wwPDB EM Validation Summary Report

Oct 27, 2026 – 09:44 PM JST

PDB ID	:	23EZ / pdb_000023ez
EMDB ID	:	EMD-68916
Title	:	semi-rotated 80S with A/A-P/P tRNA
Authors	:	Wu, M.; Yuan, S.
Deposited on	:	2026-02-04
Resolution	:	3.35 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:

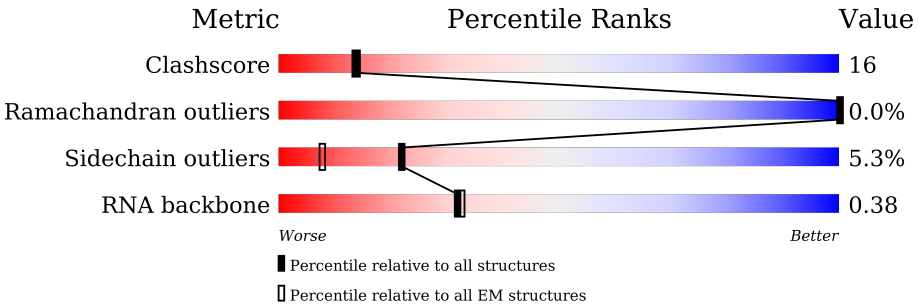
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

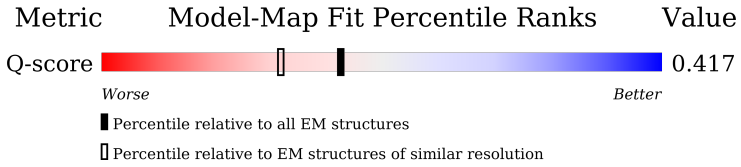
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.35 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	14390 (2.85 - 3.85)

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	S2	1800	10% 24% 49% 24% ••
2	SL	63	30% 65% 35%
3	SM	53	6% 43% 57%

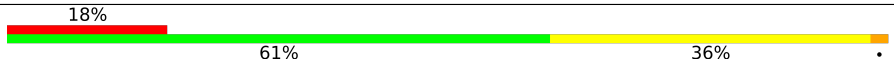
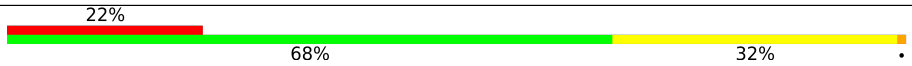
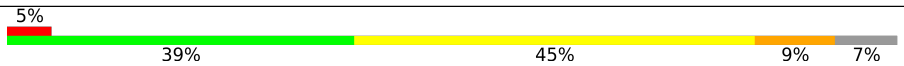
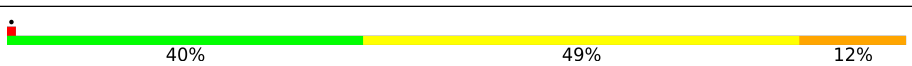
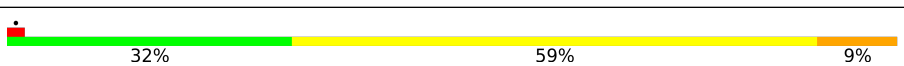
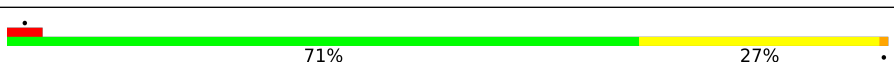
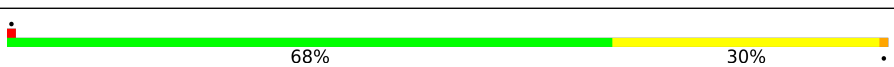
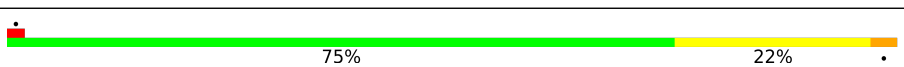
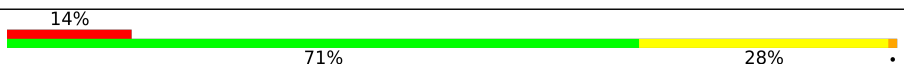
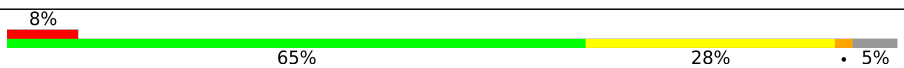
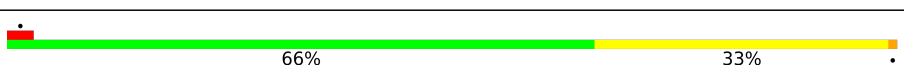
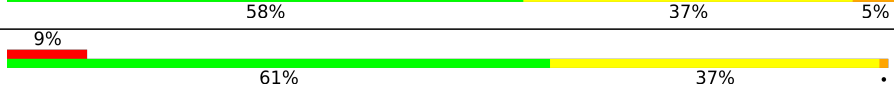
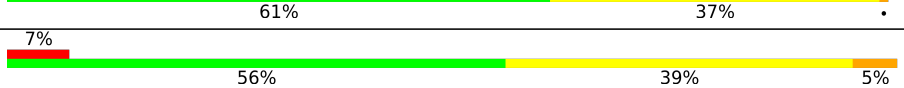
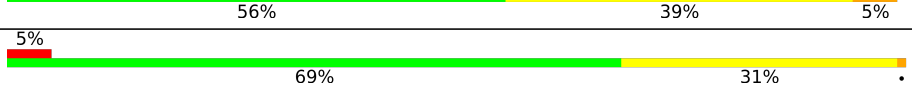
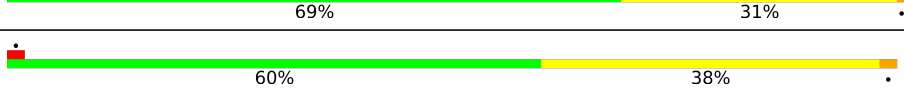
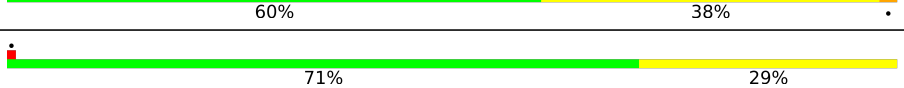
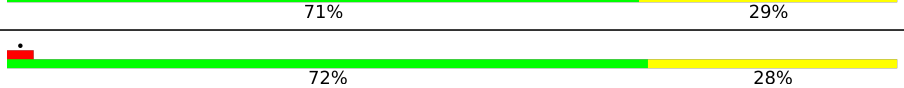
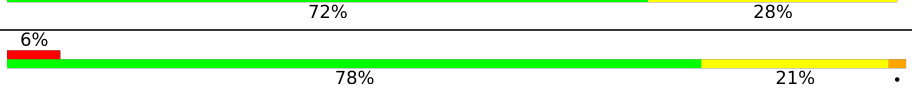
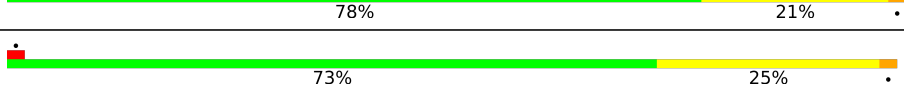
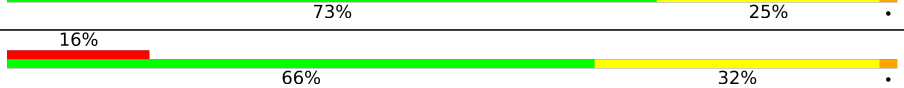
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Mol	Chain	Length	Quality of chain
4	SN	73	70% 58% 36% 5%
5	SO	312	46% 53% 44%
6	SP	206	16% 53% 44%
7	SQ	214	14% 44% 51%
8	SR	216	53% 46%
9	SS	258	7% 59% 40%
10	ST	228	14% 53% 45%
11	SU	184	21% 55% 45%
12	SV	198	7% 61% 33% 6%
13	SW	184	7% 55% 42%
14	SX	142	7% 65% 32%
15	SY	150	7% 57% 40%
16	SZ	127	12% 60% 37%
17	Sa	87	13% 63% 36%
18	Sf	81	16% 67% 33%
19	Sb	129	61% 37%
20	Sc	144	6% 62% 34%
21	SD	121	76% 41% 55%
22	Sd	134	8% 56% 42%
23	Sg	57	21% 67% 33%
24	Se	97	70% 28%
25	SF	141	24% 55% 41%
26	SG	94	16% 54% 46%
27	SH	145	18% 44% 54%
28	SI	143	22% 50% 46%

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Mol	Chain	Length	Quality of chain
29	SJ	100	
30	SK	82	
31	SA	222	
32	SB	206	
33	SE	117	
34	LA	3393	
35	LB	121	
36	LC	158	
37	LD	251	
38	LE	386	
39	LF	361	
40	LG	294	
41	LH	175	
42	LI	222	
43	LJ	233	
44	LK	191	
45	LL	218	
46	LM	169	
47	LN	193	
48	LO	136	
49	LP	203	
50	LQ	197	
51	LR	183	
52	LS	185	
53	LT	188	

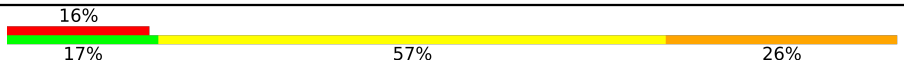
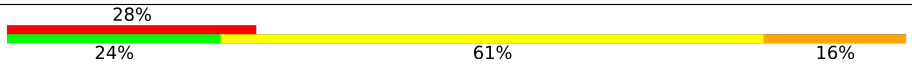
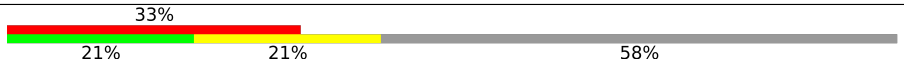
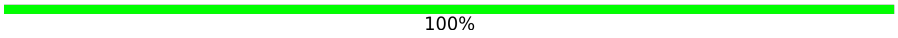
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Mol	Chain	Length	Quality of chain
54	LU	171	58% 39%
55	LV	159	63% 36%
56	LW	100	12% 65% 34%
57	LX	136	5% 68% 31%
58	LY	65	8% 72% 26%
59	LZ	121	74% 23%
60	La	125	7% 52% 44%
61	Lb	135	61% 38%
62	Lc	148	62% 36%
63	Ld	58	5% 78% 21%
64	Le	96	51% 45%
65	Lf	109	11% 66% 32%
66	Lg	127	7% 69% 28%
67	Lh	106	58% 40%
68	Li	112	59% 38%
69	Lj	119	66% 32%
70	Lk	99	5% 67% 31%
71	Ll	81	73% 27%
72	Lm	77	17% 58% 40%
73	Ln	50	70% 28%
74	Lo	52	60% 38%
75	Lp	25	72% 28%
76	Lq	103	75% 25%
77	Lr	91	7% 77% 22%
78	SC	92	23% 50% 47%

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Mol	Chain	Length	Quality of chain
79	Bb	76	
80	Cc	76	
81	pp	24	
82	mR	10	

2 Entry composition (i)

There are 82 unique types of molecules in this entry. The entry contains 201842 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 RNA (1800-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	S2	1770	37719	16863	6681	12405	1770	0	0

- Molecule 2 is a protein called Small ribosomal subunit protein eS28A.

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

- Molecule 3 is a protein called Small ribosomal subunit protein uS14A.

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

- Molecule 4 is a protein called Small ribosomal subunit protein eS31.

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

- Molecule 5 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 6 is a protein called Small ribosomal subunit protein uS2A.

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

- Molecule 7 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SQ	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 8 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 9 is a protein called Small ribosomal subunit protein eS4A.

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

- Molecule 10 is a protein called Small ribosomal subunit protein eS6A.

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

- Molecule 11 is a protein called Small ribosomal subunit protein eS7A.

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

- Molecule 12 is a protein called Small ribosomal subunit protein eS8A.

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

- Molecule 13 is a protein called Small ribosomal subunit protein uS4A.

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

- Molecule 14 is a protein called Small ribosomal subunit protein uS17A.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 16 is a protein called Small ribosomal subunit protein uS11B.

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

- Molecule 17 is a protein called Small ribosomal subunit protein eS21A.

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

- Molecule 18 is a protein called Small ribosomal subunit protein eS27A.

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

- Molecule 19 is a protein called Small ribosomal subunit protein uS8A.

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

- Molecule 20 is a protein called Small ribosomal subunit protein uS12A.

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

- Molecule 21 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 22 is a protein called Small ribosomal subunit protein eS24A.

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

- Molecule 23 is a protein called Small ribosomal subunit protein eS30A.

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

- Molecule 24 is a protein called Small ribosomal subunit protein eS26B.

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

- Molecule 25 is a protein called Small ribosomal subunit protein uS9A.

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

- Molecule 26 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SG	94	Total	C	N	O	S	0	0
			764	480	147	135	2		

- Molecule 27 is a protein called Small ribosomal subunit protein uS13A.

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

- Molecule 28 is a protein called Small ribosomal subunit protein eS19A.

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

- Molecule 29 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 30 is a protein called Small ribosomal subunit protein eS25A.

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

- Molecule 31 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 32 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 33 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 34 is a RNA chain called RNA (3393-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LA	3163	Total	C	N	O	P	0	0
			67653	30219	12193	22078	3163		

- Molecule 35 is a RNA chain called RNA (121-MER).

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

- Molecule 36 is a RNA chain called RNA (158-MER).

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

- Molecule 37 is a protein called Large ribosomal subunit protein uL2A.

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

- Molecule 38 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 39 is a protein called Large ribosomal subunit protein uL4A.

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

- Molecule 40 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL6B.

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

- Molecule 42 is a protein called Large ribosomal subunit protein uL30A.

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

- Molecule 43 is a protein called Large ribosomal subunit protein eL8A.

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

- Molecule 44 is a protein called Large ribosomal subunit protein uL6A.

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

- Molecule 45 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 46 is a protein called Large ribosomal subunit protein uL5B.

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

- Molecule 47 is a protein called Large ribosomal subunit protein eL13A.

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

- Molecule 48 is a protein called Large ribosomal subunit protein eL14A.

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

- Molecule 49 is a protein called Large ribosomal subunit protein eL15A.

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

- Molecule 50 is a protein called Large ribosomal subunit protein uL13A.

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

- Molecule 51 is a protein called Large ribosomal subunit protein uL22A.

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

- Molecule 52 is a protein called Large ribosomal subunit protein eL18A.

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

- Molecule 53 is a protein called Large ribosomal subunit protein eL19A.

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

- Molecule 54 is a protein called Large ribosomal subunit protein eL20A.

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

- Molecule 55 is a protein called Large ribosomal subunit protein eL21A.

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

- Molecule 56 is a protein called Large ribosomal subunit protein eL22A.

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

- Molecule 57 is a protein called Large ribosomal subunit protein uL14A.

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

- Molecule 58 is a protein called Large ribosomal subunit protein eL24A.

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

- Molecule 59 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 60 is a protein called Large ribosomal subunit protein uL24A.

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

- Molecule 61 is a protein called Large ribosomal subunit protein eL27A.

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

- Molecule 62 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 63 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 64 is a protein called Large ribosomal subunit protein eL30.

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

- Molecule 65 is a protein called Large ribosomal subunit protein eL31A.

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

- Molecule 66 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 67 is a protein called Large ribosomal subunit protein eL33A.

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

- Molecule 68 is a protein called Large ribosomal subunit protein eL34A.

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

- Molecule 69 is a protein called Large ribosomal subunit protein uL29A.

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

- Molecule 70 is a protein called Large ribosomal subunit protein eL36A.

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

- Molecule 71 is a protein called Large ribosomal subunit protein eL37A.

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

- Molecule 72 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 73 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 74 is a protein called Large ribosomal subunit protein eL40A.

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

- Molecule 75 is a protein called Large ribosomal subunit protein eL41A.

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

- Molecule 76 is a protein called Large ribosomal subunit protein eL42A.

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

- Molecule 77 is a protein called Large ribosomal subunit protein eL43A.

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

- Molecule 78 is a protein called Small ribosomal subunit protein eS10A.

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

- Molecule 79 is a RNA chain called RNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bb	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		

- Molecule 80 is a RNA chain called RNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cc	76	Total	C	N	O	P	0	0
			1628	726	302	524	76		

- Molecule 81 is a protein called PRO-GLN-ARG-HIS-ASP-GLU-LYS-THR-LEU-VAL-GLN -SER-GLN-VAL-ASN-ALA-TYR-ASN-ALA-ASP-MET-ILE-ASP-PRO.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	pp	10	Total	C	N	O	S	0	0
			77	47	12	17	1		

- Molecule 82 is a RNA chain called RNA (5'-R(P*GP*AP*CP*CP*CP*UP*UP*AP*AP*C) -3').

Mol	Chain	Residues	Atoms					AltConf	Trace
82	mR	10	Total	C	N	O	P	0	0
			209	94	36	69	10		

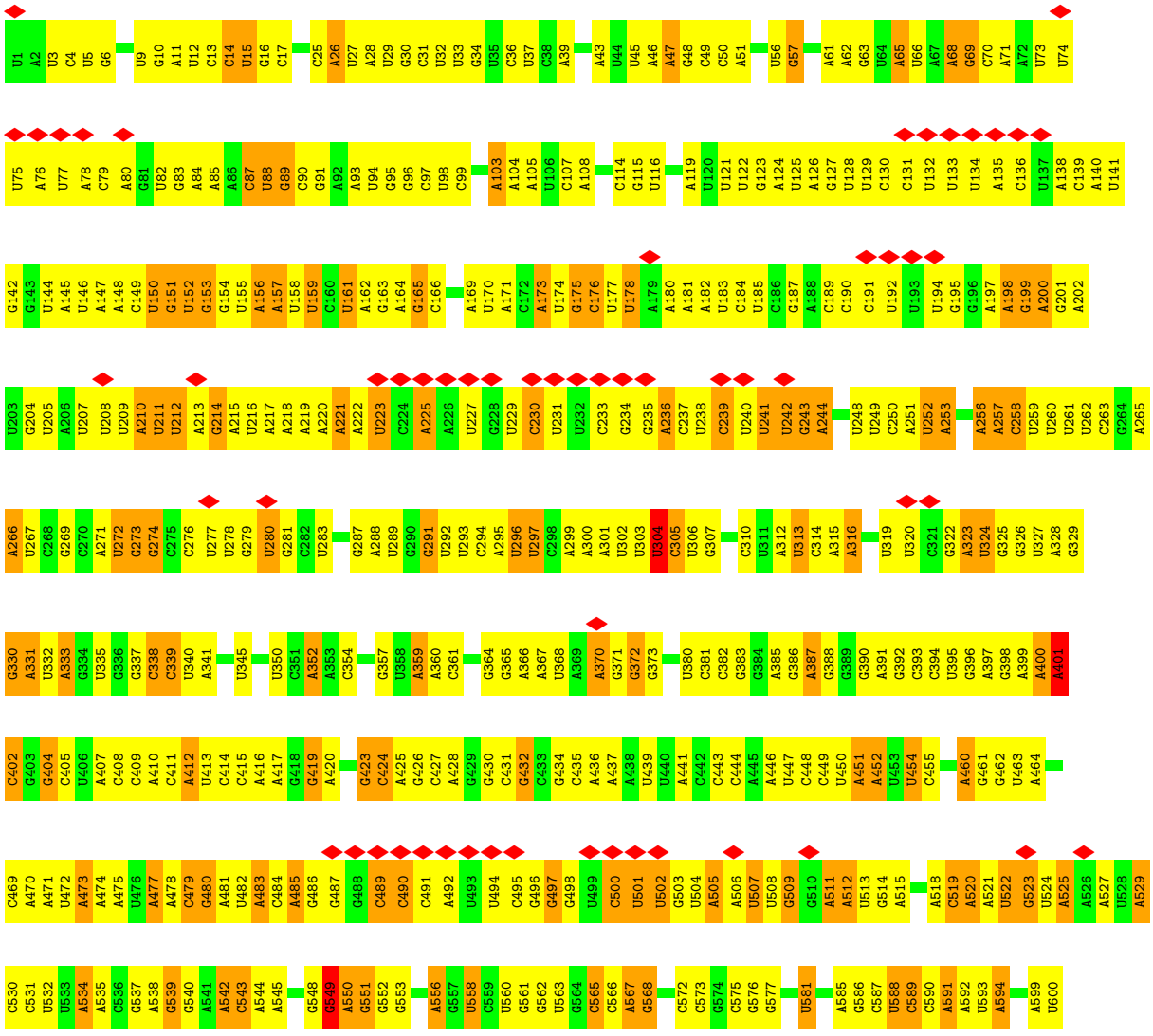
3 Residue-property plots

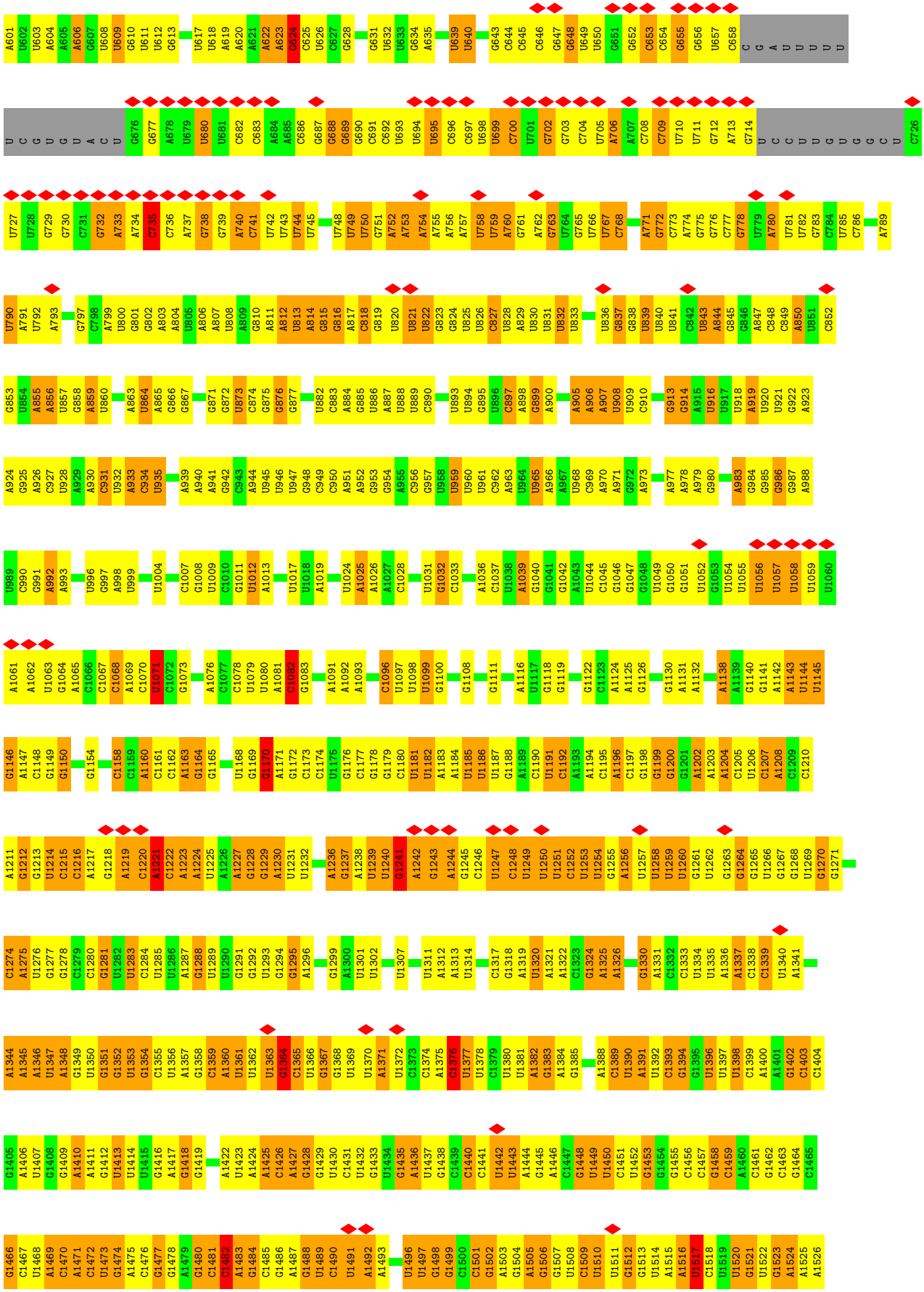
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

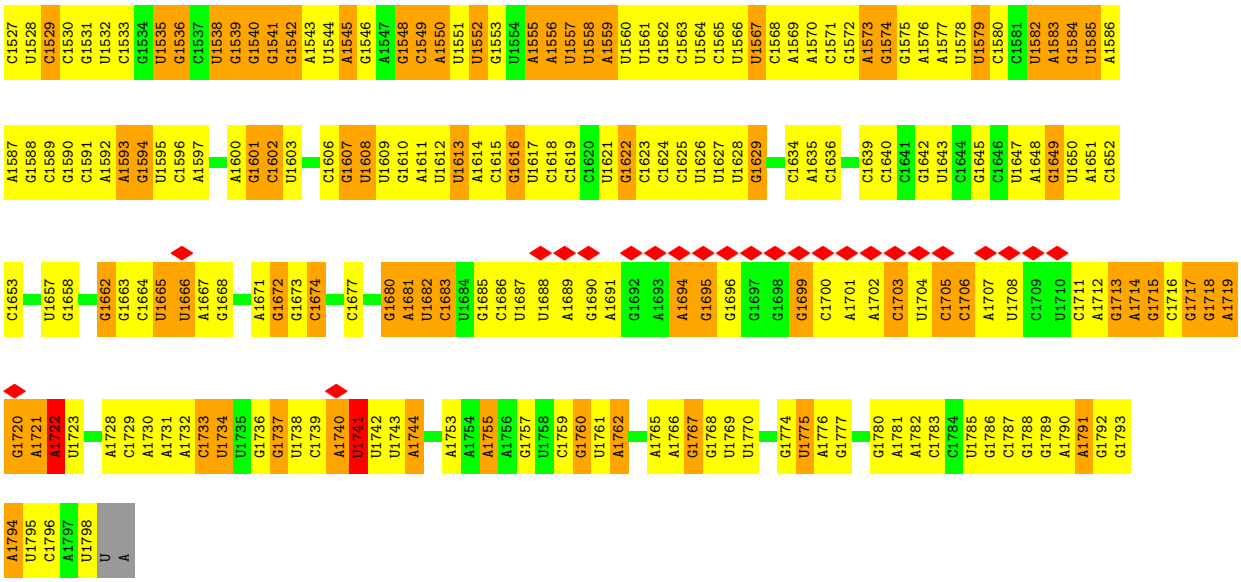
- Molecule 1: RNA (1800-MER)

Chain S2:





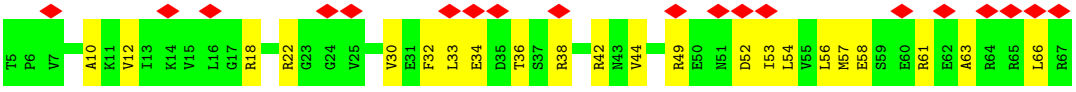




• Molecule 2: Small ribosomal subunit protein eS28A

Chain SL:

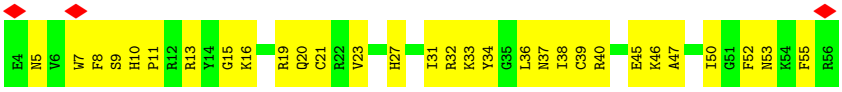




• Molecule 3: Small ribosomal subunit protein uS14A

Chain SM:

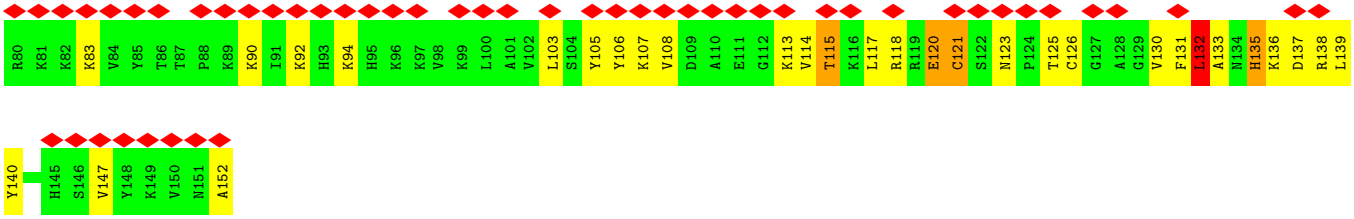




• Molecule 4: Small ribosomal subunit protein eS31

Chain SN:

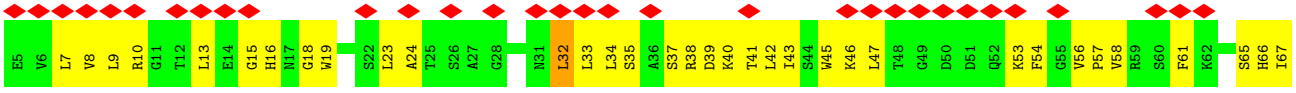


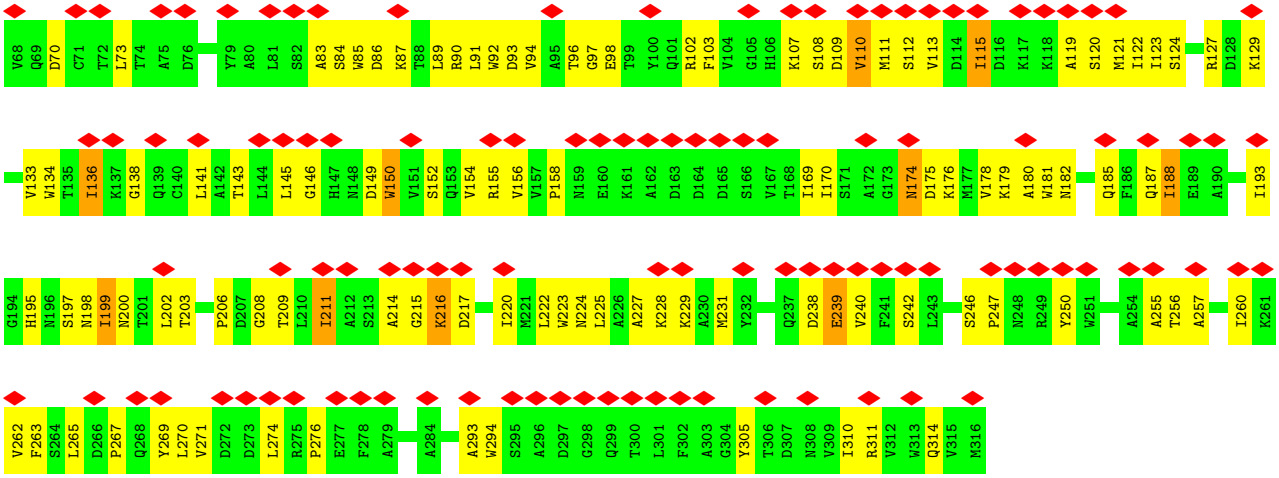


• Molecule 5: Small ribosomal subunit protein RACK1

Chain SO:



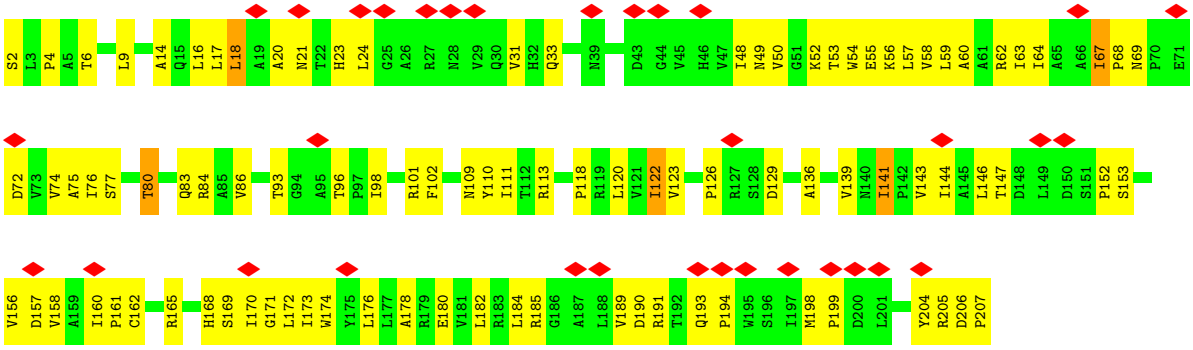




• Molecule 6: Small ribosomal subunit protein uS2A

Chain SP:

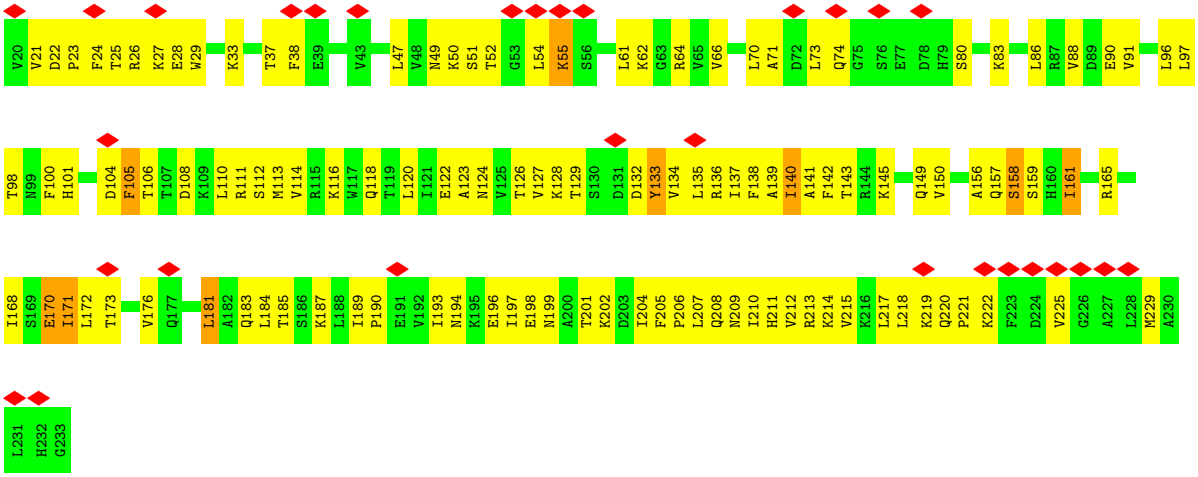




• Molecule 7: Small ribosomal subunit protein eS1A

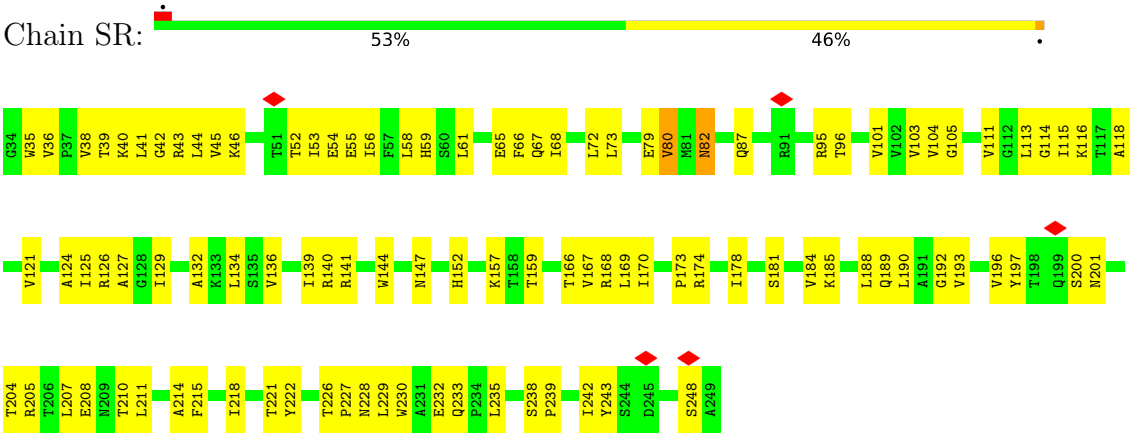
Chain SQ:





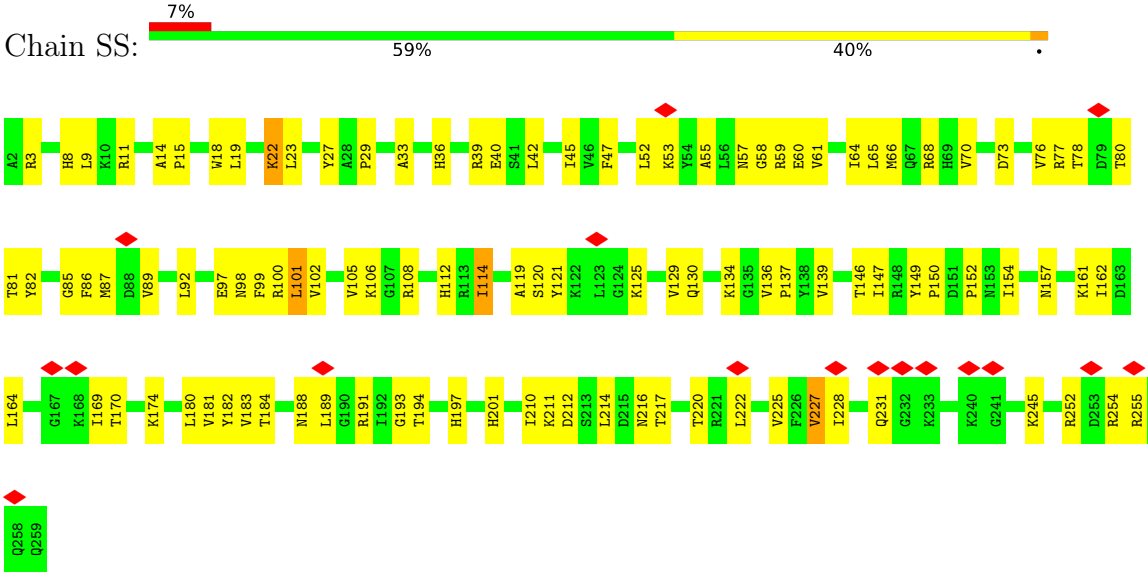
• Molecule 8: Small ribosomal subunit protein uS5

Chain SR:



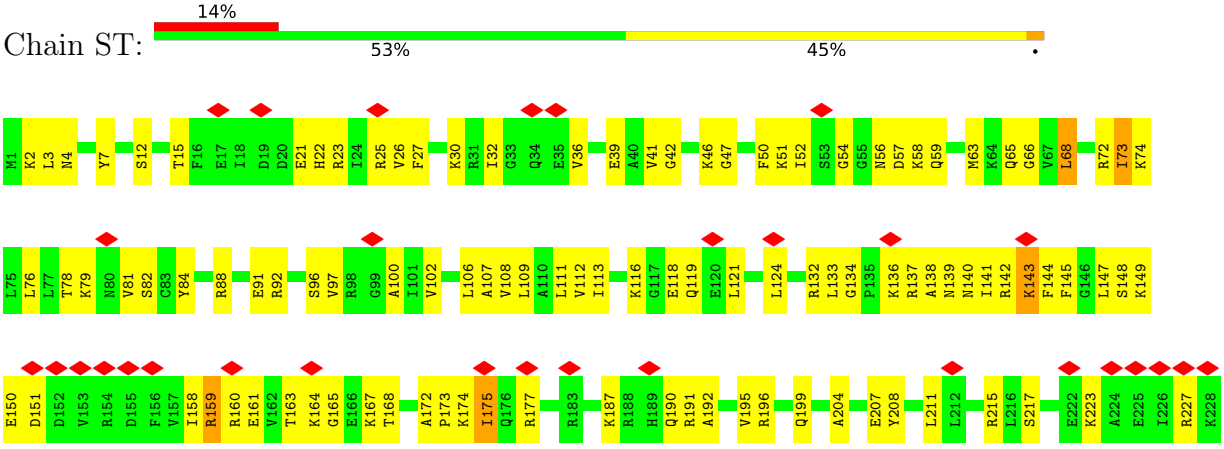
• Molecule 9: Small ribosomal subunit protein eS4A

Chain SS:



• Molecule 10: Small ribosomal subunit protein eS6A

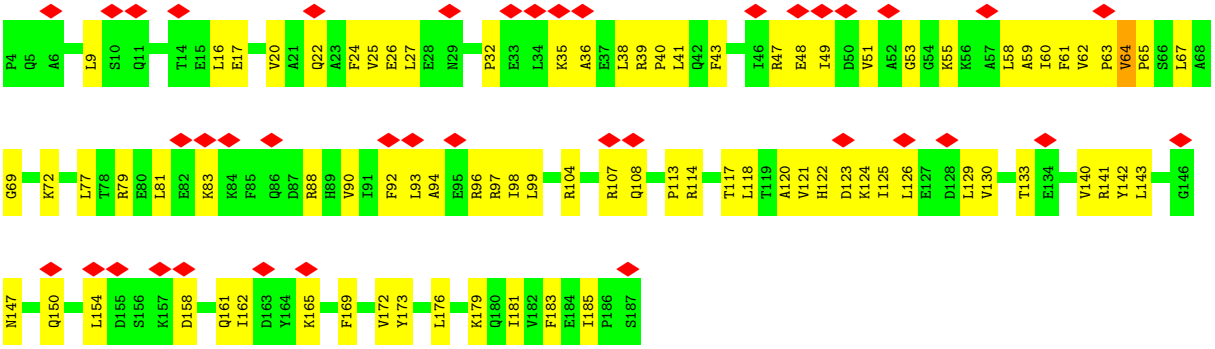
Chain ST:



• Molecule 11: Small ribosomal subunit protein eS7A

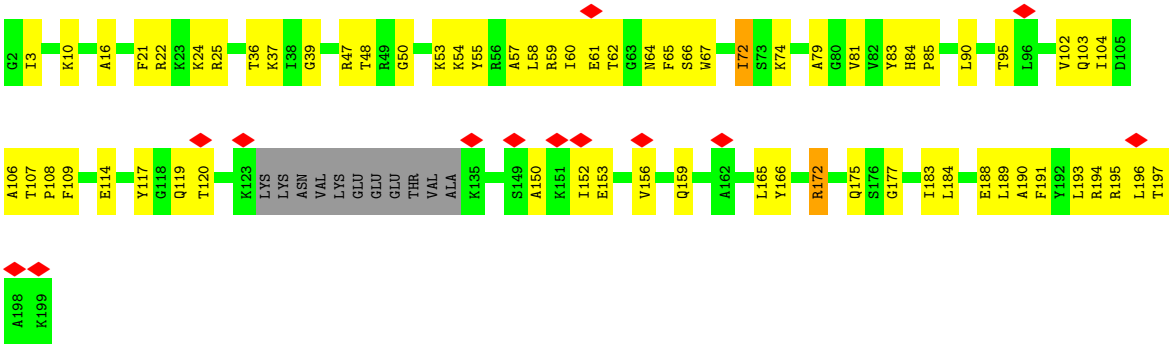
Chain SU:





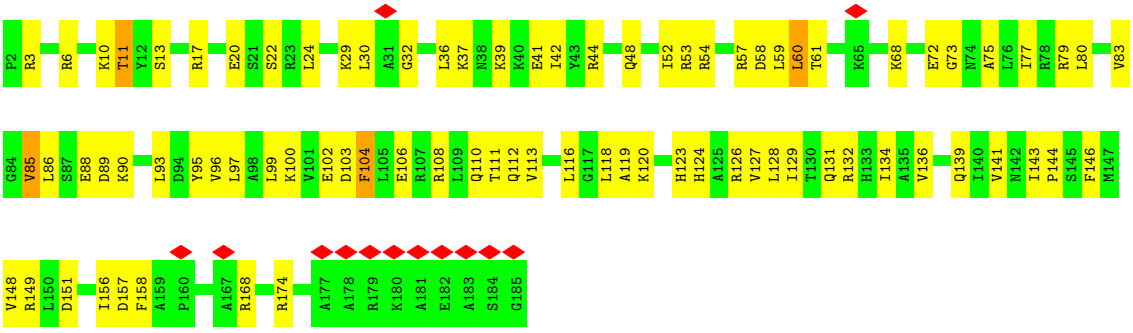
• Molecule 12: Small ribosomal subunit protein eS8A





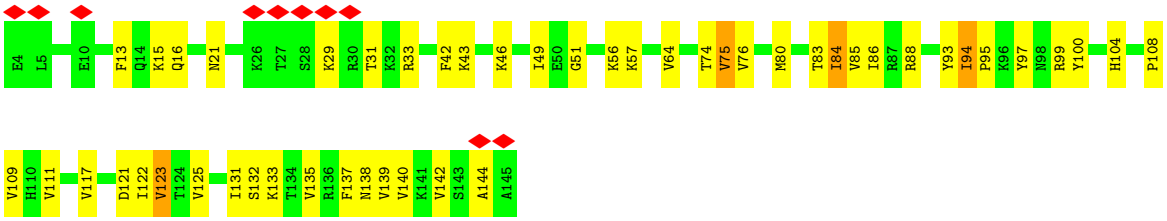
• Molecule 13: Small ribosomal subunit protein uS4A





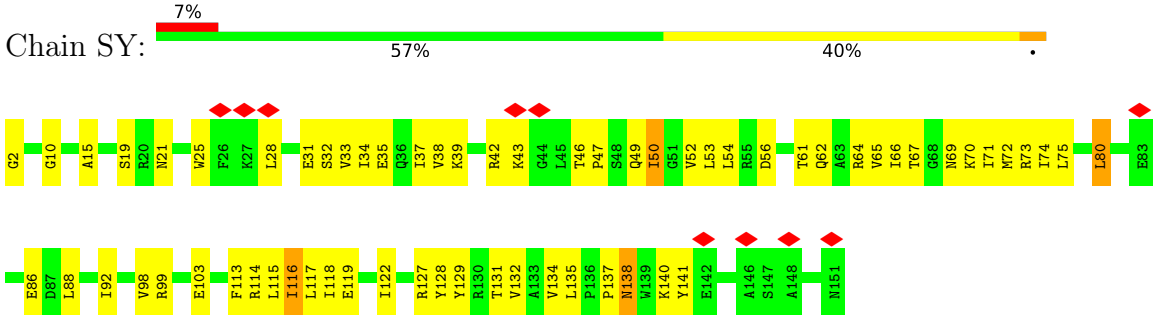
• Molecule 14: Small ribosomal subunit protein uS17A





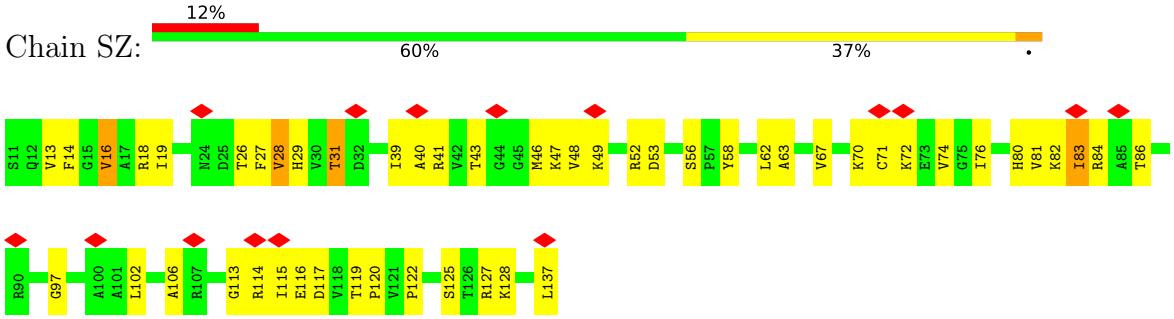
• Molecule 15: Small ribosomal subunit protein uS15

Chain SY:



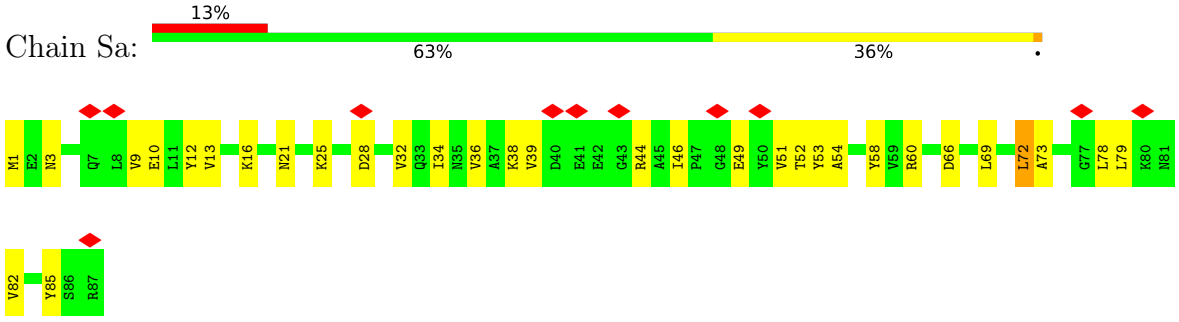
• Molecule 16: Small ribosomal subunit protein uS11B

Chain SZ:



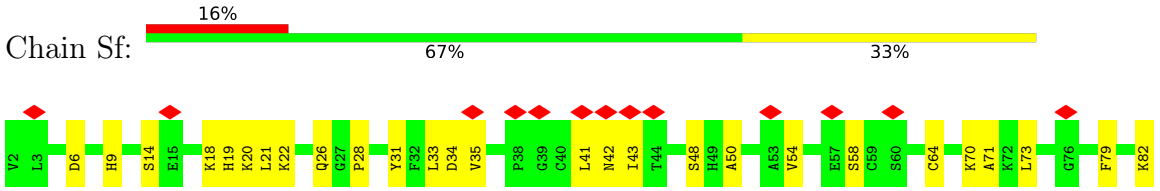
• Molecule 17: Small ribosomal subunit protein eS21A

Chain Sa:



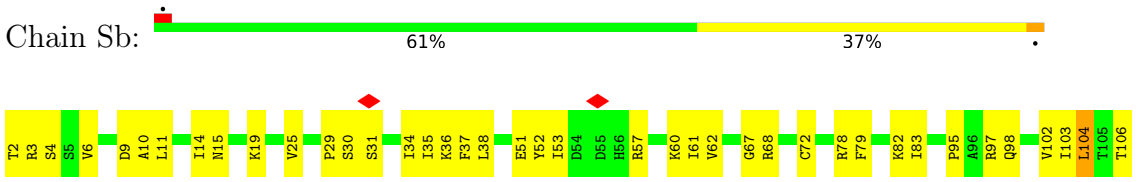
• Molecule 18: Small ribosomal subunit protein eS27A

Chain Sf:



• Molecule 19: Small ribosomal subunit protein uS8A

Chain Sb:

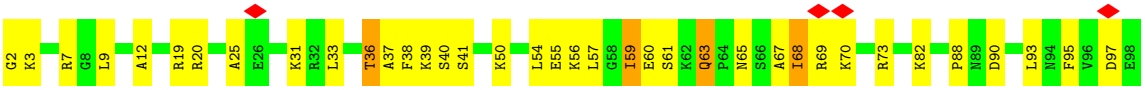




• Molecule 20: Small ribosomal subunit protein uS12A

Chain Sc:



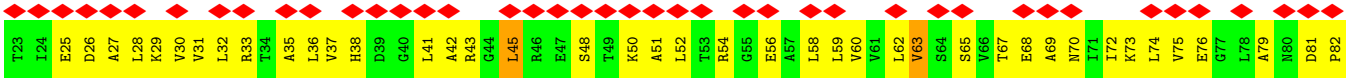


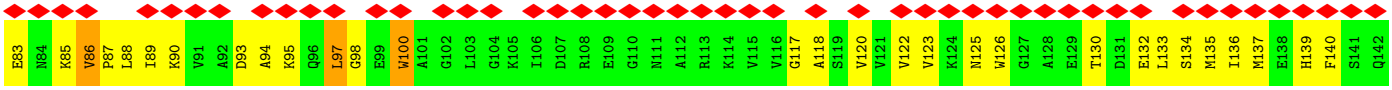


• Molecule 21: Small ribosomal subunit protein eS12

Chain SD:





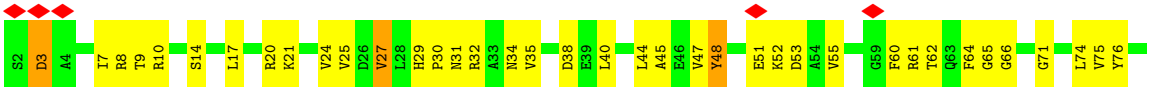


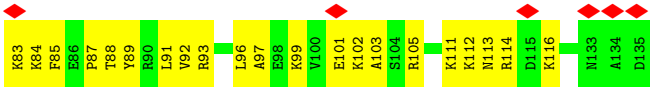


• Molecule 22: Small ribosomal subunit protein eS24A

Chain Sd:



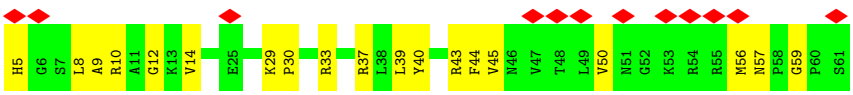




• Molecule 23: Small ribosomal subunit protein eS30A

Chain Sg:

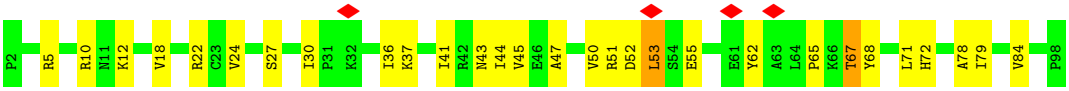




• Molecule 24: Small ribosomal subunit protein eS26B

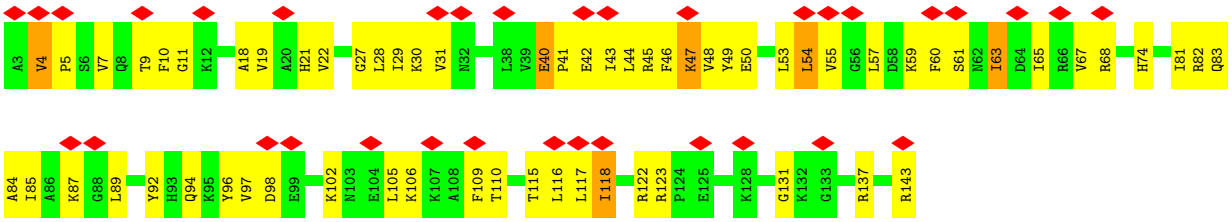
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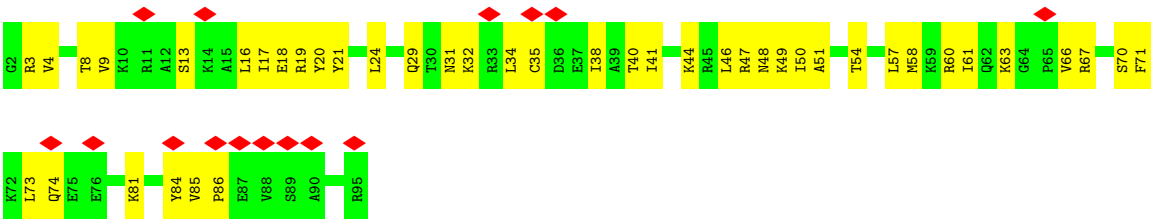
• Molecule 25: Small ribosomal subunit protein uS9A





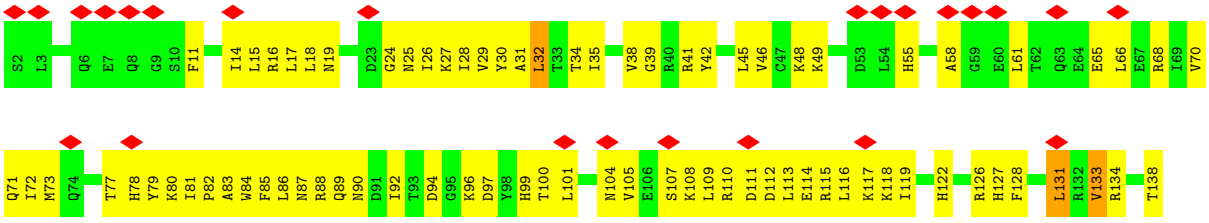
• Molecule 26: Small ribosomal subunit protein eS17A





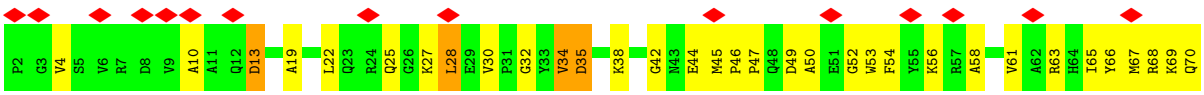
• Molecule 27: Small ribosomal subunit protein uS13A

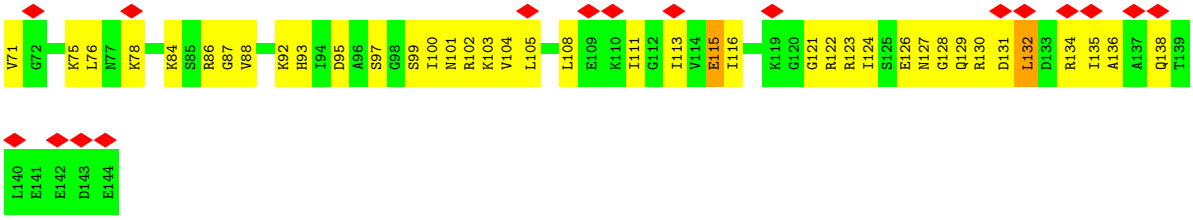




• Molecule 28: Small ribosomal subunit protein eS19A



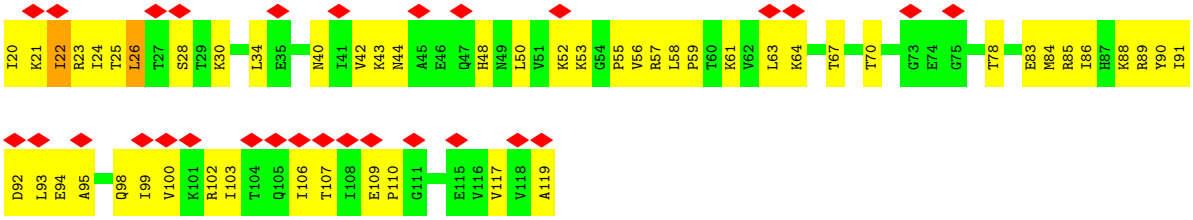




• Molecule 29: Small ribosomal subunit protein uS10

Chain SJ:

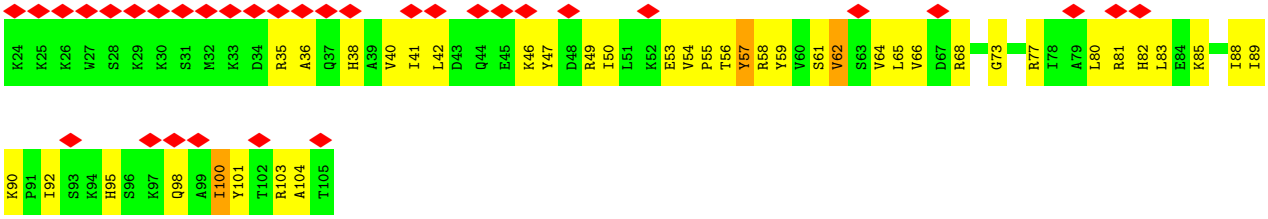




• Molecule 30: Small ribosomal subunit protein eS25A

Chain SK:

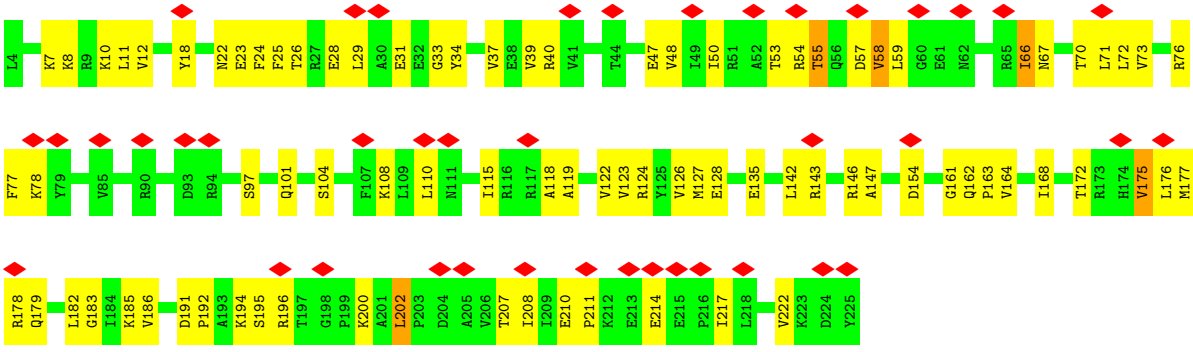




• Molecule 31: Small ribosomal subunit protein uS3

Chain SA:

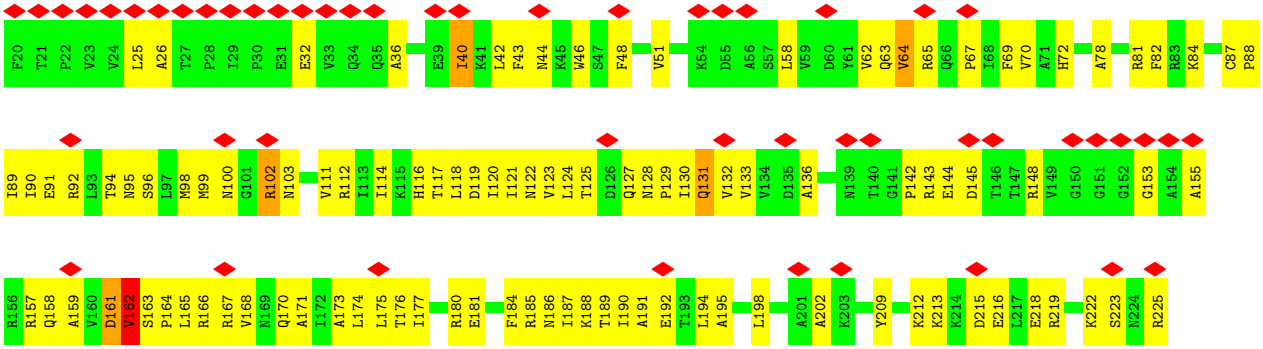




• Molecule 32: Small ribosomal subunit protein uS7

Chain SB:

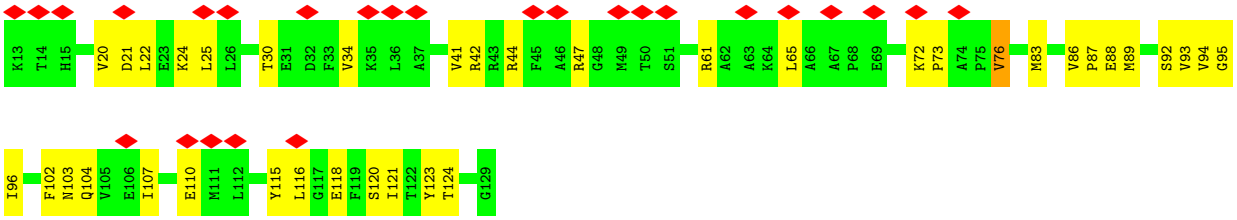




• Molecule 33: Small ribosomal subunit protein uS19

Chain SE:

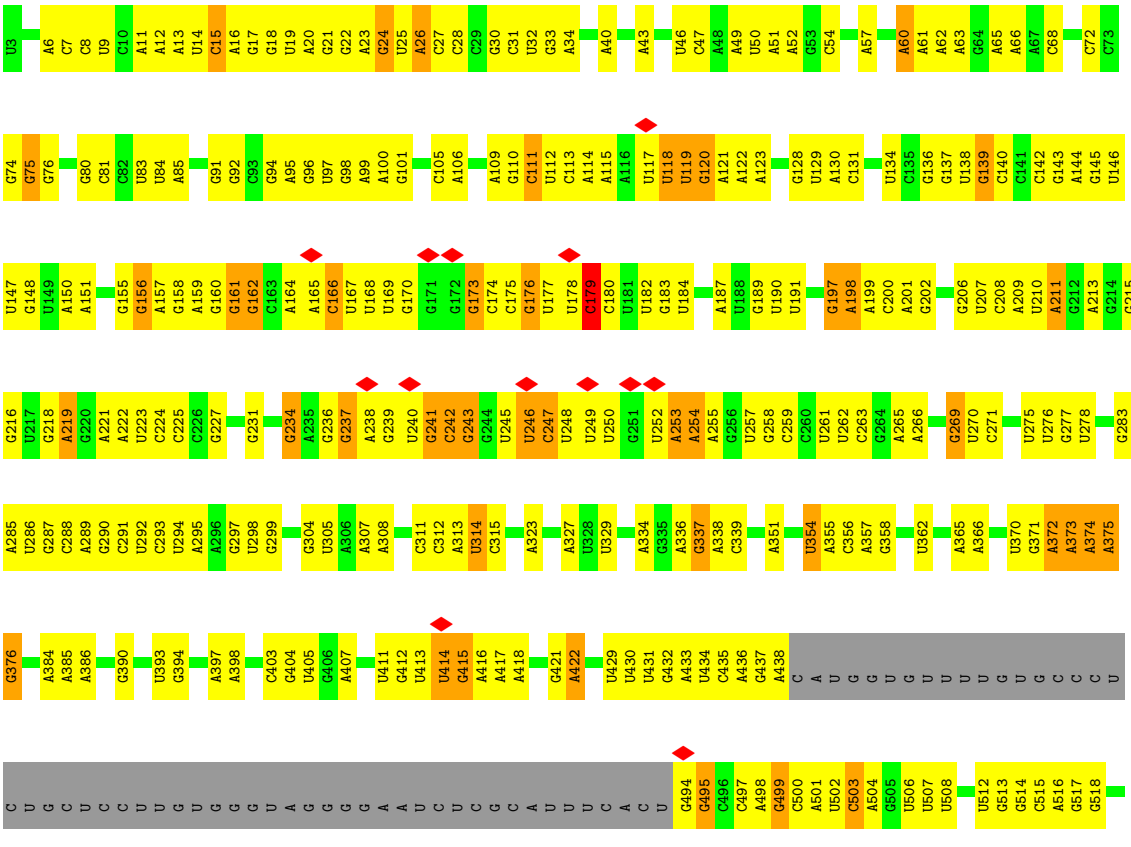


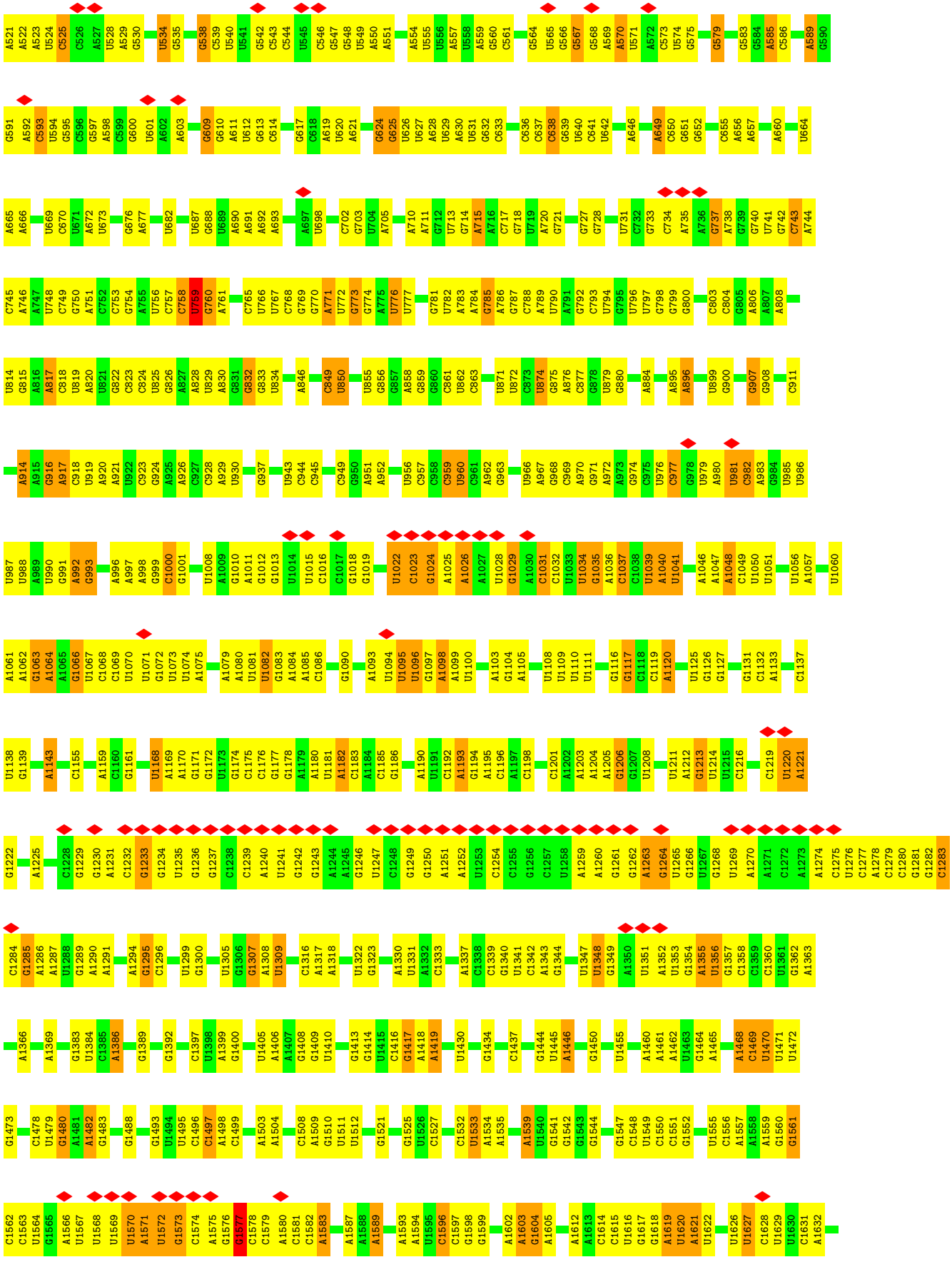


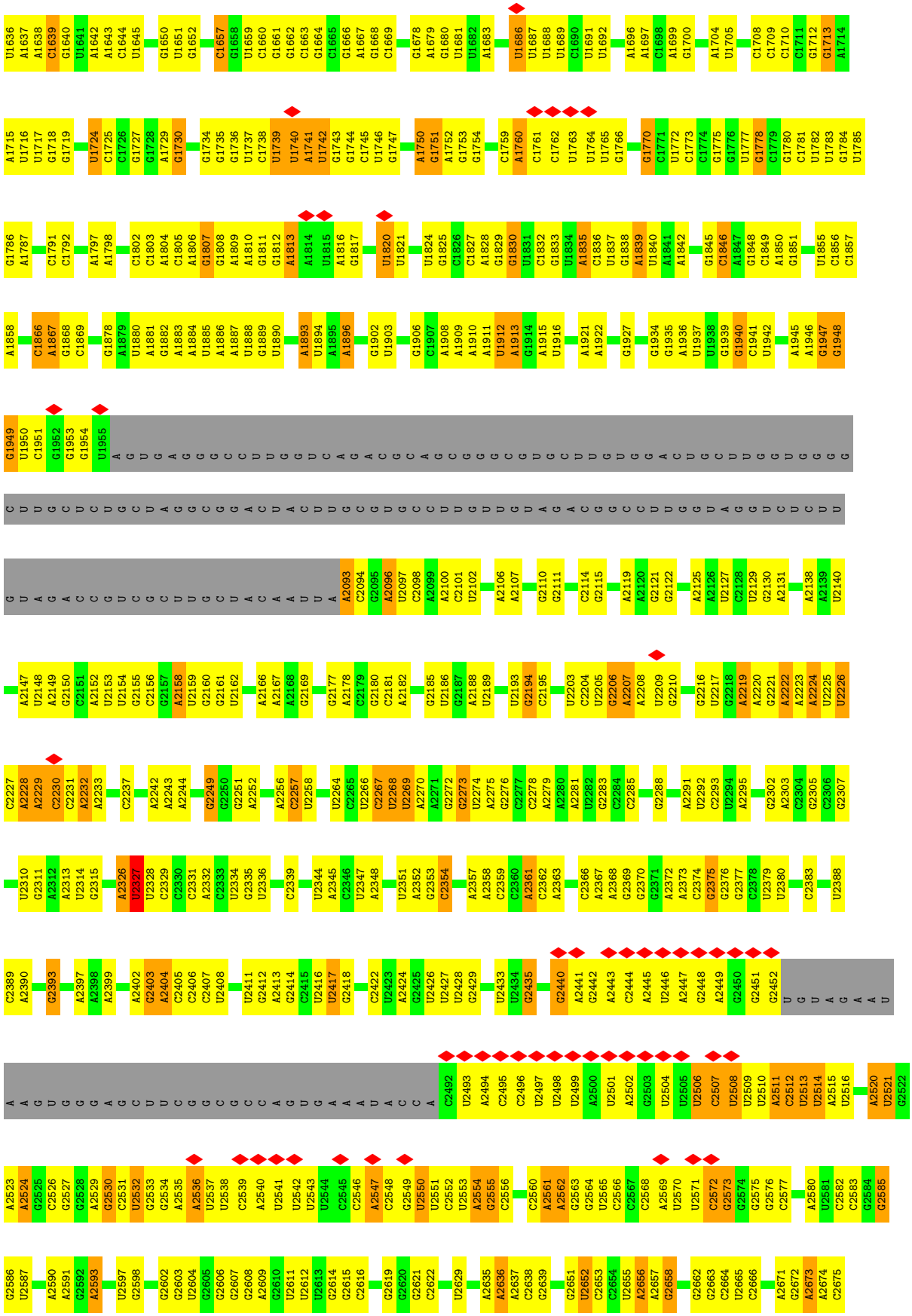
• Molecule 34: RNA (3393-MER)

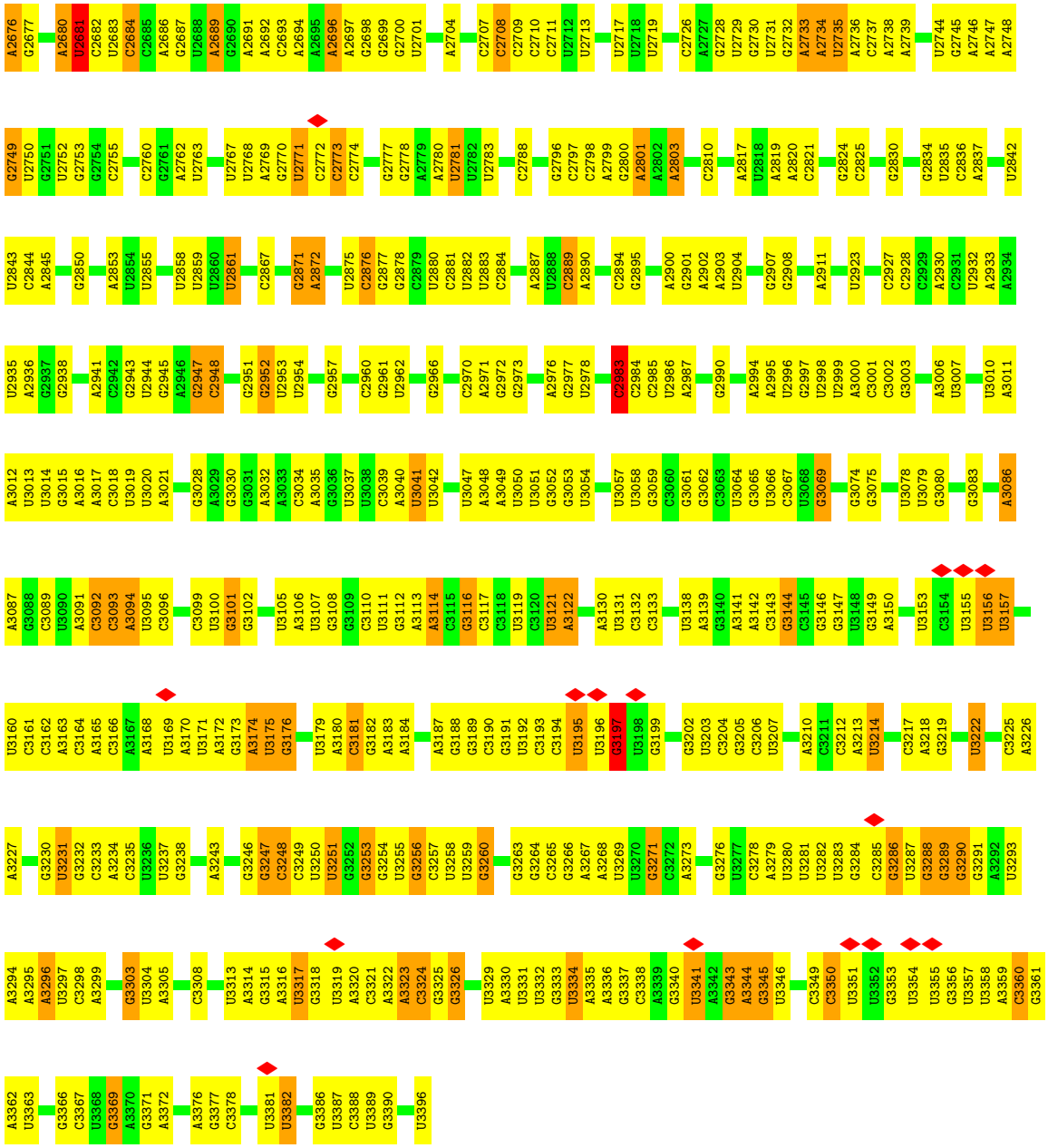
Chain LA:







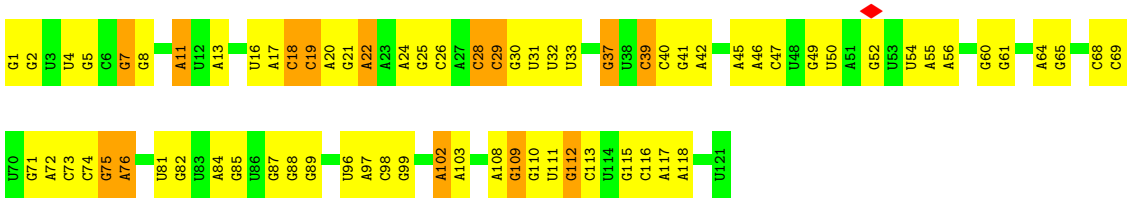




• Molecule 35: RNA (121-MER)

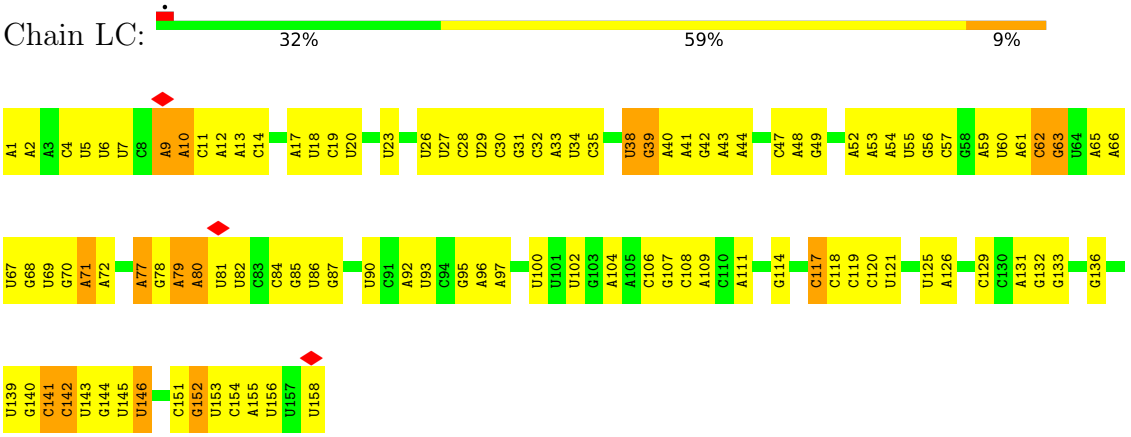
Chain LB:





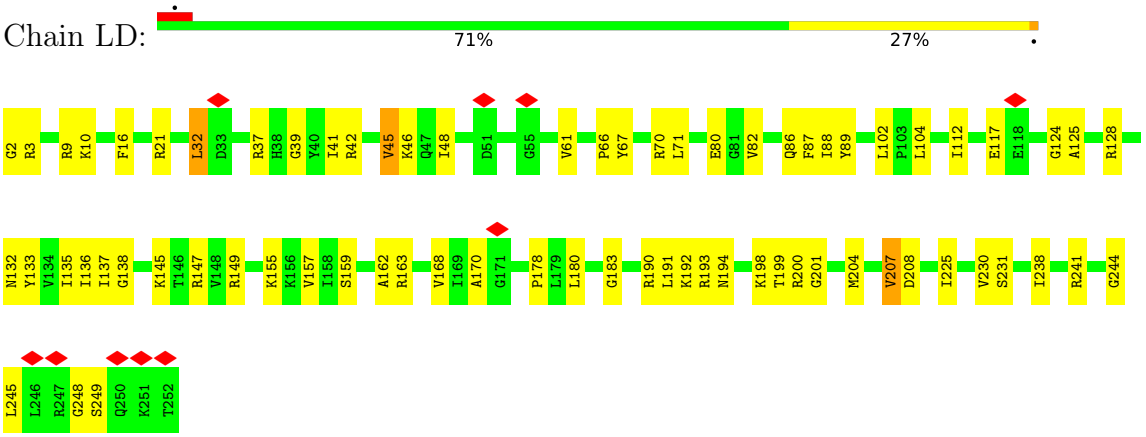
• Molecule 36: RNA (158-MER)

Chain LC:



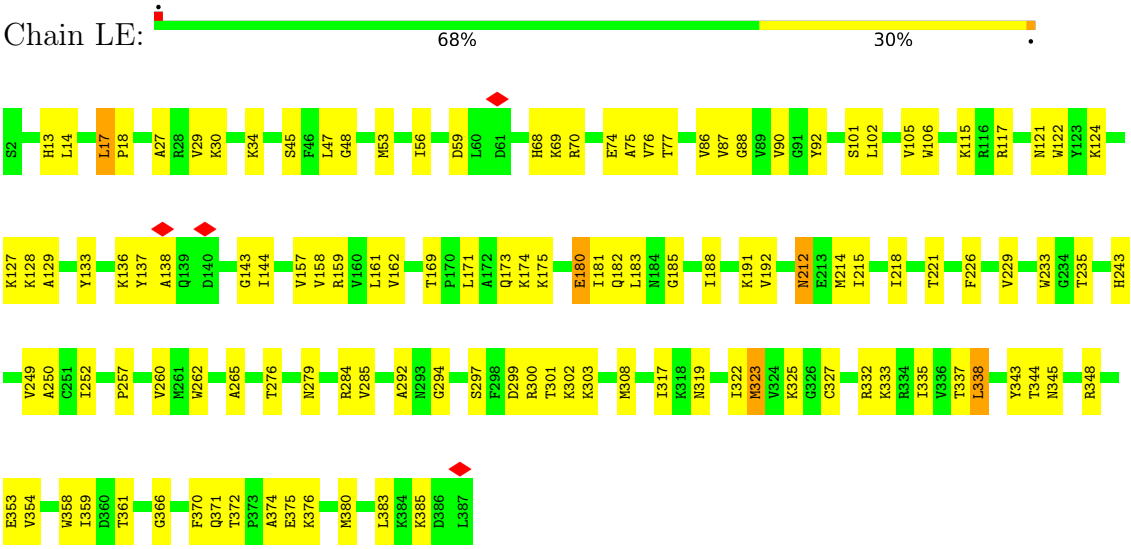
• Molecule 37: Large ribosomal subunit protein uL2A

Chain LD:



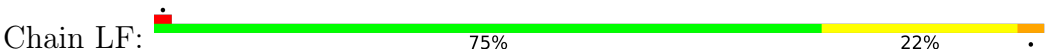
• Molecule 38: Large ribosomal subunit protein uL3

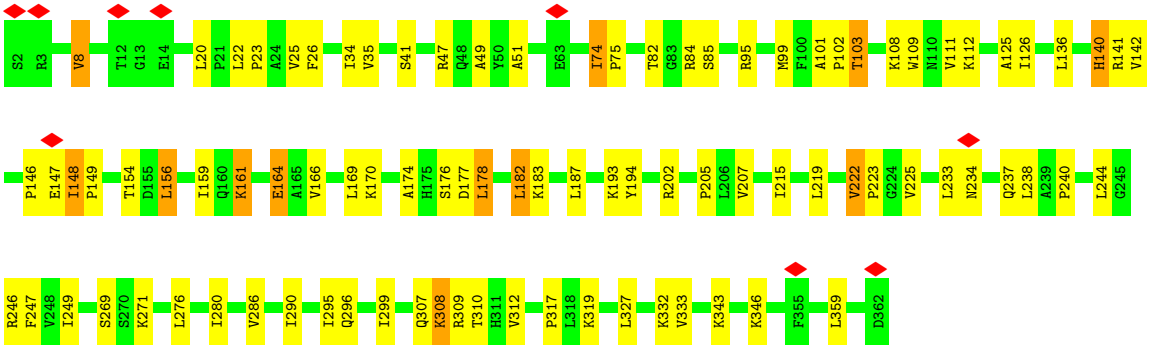
Chain LE:



• Molecule 39: Large ribosomal subunit protein uL4A

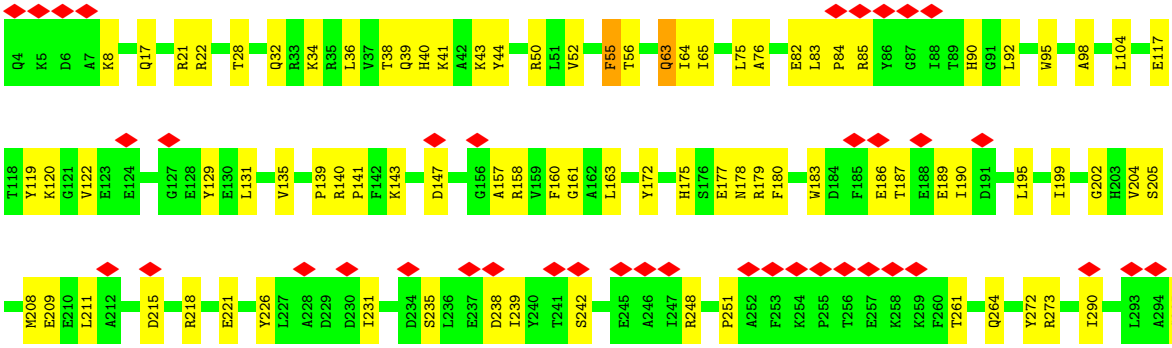
Chain LF:





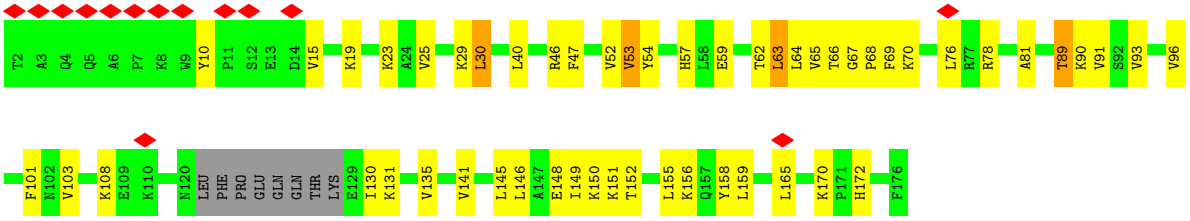
• Molecule 40: Large ribosomal subunit protein uL18





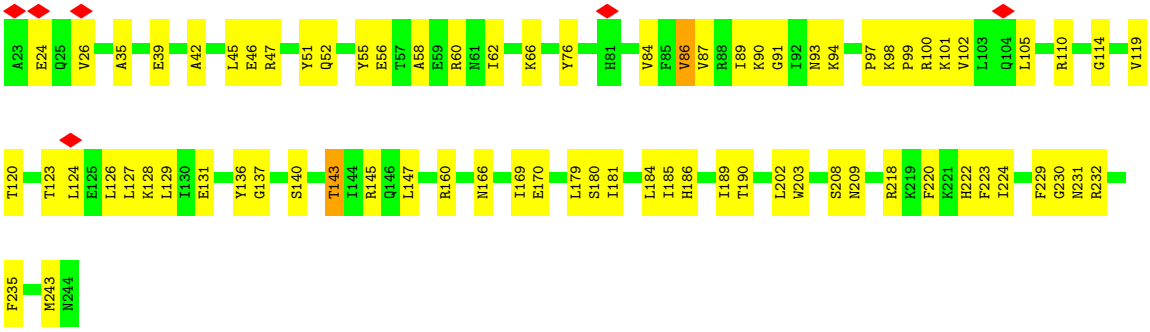
• Molecule 41: Large ribosomal subunit protein eL6B





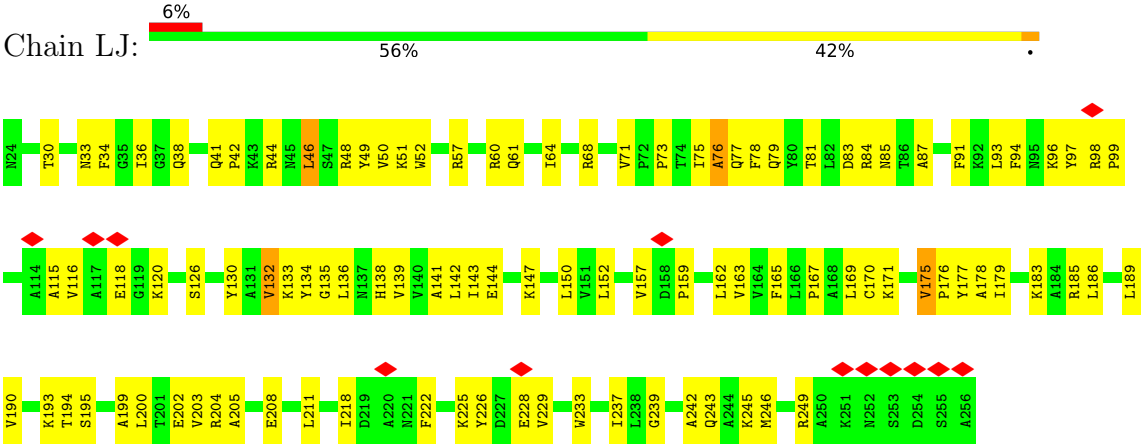
• Molecule 42: Large ribosomal subunit protein uL30A





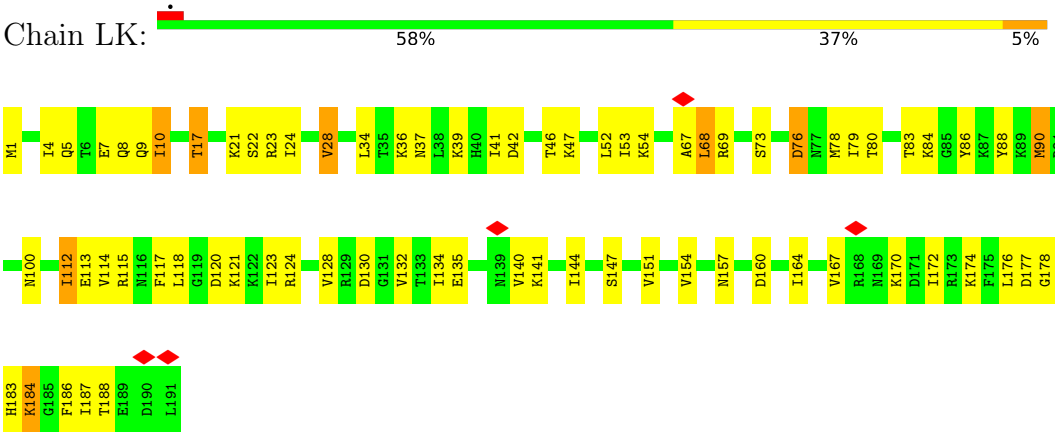
• Molecule 43: Large ribosomal subunit protein eL8A

Chain LJ:



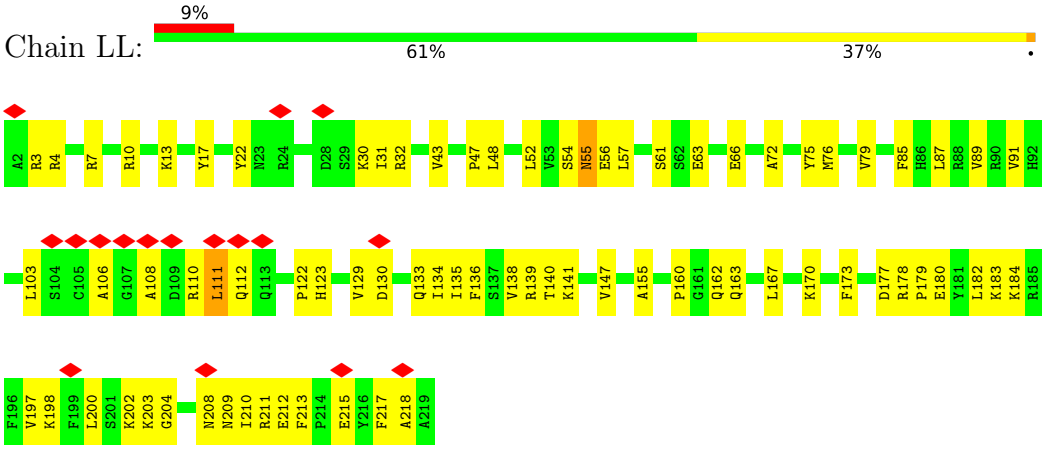
• Molecule 44: Large ribosomal subunit protein uL6A

Chain LK:



• Molecule 45: Large ribosomal subunit protein uL16

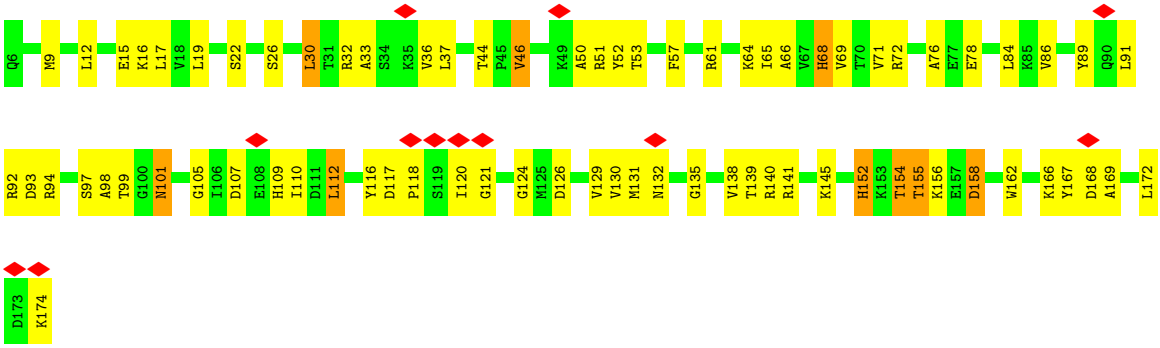
Chain LL:



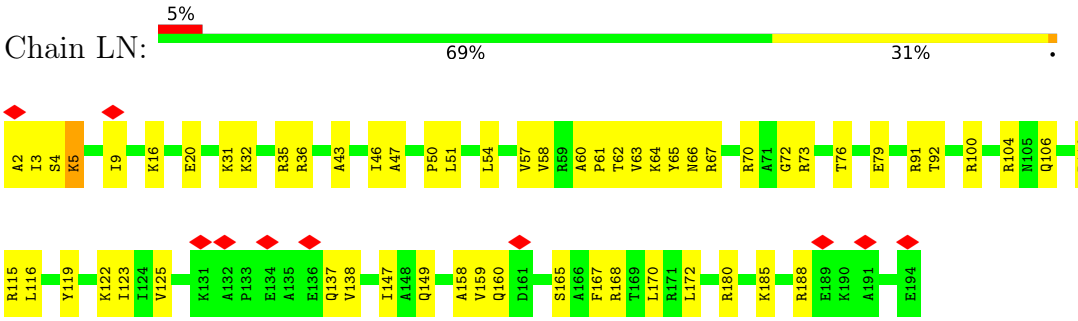
• Molecule 46: Large ribosomal subunit protein uL5B

Chain LM:

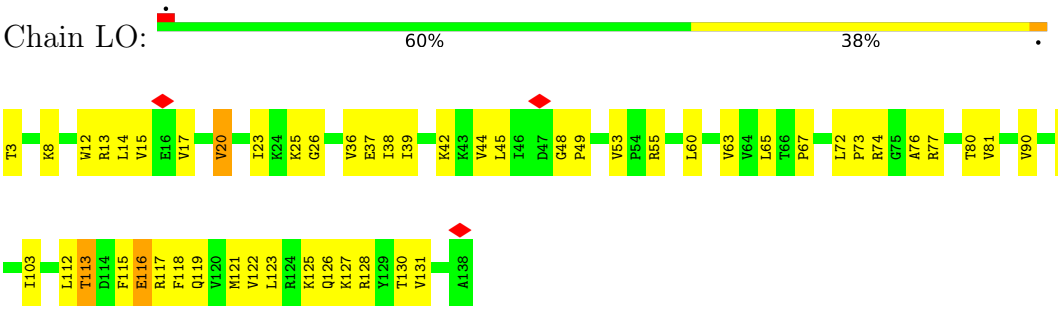




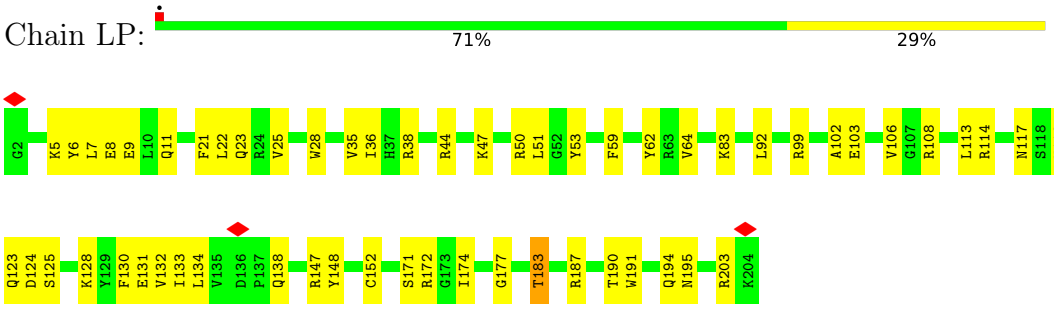
• Molecule 47: Large ribosomal subunit protein eL13A



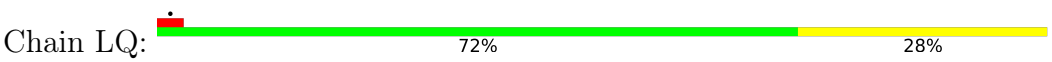
• Molecule 48: Large ribosomal subunit protein eL14A

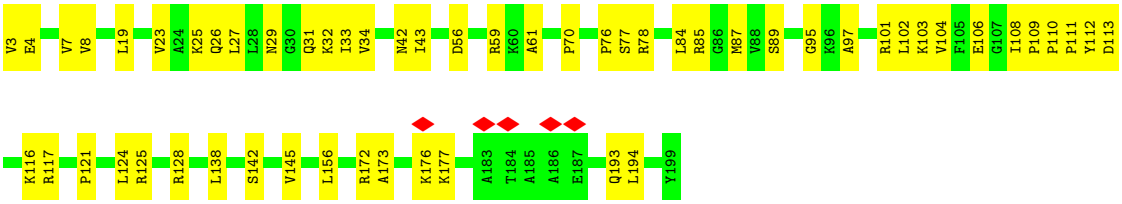


• Molecule 49: Large ribosomal subunit protein eL15A

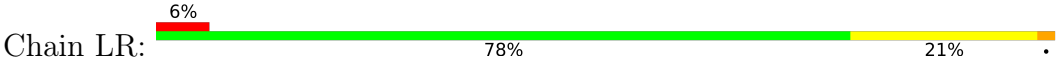


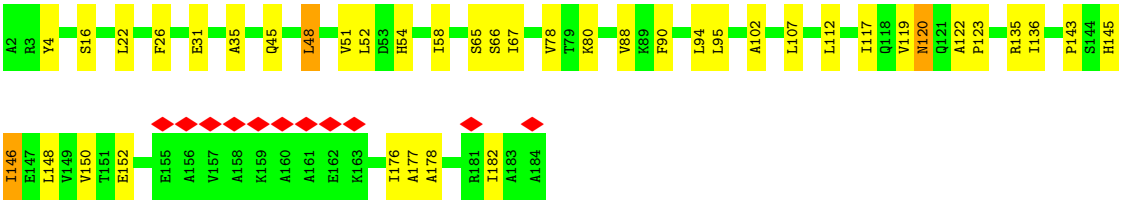
• Molecule 50: Large ribosomal subunit protein uL13A





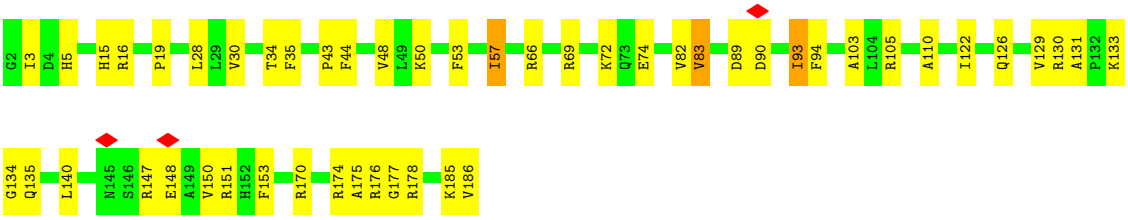
• Molecule 51: Large ribosomal subunit protein uL22A





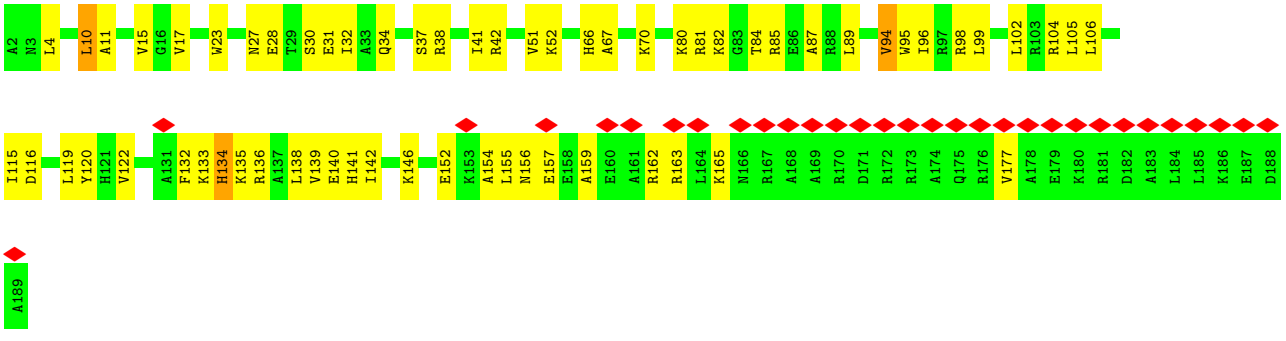
• Molecule 52: Large ribosomal subunit protein eL18A





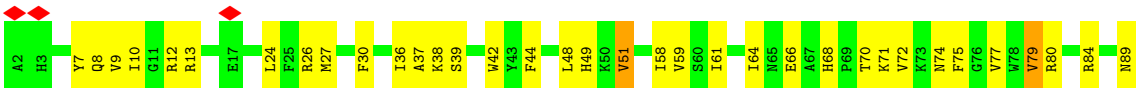
• Molecule 53: Large ribosomal subunit protein eL19A

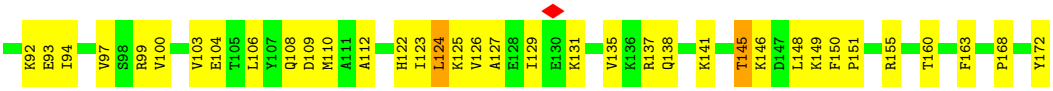




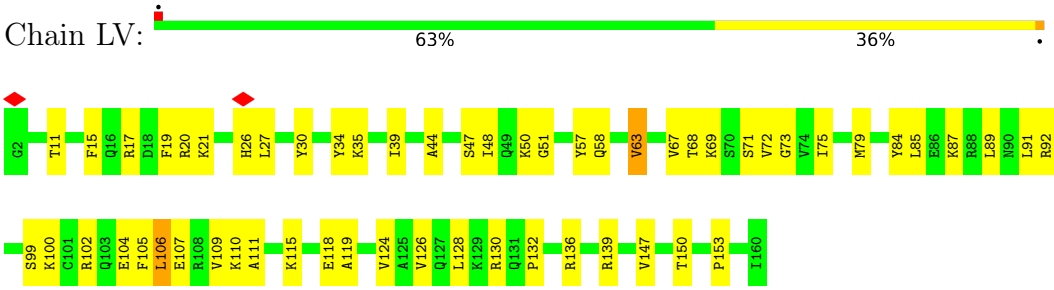
• Molecule 54: Large ribosomal subunit protein eL20A



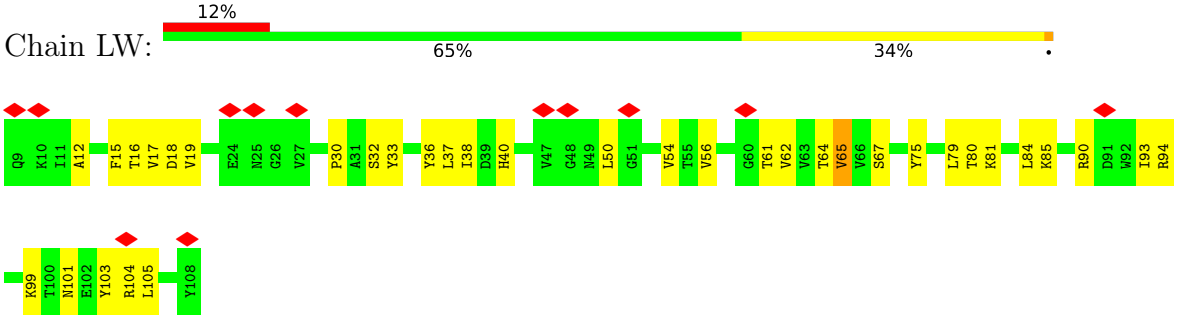




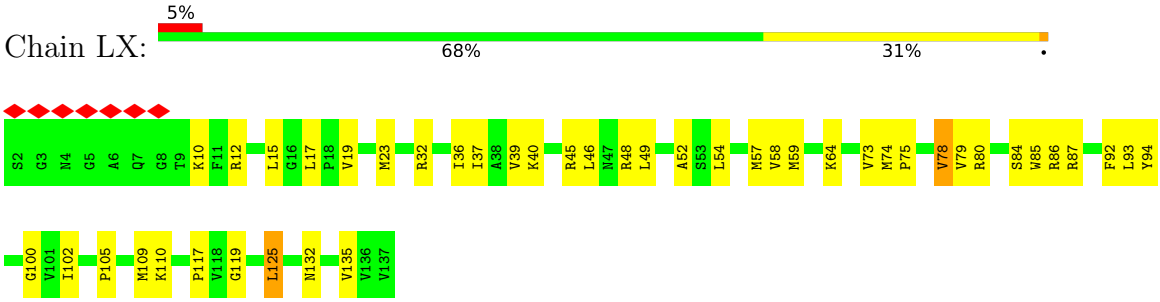
• Molecule 55: Large ribosomal subunit protein eL21A



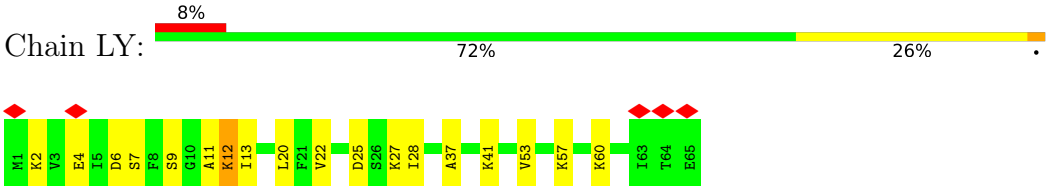
• Molecule 56: Large ribosomal subunit protein eL22A



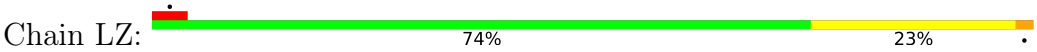
• Molecule 57: Large ribosomal subunit protein uL14A

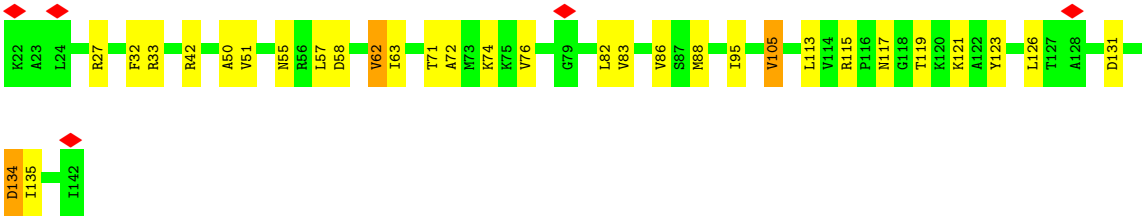


• Molecule 58: Large ribosomal subunit protein eL24A

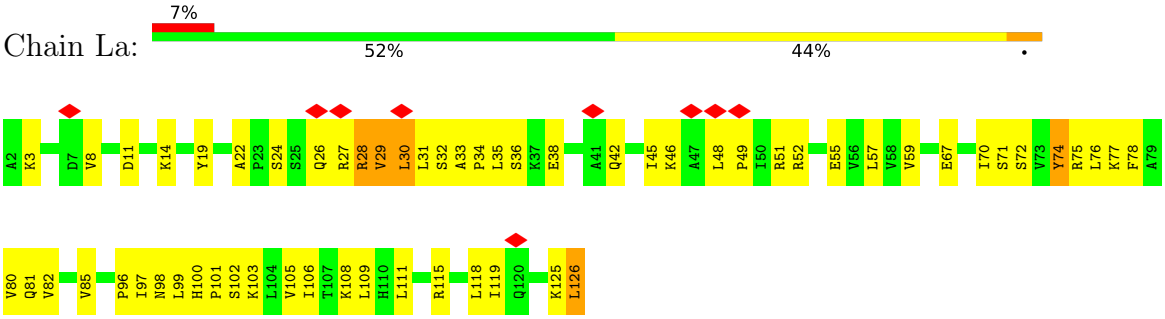


• Molecule 59: Large ribosomal subunit protein uL23

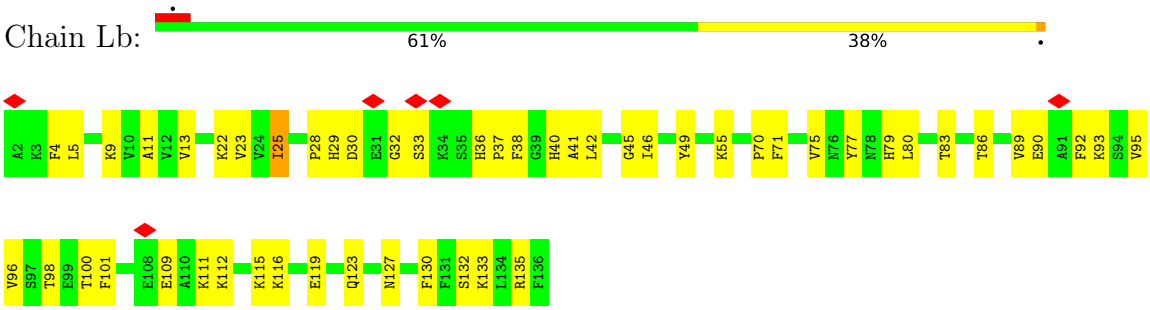




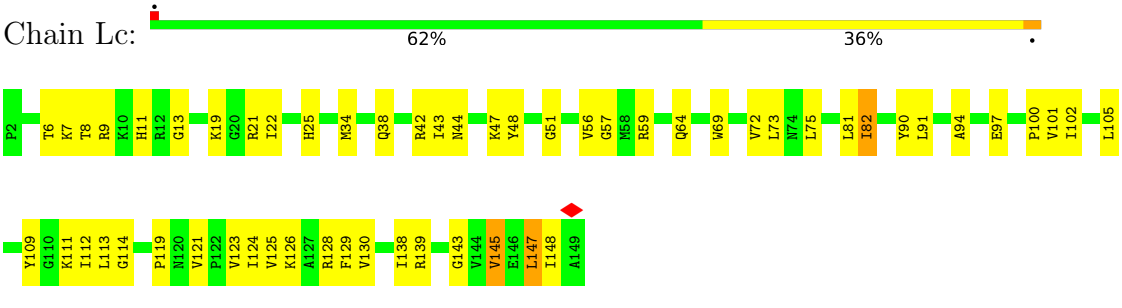
• Molecule 60: Large ribosomal subunit protein uL24A



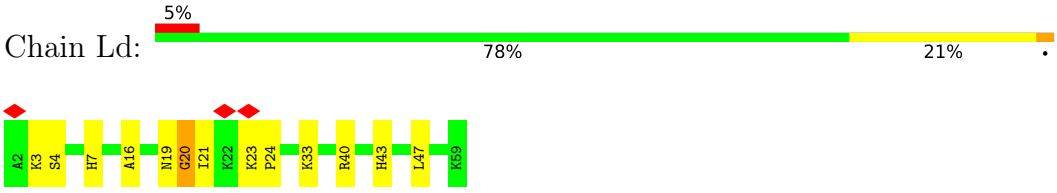
• Molecule 61: Large ribosomal subunit protein eL27A



• Molecule 62: Large ribosomal subunit protein uL15

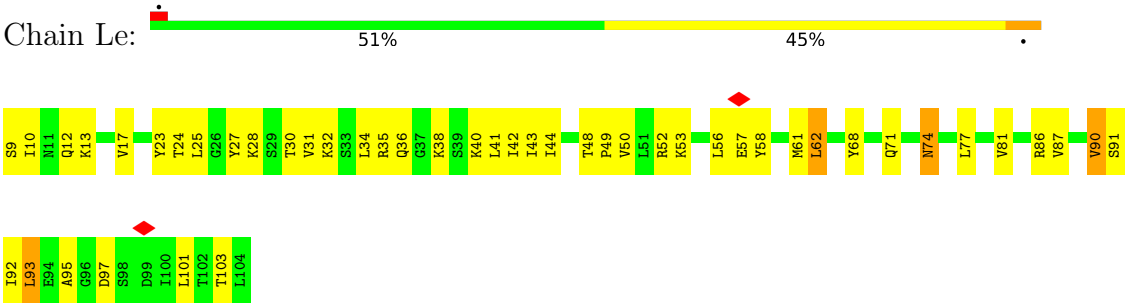


• Molecule 63: Large ribosomal subunit protein eL29



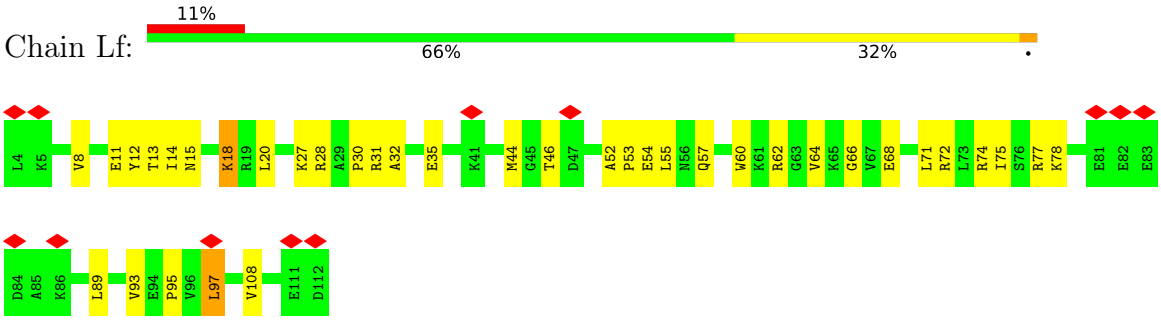
• Molecule 64: Large ribosomal subunit protein eL30

Chain Le:



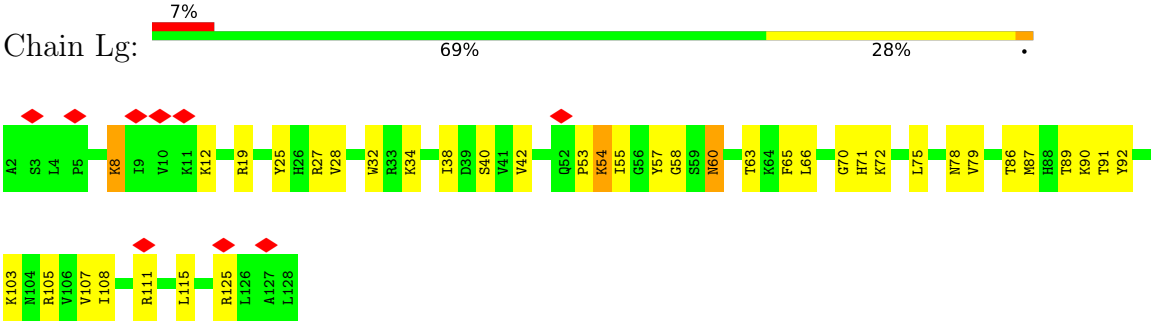
• Molecule 65: Large ribosomal subunit protein eL31A

Chain Lf:



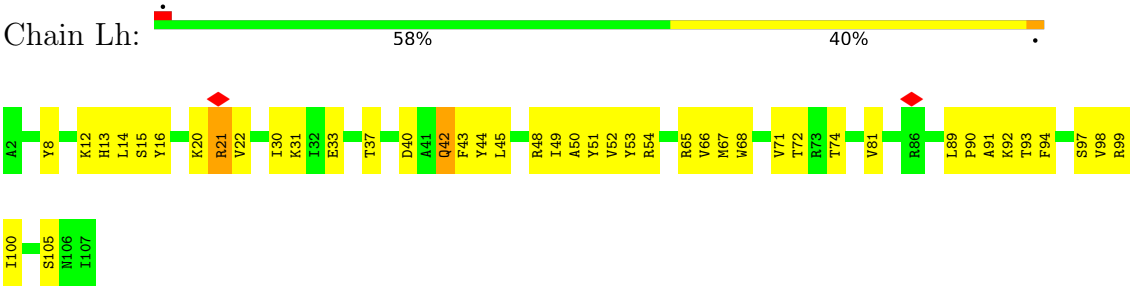
• Molecule 66: Large ribosomal subunit protein eL32

Chain Lg:



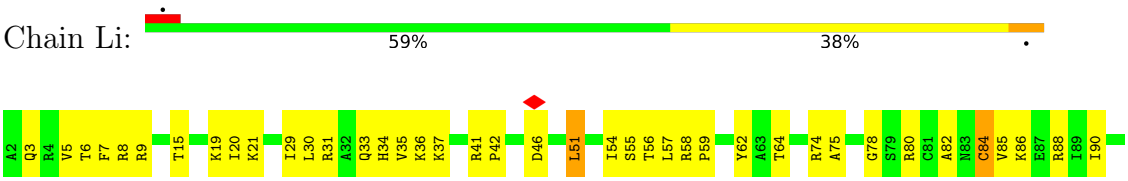
• Molecule 67: Large ribosomal subunit protein eL33A

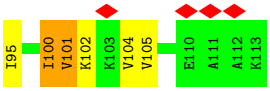
Chain Lh:



• Molecule 68: Large ribosomal subunit protein eL34A

Chain Li:

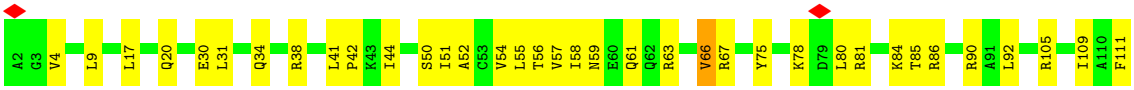


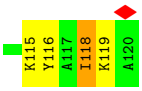


• Molecule 69: Large ribosomal subunit protein uL29A

Chain Lj:



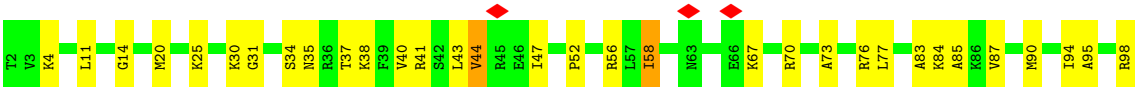




• Molecule 70: Large ribosomal subunit protein eL36A

Chain Lk:



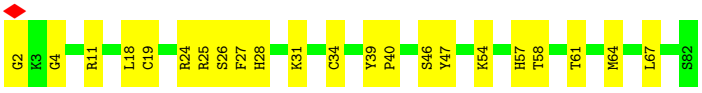




• Molecule 71: Large ribosomal subunit protein eL37A

Chain Ll:

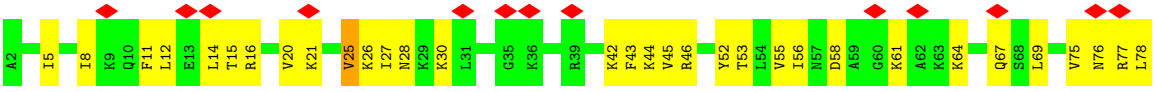




• Molecule 72: Large ribosomal subunit protein eL38

Chain Lm:

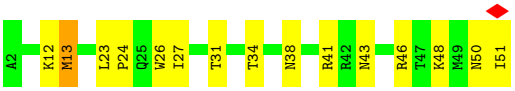




• Molecule 73: Large ribosomal subunit protein eL39

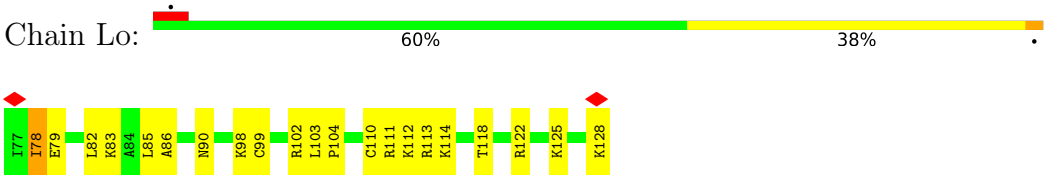
Chain Ln:





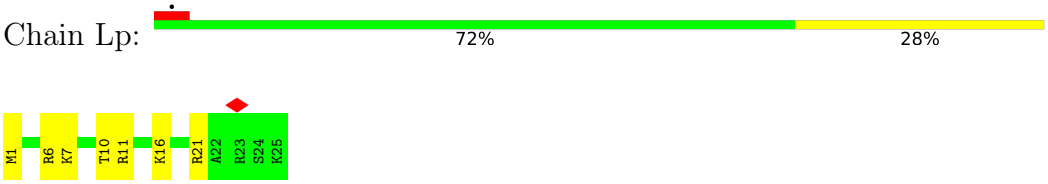
• Molecule 74: Large ribosomal subunit protein eL40A

Chain Lo:



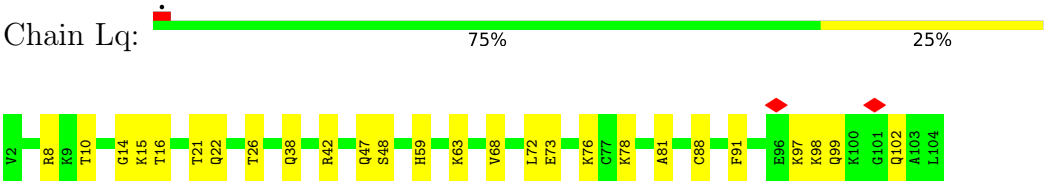
• Molecule 75: Large ribosomal subunit protein eL41A

Chain Lp:



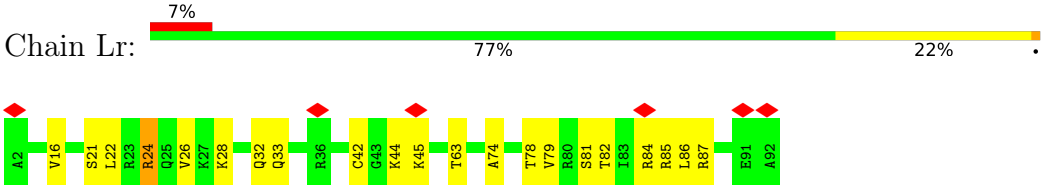
• Molecule 76: Large ribosomal subunit protein eL42A

Chain Lq:



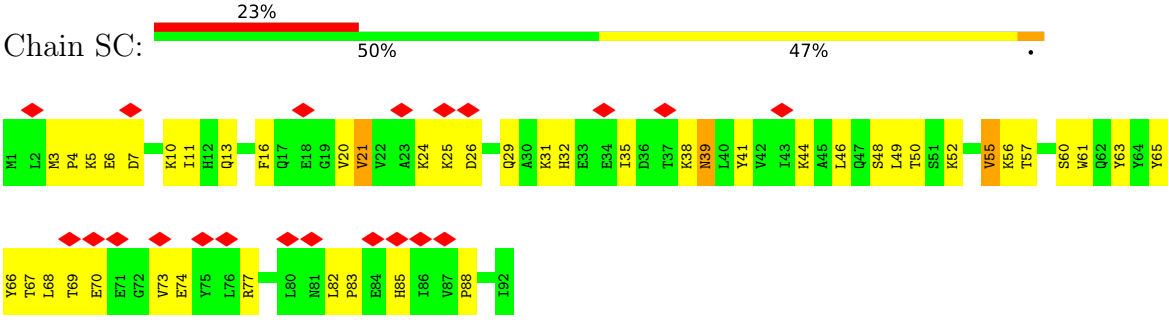
• Molecule 77: Large ribosomal subunit protein eL43A

Chain Lr:



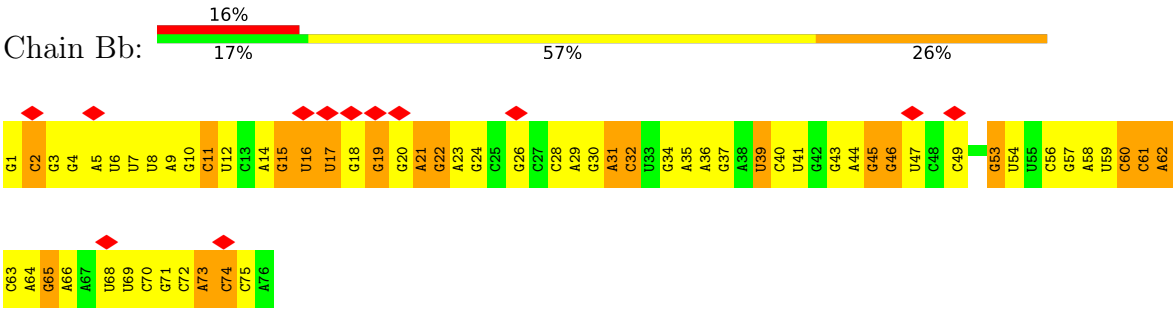
• Molecule 78: Small ribosomal subunit protein eS10A

Chain SC:



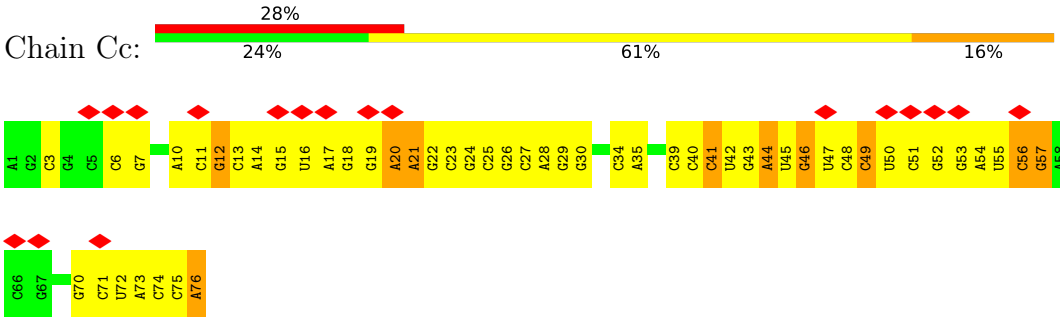
• Molecule 79: RNA (76-MER)

Chain Bb:



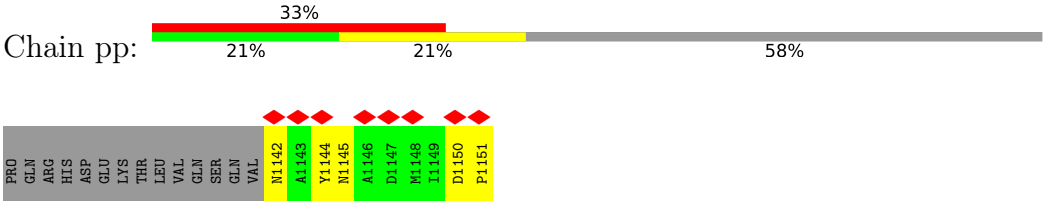
• Molecule 80: RNA (76-MER)

Chain Cc:



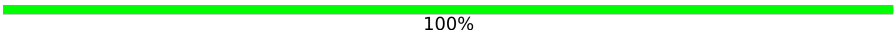
• Molecule 81: PRO-GLN-ARG-HIS-ASP-GLU-LYS-THR-LEU-VAL-GLN-SER-GLN-VAL-ASN-ALA-TYR-ASN-ALA-ASP-MET-ILE-ASP-PRO

Chain pp:



• Molecule 82: RNA (5'-R(P*GP*AP*CP*CP*CP*UP*UP*AP*AP*C)-3')

Chain mR:



There are no outlier residues recorded for this chain.

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5985	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	0.917	Depositor
Minimum map value	-0.535	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.16	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	S2	0.53	0/42189	0.86	63/65739 (0.1%)
2	SL	0.19	0/493	0.48	0/663
3	SM	0.27	0/452	0.51	0/600
4	SN	0.28	0/567	0.75	3/764 (0.4%)
5	SO	0.20	0/2436	0.48	0/3318
6	SP	0.24	0/1644	0.50	0/2249
7	SQ	0.25	0/1735	0.53	1/2335 (0.0%)
8	SR	0.28	0/1656	0.51	0/2251
9	SS	0.23	0/2097	0.45	0/2823
10	ST	0.22	0/1839	0.44	0/2460
11	SU	0.20	0/1498	0.46	0/2019
12	SV	0.24	0/1501	0.40	0/2006
13	SW	0.23	0/1504	0.43	0/2016
14	SX	0.26	0/1168	0.38	0/1575
15	SY	0.26	0/1215	0.46	0/1638
16	SZ	0.22	0/934	0.46	0/1257
17	Sa	0.26	0/682	0.53	0/921
18	Sf	0.22	0/620	0.41	0/838
19	Sb	0.28	0/1038	0.45	0/1395
20	Sc	0.27	0/1139	0.49	0/1518
21	SD	0.22	0/883	0.58	0/1199
22	Sd	0.31	0/1046	0.54	0/1401
23	Sg	0.20	0/459	0.42	0/611
24	Se	0.24	0/778	0.41	0/1042
25	SF	0.22	0/1125	0.51	0/1510
26	SG	0.25	0/773	0.63	0/1033
27	SH	0.21	0/1207	0.47	0/1623
28	SI	0.30	0/1130	0.53	0/1517
29	SJ	0.22	0/807	0.47	0/1091
30	SK	0.21	0/661	0.46	0/888
31	SA	0.22	0/1754	0.44	0/2361
32	SB	0.21	0/1625	0.45	0/2197
33	SE	0.18	0/936	0.40	0/1259
34	LA	0.64	0/75727	0.80	45/118064 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	LB	0.55	0/2883	0.74	0/4491
36	LC	0.63	0/3746	0.81	0/5832
37	LD	0.30	0/1933	0.40	0/2598
38	LE	0.28	0/3146	0.40	0/4228
39	LF	0.28	0/2800	0.39	0/3790
40	LG	0.22	0/2400	0.41	0/3239
41	LH	0.24	0/1329	0.40	0/1794
42	LI	0.30	0/1821	0.46	0/2451
43	LJ	0.26	0/1836	0.45	0/2481
44	LK	0.27	0/1529	0.46	0/2060
45	LL	0.25	0/1801	0.39	0/2416
46	LM	0.23	0/1367	0.45	0/1834
47	LN	0.26	0/1568	0.43	0/2106
48	LO	0.26	0/1068	0.45	0/1438
49	LP	0.30	0/1757	0.40	0/2354
50	LQ	0.29	0/1585	0.42	0/2128
51	LR	0.28	0/1439	0.40	0/1938
52	LS	0.28	0/1465	0.41	0/1965
53	LT	0.28	0/1532	0.47	0/2043
54	LU	0.30	0/1473	0.45	0/1980
55	LV	0.27	0/1296	0.44	0/1739
56	LW	0.22	0/812	0.41	0/1099
57	LX	0.30	0/1018	0.40	0/1369
58	LY	0.38	0/540	0.55	1/717 (0.1%)
59	LZ	0.27	0/979	0.41	0/1321
60	La	0.26	0/995	0.54	0/1329
61	Lb	0.31	0/1106	0.48	0/1485
62	Lc	0.30	0/1200	0.39	0/1607
63	Ld	0.25	0/473	0.43	0/629
64	Le	0.28	0/745	0.50	0/1001
65	Lf	0.26	0/890	0.39	0/1196
66	Lg	0.29	0/1038	0.43	0/1390
67	Lh	0.33	0/868	0.48	0/1168
68	Li	0.28	0/890	0.43	0/1189
69	Lj	0.26	0/978	0.40	0/1301
70	Lk	0.24	0/772	0.40	0/1026
71	Ll	0.29	0/660	0.39	0/875
72	Lm	0.22	0/618	0.45	0/826
73	Ln	0.25	0/443	0.33	0/588
74	Lo	0.27	0/416	0.45	0/553
75	Lp	0.23	0/230	0.43	0/296
76	Lq	0.25	0/836	0.38	0/1104
77	Lr	0.27	0/701	0.47	0/934

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	SC	0.25	0/769	0.52	0/1039
79	Bb	0.40	0/1814	0.86	0/2827
80	Cc	0.37	0/1821	0.78	0/2838
81	pp	0.27	0/78	0.62	0/106
All	All	0.49	0/216782	0.71	113/318899 (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
6	SP	0	1
11	SU	0	1
20	Sc	0	1
25	SF	0	1
32	SB	0	1
43	LJ	0	2
48	LO	0	1
60	La	0	1
63	Ld	0	2
All	All	0	11

There are no bond length outliers.

The worst 5 of 113 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	SN	132	LEU	CD1-CG-CD2	-8.30	92.54	110.80
1	S2	1585	U	C5-C6-N1	8.09	126.75	122.70
34	LA	179	C	N1-C2-O2	7.80	123.58	118.90
1	S2	1482	C	C2-N1-C1'	7.59	127.15	118.80
1	S2	735	C	N1-C2-O2	7.56	123.44	118.90

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
32	SB	162	VAL	Peptide
25	SF	40	GLU	Peptide
6	SP	193	GLN	Peptide
11	SU	64	VAL	Peptide

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Mol	Chain	Res	Type	Group
20	Sc	63	GLN	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	S2	37719	0	18978	1102	0
2	SL	491	0	524	21	0
3	SM	442	0	432	28	0
4	SN	556	0	544	35	0
5	SO	2383	0	2332	117	0
6	SP	1603	0	1610	72	0
7	SQ	1709	0	1784	92	0
8	SR	1626	0	1715	79	0
9	SS	2056	0	2140	79	0
10	ST	1815	0	1894	89	0
11	SU	1473	0	1553	63	0
12	SV	1476	0	1501	53	0
13	SW	1479	0	1556	76	0
14	SX	1142	0	1209	41	0
15	SY	1192	0	1255	53	0
16	SZ	923	0	948	44	0
17	Sa	673	0	662	29	0
18	Sf	610	0	633	17	0
19	Sb	1021	0	1060	41	0
20	Sc	1121	0	1195	52	0
21	SD	875	0	878	63	0
22	Sd	1032	0	1044	53	0
23	Sg	451	0	494	14	0
24	Se	765	0	814	22	0
25	SF	1105	0	1166	61	0
26	SG	764	0	808	42	0
27	SH	1188	0	1216	88	0
28	SI	1112	0	1124	63	0
29	SJ	797	0	863	45	0
30	SK	651	0	682	36	0
31	SA	1729	0	1812	65	0
32	SB	1605	0	1669	98	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	SE	916	0	941	33	0
34	LA	67653	0	33997	1279	0
35	LB	2579	0	1304	67	0
36	LC	3353	0	1695	74	0
37	LD	1899	0	1957	72	0
38	LE	3075	0	3142	94	0
39	LF	2748	0	2859	76	0
40	LG	2351	0	2294	77	0
41	LH	1307	0	1377	50	0
42	LI	1784	0	1862	56	0
43	LJ	1804	0	1877	83	0
44	LK	1508	0	1571	53	0
45	LL	1764	0	1804	63	0
46	LM	1346	0	1370	48	0
47	LN	1543	0	1608	48	0
48	LO	1053	0	1149	47	0
49	LP	1720	0	1779	50	0
50	LQ	1555	0	1659	48	0
51	LR	1416	0	1433	27	0
52	LS	1441	0	1543	42	0
53	LT	1515	0	1606	50	0
54	LU	1437	0	1475	56	0
55	LV	1272	0	1312	54	0
56	LW	796	0	812	25	0
57	LX	1003	0	1048	32	0
58	LY	528	0	544	12	0
59	LZ	964	0	1025	28	0
60	La	984	0	1074	52	0
61	Lb	1080	0	1118	38	0
62	Lc	1169	0	1211	55	0
63	Ld	462	0	491	10	0
64	Le	737	0	792	41	0
65	Lf	876	0	912	20	0
66	Lg	1017	0	1081	29	0
67	Lh	850	0	880	32	0
68	Li	880	0	945	33	0
69	Lj	969	0	1078	29	0
70	Lk	766	0	844	28	0
71	Ll	645	0	649	18	0
72	Lm	612	0	682	25	0
73	Ln	436	0	475	13	0
74	Lo	410	0	446	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
75	Lp	229	0	273	6	0
76	Lq	824	0	892	18	0
77	Lr	694	0	738	16	0
78	SC	752	0	719	48	0
79	Bb	1622	0	821	43	0
80	Cc	1628	0	827	57	0
81	pp	77	0	65	3	0
82	mR	209	0	0	0	0
All	All	201842	0	148151	5466	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 16.

The worst 5 of 5466 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)
1:S2:1673:G:N1	1:S2:1728:A:H2	1.28	1.31
1:S2:1673:G:N1	1:S2:1728:A:C2	2.02	1.20
1:S2:229:U:H3	1:S2:237:C:N4	1.44	1.14
34:LA:3234:A:N6	34:LA:3253:G:H1	1.46	1.13
34:LA:2216:G:H1	34:LA:2228:A:H61	1.06	1.02

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	
2	SL	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
3	SM	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
4	SN	71/73 (97%)	52 (73%)	19 (27%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	SO	310/312 (99%)	278 (90%)	32 (10%)	0	100	100
6	SP	204/206 (99%)	173 (85%)	31 (15%)	0	100	100
7	SQ	212/214 (99%)	186 (88%)	26 (12%)	0	100	100
8	SR	214/216 (99%)	201 (94%)	13 (6%)	0	100	100
9	SS	256/258 (99%)	233 (91%)	23 (9%)	0	100	100
10	ST	226/228 (99%)	207 (92%)	18 (8%)	1 (0%)	30	58
11	SU	182/184 (99%)	171 (94%)	11 (6%)	0	100	100
12	SV	183/198 (92%)	171 (93%)	12 (7%)	0	100	100
13	SW	182/184 (99%)	167 (92%)	15 (8%)	0	100	100
14	SX	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
15	SY	148/150 (99%)	136 (92%)	12 (8%)	0	100	100
16	SZ	125/127 (98%)	117 (94%)	8 (6%)	0	100	100
17	Sa	85/87 (98%)	73 (86%)	12 (14%)	0	100	100
18	Sf	79/81 (98%)	69 (87%)	10 (13%)	0	100	100
19	Sb	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
20	Sc	142/144 (99%)	125 (88%)	17 (12%)	0	100	100
21	SD	119/121 (98%)	92 (77%)	26 (22%)	1 (1%)	16	44
22	Sd	132/134 (98%)	124 (94%)	8 (6%)	0	100	100
23	Sg	55/57 (96%)	49 (89%)	6 (11%)	0	100	100
24	Se	95/97 (98%)	89 (94%)	6 (6%)	0	100	100
25	SF	139/141 (99%)	128 (92%)	11 (8%)	0	100	100
26	SG	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
27	SH	143/145 (99%)	132 (92%)	11 (8%)	0	100	100
28	SI	141/143 (99%)	134 (95%)	7 (5%)	0	100	100
29	SJ	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
30	SK	80/82 (98%)	70 (88%)	10 (12%)	0	100	100
31	SA	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
32	SB	204/206 (99%)	182 (89%)	21 (10%)	1 (0%)	24	52
33	SE	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
37	LD	249/251 (99%)	232 (93%)	17 (7%)	0	100	100
38	LE	384/386 (100%)	352 (92%)	32 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	LF	359/361 (99%)	337 (94%)	22 (6%)	0	100	100
40	LG	292/294 (99%)	278 (95%)	14 (5%)	0	100	100
41	LH	163/175 (93%)	154 (94%)	9 (6%)	0	100	100
42	LI	220/222 (99%)	207 (94%)	13 (6%)	0	100	100
43	LJ	231/233 (99%)	217 (94%)	14 (6%)	0	100	100
44	LK	189/191 (99%)	167 (88%)	22 (12%)	0	100	100
45	LL	216/218 (99%)	206 (95%)	10 (5%)	0	100	100
46	LM	167/169 (99%)	154 (92%)	13 (8%)	0	100	100
47	LN	191/193 (99%)	175 (92%)	16 (8%)	0	100	100
48	LO	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
49	LP	201/203 (99%)	191 (95%)	10 (5%)	0	100	100
50	LQ	195/197 (99%)	188 (96%)	7 (4%)	0	100	100
51	LR	181/183 (99%)	167 (92%)	14 (8%)	0	100	100
52	LS	183/185 (99%)	166 (91%)	17 (9%)	0	100	100
53	LT	186/188 (99%)	180 (97%)	6 (3%)	0	100	100
54	LU	169/171 (99%)	160 (95%)	9 (5%)	0	100	100
55	LV	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
56	LW	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
57	LX	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
58	LY	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
59	LZ	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
60	La	123/125 (98%)	111 (90%)	11 (9%)	1 (1%)	16	44
61	Lb	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
62	Lc	146/148 (99%)	133 (91%)	13 (9%)	0	100	100
63	Ld	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
64	Le	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
65	Lf	107/109 (98%)	100 (94%)	7 (6%)	0	100	100
66	Lg	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
67	Lh	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
68	Li	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
69	Lj	117/119 (98%)	109 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	Lk	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
71	Ll	79/81 (98%)	74 (94%)	5 (6%)	0	100	100
72	Lm	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
73	Ln	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
74	Lo	50/52 (96%)	45 (90%)	5 (10%)	0	100	100
75	Lp	23/25 (92%)	23 (100%)	0	0	100	100
76	Lq	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
77	Lr	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
78	SC	90/92 (98%)	75 (83%)	14 (16%)	1 (1%)	11	36
81	pp	8/24 (33%)	6 (75%)	2 (25%)	0	100	100
All	All	10887/11074 (98%)	10064 (92%)	818 (8%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	SD	82	PRO
60	La	28	ARG
10	ST	175	ILE
32	SB	162	VAL
78	SC	5	LYS

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	
2	SL	55/56 (98%)	53 (96%)	2 (4%)	31	56
3	SM	47/47 (100%)	46 (98%)	1 (2%)	47	64
4	SN	56/64 (88%)	50 (89%)	6 (11%)	6	23
5	SO	250/257 (97%)	230 (92%)	20 (8%)	11	36
6	SP	170/173 (98%)	161 (95%)	9 (5%)	20	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
7	SQ	191/191 (100%)	175 (92%)	16 (8%)	10 34
8	SR	175/175 (100%)	166 (95%)	9 (5%)	21 48
9	SS	220/220 (100%)	210 (96%)	10 (4%)	24 51
10	ST	189/195 (97%)	174 (92%)	15 (8%)	11 37
11	SU	163/165 (99%)	160 (98%)	3 (2%)	51 66
12	SV	148/159 (93%)	140 (95%)	8 (5%)	20 47
13	SW	156/157 (99%)	147 (94%)	9 (6%)	18 45
14	SX	126/127 (99%)	118 (94%)	8 (6%)	16 43
15	SY	127/127 (100%)	118 (93%)	9 (7%)	13 39
16	SZ	90/96 (94%)	82 (91%)	8 (9%)	9 31
17	Sa	71/74 (96%)	66 (93%)	5 (7%)	14 40
18	Sf	70/70 (100%)	68 (97%)	2 (3%)	37 60
19	Sb	110/110 (100%)	107 (97%)	3 (3%)	39 60
20	Sc	119/119 (100%)	112 (94%)	7 (6%)	18 44
21	SD	88/98 (90%)	81 (92%)	7 (8%)	11 36
22	Sd	102/112 (91%)	96 (94%)	6 (6%)	18 44
23	Sg	48/49 (98%)	41 (85%)	7 (15%)	3 12
24	Se	82/83 (99%)	77 (94%)	5 (6%)	17 44
25	SF	117/117 (100%)	111 (95%)	6 (5%)	21 48
26	SG	82/85 (96%)	78 (95%)	4 (5%)	22 49
27	SH	127/128 (99%)	120 (94%)	7 (6%)	19 47
28	SI	115/115 (100%)	105 (91%)	10 (9%)	9 32
29	SJ	93/93 (100%)	86 (92%)	7 (8%)	12 38
30	SK	67/73 (92%)	63 (94%)	4 (6%)	17 44
31	SA	182/182 (100%)	173 (95%)	9 (5%)	22 49
32	SB	172/173 (99%)	163 (95%)	9 (5%)	21 48
33	SE	95/98 (97%)	92 (97%)	3 (3%)	34 58
37	LD	190/193 (98%)	185 (97%)	5 (3%)	40 61
38	LE	318/322 (99%)	306 (96%)	12 (4%)	29 55
39	LF	288/288 (100%)	273 (95%)	15 (5%)	21 48
40	LG	241/243 (99%)	236 (98%)	5 (2%)	47 64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
41	LH	139/154 (90%)	130 (94%)	9 (6%)	15 42
42	LI	186/186 (100%)	180 (97%)	6 (3%)	34 58
43	LJ	187/191 (98%)	179 (96%)	8 (4%)	26 52
44	LK	168/171 (98%)	148 (88%)	20 (12%)	5 19
45	LL	185/185 (100%)	175 (95%)	10 (5%)	20 47
46	LM	145/147 (99%)	133 (92%)	12 (8%)	10 35
47	LN	154/154 (100%)	148 (96%)	6 (4%)	28 54
48	LO	107/107 (100%)	103 (96%)	4 (4%)	30 55
49	LP	175/175 (100%)	169 (97%)	6 (3%)	32 58
50	LQ	160/160 (100%)	159 (99%)	1 (1%)	78 79
51	LR	138/145 (95%)	131 (95%)	7 (5%)	21 48
52	LS	150/150 (100%)	142 (95%)	8 (5%)	20 48
53	LT	152/153 (99%)	144 (95%)	8 (5%)	20 48
54	LU	155/155 (100%)	149 (96%)	6 (4%)	28 54
55	LV	135/136 (99%)	128 (95%)	7 (5%)	21 48
56	LW	87/87 (100%)	83 (95%)	4 (5%)	24 50
57	LX	104/104 (100%)	101 (97%)	3 (3%)	37 60
58	LY	54/57 (95%)	53 (98%)	1 (2%)	50 66
59	LZ	104/105 (99%)	100 (96%)	4 (4%)	29 55
60	La	108/108 (100%)	101 (94%)	7 (6%)	15 42
61	Lb	112/115 (97%)	107 (96%)	5 (4%)	24 51
62	Lc	117/118 (99%)	111 (95%)	6 (5%)	21 48
63	Ld	46/46 (100%)	45 (98%)	1 (2%)	45 63
64	Le	81/81 (100%)	74 (91%)	7 (9%)	10 33
65	Lf	92/96 (96%)	87 (95%)	5 (5%)	20 47
66	Lg	108/109 (99%)	103 (95%)	5 (5%)	24 50
67	Lh	90/90 (100%)	82 (91%)	8 (9%)	9 31
68	Li	95/95 (100%)	85 (90%)	10 (10%)	6 24
69	Lj	104/104 (100%)	94 (90%)	10 (10%)	8 29
70	Lk	80/81 (99%)	78 (98%)	2 (2%)	42 61
71	Ll	67/67 (100%)	66 (98%)	1 (2%)	57 68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	Lm	68/68 (100%)	67 (98%)	1 (2%)	57	68
73	Ln	45/45 (100%)	43 (96%)	2 (4%)	25	51
74	Lo	45/47 (96%)	44 (98%)	1 (2%)	45	63
75	Lp	22/23 (96%)	21 (96%)	1 (4%)	24	51
76	Lq	87/88 (99%)	84 (97%)	3 (3%)	32	58
77	Lr	71/71 (100%)	67 (94%)	4 (6%)	19	46
78	SC	77/85 (91%)	72 (94%)	5 (6%)	15	42
81	pp	8/22 (36%)	8 (100%)	0	100	100
All	All	9148/9315 (98%)	8663 (95%)	485 (5%)	22	48

5 of 485 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	SE	41	VAL
67	Lh	98	VAL
43	LJ	46	LEU
67	Lh	22	VAL
76	Lq	26	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
40	LG	178	ASN
81	pp	1142	ASN
45	LL	92	HIS
78	SC	81	ASN
68	Li	33	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S2	1767/1800 (98%)	761 (43%)	20 (1%)
34	LA	3159/3393 (93%)	795 (25%)	30 (0%)
35	LB	120/121 (99%)	19 (15%)	1 (0%)
36	LC	157/158 (99%)	46 (29%)	1 (0%)
79	Bb	75/76 (98%)	36 (48%)	0
80	Cc	75/76 (98%)	29 (38%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
82	mR	0/10	-	-
All	All	5353/5634 (95%)	1686 (31%)	52 (0%)

5 of 1686 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S2	3	U
1	S2	4	C
1	S2	9	U
1	S2	14	C
1	S2	15	U

5 of 52 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	LA	1307	G
34	LA	1947	G
34	LA	3350	C
34	LA	1468	A
34	LA	1739	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

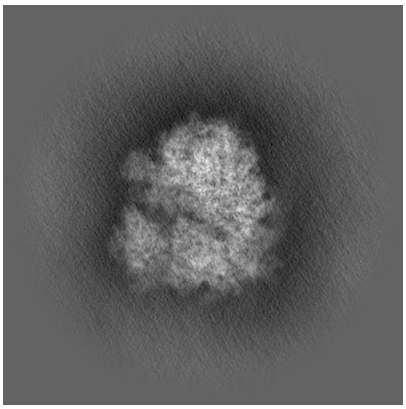
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-68916. These allow visual inspection of the internal detail of the map and identification of artifacts.

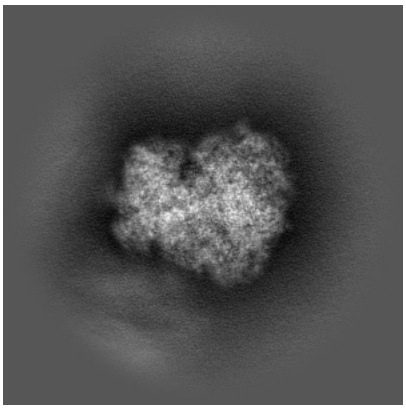
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

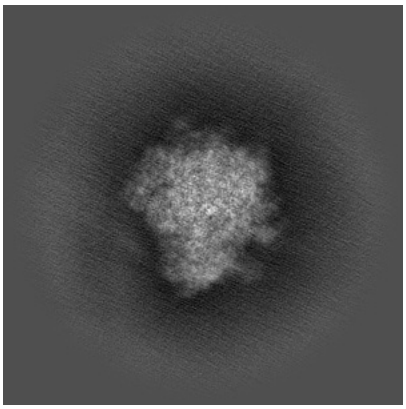
6.1.1 Primary map



X

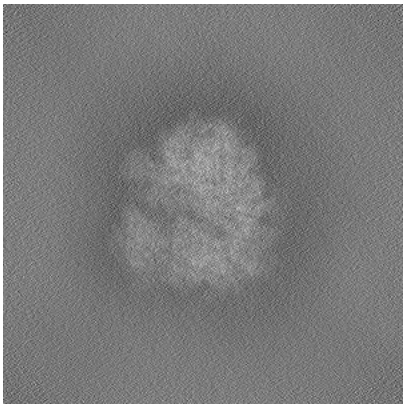


Y

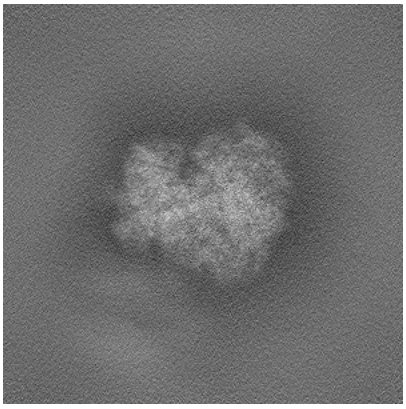


Z

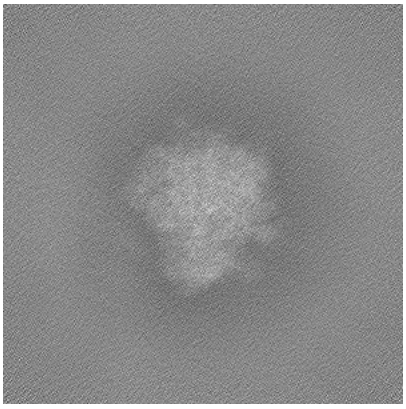
6.1.2 Raw map



X



Y

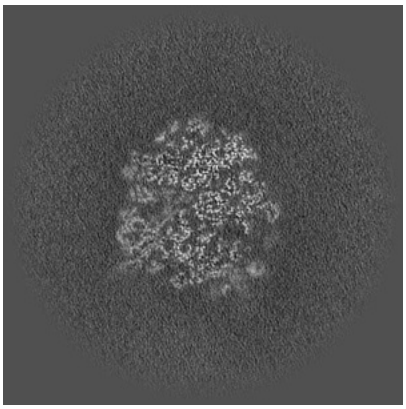


Z

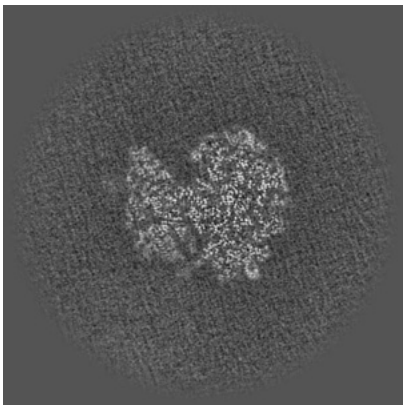
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

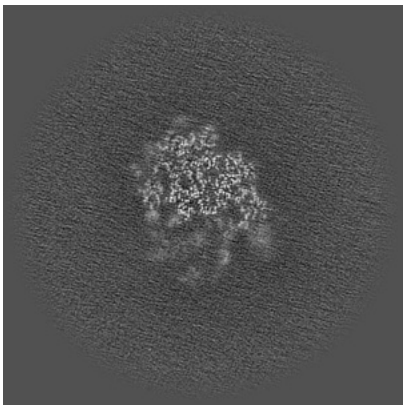
6.2.1 Primary map



X Index: 300

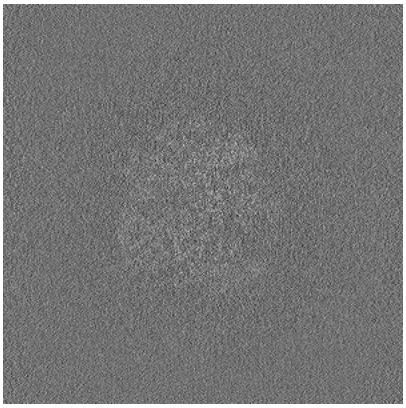


Y Index: 300

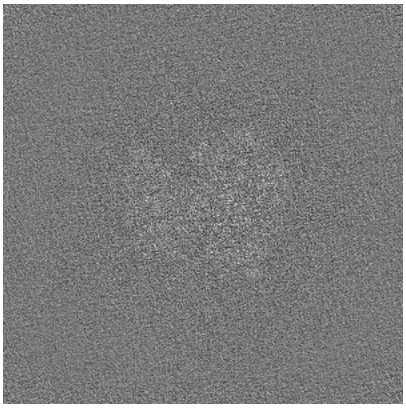


Z Index: 300

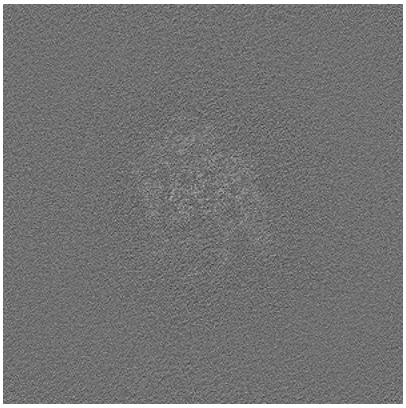
6.2.2 Raw map



X Index: 300



Y Index: 300

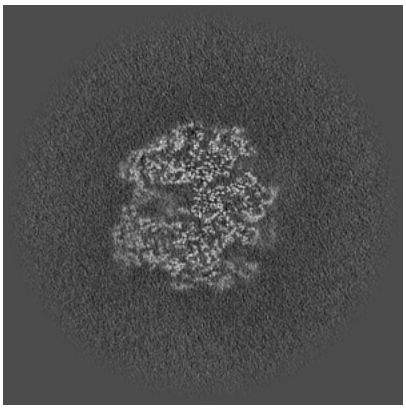


Z Index: 300

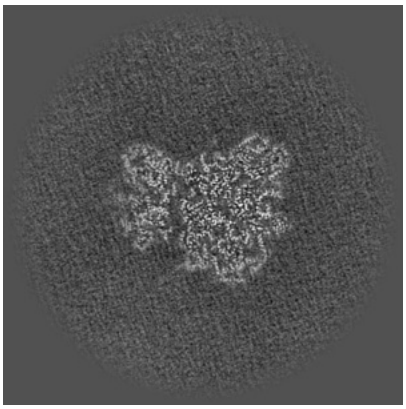
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

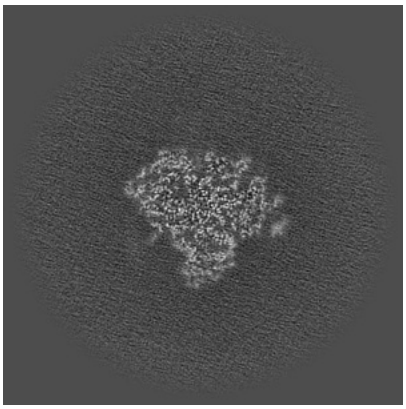
6.3.1 Primary map



X Index: 288

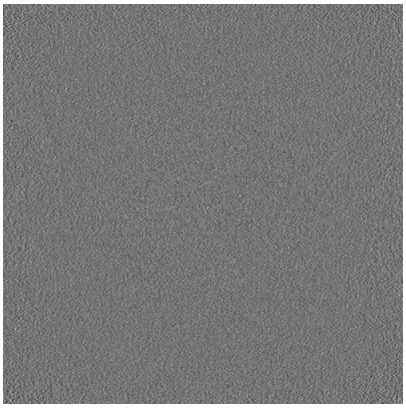


Y Index: 320

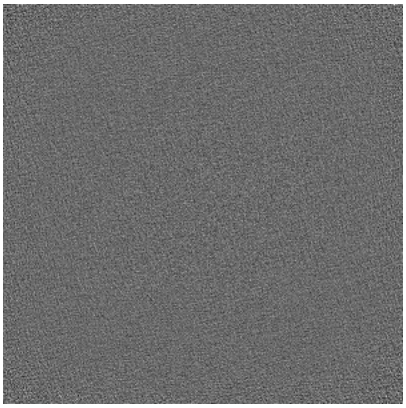


Z Index: 356

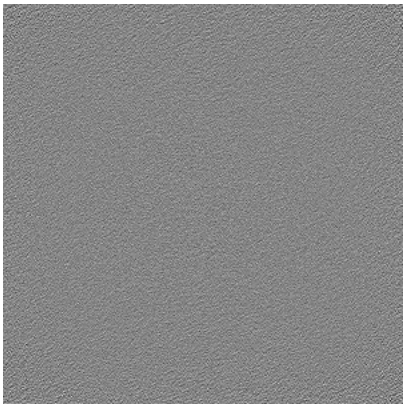
6.3.2 Raw map



X Index: 0



Y Index: 0

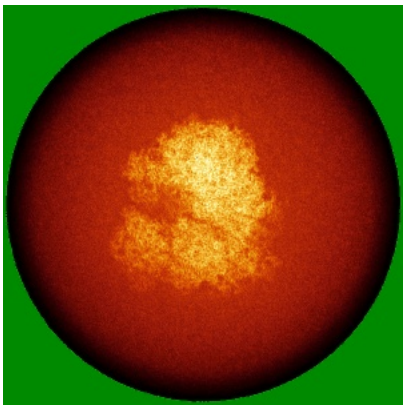


Z Index: 0

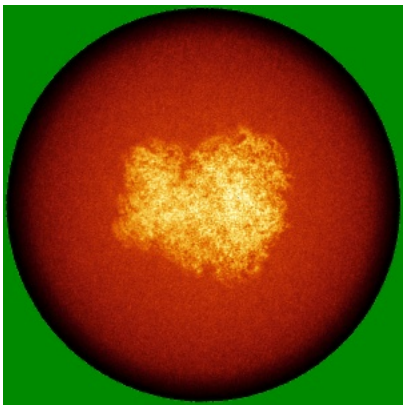
The images above show the largest variance slices of the map in three orthogonal directions.

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

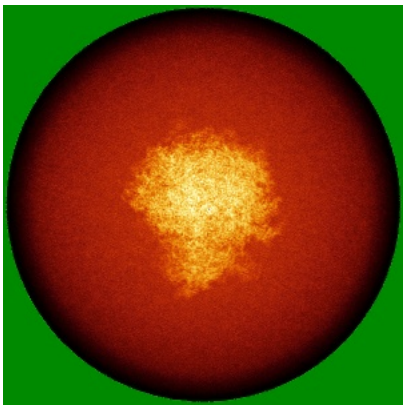
6.4.1 Primary map



X

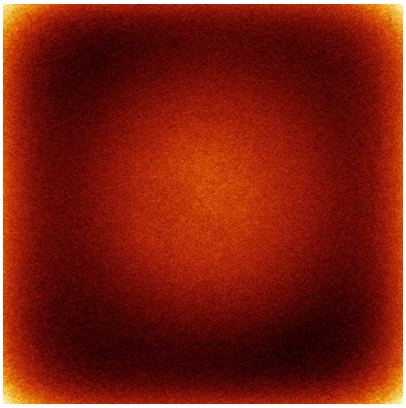


Y

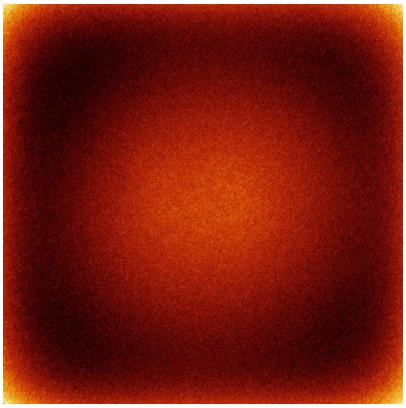


Z

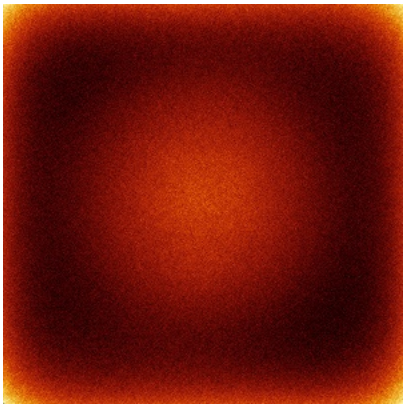
6.4.2 Raw map



X



Y

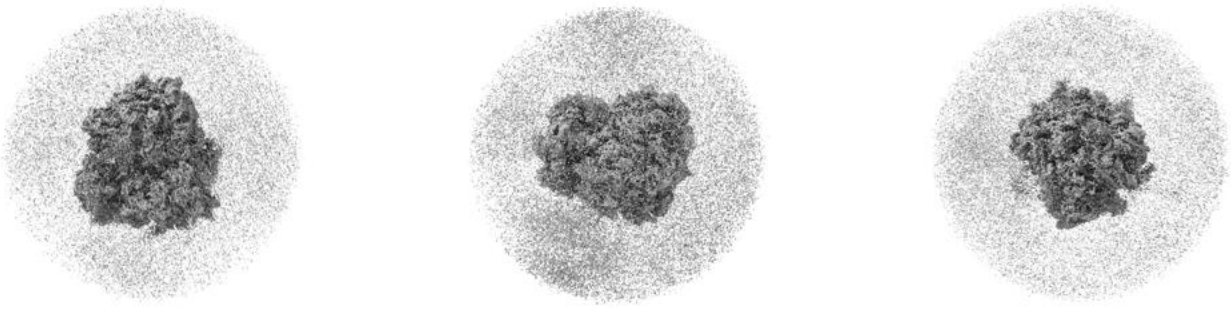


Z

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)

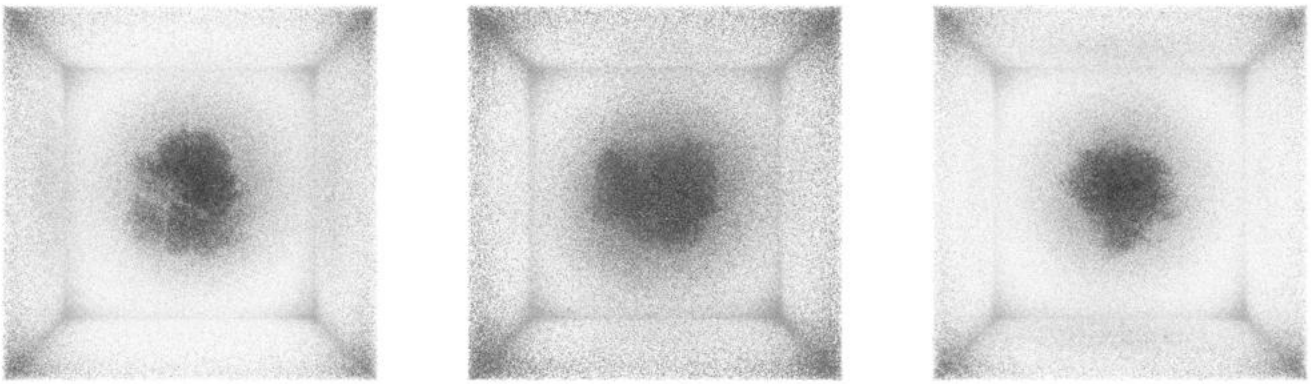
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

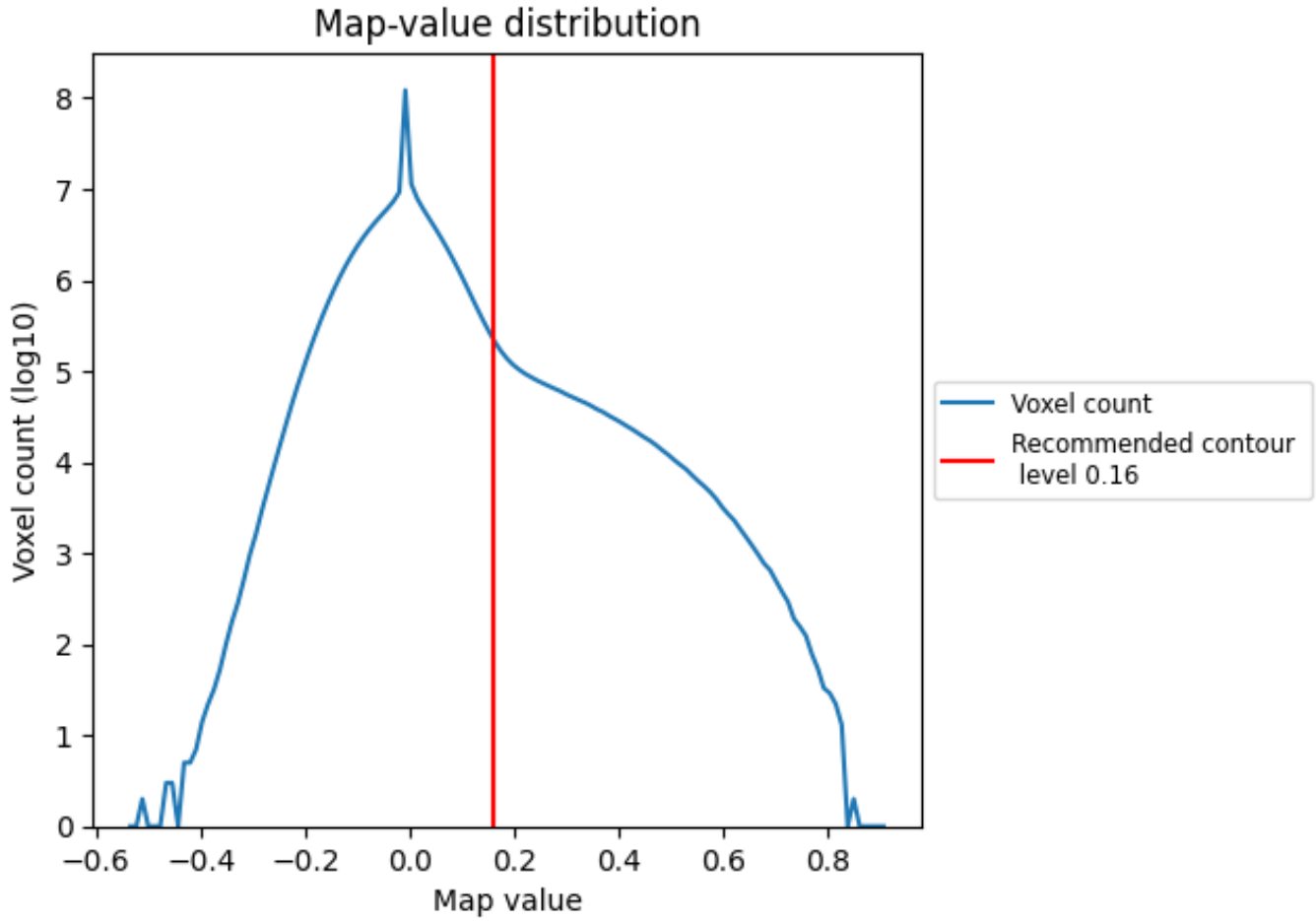
6.6 Mask visualisation (i)

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

7 Map analysis

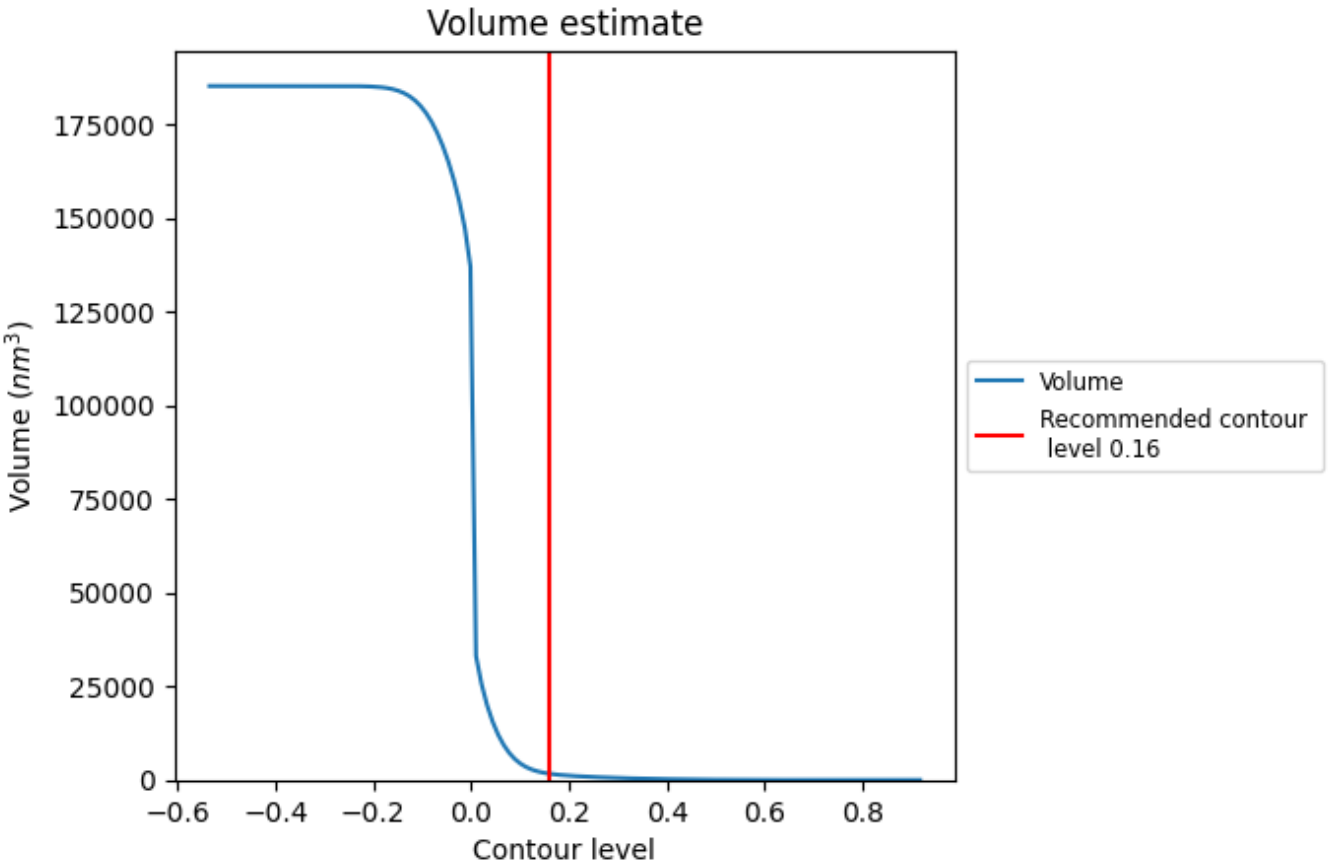
This section contains the results of statistical analysis of the map.

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.

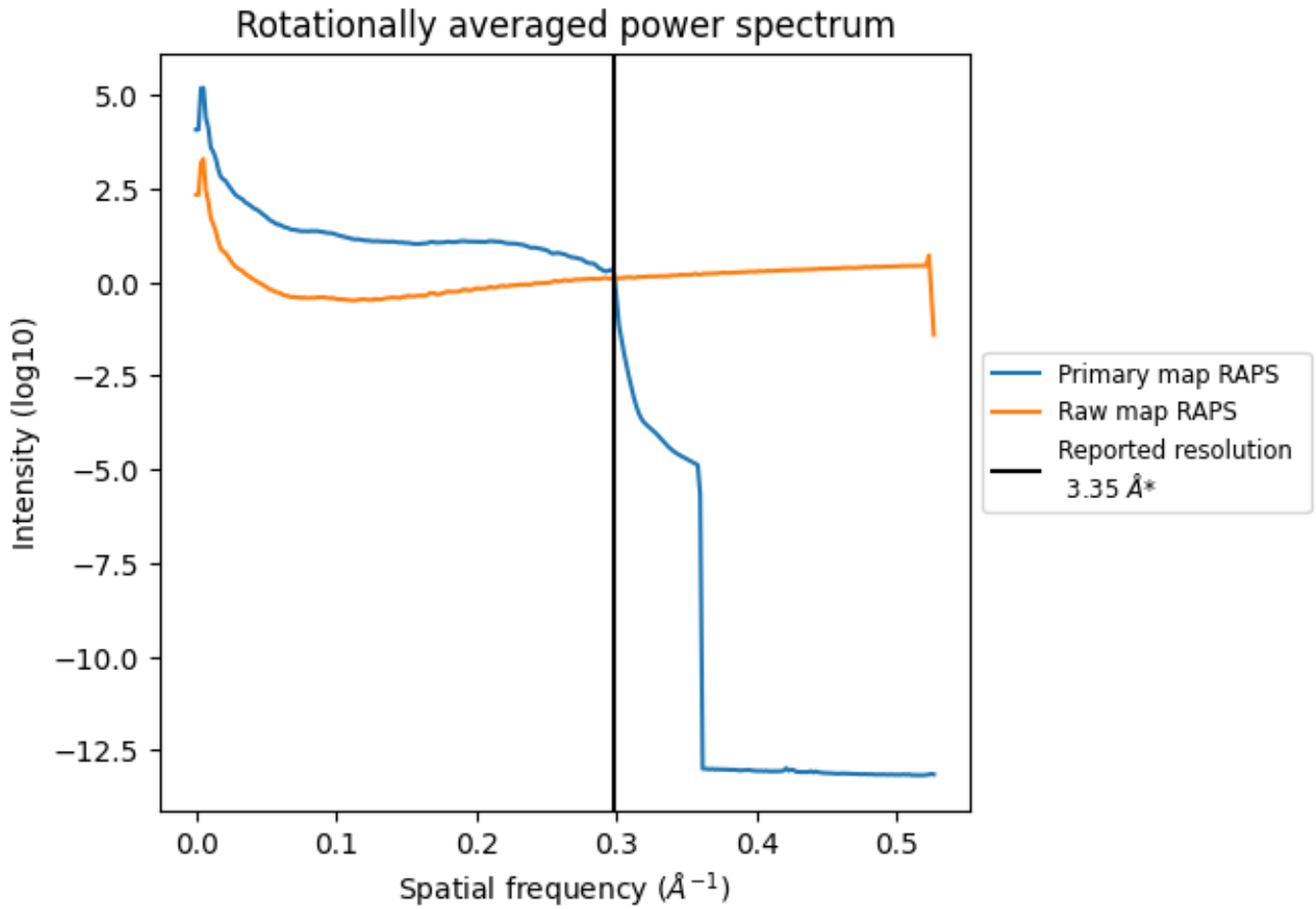
7.2 Volume estimate (i)



The volume at the recommended contour level is 1670 nm^3; this corresponds to an approximate mass of 1508 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)

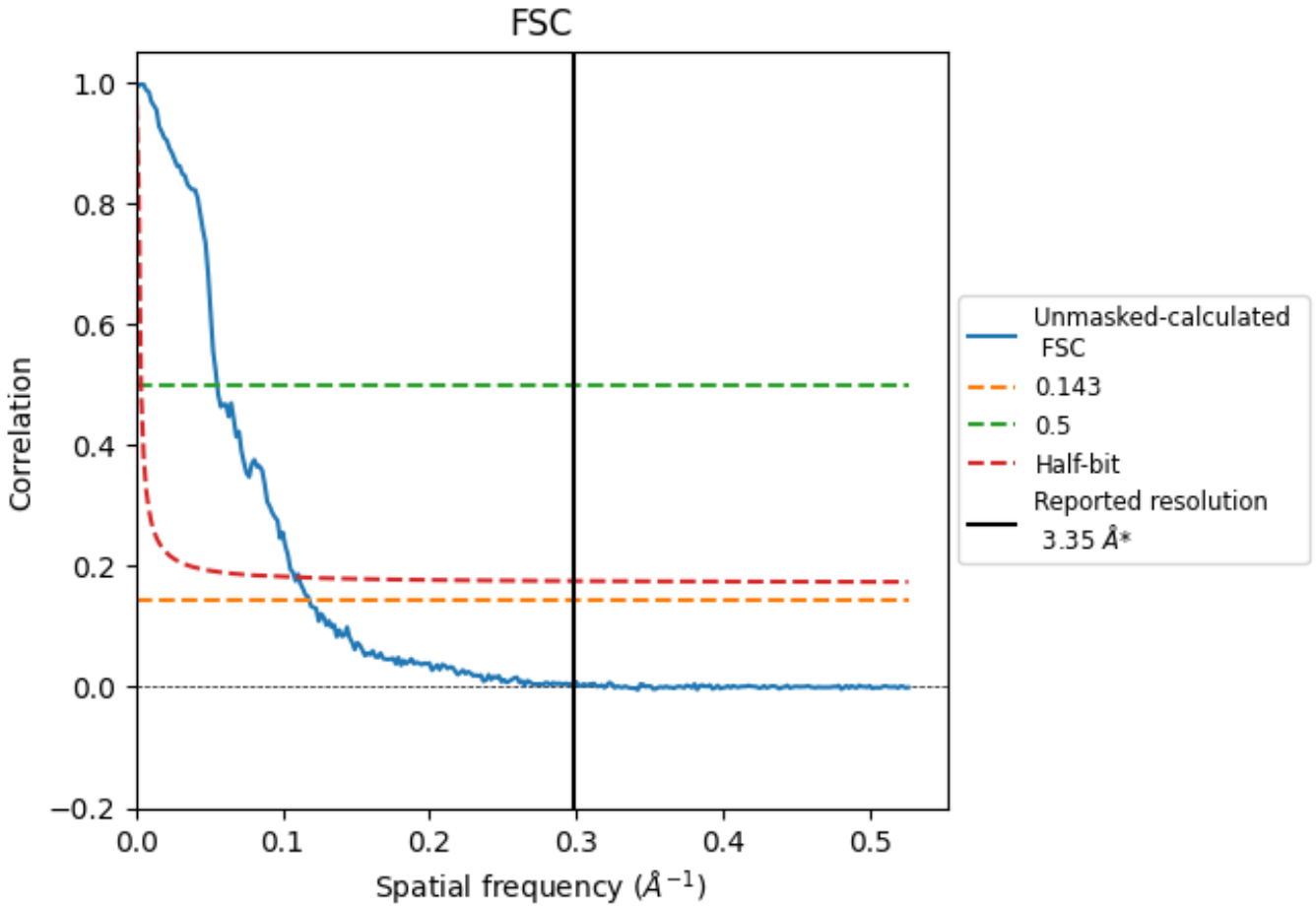


*Reported resolution corresponds to spatial frequency of 0.299 $Å^{-1}$

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 0.299 Å^{-1}

8.2 Resolution estimates (i)

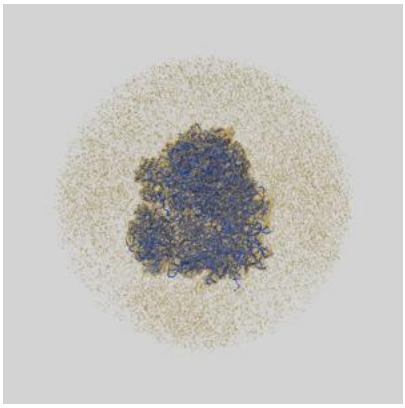
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.35	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.46	18.05	9.26

*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 8.46 differs from the reported value 3.35 by more than 10 %

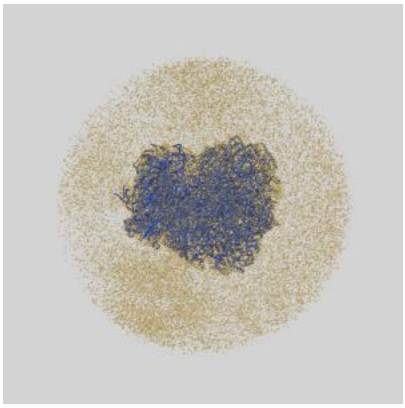
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-68916 and PDB model 23EZ. Per-residue inclusion information can be found in section 3 on page 19.

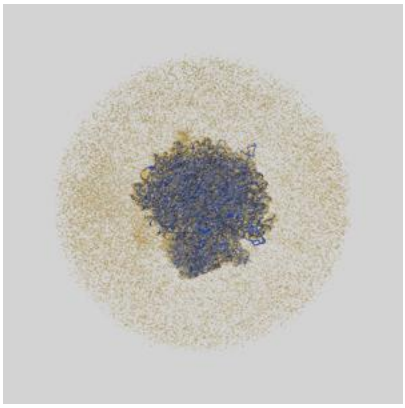
9.1 Map-model overlay



X



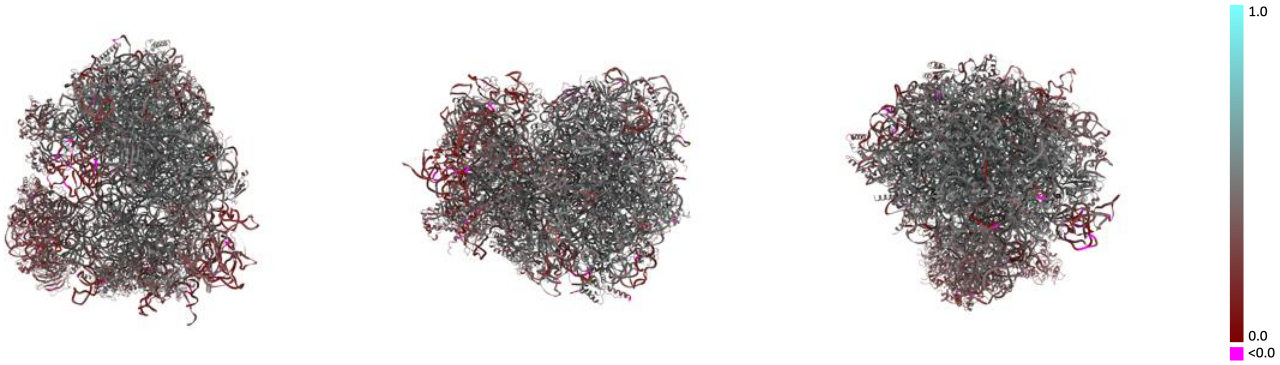
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

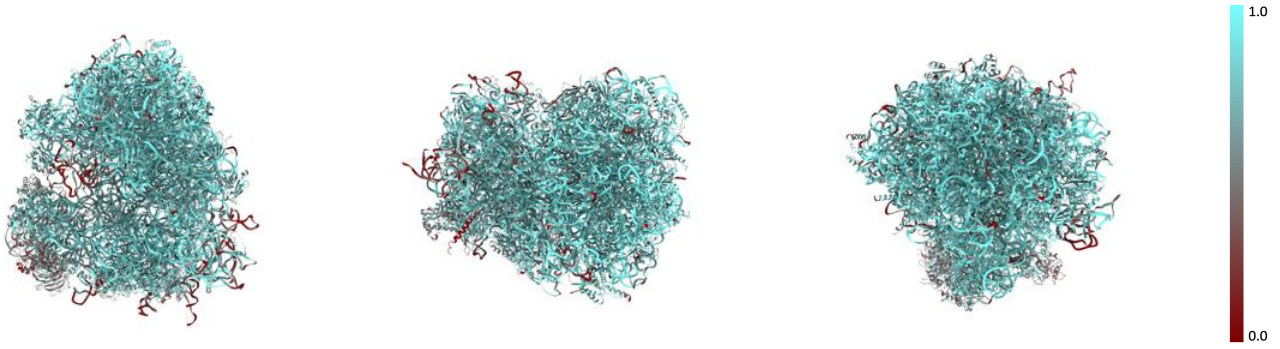
9.2 Q-score mapped to coordinate model (i)



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.

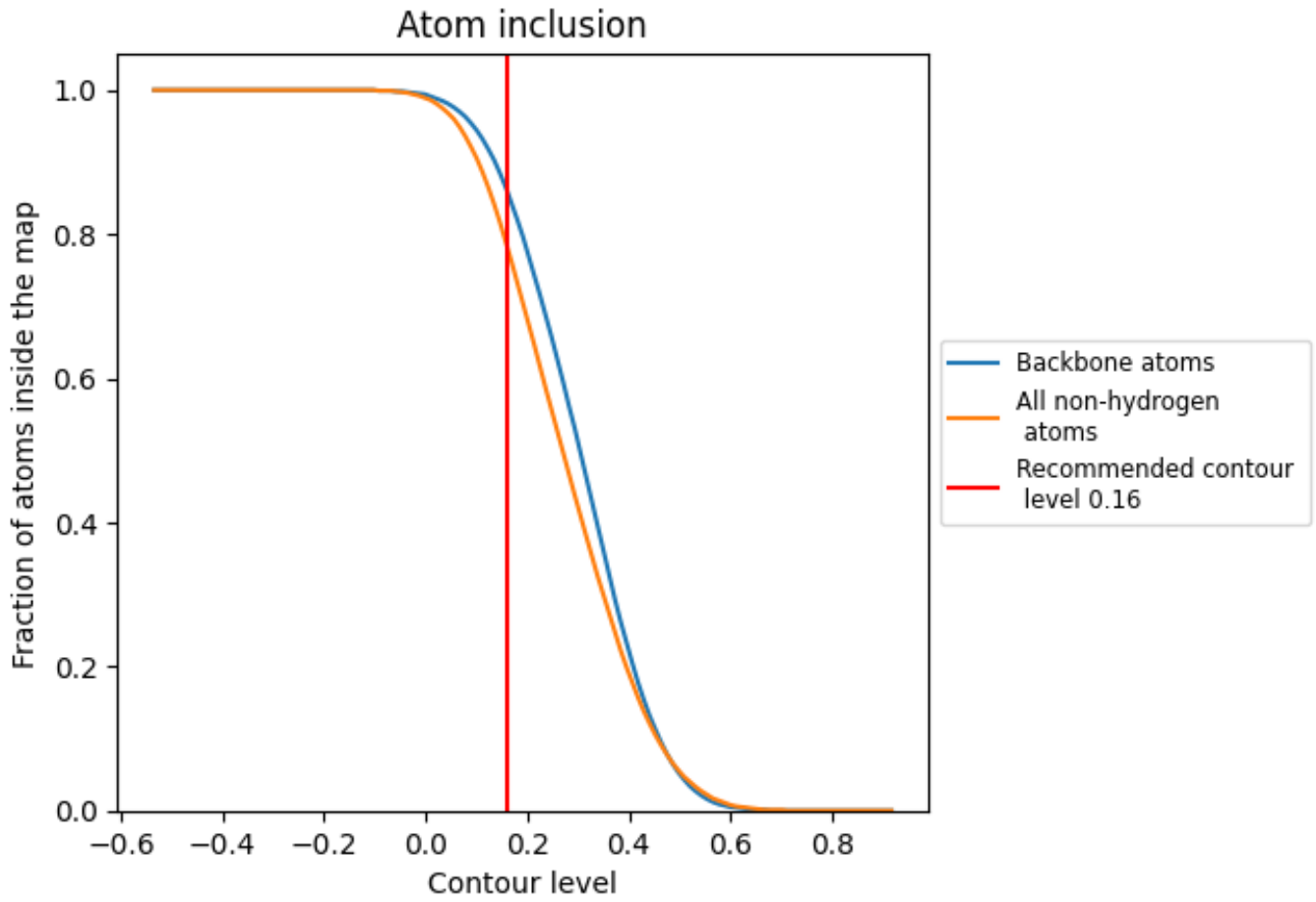
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.16).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 78% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7840	0.4170
Bb	0.5330	0.3010
Cc	0.5540	0.3100
LA	0.8720	0.4350
LB	0.9190	0.4170
LC	0.8970	0.4420
LD	0.7760	0.5070
LE	0.8130	0.4890
LF	0.8230	0.4860
LG	0.6800	0.3820
LH	0.7520	0.4370
LI	0.8030	0.4810
LJ	0.7390	0.4280
LK	0.7620	0.4600
LL	0.7520	0.4560
LM	0.7190	0.3850
LN	0.8040	0.4770
LO	0.7770	0.4430
LP	0.8190	0.5100
LQ	0.7860	0.4800
LR	0.7990	0.4850
LS	0.8190	0.5010
LT	0.6780	0.4220
LU	0.7950	0.4810
LV	0.8170	0.4870
LW	0.7070	0.3920
LX	0.7540	0.5010
LY	0.8030	0.4830
LZ	0.7810	0.4620
La	0.7550	0.4280
Lb	0.7250	0.4280
Lc	0.8300	0.5020
Ld	0.8030	0.4760
Le	0.7280	0.4490
Lf	0.7690	0.4620



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Chain	Atom inclusion	Q-score
Lg	0.7610	0.4760
Lh	0.8100	0.5050
Li	0.7540	0.4850
Lj	0.8090	0.4600
Lk	0.7630	0.4450
Ll	0.8630	0.5110
Lm	0.6330	0.4020
Ln	0.7900	0.4950
Lo	0.8460	0.4900
Lp	0.6540	0.4860
Lq	0.7900	0.4990
Lr	0.7400	0.4800
S2	0.7990	0.3640
SA	0.5790	0.3880
SB	0.5390	0.3230
SC	0.5890	0.3540
SD	0.2680	0.2660
SE	0.6350	0.3360
SF	0.5600	0.3300
SG	0.6400	0.3650
SH	0.6130	0.3540
SI	0.5900	0.3340
SJ	0.5490	0.3460
SK	0.4570	0.2870
SL	0.5010	0.3400
SM	0.6880	0.4050
SN	0.3190	0.2140
SO	0.4450	0.2650
SP	0.6220	0.3850
SQ	0.6100	0.3930
SR	0.7220	0.4400
SS	0.7070	0.4250
ST	0.6520	0.3790
SU	0.5670	0.3760
SV	0.7320	0.4300
SW	0.7100	0.3960
SX	0.7360	0.4540
SY	0.7120	0.4320
SZ	0.6720	0.4220
Sa	0.6660	0.4200
Sb	0.7680	0.4630
Sc	0.7220	0.4650

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Chain	Atom inclusion	Q-score
Sd	0.7270	0.4050
Se	0.7500	0.4650
Sf	0.6540	0.4130
Sg	0.6600	0.4070
mR	0.8520	0.3900
pp	0.3550	0.4180