



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 05:43 PM UTC

PDB ID : 3JAN / pdb_00003jan
EMDB ID : EMD-3045
Title : Structure of the scanning state of the mammalian SRP-ribosome complex
Authors : Voorhees, R.M.; Hegde, R.S.
Deposited on : 2015-06-17
Resolution : 3.75 Å (reported)
Based on initial model : 3JAJ

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

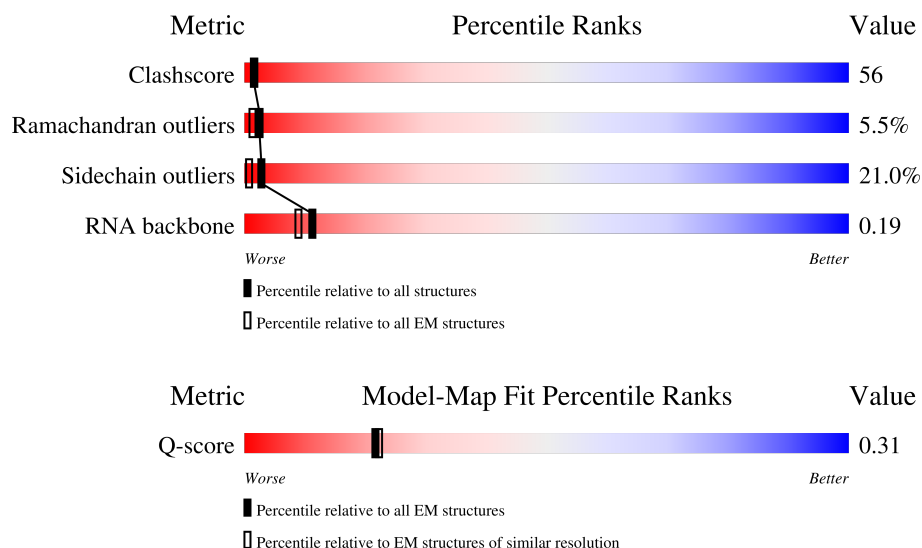
1 Overall quality at a glance i

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.



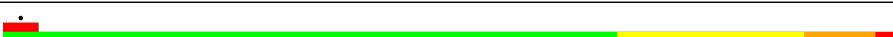
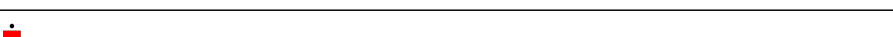
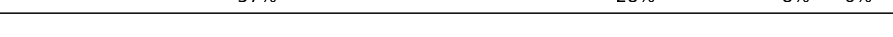
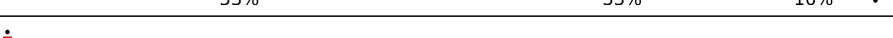
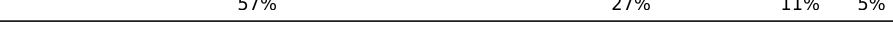
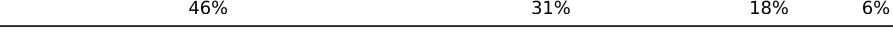
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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

Mol	Chain	Length	Quality of chain
1	A	244	
2	D	292	
3	G	238	

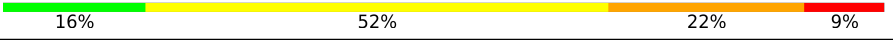
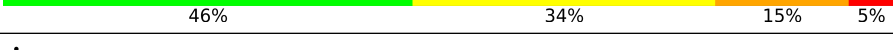
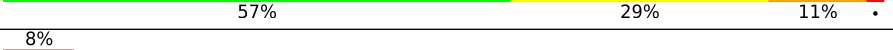
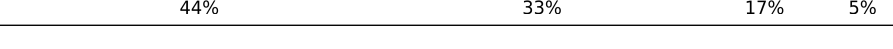
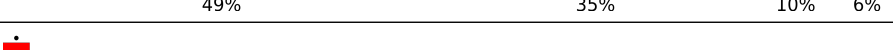
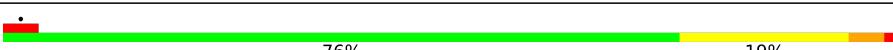
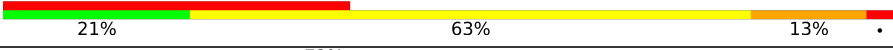
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Mol	Chain	Length	Quality of chain
4	H	190	
5	J	170	
6	L	210	
7	M	138	
8	N	203	
9	O	201	
10	Q	187	
11	R	180	
12	S	175	
13	T	159	
14	U	99	
15	V	131	
16	X	119	
17	Y	134	
18	Z	135	
19	a	147	
20	b	75	
21	c	94	
22	d	107	
23	e	128	
24	f	109	
25	g	114	
26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

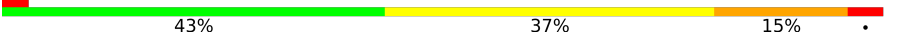
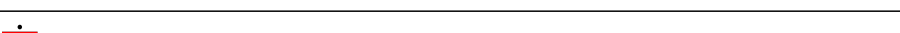
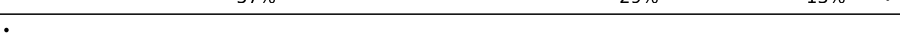
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Mol	Chain	Length	Quality of chain
29	l	50	
30	m	52	
31	o	104	
32	5	3658	
33	7	120	
34	8	156	
35	B	394	
36	C	367	
37	E	236	
38	F	225	
39	I	213	
40	P	153	
41	W	63	
42	j	86	
43	n	23	
44	p	91	
45	r	125	
46	K	163	
47	q	202	
48	z	426	
49	3	76	
50	4	206	
51	9	105	
52	6	179	
53	S2	1742	

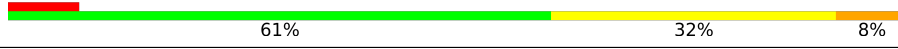
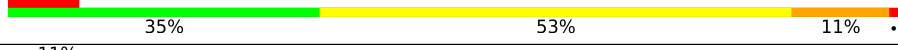
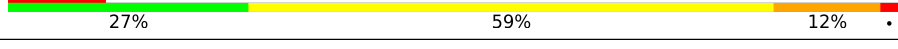
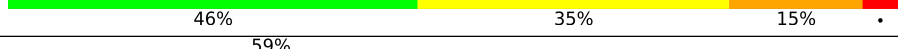
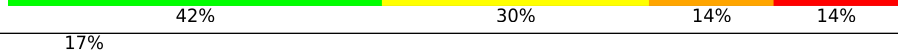
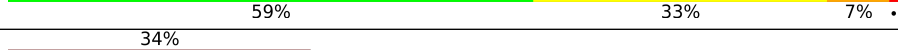
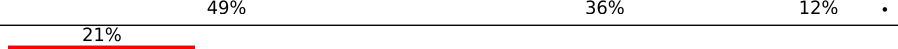
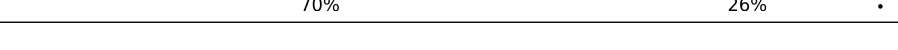
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Mol	Chain	Length	Quality of chain
54	SA	208	
55	SB	213	
56	SC	218	
57	SE	262	
58	SG	237	
59	SH	189	
60	SI	206	
61	SJ	185	
62	SL	152	
63	SN	149	
64	SO	136	
65	SV	82	
66	SW	129	
67	SX	141	
68	SY	126	
69	Sa	98	
70	Sb	83	
71	Se	57	
72	SD	227	
73	SF	191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

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

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

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

2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 227964 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ribosomal protein uL2.

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

- Molecule 2 is a protein called Ribosomal protein uL18.

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

- Molecule 3 is a protein called Ribosomal protein eL8.

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

- Molecule 4 is a protein called Ribosomal protein uL6.

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

- Molecule 5 is a protein called Ribosomal protein uL5.

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

- Molecule 6 is a protein called Ribosomal protein eL13.

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

- Molecule 7 is a protein called Ribosomal protein eL14.

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

- Molecule 8 is a protein called Ribosomal protein eL15.

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

- Molecule 9 is a protein called Ribosomal protein uL13.

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

- Molecule 10 is a protein called Ribosomal protein eL18.

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

- Molecule 11 is a protein called Ribosomal protein eL19.

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

- Molecule 12 is a protein called Ribosomal protein eL20.

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

- Molecule 13 is a protein called Ribosomal protein eL21.

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

- Molecule 14 is a protein called Ribosomal protein eL22.

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

- Molecule 15 is a protein called Ribosomal protein uL14.

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

- Molecule 16 is a protein called Ribosomal protein uL23.

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

- Molecule 17 is a protein called Ribosomal protein uL24.

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

- Molecule 18 is a protein called Ribosomal protein eL27.

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

- Molecule 19 is a protein called Ribosomal protein uL15.

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

- Molecule 20 is a protein called Ribosomal protein eL29.

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

- Molecule 21 is a protein called Ribosomal protein eL30.

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

- Molecule 22 is a protein called Ribosomal protein eL31.

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

- Molecule 23 is a protein called Ribosomal protein eL32.

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

- Molecule 24 is a protein called Ribosomal protein eL33.

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

- Molecule 25 is a protein called Ribosomal protein eL34.

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

- Molecule 26 is a protein called Ribosomal protein uL29.

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

- Molecule 27 is a protein called Ribosomal protein eL36.

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

- Molecule 28 is a protein called Ribosomal protein eL38.

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

- Molecule 29 is a protein called Ribosomal protein eL39.

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

- Molecule 30 is a protein called Ribosomal protein eL40.

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

- Molecule 31 is a protein called Ribosomal protein eL42.

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

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

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

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

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

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

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

- Molecule 35 is a protein called Ribosomal protein uL3.

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

- Molecule 36 is a protein called Ribosomal protein uL4.

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

- Molecule 37 is a protein called Ribosomal protein eL6.

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

- Molecule 38 is a protein called Ribosomal protein uL30.

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

- Molecule 39 is a protein called Ribosomal protein uL16.

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

- Molecule 40 is a protein called Ribosomal protein uL22.

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

- Molecule 41 is a protein called Ribosomal protein eL24.

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

- Molecule 42 is a protein called Ribosomal protein eL37.

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

- Molecule 43 is a protein called Ribosomal protein eL41.

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

- Molecule 44 is a protein called Ribosomal protein eL43.

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

- Molecule 45 is a protein called Ribosomal protein eL28.

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

- Molecule 46 is a protein called Ribosomal protein uL11.

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

- Molecule 47 is a protein called Ribosomal protein uL10.

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

- Molecule 48 is a protein called SRP54.

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

- Molecule 49 is a RNA chain called Val tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	3	76	Total	C	N	O	P	0	0
			1616	723	290	528	75		

- Molecule 50 is a RNA chain called SRP 7S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	4	206	Total	C	N	O	P	6	0
			4551	2026	836	1477	212		

- Molecule 51 is a protein called SRP19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	9	105	Total	C	N	O	S	0	0
			844	534	152	152	6		

- Molecule 52 is a protein called SRP68.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	6	179	Total	C	N	O	S	0	0
			1497	939	280	271	7		

- Molecule 53 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 54 is a protein called Ribosomal protein uS2.

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

- Molecule 55 is a protein called Ribosomal protein eS1.

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

- Molecule 56 is a protein called Ribosomal protein uS5.

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

- Molecule 57 is a protein called Ribosomal protein eS4.

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

- Molecule 58 is a protein called Ribosomal protein eS6.

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

- Molecule 59 is a protein called Ribosomal protein eS7.

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

- Molecule 60 is a protein called Ribosomal protein eS8.

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

- Molecule 61 is a protein called Ribosomal protein uS4.

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

- Molecule 62 is a protein called Ribosomal protein uS17.

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

- Molecule 63 is a protein called Ribosomal protein uS15.

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

- Molecule 64 is a protein called Ribosomal protein uS11.

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

- Molecule 65 is a protein called Ribosomal protein eS21.

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

- Molecule 66 is a protein called Ribosomal protein uS8.

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

- Molecule 67 is a protein called Ribosomal protein uS12.

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

- Molecule 68 is a protein called Ribosomal protein eS24.

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

- Molecule 69 is a protein called Ribosomal protein eS26.

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

- Molecule 70 is a protein called Ribosomal protein eS27.

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

- Molecule 71 is a protein called Ribosomal protein eS30.

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

- Molecule 72 is a protein called Ribosomal protein uS3.

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

- Molecule 73 is a protein called Ribosomal protein uS7.

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

- Molecule 74 is a protein called Ribosomal protein eS10.

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

- Molecule 75 is a protein called Ribosomal protein eS12.

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

- Molecule 76 is a protein called Ribosomal protein uS19.

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

- Molecule 77 is a protein called Ribosomal protein uS9.

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

- Molecule 78 is a protein called Ribosomal protein eS17.

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

- Molecule 79 is a protein called Ribosomal protein uS13.

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

- Molecule 80 is a protein called Ribosomal protein eS19.

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

- Molecule 81 is a protein called Ribosomal protein uS10.

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

- Molecule 82 is a protein called Ribosomal protein es25.

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

- Molecule 83 is a protein called Ribosomal protein eS28.

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

- Molecule 84 is a protein called Ribosomal protein uS14.

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

- Molecule 85 is a protein called Ribosomal protein eS31.

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

- Molecule 86 is a protein called Ribosomal protein RACK1.

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

- Molecule 87 is a protein called SRP9.

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

- Molecule 88 is a protein called SRP14.

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

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	D	1	Total	Mg	0
			1	1	
89	V	1	Total	Mg	0
			1	1	
89	g	1	Total	Mg	0
			1	1	
89	5	116	Total	Mg	0
			116	116	
89	7	5	Total	Mg	0
			5	5	
89	8	6	Total	Mg	0
			6	6	

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Mol	Chain	Residues	Atoms		AltConf
89	S2	36	Total 36	Mg 36	0

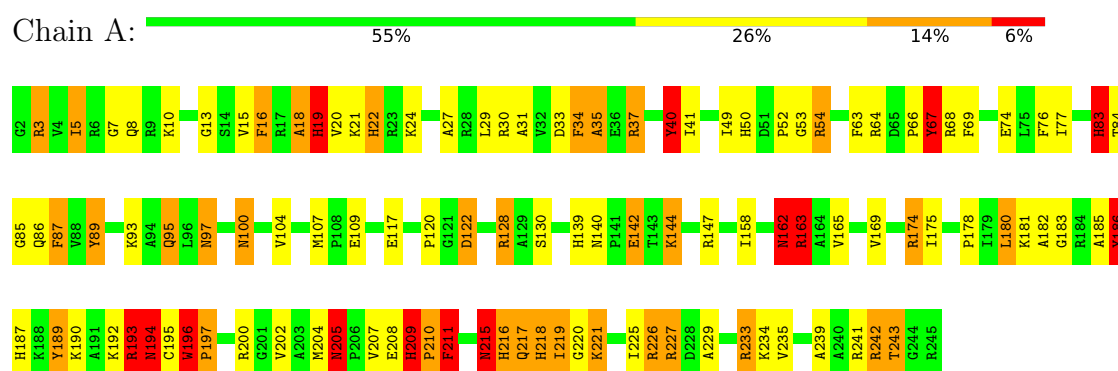
- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

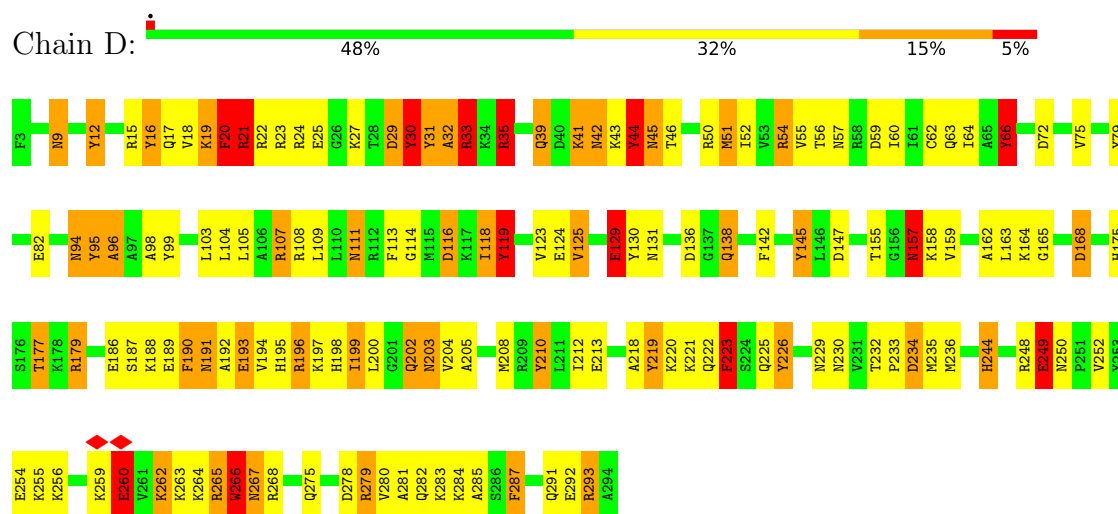
3 Residue-property plots

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

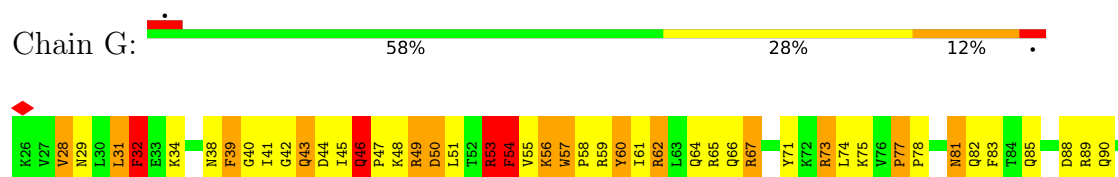
• Molecule 1: Ribosomal protein uL2

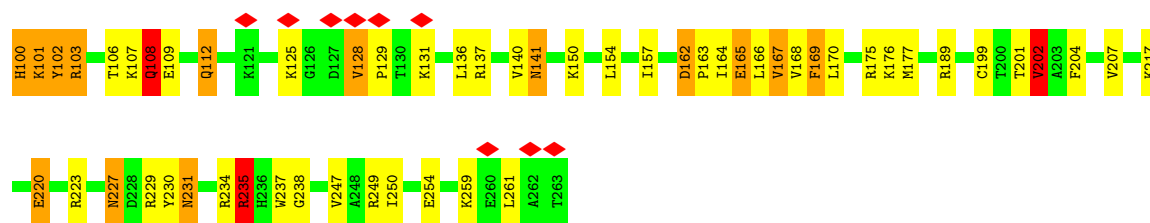


• Molecule 2: Ribosomal protein uL18

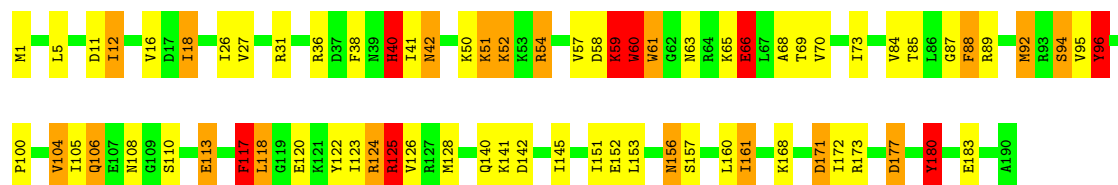


• Molecule 3: Ribosomal protein eL8

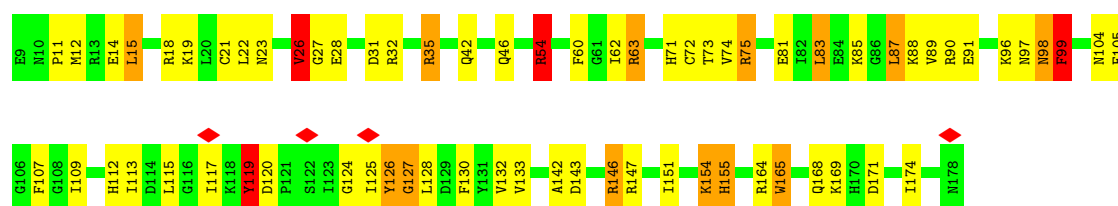




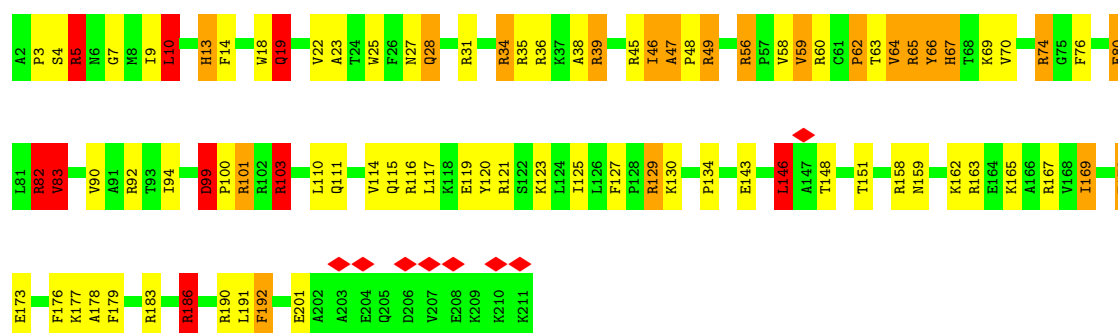
• Molecule 4: Ribosomal protein uL6



• Molecule 5: Ribosomal protein uL5

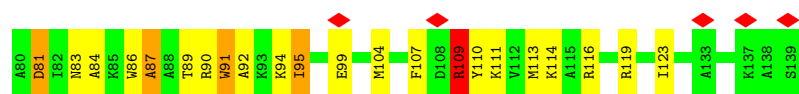


• Molecule 6: Ribosomal protein eL13



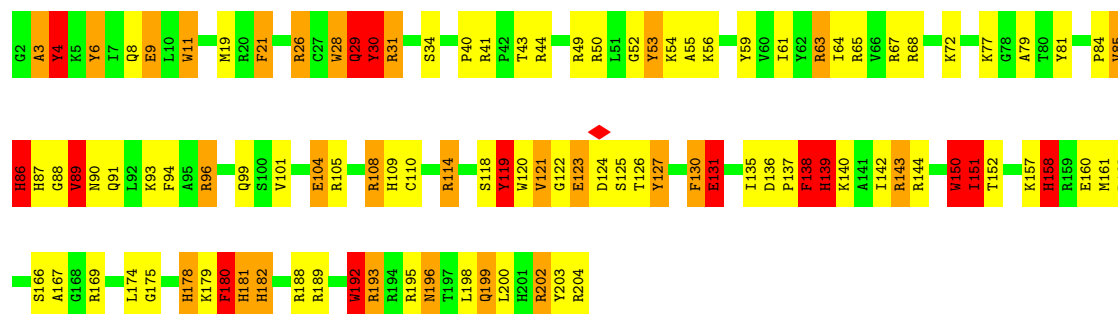
• Molecule 7: Ribosomal protein eL14





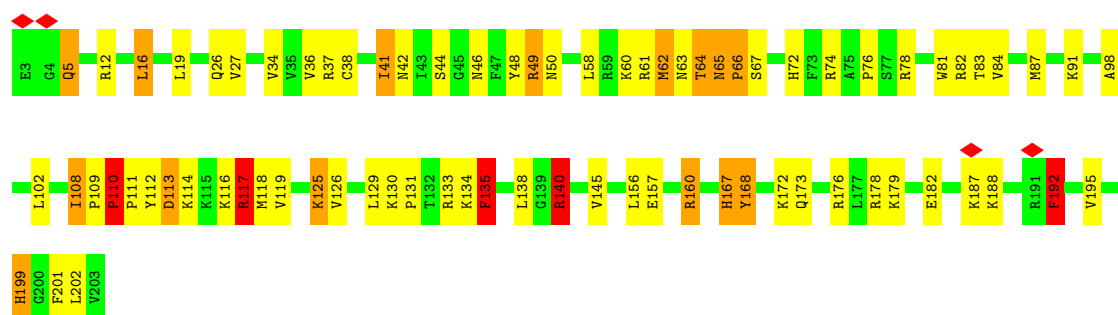
• Molecule 8: Ribosomal protein eL15

Chain N: 48% 32% 13% 7%



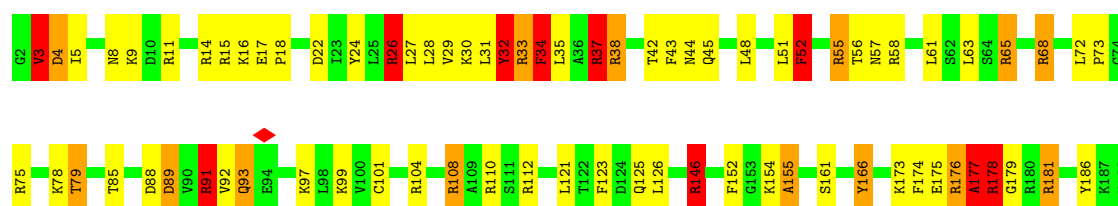
• Molecule 9: Ribosomal protein uL13

Chain O: 60% 30% 7%



• Molecule 10: Ribosomal protein eL18

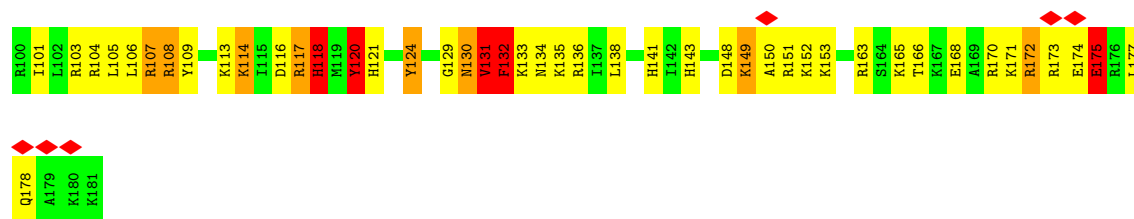
Chain Q: 59% 28% 7% 5%



• Molecule 11: Ribosomal protein eL19

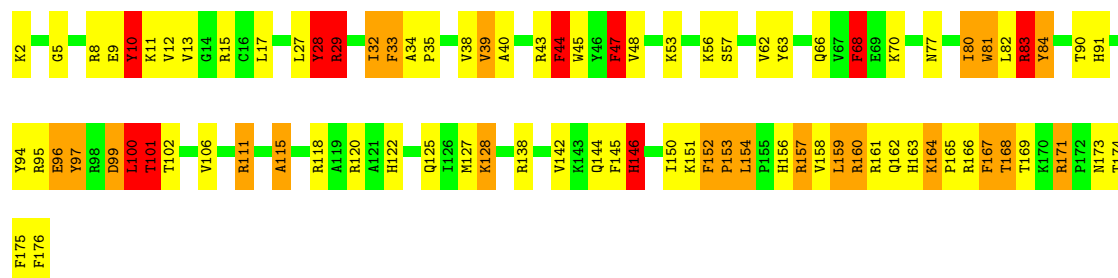
Chain R: 52% 33% 12%





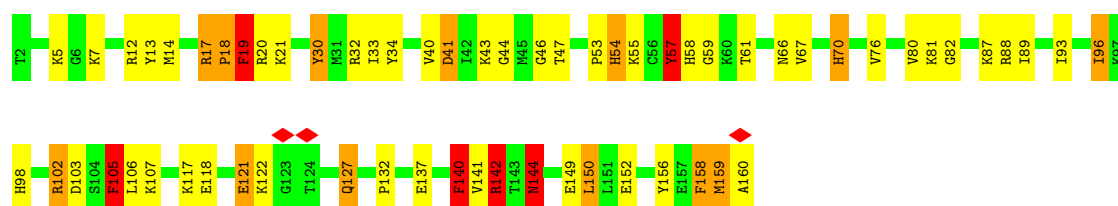
• Molecule 12: Ribosomal protein eL20

Chain S: 50% 31% 13% 6%



• Molecule 13: Ribosomal protein eL21

Chain T: 60% 28% 8%



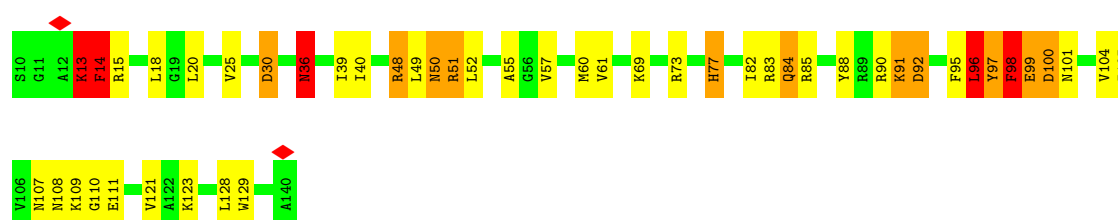
• Molecule 14: Ribosomal protein eL22

Chain U: 69% 21% 8%



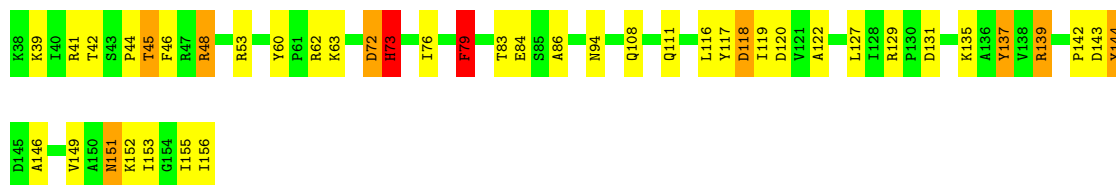
• Molecule 15: Ribosomal protein uL14

Chain V: 63% 24% 8%



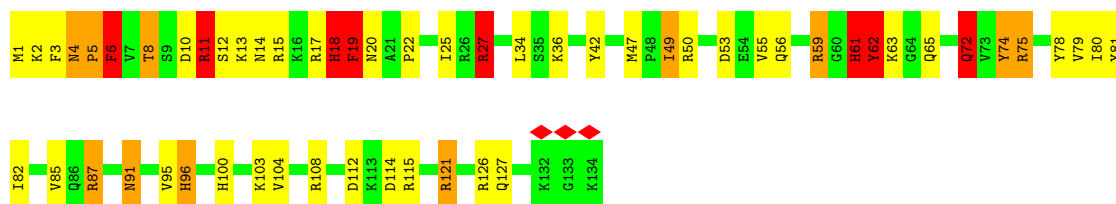
• Molecule 16: Ribosomal protein uL23

Chain X: 



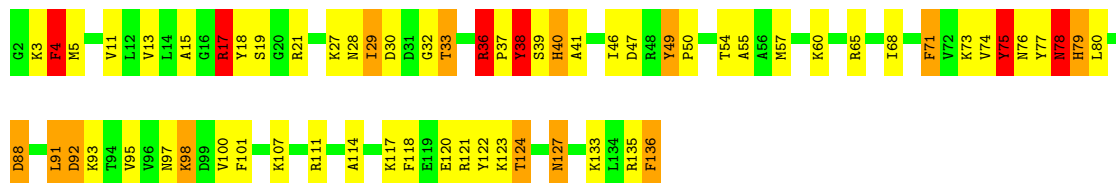
- Molecule 17: Ribosomal protein uL24

Chain Y: 



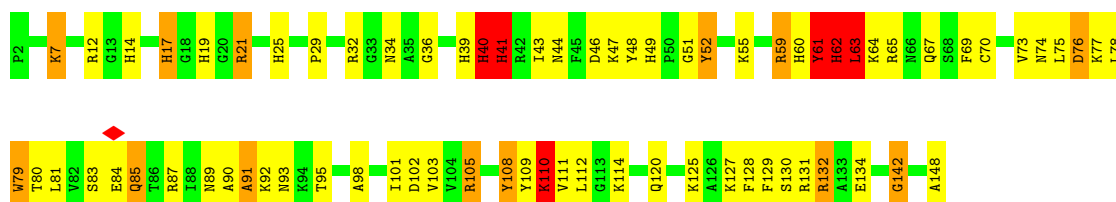
- Molecule 18: Ribosomal protein eL27

Chain Z: 



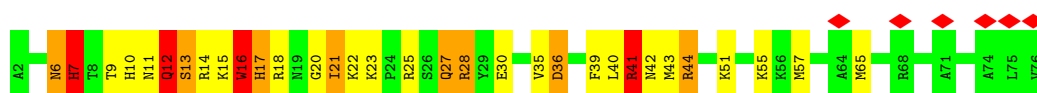
- Molecule 19: Ribosomal protein uL15

Chain a: 



- Molecule 20: Ribosomal protein eL29

Chain b: 

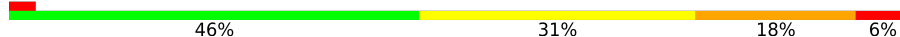


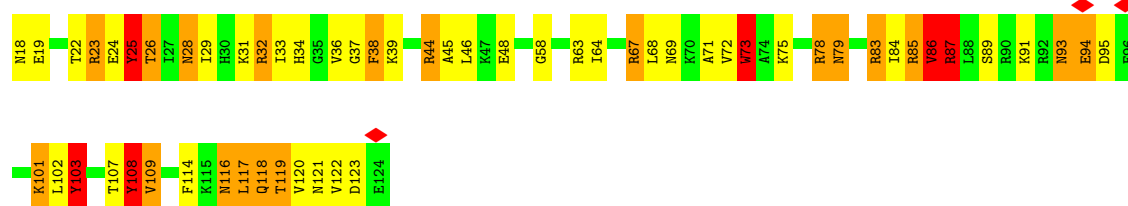
- Molecule 21: Ribosomal protein eL30

Chain c: 



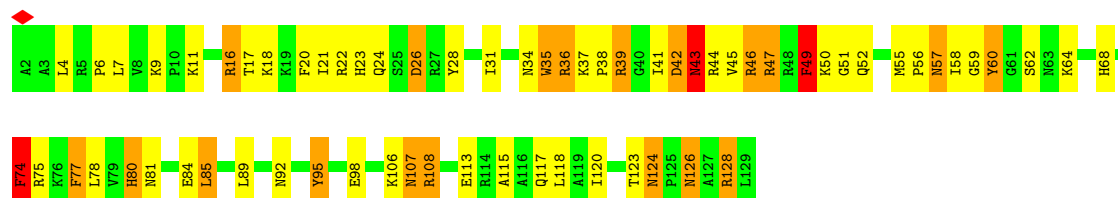
- Molecule 22: Ribosomal protein eL31

Chain d: 



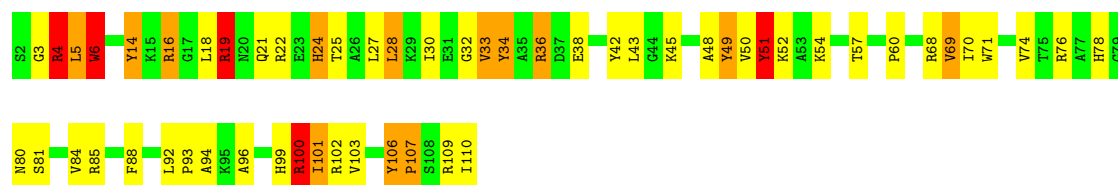
- Molecule 23: Ribosomal protein eL32

Chain e: 



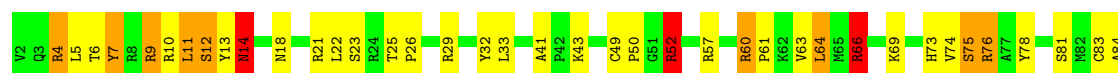
- Molecule 24: Ribosomal protein eL33

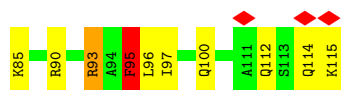
Chain f: 



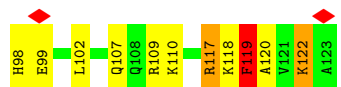
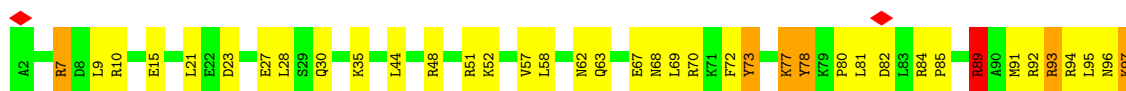
- Molecule 25: Ribosomal protein eL34

Chain g: 





- Molecule 26: Ribosomal protein uL29



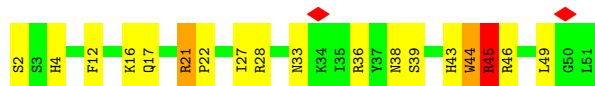
- Molecule 27: Ribosomal protein eL36



- Molecule 28: Ribosomal protein eL38



- Molecule 29: Ribosomal protein eL39

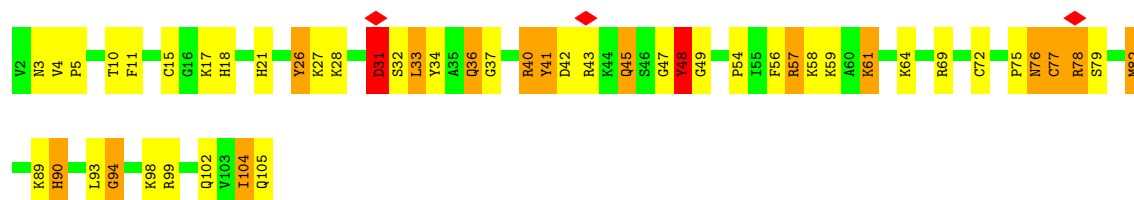


- Molecule 30: Ribosomal protein eL40

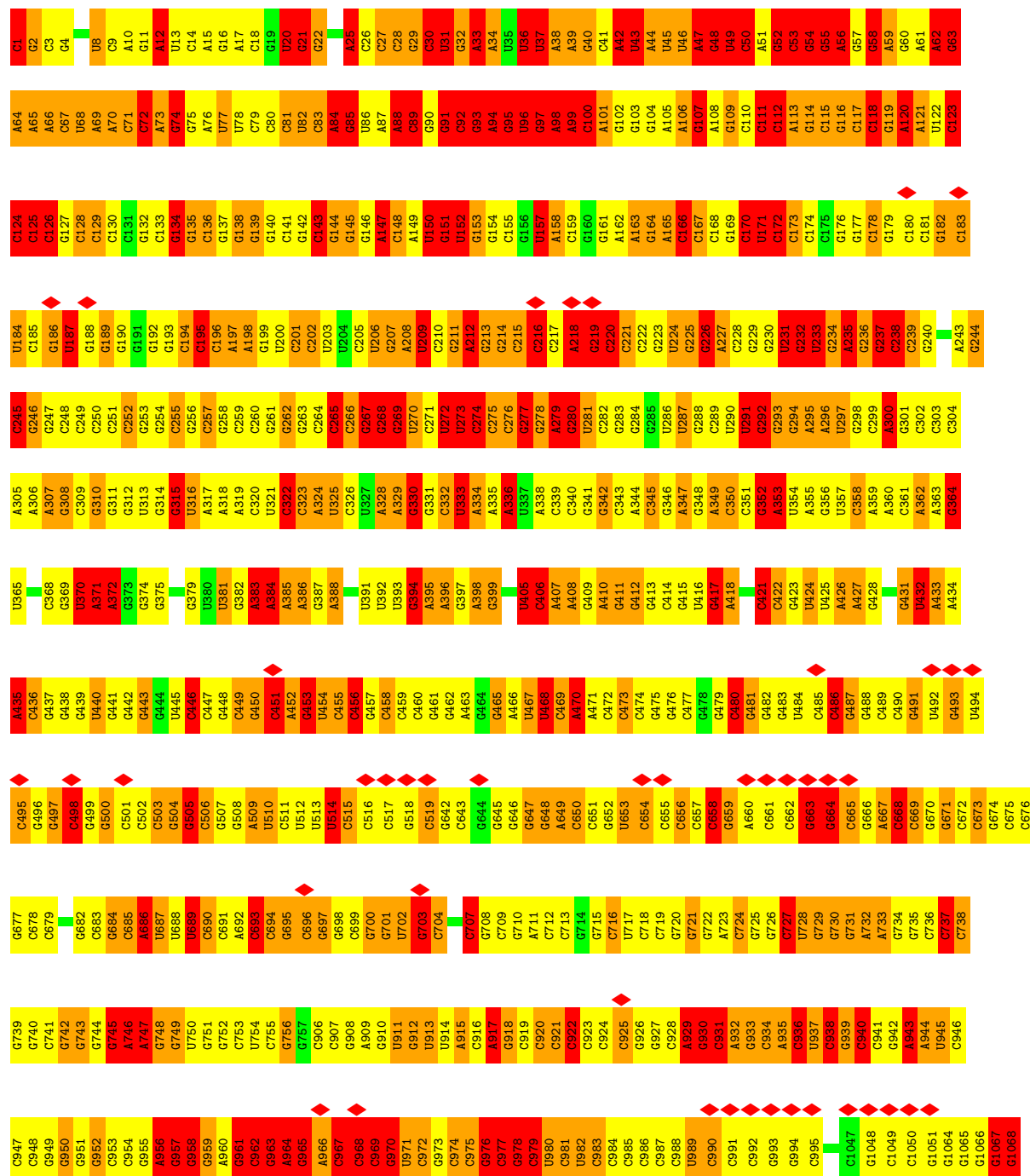


- Molecule 31: Ribosomal protein eL42





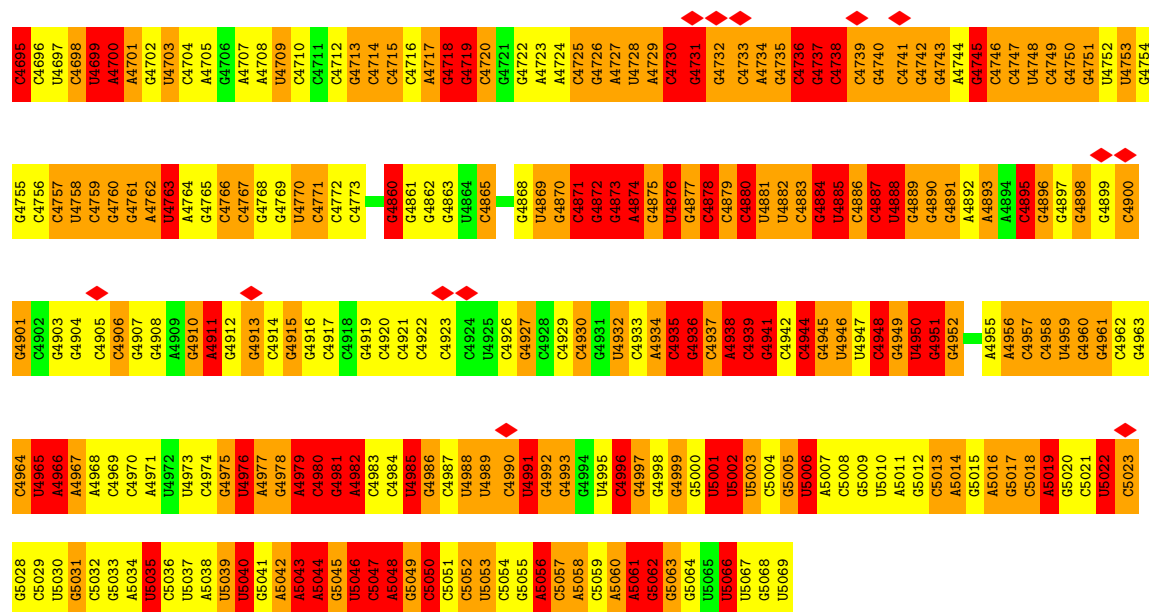
• Molecule 32: 28S ribosomal RNA



G1069	G1070	G1071	G1072	G1073	G1074	G1075	G1076	G1077	G1078	G1079	G1080	G1081	G1082	G1083	G1084	G1085	G1086	G1089	G1090	G1091	G1092	G1093	G1094	G1095	G1096	G1097	G1098	G1099	G1100	G1167	G1168	G1169	G1170	G1171	G1172	G1173	G1174	G1175	G1176	G1177	G1178	G1179	G1180	G1181	G1182	G1183	G1184	G1185	G1186	G1187	G1188	G1189	G1190	G1191	G1192	G1193	G1194	G1195																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
G1196	G1197	G1198	G1199	G1200	G1201	G1202	G1203	G1204	G1205	G1206	G1207	G1208	G1209	G1210	G1211	G1212	G1213	G1214	G1215	G1216	G1217	G1218	G1219	G1220	G1221	G1222	G1223	G1224	G1225	G1226	G1227	G1228	G1229	G1230	G1231	G1232	G1233	G1234	G1235	G1236	G1237	G1238	G1239	G1240	G1241	G1242	G1243	G1244	G1245	G1246	G1247	G1248	G1249	G1250	G1251	G1252	G1253	G1254	G1255	G1256	G1257	G1258	G1259	G1260	G1261	G1262	G1263	G1264																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		

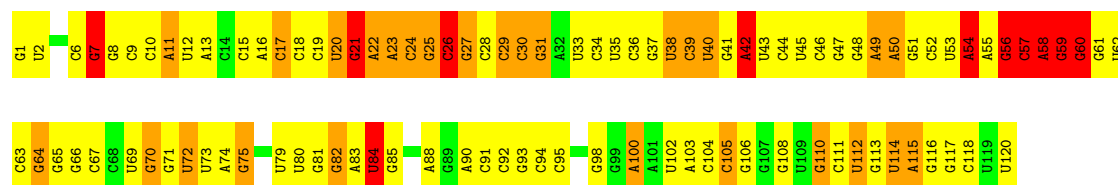
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G3600	G2862	C2802	C2738	A2674	C2613	A2653	G2493	G2433	A2307	C2247	G2076	A2013
C3601	C2863	U2802	C2739	A2675	C2614	G2554	U2494	G2434	A2308	C2248	C2077	C2014
G3603	U2864	U2803	U2740	A2676	G2555	G2556	U2495	G2435	G2309	C2249	C2078	U2015
G3604	U2865	C2804	U2741	G2677	G2556	G2557	G2496	U2436	C2310	C2250	G2079	C2016
A3604	C2866	C2805	G2742	A2678	G2558	C2558	G2498	A2438	C2311	C2251	U2080	A2017
C3605	C2867	A2806	A2743	G2679	G2618	G2559	C2499	G2439	U2312	G2252	C2081	C2018
U3606	U2868	A2807	A2744	G2682	G2619	C2560	U2500	A2439	A2313	G2253	G2082	C2019
U3607	U2869	G2808	A2745	C2683	G2620	C2561	C2501	U2440	A2253	A2254	C2083	U2020
A3608	A2870	C2809	A2746	C2684	A2621	G2562	G2502	G2442	G2316	C2255	C2084	G2021
G3609	A2871	G2811	U2747	C2685	A2622	C2563	C2503	G2443	G2317	C2256	G2085	G2022
C3610	C2872	A2812	C2748	G2686	G2623	G2564	G2504	U2444	C2318	C2257	A2086	A2024
A3611	U2873	A2813	C2749	U2686	G2624	G2565	C2505	C2445	C2319	C2258	A2088	A2025
C3612	U2874	C2814	G2750	U2687	U2625	A2566	G2506	U2446	C2320	G2259	G2089	A2026
U3613	C2875	A2815	G2751	G2688	U2626	G2567	C2507	U2447	G2321	C2260	U2090	U2027
G3614	G2876	G2816	G2752	G2689	C2627	G2568	A2507	U2448	C2322	G2261	C2091	
C3615	A2878	C2817	G2753	C2690	U2628	C2569	G2508	G2449	C2323	G2262	G2092	U2032
U3616	U2879	A2818	U2754	U2691	G2629	G2569	C2509	A2449	C2324	G2263	A2093	A2033
G3617	U2880	U2819	U2755	U2692	U2630	U2570	G2510	G2450	C2325	A2263	G2094	A2034
C3618		C2820	A2756	G2693	U2631	C2571	A2511	A2451	C2326	C2264	A2095	C2035
G3619	G2884	U2821	A2757	G2694	U2632	C2572	A2512	G2452	C2327	G2265	G2096	C2036
C3620	C2889	G2822	G2758	A2695	U2633	A2573	A2513	A2453	C2328	C2266	U2097	C2037
A3621	A2890	C2823	G2759	A2696	C2634	G2574	G2514	U2454	C2329	U2267	G2098	U2038
C3622	C2891	A2824	U2760	A2697	U2635	U2575	G2515	G2455	U2330	A2268	G2099	A2040
G3623	C2892	C2825	U2761	G2698	U2636	U2576	G2516	G2456	C2331	C2269	A2100	A2041
A3624	U2893	U2826	G2762	C2699	U2637	C2577	A2517	G2457	G2332	G2270	C2101	A2042
G3625	G2894	G2827	U2763	G2700	U2638	G2578	G2518	C2458	A2333	C2271	G2102	A2043
C3626	A2894	U2828	A2764	U2701	G2640	G2579	U2519	G2459	C2334	C2272	G2103	U2044
G3627	A2895	U2829	A2765	C2702	A2641	U2580	G2520	A2460	C2335	C2273	G2104	G2045
C3628	G2896	G2830	A2766	G2703	A2642	A2581	G2521	G2461	C2336	G2274	A2105	G2046
A3629	C2897	U2831	U2767	C2704	G2643	A2582	G2522	C2462	C2337	G2275	G2106	A2047
U3630	G2898	A2832	C2768	G2705	G2644	C2583	G2523	G2463	C2338	A2276	G2107	U2048
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C3632	U2900	A2834	C2770	U2707	C2646	G2585	U2525	C2465	C2340	G2278	G2109	G2050
C3633	G2901	C2835	G2771	U2708	A2647	A2586	A2526	G2466	A2341	A2279	G2110	C2051
G3634	C2902	A2836	C2772	C2709	G2648	C2588	G2528	U2468	G2342	G2280	G2111	C2052
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C3636	U2904	G2838	C2774	G2711	C2650	G2590	C2530	C2470	G2344	A2282	G2113	G2055
U3637	C2905	U2839	C2775	G2712	G2651	A2591	C2531	A2471	C2345	G2283	G2114	A2057
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A3642	C2909	U2843	G2779	G2716	U2655	C2595	G2535	G2475	U2349	G2287	G2118	U2061
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G3645	C2847	G2846	C2784	G2721	G2657	C2597	A2537	A2477	U2351	C2289	G2120	G2063
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	U3595	C2860	A2798	G2736	C2672	A2611	A2551	C2491		U2305		
	A3596											
	G3597											
	C3598											

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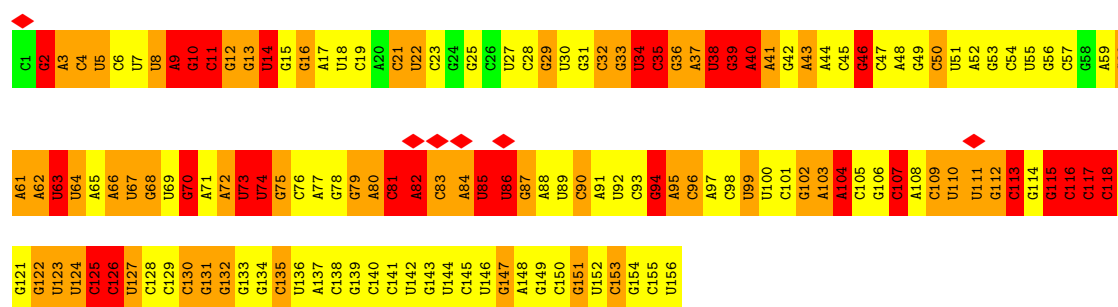
• Molecule 33: 5S ribosomal RNA

Chain 7: 16% 52% 22% 9%



• Molecule 34: 5.8S ribosomal RNA

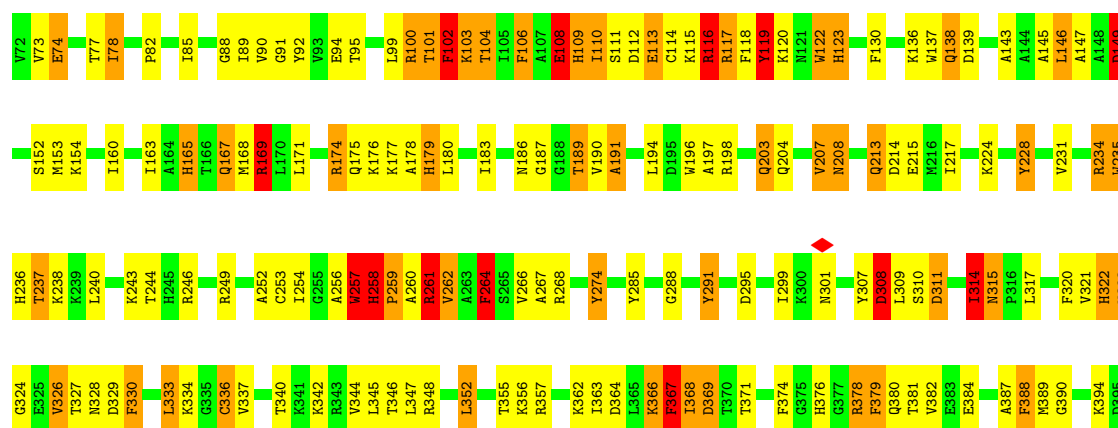
Chain 8: 45% 33% 19%



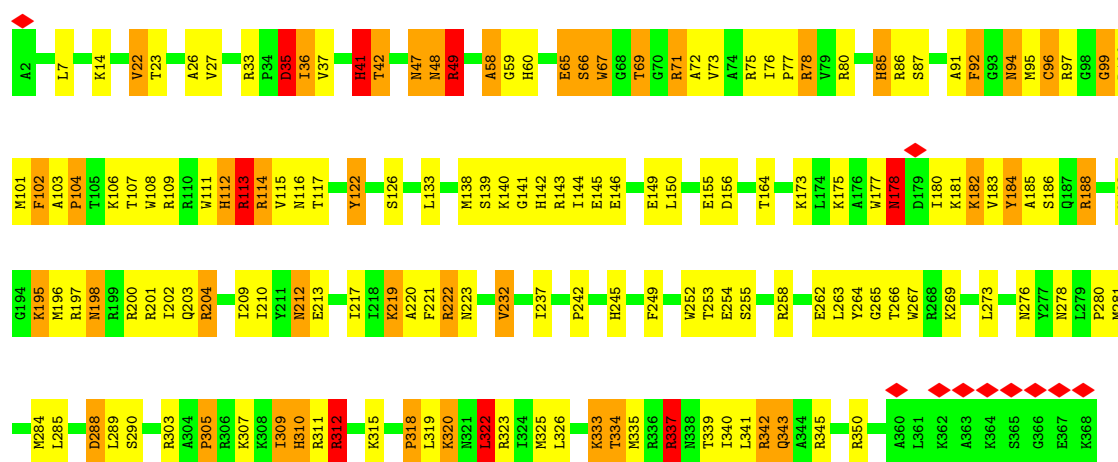
• Molecule 35: Ribosomal protein uL3

Chain B: 46% 34% 15% 5%

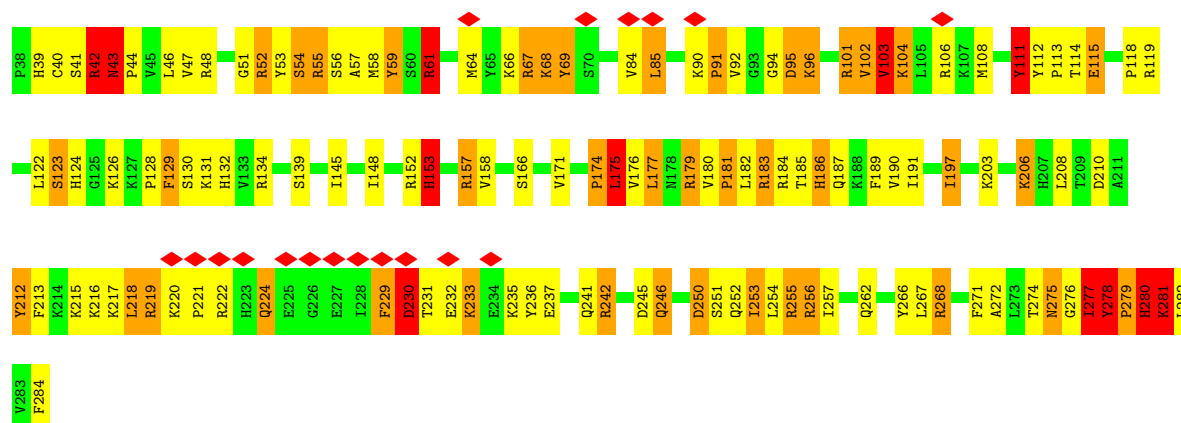
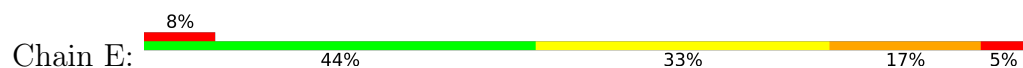




• Molecule 36: Ribosomal protein uL4

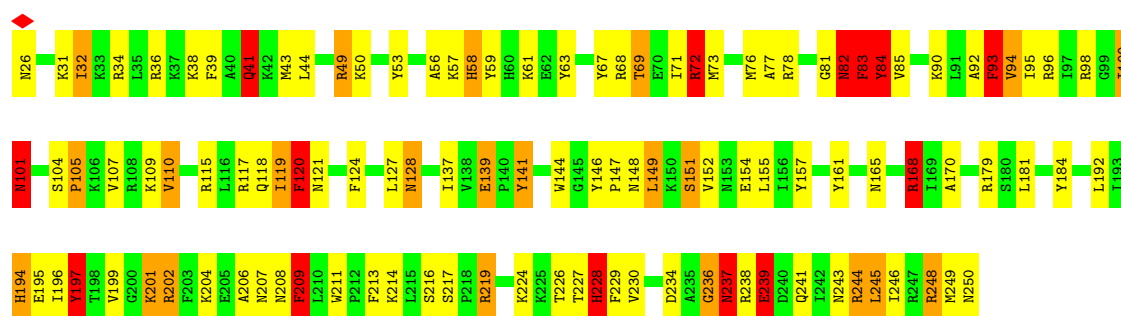


• Molecule 37: Ribosomal protein eL6



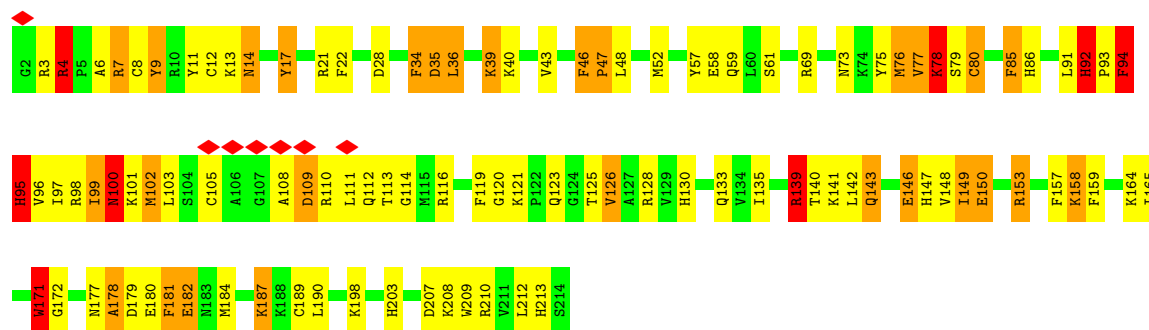
• Molecule 38: Ribosomal protein uL30

Chain F: 



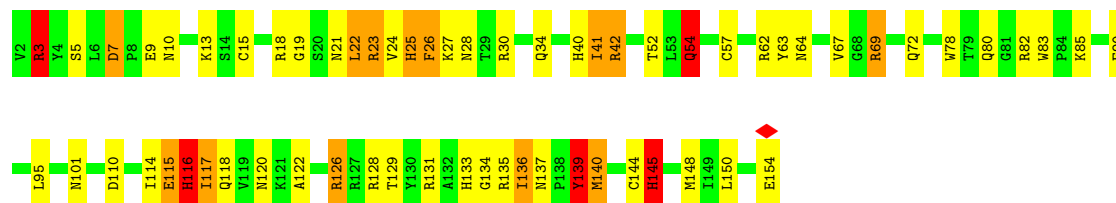
• Molecule 39: Ribosomal protein uL16

Chain I: 



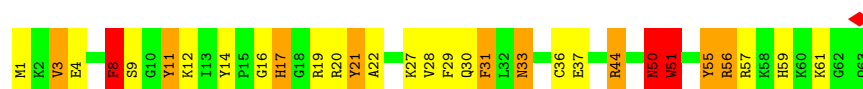
• Molecule 40: Ribosomal protein uL22

Chain P: 



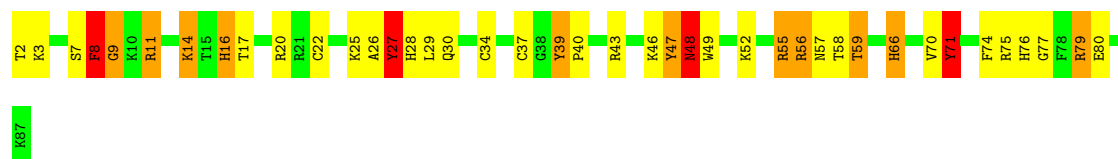
• Molecule 41: Ribosomal protein eL24

Chain W: 

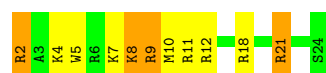


• Molecule 42: Ribosomal protein eL37

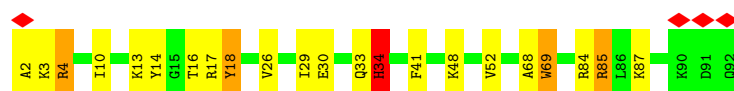
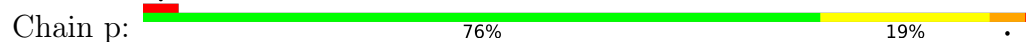
Chain j: 



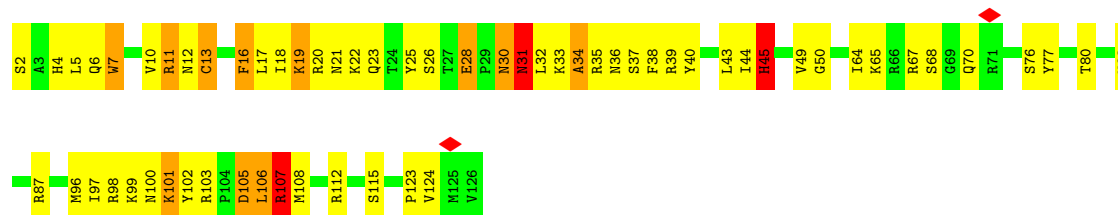
- Molecule 43: Ribosomal protein eL41



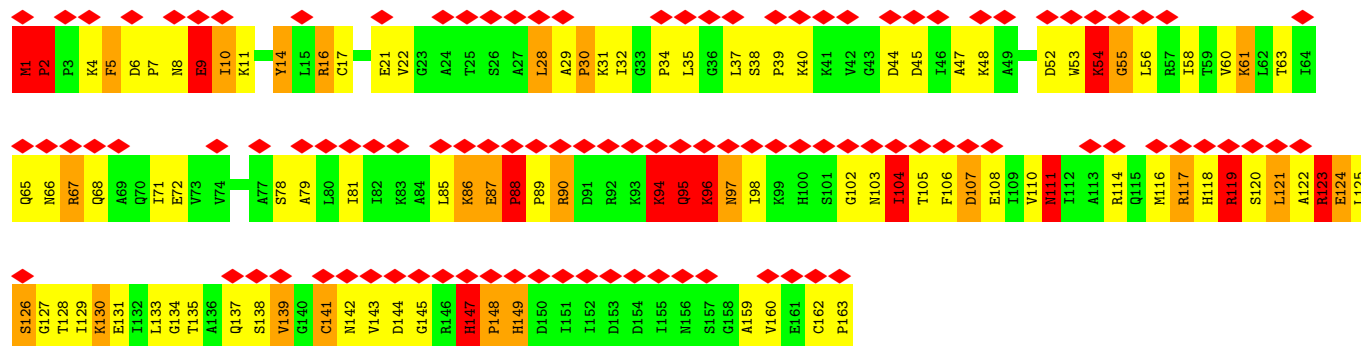
- Molecule 44: Ribosomal protein eL43



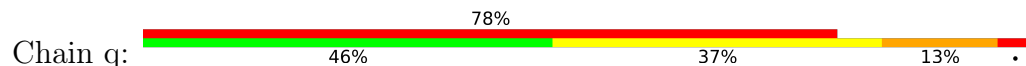
- Molecule 45: Ribosomal protein eL28

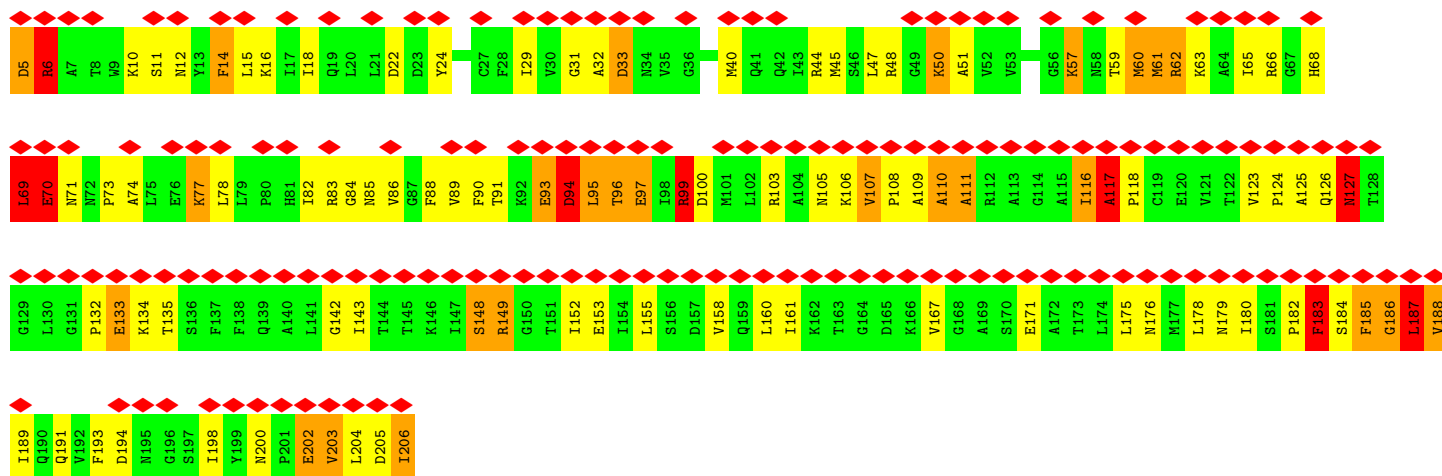


- Molecule 46: Ribosomal protein uL11

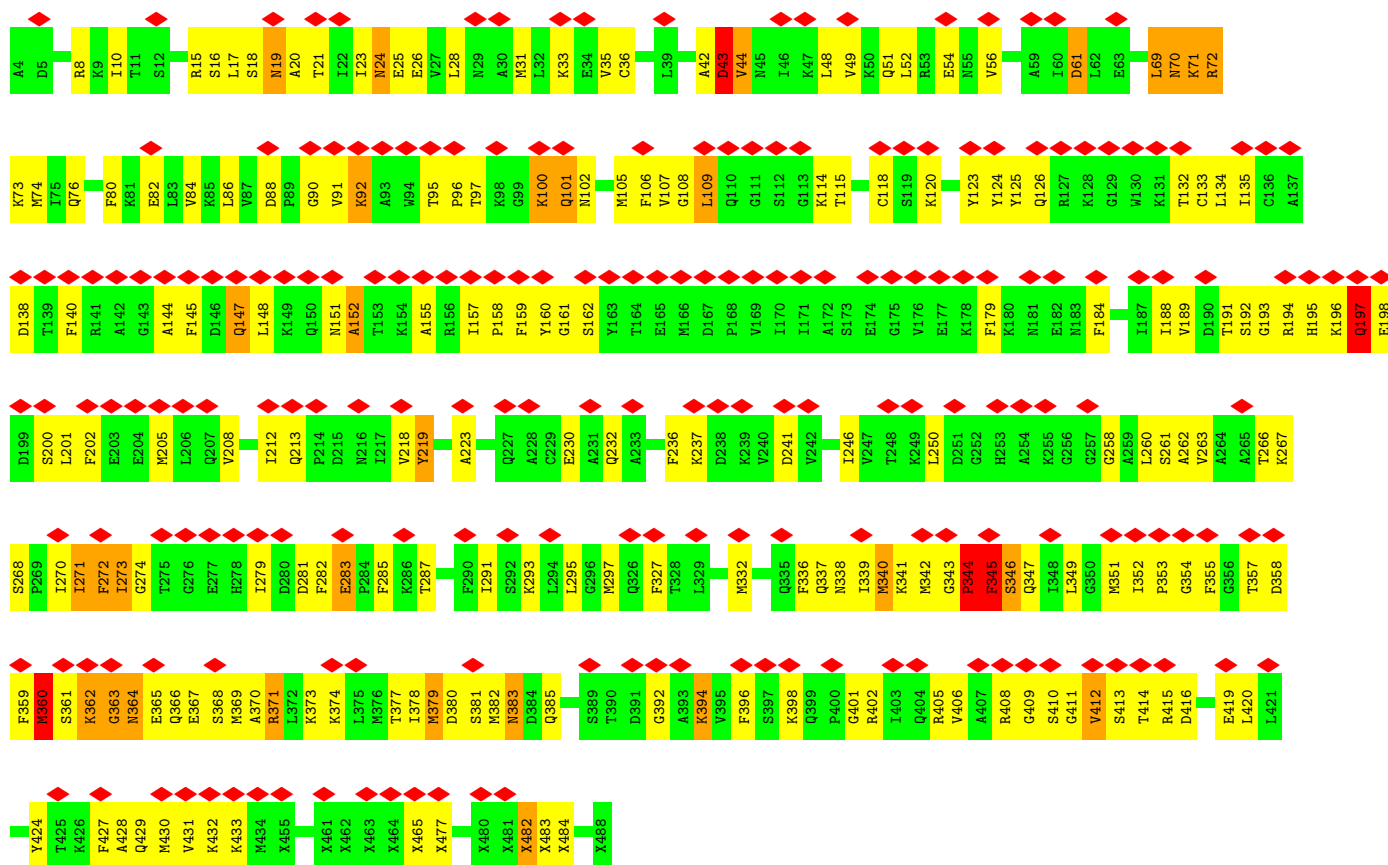


- Molecule 47: Ribosomal protein uL10

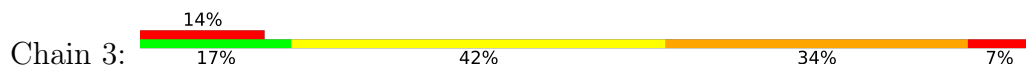




• Molecule 48: SRP54

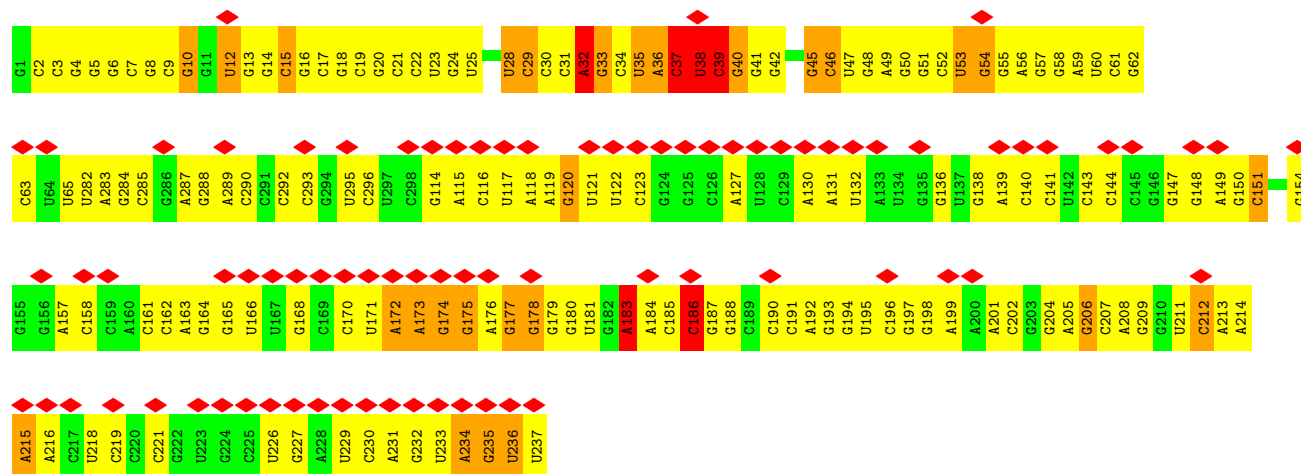


• Molecule 49: Val tRNA

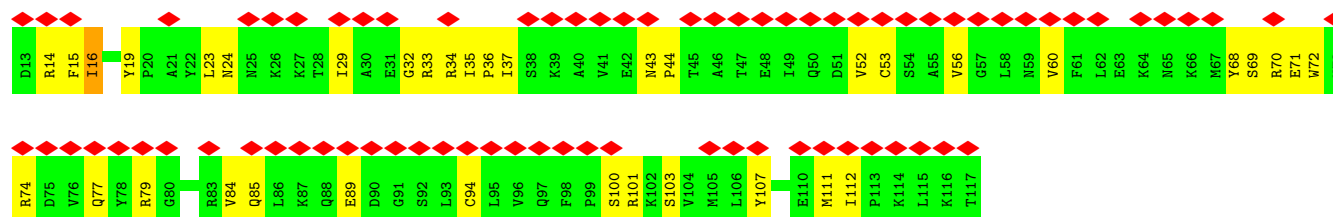




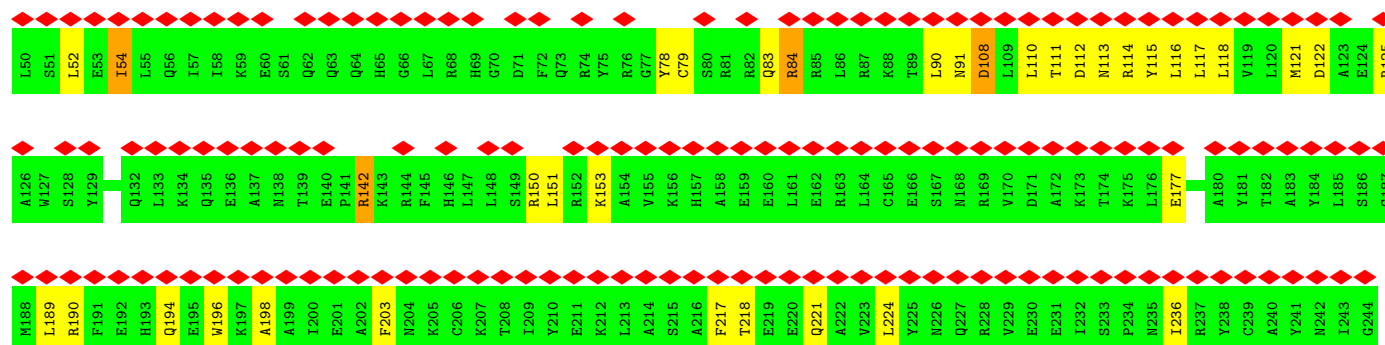
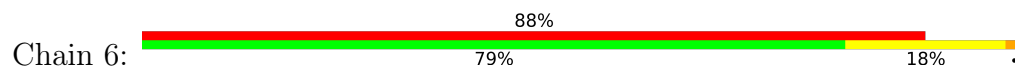
• Molecule 50: SRP 7S RNA



• Molecule 51: SRP19

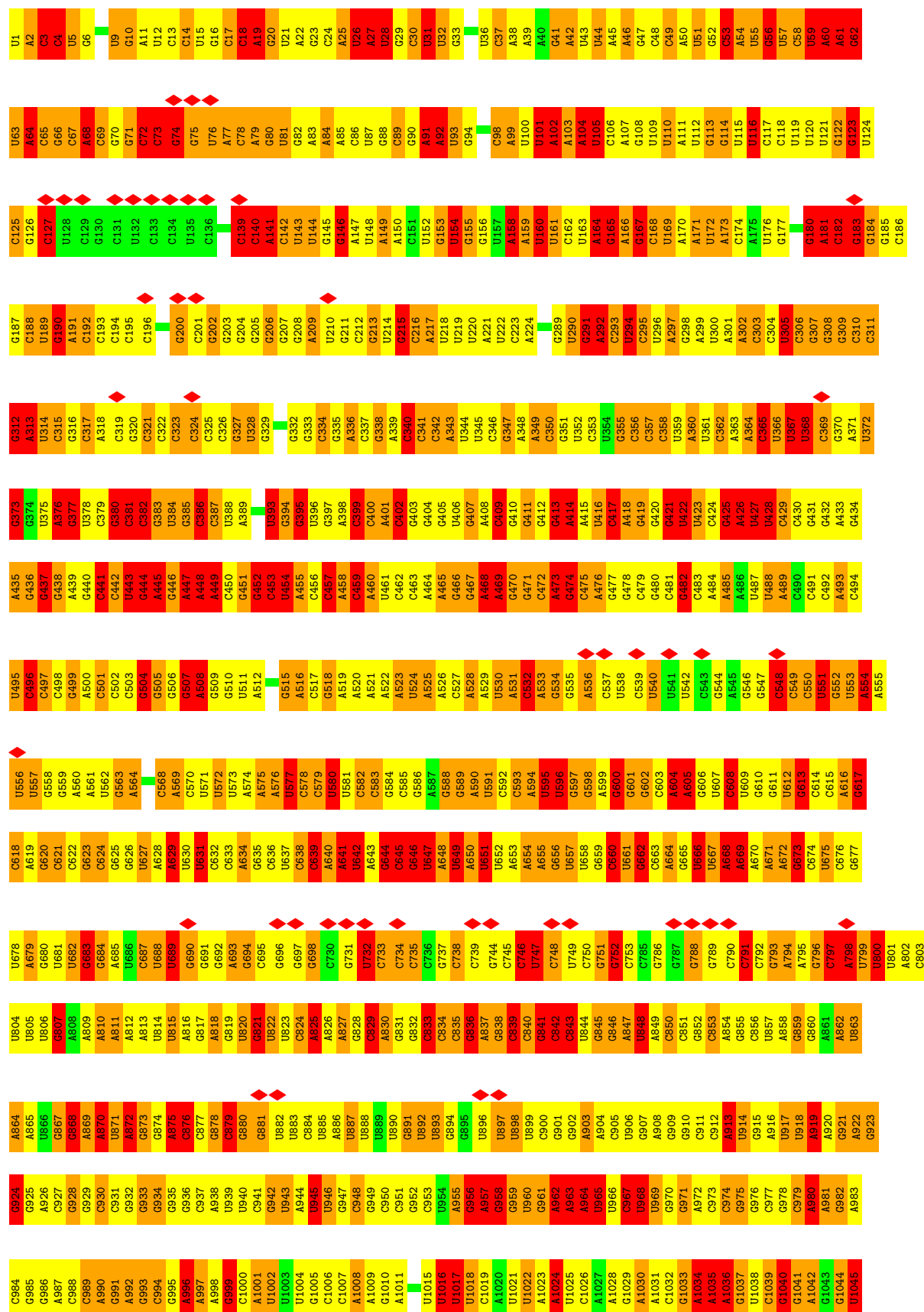


• Molecule 52: SRP68

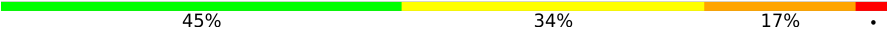


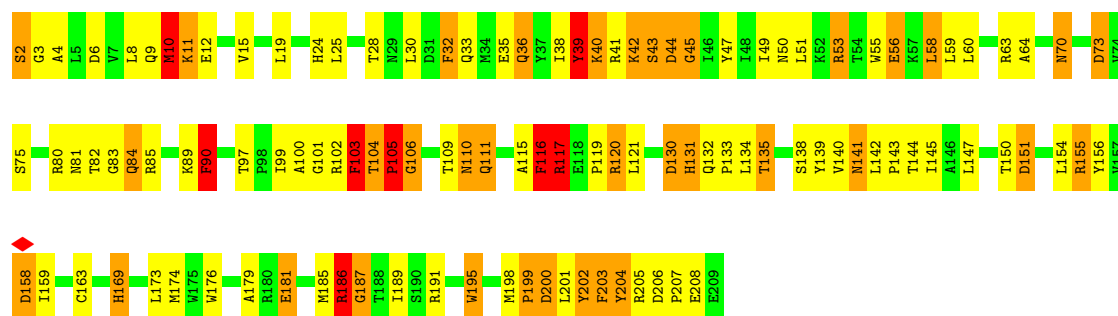
• Molecule 53: 18S ribosomal RNA





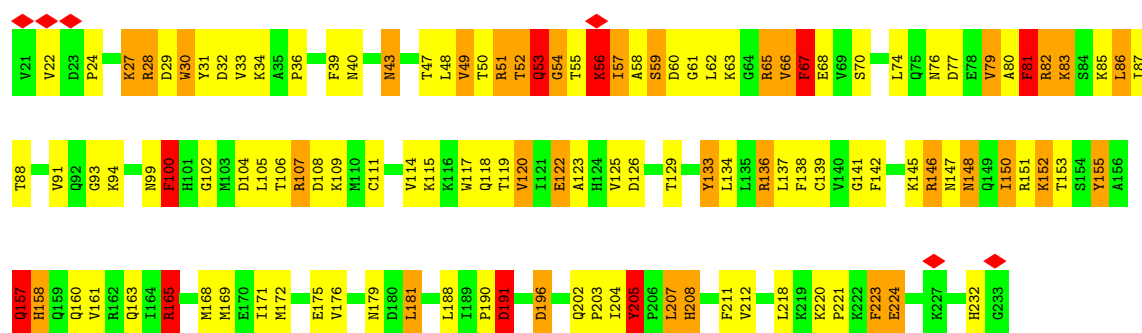


Chain SA: 



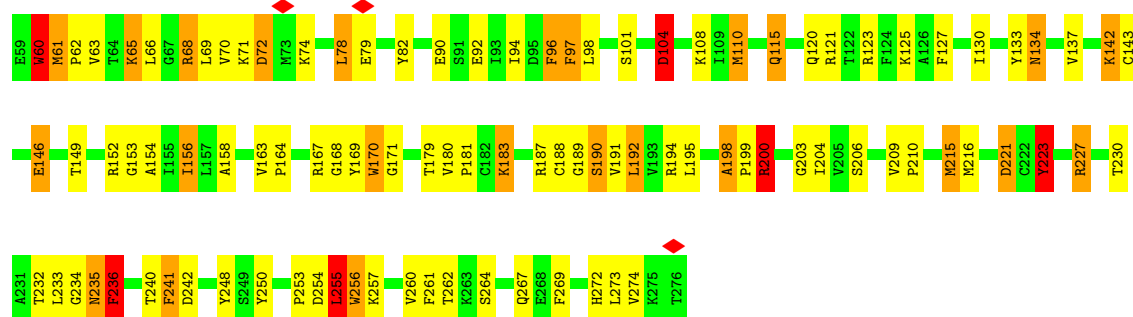
• Molecule 55: Ribosomal protein eS1

Chain SB: 



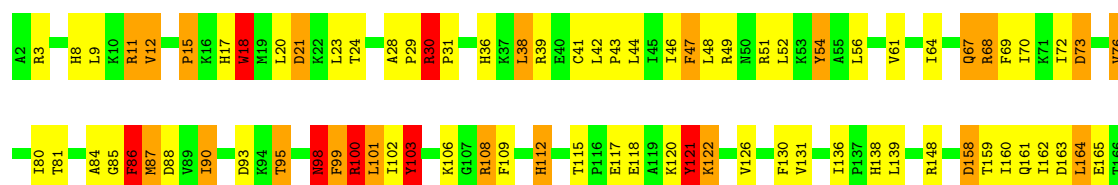
• Molecule 56: Ribosomal protein uS5

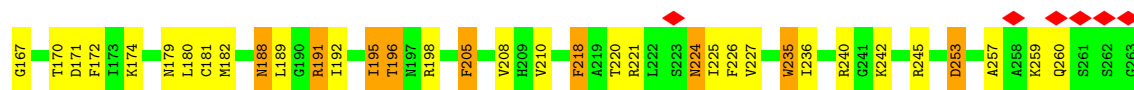
Chain SC: 



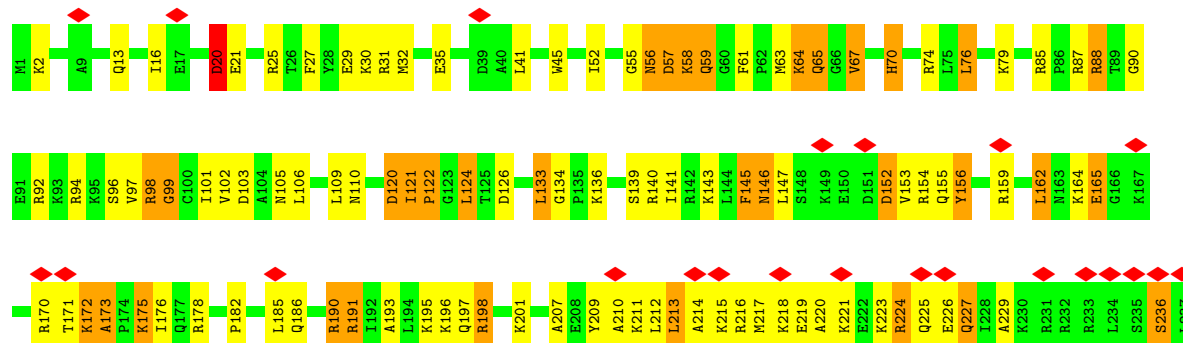
• Molecule 57: Ribosomal protein eS4

Chain SE: 

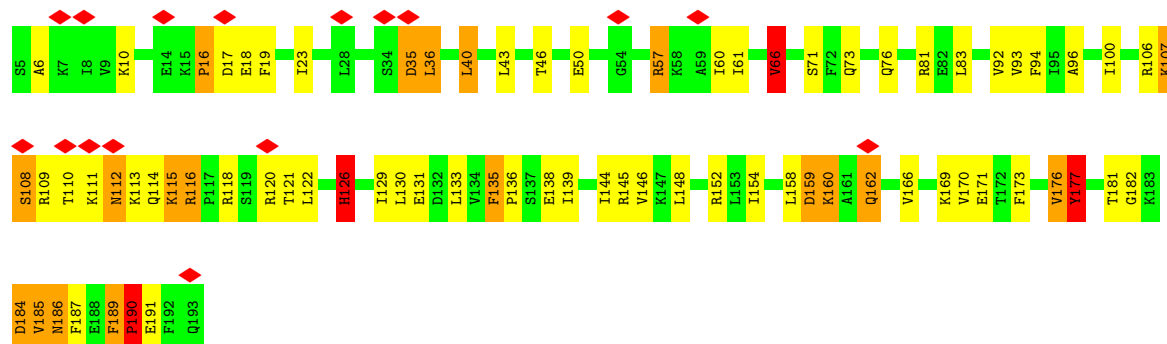




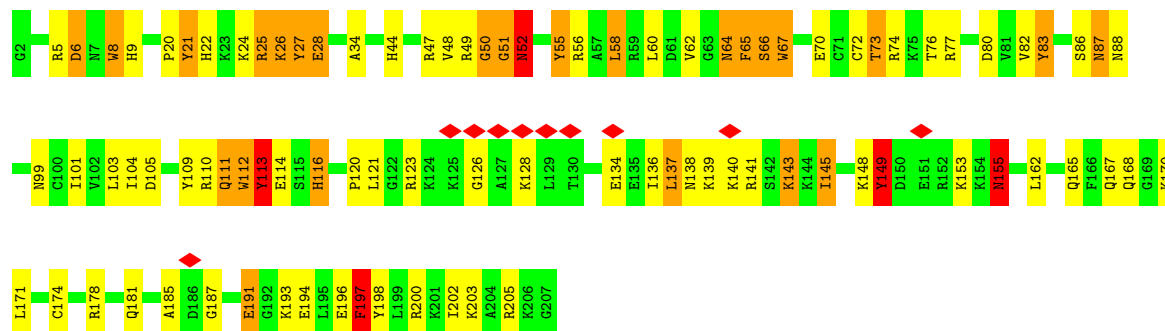
• Molecule 58: Ribosomal protein eS6



• Molecule 59: Ribosomal protein eS7

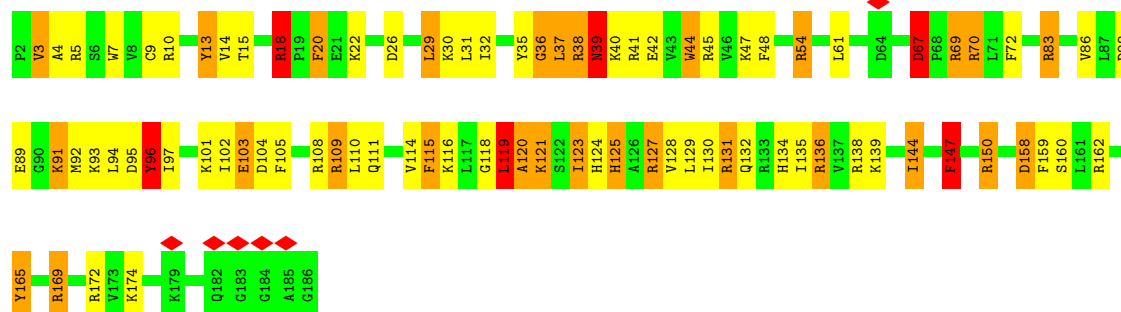


• Molecule 60: Ribosomal protein eS8



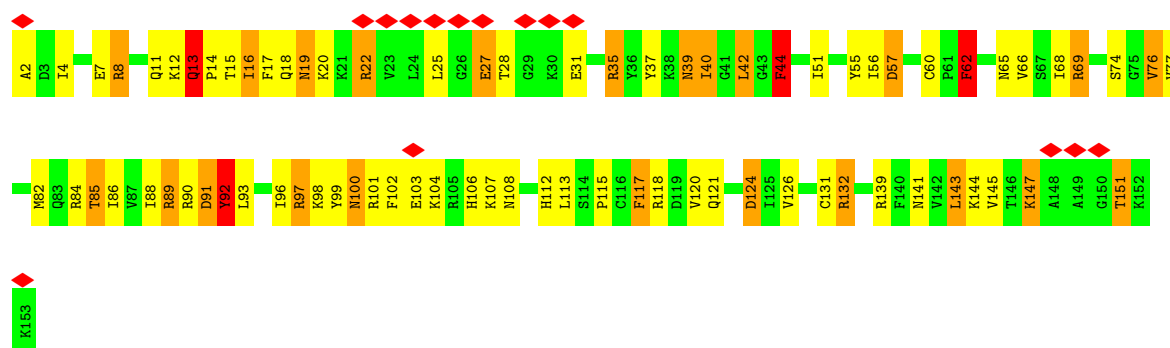
• Molecule 61: Ribosomal protein uS4

Chain SJ:  53% 29% 15% .



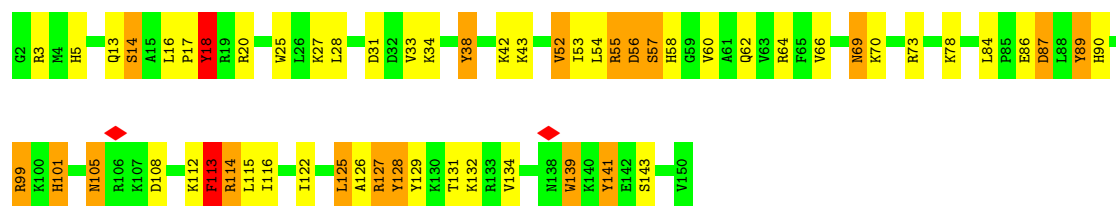
- Molecule 62: Ribosomal protein uS17

Chain SL:  10% 49% 34% 15% .



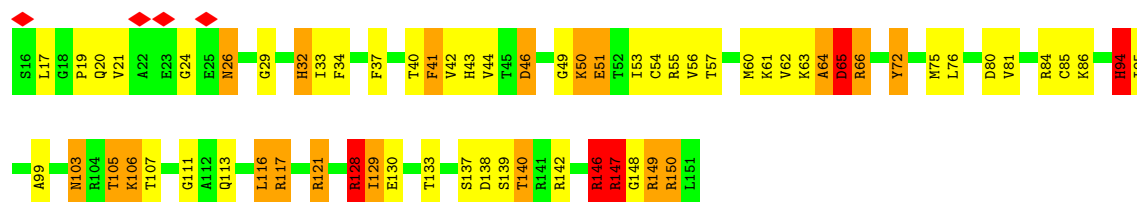
- Molecule 63: Ribosomal protein uS15

Chain SN:  61% 26% 12% .



- Molecule 64: Ribosomal protein uS11

Chain SO:  51% 31% 14% .



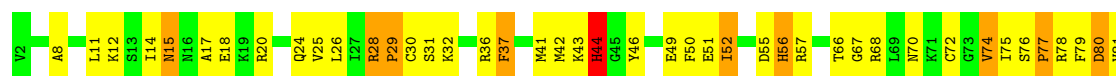
- Molecule 65: Ribosomal protein eS21

Chain SV: 



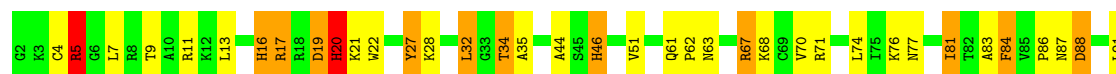
• Molecule 66: Ribosomal protein uS8

Chain SW: 



• Molecule 67: Ribosomal protein uS12

Chain SX: 



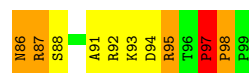
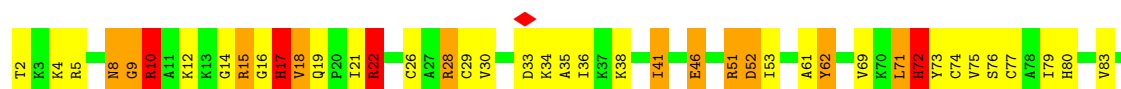
• Molecule 68: Ribosomal protein eS24

Chain SY: 

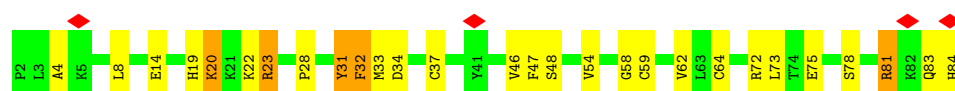


• Molecule 69: Ribosomal protein eS26

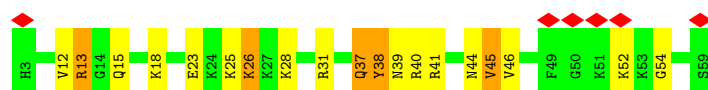
Chain Sa: 



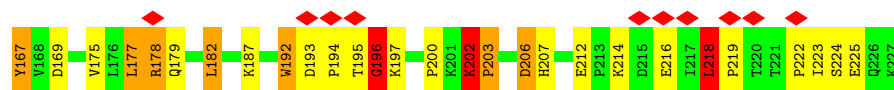
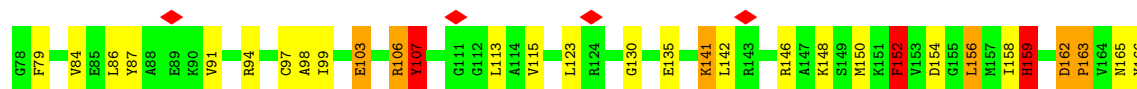
• Molecule 70: Ribosomal protein eS27



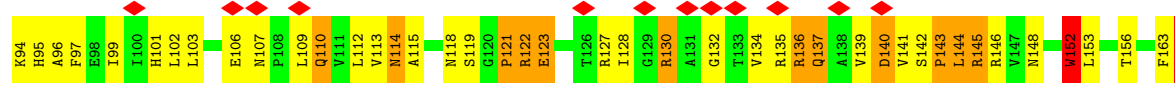
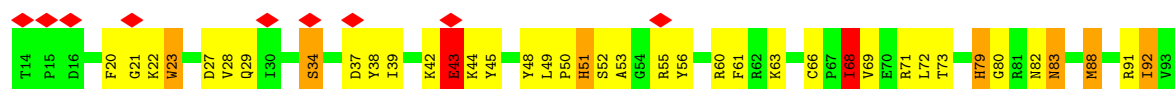
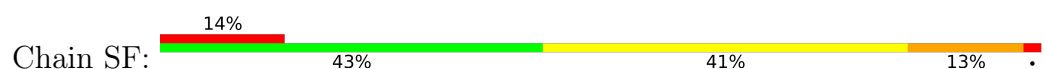
- Molecule 71: Ribosomal protein eS30



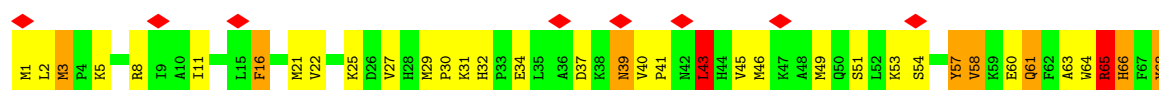
- Molecule 72: Ribosomal protein uS3

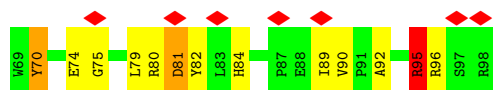


- Molecule 73: Ribosomal protein uS7

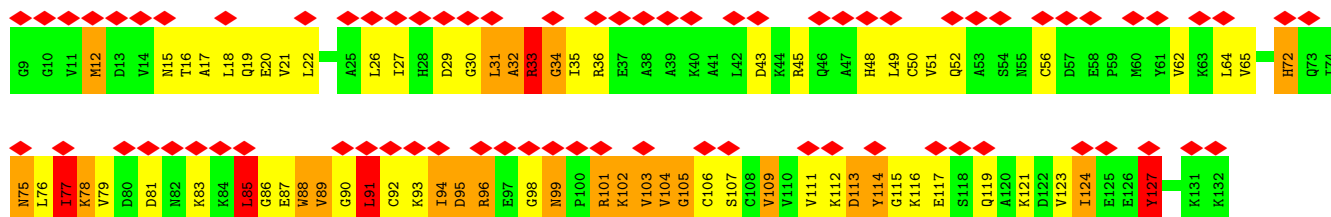


- Molecule 74: Ribosomal protein eS10

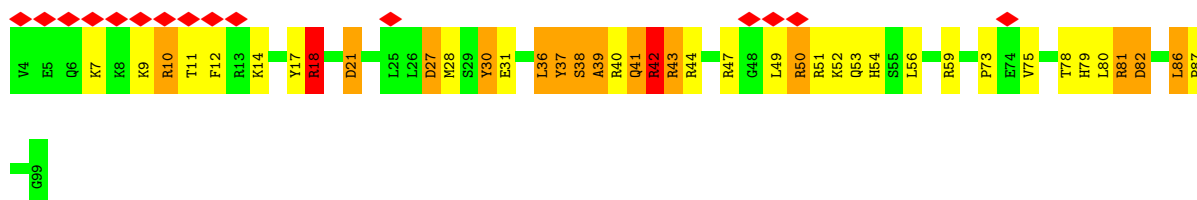




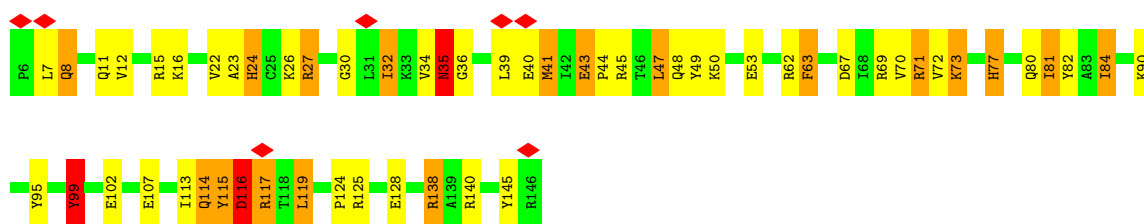
• Molecule 75: Ribosomal protein eS12



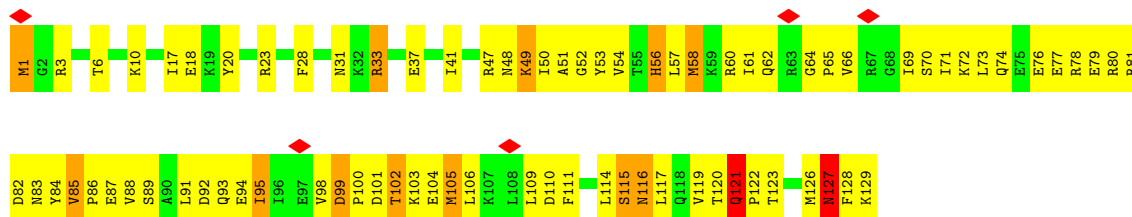
• Molecule 76: Ribosomal protein uS19



• Molecule 77: Ribosomal protein uS9

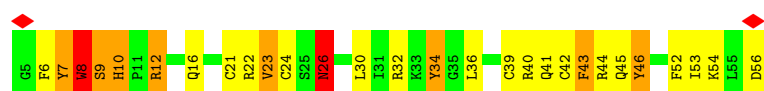


• Molecule 78: Ribosomal protein eS17



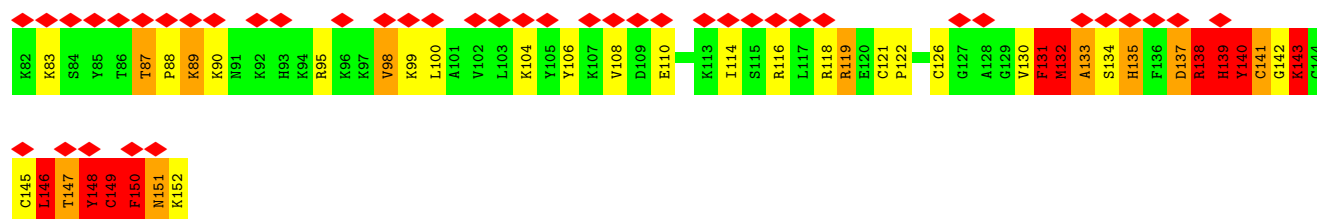
• Molecule 79: Ribosomal protein uS13

Chain Sd: 



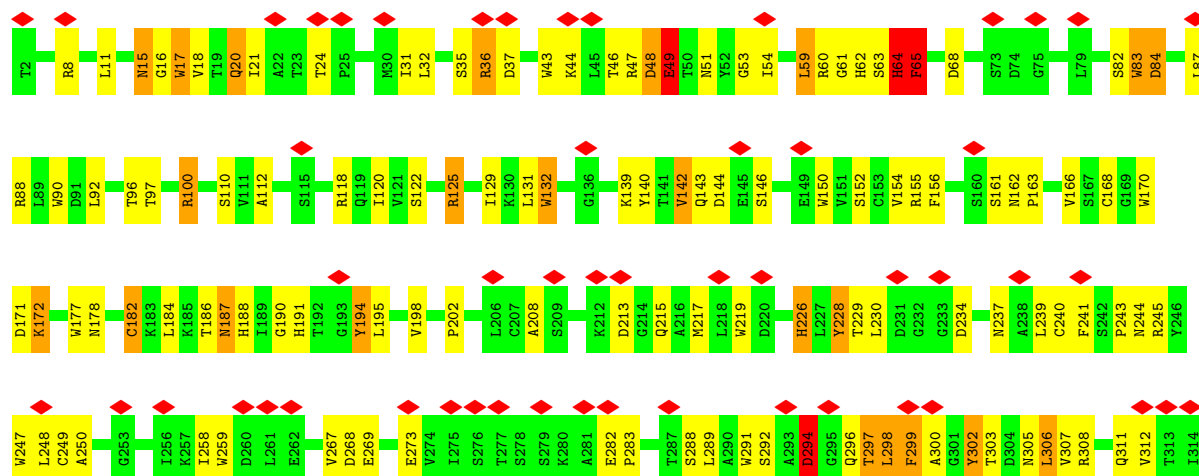
• Molecule 85: Ribosomal protein eS31

Chain Sf: 



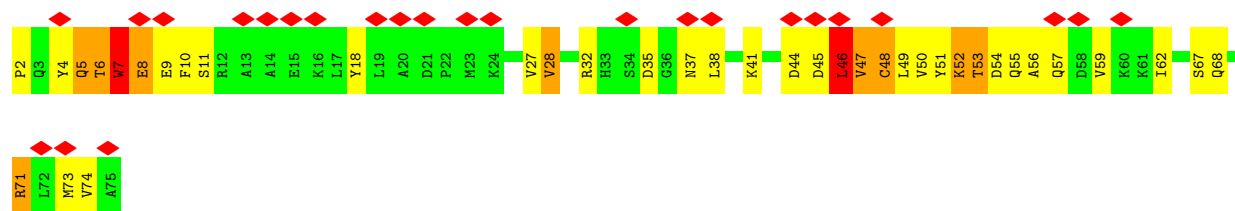
• Molecule 86: Ribosomal protein RACK1

Chain Sg: 



• Molecule 87: SRP9

Chain S1: 



• Molecule 88: SRP14

Chain S4: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	27627	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)	2000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.577	Depositor
Minimum map value	-0.384	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3399999, 1.3399999, 1.3399999	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.99	7/1906 (0.4%)	1.41	29/2556 (1.1%)
2	D	0.91	9/2426 (0.4%)	1.37	31/3252 (1.0%)
3	G	0.96	9/1944 (0.5%)	1.24	16/2618 (0.6%)
4	H	0.83	3/1537 (0.2%)	1.20	10/2066 (0.5%)
5	J	0.79	2/1382 (0.1%)	1.12	8/1849 (0.4%)
6	L	0.81	2/1734 (0.1%)	1.19	7/2318 (0.3%)
7	M	0.80	1/1152 (0.1%)	1.22	8/1539 (0.5%)
8	N	0.93	3/1746 (0.2%)	1.43	25/2338 (1.1%)
9	O	0.83	2/1684 (0.1%)	1.30	15/2251 (0.7%)
10	Q	0.89	6/1530 (0.4%)	1.37	19/2041 (0.9%)
11	R	1.15	3/1524 (0.2%)	1.41	13/2013 (0.6%)
12	S	1.21	10/1493 (0.7%)	1.50	25/2002 (1.2%)
13	T	0.77	2/1326 (0.2%)	1.14	8/1770 (0.5%)
14	U	0.87	3/822 (0.4%)	1.11	2/1103 (0.2%)
15	V	0.78	0/993	1.16	3/1332 (0.2%)
16	X	0.80	0/993	1.15	4/1334 (0.3%)
17	Y	0.87	3/1132 (0.3%)	1.30	16/1504 (1.1%)
18	Z	0.88	3/1130 (0.3%)	1.27	9/1507 (0.6%)
19	a	0.92	7/1192 (0.6%)	1.38	14/1591 (0.9%)
20	b	0.94	1/620 (0.2%)	1.43	8/819 (1.0%)
21	c	0.83	1/742 (0.1%)	1.30	9/996 (0.9%)
22	d	0.92	3/903 (0.3%)	1.32	12/1216 (1.0%)
23	e	0.92	3/1071 (0.3%)	1.31	15/1429 (1.0%)
24	f	1.01	5/895 (0.6%)	1.37	6/1198 (0.5%)
25	g	0.81	0/916	1.25	10/1220 (0.8%)
26	h	0.73	1/1023 (0.1%)	1.22	8/1350 (0.6%)
27	i	0.84	3/843 (0.4%)	1.26	7/1115 (0.6%)
28	k	0.68	0/575	1.07	1/761 (0.1%)
29	l	0.74	0/454	1.21	4/599 (0.7%)
30	m	0.67	0/435	1.13	1/575 (0.2%)
31	o	0.81	2/864 (0.2%)	1.33	12/1140 (1.1%)
32	5	0.58	12/87703 (0.0%)	1.26	1308/136805 (1.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	7	0.53	0/2858	1.13	22/4455 (0.5%)
34	8	0.59	1/3701 (0.0%)	1.27	62/5766 (1.1%)
35	B	0.93	10/3214 (0.3%)	1.26	29/4308 (0.7%)
36	C	0.88	4/2973 (0.1%)	1.23	17/3990 (0.4%)
37	E	0.96	5/1941 (0.3%)	1.35	24/2601 (0.9%)
38	F	0.89	0/1905	1.41	30/2539 (1.2%)
39	I	0.77	2/1753 (0.1%)	1.25	17/2343 (0.7%)
40	P	0.99	4/1268 (0.3%)	1.31	15/1701 (0.9%)
41	W	0.92	1/541 (0.2%)	1.30	3/720 (0.4%)
42	j	0.94	1/721 (0.1%)	1.43	16/953 (1.7%)
43	n	0.96	0/223	1.18	0/284
44	p	0.74	1/718 (0.1%)	1.19	3/953 (0.3%)
45	r	0.79	1/1017 (0.1%)	1.23	9/1365 (0.7%)
46	K	1.22	3/1256 (0.2%)	1.59	19/1694 (1.1%)
47	q	0.97	1/1580 (0.1%)	1.16	8/2133 (0.4%)
48	z	1.26	11/3171 (0.3%)	1.41	13/4257 (0.3%)
49	3	1.29	2/1804 (0.1%)	1.18	12/2805 (0.4%)
50	4	0.61	1/5090 (0.0%)	0.76	6/7936 (0.1%)
51	9	0.45	0/858	0.90	0/1156
52	6	0.38	0/1521	0.80	2/2039 (0.1%)
53	S2	0.59	11/41241 (0.0%)	1.26	593/64249 (0.9%)
54	SA	0.86	2/1679 (0.1%)	1.25	14/2283 (0.6%)
55	SB	0.92	5/1753 (0.3%)	1.30	17/2350 (0.7%)
56	SC	0.84	3/1726 (0.2%)	1.23	15/2332 (0.6%)
57	SE	0.85	5/2118 (0.2%)	1.26	15/2849 (0.5%)
58	SG	0.81	1/1946 (0.1%)	1.17	10/2590 (0.4%)
59	SH	0.70	0/1544	1.13	4/2068 (0.2%)
60	SI	0.97	5/1715 (0.3%)	1.29	14/2287 (0.6%)
61	SJ	0.80	0/1550	1.27	10/2069 (0.5%)
62	SL	0.84	2/1259 (0.2%)	1.25	13/1684 (0.8%)
63	SN	0.82	2/1226 (0.2%)	1.23	11/1649 (0.7%)
64	SO	0.84	0/1029	1.32	7/1380 (0.5%)
65	SV	0.72	0/631	1.08	2/844 (0.2%)
66	SW	0.82	0/1051	1.21	6/1406 (0.4%)
67	SX	0.86	3/1118 (0.3%)	1.18	6/1493 (0.4%)
68	SY	0.75	1/1040 (0.1%)	1.12	5/1382 (0.4%)
69	Sa	0.93	2/794 (0.3%)	1.37	9/1065 (0.8%)
70	Sb	0.71	0/665	1.05	2/891 (0.2%)
71	Se	0.66	0/458	1.05	2/602 (0.3%)
72	SD	0.83	0/1793	1.19	11/2414 (0.5%)
73	SF	0.82	2/1531 (0.1%)	1.25	9/2059 (0.4%)
74	SK	0.83	0/851	1.21	7/1147 (0.6%)
75	SM	1.09	1/970 (0.1%)	1.27	7/1300 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SP	1.16	3/816 (0.4%)	1.20	5/1084 (0.5%)
77	SQ	0.71	0/1142	1.13	6/1528 (0.4%)
78	SR	0.69	0/1060	1.04	4/1421 (0.3%)
79	SS	0.65	0/1157	1.16	5/1548 (0.3%)
80	ST	0.81	2/1119 (0.2%)	1.29	11/1499 (0.7%)
81	SU	0.76	0/828	1.06	2/1112 (0.2%)
82	SZ	0.71	0/604	1.07	0/810
83	Sc	0.75	2/507 (0.4%)	1.01	2/677 (0.3%)
84	Sd	0.87	1/445 (0.2%)	1.20	3/589 (0.5%)
85	Sf	1.39	8/593 (1.3%)	1.68	14/786 (1.8%)
86	Sg	0.76	1/2493 (0.0%)	1.02	9/3394 (0.3%)
87	S1	1.15	5/619 (0.8%)	1.16	5/832 (0.6%)
88	S4	0.78	2/608 (0.3%)	1.00	0/809
All	All	0.73	223/244482 (0.1%)	1.25	2825/358687 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

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

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Mol	Chain	#Chirality outliers	#Planarity outliers
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	173
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	1
45	r	0	3
46	K	0	10
47	q	0	8
48	z	0	7
53	S2	0	59
54	SA	0	5
55	SB	0	7
56	SC	0	7
57	SE	0	6
58	SG	0	1
59	SH	0	2
60	SI	0	9
61	SJ	0	3
62	SL	0	3
63	SN	0	5
64	SO	0	1
65	SV	0	3
66	SW	0	3
67	SX	0	2
68	SY	0	1
69	Sa	0	3
70	Sb	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
72	SD	0	3
73	SF	0	4
74	SK	0	1
75	SM	0	2
76	SP	0	3
77	SQ	0	1
79	SS	0	1
80	ST	0	2
81	SU	0	1
82	SZ	0	1
84	Sd	0	3
85	Sf	0	4
86	Sg	0	3
87	S1	0	4
All	All	0	525

The worst 5 of 223 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	3	31	C	O3'-P	-49.80	0.86	1.61
48	z	340	MET	C-N	41.61	1.86	1.33
50	4	183	A	O3'-P	-35.37	1.08	1.61
48	z	345	PHE	C-N	-29.98	0.91	1.33
32	5	1823	G	O3'-P	28.51	2.04	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	z	340	MET	CA-C-N	-30.44	75.16	120.82
48	z	340	MET	C-N-CA	-30.44	75.16	120.82
48	z	340	MET	O-C-N	29.41	153.86	122.09
49	3	31	C	O3'-P-O5'	-23.73	68.41	104.00
46	K	1	MET	CA-C-N	-18.12	101.72	120.38

There are no chirality outliers.

5 of 525 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	18	ALA	Peptide
1	A	194	ASN	Peptide
1	A	196	TRP	Peptide

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Mol	Chain	Res	Type	Group
1	A	66	PRO	Peptide
1	A	67	TYR	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1868	0	1959	135	0
2	D	2380	0	2412	129	0
3	G	1912	0	2059	95	0
4	H	1518	0	1601	69	0
5	J	1359	0	1390	58	0
6	L	1703	0	1818	75	0
7	M	1131	0	1209	62	0
8	N	1701	0	1749	122	0
9	O	1651	0	1786	68	0
10	Q	1506	0	1623	70	0
11	R	1508	0	1664	115	0
12	S	1454	0	1496	118	0
13	T	1298	0	1366	60	0
14	U	808	0	831	15	0
15	V	979	0	1039	44	0
16	X	976	0	1053	39	0
17	Y	1115	0	1205	51	0
18	Z	1107	0	1182	57	0
19	a	1163	0	1211	82	0
20	b	610	0	650	39	0
21	c	732	0	769	53	0
22	d	888	0	930	52	0
23	e	1053	0	1147	69	0
24	f	876	0	912	48	0
25	g	906	0	1002	43	0
26	h	1015	0	1150	48	0
27	i	832	0	917	26	0
28	k	569	0	637	12	0
29	l	444	0	483	11	0
30	m	429	0	466	17	0
31	o	851	0	923	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	5	78406	0	39609	10946	0
33	7	2558	0	1296	326	0
34	8	3314	0	1683	566	0
35	B	3147	0	3280	203	0
36	C	2919	0	3100	130	0
37	E	1904	0	2055	119	0
38	F	1870	0	1996	131	0
39	I	1713	0	1752	133	0
40	P	1242	0	1269	63	0
41	W	528	0	541	55	0
42	j	706	0	742	41	0
43	n	222	0	258	39	0
44	p	708	0	760	18	0
45	r	1001	0	1062	50	0
46	K	1238	0	1293	99	0
47	q	1556	0	1612	116	0
48	z	3241	0	3210	498	0
49	3	1616	0	824	168	0
50	4	4551	0	2299	450	0
51	9	844	0	861	54	0
52	6	1497	0	1504	25	0
53	S2	36900	0	18593	5342	0
54	SA	1642	0	1646	175	0
55	SB	1725	0	1794	161	0
56	SC	1690	0	1777	77	0
57	SE	2076	0	2177	79	0
58	SG	1923	0	2089	75	0
59	SH	1521	0	1615	93	0
60	SI	1686	0	1772	85	0
61	SJ	1525	0	1640	67	0
62	SL	1238	0	1313	67	0
63	SN	1202	0	1289	62	0
64	SO	1016	0	1037	68	0
65	SV	625	0	628	21	0
66	SW	1034	0	1080	52	0
67	SX	1099	0	1166	47	0
68	SY	1023	0	1090	42	0
69	Sa	781	0	832	60	0
70	Sb	651	0	672	13	0
71	Se	452	0	494	12	0
72	SD	1765	0	1865	66	0
73	SF	1509	0	1563	141	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
74	SK	827	0	854	30	0
75	SM	960	0	989	66	0
76	SP	805	0	861	21	0
77	SQ	1124	0	1193	39	0
78	SR	1047	0	1101	222	0
79	SS	1139	0	1190	146	0
80	ST	1101	0	1135	61	0
81	SU	818	0	883	25	0
82	SZ	598	0	655	128	0
83	Sc	506	0	531	208	0
84	Sd	434	0	427	29	0
85	Sf	581	0	599	199	0
86	Sg	2436	0	2393	89	0
87	S1	608	0	617	32	0
88	S4	604	0	638	16	0
89	5	116	0	0	0	0
89	7	5	0	0	0	0
89	8	6	0	0	0	0
89	D	1	0	0	0	0
89	S2	36	0	0	1	0
89	V	1	0	0	0	0
89	g	1	0	0	0	0
90	Sa	1	0	0	2	0
90	j	1	0	0	2	0
90	m	1	0	0	0	0
90	o	1	0	0	2	0
All	All	227964	0	169843	21978	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 56.

The worst 5 of 21978 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:z:297:MET:HE3	48:z:355:PHE:CD1	1.21	1.70
32:5:294:G:C5'	32:5:296:A:H4'	1.20	1.68
49:3:31:C:H4'	53:S2:1640:A:C2	1.31	1.65
11:R:166:THR:HG21	53:S2:872:A:C3'	1.21	1.64
11:R:172:ARG:HG2	53:S2:909:G:P	1.35	1.61

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	242/244 (99%)	194 (80%)	38 (16%)	10 (4%)	2	19
2	D	290/292 (99%)	228 (79%)	41 (14%)	21 (7%)	1	12
3	G	236/238 (99%)	188 (80%)	41 (17%)	7 (3%)	3	25
4	H	188/190 (99%)	162 (86%)	20 (11%)	6 (3%)	3	24
5	J	168/170 (99%)	126 (75%)	33 (20%)	9 (5%)	1	16
6	L	208/210 (99%)	166 (80%)	29 (14%)	13 (6%)	1	13
7	M	136/138 (99%)	111 (82%)	21 (15%)	4 (3%)	3	25
8	N	201/203 (99%)	159 (79%)	31 (15%)	11 (6%)	1	15
9	O	199/201 (99%)	177 (89%)	19 (10%)	3 (2%)	8	35
10	Q	185/187 (99%)	154 (83%)	24 (13%)	7 (4%)	2	20
11	R	178/180 (99%)	148 (83%)	23 (13%)	7 (4%)	2	20
12	S	173/175 (99%)	139 (80%)	27 (16%)	7 (4%)	2	20
13	T	157/159 (99%)	132 (84%)	20 (13%)	5 (3%)	3	24
14	U	97/99 (98%)	80 (82%)	14 (14%)	3 (3%)	3	24
15	V	129/131 (98%)	110 (85%)	14 (11%)	5 (4%)	2	20
16	X	117/119 (98%)	102 (87%)	12 (10%)	3 (3%)	4	27
17	Y	132/134 (98%)	105 (80%)	21 (16%)	6 (4%)	2	18
18	Z	133/135 (98%)	111 (84%)	15 (11%)	7 (5%)	1	16
19	a	145/147 (99%)	114 (79%)	24 (17%)	7 (5%)	2	17
20	b	73/75 (97%)	60 (82%)	10 (14%)	3 (4%)	2	19
21	c	92/94 (98%)	78 (85%)	10 (11%)	4 (4%)	2	19
22	d	105/107 (98%)	85 (81%)	16 (15%)	4 (4%)	2	20
23	e	126/128 (98%)	110 (87%)	14 (11%)	2 (2%)	7	34
24	f	107/109 (98%)	89 (83%)	11 (10%)	7 (6%)	1	13
25	g	112/114 (98%)	100 (89%)	10 (9%)	2 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	h	120/122 (98%)	97 (81%)	21 (18%)	2 (2%)	7	33
27	i	100/102 (98%)	85 (85%)	13 (13%)	2 (2%)	6	31
28	k	67/69 (97%)	53 (79%)	11 (16%)	3 (4%)	2	18
29	l	48/50 (96%)	42 (88%)	5 (10%)	1 (2%)	5	30
30	m	50/52 (96%)	44 (88%)	6 (12%)	0	100	100
31	o	102/104 (98%)	79 (78%)	17 (17%)	6 (6%)	1	14
35	B	392/394 (100%)	309 (79%)	54 (14%)	29 (7%)	1	11
36	C	365/367 (100%)	292 (80%)	55 (15%)	18 (5%)	1	17
37	E	232/236 (98%)	144 (62%)	55 (24%)	33 (14%)	0	3
38	F	223/225 (99%)	180 (81%)	35 (16%)	8 (4%)	2	21
39	I	211/213 (99%)	170 (81%)	28 (13%)	13 (6%)	1	14
40	P	151/153 (99%)	134 (89%)	15 (10%)	2 (1%)	9	37
41	W	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
42	j	84/86 (98%)	64 (76%)	18 (21%)	2 (2%)	4	28
43	n	21/23 (91%)	20 (95%)	1 (5%)	0	100	100
44	p	89/91 (98%)	75 (84%)	14 (16%)	0	100	100
45	r	123/125 (98%)	96 (78%)	20 (16%)	7 (6%)	1	14
46	K	159/163 (98%)	91 (57%)	34 (21%)	34 (21%)	0	1
47	q	200/202 (99%)	141 (70%)	31 (16%)	28 (14%)	0	3
48	z	399/426 (94%)	348 (87%)	30 (8%)	21 (5%)	1	16
51	9	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
52	6	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
54	SA	206/208 (99%)	163 (79%)	29 (14%)	14 (7%)	1	12
55	SB	211/213 (99%)	154 (73%)	36 (17%)	21 (10%)	0	7
56	SC	216/218 (99%)	182 (84%)	27 (12%)	7 (3%)	3	24
57	SE	260/262 (99%)	198 (76%)	44 (17%)	18 (7%)	1	12
58	SG	235/237 (99%)	195 (83%)	32 (14%)	8 (3%)	3	23
59	SH	187/189 (99%)	140 (75%)	30 (16%)	17 (9%)	0	8
60	SI	204/206 (99%)	165 (81%)	30 (15%)	9 (4%)	2	19
61	SJ	183/185 (99%)	134 (73%)	34 (19%)	15 (8%)	0	9
62	SL	150/152 (99%)	122 (81%)	22 (15%)	6 (4%)	2	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	SN	147/149 (99%)	115 (78%)	28 (19%)	4 (3%)	4	26
64	SO	134/136 (98%)	99 (74%)	21 (16%)	14 (10%)	0	6
65	SV	80/82 (98%)	58 (72%)	15 (19%)	7 (9%)	0	8
66	SW	127/129 (98%)	108 (85%)	16 (13%)	3 (2%)	4	28
67	SX	139/141 (99%)	109 (78%)	26 (19%)	4 (3%)	3	25
68	SY	124/126 (98%)	101 (82%)	16 (13%)	7 (6%)	1	15
69	Sa	96/98 (98%)	69 (72%)	18 (19%)	9 (9%)	0	8
70	Sb	81/83 (98%)	61 (75%)	16 (20%)	4 (5%)	1	17
71	Se	55/57 (96%)	41 (74%)	12 (22%)	2 (4%)	2	21
72	SD	225/227 (99%)	174 (77%)	41 (18%)	10 (4%)	2	19
73	SF	189/191 (99%)	146 (77%)	33 (18%)	10 (5%)	1	16
74	SK	96/98 (98%)	58 (60%)	26 (27%)	12 (12%)	0	4
75	SM	122/124 (98%)	78 (64%)	24 (20%)	20 (16%)	0	2
76	SP	94/96 (98%)	67 (71%)	17 (18%)	10 (11%)	0	6
77	SQ	139/141 (99%)	111 (80%)	20 (14%)	8 (6%)	1	14
78	SR	127/129 (98%)	111 (87%)	11 (9%)	5 (4%)	2	20
79	SS	135/137 (98%)	114 (84%)	12 (9%)	9 (7%)	1	13
80	ST	139/141 (99%)	115 (83%)	18 (13%)	6 (4%)	2	19
81	SU	102/104 (98%)	83 (81%)	13 (13%)	6 (6%)	1	14
82	SZ	73/75 (97%)	59 (81%)	9 (12%)	5 (7%)	1	12
83	Sc	60/64 (94%)	47 (78%)	12 (20%)	1 (2%)	7	33
84	Sd	50/52 (96%)	36 (72%)	11 (22%)	3 (6%)	1	14
85	Sf	69/71 (97%)	42 (61%)	15 (22%)	12 (17%)	0	2
86	Sg	311/313 (99%)	240 (77%)	56 (18%)	15 (5%)	2	17
87	S1	72/74 (97%)	61 (85%)	6 (8%)	5 (7%)	1	12
88	S4	72/76 (95%)	68 (94%)	4 (6%)	0	100	100
All	All	12314/12513 (98%)	9837 (80%)	1799 (15%)	678 (6%)	2	15

5 of 678 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	HIS
1	A	196	TRP

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

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	187/187 (100%)	136 (73%)	51 (27%)	0	3
2	D	246/247 (100%)	182 (74%)	64 (26%)	0	4
3	G	204/206 (99%)	151 (74%)	53 (26%)	0	4
4	H	169/169 (100%)	129 (76%)	40 (24%)	1	5
5	J	143/143 (100%)	108 (76%)	35 (24%)	1	4
6	L	176/176 (100%)	138 (78%)	38 (22%)	1	6
7	M	116/116 (100%)	90 (78%)	26 (22%)	1	6
8	N	171/171 (100%)	130 (76%)	41 (24%)	1	5
9	O	172/172 (100%)	143 (83%)	29 (17%)	2	13
10	Q	163/163 (100%)	126 (77%)	37 (23%)	1	5
11	R	159/159 (100%)	117 (74%)	42 (26%)	0	3
12	S	156/156 (100%)	126 (81%)	30 (19%)	1	9
13	T	139/139 (100%)	110 (79%)	29 (21%)	1	7
14	U	89/89 (100%)	69 (78%)	20 (22%)	1	6
15	V	101/101 (100%)	77 (76%)	24 (24%)	1	5
16	X	107/107 (100%)	89 (83%)	18 (17%)	2	13
17	Y	124/124 (100%)	94 (76%)	30 (24%)	1	5
18	Z	117/117 (100%)	92 (79%)	25 (21%)	1	6
19	a	119/119 (100%)	97 (82%)	22 (18%)	1	11
20	b	63/63 (100%)	48 (76%)	15 (24%)	1	5
21	c	79/79 (100%)	61 (77%)	18 (23%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	d	98/98 (100%)	66 (67%)	32 (33%)	0	1
23	e	114/114 (100%)	88 (77%)	26 (23%)	1	5
24	f	88/88 (100%)	72 (82%)	16 (18%)	2	12
25	g	98/98 (100%)	78 (80%)	20 (20%)	1	8
26	h	109/109 (100%)	89 (82%)	20 (18%)	2	11
27	i	86/86 (100%)	69 (80%)	17 (20%)	1	8
28	k	64/64 (100%)	53 (83%)	11 (17%)	2	12
29	l	47/47 (100%)	38 (81%)	9 (19%)	1	10
30	m	48/48 (100%)	33 (69%)	15 (31%)	0	1
31	o	92/92 (100%)	70 (76%)	22 (24%)	1	5
35	B	335/335 (100%)	256 (76%)	79 (24%)	1	5
36	C	305/305 (100%)	233 (76%)	72 (24%)	1	5
37	E	209/209 (100%)	159 (76%)	50 (24%)	1	5
38	F	194/194 (100%)	147 (76%)	47 (24%)	1	5
39	I	180/180 (100%)	132 (73%)	48 (27%)	0	3
40	P	134/134 (100%)	109 (81%)	25 (19%)	1	10
41	W	55/55 (100%)	40 (73%)	15 (27%)	0	3
42	j	73/73 (100%)	62 (85%)	11 (15%)	3	16
43	n	22/22 (100%)	17 (77%)	5 (23%)	1	5
44	p	74/74 (100%)	64 (86%)	10 (14%)	4	18
45	r	109/109 (100%)	90 (83%)	19 (17%)	2	12
46	K	136/136 (100%)	115 (85%)	21 (15%)	2	15
47	q	170/170 (100%)	134 (79%)	36 (21%)	1	7
48	z	340/340 (100%)	318 (94%)	22 (6%)	15	41
51	9	92/94 (98%)	87 (95%)	5 (5%)	20	45
52	6	157/157 (100%)	151 (96%)	6 (4%)	29	52
54	SA	174/174 (100%)	130 (75%)	44 (25%)	0	4
55	SB	194/194 (100%)	155 (80%)	39 (20%)	1	8
56	SC	184/184 (100%)	147 (80%)	37 (20%)	1	8
57	SE	224/224 (100%)	173 (77%)	51 (23%)	1	5
58	SG	207/207 (100%)	158 (76%)	49 (24%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	SH	169/169 (100%)	145 (86%)	24 (14%)	3	17
60	SI	178/178 (100%)	148 (83%)	30 (17%)	2	13
61	SJ	161/161 (100%)	116 (72%)	45 (28%)	0	2
62	SL	136/136 (100%)	100 (74%)	36 (26%)	0	3
63	SN	130/130 (100%)	100 (77%)	30 (23%)	1	5
64	SO	106/106 (100%)	74 (70%)	32 (30%)	0	2
65	SV	66/66 (100%)	52 (79%)	14 (21%)	1	7
66	SW	112/112 (100%)	89 (80%)	23 (20%)	1	8
67	SX	113/113 (100%)	99 (88%)	14 (12%)	4	21
68	SY	108/108 (100%)	83 (77%)	25 (23%)	1	5
69	Sa	85/85 (100%)	73 (86%)	12 (14%)	3	18
70	Sb	75/75 (100%)	62 (83%)	13 (17%)	2	12
71	Se	46/46 (100%)	34 (74%)	12 (26%)	0	4
72	SD	190/190 (100%)	145 (76%)	45 (24%)	1	5
73	SF	161/161 (100%)	120 (74%)	41 (26%)	0	4
74	SK	89/89 (100%)	68 (76%)	21 (24%)	1	5
75	SM	104/104 (100%)	75 (72%)	29 (28%)	0	2
76	SP	88/88 (100%)	71 (81%)	17 (19%)	1	9
77	SQ	117/117 (100%)	91 (78%)	26 (22%)	1	6
78	SR	117/117 (100%)	102 (87%)	15 (13%)	4	20
79	SS	119/119 (100%)	101 (85%)	18 (15%)	3	16
80	ST	112/112 (100%)	82 (73%)	30 (27%)	0	3
81	SU	94/94 (100%)	79 (84%)	15 (16%)	2	14
82	SZ	66/66 (100%)	56 (85%)	10 (15%)	3	16
83	Sc	57/57 (100%)	45 (79%)	12 (21%)	1	7
84	Sd	45/45 (100%)	31 (69%)	14 (31%)	0	1
85	Sf	64/64 (100%)	44 (69%)	20 (31%)	0	1
86	Sg	272/272 (100%)	236 (87%)	36 (13%)	4	19
87	S1	67/67 (100%)	54 (81%)	13 (19%)	1	9
88	S4	69/69 (100%)	59 (86%)	10 (14%)	3	17
All	All	10728/10733 (100%)	8480 (79%)	2248 (21%)	3	7

5 of 2248 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
70	Sb	20	LYS
72	SD	165	ASN
69	Sa	95	ARG
79	SS	87	GLN
25	g	93	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 296 such sidechains are listed below:

Mol	Chain	Res	Type
68	SY	94	HIS
85	Sf	111	ASN
72	SD	4	GLN
77	SQ	142	GLN
26	h	68	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	5	3646/3658 (99%)	1720 (47%)	665 (18%)
33	7	119/120 (99%)	39 (32%)	13 (10%)
34	8	155/156 (99%)	65 (41%)	29 (18%)
49	3	74/76 (97%)	30 (40%)	5 (6%)
50	4	197/206 (95%)	45 (22%)	10 (5%)
53	S2	1715/1742 (98%)	861 (50%)	303 (17%)
All	All	5906/5958 (99%)	2760 (46%)	1025 (17%)

5 of 2760 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 1025 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	S2	1355	C

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Mol	Chain	Res	Type
53	S2	1452	A
53	S2	1352	G
32	5	2517	A
32	5	2470	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
53	S2	6
48	z	5
50	4	3

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Mol	Chain	Number of breaks
49	3	3
46	K	2
37	E	1
88	S4	1
52	6	1
83	Sc	1
11	R	1

The worst 5 of 40 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	141.53
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
1	S2	698:G	O3'	730:C	P	20.30

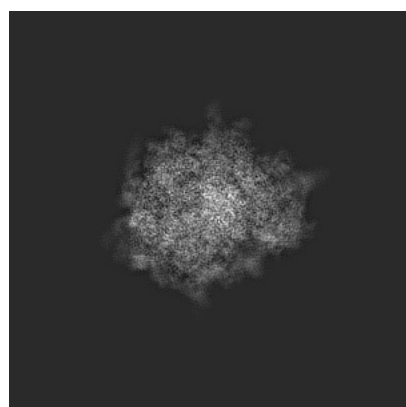
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3045. These allow visual inspection of the internal detail of the map and identification of artifacts.

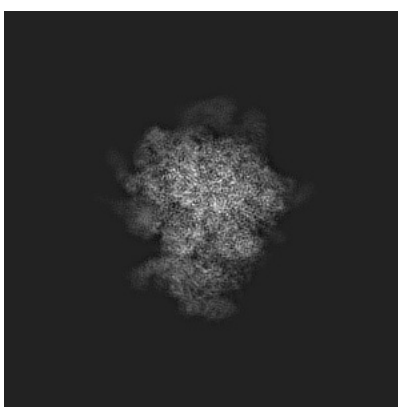
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

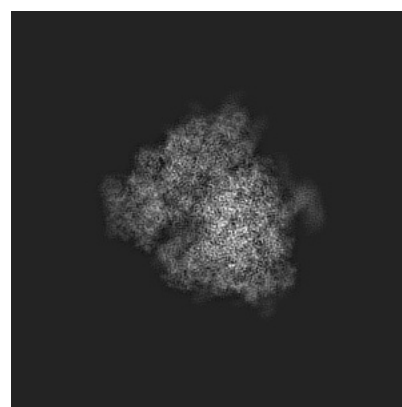
6.1.1 Primary map



X



Y

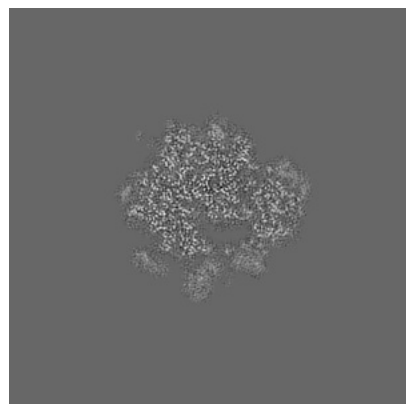


Z

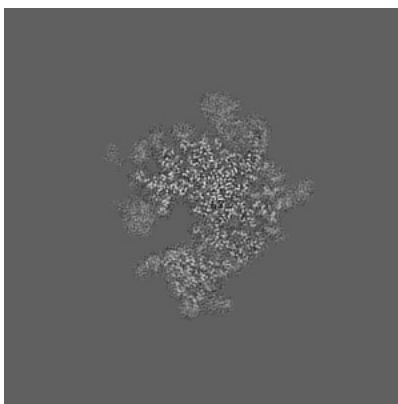
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

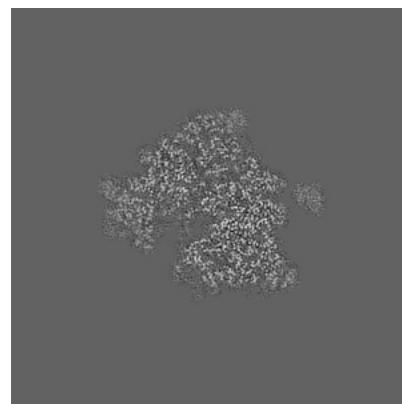
6.2.1 Primary map



X Index: 210



Y Index: 210

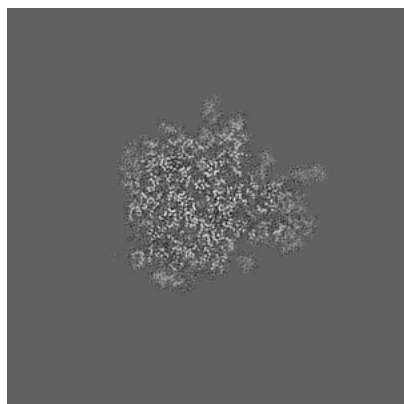


Z Index: 210

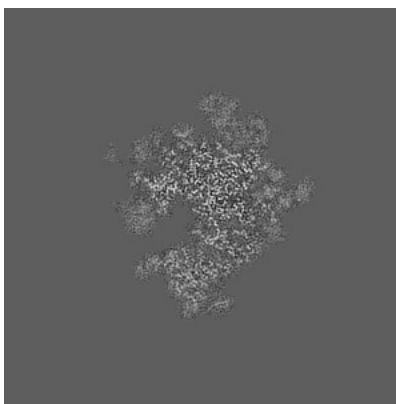
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

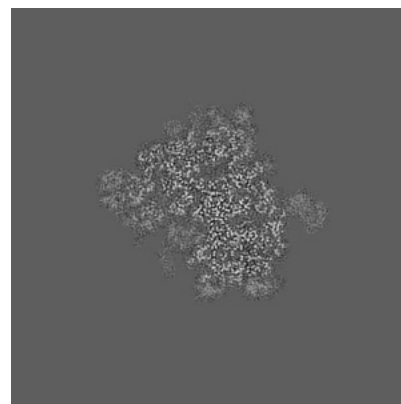
6.3.1 Primary map



X Index: 230



Y Index: 211

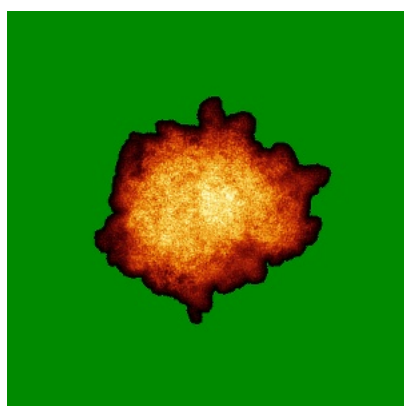


Z Index: 227

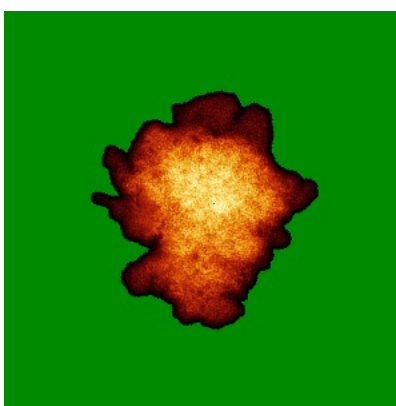
The images above show the largest variance slices of the map in three orthogonal directions.

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

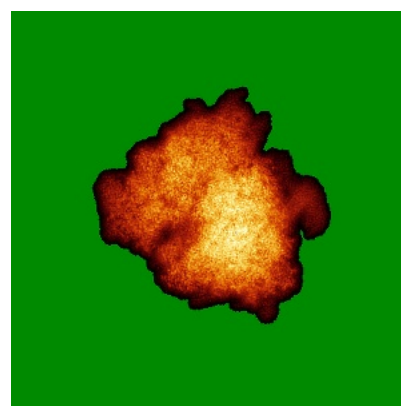
6.4.1 Primary map



X



Y

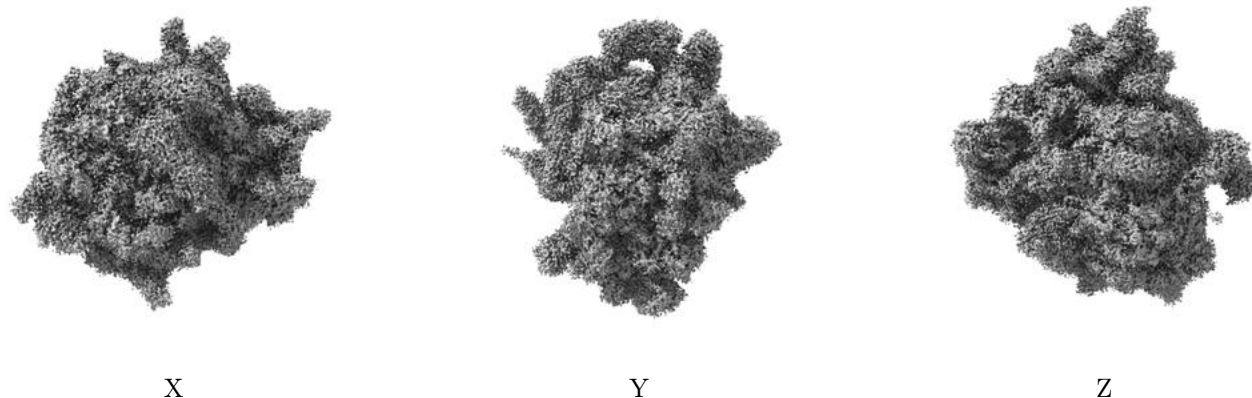


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

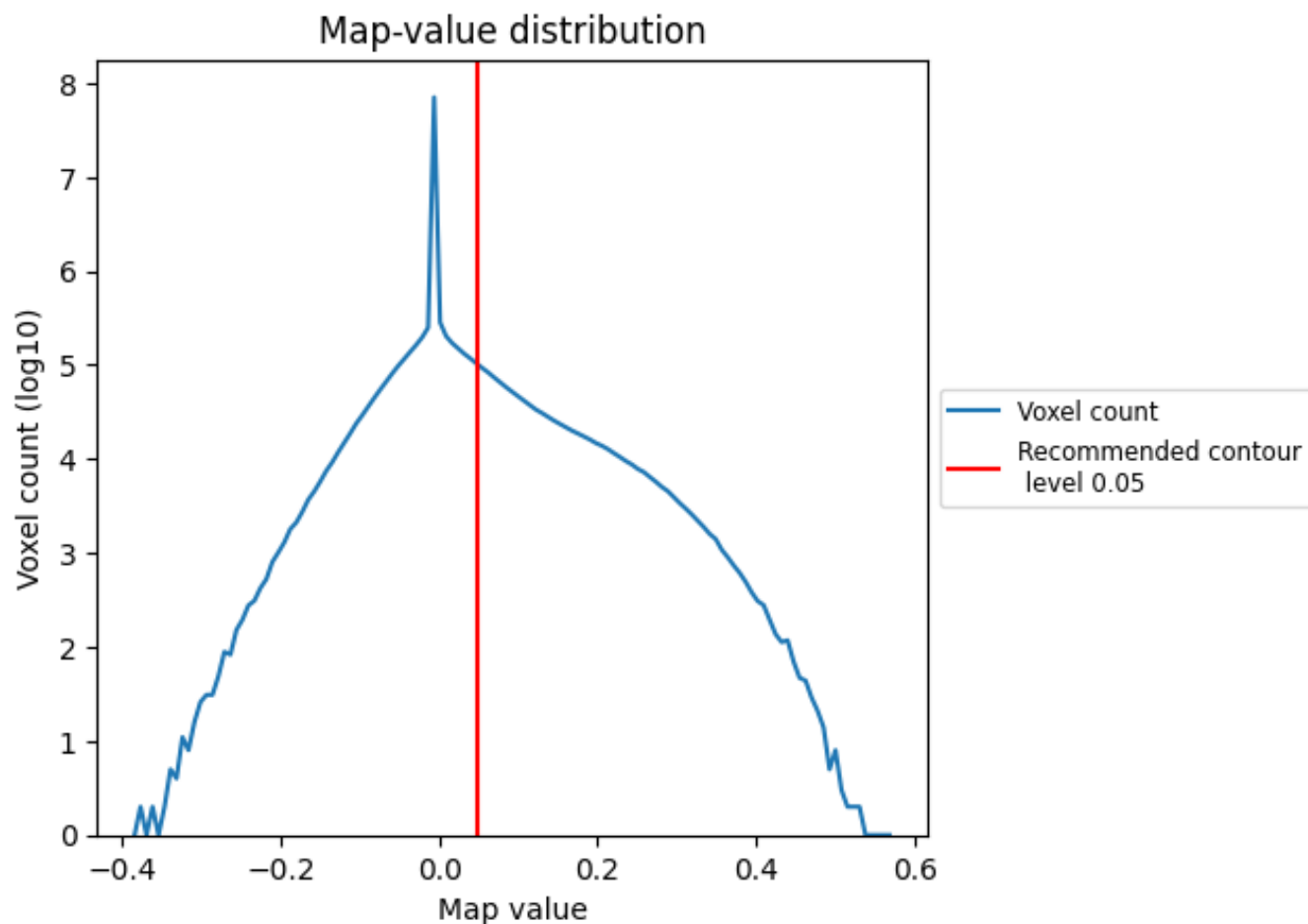
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

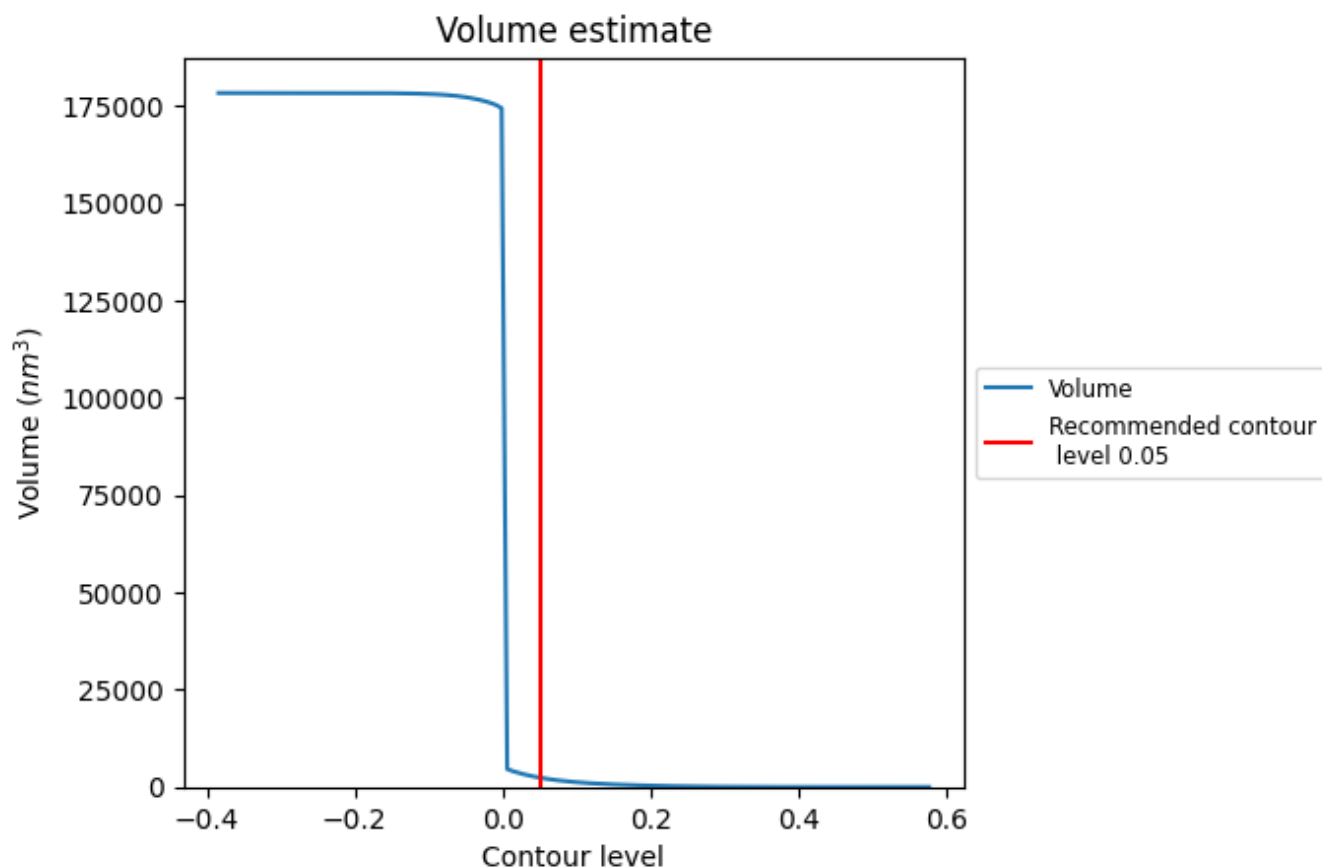
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

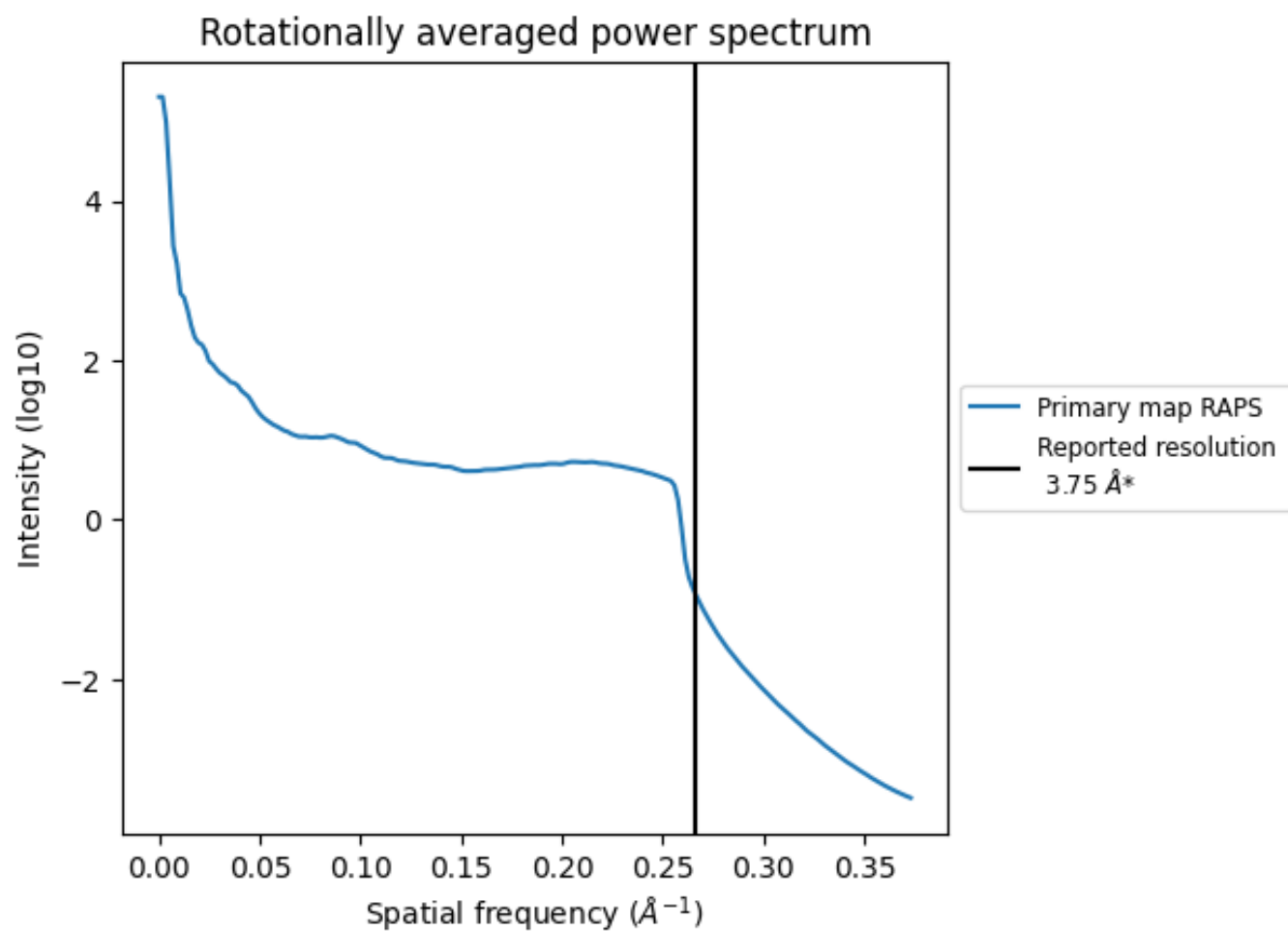
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2397 nm³; this corresponds to an approximate mass of 2166 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

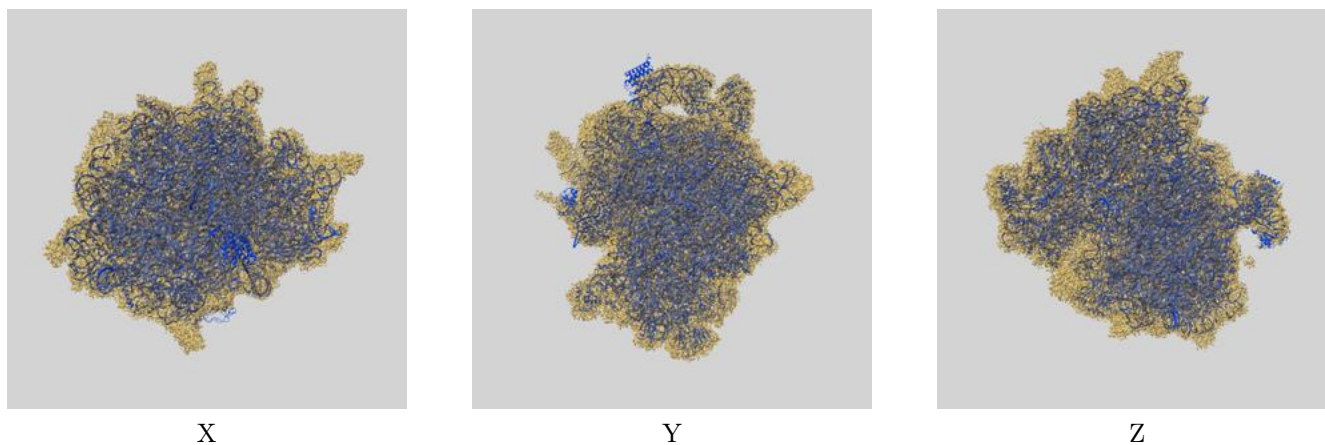
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

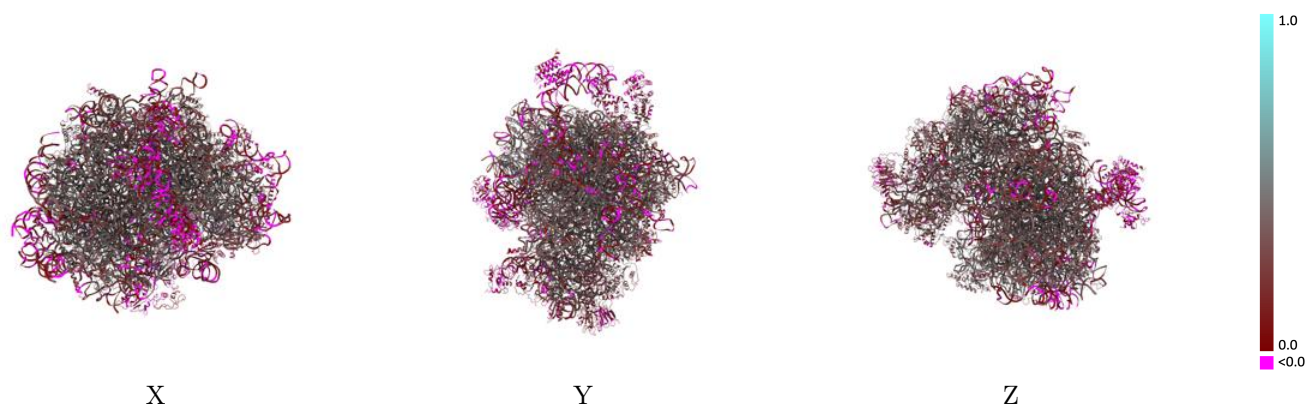
This section contains information regarding the fit between EMDB map EMD-3045 and PDB model 3JAN. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



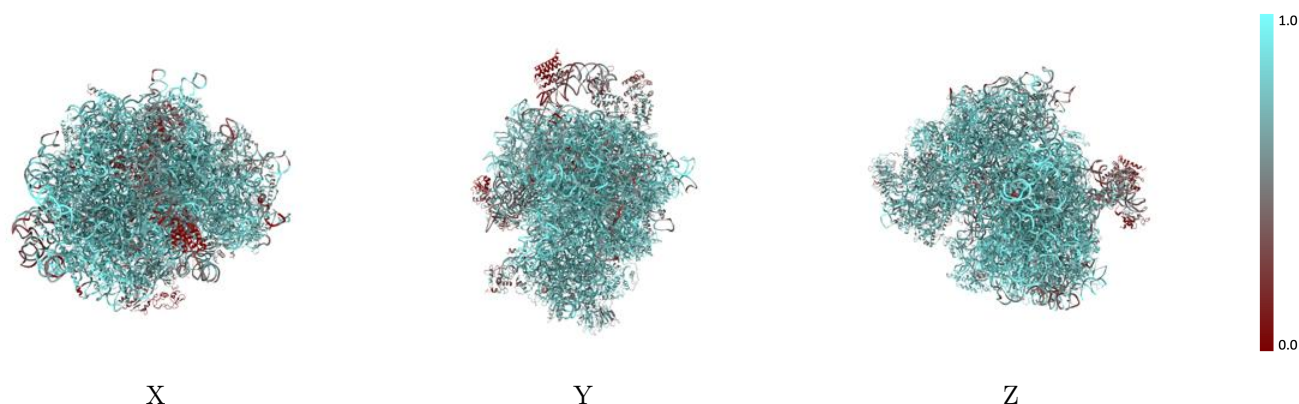
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



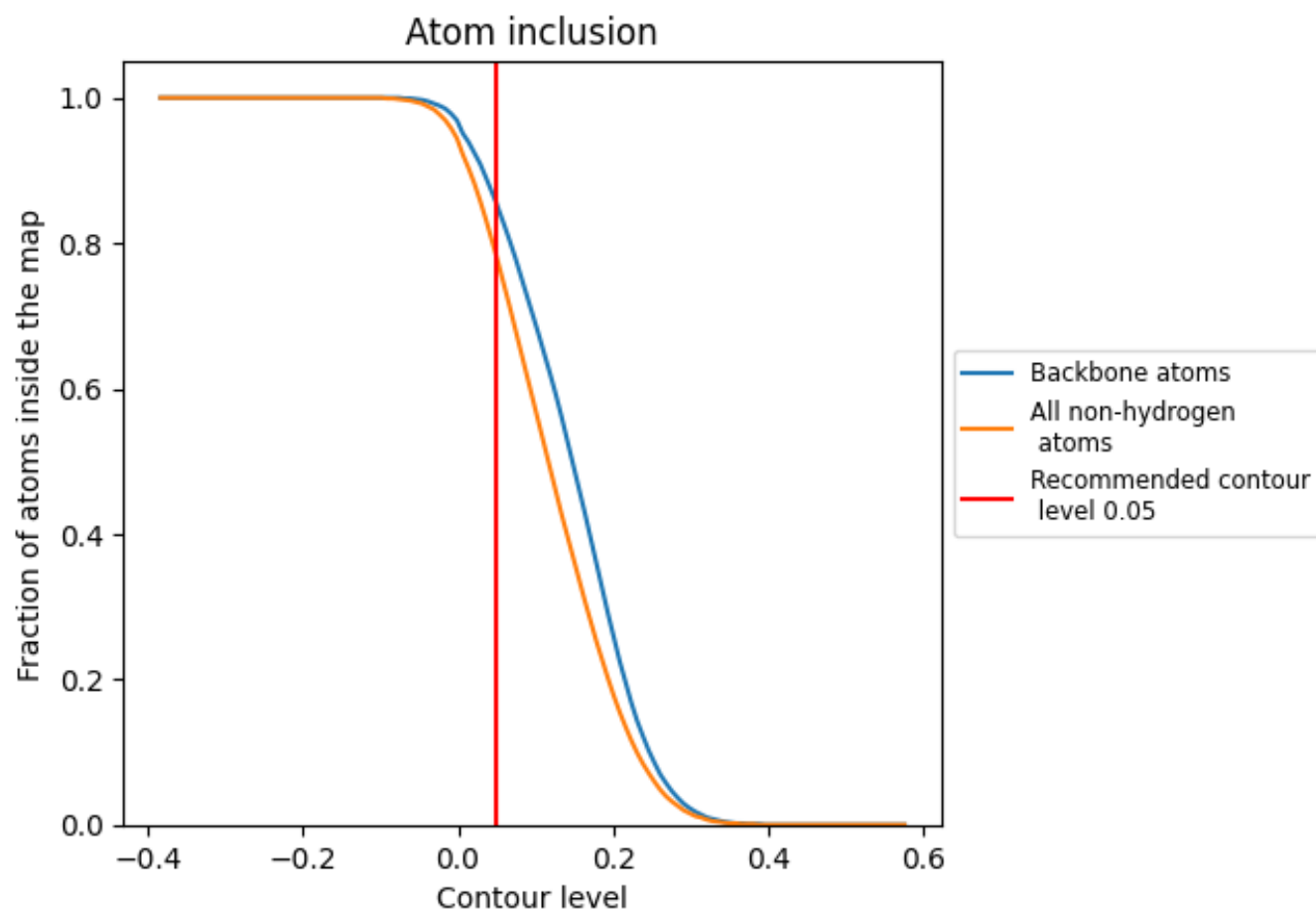
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7810	 0.3100
3	 0.6100	 0.2280
4	 0.4710	 0.0380
5	 0.8340	 0.3180
6	 0.1320	 -0.0170
7	 0.9190	 0.3910
8	 0.8530	 0.3370
9	 0.2290	 0.0070
A	 0.8070	 0.4030
B	 0.8300	 0.4050
C	 0.8150	 0.3970
D	 0.8160	 0.3580
E	 0.7530	 0.3300
F	 0.8200	 0.4010
G	 0.7650	 0.3270
H	 0.8110	 0.3960
I	 0.8110	 0.3990
J	 0.7920	 0.3570
K	 0.2840	 0.0300
L	 0.8020	 0.3780
M	 0.8110	 0.3860
N	 0.8240	 0.4030
O	 0.8200	 0.3970
P	 0.8080	 0.4020
Q	 0.8350	 0.4290
R	 0.7760	 0.3180
S	 0.8450	 0.4160
S1	 0.4960	 0.1160
S2	 0.8390	 0.3050
S4	 0.5350	 0.1840
SA	 0.7930	 0.3490
SB	 0.7830	 0.3560
SC	 0.8070	 0.3740
SD	 0.6840	 0.2600
SE	 0.7960	 0.3680



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Chain	Atom inclusion	Q-score
SF	 0.6790	 0.2380
SG	 0.6990	 0.2550
SH	 0.7120	 0.2850
SI	 0.7650	 0.3370
SJ	 0.8080	 0.3600
SK	 0.6520	 0.1880
SL	 0.7490	 0.3590
SM	 0.3470	 0.0280
SN	 0.7970	 0.3810
SO	 0.7920	 0.3700
SP	 0.6360	 0.1910
SQ	 0.7300	 0.2920
SR	 0.6950	 0.2680
SS	 0.7380	 0.2770
ST	 0.7540	 0.2710
SU	 0.6900	 0.2620
SV	 0.7900	 0.3450
SW	 0.8190	 0.3930
SX	 0.8080	 0.4050
SY	 0.7460	 0.3210
SZ	 0.6960	 0.2200
Sa	 0.8350	 0.4050
Sb	 0.7780	 0.3510
Sc	 0.6630	 0.2580
Sd	 0.7810	 0.3360
Se	 0.6980	 0.2810
Sf	 0.3380	 0.0080
Sg	 0.6310	 0.1620
T	 0.8100	 0.4050
U	 0.7390	 0.2920
V	 0.8040	 0.4050
W	 0.7900	 0.3870
X	 0.7810	 0.3700
Y	 0.7750	 0.3520
Z	 0.8030	 0.3530
a	 0.8360	 0.4230
b	 0.7360	 0.3130
c	 0.7890	 0.3550
d	 0.7850	 0.3600
e	 0.8320	 0.4190
f	 0.8410	 0.4190
g	 0.7750	 0.3580

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Chain	Atom inclusion	Q-score
h	 0.7650	 0.3490
i	 0.8200	 0.3780
j	 0.8560	 0.4180
k	 0.7400	 0.2830
l	 0.7730	 0.3740
m	 0.8340	 0.4170
n	 0.7910	 0.3390
o	 0.8180	 0.4060
p	 0.7940	 0.3960
q	 0.2150	 0.0080
r	 0.8380	 0.4080
z	 0.4250	 0.0860