wwPDB EM Validation Summary Report

Mar 9, 2026 – 10:13 AM UTC

PDB ID	:	8ZHB / pdb_00008zhb
EMDB ID	:	EMD-60097
Title	:	80S ribosome with A/A P/E tRNA and mRNA of WNV
Authors	:	Wu, M.; Yuan, S.
Deposited on	:	2024-05-10
Resolution	:	2.60 Å(reported)

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:

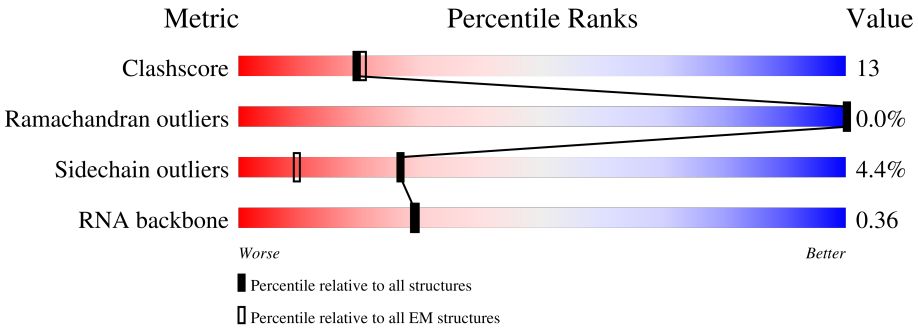
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

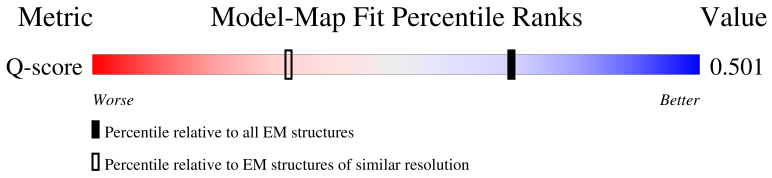
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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	8728 (2.10 - 3.10)

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 <=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	LA	3393	9% 43% 41% 10% 6%
2	LB	121	50% 45% 5%
3	LC	158	5% 42% 45% 13%

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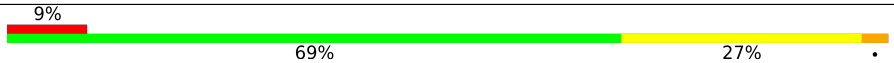
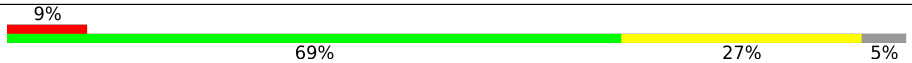
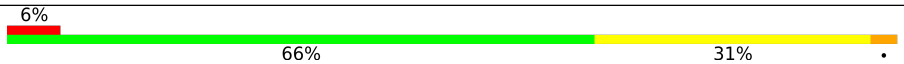
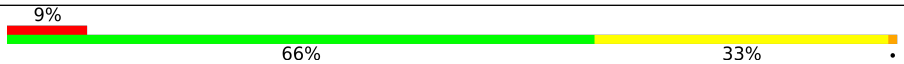
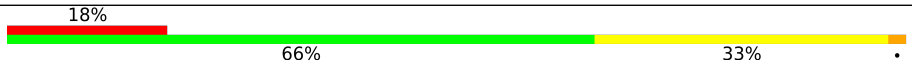
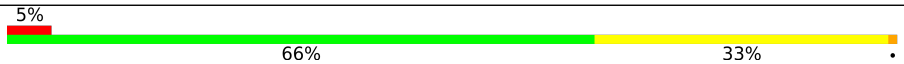
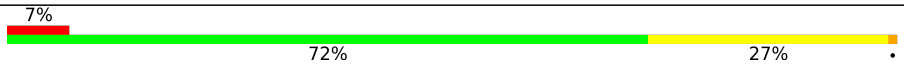
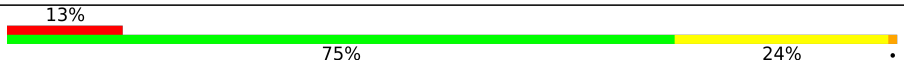
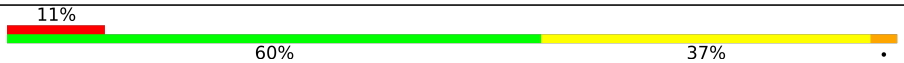
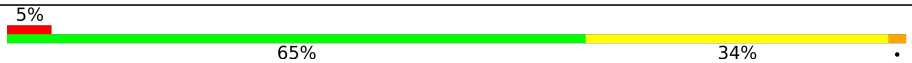
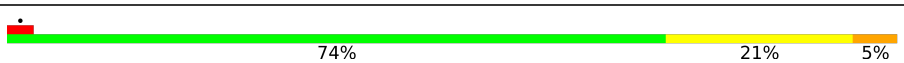
Mol	Chain	Length	Quality of chain
4	LD	251	
5	LE	386	
6	LF	361	
7	LG	294	
8	LH	175	
9	LI	222	
10	LJ	233	
11	LK	191	
12	LL	218	
13	LM	169	
14	LN	193	
15	LO	136	
16	LP	203	
17	LQ	197	
18	LR	183	
19	LS	185	
20	LT	188	
21	LU	171	
22	LV	159	
23	LW	100	
24	LX	136	
25	LY	65	
26	LZ	121	
27	La	125	
28	Lb	135	

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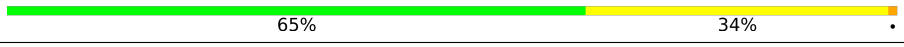
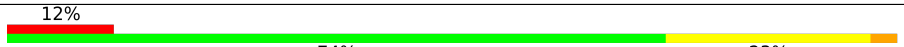
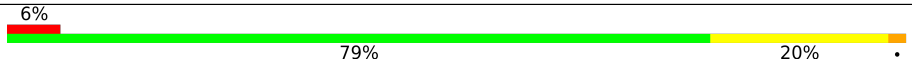
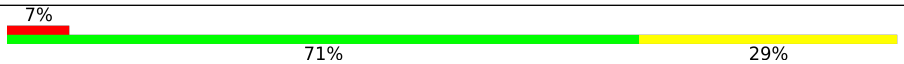
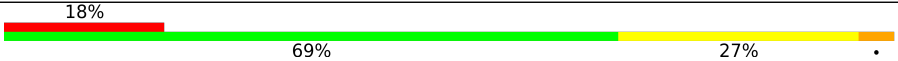
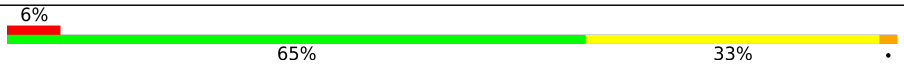
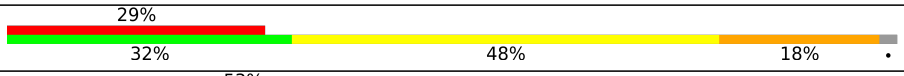
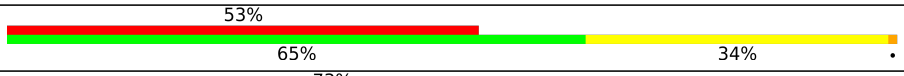
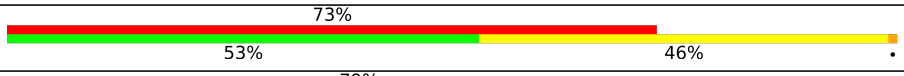
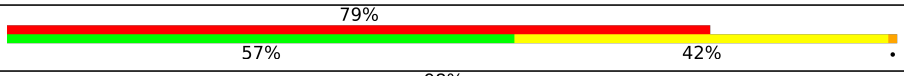
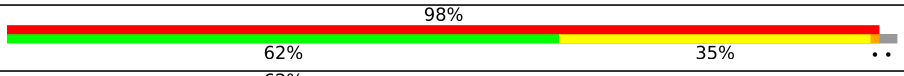
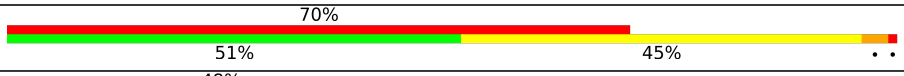
Mol	Chain	Length	Quality of chain
29	Lc	148	
30	Ld	58	
31	Le	96	
32	Lf	109	
33	Lg	127	
34	Lh	106	
35	Li	112	
36	Lj	119	
37	Lk	99	
38	Ll	81	
39	Lm	77	
40	Ln	50	
41	Lo	52	
42	Lp	25	
43	Lq	103	
44	Lr	91	
45	S2	1799	
46	SA	223	
47	SB	206	
48	SC	92	
49	SD	124	
50	SE	117	
51	SF	141	
52	SG	125	
53	SH	145	

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Mol	Chain	Length	Quality of chain
54	SI	143	69% 64% 34%
55	SJ	101	66% 51% 48%
56	SK	82	95% 61% 39%
57	SL	63	63% 54% 43%
58	SM	53	45% 75% 25%
59	SN	73	99% 81% 18%
60	SO	312	91% 63% 36%
61	SP	206	15% 58% 40%
62	SQ	232	11% 57% 38%
63	SR	217	6% 66% 30%
64	SS	260	23% 54% 42%
65	ST	228	52% 59% 38%
66	SU	185	29% 59% 38%
67	SV	199	28% 57% 37% 6%
68	SW	185	32% 49% 48%
69	SX	146	15% 73% 23%
70	SY	150	5% 72% 25%
71	SZ	128	59% 38%
72	Sa	87	9% 55% 45%
73	Sb	129	74% 26%
74	Sc	144	14% 67% 32%
75	Sd	134	39% 60% 38%
76	Se	97	7% 76% 23%
77	Sf	81	16% 69% 28%
78	Sg	57	44% 72% 28%

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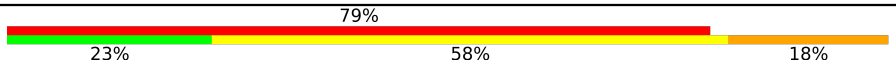
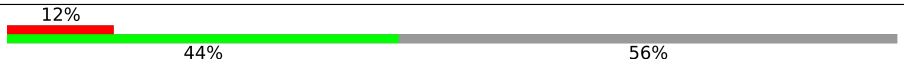
Mol	Chain	Length	Quality of chain
79	Ta	77	
80	Tb	77	
81	mR	25	

2 Entry composition (i)

There are 81 unique types of molecules in this entry. The entry contains 202562 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S rRNA (3393-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	LA	3184	68091	30415	12259	22233	3184	0	0

- Molecule 2 is a RNA chain called 5S rRNA (121-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	LB	121	2579	1152	461	845	121	0	0

- Molecule 3 is a RNA chain called 5.8S rRNA (158-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	LC	158	3353	1500	586	1109	158	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein uL2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	LD	251	1899	1182	385	331	1	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LE	386	3075	1950	584	533	8	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LF	361	2748	1729	522	494	3	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LG	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	LH	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 9 is a protein called Large ribosomal subunit protein uL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 10 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 11 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LK	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 12 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 13 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	LN	193	Total 1543	C 962	N 315	O 266	0	0

- Molecule 15 is a protein called Large ribosomal subunit protein eL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LO	136	Total 1053	C 675	N 199	O 177	S 2	0	0

- Molecule 16 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LP	203	Total 1720	C 1077	N 361	O 281	S 1	0	0

- Molecule 17 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LQ	197	Total 1555	C 1003	N 289	O 262	S 1	197	0

- Molecule 18 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	LR	183	Total 1416	C 879	N 284	O 253	0	0

- Molecule 19 is a protein called Large ribosomal subunit protein eL18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	185	Total 1441	C 908	N 290	O 241	S 2	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein eL19A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	LT	188	Total 1515	C 932	N 323	O 260	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 22 is a protein called Large ribosomal subunit protein eL21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	LW	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 24 is a protein called Large ribosomal subunit protein uL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LX	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 25 is a protein called Large ribosomal subunit protein eL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	65	Total	C	N	O	S	0	0
			528	339	104	84	1		

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LZ	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 27 is a protein called Large ribosomal subunit protein uL24A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	La	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 28 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Lb	135	Total 1080	C 701	N 199	O 180	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	148	Total 1169	C 747	N 231	O 188	S 3	0	0

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Ld	58	Total 462	C 289	N 100	O 73	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Le	96	Total 737	C 476	N 123	O 137	S 1	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein eL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	109	Total 876	C 556	N 167	O 152	S 1	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lg	127	Total 1017	C 644	N 205	O 167	S 1	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lh	106	Total 850	C 540	N 165	O 144	S 1	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein eL34A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 36 is a protein called Large ribosomal subunit protein uL29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 37 is a protein called Large ribosomal subunit protein eL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lk	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 38 is a protein called Large ribosomal subunit protein eL37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ll	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Lm	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ln	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 41 is a protein called Large ribosomal subunit protein eL40A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lo	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 42 is a protein called Large ribosomal subunit protein eL41A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lp	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 43 is a protein called Large ribosomal subunit protein eL42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lq	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 44 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lr	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 45 is a RNA chain called chain 2 18S rRNA (1799-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
45	S2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

- Molecule 46 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SA	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 47 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SB	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 48 is a protein called Small ribosomal subunit protein eS10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SC	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 49 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	121	Total 875	C 551	N 153	O 169	S 2	0	0

- Molecule 50 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SE	117	Total 916	C 583	N 171	O 155	S 7	0	0

- Molecule 51 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	SF	141	Total 1105	C 708	N 203	O 194	0	0

- Molecule 52 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SG	121	Total 948	C 596	N 179	O 171	S 2	0	0

- Molecule 53 is a protein called Small ribosomal subunit protein uS13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SH	145	Total 1188	C 741	N 237	O 208	S 2	0	0

- Molecule 54 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SI	143	Total 1112	C 694	N 208	O 208	S 2	0	0

- Molecule 55 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SJ	100	Total 797	C 506	N 144	O 146	S 1	0	0

- Molecule 56 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	SK	82	Total 651	C 416	N 123	O 112	0	0

- Molecule 57 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SL	63	Total 491	C 303	N 96	O 91	S 1	0	0

- Molecule 58 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SM	53	Total 442	C 274	N 92	O 72	S 4	0	0

- Molecule 59 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SN	73	Total 556	C 352	N 105	O 95	S 4	0	0

- Molecule 60 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SO	312	Total 2383	C 1514	N 409	O 452	S 8	0	0

- Molecule 61 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SP	206	Total 1603	C 1030	N 284	O 287	S 2	0	0

- Molecule 62 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SQ	226	Total 1798	C 1139	N 330	O 325	S 4	0	0

- Molecule 63 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SR	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 64 is a protein called Small ribosomal subunit protein eS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SS	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 65 is a protein called Small ribosomal subunit protein eS6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	ST	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 66 is a protein called Small ribosomal subunit protein eS7A.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	SU	184	Total	C	N	O	0	0
			1473	946	263	264		

- Molecule 67 is a protein called Small ribosomal subunit protein eS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SV	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 68 is a protein called Small ribosomal subunit protein uS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SW	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 69 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SX	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 70 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SY	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 71 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SZ	127	Total	C	N	O	S	0	0
			923	568	185	167	3		

- Molecule 72 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sa	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 73 is a protein called Small ribosomal subunit protein uS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sb	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 74 is a protein called Small ribosomal subunit protein uS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sc	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 75 is a protein called Small ribosomal subunit protein eS24A.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	Sd	134	Total	C	N	O	0	0
			1032	651	195	186		

- Molecule 76 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Se	97	Total	C	N	O	S	0	0
			765	473	160	127	5		

- Molecule 77 is a protein called Small ribosomal subunit protein eS27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sf	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 78 is a protein called Small ribosomal subunit protein eS30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sg	57	Total	C	N	O	S	0	0
			451	284	93	73	1		

- Molecule 79 is a RNA chain called tRNA (77-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Ta	77	Total	C	N	O	P	0	0
			1650	734	303	536	77		

- Molecule 80 is a RNA chain called tRNA (77-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Tb	77	Total	C	N	O	P	0	0
			1645	732	298	538	77		

- Molecule 81 is a RNA chain called RNA (5'-R(P*GP*AP*UP*UP*GP*AP*CP*CP*CP*UP*U)-3').

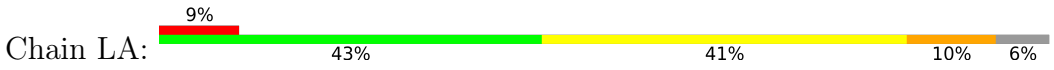
Mol	Chain	Residues	Atoms					AltConf	Trace
81	mR	11	Total	C	N	O	P	0	0
			230	103	37	79	11		

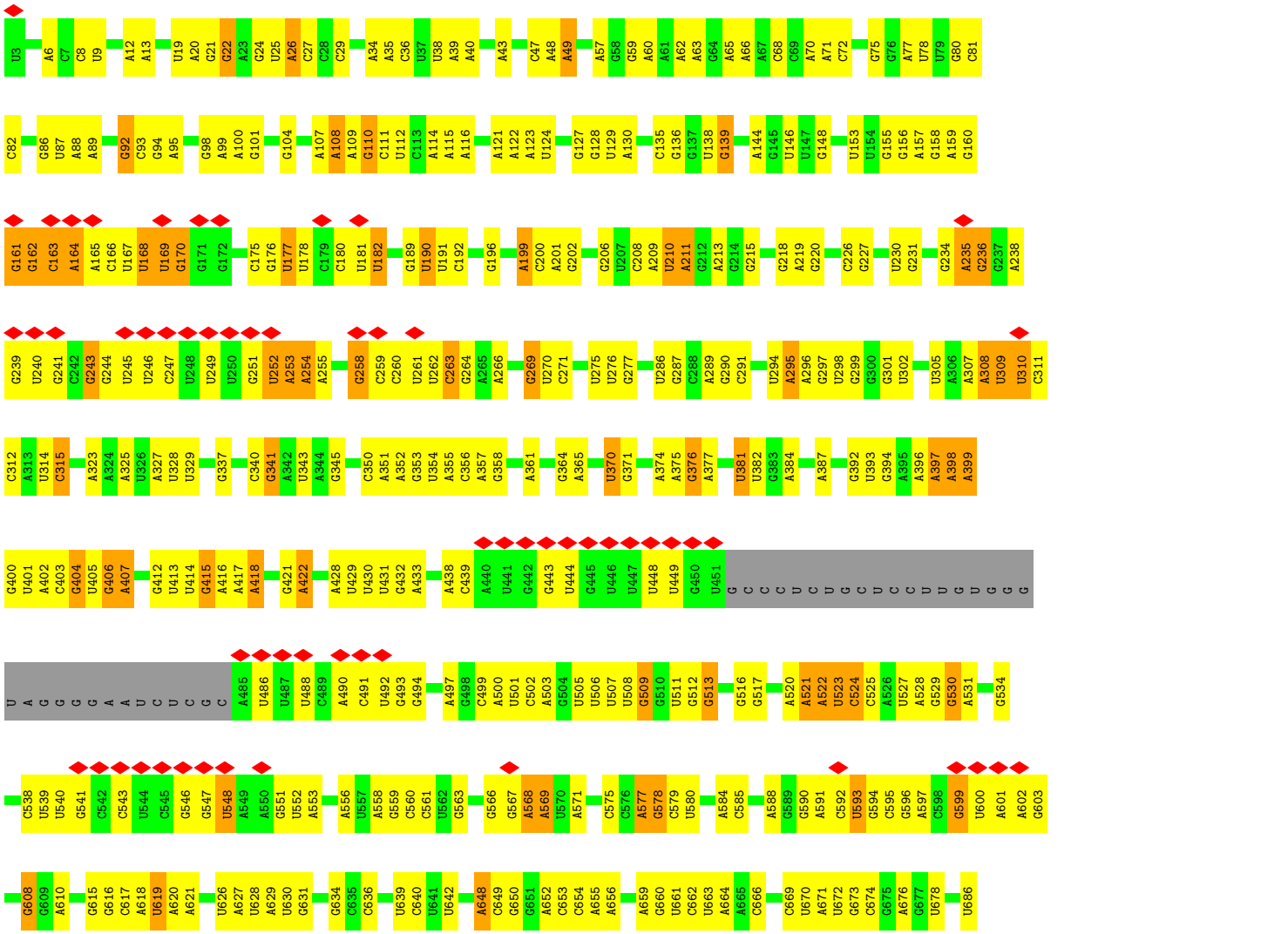
3 Residue-property plots (i)

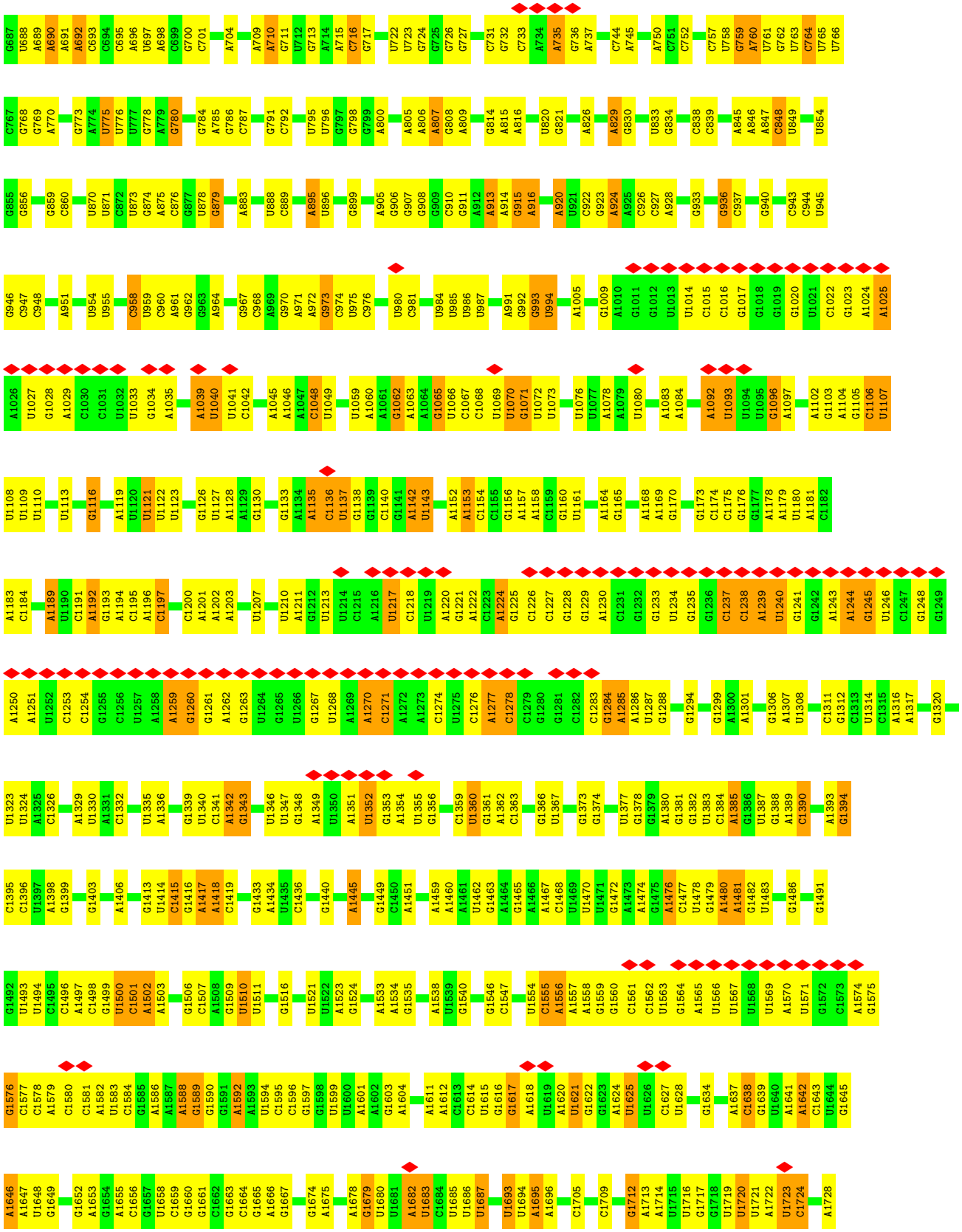
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

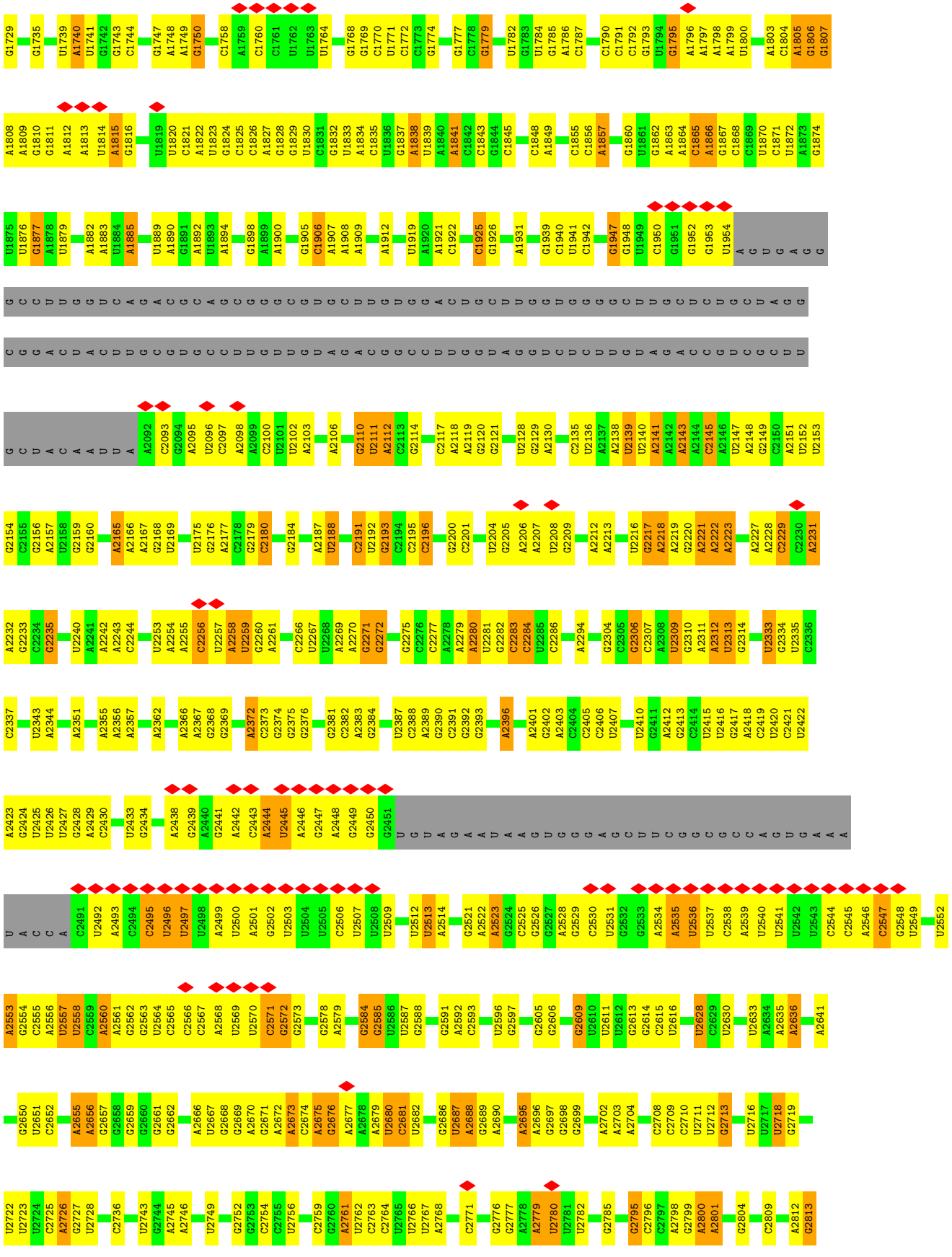
- Molecule 1: 25S rRNA (3393-MER)

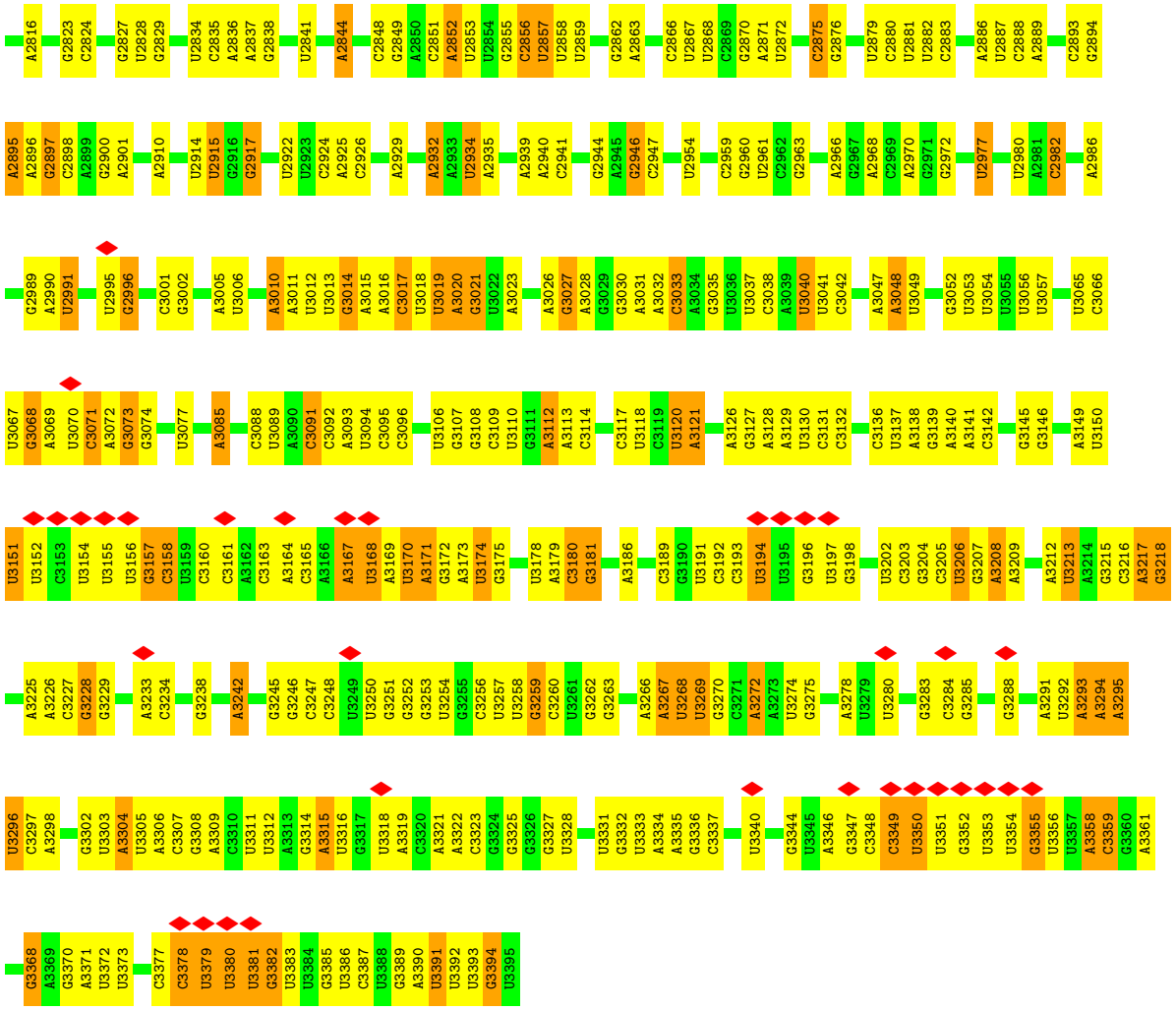
Chain LA:







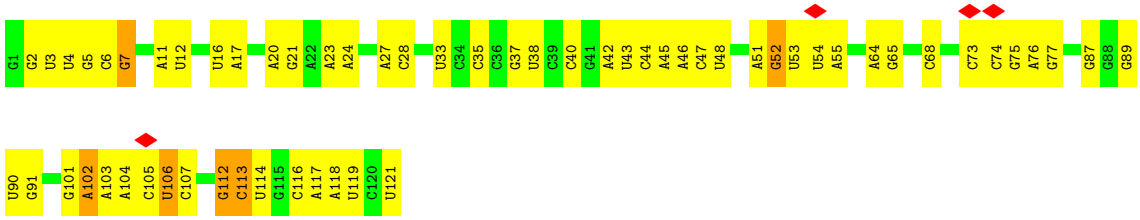




• Molecule 2: 5S rRNA (121-MER)

Chain LB:

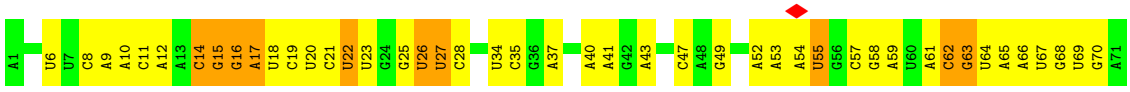


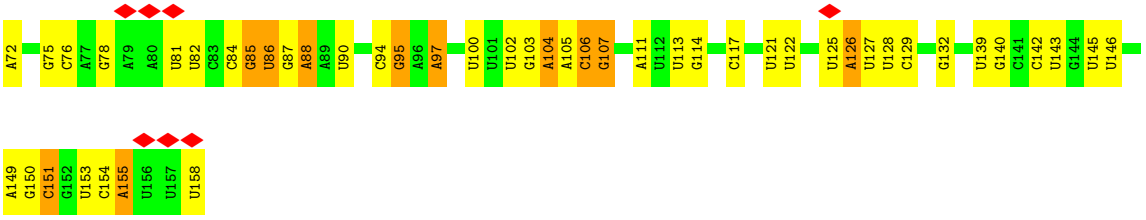


• Molecule 3: 5.8S rRNA (158-MER)

Chain LC:



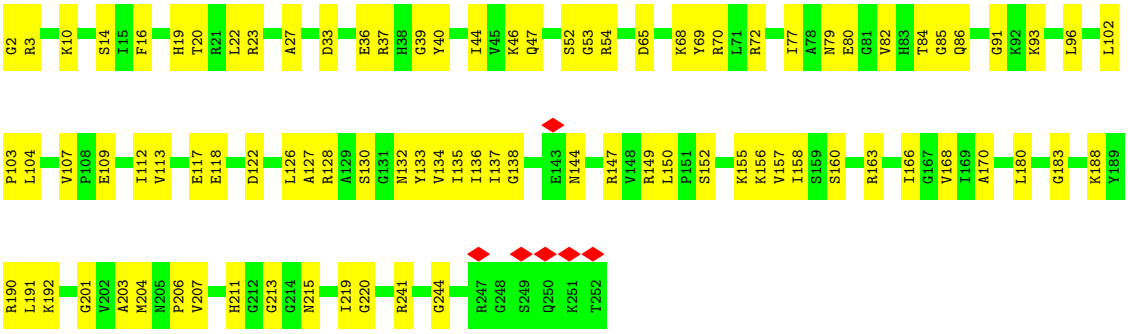




• Molecule 4: Large ribosomal subunit protein uL2A

Chain LD:

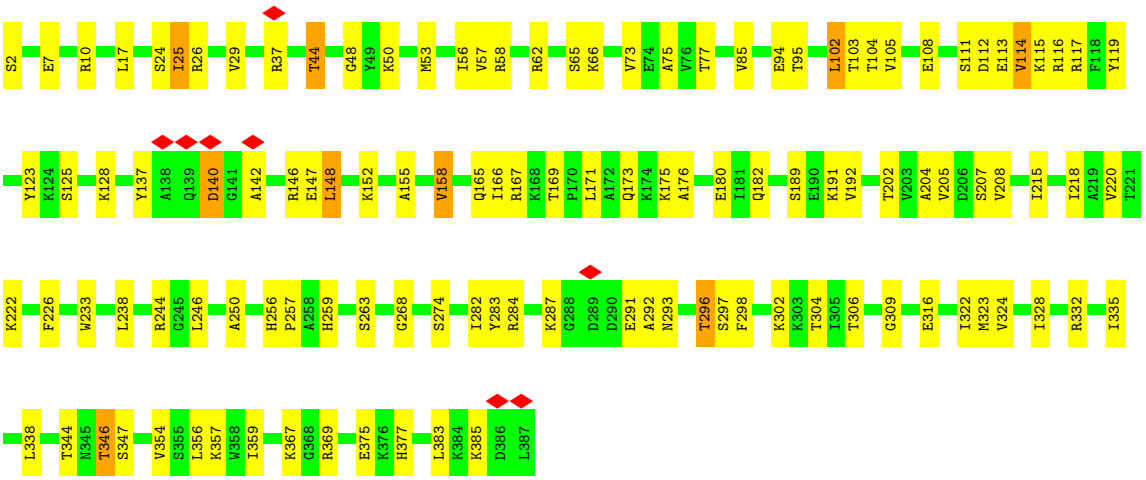




• Molecule 5: Large ribosomal subunit protein uL3

Chain LE:

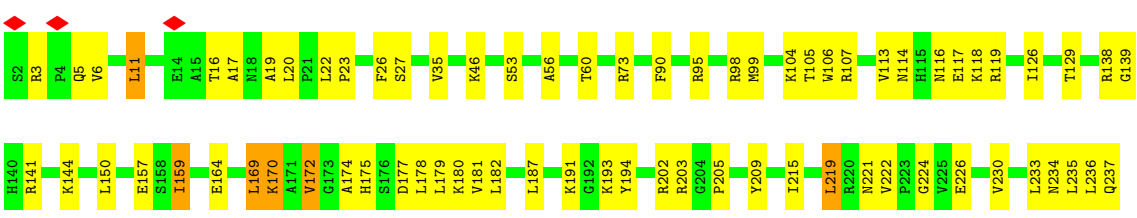


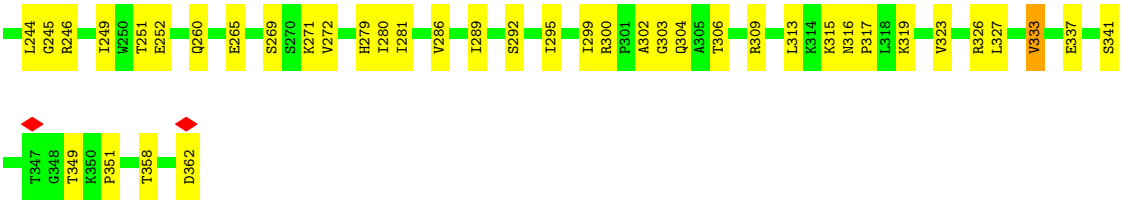


• Molecule 6: Large ribosomal subunit protein uL4A

Chain LF:

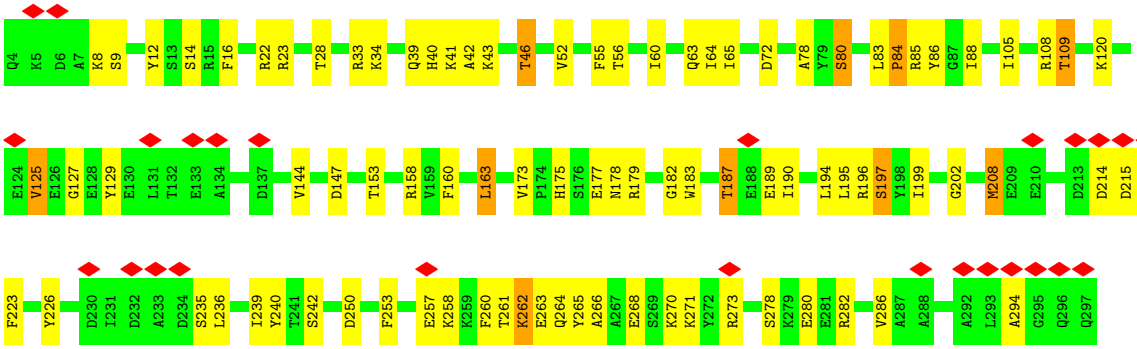






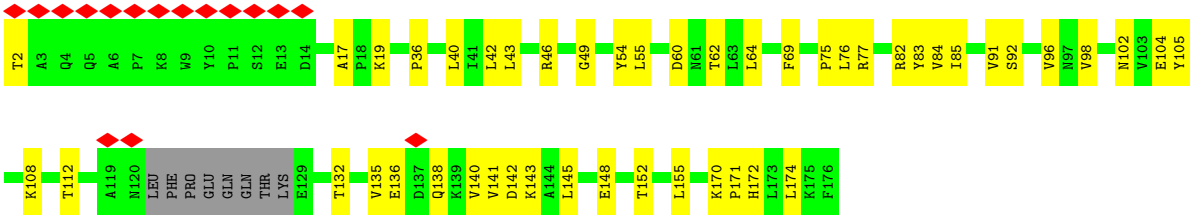
• Molecule 7: Large ribosomal subunit protein uL18





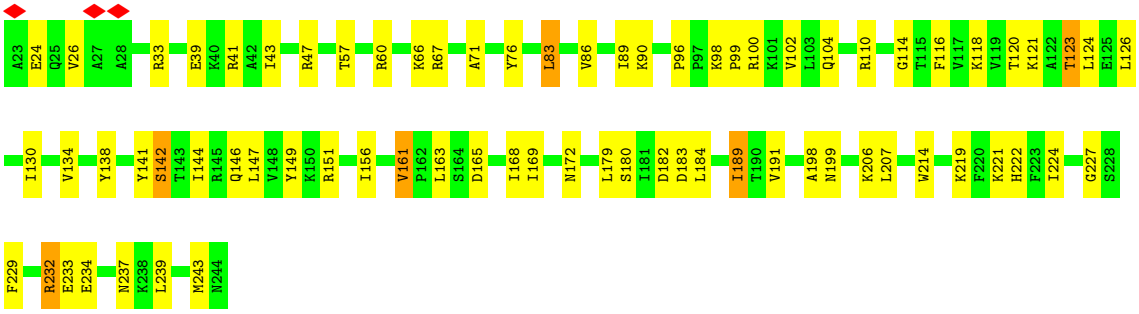
• Molecule 8: Large ribosomal subunit protein eL6B





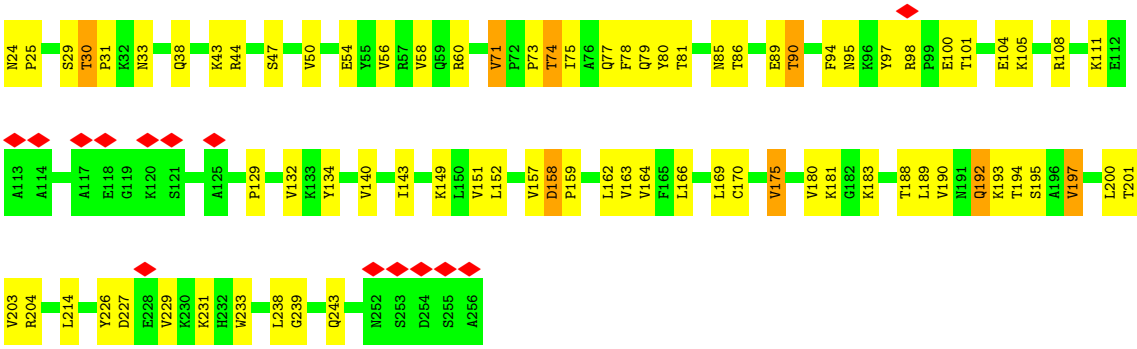
• Molecule 9: Large ribosomal subunit protein uL30A



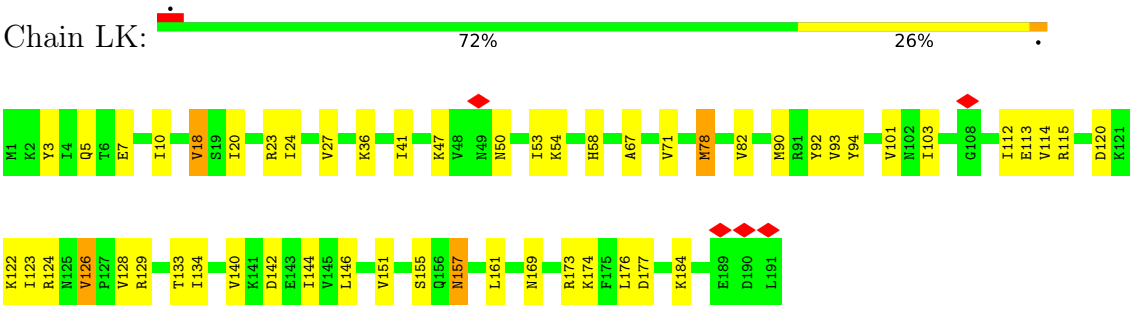


• Molecule 10: Large ribosomal subunit protein eL8A

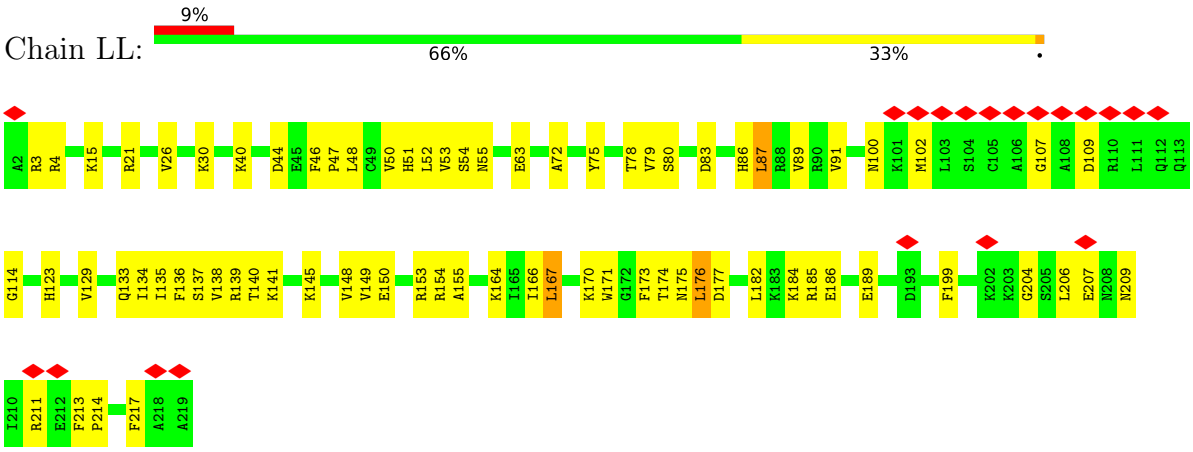




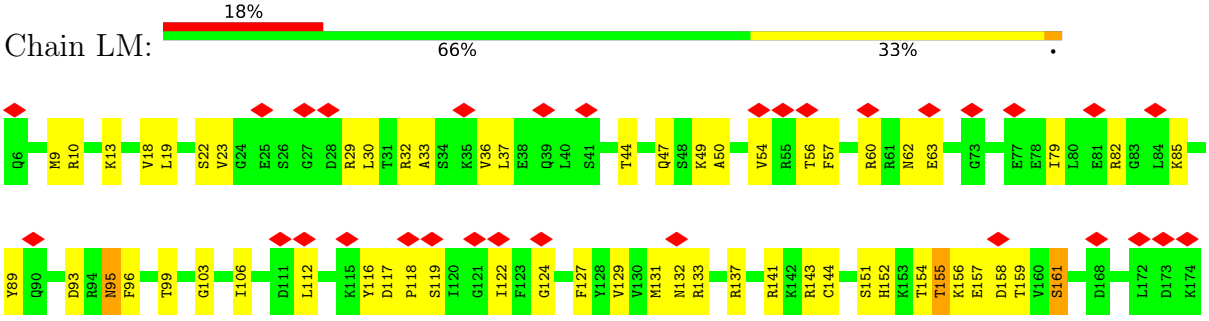
• Molecule 11: Large ribosomal subunit protein uL6A



• Molecule 12: Large ribosomal subunit protein uL16

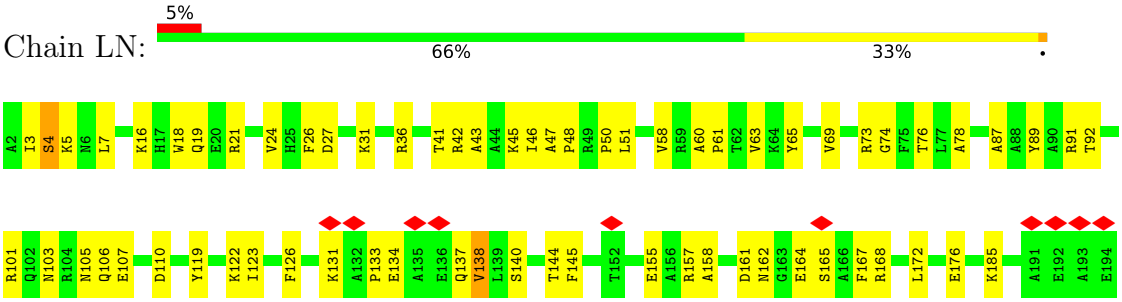


• Molecule 13: Large ribosomal subunit protein uL5B



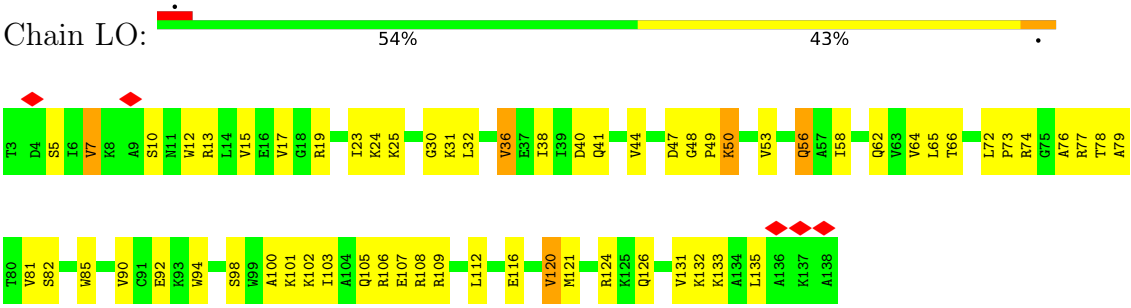
• Molecule 14: Large ribosomal subunit protein eL13A

Chain LN:



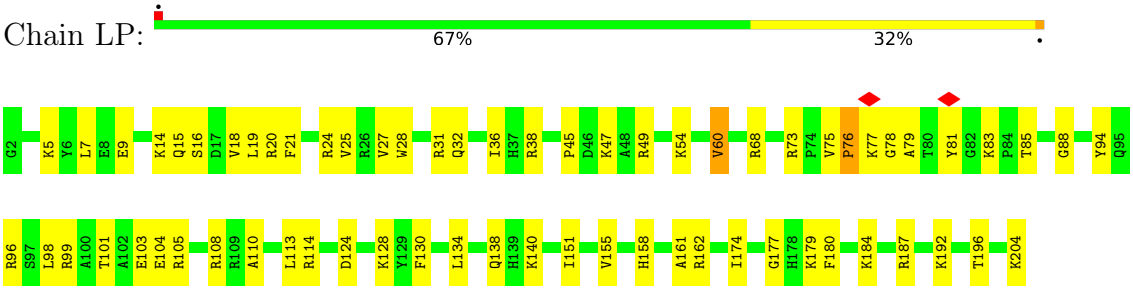
• Molecule 15: Large ribosomal subunit protein eL14A

Chain LO:



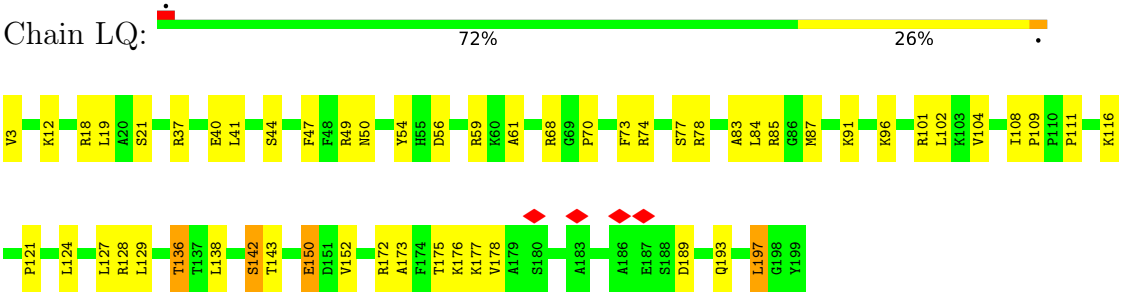
• Molecule 16: Large ribosomal subunit protein eL15A

Chain LP:



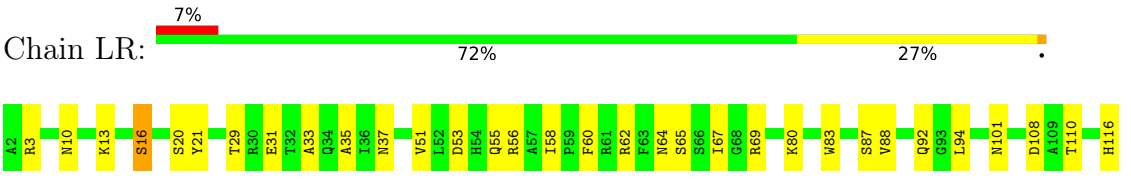
• Molecule 17: Large ribosomal subunit protein uL13A

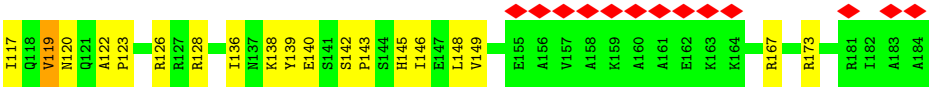
Chain LQ:



• Molecule 18: Large ribosomal subunit protein uL22A

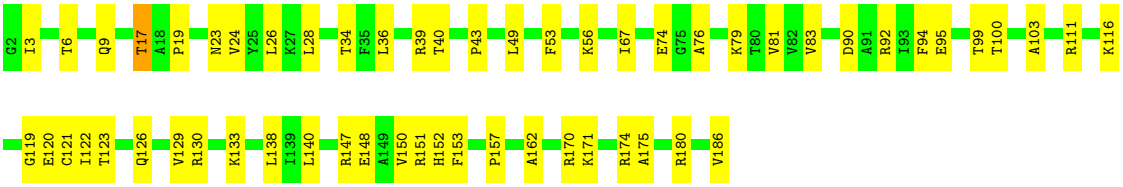
Chain LR:



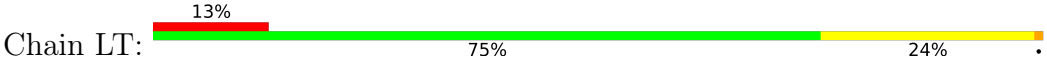


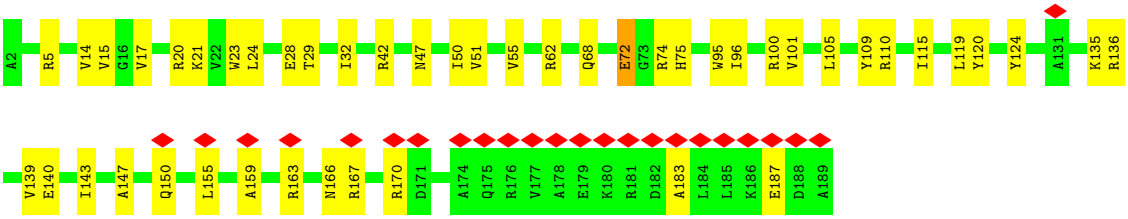
• Molecule 19: Large ribosomal subunit protein eL18A





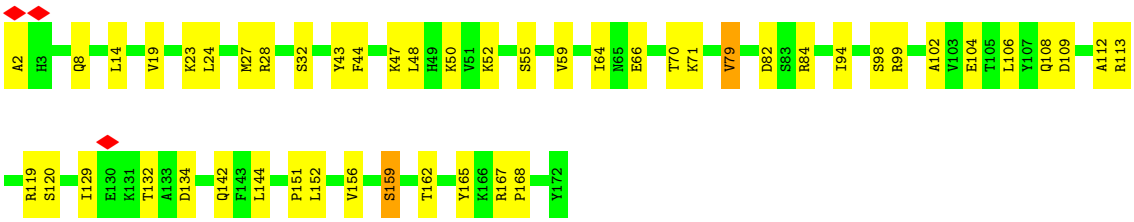
• Molecule 20: Large ribosomal subunit protein eL19A





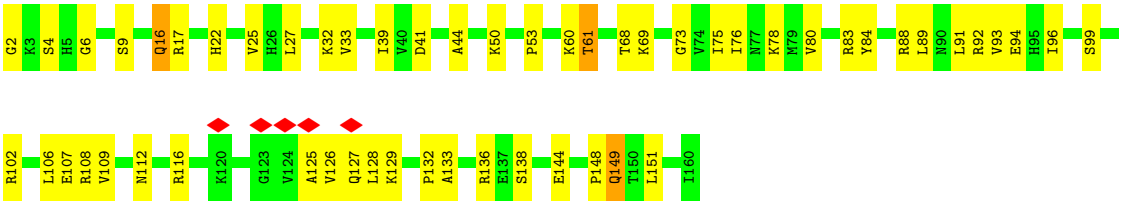
• Molecule 21: Large ribosomal subunit protein eL20A





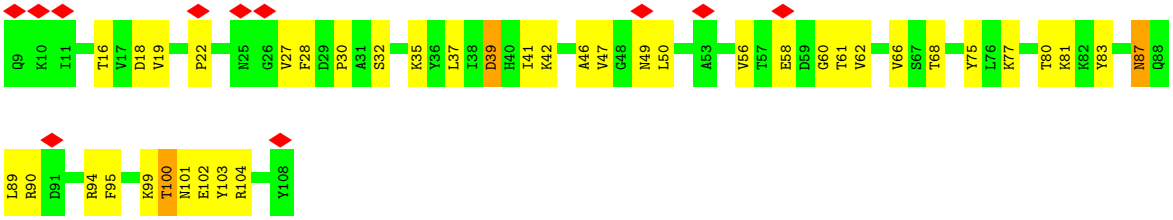
• Molecule 22: Large ribosomal subunit protein eL21A





• Molecule 23: Large ribosomal subunit protein eL22A

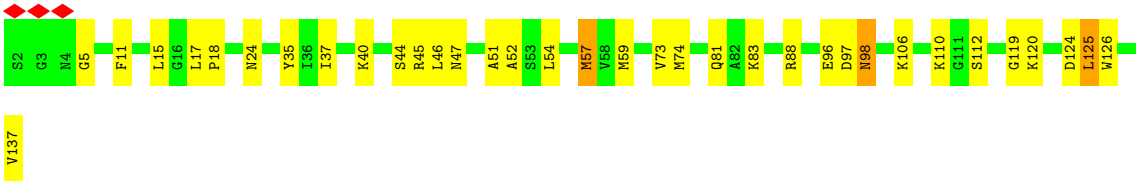




• Molecule 24: Large ribosomal subunit protein uL14A

Chain LX:

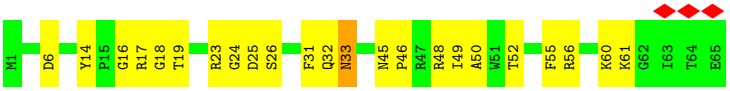




• Molecule 25: Large ribosomal subunit protein eL24A

Chain LY:

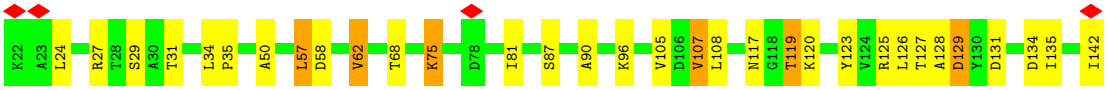




• Molecule 26: Large ribosomal subunit protein uL23

Chain LZ:

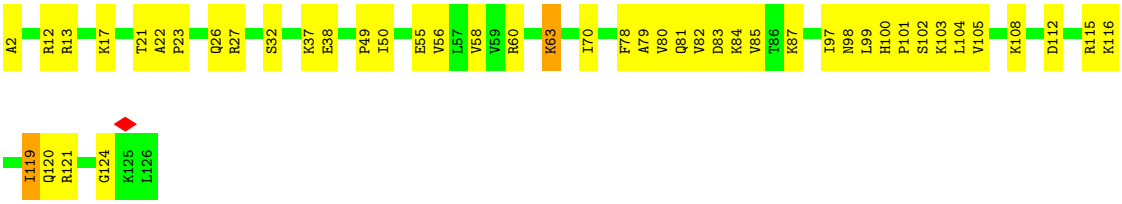




• Molecule 27: Large ribosomal subunit protein uL24A

Chain La:

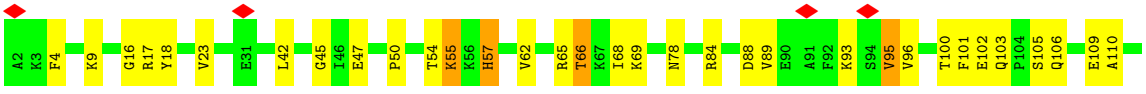


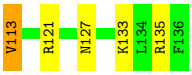


• Molecule 28: Large ribosomal subunit protein eL27A

Chain Lb:



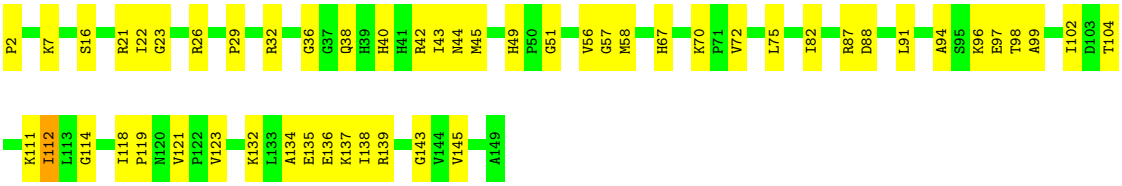




• Molecule 29: Large ribosomal subunit protein uL15

Chain Lc:

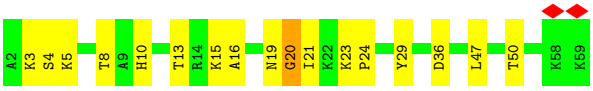




• Molecule 30: Large ribosomal subunit protein eL29

Chain Ld:

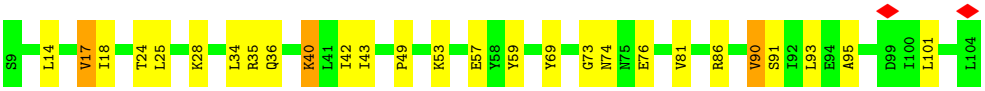




• Molecule 31: Large ribosomal subunit protein eL30

Chain Le:

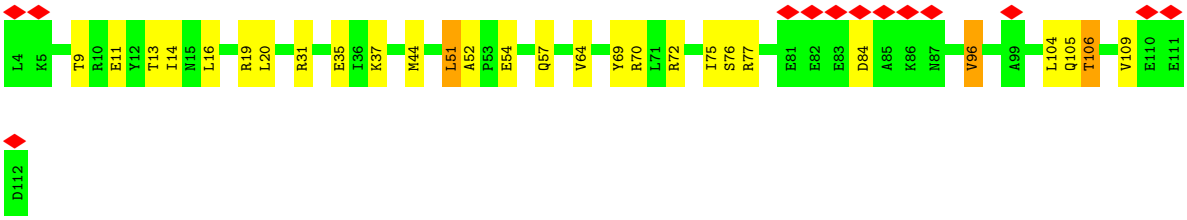




• Molecule 32: Large ribosomal subunit protein eL31A

Chain Lf:

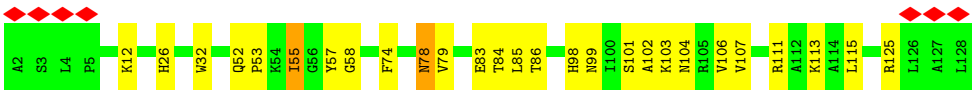




• Molecule 33: Large ribosomal subunit protein eL32

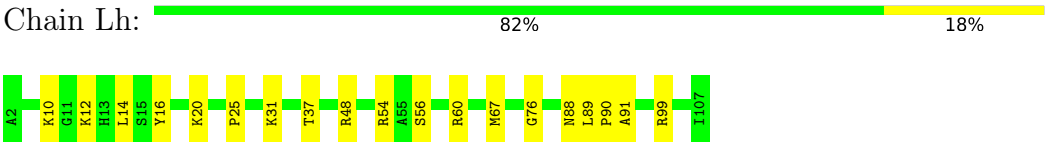
Chain Lg:





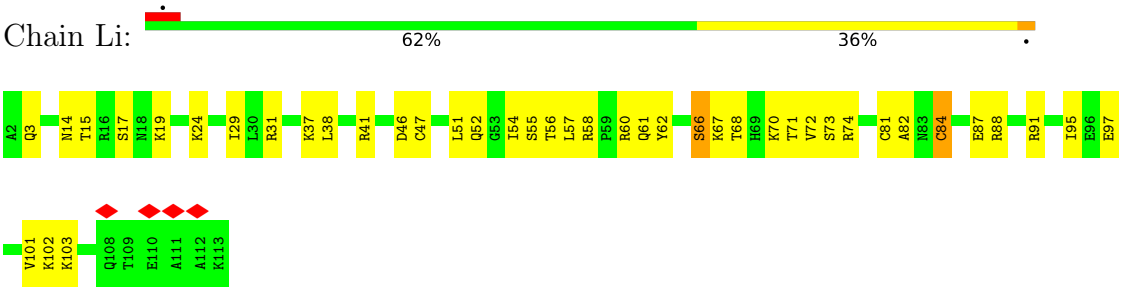
• Molecule 34: Large ribosomal subunit protein eL33A

Chain Lh:



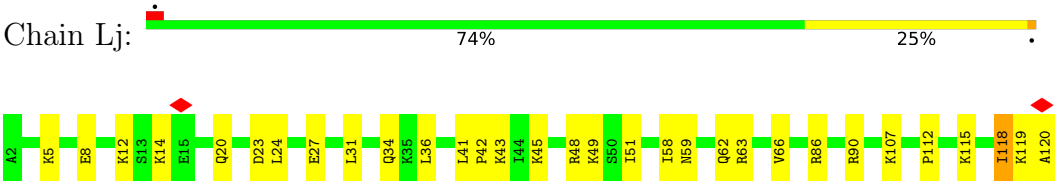
• Molecule 35: Large ribosomal subunit protein eL34A

Chain Li:



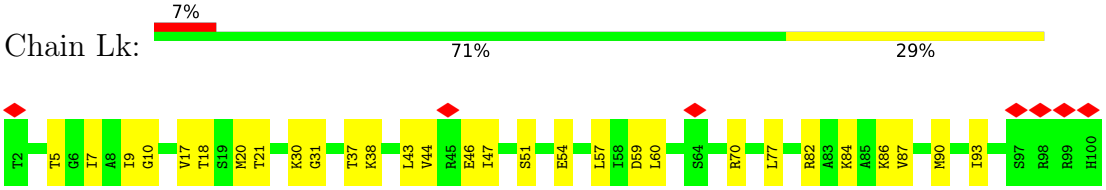
• Molecule 36: Large ribosomal subunit protein uL29A

Chain Lj:



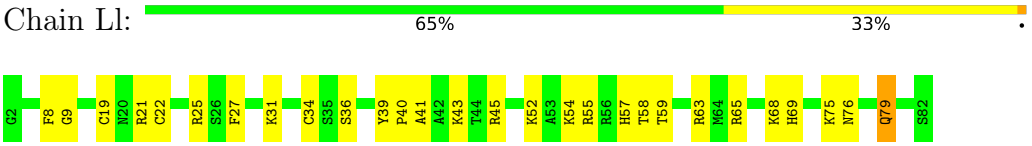
• Molecule 37: Large ribosomal subunit protein eL36A

Chain Lk:



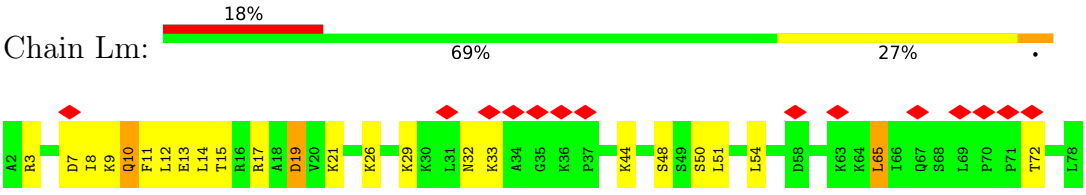
• Molecule 38: Large ribosomal subunit protein eL37A

Chain Ll:



• Molecule 39: Large ribosomal subunit protein eL38

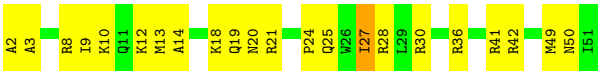
Chain Lm:



• Molecule 40: Large ribosomal subunit protein eL39

Chain Ln:





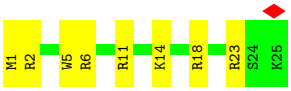
• Molecule 41: Large ribosomal subunit protein eL40A





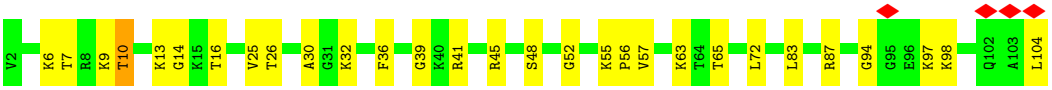
• Molecule 42: Large ribosomal subunit protein eL41A





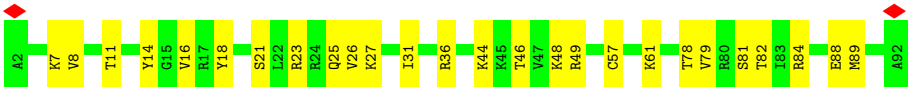
• Molecule 43: Large ribosomal subunit protein eL42A





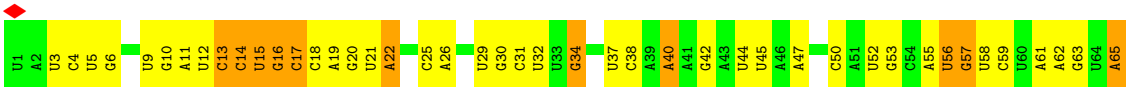
• Molecule 44: Large ribosomal subunit protein eL43A

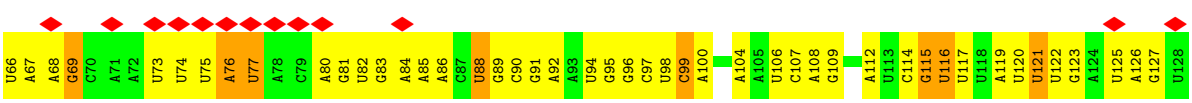


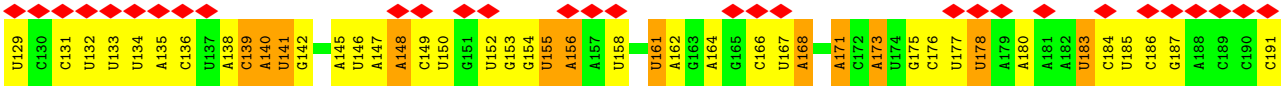


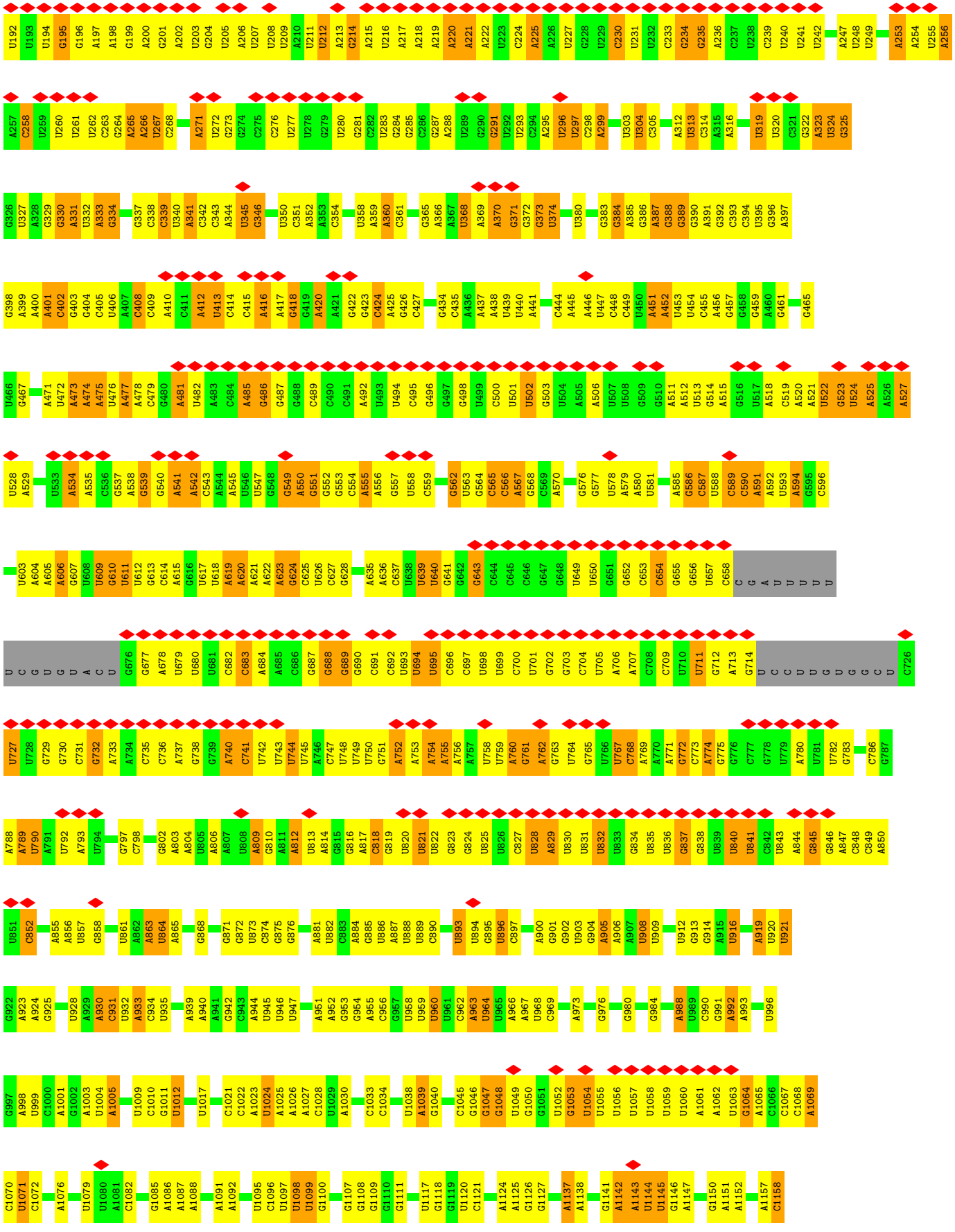
• Molecule 45: chain 2 18S rRNA (1799-MER)







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A257 C258 U259 U260 U261 U262 C263 G264 A265 A266 U267 C268 A271 U272 G273 G274 C275 C276 U277 U278 C279 U280 G281 C282 U283 G284 G285 C286 G287 A288 U289 G290 G291 U292 U293 C294 A295 U296 U297 C298 A299 U303 U304 C305 A312 U313 C314 A315 A316 U319 U320 C321 G322 A323 U324 G325
G326 U327 A328 G329 G330 A331 U332 A333 G334 G337 C338 G339 U340 A341 C342 C343 A344 U345 G346 U350 C351 A352 A353 C354 U358 A359 A360 C361 G365 A366 A367 U368 A369 A370 G371 G372 G373 U374 U380 G383 G384 A385 G386 A387 G388 G389 G390 A391 G392 C393 C394 U395 G396 A397
G398 A399 A400 A401 C402 G403 G404 C405 U406 A407 C408 C409 A410 C411 A412 U413 C414 C415 A416 A417 G418 G419 A420 A421 G422 G423 C424 A425 G426 C427 G434 C435 A436 A437 A438 U439 U440 A441 C444 A445 A446 U447 C448 C449 U450 A451 A452 U453 U454 C455 A456 G457 G458 G459 A460 G461 G465
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U528 A529 U533 A534 A535 C536 G537 A538 G539 G540 A541 A542 C543 A544 A545 U546 U547 G548 G549 A550 G551 G552 G553 C554 A555 A556 G557 U558 C559 G562 U563 G564 C565 C566 A567 G568 C569 A570 G576 G577 U578 A579 A580 U581 A585 G586 C587 U588 C589 C590 A591 A592 U593 A594 G595 C596
U603 A604 A605 A606 G607 U608 U609 C610 U611 U612 C613 C614 A615 G616 U617 U618 A619 A620 A621 A622 A623 G624 C625 U626 C627 G628 A635 A636 C637 U638 U639 U640 G641 G642 G643 C644 C645 C646 G647 G648 U649 U650 G651 C652 C653 C654 G655 G656 U657 C658 C G A U U U U U
U G676 G677 A678 U679 U680 U681 C682 C683 A684 A685 C686 G687 G688 G689 G690 C691 C692 U693 U694 U695 C696 C697 U698 U699 C700 U701 G702 G703 C704 U705 A706 A707 C708 C709 U710 U711 G712 A713 G714 U C C U U G U G G C U C726
U727 U728 G729 G730 C731 G732 A733 A734 C735 C736 A737 G738 G739 A740 C741 U742 U743 U744 U745 A746 C747 U748 U749 U750 G751 A752 A753 A754 A755 A756 A757 U758 U759 A760 G761 A762 G763 U764 G765 U766 U767 C768 A769 A770 A771 G772 C773 A774 G775 G776 C777 G778 U779 A780 U781 U782 G783 C786 G787
A788 A789 U790 A791 U792 A793 U794 G797 C798 G802 A803 A804 U805 A806 A807 U808 A809 G810 A811 A812 U813 A814 G815 G816 A817 C818 G819 U820 U821 U822 G823 G824 U825 U826 C827 U828 A829 U830 U831 U832 U833 G834 U835 U836 G837 G838 U839 U840 U841 C842 A843 A844 G845 G846 A847 C848 C849 A850
U851 C852 A855 A856 U857 G858 U861 A862 A863 U864 A865 G868 G871 G872 U873 C874 G875 G876 A881 U882 C883 A884 G885 U886 A887 U888 U889 C890 U893 U894 G895 U896 C897 A900 G901 G902 U903 G904 A905 A906 A907 U908 U909 U912 G913 G914 A915 U916 A919 U920 U921
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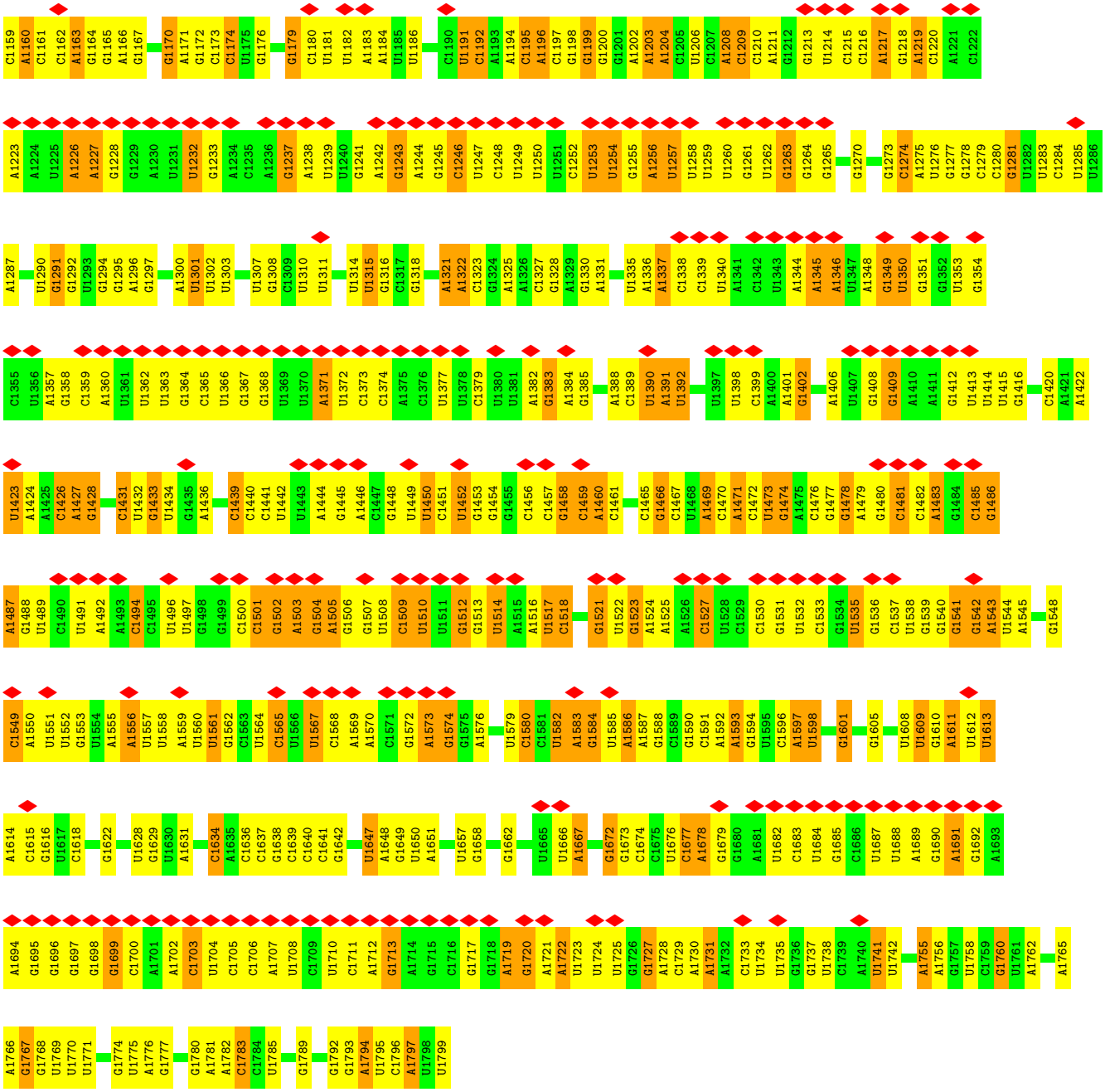
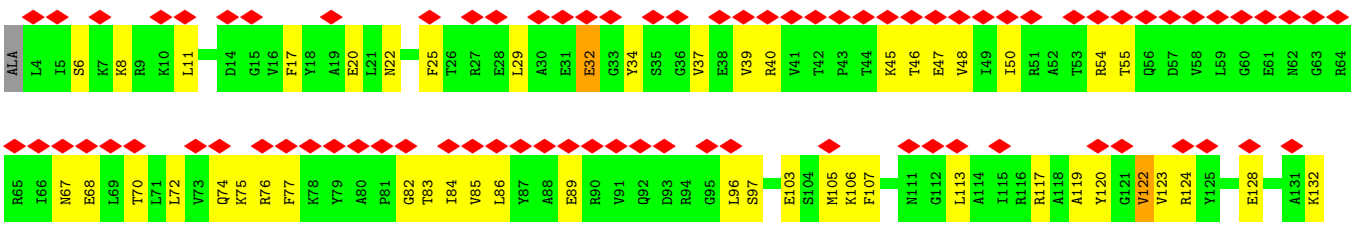
C1070 U1071 C1072 A1076 U1079 U1080 A1081 C1082 G1085 A1086 A1087 A1088 A1091 A1092 U1095 C1096 U1097 U1098 U1099 G1100 G1107 G1108 G1109 G1110 G1111 U1117 G1118 G1119 U1120 C1121 A1124 A1125 G1126 G1127 A1137 A1138 G1141 A1142 A1143 U1144 U1145 G1146 A1147 G1150 A1151 A1152 A1157 C1158

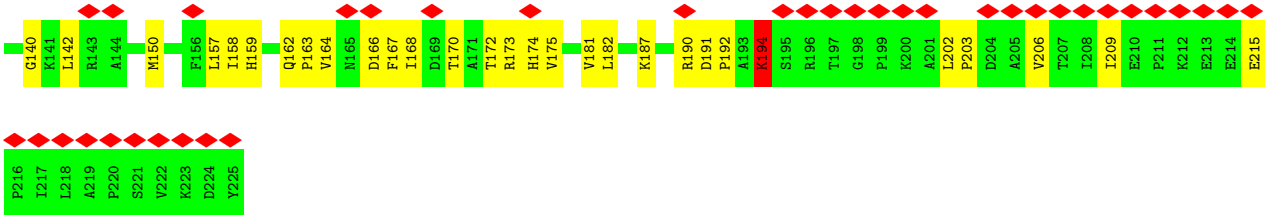


• Molecule 46: Small ribosomal subunit protein uS3

Chain SA:







• Molecule 47: Small ribosomal subunit protein uS7

Chain SB:

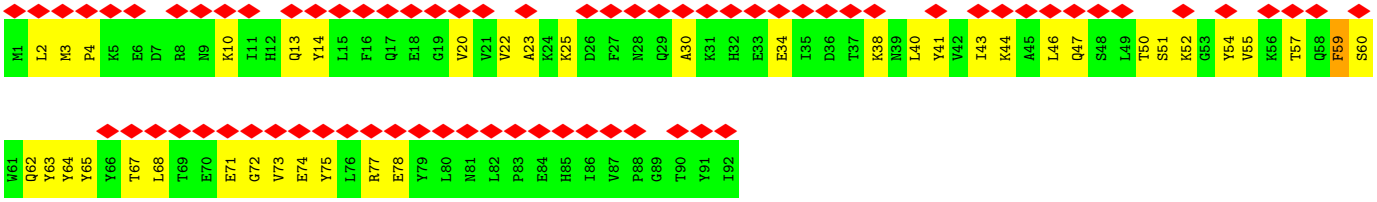




• Molecule 48: Small ribosomal subunit protein eS10A

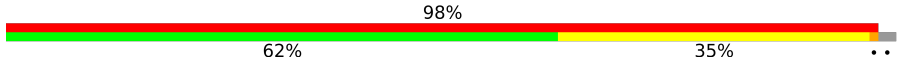
Chain SC:

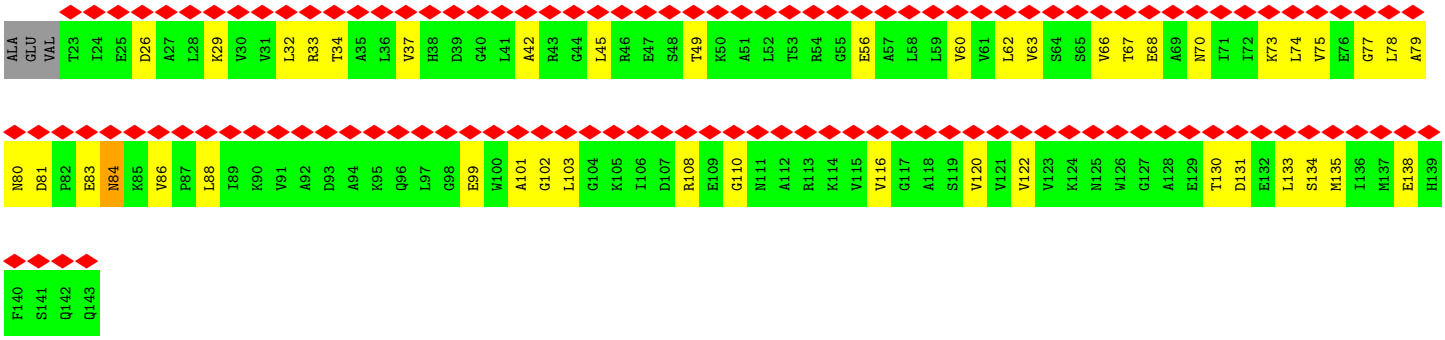




• Molecule 49: Small ribosomal subunit protein eS12

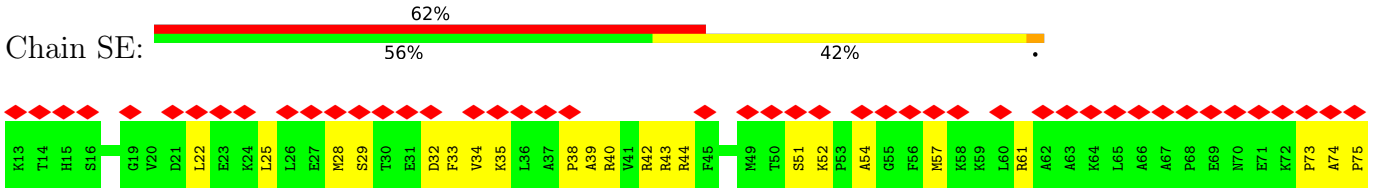
Chain SD:





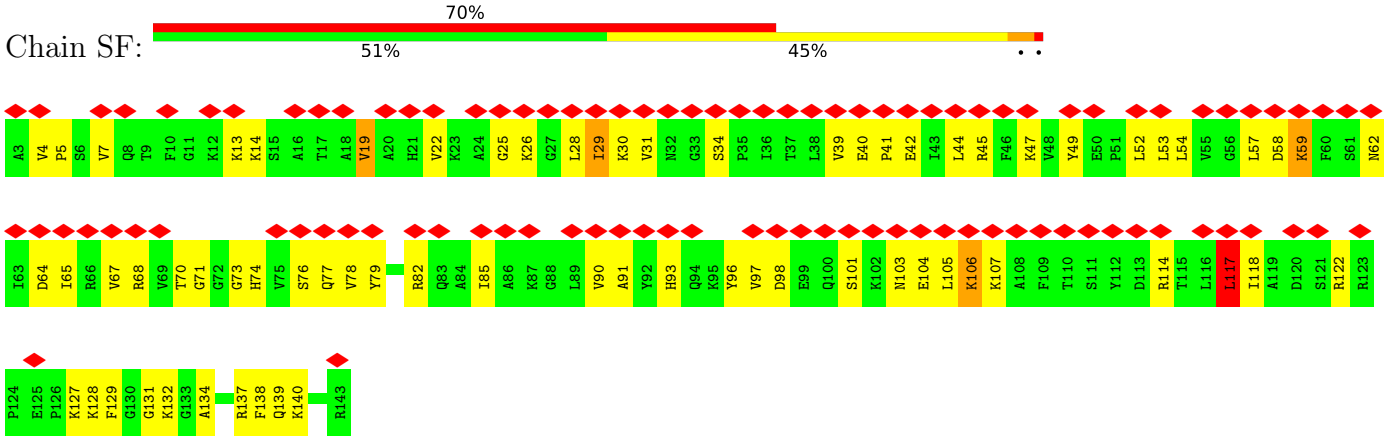
• Molecule 50: Small ribosomal subunit protein uS19

Chain SE:



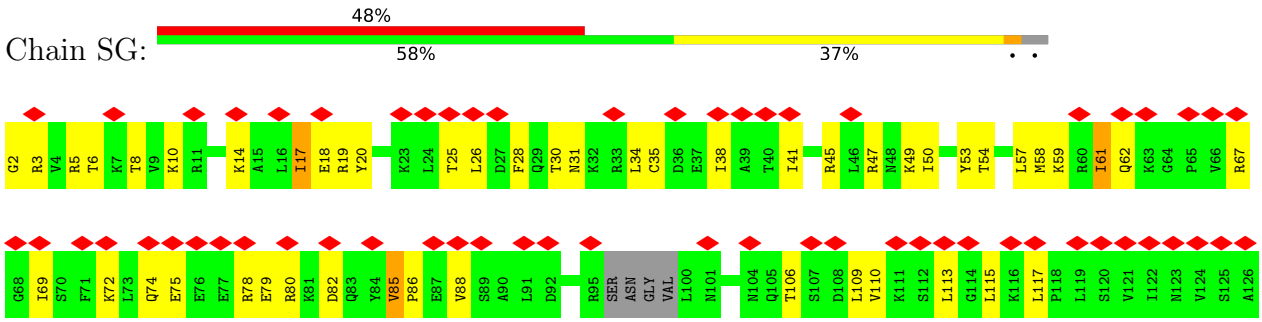
• Molecule 51: Small ribosomal subunit protein uS9A

Chain SF:



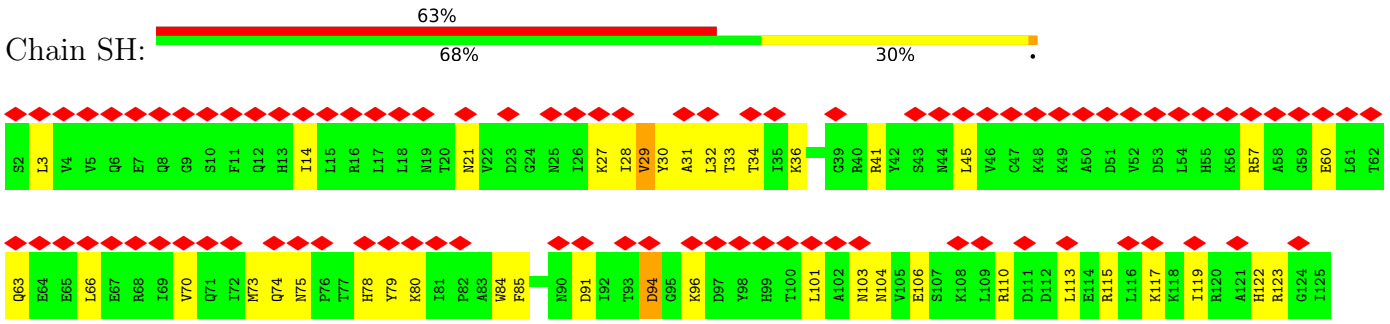
• Molecule 52: Small ribosomal subunit protein eS17A

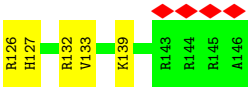
Chain SG:



• Molecule 53: Small ribosomal subunit protein uS13A

Chain SH:

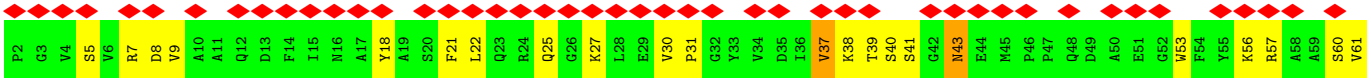


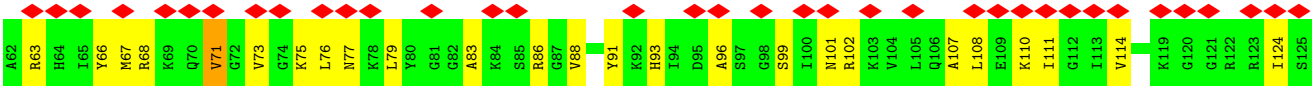


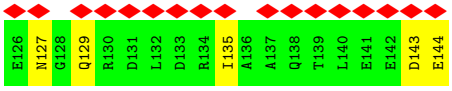
• Molecule 54: Small ribosomal subunit protein eS19A

Chain SI:





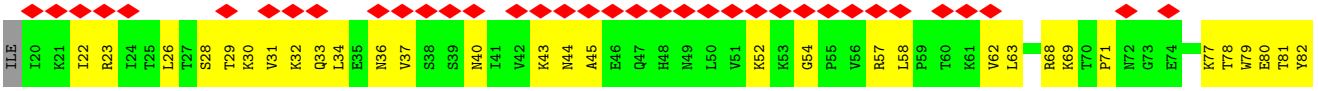




• Molecule 55: Small ribosomal subunit protein uS10

Chain SJ:

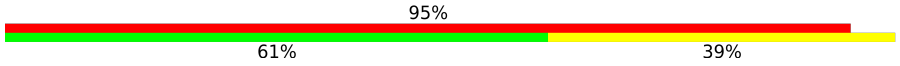


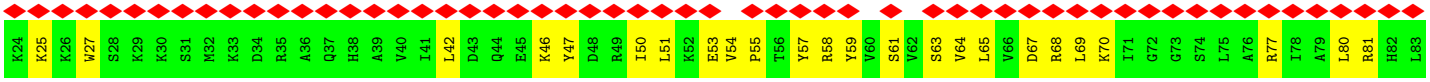


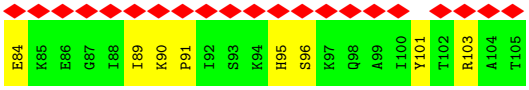


• Molecule 56: Small ribosomal subunit protein eS25A

Chain SK:



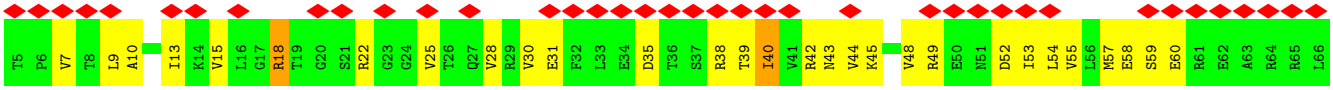




• Molecule 57: Small ribosomal subunit protein eS28A

Chain SL:



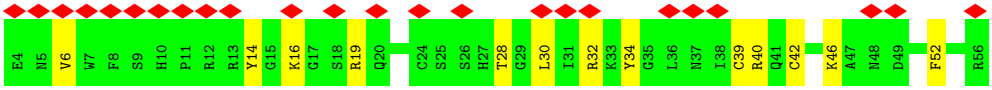




• Molecule 58: Small ribosomal subunit protein uS14A

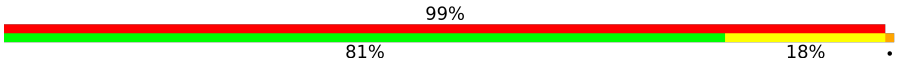
Chain SM:

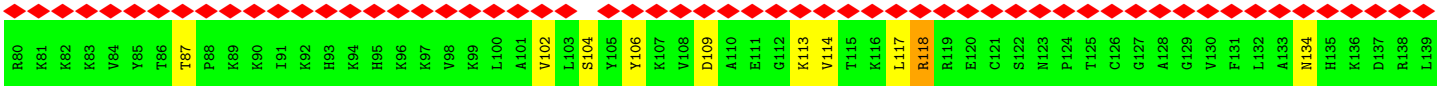


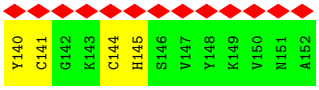


• Molecule 59: Small ribosomal subunit protein eS31

Chain SN:

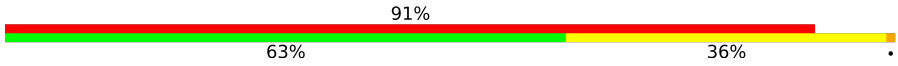




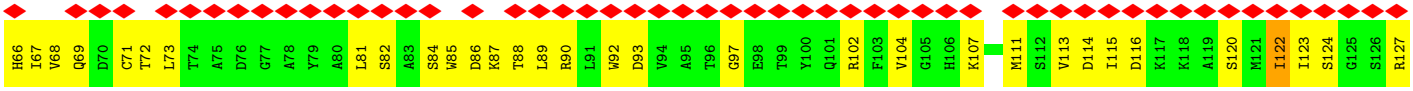


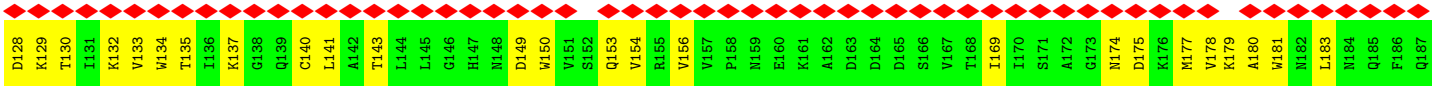
• Molecule 60: Small ribosomal subunit protein RACK1

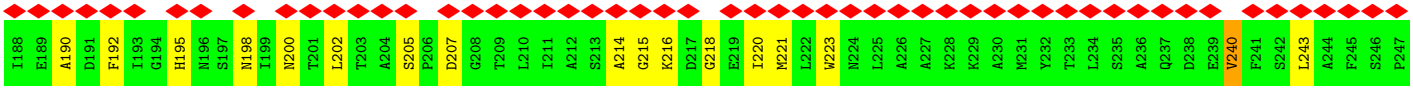
Chain SO:

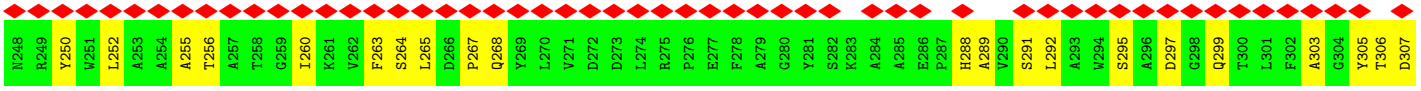


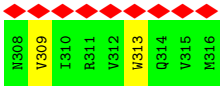






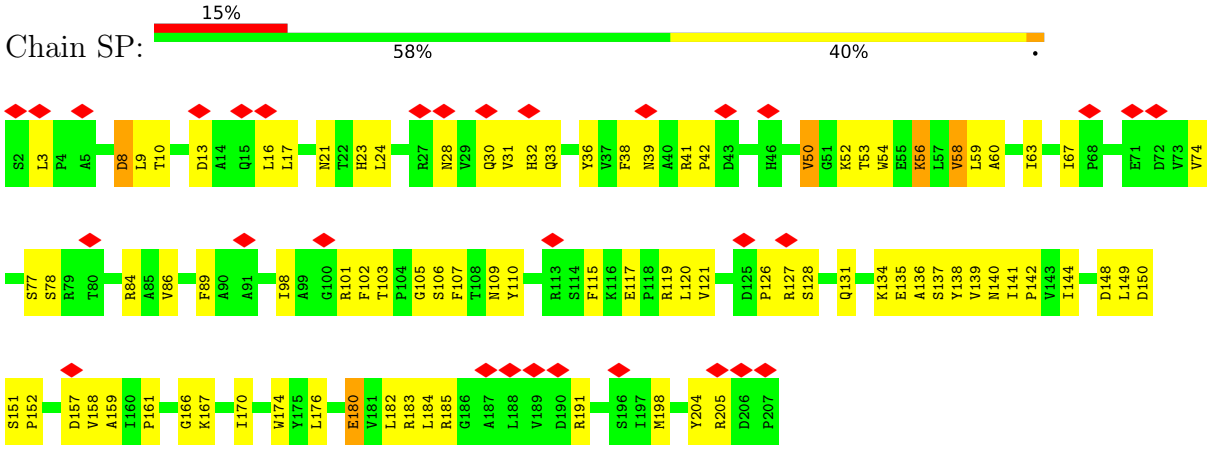






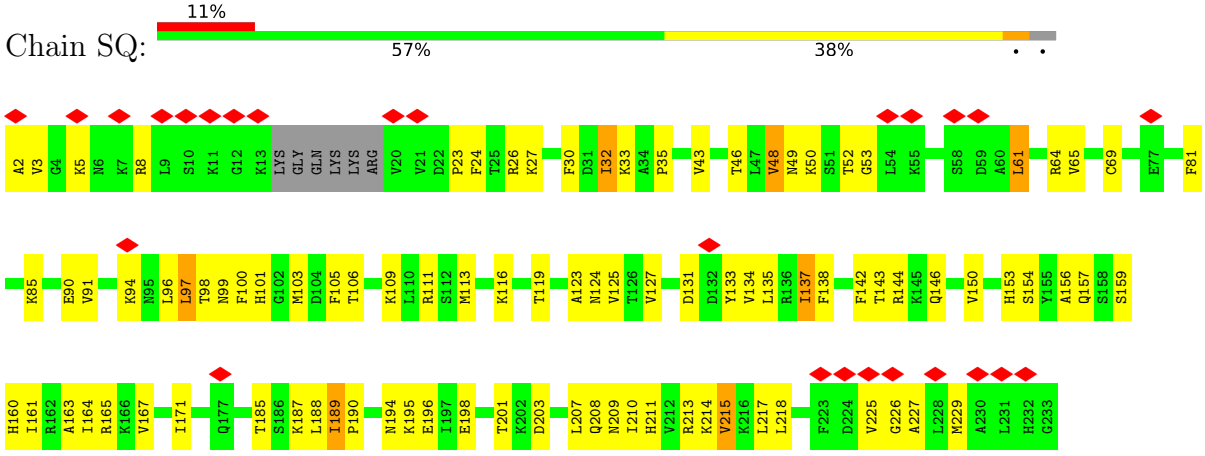
• Molecule 61: Small ribosomal subunit protein uS2A

Chain SP:



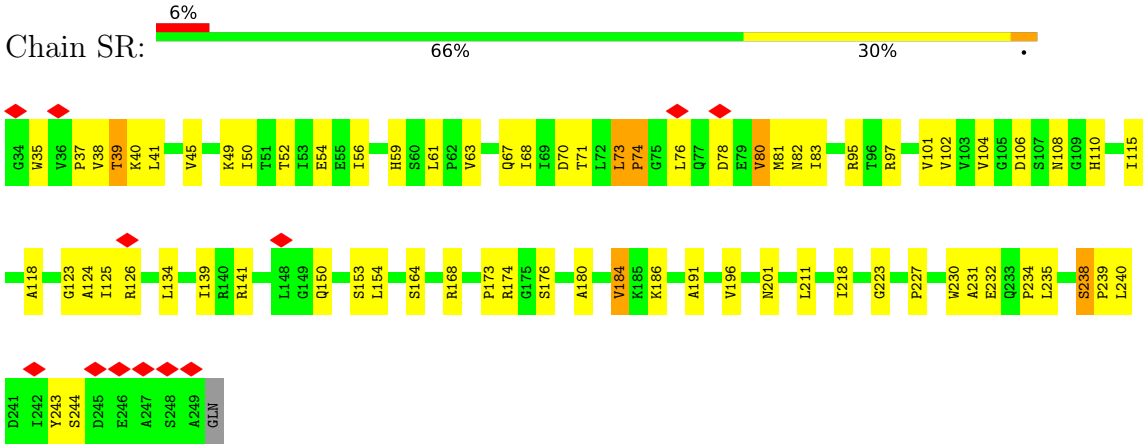
• Molecule 62: Small ribosomal subunit protein eS1A

Chain SQ:



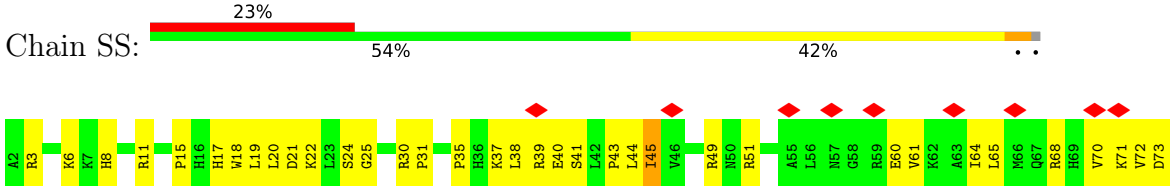
• Molecule 63: Small ribosomal subunit protein uS5

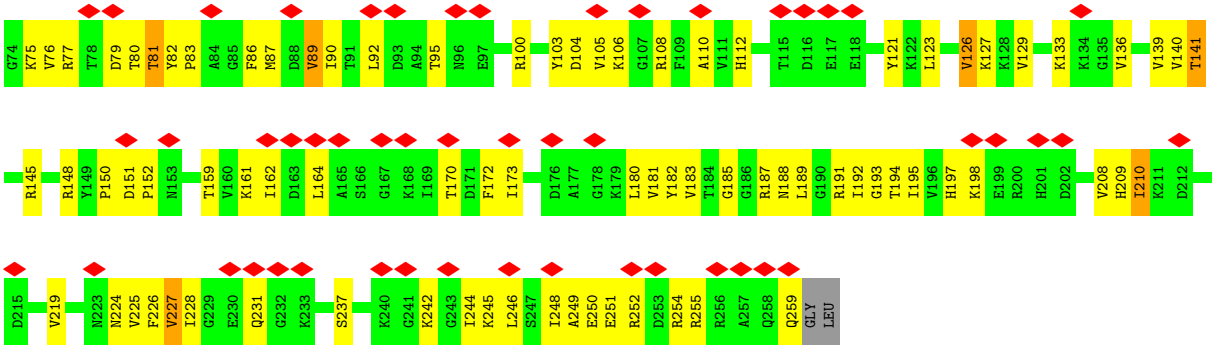
Chain SR:



• Molecule 64: Small ribosomal subunit protein eS4A

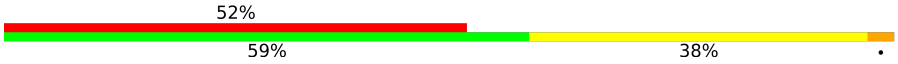
Chain SS:

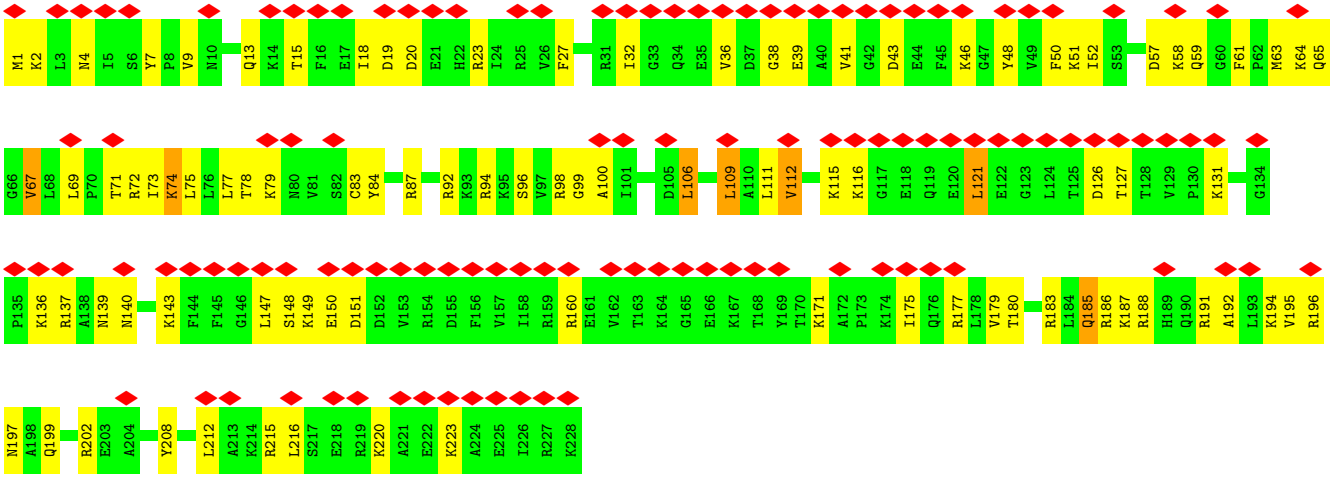




• Molecule 65: Small ribosomal subunit protein eS6A

Chain ST:

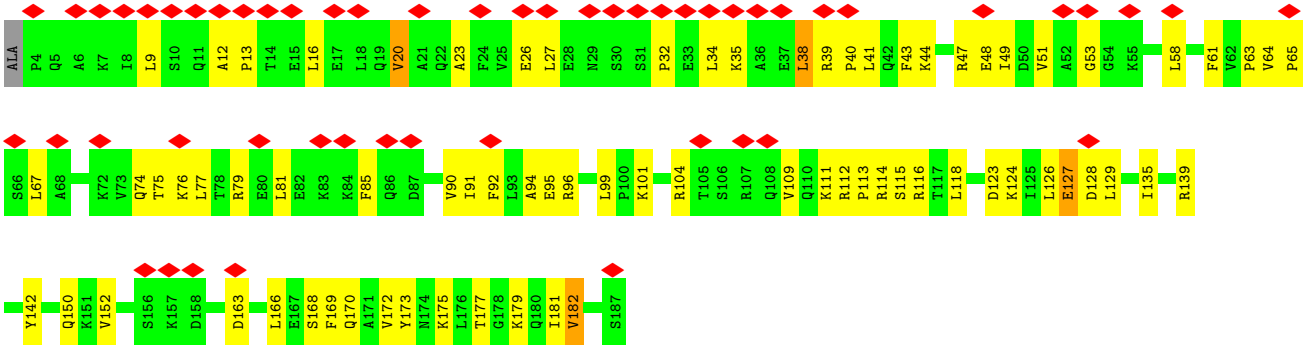




• Molecule 66: Small ribosomal subunit protein eS7A

Chain SU:

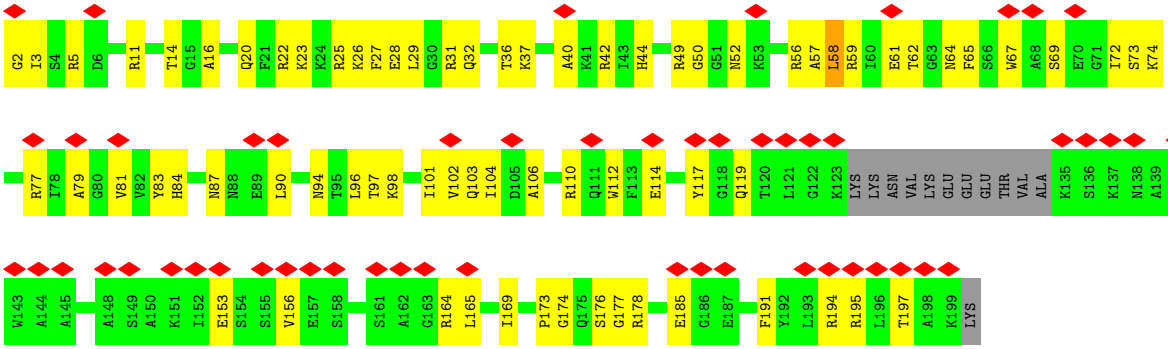




• Molecule 67: Small ribosomal subunit protein eS8A

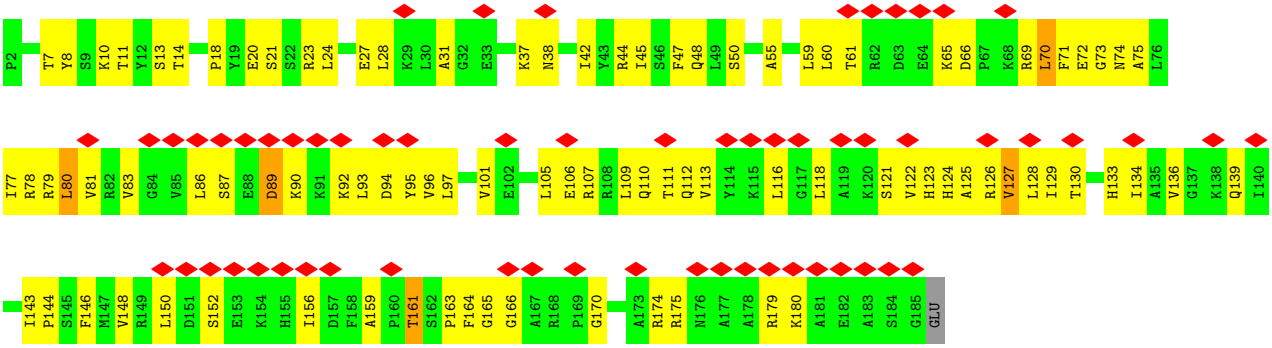
Chain SV:



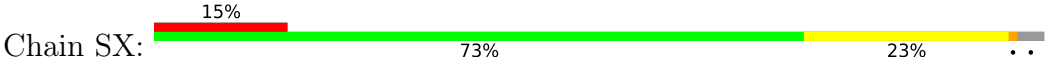


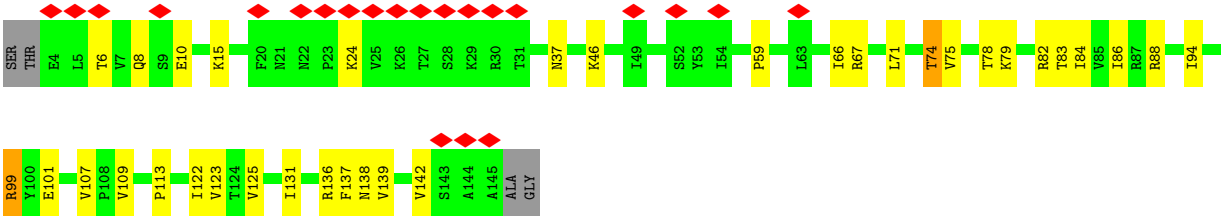
• Molecule 68: Small ribosomal subunit protein uS4A





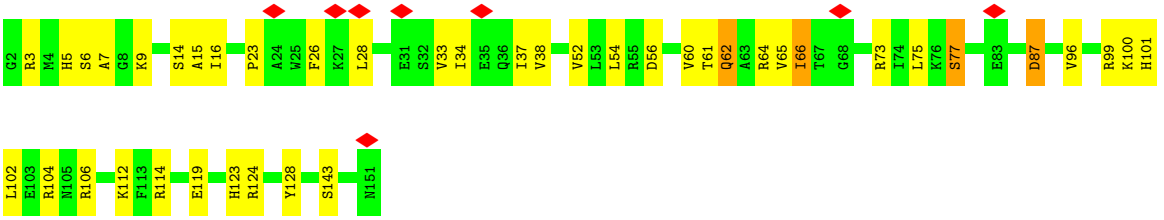
• Molecule 69: Small ribosomal subunit protein uS17A





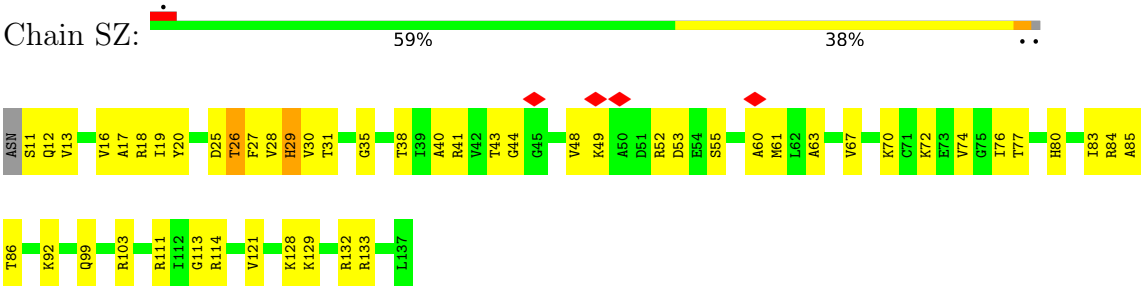
• Molecule 70: Small ribosomal subunit protein uS15





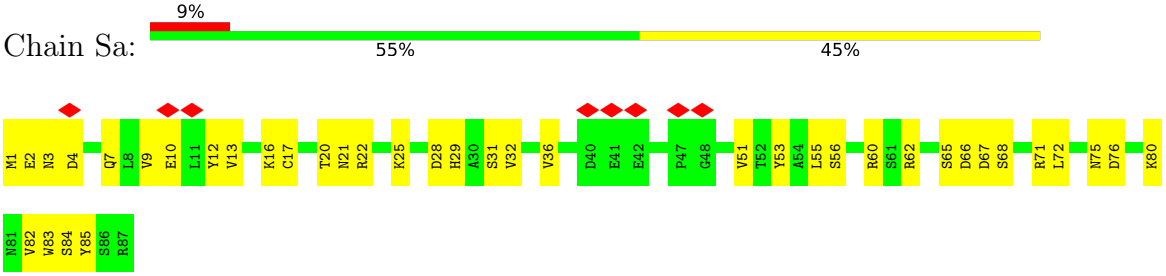
• Molecule 71: Small ribosomal subunit protein uS11B

Chain SZ:



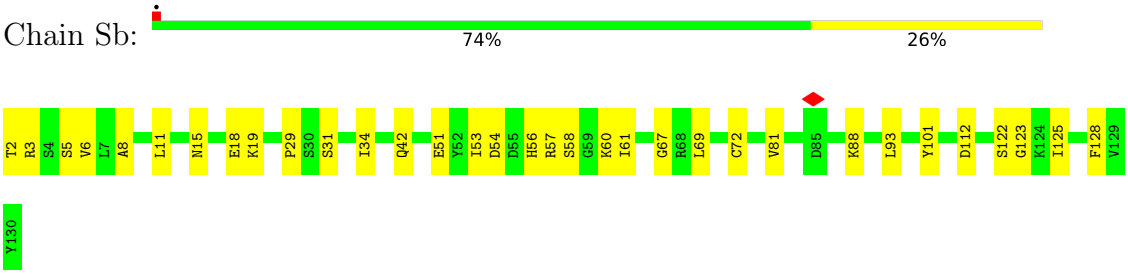
• Molecule 72: Small ribosomal subunit protein eS21A

Chain Sa:



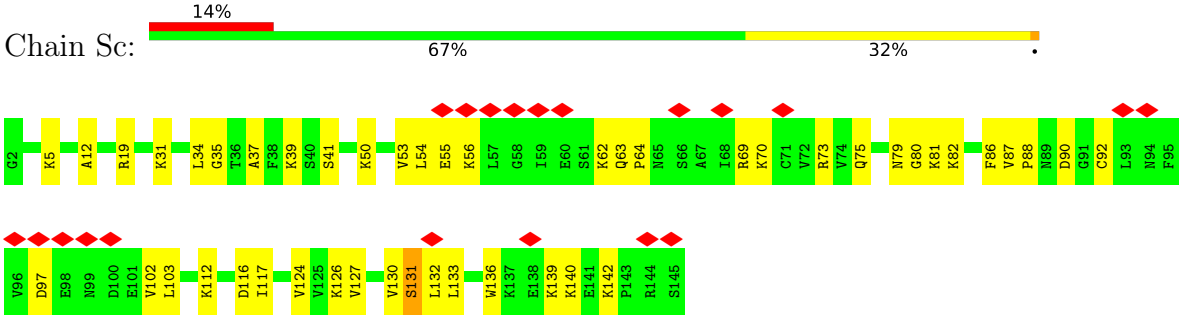
• Molecule 73: Small ribosomal subunit protein uS8A

Chain Sb:



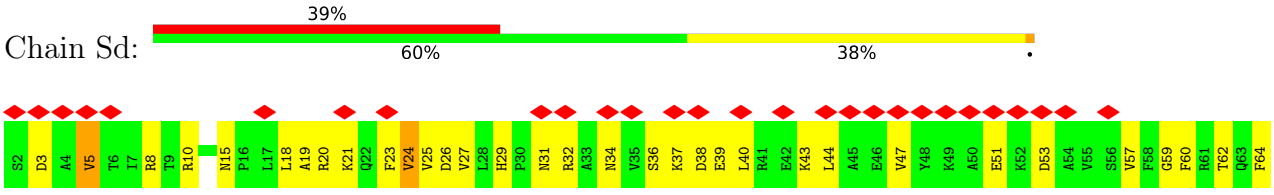
• Molecule 74: Small ribosomal subunit protein uS12A

Chain Sc:



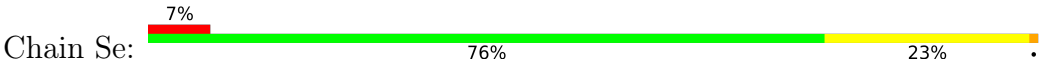
• Molecule 75: Small ribosomal subunit protein eS24A

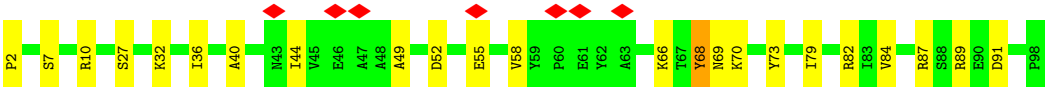
Chain Sd:





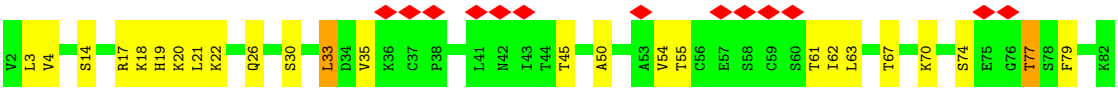
• Molecule 76: Small ribosomal subunit protein eS26B



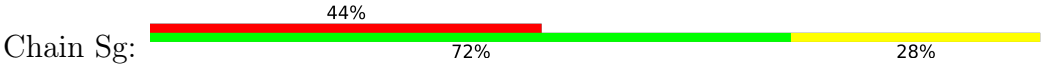


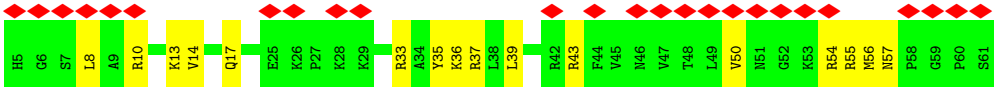
• Molecule 77: Small ribosomal subunit protein eS27A



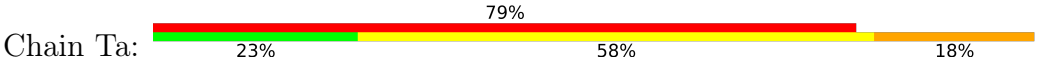


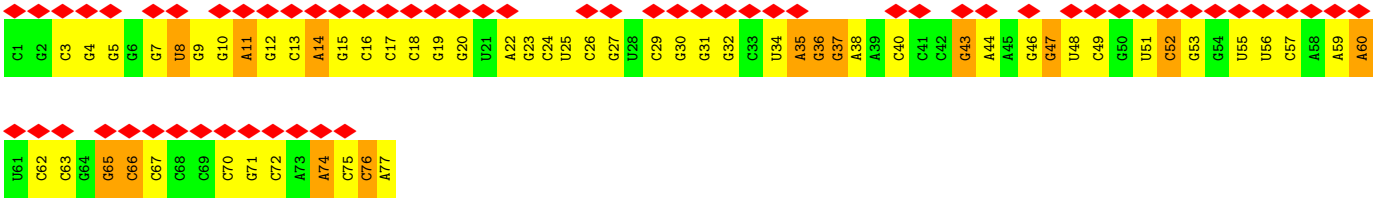
• Molecule 78: Small ribosomal subunit protein eS30A





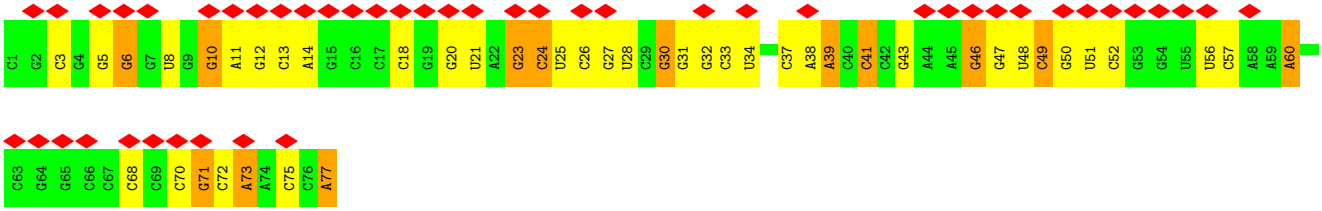
• Molecule 79: tRNA (77-MER)





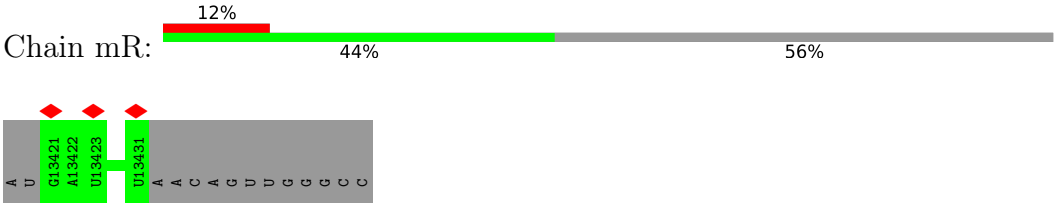
• Molecule 80: tRNA (77-MER)





• Molecule 81: RNA (5'-R(P*GP*AP*UP*UP*GP*AP*CP*CP*CP*UP*U)-3')

Chain mR:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84473	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.367	Depositor
Minimum map value	-1.707	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.085	Depositor
Recommended contour level	0.26	Depositor
Map size (Å)	570.0, 570.0, 570.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	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	LA	0.14	0/76214	0.32	0/118821
2	LB	0.13	0/2883	0.29	0/4491
3	LC	0.13	0/3746	0.30	0/5832
4	LD	0.17	0/1933	0.39	0/2598
5	LE	0.16	0/3146	0.38	0/4228
6	LF	0.17	0/2800	0.39	0/3790
7	LG	0.16	0/2400	0.40	1/3239 (0.0%)
8	LH	0.16	0/1329	0.36	0/1794
9	LI	0.16	0/1821	0.37	0/2451
10	LJ	0.16	0/1836	0.39	0/2481
11	LK	0.20	0/1529	0.40	0/2060
12	LL	0.27	2/1801 (0.1%)	0.43	2/2416 (0.1%)
13	LM	0.17	0/1367	0.39	0/1834
14	LN	0.19	0/1568	0.40	0/2106
15	LO	0.30	1/1068 (0.1%)	0.43	1/1438 (0.1%)
16	LP	0.16	0/1757	0.38	0/2354
17	LQ	0.18	0/1585	0.37	0/2128
18	LR	0.15	0/1439	0.36	0/1938
19	LS	0.16	0/1465	0.38	0/1965
20	LT	0.17	0/1532	0.32	0/2043
21	LU	0.19	0/1473	0.37	0/1980
22	LV	0.17	0/1296	0.34	0/1739
23	LW	0.14	0/812	0.39	0/1099
24	LX	0.15	0/1018	0.36	0/1369
25	LY	0.14	0/540	0.31	0/717
26	LZ	0.14	0/979	0.34	0/1321
27	La	0.14	0/995	0.33	0/1329
28	Lb	0.17	0/1106	0.38	0/1485
29	Lc	0.17	0/1200	0.38	0/1607
30	Ld	0.19	0/473	0.38	0/629
31	Le	0.14	0/745	0.33	0/1001
32	Lf	0.25	1/890 (0.1%)	0.34	0/1196
33	Lg	0.16	0/1038	0.34	0/1390
34	Lh	0.15	0/868	0.36	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	Li	0.15	0/890	0.33	0/1189
36	Lj	0.17	0/978	0.41	1/1301 (0.1%)
37	Lk	0.17	0/772	0.39	0/1026
38	Ll	0.18	0/660	0.37	0/875
39	Lm	0.15	0/618	0.42	1/826 (0.1%)
40	Ln	0.18	0/443	0.33	0/588
41	Lo	0.13	0/416	0.34	0/553
42	Lp	0.14	0/230	0.35	0/296
43	Lq	0.52	2/836 (0.2%)	0.52	1/1104 (0.1%)
44	Lr	0.15	0/701	0.36	0/934
45	S2	0.12	0/42211	0.31	0/65773
46	SA	0.28	0/1754	0.47	1/2361 (0.0%)
47	SB	0.18	0/1625	0.44	0/2197
48	SC	0.12	0/769	0.36	0/1039
49	SD	0.26	0/883	0.61	0/1199
50	SE	0.15	0/936	0.39	0/1259
51	SF	0.24	0/1125	0.49	2/1510 (0.1%)
52	SG	0.18	0/957	0.38	0/1283
53	SH	0.17	0/1207	0.38	0/1623
54	SI	0.17	0/1130	0.42	0/1517
55	SJ	0.15	0/807	0.40	0/1091
56	SK	0.20	0/661	0.41	0/888
57	SL	0.19	0/493	0.40	0/663
58	SM	0.10	0/452	0.28	0/600
59	SN	0.13	0/567	0.47	1/764 (0.1%)
60	SO	0.18	0/2436	0.43	0/3318
61	SP	0.18	0/1644	0.42	0/2249
62	SQ	0.32	1/1823 (0.1%)	0.48	1/2447 (0.0%)
63	SR	0.28	0/1656	0.56	4/2251 (0.2%)
64	SS	0.17	0/2097	0.43	0/2823
65	ST	0.15	0/1839	0.39	0/2460
66	SU	0.19	0/1498	0.45	0/2019
67	SV	0.17	0/1501	0.36	0/2006
68	SW	0.33	1/1504 (0.1%)	0.59	4/2016 (0.2%)
69	SX	0.15	0/1168	0.35	0/1575
70	SY	0.16	0/1215	0.39	0/1638
71	SZ	0.21	0/934	0.46	0/1257
72	Sa	0.15	0/682	0.37	0/921
73	Sb	0.18	0/1038	0.44	0/1395
74	Sc	0.16	0/1139	0.44	0/1518
75	Sd	0.15	0/1046	0.32	0/1401
76	Se	0.14	0/778	0.42	0/1042
77	Sf	0.15	0/620	0.37	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	Sg	0.15	0/459	0.38	0/611
79	Ta	0.13	0/1844	0.36	0/2873
80	Tb	0.11	0/1837	0.28	0/2861
All	All	0.16	8/217531 (0.0%)	0.35	20/320015 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	LJ	0	1
16	LP	0	1
30	Ld	0	1
73	Sb	0	1
All	All	0	4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	Lq	55	LYS	C-O	-9.04	1.16	1.24
62	SQ	189	ILE	CA-CB	-7.25	1.50	1.54
12	LL	213	PHE	C-O	6.68	1.27	1.23
68	SW	159	ALA	C-N	6.08	1.39	1.33
32	Lf	51	LEU	C-N	-5.79	1.24	1.33

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
12	LL	214	PRO	N-CD-CG	-10.43	87.55	103.20
68	SW	166	GLY	N-CA-C	9.91	123.74	111.85
68	SW	165	GLY	N-CA-C	-9.02	91.80	113.18
51	SF	117	LEU	CB-CG-CD1	-8.99	83.72	110.70
46	SA	194	LYS	N-CA-C	-8.32	101.56	113.21

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	LJ	30	THR	Peptide
16	LP	75	VAL	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
30	Ld	20	GLY	Peptide
73	Sb	54	ASP	Peptide

5.2 Too-close contacts (i)

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	LA	68091	0	34217	1099	0
2	LB	2579	0	1304	37	0
3	LC	3353	0	1695	73	0
4	LD	1899	0	1957	68	0
5	LE	3075	0	3142	86	0
6	LF	2748	0	2859	85	0
7	LG	2351	0	2294	74	0
8	LH	1307	0	1377	35	0
9	LI	1784	0	1862	52	0
10	LJ	1804	0	1877	51	0
11	LK	1508	0	1572	41	0
12	LL	1764	0	1804	57	0
13	LM	1346	0	1370	50	0
14	LN	1543	0	1608	58	0
15	LO	1053	0	1149	53	0
16	LP	1720	0	1779	55	0
17	LQ	1555	0	1659	44	0
18	LR	1416	0	1433	36	0
19	LS	1441	0	1543	44	0
20	LT	1515	0	1606	34	0
21	LU	1437	0	1475	36	0
22	LV	1272	0	1312	42	0
23	LW	796	0	812	27	0
24	LX	1003	0	1048	23	0
25	LY	528	0	546	19	0
26	LZ	964	0	1025	28	0
27	La	984	0	1075	35	0
28	Lb	1080	0	1122	28	0
29	Lc	1169	0	1211	49	0
30	Ld	462	0	491	16	0
31	Le	737	0	792	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	Lf	876	0	912	22	0
33	Lg	1017	0	1081	25	0
34	Lh	850	0	880	18	0
35	Li	880	0	945	35	0
36	Lj	969	0	1078	31	0
37	Lk	766	0	844	23	0
38	Ll	645	0	649	29	0
39	Lm	612	0	682	18	0
40	Ln	436	0	475	19	0
41	Lo	410	0	446	15	0
42	Lp	229	0	273	9	0
43	Lq	824	0	892	22	0
44	Lr	694	0	738	21	0
45	S2	37739	0	18988	798	0
46	SA	1729	0	1812	63	0
47	SB	1605	0	1669	101	0
48	SC	752	0	719	33	0
49	SD	875	0	878	33	0
50	SE	916	0	941	46	0
51	SF	1105	0	1166	61	0
52	SG	948	0	990	44	0
53	SH	1188	0	1218	44	0
54	SI	1112	0	1124	55	0
55	SJ	797	0	863	43	0
56	SK	651	0	682	30	0
57	SL	491	0	524	35	0
58	SM	442	0	432	12	0
59	SN	556	0	549	11	0
60	SO	2383	0	2332	96	0
61	SP	1603	0	1610	64	0
62	SQ	1798	0	1890	99	0
63	SR	1626	0	1715	47	0
64	SS	2056	0	2140	103	0
65	ST	1815	0	1894	72	0
66	SU	1473	0	1555	72	0
67	SV	1476	0	1501	61	0
68	SW	1479	0	1556	81	0
69	SX	1142	0	1209	28	0
70	SY	1192	0	1255	33	0
71	SZ	923	0	948	54	0
72	Sa	673	0	662	30	0
73	Sb	1021	0	1060	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
74	Sc	1121	0	1196	37	0
75	Sd	1032	0	1044	46	0
76	Se	765	0	814	20	0
77	Sf	610	0	633	22	0
78	Sg	451	0	494	20	0
79	Ta	1650	0	838	21	0
80	Tb	1645	0	837	16	0
81	mR	230	0	0	0	0
All	All	202562	0	148649	4350	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 13.

The worst 5 of 4350 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)
45:S2:752:A:N6	45:S2:797:G:H1	1.31	1.26
1:LA:3233:A:N6	1:LA:3252:G:H1	1.43	1.15
1:LA:1645:G:N2	1:LA:1808:A:H62	1.51	1.07
45:S2:220:A:N6	45:S2:841:U:H3	1.53	1.05
45:S2:761:G:N2	45:S2:789:A:H62	1.54	1.04

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LD	249/251 (99%)	236 (95%)	13 (5%)	0	100	100
5	LE	384/386 (100%)	356 (93%)	28 (7%)	0	100	100
6	LF	359/361 (99%)	333 (93%)	26 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	LG	292/294 (99%)	275 (94%)	17 (6%)	0	100	100
8	LH	163/175 (93%)	154 (94%)	9 (6%)	0	100	100
9	LI	220/222 (99%)	210 (96%)	10 (4%)	0	100	100
10	LJ	231/233 (99%)	217 (94%)	14 (6%)	0	100	100
11	LK	189/191 (99%)	176 (93%)	13 (7%)	0	100	100
12	LL	216/218 (99%)	208 (96%)	8 (4%)	0	100	100
13	LM	167/169 (99%)	158 (95%)	9 (5%)	0	100	100
14	LN	191/193 (99%)	174 (91%)	17 (9%)	0	100	100
15	LO	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
16	LP	201/203 (99%)	188 (94%)	11 (6%)	2 (1%)	12	28
17	LQ	195/197 (99%)	193 (99%)	2 (1%)	0	100	100
18	LR	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
19	LS	183/185 (99%)	174 (95%)	9 (5%)	0	100	100
20	LT	186/188 (99%)	181 (97%)	5 (3%)	0	100	100
21	LU	169/171 (99%)	162 (96%)	7 (4%)	0	100	100
22	LV	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
23	LW	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
24	LX	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
25	LY	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
26	LZ	119/121 (98%)	117 (98%)	2 (2%)	0	100	100
27	La	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
28	Lb	133/135 (98%)	122 (92%)	11 (8%)	0	100	100
29	Lc	146/148 (99%)	136 (93%)	10 (7%)	0	100	100
30	Ld	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
31	Le	94/96 (98%)	94 (100%)	0	0	100	100
32	Lf	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
33	Lg	125/127 (98%)	119 (95%)	6 (5%)	0	100	100
34	Lh	104/106 (98%)	99 (95%)	5 (5%)	0	100	100
35	Li	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
36	Lj	117/119 (98%)	110 (94%)	7 (6%)	0	100	100
37	Lk	97/99 (98%)	91 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	Ll	79/81 (98%)	77 (98%)	2 (2%)	0	100	100
39	Lm	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
40	Ln	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
41	Lo	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
42	Lp	23/25 (92%)	23 (100%)	0	0	100	100
43	Lq	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
44	Lr	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
46	SA	220/223 (99%)	211 (96%)	9 (4%)	0	100	100
47	SB	204/206 (99%)	191 (94%)	12 (6%)	1 (0%)	24	46
48	SC	90/92 (98%)	81 (90%)	9 (10%)	0	100	100
49	SD	119/124 (96%)	90 (76%)	29 (24%)	0	100	100
50	SE	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
51	SF	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
52	SG	117/125 (94%)	117 (100%)	0	0	100	100
53	SH	143/145 (99%)	137 (96%)	6 (4%)	0	100	100
54	SI	141/143 (99%)	131 (93%)	10 (7%)	0	100	100
55	SJ	98/101 (97%)	93 (95%)	5 (5%)	0	100	100
56	SK	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
57	SL	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
58	SM	51/53 (96%)	50 (98%)	1 (2%)	0	100	100
59	SN	71/73 (97%)	56 (79%)	15 (21%)	0	100	100
60	SO	310/312 (99%)	283 (91%)	27 (9%)	0	100	100
61	SP	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
62	SQ	222/232 (96%)	201 (90%)	21 (10%)	0	100	100
63	SR	214/217 (99%)	202 (94%)	12 (6%)	0	100	100
64	SS	256/260 (98%)	229 (90%)	27 (10%)	0	100	100
65	ST	226/228 (99%)	213 (94%)	11 (5%)	2 (1%)	14	30
66	SU	182/185 (98%)	169 (93%)	13 (7%)	0	100	100
67	SV	183/199 (92%)	176 (96%)	7 (4%)	0	100	100
68	SW	182/185 (98%)	172 (94%)	10 (6%)	0	100	100
69	SX	140/146 (96%)	134 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	SY	148/150 (99%)	136 (92%)	12 (8%)	0	100	100
71	SZ	125/128 (98%)	114 (91%)	11 (9%)	0	100	100
72	Sa	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
73	Sb	127/129 (98%)	115 (91%)	12 (9%)	0	100	100
74	Sc	142/144 (99%)	126 (89%)	16 (11%)	0	100	100
75	Sd	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
76	Se	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
77	Sf	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
78	Sg	55/57 (96%)	47 (86%)	8 (14%)	0	100	100
All	All	10914/11115 (98%)	10242 (94%)	667 (6%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
65	ST	177	ARG
65	ST	175	ILE
47	SB	162	VAL
16	LP	78	GLY
16	LP	76	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LD	190/193 (98%)	187 (98%)	3 (2%)	55	79
5	LE	318/322 (99%)	300 (94%)	18 (6%)	18	40
6	LF	288/288 (100%)	275 (96%)	13 (4%)	24	50
7	LG	241/243 (99%)	227 (94%)	14 (6%)	18	39
8	LH	139/154 (90%)	135 (97%)	4 (3%)	37	65
9	LI	186/186 (100%)	178 (96%)	8 (4%)	26	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	LJ	187/191 (98%)	173 (92%)	14 (8%)	12	28
11	LK	168/171 (98%)	160 (95%)	8 (5%)	23	47
12	LL	185/185 (100%)	177 (96%)	8 (4%)	26	51
13	LM	145/147 (99%)	139 (96%)	6 (4%)	27	54
14	LN	154/154 (100%)	146 (95%)	8 (5%)	21	44
15	LO	107/107 (100%)	97 (91%)	10 (9%)	8	18
16	LP	175/175 (100%)	170 (97%)	5 (3%)	37	65
17	LQ	160/160 (100%)	154 (96%)	6 (4%)	29	56
18	LR	138/145 (95%)	134 (97%)	4 (3%)	37	65
19	LS	150/150 (100%)	145 (97%)	5 (3%)	33	61
20	LT	152/153 (99%)	146 (96%)	6 (4%)	28	55
21	LU	155/155 (100%)	145 (94%)	10 (6%)	15	35
22	LV	135/136 (99%)	129 (96%)	6 (4%)	25	50
23	LW	87/87 (100%)	81 (93%)	6 (7%)	14	32
24	LX	104/104 (100%)	97 (93%)	7 (7%)	15	33
25	LY	54/57 (95%)	51 (94%)	3 (6%)	19	40
26	LZ	104/105 (99%)	97 (93%)	7 (7%)	15	33
27	La	108/108 (100%)	105 (97%)	3 (3%)	38	66
28	Lb	112/115 (97%)	106 (95%)	6 (5%)	20	42
29	Lc	117/118 (99%)	114 (97%)	3 (3%)	40	68
30	Ld	46/46 (100%)	45 (98%)	1 (2%)	45	72
31	Le	81/81 (100%)	77 (95%)	4 (5%)	22	47
32	Lf	92/96 (96%)	88 (96%)	4 (4%)	26	51
33	Lg	108/109 (99%)	105 (97%)	3 (3%)	38	66
34	Lh	90/90 (100%)	89 (99%)	1 (1%)	65	84
35	Li	95/95 (100%)	90 (95%)	5 (5%)	20	43
36	Lj	104/104 (100%)	104 (100%)	0	100	100
37	Lk	80/81 (99%)	77 (96%)	3 (4%)	29	56
38	Ll	67/67 (100%)	64 (96%)	3 (4%)	24	50
39	Lm	68/68 (100%)	64 (94%)	4 (6%)	18	38
40	Ln	45/45 (100%)	42 (93%)	3 (7%)	15	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	Lo	45/47 (96%)	44 (98%)	1 (2%)	45	72
42	Lp	22/23 (96%)	21 (96%)	1 (4%)	24	50
43	Lq	87/88 (99%)	84 (97%)	3 (3%)	32	60
44	Lr	71/71 (100%)	70 (99%)	1 (1%)	59	81
46	SA	182/182 (100%)	170 (93%)	12 (7%)	15	34
47	SB	172/173 (99%)	169 (98%)	3 (2%)	53	78
48	SC	77/85 (91%)	73 (95%)	4 (5%)	21	44
49	SD	88/100 (88%)	82 (93%)	6 (7%)	14	32
50	SE	95/98 (97%)	91 (96%)	4 (4%)	26	52
51	SF	117/117 (100%)	109 (93%)	8 (7%)	14	32
52	SG	101/113 (89%)	96 (95%)	5 (5%)	22	46
53	SH	127/128 (99%)	123 (97%)	4 (3%)	35	63
54	SI	115/115 (100%)	111 (96%)	4 (4%)	32	59
55	SJ	93/94 (99%)	89 (96%)	4 (4%)	26	51
56	SK	67/73 (92%)	67 (100%)	0	100	100
57	SL	55/56 (98%)	51 (93%)	4 (7%)	13	29
58	SM	47/47 (100%)	46 (98%)	1 (2%)	47	73
59	SN	56/64 (88%)	55 (98%)	1 (2%)	51	76
60	SO	250/257 (97%)	243 (97%)	7 (3%)	38	66
61	SP	170/173 (98%)	163 (96%)	7 (4%)	27	54
62	SQ	200/205 (98%)	190 (95%)	10 (5%)	22	46
63	SR	175/176 (99%)	166 (95%)	9 (5%)	21	45
64	SS	220/221 (100%)	206 (94%)	14 (6%)	16	35
65	ST	189/195 (97%)	176 (93%)	13 (7%)	14	32
66	SU	163/165 (99%)	158 (97%)	5 (3%)	35	63
67	SV	148/160 (92%)	145 (98%)	3 (2%)	48	74
68	SW	156/158 (99%)	145 (93%)	11 (7%)	13	31
69	SX	126/129 (98%)	122 (97%)	4 (3%)	34	62
70	SY	127/127 (100%)	119 (94%)	8 (6%)	16	36
71	SZ	90/97 (93%)	87 (97%)	3 (3%)	33	61
72	Sa	71/74 (96%)	66 (93%)	5 (7%)	14	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
73	Sb	110/110 (100%)	109 (99%)	1 (1%)	70 87
74	Sc	119/119 (100%)	116 (98%)	3 (2%)	42 69
75	Sd	102/112 (91%)	94 (92%)	8 (8%)	11 26
76	Se	82/83 (99%)	81 (99%)	1 (1%)	63 83
77	Sf	70/70 (100%)	64 (91%)	6 (9%)	10 22
78	Sg	48/49 (98%)	47 (98%)	1 (2%)	47 73
All	All	9168/9345 (98%)	8761 (96%)	407 (4%)	27 50

5 of 407 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	SA	96	LEU
58	SM	28	THR
76	Se	68	TYR
46	SA	194	LYS
51	SF	52	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
36	Lj	62	GLN
71	SZ	65	GLN
49	SD	143	GLN
71	SZ	24	ASN
67	SV	64	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	LA	3180/3393 (93%)	852 (26%)	36 (1%)
2	LB	120/121 (99%)	24 (20%)	1 (0%)
3	LC	157/158 (99%)	43 (27%)	2 (1%)
45	S2	1768/1799 (98%)	720 (40%)	26 (1%)
79	Ta	76/77 (98%)	48 (63%)	0
80	Tb	76/77 (98%)	38 (50%)	0
81	mR	0/25	-	-
All	All	5377/5650 (95%)	1725 (32%)	65 (1%)

5 of 1725 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	LA	6	A
1	LA	22	G
1	LA	26	A
1	LA	34	A
1	LA	40	A

5 of 65 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	S2	1226	A
45	S2	1256	A
1	LA	2444	A
1	LA	2443	C
45	S2	1274	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

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

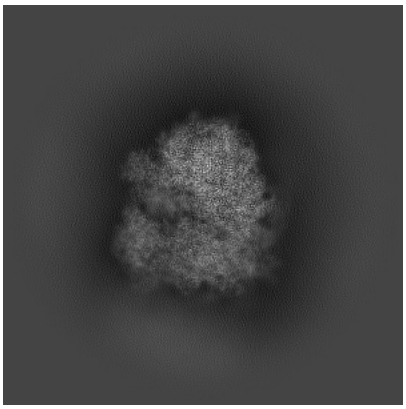
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-60097. These allow visual inspection of the internal detail of the map and identification of artifacts.

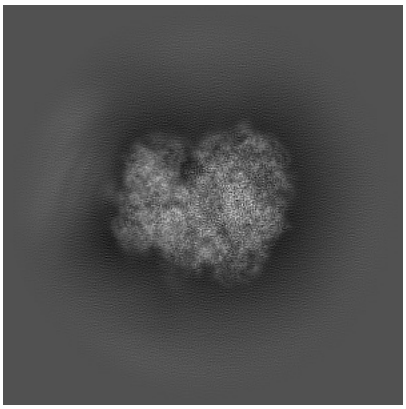
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

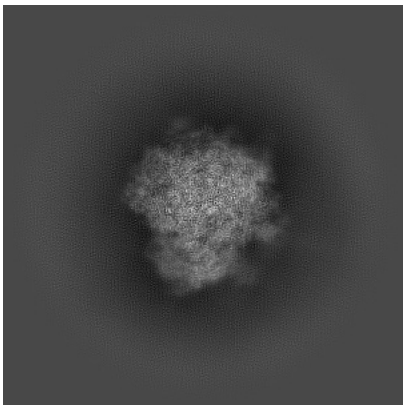
6.1.1 Primary map



X

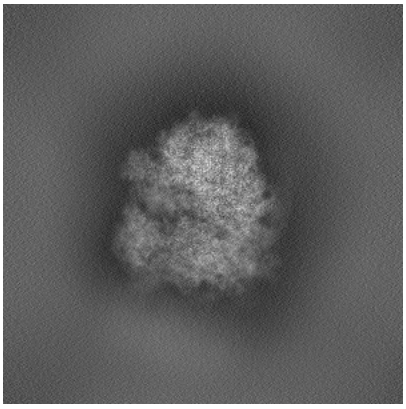


Y

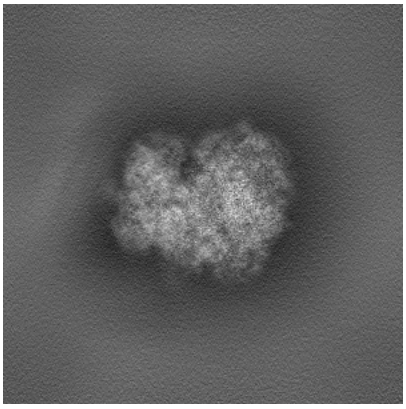


Z

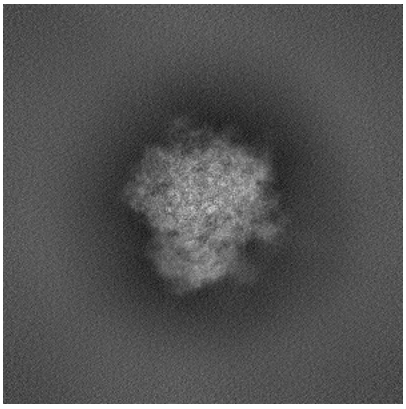
6.1.2 Raw map



X



Y

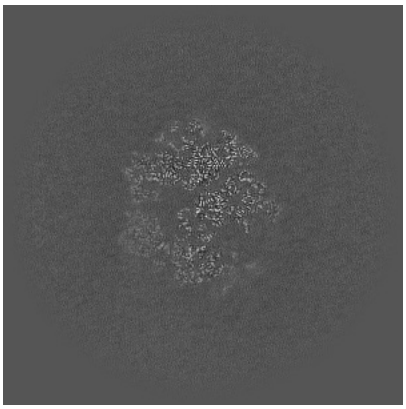


Z

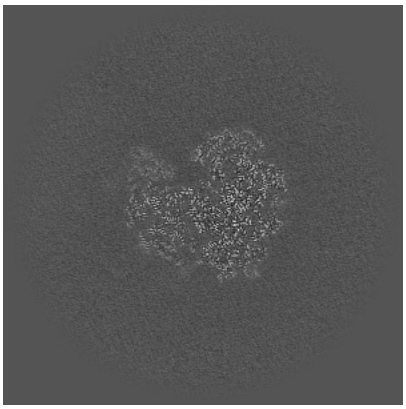
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

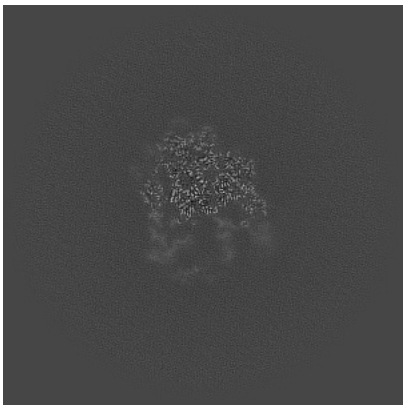
6.2.1 Primary map



X Index: 300

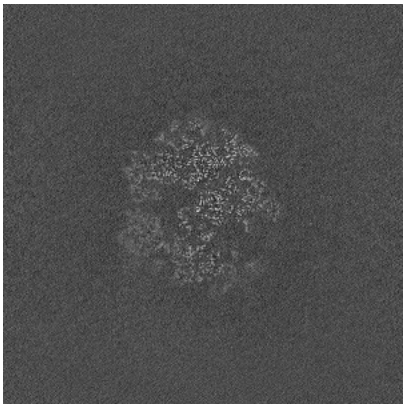


Y Index: 300

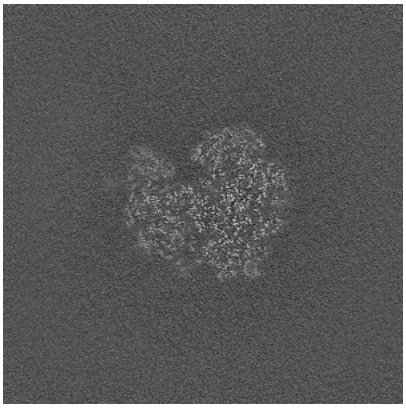


Z Index: 300

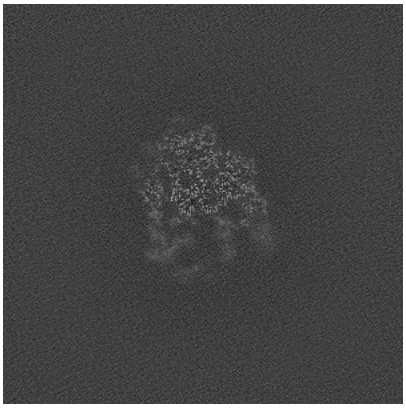
6.2.2 Raw map



X Index: 300



Y Index: 300

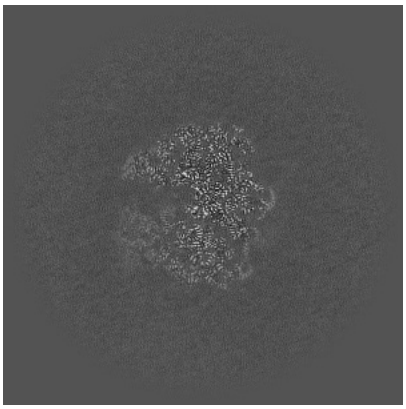


Z Index: 300

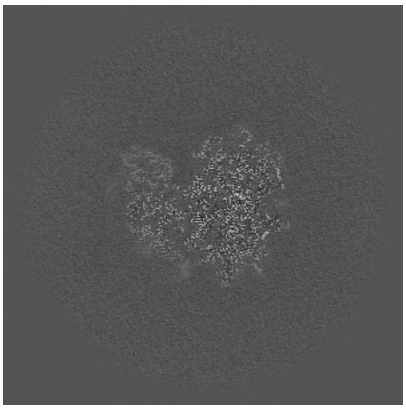
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

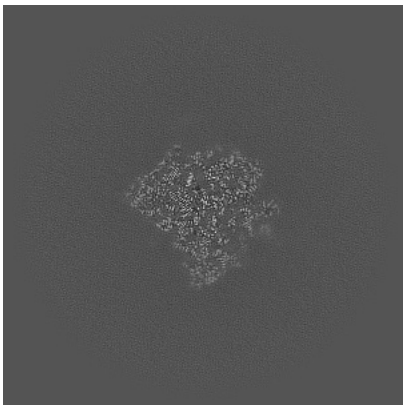
6.3.1 Primary map



X Index: 283

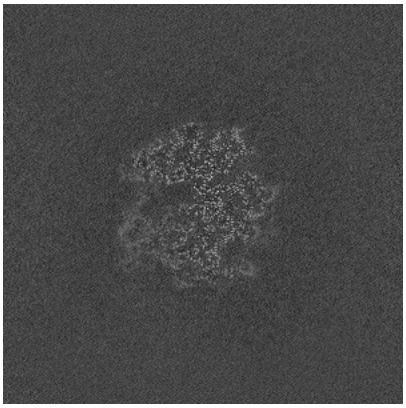


Y Index: 307

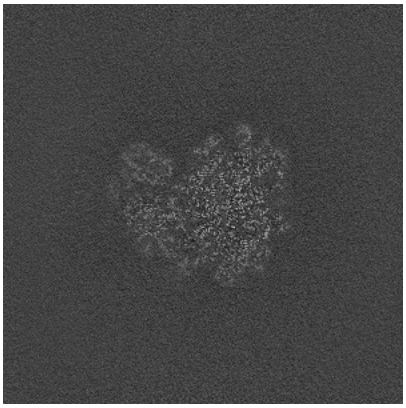


Z Index: 345

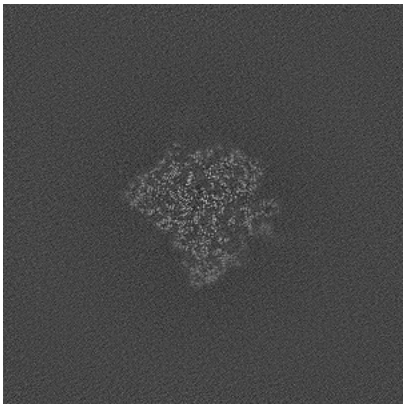
6.3.2 Raw map



X Index: 288



Y Index: 310

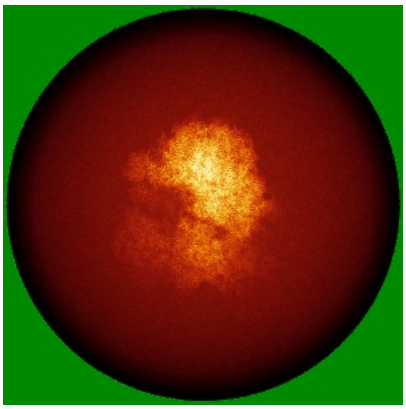


Z Index: 345

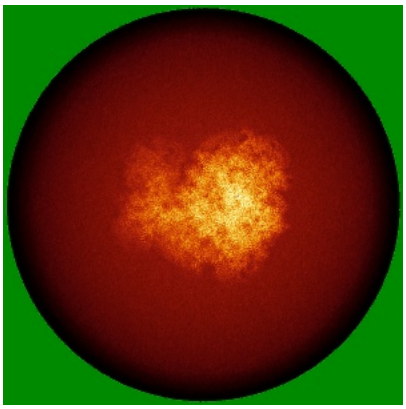
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

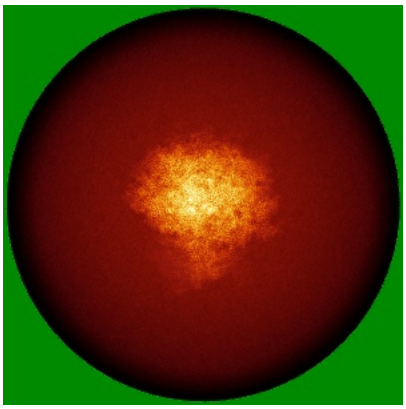
6.4.1 Primary map



X

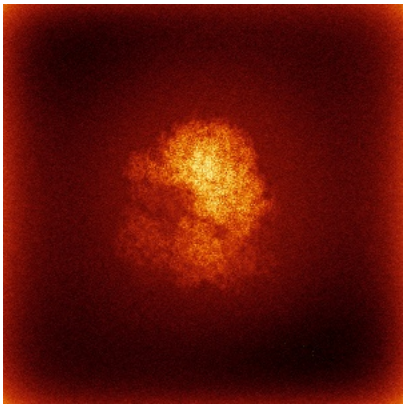


Y

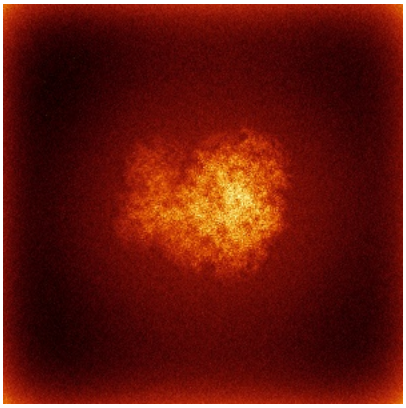


Z

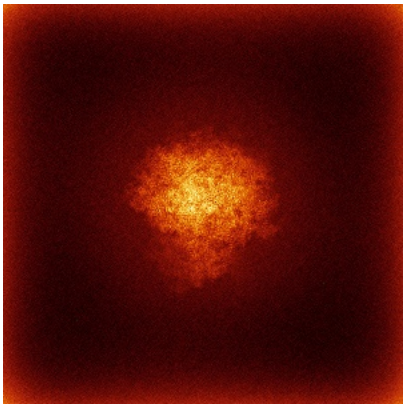
6.4.2 Raw map



X



Y

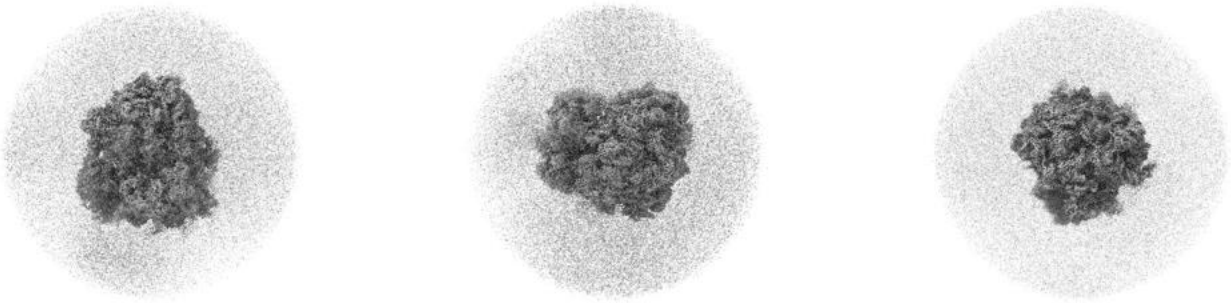


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.26. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

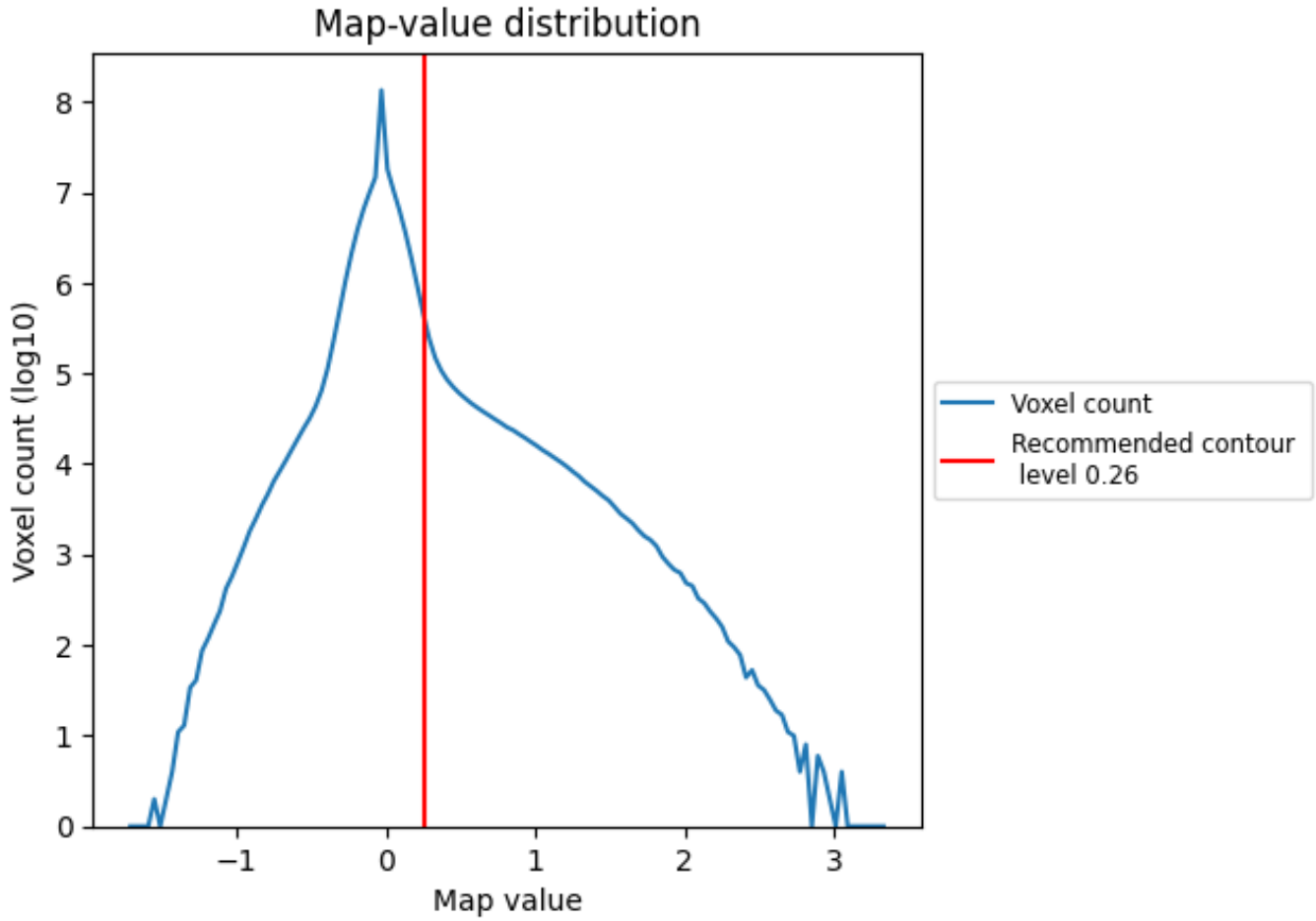
6.6 Mask visualisation (i)

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

7 Map analysis

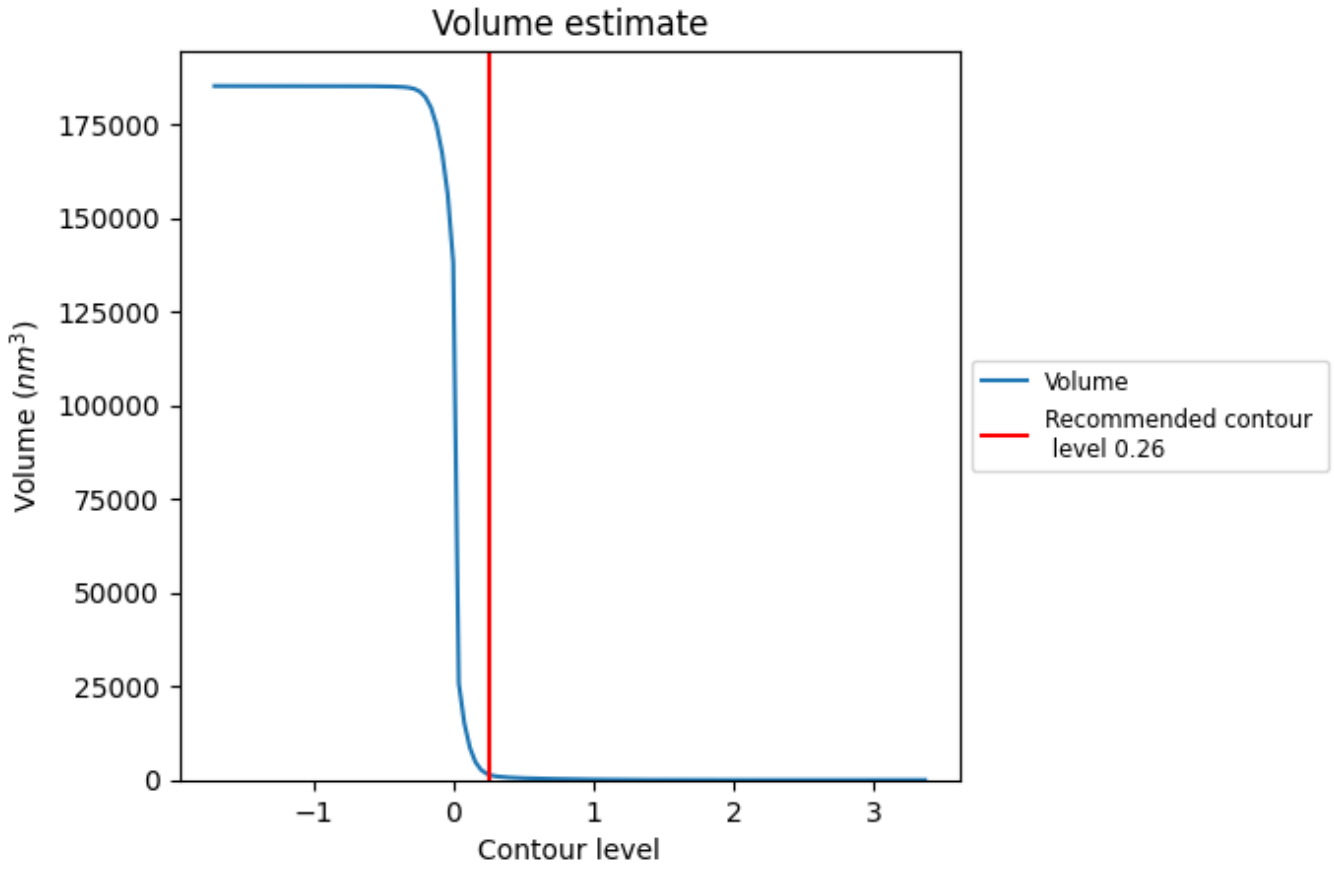
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

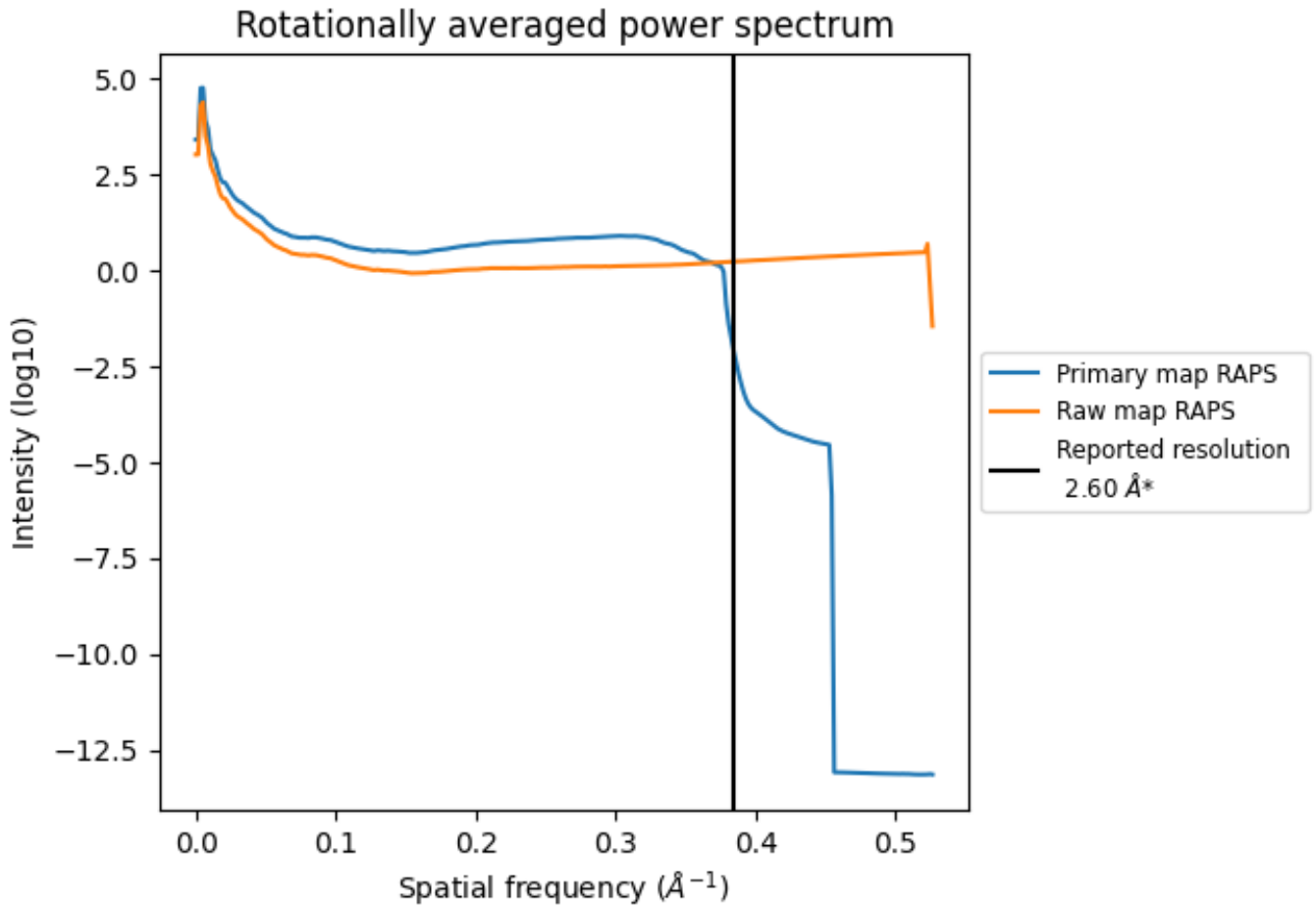
7.2 Volume estimate (i)



The volume at the recommended contour level is 1368 nm^3; this corresponds to an approximate mass of 1236 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)

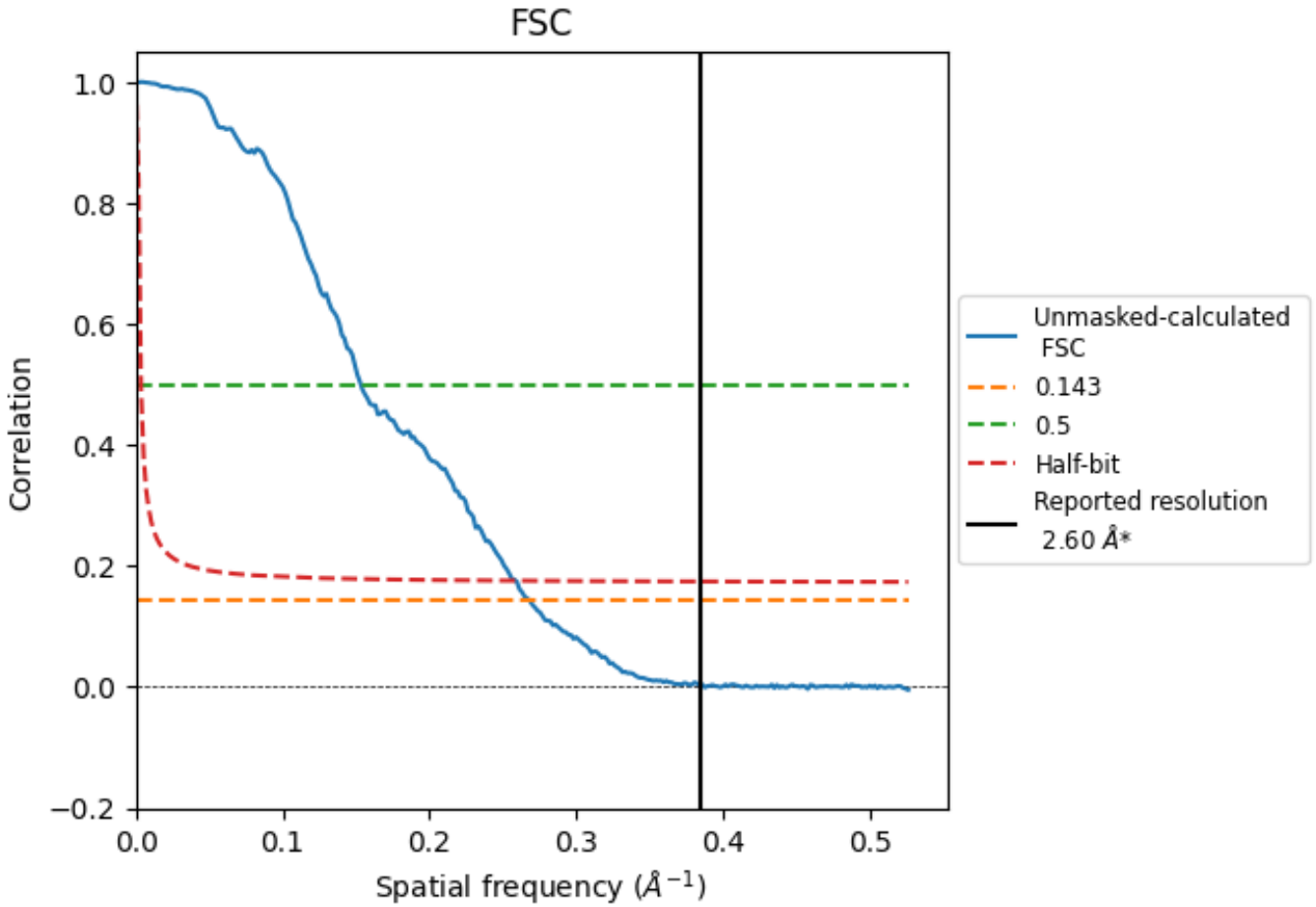


*Reported resolution corresponds to spatial frequency of 0.385 $Å^{-1}$

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.385 Å^{-1}

8.2 Resolution estimates (i)

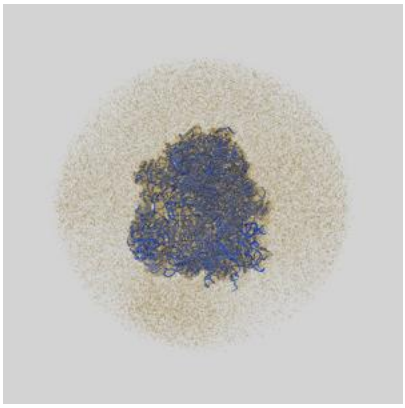
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.73	6.52	3.87

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.73 differs from the reported value 2.6 by more than 10 %

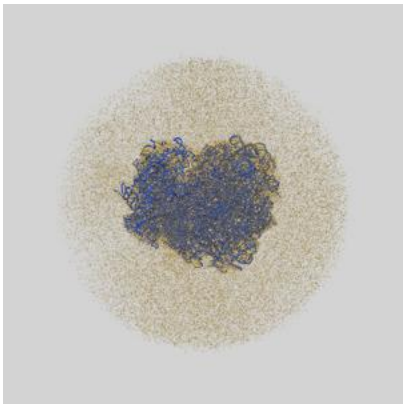
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-60097 and PDB model 8ZHB. Per-residue inclusion information can be found in section 3 on page 19.

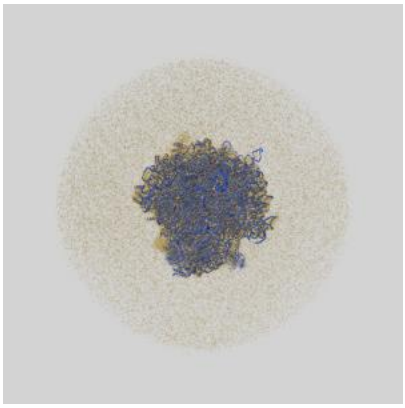
9.1 Map-model overlay



X



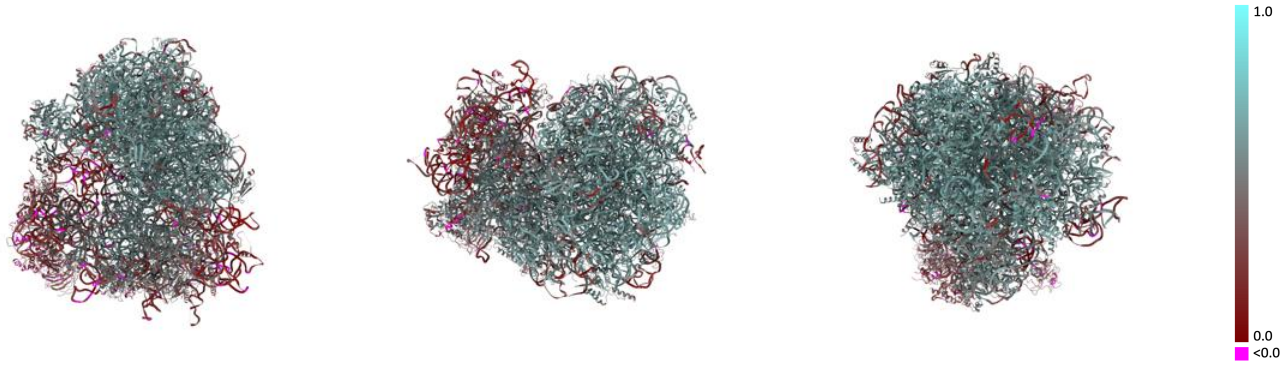
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.26 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.

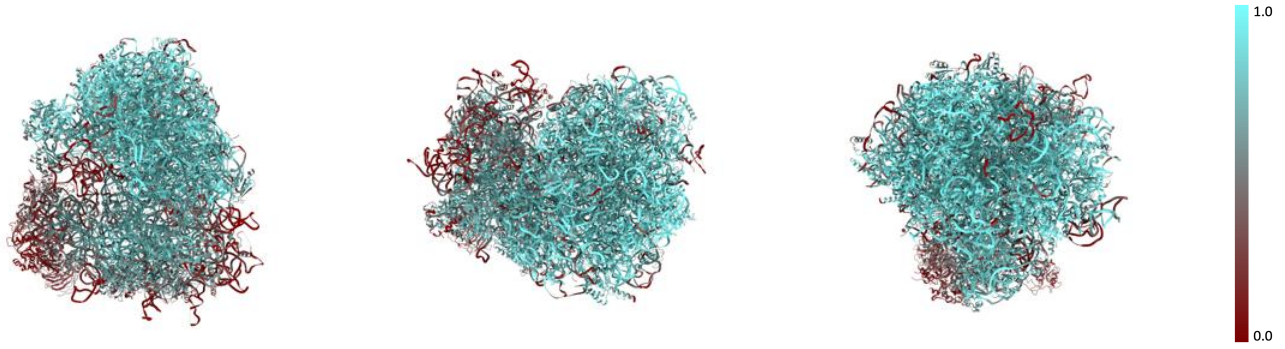
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

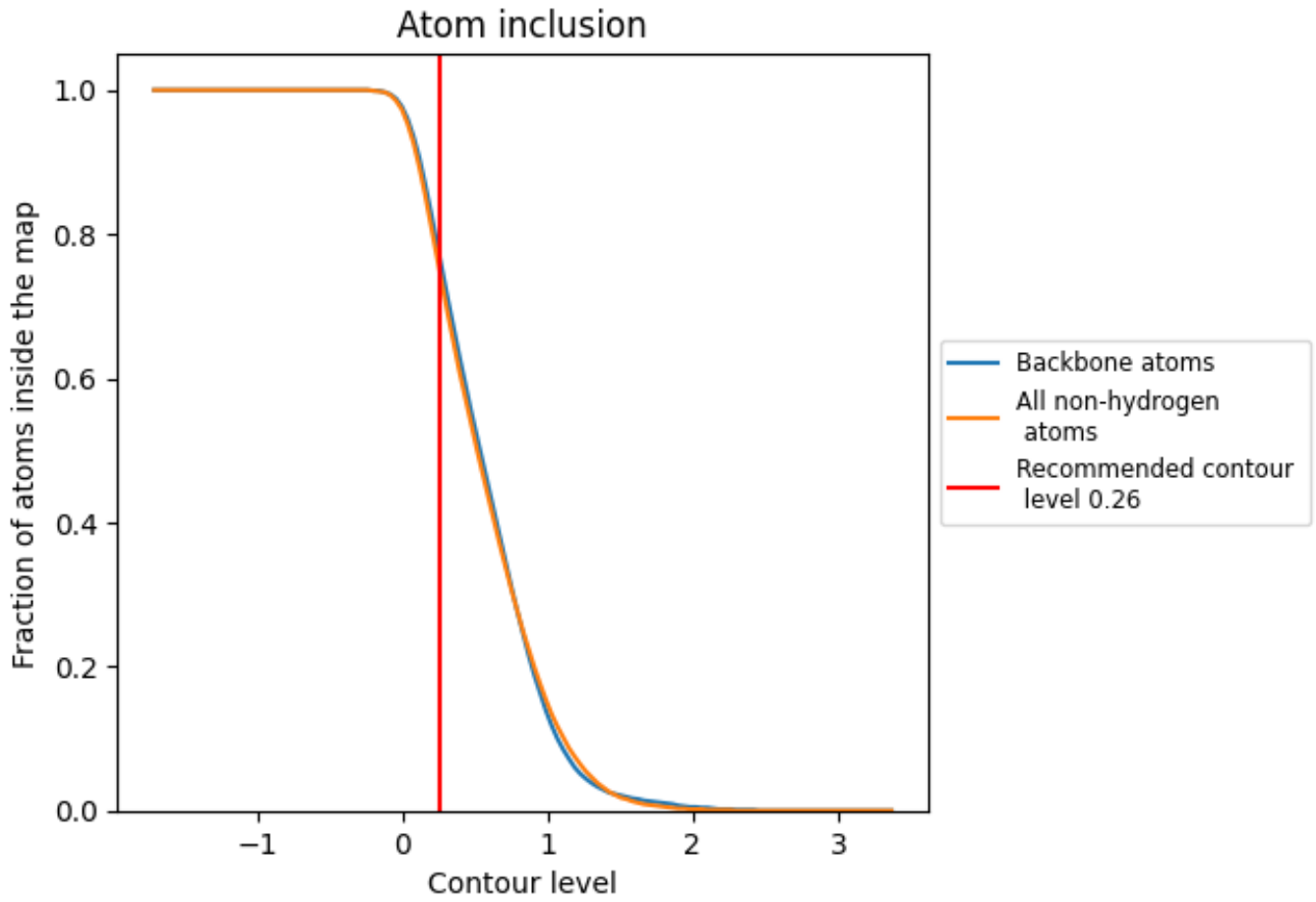
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.26).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 74% 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 (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7450	0.5010
LA	0.8730	0.5600
LB	0.9030	0.5570
LC	0.9190	0.5920
LD	0.9350	0.6380
LE	0.9030	0.6050
LF	0.9080	0.6130
LG	0.7830	0.5400
LH	0.7970	0.5500
LI	0.9200	0.6200
LJ	0.8190	0.5620
LK	0.8410	0.5750
LL	0.8160	0.5790
LM	0.6630	0.4660
LN	0.8780	0.5980
LO	0.8590	0.5750
LP	0.9450	0.6320
LQ	0.8980	0.6050
LR	0.8900	0.6050
LS	0.9380	0.6320
LT	0.7870	0.5450
LU	0.9030	0.6120
LV	0.9010	0.6070
LW	0.6960	0.4940
LX	0.8890	0.6150
LY	0.9020	0.6160
LZ	0.8570	0.6010
La	0.9100	0.6170
Lb	0.8590	0.5870
Lc	0.9360	0.6300
Ld	0.8520	0.5850
Le	0.8650	0.5920
Lf	0.8320	0.5780
Lg	0.8780	0.6090
Lh	0.9390	0.6330



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Chain	Atom inclusion	Q-score
Li	0.8850	0.6070
Lj	0.8820	0.5940
Lk	0.8370	0.5580
Ll	0.9660	0.6460
Lm	0.6490	0.4910
Ln	0.9130	0.6240
Lo	0.8810	0.6060
Lp	0.8460	0.6160
Lq	0.8960	0.6160
Lr	0.8710	0.6280
S2	0.6190	0.3850
SA	0.3760	0.3680
SB	0.2820	0.3250
SC	0.2740	0.2810
SD	0.0380	0.1800
SE	0.3460	0.3000
SF	0.3070	0.3280
SG	0.4600	0.3990
SH	0.3370	0.3190
SI	0.2980	0.3150
SJ	0.3020	0.3170
SK	0.1230	0.2190
SL	0.3340	0.3290
SM	0.4440	0.3690
SN	0.0660	0.1860
SO	0.1650	0.2310
SP	0.6650	0.4900
SQ	0.7030	0.5060
SR	0.7710	0.5580
SS	0.5860	0.4520
ST	0.3940	0.3540
SU	0.5800	0.4630
SV	0.5810	0.4360
SW	0.5180	0.3950
SX	0.7170	0.5210
SY	0.8050	0.5670
SZ	0.7800	0.5420
Sa	0.7370	0.5330
Sb	0.8940	0.6110
Sc	0.7000	0.4990
Sd	0.4770	0.3820
Se	0.8350	0.5660

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Chain	Atom inclusion	Q-score
Sf	0.7260	0.4980
Sg	0.4440	0.3480
Ta	0.2480	0.1590
Tb	0.3430	0.2300
mR	0.5870	0.3670