wwPDB EM Validation Summary Report

Oct 28, 2026 – 01:22 AM JST

PDB ID	:	23AR / pdb_000023ar
EMDB ID	:	EMD-68804
Title	:	Rotated 80S with A/P-P/E tRNA
Authors	:	Wu, M.; Yuan, S.
Deposited on	:	2026-01-30
Resolution	:	2.75 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:

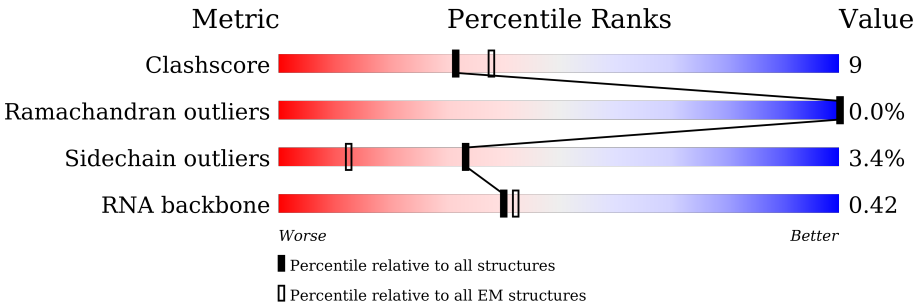
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

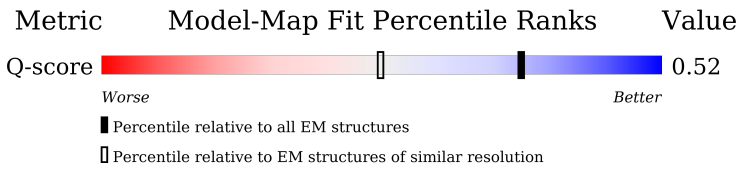
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.75 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	10570 (2.25 - 3.25)

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	49% 38% 6% 7%
2	LB	121	54% 41% 5%
3	LC	158	46% 46% 8%

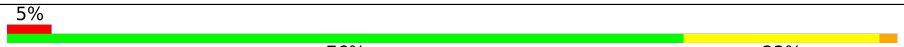
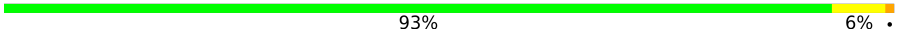
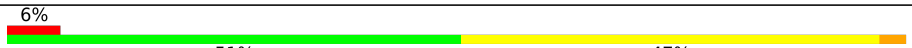
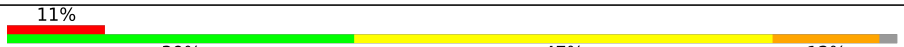
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Mol	Chain	Length	Quality of chain
4	LD	251	79% 20%
5	LE	386	77% 23%
6	LF	361	79% 20%
7	LG	294	78% 21%
8	LH	175	6% 77% 18% 5%
9	LI	222	81% 18%
10	LJ	233	76% 23%
11	LK	191	76% 23%
12	LL	218	78% 22%
13	LM	169	64% 34%
14	LN	193	79% 21%
15	LO	136	78% 21%
16	LP	203	76% 23%
17	LQ	197	75% 25%
18	LR	183	79% 21%
19	LS	185	77% 23%
20	LT	188	8% 82% 18%
21	LU	171	75% 23%
22	LV	159	77% 22%
23	LW	100	64% 30% 6%
24	LX	136	82% 18%
25	LY	65	72% 28%
26	LZ	121	80% 19%
27	La	125	78% 22%
28	Lb	135	73% 27%

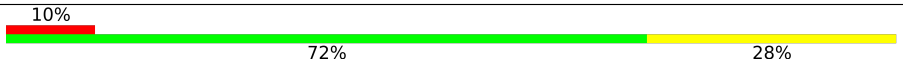
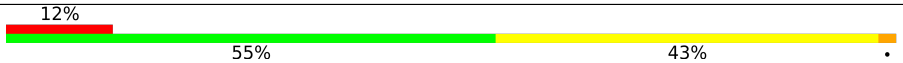
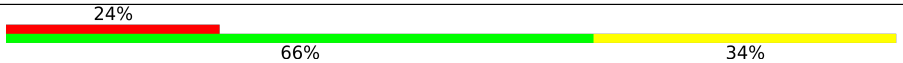
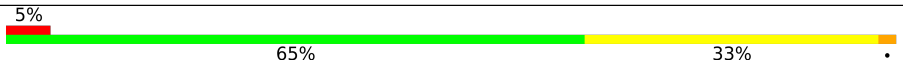
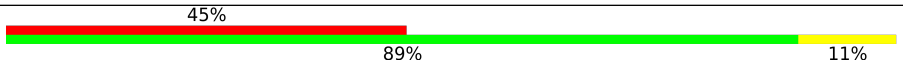
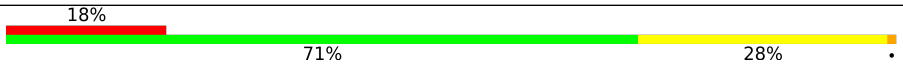
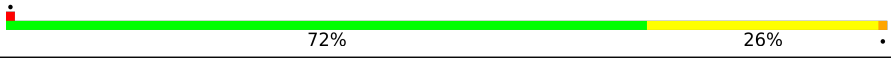
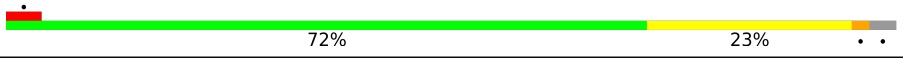
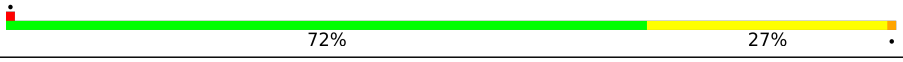
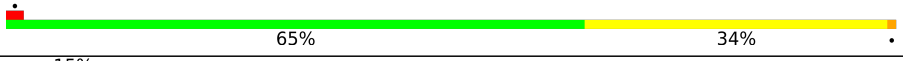
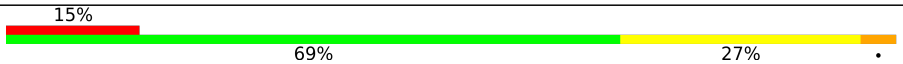
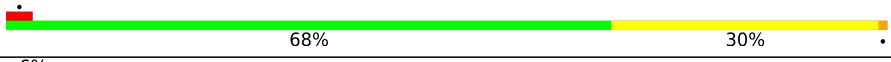
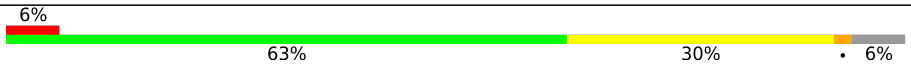
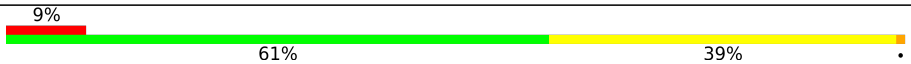
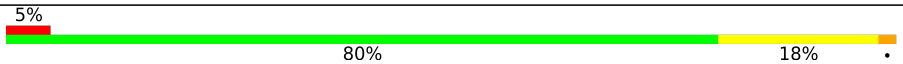
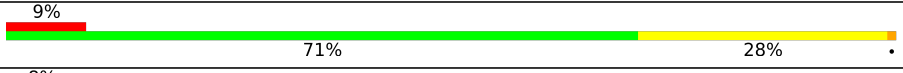
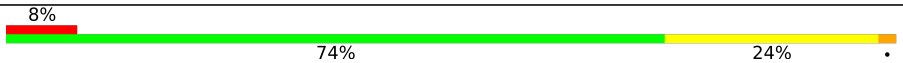
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Mol	Chain	Length	Quality of chain
29	Lc	148	
30	Ld	58	
31	Le	96	
32	Lf	109	
33	Lg	127	
34	Lh	106	
35	Li	112	
36	Lj	119	
37	Lk	99	
38	Ll	81	
39	Lm	77	
40	Ln	50	
41	Lo	52	
42	Lp	25	
43	Lq	103	
44	Lr	91	
45	mR	11	
46	Cc	77	
47	S2	1800	
48	SA	222	
49	SB	206	
50	SC	92	
51	SD	121	
52	SE	117	
53	SF	141	

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Mol	Chain	Length	Quality of chain
54	SG	125	
55	SH	145	
56	SI	143	
57	SJ	100	
58	SK	82	
59	SL	63	
60	SM	53	
61	SN	73	
62	SO	312	
63	SP	206	
64	SQ	232	
65	SR	216	
66	SS	258	
67	ST	228	
68	SU	184	
69	SV	198	
70	SW	184	
71	SX	142	
72	SY	150	
73	SZ	127	
74	Sa	87	
75	Sb	129	
76	Sc	144	
77	Sd	134	
78	Se	97	

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Mol	Chain	Length	Quality of chain
79	Sf	81	
80	Sg	57	
81	Bb	76	

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 (3184-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	C	N	O	0	0
			1080	701	199	180		

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

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

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

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

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

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

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

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

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

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

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

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

- 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 (77-MER).

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

- Molecule 47 is a RNA chain called RNA (1800-MER).

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

- Molecule 48 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 49 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 50 is a protein called Small ribosomal subunit protein eS10A.

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

- Molecule 51 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 52 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 53 is a protein called Small ribosomal subunit protein uS9A.

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

- Molecule 54 is a protein called Small ribosomal subunit protein eS17B.

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

- Molecule 55 is a protein called Small ribosomal subunit protein uS13A.

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

- Molecule 56 is a protein called Small ribosomal subunit protein eS19A.

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

- Molecule 57 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 58 is a protein called Small ribosomal subunit protein eS25A.

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

- Molecule 59 is a protein called Small ribosomal subunit protein eS28A.

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

- Molecule 60 is a protein called Small ribosomal subunit protein uS14A.

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

- Molecule 61 is a protein called Small ribosomal subunit protein eS31.

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

- Molecule 62 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 63 is a protein called Small ribosomal subunit protein uS2A.

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

- Molecule 64 is a protein called Small ribosomal subunit protein eS1A.

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

- Molecule 65 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 66 is a protein called Small ribosomal subunit protein eS4A.

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

- Molecule 67 is a protein called Small ribosomal subunit protein eS6A.

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

- Molecule 68 is a protein called Small ribosomal subunit protein eS7A.

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

- Molecule 69 is a protein called Small ribosomal subunit protein eS8A.

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

- Molecule 70 is a protein called Small ribosomal subunit protein uS4A.

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

- Molecule 71 is a protein called Small ribosomal subunit protein uS17A.

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

- Molecule 72 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 73 is a protein called Small ribosomal subunit protein uS11B.

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

- Molecule 74 is a protein called Small ribosomal subunit protein eS21A.

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

- Molecule 75 is a protein called Small ribosomal subunit protein uS8A.

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

- Molecule 76 is a protein called Small ribosomal subunit protein uS12A.

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS24A.

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

- Molecule 78 is a protein called Small ribosomal subunit protein eS26B.

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

- Molecule 79 is a protein called Small ribosomal subunit protein eS27A.

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

- Molecule 80 is a protein called Small ribosomal subunit protein eS30A.

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

- Molecule 81 is a RNA chain called RNA (76-MER).

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

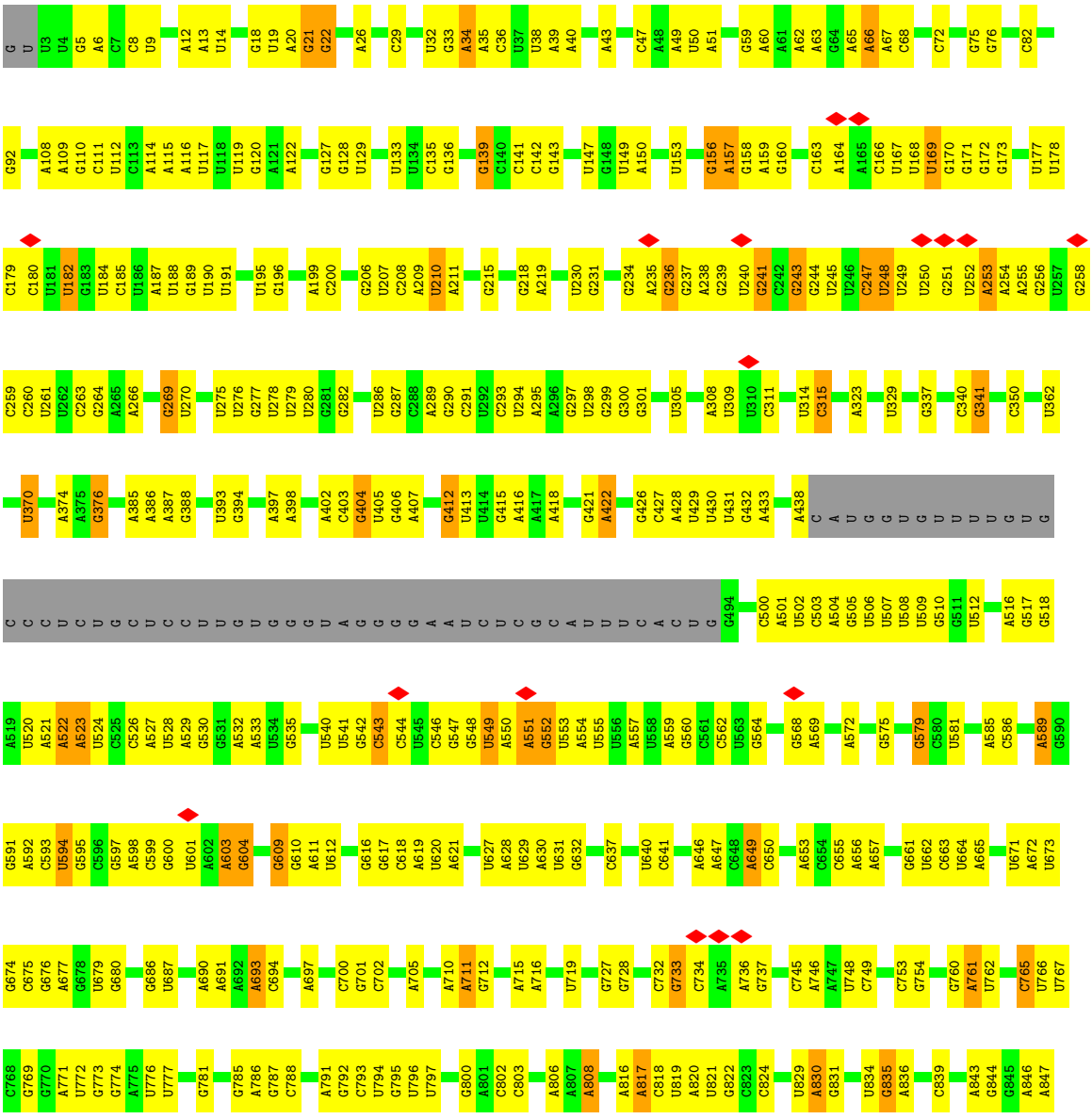
3 Residue-property plots (i)

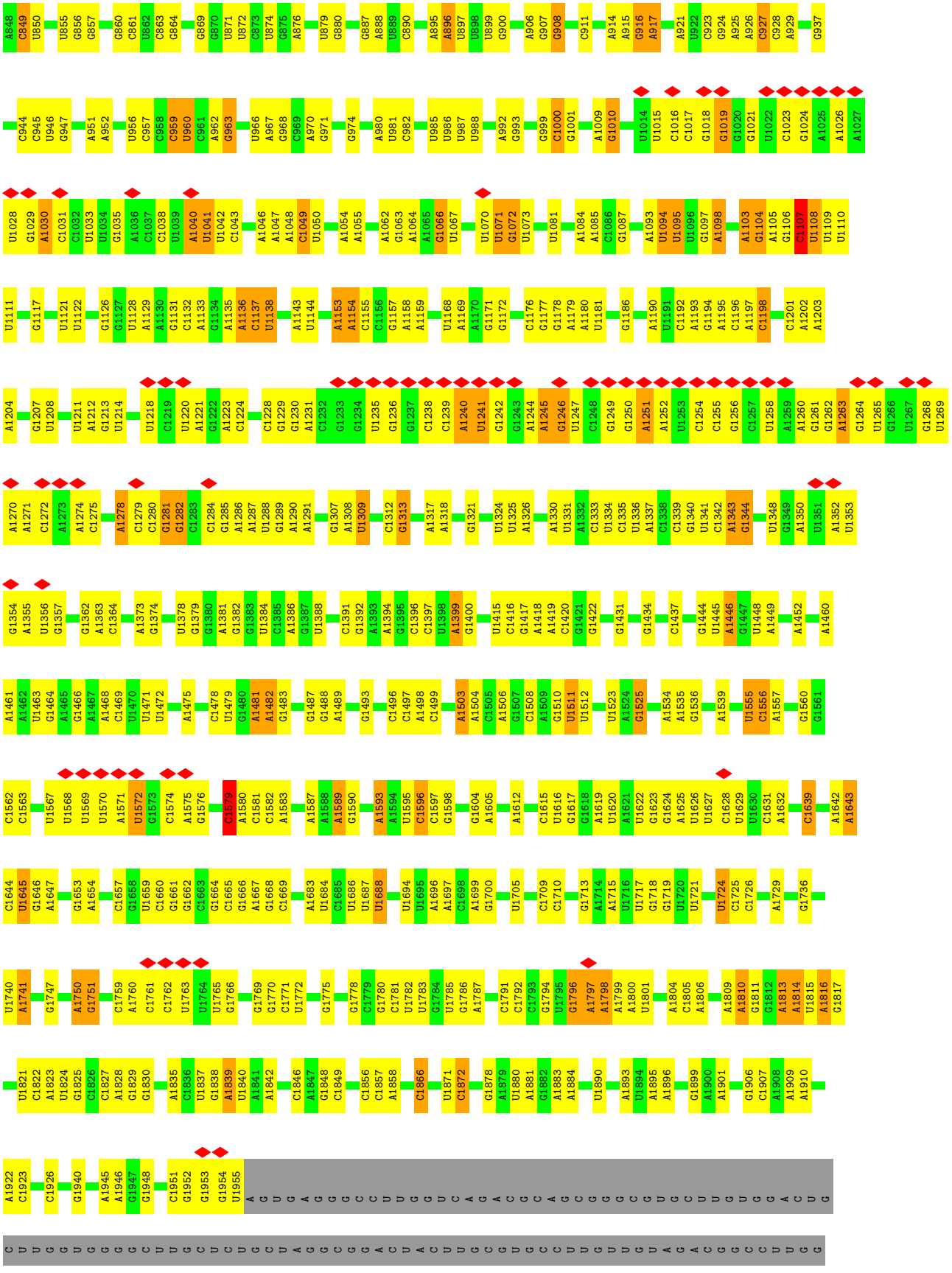
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

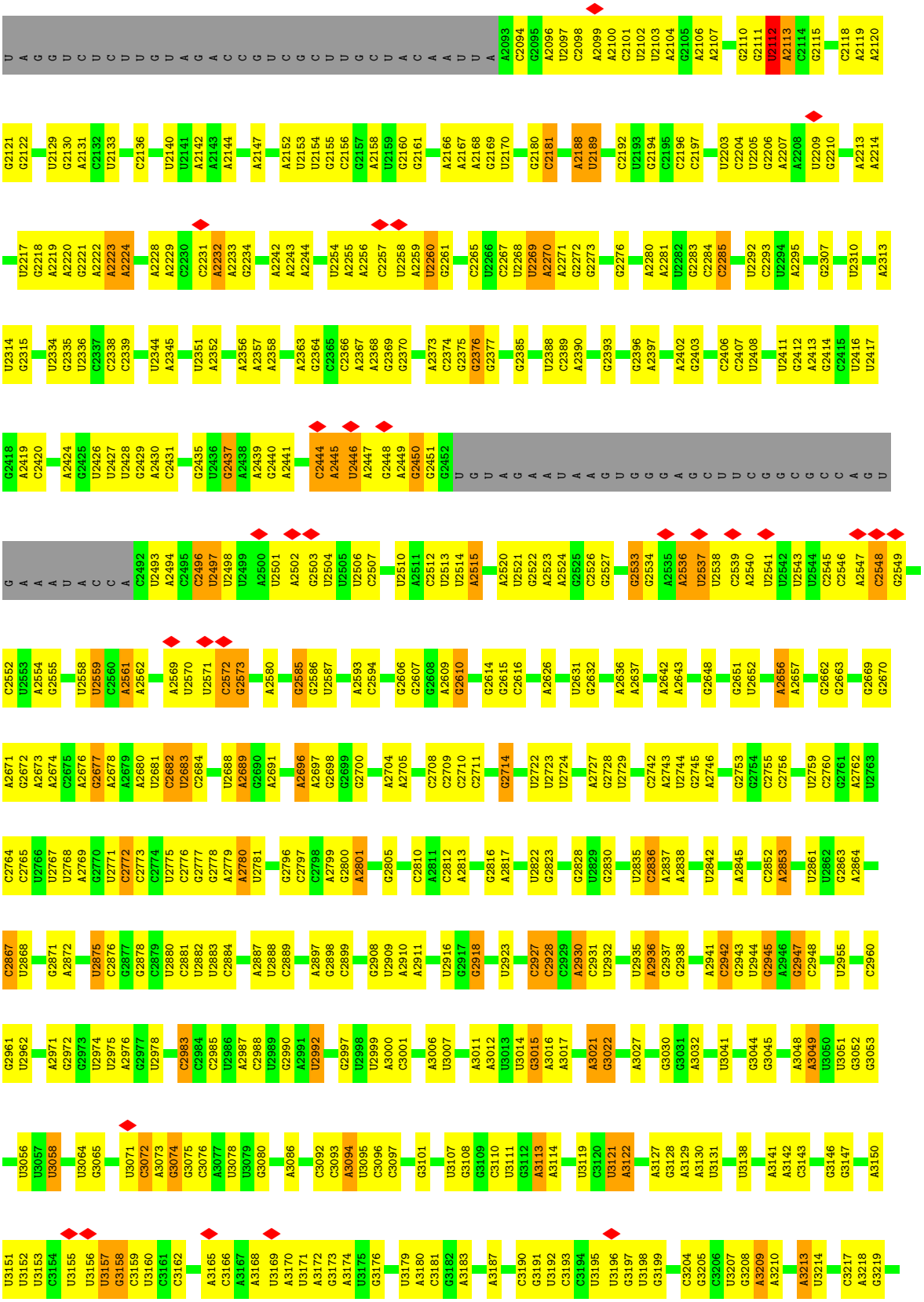
- Molecule 1: RNA (3184-MER)

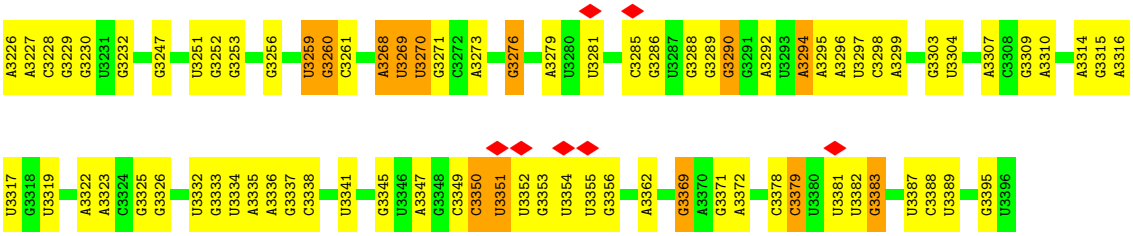
Chain LA:






A848 C849 U850 U855 G856 G857 G860 C861 U862 C863 G864 G869 G870 U871 U872 C873 U874 G875 A876 U879 G880 G887 A888 U889 C890 A895 A896 U897 U898 U899 G900 A906 G907 G908 C911 A914 A915 G916 A917 A921 U922 C923 G924 A925 A926 C927 C928 A929 G937
C944 C945 U946 G947 A951 A952 U956 C957 C958 C959 U960 C961 A962 G963 U966 A967 G968 C969 A970 G971 G974 A980 U981 C982 U985 U986 U987 U988 A992 G993 G999 C1000 G1001 A1009 G1010 U1014 U1015 C1016 C1017 G1018 G1019 G1020 G1021 U1022 C1023 G1024 A1025 A1026 A1027
U1028 G1029 A1030 C1031 C1032 U1033 U1034 G1035 A1036 C1037 C1038 U1039 A1040 U1041 U1042 C1043 A1046 A1047 A1048 C1049 U1050 A1054 A1055 A1062 G1063 A1064 A1065 G1066 U1067 U1070 U1071 G1072 U1073 U1081 A1084 A1085 C1086 G1087 A1093 U1094 U1095 U1096 G1097 A1098 A1103 G1104 A1105 G1106 C1107 U1108 U1109 U1110
U1111 G1117 U1121 U1122 G1126 G1127 U1128 A1129 A1130 G1131 C1132 A1133 G1134 A1135 A1136 C1137 U1138 A1143 U1144 A1153 A1154 C1155 C1156 G1157 A1158 A1159 U1168 A1169 A1170 G1171 G1172 C1176 G1177 G1178 A1179 A1180 U1181 G1186 A1190 U1191 C1192 A1193 G1194 A1195 C1196 A1197 C1198 C1201 A1202 A1203
A1204 G1207 U1208 U1211 A1212 G1213 U1214 U1218 C1219 U1220 A1221 G1222 A1223 C1224 C1228 G1229 G1230 A1231 C1232 G1233 G1234 U1235 G1236 G1237 C1238 C1239 A1240 U1241 G1242 G1243 A1244 A1245 G1246 U1247 C1248 G1249 G1250 A1251 A1252 U1253 C1254 C1255 G1256 C1257 U1258 A1259 A1260 G1261 G1262 A1263 G1264 U1265 G1266 U1267 G1268 U1269
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A1461 A1462 U1463 G1464 A1465 G1466 A1467 A1468 C1469 U1470 U1471 U1472 A1475 C1478 U1479 G1480 A1481 A1482 G1483 G1487 G1488 A1489 G1493 C1496 C1497 A1498 C1499 A1503 A1504 C1505 A1506 G1507 C1508 A1509 G1510 U1511 U1512 U1523 A1524 G1525 A1534 A1535 G1536 A1539 U1555 C1556 A1557 G1560 G1561
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C1644 U1645 G1646 A1647 G1653 A1654 C1657 G1658 U1659 C1660 G1661 G1662 C1663 G1664 C1665 G1666 A1667 G1668 C1669 A1683 U1684 C1685 U1686 U1687 U1688 U1694 U1695 A1696 A1697 C1698 A1699 G1700 U1705 C1709 C1710 G1713 A1714 A1715 U1716 U1717 G1718 G1719 U1720 U1721 U1724 C1725 C1726 A1729 G1736
U1740 A1741 G1747 A1750 G1751 C1759 A1760 C1761 C1762 U1763 U1764 U1765 G1766 G1769 G1770 C1771 U1772 G1775 G1778 C1779 G1780 C1781 U1782 U1783 G1784 U1785 G1786 A1787 C1791 C1792 C1793 G1794 U1795 G1796 A1797 A1798 A1799 A1800 U1801 A1804 C1805 A1806 A1809 A1810 G1811 G1812 A1813 A1814 U1815 A1816 G1817
U1821 C1822 A1823 U1824 G1825 C1826 C1827 A1828 G1829 G1830 A1835 C1836 U1837 G1838 A1839 U1840 A1841 A1842 C1846 A1847 G1848 C1849 C1856 C1857 A1858 C1866 U1871 C1872 G1878 A1879 U1880 A1881 G1882 A1883 A1884 U1890 A1893 U1894 A1895 A1896 G1899 A1900 A1901 G1906 C1907 A1908 A1909 A1910
A1922 C1923 C1926 G1940 A1945 A1946 G1947 G1948 C1951 G1952 G1953 G1954 U1955 A G U G A G G C C U U G C U G U G G G C U U G C U C U U G C U A A G G G C C U G U G A C U U A G G G U C A G A C U G C U G C C A G C U U G U G G U U G C U G U A G A C G U U G G C C U A C U G G



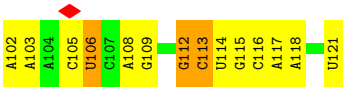


• Molecule 2: RNA (121-MER)

Chain LB:



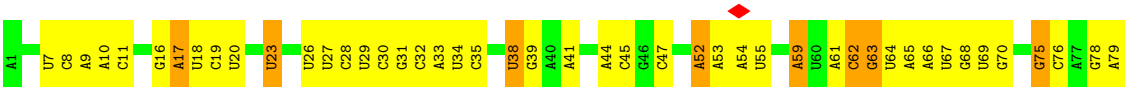


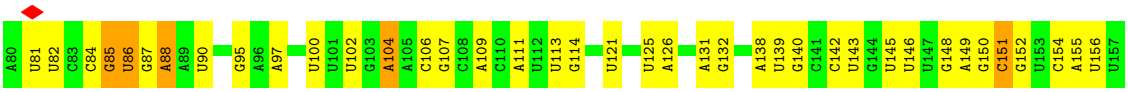


• Molecule 3: RNA (158-MER)

Chain LC:





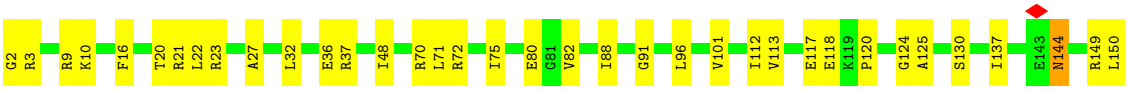


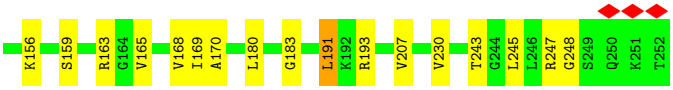


• Molecule 4: Large ribosomal subunit protein uL2A

Chain LD:



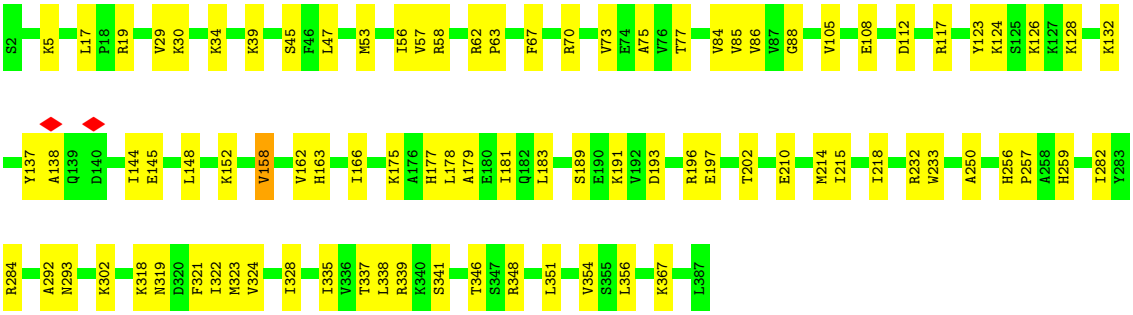




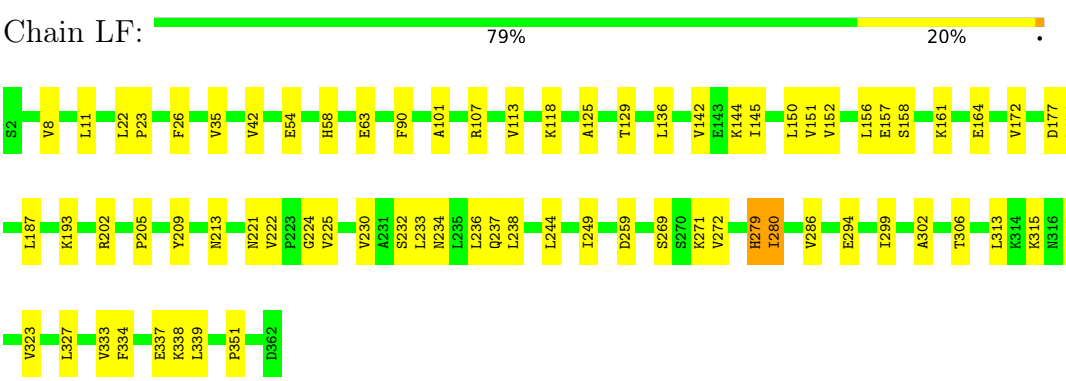
• Molecule 5: Large ribosomal subunit protein uL3

Chain LE:

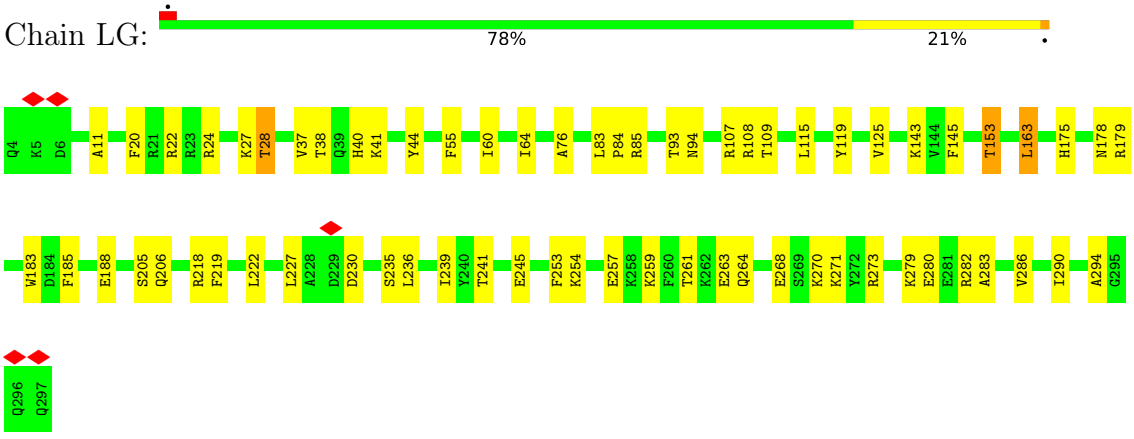




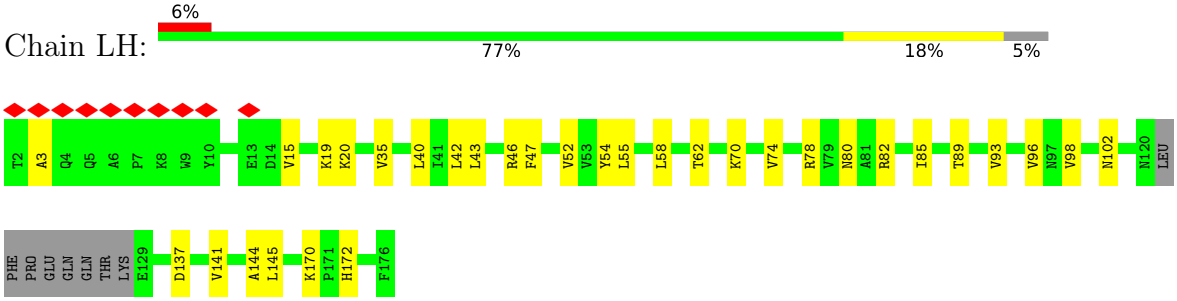
• Molecule 6: Large ribosomal subunit protein uL4A



• Molecule 7: Large ribosomal subunit protein uL18

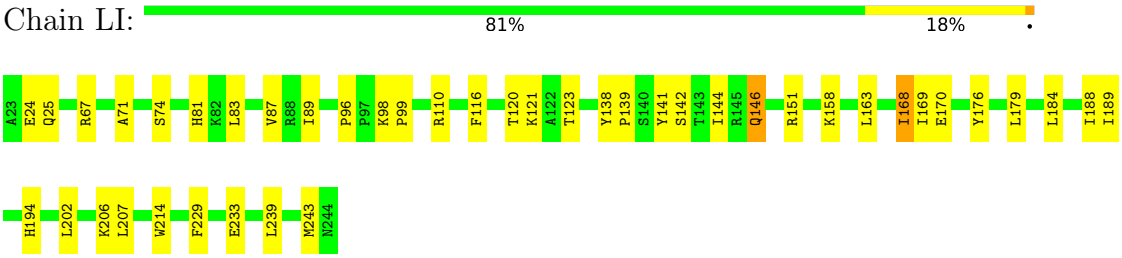


• Molecule 8: Large ribosomal subunit protein eL6B



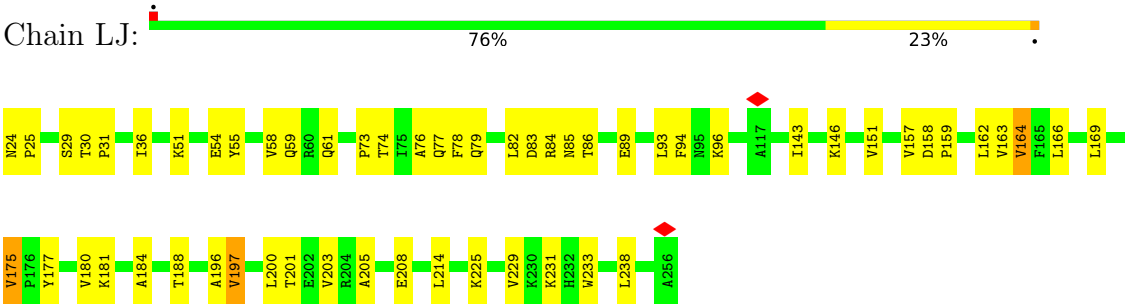
• Molecule 9: Large ribosomal subunit protein uL30A

Chain LI:



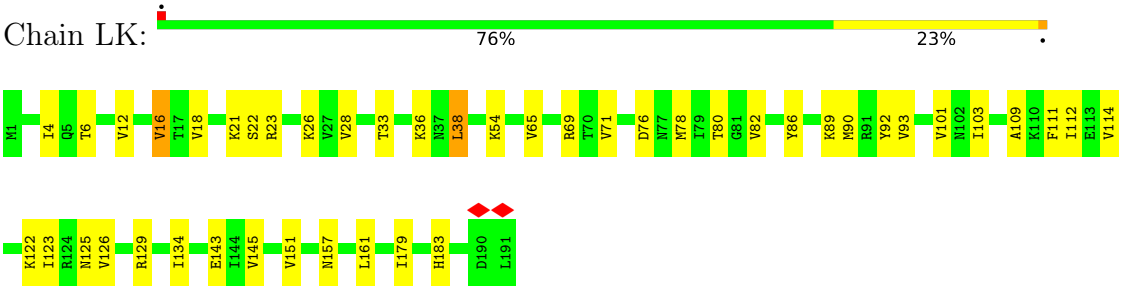
• Molecule 10: Large ribosomal subunit protein eL8A

Chain LJ:



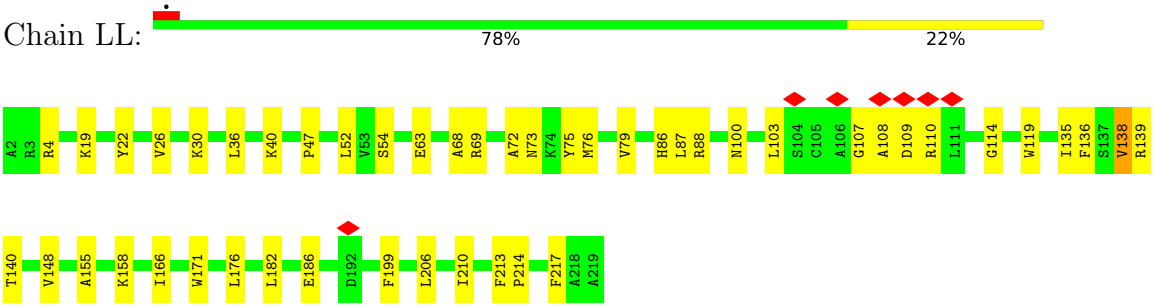
• Molecule 11: Large ribosomal subunit protein uL6A

Chain LK:



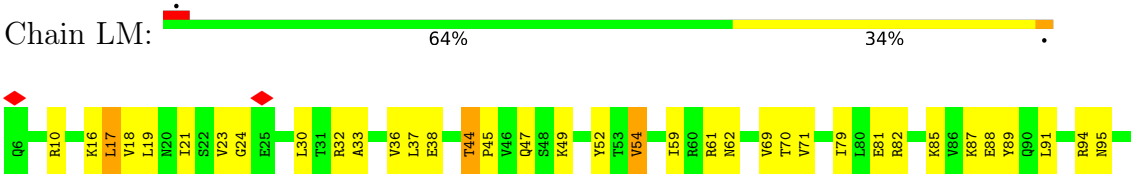
• Molecule 12: Large ribosomal subunit protein uL16

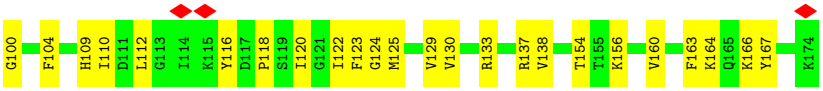
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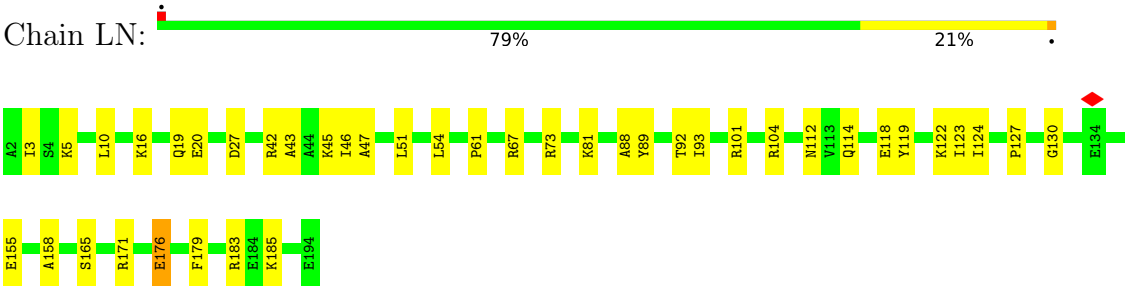
• Molecule 13: Large ribosomal subunit protein uL5B

Chain LM:

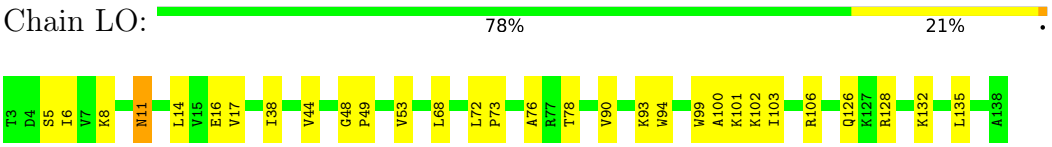




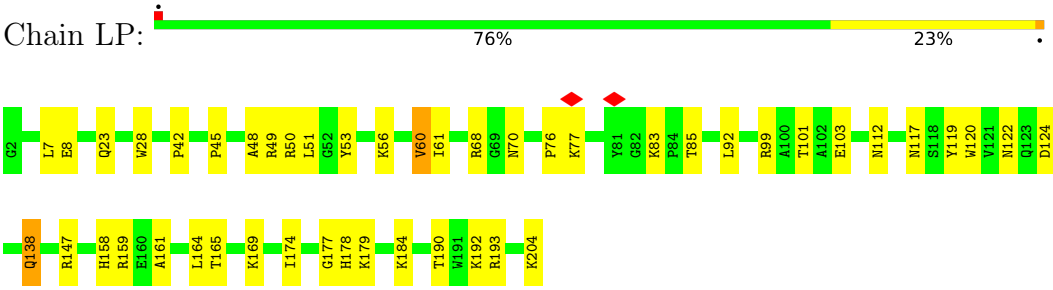
• Molecule 14: Large ribosomal subunit protein eL13A



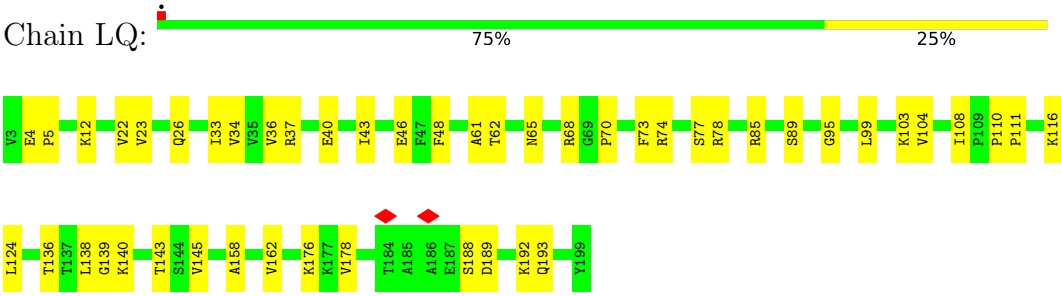
• Molecule 15: Large ribosomal subunit protein eL14A



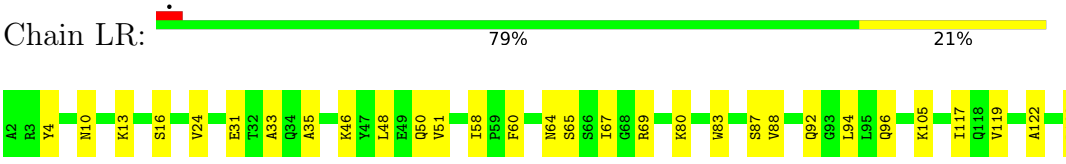
• Molecule 16: Large ribosomal subunit protein eL15A

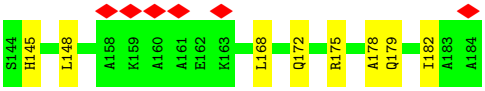


• Molecule 17: Large ribosomal subunit protein uL13A



• Molecule 18: Large ribosomal subunit protein uL22A





• Molecule 19: Large ribosomal subunit protein eL18A

Chain LS:



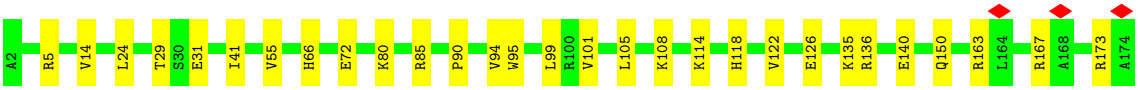


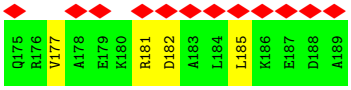


• Molecule 20: Large ribosomal subunit protein eL19A

Chain LT:



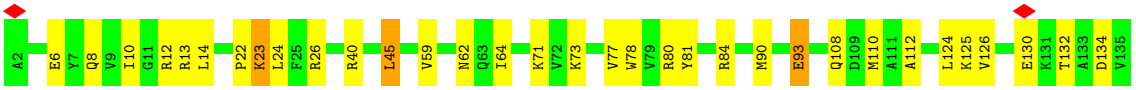


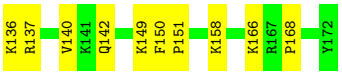


• Molecule 21: Large ribosomal subunit protein eL20A

Chain LU:





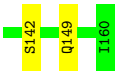


• Molecule 22: Large ribosomal subunit protein eL21A

Chain LV:



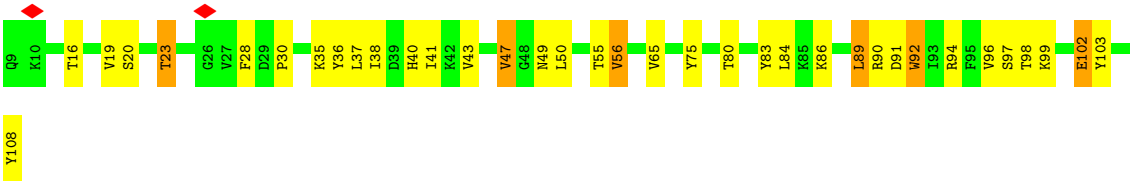




• Molecule 23: Large ribosomal subunit protein eL22A

Chain LW:

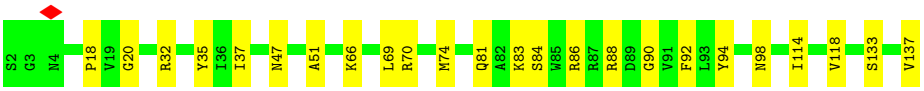




• Molecule 24: Large ribosomal subunit protein uL14A

Chain LX:

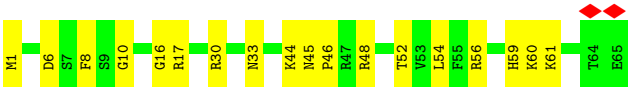




• Molecule 25: Large ribosomal subunit protein eL24A

Chain LY:

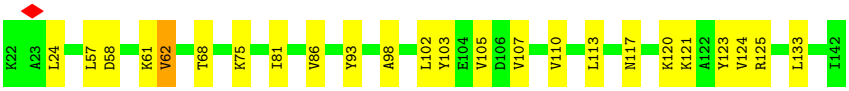




• Molecule 26: Large ribosomal subunit protein uL23

Chain LZ:

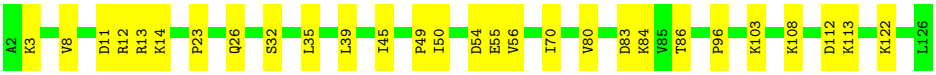




• Molecule 27: Large ribosomal subunit protein uL24A

Chain La:





• Molecule 28: Large ribosomal subunit protein eL27A

Chain Lb:

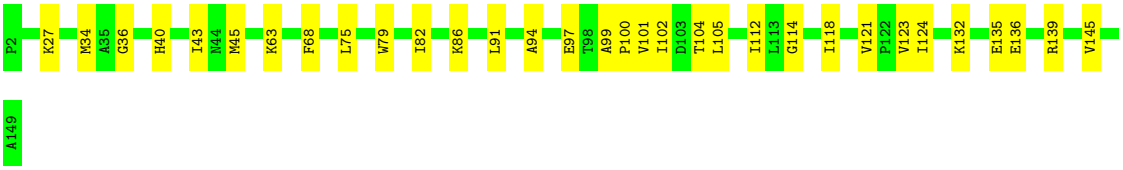




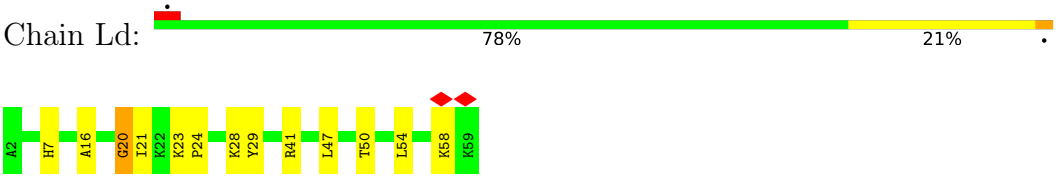
• Molecule 29: Large ribosomal subunit protein uL15

Chain Lc:

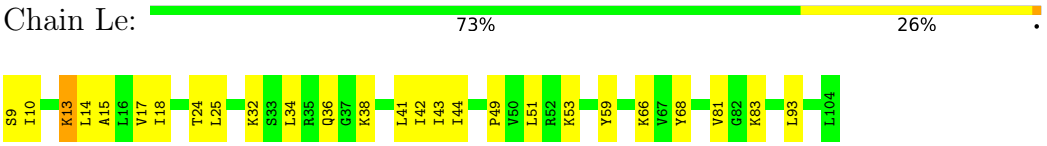




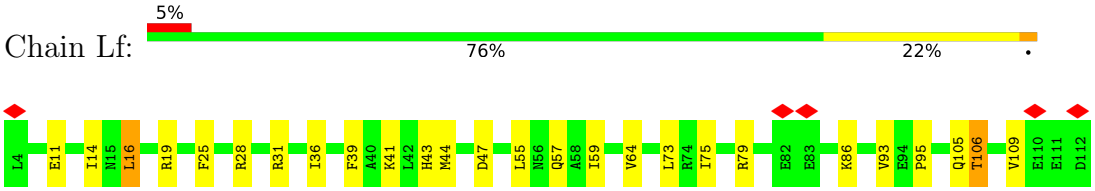
• Molecule 30: Large ribosomal subunit protein eL29



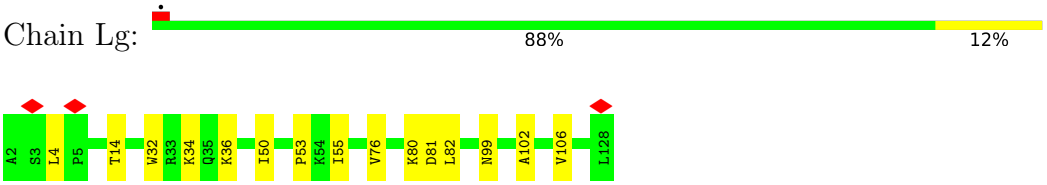
• Molecule 31: Large ribosomal subunit protein eL30



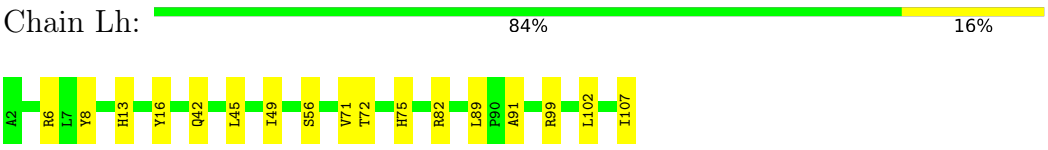
• Molecule 32: Large ribosomal subunit protein eL31A



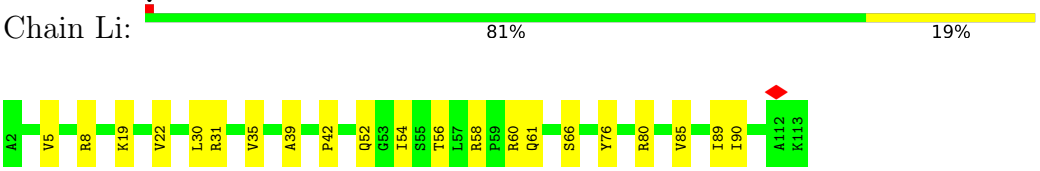
• Molecule 33: Large ribosomal subunit protein eL32



• Molecule 34: Large ribosomal subunit protein eL33A



• Molecule 35: Large ribosomal subunit protein eL34A



• Molecule 36: Large ribosomal subunit protein uL29A

Chain Lj:

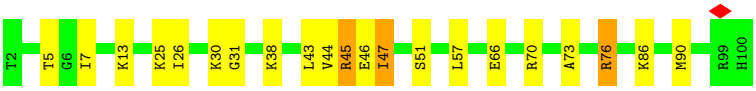




• Molecule 37: Large ribosomal subunit protein eL36A

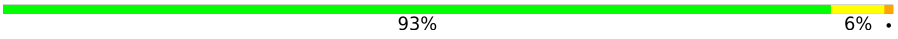
Chain Lk:

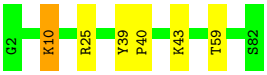




• Molecule 38: Large ribosomal subunit protein eL37A

Chain Ll:

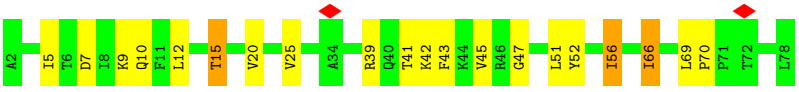




• Molecule 39: Large ribosomal subunit protein eL38

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:

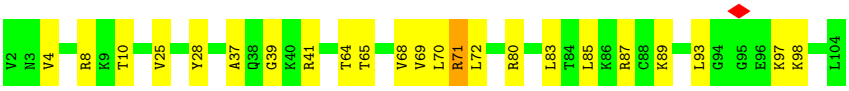




• Molecule 43: Large ribosomal subunit protein eL42A

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:

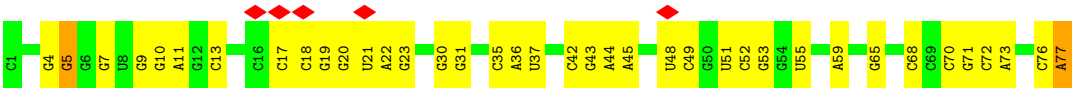


There are no outlier residues recorded for this chain.

• Molecule 46: RNA (77-MER)

Chain Cc:

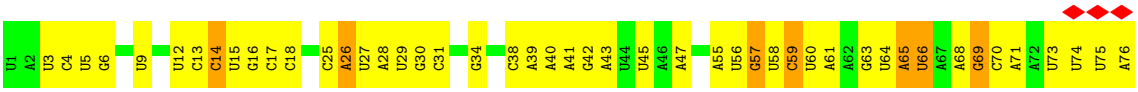


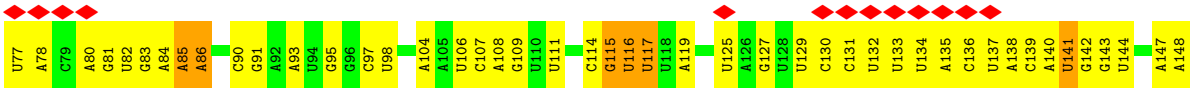


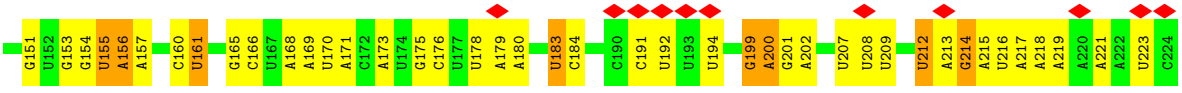
• Molecule 47: RNA (1800-MER)

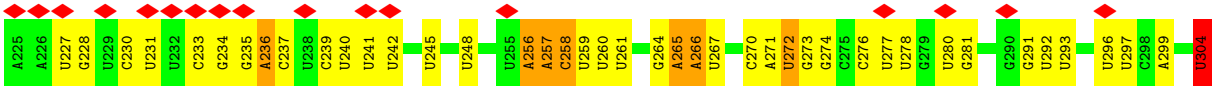
Chain S2:

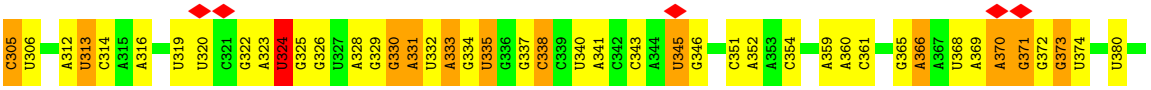


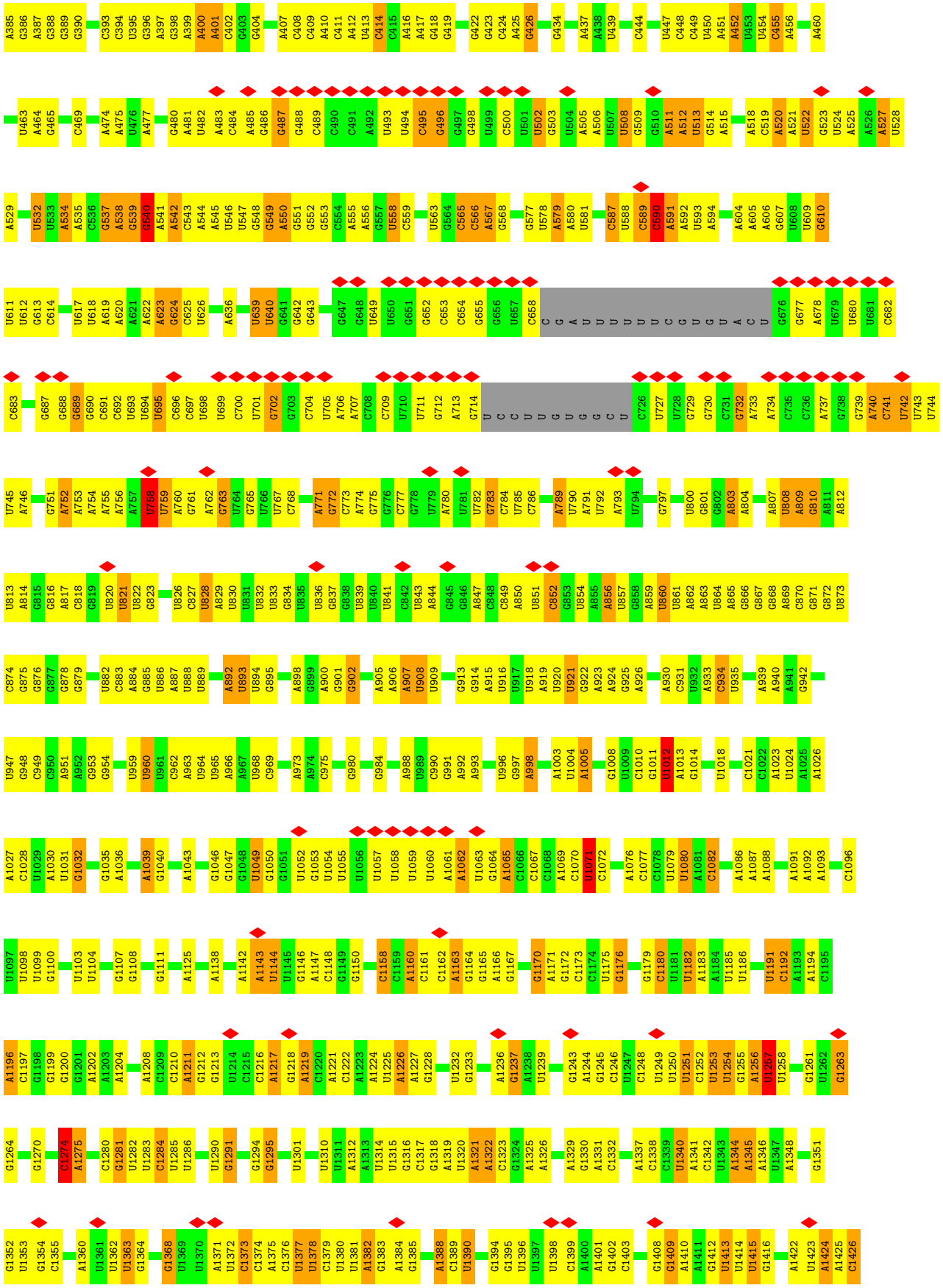


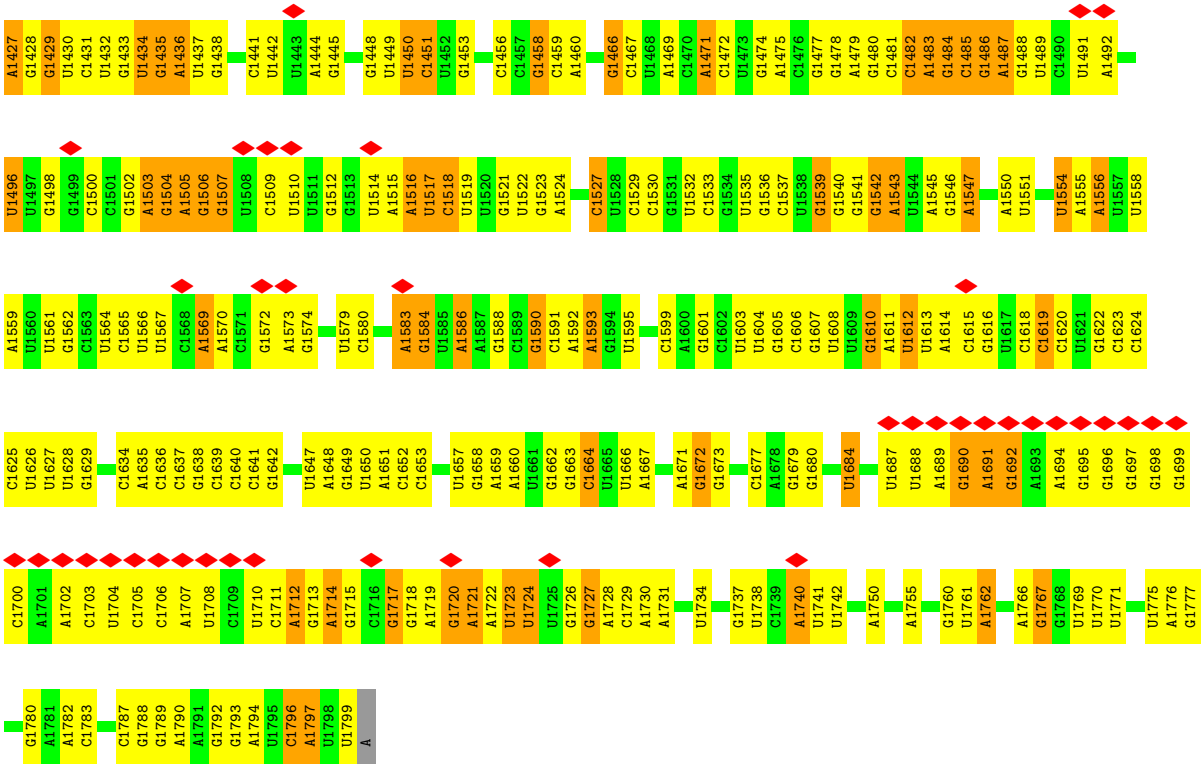








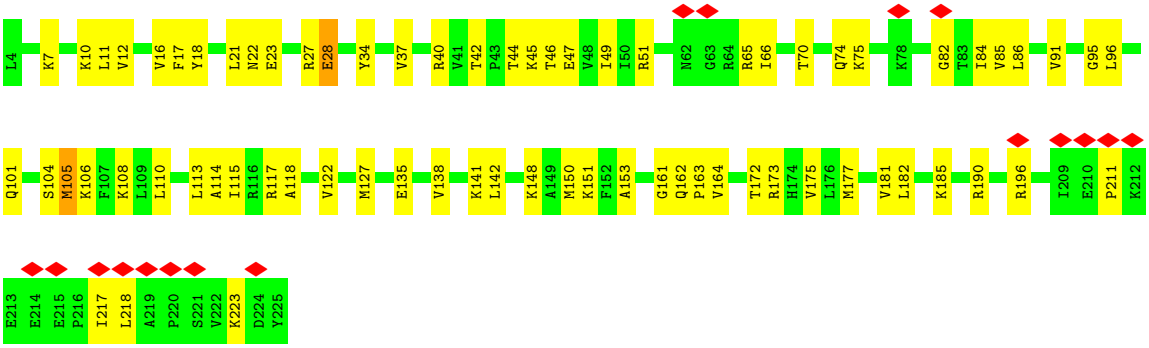




• Molecule 48: Small ribosomal subunit protein uS3

Chain SA:

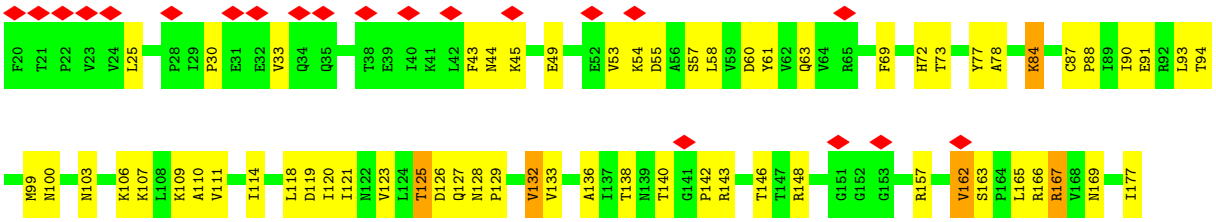


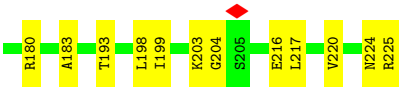


• Molecule 49: Small ribosomal subunit protein uS7

Chain SB:



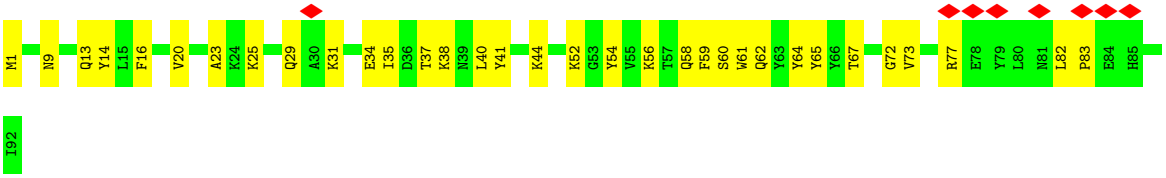




• Molecule 50: Small ribosomal subunit protein eS10A

Chain SC:

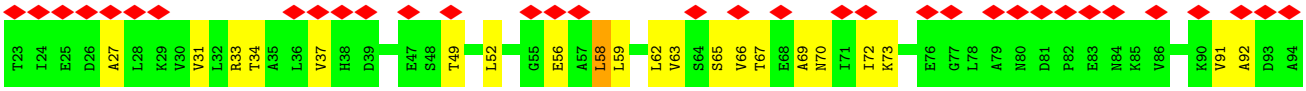


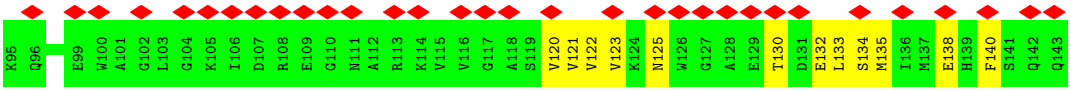


• Molecule 51: Small ribosomal subunit protein eS12

Chain SD:



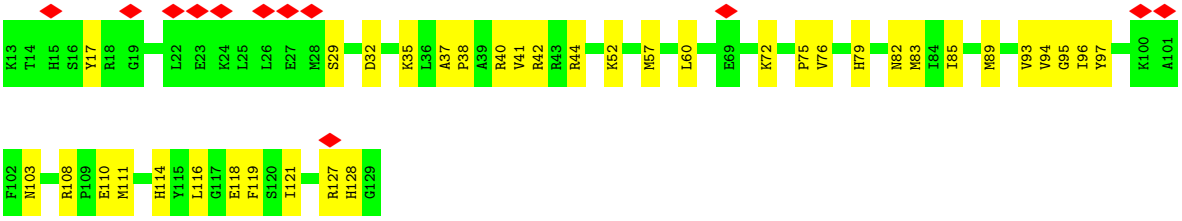




• Molecule 52: Small ribosomal subunit protein uS19

Chain SE:

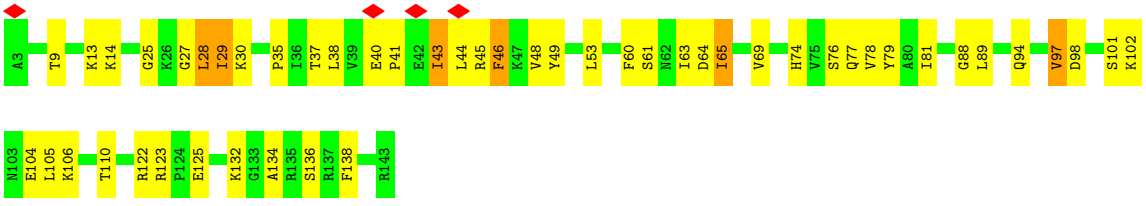




• Molecule 53: Small ribosomal subunit protein uS9A

Chain SF:





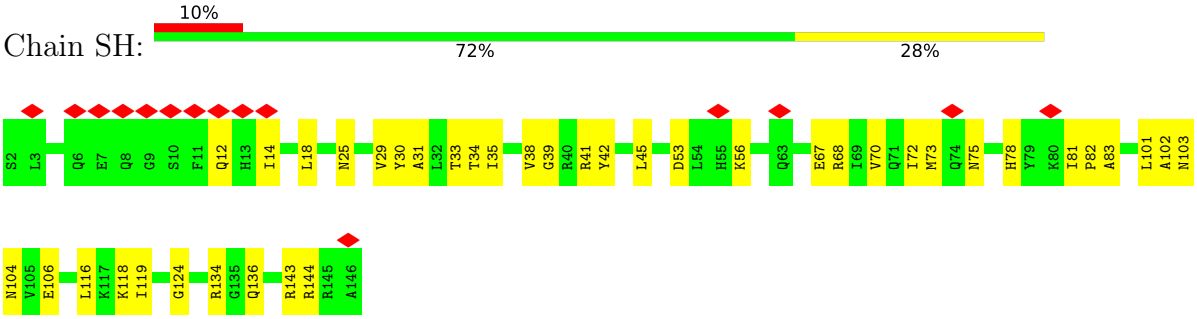
• Molecule 54: Small ribosomal subunit protein eS17B

Chain SG:

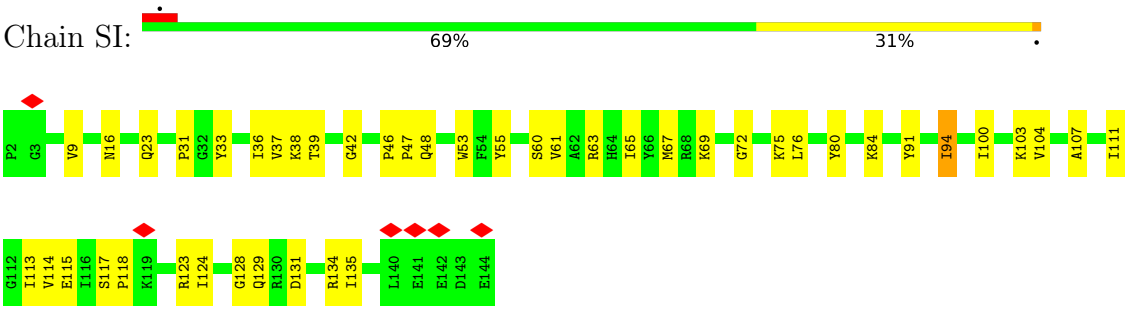




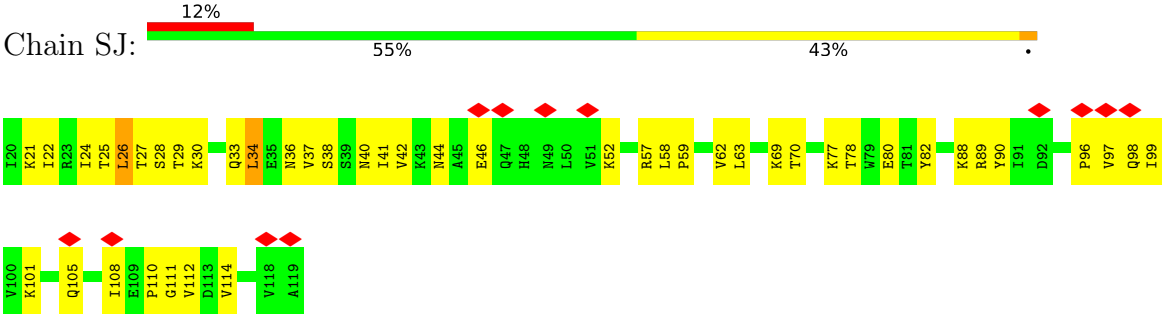
• Molecule 55: Small ribosomal subunit protein uS13A



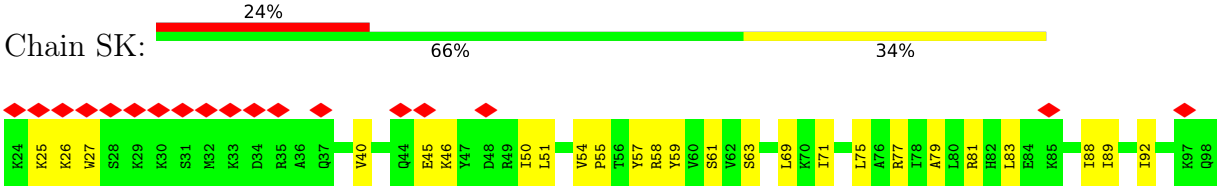
• Molecule 56: Small ribosomal subunit protein eS19A

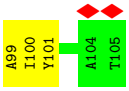


• Molecule 57: Small ribosomal subunit protein uS10



• Molecule 58: Small ribosomal subunit protein eS25A

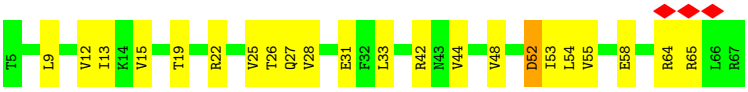




• Molecule 59: Small ribosomal subunit protein eS28A

Chain SL:

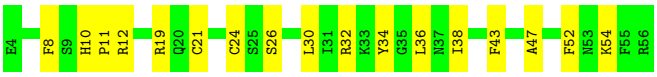




• Molecule 60: Small ribosomal subunit protein uS14A

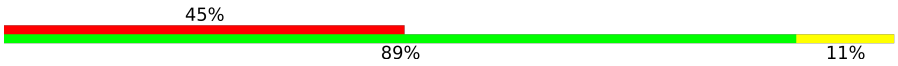
Chain SM:

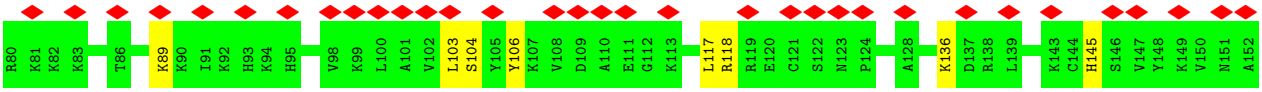




• Molecule 61: Small ribosomal subunit protein eS31

Chain SN:

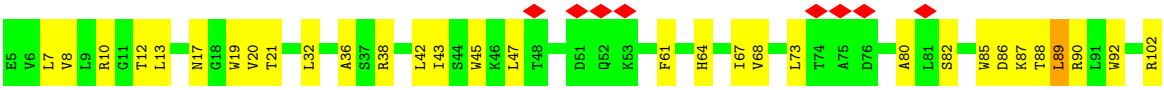


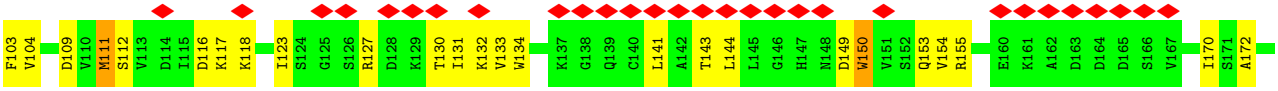


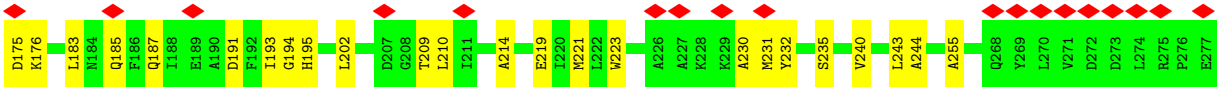
• Molecule 62: Small ribosomal subunit protein RACK1

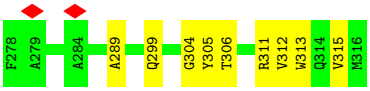
Chain SO:







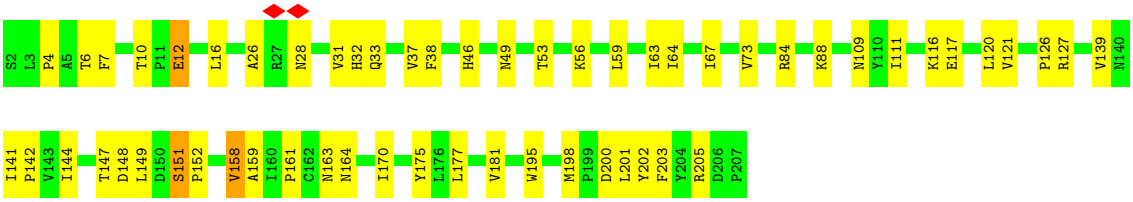




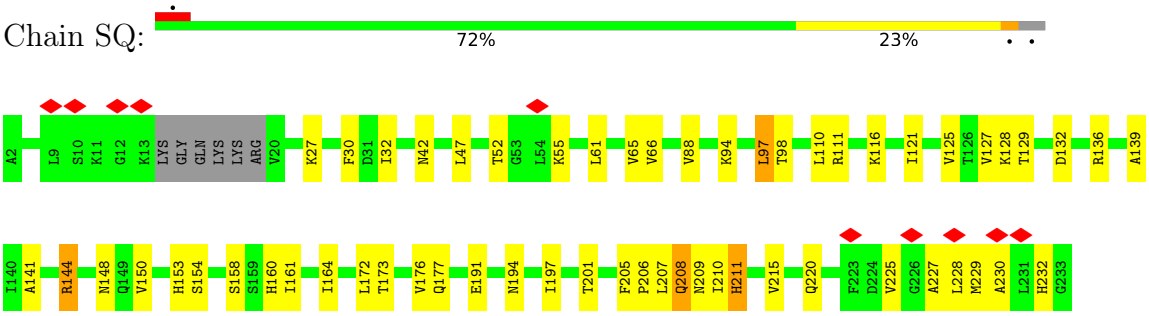
• Molecule 63: Small ribosomal subunit protein uS2A

Chain SP:

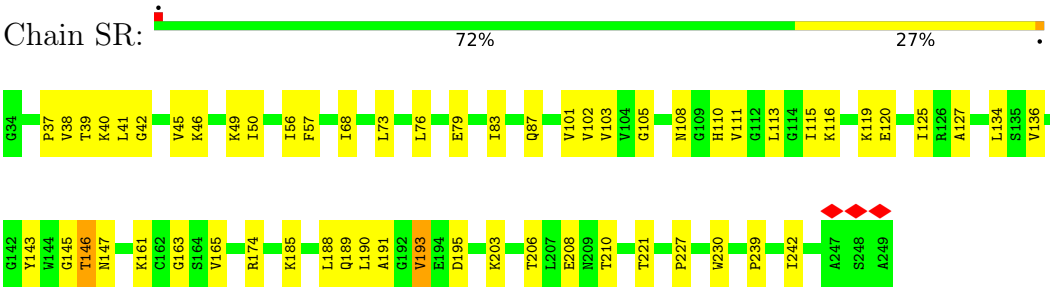




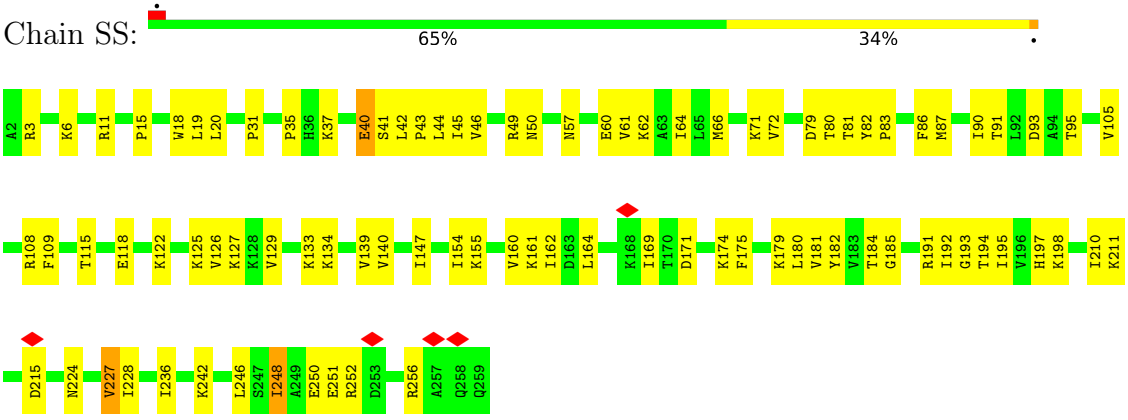
• Molecule 64: Small ribosomal subunit protein eS1A



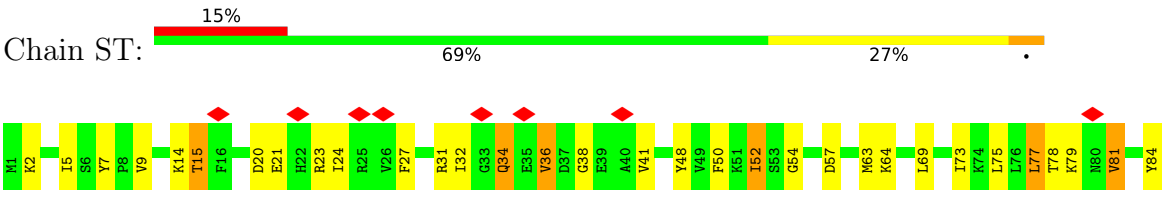
• Molecule 65: Small ribosomal subunit protein uS5

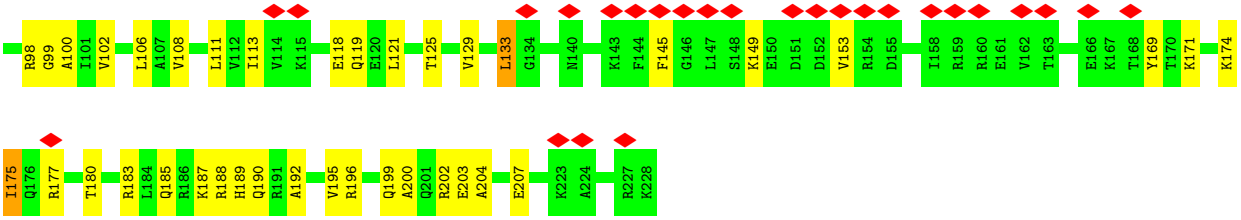


• Molecule 66: Small ribosomal subunit protein eS4A



• Molecule 67: Small ribosomal subunit protein eS6A





• Molecule 68: Small ribosomal subunit protein eS7A

Chain SU:



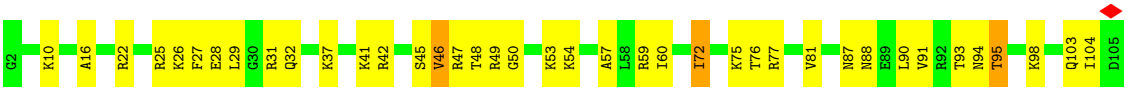




• Molecule 69: Small ribosomal subunit protein eS8A

Chain SV:





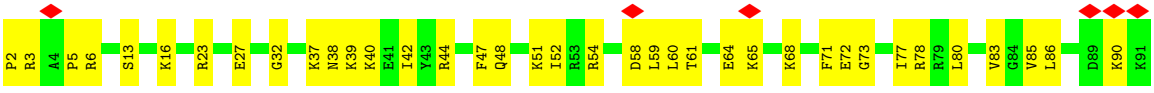




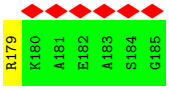
• Molecule 70: Small ribosomal subunit protein uS4A

Chain SW:



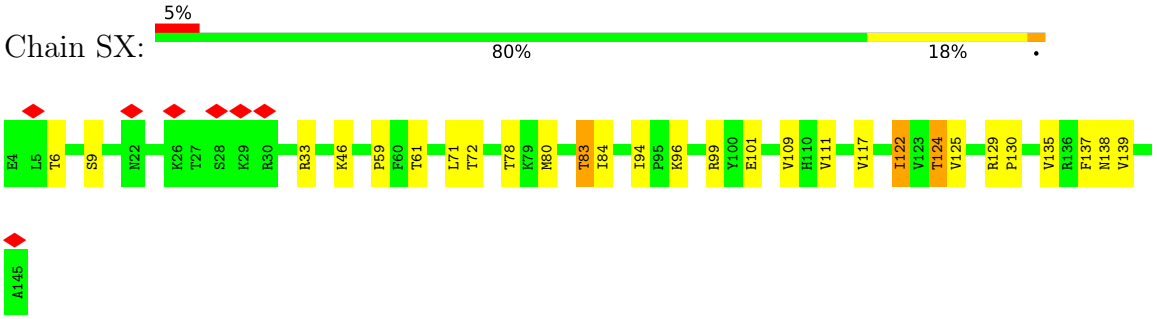






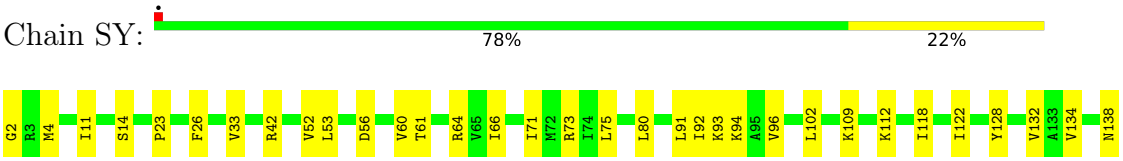
• Molecule 71: Small ribosomal subunit protein uS17A

Chain SX:



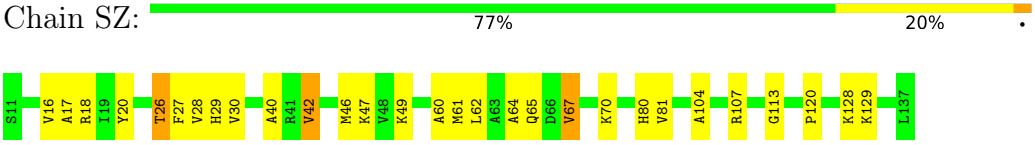
• Molecule 72: Small ribosomal subunit protein uS15

Chain SY:



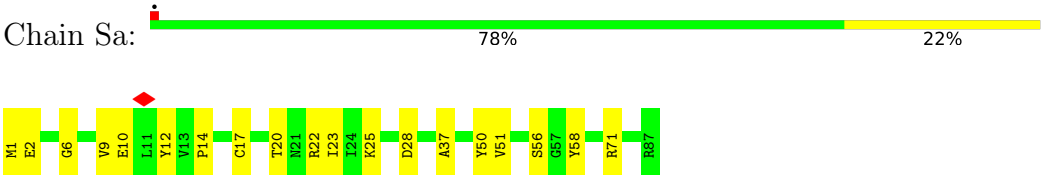
• Molecule 73: Small ribosomal subunit protein uS11B

Chain SZ:



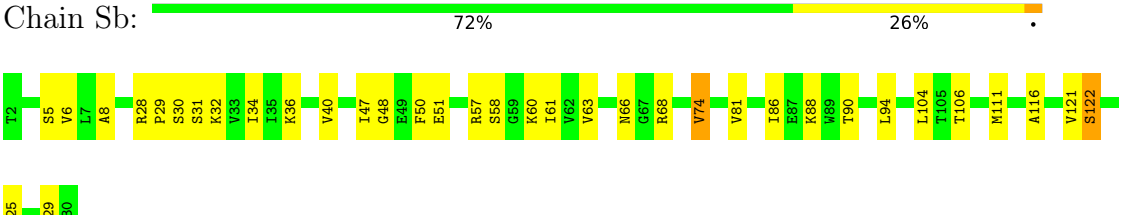
• Molecule 74: Small ribosomal subunit protein eS21A

Chain Sa:



• Molecule 75: Small ribosomal subunit protein uS8A

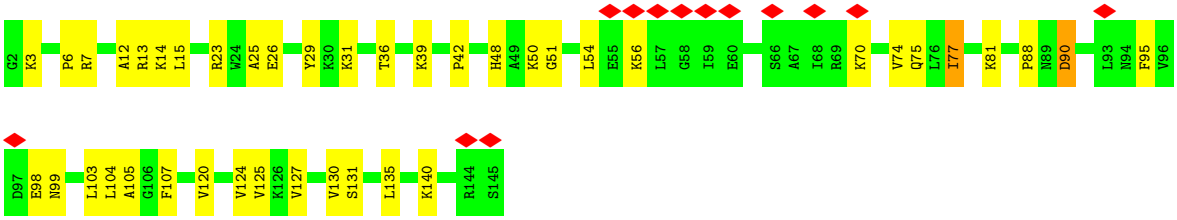
Chain Sb:



• Molecule 76: Small ribosomal subunit protein uS12A

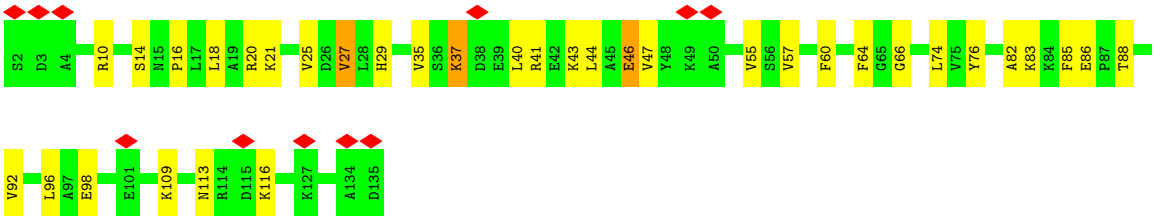
Chain Sc:



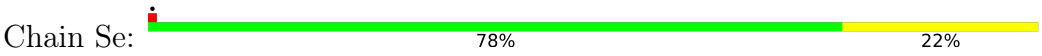


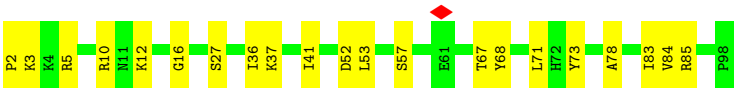
• Molecule 77: Small ribosomal subunit protein eS24A



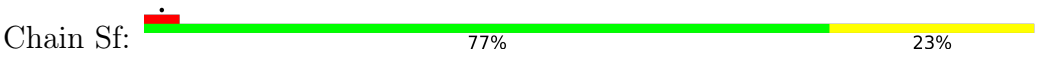


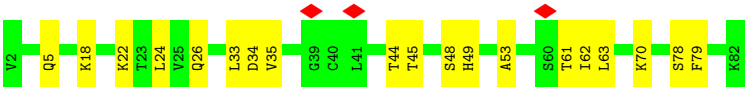
• Molecule 78: Small ribosomal subunit protein eS26B



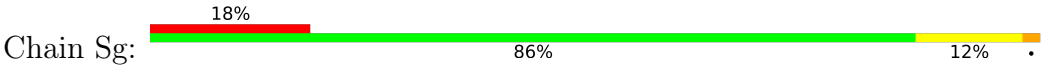


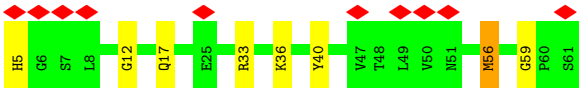
• Molecule 79: Small ribosomal subunit protein eS27A



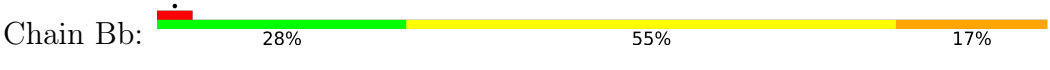


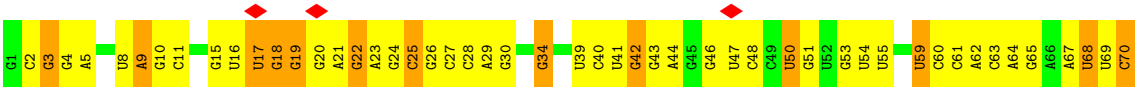
• Molecule 80: Small ribosomal subunit protein eS30A

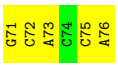




• Molecule 81: RNA (76-MER)






G71
C72
A73
C74
C75
A76

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33691	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	2.586	Depositor
Minimum map value	-1.363	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.082	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	LA	0.26	0/75727	0.71	12/118064 (0.0%)
2	LB	0.24	0/2883	0.69	1/4491 (0.0%)
3	LC	0.25	0/3746	0.68	0/5832
4	LD	0.14	0/1933	0.34	0/2598
5	LE	0.15	0/3146	0.33	0/4228
6	LF	0.14	0/2800	0.34	0/3790
7	LG	0.13	0/2400	0.35	0/3239
8	LH	0.15	0/1329	0.38	0/1794
9	LI	0.15	0/1821	0.35	0/2451
10	LJ	0.14	0/1836	0.38	0/2481
11	LK	0.17	0/1529	0.39	0/2060
12	LL	0.12	0/1801	0.30	0/2416
13	LM	0.13	0/1367	0.39	0/1834
14	LN	0.15	0/1568	0.38	0/2106
15	LO	0.15	0/1068	0.33	0/1438
16	LP	0.14	0/1757	0.32	0/2354
17	LQ	0.16	0/1585	0.37	0/2128
18	LR	0.13	0/1439	0.34	0/1938
19	LS	0.13	0/1465	0.34	0/1965
20	LT	0.12	0/1532	0.29	0/2043
21	LU	0.15	0/1473	0.34	0/1980
22	LV	0.14	0/1296	0.32	0/1739
23	LW	0.14	0/812	0.43	0/1099
24	LX	0.12	0/1018	0.29	0/1369
25	LY	0.13	0/540	0.34	0/717
26	LZ	0.12	0/979	0.30	0/1321
27	La	0.12	0/995	0.30	0/1329
28	Lb	0.11	0/1106	0.31	0/1485
29	Lc	0.14	0/1200	0.33	0/1607
30	Ld	0.12	0/473	0.32	0/629
31	Le	0.12	0/745	0.30	0/1001
32	Lf	0.13	0/890	0.31	0/1196
33	Lg	0.14	0/1038	0.30	0/1390
34	Lh	0.12	0/868	0.30	0/1168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	Li	0.13	0/890	0.31	0/1189
36	Lj	0.13	0/978	0.35	0/1301
37	Lk	0.12	0/772	0.29	0/1026
38	Ll	0.12	0/660	0.30	0/875
39	Lm	0.11	0/618	0.32	0/826
40	Ln	0.13	0/443	0.31	0/588
41	Lo	0.10	0/416	0.28	0/553
42	Lp	0.11	0/230	0.25	0/296
43	Lq	0.13	0/836	0.35	0/1104
44	Lr	0.14	0/701	0.37	0/934
46	Cc	0.20	0/1836	0.69	0/2859
47	S2	0.25	0/42211	0.75	33/65773 (0.1%)
48	SA	0.17	0/1754	0.43	0/2361
49	SB	0.15	0/1625	0.38	0/2197
50	SC	0.14	0/769	0.40	0/1039
51	SD	0.17	0/883	0.52	0/1199
52	SE	0.14	0/936	0.37	0/1259
53	SF	0.13	0/1125	0.39	0/1510
54	SG	0.12	0/957	0.35	0/1283
55	SH	0.13	0/1207	0.36	0/1623
56	SI	0.15	0/1130	0.38	0/1517
57	SJ	0.15	0/807	0.40	0/1091
58	SK	0.11	0/661	0.30	0/888
59	SL	0.10	0/493	0.34	0/663
60	SM	0.11	0/452	0.33	0/600
61	SN	0.11	0/567	0.34	0/764
62	SO	0.15	0/2436	0.42	0/3318
63	SP	0.15	0/1644	0.38	0/2249
64	SQ	0.14	0/1823	0.39	0/2447
65	SR	0.15	0/1656	0.38	0/2251
66	SS	0.18	0/2097	0.42	0/2823
67	ST	0.14	0/1839	0.39	0/2460
68	SU	0.15	0/1498	0.38	0/2019
69	SV	0.13	0/1501	0.34	0/2006
70	SW	0.16	0/1504	0.45	0/2016
71	SX	0.12	0/1168	0.31	0/1575
72	SY	0.15	0/1215	0.35	0/1638
73	SZ	0.14	0/934	0.33	0/1257
74	Sa	0.12	0/682	0.31	0/921
75	Sb	0.15	0/1038	0.35	0/1395
76	Sc	0.12	0/1139	0.36	0/1518
77	Sd	0.14	0/1046	0.35	0/1401
78	Se	0.12	0/778	0.33	0/1042

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
79	Sf	0.18	0/620	0.40	0/838
80	Sg	0.13	0/459	0.44	0/611
81	Bb	0.23	0/1814	0.74	1/2827 (0.0%)
All	All	0.21	0/217013	0.61	47/319210 (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
10	LJ	0	2
30	Ld	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	S2	590	C	C2-N1-C1'	8.26	127.88	118.80
47	S2	1182	U	C2-N1-C1'	7.96	127.25	117.70
47	S2	692	C	N3-C2-O2	-7.23	116.84	121.90
47	S2	1482	C	N1-C2-O2	7.19	123.22	118.90
47	S2	758	U	C2-N1-C1'	6.86	125.94	117.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	LJ	30	THR	Peptide
10	LJ	76	ALA	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	767	0
2	LB	2579	0	1304	38	0
3	LC	3353	0	1695	53	0
4	LD	1899	0	1957	43	0
5	LE	3075	0	3142	60	0
6	LF	2748	0	2859	54	0
7	LG	2351	0	2294	50	0
8	LH	1307	0	1377	19	0
9	LI	1784	0	1862	33	0
10	LJ	1804	0	1877	34	0
11	LK	1508	0	1572	35	0
12	LL	1764	0	1804	33	0
13	LM	1346	0	1370	43	0
14	LN	1543	0	1608	30	0
15	LO	1053	0	1149	21	0
16	LP	1720	0	1779	35	0
17	LQ	1555	0	1659	29	0
18	LR	1416	0	1433	25	0
19	LS	1441	0	1543	31	0
20	LT	1515	0	1606	20	0
21	LU	1437	0	1475	31	0
22	LV	1272	0	1312	25	0
23	LW	796	0	812	24	0
24	LX	1003	0	1048	15	0
25	LY	528	0	546	13	0
26	LZ	964	0	1025	14	0
27	La	984	0	1075	16	0
28	Lb	1080	0	1122	23	0
29	Lc	1169	0	1211	24	0
30	Ld	462	0	491	8	0
31	Le	737	0	792	16	0
32	Lf	876	0	912	14	0
33	Lg	1017	0	1081	9	0
34	Lh	850	0	880	11	0
35	Li	880	0	945	17	0
36	Lj	969	0	1078	22	0
37	Lk	766	0	844	16	0
38	Ll	645	0	649	7	0
39	Lm	612	0	682	15	0
40	Ln	436	0	475	13	0
41	Lo	410	0	446	5	0
42	Lp	229	0	273	3	0
43	Lq	824	0	892	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Lr	694	0	738	10	0
45	mR	228	0	0	0	0
46	Cc	1644	0	837	16	0
47	S2	37739	0	18988	532	0
48	SA	1729	0	1812	55	0
49	SB	1605	0	1669	63	0
50	SC	752	0	719	28	0
51	SD	875	0	878	21	0
52	SE	916	0	941	28	0
53	SF	1105	0	1166	37	0
54	SG	948	0	990	26	0
55	SH	1188	0	1218	29	0
56	SI	1112	0	1124	34	0
57	SJ	797	0	863	36	0
58	SK	651	0	682	21	0
59	SL	491	0	524	20	0
60	SM	442	0	432	13	0
61	SN	556	0	549	7	0
62	SO	2383	0	2332	66	0
63	SP	1603	0	1610	39	0
64	SQ	1798	0	1890	43	0
65	SR	1626	0	1715	40	0
66	SS	2056	0	2140	73	0
67	ST	1815	0	1894	48	0
68	SU	1473	0	1555	35	0
69	SV	1476	0	1501	49	0
70	SW	1479	0	1556	58	0
71	SX	1142	0	1209	23	0
72	SY	1192	0	1255	22	0
73	SZ	923	0	948	19	0
74	Sa	673	0	662	12	0
75	Sb	1021	0	1060	24	0
76	Sc	1121	0	1196	26	0
77	Sd	1032	0	1044	27	0
78	Se	765	0	814	14	0
79	Sf	610	0	633	12	0
80	Sg	451	0	494	8	0
81	Bb	1622	0	821	31	0
All	All	202093	0	148412	3049	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 9.

The worst 5 of 3049 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)
47:S2:1673:G:N1	47:S2:1728:A:H2	1.60	1.00
3:LC:121:U:H3	3:LC:132:G:H1	1.11	0.97
46:Cc:51:U:H3	46:Cc:65:G:H1	1.00	0.96
47:S2:1673:G:N1	47:S2:1728:A:C2	2.33	0.96
47:S2:752:A:N6	47:S2:797:G:H1	1.65	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	
4	LD	249/251 (99%)	234 (94%)	15 (6%)	0	100	100
5	LE	384/386 (100%)	360 (94%)	24 (6%)	0	100	100
6	LF	359/361 (99%)	336 (94%)	23 (6%)	0	100	100
7	LG	292/294 (99%)	278 (95%)	14 (5%)	0	100	100
8	LH	163/175 (93%)	155 (95%)	8 (5%)	0	100	100
9	LI	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
10	LJ	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
11	LK	189/191 (99%)	175 (93%)	14 (7%)	0	100	100
12	LL	216/218 (99%)	209 (97%)	7 (3%)	0	100	100
13	LM	167/169 (99%)	160 (96%)	7 (4%)	0	100	100
14	LN	191/193 (99%)	173 (91%)	18 (9%)	0	100	100
15	LO	134/136 (98%)	129 (96%)	5 (4%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LR	181/183 (99%)	170 (94%)	11 (6%)	0	100	100
19	LS	183/185 (99%)	177 (97%)	6 (3%)	0	100	100
20	LT	186/188 (99%)	183 (98%)	3 (2%)	0	100	100
21	LU	169/171 (99%)	160 (95%)	9 (5%)	0	100	100
22	LV	157/159 (99%)	145 (92%)	12 (8%)	0	100	100
23	LW	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
24	LX	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
25	LY	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
26	LZ	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
27	La	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
28	Lb	133/135 (98%)	126 (95%)	7 (5%)	0	100	100
29	Lc	146/148 (99%)	134 (92%)	12 (8%)	0	100	100
30	Ld	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
31	Le	94/96 (98%)	94 (100%)	0	0	100	100
32	Lf	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
33	Lg	125/127 (98%)	123 (98%)	2 (2%)	0	100	100
34	Lh	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
35	Li	110/112 (98%)	109 (99%)	1 (1%)	0	100	100
36	Lj	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
37	Lk	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
38	Ll	79/81 (98%)	79 (100%)	0	0	100	100
39	Lm	75/77 (97%)	75 (100%)	0	0	100	100
40	Ln	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
41	Lo	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
42	Lp	23/25 (92%)	23 (100%)	0	0	100	100
43	Lq	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
44	Lr	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
48	SA	220/222 (99%)	213 (97%)	7 (3%)	0	100	100
49	SB	204/206 (99%)	191 (94%)	12 (6%)	1 (0%)	24	43
50	SC	90/92 (98%)	79 (88%)	11 (12%)	0	100	100
51	SD	119/121 (98%)	95 (80%)	24 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	SE	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
53	SF	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
54	SG	117/125 (94%)	113 (97%)	4 (3%)	0	100	100
55	SH	143/145 (99%)	139 (97%)	4 (3%)	0	100	100
56	SI	141/143 (99%)	130 (92%)	11 (8%)	0	100	100
57	SJ	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
58	SK	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
59	SL	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
60	SM	51/53 (96%)	51 (100%)	0	0	100	100
61	SN	71/73 (97%)	59 (83%)	12 (17%)	0	100	100
62	SO	310/312 (99%)	277 (89%)	33 (11%)	0	100	100
63	SP	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
64	SQ	222/232 (96%)	204 (92%)	18 (8%)	0	100	100
65	SR	214/216 (99%)	201 (94%)	13 (6%)	0	100	100
66	SS	256/258 (99%)	236 (92%)	20 (8%)	0	100	100
67	ST	226/228 (99%)	206 (91%)	19 (8%)	1 (0%)	30	50
68	SU	182/184 (99%)	171 (94%)	11 (6%)	0	100	100
69	SV	183/198 (92%)	175 (96%)	8 (4%)	0	100	100
70	SW	182/184 (99%)	168 (92%)	14 (8%)	0	100	100
71	SX	140/142 (99%)	131 (94%)	9 (6%)	0	100	100
72	SY	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
73	SZ	125/127 (98%)	113 (90%)	12 (10%)	0	100	100
74	Sa	85/87 (98%)	79 (93%)	6 (7%)	0	100	100
75	Sb	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
76	Sc	142/144 (99%)	128 (90%)	14 (10%)	0	100	100
77	Sd	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
78	Se	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
79	Sf	79/81 (98%)	71 (90%)	8 (10%)	0	100	100
80	Sg	55/57 (96%)	49 (89%)	6 (11%)	0	100	100
All	All	10914/11099 (98%)	10282 (94%)	630 (6%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
67	ST	175	ILE
49	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%)	185 (97%)	5 (3%)	40	63
5	LE	318/322 (99%)	309 (97%)	9 (3%)	38	61
6	LF	288/288 (100%)	279 (97%)	9 (3%)	35	59
7	LG	241/243 (99%)	234 (97%)	7 (3%)	37	61
8	LH	139/154 (90%)	134 (96%)	5 (4%)	31	55
9	LI	186/186 (100%)	182 (98%)	4 (2%)	45	67
10	LJ	187/191 (98%)	182 (97%)	5 (3%)	39	62
11	LK	168/171 (98%)	161 (96%)	7 (4%)	26	49
12	LL	185/185 (100%)	181 (98%)	4 (2%)	45	67
13	LM	145/147 (99%)	141 (97%)	4 (3%)	38	61
14	LN	154/154 (100%)	147 (96%)	7 (4%)	24	46
15	LO	107/107 (100%)	105 (98%)	2 (2%)	50	70
16	LP	175/175 (100%)	171 (98%)	4 (2%)	44	66
17	LQ	160/160 (100%)	159 (99%)	1 (1%)	78	88
18	LR	138/145 (95%)	135 (98%)	3 (2%)	45	67
19	LS	150/150 (100%)	147 (98%)	3 (2%)	48	69
20	LT	152/153 (99%)	146 (96%)	6 (4%)	28	51
21	LU	155/155 (100%)	149 (96%)	6 (4%)	28	51
22	LV	135/136 (99%)	130 (96%)	5 (4%)	30	54
23	LW	87/87 (100%)	77 (88%)	10 (12%)	5	10
24	LX	104/104 (100%)	100 (96%)	4 (4%)	29	52
25	LY	54/57 (95%)	53 (98%)	1 (2%)	50	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	LZ	104/105 (99%)	100 (96%)	4 (4%)	29	52
27	La	108/108 (100%)	106 (98%)	2 (2%)	50	70
28	Lb	112/115 (97%)	111 (99%)	1 (1%)	70	82
29	Lc	117/118 (99%)	115 (98%)	2 (2%)	53	71
30	Ld	46/46 (100%)	45 (98%)	1 (2%)	45	67
31	Le	81/81 (100%)	80 (99%)	1 (1%)	63	78
32	Lf	92/96 (96%)	85 (92%)	7 (8%)	12	23
33	Lg	108/109 (99%)	106 (98%)	2 (2%)	50	70
34	Lh	90/90 (100%)	89 (99%)	1 (1%)	65	79
35	Li	95/95 (100%)	94 (99%)	1 (1%)	65	79
36	Lj	104/104 (100%)	100 (96%)	4 (4%)	29	52
37	Lk	80/81 (99%)	76 (95%)	4 (5%)	22	42
38	Ll	67/67 (100%)	66 (98%)	1 (2%)	57	74
39	Lm	68/68 (100%)	65 (96%)	3 (4%)	25	47
40	Ln	45/45 (100%)	42 (93%)	3 (7%)	15	28
41	Lo	45/47 (96%)	45 (100%)	0	100	100
42	Lp	22/23 (96%)	21 (96%)	1 (4%)	24	46
43	Lq	87/88 (99%)	85 (98%)	2 (2%)	44	66
44	Lr	71/71 (100%)	71 (100%)	0	100	100
48	SA	182/182 (100%)	176 (97%)	6 (3%)	33	57
49	SB	172/173 (99%)	165 (96%)	7 (4%)	27	49
50	SC	77/85 (91%)	77 (100%)	0	100	100
51	SD	88/98 (90%)	84 (96%)	4 (4%)	24	46
52	SE	95/98 (97%)	93 (98%)	2 (2%)	47	67
53	SF	117/117 (100%)	110 (94%)	7 (6%)	17	32
54	SG	101/113 (89%)	93 (92%)	8 (8%)	11	21
55	SH	127/128 (99%)	126 (99%)	1 (1%)	73	84
56	SI	115/115 (100%)	110 (96%)	5 (4%)	26	47
57	SJ	93/93 (100%)	87 (94%)	6 (6%)	15	29
58	SK	67/73 (92%)	65 (97%)	2 (3%)	36	60
59	SL	55/56 (98%)	53 (96%)	2 (4%)	31	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	SM	47/47 (100%)	47 (100%)	0	100	100
61	SN	56/64 (88%)	56 (100%)	0	100	100
62	SO	250/257 (97%)	243 (97%)	7 (3%)	38	61
63	SP	170/173 (98%)	164 (96%)	6 (4%)	32	56
64	SQ	200/205 (98%)	188 (94%)	12 (6%)	17	32
65	SR	175/175 (100%)	167 (95%)	8 (5%)	24	45
66	SS	220/220 (100%)	214 (97%)	6 (3%)	39	62
67	ST	189/195 (97%)	175 (93%)	14 (7%)	13	24
68	SU	163/165 (99%)	154 (94%)	9 (6%)	19	37
69	SV	148/159 (93%)	141 (95%)	7 (5%)	23	45
70	SW	156/157 (99%)	150 (96%)	6 (4%)	29	52
71	SX	126/127 (99%)	122 (97%)	4 (3%)	34	58
72	SY	127/127 (100%)	124 (98%)	3 (2%)	43	65
73	SZ	90/96 (94%)	86 (96%)	4 (4%)	25	47
74	Sa	71/74 (96%)	70 (99%)	1 (1%)	59	75
75	Sb	110/110 (100%)	105 (96%)	5 (4%)	24	46
76	Sc	119/119 (100%)	114 (96%)	5 (4%)	26	49
77	Sd	102/112 (91%)	97 (95%)	5 (5%)	22	43
78	Se	82/83 (99%)	80 (98%)	2 (2%)	43	65
79	Sf	70/70 (100%)	65 (93%)	5 (7%)	13	25
80	Sg	48/49 (98%)	46 (96%)	2 (4%)	26	49
All	All	9168/9335 (98%)	8856 (97%)	312 (3%)	33	57

5 of 312 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
65	SR	146	THR
73	SZ	67	VAL
66	SS	248	ILE
68	SU	107	ARG
77	Sd	27	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
53	SF	83	GLN
64	SQ	160	HIS
54	SG	42	GLN
62	SO	17	ASN
66	SS	57	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	LA	3159/3396 (93%)	749 (23%)	27 (0%)
2	LB	120/121 (99%)	17 (14%)	1 (0%)
3	LC	157/158 (99%)	36 (22%)	1 (0%)
45	mR	0/11	-	-
46	Cc	76/77 (98%)	22 (28%)	0
47	S2	1768/1800 (98%)	671 (37%)	21 (1%)
81	Bb	75/76 (98%)	33 (44%)	0
All	All	5355/5639 (94%)	1528 (28%)	50 (0%)

5 of 1528 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	LA	5	G
1	LA	6	A
1	LA	14	U
1	LA	21	G
1	LA	22	G

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	LC	85	G
47	S2	539	G
47	S2	1471	A
47	S2	139	C
47	S2	400	A

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.

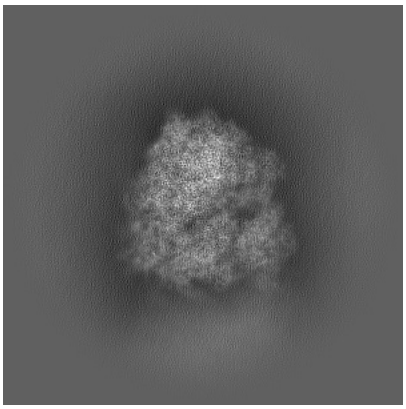
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-68804. These allow visual inspection of the internal detail of the map and identification of artifacts.

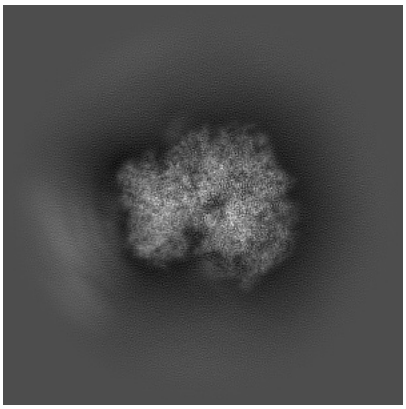
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

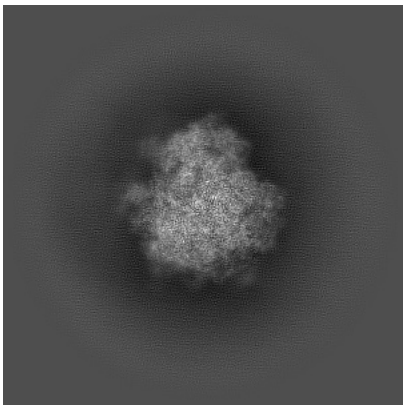
6.1.1 Primary map



X

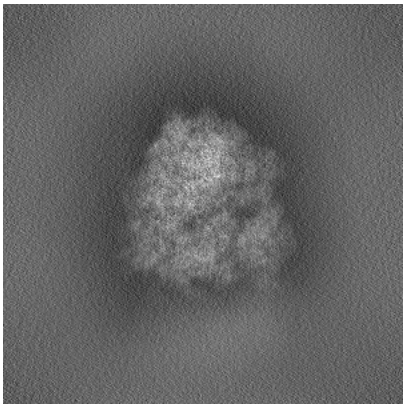


Y

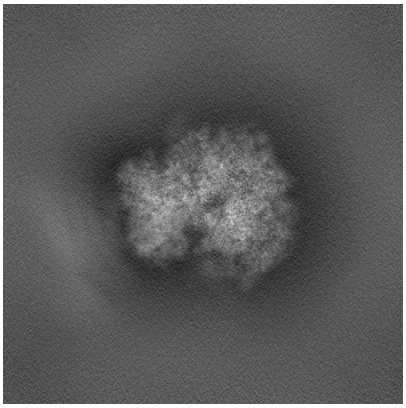


Z

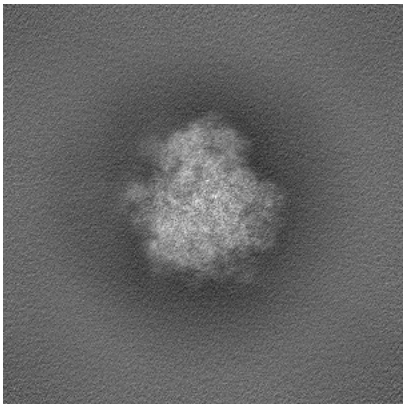
6.1.2 Raw map



X



Y

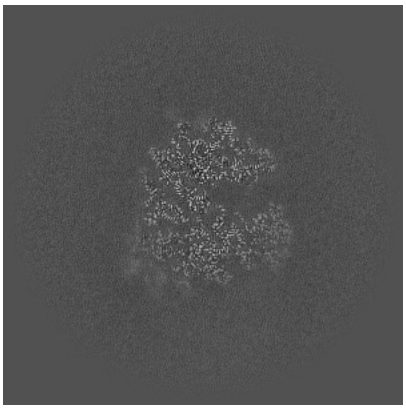


Z

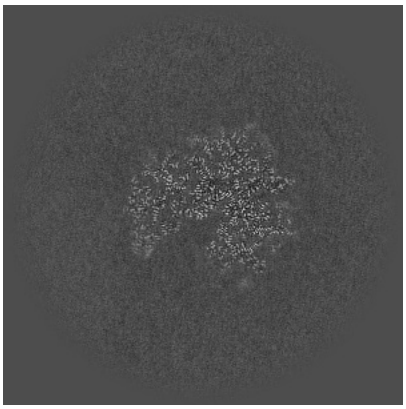
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

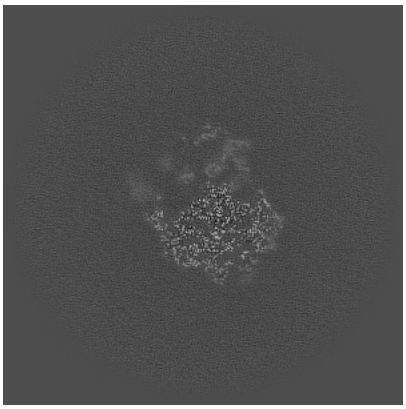
6.2.1 Primary map



X Index: 300

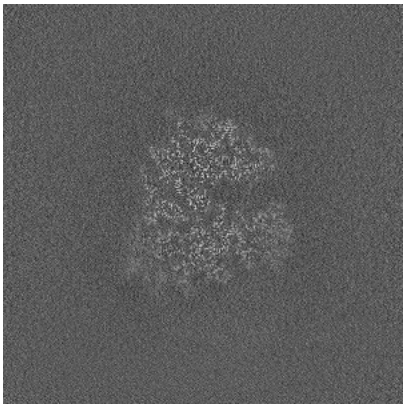


Y Index: 300

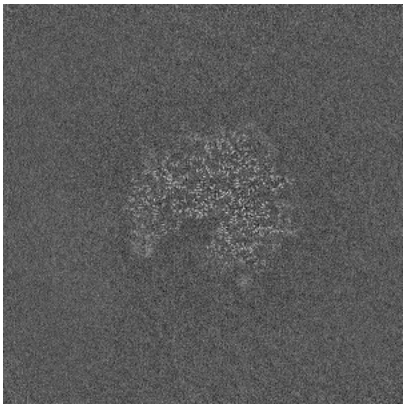


Z Index: 300

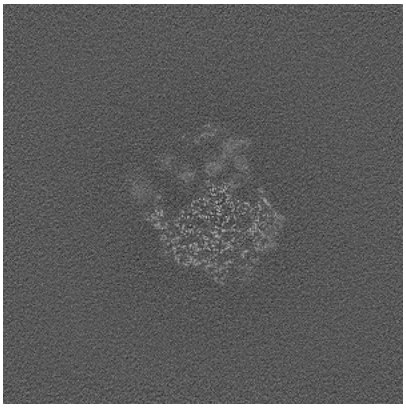
6.2.2 Raw map



X Index: 300



Y Index: 300

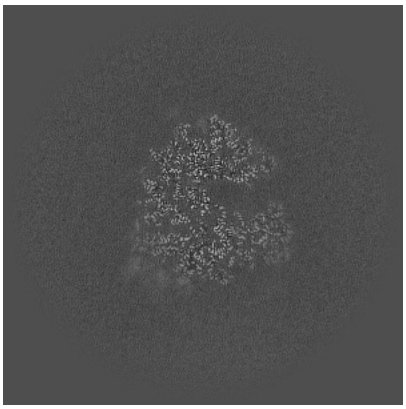


Z Index: 300

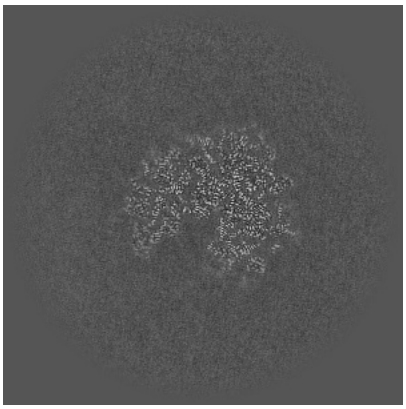
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

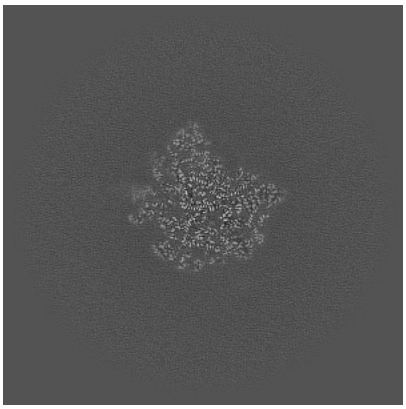
6.3.1 Primary map



X Index: 302

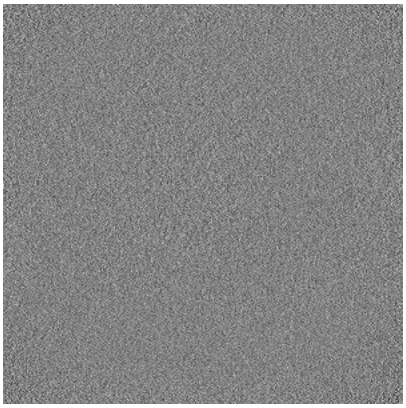


Y Index: 302

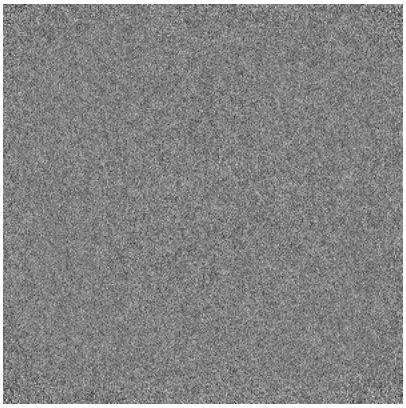


Z Index: 344

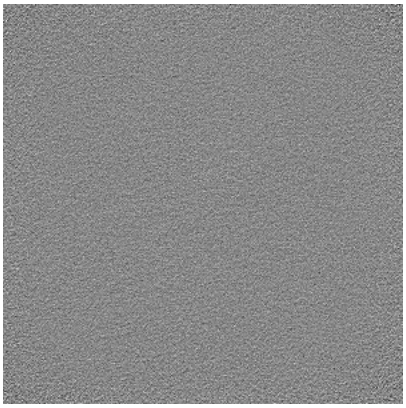
6.3.2 Raw map



X Index: 0



Y Index: 0

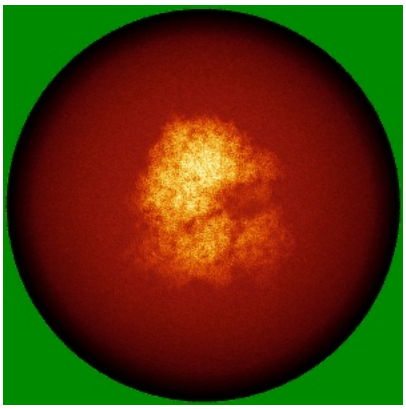


Z Index: 599

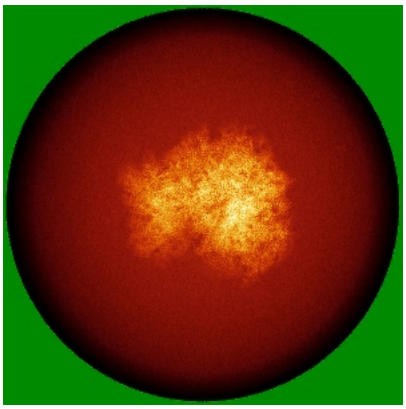
The images above show the largest variance slices of the map in three orthogonal directions.

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

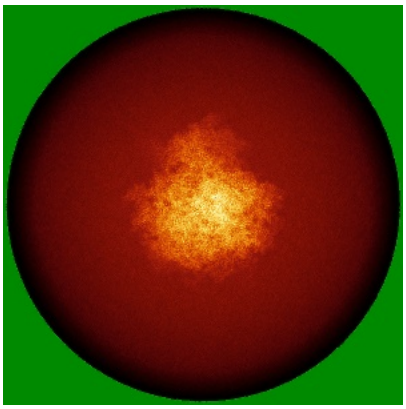
6.4.1 Primary map



X

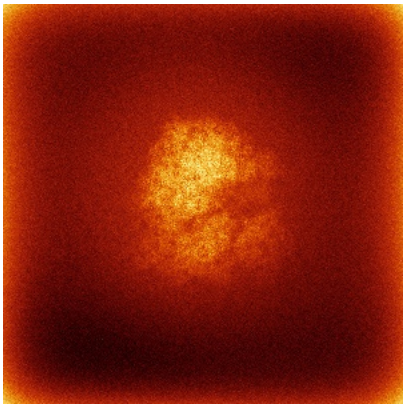


Y

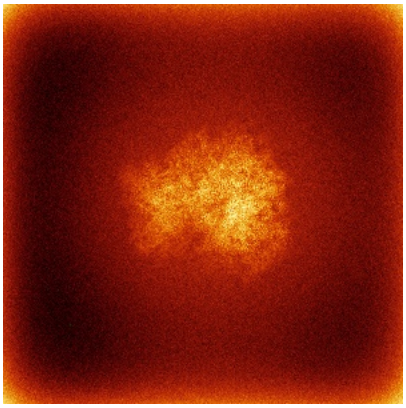


Z

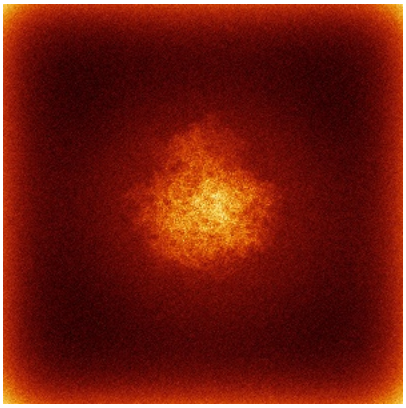
6.4.2 Raw map



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)

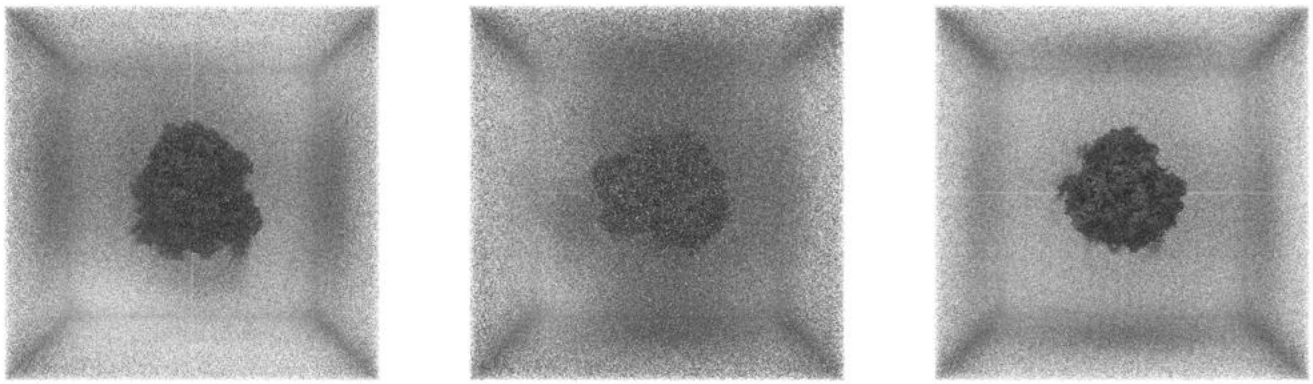
6.5.1 Primary map



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.

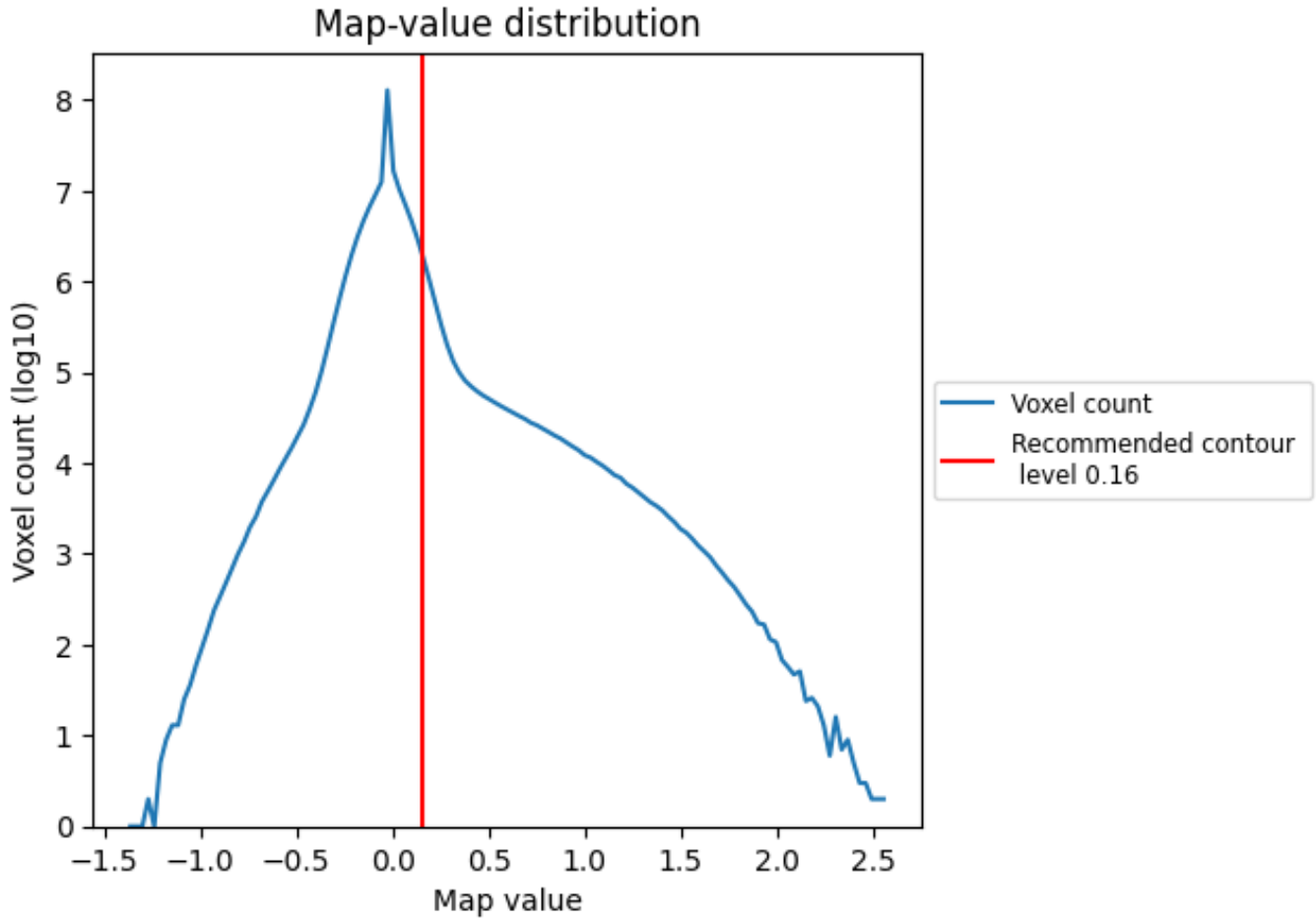
6.6 Mask visualisation (i)

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

7 Map analysis

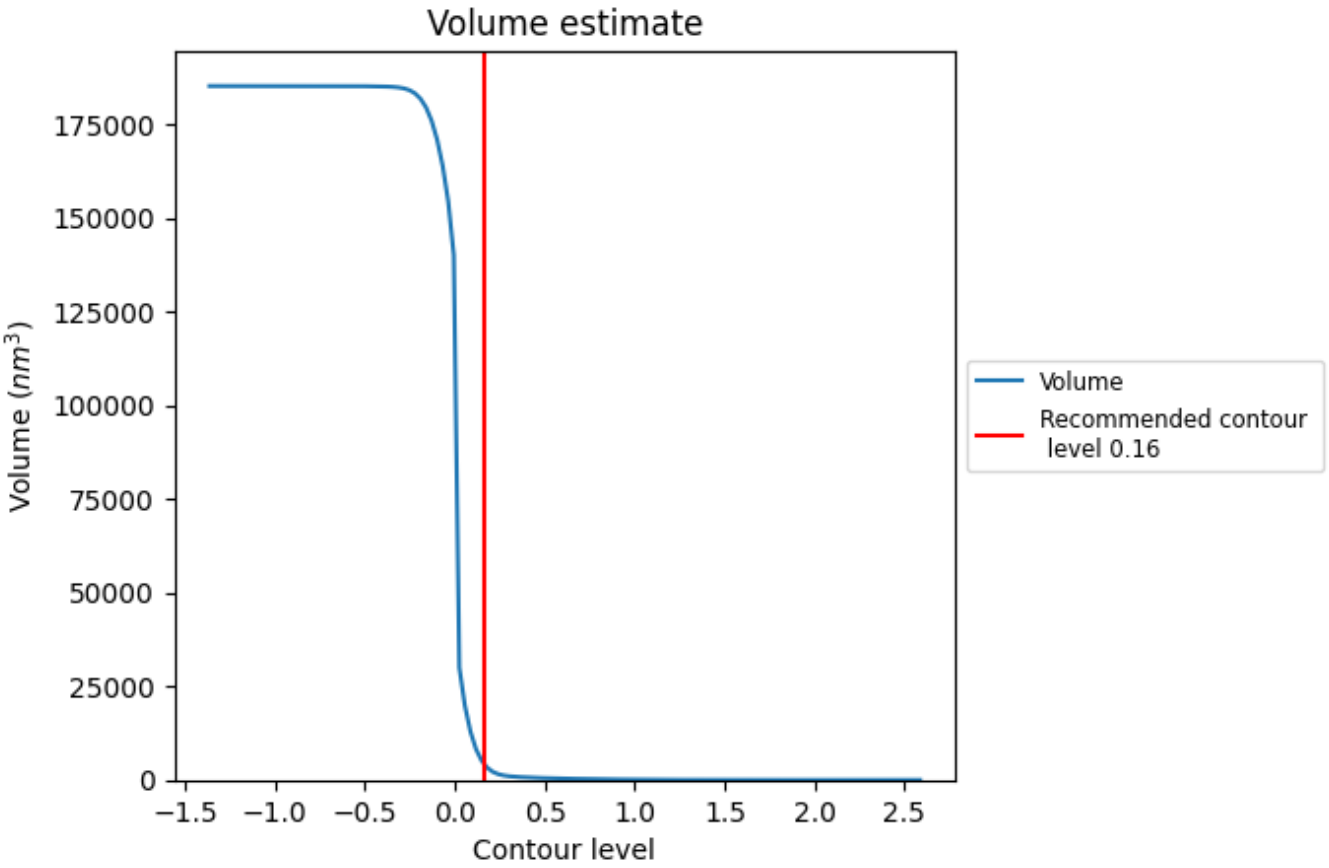
This section contains the results of statistical analysis of the map.

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.

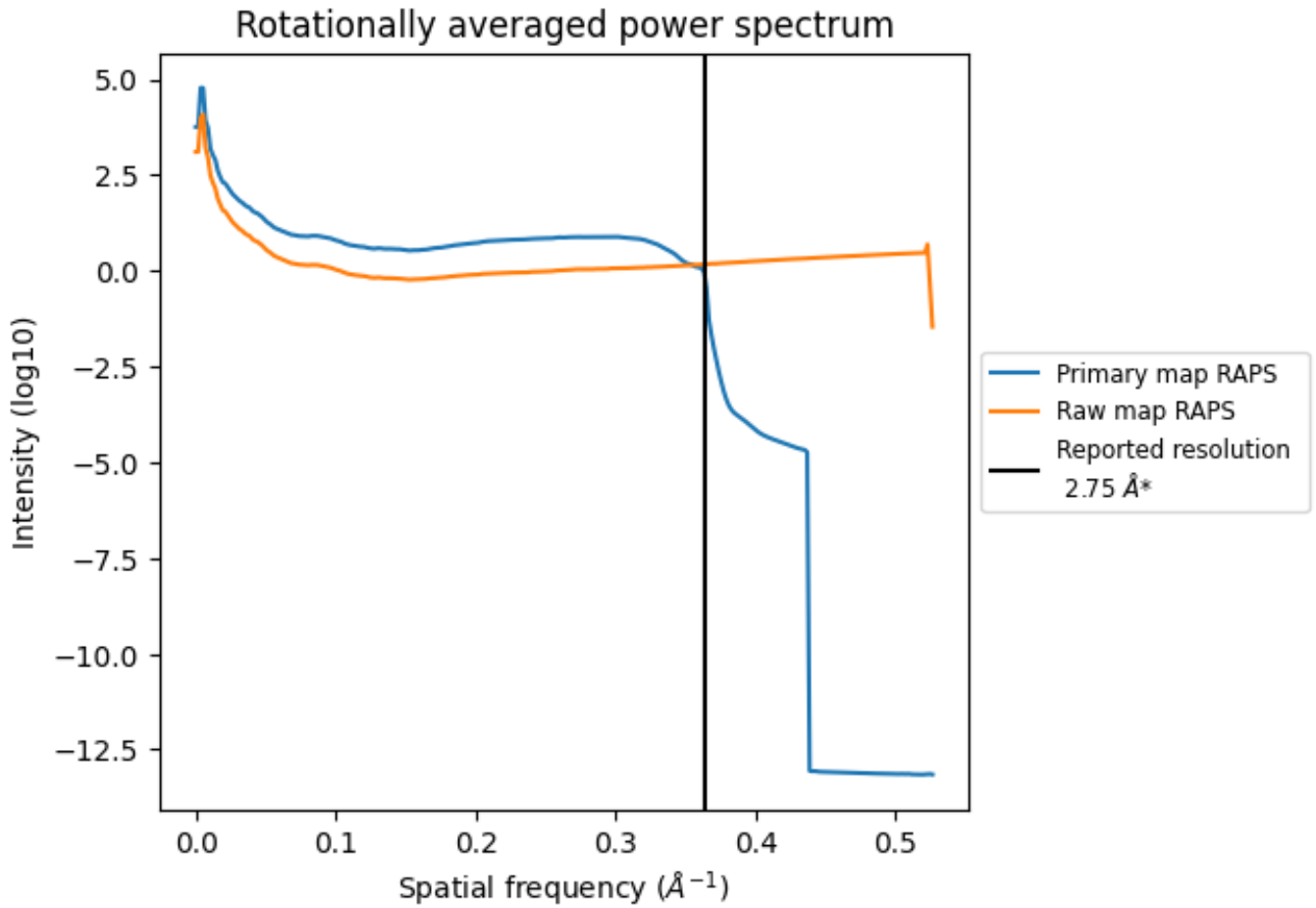
7.2 Volume estimate (i)



The volume at the recommended contour level is 4509 nm^3; this corresponds to an approximate mass of 4073 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)

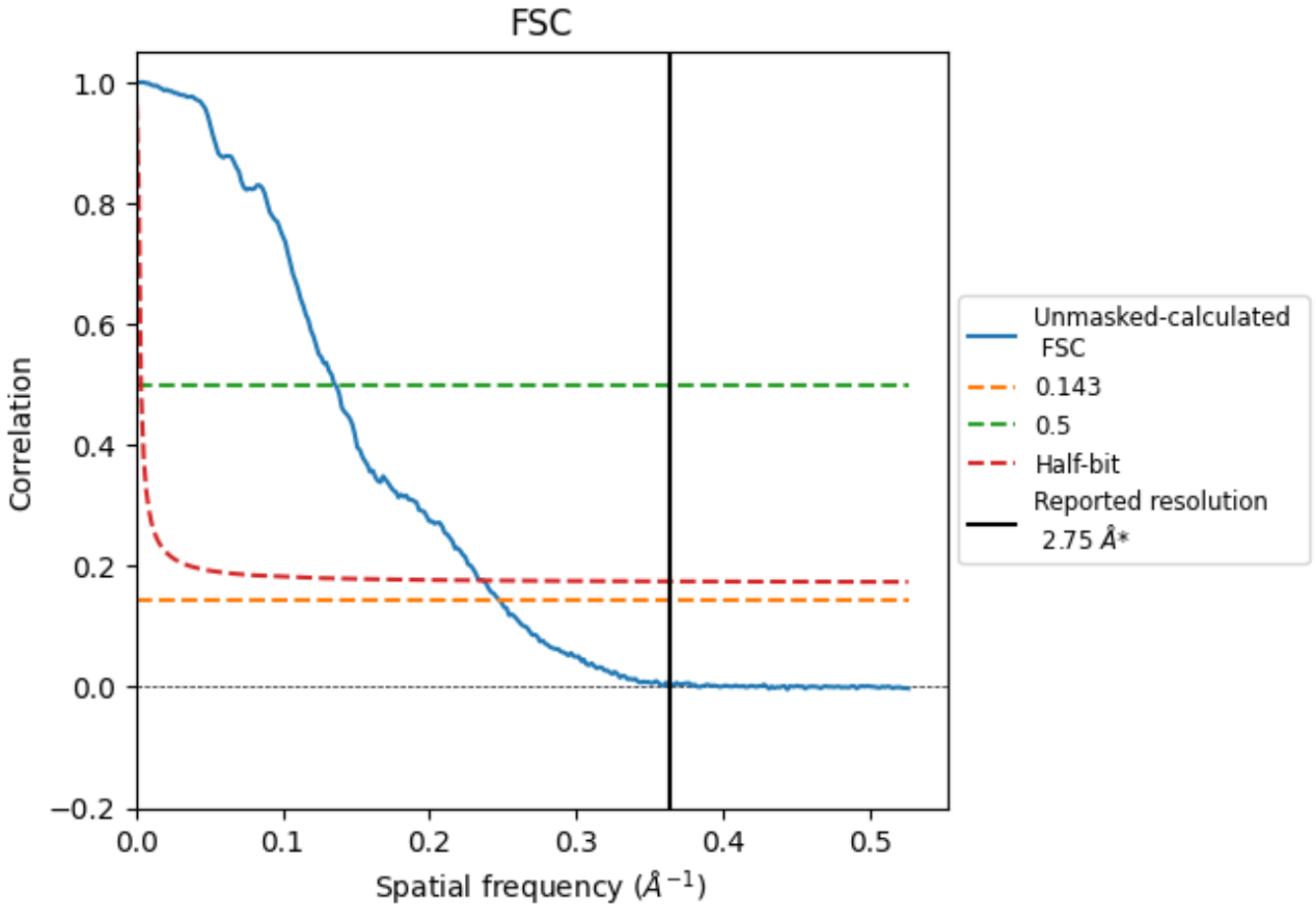


*Reported resolution corresponds to spatial frequency of 0.364 $Å^{-1}$

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 0.364 Å^{-1}

8.2 Resolution estimates (i)

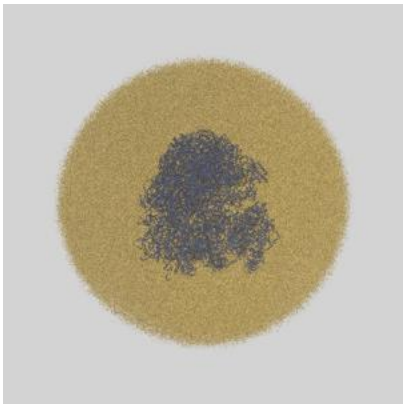
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.75	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.04	7.38	4.23

*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 4.04 differs from the reported value 2.75 by more than 10 %

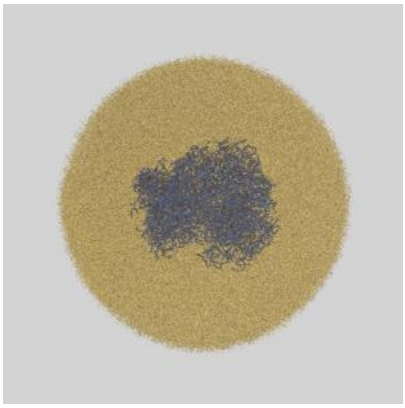
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-68804 and PDB model 23AR. Per-residue inclusion information can be found in section 3 on page 19.

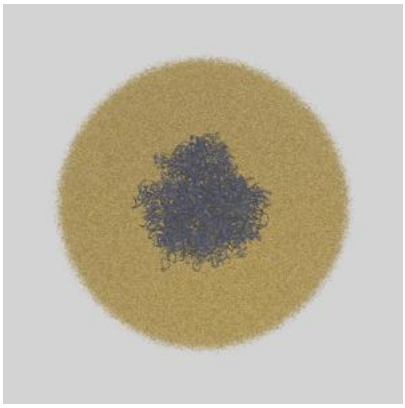
9.1 Map-model overlay



X



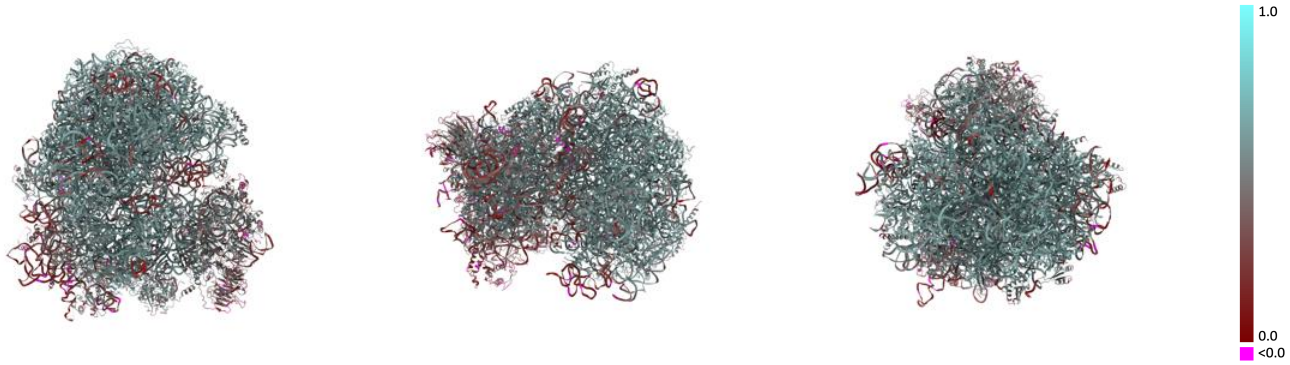
Y



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.

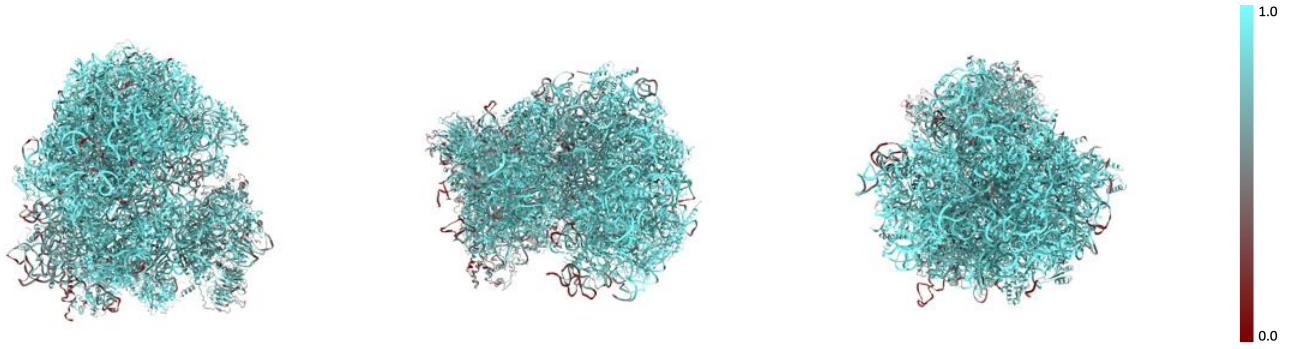
9.2 Q-score mapped to coordinate model (i)



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.

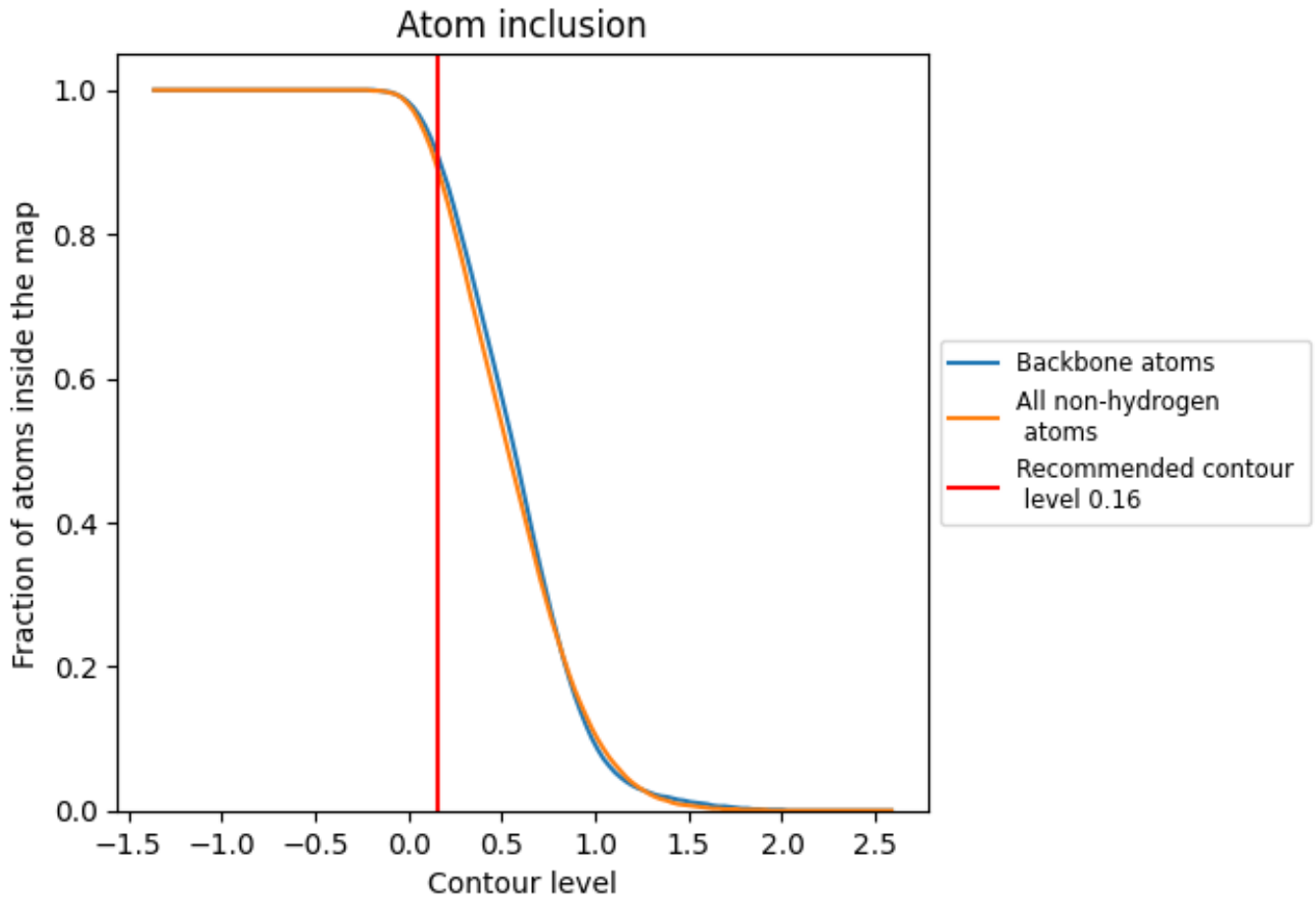
9.3 Atom inclusion mapped to coordinate model (i)



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, 91% of all backbone atoms, 89% 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	0.8870	0.5200
Bb	0.8470	0.3970
Cc	0.8690	0.4160
LA	0.9300	0.5550
LB	0.9640	0.5610
LC	0.9560	0.5750
LD	0.9640	0.6240
LE	0.9580	0.6020
LF	0.9490	0.5940
LG	0.9100	0.5450
LH	0.8870	0.5340
LI	0.9470	0.5970
LJ	0.9100	0.5530
LK	0.9200	0.5640
LL	0.9220	0.5780
LM	0.8840	0.5170
LN	0.9380	0.5860
LO	0.9270	0.5650
LP	0.9610	0.6180
LQ	0.9450	0.5840
LR	0.9360	0.5970
LS	0.9710	0.6110
LT	0.8560	0.5380
LU	0.9460	0.5960
LV	0.9420	0.5860
LW	0.8730	0.4870
LX	0.9540	0.6080
LY	0.9410	0.5980
LZ	0.9360	0.5900
La	0.9720	0.6030
Lb	0.9200	0.5620
Lc	0.9710	0.6160
Ld	0.9140	0.5590
Le	0.9200	0.5720
Lf	0.9230	0.5760



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Chain	Atom inclusion	Q-score
Lg	0.9250	0.5850
Lh	0.9720	0.6260
Li	0.9360	0.5960
Lj	0.9580	0.5850
Lk	0.9200	0.5500
Ll	0.9740	0.6250
Lm	0.8210	0.4870
Ln	0.9400	0.5940
Lo	0.9500	0.6020
Lp	0.9280	0.5940
Lq	0.9540	0.6050
Lr	0.9430	0.6090
S2	0.8190	0.4380
SA	0.7950	0.4680
SB	0.7840	0.4450
SC	0.7450	0.3870
SD	0.3880	0.1970
SE	0.7970	0.4280
SF	0.8370	0.4810
SG	0.8470	0.4860
SH	0.7830	0.4290
SI	0.8200	0.4510
SJ	0.7120	0.3970
SK	0.6440	0.3630
SL	0.7610	0.4350
SM	0.9050	0.5220
SN	0.4180	0.1970
SO	0.6650	0.3260
SP	0.8870	0.5210
SQ	0.8740	0.5200
SR	0.9130	0.5700
SS	0.8520	0.4900
ST	0.7090	0.3530
SU	0.8090	0.4650
SV	0.8290	0.4690
SW	0.8100	0.4580
SX	0.8860	0.5350
SY	0.9300	0.5660
SZ	0.9250	0.5600
Sa	0.9050	0.5450
Sb	0.9530	0.6000
Sc	0.8650	0.5340

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Chain	Atom inclusion	Q-score
Sd	0.7980	0.4280
Se	0.9480	0.5910
Sf	0.8870	0.5180
Sg	0.7520	0.4350
mR	0.9430	0.5550