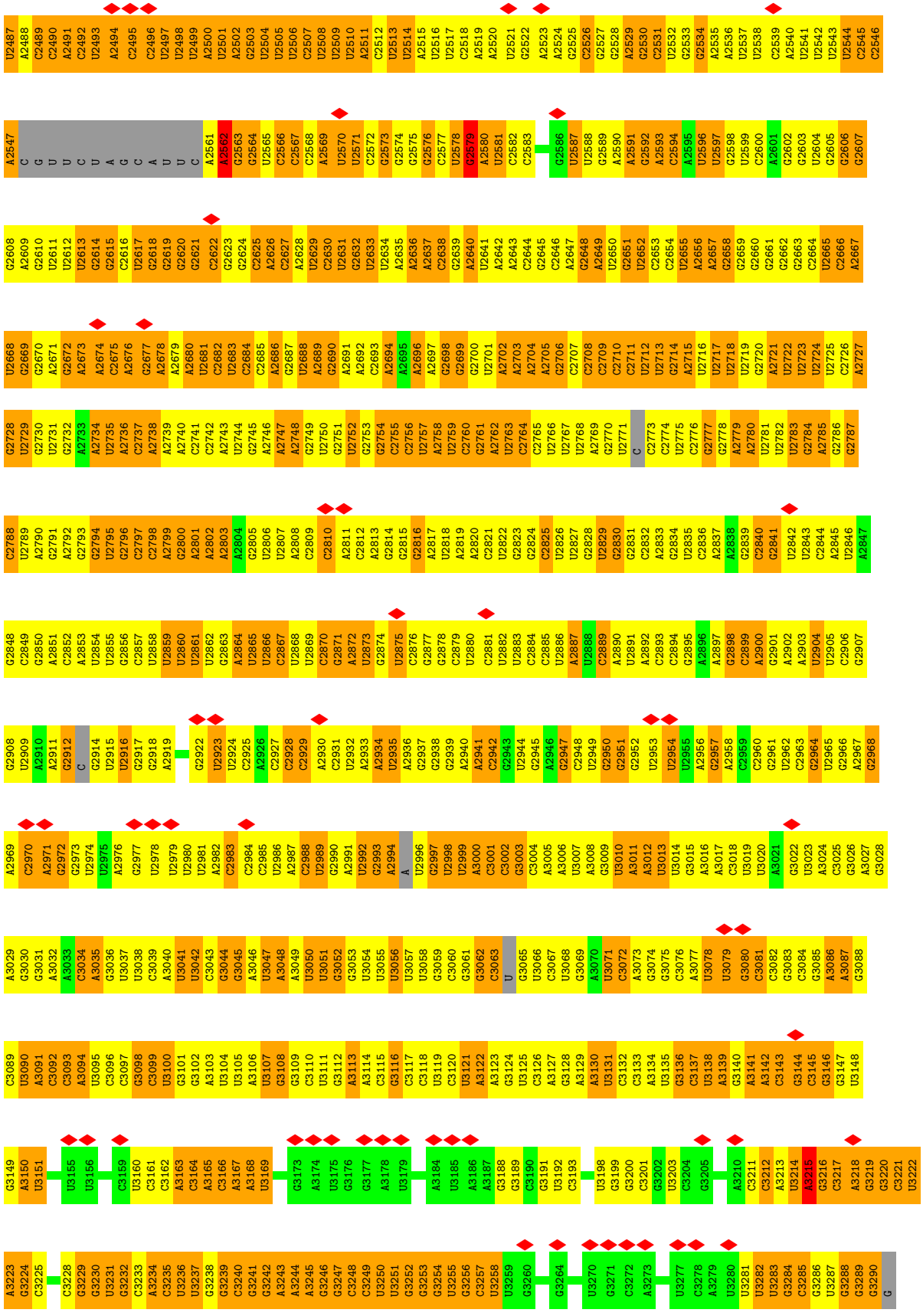
• Molecule 81: 25S rRNA

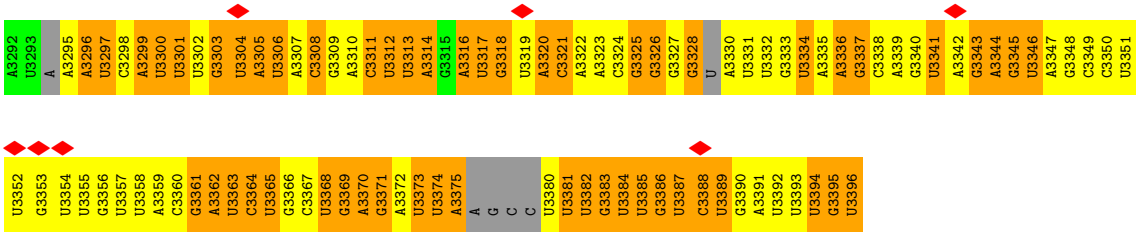






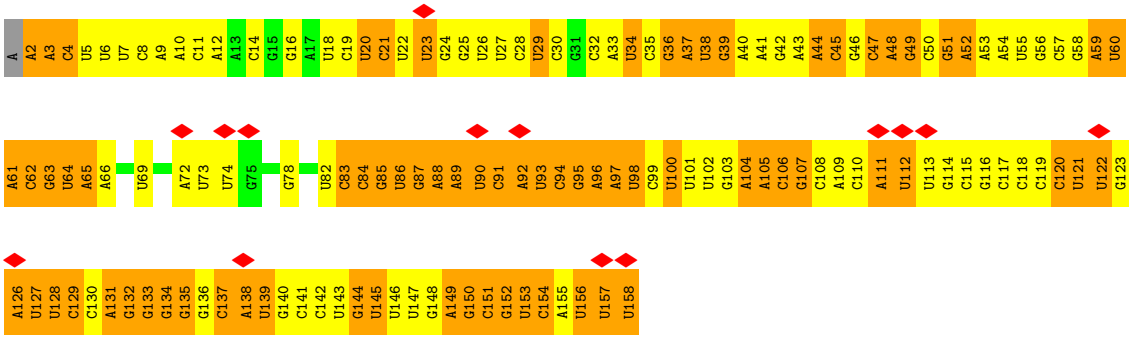






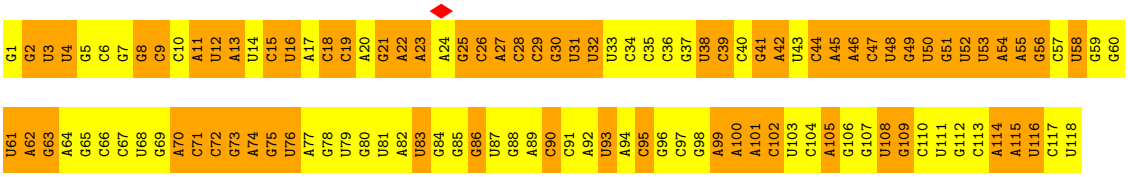
• Molecule 82: 5.8S rRNA

Chain DB:



• Molecule 83: 5S rRNA

Chain DC:



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

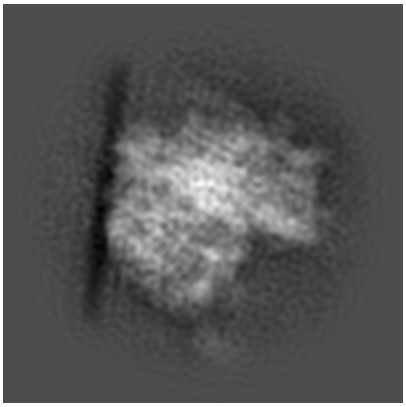
6 Map visualisation

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.

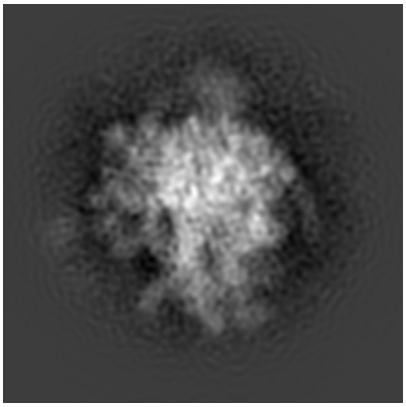
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

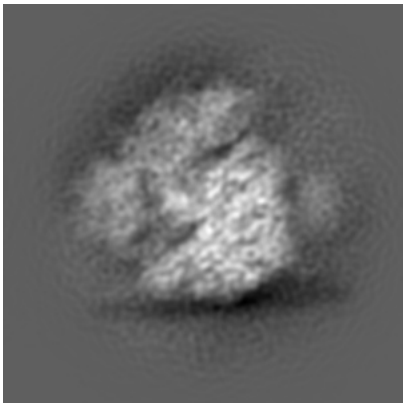
6.1.1 Primary map



X



Y

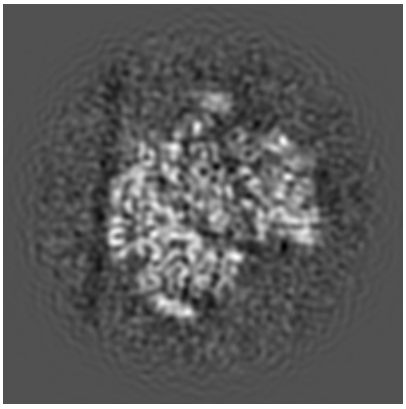


Z

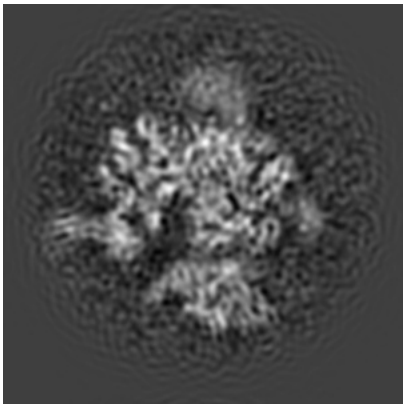
The images above show the map projected in three orthogonal directions.

6.2 Central slices

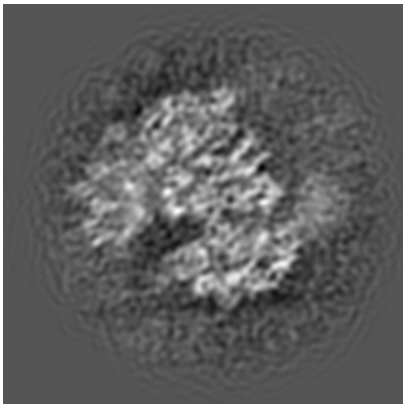
6.2.1 Primary map



X Index: 184



Y Index: 184

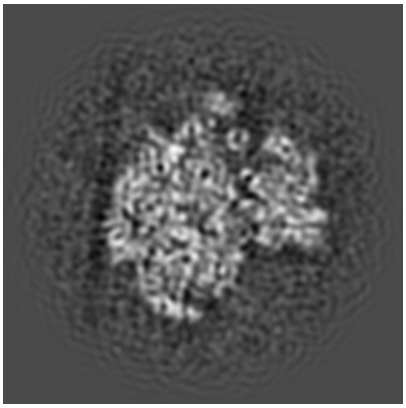


Z Index: 184

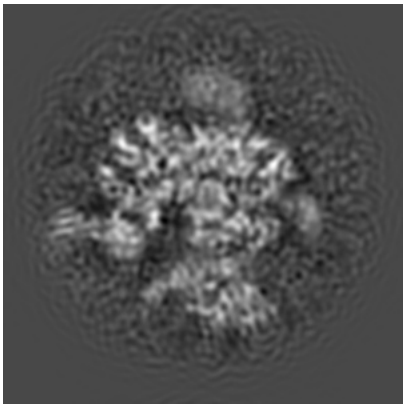
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

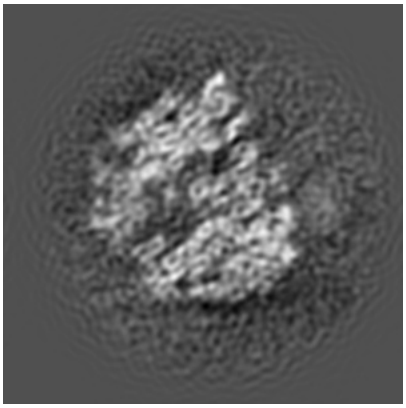
6.3.1 Primary map



X Index: 188



Y Index: 187

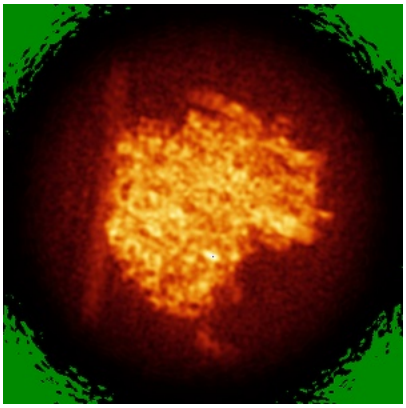


Z Index: 172

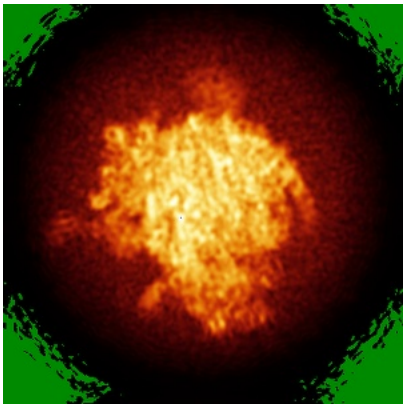
The images above show the largest variance slices of the map in three orthogonal directions.

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

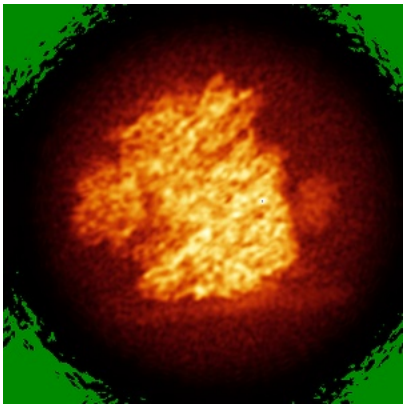
6.4.1 Primary map



X



Y

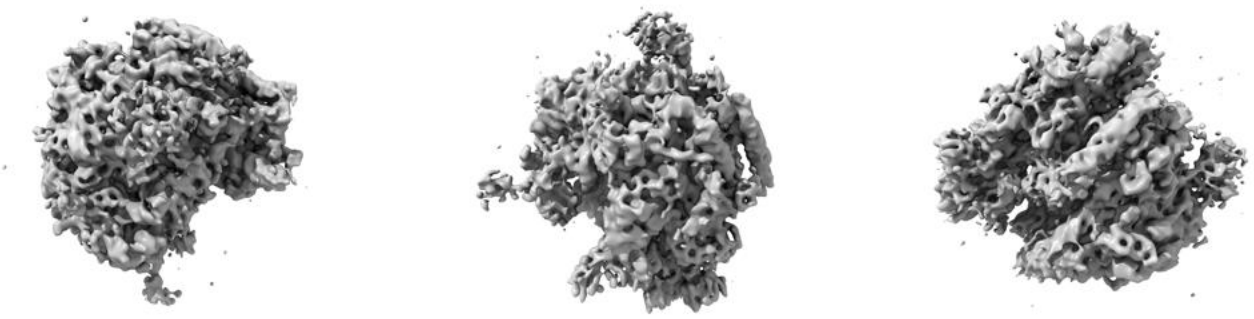


Z

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.

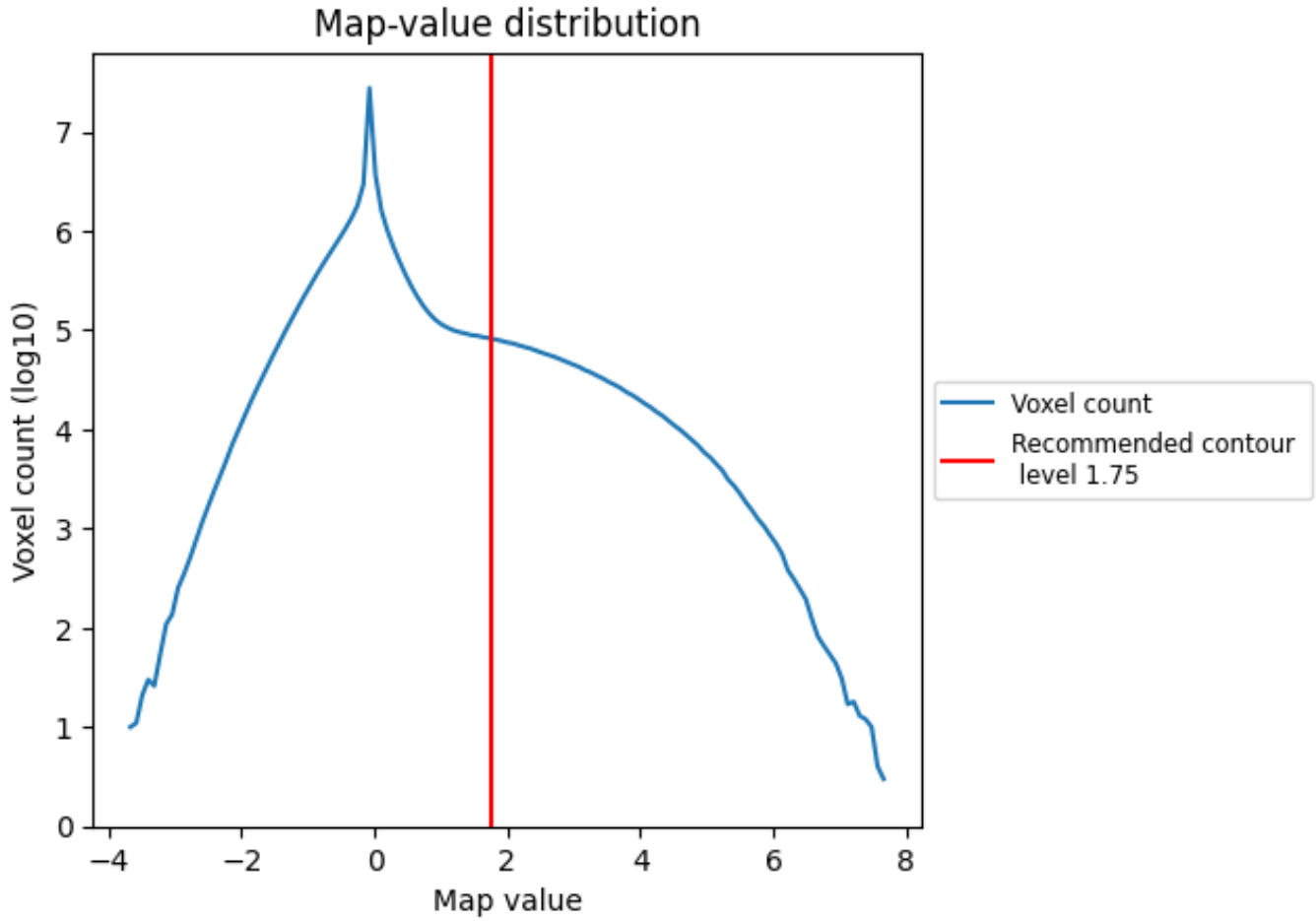
6.6 Mask visualisation (i)

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

7 Map analysis

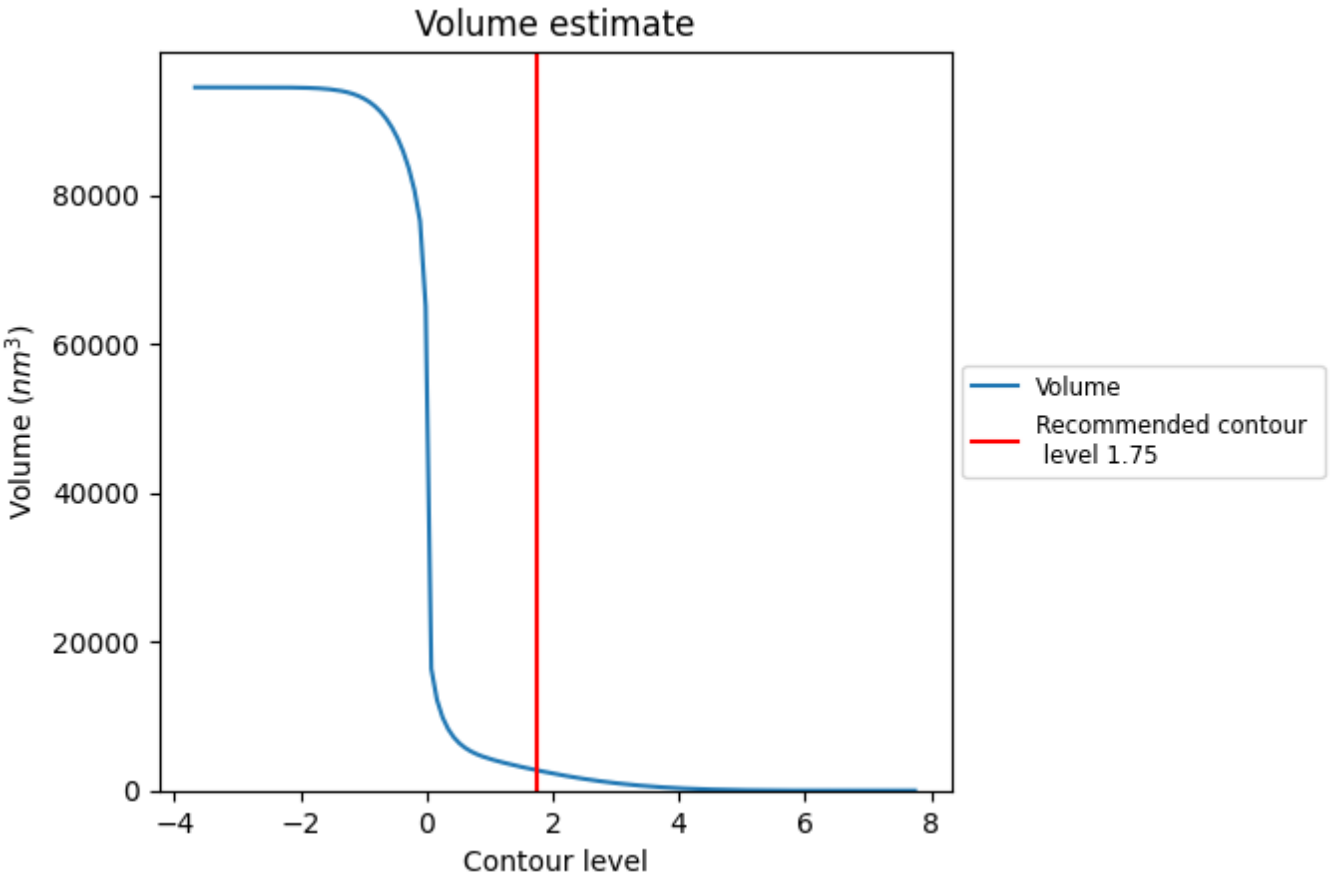
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

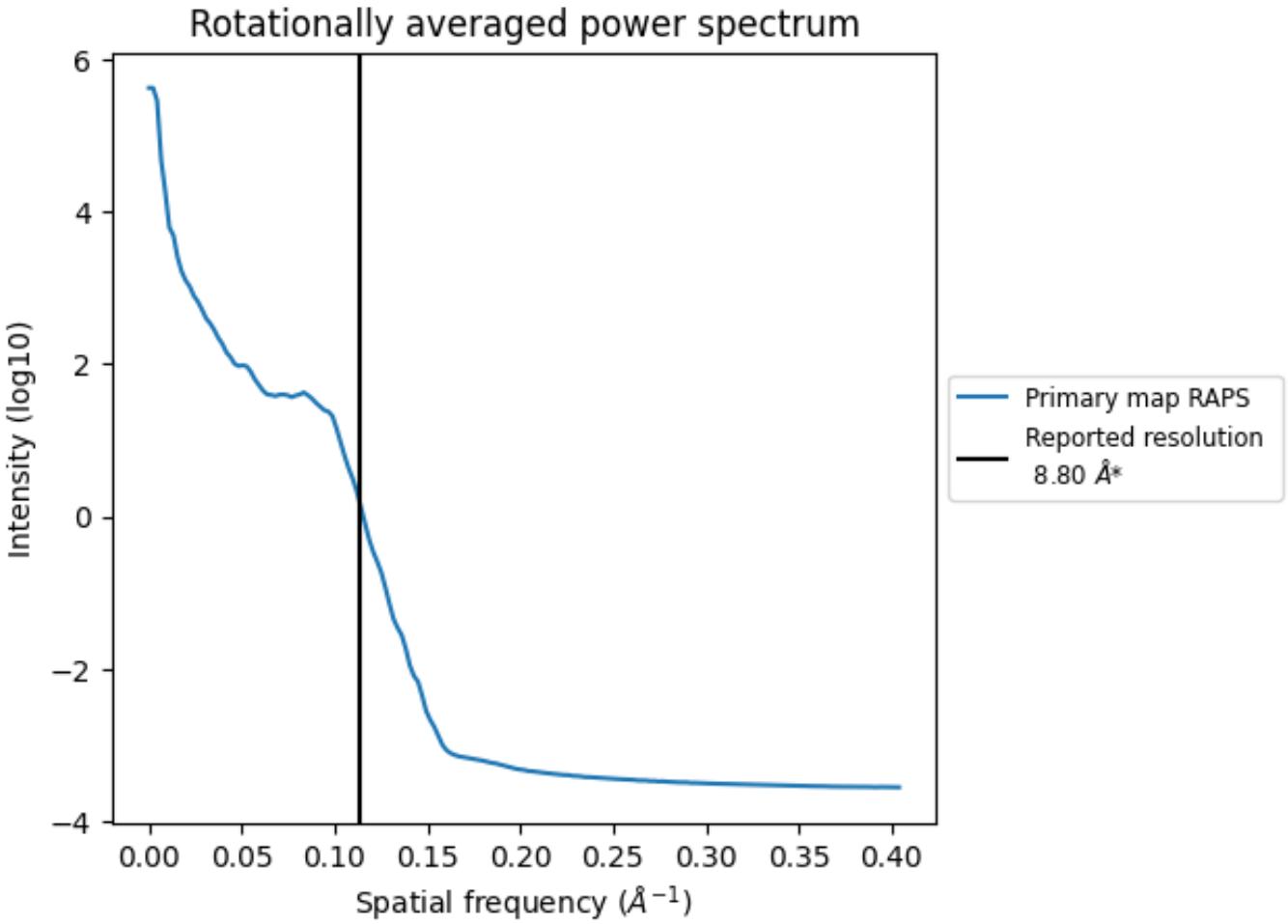
7.2 Volume estimate (i)



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}

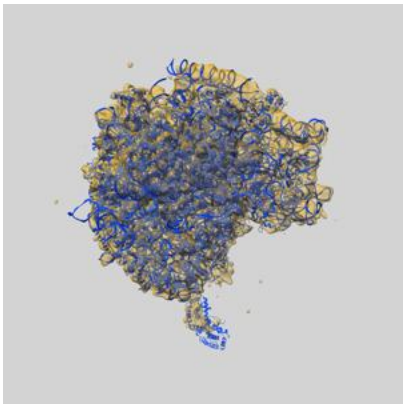
8 Fourier-Shell correlation (i)

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

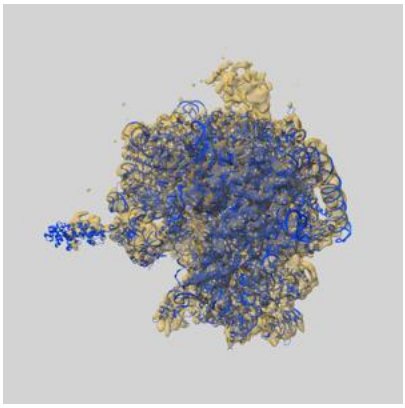
9 Map-model fit

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.

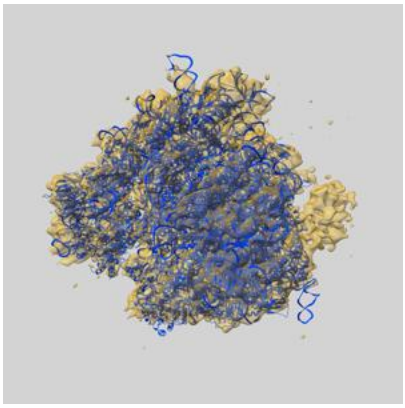
9.1 Map-model overlay



X



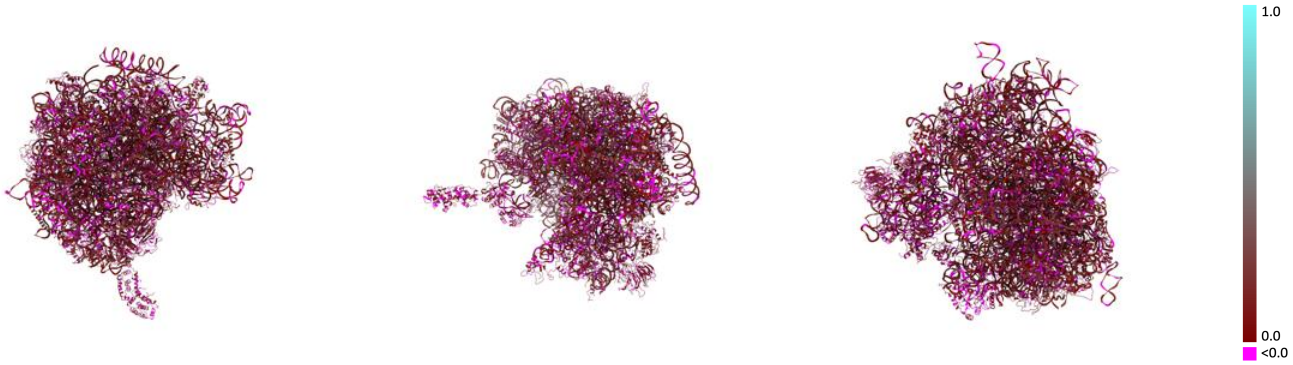
Y



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.

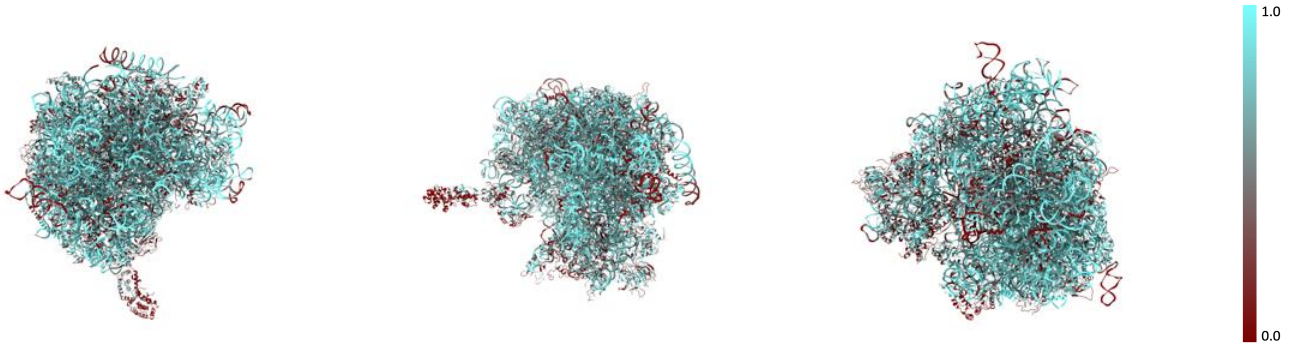
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

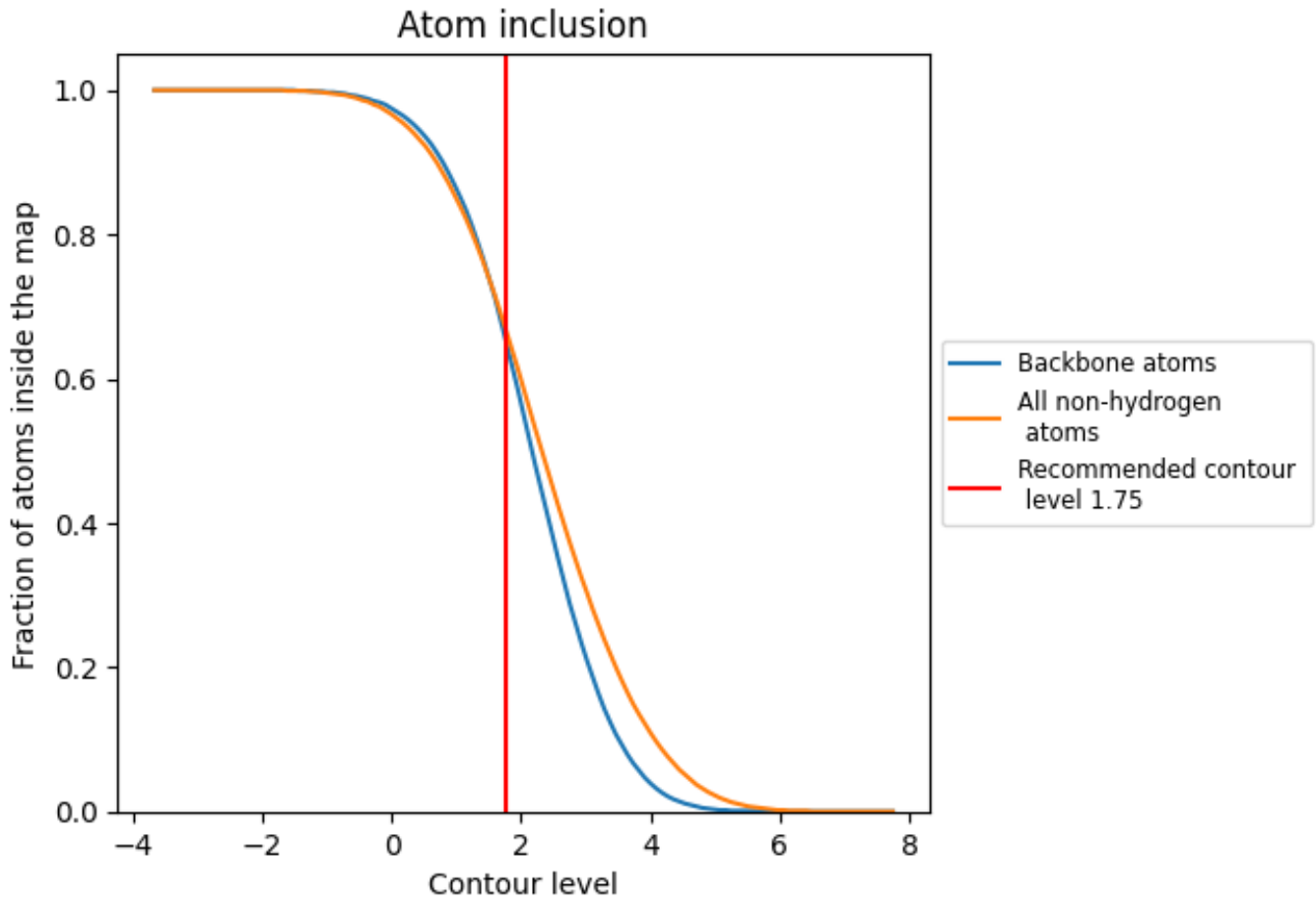
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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

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