wwPDB EM Validation Summary Report (i)

Feb 13, 2024 – 01:18 AM EST

PDB ID	:	3J6X
EMDB ID	:	EMD-5942
Title	:	S. cerevisiae 80S ribosome bound with Taura syndrome virus (TSV) IRES, 5 degree rotation (Class II)
Authors	:	Koh, C.S.; Brilot, A.F.; Grigorieff, N.; Korostelev, A.A.
Deposited on	:	2014-04-16
Resolution	:	6.10 Å(reported)
Based on initial models	:	3U5B, 3U5C, 3U5D, 3U5E

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:

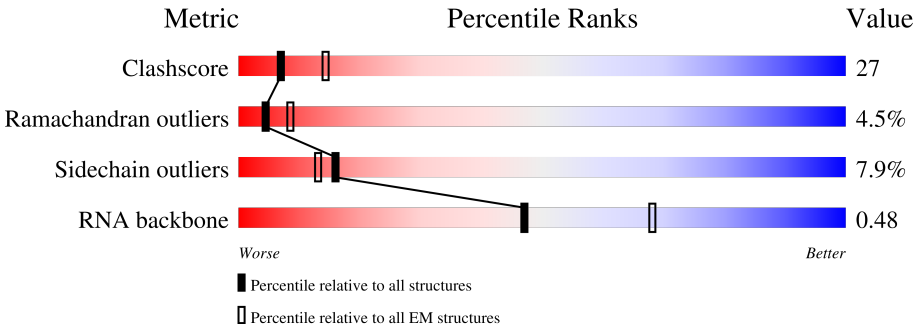
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 6.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
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	2S	3395	32% 52% 12%
2	8S	158	32% 55% 12%
3	5S	121	35% 59% 7%
4	L1	217	30% 36% 48% 9% 6%
5	L2	254	37% 59%
6	L3	387	41% 51% 8%
7	L4	362	43% 46% 10%

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Mol	Chain	Length	Quality of chain
8	L5	297	8% 52% 43% 5%
9	L6	176	39% 45% 5% 11%
10	L7	244	37% 48% 5% 9%
11	L8	256	5% 43% 42% 6% 9%
12	L9	191	5% 45% 46% 9%
13	50	221	45% 45% 6% 5%
14	51	174	39% 51% 7%
15	53	199	46% 46% 6%
16	54	138	6% 53% 42%
17	55	204	40% 51% 7%
18	56	199	42% 52% 5%
19	57	184	9% 41% 53% 5%
20	58	186	41% 52% 5%
21	59	189	8% 46% 50%
22	60	172	40% 49% 11%
23	61	160	44% 48% 8%
24	62	121	40% 38% 5% 17%
25	63	137	5% 39% 54% 6%
26	64	155	16% 21% 61%
27	65	142	6% 31% 48% 6% 15%
28	66	127	46% 49%
29	67	136	7% 38% 59%
30	68	149	38% 57%
31	69	59	8% 53% 41% 5%
32	70	105	6% 37% 53% 8%

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Mol	Chain	Length	Quality of chain
33	71	113	44% 49%
34	72	130	40% 54%
35	73	107	34% 55% 10%
36	74	121	37% 50% 5% 7%
37	75	120	6% 44% 52%
38	76	100	36% 50% 13%
39	77	88	43% 49% 7%
40	78	78	13% 45% 47% 6%
41	79	51	49% 41% 8%
42	80	128	15% 23% 59%
43	81	25	100% 24% 60% 16%
44	82	106	39% 51% 7%
45	83	92	41% 55%
46	1S	1798	33% 50% 15%
47	S0	252	12% 36% 40% 6% 18%
48	S1	255	14% 34% 39% 11% 16%
49	S2	254	37% 44% 15%
50	S3	240	10% 55% 32% 6% 7%
51	S4	261	42% 50% 7%
52	S5	225	12% 41% 44% 6% 8%
53	S6	236	8% 45% 47%
54	S7	190	18% 36% 54% 6%
55	S8	200	36% 53% 5% 6%
56	S9	197	37% 51% 6% 6%
57	10	105	12% 30% 48% 13% 9%

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Mol	Chain	Length	Quality of chain
58	11	156	12% 40% 53% 6%
59	12	143	69% 35% 41% 10% 13%
60	13	151	5% 36% 58% 5%
61	14	137	10% 39% 48% 6% 7%
62	15	142	23% 46% 37% 13%
63	16	143	14% 42% 52%
64	17	136	25% 49% 34% 6% 12%
65	18	146	14% 40% 46% 12%
66	19	144	12% 40% 51% 8%
67	20	121	19% 37% 45% 6% 12%
68	21	87	7% 43% 49% 8%
69	22	130	38% 55% 6%
70	23	145	32% 54% 12%
71	24	135	6% 38% 52% 10%
72	25	108	12% 21% 35% 6% 35%
73	26	119	10% 29% 42% 9% 18%
74	27	82	15% 51% 39% 9%
75	28	67	16% 33% 54% 7% 6%
76	29	56	7% 34% 57% 5%
77	30	63	8% 51% 37% 6% 5%
78	31	152	36% 26% 18% 53%
79	RA	319	22% 57% 36% 6%
80	IR	201	47% 99%

2 Entry composition (i)

There are 80 unique types of molecules in this entry. The entry contains 204247 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2S	3308	70742	31596	12731	23107	3308	0	0

- Molecule 2 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	8S	158	3354	1500	586	1110	158	0	0

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	5S	121	2580	1152	461	846	121	0	0

- Molecule 4 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	L1	204	1609	1031	279	290	9	0	0

- Molecule 5 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	L2	252	1918	1193	389	335	1	0	0

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	L3	386	3082	1956	584	534	8	0	0

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L4	361	Total	C	N	O	S	0	0
			2750	1730	522	495	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L5	296	Total	C	N	O	S	0	0
			2376	1501	414	459	2		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L6	156	Total	C	N	O	S	0	0
			1240	800	222	217	1		

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L7	222	Total	C	N	O	S	0	0
			1785	1151	324	309	1		

- Molecule 11 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L8	233	Total	C	N	O	S	0	0
			1818	1159	326	330	3		

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L9	191	Total	C	N	O	S	0	0
			1519	963	274	278	4		

- Molecule 13 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	50	211	Total	C	N	O	S	0	0
			1718	1089	325	298	6		

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	51	169	Total	C	N	O	S	0	0
			1354	847	253	250	4		

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	53	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	54	136	Total	C	N	O	S	0	0
			1054	675	199	178	2		

- Molecule 17 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	55	203	Total	C	N	O	S	0	0
			1721	1077	361	282	1		

- Molecule 18 is a protein called 60S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	56	197	Total	C	N	O	S	0	0
			1556	1003	289	263	1		

- Molecule 19 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	57	183	Total	C	N	O	0	0
			1443	896	287	260		

- Molecule 20 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	58	185	Total	C	N	O	S	0	0
			1442	908	290	242	2		

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	59	188	Total	C	N	O	0	0
			1522	935	326	261		

- Molecule 22 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	60	172	Total	C	N	O	S	0	0
			1446	930	267	245	4		

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	61	159	Total	C	N	O	S	0	0
			1277	805	246	222	4		

- Molecule 24 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	62	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 25 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	63	136	Total	C	N	O	S	0	0
			1004	628	189	180	7		

- Molecule 26 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	64	61	Total	C	N	O	S	0	0
			509	328	100	80	1		

- Molecule 27 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	65	121	Total	C	N	O	S	0	0
			969	623	170	174	2		

- Molecule 28 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	66	126	Total 994	C 625	N 192	O 177	0	0

- Molecule 29 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	67	135	Total 1093	C 710	N 202	O 181	0	0

- Molecule 30 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	68	148	Total 1174	C 749	N 231	O 191	S 3	0	0

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	69	58	Total 463	C 289	N 100	O 74	0	0

- Molecule 32 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	70	97	Total 743	C 479	N 124	O 139	S 1	0	0

- Molecule 33 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	71	109	Total 890	C 565	N 168	O 156	S 1	0	0

- Molecule 34 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	72	127	Total 1020	C 647	N 205	O 167	S 1	0	0

- Molecule 35 is a protein called 60S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	73	106	Total	C	N	O	S	0	0
			851	540	165	145	1		

- Molecule 36 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	74	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 37 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	75	119	Total	C	N	O	S	0	0
			970	615	186	168	1		

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	76	99	Total	C	N	O	S	0	0
			772	481	156	133	2		

- Molecule 39 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	77	87	Total	C	N	O	S	0	0
			682	414	148	115	5		

- Molecule 40 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	78	77	Total	C	N	O	0	0
			613	391	115	107		

- Molecule 41 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	79	50	Total	C	N	O	S	0	0
			437	272	97	66	2		

- Molecule 42 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	80	52	Total	C	N	O	S	0	0
			418	259	86	68	5		

- Molecule 43 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	81	25	Total	C	N	O	S	0	0
			234	142	63	28	1		

- Molecule 44 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	82	103	Total	C	N	O	S	0	0
			827	520	167	135	5		

- Molecule 45 is a protein called 60S ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	83	91	Total	C	N	O	S	0	0
			695	429	138	122	6		

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1S	1781	Total	C	N	O	P	0	0
			37949	16965	6715	12488	1781		

- Molecule 47 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S0	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 48 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S1	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 49 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 50 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S3	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S4	260	Total	C	N	O	S	0	0
			2069	1316	389	361	3		

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S5	206	Total	C	N	O	S	0	0
			1610	1007	300	300	3		

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S6	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	S7	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S8	188	Total	C	N	O	S	0	0
			1490	925	298	265	2		

- Molecule 56 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S9	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 57 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	10	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 58 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	11	155	Total	C	N	O	S	0	0
			1245	798	235	209	3		

- Molecule 59 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	12	124	Total	C	N	O	S	0	0
			935	587	165	181	2		

- Molecule 60 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	13	150	Total	C	N	O	S	0	0
			1193	759	224	208	2		

- Molecule 61 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	14	127	Total	C	N	O	S	0	0
			942	578	186	175	3		

- Molecule 62 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	15	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 63 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	16	141	Total	C	N	O	0	0
			1106	708	203	195		

- Molecule 64 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	17	120	Total	C	N	O	S	0	0
			965	603	183	177	2		

- Molecule 65 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	18	145	Total	C	N	O	S	0	0
			1193	743	237	211	2		

- Molecule 66 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	19	143	Total	C	N	O	S	0	0
			1113	694	208	209	2		

- Molecule 67 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	20	107	Total	C	N	O	S	0	0
			856	539	156	160	1		

- Molecule 68 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	21	87	Total	C	N	O	S	0	0
			685	420	125	138	2		

- Molecule 69 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	22	129	Total	C	N	O	S	0	0
			1022	650	188	181	3		

- Molecule 70 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	23	144	Total	C	N	O	S	0	0
			1122	708	220	192	2		

- Molecule 71 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	24	134	Total	C	N	O	0	0
			1074	676	208	190		

- Molecule 72 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	25	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 73 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	26	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 74 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	27	81	Total	C	N	O	S	0	0
			611	382	110	114	5		

- Molecule 75 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	28	63	Total	C	N	O	S	0	0
			498	306	99	92	1		

- Molecule 76 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	29	53	Total	C	N	O	S	0	0
			444	275	92	73	4		

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	30	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 78 is a protein called 40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	31	71	Total	C	N	O	S	0	0
			498	309	93	92	4		

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	RA	318	Total	C	N	O	S	0	0
			2445	1546	419	472	8		

- Molecule 80 is a RNA chain called TSV IRES mRNA.

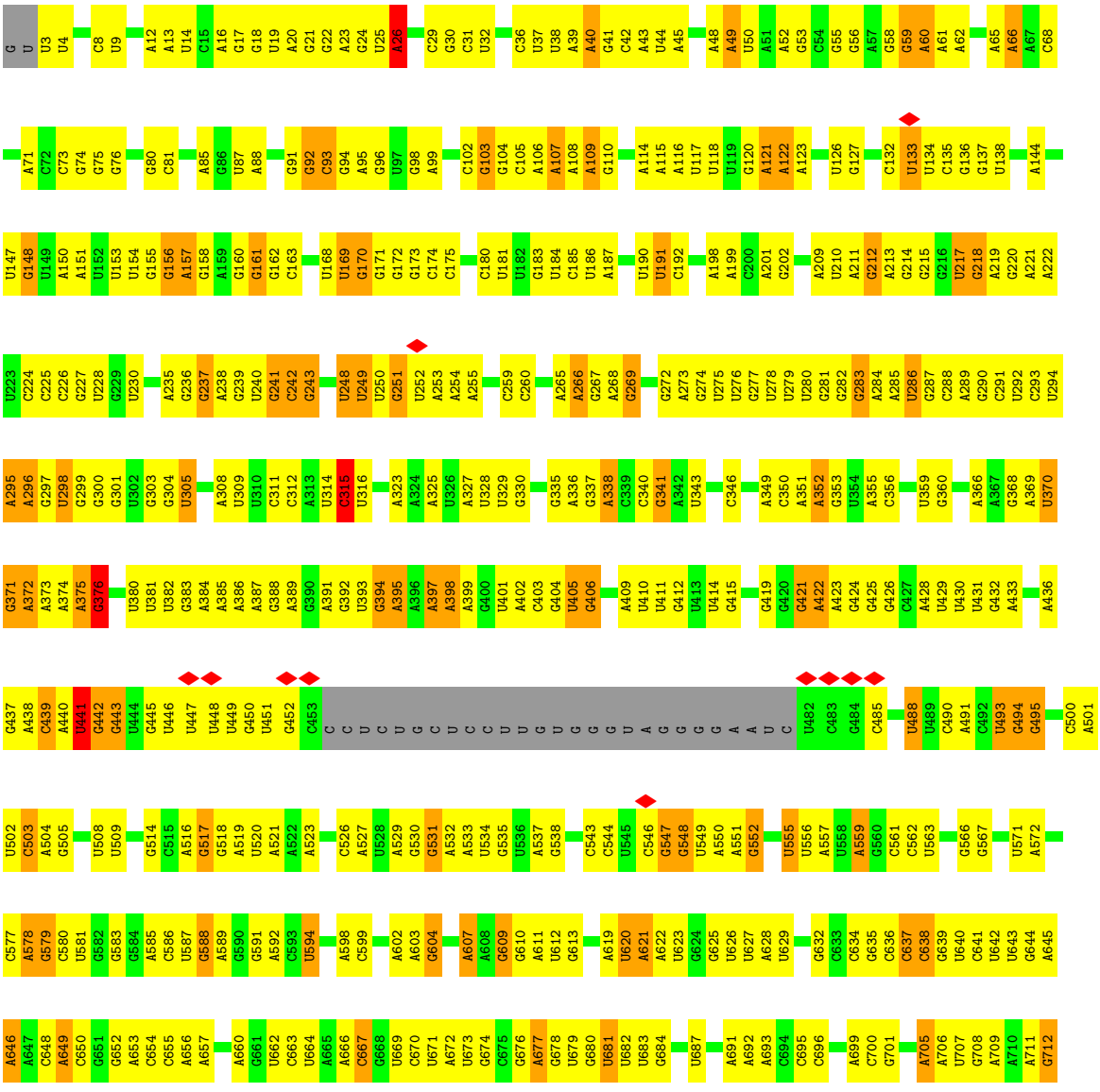
Mol	Chain	Residues	Atoms		AltConf	Trace
80	IR	198	Total	P	0	198
			198	198		

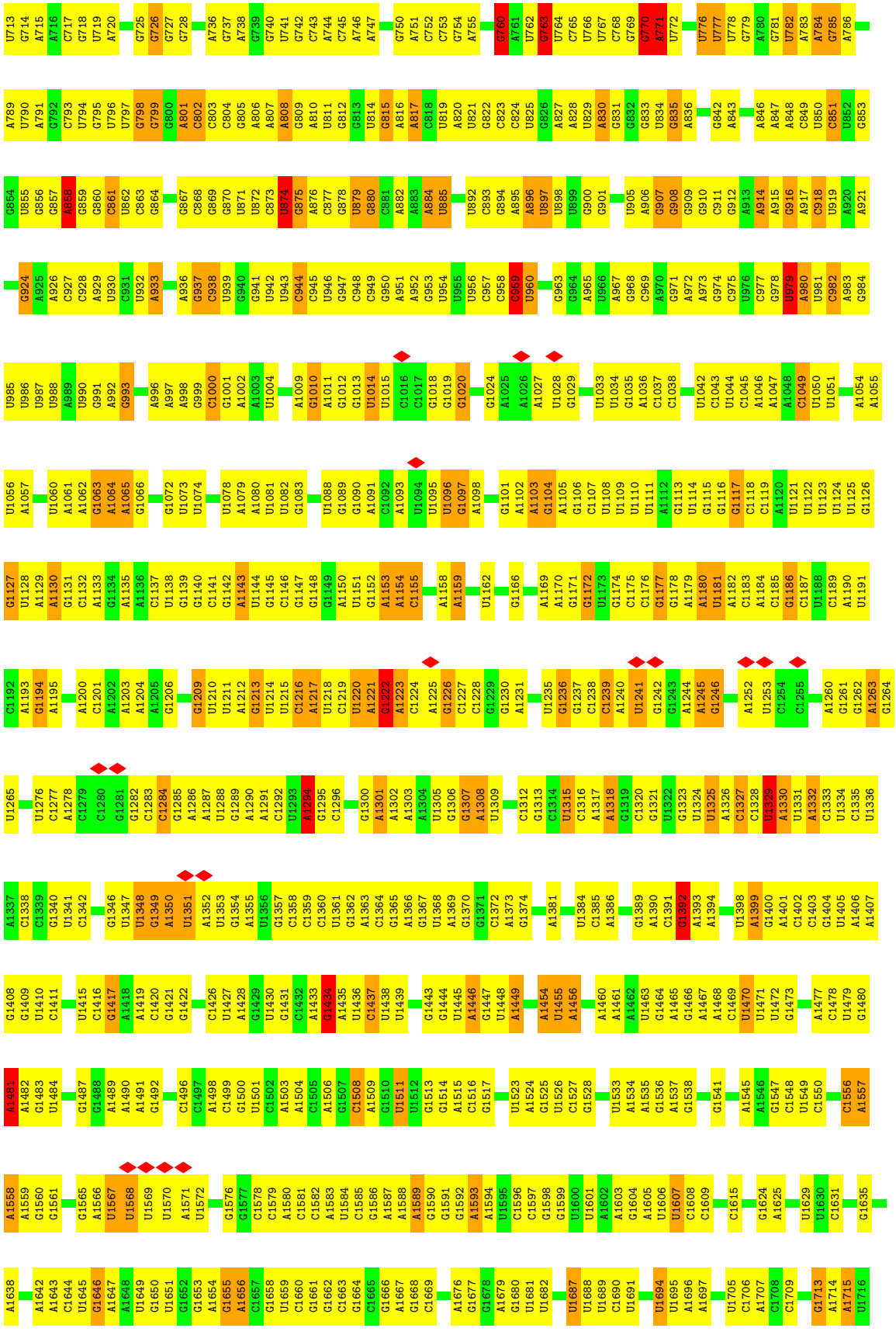
3 Residue-property plots (i)

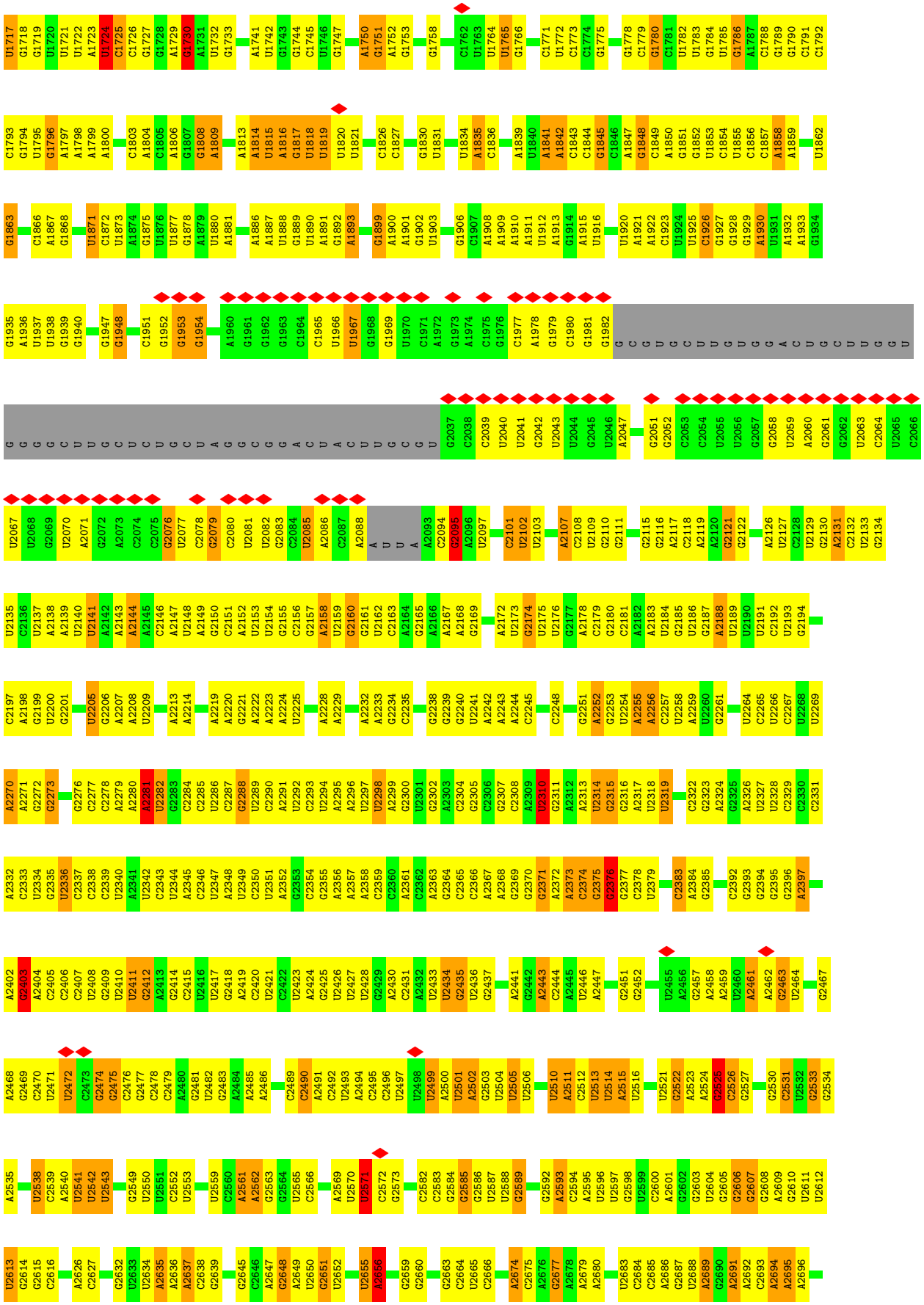
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

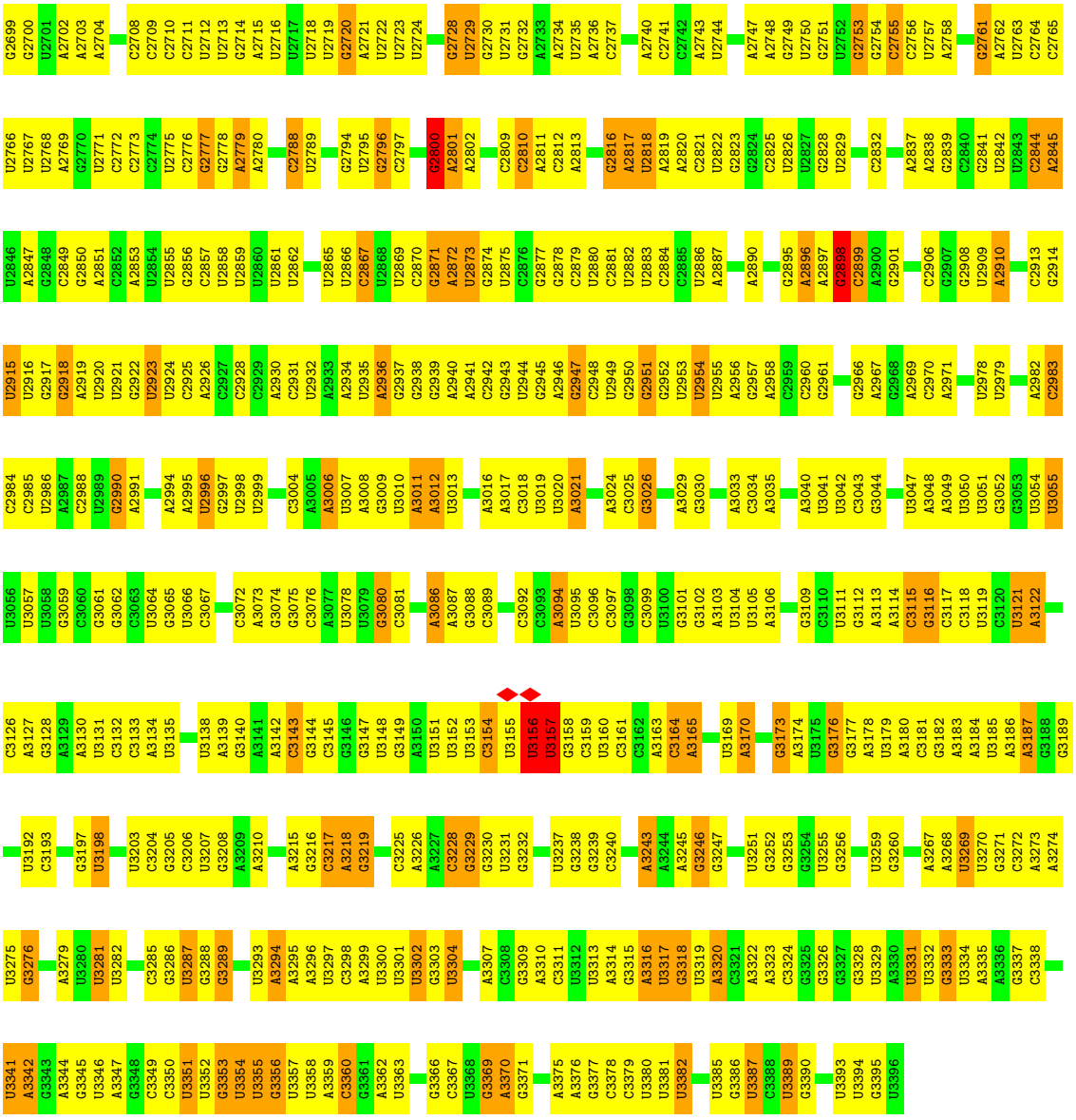
- Molecule 1: 25S ribosomal RNA

Chain 2S:



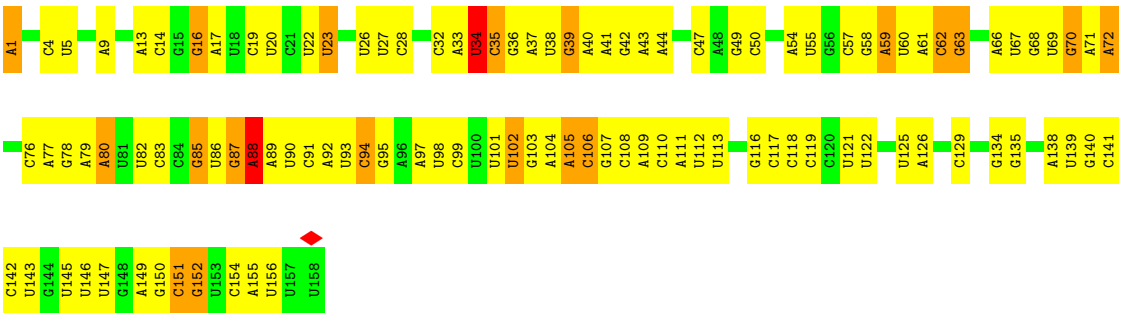






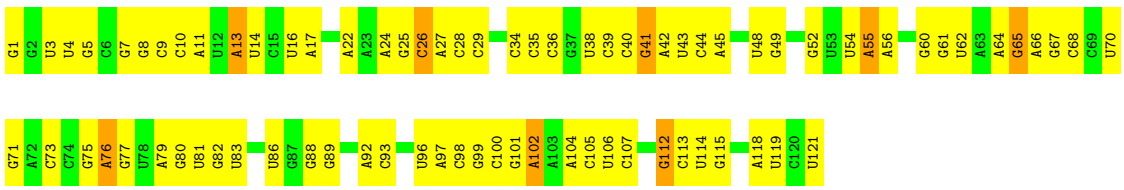
• Molecule 2: 5.8S ribosomal RNA

Chain 8S:



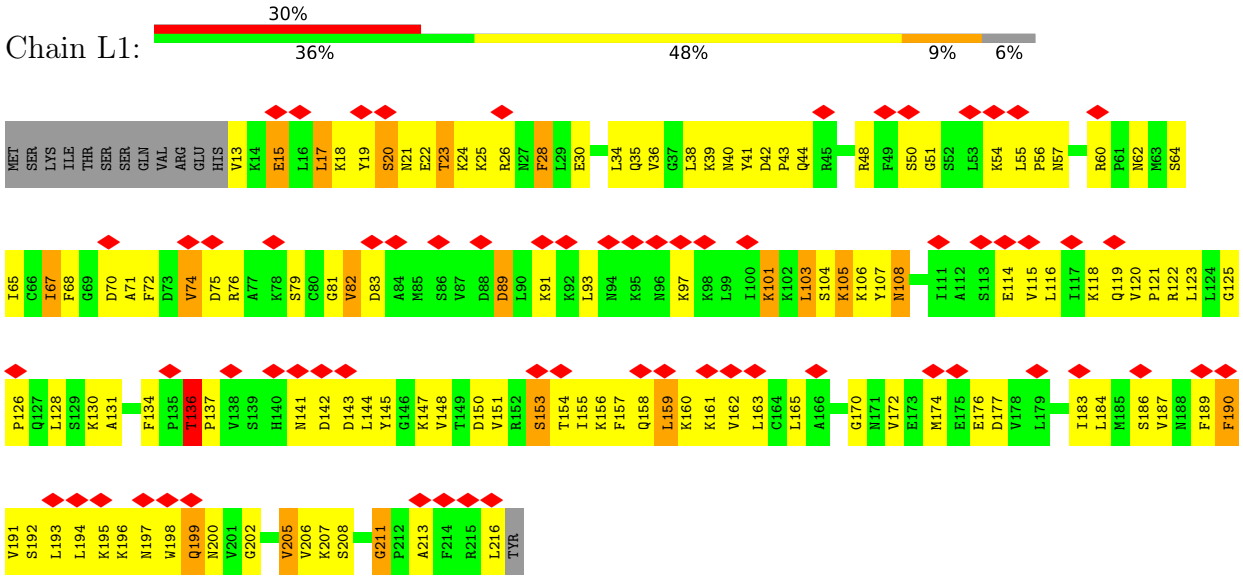
• Molecule 3: 5S ribosomal RNA

Chain 5S:



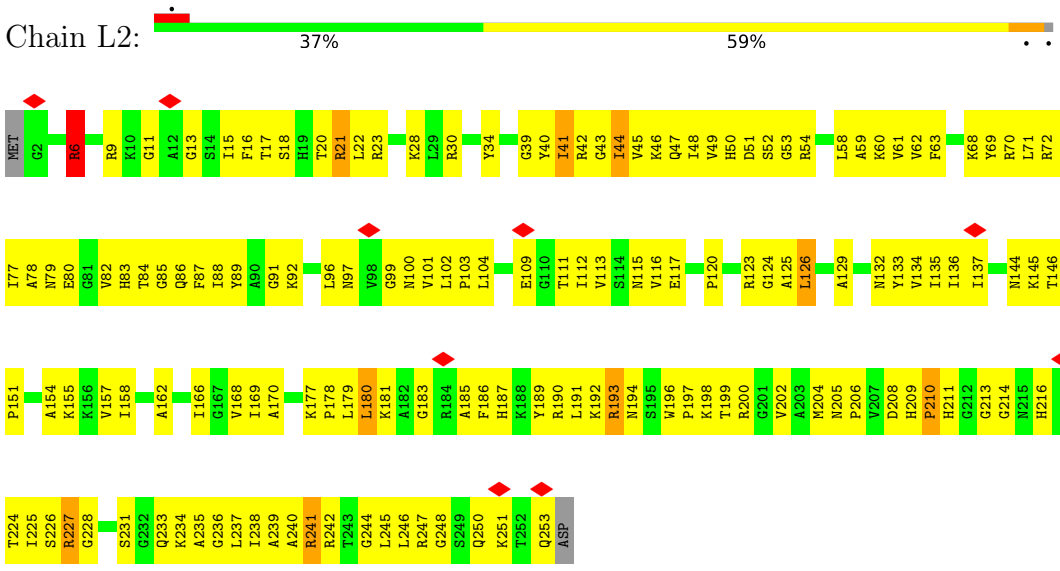
• Molecule 4: 60S ribosomal protein L1

Chain L1:



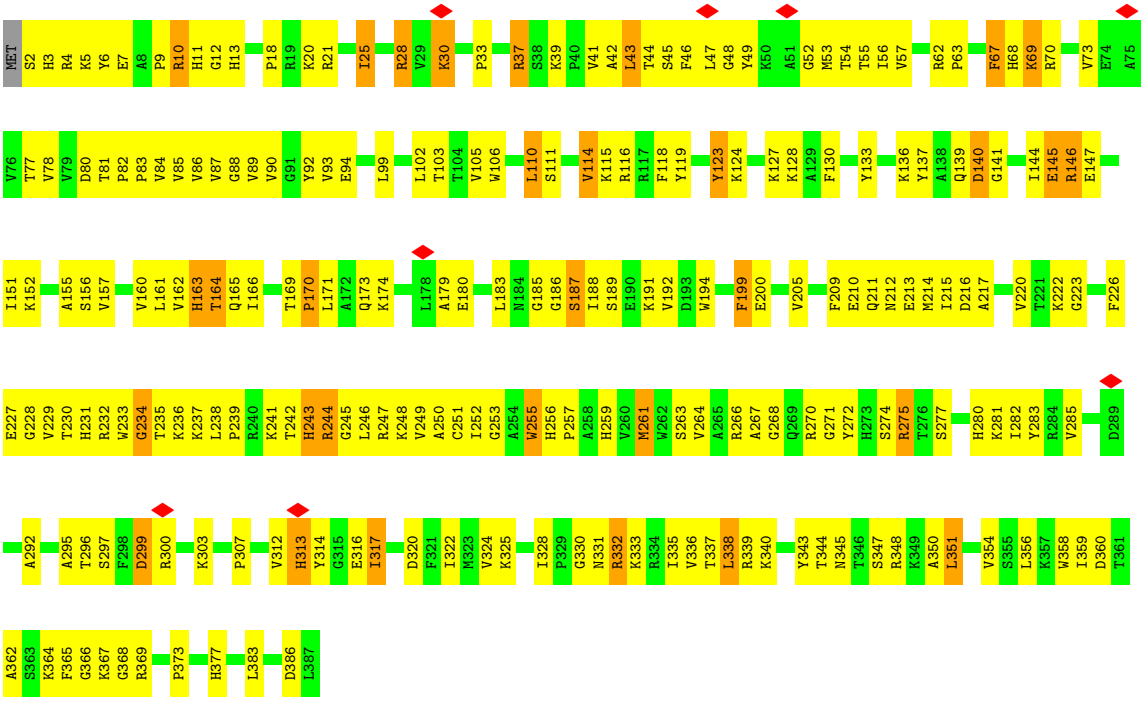
• Molecule 5: 60S ribosomal protein L2

Chain L2:



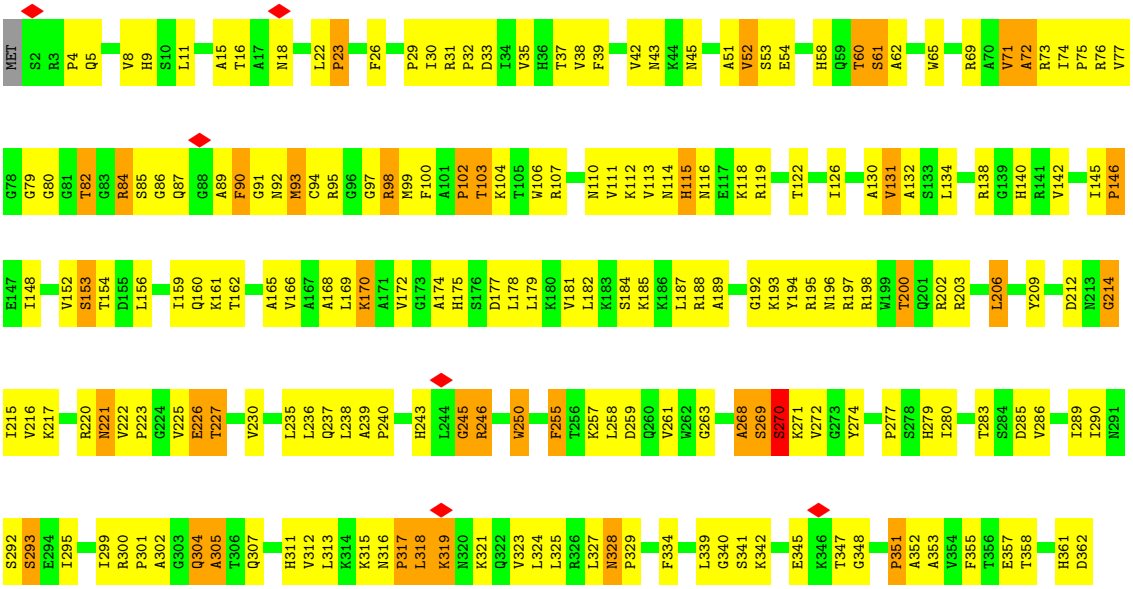
• Molecule 6: 60S ribosomal protein L3

Chain L3:



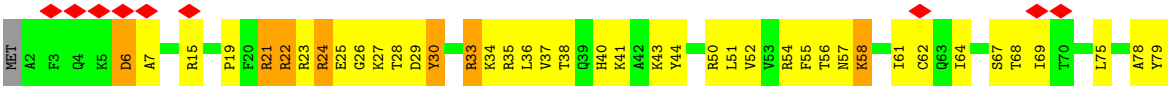
• Molecule 7: 60S ribosomal protein L4

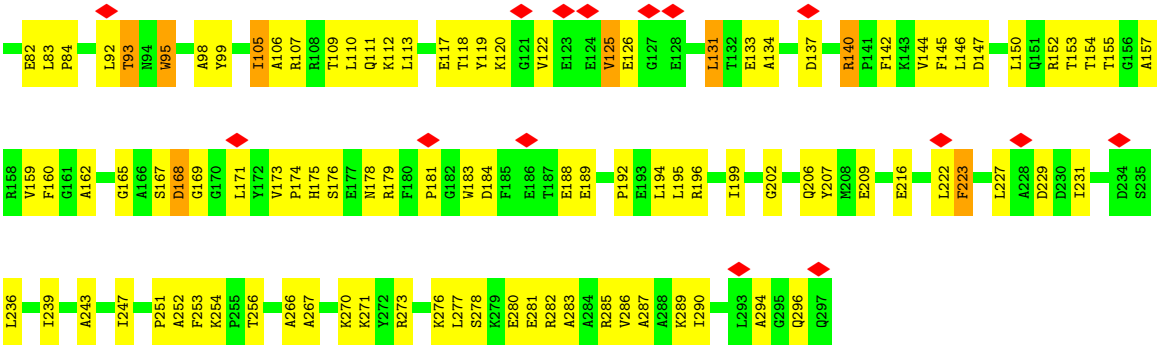
Chain L4:



• Molecule 8: 60S ribosomal protein L5

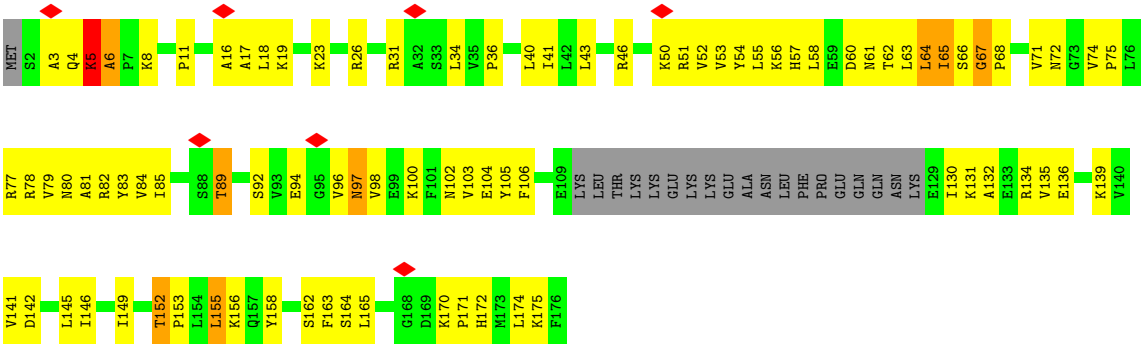
Chain L5:





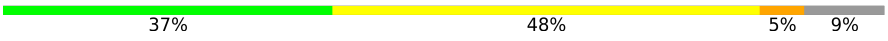
• Molecule 9: 60S ribosomal protein L6

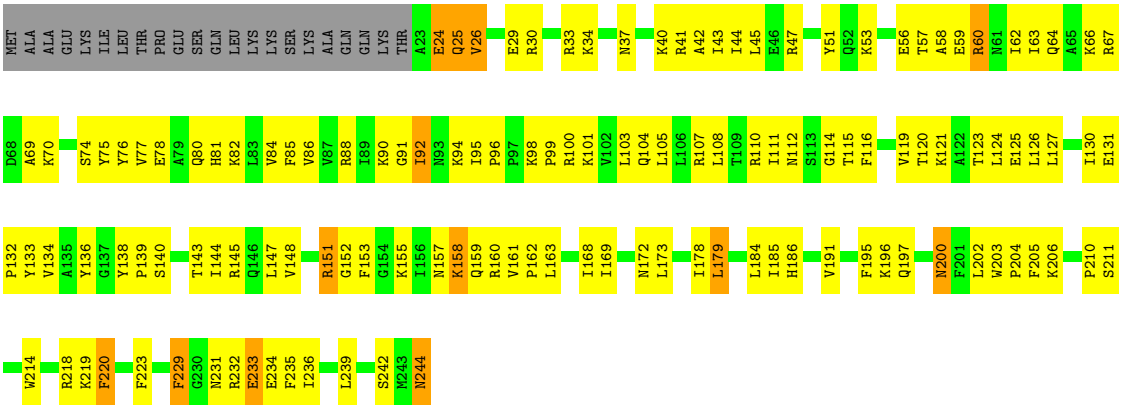
Chain L6:



• Molecule 10: 60S ribosomal protein L7

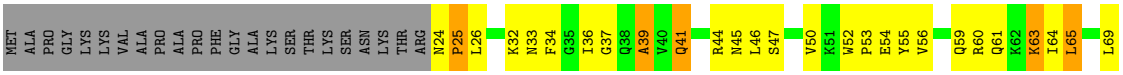
Chain L7:

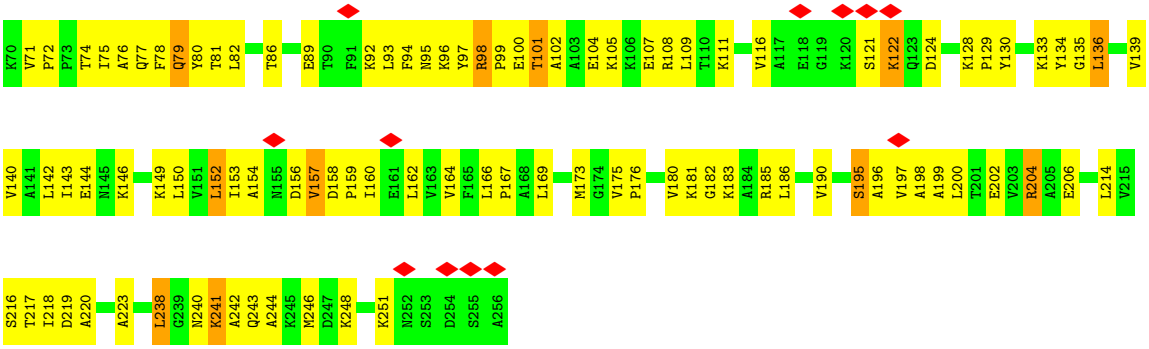




• Molecule 11: 60S ribosomal protein L8

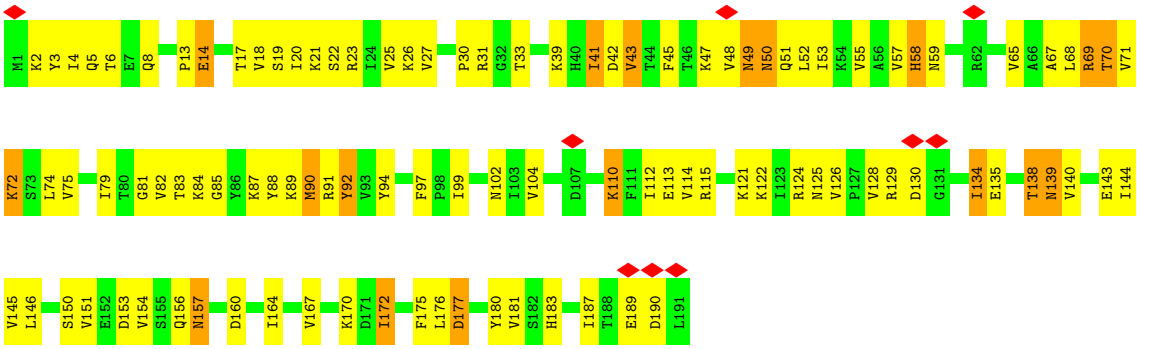
Chain L8:





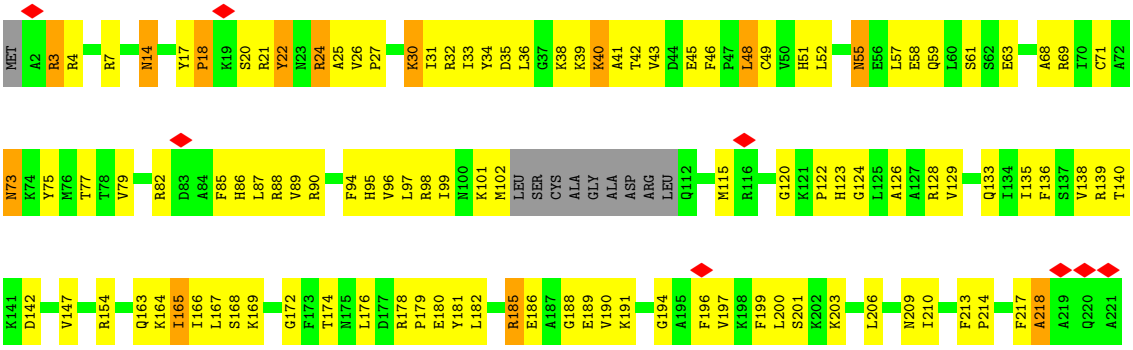
• Molecule 12: 60S ribosomal protein L9

Chain L9:



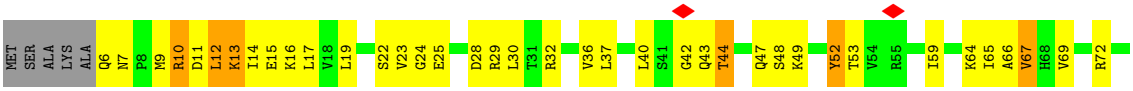
• Molecule 13: 60S ribosomal protein L10

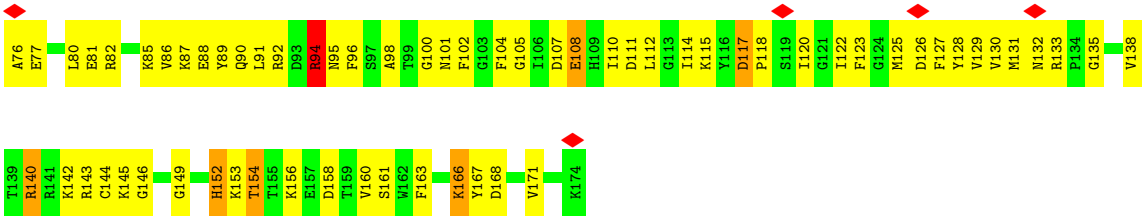
Chain 50:



• Molecule 14: 60S ribosomal protein L11

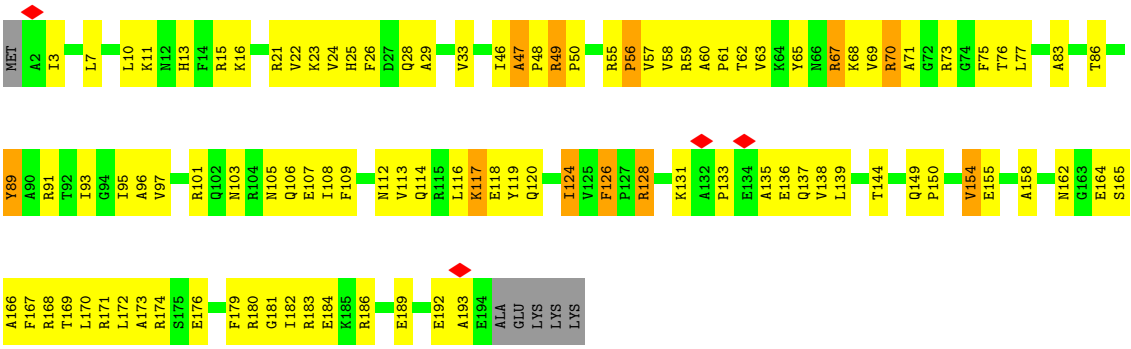
Chain 51:





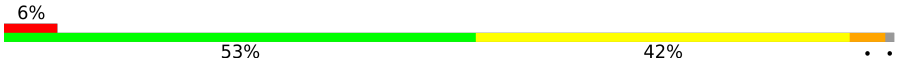
• Molecule 15: 60S ribosomal protein L13

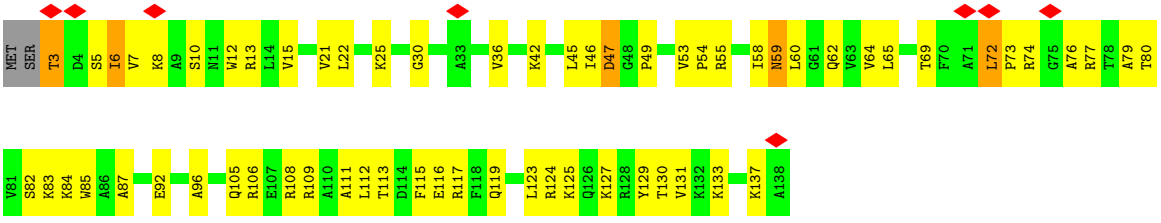
Chain 53:



• Molecule 16: 60S ribosomal protein L14

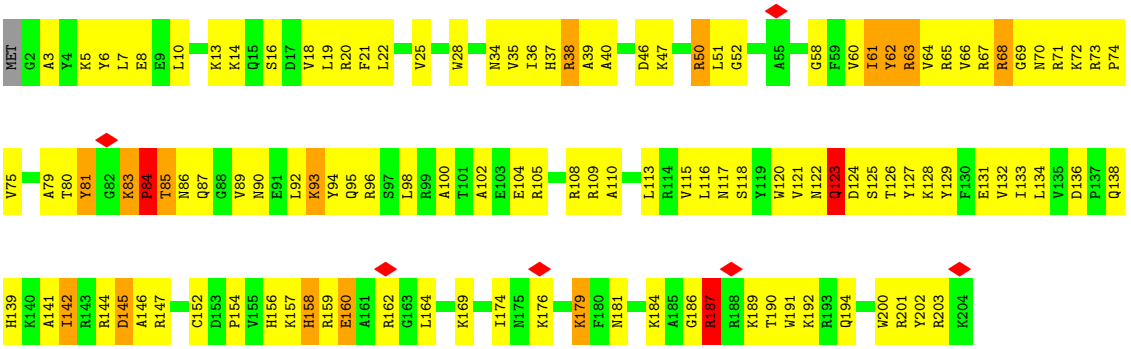
Chain 54:





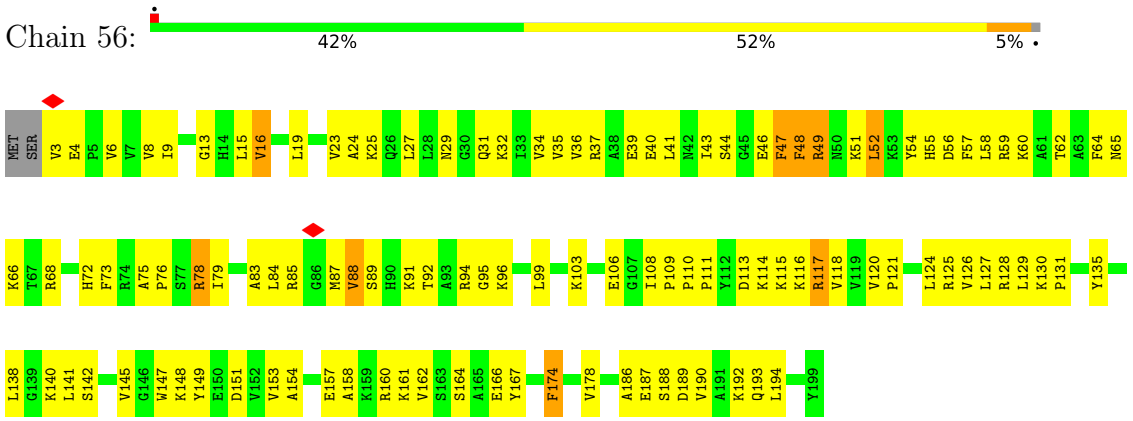
• Molecule 17: 60S ribosomal protein L15

Chain 55:



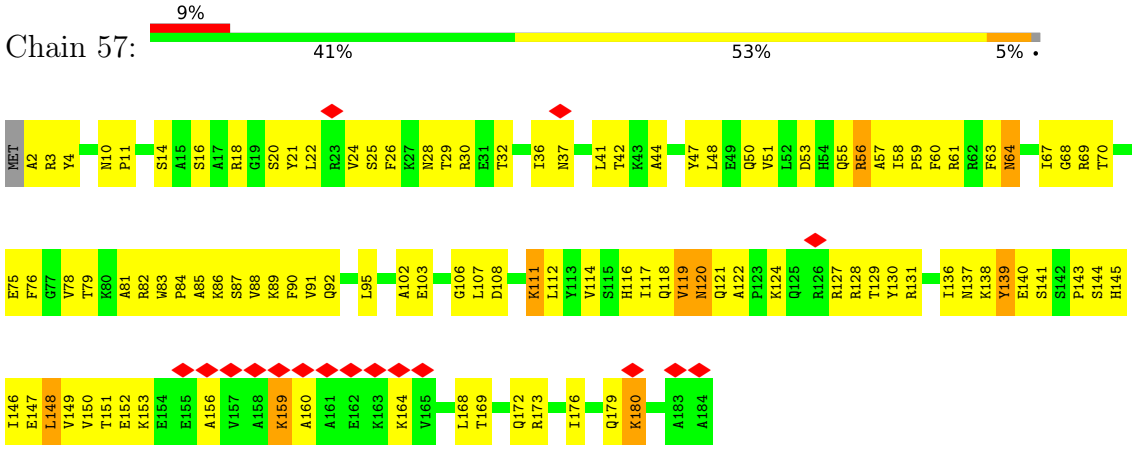
• Molecule 18: 60S ribosomal protein L16

Chain 56:



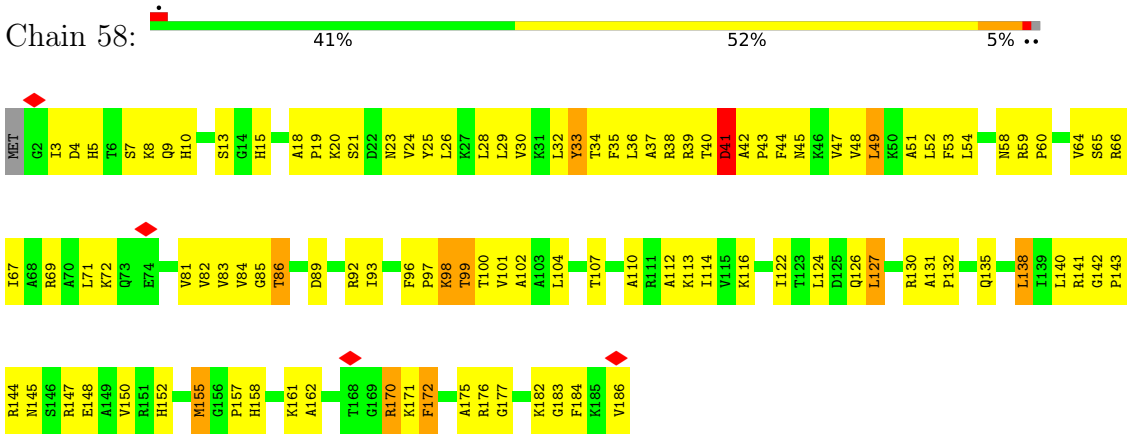
• Molecule 19: 60S ribosomal protein L17

Chain 57:



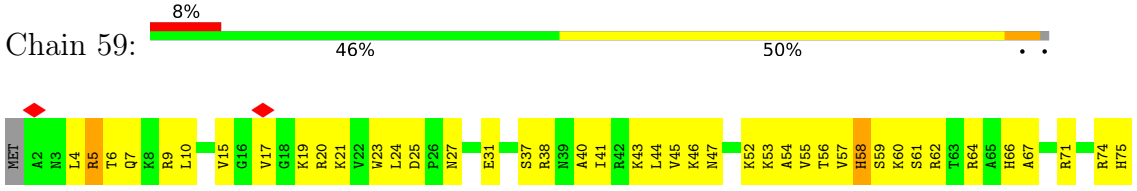
• Molecule 20: 60S ribosomal protein L18

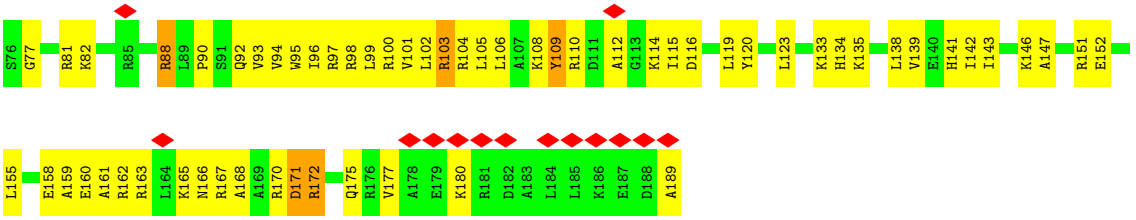
Chain 58:



• Molecule 21: 60S ribosomal protein L19

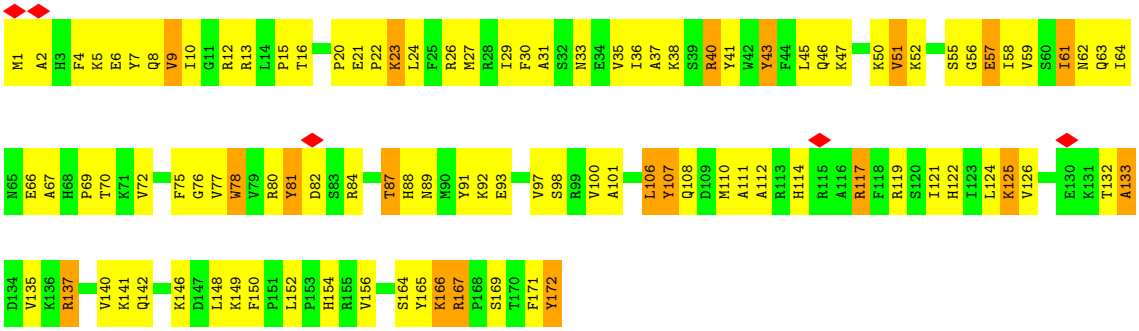
Chain 59:





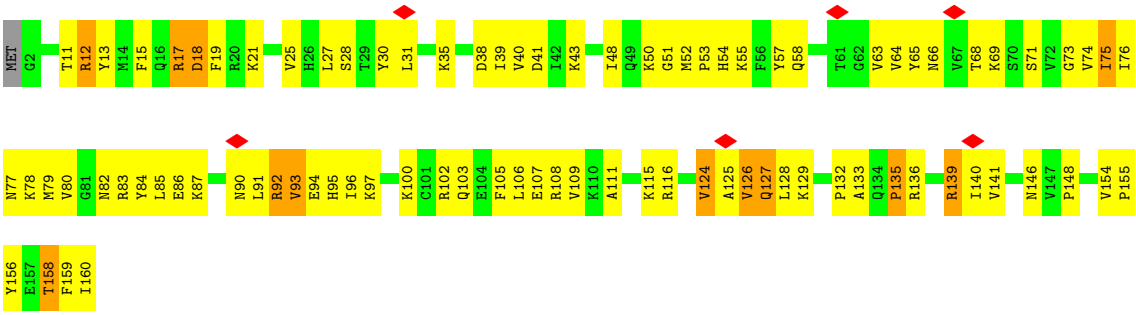
• Molecule 22: 60S ribosomal protein L20

Chain 60:



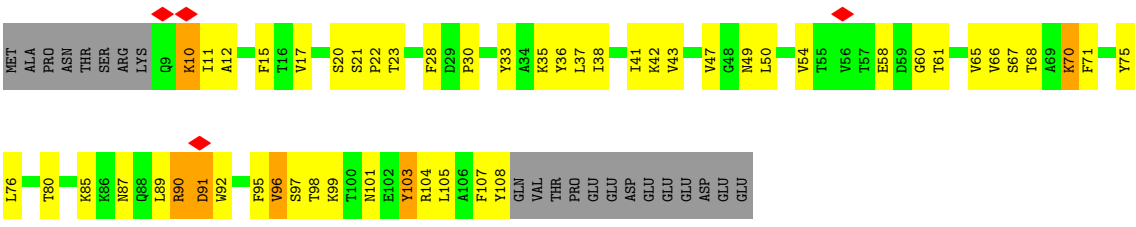
• Molecule 23: 60S ribosomal protein L21

Chain 61:



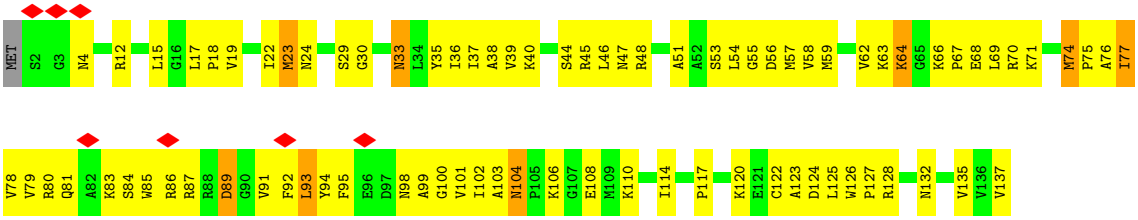
• Molecule 24: 60S ribosomal protein L22

Chain 62:



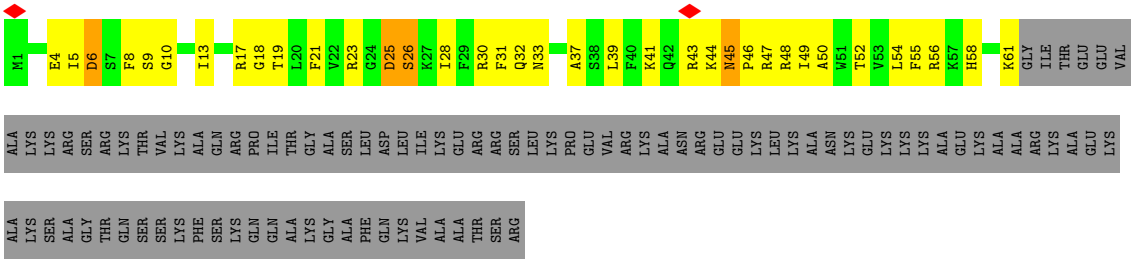
• Molecule 25: 60S ribosomal protein L23

Chain 63:



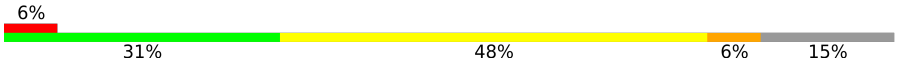
• Molecule 26: 60S ribosomal protein L24

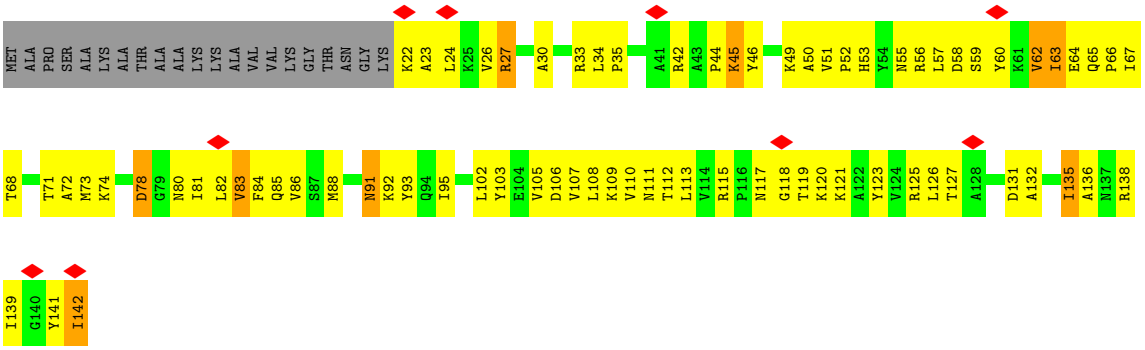
Chain 64:



• Molecule 27: 60S ribosomal protein L25

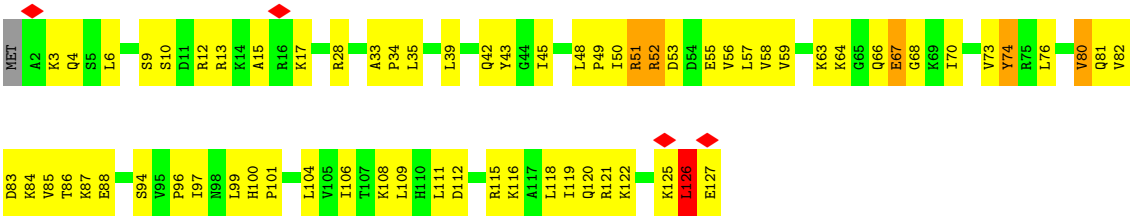
Chain 65:





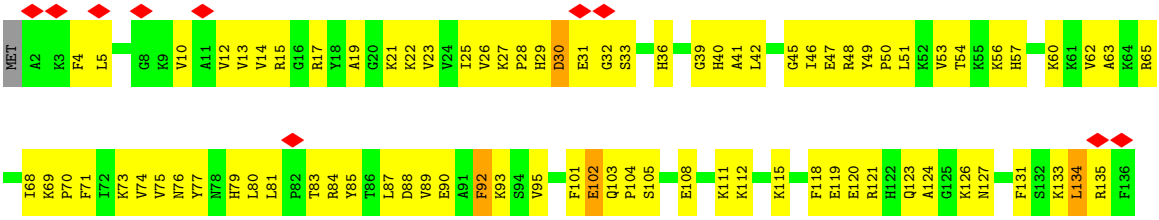
• Molecule 28: 60S ribosomal protein L26

Chain 66:



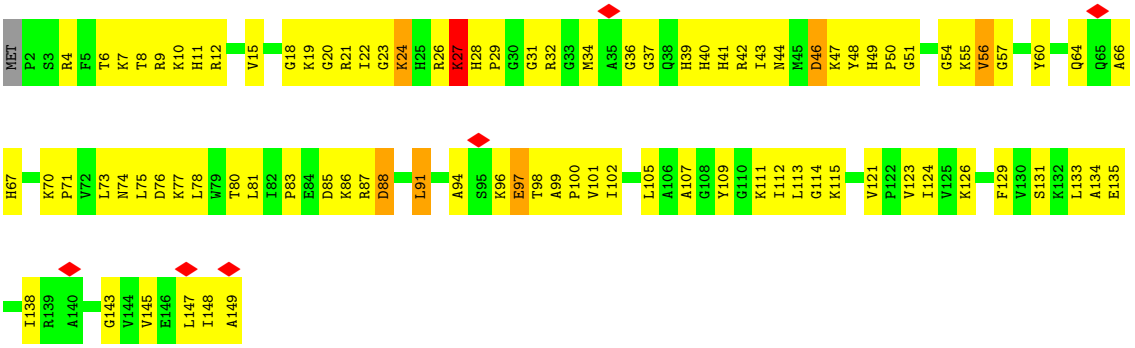
• Molecule 29: 60S ribosomal protein L27

Chain 67:



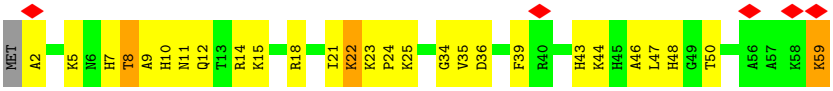
• Molecule 30: 60S ribosomal protein L28

Chain 68:



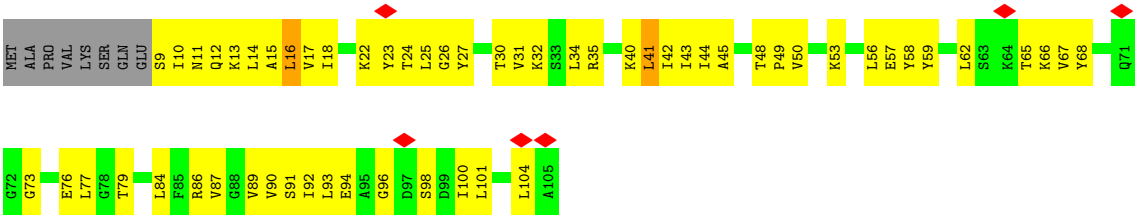
• Molecule 31: 60S ribosomal protein L29

Chain 69:



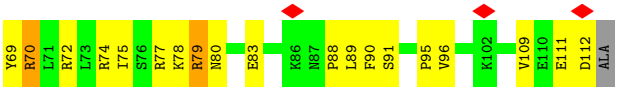
• Molecule 32: 60S ribosomal protein L30

Chain 70:



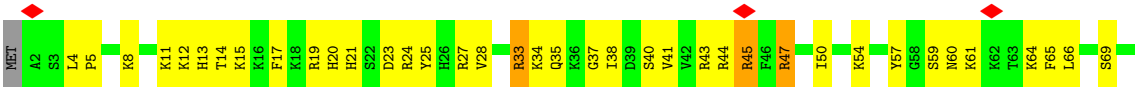
• Molecule 33: 60S ribosomal protein L31

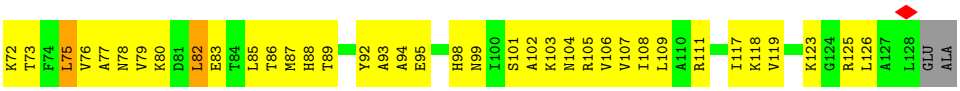
Chain 71:



• Molecule 34: 60S ribosomal protein L32

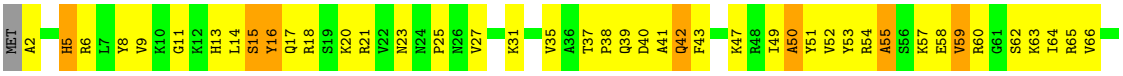
Chain 72:

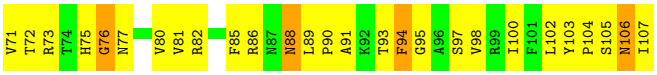




• Molecule 35: 60S ribosomal protein L33

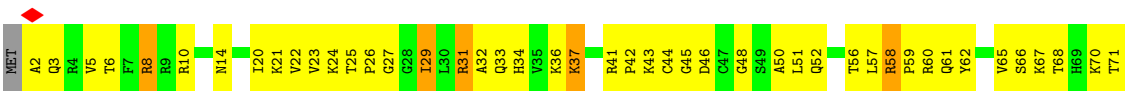
Chain 73:

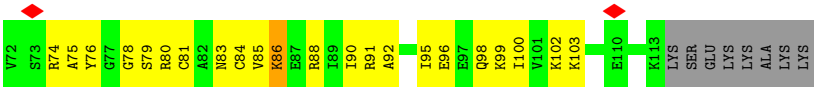




• Molecule 36: 60S ribosomal protein L34

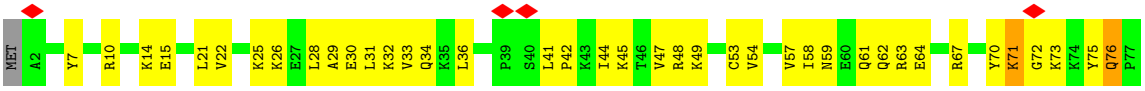
Chain 74:

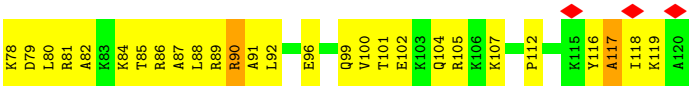




• Molecule 37: 60S ribosomal protein L35

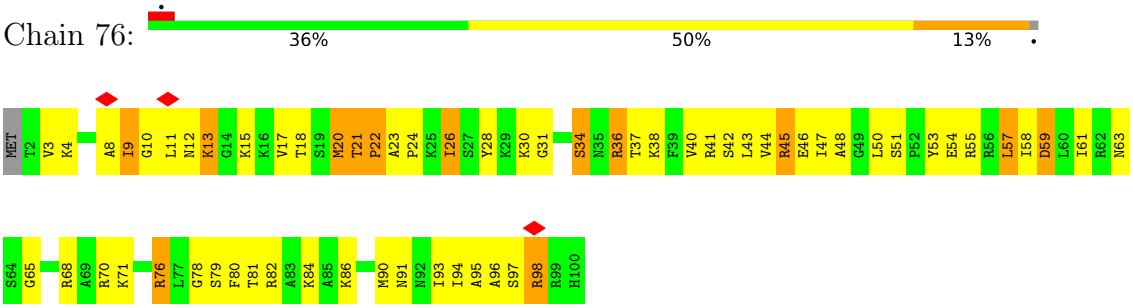
Chain 75:





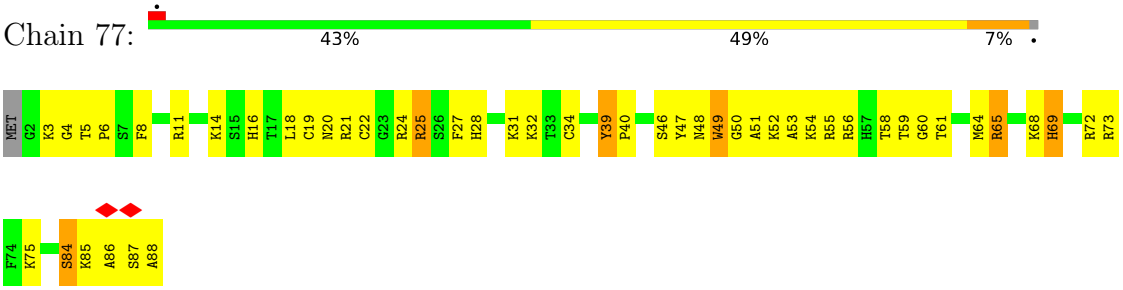
• Molecule 38: 60S ribosomal protein L36

Chain 76:



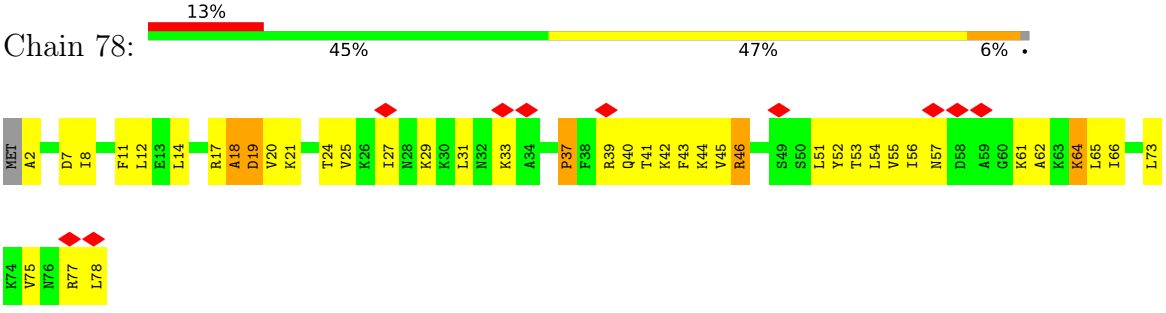
• Molecule 39: 60S ribosomal protein L37

Chain 77:



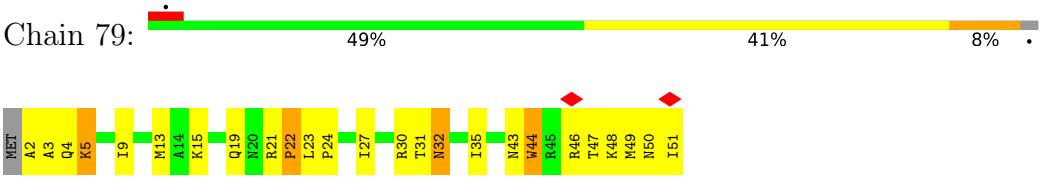
• Molecule 40: 60S ribosomal protein L38

Chain 78:



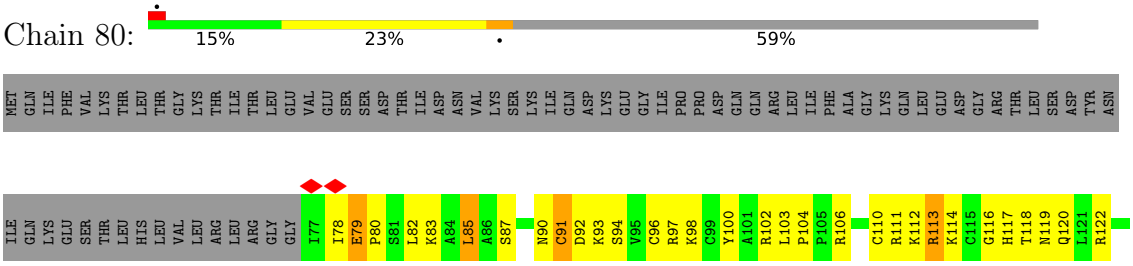
• Molecule 41: 60S ribosomal protein L39

Chain 79:



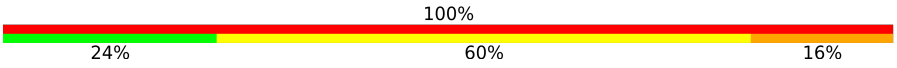
• Molecule 42: 60S ribosomal protein L40

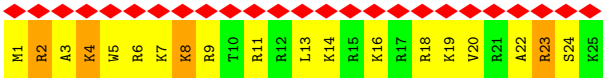
Chain 80:



• Molecule 43: 60S ribosomal protein L41

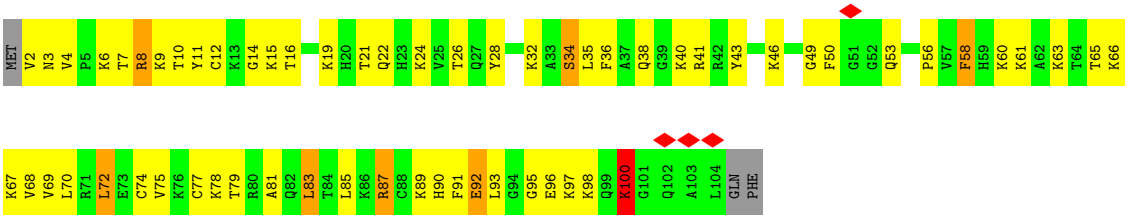
Chain 81:





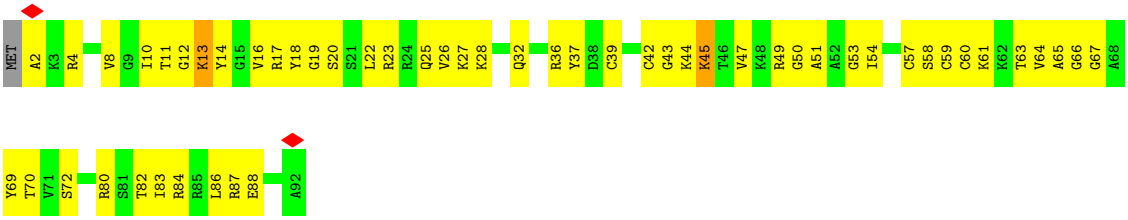
• Molecule 44: 60S ribosomal protein L42

Chain 82:



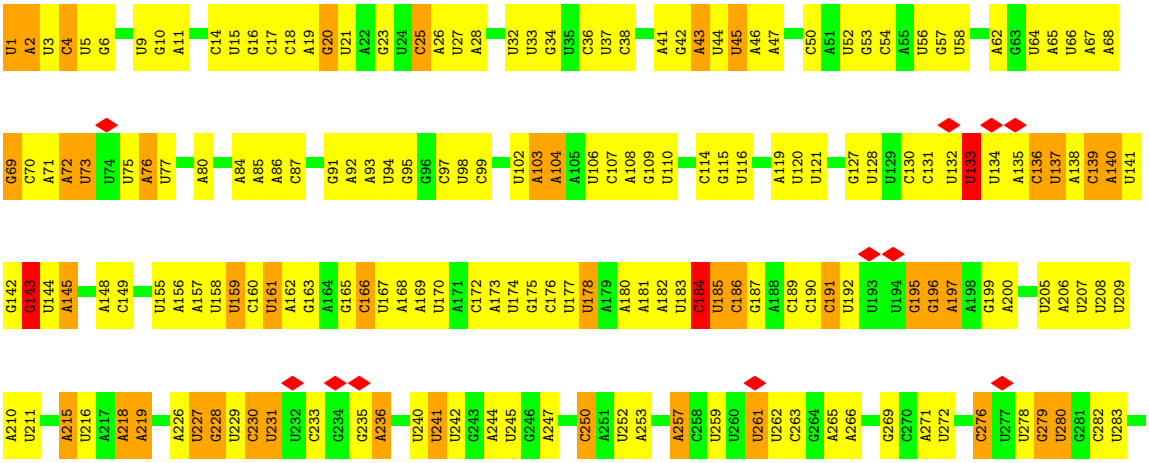
• Molecule 45: 60S ribosomal protein L43

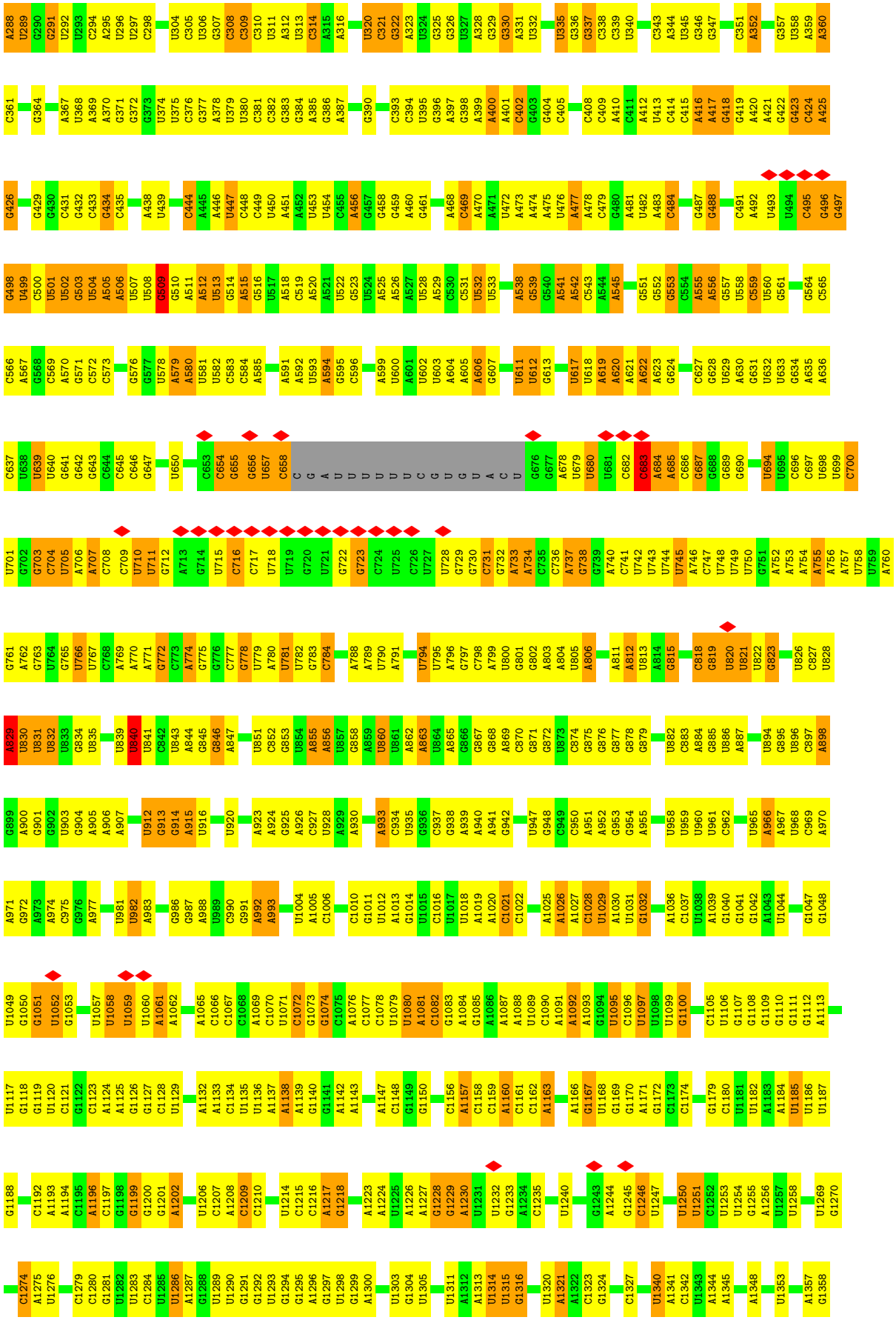
Chain 83:

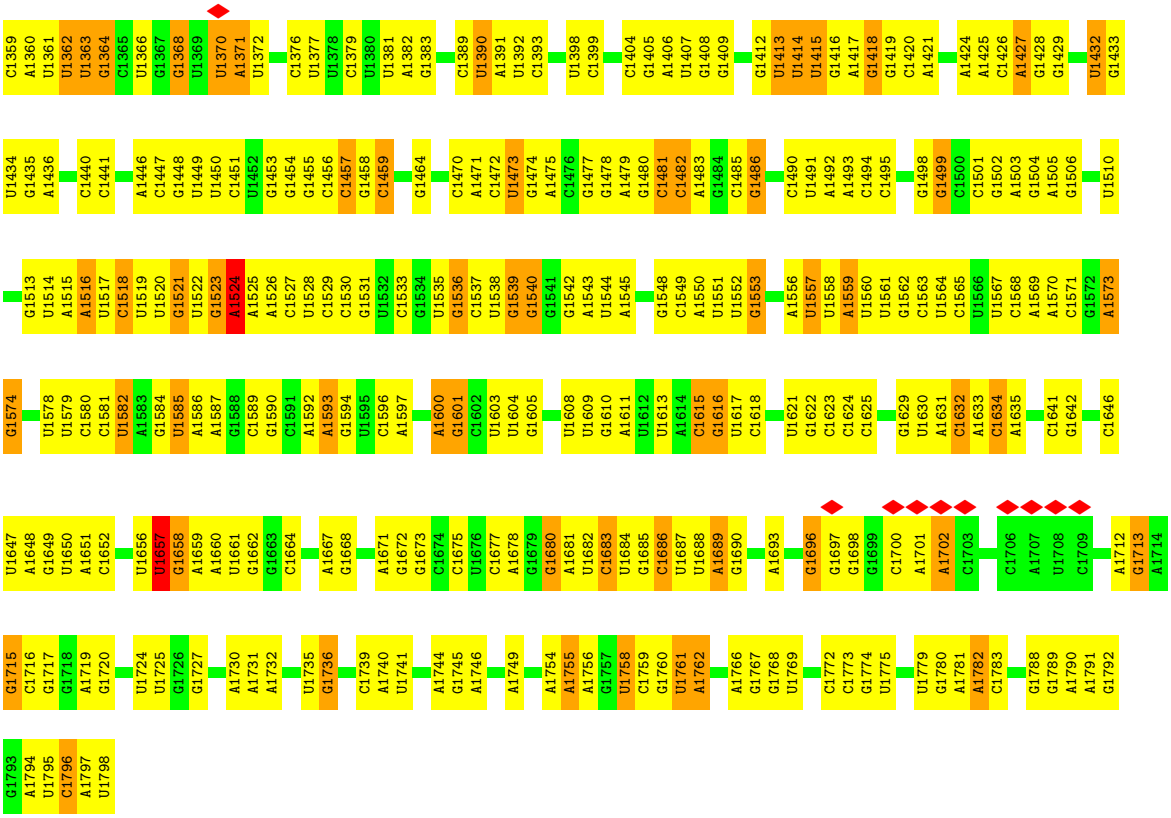


• Molecule 46: 18S ribosomal RNA

Chain 1S:

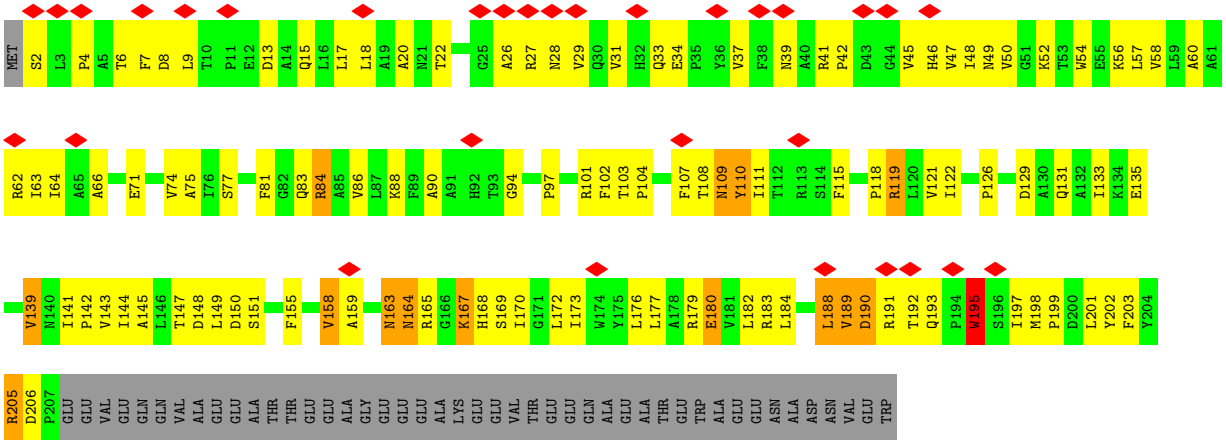






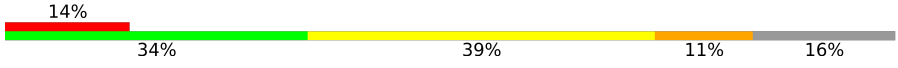
• Molecule 47: 40S ribosomal protein S0

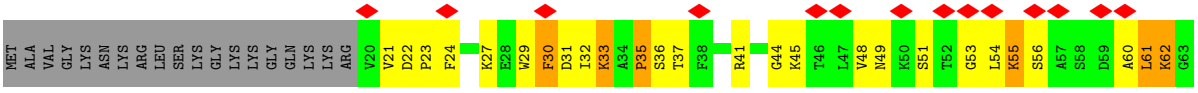
Chain S0:

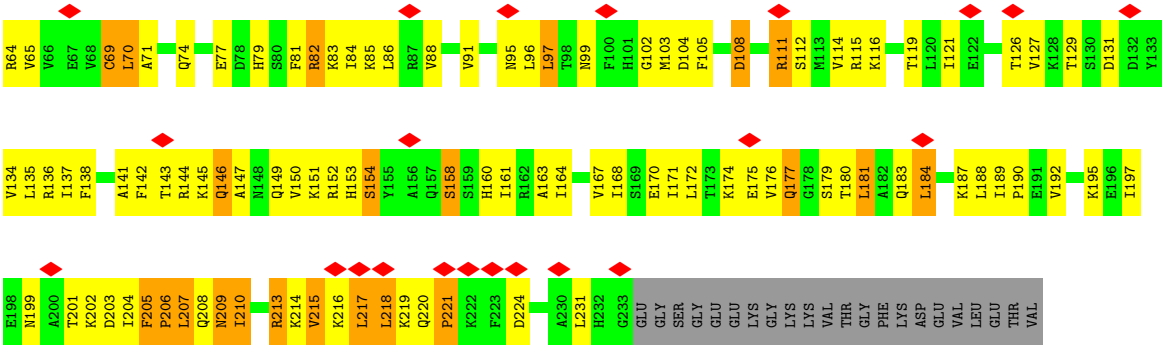


• Molecule 48: 40S ribosomal protein S1

Chain S1:

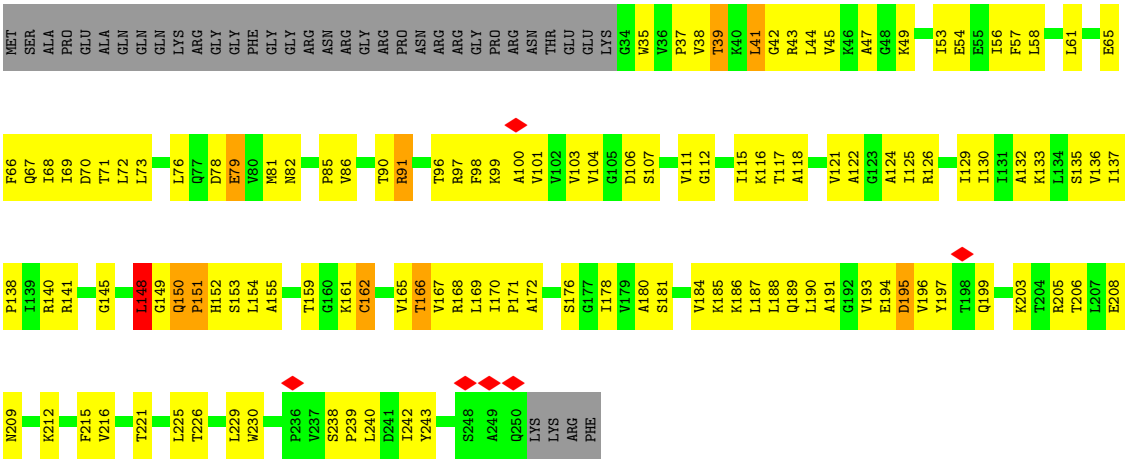






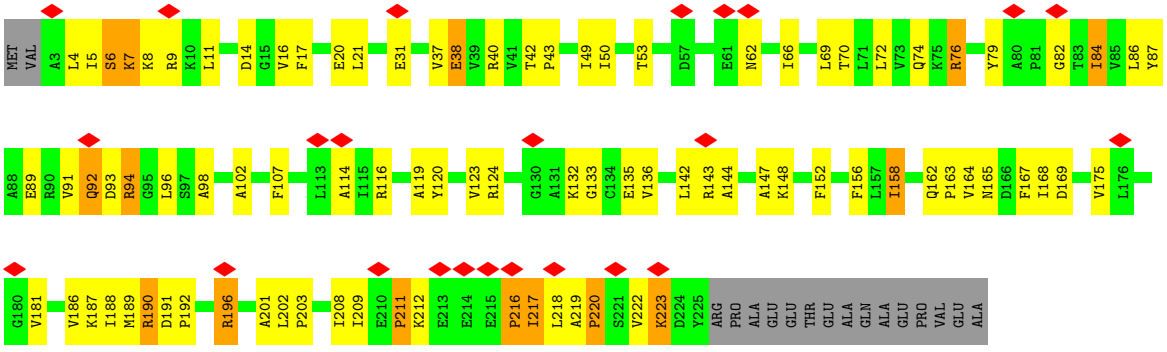
• Molecule 49: 40S ribosomal protein S2

Chain S2:



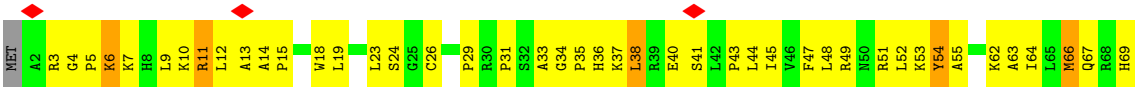
• Molecule 50: 40S ribosomal protein S3

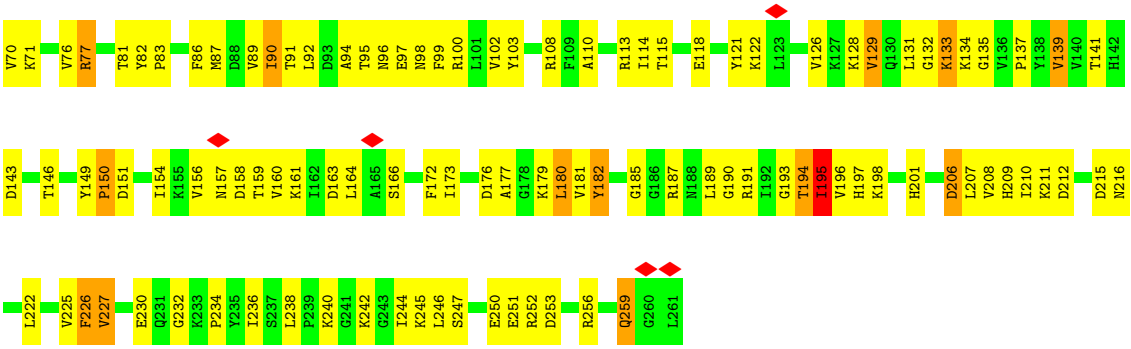
Chain S3:



• Molecule 51: 40S ribosomal protein S4

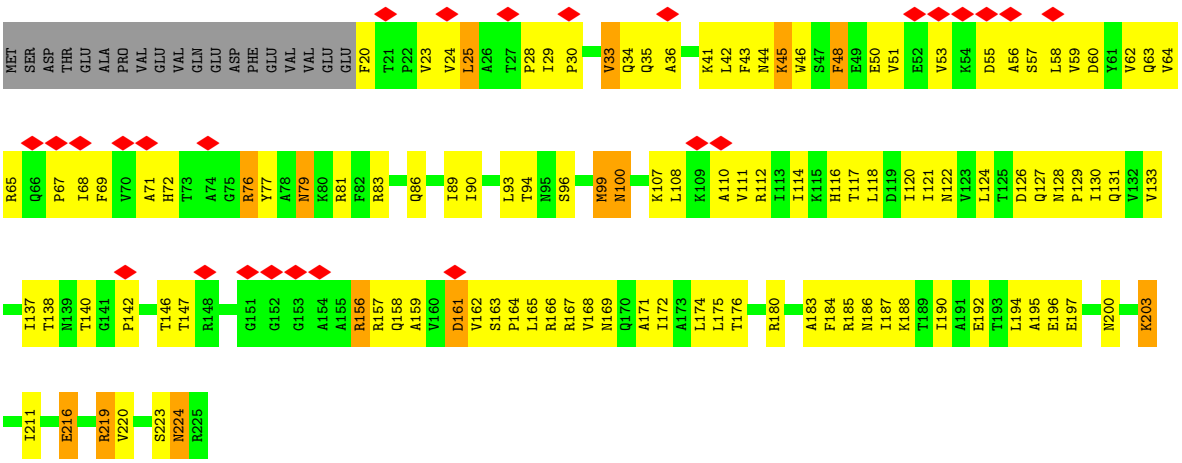
Chain S4:





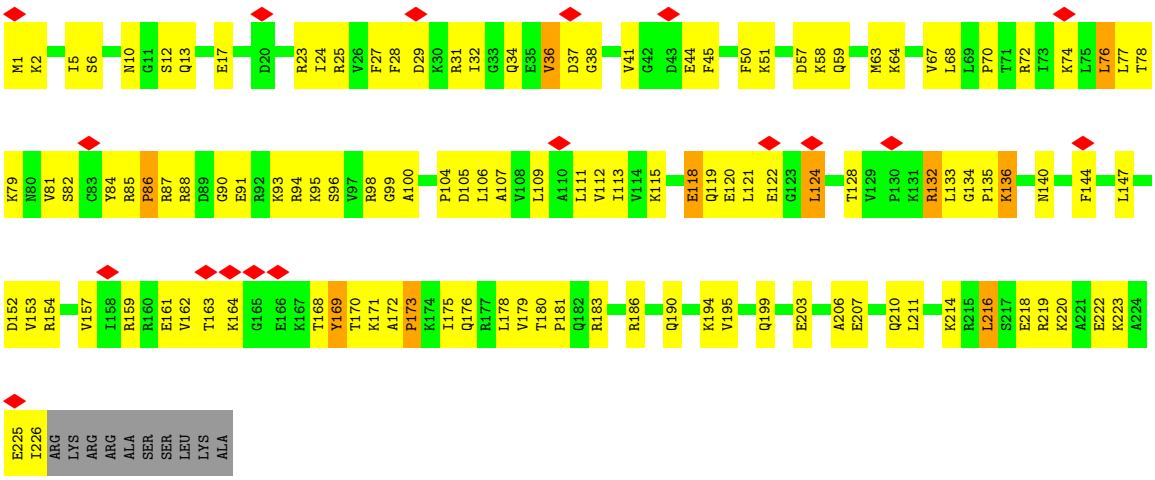
• Molecule 52: 40S ribosomal protein S5

Chain S5:



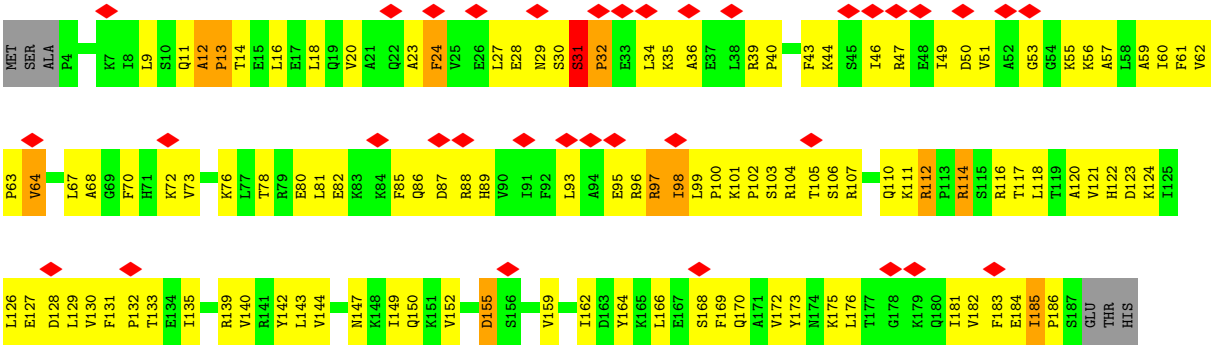
• Molecule 53: 40S ribosomal protein S6

Chain S6:



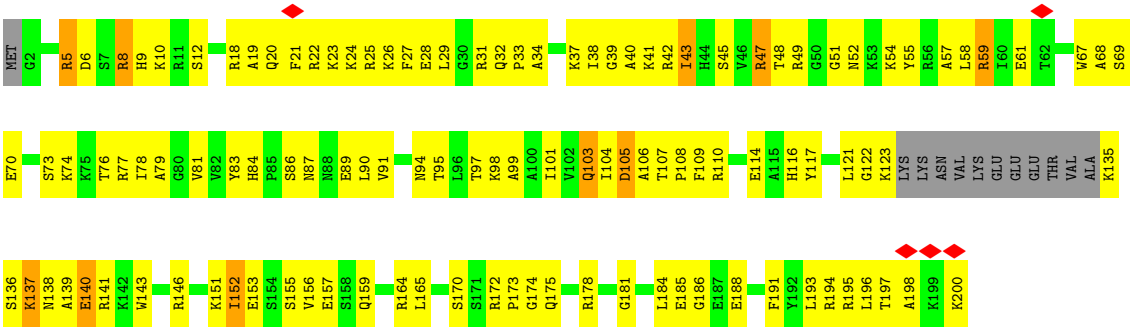
• Molecule 54: 40S ribosomal protein S7

Chain S7:



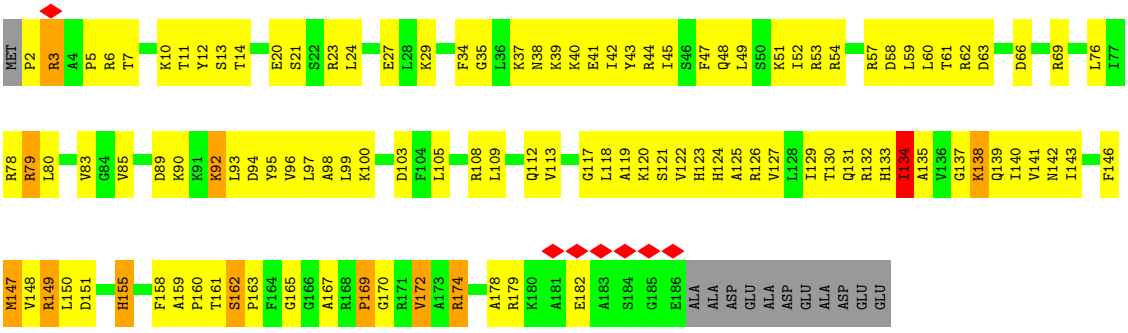
• Molecule 55: 40S ribosomal protein S8

Chain S8:



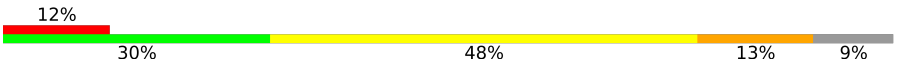
• Molecule 56: 40S ribosomal protein S9

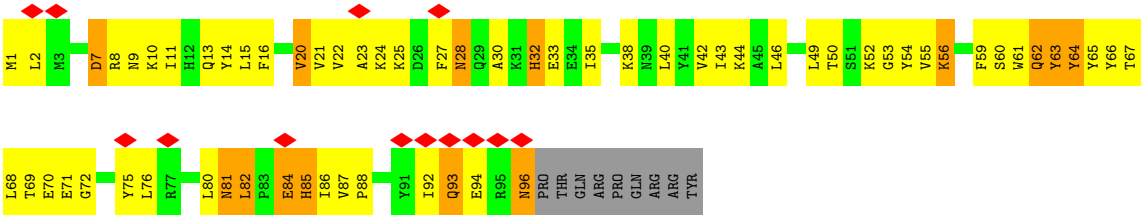
Chain S9:



• Molecule 57: 40S ribosomal protein S10

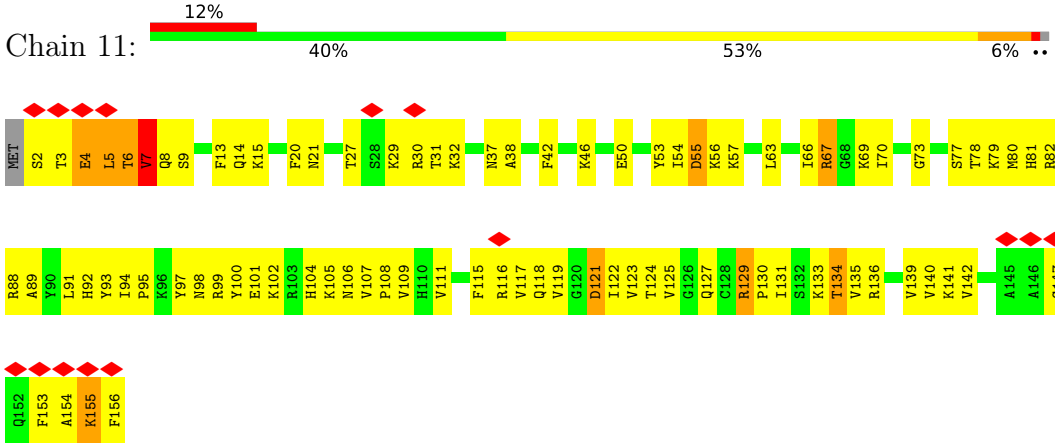
Chain 10:





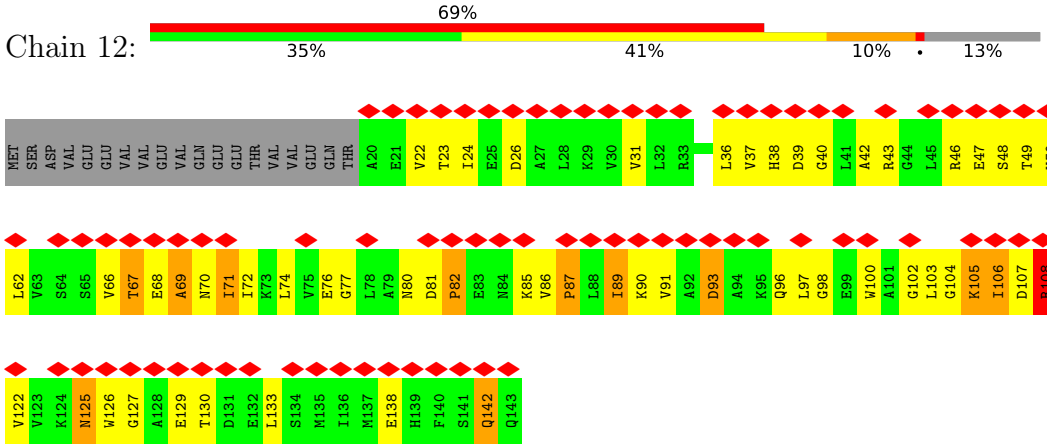
• Molecule 58: 40S ribosomal protein S11

Chain 11:



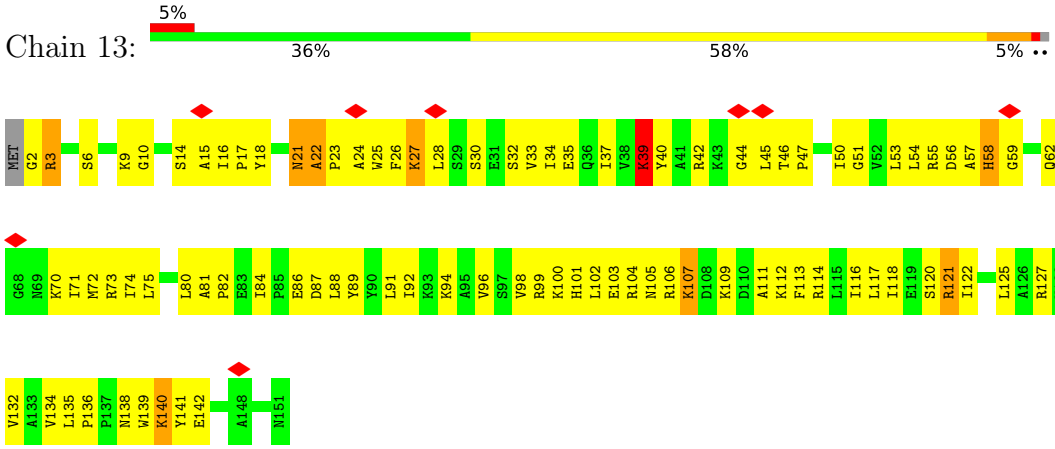
• Molecule 59: 40S ribosomal protein S12

Chain 12:



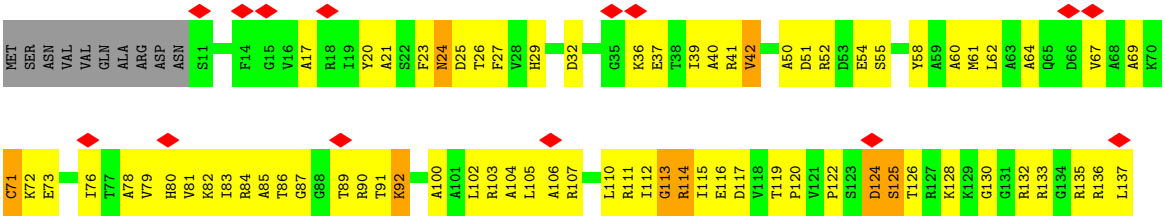
• Molecule 60: 40S ribosomal protein S13

Chain 13:



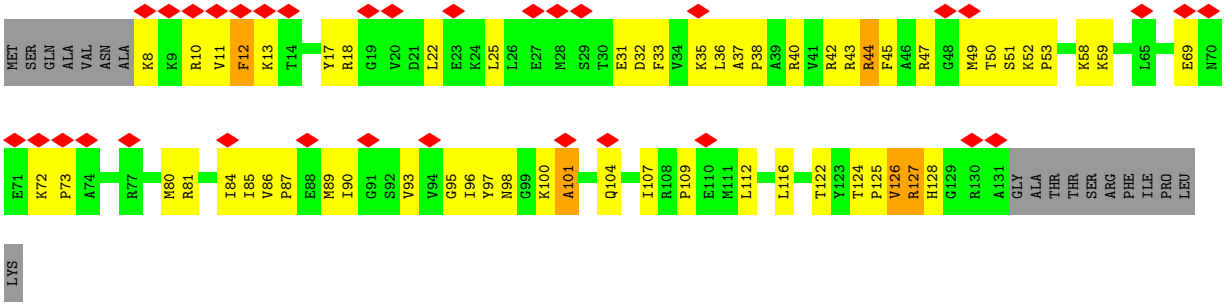
• Molecule 61: 40S ribosomal protein S14

Chain 14:



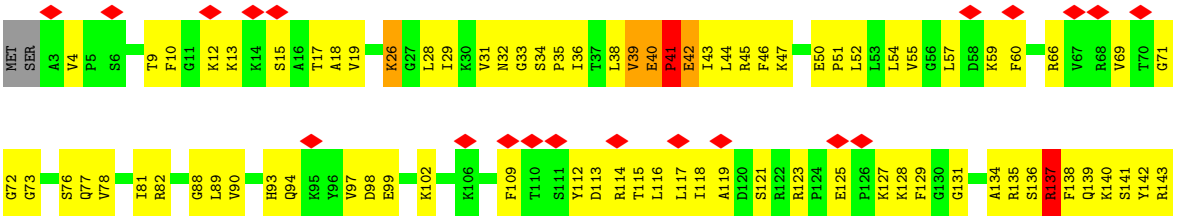
• Molecule 62: 40S ribosomal protein S15

Chain 15:



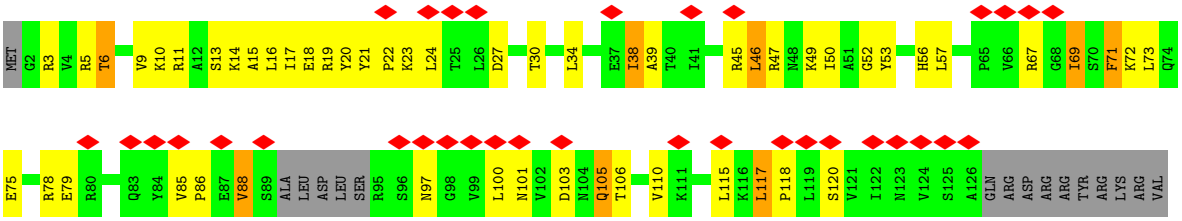
• Molecule 63: 40S ribosomal protein S16

Chain 16:



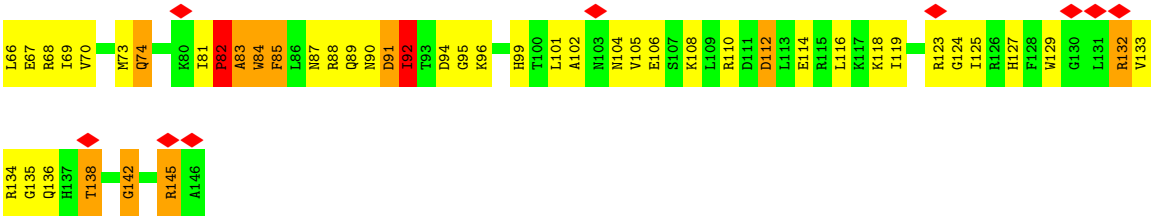
• Molecule 64: 40S ribosomal protein S17

Chain 17:

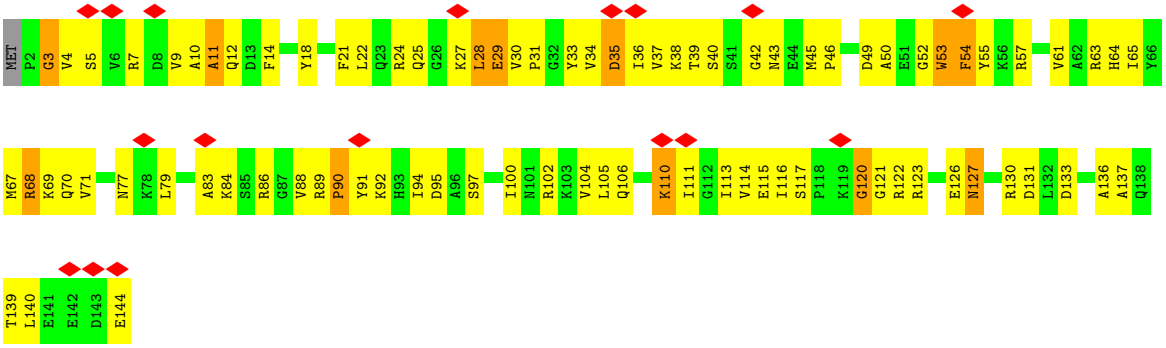


• Molecule 65: 40S ribosomal protein S18

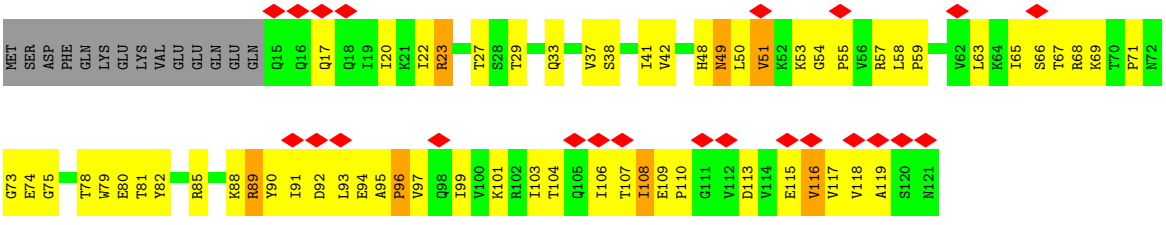
Chain 18:



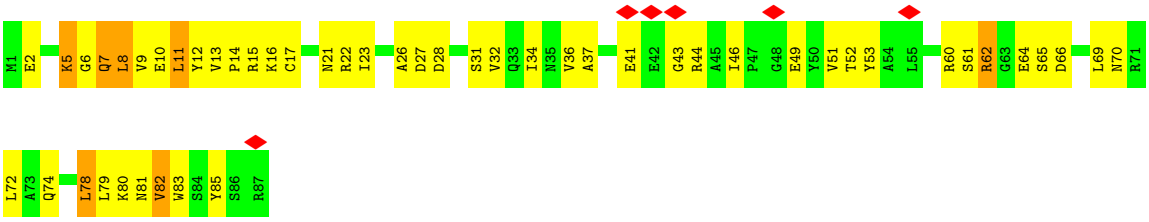
• Molecule 66: 40S ribosomal protein S19



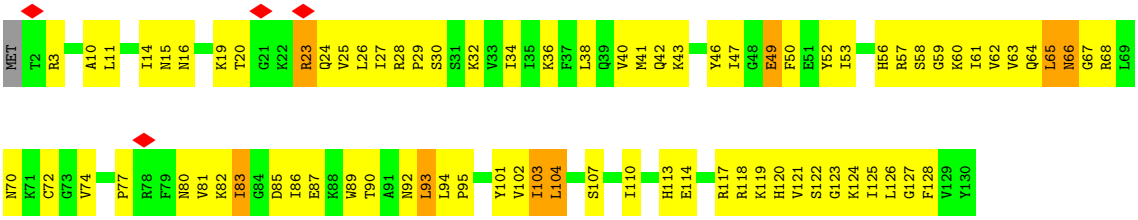
• Molecule 67: 40S ribosomal protein S20



• Molecule 68: 40S ribosomal protein S21

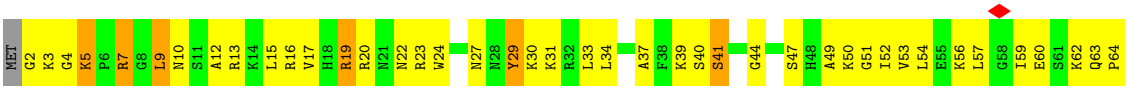


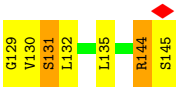
• Molecule 69: 40S ribosomal protein S22



• Molecule 70: 40S ribosomal protein S23

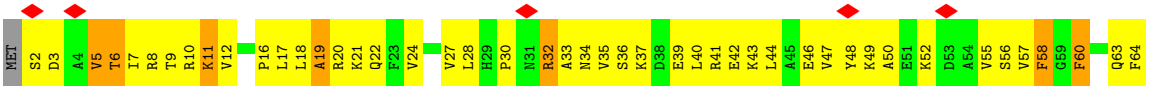
Chain 23:

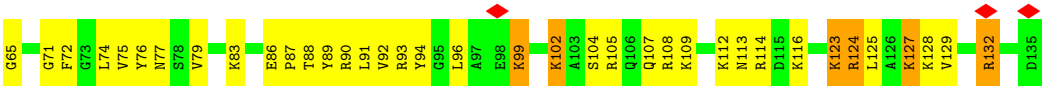




• Molecule 71: 40S ribosomal protein S24

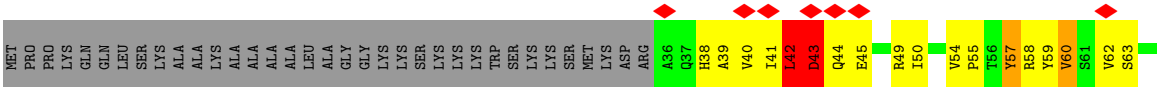
Chain 24:

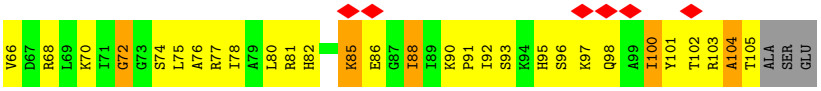




• Molecule 72: 40S ribosomal protein S25

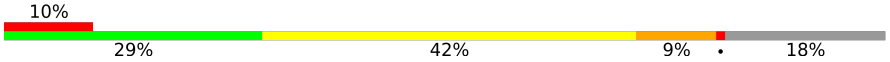
Chain 25:

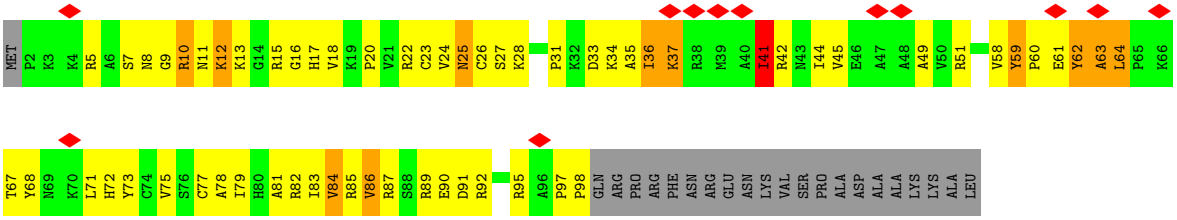




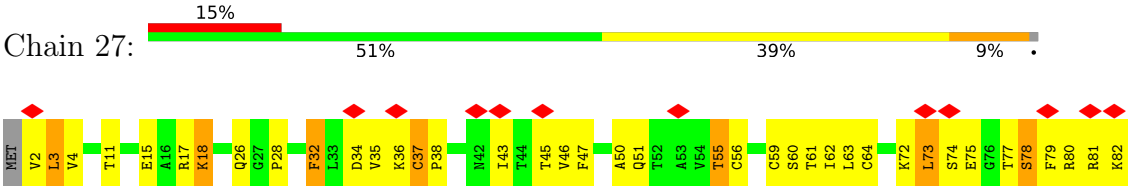
• Molecule 73: 40S ribosomal protein S26

Chain 26:

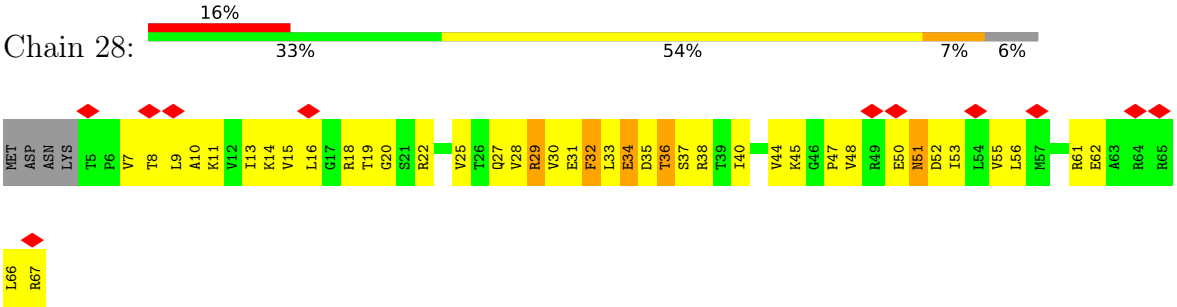




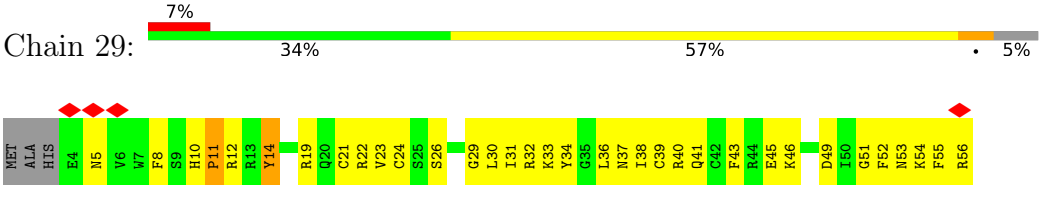
• Molecule 74: 40S ribosomal protein S27



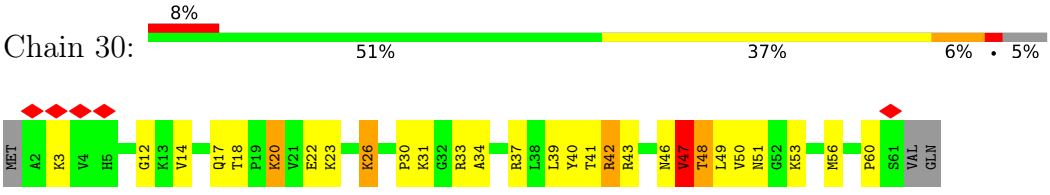
• Molecule 75: 40S ribosomal protein S28



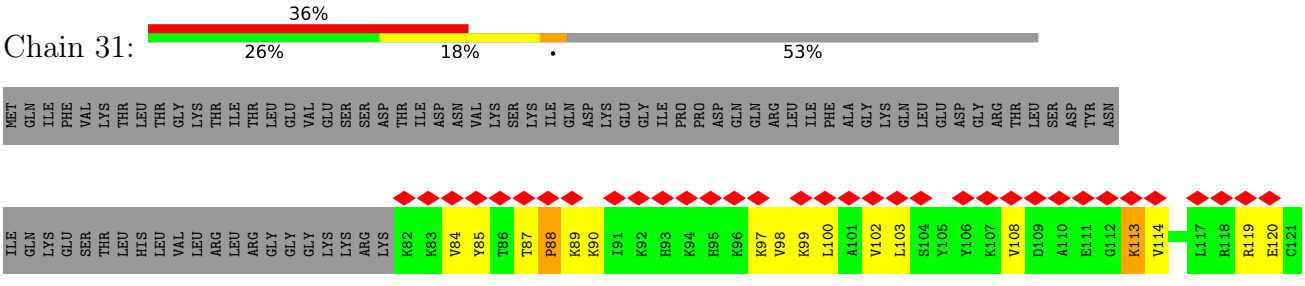
• Molecule 76: 40S ribosomal protein S29

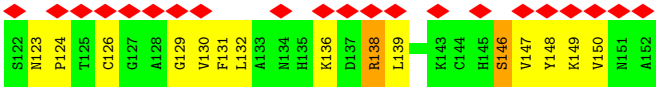


• Molecule 77: 40S ribosomal protein S30



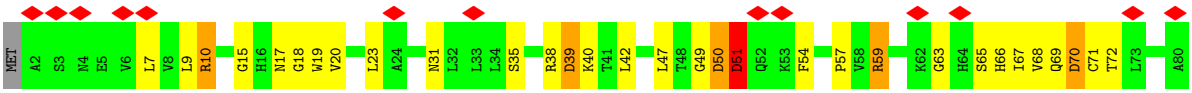
• Molecule 78: 40S ribosomal protein S31

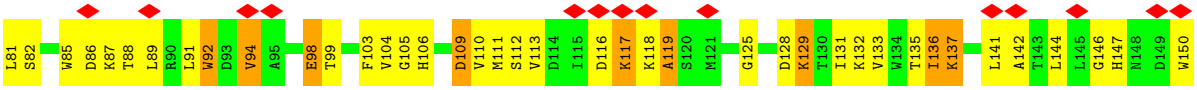


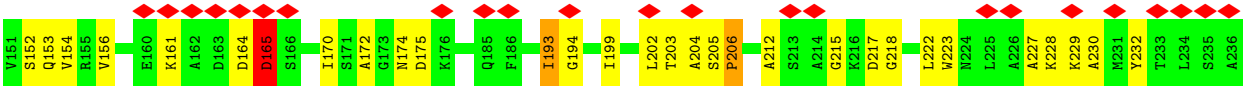


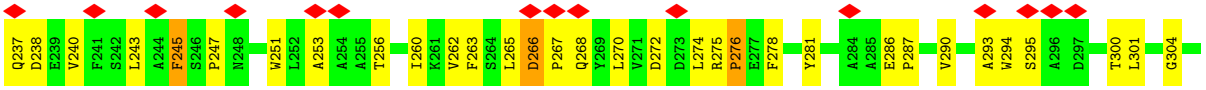
• Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein

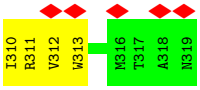
Chain RA:





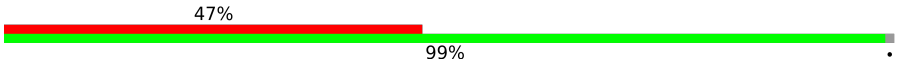


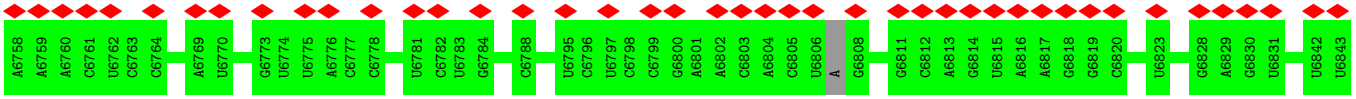


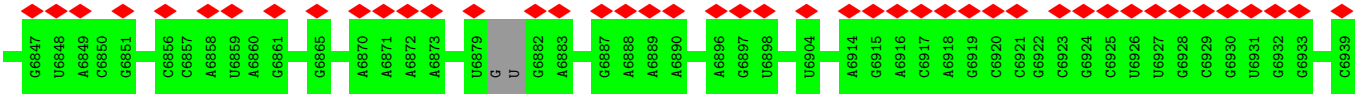


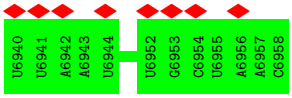
• Molecule 80: TSV IRES mRNA

Chain IR:









4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	52444	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	CTFFIND3, FREALIGN per micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	1150	Depositor
Maximum defocus (nm)	6530	Depositor
Magnification	132138	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	4.026	Depositor
Minimum map value	-1.575	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.284	Depositor
Recommended contour level	0.815	Depositor
Map size (Å)	444.99, 444.99, 444.99	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0595, 1.0595, 1.0595	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	2S	0.87	4/79178 (0.0%)	0.76	26/123444 (0.0%)
2	8S	0.84	2/3747 (0.1%)	0.75	3/5832 (0.1%)
3	5S	0.85	1/2884 (0.0%)	0.72	0/4491
4	L1	0.55	0/1634	0.69	0/2195
5	L2	0.51	0/1952	0.71	0/2622
6	L3	0.55	0/3153	0.68	0/4239
7	L4	0.58	0/2802	0.71	0/3792
8	L5	0.55	0/2426	0.63	0/3271
9	L6	0.62	0/1261	0.72	1/1694 (0.1%)
10	L7	0.57	0/1822	0.70	0/2451
11	L8	0.53	0/1850	0.69	0/2495
12	L9	0.57	0/1540	0.71	0/2073
13	50	0.53	0/1754	0.67	0/2350
14	51	0.50	0/1375	0.66	0/1842
15	53	0.57	0/1568	0.72	0/2106
16	54	0.62	0/1069	0.68	0/1438
17	55	0.57	0/1758	0.67	0/2354
18	56	0.57	0/1586	0.70	0/2128
19	57	0.59	0/1466	0.72	0/1968
20	58	0.56	0/1466	0.73	1/1965 (0.1%)
21	59	0.48	0/1539	0.68	0/2050
22	60	0.59	0/1482	0.67	0/1990
23	61	0.57	0/1301	0.68	0/1743
24	62	0.52	0/812	0.63	0/1099
25	63	0.54	0/1019	0.70	0/1369
26	64	0.53	0/521	0.66	0/691
27	65	0.53	0/984	0.69	0/1325
28	66	0.54	0/1005	0.68	0/1341
29	67	0.47	0/1119	0.61	0/1497
30	68	0.56	0/1205	0.72	0/1612
31	69	0.53	0/474	0.71	0/629
32	70	0.49	0/751	0.64	0/1008
33	71	0.52	0/904	0.66	0/1213
34	72	0.58	0/1041	0.70	0/1394

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
35	73	0.64	0/869	0.70	0/1168
36	74	0.50	0/891	0.66	0/1191
37	75	0.52	0/979	0.68	0/1301
38	76	0.54	0/779	0.74	0/1034
39	77	0.56	0/697	0.70	0/923
40	78	0.49	0/619	0.62	0/826
41	79	0.54	0/444	0.70	0/588
42	80	0.53	0/424	0.66	0/562
43	81	0.74	0/235	0.76	0/300
44	82	0.57	0/839	0.71	0/1108
45	83	0.51	0/702	0.66	0/934
46	1S	0.78	1/42445 (0.0%)	0.75	12/66138 (0.0%)
47	S0	0.49	0/1653	0.64	0/2261
48	S1	0.47	0/1735	0.62	0/2335
49	S2	0.45	0/1665	0.65	0/2263
50	S3	0.49	0/1759	0.63	0/2368
51	S4	0.45	0/2110	0.64	0/2839
52	S5	0.48	0/1630	0.63	0/2202
53	S6	0.47	0/1844	0.67	0/2464
54	S7	0.49	0/1506	0.67	1/2028 (0.0%)
55	S8	0.49	0/1515	0.65	0/2021
56	S9	0.43	0/1519	0.67	0/2035
57	10	0.58	0/837	0.65	0/1131
58	11	0.52	0/1273	0.63	0/1712
59	12	0.63	0/943	0.74	0/1274
60	13	0.48	0/1216	0.61	0/1638
61	14	0.49	0/953	0.66	0/1279
62	15	0.52	0/1012	0.65	0/1356
63	16	0.50	0/1126	0.64	0/1510
64	17	0.52	0/974	0.67	0/1304
65	18	0.51	0/1212	0.67	0/1628
66	19	0.51	0/1131	0.64	0/1517
67	20	0.52	0/866	0.61	0/1169
68	21	0.50	0/694	0.63	0/935
69	22	0.46	0/1039	0.65	0/1395
70	23	0.46	0/1140	0.66	1/1518 (0.1%)
71	24	0.47	0/1088	0.59	0/1449
72	25	0.52	0/571	0.71	0/768
73	26	0.46	0/782	0.61	0/1047
74	27	0.50	0/621	0.67	0/838
75	28	0.47	0/500	0.65	0/670
76	29	0.51	0/454	0.59	0/602
77	30	0.48	0/483	0.62	0/643

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	31	0.56	0/505	0.68	1/682 (0.1%)
79	RA	0.53	0/2498	0.64	0/3398
All	All	0.73	8/219225 (0.0%)	0.73	46/322063 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	2S	0	108
2	8S	0	5
3	5S	0	1
6	L3	0	1
46	1S	0	45
All	All	0	160

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	1S	1	U	OP3-P	-7.30	1.52	1.61
2	8S	1	A	OP3-P	-6.88	1.52	1.61
3	5S	1	G	OP3-P	-6.71	1.53	1.61
1	2S	485	C	N1-C2	6.21	1.46	1.40
1	2S	2095	G	C5-C6	-5.33	1.37	1.42

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
46	1S	1600	A	N9-C1'-C2'	7.24	123.41	114.00
46	1S	1524	A	O4'-C1'-N9	7.00	113.80	108.20
46	1S	143	G	N9-C1'-C2'	6.38	122.29	114.00
1	2S	315	C	N1-C1'-C2'	6.28	122.16	114.00
1	2S	1172	G	N9-C1'-C2'	6.16	122.00	114.00

There are no chirality outliers.

5 of 160 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2S	107	A	Sidechain
1	2S	26	A	Sidechain

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Mol	Chain	Res	Type	Group
1	2S	40	A	Sidechain
1	2S	59	G	Sidechain
1	2S	93	C	Sidechain

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2S	70742	0	35551	2329	0
2	8S	3354	0	1695	110	0
3	5S	2580	0	1304	89	0
4	L1	1609	0	1701	132	0
5	L2	1918	0	1987	194	0
6	L3	3082	0	3165	270	0
7	L4	2750	0	2863	230	0
8	L5	2376	0	2325	135	0
9	L6	1240	0	1326	100	0
10	L7	1785	0	1862	137	0
11	L8	1818	0	1908	131	0
12	L9	1519	0	1587	117	0
13	50	1718	0	1754	106	0
14	51	1354	0	1383	100	0
15	53	1543	0	1608	131	0
16	54	1054	0	1149	69	0
17	55	1721	0	1779	162	0
18	56	1556	0	1659	122	0
19	57	1443	0	1485	119	0
20	58	1442	0	1543	133	0
21	59	1522	0	1617	104	0
22	60	1446	0	1487	124	0
23	61	1277	0	1323	107	0
24	62	796	0	812	46	0
25	63	1004	0	1048	94	0
26	64	509	0	537	36	0
27	65	969	0	1036	82	0
28	66	994	0	1081	74	0
29	67	1093	0	1155	81	0
30	68	1174	0	1215	109	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	69	463	0	491	31	0
32	70	743	0	797	52	0
33	71	890	0	938	66	0
34	72	1020	0	1090	76	0
35	73	851	0	880	76	0
36	74	881	0	949	77	0
37	75	970	0	1078	70	0
38	76	772	0	849	73	0
39	77	682	0	687	57	0
40	78	613	0	682	36	0
41	79	437	0	475	26	0
42	80	418	0	459	32	0
43	81	234	0	284	24	0
44	82	827	0	901	63	0
45	83	695	0	738	68	0
46	1S	37949	0	19093	1253	0
47	S0	1612	0	1623	101	0
48	S1	1709	0	1784	147	0
49	S2	1635	0	1723	130	0
50	S3	1734	0	1817	103	0
51	S4	2069	0	2154	156	0
52	S5	1610	0	1675	130	0
53	S6	1820	0	1918	125	0
54	S7	1481	0	1572	142	0
55	S8	1490	0	1525	124	0
56	S9	1494	0	1573	120	0
57	10	817	0	804	76	0
58	11	1245	0	1314	108	0
59	12	935	0	975	67	0
60	13	1193	0	1255	107	0
61	14	942	0	979	84	0
62	15	991	0	1035	60	0
63	16	1106	0	1166	79	0
64	17	965	0	1026	64	0
65	18	1193	0	1222	93	0
66	19	1113	0	1124	98	0
67	20	856	0	917	73	0
68	21	685	0	672	44	0
69	22	1022	0	1060	114	0
70	23	1122	0	1196	122	0
71	24	1074	0	1132	81	0
72	25	563	0	603	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	26	769	0	818	76	0
74	27	611	0	633	32	0
75	28	498	0	535	46	0
76	29	444	0	436	36	0
77	30	475	0	525	43	0
78	31	498	0	441	25	0
79	RA	2445	0	2401	111	0
80	IR	198	0	0	0	0
All	All	204247	0	150969	9608	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 27.

The worst 5 of 9608 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:S3:209:ILE:HG22	64:17:38:ILE:HG13	1.29	1.15
46:1S:1701:A:H3'	46:1S:1702:A:H5"	1.25	1.14
6:L3:86:VAL:HA	6:L3:162:VAL:HG12	1.21	1.13
1:2S:632:G:H5"	18:56:94:ARG:HD2	1.26	1.13
9:L6:43:LEU:HD13	35:73:103:TYR:HB3	1.31	1.13

There are no symmetry-related clashes.

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
4	L1	202/217 (93%)	137 (68%)	50 (25%)	15 (7%)	1 13
5	L2	250/254 (98%)	196 (78%)	44 (18%)	10 (4%)	3 23
6	L3	384/387 (99%)	322 (84%)	51 (13%)	11 (3%)	4 29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	L4	359/362 (99%)	284 (79%)	48 (13%)	27 (8%)	1	13
8	L5	294/297 (99%)	244 (83%)	40 (14%)	10 (3%)	3	26
9	L6	152/176 (86%)	131 (86%)	16 (10%)	5 (3%)	4	26
10	L7	220/244 (90%)	192 (87%)	19 (9%)	9 (4%)	3	22
11	L8	231/256 (90%)	184 (80%)	38 (16%)	9 (4%)	3	23
12	L9	189/191 (99%)	153 (81%)	30 (16%)	6 (3%)	4	26
13	50	207/221 (94%)	166 (80%)	36 (17%)	5 (2%)	6	33
14	51	167/174 (96%)	130 (78%)	29 (17%)	8 (5%)	2	20
15	53	191/199 (96%)	150 (78%)	35 (18%)	6 (3%)	4	27
16	54	134/138 (97%)	114 (85%)	17 (13%)	3 (2%)	6	35
17	55	201/204 (98%)	156 (78%)	36 (18%)	9 (4%)	2	22
18	56	195/199 (98%)	177 (91%)	14 (7%)	4 (2%)	7	36
19	57	181/184 (98%)	143 (79%)	34 (19%)	4 (2%)	6	35
20	58	183/186 (98%)	153 (84%)	23 (13%)	7 (4%)	3	24
21	59	186/189 (98%)	168 (90%)	14 (8%)	4 (2%)	6	35
22	60	170/172 (99%)	140 (82%)	25 (15%)	5 (3%)	4	29
23	61	157/160 (98%)	128 (82%)	19 (12%)	10 (6%)	1	16
24	62	98/121 (81%)	76 (78%)	18 (18%)	4 (4%)	3	22
25	63	134/137 (98%)	105 (78%)	24 (18%)	5 (4%)	3	24
26	64	59/155 (38%)	43 (73%)	13 (22%)	3 (5%)	2	19
27	65	119/142 (84%)	97 (82%)	17 (14%)	5 (4%)	3	22
28	66	124/127 (98%)	104 (84%)	16 (13%)	4 (3%)	4	26
29	67	133/136 (98%)	110 (83%)	20 (15%)	3 (2%)	6	34
30	68	146/149 (98%)	117 (80%)	26 (18%)	3 (2%)	7	36
31	69	56/59 (95%)	43 (77%)	11 (20%)	2 (4%)	3	25
32	70	95/105 (90%)	89 (94%)	4 (4%)	2 (2%)	7	36
33	71	107/113 (95%)	91 (85%)	14 (13%)	2 (2%)	8	38
34	72	125/130 (96%)	109 (87%)	15 (12%)	1 (1%)	19	60
35	73	104/107 (97%)	79 (76%)	17 (16%)	8 (8%)	1	13
36	74	110/121 (91%)	88 (80%)	18 (16%)	4 (4%)	3	25
37	75	117/120 (98%)	107 (92%)	6 (5%)	4 (3%)	3	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
38	76	97/100 (97%)	76 (78%)	13 (13%)	8 (8%)	1 12
39	77	85/88 (97%)	67 (79%)	16 (19%)	2 (2%)	6 33
40	78	75/78 (96%)	64 (85%)	7 (9%)	4 (5%)	2 19
41	79	48/51 (94%)	39 (81%)	8 (17%)	1 (2%)	7 36
42	80	50/128 (39%)	42 (84%)	6 (12%)	2 (4%)	3 23
43	81	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2 22
44	82	101/106 (95%)	79 (78%)	18 (18%)	4 (4%)	3 23
45	83	89/92 (97%)	75 (84%)	13 (15%)	1 (1%)	14 52
47	S0	204/252 (81%)	163 (80%)	29 (14%)	12 (6%)	1 17
48	S1	212/255 (83%)	154 (73%)	45 (21%)	13 (6%)	1 16
49	S2	215/254 (85%)	177 (82%)	30 (14%)	8 (4%)	3 24
50	S3	221/240 (92%)	184 (83%)	24 (11%)	13 (6%)	1 17
51	S4	258/261 (99%)	203 (79%)	45 (17%)	10 (4%)	3 23
52	S5	204/225 (91%)	165 (81%)	32 (16%)	7 (3%)	3 26
53	S6	224/236 (95%)	192 (86%)	26 (12%)	6 (3%)	5 31
54	S7	182/190 (96%)	137 (75%)	34 (19%)	11 (6%)	1 16
55	S8	184/200 (92%)	147 (80%)	28 (15%)	9 (5%)	2 20
56	S9	183/197 (93%)	153 (84%)	21 (12%)	9 (5%)	2 20
57	10	94/105 (90%)	74 (79%)	13 (14%)	7 (7%)	1 13
58	11	153/156 (98%)	107 (70%)	37 (24%)	9 (6%)	1 17
59	12	122/143 (85%)	76 (62%)	29 (24%)	17 (14%)	0 4
60	13	148/151 (98%)	125 (84%)	20 (14%)	3 (2%)	7 38
61	14	125/137 (91%)	96 (77%)	22 (18%)	7 (6%)	2 18
62	15	122/142 (86%)	101 (83%)	16 (13%)	5 (4%)	3 22
63	16	139/143 (97%)	112 (81%)	20 (14%)	7 (5%)	2 20
64	17	116/136 (85%)	92 (79%)	20 (17%)	4 (3%)	3 26
65	18	143/146 (98%)	120 (84%)	16 (11%)	7 (5%)	2 20
66	19	141/144 (98%)	118 (84%)	15 (11%)	8 (6%)	1 18
67	20	105/121 (87%)	85 (81%)	14 (13%)	6 (6%)	1 18
68	21	85/87 (98%)	68 (80%)	13 (15%)	4 (5%)	2 21
69	22	127/130 (98%)	106 (84%)	19 (15%)	2 (2%)	9 43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
70	23	142/145 (98%)	108 (76%)	24 (17%)	10 (7%)	1 14
71	24	132/135 (98%)	106 (80%)	20 (15%)	6 (4%)	2 22
72	25	68/108 (63%)	45 (66%)	14 (21%)	9 (13%)	0 4
73	26	95/119 (80%)	64 (67%)	19 (20%)	12 (13%)	0 5
74	27	79/82 (96%)	58 (73%)	15 (19%)	6 (8%)	1 13
75	28	61/67 (91%)	50 (82%)	9 (15%)	2 (3%)	4 26
76	29	51/56 (91%)	44 (86%)	5 (10%)	2 (4%)	3 23
77	30	58/63 (92%)	47 (81%)	8 (14%)	3 (5%)	2 19
78	31	69/152 (45%)	37 (54%)	20 (29%)	12 (17%)	0 2
79	RA	316/319 (99%)	252 (80%)	53 (17%)	11 (4%)	3 25
All	All	11126/12097 (92%)	8955 (80%)	1674 (15%)	497 (4%)	4 22

5 of 497 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	L1	15	GLU
4	L1	20	SER
4	L1	23	THR
4	L1	136	THR
4	L1	199	GLN

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
4	L1	185/198 (93%)	166 (90%)	19 (10%)	7 25
5	L2	194/196 (99%)	183 (94%)	11 (6%)	20 46
6	L3	322/323 (100%)	290 (90%)	32 (10%)	8 26
7	L4	288/289 (100%)	260 (90%)	28 (10%)	8 27
8	L5	244/245 (100%)	222 (91%)	22 (9%)	9 30
9	L6	134/153 (88%)	127 (95%)	7 (5%)	23 48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	L7	186/205 (91%)	174 (94%)	12 (6%)	17	42
11	L8	191/208 (92%)	177 (93%)	14 (7%)	14	39
12	L9	171/171 (100%)	153 (90%)	18 (10%)	7	24
13	50	180/187 (96%)	164 (91%)	16 (9%)	9	31
14	51	147/150 (98%)	133 (90%)	14 (10%)	8	28
15	53	154/159 (97%)	140 (91%)	14 (9%)	9	30
16	54	107/109 (98%)	102 (95%)	5 (5%)	26	51
17	55	175/176 (99%)	161 (92%)	14 (8%)	12	35
18	56	160/162 (99%)	153 (96%)	7 (4%)	28	53
19	57	145/146 (99%)	134 (92%)	11 (8%)	13	37
20	58	150/151 (99%)	141 (94%)	9 (6%)	19	44
21	59	153/154 (99%)	145 (95%)	8 (5%)	23	48
22	60	156/156 (100%)	134 (86%)	22 (14%)	3	17
23	61	136/137 (99%)	128 (94%)	8 (6%)	19	45
24	62	87/107 (81%)	82 (94%)	5 (6%)	20	46
25	63	104/105 (99%)	93 (89%)	11 (11%)	6	24
26	64	54/129 (42%)	51 (94%)	3 (6%)	21	46
27	65	105/118 (89%)	91 (87%)	14 (13%)	4	18
28	66	109/110 (99%)	105 (96%)	4 (4%)	34	58
29	67	115/116 (99%)	111 (96%)	4 (4%)	36	59
30	68	118/119 (99%)	108 (92%)	10 (8%)	10	33
31	69	46/47 (98%)	42 (91%)	4 (9%)	10	31
32	70	81/88 (92%)	77 (95%)	4 (5%)	25	50
33	71	96/97 (99%)	85 (88%)	11 (12%)	5	21
34	72	109/111 (98%)	101 (93%)	8 (7%)	14	39
35	73	90/91 (99%)	82 (91%)	8 (9%)	9	31
36	74	95/103 (92%)	88 (93%)	7 (7%)	13	38
37	75	104/105 (99%)	97 (93%)	7 (7%)	16	41
38	76	81/82 (99%)	71 (88%)	10 (12%)	4	20
39	77	70/71 (99%)	65 (93%)	5 (7%)	14	39
40	78	68/69 (99%)	63 (93%)	5 (7%)	13	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
41	79	45/46 (98%)	40 (89%)	5 (11%)	6 22
42	80	47/116 (40%)	43 (92%)	4 (8%)	10 33
43	81	23/23 (100%)	18 (78%)	5 (22%)	1 6
44	82	88/91 (97%)	80 (91%)	8 (9%)	9 30
45	83	71/72 (99%)	70 (99%)	1 (1%)	67 80
47	S0	173/210 (82%)	161 (93%)	12 (7%)	15 40
48	S1	191/224 (85%)	174 (91%)	17 (9%)	9 31
49	S2	176/205 (86%)	168 (96%)	8 (4%)	27 52
50	S3	182/195 (93%)	172 (94%)	10 (6%)	21 47
51	S4	221/222 (100%)	200 (90%)	21 (10%)	8 28
52	S5	173/191 (91%)	162 (94%)	11 (6%)	17 42
53	S6	193/201 (96%)	180 (93%)	13 (7%)	16 41
54	S7	165/170 (97%)	157 (95%)	8 (5%)	25 51
55	S8	150/161 (93%)	140 (93%)	10 (7%)	16 41
56	S9	158/166 (95%)	143 (90%)	15 (10%)	8 28
57	10	89/98 (91%)	78 (88%)	11 (12%)	4 19
58	11	136/137 (99%)	126 (93%)	10 (7%)	13 38
59	12	100/119 (84%)	87 (87%)	13 (13%)	4 18
60	13	127/128 (99%)	117 (92%)	10 (8%)	12 36
61	14	96/105 (91%)	91 (95%)	5 (5%)	23 48
62	15	104/118 (88%)	100 (96%)	4 (4%)	33 57
63	16	117/119 (98%)	107 (92%)	10 (8%)	10 33
64	17	109/124 (88%)	101 (93%)	8 (7%)	14 39
65	18	128/129 (99%)	108 (84%)	20 (16%)	2 14
66	19	115/116 (99%)	108 (94%)	7 (6%)	18 44
67	20	100/114 (88%)	96 (96%)	4 (4%)	31 55
68	21	74/74 (100%)	63 (85%)	11 (15%)	3 15
69	22	110/111 (99%)	103 (94%)	7 (6%)	17 42
70	23	119/120 (99%)	110 (92%)	9 (8%)	13 37
71	24	112/113 (99%)	101 (90%)	11 (10%)	8 27
72	25	61/89 (68%)	54 (88%)	7 (12%)	5 21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
73	26	83/101 (82%)	77 (93%)	6 (7%)	14 39
74	27	70/71 (99%)	67 (96%)	3 (4%)	29 53
75	28	56/60 (93%)	50 (89%)	6 (11%)	6 24
76	29	47/49 (96%)	44 (94%)	3 (6%)	17 42
77	30	51/54 (94%)	45 (88%)	6 (12%)	5 21
78	31	43/135 (32%)	40 (93%)	3 (7%)	15 40
79	RA	261/262 (100%)	241 (92%)	20 (8%)	13 37
All	All	9474/10182 (93%)	8721 (92%)	753 (8%)	16 36

5 of 753 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	S2	41	LEU
58	11	116	ARG
50	S3	92	GLN
48	S1	224	ASP
53	S6	132	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 249 such sidechains are listed below:

Mol	Chain	Res	Type
30	68	28	HIS
68	21	70	ASN
44	82	99	GLN
68	21	7	GLN
71	24	15	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2S	3304/3395 (97%)	553 (16%)	30 (0%)
2	8S	157/158 (99%)	27 (17%)	1 (0%)
3	5S	120/121 (99%)	12 (10%)	0
46	1S	1779/1798 (98%)	346 (19%)	19 (1%)
80	IR	0/201	-	-
All	All	5360/5673 (94%)	938 (17%)	50 (0%)

5 of 938 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2S	13	A
1	2S	14	U
1	2S	26	A
1	2S	40	A
1	2S	43	A

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2S	3351	U
46	1S	497	G
46	1S	1761	U
1	2S	3353	G
46	1S	139	C

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)

There are no chain breaks in this entry.

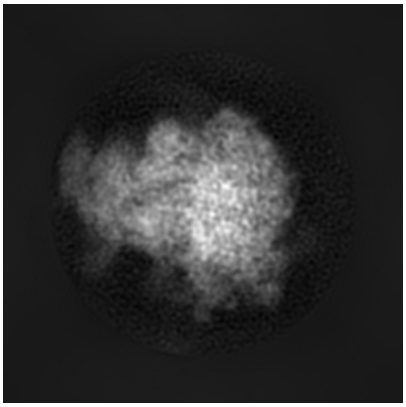
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-5942. These allow visual inspection of the internal detail of the map and identification of artifacts.

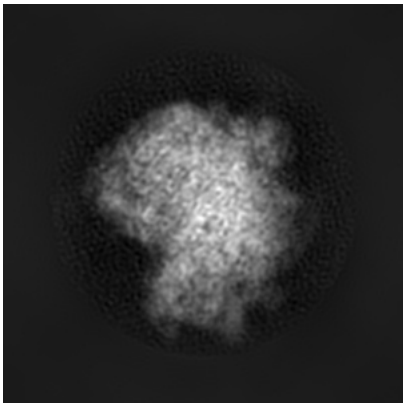
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

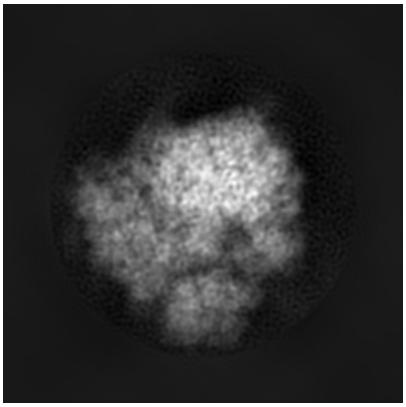
6.1.1 Primary map



X



Y

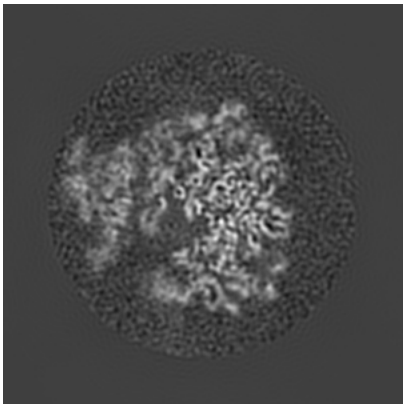


Z

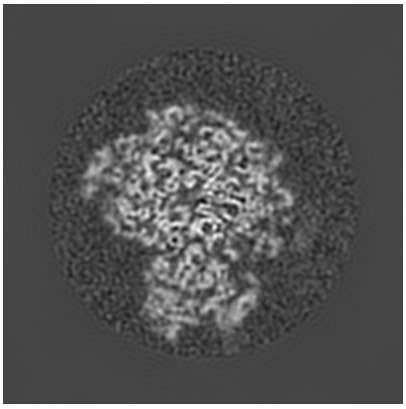
The images above show the map projected in three orthogonal directions.

6.2 Central slices

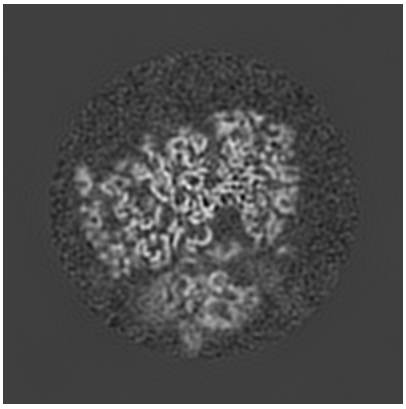
6.2.1 Primary map



X Index: 210



Y Index: 210

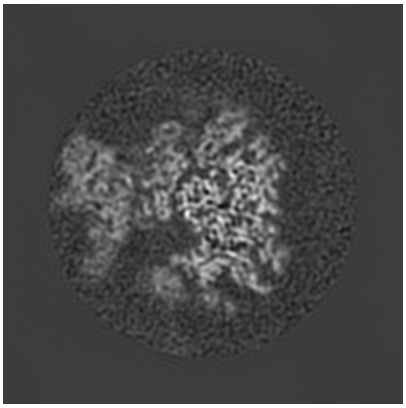


Z Index: 210

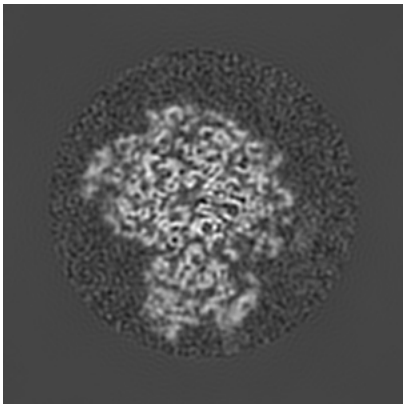
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

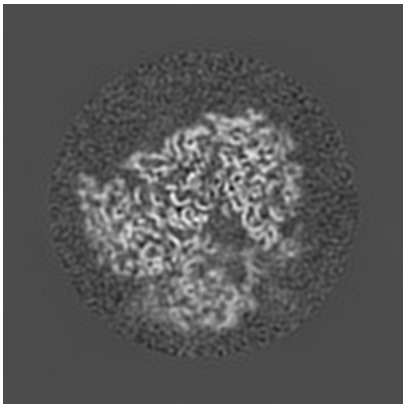
6.3.1 Primary map



X Index: 200



Y Index: 210

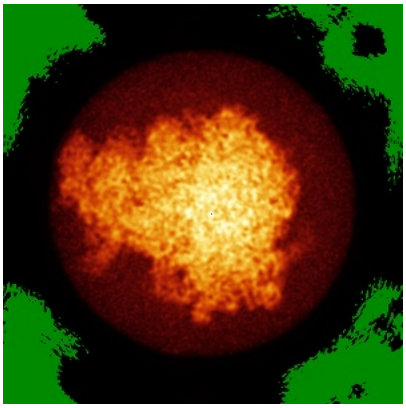


Z Index: 203

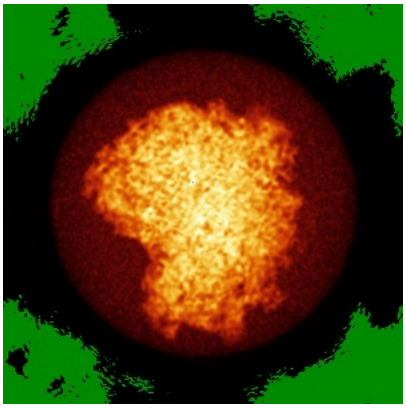
The images above show the largest variance slices of the map in three orthogonal directions.

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

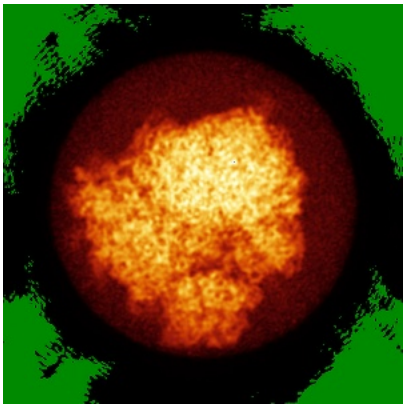
6.4.1 Primary map



X



Y

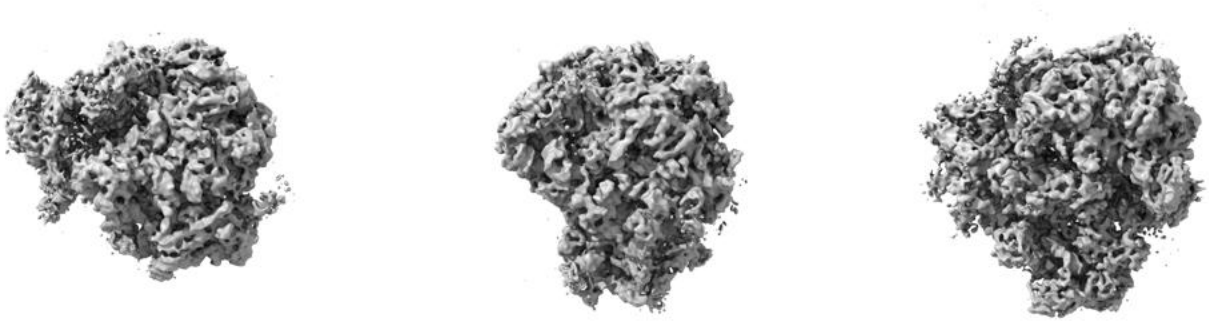


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.815. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

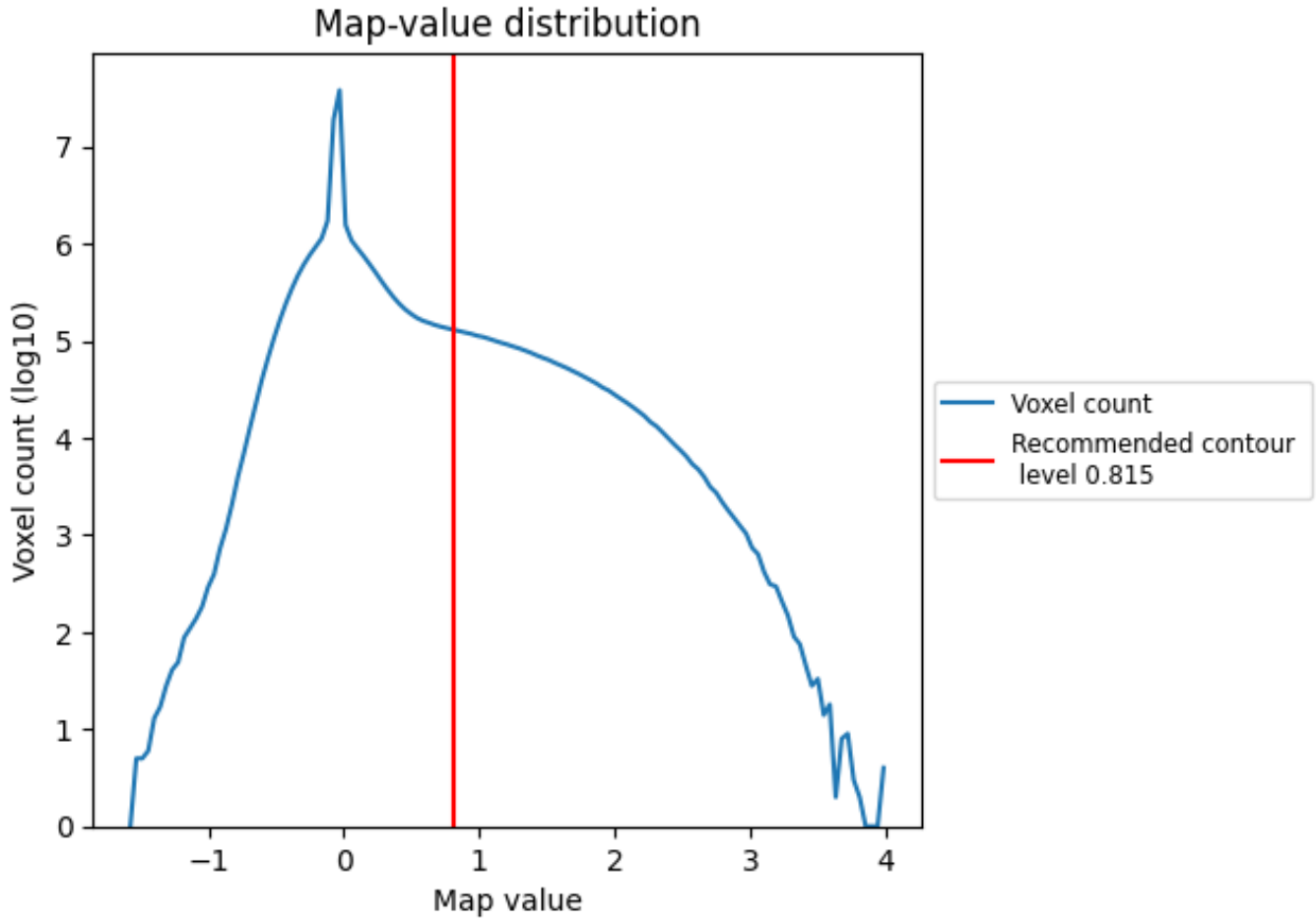
6.6 Mask visualisation (i)

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

7 Map analysis

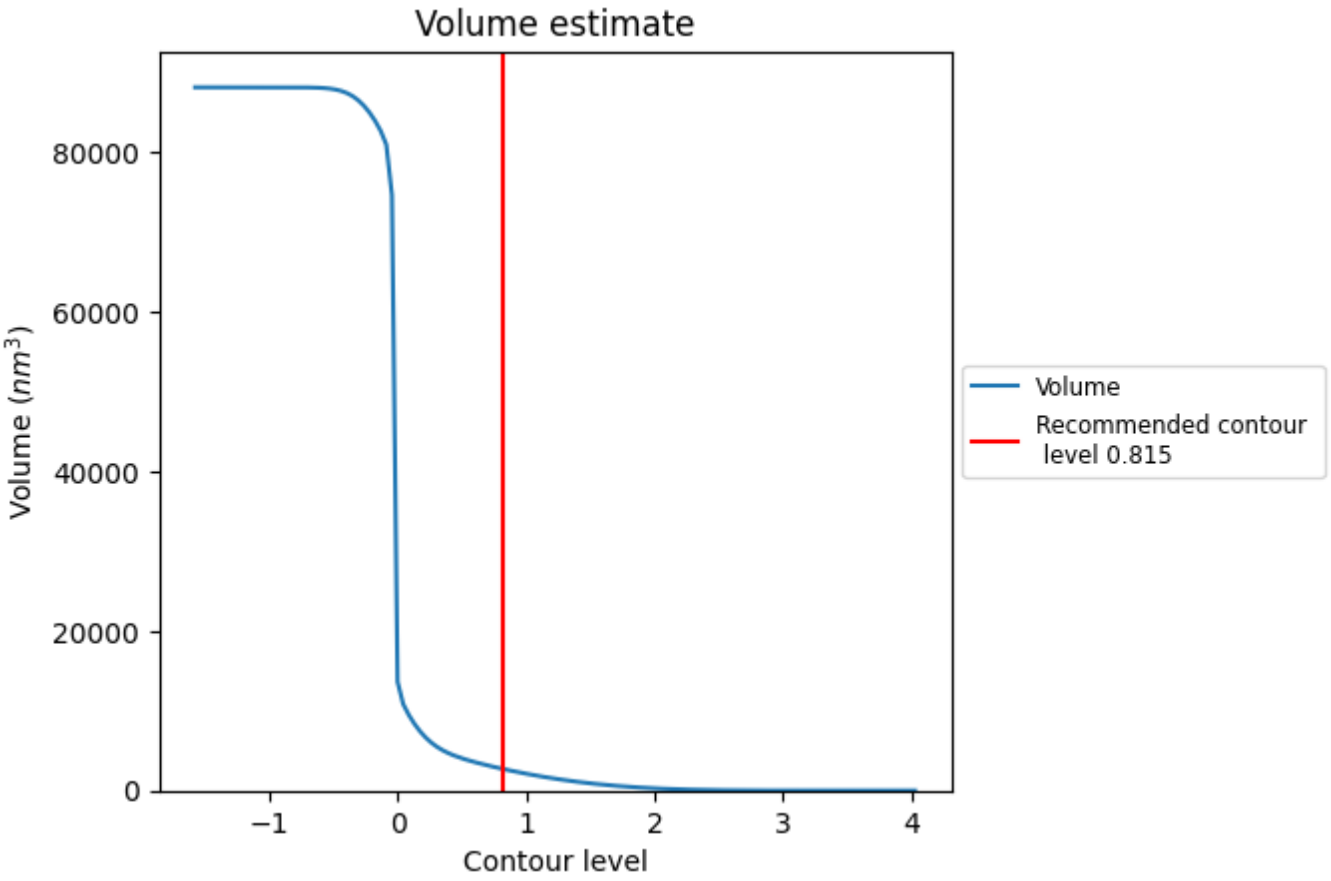
This section contains the results of statistical analysis of the map.

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.

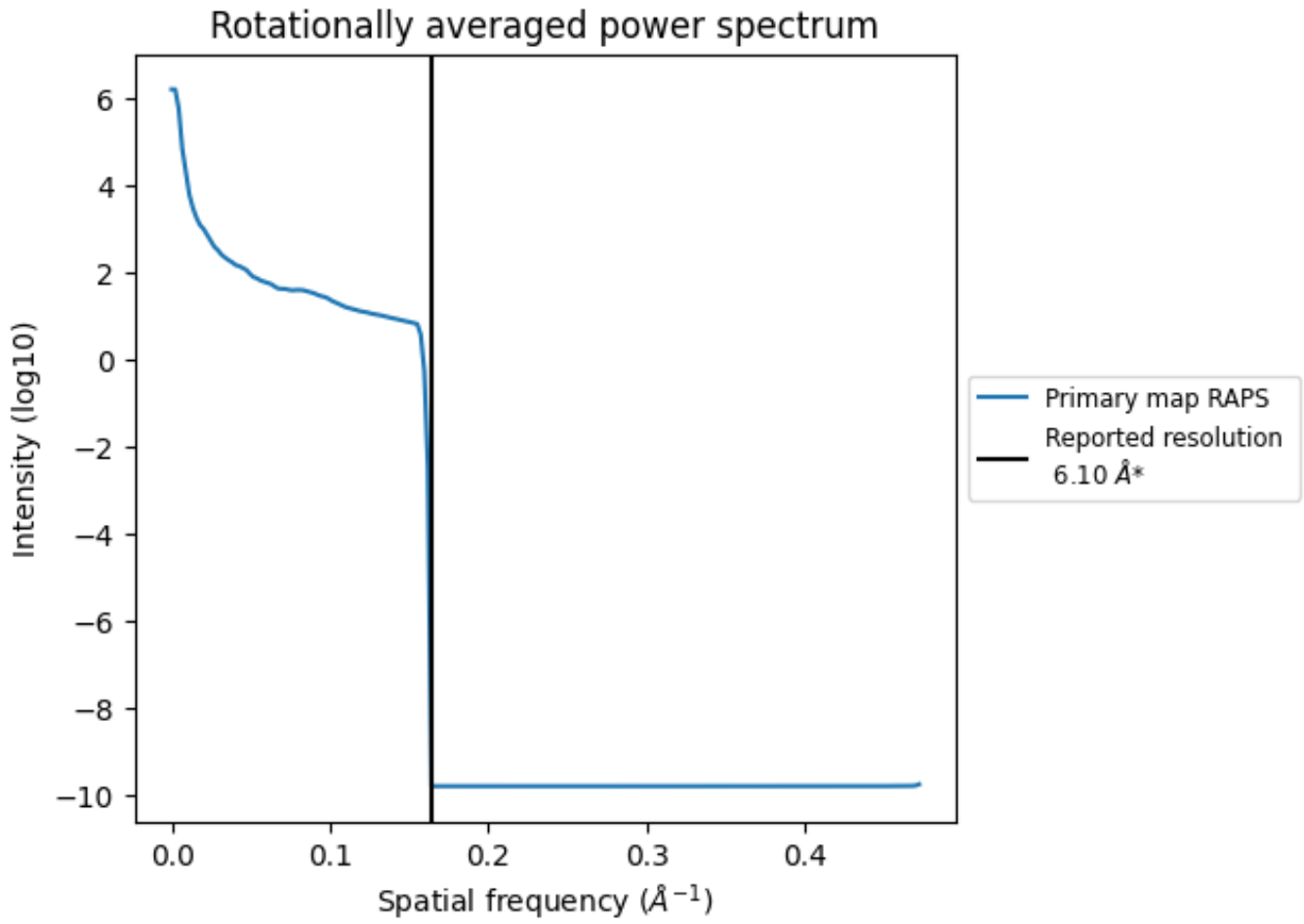
7.2 Volume estimate (i)



The volume at the recommended contour level is 2726 nm^3; this corresponds to an approximate mass of 2462 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 0.164 Å^{-1}

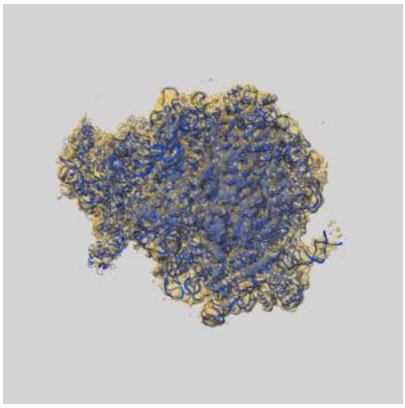
8 Fourier-Shell correlation (i)

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

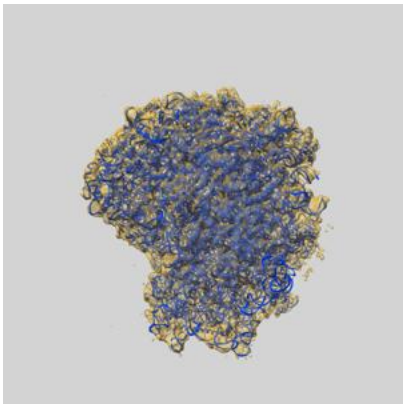
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-5942 and PDB model 3J6X. Per-residue inclusion information can be found in section 3 on page 18.

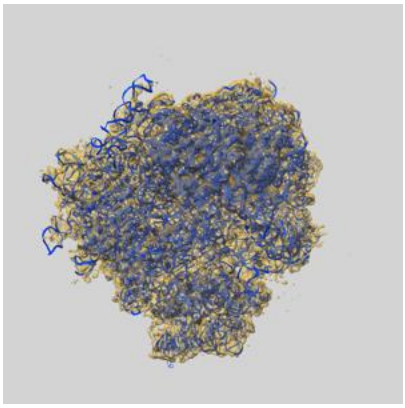
9.1 Map-model overlay



X



Y



Z

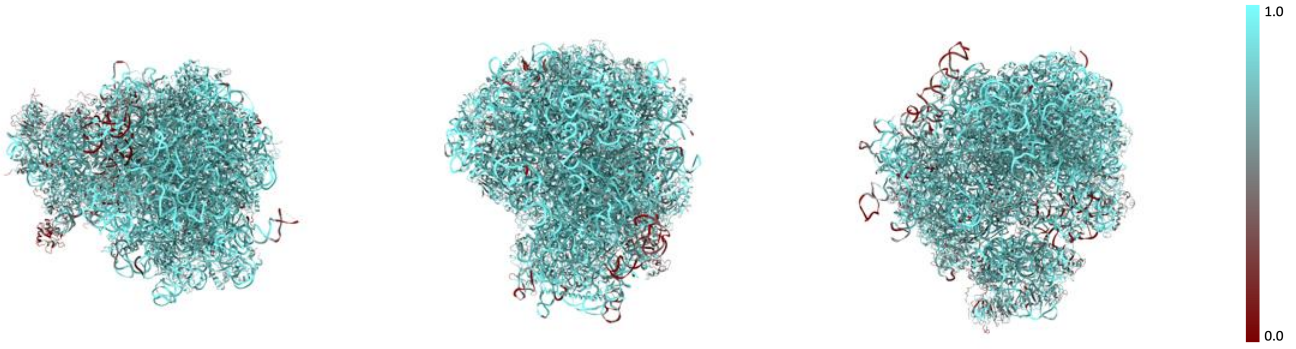
The images above show the 3D surface view of the map at the recommended contour level 0.815 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model

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.

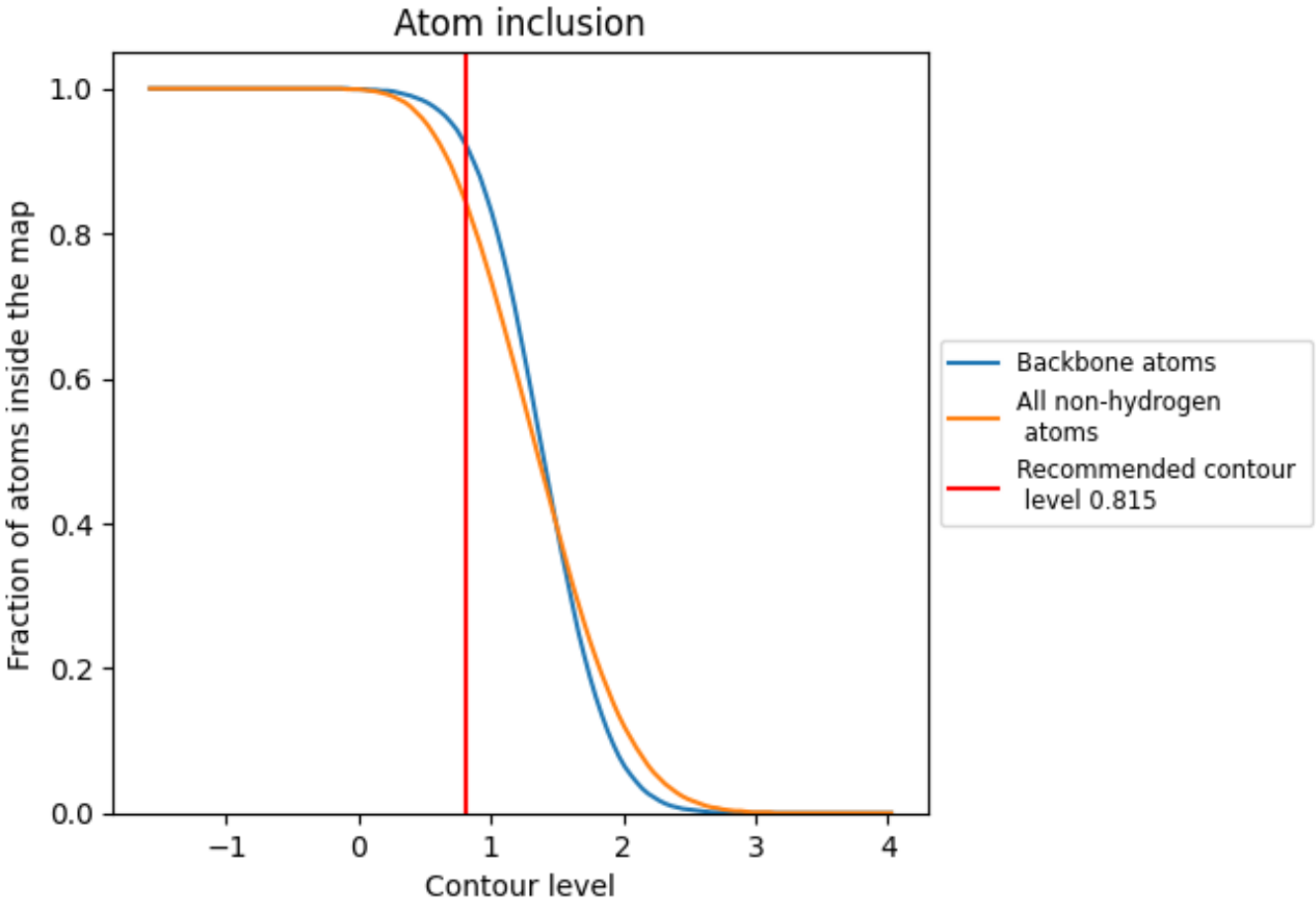
9.3 Atom inclusion mapped to coordinate model



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 (0.815).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 84% 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 (0.815) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8410	0.2030
10	0.6850	0.1560
11	0.7110	0.1900
12	0.1720	0.1050
13	0.7290	0.1890
14	0.6900	0.1560
15	0.5990	0.1550
16	0.6800	0.1420
17	0.5650	0.1670
18	0.6390	0.1410
19	0.7190	0.1420
1S	0.9170	0.2170
20	0.6010	0.1460
21	0.6900	0.1880
22	0.7490	0.1760
23	0.7840	0.1960
24	0.7340	0.1600
25	0.6910	0.1490
26	0.6810	0.1960
27	0.6810	0.1870
28	0.6530	0.1710
29	0.7410	0.1490
2S	0.9370	0.2340
30	0.7320	0.1820
31	0.2360	0.1600
50	0.7930	0.1840
51	0.7490	0.1620
53	0.7740	0.1760
54	0.7550	0.1750
55	0.7720	0.1580
56	0.7810	0.1680
57	0.7540	0.1820
58	0.7680	0.1800
59	0.7280	0.1860
5S	0.9820	0.2240

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Chain	Atom inclusion	Q-score
60	0.7650	0.1710
61	0.7720	0.1890
62	0.7560	0.1790
63	0.7800	0.2000
64	0.7650	0.1770
65	0.7330	0.1950
66	0.7960	0.1830
67	0.7170	0.1840
68	0.7920	0.1820
69	0.7700	0.1990
70	0.7320	0.1960
71	0.7710	0.1830
72	0.7920	0.2050
73	0.8160	0.1700
74	0.7410	0.1700
75	0.7390	0.1720
76	0.7720	0.1660
77	0.8190	0.1610
78	0.6200	0.1860
79	0.7640	0.2040
80	0.7300	0.1800
81	0.0380	0.0070
82	0.7970	0.1930
83	0.7790	0.1850
8S	0.9670	0.2440
IR	0.5200	0.1120
L1	0.5570	0.1210
L2	0.8000	0.1880
L3	0.7920	0.1880
L4	0.7900	0.1810
L5	0.7180	0.1590
L6	0.7630	0.1810
L7	0.7870	0.1770
L8	0.7360	0.1740
L9	0.7310	0.1850
RA	0.6280	0.1270
S0	0.6600	0.1790
S1	0.6160	0.1720
S2	0.7750	0.1930
S3	0.7050	0.1740
S4	0.7650	0.1820
S5	0.6720	0.1530

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Chain	Atom inclusion	Q-score
S6	0.7480	0.1610
S7	0.5990	0.1640
S8	0.7810	0.1670
S9	0.7430	0.1740