wwPDB EM Validation Summary Report (i)

Feb 13, 2024 – 04:44 AM EST

PDB ID	:	3J6Y
EMDB ID	:	EMD-5943
Title	:	S. cerevisiae 80S ribosome bound with Taura syndrome virus (TSV) IRES, 2 degree rotation (Class I)
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	:	3U5D, 3U5E, 3U5B, 3U5C

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:

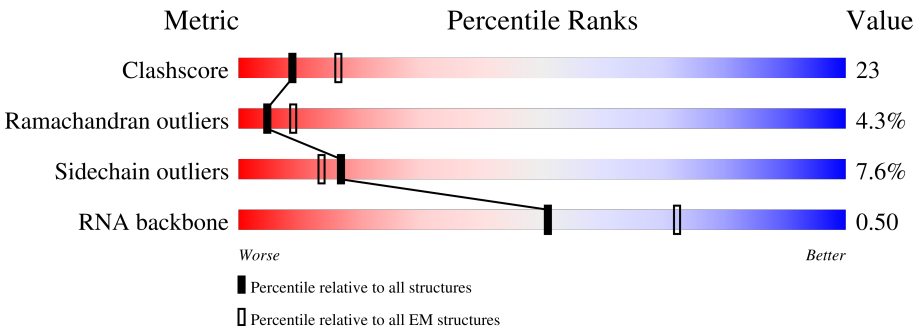
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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	34% 52% 11% • •
2	8S	158	32% 56% 10% •
3	5S	121	36% 60% 5%
4	L1	217	47% 41% 47% 6% • 6%
5	L2	254	37% 57% 6% •
6	L3	387	44% 51% 5%
7	L4	362	47% 45% 8%

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Mol	Chain	Length	Quality of chain
8	L5	297	9% 54% 40% 6%
9	L6	176	45% 38% 5% 11%
10	L7	244	38% 46% 7% 9%
11	L8	256	46% 39% 5% 9%
12	L9	191	48% 46% 6%
13	50	221	45% 46% 5% 5%
14	51	174	49% 44%
15	53	199	7% 46% 43% 7%
16	54	138	55% 40%
17	55	204	43% 50% 6%
18	56	199	42% 50% 7%
19	57	184	7% 47% 48%
20	58	186	51% 44% 5%
21	59	189	8% 43% 53%
22	60	172	47% 48% 5%
23	61	160	46% 44% 9%
24	62	121	42% 38% 17%
25	63	137	40% 55%
26	64	155	20% 18% 61%
27	65	142	42% 38% 6% 15%
28	66	127	56% 41%
29	67	136	51% 46%
30	68	149	39% 53% 7%
31	69	59	5% 42% 47% 8%
32	70	105	5% 34% 54% 8%

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Mol	Chain	Length	Quality of chain
33	71	113	40% 50% 7%
34	72	130	48% 44% 5%
35	73	107	56% 36% 7%
36	74	121	31% 57% 7%
37	75	120	42% 53%
38	76	100	52% 43%
39	77	88	43% 51%
40	78	78	5% 54% 38% 6%
41	79	51	39% 57%
42	80	128	20% 18% 59%
43	81	25	96% 56% 36% 8%
44	82	106	48% 41% 8%
45	83	92	38% 57%
46	1S	1798	35% 50% 13%
47	S0	252	9% 36% 40% 6% 18%
48	S1	255	11% 33% 41% 10% 16%
49	S2	254	47% 35% 15%
50	S3	240	10% 53% 34% 5% 7%
51	S4	261	5% 39% 54% 7%
52	S5	225	14% 44% 43% 5% 8%
53	S6	236	8% 53% 39%
54	S7	190	27% 39% 51% 6%
55	S8	200	42% 47% 6%
56	S9	197	7% 34% 53% 6% 6%
57	10	105	13% 29% 53% 9% 9%

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Mol	Chain	Length	Quality of chain
58	11	156	12% 51% 42% 5%
59	12	143	69% 34% 42% 10% 13%
60	13	151	13% 49% 44% 6%
61	14	137	7% 44% 44% 7%
62	15	142	37% 46% 35% 6% 13%
63	16	143	13% 37% 55% 6%
64	17	136	22% 38% 40% 10% 12%
65	18	146	18% 42% 48% 8%
66	19	144	18% 46% 49% 5%
67	20	121	21% 33% 49% 7% 12%
68	21	87	9% 49% 41% 9%
69	22	130	32% 59% 8%
70	23	145	39% 52% 8%
71	24	135	19% 46% 50%
72	25	108	9% 23% 31% 9% 35%
73	26	119	5% 27% 45% 10% 18%
74	27	82	15% 59% 35% 5%
75	28	67	18% 37% 55% 6%
76	29	56	16% 68% 25% 5%
77	30	63	10% 40% 46% 10% 5%
78	31	152	34% 30% 14% 53%
79	RA	319	21% 49% 47%
80	IR	201	35% 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
			Total	C	N	O	S		
7	L4	361	2750	1730	522	495	3	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

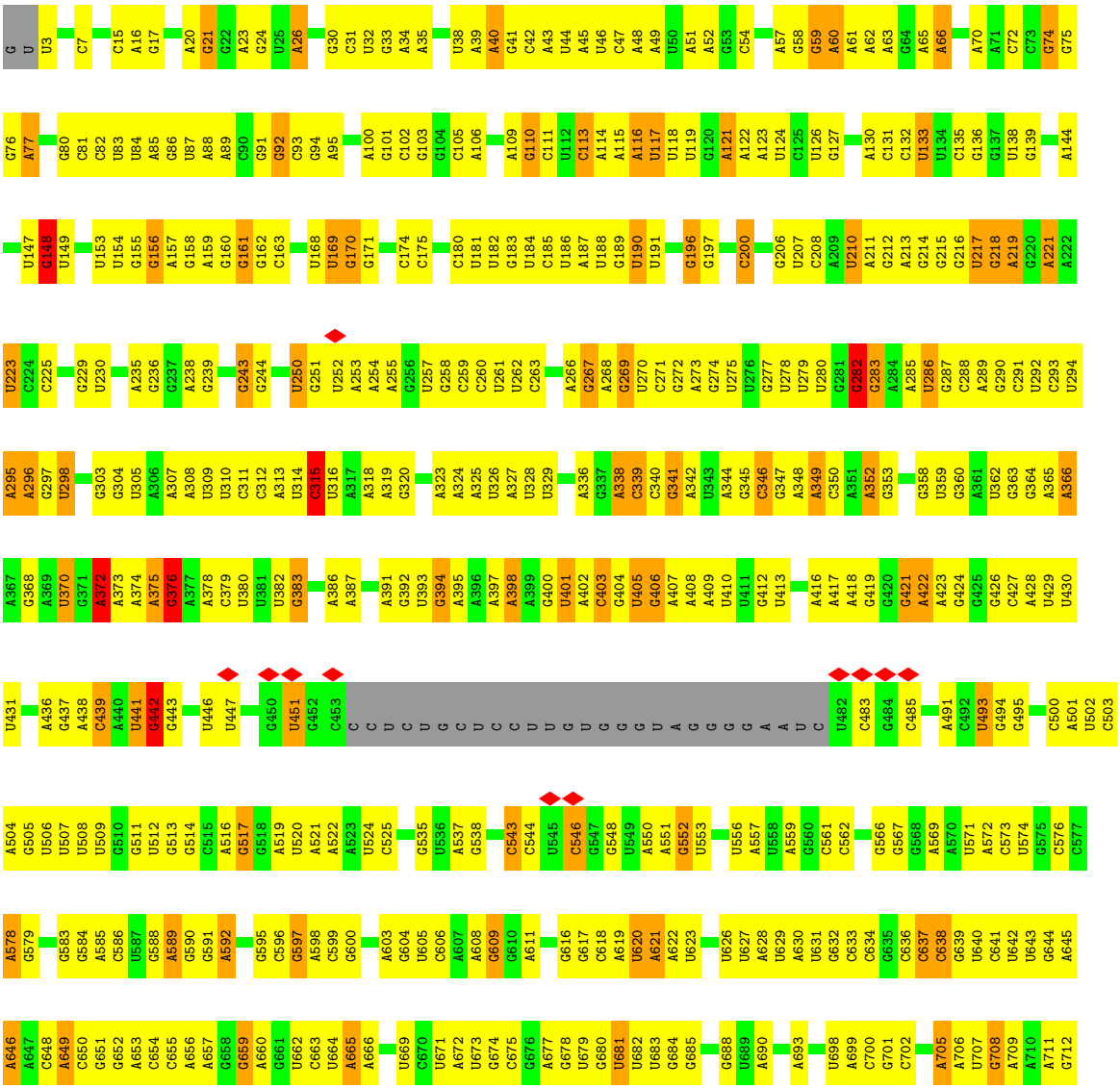
Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	P		
80	IR	198	198	198	0	198

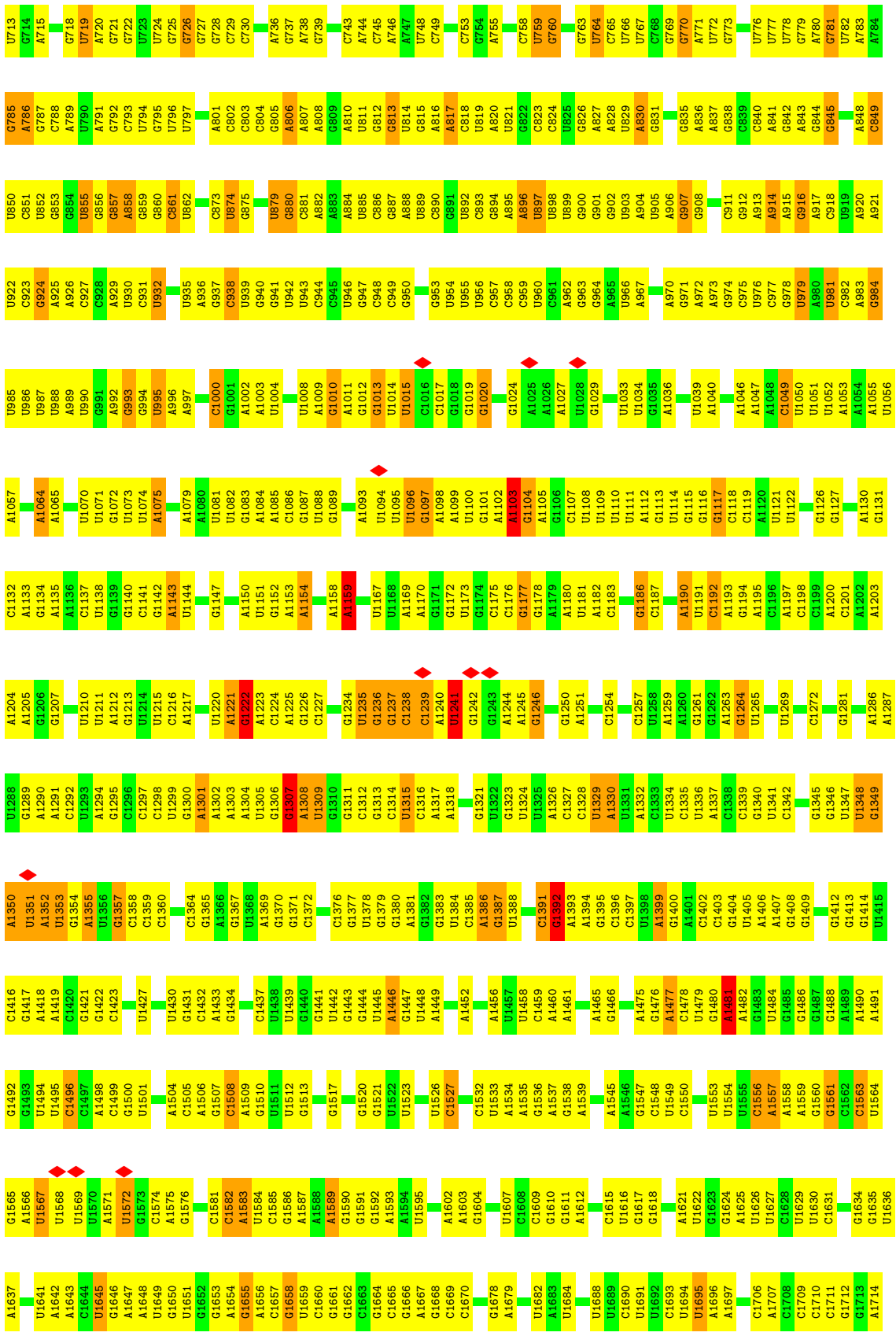
3 Residue-property plots (i)

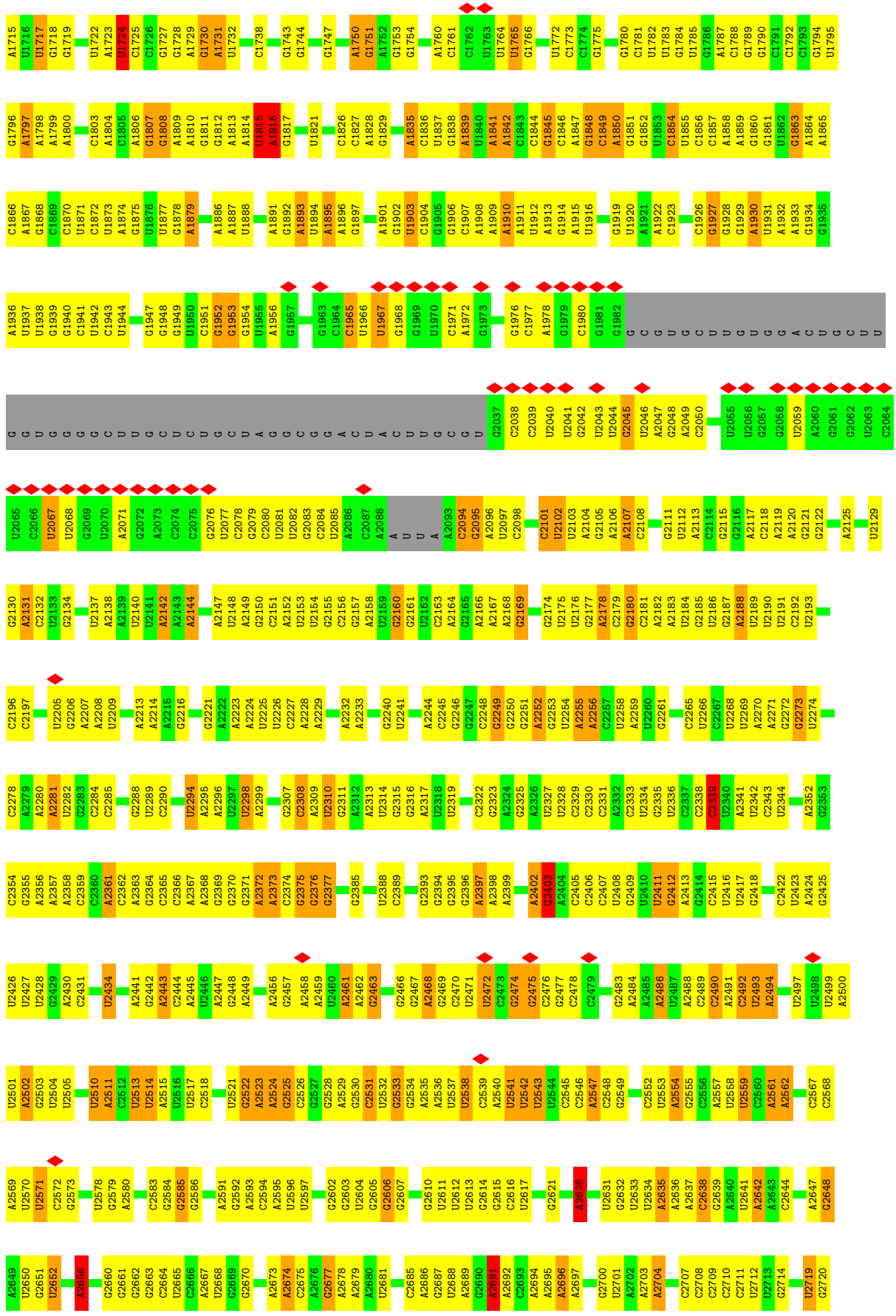
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

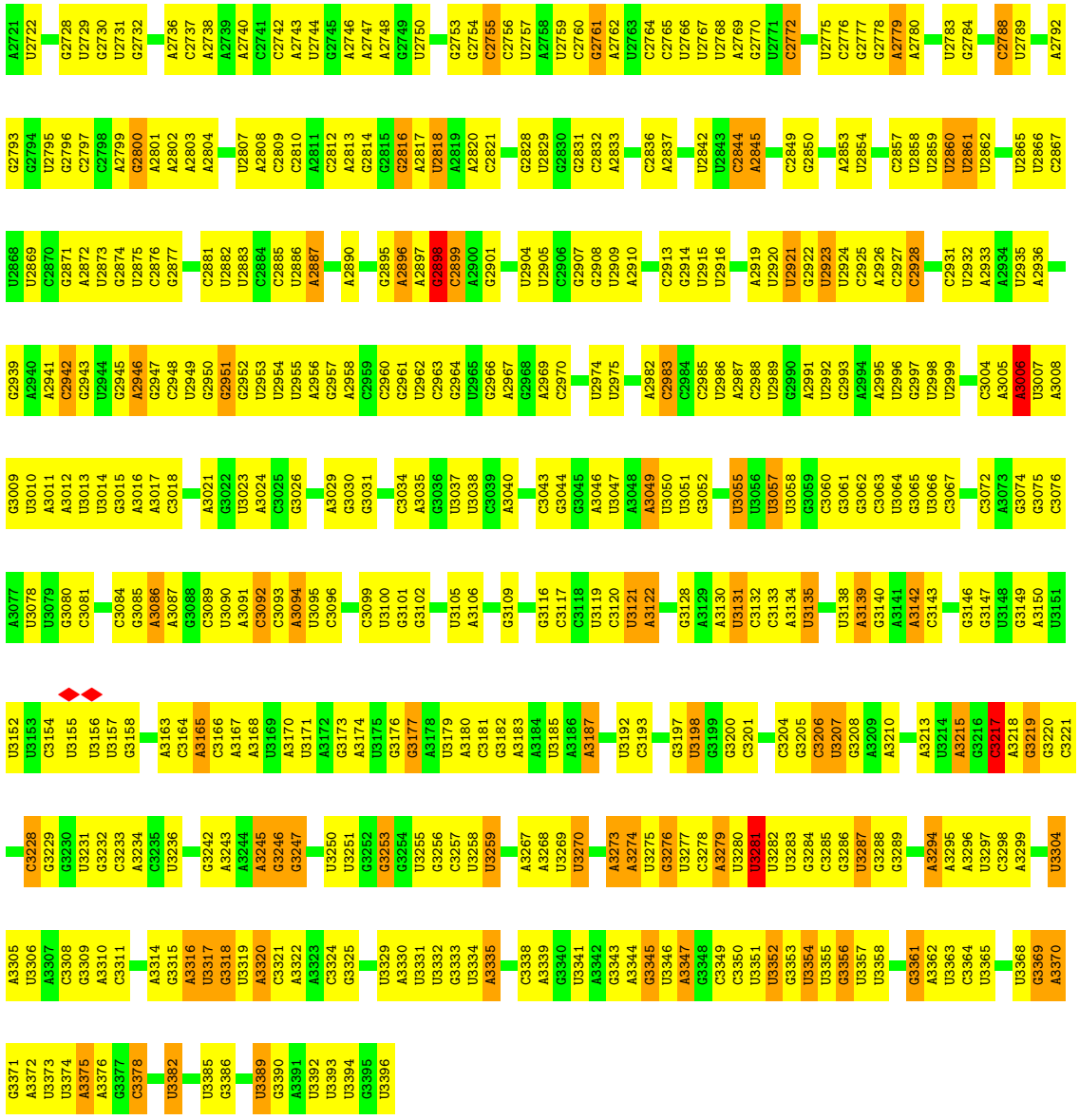
- Molecule 1: 25S ribosomal RNA

Chain 2S:



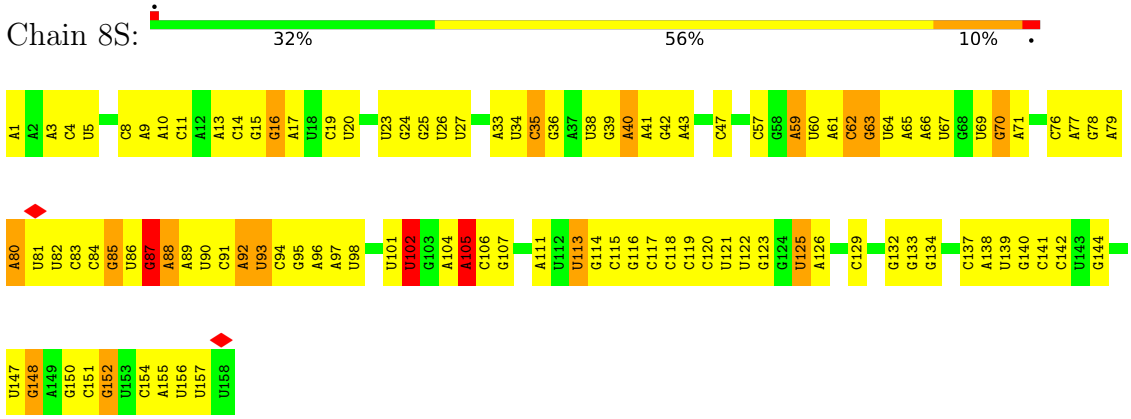



A1715 U1716 U1717 G1718 G1719 U1722 A1723 U1724 C1725 C1726 G1727 G1728 A1729 G1730 A1731 U1732 C1738 G1743 G1744 G1747 A1750 G1751 A1752 G1753 G1754 A1760 C1761 C1762 U1763 U1764 U1765 G1766 U1772 C1773 C1774 G1775 G1780 C1781 U1782 U1783 G1784 U1785 G1786 A1787 C1788 G1789 G1790 C1791 C1792 C1793 G1794 U1795
G1796 A1797 A1798 A1799 A1800 C1803 A1804 C1805 A1806 G1807 G1808 A1809 A1810 G1811 G1812 A1813 A1814 U1815 A1816 G1817 U1821 C1826 C1827 A1828 G1829 A1835 C1836 U1837 G1838 A1839 U1840 A1841 A1842 C1843 C1844 G1845 C1846 A1847 G1848 C1849 A1850 G1851 G1852 U1853 C1854 U1855 C1856 C1857 A1858 A1859 G1860 G1861 U1862 G1863 A1864 A1865
C1866 A1867 G1868 C1869 C1870 U1871 C1872 U1873 A1874 G1875 U1876 U1877 G1878 A1879 A1886 A1887 U1888 A1891 G1892 A1893 U1894 A1895 A1896 G1897 A1901 G1902 U1903 C1904 G1905 G1906 C1907 A1908 A1909 A1910 A1911 U1912 A1913 G1914 A1915 U1916 G1919 U1920 A1921 A1922 C1923 C1926 G1927 G1928 G1929 A1930 U1931 A1932 A1933 G1934 G1935
A1936 U1937 U1938 G1939 G1940 C1941 U1942 C1943 U1944 G1947 G1948 G1949 U1950 C1951 G1952 G1953 G1954 U1955 A1956 G1957 G1963 C1964 C1965 U1966 U1967 G1968 G1969 U1970 C1971 A1972 G1973 G1976 C1977 A1978 G1979 C1980 G1981 G1982 G C G U G C U U G U G A C U G C U
G G U G G G C U U G C U C U G C G G A C U U G C A C U A G U G2037 C2038 C2039 U2040 U2041 G2042 U2043 U2044 G2045 U2046 A2047 G2048 A2049 C2050 U2055 U2056 G2057 G2058 U2059 A2060 G2061 G2062 U2063 C2064
U2065 C2066 U2067 U2068 G2069 U2070 A2071 G2072 A2073 C2074 C2075 G2076 U2077 C2078 G2079 C2080 U2081 U2082 G2083 C2084 U2085 A2086 C2087 A2088 A U U A A2093 C2094 G2095 A2096 U2097 C2098 C2101 U2102 U2103 A2104 G2105 A2106 A2107 C2108 G2111 U2112 A2113 C2114 G2115 G2116 A2117 C2118 A2119 A2120 G2121 G2122 A2125 U2129
G2130 A2131 C2132 U2133 G2134 U2137 A2138 A2139 U2140 U2141 A2142 A2143 A2144 A2147 U2148 A2149 G2150 C2151 A2152 U2153 U2154 G2155 C2156 G2157 A2158 U2159 G2160 G2161 U2162 C2163 A2164 G2165 A2166 A2167 A2168 G2169 G2174 U2175 U2176 G2177 A2178 C2179 G2180 C2181 A2182 A2183 U2184 G2185 U2186 G2187 A2188 U2189 U2190 U2191 C2192 U2193
C2196 C2197 U2205 G2206 A2207 A2208 U2209 A2213 A2214 A2215 G2216 G2221 A2222 A2223 A2224 U2225 U2226 C2227 A2228 A2229 A2232 A2233 G2240 U2241 A2244 C2245 G2246 G2247 C2248 G2249 G2250 G2251 A2252 G2253 U2254 A2255 A2256 C2257 U2258 A2259 U2260 G2261 C2265 U2266 C2267 U2268 U2269 A2270 A2271 G2272 G2273 U2274
C2278 A2279 A2280 A2281 U2282 G2283 C2284 C2285 G2288 U2289 C2290 U2294 A2295 A2296 U2297 U2298 A2299 G2307 C2308 A2309 U2310 G2311 A2312 A2313 U2314 G2315 G2316 A2317 U2318 U2319 C2322 C2323 A2324 G2325 A2326 U2327 U2328 C2329 C2330 C2331 A2332 C2333 U2334 G2335 U2336 C2337 C2338 C2339 U2340 A2341 U2342 C2343 U2344 A2352 G2353
C2354 G2355 A2356 A2357 A2358 C2359 C2360 A2361 C2362 A2363 G2364 C2365 C2366 A2367 A2368 G2369 G2370 G2371 A2372 A2373 C2374 G2375 G2376 G2377 G2385 U2388 C2389 G2393 G2394 G2395 G2396 A2397 A2398 A2399 A2402 G2403 A2404 C2405 C2406 C2407 U2408 G2409 U2410 U2411 G2412 A2413 G2414 C2415 U2416 U2417 G2418 C2422 U2423 A2424 G2425
U2426 U2427 U2428 G2429 A2430 C2431 U2434 A2441 G2442 A2443 C2444 A2445 U2446 A2447 G2448 A2449 A2456 G2457 A2458 A2459 U2460 A2461 A2462 G2463 G2466 G2467 A2468 G2469 C2470 U2471 U2472 C2473 G2474 G2475 C2476 G2477 C2478 C2479 G2483 A2484 A2485 A2486 U2487 A2488 C2489 C2490 A2491 C2492 U2493 A2494 U2497 U2498 U2499 A2500
U2501 A2502 G2503 U2504 U2505 U2510 A2511 C2512 U2513 U2514 A2515 U2516 U2517 C2518 U2521 G2522 A2523 A2524 G2525 C2526 G2527 G2528 A2529 G2530 C2531 U2532 G2533 C2534 A2535 A2536 U2537 U2538 C2539 A2540 U2541 U2542 U2543 U2544 C2545 C2546 A2547 C2548 G2549 C2552 U2553 A2554 G2555 C2556 A2557 U2558 U2559 C2560 A2561 A2562 C2567 C2568
A2569 U2570 U2571 C2572 G2573 U2578 G2579 A2580 C2583 G2584 G2585 G2586 A2591 G2592 A2593 C2594 A2595 U2596 U2597 G2602 G2603 U2604 G2605 G2606 G2607 G2610 U2611 U2612 U2613 G2614 G2615 C2616 U2617 G2621 A2626 U2631 G2632 U2633 U2634 A2635 A2636 A2637 C2638 G2639 A2640 U2641 A2642 A2643 C2644 A2647 G2648
A2649 U2650 G2651 U2652 A2656 G2660 G2661 G2662 G2663 C2664 U2665 C2666 A2667 U2668 G2669 G2670 A2673 A2674 C2675 A2676 G2677 A2678 A2679 A2680 U2681 C2685 A2686 G2687 U2688 A2689 G2690 A2691 A2692 C2693 A2694 A2695 A2696 A2697 G2700 U2701 A2702 A2703 A2704 C2707 C2708 C2709 C2710 C2711 U2712 U2713 G2714 U2719 G2720



- Molecule 2: 5.8S ribosomal RNA

Chain 8S:



- Molecule 3: 5S ribosomal RNA

Chain 5S: 36% 60% 5%

G1 U4 G5 C6 G7 G8 C9 C10 A11 U12 A13 U14 C15 U16 A17 C18 C19 A20 G21 A22 C28 C29 G30 U31 U32 U33 C34 C35 C36 G37 U38 C39 C40 C41 A42 U43 C44 A45 A46 C47 U48 G49 U54 C58 U59 G60 G61 G65 A66 G67 C68 G75 A76 G77

U78 A79 G80 U81 A84 G85 U86 G87 G88 G89 A92 C93 C94 A95 U96 A97 C98 G99 C100 G101 A102 A103 A104 A108 G109 G110 U111 G112 C113 U114 G115 C116 A117 A118 U119 C120 U121

- Molecule 4: 60S ribosomal protein L1

Chain L1: 47% 41% 47% 6% • 6%

MET SER LYS ILE THR SER SER GLN VAL ARG GLU HIS V13 K14 E15 L16 L17 K18 Y19 S20 N21 E22 T23 K24 K25 R26 N27 F28 L29 E30 T31 V32 E33 V36 G37 L38 K39 N40 Y41 D42 P43 Q44 R45 D46 K47 R48 F49 S50 G51 S52 L53 K54 L55 P56 N57 C58 P59 R60 P61

N62 M63 S64 I65 F68 G69 D70 A71 F72 D73 V74 D75 R76 A77 K78 S79 C80 G81 V82 D83 A84 M85 D88 D89 L90 K91 K92 L93 N94 K95 N96 K97 K98 L99 I100 K101 K102 L103 S104 K105 K106 Y107 N108 A109 F110 I111 A112 S113 E114 V115 K118 Q119 V120 P121 R122 L123

Q127 L128 S129 K130 A131 G132 K133 F134 P135 T136 P137 V138 S139 H140 N141 D142 D143 L144 Y145 G146 K147 D150 V151 R152 S153 T154 I155 K156 F157 Q158 L159 K160 K161 V162 L163 C164 L165 A166 V167 A168 V169 G170 N171 V172 E173 M174 E175 E176 D177 V178 L179 V180 N181 Q182 I183 L184 M185 S186 V187

N188 F189 F190 V191 S192 L193 L194 K195 K196 N197 W198 Q199 N200 V201 G202 S203 L204 V205 V206 K207 S208 S209 M210 G211 P212 A213 F214 R215 L216 TYR

- Molecule 5: 60S ribosomal protein L2

Chain L2: 37% 57% 6% •

MET G2 R3 V4 I5 R6 N7 Q8 R9 K10 G11 I15 T20 R21 L22 R23 A26 A27 T31 L32 D33 Y34 R37 H38 G39 R42 G43 I44 V45 I48 V49 H50 G53 R54 V61 V62 D65 P66 Y67 K68 Y69 R70 L71 R72 E73 E74 I75 F76 I77 A78

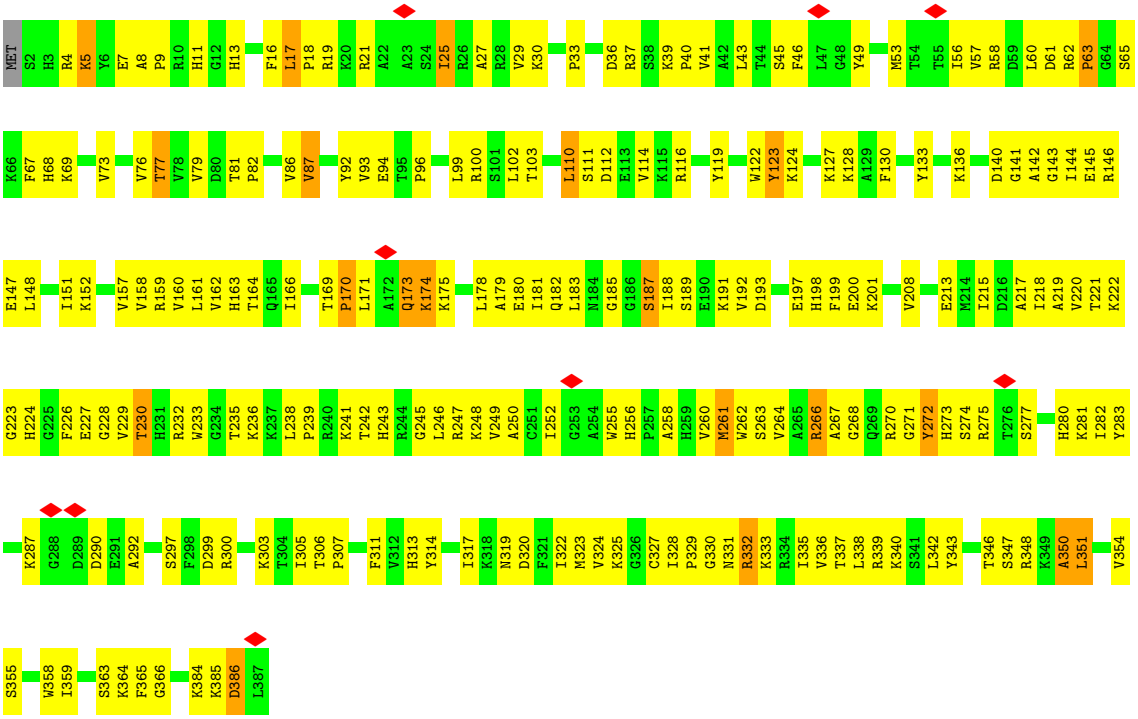
N79 E80 G81 V82 H83 T84 G85 Q86 F87 I88 G91 K92 K93 L96 N97 N100 V101 L102 P103 L104 V107 P108 E109 G110 T111 I112 V113 S114 N115 V116 E117 E118 K119 P120 G121 D122 R123 G124 A125 L126 A127 R128 A129 S130 G131 N132 Y133 V134 I135 I136 I137 G138 H139 N140 P141 D142

E143 M144 K145 T146 R147 V148 R149 L150 P151 A154 K155 K156 V157 I158 S159 S160 D161 A162 V165 I166 G167 V168 I169 A170 G173 R174 V175 D176 K177 P178 L179 L180 K181 A182 G183 R184 A185 F186 H187 K188 Y189 R190 L191 K192 R193 N194 S195 W196 P197 K198 T199 R200 M204 N205 P206 V207

D208 H209 P210 H211 G212 G213 H216 Q217 H218 I219 G220 K221 A222 S223 T224 I225 S226 R227 G228 A229 V230 S231 G232 Q233 K234 A235 G236 L237 I238 A239 A240 R241 G244 R247 G248 S249 Q250 K251 T252 Q253 ASP

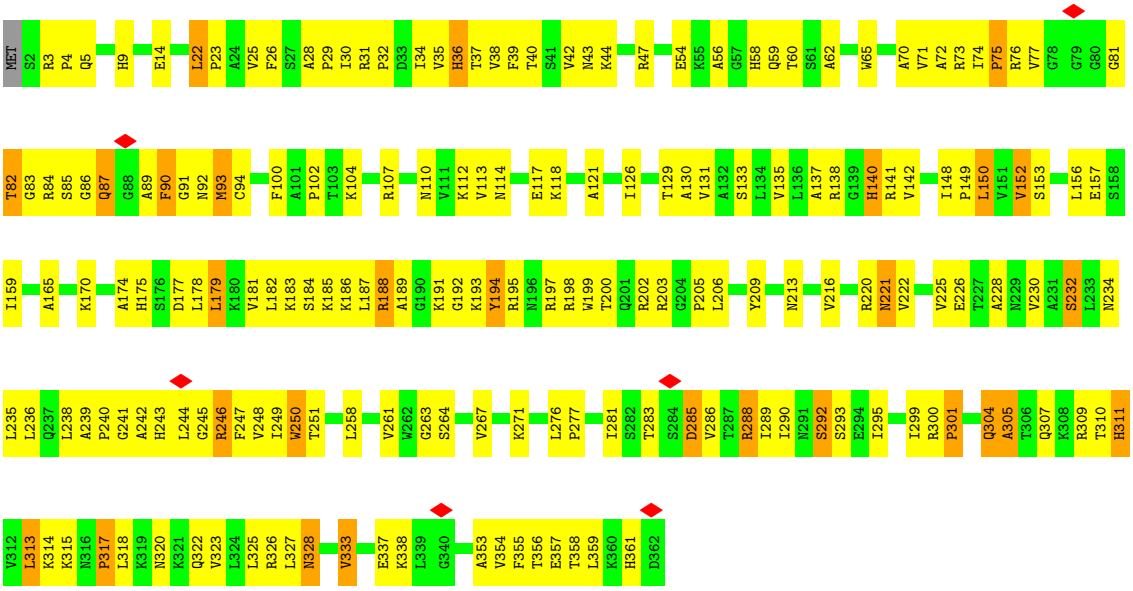
- Molecule 6: 60S ribosomal protein L3

Chain L3: 44% 51% 5%



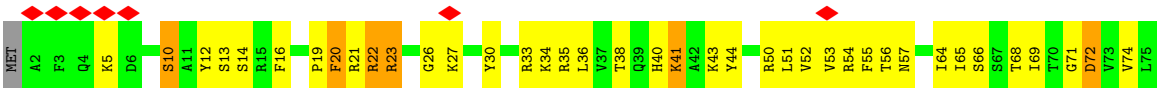
- Molecule 7: 60S ribosomal protein L4

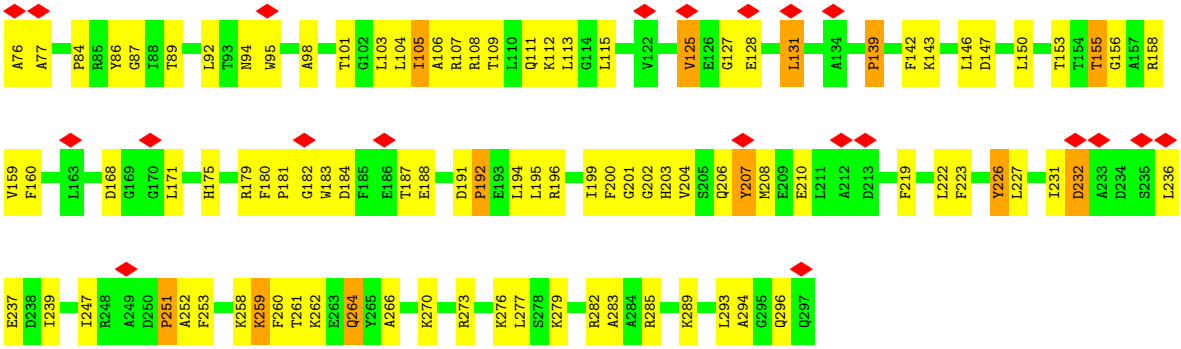
Chain L4:



- Molecule 8: 60S ribosomal protein L5

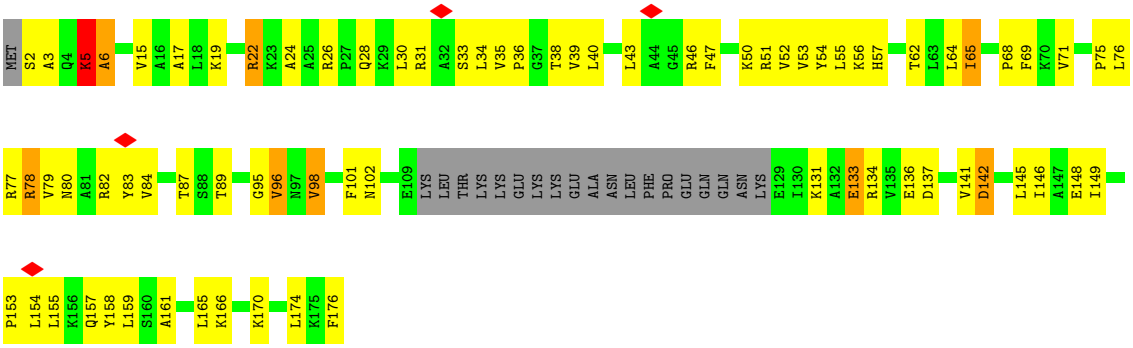
Chain L5:





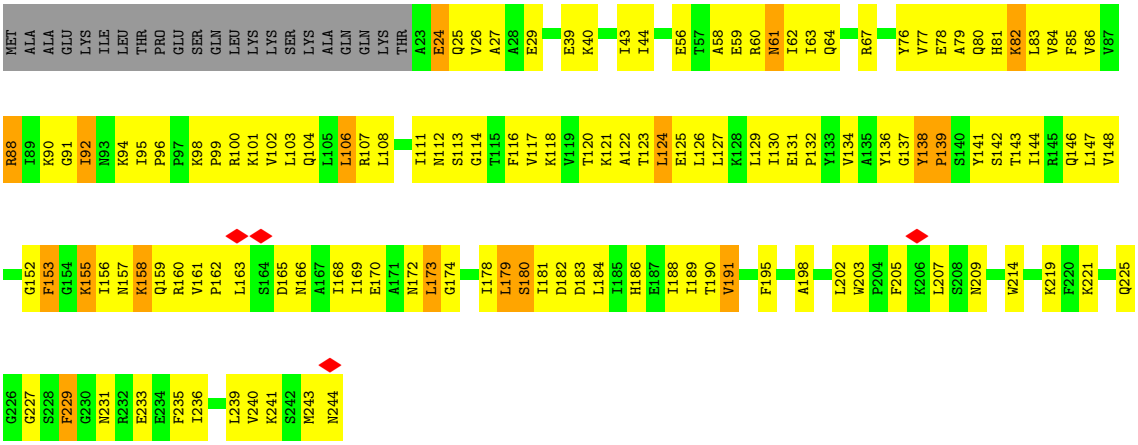
- Molecule 9: 60S ribosomal protein L6

Chain L6:



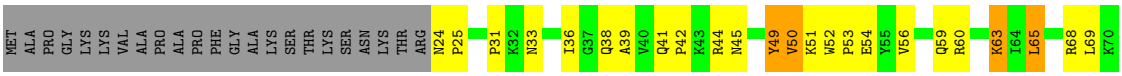
- Molecule 10: 60S ribosomal protein L7

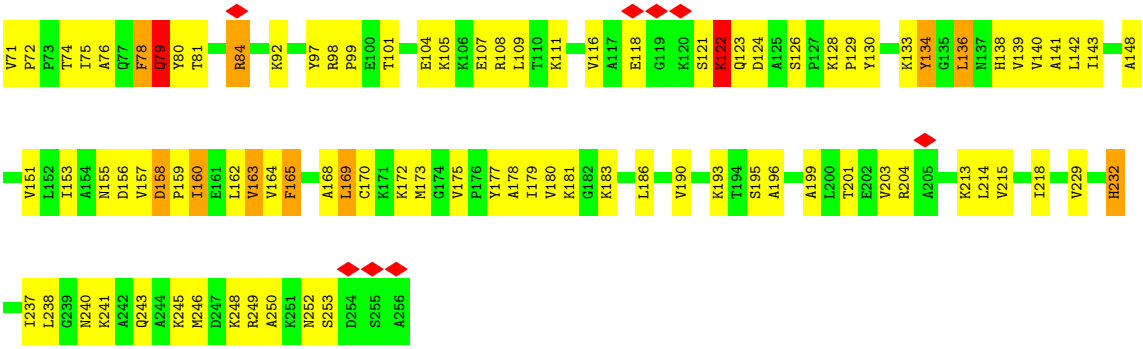
Chain L7:



- Molecule 11: 60S ribosomal protein L8

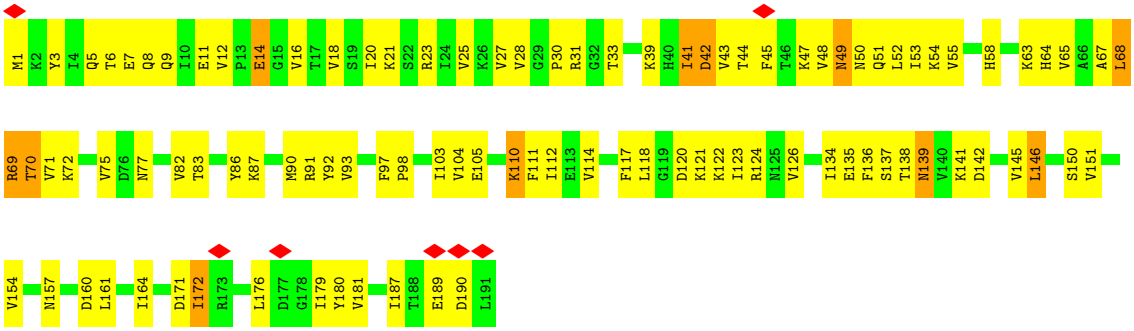
Chain L8:





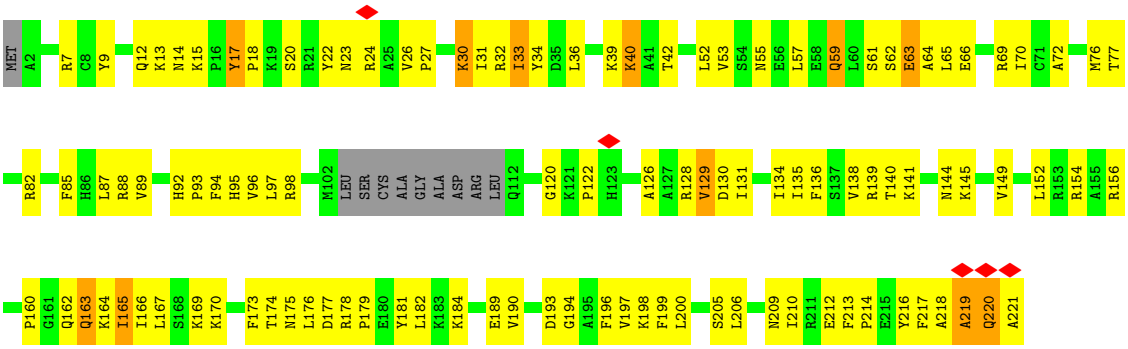
- Molecule 12: 60S ribosomal protein L9

Chain L9:



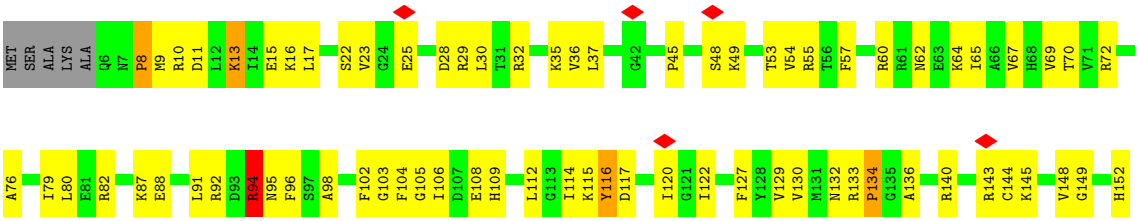
- Molecule 13: 60S ribosomal protein L10

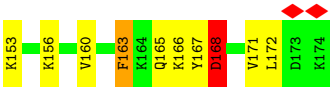
Chain 50:



- Molecule 14: 60S ribosomal protein L11

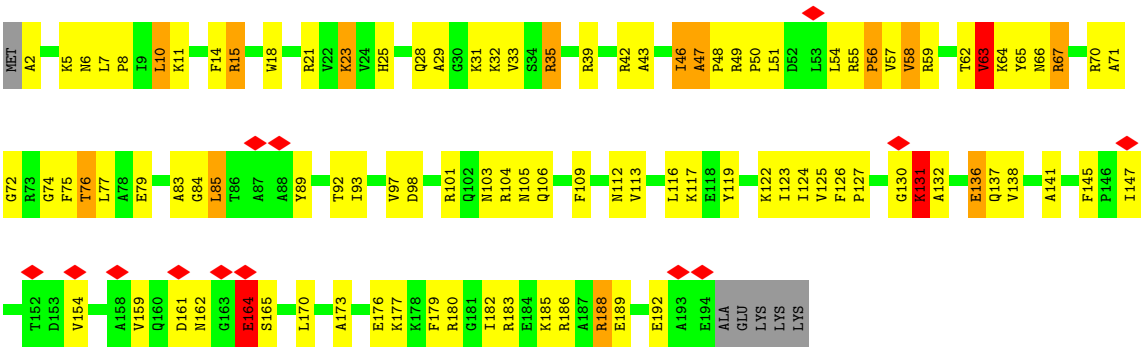
Chain 51:





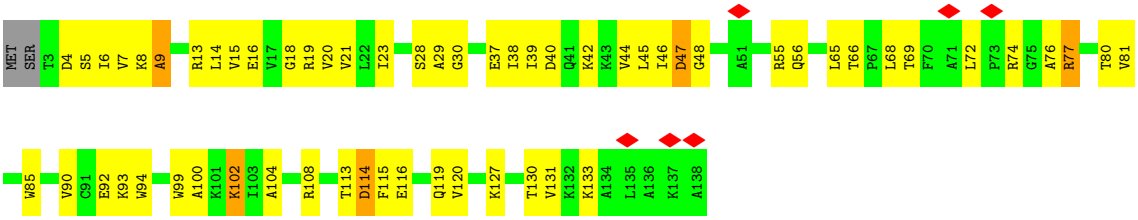
• Molecule 15: 60S ribosomal protein L13

Chain 53:



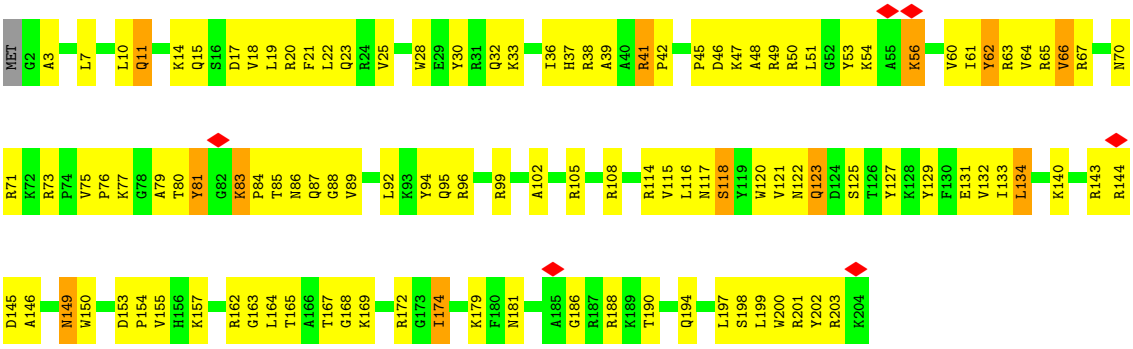
• Molecule 16: 60S ribosomal protein L14

Chain 54:



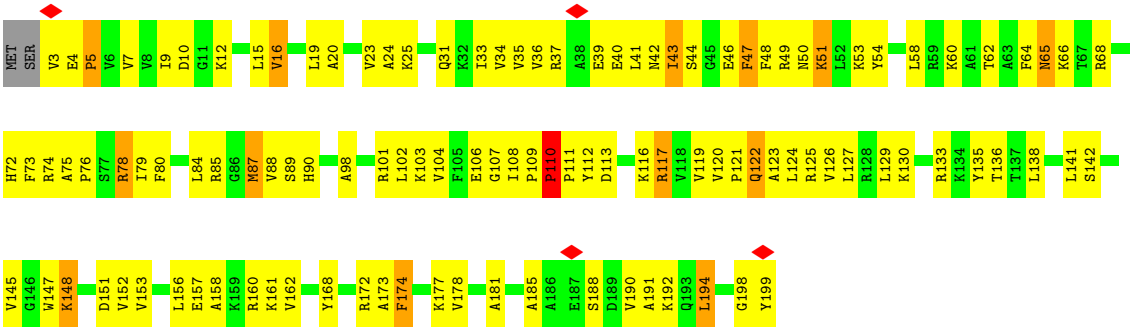
• Molecule 17: 60S ribosomal protein L15

Chain 55:



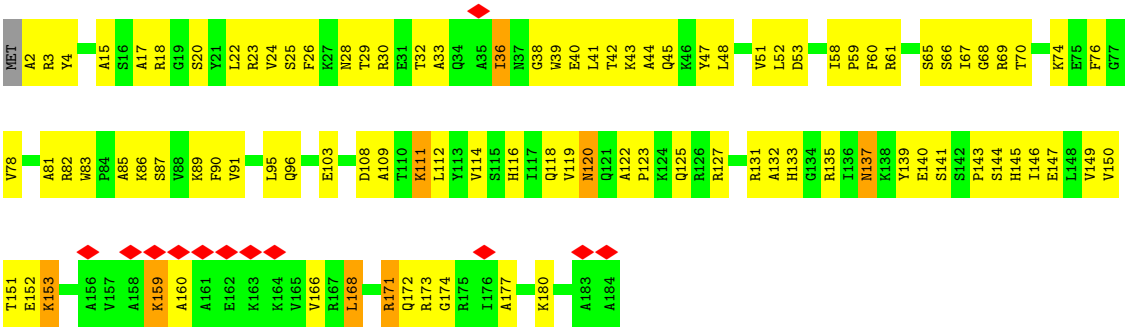
• Molecule 18: 60S ribosomal protein L16

Chain 56:



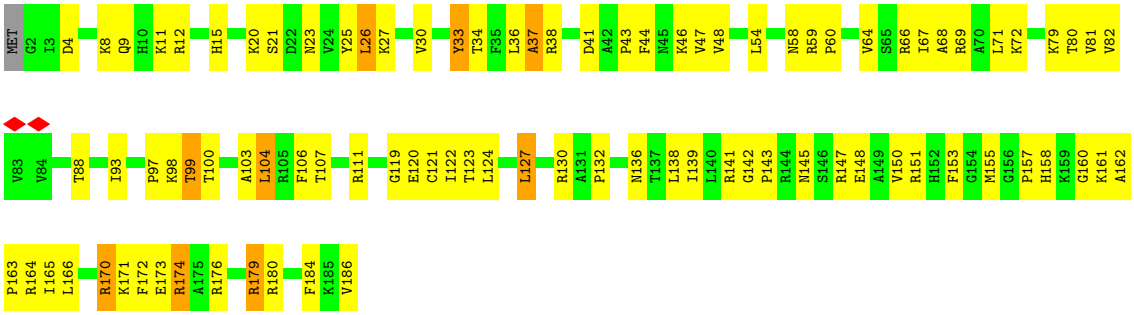
• Molecule 19: 60S ribosomal protein L17

Chain 57:



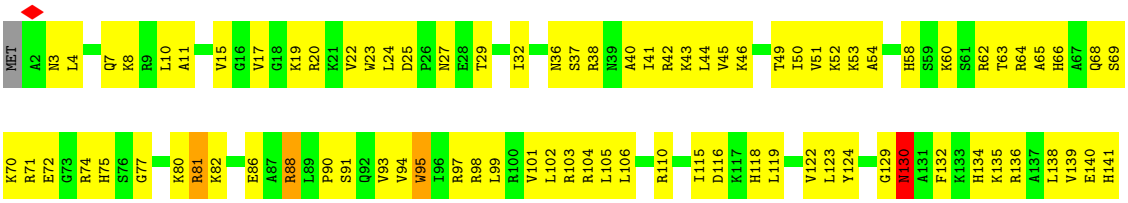
• Molecule 20: 60S ribosomal protein L18

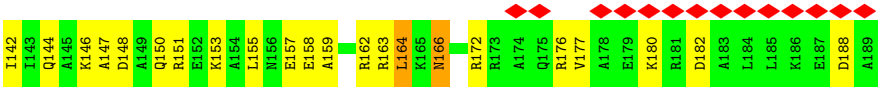
Chain 58:



• Molecule 21: 60S ribosomal protein L19

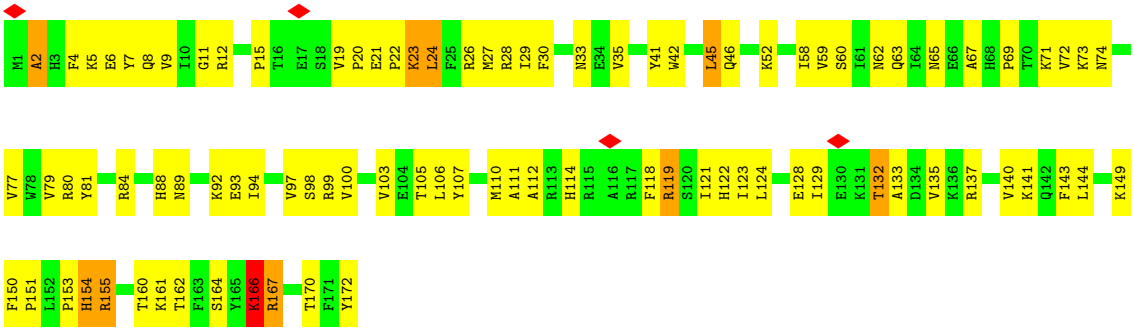
Chain 59:





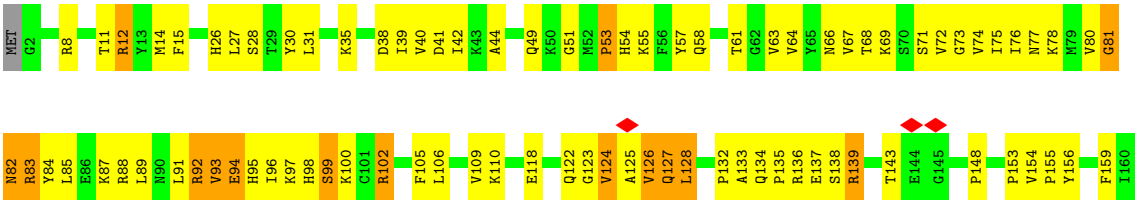
- Molecule 22: 60S ribosomal protein L20

Chain 60:



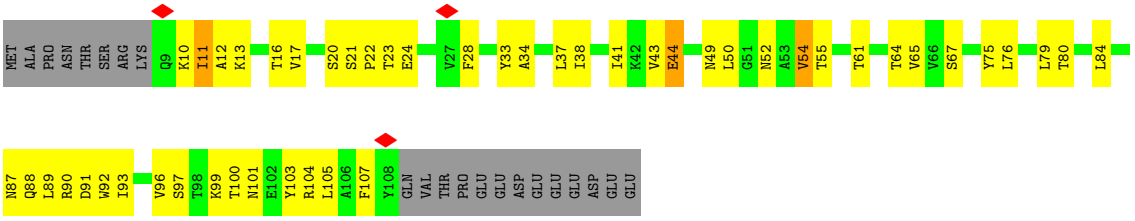
- Molecule 23: 60S ribosomal protein L21

Chain 61:



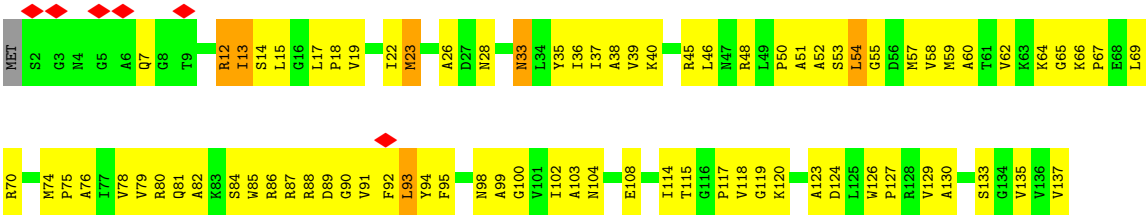
- Molecule 24: 60S ribosomal protein L22

Chain 62:



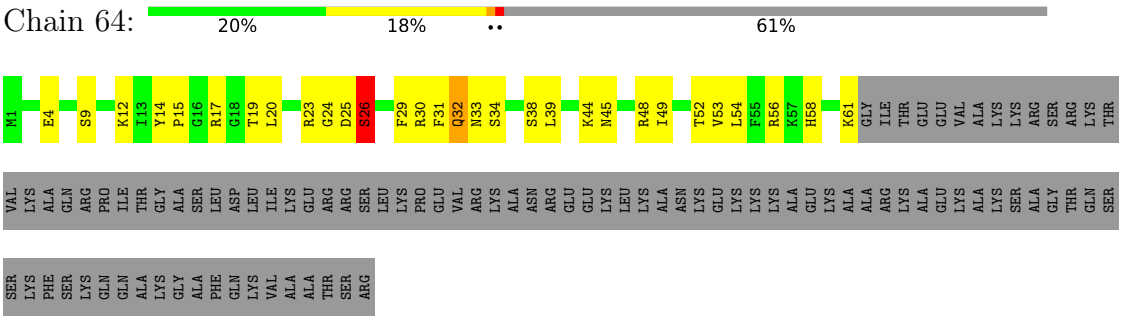
- Molecule 25: 60S ribosomal protein L23

Chain 63:



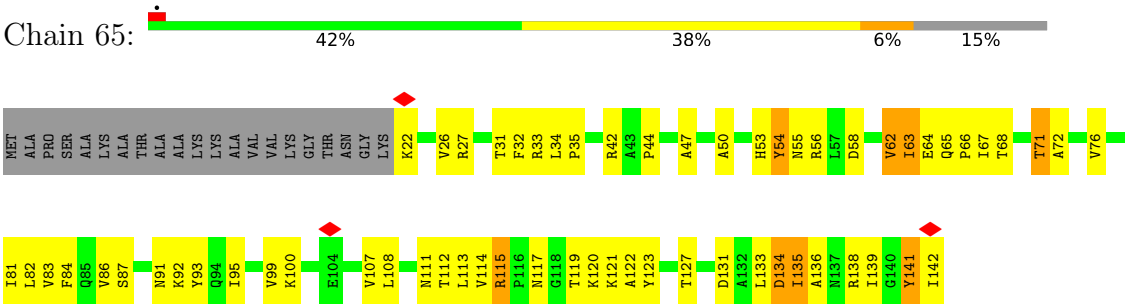
- Molecule 26: 60S ribosomal protein L24

Chain 64:



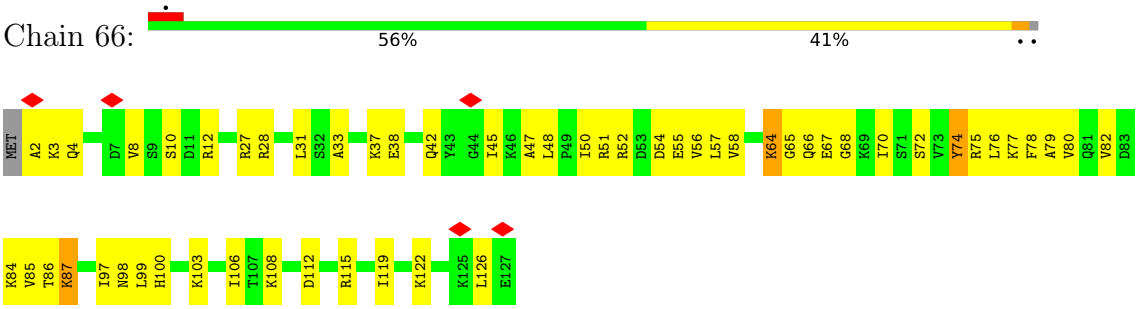
- Molecule 27: 60S ribosomal protein L25

Chain 65:



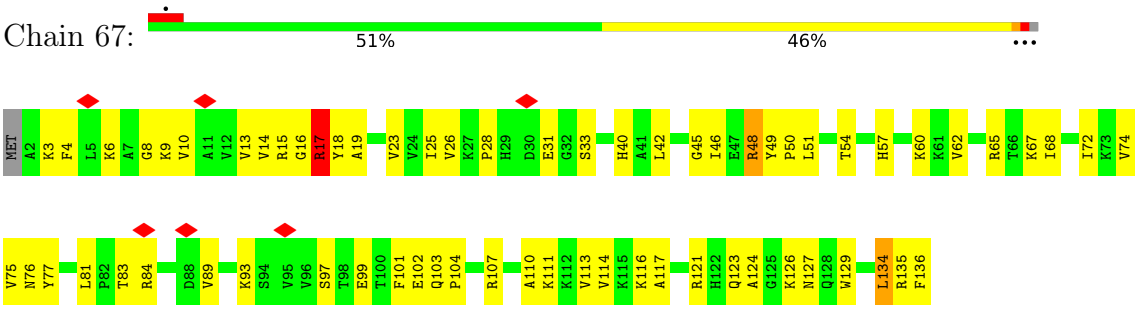
- Molecule 28: 60S ribosomal protein L26

Chain 66:



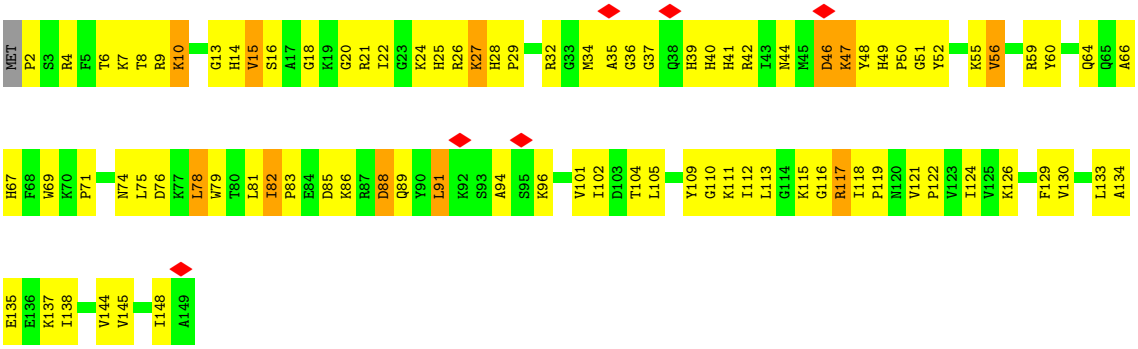
- Molecule 29: 60S ribosomal protein L27

Chain 67:



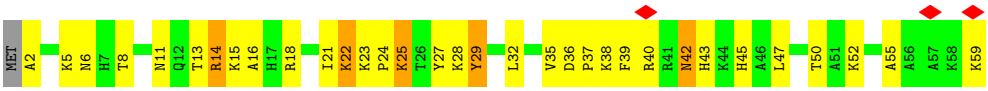
- Molecule 30: 60S ribosomal protein L28

Chain 68:



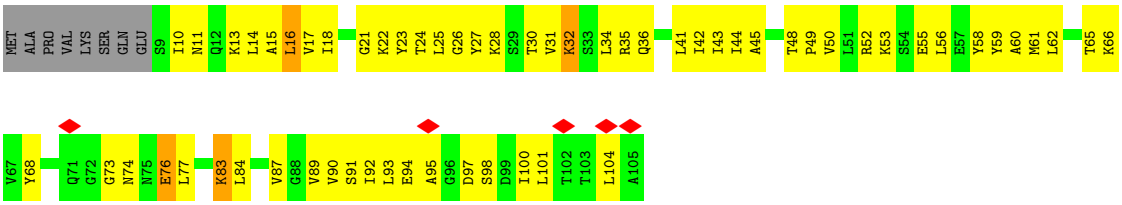
- Molecule 31: 60S ribosomal protein L29

Chain 69:



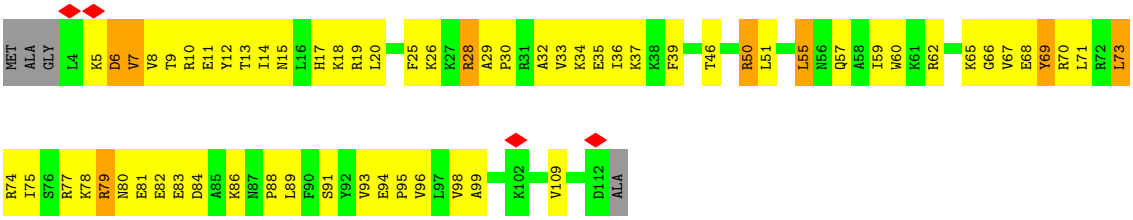
- Molecule 32: 60S ribosomal protein L30

Chain 70:



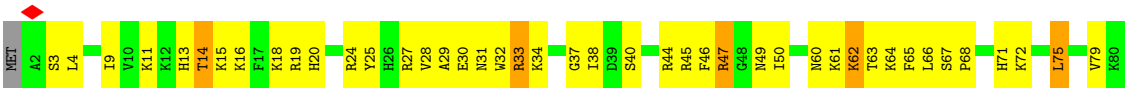
- Molecule 33: 60S ribosomal protein L31

Chain 71:



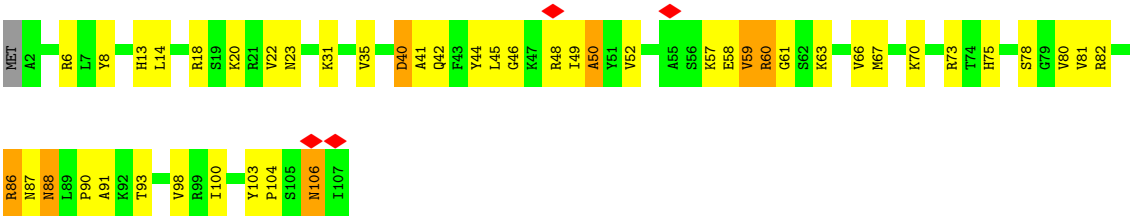
- Molecule 34: 60S ribosomal protein L32

Chain 72:



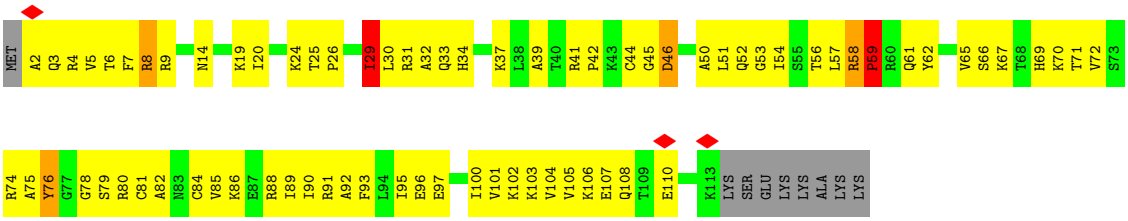
- Molecule 35: 60S ribosomal protein L33

Chain 73:



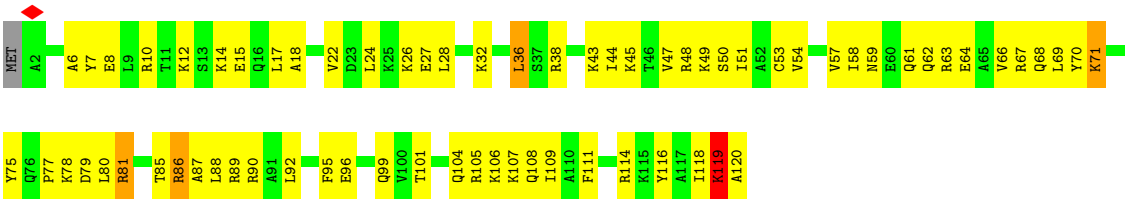
- Molecule 36: 60S ribosomal protein L34

Chain 74:



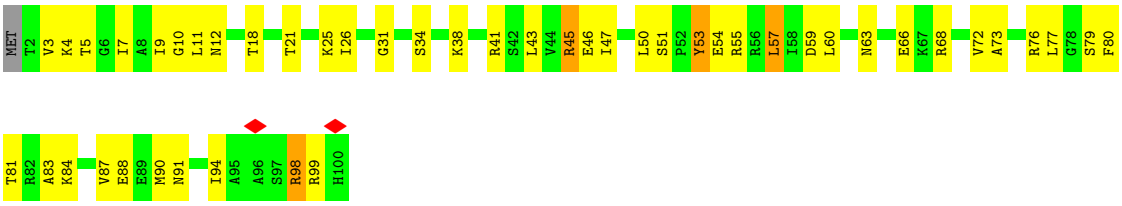
- Molecule 37: 60S ribosomal protein L35

Chain 75:



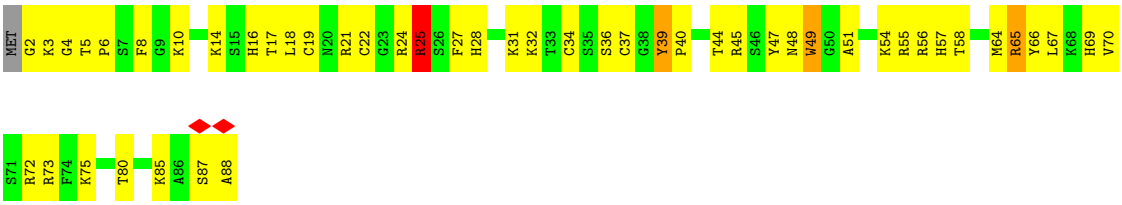
- Molecule 38: 60S ribosomal protein L36

Chain 76:



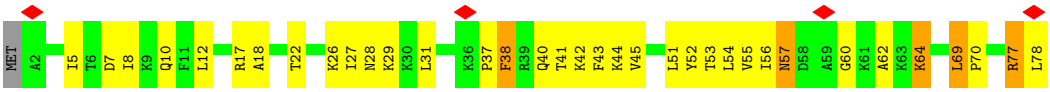
- Molecule 39: 60S ribosomal protein L37

Chain 77:



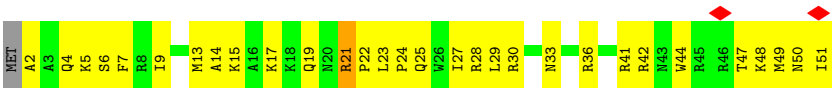
- Molecule 40: 60S ribosomal protein L38

Chain 78:



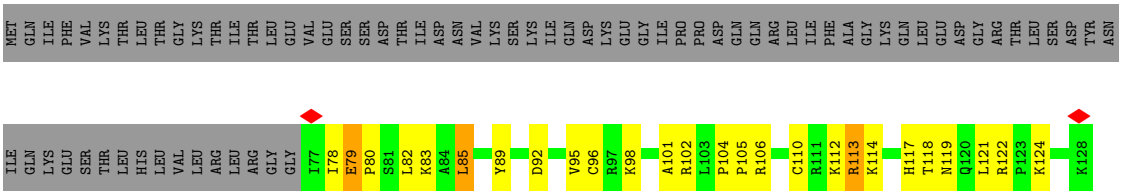
- Molecule 41: 60S ribosomal protein L39

Chain 79:



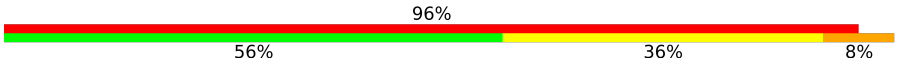
- Molecule 42: 60S ribosomal protein L40

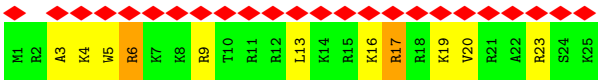
Chain 80:



- Molecule 43: 60S ribosomal protein L41

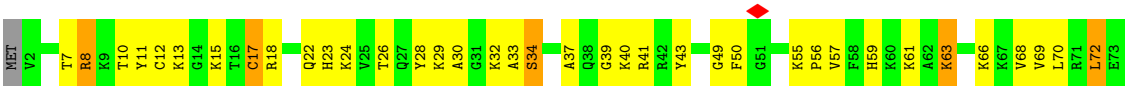
Chain 81:

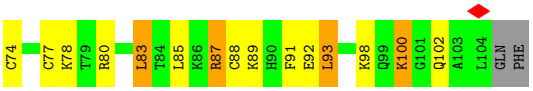




- Molecule 44: 60S ribosomal protein L42

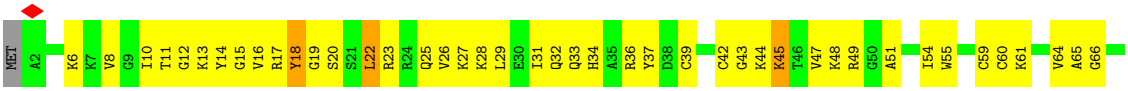
Chain 82:

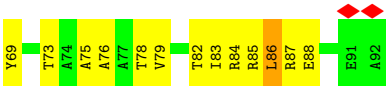




- Molecule 45: 60S ribosomal protein L43

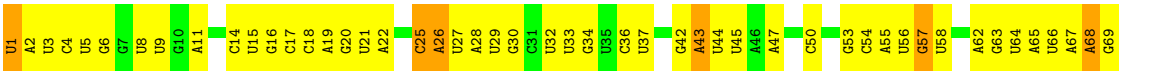
Chain 83:

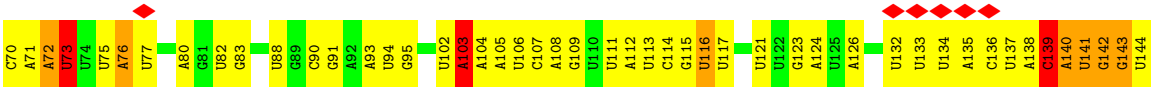


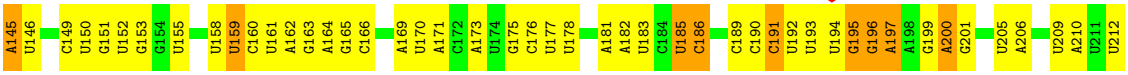


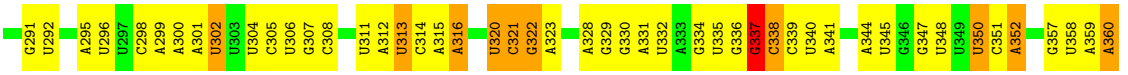
- Molecule 46: 18S ribosomal RNA

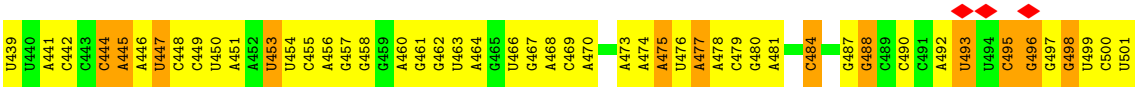
Chain 1S:

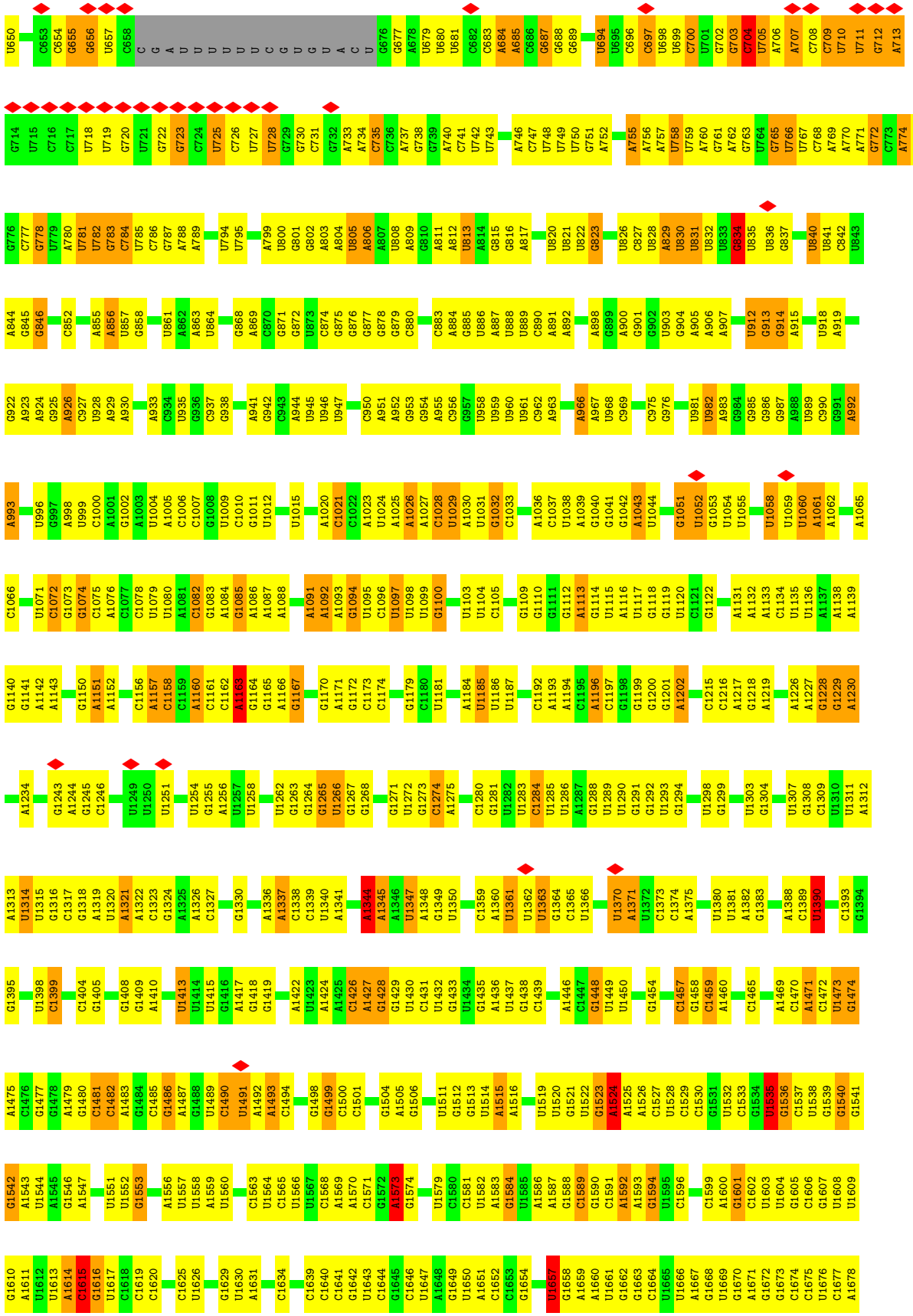








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G714 U715 C716 C717 U718 U719 G720 U721 G722 G723 C724 U725 C726 U727 U728 G729 G730 C731 G732 A733 A734 C735 C736 A737 G738 G739 A740 C741 U742 U743 A746 C747 U748 U749 U750 G751 A752 A755 A756 A757 U758 U759 A760 G761 A762 G763 U764 G765 U766 U767 C768 A769 A770 A771 G772 C773 A774 G775
G776 C777 G778 U779 A780 U781 U782 G783 C784 U785 C786 G787 A788 A789 U794 U795 A799 U800 G801 G802 A803 A804 U805 A806 A807 U808 A809 G810 A811 A812 U813 A814 G815 A816 A817 U820 U821 U822 G823 U826 C827 U828 A829 U830 U831 U832 U833 G834 U835 U836 G837 U840 U841 C842 U843
A844 G845 G846 C852 A855 A856 U857 G858 U861 A862 A863 U864 G868 A869 C870 G871 G872 U873 C874 G875 G876 G877 G878 G879 C880 C883 A884 G885 U886 A887 U888 U889 C890 A891 A892 A898 G899 A900 G901 G902 U903 G904 A905 A906 A907 U912 G913 G914 A915 U918 A919
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A993 U996 G997 A998 U999 C1000 A1001 G1002 A1003 U1004 A1005 C1006 C1007 G1008 U1009 C1010 G1011 U1012 U1015 A1020 C1021 C1022 A1023 U1024 A1025 A1026 A1027 C1028 U1029 A1030 U1031 G1032 C1033 A1036 C1037 U1038 A1039 G1040 G1041 G1042 A1043 U1044 G1051 U1052 G1053 U1054 U1055 U1058 U1059 U1060 A1061 A1062 A1065
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G1140 G1141 A1142 A1143 G1150 A1151 A1152 C1156 A1157 C1158 C1159 A1160 C1161 C1162 A1163 G1164 G1165 A1166 G1167 G1170 A1171 G1172 C1173 C1174 G1179 C1180 U1181 A1184 U1185 U1186 U1187 C1192 A1193 A1194 C1195 A1196 C1197 G1198 G1199 G1200 G1201 A1202 C1215 C1216 A1217 G1218 A1219 A1226 A1227 G1228 G1229 A1230
A1234 G1243 A1244 G1245 C1246 U1249 U1250 U1251 U1254 G1255 A1256 U1257 U1258 U1262 G1263 G1264 G1265 U1266 G1267 G1268 G1271 U1272 G1273 C1274 A1275 C1280 G1281 U1282 U1283 C1284 U1285 U1286 A1287 G1288 U1289 U1290 G1291 G1292 U1293 G1294 U1298 G1299 U1303 G1304 U1307 G1308 G1309 U1310 U1311 A1312
A1313 U1314 U1315 G1316 C1317 G1318 A1319 U1320 A1321 A1322 C1323 G1324 A1325 A1326 C1327 G1330 A1336 A1337 C1338 C1339 U1340 A1341 A1344 A1345 A1346 U1347 U1348 G1349 U1350 C1359 A1360 U1361 U1362 G1363 G1364 C1365 U1366 U1370 A1371 U1372 C1373 C1374 A1375 U1380 U1381 A1382 G1383 A1388 C1389 U1390 C1393 G1394
G1395 U1398 C1399 C1404 G1405 G1408 G1409 A1410 U1413 U1414 U1415 G1416 A1417 G1418 G1419 A1422 U1423 A1424 A1425 C1426 A1427 G1428 G1429 U1430 C1431 U1432 G1433 U1434 G1435 A1436 U1437 G1438 C1439 A1446 C1447 G1448 U1449 U1450 G1454 C1457 G1458 C1459 A1460 C1465 A1469 C1470 A1471 C1472 U1473 G1474
A1475 C1476 G1477 G1478 A1479 G1480 C1481 C1482 A1483 G1484 C1485 G1486 A1487 G1488 U1489 C1490 U1491 A1492 A1493 C1494 G1498 G1499 C1500 C1501 G1504 A1505 G1506 U1511 G1512 G1513 U1514 A1515 A1516 U1519 U1520 G1521 U1522 G1523 A1524 A1525 A1526 C1527 U1528 C1529 C1530 G1531 U1532 C1533 G1534 U1535 G1536 C1537 U1538 G1539 G1540 G1541
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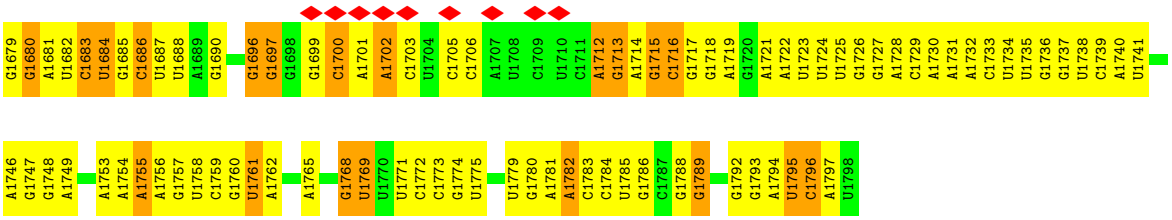
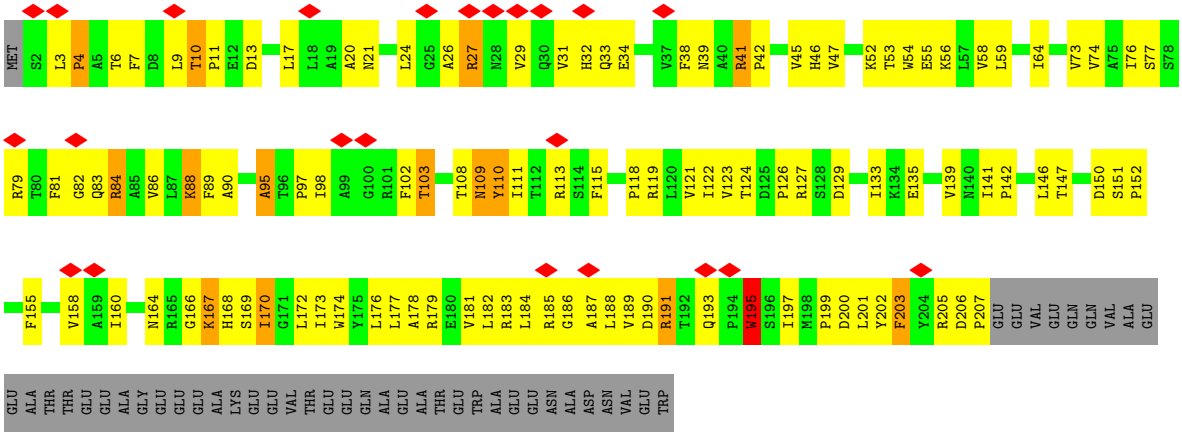


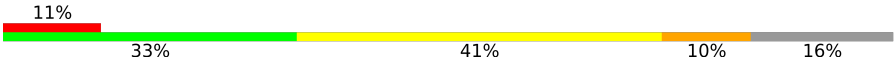
• Molecule 47: 40S ribosomal protein S0

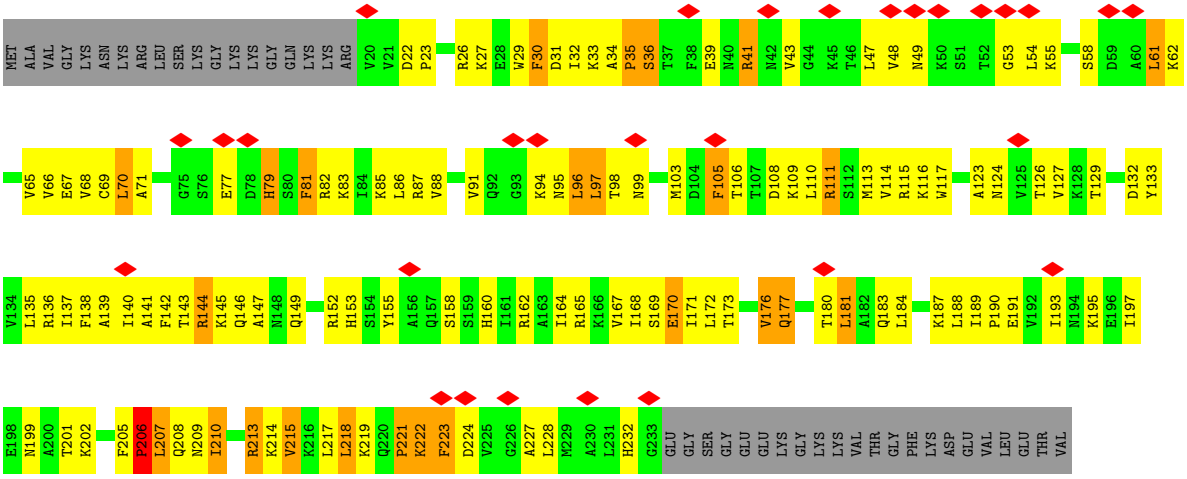
Chain S0:



• Molecule 48: 40S ribosomal protein S1

Chain S1:



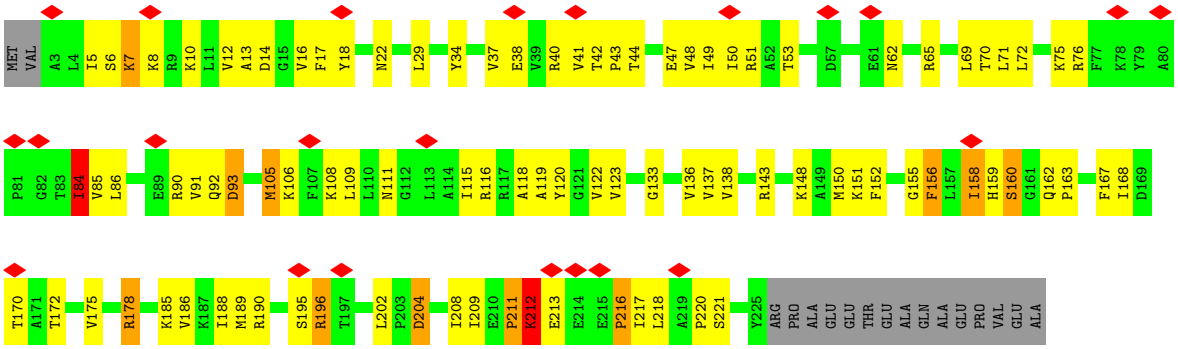


• Molecule 49: 40S ribosomal protein S2

Chain S2:

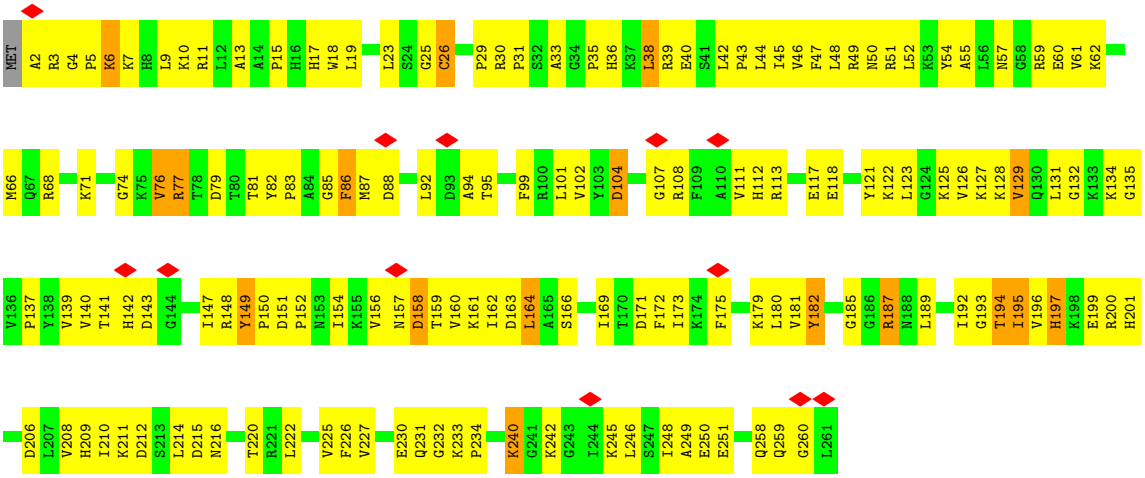
- Molecule 50: 40S ribosomal protein S3

Chain S3:



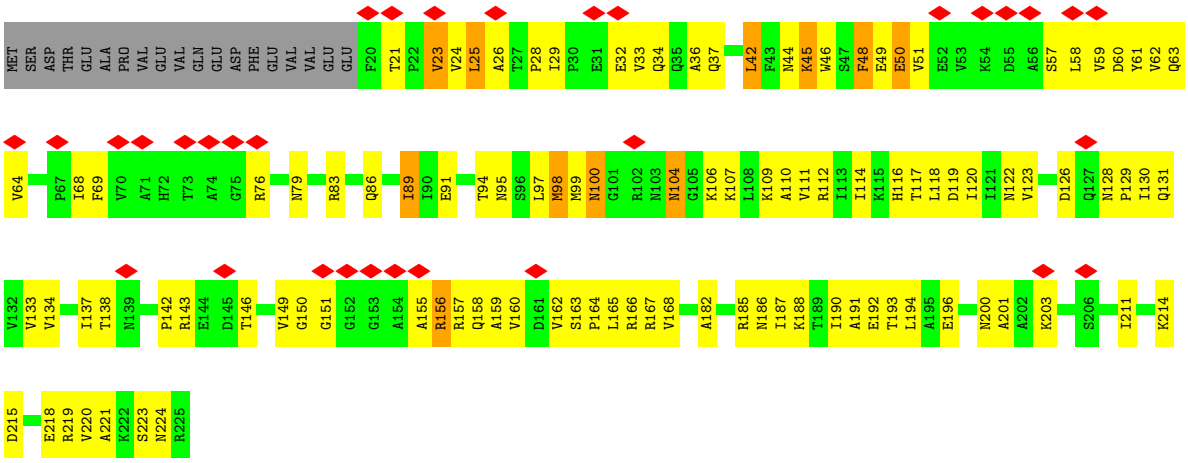
- Molecule 51: 40S ribosomal protein S4

Chain S4:



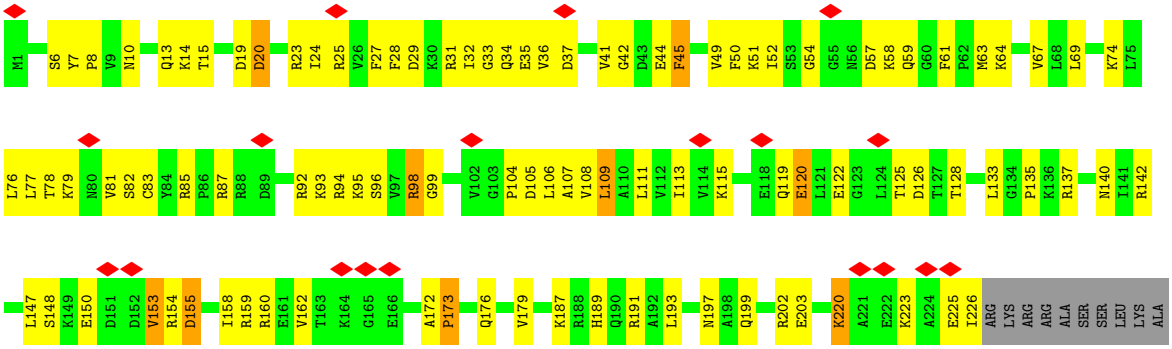
- Molecule 52: 40S ribosomal protein S5

Chain S5:



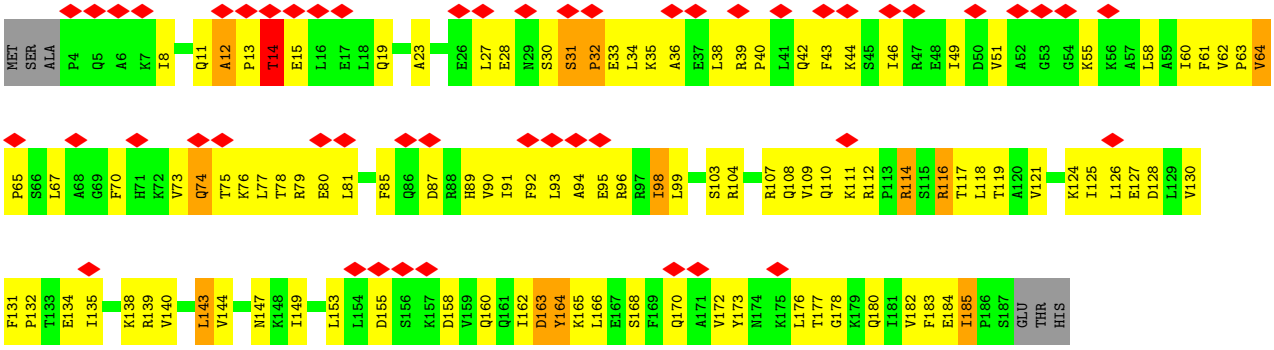
- Molecule 53: 40S ribosomal protein S6

Chain S6:



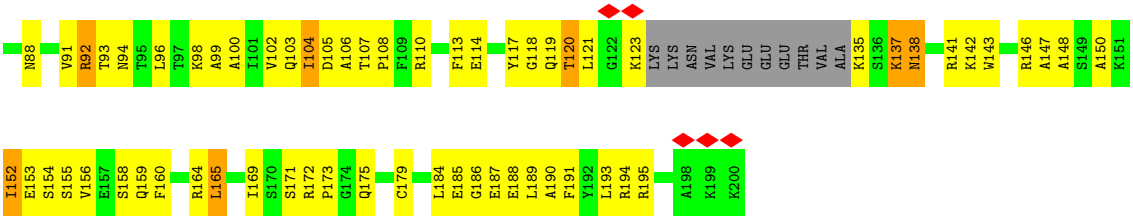
- Molecule 54: 40S ribosomal protein S7

Chain S7:



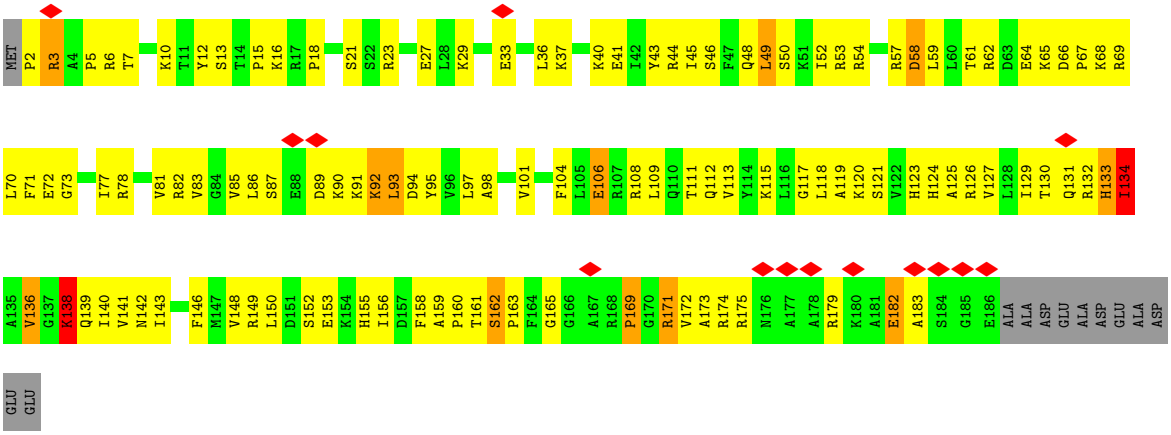
- Molecule 55: 40S ribosomal protein S8

Chain S8:



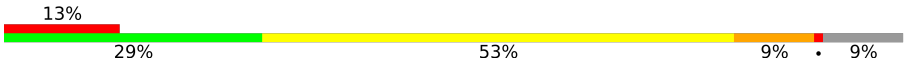
• Molecule 56: 40S ribosomal protein S9

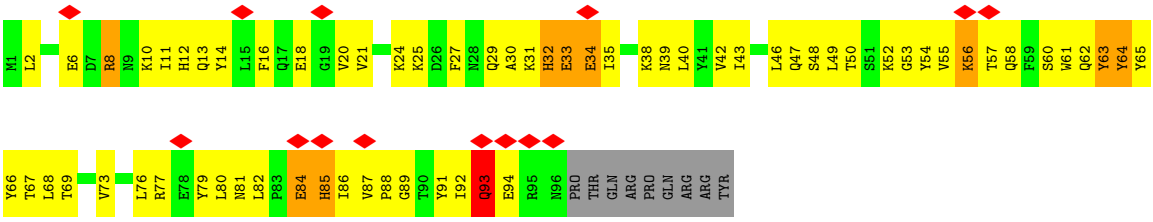
Chain S9:



• Molecule 57: 40S ribosomal protein S10

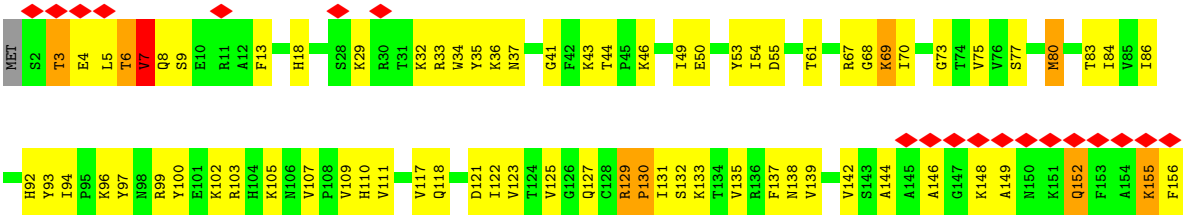
Chain 10:





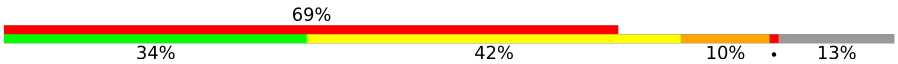
• Molecule 58: 40S ribosomal protein S11

Chain 11:



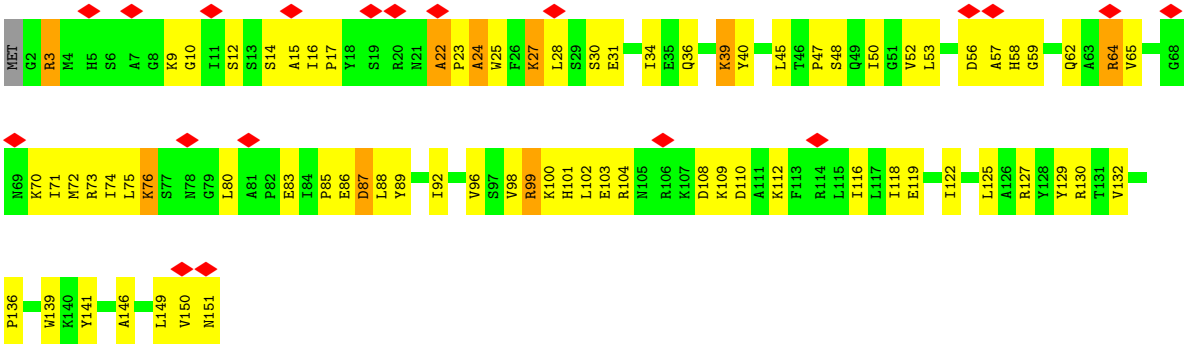
• Molecule 59: 40S ribosomal protein S12

Chain 12:



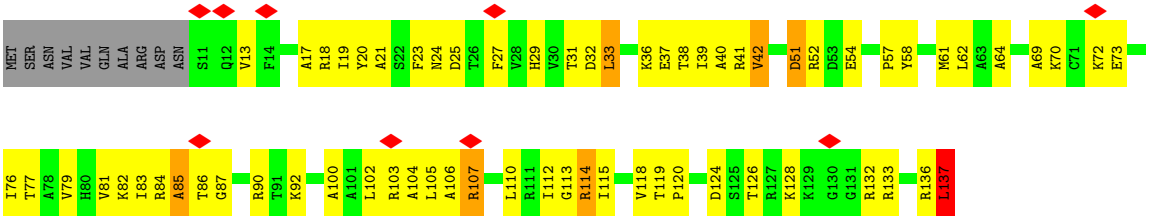
- Molecule 60: 40S ribosomal protein S13

Chain 13:



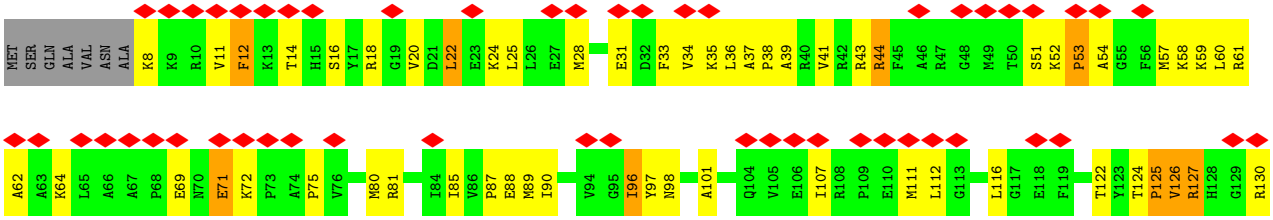
- Molecule 61: 40S ribosomal protein S14

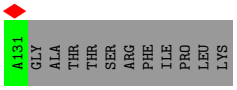
Chain 14:



- Molecule 62: 40S ribosomal protein S15

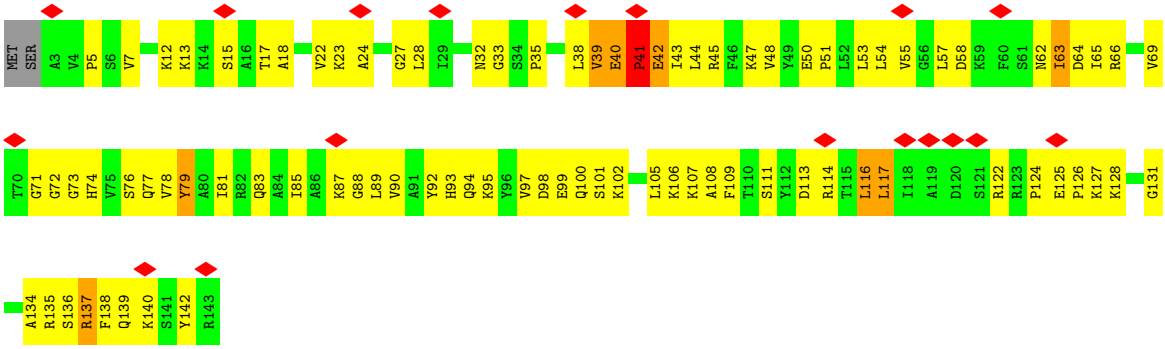
Chain 15:





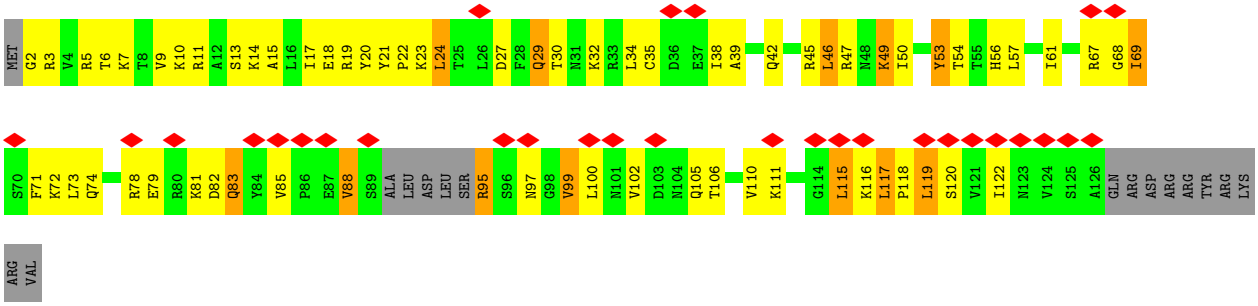
- Molecule 63: 40S ribosomal protein S16

Chain 16:



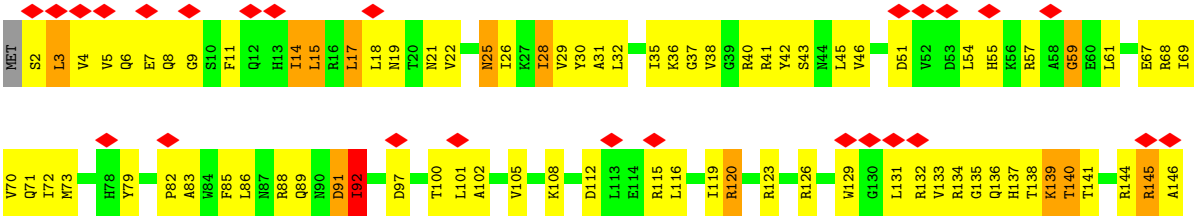
- Molecule 64: 40S ribosomal protein S17

Chain 17:



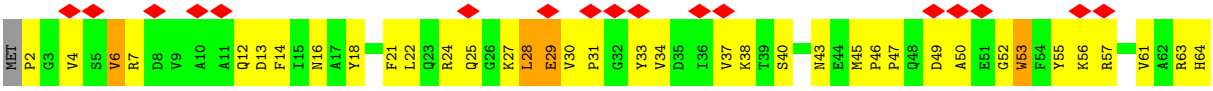
- Molecule 65: 40S ribosomal protein S18

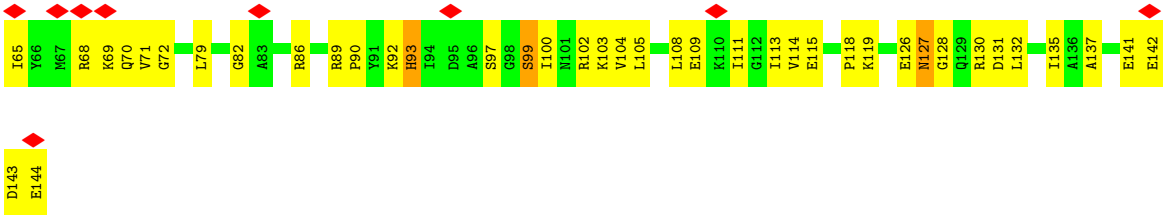
Chain 18:



- Molecule 66: 40S ribosomal protein S19

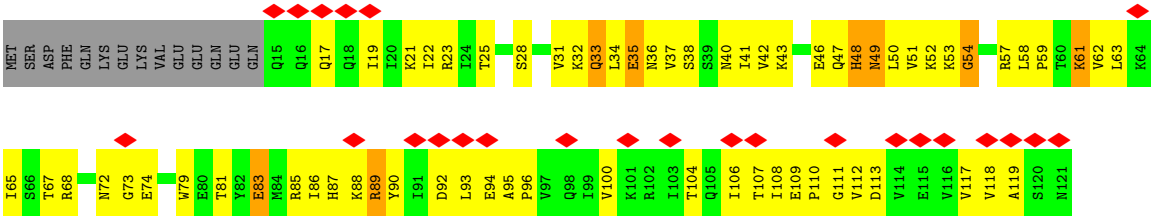
Chain 19:





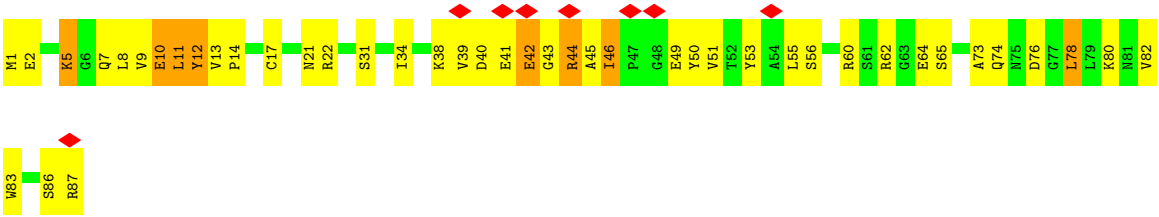
- Molecule 67: 40S ribosomal protein S20

Chain 20:



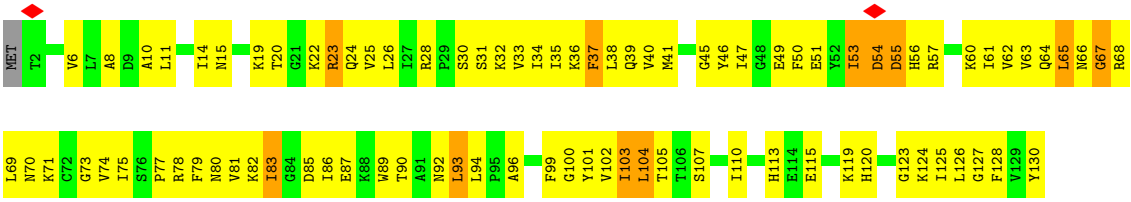
- Molecule 68: 40S ribosomal protein S21

Chain 21:



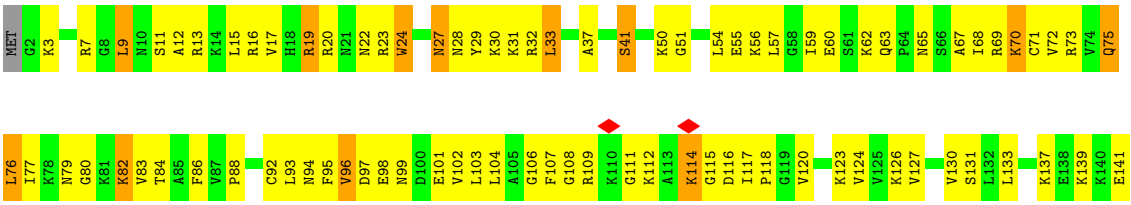
- Molecule 69: 40S ribosomal protein S22

Chain 22:



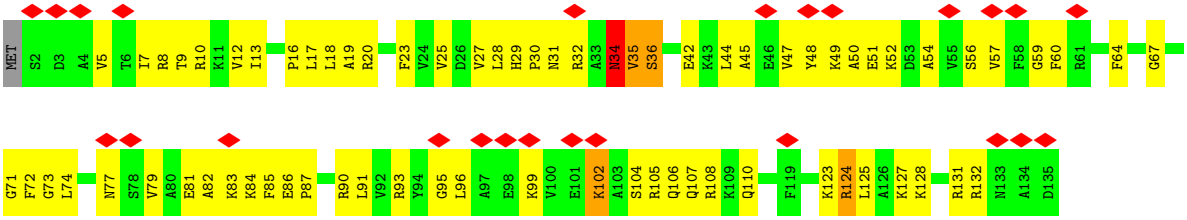
- Molecule 70: 40S ribosomal protein S23

Chain 23:



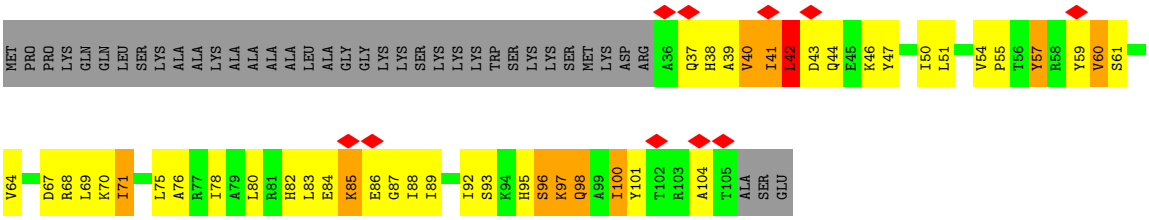
- Molecule 71: 40S ribosomal protein S24

Chain 24:



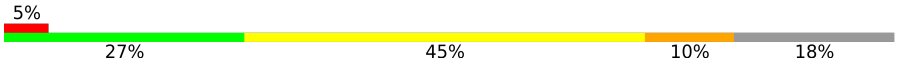
- Molecule 72: 40S ribosomal protein S25

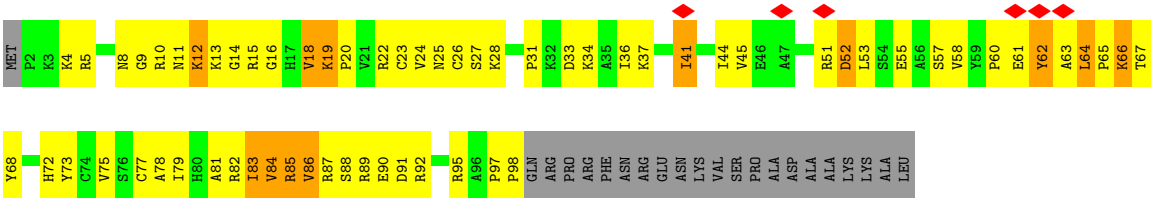
Chain 25:



- Molecule 73: 40S ribosomal protein S26

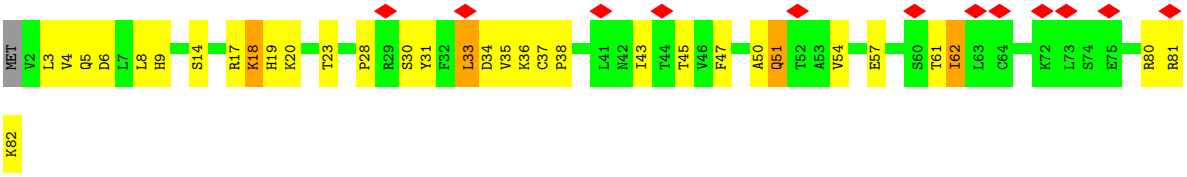
Chain 26:





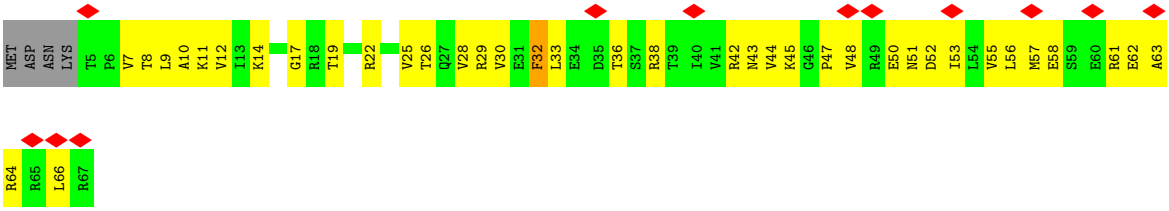
- Molecule 74: 40S ribosomal protein S27

Chain 27:



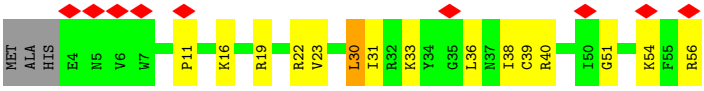
- Molecule 75: 40S ribosomal protein S28

Chain 28:



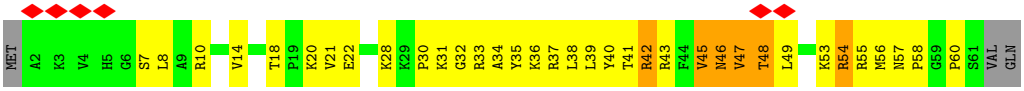
- Molecule 76: 40S ribosomal protein S29

Chain 29:



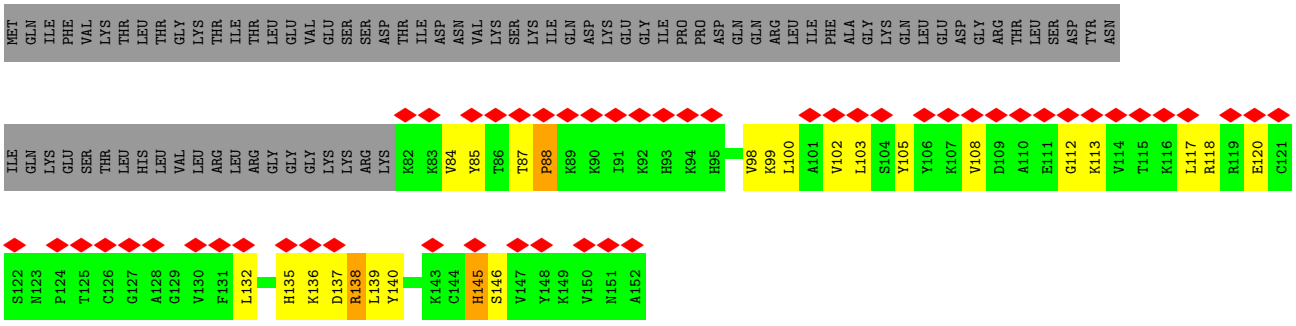
- Molecule 77: 40S ribosomal protein S30

Chain 30:



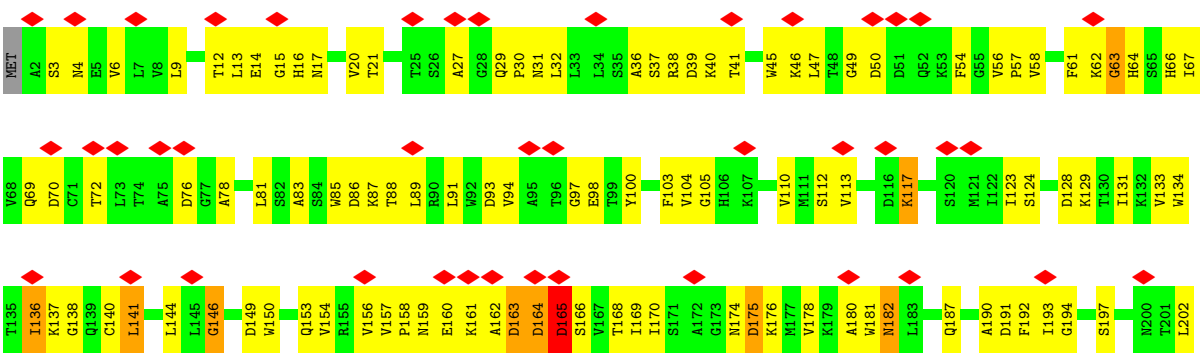
- Molecule 78: 40S ribosomal protein S31

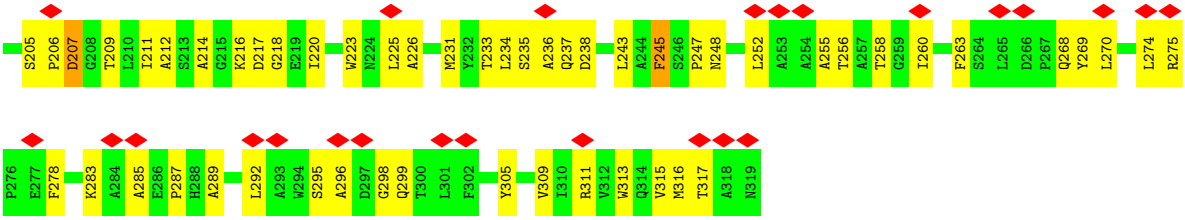
Chain 31:



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

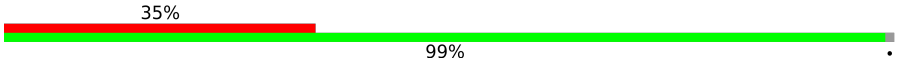
Chain RA:

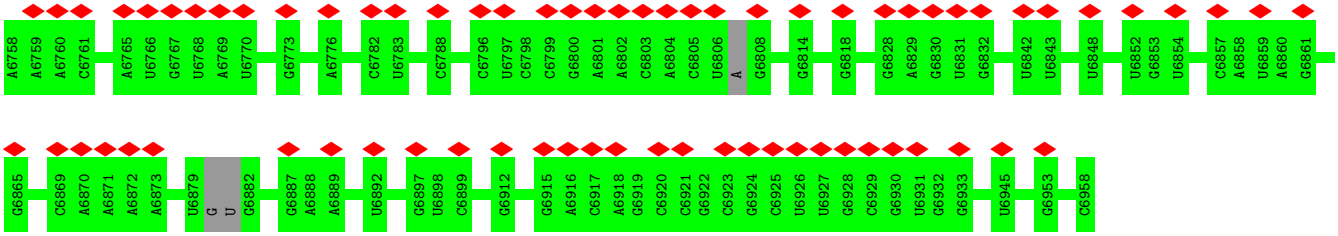




• Molecule 80: TSV IRES mRNA

Chain IR:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	51373	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	4.067	Depositor
Minimum map value	-1.662	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.283	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	0.83	7/79178 (0.0%)	0.75	31/123444 (0.0%)
2	8S	0.80	1/3747 (0.0%)	0.73	2/5832 (0.0%)
3	5S	0.79	1/2884 (0.0%)	0.71	0/4491
4	L1	0.59	0/1634	0.71	0/2195
5	L2	0.50	0/1952	0.65	0/2622
6	L3	0.57	0/3153	0.64	1/4239 (0.0%)
7	L4	0.58	0/2802	0.67	0/3792
8	L5	0.58	0/2426	0.61	0/3271
9	L6	0.62	0/1261	0.68	0/1694
10	L7	0.59	0/1822	0.64	0/2451
11	L8	0.54	0/1850	0.63	0/2495
12	L9	0.57	0/1540	0.62	0/2073
13	50	0.56	0/1754	0.65	0/2350
14	51	0.53	0/1375	0.59	0/1842
15	53	0.56	0/1568	0.67	0/2106
16	54	0.60	0/1069	0.63	0/1438
17	55	0.55	0/1758	0.62	0/2354
18	56	0.56	0/1586	0.65	0/2128
19	57	0.57	0/1466	0.66	0/1968
20	58	0.57	0/1466	0.68	0/1965
21	59	0.46	0/1539	0.63	0/2050
22	60	0.62	0/1482	0.63	0/1990
23	61	0.58	0/1301	0.66	0/1743
24	62	0.54	0/812	0.60	0/1099
25	63	0.55	0/1019	0.64	0/1369
26	64	0.60	0/521	0.61	0/691
27	65	0.54	0/984	0.61	0/1325
28	66	0.54	0/1005	0.64	0/1341
29	67	0.52	0/1119	0.58	0/1497
30	68	0.57	0/1205	0.70	1/1612 (0.1%)
31	69	0.52	0/474	0.64	0/629
32	70	0.51	0/751	0.58	0/1008
33	71	0.53	0/904	0.64	0/1213
34	72	0.59	0/1041	0.67	1/1394 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	73	0.63	0/869	0.67	0/1168
36	74	0.50	0/891	0.65	0/1191
37	75	0.52	0/979	0.61	0/1301
38	76	0.52	0/779	0.66	0/1034
39	77	0.55	0/697	0.61	0/923
40	78	0.50	0/619	0.58	0/826
41	79	0.52	0/444	0.61	0/588
42	80	0.59	0/424	0.65	0/562
43	81	0.73	0/235	0.72	0/300
44	82	0.57	0/839	0.63	0/1108
45	83	0.48	0/702	0.63	0/934
46	1S	0.74	1/42445 (0.0%)	0.75	20/66138 (0.0%)
47	S0	0.50	0/1653	0.62	0/2261
48	S1	0.51	0/1735	0.61	0/2335
49	S2	0.46	0/1665	0.59	0/2263
50	S3	0.53	0/1759	0.60	0/2368
51	S4	0.49	0/2110	0.62	0/2839
52	S5	0.50	0/1630	0.60	0/2202
53	S6	0.51	0/1844	0.61	0/2464
54	S7	0.51	0/1506	0.62	0/2028
55	S8	0.51	0/1515	0.58	0/2021
56	S9	0.47	0/1519	0.63	0/2035
57	10	0.58	0/837	0.61	0/1131
58	11	0.54	0/1273	0.60	0/1712
59	12	0.61	0/943	0.70	1/1274 (0.1%)
60	13	0.51	0/1216	0.62	0/1638
61	14	0.48	0/953	0.63	1/1279 (0.1%)
62	15	0.60	0/1012	0.67	0/1356
63	16	0.53	0/1126	0.64	1/1510 (0.1%)
64	17	0.52	0/974	0.62	0/1304
65	18	0.53	0/1212	0.62	0/1628
66	19	0.54	0/1131	0.62	0/1517
67	20	0.55	0/866	0.61	0/1169
68	21	0.49	0/694	0.61	0/935
69	22	0.46	0/1039	0.58	0/1395
70	23	0.49	0/1140	0.65	1/1518 (0.1%)
71	24	0.52	0/1088	0.55	0/1449
72	25	0.53	0/571	0.65	0/768
73	26	0.47	0/782	0.59	0/1047
74	27	0.53	0/621	0.66	0/838
75	28	0.49	0/500	0.61	0/670
76	29	0.57	0/454	0.56	0/602
77	30	0.51	0/483	0.62	0/643

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	31	0.57	0/505	0.71	1/682 (0.1%)
79	RA	0.54	0/2498	0.61	0/3398
All	All	0.70	10/219225 (0.0%)	0.70	61/322063 (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	92
2	8S	0	10
46	1S	1	37
All	All	1	139

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	1S	1	U	OP3-P	-6.84	1.52	1.61
3	5S	1	G	OP3-P	-6.79	1.53	1.61
2	8S	1	A	OP3-P	-6.58	1.53	1.61
1	2S	485	C	N1-C2	6.43	1.46	1.40
1	2S	483	C	N1-C2	5.87	1.46	1.40

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2S	1103	A	C5'-C4'-O4'	9.19	120.13	109.10
46	1S	1573	A	C2'-C3'-O3'	8.81	128.88	109.50
46	1S	1761	U	C2'-C3'-O3'	8.18	127.50	109.50
1	2S	282	G	C2'-C3'-O3'	7.58	126.18	109.50
46	1S	704	C	N1-C1'-C2'	7.44	123.67	114.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
46	1S	1573	A	C3'

5 of 139 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2S	148	G	Sidechain
1	2S	26	A	Sidechain
1	2S	40	A	Sidechain
1	2S	59	G	Sidechain
1	2S	91	G	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	2043	0
2	8S	3354	0	1695	102	0
3	5S	2580	0	1304	65	0
4	L1	1609	0	1701	103	0
5	L2	1918	0	1987	169	0
6	L3	3082	0	3165	234	0
7	L4	2750	0	2863	188	0
8	L5	2376	0	2325	114	0
9	L6	1240	0	1326	93	0
10	L7	1785	0	1862	134	0
11	L8	1818	0	1908	109	0
12	L9	1519	0	1587	105	0
13	50	1718	0	1754	90	0
14	51	1354	0	1383	73	0
15	53	1543	0	1608	100	0
16	54	1054	0	1149	58	0
17	55	1721	0	1779	129	0
18	56	1556	0	1659	119	0
19	57	1443	0	1485	104	0
20	58	1442	0	1543	92	0
21	59	1522	0	1617	96	0
22	60	1446	0	1487	97	0
23	61	1277	0	1323	94	0
24	62	796	0	812	41	0
25	63	1004	0	1048	91	0
26	64	509	0	537	20	0
27	65	969	0	1036	62	0
28	66	994	0	1081	57	0
29	67	1093	0	1155	67	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	68	1174	0	1215	96	0
31	69	463	0	491	37	0
32	70	743	0	797	56	0
33	71	890	0	938	68	0
34	72	1020	0	1090	57	0
35	73	851	0	880	47	0
36	74	881	0	949	98	0
37	75	970	0	1078	62	0
38	76	772	0	849	46	0
39	77	682	0	687	68	0
40	78	613	0	682	36	0
41	79	437	0	475	25	0
42	80	418	0	459	26	0
43	81	234	0	284	9	0
44	82	827	0	901	46	0
45	83	695	0	738	63	0
46	1S	37949	0	19093	1110	0
47	S0	1612	0	1623	120	0
48	S1	1709	0	1784	128	0
49	S2	1635	0	1723	80	0
50	S3	1734	0	1817	85	0
51	S4	2069	0	2154	160	0
52	S5	1610	0	1675	111	0
53	S6	1820	0	1918	84	0
54	S7	1481	0	1572	100	0
55	S8	1490	0	1525	112	0
56	S9	1494	0	1573	121	0
57	10	817	0	804	63	0
58	11	1245	0	1314	68	0
59	12	935	0	975	64	0
60	13	1193	0	1255	85	0
61	14	942	0	979	88	0
62	15	991	0	1035	49	0
63	16	1106	0	1166	102	0
64	17	965	0	1026	77	0
65	18	1193	0	1222	87	0
66	19	1113	0	1124	71	0
67	20	856	0	917	67	0
68	21	685	0	672	43	0
69	22	1022	0	1060	96	0
70	23	1122	0	1196	102	0
71	24	1074	0	1132	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	25	563	0	603	50	0
73	26	769	0	818	82	0
74	27	611	0	633	33	0
75	28	498	0	535	47	0
76	29	444	0	436	13	0
77	30	475	0	525	48	0
78	31	498	0	441	13	0
79	RA	2445	0	2401	121	0
80	IR	198	0	0	0	0
All	All	204247	0	150969	8302	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 23.

The worst 5 of 8302 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)
1:2S:250:U:H5'	1:2S:251:G:H5"	1.25	1.16
46:1S:1712:A:H3'	46:1S:1713:G:H5"	1.26	1.15
60:13:22:ALA:HB1	60:13:23:PRO:HA	1.28	1.12
19:57:122:ALA:HB3	19:57:143:PRO:HB2	1.23	1.11
46:1S:845:G:H2'	46:1S:846:G:H5"	1.32	1.11

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%)	133 (66%)	52 (26%)	17 (8%)	1 11
5	L2	250/254 (98%)	199 (80%)	41 (16%)	10 (4%)	3 23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	L3	384/387 (99%)	321 (84%)	52 (14%)	11 (3%)	4	29
7	L4	359/362 (99%)	290 (81%)	47 (13%)	22 (6%)	1	16
8	L5	294/297 (99%)	240 (82%)	41 (14%)	13 (4%)	2	22
9	L6	152/176 (86%)	132 (87%)	16 (10%)	4 (3%)	5	31
10	L7	220/244 (90%)	196 (89%)	19 (9%)	5 (2%)	6	34
11	L8	231/256 (90%)	190 (82%)	31 (13%)	10 (4%)	2	22
12	L9	189/191 (99%)	157 (83%)	27 (14%)	5 (3%)	5	31
13	50	207/221 (94%)	173 (84%)	30 (14%)	4 (2%)	8	38
14	51	167/174 (96%)	131 (78%)	27 (16%)	9 (5%)	2	19
15	53	191/199 (96%)	152 (80%)	25 (13%)	14 (7%)	1	13
16	54	134/138 (97%)	114 (85%)	14 (10%)	6 (4%)	2	22
17	55	201/204 (98%)	168 (84%)	28 (14%)	5 (2%)	5	32
18	56	195/199 (98%)	175 (90%)	15 (8%)	5 (3%)	5	31
19	57	181/184 (98%)	150 (83%)	26 (14%)	5 (3%)	5	30
20	58	183/186 (98%)	154 (84%)	25 (14%)	4 (2%)	6	35
21	59	186/189 (98%)	166 (89%)	16 (9%)	4 (2%)	6	35
22	60	170/172 (99%)	139 (82%)	26 (15%)	5 (3%)	4	29
23	61	157/160 (98%)	126 (80%)	19 (12%)	12 (8%)	1	13
24	62	98/121 (81%)	83 (85%)	12 (12%)	3 (3%)	4	27
25	63	134/137 (98%)	113 (84%)	20 (15%)	1 (1%)	22	62
26	64	59/155 (38%)	44 (75%)	14 (24%)	1 (2%)	9	42
27	65	119/142 (84%)	100 (84%)	16 (13%)	3 (2%)	5	32
28	66	124/127 (98%)	110 (89%)	13 (10%)	1 (1%)	19	60
29	67	133/136 (98%)	106 (80%)	23 (17%)	4 (3%)	4	28
30	68	146/149 (98%)	110 (75%)	27 (18%)	9 (6%)	1	16
31	69	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	8	40
32	70	95/105 (90%)	89 (94%)	5 (5%)	1 (1%)	14	52
33	71	107/113 (95%)	84 (78%)	20 (19%)	3 (3%)	5	30
34	72	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
35	73	104/107 (97%)	80 (77%)	21 (20%)	3 (3%)	4	29
36	74	110/121 (91%)	92 (84%)	14 (13%)	4 (4%)	3	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	75	117/120 (98%)	108 (92%)	8 (7%)	1 (1%)	17	56
38	76	97/100 (97%)	81 (84%)	14 (14%)	2 (2%)	7	36
39	77	85/88 (97%)	70 (82%)	13 (15%)	2 (2%)	6	33
40	78	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
41	79	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	7	36
42	80	50/128 (39%)	40 (80%)	9 (18%)	1 (2%)	7	38
43	81	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
44	82	101/106 (95%)	88 (87%)	9 (9%)	4 (4%)	3	23
45	83	89/92 (97%)	74 (83%)	11 (12%)	4 (4%)	2	22
47	S0	204/252 (81%)	163 (80%)	30 (15%)	11 (5%)	2	19
48	S1	212/255 (83%)	152 (72%)	41 (19%)	19 (9%)	1	11
49	S2	215/254 (85%)	178 (83%)	27 (13%)	10 (5%)	2	21
50	S3	221/240 (92%)	181 (82%)	29 (13%)	11 (5%)	2	20
51	S4	258/261 (99%)	214 (83%)	35 (14%)	9 (4%)	3	25
52	S5	204/225 (91%)	164 (80%)	30 (15%)	10 (5%)	2	20
53	S6	224/236 (95%)	193 (86%)	25 (11%)	6 (3%)	5	31
54	S7	182/190 (96%)	138 (76%)	29 (16%)	15 (8%)	1	12
55	S8	184/200 (92%)	151 (82%)	29 (16%)	4 (2%)	6	35
56	S9	183/197 (93%)	153 (84%)	21 (12%)	9 (5%)	2	20
57	10	94/105 (90%)	75 (80%)	13 (14%)	6 (6%)	1	16
58	11	153/156 (98%)	108 (71%)	36 (24%)	9 (6%)	1	17
59	12	122/143 (85%)	85 (70%)	23 (19%)	14 (12%)	0	6
60	13	148/151 (98%)	123 (83%)	22 (15%)	3 (2%)	7	38
61	14	125/137 (91%)	95 (76%)	24 (19%)	6 (5%)	2	20
62	15	122/142 (86%)	90 (74%)	22 (18%)	10 (8%)	1	12
63	16	139/143 (97%)	114 (82%)	18 (13%)	7 (5%)	2	20
64	17	116/136 (85%)	98 (84%)	14 (12%)	4 (3%)	3	26
65	18	143/146 (98%)	115 (80%)	19 (13%)	9 (6%)	1	16
66	19	141/144 (98%)	117 (83%)	20 (14%)	4 (3%)	5	30
67	20	105/121 (87%)	88 (84%)	13 (12%)	4 (4%)	3	24
68	21	85/87 (98%)	69 (81%)	10 (12%)	6 (7%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	22	127/130 (98%)	108 (85%)	16 (13%)	3 (2%)	6	33
70	23	142/145 (98%)	102 (72%)	32 (22%)	8 (6%)	2	18
71	24	132/135 (98%)	103 (78%)	23 (17%)	6 (4%)	2	22
72	25	68/108 (63%)	46 (68%)	16 (24%)	6 (9%)	1	11
73	26	95/119 (80%)	62 (65%)	21 (22%)	12 (13%)	0	5
74	27	79/82 (96%)	59 (75%)	16 (20%)	4 (5%)	2	19
75	28	61/67 (91%)	50 (82%)	10 (16%)	1 (2%)	9	43
76	29	51/56 (91%)	44 (86%)	5 (10%)	2 (4%)	3	23
77	30	58/63 (92%)	42 (72%)	11 (19%)	5 (9%)	1	11
78	31	69/152 (45%)	42 (61%)	18 (26%)	9 (13%)	0	5
79	RA	316/319 (99%)	250 (79%)	53 (17%)	13 (4%)	3	22
All	All	11126/12097 (92%)	9048 (81%)	1604 (14%)	474 (4%)	5	22

5 of 474 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	L1	20	SER
4	L1	153	SER
4	L1	193	LEU
4	L1	199	GLN
4	L1	209	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	
4	L1	185/198 (93%)	169 (91%)	16 (9%)	10	32
5	L2	194/196 (99%)	181 (93%)	13 (7%)	16	41
6	L3	322/323 (100%)	301 (94%)	21 (6%)	17	42
7	L4	288/289 (100%)	268 (93%)	20 (7%)	15	40
8	L5	244/245 (100%)	225 (92%)	19 (8%)	12	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	L6	134/153 (88%)	126 (94%)	8 (6%)	19	44
10	L7	186/205 (91%)	172 (92%)	14 (8%)	13	38
11	L8	191/208 (92%)	174 (91%)	17 (9%)	9	31
12	L9	171/171 (100%)	159 (93%)	12 (7%)	15	40
13	50	180/187 (96%)	165 (92%)	15 (8%)	11	34
14	51	147/150 (98%)	139 (95%)	8 (5%)	22	47
15	53	154/159 (97%)	137 (89%)	17 (11%)	6	23
16	54	107/109 (98%)	100 (94%)	7 (6%)	17	42
17	55	175/176 (99%)	162 (93%)	13 (7%)	13	38
18	56	160/162 (99%)	145 (91%)	15 (9%)	8	28
19	57	145/146 (99%)	136 (94%)	9 (6%)	18	43
20	58	150/151 (99%)	138 (92%)	12 (8%)	12	35
21	59	153/154 (99%)	139 (91%)	14 (9%)	9	29
22	60	156/156 (100%)	145 (93%)	11 (7%)	14	39
23	61	136/137 (99%)	125 (92%)	11 (8%)	11	35
24	62	87/107 (81%)	85 (98%)	2 (2%)	50	70
25	63	104/105 (99%)	94 (90%)	10 (10%)	8	27
26	64	54/129 (42%)	50 (93%)	4 (7%)	13	38
27	65	105/118 (89%)	95 (90%)	10 (10%)	8	28
28	66	109/110 (99%)	102 (94%)	7 (6%)	17	42
29	67	115/116 (99%)	111 (96%)	4 (4%)	36	59
30	68	118/119 (99%)	107 (91%)	11 (9%)	9	29
31	69	46/47 (98%)	40 (87%)	6 (13%)	4	18
32	70	81/88 (92%)	76 (94%)	5 (6%)	18	43
33	71	96/97 (99%)	88 (92%)	8 (8%)	11	34
34	72	109/111 (98%)	100 (92%)	9 (8%)	11	34
35	73	90/91 (99%)	83 (92%)	7 (8%)	12	36
36	74	95/103 (92%)	89 (94%)	6 (6%)	18	43
37	75	104/105 (99%)	95 (91%)	9 (9%)	10	31
38	76	81/82 (99%)	75 (93%)	6 (7%)	13	38
39	77	70/71 (99%)	64 (91%)	6 (9%)	10	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	78	68/69 (99%)	62 (91%)	6 (9%)	10	31
41	79	45/46 (98%)	41 (91%)	4 (9%)	9	31
42	80	47/116 (40%)	45 (96%)	2 (4%)	29	53
43	81	23/23 (100%)	18 (78%)	5 (22%)	1	6
44	82	88/91 (97%)	77 (88%)	11 (12%)	4	19
45	83	71/72 (99%)	68 (96%)	3 (4%)	30	54
47	S0	173/210 (82%)	163 (94%)	10 (6%)	20	45
48	S1	191/224 (85%)	173 (91%)	18 (9%)	8	28
49	S2	176/205 (86%)	170 (97%)	6 (3%)	37	60
50	S3	182/195 (93%)	168 (92%)	14 (8%)	13	37
51	S4	221/222 (100%)	199 (90%)	22 (10%)	7	26
52	S5	173/191 (91%)	163 (94%)	10 (6%)	20	45
53	S6	193/201 (96%)	184 (95%)	9 (5%)	26	51
54	S7	165/170 (97%)	154 (93%)	11 (7%)	16	41
55	S8	150/161 (93%)	142 (95%)	8 (5%)	22	47
56	S9	158/166 (95%)	146 (92%)	12 (8%)	13	37
57	10	89/98 (91%)	82 (92%)	7 (8%)	12	36
58	11	136/137 (99%)	127 (93%)	9 (7%)	16	41
59	12	100/119 (84%)	88 (88%)	12 (12%)	5	20
60	13	127/128 (99%)	114 (90%)	13 (10%)	7	25
61	14	96/105 (91%)	93 (97%)	3 (3%)	40	62
62	15	104/118 (88%)	96 (92%)	8 (8%)	13	37
63	16	117/119 (98%)	111 (95%)	6 (5%)	24	49
64	17	109/124 (88%)	94 (86%)	15 (14%)	3	17
65	18	128/129 (99%)	119 (93%)	9 (7%)	15	40
66	19	115/116 (99%)	103 (90%)	12 (10%)	7	25
67	20	100/114 (88%)	91 (91%)	9 (9%)	9	30
68	21	74/74 (100%)	70 (95%)	4 (5%)	22	47
69	22	110/111 (99%)	101 (92%)	9 (8%)	11	34
70	23	119/120 (99%)	106 (89%)	13 (11%)	6	23
71	24	112/113 (99%)	107 (96%)	5 (4%)	27	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	25	61/89 (68%)	50 (82%)	11 (18%)	1	10
73	26	83/101 (82%)	75 (90%)	8 (10%)	8	27
74	27	70/71 (99%)	69 (99%)	1 (1%)	67	80
75	28	56/60 (93%)	53 (95%)	3 (5%)	22	47
76	29	47/49 (96%)	46 (98%)	1 (2%)	53	72
77	30	51/54 (94%)	47 (92%)	4 (8%)	12	36
78	31	43/135 (32%)	38 (88%)	5 (12%)	5	21
79	RA	261/262 (100%)	241 (92%)	20 (8%)	13	37
All	All	9474/10182 (93%)	8754 (92%)	720 (8%)	17	37

5 of 720 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	S4	38	LEU
60	13	149	LEU
51	S4	212	ASP
51	S4	11	ARG
55	S8	187	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 263 such sidechains are listed below:

Mol	Chain	Res	Type
66	19	138	GLN
69	22	16	ASN
79	RA	195	HIS
20	58	145	ASN
19	57	120	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2S	3304/3395 (97%)	521 (15%)	26 (0%)
2	8S	157/158 (99%)	22 (14%)	1 (0%)
3	5S	120/121 (99%)	10 (8%)	0
46	1S	1779/1798 (98%)	332 (18%)	21 (1%)
80	IR	0/201	-	-
All	All	5360/5673 (94%)	885 (16%)	48 (0%)

5 of 885 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2S	21	G
1	2S	26	A
1	2S	40	A
1	2S	43	A
1	2S	49	A

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	1S	103	A
46	1S	555	A
46	1S	139	C
46	1S	498	G
46	1S	794	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)

There are no chain breaks in this entry.

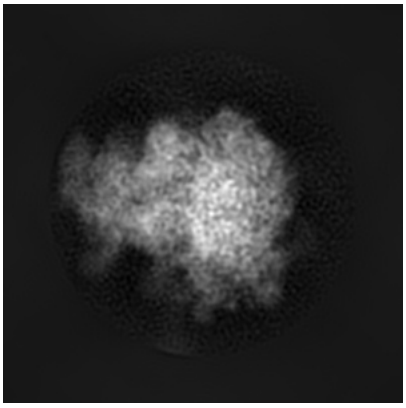
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-5943. These allow visual inspection of the internal detail of the map and identification of artifacts.

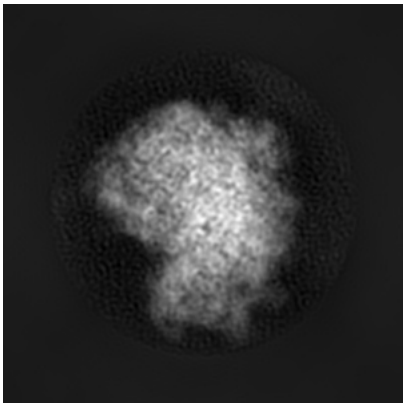
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

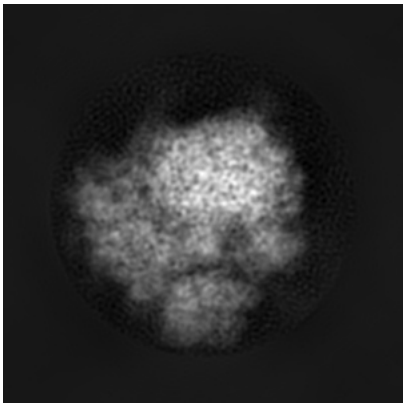
6.1.1 Primary map



X



Y

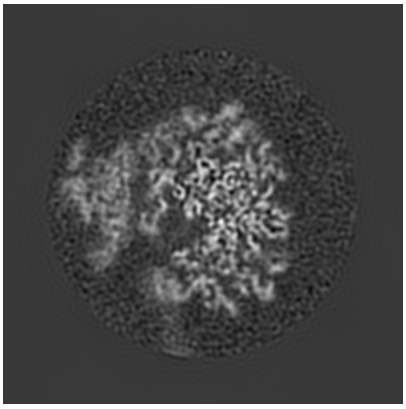


Z

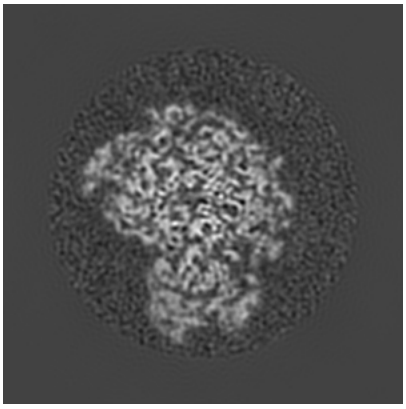
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

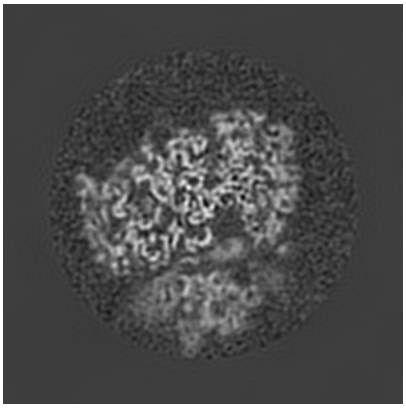
6.2.1 Primary map



X Index: 210



Y Index: 210

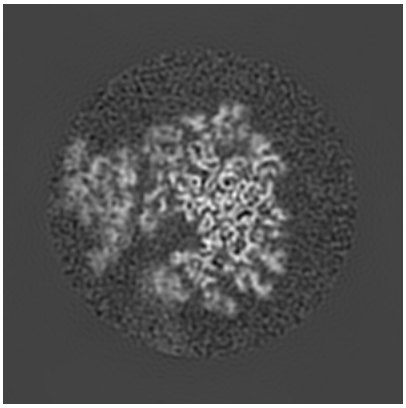


Z Index: 210

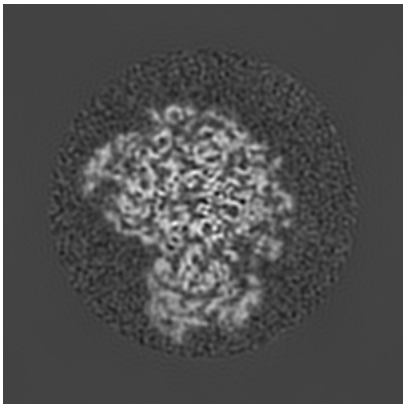
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

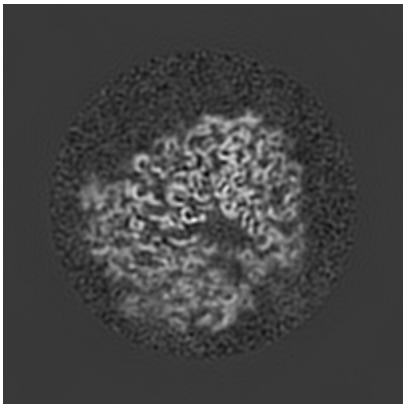
6.3.1 Primary map



X Index: 206



Y Index: 209

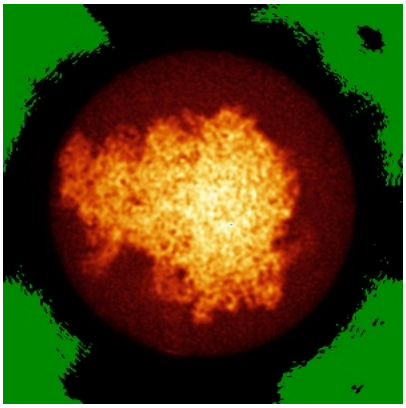


Z Index: 199

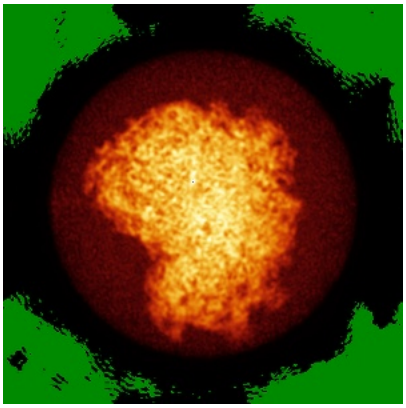
The images above show the largest variance slices of the map in three orthogonal directions.

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

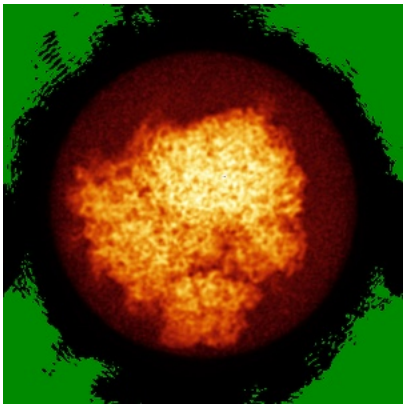
6.4.1 Primary map



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.

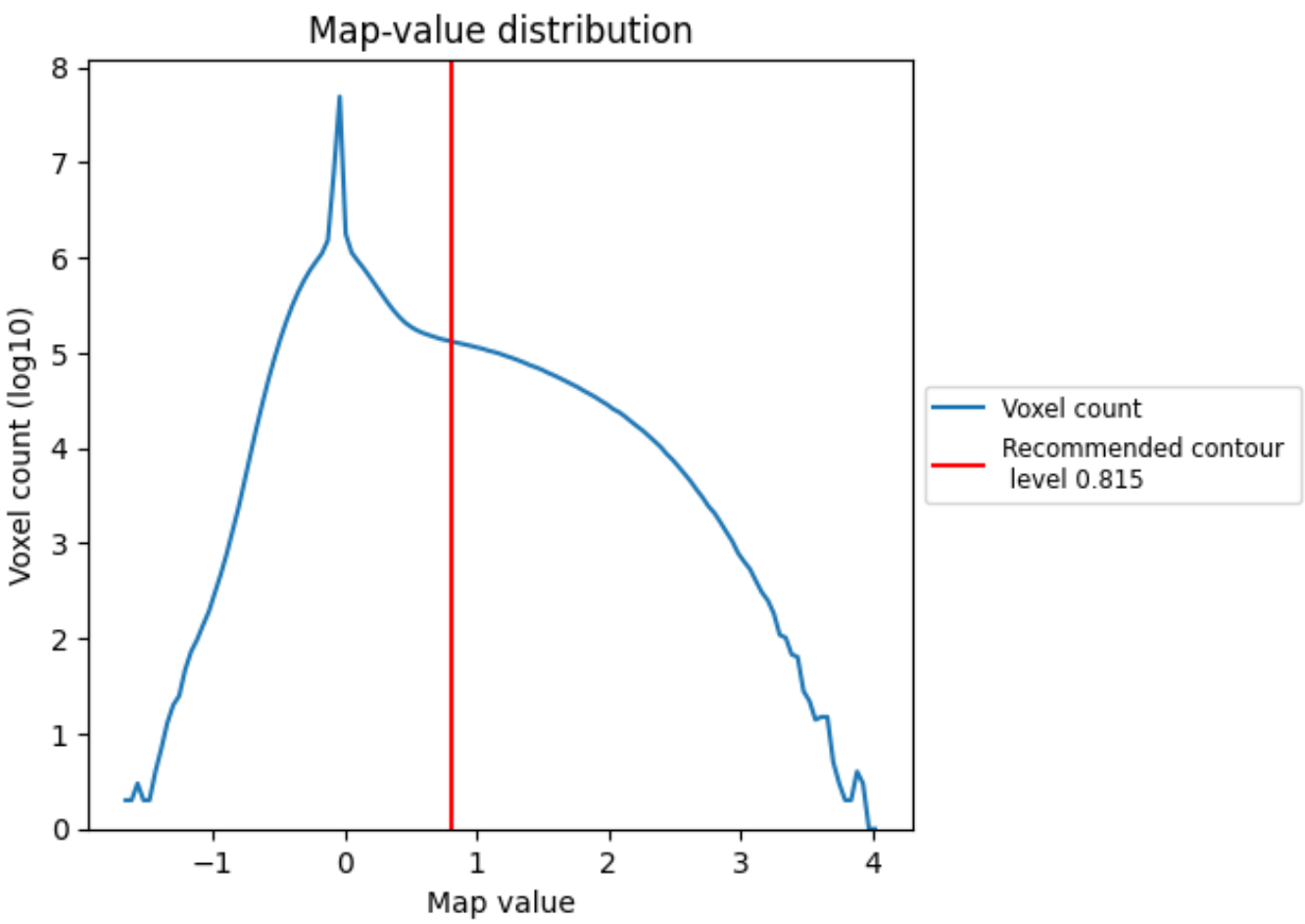
6.6 Mask visualisation (i)

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

7 Map analysis (i)

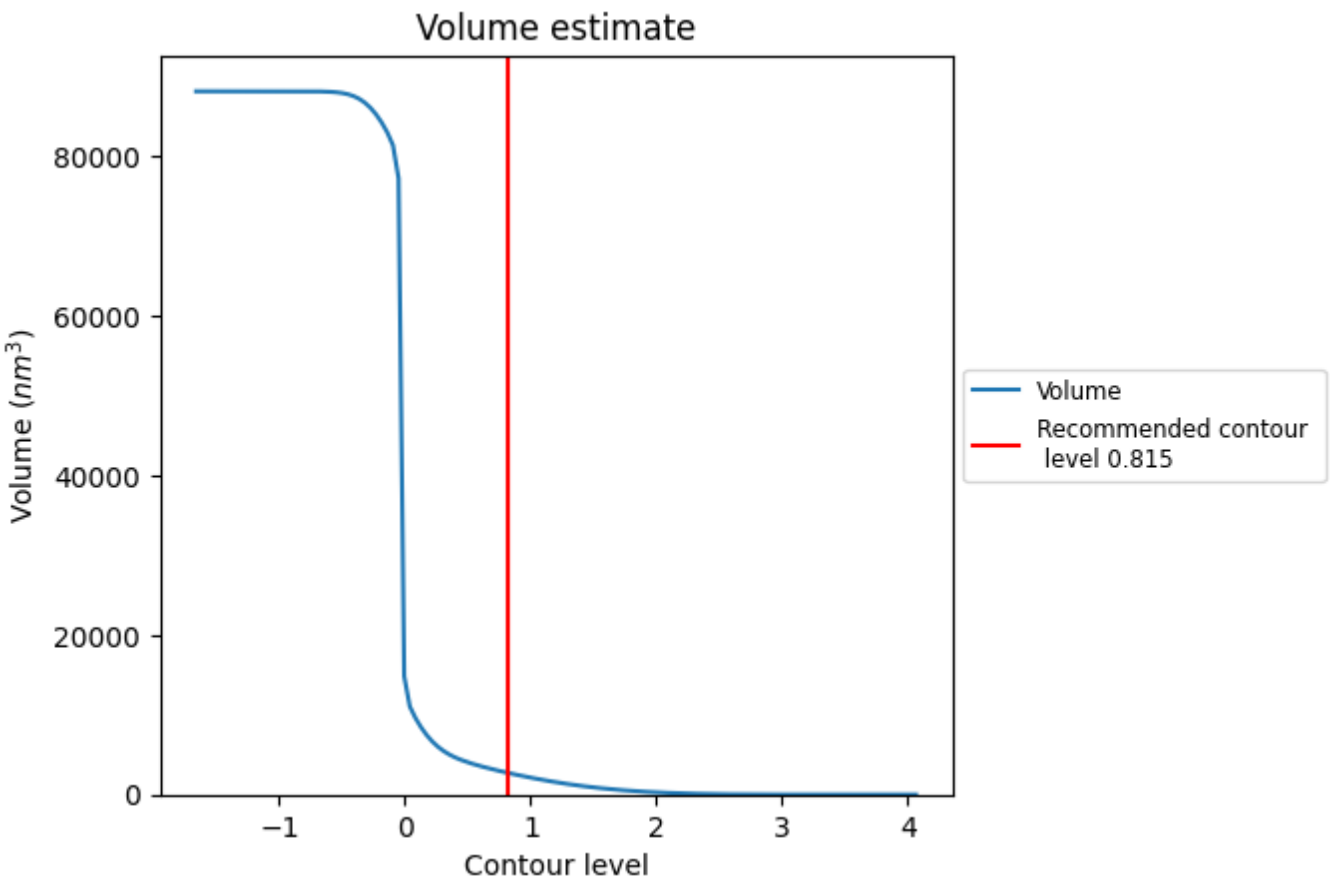
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

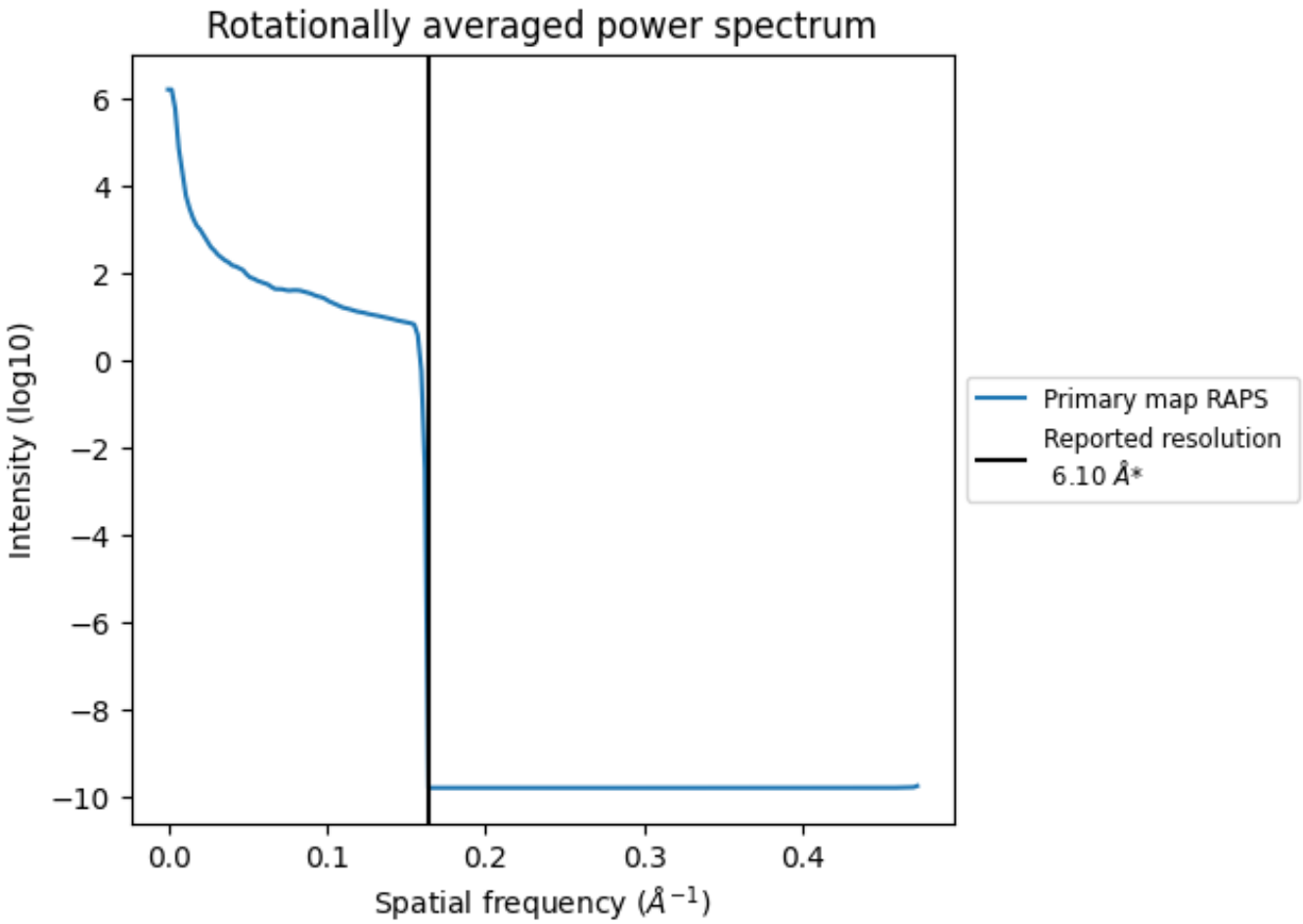
7.2 Volume estimate (i)



The volume at the recommended contour level is 2733 nm^3; this corresponds to an approximate mass of 2468 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}

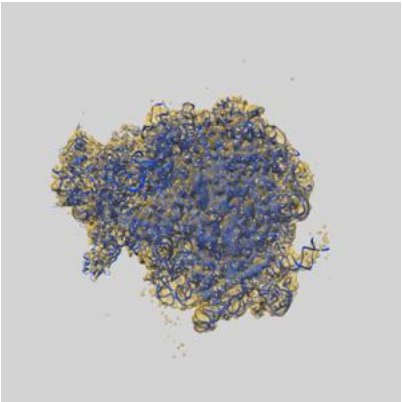
8 Fourier-Shell correlation (i)

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

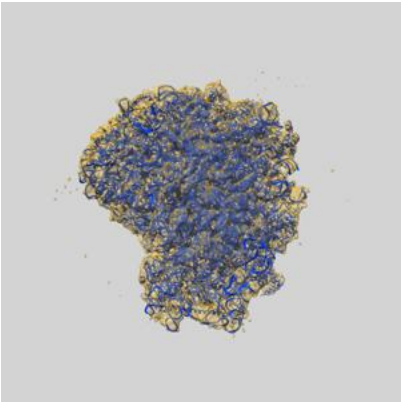
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-5943 and PDB model 3J6Y. Per-residue inclusion information can be found in section 3 on page 18.

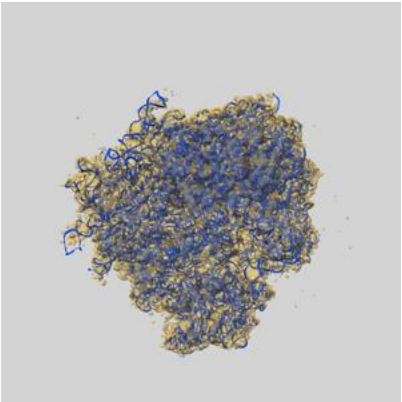
9.1 Map-model overlay (i)



X



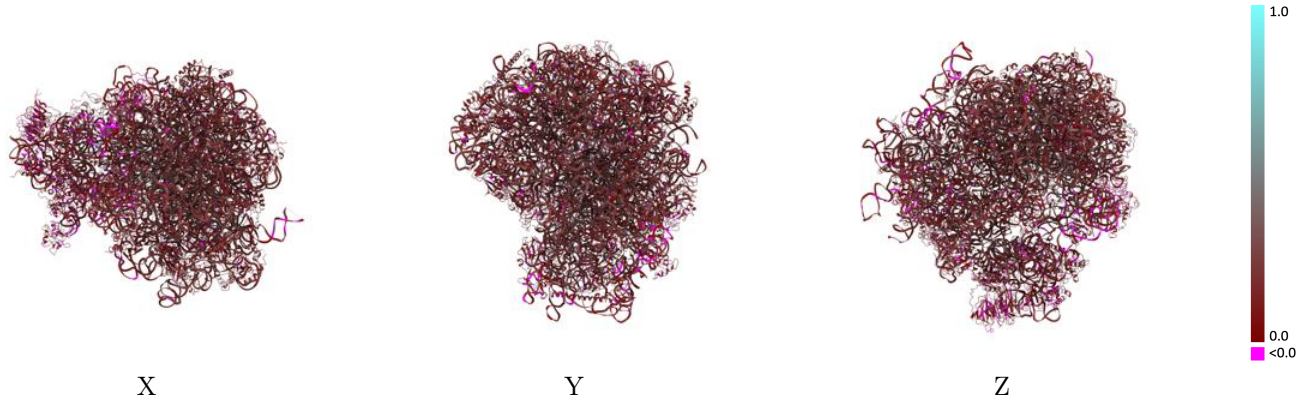
Y



Z

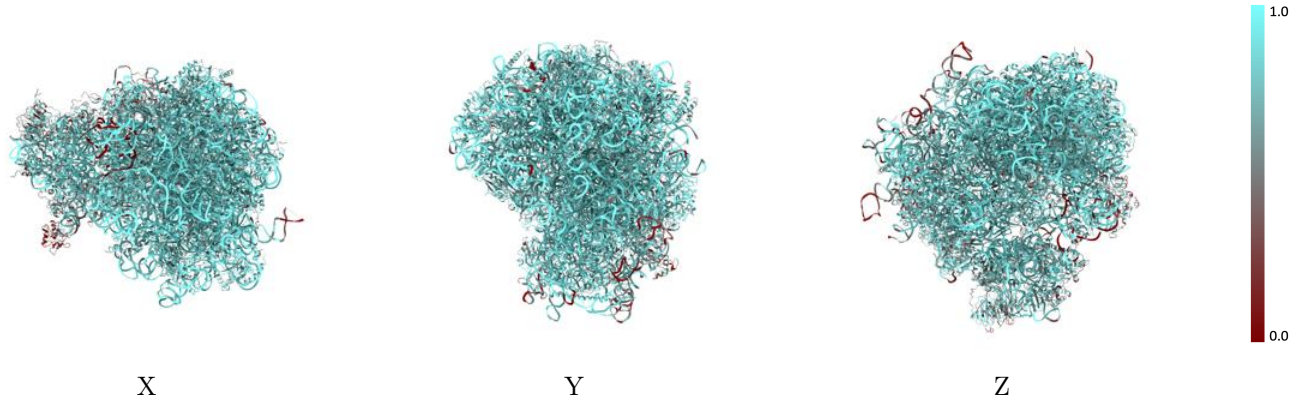
The images above show the 3D surface view of the map at the recommended contour level 0.815 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



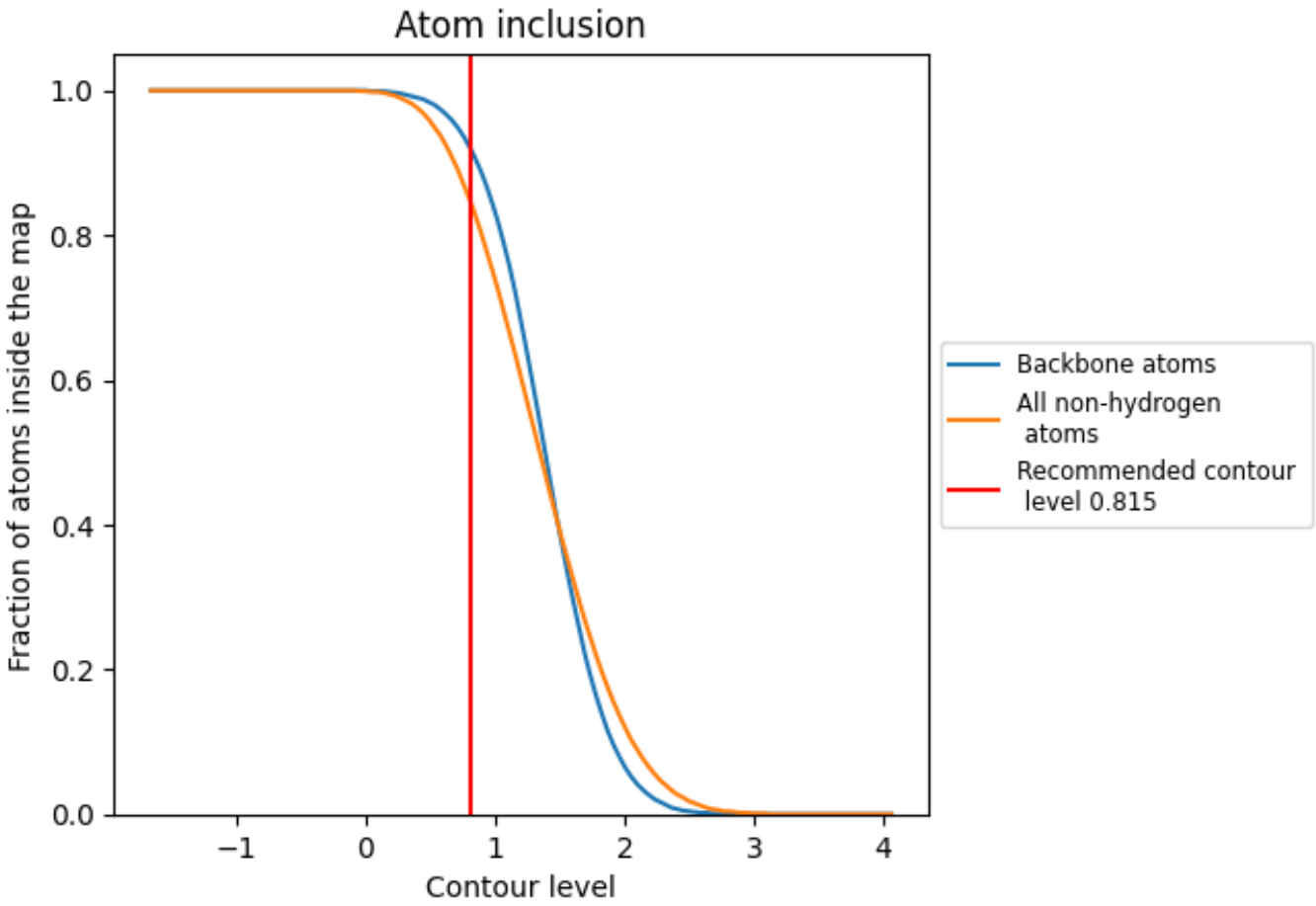
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



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

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	0.8440	0.2020
10	0.6900	0.1580
11	0.7270	0.1970
12	0.1660	0.1130
13	0.6980	0.1670
14	0.7520	0.1680
15	0.5220	0.1310
16	0.6880	0.1380
17	0.5910	0.1590
18	0.6440	0.1380
19	0.6520	0.1110
1S	0.9160	0.2110
20	0.6120	0.1440
21	0.7070	0.1910
22	0.7540	0.1790
23	0.7750	0.1890
24	0.6710	0.1500
25	0.6560	0.1670
26	0.7380	0.1850
27	0.6730	0.1710
28	0.6510	0.1470
29	0.6990	0.1240
2S	0.9440	0.2330
30	0.7450	0.2020
31	0.2810	0.1520
50	0.7770	0.1990
51	0.7460	0.1640
53	0.7630	0.1880
54	0.7540	0.1740
55	0.7670	0.1580
56	0.7850	0.1730
57	0.7690	0.1840
58	0.7760	0.1800
59	0.7490	0.1840
5S	0.9710	0.2270

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Chain	Atom inclusion	Q-score
60	0.7610	0.1720
61	0.7940	0.1990
62	0.7420	0.1890
63	0.7860	0.1940
64	0.8010	0.1850
65	0.7740	0.1930
66	0.7770	0.1750
67	0.7500	0.1800
68	0.7790	0.1840
69	0.7770	0.2060
70	0.7520	0.1950
71	0.7800	0.1930
72	0.8040	0.1970
73	0.7930	0.1680
74	0.7720	0.1700
75	0.7610	0.1750
76	0.7450	0.1760
77	0.8160	0.1630
78	0.7120	0.1760
79	0.7740	0.1920
80	0.7330	0.1660
81	0.0470	0.0400
82	0.7720	0.1930
83	0.8100	0.1920
8S	0.9710	0.2410
IR	0.6460	0.1160
L1	0.4280	0.0990
L2	0.8020	0.1960
L3	0.7860	0.1840
L4	0.8050	0.1940
L5	0.7070	0.1560
L6	0.7820	0.1880
L7	0.7840	0.1790
L8	0.7500	0.1840
L9	0.7540	0.1760
RA	0.6500	0.1330
S0	0.6920	0.1850
S1	0.6750	0.1730
S2	0.7680	0.1920
S3	0.7040	0.1830
S4	0.7660	0.1680
S5	0.6510	0.1450

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Chain	Atom inclusion	Q-score
S6	0.7290	0.1530
S7	0.5870	0.1690
S8	0.7820	0.1770
S9	0.7450	0.1600