wwPDB EM Validation Summary Report

Oct 27, 2026 – 09:44 PM JST

PDB ID	:	22YP / pdb_000022yp
EMDB ID	:	EMD-68778
Title	:	Rotated 80S with A/A-P/E tRNA
Authors	:	Wu, M.; Yuan, S.
Deposited on	:	2026-01-28
Resolution	:	2.93 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:

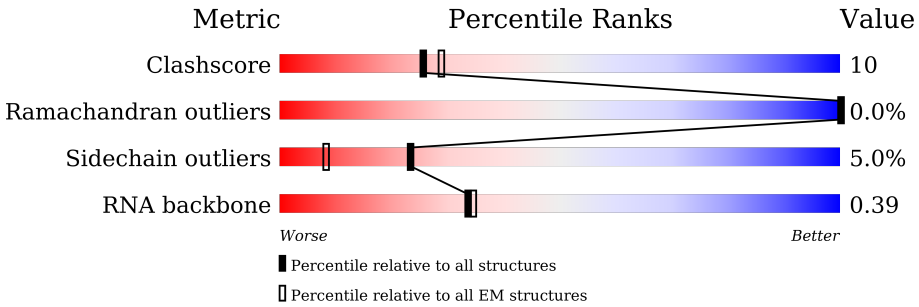
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

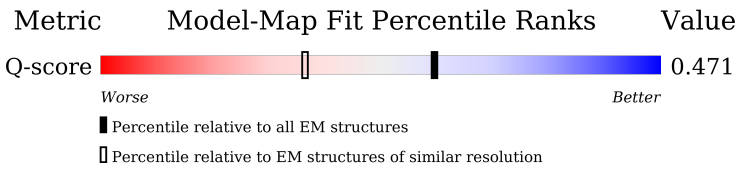
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.93 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.





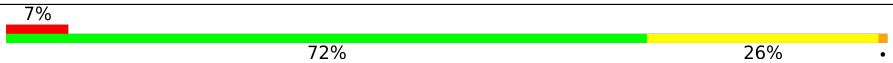
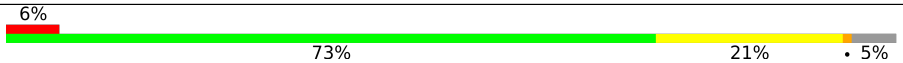
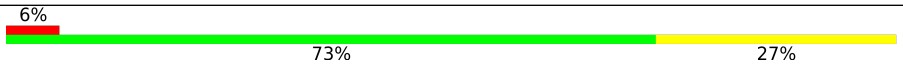
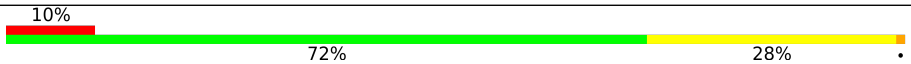
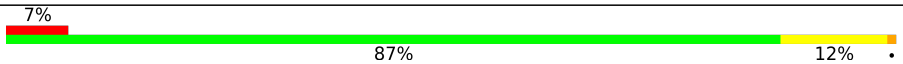
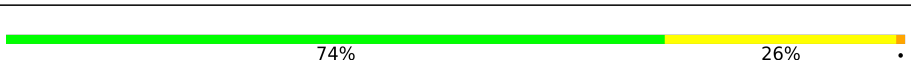
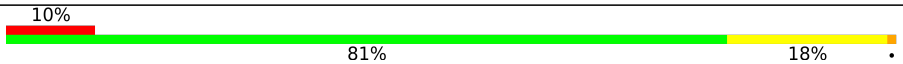
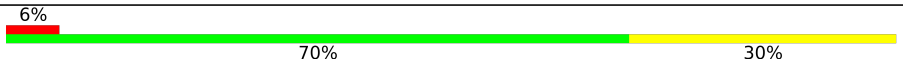
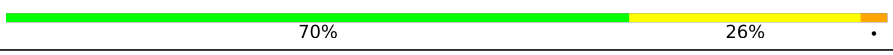
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13037 (2.43 - 3.43)

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

Mol	Chain	Length	Quality of chain
1	LA	3396	5% 48% 38% 6% 7%
2	LB	121	55% 37% 8%
3	LC	158	49% 42% 8%

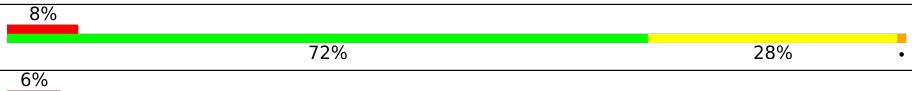
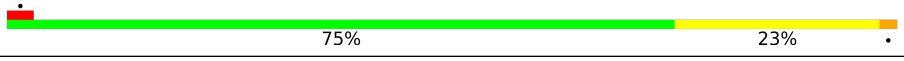
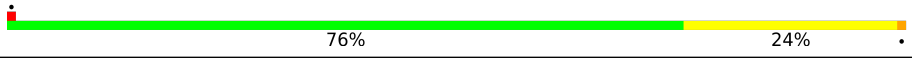
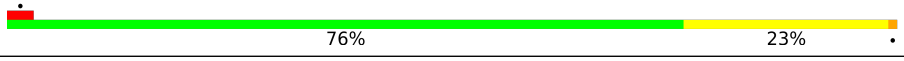
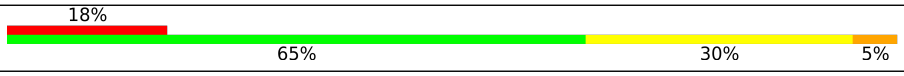
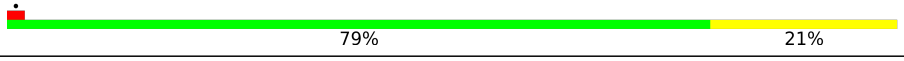
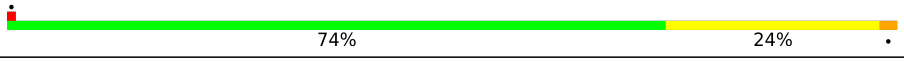
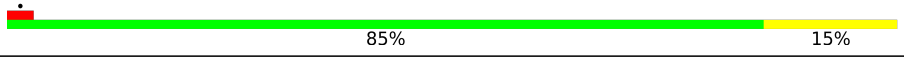
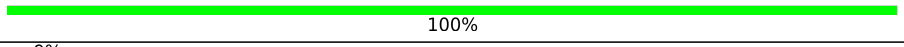
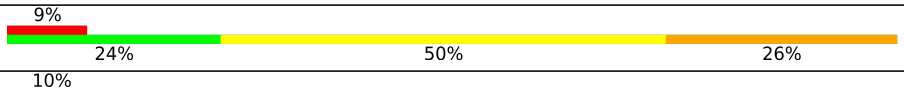
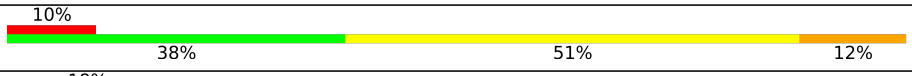
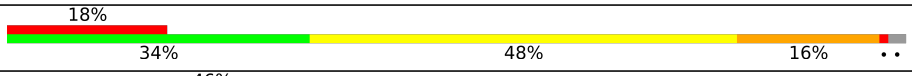
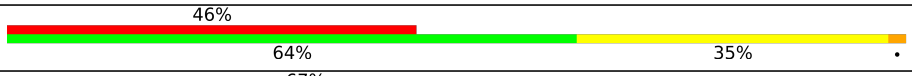
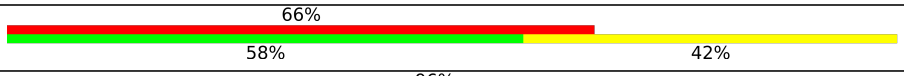
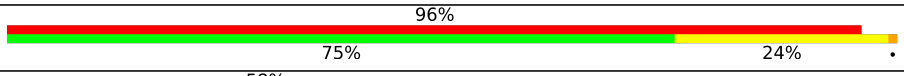
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Mol	Chain	Length	Quality of chain
4	LD	251	
5	LE	386	
6	LF	361	
7	LG	294	
8	LH	175	
9	LI	222	
10	LJ	233	
11	LK	191	
12	LL	218	
13	LM	169	
14	LN	193	
15	LO	136	
16	LP	203	
17	LQ	197	
18	LR	183	
19	LS	185	
20	LT	188	
21	LU	171	
22	LV	159	
23	LW	100	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

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Mol	Chain	Length	Quality of chain
29	Lc	148	
30	Ld	58	
31	Le	96	
32	Lf	109	
33	Lg	127	
34	Lh	106	
35	Li	112	
36	Lj	119	
37	Lk	99	
38	Ll	81	
39	Lm	77	
40	Ln	50	
41	Lo	52	
42	Lp	25	
43	Lq	103	
44	Lr	91	
45	mR	11	
46	Bb	76	
47	Cc	77	
48	S2	1800	
49	SA	222	
50	SB	206	
51	SC	92	
52	SD	121	
53	SE	117	

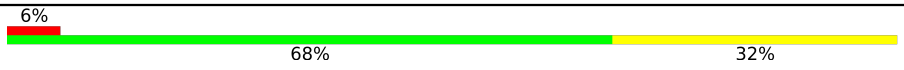
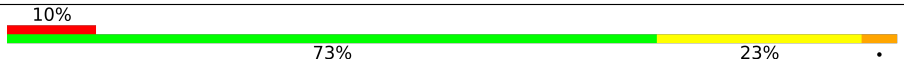
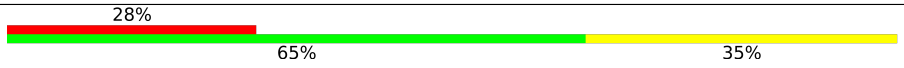
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Mol	Chain	Length	Quality of chain
54	SF	141	64% 56% 43%
55	SG	125	34% 74% 21%
56	SH	145	57% 60% 38%
57	SI	143	55% 67% 33%
58	SJ	100	54% 57% 39%
59	SK	82	79% 68% 29%
60	SL	63	65% 63% 35%
61	SM	53	30% 51% 45%
62	SN	73	90% 81% 19%
63	SO	312	76% 66% 32%
64	SP	206	14% 63% 36%
65	SQ	232	13% 63% 31%
66	SR	216	63% 35%
67	SS	258	16% 59% 39%
68	ST	228	40% 59% 38%
69	SU	184	17% 54% 44%
70	SV	198	22% 56% 37% 6%
71	SW	184	25% 61% 38%
72	SX	142	17% 68% 30%
73	SY	150	5% 66% 31%
74	SZ	127	6% 62% 36%
75	Sa	87	63% 34%
76	Sb	129	65% 33%
77	Sc	144	10% 73% 25%
78	Sd	134	34% 63% 37%

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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 (3393-MER).

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 45 is a RNA chain called RNA (5'-R(P*UP*GP*AP*CP*GP*CP*UP*UP*UP*UP*C)-3').

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

- Molecule 46 is a RNA chain called RNA (76-MER).

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

- Molecule 47 is a RNA chain called RNA (77-MER).

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 (1800-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.

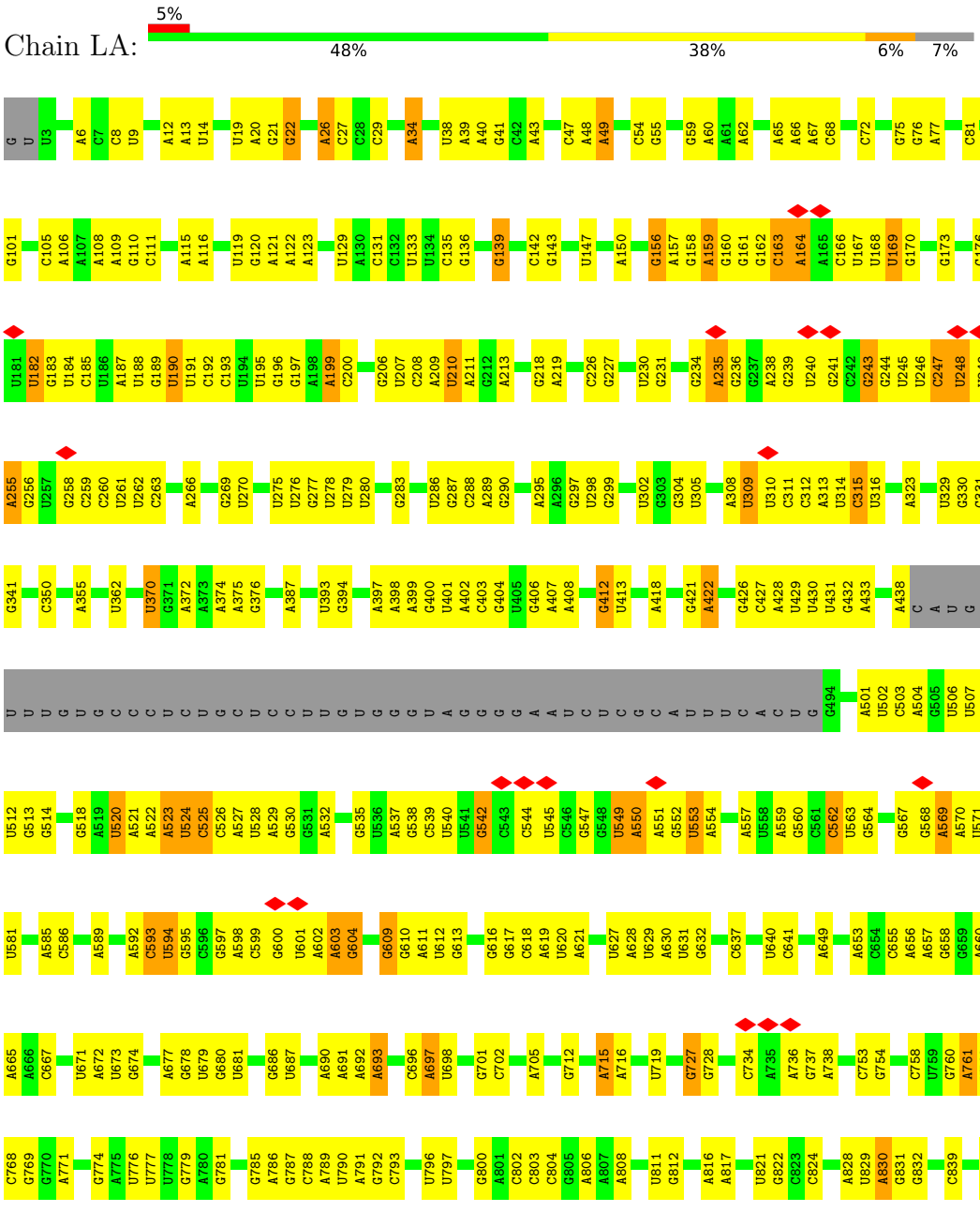
Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sg	57	Total	C	N	O	S	0	0
			451	284	93	73	1		

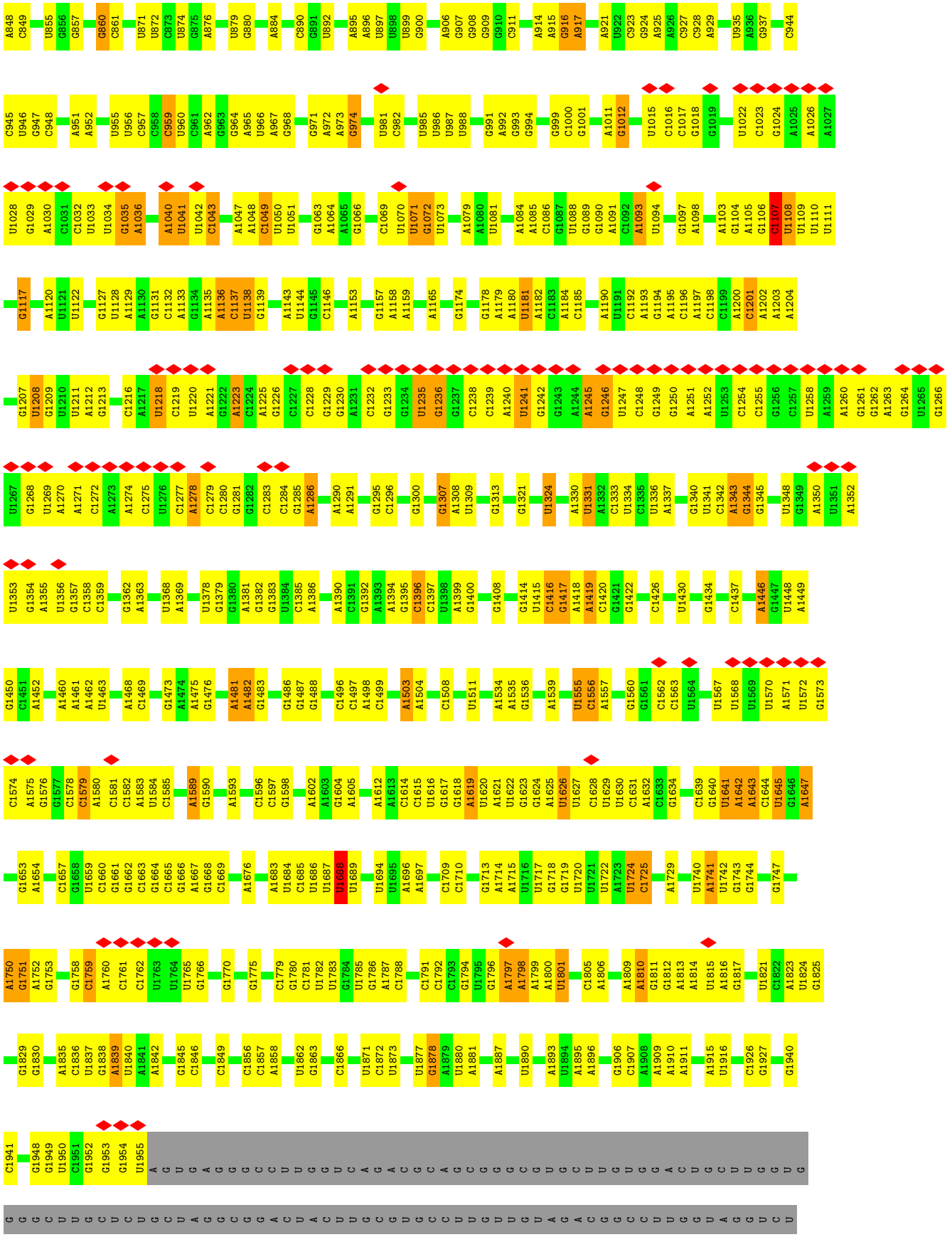
3 Residue-property plots (i)

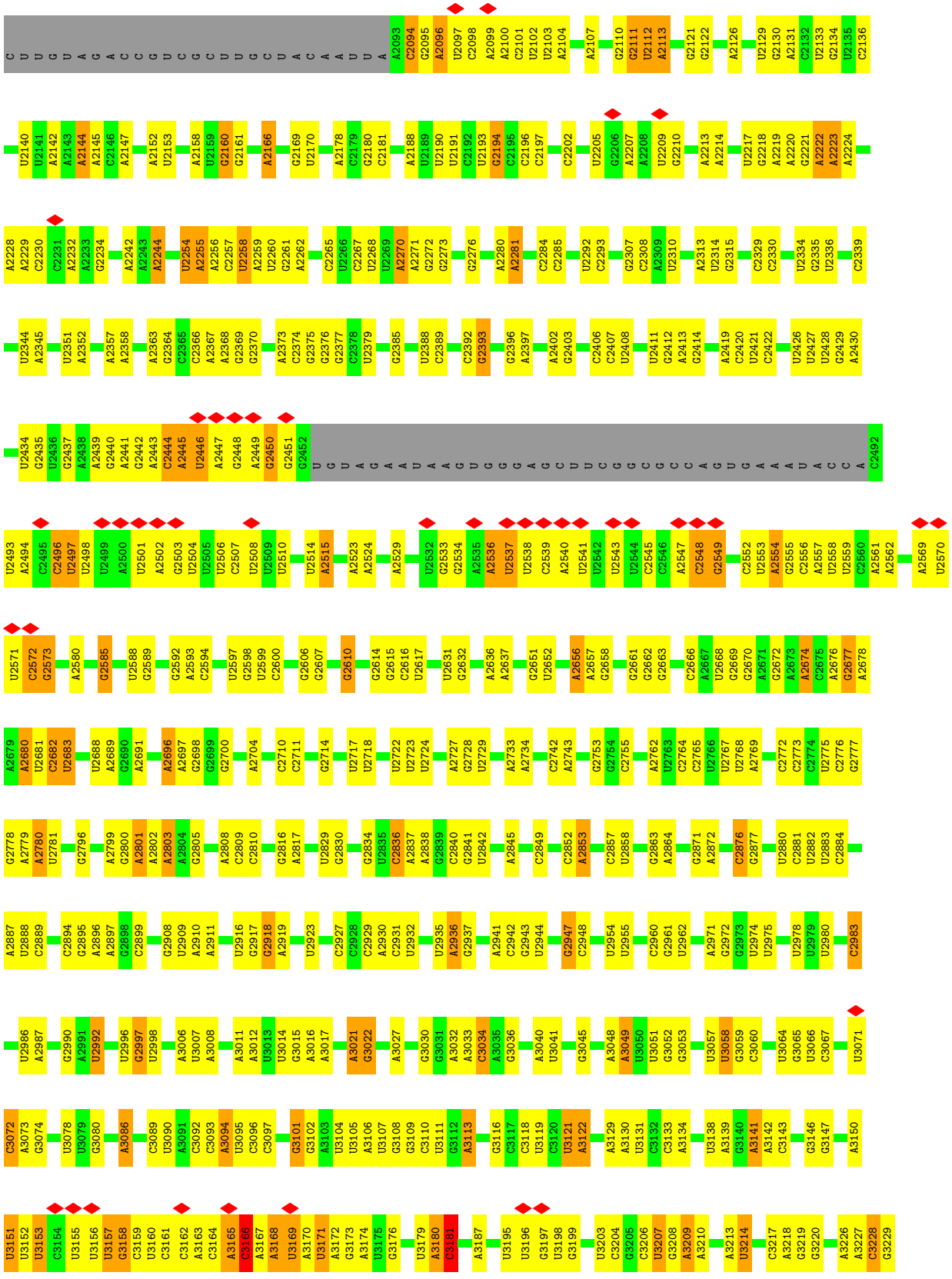
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

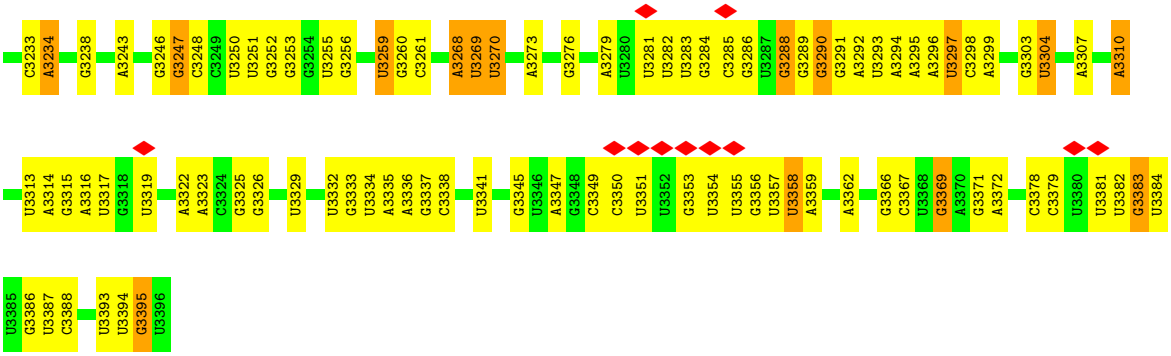
- Molecule 1: RNA (3393-MER)

Chain LA:





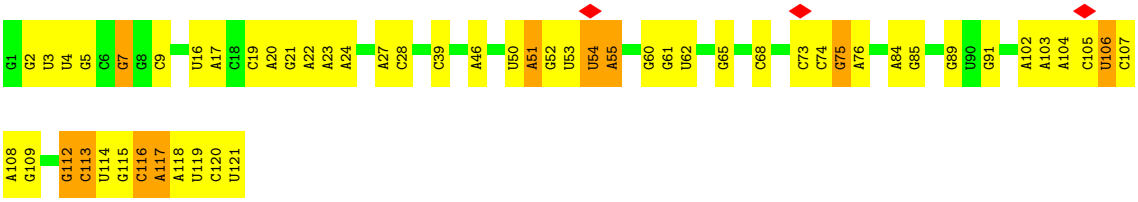




• Molecule 2: RNA (121-MER)

Chain LB:

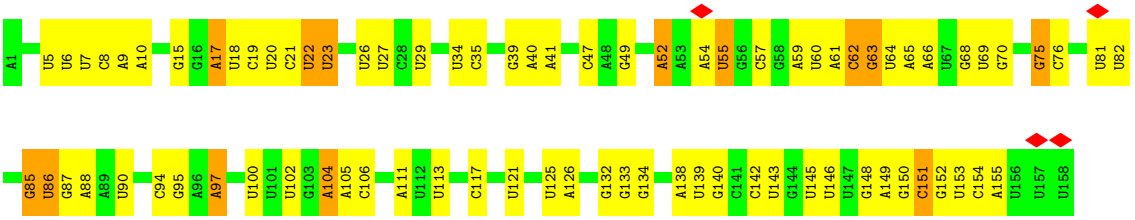




• Molecule 3: RNA (158-MER)

Chain LC:

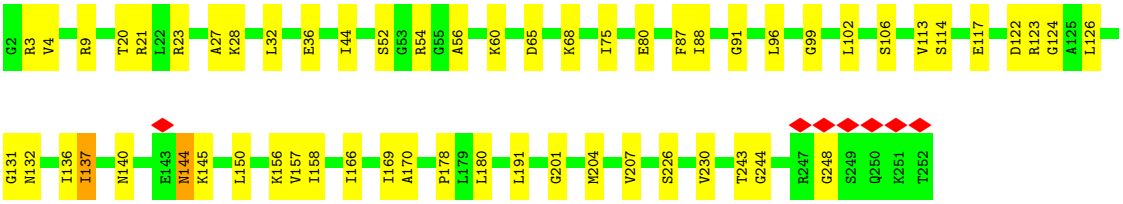




• Molecule 4: Large ribosomal subunit protein uL2A

Chain LD:

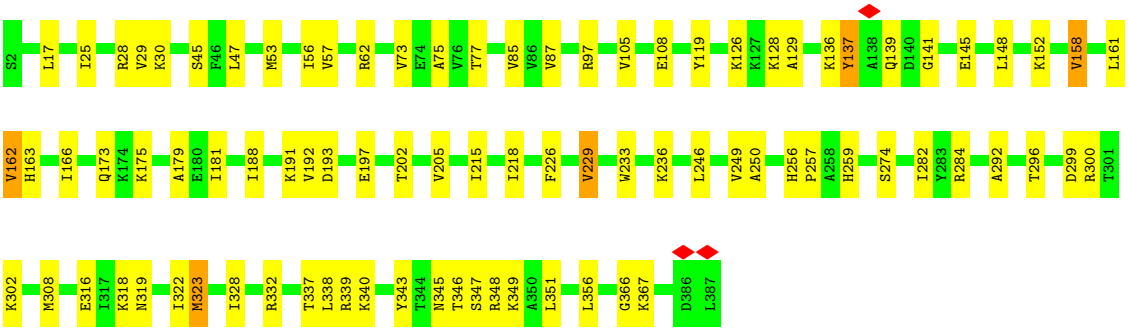




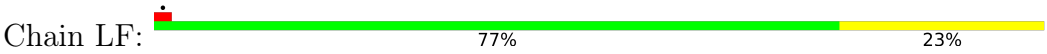
• Molecule 5: Large ribosomal subunit protein uL3

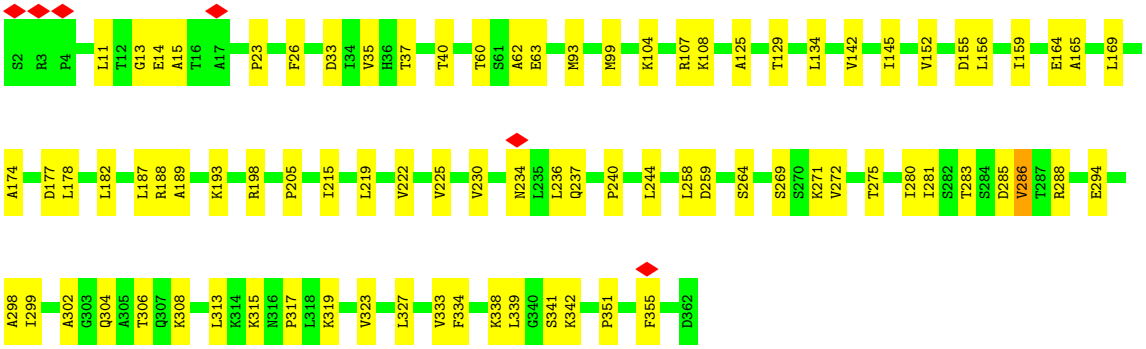
Chain LE:



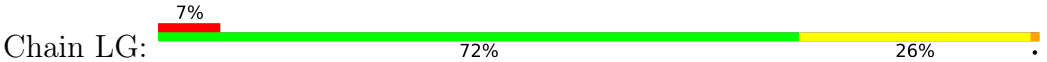


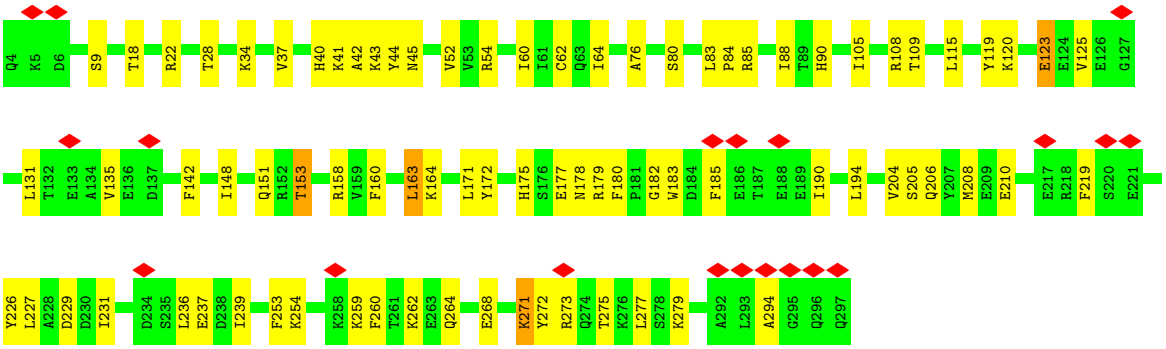
• Molecule 6: Large ribosomal subunit protein uL4A



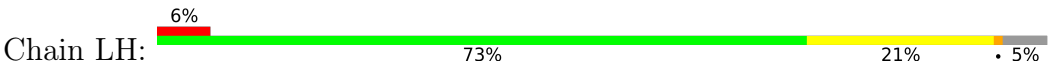


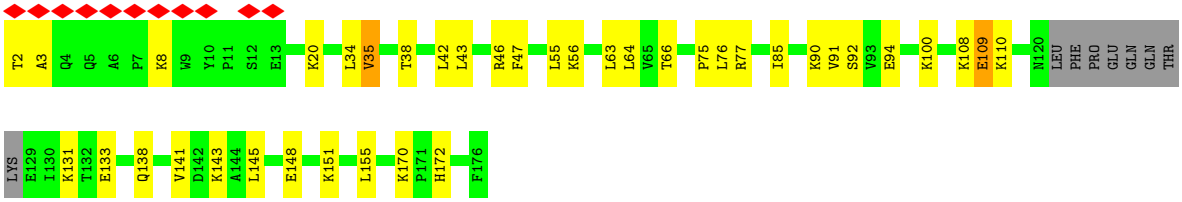
• Molecule 7: Large ribosomal subunit protein uL18





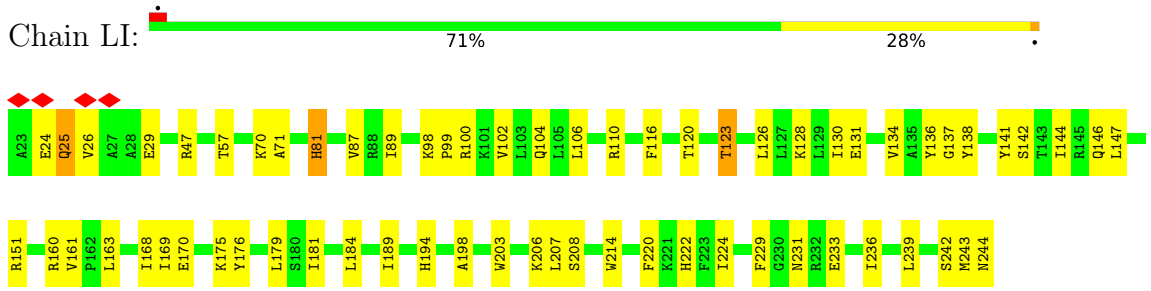
• Molecule 8: Large ribosomal subunit protein eL6B





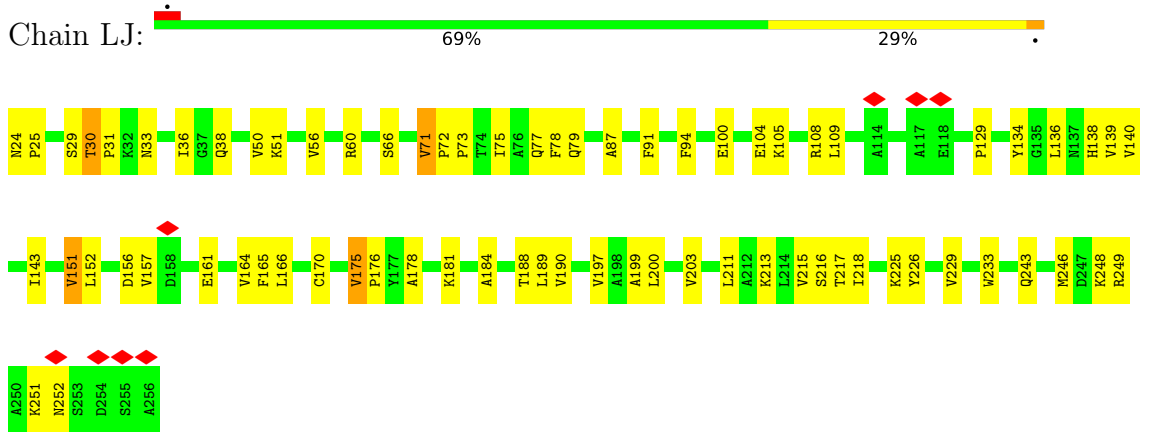
• Molecule 9: Large ribosomal subunit protein uL30A

Chain LI:



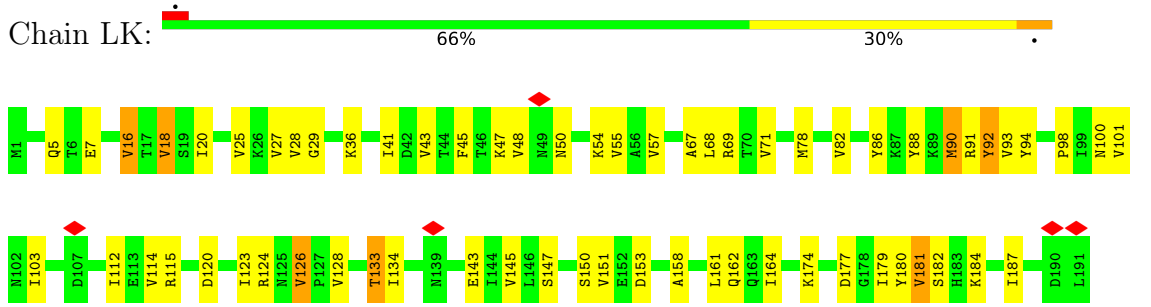
• Molecule 10: Large ribosomal subunit protein eL8A

Chain LJ:



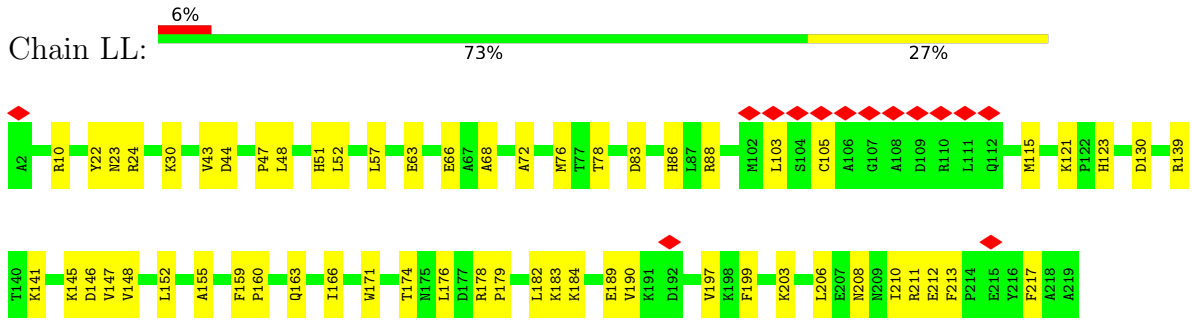
• Molecule 11: Large ribosomal subunit protein uL6A

Chain LK:



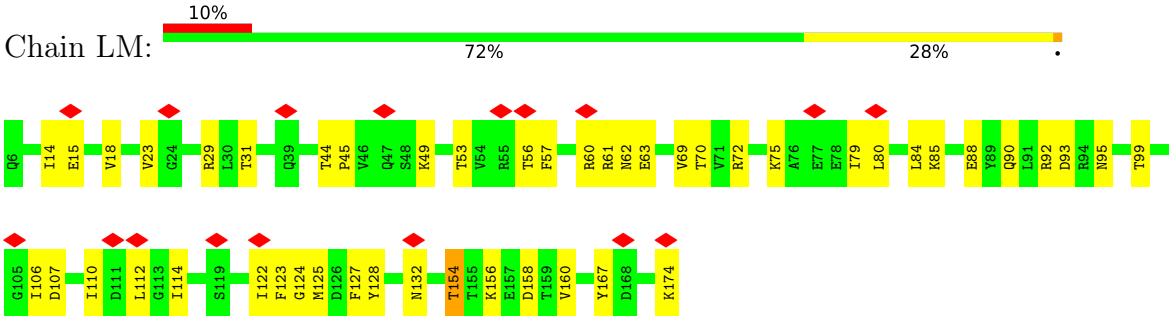
• Molecule 12: Large ribosomal subunit protein uL16

Chain LL:



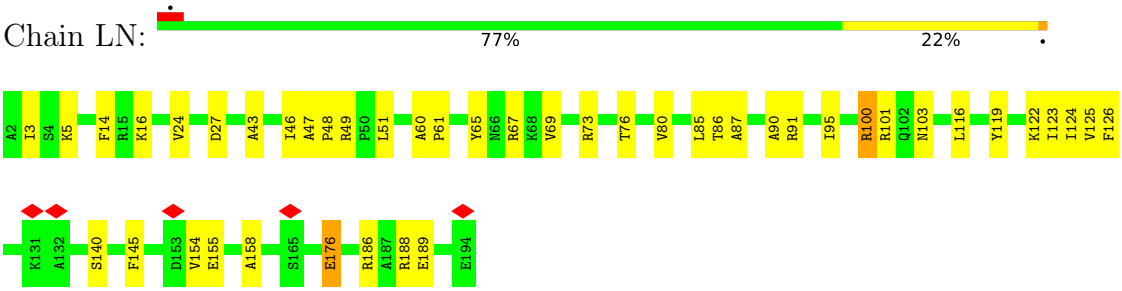
• Molecule 13: Large ribosomal subunit protein uL5B

Chain LM:



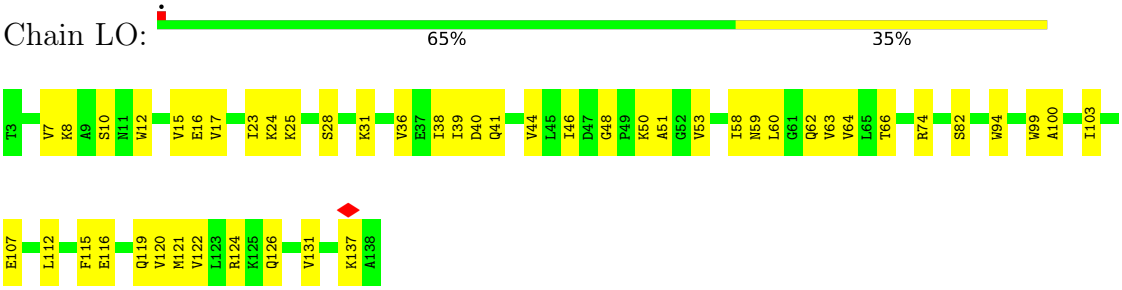
• Molecule 14: Large ribosomal subunit protein eL13A

Chain LN:



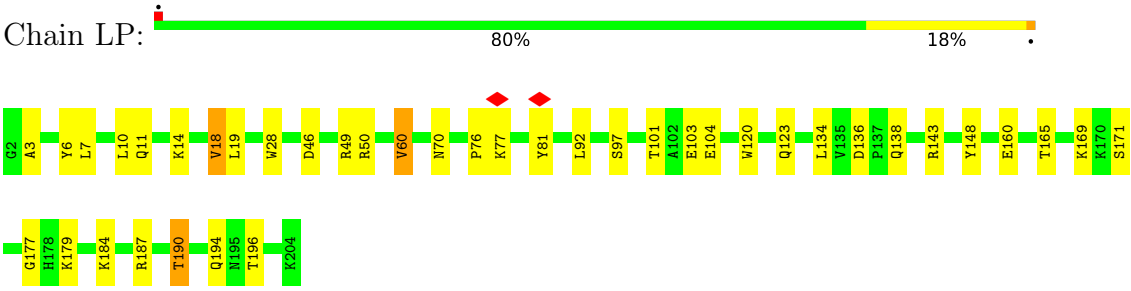
• Molecule 15: Large ribosomal subunit protein eL14A

Chain LO:



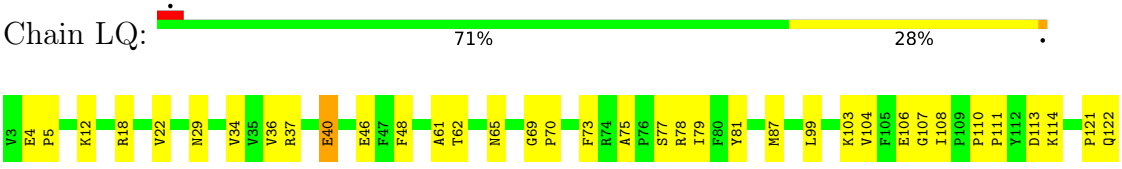
• Molecule 16: Large ribosomal subunit protein eL15A

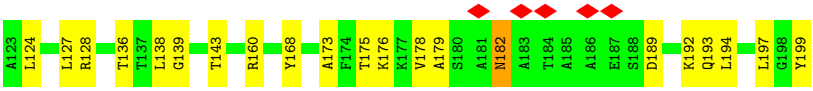
Chain LP:



• Molecule 17: Large ribosomal subunit protein uL13A

Chain LQ:





• Molecule 18: Large ribosomal subunit protein uL22A

Chain LR:

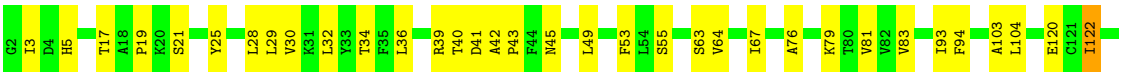




• Molecule 19: Large ribosomal subunit protein eL18A

Chain LS:



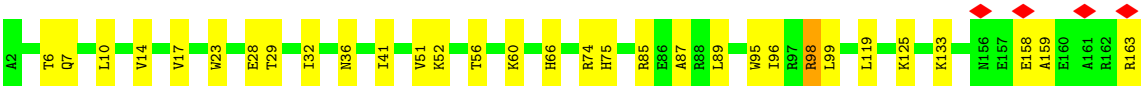


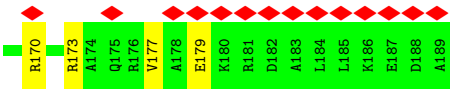


• Molecule 20: Large ribosomal subunit protein eL19A

Chain LT:



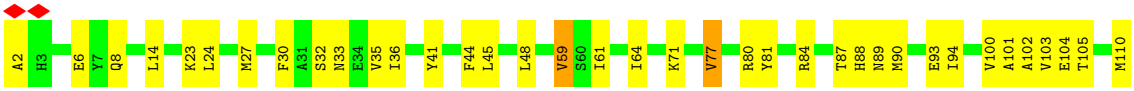




• Molecule 21: Large ribosomal subunit protein eL20A

Chain LU:



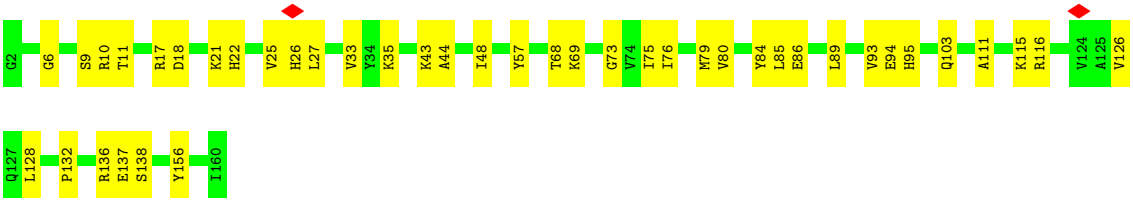




• Molecule 22: Large ribosomal subunit protein eL21A

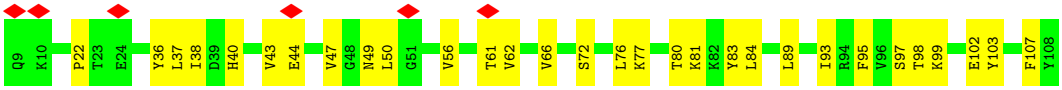
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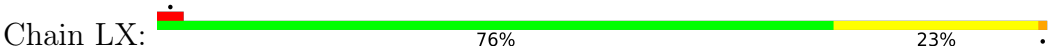


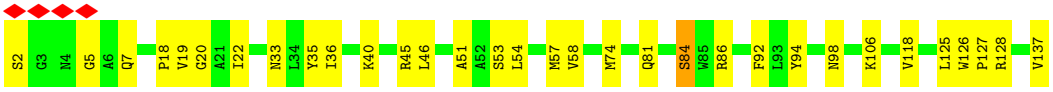
• Molecule 23: Large ribosomal subunit protein eL22A



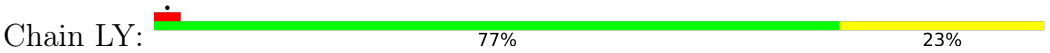


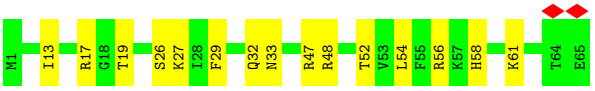
• Molecule 24: Large ribosomal subunit protein uL14A





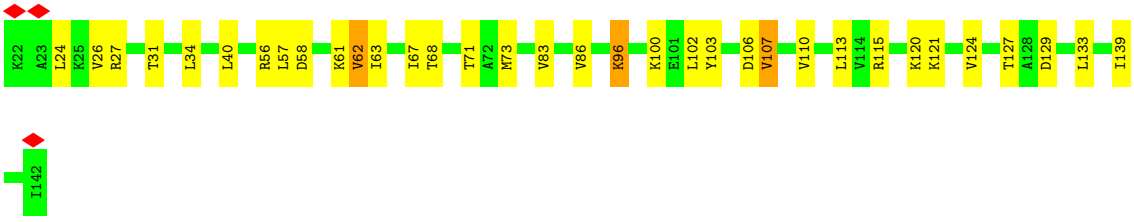
• Molecule 25: Large ribosomal subunit protein eL24A





• Molecule 26: Large ribosomal subunit protein uL23





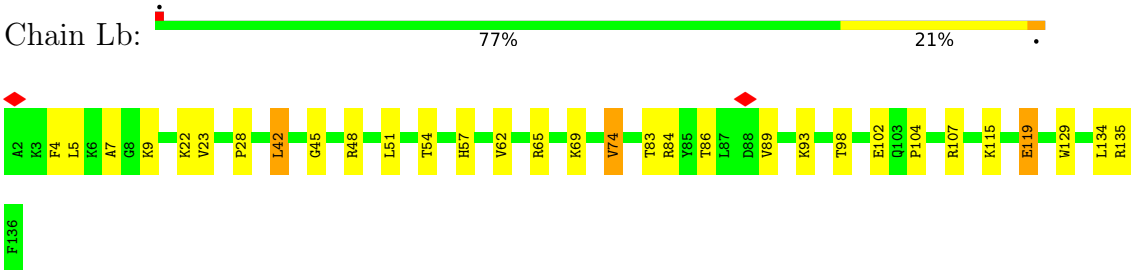
• Molecule 27: Large ribosomal subunit protein uL24A





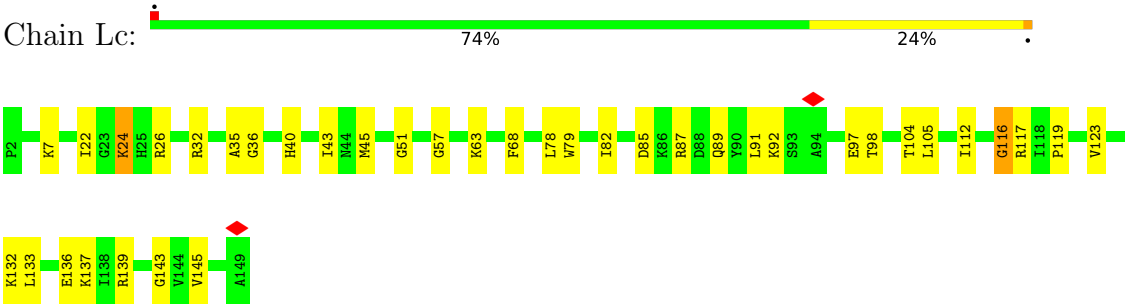
• Molecule 28: Large ribosomal subunit protein eL27A

Chain Lb:



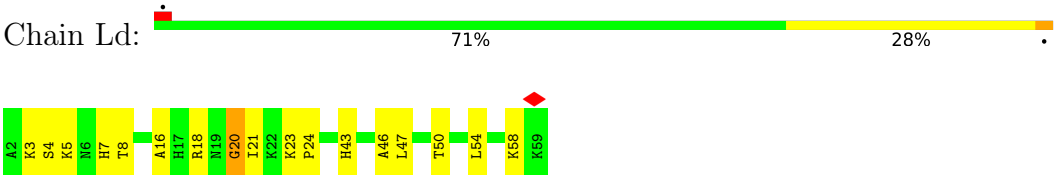
• Molecule 29: Large ribosomal subunit protein uL15

Chain Lc:



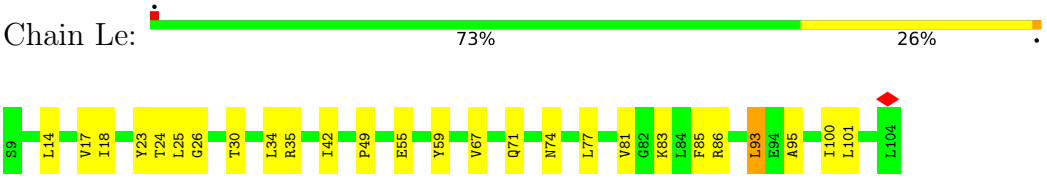
• Molecule 30: Large ribosomal subunit protein eL29

Chain Ld:



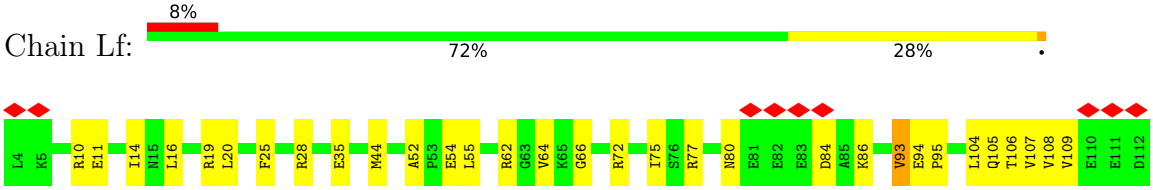
• Molecule 31: Large ribosomal subunit protein eL30

Chain Le:



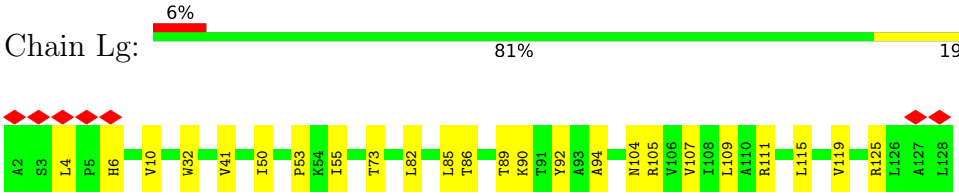
• Molecule 32: Large ribosomal subunit protein eL31A

Chain Lf:



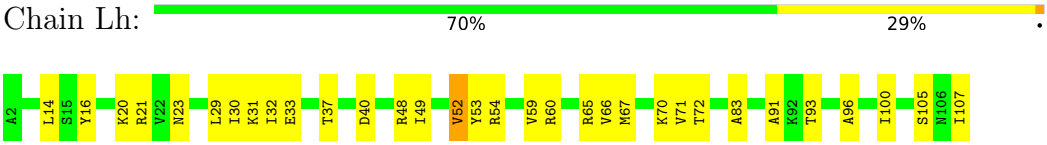
• Molecule 33: Large ribosomal subunit protein eL32

Chain Lg:



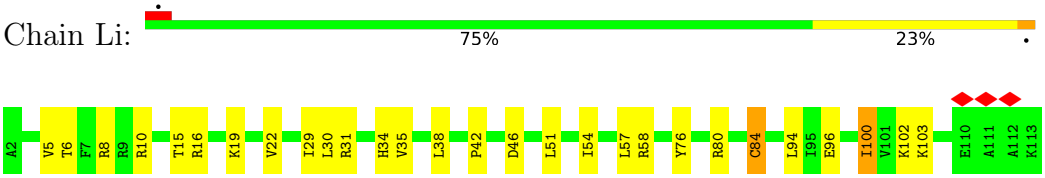
• Molecule 34: Large ribosomal subunit protein eL33A

Chain Lh:



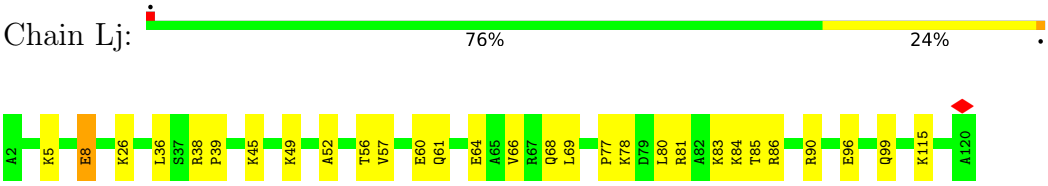
• Molecule 35: Large ribosomal subunit protein eL34A

Chain Li:



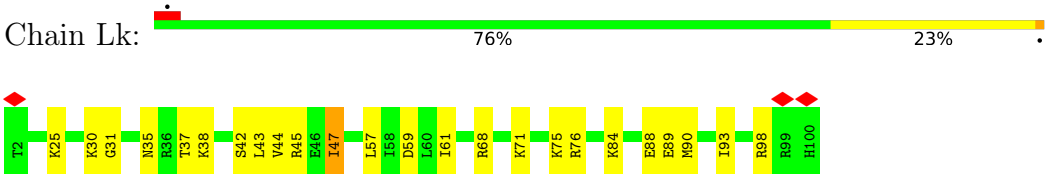
• Molecule 36: Large ribosomal subunit protein uL29A

Chain Lj:



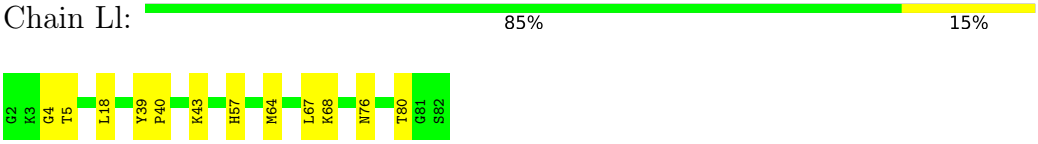
• Molecule 37: Large ribosomal subunit protein eL36A

Chain Lk:



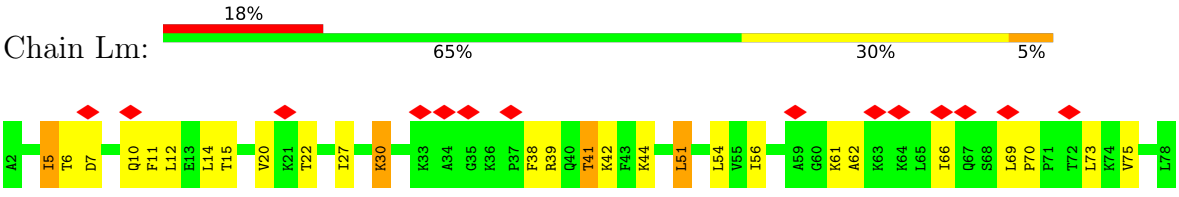
• Molecule 38: Large ribosomal subunit protein eL37A

Chain Ll:



• Molecule 39: Large ribosomal subunit protein eL38

Chain Lm:



• Molecule 40: Large ribosomal subunit protein eL39

Chain Ln:





• Molecule 41: Large ribosomal subunit protein eL40A

Chain Lo:





• Molecule 42: Large ribosomal subunit protein eL41A

Chain Lp:

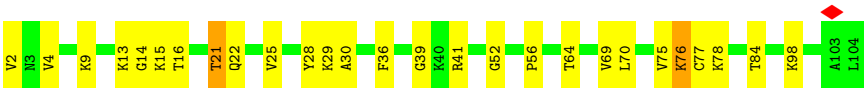




• Molecule 43: Large ribosomal subunit protein eL42A

Chain Lq:

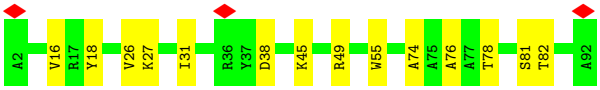




• Molecule 44: Large ribosomal subunit protein eL43A

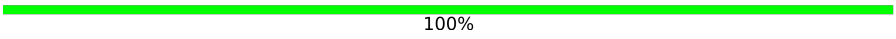
Chain Lr:





• Molecule 45: RNA (5'-R(P*UP*GP*AP*CP*GP*CP*UP*UP*UP*UP*C)-3')

Chain mR:

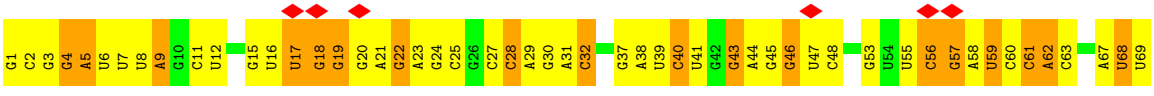


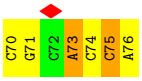
There are no outlier residues recorded for this chain.

• Molecule 46: RNA (76-MER)

Chain Bb:

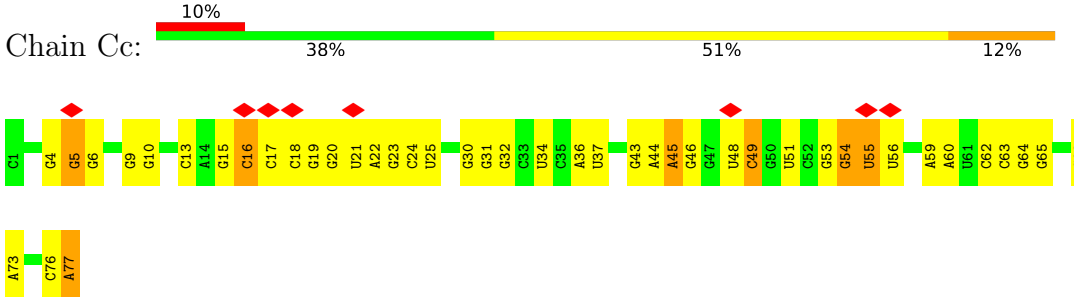






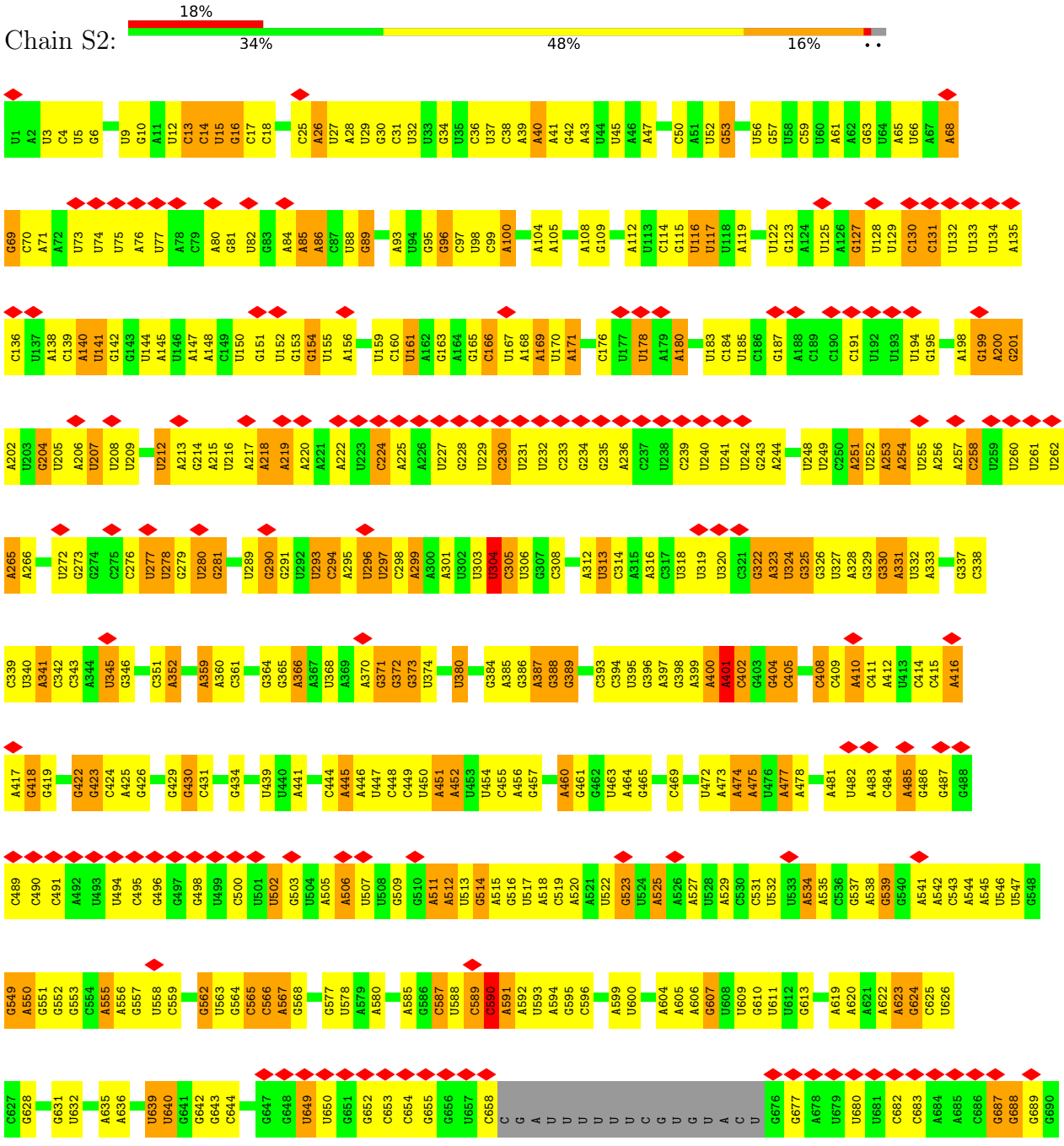
• Molecule 47: RNA (77-MER)

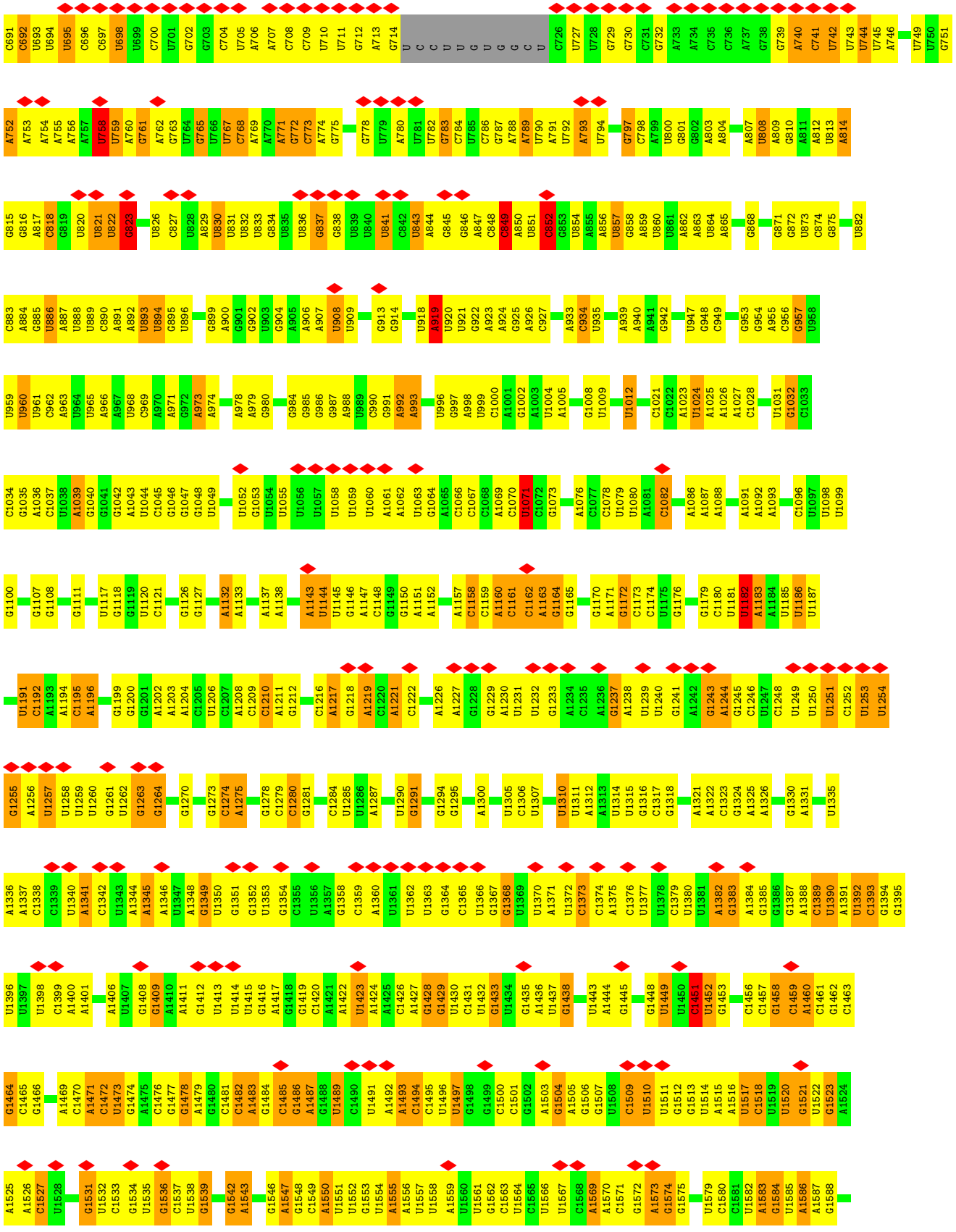
Chain Cc:

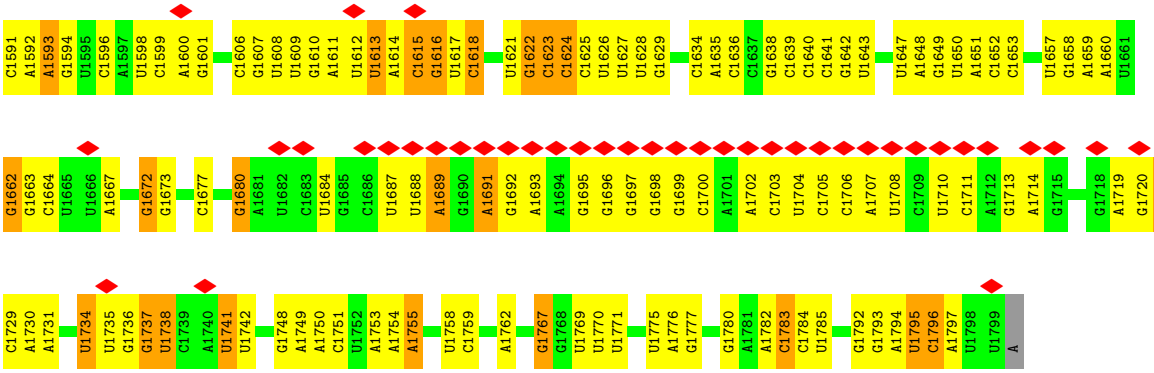


• Molecule 48: RNA (1800-MER)

Chain S2:



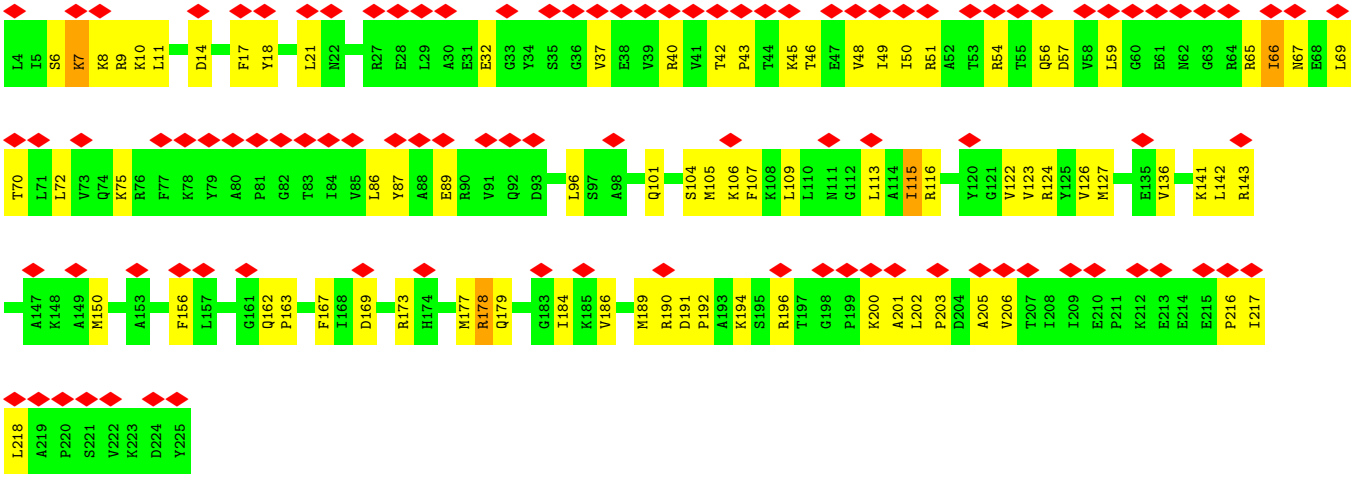




• Molecule 49: Small ribosomal subunit protein uS3

Chain SA:

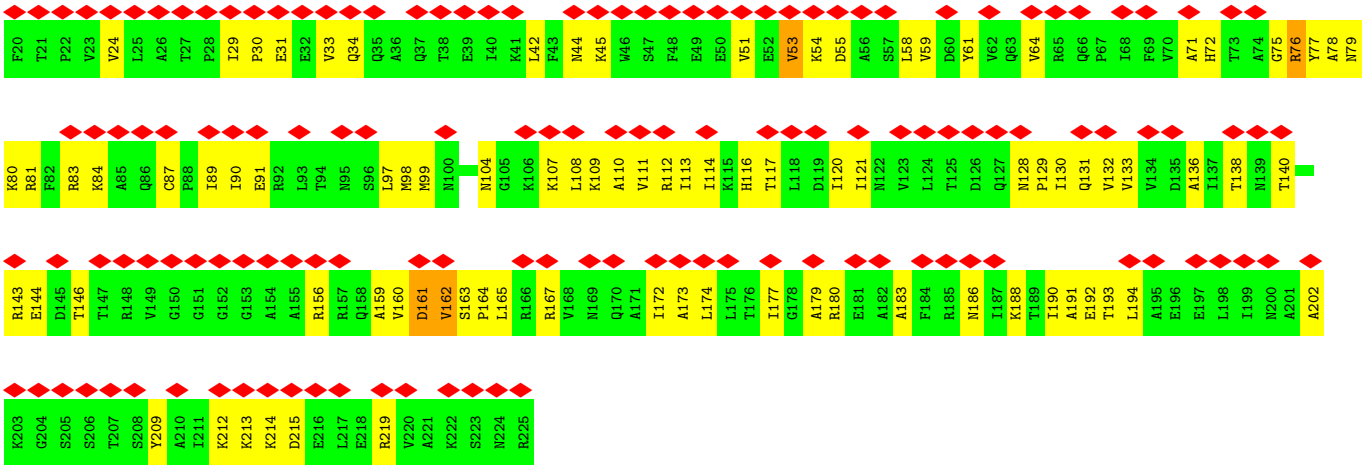




• Molecule 50: Small ribosomal subunit protein uS7

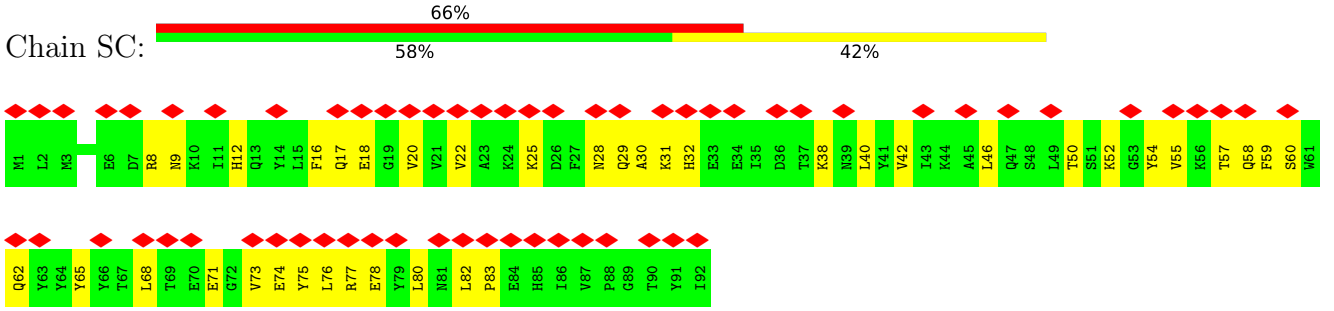
Chain SB:





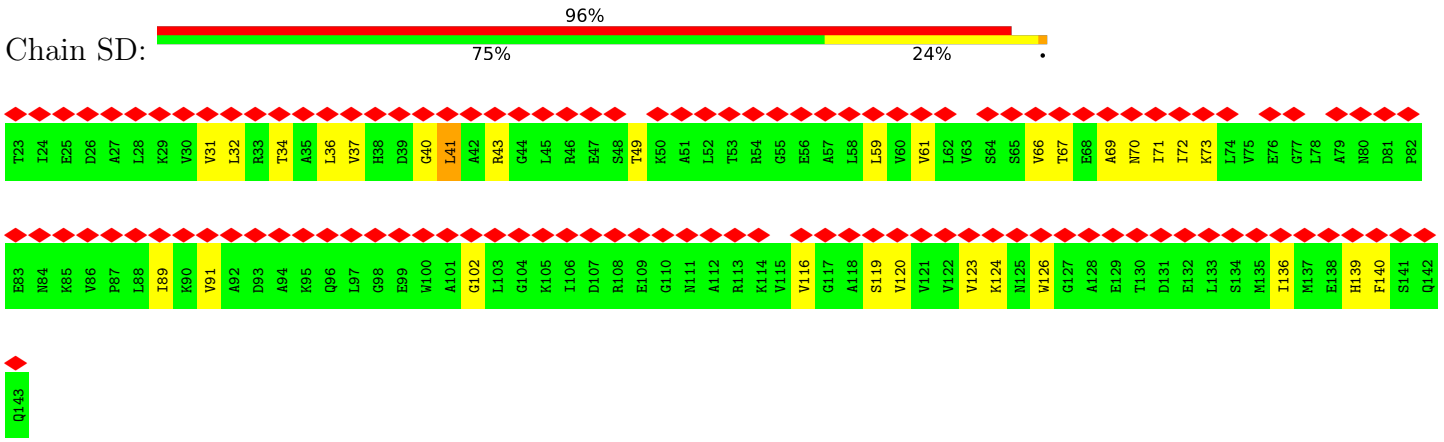
• Molecule 51: Small ribosomal subunit protein eS10A

Chain SC:



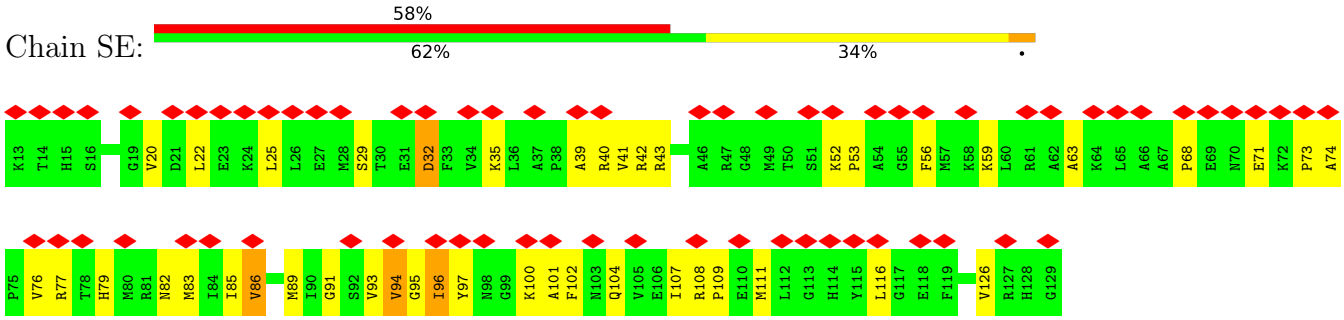
• Molecule 52: Small ribosomal subunit protein eS12

Chain SD:



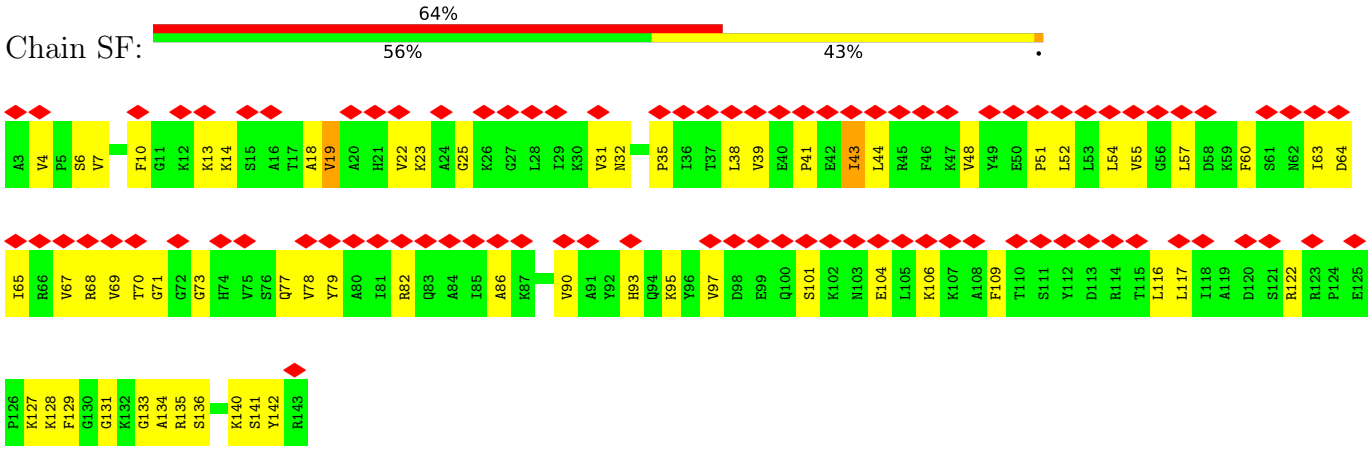
• Molecule 53: Small ribosomal subunit protein uS19

Chain SE:



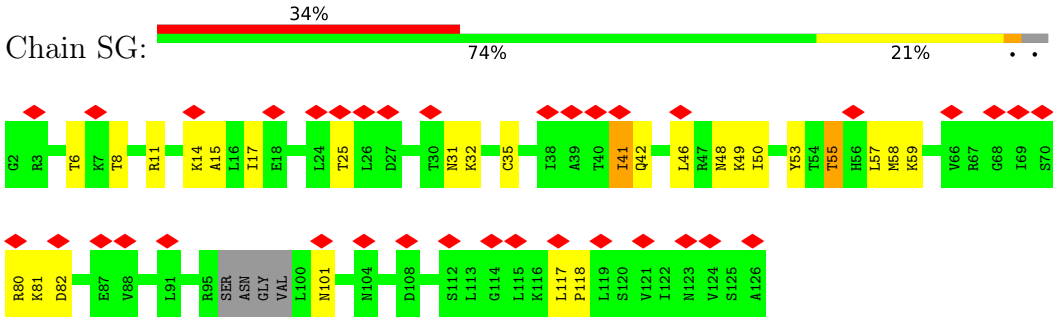
• Molecule 54: Small ribosomal subunit protein uS9A

Chain SF:



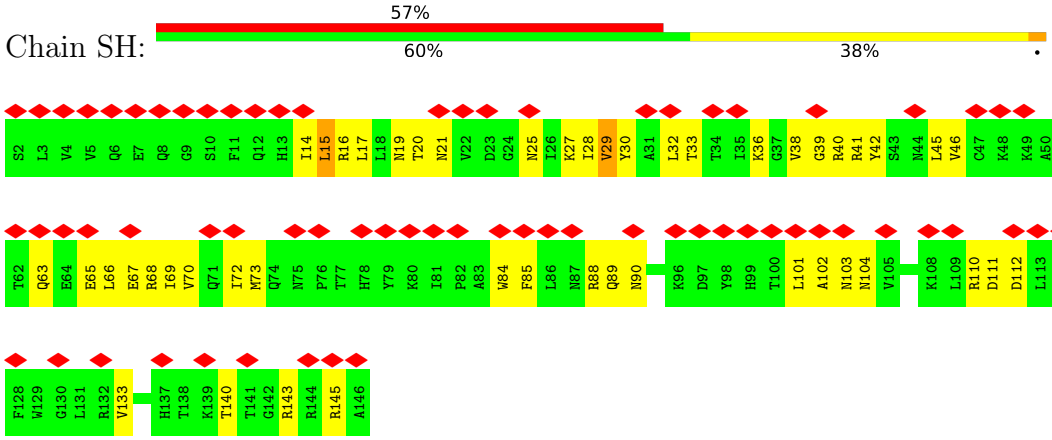
• Molecule 55: Small ribosomal subunit protein eS17B

Chain SG:



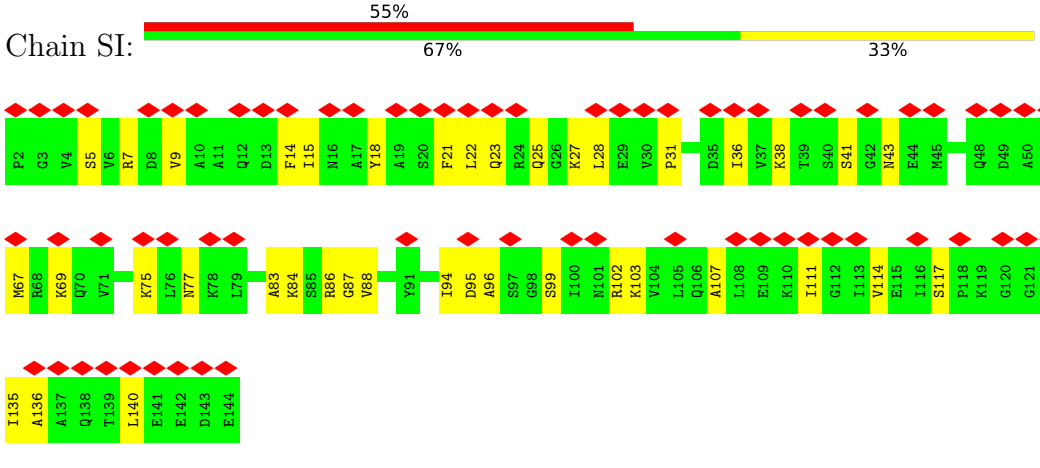
• Molecule 56: Small ribosomal subunit protein uS13A

Chain SH:



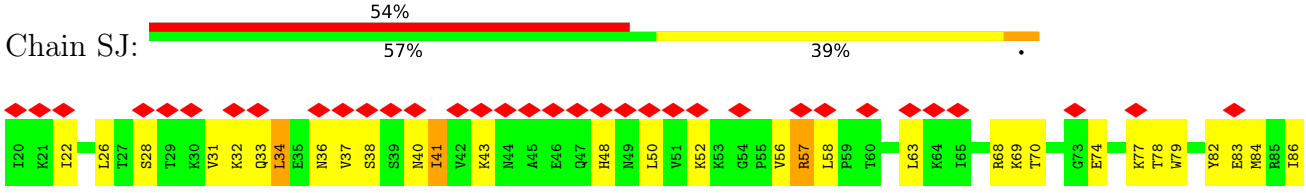
• Molecule 57: Small ribosomal subunit protein eS19A

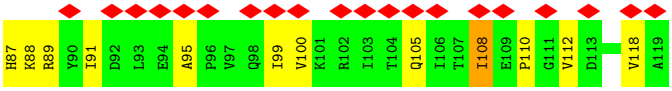
Chain SI:



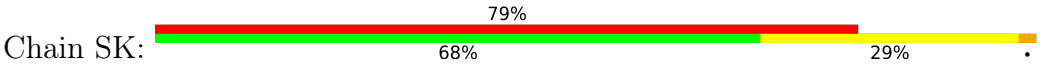
• Molecule 58: Small ribosomal subunit protein uS10

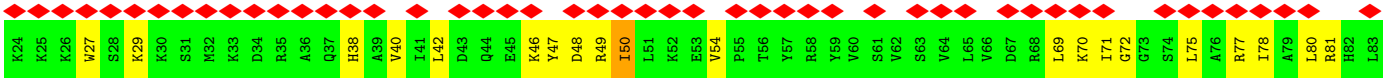
Chain SJ:

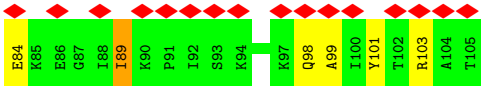




• Molecule 59: Small ribosomal subunit protein eS25A

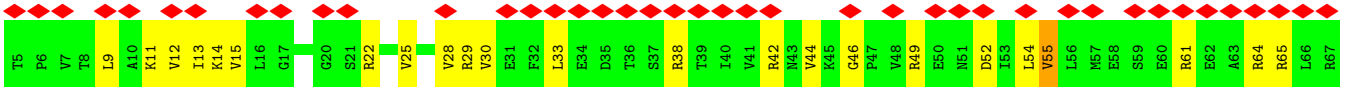






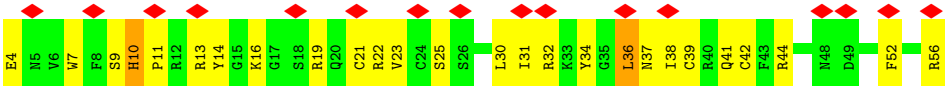
• Molecule 60: Small ribosomal subunit protein eS28A



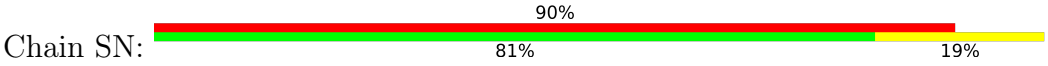


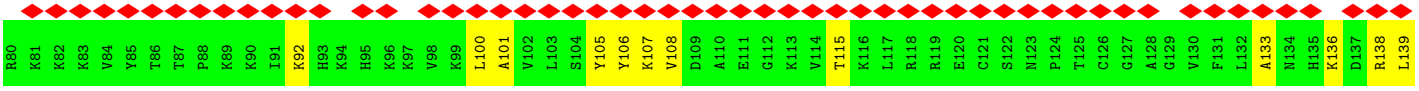
• Molecule 61: Small ribosomal subunit protein uS14A

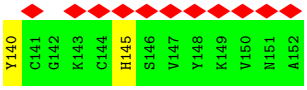




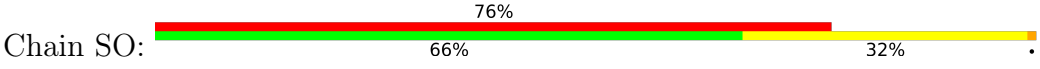
• Molecule 62: Small ribosomal subunit protein eS31

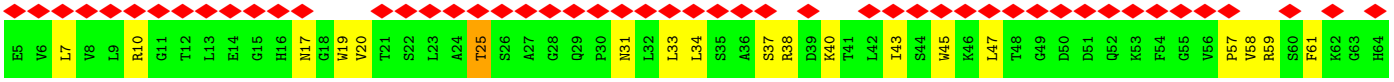


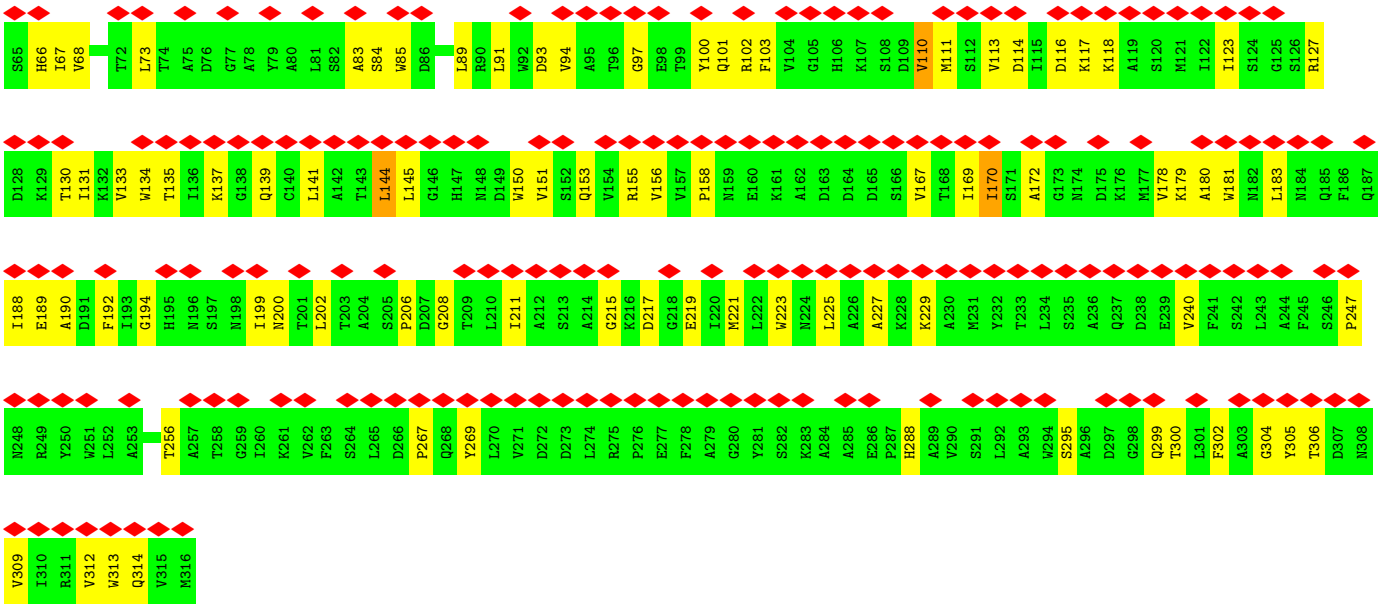




• Molecule 63: Small ribosomal subunit protein RACK1



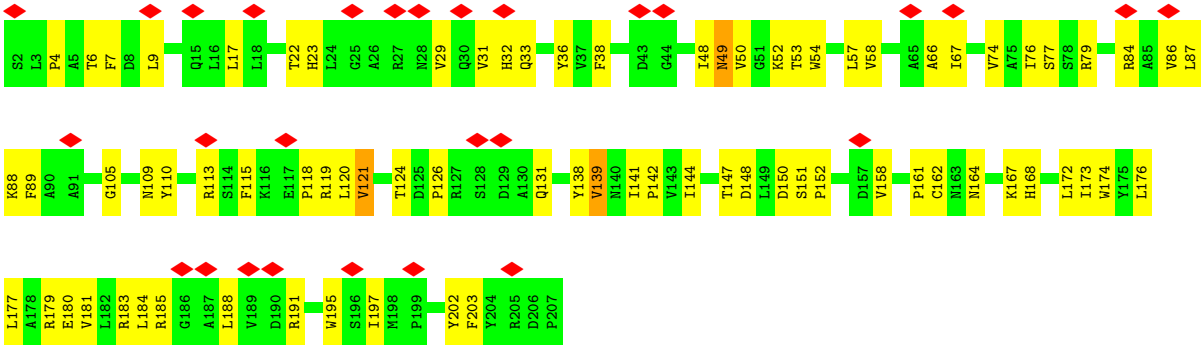




• Molecule 64: Small ribosomal subunit protein uS2A

Chain SP:

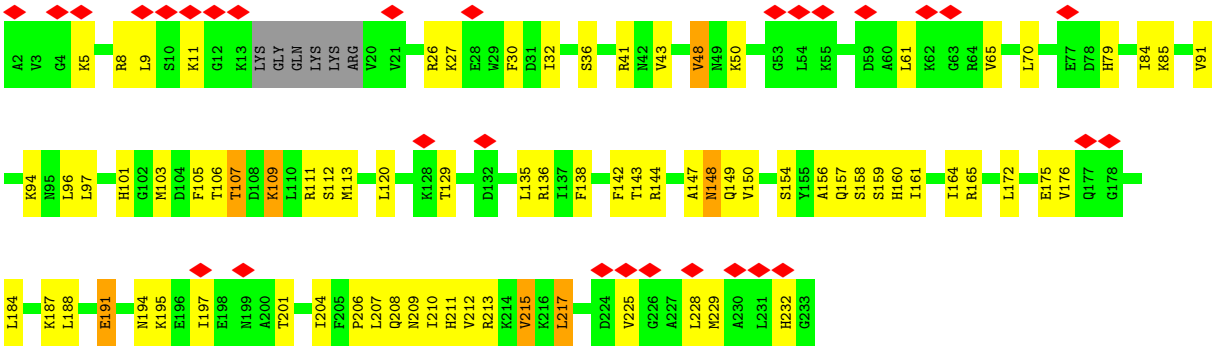




• Molecule 65: Small ribosomal subunit protein eS1A

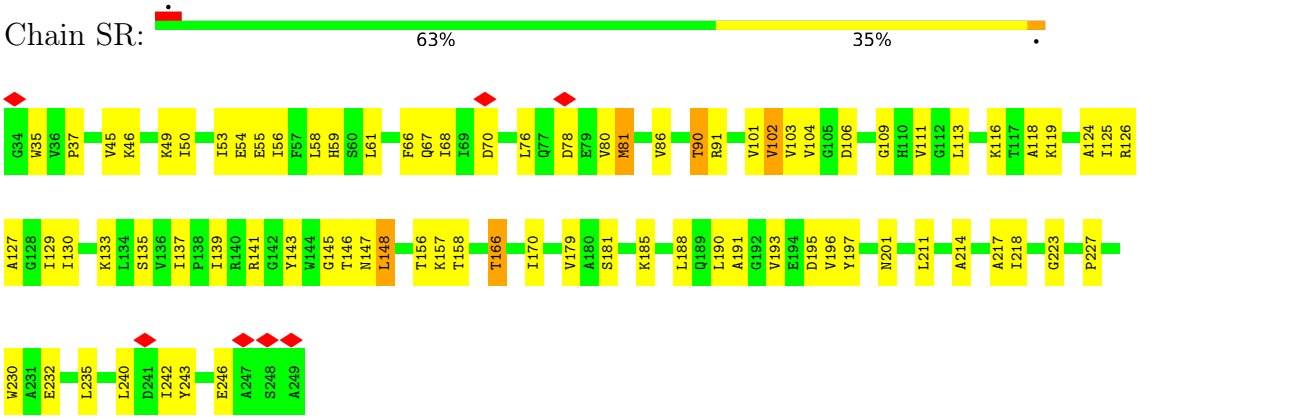
Chain SQ:





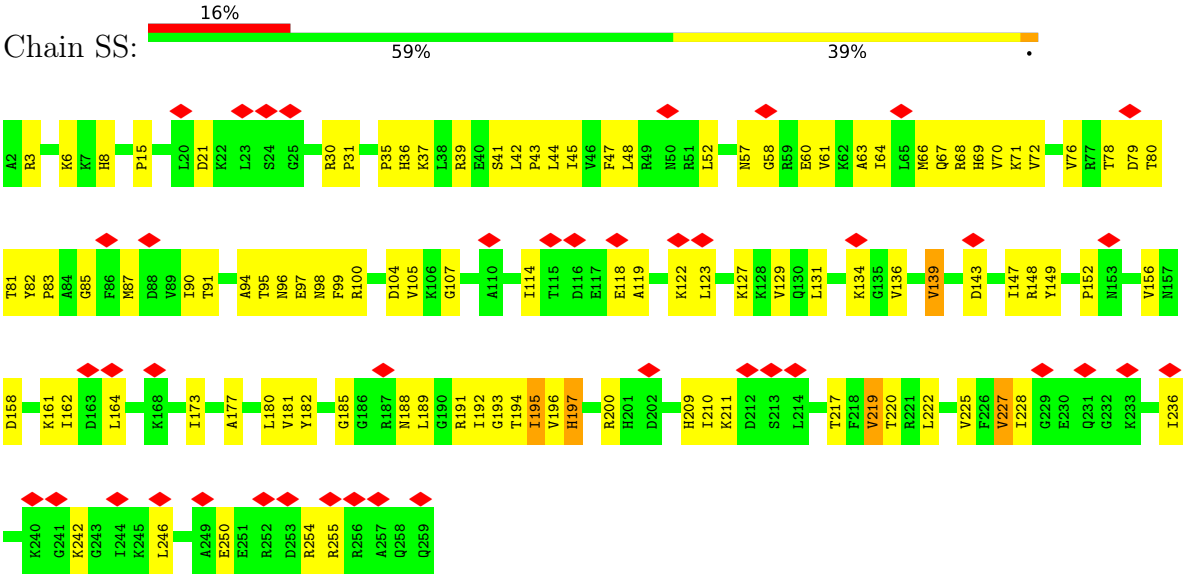
• Molecule 66: Small ribosomal subunit protein uS5

Chain SR:



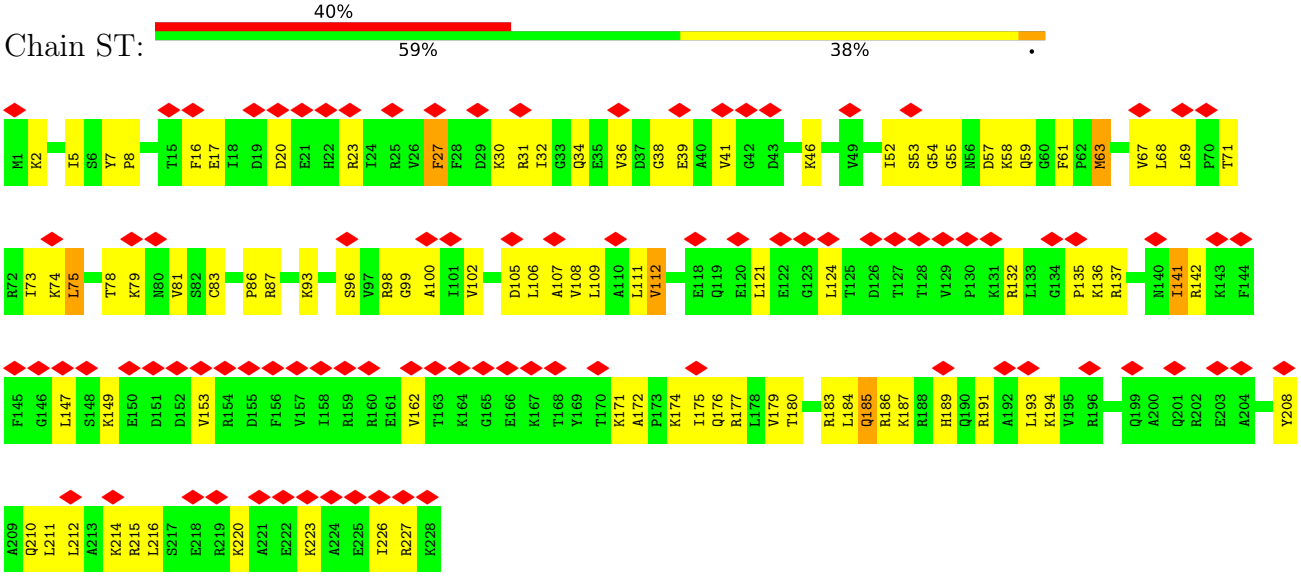
• Molecule 67: Small ribosomal subunit protein eS4A

Chain SS:



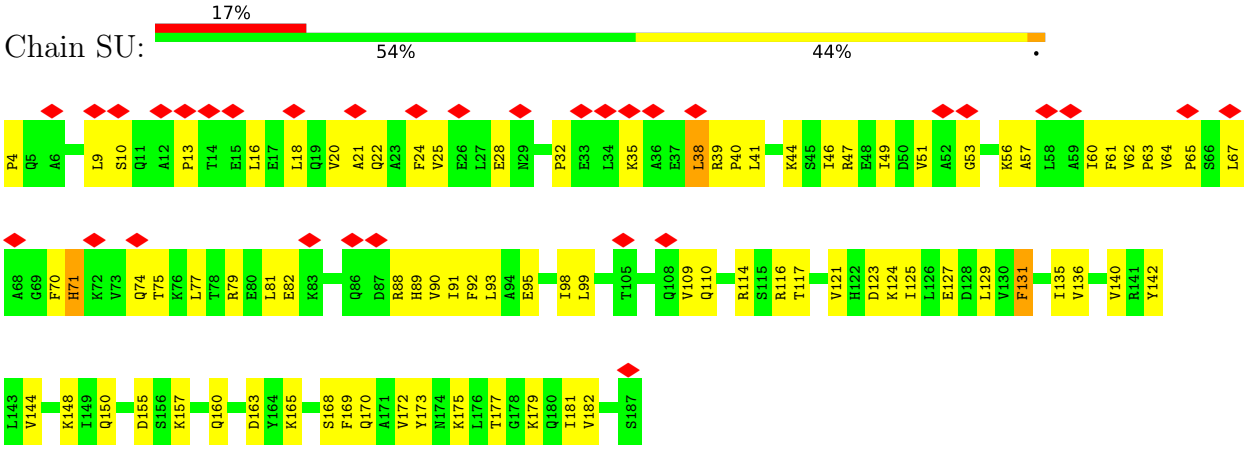
• Molecule 68: Small ribosomal subunit protein eS6A

Chain ST:



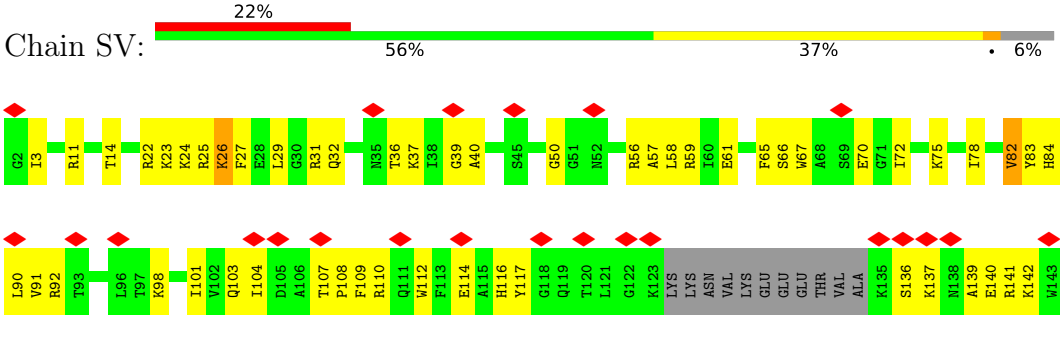
• Molecule 69: Small ribosomal subunit protein eS7A

Chain SU:



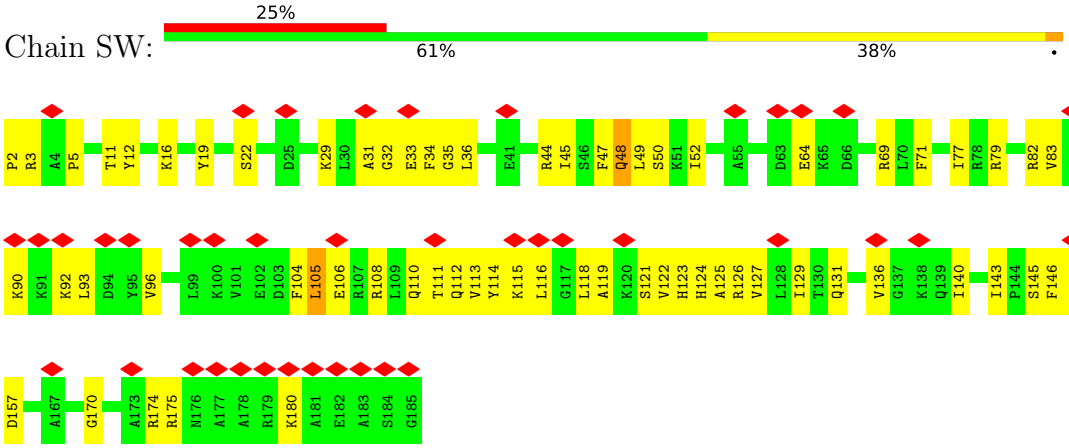
• Molecule 70: Small ribosomal subunit protein eS8A

Chain SV:



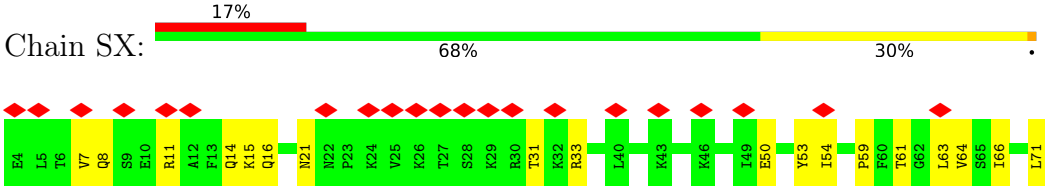
• Molecule 71: Small ribosomal subunit protein uS4A

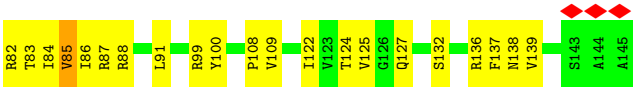
Chain SW:



• Molecule 72: Small ribosomal subunit protein uS17A

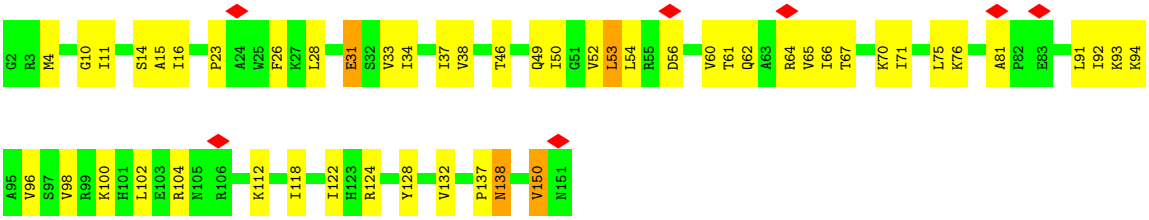
Chain SX:





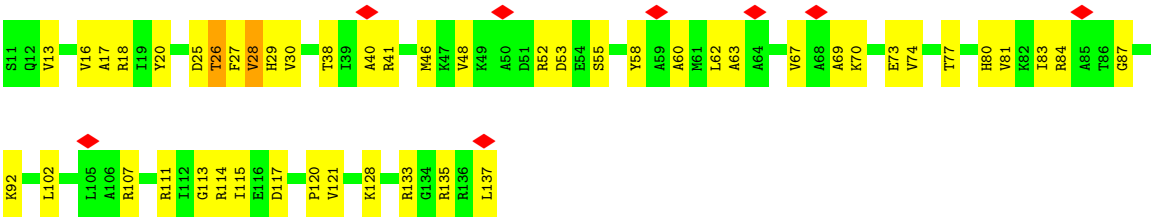
• Molecule 73: Small ribosomal subunit protein uS15





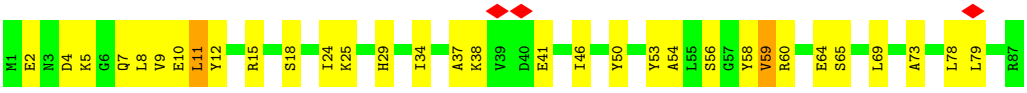
• Molecule 74: Small ribosomal subunit protein uS11B





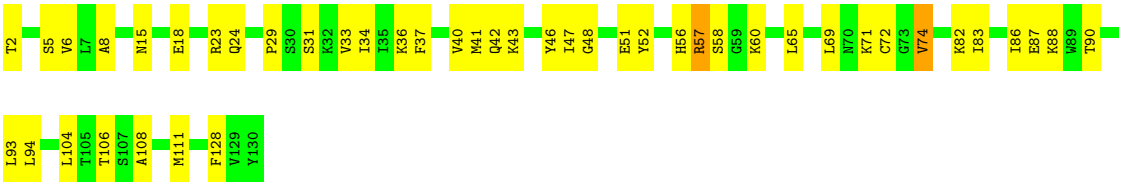
• Molecule 75: Small ribosomal subunit protein eS21A



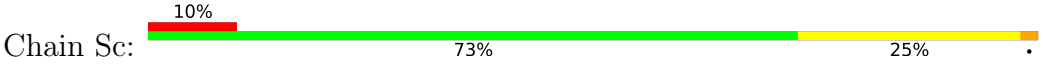


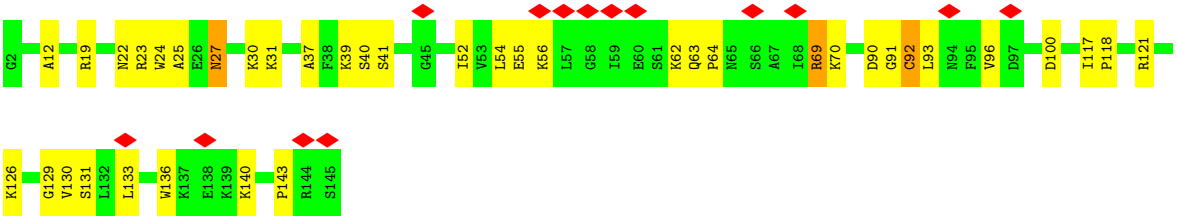
• Molecule 76: Small ribosomal subunit protein uS8A



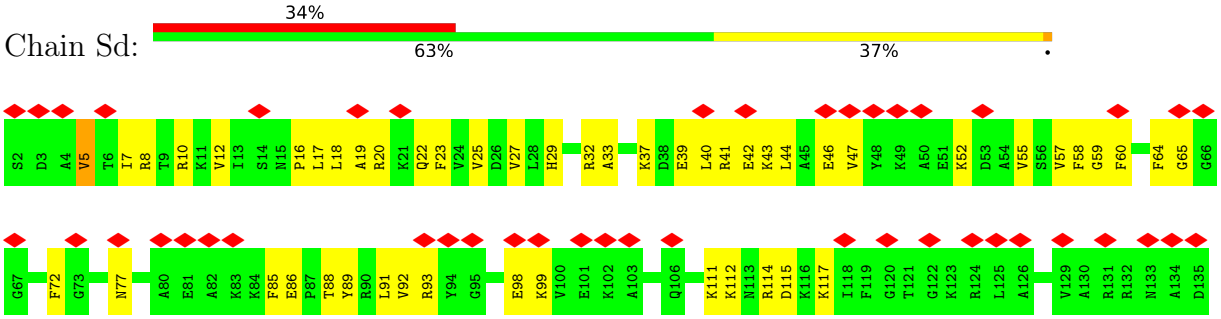


• Molecule 77: Small ribosomal subunit protein uS12A

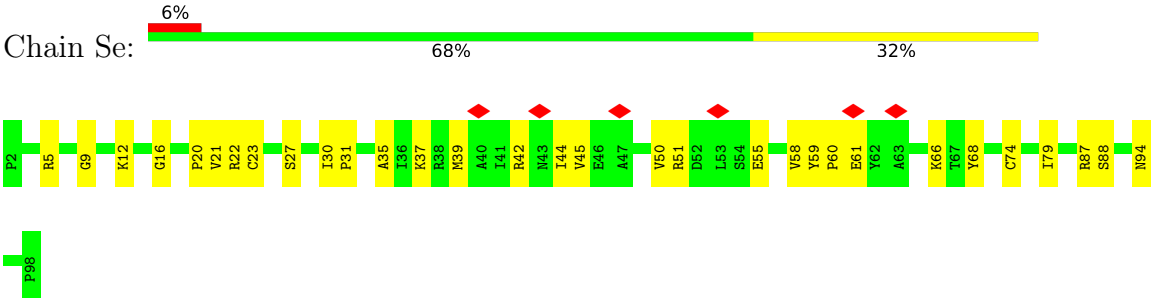




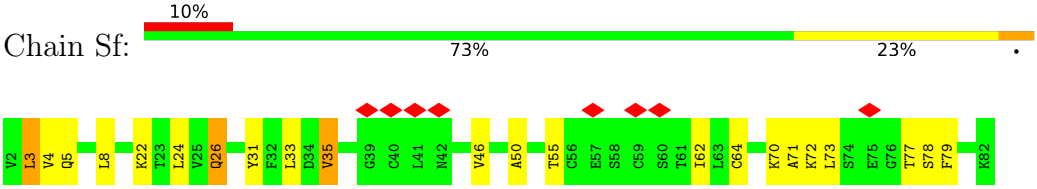
• Molecule 78: Small ribosomal subunit protein eS24A



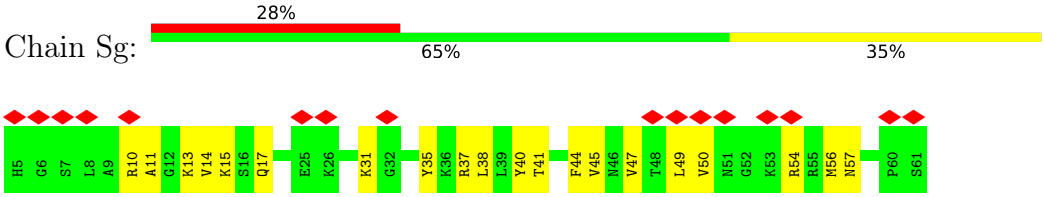
• Molecule 79: Small ribosomal subunit protein eS26B



• Molecule 80: Small ribosomal subunit protein eS27A



• Molecule 81: Small ribosomal subunit protein eS30A



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12559	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	1.692	Depositor
Minimum map value	-0.827	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	570.0, 570.0, 570.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	LA	0.43	0/75727	0.75	25/118064 (0.0%)
2	LB	0.38	0/2883	0.74	2/4491 (0.0%)
3	LC	0.42	0/3746	0.71	0/5832
4	LD	0.22	0/1933	0.39	0/2598
5	LE	0.20	0/3146	0.37	0/4228
6	LF	0.21	0/2800	0.36	0/3790
7	LG	0.17	0/2400	0.38	0/3239
8	LH	0.19	0/1329	0.43	0/1794
9	LI	0.23	0/1821	0.39	0/2451
10	LJ	0.18	0/1836	0.38	0/2481
11	LK	0.18	0/1529	0.38	0/2060
12	LL	0.22	0/1801	0.46	0/2416
13	LM	0.18	0/1367	0.43	0/1834
14	LN	0.20	0/1568	0.39	0/2106
15	LO	0.19	0/1068	0.42	0/1438
16	LP	0.21	0/1757	0.36	0/2354
17	LQ	0.21	0/1585	0.37	0/2128
18	LR	0.20	0/1439	0.34	0/1938
19	LS	0.21	0/1465	0.36	0/1965
20	LT	0.19	0/1532	0.35	0/2043
21	LU	0.21	0/1473	0.39	0/1980
22	LV	0.20	0/1296	0.37	0/1739
23	LW	0.21	0/812	0.55	0/1099
24	LX	0.21	0/1018	0.36	0/1369
25	LY	0.19	0/540	0.35	0/717
26	LZ	0.19	0/979	0.38	0/1321
27	La	0.18	0/995	0.35	0/1329
28	Lb	0.18	0/1106	0.35	0/1485
29	Lc	0.22	0/1200	0.43	1/1607 (0.1%)
30	Ld	0.19	0/473	0.40	0/629
31	Le	0.18	0/745	0.39	0/1001
32	Lf	0.17	0/890	0.35	0/1196
33	Lg	0.19	0/1038	0.32	0/1390
34	Lh	0.22	0/868	0.38	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
35	Li	0.19	0/890	0.33	0/1189
36	Lj	0.19	0/978	0.44	0/1301
37	Lk	0.20	0/772	0.41	0/1026
38	Ll	0.22	0/660	0.35	0/875
39	Lm	0.17	0/618	0.42	0/826
40	Ln	0.21	0/443	0.32	0/588
41	Lo	0.20	0/416	0.41	0/553
42	Lp	0.17	0/230	0.35	0/296
43	Lq	0.19	0/836	0.38	0/1104
44	Lr	0.20	0/701	0.40	0/934
46	Bb	0.30	0/1814	0.81	0/2827
47	Cc	0.26	0/1836	0.72	0/2859
48	S2	0.33	1/42211 (0.0%)	0.82	56/65773 (0.1%)
49	SA	0.16	0/1754	0.45	0/2361
50	SB	0.16	0/1625	0.47	0/2197
51	SC	0.15	0/769	0.38	0/1039
52	SD	0.17	0/883	0.50	0/1199
53	SE	0.14	0/936	0.41	0/1259
54	SF	0.15	0/1125	0.45	0/1510
55	SG	0.17	0/957	0.46	0/1283
56	SH	0.16	0/1207	0.42	0/1623
57	SI	0.16	0/1130	0.42	0/1517
58	SJ	0.15	0/807	0.39	0/1091
59	SK	0.16	0/661	0.46	0/888
60	SL	0.15	0/493	0.44	0/663
61	SM	0.12	0/452	0.33	0/600
62	SN	0.15	0/567	0.46	0/764
63	SO	0.15	0/2436	0.44	0/3318
64	SP	0.18	0/1644	0.45	0/2249
65	SQ	0.16	0/1823	0.42	0/2447
66	SR	0.19	0/1656	0.46	0/2251
67	SS	0.16	0/2097	0.42	0/2823
68	ST	0.14	0/1839	0.40	0/2460
69	SU	0.18	0/1498	0.44	0/2019
70	SV	0.16	0/1501	0.40	0/2006
71	SW	0.17	0/1504	0.46	0/2016
72	SX	0.17	0/1168	0.35	0/1575
73	SY	0.25	0/1215	0.44	0/1638
74	SZ	0.17	0/934	0.38	0/1257
75	Sa	0.21	0/682	0.50	0/921
76	Sb	0.21	0/1038	0.41	0/1395
77	Sc	0.17	0/1139	0.43	0/1518
78	Sd	0.14	0/1046	0.36	0/1401

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
79	Se	0.19	0/778	0.40	0/1042
80	Sf	0.21	0/620	0.43	0/838
81	Sg	0.16	0/459	0.48	0/611
All	All	0.33	1/217013 (0.0%)	0.66	84/319210 (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
6	LF	0	1
10	LJ	0	1
30	Ld	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	S2	823	G	C6-N1	-5.05	1.36	1.39

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
48	S2	849	C	N3-C4-N4	-19.82	104.13	118.00
48	S2	823	G	N1-C6-O6	-18.52	108.79	119.90
48	S2	823	G	C5-C6-O6	15.94	138.16	128.60
48	S2	849	C	C5-C4-N4	14.02	130.01	120.20
48	S2	893	U	N3-C4-O4	-11.45	111.39	119.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	LF	13	GLY	Peptide
10	LJ	30	THR	Peptide
30	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	LA	67653	0	33997	775	0
2	LB	2579	0	1304	38	0
3	LC	3353	0	1695	46	0
4	LD	1899	0	1957	42	0
5	LE	3075	0	3142	60	0
6	LF	2748	0	2859	64	0
7	LG	2351	0	2294	59	0
8	LH	1307	0	1377	31	0
9	LI	1784	0	1862	44	0
10	LJ	1804	0	1877	47	0
11	LK	1508	0	1572	42	0
12	LL	1764	0	1804	42	0
13	LM	1346	0	1370	28	0
14	LN	1543	0	1608	31	0
15	LO	1053	0	1149	32	0
16	LP	1720	0	1779	28	0
17	LQ	1555	0	1659	36	0
18	LR	1416	0	1433	13	0
19	LS	1441	0	1543	33	0
20	LT	1515	0	1606	25	0
21	LU	1437	0	1475	33	0
22	LV	1272	0	1312	31	0
23	LW	796	0	812	20	0
24	LX	1003	0	1048	14	0
25	LY	528	0	546	10	0
26	LZ	964	0	1025	21	0
27	La	984	0	1075	24	0
28	Lb	1080	0	1122	17	0
29	Lc	1169	0	1211	29	0
30	Ld	462	0	491	15	0
31	Le	737	0	792	18	0
32	Lf	876	0	912	16	0
33	Lg	1017	0	1081	14	0
34	Lh	850	0	880	19	0
35	Li	880	0	945	19	0
36	Lj	969	0	1078	20	0
37	Lk	766	0	844	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Ll	645	0	649	9	0
39	Lm	612	0	682	20	0
40	Ln	436	0	475	12	0
41	Lo	410	0	446	13	0
42	Lp	229	0	273	9	0
43	Lq	824	0	892	16	0
44	Lr	694	0	738	10	0
45	mR	228	0	0	0	0
46	Bb	1622	0	821	39	0
47	Cc	1644	0	837	27	0
48	S2	37739	0	18988	685	0
49	SA	1729	0	1812	70	0
50	SB	1605	0	1669	74	0
51	SC	752	0	719	29	0
52	SD	875	0	878	15	0
53	SE	916	0	941	35	0
54	SF	1105	0	1166	50	0
55	SG	948	0	990	21	0
56	SH	1188	0	1218	46	0
57	SI	1112	0	1124	37	0
58	SJ	797	0	863	35	0
59	SK	651	0	682	22	0
60	SL	491	0	524	22	0
61	SM	442	0	432	24	0
62	SN	556	0	549	8	0
63	SO	2383	0	2332	65	0
64	SP	1603	0	1610	62	0
65	SQ	1798	0	1890	67	0
66	SR	1626	0	1715	60	0
67	SS	2056	0	2140	79	0
68	ST	1815	0	1894	68	0
69	SU	1473	0	1555	59	0
70	SV	1476	0	1501	59	0
71	SW	1479	0	1556	58	0
72	SX	1142	0	1209	33	0
73	SY	1192	0	1255	37	0
74	SZ	923	0	948	44	0
75	Sa	673	0	662	21	0
76	Sb	1021	0	1060	32	0
77	Sc	1121	0	1196	27	0
78	Sd	1032	0	1044	39	0
79	Se	765	0	814	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	Sf	610	0	633	21	0
81	Sg	451	0	494	17	0
All	All	202093	0	148412	3590	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 10.

The worst 5 of 3590 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:S2:1673:G:N1	48:S2:1728:A:H2	1.49	1.09
48:S2:1673:G:N1	48:S2:1728:A:C2	2.21	1.09
48:S2:550:A:N6	48:S2:587:C:C4	2.25	1.05
48:S2:698:U:H3	48:S2:741:C:N4	1.54	1.05
48:S2:1374:C:N4	48:S2:1375:A:N6	2.06	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	
4	LD	249/251 (99%)	234 (94%)	15 (6%)	0	100	100
5	LE	384/386 (100%)	358 (93%)	26 (7%)	0	100	100
6	LF	359/361 (99%)	334 (93%)	25 (7%)	0	100	100
7	LG	292/294 (99%)	279 (96%)	13 (4%)	0	100	100
8	LH	163/175 (93%)	153 (94%)	10 (6%)	0	100	100
9	LI	220/222 (99%)	207 (94%)	13 (6%)	0	100	100
10	LJ	231/233 (99%)	217 (94%)	14 (6%)	0	100	100
11	LK	189/191 (99%)	176 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	LL	216/218 (99%)	202 (94%)	14 (6%)	0	100	100
13	LM	167/169 (99%)	157 (94%)	10 (6%)	0	100	100
14	LN	191/193 (99%)	176 (92%)	15 (8%)	0	100	100
15	LO	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
16	LP	201/203 (99%)	192 (96%)	9 (4%)	0	100	100
17	LQ	195/197 (99%)	191 (98%)	4 (2%)	0	100	100
18	LR	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
19	LS	183/185 (99%)	173 (94%)	10 (6%)	0	100	100
20	LT	186/188 (99%)	182 (98%)	4 (2%)	0	100	100
21	LU	169/171 (99%)	157 (93%)	12 (7%)	0	100	100
22	LV	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
23	LW	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
24	LX	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
25	LY	63/65 (97%)	62 (98%)	1 (2%)	0	100	100
26	LZ	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
27	La	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
28	Lb	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
29	Lc	146/148 (99%)	134 (92%)	12 (8%)	0	100	100
30	Ld	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
31	Le	94/96 (98%)	94 (100%)	0	0	100	100
32	Lf	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
33	Lg	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
34	Lh	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
35	Li	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
36	Lj	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
37	Lk	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
38	Ll	79/81 (98%)	77 (98%)	2 (2%)	0	100	100
39	Lm	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
40	Ln	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
41	Lo	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
42	Lp	23/25 (92%)	23 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	Lq	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
44	Lr	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
49	SA	220/222 (99%)	214 (97%)	6 (3%)	0	100	100
50	SB	204/206 (99%)	189 (93%)	14 (7%)	1 (0%)	24	49
51	SC	90/92 (98%)	84 (93%)	6 (7%)	0	100	100
52	SD	119/121 (98%)	90 (76%)	29 (24%)	0	100	100
53	SE	115/117 (98%)	107 (93%)	8 (7%)	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%)	133 (93%)	10 (7%)	0	100	100
57	SI	141/143 (99%)	134 (95%)	7 (5%)	0	100	100
58	SJ	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
59	SK	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
60	SL	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
61	SM	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
62	SN	71/73 (97%)	56 (79%)	15 (21%)	0	100	100
63	SO	310/312 (99%)	281 (91%)	29 (9%)	0	100	100
64	SP	204/206 (99%)	183 (90%)	21 (10%)	0	100	100
65	SQ	222/232 (96%)	201 (90%)	21 (10%)	0	100	100
66	SR	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
67	SS	256/258 (99%)	231 (90%)	25 (10%)	0	100	100
68	ST	226/228 (99%)	210 (93%)	15 (7%)	1 (0%)	30	54
69	SU	182/184 (99%)	171 (94%)	11 (6%)	0	100	100
70	SV	183/198 (92%)	170 (93%)	13 (7%)	0	100	100
71	SW	182/184 (99%)	168 (92%)	14 (8%)	0	100	100
72	SX	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
73	SY	148/150 (99%)	138 (93%)	10 (7%)	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%)	118 (93%)	9 (7%)	0	100	100
77	Sc	142/144 (99%)	126 (89%)	16 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	Sd	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
79	Se	95/97 (98%)	89 (94%)	6 (6%)	0	100	100
80	Sf	79/81 (98%)	71 (90%)	8 (10%)	0	100	100
81	Sg	55/57 (96%)	46 (84%)	9 (16%)	0	100	100
All	All	10914/11099 (98%)	10209 (94%)	703 (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	
4	LD	190/193 (98%)	186 (98%)	4 (2%)	47	70
5	LE	318/322 (99%)	305 (96%)	13 (4%)	27	52
6	LF	288/288 (100%)	279 (97%)	9 (3%)	35	60
7	LG	241/243 (99%)	232 (96%)	9 (4%)	30	55
8	LH	139/154 (90%)	134 (96%)	5 (4%)	31	56
9	LI	186/186 (100%)	177 (95%)	9 (5%)	23	47
10	LJ	187/191 (98%)	178 (95%)	9 (5%)	23	47
11	LK	168/171 (98%)	154 (92%)	14 (8%)	10	26
12	LL	185/185 (100%)	181 (98%)	4 (2%)	45	69
13	LM	145/147 (99%)	133 (92%)	12 (8%)	10	26
14	LN	154/154 (100%)	143 (93%)	11 (7%)	13	31
15	LO	107/107 (100%)	104 (97%)	3 (3%)	38	63
16	LP	175/175 (100%)	167 (95%)	8 (5%)	24	49
17	LQ	160/160 (100%)	154 (96%)	6 (4%)	29	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
18	LR	138/145 (95%)	133 (96%)	5 (4%)	31 56
19	LS	150/150 (100%)	140 (93%)	10 (7%)	15 34
20	LT	152/153 (99%)	143 (94%)	9 (6%)	18 39
21	LU	155/155 (100%)	147 (95%)	8 (5%)	21 44
22	LV	135/136 (99%)	132 (98%)	3 (2%)	45 69
23	LW	87/87 (100%)	82 (94%)	5 (6%)	18 41
24	LX	104/104 (100%)	97 (93%)	7 (7%)	15 34
25	LY	54/57 (95%)	52 (96%)	2 (4%)	30 55
26	LZ	104/105 (99%)	93 (89%)	11 (11%)	6 18
27	La	108/108 (100%)	103 (95%)	5 (5%)	24 49
28	Lb	112/115 (97%)	104 (93%)	8 (7%)	13 31
29	Lc	117/118 (99%)	113 (97%)	4 (3%)	32 58
30	Ld	46/46 (100%)	45 (98%)	1 (2%)	45 69
31	Le	81/81 (100%)	78 (96%)	3 (4%)	30 55
32	Lf	92/96 (96%)	87 (95%)	5 (5%)	20 42
33	Lg	108/109 (99%)	104 (96%)	4 (4%)	30 55
34	Lh	90/90 (100%)	84 (93%)	6 (7%)	15 34
35	Li	95/95 (100%)	90 (95%)	5 (5%)	20 43
36	Lj	104/104 (100%)	103 (99%)	1 (1%)	68 81
37	Lk	80/81 (99%)	77 (96%)	3 (4%)	29 54
38	Ll	67/67 (100%)	65 (97%)	2 (3%)	36 61
39	Lm	68/68 (100%)	59 (87%)	9 (13%)	4 11
40	Ln	45/45 (100%)	41 (91%)	4 (9%)	9 23
41	Lo	45/47 (96%)	45 (100%)	0	100 100
42	Lp	22/23 (96%)	22 (100%)	0	100 100
43	Lq	87/88 (99%)	81 (93%)	6 (7%)	14 33
44	Lr	71/71 (100%)	70 (99%)	1 (1%)	59 76
49	SA	182/182 (100%)	175 (96%)	7 (4%)	29 54
50	SB	172/173 (99%)	163 (95%)	9 (5%)	21 44
51	SC	77/85 (91%)	75 (97%)	2 (3%)	40 65
52	SD	88/98 (90%)	83 (94%)	5 (6%)	18 41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	SE	95/98 (97%)	90 (95%)	5 (5%)	20	43
54	SF	117/117 (100%)	113 (97%)	4 (3%)	32	58
55	SG	101/113 (89%)	98 (97%)	3 (3%)	36	61
56	SH	127/128 (99%)	120 (94%)	7 (6%)	19	41
57	SI	115/115 (100%)	114 (99%)	1 (1%)	70	82
58	SJ	93/93 (100%)	84 (90%)	9 (10%)	8	20
59	SK	67/73 (92%)	62 (92%)	5 (8%)	12	29
60	SL	55/56 (98%)	53 (96%)	2 (4%)	31	56
61	SM	47/47 (100%)	44 (94%)	3 (6%)	16	36
62	SN	56/64 (88%)	54 (96%)	2 (4%)	31	56
63	SO	250/257 (97%)	237 (95%)	13 (5%)	21	44
64	SP	170/173 (98%)	165 (97%)	5 (3%)	37	62
65	SQ	200/205 (98%)	187 (94%)	13 (6%)	15	35
66	SR	175/175 (100%)	162 (93%)	13 (7%)	13	30
67	SS	220/220 (100%)	210 (96%)	10 (4%)	24	49
68	ST	189/195 (97%)	174 (92%)	15 (8%)	11	27
69	SU	163/165 (99%)	157 (96%)	6 (4%)	30	55
70	SV	148/159 (93%)	138 (93%)	10 (7%)	14	33
71	SW	156/157 (99%)	147 (94%)	9 (6%)	18	40
72	SX	126/127 (99%)	118 (94%)	8 (6%)	16	36
73	SY	127/127 (100%)	118 (93%)	9 (7%)	13	31
74	SZ	90/96 (94%)	88 (98%)	2 (2%)	45	69
75	Sa	71/74 (96%)	65 (92%)	6 (8%)	10	24
76	Sb	110/110 (100%)	104 (94%)	6 (6%)	19	41
77	Sc	119/119 (100%)	111 (93%)	8 (7%)	15	34
78	Sd	102/112 (91%)	98 (96%)	4 (4%)	28	53
79	Se	82/83 (99%)	79 (96%)	3 (4%)	30	55
80	Sf	70/70 (100%)	65 (93%)	5 (7%)	13	31
81	Sg	48/49 (98%)	43 (90%)	5 (10%)	7	18
All	All	9168/9335 (98%)	8711 (95%)	457 (5%)	23	46

5 of 457 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	Lm	75	VAL
78	Sd	25	VAL
58	SJ	34	LEU
77	Sc	117	ILE
71	SW	156	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
50	SB	116	HIS
59	SK	98	GLN
50	SB	169	ASN
55	SG	31	ASN
63	SO	288	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	LA	3159/3396 (93%)	777 (24%)	30 (0%)
2	LB	120/121 (99%)	22 (18%)	1 (0%)
3	LC	157/158 (99%)	36 (22%)	1 (0%)
45	mR	0/11	-	-
46	Bb	75/76 (98%)	34 (45%)	0
47	Cc	76/77 (98%)	27 (35%)	0
48	S2	1768/1800 (98%)	709 (40%)	20 (1%)
All	All	5355/5639 (94%)	1605 (29%)	52 (0%)

5 of 1605 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	LA	6	A
1	LA	14	U
1	LA	22	G
1	LA	26	A
1	LA	34	A

5 of 52 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	LA	3269	U
48	S2	400	A

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Mol	Chain	Res	Type
48	S2	1274	C
1	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.

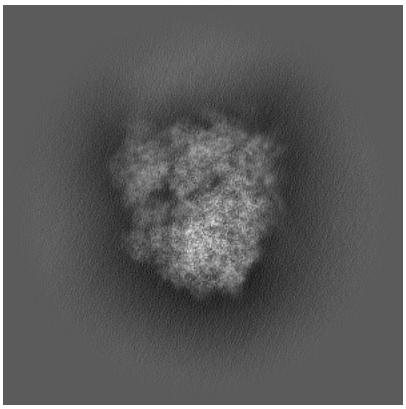
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-68778. These allow visual inspection of the internal detail of the map and identification of artifacts.

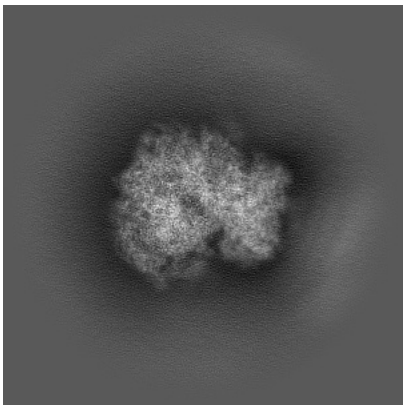
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

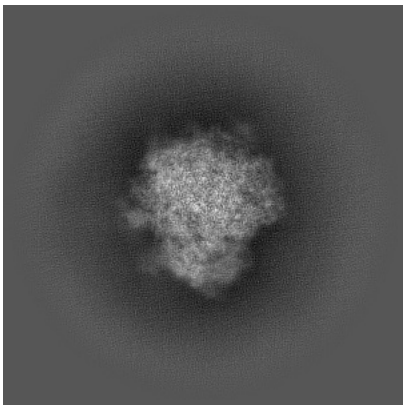
6.1.1 Primary map



X

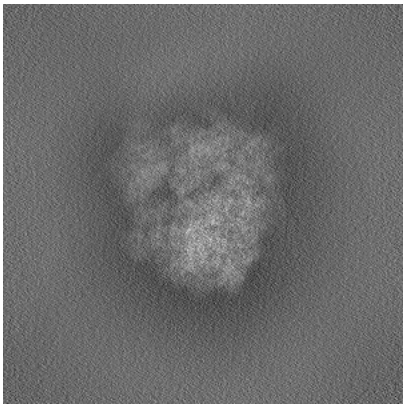


Y

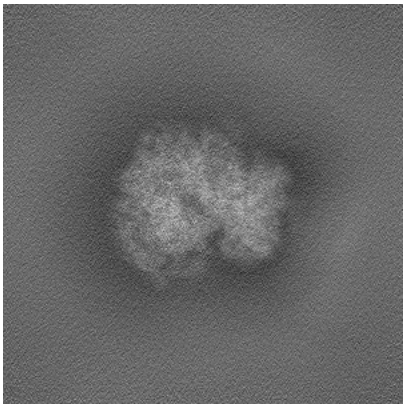


Z

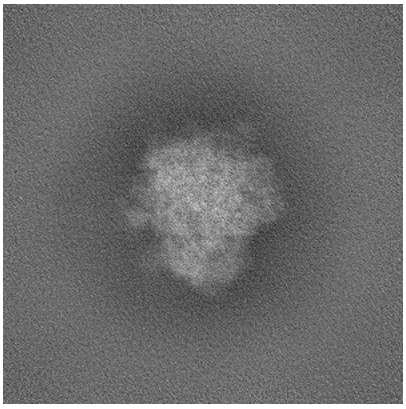
6.1.2 Raw map



X



Y

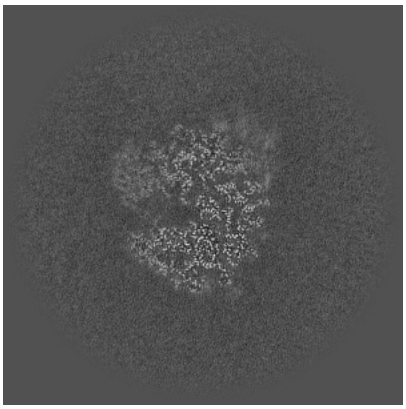


Z

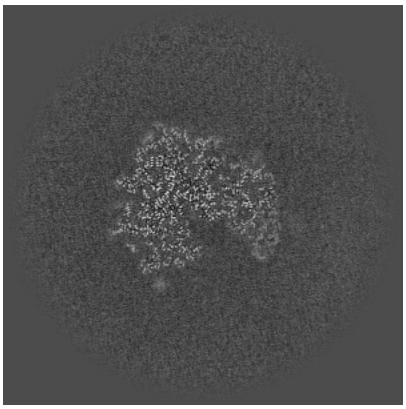
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

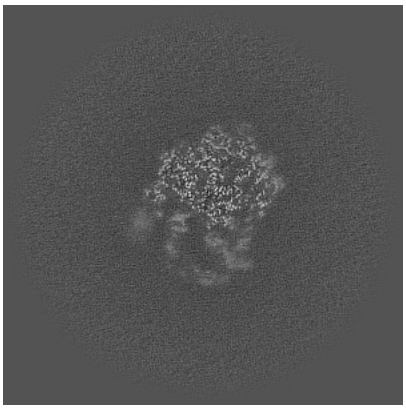
6.2.1 Primary map



X Index: 300

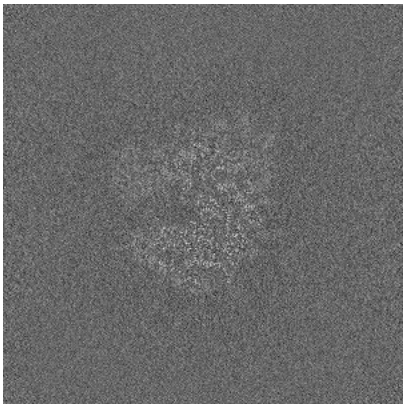


Y Index: 300

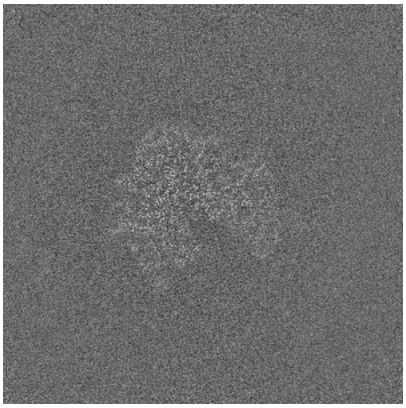


Z Index: 300

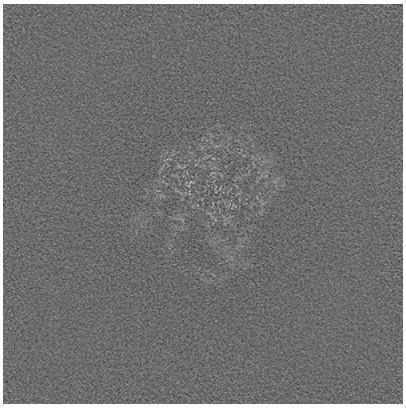
6.2.2 Raw map



X Index: 300



Y Index: 300

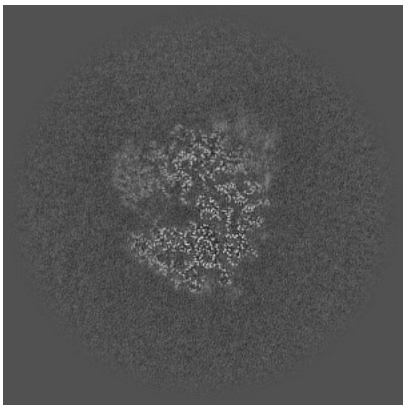


Z Index: 300

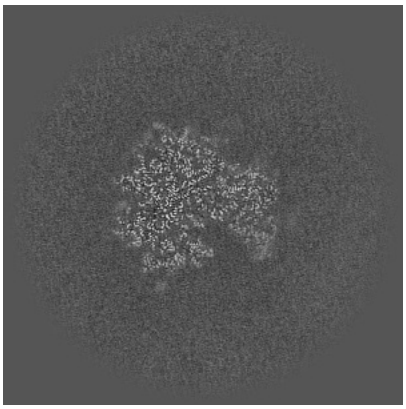
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

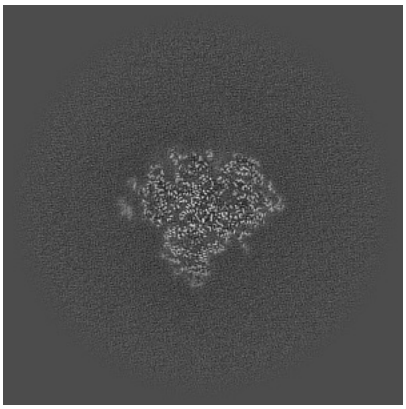
6.3.1 Primary map



X Index: 300

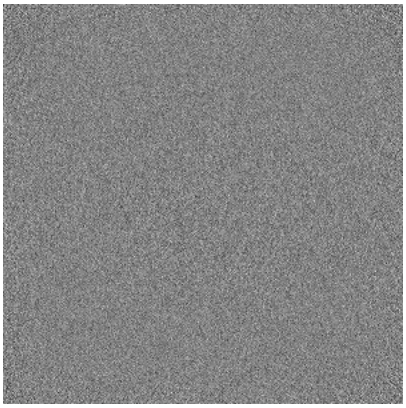


Y Index: 306

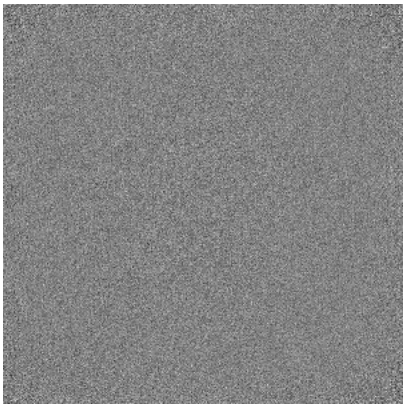


Z Index: 240

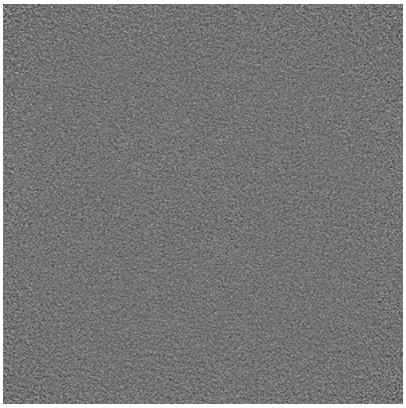
6.3.2 Raw map



X Index: 0



Y Index: 0

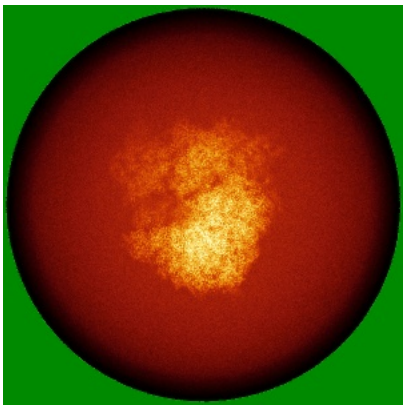


Z Index: 0

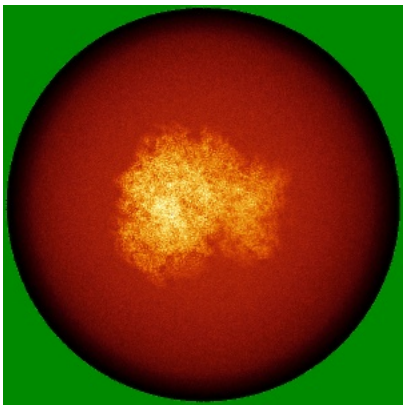
The images above show the largest variance slices of the map in three orthogonal directions.

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

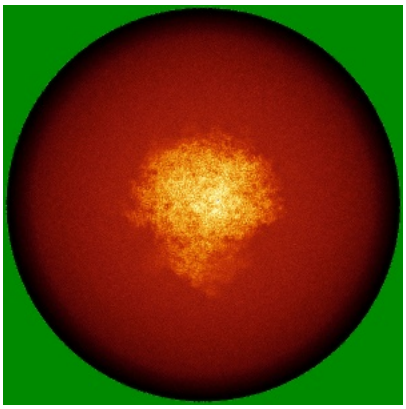
6.4.1 Primary map



X

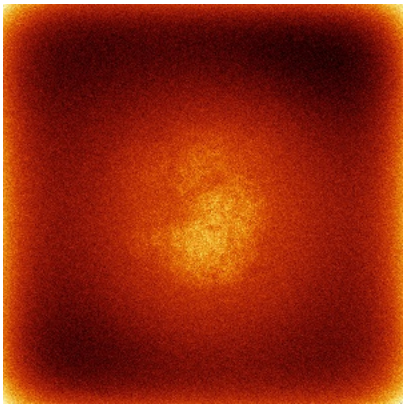


Y

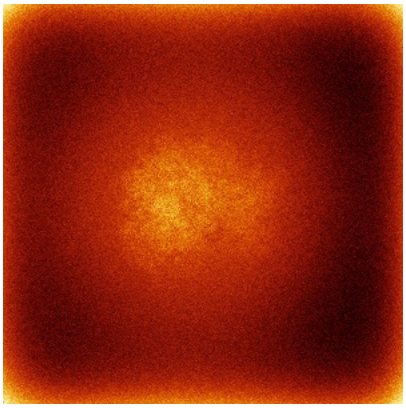


Z

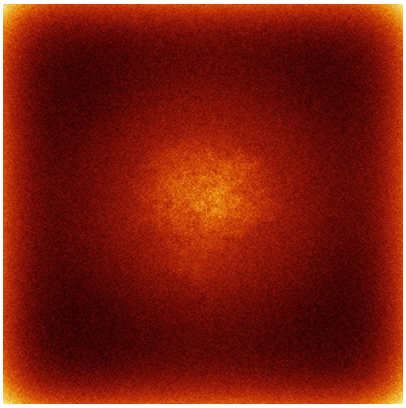
6.4.2 Raw map



X



Y

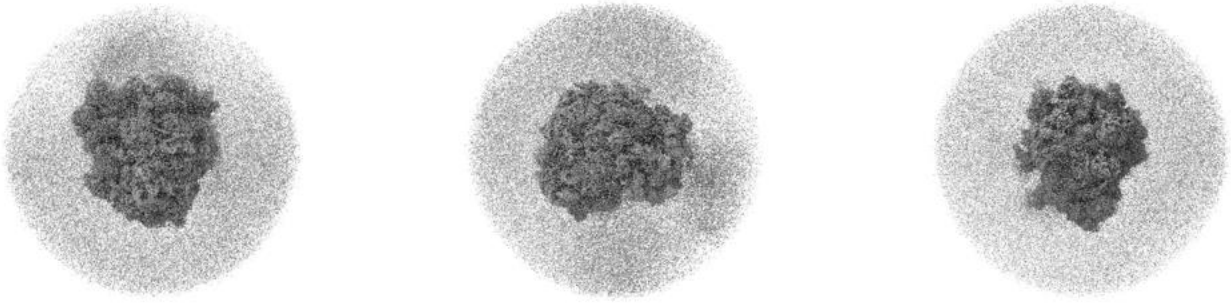


Z

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)

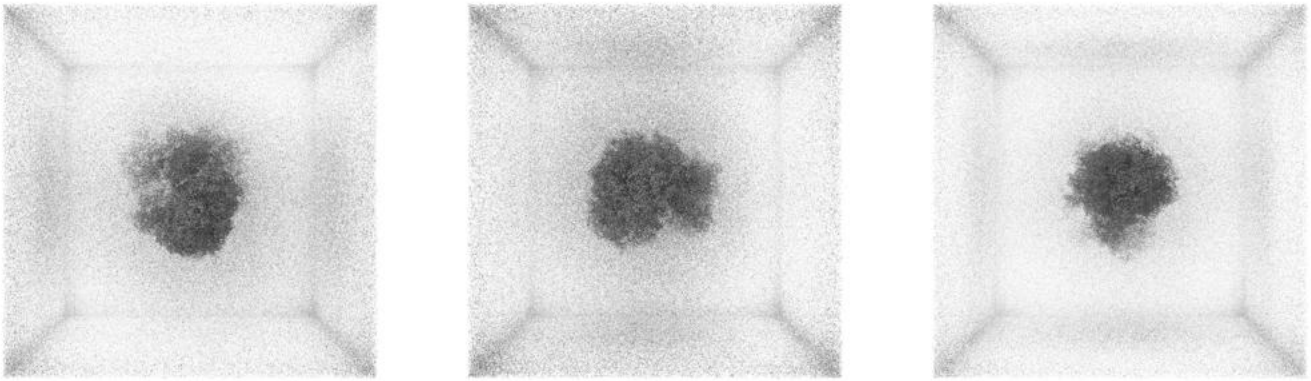
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. 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.

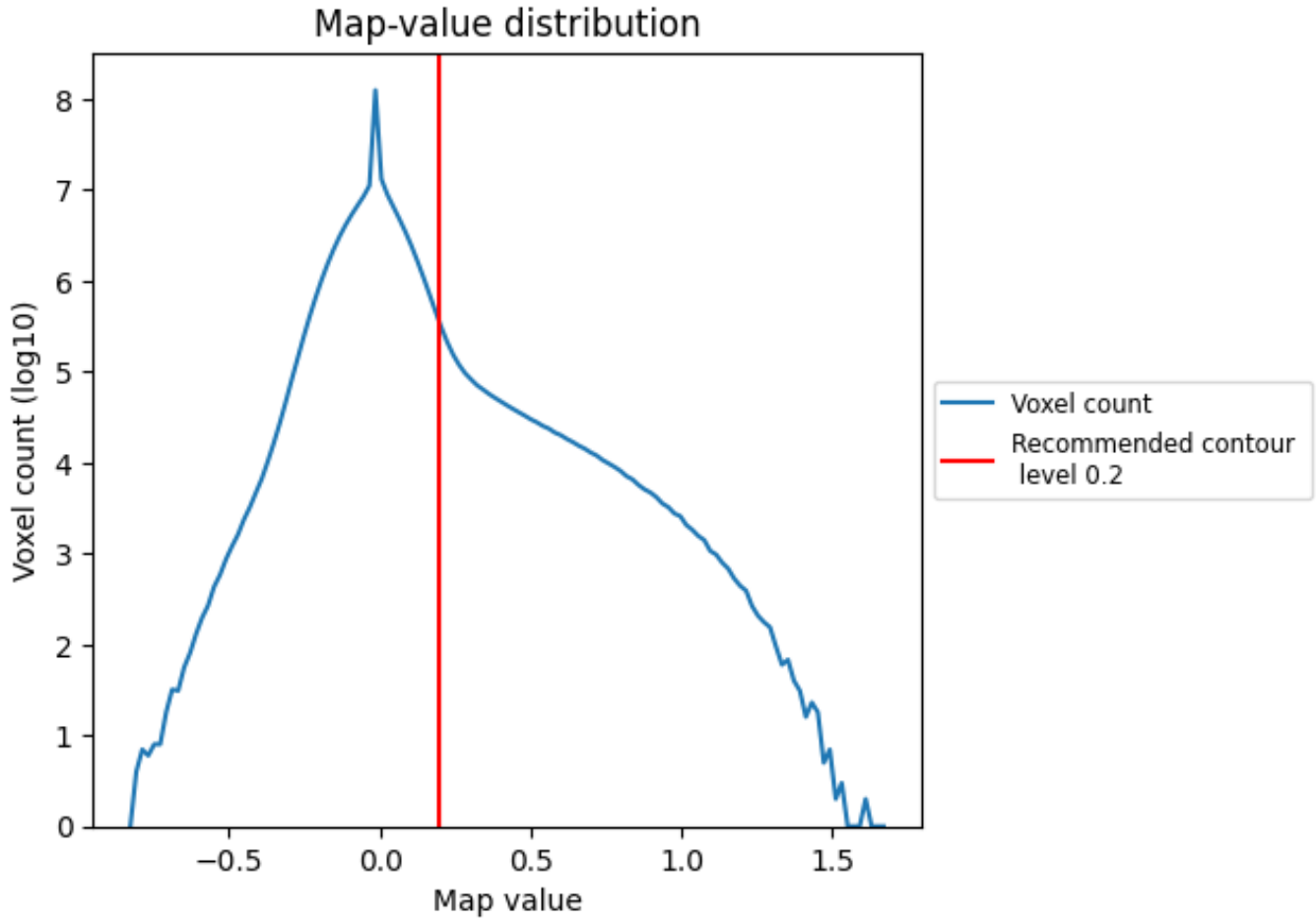
6.6 Mask visualisation (i)

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

7 Map analysis

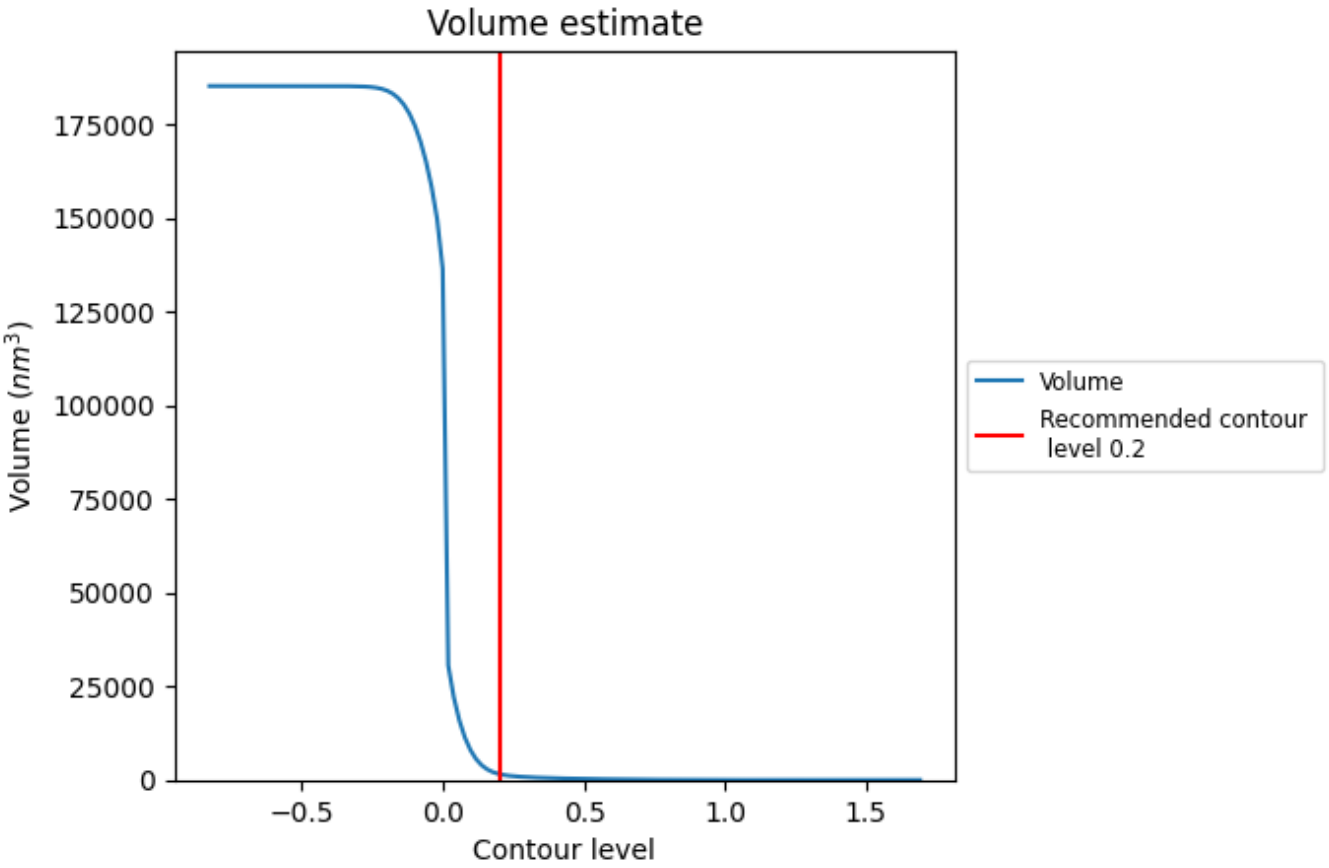
This section contains the results of statistical analysis of the map.

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.

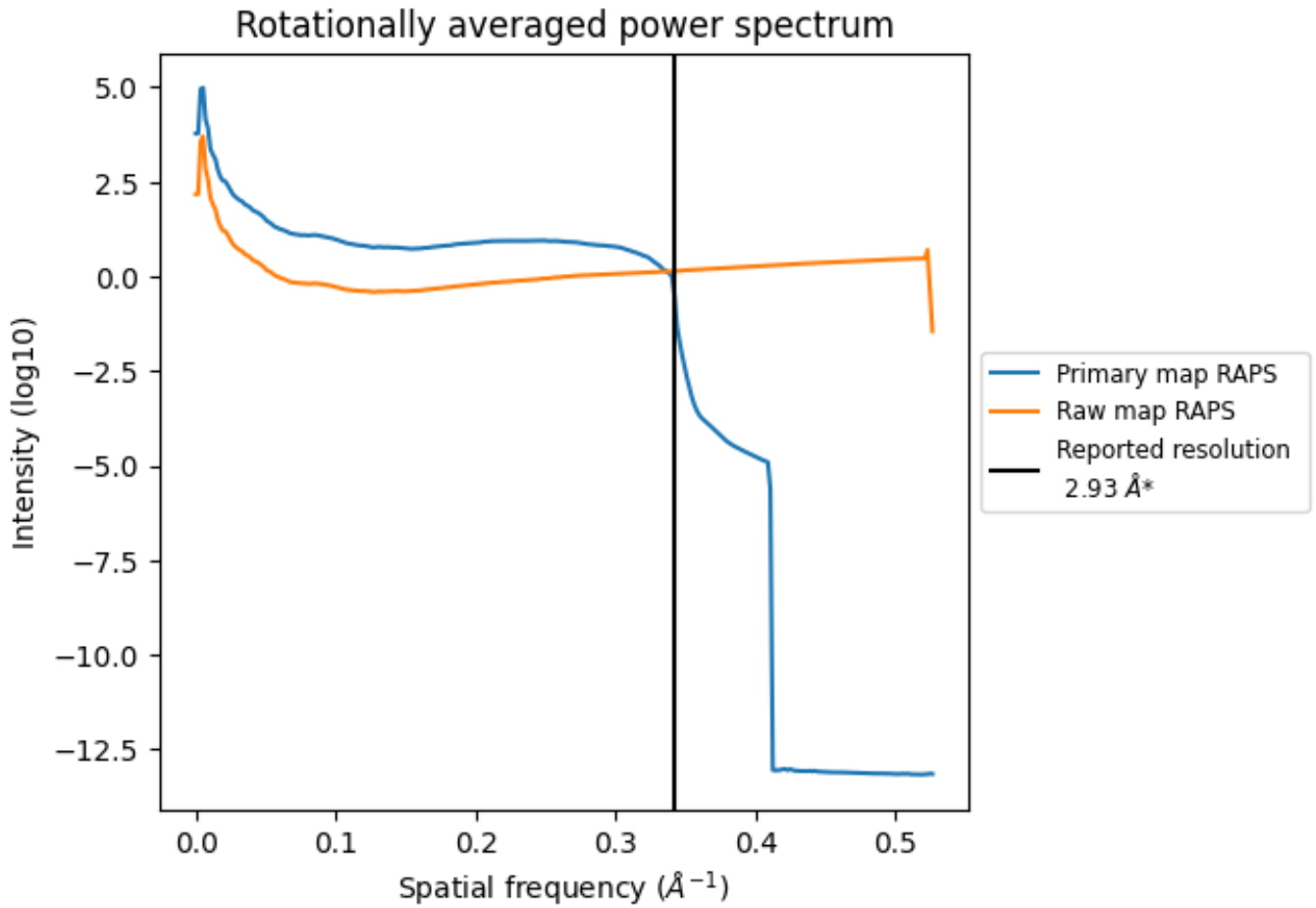
7.2 Volume estimate



The volume at the recommended contour level is 1582 nm^3; this corresponds to an approximate mass of 1429 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)

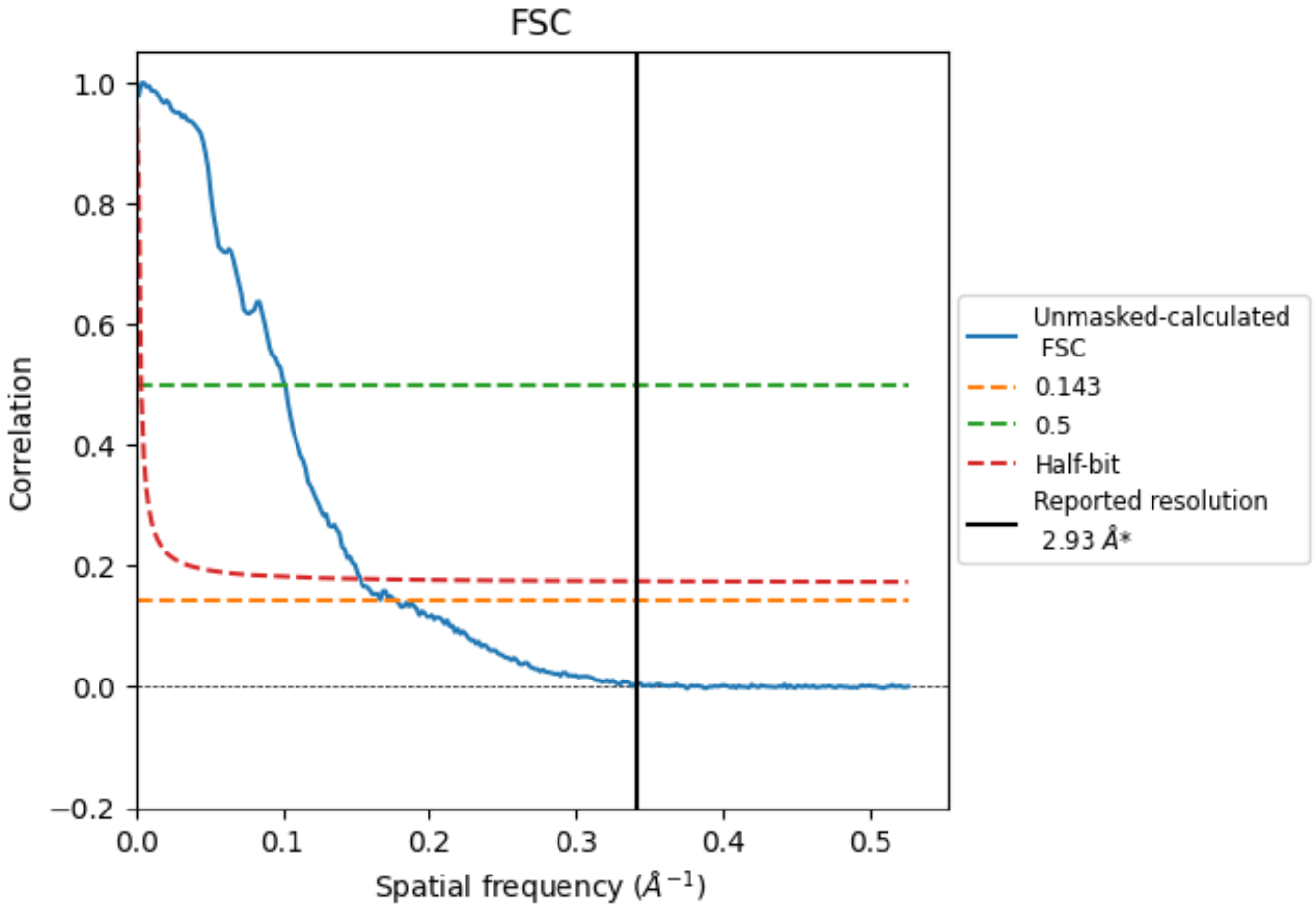


*Reported resolution corresponds to spatial frequency of 0.341 $Å^{-1}$

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 0.341 Å^{-1}

8.2 Resolution estimates (i)

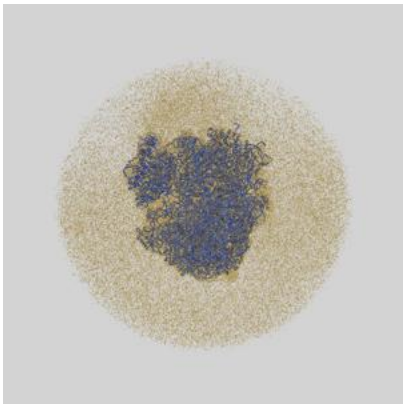
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.93	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.63	9.89	6.54

*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 5.63 differs from the reported value 2.93 by more than 10 %

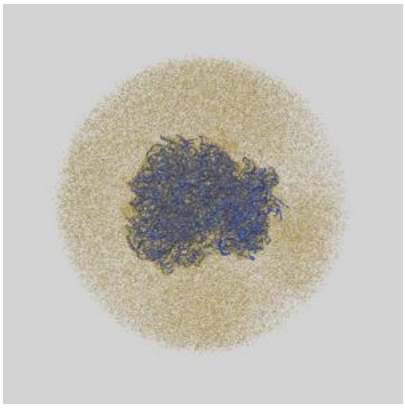
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-68778 and PDB model 22YP. Per-residue inclusion information can be found in section 3 on page 19.

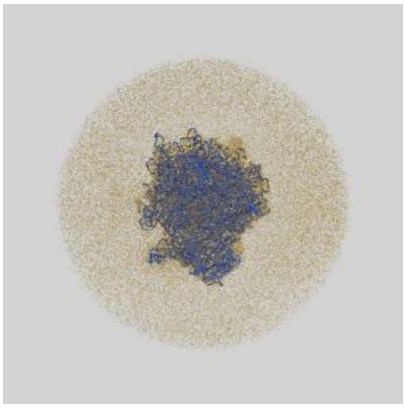
9.1 Map-model overlay



X



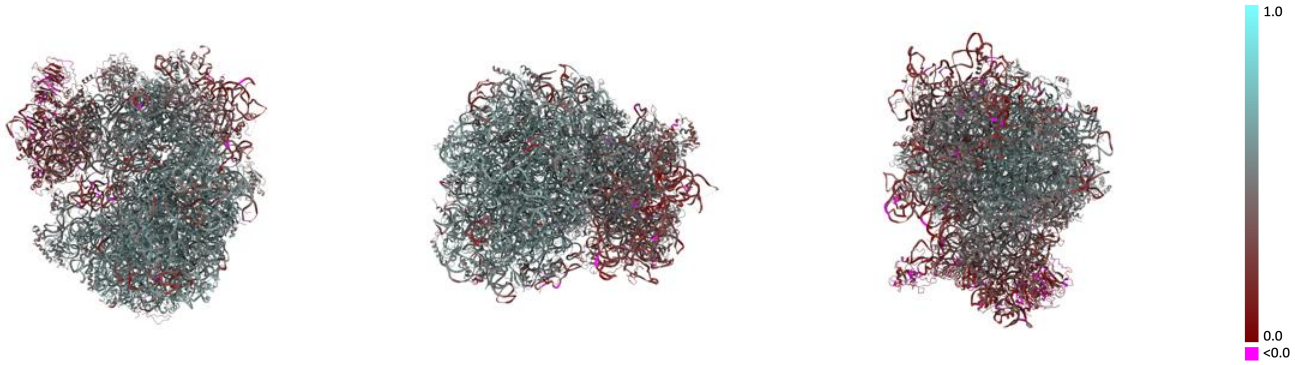
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2 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.

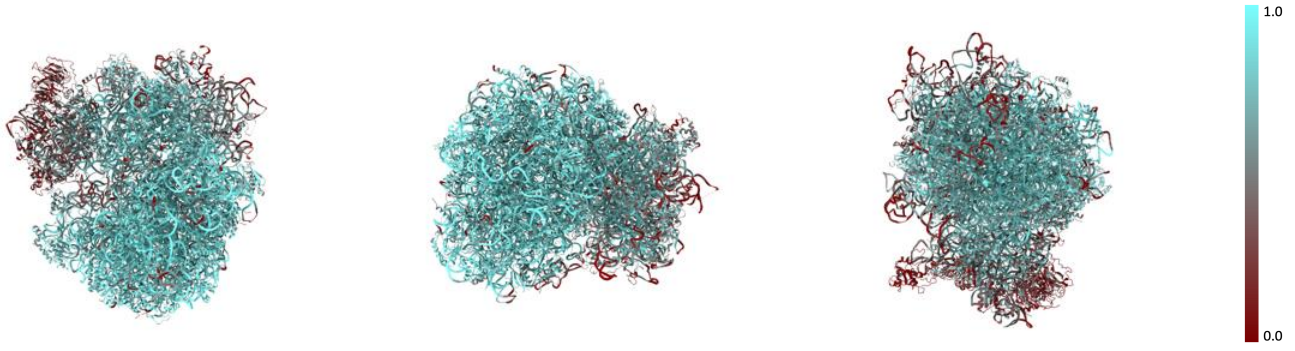
9.2 Q-score mapped to coordinate model (i)



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.

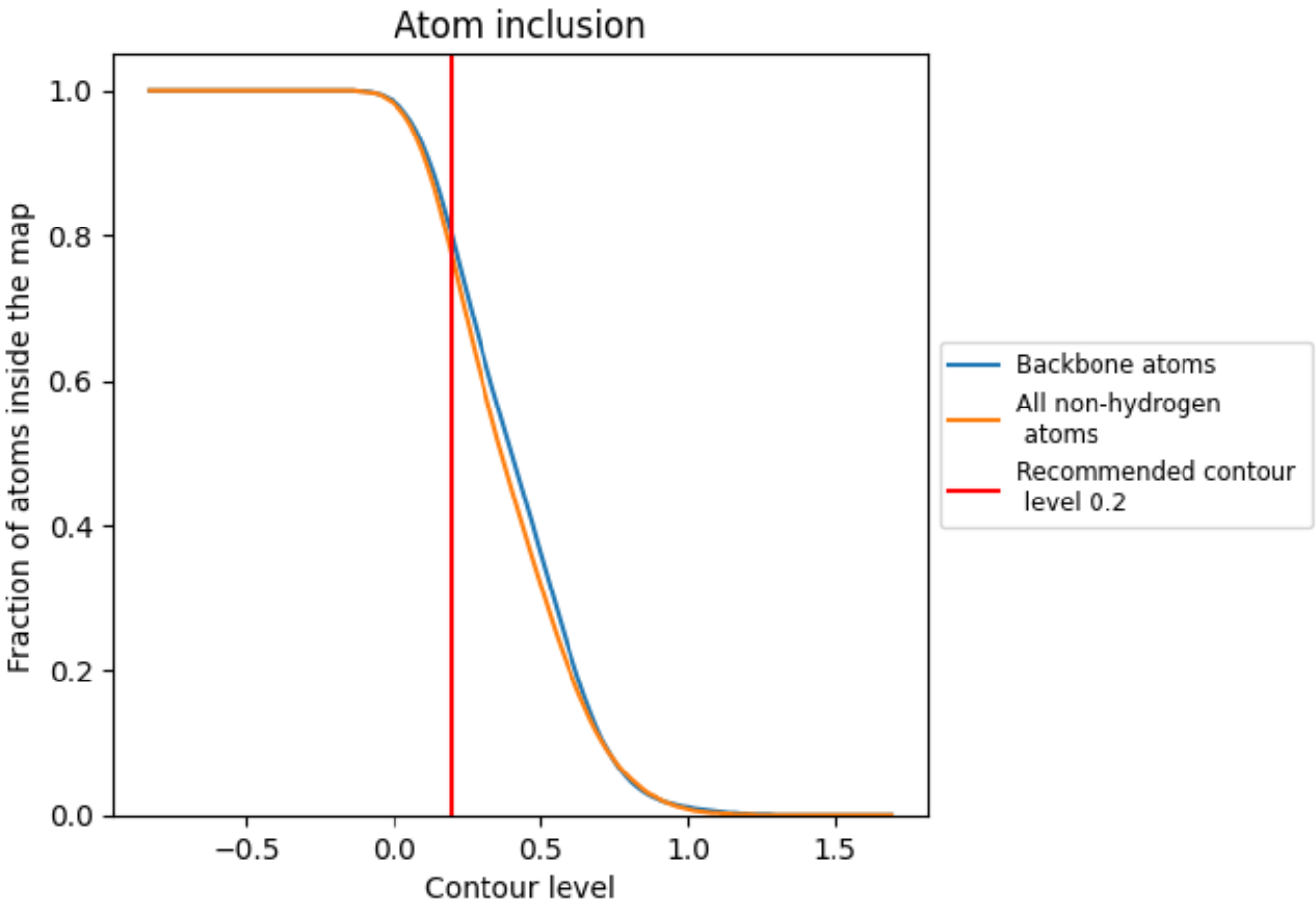
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.2).

9.4 Atom inclusion (i)



At the recommended contour level, 80% of all backbone atoms, 77% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7700	0.4710
Bb	0.6950	0.3040
Cc	0.6610	0.3260
LA	0.8910	0.5270
LB	0.9130	0.5140
LC	0.9170	0.5460
LD	0.8710	0.5900
LE	0.8800	0.5710
LF	0.8710	0.5620
LG	0.7760	0.4970
LH	0.7990	0.5160
LI	0.8650	0.5650
LJ	0.8200	0.5350
LK	0.8170	0.5420
LL	0.7970	0.5270
LM	0.7130	0.4570
LN	0.8600	0.5490
LO	0.8470	0.5360
LP	0.8990	0.5880
LQ	0.8710	0.5620
LR	0.8560	0.5640
LS	0.9010	0.5850
LT	0.7780	0.5160
LU	0.8560	0.5640
LV	0.8630	0.5610
LW	0.7520	0.4710
LX	0.8560	0.5700
LY	0.8810	0.5710
LZ	0.8130	0.5520
La	0.8730	0.5650
Lb	0.8290	0.5430
Lc	0.8970	0.5830
Ld	0.8430	0.5410
Le	0.8300	0.5480
Lf	0.8260	0.5420



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Chain	Atom inclusion	Q-score
Lg	0.8400	0.5540
Lh	0.8980	0.5950
Li	0.8360	0.5600
Lj	0.8460	0.5430
Lk	0.8120	0.5230
Ll	0.9000	0.5890
Lm	0.6610	0.4730
Ln	0.8550	0.5770
Lo	0.8510	0.5610
Lp	0.7640	0.5450
Lq	0.8530	0.5680
Lr	0.8310	0.5750
S2	0.6860	0.3700
SA	0.4300	0.3360
SB	0.3200	0.2860
SC	0.3400	0.2700
SD	0.0900	0.1840
SE	0.3640	0.2450
SF	0.3450	0.2470
SG	0.5160	0.3650
SH	0.3790	0.2720
SI	0.3640	0.2600
SJ	0.3680	0.2930
SK	0.2040	0.2360
SL	0.3550	0.2960
SM	0.5320	0.3560
SN	0.1360	0.1850
SO	0.2540	0.2140
SP	0.6520	0.4380
SQ	0.6700	0.4650
SR	0.7550	0.5070
SS	0.6280	0.4240
ST	0.4690	0.3470
SU	0.6040	0.4310
SV	0.5920	0.3880
SW	0.5890	0.3840
SX	0.6890	0.4690
SY	0.7670	0.5030
SZ	0.7380	0.4780
Sa	0.7340	0.4940
Sb	0.8440	0.5510
Sc	0.7160	0.4770

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Chain	Atom inclusion	Q-score
Sd	0.5380	0.3570
Se	0.7920	0.5220
Sf	0.6970	0.4510
Sg	0.5910	0.3940
mR	0.8640	0.5110