



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:02 pm GMT

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 PDB ID : 3U5E, 3U5D, 3U5C, 3U5B

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc29047

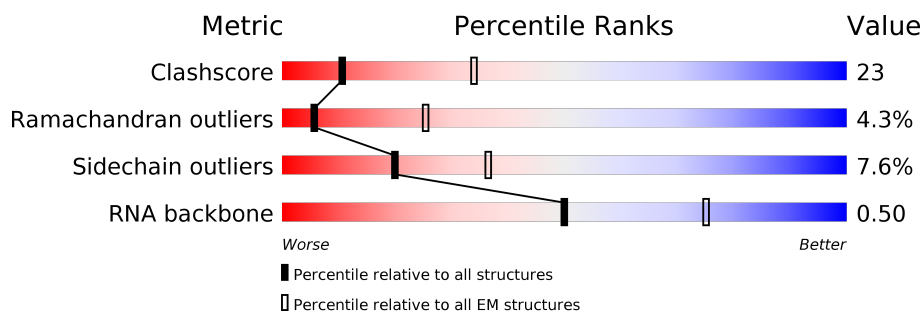
# 1 Overall quality at a glance

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.







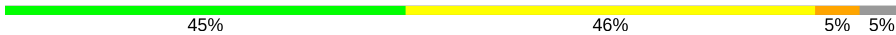

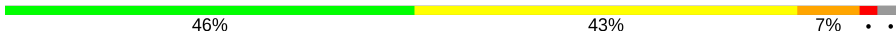

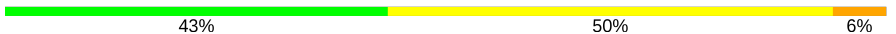
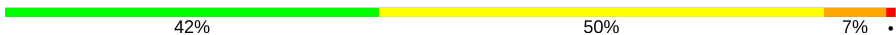
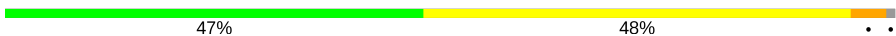

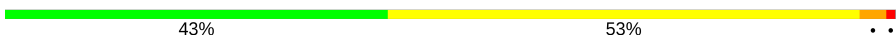












Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	2S	3395	34% 52% 10% . .
2	8S	158	32% 56% 9% .
3	5S	121	36% 60% 5%
4	L1	217	41% 47% 6% . 6%
5	L2	254	37% 57% 6% .
6	L3	387	44% 51% 5%
7	L4	362	47% 45% 8%
8	L5	297	54% 40% 6%




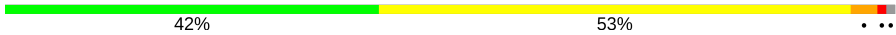

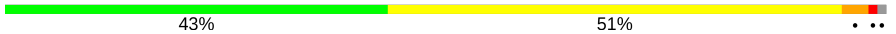

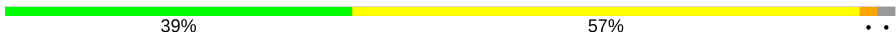



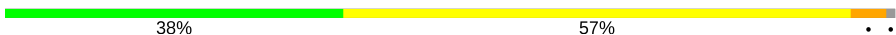
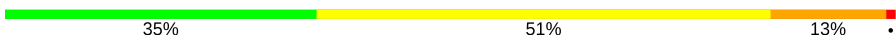












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Mol	Chain	Length	Quality of chain
9	L6	176	
10	L7	244	
11	L8	256	
12	L9	191	
13	50	221	
14	51	174	
15	53	199	
16	54	138	
17	55	204	
18	56	199	
19	57	184	
20	58	186	
21	59	189	
22	60	172	
23	61	160	
24	62	121	
25	63	137	
26	64	155	
27	65	142	
28	66	127	
29	67	136	
30	68	149	
31	69	59	
32	70	105	
33	71	113	





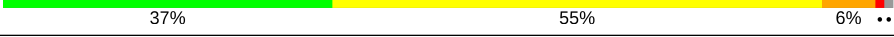
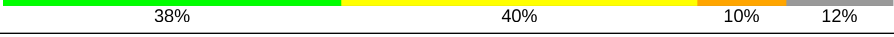
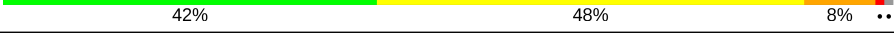

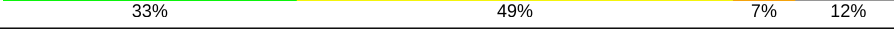


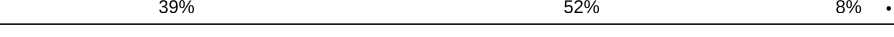

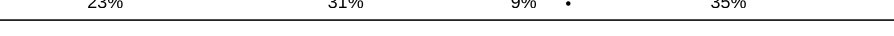
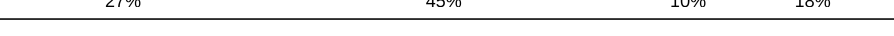

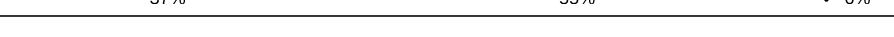

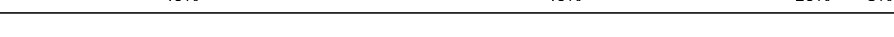
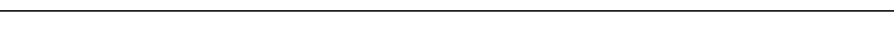

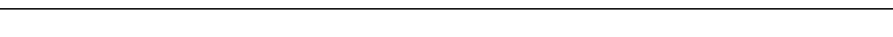
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Mol	Chain	Length	Quality of chain
34	72	130	
35	73	107	
36	74	121	
37	75	120	
38	76	100	
39	77	88	
40	78	78	
41	79	51	
42	80	128	
43	81	25	
44	82	106	
45	83	92	
46	1S	1798	
47	S0	252	
48	S1	255	
49	S2	254	
50	S3	240	
51	S4	261	
52	S5	225	
53	S6	236	
54	S7	190	
55	S8	200	
56	S9	197	
57	10	105	
58	11	156	

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Mol	Chain	Length	Quality of chain
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	0	0
			1106	708	203	195		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

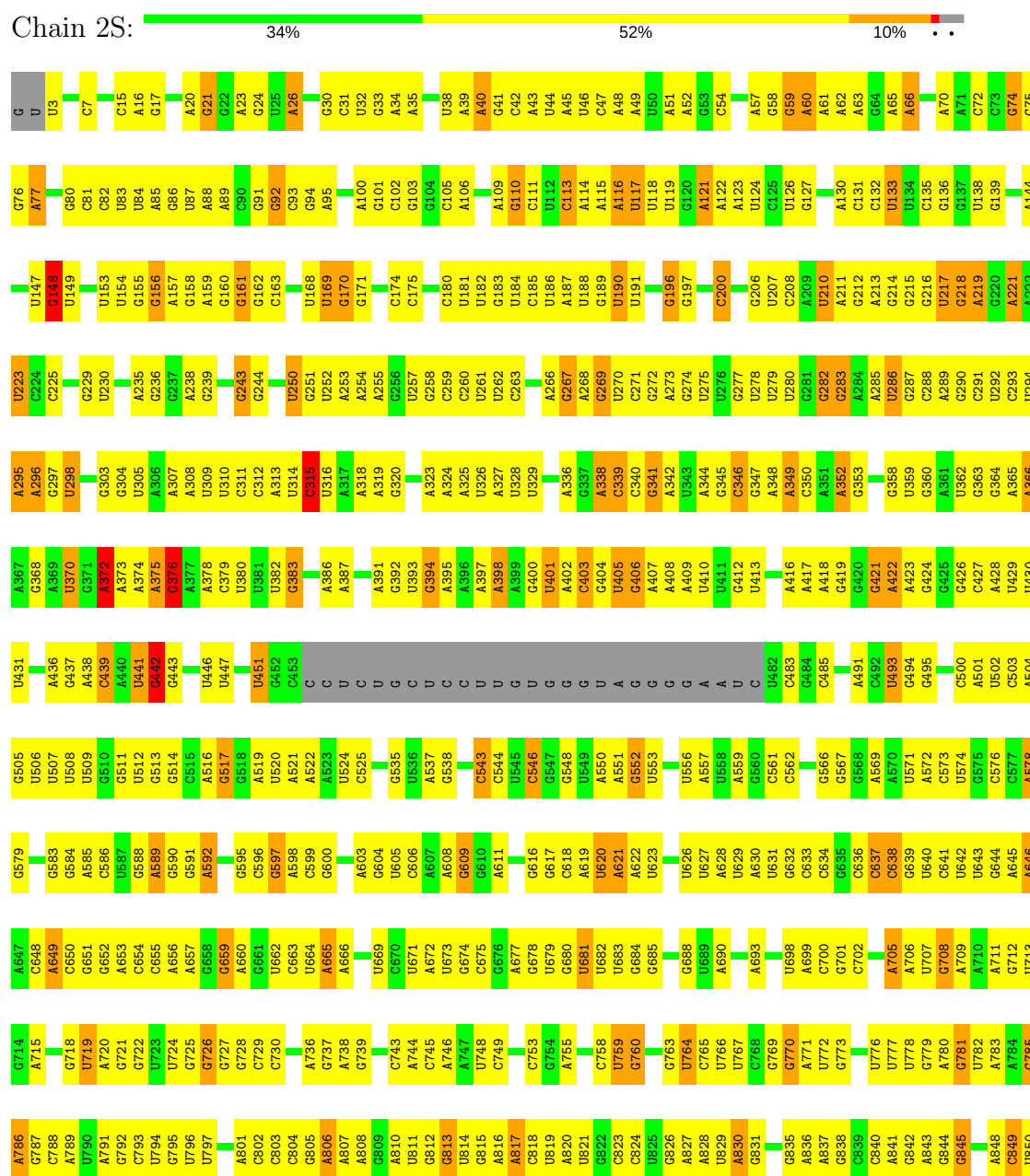
- Molecule 80 is a RNA chain called TSV IRES mRNA.

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

### 3 Residue-property plots

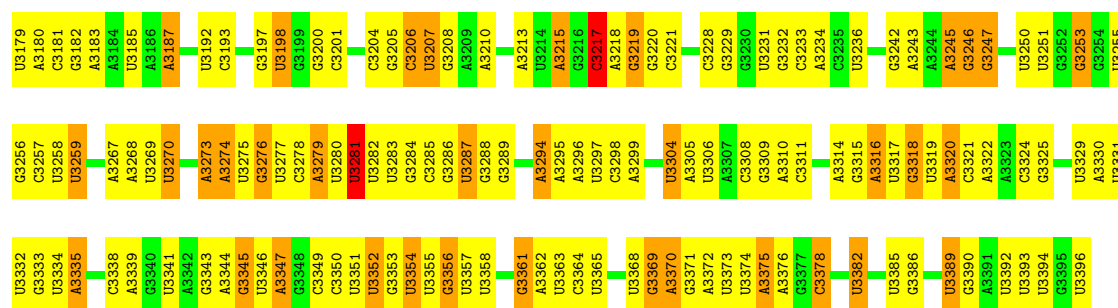
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according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

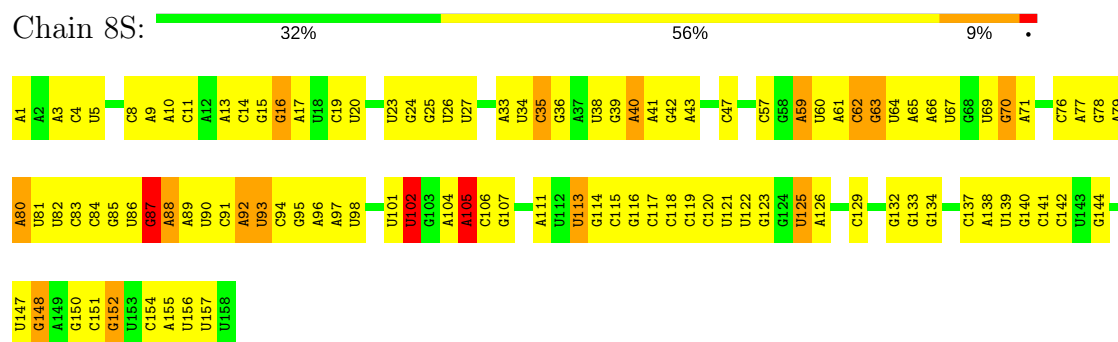


G1939	C1869	A1799	U1717	U1641	U1567	U1494	A1418	A1352	A1290	G1206	G1134	A1064	U986	C923	C851
G1940	C1870	A1800	G1718	A1642	U1568	U1495	A1419	U1353	A1291	G1207	A1136	A1065	U987	G924	U852
C1941	C1871	C1803	G1719	A1643	U1569	C1496	G1420	G1354	C1292	U1210	C1137	U1070	U988	A925	C853
C1942	C1872	A1804	U1723	U1645	U1570	C1497	G1421	A1355	U1293	U1211	U1138	U1071	A989	U926	U854
C1943	C1873	A1805	A1722	G1646	A1571	A1498	G1422	G1356	A1294	A1212	G1139	G1072	U990	C927	U855
U1944	C1874	A1806	U1723	G1646	A1572	A1499	G1423	G1357	G1295	G1213	G1140	G1073	C928	C928	C856
	U1876	G1807	U1724	A1647	G1573	U1501	U1427	C1358	C1297	U1214	C1141	U1074	A982	A929	C857
G1947	C1877	G1808	C1725	A1648	C1574	U1504	U1430	C1359	C1298	U1215	C1142	A1075	U993	U930	A858
G1948	C1878	A1809	G1726	U1649	A1575	A1505	A1431	C1360	U1299	G1216	A1143	U1076	C994	C931	C859
G1949	C1879	A1810	U1727	U1650	G1576	A1506	A1432	C1361	U1299	G1216	A1144	A1079	U995	U932	C860
C1950	C1880	A1811	U1728	U1651	G1577	A1507	A1433	C1362	A1301	A1217	G1147	A1080	U996	C936	C861
G1951	C1881	G1812	A1729	G1653	C1582	A1508	U1434	C1363	A1302	U1220		U1081	A997	A936	U862
G1952	C1882	A1813	U1730	A1654	U1583	C1508	G1434	C1364	A1303	A1221		U1082	C1000	C937	C873
C1953	C1883	A1814	U1732	G1655	A1584	A1509	U1437	C1365	A1304	G1222	A1150	G1083	U938	C938	C874
U1954	C1884	A1815	U1733	A1656	C1585	A1510	U1438	U1366	U1305	G1223	U1151	A1084	U939	U939	C875
U1955	C1885	A1816	G1738	G1657	U1586	U1511	U1439	G1370	G1306	A1224	G1152	C1085	A1003	G940	
A1956	C1886	A1817	U1739	G1658	A1587	U1512	G1440	G1371	G1307	A1225	A1153	C1086	G941	G941	U879
	C1887	G1743	U1740	U1659	U1588	G1513	G1441	C1372	A1308	G1226	A1154	U1087	U942	U942	C880
C1965	C1888	G1744	U1741	C1660	A1589		U1442	C1376	U1309	C1227		U1088	U943	U943	C881
U1966	C1889	G1745	U1742	G1661	U1590	G1517	U1443	G1377	G1310		A1158	U1089	C944	C944	C882
U1967	C1890	G1746	U1743	G1662	G1591	U1520	G1444	U1378	G1311	U1234	A1159	C945	U946	U946	A883
U1968	C1891	A1826	U1747	G1663	G1592	G1521	U1445	G1379	G1312	U1235	U1167	U1094	U947	U947	A884
	C1892	A1827	U1748	G1664	A1593	G1522	U1446	G1380	G1313	G1236	U1168	U1095	C948	C948	U885
C1971	C1893	A1828	U1749	G1665	U1594	U1523	U1447	G1381	U1314	G1237	A1169	U1096	C949	C949	C886
	C1894	A1829	U1750	G1666	U1595		U1448	G1382	U1315	C1238	A1170	U1097	G950	G950	C887
	C1895	A1830	U1751	C1667	U1596		U1449	G1383	C1316	C1239	A1171	G1098			A888
	C1896	A1831	U1752	U1667	U1597	U1526	A1450	U1384	G1317	U1240	G1172	A1099	C951	C951	U889
	C1897	A1832	U1753	C1668	A1603	C1527	U1451	G1385	A1318	U1241	G1173	U1100	C952	C952	C890
	C1898	A1833	U1754	U1669	G1604		U1452	C1386	G1321	G1243	G1174	G1101	U954	U954	U892
	C1899	A1834	U1755	U1670	U1605	U1532	U1453	G1387	U1322	U1244	C1175	A1102	U955	U955	C893
	C1900	A1835	U1756	G1671	C1606	U1533	U1454	U1388	G1323	A1245	G1176	A1103	U956	U956	C894
	C1901	A1836	U1757	U1672	U1607	A1534	U1455	C1391	G1324	G1246	G1177	G1104	C957	C957	C895
	C1902	A1837	U1758	U1673	C1608	A1535	U1456	C1392	U1325	A1251	G1178	A1105	C958	C958	A895
	C1903	A1838	U1759	U1674	U1609	G1536	U1457	C1393	U1326		A1179	G1106	U959	U959	A896
	C1904	A1839	U1760	U1675	G1610	U1537	U1458	C1394	U1327	G1250	A1180	C1107	U960	U960	U897
	C1905	A1840	U1761	U1676	G1611	U1538	U1459	A1395	C1328	U1254	U1181	U1108	U961	U961	U898
	C1906	A1841	U1762	U1677	A1612	A1539	U1460	C1396	U1329		U1182	U1109	U962	U962	U899
	C1907	A1842	U1763	U1678	C1613		U1461	C1397	U1330	C1257	U1183	U1110	G900	G900	G900
	C1908	A1843	U1764	U1679	U1614	A1545	U1462	U1398	U1331	U1258	G1186	A1112	G901	G901	G901
	C1909	A1844	U1765	U1680	G1615	U1546	U1463	U1399	U1332	U1259	C1187	U1113	U902	U902	U902
	C1910	A1845	U1766	U1681	U1616	G1547	U1464	U1400	U1333	A1260		U1114	U903	U903	U903
	C1911	A1846	U1767	U1682	C1617	U1548	U1465	A1401	U1334	G1261	A1190	U1115	U904	U904	U904
	C1912	A1847	U1768	U1683	U1618	U1549	U1466	U1402	U1335	U1262	U1191	G1116	U905	U905	U905
	C1913	A1848	U1769	U1684	G1619	U1550	U1467	C1403	C1336	G1263	U1192	G1117	A906	A906	A906
	C1914	A1849	U1770	U1685	U1620	U1551	U1468	U1404	U1337	U1264	U1193	G1118	U907	U907	U907
	C1915	A1850	U1771	U1686	G1621	U1552	U1469	U1405	U1338	U1265	U1194	C1119	G908	G908	G908
	C1916	A1851	U1772	U1687	U1622	U1553	U1470	U1406	C1339		A1195	A1120			C911
	C1917	A1852	U1773	U1688	U1623	U1554	U1471	U1407	U1340	U1269	C1196	U1121	G912	G912	G912
	C1918	A1853	U1774	U1689	C1624	U1555	U1472	U1408	U1341		U1197	U1122	U976	U976	U976
	C1919	A1854	U1775	U1690	U1625	U1556	U1473	U1409	C1342	C1272	U1198	G1126	C977	C977	A914
	C1920	A1855	U1776	U1691	U1626	U1557	U1474	U1410	G1343	G1281	C1199	U1051	U978	U978	A915
	C1921	A1856	U1777	U1692	U1627	U1558	U1475	U1411	G1344	U1282	U1201	A1053	U979	U979	G916
	C1922	A1857	U1778	U1693	U1628	U1559	U1476	U1412	G1345		A1202	A1054	A980	A980	A917
	C1923	A1858	U1779	U1694	U1629	U1560	U1477	U1413	U1346	G1283	U1202	A1055	C981	C981	U919
	C1924	A1859	U1780	U1695	U1630	U1561	U1478	U1414	U1347	U1284	A1203	A1056	C982	C982	U919
	C1925	A1860	U1781	U1696	U1631	U1562	U1479	U1415	U1348	U1285	A1204	A1057	A983	A983	A920
	C1926	A1861	U1782	U1697	U1632	U1563	U1480	U1416	U1349	U1286	A1205	A1058	A984	A984	A921
	C1927	A1862	U1783	U1698	U1633	U1564	U1481	U1417	U1350	U1287			U985	U985	U922
	C1928	U1863	U1784	U1699	U1634	U1565	U1482	U1418	U1351	U1288					
	C1929	A1864	U1785	U1700	G1634	U1566	U1483	U1419		U1289					
	C1930	A1865	U1786	U1701	G1635	U1567	U1484	U1420							
	C1931	A1866	U1787	U1702	G1636	U1568	U1485	U1421							
	C1932	A1867	U1788	U1703	G1637	U1569	U1486	U1422							
	C1933	A1868	U1789	U1704	G1638	U1570	U1487	U1423							
	C1934	A1869	U1790	U1705	G1639	U1571	U1488	U1424							
	C1935	A1870	U1791	U1706	G1640	U1572	U1489	U1425							
	C1936	A1871	U1792	U1707	G1641	U1573	U1490	U1426							
	C1937	A1872	U1793	U1708	G1642	U1574	U1491	U1427							
	C1938	A1873	U1794	U1709	G1643	U1575	U1492	U1428							
	C1939	A1874	U1795	U1710	G1644	U1576	U1493	U1429							
	C1940	A1875	U1796	U1711	G1645	U1577	U1494	U1430							
	C1941	A1876	U1797	U1712	G1646	U1578	U1495	U1431							
	C1942	A1877	U1798	U1713	G1647	U1579	U1496	U1432							
	C1943	A1878	U1799	U1714	G1648	U1580	U1497	U1433							
	C1944	A1879	U1800	U1715	G1649	U1581	U1498	U1434							
	C1945	A1880	U1801	U1716	G1650	U1582	U1499	U1435							
	C1946	A1881	U1802	U1717	G1651	U1583	U1500	U1436							
	C1947	A1882	U1803	U1718	G1652	U1584	U1501	U1437							
	C1948	A1883	U1804	U1719	G1653	U1585	U1502	U1438							
	C1949	A1884	U1805	U1720	G1654	U1586	U1503	U1439							
	C1950	A1885	U1806	U1721	G1655	U1587	U1504	U1440							
	C1951	A1886	U1807	U1722	G1656	U1588	U1505	U1441							
	C1952	A1887	U1808	U1723	G1657	U1589	U1506	U1442							
	C1953	A1888	U1809	U1724	G1658	U1590	U1507	U1443							
	C1954	A1889	U1810	U1725	G1659	U1591	U1508	U1444							
	C1955	A1890	U1811	U1726	G1660	U1592	U1509	U1445							
	C1956	A1891	U1812	U1727	G1661	U1593	U1510	U1446							
	C1957	A1892	U1813	U1728	G1662	U1594	U1511	U1447							
	C1958	A1893	U1814	U1729	G1663	U1595	U1512	U1448							
	C1959	A1894	U1815	U1730	G1664	U1596	U1513	U1449							
	C1960	A1895	U1816	U1731	G1665	U1597	U1514	U1450							

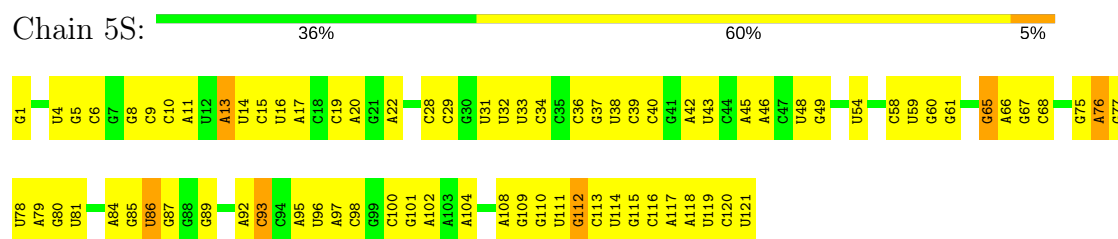


• Molecule 2: 5.8S ribosomal RNA



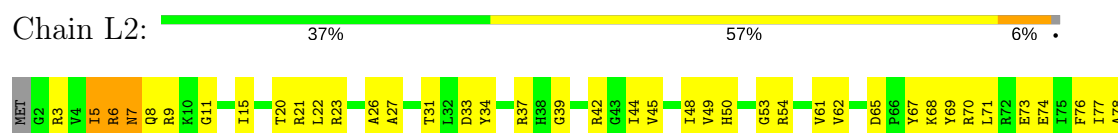
• Molecule 3: 5S ribosomal RNA

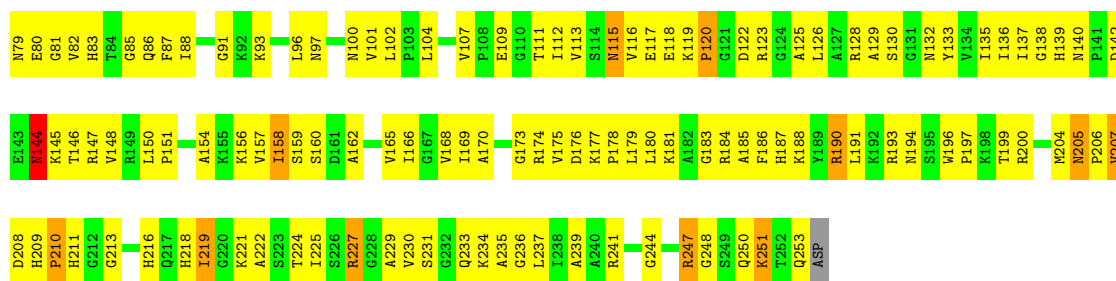


• Molecule 4: 60S ribosomal protein L1



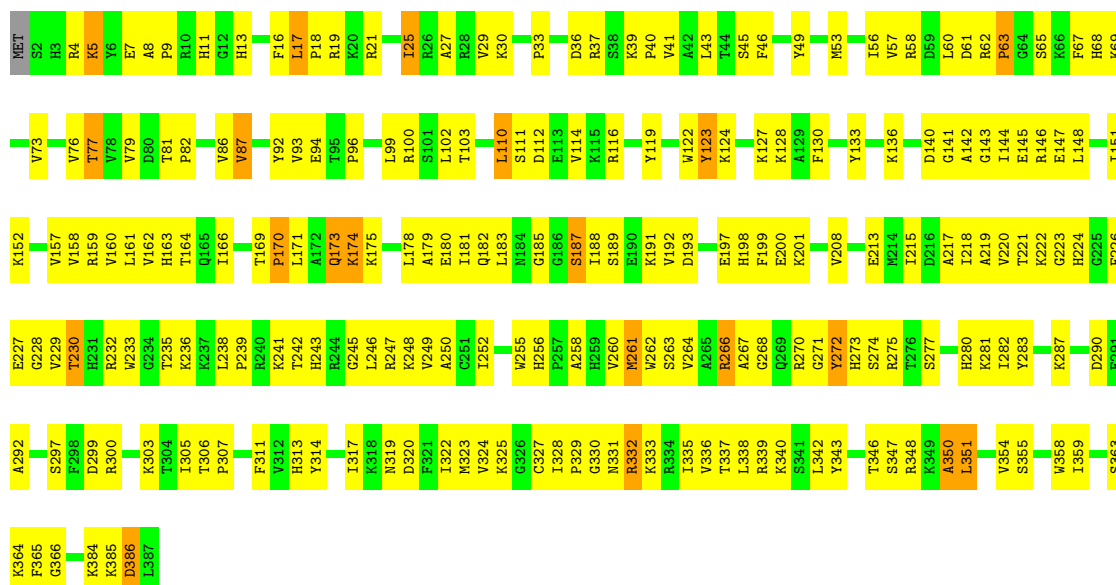
• Molecule 5: 60S ribosomal protein L2





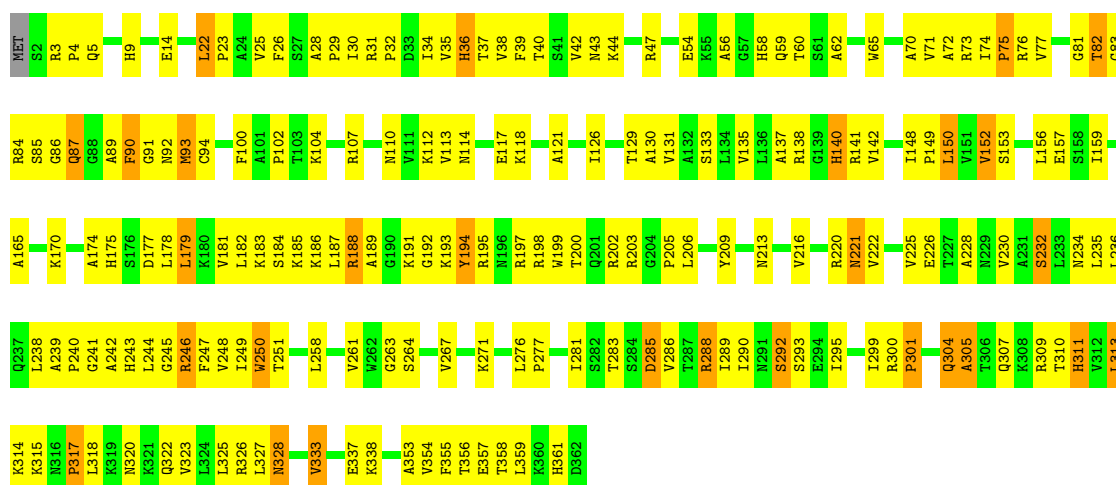
• Molecule 6: 60S ribosomal protein L3

Chain L3: 44% 51% 5%

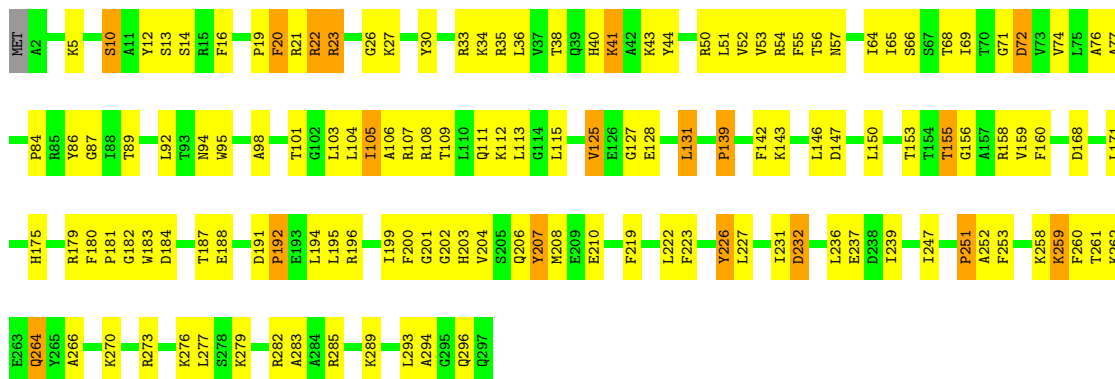


• Molecule 7: 60S ribosomal protein L4

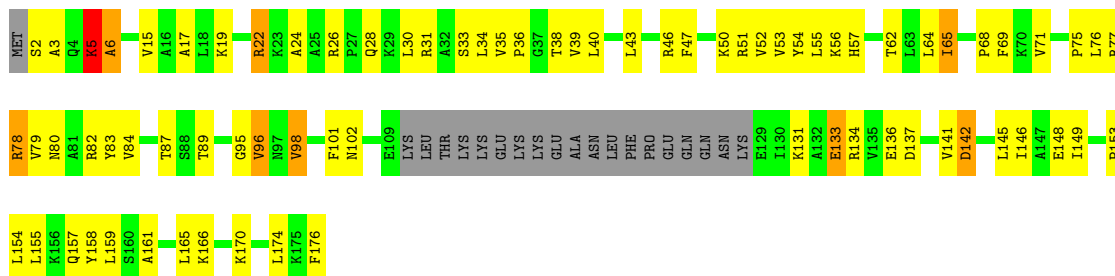
Chain L4: 47% 45% 8%



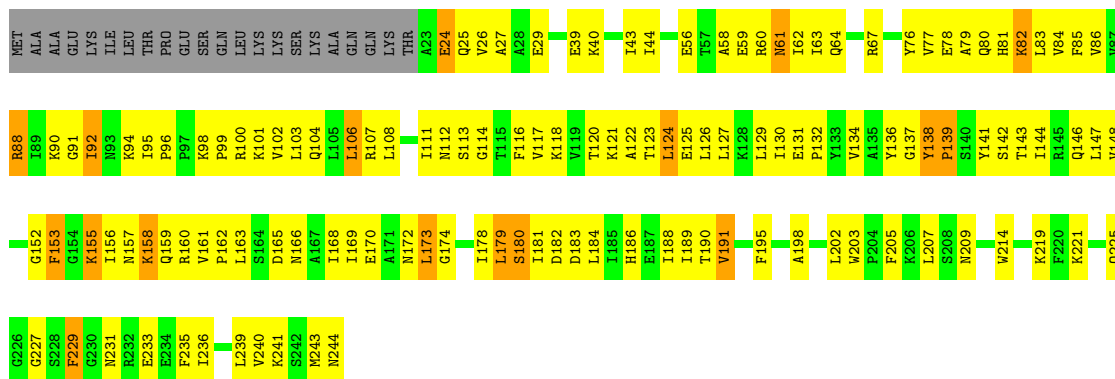
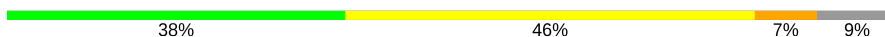
• Molecule 8: 60S ribosomal protein L5



- Molecule 9: 60S ribosomal protein L6

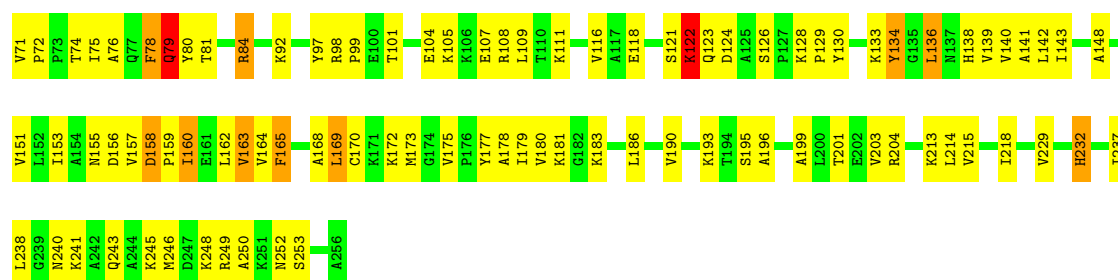


- Molecule 10: 60S ribosomal protein L7



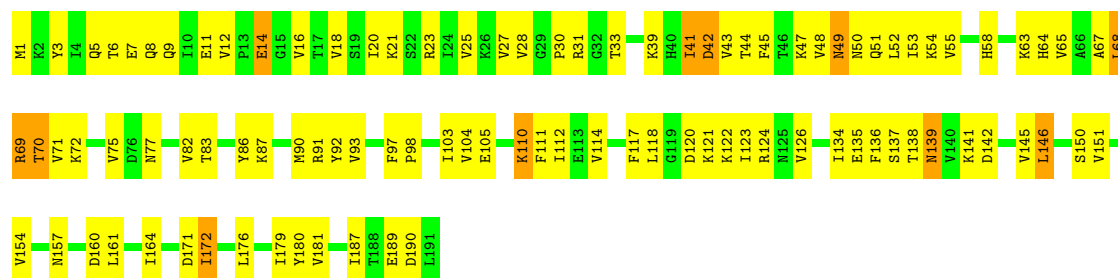
- Molecule 11: 60S ribosomal protein L8





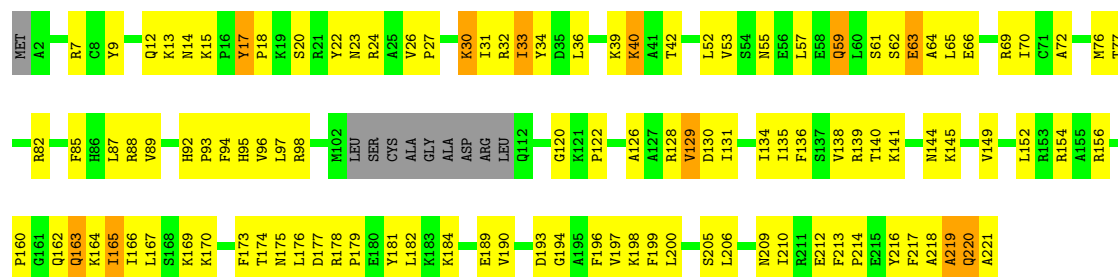
• Molecule 12: 60S ribosomal protein L9

Chain L9: 48% 46% 6%



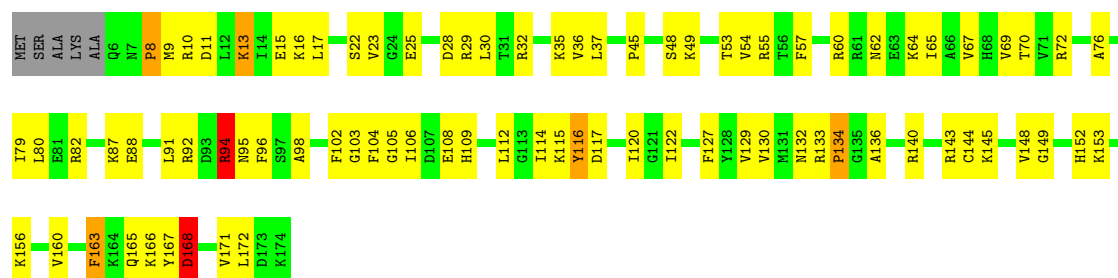
• Molecule 13: 60S ribosomal protein L10

Chain 50: 45% 46% 5% 5%



• Molecule 14: 60S ribosomal protein L11

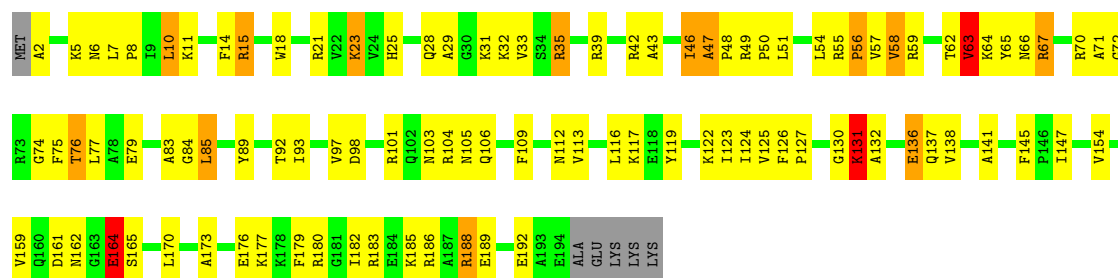
Chain 51: 49% 44%



• Molecule 15: 60S ribosomal protein L13

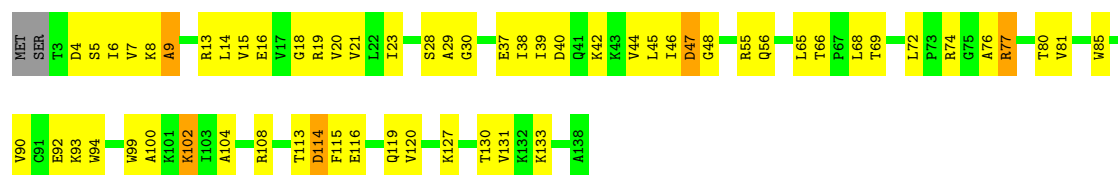
Chain 53: 46% 43% 7%





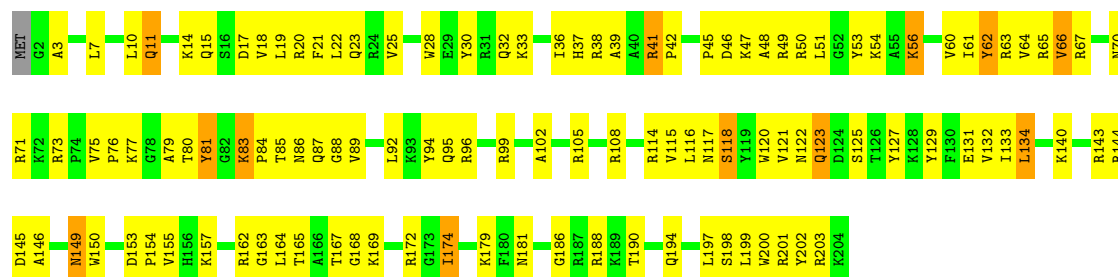
• Molecule 16: 60S ribosomal protein L14

Chain 54: 55% 40% ..



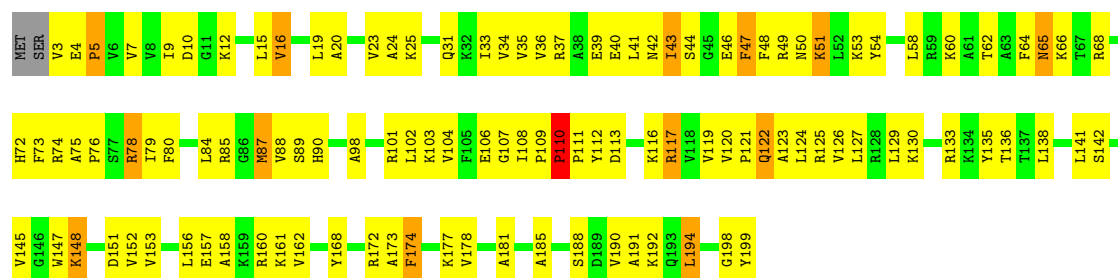
• Molecule 17: 60S ribosomal protein L15

Chain 55: 43% 50% 6% ..



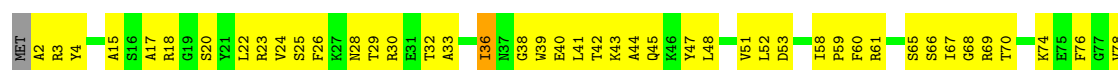
• Molecule 18: 60S ribosomal protein L16

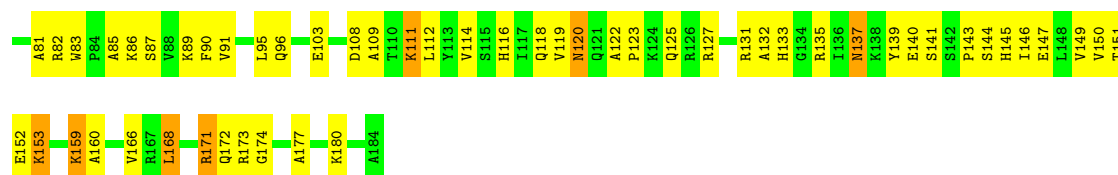
Chain 56: 42% 50% 7% ..



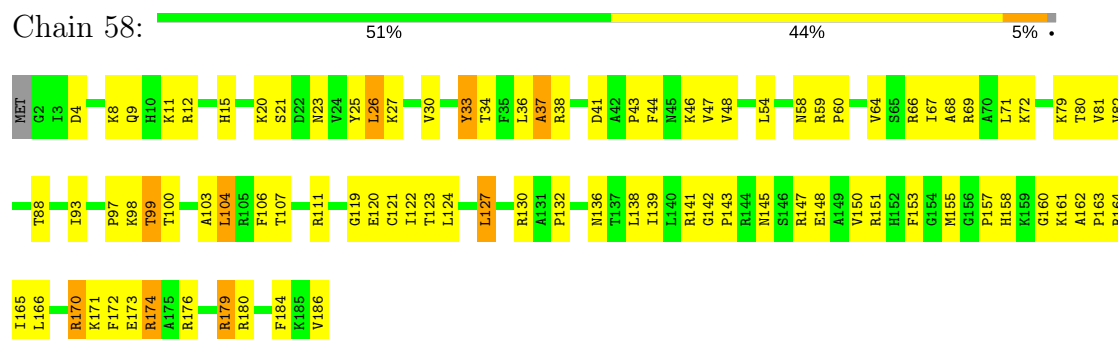
• Molecule 19: 60S ribosomal protein L17

Chain 57: 47% 48% ..

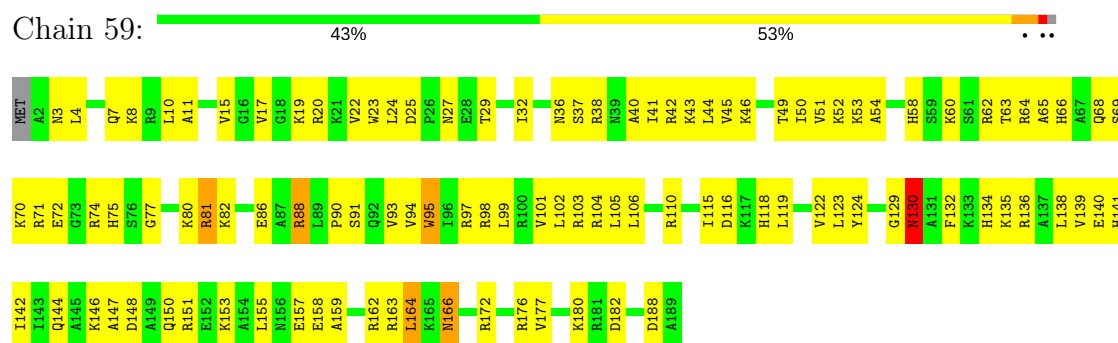




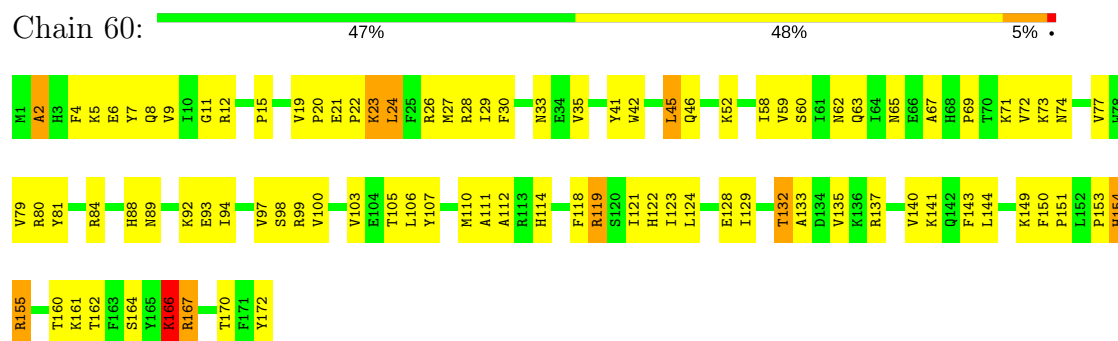
- Molecule 20: 60S ribosomal protein L18



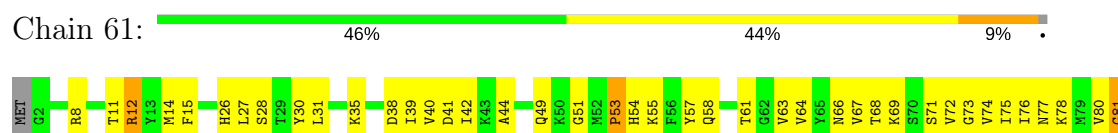
- Molecule 21: 60S ribosomal protein L19



- Molecule 22: 60S ribosomal protein L20



- Molecule 23: 60S ribosomal protein L21

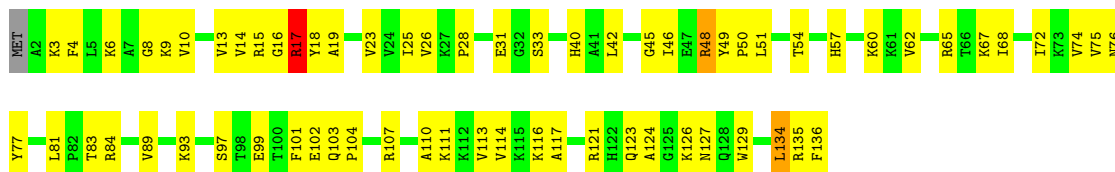






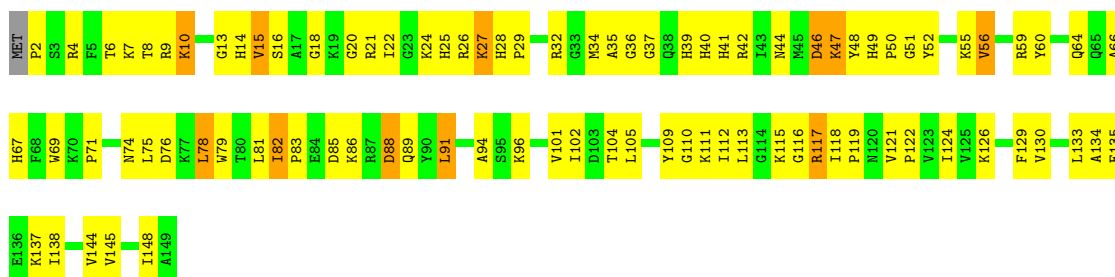
• Molecule 29: 60S ribosomal protein L27

Chain 67: 51% 46% ...



• Molecule 30: 60S ribosomal protein L28

Chain 68: 39% 53% 7% •



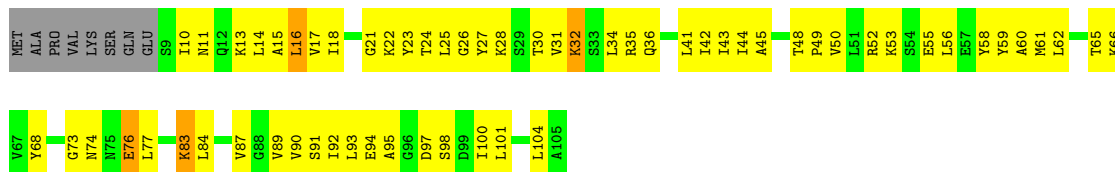
• Molecule 31: 60S ribosomal protein L29

Chain 69: 42% 47% 8% •



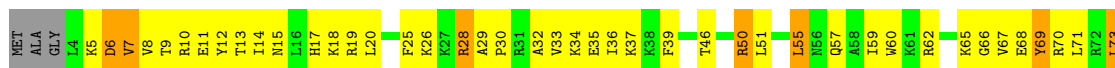
• Molecule 32: 60S ribosomal protein L30

Chain 70: 34% 54% 8% •



• Molecule 33: 60S ribosomal protein L31

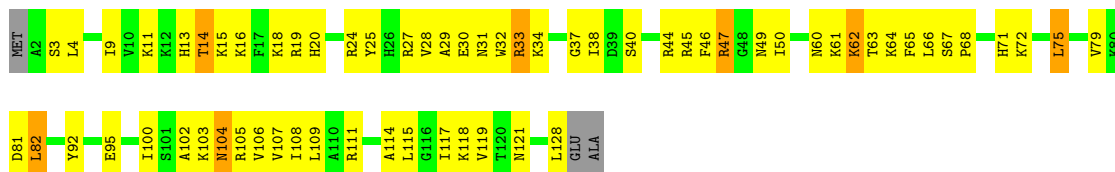
Chain 71: 40% 50% 7% •





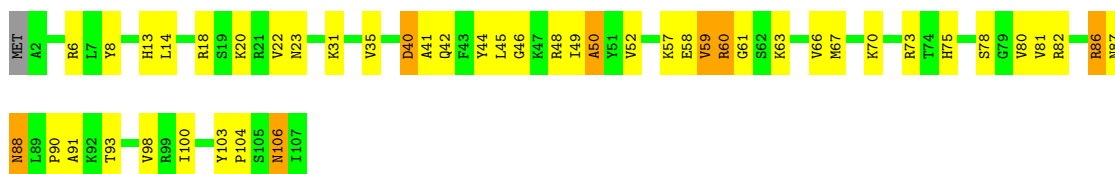
• Molecule 34: 60S ribosomal protein L32

Chain 72: 48% 44% 5%



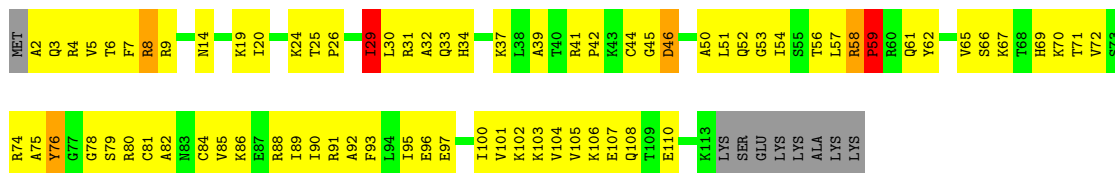
• Molecule 35: 60S ribosomal protein L33

Chain 73: 56% 36% 7%



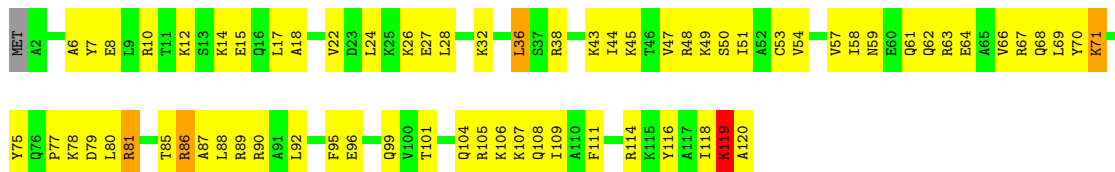
• Molecule 36: 60S ribosomal protein L34

Chain 74: 31% 57% 7%



• Molecule 37: 60S ribosomal protein L35

Chain 75: 42% 53% 2%



• Molecule 38: 60S ribosomal protein L36

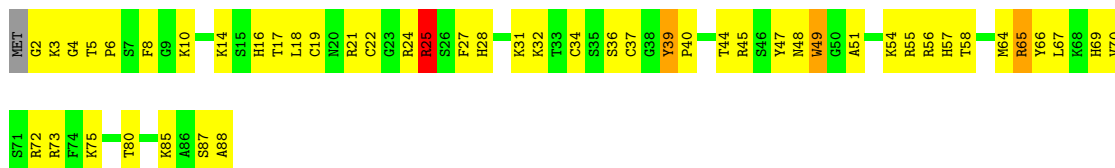
Chain 76: 52% 43% 2%





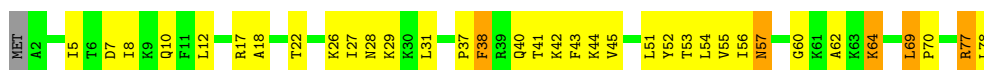
• Molecule 39: 60S ribosomal protein L37

Chain 77: 43% 51% 6%



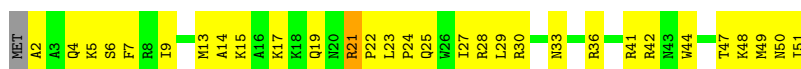
• Molecule 40: 60S ribosomal protein L38

Chain 78: 54% 38% 6%



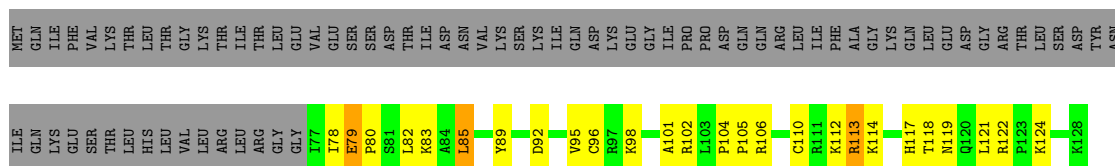
• Molecule 41: 60S ribosomal protein L39

Chain 79: 39% 57% 4%



• Molecule 42: 60S ribosomal protein L40

Chain 80: 20% 18% 62%



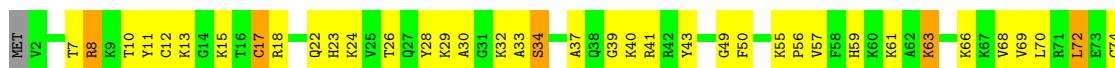
• Molecule 43: 60S ribosomal protein L41

Chain 81: 56% 36% 8%



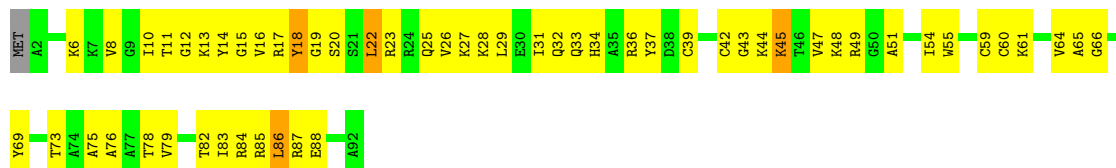
• Molecule 44: 60S ribosomal protein L42

Chain 82: 48% 41% 11%

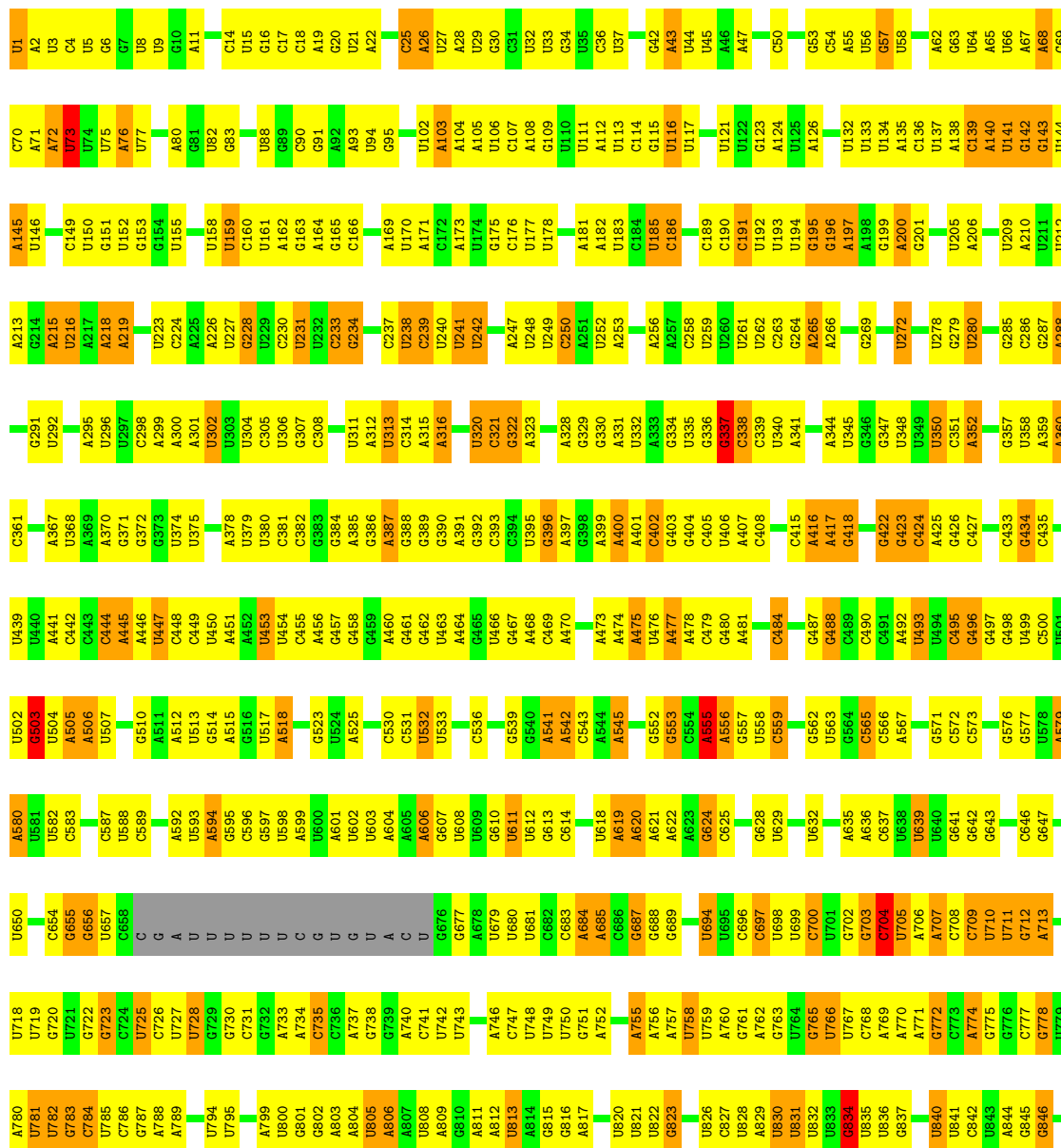


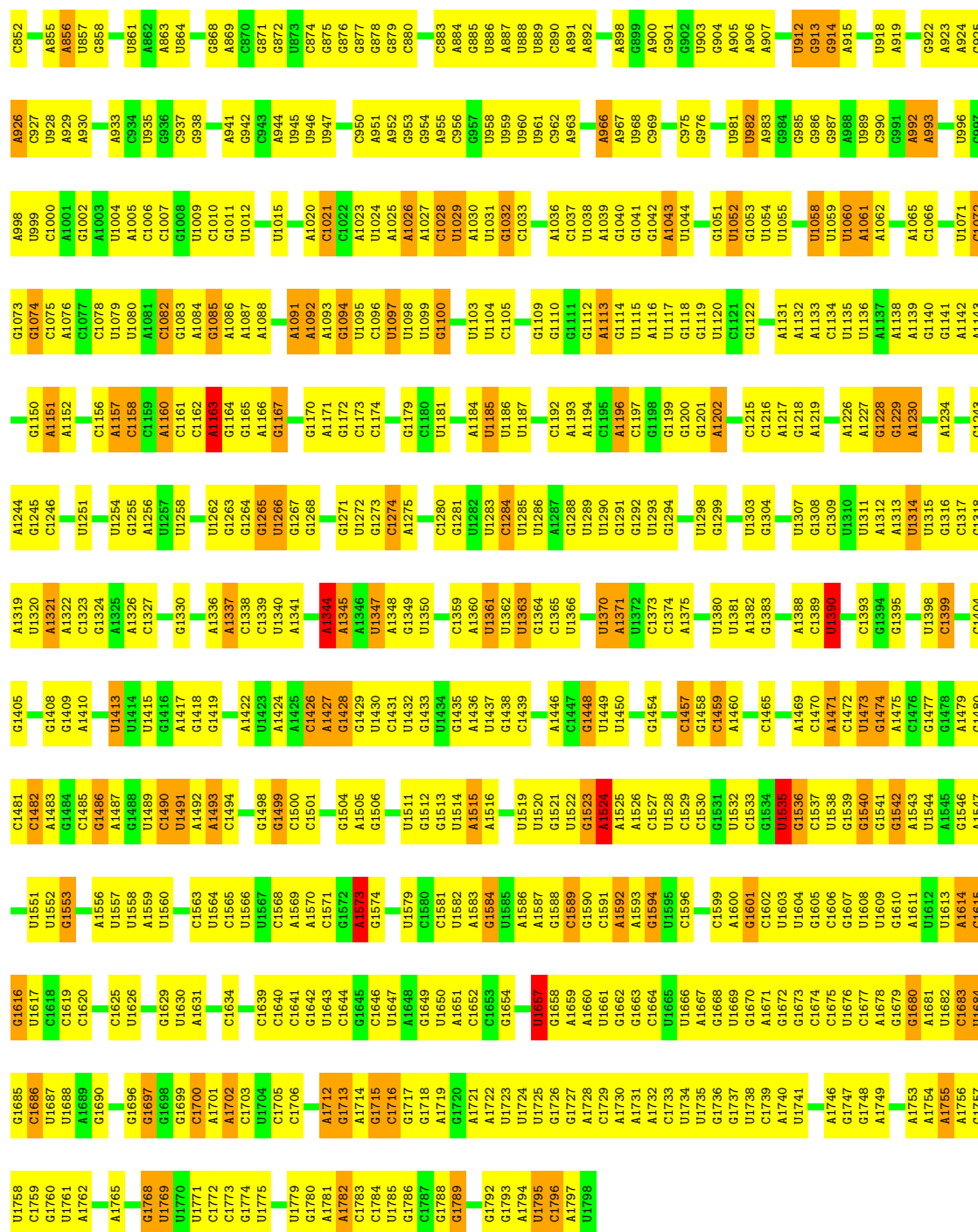


- Molecule 45: 60S ribosomal protein L43

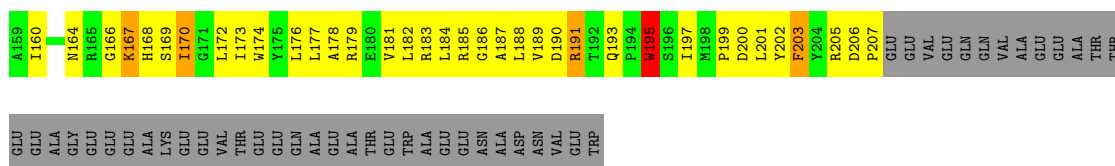


- Molecule 46: 18S ribosomal RNA

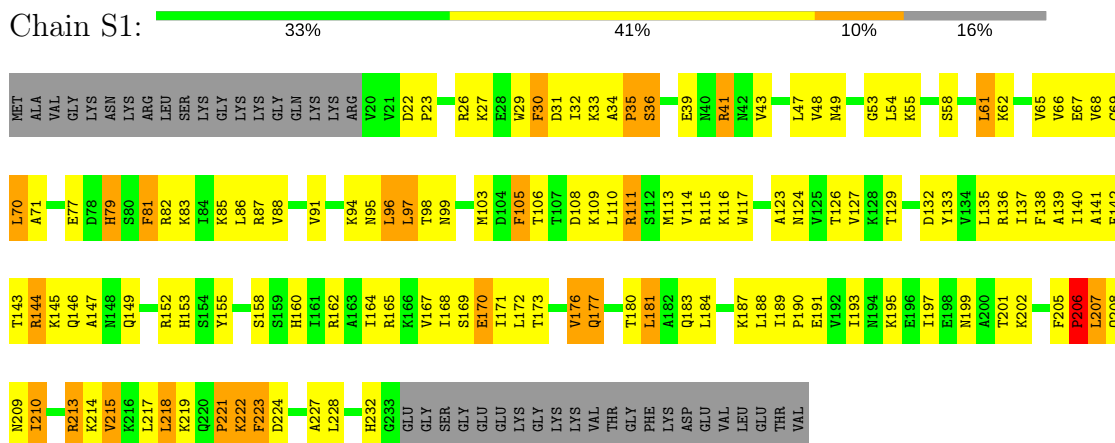




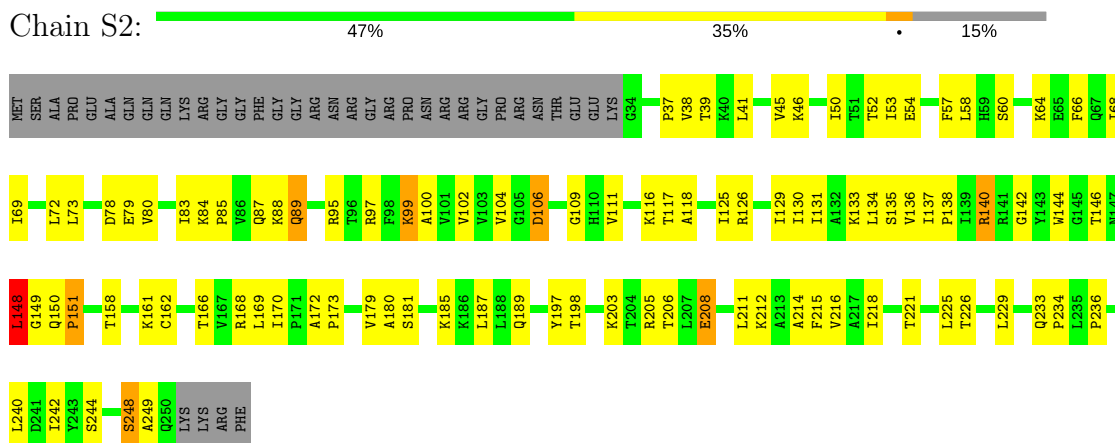




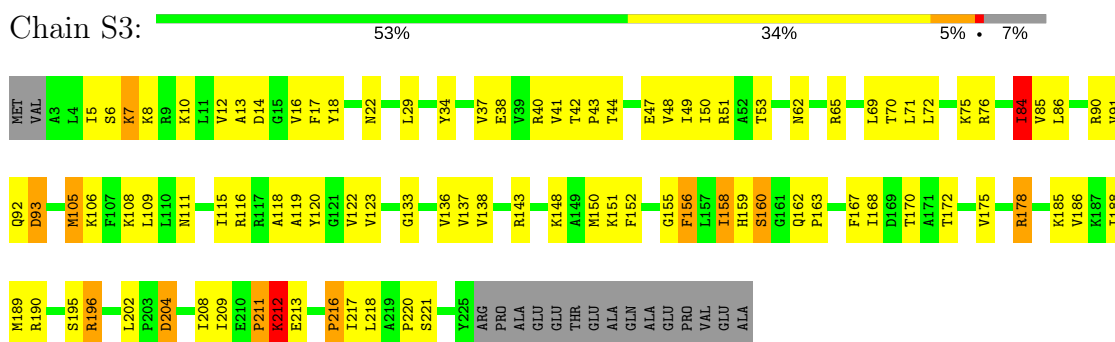
- Molecule 48: 40S ribosomal protein S1



- Molecule 49: 40S ribosomal protein S2

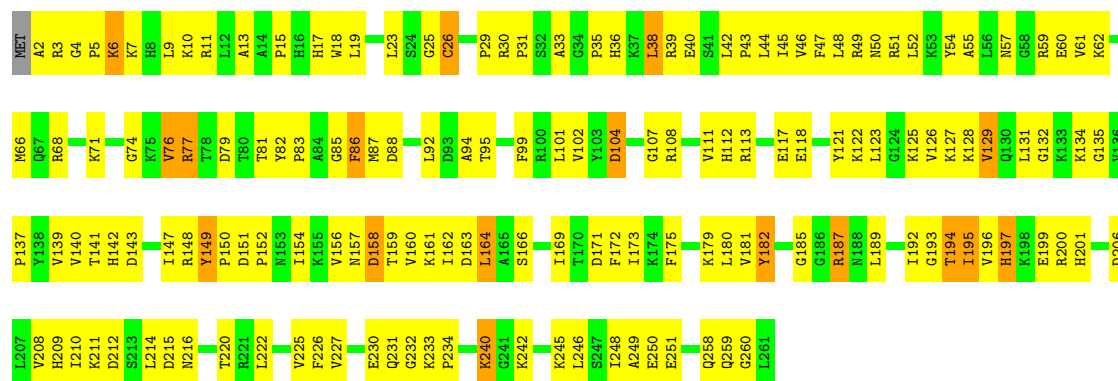


- Molecule 50: 40S ribosomal protein S3



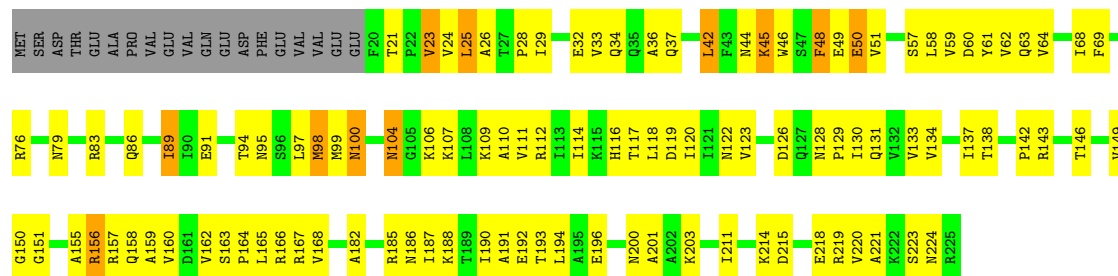
- Molecule 51: 40S ribosomal protein S4

Chain S4: 



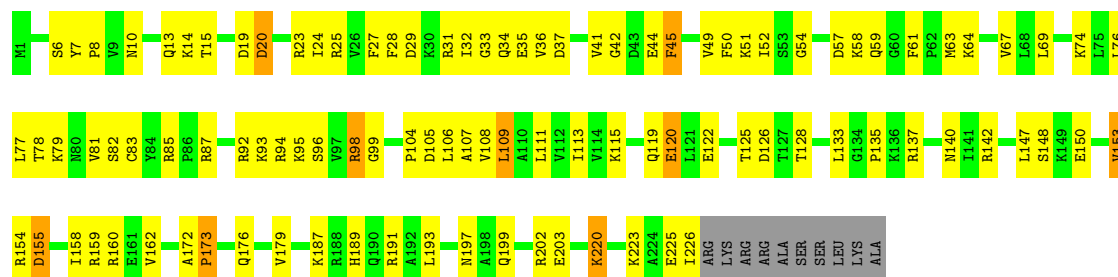
• Molecule 52: 40S ribosomal protein S5

Chain S5: 



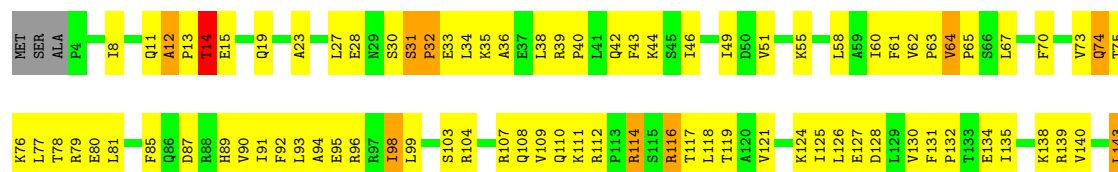
• Molecule 53: 40S ribosomal protein S6

Chain S6: 



• Molecule 54: 40S ribosomal protein S7

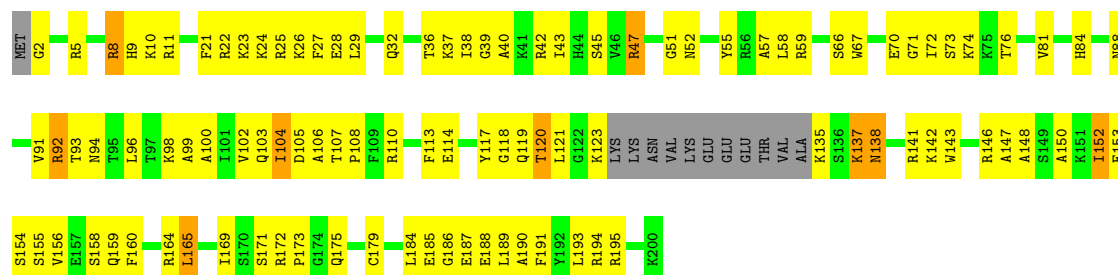
Chain S7: 





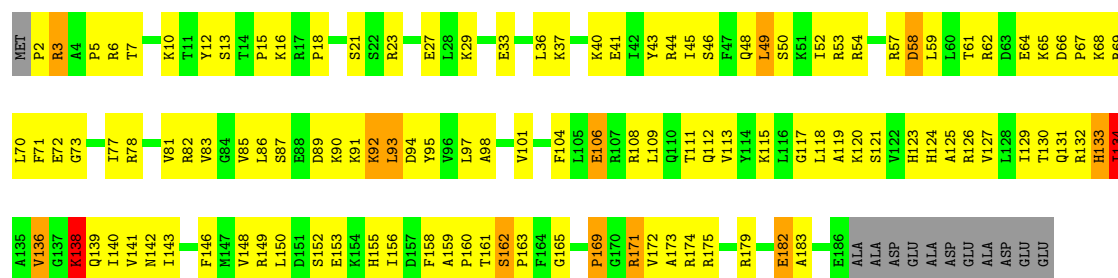
• Molecule 55: 40S ribosomal protein S8

Chain S8: 43% 47% 5% 6%



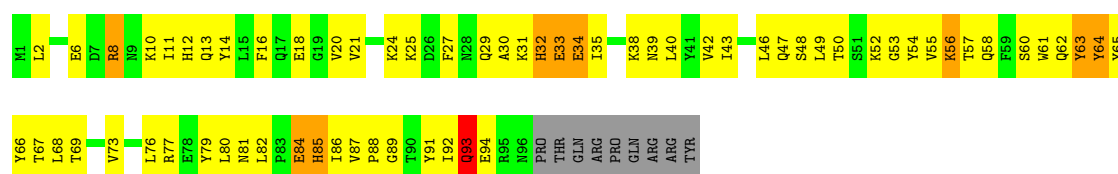
• Molecule 56: 40S ribosomal protein S9

Chain S9: 34% 53% 6% 6%



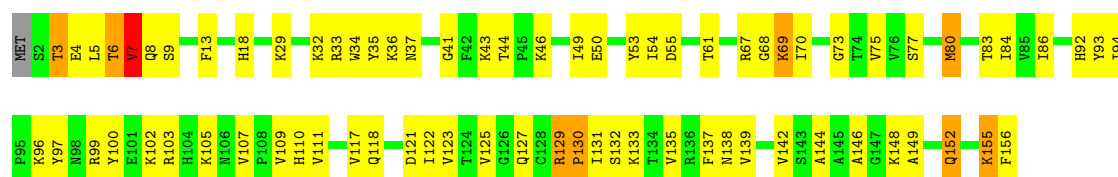
• Molecule 57: 40S ribosomal protein S10

Chain 10: 29% 53% 9% 9%



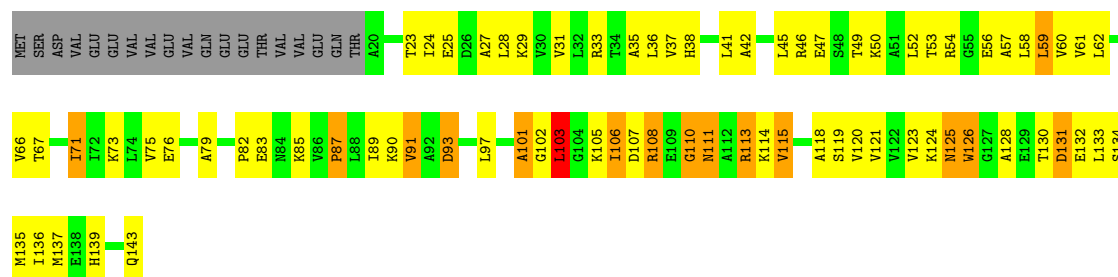
• Molecule 58: 40S ribosomal protein S11

Chain 11: 51% 42% 5% ..



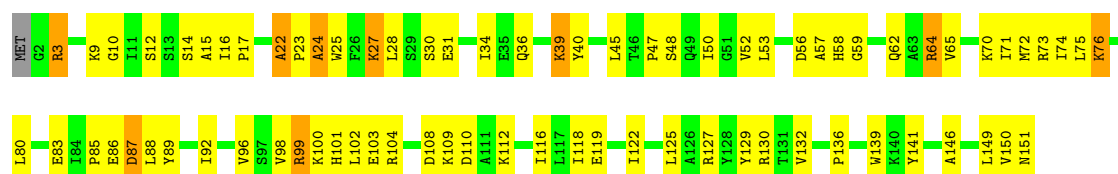
• Molecule 59: 40S ribosomal protein S12

Chain 12: 



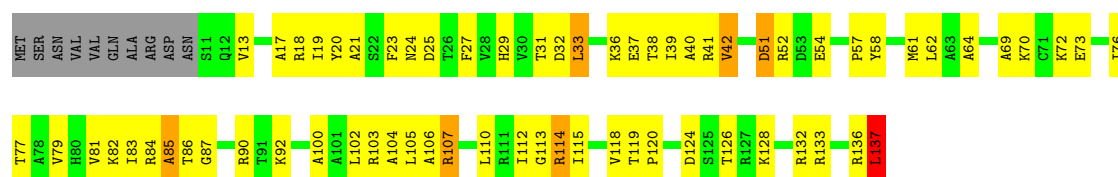
- Molecule 60: 40S ribosomal protein S13

Chain 13: 



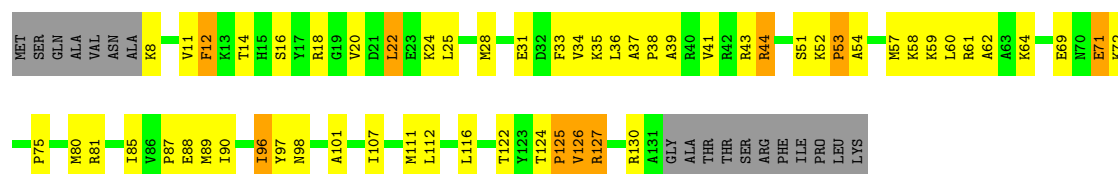
- Molecule 61: 40S ribosomal protein S14

Chain 14: 




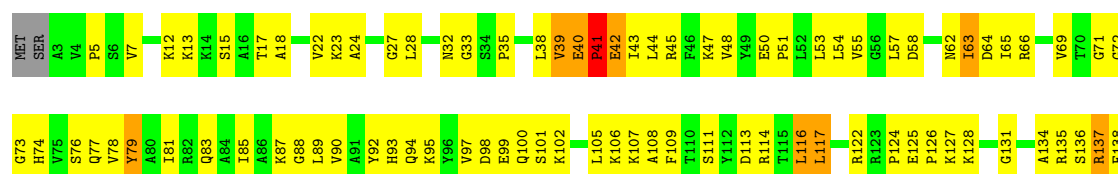
- Molecule 62: 40S ribosomal protein S15

Chain 15: 



- Molecule 63: 40S ribosomal protein S16

Chain 16: 



Q139  
K140  
S141  
Y142  
R143

• Molecule 64: 40S ribosomal protein S17

Chain 17: 38% 40% 10% 12%

MET G2 G3 V4 T6 T7 T8 T9 K10 R11 R12 S13 S14 K14 A15 A16 L17 L18 ASP L19 LEU Y20 Y21 P22 P23 K24 L24 D27 F28 Q29 Q30 T30 Q31 Q32 Q33 L34 C35 I38 A39 Q42 R45 L46 R47 R48 R49 I50 Y53 T54 T55 H56 L57 L58 I61 R67 G68 I69 S70 F71

K72 L73 Q74 R78 R79 R80 R81 R82 Q83 Q84 Y85 V88 S89 A89 LEU L18 ASP L19 LEU Y20 Y21 P22 P23 K24 L24 D27 F28 Q29 Q30 T30 Q31 Q32 Q33 L34 C35 I38 A39 Q42 R45 L46 R47 R48 R49 I50 Y53 T54 T55 H56 L57 L58 I61 R67 G68 I69 S70 F71

• Molecule 65: 40S ribosomal protein S18

Chain 18: 42% 48% 8% ..

MET S2 L3 V4 V5 Q6 E7 Q8 Q9 F11 I14 L15 L16 L17 L18 L19 N19 T20 N21 V22 N25 I26 I27 I28 I29 Y30 Y31 A31 L32 L33 I35 K36 G37 V38 G39 R40 R41 Y42 S43 M44 L45 V46 D51 L54 H55 K56 R57 A58 G59 L61 E67 R68 I69 V70 Q71

I72 M73 Y79 P82 A83 A84 R85 R86 R87 R88 R89 R90 R91 R92 D97 T100 L101 A102 V105 K108 D112 R115 L116 I119 R120 R123 R126 W129 G130 L131 R132 V133 R134 G135 Q136 H137 T138 K139 T140 T141 R144 R145 A146

• Molecule 66: 40S ribosomal protein S19

Chain 19: 46% 49% 5% .

MET F2 G3 V4 V5 V6 R7 Q12 D13 F14 I15 I16 A17 Y18 F21 L22 L23 Q24 R24 Q25 Q26 K27 L28 E29 V30 F31 G32 Y33 V34 V37 K38 T39 S40 M43 E44 M45 P46 P47 Q48 Q49 A50 E51 G52 M53 F54 Y55 K56 R57 V61 A62 R63 R64 T65 R68 K69

Q70 V71 G72 L79 G82 R86 R89 P90 Y91 K92 H93 S97 G98 G99 I100 N101 K102 K103 V104 L105 L108 E109 K110 I111 G112 I113 V114 E115 P118 K119 E126 M127 G128 Q129 R130 D131 L132 I135 A136 A137 E141 E142 D143 E144

• Molecule 67: 40S ribosomal protein S20

Chain 20: 33% 49% 7% 12%

MET SER ASP PHE GLN LYS LYS VAL GLU GLU GLN Q15 Q16 Q17 Q18 Q19 I20 I21 I22 I23 I24 I25 S28 V31 K32 Q33 L34 L35 N36 V37 S38 N40 I41 V42 K43 E46 Q47 H48 L50 V51 K52 K53 G54 R57 L58 P59 T60 K61 V62 L63 K64

I65 S66 T67 R68 M72 G73 E74 W79 E80 E81 Y82 E83 R84 R85 R86 R87 R88 R89 Y90 I91 I92 I93 I94 I95 P96 V100 T104 Q105 I106 T107 T108 E109 P110 G111 V112 D113 V117 V118 A119 S120 R121

• Molecule 68: 40S ribosomal protein S21

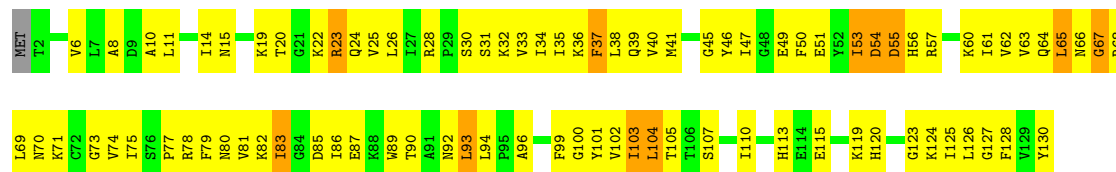
Chain 21: 49% 41% 9%

K1 E2 K5 G6 G7 L8 L9 V9 E10 E11 L12 Y13 V14 C17 N21 R22 S31 I34 K38 V39 D40 E41 G43 R44 A45 T46 E49 Y50 T51 T52 Y53 A54 L55 S56 R60 R61 R62 G63 E64 S65 A73 Q74 R75 D76 D77 L78 L79 R80 R81 R82 V83



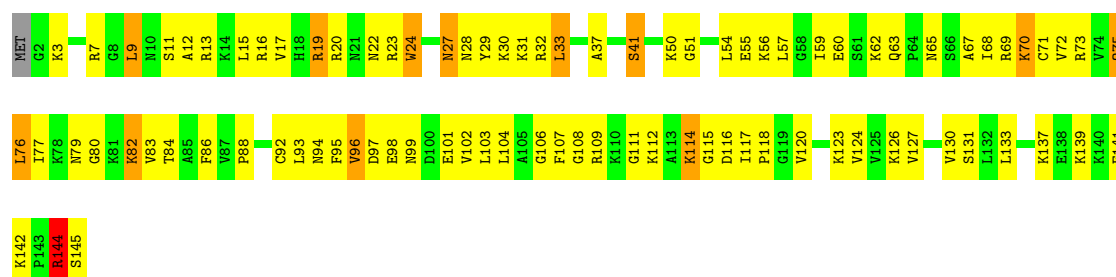
• Molecule 69: 40S ribosomal protein S22

Chain 22: 32% 59% 8% .



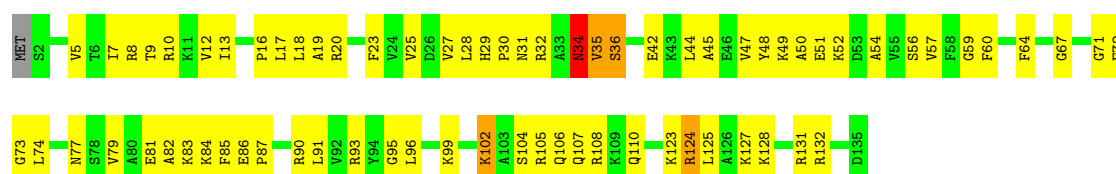
• Molecule 70: 40S ribosomal protein S23

Chain 23: 39% 52% 8% ..



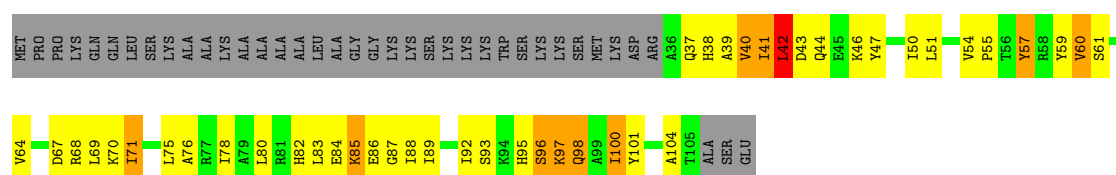
• Molecule 71: 40S ribosomal protein S24

Chain 24: 46% 50% ..



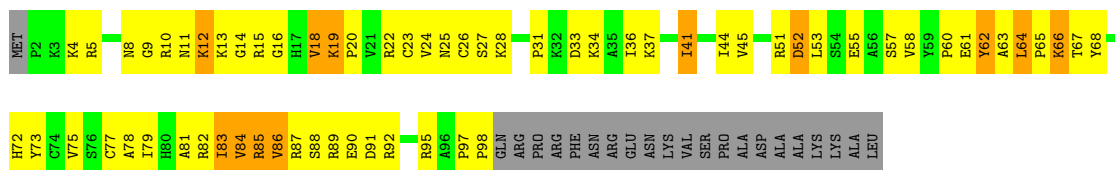
• Molecule 72: 40S ribosomal protein S25

Chain 25: 23% 31% 9% 35%



• Molecule 73: 40S ribosomal protein S26

Chain 26: 27% 45% 10% 18%



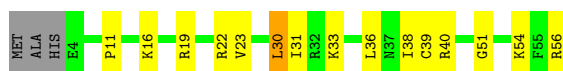
- Molecule 74: 40S ribosomal protein S27



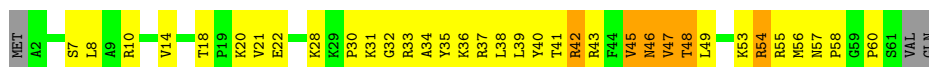
- Molecule 75: 40S ribosomal protein S28



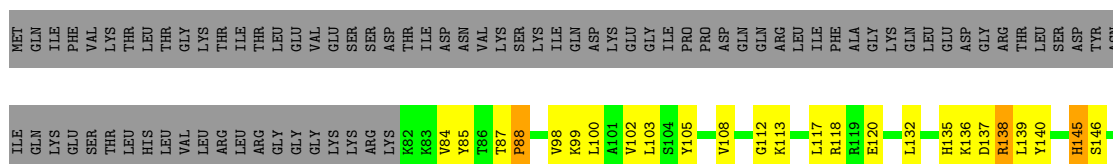
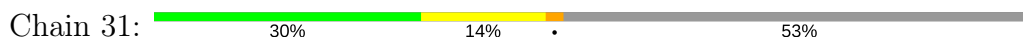
- Molecule 76: 40S ribosomal protein S29



- Molecule 77: 40S ribosomal protein S30

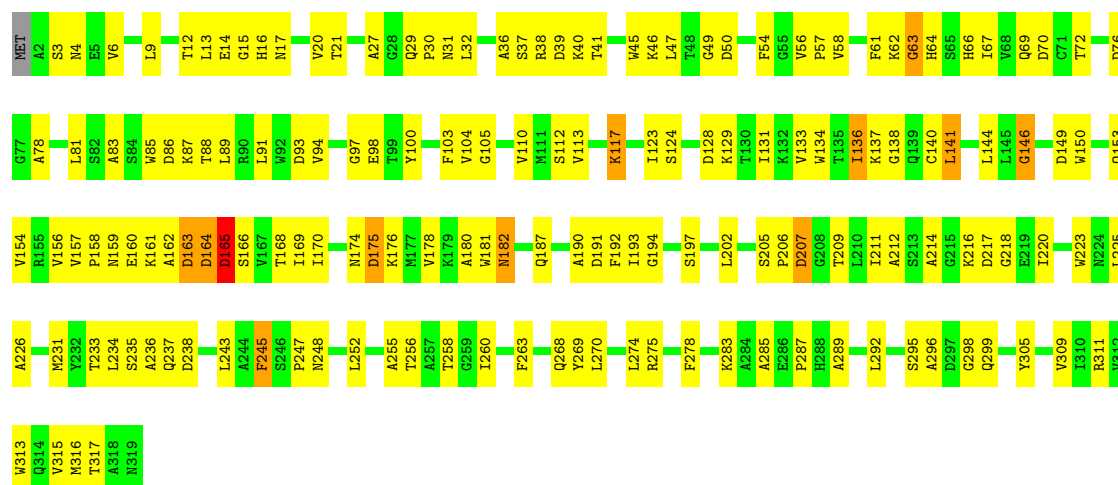


- Molecule 78: 40S ribosomal protein S31



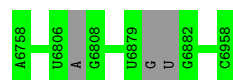
- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein





- Molecule 80: TSV IRES mRNA

Chain IR:  99%





## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	51373	Depositor
Resolution determination method	FSC 0.143	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

## 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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	2S	0.83	7/79178 (0.0%)	0.75	31/123444 (0.0%)
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
2	8S	0.80	1/3747 (0.0%)	0.73	2/5832 (0.0%)
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
3	5S	0.79	1/2884 (0.0%)	0.71	0/4491
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%)
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
4	L1	0.59	0/1634	0.71	0/2195

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
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
5	L2	0.50	0/1952	0.65	0/2622
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%)
6	L3	0.57	0/3153	0.64	1/4239 (0.0%)
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
7	L4	0.58	0/2802	0.67	0/3792
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
78	31	0.57	0/505	0.71	1/682 (0.1%)
79	RA	0.54	0/2498	0.61	0/3398

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
8	L5	0.58	0/2426	0.61	0/3271
9	L6	0.62	0/1261	0.68	0/1694
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
46:1S:845:G:H2'	46:1S:846:G:H5''	1.32	1.11
19:57:122:ALA:HB3	19:57:143:PRO:HB2	1.23	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	15
5	L2	250/254 (98%)	199 (80%)	41 (16%)	10 (4%)	3	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	L3	384/387 (99%)	321 (84%)	52 (14%)	11 (3%)	5	38
7	L4	359/362 (99%)	290 (81%)	47 (13%)	22 (6%)	2	22
8	L5	294/297 (99%)	240 (82%)	41 (14%)	13 (4%)	3	29
9	L6	152/176 (86%)	132 (87%)	16 (10%)	4 (3%)	6	40
10	L7	220/244 (90%)	196 (89%)	19 (9%)	5 (2%)	7	43
11	L8	231/256 (90%)	190 (82%)	31 (13%)	10 (4%)	3	29
12	L9	189/191 (99%)	157 (83%)	27 (14%)	5 (3%)	6	40
13	50	207/221 (94%)	173 (84%)	30 (14%)	4 (2%)	9	47
14	51	167/174 (96%)	131 (78%)	27 (16%)	9 (5%)	2	25
15	53	191/199 (96%)	152 (80%)	25 (13%)	14 (7%)	1	19
16	54	134/138 (97%)	114 (85%)	14 (10%)	6 (4%)	3	28
17	55	201/204 (98%)	168 (84%)	28 (14%)	5 (2%)	6	40
18	56	195/199 (98%)	175 (90%)	15 (8%)	5 (3%)	6	40
19	57	181/184 (98%)	150 (83%)	26 (14%)	5 (3%)	6	39
20	58	183/186 (98%)	154 (84%)	25 (14%)	4 (2%)	8	44
21	59	186/189 (98%)	166 (89%)	16 (9%)	4 (2%)	8	44
22	60	170/172 (99%)	139 (82%)	26 (15%)	5 (3%)	5	38
23	61	157/160 (98%)	126 (80%)	19 (12%)	12 (8%)	1	18
24	62	98/121 (81%)	83 (85%)	12 (12%)	3 (3%)	5	36
25	63	134/137 (98%)	113 (84%)	20 (15%)	1 (1%)	25	68
26	64	59/155 (38%)	44 (75%)	14 (24%)	1 (2%)	11	50
27	65	119/142 (84%)	100 (84%)	16 (13%)	3 (2%)	6	40
28	66	124/127 (98%)	110 (89%)	13 (10%)	1 (1%)	22	66
29	67	133/136 (98%)	106 (80%)	23 (17%)	4 (3%)	5	37
30	68	146/149 (98%)	110 (75%)	27 (18%)	9 (6%)	2	22
31	69	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	10	48
32	70	95/105 (90%)	89 (94%)	5 (5%)	1 (1%)	17	59
33	71	107/113 (95%)	84 (78%)	20 (19%)	3 (3%)	6	39
34	72	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
35	73	104/107 (97%)	80 (77%)	21 (20%)	3 (3%)	5	38
36	74	110/121 (91%)	92 (84%)	14 (13%)	4 (4%)	4	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	75	117/120 (98%)	108 (92%)	8 (7%)	1 (1%)	20	63
38	76	97/100 (97%)	81 (84%)	14 (14%)	2 (2%)	8	45
39	77	85/88 (97%)	70 (82%)	13 (15%)	2 (2%)	7	42
40	78	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
41	79	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	8	45
42	80	50/128 (39%)	40 (80%)	9 (18%)	1 (2%)	9	46
43	81	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
44	82	101/106 (95%)	88 (87%)	9 (9%)	4 (4%)	3	31
45	83	89/92 (97%)	74 (83%)	11 (12%)	4 (4%)	3	28
47	S0	204/252 (81%)	163 (80%)	30 (15%)	11 (5%)	2	25
48	S1	212/255 (83%)	152 (72%)	41 (19%)	19 (9%)	1	15
49	S2	215/254 (85%)	178 (83%)	27 (13%)	10 (5%)	3	28
50	S3	221/240 (92%)	181 (82%)	29 (13%)	11 (5%)	2	27
51	S4	258/261 (99%)	214 (83%)	35 (14%)	9 (4%)	4	34
52	S5	204/225 (91%)	164 (80%)	30 (15%)	10 (5%)	2	27
53	S6	224/236 (95%)	193 (86%)	25 (11%)	6 (3%)	6	39
54	S7	182/190 (96%)	138 (76%)	29 (16%)	15 (8%)	1	16
55	S8	184/200 (92%)	151 (82%)	29 (16%)	4 (2%)	8	44
56	S9	183/197 (93%)	153 (84%)	21 (12%)	9 (5%)	2	27
57	10	94/105 (90%)	75 (80%)	13 (14%)	6 (6%)	1	22
58	11	153/156 (98%)	108 (71%)	36 (24%)	9 (6%)	2	23
59	12	122/143 (85%)	85 (70%)	23 (19%)	14 (12%)	0	8
60	13	148/151 (98%)	123 (83%)	22 (15%)	3 (2%)	9	46
61	14	125/137 (91%)	95 (76%)	24 (19%)	6 (5%)	2	27
62	15	122/142 (86%)	90 (74%)	22 (18%)	10 (8%)	1	16
63	16	139/143 (97%)	114 (82%)	18 (13%)	7 (5%)	2	27
64	17	116/136 (85%)	98 (84%)	14 (12%)	4 (3%)	4	34
65	18	143/146 (98%)	115 (80%)	19 (13%)	9 (6%)	1	22
66	19	141/144 (98%)	117 (83%)	20 (14%)	4 (3%)	6	39
67	20	105/121 (87%)	88 (84%)	13 (12%)	4 (4%)	4	32
68	21	85/87 (98%)	69 (81%)	10 (12%)	6 (7%)	1	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	22	127/130 (98%)	108 (85%)	16 (13%)	3 (2%)	7	42
70	23	142/145 (98%)	102 (72%)	32 (22%)	8 (6%)	2	24
71	24	132/135 (98%)	103 (78%)	23 (17%)	6 (4%)	3	28
72	25	68/108 (63%)	46 (68%)	16 (24%)	6 (9%)	1	15
73	26	95/119 (80%)	62 (65%)	21 (22%)	12 (13%)	0	7
74	27	79/82 (96%)	59 (75%)	16 (20%)	4 (5%)	2	26
75	28	61/67 (91%)	50 (82%)	10 (16%)	1 (2%)	11	51
76	29	51/56 (91%)	44 (86%)	5 (10%)	2 (4%)	3	31
77	30	58/63 (92%)	42 (72%)	11 (19%)	5 (9%)	1	15
78	31	69/152 (45%)	42 (61%)	18 (26%)	9 (13%)	0	6
79	RA	316/319 (99%)	250 (79%)	53 (17%)	13 (4%)	3	30
All	All	11126/12097 (92%)	9048 (81%)	1604 (14%)	474 (4%)	6	29

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%)	12	42
5	L2	194/196 (99%)	181 (93%)	13 (7%)	19	51
6	L3	322/323 (100%)	301 (94%)	21 (6%)	20	52
7	L4	288/289 (100%)	268 (93%)	20 (7%)	18	50
8	L5	244/245 (100%)	225 (92%)	19 (8%)	15	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	L6	134/153 (88%)	126 (94%)	8 (6%)	22	55
10	L7	186/205 (91%)	172 (92%)	14 (8%)	16	48
11	L8	191/208 (92%)	174 (91%)	17 (9%)	11	39
12	L9	171/171 (100%)	159 (93%)	12 (7%)	18	50
13	50	180/187 (96%)	165 (92%)	15 (8%)	13	43
14	51	147/150 (98%)	139 (95%)	8 (5%)	26	58
15	53	154/159 (97%)	137 (89%)	17 (11%)	7	30
16	54	107/109 (98%)	100 (94%)	7 (6%)	20	52
17	55	175/176 (99%)	162 (93%)	13 (7%)	16	48
18	56	160/162 (99%)	145 (91%)	15 (9%)	10	37
19	57	145/146 (99%)	136 (94%)	9 (6%)	21	54
20	58	150/151 (99%)	138 (92%)	12 (8%)	14	45
21	59	153/154 (99%)	139 (91%)	14 (9%)	11	38
22	60	156/156 (100%)	145 (93%)	11 (7%)	17	49
23	61	136/137 (99%)	125 (92%)	11 (8%)	14	44
24	62	87/107 (81%)	85 (98%)	2 (2%)	56	79
25	63	104/105 (99%)	94 (90%)	10 (10%)	10	35
26	64	54/129 (42%)	50 (93%)	4 (7%)	16	48
27	65	105/118 (89%)	95 (90%)	10 (10%)	10	36
28	66	109/110 (99%)	102 (94%)	7 (6%)	20	53
29	67	115/116 (99%)	111 (96%)	4 (4%)	41	69
30	68	118/119 (99%)	107 (91%)	11 (9%)	10	37
31	69	46/47 (98%)	40 (87%)	6 (13%)	5	25
32	70	81/88 (92%)	76 (94%)	5 (6%)	21	54
33	71	96/97 (99%)	88 (92%)	8 (8%)	13	43
34	72	109/111 (98%)	100 (92%)	9 (8%)	13	43
35	73	90/91 (99%)	83 (92%)	7 (8%)	15	46
36	74	95/103 (92%)	89 (94%)	6 (6%)	21	53
37	75	104/105 (99%)	95 (91%)	9 (9%)	12	40
38	76	81/82 (99%)	75 (93%)	6 (7%)	16	48
39	77	70/71 (99%)	64 (91%)	6 (9%)	12	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	78	68/69 (99%)	62 (91%)	6 (9%)	12	40
41	79	45/46 (98%)	41 (91%)	4 (9%)	11	39
42	80	47/116 (40%)	45 (96%)	2 (4%)	33	64
43	81	23/23 (100%)	18 (78%)	5 (22%)	1	7
44	82	88/91 (97%)	77 (88%)	11 (12%)	5	26
45	83	71/72 (99%)	68 (96%)	3 (4%)	34	64
47	S0	173/210 (82%)	163 (94%)	10 (6%)	23	56
48	S1	191/224 (85%)	173 (91%)	18 (9%)	10	37
49	S2	176/205 (86%)	170 (97%)	6 (3%)	42	69
50	S3	182/195 (93%)	168 (92%)	14 (8%)	15	47
51	S4	221/222 (100%)	199 (90%)	22 (10%)	9	33
52	S5	173/191 (91%)	163 (94%)	10 (6%)	23	56
53	S6	193/201 (96%)	184 (95%)	9 (5%)	30	62
54	S7	165/170 (97%)	154 (93%)	11 (7%)	19	51
55	S8	150/161 (93%)	142 (95%)	8 (5%)	26	59
56	S9	158/166 (95%)	146 (92%)	12 (8%)	15	47
57	10	89/98 (91%)	82 (92%)	7 (8%)	14	45
58	11	136/137 (99%)	127 (93%)	9 (7%)	19	52
59	12	100/119 (84%)	88 (88%)	12 (12%)	6	27
60	13	127/128 (99%)	114 (90%)	13 (10%)	8	33
61	14	96/105 (91%)	93 (97%)	3 (3%)	45	71
62	15	104/118 (88%)	96 (92%)	8 (8%)	15	47
63	16	117/119 (98%)	111 (95%)	6 (5%)	28	60
64	17	109/124 (88%)	94 (86%)	15 (14%)	4	23
65	18	128/129 (99%)	119 (93%)	9 (7%)	18	50
66	19	115/116 (99%)	103 (90%)	12 (10%)	8	32
67	20	100/114 (88%)	91 (91%)	9 (9%)	11	39
68	21	74/74 (100%)	70 (95%)	4 (5%)	26	58
69	22	110/111 (99%)	101 (92%)	9 (8%)	13	44
70	23	119/120 (99%)	106 (89%)	13 (11%)	7	30
71	24	112/113 (99%)	107 (96%)	5 (4%)	32	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	25	61/89 (68%)	50 (82%)	11 (18%)	2	13
73	26	83/101 (82%)	75 (90%)	8 (10%)	10	35
74	27	70/71 (99%)	69 (99%)	1 (1%)	71	86
75	28	56/60 (93%)	53 (95%)	3 (5%)	26	58
76	29	47/49 (96%)	46 (98%)	1 (2%)	59	80
77	30	51/54 (94%)	47 (92%)	4 (8%)	15	46
78	31	43/135 (32%)	38 (88%)	5 (12%)	6	28
79	RA	261/262 (100%)	241 (92%)	20 (8%)	15	47
All	All	9474/10182 (93%)	8754 (92%)	720 (8%)	20	47

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

Mol	Chain	Res	Type
31	69	59	LYS
44	82	83	LEU
71	24	102	LYS
33	71	69	TYR
37	75	79	ASP

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

Mol	Chain	Res	Type
25	63	132	ASN
40	78	10	GLN
70	23	21	ASN
28	66	26	GLN
34	72	35	GLN

### 5.3.3 RNA ⓘ

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

There are no RNA pucker outliers to report.

## 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 carbohydrates 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.