wwPDB EM Validation Summary Report (i)

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 (i) 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 (i)) were used in the production of this report:

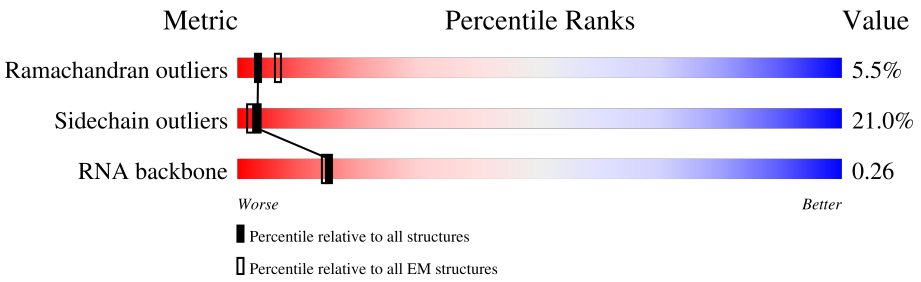
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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 <=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%
39	I	213	68% 28%
40	P	153	78% 18%
41	W	63	71% 24% 5%
42	j	86	76% 17% 7%
43	n	23	74% 26%
44	p	91	86% 11%
45	r	125	74% 24%
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%
51	4	206	10% 76% 21%
52	9	105	50% 96%
53	6	179	79% 97%
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	8% 84% 12%
85	Sd	52	77% 17%
86	Sf	71	48% 56% 30% 10%
87	Sg	313	83% 15%
88	S1	74	7% 77% 22%
89	S4	76	87% 13%

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
			Total	C	N	O	S		
21	c	94	732	465	130	131	6	0	0

- Molecule 22 is a protein called Ribosomal protein eL31.

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

- Molecule 23 is a protein called Ribosomal protein eL32.

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

- Molecule 24 is a protein called Ribosomal protein eL33.

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

- Molecule 25 is a protein called Ribosomal protein eL34.

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

- Molecule 26 is a protein called Ribosomal protein uL29.

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

- Molecule 27 is a protein called Ribosomal protein eL36.

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

- Molecule 28 is a protein called Ribosomal protein eL38.

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

- Molecule 29 is a protein called Ribosomal protein eL39.

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

- Molecule 30 is a protein called Ribosomal protein eL40.

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

- Molecule 31 is a protein called Ribosomal protein eL42.

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
42	j	86	706	436	155	110	5	0	0

- Molecule 43 is a protein called Ribosomal protein eL41.

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

- Molecule 44 is a protein called Ribosomal protein eL43.

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

- Molecule 45 is a protein called Ribosomal protein eL28.

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

- Molecule 46 is a protein called Ribosomal protein uL11.

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

- Molecule 47 is a protein called Ribosomal protein uL10.

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

- Molecule 48 is a protein called SRP54.

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

- Molecule 49 is a protein called Nascent chain.

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

- Molecule 50 is a RNA chain called Val tRNA.

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

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

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

- Molecule 52 is a protein called SRP19.

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

- Molecule 53 is a protein called SRP68.

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

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

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

- Molecule 55 is a protein called Ribosomal protein uS2.

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

- 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
			Total	C	N	O	S		
70	Sa	98	781	486	161	129	5	0	0

- Molecule 71 is a protein called Ribosomal protein eS27.

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

- Molecule 72 is a protein called Ribosomal protein eS30.

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

- Molecule 73 is a protein called Ribosomal protein uS3.

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

- Molecule 74 is a protein called Ribosomal protein uS7.

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

- Molecule 75 is a protein called Ribosomal protein eS10.

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

- Molecule 76 is a protein called Ribosomal protein eS12.

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

- 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
			Total	C	N	O	S		
84	Sc	64	506	308	102	94	2	0	0

- Molecule 85 is a protein called Ribosomal protein uS14.

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

- Molecule 86 is a protein called Ribosomal protein eS31.

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

- Molecule 87 is a protein called Ribosomal protein RACK1.

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

- Molecule 88 is a protein called SRP9.

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

- Molecule 89 is a protein called SRP14.

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

- Molecule 90 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

Continued on next page...

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

- Molecule 91 is ZINC ION (three-letter code: ZN) (formula: Zn).

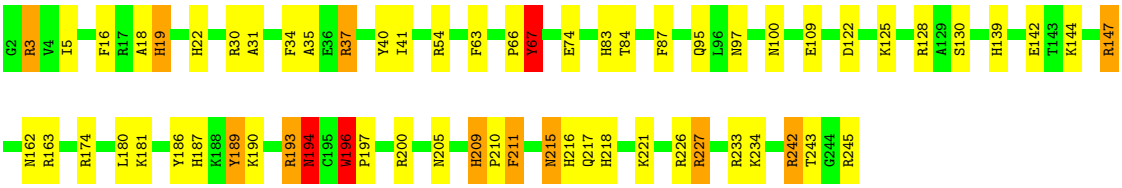
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
91	m	1	1	1	0
			Total	Zn	
91	o	1	1	1	0
			Total	Zn	
91	j	1	1	1	0
			Total	Zn	
91	Sa	1	1	1	0

3 Residue-property plots (i)

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

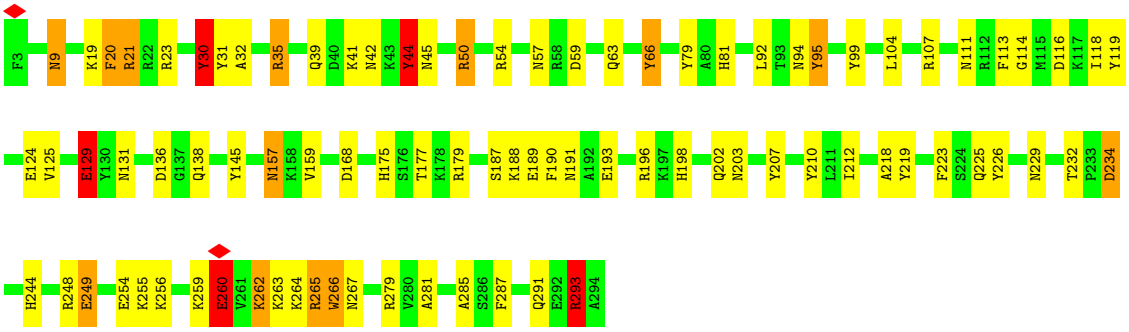
• Molecule 1: Ribosomal protein uL2

Chain A:



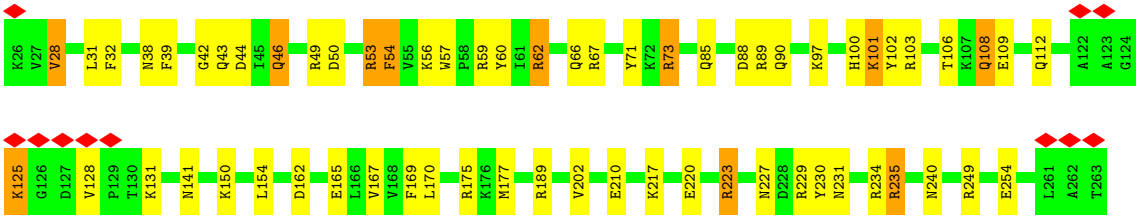
• Molecule 2: Ribosomal protein uL18

Chain D:



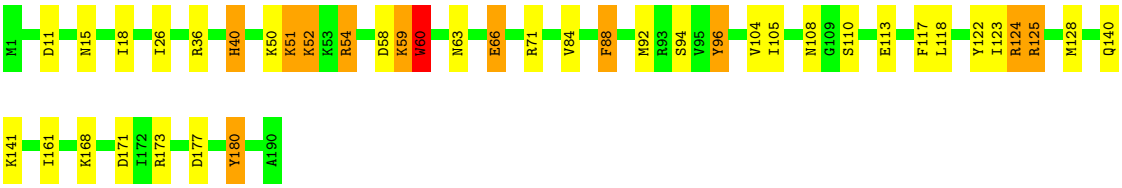
• Molecule 3: Ribosomal protein eL8

Chain G:



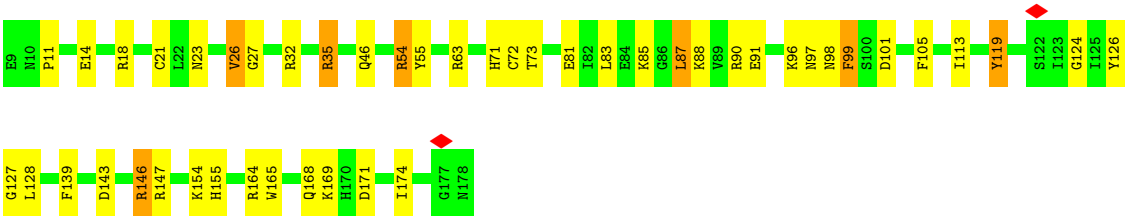
• Molecule 4: Ribosomal protein uL6

Chain H:



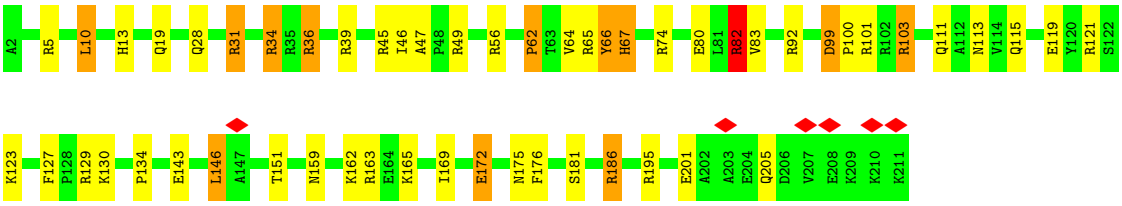
- Molecule 5: Ribosomal protein uL5

Chain J:



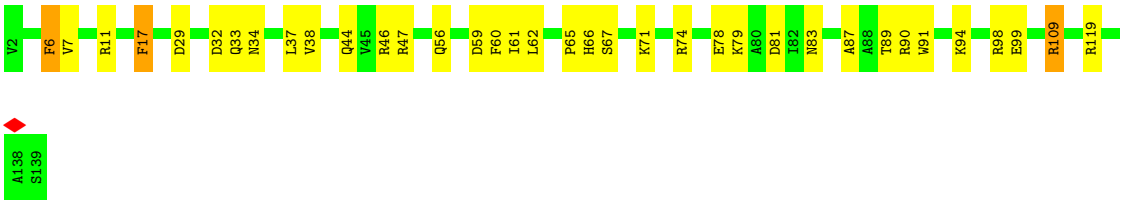
- Molecule 6: Ribosomal protein eL13

Chain L:



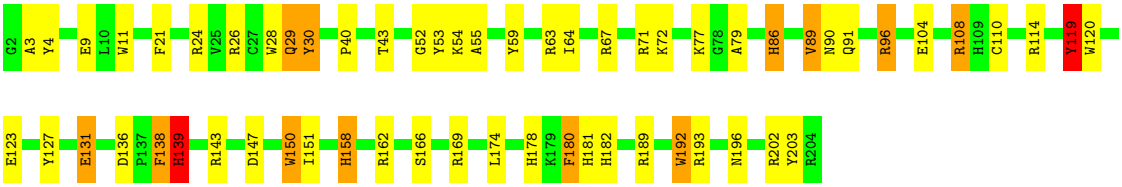
- Molecule 7: Ribosomal protein eL14

Chain M:



- Molecule 8: Ribosomal protein eL15

Chain N:



• Molecule 9: Ribosomal protein uL13

Chain O: 80% 15%

E3 G4 Q5 L16 R31 R37 C38 I41 N42 N46 R49 N50 F57 K60 R61 M62 N63 T64 H72 F73 R74 R78 R82 R85 D106 P110 P111 Y112 D113 R117 K125 F135 R140 W147 R160 K161 E162 H167

Q173 R178 K187 K188 F192 T198 H199 L202 V203

• Molecule 10: Ribosomal protein eL18

Chain Q: 74% 17% 7%

G2 V3 D4 I5 K9 R14 R15 K16 R26 Y32 R33 F34 R37 R38 T39 N40 N44 L51 F52 R55 R58 L63 S64 R65 R68 L72 R75 T79 T85 D89 V90 R91 V92 Q93 K97 R108 A109 R110 S111 R112 K119

D129 R146 A155 P159 H160 S161 Y166 V167 R168 K173 F174 E175 R176 A177 R178 G179 R180 R181 N188

• Molecule 11: Ribosomal protein eL19

Chain R: 70% 25% 5%

S2 L6 R9 C17 G18 K19 W23 N30 E31 N36 Q39 Q40 I41 R42 I50 I51 R52 H58 N66 R71 R74 R81 R88 M89 T94 W95 M96 M99 R103 R104 L105 L106 R107 R108 K113 D116 R117 H118 H119 Y120

Y124 N130 V131 F132 K133 R136 I137 L138 H141 K149 L155 E168 A169 R170 K171 R172 R173 E174 E175 R176 L177 Q178 A179 K180 K181

• Molecule 12: Ribosomal protein eL20

Chain S: 71% 20% 7%

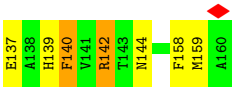
K2 G5 Y10 L17 Y28 R29 I32 F33 R43 F44 F47 V48 K53 C64 F68 E69 K70 N77 I80 W81 L82 R83 Y84 Y94 R95 E96 Y97 R98 D99 L100 T101 R111 R116 K128 R138 F145 H146 K149 I150 K151 F152

P153 L154 P155 H156 R157 Y158 L159 Q162 H163 K164 P165 R166 F167 T168 R171 F176

• Molecule 13: Ribosomal protein eL21

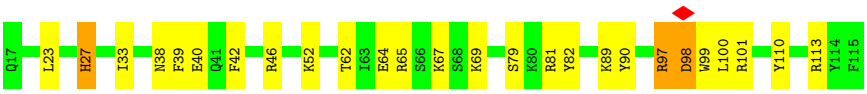
Chain T: 74% 24%

T2 K5 R9 Y13 R17 P18 F19 Y30 M31 R32 I33 Y34 K35 K36 D41 G44 P53 H54 K55 C56 Y57 K60 T61 V67 H70 V76 R88 R102 D103 S104 F105 L106 K107 E111 N112 D113 K117 E118 E121 Q127 R136



• Molecule 14: Ribosomal protein eL22

Chain U:

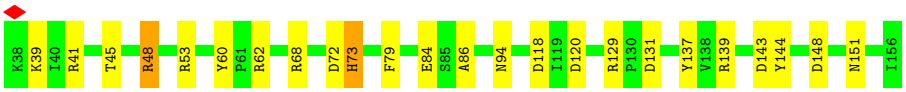


• Molecule 15: Ribosomal protein uL14

Chain V:

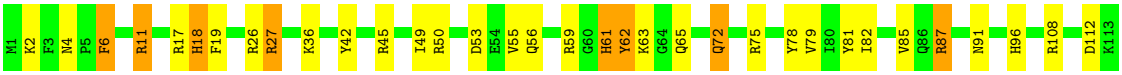
• Molecule 16: Ribosomal protein uL23

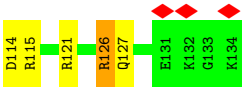
Chain X:



• Molecule 17: Ribosomal protein uL24

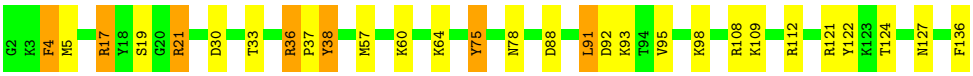
Chain Y:





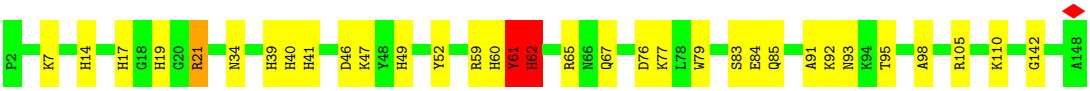
• Molecule 18: Ribosomal protein eL27

Chain Z:



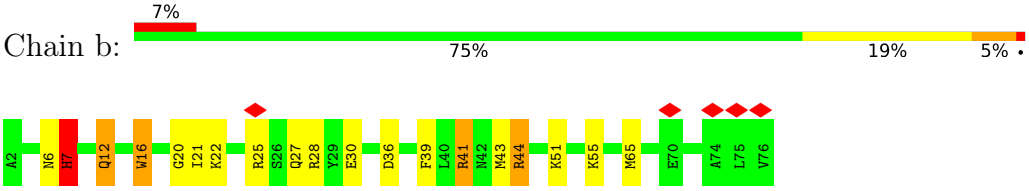
• Molecule 19: Ribosomal protein uL15

Chain a:



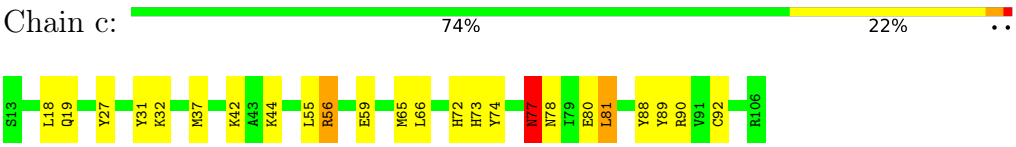
- Molecule 20: Ribosomal protein eL29

Chain b:



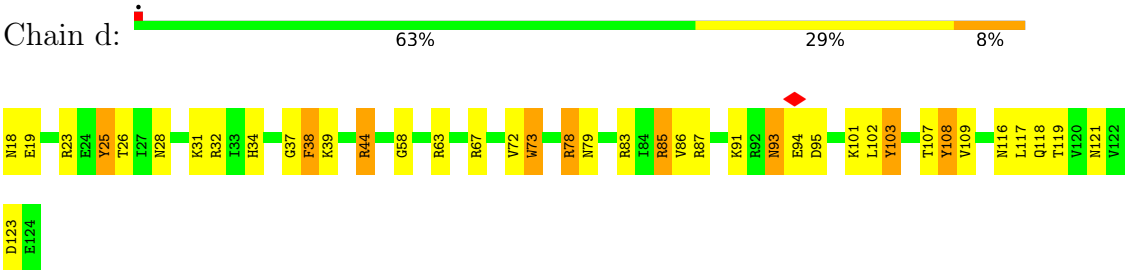
- Molecule 21: Ribosomal protein eL30

Chain c:



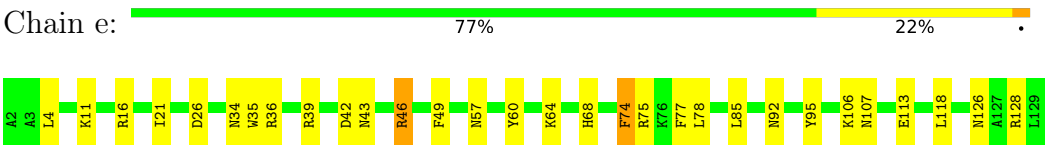
- Molecule 22: Ribosomal protein eL31

Chain d:



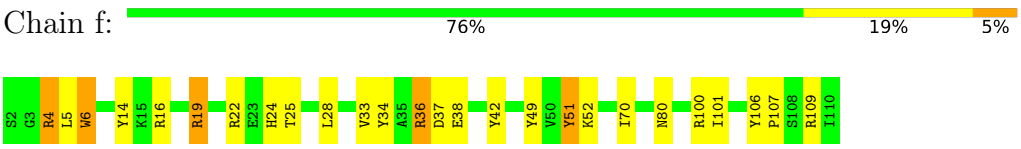
- Molecule 23: Ribosomal protein eL32

Chain e:



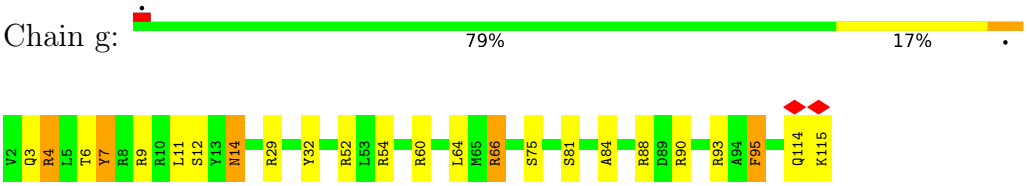
- Molecule 24: Ribosomal protein eL33

Chain f:



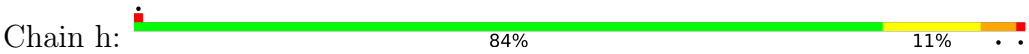
- Molecule 25: Ribosomal protein eL34

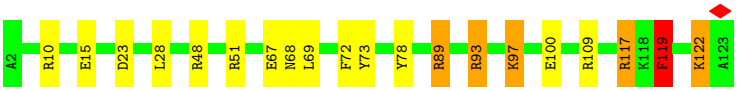
Chain g:



- Molecule 26: Ribosomal protein uL29

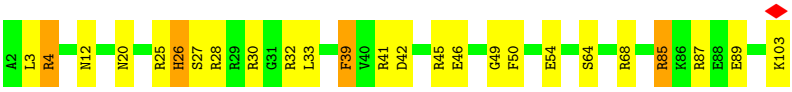
Chain h:





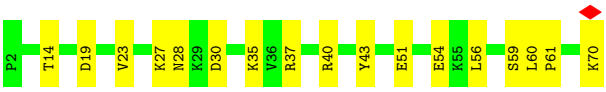
• Molecule 27: Ribosomal protein eL36

Chain i:



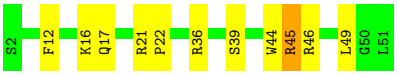
• Molecule 28: Ribosomal protein eL38

Chain k:



• Molecule 29: Ribosomal protein eL39

Chain l:

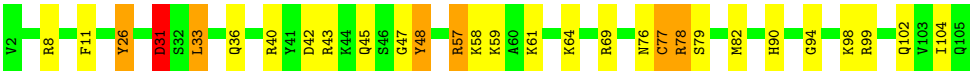


• Molecule 30: Ribosomal protein eL40

Chain m:

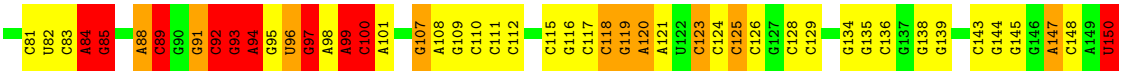
• Molecule 31: Ribosomal protein eL42

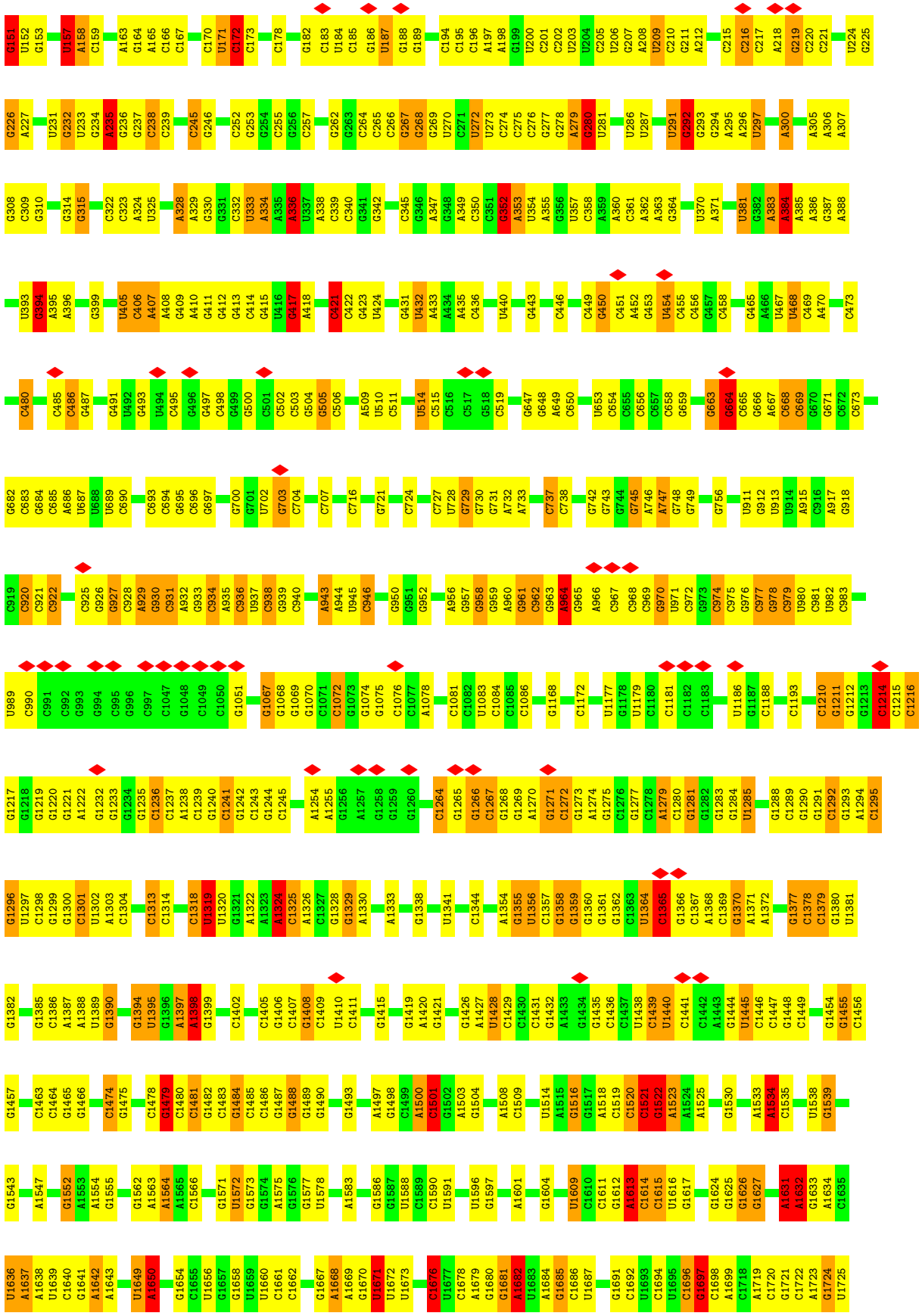
Chain o:



• Molecule 32: 28S ribosomal RNA

Chain 5:




G151 U152 G153 U157 A158 C159 A163 G164 A165 C166 C167 C170 U171 C172 C173 C178 G182 C183 U184 C185 G186 U187 G188 G189 C194 C195 C196 A197 A198 G199 U200 C201 C202 U203 U204 C205 U206 G207 A208 U209 C210 G211 A212 C215 C216 C217 A218 G219 C220 C221 U224 G225
G226 A227 U231 G232 U233 G234 A235 G236 G237 C238 C239 C245 G246 C252 G253 G254 C255 G256 C257 G262 G263 C264 C265 C266 G267 G268 G269 U270 C271 U272 U273 C274 C275 C276 G277 G278 A279 G280 U281 U286 U287 U291 G292 G293 G294 A295 A296 U297 A300 A305 A306 A307
G308 C309 G310 G314 G315 C322 C323 A324 U325 A328 A329 G330 G331 C332 U333 A334 A335 A336 U337 A338 C339 C340 G341 G342 C345 G346 A347 G348 A349 C350 C351 G352 A353 U354 A355 G356 U357 C358 A359 A360 C361 A362 A363 G364 U370 A371 U381 G382 A383 A384 A385 A386 G387 A388
U393 G394 A395 A396 G399 U405 C406 A407 A408 G409 A410 G411 G412 C413 C414 G415 U416 G417 A418 C421 C422 G423 U424 G431 U432 A433 A434 A435 C436 U440 G443 C446 C449 G450 C451 A452 G453 U454 C455 C456 G457 C458 G465 A466 U467 U468 C469 A470 C473
G480 C485 C486 G487 G491 U492 G493 U494 C495 G496 G497 C498 G499 G500 C501 C502 C503 G504 G505 C506 A509 U510 C511 U514 C515 C516 C517 G518 C519 G647 G648 A649 C650 U653 C654 C655 C656 C657 C658 G659 G663 G664 C665 G666 A667 C668 C669 G670 G671 C672 C673
G682 C683 G684 C685 A686 U687 U688 U689 C690 C693 C694 G695 C696 G697 G700 G701 U702 G703 C704 C707 C716 G721 C724 C727 U728 G729 G730 G731 A732 A733 C737 C738 G742 G743 G744 G745 A746 A747 G748 G749 G756 U911 G912 U913 U914 A915 C916 A917 G918
C919 C920 C921 C922 C925 G926 G927 C928 A929 G930 C931 A932 G933 C934 A935 C936 U937 C938 G939 C940 A943 A944 U945 C946 G950 G951 G952 A956 G957 G958 G959 A960 G961 C962 G963 A964 G965 A966 C967 C968 G969 G970 U971 G972 G973 C974 C975 G976 C977 G978 C979 U980 C981 U982 C983
U989 C990 C991 C992 G993 G994 C995 G996 C997 C1047 G1048 C1049 C1050 G1051 G1067 G1068 G1069 G1070 C1071 C1072 G1073 G1074 G1075 C1076 C1077 A1078 C1081 C1082 U1083 C1084 C1085 C1086 G1168 C1172 U1177 G1178 U1179 C1180 C1181 C1182 C1183 U1186 G1187 C1188 C1193 C1210 G1211 G1212 G1213 C1214 C1215 C1216
G1217 G1218 G1219 G1220 G1221 A1222 G1232 G1233 G1234 G1235 C1236 C1237 A1238 C1239 G1240 C1241 G1242 C1243 G1244 C1245 A1254 A1255 G1256 A1257 G1258 G1259 G1260 C1264 G1265 G1266 C1267 G1268 G1269 A1270 G1271 C1272 G1273 A1274 G1275 C1276 G1277 C1278 A1279 C1280 G1281 G1282 G1283 G1284 U1285 G1288 C1289 G1290 G1291 C1292 G1293 A1294 C1295
G1296 U1297 C1298 G1299 G1300 C1301 U1302 A1303 C1304 C1313 C1314 C1318 U1319 U1320 G1321 A1322 A1323 A1324 C1325 A1326 C1327 G1328 G1329 A1330 A1333 G1338 U1341 C1344 A1354 G1355 U1356 C1357 G1358 G1359 G1360 G1361 G1362 C1363 U1364 C1365 G1366 C1367 A1368 C1369 G1370 A1371 A1372 G1377 C1378 C1379 G1380 U1381
G1382 G1385 C1386 A1387 A1388 U1389 G1390 G1394 U1395 G1396 A1397 A1398 G1399 C1402 C1405 G1406 C1407 G1408 C1409 U1410 C1411 G1415 G1419 A1420 G1421 G1426 A1427 U1428 G1429 C1430 C1431 G1432 A1433 G1434 G1435 C1436 C1437 U1438 C1439 U1440 C1441 C1442 A1443 G1444 U1445 C1446 C1447 G1448 C1449 G1454 G1455 C1456
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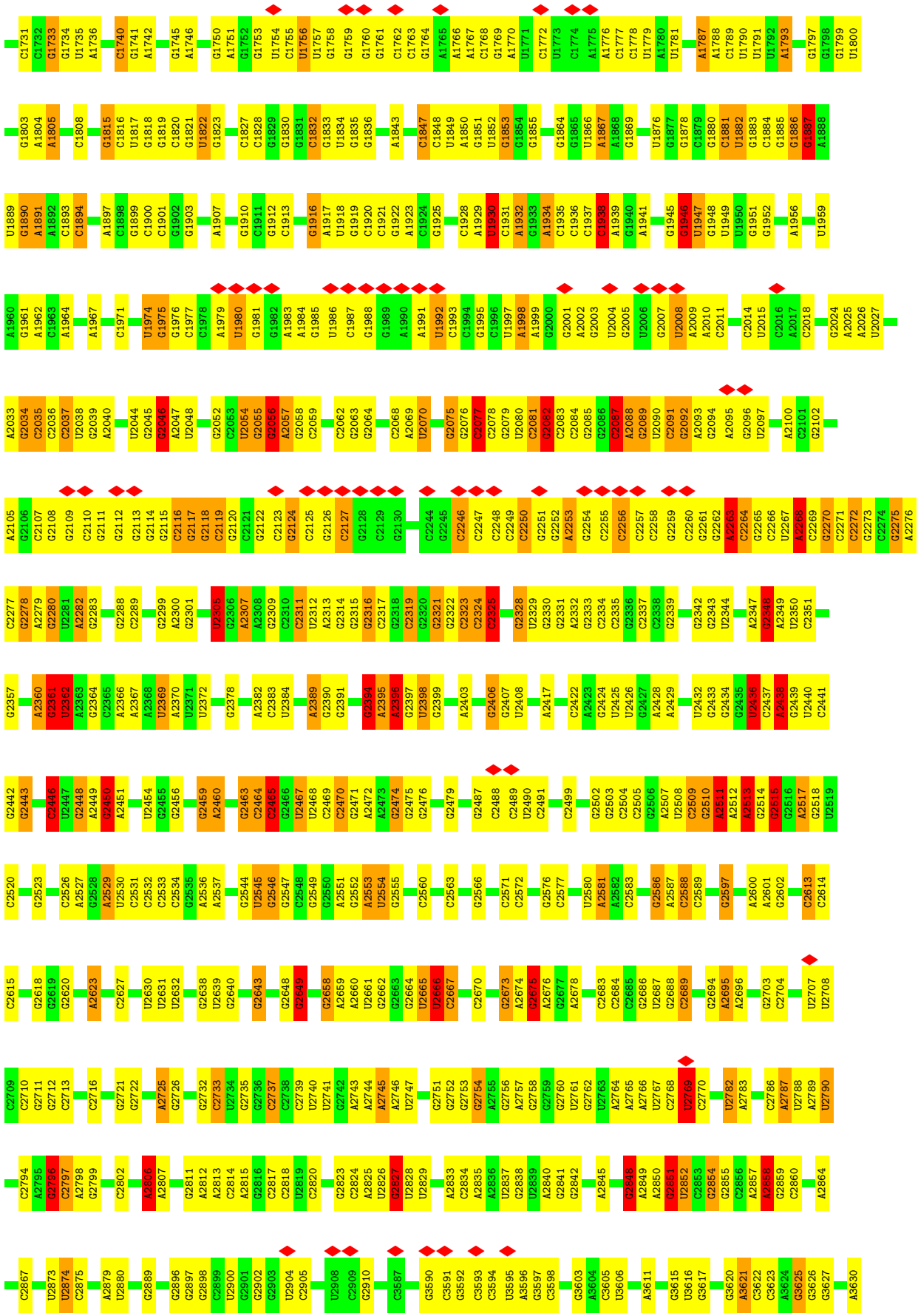
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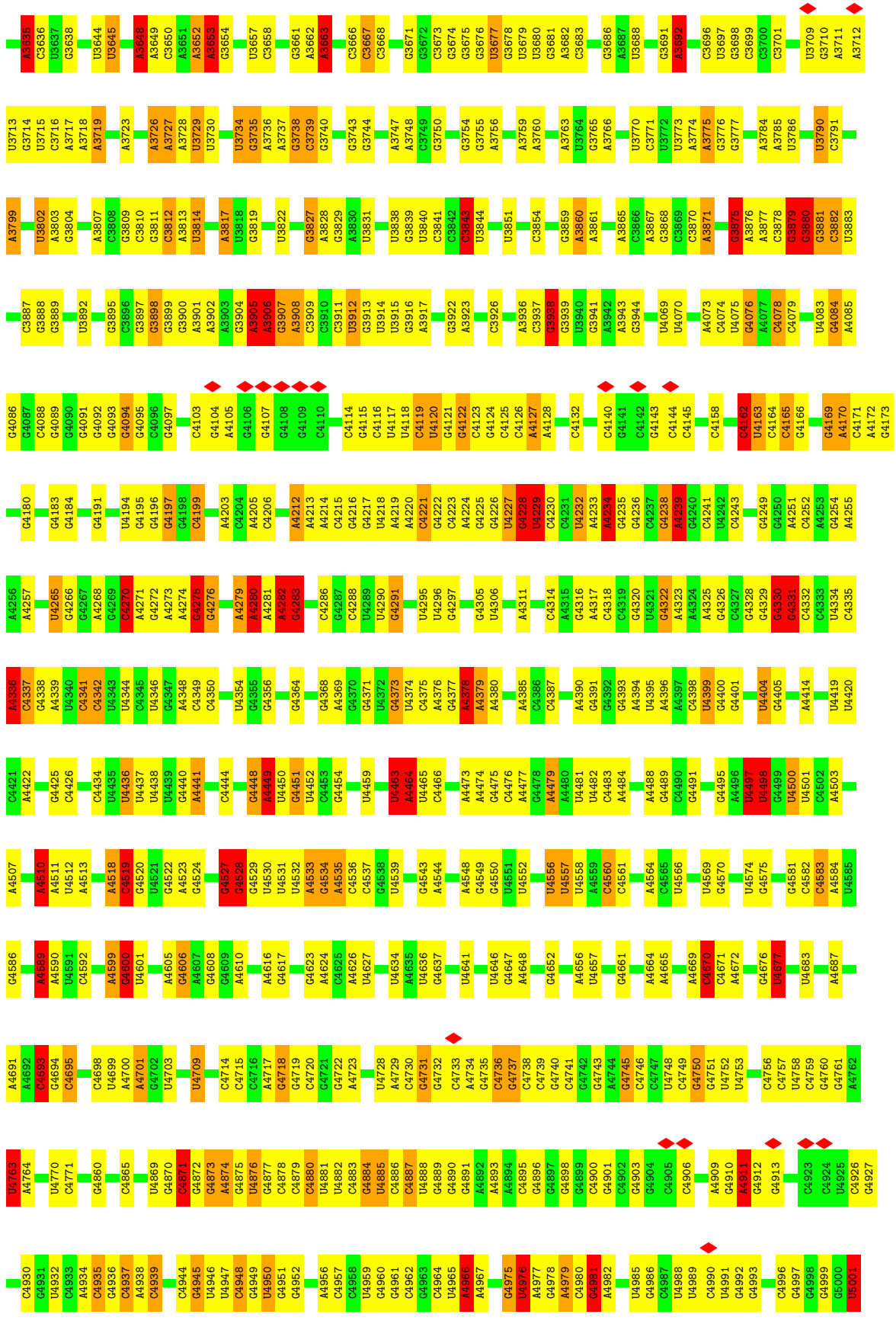
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- Molecule 33: 5S ribosomal RNA

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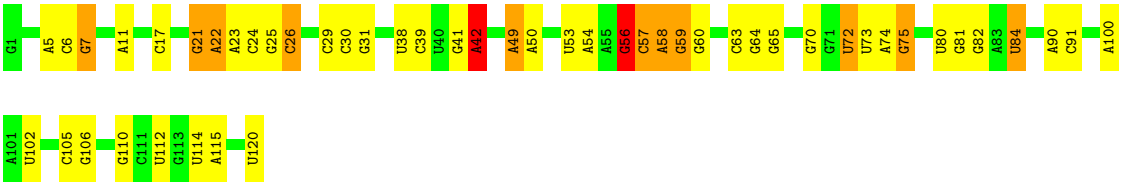

- Molecule 34: 5.8S ribosomal RNA

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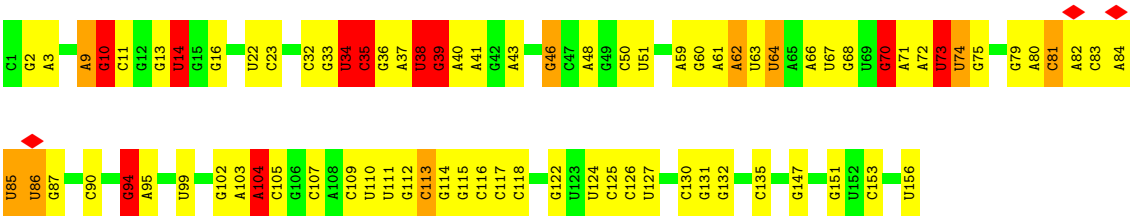

- Molecule 35: Ribosomal protein uL3

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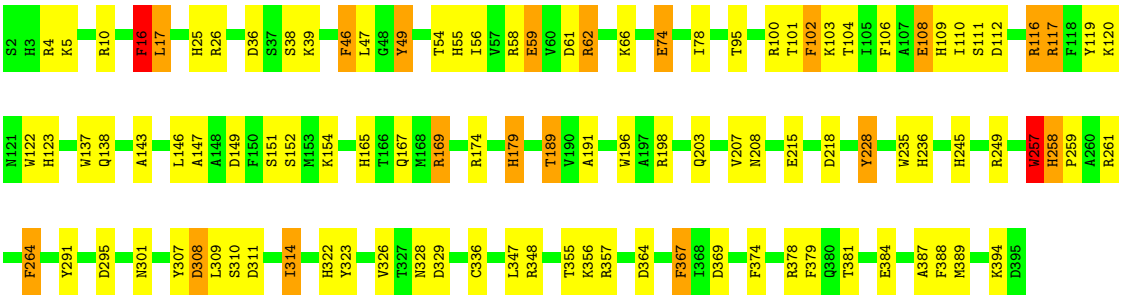

- Molecule 36: Ribosomal protein uL4

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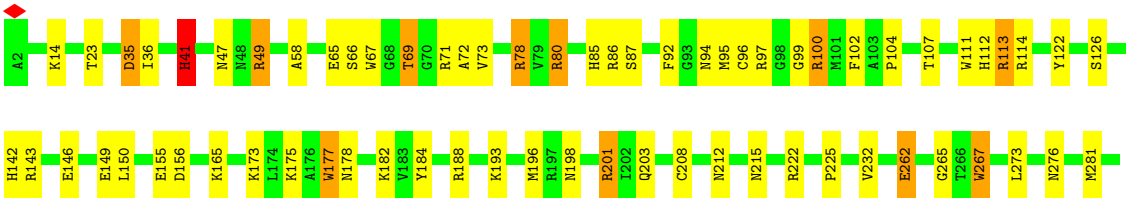

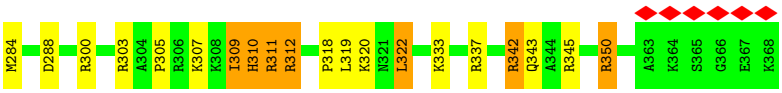

• Molecule 37: Ribosomal protein eL6

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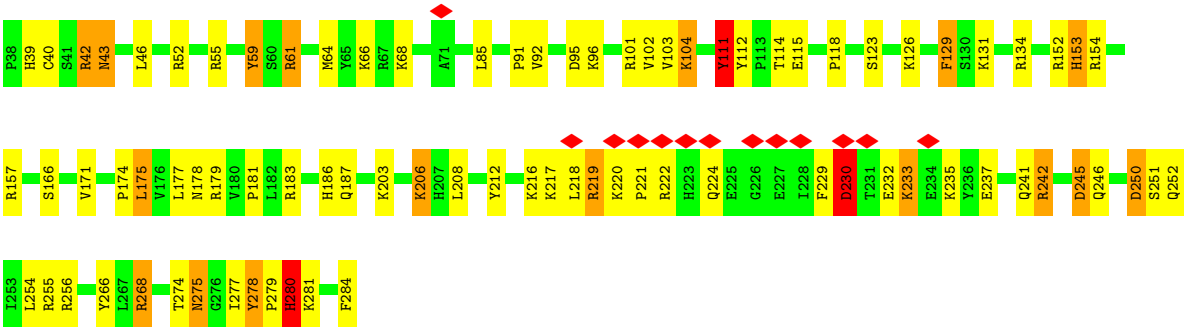

• Molecule 38: Ribosomal protein uL30

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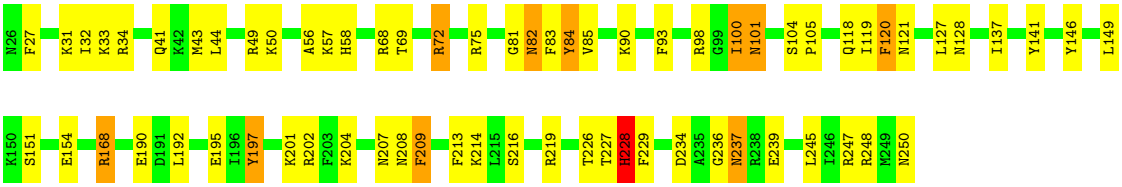

• Molecule 39: Ribosomal protein uL16

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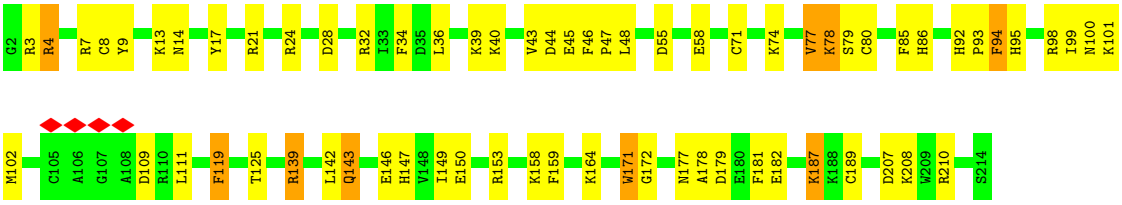
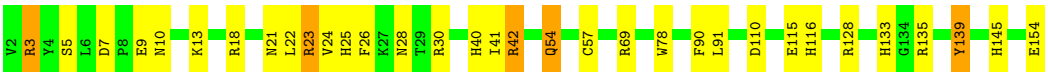


• Molecule 40: Ribosomal protein uL22

Chain P:



• Molecule 41: Ribosomal protein eL24

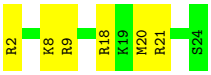
Chain W:

• Molecule 42: Ribosomal protein eL37

Chain j:

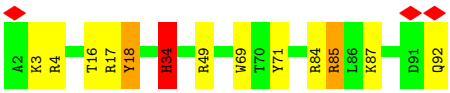
• Molecule 43: Ribosomal protein eL41

Chain n:



• Molecule 44: Ribosomal protein eL43

Chain p:

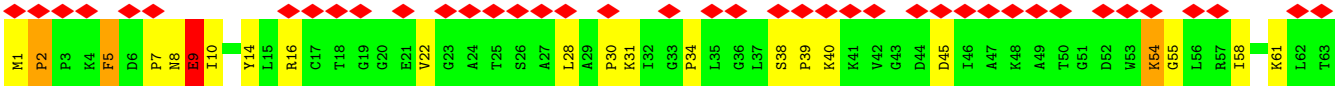


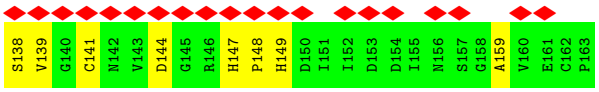
• Molecule 45: Ribosomal protein eL28

Chain r:

• Molecule 46: Ribosomal protein uL11

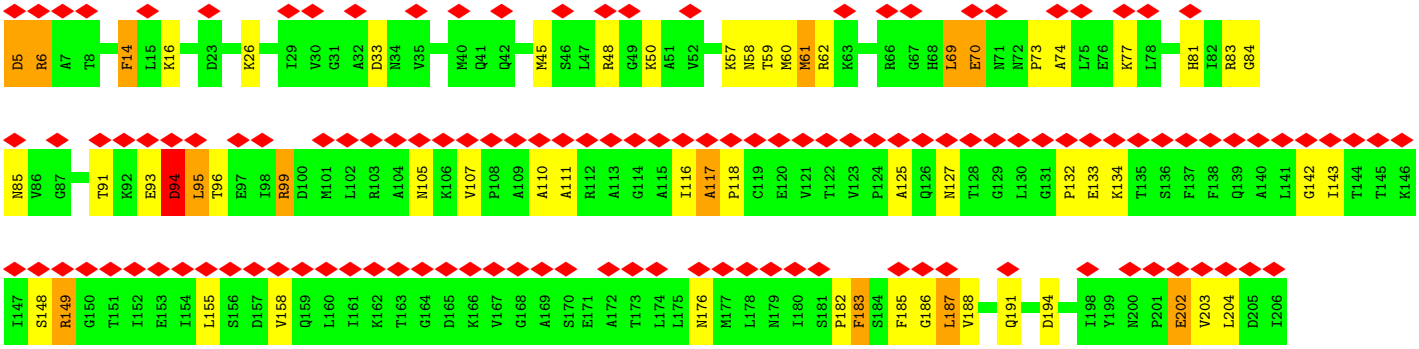
Chain K:





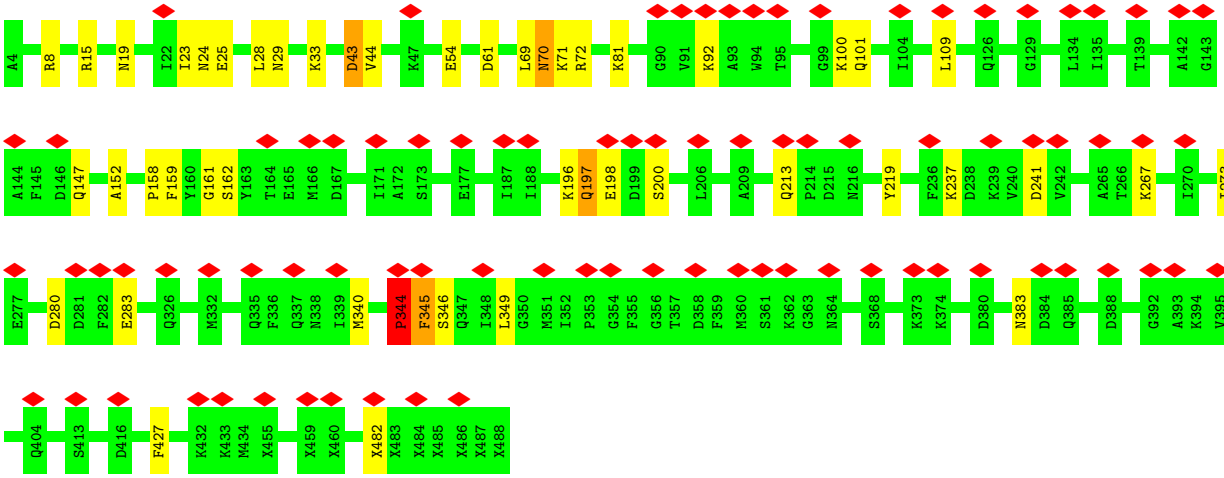
• Molecule 47: Ribosomal protein uL10

Chain q:



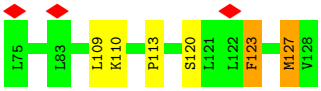
- Molecule 48: SRP54

Chain z:



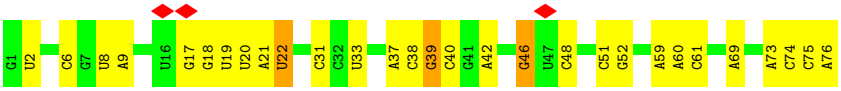
- Molecule 49: Nascent chain

Chain 2:



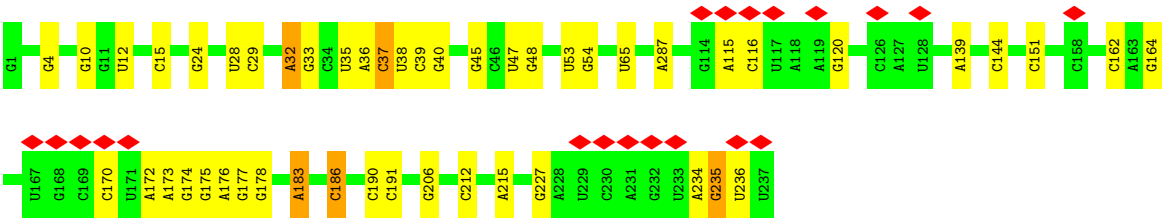
- Molecule 50: Val tRNA

Chain 3:



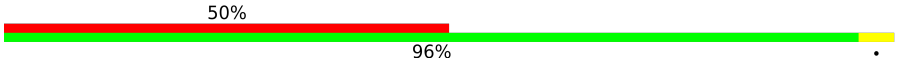
- Molecule 51: SRP 7S RNA

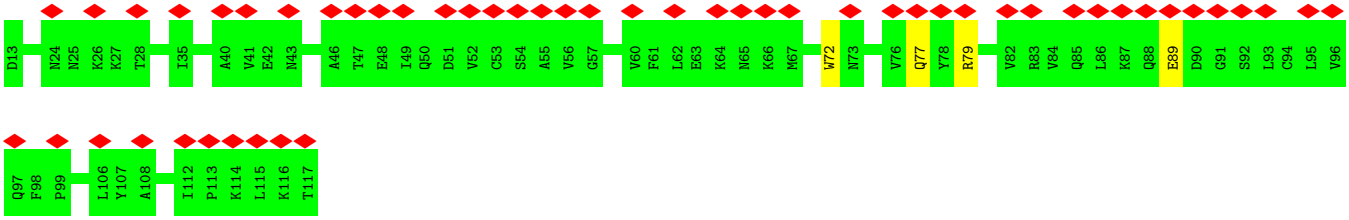
Chain 4:



- Molecule 52: SRP19

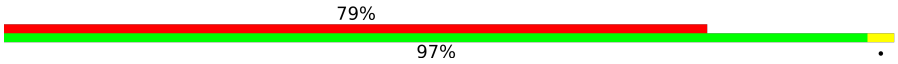
Chain 9:

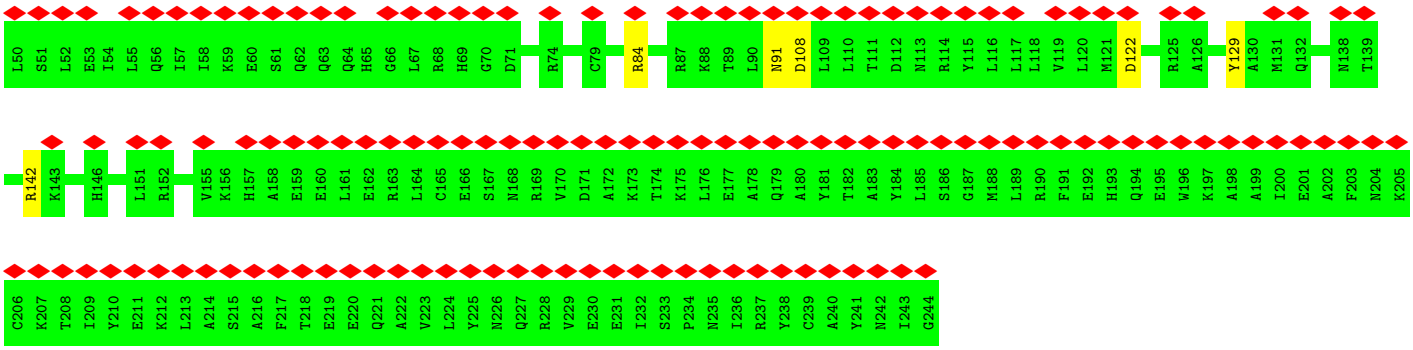




- Molecule 53: SRP68

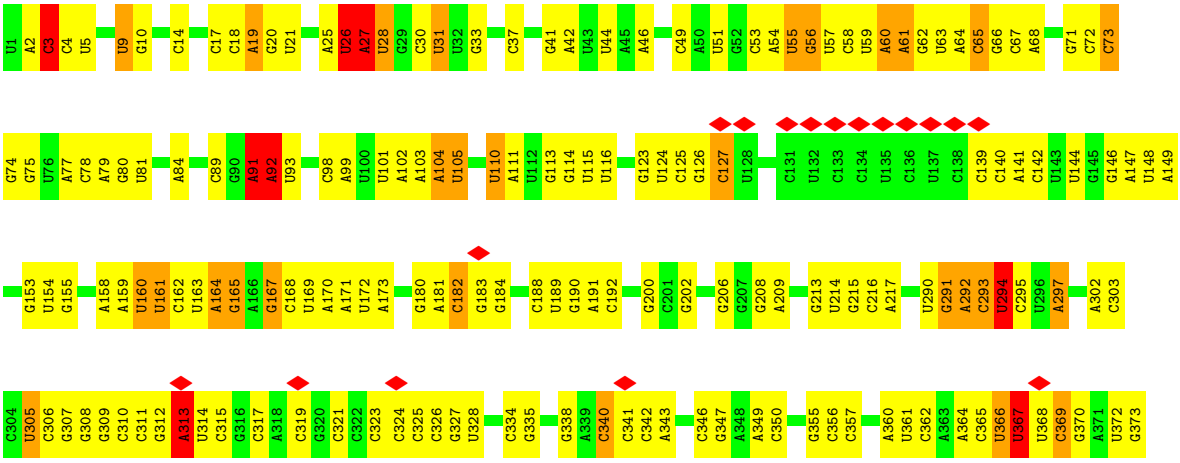
Chain 6:

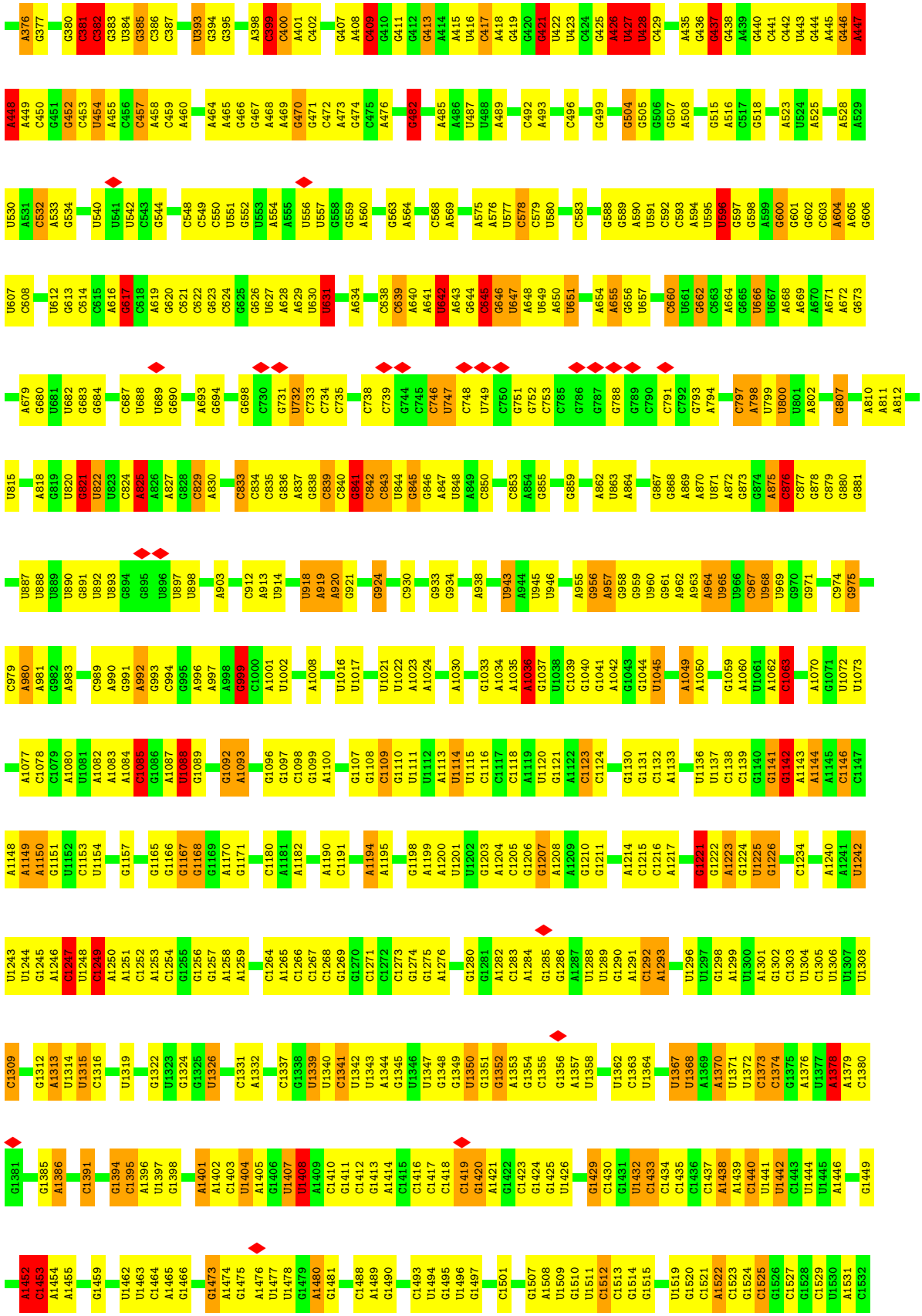




- Molecule 54: 18S ribosomal RNA

Chain S2:

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A448 A449 C450 G451 G452 C453 U454 A455 C456 C457 A458 C459 A460 A464 A465 C466 G467 A468 A469 G470 G471 C472 A473 G474 C475 A476 G482 A485 A486 U487 U488 A489 C492 A493 C496 G499 G504 G505 G506 G507 A508 G515 A516 C517 G518 A523 U524 A525 A528 A529
U530 A531 C532 A533 G534 U540 U541 U542 C543 G544 C548 C549 C550 U551 G552 U553 A554 A555 U556 U557 G558 G559 A560 G563 A564 C568 A569 A575 A576 U577 C578 C579 U580 C583 G588 G589 A590 U591 C592 C593 A594 U595 U596 G597 G598 A599 G600 G601 G602 C603 A604 A605 G606
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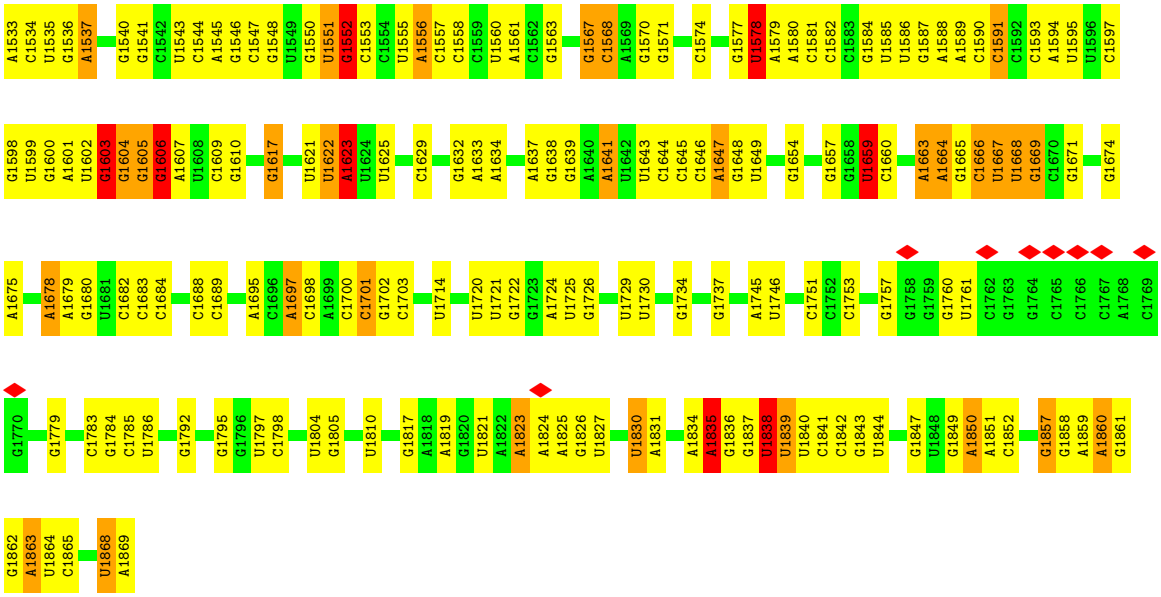
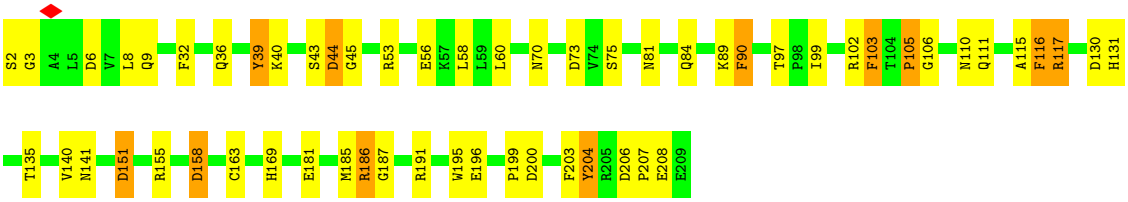
A1148 A1149 A1150 G1151 U1152 C1153 U1154 G1157 G1165 G1166 G1167 G1168 G1169 A1170 G1171 C1180 A1181 A1182 A1190 C1191 A1194 A1195 G1198 A1199 A1200 U1201 U1202 G1203 A1204 C1205 G1206 G1207 A1208 A1209 G1210 G1211 A1214 C1215 C1216 A1217 G1221 G1222 A1223 G1224 U1225 G1226 C1234 A1240 A1241 U1242
U1243 U1244 G1245 A1246 C1247 U1248 C1249 A1250 A1251 C1252 A1253 C1254 G1255 G1256 G1257 A1258 A1259 C1264 A1265 C1266 C1267 C1268 G1269 G1270 C1271 C1272 C1273 G1274 G1275 A1276 G1280 G1281 A1282 C1283 A1284 G1285 G1286 A1287 U1288 U1289 G1290 A1291 C1292 A1293 U1296 U1297 G1298 A1299 U1300 A1301 G1302 C1303 U1304 C1305 U1306 U1307 U1308
C1309 G1312 A1313 U1314 U1315 C1316 U1319 G1322 U1323 G1324 G1325 U1326 C1331 A1332 C1337 G1338 U1339 U1340 C1341 U1342 U1343 A1344 G1345 U1346 U1347 G1348 G1349 U1350 G1351 G1352 A1353 G1354 C1355 G1356 A1357 U1358 U1362 C1363 U1364 U1367 U1368 A1369 A1370 U1371 U1372 C1373 C1374 G1375 A1376 U1377 A1378 A1379 C1380
G1381 G1385 A1386 C1391 G1394 C1395 A1396 U1397 G1398 A1401 A1402 C1403 A1404 A1405 G1406 U1407 U1408 A1409 C1410 G1411 C1412 G1413 A1414 C1415 C1416 C1417 C1418 C1419 G1420 A1421 G1422 C1423 G1424 G1425 U1426 G1429 C1430 G1431 U1432 C1433 C1434 C1435 C1436 C1437 A1438 A1439 C1440 U1441 U1442 C1443 U1444 U1445 A1446 G1449
A1452 C1453 A1454 A1455 G1459 U1462 U1463 C1464 A1465 G1466 G1473 A1474 G1475 A1476 U1477 U1478 G1479 A1480 G1481 C1488 A1489 G1490 G1493 U1494 G1495 U1496 G1497 C1501 G1507 A1508 U1509 G1510 U1511 C1512 C1513 G1514 G1515 U1519 G1520 C1521 A1522 C1523 G1524 C1525 G1526 C1527 G1528 G1529 U1530 A1531 C1532



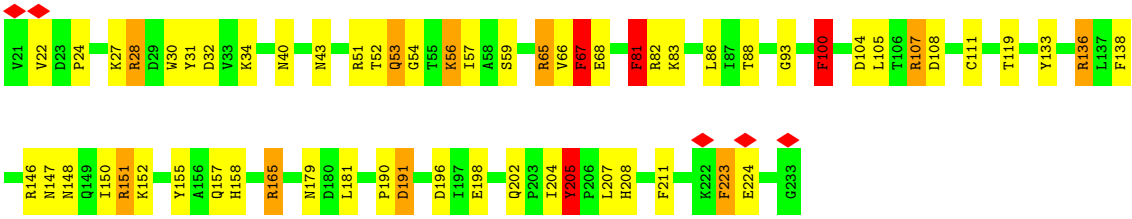
- Molecule 55: Ribosomal protein uS2

Chain SA:



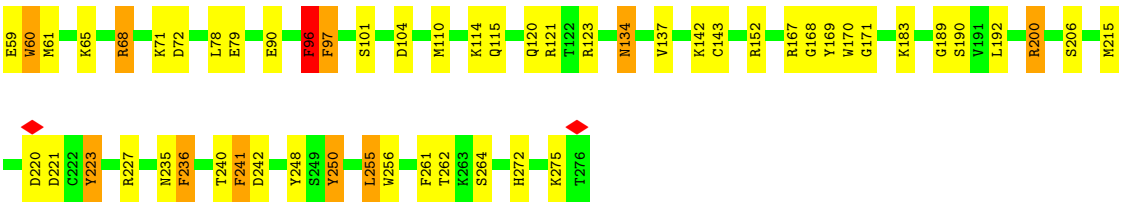
- Molecule 56: Ribosomal protein eS1

Chain SB:



- Molecule 57: Ribosomal protein uS5

Chain SC:

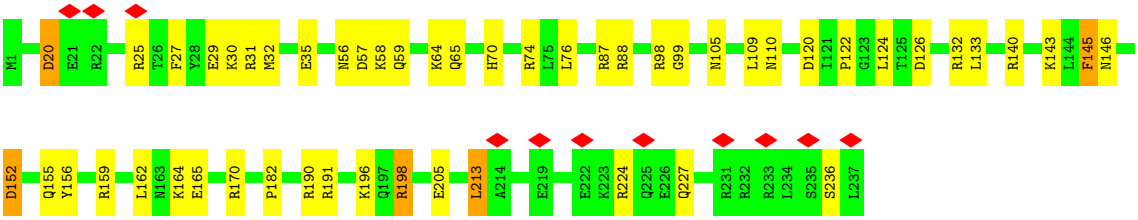


• Molecule 58: Ribosomal protein eS4

Chain SE:

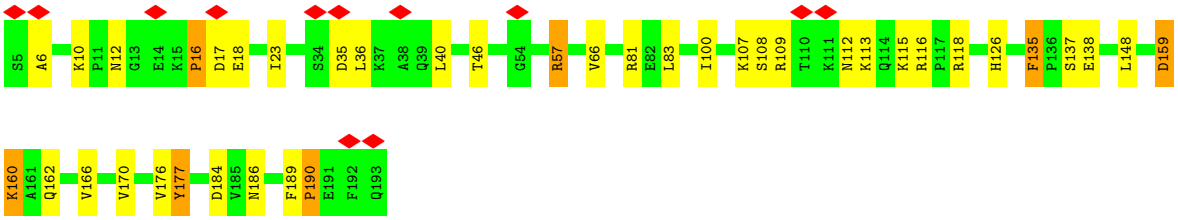
• Molecule 59: Ribosomal protein eS6

Chain SG:



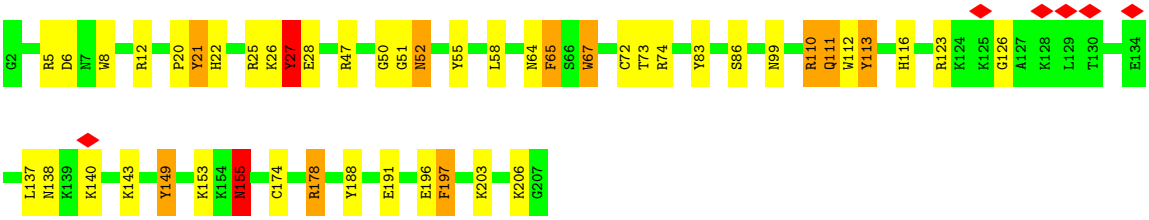
• Molecule 60: Ribosomal protein eS7

Chain SH:



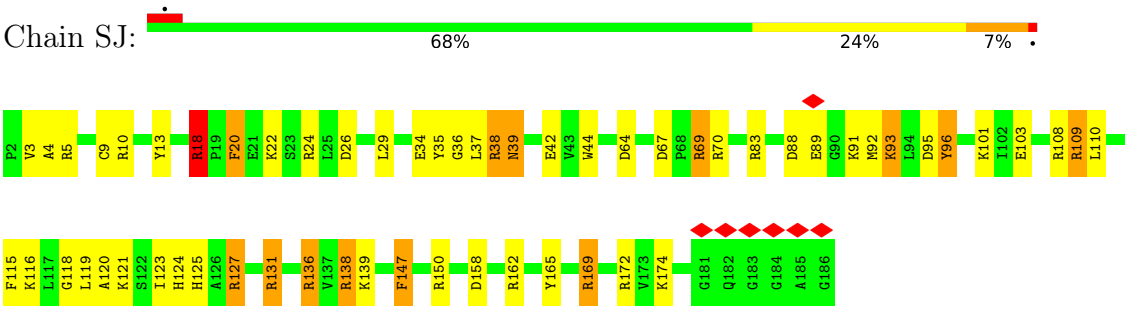
• Molecule 61: Ribosomal protein eS8

Chain SI:



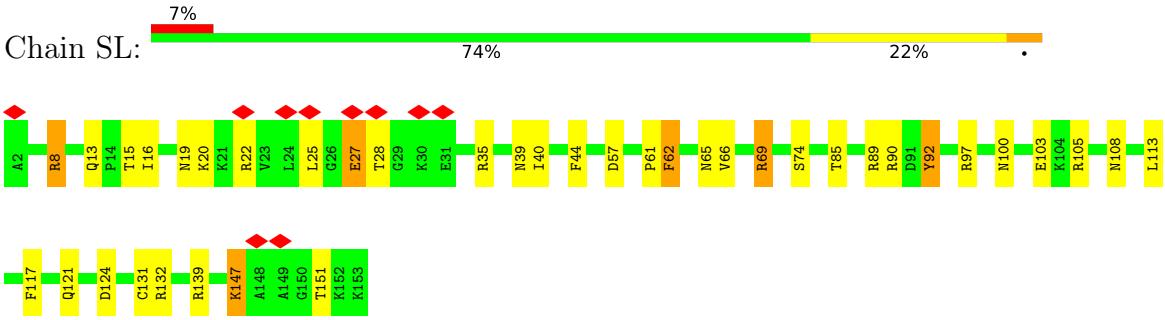
• Molecule 62: Ribosomal protein uS4

Chain SJ:



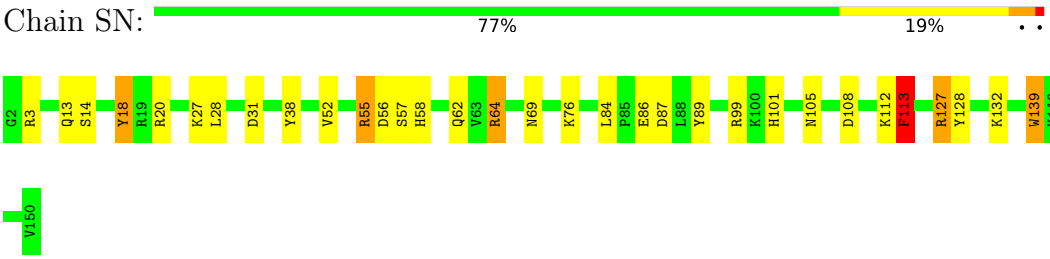
- Molecule 63: Ribosomal protein uS17

Chain SL:



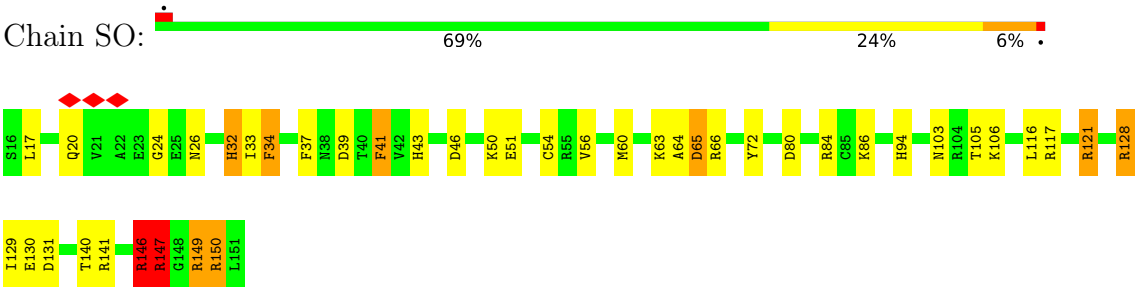
- Molecule 64: Ribosomal protein uS15

Chain SN:



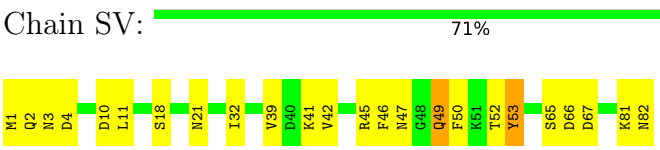
- Molecule 65: Ribosomal protein uS11

Chain SO:



- Molecule 66: Ribosomal protein eS21

Chain SV:



- Molecule 67: Ribosomal protein uS8

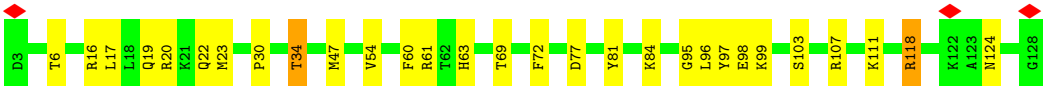
Chain SW: 76% 22%

• Molecule 68: Ribosomal protein uS12

Chain SX: 82% 15%

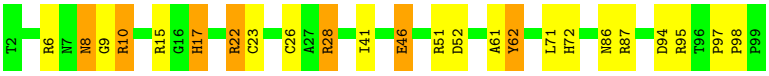
• Molecule 69: Ribosomal protein eS24

Chain SY: 77% 21%



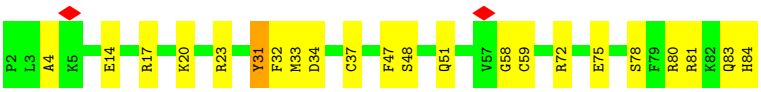
• Molecule 70: Ribosomal protein eS26

Chain Sa: 76% 17% 7%



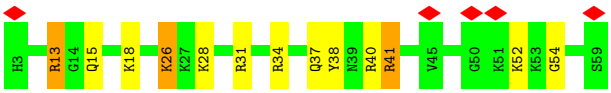
• Molecule 71: Ribosomal protein eS27

Chain Sb: 73% 25%



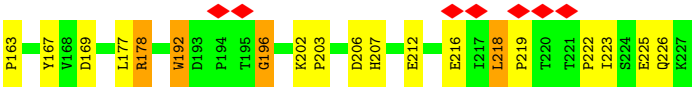
• Molecule 72: Ribosomal protein eS30

Chain Se: 9% 77% 18% 5%



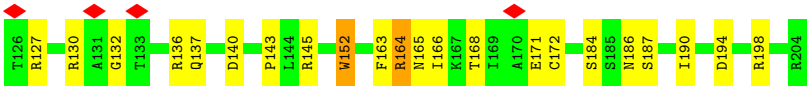
• Molecule 73: Ribosomal protein uS3

Chain SD: 78% 17%



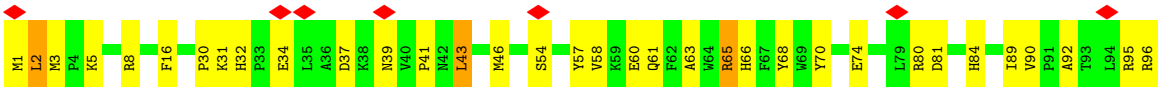
• Molecule 74: Ribosomal protein uS7

Chain SF:



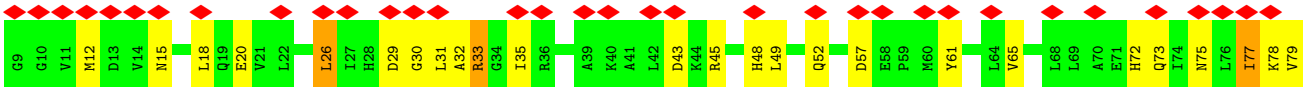
• Molecule 75: Ribosomal protein eS10

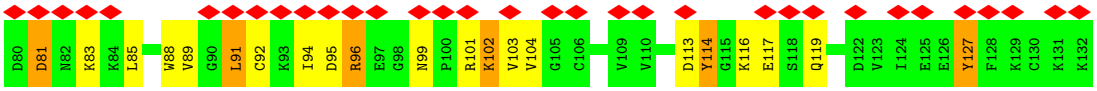
Chain SK:



• Molecule 76: Ribosomal protein eS12

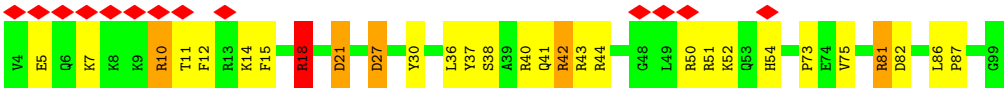
Chain SM:





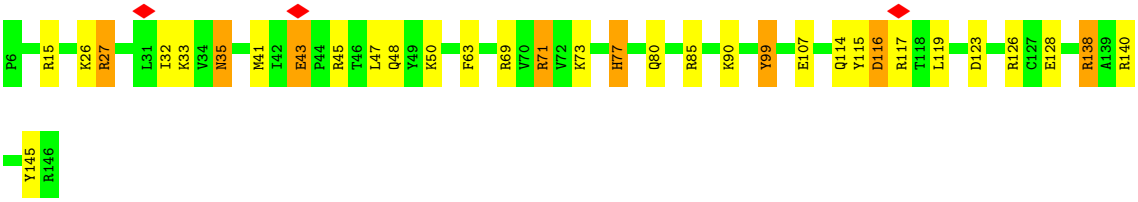
• Molecule 77: Ribosomal protein uS19

Chain SP:



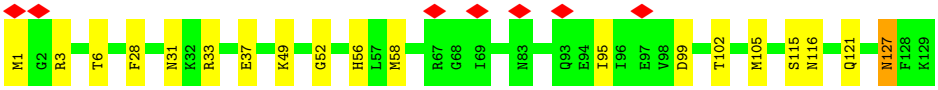
• Molecule 78: Ribosomal protein uS9

Chain SQ:



• Molecule 79: Ribosomal protein eS17

Chain SR:

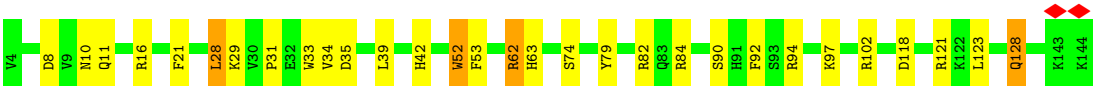


• Molecule 80: Ribosomal protein uS13

Chain SS:

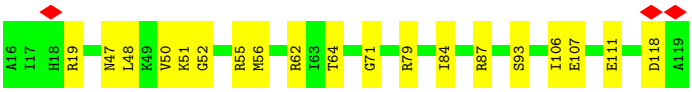
• Molecule 81: Ribosomal protein eS19

Chain ST:



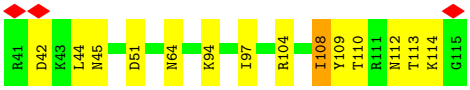
• Molecule 82: Ribosomal protein uS10

Chain SU:



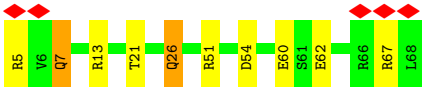
• Molecule 83: Ribosomal protein es25

Chain SZ:



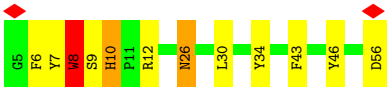
• Molecule 84: Ribosomal protein eS28

Chain Sc:



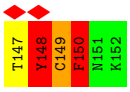
- Molecule 85: Ribosomal protein uS14

Chain Sd:



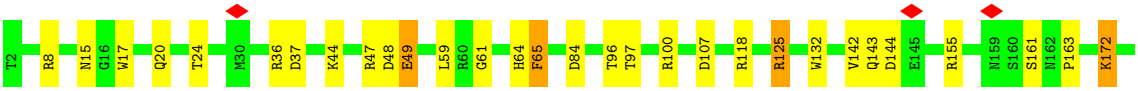
- Molecule 86: Ribosomal protein eS31

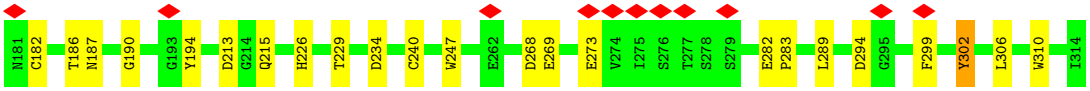
Chain Sf:



- Molecule 87: Ribosomal protein RACK1

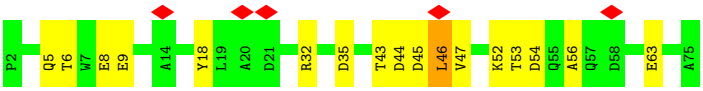
Chain Sg:





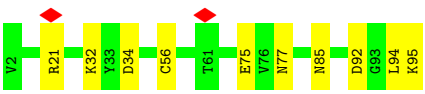
- Molecule 88: SRP9

Chain S1:



- Molecule 89: SRP14

Chain S4:



4 Experimental information (i)

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 ($e^-/Å^2$)	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 (Å)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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(^{o})	Ideal(^{o})
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

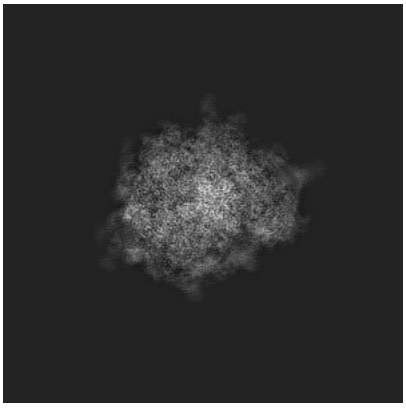
6 Map visualisation (i)

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.

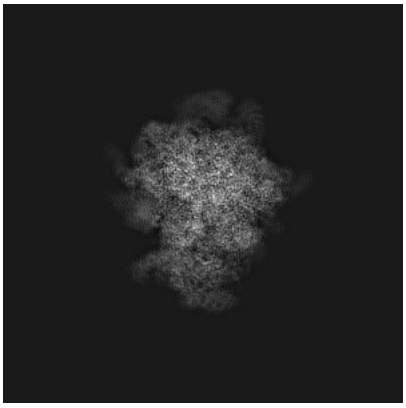
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

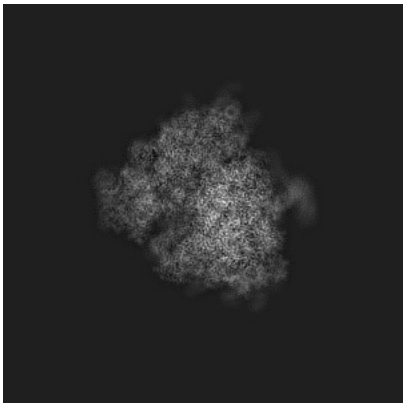
6.1.1 Primary map



X



Y

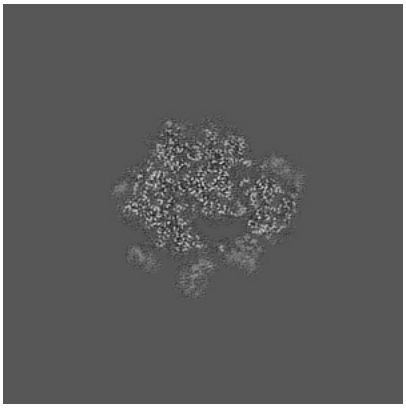


Z

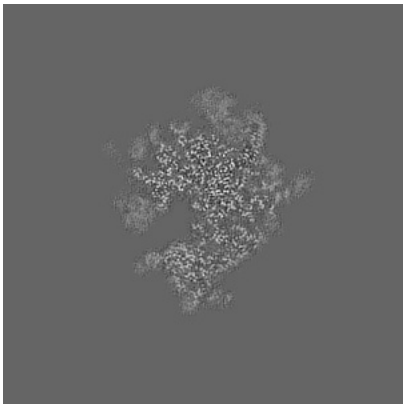
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

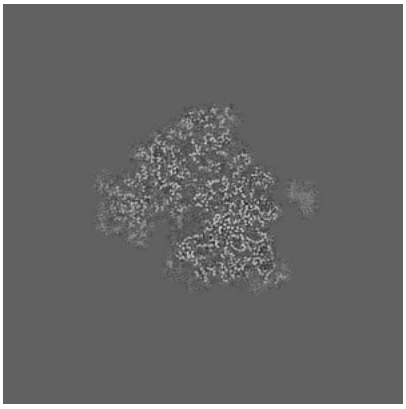
6.2.1 Primary map



X Index: 210



Y Index: 210

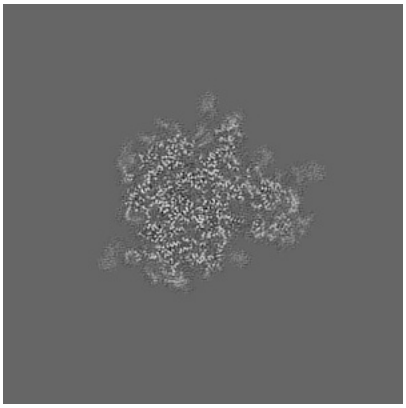


Z Index: 210

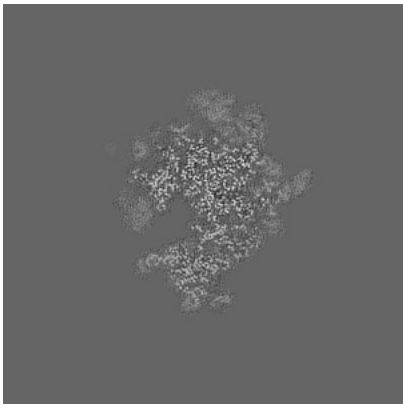
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

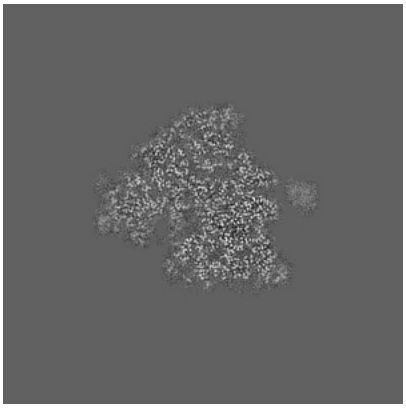
6.3.1 Primary map



X Index: 234



Y Index: 212

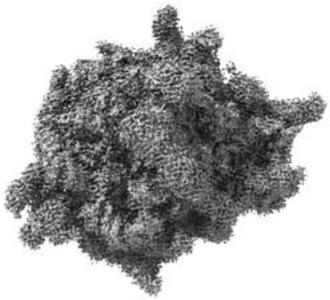


Z Index: 208

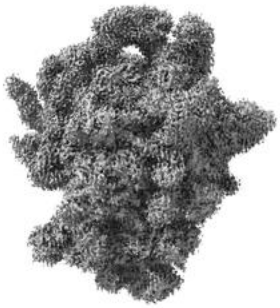
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal 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.

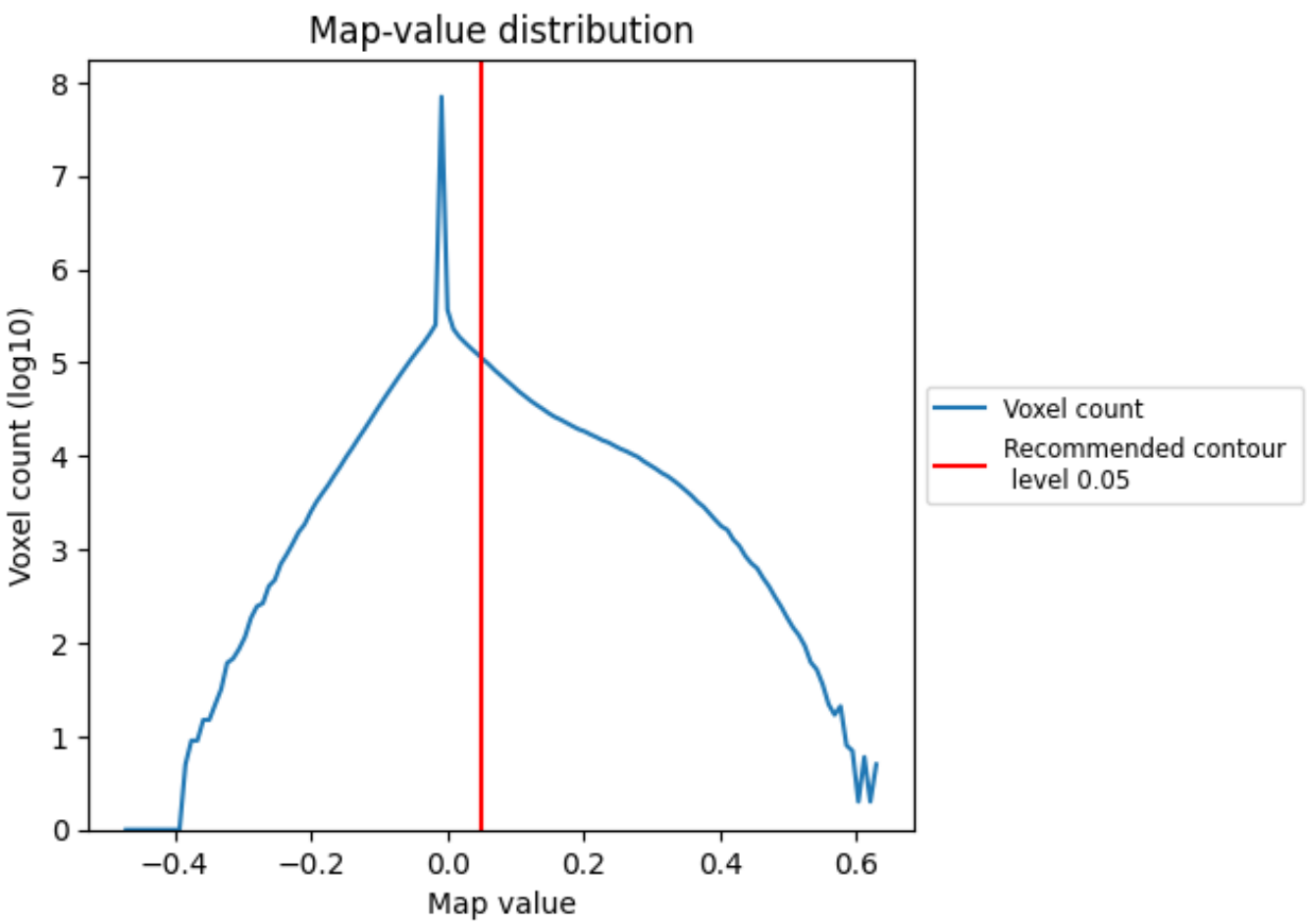
6.5 Mask visualisation (i)

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

7 Map analysis (i)

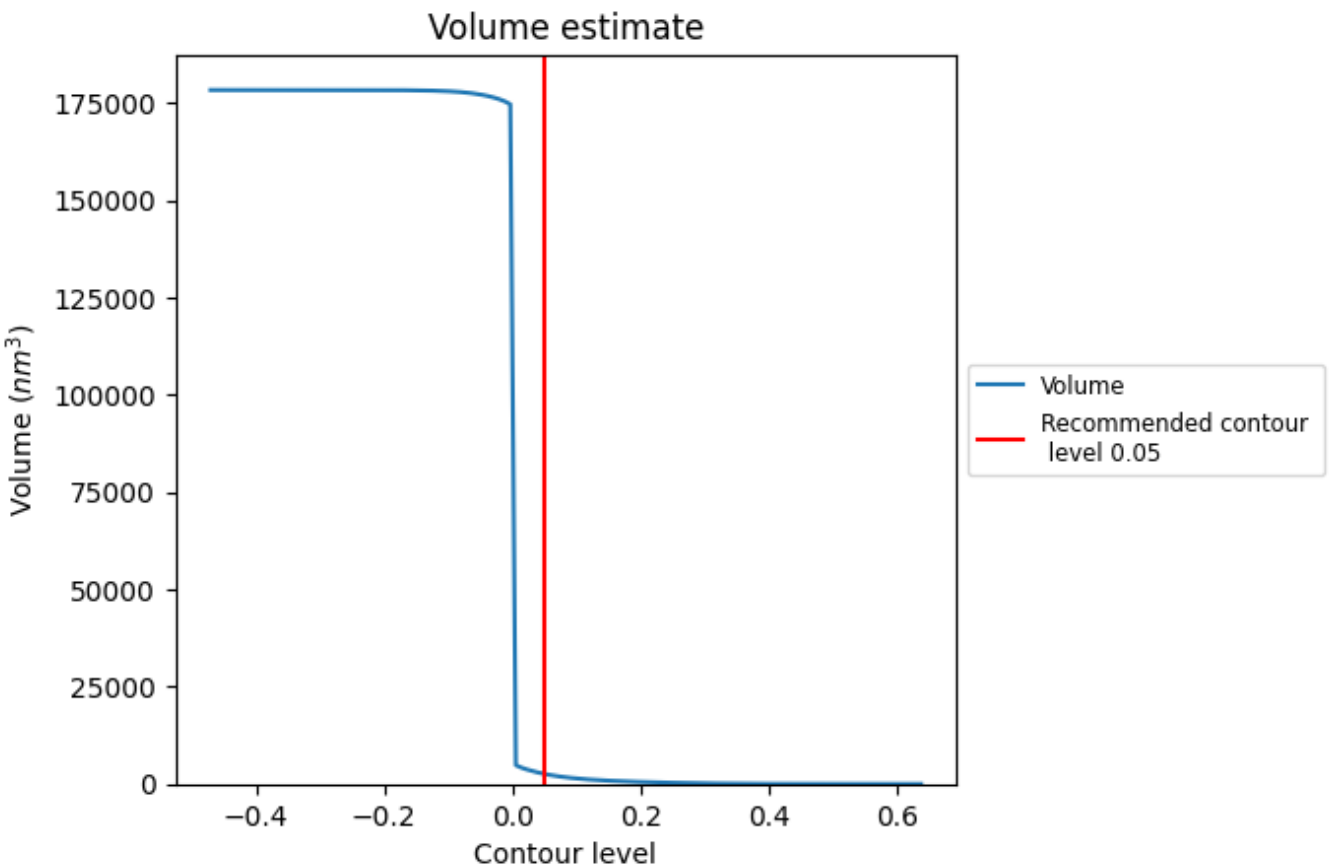
This section contains the results of statistical analysis of the map.

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.

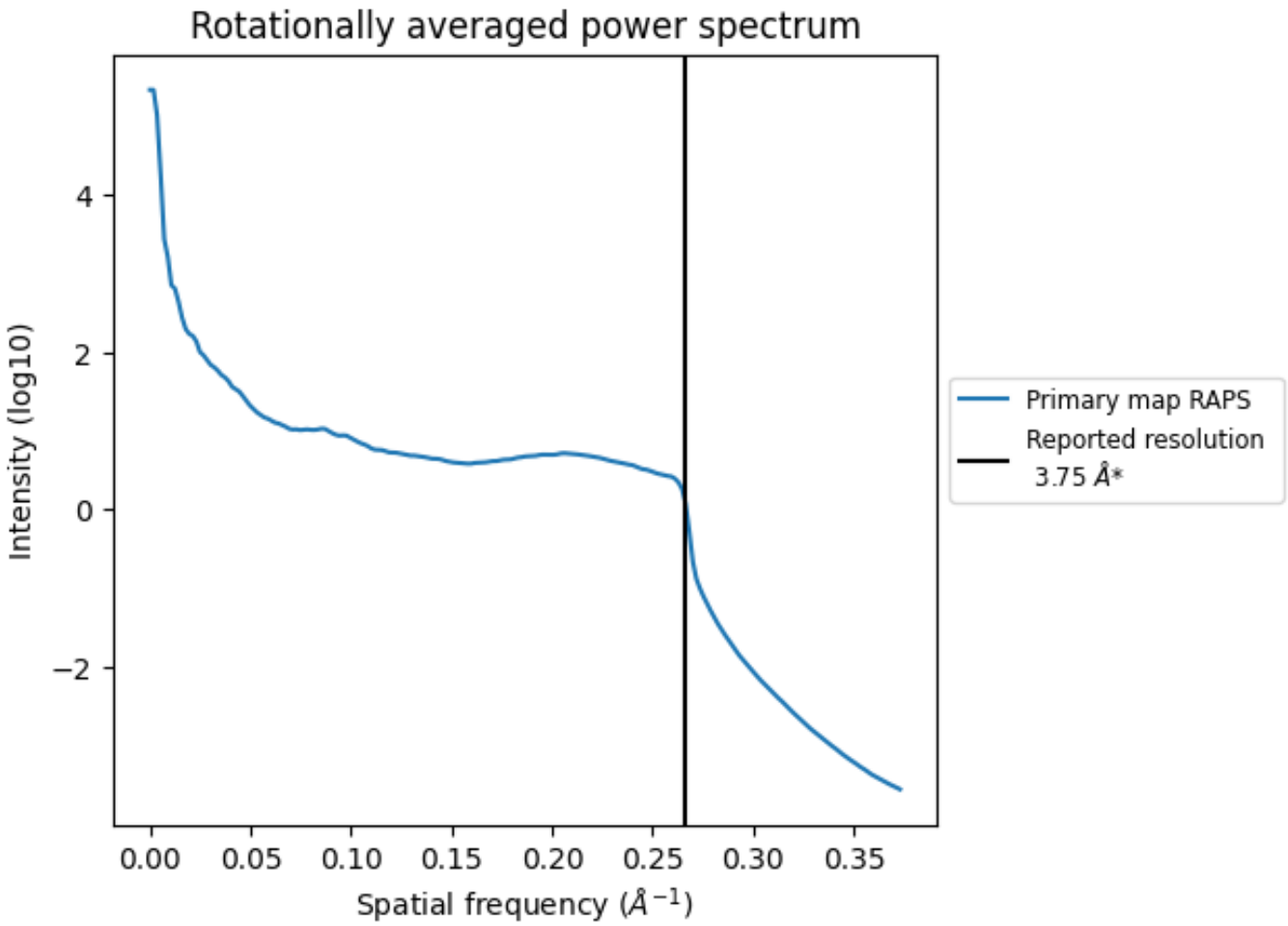
7.2 Volume estimate (i)



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 (i)



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

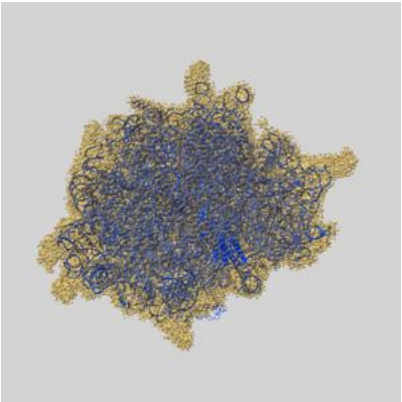
8 Fourier-Shell correlation (i)

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

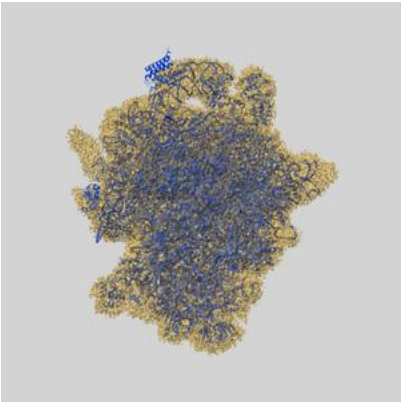
9 Map-model fit (i)

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.

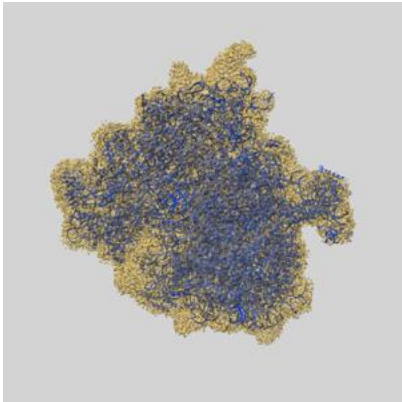
9.1 Map-model overlay (i)



X



Y



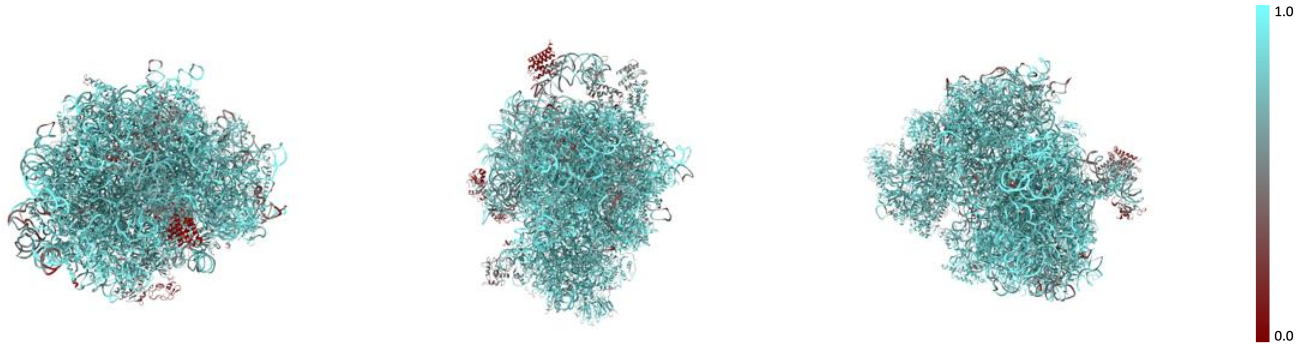
Z

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.

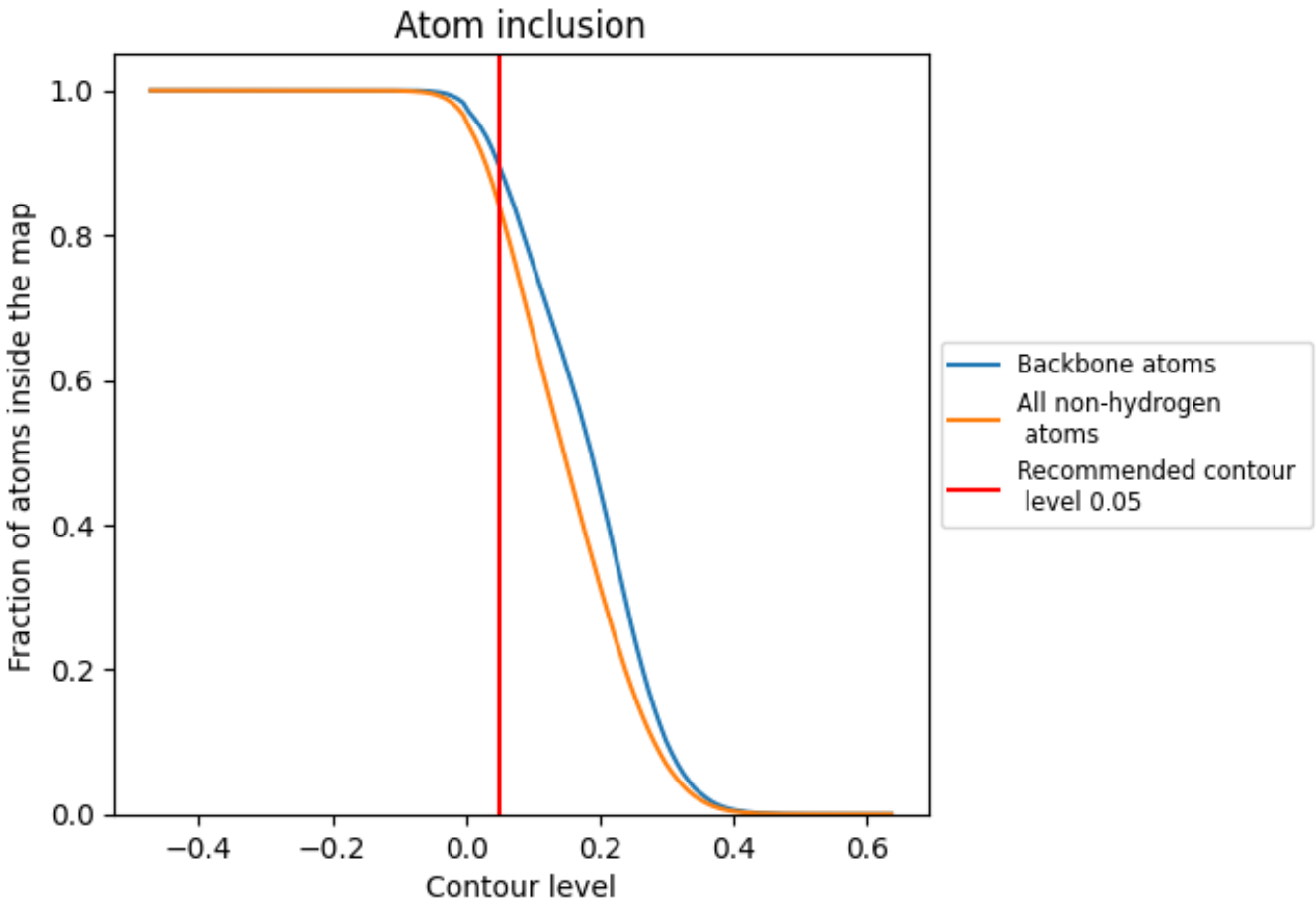
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

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