



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Aug 17, 2017 – 02:06 PM EDT

PDB ID : 4V3P
EMDB ID: : EMD-2790
Title : The molecular structure of the left-handed supra-molecular helix of eukaryotic polyribosomes
Authors : Myasnikov, A.G.; Afonina, Z.A.; Menetret, J.F.; Shirokov, V.A.; Spirin, A.S.; Klaholz, B.P.
Deposited on : unknown
Resolution : 34.00 Å(reported)
Based on PDB ID : 3IZ6

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
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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) : rb-20029824

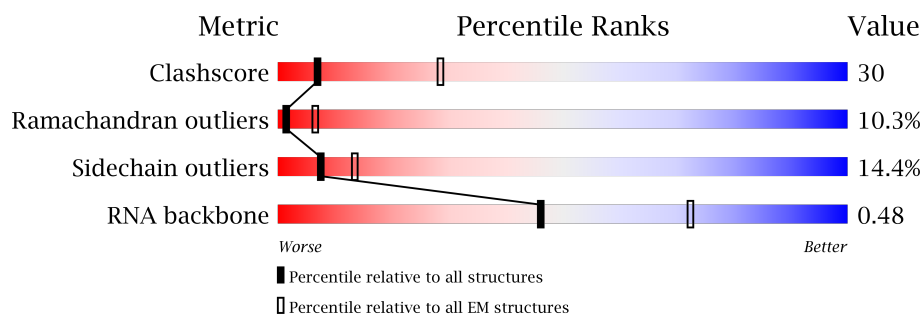
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 34.00 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.



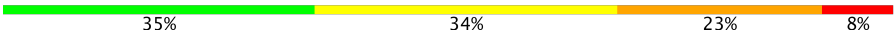

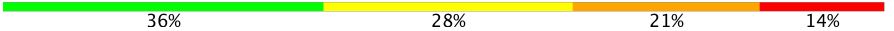

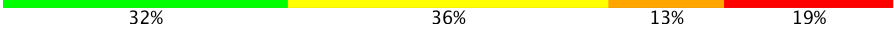



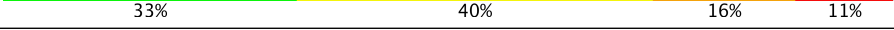


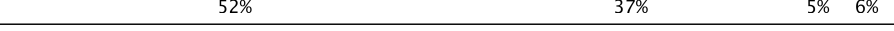
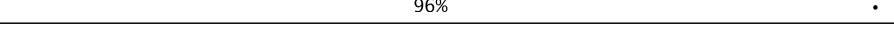
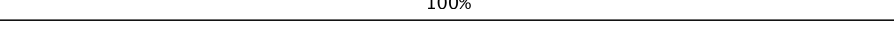





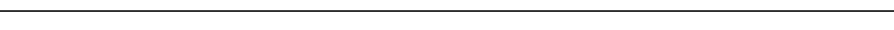

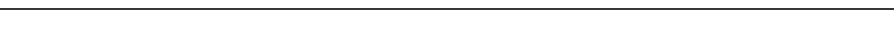
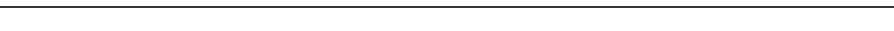


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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 ≥ 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	Sa	380	65% 26% 7% .
2	SA	260	35% 40% 18% 6%
3	SB	208	32% 34% 25% 9%
4	SD	200	31% 46% 13% 12%
5	SE	263	52% 30% 15% .
6	SF	191	61% 27% 10% .
7	SI	126	53% 30% 11% 6%
8	SJ	128	59% 30% 8% .




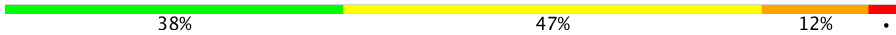
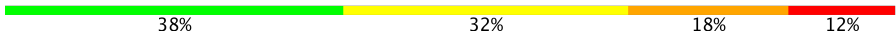






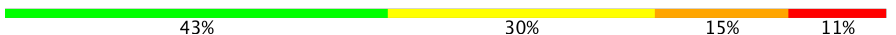
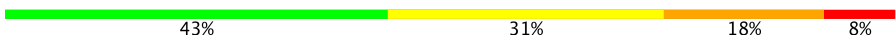

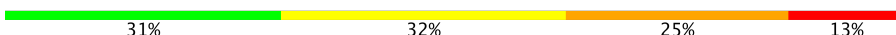










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Mol	Chain	Length	Quality of chain
9	SK	119	
10	SL	142	
11	SM	152	
12	SO	121	
13	SQ	141	
14	SP	85	
15	SS	146	
16	SR	91	
17	SV	100	
18	SW	92	
19	SY	58	
20	SZ	62	
21	Sc	25	
22	Sb	36	
23	SU	98	
24	SX	50	
25	SC	195	
26	SG	143	
27	SH	130	
28	SN	48	
29	ST	82	
30	S3	11	
31	S2	75	
32	S1	1743	
33	L1	3352	

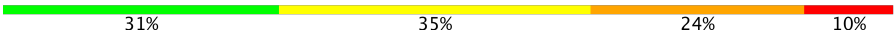



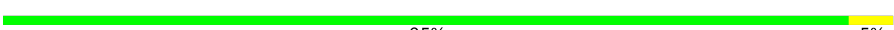





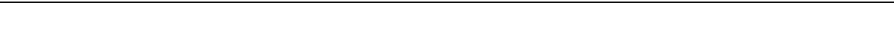

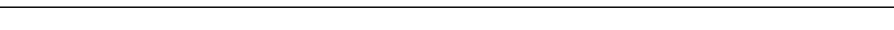
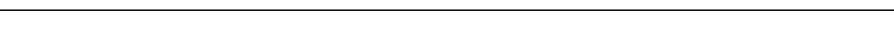





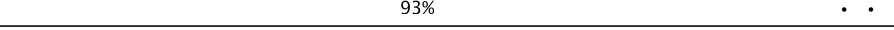





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Mol	Chain	Length	Quality of chain
34	L3	120	
35	L2	159	
36	LA	216	
37	LB	255	
38	LE	170	
39	LF	190	
40	LH	201	
41	LM	140	
42	LP	194	
43	LO	144	
44	LR	163	
45	LQ	304	
46	LT	189	
47	LU	164	
48	LV	171	
49	LX	122	
50	LZ	75	
51	LY	130	
52	Lb	73	
53	Ld	23	
54	Lf	112	
55	Lg	120	
56	Lh	133	
57	Li	94	
58	Ln	69	

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Mol	Chain	Length	Quality of chain
59	Lo	51	
60	Lr	105	
61	Lq	25	
62	Lx	20	
62	Ly	20	
63	Lz	14	
64	LG	219	
65	LL	182	
66	LN	134	
67	LS	167	
68	LW	108	
69	La	99	
70	Li	119	
71	Lj	104	
72	Lk	77	
73	Lp	41	
74	LJ	128	
75	Lt	58	
75	Lu	58	
76	Lv	59	
76	Lw	59	
77	Lc	124	
78	Le	244	
79	Ls	262	
80	LC	389	

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Mol	Chain	Length	Quality of chain
81	LD	372	<div><div></div><div>52%</div><div>29%</div><div>10%</div><div>9%</div></div>
82	LK	206	<div><div></div><div>59%</div><div>23%</div><div>13%</div><div></div></div>
83	Lm	92	<div><div></div><div>71%</div><div>18%</div><div>10%</div><div></div></div>
84	LI	184	<div><div></div><div>68%</div><div>20%</div><div>9%</div><div></div></div>

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 195694 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 protein called G protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Sa	380	Total	C	N	O	S	0	0
			2842	1758	512	553	19		

- Molecule 2 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	260	Total	C	N	O	S	0	0
			1946	1220	349	367	10		

- Molecule 3 is a protein called Putative 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SB	208	Total	C	N	O	S	0	0
			1539	964	288	279	8		

- Molecule 4 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SD	200	Total	C	N	O	S	0	0
			1607	1030	290	283	4		

- Molecule 5 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SE	263	Total	C	N	O	S	0	0
			2028	1283	385	352	8		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SF	191	Total	C	N	O	S	0	0
			1485	925	281	272	7		

- Molecule 7 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SI	126	Total	C	N	O	S	0	0
			1017	648	195	170	4		

- Molecule 8 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SJ	128	Total	C	N	O	S	0	0
			887	541	171	171	4		

- Molecule 9 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SK	119	Total	C	N	O	S	0	0
			830	508	159	159	4		

- Molecule 10 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SL	142	Total	C	N	O	S	0	0
			952	576	197	175	4		

- Molecule 11 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SM	152	Total	C	N	O	S	0	0
			1167	722	233	206	6		

- Molecule 12 is a protein called 40S ribosomal protein S13-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SO	121	Total	C	N	O	S	0	0
			977	627	180	167	3		

- Molecule 13 is a protein called 40S ribosomal protein S17-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SQ	141	Total	C	N	O	S	0	0
			1129	699	214	210	6		

- Molecule 14 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SP	85	Total	C	N	O	S	0	0
			639	399	130	107	3		

- Molecule 15 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SS	146	Total	C	N	O	S	0	0
			1155	726	218	207	4		

- Molecule 16 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SR	91	Total	C	N	O	S	0	0
			711	457	130	120	4		

- Molecule 17 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SV	100	Total	C	N	O	S	0	0
			740	458	142	140			

- Molecule 18 is a protein called 40S WHEAT GERM RIBOSOME1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SW	92	Total	C	N	O	S	0	0
			460	276	92	92			

- Molecule 19 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SY	58	Total	C	N	O	S	0	0
			442	274	83	82	3		

- Molecule 20 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SZ	62	Total	C	N	O	S	0	0
			469	289	105	73	2		

- Molecule 21 is a protein called Unknown 40S wheat germ ribosome protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Sc	25	Total	C	N	O	0	0
			126	75	25	26		

- Molecule 22 is a protein called Unknown 40S wheat germ ribosome protein 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Sb	36	Total	C	N	O	0	0
			181	108	36	37		

- Molecule 23 is a protein called Unknown 40S wheat germ ribosome protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SU	98	Total	C	N	O	S	0	0
			732	466	142	123	1		

- Molecule 24 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SX	50	Total	C	N	O	S	0	0
			375	235	65	68	7		

- Molecule 25 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SC	195	Total	C	N	O	S	0	0
			1535	958	307	265	5		

- Molecule 26 is a protein called Unknown 40S wheat germ ribosome protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	SG	143	Total	C	N	O	0	0
			716	429	143	144		

- Molecule 27 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SH	130	Total	C	N	O	S	0	0
			1042	667	189	181	5		

- Molecule 28 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SN	48	Total	C	N	O	S	0	0
			313	184	67	56	6		

- Molecule 29 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	ST	82	Total	C	N	O	S	0	0
			650	400	121	126	3		

- Molecule 30 is a RNA chain called 40S WHEAT GERM RIBOSOME protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	S3	11	Total	C	N	O	P	0	0
			236	106	45	74	11		

- Molecule 31 is a RNA chain called 40S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	S2	75	Total	C	N	O	P	0	0
			1599	712	280	532	75		

- Molecule 32 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S1	1743	Total	C	N	O	P	0	11
			33897	14994	5742	11418	1743		

- Molecule 33 is a RNA chain called 26S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L1	3352	Total	C	N	O	P	0	39
			69592	30953	12564	22725	3350		

- Molecule 34 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L3	120	Total	C	N	O	P	0	0
			2565	1144	461	840	120		

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L2	159	Total	C	N	O	P	0	0
			3192	1415	555	1063	159		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L2	136	G	C	conflict	GB 17016972

- Molecule 36 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LA	216	Total	C	N	O	S	0	0
			1718	1092	309	304	13		

- Molecule 37 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LB	255	Total	C	N	O	S	0	0
			1933	1200	398	326	9		

- Molecule 38 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LE	170	Total	C	N	O	S	0	0
			1376	867	256	244	9		

- Molecule 39 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LF	190	Total	C	N	O	S	0	0
			1500	947	270	277	6		

- Molecule 40 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LH	201	Total	C	N	O	S	0	0
			1564	996	289	273	6		

- Molecule 41 is a protein called Ribosomal Pr 117.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LM	140	Total	C	N	O	S	0	0
			1020	640	192	179	9		

- Molecule 42 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LP	194	Total	C	N	O	S	0	0
			1630	1027	342	257	4		

- Molecule 43 is a protein called 60S ribosomal protein L27a-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LO	144	Total	C	N	O	S	0	0
			1086	691	217	173	5		

- Molecule 44 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LR	163	Total	C	N	O	S	0	0
			1284	810	248	219	7		

- Molecule 45 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LQ	304	Total	C	N	O	S	0	0
			2395	1497	430	461	7		

- Molecule 46 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LT	189	Total	C	N	O	S	0	0
			1569	972	330	257	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LT	184	GLY	UNK	variant	UNP Q7XY20

- Molecule 47 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LU	164	Total	C	N	O	S	0	0
			1266	789	250	225	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LU	65	TRP	CYS	conflict	UNP W5EIT2

- Molecule 48 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LV	171	Total	C	N	O	S	0	0
			1335	826	266	238	5		

- Molecule 49 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LX	122	Total	C	N	O	S	0	0
			987	634	178	173	2		

- Molecule 50 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LZ	75	Total	C	N	O	S	0	0
			578	366	115	94	3		

- Molecule 51 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LY	130	Total	C	N	O	S	0	0
			1048	647	220	178	3		

- Molecule 52 is a protein called 60S ribosomal protein l28.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Lb	73	Total	C	N	O	S	0	0
			576	364	107	103	2		

- Molecule 53 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	Ld	23	Total	C	N	O	0	0
			199	119	41	39		

- Molecule 54 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Lf	112	Total	C	N	O	S	0	0
			825	516	146	157	6		

- Molecule 55 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Lg	120	Total	C	N	O	S	0	0
			944	585	185	171	3		

- Molecule 56 is a protein called Ribosomal L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lh	133	Total	C	N	O	S	0	0
			1089	688	216	179	6		

- Molecule 57 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ll	94	Total	C	N	O	S	0	0
			725	438	158	122	7		

- Molecule 58 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ln	69	Total	C	N	O	S	0	0
			547	347	102	96	2		

- Molecule 59 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Lo	51	Total	C	N	O	S	0	0
			460	291	100	67	2		

- Molecule 60 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Lr	105	Total	C	N	O	S	0	0
			838	523	166	143	6		

- Molecule 61 is a protein called Unknown 60S wheat germ ribosome protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Lq	25	Total	C	N	O	S	0	0
			238	145	62	28	3		

- Molecule 62 is a protein called Unknown 60S wheat germ ribosome protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	Ly	20	Total	C	N	O	0	0
			101	60	20	21		
62	Lx	20	Total	C	N	O	0	0
			101	60	20	21		

- Molecule 63 is a protein called Unknown 60S wheat germ ribosome protein 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	Lz	14	Total	C	N	O	0	0
			71	42	14	15		

- Molecule 64 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	LG	219	Total	C	N	O	S	0	0
			1730	1106	314	306	4		

- Molecule 65 is a protein called Unknown 60S wheat germ ribosome protein 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	LL	182	Total	C	N	O	0	0
			910	545	182	183		

- Molecule 66 is a protein called Unknown 60S wheat germ ribosome protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	LN	134	Total	C	N	O	S	0	0
			1081	690	201	185	5		

- Molecule 67 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	LS	167	Total	C	N	O	S	0	0
			1419	916	263	233	7		

- Molecule 68 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	LW	108	Total	C	N	O	S	0	0
			839	530	152	155	2		

- Molecule 69 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	La	99	Total	C	N	O	S	0	0
			732	463	140	126	3		

- Molecule 70 is a protein called Ribosomal protein l34.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Li	119	Total	C	N	O	S	0	0
			964	606	195	161	2		

- Molecule 71 is a protein called ribosomal protein L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lj	104	Total	C	N	O	S	0	0
			797	498	158	138	3		

- Molecule 72 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Lk	77	Total	C	N	O	S	0	0
			613	383	128	100	2		

- Molecule 73 is a protein called Ubiquitin-60S ribosomal protein L40-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Lp	41	Total	C	N	O	S	0	0
			344	211	75	53	5		

- Molecule 74 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	LJ	128	Total	C	N	O	S	0	0
			959	601	177	177	4		

- Molecule 75 is a protein called Ribosomal protein P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Lt	58	Total	C	N	O	S	0	0
			432	283	69	79	1		
75	Lu	58	Total	C	N	O	S	0	0
			432	283	69	79	1		

- Molecule 76 is a protein called 60S acidic ribosomal protein P2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Lv	59	Total	C	N	O	S	0	0
			441	278	69	90	4		
76	Lw	59	Total	C	N	O	S	0	0
			441	278	69	90	4		

- Molecule 77 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Lc	124	Total	C	N	O		0	0
			1006	632	202	172			

- Molecule 78 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Le	244	Total	C	N	O	S	0	0
			1984	1271	368	339	6		

- Molecule 79 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Ls	262	Total	C	N	O	S	0	0
			1993	1278	330	377	8		

- Molecule 80 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	LC	389	Total	C	N	O	S	0	0
			3102	1968	578	538	18		

- Molecule 81 is a protein called 60S ribosomal protein L4/L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	LD	372	Total	C	N	O	S	0	0
			2866	1802	555	502	7		

- Molecule 82 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	LK	206	Total	C	N	O	S	0	0
			1650	1045	320	274	11		

- Molecule 83 is a protein called 60S ribosomal protein L37a, expressed.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Lm	92	Total	C	N	O	S	0	0
			715	447	137	124	7		

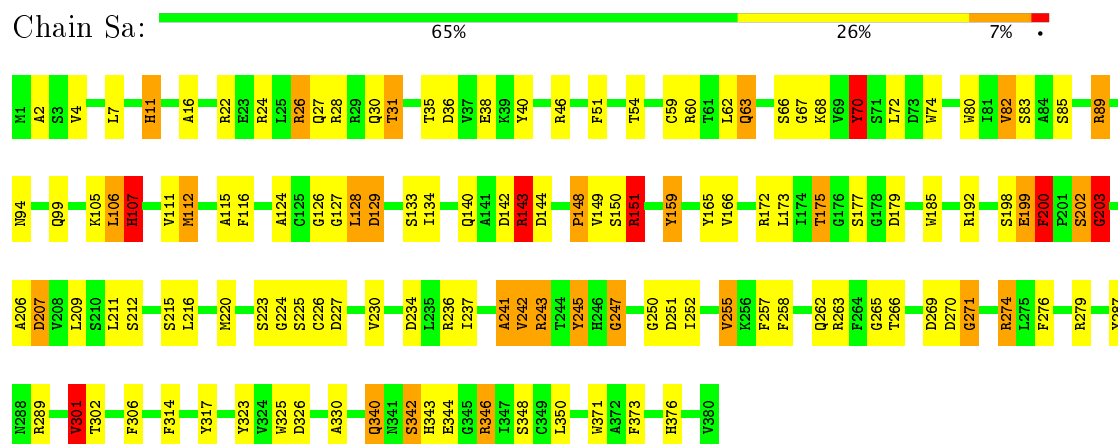
- Molecule 84 is a protein called 60S ribosomal protein L10-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	LI	184	Total	C	N	O	S	0	0
			1468	923	288	245	12		

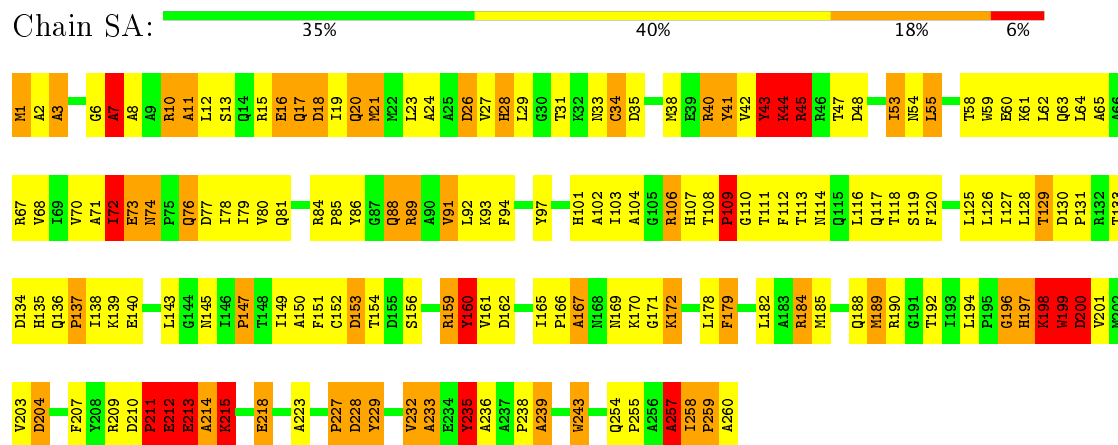
3 Residue-property plots

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.

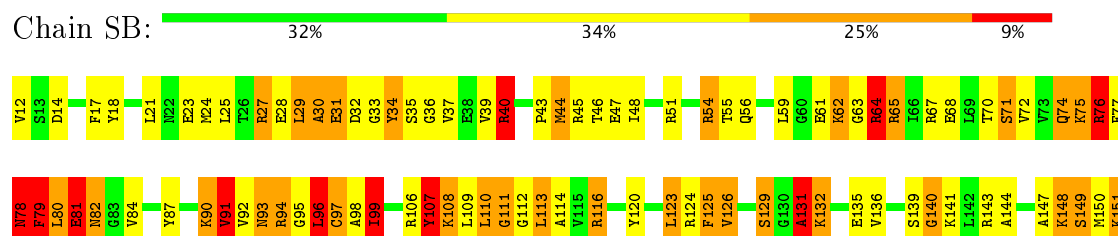
- Molecule 1: G protein beta subunit



- Molecule 2: 40S ribosomal protein SA



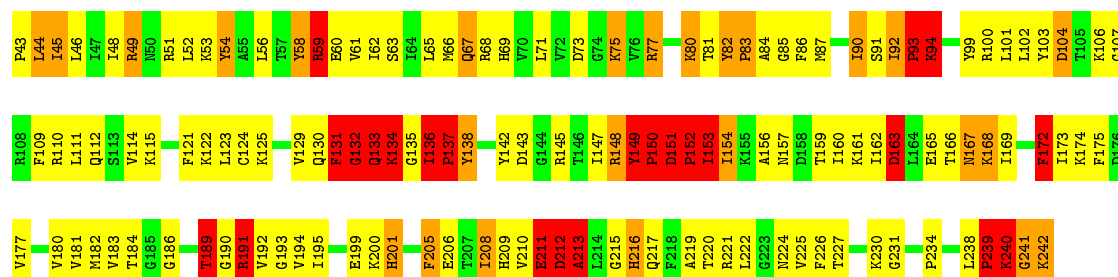
- Molecule 3: Putative 40S ribosomal protein S3





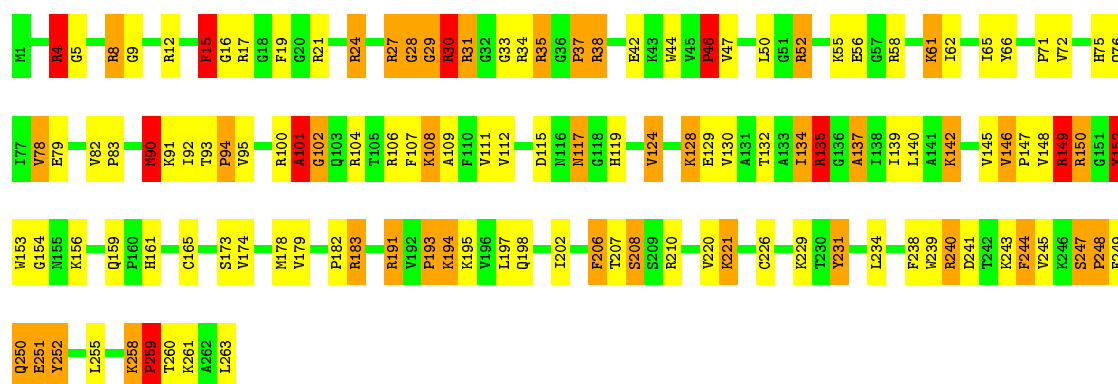
• Molecule 4: 40S ribosomal protein S4

Chain SD: 31% 46% 13% 12%



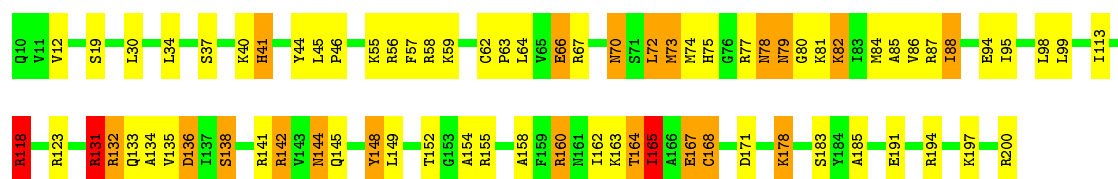
• Molecule 5: 40S ribosomal protein S2

Chain SE: 52% 30% 15%



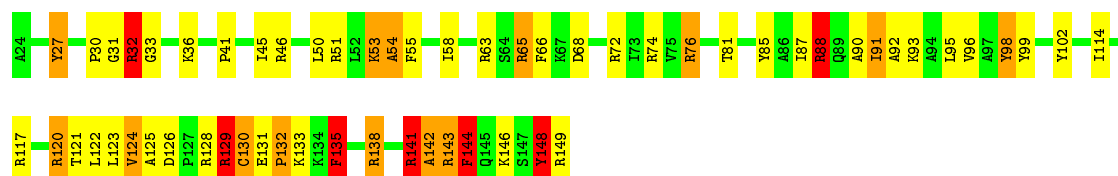
• Molecule 6: 40S ribosomal protein S5

Chain SF: 61% 27% 10%

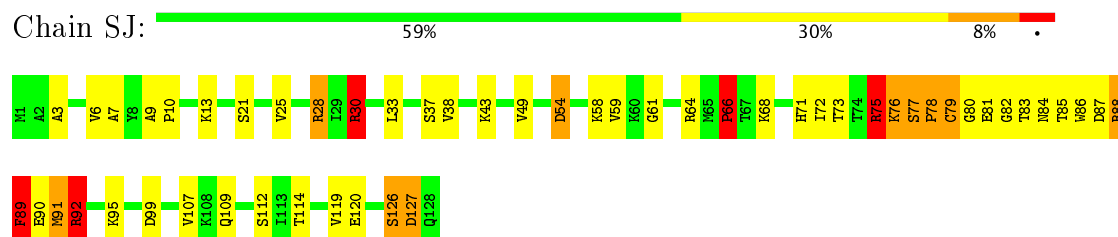


• Molecule 7: 40S ribosomal protein S16

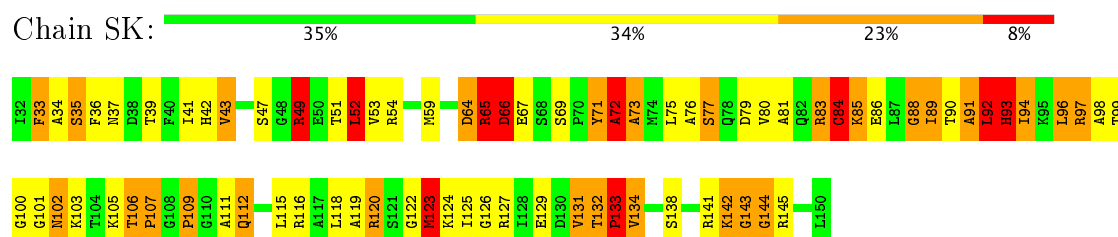
Chain SI: 53% 30% 11% 6%



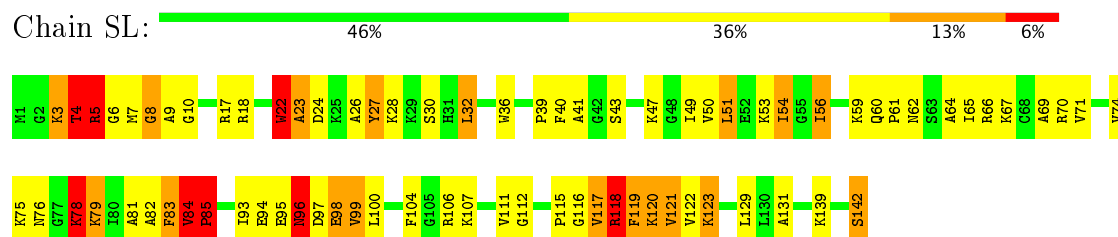
- Molecule 8: 40S ribosomal protein S20



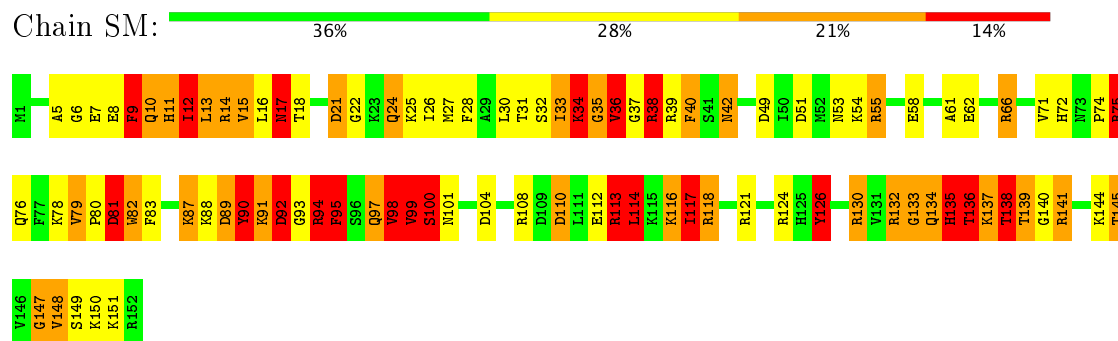
- Molecule 9: 40S ribosomal protein S14



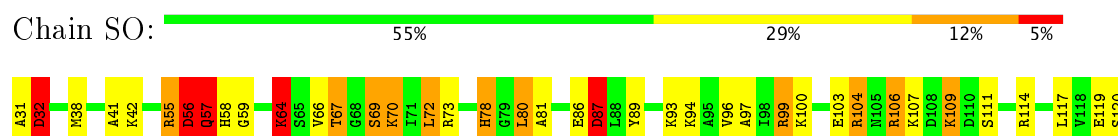
- Molecule 10: 40S ribosomal protein S23

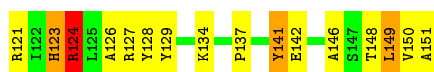


- Molecule 11: 40S ribosomal protein S18



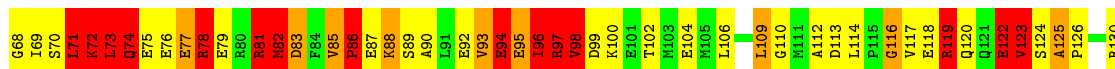
- Molecule 12: 40S ribosomal protein S13-1





- Molecule 13: 40S ribosomal protein S17-4

Chain SQ: 32% 36% 13% 19%



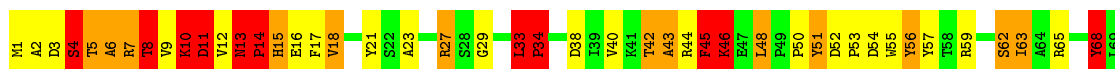
- Molecule 14: 40S ribosomal protein S11

Chain SP: 25% 41% 24% 11%



- Molecule 15: 40S ribosomal protein S19

Chain SS: 47% 27% 16% 10%



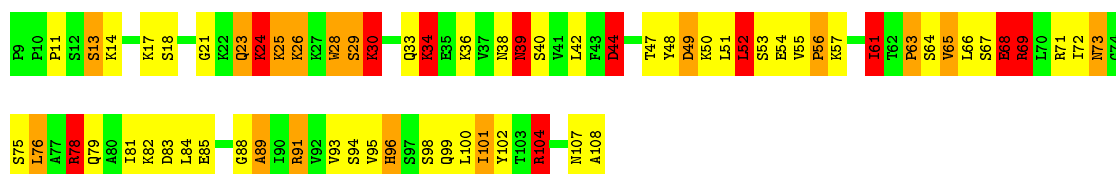
- Molecule 16: 40S ribosomal protein S15

Chain SR: 55% 30% 12%



- Molecule 17: 40S ribosomal protein S25

Chain SV: 33% 40% 16% 11%



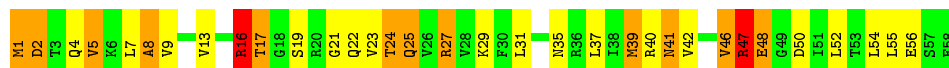
- Molecule 18: 40S WHEAT GERM RIBOSOME1

Chain SW: 67% 29% .



- Molecule 19: 40S ribosomal protein S28

Chain SY: 43% 33% 21% .



- Molecule 20: 40S ribosomal protein S30

Chain SZ: 52% 37% 5% 6% .



- Molecule 21: Unknown 40S wheat germ ribosome protein 2

Chain Sc: 96% .



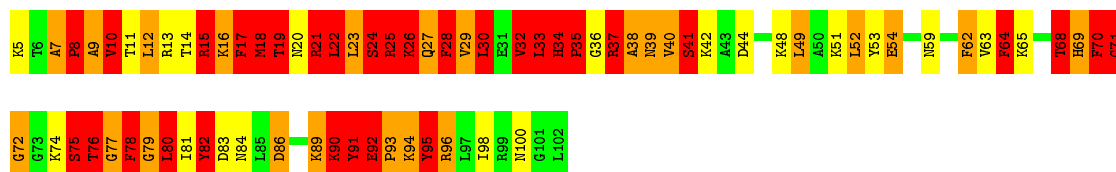
- Molecule 22: Unknown 40S wheat germ ribosome protein 3

Chain Sb: 100%

There are no outlier residues recorded for this chain.

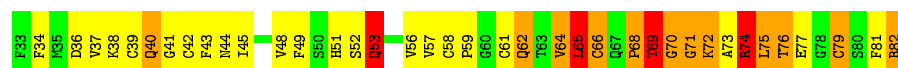
- Molecule 23: Unknown 40S wheat germ ribosome protein 3

Chain SU: 23% 20% 23% 33%



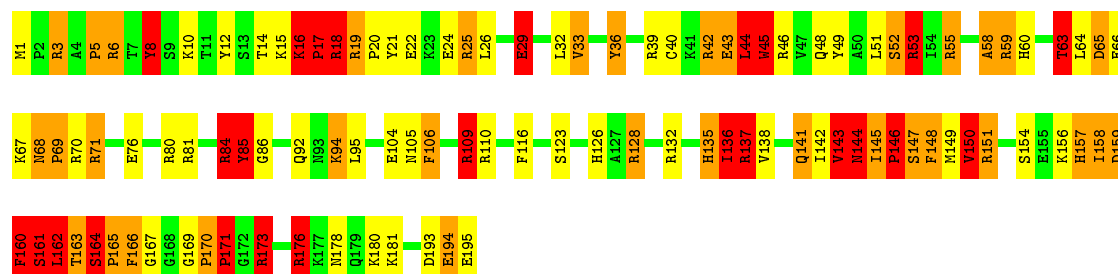
- Molecule 24: 40S ribosomal protein S27

Chain SX: 



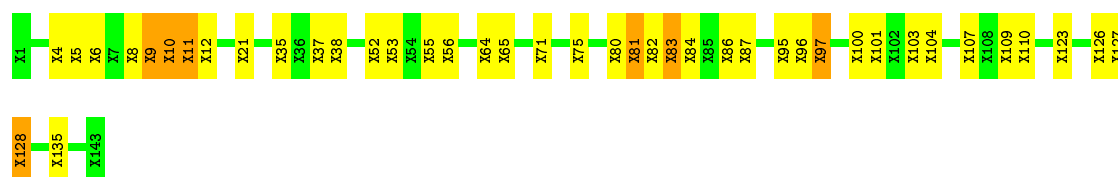
- Molecule 25: 40S ribosomal protein S9

Chain SC: 




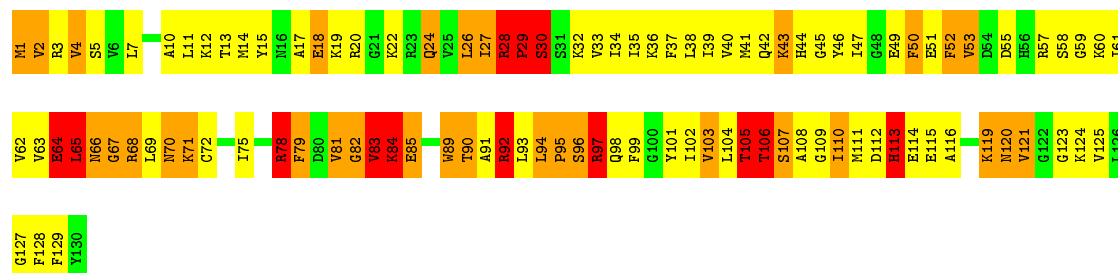
- Molecule 26: Unknown 40S wheat germ ribosome protein 4

Chain SG: 



- Molecule 27: Ribosomal protein S15

Chain SH: 



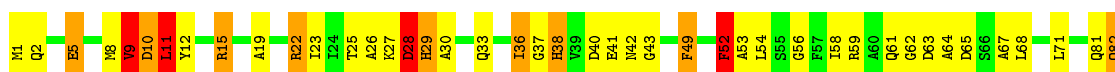
- Molecule 28: 40S ribosomal protein S29

Chain SN: 



- Molecule 29: 40S ribosomal protein S21

Chain ST: 



• Molecule 30: 40S WHEAT GERM RIBOSOME protein 4

Chain S3: 9% 36% 36% 18%



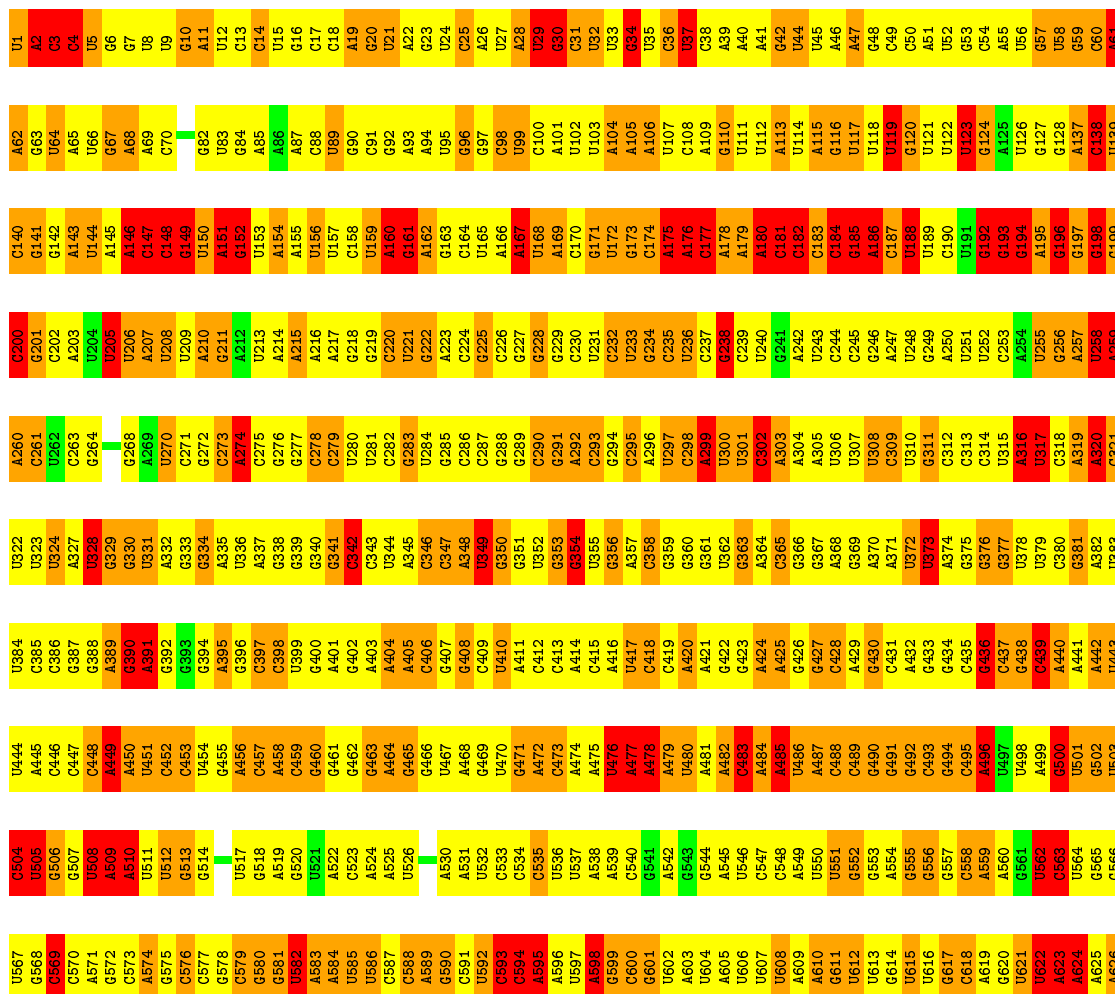
• Molecule 31: 40S ribosomal RNA

Chain S2: 41% 35% 23%

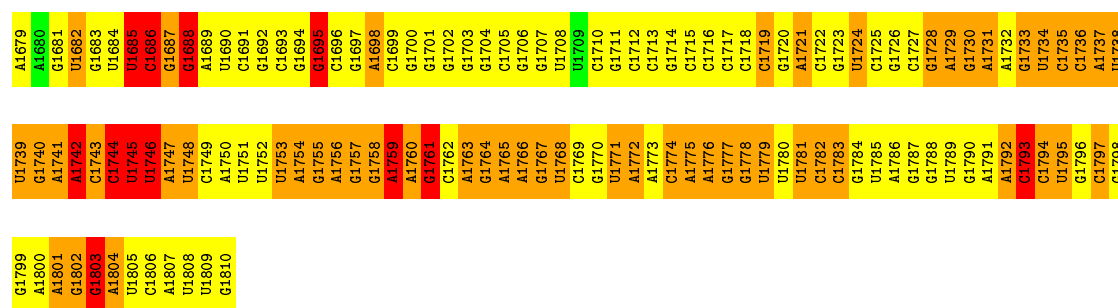


• Molecule 32: 18S ribosomal RNA

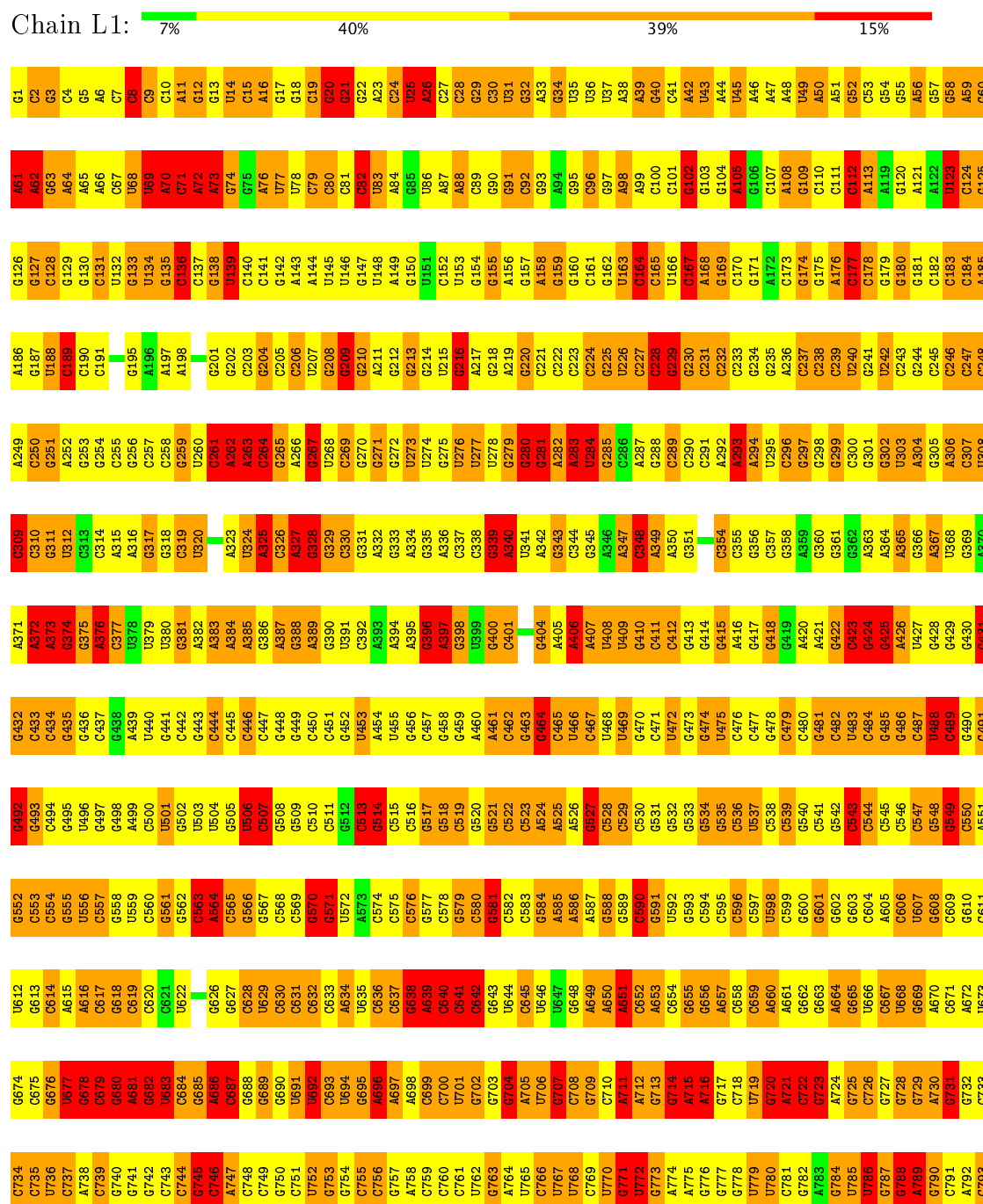
Chain S1: 7% 47% 35% 11%



A1619	U1559	A1489	C1426	C1365	U1305	U1244	C1184	G1124	U1063	A1003	G943	G883	U796	C687	A627
C1620	U1560	G1492	A1427	A1366	U1306	G1245	U1185	U1125	U1064	U1004	A944	G884	A796	U688	A628
A1621	C1561	A1493	A1428	C1367	U1307	A1246	U1186	C1126	A1065	C1005	A945	C885	C798	C689	A629
A1622	C1562	A1494	U1429	C1368	G1308	G1247	A1187	G1127	U1066	A1006	A946	A886	A799	G690	U630
C1623	A1563	G1494	A1430	C1369	U1309	A1248	U1188	C1128	A1067	G1007	A947	U887	U800	A691	A631
G1624	A1564	C1494	A1431	C1370	C1310	G1249	U1189	A1129	G1068	A1008	C948	U888	U801	G692	A632
U1625	U1565	A1496	C1432	U1371	U1311	C1250	U1190	A1130	G1069	U1009	A949	C889	A802	C693	U633
C1626	U1566	U1497	A1433	C1372	G1312	U1251	U1191	G1131	A1070	A1010	U850	C890	G803	C694	U634
C1627	U1567	A1498	C1373	G1313	G1313	U1252	U1192	G1132	C1071	C1011	U851	U891	A823	U715	U635
C1628	U1568	G1498	G1374	U1314	U1254	U1255	A1193	C1133	U1072	C1012	U852	A892	U824	U716	U636
U1629	U1569	A1500	A1436	C1375	U1315	U1256	C1194	C1073	G1073	U1013	G953	U893	U825	U717	U637
G1630	G1570	U1501	A1437	A1376	A1316	U1257	U1195	G1135	G1074	U1014	C954	U894	C826	A718	U638
C1631	G1571	C1503	C1437	G1377	A1317	U1258	U1196	A1136	G1075	C1015	C955	U895	C827	G717	U639
C1632	U1572	U1504	C1438	C1378	U1318	U1259	A1197	A1137	C1076	C1016	A956	C896	G828	C718	A640
C1633	C1573	U1505	U1440	U1379	U1319	G1260	A1198	A1138	C1077	U1017	A957	A897	G829	C719	U641
C1634	U1574	G1506	A1441	A1380	C1320	A1261	C1199	A1139	G1078	A1018	U958	U898	U830	U720	U642
U1635	U1575	A1442	A1442	G1381	C1321	U1262	A1200	U1140	G1079	U1019	G959	A899	C831	U724	U643
U1636	C1576	U1443	U1443	C1382	G1322	G1263	C1201	U1141	C1080	U1020	A960	G900	C832	U725	U644
C1637	A1577	U1508	G1444	U1383	U1323	U1264	G1202	A1142	A1081	C1021	U961	U901	U833	U726	U645
U1638	A1578	G1510	C1445	U1384	U1324	U1265	G1203	A1143	C1082	U1022	G962	C902	A834	U731	U646
A1639	C1579	U1511	C1446	C1385	A1325	U1266	G1204	A1144	C1083	C1023	U963	A903	U835	U732	U647
C1640	U1580	A1512	U1447	U1386	A1326	G1267	G1205	G1145	U1084	A1024	U964	G904	U836	U733	U648
A1641	A1581	C1513	U1448	C1387	C1327	U1268	A1206	G1146	U1085	A1025	U965	A905	G837	U734	U649
C1642	G1582	U1514	U1449	A1388	G1328	G1269	A1207	A1147	A1086	C1026	U966	G906	U838	C734	U650
A1643	G1583	G1515	A1450	G1389	A1329	G1270	A1208	A1148	G1088	C1027	C967	G907	G839	C735	U651
C1644	A1584	C1516	A1452	A1390	A1330	U1271	C1209	U1149	A1089	A1028	A968	U908	U840	U736	U652
C1645	U1585	C1517	U1453	G1391	C1331	G1272	U1210	U1150	G1090	U1029	U969	G909	U841	U740	U653
G1646	C1586	U1518	G1454	C1392	C1332	G1273	U1211	G1151	A1091	A1030	U970	A910	G842	C741	U654
C1647	G1587	G1519	U1455	G1393	A1333	G1274	A1212	A1152	A1092	A1031	G971	A911	G843	U742	U655
C1648	C1588	G1520	U1456	A1394	G1334	G1275	C1213	C1153	A1093	A1032	A972	A912	C844	U743	U656
C1649	U1589	G1521	C1457	C1395	A1335	G1276	C1214	G1154	U1094	C1033	U973	U913	C845	U744	U657
U1650	U1590	U1522	U1458	U1396	C1336	U1277	A1215	G1155	C1095	G1034	C974	U914	U846	U745	U658
U1651	A1591	A1524	G1459	A1397	C1337	G1278	G1216	A1156	A1096	A1035	A975	C915	U847	A766	U659
C1652	U1592	C1525	G1460	U1398	U1338	A1279	U1217	A1157	A1097	U1036	U976	U916	C848	A767	U660
C1653	U1593	C1526	G1461	G1399	C1339	U1280	U1218	G1158	A1098	G1037	G977	U917	G849	A768	U661
C1654	A1594	U1535	C1462	G1400	A1340	G1281	C1219	G1159	G1099	C1038	A978	G918	G850	G769	U662
U1655	A1595	U1536	G1464	C1401	G1341	G1282	C1220	G1160	U1100	C1039	A979	G919	G851	U770	U663
C1656	G1596	U1537	C1465	C1402	C1342	G1283	A1221	C1161	C1101	G1040	C980	A920	A852	G771	U664
C1657	C1597	U1538	A1466	U1403	C1343	C1284	G1222	A1162	U1102	A1041	G981	U921	U853	C772	U665
U1658	G1598	U1539	C1467	U1404	U1344	C1285	A1223	C1163	U1103	C1042	A982	U922	C854	U773	U666
A1659	C1599	U1540	G1468	U1405	G1345	G1286	C1224	C1164	U1104	C1043	A983	U923	G855	C774	U667
C1660	G1600	U1541	C1469	U1406	C1346	U1287	A1225	A1165	G1105	A1044	A984	A924	G856	A775	U668
C1661	A1601	G1542	A1470	A1407	U1347	G1288	U1226	C1166	G1106	G1045	G985	U925	A857	A776	U669
C1662	G1602	U1543	C1471	A1408	A1348	U1289	A1227	C1167	G1107	G1046	U986	G926	G858	A777	U670
A1663	U1603	U1544	G1472	G1409	A1349	U1290	G1228	A1168	U1108	G1047	U987	A927	U859	G778	U671
U1664	C1604	G1544	C1473	C1410	C1350	U1291	C1229	A1169	U1109	A1048	A988	A928	A860	C779	U672
U1665	A1605	U1545	U1474	C1411	U1351	G1292	A1230	G1170	C1110	U1049	G989	A929	A861	U783	U673
G1666	U1606	U1546	A1475	A1412	A1352	G1293	A1231	G1171	C1111	C1050	G990	G930	U862	C784	U674
A1667	G1607	G1547	C1476	C1413	G1353	U1294	G1232	G1172	G1112	G1051	G991	A931	G871	C785	A675
A1668	A1608	U1548	A1477	G1414	C1354	U1295	G1233	U1173	G1113	G1052	G992	C932	G872	A786	U676
U1669	G1609	G1549	C1478	G1415	U1355	G1296	A1234	G1174	G1114	C1053	C993	G933	G873	U786	U677
G1670	U1610	U1550	U1479	A1416	A1356	U1297	U1235	G1175	G1115	G1054	A994	A934	A874	C787	A678
U1671	U1611	A1551	G1480	A1417	U1357	G1298	U1236	A1176	G1116	G1055	C995	A935	C875	C788	U679
U1672	C1612	U1552	A1481	G1418	G1358	U1299	G1237	G1177	G1117	A1056	G996	C936	A876	C789	U680
C1673	G1613	A1553	U1482	U1419	C1359	U1299	A1238	C1178	A1118	U1057	A997	A937	G877	U790	U681
C1674	C1614	U1554	U1483	U1421	G1360	A1300	C1239	C1179	G1119	G1058	A998	A938	U878	C791	A682
G1675	G1615	U1555	U1484	G1422	G1361	G1301	A1240	U1180	U1120	U1059	G999	C939	C879	U792	U683
G1676	U1616	A1423	A1485	A1424	A1362	C1302	G1241	G1181	A1121	U1060	A1000	U940	G880	U793	U684
U1677	U1617	G1424	C1424	G1303	G1363	C1303	A1242	G1182	U1122	G1061	C1001	G941	G881	G793	U685
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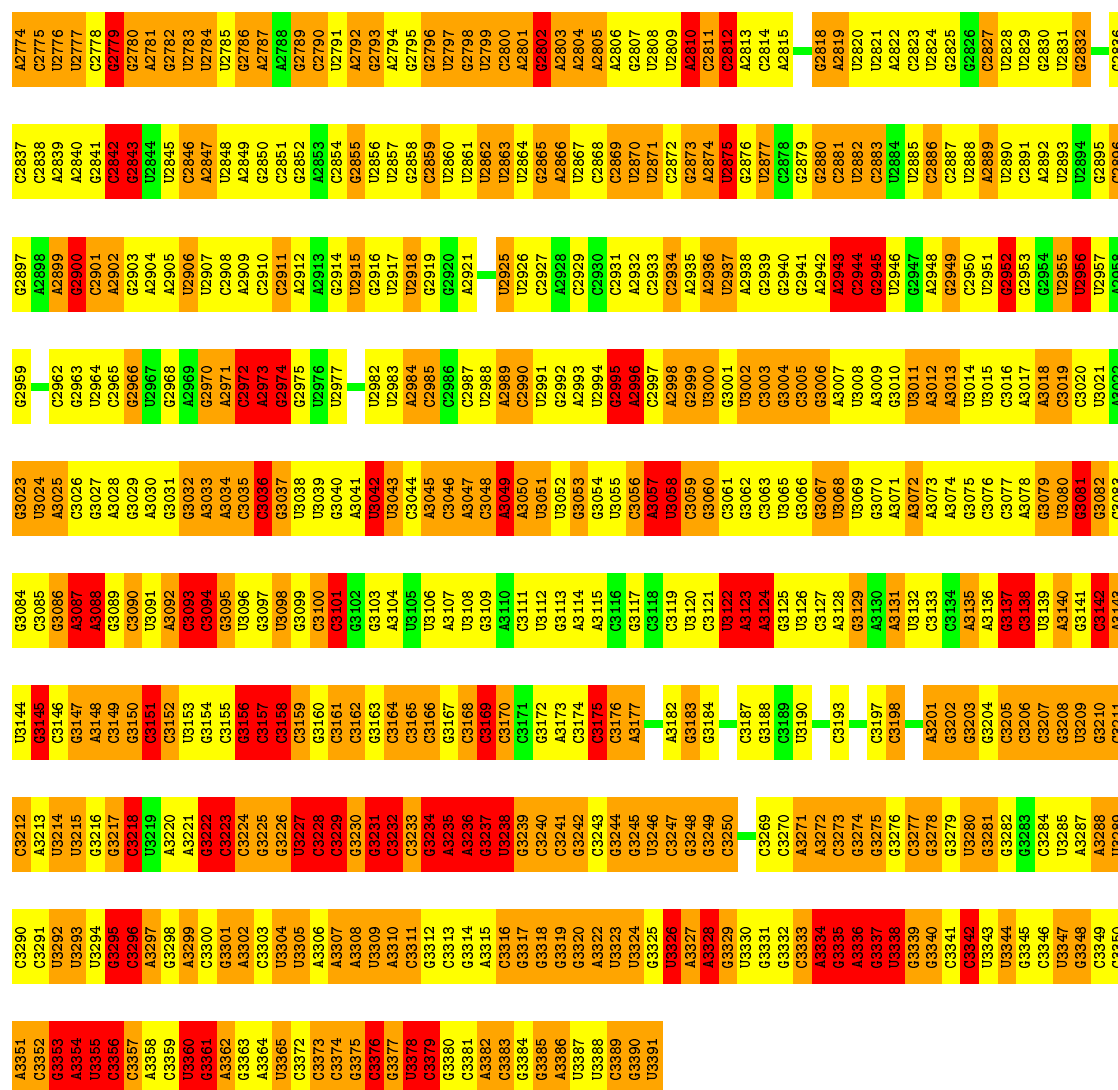


- Molecule 33: 26S ribosomal RNA

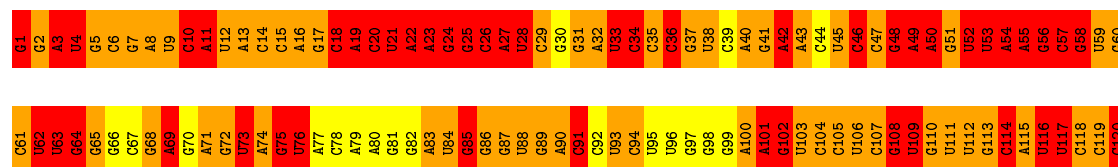
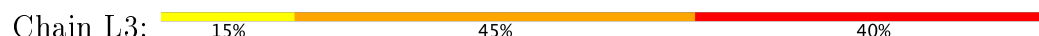


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C1720	C1660	A1537	G1476	G1340	C1279	C1219	C1159	G1099	G1038	6975	G915	U885	C795
A1721	A1561	A1538	A1477	G1341	U1280	G1220	G1160	G1100	A1040	A976	A916	G856	C796
G1722	G1662	G1539	A1478	C1342	C1281	A1221	A1161	A1101	C1041	6977	A917	G857	U797
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C1724	C1664	G1541	G1480	A1344	C1283	U1223	A1163	U1103	U1043	C979	G919	G859	U799
G1665	G1665	A1542	C1481	U1345	C1284	A1224	G1164	C1104	A1044	C980	A920	G860	C800
C1666	U1604	G1420	C1482	U1346	U1285	A1225	G1165	G1105	A1045	A981	G921	A861	G801
A1726	C1667	G1544	C1483	U1347	G1286	G1226	C1166	G1106	U1046	U982	U922	G862	G802
G1728	U1668	G1545	A1484	C1348	C1287	A1227	G1167	G1107	U1047	U983	A923	G863	A803
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U1730	G1670	G1547	G1486	G1350	C1289	U1229	G1169	G1109	U1049	C985	U925	U865	C805
A1731	U1671	U1610	A1487	C1351	A1290	G1230	U1170	C1110	A1050	G986	C926	C866	C806
G1732	G1672	C1426	G1488	C1351	A1291	C1231	U1171	U1111	A1051	A987	G927	G867	C807
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A1764	C1703	C1582	U1522	A1395	C1323	A1263	A1204	G1144	G1084	U1020	C960	C900	A840
G1765	U1704	G1583	G1522	C1395	G1324	U1264	G1145	G1145	G1085	U1021	C961	U901	C841
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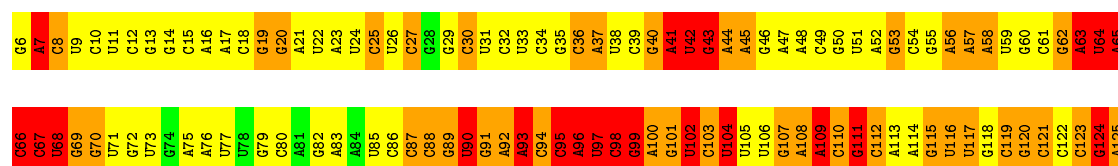


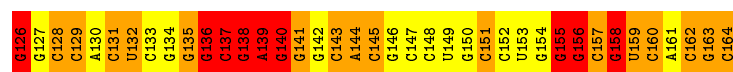



- Molecule 34: 5S ribosomal RNA



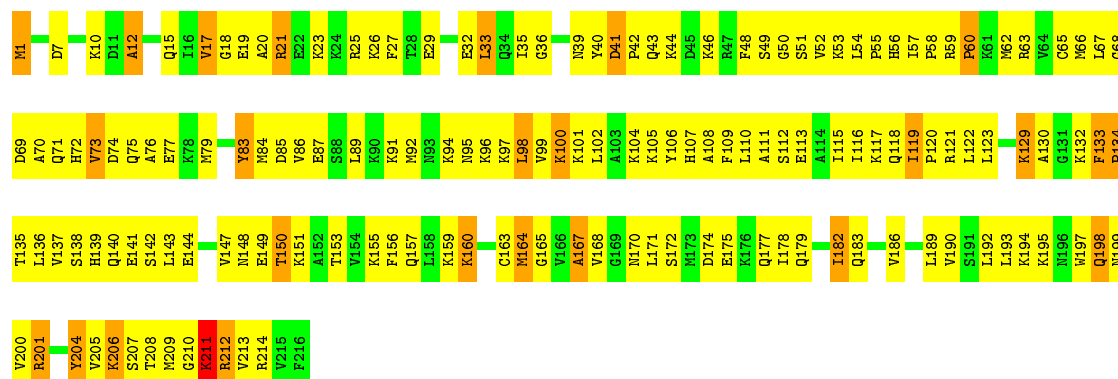
- Molecule 35: 5.8S ribosomal RNA





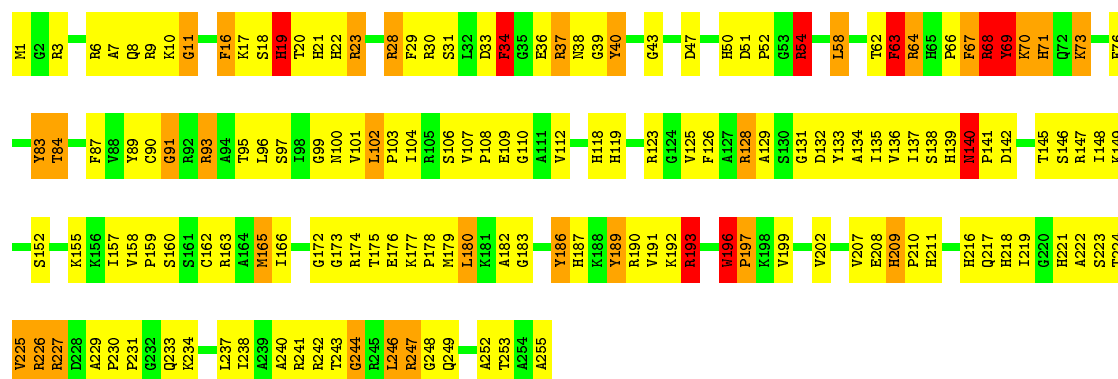
• Molecule 36: Ribosomal protein

Chain LA: 28% 60% 12%



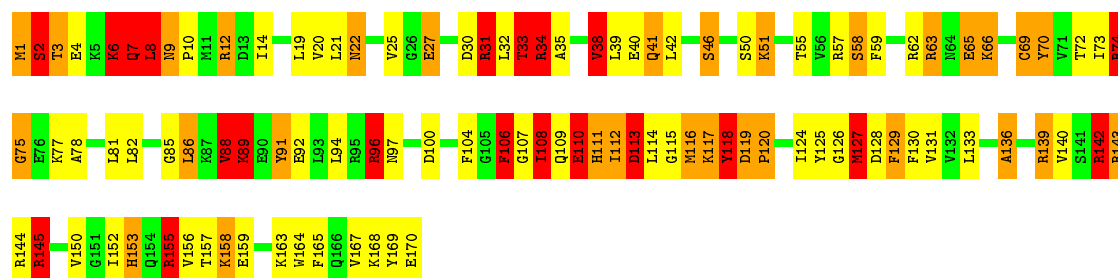
• Molecule 37: 60S ribosomal protein L2

Chain LB: 38% 47% 12%



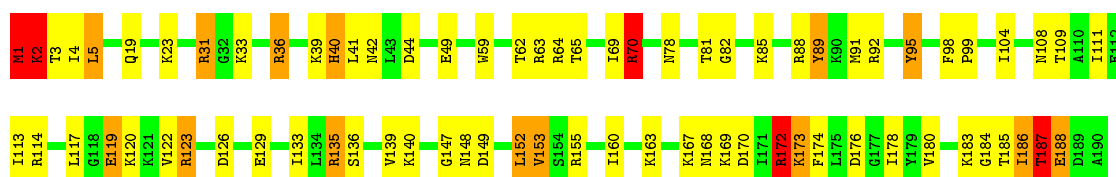
• Molecule 38: Ribosomal protein L11

Chain LE: 38% 32% 18% 12%

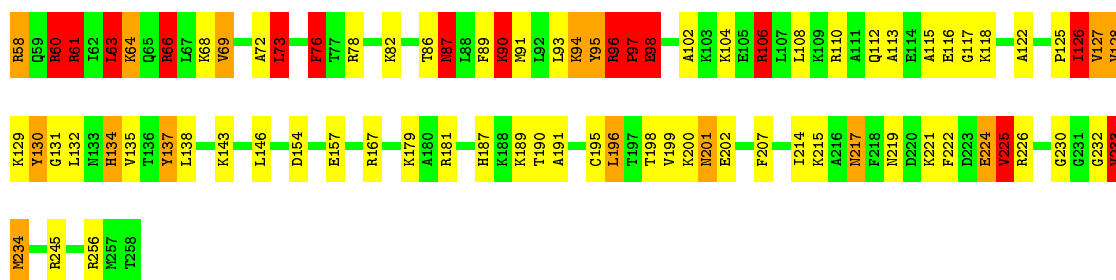


• Molecule 39: 60S ribosomal protein L9

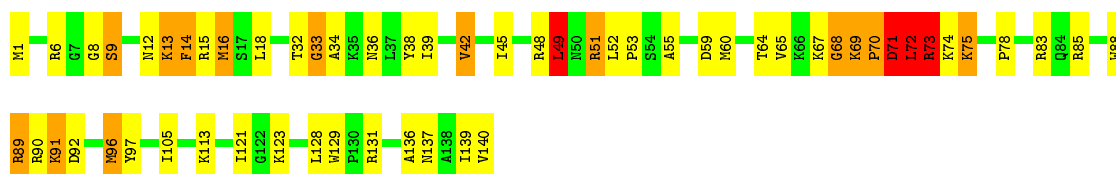
Chain LF: 60% 30% 7%



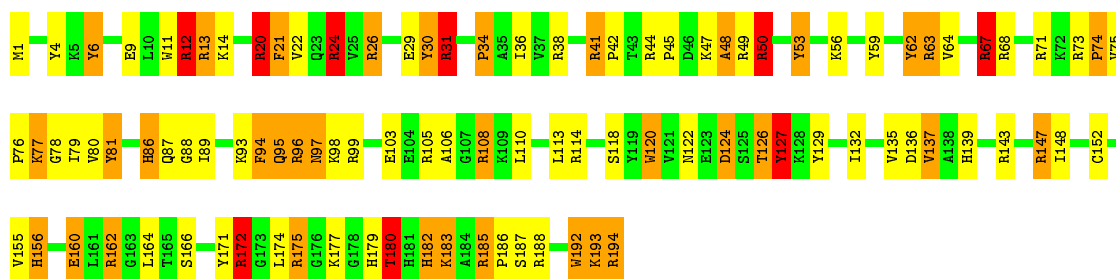
• Molecule 40: 60S ribosomal protein L7a



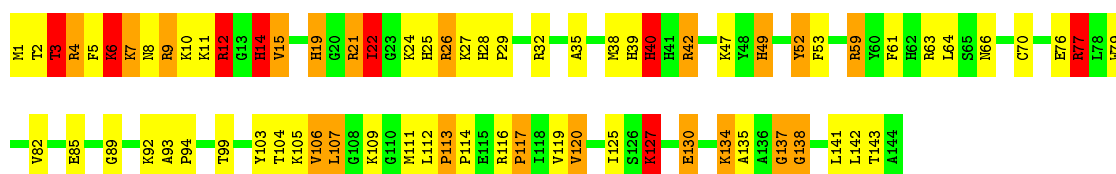
• Molecule 41: Ribosomal Pr 117



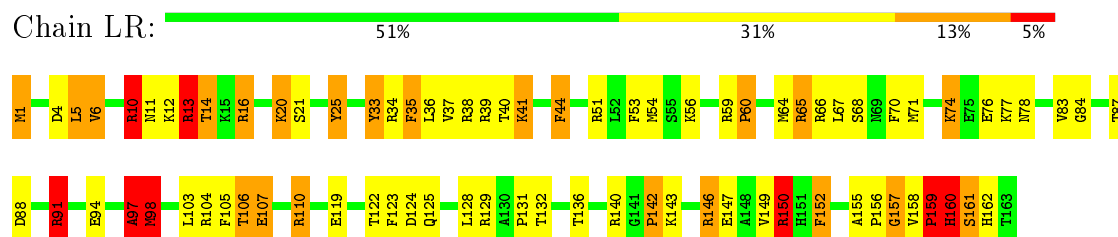
• Molecule 42: Ribosomal protein L15



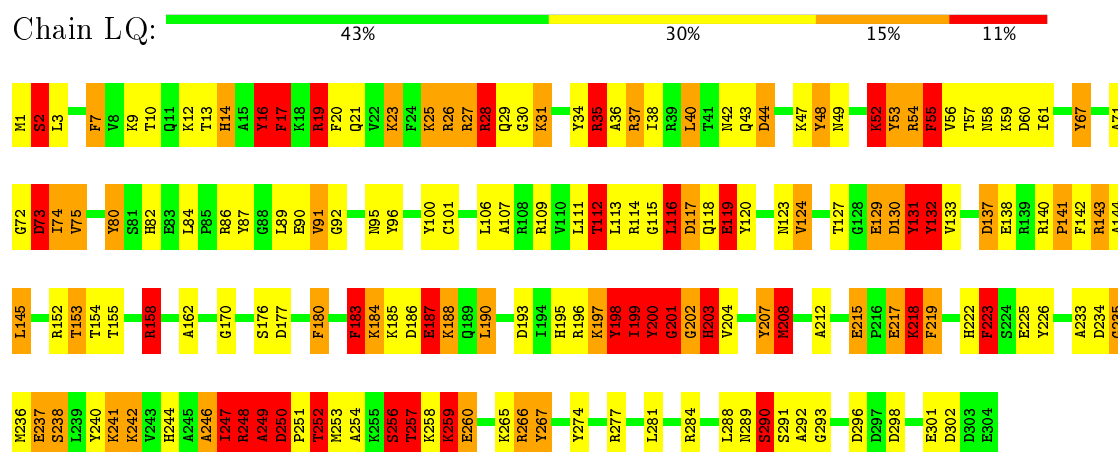
• Molecule 43: 60S ribosomal protein L27a-3



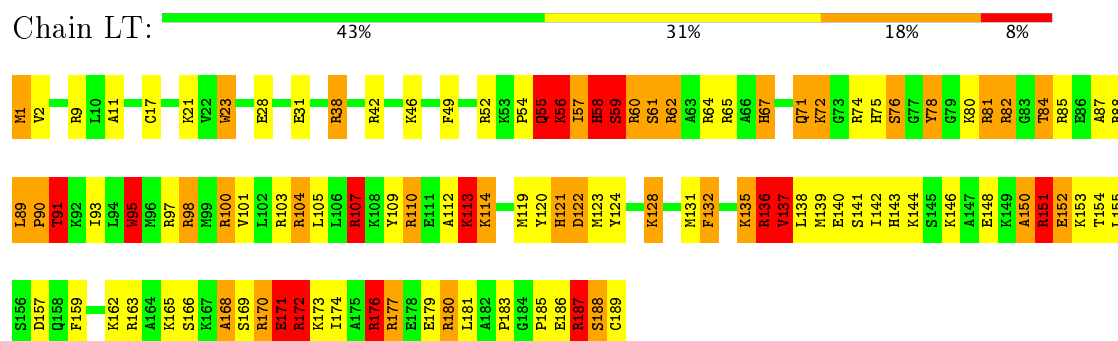
- Molecule 44: 60S ribosomal protein L18



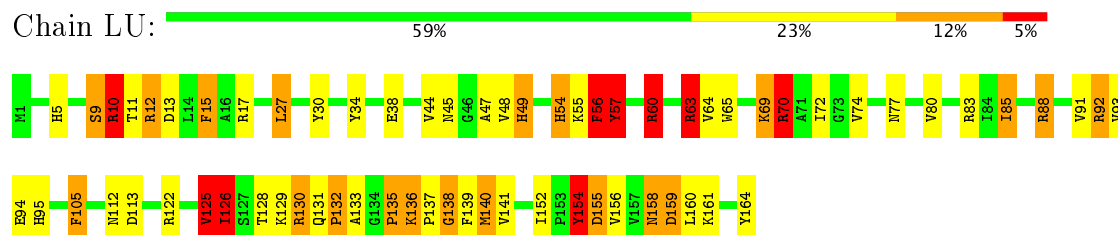
- Molecule 45: 60S ribosomal protein L5



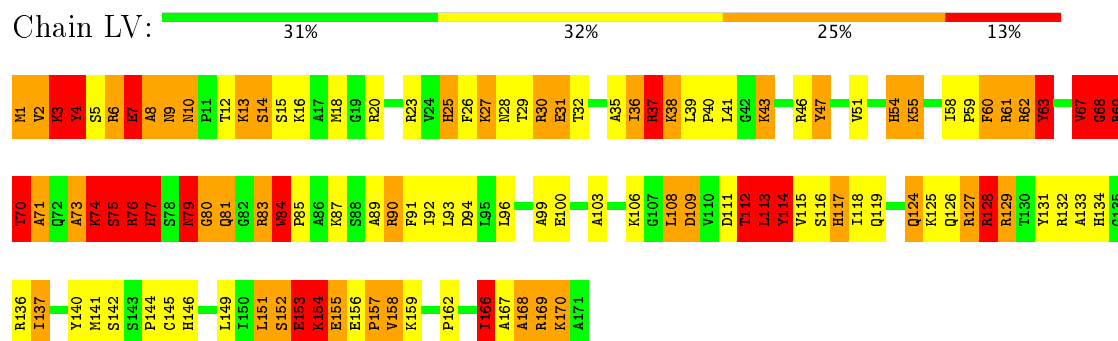
- Molecule 46: Ribosomal protein L19



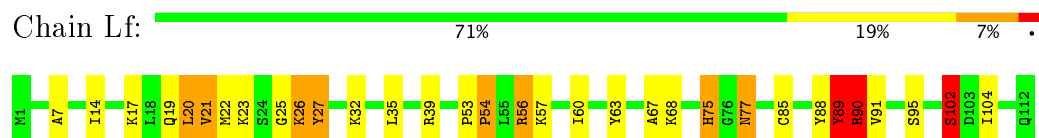
- Molecule 47: 60S ribosomal protein L21



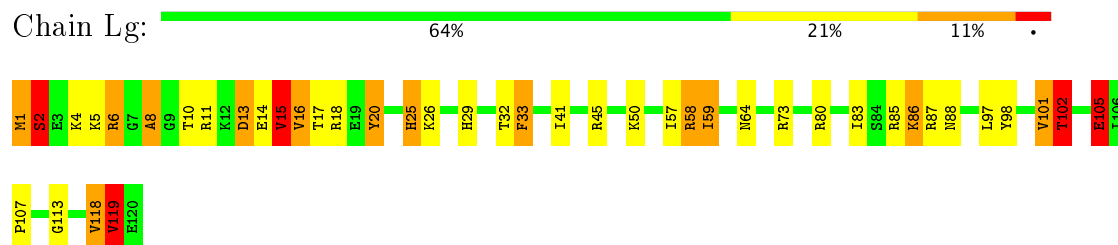
- Molecule 48: 60S ribosomal protein L17



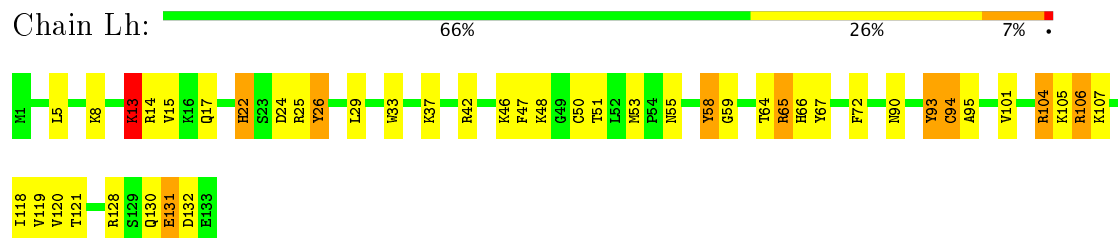
- Molecule 54: 60S ribosomal protein L30



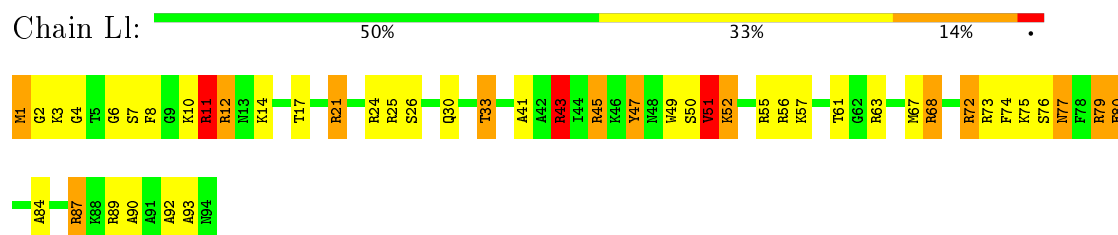
- Molecule 55: 60S ribosomal protein L31



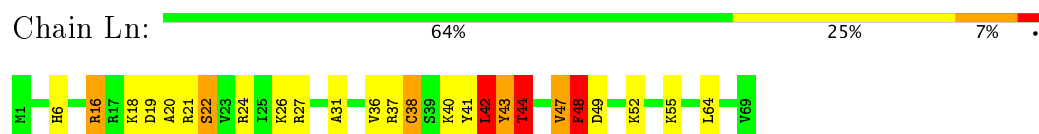
- Molecule 56: Ribosomal L32



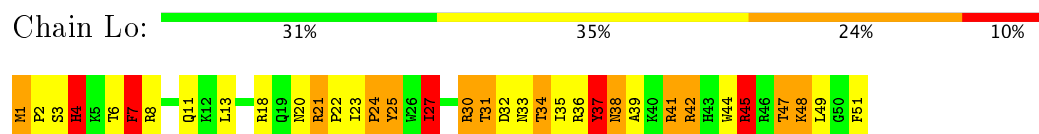
- Molecule 57: Ribosomal protein L37



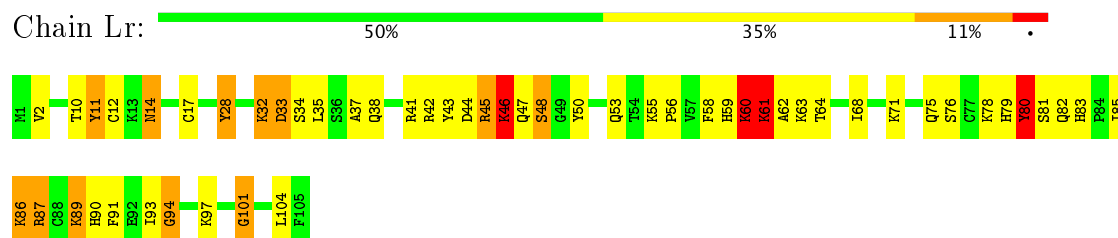
- Molecule 58: 60S ribosomal protein L38



- Molecule 59: Ribosomal protein L39



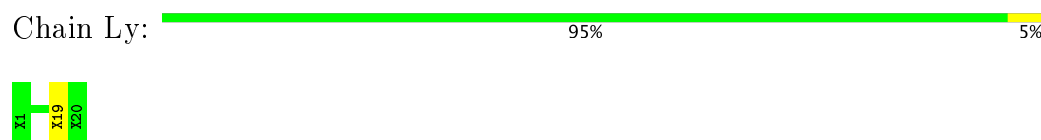
- Molecule 60: 60S ribosomal protein L44



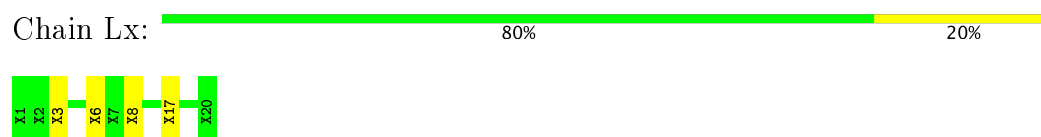
- Molecule 61: Unknown 60S wheat germ ribosome protein 1



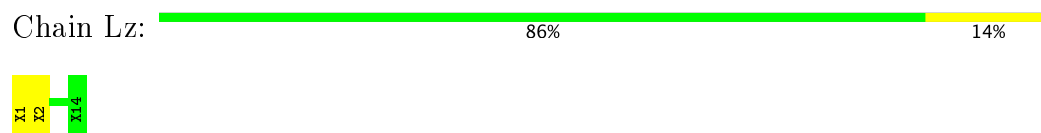
- Molecule 62: Unknown 60S wheat germ ribosome protein 2



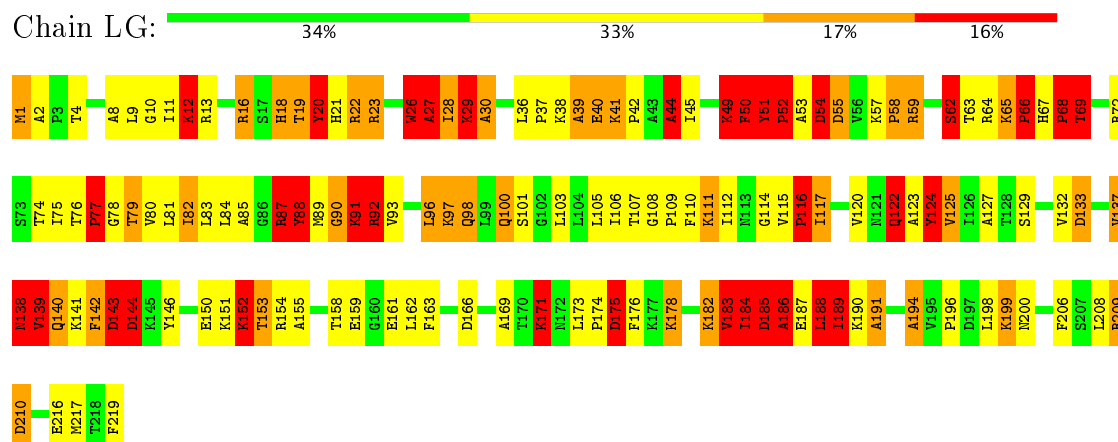
- Molecule 62: Unknown 60S wheat germ ribosome protein 2



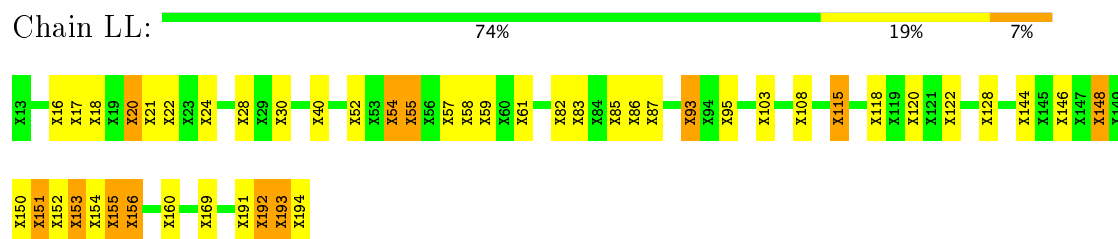
- Molecule 63: Unknown 60S wheat germ ribosome protein 3



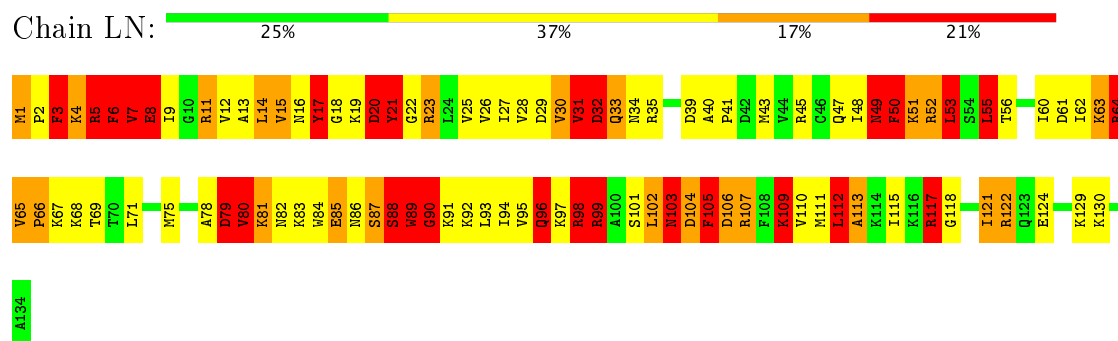
- Molecule 64: 60S ribosomal protein L6



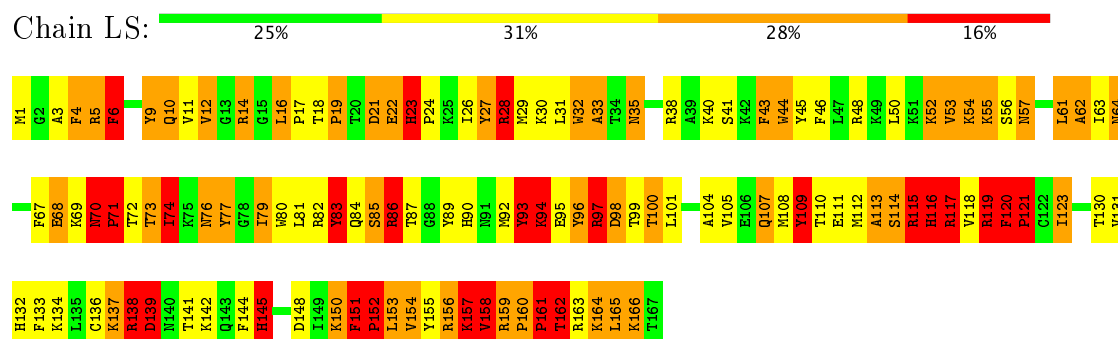
- Molecule 65: Unknown 60S wheat germ ribosome protein 5



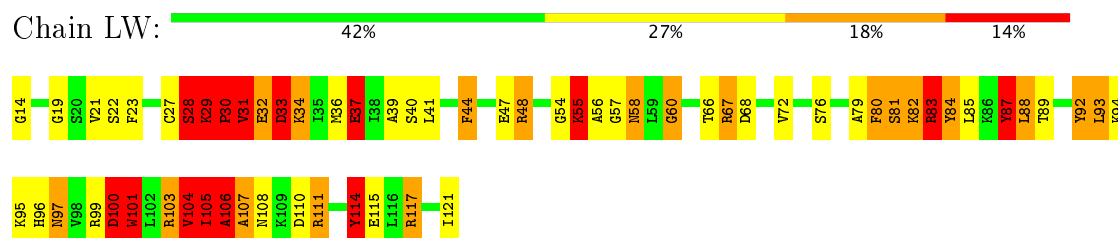
- Molecule 66: Unknown 60S wheat germ ribosome protein 6



- Molecule 67: 60S ribosomal protein L18a

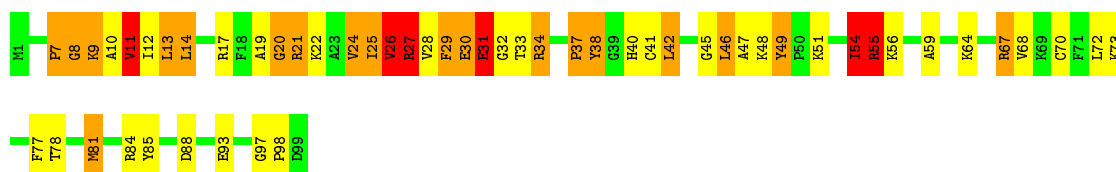


- Molecule 68: 60S ribosomal protein L22



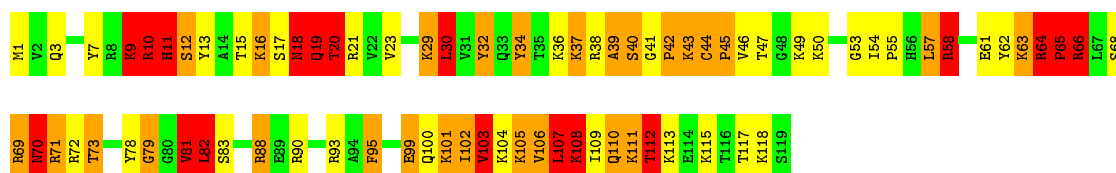
- Molecule 69: 60S ribosomal protein L27





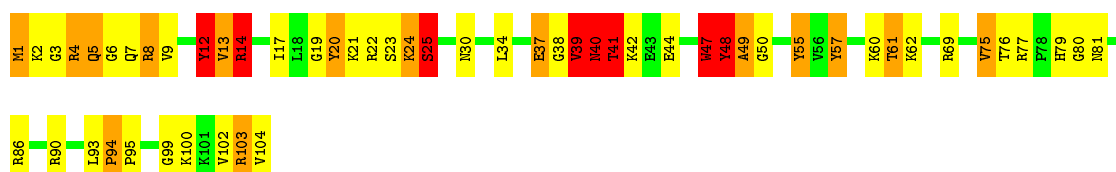
- Molecule 70: Ribosomal protein l34

Chain Li:



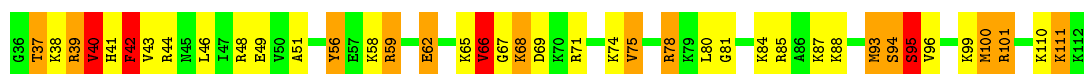
- Molecule 71: ribosomal protein L35A

Chain Lj:



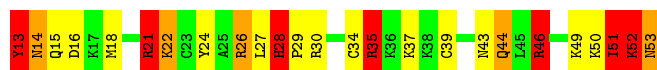
- Molecule 72: 60S ribosomal protein L36

Chain Lk:



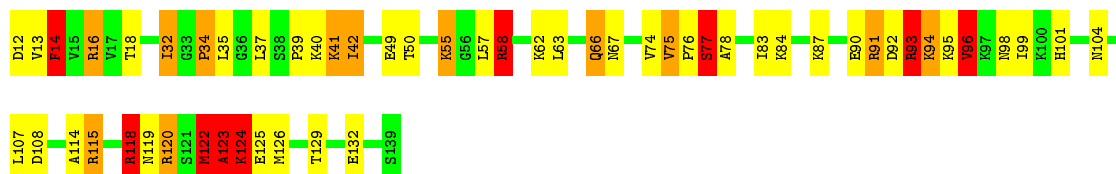
- Molecule 73: Ubiquitin-60S ribosomal protein L40-1

Chain Lp:



- Molecule 74: 60S ribosomal protein L12

Chain LJ:



- Molecule 75: Ribosomal protein P1

Chain Lt:  91% 5%



- Molecule 75: Ribosomal protein P1

Chain Lu:  93%



- Molecule 76: 60S acidic ribosomal protein P2A

Chain Lv:  88% 10%



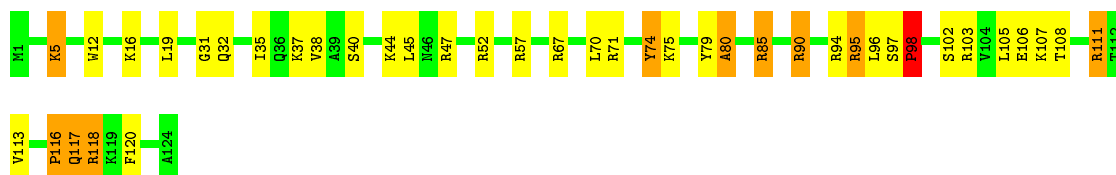
- Molecule 76: 60S acidic ribosomal protein P2A

Chain Lw:  86% 8% 5%



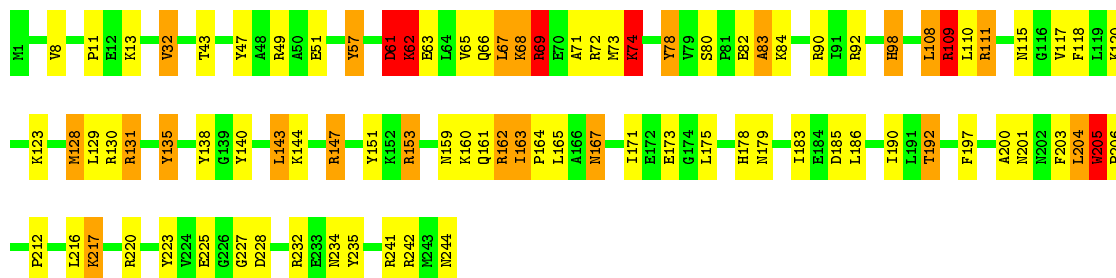
- Molecule 77: 60S ribosomal protein L35

Chain Lc:  67% 24% 8%




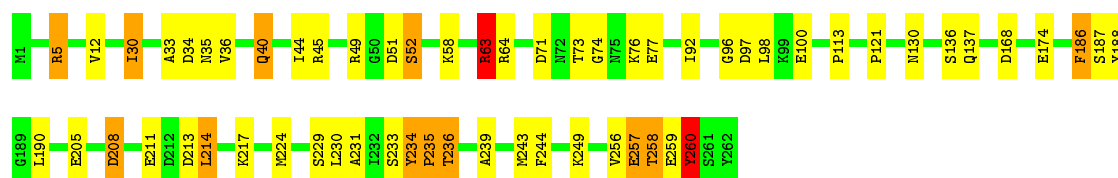
- Molecule 78: Ribosomal protein L7

Chain Le:  64% 25% 9%



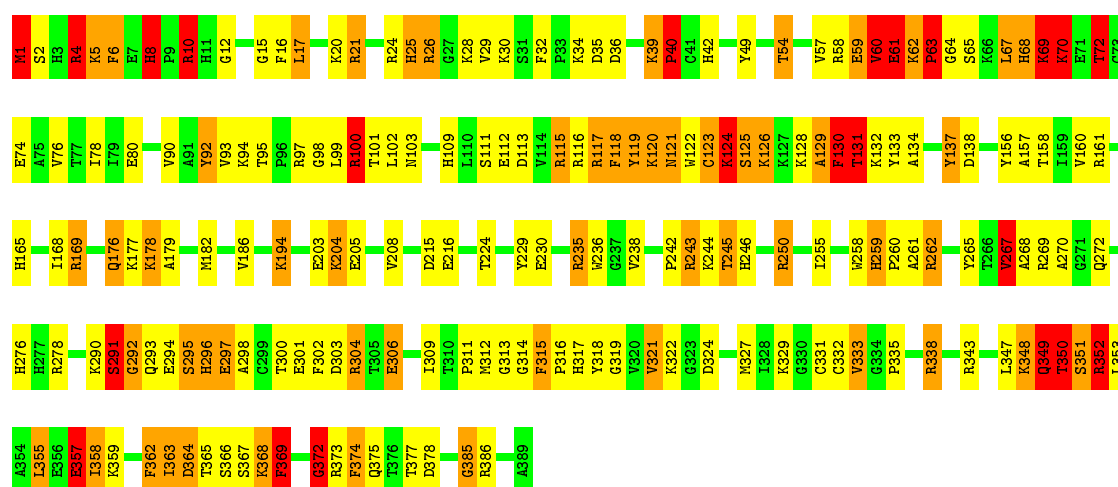
- Molecule 79: 60S acidic ribosomal protein P0

Chain Ls: 



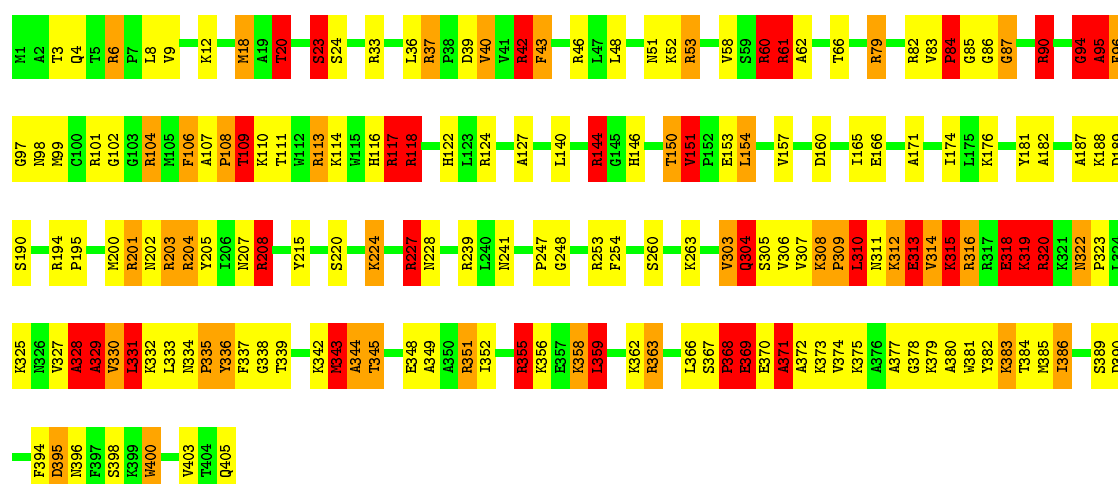
• Molecule 80: Ribosomal protein L3

Chain LC: 



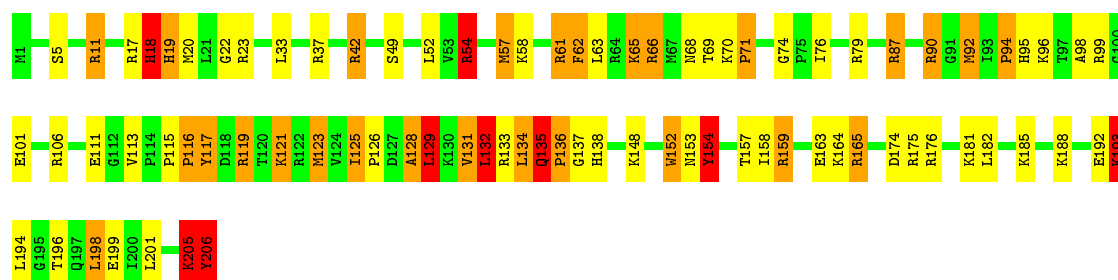
• Molecule 81: 60S ribosomal protein L4/L1

Chain LD: 



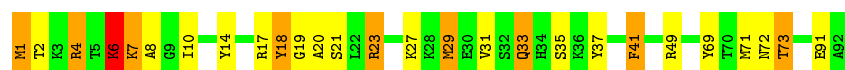
• Molecule 82: Ribosomal protein L13a

Chain LK: 



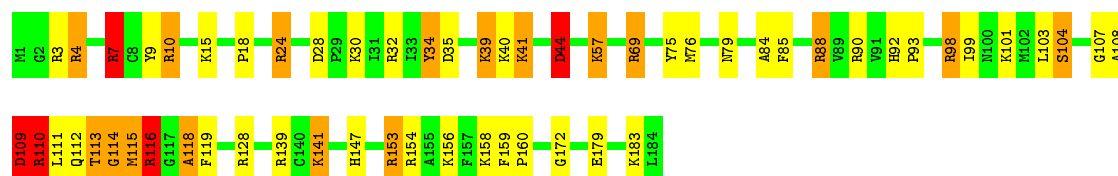
- Molecule 83: 60S ribosomal protein L37a, expressed

Chain Lm: 71% 18% 10% .



- Molecule 84: 60S ribosomal protein L10-1

Chain LI: 68% 20% 9% .



4 Experimental information

Property	Value	Source
Reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of subtomograms used	106	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	150	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	41176	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	Sa	1.90	33/2897 (1.1%)	2.28	124/3917 (3.2%)
10	SL	1.68	18/965 (1.9%)	2.24	35/1271 (2.8%)
11	SM	3.93	25/1185 (2.1%)	3.78	113/1574 (7.2%)
12	SO	0.90	2/994 (0.2%)	2.31	29/1332 (2.2%)
13	SQ	1.81	23/1145 (2.0%)	3.16	96/1531 (6.3%)
14	SP	1.91	10/653 (1.5%)	2.85	41/871 (4.7%)
15	SS	1.88	24/1179 (2.0%)	3.02	80/1586 (5.0%)
16	SR	1.50	6/727 (0.8%)	1.91	29/975 (3.0%)
17	SV	1.18	3/748 (0.4%)	1.77	31/994 (3.1%)
19	SY	1.98	8/443 (1.8%)	2.41	20/592 (3.4%)
2	SA	1.63	11/1988 (0.6%)	2.25	83/2697 (3.1%)
20	SZ	1.54	4/476 (0.8%)	2.82	22/623 (3.5%)
23	SU	2.45	34/745 (4.6%)	3.90	126/988 (12.8%)
24	SX	1.65	9/382 (2.4%)	1.96	15/515 (2.9%)
25	SC	3.58	34/1563 (2.2%)	3.62	136/2086 (6.5%)
27	SH	1.53	10/1060 (0.9%)	2.45	52/1419 (3.7%)
28	SN	2.18	7/317 (2.2%)	2.71	27/414 (6.5%)
29	ST	1.52	4/659 (0.6%)	2.09	29/884 (3.3%)
3	SB	2.02	27/1555 (1.7%)	2.91	115/2077 (5.5%)
30	S3	2.62	16/264 (6.1%)	2.41	16/407 (3.9%)
31	S2	3.33	165/1785 (9.2%)	2.83	192/2779 (6.9%)
32	S1	2.97	2435/37672 (6.5%)	2.60	3313/58357 (5.7%)
33	L1	3.27	5613/77720 (7.2%)	2.85	8211/121026 (6.8%)
34	L3	3.13	166/2868 (5.8%)	2.95	328/4468 (7.3%)
35	L2	3.74	298/3553 (8.4%)	3.05	429/5515 (7.8%)
36	LA	1.27	7/1741 (0.4%)	1.66	27/2323 (1.2%)
37	LB	1.57	15/1979 (0.8%)	2.30	63/2659 (2.4%)
38	LE	2.68	30/1397 (2.1%)	2.43	86/1864 (4.6%)
39	LF	1.25	10/1519 (0.7%)	1.98	45/2042 (2.2%)
4	SD	1.94	35/1637 (2.1%)	3.00	96/2202 (4.4%)
40	LH	1.24	9/1586 (0.6%)	2.43	41/2120 (1.9%)
41	LM	1.36	7/1036 (0.7%)	1.97	40/1388 (2.9%)
42	LP	1.72	23/1669 (1.4%)	2.57	80/2235 (3.6%)
43	LO	1.49	11/1113 (1.0%)	2.62	32/1485 (2.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
44	LR	1.36	7/1303 (0.5%)	2.09	41/1748 (2.3%)
45	LQ	1.69	24/2438 (1.0%)	3.26	131/3271 (4.0%)
46	LT	1.73	12/1590 (0.8%)	2.57	88/2100 (4.2%)
47	LU	1.75	9/1290 (0.7%)	2.66	55/1728 (3.2%)
48	LV	2.47	27/1359 (2.0%)	3.07	111/1816 (6.1%)
49	LX	1.71	9/1002 (0.9%)	2.28	42/1340 (3.1%)
5	SE	2.09	32/2068 (1.5%)	2.98	73/2776 (2.6%)
50	LZ	1.42	5/591 (0.8%)	2.45	20/782 (2.6%)
51	LY	1.65	15/1061 (1.4%)	2.37	37/1418 (2.6%)
52	Lb	1.79	9/585 (1.5%)	2.16	31/786 (3.9%)
53	Ld	1.12	0/201	1.55	3/261 (1.1%)
54	Lf	1.22	1/836 (0.1%)	1.85	23/1121 (2.1%)
55	Lg	1.52	7/954 (0.7%)	2.14	42/1272 (3.3%)
56	Lh	1.50	4/1108 (0.4%)	2.35	37/1477 (2.5%)
57	Li	1.67	8/738 (1.1%)	2.57	49/974 (5.0%)
58	Ln	1.11	1/554 (0.2%)	2.46	15/738 (2.0%)
59	Lo	1.87	7/472 (1.5%)	3.05	44/627 (7.0%)
6	SF	0.99	2/1505 (0.1%)	1.58	29/2027 (1.4%)
60	Lr	1.99	14/853 (1.6%)	3.17	41/1124 (3.6%)
61	Lq	1.77	5/239 (2.1%)	3.70	15/302 (5.0%)
64	LG	1.72	25/1765 (1.4%)	3.20	140/2372 (5.9%)
66	LN	1.57	13/1094 (1.2%)	3.36	81/1461 (5.5%)
67	LS	1.93	21/1457 (1.4%)	2.83	120/1957 (6.1%)
68	LW	1.76	14/850 (1.6%)	2.74	55/1135 (4.8%)
69	La	1.69	12/743 (1.6%)	2.67	65/992 (6.6%)
7	SI	1.85	14/1034 (1.4%)	2.36	42/1379 (3.0%)
70	Li	1.87	15/979 (1.5%)	2.91	91/1305 (7.0%)
71	Lj	1.89	20/811 (2.5%)	3.14	58/1083 (5.4%)
72	Lk	1.74	7/618 (1.1%)	3.73	52/809 (6.4%)
73	Lp	2.33	11/349 (3.2%)	3.33	37/458 (8.1%)
74	LJ	1.36	1/967 (0.1%)	2.08	29/1298 (2.2%)
75	Lt	0.83	0/438	1.67	4/596 (0.7%)
75	Lu	0.69	0/438	1.28	2/596 (0.3%)
76	Lv	0.83	0/444	1.42	6/596 (1.0%)
76	Lw	0.97	1/444 (0.2%)	1.61	8/596 (1.3%)
77	Lc	1.69	10/1017 (1.0%)	2.53	27/1351 (2.0%)
78	Le	1.52	13/2018 (0.6%)	2.44	77/2702 (2.8%)
79	Ls	0.90	0/2023	1.71	40/2739 (1.5%)
8	SJ	1.78	13/896 (1.5%)	2.78	34/1193 (2.8%)
80	LC	1.56	35/3168 (1.1%)	3.16	134/4234 (3.2%)
81	LD	1.47	27/2919 (0.9%)	3.04	129/3924 (3.3%)
82	LK	1.33	12/1678 (0.7%)	2.08	44/2246 (2.0%)
83	Lm	1.32	4/724 (0.6%)	2.06	28/958 (2.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
84	LI	0.93	6/1499 (0.4%)	1.88	31/2001 (1.5%)
9	SK	2.29	11/839 (1.3%)	2.92	43/1120 (3.8%)
All	All	2.71	9615/207179 (4.6%)	2.73	16506/304005 (5.4%)

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	Sa	1	25
10	SL	0	11
11	SM	1	24
12	SO	0	14
13	SQ	1	37
14	SP	3	6
15	SS	1	25
16	SR	0	4
17	SV	0	5
18	SW	0	12
19	SY	0	6
2	SA	1	24
20	SZ	1	9
21	Sc	0	1
23	SU	3	38
24	SX	0	3
25	SC	6	43
26	SG	8	43
27	SH	0	11
28	SN	1	6
29	ST	2	6
3	SB	0	32
32	S1	9	0
33	L1	49	0
34	L3	2	0
35	L2	4	0
36	LA	0	4
37	LB	0	25
38	LE	1	18
39	LF	0	15
4	SD	1	31
40	LH	0	28

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Mol	Chain	#Chirality outliers	#Planarity outliers
41	LM	0	5
42	LP	0	29
43	LO	0	20
44	LR	0	27
45	LQ	4	59
46	LT	1	26
47	LU	1	21
48	LV	0	29
49	LX	1	11
5	SE	0	23
50	LZ	0	12
51	LY	0	12
52	Lb	0	2
53	Ld	0	2
54	Lf	0	6
55	Lg	0	11
56	Lh	1	13
57	Li	0	11
58	Ln	0	11
59	Lo	0	12
6	SF	0	14
60	Lr	1	28
61	Lq	0	5
62	Lx	0	5
62	Ly	0	1
63	Lz	0	2
64	LG	2	59
65	LL	1	39
66	LN	2	21
67	LS	2	41
68	LW	0	24
69	La	0	28
7	SI	0	5
70	Li	2	43
71	Lj	0	26
72	Lk	1	10
73	Lp	2	10
74	LJ	1	12
75	Lt	0	2
75	Lu	0	3
76	Lv	0	1
76	Lw	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
77	Lc	0	16
78	Le	0	23
79	Ls	1	13
8	SJ	0	16
80	LC	5	58
81	LD	2	58
82	LK	2	26
83	Lm	0	12
84	LI	0	17
9	SK	0	14
All	All	127	1482

The worst 5 of 9615 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	SM	126	TYR	CD2-CE2	112.90	3.08	1.39
25	SC	171	PRO	N-CD	81.71	2.62	1.47
32	S1	1315	U	O3'-P	-72.15	0.74	1.61
32	S1	860	A	O3'-P	-63.70	0.84	1.61
33	L1	2398	A	O3'-P	-57.14	0.92	1.61

The worst 5 of 16506 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	SE	30	ARG	NE-CZ-NH2	-75.84	82.38	120.30
66	LN	64	ARG	NE-CZ-NH2	-64.81	87.90	120.30
11	SM	126	TYR	CZ-CE2-CD2	-63.49	62.66	119.80
33	L1	1395	A	O4'-C1'-N9	60.43	156.54	108.20
33	L1	62	A	O4'-C1'-N9	55.67	152.73	108.20

5 of 127 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	Sa	128	LEU	CA
2	SA	199	TRP	CA
4	SD	56	LEU	CA
11	SM	116	LYS	CA
13	SQ	139	ASP	CA

5 of 1482 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Sa	105	LYS	Peptide
1	Sa	26	ARG	Sidechain
1	Sa	63	GLN	Sidechain
1	Sa	70	TYR	Sidechain
1	Sa	82	VAL	Mainchain

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	Sa	2842	0	2691	0	0
2	SA	1946	0	1876	281	0
3	SB	1539	0	1537	60	0
4	SD	1607	0	1675	235	0
5	SE	2028	0	2104	259	0
6	SF	1485	0	1525	103	0
7	SI	1017	0	1080	68	0
8	SJ	887	0	861	48	0
9	SK	830	0	806	104	0
10	SL	952	0	875	82	0
11	SM	1167	0	1141	137	0
12	SO	977	0	1056	106	0
13	SQ	1129	0	1160	66	0
14	SP	639	0	625	269	0
15	SS	1155	0	1173	103	0
16	SR	711	0	758	24	0
17	SV	740	0	746	196	0
18	SW	460	0	111	24	0
19	SY	442	0	467	34	0
20	SZ	469	0	500	24	0
21	Sc	126	0	26	0	0
22	Sb	181	0	39	0	0
23	SU	732	0	740	108	0
24	SX	375	0	367	96	0
25	SC	1535	0	1556	106	0
26	SG	716	0	160	74	0
27	SH	1042	0	1086	309	0
28	SN	313	0	269	33	0
29	ST	650	0	636	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	S3	236	0	120	15	0
31	S2	1599	0	797	277	0
32	S1	33897	0	16592	1570	0
33	L1	69592	0	34889	2808	0
34	L3	2565	0	1293	389	0
35	L2	3192	0	1590	113	0
36	LA	1718	0	1841	311	0
37	LB	1933	0	1932	305	0
38	LE	1376	0	1417	206	0
39	LF	1500	0	1564	88	0
40	LH	1564	0	1658	26	0
41	LM	1020	0	1059	88	0
42	LP	1630	0	1704	74	0
43	LO	1086	0	1127	63	0
44	LR	1284	0	1376	74	0
45	LQ	2395	0	2337	196	0
46	LT	1569	0	1676	382	0
47	LU	1266	0	1268	26	0
48	LV	1335	0	1337	168	0
49	LX	987	0	1083	37	0
50	LZ	578	0	566	27	0
51	LY	1048	0	1130	66	0
52	Lb	576	0	616	0	0
53	Ld	199	0	193	0	0
54	Lf	825	0	830	0	0
55	Lg	944	0	992	0	0
56	Lh	1089	0	1164	0	0
57	Li	725	0	718	0	0
58	Ln	547	0	578	0	0
59	Lo	460	0	490	0	0
60	Lr	838	0	887	0	0
61	Lq	238	0	289	0	0
62	Lx	101	0	24	0	0
62	Ly	101	0	23	0	0
63	Lz	71	0	16	0	0
64	LG	1730	0	1824	123	0
65	LL	910	0	202	82	0
66	LN	1081	0	1170	199	0
67	LS	1419	0	1465	179	0
68	LW	839	0	863	36	0
69	La	732	0	754	0	0
70	Li	964	0	1053	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	Lj	797	0	804	0	0
72	Lk	613	0	684	0	0
73	Lp	344	0	371	0	0
74	LJ	959	0	1039	22	0
75	Lt	432	0	463	0	0
75	Lu	432	0	463	0	0
76	Lv	441	0	453	0	0
76	Lw	441	0	453	0	0
77	Lc	1006	0	1100	0	0
78	Le	1984	0	2090	0	0
79	Ls	1993	0	2086	0	0
80	LC	3102	0	3191	69	0
81	LD	2866	0	2967	261	0
82	LK	1650	0	1771	118	0
83	Lm	715	0	756	0	0
84	LI	1468	0	1506	83	0
All	All	195694	0	140350	8316	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 30.

The worst 5 of 8316 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)
38:LE:91:TYR:CG	38:LE:91:TYR:CD1	1.78	1.70
38:LE:91:TYR:CD2	38:LE:91:TYR:CE2	1.75	1.69
38:LE:91:TYR:CZ	38:LE:91:TYR:CE2	1.80	1.68
38:LE:91:TYR:CD1	38:LE:91:TYR:CE1	1.78	1.68
17:SV:48:TYR:CD1	17:SV:81:ILE:HG23	1.16	1.66

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	
1	Sa	376/380 (99%)	330 (88%)	24 (6%)	22 (6%)	2	23
2	SA	258/260 (99%)	194 (75%)	31 (12%)	33 (13%)	0	6
3	SB	206/208 (99%)	117 (57%)	35 (17%)	54 (26%)	0	1
4	SD	198/200 (99%)	164 (83%)	17 (9%)	17 (9%)	1	15
5	SE	261/263 (99%)	186 (71%)	45 (17%)	30 (12%)	0	8
6	SF	189/191 (99%)	157 (83%)	25 (13%)	7 (4%)	4	33
7	SI	124/126 (98%)	90 (73%)	17 (14%)	17 (14%)	0	6
8	SJ	126/128 (98%)	103 (82%)	14 (11%)	9 (7%)	1	19
9	SK	117/119 (98%)	85 (73%)	13 (11%)	19 (16%)	0	4
10	SL	140/142 (99%)	93 (66%)	18 (13%)	29 (21%)	0	2
11	SM	150/152 (99%)	101 (67%)	22 (15%)	27 (18%)	0	3
12	SO	119/121 (98%)	95 (80%)	11 (9%)	13 (11%)	0	10
13	SQ	139/141 (99%)	87 (63%)	27 (19%)	25 (18%)	0	3
14	SP	83/85 (98%)	64 (77%)	12 (14%)	7 (8%)	1	15
15	SS	144/146 (99%)	119 (83%)	13 (9%)	12 (8%)	1	16
16	SR	89/91 (98%)	65 (73%)	15 (17%)	9 (10%)	1	12
17	SV	98/100 (98%)	70 (71%)	12 (12%)	16 (16%)	0	4
19	SY	56/58 (97%)	38 (68%)	8 (14%)	10 (18%)	0	3
20	SZ	60/62 (97%)	43 (72%)	9 (15%)	8 (13%)	0	6
23	SU	96/98 (98%)	70 (73%)	12 (12%)	14 (15%)	0	5
24	SX	48/50 (96%)	36 (75%)	8 (17%)	4 (8%)	1	16
25	SC	193/195 (99%)	127 (66%)	34 (18%)	32 (17%)	0	4
27	SH	128/130 (98%)	100 (78%)	17 (13%)	11 (9%)	1	15
28	SN	46/48 (96%)	30 (65%)	4 (9%)	12 (26%)	0	1
29	ST	80/82 (98%)	67 (84%)	4 (5%)	9 (11%)	0	8
36	LA	214/216 (99%)	191 (89%)	14 (6%)	9 (4%)	3	30
37	LB	253/255 (99%)	224 (88%)	18 (7%)	11 (4%)	3	29
38	LE	168/170 (99%)	129 (77%)	16 (10%)	23 (14%)	0	6
39	LF	188/190 (99%)	165 (88%)	16 (8%)	7 (4%)	4	33
40	LH	199/201 (99%)	149 (75%)	26 (13%)	24 (12%)	0	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	LM	138/140 (99%)	123 (89%)	9 (6%)	6 (4%)	3	29
42	LP	192/194 (99%)	169 (88%)	18 (9%)	5 (3%)	6	40
43	LO	142/144 (99%)	106 (75%)	17 (12%)	19 (13%)	0	6
44	LR	161/163 (99%)	127 (79%)	18 (11%)	16 (10%)	1	12
45	LQ	302/304 (99%)	218 (72%)	39 (13%)	45 (15%)	0	5
46	LT	187/189 (99%)	167 (89%)	12 (6%)	8 (4%)	3	29
47	LU	162/164 (99%)	136 (84%)	18 (11%)	8 (5%)	2	27
48	LV	169/171 (99%)	131 (78%)	20 (12%)	18 (11%)	0	10
49	LX	120/122 (98%)	98 (82%)	12 (10%)	10 (8%)	1	16
50	LZ	73/75 (97%)	53 (73%)	13 (18%)	7 (10%)	1	13
51	LY	128/130 (98%)	113 (88%)	9 (7%)	6 (5%)	3	28
52	Lb	71/73 (97%)	48 (68%)	12 (17%)	11 (16%)	0	4
53	Ld	21/23 (91%)	18 (86%)	2 (10%)	1 (5%)	2	28
54	Lf	110/112 (98%)	95 (86%)	8 (7%)	7 (6%)	1	22
55	Lg	118/120 (98%)	96 (81%)	13 (11%)	9 (8%)	1	18
56	Lh	131/133 (98%)	113 (86%)	9 (7%)	9 (7%)	1	20
57	Ll	92/94 (98%)	60 (65%)	18 (20%)	14 (15%)	0	5
58	Ln	67/69 (97%)	51 (76%)	11 (16%)	5 (8%)	1	18
59	Lo	49/51 (96%)	33 (67%)	6 (12%)	10 (20%)	0	2
60	Lr	103/105 (98%)	75 (73%)	16 (16%)	12 (12%)	0	8
61	Lq	23/25 (92%)	20 (87%)	3 (13%)	0	100	100
64	LG	217/219 (99%)	149 (69%)	24 (11%)	44 (20%)	0	2
66	LN	132/134 (98%)	96 (73%)	15 (11%)	21 (16%)	0	4
67	LS	165/167 (99%)	115 (70%)	24 (14%)	26 (16%)	0	4
68	LW	106/108 (98%)	73 (69%)	15 (14%)	18 (17%)	0	4
69	La	97/99 (98%)	68 (70%)	15 (16%)	14 (14%)	0	5
70	Li	117/119 (98%)	72 (62%)	13 (11%)	32 (27%)	0	0
71	Lj	102/104 (98%)	74 (72%)	17 (17%)	11 (11%)	0	10
72	Lk	75/77 (97%)	60 (80%)	5 (7%)	10 (13%)	0	6
73	Lp	39/41 (95%)	28 (72%)	8 (20%)	3 (8%)	1	18
74	LJ	126/128 (98%)	97 (77%)	15 (12%)	14 (11%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	Lt	56/58 (97%)	54 (96%)	1 (2%)	1 (2%)	10	49
75	Lu	56/58 (97%)	54 (96%)	1 (2%)	1 (2%)	10	49
76	Lv	57/59 (97%)	54 (95%)	2 (4%)	1 (2%)	10	49
76	Lw	57/59 (97%)	54 (95%)	2 (4%)	1 (2%)	10	49
77	Lc	122/124 (98%)	106 (87%)	7 (6%)	9 (7%)	1	18
78	Le	239/244 (98%)	212 (89%)	17 (7%)	10 (4%)	3	30
79	Ls	260/262 (99%)	233 (90%)	17 (6%)	10 (4%)	4	32
80	LC	387/389 (100%)	298 (77%)	43 (11%)	46 (12%)	0	7
81	LD	368/372 (99%)	306 (83%)	38 (10%)	24 (6%)	1	22
82	LK	204/206 (99%)	179 (88%)	15 (7%)	10 (5%)	2	27
83	Lm	90/92 (98%)	77 (86%)	9 (10%)	4 (4%)	3	29
84	LI	182/184 (99%)	140 (77%)	26 (14%)	16 (9%)	1	15
All	All	10359/10512 (98%)	8138 (79%)	1149 (11%)	1072 (10%)	1	11

5 of 1072 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Sa	2	ALA
1	Sa	112	MET
1	Sa	129	ASP
1	Sa	149	VAL
1	Sa	150	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	
1	Sa	301/323 (93%)	275 (91%)	26 (9%)	12	42
2	SA	190/204 (93%)	161 (85%)	29 (15%)	3	19
3	SB	150/175 (86%)	126 (84%)	24 (16%)	3	18
4	SD	176/176 (100%)	152 (86%)	24 (14%)	4	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	SE	211/211 (100%)	190 (90%)	21 (10%)	9	33
6	SF	158/159 (99%)	144 (91%)	14 (9%)	11	39
7	SI	103/103 (100%)	91 (88%)	12 (12%)	6	27
8	SJ	91/113 (80%)	84 (92%)	7 (8%)	15	47
9	SK	78/94 (83%)	66 (85%)	12 (15%)	3	19
10	SL	79/113 (70%)	71 (90%)	8 (10%)	9	33
11	SM	116/133 (87%)	91 (78%)	25 (22%)	1	7
12	SO	106/106 (100%)	97 (92%)	9 (8%)	12	42
13	SQ	123/127 (97%)	100 (81%)	23 (19%)	2	11
14	SP	63/74 (85%)	53 (84%)	10 (16%)	3	18
15	SS	121/121 (100%)	96 (79%)	25 (21%)	1	8
16	SR	77/77 (100%)	64 (83%)	13 (17%)	2	16
17	SV	76/87 (87%)	70 (92%)	6 (8%)	14	45
19	SY	49/52 (94%)	41 (84%)	8 (16%)	3	17
20	SZ	44/49 (90%)	38 (86%)	6 (14%)	4	23
23	SU	70/84 (83%)	42 (60%)	28 (40%)	0	0
24	SX	44/44 (100%)	40 (91%)	4 (9%)	11	38
25	SC	154/167 (92%)	136 (88%)	18 (12%)	6	27
27	SH	113/113 (100%)	95 (84%)	18 (16%)	3	18
28	SN	27/40 (68%)	24 (89%)	3 (11%)	7	29
29	ST	68/68 (100%)	59 (87%)	9 (13%)	5	24
36	LA	192/192 (100%)	179 (93%)	13 (7%)	18	51
37	LB	193/195 (99%)	175 (91%)	18 (9%)	10	37
38	LE	148/149 (99%)	126 (85%)	22 (15%)	3	20
39	LF	164/164 (100%)	152 (93%)	12 (7%)	16	49
40	LH	164/173 (95%)	135 (82%)	29 (18%)	2	13
41	LM	103/109 (94%)	91 (88%)	12 (12%)	6	27
42	LP	167/167 (100%)	143 (86%)	24 (14%)	4	22
43	LO	104/110 (94%)	88 (85%)	16 (15%)	3	19
44	LR	138/138 (100%)	117 (85%)	21 (15%)	3	19
45	LQ	242/251 (96%)	196 (81%)	46 (19%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	LT	166/166 (100%)	144 (87%)	22 (13%)	4	24
47	LU	129/140 (92%)	110 (85%)	19 (15%)	3	20
48	LV	136/144 (94%)	112 (82%)	24 (18%)	2	14
49	LX	109/109 (100%)	95 (87%)	14 (13%)	5	25
50	LZ	54/66 (82%)	49 (91%)	5 (9%)	10	37
51	LY	115/115 (100%)	98 (85%)	17 (15%)	3	20
52	Lb	64/64 (100%)	57 (89%)	7 (11%)	7	30
53	Ld	21/21 (100%)	20 (95%)	1 (5%)	30	61
54	Lf	90/98 (92%)	72 (80%)	18 (20%)	1	9
55	Lg	99/103 (96%)	85 (86%)	14 (14%)	4	22
56	Lh	119/122 (98%)	111 (93%)	8 (7%)	19	51
57	Ll	72/77 (94%)	61 (85%)	11 (15%)	3	19
58	Ln	59/63 (94%)	48 (81%)	11 (19%)	2	11
59	Lo	48/48 (100%)	37 (77%)	11 (23%)	1	6
60	Lr	91/94 (97%)	75 (82%)	16 (18%)	2	14
61	Lq	24/24 (100%)	22 (92%)	2 (8%)	13	43
64	LG	185/185 (100%)	152 (82%)	33 (18%)	2	13
66	LN	116/116 (100%)	88 (76%)	28 (24%)	1	5
67	LS	153/153 (100%)	123 (80%)	30 (20%)	1	10
68	LW	89/94 (95%)	75 (84%)	14 (16%)	3	18
69	La	73/83 (88%)	56 (77%)	17 (23%)	1	6
70	Li	105/107 (98%)	78 (74%)	27 (26%)	0	4
71	Lj	80/89 (90%)	63 (79%)	17 (21%)	1	8
72	Lk	62/62 (100%)	45 (73%)	17 (27%)	0	4
73	Lp	38/38 (100%)	26 (68%)	12 (32%)	0	2
74	LJ	104/105 (99%)	80 (77%)	24 (23%)	1	6
75	Lt	46/46 (100%)	45 (98%)	1 (2%)	57	79
75	Lu	46/46 (100%)	46 (100%)	0	100	100
76	Lv	48/48 (100%)	47 (98%)	1 (2%)	59	80
76	Lw	48/48 (100%)	46 (96%)	2 (4%)	34	64
77	Lc	107/109 (98%)	99 (92%)	8 (8%)	16	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	Le	206/206 (100%)	171 (83%)	35 (17%)	2	15
79	Ls	222/222 (100%)	199 (90%)	23 (10%)	8	32
80	LC	328/335 (98%)	276 (84%)	52 (16%)	3	18
81	LD	294/302 (97%)	257 (87%)	37 (13%)	5	26
82	LK	173/173 (100%)	141 (82%)	32 (18%)	2	12
83	Lm	73/73 (100%)	67 (92%)	6 (8%)	13	43
84	LI	152/156 (97%)	135 (89%)	17 (11%)	7	29
All	All	8547/8911 (96%)	7319 (86%)	1228 (14%)	7	22

5 of 1228 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	LQ	31	LYS
51	LY	51	LYS
80	LC	369	PHE
45	LQ	183	PHE
47	LU	60	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 143 such sidechains are listed below:

Mol	Chain	Res	Type
37	LB	71	HIS
43	LO	39	HIS
79	Ls	137	GLN
37	LB	168	GLN
39	LF	162	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	S3	10/11 (90%)	3 (30%)	1 (10%)
31	S2	74/75 (98%)	22 (29%)	5 (6%)
32	S1	1492/1743 (85%)	439 (29%)	156 (10%)
33	L1	3192/3352 (95%)	903 (28%)	413 (12%)
34	L3	120/120 (100%)	49 (40%)	17 (14%)
35	L2	143/159 (89%)	55 (38%)	28 (19%)
All	All	5031/5460 (92%)	1471 (29%)	620 (12%)

5 of 1471 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	S3	13	A
30	S3	14	A
30	S3	18	C
31	S2	2	C
31	S2	8	U

5 of 620 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
33	L1	1057	A
33	L1	1598	U
33	L1	3389	C
33	L1	1126	U
33	L1	1312	A

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	S1	23

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Mol	Chain	Number of breaks
33	L1	20
26	SG	3
9	SK	2
78	Le	2
2	SA	2
19	SY	2
25	SC	2
14	SP	1
4	SD	1
16	SR	1
5	SE	1
81	LD	1
15	SS	1
28	SN	1
1	Sa	1
3	SB	1
10	SL	1
24	SX	1
18	SW	1

The worst 5 of 68 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S1	694:C	O3'	701:C	P	33.58
1	S1	803:G	O3'	823:A	P	30.95
1	L1	2547:C	O3'	2561:A	P	30.63
1	S1	744:G	O3'	764:U	P	27.26
1	S1	862:U	O3'	871:G	P	24.78