



wwPDB EM Validation Summary Report ⓘ

Apr 2, 2025 – 03:16 am BST

PDB ID : 4V3P / pdb_00004v3p
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 : 2014-10-20
Resolution : 34.00 Å (reported)
Based on initial model : 3IZ6

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

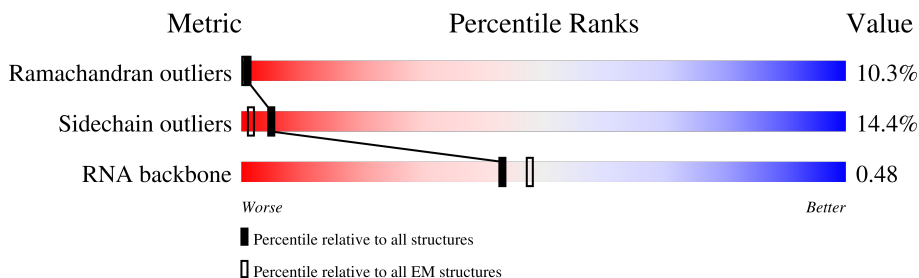
1 Overall quality at a glance

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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	Sa	380	<div> <div>34%</div> <div>65%</div> <div>26%</div> <div>7%</div> <div>.</div> </div>
2	SA	260	<div> <div>30%</div> <div>62%</div> <div>23%</div> <div>13%</div> <div>.</div> </div>
3	SB	208	<div> <div>34%</div> <div>41%</div> <div>33%</div> <div>22%</div> <div>.</div> </div>
4	SD	200	<div> <div>65%</div> <div>21%</div> <div>8%</div> <div>6%</div> </div>
5	SE	263	<div> <div>5%</div> <div>62%</div> <div>28%</div> <div>8%</div> <div>.</div> </div>
6	SF	191	<div> <div>63%</div> <div>76%</div> <div>19%</div> <div>5%</div> </div>
7	SI	126	<div> <div>10%</div> <div>61%</div> <div>30%</div> <div>6%</div> <div>.</div> </div>
8	SJ	128	<div> <div>30%</div> <div>68%</div> <div>23%</div> <div>8%</div> <div>.</div> </div>



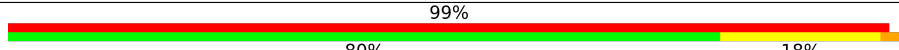


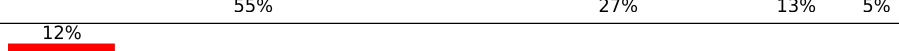
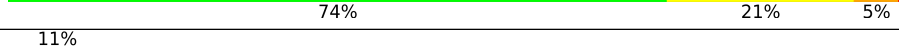








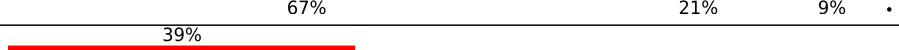








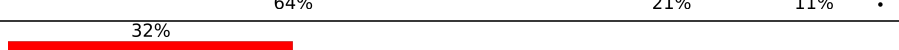
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Mol	Chain	Length	Quality of chain
9	SK	119	
10	SL	142	
11	SM	152	
12	SO	121	
13	SQ	141	
14	SP	85	
15	SS	146	
16	SR	91	
17	SV	100	
18	SW	92	
19	SY	58	
20	SZ	62	
21	Sc	25	
22	Sb	36	
23	SU	98	
24	SX	50	
25	SC	195	
26	SG	143	
27	SH	130	
28	SN	48	
29	ST	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>25%</div><div>66%</div><div>21%</div><div>9%</div><div></div></div>
82	LK	206	<div><div></div><div>45%</div><div>68%</div><div>20%</div><div>10%</div><div></div></div>
83	Lm	92	<div><div></div><div>87%</div><div>71%</div><div>18%</div><div>10%</div><div></div></div>
84	LI	184	<div><div></div><div>42%</div><div>73%</div><div>20%</div><div>5%</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		

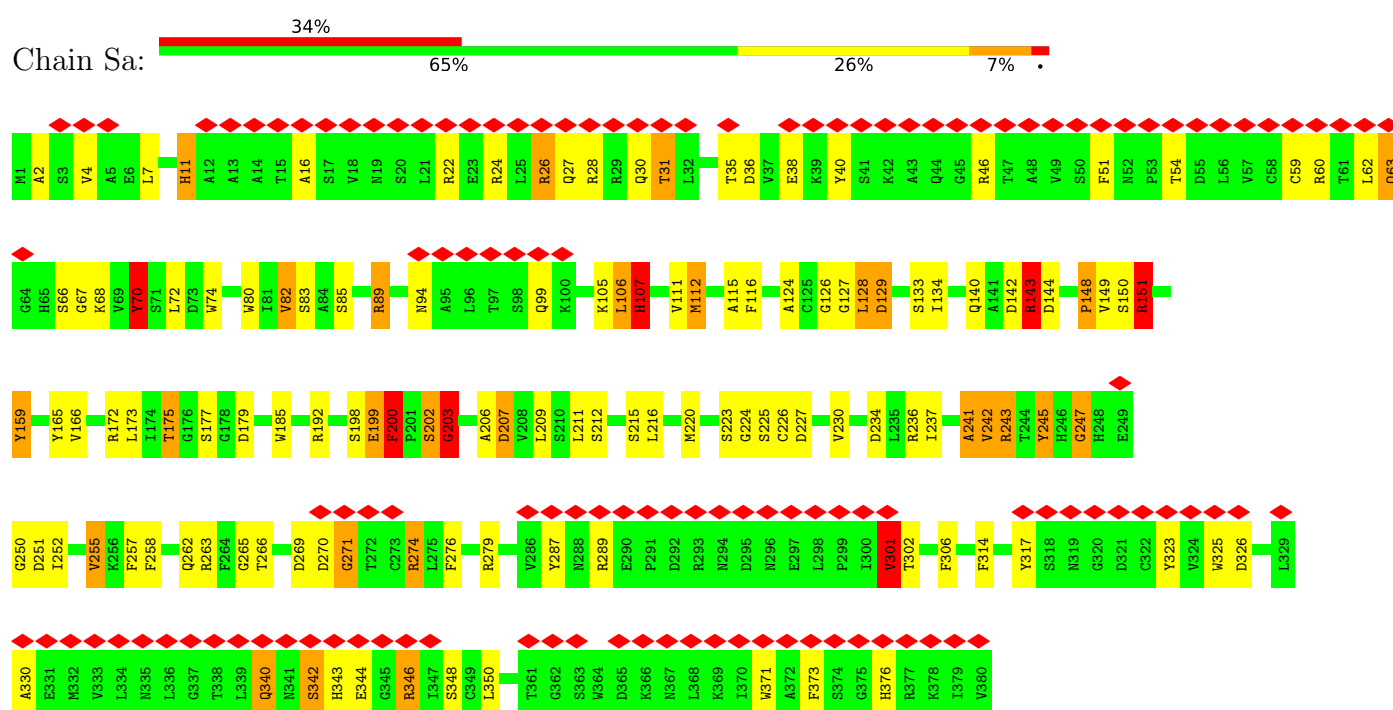
- Molecule 84 is a protein called 60S ribosomal protein L10-1.

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

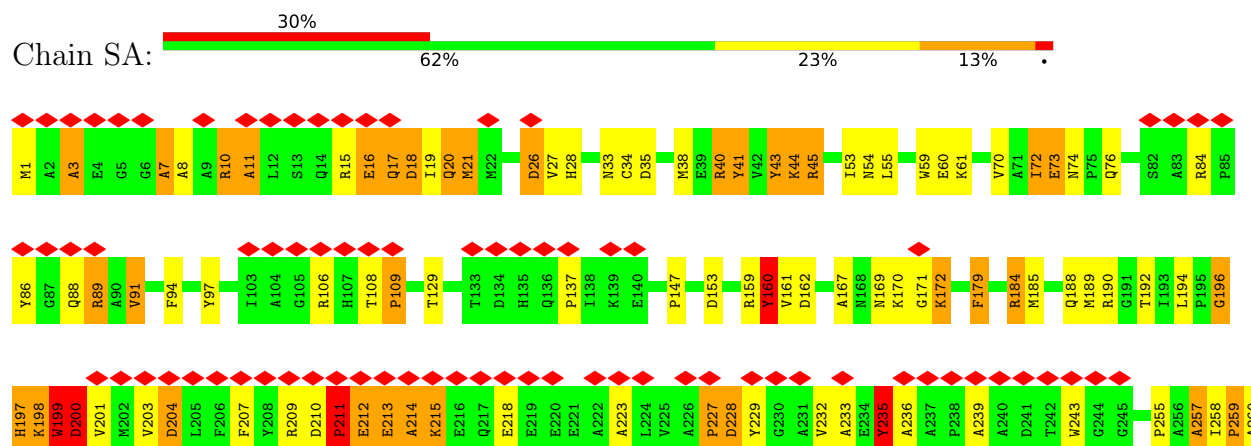
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.


• Molecule 1: G protein beta subunit

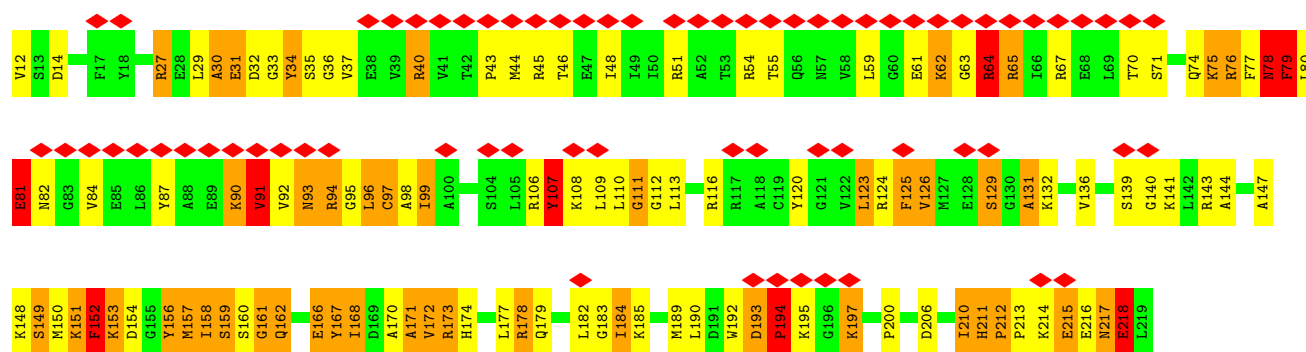


• Molecule 2: 40S ribosomal protein SA



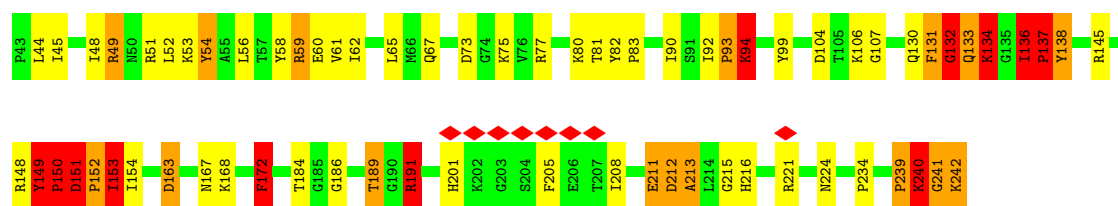
• Molecule 3: Putative 40S ribosomal protein S3

Chain SB: 



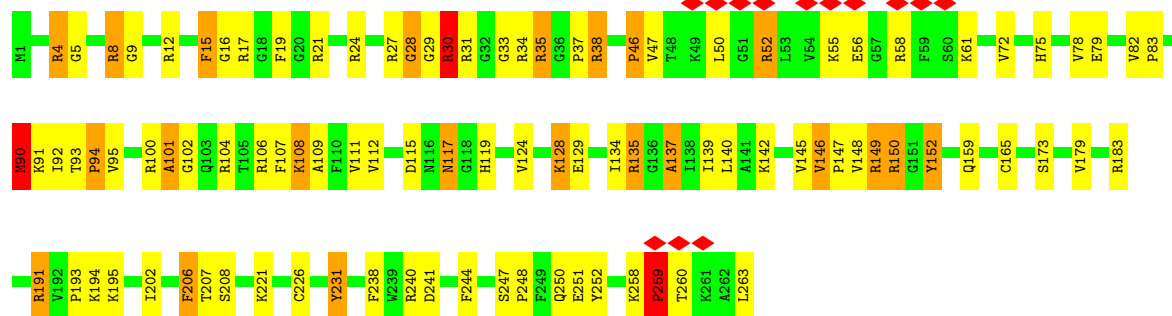
• Molecule 4: 40S ribosomal protein S4

Chain SD: 




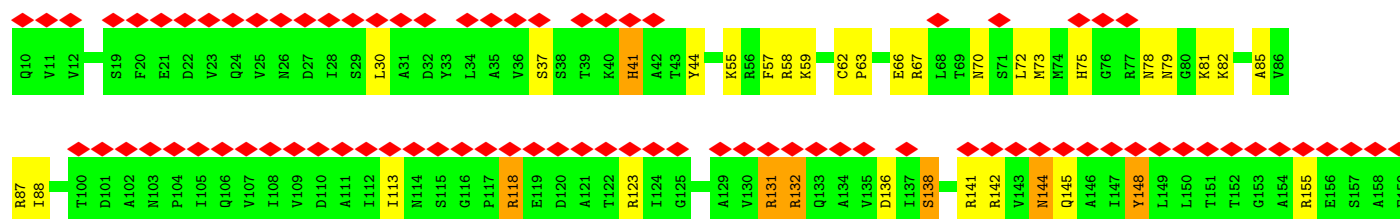
• Molecule 5: 40S ribosomal protein S2

Chain SE: 



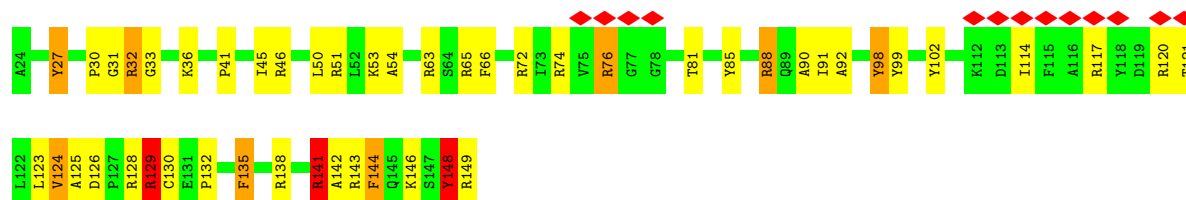
• Molecule 6: 40S ribosomal protein S5

Chain SF: 

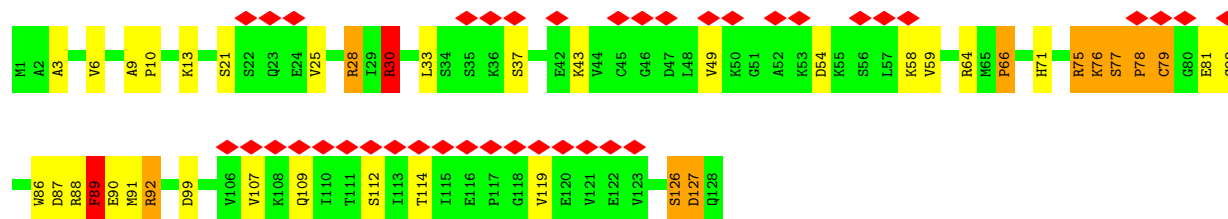




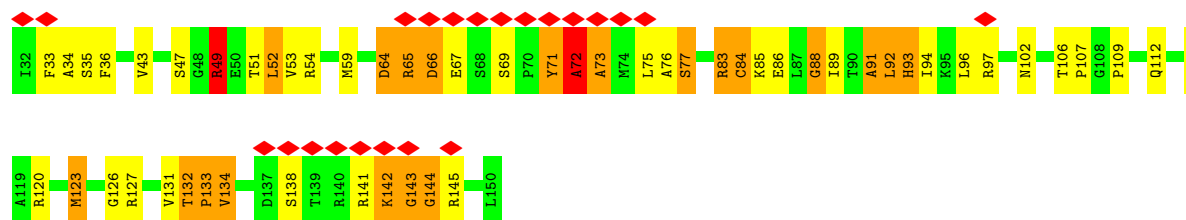
• Molecule 7: 40S ribosomal protein S16



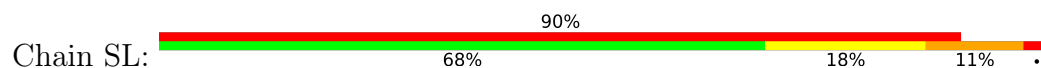
• Molecule 8: 40S ribosomal protein S20



• Molecule 9: 40S ribosomal protein S14

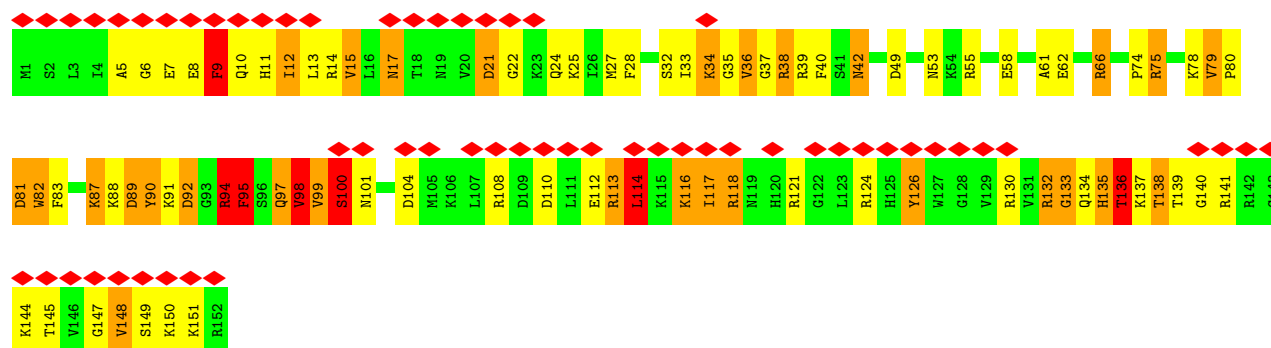
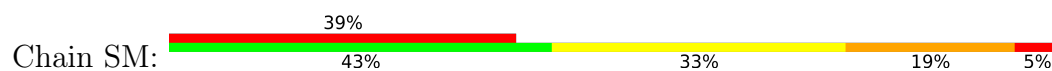


• Molecule 10: 40S ribosomal protein S23

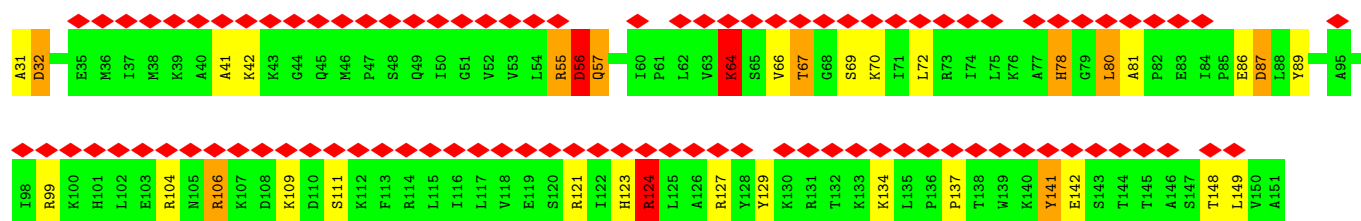
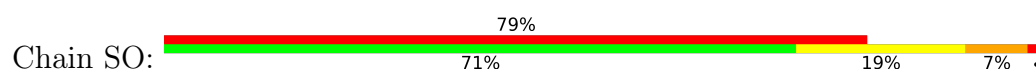




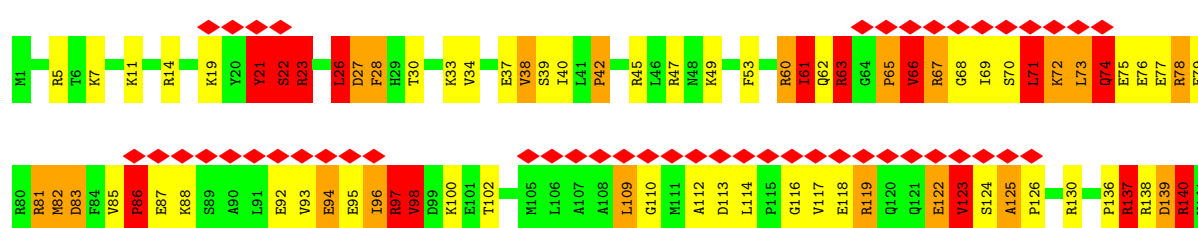
• Molecule 11: 40S ribosomal protein S18



• Molecule 12: 40S ribosomal protein S13-1



• Molecule 13: 40S ribosomal protein S17-4



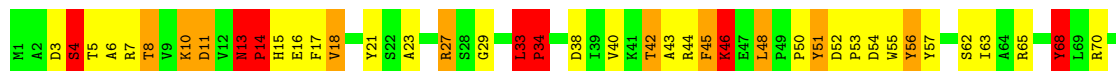
• Molecule 14: 40S ribosomal protein S11





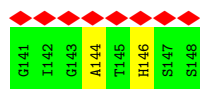
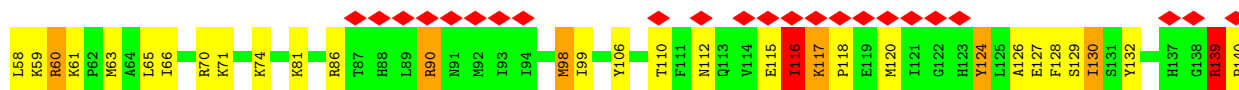
- Molecule 15: 40S ribosomal protein S19

Chain SS: 55% 27% 12% 5%



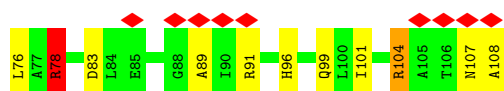
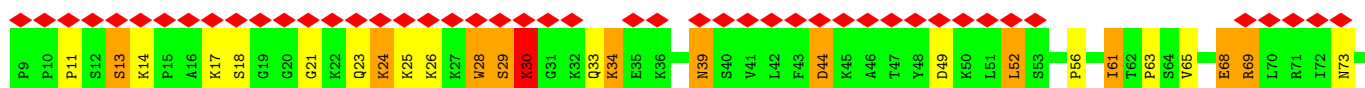
- Molecule 16: 40S ribosomal protein S15

Chain SR: 34% 63% 29% 7%



- Molecule 17: 40S ribosomal protein S25

Chain SV: 55% 63% 23% 12%



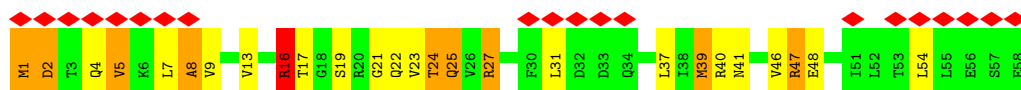
- Molecule 18: 40S WHEAT GERM RIBOSOME1

Chain SW: 89% 11%

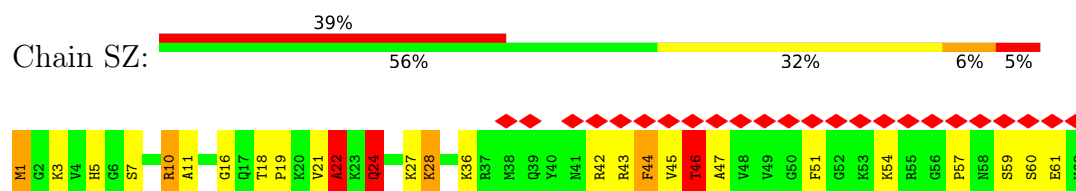


- Molecule 19: 40S ribosomal protein S28

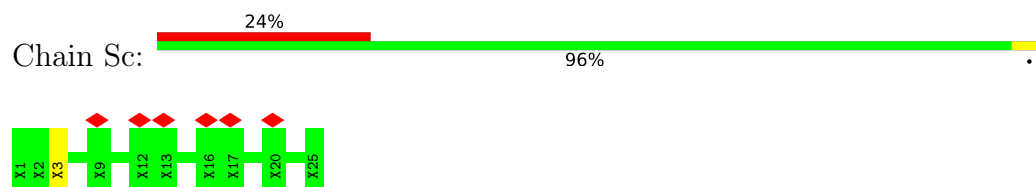
Chain SY: 34% 55% 28% 16%



- Molecule 20: 40S ribosomal protein S30



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

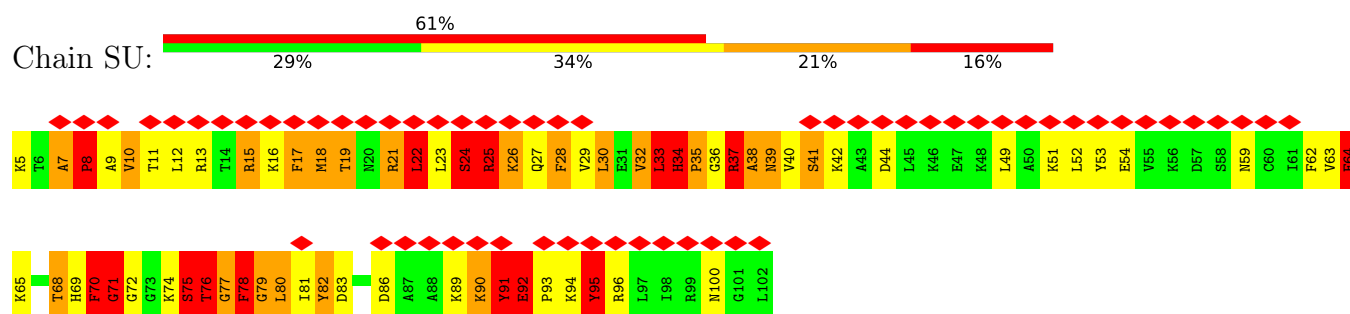


- Molecule 22: Unknown 40S wheat germ ribosome protein 3

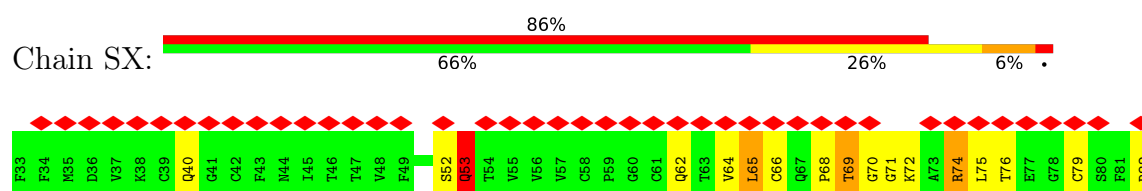


There are no outlier residues recorded for this chain.

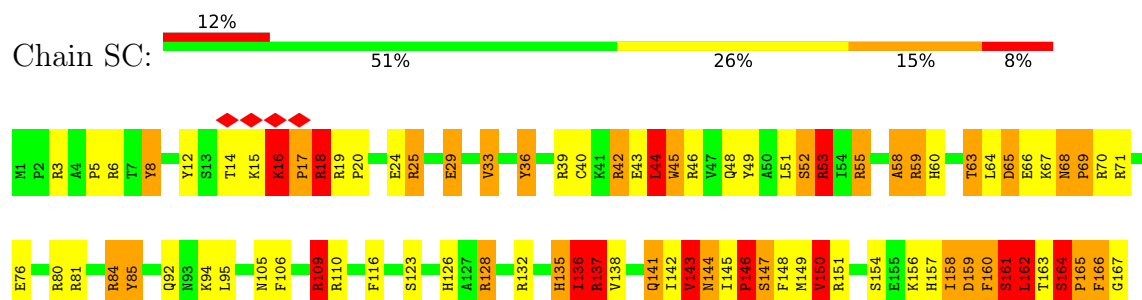
- Molecule 23: Unknown 40S wheat germ ribosome protein 3

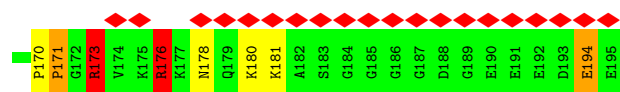


- Molecule 24: 40S ribosomal protein S27

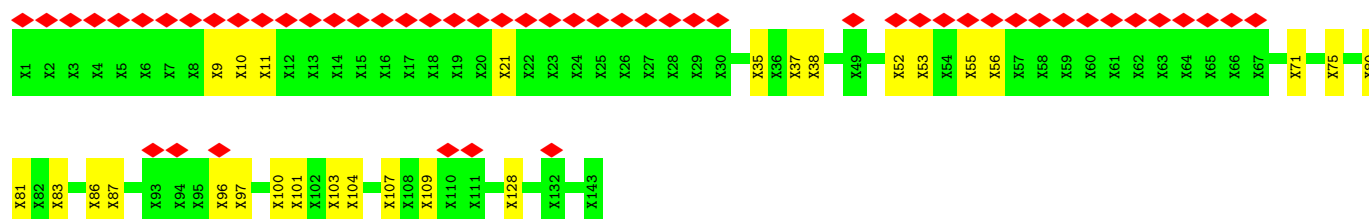
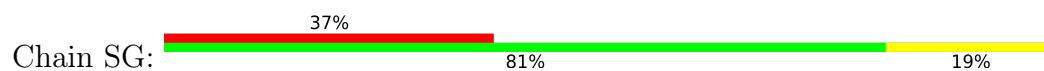


- Molecule 25: 40S ribosomal protein S9





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



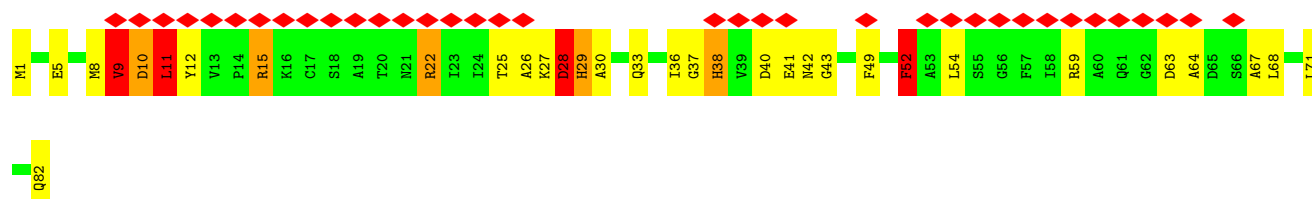
- Molecule 27: Ribosomal protein S15



- Molecule 28: 40S ribosomal protein S29



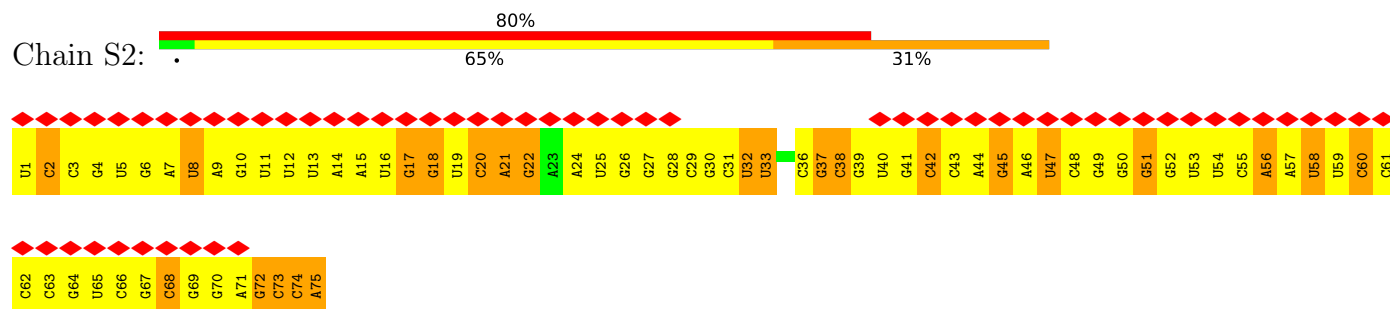
- Molecule 29: 40S ribosomal protein S21



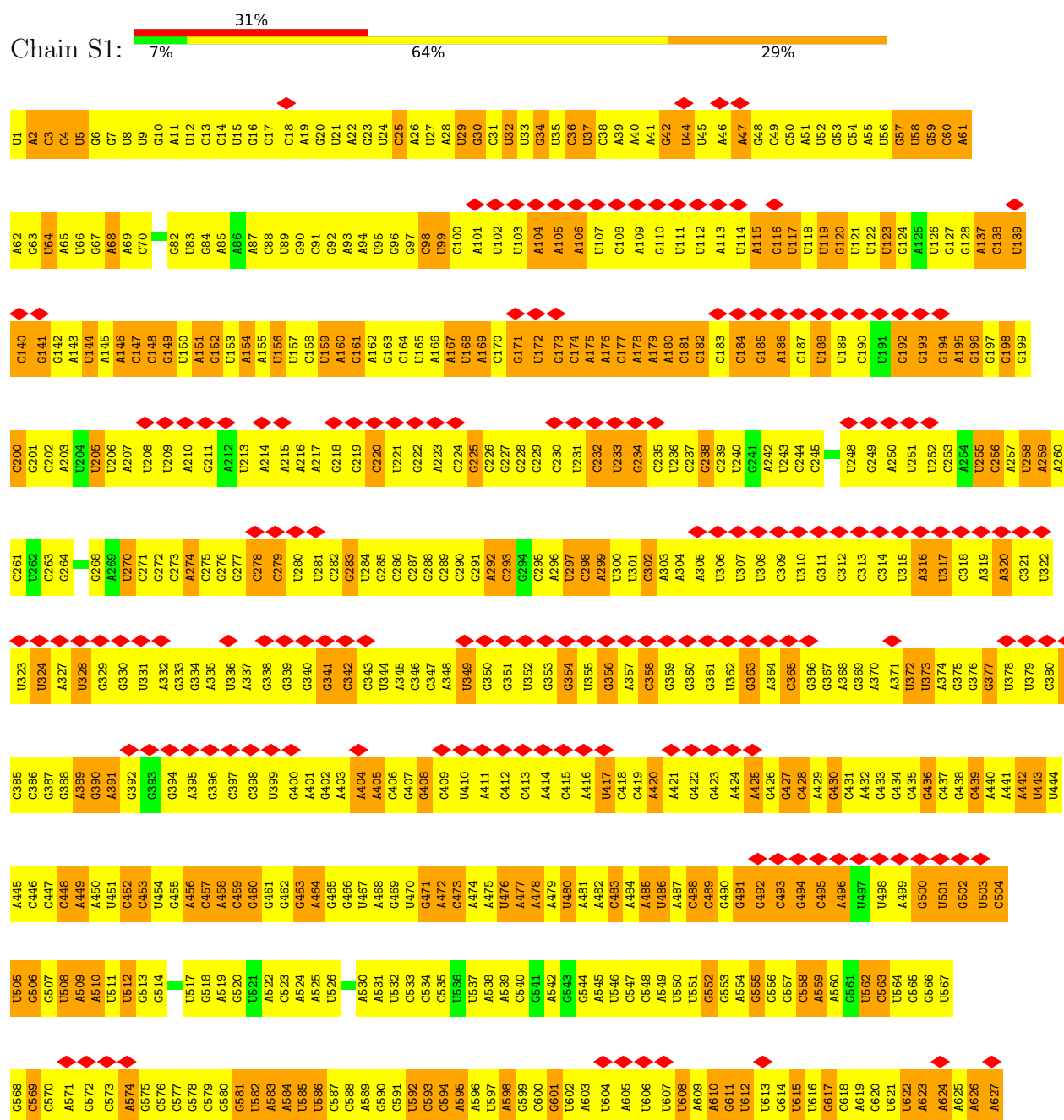
- Molecule 30: 40S WHEAT GERM RIBOSOME protein 4



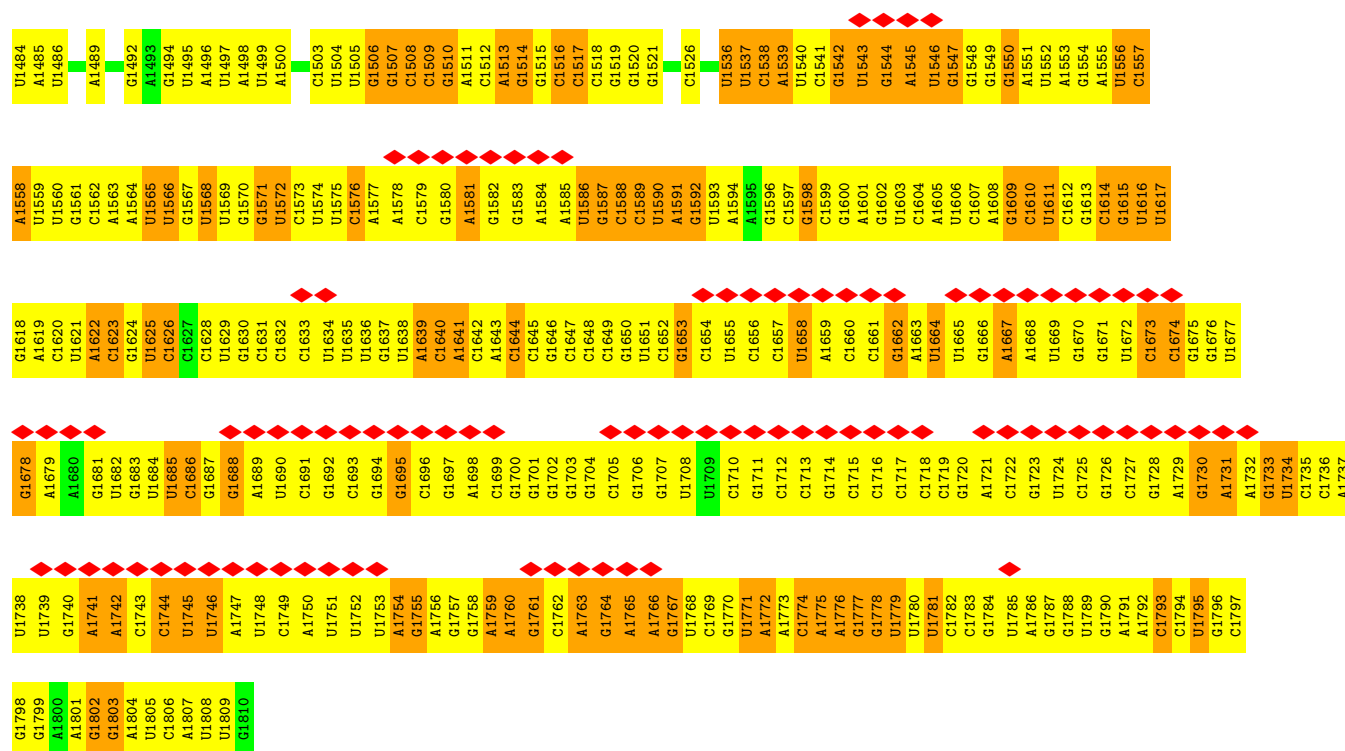
• Molecule 31: 40S ribosomal RNA



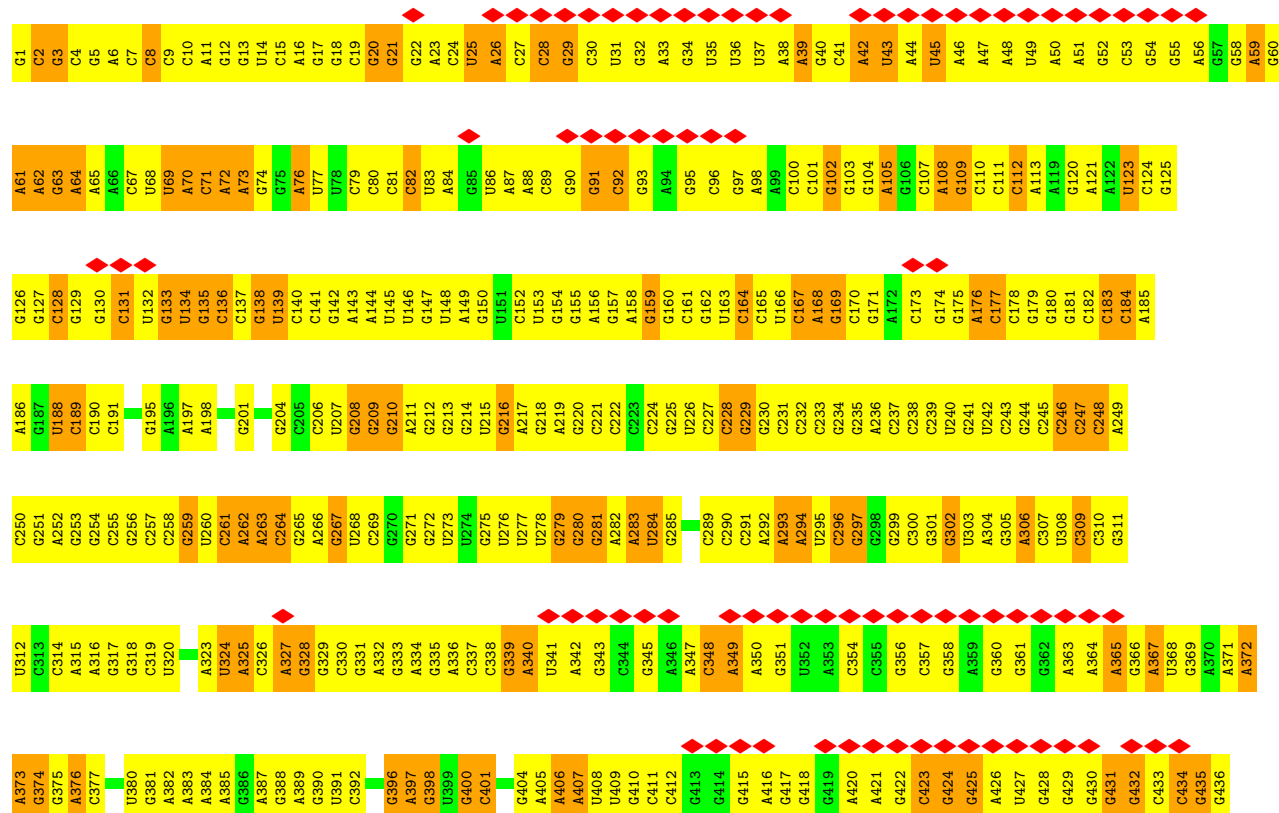
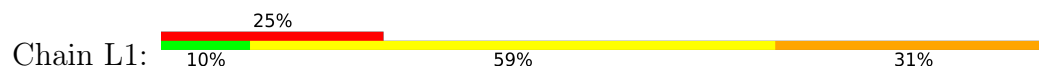
• Molecule 32: 18S ribosomal RNA



G1422	G1361	G1301	A1240	U1059	G999	C939	C879	U792	U688	G628
A1423	A1362	C1302	G1241	U1060	A1000	U940	G880	G793	C629	U636
G1424	G1363	G1303	A1242	G1061	G1001	G941	G881	G794	C629	U637
G1425	C1364	A1304	G1123	C1062	G1002	C942	G882	A795	U630	G638
C1426	C1365	U1305	U1243	U1063	A1003	G943	G883	U796	G631	G639
A1427	A1366	U1306	G1124	U1064	U1004	A944	G884	A797	C632	A640
A1428	U1367	U1307	U1246	A1065	C1005	A945	G885	C798	G633	C641
U1429	C1368	G1308	G1247	U1066	A1006	A946	C886	A799	U634	C642
A1430	A1369	U1309	A1187	U1067	G1007	G947	A886	U800	A634	U643
A1431	C1370	C1310	A1188	U1067	A1008	C948	U887	U801	G635	U644
C1432	G1371	U1311	U1129	A1067	U1009	A949	U887	A802	G636	U645
A1433	C1372	U1312	A1129	G1068	A1010	U950	U888	G803	U637	G646
G1434	U1253	G1312	A1130	G1069	C1011	U951	C889	A823	C713	G647
G1435	U1254	G1313	G1131	A1070	C1012	U952	G890	U824	C714	G638
U1436	U1255	U1314	U1071	C1071	G1013	U953	U891	U825	U715	G639
C1437	C1256	U1315	G1132	U1072	U1014	G953	U892	U826	A716	A640
U1438	U1257	U1316	C1133	C1073	C1015	C954	A892	C827	G717	C641
G1439	U1258	A1316	U1134	G1074	C1016	C955	U893	C827	C718	C642
U1440	C1196	U1135	G1135	C1075	U1017	A956	U894	G828	C719	U643
A1441	A1197	G1136	U1076	C1076	A1018	A957	U895	G829	U720	U644
C1442	U1198	A1136	C1077	C1077	G1019	G958	C896	U830	A723	G645
U1443	U1199	A1137	G1078	G1078	U1020	G959	A897	C831	U724	G646
U1444	C1201	G1137	C1079	C1079	C1021	A960	U898	C832	U725	G647
G1445	G1192	A1138	C1080	C1080	U1022	U961	A899	U833	U731	C648
U1446	A1193	U1139	A1081	C1081	C1023	G962	G900	U834	G732	C649
C1447	C1194	U1140	C1082	C1082	A1024	U963	U901	U835	G733	G650
U1448	U1195	U1141	C1083	C1083	A1025	U964	C902	U836	G734	G651
A1449	C1196	A1142	U1084	U1084	G1026	U965	A903	G837	G735	C652
U1450	U1207	A1143	U1085	U1085	C1027	C967	G904	U838	U736	U653
U1451	A1208	A1144	G1086	G1086	U1028	A968	A905	G839	G743	C654
G1452	C1209	G1145	A1089	C1089	C1029	U969	A906	U840	G744	G655
U1453	U1210	U1146	G1090	C1090	U1029	U970	G907	G842	U764	C656
C1454	U1211	A1147	A1091	C1091	A1030	A971	U908	G843	U765	C657
U1455	A1212	U1148	A1092	C1092	A1031	U973	G909	G843	U766	G658
U1456	C1213	U1149	C1093	C1093	A1032	C974	A910	G844	A766	G659
C1457	U1214	G1151	C1094	C1094	G1033	A975	A911	G845	G767	U661
U1458	C1215	C1153	A1097	C1097	C1034	A976	A912	U846	A768	C662
G1459	G1216	G1154	A1098	C1098	A1035	G977	A913	U847	G769	C663
U1460	G1217	G1155	G1099	C1099	U1036	A978	U913	U847	U770	C664
G1461	U1218	A1156	U1100	C1100	G1037	A979	U914	C948	G771	C665
C1462	C1219	U1157	C1101	C1101	C1038	A980	C915	G849	C772	C666
U1463	G1220	G1158	U1102	C1102	C1039	C980	U916	G850	C773	C667
G1464	G1221	G1159	U1103	C1103	G1040	G981	A917	G851	C774	A669
C1465	C1222	C1160	U1104	C1104	A1041	G982	U917	A852	A775	C670
U1466	A1223	G1161	G1105	C1105	C1042	A983	G918	G853	A776	G671
G1467	G1224	A1162	G1106	C1106	A1043	A984	G919	C854	C777	G672
U1468	U1225	C1163	U1107	C1107	G1045	A985	A920	G854	G778	C673
C1469	U1226	A1164	U1108	C1108	G1046	G985	U921	G855	A780	G674
U1470	C1227	U1165	U1109	C1109	G1047	U986	U922	G856	A781	A675
G1471	U1228	C1166	C1110	C1110	A1048	U987	U923	G857	C677	G676
C1472	A1229	G1167	C1111	C1111	U1049	G988	A924	G858	C678	C677
U1473	G1230	A1168	G1112	C1112	G1050	G989	U925	G859	C679	A678
G1474	C1231	G1169	G1113	C1113	G1051	G990	G926	A860	C680	C680
C1475	U1232	G1170	G1114	C1114	C1052	G991	A927	U861	G881	G881
U1476	U1233	C1171	G1115	C1115	G1053	G992	A928	A861	A785	A682
G1477	G1234	G1172	G1116	C1116	G1054	G993	A929	U862	C786	C683
U1478	C1235	U1173	G1117	C1117	G1055	G994	G930	G871	A786	C684
C1479	U1236	G1174	G1118	C1118	G1056	U995	A931	A874	U787	U685
U1480	G1237	A1175	G1119	C1119	G1057	G996	C932	G875	C787	C686
A1481	U1238	C1176	G1177	C1177	U1058	A997	A933	A876	G788	C687
G1482	A1300	C1178	C1179	C1179	G1059	A998	C934	G877	G789	G687
U1483							C935	A878	U790	
							A936	G879	C791	
							A937			
							A938			



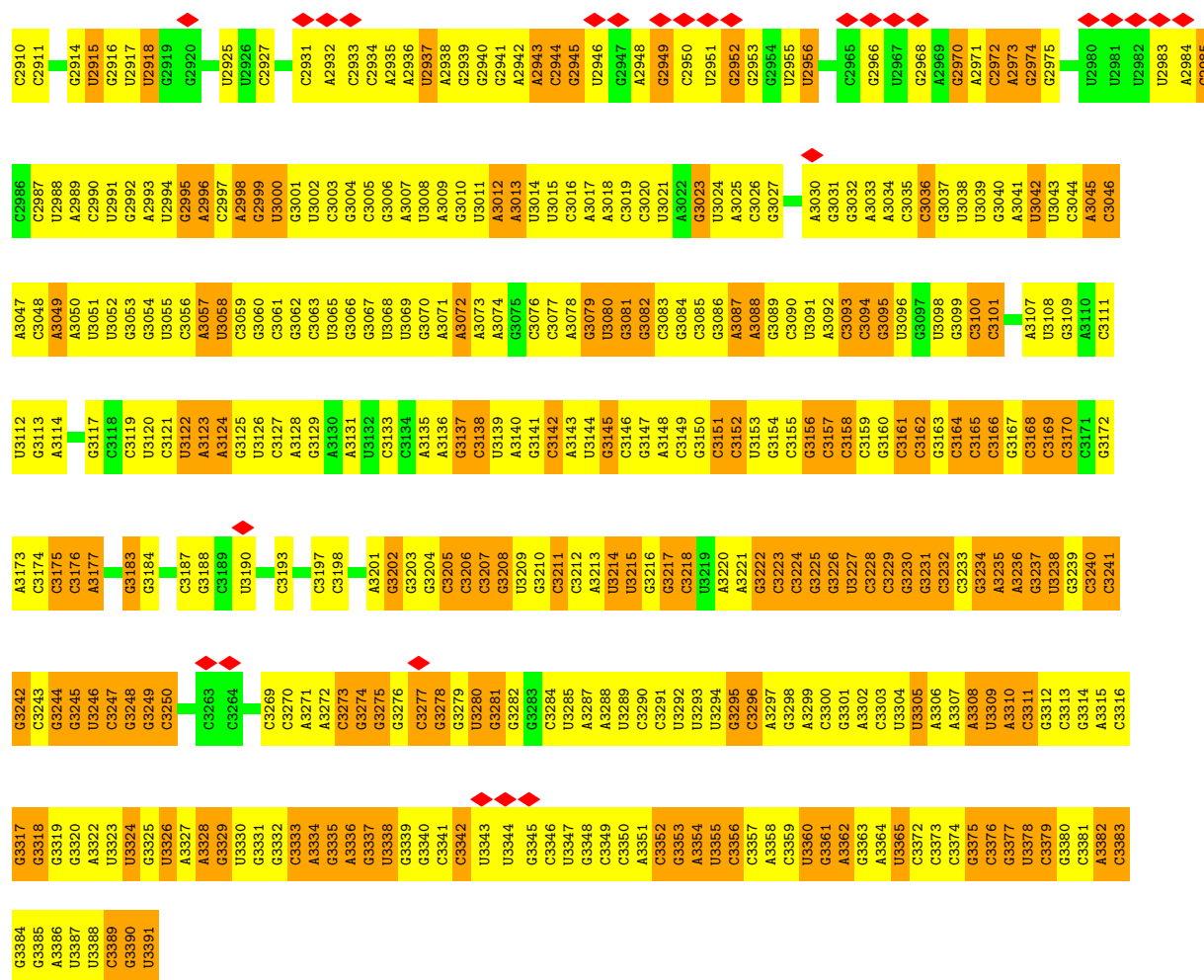
• Molecule 33: 26S ribosomal RNA



A1224	A1225	G1226	A1227	A1228	A1229	A1232	A1233	G1234	A1235	A1236	G1237	A1238	G1239	A1240	A1241	A1242	A1243	A1244	A1245	A1246	A1247	A1248	A1249	G1250	U1251	C1252	G1253	A1254	A1255	A1256	U1257	C1258	C1259	G1260	C1261	A1262	A1263	A1264	G1265	G1266	A1267	G1268	A1269	G1270	U1271	G1272	A1273	A1274	A1275	C1276	A1277	A1278	C1279	A1280	C1281	A1282	C1283	C1284										
A1102	U1103	C1104	G1105	G1106	G1107	U1108	U1109	C1110	U1111	C1112	C1113	A1114	A1115	G1116	U1117	G1118	G1119	G1120	C1121	C1122	A1123	U1124	U1125	U1126	U1127	U1128	A1129	U1130	U1131	A1132	A1133	G1134	C1135	A1136	G1137	U1081	U1082	C1083	G1084	G1085	U1086	G1087	A1088	G1089	C1090	C1091	U1092	U1093	G1094	C1095	C1096	U1097	U1098	G1099	G1100	A1101												
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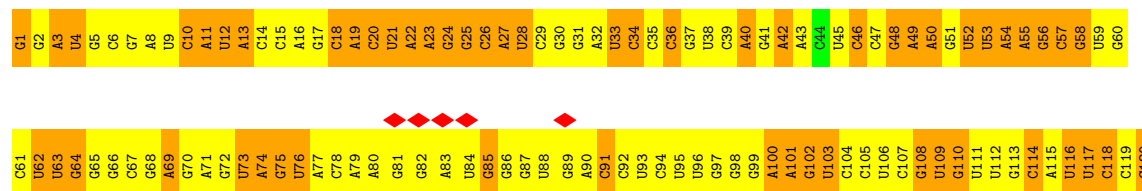
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G2041	U1921	A1861	A1796	G1677	G1616	C1554	A1494	G1428	C1364	A1295
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- Molecule 34: 5S ribosomal RNA

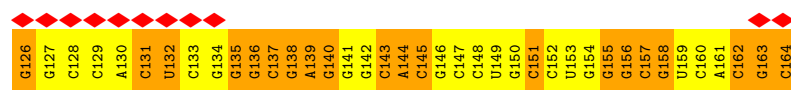
Chain L3: . 52% 47%



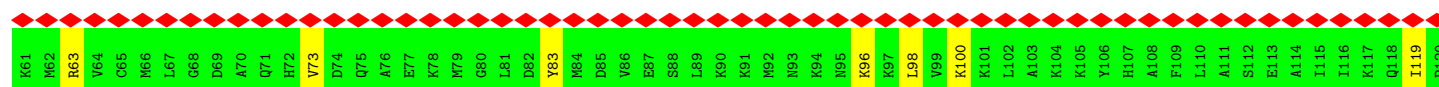
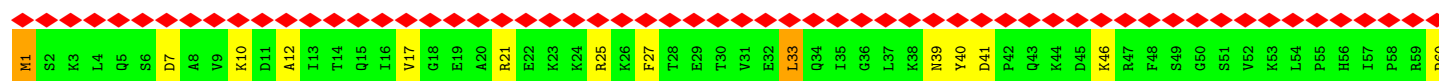
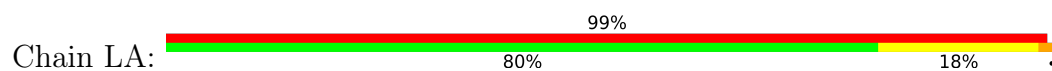
- Molecule 35: 5.8S ribosomal RNA

Chain L2: . 15% 56% 40%

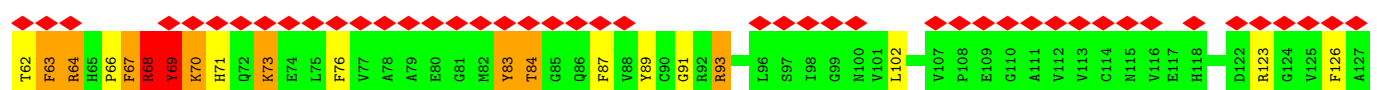
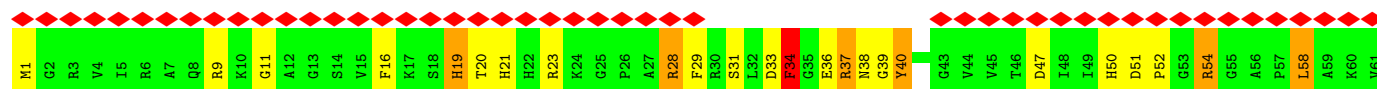
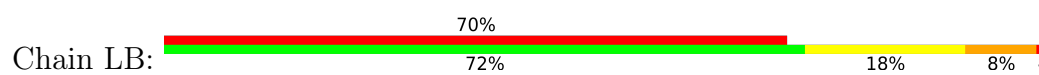




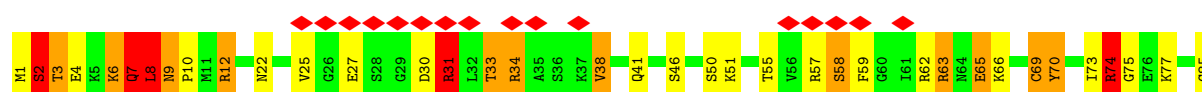
• Molecule 36: Ribosomal protein



• Molecule 37: 60S ribosomal protein L2

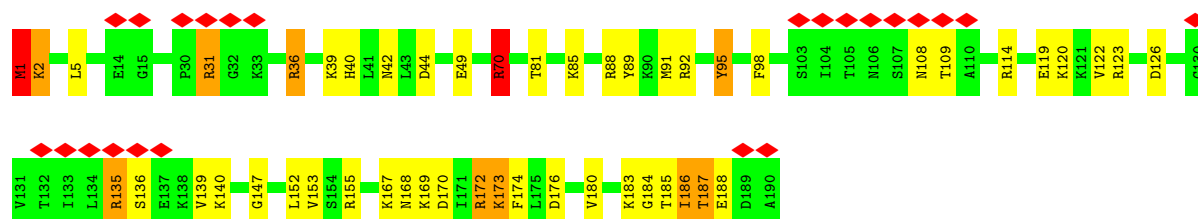
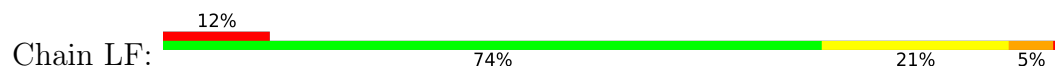


• Molecule 38: Ribosomal protein L11

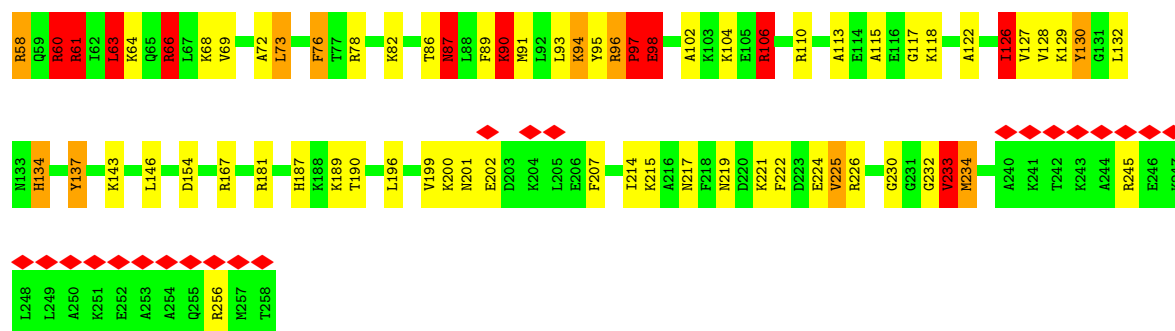




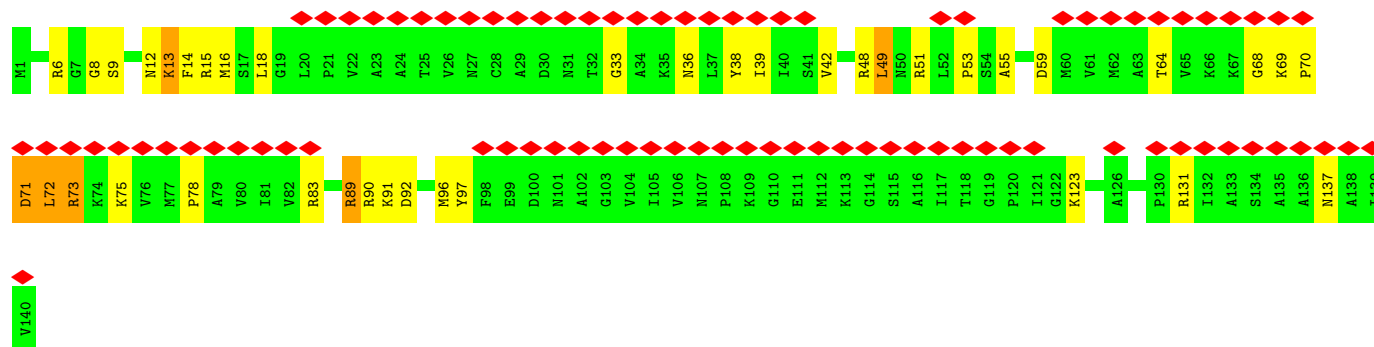
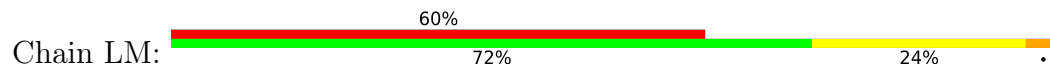
- Molecule 39: 60S ribosomal protein L9



- Molecule 40: 60S ribosomal protein L7a

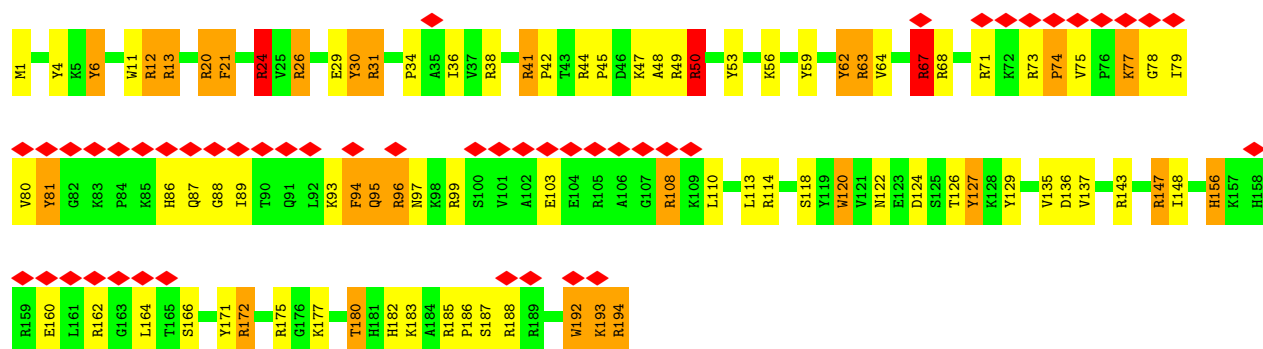


- Molecule 41: Ribosomal Pr 117

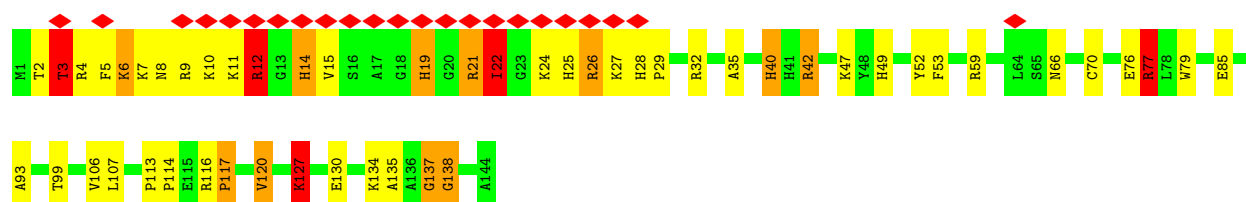


- Molecule 42: Ribosomal protein L15

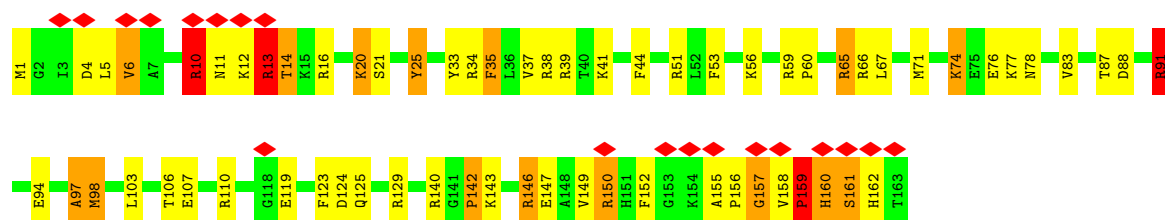




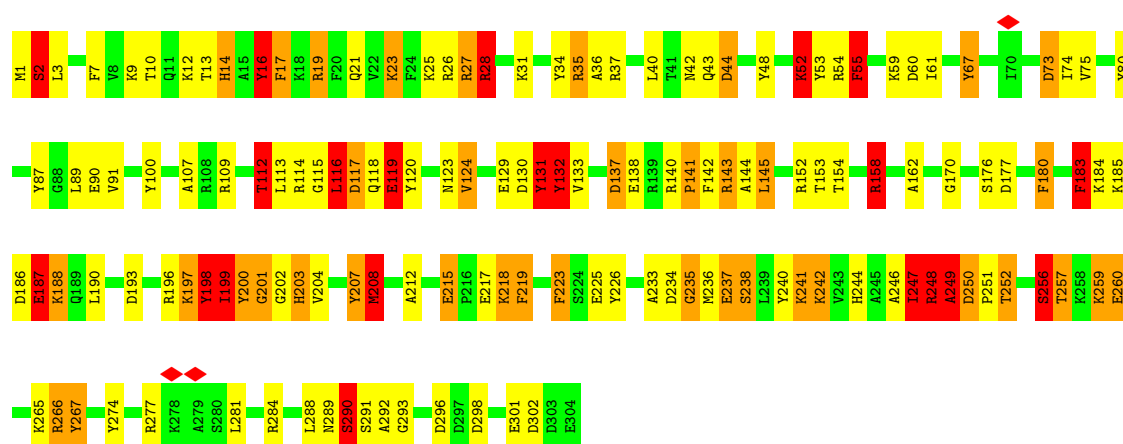
• Molecule 43: 60S ribosomal protein L27a-3



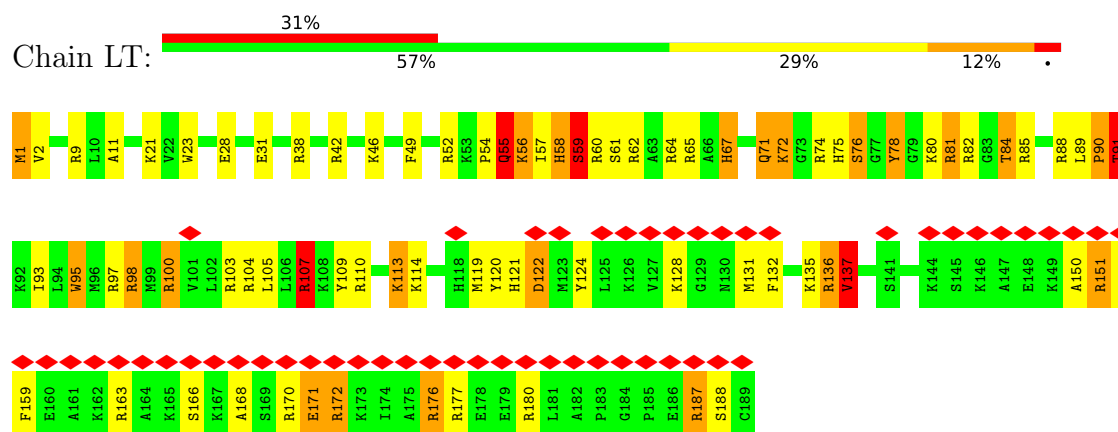
• Molecule 44: 60S ribosomal protein L18



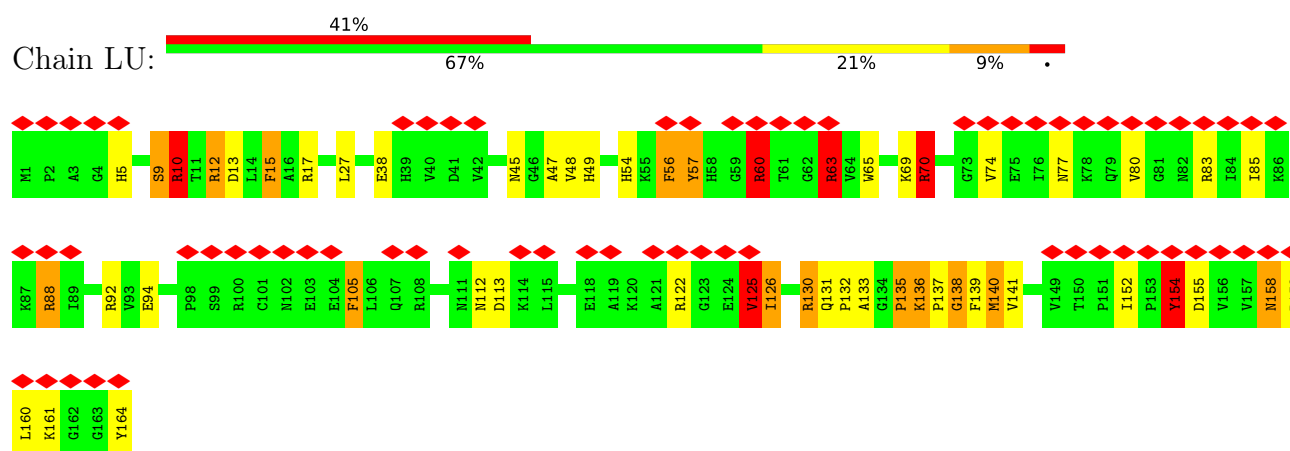
• Molecule 45: 60S ribosomal protein L5



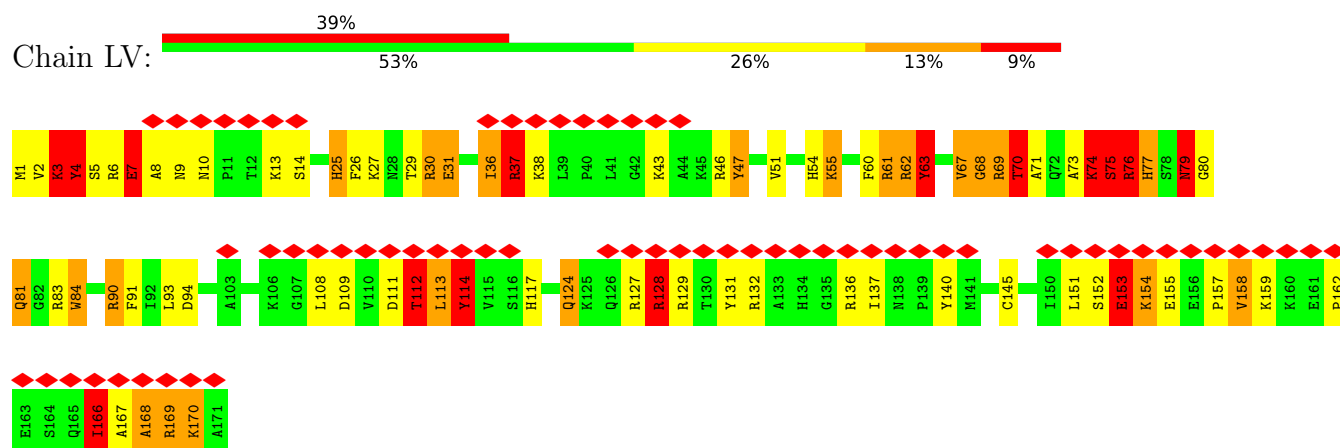
- Molecule 46: Ribosomal protein L19



- Molecule 47: 60S ribosomal protein L21

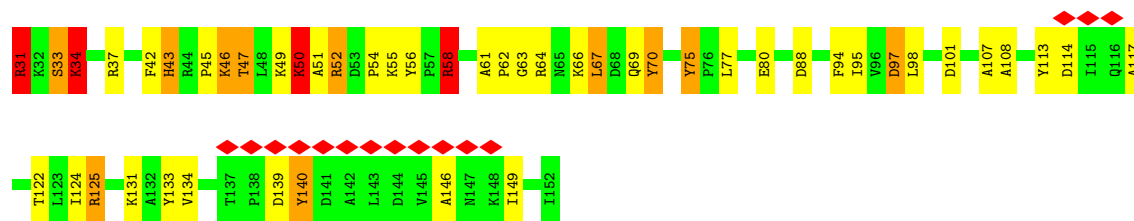


- Molecule 48: 60S ribosomal protein L17



- Molecule 49: 60S ribosomal protein L23a





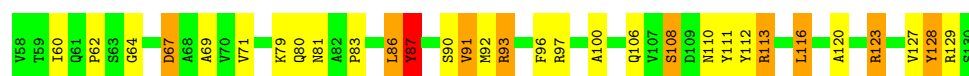
• Molecule 50: 60S ribosomal protein L24



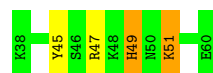
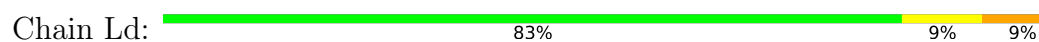
• Molecule 51: 60S ribosomal protein L26



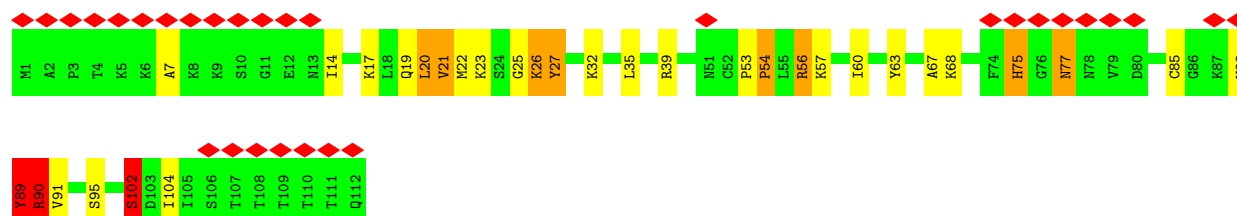
• Molecule 52: 60S ribosomal protein L28



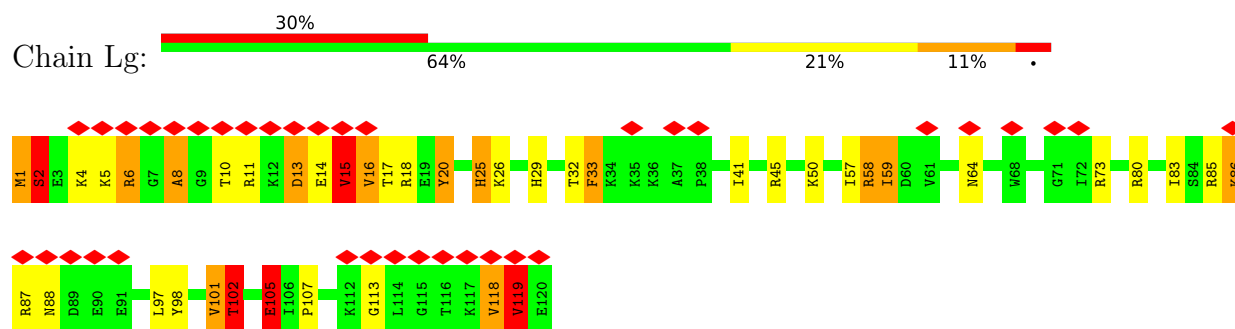
• Molecule 53: 60S ribosomal protein L29



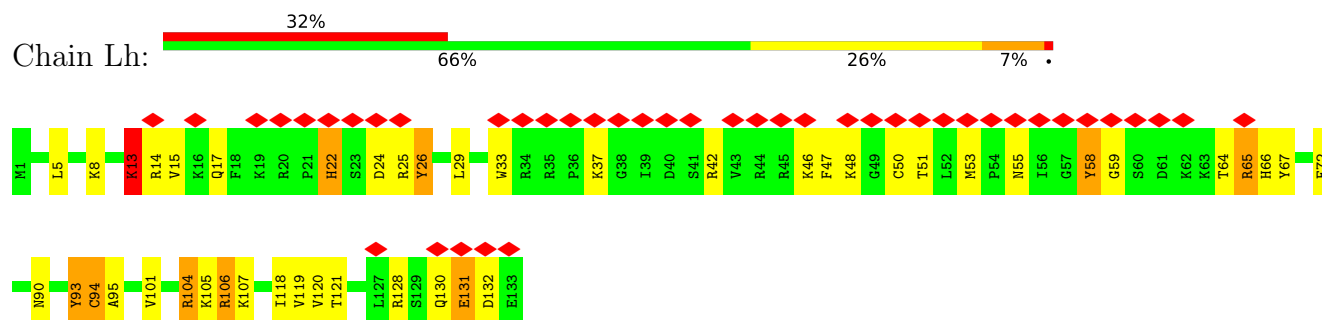
• Molecule 54: 60S ribosomal protein L30



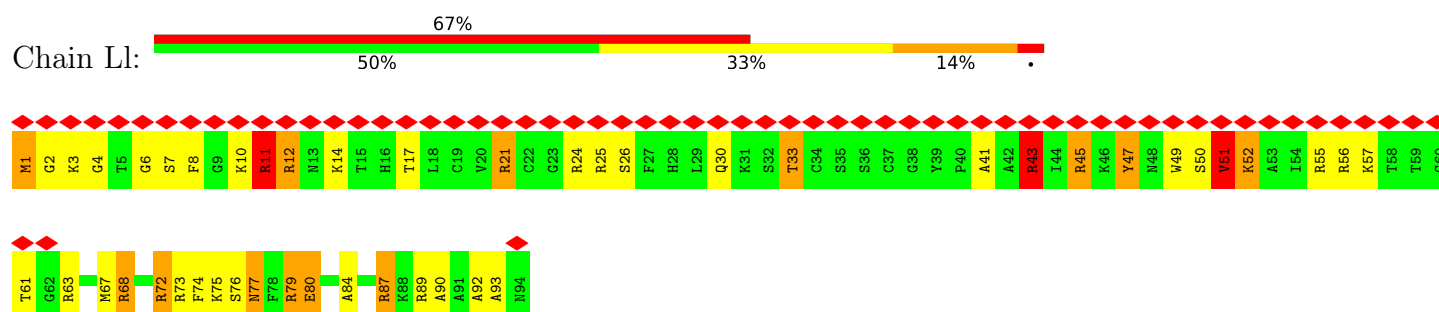
- Molecule 55: 60S ribosomal protein L31



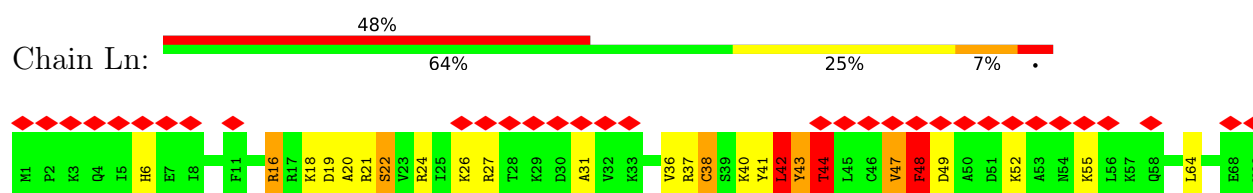
- Molecule 56: Ribosomal L32



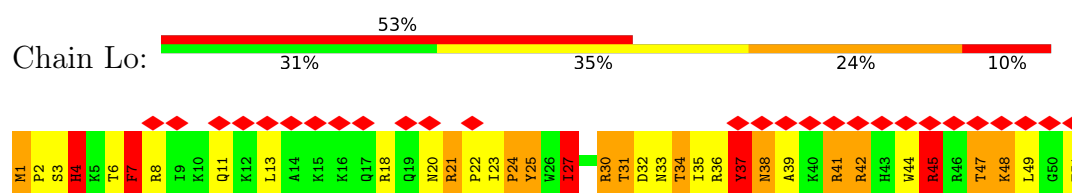
- Molecule 57: Ribosomal protein L37



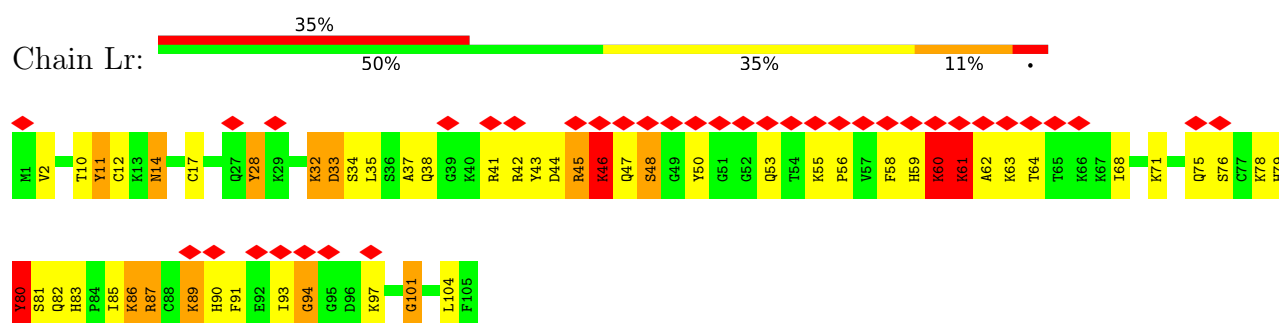
- Molecule 58: 60S ribosomal protein L38



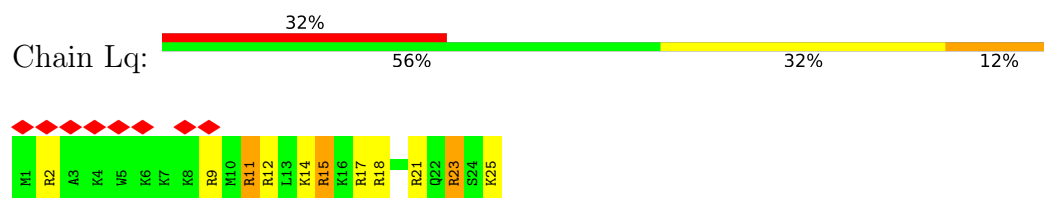
- Molecule 59: Ribosomal protein L39



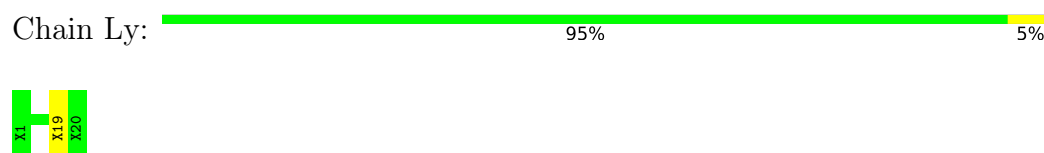
- Molecule 60: 60S ribosomal protein L44



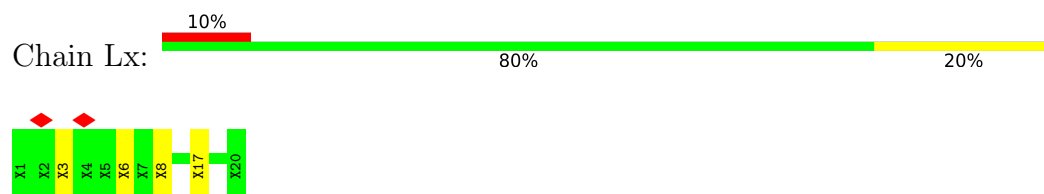
- Molecule 61: Unknown 60S wheat germ ribosome protein 1



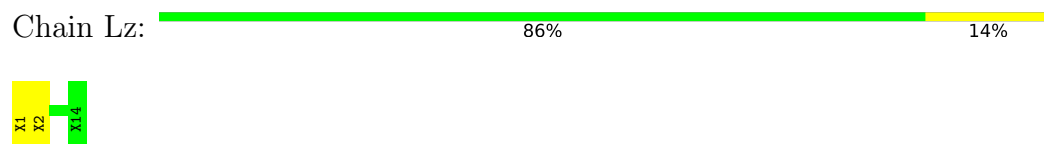
- Molecule 62: Unknown 60S wheat germ ribosome protein 2



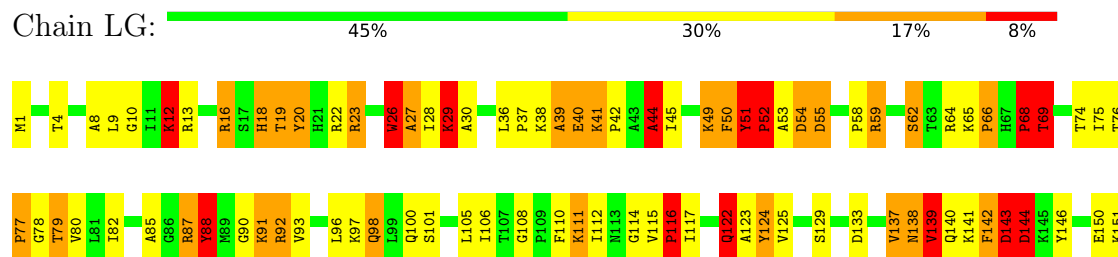
- Molecule 62: Unknown 60S wheat germ ribosome protein 2

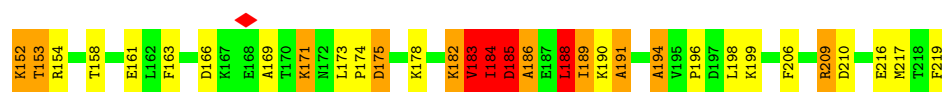


- Molecule 63: Unknown 60S wheat germ ribosome protein 3

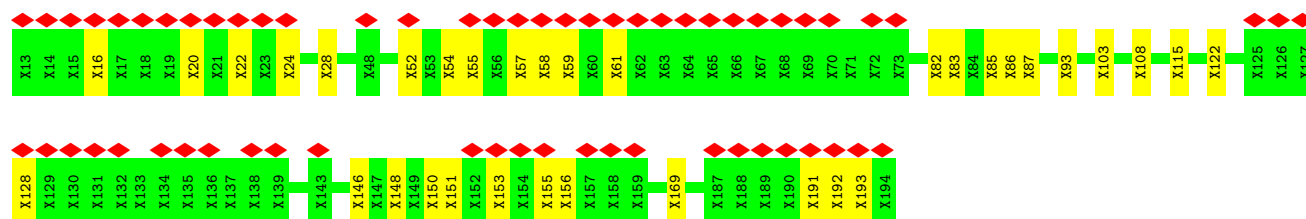
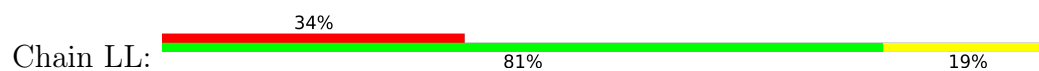


- Molecule 64: 60S ribosomal protein L6

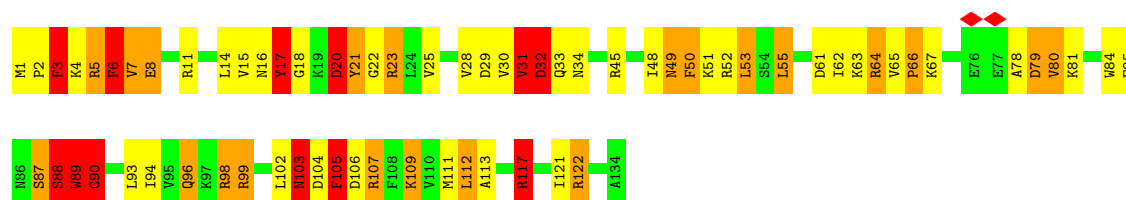




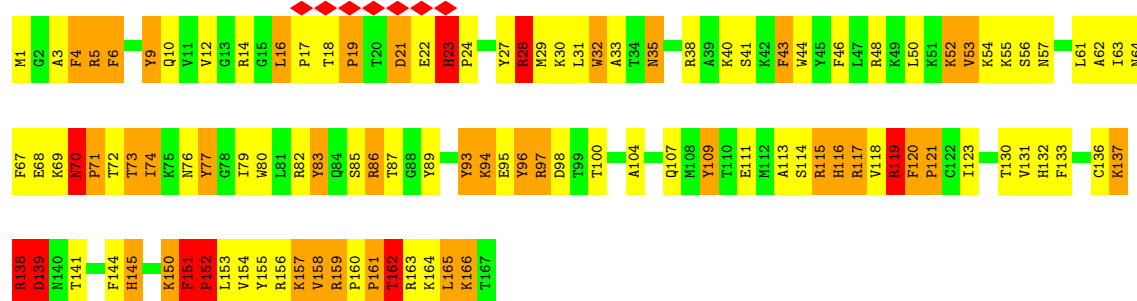
- Molecule 65: Unknown 60S wheat germ ribosome protein 5



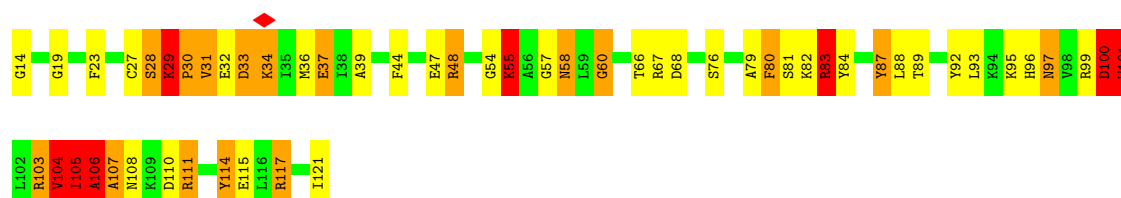
- Molecule 66: Unknown 60S wheat germ ribosome protein 6



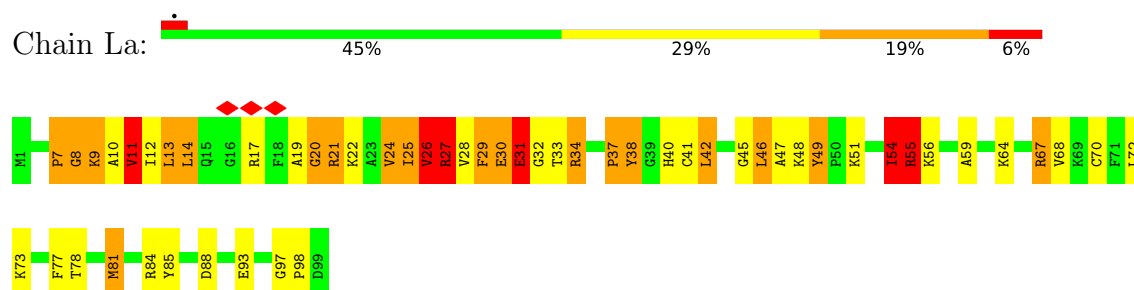
- Molecule 67: 60S ribosomal protein L18a



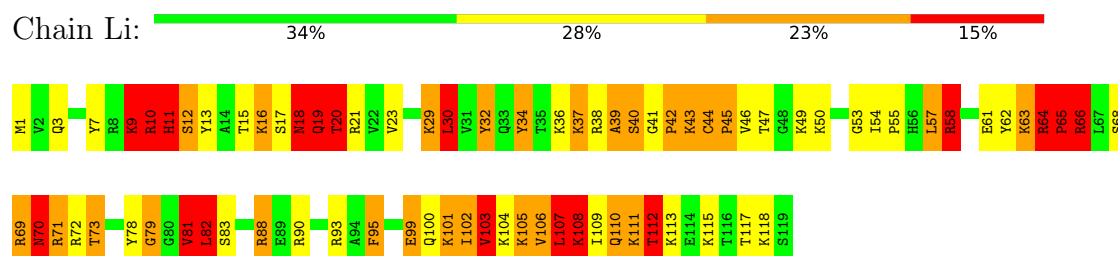
- Molecule 68: 60S ribosomal protein L22



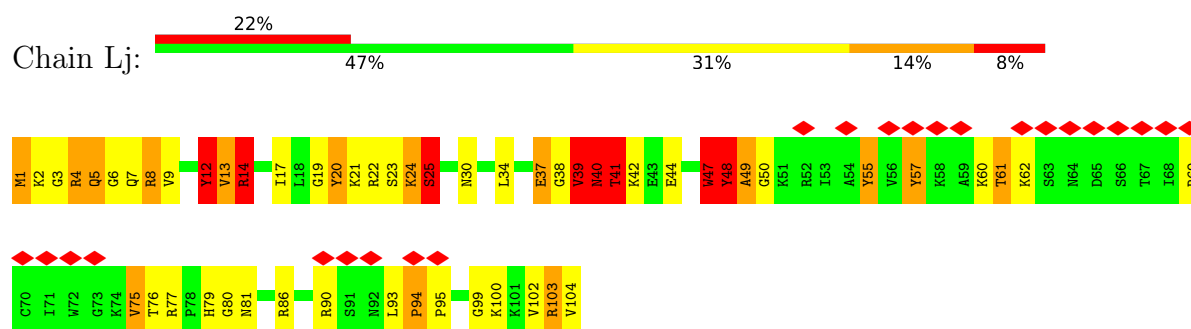
- Molecule 69: 60S ribosomal protein L27



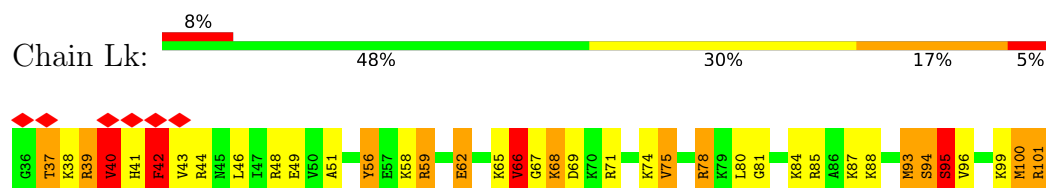
- Molecule 70: Ribosomal protein l34



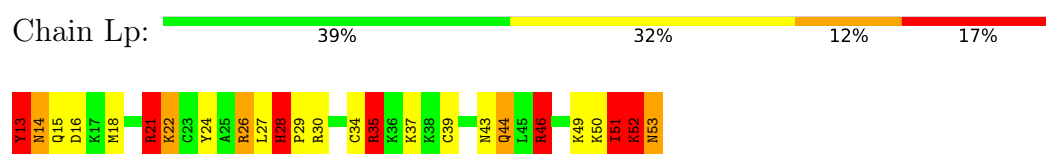
- Molecule 71: ribosomal protein L35A



- Molecule 72: 60S ribosomal protein L36

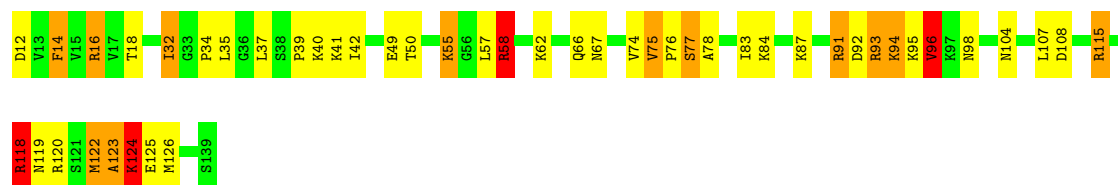


- Molecule 73: Ubiquitin-60S ribosomal protein L40-1



- Molecule 74: 60S ribosomal protein L12





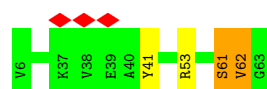
- Molecule 75: Ribosomal protein P1

Chain Lt: 91% 5% .



- Molecule 75: Ribosomal protein P1

Chain Lu: 93% 5% . .



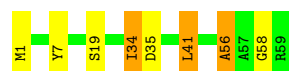
- Molecule 76: 60S acidic ribosomal protein P2A

Chain Lv: 88% 10% .



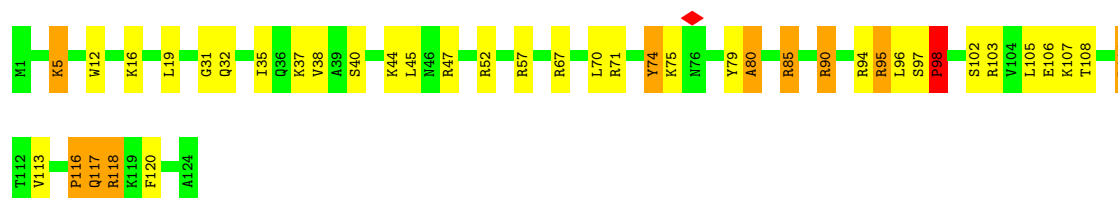
- Molecule 76: 60S acidic ribosomal protein P2A

Chain Lw: 86% 8% 5%



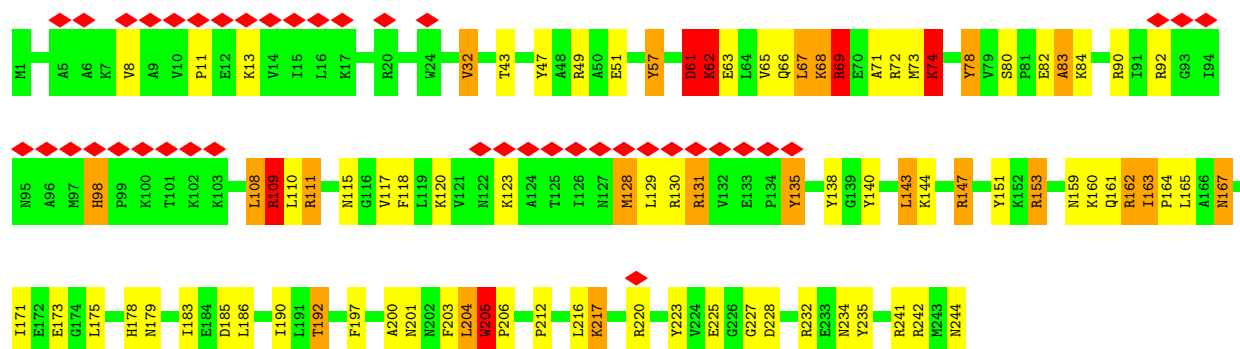
- Molecule 77: 60S ribosomal protein L35

Chain Lc: 67% 24% 8% .



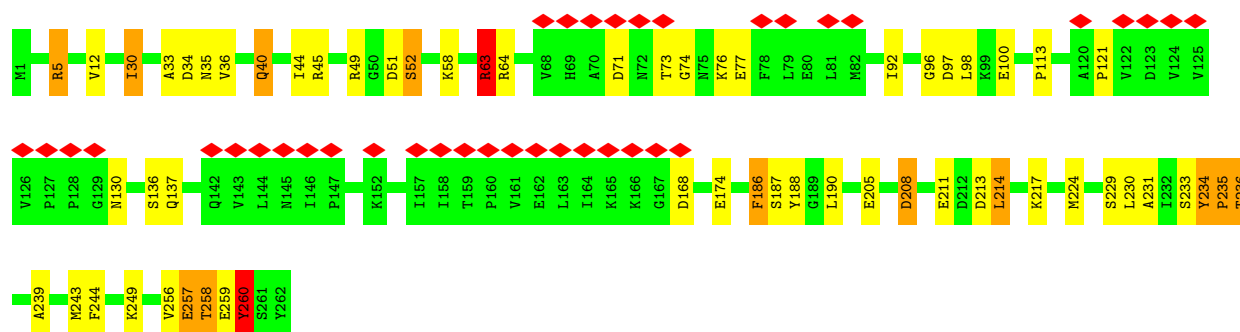
- Molecule 78: Ribosomal protein L7

Chain Le: 17% 64% 25% 9% .



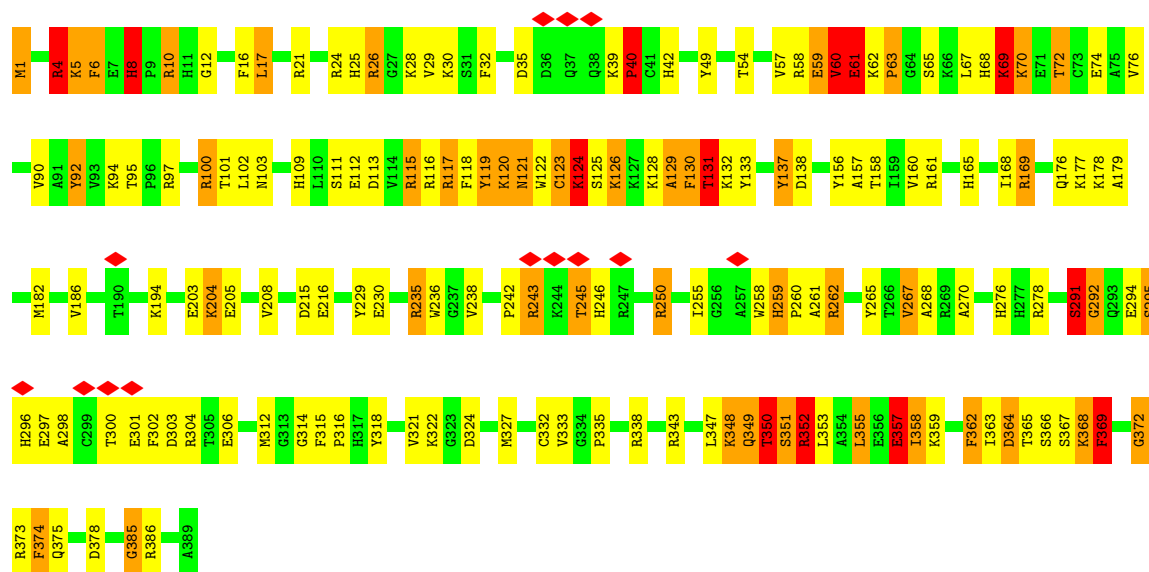
• Molecule 79: 60S acidic ribosomal protein P0

Chain Ls: 15% 77% 18% 5% .



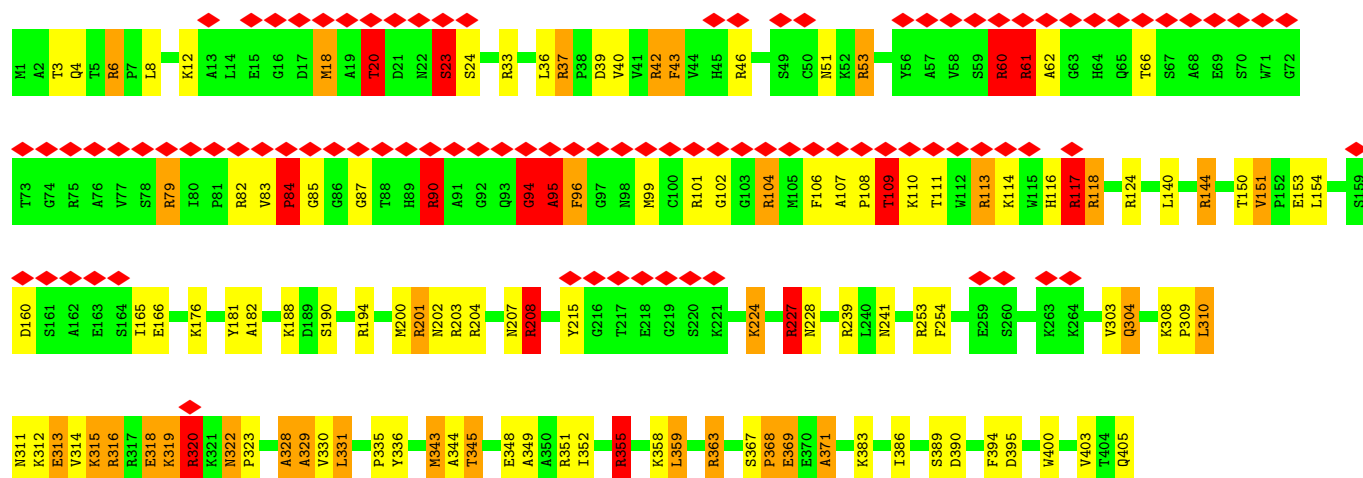
• Molecule 80: Ribosomal protein L3

Chain LC: 57% 28% 11% .

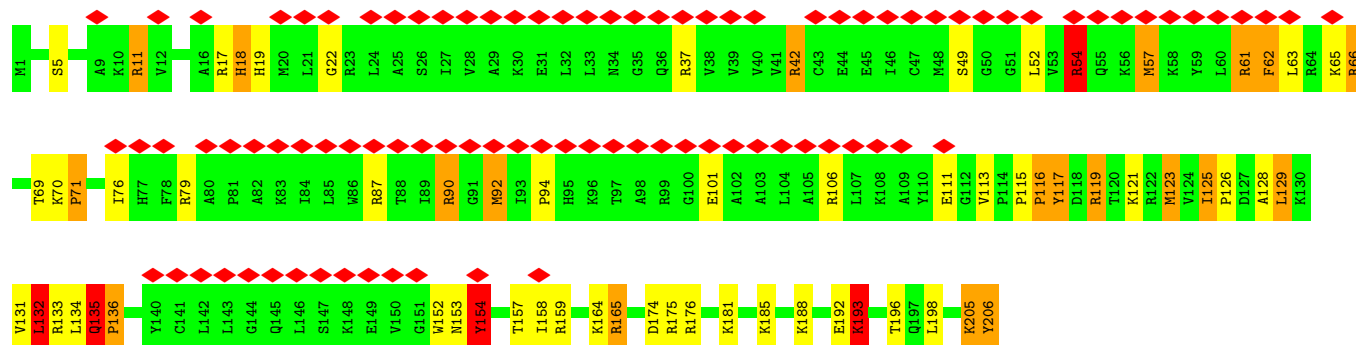


• Molecule 81: 60S ribosomal protein L4/L1

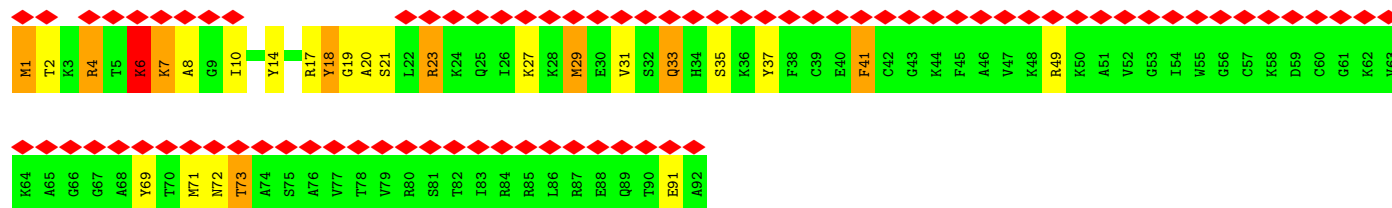
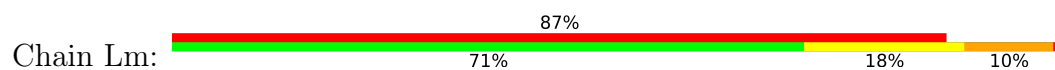
Chain LD: 25% 66% 21% 9% .



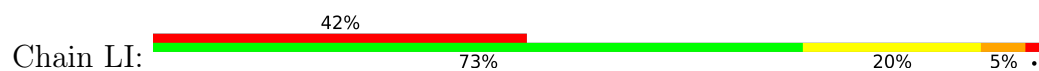
• Molecule 82: Ribosomal protein L13a

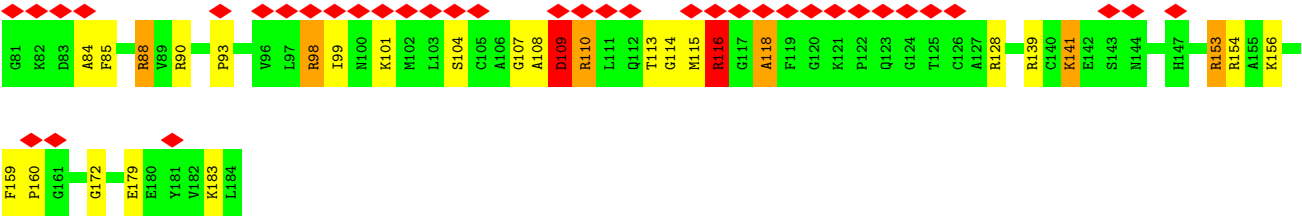


• Molecule 83: 60S ribosomal protein L37a, expressed



• Molecule 84: 60S ribosomal protein L10-1





4 Experimental information

Property	Value	Source
EM 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	
CTF correction method	Not provided	
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
Maximum map value	16.279	Depositor
Minimum map value	-14.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1	Depositor
Map size (Å)	1740.8, 1740.8, 1360.0	wwPDB
Map dimensions	256, 256, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	6.8, 6.8, 6.8	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	Sa	1.90	33/2897 (1.1%)	2.28	124/3917 (3.2%)
2	SA	1.63	11/1988 (0.6%)	2.25	83/2697 (3.1%)
3	SB	2.02	27/1555 (1.7%)	2.91	115/2077 (5.5%)
4	SD	1.94	35/1637 (2.1%)	3.00	96/2202 (4.4%)
5	SE	2.09	32/2068 (1.5%)	2.98	73/2776 (2.6%)
6	SF	0.99	2/1505 (0.1%)	1.58	29/2027 (1.4%)
7	SI	1.85	14/1034 (1.4%)	2.36	42/1379 (3.0%)
8	SJ	1.78	13/896 (1.5%)	2.78	34/1193 (2.8%)
9	SK	2.29	11/839 (1.3%)	2.92	43/1120 (3.8%)
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%)
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%)
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%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	LF	1.25	10/1519 (0.7%)	1.98	45/2042 (2.2%)
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%)
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%)
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%)
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%)
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%)
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%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
83	Lm	1.32	4/724 (0.6%)	2.06	28/958 (2.9%)
84	LI	0.93	6/1499 (0.4%)	1.88	31/2001 (1.5%)
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
2	SA	1	24
3	SB	0	32
4	SD	1	31
5	SE	0	23
6	SF	0	14
7	SI	0	5
8	SJ	0	16
9	SK	0	14
10	SL	0	11
11	SM	1	24
12	SO	0	14
13	SQ	1	37
14	SP	0	6
15	SS	1	25
16	SR	0	4
17	SV	0	5
18	SW	0	12
19	SY	0	6
20	SZ	1	9
21	Sc	0	1
23	SU	3	38
24	SX	0	3
25	SC	6	43
26	SG	0	43
27	SH	0	11
28	SN	1	6
29	ST	2	6
32	S1	9	0
33	L1	45	0
34	L3	2	0
35	L2	4	0

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Mol	Chain	#Chirality outliers	#Planarity outliers
36	LA	0	4
37	LB	0	25
38	LE	1	18
39	LF	0	15
40	LH	0	28
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
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
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	0	39
66	LN	2	21
67	LS	2	41
68	LW	0	24
69	La	0	28
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

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Mol	Chain	#Chirality outliers	#Planarity outliers
76	Lv	0	1
76	Lw	0	2
77	Lc	0	16
78	Le	0	23
79	Ls	1	13
80	LC	5	58
81	LD	2	58
82	LK	2	26
83	Lm	0	12
84	LI	0	17
All	All	111	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 111 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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	1	13
2	SA	258/260 (99%)	194 (75%)	31 (12%)	33 (13%)	0	4
3	SB	206/208 (99%)	117 (57%)	35 (17%)	54 (26%)	0	1
4	SD	198/200 (99%)	164 (83%)	17 (9%)	17 (9%)	0	9
5	SE	261/263 (99%)	186 (71%)	45 (17%)	30 (12%)	0	5
6	SF	189/191 (99%)	157 (83%)	25 (13%)	7 (4%)	2	20
7	SI	124/126 (98%)	90 (73%)	17 (14%)	17 (14%)	0	4
8	SJ	126/128 (98%)	103 (82%)	14 (11%)	9 (7%)	1	11
9	SK	117/119 (98%)	85 (73%)	13 (11%)	19 (16%)	0	2
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	2
12	SO	119/121 (98%)	95 (80%)	11 (9%)	13 (11%)	0	6
13	SQ	139/141 (99%)	87 (63%)	27 (19%)	25 (18%)	0	2
14	SP	83/85 (98%)	64 (77%)	12 (14%)	7 (8%)	0	9
15	SS	144/146 (99%)	119 (83%)	13 (9%)	12 (8%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	SR	89/91 (98%)	65 (73%)	15 (17%)	9 (10%)	0	7
17	SV	98/100 (98%)	70 (71%)	12 (12%)	16 (16%)	0	2
19	SY	56/58 (97%)	38 (68%)	8 (14%)	10 (18%)	0	2
20	SZ	60/62 (97%)	43 (72%)	9 (15%)	8 (13%)	0	4
23	SU	96/98 (98%)	70 (73%)	12 (12%)	14 (15%)	0	3
24	SX	48/50 (96%)	36 (75%)	8 (17%)	4 (8%)	0	9
25	SC	193/195 (99%)	127 (66%)	34 (18%)	32 (17%)	0	2
27	SH	128/130 (98%)	100 (78%)	17 (13%)	11 (9%)	0	9
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	5
36	LA	214/216 (99%)	191 (89%)	14 (6%)	9 (4%)	2	17
37	LB	253/255 (99%)	224 (88%)	18 (7%)	11 (4%)	2	17
38	LE	168/170 (99%)	129 (77%)	16 (10%)	23 (14%)	0	4
39	LF	188/190 (99%)	165 (88%)	16 (8%)	7 (4%)	2	20
40	LH	199/201 (99%)	149 (75%)	26 (13%)	24 (12%)	0	4
41	LM	138/140 (99%)	123 (89%)	9 (6%)	6 (4%)	2	17
42	LP	192/194 (99%)	169 (88%)	18 (9%)	5 (3%)	4	26
43	LO	142/144 (99%)	106 (75%)	17 (12%)	19 (13%)	0	4
44	LR	161/163 (99%)	127 (79%)	18 (11%)	16 (10%)	0	7
45	LQ	302/304 (99%)	218 (72%)	39 (13%)	45 (15%)	0	3
46	LT	187/189 (99%)	167 (89%)	12 (6%)	8 (4%)	2	17
47	LU	162/164 (99%)	136 (84%)	18 (11%)	8 (5%)	2	16
48	LV	169/171 (99%)	131 (78%)	20 (12%)	18 (11%)	0	6
49	LX	120/122 (98%)	98 (82%)	12 (10%)	10 (8%)	0	9
50	LZ	73/75 (97%)	53 (73%)	13 (18%)	7 (10%)	0	7
51	LY	128/130 (98%)	113 (88%)	9 (7%)	6 (5%)	2	16
52	Lb	71/73 (97%)	48 (68%)	12 (17%)	11 (16%)	0	3
53	Ld	21/23 (91%)	18 (86%)	2 (10%)	1 (5%)	2	16
54	Lf	110/112 (98%)	95 (86%)	8 (7%)	7 (6%)	1	13
55	Lg	118/120 (98%)	96 (81%)	13 (11%)	9 (8%)	1	10
56	Lh	131/133 (98%)	113 (86%)	9 (7%)	9 (7%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	Ll	92/94 (98%)	60 (65%)	18 (20%)	14 (15%)	0	3
58	Ln	67/69 (97%)	51 (76%)	11 (16%)	5 (8%)	1	10
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	4
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	2
67	LS	165/167 (99%)	115 (70%)	24 (14%)	26 (16%)	0	2
68	LW	106/108 (98%)	73 (69%)	15 (14%)	18 (17%)	0	2
69	La	97/99 (98%)	68 (70%)	15 (16%)	14 (14%)	0	3
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	6
72	Lk	75/77 (97%)	60 (80%)	5 (7%)	10 (13%)	0	4
73	Lp	39/41 (95%)	28 (72%)	8 (20%)	3 (8%)	1	10
74	LJ	126/128 (98%)	97 (77%)	15 (12%)	14 (11%)	0	5
75	Lt	56/58 (97%)	54 (96%)	1 (2%)	1 (2%)	7	35
75	Lu	56/58 (97%)	54 (96%)	1 (2%)	1 (2%)	7	35
76	Lv	57/59 (97%)	54 (95%)	2 (4%)	1 (2%)	7	35
76	Lw	57/59 (97%)	54 (95%)	2 (4%)	1 (2%)	7	35
77	Lc	122/124 (98%)	106 (87%)	7 (6%)	9 (7%)	1	10
78	Le	239/244 (98%)	212 (89%)	17 (7%)	10 (4%)	2	17
79	Ls	260/262 (99%)	233 (90%)	17 (6%)	10 (4%)	2	19
80	LC	387/389 (100%)	298 (77%)	43 (11%)	46 (12%)	0	4
81	LD	368/372 (99%)	306 (83%)	38 (10%)	24 (6%)	1	12
82	LK	204/206 (99%)	179 (88%)	15 (7%)	10 (5%)	2	16
83	Lm	90/92 (98%)	77 (86%)	9 (10%)	4 (4%)	2	17
84	LI	182/184 (99%)	140 (77%)	26 (14%)	16 (9%)	0	9
All	All	10359/10512 (98%)	8138 (79%)	1149 (11%)	1072 (10%)	1	6

5 of 1072 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Sa	2	ALA

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Mol	Chain	Res	Type
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%)	8	26
2	SA	190/204 (93%)	161 (85%)	29 (15%)	2	11
3	SB	150/175 (86%)	126 (84%)	24 (16%)	2	10
4	SD	176/176 (100%)	152 (86%)	24 (14%)	3	13
5	SE	211/211 (100%)	190 (90%)	21 (10%)	6	20
6	SF	158/159 (99%)	144 (91%)	14 (9%)	8	25
7	SI	103/103 (100%)	91 (88%)	12 (12%)	4	16
8	SJ	91/113 (80%)	84 (92%)	7 (8%)	10	30
9	SK	78/94 (83%)	66 (85%)	12 (15%)	2	11
10	SL	79/113 (70%)	71 (90%)	8 (10%)	6	20
11	SM	116/133 (87%)	91 (78%)	25 (22%)	1	5
12	SO	106/106 (100%)	97 (92%)	9 (8%)	8	27
13	SQ	123/127 (97%)	100 (81%)	23 (19%)	1	7
14	SP	63/74 (85%)	53 (84%)	10 (16%)	2	10
15	SS	121/121 (100%)	96 (79%)	25 (21%)	1	6
16	SR	77/77 (100%)	64 (83%)	13 (17%)	1	9
17	SV	76/87 (87%)	70 (92%)	6 (8%)	10	29
19	SY	49/52 (94%)	41 (84%)	8 (16%)	2	10
20	SZ	44/49 (90%)	38 (86%)	6 (14%)	3	13
23	SU	70/84 (83%)	42 (60%)	28 (40%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	SX	44/44 (100%)	40 (91%)	4 (9%)	7	24
25	SC	154/167 (92%)	136 (88%)	18 (12%)	4	16
27	SH	113/113 (100%)	95 (84%)	18 (16%)	2	10
28	SN	27/40 (68%)	24 (89%)	3 (11%)	5	17
29	ST	68/68 (100%)	59 (87%)	9 (13%)	3	14
36	LA	192/192 (100%)	179 (93%)	13 (7%)	13	34
37	LB	193/195 (99%)	175 (91%)	18 (9%)	7	23
38	LE	148/149 (99%)	126 (85%)	22 (15%)	2	11
39	LF	164/164 (100%)	152 (93%)	12 (7%)	11	31
40	LH	164/173 (95%)	135 (82%)	29 (18%)	1	8
41	LM	103/109 (94%)	91 (88%)	12 (12%)	4	16
42	LP	167/167 (100%)	143 (86%)	24 (14%)	2	12
43	LO	104/110 (94%)	88 (85%)	16 (15%)	2	11
44	LR	138/138 (100%)	117 (85%)	21 (15%)	2	11
45	LQ	242/251 (96%)	196 (81%)	46 (19%)	1	7
46	LT	166/166 (100%)	144 (87%)	22 (13%)	3	13
47	LU	129/140 (92%)	110 (85%)	19 (15%)	2	12
48	LV	136/144 (94%)	112 (82%)	24 (18%)	1	8
49	LX	109/109 (100%)	95 (87%)	14 (13%)	3	14
50	LZ	54/66 (82%)	49 (91%)	5 (9%)	7	23
51	LY	115/115 (100%)	98 (85%)	17 (15%)	2	12
52	Lb	64/64 (100%)	57 (89%)	7 (11%)	5	18
53	Ld	21/21 (100%)	20 (95%)	1 (5%)	21	43
54	Lf	90/98 (92%)	72 (80%)	18 (20%)	1	6
55	Lg	99/103 (96%)	85 (86%)	14 (14%)	3	12
56	Lh	119/122 (98%)	111 (93%)	8 (7%)	13	34
57	Li	72/77 (94%)	61 (85%)	11 (15%)	2	11
58	Ln	59/63 (94%)	48 (81%)	11 (19%)	1	7
59	Lo	48/48 (100%)	37 (77%)	11 (23%)	0	4
60	Lr	91/94 (97%)	75 (82%)	16 (18%)	1	8
61	Lq	24/24 (100%)	22 (92%)	2 (8%)	9	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	LG	185/185 (100%)	152 (82%)	33 (18%)	1	8
66	LN	116/116 (100%)	88 (76%)	28 (24%)	0	3
67	LS	153/153 (100%)	123 (80%)	30 (20%)	1	7
68	LW	89/94 (95%)	75 (84%)	14 (16%)	2	11
69	La	73/83 (88%)	56 (77%)	17 (23%)	0	4
70	Li	105/107 (98%)	78 (74%)	27 (26%)	0	3
71	Lj	80/89 (90%)	63 (79%)	17 (21%)	1	5
72	Lk	62/62 (100%)	45 (73%)	17 (27%)	0	2
73	Lp	38/38 (100%)	26 (68%)	12 (32%)	0	2
74	LJ	104/105 (99%)	80 (77%)	24 (23%)	0	4
75	Lt	46/46 (100%)	45 (98%)	1 (2%)	47	65
75	Lu	46/46 (100%)	46 (100%)	0	100	100
76	Lv	48/48 (100%)	47 (98%)	1 (2%)	48	66
76	Lw	48/48 (100%)	46 (96%)	2 (4%)	25	46
77	Lc	107/109 (98%)	99 (92%)	8 (8%)	11	31
78	Le	206/206 (100%)	171 (83%)	35 (17%)	1	9
79	Ls	222/222 (100%)	199 (90%)	23 (10%)	5	19
80	LC	328/335 (98%)	276 (84%)	52 (16%)	2	10
81	LD	294/302 (97%)	257 (87%)	37 (13%)	3	14
82	LK	173/173 (100%)	141 (82%)	32 (18%)	1	8
83	Lm	73/73 (100%)	67 (92%)	6 (8%)	9	28
84	LI	152/156 (97%)	135 (89%)	17 (11%)	5	17
All	All	8547/8911 (96%)	7319 (86%)	1228 (14%)	5	12

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

Mol	Chain	Res	Type
70	Li	45	PRO
81	LD	99	MET
71	Lj	40	ASN
70	Li	29	LYS
78	Le	98	HIS

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

Mol	Chain	Res	Type
64	LG	18	HIS
67	LS	145	HIS
79	Ls	35	ASN
27	SH	8	ASN
25	SC	178	ASN

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	2468	G
33	L1	3389	C
33	L1	2504	A
33	L1	2467	A
33	L1	2842	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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
33	L1	20
26	SG	3
78	Le	2
25	SC	2
9	SK	2
19	SY	2
2	SA	2
81	LD	1
18	SW	1
1	Sa	1
4	SD	1
16	SR	1
3	SB	1
28	SN	1
5	SE	1
24	SX	1
15	SS	1
10	SL	1
14	SP	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

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
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

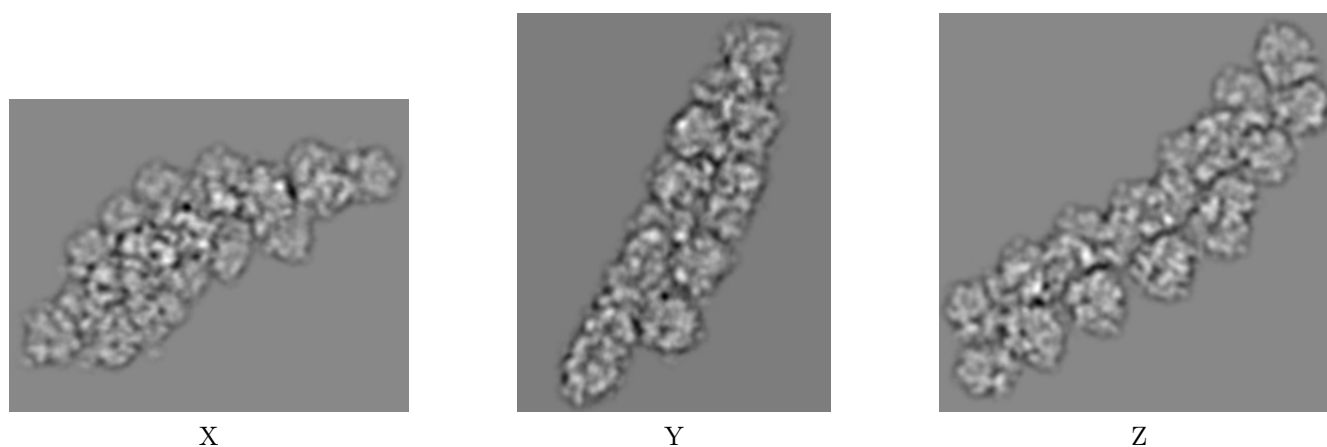
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2790. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

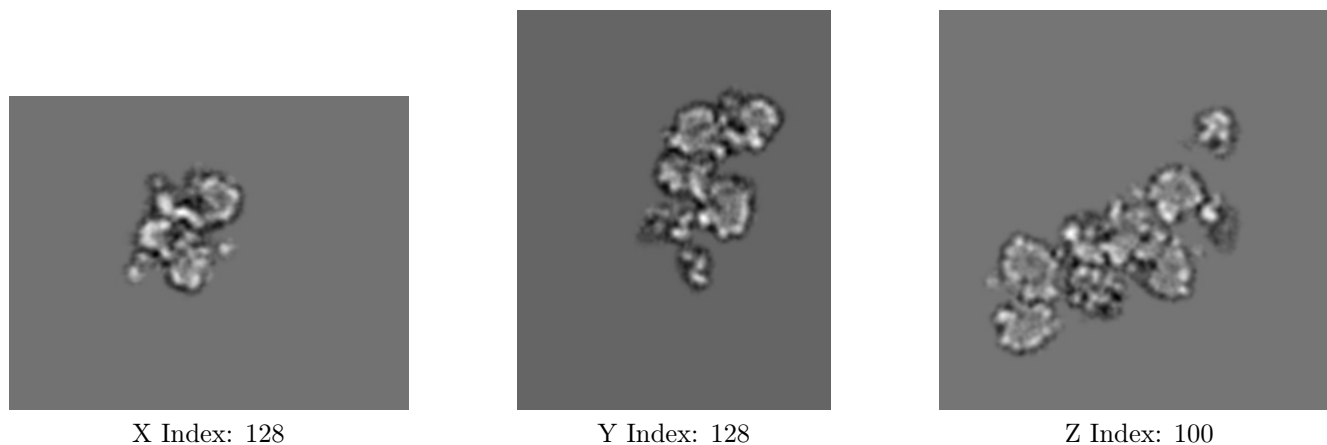
6.1.1 Primary map



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

6.2 Central slices [i](#)

6.2.1 Primary map



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

6.3 Largest variance slices [i](#)

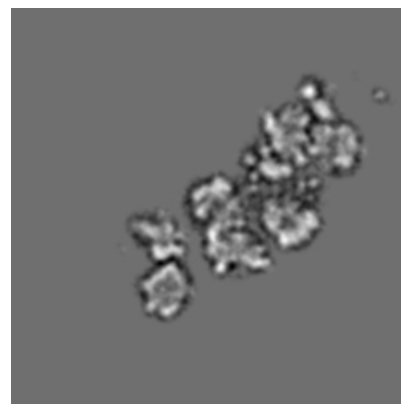
6.3.1 Primary map



X Index: 44



Y Index: 93

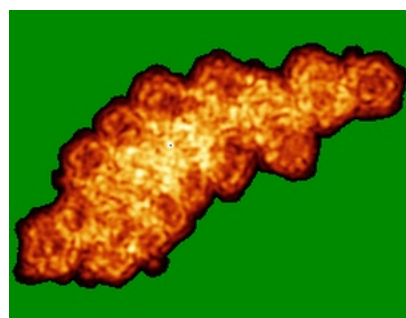


Z Index: 126

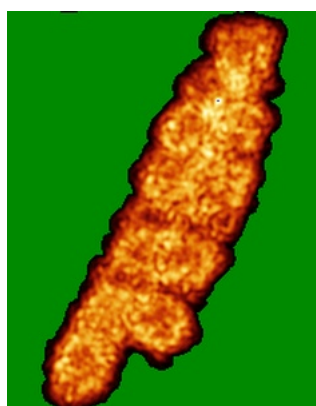
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

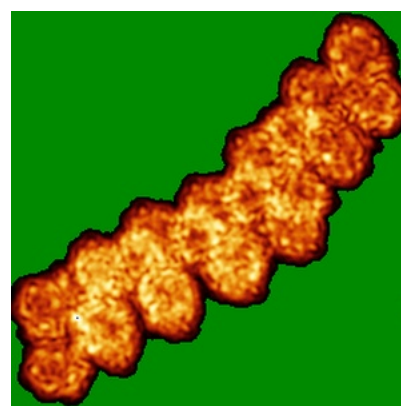
6.4.1 Primary map



X



Y

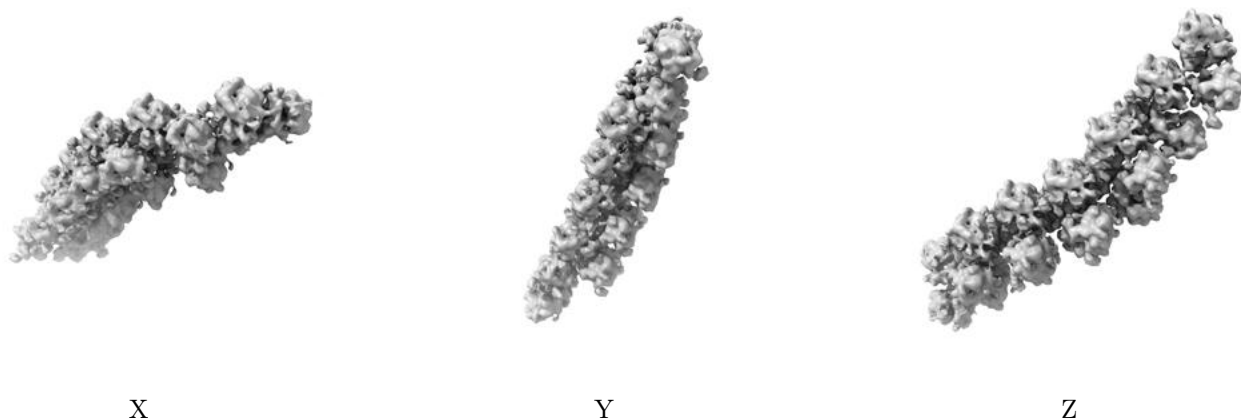


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

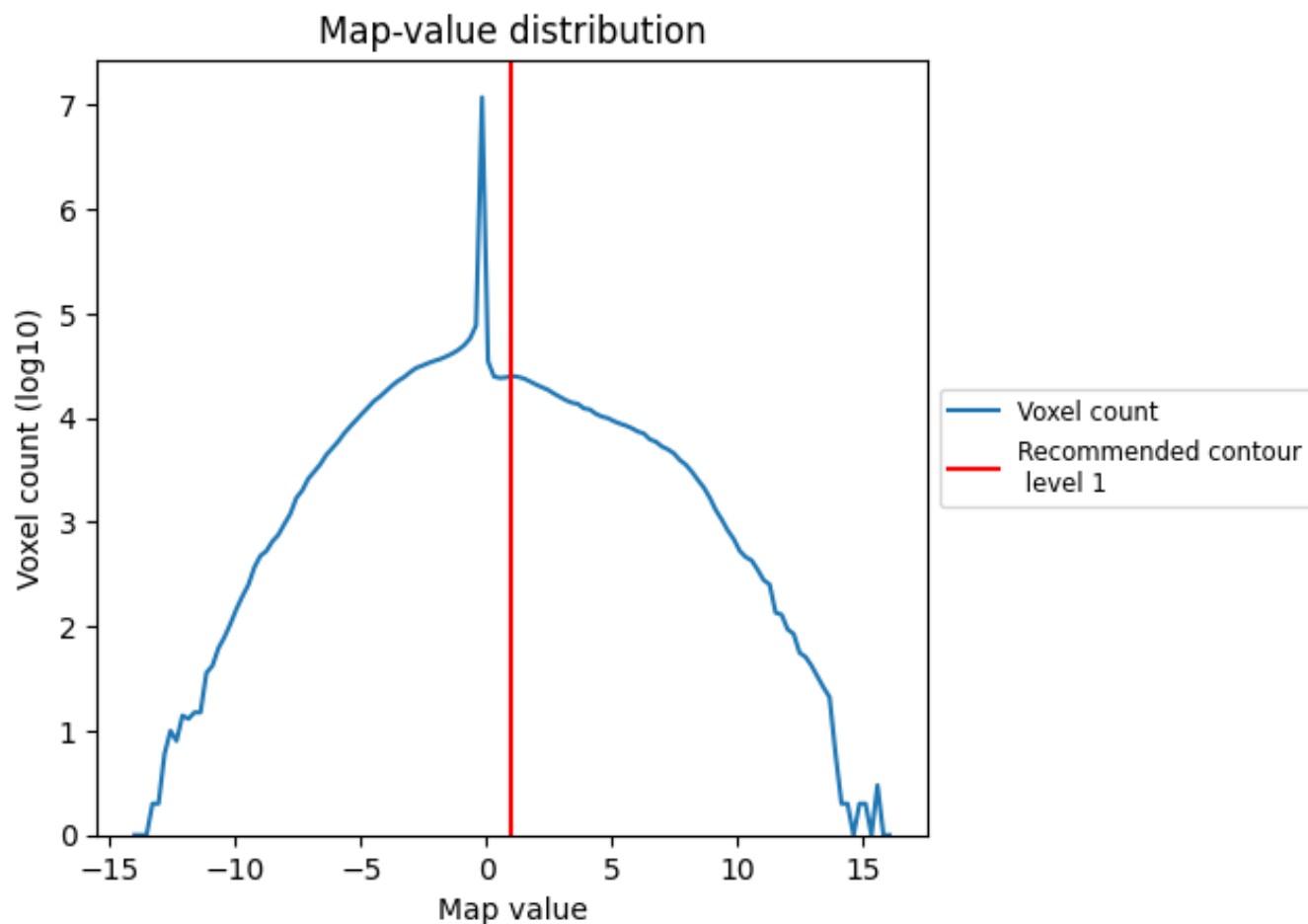
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

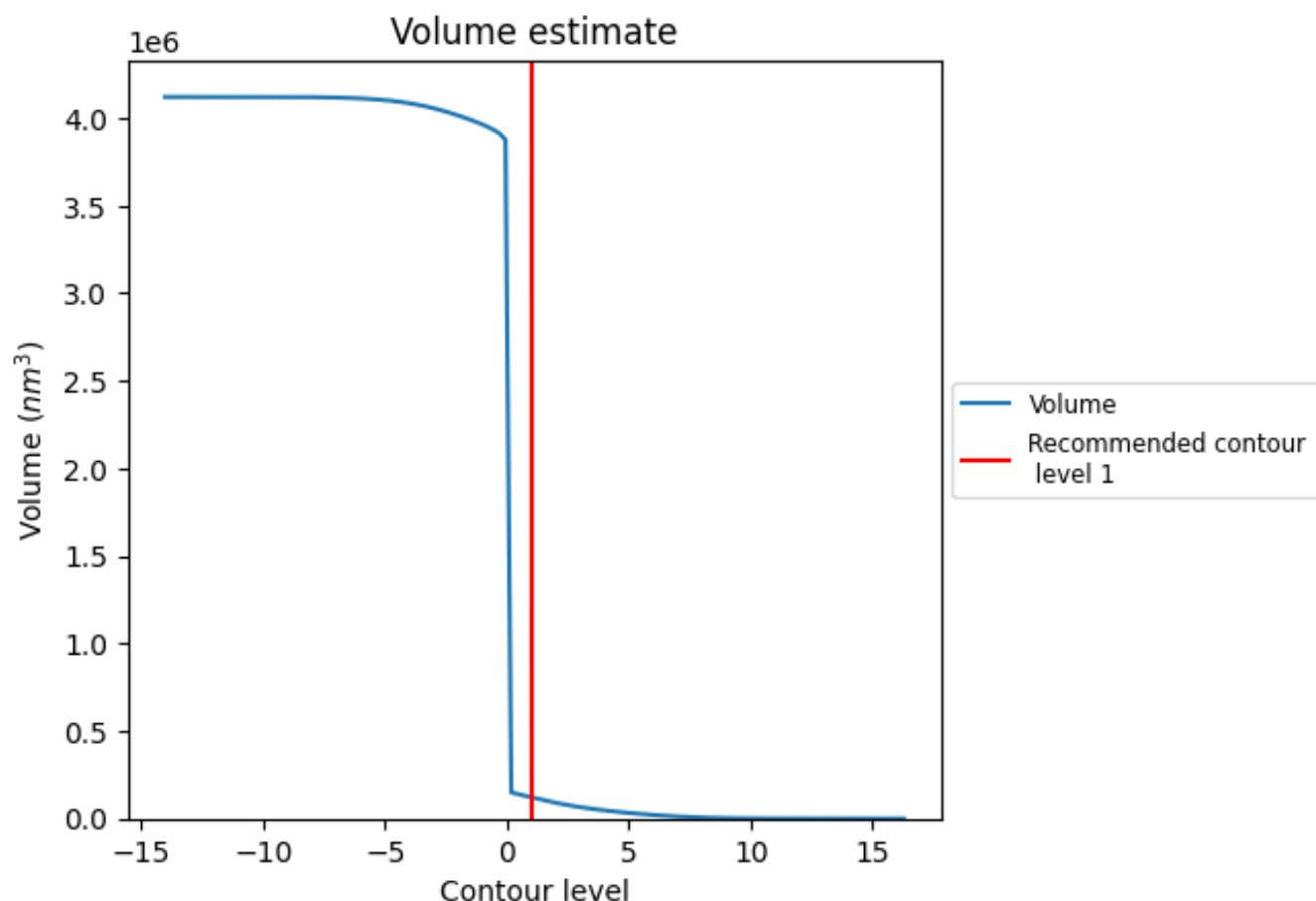
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 122092 nm³; this corresponds to an approximate mass of 110289 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation

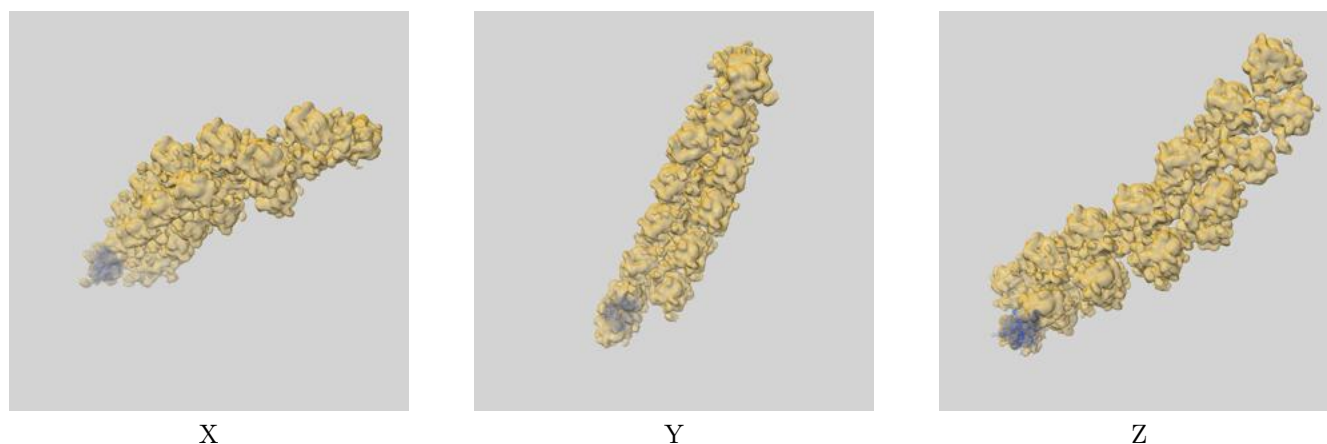
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

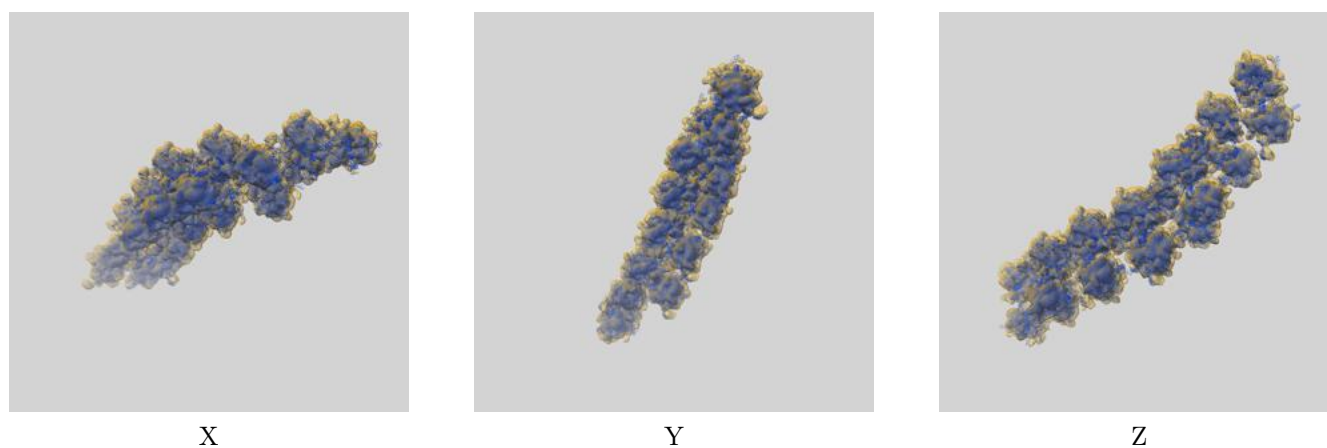
This section contains information regarding the fit between EMDB map EMD-2790 and PDB model 4V3P. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

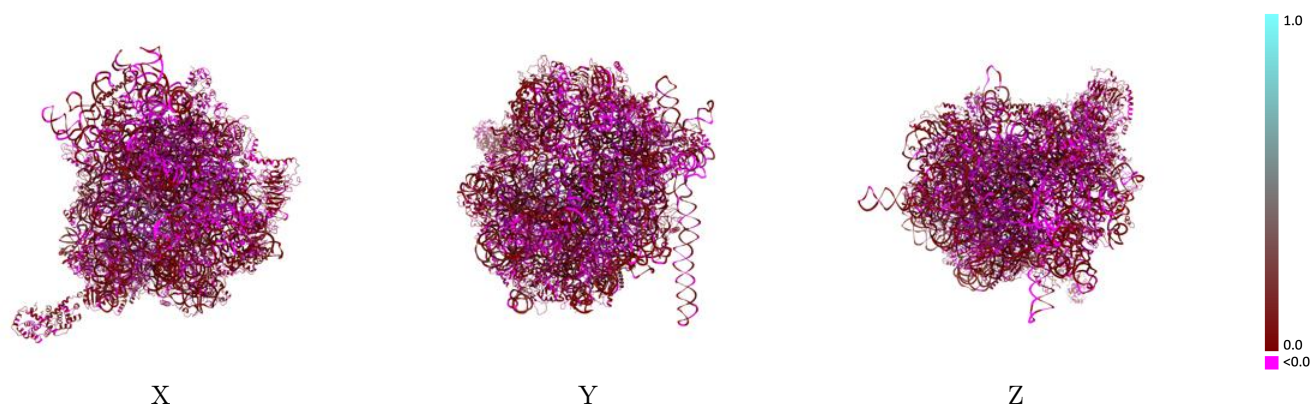


9.1.2 Map-model assembly overlay [i](#)



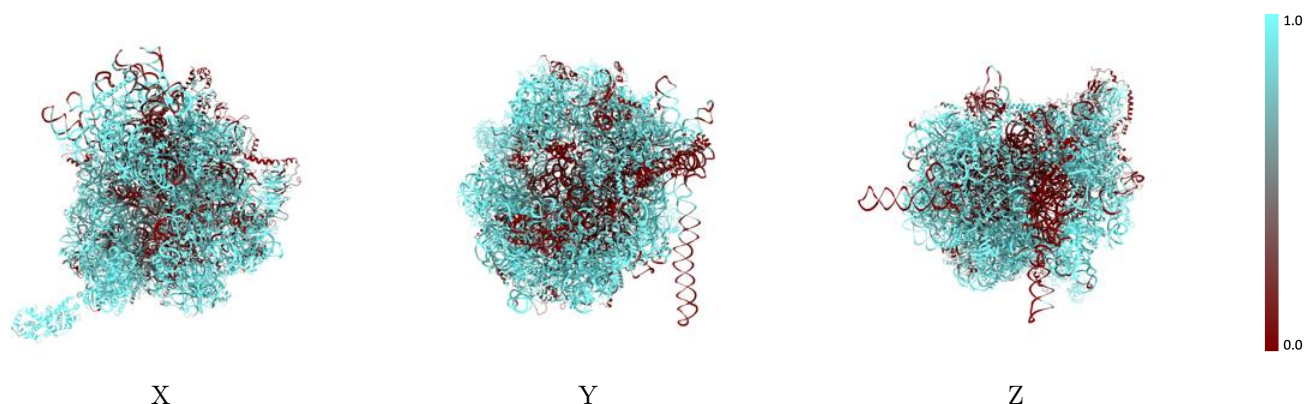
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



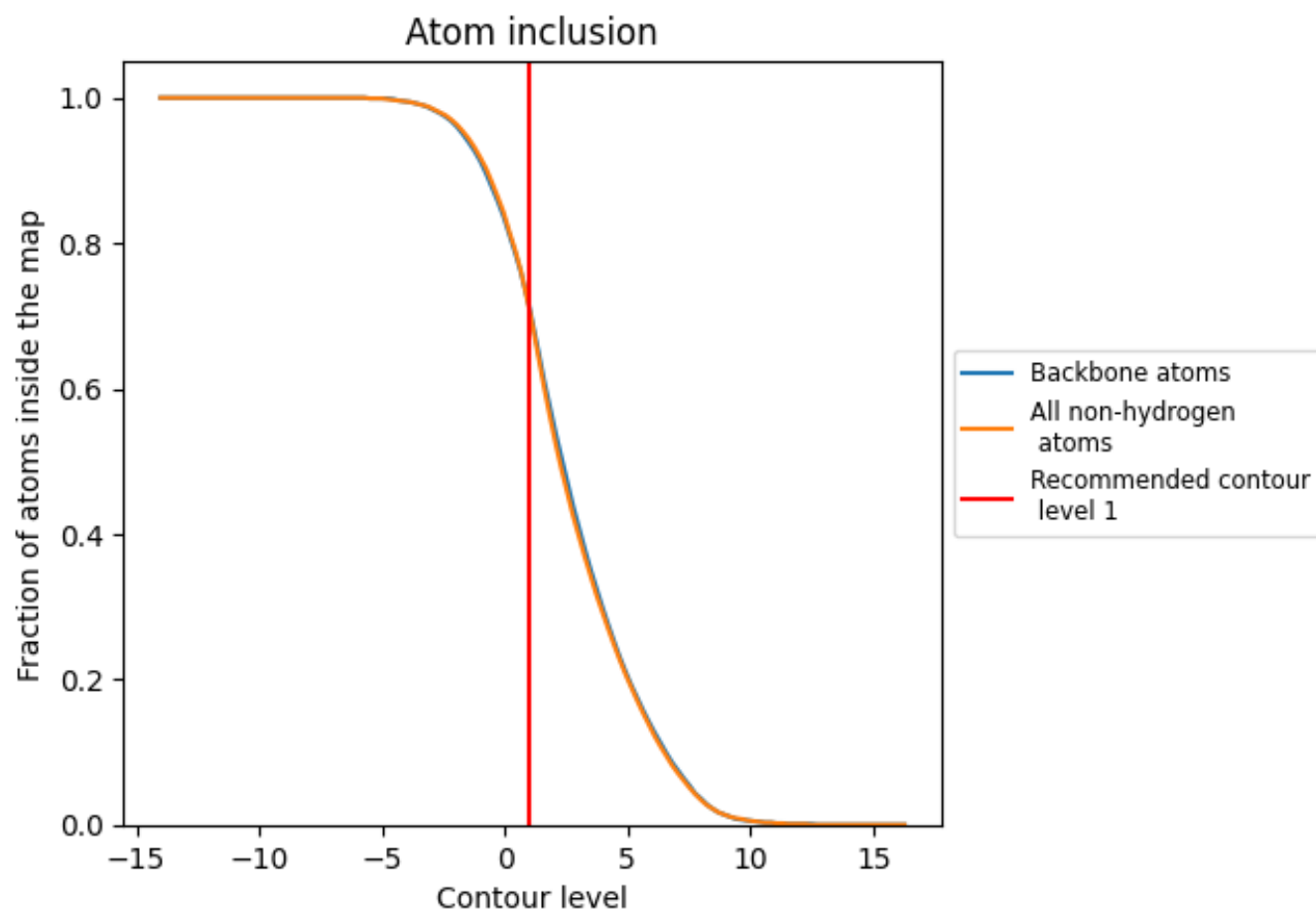
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7100	 0.0160
L1	 0.7200	 0.0180
L2	 0.8090	 0.0040
L3	 0.9400	 0.0370
LA	 0.0140	 -0.0110
LB	 0.2940	 -0.0160
LC	 0.9570	 0.0250
LD	 0.7450	 0.0060
LE	 0.8460	 0.0270
LF	 0.8750	 0.0510
LG	 0.9890	 0.0500
LH	 0.8810	 0.0350
LI	 0.5720	 0.0040
LJ	 0.9850	 0.0470
LK	 0.5420	 -0.0260
LL	 0.6670	 0.0050
LM	 0.3940	 -0.0240
LN	 0.9660	 0.0150
LO	 0.8240	 0.0400
LP	 0.7390	 -0.0220
LQ	 0.9860	 0.0420
LR	 0.8750	 0.0340
LS	 0.9620	 0.0030
LT	 0.6820	 0.0060
LU	 0.5640	 -0.0170
LV	 0.6150	 0.0030
LW	 0.9610	 0.0590
LX	 0.8670	 0.0280
LY	 1.0000	 0.0440
LZ	 0.7770	 -0.0020
La	 0.9400	 0.0030
Lb	 1.0000	 0.0500
Lc	 0.9810	 0.0470
Ld	 1.0000	 -0.0110
Le	 0.8050	 -0.0040

























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Chain	Atom inclusion	Q-score
Lf	 0.7330	 0.0220
Lg	 0.6920	 0.0010
Lh	 0.6700	 -0.0050
Li	 1.0000	 0.0700
Lj	 0.7760	 -0.0140
Lk	 0.9050	 0.0460
Ll	 0.3230	 -0.0400
Lm	 0.1080	 -0.0130
Ln	 0.5370	 0.0300
Lo	 0.4590	 -0.0550
Lp	 0.9850	 -0.0140
Lq	 0.7030	 0.0370
Lr	 0.6040	 0.0130
Ls	 0.8260	 0.0350
Lt	 1.0000	 0.0840
Lu	 0.9440	 0.0330
Lv	 0.9980	 0.0540
Lw	 0.9930	 0.0220
Lx	 0.9210	 0.0120
Ly	 1.0000	 0.0200
Lz	 1.0000	 -0.0620
S1	 0.6480	 0.0130
S2	 0.1920	 -0.0060
S3	 1.0000	 0.0580
SA	 0.7040	 0.0150
SB	 0.6260	 0.0000
SC	 0.8900	 0.0220
SD	 0.9500	 0.0040
SE	 0.9360	 0.0110
SF	 0.3650	 0.0150
SG	 0.6270	 0.0250
SH	 0.9650	 0.0030
SI	 0.8920	 0.0190
SJ	 0.6790	 -0.0170
SK	 0.8190	 0.0470
SL	 0.0780	 -0.0180
SM	 0.6310	 0.0160
SN	 1.0000	 0.0080
SO	 0.2030	 -0.0070
SP	 0.0080	 -0.0010
SQ	 0.6640	 0.0240
SR	 0.6480	 0.0330

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Chain	Atom inclusion	Q-score
SS	 1.0000	 0.0720
ST	 0.5200	 0.0230
SU	 0.3720	 -0.0060
SV	 0.4420	 0.0210
SW	 0.9540	 0.0840
SX	 0.1540	 -0.0240
SY	 0.6200	 0.0330
SZ	 0.6280	 0.0340
Sa	 0.6630	 0.0350
Sb	 1.0000	 0.1390
Sc	 0.7620	 0.0180