



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:53 PM BST

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

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

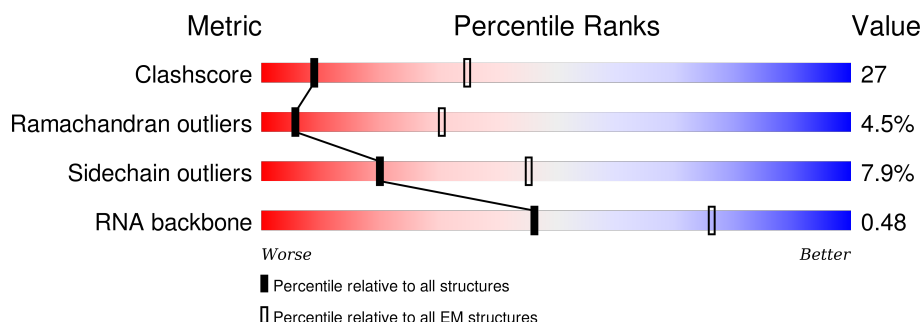
1 Overall quality at a glance

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.




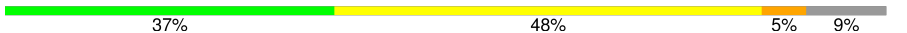
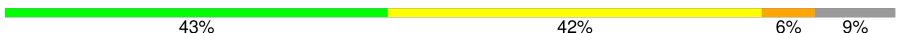


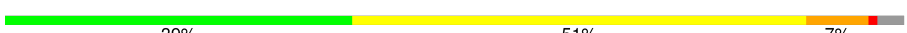
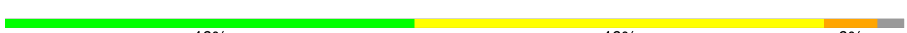




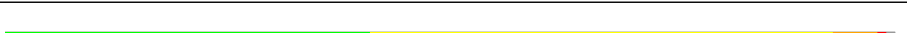













Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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 ≥ 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	32% 52% 12% . .
2	8S	158	32% 55% 12% .
3	5S	121	35% 59% 7%
4	L1	217	36% 48% 9% 6%
5	L2	254	37% 59% . .
6	L3	387	41% 51% 8%
7	L4	362	43% 46% 10%
8	L5	297	52% 43% 5%




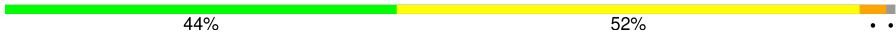
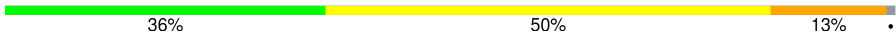
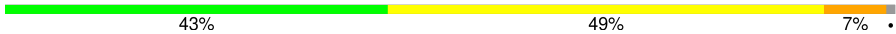
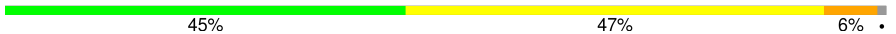


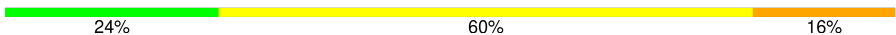
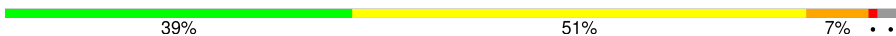
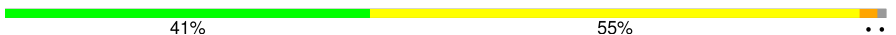
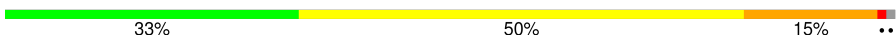
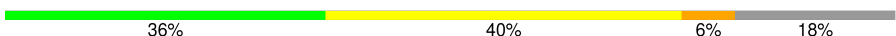
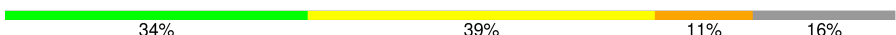










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Mol	Chain	Length	Quality of chain
9	L6	176	
10	L7	244	
11	L8	256	
12	L9	191	
13	50	221	
14	51	174	
15	53	199	
16	54	138	
17	55	204	
18	56	199	
19	57	184	
20	58	186	
21	59	189	
22	60	172	
23	61	160	
24	62	121	
25	63	137	
26	64	155	
27	65	142	
28	66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


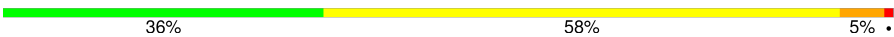




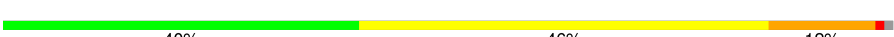
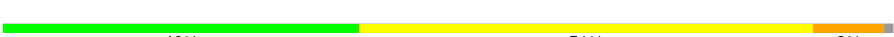
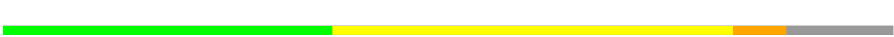

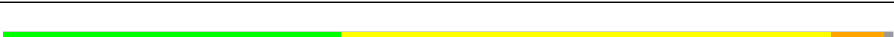
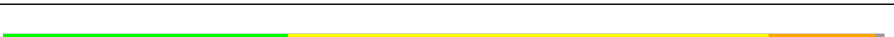

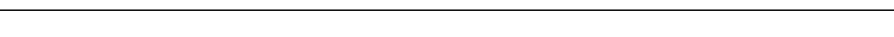
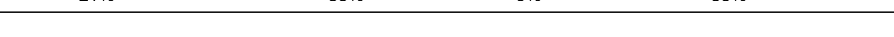
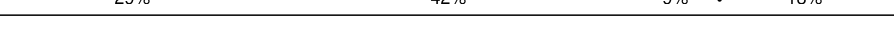






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Mol	Chain	Length	Quality of chain
34	72	130	
35	73	107	
36	74	121	
37	75	120	
38	76	100	
39	77	88	
40	78	78	
41	79	51	
42	80	128	
43	81	25	
44	82	106	
45	83	92	
46	1S	1798	
47	S0	252	
48	S1	255	
49	S2	254	
50	S3	240	
51	S4	261	
52	S5	225	
53	S6	236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

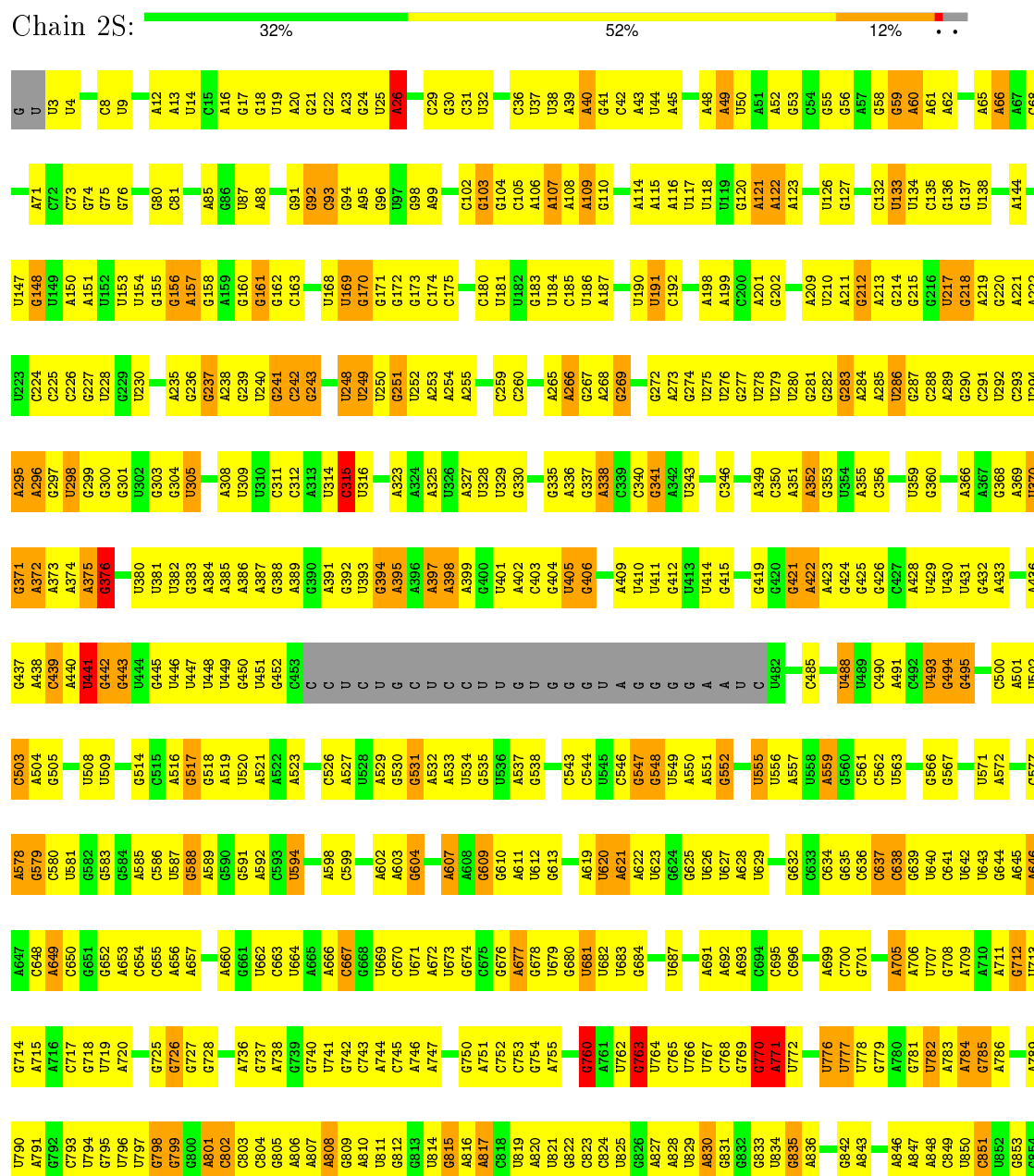
- Molecule 80 is a RNA chain called TSV IRES mRNA.

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 errors 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.

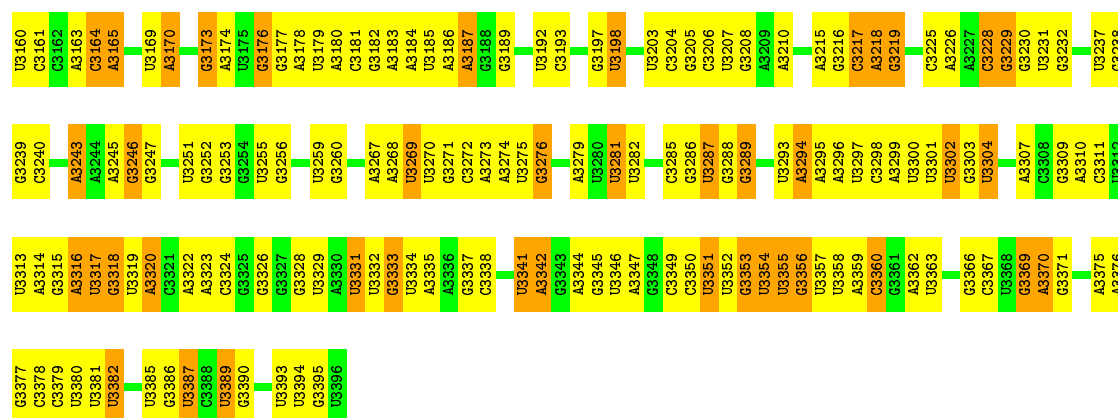
• Molecule 1: 25S ribosomal RNA





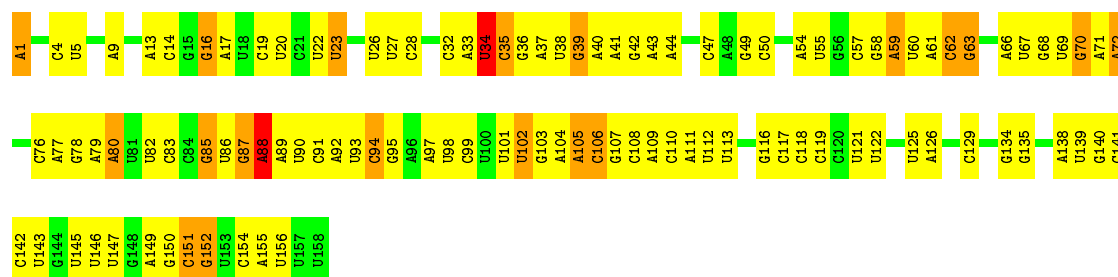






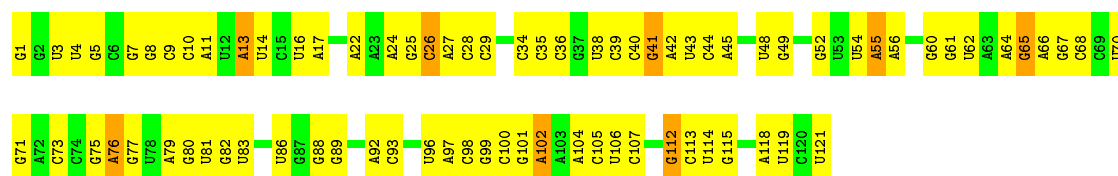
• Molecule 2: 5.8S ribosomal RNA

Chain 8S: 32% 55% 12%



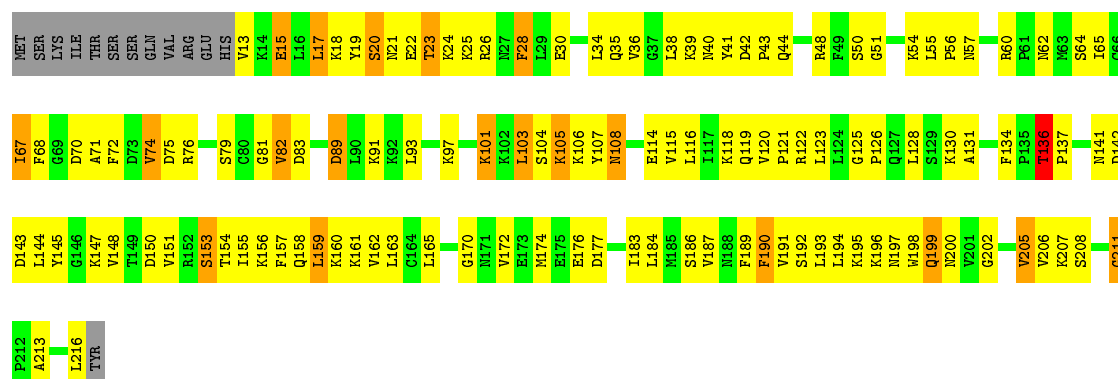
• Molecule 3: 5S ribosomal RNA

Chain 5S: 35% 59% 7%

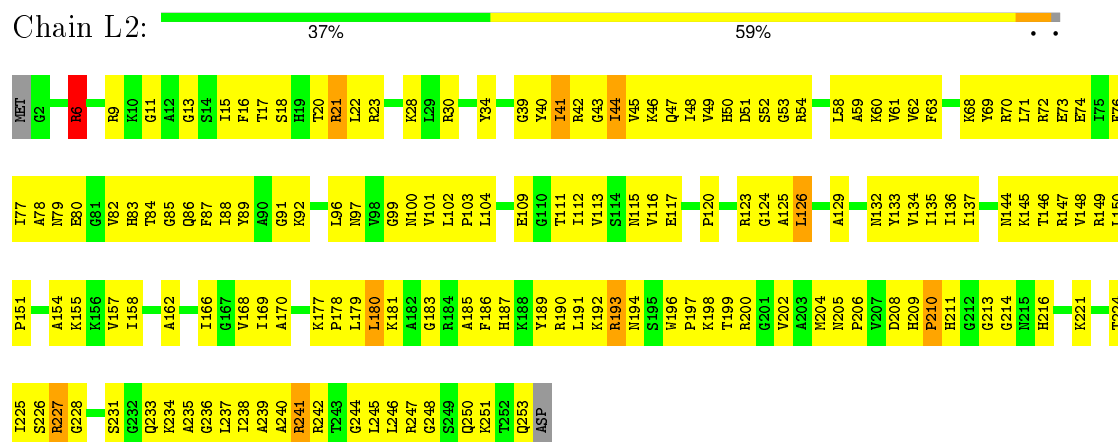


• Molecule 4: 60S ribosomal protein L1

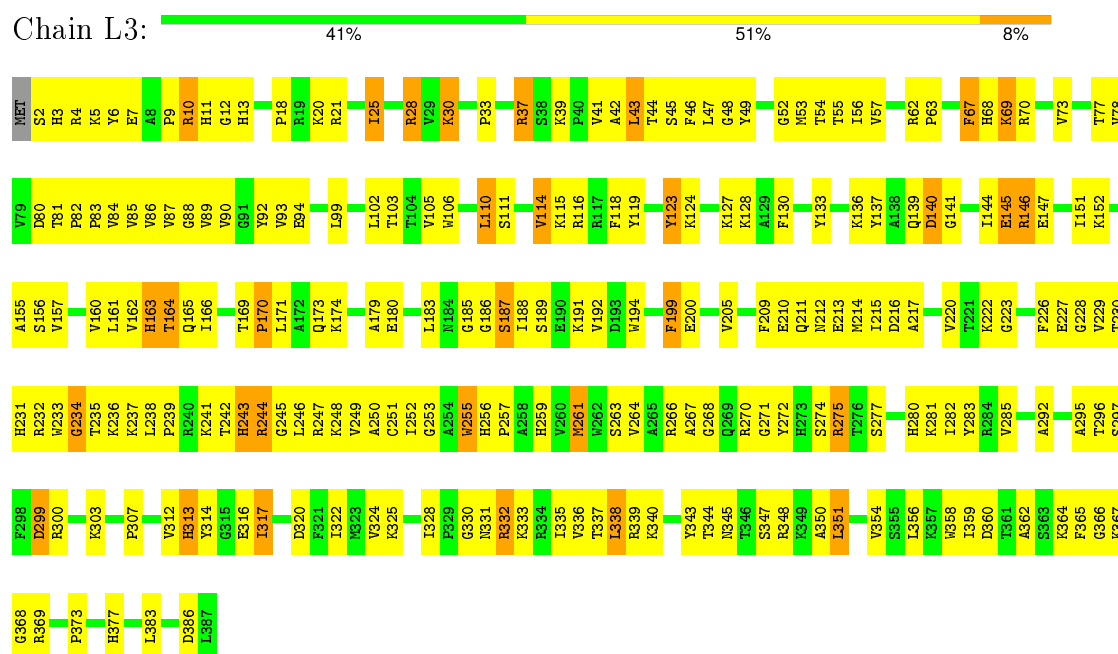
Chain L1: 36% 48% 9% 6%



- Molecule 5: 60S ribosomal protein L2

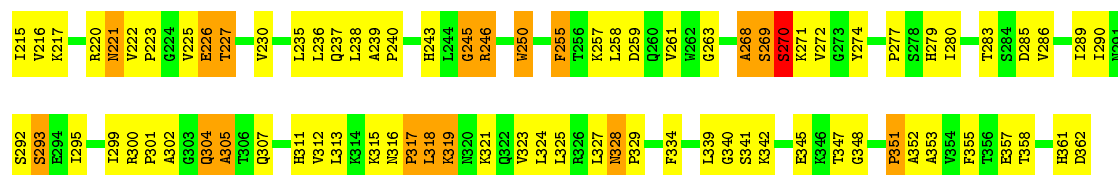


- Molecule 6: 60S ribosomal protein L3

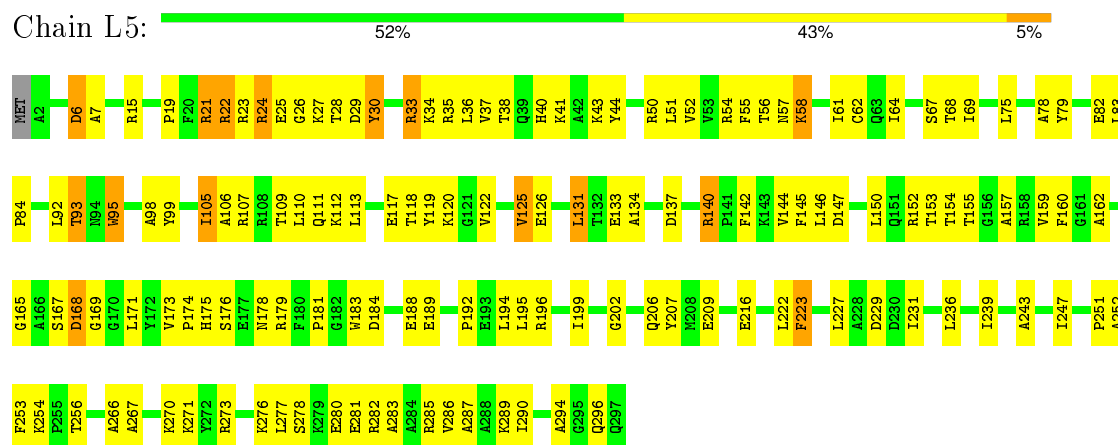


- Molecule 7: 60S ribosomal protein L4

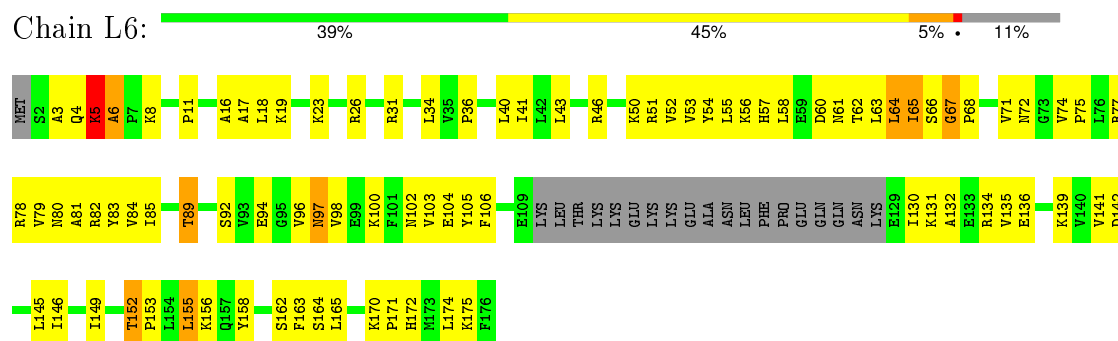




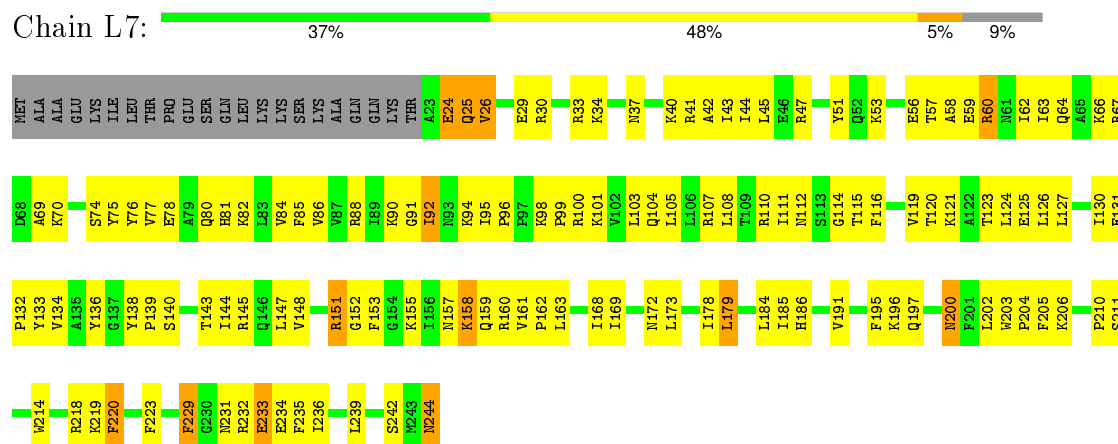
• Molecule 8: 60S ribosomal protein L5



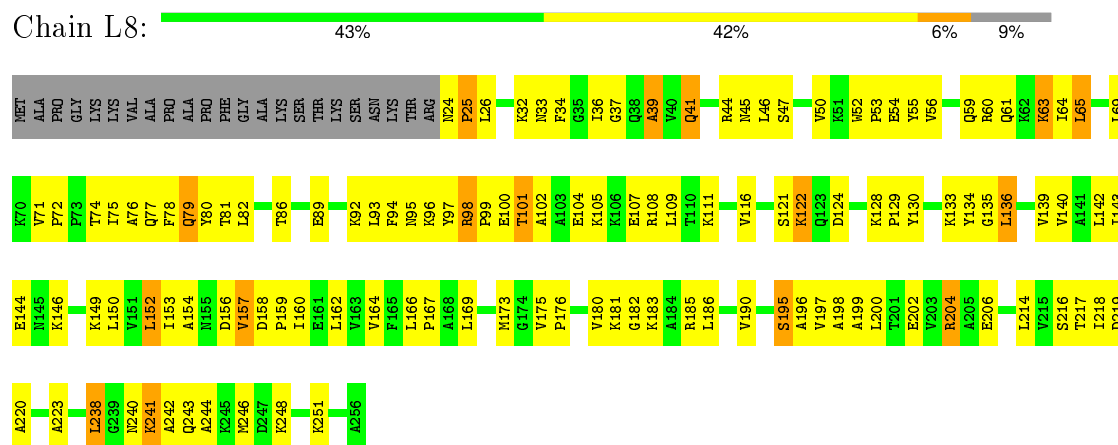
• Molecule 9: 60S ribosomal protein L6



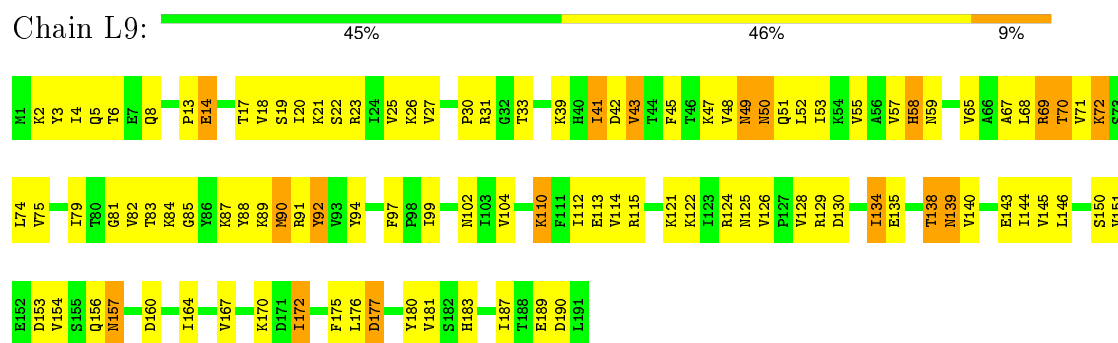
• Molecule 10: 60S ribosomal protein L7



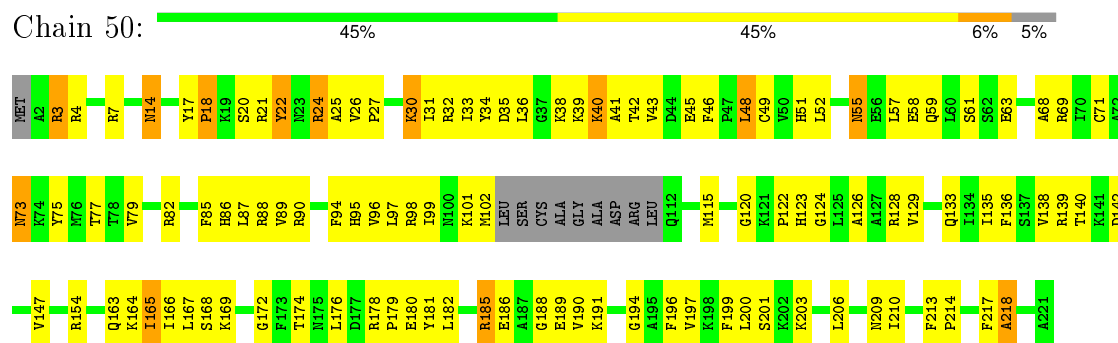
• Molecule 11: 60S ribosomal protein L8



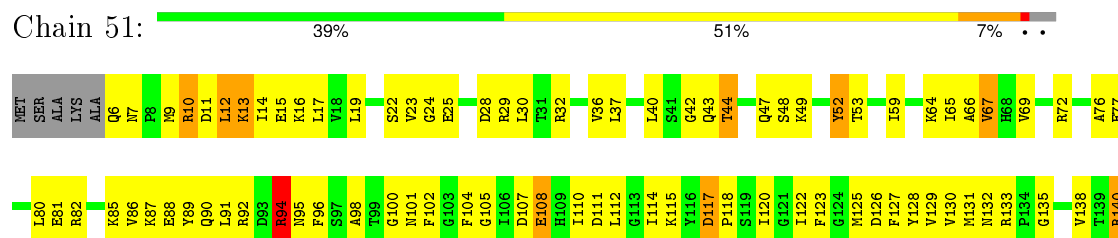
- Molecule 12: 60S ribosomal protein L9



- Molecule 13: 60S ribosomal protein L10



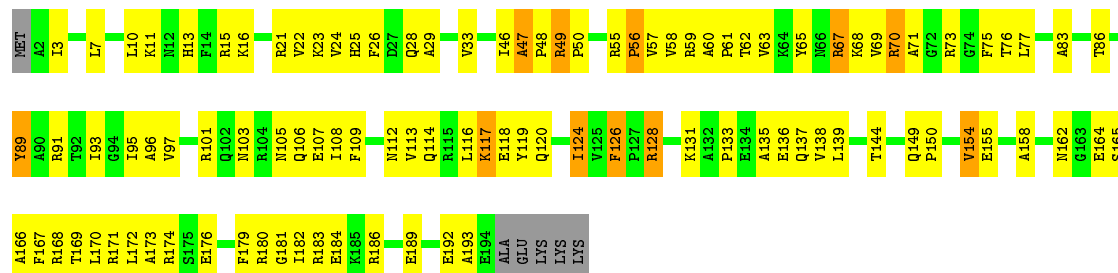
- Molecule 14: 60S ribosomal protein L11





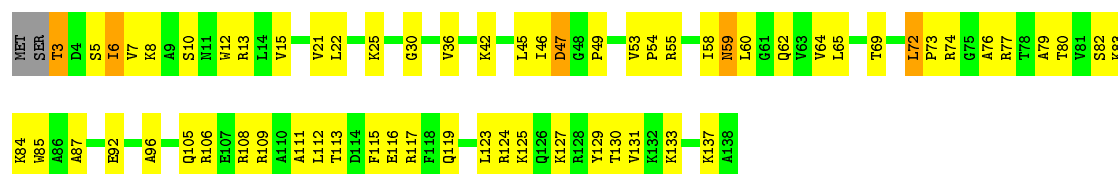
• Molecule 15: 60S ribosomal protein L13

Chain 53: 46% 46% 6% .



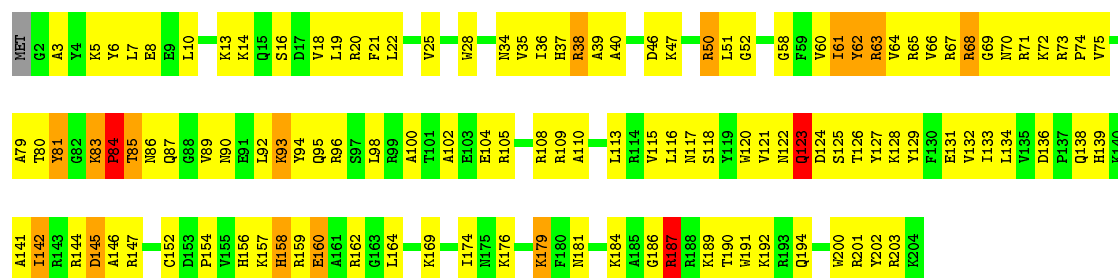
• Molecule 16: 60S ribosomal protein L14

Chain 54: 53% 42% . .



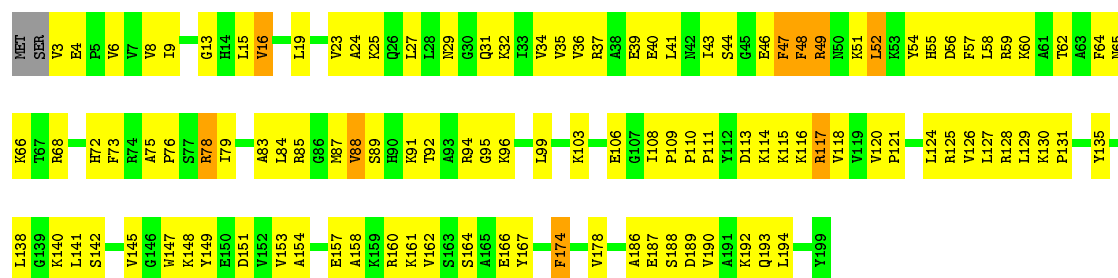
• Molecule 17: 60S ribosomal protein L15

Chain 55: 40% 51% 7% .

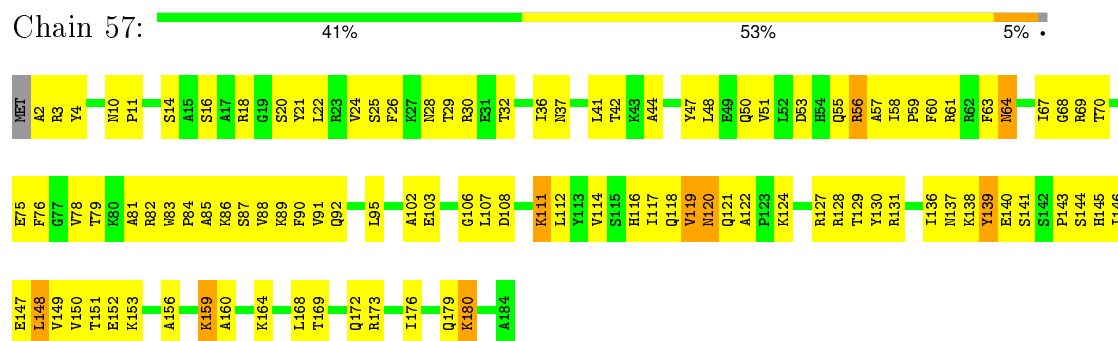


• Molecule 18: 60S ribosomal protein L16

Chain 56: 42% 52% 5% .



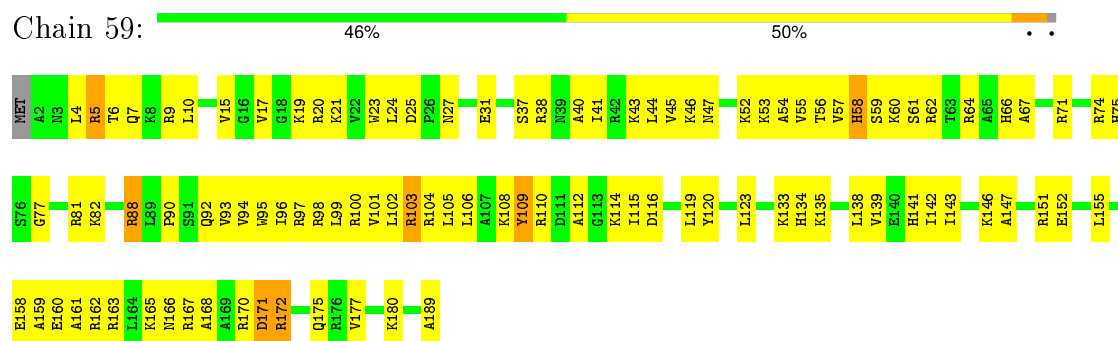
- Molecule 19: 60S ribosomal protein L17



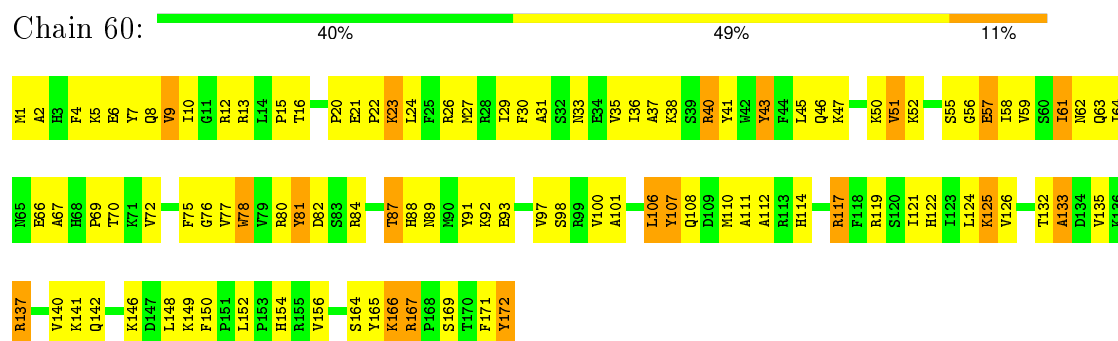
- Molecule 20: 60S ribosomal protein L18



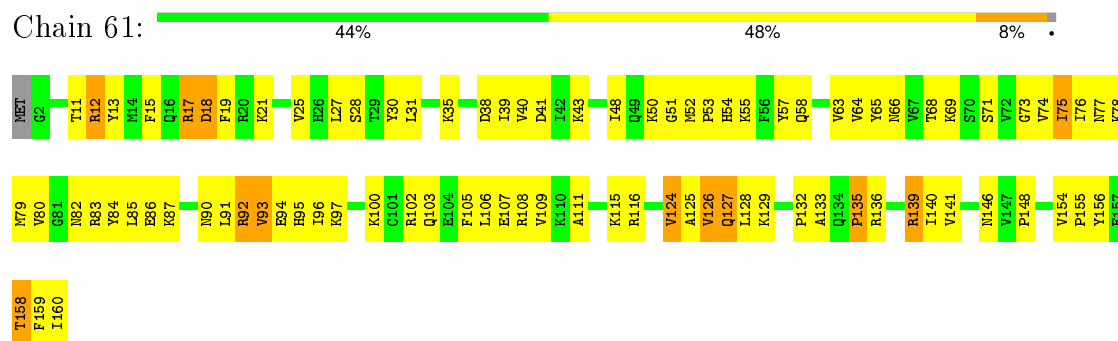
- Molecule 21: 60S ribosomal protein L19



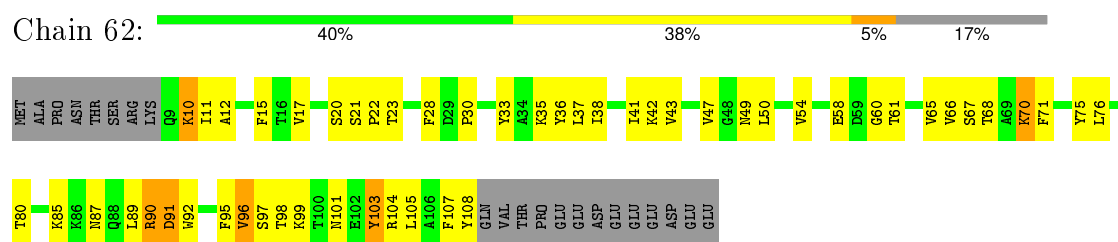
- Molecule 22: 60S ribosomal protein L20



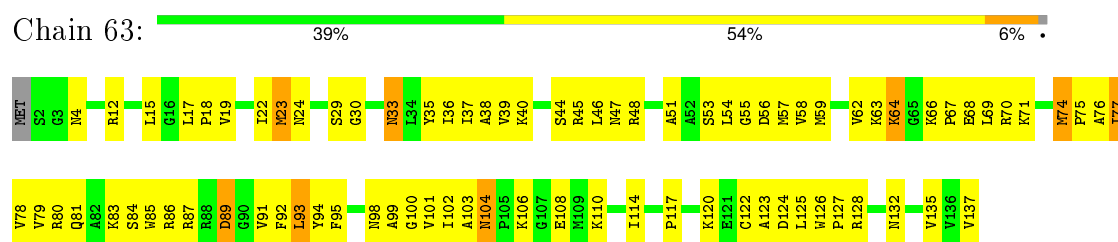
- Molecule 23: 60S ribosomal protein L21



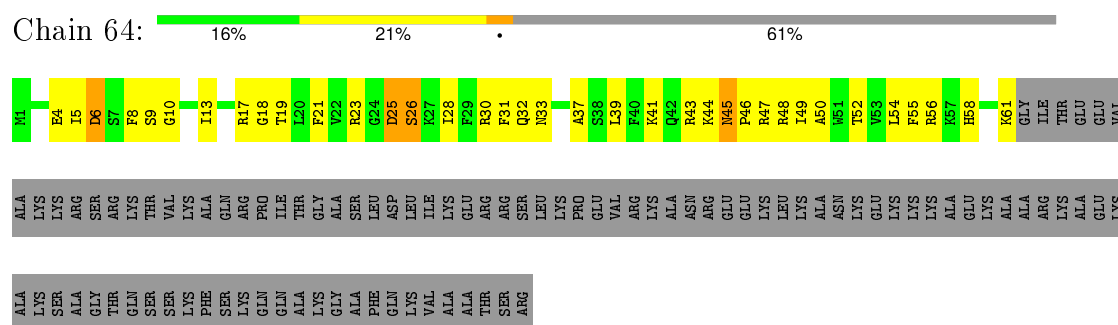
- Molecule 24: 60S ribosomal protein L22



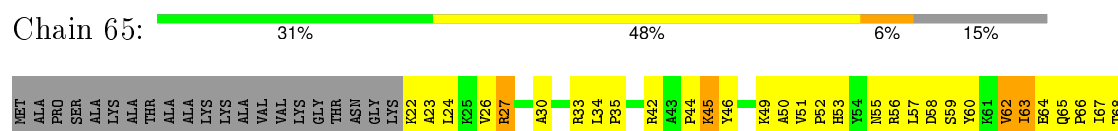
- Molecule 25: 60S ribosomal protein L23

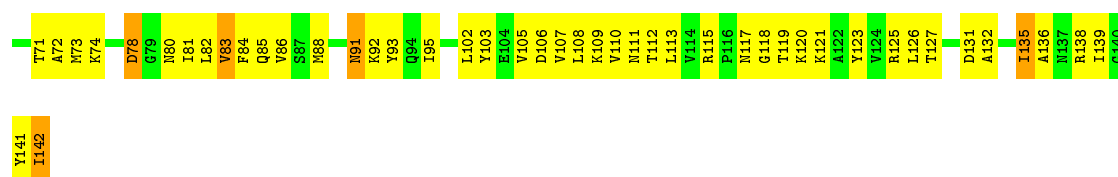


- Molecule 26: 60S ribosomal protein L24



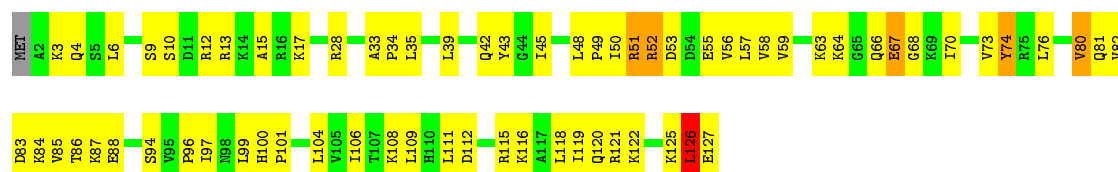
- Molecule 27: 60S ribosomal protein L25





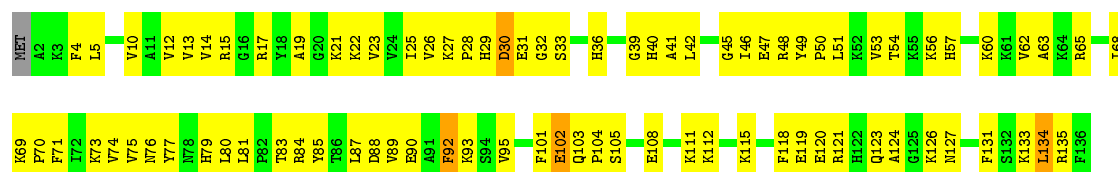
- Molecule 28: 60S ribosomal protein L26

Chain 66: 46% 49% . .



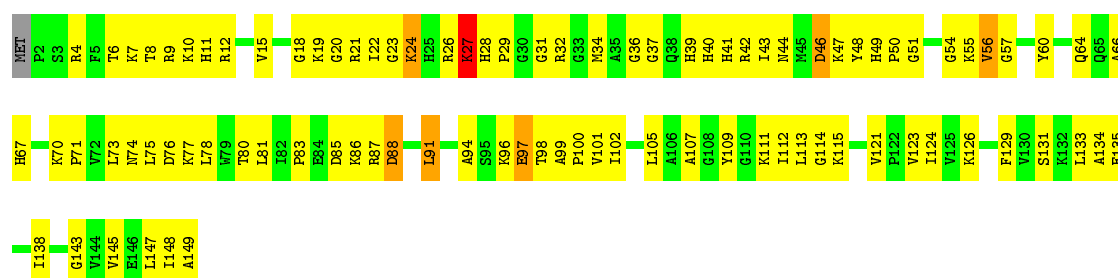
- Molecule 29: 60S ribosomal protein L27

Chain 67: 38% 59% . .



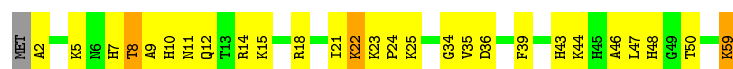
- Molecule 30: 60S ribosomal protein L28

Chain 68: 38% 57% . .



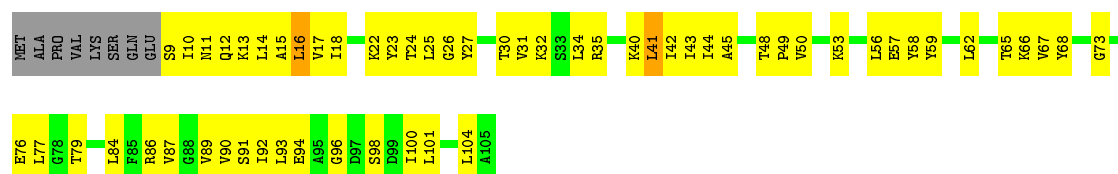
- Molecule 31: 60S ribosomal protein L29

Chain 69: 53% 41% 5% .



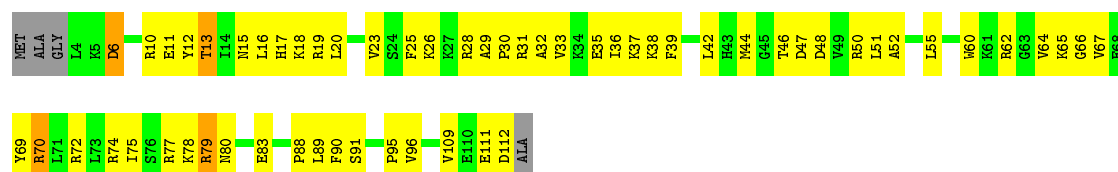
- Molecule 32: 60S ribosomal protein L30

Chain 70: 37% 53% 8% .



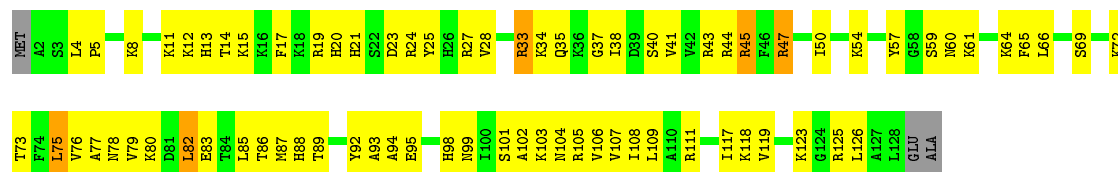
- Molecule 33: 60S ribosomal protein L31

Chain 71: 44% 49% . .



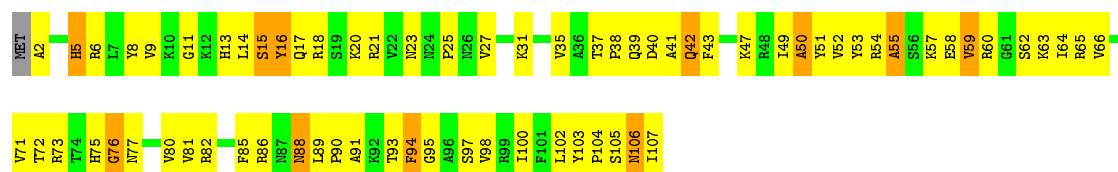
- Molecule 34: 60S ribosomal protein L32

Chain 72: 40% 54% . .



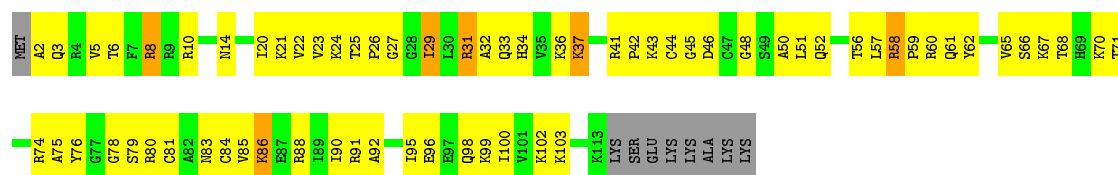
- Molecule 35: 60S ribosomal protein L33

Chain 73: 34% 55% 10% .



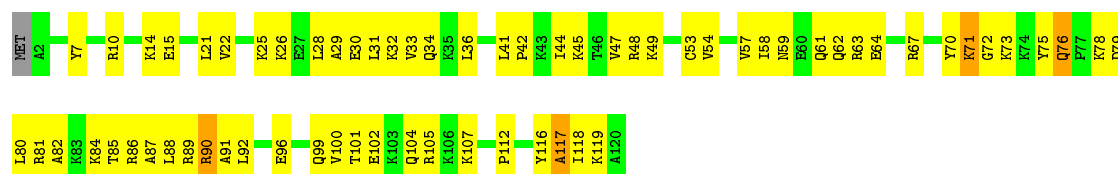
- Molecule 36: 60S ribosomal protein L34

Chain 74: 37% 50% 5% 7%



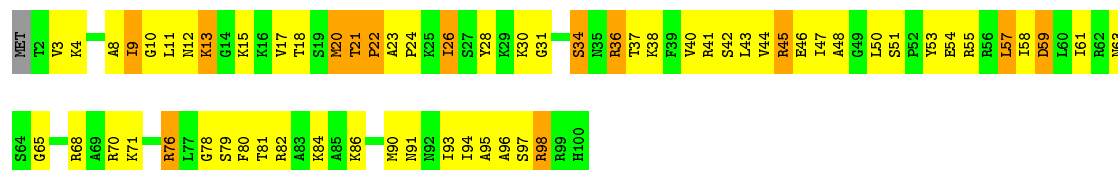
- Molecule 37: 60S ribosomal protein L35

Chain 75: 44% 52% . .



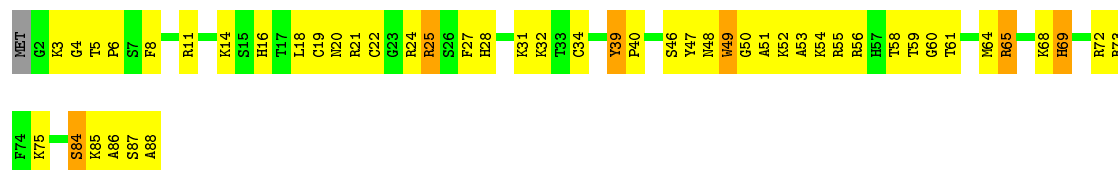
- Molecule 38: 60S ribosomal protein L36

Chain 76: .



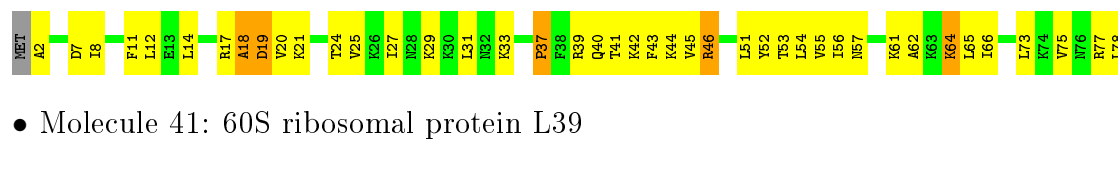
- Molecule 39: 60S ribosomal protein L37

Chain 77: .



- Molecule 40: 60S ribosomal protein L38

Chain 78: .



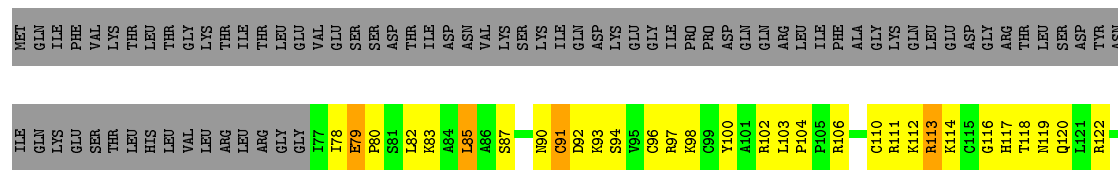
- Molecule 41: 60S ribosomal protein L39

Chain 79: .



- Molecule 42: 60S ribosomal protein L40

Chain 80: .



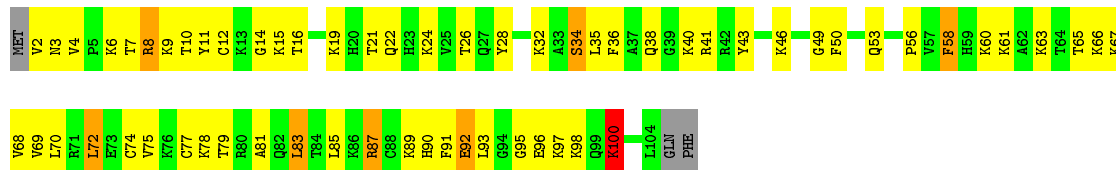
- Molecule 43: 60S ribosomal protein L41

Chain 81: 24% 60% 16%



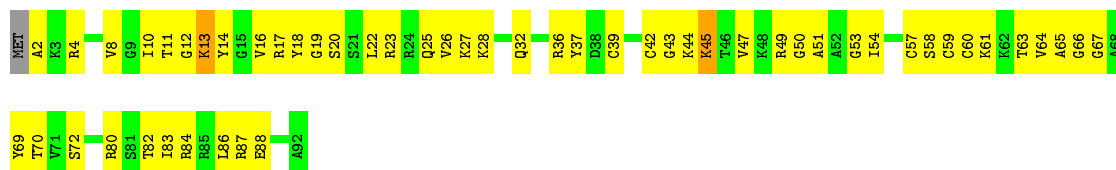
- Molecule 44: 60S ribosomal protein L42

Chain 82: 39% 51% 7% ..



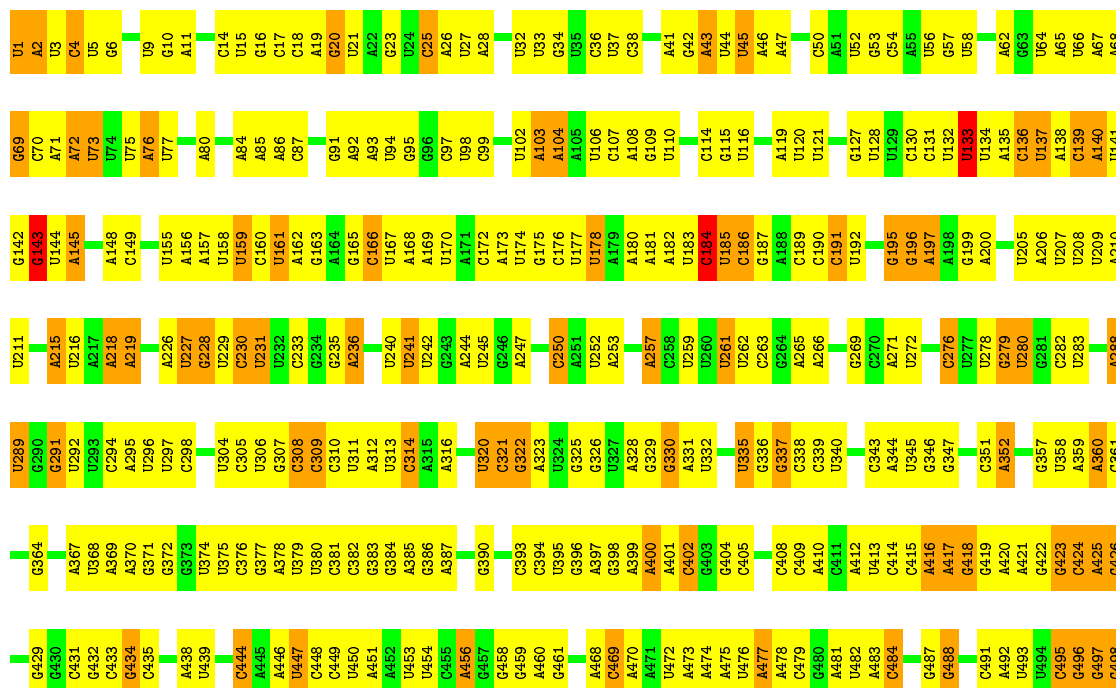
- Molecule 45: 60S ribosomal protein L43

Chain 83: 41% 55% ..

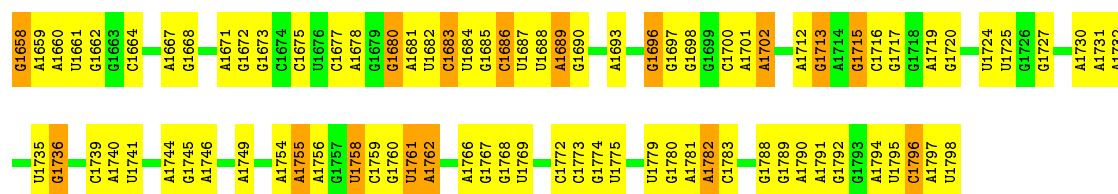


- Molecule 46: 18S ribosomal RNA

Chain 1S: 33% 50% 15% ..

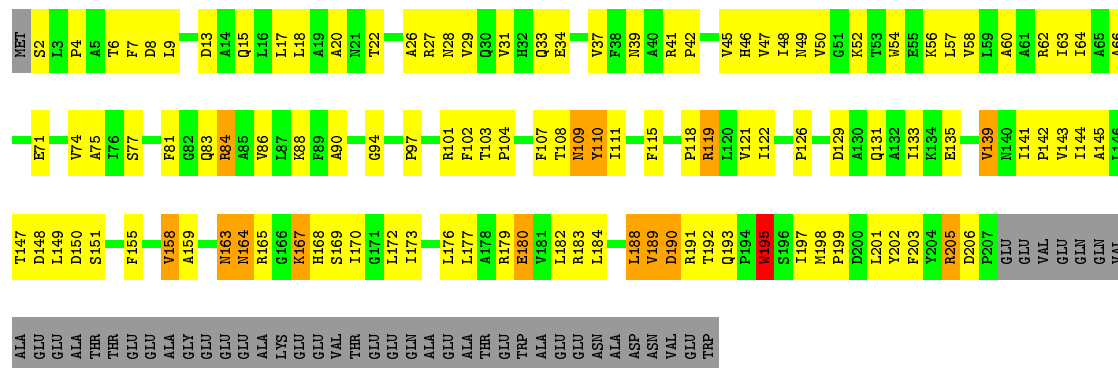


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A1587	G1523	U1450	U1370	U1285	G1200	G1127	A1061	U983	U912	U841	A771	U705	U640	C569	U501
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C1589	U1525	U1452	U1372	A1287	A1202	U1129	A1065	G986	G914	U843	C773	A707	G642	C571	G503
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G1601	G1536			A1300	A1223	A1143	U1076	G1010	A930	U858	G785	G722	C658	A585	G516
C1602	U1537			U1303	A1224		C1077	G1011	A933	A859	A788	G723	C	U	U517
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G1604	U1539			U1305	A1226	C1148	U1079	A1013	C935	U861	U790	G729	A	A592	A519
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U1612	G1546			U1315	U1232	C1159	A1087	A1019	A940	G867	C798	G735	U	A599	A525
G1613	C1548			G1316	G1233	A1160	U1088	A1020	A941	G868	A799	G736	C	U590	A526
C1614	U1550			U1317	A1234	A1161	U1089	C1021	G942	U869	U737	G737	G	A601	A527
G1615	U1551			U1318	G1235	C1162	C1090	C1022		C870	G801	U738	U	U602	U528
C1616	U1552			U1319	U1236	A1163	A1091		U947	G871	G802	G739	U	U603	A529
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	A1555			G1323	A1242	A1166	G1094	C1027	C950	G874	U805	U742	C	A606	U532
U1621	U1556			A1244	U1243	A1167	U1095	U1028	A951	G875	A806	U743	U	G607	U533
G1622	U1557			G1324	U1244	U1168	U1096	U1029	A952	G876		U744	G676	U611	A538
C1623	A1558			U1327	G1245	G1169	C1096	A1030	G953	G877	A811	U745	G677	U612	G539
C1624	U1559			U1328	U1246	G1170	U1097	U1031	G954	G878	A812	A746	A673	U613	G540
G1625	U1560			U1329	U1247	G1171	U1098	U1032	A955	G879	A813	C747	U679	G613	A541
	U1561			U1330	U1248	A1172	U1099				A814	U748	U680	U617	A542
U1629	G1562			A1341	U1250	G1173	G1100	A1036	U958	U882	G815	U749	U681	U618	C543
G1630	U1563			U1342	C1251	C1174		C1037	U959	C883	U750	U750	C682	A619	A544
A1631	U1564			U1343	U1252	U1174	G1105	U1038	U960	A884		G751	C683	A620	A545
G1632	U1565			A1344	U1253	G1179	U1106	A1039	U961	G885	C818	A752	A684	A621	
A1633	U1566			A1345	U1254	C1180	G1107	U1040	C962	U886	G819	A753	A685	A622	G551
C1634	U1567			U1346	G1255	U1181	G1108	G1041		U887	U820	A754	C686	A623	G552
	C1568			A1348	U1256	U1182	G1109	U1042	U965	U888	U822	A755	G687	A624	G553
U1635	U1569			U1349	U1257	A1183	G1110	A1043		U889	G823	A756	G688	G627	C554
G1641	A1570			U1350	U1258	A1184	G1111	U1044	A966	G895	A757	A757	G689	U619	A555
U1642	G1571			U1351	U1259	U1185	G1112		A967	U896	U826	U758	G690	G628	A556
	G1572			A1357	U1260	U1186	A1113	G1047	C969	C897	C827	U759		U629	G557
G1646	A1573			G1358	G1270	U1187		U1048	A970	A898	U828	A760	U694	A630	U558
U1647	U1574			C1359	U1271	U1188	U1117	U1049	A971	G899	A929	G761	C695	G631	C559
A1648				A1360	C1272	G1189	U1118	G1050	G972	A900	U830	A762	C696	U632	U560
G1649	U1578			U1361	A1273	G1192	G1119	U1051	A973	G901	U831	G763	C697	U633	G561
U1650	U1579			U1362	U1276	A1193	G1120	U1052	A974	G902	U832	U764	U698	G634	
A1651	U1580			U1363	U1277	A1194	C1121	G1053	C975	U903	U833	G765	U699	A635	
C1652	C1581			G1364	C1279	A1195	C1122	U1057	A976	U904	U834	U766	C700	A636	
	U1582			C1365	G1280	C1196	G1123		G977	A905	U835	U767	U701	C637	G564
U1656	A1583			U1366	G1281	A1196	C1124	U1058		A906		C768	G702		C566
U1657	G1584			G1367	U1282	C1197	A1124								



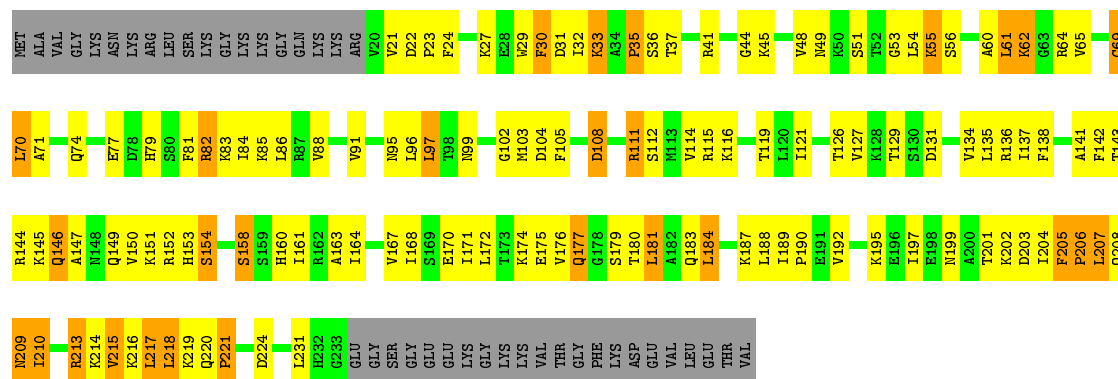
• Molecule 47: 40S ribosomal protein S0

Chain S0: 36% 40% 6% 18%



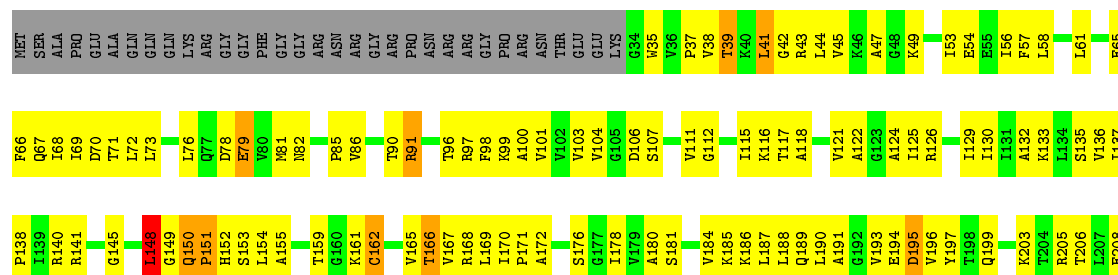
• Molecule 48: 40S ribosomal protein S1

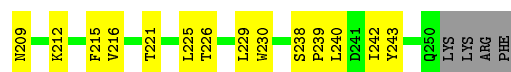
Chain S1: 34% 39% 11% 16%



• Molecule 49: 40S ribosomal protein S2

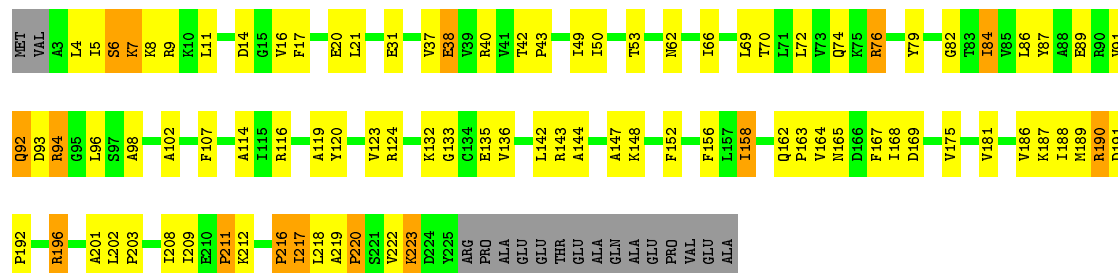
Chain S2: 37% 44% 15% 4%





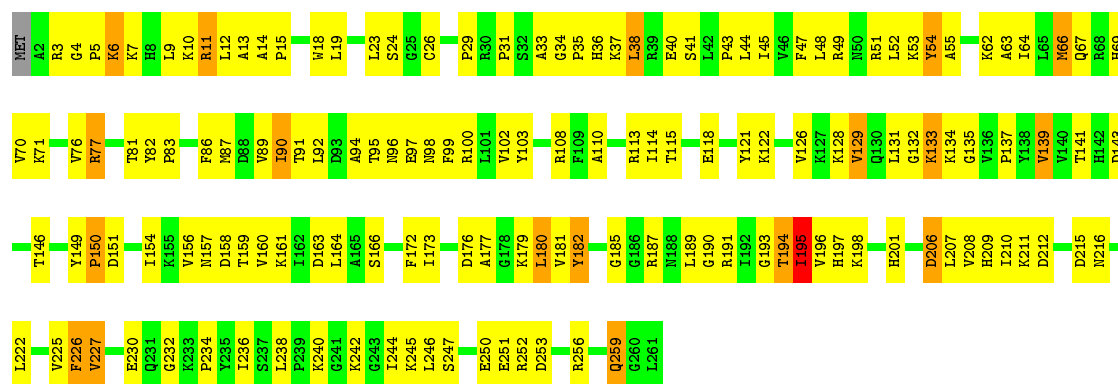
- Molecule 50: 40S ribosomal protein S3

Chain S3: 55% 32% 6% 7%



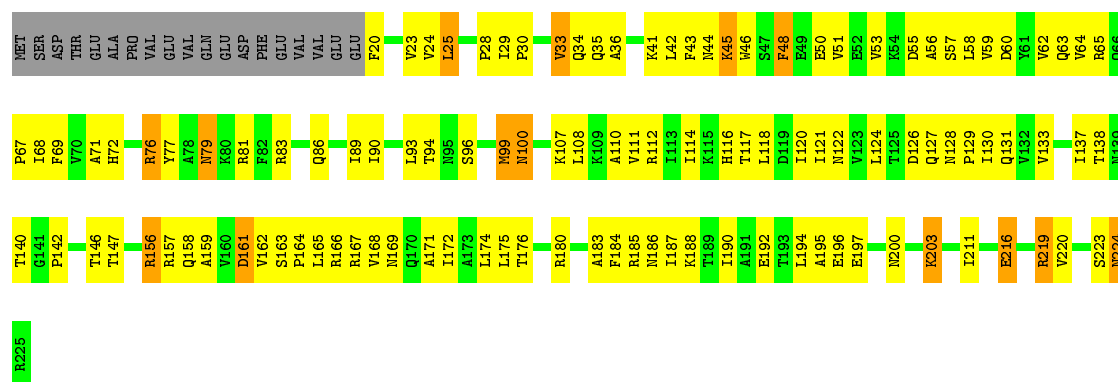
- Molecule 51: 40S ribosomal protein S4

Chain S4: 42% 50% 7%



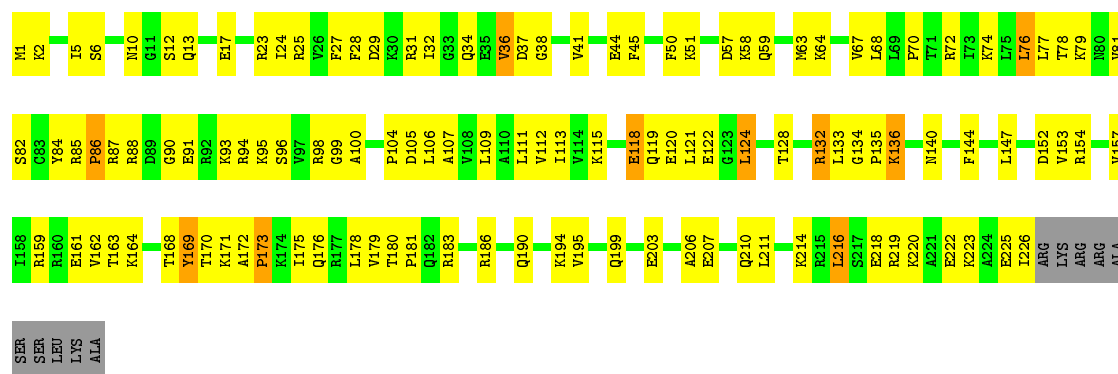
- Molecule 52: 40S ribosomal protein S5

Chain S5: 41% 44% 6% 8%



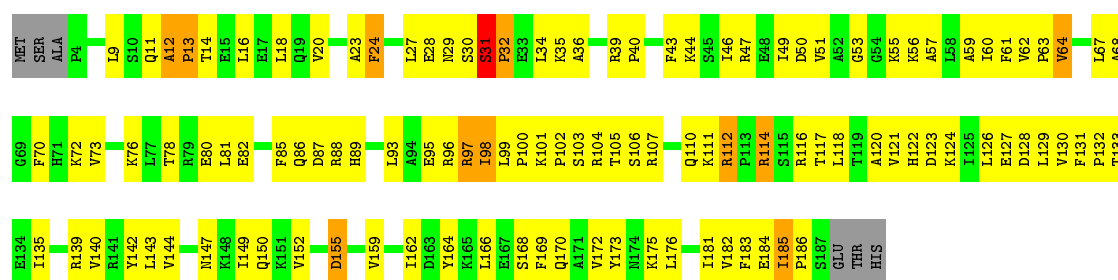
- Molecule 53: 40S ribosomal protein S6

Chain S6: 45% 47% 2%



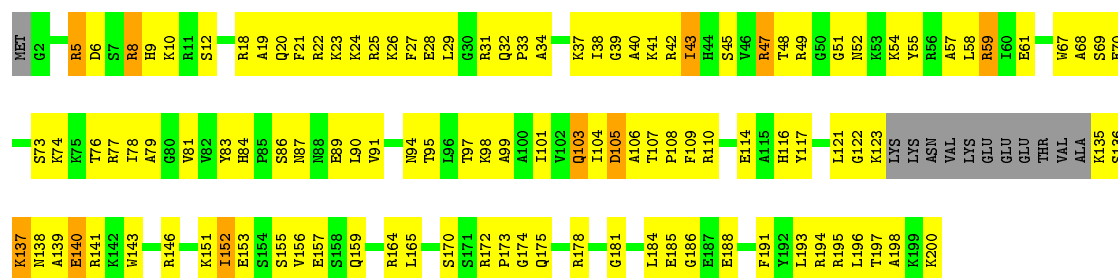
• Molecule 54: 40S ribosomal protein S7

Chain S7: 36% 54% 6% • •



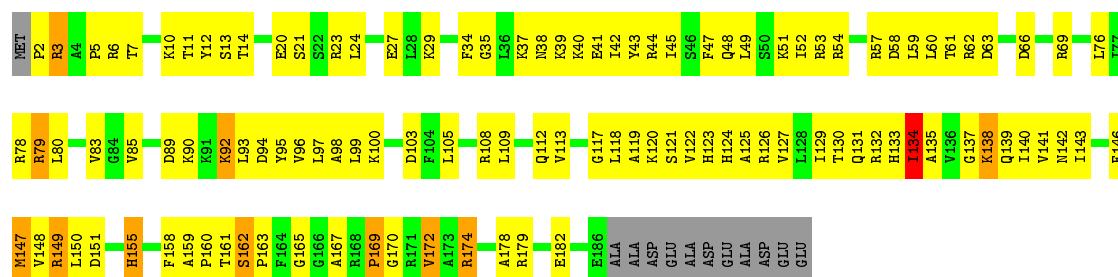
• Molecule 55: 40S ribosomal protein S8

Chain S8: 36% 53% 5% 6%

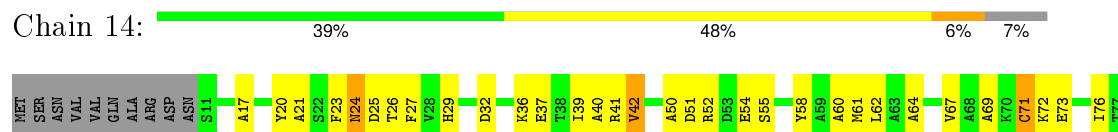


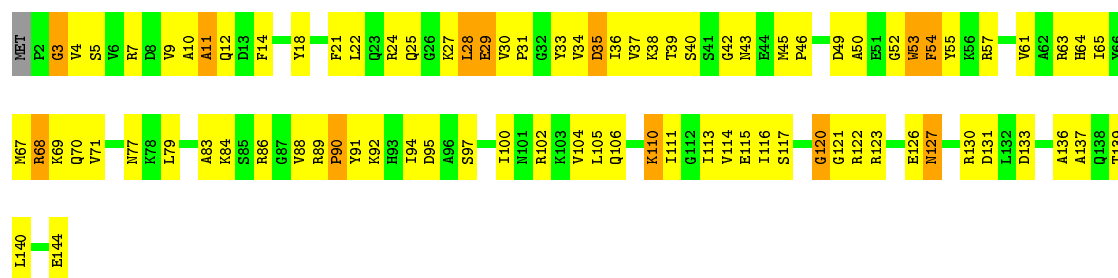
• Molecule 56: 40S ribosomal protein S9

Chain S9: 37% 51% 6% • 6%

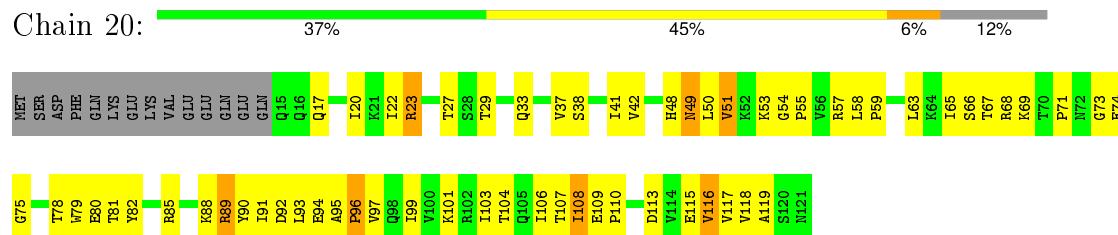


• Molecule 57: 40S ribosomal protein S10

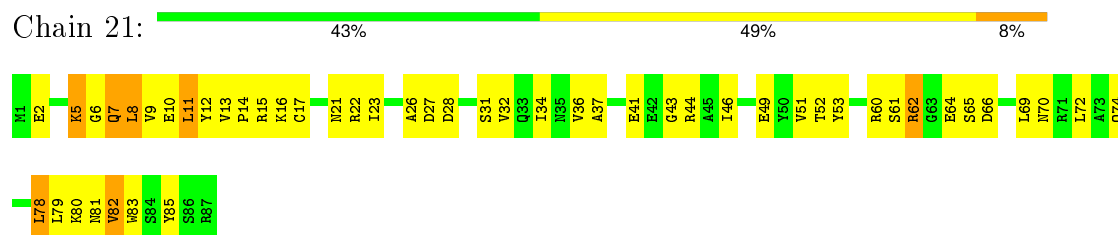




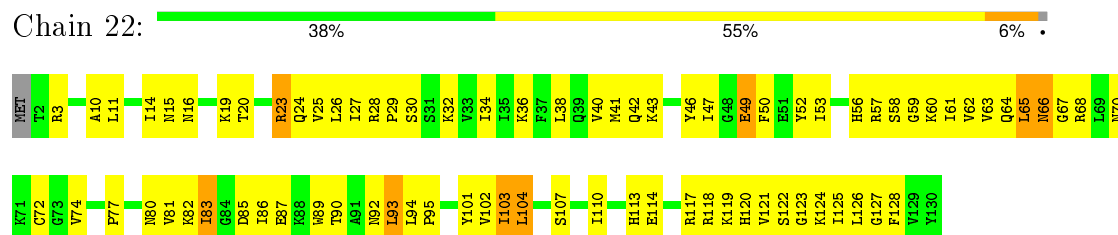
- Molecule 67: 40S ribosomal protein S20



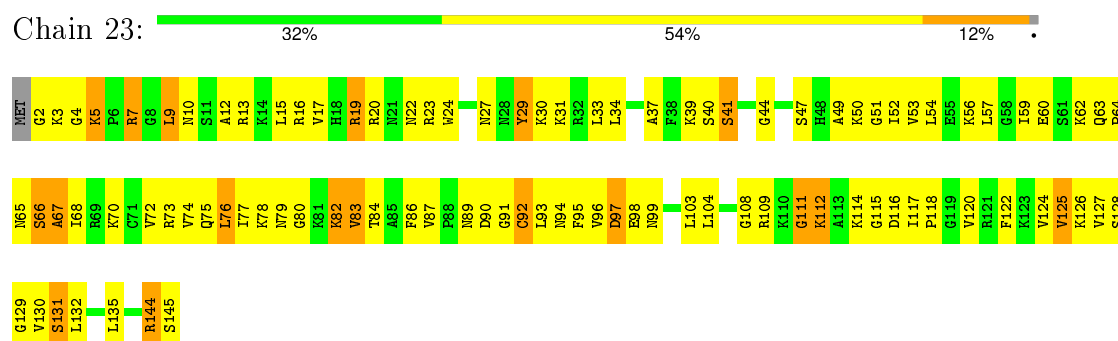
- Molecule 68: 40S ribosomal protein S21



- Molecule 69: 40S ribosomal protein S22

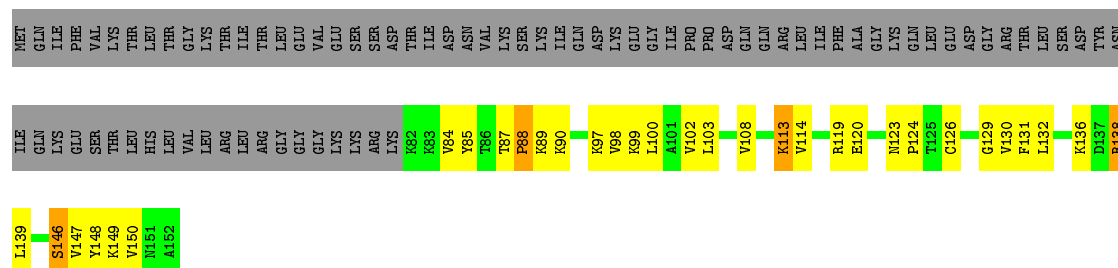


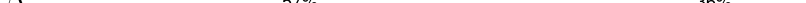
- Molecule 70: 40S ribosomal protein S23

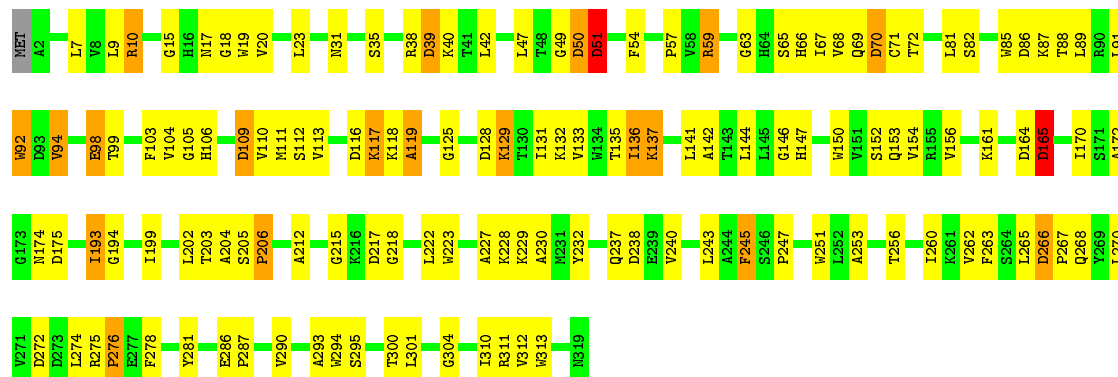




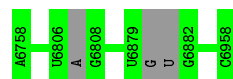
- Chain 31:  26% 18% . 53%



- Chain RA: 



- Chain IR: 99%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	52444	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	133333	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	0.87	4/79178 (0.0%)	0.76	26/123444 (0.0%)
10	L7	0.57	0/1822	0.70	0/2451
11	L8	0.53	0/1850	0.69	0/2495
12	L9	0.57	0/1540	0.71	0/2073
13	50	0.53	0/1754	0.67	0/2350
14	51	0.50	0/1375	0.66	0/1842
15	53	0.57	0/1568	0.72	0/2106
16	54	0.62	0/1069	0.68	0/1438
17	55	0.57	0/1758	0.67	0/2354
18	56	0.57	0/1586	0.70	0/2128
19	57	0.59	0/1466	0.72	0/1968
2	8S	0.84	2/3747 (0.1%)	0.75	3/5832 (0.1%)
20	58	0.56	0/1466	0.73	1/1965 (0.1%)
21	59	0.48	0/1539	0.68	0/2050
22	60	0.59	0/1482	0.67	0/1990
23	61	0.57	0/1301	0.68	0/1743
24	62	0.52	0/812	0.63	0/1099
25	63	0.54	0/1019	0.70	0/1369
26	64	0.53	0/521	0.66	0/691
27	65	0.53	0/984	0.69	0/1325
28	66	0.54	0/1005	0.68	0/1341
29	67	0.47	0/1119	0.61	0/1497
3	5S	0.85	1/2884 (0.0%)	0.72	0/4491
30	68	0.56	0/1205	0.72	0/1612
31	69	0.53	0/474	0.71	0/629
32	70	0.49	0/751	0.64	0/1008
33	71	0.52	0/904	0.66	0/1213
34	72	0.58	0/1041	0.70	0/1394
35	73	0.64	0/869	0.70	0/1168
36	74	0.50	0/891	0.66	0/1191
37	75	0.52	0/979	0.68	0/1301
38	76	0.54	0/779	0.74	0/1034
39	77	0.56	0/697	0.70	0/923
4	L1	0.55	0/1634	0.69	0/2195

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	78	0.49	0/619	0.62	0/826
41	79	0.54	0/444	0.70	0/588
42	80	0.53	0/424	0.66	0/562
43	81	0.74	0/235	0.76	0/300
44	82	0.57	0/839	0.71	0/1108
45	83	0.51	0/702	0.66	0/934
46	1S	0.78	1/42445 (0.0%)	0.75	12/66138 (0.0%)
47	S0	0.49	0/1653	0.64	0/2261
48	S1	0.47	0/1735	0.62	0/2335
49	S2	0.45	0/1665	0.65	0/2263
5	L2	0.51	0/1952	0.71	0/2622
50	S3	0.49	0/1759	0.63	0/2368
51	S4	0.45	0/2110	0.64	0/2839
52	S5	0.48	0/1630	0.63	0/2202
53	S6	0.47	0/1844	0.67	0/2464
54	S7	0.49	0/1506	0.67	1/2028 (0.0%)
55	S8	0.49	0/1515	0.65	0/2021
56	S9	0.43	0/1519	0.67	0/2035
57	10	0.58	0/837	0.65	0/1131
58	11	0.52	0/1273	0.63	0/1712
59	12	0.63	0/943	0.74	0/1274
6	L3	0.55	0/3153	0.68	0/4239
60	13	0.48	0/1216	0.61	0/1638
61	14	0.49	0/953	0.66	0/1279
62	15	0.52	0/1012	0.65	0/1356
63	16	0.50	0/1126	0.64	0/1510
64	17	0.52	0/974	0.67	0/1304
65	18	0.51	0/1212	0.67	0/1628
66	19	0.51	0/1131	0.64	0/1517
67	20	0.52	0/866	0.61	0/1169
68	21	0.50	0/694	0.63	0/935
69	22	0.46	0/1039	0.65	0/1395
7	L4	0.58	0/2802	0.71	0/3792
70	23	0.46	0/1140	0.66	1/1518 (0.1%)
71	24	0.47	0/1088	0.59	0/1449
72	25	0.52	0/571	0.71	0/768
73	26	0.46	0/782	0.61	0/1047
74	27	0.50	0/621	0.67	0/838
75	28	0.47	0/500	0.65	0/670
76	29	0.51	0/454	0.59	0/602
77	30	0.48	0/483	0.62	0/643
78	31	0.56	0/505	0.68	1/682 (0.1%)
79	RA	0.53	0/2498	0.64	0/3398

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
8	L5	0.55	0/2426	0.63	0/3271
9	L6	0.62	0/1261	0.72	1/1694 (0.1%)
All	All	0.73	8/219225 (0.0%)	0.73	46/322063 (0.0%)

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

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

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

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

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

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

There are no chirality outliers.

5 of 160 planarity outliers are listed below:

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

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

5.2 Too-close contacts

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

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

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

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

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

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

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

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	L1	202/217 (93%)	137 (68%)	50 (25%)	15 (7%)	1	21
5	L2	250/254 (98%)	196 (78%)	44 (18%)	10 (4%)	4	35
6	L3	384/387 (99%)	322 (84%)	51 (13%)	11 (3%)	6	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	L4	359/362 (99%)	284 (79%)	48 (13%)	27 (8%)	1	20
8	L5	294/297 (99%)	244 (83%)	40 (14%)	10 (3%)	5	39
9	L6	152/176 (86%)	131 (86%)	16 (10%)	5 (3%)	5	40
10	L7	220/244 (90%)	192 (87%)	19 (9%)	9 (4%)	3	34
11	L8	231/256 (90%)	184 (80%)	38 (16%)	9 (4%)	4	36
12	L9	189/191 (99%)	153 (81%)	30 (16%)	6 (3%)	5	40
13	50	207/221 (94%)	166 (80%)	36 (17%)	5 (2%)	7	47
14	51	167/174 (96%)	130 (78%)	29 (17%)	8 (5%)	3	31
15	53	191/199 (96%)	150 (78%)	35 (18%)	6 (3%)	5	41
16	54	134/138 (97%)	114 (85%)	17 (13%)	3 (2%)	8	49
17	55	201/204 (98%)	156 (78%)	36 (18%)	9 (4%)	3	33
18	56	195/199 (98%)	177 (91%)	14 (7%)	4 (2%)	9	50
19	57	181/184 (98%)	143 (79%)	34 (19%)	4 (2%)	8	49
20	58	183/186 (98%)	153 (84%)	23 (13%)	7 (4%)	4	36
21	59	186/189 (98%)	168 (90%)	14 (8%)	4 (2%)	8	49
22	60	170/172 (99%)	140 (82%)	25 (15%)	5 (3%)	6	42
23	61	157/160 (98%)	128 (82%)	19 (12%)	10 (6%)	2	25
24	62	98/121 (81%)	76 (78%)	18 (18%)	4 (4%)	3	34
25	63	134/137 (98%)	105 (78%)	24 (18%)	5 (4%)	4	37
26	64	59/155 (38%)	43 (73%)	13 (22%)	3 (5%)	2	30
27	65	119/142 (84%)	97 (82%)	17 (14%)	5 (4%)	3	34
28	66	124/127 (98%)	104 (84%)	16 (13%)	4 (3%)	5	40
29	67	133/136 (98%)	110 (83%)	20 (15%)	3 (2%)	8	48
30	68	146/149 (98%)	117 (80%)	26 (18%)	3 (2%)	9	50
31	69	56/59 (95%)	43 (77%)	11 (20%)	2 (4%)	4	38
32	70	95/105 (90%)	89 (94%)	4 (4%)	2 (2%)	9	50
33	71	107/113 (95%)	91 (85%)	14 (13%)	2 (2%)	10	51
34	72	125/130 (96%)	109 (87%)	15 (12%)	1 (1%)	24	69
35	73	104/107 (97%)	79 (76%)	17 (16%)	8 (8%)	1	20
36	74	110/121 (91%)	88 (80%)	18 (16%)	4 (4%)	4	38
37	75	117/120 (98%)	107 (92%)	6 (5%)	4 (3%)	5	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	76	97/100 (97%)	76 (78%)	13 (13%)	8 (8%)	1	18
39	77	85/88 (97%)	67 (79%)	16 (19%)	2 (2%)	7	47
40	78	75/78 (96%)	64 (85%)	7 (9%)	4 (5%)	2	29
41	79	48/51 (94%)	39 (81%)	8 (17%)	1 (2%)	9	50
42	80	50/128 (39%)	42 (84%)	6 (12%)	2 (4%)	4	35
43	81	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	3	34
44	82	101/106 (95%)	79 (78%)	18 (18%)	4 (4%)	4	35
45	83	89/92 (97%)	75 (84%)	13 (15%)	1 (1%)	17	63
47	S0	204/252 (81%)	163 (80%)	29 (14%)	12 (6%)	2	26
48	S1	212/255 (83%)	154 (73%)	45 (21%)	13 (6%)	2	25
49	S2	215/254 (85%)	177 (82%)	30 (14%)	8 (4%)	4	37
50	S3	221/240 (92%)	184 (83%)	24 (11%)	13 (6%)	2	26
51	S4	258/261 (99%)	203 (79%)	45 (17%)	10 (4%)	4	36
52	S5	204/225 (91%)	165 (81%)	32 (16%)	7 (3%)	5	39
53	S6	224/236 (95%)	192 (86%)	26 (12%)	6 (3%)	6	44
54	S7	182/190 (96%)	137 (75%)	34 (19%)	11 (6%)	2	26
55	S8	184/200 (92%)	147 (80%)	28 (15%)	9 (5%)	3	31
56	S9	183/197 (93%)	153 (84%)	21 (12%)	9 (5%)	3	31
57	10	94/105 (90%)	74 (79%)	13 (14%)	7 (7%)	1	21
58	11	153/156 (98%)	107 (70%)	37 (24%)	9 (6%)	2	26
59	12	122/143 (85%)	76 (62%)	29 (24%)	17 (14%)	0	6
60	13	148/151 (98%)	125 (84%)	20 (14%)	3 (2%)	9	51
61	14	125/137 (91%)	96 (77%)	22 (18%)	7 (6%)	2	28
62	15	122/142 (86%)	101 (83%)	16 (13%)	5 (4%)	3	34
63	16	139/143 (97%)	112 (81%)	20 (14%)	7 (5%)	3	30
64	17	116/136 (85%)	92 (79%)	20 (17%)	4 (3%)	5	39
65	18	143/146 (98%)	120 (84%)	16 (11%)	7 (5%)	3	31
66	19	141/144 (98%)	118 (84%)	15 (11%)	8 (6%)	2	27
67	20	105/121 (87%)	85 (81%)	14 (13%)	6 (6%)	2	27
68	21	85/87 (98%)	68 (80%)	13 (15%)	4 (5%)	3	32
69	22	127/130 (98%)	106 (84%)	19 (15%)	2 (2%)	12	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	23	142/145 (98%)	108 (76%)	24 (17%)	10 (7%)	1	22
71	24	132/135 (98%)	106 (80%)	20 (15%)	6 (4%)	3	33
72	25	68/108 (63%)	45 (66%)	14 (21%)	9 (13%)	0	7
73	26	95/119 (80%)	64 (67%)	19 (20%)	12 (13%)	0	8
74	27	79/82 (96%)	58 (73%)	15 (19%)	6 (8%)	1	20
75	28	61/67 (91%)	50 (82%)	9 (15%)	2 (3%)	5	40
76	29	51/56 (91%)	44 (86%)	5 (10%)	2 (4%)	4	36
77	30	58/63 (92%)	47 (81%)	8 (14%)	3 (5%)	2	29
78	31	69/152 (45%)	37 (54%)	20 (29%)	12 (17%)	0	4
79	RA	316/319 (99%)	252 (80%)	53 (17%)	11 (4%)	4	39
All	All	11126/12097 (92%)	8955 (80%)	1674 (15%)	497 (4%)	6	33

5 of 497 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	L1	185/198 (93%)	166 (90%)	19 (10%)	9	37
5	L2	194/196 (99%)	183 (94%)	11 (6%)	25	62
6	L3	322/323 (100%)	290 (90%)	32 (10%)	10	39
7	L4	288/289 (100%)	260 (90%)	28 (10%)	10	40
8	L5	244/245 (100%)	222 (91%)	22 (9%)	12	44
9	L6	134/153 (88%)	127 (95%)	7 (5%)	29	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	L7	186/205 (91%)	174 (94%)	12 (6%)	21	58
11	L8	191/208 (92%)	177 (93%)	14 (7%)	17	55
12	L9	171/171 (100%)	153 (90%)	18 (10%)	8	36
13	50	180/187 (96%)	164 (91%)	16 (9%)	12	44
14	51	147/150 (98%)	133 (90%)	14 (10%)	11	41
15	53	154/159 (97%)	140 (91%)	14 (9%)	12	44
16	54	107/109 (98%)	102 (95%)	5 (5%)	32	68
17	55	175/176 (99%)	161 (92%)	14 (8%)	15	51
18	56	160/162 (99%)	153 (96%)	7 (4%)	35	69
19	57	145/146 (99%)	134 (92%)	11 (8%)	16	53
20	58	150/151 (99%)	141 (94%)	9 (6%)	24	61
21	59	153/154 (99%)	145 (95%)	8 (5%)	29	65
22	60	156/156 (100%)	134 (86%)	22 (14%)	4	26
23	61	136/137 (99%)	128 (94%)	8 (6%)	24	61
24	62	87/107 (81%)	82 (94%)	5 (6%)	25	62
25	63	104/105 (99%)	93 (89%)	11 (11%)	8	36
26	64	54/129 (42%)	51 (94%)	3 (6%)	26	62
27	65	105/118 (89%)	91 (87%)	14 (13%)	5	28
28	66	109/110 (99%)	105 (96%)	4 (4%)	41	73
29	67	115/116 (99%)	111 (96%)	4 (4%)	43	74
30	68	118/119 (99%)	108 (92%)	10 (8%)	13	48
31	69	46/47 (98%)	42 (91%)	4 (9%)	13	45
32	70	81/88 (92%)	77 (95%)	4 (5%)	31	67
33	71	96/97 (99%)	85 (88%)	11 (12%)	7	32
34	72	109/111 (98%)	101 (93%)	8 (7%)	17	55
35	73	90/91 (99%)	82 (91%)	8 (9%)	12	44
36	74	95/103 (92%)	88 (93%)	7 (7%)	17	54
37	75	104/105 (99%)	97 (93%)	7 (7%)	20	57
38	76	81/82 (99%)	71 (88%)	10 (12%)	6	30
39	77	70/71 (99%)	65 (93%)	5 (7%)	18	55
40	78	68/69 (99%)	63 (93%)	5 (7%)	17	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	79	45/46 (98%)	40 (89%)	5 (11%)	8	34
42	80	47/116 (40%)	43 (92%)	4 (8%)	13	48
43	81	23/23 (100%)	18 (78%)	5 (22%)	1	9
44	82	88/91 (97%)	80 (91%)	8 (9%)	12	44
45	83	71/72 (99%)	70 (99%)	1 (1%)	74	89
47	S0	173/210 (82%)	161 (93%)	12 (7%)	19	56
48	S1	191/224 (85%)	174 (91%)	17 (9%)	12	44
49	S2	176/205 (86%)	168 (96%)	8 (4%)	34	69
50	S3	182/195 (93%)	172 (94%)	10 (6%)	27	64
51	S4	221/222 (100%)	200 (90%)	21 (10%)	11	41
52	S5	173/191 (91%)	162 (94%)	11 (6%)	22	58
53	S6	193/201 (96%)	180 (93%)	13 (7%)	20	57
54	S7	165/170 (97%)	157 (95%)	8 (5%)	31	67
55	S8	150/161 (93%)	140 (93%)	10 (7%)	20	57
56	S9	158/166 (95%)	143 (90%)	15 (10%)	11	41
57	10	89/98 (91%)	78 (88%)	11 (12%)	6	30
58	11	136/137 (99%)	126 (93%)	10 (7%)	17	54
59	12	100/119 (84%)	87 (87%)	13 (13%)	5	28
60	13	127/128 (99%)	117 (92%)	10 (8%)	15	51
61	14	96/105 (91%)	91 (95%)	5 (5%)	29	65
62	15	104/118 (88%)	100 (96%)	4 (4%)	40	73
63	16	117/119 (98%)	107 (92%)	10 (8%)	13	48
64	17	109/124 (88%)	101 (93%)	8 (7%)	17	55
65	18	128/129 (99%)	108 (84%)	20 (16%)	3	22
66	19	115/116 (99%)	108 (94%)	7 (6%)	23	60
67	20	100/114 (88%)	96 (96%)	4 (4%)	38	71
68	21	74/74 (100%)	63 (85%)	11 (15%)	4	24
69	22	110/111 (99%)	103 (94%)	7 (6%)	22	58
70	23	119/120 (99%)	110 (92%)	9 (8%)	16	53
71	24	112/113 (99%)	101 (90%)	11 (10%)	10	39
72	25	61/89 (68%)	54 (88%)	7 (12%)	7	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	26	83/101 (82%)	77 (93%)	6 (7%)	18	55
74	27	70/71 (99%)	67 (96%)	3 (4%)	35	70
75	28	56/60 (93%)	50 (89%)	6 (11%)	8	36
76	29	47/49 (96%)	44 (94%)	3 (6%)	22	58
77	30	51/54 (94%)	45 (88%)	6 (12%)	6	32
78	31	43/135 (32%)	40 (93%)	3 (7%)	19	56
79	RA	261/262 (100%)	241 (92%)	20 (8%)	16	52
All	All	9474/10182 (93%)	8721 (92%)	753 (8%)	20	51

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

Mol	Chain	Res	Type
30	68	97	GLU
43	81	4	LYS
71	24	124	ARG
33	71	6	ASP
36	74	86	LYS

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

Mol	Chain	Res	Type
29	67	36	HIS
41	79	32	ASN
69	22	98	GLN
30	68	28	HIS
35	73	26	ASN

5.3.3 RNA ⓘ

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

5 of 938 RNA backbone outliers are listed below:

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

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2S	2896	A
1	2S	3317	U
46	1S	1481	C
1	2S	3121	U
1	2S	3228	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no 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.