



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 12:53 AM UTC

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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

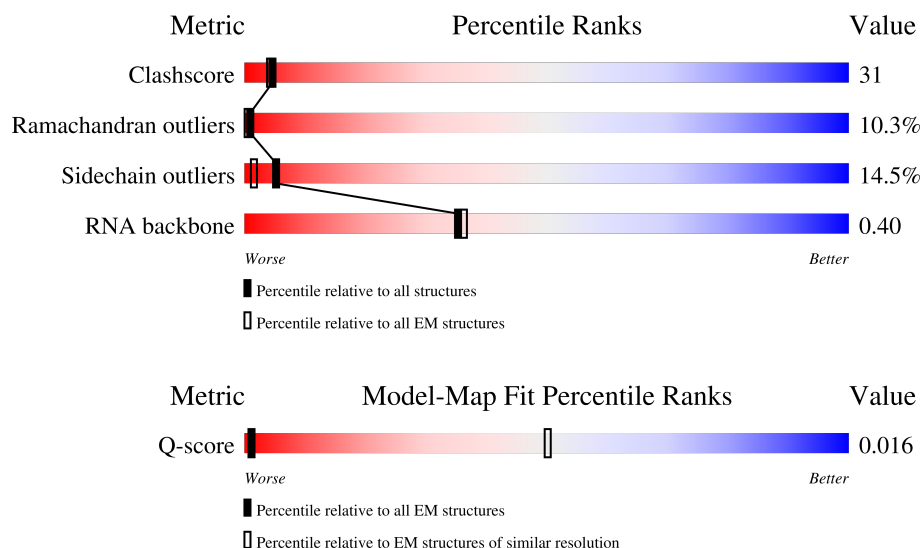
1 Overall quality at a glance i

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.



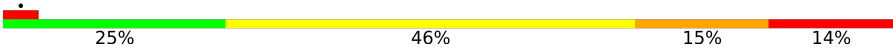
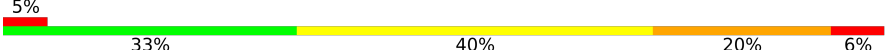
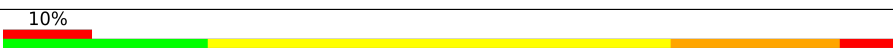
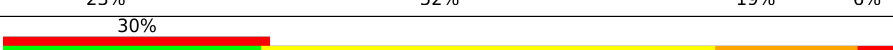
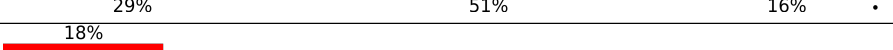
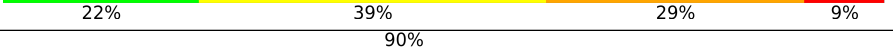
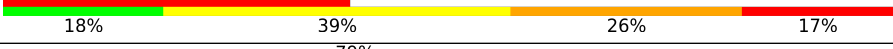
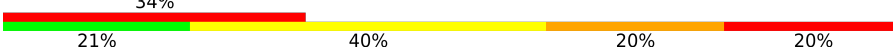
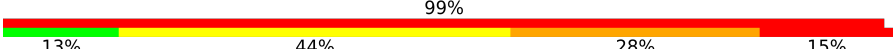
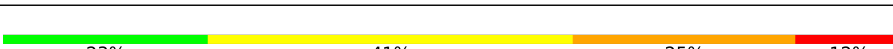
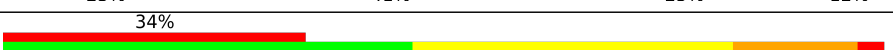
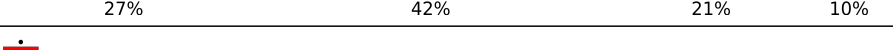
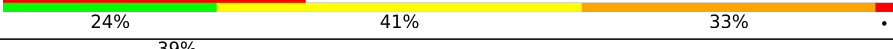
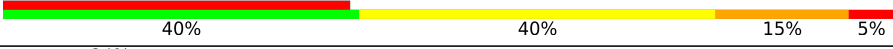
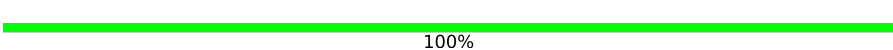
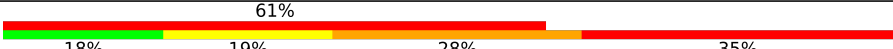
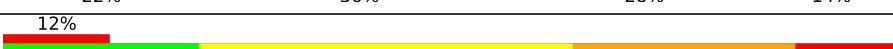
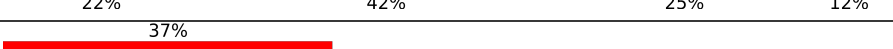
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4 (34.00 - 34.00)

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	34% 34% 47% 13% 6%
2	SA	260	30% 21% 47% 25% 7%
3	SB	208	34% 18% 40% 30% 12%

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Mol	Chain	Length	Quality of chain
4	SD	200	
5	SE	263	
6	SF	191	
7	SI	126	
8	SJ	128	
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	

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Mol	Chain	Length	Quality of chain
29	ST	82	
30	S3	11	
31	S2	75	
32	S1	1743	
33	L1	3352	
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	

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Mol	Chain	Length	Quality of chain
54	Lf	112	
55	Lg	120	
56	Lh	133	
57	Ll	94	
58	Ln	69	
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	

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Mol	Chain	Length	Quality of chain
76	Lw	59	
77	Lc	124	
78	Le	244	
79	Ls	262	
80	LC	389	
81	LD	372	
82	LK	206	
83	Lm	92	
84	LI	184	

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		

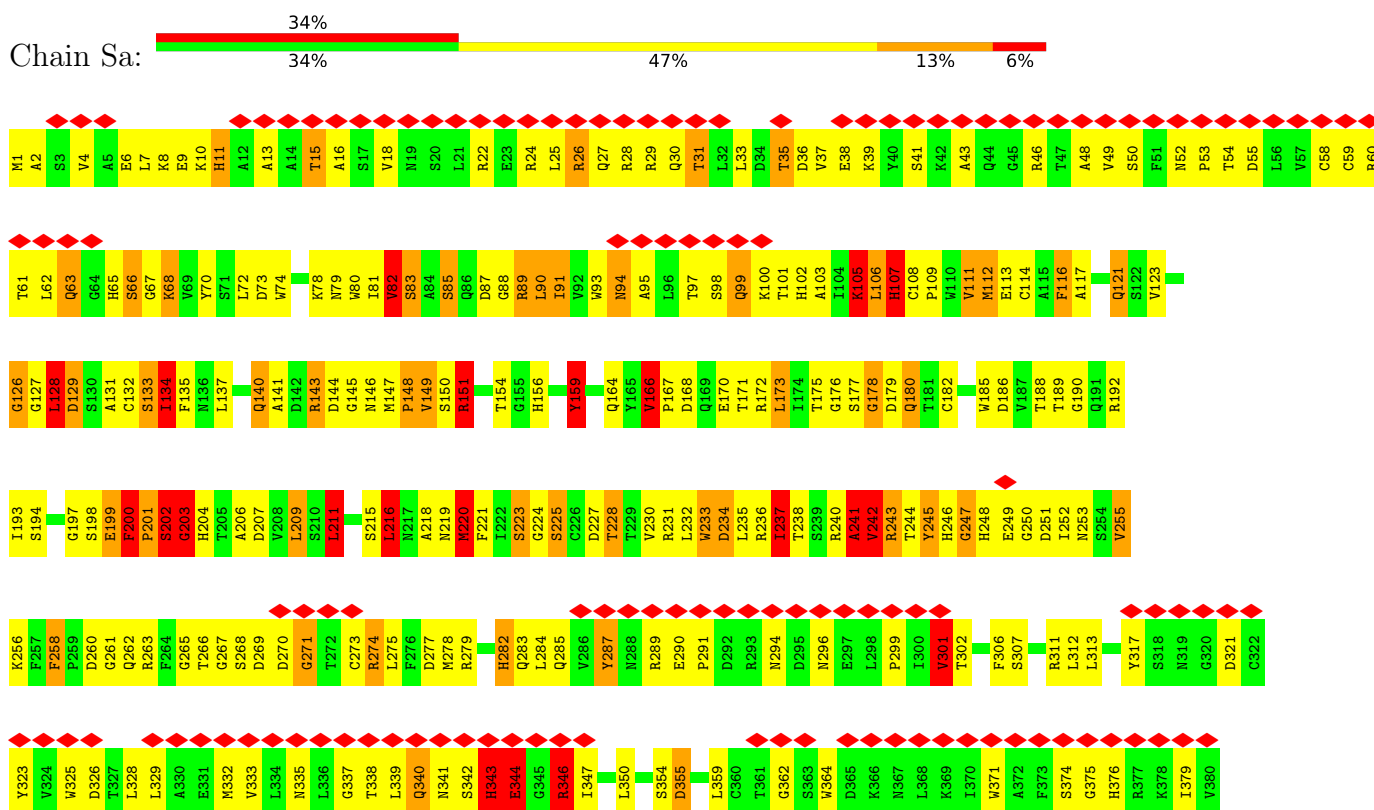
- Molecule 84 is a protein called 60S ribosomal protein L10-1.

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

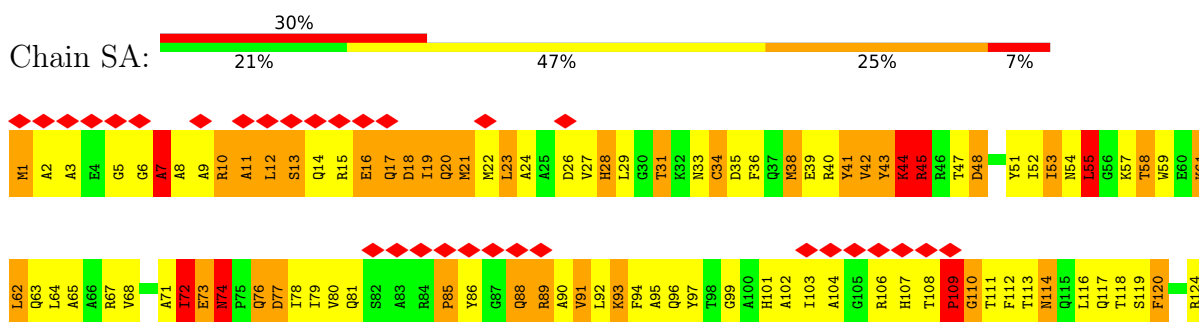
3 Residue-property plots

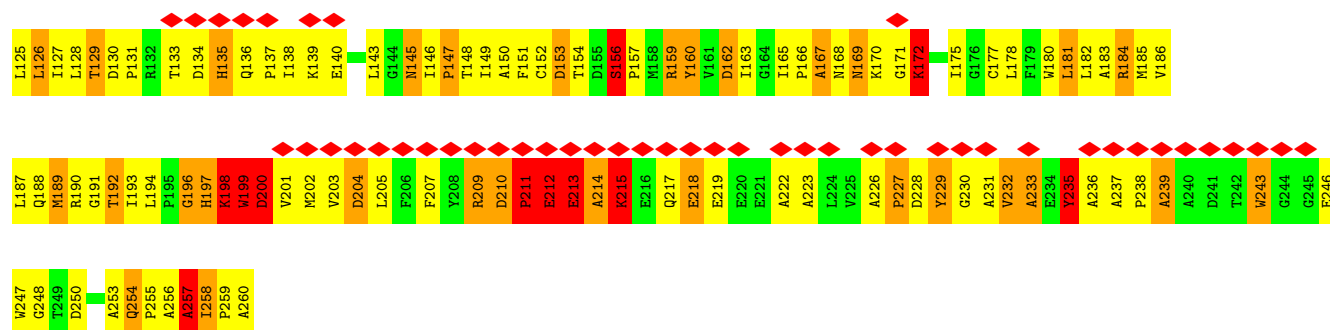
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

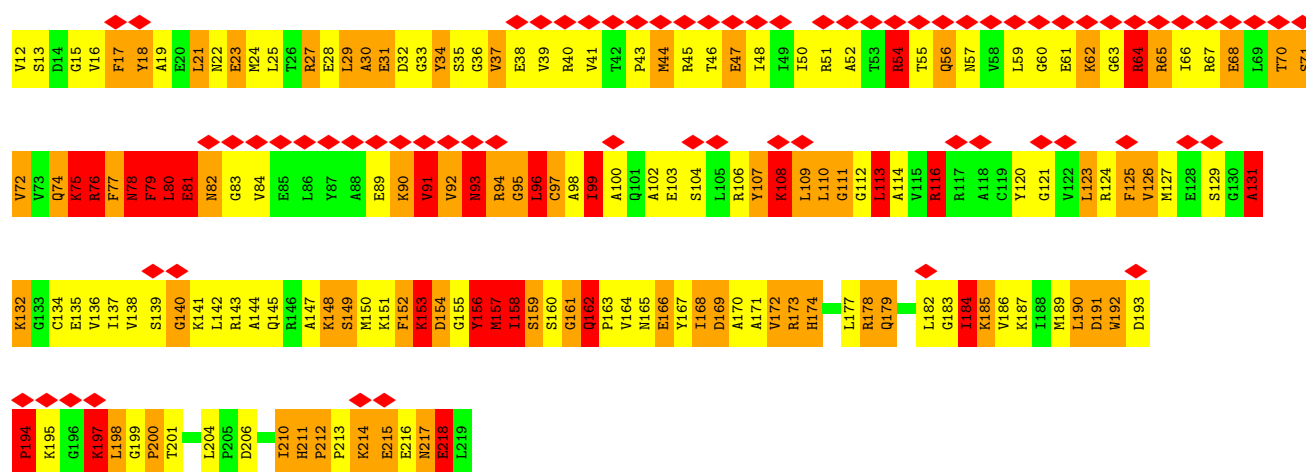


• Molecule 2: 40S ribosomal protein SA

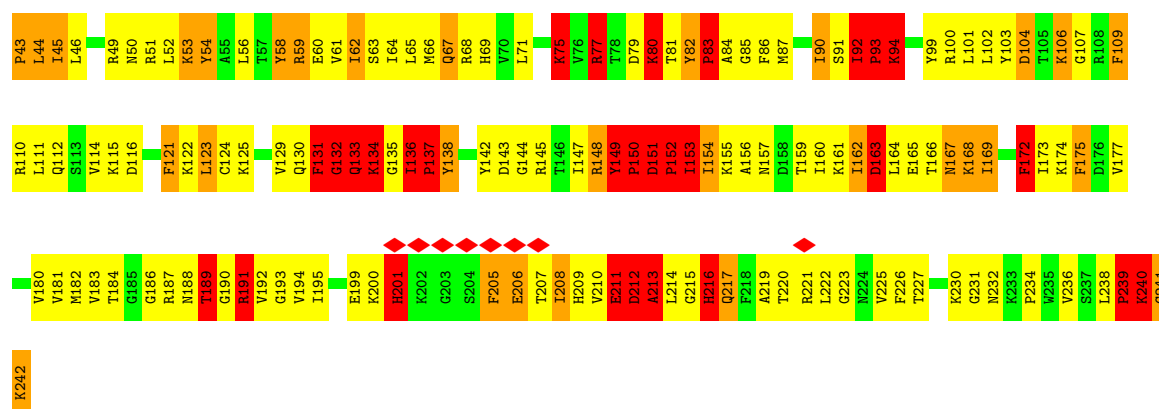




• Molecule 3: Putative 40S ribosomal protein S3

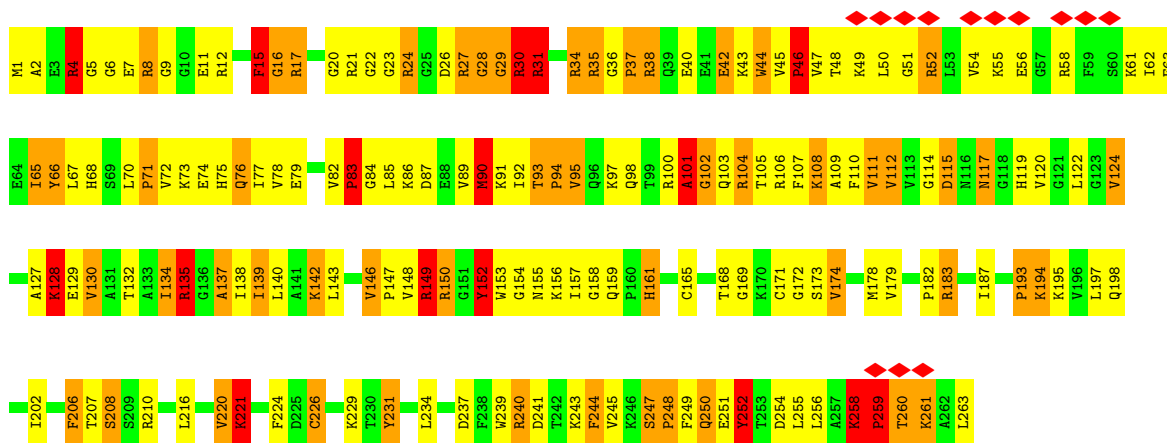


• Molecule 4: 40S ribosomal protein S4

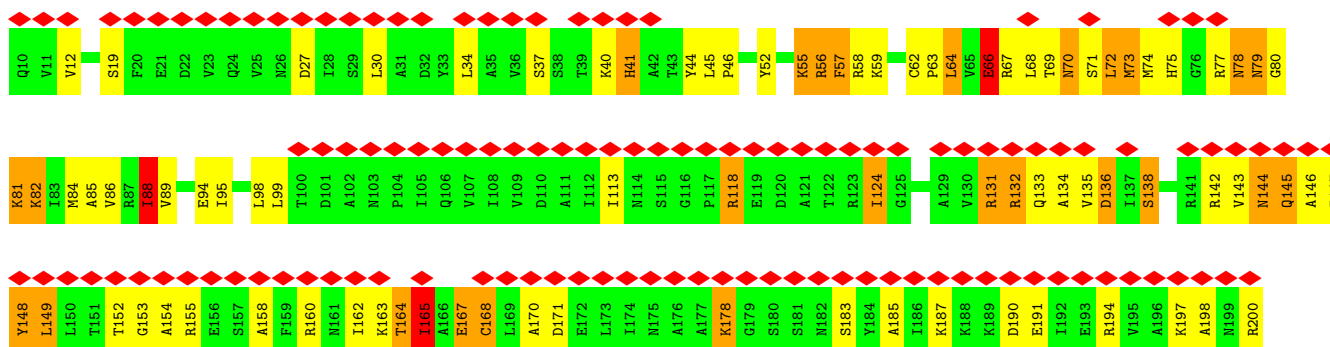


• Molecule 5: 40S ribosomal protein S2

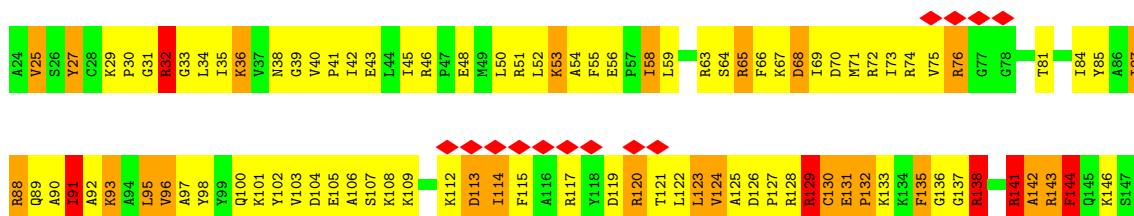




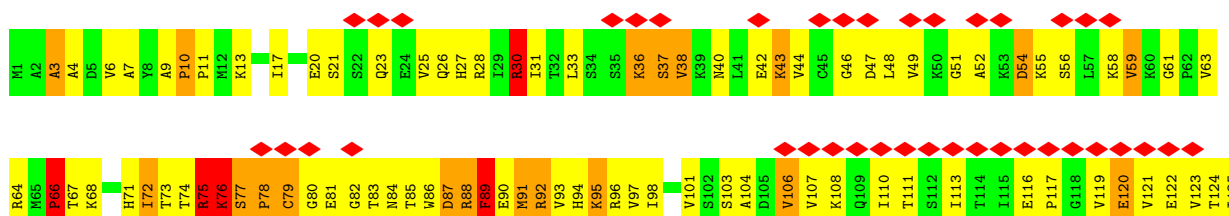
• Molecule 6: 40S ribosomal protein S5



• Molecule 7: 40S ribosomal protein S16



• Molecule 8: 40S ribosomal protein S20



S126
D127
Q128

• Molecule 9: 40S ribosomal protein S14

Chain SK: 18%
22% 39% 29% 9%

I32 F33 A34 S35 F36 N37 D38 T39 F40 L46 L45 S47 G48 R49 E50 T51 L52 V53 R54 M59 K60 V61 K62 K63 D64 R65 R66 E67 S68 S69 P70 Y71 A72 A73 R74 L75 A76 S77 Q78 D79 V80 A81 Q82 Q83 R84 R85 E86 L87 G88 T89 A91 L92 H93 I94 K95

L96 R97 T99 G100 G101 M102 K103 T104 K105 T106 P107 P109 A110 A111 Q112 S113 A114 L115 L116 A117 L118 A119 I120 S121 G122 M123 K124 I125 G126 I127 I128 E129 D130 V131 T132 P133 V134 P135 T136 D137 S138 T139 R140 R141 K142 A143 G144 R145 R146 G147 R148 R149 L150

• Molecule 10: 40S ribosomal protein S23

Chain SL: 90%
38% 37% 17% 8%

M1 G2 K3 T4 R5 G6 M7 G8 A9 G10 R11 K12 L13 L14 T15 H16 R17 R18 N19 Q20 R21 V22 A23 D24 K25 A26 Y27 K28 K29 S30 H31 L32 G33 N34 E35 W36 K37 K38 P39 F40 A41 G42 S44 H45 A46 K47 G48 I49 V50 L51 E52 K53 I54 G55 I56 E57 A58 K59 Q60

P61 M62 S63 A64 I65 R66 K67 C68 A69 R70 V71 Q72 L73 V74 K75 N76 G77 K78 K79 I80 A81 F82 V84 P85 N86 D87 G88 C89 L90 N91 F92 I93 E94 E95 N96 D97 E98 V99 L100 I101 A102 G103 F104 G105 R106 K107 G108 H109 V110 V111 G112 I114 P115 G116 V117 R118 F119 K120

V121 V122 K123 V124 S125 G126 V127 S128 L129 L130 A131 F132 K134 E135 K136 K137 E138 K139 P140 R141 S142

• Molecule 11: 40S ribosomal protein S18

Chain SM: 39%
18% 39% 26% 17%

M1 S2 L3 I4 A5 G6 E7 E8 F9 Q10 H11 I12 L13 R14 L15 L16 N17 T18 N19 V20 D21 Q22 K23 K24 K25 I26 M27 F28 A29 L30 T31 S32 I33 K34 V35 V36 R37 R38 S39 F40 N42 T43 V44 C45 R46 K47 A48 D49 E50 D51 M52 N53 K54 R55 A56 G57 E58 A61

E62 E63 M64 M68 A69 V70 V71 H72 N73 R74 R75 Q76 F77 K78 V79 P80 D81 R82 W82 F83 K87 K88 D89 Y90 K91 D92 G93 R94 R95 S96 Q97 V98 V99 S100 N101 A102 V103 I104 M105 K106 L107 R108 D109 N110 L111 E112 R113 L114 K115 K116 I117 R118 N119 H120 R121 G122 L123 R124 H125

Y126 W127 G128 V129 R130 V131 R132 G133 Q134 H135 T136 K137 T138 T139 G140 R141 G142 G143 K144 T145 V146 G147 V148 S149 K150 K151 R152

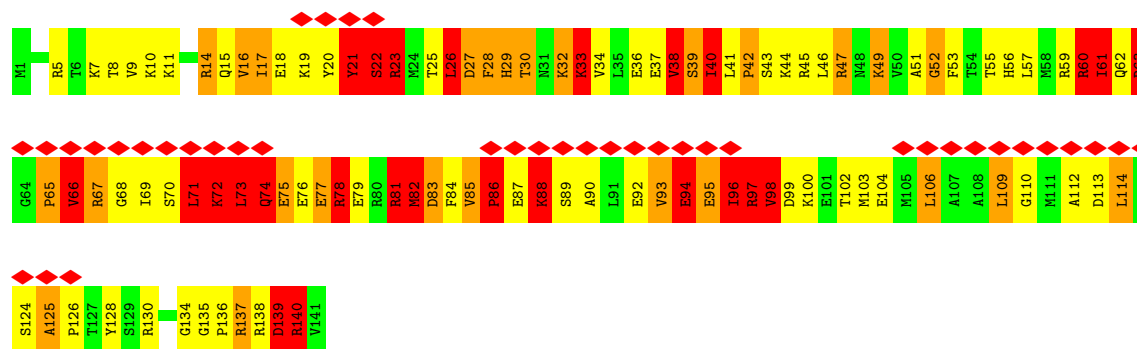
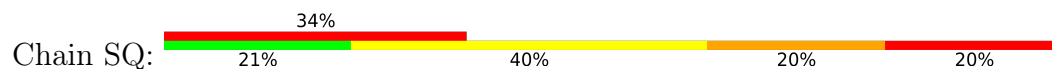
• Molecule 12: 40S ribosomal protein S13-1

Chain SO: 79%
47% 36% 12%

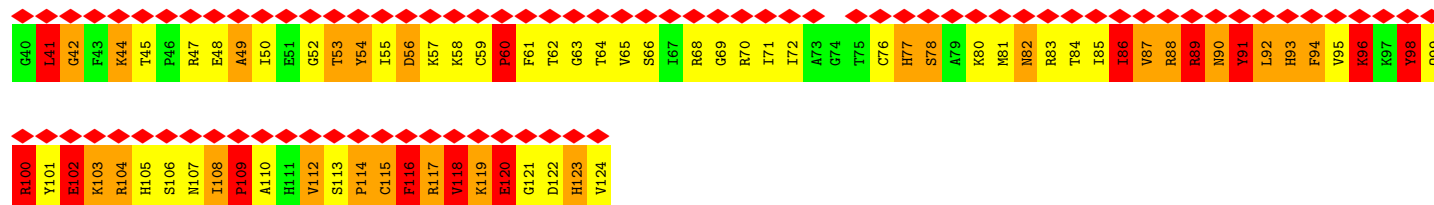
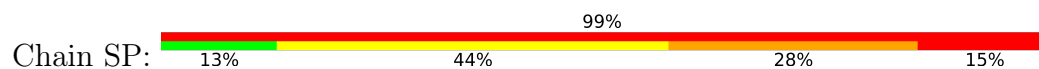
A31 D32 V33 E34 E35 N36 I37 N38 K39 A40 A41 K42 K43 G44 Q45 M46 P47 S48 Q49 I50 G51 V52 V53 L54 R55 D56 Q57 H58 G59 I60 P61 L62 V63 K64 S65 V66 T67 G68 S69 K70 I71 L72 R73 I74 L75 K76 A77 H78 G79 L80 A81 P82 E83 I84 P85 E86 D87 F90



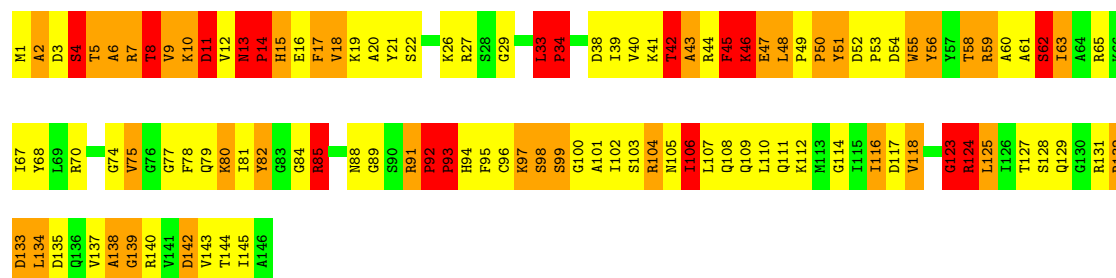
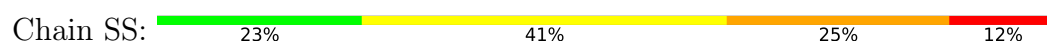
• Molecule 13: 40S ribosomal protein S17-4



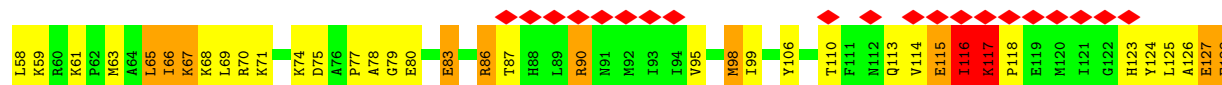
• Molecule 14: 40S ribosomal protein S11



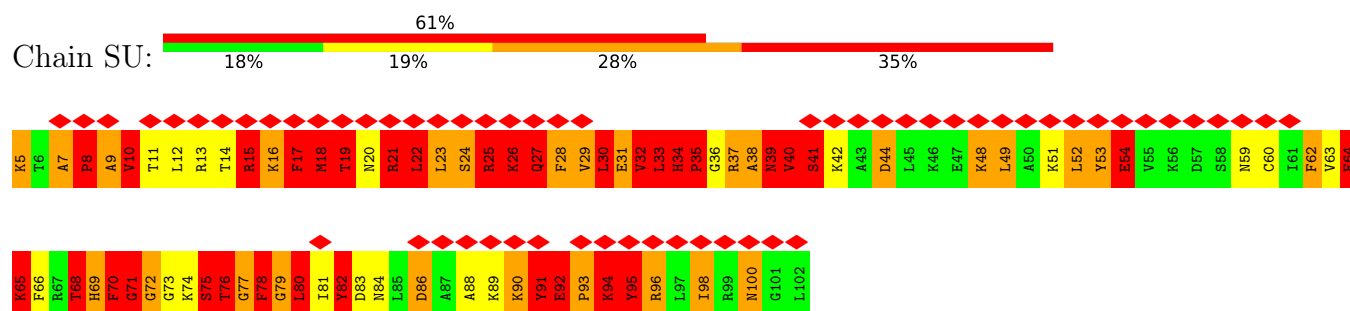
• Molecule 15: 40S ribosomal protein S19



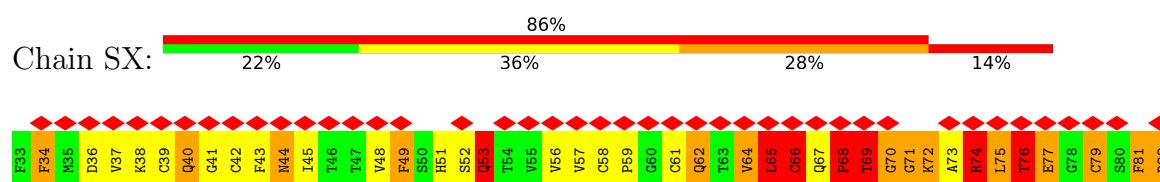
• Molecule 16: 40S ribosomal protein S15



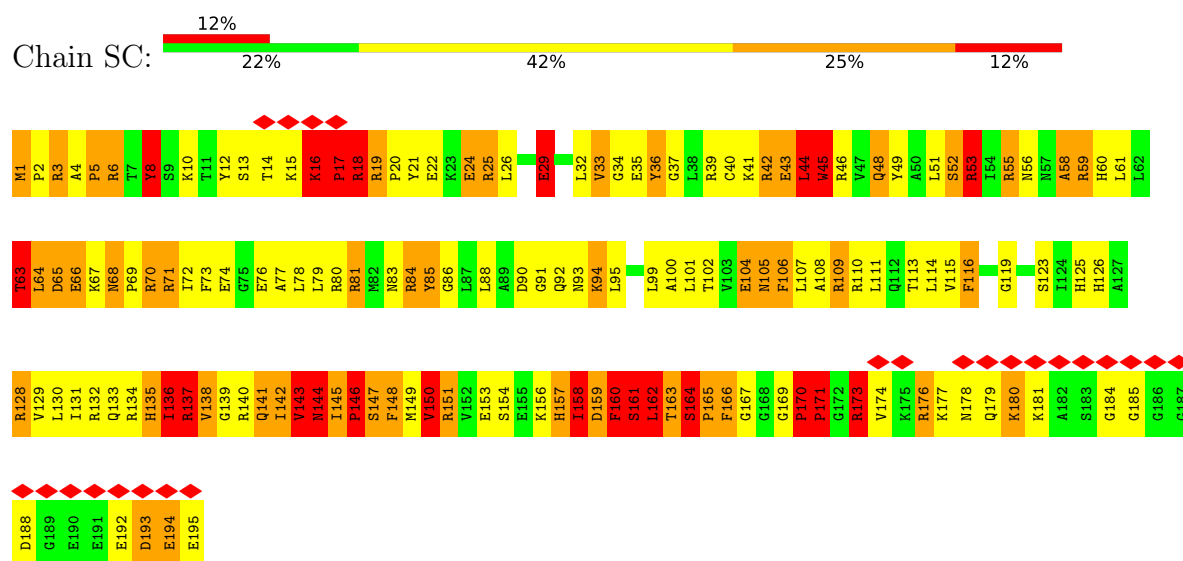
- Molecule 23: Unknown 40S wheat germ ribosome protein 3



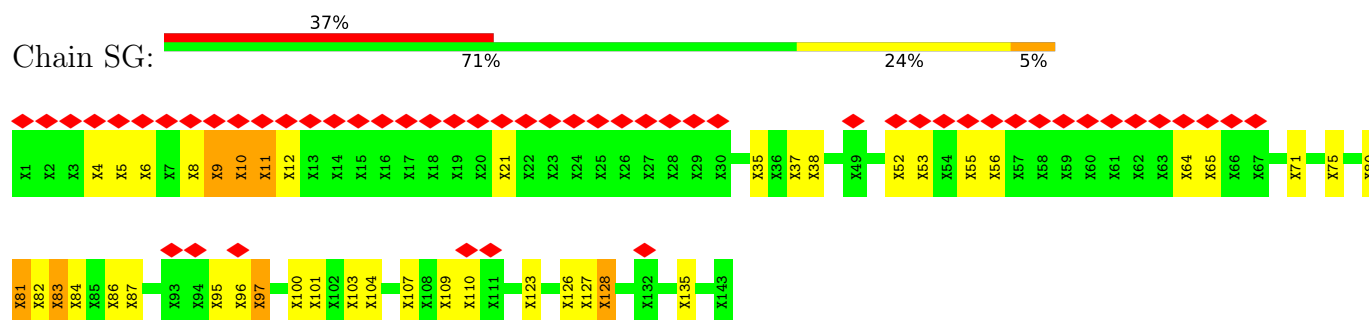
- Molecule 24: 40S ribosomal protein S27



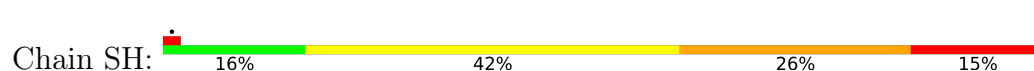
- Molecule 25: 40S ribosomal protein S9

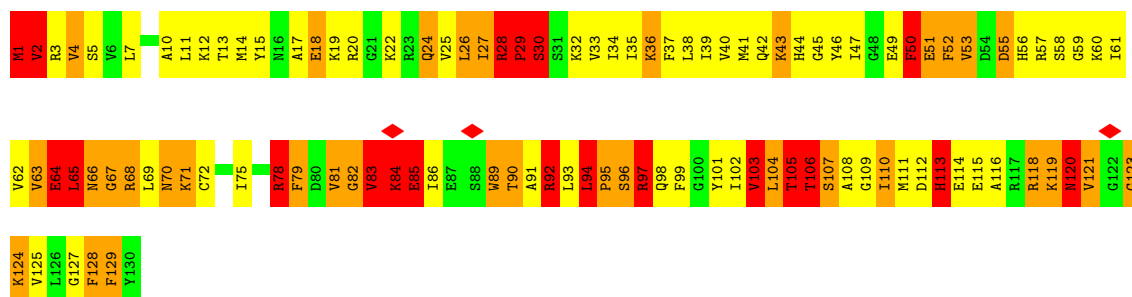


- Molecule 26: Unknown 40S wheat germ ribosome protein 4



- Molecule 27: Ribosomal protein S15

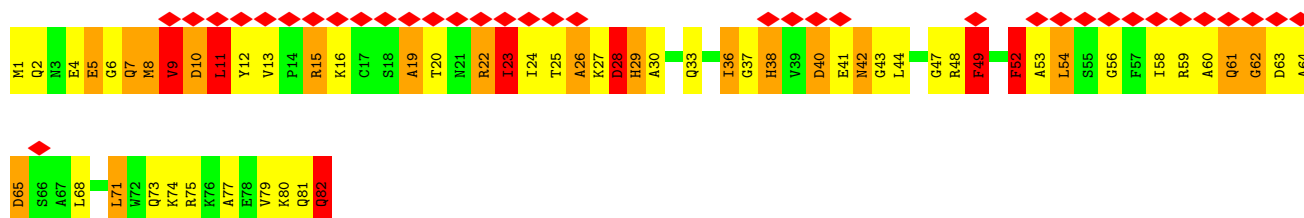




- Molecule 28: 40S ribosomal protein S29



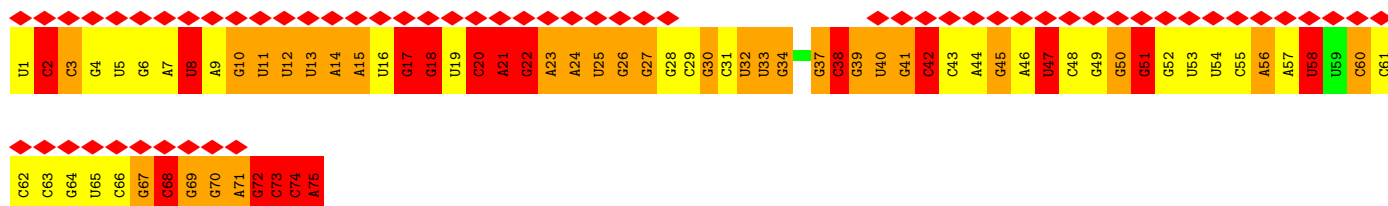
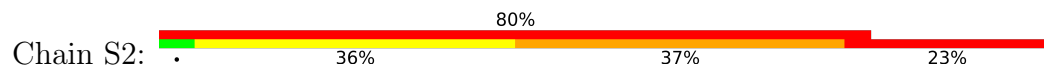
- Molecule 29: 40S ribosomal protein S21



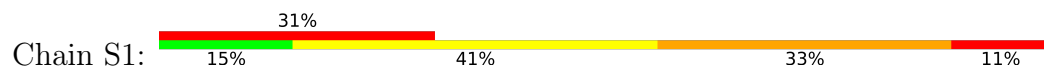
- Molecule 30: 40S WHEAT GERM RIBOSOME protein 4



- Molecule 31: 40S ribosomal RNA



- Molecule 32: 18S ribosomal RNA

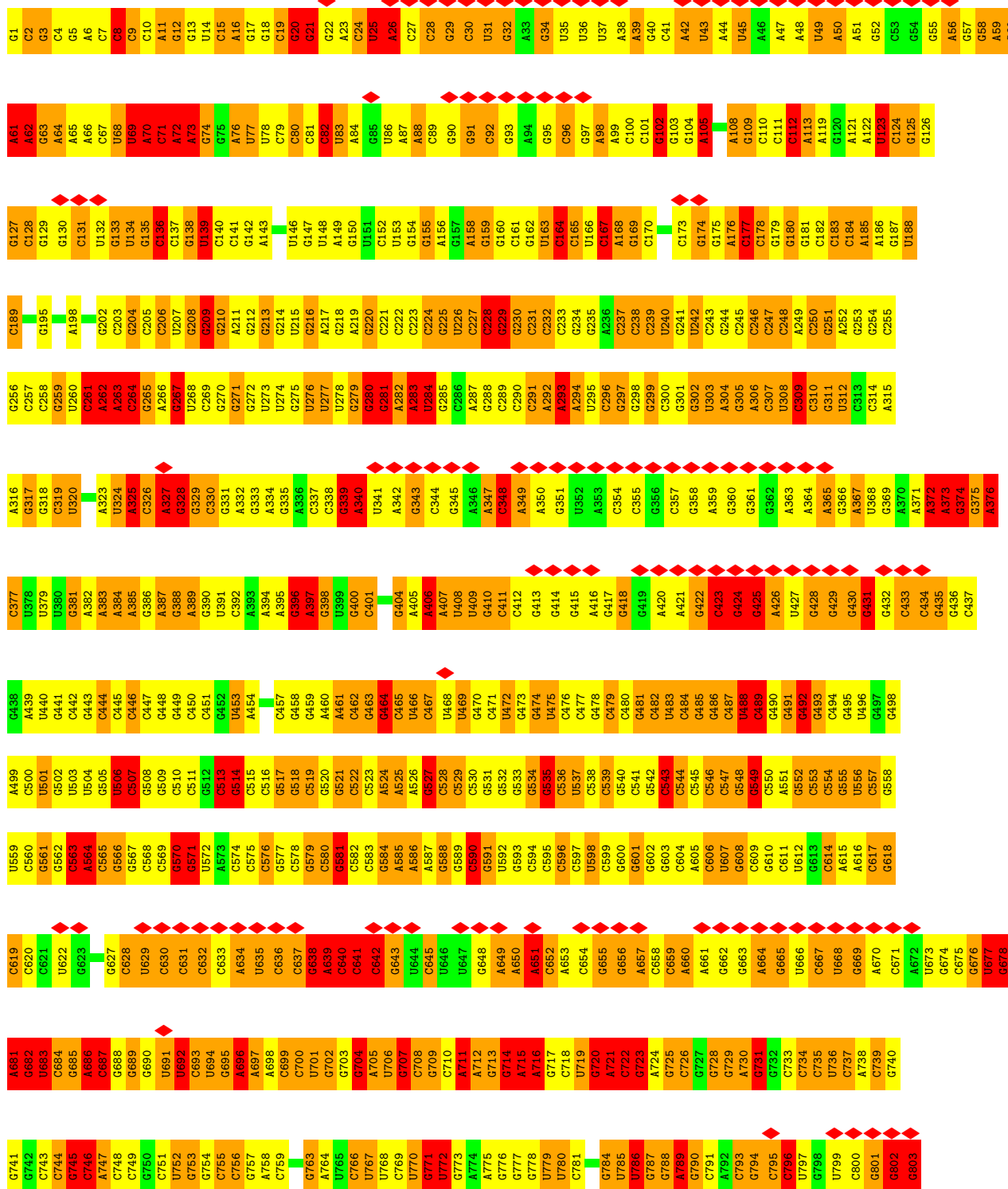
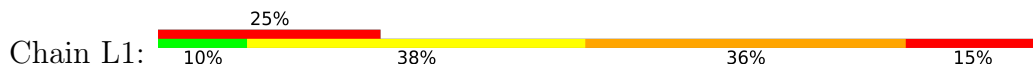


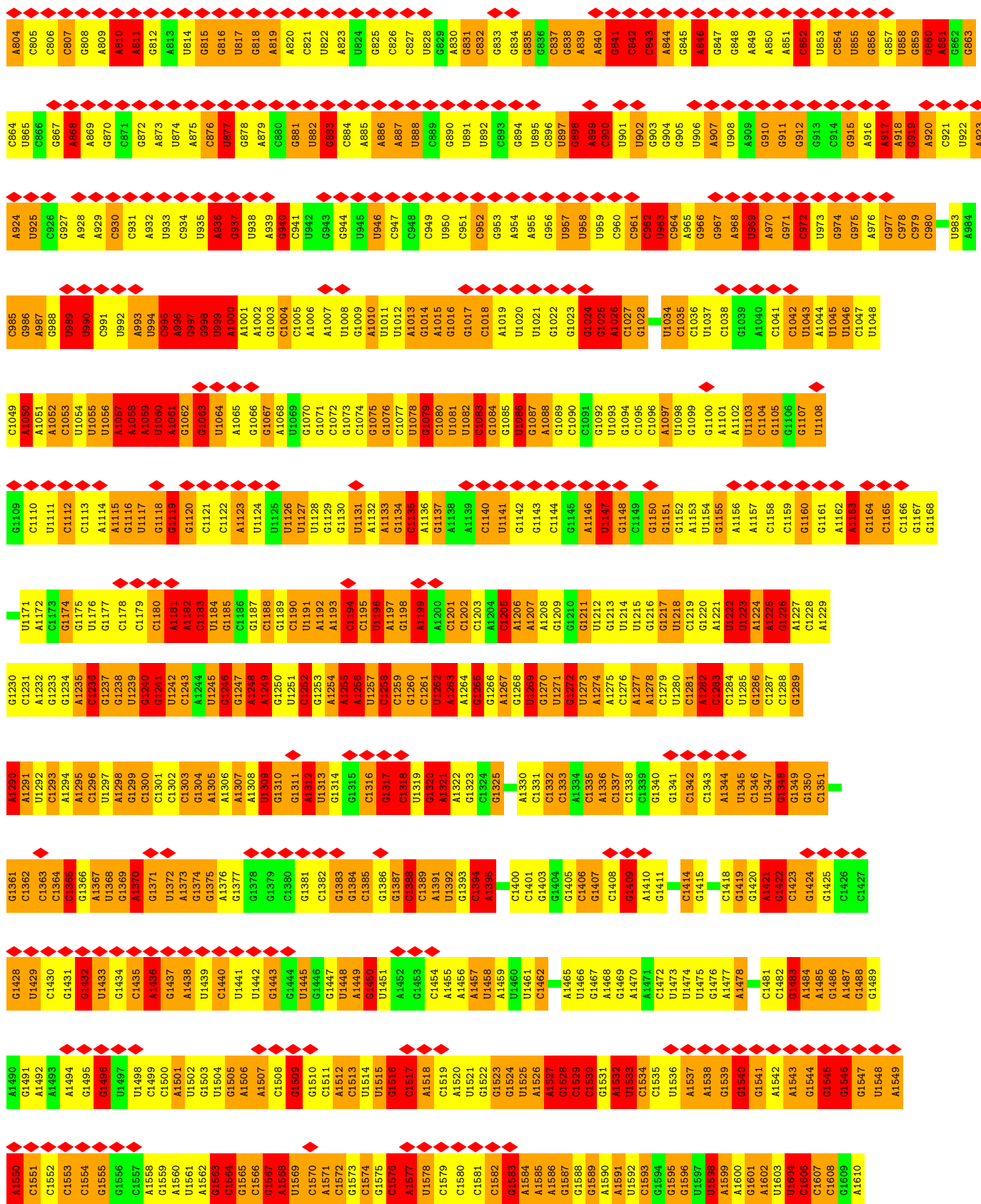


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C1716	C1656	G1596	U1537	U1458	C1395	G1331	G1271	G1204	A1143	C1082	U1020	A960
C1717	C1657	G1597	U1538	U1459	G1396	G1332	G1272	G1205	A1144	C1083	C1021	U961
C1718	C1658	G1598	G1538	G1460	A1397	A1333	U1273	A1206	G1145	U1085	U1022	G962
C1719	A1658	C1599	A1539	G1461	U1398	G1336	G1274	A1207	A1146	U1086	U963	U963
A1659	U1659	G1600	U1540	C1462	G1399	C1337	G1275	A1208	A1147	A1088	C1023	U964
G1720	C1660	A1601	C1541	G1464	G1400	U1338	U1276	C1209	A1148	U1089	A1024	U965
A1721	C1661	U1603	U1542	C1465	C1401	C1339	G1277	C1210	U1149	A1091	A1025	U966
C1722	G1662	G1604	U1543	A1466	C1402	A1340	A1278	A1212	U1150	G1090	A1026	C967
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C1742	G1681	G1627	G1494	G1494	G1424	C1363	G1301	G1237	U1173	G1113	U1049	U986
C1743	G1682	U1628	G1494	G1494	G1425	G1363	G1302	A1238	G1174	G1114	C1050	U987
C1744	U1683	U1629	A1498	A1498	A1427	G1363	A1303	C1239	A1176	G1115	C1053	C988
U1745	U1685	G1630	C1503	C1503	U1429	C1370	U1305	A1240	G1177	G1116	G1054	C989
U1746	C1686	C1631	U1504	U1504	A1430	U1371	U1306	G1241	C1178	G1117	G1055	C990
A1747	G1687	C1632	U1505	U1505	A1431	C1372	U1307	A1242	U1179	G1118	A1056	C991
C1748	U1688	U1634	G1506	G1506	A1432	C1373	U1308	C1243	U1180	G1119	U1057	C992
C1749	A1689	U1635	G1507	G1507	A1433	G1374	U1309	U1244	G1181	U1120	G1058	C993
A1750	U1690	U1636	C1508	C1508	G1434	C1375	U1309	G1245	G1182	U1121	U1059	U994
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U1752	G1692	U1638	G1510	G1510	U1436	C1377	U1311	G1247	U1185	U1122	G1061	C996
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A1754	U1694	C1642	U1512	U1512	U1438	A1380	G1312	C1249	U1187	G1124	U1063	A998
C1755	G1695	C1643	A1513	A1513	G1439	G1381	G1313	C1250	A1187	U1125	U1064	C999
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A1759	C1699	C1647	C1517	C1517	U1443	C1385	A1317	A1260	U1191	A1129	G1068	C1005
A1760	U1699	U1648	U1518	U1518	C1444	U1386	U1318	U1261	A1193	G1069	A1006	A1006
G1761	G1700	C1649	G1519	G1519	C1445	A1387	U1319	U1262	G1194	A1130	G1070	G1007
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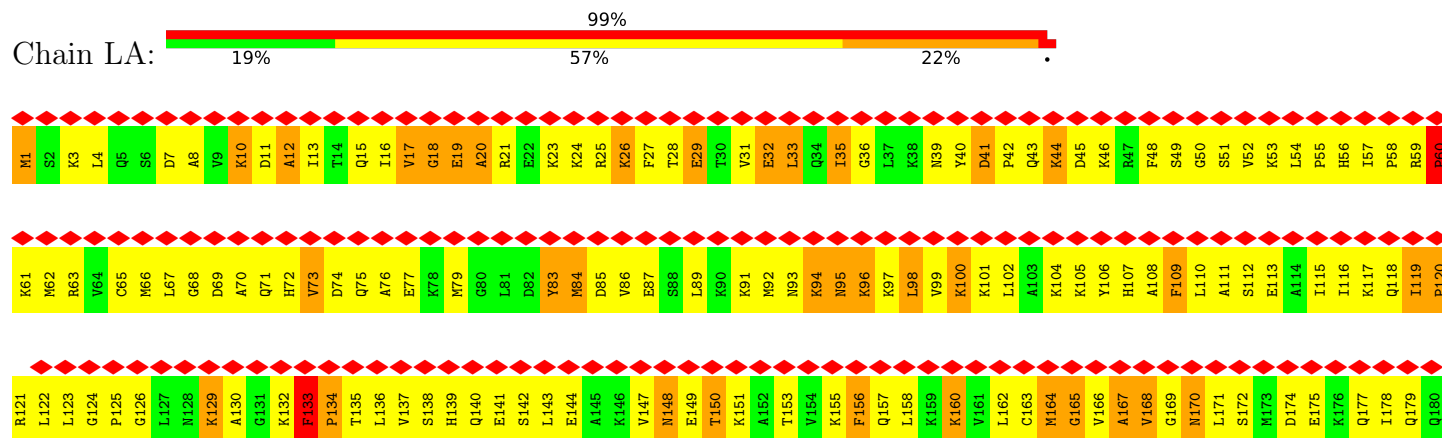
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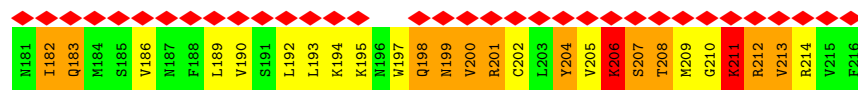




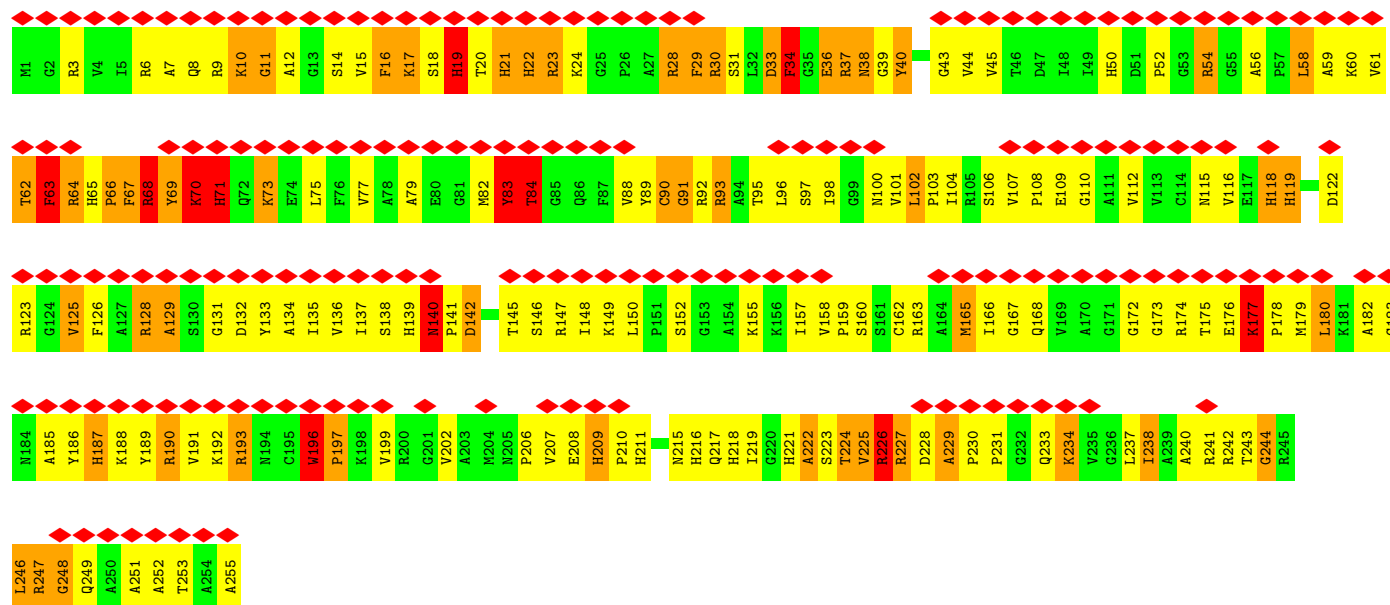
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C2413	C2414	U2415	U2416	C2417	A2418	C2419	U2420	C2421	U2422	A2423	C2424	U2425	C2426	C2427	A2428	A2429	C2430	U2431	U2432	U2433	C2434	U2435	C2436	C2437	A2438	C2439	U2440	C2441	A2442	C2443	U2444	U2445	C2446	C2447	C2448	A2449	C2450	C2451	U2452	C2453	A2454	A2455	C2456	C2457	C2458	U2459	A2460	A2461	C2462	U2463	C2464	C2465	A2466	A2467	C2468	C2469	C2470	C2471	U2472

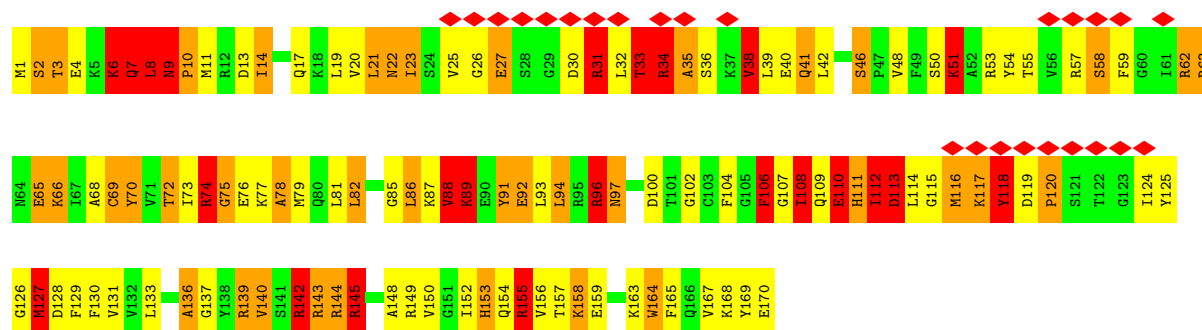
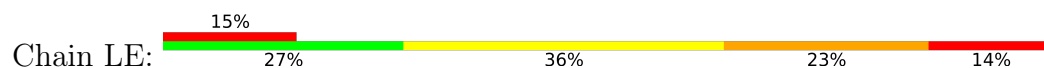




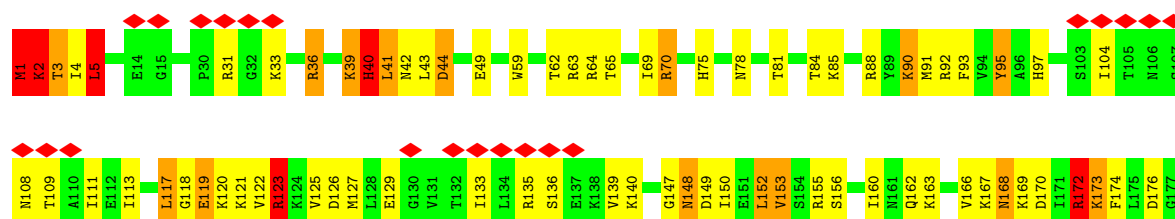
• Molecule 37: 60S ribosomal protein L2

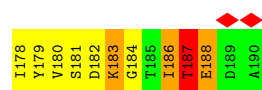


• Molecule 38: Ribosomal protein L11

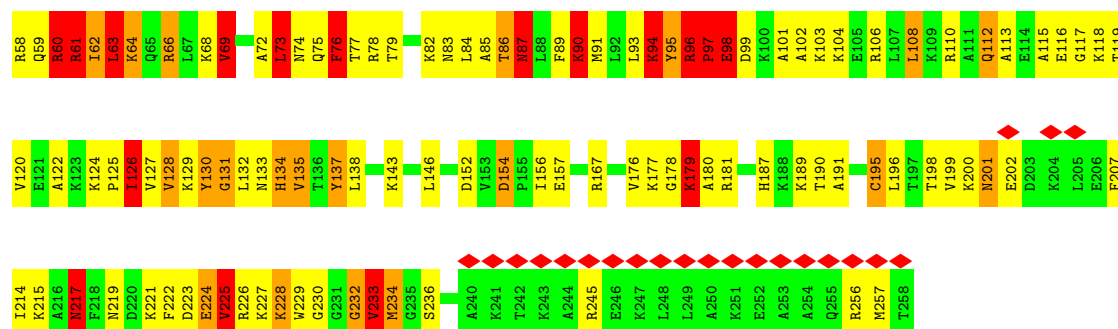


• Molecule 39: 60S ribosomal protein L9

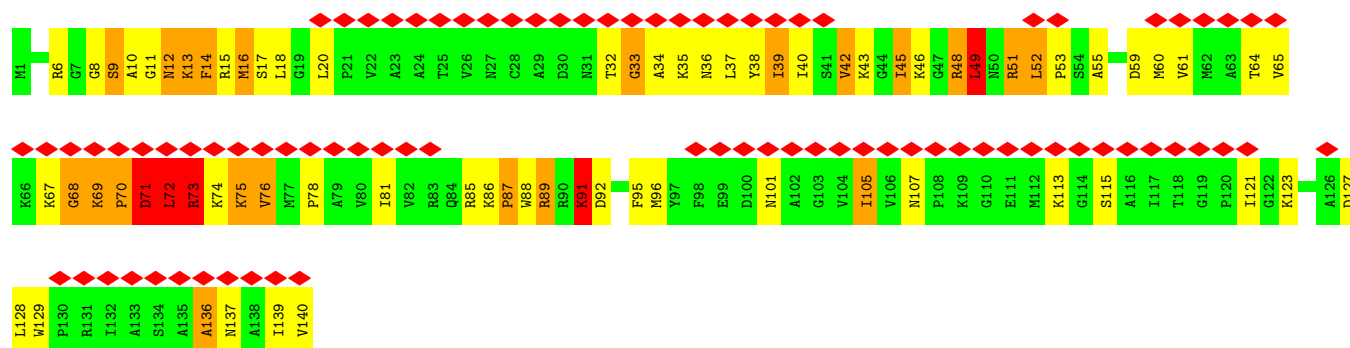




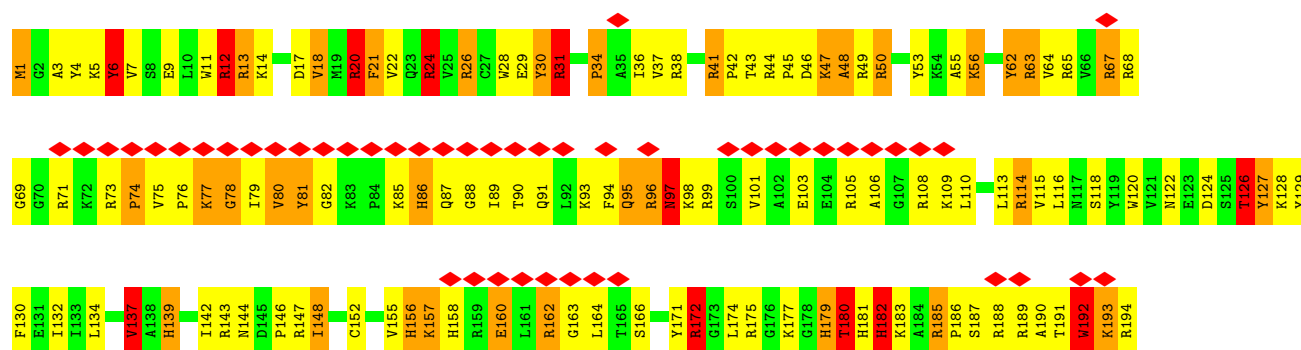
- Molecule 40: 60S ribosomal protein L7a



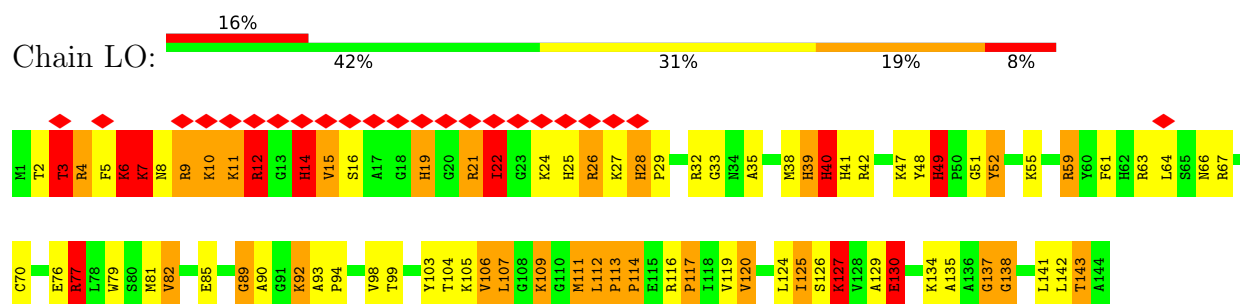
- Molecule 41: Ribosomal Pr 117



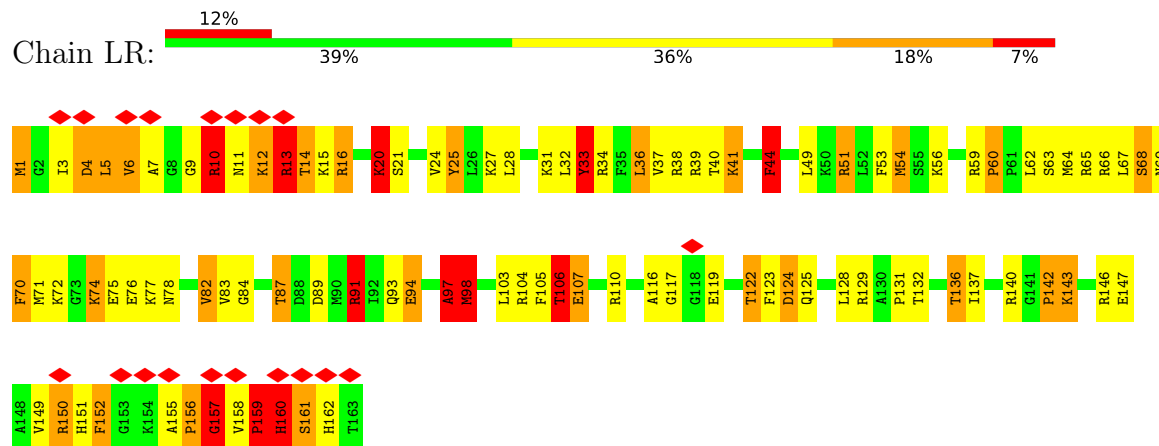
- Molecule 42: Ribosomal protein L15



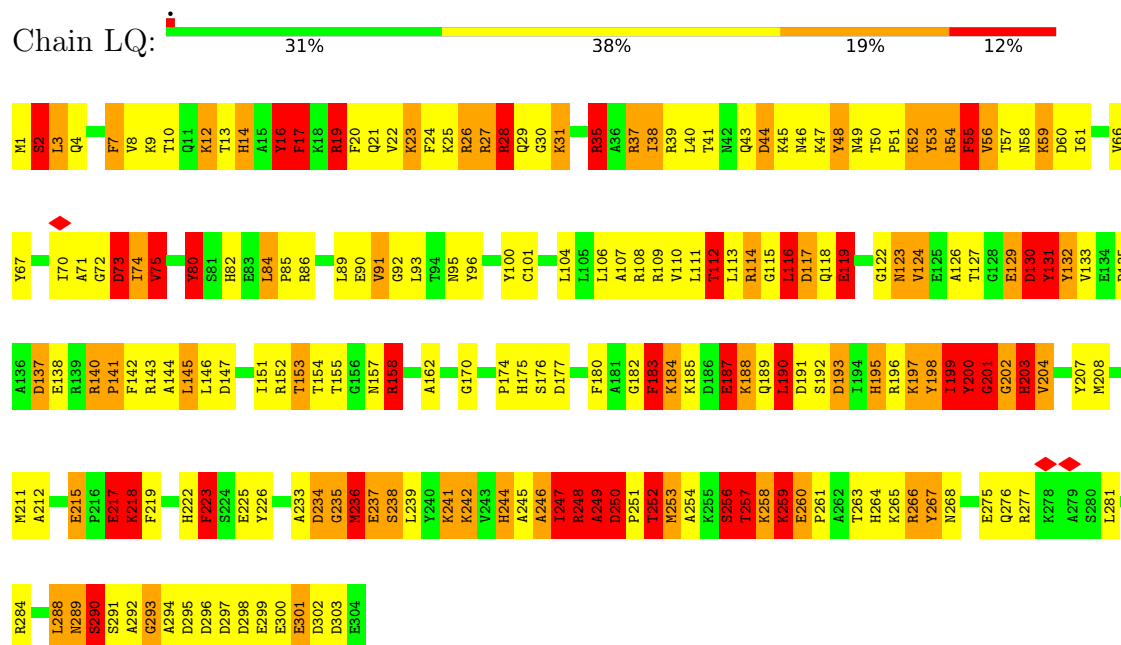
- Molecule 43: 60S ribosomal protein L27a-3



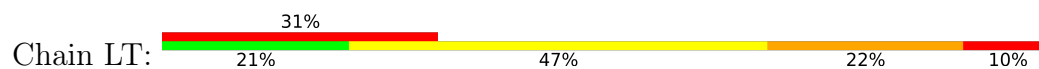
• Molecule 44: 60S ribosomal protein L18

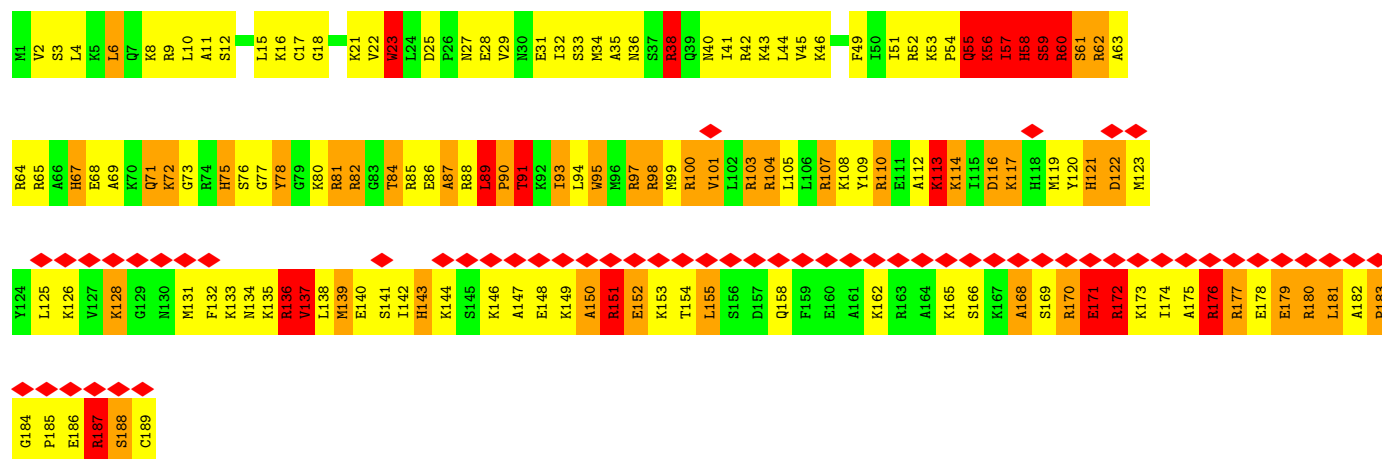


• Molecule 45: 60S ribosomal protein L5

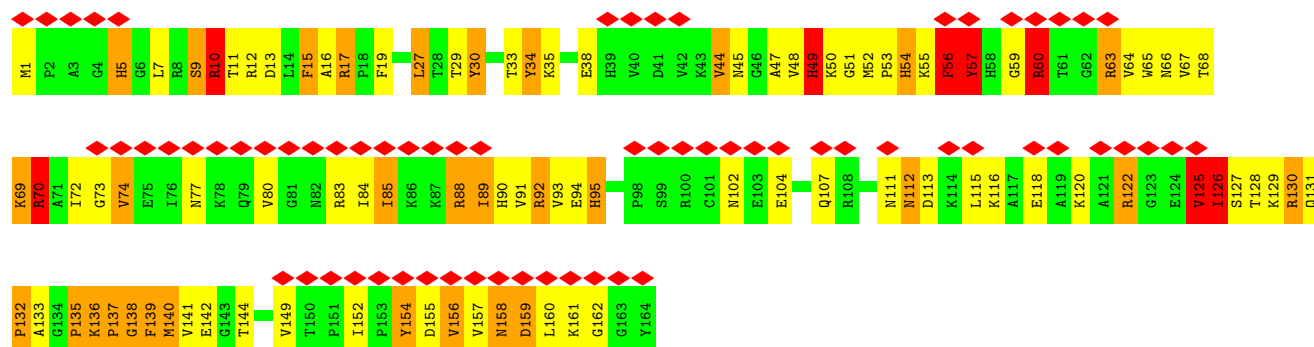
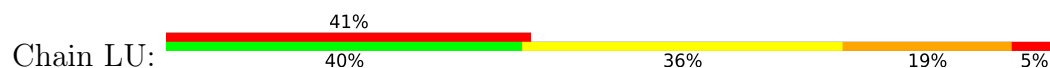


• Molecule 46: Ribosomal protein L19

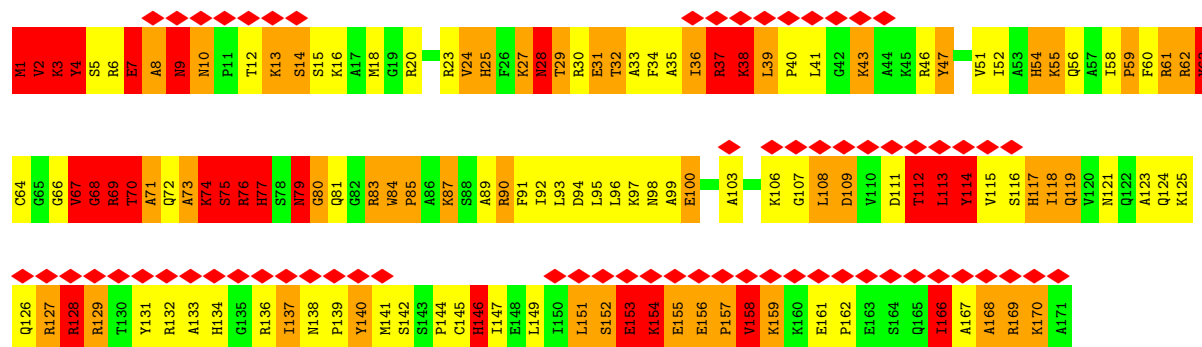
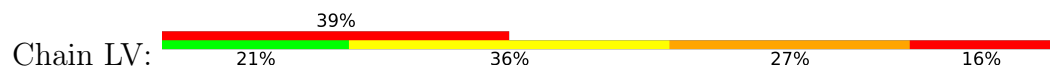




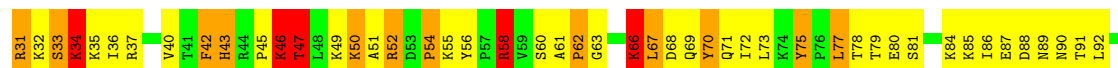
• Molecule 47: 60S ribosomal protein L21

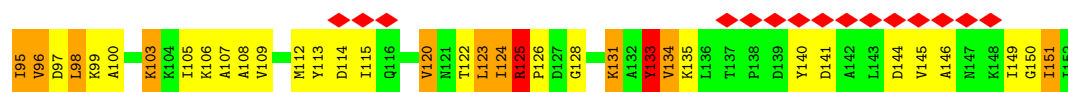


• Molecule 48: 60S ribosomal protein L17

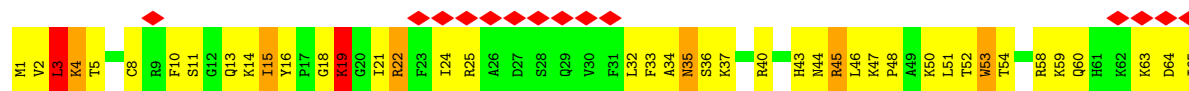


• Molecule 49: 60S ribosomal protein L23a

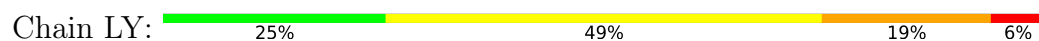




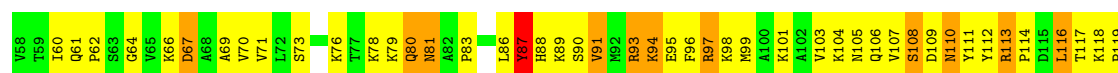
- Molecule 50: 60S ribosomal protein L24



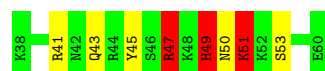
- Molecule 51: 60S ribosomal protein L26



- Molecule 52: 60S ribosomal protein L28

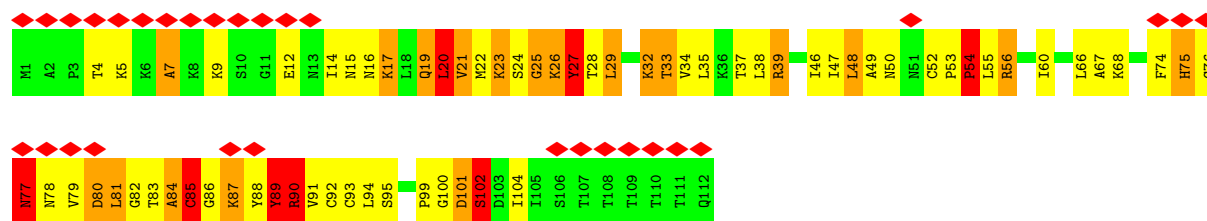


- Molecule 53: 60S ribosomal protein L29

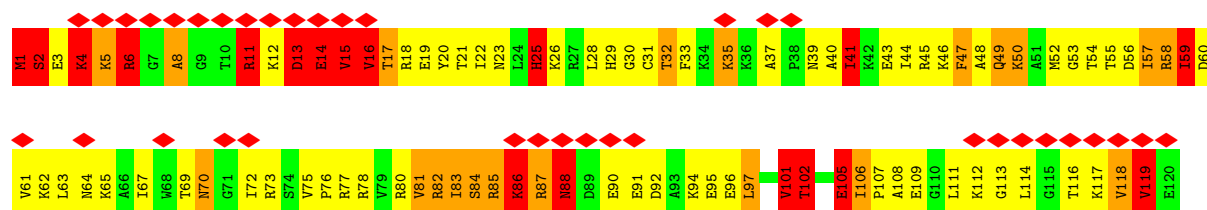
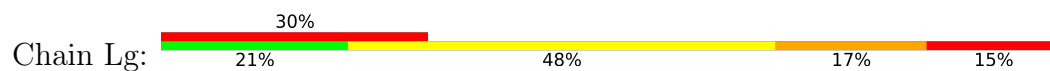


- Molecule 54: 60S ribosomal protein L30

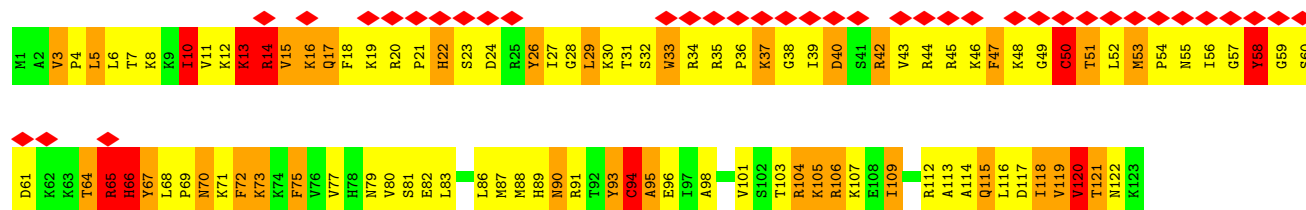
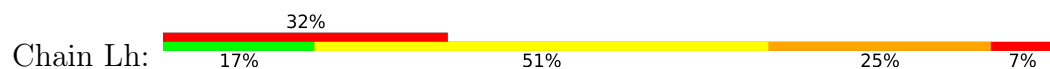




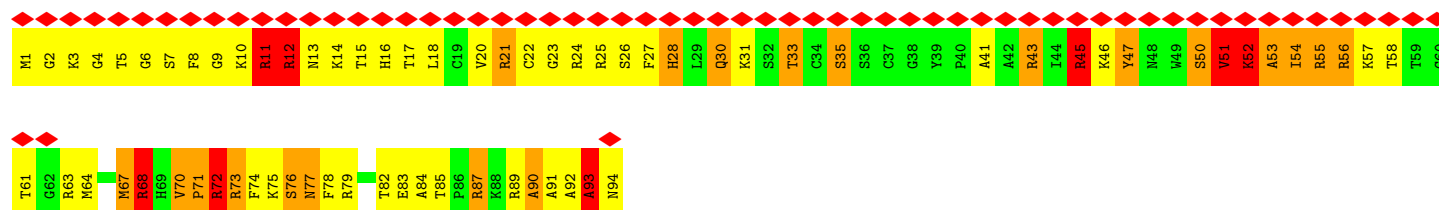
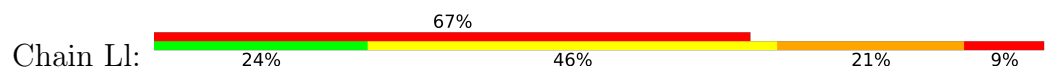
• Molecule 55: 60S ribosomal protein L31



• Molecule 56: Ribosomal L32

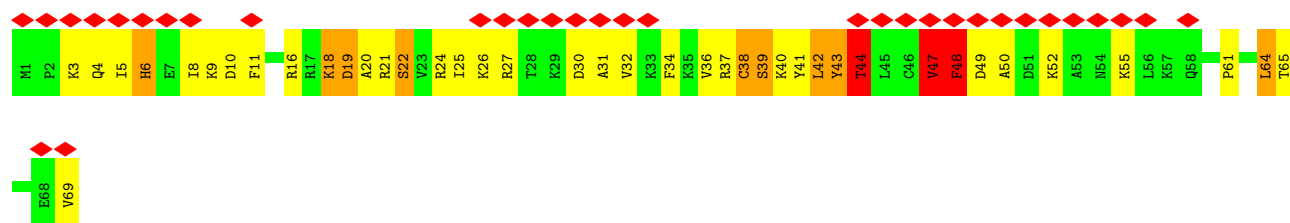


• Molecule 57: Ribosomal protein L37



• Molecule 58: 60S ribosomal protein L38





- Molecule 59: Ribosomal protein L39



- Molecule 60: 60S ribosomal protein L44



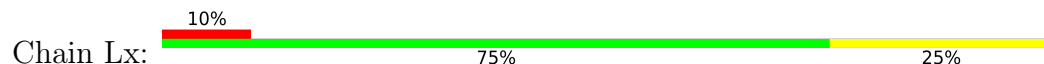
- Molecule 61: Unknown 60S wheat germ ribosome protein 1



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



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

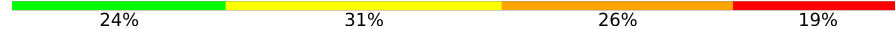


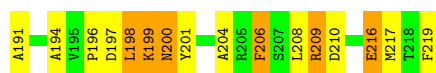
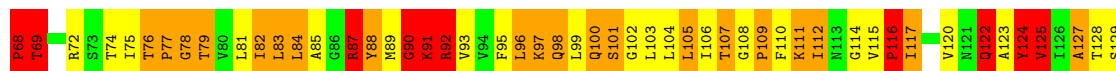
- Molecule 63: Unknown 60S wheat germ ribosome protein 3

Chain Lz: 



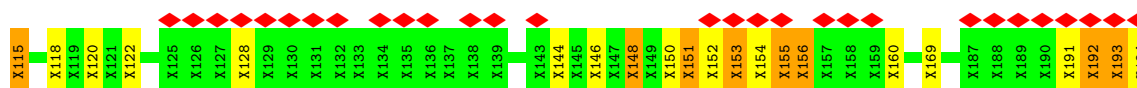
• Molecule 64: 60S ribosomal protein L6

Chain LG: 



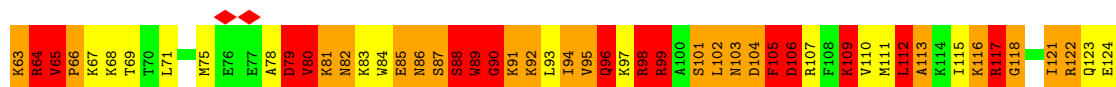
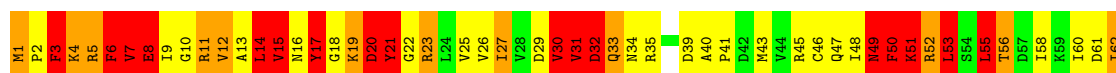
• Molecule 65: Unknown 60S wheat germ ribosome protein 5

Chain LL: 



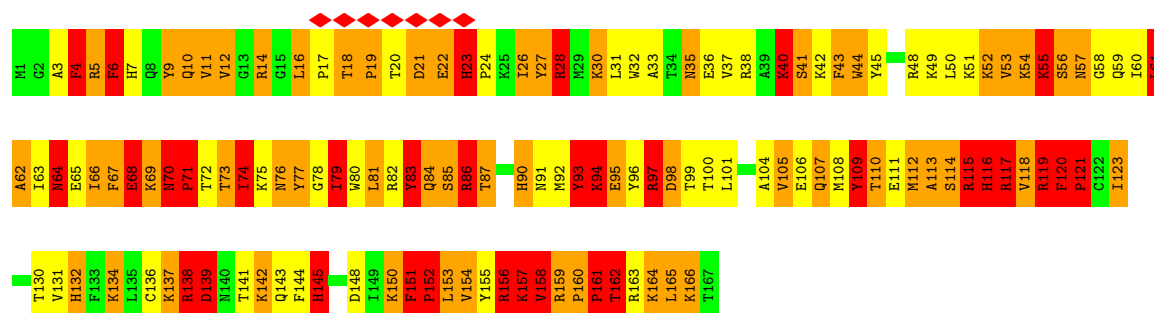
• Molecule 66: Unknown 60S wheat germ ribosome protein 6

Chain LN: 

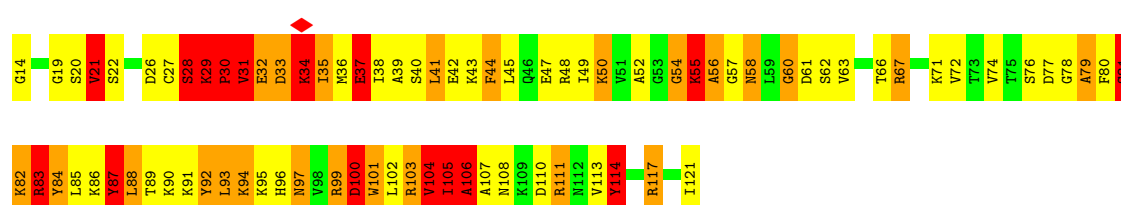
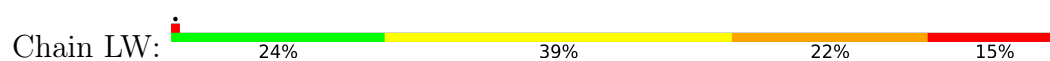


• Molecule 67: 60S ribosomal protein L18a

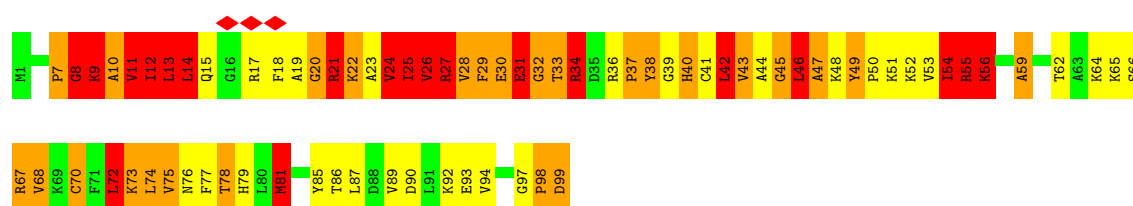
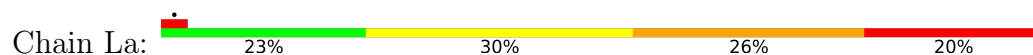
Chain LS: 



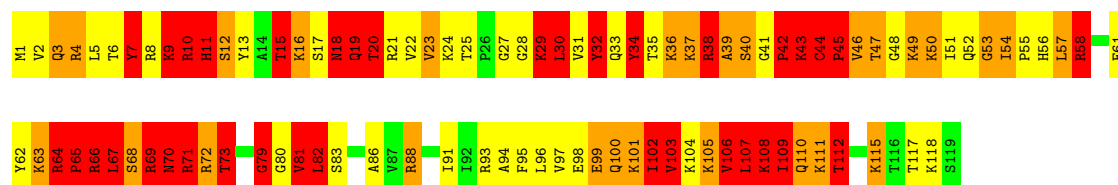
• Molecule 68: 60S ribosomal protein L22



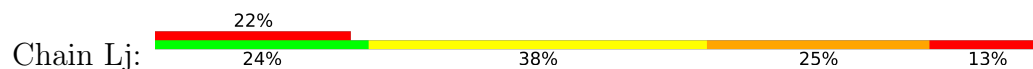
• Molecule 69: 60S ribosomal protein L27

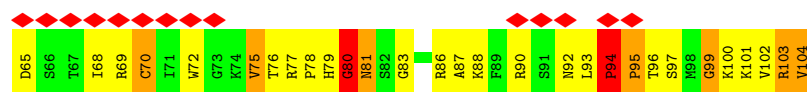


• Molecule 70: Ribosomal protein l34

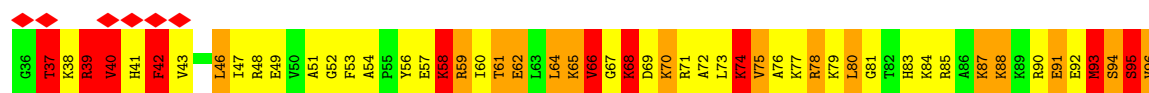
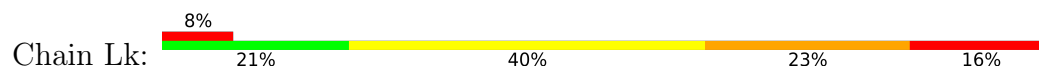


• Molecule 71: ribosomal protein L35A





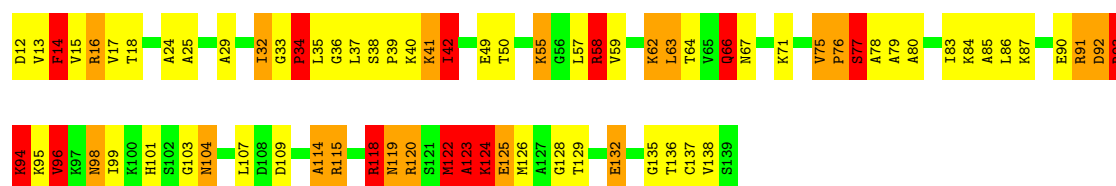
- Molecule 72: 60S ribosomal protein L36



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



- Molecule 74: 60S ribosomal protein L12



- Molecule 75: Ribosomal protein P1

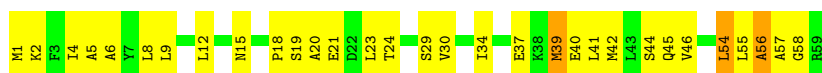


- Molecule 75: Ribosomal protein P1



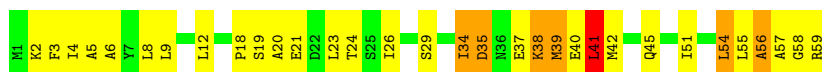
- Molecule 76: 60S acidic ribosomal protein P2A





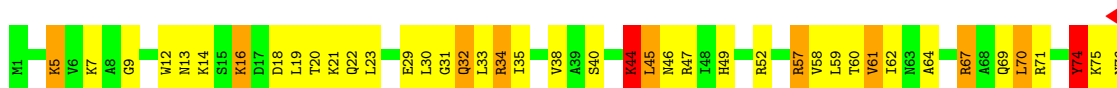
- Molecule 76: 60S acidic ribosomal protein P2A

Chain Lw: 46% 42% 10%



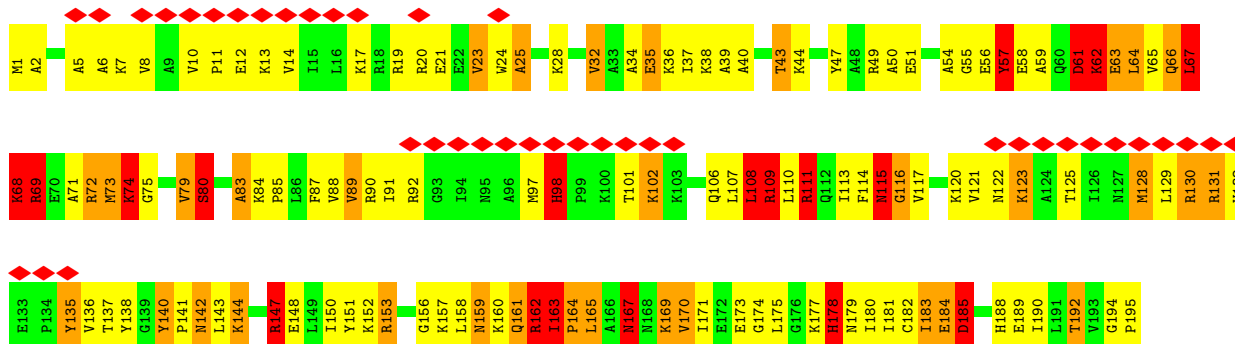
- Molecule 77: 60S ribosomal protein L35

Chain Lc: 40% 36% 19% 5%



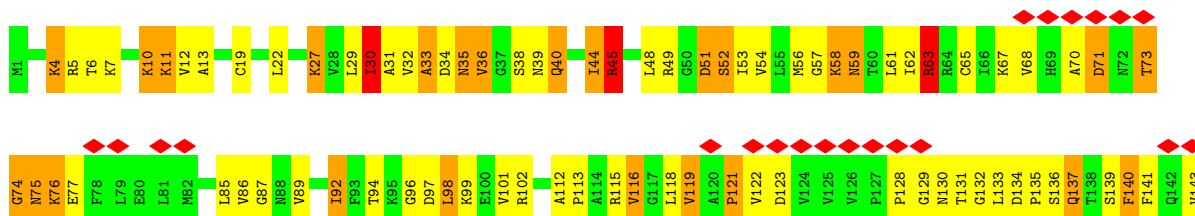
- Molecule 78: Ribosomal protein L7

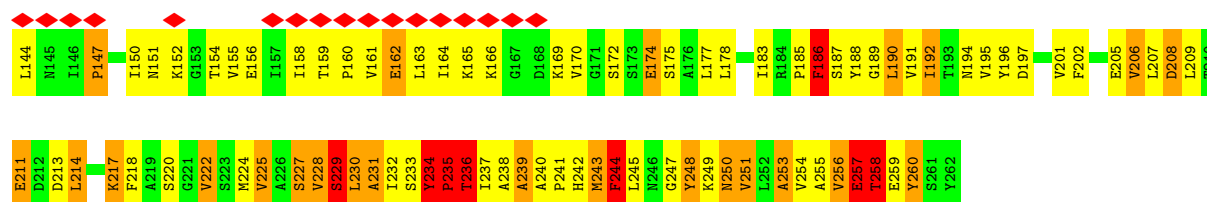
Chain Le: 17% 32% 44% 16% 8%



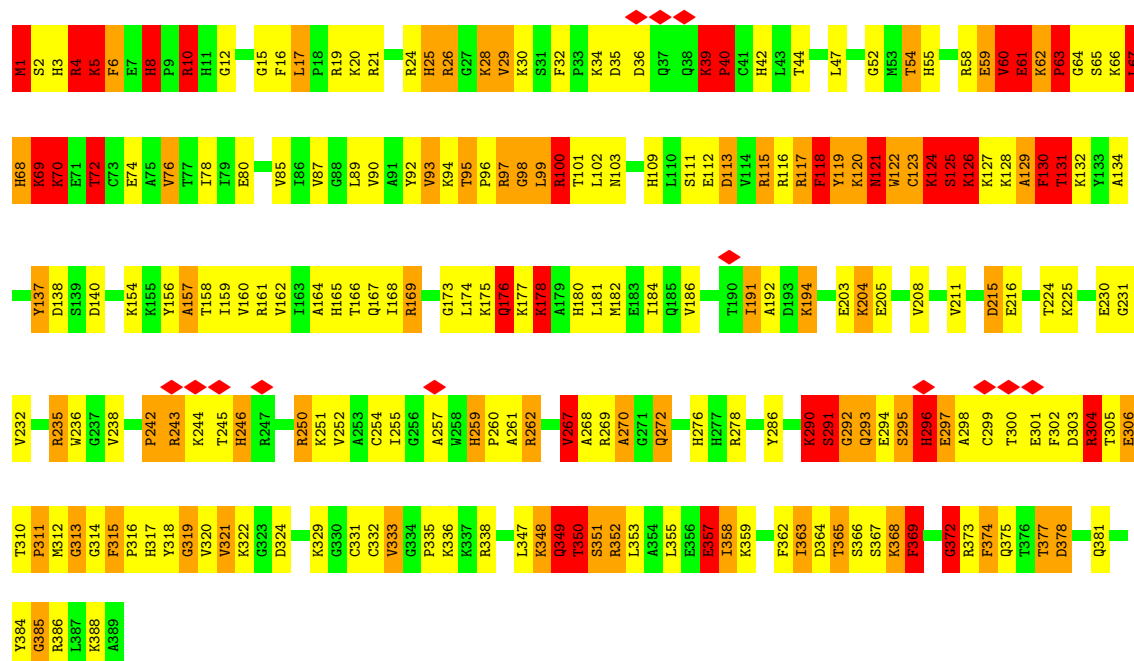
- Molecule 79: 60S acidic ribosomal protein P0

Chain Ls: 15% 36% 41% 19%

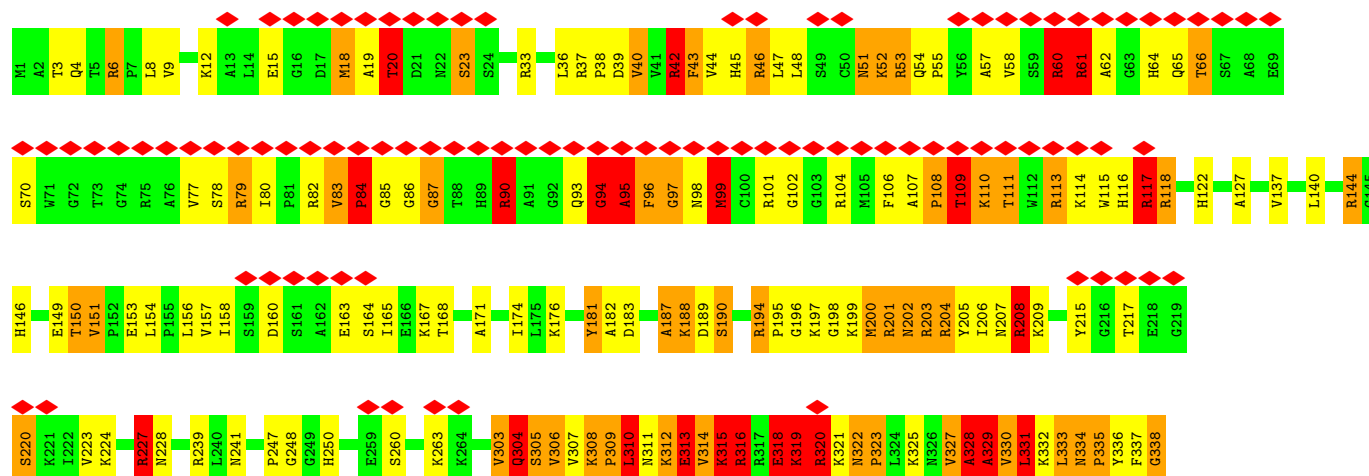
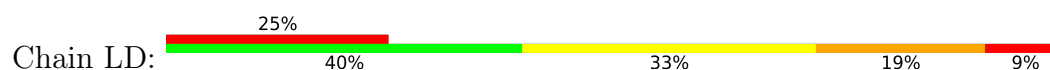




• Molecule 80: Ribosomal protein L3

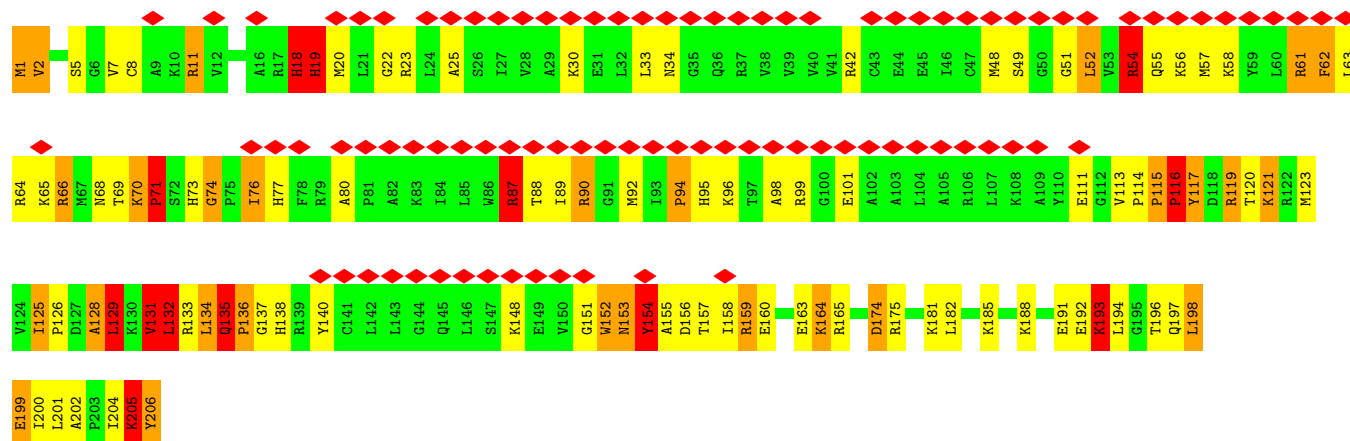


• Molecule 81: 60S ribosomal protein L4/L1

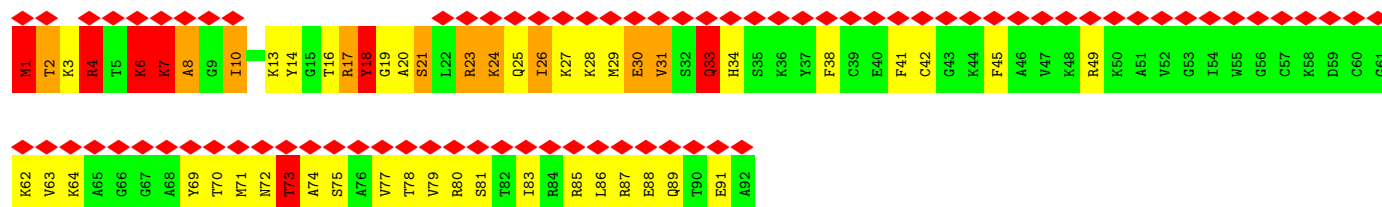
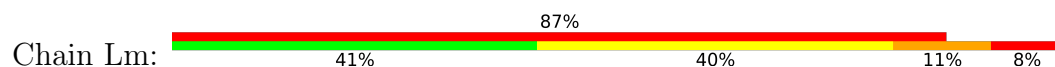




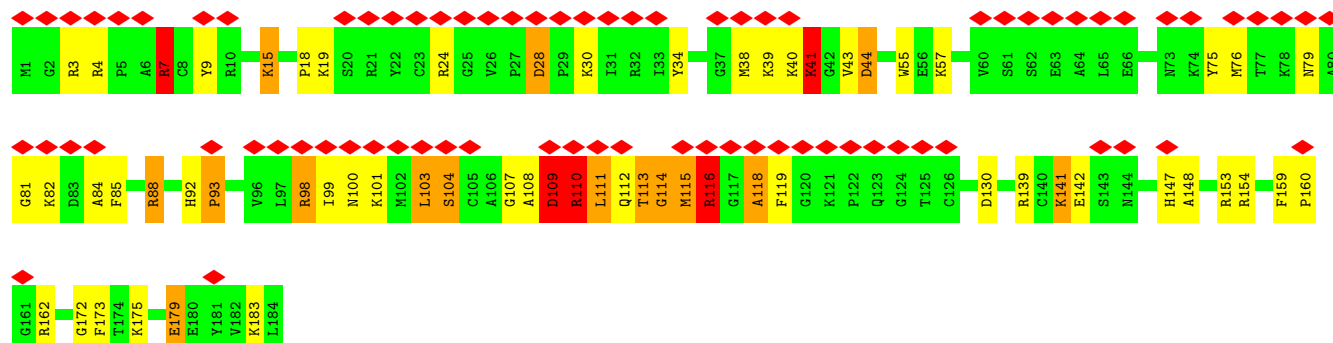
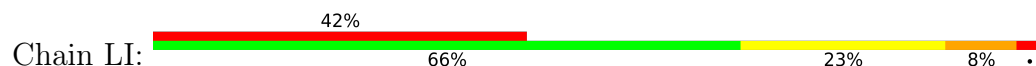
• Molecule 82: Ribosomal protein L13a



• 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	2.51	114/2897 (3.9%)	2.93	280/3917 (7.1%)
2	SA	2.25	65/1988 (3.3%)	3.27	204/2697 (7.6%)
3	SB	2.68	93/1555 (6.0%)	3.70	244/2077 (11.7%)
4	SD	2.94	64/1637 (3.9%)	4.11	161/2202 (7.3%)
5	SE	2.54	67/2068 (3.2%)	3.57	199/2776 (7.2%)
6	SF	1.40	14/1505 (0.9%)	2.21	64/2027 (3.2%)
7	SI	2.43	53/1034 (5.1%)	2.75	92/1379 (6.7%)
8	SJ	2.58	45/896 (5.0%)	3.76	91/1193 (7.6%)
9	SK	2.88	33/839 (3.9%)	3.58	99/1120 (8.8%)
10	SL	2.34	31/965 (3.2%)	3.21	78/1271 (6.1%)
11	SM	3.20	71/1185 (6.0%)	4.14	196/1574 (12.5%)
12	SO	1.22	5/994 (0.5%)	3.12	39/1332 (2.9%)
13	SQ	2.60	59/1145 (5.2%)	4.40	176/1531 (11.5%)
14	SP	2.64	34/653 (5.2%)	3.44	59/871 (6.8%)
15	SS	2.61	57/1179 (4.8%)	4.24	166/1586 (10.5%)
16	SR	2.25	15/727 (2.1%)	2.57	47/975 (4.8%)
17	SV	1.68	10/748 (1.3%)	2.19	53/994 (5.3%)
19	SY	2.80	19/443 (4.3%)	3.27	39/592 (6.6%)
20	SZ	2.11	13/476 (2.7%)	4.13	45/623 (7.2%)
23	SU	3.61	64/745 (8.6%)	5.11	176/988 (17.8%)
24	SX	2.35	17/382 (4.5%)	2.42	33/515 (6.4%)
25	SC	3.74	87/1563 (5.6%)	4.37	255/2086 (12.2%)
27	SH	2.23	33/1060 (3.1%)	3.17	110/1419 (7.8%)
28	SN	3.21	25/317 (7.9%)	3.76	59/414 (14.3%)
29	ST	2.26	26/659 (3.9%)	3.13	93/884 (10.5%)
30	S3	2.00	10/264 (3.8%)	2.12	16/407 (3.9%)
31	S2	2.64	101/1785 (5.7%)	2.47	175/2779 (6.3%)
32	S1	2.35	1648/37672 (4.4%)	2.24	2742/58357 (4.7%)
33	L1	2.58	3984/77720 (5.1%)	2.47	7259/121026 (6.0%)
34	L3	2.44	128/2868 (4.5%)	2.55	285/4468 (6.4%)
35	L2	2.93	216/3553 (6.1%)	2.66	376/5515 (6.8%)
36	LA	1.79	30/1741 (1.7%)	2.24	97/2323 (4.2%)
37	LB	2.13	60/1979 (3.0%)	2.97	144/2659 (5.4%)
38	LE	3.03	65/1397 (4.7%)	2.89	151/1864 (8.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	LF	1.74	36/1519 (2.4%)	2.38	60/2042 (2.9%)
40	LH	1.69	30/1586 (1.9%)	3.03	91/2120 (4.3%)
41	LM	1.87	24/1036 (2.3%)	2.61	80/1388 (5.8%)
42	LP	2.20	50/1669 (3.0%)	2.91	123/2235 (5.5%)
43	LO	1.98	29/1113 (2.6%)	3.63	66/1485 (4.4%)
44	LR	1.85	28/1303 (2.1%)	2.48	75/1748 (4.3%)
45	LQ	2.24	77/2438 (3.2%)	4.09	235/3271 (7.2%)
46	LT	2.30	66/1590 (4.2%)	3.20	183/2100 (8.7%)
47	LU	2.29	44/1290 (3.4%)	3.59	130/1728 (7.5%)
48	LV	2.64	71/1359 (5.2%)	4.33	193/1816 (10.6%)
49	LX	2.32	35/1002 (3.5%)	2.88	86/1340 (6.4%)
50	LZ	1.93	18/591 (3.0%)	3.21	40/782 (5.1%)
51	LY	2.23	36/1061 (3.4%)	2.92	71/1418 (5.0%)
52	Lb	2.29	19/585 (3.2%)	2.64	43/786 (5.5%)
53	Ld	1.40	1/201 (0.5%)	2.19	12/261 (4.6%)
54	Lf	1.68	22/836 (2.6%)	2.39	47/1121 (4.2%)
55	Lg	2.16	36/954 (3.8%)	2.74	95/1272 (7.5%)
56	Lh	2.08	32/1108 (2.9%)	3.10	87/1477 (5.9%)
57	Li	2.23	31/738 (4.2%)	3.06	89/974 (9.1%)
58	Ln	1.57	9/554 (1.6%)	3.33	35/738 (4.7%)
59	Lo	2.53	24/472 (5.1%)	3.70	73/627 (11.6%)
60	Lr	2.74	37/853 (4.3%)	4.60	118/1124 (10.5%)
61	Lq	2.27	10/239 (4.2%)	4.16	11/302 (3.6%)
64	LG	2.49	69/1765 (3.9%)	4.39	262/2372 (11.0%)
66	LN	2.18	40/1094 (3.7%)	3.80	150/1461 (10.3%)
67	LS	2.37	54/1457 (3.7%)	3.67	203/1957 (10.4%)
68	LW	2.43	30/850 (3.5%)	3.67	99/1135 (8.7%)
69	La	2.64	34/743 (4.6%)	3.80	125/992 (12.6%)
70	Li	2.57	49/979 (5.0%)	3.71	149/1305 (11.4%)
71	Lj	2.60	37/811 (4.6%)	3.88	98/1083 (9.0%)
72	Lk	2.32	29/618 (4.7%)	5.17	88/809 (10.9%)
73	Lp	3.38	23/349 (6.6%)	4.34	58/458 (12.7%)
74	LJ	1.88	17/967 (1.8%)	2.62	80/1298 (6.2%)
75	Lt	1.09	1/438 (0.2%)	1.91	10/596 (1.7%)
75	Lu	0.93	0/438	1.78	6/596 (1.0%)
76	Lv	1.04	0/444	1.97	12/596 (2.0%)
76	Lw	1.30	2/444 (0.5%)	2.27	25/596 (4.2%)
77	Lc	2.30	38/1017 (3.7%)	3.54	72/1351 (5.3%)
78	Le	2.03	58/2018 (2.9%)	3.23	196/2702 (7.3%)
79	Ls	1.27	11/2023 (0.5%)	2.38	119/2739 (4.3%)
80	LC	2.05	94/3168 (3.0%)	4.14	240/4234 (5.7%)
81	LD	1.96	80/2919 (2.7%)	4.10	279/3924 (7.1%)
82	LK	1.79	29/1678 (1.7%)	2.66	102/2246 (4.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
83	Lm	1.86	11/724 (1.5%)	2.68	37/958 (3.9%)
84	LI	1.65	7/1499 (0.5%)	2.48	49/2001 (2.4%)
All	All	2.43	8834/207179 (4.3%)	2.82	18805/304005 (6.2%)

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 8834 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	SC	171	PRO	N-CD	81.78	2.62	1.47
32	S1	1315	U	O3'-P	-57.72	0.74	1.61
11	SM	126	TYR	CD2-CE2	56.68	3.08	1.38
1	Sa	140	GLN	CD-NE2	51.16	2.40	1.33
32	S1	860	A	O3'-P	-50.96	0.84	1.61

The worst 5 of 18805 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
72	Lk	93	MET	CA-C-O	-67.87	58.55	121.67
60	Lr	101	GLY	CA-C-O	-65.35	56.59	120.64
48	LV	36	ILE	O-C-N	-60.24	64.59	123.03
2	SA	204	ASP	O-C-N	-58.77	68.01	123.26
23	SU	82	TYR	CA-C-O	-57.12	48.95	122.63

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

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	2692	125	0
2	SA	1946	0	1877	290	0
3	SB	1539	0	1537	63	0
4	SD	1607	0	1677	243	0
5	SE	2028	0	2104	263	0
6	SF	1485	0	1525	105	0
7	SI	1017	0	1080	77	0
8	SJ	887	0	861	49	0
9	SK	830	0	808	110	0
10	SL	952	0	875	85	0
11	SM	1167	0	1142	137	0
12	SO	977	0	1056	201	0
13	SQ	1129	0	1160	68	0
14	SP	639	0	625	272	0
15	SS	1155	0	1173	104	0
16	SR	711	0	758	23	0
17	SV	740	0	746	201	0
18	SW	460	0	111	24	0
19	SY	442	0	467	35	0
20	SZ	469	0	501	26	0
21	Sc	126	0	26	9	0
22	Sb	181	0	39	0	0
23	SU	732	0	740	113	0
24	SX	375	0	368	97	0
25	SC	1535	0	1556	109	0
26	SG	716	0	160	75	0
27	SH	1042	0	1086	318	0
28	SN	313	0	269	32	0
29	ST	650	0	636	33	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	276	0
32	S1	33897	0	16592	1750	0
33	L1	69592	0	34889	3160	0
34	L3	2565	0	1293	390	0
35	L2	3192	0	1590	160	0
36	LA	1718	0	1841	321	0
37	LB	1933	0	1932	338	0
38	LE	1376	0	1417	202	0
39	LF	1500	0	1564	35	0
40	LH	1564	0	1658	26	0
41	LM	1020	0	1059	64	0
42	LP	1630	0	1704	88	0
43	LO	1086	0	1127	61	0
44	LR	1284	0	1376	79	0
45	LQ	2395	0	2338	200	0
46	LT	1569	0	1676	389	0
47	LU	1266	0	1268	24	0
48	LV	1335	0	1339	175	0
49	LX	987	0	1083	39	0
50	LZ	578	0	566	25	0
51	LY	1048	0	1130	69	0
52	Lb	576	0	616	22	0
53	Ld	199	0	193	6	0
54	Lf	825	0	830	217	0
55	Lg	944	0	992	124	0
56	Lh	1089	0	1164	152	0
57	Li	725	0	718	63	0
58	Ln	547	0	578	5	0
59	Lo	460	0	490	26	0
60	Lr	838	0	887	21	0
61	Lq	238	0	289	2	0
62	Lx	101	0	24	1	0
62	Ly	101	0	23	0	0
63	Lz	71	0	16	3	0
64	LG	1730	0	1824	120	0
65	LL	910	0	202	83	0
66	LN	1081	0	1171	203	0
67	LS	1419	0	1466	220	0
68	LW	839	0	863	36	0
69	La	732	0	754	94	0
70	Li	964	0	1054	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	Lj	797	0	804	116	0
72	Lk	613	0	684	93	0
73	Lp	344	0	371	69	0
74	LJ	959	0	1039	21	0
75	Lt	432	0	463	109	0
75	Lu	432	0	463	90	0
76	Lv	441	0	453	120	0
76	Lw	441	0	453	97	0
77	Lc	1006	0	1100	25	0
78	Le	1984	0	2090	158	0
79	Ls	1993	0	2086	220	0
80	LC	3102	0	3191	71	0
81	LD	2866	0	2968	338	0
82	LK	1650	0	1771	135	0
83	Lm	715	0	756	171	0
84	LI	1468	0	1506	78	0
All	All	195694	0	140366	10229	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 31.

The worst 5 of 10229 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:CD1	38:LE:91:TYR:CG	1.78	1.70
38:LE:91:TYR:CD2	38:LE:91:TYR:CE2	1.75	1.69
38:LE:91:TYR:CE2	38:LE:91:TYR:CZ	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%)	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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	25
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%)	1	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	12
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
57	Li	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	Lt	56/58 (97%)	54 (96%)	1 (2%)	1 (2%)	6	34
75	Lu	56/58 (97%)	54 (96%)	1 (2%)	1 (2%)	6	34
76	Lv	57/59 (97%)	54 (95%)	2 (4%)	1 (2%)	6	34
76	Lw	57/59 (97%)	54 (95%)	2 (4%)	1 (2%)	6	34
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%)	1	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	8
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
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%)	272 (90%)	29 (10%)	8	25
2	SA	190/204 (93%)	167 (88%)	23 (12%)	5	17
3	SB	150/175 (86%)	130 (87%)	20 (13%)	4	14
4	SD	176/176 (100%)	150 (85%)	26 (15%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	SE	211/211 (100%)	188 (89%)	23 (11%)	6	21
6	SF	158/159 (99%)	142 (90%)	16 (10%)	7	23
7	SI	103/103 (100%)	93 (90%)	10 (10%)	8	24
8	SJ	91/113 (80%)	81 (89%)	10 (11%)	6	20
9	SK	78/94 (83%)	67 (86%)	11 (14%)	3	13
10	SL	79/113 (70%)	70 (89%)	9 (11%)	5	18
11	SM	116/133 (87%)	87 (75%)	29 (25%)	0	4
12	SO	106/106 (100%)	95 (90%)	11 (10%)	7	22
13	SQ	123/127 (97%)	101 (82%)	22 (18%)	2	9
14	SP	63/74 (85%)	53 (84%)	10 (16%)	2	11
15	SS	121/121 (100%)	96 (79%)	25 (21%)	1	6
16	SR	77/77 (100%)	65 (84%)	12 (16%)	2	12
17	SV	76/87 (87%)	71 (93%)	5 (7%)	15	37
19	SY	49/52 (94%)	44 (90%)	5 (10%)	7	23
20	SZ	44/49 (90%)	38 (86%)	6 (14%)	3	14
23	SU	70/84 (83%)	42 (60%)	28 (40%)	0	1
24	SX	44/44 (100%)	40 (91%)	4 (9%)	9	27
25	SC	154/167 (92%)	134 (87%)	20 (13%)	4	15
27	SH	113/113 (100%)	93 (82%)	20 (18%)	2	9
28	SN	27/40 (68%)	23 (85%)	4 (15%)	3	13
29	ST	68/68 (100%)	58 (85%)	10 (15%)	3	13
36	LA	192/192 (100%)	175 (91%)	17 (9%)	9	28
37	LB	193/195 (99%)	179 (93%)	14 (7%)	13	34
38	LE	148/149 (99%)	125 (84%)	23 (16%)	2	12
39	LF	164/164 (100%)	150 (92%)	14 (8%)	10	29
40	LH	164/173 (95%)	135 (82%)	29 (18%)	2	9
41	LM	103/109 (94%)	90 (87%)	13 (13%)	4	16
42	LP	167/167 (100%)	149 (89%)	18 (11%)	6	21
43	LO	104/110 (94%)	87 (84%)	17 (16%)	2	10
44	LR	138/138 (100%)	115 (83%)	23 (17%)	2	10
45	LQ	242/251 (96%)	199 (82%)	43 (18%)	2	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	LT	166/166 (100%)	143 (86%)	23 (14%)	3	14
47	LU	129/140 (92%)	111 (86%)	18 (14%)	3	13
48	LV	136/144 (94%)	113 (83%)	23 (17%)	2	10
49	LX	109/109 (100%)	97 (89%)	12 (11%)	6	20
50	LZ	54/66 (82%)	48 (89%)	6 (11%)	6	20
51	LY	115/115 (100%)	98 (85%)	17 (15%)	3	13
52	Lb	64/64 (100%)	59 (92%)	5 (8%)	11	32
53	Ld	21/21 (100%)	19 (90%)	2 (10%)	8	25
54	Lf	90/98 (92%)	72 (80%)	18 (20%)	1	7
55	Lg	99/103 (96%)	83 (84%)	16 (16%)	2	11
56	Lh	119/122 (98%)	111 (93%)	8 (7%)	15	36
57	Ll	72/77 (94%)	63 (88%)	9 (12%)	4	16
58	Ln	59/63 (94%)	48 (81%)	11 (19%)	1	8
59	Lo	48/48 (100%)	38 (79%)	10 (21%)	1	6
60	Lr	91/94 (97%)	74 (81%)	17 (19%)	1	8
61	Lq	24/24 (100%)	22 (92%)	2 (8%)	10	30
64	LG	185/185 (100%)	151 (82%)	34 (18%)	1	8
66	LN	116/116 (100%)	85 (73%)	31 (27%)	0	3
67	LS	153/153 (100%)	119 (78%)	34 (22%)	1	6
68	LW	89/94 (95%)	70 (79%)	19 (21%)	1	6
69	La	73/83 (88%)	55 (75%)	18 (25%)	1	4
70	Li	105/107 (98%)	75 (71%)	30 (29%)	0	2
71	Lj	80/89 (90%)	63 (79%)	17 (21%)	1	6
72	Lk	62/62 (100%)	46 (74%)	16 (26%)	0	3
73	Lp	38/38 (100%)	26 (68%)	12 (32%)	0	2
74	LJ	104/105 (99%)	79 (76%)	25 (24%)	1	4
75	Lt	46/46 (100%)	44 (96%)	2 (4%)	26	47
75	Lu	46/46 (100%)	45 (98%)	1 (2%)	45	64
76	Lv	48/48 (100%)	48 (100%)	0	100	100
76	Lw	48/48 (100%)	47 (98%)	1 (2%)	47	65
77	Lc	107/109 (98%)	99 (92%)	8 (8%)	12	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
78	Le	206/206 (100%)	175 (85%)	31 (15%)	3	12
79	Ls	222/222 (100%)	197 (89%)	25 (11%)	5	19
80	LC	328/335 (98%)	271 (83%)	57 (17%)	2	9
81	LD	294/302 (97%)	257 (87%)	37 (13%)	4	16
82	LK	173/173 (100%)	142 (82%)	31 (18%)	2	9
83	Lm	73/73 (100%)	65 (89%)	8 (11%)	6	20
84	LI	152/156 (97%)	142 (93%)	10 (7%)	15	37
All	All	8547/8911 (96%)	7304 (86%)	1243 (14%)	5	13

5 of 1243 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	La	55	ARG
80	LC	316	PRO
70	Li	99	GLU
69	La	54	ILE
77	Lc	70	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 207 such sidechains are listed below:

Mol	Chain	Res	Type
45	LQ	82	HIS
54	Lf	13	ASN
80	LC	381	GLN
45	LQ	286	ASN
48	LV	9	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	1477/1743 (84%)	431 (29%)	156 (10%)
33	L1	3179/3352 (94%)	906 (28%)	414 (13%)
34	L3	120/120 (100%)	49 (40%)	17 (14%)
35	L2	142/159 (89%)	56 (39%)	28 (19%)
All	All	5002/5460 (91%)	1467 (29%)	621 (12%)

5 of 1467 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 621 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
33	L1	2467	A
33	L1	3378	U
33	L1	2503	A
33	L1	2466	G
33	L1	2818	G

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 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

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Mol	Chain	Number of breaks
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
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

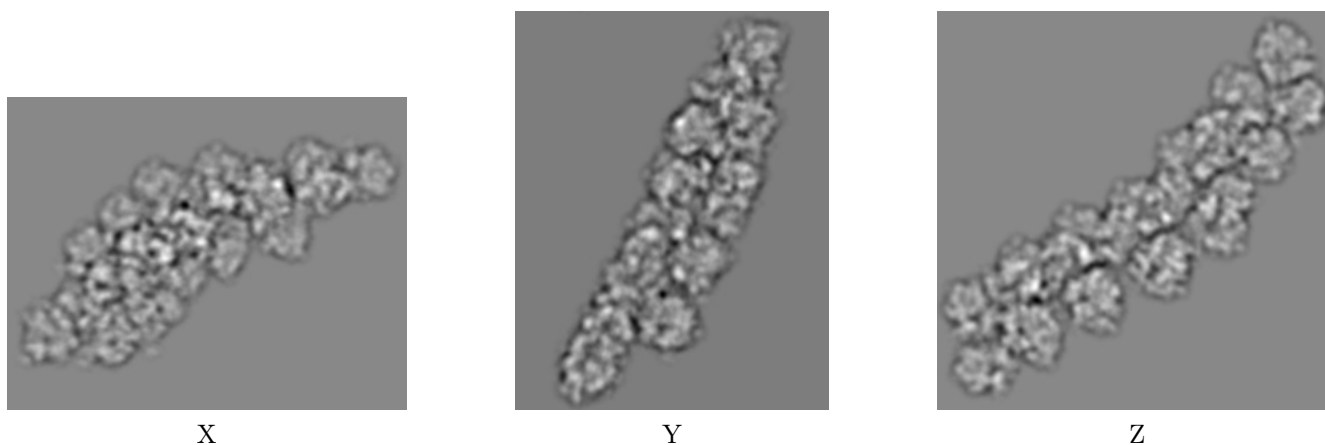
6 Map visualisation [i](#)

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](#)

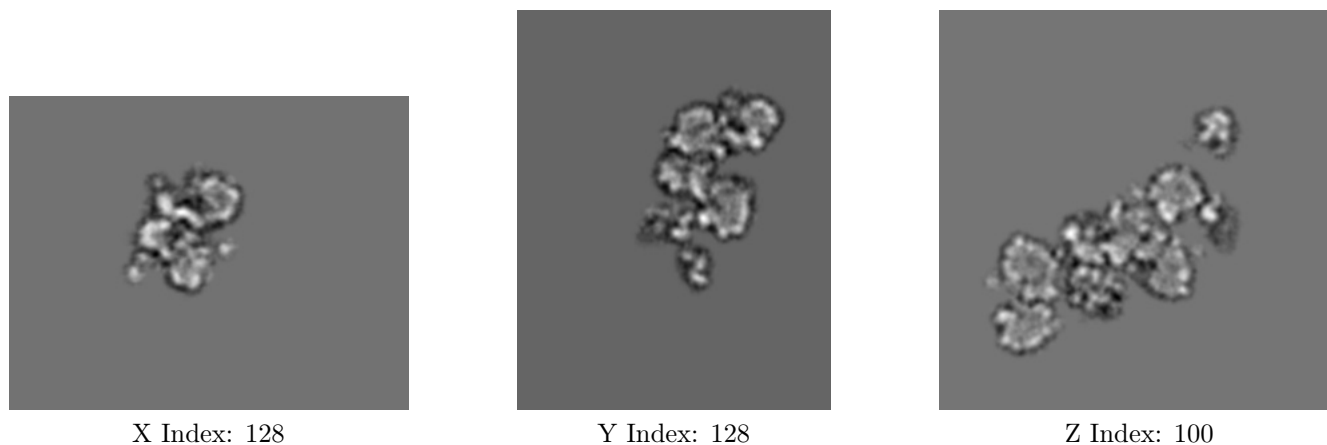
6.1.1 Primary map



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](#)

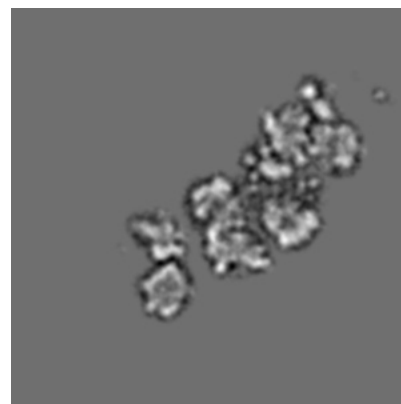
6.3.1 Primary map



X Index: 44



Y Index: 93

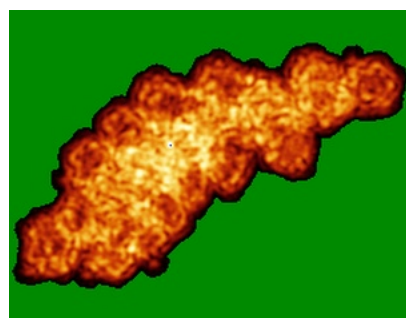


Z Index: 126

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

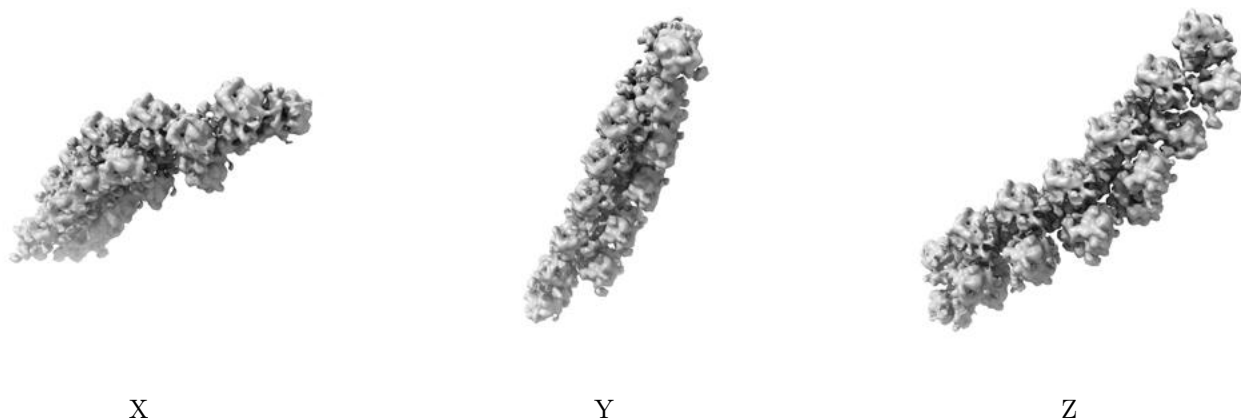


Z

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.

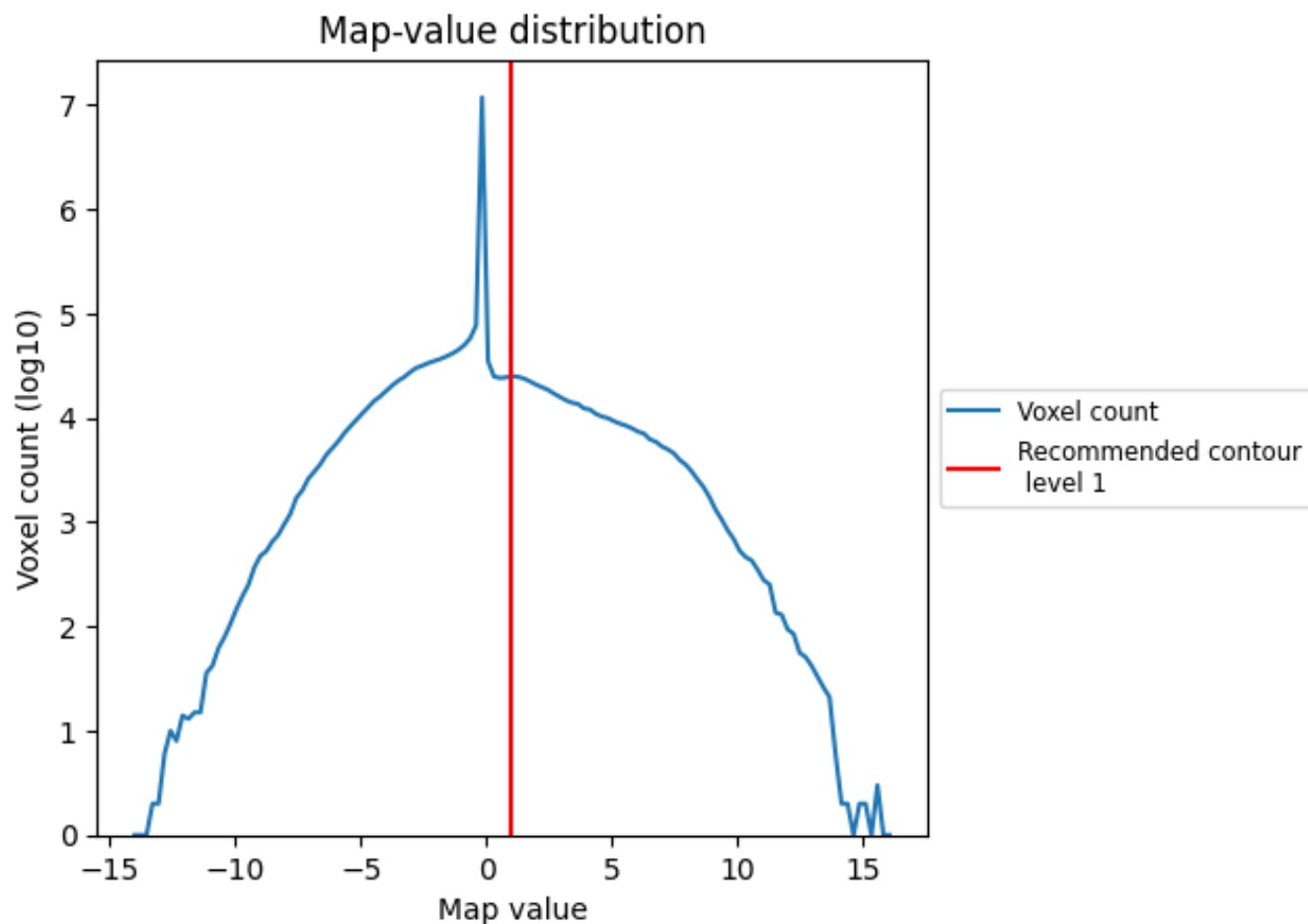
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

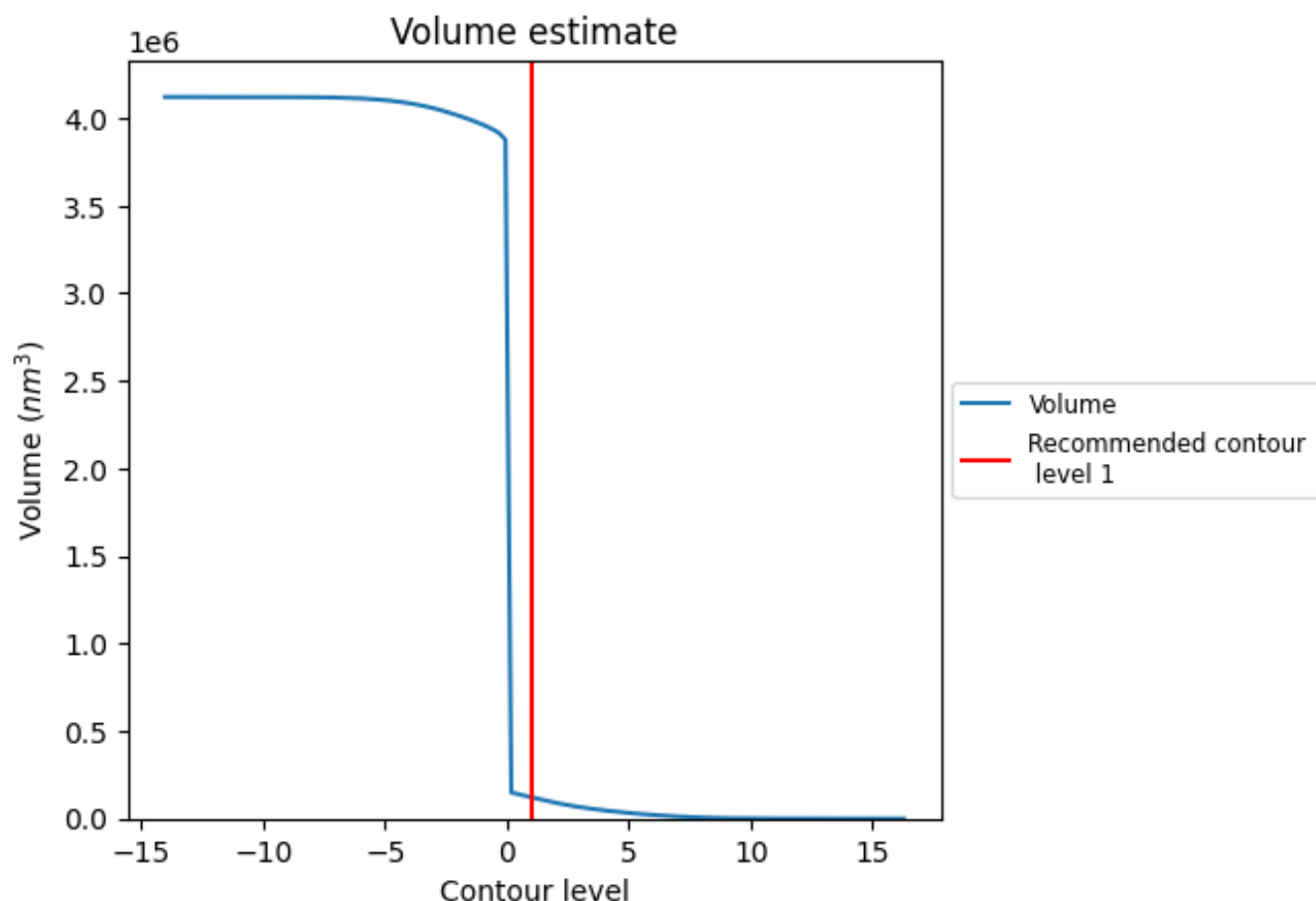
This section contains the results of statistical analysis of the map.

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

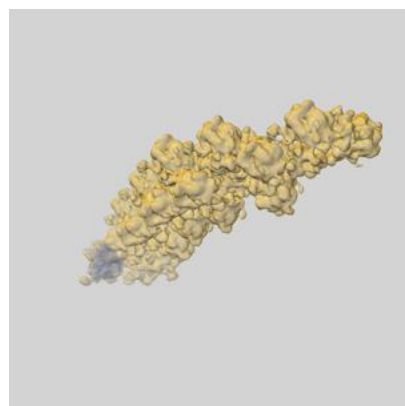
This section was not generated. No FSC curve or half-maps provided.

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

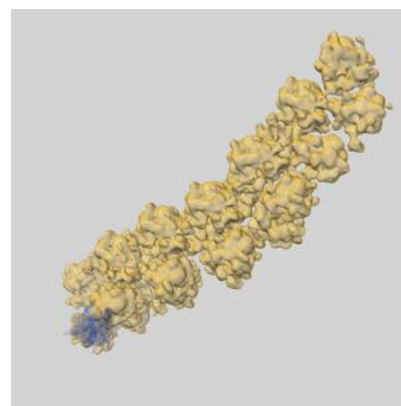
9.1.1 Map-model overlay [i](#)



X



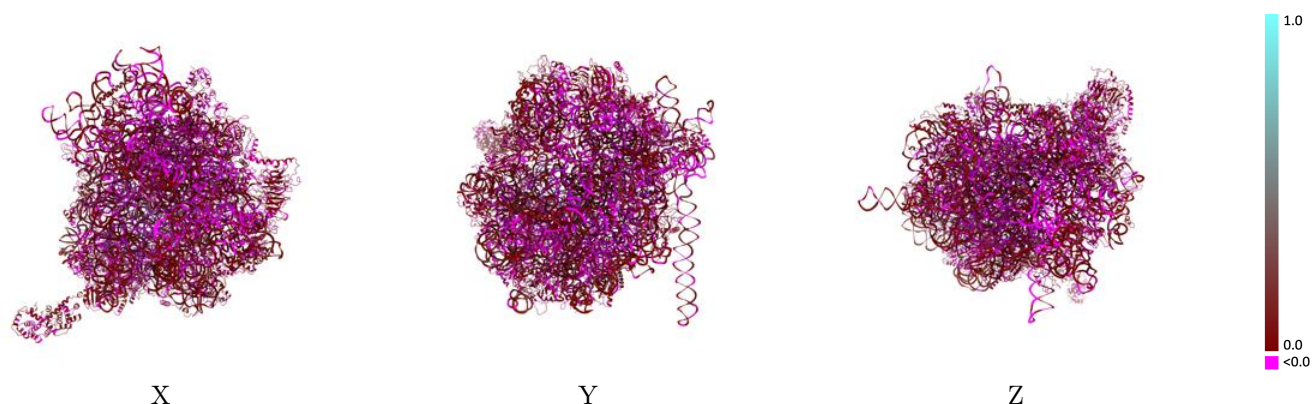
Y



Z

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](#)

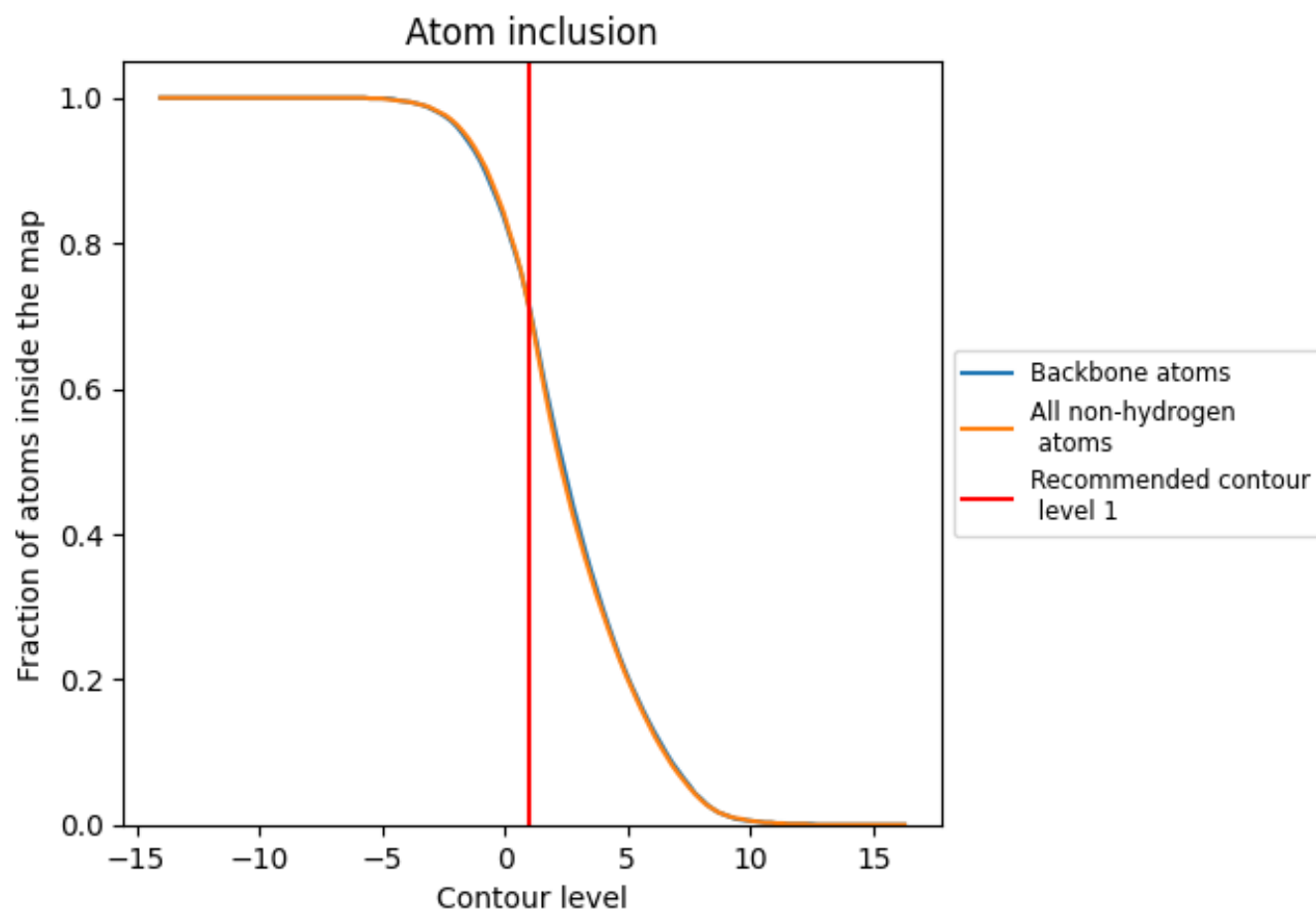


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

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