



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:02 AM UTC

PDB ID : 3JAJ / pdb_00003jaj
EMDB ID : EMD-3037
Title : Structure of the engaged state of the mammalian SRP-ribosome complex
Authors : Voorhees, R.M.; Hegde, R.S.
Deposited on : 2015-06-16
Resolution : 3.75 Å (reported)
Based on initial models : 1QB2, 3J7P, 3J7O, 4P3E, 1WGW, 1E8S, 1E80

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

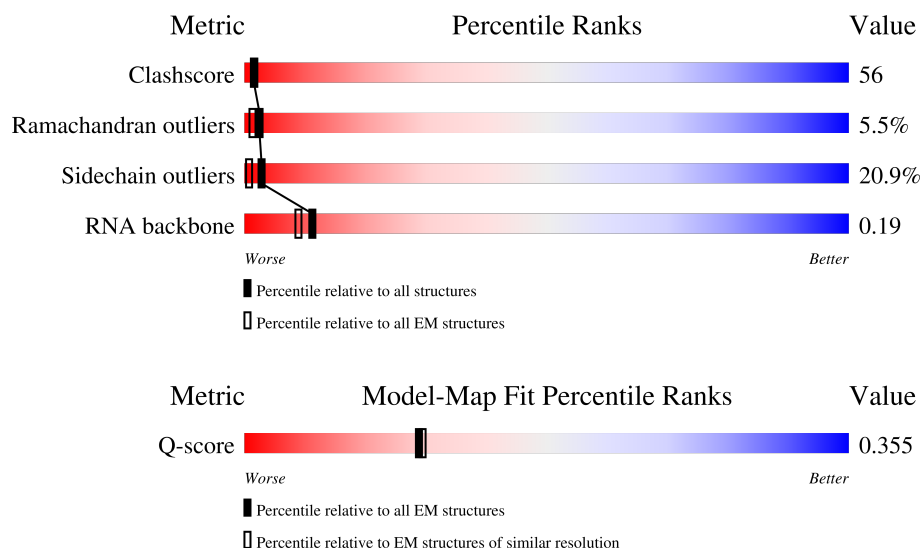
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 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.



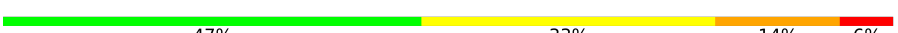
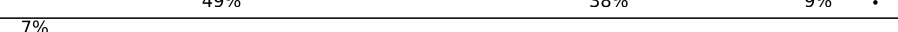
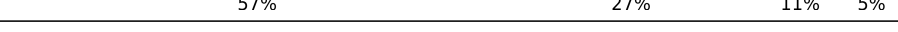
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10301 (3.25 - 4.25)

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 $\leq 5\%$. 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	A	244	
2	D	292	
3	G	238	

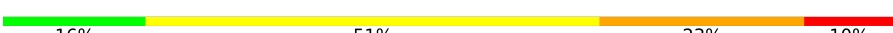
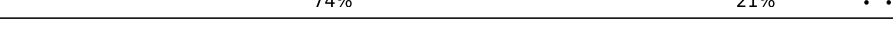
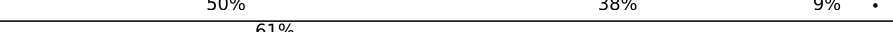
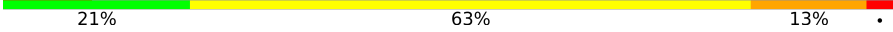
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Mol	Chain	Length	Quality of chain
4	H	190	
5	J	170	
6	L	210	
7	M	138	
8	N	203	
9	O	201	
10	Q	187	
11	R	180	
12	S	175	
13	T	159	
14	U	99	
15	V	131	
16	X	119	
17	Y	134	
18	Z	135	
19	a	147	
20	b	75	
21	c	94	
22	d	107	
23	e	128	
24	f	109	
25	g	114	
26	h	122	
27	i	102	
28	k	69	

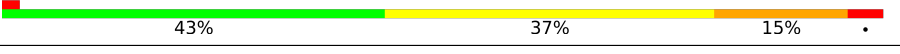
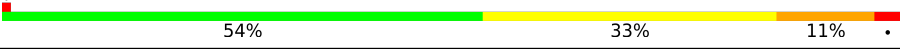
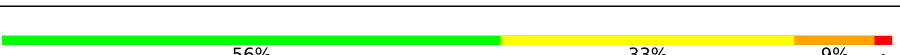
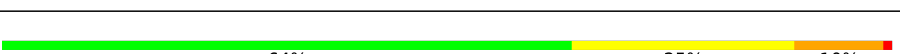
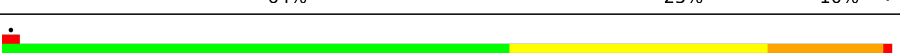
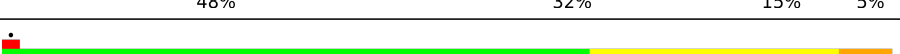
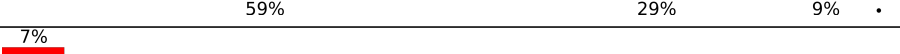
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Mol	Chain	Length	Quality of chain
29	l	50	
30	m	52	
31	o	104	
32	5	3658	
33	7	120	
34	8	156	
35	B	394	
36	C	367	
37	E	236	
38	F	225	
39	I	213	
40	P	153	
41	W	63	
42	j	86	
43	n	23	
44	p	91	
45	r	125	
46	K	163	
47	q	202	
48	z	426	
49	2	31	
50	3	76	
51	4	206	
52	9	105	
53	6	179	

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Mol	Chain	Length	Quality of chain
54	S2	1742	
55	SA	208	
56	SB	213	
57	SC	218	
58	SE	262	
59	SG	237	
60	SH	189	
61	SI	206	
62	SJ	185	
63	SL	152	
64	SN	149	
65	SO	136	
66	SV	82	
67	SW	129	
68	SX	141	
69	SY	126	
70	Sa	98	
71	Sb	83	
72	Se	57	
73	SD	227	
74	SF	191	
75	SK	98	
76	SM	124	
77	SP	96	
78	SQ	141	

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Mol	Chain	Length	Quality of chain
79	SR	129	
80	SS	137	
81	ST	141	
82	SU	104	
83	SZ	75	
84	Sc	64	
85	Sd	52	
86	Sf	71	
87	Sg	313	
88	S1	74	
89	S4	76	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
91	ZN	Sa	101	-	-	X	-
91	ZN	o	201	-	-	X	-

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 228197 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 protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 2 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 3 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	238	Total	C	N	O	S	0	0
			1912	1218	368	322	4		

- Molecule 4 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 5 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 6 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 7 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 8 is a protein called Ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 9 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 10 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 11 is a protein called Ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 12 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 13 is a protein called Ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 14 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 15 is a protein called Ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 16 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 17 is a protein called Ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 18 is a protein called Ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 19 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 20 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 21 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 22 is a protein called Ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 23 is a protein called Ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 24 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 25 is a protein called Ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 26 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 27 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 28 is a protein called Ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 29 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 30 is a protein called Ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 31 is a protein called Ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 32 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	3658	Total	C	N	O	P	0	0
			78406	34911	14352	25486	3657		

- Molecule 33 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 34 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 35 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 36 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 37 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 38 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 39 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 40 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 41 is a protein called Ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 42 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 43 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 44 is a protein called Ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 46 is a protein called Ribosomal protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	K	163	Total	C	N	O	S	0	0
			1238	773	230	230	5		

- Molecule 47 is a protein called Ribosomal protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	202	Total	C	N	O	S	0	0
			1556	989	272	286	9		

- Molecule 48 is a protein called SRP54.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	z	426	Total	C	N	O	S	0	0
			3241	2047	555	615	24		

- Molecule 49 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	31	Total	C	N	O	S	0	0
			233	167	32	32	2		

- Molecule 50 is a RNA chain called Val tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	76	Total	C	N	O	P	0	0
			1616	723	290	528	75		

- Molecule 51 is a RNA chain called SRP 7S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	206	Total	C	N	O	P	6	0
			4551	2026	836	1477	212		

- Molecule 52 is a protein called SRP19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	9	105	Total	C	N	O	S	0	0
			844	534	152	152	6		

- Molecule 53 is a protein called SRP68.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	179	Total	C	N	O	S	0	0
			1497	939	280	271	7		

- Molecule 54 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S2	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 55 is a protein called Ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 56 is a protein called Ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SB	213	Total	C	N	O	S	0	0
			1725	1093	311	308	13		

- Molecule 57 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SC	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 58 is a protein called Ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 59 is a protein called Ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 60 is a protein called Ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 61 is a protein called Ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 62 is a protein called Ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 63 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SL	152	Total	C	N	O	S	0	0
			1238	788	232	212	6		

- Molecule 64 is a protein called Ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 65 is a protein called Ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 66 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 67 is a protein called Ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 68 is a protein called Ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SX	141	Total	C	N	O	S	0	0
			1099	694	220	182	3		

- Molecule 69 is a protein called Ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- Molecule 70 is a protein called Ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sa	98	Total	C	N	O	S	0	0
			781	486	161	129	5		

- Molecule 71 is a protein called Ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 72 is a protein called Ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Se	57	Total	C	N	O	S	0	0
			452	279	99	73	1		

- Molecule 73 is a protein called Ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 74 is a protein called Ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 75 is a protein called Ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 76 is a protein called Ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SM	124	Total	C	N	O	S	0	0
			960	600	171	181	8		

- Molecule 77 is a protein called Ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SP	96	Total	C	N	O	S	0	0
			805	506	158	135	6		

- Molecule 78 is a protein called Ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 79 is a protein called Ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SR	129	Total	C	N	O	S	0	0
			1047	658	193	191	5		

- Molecule 80 is a protein called Ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	SS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 81 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	ST	141	Total	C	N	O	S	0	0
			1101	690	212	196	3		

- Molecule 82 is a protein called Ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	SU	104	Total	C	N	O	S	0	0
			818	513	153	148	4		

- Molecule 83 is a protein called Ribosomal protein es25.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 84 is a protein called Ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 85 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Sd	52	Total	C	N	O	S	0	0
			434	273	87	69	5		

- Molecule 86 is a protein called Ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Sf	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 87 is a protein called Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 88 is a protein called SRP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	S1	74	Total	C	N	O	S	0	0
			608	388	105	110	5		

- Molecule 89 is a protein called SRP14.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	S4	76	Total	C	N	O	S	0	0
			604	382	105	113	4		

- Molecule 90 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
90	D	1	Total	Mg	0
			1	1	
90	V	1	Total	Mg	0
			1	1	
90	g	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
90	5	116	Total 116	Mg 116	0
90	7	5	Total 5	Mg 5	0
90	8	6	Total 6	Mg 6	0
90	S2	36	Total 36	Mg 36	0

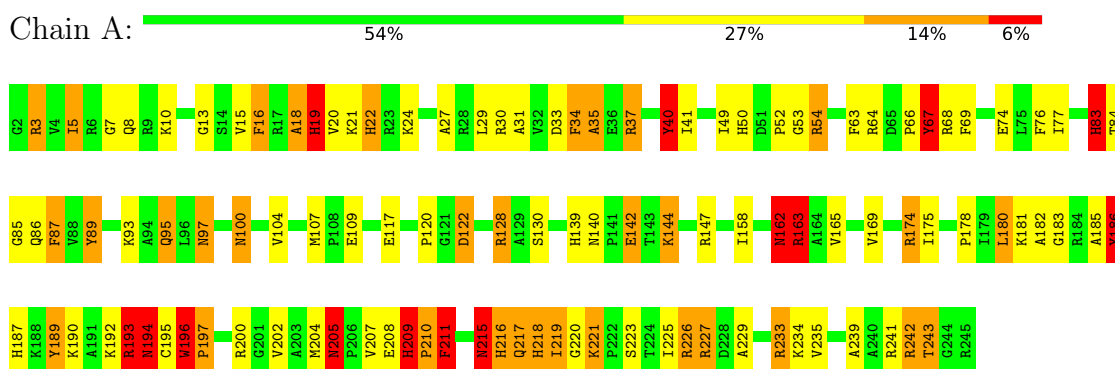
- Molecule 91 is ZINC ION (CCD ID: ZN) (formula: Zn).

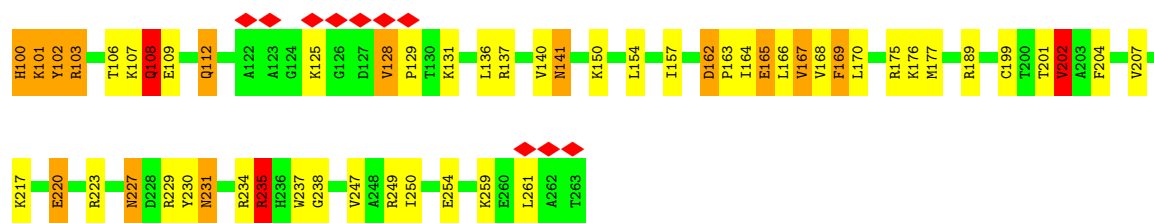
Mol	Chain	Residues	Atoms		AltConf
91	m	1	Total 1	Zn 1	0
91	o	1	Total 1	Zn 1	0
91	j	1	Total 1	Zn 1	0
91	Sa	1	Total 1	Zn 1	0

3 Residue-property plots

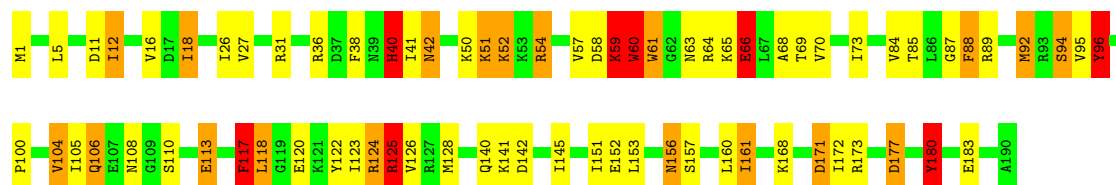
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Ribosomal protein uL2

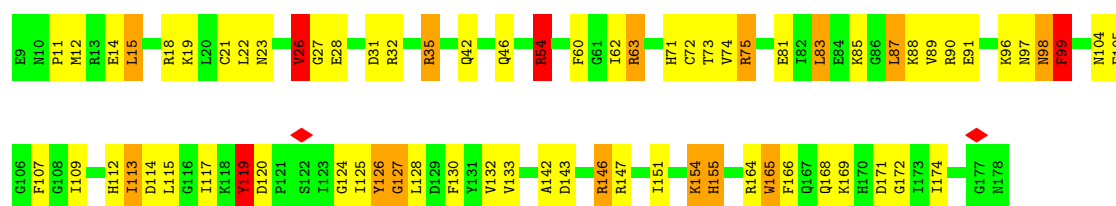




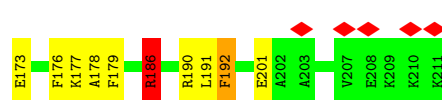
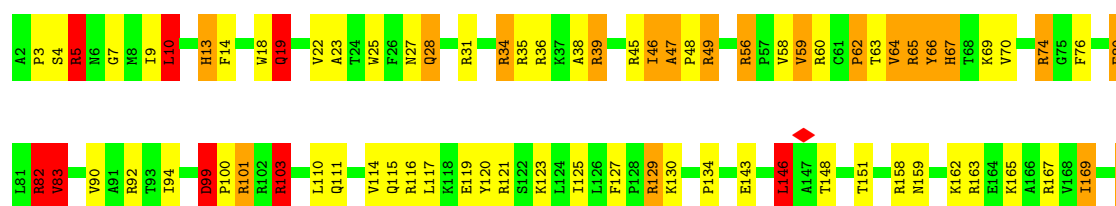
• Molecule 4: Ribosomal protein uL6



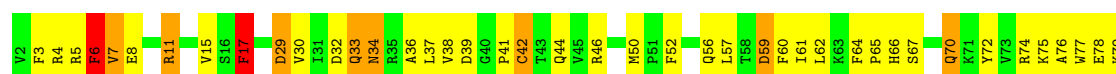
• Molecule 5: Ribosomal protein uL5

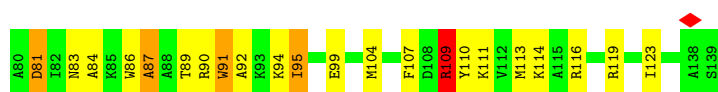


• Molecule 6: Ribosomal protein eL13

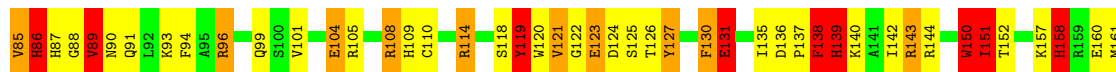
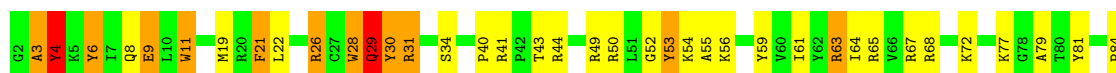


• Molecule 7: Ribosomal protein eL14

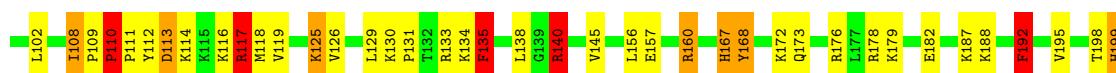
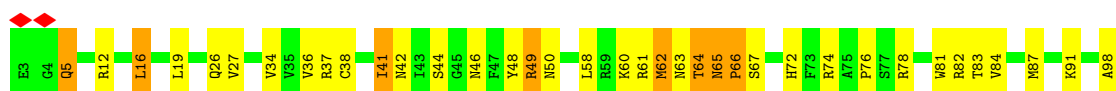




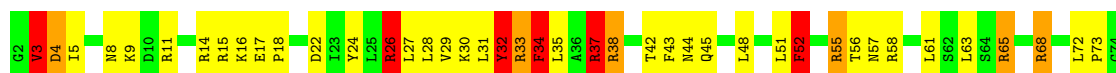
• Molecule 8: Ribosomal protein eL15



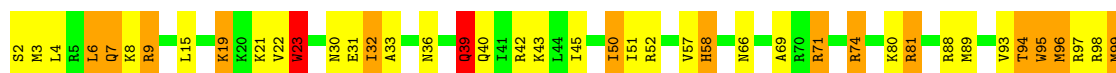
• Molecule 9: Ribosomal protein uL13

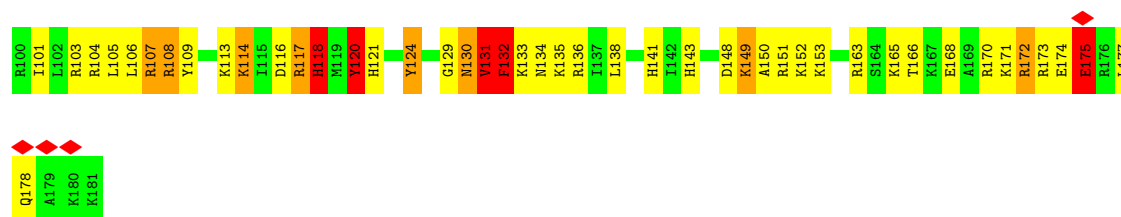


• Molecule 10: Ribosomal protein eL18



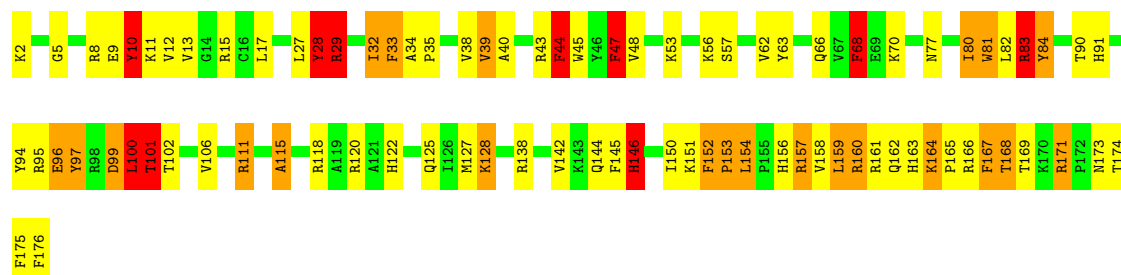
• Molecule 11: Ribosomal protein eL19





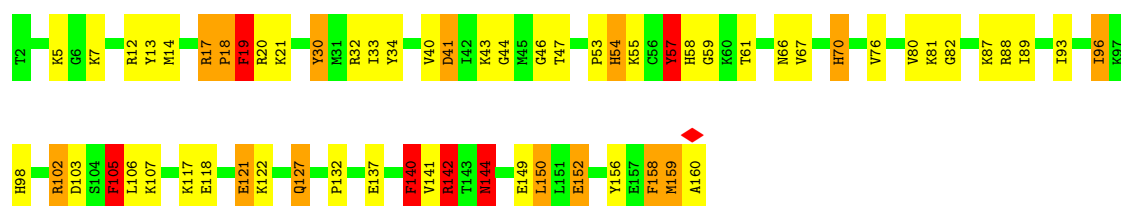
• Molecule 12: Ribosomal protein eL20

Chain S: 50% 31% 13% 6%



• Molecule 13: Ribosomal protein eL21

Chain T: 60% 27% 9%



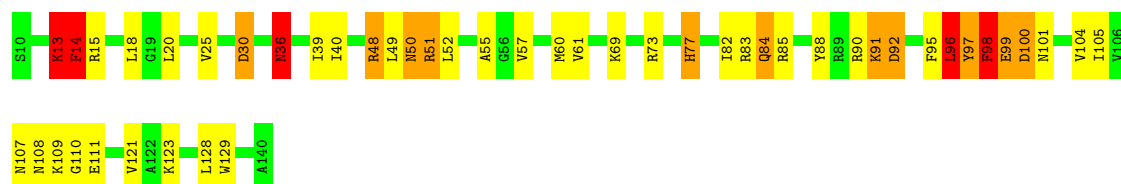
• Molecule 14: Ribosomal protein eL22

Chain U: 69% 21% 8%



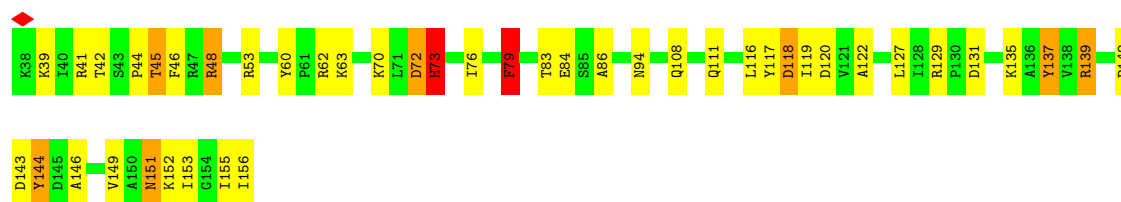
• Molecule 15: Ribosomal protein uL14

Chain V: 63% 24% 8%



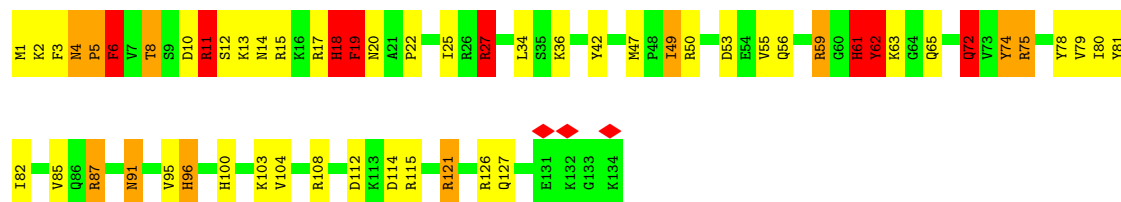
• Molecule 16: Ribosomal protein uL23

Chain X: 



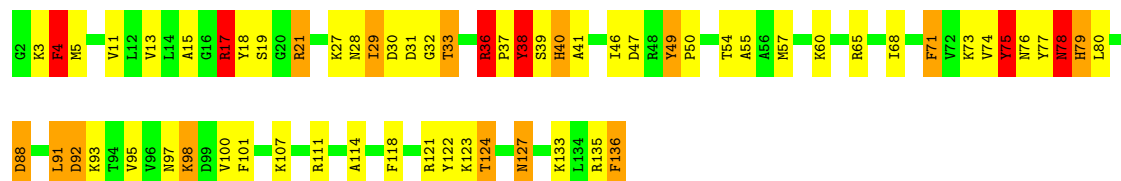
- Molecule 17: Ribosomal protein uL24

Chain Y: 



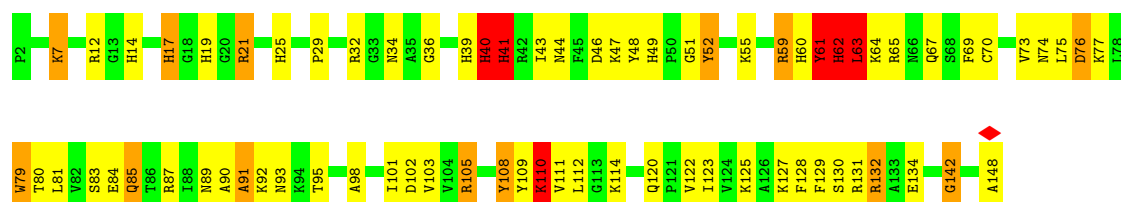
- Molecule 18: Ribosomal protein eL27

Chain Z: 



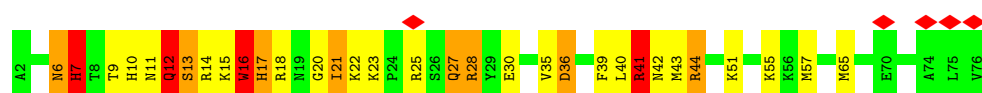
- Molecule 19: Ribosomal protein uL15

Chain a: 



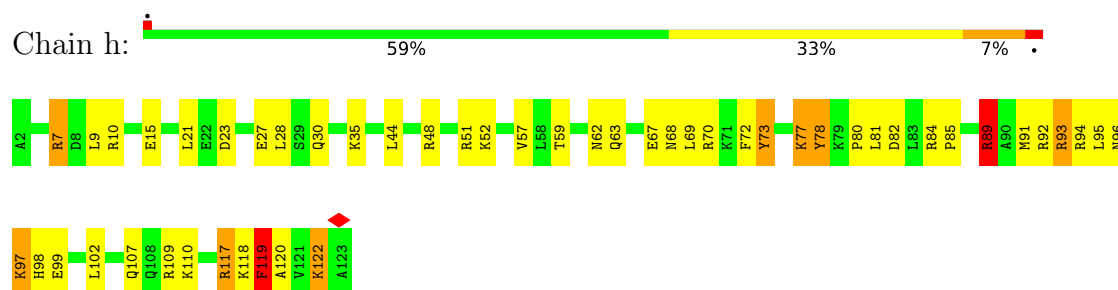
- Molecule 20: Ribosomal protein eL29

Chain b: 

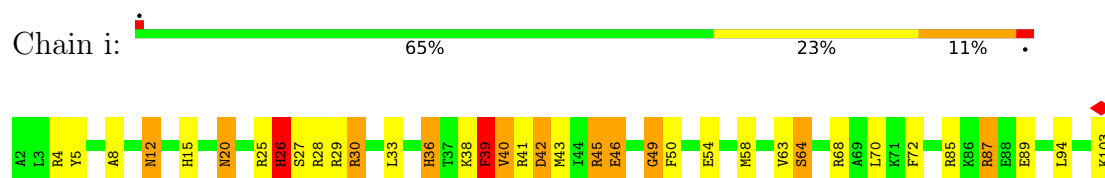


- Molecule 21: Ribosomal protein eL30

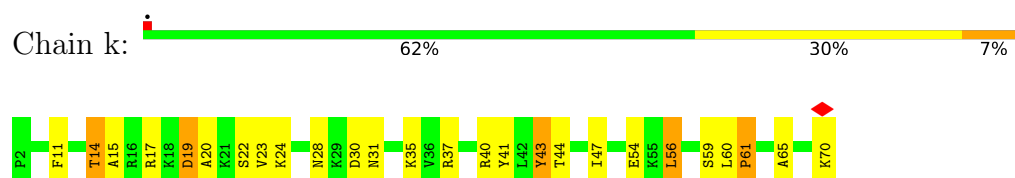
- Molecule 26: Ribosomal protein uL29



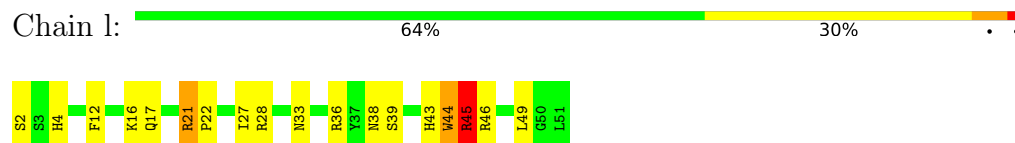
- Molecule 27: Ribosomal protein eL36



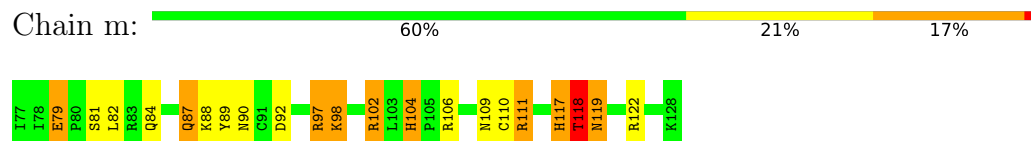
- Molecule 28: Ribosomal protein eL38



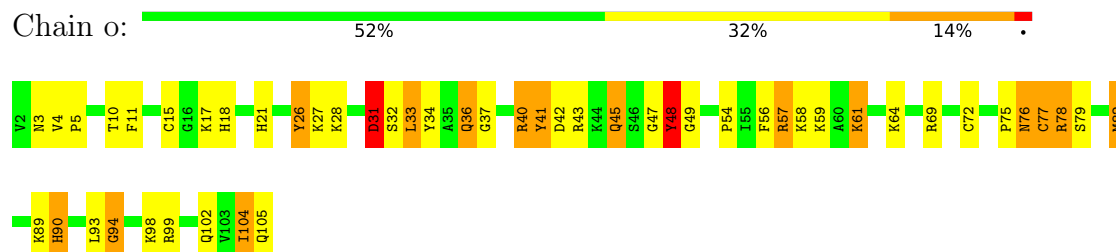
- Molecule 29: Ribosomal protein eL39



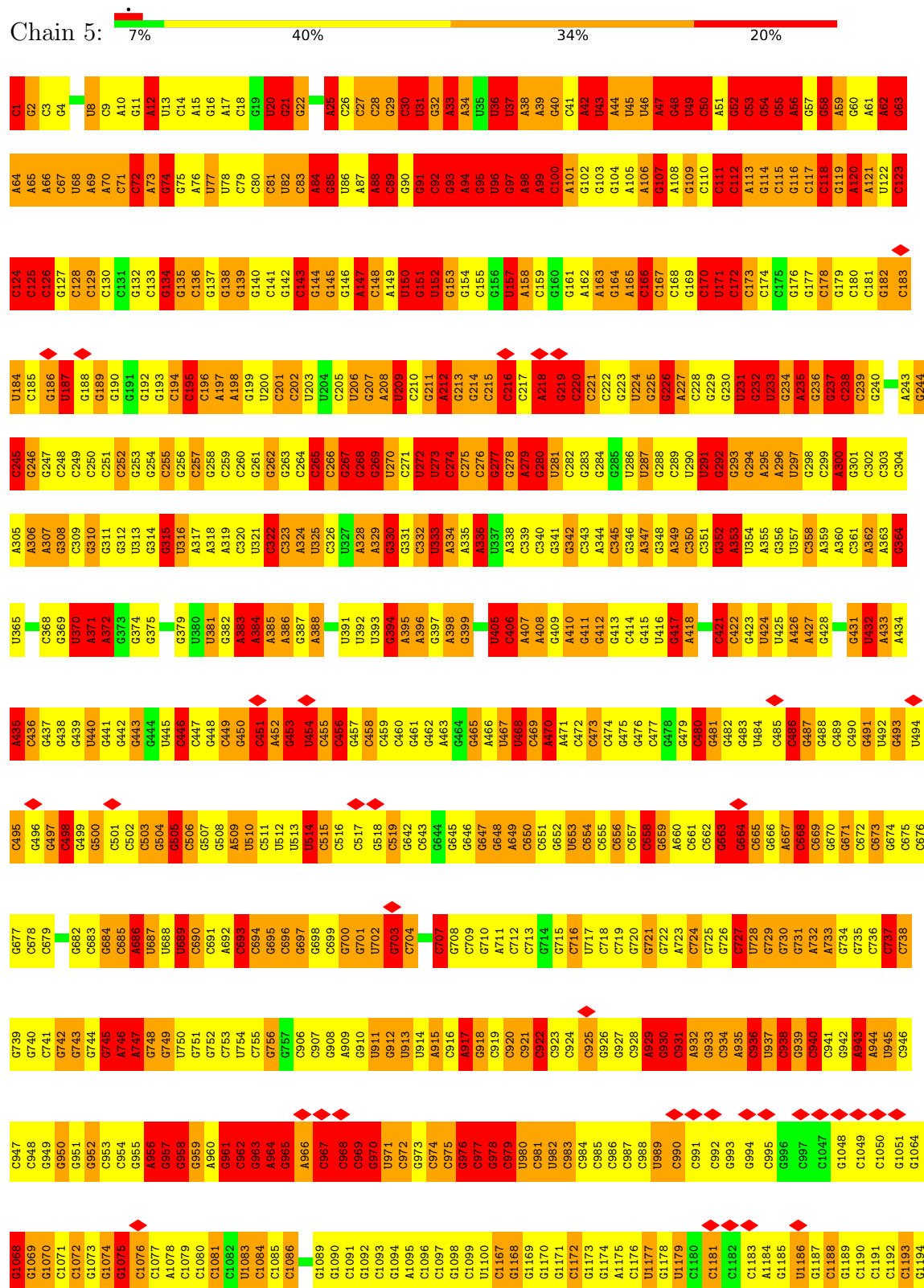
- Molecule 30: Ribosomal protein eL40



- Molecule 31: Ribosomal protein eL42



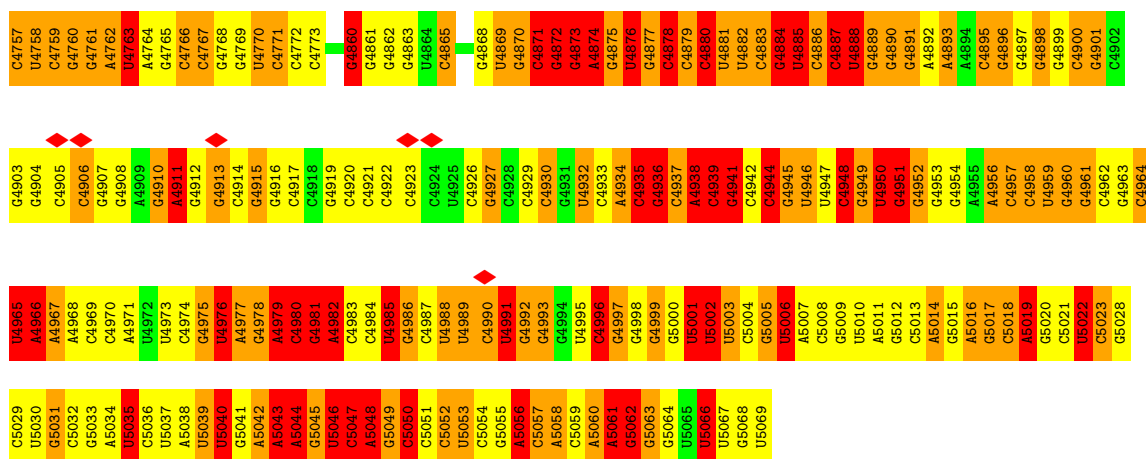
• Molecule 32: 28S ribosomal RNA



C2011	G1951	G1830	G1769	G1891	G1506	G1444	C1384	A1324	C1264	G1195
A2012	G1952	G1831	A1770	C1892	C1507	U1445	G1385	C1525	G1265	G1196
A2013	U1953	C1832	U1771	U1893	U1508	C1446	A1508	A1526	G1266	C1197
C2014	C1894	C1833	C1772	U1894	C1509	C1447	C1386	C1327	G1198	G1199
U2015	G1955	U1834	U1773	U1895	U1510	G1448	A1388	G1328	C1267	G1200
C2016	A1956	G1835	C1774	C1896	U1511	C1449	U1389	G1329	G1268	G1201
A2017	U1957	G1836	C1775	G1897	G1512	C1450	G1390	A1330	G1269	U1201
C2018	C1898	A1837	A1776	C1898	U1513	C1451	A1391	G1331	A1270	C1202
C2019	G1899	A1838	A1777	A1899	U1514	G1452	A1392	C1332	G1271	C1203
U2020	A1900	C1839	C1777	C1718	U1515	G1453	G1393	A1333	C1272	C1204
C2021	C1901	G1840	C1778	A1719	G1516	G1454	G1394	A1334	C1273	G1205
C2022	A1962	G1842	U1779	G1720	G1517	G1455	U1395	G1335	A1274	C1206
C2023	C1903	A1843	A1780	G1721	A1518	G1456	G1396	G1336	G1275	C1207
G2024	G1904	G1844	U1781	C1722	C1519	G1457	A1397	A1337	C1276	G1208
A2025	U1905	U1945	U1782	A1723	C1520	C1458	A1398	G1338	G1277	U1209
C2026	C1906	G1846	C1783	G1724	C1521	A1459	G1399	U1339	C1278	C1210
A2027	A1907	C1847	U1784	U1725	G1522	C1460	G1400	C1340	A1279	G1211
G1968	A1908	G1848	C1785	C1585	A1523	C1461	C1401	U1341	C1280	G1212
G1969	G1909	U1849	A1786	G1586	A1524	C1463	G1402	A1342	G1281	G1213
A1970	G1910	A1850	U1787	G1587	A1525	C1464	G1403	A1343	G1282	C1214
C2034	C1911	G1851	A1788	U1588	G1526	C1465	G1404	C1344	G1283	C1215
G1972	G1912	U1852	C1789	C1589	U1528	G1466	C1405	C1345	G1284	G1216
G1973	C1913	G1853	U1790	C1590	U1529	C1467	G1406	C1346	U1285	G1217
U1974	C1914	G1854	U1791	U1591	G1530	C1468	C1407	G1347	G1286	G1218
G1975	C1915	G1855	U1792	G1592	G1531	C1469	G1408	U1348	G1287	G1219
G1976	G1916	C1856	A1793	A1593	A1533	G1470	C1409	G1349	G1288	G1220
C1977	A1917	C1857	A1794	C1594	A1534	U1471	U1410	C1350	C1289	U1221
C1978	A1918	A1858	U1795	C1595	U1535	C1472	C1411	G1351	G1290	A1222
A1979	G1919	G1859	U1796	U1596	U1536	U1473	G1412	C1352	G1291	G1232
C1920	U1960	U1860	G1797	G1597	U1537	C1474	G1413	G1353	C1292	G1233
G1921	G1921	U1861	G1798	C1598	U1538	G1475	C1414	A1354	G1293	G1234
G1922	G1922	U1862	G1799	A1599	G1539	C1476	G1415	G1355	A1294	G1235
A1923	G1923	U1863	C1740	C1600	C1540	C1477	G1416	U1356	C1295	C1236
C1924	G1924	C1864	A1742	A1601	U1541	C1478	C1417	C1357	G1296	C1237
A1984	G1925	G1865	A1743	U1602	U1542	G1479	G1418	G1358	U1297	A1238
U1866	U1866	U1866	U1744	C1603	G1543	C1480	G1419	G1359	C1298	C1239
U1927	U1927	A1867	G1745	G1604	G1544	G1481	A1420	G1360	G1299	G1240
A1904	C1928	A1868	A1746	G1605	G1545	C1482	G1421	G1361	G1300	C1241
G1869	A1929	A1669	U1747	G1608	C1546	C1483	G1422	G1362	C1301	G1242
U1930	U1930	G1670	U1748	U1609	A1547	G1484	U1423	C1363	U1302	C1243
C1931	C1931	U1671	A1749	C1610	G1548	C1485	G1424	A1364	A1303	G1244
A1932	A1932	G1672	G1750	C1611	G1549	C1486	G1425	C1365	C1304	G1245
G1933	G1933	A1872	G1751	G1612	U1550	G1487	G1426	G1366	C1305	G1246
A1934	A1934	G1674	A1751	A1613	C1551	G1488	A1427	G1367	A1307	U1247
C1935	C1935	C1675	G1752	C1614	G1552	G1489	U1428	C1368	C1308	C1248
C1936	C1936	C1676	G1753	C1615	A1553	G1490	U1429	C1369	C1309	C1249
C1937	C1937	C1677	U1754	U1616	A1554	A1491	C1430	G1370	C1310	C1250
C1938	C1938	C1678	U1755	U1617	G1555	G1492	C1431	A1371	G1311	C1251
A1939	A1939	A1816	U1756	G1618	C1556	G1493	G1432	A1372	C1312	G1252
G1940	G1940	G1680	U1757	G1619	C1557	U1494	A1433	A1373	C1313	G1253
A1941	A1941	G1681	G1758	U1820	A1558	A1497	G1434	G1374	C1314	A1254
A1942	A1942	A1682	G1759	A1621	G1559	A1498	G1435	C1375	C1315	A1255
G1883	G1883	U1683	G1760	U1622	A1560	C1499	C1436	C1376	G1316	G1256
A1944	A1944	A1684	G1761	A1623	G1561	U1500	U1437	G1377	U1317	A1257
G1945	G1945	G1685	C1762	G1625	U1562	A1501	C1438	C1378	C1318	G1258
G1886	G1886	C1686	C1763	G1626	A1563	C1501	U1439	C1379	G1319	G1259
C1887	C1887	U1687	G1764	G1627	A1564	G1502	U1440	C1380	U1320	G1260
A1988	A1988	U1688	A1765	G1628	A1565	A1503	C1441	U1381	G1321	G1261
U1949	U1949	G1689	U1766	C1629	C1566	G1504	C1442	A1382	A1322	G1262
G1890	G1890	C1690	A1767	G1629	U1567	C1505	A1443	G1383	A1323	A1263
C2007	G2007									
U2008	U2008									
A2009	A2009									
A2010	A2010									

C3568	C3569	C3598	C3660	C3661	C3660	A2798	G2736	C2672	A2611	A2551	C2491	A2431	G2305	G2245	C2074
G3660	G3661	A3599	C2861	C2862	C2863	G2799	C2737	G2673	C2612	G2552	C2492	U2432	G2306	G2246	G2075
C3660	C3661	C3600	G2863	G2864	G2865	C2802	C2738	A2674	C2613	A2553	G2493	G2433	A2307	C2247	C2076
C3662	C3663	C3602	A2864	A2865	A2866	G2803	G2739	G2675	C2614	G2554	U2494	G2434	A2308	C2248	C2077
A3663	A3664	G3603	U2865	U2866	U2867	G2804	U2741	A2677	C2615	G2555	G2495	G2435	C2309	C2249	G2078
G3664	G3665	A3604	C2866	C2867	C2868	G2805	G2742	A2678	C2616	G2557	G2497	G2436	C2310	C2250	G2079
C3666	C3667	C3605	A2867	A2868	A2869	G2806	G2743	G2679	G2617	G2558	C2498	G2437	C2311	G2251	U2080
C3668	C3669	U3606	G2870	G2871	G2872	G2807	A2744	G2680	G2618	G2559	C2499	A2376	U2312	G2252	G2081
G3669	G3670	A3608	U2871	U2872	U2873	G2808	A2745	C2682	U2620	C2560	U2500	G2377	G2313	A2253	G2082
C3670	C3671	A3610	A2873	A2874	A2875	G2811	U2746	C2683	A2621	C2561	C2501	G2378	G2314	G2254	C2083
G3671	G3672	A3611	G2876	G2877	G2878	G2812	G2747	C2684	G2622	C2562	G2502	A2382	G2315	G2255	C2084
C3673	C3674	C3612	U2879	U2880	U2881	A2813	U2748	G2685	G2623	C2563	G2503	C2383	G2316	G2256	G2085
G3675	G3676	G3613	G2880	G2881	G2882	A2814	G2749	G2686	G2624	C2564	C2504	C2384	G2317	G2257	G2086
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C3679	C3680	G3616	G2889	G2890	G2891	G2817	G2752	C2689	G2627	C2567	G2507	G2387	G2320	G2260	U2090
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C3683	C3684	C3621	U2893	U2894	U2895	U2819	G2754	U2691	C2629	C2569	G2509	A2449	G2322	G2262	G2092
G3685	G3686	A3622	G2896	G2897	G2898	G2820	A2755	U2692	U2630	C2570	G2510	G2450	G2323	G2263	A2093
C3687	C3688	C3623	G2899	G2900	G2901	C2821	G2756	G2693	U2631	C2571	A2511	A2451	C2324	G2264	G2094
G3689	G3690	G3624	U2902	U2903	U2904	G2822	U2757	U2632	U2632	C2572	A2512	G2452	G2325	A2265	A2095
C3691	C3692	A3624	G2905	G2906	G2907	G2823	G2758	A2694	U2633	A2573	A2513	A2453	G2326	C2266	G2096
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U3695	U3696	G3634	G2911	G2912	G2913	G2825	U2760	A2696	U2635	C2575	G2515	G2455	G2328	U2268	G2098
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C3701	C3702	U3637	G2910	G2911	G2912	G2828	U2763	G2706	C2645	G2578	G2518	G2458	G2331	A2271	A2101
A3702	A3703	G3638	U2904	U2905	U2906	G2829	U2764	U2707	G2646	C2579	G2519	G2459	G2332	G2272	G2102
G3704	G3705	U3640	G2907	G2908	G2909	G2830	U2765	U2708	C2647	G2580	G2520	A2460	G2333	C2271	G2103
C3706	C3707	A3641	G2910	G2911	G2912	G2831	U2766	U2709	G2648	C2581	G2521	G2461	G2334	G2272	G2104
U3707	U3708	G3642	G2913	G2914	G2915	G2832	U2767	G2710	G2649	C2582	G2522	G2462	G2335	G2273	G2105
C3709	C3710	A3643	U2904	U2905	U2906	G2833	U2768	G2711	G2650	C2583	G2523	G2463	G2336	G2274	A2106
G3711	G3712	G3644	G2907	G2908	G2909	G2834	U2769	U2712	C2651	G2584	U2524	G2464	G2337	G2275	C2107
A3713	A3714	U3645	G2910	G2911	G2912	G2835	U2770	G2713	C2652	G2585	G2525	G2465	G2338	A2276	G2108
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G3717	G3718	G3647	G2913	G2914	G2915	G2837	U2772	G2715	C2654	C2587	G2527	G2467	G2340	G2278	G2110
C3719	C3720	A3648	U2904	U2905	U2906	G2838	U2773	G2716	G2655	C2588	G2528	U2468	G2341	A2279	G2111
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C3765	C3766	C3670	G2907	G2908	G2909	G2861	U2796	G2739	G2671	G2611	G2551	G2491	A2369	G2303	G2134
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G3771	G3772	G3673	U2904	U2905	U2906	G2864	U2799	G2742	G2674	G2614	G2554	G2494	A2372	G2306	G2137
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U3787	U3788	G3681	U2904	U2905	U2906	G2872	U2807	G2750	U2679	C2562	G2502	G2502	A2380	G2314	G2145
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U4699	A4570	A4510	C4387	G4267	U4202	G4141	G4081	G3904	U3844	C3781	G3720
A4700	A4571	A4511	A4388	A4268	A4203	C4142	G4082	A3905	A3845	G3782	G3721
G4701	U4572	U4512	C4389	G4269	C4204	C4143	U4083	A3906	C3846	A3783	G3722
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U4703	G4514	G4514	C4391	A4271	C4206	C4144	A4085	A3908	U3848	A3785	G3725
C4704	A4574	G4515	G4392	G4272	C4207	C4145	G4086	C3909	C3849	U3786	
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G4694	U4629	G4566	C4444	A4324	A4324	C4199	C4136	A4078	G3901	A3775	
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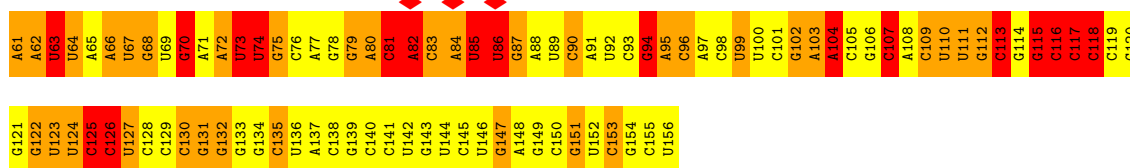
• Molecule 33: 5S ribosomal RNA

Chain 7: 16% 51% 23% 10%



• Molecule 34: 5.8S ribosomal RNA

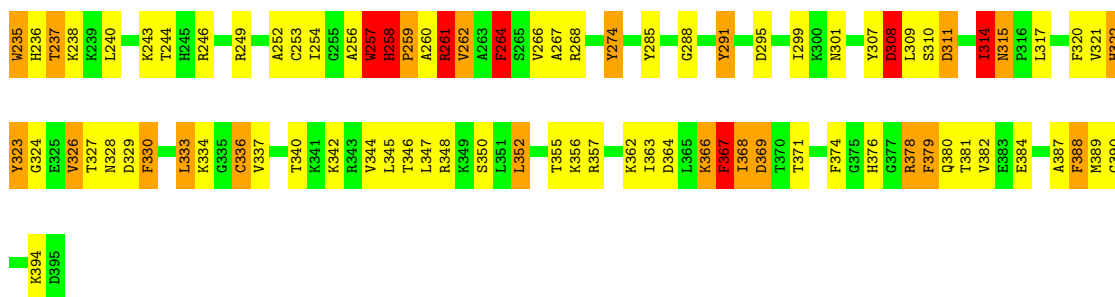
Chain 8: 45% 34% 19%



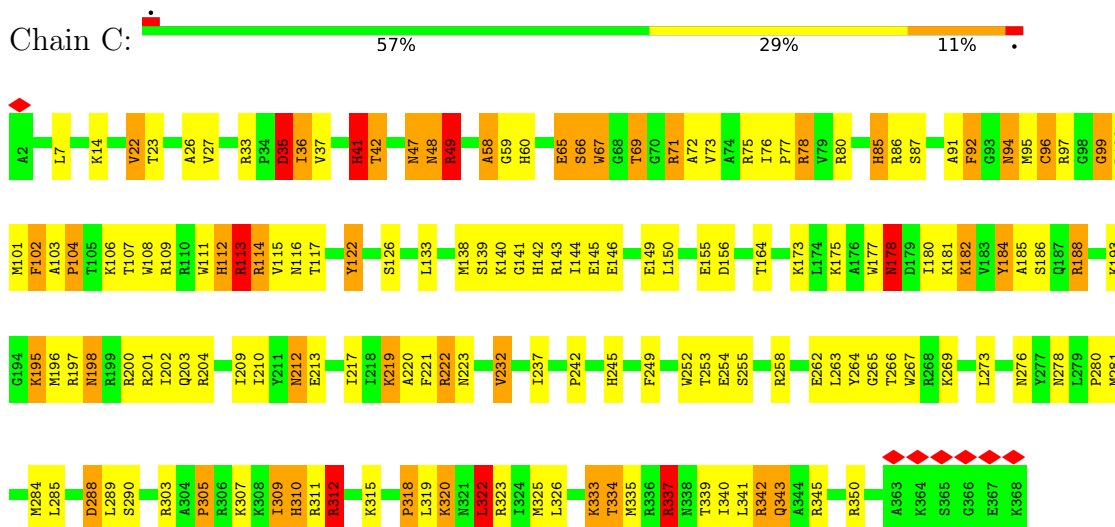
• Molecule 35: Ribosomal protein uL3

Chain B: 46% 34% 14% 5%

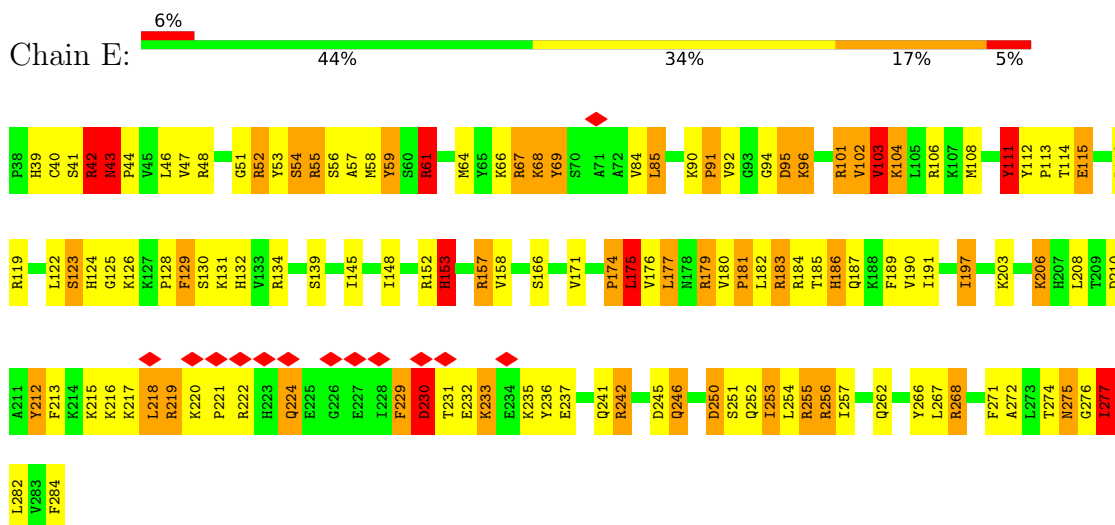




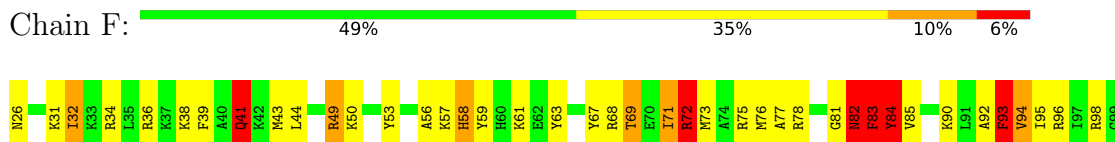
• Molecule 36: Ribosomal protein uL4

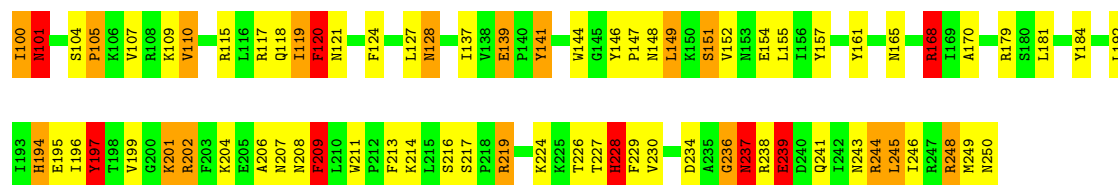


• Molecule 37: Ribosomal protein eL6

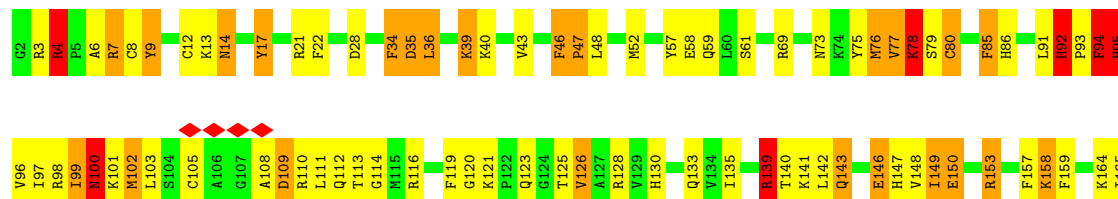


• Molecule 38: Ribosomal protein uL30

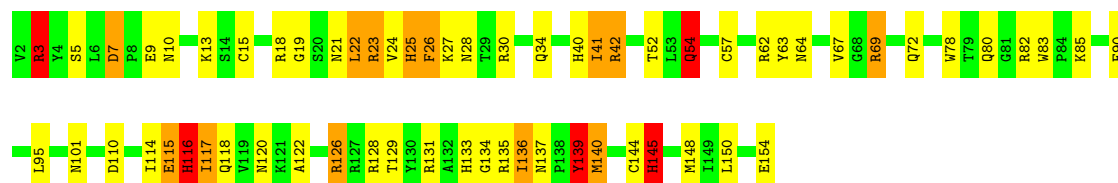




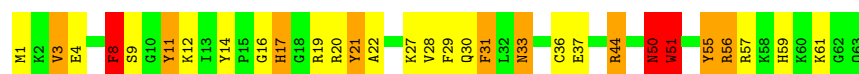
• Molecule 39: Ribosomal protein uL16



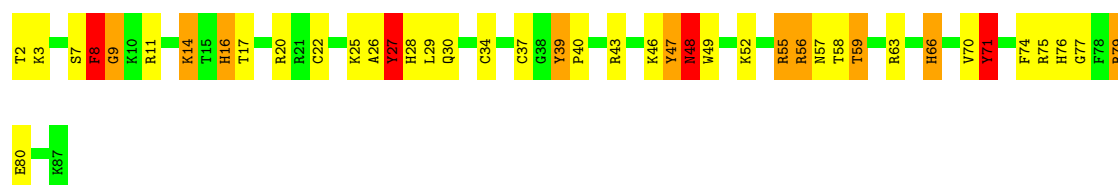
• Molecule 40: Ribosomal protein uL22



• Molecule 41: Ribosomal protein eL24

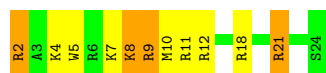


• Molecule 42: Ribosomal protein eL37



• Molecule 43: Ribosomal protein eL41

Chain n: 



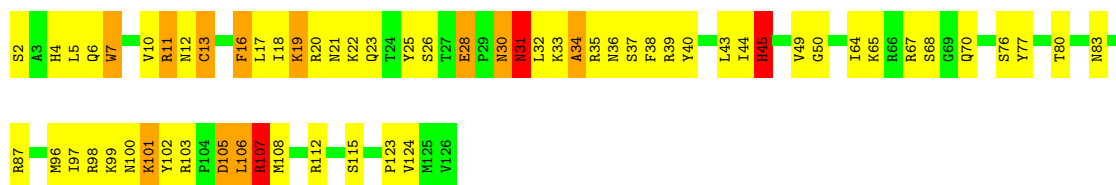
• Molecule 44: Ribosomal protein eL43

Chain p: 



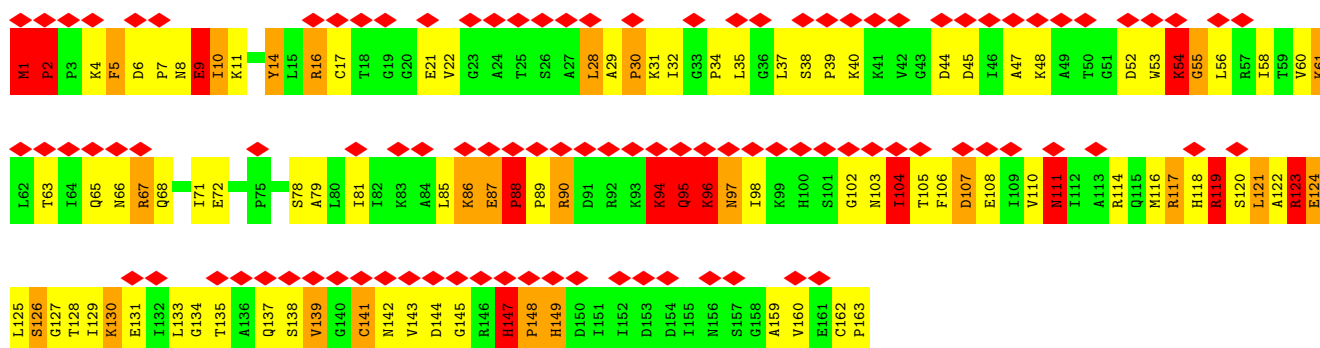
• Molecule 45: Ribosomal protein eL28

Chain r: 



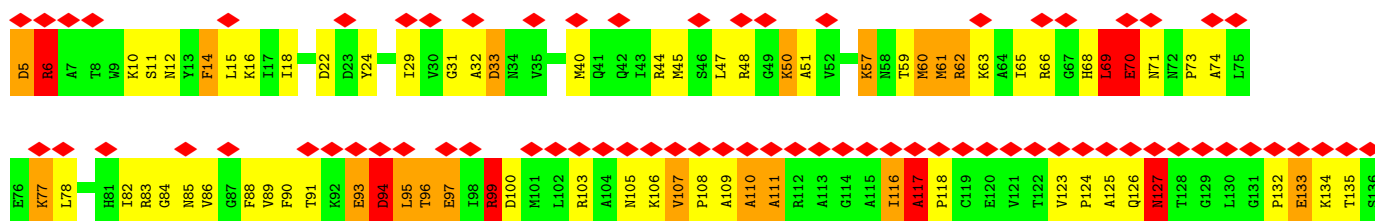
• Molecule 46: Ribosomal protein uL11

Chain K: 



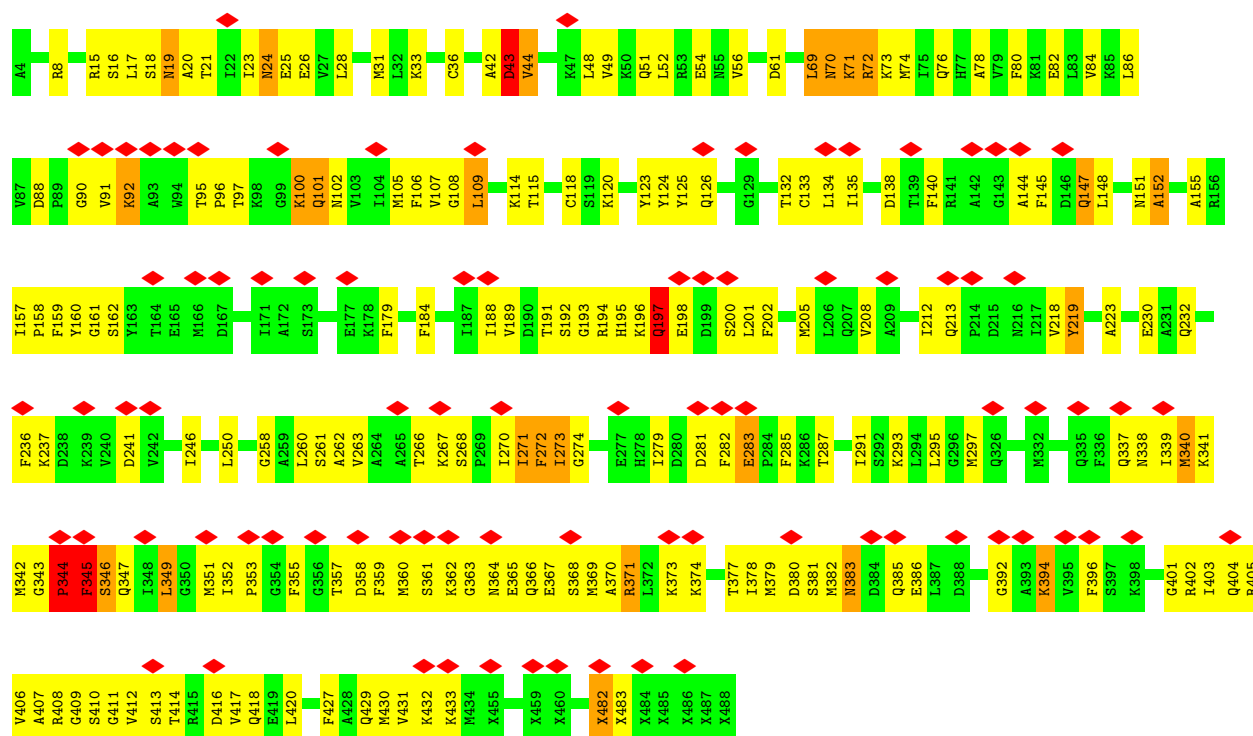
• Molecule 47: Ribosomal protein uL10

Chain q: 





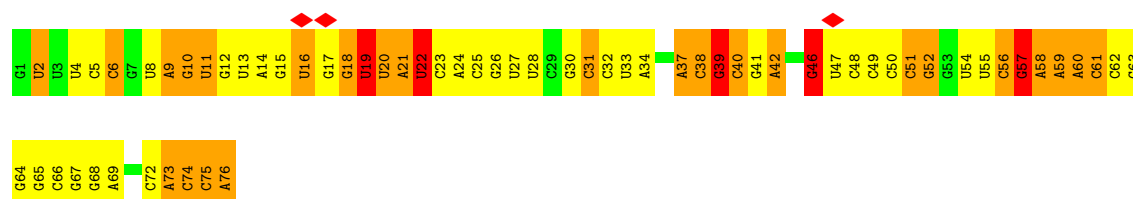
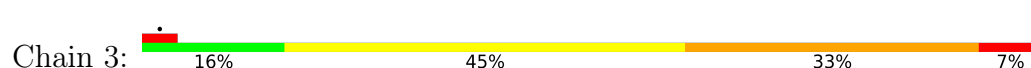
• Molecule 48: SRP54



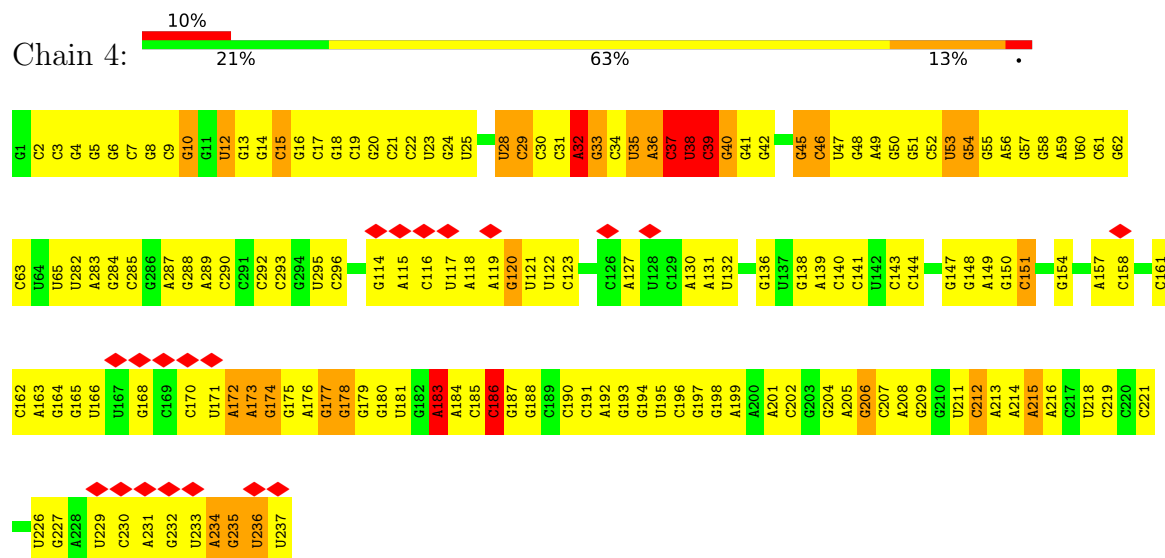
• Molecule 49: Nascent chain



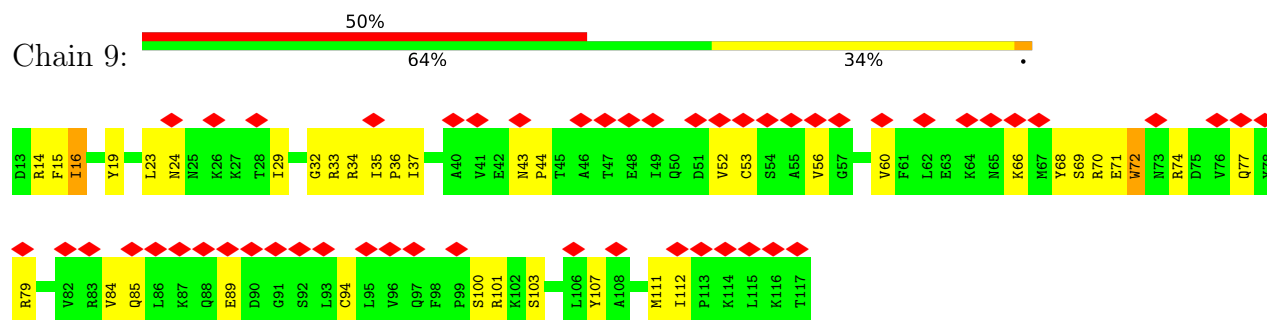
• Molecule 50: Val tRNA



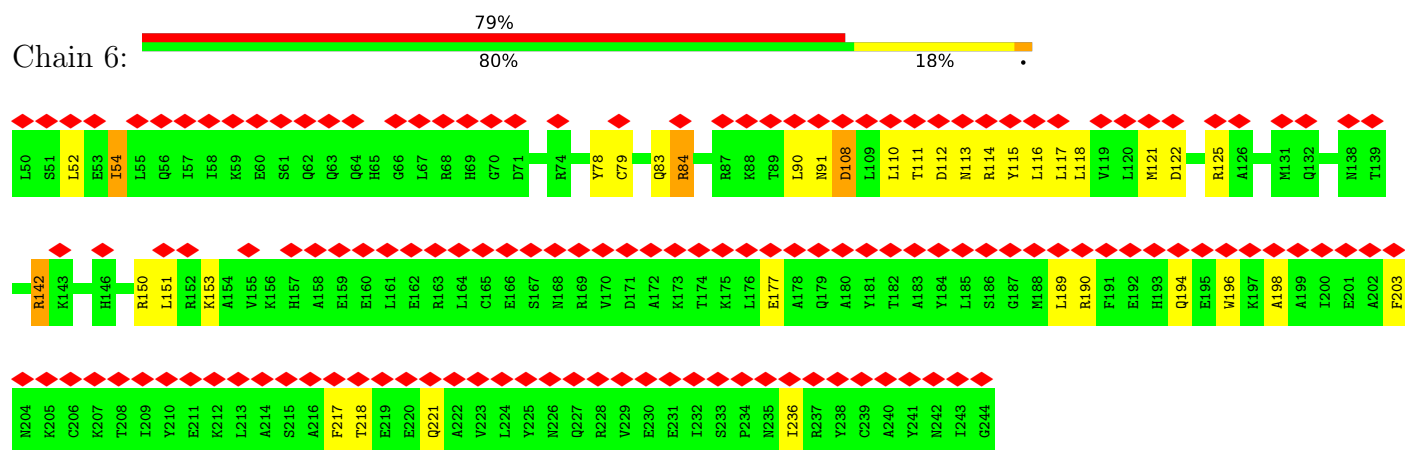
- Molecule 51: SRP 7S RNA



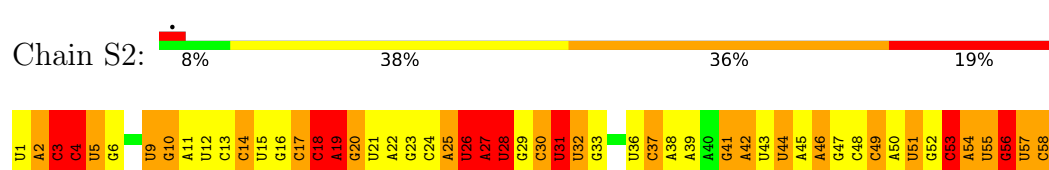
- Molecule 52: SRP19



- Molecule 53: SRP68

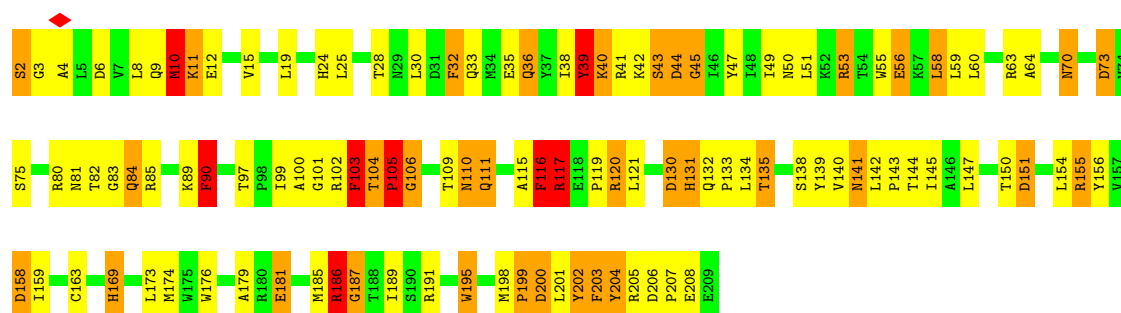


- Molecule 54: 18S ribosomal RNA

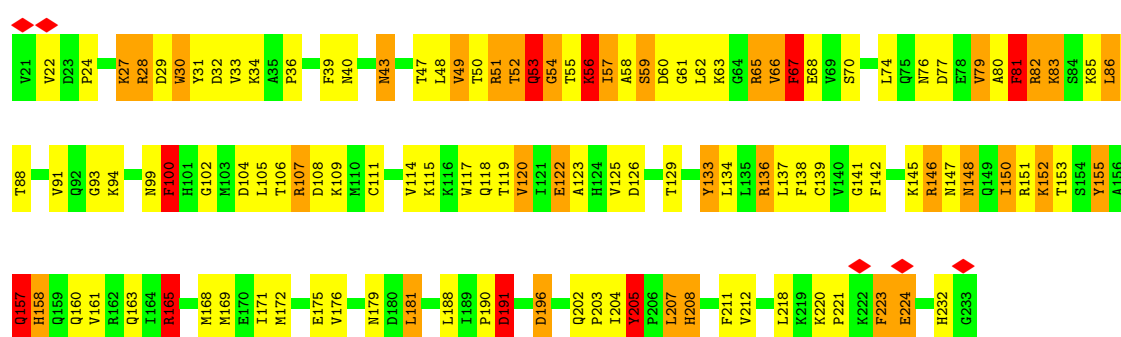


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U804	U805	U806	G807	U808	A809	G810	A811	U812	G813	U814	U815	A816	G817	U818	A819	U820	G821	U822	U823	C824	U825	A826	U827	U828	G829	C830	U831	C832	U833	G834	U835	C836	U837	G838	U839	C840	U841	C842	U843	G844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	U901	U902	U903	U904	U905	U906	U907	U908	U909	U910	U911	U912	U913	U914	U915	U916	U917	U918	U919	U920	U921	U922	U923	U924	U925	U926	U927	U928	U929	U930	U931	U932	U933	U934	U935	U936	U937	U938	U939	U940	U941	U942	U943	U944	U945	U946	U947	U948	U949	U950	U951	U952	U953	U954	U955	U956	U957	U958	U959	U960	U961	U962	U963	U964	U965	U966	U967	U968	U969	U970	U971	U972	U973	U974	U975	U976	U977	U978	U979	U980	U981	U982	U983	U984	U985	U986	U987	U988	U989	U990	U991	U992	U993	U994	U995	U996	U997	U998	U999	U1000	U1001	U1002	U1003	U1004	U1005	U1006	U1007	U1008	U1009	U1010	U1011	U1012	U1013	U1014	U1015	U1016	U1017	U1018	U1019	U1020	U1021	U1022	U1023	U1024	U1025	U1026	U1027	U1028	U1029	U1030	U1031	U1032	U1033	U1034	U1035	U1036	U1037	U1038	U1039	U1040	U1041	U1042	U1043	U1044	U1045																																																																																																																																																																																																																																																																																																																					
U566	U567	U568	U569	U570	U571	U572	U573	U574	U575	U576	U577	U578	U579	U580	U581	U582	U583	U584	U585	U586	U587	U588	U589	U590	U591	U592	U593	U594	U595	U596	U597	U598	U599	U600	U601	U602	U603	U604	U605	U606	U607	U608	U609	U610	U611	U612	U613	U614	U615	U616	U617	U618	U619	U620	U621	U622	U623	U624	U625	U626	U627	U628	U629	U630	U631	U632	U633	U634	U635	U636	U637	U638	U639	U640	U641	U642	U643	U644	U645	U646	U647	U648	U649	U650	U651	U652	U653	U654	U655	U656	U657	U658	U659	U660	U661	U662	U663	U664	U665	U666	U667	U668	U669	U670	U671	U672	U673	U674	U675	U676	U677	U678	U679	U680	U681	U682	U683	U684	U685	U686	U687	U688	U689	U690	U691	U692	U693	U694	U695	U696	U697	U698	U699	U700	U701	U702	U703	U704	U705	U706	U707	U708	U709	U710	U711	U712	U713	U714	U715	U716	U717	U718	U719	U720	U721	U722	U723	U724	U725	U726	U727	U728	U729	U730	U731	U732	U733	U734	U735	U736	U737	U738	U739	U740	U741	U742	U743	U744	U745	U746	U747	U748	U749	U750	U751	U752	U753	U754	U755	U756	U757	U758	U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780	U781	U782	U783	U784	U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	U901	U902	U903	U904	U905	U906	U907	U908	U909	U910	U911	U912	U913	U914	U915	U916	U917	U918	U919	U920	U921	U922	U923	U924	U925	U926	U927	U928	U929	U930	U931	U932	U933	U934	U935	U936	U937	U938	U939	U940	U941	U942	U943	U944	U945	U946	U947	U948	U949	U950	U951	U952	U953	U954	U955	U956	U957	U958	U959	U960	U961	U962	U963	U964	U965	U966	U967	U968	U969	U970	U971	U972	U973	U974	U975	U976	U977	U978	U979	U980	U981	U982	U983	U984	U985	U986	U987	U988	U989	U990	U991	U992	U993	U994	U995	U996	U997	U998	U999	U1000	U1001	U1002	U1003	U1004	U1005	U1006	U1007	U1008	U1009	U1010	U1011	U1012	U1013	U1014	U1015	U1016	U1017	U1018	U1019	U1020	U1021	U1022	U1023	U1024	U1025	U1026	U1027	U1028	U1029	U1030	U1031	U1032	U1033	U1034	U1035	U1036	U1037	U1038	U1039	U1040	U1041	U1042	U1043	U1044	U1045																																																																							
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G373	G374	U375	A376	G377	U378	C379	G380	C381	C382	G383	U384	G385	C386	C3																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								

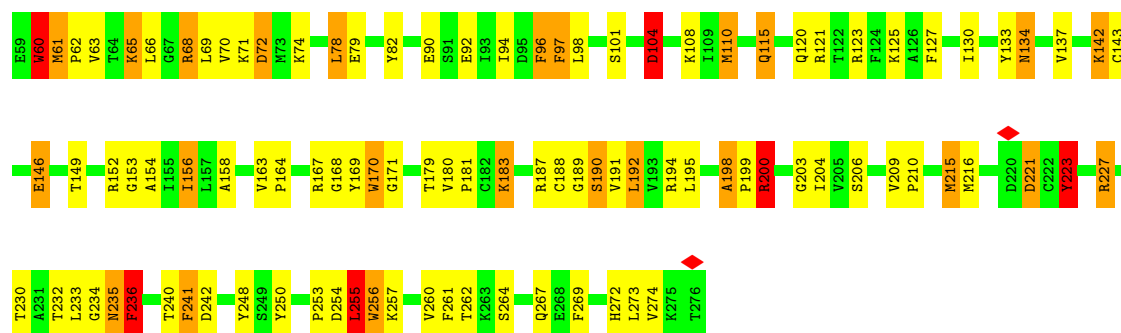




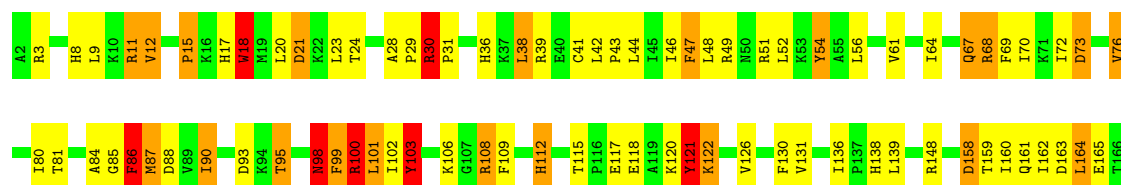
• Molecule 56: Ribosomal protein eS1

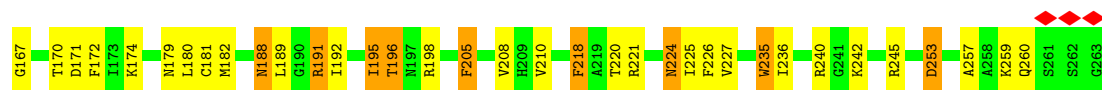


• Molecule 57: Ribosomal protein uS5

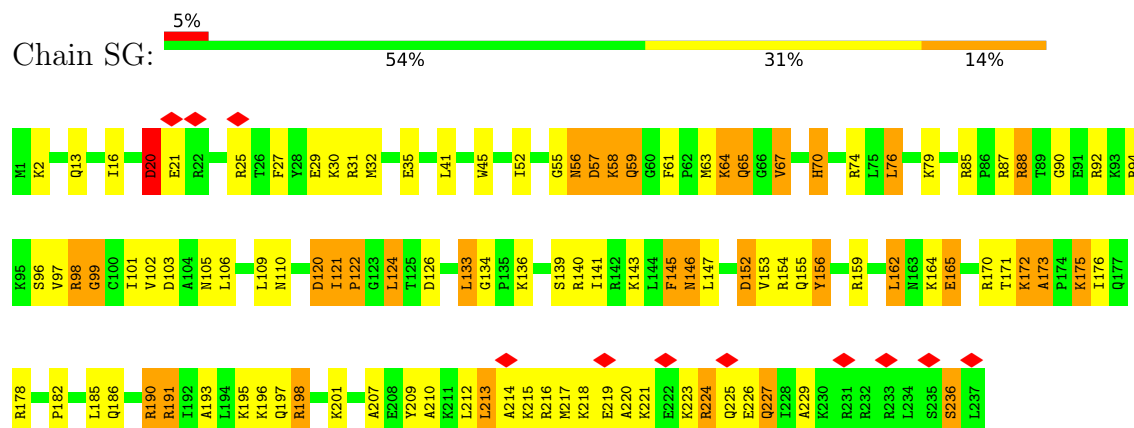


• Molecule 58: Ribosomal protein eS4

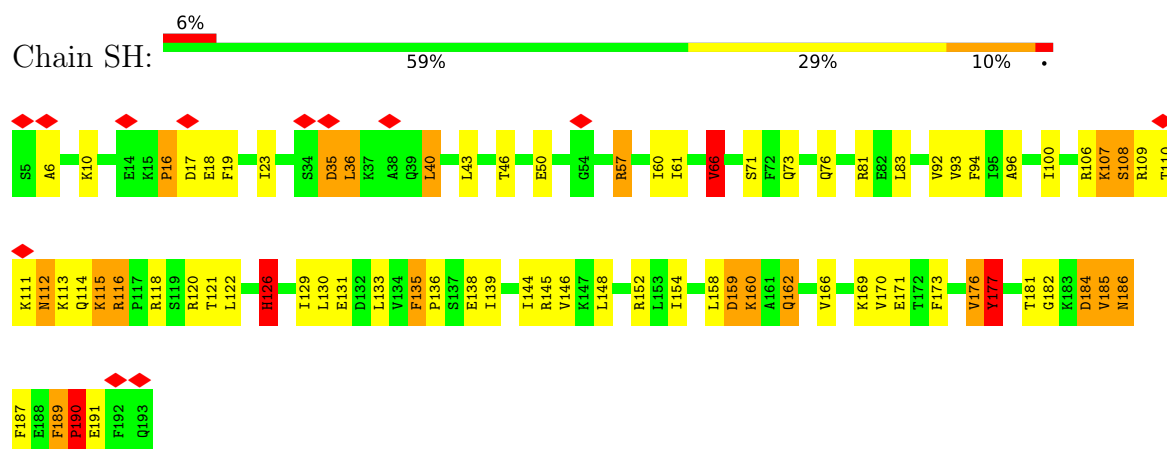




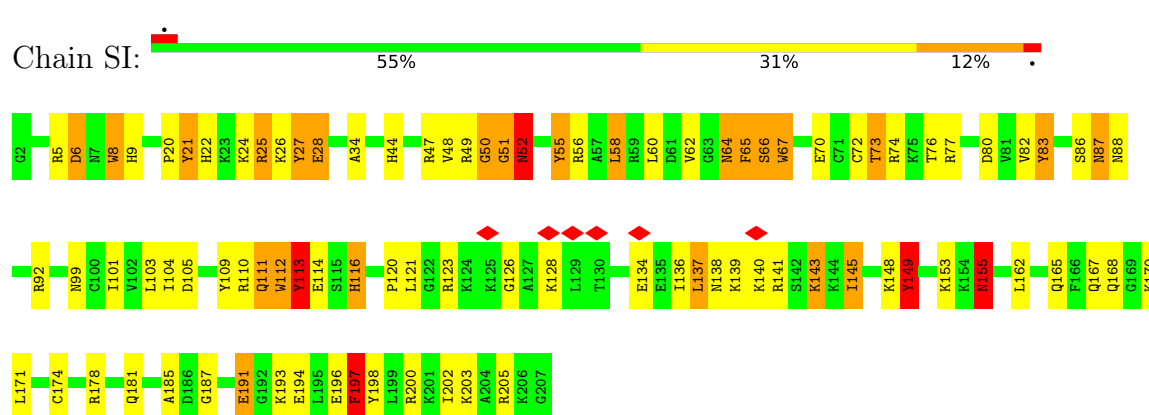
• Molecule 59: Ribosomal protein eS6



• Molecule 60: Ribosomal protein eS7

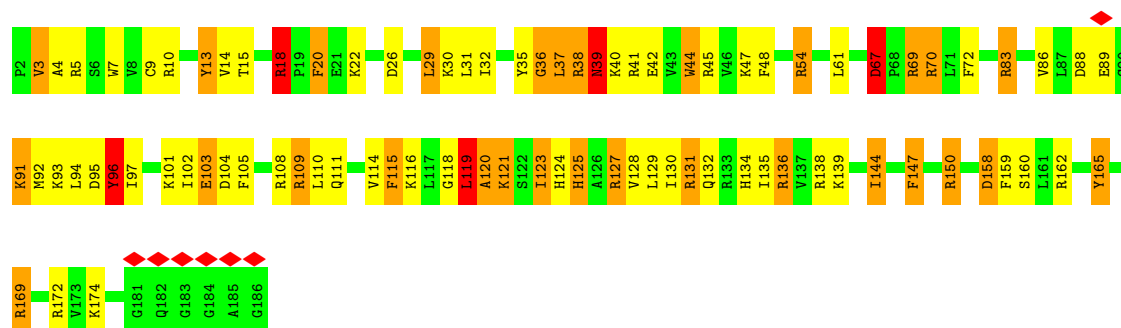


• Molecule 61: Ribosomal protein eS8

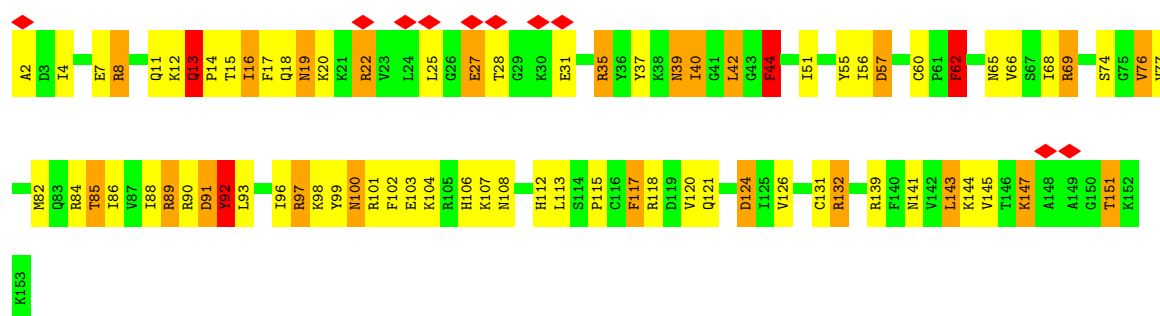


• Molecule 62: Ribosomal protein uS4

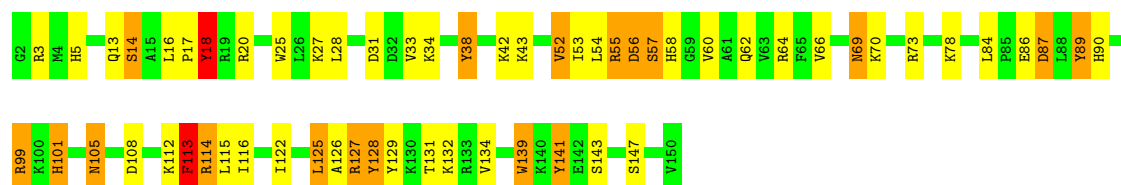




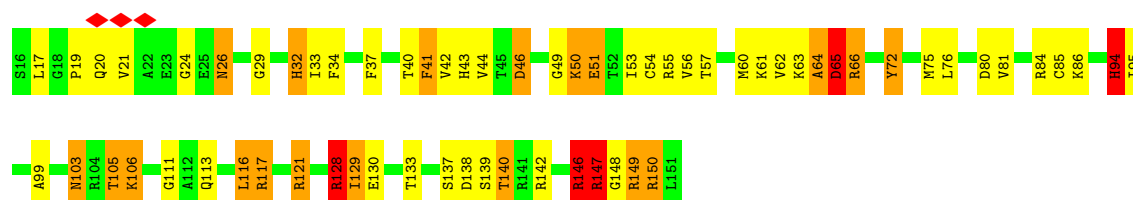
• Molecule 63: Ribosomal protein uS17



• Molecule 64: Ribosomal protein uS15



• Molecule 65: Ribosomal protein uS11



• Molecule 66: Ribosomal protein eS21





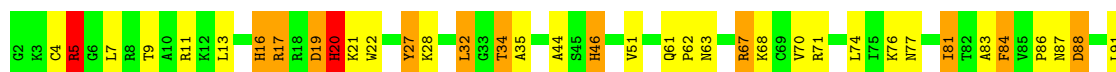
• Molecule 67: Ribosomal protein uS8

Chain SW: 50% 40% 10% .



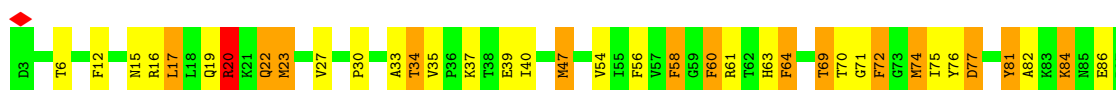
• Molecule 68: Ribosomal protein uS12

Chain SX: 64% 25% 10% .



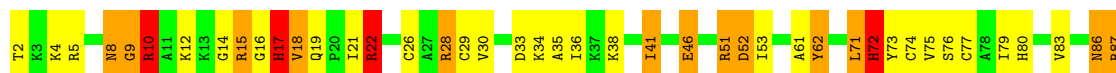
• Molecule 69: Ribosomal protein eS24

Chain SY: 57% 29% 13% .



• Molecule 70: Ribosomal protein eS26

Chain Sa: 48% 32% 15% 5%



• Molecule 71: Ribosomal protein eS27

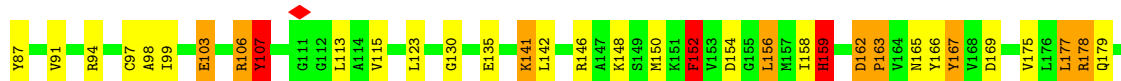
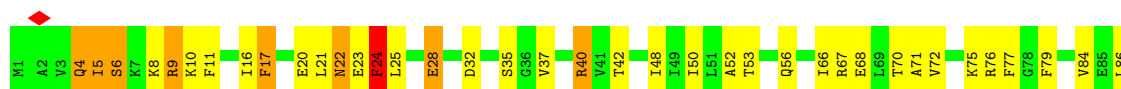
Chain Sb: 66% 28% 6%



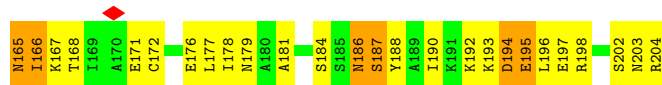
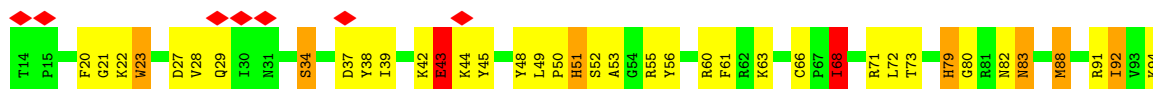
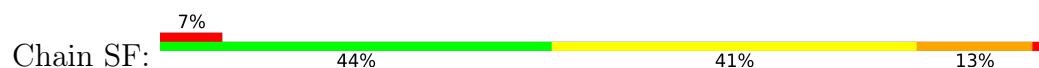
- Molecule 72: Ribosomal protein eS30



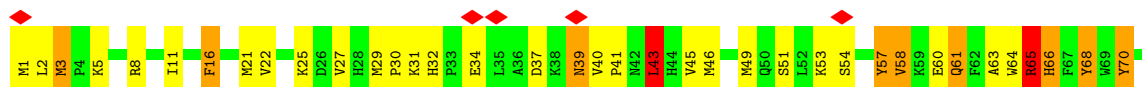
- Molecule 73: Ribosomal protein uS3



- Molecule 74: Ribosomal protein uS7

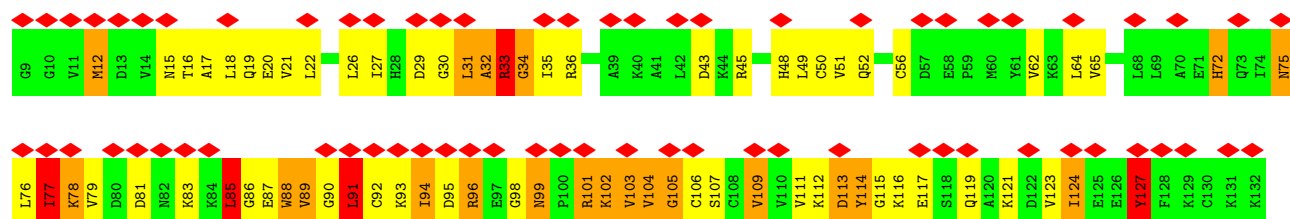


- Molecule 75: Ribosomal protein eS10

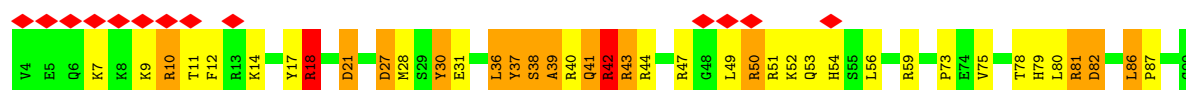




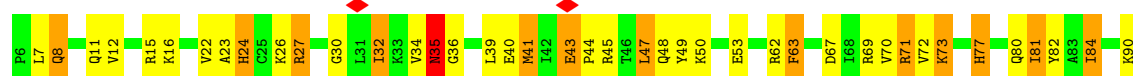
• Molecule 76: Ribosomal protein eS12



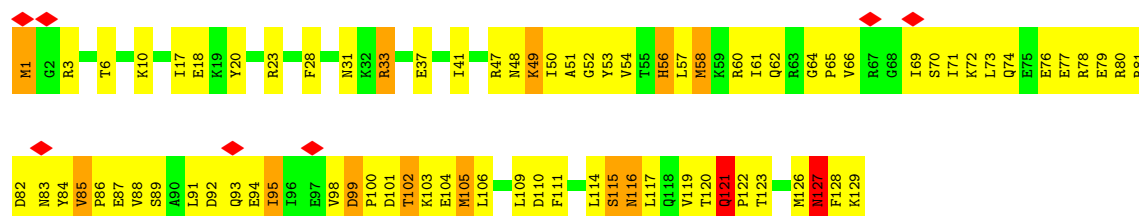
• Molecule 77: Ribosomal protein uS19



• Molecule 78: Ribosomal protein uS9

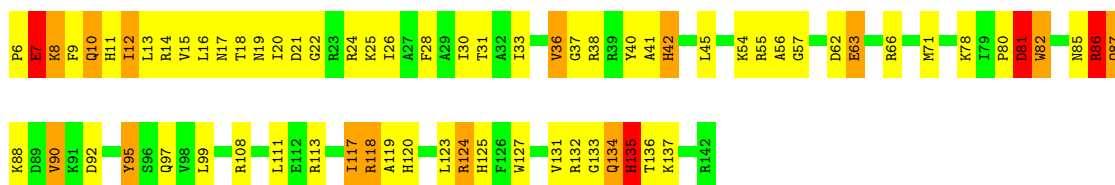


• Molecule 79: Ribosomal protein eS17

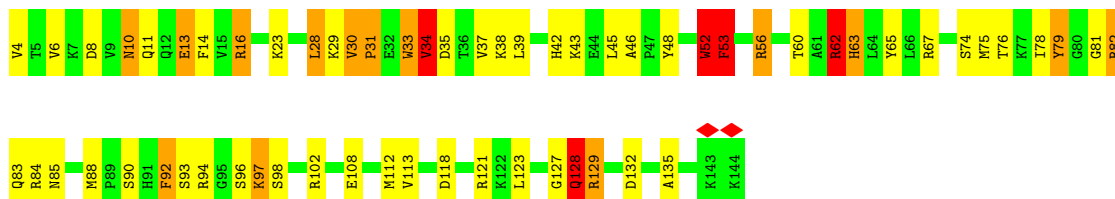


• Molecule 80: Ribosomal protein uS13





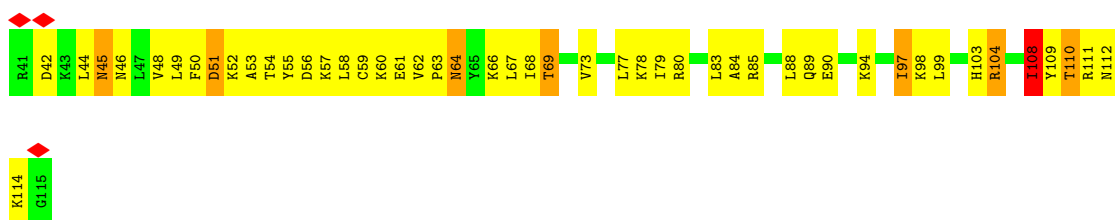
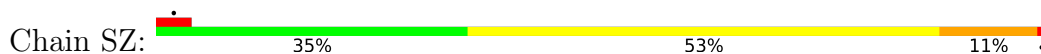
• Molecule 81: Ribosomal protein eS19



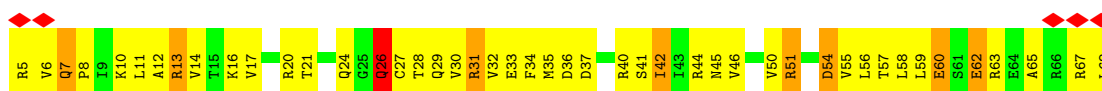
• Molecule 82: Ribosomal protein uS10



• Molecule 83: Ribosomal protein es25

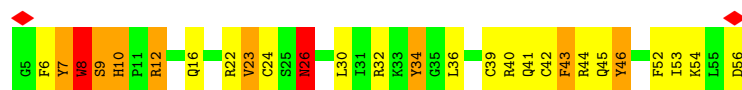


• Molecule 84: Ribosomal protein eS28

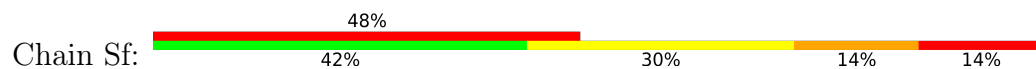


• Molecule 85: Ribosomal protein uS14

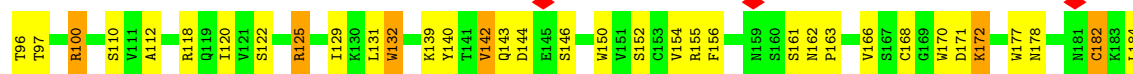
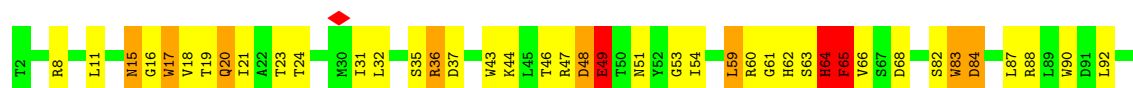




• Molecule 86: Ribosomal protein eS31



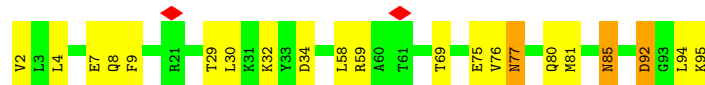
• Molecule 87: Ribosomal protein RACK1



• Molecule 88: SRP9



• Molecule 89: SRP14



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	52061	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.638	Depositor
Minimum map value	-0.471	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3399999, 1.3399999, 1.3399999	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	A	0.99	7/1906 (0.4%)	1.42	29/2556 (1.1%)
2	D	0.91	9/2426 (0.4%)	1.37	30/3252 (0.9%)
3	G	0.96	9/1944 (0.5%)	1.24	16/2618 (0.6%)
4	H	0.83	3/1537 (0.2%)	1.21	10/2066 (0.5%)
5	J	0.79	2/1382 (0.1%)	1.12	8/1849 (0.4%)
6	L	0.81	2/1734 (0.1%)	1.19	7/2318 (0.3%)
7	M	0.80	1/1152 (0.1%)	1.22	8/1539 (0.5%)
8	N	0.93	3/1746 (0.2%)	1.43	25/2338 (1.1%)
9	O	0.83	2/1684 (0.1%)	1.30	15/2251 (0.7%)
10	Q	0.89	6/1530 (0.4%)	1.37	19/2041 (0.9%)
11	R	1.14	3/1524 (0.2%)	1.41	13/2013 (0.6%)
12	S	1.21	10/1493 (0.7%)	1.50	25/2002 (1.2%)
13	T	0.78	2/1326 (0.2%)	1.14	8/1770 (0.5%)
14	U	0.88	3/822 (0.4%)	1.11	2/1103 (0.2%)
15	V	0.78	0/993	1.16	3/1332 (0.2%)
16	X	0.80	0/993	1.15	4/1334 (0.3%)
17	Y	0.87	3/1132 (0.3%)	1.30	16/1504 (1.1%)
18	Z	0.89	3/1130 (0.3%)	1.27	9/1507 (0.6%)
19	a	0.92	7/1192 (0.6%)	1.38	14/1591 (0.9%)
20	b	0.94	1/620 (0.2%)	1.43	8/819 (1.0%)
21	c	0.83	1/742 (0.1%)	1.30	9/996 (0.9%)
22	d	0.92	3/903 (0.3%)	1.32	12/1216 (1.0%)
23	e	0.91	3/1071 (0.3%)	1.31	15/1429 (1.0%)
24	f	1.01	5/895 (0.6%)	1.37	6/1198 (0.5%)
25	g	0.81	0/916	1.25	10/1220 (0.8%)
26	h	0.74	1/1023 (0.1%)	1.22	8/1350 (0.6%)
27	i	0.84	3/843 (0.4%)	1.26	7/1115 (0.6%)
28	k	0.68	0/575	1.07	1/761 (0.1%)
29	l	0.74	0/454	1.21	4/599 (0.7%)
30	m	0.67	0/435	1.13	1/575 (0.2%)
31	o	0.81	2/864 (0.2%)	1.33	12/1140 (1.1%)
32	5	0.58	12/87703 (0.0%)	1.26	1305/136805 (1.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	7	0.53	0/2858	1.13	22/4455 (0.5%)
34	8	0.59	1/3701 (0.0%)	1.27	62/5766 (1.1%)
35	B	0.93	10/3214 (0.3%)	1.26	28/4308 (0.6%)
36	C	0.88	4/2973 (0.1%)	1.23	17/3990 (0.4%)
37	E	0.95	5/1941 (0.3%)	1.35	24/2601 (0.9%)
38	F	0.89	0/1905	1.41	30/2539 (1.2%)
39	I	0.77	2/1753 (0.1%)	1.25	17/2343 (0.7%)
40	P	0.99	4/1268 (0.3%)	1.31	15/1701 (0.9%)
41	W	0.92	1/541 (0.2%)	1.30	3/720 (0.4%)
42	j	0.94	1/721 (0.1%)	1.43	15/953 (1.6%)
43	n	0.97	0/223	1.20	0/284
44	p	0.74	1/718 (0.1%)	1.18	3/953 (0.3%)
45	r	0.79	1/1017 (0.1%)	1.24	9/1365 (0.7%)
46	K	1.22	3/1256 (0.2%)	1.59	19/1694 (1.1%)
47	q	0.97	1/1580 (0.1%)	1.16	8/2133 (0.4%)
48	z	1.25	9/3171 (0.3%)	1.41	12/4257 (0.3%)
49	2	0.74	0/234	1.31	5/317 (1.6%)
50	3	1.29	2/1804 (0.1%)	1.18	11/2805 (0.4%)
51	4	0.61	1/5090 (0.0%)	0.76	6/7936 (0.1%)
52	9	0.45	0/858	0.90	0/1156
53	6	0.38	0/1521	0.80	2/2039 (0.1%)
54	S2	0.59	11/41241 (0.0%)	1.26	597/64249 (0.9%)
55	SA	0.86	2/1679 (0.1%)	1.25	14/2283 (0.6%)
56	SB	0.92	5/1753 (0.3%)	1.30	17/2350 (0.7%)
57	SC	0.84	3/1726 (0.2%)	1.23	15/2332 (0.6%)
58	SE	0.85	5/2118 (0.2%)	1.26	15/2849 (0.5%)
59	SG	0.81	1/1946 (0.1%)	1.17	10/2590 (0.4%)
60	SH	0.70	0/1544	1.13	4/2068 (0.2%)
61	SI	0.97	5/1715 (0.3%)	1.29	14/2287 (0.6%)
62	SJ	0.80	0/1550	1.27	9/2069 (0.4%)
63	SL	0.84	2/1259 (0.2%)	1.25	13/1684 (0.8%)
64	SN	0.82	3/1226 (0.2%)	1.23	11/1649 (0.7%)
65	SO	0.84	0/1029	1.32	7/1380 (0.5%)
66	SV	0.72	0/631	1.08	2/844 (0.2%)
67	SW	0.82	0/1051	1.21	6/1406 (0.4%)
68	SX	0.86	3/1118 (0.3%)	1.18	6/1493 (0.4%)
69	SY	0.75	1/1040 (0.1%)	1.12	5/1382 (0.4%)
70	Sa	0.93	2/794 (0.3%)	1.37	9/1065 (0.8%)
71	Sb	0.70	0/665	1.05	2/891 (0.2%)
72	Se	0.66	0/458	1.05	2/602 (0.3%)
73	SD	0.84	0/1793	1.19	11/2414 (0.5%)
74	SF	0.82	2/1531 (0.1%)	1.24	9/2059 (0.4%)
75	SK	0.83	0/851	1.21	7/1147 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SM	1.09	1/970 (0.1%)	1.27	7/1300 (0.5%)
77	SP	1.15	3/816 (0.4%)	1.21	5/1084 (0.5%)
78	SQ	0.71	0/1142	1.13	6/1528 (0.4%)
79	SR	0.69	0/1060	1.04	4/1421 (0.3%)
80	SS	0.65	0/1157	1.16	5/1548 (0.3%)
81	ST	0.81	2/1119 (0.2%)	1.29	11/1499 (0.7%)
82	SU	0.76	0/828	1.06	2/1112 (0.2%)
83	SZ	0.71	0/604	1.06	0/810
84	Sc	0.75	2/507 (0.4%)	1.01	2/677 (0.3%)
85	Sd	0.87	1/445 (0.2%)	1.20	3/589 (0.5%)
86	Sf	1.39	8/593 (1.3%)	1.68	14/786 (1.8%)
87	Sg	0.76	1/2493 (0.0%)	1.02	9/3394 (0.3%)
88	S1	1.15	5/619 (0.8%)	1.16	5/832 (0.6%)
89	S4	0.78	2/608 (0.3%)	1.00	0/809
All	All	0.73	222/244716 (0.1%)	1.25	2825/359004 (0.8%)

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
1	A	0	8
2	D	0	9
3	G	0	4
4	H	0	2
5	J	0	2
6	L	0	4
7	M	0	3
8	N	0	9
9	O	0	4
10	Q	0	5
11	R	0	7
12	S	0	8
13	T	0	2
15	V	0	3
16	X	0	2
17	Y	0	3
18	Z	0	1
19	a	0	6
20	b	0	2
21	c	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
22	d	0	5
23	e	0	1
24	f	0	2
25	g	0	2
26	h	0	1
27	i	0	3
28	k	0	1
30	m	0	1
31	o	0	3
32	5	0	175
33	7	0	2
34	8	0	11
35	B	0	12
36	C	0	4
37	E	0	16
38	F	0	8
39	I	0	3
40	P	0	4
41	W	0	1
42	j	0	4
44	p	0	2
45	r	0	3
46	K	0	10
47	q	0	8
48	z	0	7
49	2	0	1
54	S2	0	59
55	SA	0	5
56	SB	0	7
57	SC	0	7
58	SE	0	6
59	SG	0	1
60	SH	0	2
61	SI	0	9
62	SJ	0	3
63	SL	0	3
64	SN	0	5
65	SO	0	1
66	SV	0	3
67	SW	0	3
68	SX	0	2
69	SY	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
70	Sa	0	3
71	Sb	0	1
73	SD	0	3
74	SF	0	4
75	SK	0	1
76	SM	0	2
77	SP	0	3
78	SQ	0	1
80	SS	0	1
81	ST	0	2
82	SU	0	1
83	SZ	0	1
85	Sd	0	3
86	Sf	0	4
87	Sg	0	3
88	S1	0	4
All	All	0	529

The worst 5 of 222 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	3	31	C	O3'-P	-49.79	0.86	1.61
48	z	340	MET	C-N	41.63	1.86	1.33
51	4	183	A	O3'-P	-35.33	1.08	1.61
48	z	345	PHE	C-N	-29.97	0.91	1.33
32	5	1823	G	O3'-P	28.48	2.03	1.61

The worst 5 of 2825 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	z	340	MET	CA-C-N	-30.44	75.16	120.82
48	z	340	MET	C-N-CA	-30.44	75.16	120.82
48	z	340	MET	O-C-N	29.41	153.86	122.09
50	3	31	C	O3'-P-O5'	-23.73	68.40	104.00
46	K	1	MET	CA-C-N	-18.14	101.70	120.38

There are no chirality outliers.

5 of 529 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	18	ALA	Peptide

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Mol	Chain	Res	Type	Group
1	A	194	ASN	Peptide
1	A	196	TRP	Peptide
1	A	66	PRO	Peptide
1	A	67	TYR	Sidechain

5.2 Too-close contacts

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	A	1868	0	1959	137	0
2	D	2380	0	2412	130	0
3	G	1912	0	2059	95	0
4	H	1518	0	1601	70	0
5	J	1359	0	1390	63	0
6	L	1703	0	1818	74	0
7	M	1131	0	1209	62	0
8	N	1701	0	1749	124	0
9	O	1651	0	1786	68	0
10	Q	1506	0	1623	71	0
11	R	1508	0	1663	116	0
12	S	1454	0	1496	118	0
13	T	1298	0	1366	61	0
14	U	808	0	831	15	0
15	V	979	0	1039	44	0
16	X	976	0	1053	40	0
17	Y	1115	0	1205	50	0
18	Z	1107	0	1182	58	0
19	a	1163	0	1211	83	0
20	b	610	0	650	42	0
21	c	732	0	769	53	0
22	d	888	0	930	52	0
23	e	1053	0	1147	69	0
24	f	876	0	912	48	0
25	g	906	0	1002	42	0
26	h	1015	0	1150	49	0
27	i	832	0	917	26	0
28	k	569	0	637	12	0
29	l	444	0	483	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	m	429	0	466	17	0
31	o	851	0	923	42	0
32	5	78406	0	39609	10957	0
33	7	2558	0	1296	327	0
34	8	3314	0	1683	583	0
35	B	3147	0	3280	201	0
36	C	2919	0	3100	129	0
37	E	1904	0	2055	118	0
38	F	1870	0	1996	131	0
39	I	1713	0	1752	132	0
40	P	1242	0	1269	63	0
41	W	528	0	541	57	0
42	j	706	0	742	41	0
43	n	222	0	257	34	0
44	p	708	0	760	19	0
45	r	1001	0	1062	49	0
46	K	1238	0	1293	101	0
47	q	1556	0	1612	117	0
48	z	3241	0	3211	483	0
49	2	233	0	291	32	0
50	3	1616	0	824	177	0
51	4	4551	0	2297	408	0
52	9	844	0	861	68	0
53	6	1497	0	1504	24	0
54	S2	36900	0	18592	5345	0
55	SA	1642	0	1646	179	0
56	SB	1725	0	1794	162	0
57	SC	1690	0	1777	77	0
58	SE	2076	0	2177	79	0
59	SG	1923	0	2089	77	0
60	SH	1521	0	1615	92	0
61	SI	1686	0	1772	87	0
62	SJ	1525	0	1640	67	0
63	SL	1238	0	1313	66	0
64	SN	1202	0	1289	63	0
65	SO	1016	0	1037	67	0
66	SV	625	0	628	20	0
67	SW	1034	0	1080	52	0
68	SX	1099	0	1166	47	0
69	SY	1023	0	1090	42	0
70	Sa	781	0	832	59	0
71	Sb	651	0	672	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	Se	452	0	494	13	0
73	SD	1765	0	1865	65	0
74	SF	1509	0	1563	140	0
75	SK	827	0	854	30	0
76	SM	960	0	989	64	0
77	SP	805	0	861	20	0
78	SQ	1124	0	1193	39	0
79	SR	1047	0	1101	225	0
80	SS	1139	0	1190	147	0
81	ST	1101	0	1135	61	0
82	SU	818	0	883	25	0
83	SZ	598	0	655	129	0
84	Sc	506	0	531	207	0
85	Sd	434	0	427	28	0
86	Sf	581	0	599	198	0
87	Sg	2436	0	2393	90	0
88	S1	608	0	617	32	0
89	S4	604	0	638	15	0
90	5	116	0	0	0	0
90	7	5	0	0	0	0
90	8	6	0	0	0	0
90	D	1	0	0	0	0
90	S2	36	0	0	1	0
90	V	1	0	0	0	0
90	g	1	0	0	0	0
91	Sa	1	0	0	2	0
91	j	1	0	0	1	0
91	m	1	0	0	0	0
91	o	1	0	0	2	0
All	All	228197	0	170130	22018	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 56.

The worst 5 of 22018 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)
50:3:31:C:H4'	54:S2:1640:A:C2	1.26	1.69
48:z:297:MET:HE3	48:z:355:PHE:CD1	1.21	1.69
48:z:405:ARG:HG2	51:4:207:C:C4'	1.29	1.63
39:I:101:LYS:HE2	39:I:121:LYS:CG	1.28	1.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:z:413:SER:HB2	52:9:74:ARG:CB	1.33	1.59

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	
1	A	242/244 (99%)	194 (80%)	38 (16%)	10 (4%)	2	19
2	D	290/292 (99%)	228 (79%)	41 (14%)	21 (7%)	1	12
3	G	236/238 (99%)	188 (80%)	41 (17%)	7 (3%)	3	25
4	H	188/190 (99%)	162 (86%)	20 (11%)	6 (3%)	3	24
5	J	168/170 (99%)	126 (75%)	33 (20%)	9 (5%)	1	16
6	L	208/210 (99%)	166 (80%)	29 (14%)	13 (6%)	1	13
7	M	136/138 (99%)	111 (82%)	21 (15%)	4 (3%)	3	25
8	N	201/203 (99%)	159 (79%)	31 (15%)	11 (6%)	1	15
9	O	199/201 (99%)	177 (89%)	19 (10%)	3 (2%)	8	35
10	Q	185/187 (99%)	154 (83%)	24 (13%)	7 (4%)	2	20
11	R	178/180 (99%)	148 (83%)	23 (13%)	7 (4%)	2	20
12	S	173/175 (99%)	139 (80%)	27 (16%)	7 (4%)	2	20
13	T	157/159 (99%)	132 (84%)	20 (13%)	5 (3%)	3	24
14	U	97/99 (98%)	80 (82%)	14 (14%)	3 (3%)	3	24
15	V	129/131 (98%)	110 (85%)	14 (11%)	5 (4%)	2	20
16	X	117/119 (98%)	102 (87%)	12 (10%)	3 (3%)	4	27
17	Y	132/134 (98%)	105 (80%)	21 (16%)	6 (4%)	2	18
18	Z	133/135 (98%)	111 (84%)	15 (11%)	7 (5%)	1	16
19	a	145/147 (99%)	114 (79%)	24 (17%)	7 (5%)	2	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	b	73/75 (97%)	60 (82%)	10 (14%)	3 (4%)	2	19
21	c	92/94 (98%)	78 (85%)	10 (11%)	4 (4%)	2	19
22	d	105/107 (98%)	85 (81%)	16 (15%)	4 (4%)	2	20
23	e	126/128 (98%)	110 (87%)	14 (11%)	2 (2%)	7	34
24	f	107/109 (98%)	89 (83%)	11 (10%)	7 (6%)	1	13
25	g	112/114 (98%)	100 (89%)	10 (9%)	2 (2%)	6	32
26	h	120/122 (98%)	97 (81%)	21 (18%)	2 (2%)	7	33
27	i	100/102 (98%)	85 (85%)	13 (13%)	2 (2%)	6	31
28	k	67/69 (97%)	53 (79%)	11 (16%)	3 (4%)	2	18
29	l	48/50 (96%)	42 (88%)	5 (10%)	1 (2%)	5	30
30	m	50/52 (96%)	44 (88%)	6 (12%)	0	100	100
31	o	102/104 (98%)	79 (78%)	17 (17%)	6 (6%)	1	14
35	B	392/394 (100%)	309 (79%)	54 (14%)	29 (7%)	1	11
36	C	365/367 (100%)	292 (80%)	55 (15%)	18 (5%)	1	17
37	E	232/236 (98%)	144 (62%)	55 (24%)	33 (14%)	0	3
38	F	223/225 (99%)	180 (81%)	35 (16%)	8 (4%)	2	21
39	I	211/213 (99%)	170 (81%)	28 (13%)	13 (6%)	1	14
40	P	151/153 (99%)	134 (89%)	15 (10%)	2 (1%)	9	37
41	W	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
42	j	84/86 (98%)	64 (76%)	18 (21%)	2 (2%)	4	28
43	n	21/23 (91%)	20 (95%)	1 (5%)	0	100	100
44	p	89/91 (98%)	75 (84%)	14 (16%)	0	100	100
45	r	123/125 (98%)	96 (78%)	20 (16%)	7 (6%)	1	14
46	K	159/163 (98%)	91 (57%)	34 (21%)	34 (21%)	0	1
47	q	200/202 (99%)	141 (70%)	31 (16%)	28 (14%)	0	3
48	z	399/426 (94%)	350 (88%)	31 (8%)	18 (4%)	2	18
49	2	27/31 (87%)	15 (56%)	9 (33%)	3 (11%)	0	5
52	9	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
53	6	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
55	SA	206/208 (99%)	163 (79%)	30 (15%)	13 (6%)	1	13
56	SB	211/213 (99%)	154 (73%)	36 (17%)	21 (10%)	0	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	SC	216/218 (99%)	182 (84%)	27 (12%)	7 (3%)	3	24
58	SE	260/262 (99%)	198 (76%)	44 (17%)	18 (7%)	1	12
59	SG	235/237 (99%)	195 (83%)	32 (14%)	8 (3%)	3	23
60	SH	187/189 (99%)	141 (75%)	29 (16%)	17 (9%)	0	8
61	SI	204/206 (99%)	165 (81%)	30 (15%)	9 (4%)	2	19
62	SJ	183/185 (99%)	133 (73%)	35 (19%)	15 (8%)	0	9
63	SL	150/152 (99%)	122 (81%)	22 (15%)	6 (4%)	2	20
64	SN	147/149 (99%)	115 (78%)	28 (19%)	4 (3%)	4	26
65	SO	134/136 (98%)	99 (74%)	21 (16%)	14 (10%)	0	6
66	SV	80/82 (98%)	58 (72%)	15 (19%)	7 (9%)	0	8
67	SW	127/129 (98%)	108 (85%)	16 (13%)	3 (2%)	4	28
68	SX	139/141 (99%)	109 (78%)	26 (19%)	4 (3%)	3	25
69	SY	124/126 (98%)	101 (82%)	16 (13%)	7 (6%)	1	15
70	Sa	96/98 (98%)	69 (72%)	18 (19%)	9 (9%)	0	8
71	Sb	81/83 (98%)	61 (75%)	16 (20%)	4 (5%)	1	17
72	Se	55/57 (96%)	41 (74%)	12 (22%)	2 (4%)	2	21
73	SD	225/227 (99%)	174 (77%)	41 (18%)	10 (4%)	2	19
74	SF	189/191 (99%)	145 (77%)	34 (18%)	10 (5%)	1	16
75	SK	96/98 (98%)	58 (60%)	26 (27%)	12 (12%)	0	4
76	SM	122/124 (98%)	78 (64%)	24 (20%)	20 (16%)	0	2
77	SP	94/96 (98%)	67 (71%)	17 (18%)	10 (11%)	0	6
78	SQ	139/141 (99%)	111 (80%)	20 (14%)	8 (6%)	1	14
79	SR	127/129 (98%)	111 (87%)	11 (9%)	5 (4%)	2	20
80	SS	135/137 (98%)	114 (84%)	12 (9%)	9 (7%)	1	13
81	ST	139/141 (99%)	115 (83%)	18 (13%)	6 (4%)	2	19
82	SU	102/104 (98%)	83 (81%)	13 (13%)	6 (6%)	1	14
83	SZ	73/75 (97%)	59 (81%)	9 (12%)	5 (7%)	1	12
84	Sc	60/64 (94%)	47 (78%)	12 (20%)	1 (2%)	7	33
85	Sd	50/52 (96%)	36 (72%)	11 (22%)	3 (6%)	1	14
86	Sf	69/71 (97%)	42 (61%)	15 (22%)	12 (17%)	0	2
87	Sg	311/313 (99%)	240 (77%)	56 (18%)	15 (5%)	2	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
88	S1	72/74 (97%)	61 (85%)	6 (8%)	5 (7%)	1	12
89	S4	72/76 (95%)	68 (94%)	4 (6%)	0	100	100
All	All	12341/12544 (98%)	9853 (80%)	1811 (15%)	677 (6%)	2	15

5 of 677 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	HIS
1	A	196	TRP
1	A	197	PRO
2	D	9	ASN
2	D	19	LYS

5.3.2 Protein sidechains ⓘ

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	
1	A	187/187 (100%)	136 (73%)	51 (27%)	0	3
2	D	246/247 (100%)	183 (74%)	63 (26%)	0	4
3	G	204/206 (99%)	151 (74%)	53 (26%)	0	4
4	H	169/169 (100%)	129 (76%)	40 (24%)	1	5
5	J	143/143 (100%)	108 (76%)	35 (24%)	1	4
6	L	176/176 (100%)	138 (78%)	38 (22%)	1	6
7	M	116/116 (100%)	90 (78%)	26 (22%)	1	6
8	N	171/171 (100%)	131 (77%)	40 (23%)	1	5
9	O	172/172 (100%)	143 (83%)	29 (17%)	2	13
10	Q	163/163 (100%)	126 (77%)	37 (23%)	1	5
11	R	159/159 (100%)	117 (74%)	42 (26%)	0	3
12	S	156/156 (100%)	126 (81%)	30 (19%)	1	9
13	T	139/139 (100%)	110 (79%)	29 (21%)	1	7
14	U	89/89 (100%)	69 (78%)	20 (22%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	V	101/101 (100%)	77 (76%)	24 (24%)	1	5
16	X	107/107 (100%)	89 (83%)	18 (17%)	2	13
17	Y	124/124 (100%)	94 (76%)	30 (24%)	1	5
18	Z	117/117 (100%)	92 (79%)	25 (21%)	1	6
19	a	119/119 (100%)	97 (82%)	22 (18%)	1	11
20	b	63/63 (100%)	48 (76%)	15 (24%)	1	5
21	c	79/79 (100%)	61 (77%)	18 (23%)	1	5
22	d	98/98 (100%)	66 (67%)	32 (33%)	0	1
23	e	114/114 (100%)	88 (77%)	26 (23%)	1	5
24	f	88/88 (100%)	72 (82%)	16 (18%)	2	12
25	g	98/98 (100%)	78 (80%)	20 (20%)	1	8
26	h	109/109 (100%)	89 (82%)	20 (18%)	2	11
27	i	86/86 (100%)	69 (80%)	17 (20%)	1	8
28	k	64/64 (100%)	53 (83%)	11 (17%)	2	12
29	l	47/47 (100%)	38 (81%)	9 (19%)	1	10
30	m	48/48 (100%)	33 (69%)	15 (31%)	0	1
31	o	92/92 (100%)	70 (76%)	22 (24%)	1	5
35	B	335/335 (100%)	256 (76%)	79 (24%)	1	5
36	C	305/305 (100%)	233 (76%)	72 (24%)	1	5
37	E	209/209 (100%)	159 (76%)	50 (24%)	1	5
38	F	194/194 (100%)	147 (76%)	47 (24%)	1	5
39	I	180/180 (100%)	132 (73%)	48 (27%)	0	3
40	P	134/134 (100%)	109 (81%)	25 (19%)	1	10
41	W	55/55 (100%)	40 (73%)	15 (27%)	0	3
42	j	73/73 (100%)	62 (85%)	11 (15%)	3	16
43	n	22/22 (100%)	17 (77%)	5 (23%)	1	5
44	p	74/74 (100%)	64 (86%)	10 (14%)	4	18
45	r	109/109 (100%)	90 (83%)	19 (17%)	2	12
46	K	136/136 (100%)	115 (85%)	21 (15%)	2	15
47	q	170/170 (100%)	134 (79%)	36 (21%)	1	7
48	z	340/340 (100%)	322 (95%)	18 (5%)	20	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	2	29/29 (100%)	26 (90%)	3 (10%)	7	27
52	9	92/94 (98%)	87 (95%)	5 (5%)	20	45
53	6	157/157 (100%)	151 (96%)	6 (4%)	29	52
55	SA	174/174 (100%)	130 (75%)	44 (25%)	0	4
56	SB	194/194 (100%)	155 (80%)	39 (20%)	1	8
57	SC	184/184 (100%)	147 (80%)	37 (20%)	1	8
58	SE	224/224 (100%)	173 (77%)	51 (23%)	1	5
59	SG	207/207 (100%)	158 (76%)	49 (24%)	1	5
60	SH	169/169 (100%)	145 (86%)	24 (14%)	3	17
61	SI	178/178 (100%)	148 (83%)	30 (17%)	2	13
62	SJ	161/161 (100%)	116 (72%)	45 (28%)	0	2
63	SL	136/136 (100%)	100 (74%)	36 (26%)	0	3
64	SN	130/130 (100%)	100 (77%)	30 (23%)	1	5
65	SO	106/106 (100%)	74 (70%)	32 (30%)	0	2
66	SV	66/66 (100%)	52 (79%)	14 (21%)	1	7
67	SW	112/112 (100%)	89 (80%)	23 (20%)	1	8
68	SX	113/113 (100%)	99 (88%)	14 (12%)	4	21
69	SY	108/108 (100%)	83 (77%)	25 (23%)	1	5
70	Sa	85/85 (100%)	73 (86%)	12 (14%)	3	18
71	Sb	75/75 (100%)	62 (83%)	13 (17%)	2	12
72	Se	46/46 (100%)	34 (74%)	12 (26%)	0	4
73	SD	190/190 (100%)	145 (76%)	45 (24%)	1	5
74	SF	161/161 (100%)	120 (74%)	41 (26%)	0	4
75	SK	89/89 (100%)	68 (76%)	21 (24%)	1	5
76	SM	104/104 (100%)	75 (72%)	29 (28%)	0	2
77	SP	88/88 (100%)	71 (81%)	17 (19%)	1	9
78	SQ	117/117 (100%)	91 (78%)	26 (22%)	1	6
79	SR	117/117 (100%)	102 (87%)	15 (13%)	4	20
80	SS	119/119 (100%)	101 (85%)	18 (15%)	3	16
81	ST	112/112 (100%)	82 (73%)	30 (27%)	0	3
82	SU	94/94 (100%)	79 (84%)	15 (16%)	2	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	SZ	66/66 (100%)	56 (85%)	10 (15%)	3	16
84	Sc	57/57 (100%)	45 (79%)	12 (21%)	1	7
85	Sd	45/45 (100%)	31 (69%)	14 (31%)	0	1
86	Sf	64/64 (100%)	44 (69%)	20 (31%)	0	1
87	Sg	272/272 (100%)	236 (87%)	36 (13%)	4	19
88	S1	67/67 (100%)	54 (81%)	13 (19%)	1	9
89	S4	69/69 (100%)	59 (86%)	10 (14%)	3	17
All	All	10757/10762 (100%)	8512 (79%)	2245 (21%)	3	7

5 of 2245 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
71	Sb	33	MET
73	SD	177	LEU
71	Sb	23	ARG
80	SS	113	ARG
25	g	114	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 302 such sidechains are listed below:

Mol	Chain	Res	Type
67	SW	90	GLN
83	SZ	46	ASN
69	SY	94	HIS
76	SM	48	HIS
89	S4	54	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	5	3646/3658 (99%)	1724 (47%)	666 (18%)
33	7	119/120 (99%)	39 (32%)	15 (12%)
34	8	155/156 (99%)	66 (42%)	30 (19%)
50	3	74/76 (97%)	30 (40%)	5 (6%)
51	4	197/206 (95%)	45 (22%)	10 (5%)
54	S2	1715/1742 (98%)	860 (50%)	303 (17%)
All	All	5906/5958 (99%)	2764 (46%)	1029 (17%)

5 of 2764 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
32	5	2	G
32	5	8	U
32	5	12	A
32	5	13	U
32	5	20	U

5 of 1029 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	S2	1341	C
54	S2	1440	C
54	S2	1315	U
32	5	2515	G
32	5	2468	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 170 ligands modelled in this entry, 170 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	5	16
54	S2	6
48	z	5
51	4	3
50	3	3
46	K	2
49	2	1
37	E	1
89	S4	1
53	6	1
84	Sc	1
11	R	1

The worst 5 of 41 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	4	298:C	O3'	114:G	P	140.85
1	2	85:LEU	C	109:LEU	N	48.29
1	z	297:MET	C	326:GLN	N	33.03
1	E	72:ALA	C	84:VAL	N	24.28
1	S2	753:C	O3'	785:C	P	22.70

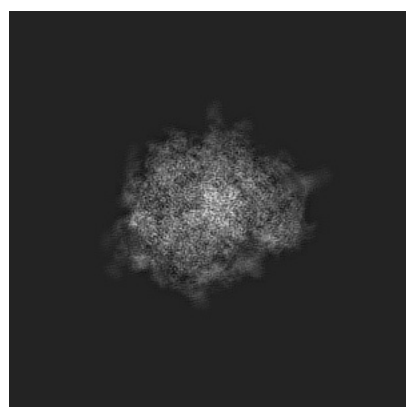
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3037. These allow visual inspection of the internal detail of the map and identification of artifacts.

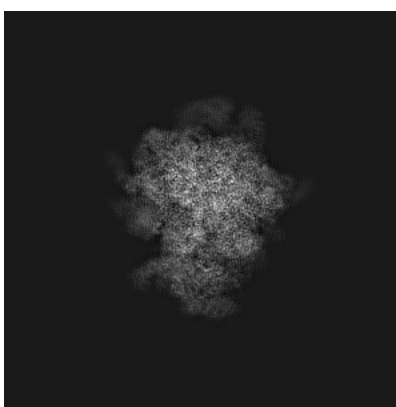
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

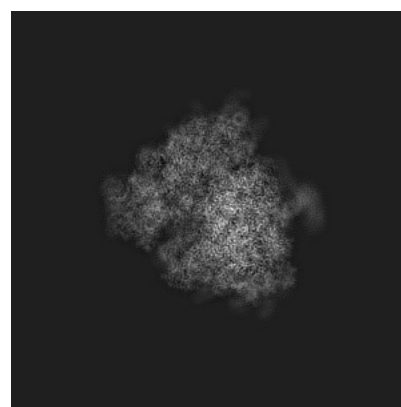
6.1.1 Primary map



X



Y

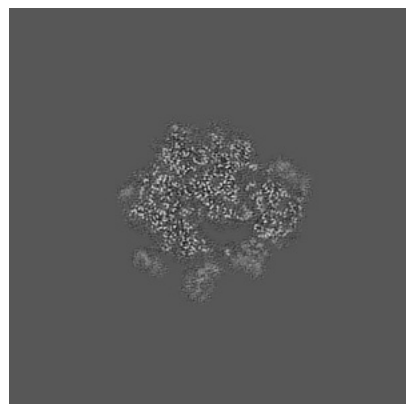


Z

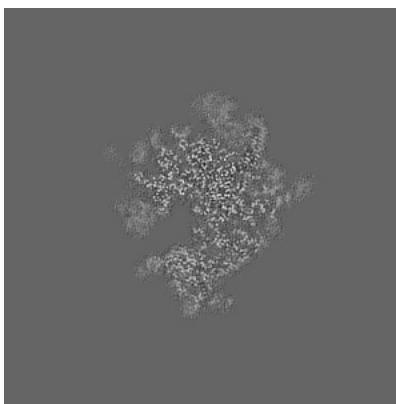
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

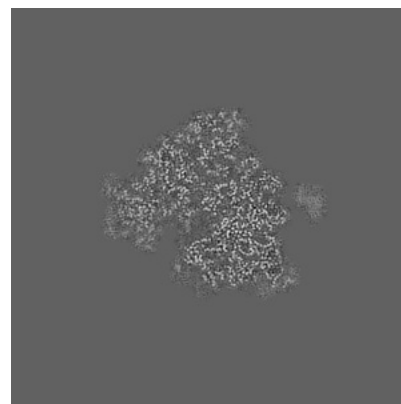
6.2.1 Primary map



X Index: 210



Y Index: 210

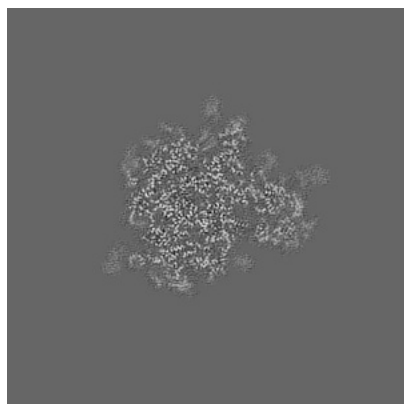


Z Index: 210

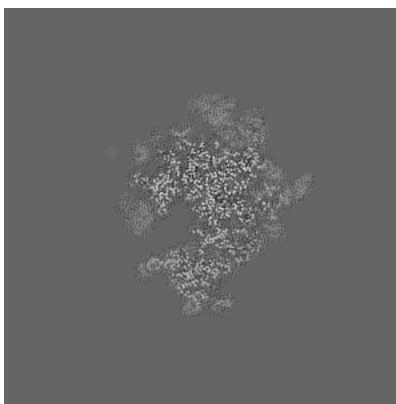
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

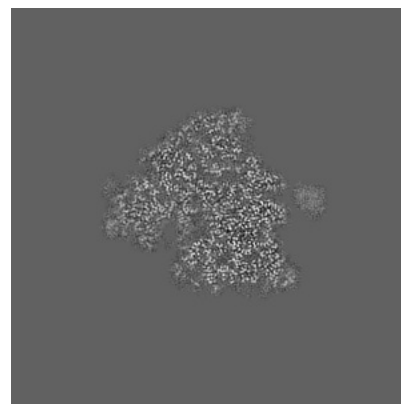
6.3.1 Primary map



X Index: 234



Y Index: 212

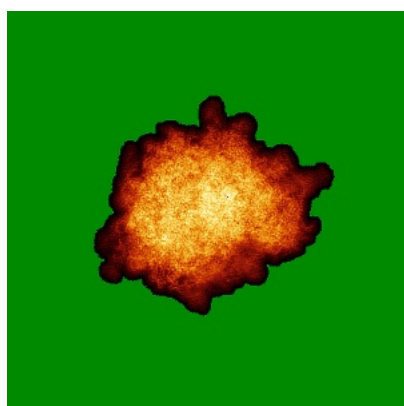


Z Index: 208

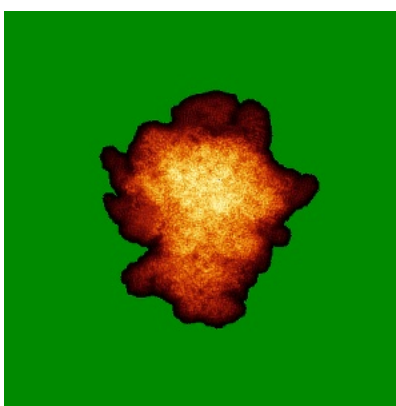
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

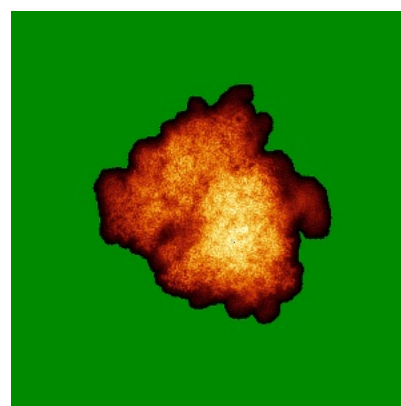
6.4.1 Primary map



X



Y

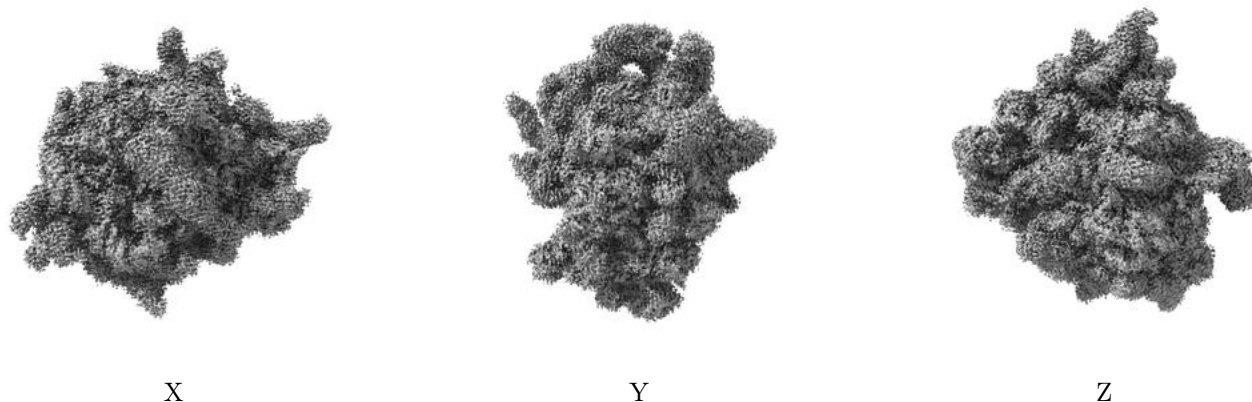


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

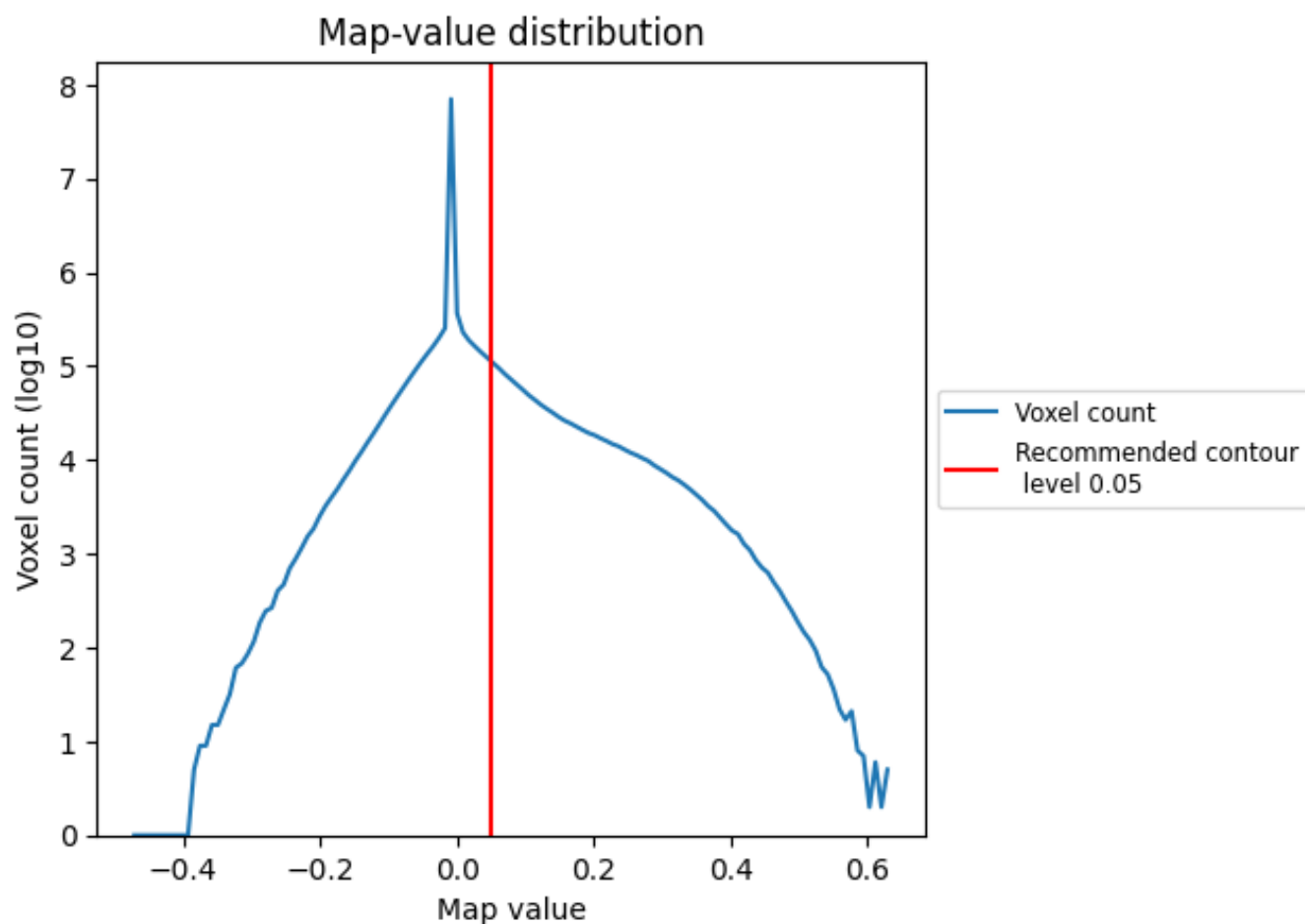
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

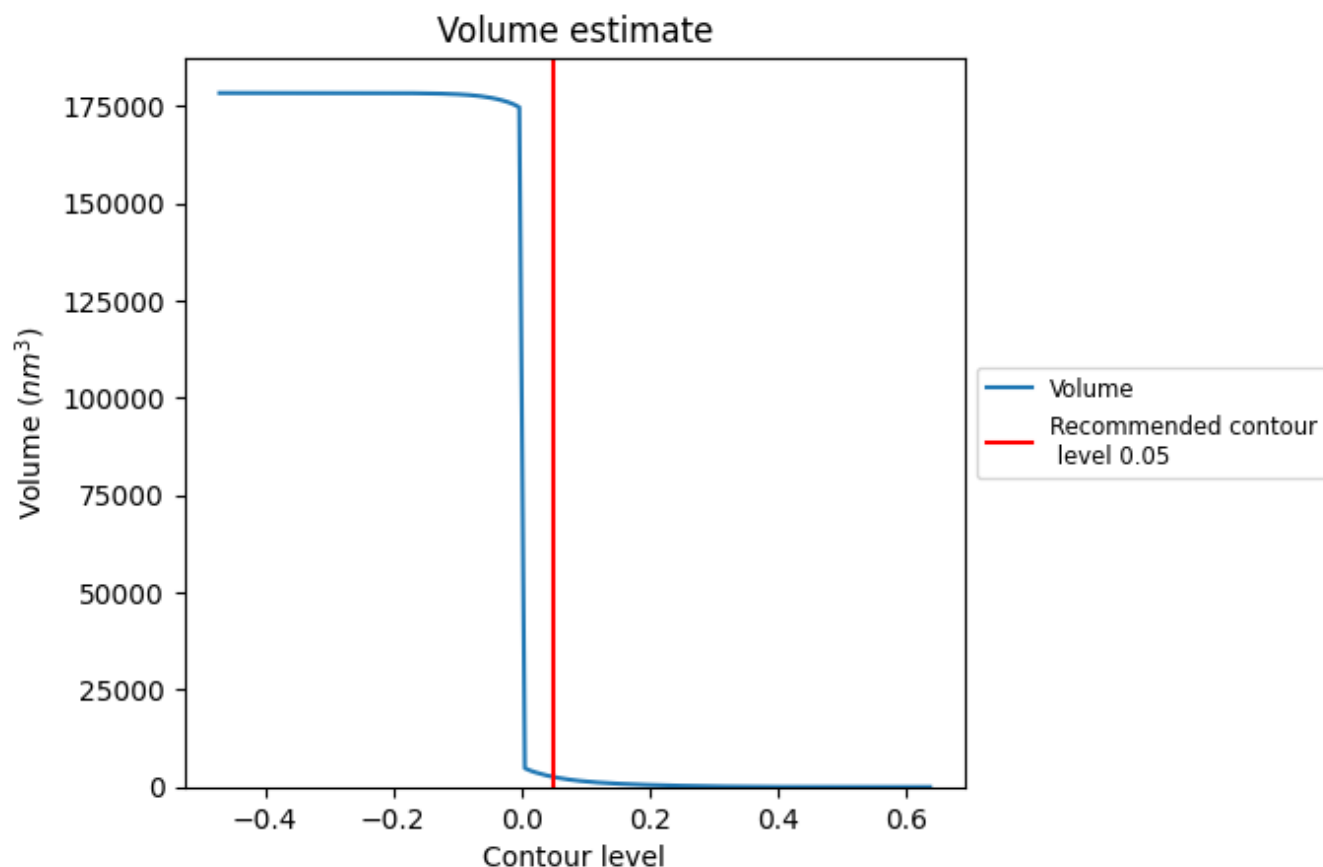
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

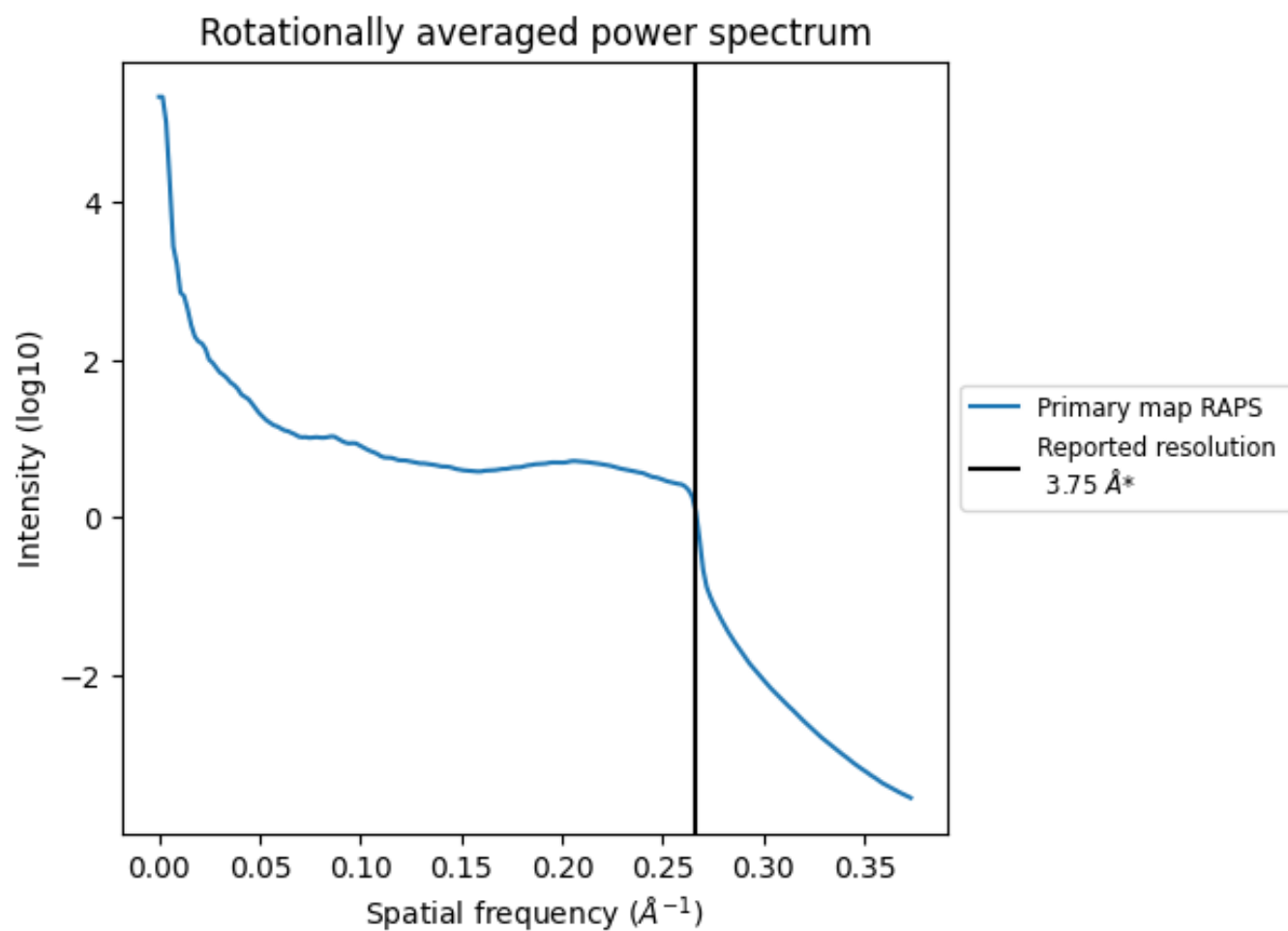
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2578 nm^3 ; this corresponds to an approximate mass of 2329 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.267 Å⁻¹

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

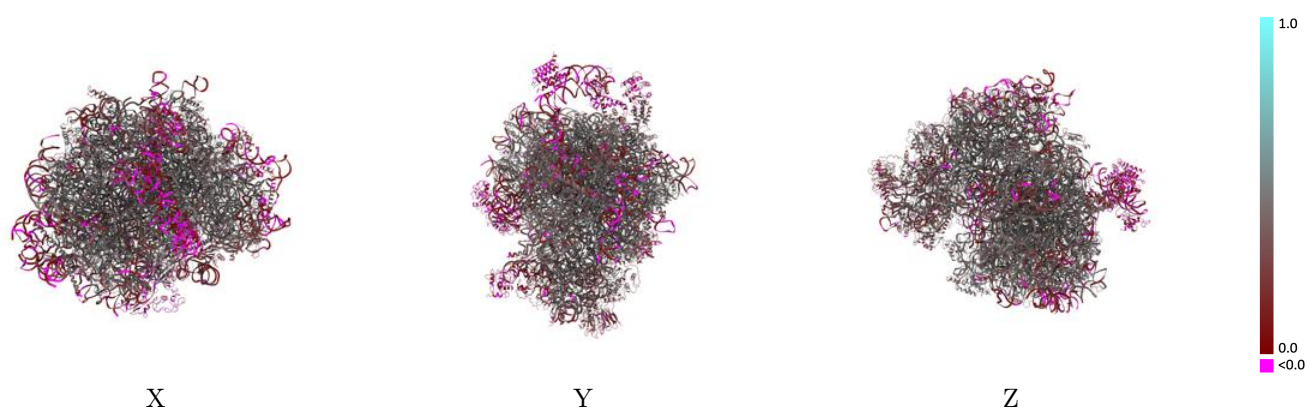
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3037 and PDB model 3JAJ. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

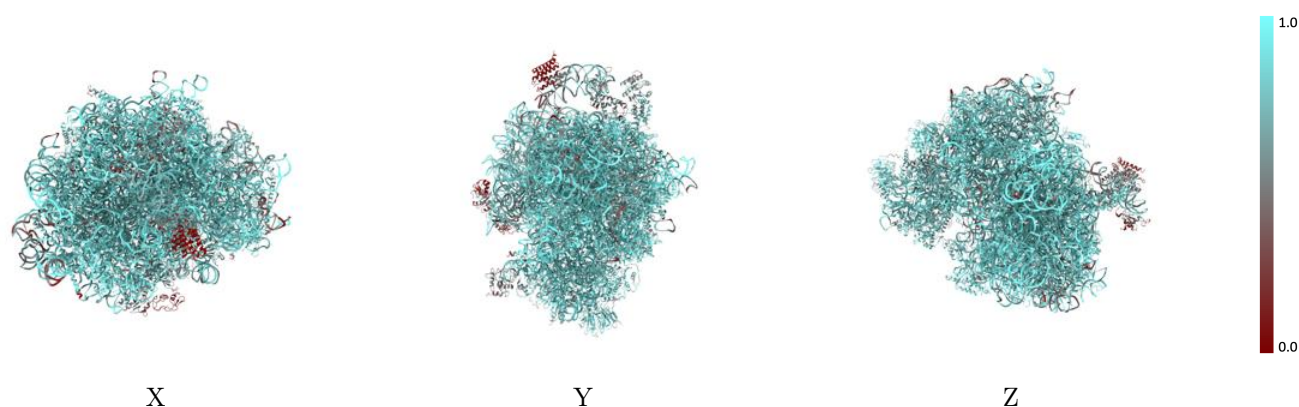
This section was not generated.

9.2 Q-score mapped to coordinate model [i](#)



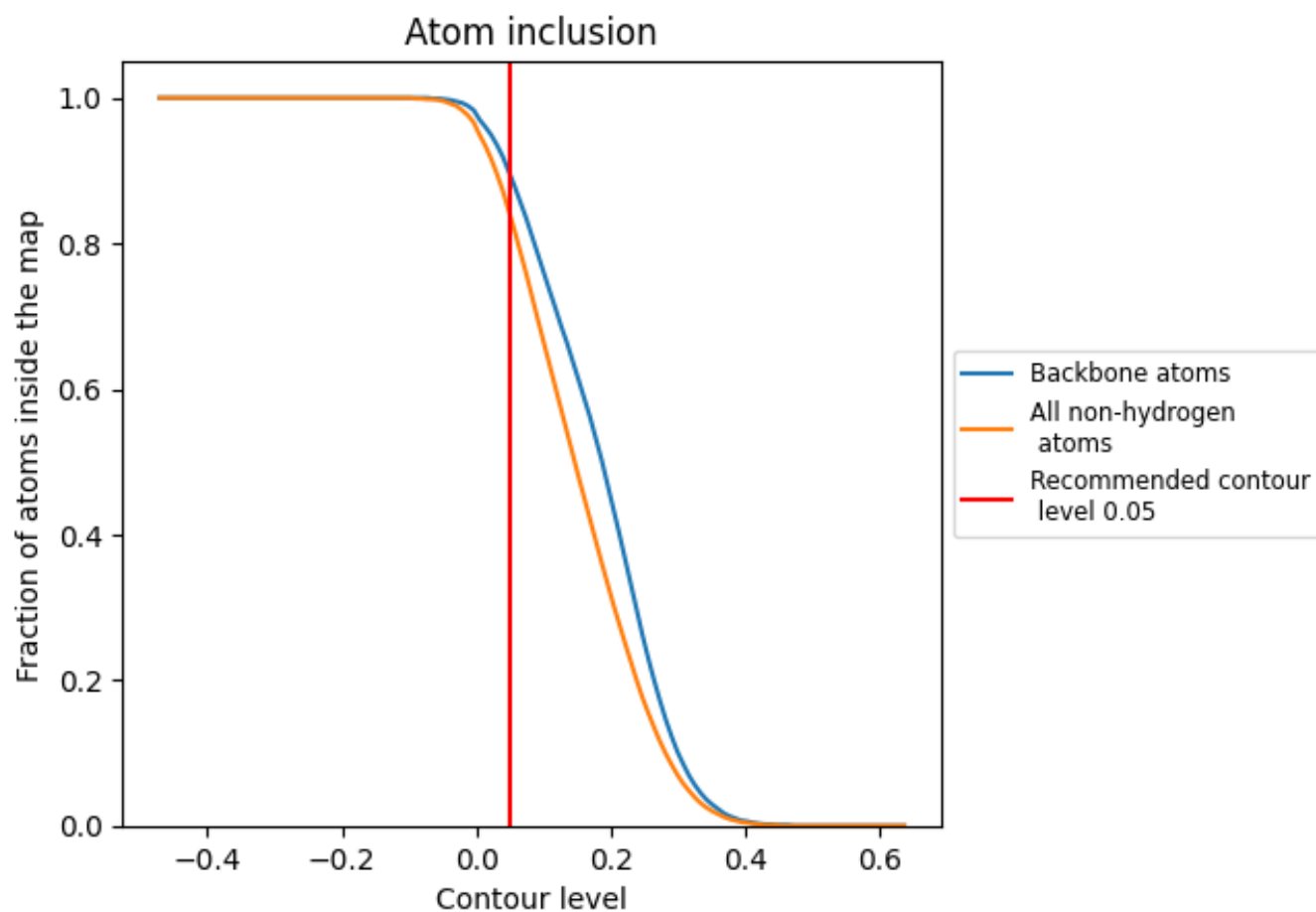
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 84% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8410	 0.3550
2	 0.6090	 0.2570
3	 0.8600	 0.3180
4	 0.6920	 0.0860
5	 0.8750	 0.3540
6	 0.1830	 0.0000
7	 0.9440	 0.4200
8	 0.9040	 0.3840
9	 0.4040	 0.0380
A	 0.8800	 0.4640
B	 0.8870	 0.4580
C	 0.8760	 0.4500
D	 0.8740	 0.4050
E	 0.8240	 0.3760
F	 0.8690	 0.4420
G	 0.8220	 0.3960
H	 0.8690	 0.4440
I	 0.8600	 0.4360
J	 0.8550	 0.4050
K	 0.3210	 0.0010
L	 0.8460	 0.4130
M	 0.8830	 0.4320
N	 0.8940	 0.4690
O	 0.8680	 0.4490
P	 0.8730	 0.4670
Q	 0.8840	 0.4620
R	 0.8490	 0.4020
S	 0.8950	 0.4590
S1	 0.7230	 0.2760
S2	 0.8780	 0.3390
S4	 0.7450	 0.3270
SA	 0.8470	 0.4070
SB	 0.8510	 0.4230
SC	 0.8660	 0.4430
SD	 0.7820	 0.3440



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Chain	Atom inclusion	Q-score
SE	 0.8720	 0.4350
SF	 0.7430	 0.2860
SG	 0.7920	 0.3240
SH	 0.7760	 0.3330
SI	 0.8370	 0.3970
SJ	 0.8700	 0.4090
SK	 0.7370	 0.2330
SL	 0.8270	 0.4230
SM	 0.3940	 0.0260
SN	 0.8650	 0.4240
SO	 0.8460	 0.4190
SP	 0.6990	 0.2310
SQ	 0.8310	 0.3800
SR	 0.7500	 0.3240
SS	 0.8240	 0.3380
ST	 0.8200	 0.3430
SU	 0.8050	 0.3520
SV	 0.8400	 0.4170
SW	 0.8920	 0.4550
SX	 0.8770	 0.4640
SY	 0.8290	 0.3870
SZ	 0.7530	 0.2770
Sa	 0.8800	 0.4460
Sb	 0.8360	 0.3870
Sc	 0.7570	 0.3270
Sd	 0.8390	 0.3930
Se	 0.7730	 0.3460
Sf	 0.4470	 0.0610
Sg	 0.7590	 0.2530
T	 0.8730	 0.4480
U	 0.8460	 0.3830
V	 0.8760	 0.4710
W	 0.8550	 0.4330
X	 0.8500	 0.4440
Y	 0.8580	 0.4280
Z	 0.8970	 0.4320
a	 0.9040	 0.4650
b	 0.8010	 0.3750
c	 0.8890	 0.4450
d	 0.8600	 0.4310
e	 0.8720	 0.4570
f	 0.9180	 0.4670

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Chain	Atom inclusion	Q-score
g	 0.8580	 0.4430
h	 0.8480	 0.4100
i	 0.8660	 0.4250
j	 0.9040	 0.4570
k	 0.7920	 0.3760
l	 0.8720	 0.4600
m	 0.8990	 0.4470
n	 0.8160	 0.3670
o	 0.8760	 0.4500
p	 0.8460	 0.4490
q	 0.3190	 0.0460
r	 0.9030	 0.4530
z	 0.6100	 0.1370