wwPDB EM Validation Summary Report

Oct 27, 2026 – 10:36 PM JST

PDB ID	:	22YN / pdb_000022yn
EMDB ID	:	EMD-68777
Title	:	Rotated 80S with A/A'-P/E tRNA
Authors	:	Wu, M.; Yuan, S.
Deposited on	:	2026-01-28
Resolution	:	2.90 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:

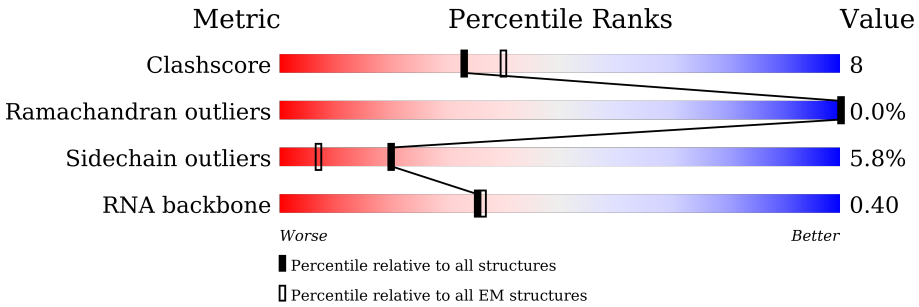
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

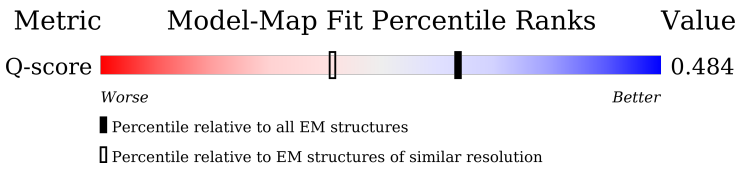
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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	Bb	76	8% 34% 53% 13%
2	LA	3396	49% 37% 7% 7%
3	LB	121	51% 42% 6%

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Mol	Chain	Length	Quality of chain
4	LC	158	52% 42% 6%
5	LD	251	78% 20%
6	LE	386	75% 24%
7	LF	361	78% 20%
8	LG	294	73% 27%
9	LH	175	6% 79% 15% 5%
10	LI	222	78% 21%
11	LJ	233	75% 25%
12	LK	191	80% 18%
13	LL	218	72% 26%
14	LM	169	5% 69% 27%
15	LN	193	80% 19%
16	LO	136	71% 26%
17	LP	203	81% 18%
18	LQ	197	81% 17%
19	LR	183	5% 84% 15%
20	LS	185	79% 20%
21	LT	188	7% 84% 15%
22	LU	171	81% 18%
23	LV	159	77% 23%
24	LW	100	82% 17%
25	LX	136	79% 20%
26	LY	65	89% 11%
27	LZ	121	83% 16%
28	La	125	70% 28%

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Mol	Chain	Length	Quality of chain
29	Lb	135	82% 16%
30	Lc	148	80% 19%
31	Ld	58	79% 19%
32	Le	96	78% 21%
33	Lf	109	6% 81% 18%
34	Lg	127	91% 9%
35	Lh	106	82% 17%
36	Li	112	91% 9%
37	Lj	119	75% 24%
38	Lk	99	82% 15%
39	Ll	81	86% 12%
40	Lm	77	6% 78% 17% 5%
41	Ln	50	70% 24% 6%
42	Lo	52	87% 13%
43	Lp	25	80% 20%
44	Lq	103	81% 19%
45	Lr	91	79% 21%
46	mR	11	100%
47	Cc	77	5% 36% 56% 8%
48	S2	1800	12% 38% 46% 13%
49	SA	222	13% 70% 28%
50	SB	206	18% 62% 36%
51	SC	92	21% 65% 34%
52	SD	121	69% 75% 21%
53	SE	117	19% 66% 31%

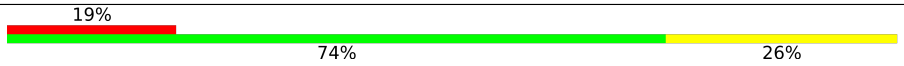
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Mol	Chain	Length	Quality of chain
54	SF	141	12% 67% 30%
55	SG	125	6% 70% 25%
56	SH	145	19% 75% 22%
57	SI	143	12% 59% 34% 6%
58	SJ	100	24% 64% 34%
59	SK	82	35% 72% 28%
60	SL	63	14% 57% 37% 6%
61	SM	53	68% 30%
62	SN	73	66% 84% 16%
63	SO	312	30% 65% 32%
64	SP	206	67% 32%
65	SQ	232	69% 26%
66	SR	216	69% 28%
67	SS	258	66% 31%
68	ST	228	20% 71% 28%
69	SU	184	7% 67% 32%
70	SV	198	9% 67% 25% 6%
71	SW	184	13% 77% 22%
72	SX	142	8% 77% 21%
73	SY	150	71% 29%
74	SZ	127	73% 27%
75	Sa	87	77% 21%
76	Sb	129	74% 25%
77	Sc	144	9% 79% 21%
78	Sd	134	8% 66% 29%

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Mol	Chain	Length	Quality of chain
79	Se	97	
80	Sf	81	
81	Sg	57	

2 Entry composition (i)

There are 81 unique types of molecules in this entry. The entry contains 202093 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 (76-MER).

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

- Molecule 2 is a RNA chain called RNA (3393-MER).

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

- Molecule 3 is a RNA chain called RNA (121-MER).

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

- Molecule 4 is a RNA chain called RNA (158-MER).

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL2A.

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

- Molecule 6 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 7 is a protein called Large ribosomal subunit protein uL4A.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 9 is a protein called Large ribosomal subunit protein eL6B.

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

- Molecule 10 is a protein called Large ribosomal subunit protein uL30A.

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

- Molecule 11 is a protein called Large ribosomal subunit protein eL8A.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL6A.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL5B.

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

- Molecule 15 is a protein called Large ribosomal subunit protein eL13A.

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

- Molecule 16 is a protein called Large ribosomal subunit protein eL14A.

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

- Molecule 17 is a protein called Large ribosomal subunit protein eL15A.

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

- Molecule 18 is a protein called Large ribosomal subunit protein uL13A.

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

- Molecule 19 is a protein called Large ribosomal subunit protein uL22A.

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

- Molecule 20 is a protein called Large ribosomal subunit protein eL18A.

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

- Molecule 21 is a protein called Large ribosomal subunit protein eL19A.

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

- Molecule 22 is a protein called Large ribosomal subunit protein eL20A.

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

- Molecule 23 is a protein called Large ribosomal subunit protein eL21A.

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

- Molecule 24 is a protein called Large ribosomal subunit protein eL22A.

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

- Molecule 25 is a protein called Large ribosomal subunit protein uL14A.

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

- Molecule 26 is a protein called Large ribosomal subunit protein eL24A.

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

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 28 is a protein called Large ribosomal subunit protein uL24A.

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

- Molecule 29 is a protein called Large ribosomal subunit protein eL27A.

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

- Molecule 30 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 31 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL30.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL31A.

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

- Molecule 34 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL33A.

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

- Molecule 36 is a protein called Large ribosomal subunit protein eL34A.

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

- Molecule 37 is a protein called Large ribosomal subunit protein uL29A.

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL36A.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL37A.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 42 is a protein called Large ribosomal subunit protein eL40A.

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

- Molecule 43 is a protein called Large ribosomal subunit protein eL41A.

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

- Molecule 44 is a protein called Large ribosomal subunit protein eL42A.

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

- Molecule 45 is a protein called Large ribosomal subunit protein eL43A.

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

- Molecule 46 is a RNA chain called RNA (5'-R(P*UP*GP*AP*CP*GP*CP*UP*UP*UP*UP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
46	mR	11	Total	C	N	O	P	0	0
			228	102	34	81	11		

- Molecule 47 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Cc	77	Total	C	N	O	P	0	0
			1644	732	298	537	77		

- Molecule 48 is a RNA chain called RNA(1770-MER).

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

- Molecule 49 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 50 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 51 is a protein called Small ribosomal subunit protein eS10A.

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

- Molecule 52 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 54 is a protein called Small ribosomal subunit protein uS9A.

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

- Molecule 55 is a protein called Small ribosomal subunit protein eS17B.

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

- Molecule 56 is a protein called Small ribosomal subunit protein uS13A.

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

- Molecule 57 is a protein called Small ribosomal subunit protein eS19A.

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

- Molecule 58 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 59 is a protein called Small ribosomal subunit protein eS25A.

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

- Molecule 60 is a protein called Small ribosomal subunit protein eS28A.

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

- Molecule 61 is a protein called Small ribosomal subunit protein uS14A.

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

- Molecule 62 is a protein called Small ribosomal subunit protein eS31.

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

- Molecule 63 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 64 is a protein called Small ribosomal subunit protein uS2A.

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

- Molecule 65 is a protein called Small ribosomal subunit protein eS1A.

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

- Molecule 66 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 67 is a protein called Small ribosomal subunit protein eS4A.

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

- Molecule 68 is a protein called Small ribosomal subunit protein eS6A.

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

- Molecule 69 is a protein called Small ribosomal subunit protein eS7A.

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

- Molecule 70 is a protein called Small ribosomal subunit protein eS8A.

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

- Molecule 71 is a protein called Small ribosomal subunit protein uS4A.

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

- Molecule 72 is a protein called Small ribosomal subunit protein uS17A.

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

- Molecule 73 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 74 is a protein called Small ribosomal subunit protein uS11B.

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

- Molecule 75 is a protein called Small ribosomal subunit protein eS21A.

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

- Molecule 76 is a protein called Small ribosomal subunit protein uS8A.

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

- Molecule 77 is a protein called Small ribosomal subunit protein uS12A.

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

- Molecule 78 is a protein called Small ribosomal subunit protein eS24A.

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

- Molecule 79 is a protein called Small ribosomal subunit protein eS26B.

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

- Molecule 80 is a protein called Small ribosomal subunit protein eS27A.

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

- Molecule 81 is a protein called Small ribosomal subunit protein eS30A.

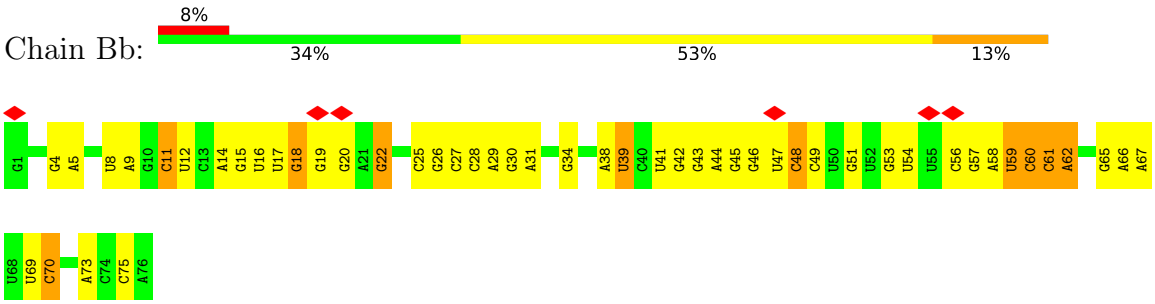
Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sg	57	Total	C	N	O	S	0	0
			451	284	93	73	1		

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.

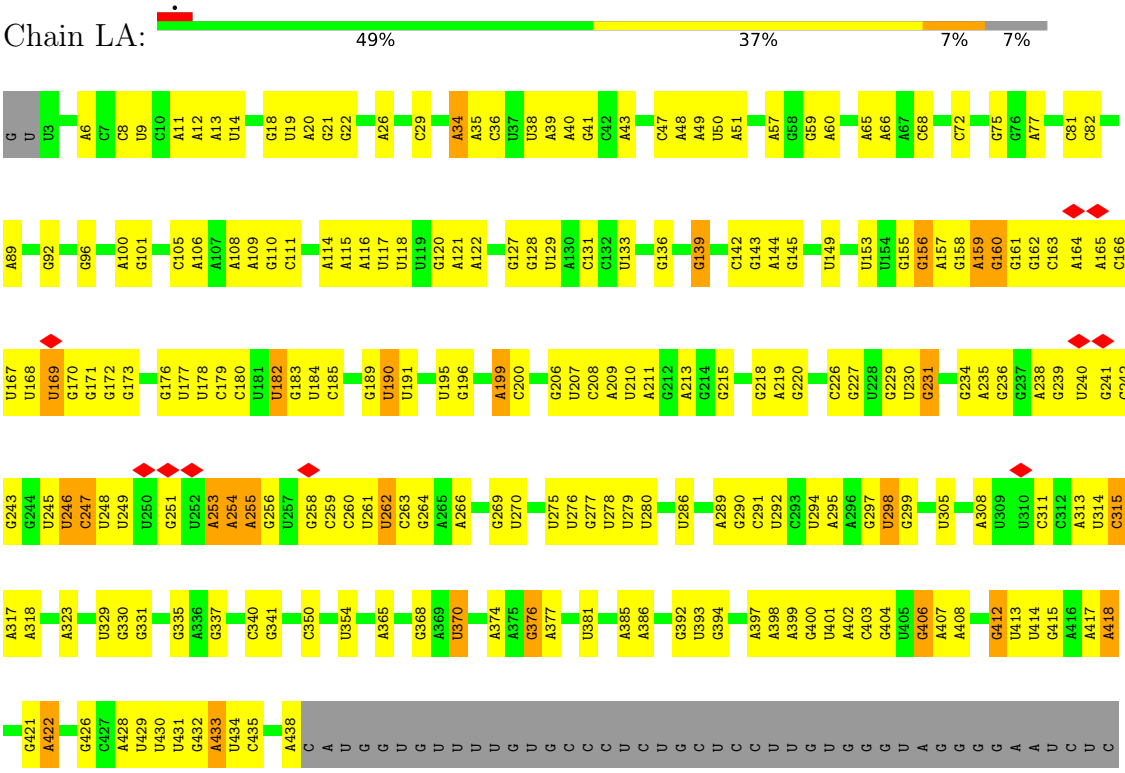
• Molecule 1: RNA (76-MER)

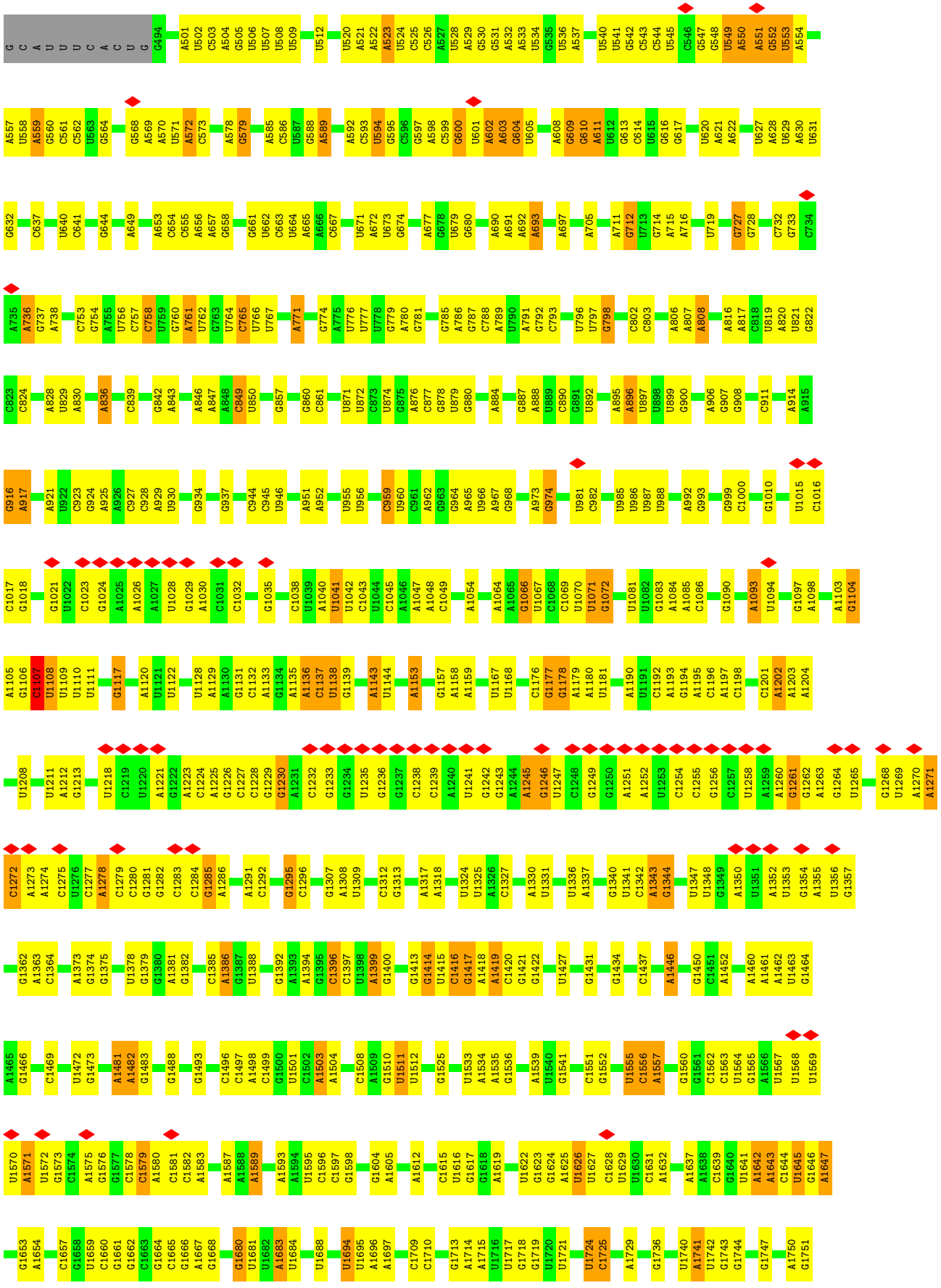
Chain Bb:

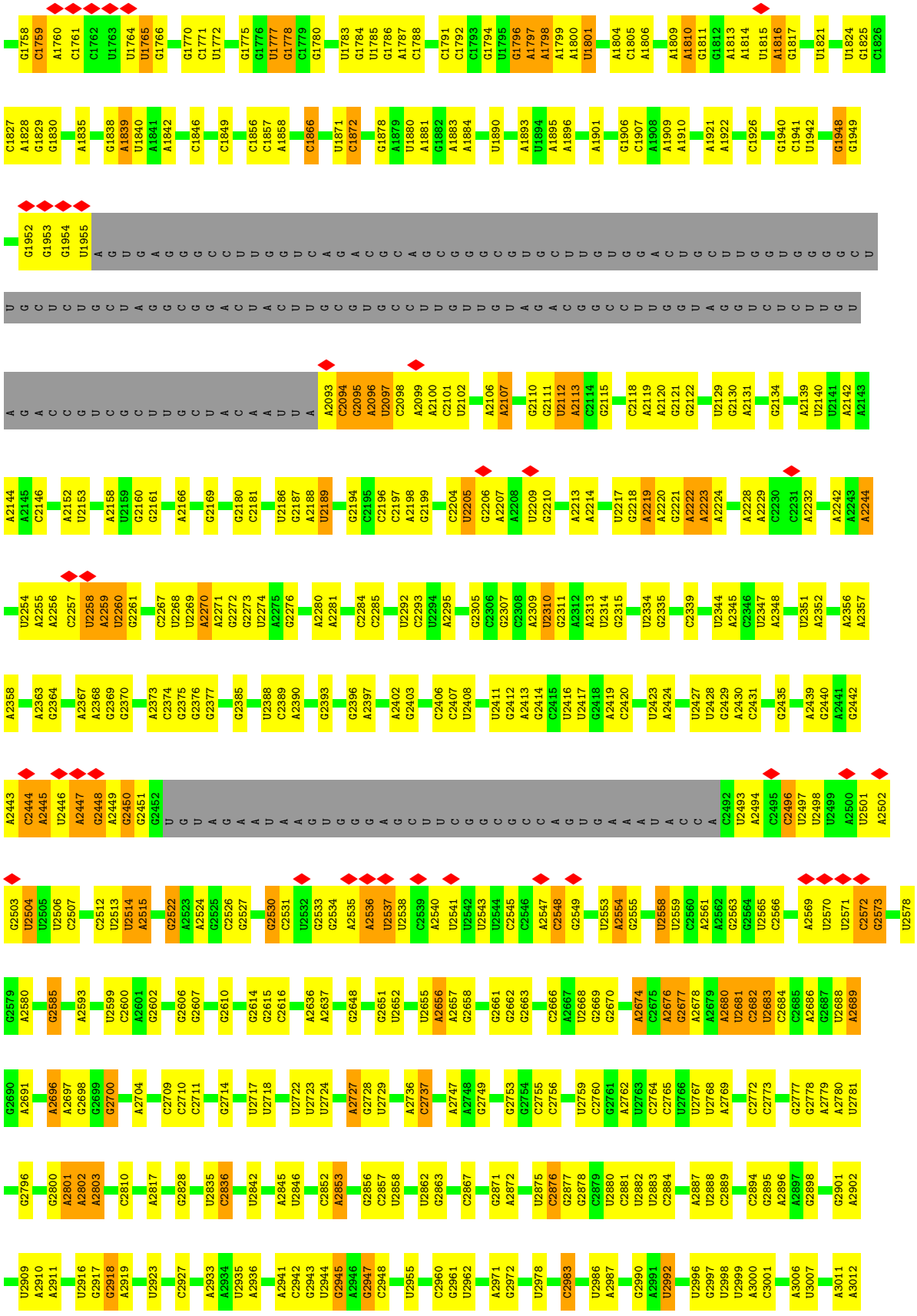


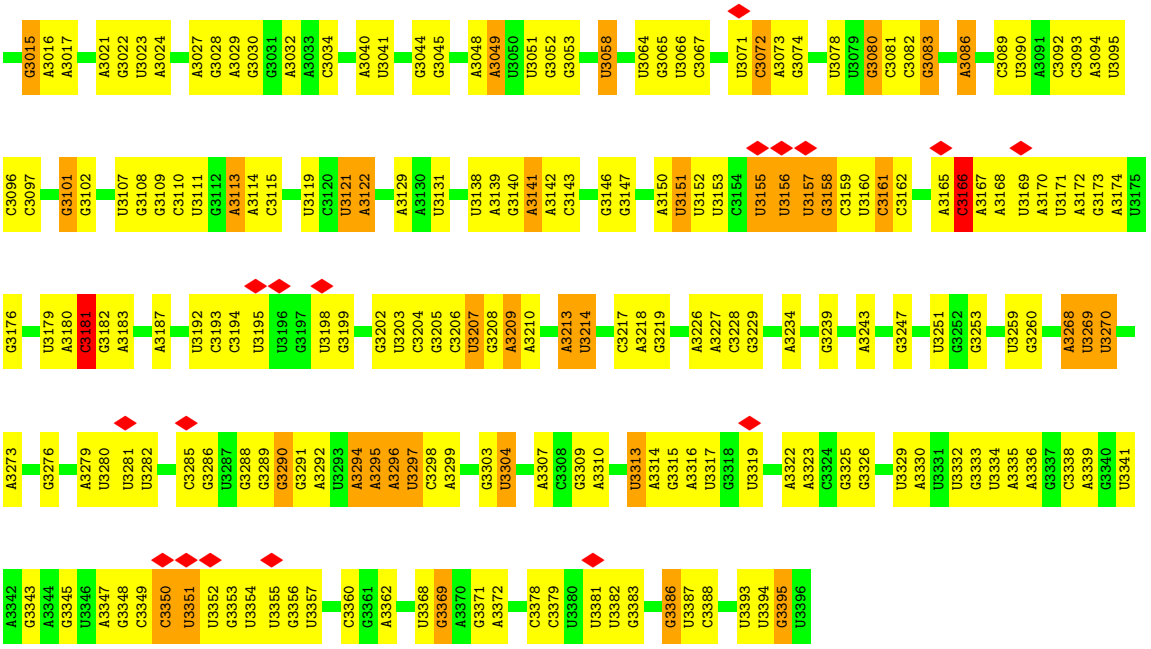
• Molecule 2: RNA (3393-MER)

Chain LA:





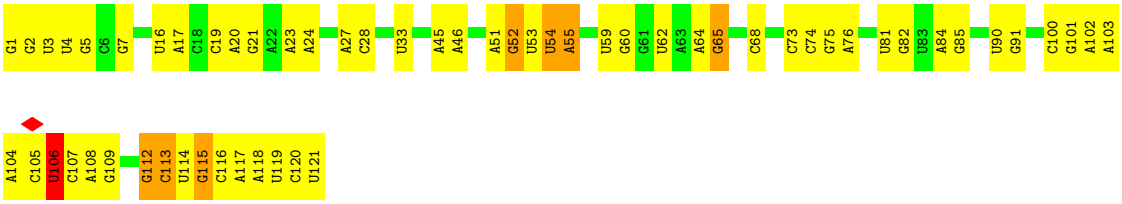

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C1827 A1828 G1829 G1830 A1835 G1838 A1839 U1840 A1841 A1842 C1846 C1849 C1856 C1857 A1858 C1866 U1871 C1872 G1878 A1879 U1880 A1881 G1882 A1883 A1884 U1890 A1893 U1894 A1895 A1896 A1901 G1906 C1907 A1908 A1909 A1910 A1921 A1922 C1926 G1940 C1941 U1942 G1948 G1949
G1952 G1953 G1954 U1955
A2093 C2094 G2095 A2096 U2097 C2098 A2099 A2100 C2101 U2102 A2106 A2107 G2110 G2111 U2112 A2113 C2114 G2115 C2118 A2119 A2120 G2121 G2122 U2129 G2130 A2131 G2134 A2139 U2140 U2141 A2142 A2143
A2144 A2145 C2146 A2152 U2153 A2158 U2159 G2160 G2161 A2166 G2169 G2180 C2181 U2186 G2187 A2188 U2189 G2194 C2195 C2196 C2197 A2198 G2199 C2204 U2205 G2206 A2207 A2208 U2209 G2210 A2213 A2214 U2217 G2218 A2219 A2220 G2221 A2222 A2223 A2224 A2228 A2229 C2230 C2231 A2232 A2242 A2243 A2244
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G2503 U2504 U2505 U2506 C2507 C2512 U2513 U2514 A2515 G2522 A2523 A2524 G2525 C2526 G2527 G2530 C2531 U2532 G2533 G2534 A2535 A2536 U2537 U2538 C2539 A2540 U2541 U2542 U2543 U2544 C2545 C2546 A2547 C2548 G2549 U2553 A2554 G2555 U2558 U2559 C2560 A2561 A2562 G2563 G2564 U2565 C2566 A2569 U2570 U2571 C2572 G2573 U2578
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• Molecule 3: RNA (121-MER)

Chain LB:

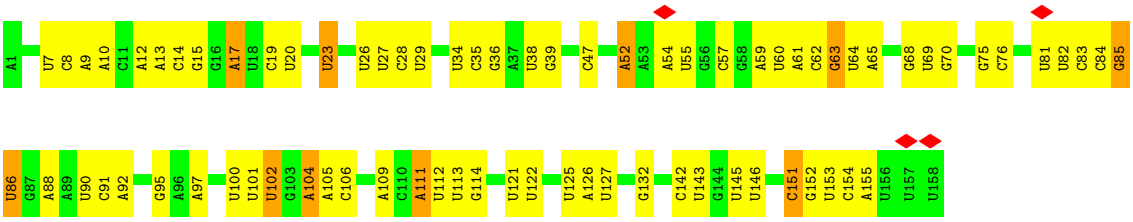




• Molecule 4: RNA (158-MER)

Chain LC:



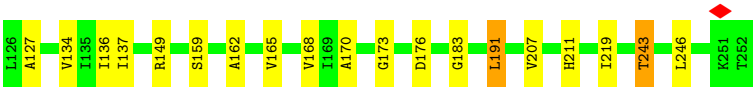


• Molecule 5: Large ribosomal subunit protein uL2A

Chain LD:



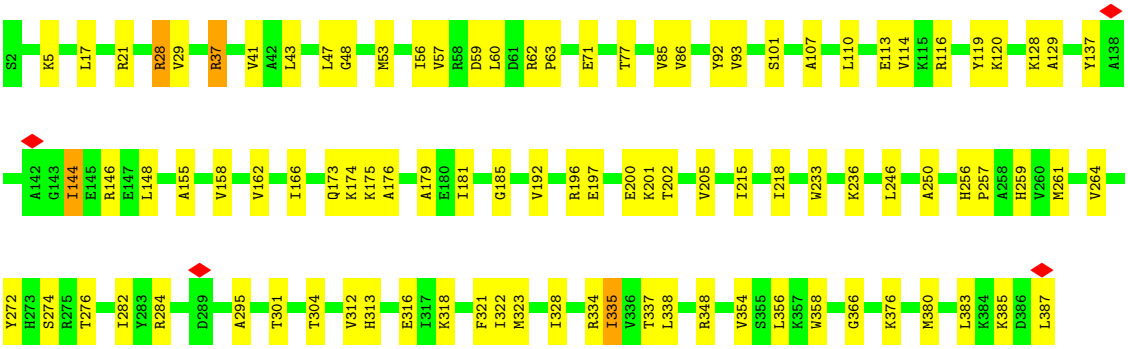




• Molecule 6: Large ribosomal subunit protein uL3

Chain LE:

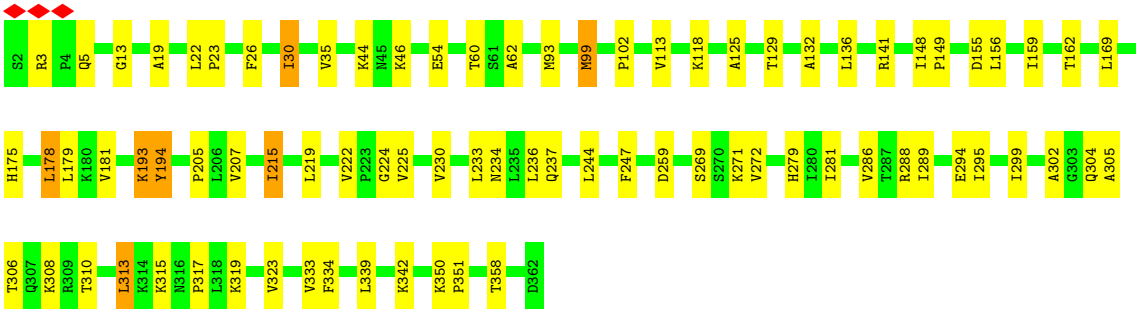




• Molecule 7: Large ribosomal subunit protein uL4A

Chain LF:

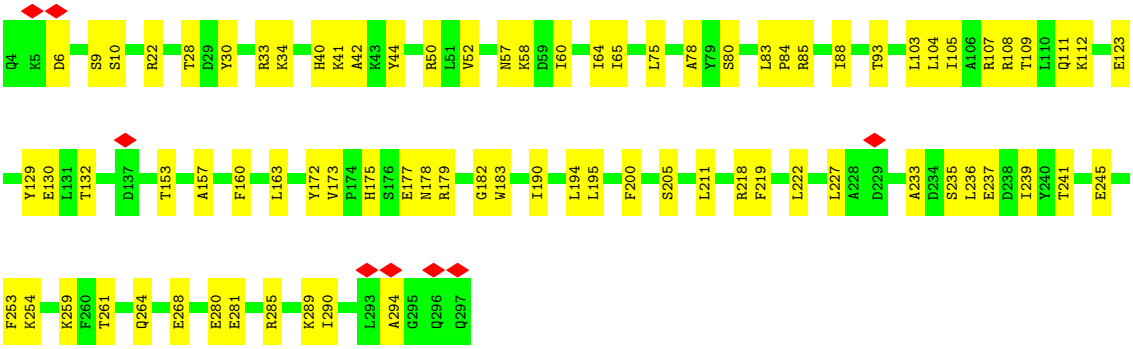




• Molecule 8: Large ribosomal subunit protein uL18

Chain LG:

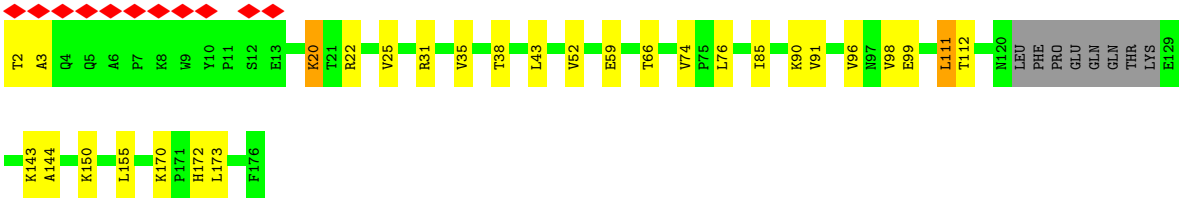




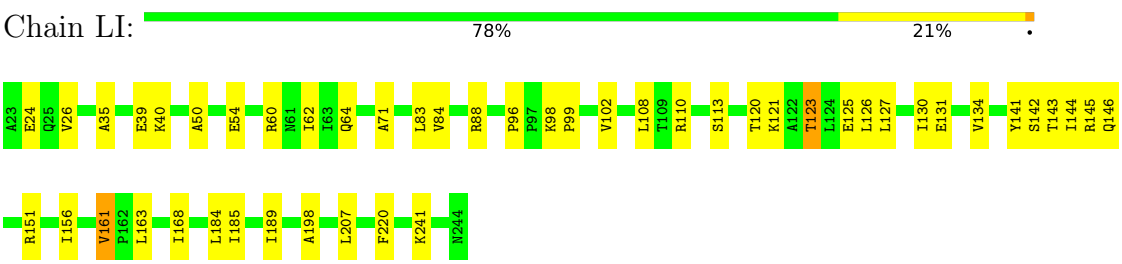
• Molecule 9: Large ribosomal subunit protein eL6B

Chain LH:

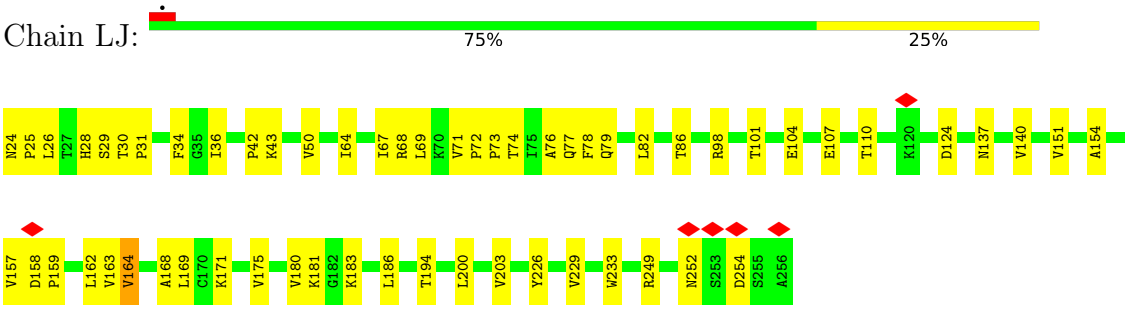




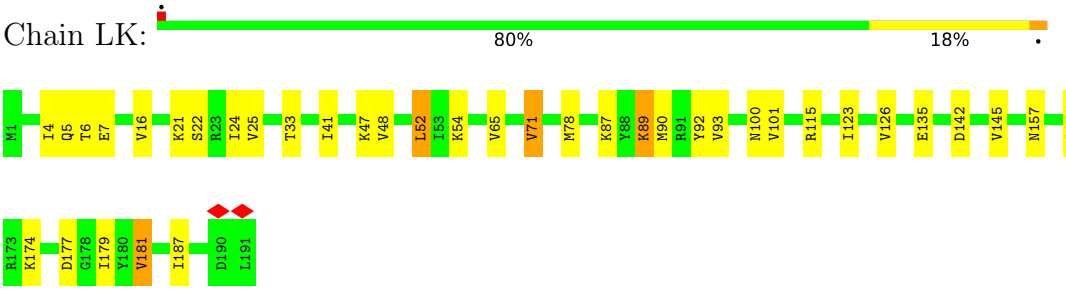
• Molecule 10: Large ribosomal subunit protein uL30A



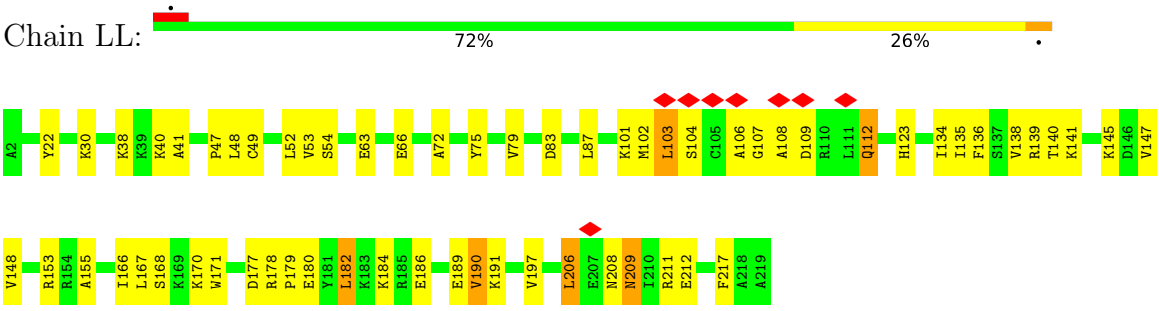
• Molecule 11: Large ribosomal subunit protein eL8A



• Molecule 12: Large ribosomal subunit protein uL6A

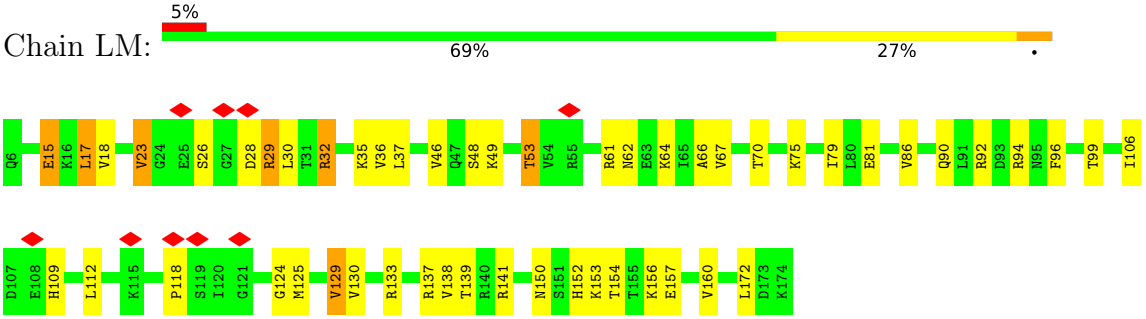


• Molecule 13: Large ribosomal subunit protein uL16



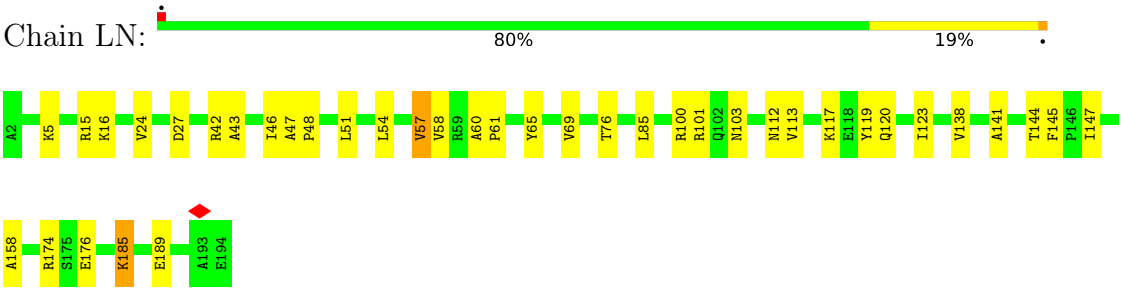
• Molecule 14: Large ribosomal subunit protein uL5B

Chain LM:



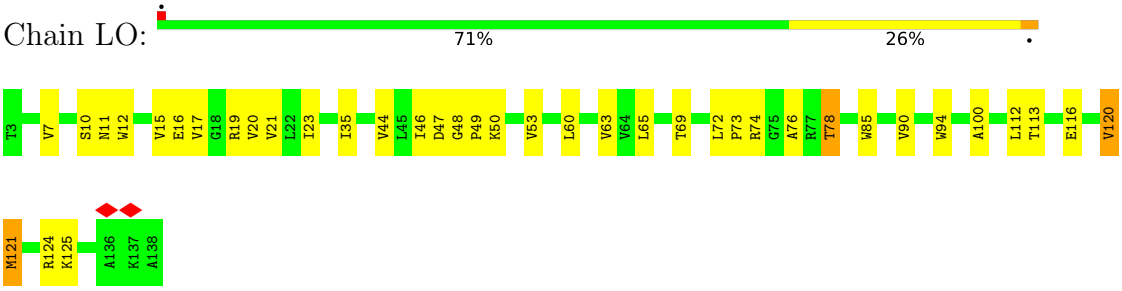
• Molecule 15: Large ribosomal subunit protein eL13A

Chain LN:



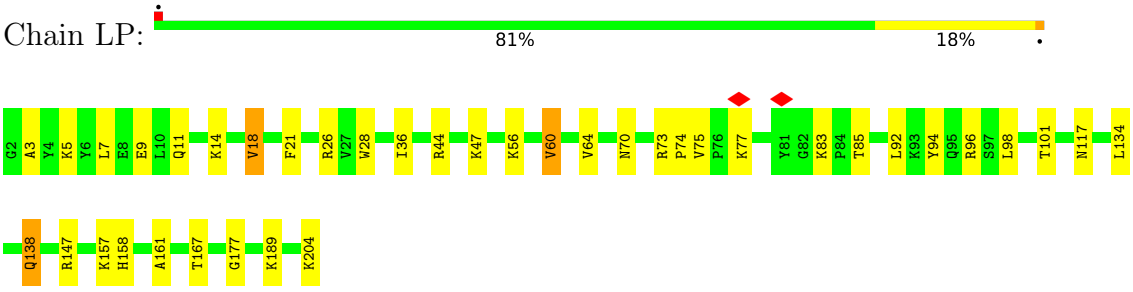
• Molecule 16: Large ribosomal subunit protein eL14A

Chain LO:



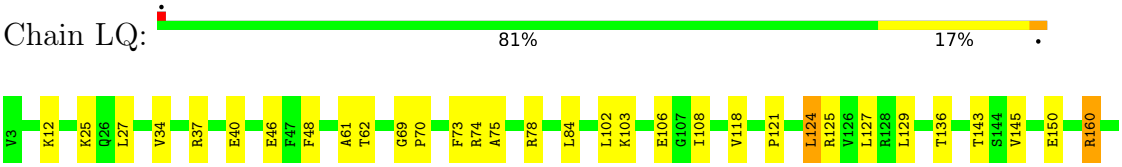
• Molecule 17: Large ribosomal subunit protein eL15A

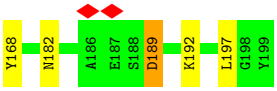
Chain LP:



• Molecule 18: Large ribosomal subunit protein uL13A

Chain LQ:

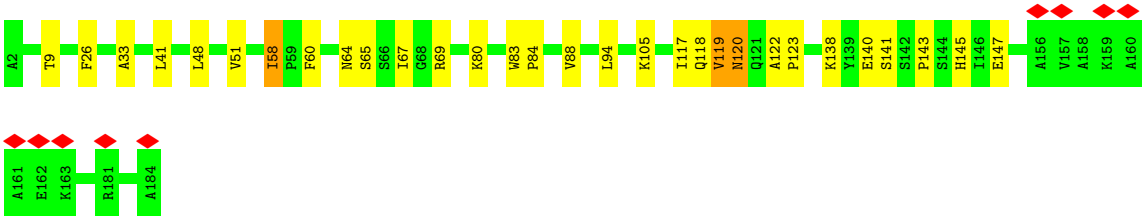




• Molecule 19: Large ribosomal subunit protein uL22A

Chain LR:

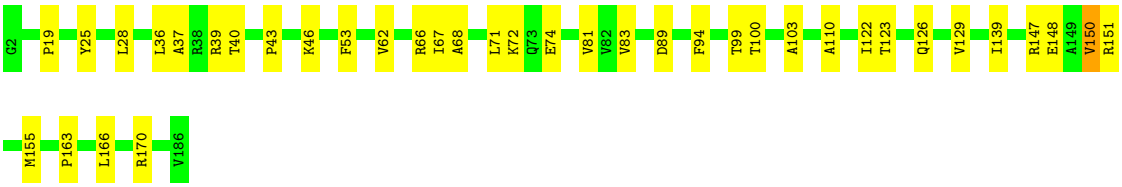




• Molecule 20: Large ribosomal subunit protein eL18A

Chain LS:

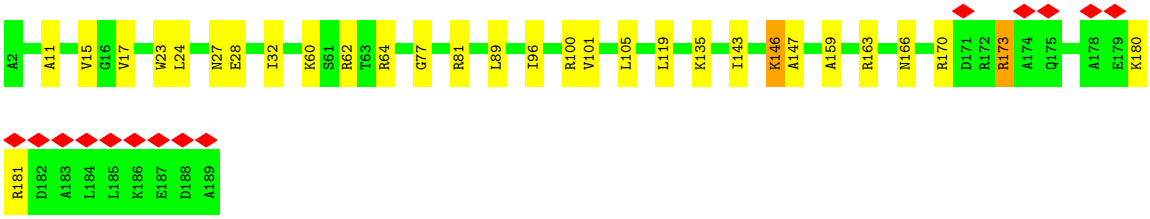




• Molecule 21: Large ribosomal subunit protein eL19A

Chain LT:





• Molecule 22: Large ribosomal subunit protein eL20A

Chain LU:

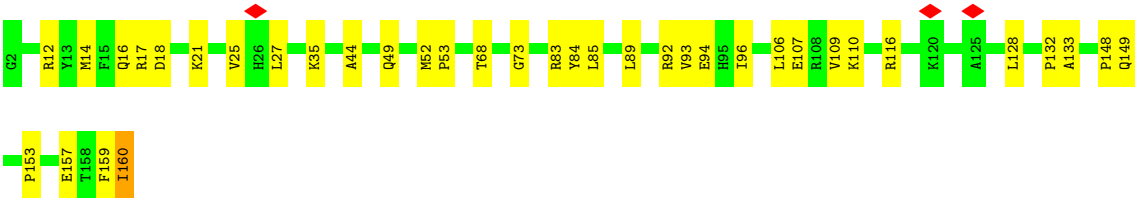




• Molecule 23: Large ribosomal subunit protein eL21A

Chain LV:

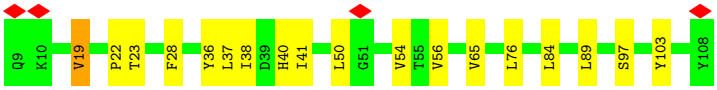




• Molecule 24: Large ribosomal subunit protein eL22A

Chain LW:

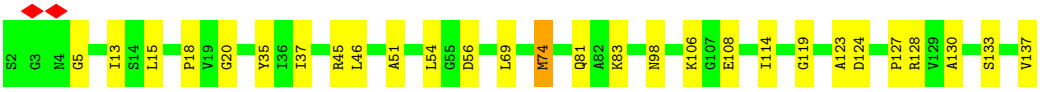




• Molecule 25: Large ribosomal subunit protein uL14A

Chain LX:

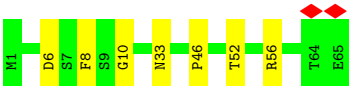




• Molecule 26: Large ribosomal subunit protein eL24A

Chain LY:

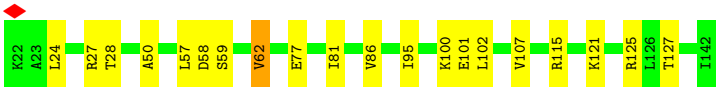




• Molecule 27: Large ribosomal subunit protein uL23

Chain LZ:

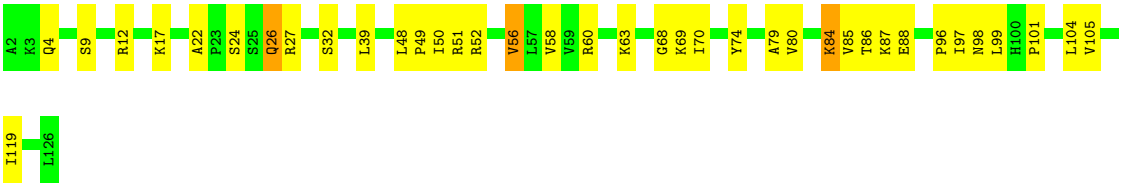




• Molecule 28: Large ribosomal subunit protein uL24A

Chain La:

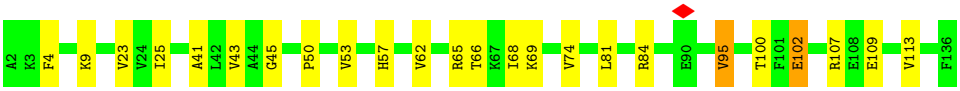




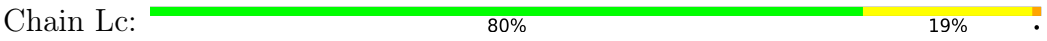
• Molecule 29: Large ribosomal subunit protein eL27A

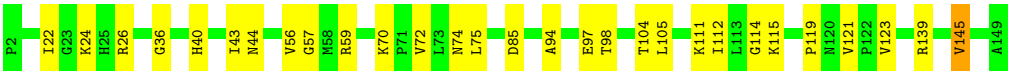
Chain Lb:



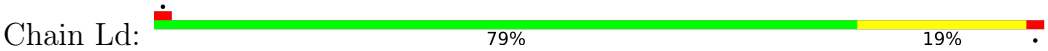


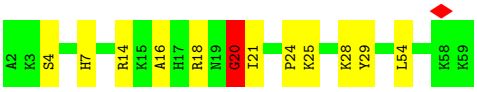
• Molecule 30: Large ribosomal subunit protein uL15



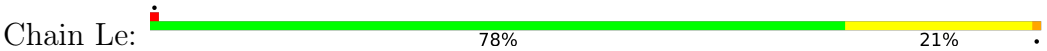


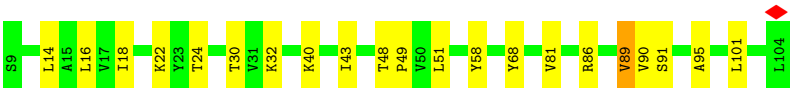
• Molecule 31: Large ribosomal subunit protein eL29



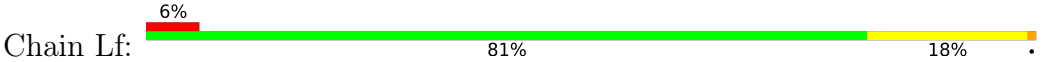


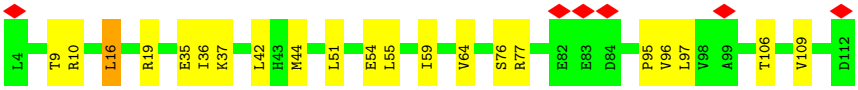
• Molecule 32: Large ribosomal subunit protein eL30



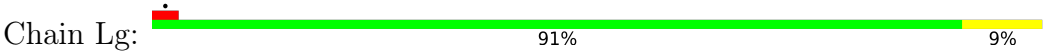


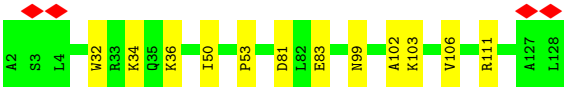
• Molecule 33: Large ribosomal subunit protein eL31A



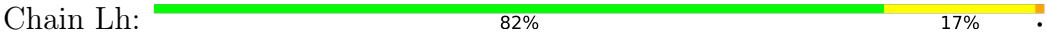


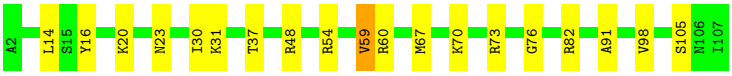
• Molecule 34: Large ribosomal subunit protein eL32





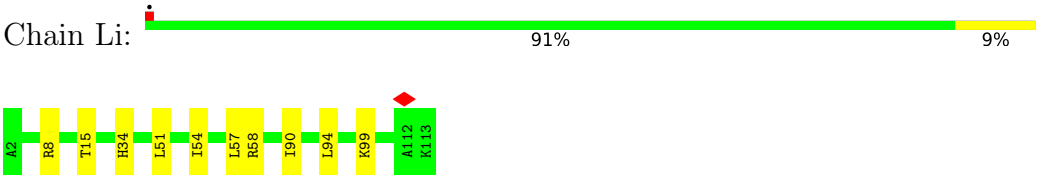
• Molecule 35: Large ribosomal subunit protein eL33A





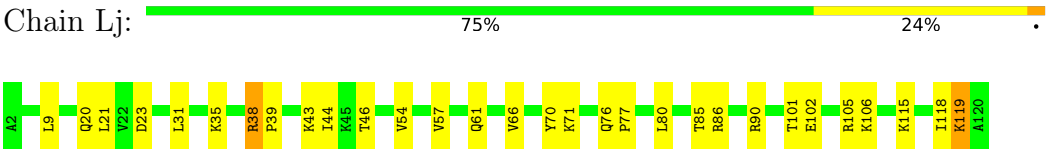
• Molecule 36: Large ribosomal subunit protein eL34A

Chain Li:



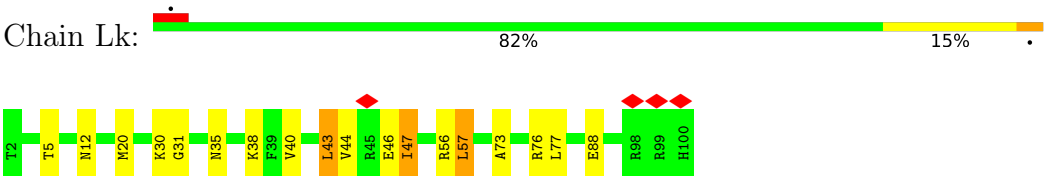
• Molecule 37: Large ribosomal subunit protein uL29A

Chain Lj:



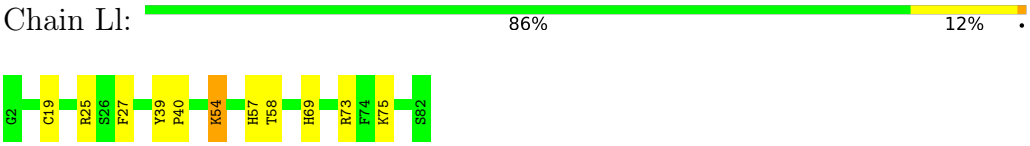
• Molecule 38: Large ribosomal subunit protein eL36A

Chain Lk:



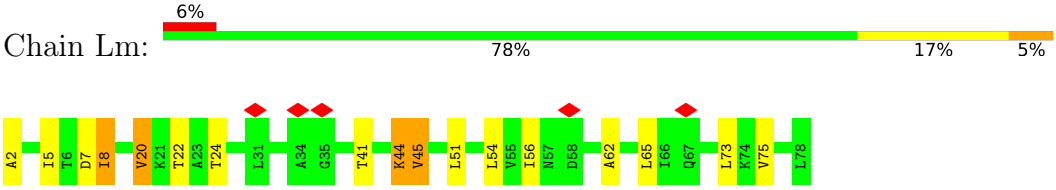
• Molecule 39: Large ribosomal subunit protein eL37A

Chain Ll:



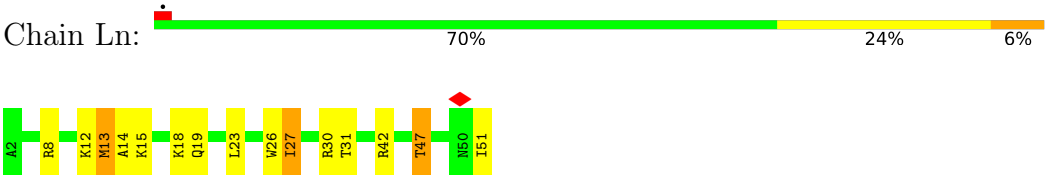
• Molecule 40: Large ribosomal subunit protein eL38

Chain Lm:



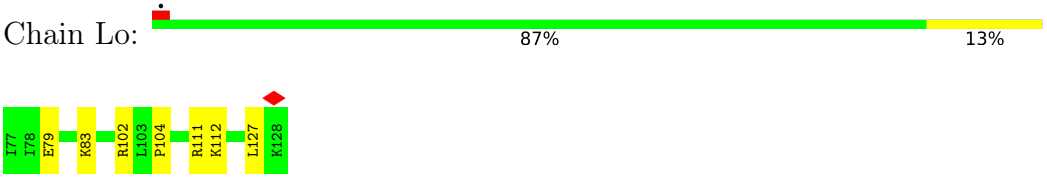
• Molecule 41: Large ribosomal subunit protein eL39

Chain Ln:



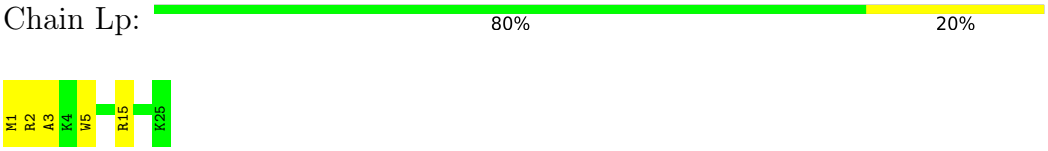
• Molecule 42: Large ribosomal subunit protein eL40A

Chain Lo:



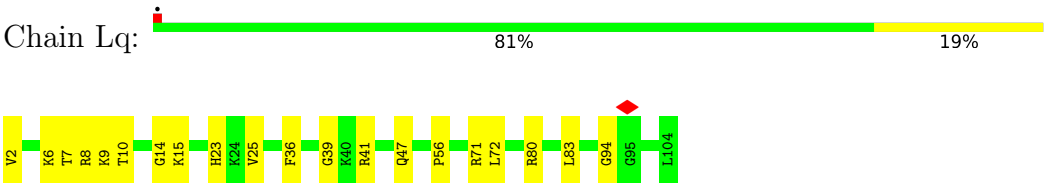
• Molecule 43: Large ribosomal subunit protein eL41A

Chain Lp:



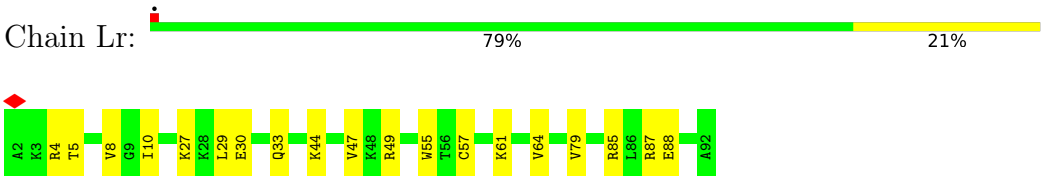
• Molecule 44: Large ribosomal subunit protein eL42A

Chain Lq:



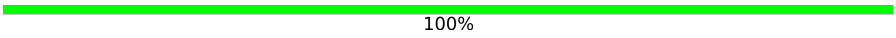
• Molecule 45: Large ribosomal subunit protein eL43A

Chain Lr:



• Molecule 46: RNA (5'-R(P*UP*GP*AP*CP*GP*CP*UP*UP*UP*UP*C)-3')

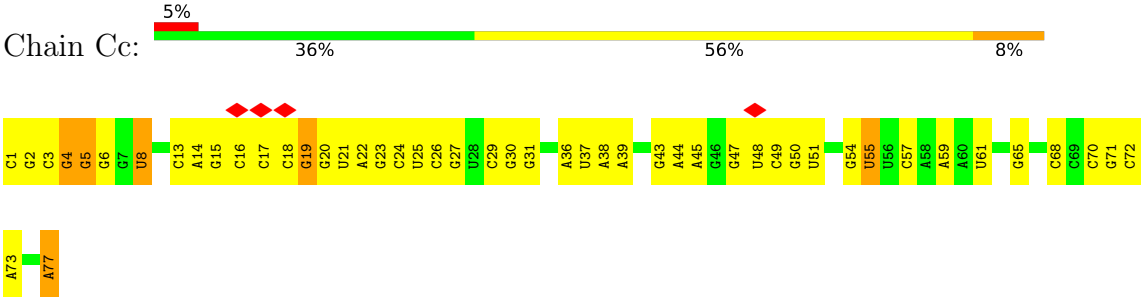
Chain mR:



There are no outlier residues recorded for this chain.

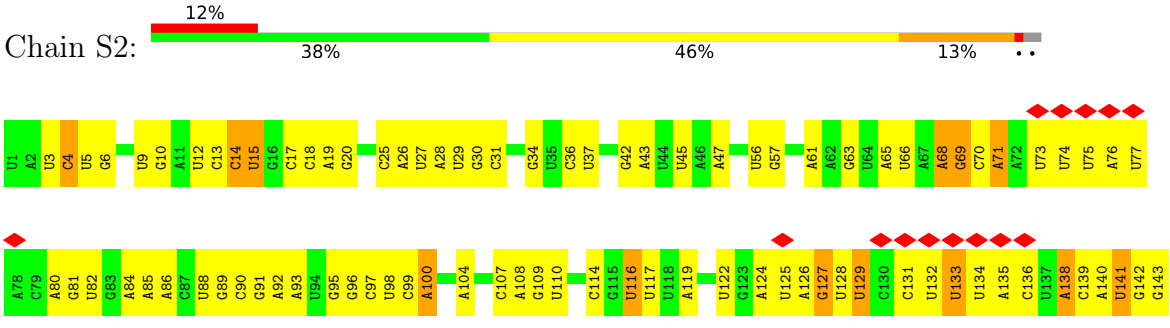
• Molecule 47: tRNA

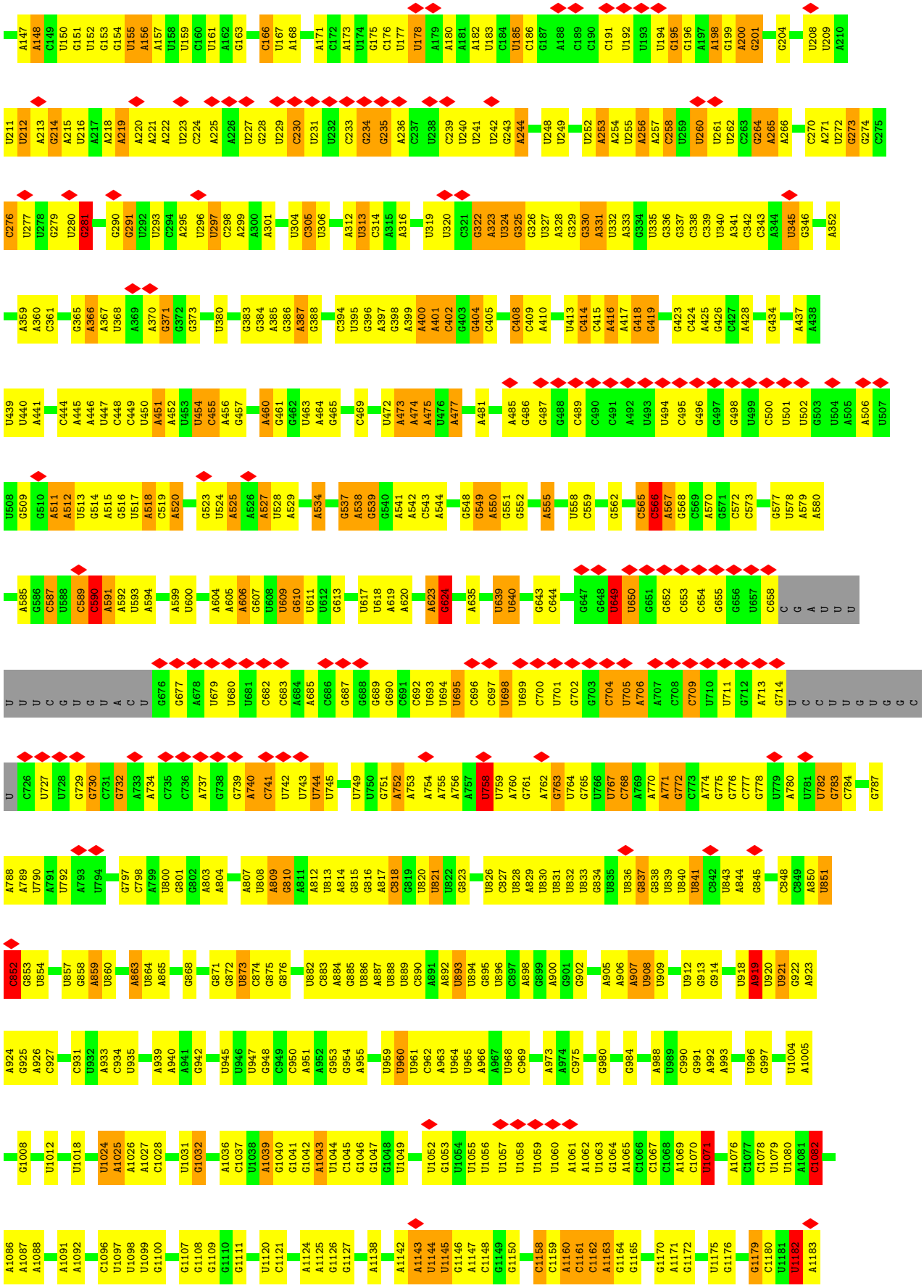
Chain Cc:

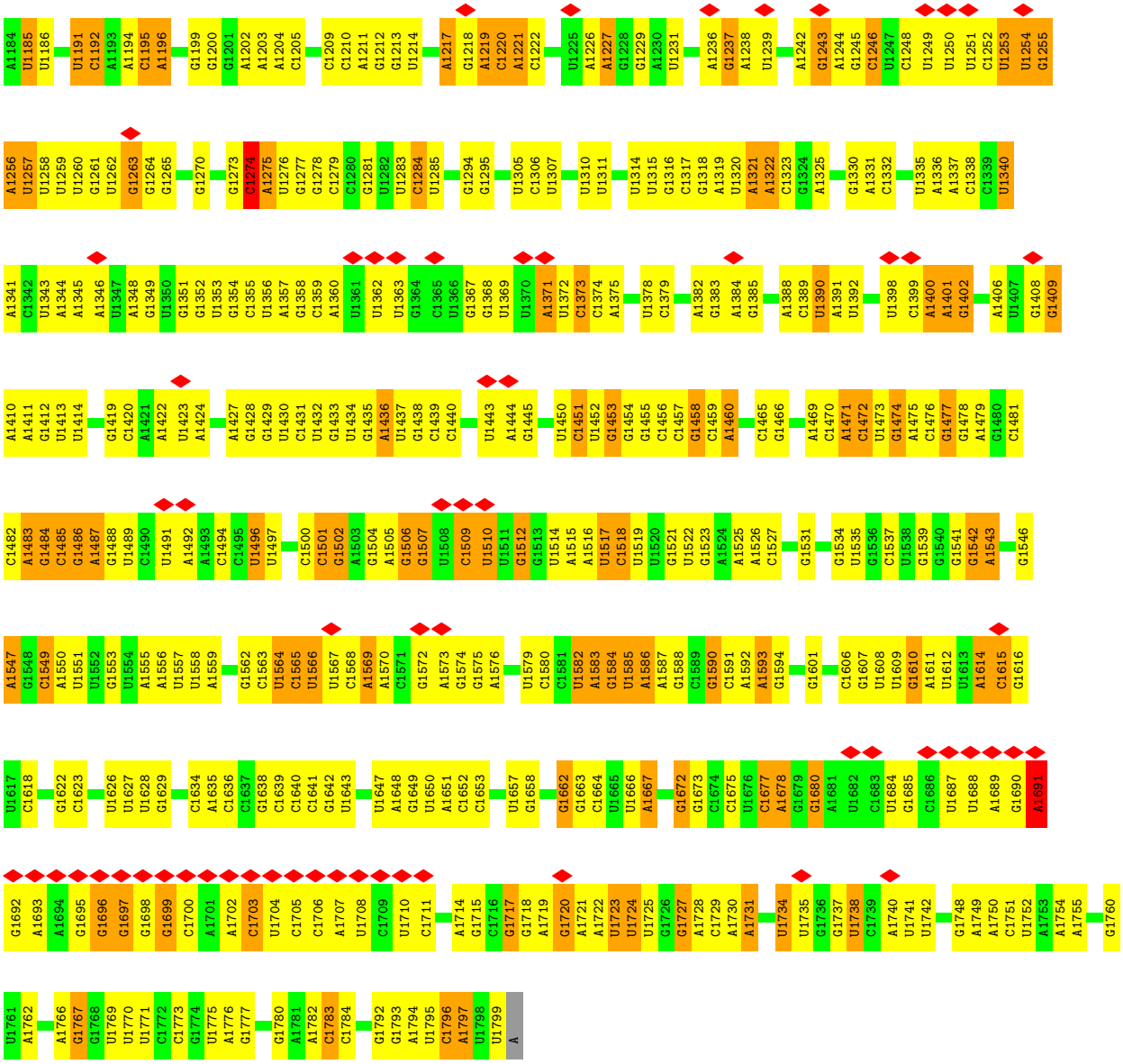


• Molecule 48: RNA(1770-MER)

Chain S2:



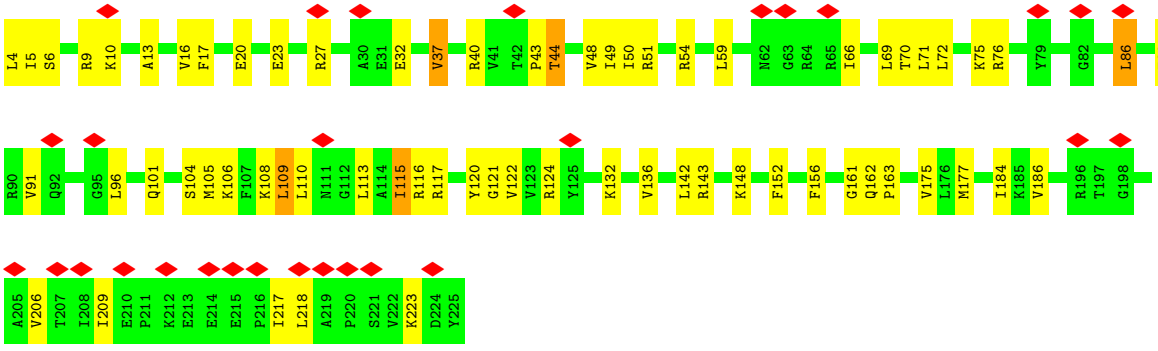




• Molecule 49: Small ribosomal subunit protein uS3

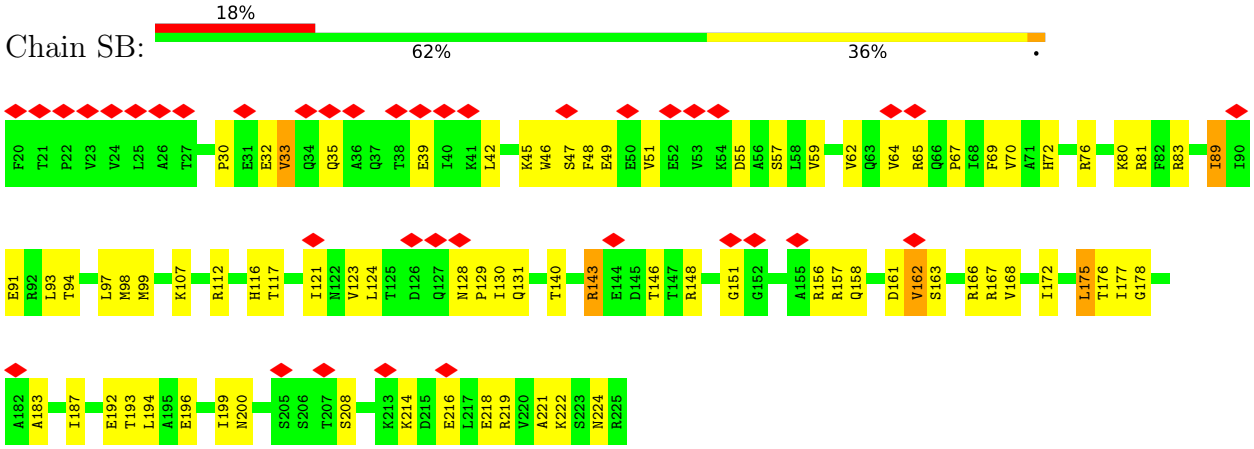
Chain SA:





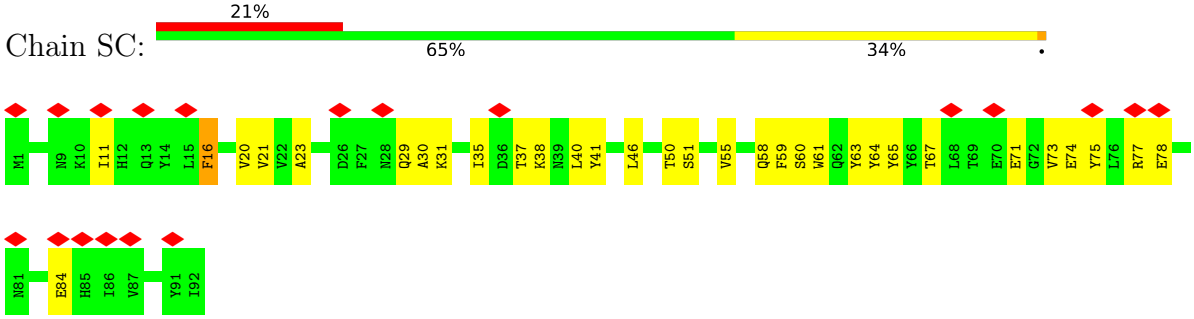
• Molecule 50: Small ribosomal subunit protein uS7

Chain SB:



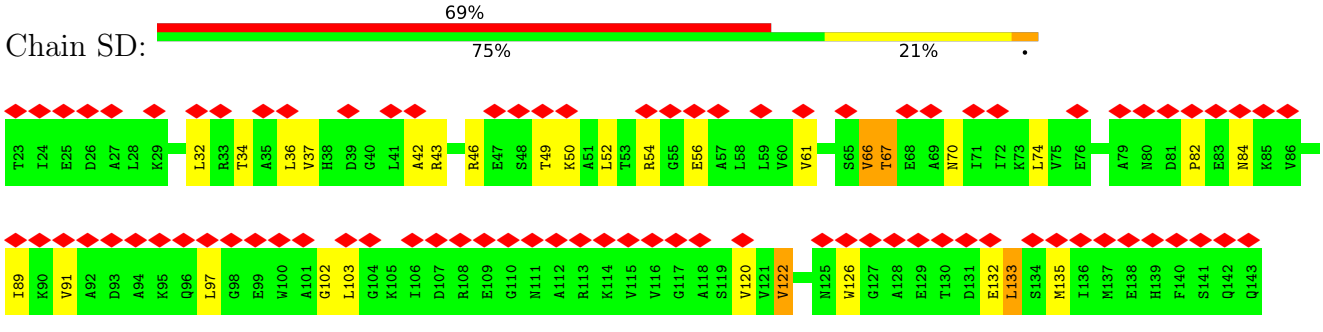
• Molecule 51: Small ribosomal subunit protein eS10A

Chain SC:



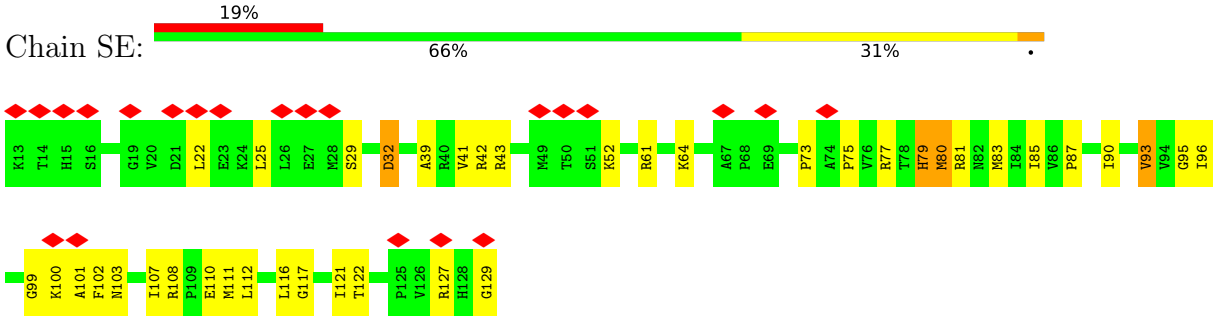
• Molecule 52: Small ribosomal subunit protein eS12

Chain SD:



• Molecule 53: Small ribosomal subunit protein uS19

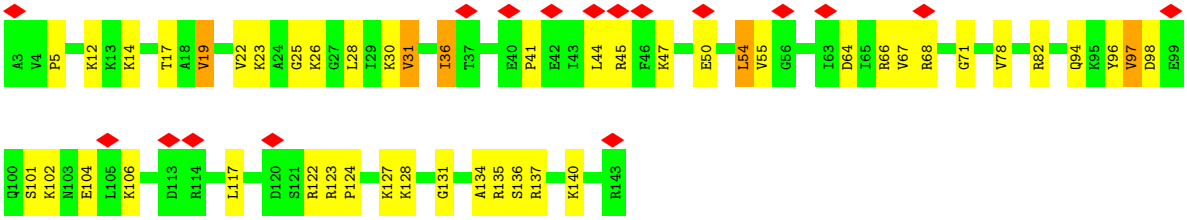
Chain SE:



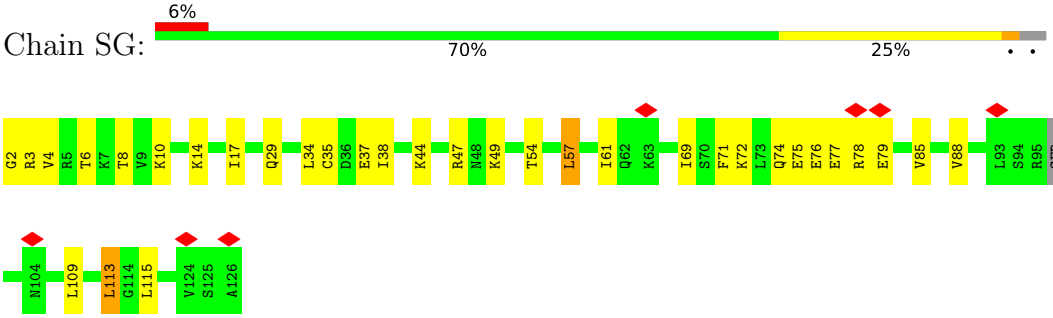
• Molecule 54: Small ribosomal subunit protein uS9A

Chain SF:

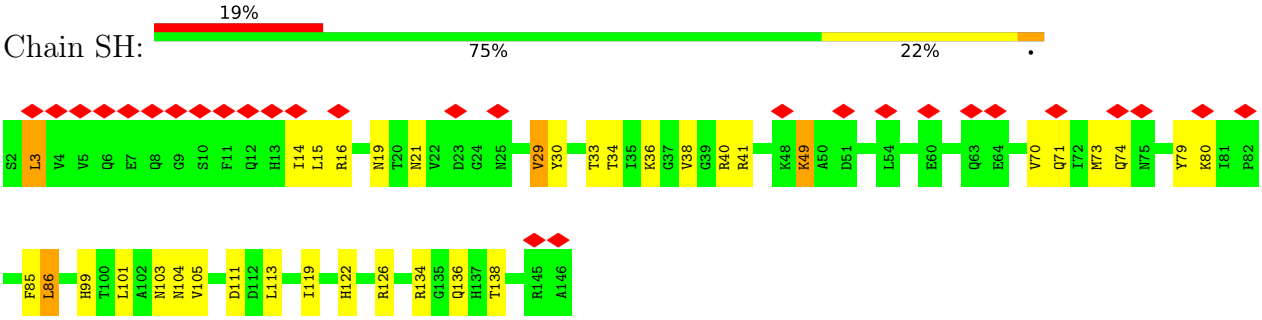




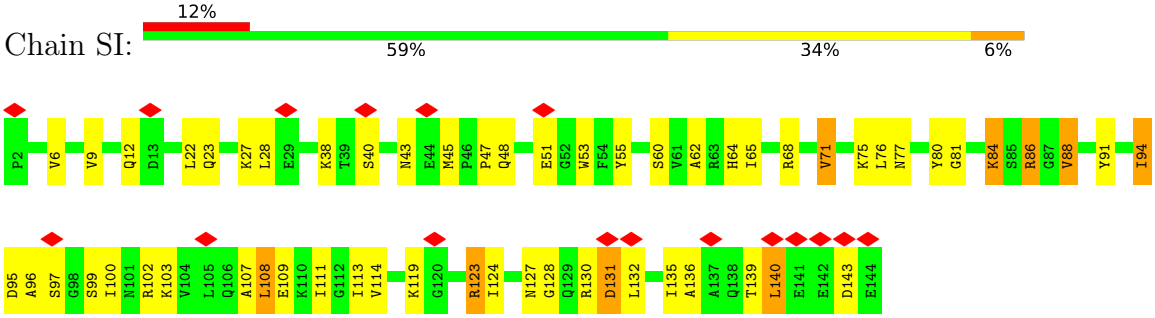
• Molecule 55: Small ribosomal subunit protein eS17B



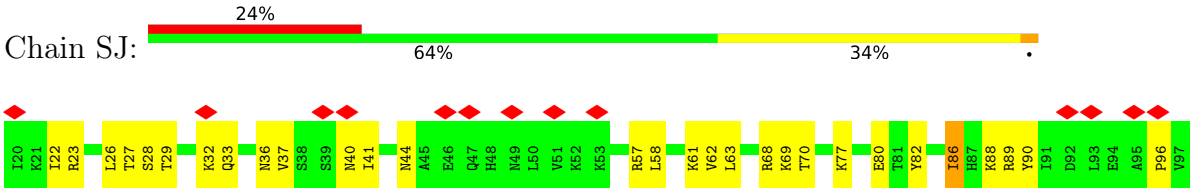
• Molecule 56: Small ribosomal subunit protein uS13A

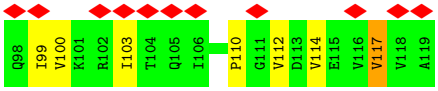


• Molecule 57: Small ribosomal subunit protein eS19A



• Molecule 58: Small ribosomal subunit protein uS10

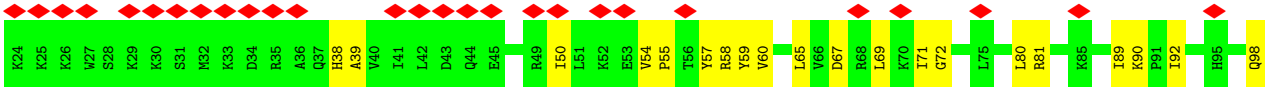


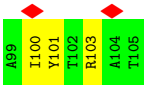


• Molecule 59: Small ribosomal subunit protein eS25A

Chain SK:



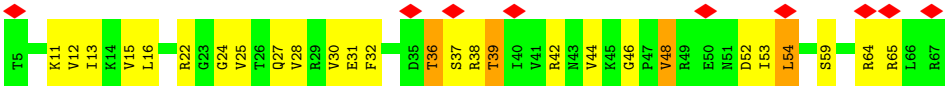




• Molecule 60: Small ribosomal subunit protein eS28A

Chain SL:

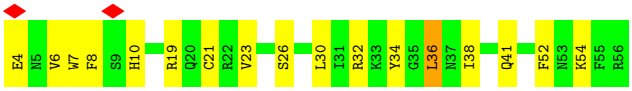




• Molecule 61: Small ribosomal subunit protein uS14A

Chain SM:

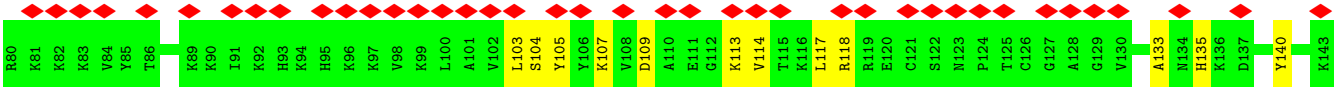


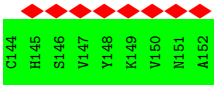


• Molecule 62: Small ribosomal subunit protein eS31

Chain SN:



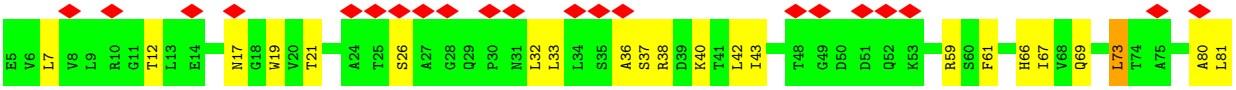


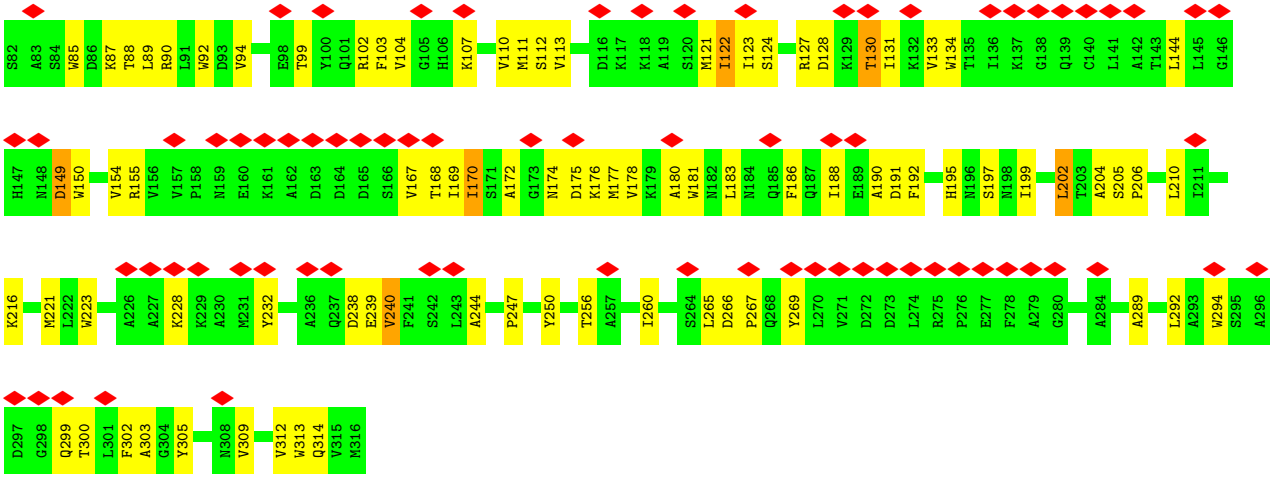


• Molecule 63: Small ribosomal subunit protein RACK1

Chain SO:



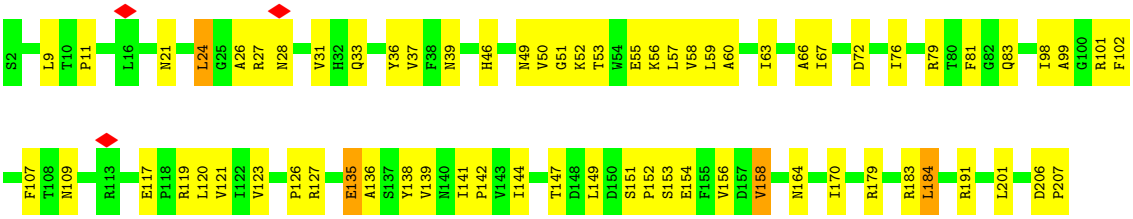




• Molecule 64: Small ribosomal subunit protein uS2A

Chain SP:

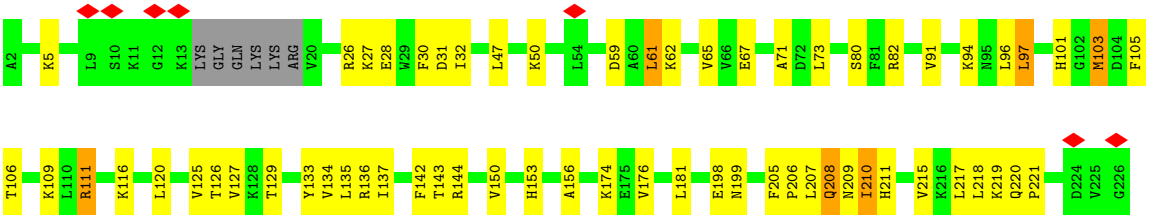




• Molecule 65: Small ribosomal subunit protein eS1A

Chain SQ:

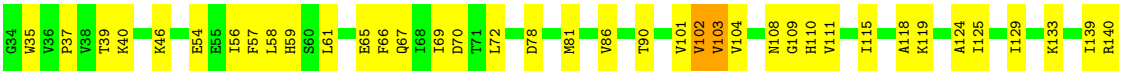


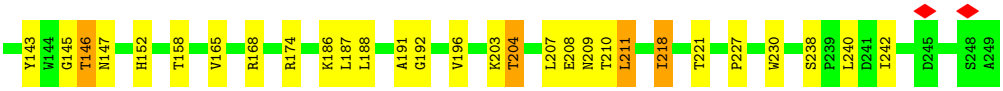


• Molecule 66: Small ribosomal subunit protein uS5

Chain SR:

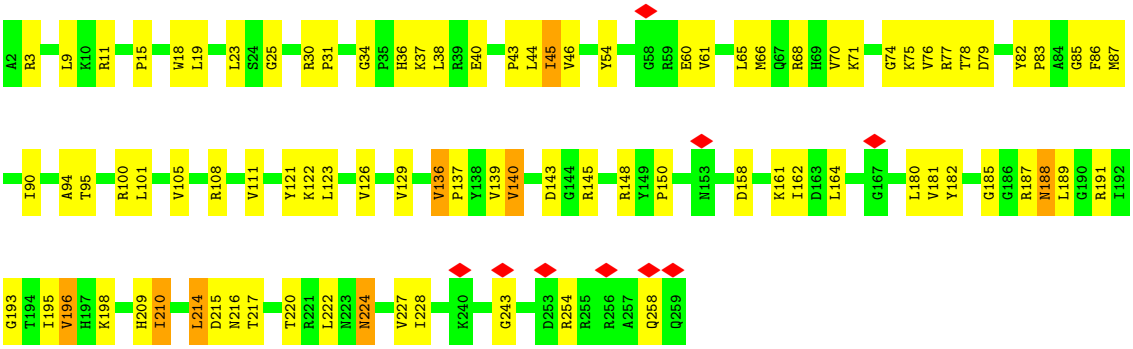






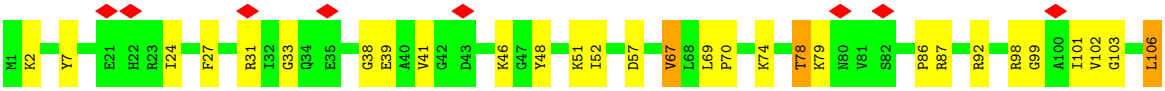
• Molecule 67: Small ribosomal subunit protein eS4A

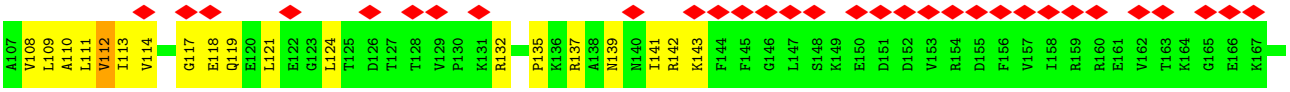


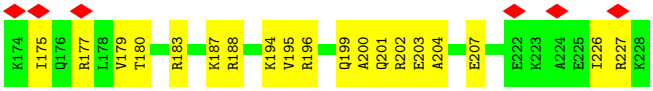


• Molecule 68: Small ribosomal subunit protein eS6A



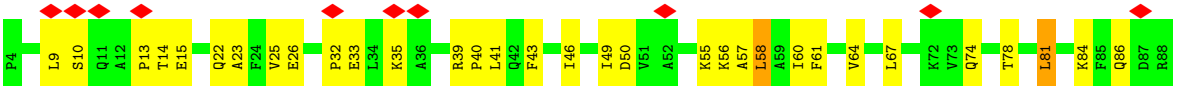


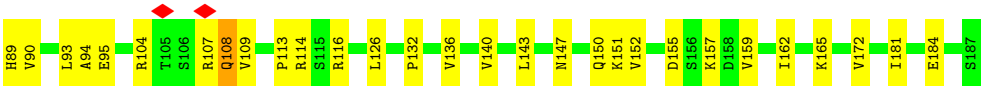




• Molecule 69: Small ribosomal subunit protein eS7A

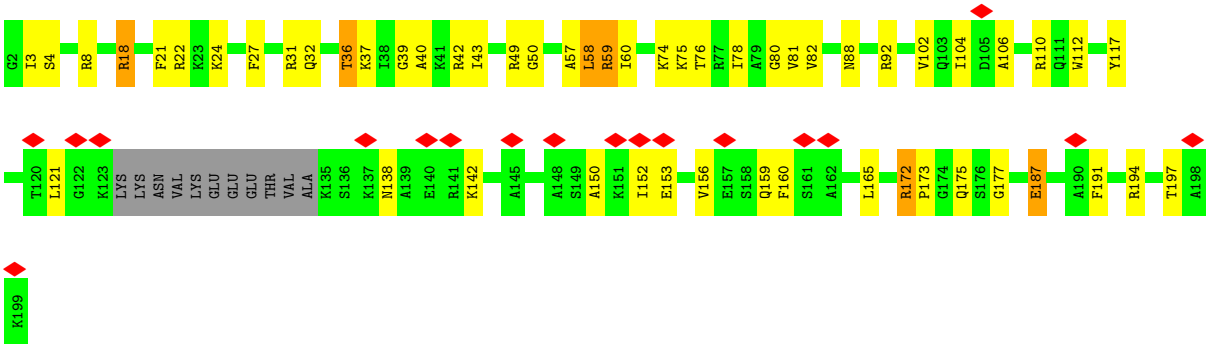




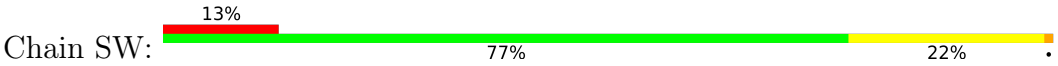


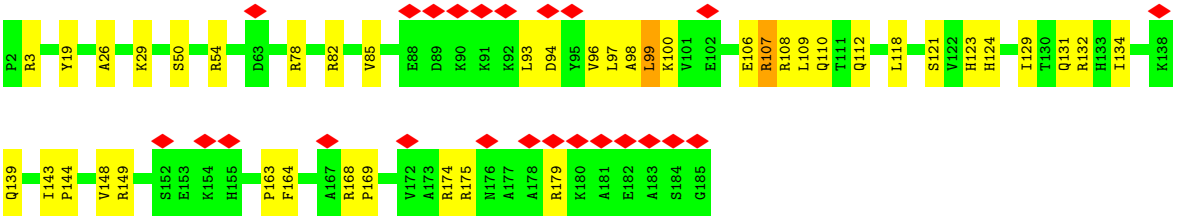
• Molecule 70: Small ribosomal subunit protein eS8A



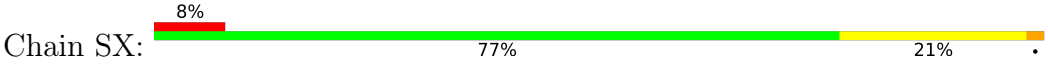


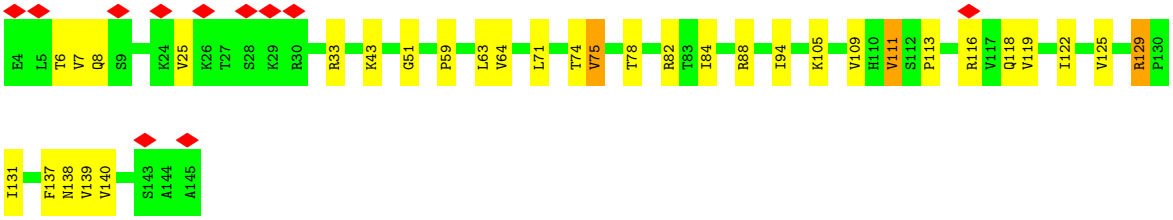
• Molecule 71: Small ribosomal subunit protein uS4A





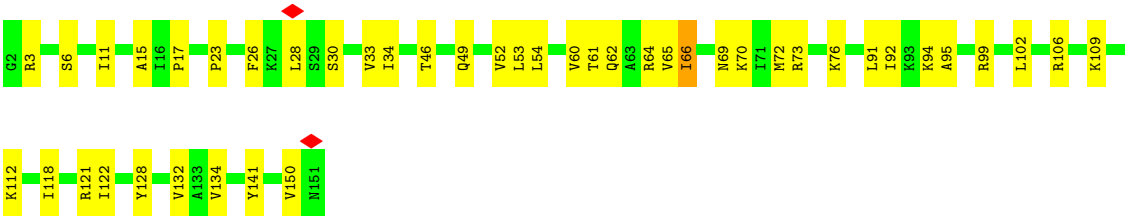
• Molecule 72: Small ribosomal subunit protein uS17A





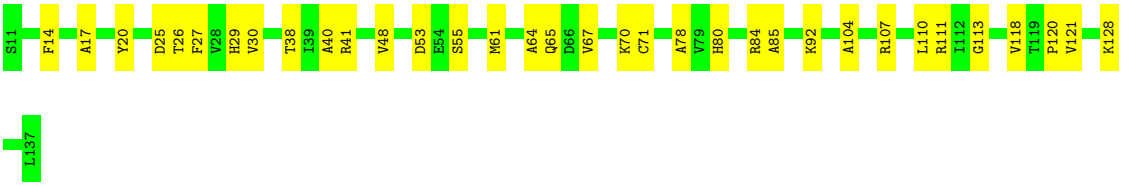
• Molecule 73: Small ribosomal subunit protein uS15



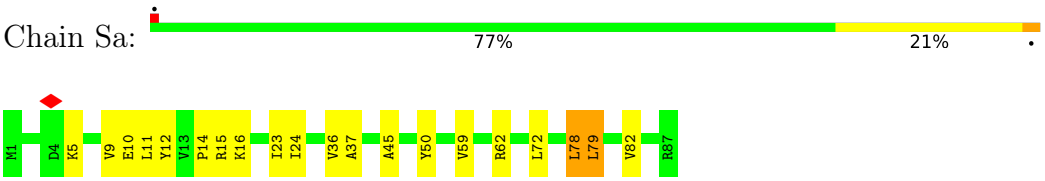


• Molecule 74: Small ribosomal subunit protein uS11B

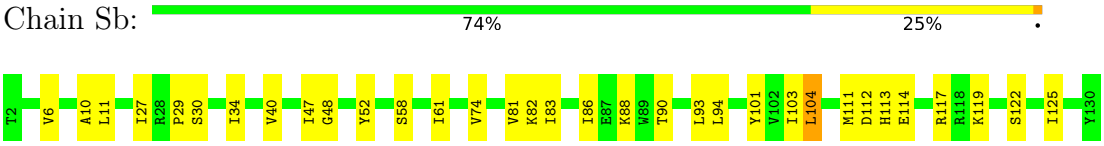




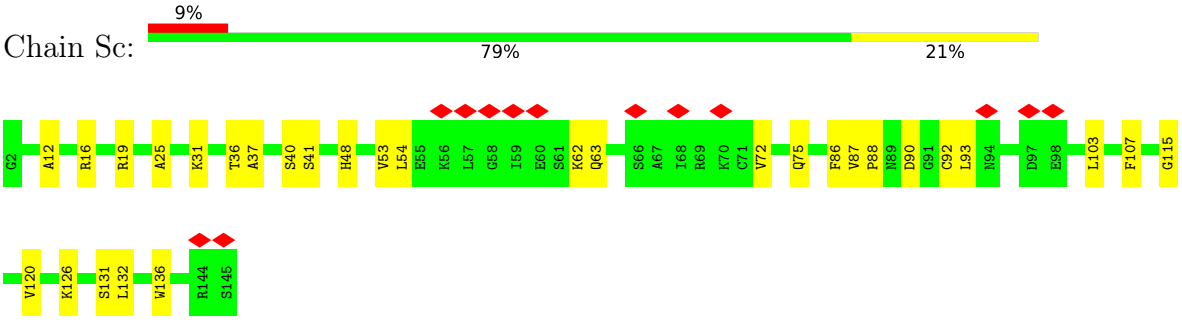
• Molecule 75: Small ribosomal subunit protein eS21A



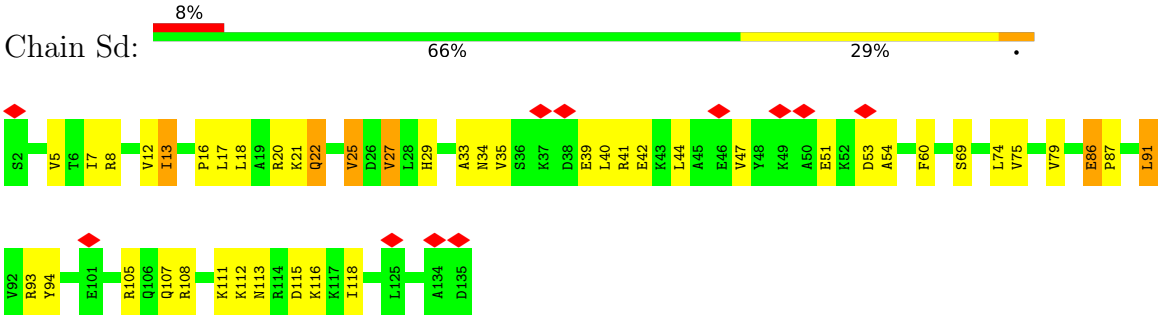
• Molecule 76: Small ribosomal subunit protein uS8A



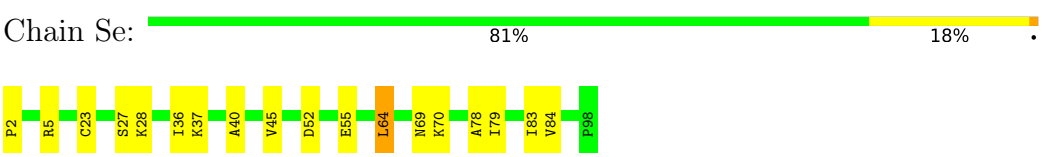
• Molecule 77: Small ribosomal subunit protein uS12A



• Molecule 78: Small ribosomal subunit protein eS24A



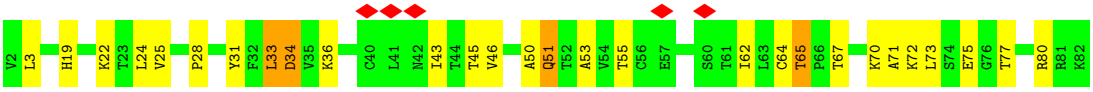
• Molecule 79: Small ribosomal subunit protein eS26B



• Molecule 80: Small ribosomal subunit protein eS27A

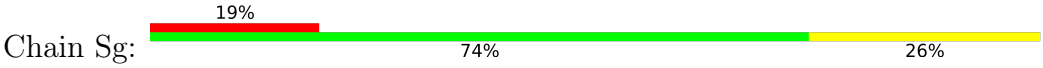
Chain Sf:





• Molecule 81: Small ribosomal subunit protein eS30A

Chain Sg:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15173	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	1.781	Depositor
Minimum map value	-0.905	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.069	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	Bb	0.27	0/1814	0.81	0/2827
2	LA	0.40	0/75727	0.75	22/118064 (0.0%)
3	LB	0.36	0/2883	0.74	2/4491 (0.0%)
4	LC	0.39	0/3746	0.71	0/5832
5	LD	0.20	0/1933	0.31	0/2598
6	LE	0.18	0/3146	0.31	0/4228
7	LF	0.17	0/2800	0.32	0/3790
8	LG	0.15	0/2400	0.32	0/3239
9	LH	0.16	0/1329	0.33	0/1794
10	LI	0.19	0/1821	0.32	0/2451
11	LJ	0.16	0/1836	0.35	0/2481
12	LK	0.15	0/1529	0.32	0/2060
13	LL	0.16	0/1801	0.32	0/2416
14	LM	0.14	0/1367	0.34	0/1834
15	LN	0.17	0/1568	0.33	0/2106
16	LO	0.14	0/1068	0.30	0/1438
17	LP	0.19	0/1757	0.33	0/2354
18	LQ	0.18	0/1585	0.30	0/2128
19	LR	0.17	0/1439	0.31	0/1938
20	LS	0.18	0/1465	0.34	0/1965
21	LT	0.15	0/1532	0.26	0/2043
22	LU	0.18	0/1473	0.34	0/1980
23	LV	0.18	0/1296	0.32	0/1739
24	LW	0.14	0/812	0.34	0/1099
25	LX	0.17	0/1018	0.29	0/1369
26	LY	0.16	0/540	0.28	0/717
27	LZ	0.16	0/979	0.30	0/1321
28	La	0.15	0/995	0.30	0/1329
29	Lb	0.16	0/1106	0.34	0/1485
30	Lc	0.18	0/1200	0.32	0/1607
31	Ld	0.17	0/473	0.51	1/629 (0.2%)
32	Le	0.15	0/745	0.31	0/1001
33	Lf	0.16	0/890	0.31	0/1196
34	Lg	0.18	0/1038	0.31	0/1390

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	Lh	0.19	0/868	0.33	0/1168
36	Li	0.16	0/890	0.28	0/1189
37	Lj	0.15	0/978	0.32	0/1301
38	Lk	0.14	0/772	0.30	0/1026
39	Ll	0.18	0/660	0.34	0/875
40	Lm	0.13	0/618	0.26	0/826
41	Ln	0.17	0/443	0.29	0/588
42	Lo	0.15	0/416	0.33	0/553
43	Lp	0.15	0/230	0.30	0/296
44	Lq	0.17	0/836	0.30	0/1104
45	Lr	0.19	0/701	0.35	0/934
47	Cc	0.26	0/1836	0.72	1/2859 (0.0%)
48	S2	0.33	0/42211	0.79	40/65773 (0.1%)
49	SA	0.14	0/1754	0.34	0/2361
50	SB	0.14	0/1625	0.34	0/2197
51	SC	0.12	0/769	0.32	0/1039
52	SD	0.15	0/883	0.46	0/1199
53	SE	0.15	0/936	0.34	0/1259
54	SF	0.13	0/1125	0.36	0/1510
55	SG	0.12	0/957	0.29	0/1283
56	SH	0.12	0/1207	0.32	0/1623
57	SI	0.13	0/1130	0.36	0/1517
58	SJ	0.14	0/807	0.37	0/1091
59	SK	0.12	0/661	0.33	0/888
60	SL	0.13	0/493	0.32	0/663
61	SM	0.13	0/452	0.34	0/600
62	SN	0.12	0/567	0.33	0/764
63	SO	0.13	0/2436	0.35	0/3318
64	SP	0.16	0/1644	0.38	0/2249
65	SQ	0.16	0/1823	0.39	0/2447
66	SR	0.16	0/1656	0.39	0/2251
67	SS	0.14	0/2097	0.37	0/2823
68	ST	0.12	0/1839	0.33	0/2460
69	SU	0.15	0/1498	0.35	0/2019
70	SV	0.12	0/1501	0.31	0/2006
71	SW	0.13	0/1504	0.36	0/2016
72	SX	0.14	0/1168	0.30	0/1575
73	SY	0.15	0/1215	0.31	0/1638
74	SZ	0.17	0/934	0.36	0/1257
75	Sa	0.14	0/682	0.33	0/921
76	Sb	0.18	0/1038	0.35	0/1395
77	Sc	0.15	0/1139	0.34	0/1518
78	Sd	0.11	0/1046	0.29	0/1401

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
79	Se	0.16	0/778	0.32	0/1042
80	Sf	0.14	0/620	0.31	0/838
81	Sg	0.12	0/459	0.34	0/611
All	All	0.31	0/217013	0.63	66/319210 (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
7	LF	0	1
11	LJ	0	2
31	Ld	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
48	S2	893	U	N3-C4-O4	-11.81	111.13	119.40
48	S2	893	U	C5-C4-O4	10.42	132.15	125.90
31	Ld	20	GLY	N-CA-C	10.22	119.51	110.21
48	S2	919	A	N1-C6-N6	-9.49	112.90	118.60
48	S2	590	C	C2-N1-C1'	9.18	128.90	118.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	LF	13	GLY	Peptide
11	LJ	30	THR	Peptide
11	LJ	76	ALA	Peptide
31	Ld	20	GLY	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	Bb	1622	0	821	27	0
2	LA	67653	0	33997	784	0
3	LB	2579	0	1304	37	0
4	LC	3353	0	1695	45	0
5	LD	1899	0	1957	37	0
6	LE	3075	0	3142	63	0
7	LF	2748	0	2859	60	0
8	LG	2351	0	2294	46	0
9	LH	1307	0	1377	16	0
10	LI	1784	0	1862	28	0
11	LJ	1804	0	1877	39	0
12	LK	1508	0	1572	26	0
13	LL	1764	0	1804	42	0
14	LM	1346	0	1370	35	0
15	LN	1543	0	1608	29	0
16	LO	1053	0	1149	22	0
17	LP	1720	0	1779	30	0
18	LQ	1555	0	1659	20	0
19	LR	1416	0	1433	18	0
20	LS	1441	0	1543	23	0
21	LT	1515	0	1606	19	0
22	LU	1437	0	1475	18	0
23	LV	1272	0	1312	28	0
24	LW	796	0	812	7	0
25	LX	1003	0	1048	14	0
26	LY	528	0	546	4	0
27	LZ	964	0	1025	13	0
28	La	984	0	1075	24	0
29	Lb	1080	0	1122	18	0
30	Lc	1169	0	1211	21	0
31	Ld	462	0	491	9	0
32	Le	737	0	792	13	0
33	Lf	876	0	912	8	0
34	Lg	1017	0	1081	6	0
35	Lh	850	0	880	12	0
36	Li	880	0	945	6	0
37	Lj	969	0	1078	20	0
38	Lk	766	0	844	14	0
39	Ll	645	0	649	4	0
40	Lm	612	0	682	8	0
41	Ln	436	0	475	15	0
42	Lo	410	0	446	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	Lp	229	0	273	5	0
44	Lq	824	0	892	10	0
45	Lr	694	0	738	14	0
46	mR	228	0	0	0	0
47	Cc	1644	0	837	30	0
48	S2	37739	0	18988	562	0
49	SA	1729	0	1812	43	0
50	SB	1605	0	1669	53	0
51	SC	752	0	719	24	0
52	SD	875	0	878	17	0
53	SE	916	0	941	27	0
54	SF	1105	0	1166	38	0
55	SG	948	0	990	21	0
56	SH	1188	0	1218	23	0
57	SI	1112	0	1124	38	0
58	SJ	797	0	863	23	0
59	SK	651	0	682	15	0
60	SL	491	0	524	24	0
61	SM	442	0	432	10	0
62	SN	556	0	549	8	0
63	SO	2383	0	2332	68	0
64	SP	1603	0	1610	53	0
65	SQ	1798	0	1890	42	0
66	SR	1626	0	1715	42	0
67	SS	2056	0	2140	61	0
68	ST	1815	0	1894	44	0
69	SU	1473	0	1555	35	0
70	SV	1476	0	1501	42	0
71	SW	1479	0	1556	31	0
72	SX	1142	0	1209	16	0
73	SY	1192	0	1255	25	0
74	SZ	923	0	948	20	0
75	Sa	673	0	662	15	0
76	Sb	1021	0	1060	20	0
77	Sc	1121	0	1196	21	0
78	Sd	1032	0	1044	27	0
79	Se	765	0	814	14	0
80	Sf	610	0	633	13	0
81	Sg	451	0	494	9	0
All	All	202093	0	148412	2924	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 8.

The worst 5 of 2924 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)
48:S2:752:A:N6	48:S2:797:G:H1	1.41	1.18
48:S2:550:A:N6	48:S2:587:C:C4	2.13	1.17
48:S2:821:U:H3	48:S2:852:C:N4	1.41	1.16
1:Bb:4:G:H1	1:Bb:69:U:H3	1.16	0.94
48:S2:69:G:H1	48:S2:82:U:H3	1.16	0.93

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	
5	LD	249/251 (99%)	230 (92%)	19 (8%)	0	100	100
6	LE	384/386 (100%)	360 (94%)	24 (6%)	0	100	100
7	LF	359/361 (99%)	335 (93%)	24 (7%)	0	100	100
8	LG	292/294 (99%)	276 (94%)	16 (6%)	0	100	100
9	LH	163/175 (93%)	155 (95%)	8 (5%)	0	100	100
10	LI	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
11	LJ	231/233 (99%)	217 (94%)	14 (6%)	0	100	100
12	LK	189/191 (99%)	177 (94%)	12 (6%)	0	100	100
13	LL	216/218 (99%)	204 (94%)	12 (6%)	0	100	100
14	LM	167/169 (99%)	157 (94%)	10 (6%)	0	100	100
15	LN	191/193 (99%)	175 (92%)	16 (8%)	0	100	100
16	LO	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
17	LP	201/203 (99%)	189 (94%)	12 (6%)	0	100	100
18	LQ	195/197 (99%)	192 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	LR	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
20	LS	183/185 (99%)	174 (95%)	9 (5%)	0	100	100
21	LT	186/188 (99%)	182 (98%)	4 (2%)	0	100	100
22	LU	169/171 (99%)	160 (95%)	9 (5%)	0	100	100
23	LV	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
24	LW	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
25	LX	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
26	LY	63/65 (97%)	62 (98%)	1 (2%)	0	100	100
27	LZ	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
28	La	123/125 (98%)	119 (97%)	4 (3%)	0	100	100
29	Lb	133/135 (98%)	126 (95%)	7 (5%)	0	100	100
30	Lc	146/148 (99%)	132 (90%)	14 (10%)	0	100	100
31	Ld	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
32	Le	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
33	Lf	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
34	Lg	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
35	Lh	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
36	Li	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
37	Lj	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
38	Lk	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
39	Ll	79/81 (98%)	78 (99%)	1 (1%)	0	100	100
40	Lm	75/77 (97%)	75 (100%)	0	0	100	100
41	Ln	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
42	Lo	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
43	Lp	23/25 (92%)	23 (100%)	0	0	100	100
44	Lq	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
45	Lr	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
49	SA	220/222 (99%)	212 (96%)	8 (4%)	0	100	100
50	SB	204/206 (99%)	189 (93%)	14 (7%)	1 (0%)	24	54
51	SC	90/92 (98%)	81 (90%)	9 (10%)	0	100	100
52	SD	119/121 (98%)	97 (82%)	22 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	SE	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
54	SF	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
55	SG	117/125 (94%)	115 (98%)	2 (2%)	0	100	100
56	SH	143/145 (99%)	135 (94%)	8 (6%)	0	100	100
57	SI	141/143 (99%)	135 (96%)	6 (4%)	0	100	100
58	SJ	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
59	SK	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
60	SL	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
61	SM	51/53 (96%)	50 (98%)	1 (2%)	0	100	100
62	SN	71/73 (97%)	55 (78%)	16 (22%)	0	100	100
63	SO	310/312 (99%)	286 (92%)	24 (8%)	0	100	100
64	SP	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
65	SQ	222/232 (96%)	203 (91%)	19 (9%)	0	100	100
66	SR	214/216 (99%)	207 (97%)	7 (3%)	0	100	100
67	SS	256/258 (99%)	234 (91%)	22 (9%)	0	100	100
68	ST	226/228 (99%)	210 (93%)	15 (7%)	1 (0%)	30	59
69	SU	182/184 (99%)	171 (94%)	11 (6%)	0	100	100
70	SV	183/198 (92%)	171 (93%)	12 (7%)	0	100	100
71	SW	182/184 (99%)	169 (93%)	13 (7%)	0	100	100
72	SX	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
73	SY	148/150 (99%)	140 (95%)	8 (5%)	0	100	100
74	SZ	125/127 (98%)	115 (92%)	10 (8%)	0	100	100
75	Sa	85/87 (98%)	78 (92%)	7 (8%)	0	100	100
76	Sb	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
77	Sc	142/144 (99%)	127 (89%)	15 (11%)	0	100	100
78	Sd	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
79	Se	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
80	Sf	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
81	Sg	55/57 (96%)	49 (89%)	6 (11%)	0	100	100
All	All	10914/11099 (98%)	10276 (94%)	636 (6%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
68	ST	175	ILE
50	SB	162	VAL

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	
5	LD	190/193 (98%)	183 (96%)	7 (4%)	30	64
6	LE	318/322 (99%)	305 (96%)	13 (4%)	27	61
7	LF	288/288 (100%)	273 (95%)	15 (5%)	21	52
8	LG	241/243 (99%)	228 (95%)	13 (5%)	20	51
9	LH	139/154 (90%)	130 (94%)	9 (6%)	15	44
10	LI	186/186 (100%)	180 (97%)	6 (3%)	34	68
11	LJ	187/191 (98%)	178 (95%)	9 (5%)	23	55
12	LK	168/171 (98%)	158 (94%)	10 (6%)	17	47
13	LL	185/185 (100%)	173 (94%)	12 (6%)	15	44
14	LM	145/147 (99%)	133 (92%)	12 (8%)	10	32
15	LN	154/154 (100%)	146 (95%)	8 (5%)	21	52
16	LO	107/107 (100%)	100 (94%)	7 (6%)	15	44
17	LP	175/175 (100%)	170 (97%)	5 (3%)	37	71
18	LQ	160/160 (100%)	153 (96%)	7 (4%)	25	59
19	LR	138/145 (95%)	129 (94%)	9 (6%)	15	44
20	LS	150/150 (100%)	145 (97%)	5 (3%)	33	67
21	LT	152/153 (99%)	148 (97%)	4 (3%)	40	73
22	LU	155/155 (100%)	149 (96%)	6 (4%)	28	63
23	LV	135/136 (99%)	131 (97%)	4 (3%)	36	70
24	LW	87/87 (100%)	80 (92%)	7 (8%)	11	34
25	LX	104/104 (100%)	98 (94%)	6 (6%)	18	49
26	LY	54/57 (95%)	53 (98%)	1 (2%)	50	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	LZ	104/105 (99%)	99 (95%)	5 (5%)	23	55
28	La	108/108 (100%)	99 (92%)	9 (8%)	10	32
29	Lb	112/115 (97%)	108 (96%)	4 (4%)	31	65
30	Lc	117/118 (99%)	111 (95%)	6 (5%)	21	53
31	Ld	46/46 (100%)	45 (98%)	1 (2%)	45	77
32	Le	81/81 (100%)	75 (93%)	6 (7%)	13	38
33	Lf	92/96 (96%)	84 (91%)	8 (9%)	9	30
34	Lg	108/109 (99%)	105 (97%)	3 (3%)	38	72
35	Lh	90/90 (100%)	86 (96%)	4 (4%)	25	59
36	Li	95/95 (100%)	92 (97%)	3 (3%)	34	68
37	Lj	104/104 (100%)	99 (95%)	5 (5%)	23	55
38	Lk	80/81 (99%)	75 (94%)	5 (6%)	16	45
39	Ll	67/67 (100%)	63 (94%)	4 (6%)	17	47
40	Lm	68/68 (100%)	60 (88%)	8 (12%)	5	17
41	Ln	45/45 (100%)	42 (93%)	3 (7%)	15	43
42	Lo	45/47 (96%)	45 (100%)	0	100	100
43	Lp	22/23 (96%)	22 (100%)	0	100	100
44	Lq	87/88 (99%)	83 (95%)	4 (5%)	24	57
45	Lr	71/71 (100%)	70 (99%)	1 (1%)	59	85
49	SA	182/182 (100%)	164 (90%)	18 (10%)	7	24
50	SB	172/173 (99%)	160 (93%)	12 (7%)	14	40
51	SC	77/85 (91%)	72 (94%)	5 (6%)	15	44
52	SD	88/98 (90%)	80 (91%)	8 (9%)	9	28
53	SE	95/98 (97%)	85 (90%)	10 (10%)	6	22
54	SF	117/117 (100%)	111 (95%)	6 (5%)	21	53
55	SG	101/113 (89%)	93 (92%)	8 (8%)	11	34
56	SH	127/128 (99%)	118 (93%)	9 (7%)	13	40
57	SI	115/115 (100%)	103 (90%)	12 (10%)	7	23
58	SJ	93/93 (100%)	88 (95%)	5 (5%)	20	51
59	SK	67/73 (92%)	65 (97%)	2 (3%)	36	70
60	SL	55/56 (98%)	50 (91%)	5 (9%)	9	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
61	SM	47/47 (100%)	43 (92%)	4 (8%)	10 31
62	SN	56/64 (88%)	55 (98%)	1 (2%)	51 80
63	SO	250/257 (97%)	233 (93%)	17 (7%)	14 42
64	SP	170/173 (98%)	162 (95%)	8 (5%)	23 56
65	SQ	200/205 (98%)	184 (92%)	16 (8%)	11 34
66	SR	175/175 (100%)	161 (92%)	14 (8%)	11 34
67	SS	220/220 (100%)	200 (91%)	20 (9%)	9 28
68	ST	189/195 (97%)	180 (95%)	9 (5%)	23 55
69	SU	163/165 (99%)	150 (92%)	13 (8%)	11 34
70	SV	148/159 (93%)	138 (93%)	10 (7%)	14 42
71	SW	156/157 (99%)	150 (96%)	6 (4%)	29 64
72	SX	126/127 (99%)	117 (93%)	9 (7%)	13 40
73	SY	127/127 (100%)	120 (94%)	7 (6%)	19 50
74	SZ	90/96 (94%)	86 (96%)	4 (4%)	25 59
75	Sa	71/74 (96%)	65 (92%)	6 (8%)	10 31
76	Sb	110/110 (100%)	106 (96%)	4 (4%)	31 65
77	Sc	119/119 (100%)	116 (98%)	3 (2%)	42 74
78	Sd	102/112 (91%)	87 (85%)	15 (15%)	3 10
79	Se	82/83 (99%)	80 (98%)	2 (2%)	43 75
80	Sf	70/70 (100%)	58 (83%)	12 (17%)	2 7
81	Sg	48/49 (98%)	46 (96%)	2 (4%)	26 60
All	All	9168/9335 (98%)	8632 (94%)	536 (6%)	20 49

5 of 536 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
70	SV	160	PHE
72	SX	78	THR
70	SV	82	VAL
79	Se	45	VAL
30	Lc	85	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
54	SF	83	GLN
67	SS	231	GLN
56	SH	99	HIS
63	SO	187	GLN
71	SW	139	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Bb	75/76 (98%)	28 (37%)	0
2	LA	3159/3396 (93%)	749 (23%)	30 (0%)
3	LB	120/121 (99%)	19 (15%)	1 (0%)
4	LC	157/158 (99%)	31 (19%)	1 (0%)
46	mR	0/11	-	-
47	Cc	76/77 (98%)	21 (27%)	0
48	S2	1768/1800 (98%)	689 (38%)	20 (1%)
All	All	5355/5639 (94%)	1537 (28%)	52 (0%)

5 of 1537 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Bb	5	A
1	Bb	8	U
1	Bb	9	A
1	Bb	11	C
1	Bb	15	G

5 of 52 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	LA	3269	U
48	S2	400	A
48	S2	1274	C
2	LA	3350	C
48	S2	139	C

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.

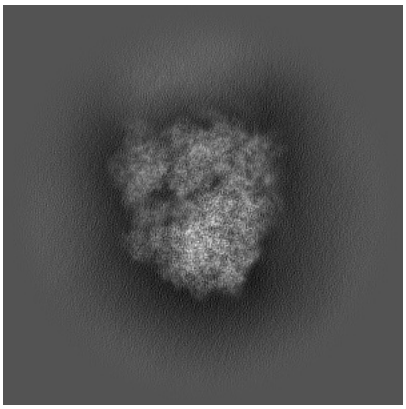
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-68777. These allow visual inspection of the internal detail of the map and identification of artifacts.

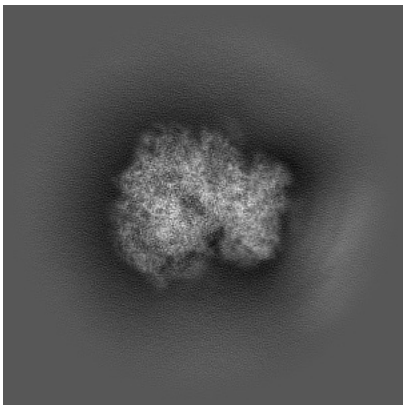
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

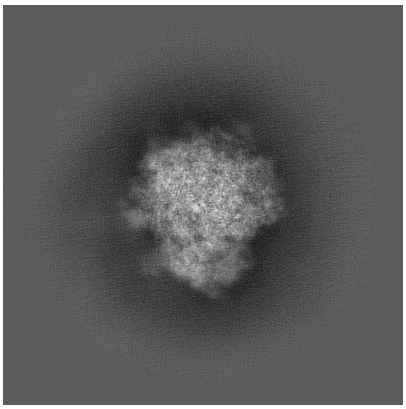
6.1.1 Primary map



X

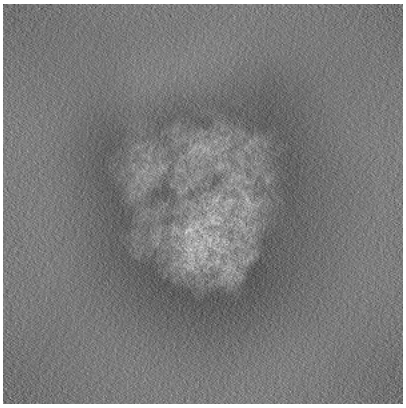


Y

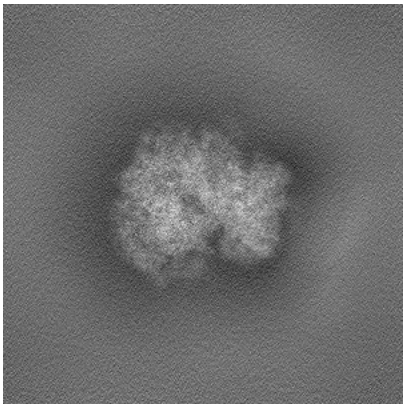


Z

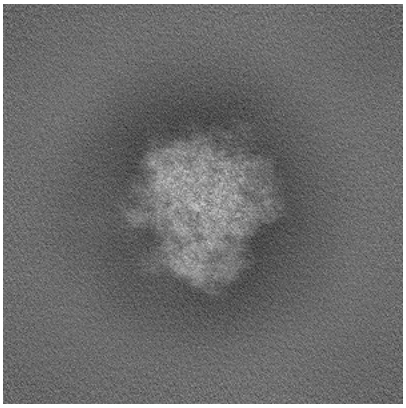
6.1.2 Raw map



X



Y

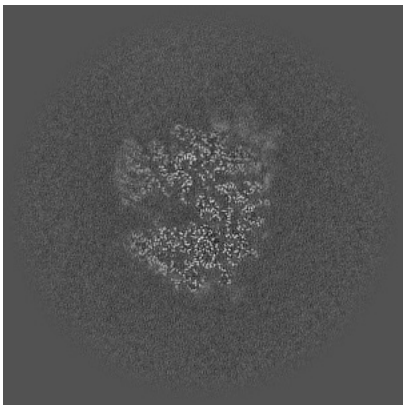


Z

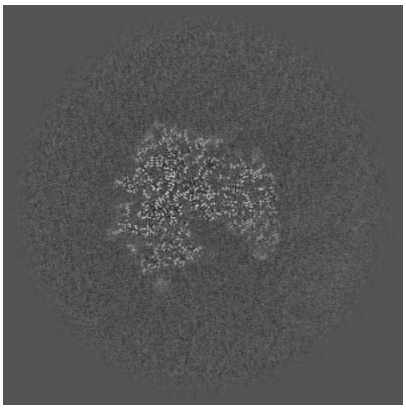
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

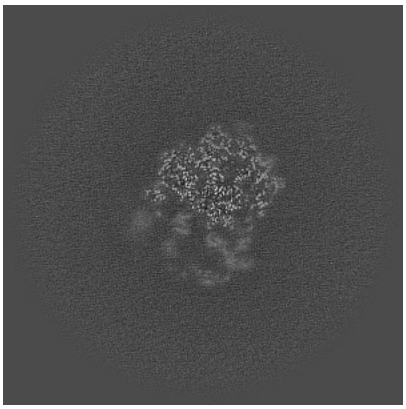
6.2.1 Primary map



X Index: 300

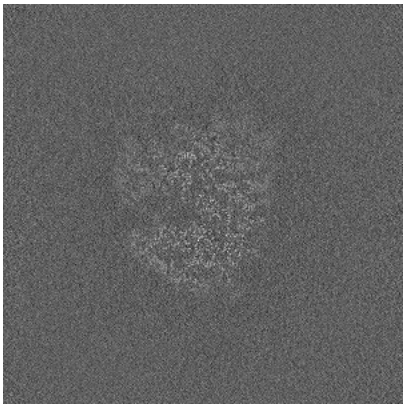


Y Index: 300

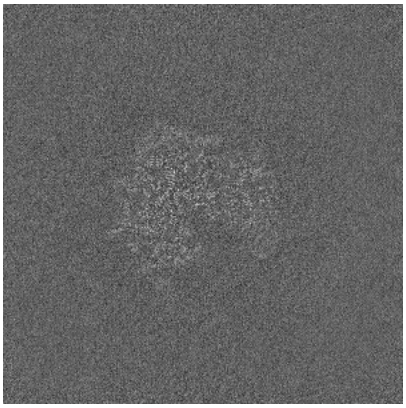


Z Index: 300

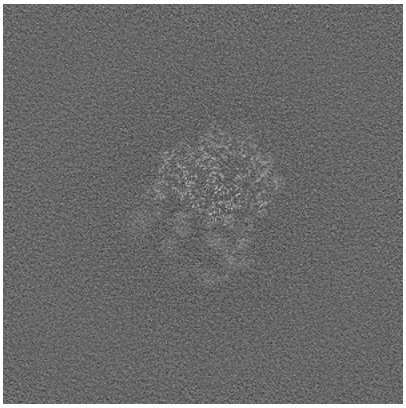
6.2.2 Raw map



X Index: 300



Y Index: 300

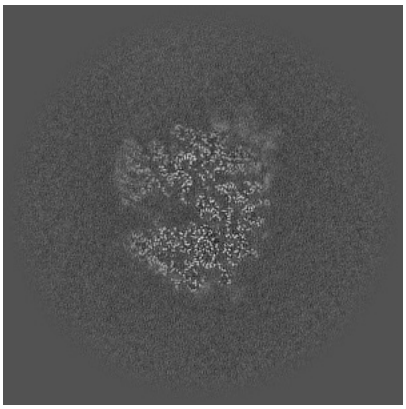


Z Index: 300

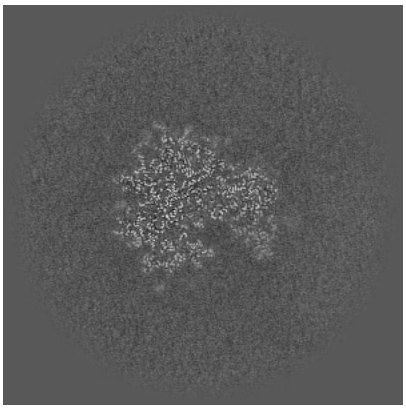
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

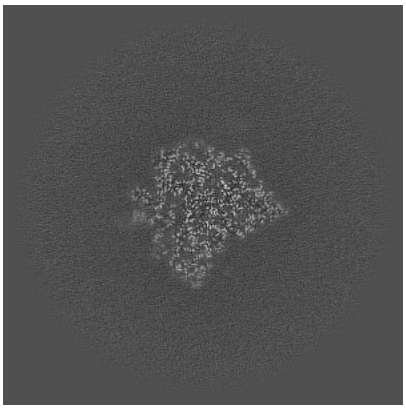
6.3.1 Primary map



X Index: 300

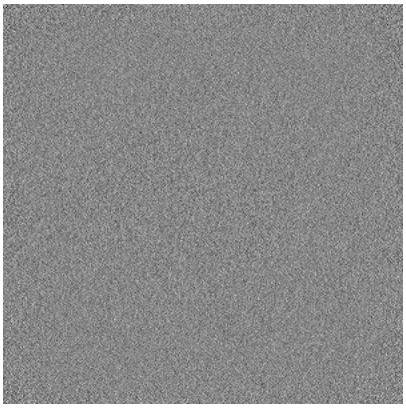


Y Index: 306

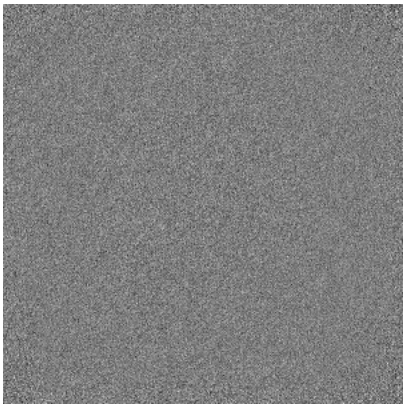


Z Index: 254

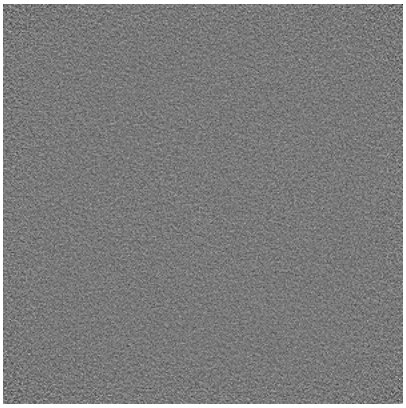
6.3.2 Raw map



X Index: 0



Y Index: 0

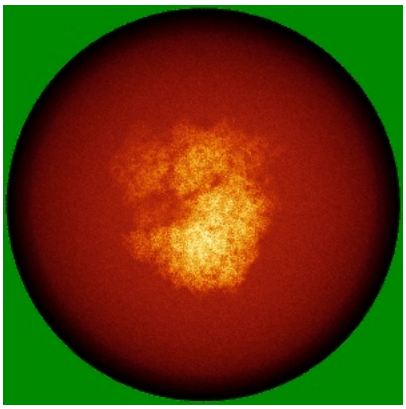


Z Index: 0

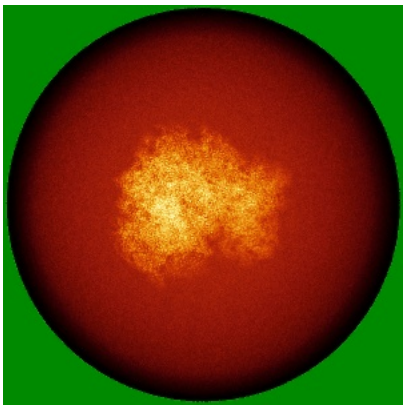
The images above show the largest variance slices of the map in three orthogonal directions.

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

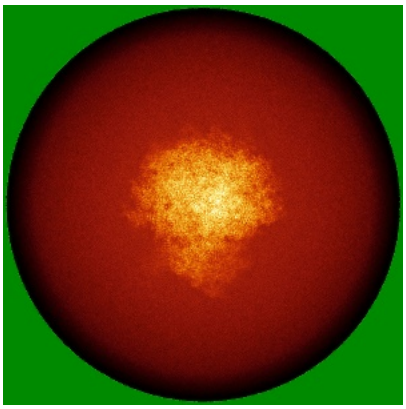
6.4.1 Primary map



X

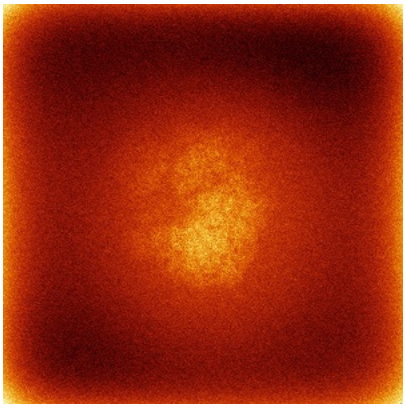


Y

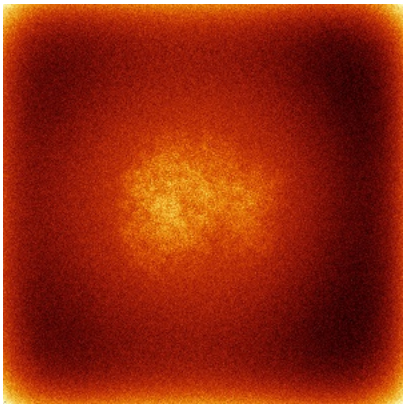


Z

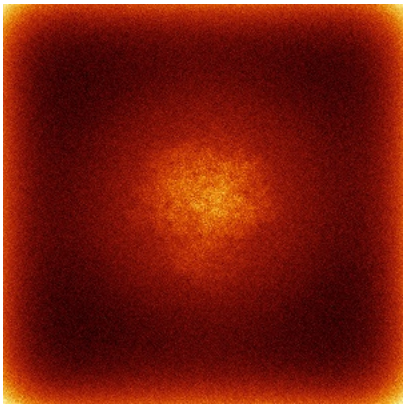
6.4.2 Raw map



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)

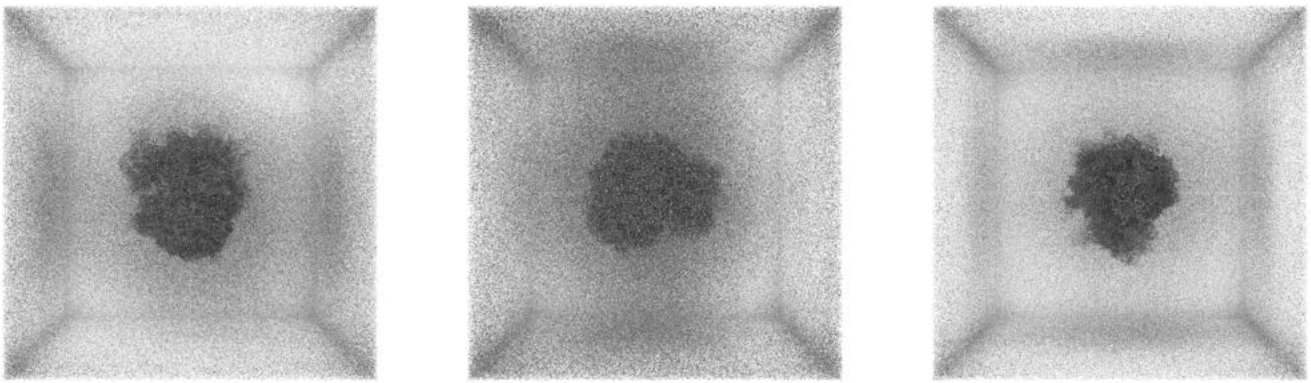
6.5.1 Primary map



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.

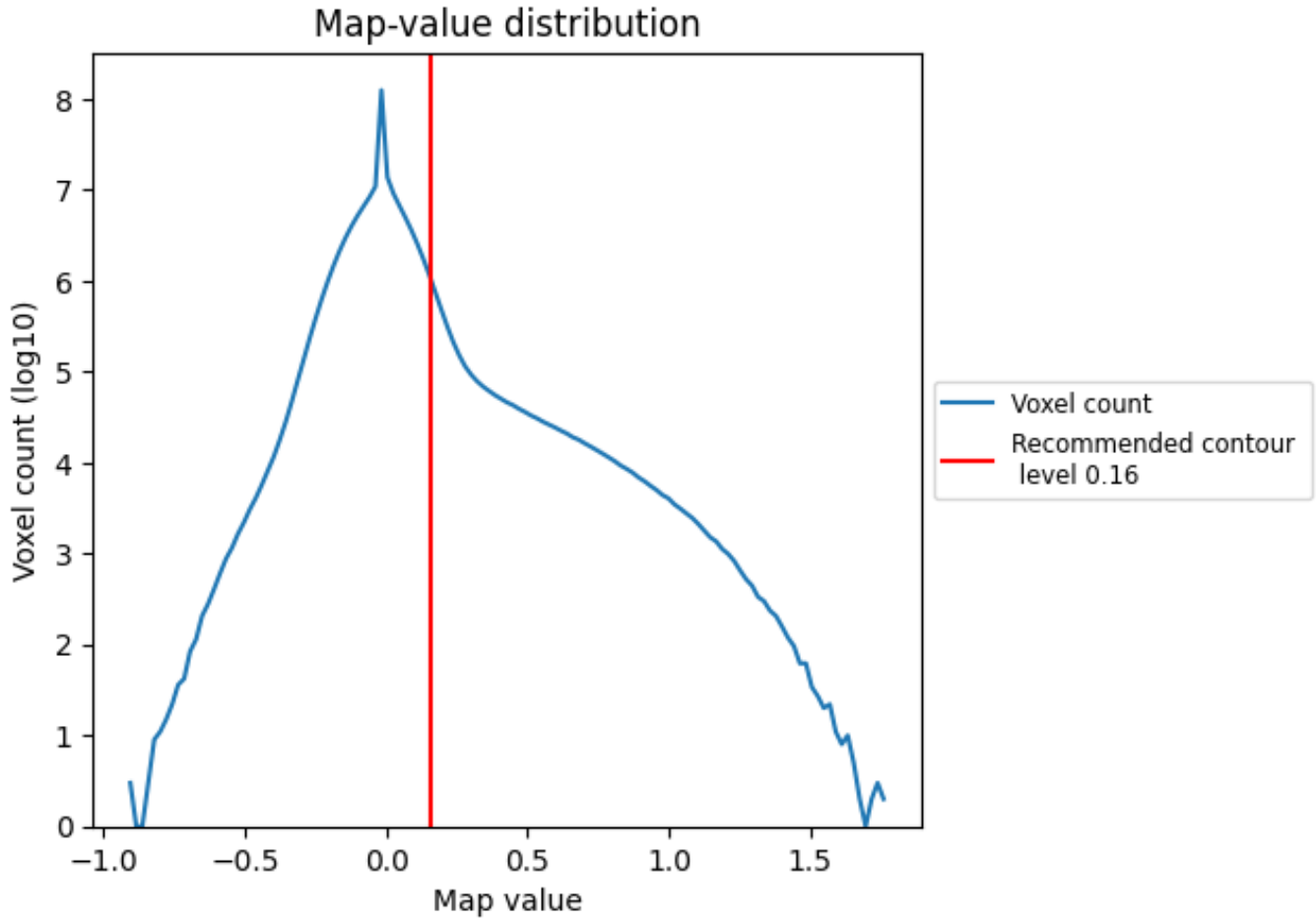
6.6 Mask visualisation (i)

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

7 Map analysis

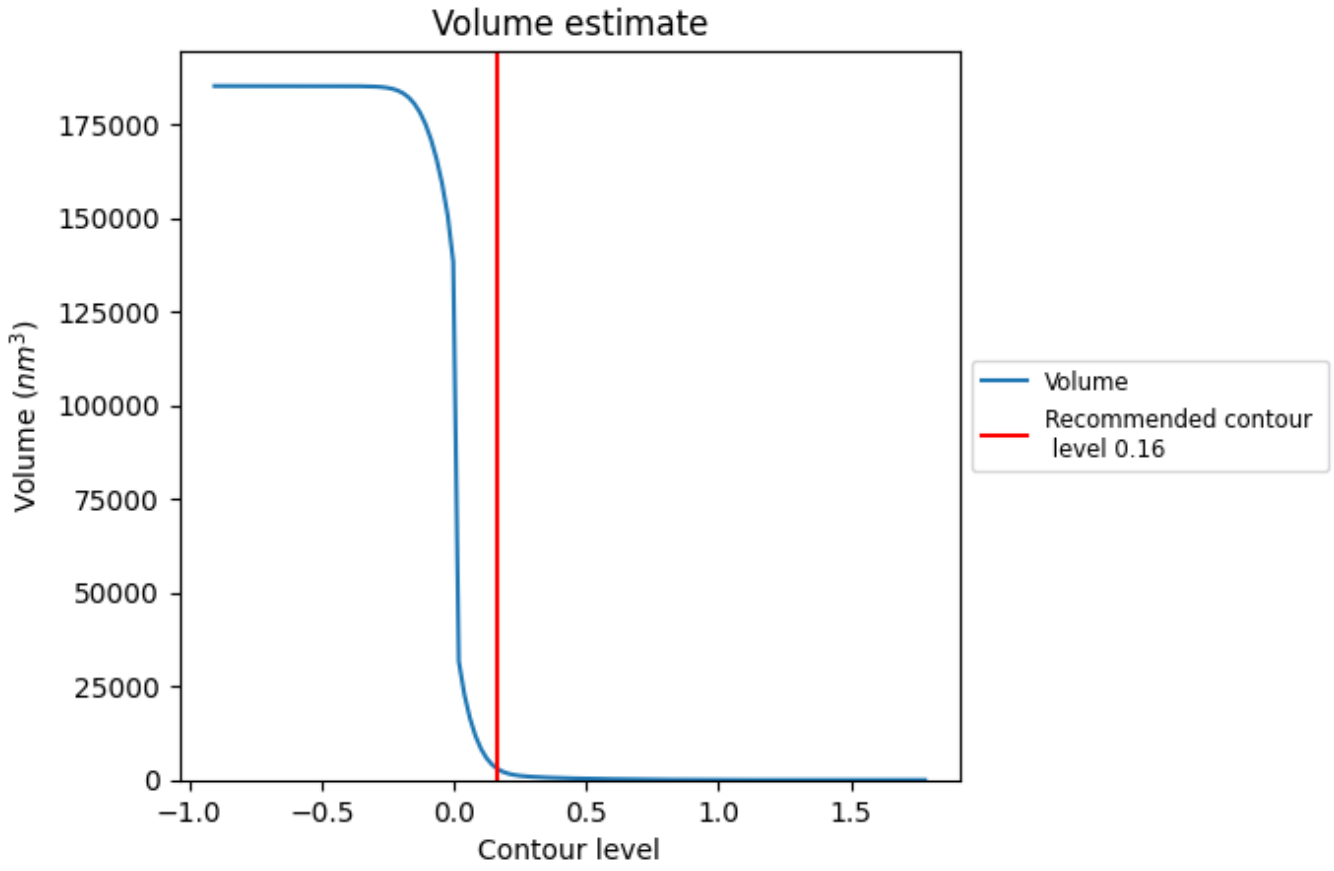
This section contains the results of statistical analysis of the map.

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.

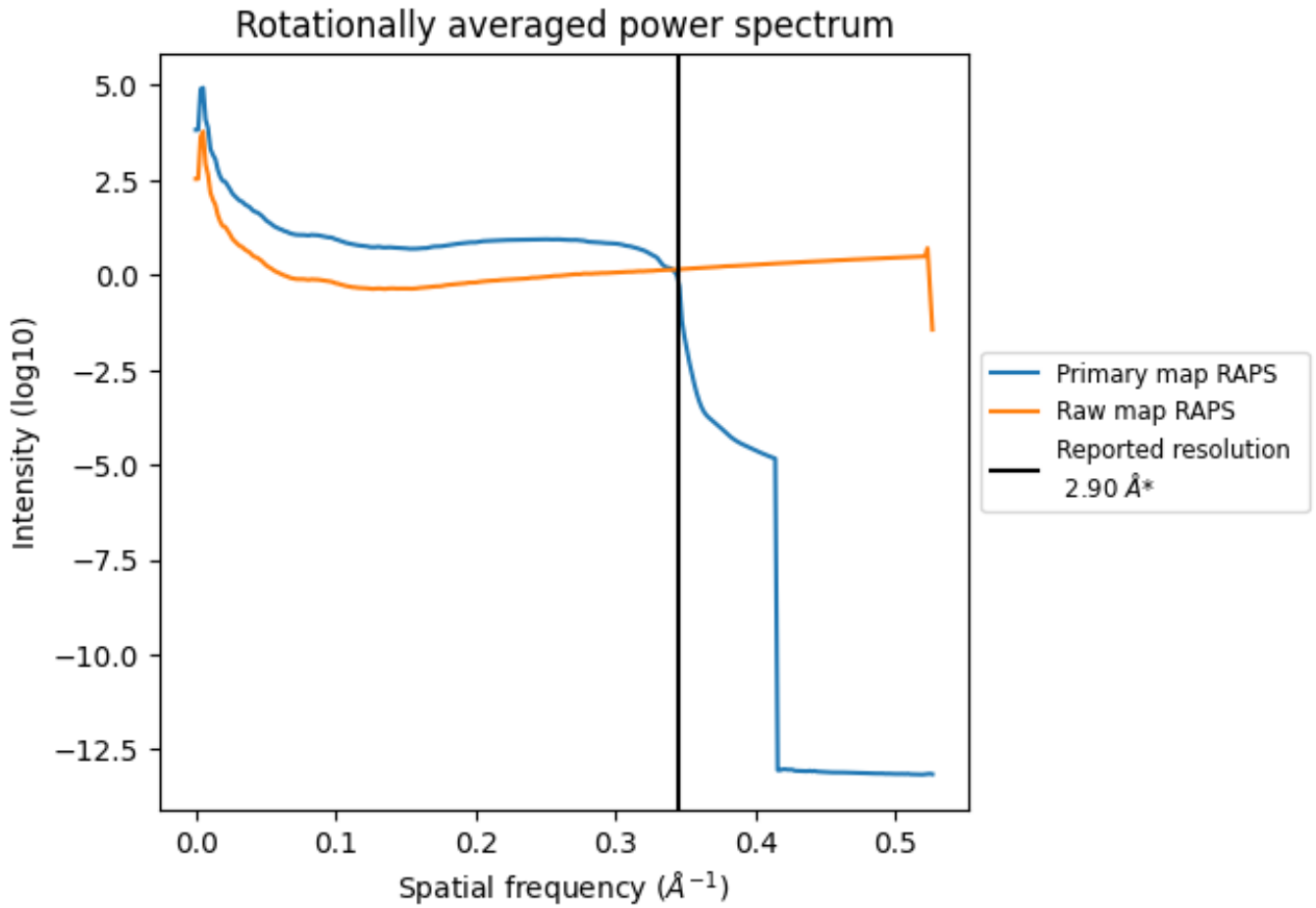
7.2 Volume estimate (i)



The volume at the recommended contour level is 3207 nm^3; this corresponds to an approximate mass of 2897 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)

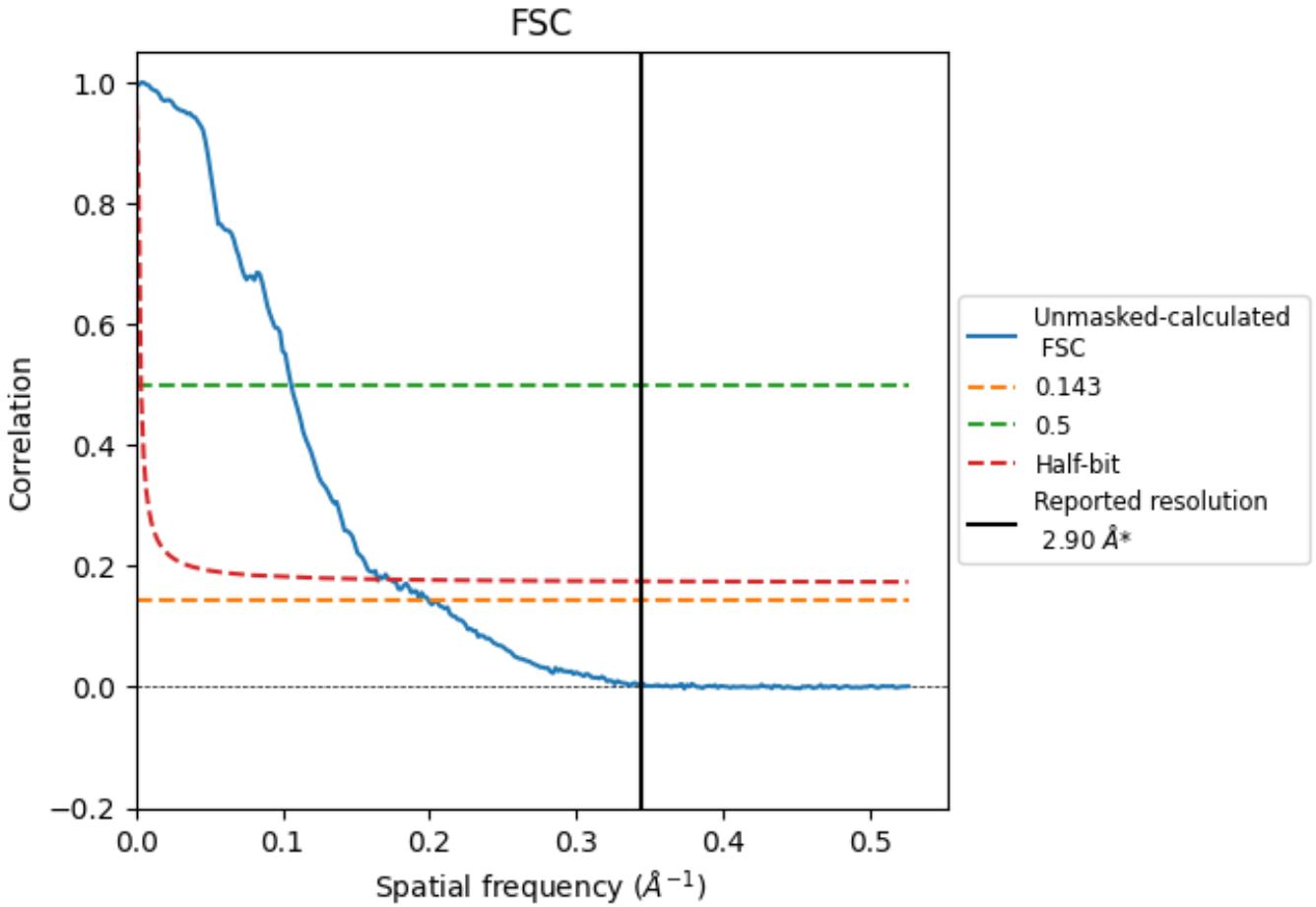


*Reported resolution corresponds to spatial frequency of 0.345 $Å^{-1}$

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 0.345 Å^{-1}

8.2 Resolution estimates (i)

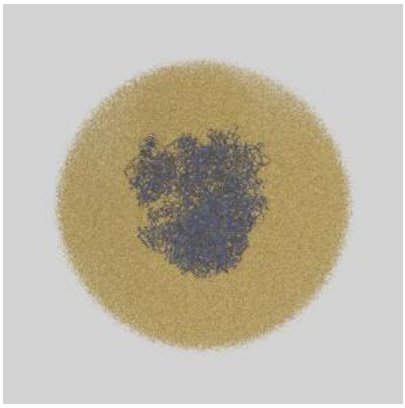
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.02	9.46	6.08

*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 5.02 differs from the reported value 2.9 by more than 10 %

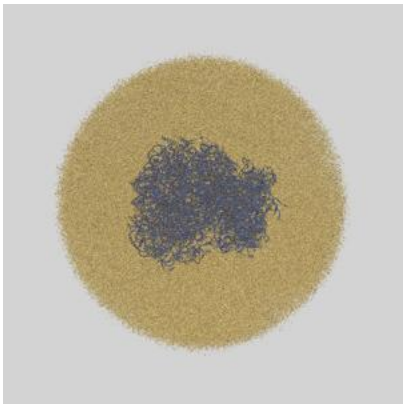
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-68777 and PDB model 22YN. Per-residue inclusion information can be found in section 3 on page 19.

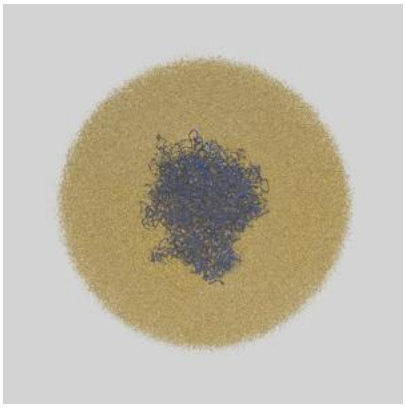
9.1 Map-model overlay



X



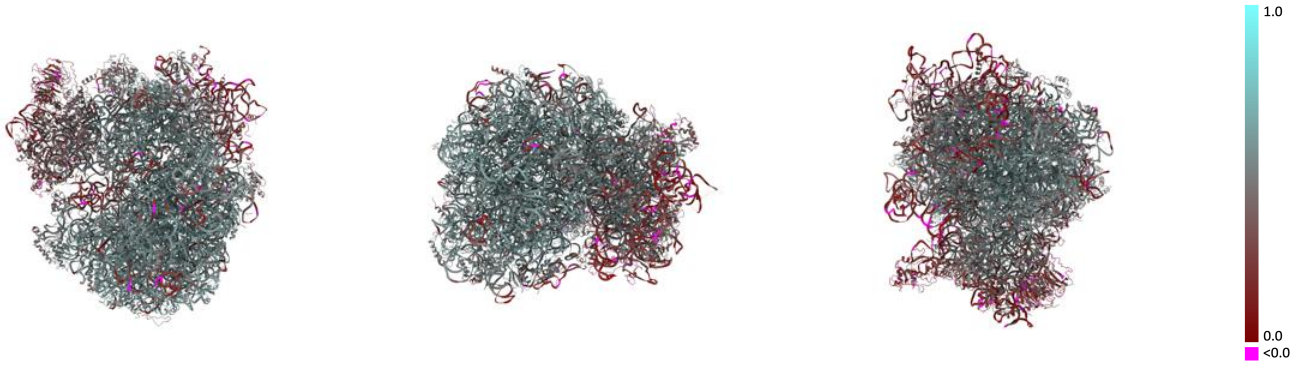
Y



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.

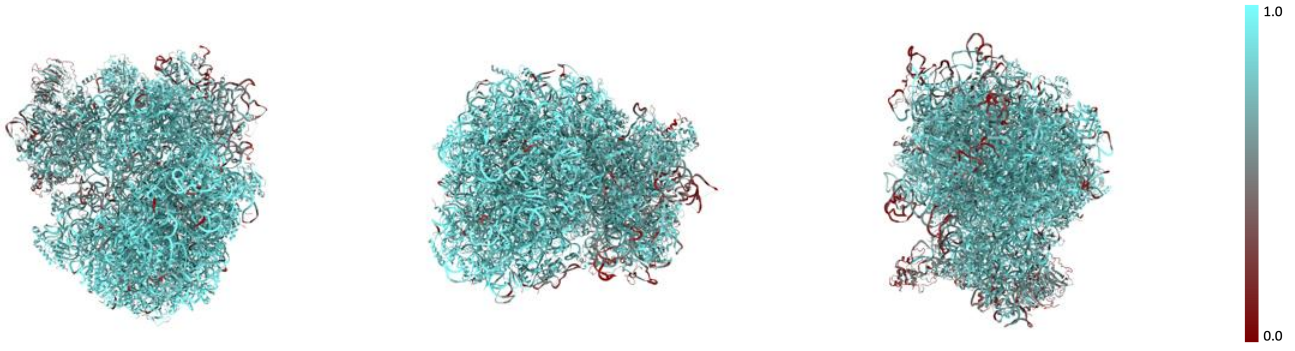
9.2 Q-score mapped to coordinate model (i)



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.

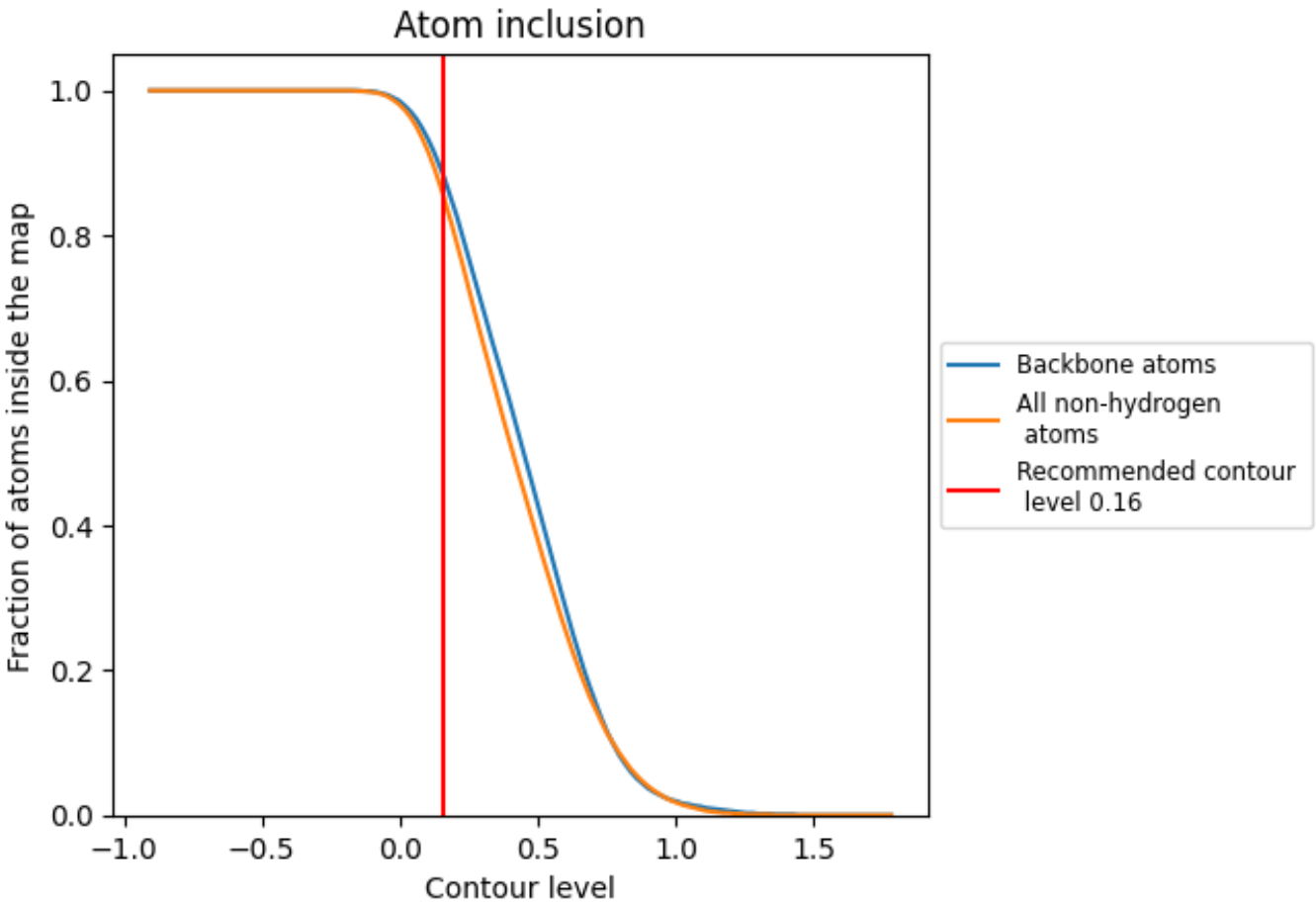
9.3 Atom inclusion mapped to coordinate model (i)



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, 88% of all backbone atoms, 85% 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	0.8530	0.4840
Bb	0.7710	0.3180
Cc	0.8260	0.3610
LA	0.9200	0.5280
LB	0.9450	0.5270
LC	0.9420	0.5470
LD	0.9330	0.5920
LE	0.9260	0.5670
LF	0.9270	0.5640
LG	0.8660	0.5050
LH	0.8580	0.5110
LI	0.9220	0.5670
LJ	0.8870	0.5210
LK	0.8780	0.5380
LL	0.8780	0.5410
LM	0.8140	0.4480
LN	0.9150	0.5590
LO	0.8990	0.5350
LP	0.9330	0.5890
LQ	0.9190	0.5650
LR	0.9110	0.5660
LS	0.9280	0.5790
LT	0.8380	0.5170
LU	0.9130	0.5660
LV	0.9090	0.5620
LW	0.8290	0.4540
LX	0.9100	0.5800
LY	0.9160	0.5640
LZ	0.9050	0.5600
La	0.9270	0.5730
Lb	0.9000	0.5410
Lc	0.9370	0.5860
Ld	0.9030	0.5360
Le	0.8770	0.5280
Lf	0.8880	0.5460



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Chain	Atom inclusion	Q-score
Lg	0.8970	0.5620
Lh	0.9340	0.5920
Li	0.8880	0.5570
Lj	0.9120	0.5450
Lk	0.8770	0.5220
Ll	0.9550	0.5950
Lm	0.7810	0.4740
Ln	0.8940	0.5700
Lo	0.9170	0.5620
Lp	0.8560	0.5520
Lq	0.9140	0.5660
Lr	0.8860	0.5760
S2	0.7880	0.3960
SA	0.6920	0.3950
SB	0.6440	0.3530
SC	0.6250	0.3070
SD	0.2950	0.1950
SE	0.6890	0.3430
SF	0.7040	0.3820
SG	0.7420	0.4120
SH	0.6690	0.3570
SI	0.7070	0.3560
SJ	0.5920	0.3050
SK	0.4650	0.2590
SL	0.6720	0.3820
SM	0.8040	0.4310
SN	0.3480	0.1950
SO	0.5350	0.2600
SP	0.8320	0.4790
SQ	0.8180	0.4920
SR	0.8610	0.5280
SS	0.7870	0.4380
ST	0.6360	0.3300
SU	0.7550	0.4400
SV	0.7810	0.4170
SW	0.7240	0.3970
SX	0.8250	0.4930
SY	0.8730	0.5230
SZ	0.8690	0.5200
Sa	0.8300	0.4970
Sb	0.9110	0.5700
Sc	0.8060	0.4950

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Chain	Atom inclusion	Q-score
Sd	0.7380	0.3720
Se	0.9010	0.5510
Sf	0.8450	0.4790
Sg	0.7080	0.3980
mR	0.9170	0.4990