



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 07:40 PM 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 : 3U5C, 3U5B, 3U5E, 3U5D

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 ⓘ 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 ⓘ](#)) were used in the production of this report:

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

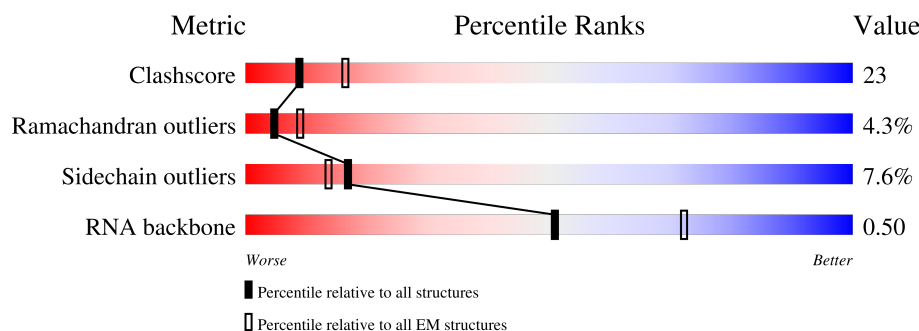
1 Overall quality at a glance

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 $\leq 5\%$. 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	
2	8S	158	
3	5S	121	
4	L1	217	
5	L2	254	
6	L3	387	
7	L4	362	




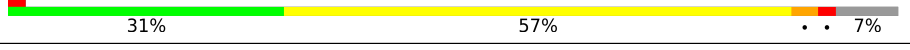
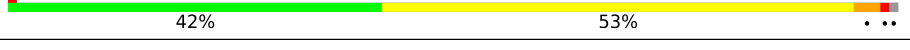


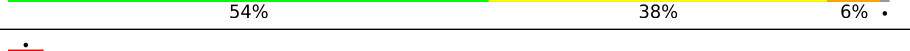
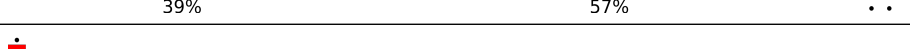
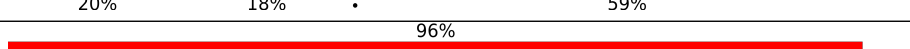

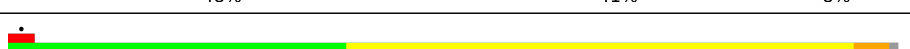
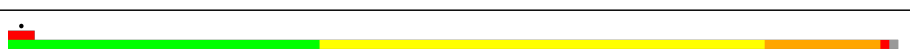
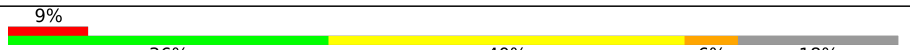
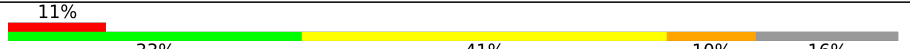
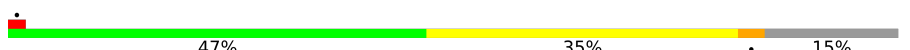




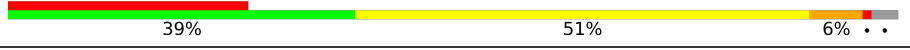

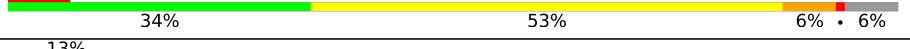


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Mol	Chain	Length	Quality of chain
8	L5	297	
9	L6	176	
10	L7	244	
11	L8	256	
12	L9	191	
13	50	221	
14	51	174	
15	53	199	
16	54	138	
17	55	204	
18	56	199	
19	57	184	
20	58	186	
21	59	189	
22	60	172	
23	61	160	
24	62	121	
25	63	137	
26	64	155	
27	65	142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

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

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Mol	Chain	Length	Quality of chain
58	11	156	
59	12	143	
60	13	151	
61	14	137	
62	15	142	
63	16	143	
64	17	136	
65	18	146	
66	19	144	
67	20	121	
68	21	87	
69	22	130	
70	23	145	
71	24	135	
72	25	108	
73	26	119	
74	27	82	
75	28	67	
76	29	56	
77	30	63	
78	31	152	
79	RA	319	
80	IR	201	

2 Entry composition

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
1	2S	3308	Total	C	N	O	P	0	0
			70742	31596	12731	23107	3308		

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

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

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

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

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

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

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

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

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

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

- 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
			1446	930	267	245	4	0

- 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
			1277	805	246	222	4	0

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

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

- 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
			1004	628	189	180	7	0

- 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
			509	328	100	80	1	0

- 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
			969	623	170	174	2	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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		
			1106	708	203	195	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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.

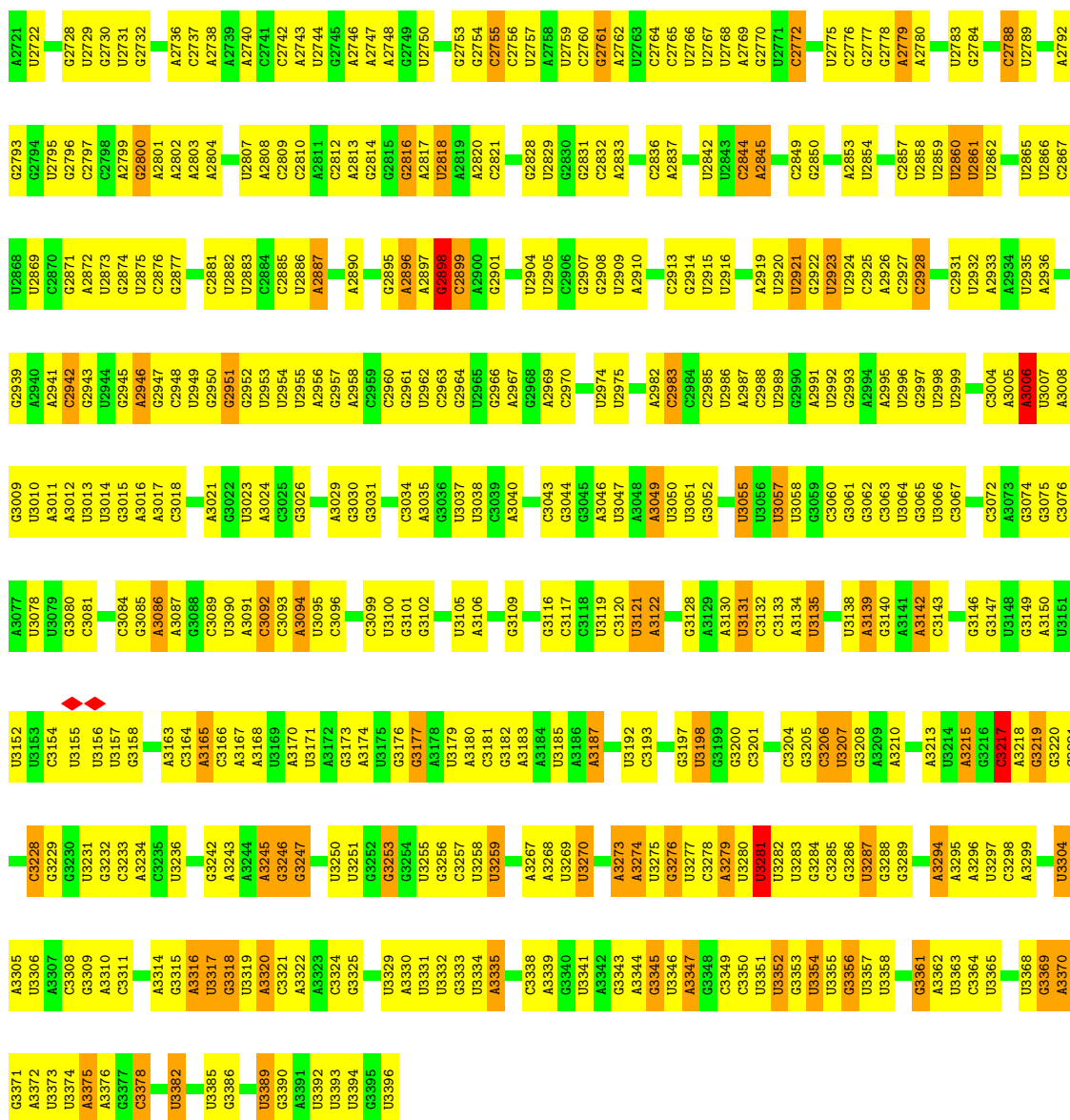
Mol	Chain	Residues	Atoms					AltConf	Trace
79	RA	318	Total	C	N	O	S	0	0
			2445	1546	419	472	8		

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

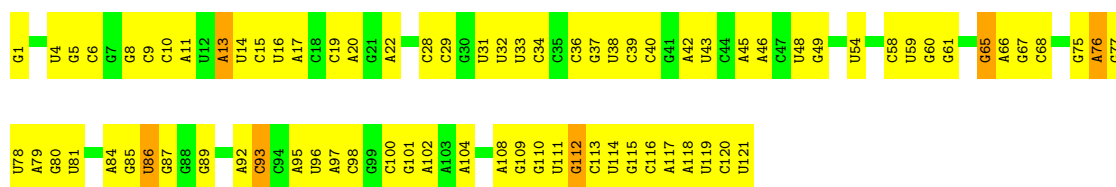
Mol	Chain	Residues	Atoms		AltConf	Trace
80	IR	198	Total	P	0	198
			198	198		

A1637	G1665	G1492	C1416	A1350	U1288	A1204	G1132	A1057	U985	U922	U850	G785	U713
A1641	A1566	G1493	G1417	U1351	G1289	A1205	A1133	A1064	U986	C923	C851	A786	G714
A1642	U1567	U1494	A1418	A1352	A1290	G1206	G1134	A1065	U987	G924	U852	G787	A715
A1643	U1568	U1495	A1419	U1353	C1292	G1207	A1135	U1070	U988	A926	G853	G788	
G1644	U1569	G1496	G1420	G1354	U1293	U1210	A1136	U1071	U990	C927	U855	A789	G718
U1645	G1497	A1355	G1421	A1355	A1294	U1211	C1137	U1072	G991	C928	G856	U790	U719
U1646	A1498	U1356	G1422	G1357	G1295	A1212	U1138	G1073	A992	A929	G857	A791	A720
G1647	C1499	G1358	C1423	G1357	C1296	G1213	G1139	U1074	G993	U930	A888	G792	G721
A1648	G1500	C1359	U1427	C1359	C1297	U1214	G1140	G1075	G994	U931	G859	G722	G722
U1649	U1501	C1360	U1430	C1360	C1298	U1215	C1141	U1076	G995	U932	G860	U723	U723
G1650	U1504	U1431	U1431	C1364	U1299	C1216	A1143	A1075	A996	U932	C861	U796	U724
A1505	C1505	G1432	C1432	U1365	G1300	A1217	U1144	A1079	A997	U935	U862	U797	G725
A1506	A1506	G1433	G1433	A1365	A1301	U1220	G1147	A1080	C1000	A936	U862	U797	G726
G1507	G1507	A1434	G1434	A1366	A1302	U1221	U1147	U1081	C1001	A937	C873	G727	G727
C1508	C1508	G1367	G1434	A1367	A1303	A1221	U1150	U1082	G1002	G938	U874	G728	G728
A1509	A1509	U1368	G1437	U1368	A1304	G1222	A1150	G1083	G1003	U939	G875	G729	C730
G1510	G1510	A1369	C1437	A1369	U1305	A1223	U1151	A1084	A1003	G940		C803	
U1511	U1511	U1370	U1438	G1370	G1306	C1224	G1152	A1085	U1004	G941	U879	G805	A736
U1512	U1512	G1371	U1439	G1371	G1307	A1225	A1153	C1086	U1008	U942	C880	A806	G737
G1513	G1513	C1372	G1440	C1372	A1308	G1226	A1154	G1087	U1009	U943	C881	A738	A738
U1517	U1517	G1376	U1441	G1376	U1309	C1227	A1158	U1088	A882	U944	A882	A808	G739
G1520	G1520	G1377	U1442	G1377	G1310	U1234	A1159	G1089	G1010	U946	A883	G809	
G1521	G1521	U1378	G1443	U1378	G1311	U1235	A1159	A1093	A1011	G947	A884	A810	C743
U1522	U1522	G1379	G1444	G1379	C1312	G1236	U1167	U1094	G1012	C948	U885	U811	A744
U1523	U1523	A1381	U1445	G1380	G1313	G1237	U1168	U1095	G1013	C948	C886	G812	C745
U1595	U1595	G1382	G1446	G1381	U1314	G1238	A1169	U1096	U1014	C949	G887	G813	A746
G1668	G1668	U1383	U1447	A1381	U1315	C1239	C1170	U1097	U1015	G950	A888	G815	U747
U1526	U1526	G1384	U1448	G1382	A1316	C1240	G1171	A1098	C1016	G953	U889	U814	U748
C1527	C1527	U1384	A1449	U1383	A1317	U1241	G1172	A1099	C1017	U954	G891	A816	C749
C1532	C1532	A1385	U1452	C1385	A1318	U1242	U1173	A1100	G1018	U955	U892	C818	C753
A1534	A1534	U1387	A1456	U1387	G1321	G1243	G1174	G1101	U1019	U956	U893	U819	G754
G1536	G1536	U1388	U1457	U1388	U1322	G1244	C1175	A1102	G1020	C957	G894	A820	A755
A1537	A1537	C1391	U1460	C1391	U1324	A1245	G1177	A1103	U1021	C958	A895	U821	
G1538	G1538	G1392	A1461	G1392	U1325	G1246	G1178	G1104	G1024	C959	A896	G823	C758
A1545	A1545	U1393	A1465	U1393	A1326	U1250	A1179	A1105	A1027	U960	U897	C824	G760
U1546	U1546	G1394	G1466	G1394	C1327	A1251	A1180	C1107	U1028	A962	U899	U825	
C1548	C1548	A1400	G1475	A1395	C1328	G1251	U1181	U1108	G1029	G963	U900	G826	G763
C1550	C1550	G1401	G1476	G1396	U1329	C1254	U1182	U1109	U1033	G964	G901	A827	U764
U1553	U1553	C1402	U1477	C1397	U1330	G1254	C1183	U1110	U1034	A965	G902	A828	C765
U1554	U1554	G1403	U1478	C1397	A1331	C1254	G1186	U1111	U1035	U966	U903	U829	U766
U1555	U1555	U1404	A1481	U1398	G1332	G1257	C1187	G1112	A1036	A967	U905	A830	U767
C1556	C1556	U1405	G1482	A1399	U1333	U1258	C1187	G1113	U1039	A970	A906	G831	C768
A1557	A1557	A1406	G1483	G1400	C1334	A1259	U1191	U1114	G1036	G971	G907	G835	G770
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G1561	G1561	G1412	G1487	G1409	G1338	G1264	A1193	C1118	A1046	C975	G912	C839	U776
C1562	C1562	G1413	G1488	G1412	C1339	U1265	G1194	C1119	A1047	U976	G913	C840	U777
U1564	U1564	U1347	A1489	G1413	G1340	U1266	A1195	U1120	A841	C977	A914	A841	U777
		G1414	G1490	U1348	U1341	U1267	C1196	U1121	C1049	G978	A915	G842	U778
		U1415	G1491	G1414	C1342	U1269	C1198	U1122	U1050	U979	G916	G843	G779
					G1345	C1272	C1199	G1126	U1051	A980	A917	G844	A780
					G1346	G1281	A1200	G1127	U1052	U981	C918	G845	G781
					U1347	G1281	C1201	U1127	A1053	C982	U919	U782	U782
					G1349	A1286	A1202	A1130	A1054	A983	A848	A783	A783
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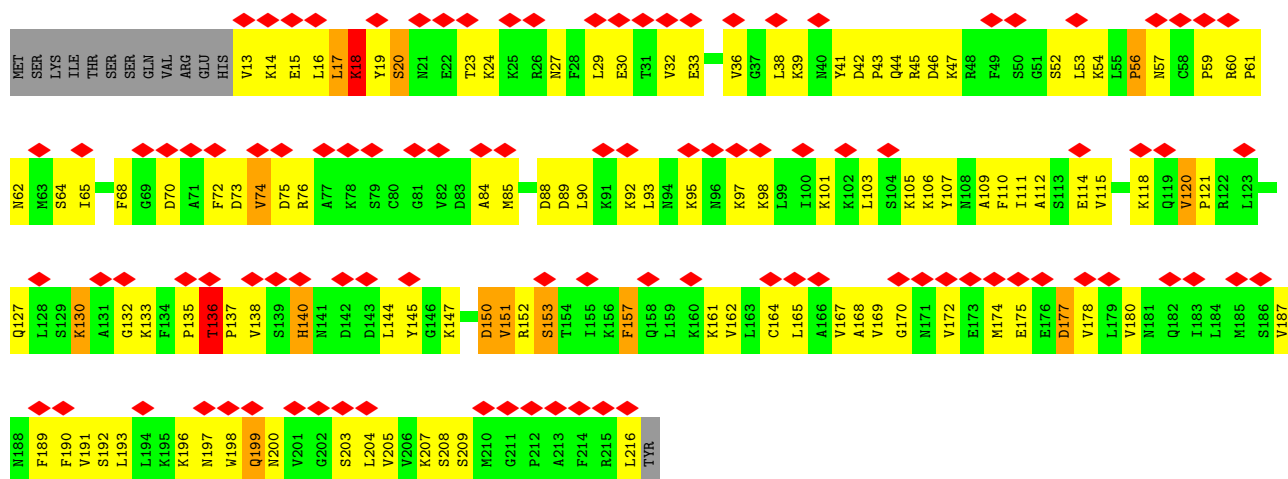


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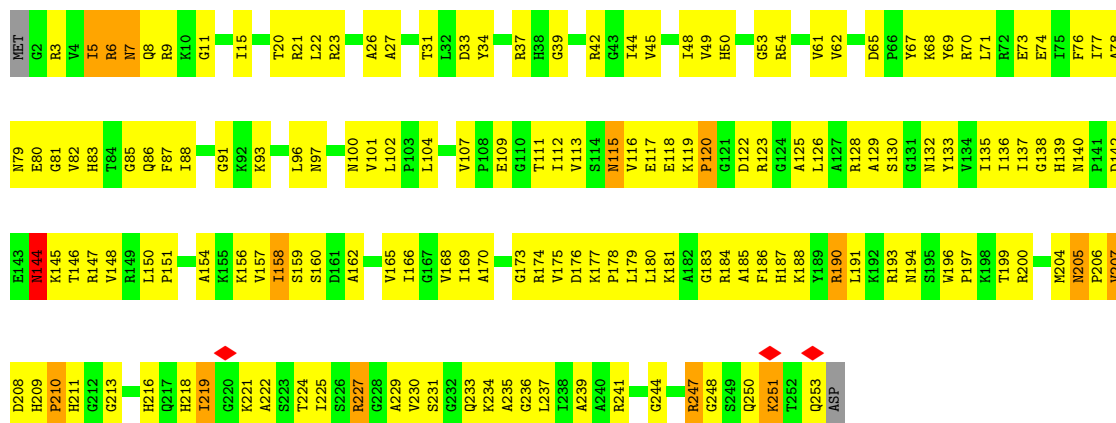
• Molecule 4: 60S ribosomal protein L1

Chain L1: 



• Molecule 5: 60S ribosomal protein L2

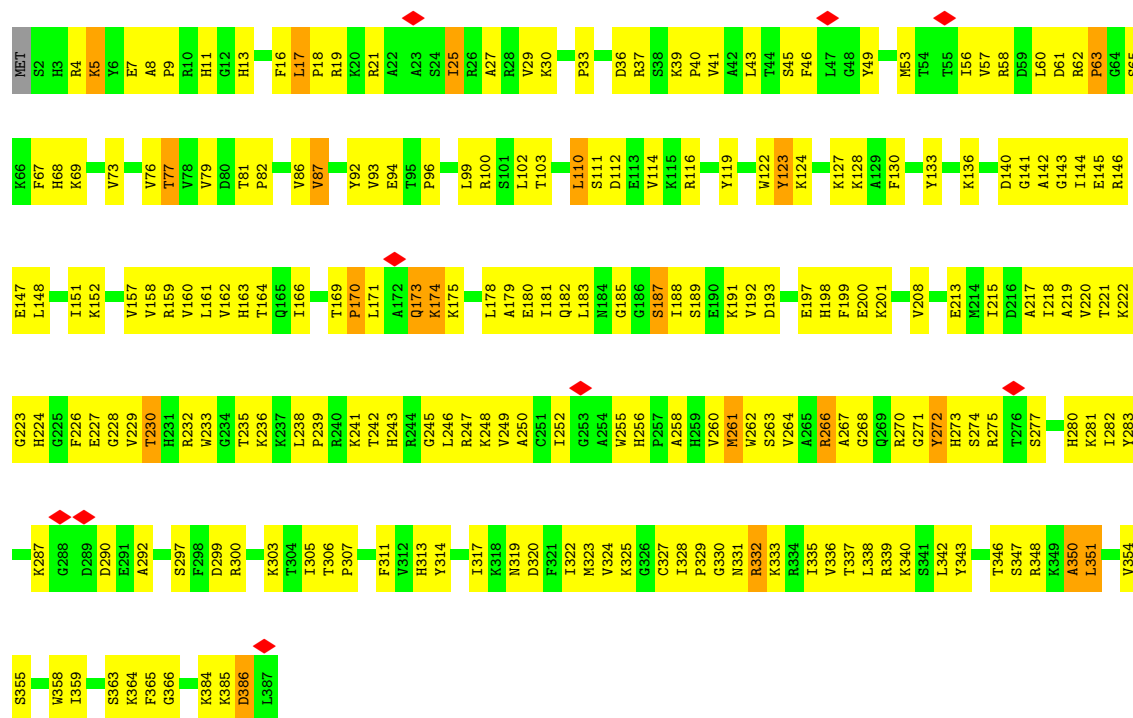
Chain L2: 



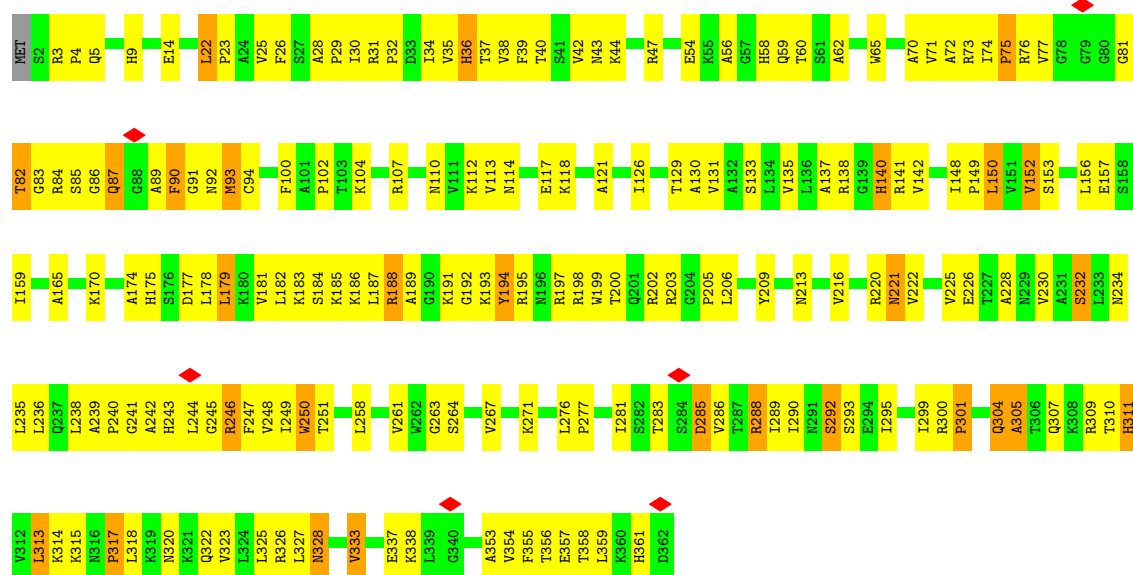
• Molecule 6: 60S ribosomal protein L3

Chain L3: 



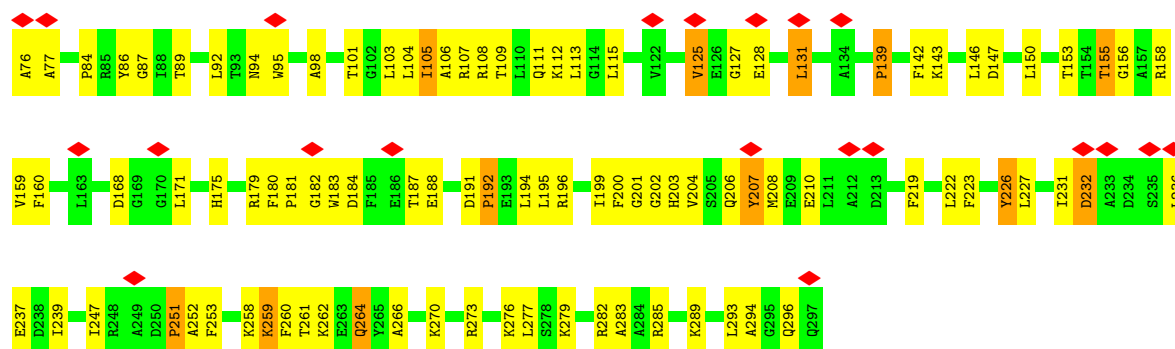


• Molecule 7: 60S ribosomal protein L4

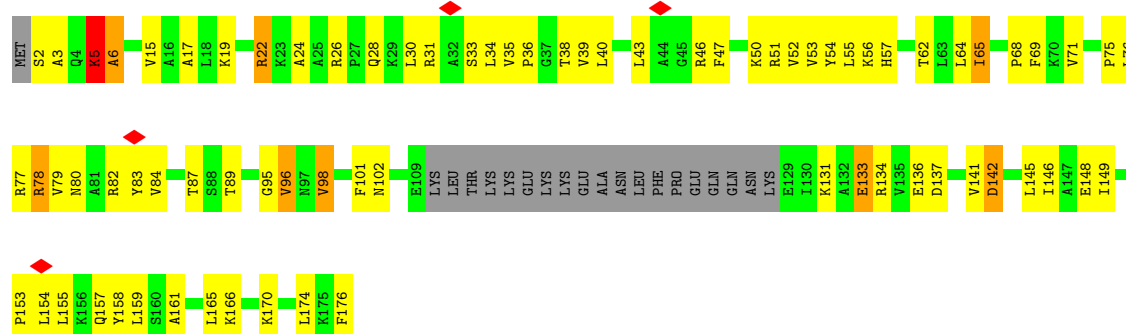


• Molecule 8: 60S ribosomal protein L5

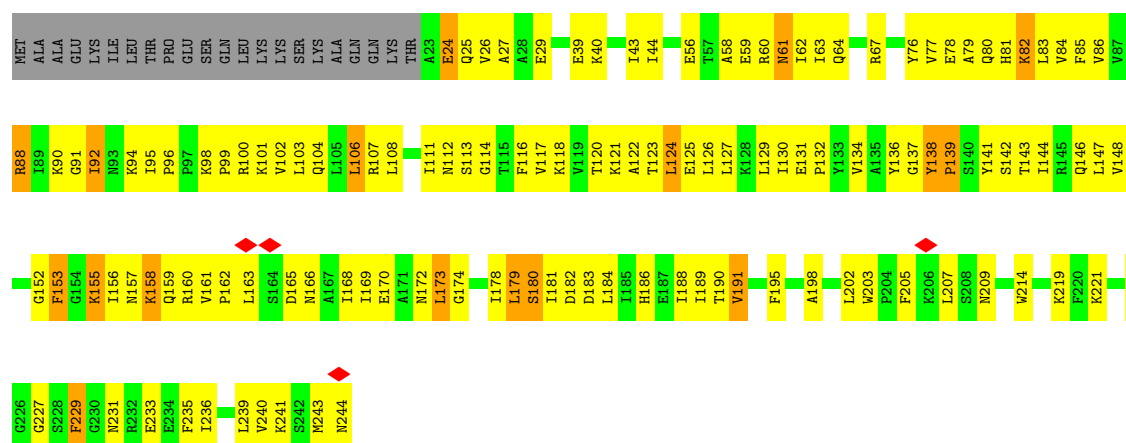




• Molecule 9: 60S ribosomal protein L6

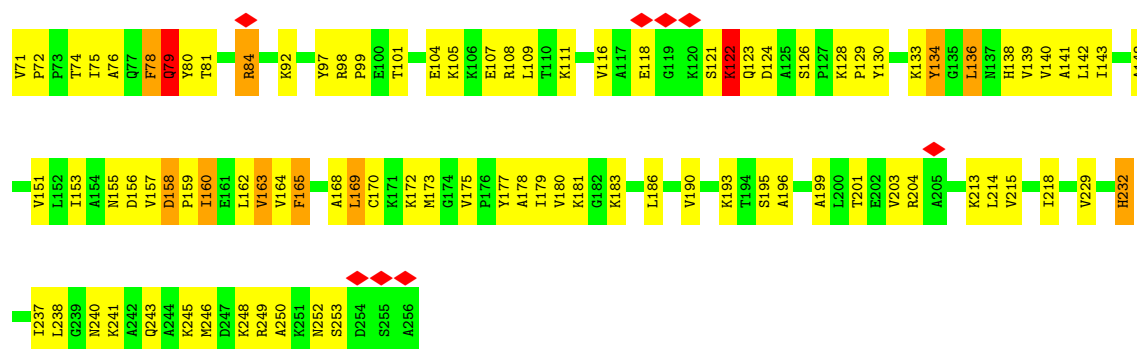


• Molecule 10: 60S ribosomal protein L7



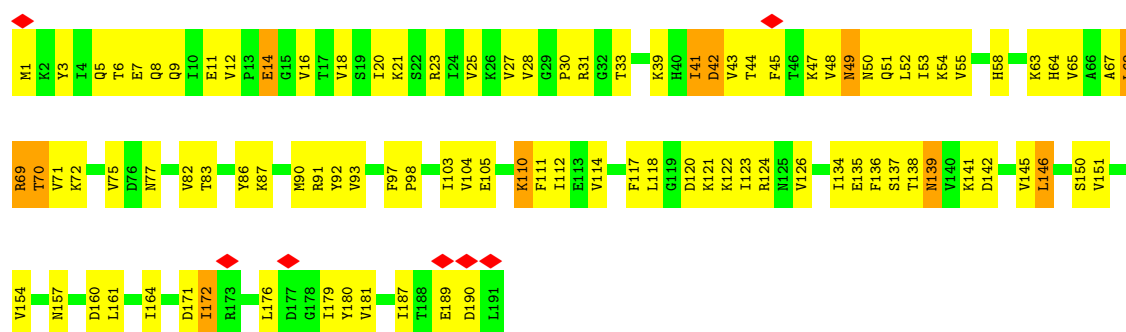
• Molecule 11: 60S ribosomal protein L8





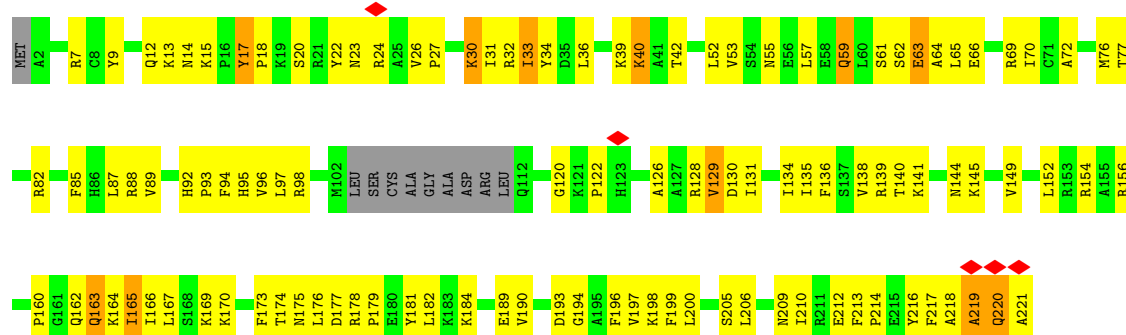
• Molecule 12: 60S ribosomal protein L9

Chain L9: 48% 46% 6%



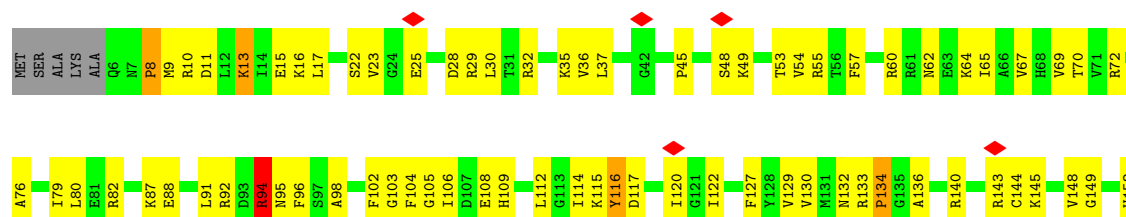
• Molecule 13: 60S ribosomal protein L10

Chain 50: 45% 46% 5% 5%



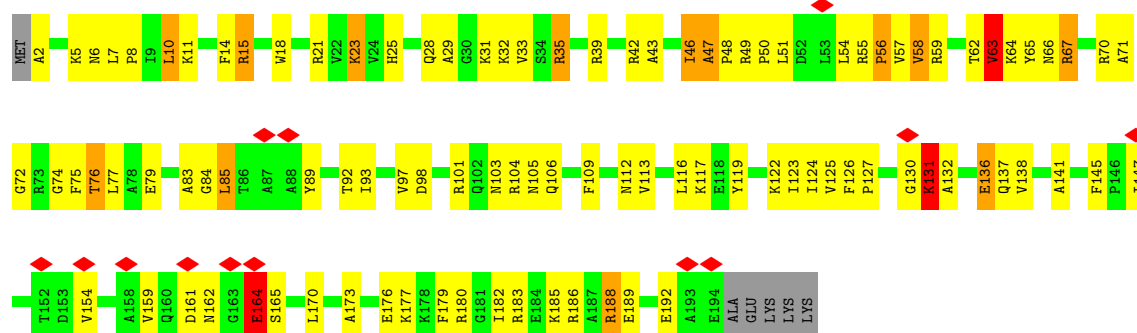
• Molecule 14: 60S ribosomal protein L11

Chain 51: 49% 44% 7%

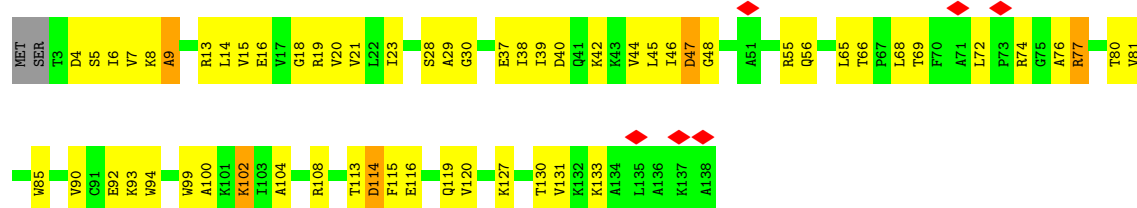




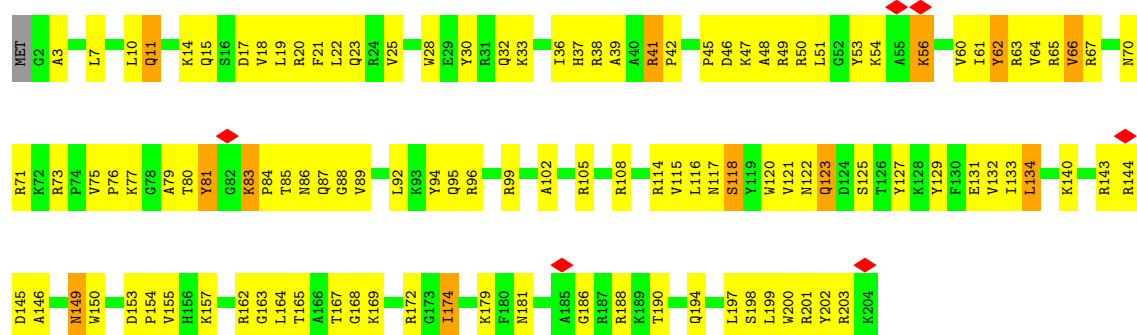
- Molecule 15: 60S ribosomal protein L13



- Molecule 16: 60S ribosomal protein L14

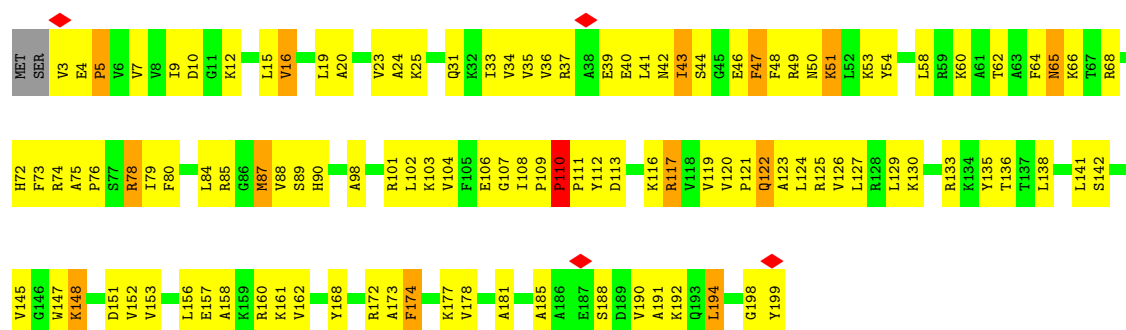


- Molecule 17: 60S ribosomal protein L15

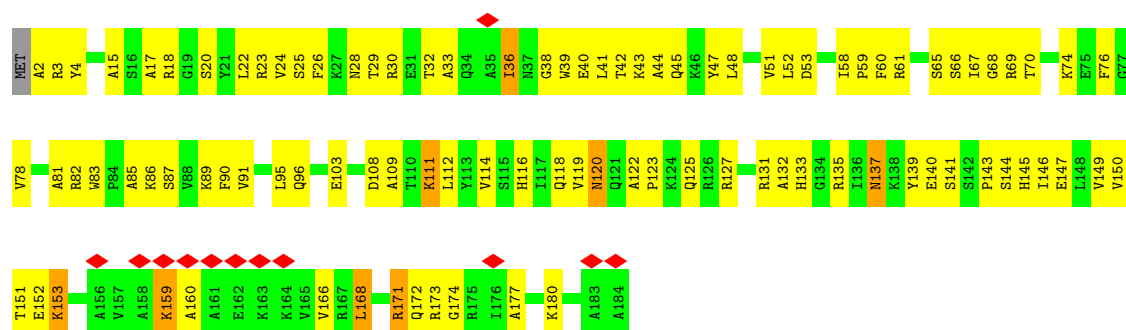


- Molecule 18: 60S ribosomal protein L16

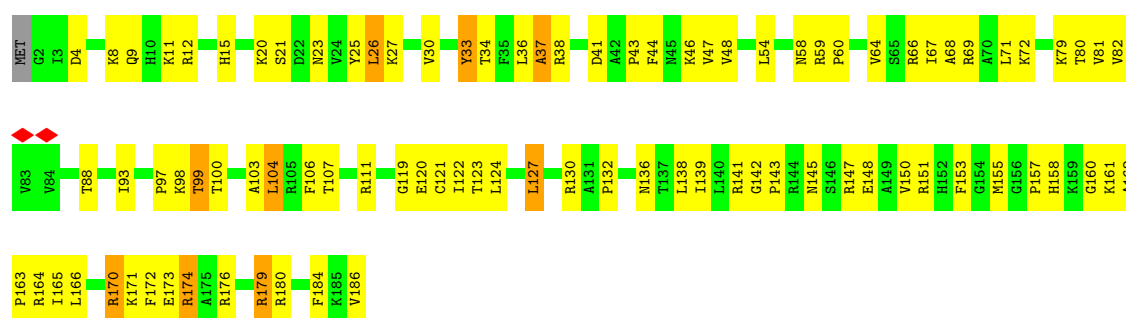




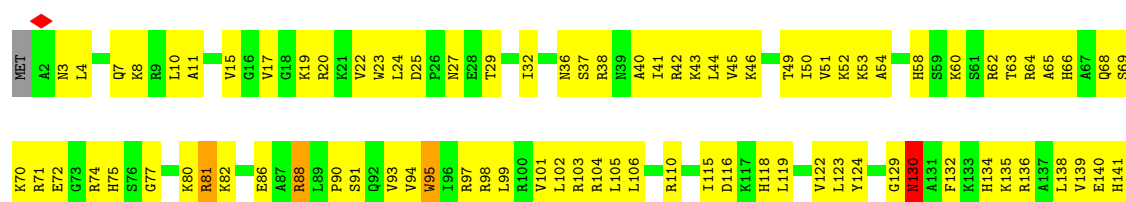
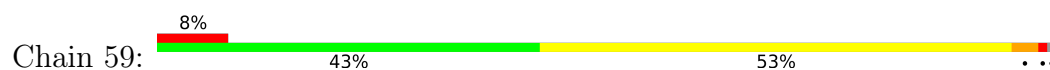
• Molecule 19: 60S ribosomal protein L17

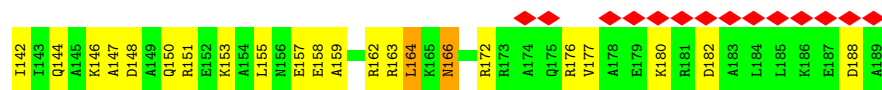


• Molecule 20: 60S ribosomal protein L18

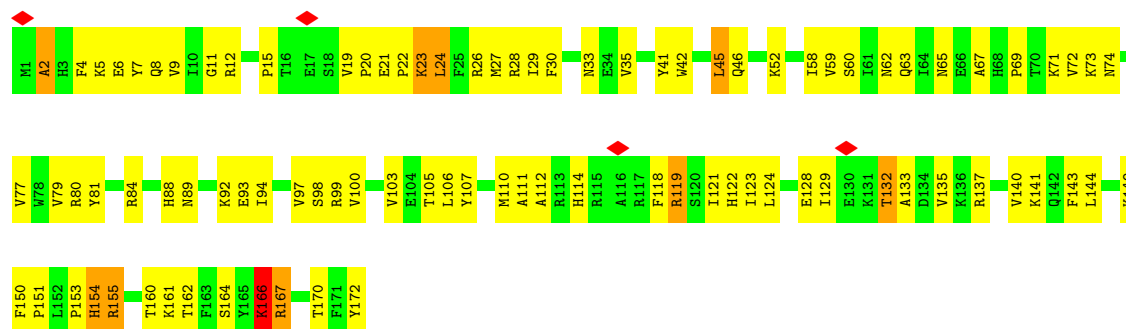


• Molecule 21: 60S ribosomal protein L19

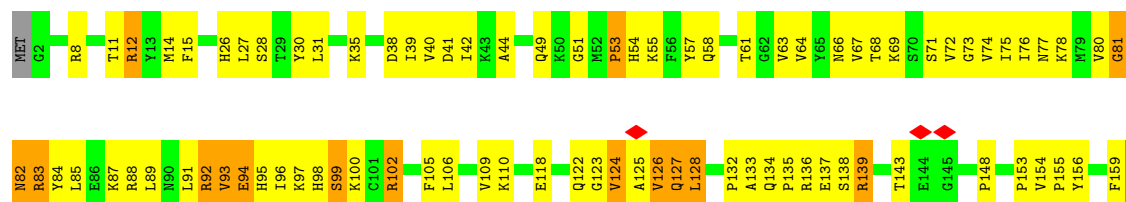




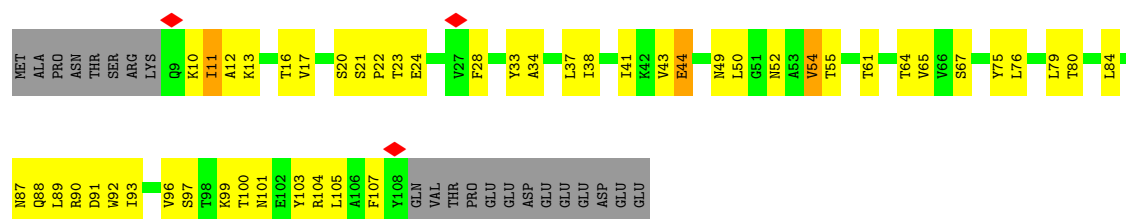
• Molecule 22: 60S ribosomal protein L20



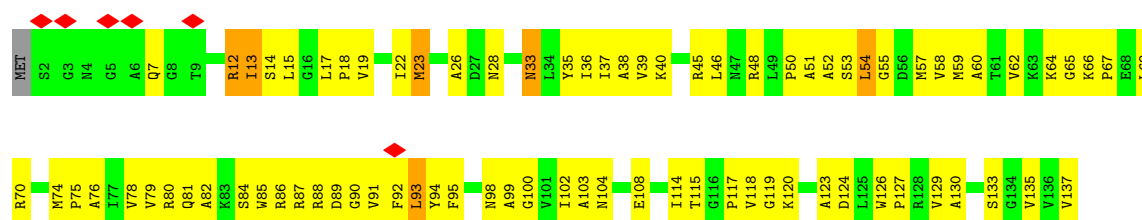
• Molecule 23: 60S ribosomal protein L21



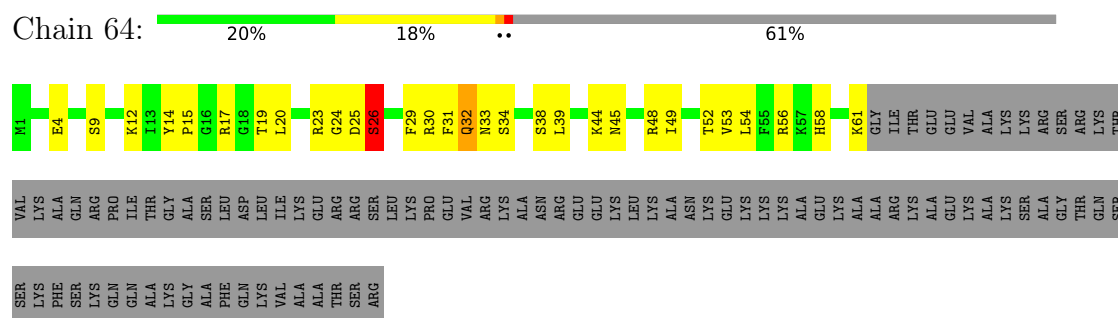
• Molecule 24: 60S ribosomal protein L22



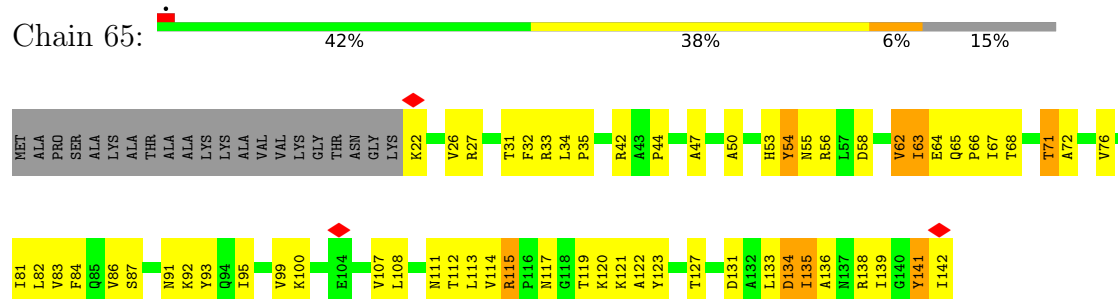
• Molecule 25: 60S ribosomal protein L23



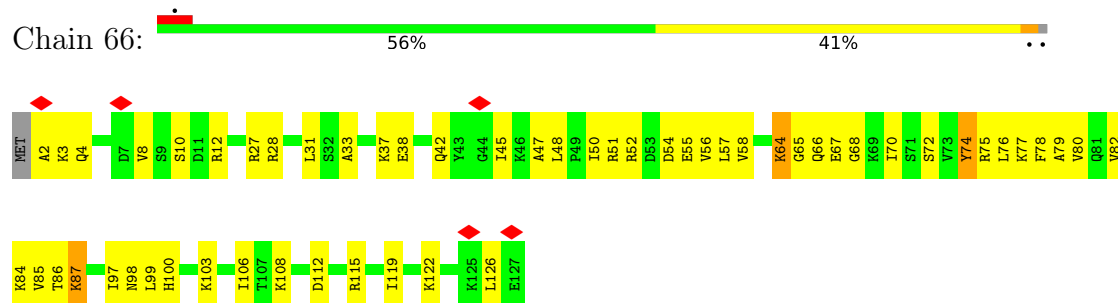
- Molecule 26: 60S ribosomal protein L24



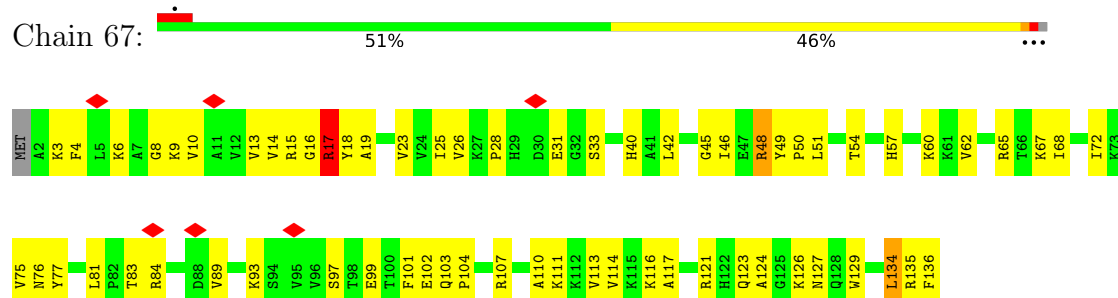
- Molecule 27: 60S ribosomal protein L25



- Molecule 28: 60S ribosomal protein L26

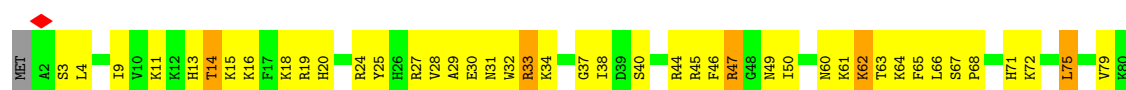


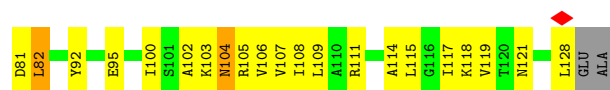
- Molecule 29: 60S ribosomal protein L27



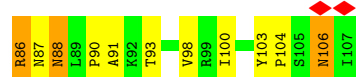
- Molecule 30: 60S ribosomal protein L28







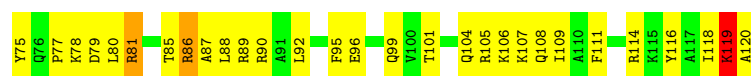
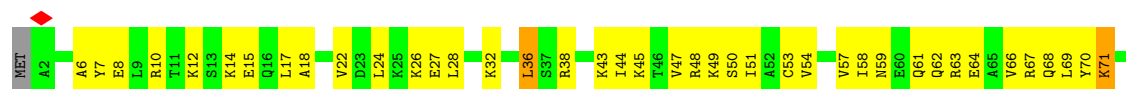
- Molecule 35: 60S ribosomal protein L33



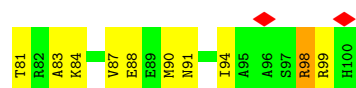
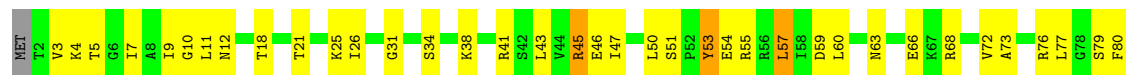
- Molecule 36: 60S ribosomal protein L34



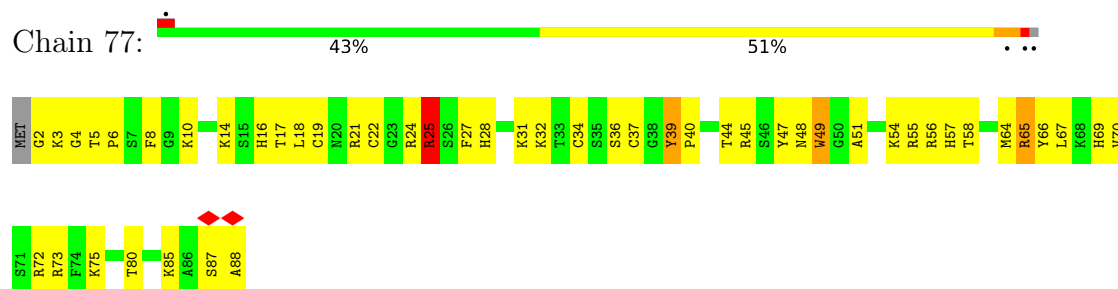
- Molecule 37: 60S ribosomal protein L35



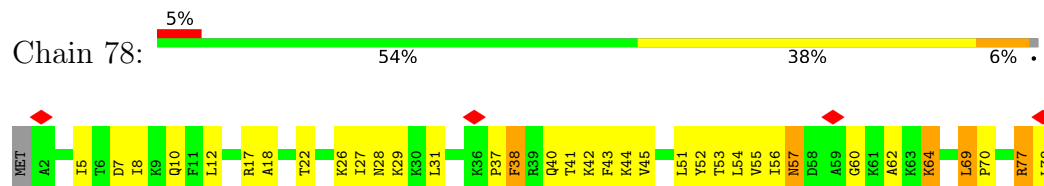
- Molecule 38: 60S ribosomal protein L36



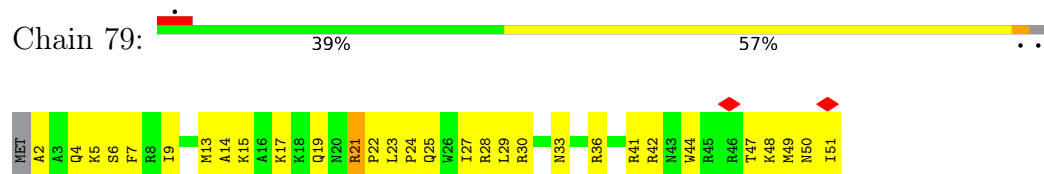
- Molecule 39: 60S ribosomal protein L37



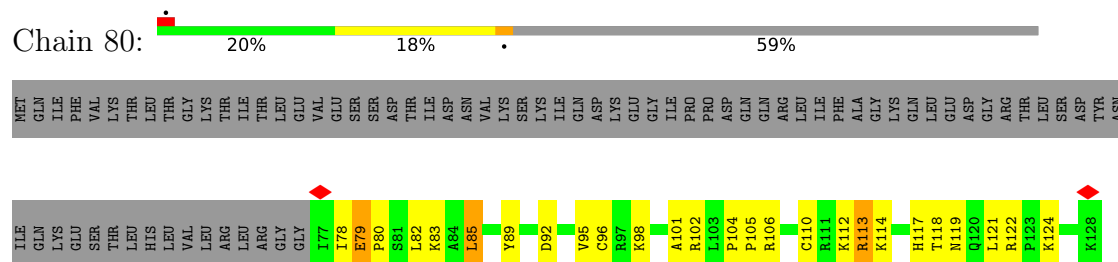
- Molecule 40: 60S ribosomal protein L38



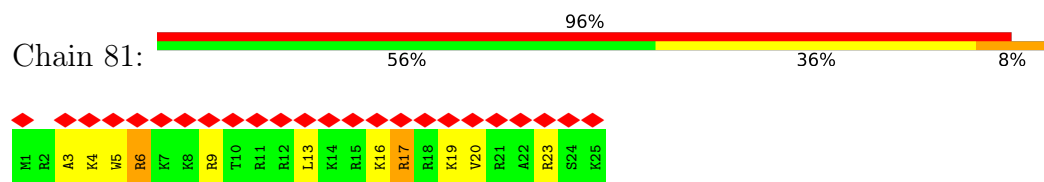
- Molecule 41: 60S ribosomal protein L39



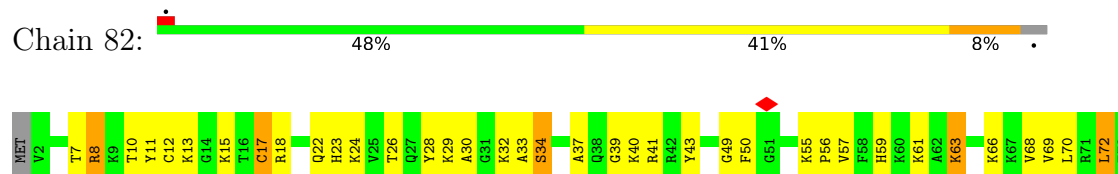
- Molecule 42: 60S ribosomal protein L40

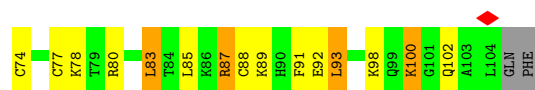


- Molecule 43: 60S ribosomal protein L41



- Molecule 44: 60S ribosomal protein L42

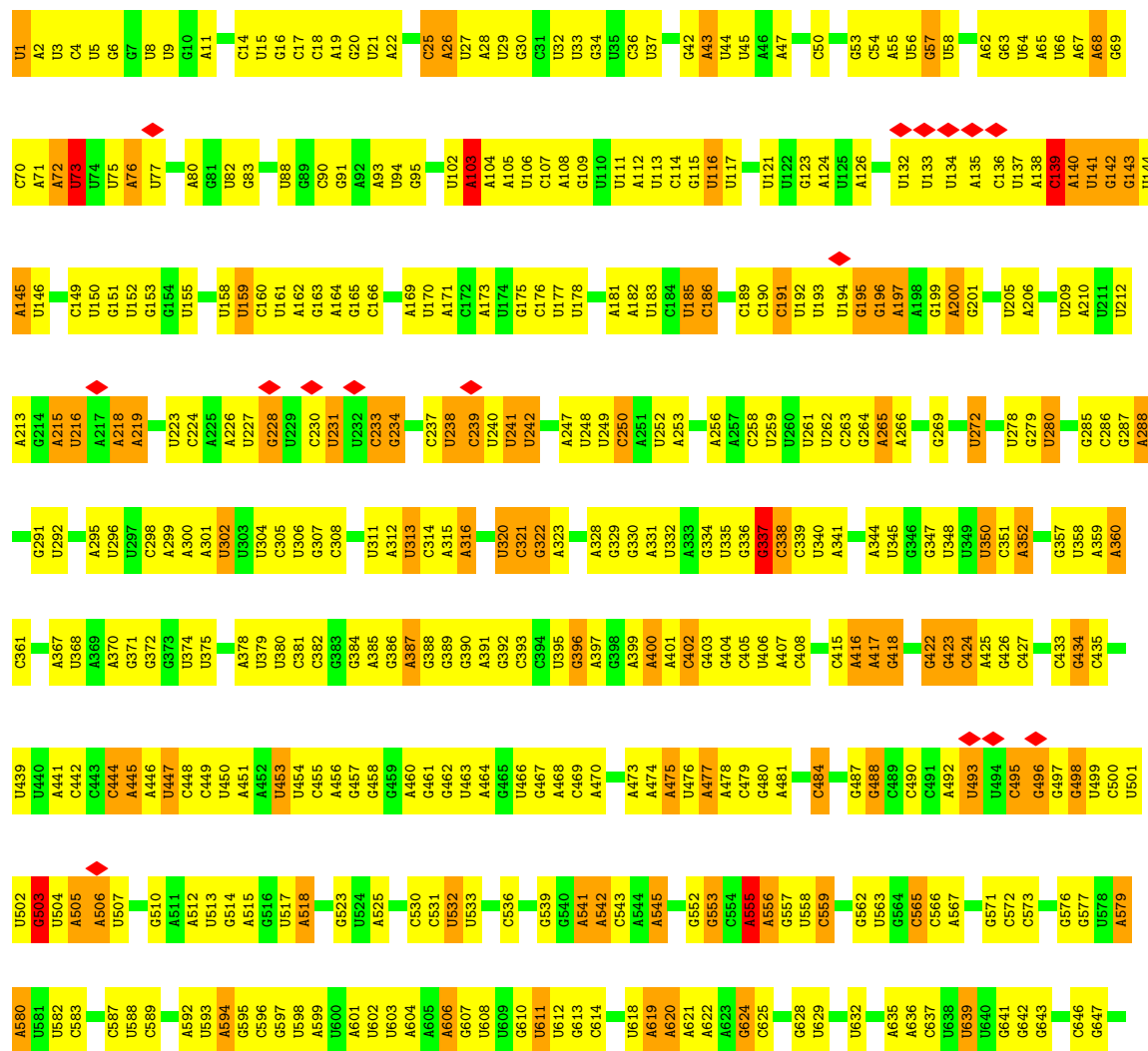


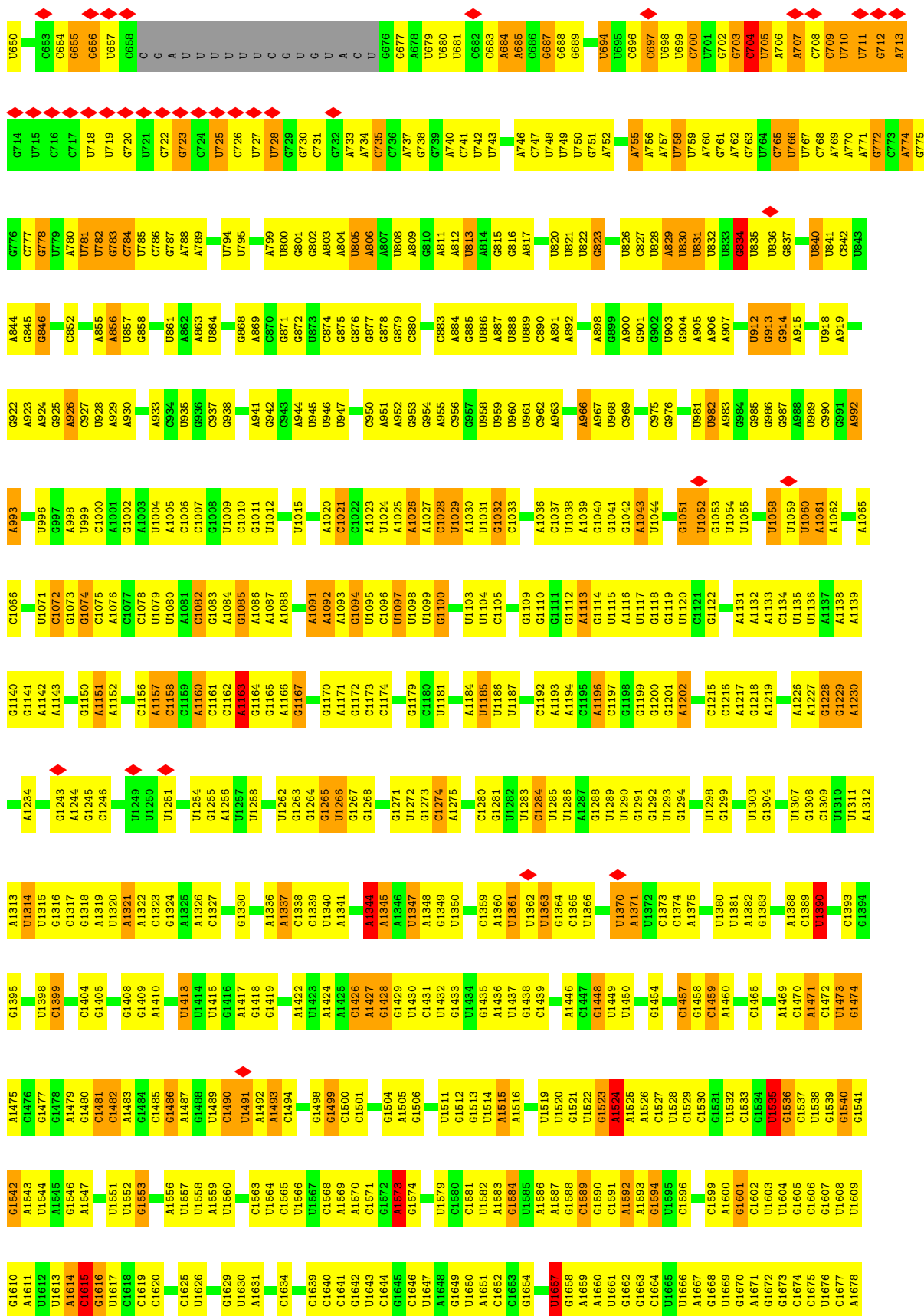


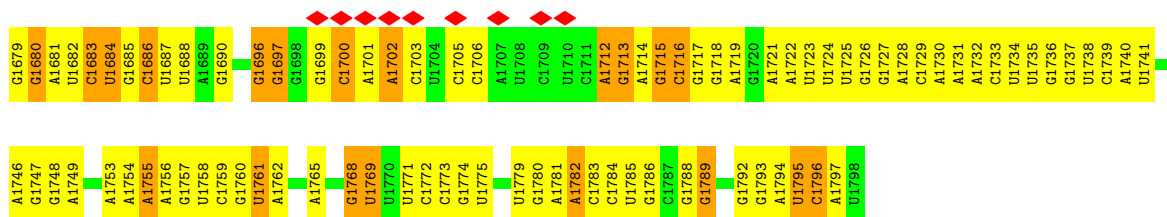
• Molecule 45: 60S ribosomal protein L43



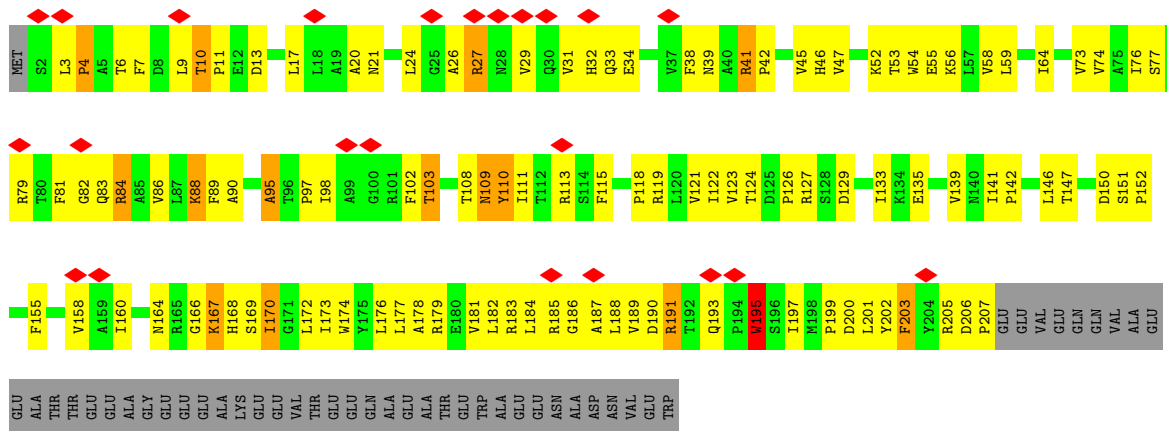
• Molecule 46: 18S ribosomal RNA



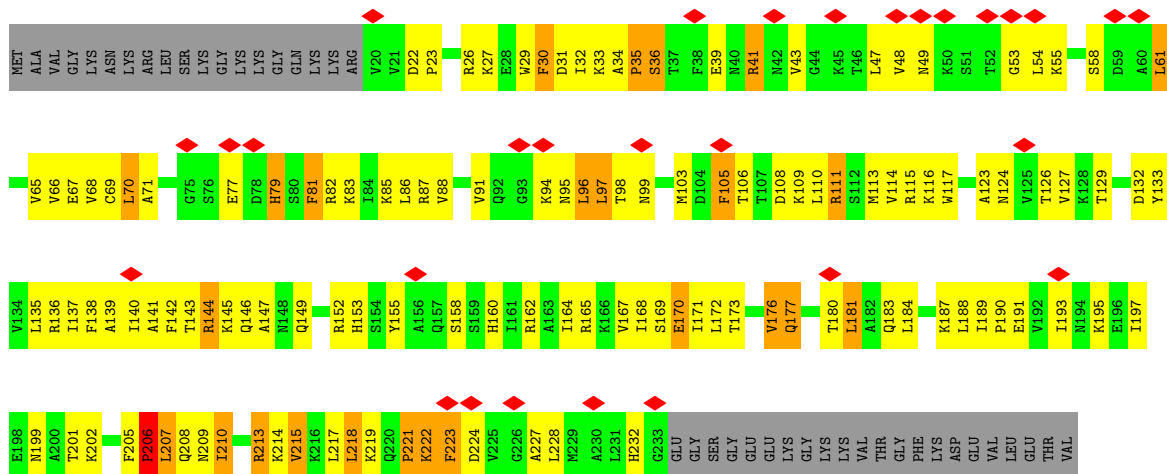




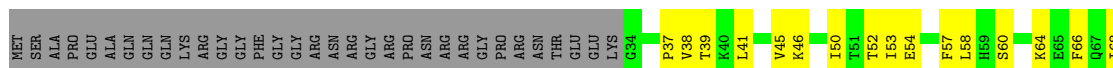
• Molecule 47: 40S ribosomal protein S0

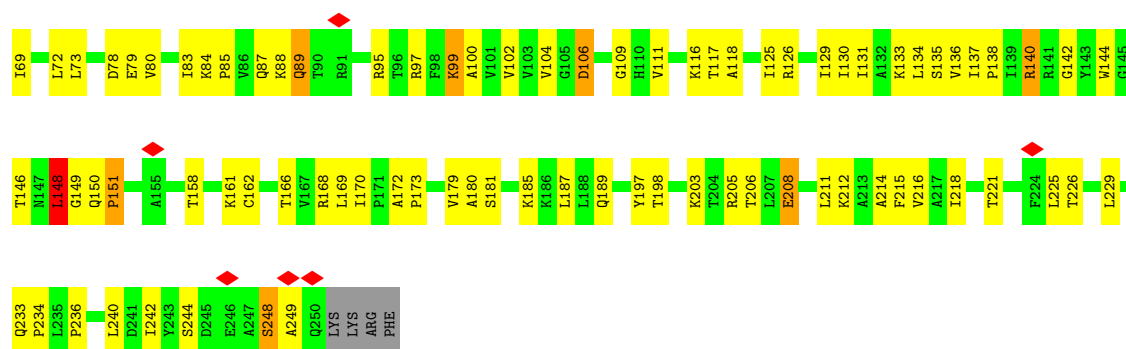


• Molecule 48: 40S ribosomal protein S1

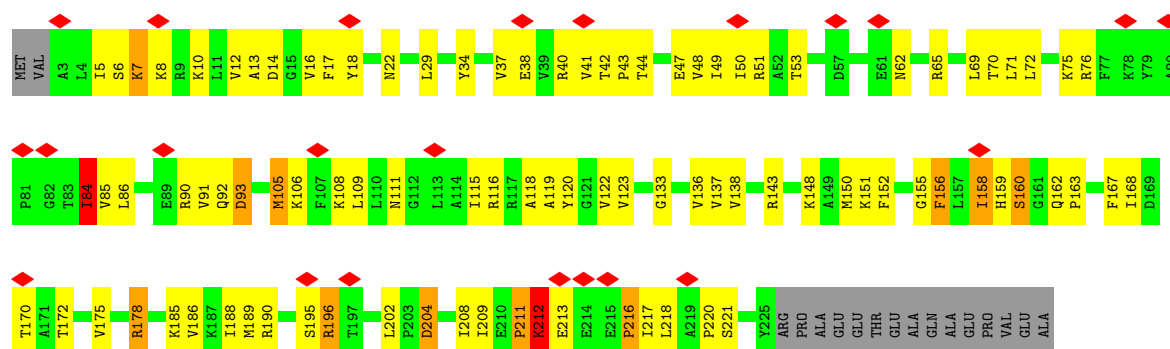


• Molecule 49: 40S ribosomal protein S2

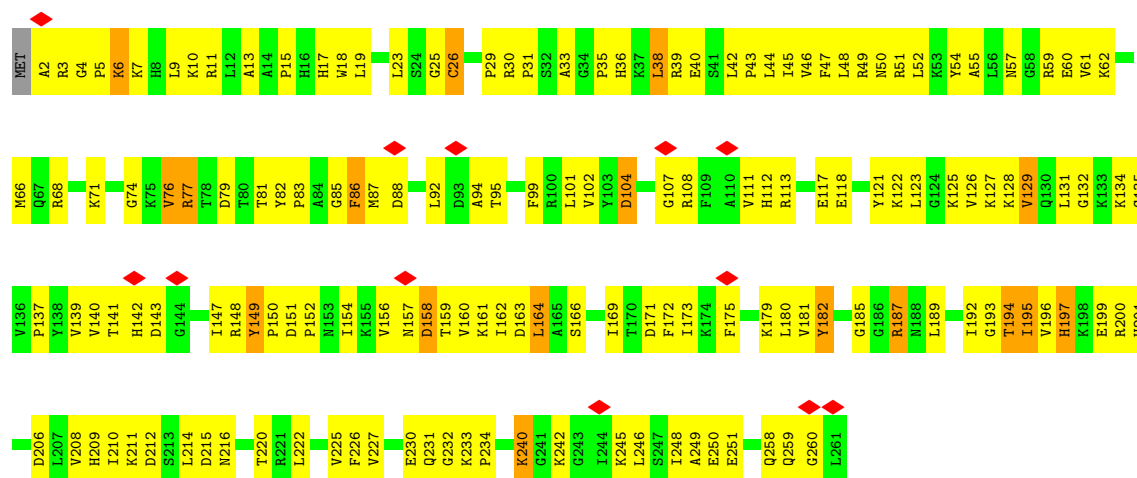
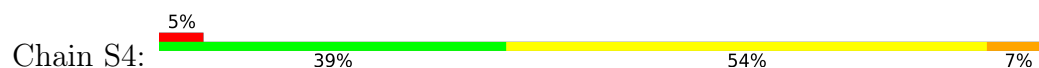




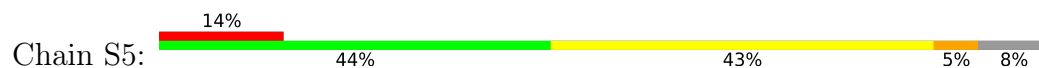
• Molecule 50: 40S ribosomal protein S3

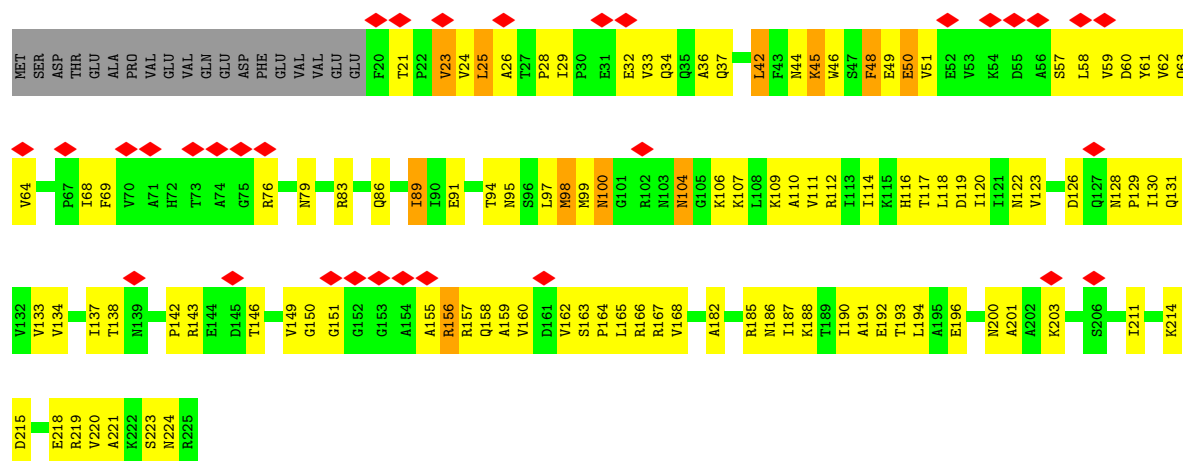


• Molecule 51: 40S ribosomal protein S4

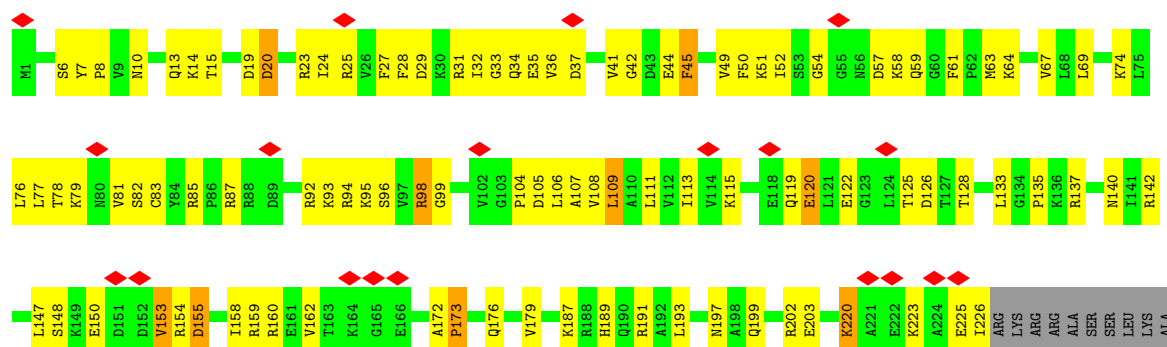


• Molecule 52: 40S ribosomal protein S5

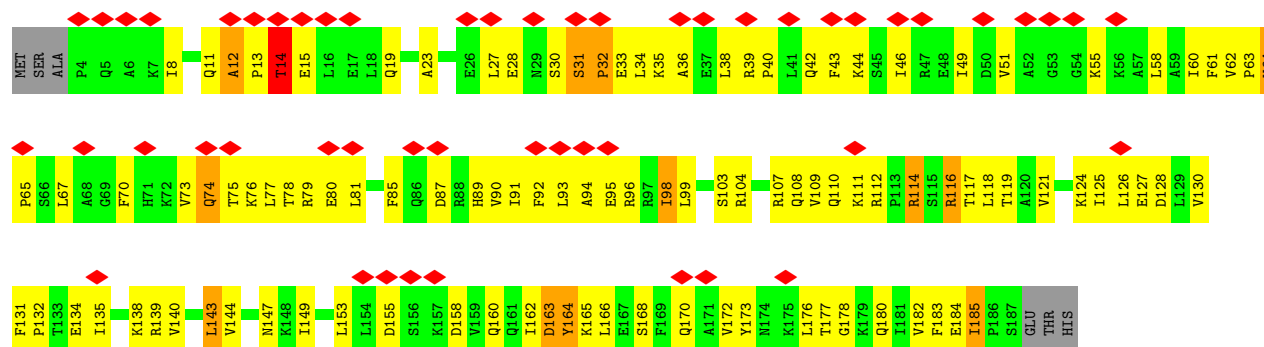




• Molecule 53: 40S ribosomal protein S6

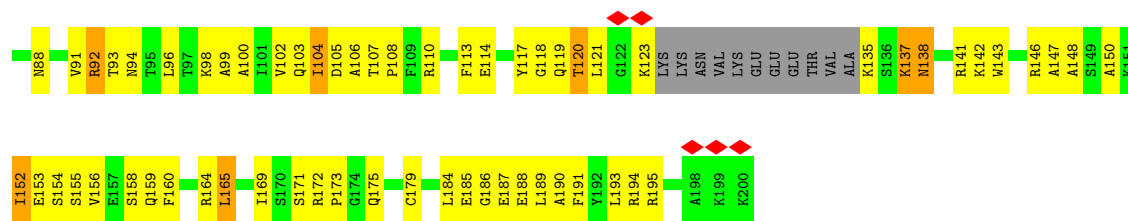


• Molecule 54: 40S ribosomal protein S7

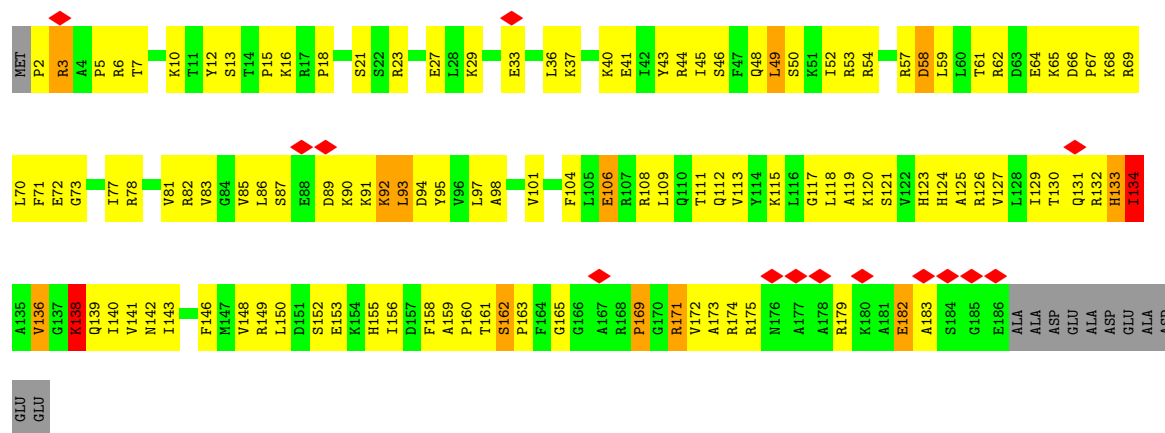


• Molecule 55: 40S ribosomal protein S8

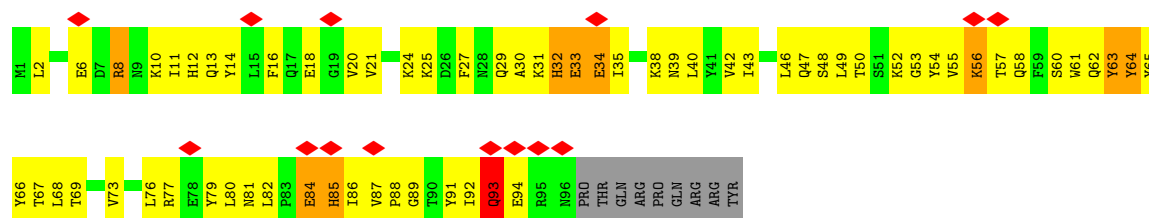




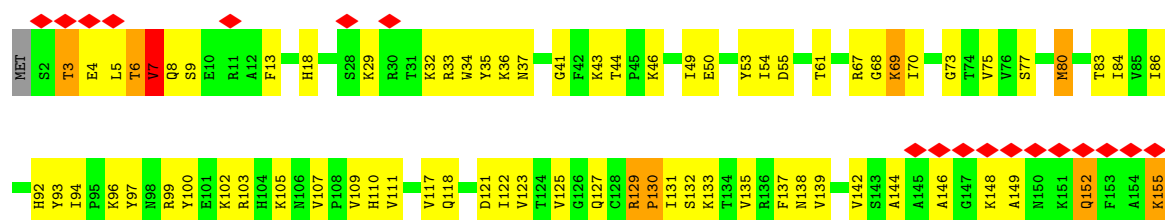
• Molecule 56: 40S ribosomal protein S9



• Molecule 57: 40S ribosomal protein S10



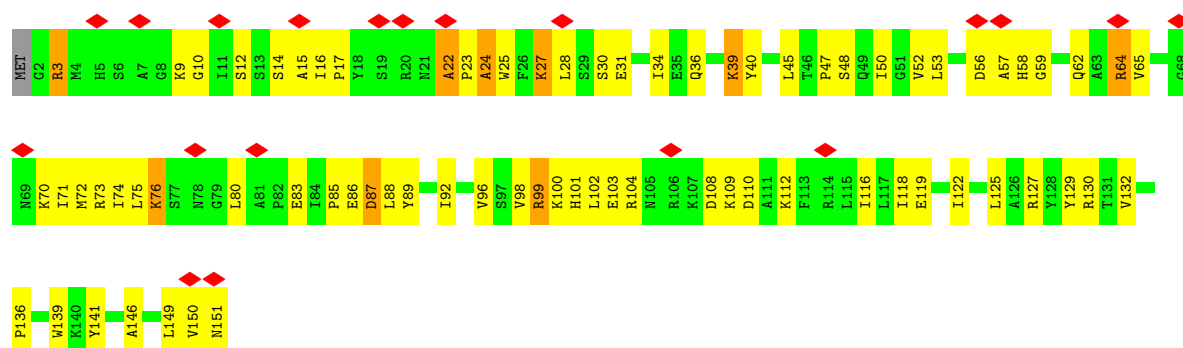
• Molecule 58: 40S ribosomal protein S11



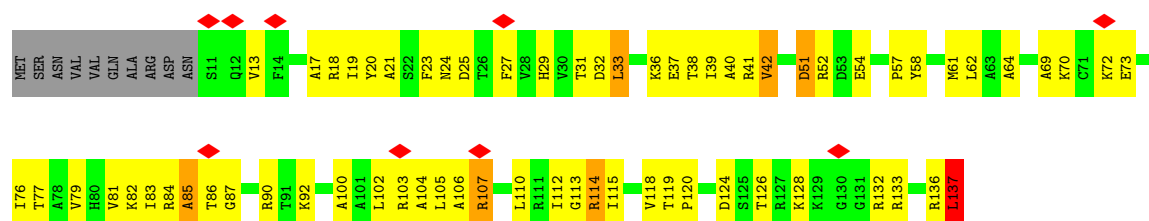
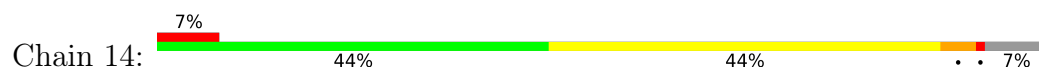
• Molecule 59: 40S ribosomal protein S12



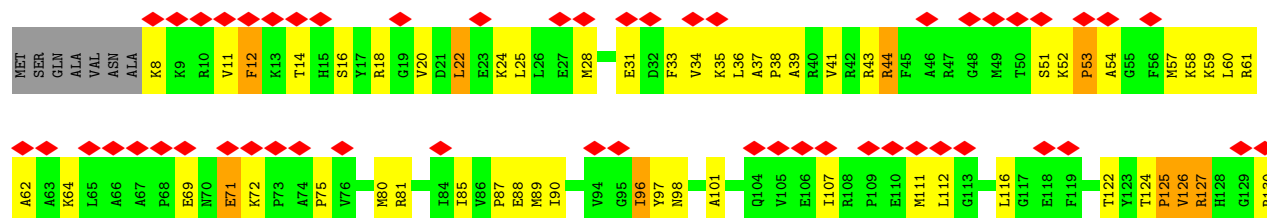
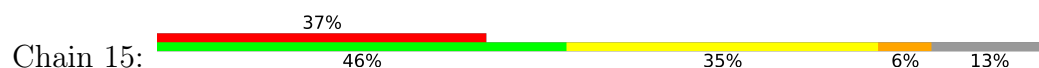
- Molecule 60: 40S ribosomal protein S13

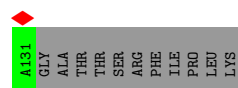


- Molecule 61: 40S ribosomal protein S14



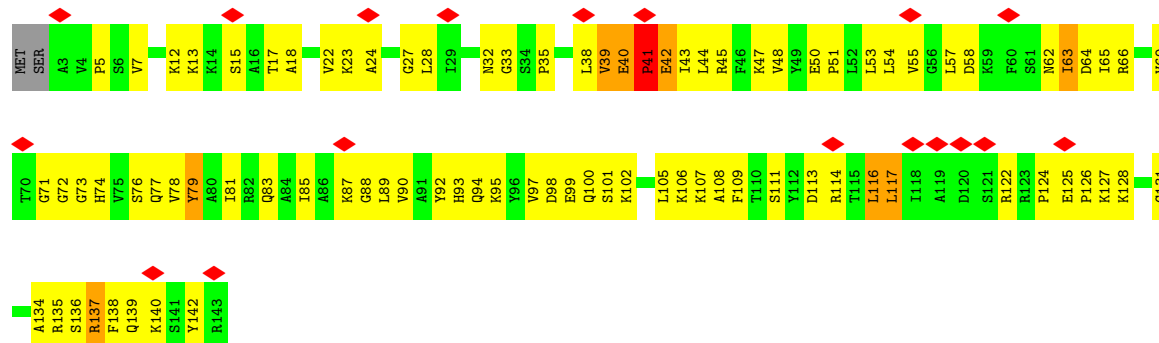
- Molecule 62: 40S ribosomal protein S15





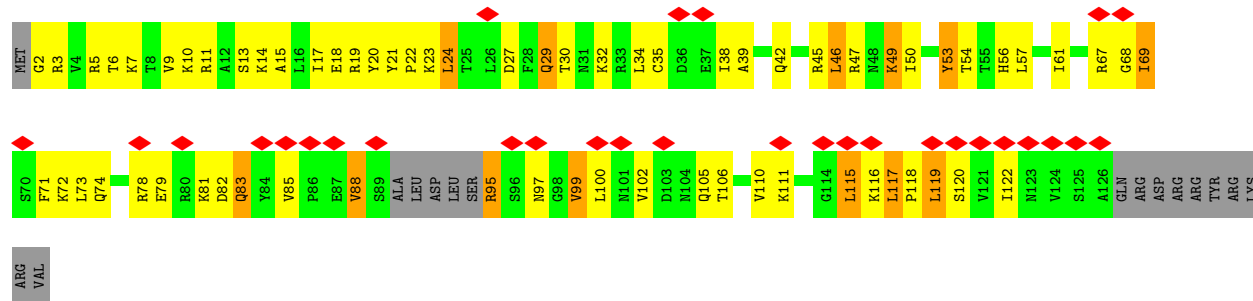
• Molecule 63: 40S ribosomal protein S16

Chain 16: 13% 37% 55% 6% ..



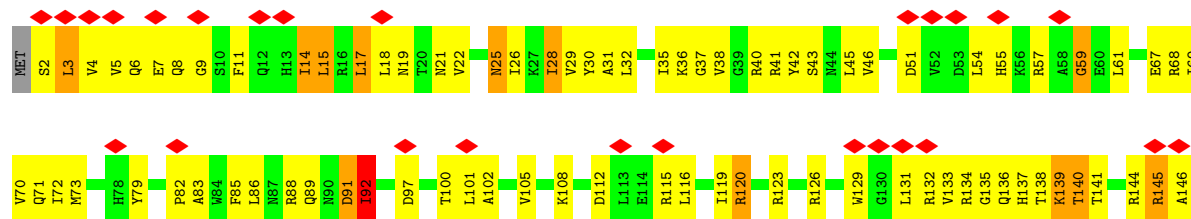
• Molecule 64: 40S ribosomal protein S17

Chain 17: 22% 38% 40% 10% 12%



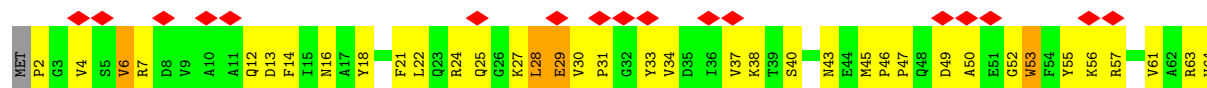
• Molecule 65: 40S ribosomal protein S18

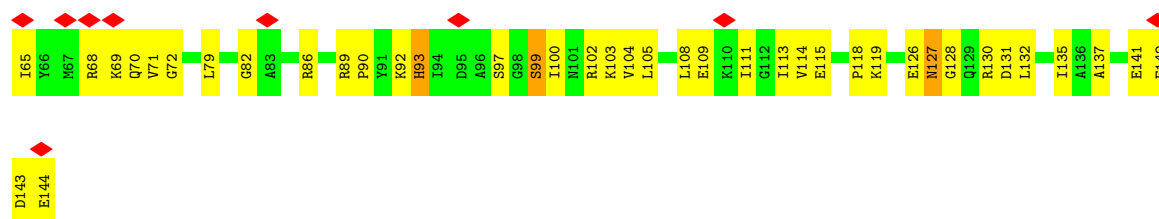
Chain 18: 18% 42% 48% 8% ..



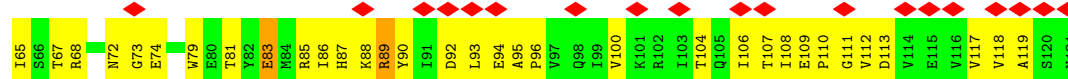
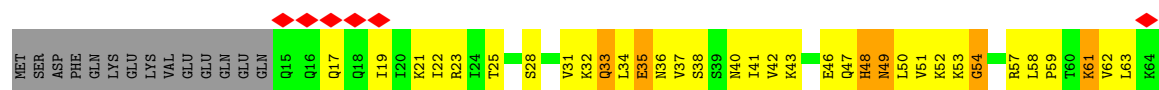
• Molecule 66: 40S ribosomal protein S19

Chain 19: 18% 46% 49% 5% .





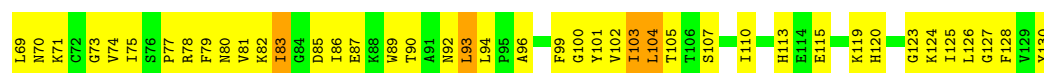
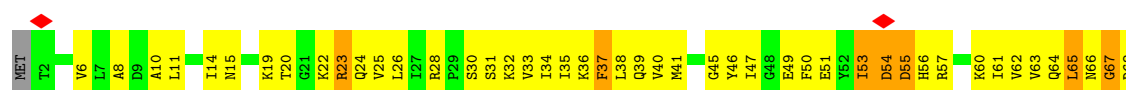
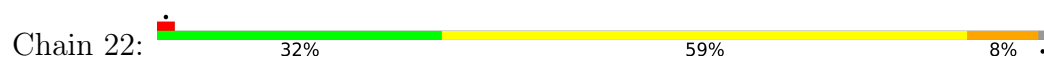
• Molecule 67: 40S ribosomal protein S20



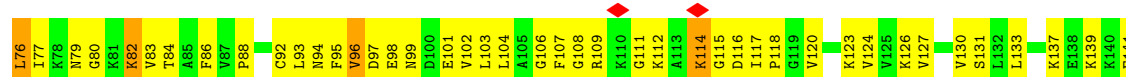
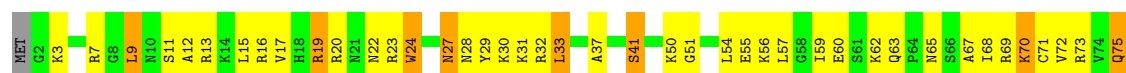
• Molecule 68: 40S ribosomal protein S21



• Molecule 69: 40S ribosomal protein S22

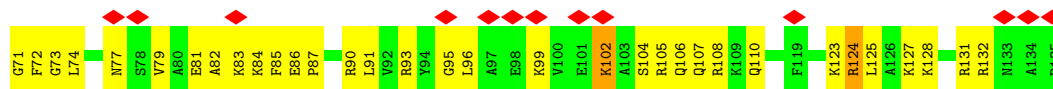
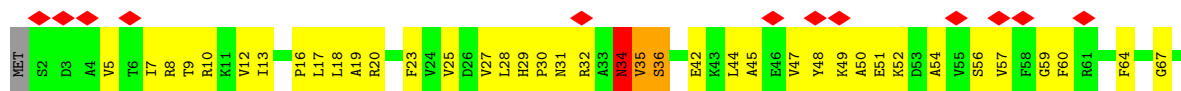


• Molecule 70: 40S ribosomal protein S23

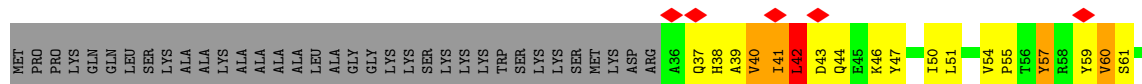
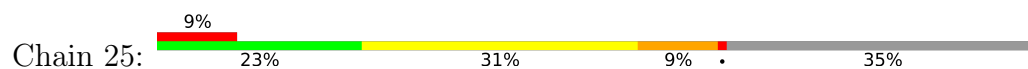




- Molecule 71: 40S ribosomal protein S24



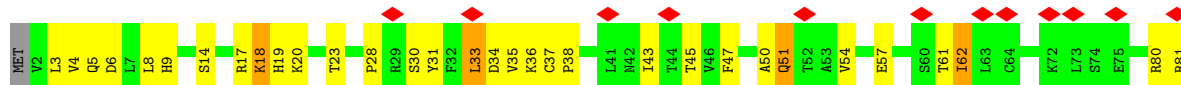
- Molecule 72: 40S ribosomal protein S25



- Molecule 73: 40S ribosomal protein S26

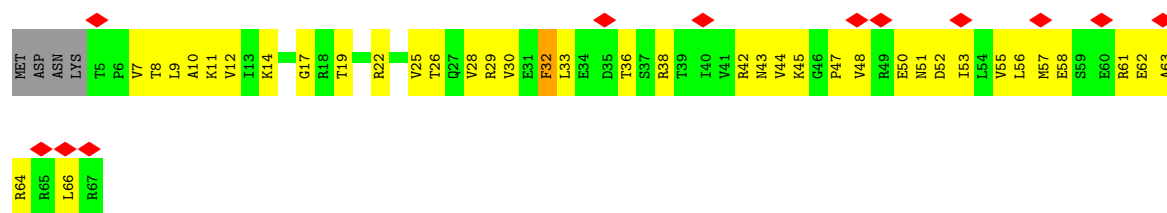


- Molecule 74: 40S ribosomal protein S27

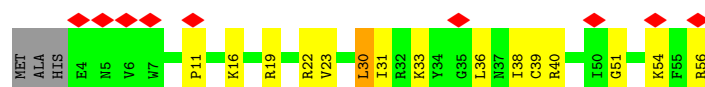


- Molecule 75: 40S ribosomal protein S28





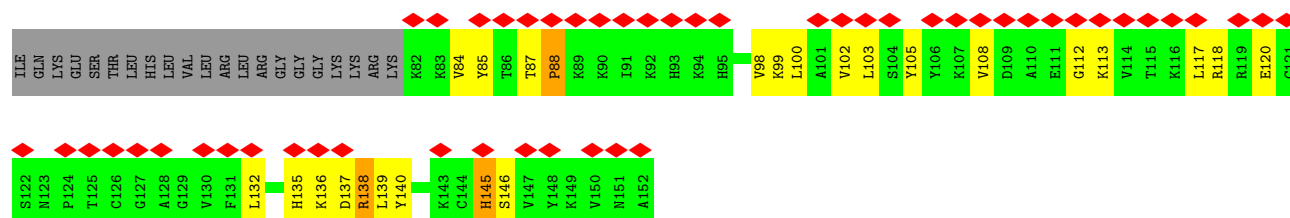
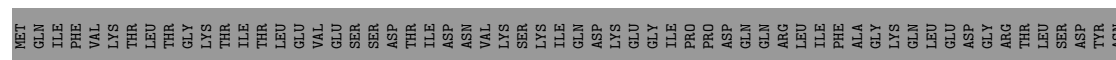
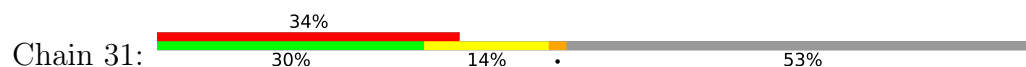
• Molecule 76: 40S ribosomal protein S29



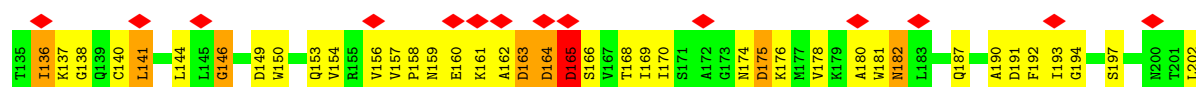
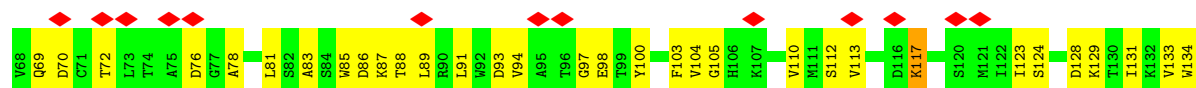
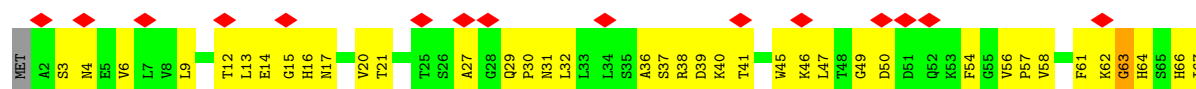
• Molecule 77: 40S ribosomal protein S30

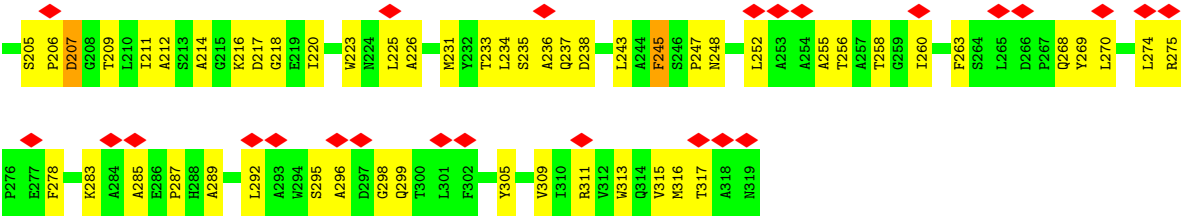


• Molecule 78: 40S ribosomal protein S31

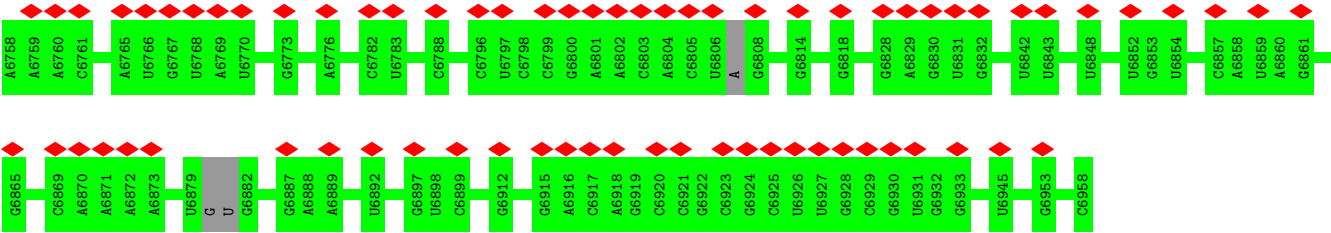


• Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein





• Molecule 80: TSV IRES mRNA



4 Experimental information

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 ($e^-/\text{\AA}^2$)	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 (\AA)	444.99, 444.99, 444.99	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0595, 1.0595, 1.0595	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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(°)	Ideal(°)
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

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 ⓘ

5.3.1 Protein backbone ⓘ

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 ⓘ

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.

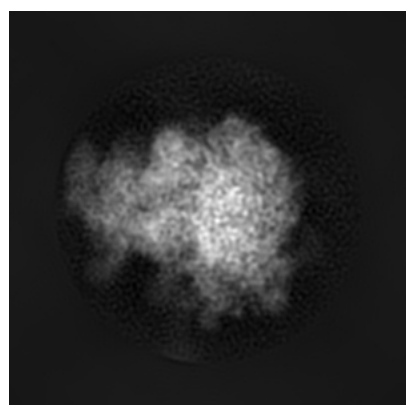
6 Map visualisation [i](#)

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.

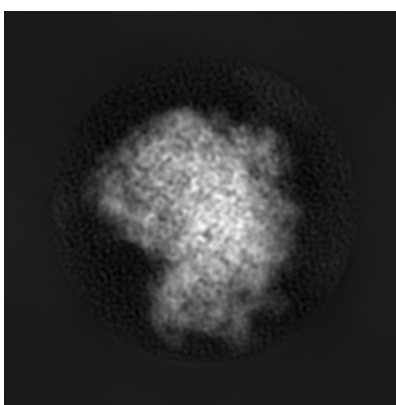
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

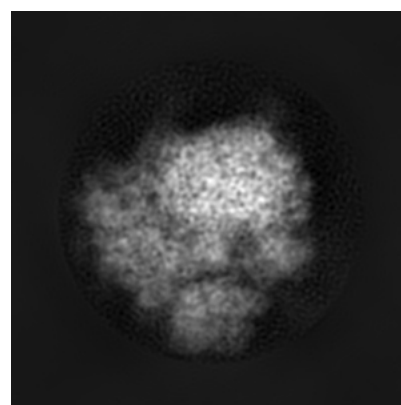
6.1.1 Primary map



X



Y

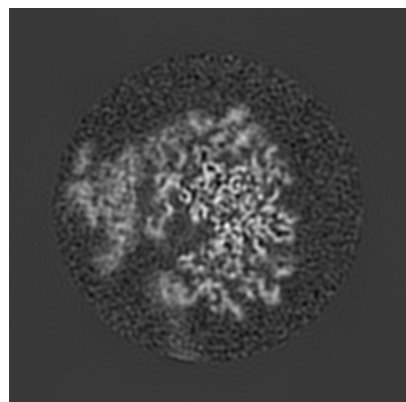


Z

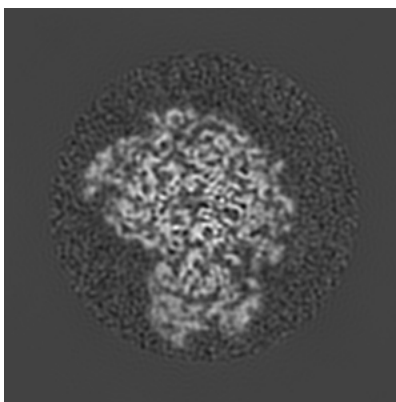
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

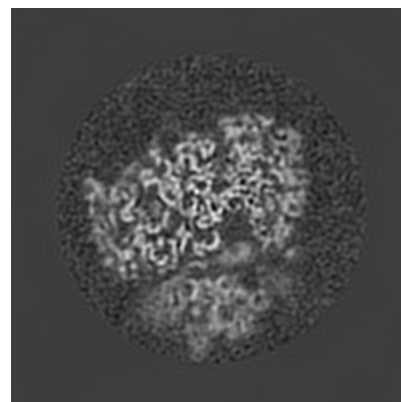
6.2.1 Primary map



X Index: 210



Y Index: 210

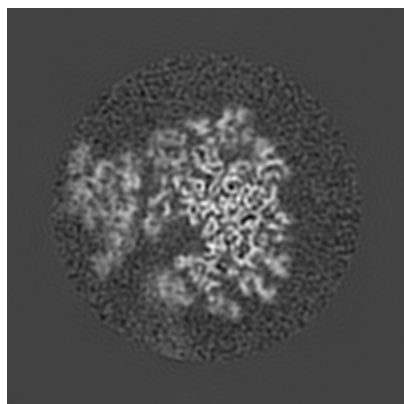


Z Index: 210

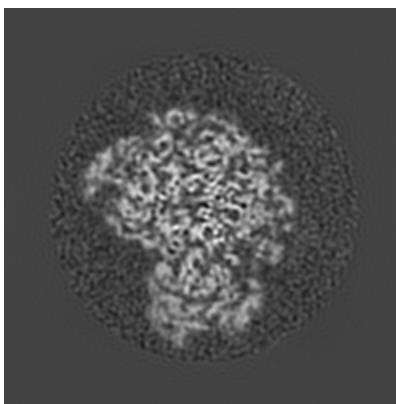
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

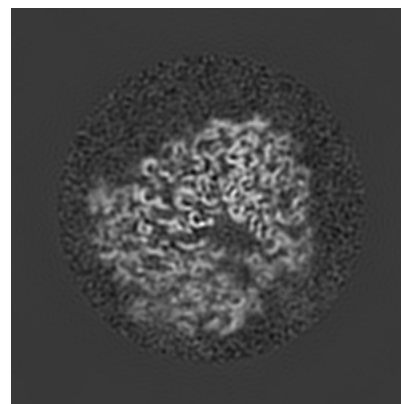
6.3.1 Primary map



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 surface views [i](#)

6.4.1 Primary map



X



Y



Z

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

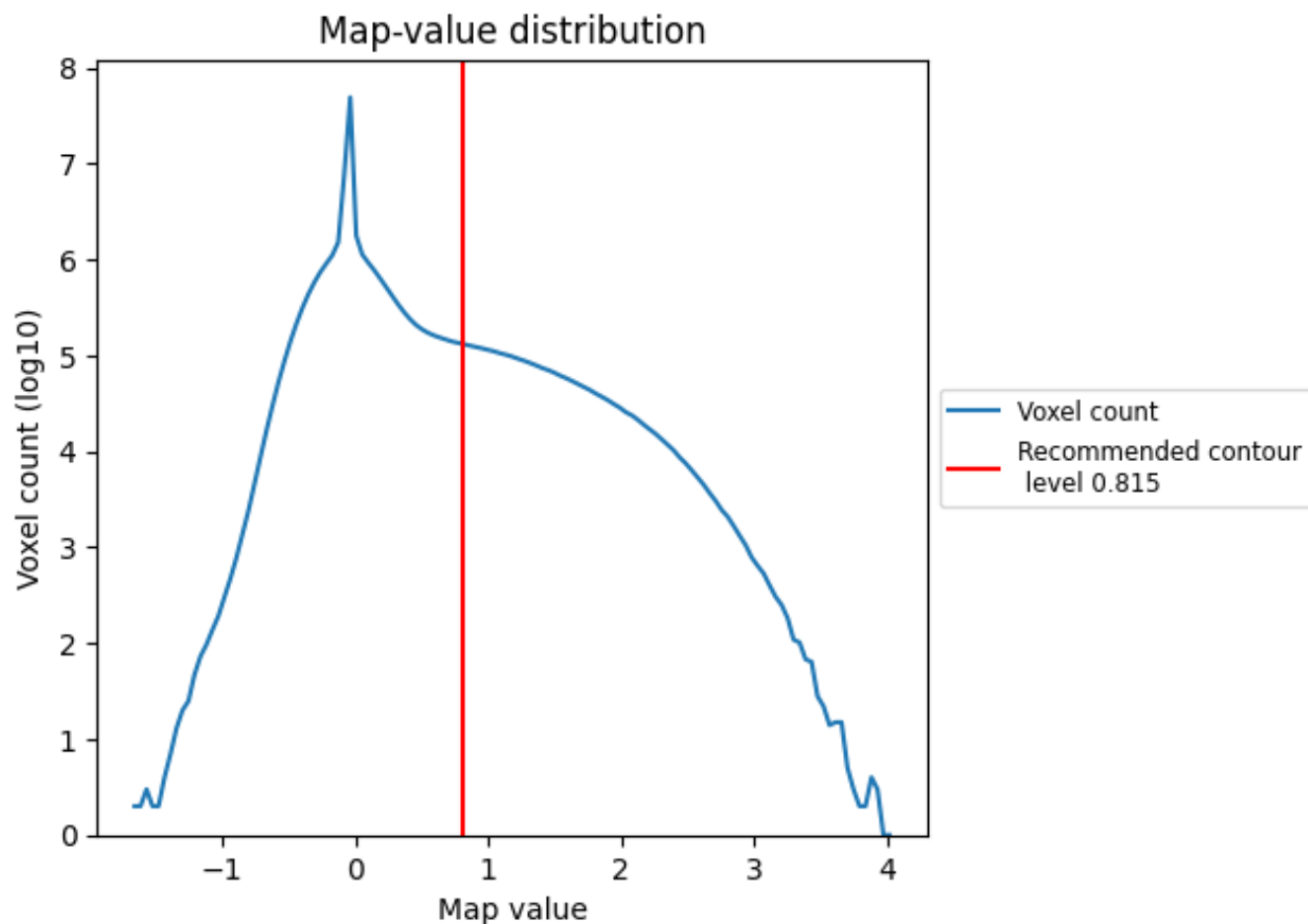
6.5 Mask visualisation

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

7 Map analysis [i](#)

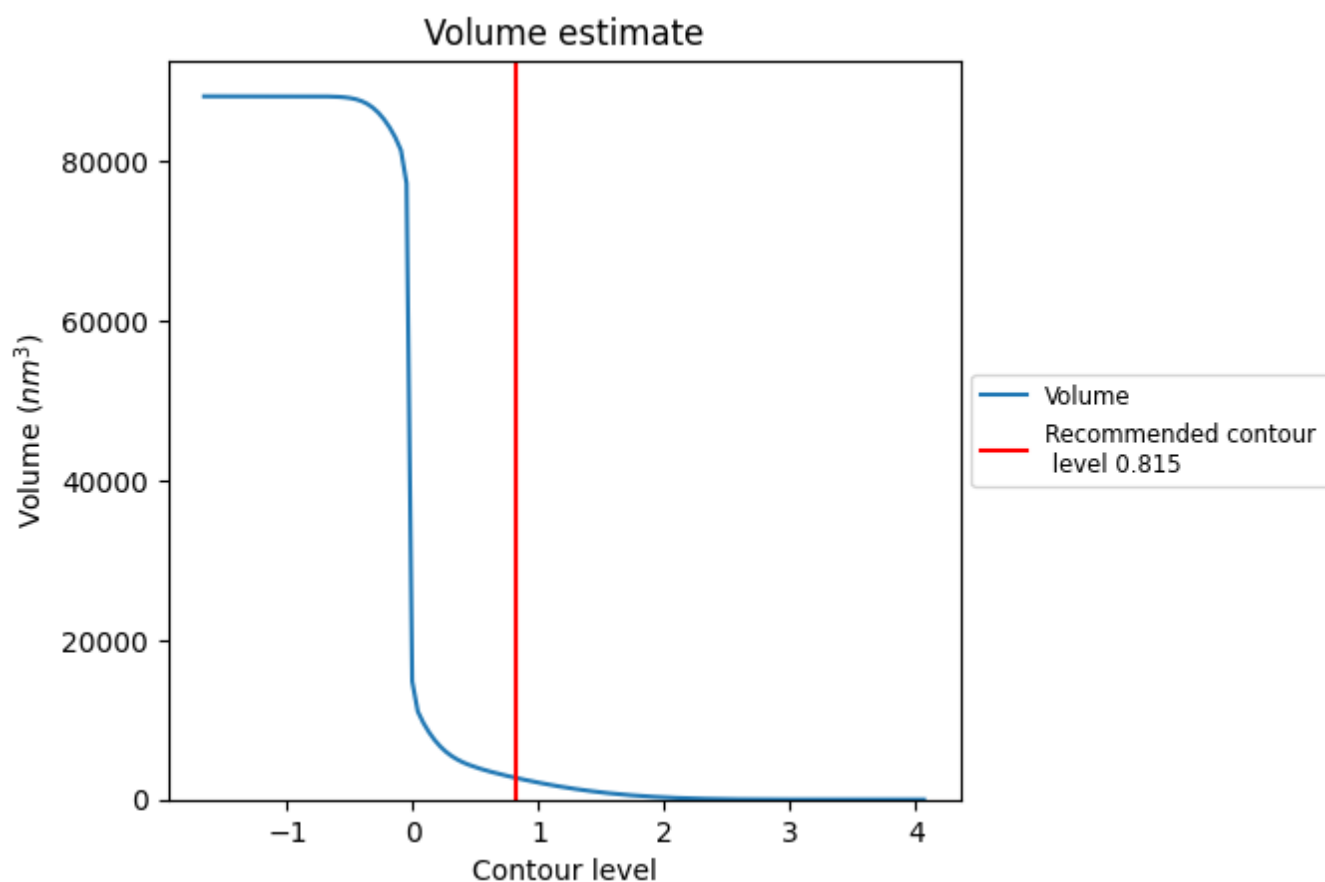
This section contains the results of statistical analysis of the map.

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.

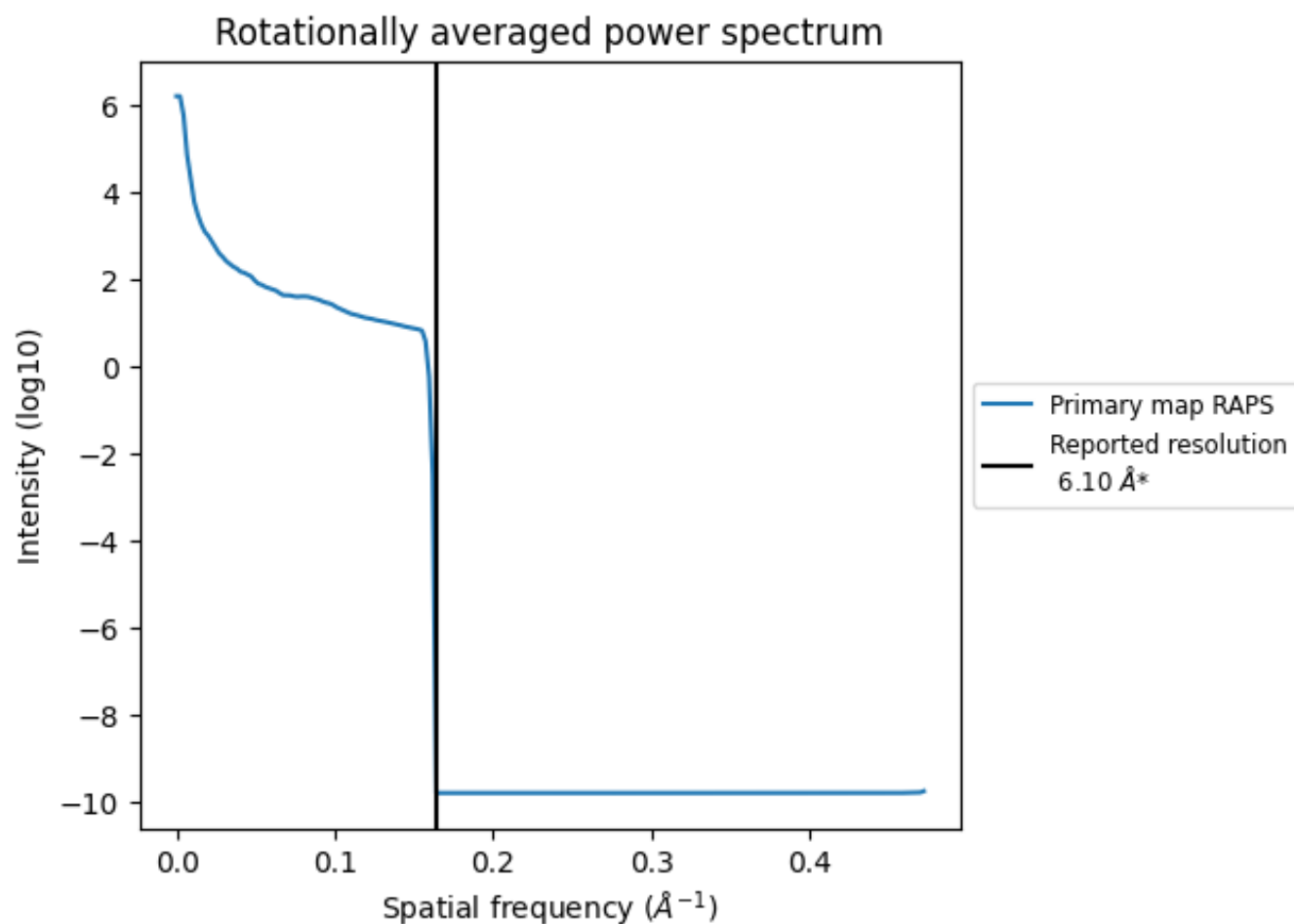
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2733 nm³; 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.164 \AA^{-1}

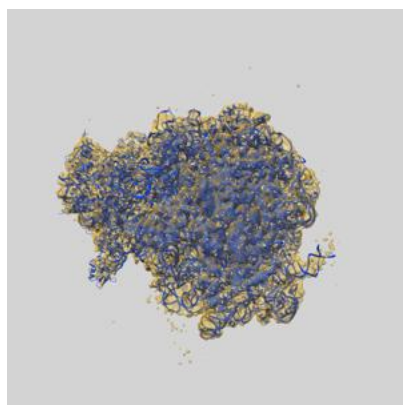
8 Fourier-Shell correlation

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

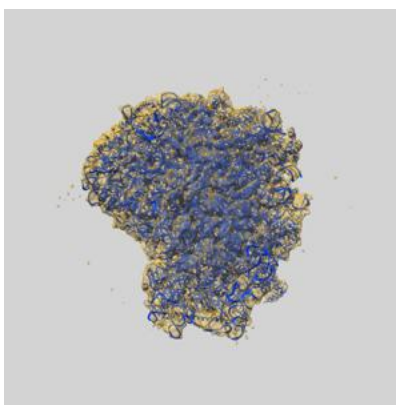
9 Map-model fit [i](#)

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](#).

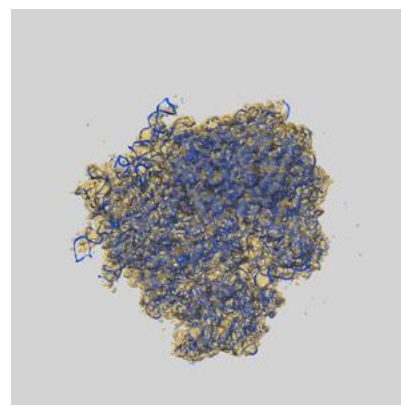
9.1 Map-model overlay [i](#)



X



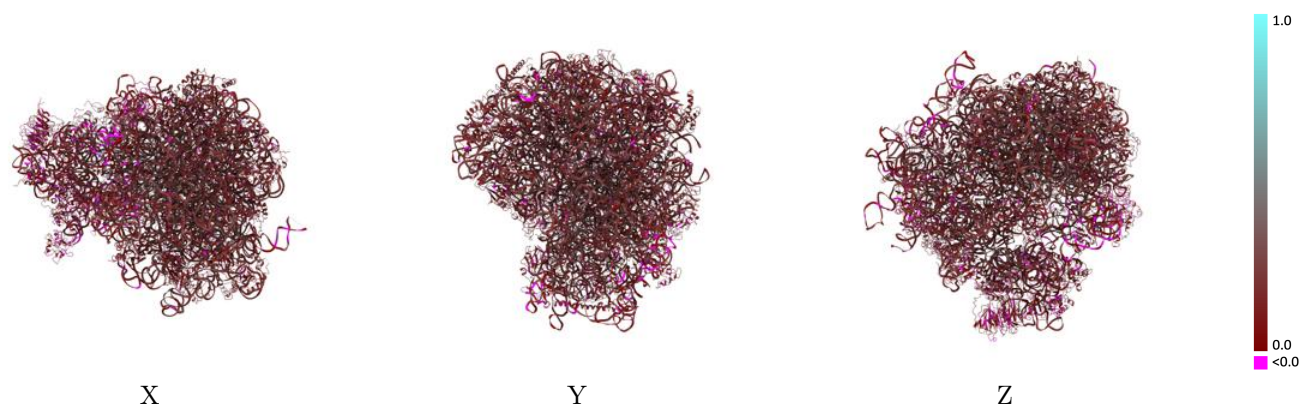
Y



Z

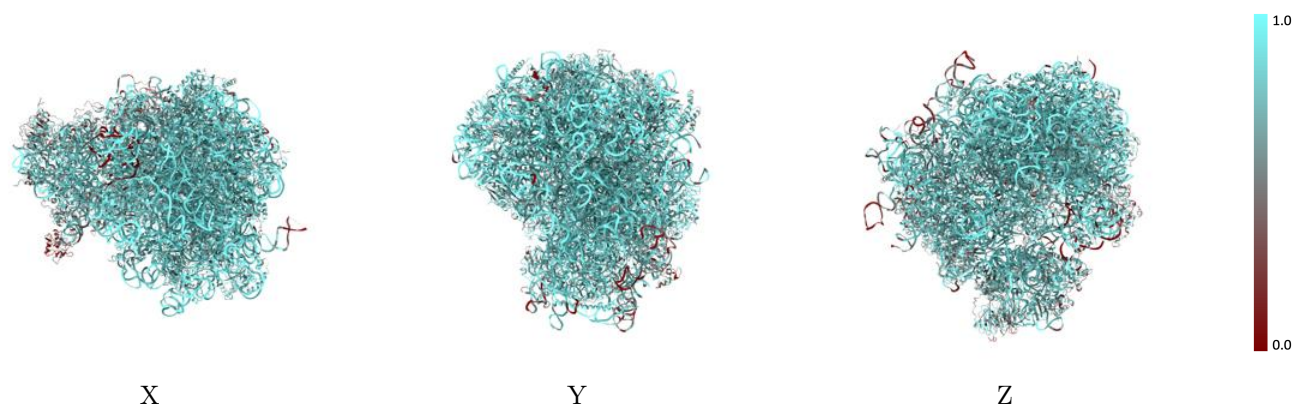
The images above show the 3D surface view of the map at the recommended contour level 0.815 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



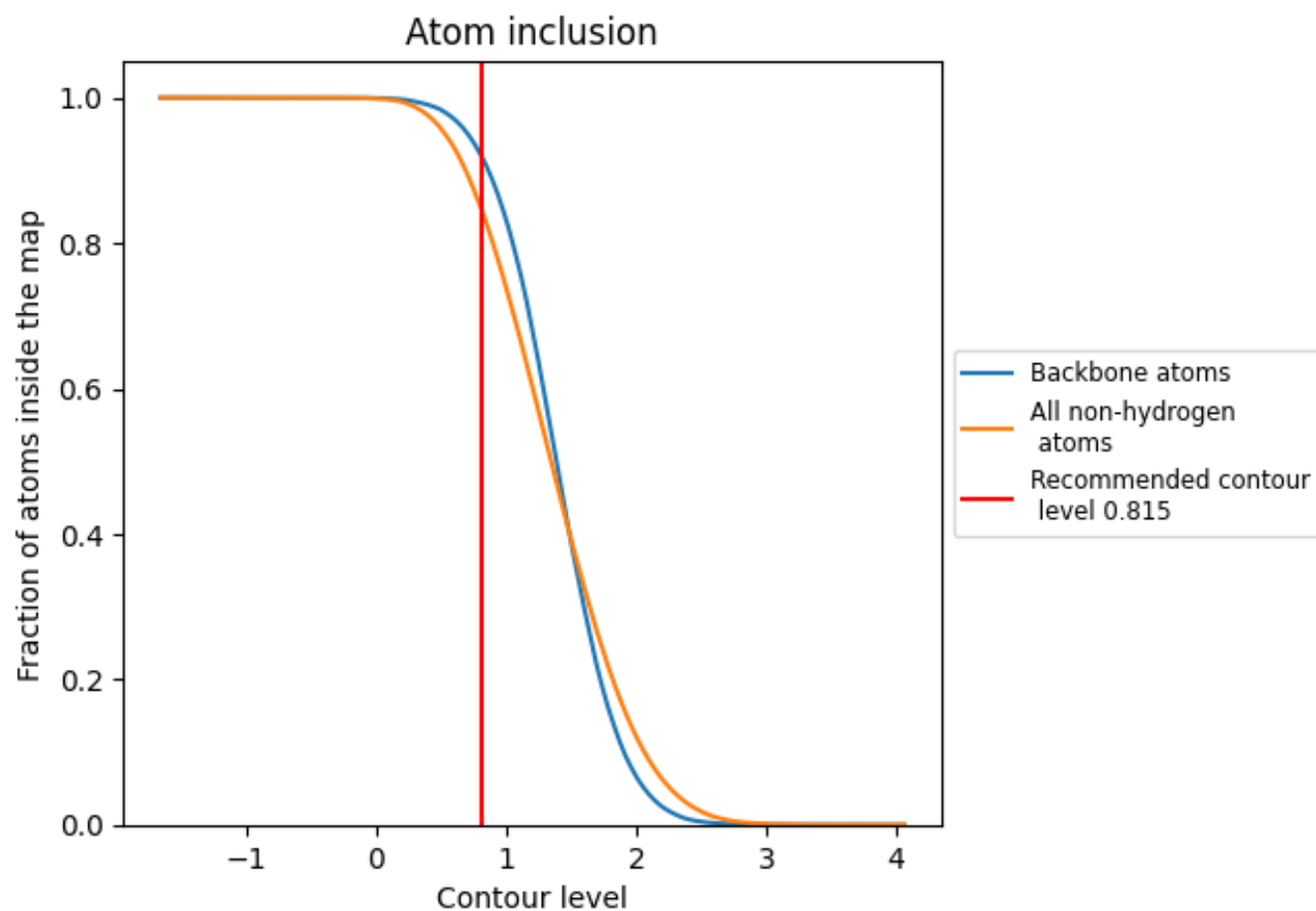
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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





















































































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	 0.8436	 0.2020
10	 0.6900	 0.1580
11	 0.7265	 0.1970
12	 0.1661	 0.1130
13	 0.6981	 0.1670
14	 0.7522	 0.1680
15	 0.5224	 0.1310
16	 0.6880	 0.1380
17	 0.5912	 0.1590
18	 0.6442	 0.1380
19	 0.6516	 0.1110
1S	 0.9162	 0.2110
20	 0.6124	 0.1440
21	 0.7068	 0.1910
22	 0.7538	 0.1790
23	 0.7753	 0.1890
24	 0.6708	 0.1500
25	 0.6563	 0.1670
26	 0.7375	 0.1850
27	 0.6728	 0.1710
28	 0.6506	 0.1470
29	 0.6988	 0.1240
2S	 0.9444	 0.2330
30	 0.7451	 0.2020
31	 0.2807	 0.1520
50	 0.7772	 0.1990
51	 0.7462	 0.1640
53	 0.7633	 0.1880
54	 0.7537	 0.1740
55	 0.7668	 0.1580
56	 0.7855	 0.1730
57	 0.7695	 0.1840
58	 0.7758	 0.1800
59	 0.7493	 0.1840
5S	 0.9709	 0.2270











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Chain	Atom inclusion	Q-score
60	 0.7612	 0.1720
61	 0.7937	 0.1990
62	 0.7417	 0.1890
63	 0.7857	 0.1940
64	 0.8012	 0.1850
65	 0.7740	 0.1930
66	 0.7766	 0.1750
67	 0.7500	 0.1800
68	 0.7787	 0.1840
69	 0.7770	 0.2060
70	 0.7524	 0.1950
71	 0.7801	 0.1930
72	 0.8038	 0.1970
73	 0.7932	 0.1680
74	 0.7723	 0.1700
75	 0.7606	 0.1750
76	 0.7453	 0.1760
77	 0.8155	 0.1630
78	 0.7117	 0.1760
79	 0.7740	 0.1920
80	 0.7327	 0.1660
81	 0.0469	 0.0400
82	 0.7723	 0.1930
83	 0.8104	 0.1920
8S	 0.9714	 0.2410
IR	 0.6465	 0.1160
L1	 0.4276	 0.0990
L2	 0.8025	 0.1960
L3	 0.7858	 0.1840
L4	 0.8047	 0.1940
L5	 0.7069	 0.1560
L6	 0.7825	 0.1880
L7	 0.7843	 0.1790
L8	 0.7497	 0.1840
L9	 0.7545	 0.1760
RA	 0.6502	 0.1330
S0	 0.6923	 0.1850
S1	 0.6748	 0.1730
S2	 0.7680	 0.1920
S3	 0.7040	 0.1830
S4	 0.7658	 0.1680
S5	 0.6508	 0.1450

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Chain	Atom inclusion	Q-score
S6	 0.7286	 0.1530
S7	 0.5868	 0.1690
S8	 0.7822	 0.1770
S9	 0.7448	 0.1600