



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 01:04 PM EST

PDB ID : 3JAJ
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 : 4P3E, 1QB2, 3J7O, 1E8S, 1E80, 3J7P, 1WGW

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:

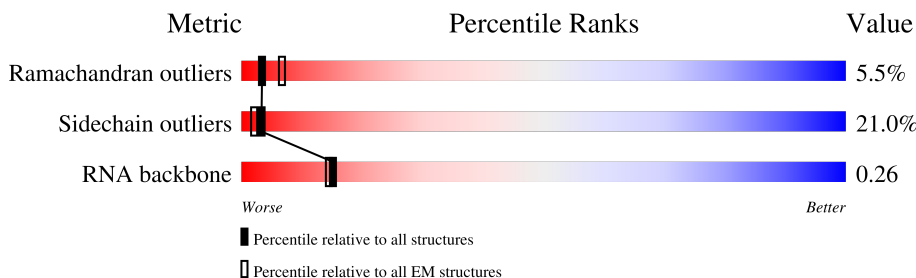
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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.




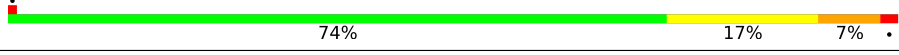

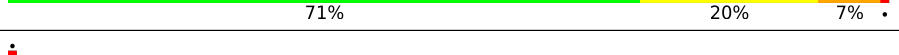
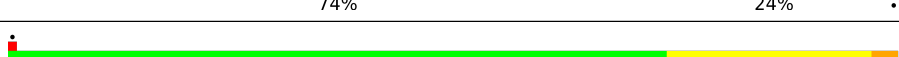
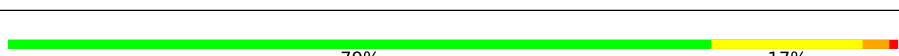












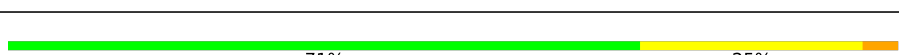
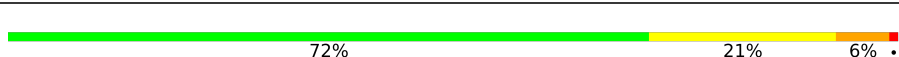

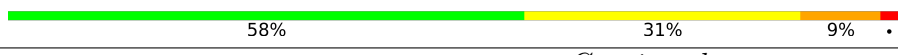



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	74% 20% 5% .
2	D	292	70% 24% . .
3	G	238	5% 74% 22% 5%
4	H	190	78% 15% 6% .
5	J	170	72% 24% .
6	L	210	74% 20% 6%
7	M	138	74% 24% .
8	N	203	70% 23% 6% .

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Mol	Chain	Length	Quality of chain
9	O	201	 80% 15%
10	Q	187	 74% 17% 7%
11	R	180	 70% 25% 5%
12	S	175	 71% 20% 7%
13	T	159	 74% 24%
14	U	99	 74% 23%
15	V	131	 79% 17%
16	X	119	 80% 18%
17	Y	134	 71% 22% 7%
18	Z	135	 79% 16% 5%
19	a	147	 78% 20%
20	b	75	 7% 75% 19% 5%
21	c	94	 74% 22%
22	d	107	 63% 29% 8%
23	e	128	 77% 22%
24	f	109	 76% 19% 5%
25	g	114	 79% 17%
26	h	122	 84% 11%
27	i	102	 75% 21%
28	k	69	 75% 25%
29	l	50	 78% 20%
30	m	52	 71% 25%
31	o	104	 72% 21% 6%
32	5	3658	 46% 40% 10%
33	7	120	 58% 31% 9%

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Mol	Chain	Length	Quality of chain
34	8	156	48% 40% 6% 6%
35	B	394	73% 22% 5%
36	C	367	76% 19% 5%
37	E	236	6% 64% 27% 7%
38	F	225	70% 25% 5%
39	I	213	68% 28% 4%
40	P	153	78% 18% 4%
41	W	63	71% 24% 5%
42	j	86	76% 17% 7%
43	n	23	74% 26%
44	p	91	86% 11% 3%
45	r	125	74% 24% 2%
46	K	163	61% 66% 28% 6%
47	q	202	62% 70% 23% 6%
48	z	426	20% 89% 10%
49	2	31	10% 81% 13% 6%
50	3	76	62% 34% 4%
51	4	206	10% 76% 21%
52	9	105	50% 96% 4%
53	6	179	79% 97% 2%
54	S2	1742	44% 44% 9%
55	SA	208	72% 23% 5%
56	SB	213	71% 22% 5%
57	SC	218	75% 20% 5%
58	SE	262	74% 21% 5%

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Mol	Chain	Length	Quality of chain
59	SG	237	5% 78% 20% .
60	SH	189	6% 79% 17% .
61	SI	206	. 77% 17% 5% .
62	SJ	185	. 68% 24% 7% .
63	SL	152	7% 74% 22% .
64	SN	149	77% 19% . .
65	SO	136	. 69% 24% 6% .
66	SV	82	71% 27% .
67	SW	129	76% 22% .
68	SX	141	82% 15% .
69	SY	126	. 77% 21% .
70	Sa	98	76% 17% 7%
71	Sb	83	. 73% 25% .
72	Se	57	9% 77% 18% 5%
73	SD	227	. 78% 17% .
74	SF	191	7% 73% 25% . .
75	SK	98	8% 65% 32% .
76	SM	124	54% 63% 30% 7%
77	SP	96	14% 70% 24% 5% .
78	SQ	141	. 77% 18% 6%
79	SR	129	5% 85% 14% .
80	SS	137	78% 18% .
81	ST	141	. 79% 18% .
82	SU	104	. 82% 18%
83	SZ	75	. 81% 17% .

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Mol	Chain	Length	Quality of chain
84	Sc	64	<p>84% 12% 8%</p>
85	Sd	52	<p>77% 17% 8%</p>
86	Sf	71	<p>56% 30% 10% 4% 48%</p>
87	Sg	313	<p>83% 15% 2%</p>
88	S1	74	<p>77% 22% 7%</p>
89	S4	76	<p>87% 13% 8%</p>

2 Entry composition [i](#)

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
			Total	C	N	O	S		
1	A	244	1868	1171	382	309	6	0	0

- Molecule 2 is a protein called Ribosomal protein uL18.

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

- Molecule 3 is a protein called Ribosomal protein eL8.

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

- Molecule 4 is a protein called Ribosomal protein uL6.

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

- Molecule 5 is a protein called Ribosomal protein uL5.

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

- Molecule 6 is a protein called Ribosomal protein eL13.

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

- Molecule 7 is a protein called Ribosomal protein eL14.

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

- Molecule 8 is a protein called Ribosomal protein eL15.

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

- Molecule 9 is a protein called Ribosomal protein uL13.

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

- Molecule 10 is a protein called Ribosomal protein eL18.

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

- Molecule 11 is a protein called Ribosomal protein eL19.

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

- Molecule 12 is a protein called Ribosomal protein eL20.

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

- Molecule 13 is a protein called Ribosomal protein eL21.

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

- Molecule 14 is a protein called Ribosomal protein eL22.

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

- Molecule 15 is a protein called Ribosomal protein uL14.

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

- Molecule 16 is a protein called Ribosomal protein uL23.

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

- Molecule 17 is a protein called Ribosomal protein uL24.

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

- Molecule 18 is a protein called Ribosomal protein eL27.

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

- Molecule 19 is a protein called Ribosomal protein uL15.

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

- Molecule 20 is a protein called Ribosomal protein eL29.

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

- 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
			Total	C	N	O	S		
35	B	394	3147	2005	591	538	13	0	0

- Molecule 36 is a protein called Ribosomal protein uL4.

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

- Molecule 37 is a protein called Ribosomal protein eL6.

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

- Molecule 38 is a protein called Ribosomal protein uL30.

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

- Molecule 39 is a protein called Ribosomal protein uL16.

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

- Molecule 40 is a protein called Ribosomal protein uL22.

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

- Molecule 41 is a protein called Ribosomal protein eL24.

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

- 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
			Total	C	N	O	S		
56	SB	213	1725	1093	311	308	13	0	0

- Molecule 57 is a protein called Ribosomal protein uS5.

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

- Molecule 58 is a protein called Ribosomal protein eS4.

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

- Molecule 59 is a protein called Ribosomal protein eS6.

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

- Molecule 60 is a protein called Ribosomal protein eS7.

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

- Molecule 61 is a protein called Ribosomal protein eS8.

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

- Molecule 62 is a protein called Ribosomal protein uS4.

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

- Molecule 63 is a protein called Ribosomal protein uS17.

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

- Molecule 64 is a protein called Ribosomal protein uS15.

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

- Molecule 65 is a protein called Ribosomal protein uS11.

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

- Molecule 66 is a protein called Ribosomal protein eS21.

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

- Molecule 67 is a protein called Ribosomal protein uS8.

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

- Molecule 68 is a protein called Ribosomal protein uS12.

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

- Molecule 69 is a protein called Ribosomal protein eS24.

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

- 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
			Total	C	N	O	S		
77	SP	96	805	506	158	135	6	0	0

- Molecule 78 is a protein called Ribosomal protein uS9.

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

- Molecule 79 is a protein called Ribosomal protein eS17.

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

- Molecule 80 is a protein called Ribosomal protein uS13.

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

- Molecule 81 is a protein called Ribosomal protein eS19.

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

- Molecule 82 is a protein called Ribosomal protein uS10.

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

- Molecule 83 is a protein called Ribosomal protein es25.

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

- 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 (three-letter code: 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 (three-letter code: ZN) (formula: Zn).

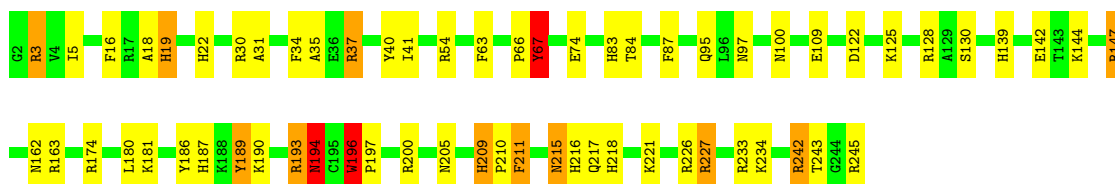
Mol	Chain	Residues	Atoms		AltConf
91	m	1	Total 1	Zn 1	0
91	o	1	Total 1	Zn 1	0
91	j	1	Total 1	Zn 1	0
91	Sa	1	Total 1	Zn 1	0

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.

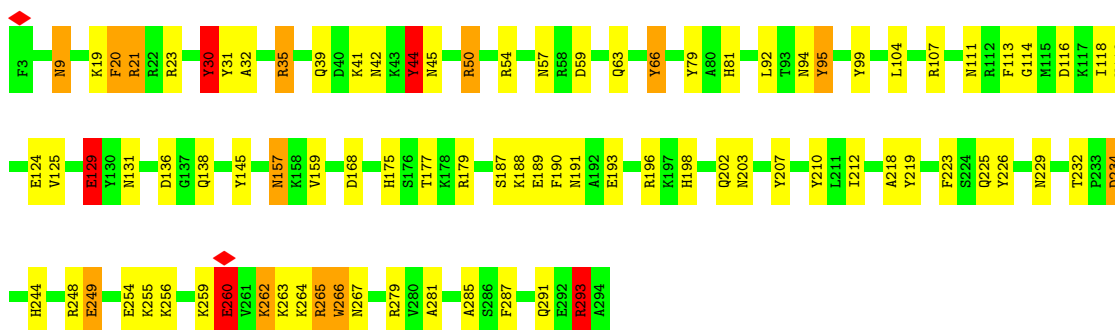
- Molecule 1: Ribosomal protein uL2

Chain A: 




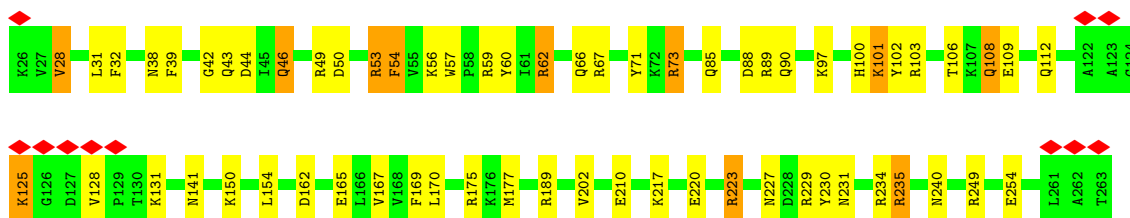
- Molecule 2: Ribosomal protein uL18

Chain D: 




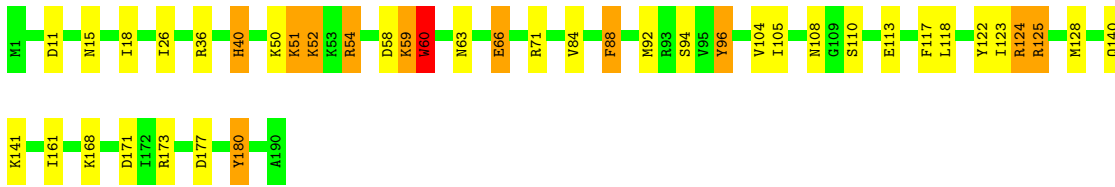
- Molecule 3: Ribosomal protein eL8

Chain G: 



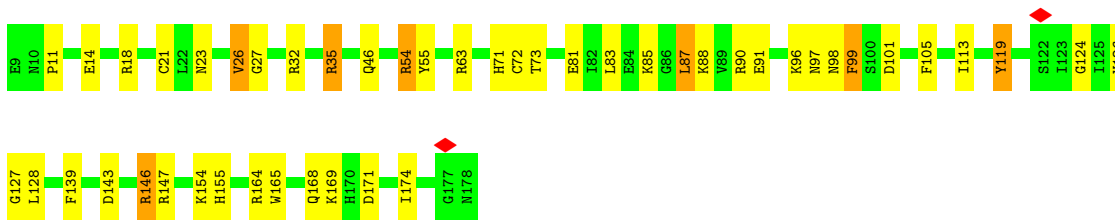
- Molecule 4: Ribosomal protein uL6

Chain H:  78% 15% 6%



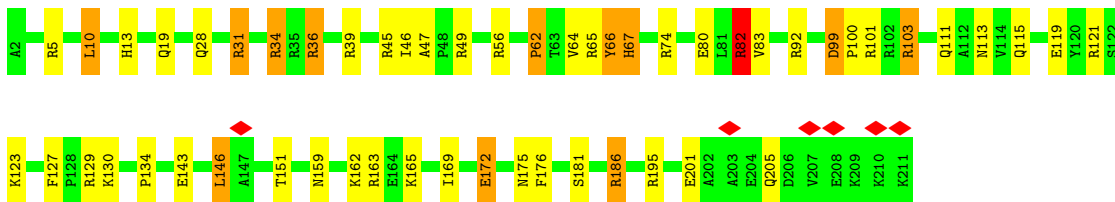
• Molecule 5: Ribosomal protein uL5

Chain J:  72% 24%



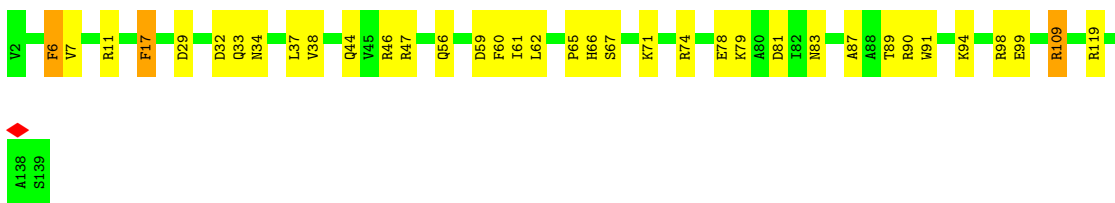
• Molecule 6: Ribosomal protein eL13

Chain L:  74% 20% 6%



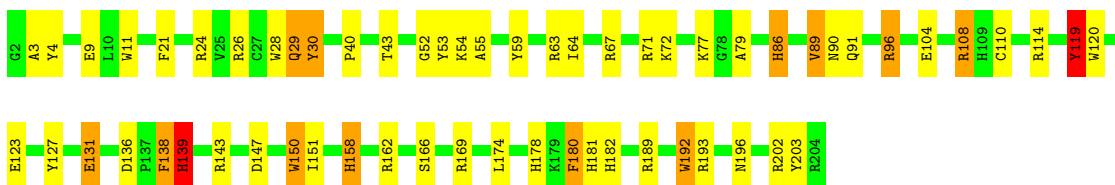
• Molecule 7: Ribosomal protein eL14

Chain M:  74% 24%

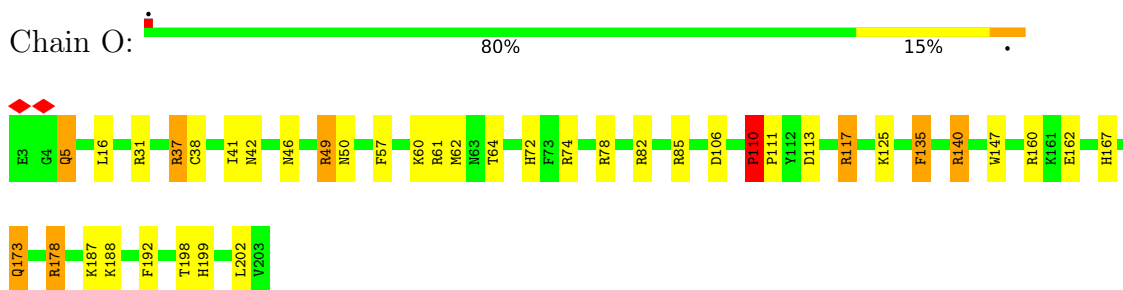


• Molecule 8: Ribosomal protein eL15

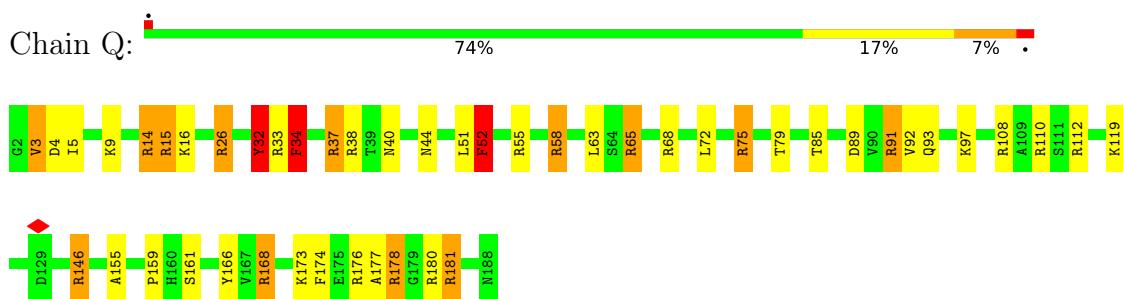
Chain N:  70% 23% 6%



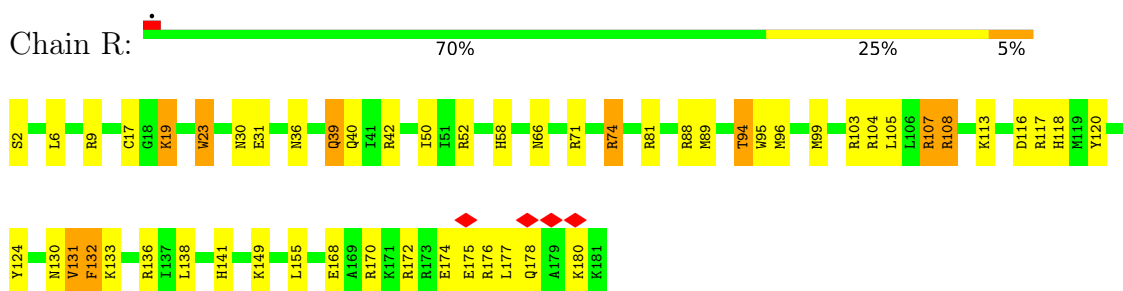
• Molecule 9: Ribosomal protein uL13



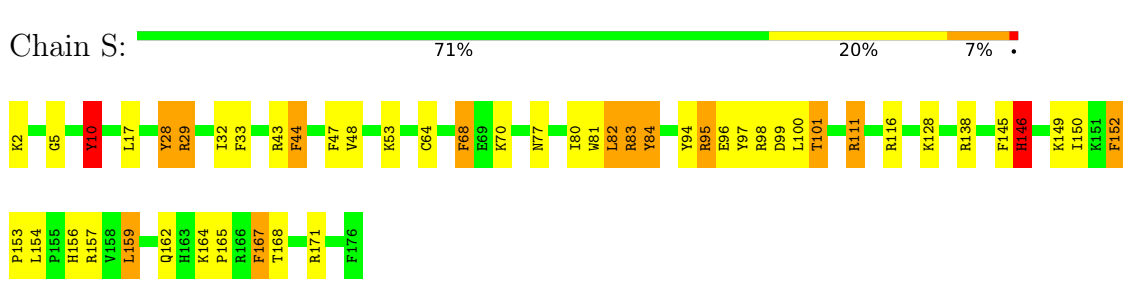
• Molecule 10: Ribosomal protein eL18



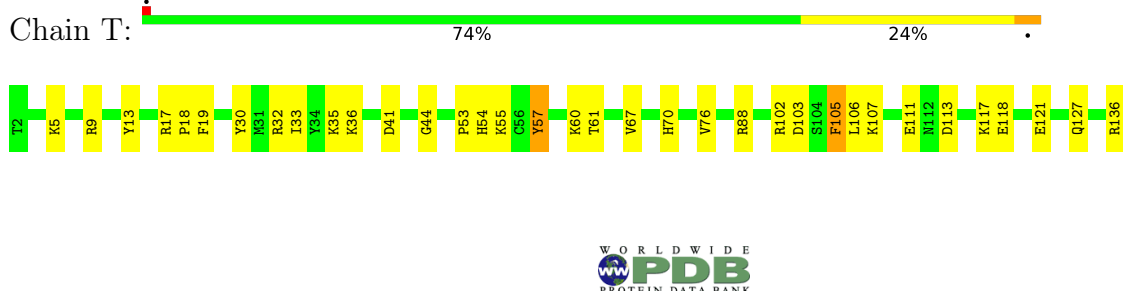
• Molecule 11: Ribosomal protein eL19

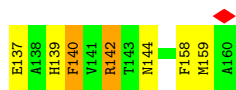


• Molecule 12: Ribosomal protein eL20

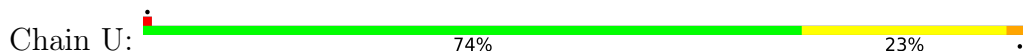


• Molecule 13: Ribosomal protein eL21

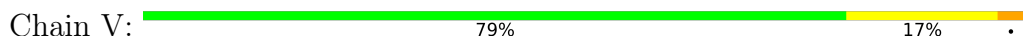




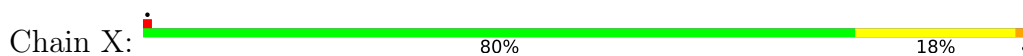
- Molecule 14: Ribosomal protein eL22



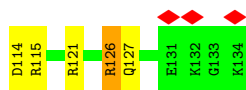
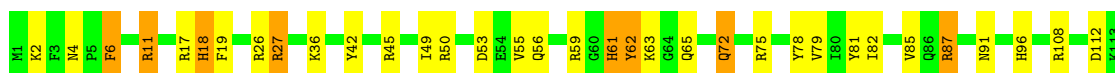
- Molecule 15: Ribosomal protein uL14



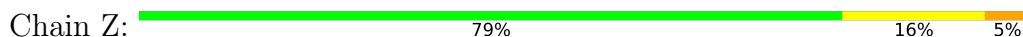
- Molecule 16: Ribosomal protein uL23



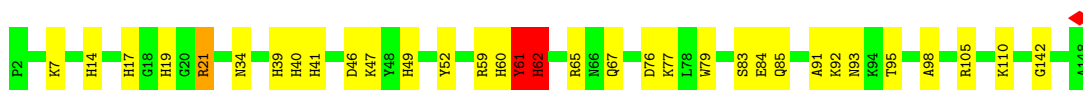
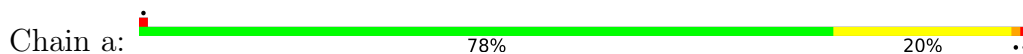
- Molecule 17: Ribosomal protein uL24



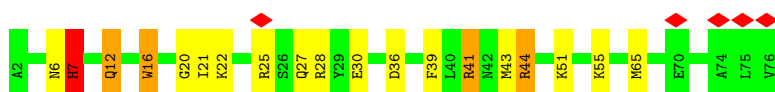
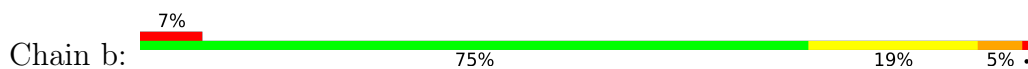
- Molecule 18: Ribosomal protein eL27



- Molecule 19: Ribosomal protein uL15



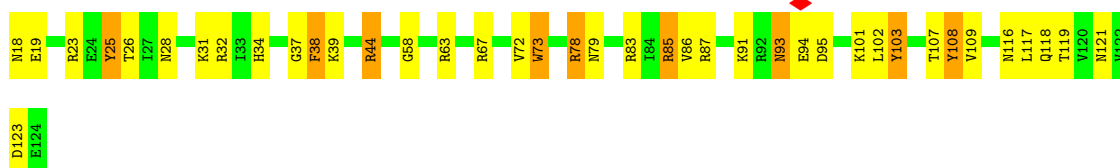
- Molecule 20: Ribosomal protein eL29



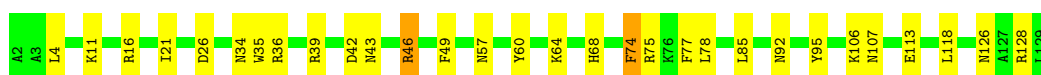
- Molecule 21: Ribosomal protein eL30



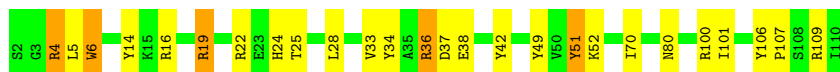
- Molecule 22: Ribosomal protein eL31



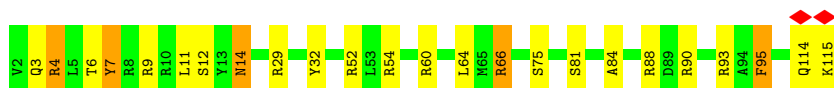
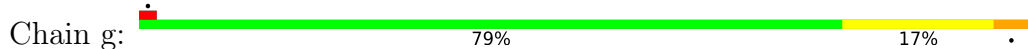
- Molecule 23: Ribosomal protein eL32



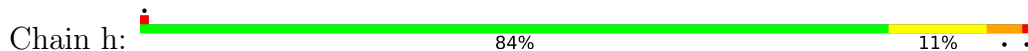
- Molecule 24: Ribosomal protein eL33



- Molecule 25: Ribosomal protein eL34

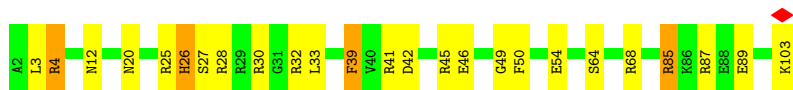


- Molecule 26: Ribosomal protein uL29

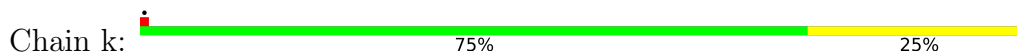




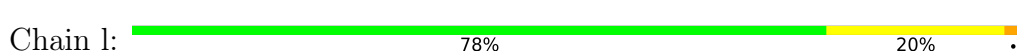
● Molecule 27: Ribosomal protein eL36



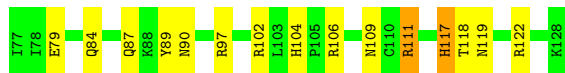
● Molecule 28: Ribosomal protein eL38



● Molecule 29: Ribosomal protein eL39



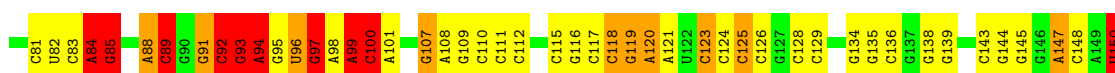
● Molecule 30: Ribosomal protein eL40

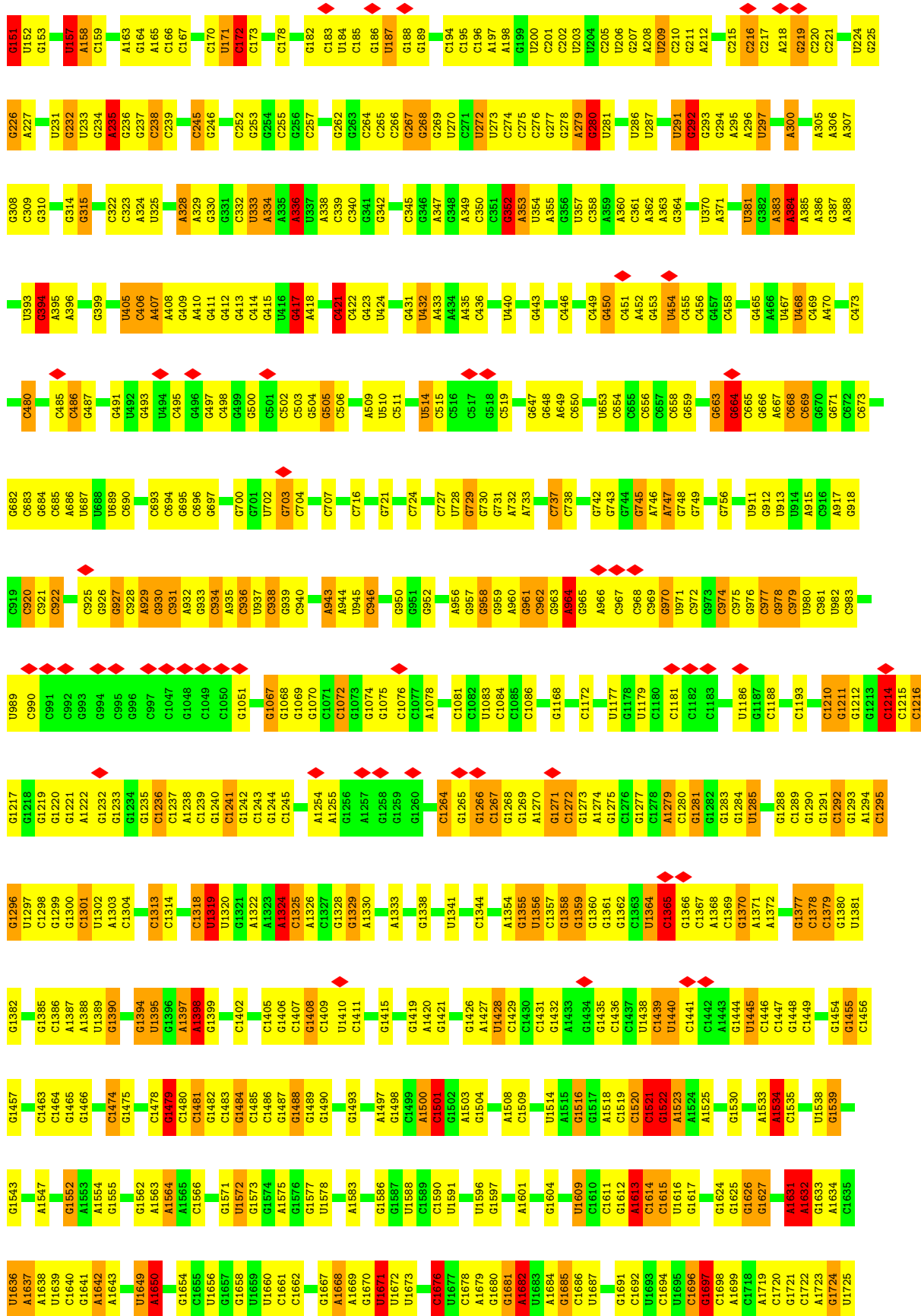


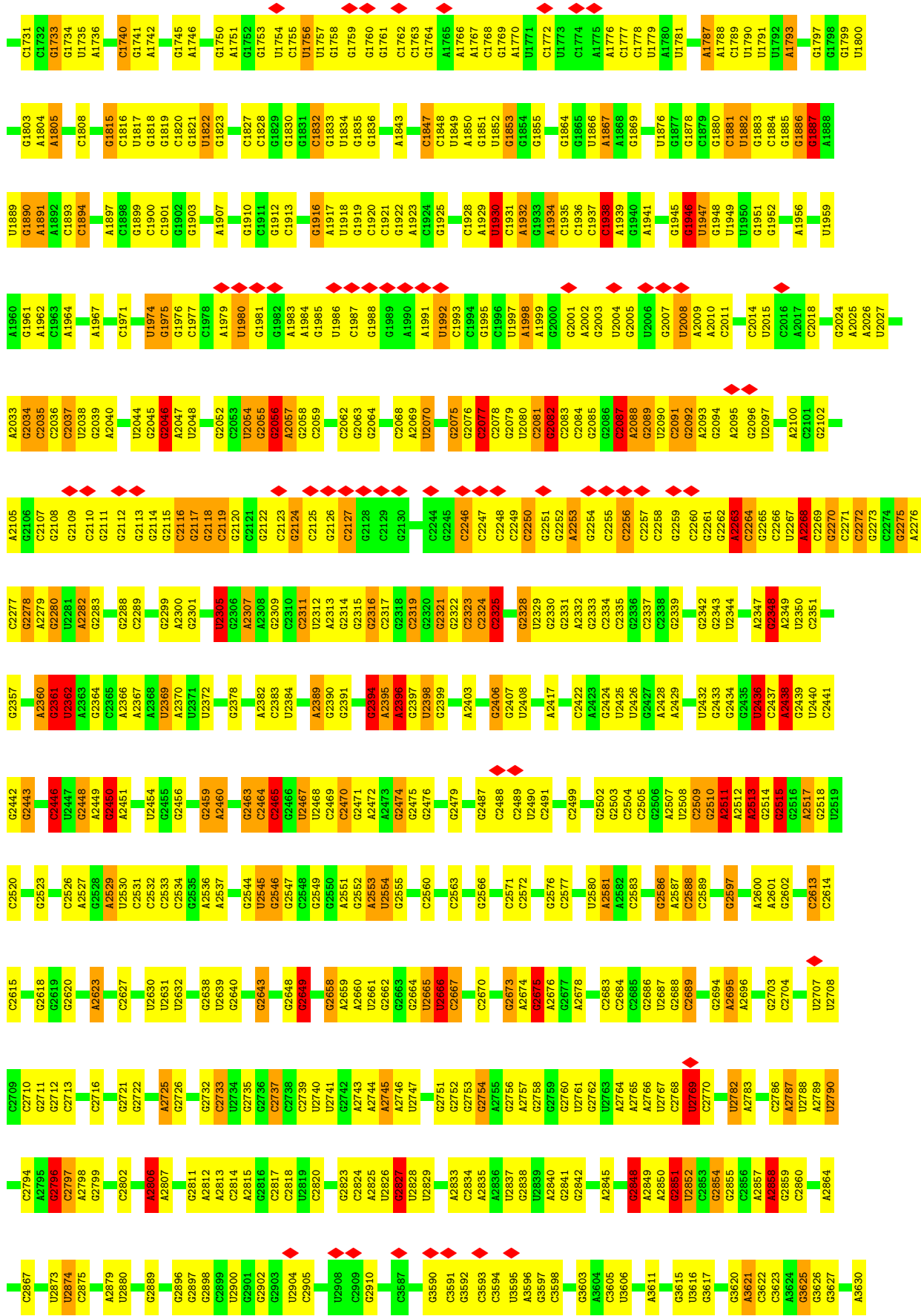
● Molecule 31: Ribosomal protein eL42

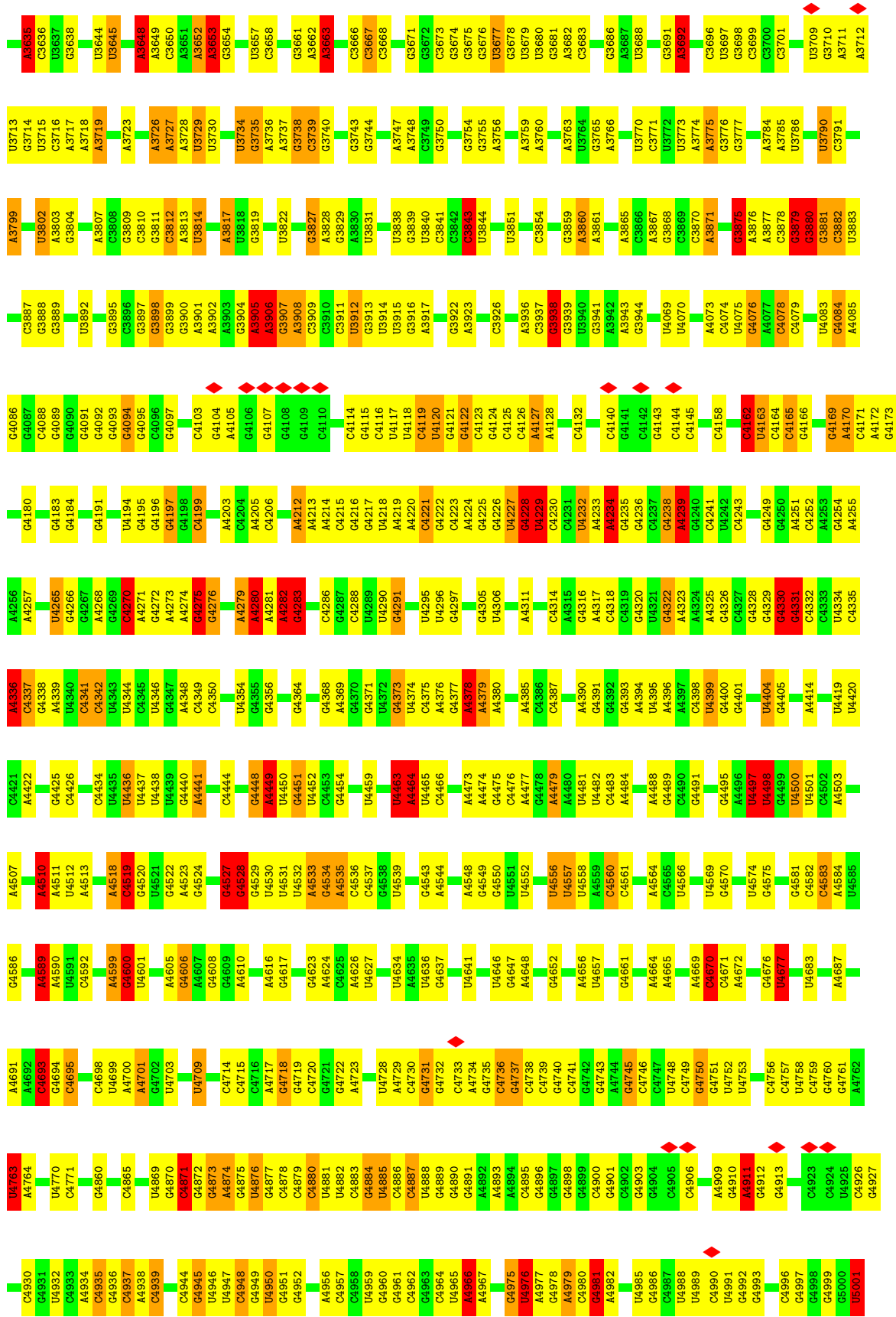


● Molecule 32: 28S ribosomal RNA



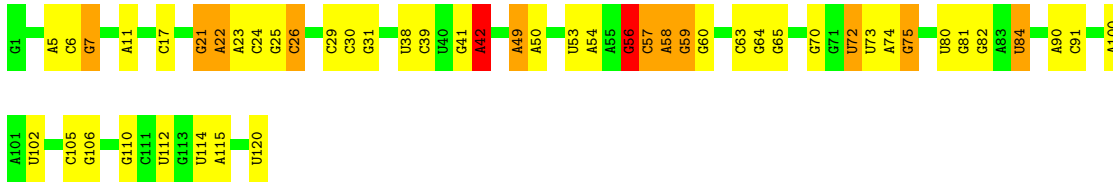




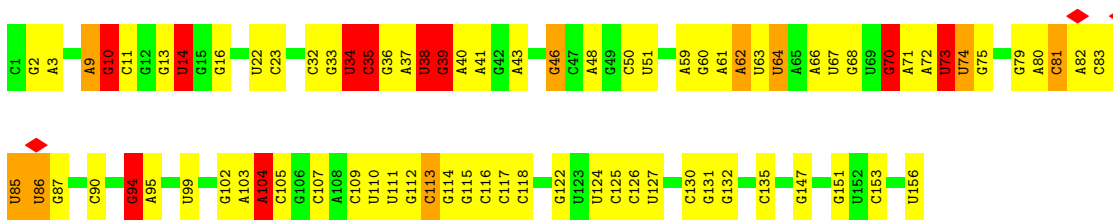




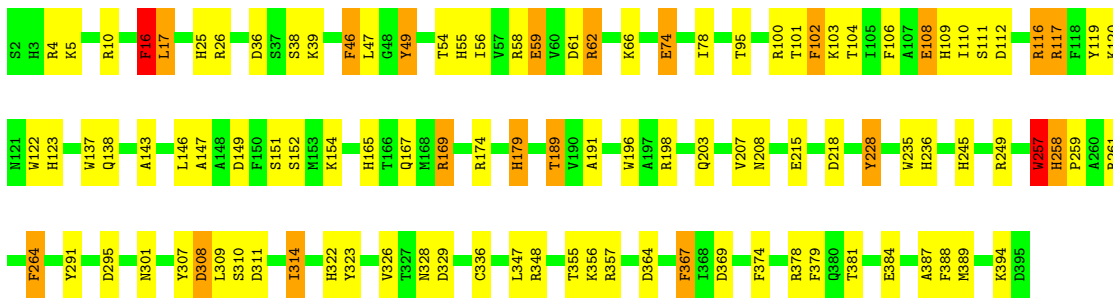
• Molecule 33: 5S ribosomal RNA



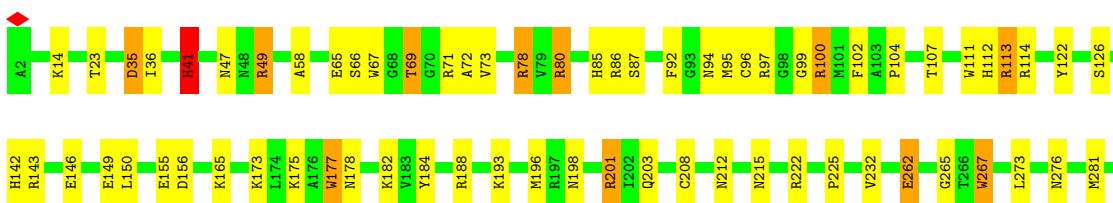
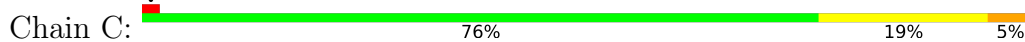
• Molecule 34: 5.8S ribosomal RNA

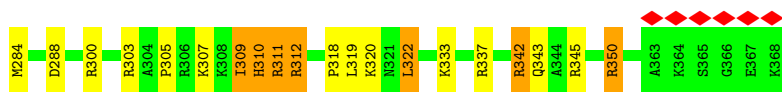


• Molecule 35: Ribosomal protein uL3

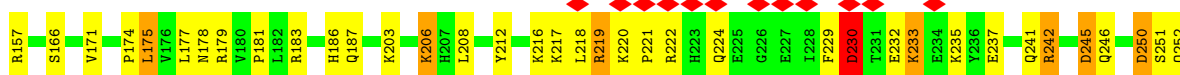
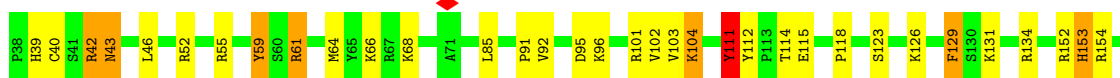


• Molecule 36: Ribosomal protein uL4





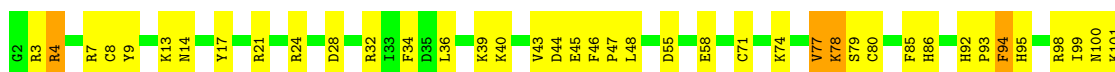
- Molecule 37: Ribosomal protein eL6



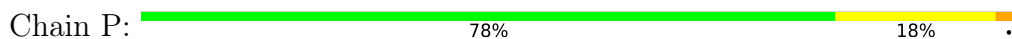
- Molecule 38: Ribosomal protein uL30



- Molecule 39: Ribosomal protein uL16



- Molecule 40: Ribosomal protein uL22



- Molecule 41: Ribosomal protein eL24

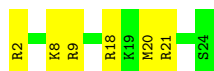




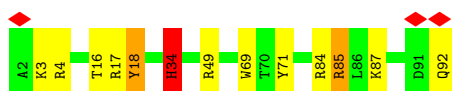
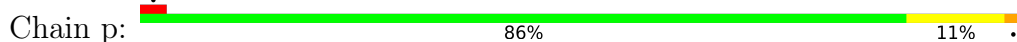
• Molecule 42: Ribosomal protein eL37



• Molecule 43: Ribosomal protein eL41



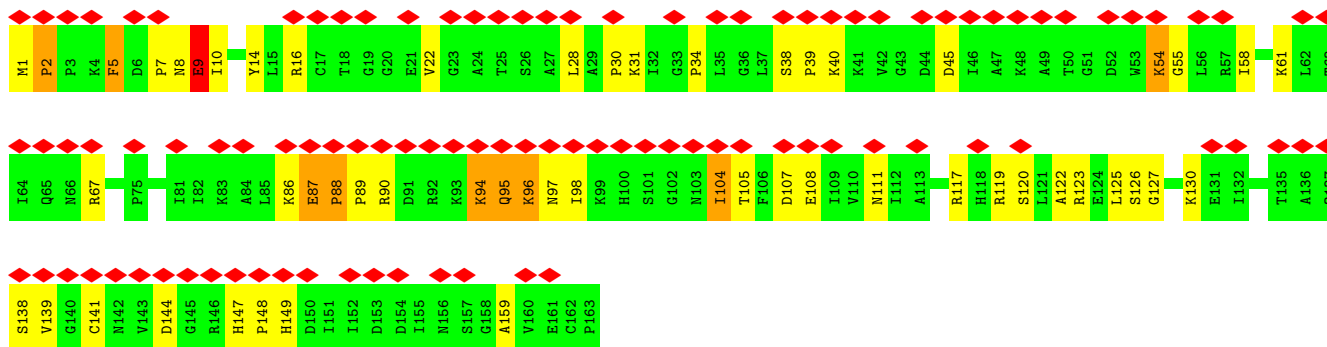
• Molecule 44: Ribosomal protein eL43



• Molecule 45: Ribosomal protein eL28

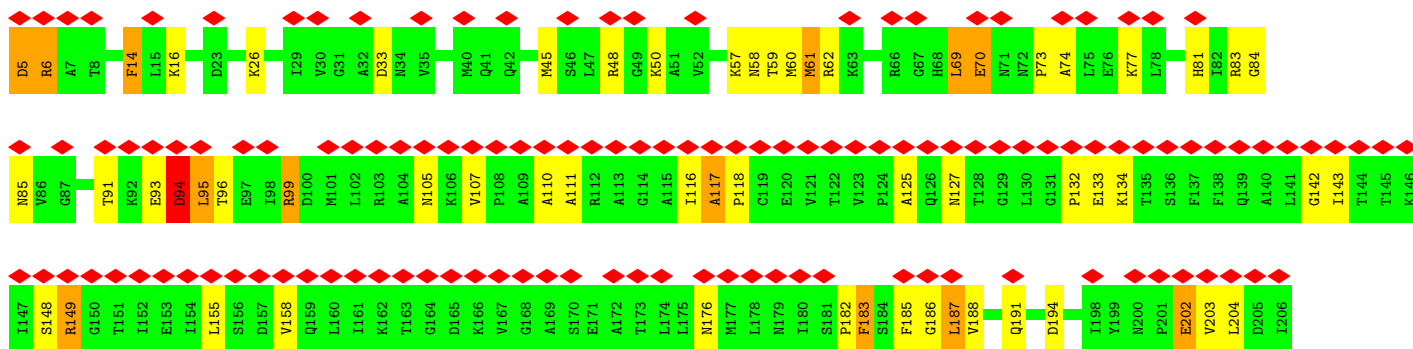


• Molecule 46: Ribosomal protein uL11

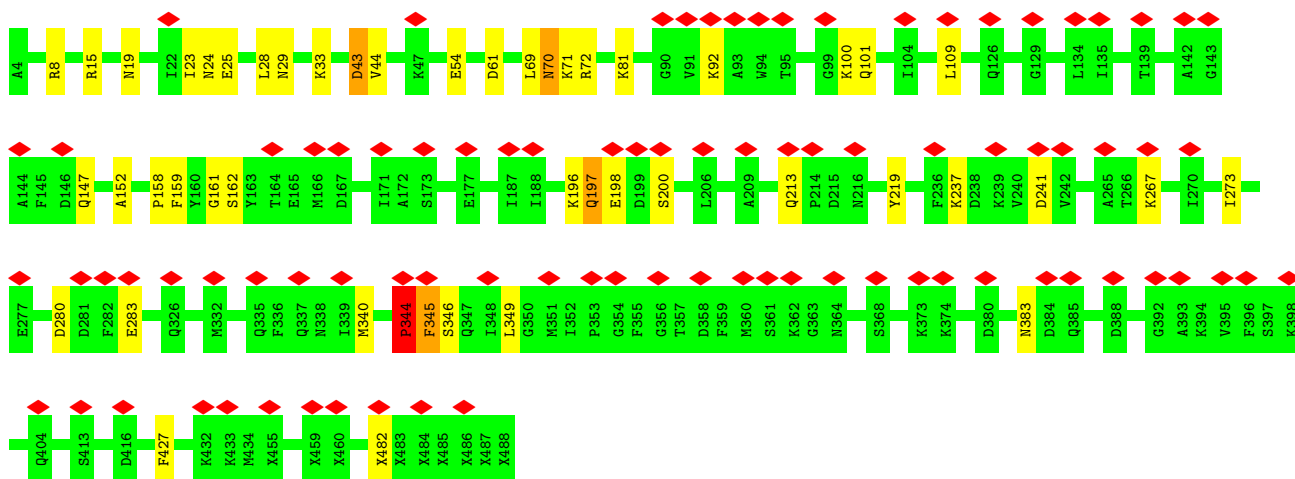
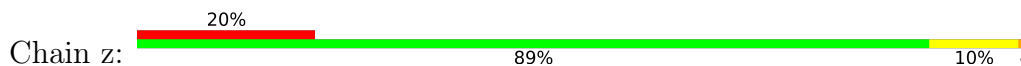


• Molecule 47: Ribosomal protein uL10

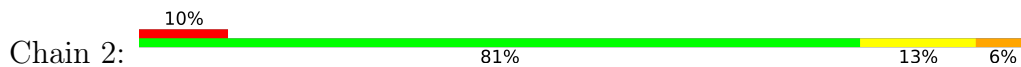




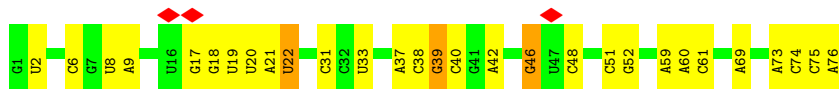
• Molecule 48: SRP54



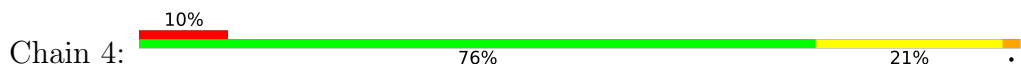
• Molecule 49: Nascent chain

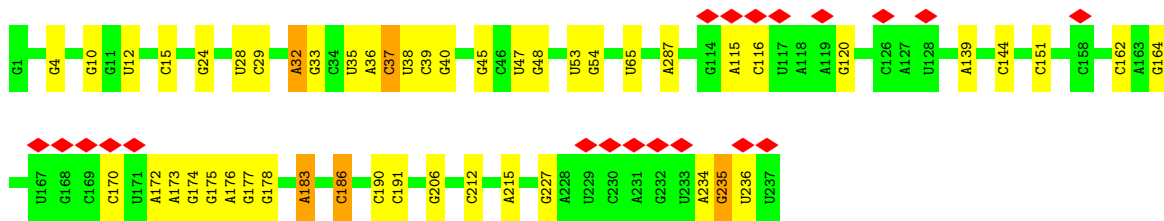


• Molecule 50: Val tRNA

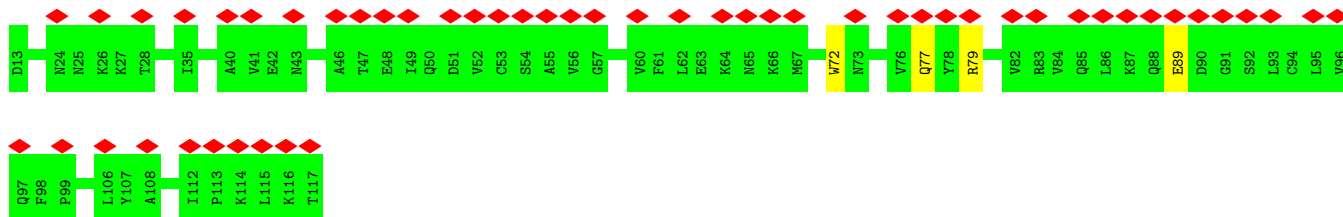


• Molecule 51: SRP 7S RNA

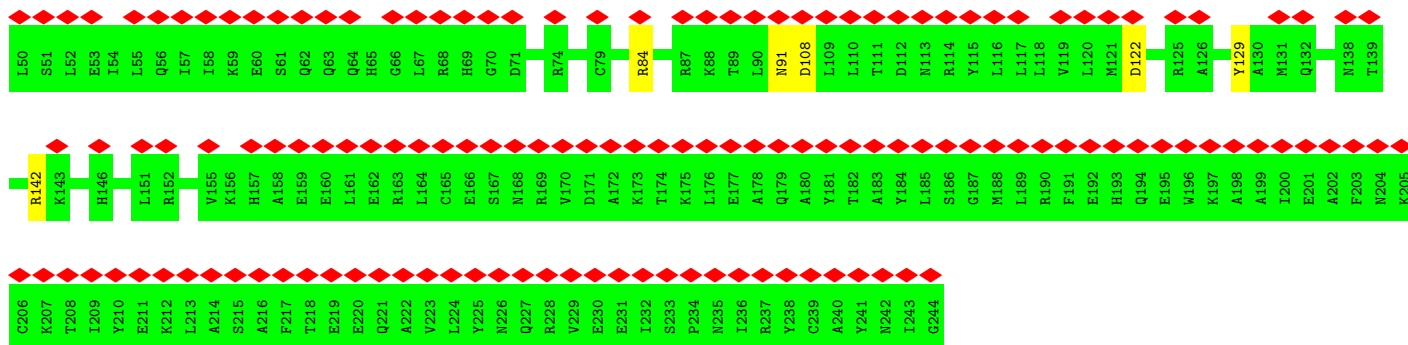
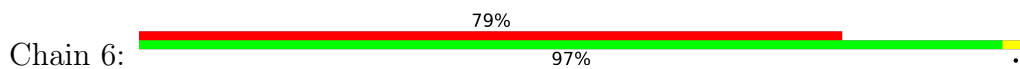




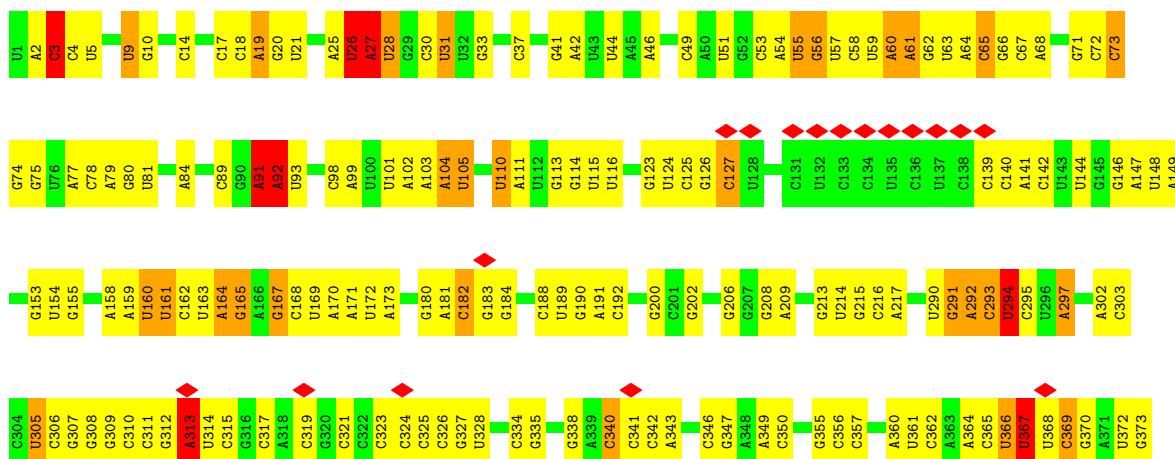
• Molecule 52: SRP19

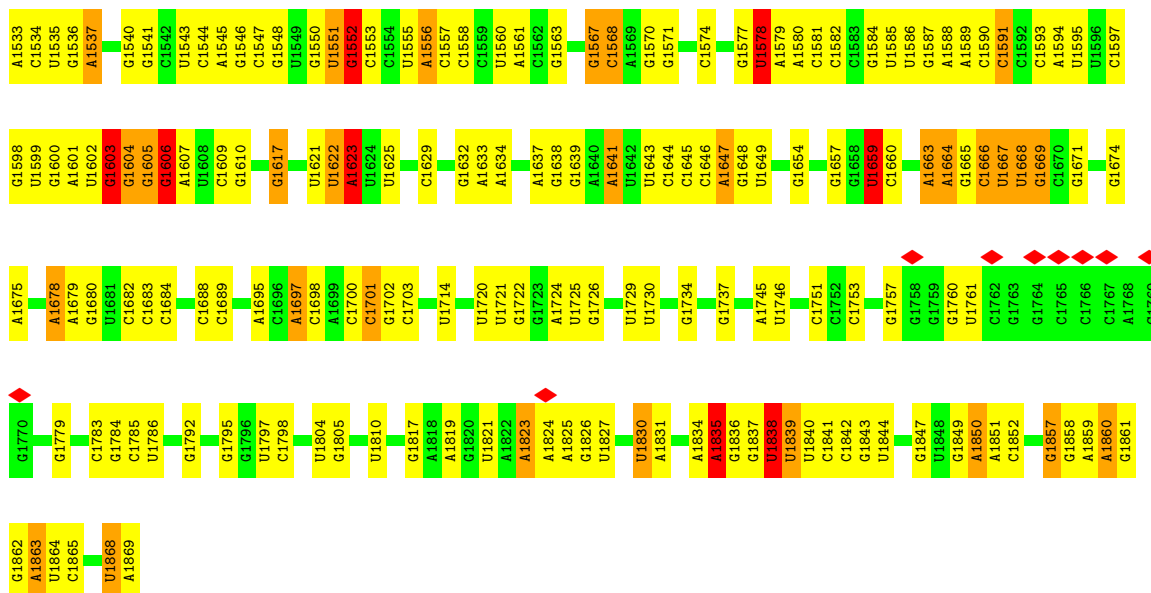


• Molecule 53: SRP68

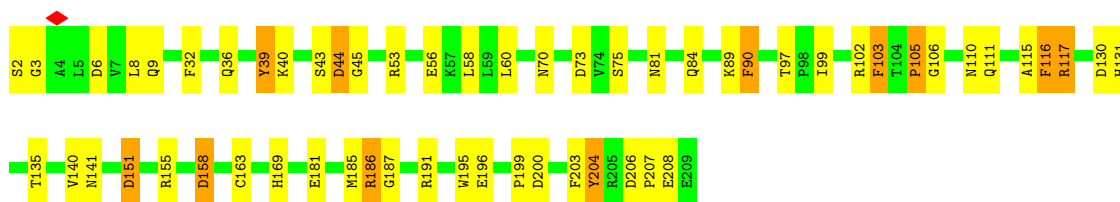


• Molecule 54: 18S ribosomal RNA

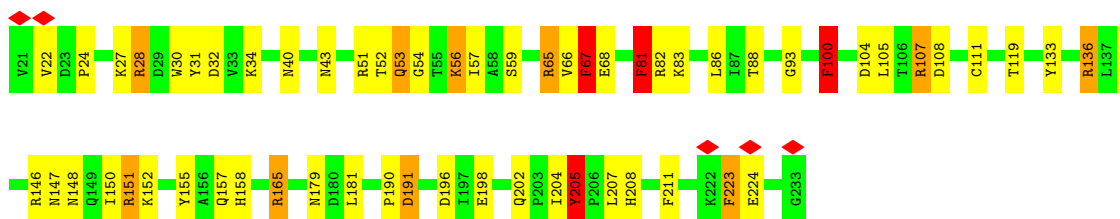




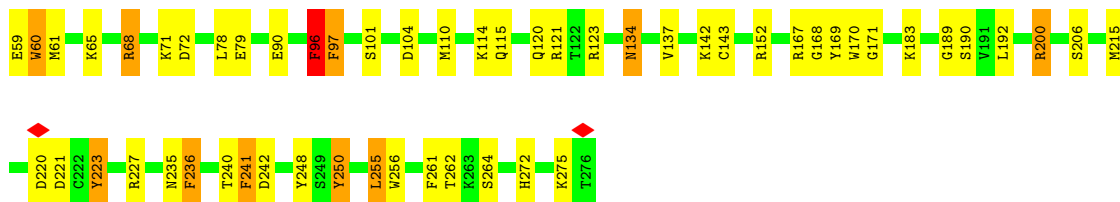
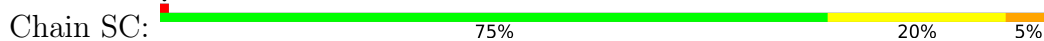
• Molecule 55: Ribosomal protein uS2



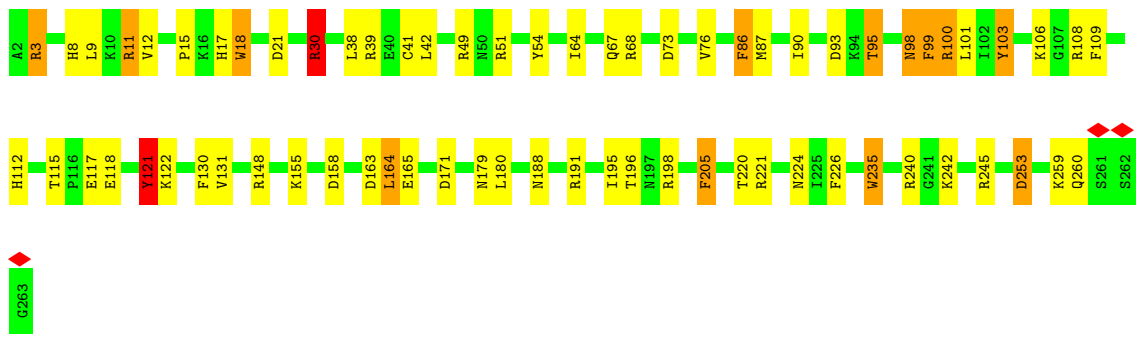
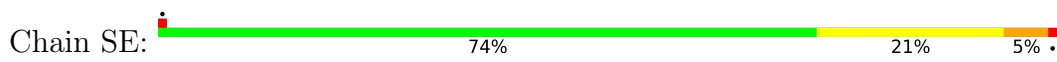
• Molecule 56: Ribosomal protein eS1



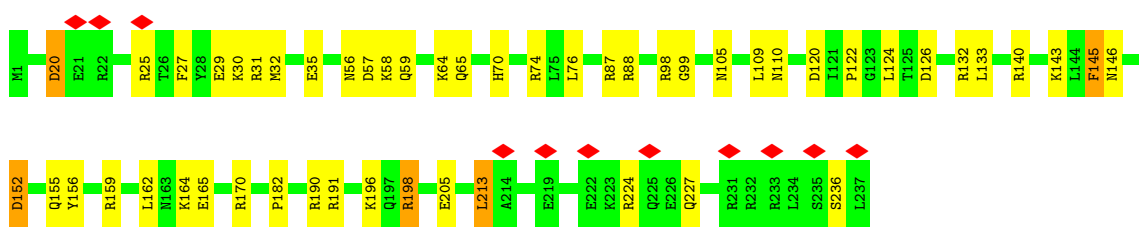
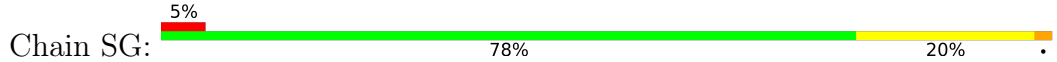
• Molecule 57: Ribosomal protein uS5



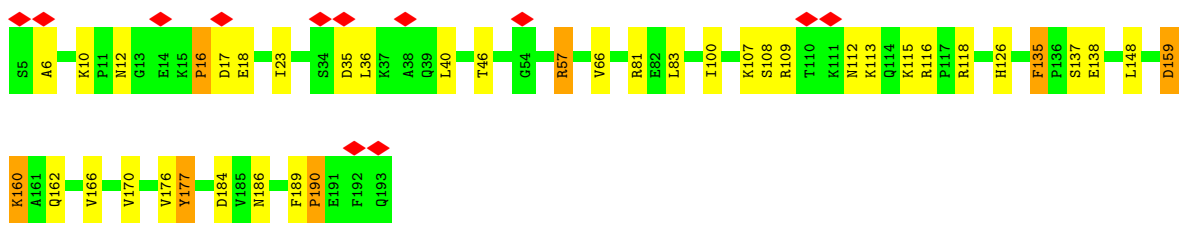
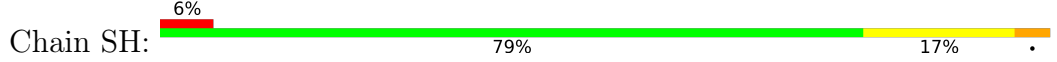
• Molecule 58: Ribosomal protein eS4



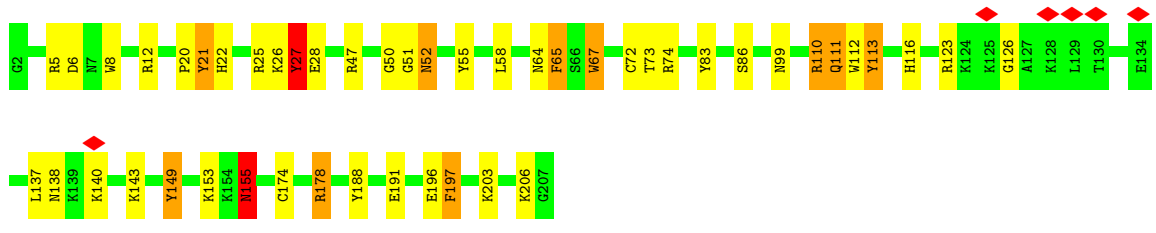
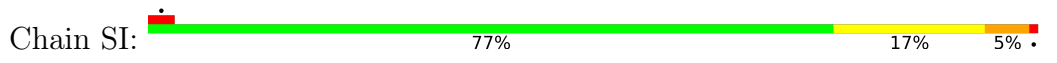
• Molecule 59: Ribosomal protein eS6



• Molecule 60: Ribosomal protein eS7

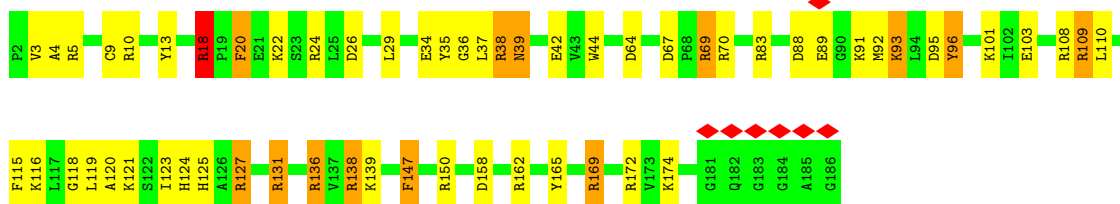


• Molecule 61: Ribosomal protein eS8




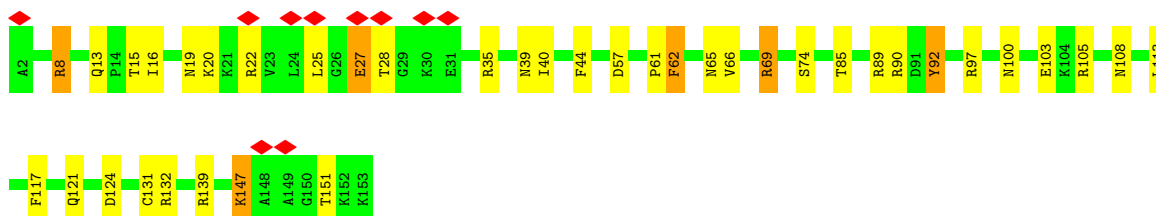
• Molecule 62: Ribosomal protein uS4

Chain SJ:  68% 24% 7%




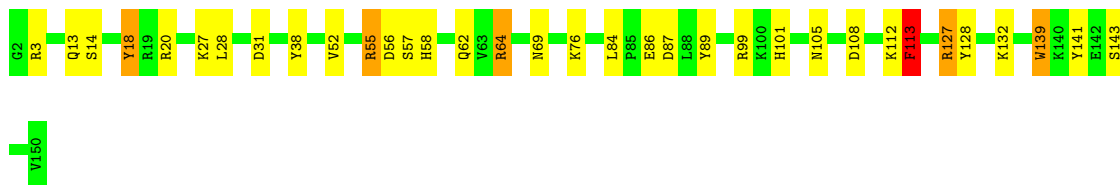
- Molecule 63: Ribosomal protein uS17

Chain SL:  74% 22% 7%



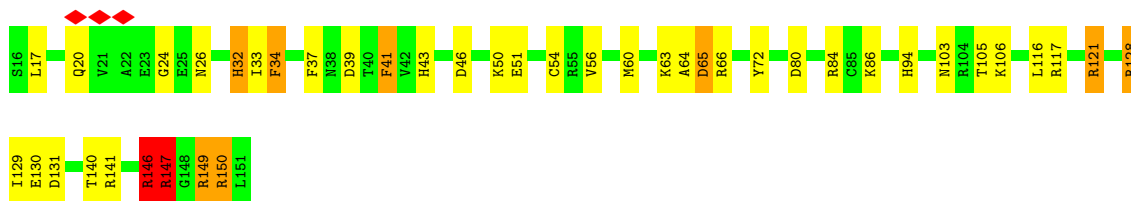
- Molecule 64: Ribosomal protein uS15

Chain SN:  77% 19% 2%



- Molecule 65: Ribosomal protein uS11

Chain SO:  69% 24% 6%




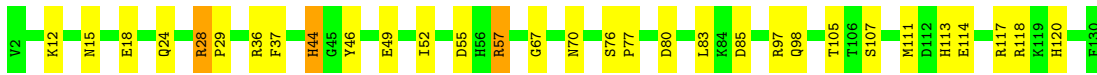
- Molecule 66: Ribosomal protein eS21

Chain SV:  71% 27% 2%




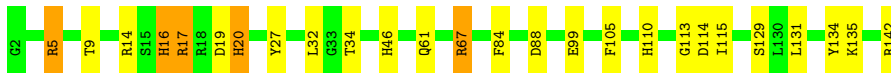
- Molecule 67: Ribosomal protein uS8

Chain SW:  76% 22%




• Molecule 68: Ribosomal protein uS12

Chain SX:  82% 15%




• Molecule 69: Ribosomal protein eS24

Chain SY:  77% 21%



• Molecule 70: Ribosomal protein eS26

Chain Sa:  76% 17% 7%




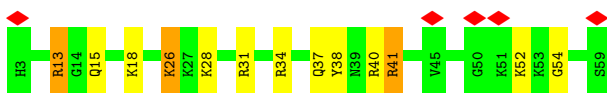
• Molecule 71: Ribosomal protein eS27

Chain Sb:  73% 25%




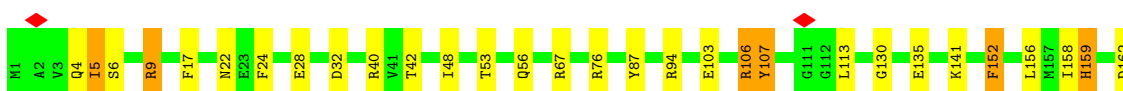
• Molecule 72: Ribosomal protein eS30

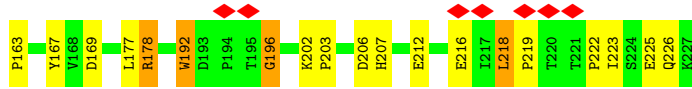
Chain Se:  9% 77% 18% 5%



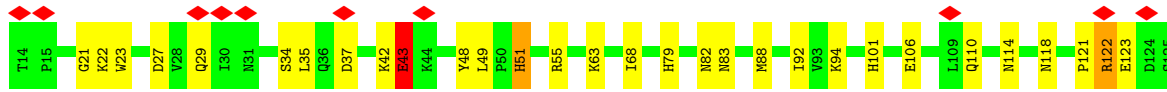
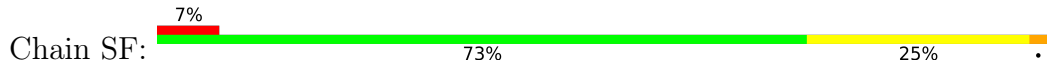
• Molecule 73: Ribosomal protein uS3

Chain SD:  78% 17%

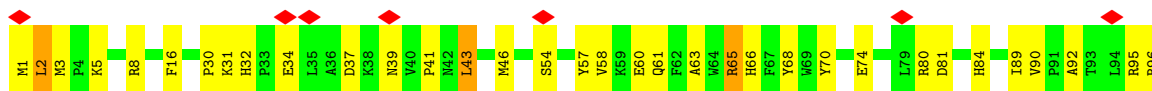




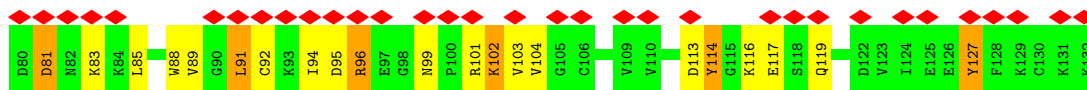
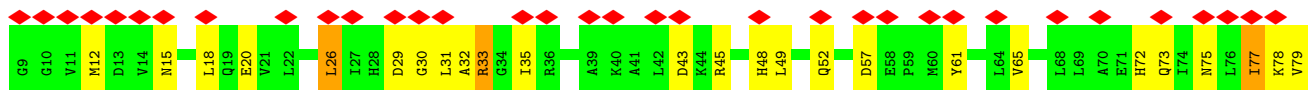
- Molecule 74: Ribosomal protein uS7



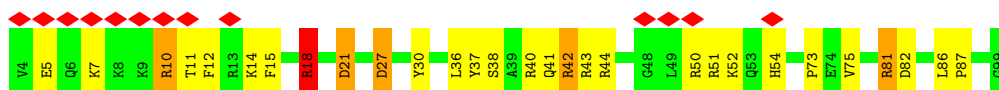
- Molecule 75: Ribosomal protein eS10



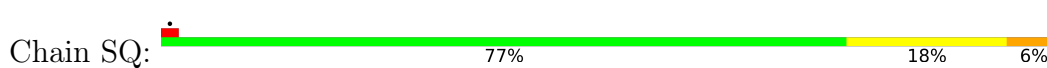
- Molecule 76: Ribosomal protein eS12

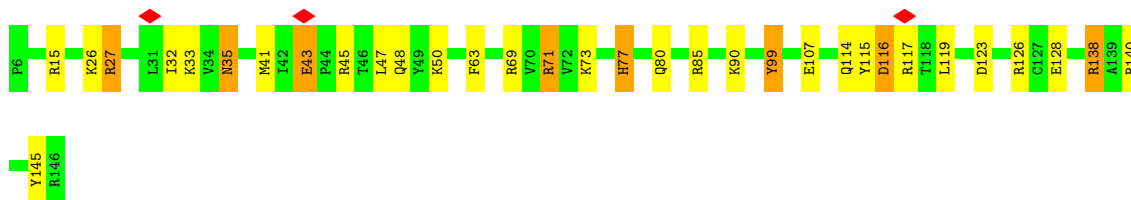


- Molecule 77: Ribosomal protein uS19

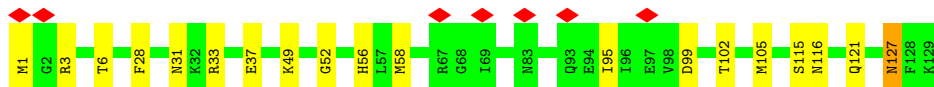
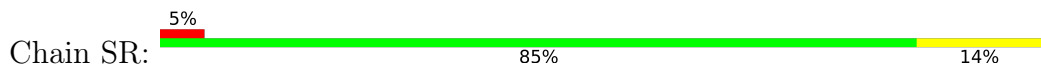


- Molecule 78: Ribosomal protein uS9

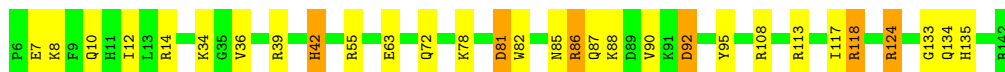
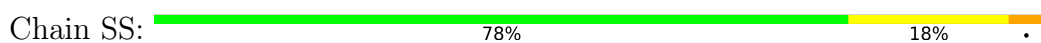




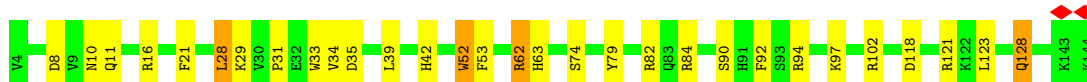
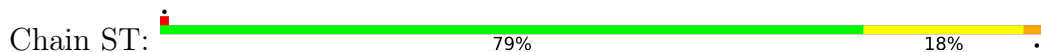
- Molecule 79: Ribosomal protein eS17



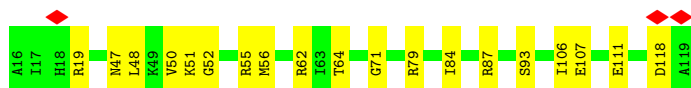
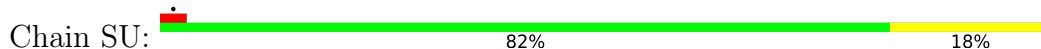
- Molecule 80: Ribosomal protein uS13



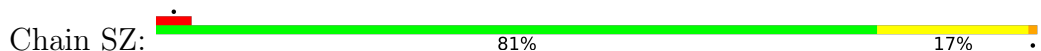
- Molecule 81: Ribosomal protein eS19



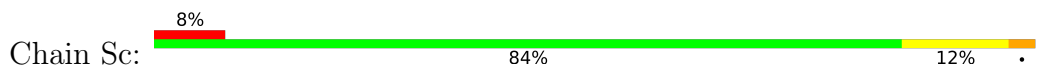
- Molecule 82: Ribosomal protein uS10

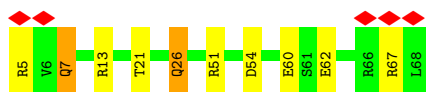


- Molecule 83: Ribosomal protein es25

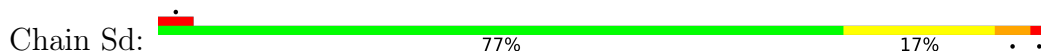


- Molecule 84: Ribosomal protein eS28

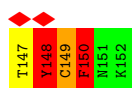




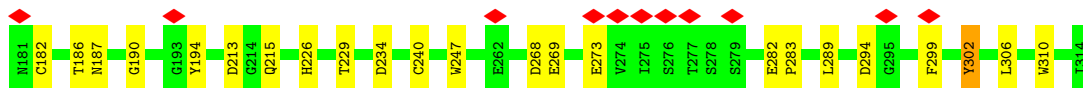
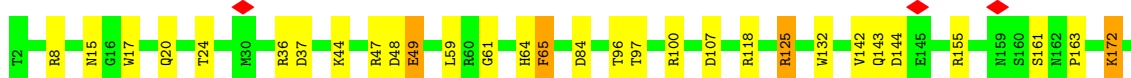
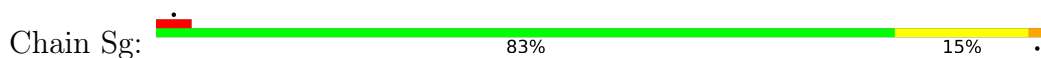
- Molecule 85: Ribosomal protein uS14



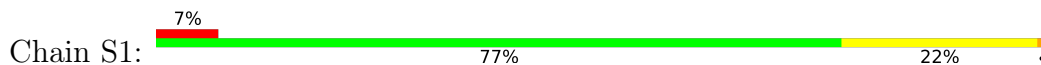
- Molecule 86: Ribosomal protein eS31



- 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 (\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 (\AA)	1.3399999, 1.3399999, 1.3399999	Depositor

5 Model quality i

5.1 Standard geometry i

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

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	0.70	1/1906 (0.1%)	1.25	19/2556 (0.7%)
2	D	0.67	2/2426 (0.1%)	1.17	25/3252 (0.8%)
3	G	0.78	8/1944 (0.4%)	1.10	14/2618 (0.5%)
4	H	0.77	2/1537 (0.1%)	1.10	10/2066 (0.5%)
5	J	0.69	2/1382 (0.1%)	1.09	15/1849 (0.8%)
6	L	0.68	3/1734 (0.2%)	1.05	7/2318 (0.3%)
7	M	0.63	1/1152 (0.1%)	1.10	5/1539 (0.3%)
8	N	0.72	3/1746 (0.2%)	1.25	11/2338 (0.5%)
9	O	0.63	2/1684 (0.1%)	1.08	11/2251 (0.5%)
10	Q	0.68	2/1530 (0.1%)	1.31	32/2041 (1.6%)
11	R	0.81	3/1524 (0.2%)	1.24	19/2013 (0.9%)
12	S	1.07	10/1493 (0.7%)	1.36	28/2002 (1.4%)
13	T	0.62	1/1326 (0.1%)	0.99	4/1770 (0.2%)
14	U	0.61	1/822 (0.1%)	0.99	2/1103 (0.2%)
15	V	0.57	0/993	0.98	2/1332 (0.2%)
16	X	0.56	0/993	0.95	3/1334 (0.2%)
17	Y	0.64	0/1132	1.17	12/1504 (0.8%)
18	Z	0.65	0/1130	1.14	8/1507 (0.5%)
19	a	0.66	0/1192	1.12	6/1591 (0.4%)
20	b	0.75	2/620 (0.3%)	1.17	7/819 (0.9%)
21	c	0.60	0/742	1.11	4/996 (0.4%)
22	d	0.69	2/903 (0.2%)	1.28	11/1216 (0.9%)
23	e	0.73	1/1071 (0.1%)	1.13	7/1429 (0.5%)
24	f	0.83	1/895 (0.1%)	1.28	10/1198 (0.8%)
25	g	0.59	0/916	1.14	8/1220 (0.7%)
26	h	0.55	0/1023	1.17	13/1350 (1.0%)
27	i	0.62	0/843	1.17	8/1115 (0.7%)
28	k	0.51	0/575	0.88	0/761
29	l	0.60	0/454	1.07	1/599 (0.2%)
30	m	0.47	0/435	0.95	1/575 (0.2%)
31	o	0.60	0/864	1.24	7/1140 (0.6%)
32	5	0.59	37/87703 (0.0%)	1.15	801/136805 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	7	0.52	0/2858	1.01	19/4455 (0.4%)
34	8	0.60	1/3701 (0.0%)	1.17	40/5766 (0.7%)
35	B	0.76	6/3214 (0.2%)	1.10	13/4308 (0.3%)
36	C	0.68	4/2973 (0.1%)	1.07	14/3990 (0.4%)
37	E	0.68	3/1941 (0.2%)	1.17	15/2601 (0.6%)
38	F	0.68	0/1905	1.17	13/2539 (0.5%)
39	I	0.59	1/1753 (0.1%)	1.05	8/2343 (0.3%)
40	P	0.77	3/1268 (0.2%)	1.15	12/1701 (0.7%)
41	W	0.73	0/541	1.17	3/720 (0.4%)
42	j	0.82	1/721 (0.1%)	1.31	12/953 (1.3%)
43	n	0.72	0/223	1.11	0/284
44	p	0.60	1/718 (0.1%)	1.00	4/953 (0.4%)
45	r	0.57	0/1017	1.05	4/1365 (0.3%)
46	K	0.76	2/1256 (0.2%)	1.17	6/1694 (0.4%)
47	q	0.73	2/1580 (0.1%)	0.93	5/2133 (0.2%)
48	z	0.92	7/3171 (0.2%)	0.95	10/4257 (0.2%)
49	2	0.50	0/234	0.99	1/317 (0.3%)
50	3	1.56	2/1804 (0.1%)	1.07	7/2805 (0.2%)
51	4	0.77	1/5090 (0.0%)	1.05	13/7936 (0.2%)
52	9	0.35	0/858	0.58	0/1156
53	6	0.29	0/1521	0.49	0/2039
54	S2	0.59	27/41241 (0.1%)	1.15	365/64249 (0.6%)
55	SA	0.63	1/1679 (0.1%)	1.05	10/2283 (0.4%)
56	SB	0.74	6/1753 (0.3%)	1.12	15/2350 (0.6%)
57	SC	0.69	1/1726 (0.1%)	1.05	14/2332 (0.6%)
58	SE	0.64	2/2118 (0.1%)	1.09	15/2849 (0.5%)
59	SG	0.69	4/1946 (0.2%)	1.05	8/2590 (0.3%)
60	SH	0.51	0/1544	0.94	5/2068 (0.2%)
61	SI	0.76	3/1715 (0.2%)	1.11	12/2287 (0.5%)
62	SJ	0.59	1/1550 (0.1%)	1.20	12/2069 (0.6%)
63	SL	0.66	1/1259 (0.1%)	1.05	4/1684 (0.2%)
64	SN	0.60	0/1226	1.05	7/1649 (0.4%)
65	SO	0.61	0/1029	1.23	13/1380 (0.9%)
66	SV	0.54	0/631	0.93	0/844
67	SW	0.65	1/1051 (0.1%)	1.04	6/1406 (0.4%)
68	SX	0.60	0/1118	1.06	9/1493 (0.6%)
69	SY	0.54	0/1040	0.94	0/1382
70	Sa	0.71	1/794 (0.1%)	1.17	6/1065 (0.6%)
71	Sb	0.48	0/665	0.90	1/891 (0.1%)
72	Se	0.50	0/458	0.97	3/602 (0.5%)
73	SD	0.60	1/1793 (0.1%)	1.01	5/2414 (0.2%)
74	SF	0.62	2/1531 (0.1%)	1.00	6/2059 (0.3%)
75	SK	0.58	0/851	1.01	5/1147 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SM	0.69	0/970	1.05	6/1300 (0.5%)
77	SP	0.87	2/816 (0.2%)	1.19	10/1084 (0.9%)
78	SQ	0.51	0/1142	1.08	12/1528 (0.8%)
79	SR	0.50	0/1060	0.73	0/1421
80	SS	0.46	0/1157	0.99	5/1548 (0.3%)
81	ST	0.61	1/1119 (0.1%)	1.05	3/1499 (0.2%)
82	SU	0.52	0/828	0.92	0/1112
83	SZ	0.47	0/604	0.84	0/810
84	Sc	0.57	2/507 (0.4%)	0.75	0/677
85	Sd	0.66	0/445	1.12	2/589 (0.3%)
86	Sf	0.96	3/593 (0.5%)	1.61	15/786 (1.9%)
87	Sg	0.56	0/2493	0.85	3/3394 (0.1%)
88	S1	1.04	4/619 (0.6%)	0.90	1/832 (0.1%)
89	S4	0.88	2/608 (0.3%)	0.77	0/809
All	All	0.64	183/244716 (0.1%)	1.12	1888/359004 (0.5%)

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 183 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	3	31	C	O3'-P	-62.24	0.86	1.61
51	4	183	A	O3'-P	-44.16	1.08	1.61
32	5	1823	G	O3'-P	35.59	2.03	1.61
48	z	340	MET	C-N	22.92	1.86	1.34
48	z	345	PHE	C-N	-18.40	0.91	1.34

The worst 5 of 1888 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	3	38	C	P-O3'-C3'	-20.63	94.95	119.70
48	z	340	MET	O-C-N	19.47	153.86	122.70
50	3	31	C	O3'-P-O5'	-18.73	68.40	104.00
48	z	340	MET	C-N-CA	-18.61	75.16	121.70
86	Sf	146	LEU	CA-CB-CG	16.39	153.01	115.30

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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	3	27
2	D	290/292 (99%)	228 (79%)	41 (14%)	21 (7%)	1	16
3	G	236/238 (99%)	188 (80%)	41 (17%)	7 (3%)	4	34
4	H	188/190 (99%)	162 (86%)	20 (11%)	6 (3%)	4	33
5	J	168/170 (99%)	126 (75%)	33 (20%)	9 (5%)	2	22
6	L	208/210 (99%)	166 (80%)	29 (14%)	13 (6%)	1	19
7	M	136/138 (99%)	111 (82%)	21 (15%)	4 (3%)	4	34
8	N	201/203 (99%)	159 (79%)	31 (15%)	11 (6%)	2	21
9	O	199/201 (99%)	177 (89%)	19 (10%)	3 (2%)	10	45
10	Q	185/187 (99%)	154 (83%)	24 (13%)	7 (4%)	3	29
11	R	178/180 (99%)	148 (83%)	23 (13%)	7 (4%)	3	28
12	S	173/175 (99%)	139 (80%)	27 (16%)	7 (4%)	3	28
13	T	157/159 (99%)	132 (84%)	20 (13%)	5 (3%)	4	33
14	U	97/99 (98%)	80 (82%)	14 (14%)	3 (3%)	4	33
15	V	129/131 (98%)	110 (85%)	14 (11%)	5 (4%)	3	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	X	117/119 (98%)	102 (87%)	12 (10%)	3 (3%)	5	36
17	Y	132/134 (98%)	105 (80%)	21 (16%)	6 (4%)	2	25
18	Z	133/135 (98%)	111 (84%)	15 (11%)	7 (5%)	2	22
19	a	145/147 (99%)	114 (79%)	24 (17%)	7 (5%)	2	24
20	b	73/75 (97%)	60 (82%)	10 (14%)	3 (4%)	3	27
21	c	92/94 (98%)	78 (85%)	10 (11%)	4 (4%)	2	26
22	d	105/107 (98%)	85 (81%)	16 (15%)	4 (4%)	3	29
23	e	126/128 (98%)	110 (87%)	14 (11%)	2 (2%)	9	44
24	f	107/109 (98%)	89 (83%)	11 (10%)	7 (6%)	1	19
25	g	112/114 (98%)	100 (89%)	10 (9%)	2 (2%)	8	42
26	h	120/122 (98%)	97 (81%)	21 (18%)	2 (2%)	9	43
27	i	100/102 (98%)	85 (85%)	13 (13%)	2 (2%)	7	41
28	k	67/69 (97%)	53 (79%)	11 (16%)	3 (4%)	2	25
29	l	48/50 (96%)	42 (88%)	5 (10%)	1 (2%)	7	40
30	m	50/52 (96%)	44 (88%)	6 (12%)	0	100	100
31	o	102/104 (98%)	79 (78%)	17 (17%)	6 (6%)	1	20
35	B	392/394 (100%)	309 (79%)	54 (14%)	29 (7%)	1	15
36	C	365/367 (100%)	292 (80%)	55 (15%)	18 (5%)	2	23
37	E	232/236 (98%)	144 (62%)	55 (24%)	33 (14%)	0	4
38	F	223/225 (99%)	180 (81%)	35 (16%)	8 (4%)	3	30
39	I	211/213 (99%)	170 (81%)	28 (13%)	13 (6%)	1	19
40	P	151/153 (99%)	134 (89%)	15 (10%)	2 (1%)	12	48
41	W	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
42	j	84/86 (98%)	64 (76%)	18 (21%)	2 (2%)	6	37
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	20
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	4
48	z	399/426 (94%)	350 (88%)	31 (8%)	18 (4%)	2	25
49	2	27/31 (87%)	15 (56%)	9 (33%)	3 (11%)	0	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	19
56	SB	211/213 (99%)	154 (73%)	36 (17%)	21 (10%)	0	9
57	SC	216/218 (99%)	182 (84%)	27 (12%)	7 (3%)	4	33
58	SE	260/262 (99%)	198 (76%)	44 (17%)	18 (7%)	1	17
59	SG	235/237 (99%)	195 (83%)	32 (14%)	8 (3%)	3	32
60	SH	187/189 (99%)	141 (75%)	29 (16%)	17 (9%)	1	11
61	SI	204/206 (99%)	165 (81%)	30 (15%)	9 (4%)	2	25
62	SJ	183/185 (99%)	133 (73%)	35 (19%)	15 (8%)	1	12
63	SL	150/152 (99%)	122 (81%)	22 (15%)	6 (4%)	3	28
64	SN	147/149 (99%)	115 (78%)	28 (19%)	4 (3%)	5	35
65	SO	134/136 (98%)	99 (74%)	21 (16%)	14 (10%)	0	8
66	SV	80/82 (98%)	58 (72%)	15 (19%)	7 (9%)	1	11
67	SW	127/129 (98%)	108 (85%)	16 (13%)	3 (2%)	6	37
68	SX	139/141 (99%)	109 (78%)	26 (19%)	4 (3%)	4	34
69	SY	124/126 (98%)	101 (82%)	16 (13%)	7 (6%)	2	21
70	Sa	96/98 (98%)	69 (72%)	18 (19%)	9 (9%)	0	10
71	Sb	81/83 (98%)	61 (75%)	16 (20%)	4 (5%)	2	23
72	Se	55/57 (96%)	41 (74%)	12 (22%)	2 (4%)	3	30
73	SD	225/227 (99%)	174 (77%)	41 (18%)	10 (4%)	2	25
74	SF	189/191 (99%)	145 (77%)	34 (18%)	10 (5%)	2	22
75	SK	96/98 (98%)	58 (60%)	26 (27%)	12 (12%)	0	5
76	SM	122/124 (98%)	78 (64%)	24 (20%)	20 (16%)	0	3
77	SP	94/96 (98%)	67 (71%)	17 (18%)	10 (11%)	0	7
78	SQ	139/141 (99%)	111 (80%)	20 (14%)	8 (6%)	1	20
79	SR	127/129 (98%)	111 (87%)	11 (9%)	5 (4%)	3	28
80	SS	135/137 (98%)	114 (84%)	12 (9%)	9 (7%)	1	18
81	ST	139/141 (99%)	115 (83%)	18 (13%)	6 (4%)	2	26
82	SU	102/104 (98%)	83 (81%)	13 (13%)	6 (6%)	1	20
83	SZ	73/75 (97%)	59 (81%)	9 (12%)	5 (7%)	1	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
84	Sc	60/64 (94%)	47 (78%)	12 (20%)	1 (2%)	9	43
85	Sd	50/52 (96%)	36 (72%)	11 (22%)	3 (6%)	1	20
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	24
88	S1	72/74 (97%)	61 (85%)	6 (8%)	5 (7%)	1	17
89	S4	72/76 (95%)	68 (94%)	4 (6%)	0	100	100
All	All	12341/12544 (98%)	9853 (80%)	1811 (15%)	677 (6%)	3	21

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 [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	
1	A	187/187 (100%)	137 (73%)	50 (27%)	0	3
2	D	246/247 (100%)	183 (74%)	63 (26%)	0	4
3	G	204/206 (99%)	150 (74%)	54 (26%)	0	3
4	H	169/169 (100%)	131 (78%)	38 (22%)	1	6
5	J	143/143 (100%)	108 (76%)	35 (24%)	0	5
6	L	176/176 (100%)	133 (76%)	43 (24%)	0	5
7	M	116/116 (100%)	87 (75%)	29 (25%)	0	4
8	N	171/171 (100%)	126 (74%)	45 (26%)	0	3
9	O	172/172 (100%)	138 (80%)	34 (20%)	1	9
10	Q	163/163 (100%)	126 (77%)	37 (23%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	R	159/159 (100%)	120 (76%)	39 (24%)	0	5
12	S	156/156 (100%)	124 (80%)	32 (20%)	1	8
13	T	139/139 (100%)	105 (76%)	34 (24%)	0	5
14	U	89/89 (100%)	65 (73%)	24 (27%)	0	3
15	V	101/101 (100%)	78 (77%)	23 (23%)	1	6
16	X	107/107 (100%)	88 (82%)	19 (18%)	2	12
17	Y	124/124 (100%)	94 (76%)	30 (24%)	0	5
18	Z	117/117 (100%)	93 (80%)	24 (20%)	1	8
19	a	119/119 (100%)	99 (83%)	20 (17%)	2	14
20	b	63/63 (100%)	48 (76%)	15 (24%)	0	5
21	c	79/79 (100%)	59 (75%)	20 (25%)	0	4
22	d	98/98 (100%)	65 (66%)	33 (34%)	0	1
23	e	114/114 (100%)	91 (80%)	23 (20%)	1	8
24	f	88/88 (100%)	73 (83%)	15 (17%)	2	14
25	g	98/98 (100%)	78 (80%)	20 (20%)	1	8
26	h	109/109 (100%)	91 (84%)	18 (16%)	2	14
27	i	86/86 (100%)	68 (79%)	18 (21%)	1	7
28	k	64/64 (100%)	51 (80%)	13 (20%)	1	8
29	l	47/47 (100%)	37 (79%)	10 (21%)	1	7
30	m	48/48 (100%)	33 (69%)	15 (31%)	0	1
31	o	92/92 (100%)	70 (76%)	22 (24%)	0	5
35	B	335/335 (100%)	260 (78%)	75 (22%)	1	6
36	C	305/305 (100%)	233 (76%)	72 (24%)	1	5
37	E	209/209 (100%)	163 (78%)	46 (22%)	1	6
38	F	194/194 (100%)	141 (73%)	53 (27%)	0	3
39	I	180/180 (100%)	126 (70%)	54 (30%)	0	2
40	P	134/134 (100%)	108 (81%)	26 (19%)	1	9
41	W	55/55 (100%)	38 (69%)	17 (31%)	0	2
42	j	73/73 (100%)	60 (82%)	13 (18%)	2	12
43	n	22/22 (100%)	16 (73%)	6 (27%)	0	3
44	p	74/74 (100%)	62 (84%)	12 (16%)	2	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	r	109/109 (100%)	83 (76%)	26 (24%)	0	5
46	K	136/136 (100%)	118 (87%)	18 (13%)	4	23
47	q	170/170 (100%)	134 (79%)	36 (21%)	1	7
48	z	340/340 (100%)	321 (94%)	19 (6%)	21	53
49	2	29/29 (100%)	26 (90%)	3 (10%)	7	31
52	9	92/94 (98%)	88 (96%)	4 (4%)	29	58
53	6	157/157 (100%)	151 (96%)	6 (4%)	33	61
55	SA	174/174 (100%)	132 (76%)	42 (24%)	0	5
56	SB	194/194 (100%)	155 (80%)	39 (20%)	1	8
57	SC	184/184 (100%)	141 (77%)	43 (23%)	1	5
58	SE	224/224 (100%)	172 (77%)	52 (23%)	1	6
59	SG	207/207 (100%)	166 (80%)	41 (20%)	1	9
60	SH	169/169 (100%)	145 (86%)	24 (14%)	3	21
61	SI	178/178 (100%)	144 (81%)	34 (19%)	1	9
62	SJ	161/161 (100%)	116 (72%)	45 (28%)	0	2
63	SL	136/136 (100%)	104 (76%)	32 (24%)	1	5
64	SN	130/130 (100%)	103 (79%)	27 (21%)	1	7
65	SO	106/106 (100%)	74 (70%)	32 (30%)	0	2
66	SV	66/66 (100%)	50 (76%)	16 (24%)	0	5
67	SW	112/112 (100%)	90 (80%)	22 (20%)	1	9
68	SX	113/113 (100%)	95 (84%)	18 (16%)	2	16
69	SY	108/108 (100%)	85 (79%)	23 (21%)	1	7
70	Sa	85/85 (100%)	71 (84%)	14 (16%)	2	14
71	Sb	75/75 (100%)	58 (77%)	17 (23%)	1	6
72	Se	46/46 (100%)	35 (76%)	11 (24%)	0	5
73	SD	190/190 (100%)	149 (78%)	41 (22%)	1	7
74	SF	161/161 (100%)	123 (76%)	38 (24%)	1	5
75	SK	89/89 (100%)	68 (76%)	21 (24%)	1	5
76	SM	104/104 (100%)	74 (71%)	30 (29%)	0	2
77	SP	88/88 (100%)	70 (80%)	18 (20%)	1	8
78	SQ	117/117 (100%)	91 (78%)	26 (22%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
79	SR	117/117 (100%)	102 (87%)	15 (13%)	4	23
80	SS	119/119 (100%)	96 (81%)	23 (19%)	1	9
81	ST	112/112 (100%)	88 (79%)	24 (21%)	1	7
82	SU	94/94 (100%)	82 (87%)	12 (13%)	4	23
83	SZ	66/66 (100%)	57 (86%)	9 (14%)	3	22
84	Sc	57/57 (100%)	47 (82%)	10 (18%)	2	12
85	Sd	45/45 (100%)	36 (80%)	9 (20%)	1	8
86	Sf	64/64 (100%)	45 (70%)	19 (30%)	0	2
87	Sg	272/272 (100%)	235 (86%)	37 (14%)	3	22
88	S1	67/67 (100%)	59 (88%)	8 (12%)	5	26
89	S4	69/69 (100%)	60 (87%)	9 (13%)	4	23
All	All	10757/10762 (100%)	8495 (79%)	2262 (21%)	3	7

5 of 2262 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	SY	22	GLN
72	Se	31	ARG
69	SY	19	GLN
78	SQ	117	ARG
24	f	101	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 269 such sidechains are listed below:

Mol	Chain	Res	Type
75	SK	32	HIS
78	SQ	80	GLN
87	Sg	64	HIS
31	o	45	GLN
27	i	26	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	5	3642/3658 (99%)	1678 (46%)	666 (18%)
33	7	119/120 (99%)	38 (31%)	15 (12%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	8	155/156 (99%)	63 (40%)	30 (19%)
50	3	73/76 (96%)	27 (36%)	5 (6%)
51	4	197/206 (95%)	43 (21%)	10 (5%)
54	S2	1714/1742 (98%)	829 (48%)	303 (17%)
All	All	5900/5958 (99%)	2678 (45%)	1029 (17%)

5 of 2678 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 monosaccharides 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 [i](#)

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

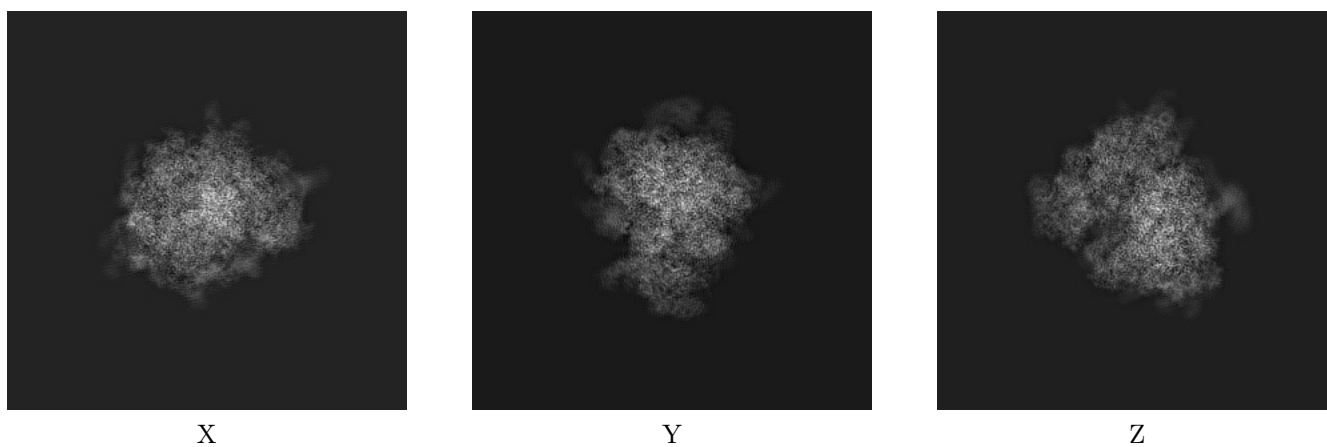
6 Map visualisation [i](#)

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](#)

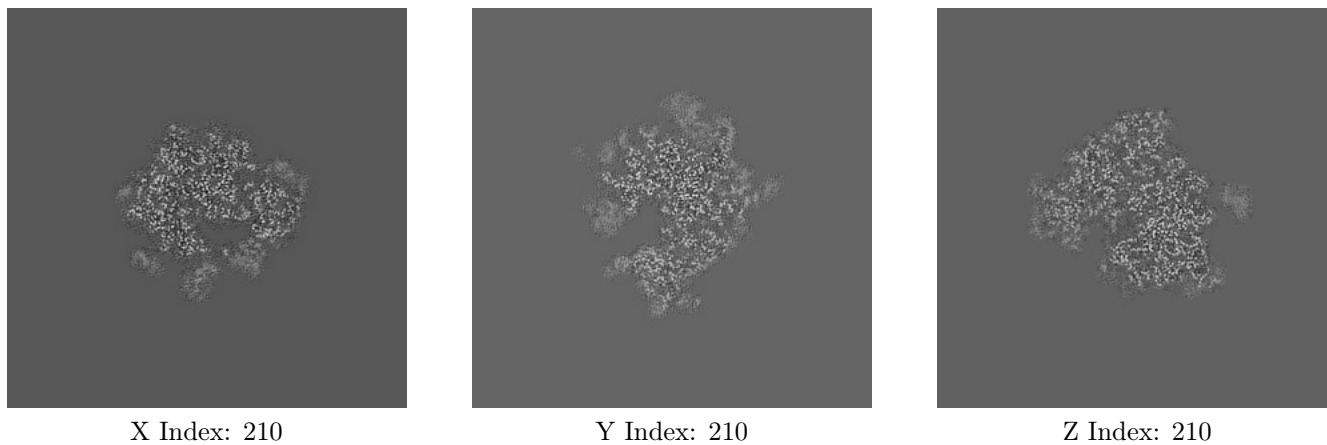
6.1.1 Primary map



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

6.2 Central slices [i](#)

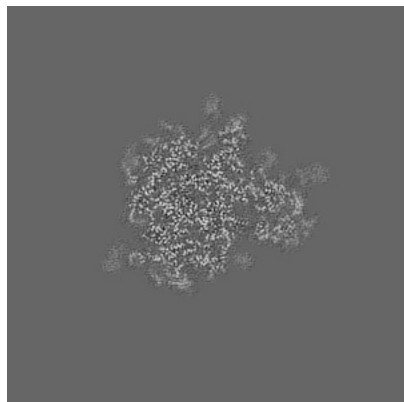
6.2.1 Primary map



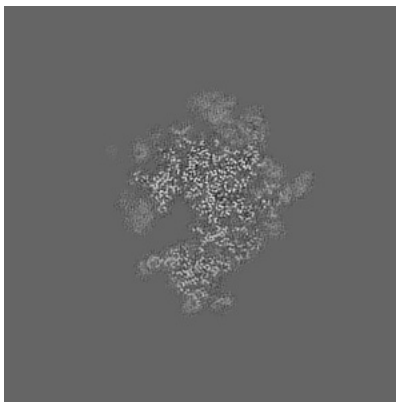
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

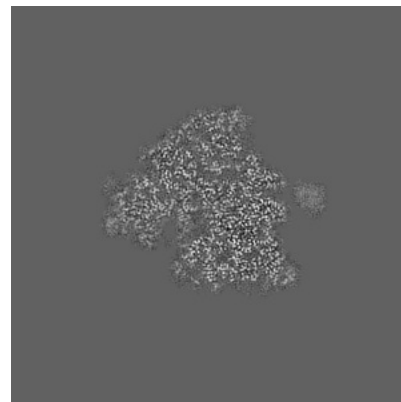
6.3.1 Primary map



X Index: 234



Y Index: 212

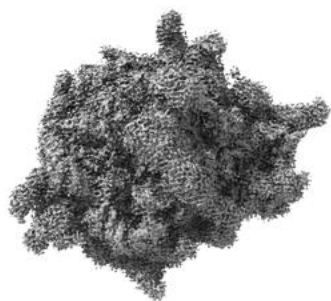


Z Index: 208

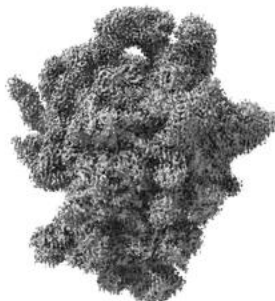
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

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.

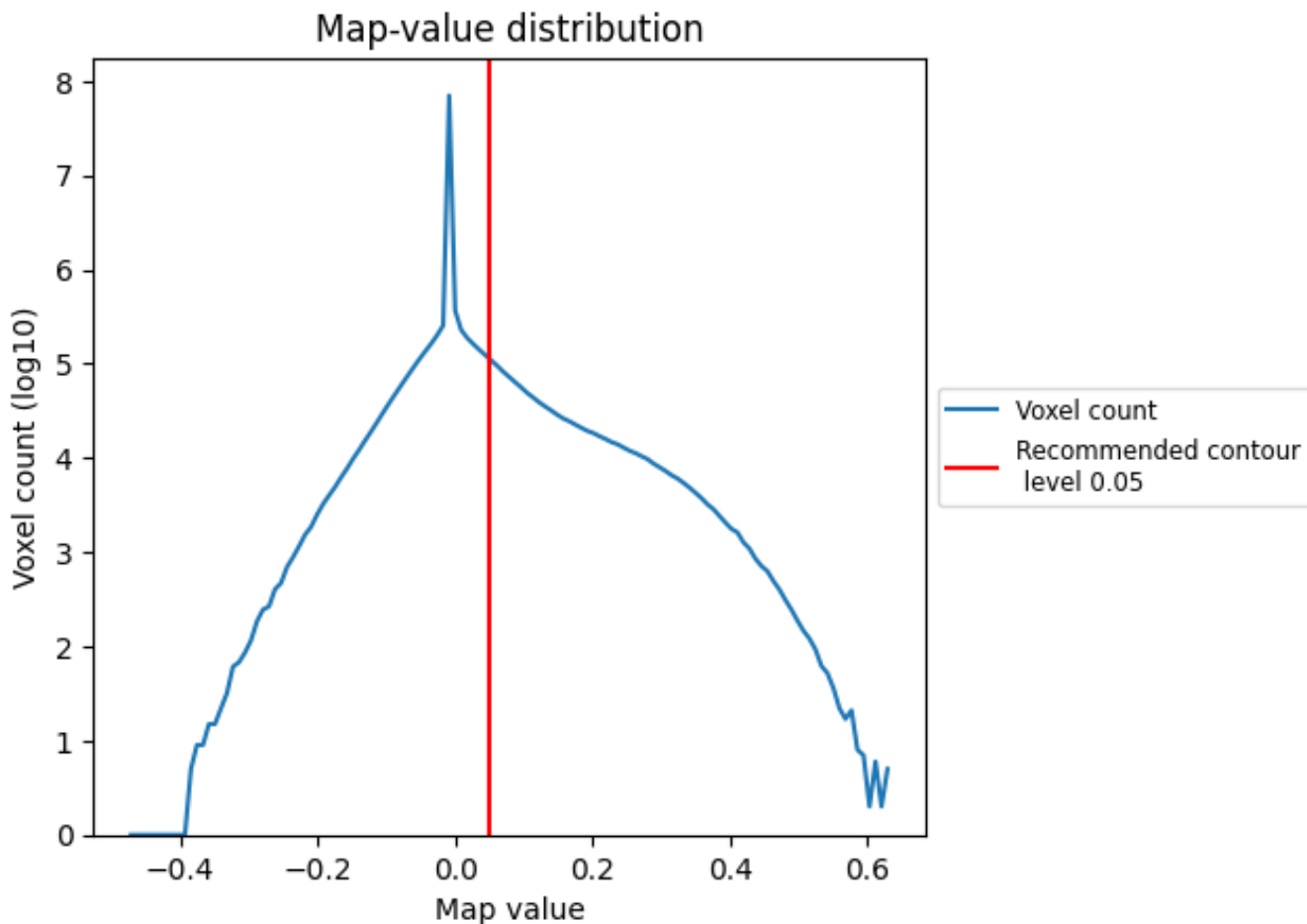
6.5 Mask visualisation

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

7 Map analysis [i](#)

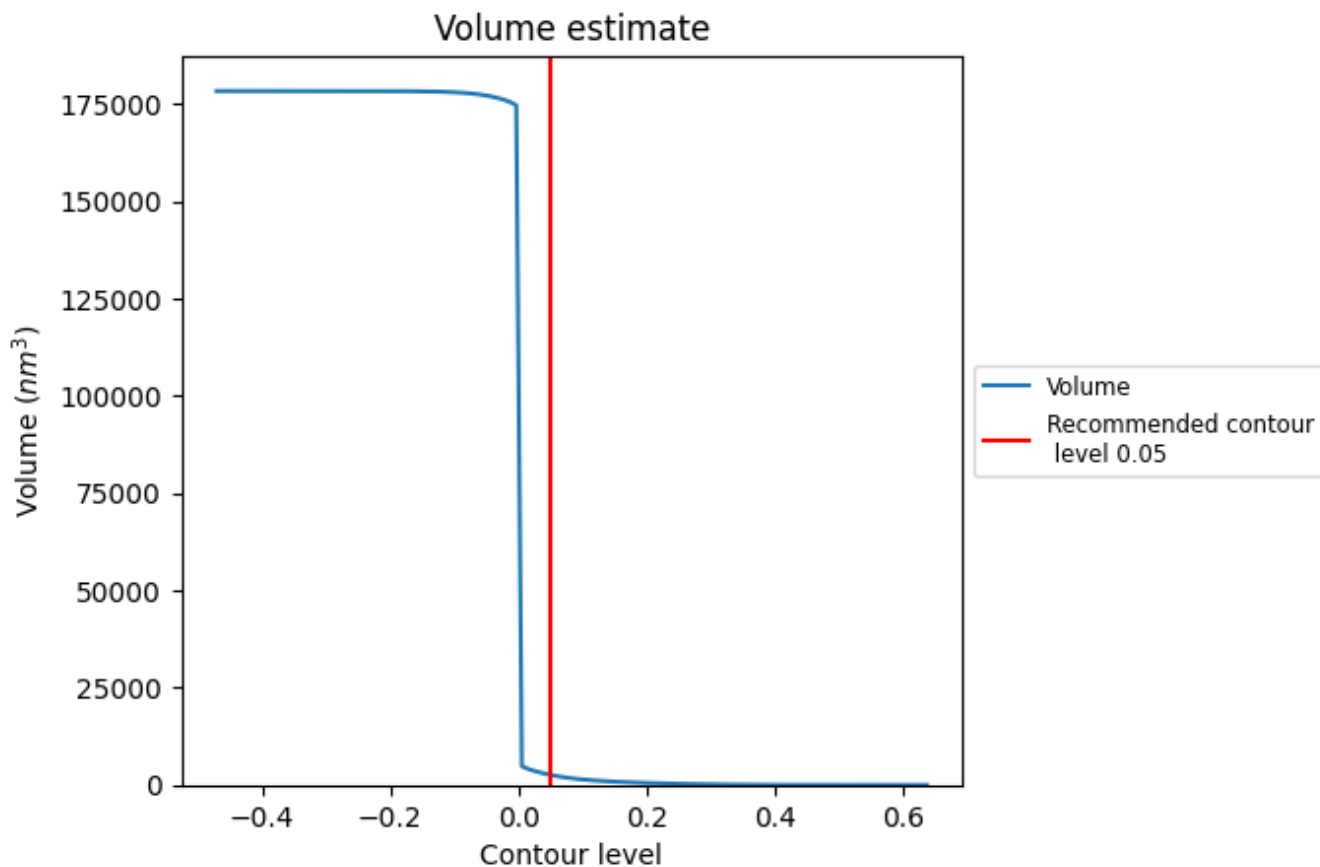
This section contains the results of statistical analysis of the map.

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.

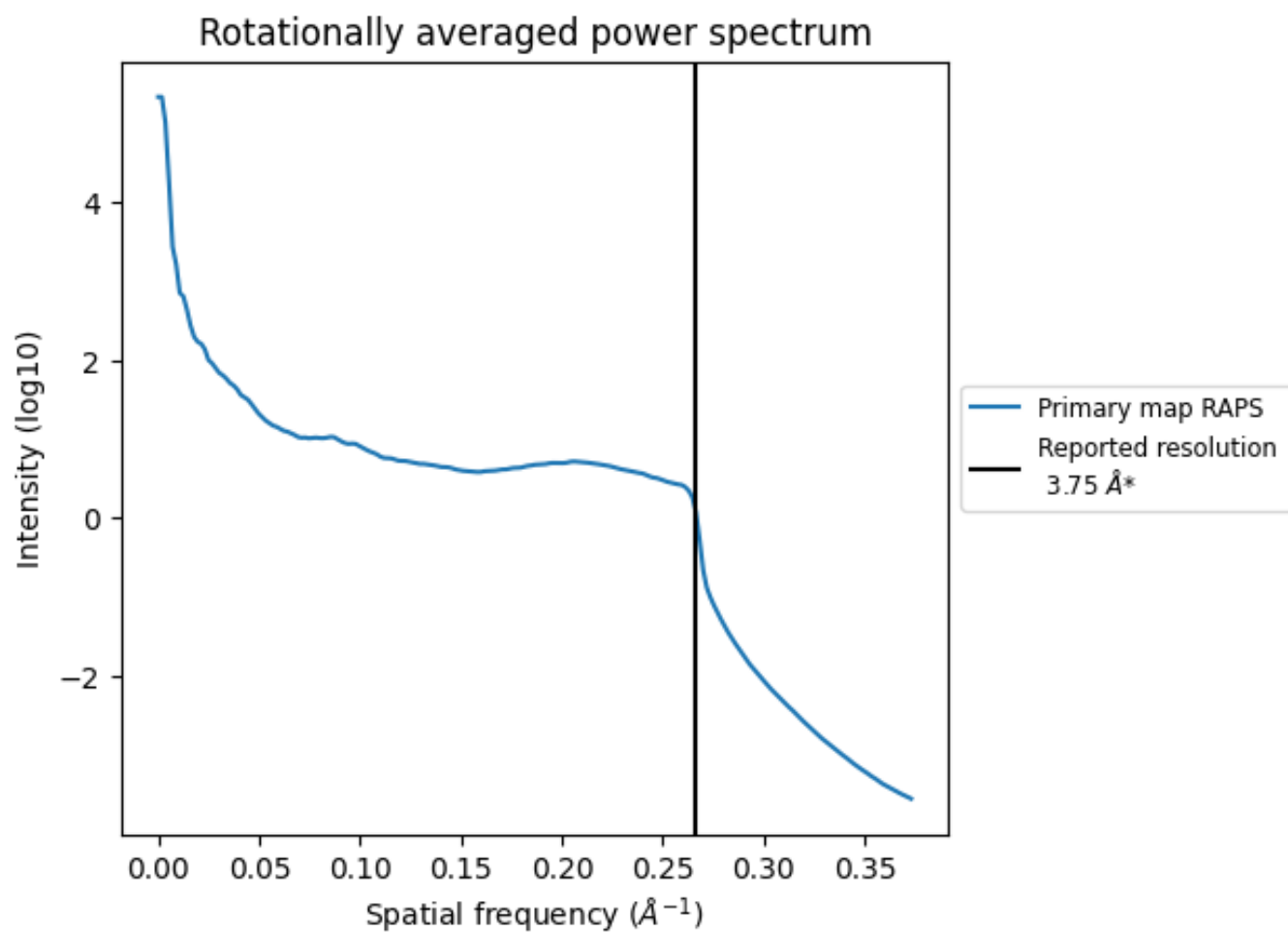
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2578 nm³; 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.267\AA^{-1}

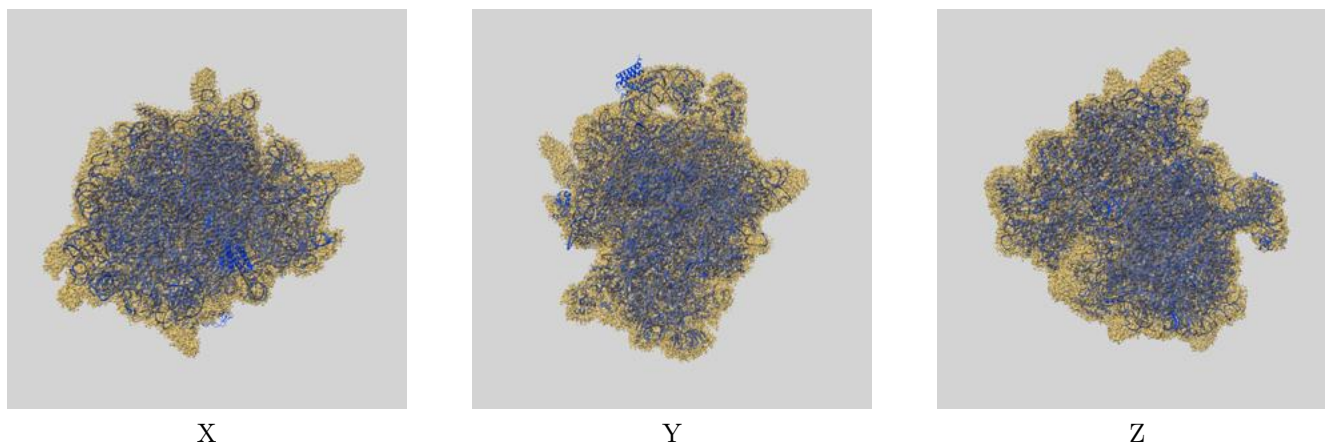
8 Fourier-Shell correlation

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](#)

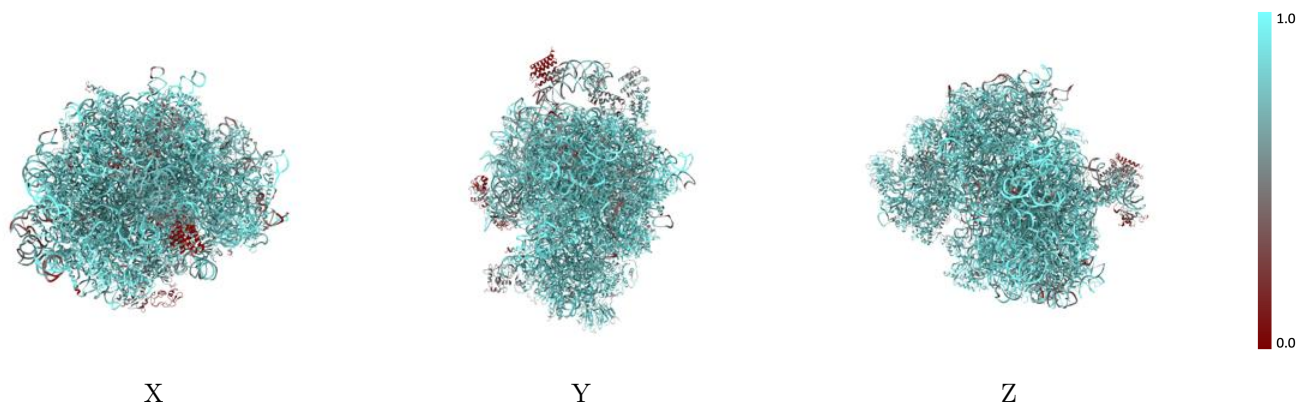


The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

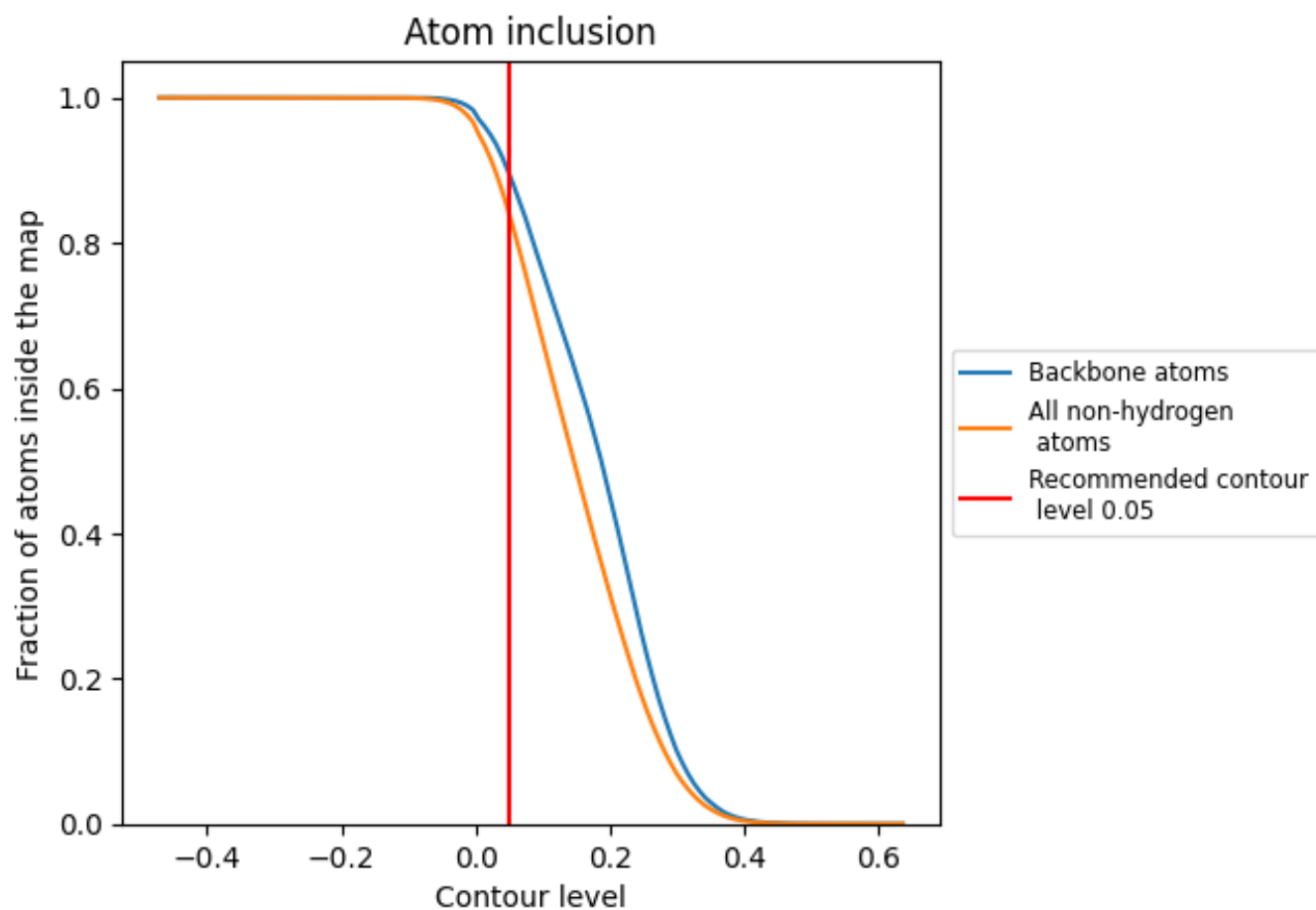
This section was not generated.

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 [i](#)











































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
All	 0.8414
2	 0.6094
3	 0.8595
4	 0.6918
5	 0.8748
6	 0.1831
7	 0.9442
8	 0.9045
9	 0.4037
A	 0.8799
B	 0.8868
C	 0.8763
D	 0.8736
E	 0.8239
F	 0.8688
G	 0.8219
H	 0.8689
I	 0.8599
J	 0.8552
K	 0.3207
L	 0.8458
M	 0.8833
N	 0.8938
O	 0.8684
P	 0.8731
Q	 0.8836
R	 0.8487
S	 0.8950
S1	 0.7227
S2	 0.8780
S4	 0.7454
SA	 0.8470
SB	 0.8512
SC	 0.8655
SD	 0.7822
















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Chain	Atom inclusion
SE	 0.8721
SF	 0.7432
SG	 0.7919
SH	 0.7761
SI	 0.8371
SJ	 0.8696
SK	 0.7366
SL	 0.8271
SM	 0.3943
SN	 0.8645
SO	 0.8460
SP	 0.6994
SQ	 0.8309
SR	 0.7498
SS	 0.8239
ST	 0.8198
SU	 0.8055
SV	 0.8396
SW	 0.8921
SX	 0.8769
SY	 0.8288
SZ	 0.7530
Sa	 0.8805
Sb	 0.8357
Sc	 0.7572
Sd	 0.8389
Se	 0.7735
Sf	 0.4470
Sg	 0.7587
T	 0.8733
U	 0.8456
V	 0.8758
W	 0.8546
X	 0.8504
Y	 0.8581
Z	 0.8966
a	 0.9043
b	 0.8013
c	 0.8895
d	 0.8600
e	 0.8722
f	 0.9181

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Chain	Atom inclusion
g	 0.8575
h	 0.8483
i	 0.8659
j	 0.9036
k	 0.7917
l	 0.8723
m	 0.8990
n	 0.8159
o	 0.8765
p	 0.8459
q	 0.3192
r	 0.9035
z	 0.6097