



## wwPDB EM Validation Summary Report ⓘ

Oct 29, 2024 – 11:24 PM EDT

PDB ID : 3JAN  
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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

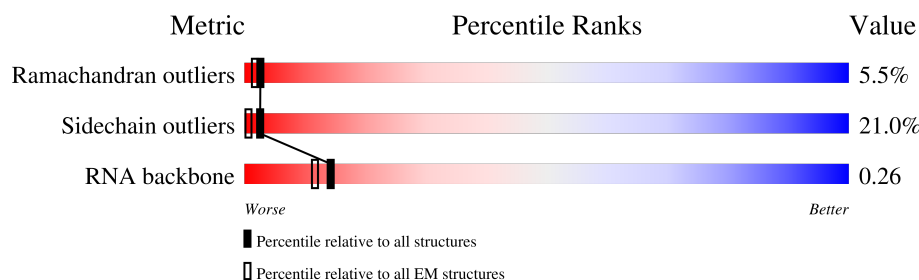
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.75 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.









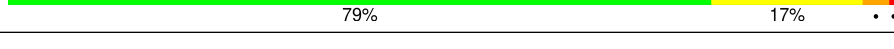
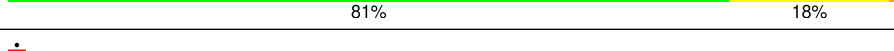
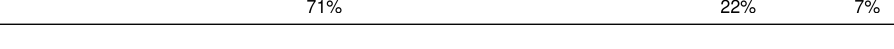
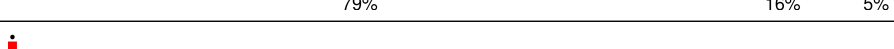
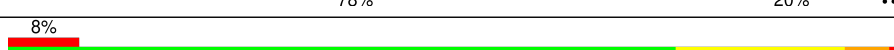

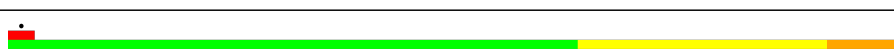

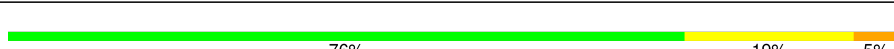





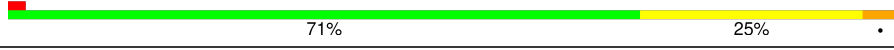
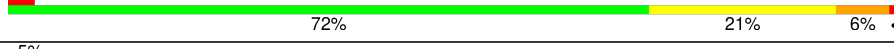
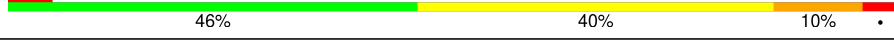


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	
4	H	190	
5	J	170	
6	L	210	
7	M	138	
8	N	203	



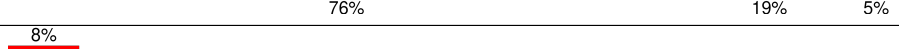
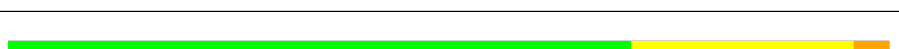



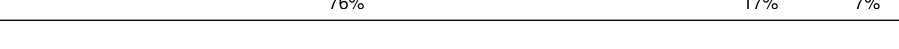



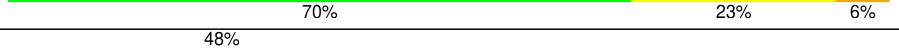

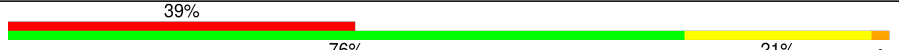
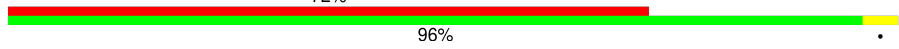
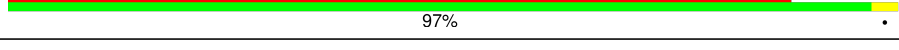
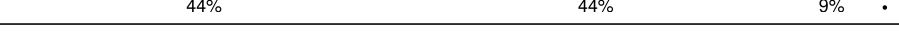







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Mol	Chain	Length	Quality of chain
9	O	201	
10	Q	187	
11	R	180	
12	S	175	
13	T	159	
14	U	99	
15	V	131	
16	X	119	
17	Y	134	
18	Z	135	
19	a	147	
20	b	75	
21	c	94	
22	d	107	
23	e	128	
24	f	109	
25	g	114	
26	h	122	
27	i	102	
28	k	69	
29	l	50	
30	m	52	
31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

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Mol	Chain	Length	Quality of chain
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	
54	SA	208	
55	SB	213	
56	SC	218	
57	SE	262	
58	SG	237	



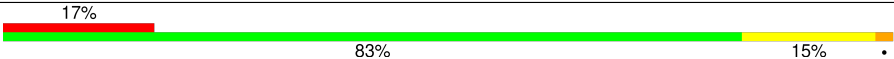
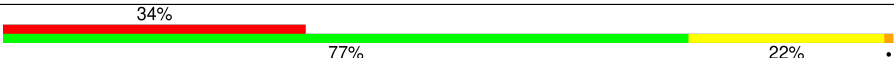
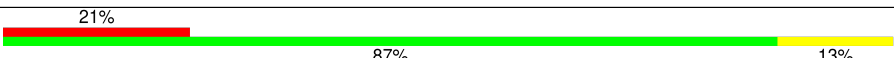
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Mol	Chain	Length	Quality of chain
59	SH	189	
60	SI	206	
61	SJ	185	
62	SL	152	
63	SN	149	
64	SO	136	
65	SV	82	
66	SW	129	
67	SX	141	
68	SY	126	
69	Sa	98	
70	Sb	83	
71	Se	57	
72	SD	227	
73	SF	191	
74	SK	98	
75	SM	124	
76	SP	96	
77	SQ	141	
78	SR	129	
79	SS	137	
80	ST	141	
81	SU	104	
82	SZ	75	
83	Sc	64	

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Mol	Chain	Length	Quality of chain
84	Sd	52	
85	Sf	71	
86	Sg	313	
87	S1	74	
88	S4	76	

## 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 (three-letter code: 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

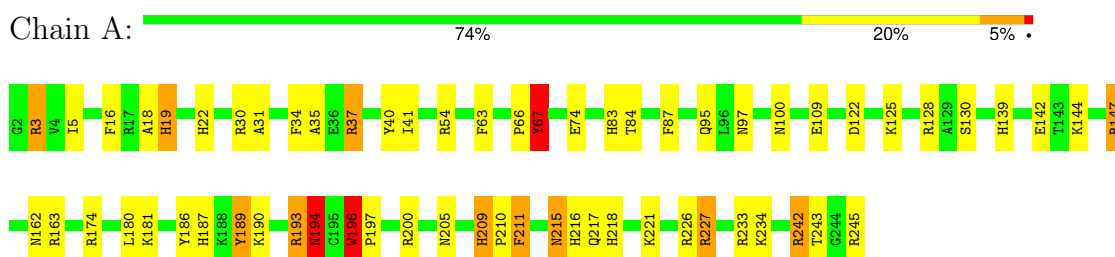
- Molecule 90 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

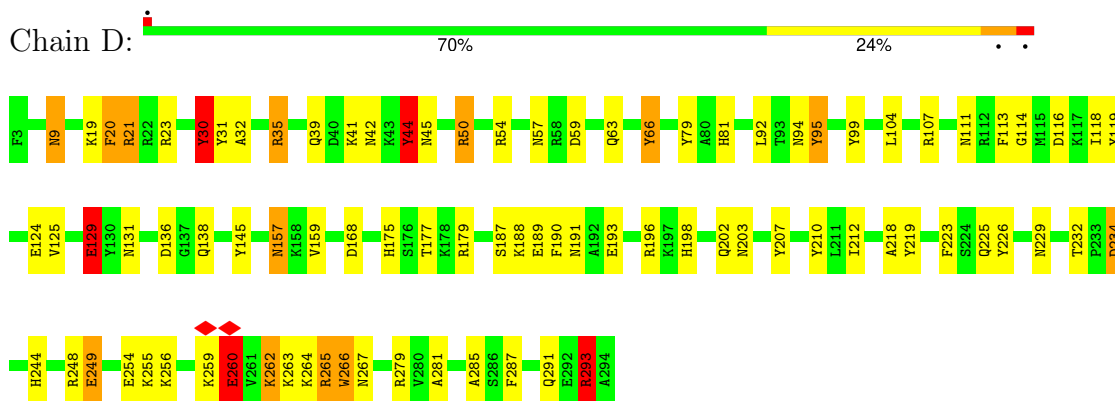
### 3 Residue-property plots

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.

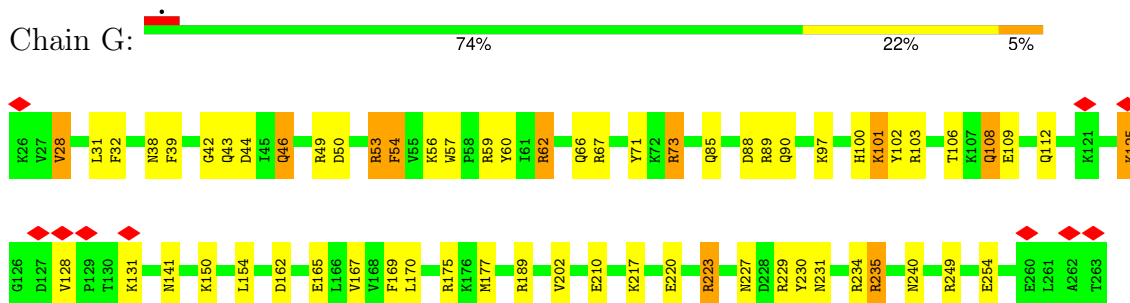
#### • Molecule 1: Ribosomal protein uL2




#### • Molecule 2: Ribosomal protein uL18

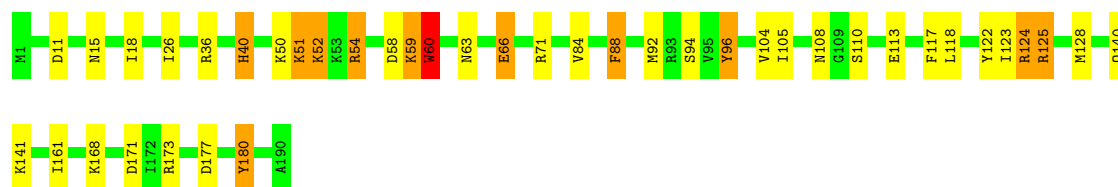


#### • Molecule 3: Ribosomal protein eL8



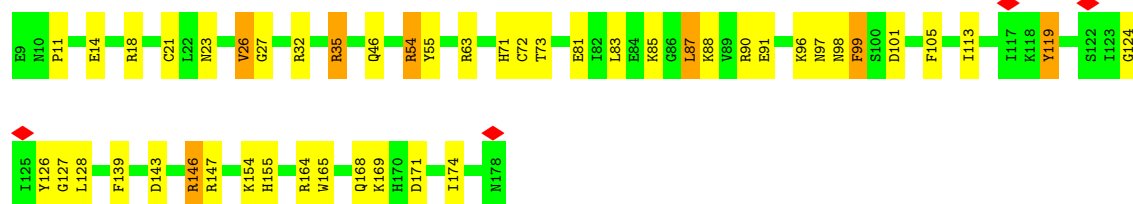
#### • Molecule 4: Ribosomal protein uL6

Chain H:  78% 15% 6% •



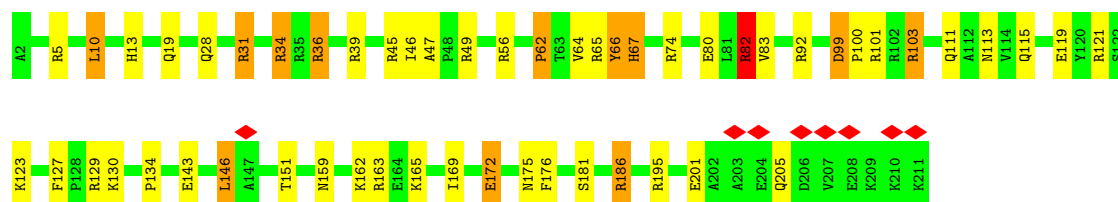
- Molecule 5: Ribosomal protein uL5

Chain J:  72% 24% •




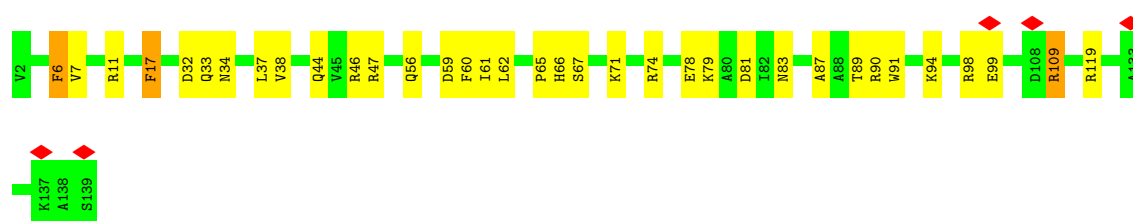
- Molecule 6: Ribosomal protein eL13

Chain L:  74% 20% 6% •



- Molecule 7: Ribosomal protein eL14

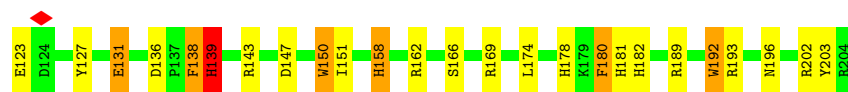
Chain M:  75% 23% •



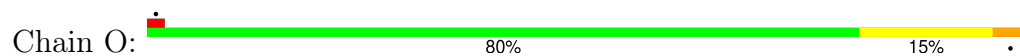
- Molecule 8: Ribosomal protein eL15

Chain N:  70% 23% 6% •

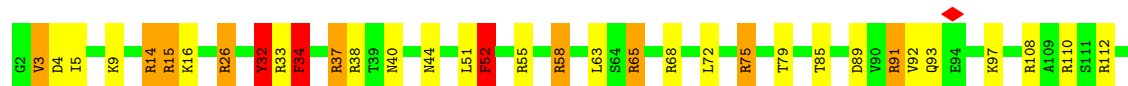
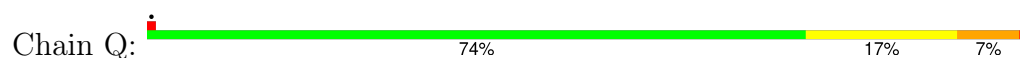




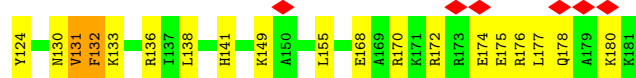
• Molecule 9: Ribosomal protein uL13



• Molecule 10: Ribosomal protein eL18



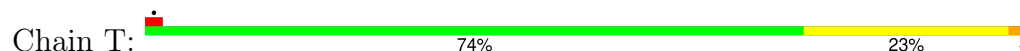
• Molecule 11: Ribosomal protein eL19

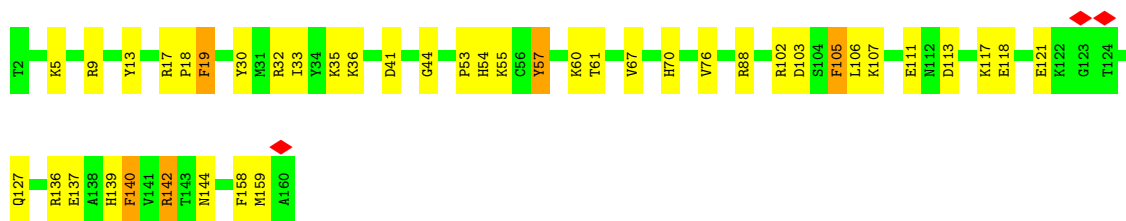


• Molecule 12: Ribosomal protein eL20

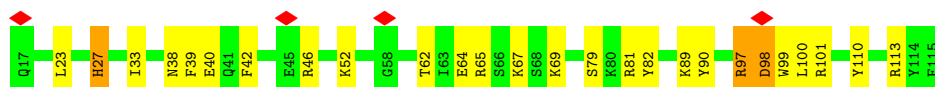


• Molecule 13: Ribosomal protein eL21

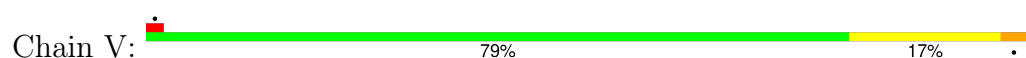




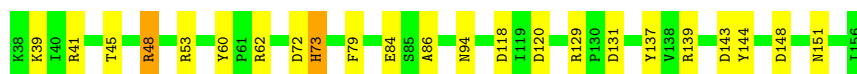
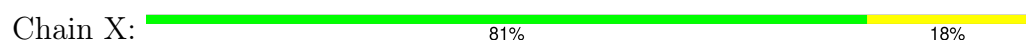
• Molecule 14: Ribosomal protein eL22



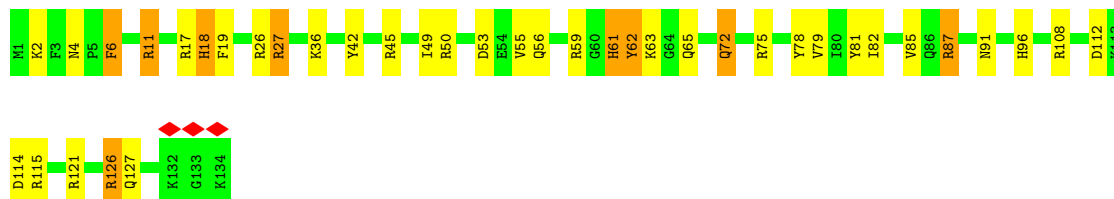
• Molecule 15: Ribosomal protein uL14



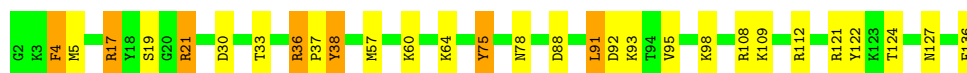
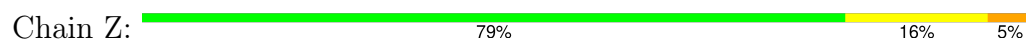
• Molecule 16: Ribosomal protein uL23



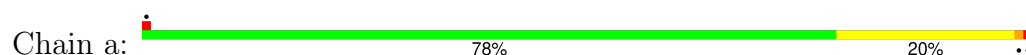
• Molecule 17: Ribosomal protein uL24



• Molecule 18: Ribosomal protein eL27



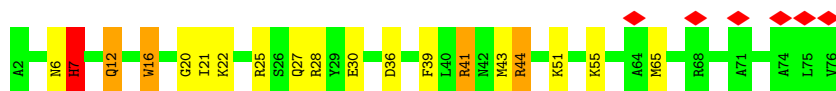
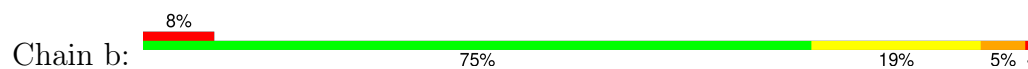
• Molecule 19: Ribosomal protein uL15







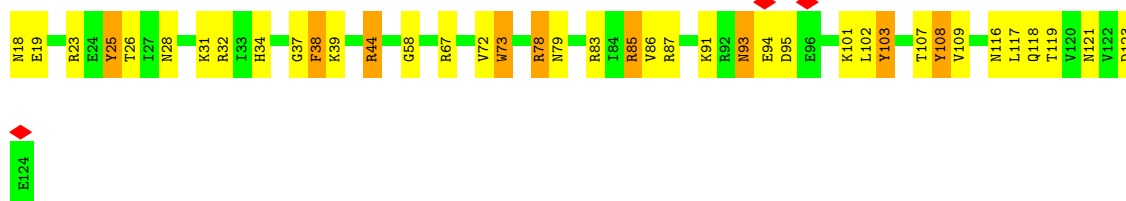
- Molecule 20: Ribosomal protein eL29



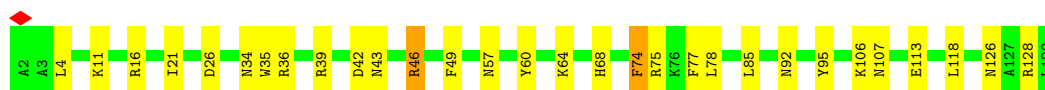
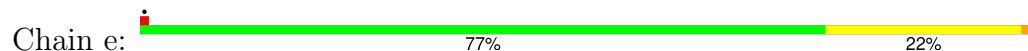
- Molecule 21: Ribosomal protein eL30



- Molecule 22: Ribosomal protein eL31



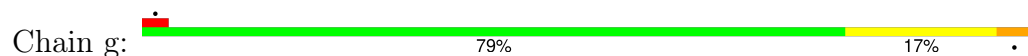
- Molecule 23: Ribosomal protein eL32

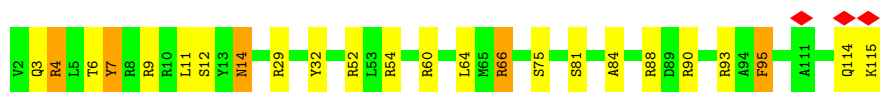


- Molecule 24: Ribosomal protein eL33

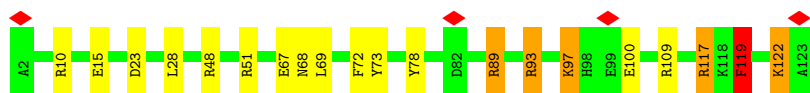
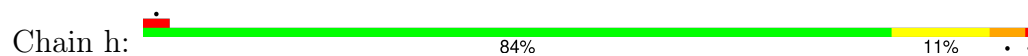


- Molecule 25: Ribosomal protein eL34

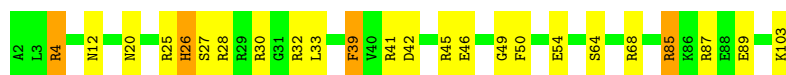




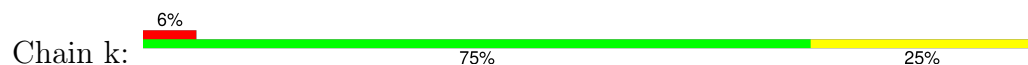
- Molecule 26: Ribosomal protein uL29



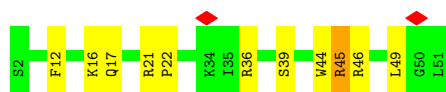
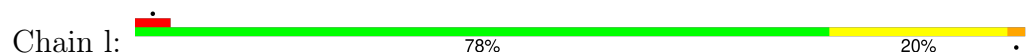
- Molecule 27: Ribosomal protein eL36



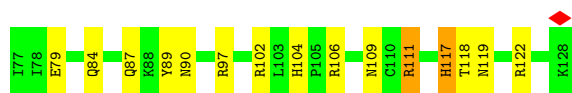
- Molecule 28: Ribosomal protein eL38



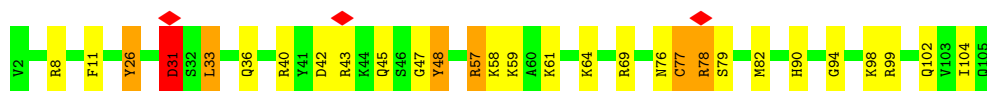
- Molecule 29: Ribosomal protein eL39



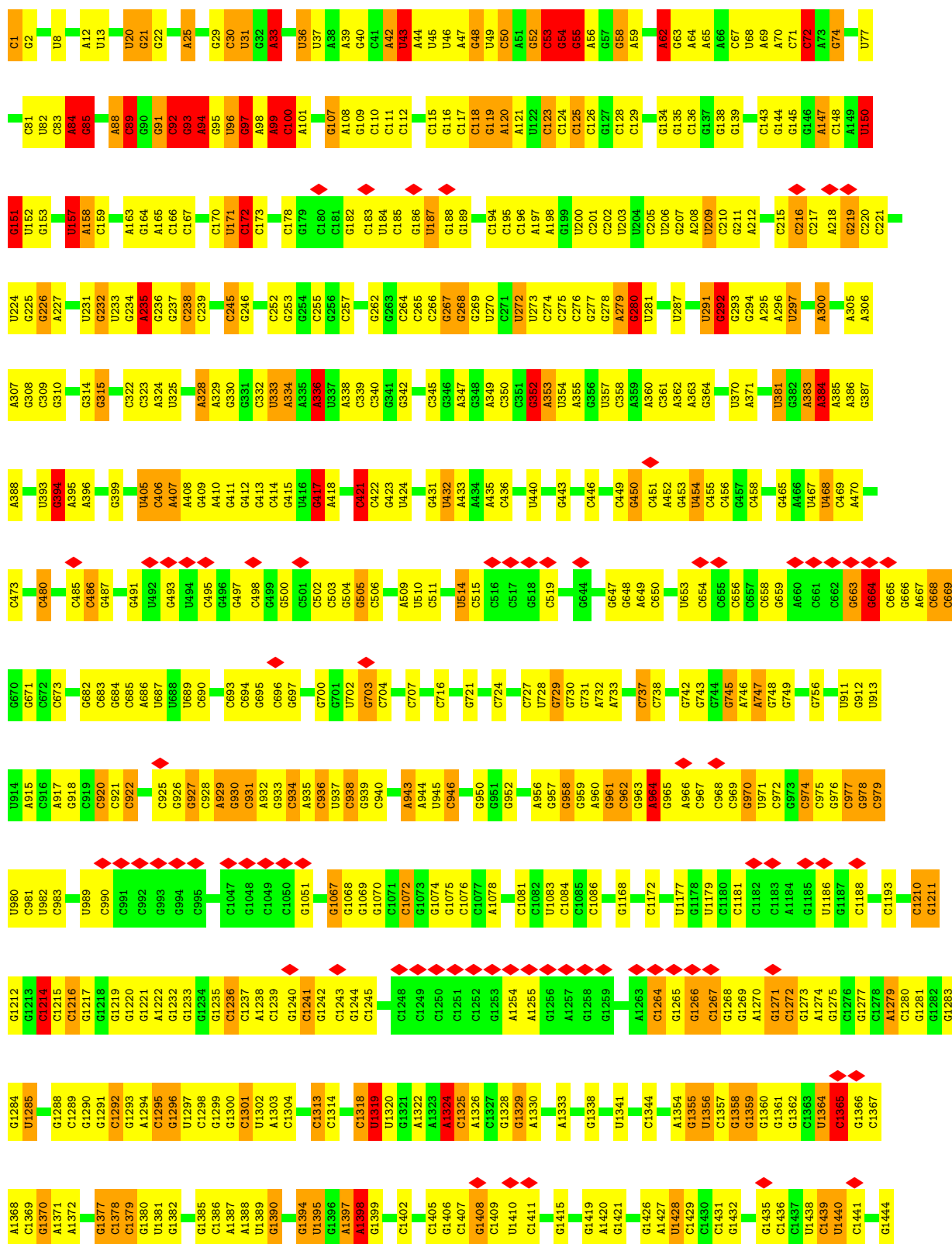
- Molecule 30: Ribosomal protein eL40



- Molecule 31: Ribosomal protein eL42

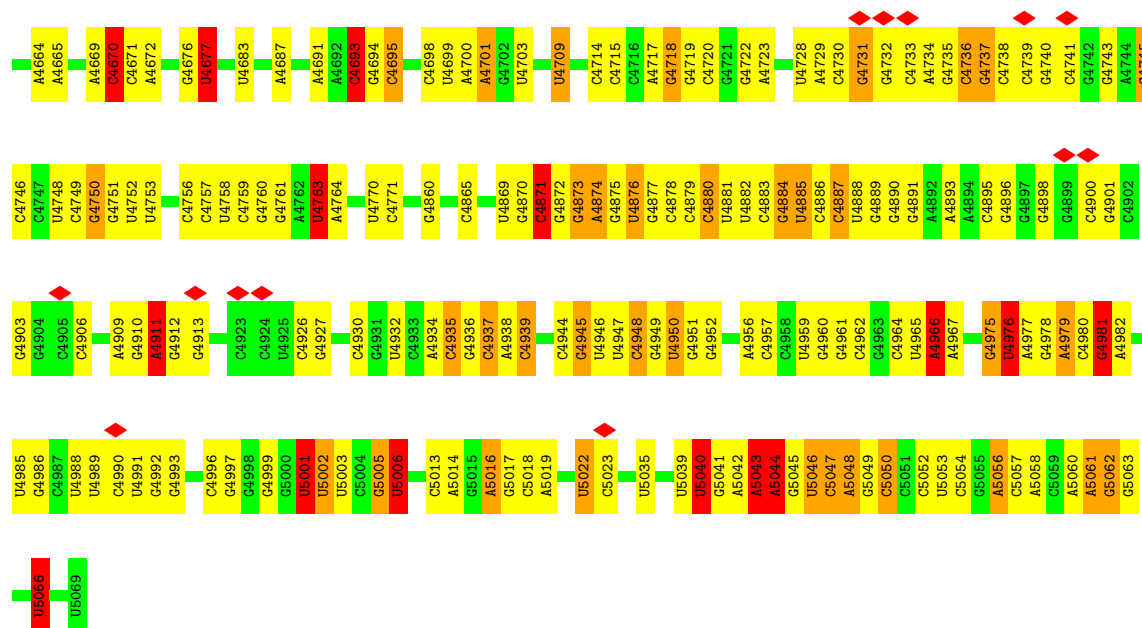


- Molecule 32: 28S ribosomal RNA



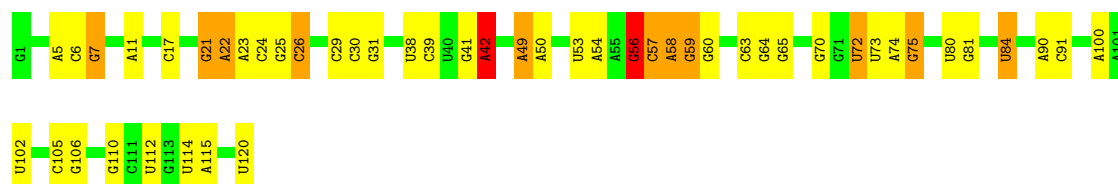
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C2509	G2510	A2511	A2512	A2513	A2514	G2515	G2516	G2518	U2519	G2520	G2523	C2526	A2527	G2528	A2529	U2530	C2531	C2532	C2533	G2534	G2535	A2536	A2537	G2544	U2545	U2546	G2547	G2548	G2549	A2550	A2551	G2552	A2553	U2554	G2555	C2560	C2563	G2566	C2571	C2572	G2576	C2577	U2580	A2581	A2582	C2583	G2586	A2587																																																																																																																									
U2432	G2433	G2434	G2435	U2436	G2437	A2438	G2439	U2440	C2441	G2442	G2443	C2446	G2447	G2448	A2449	G2450	A2451	U2454	G2455	G2456	G2459	A2460	G2463	C2464	G2465	G2466	U2467	U2468	C2469	G2470	C2471	A2472	U2473	G2474	G2475	G2476	G2479	G2487	C2488	C2489	U2490	C2491	C2499	G2502	G2503	C2504	C2505	G2506	U2507	U2508																																																																																																																							
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C2266	U2267	A2268	C2269	G2270	C2271	C2272	C2273	C2274	A2275	A2276	C2277	C2278	C2279	U2280	U2281	A2282	G2283	G2288	C2289	G2299	G2300	G2301	U2305	G2306	A2307	G2308	C2309	G2310	C2311	U2312	G2313	G2314	G2315	G2316	G2317	G2318	A2319	G2320	C2321	C2322	C2323	C2324	C2325	G2328	U2329	G2330	G2331	A2332	G2333	G2334	C2335	G2336	C2337	U2338	G2339																																																																																																																		
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C2016	A2017	C2018	G2024	A2025	A2026	U2027	A2033	G2034	C2035	C2036	C2037	U2038	G2039	A2040	U2044	G2045	G2046	A2047	U2048	C2052	G2053	U2054	G2055	G2056	A2057	G2058	C2059	C2062	G2063	G2064	C2068	A2069	U2070	G2075	C2076	C2077	G2078	G2079	U2080	C2081	C2082	C2083	C2084	G2085	G2086	A2087	C2088	G2089	U2090	C2091	G2092	A2093																																																																																																																					
G1948	U1949	U1950	G1951	G1952	A1956	U1959	A1960	U1961	A1962	A1963	A1964	A1967	C1971	U1974	G1975	G1976	C1977	G1978	A1979	U1980	G1981	G1982	A1983	G1984	G1985	U1986	G1987	G1988	G1989	A1990	A1991	U1992	C1993	G1994	G1995	C1996	U1997	A1998	A1999	G2000	G2001	A2002	G2003	U2004	G2005	U2006	G2007	U2008	A2009	A2010	C2011	C2014	U2015																																																																																																																				
G1880	C1881	U1882	G1883	C1884	G1885	G1886	G1887	U1889	U1890	A1891	A1892	C1893	C1894	A1897	G1898	G1899	C1900	G1901	G1902	G1903	A1907	G1916	A1917	U1918	G1919	G1920	C1921	G1922	A1923	G1924	G1925	C1928	A1929	U1930	A1931	C1932	G1933	C1935	C1936	C1937	C1938	C1939	G1940	A1941	G1945	G1946	U1947																																																																																																																										
U1790	U1791	U1792	A1793	G1797	G1798	G1799	U1800	G1803	A1804	A1805	C1808	G1815	C1816	U1817	G1818	G1819	C1820	G1821	U1822	G1823	C1827	G1828	G1829	G1830	G1831	G1832	G1833	U1834	G1835	G1836	A1843	C1847	C1848	U1849	G1851	U1852	G1853	G1854	G1855	G1864	G1865	U1866	A1867	A1868	G1869	U1876	G1877	G1878	C1879																																																																																																																								
A1699	C1718	C1719	C1720	G1721	C1722	A1632	G1633	A1634	C1635	U1636	A1637	A1638	U1639	C1640	G1641	A1642	A1643	C1649	A1650	G1654	C1655	U1656	G1657	G1658	U1659	G1660	C1661	C1662	G1667	A1668	A1669	G1670	U1671	U1672	U1673	C1676	U1677	C1678	A1679	C1680	G1681	A1682	U1683	A1684	G1685	C1686	U1687	G1691	C1692	U1693	C1694	U1695	C1696	G1697	C1698																																																																																																																		
G1530	A1533	A1534	C1535	U1538	U1539	G1543	U1547	G1582	A1553	A1554	G1555	G1562	A1563	A1564	A1565	C1566	G1571	U1572	G1573	G1574	A1575	G1576	G1577	U1578	A1583	G1586	G1587	U1588	C1589	U1591	U1596	G1597	A1601	G1604	U1609	G1610	G1611	G1612	A1613	C1614	G1615	G1616	G1617	G1624																																																																																																																													
G1445	C1446	C1447	G1448	C1449	G1454	G1455	G1456	G1457	C1463	A1464	G1465	G1466	C1474	G1475	C1478	G1479	C1480	C1481	G1482	C1483	A1484	C1485	C1486	C1487	G1488	G1489	G1490	G1493	A1497	G1498	C1499	A1500	C1501	G1502	A1503	G1504	A1508	C1509	U1514	A1515	G1516	G1517	A1518	C1519	C1520	G1521	G1522	A1523	U1524	A1525																																																																																																																							





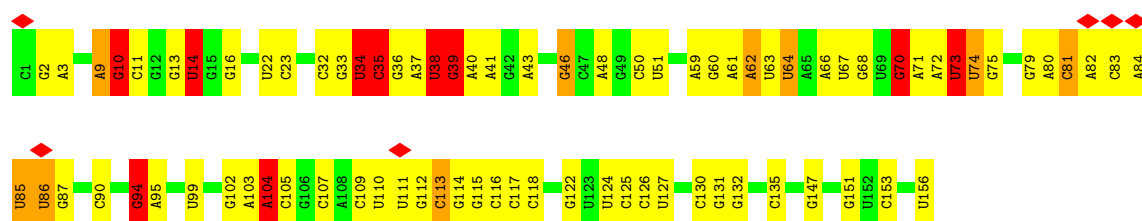
• Molecule 33: 5S ribosomal RNA

Chain 7: 59% 30% 9% .



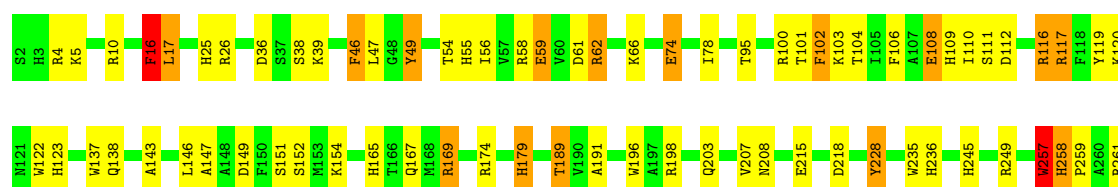
• Molecule 34: 5.8S ribosomal RNA

Chain 8: 48% 40% 6% 6% .



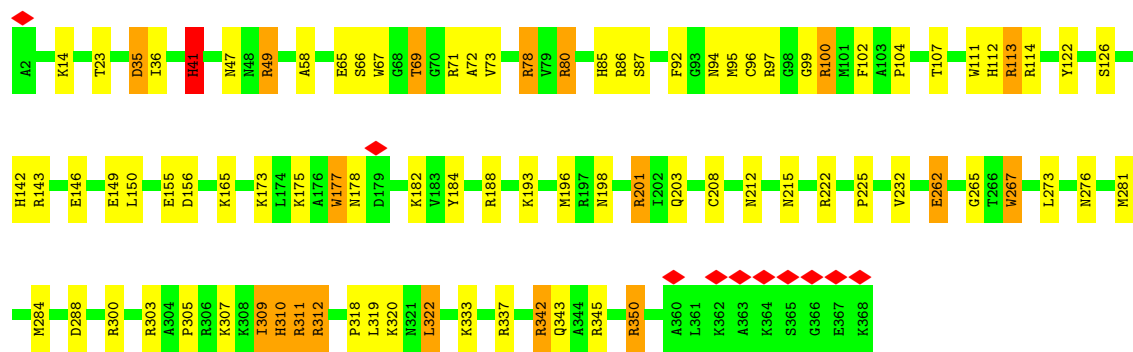
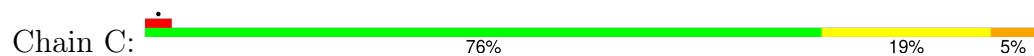
• Molecule 35: Ribosomal protein uL3

Chain B: 73% 22% 5% .

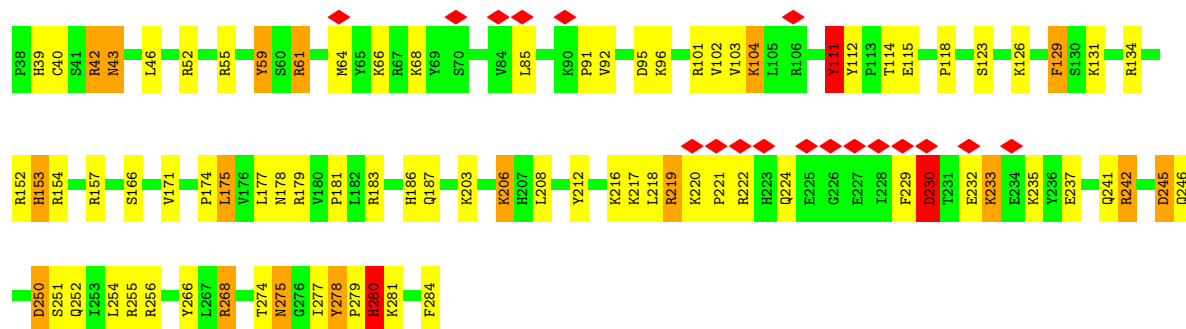




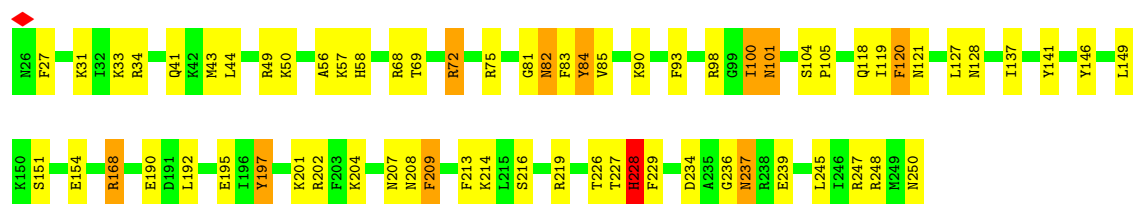
• Molecule 36: Ribosomal protein uL4



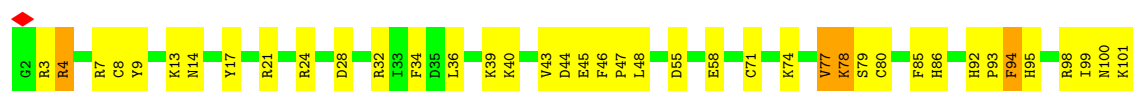
• Molecule 37: Ribosomal protein eL6

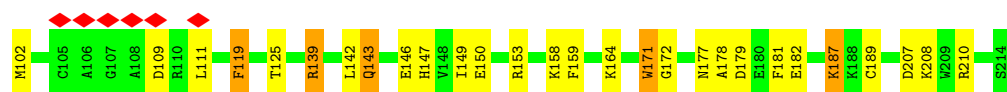


• Molecule 38: Ribosomal protein uL30

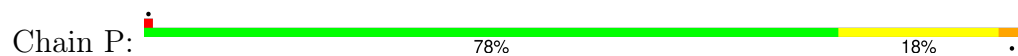


• Molecule 39: Ribosomal protein uL16





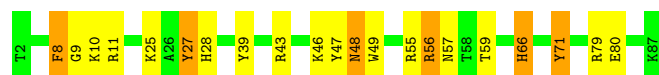
- Molecule 40: Ribosomal protein uL22



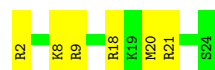
- Molecule 41: Ribosomal protein eL24



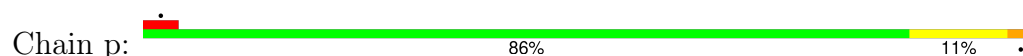
- Molecule 42: Ribosomal protein eL37



- Molecule 43: Ribosomal protein eL41



- Molecule 44: Ribosomal protein eL43

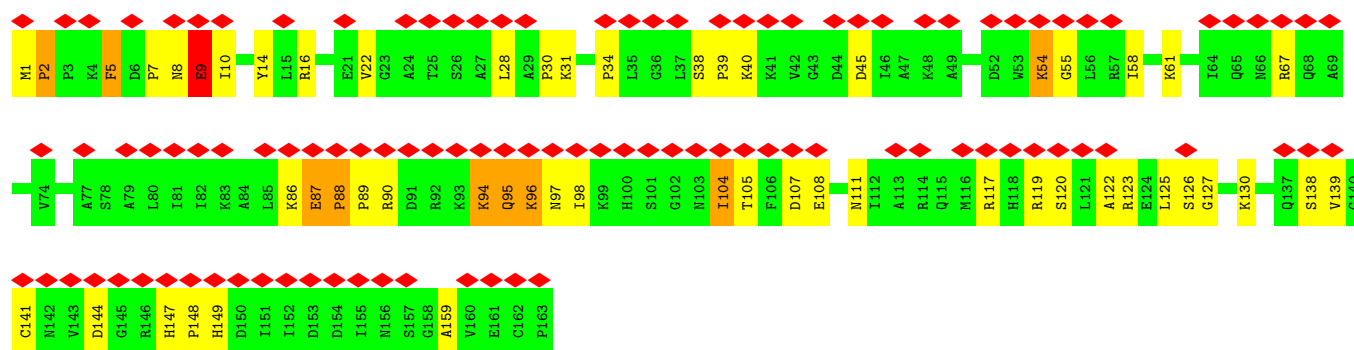


- Molecule 45: Ribosomal protein eL28

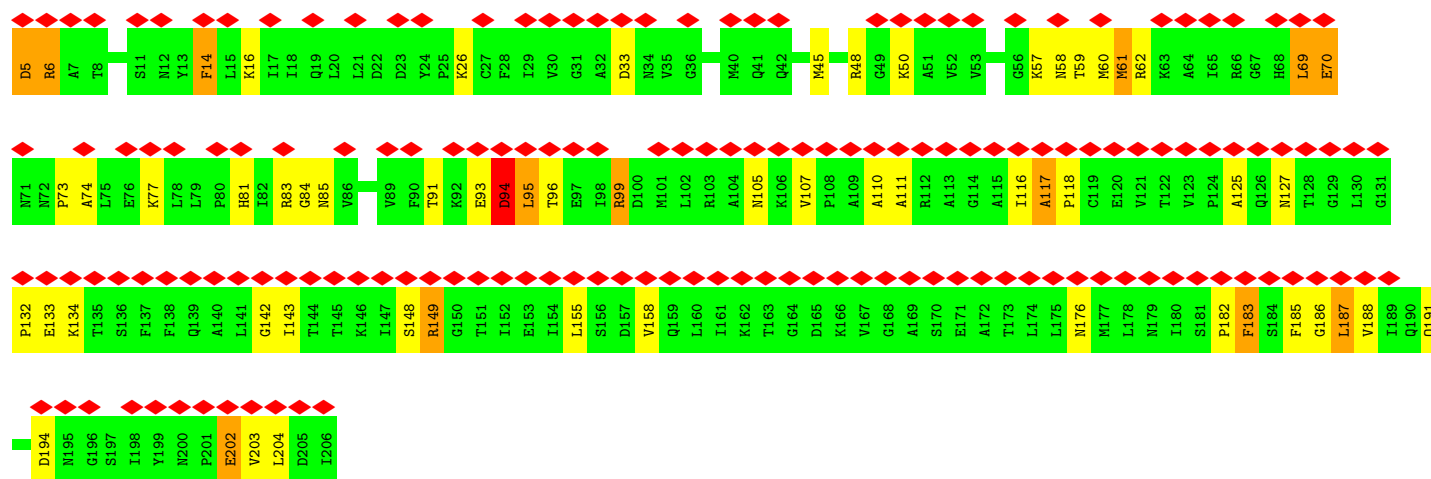
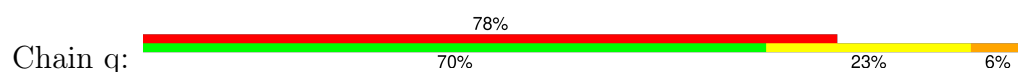


- Molecule 46: Ribosomal protein uL11

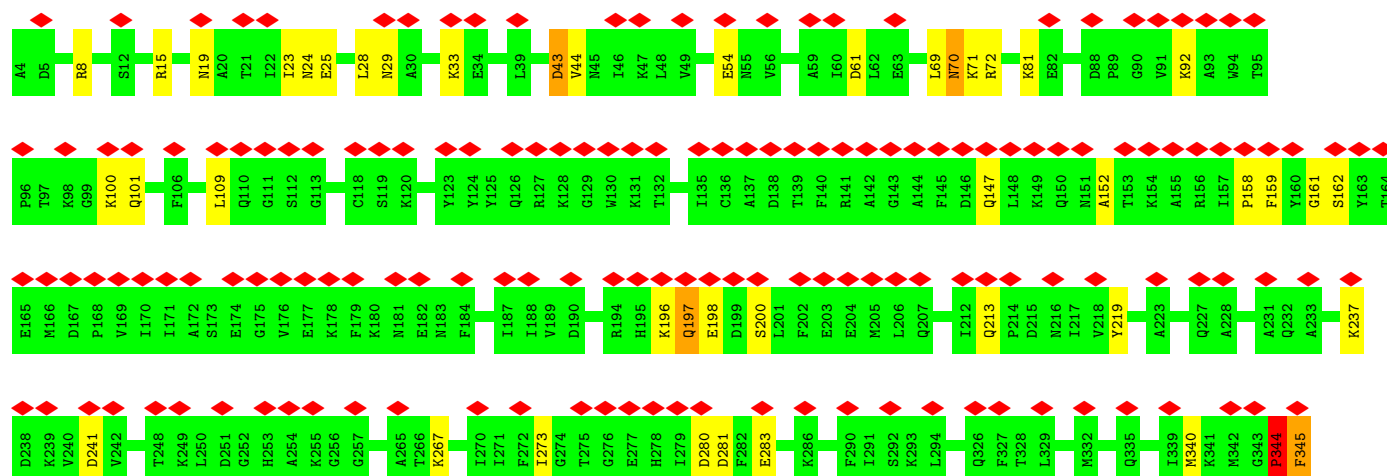
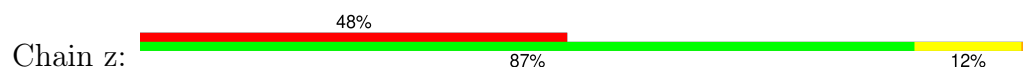


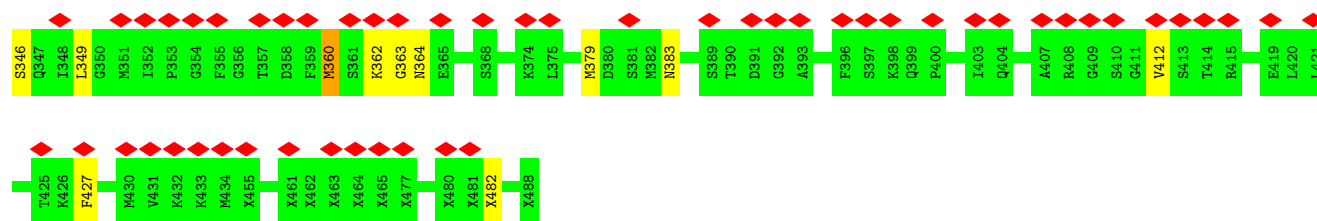


• Molecule 47: Ribosomal protein uL10

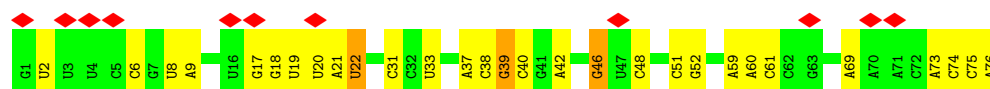


• Molecule 48: SRP54

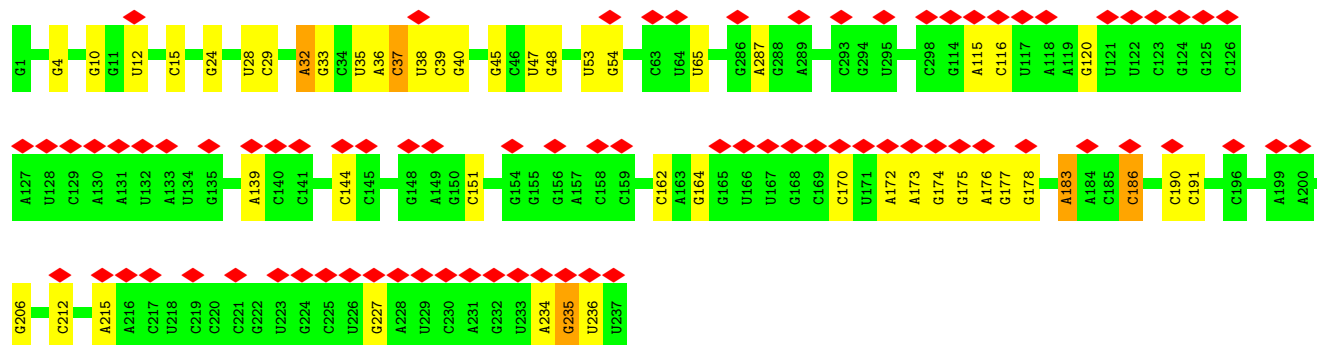
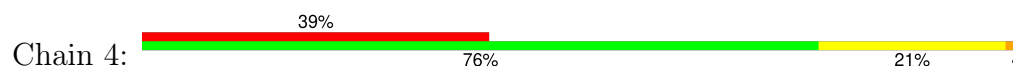




• Molecule 49: Val tRNA



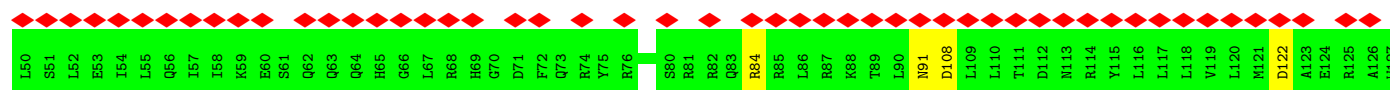
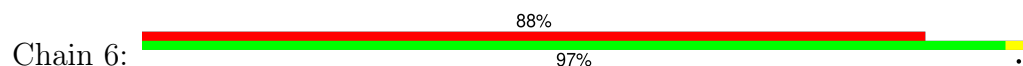
• Molecule 50: SRP 7S RNA

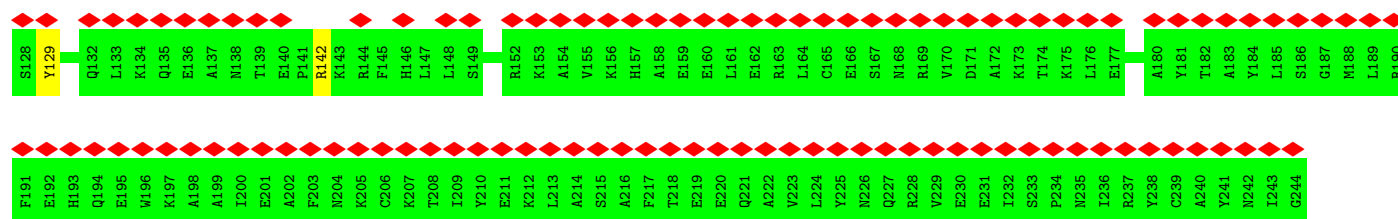


• Molecule 51: SRP19

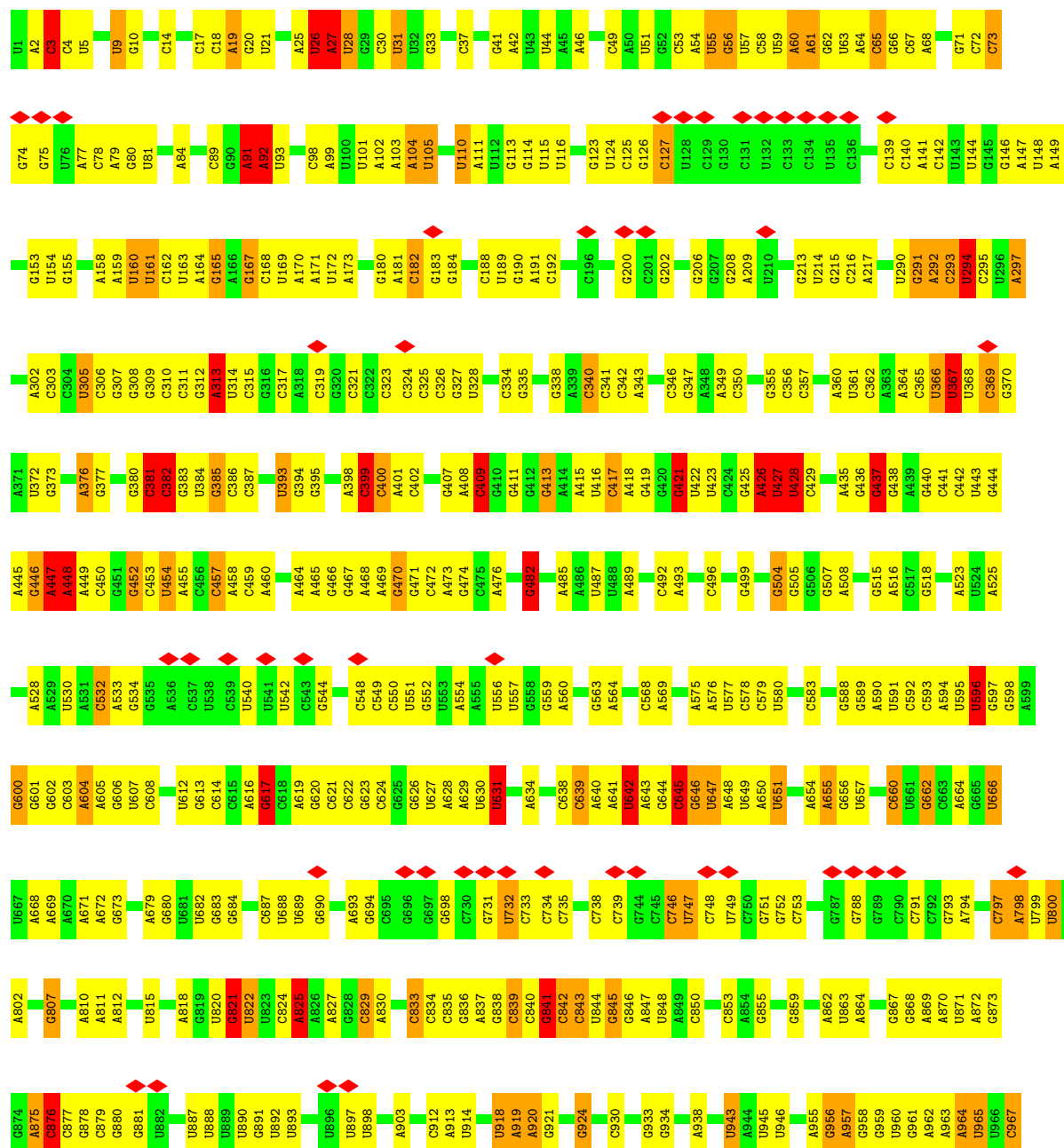


• Molecule 52: SRP68





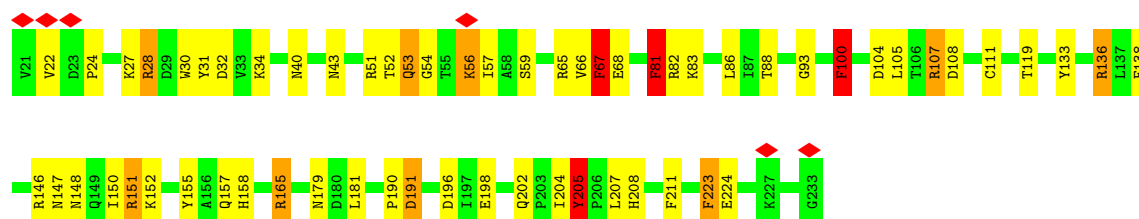
• Molecule 53: 18S ribosomal RNA



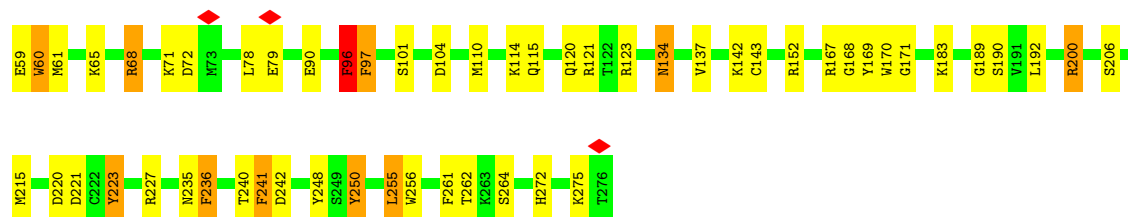
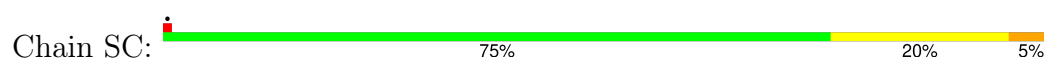




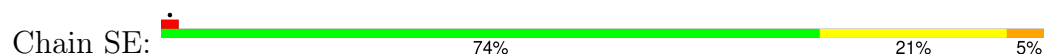
- Molecule 55: Ribosomal protein eS1



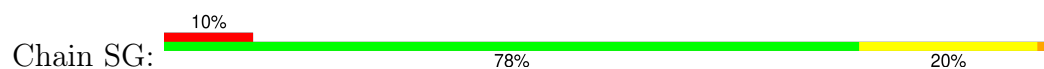
- Molecule 56: Ribosomal protein uS5



- Molecule 57: Ribosomal protein eS4

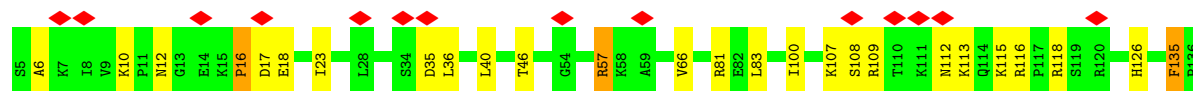
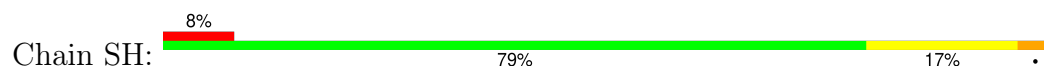


- Molecule 58: Ribosomal protein eS6

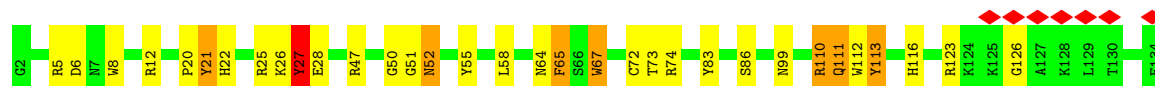
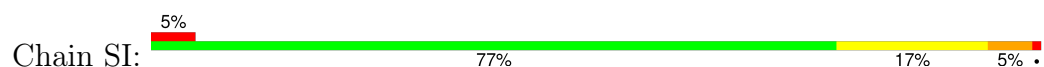




• Molecule 59: Ribosomal protein eS7



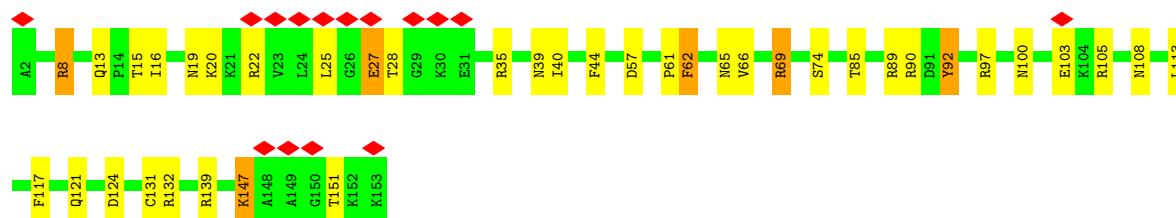
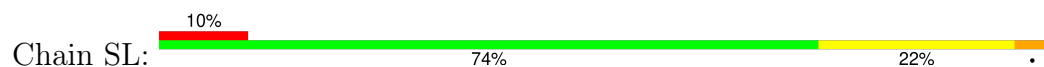
• Molecule 60: Ribosomal protein eS8




• Molecule 61: Ribosomal protein uS4

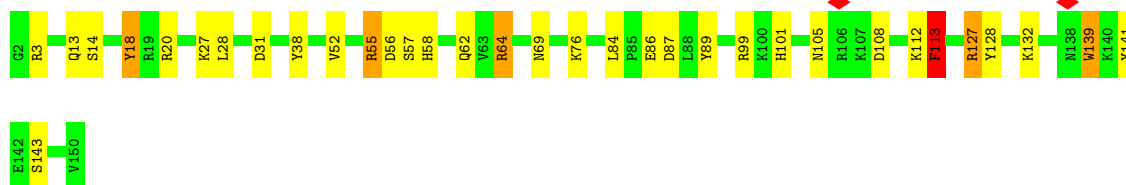


• Molecule 62: Ribosomal protein uS17



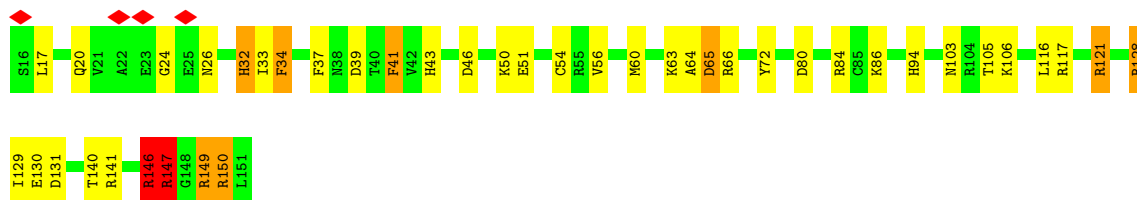
• Molecule 63: Ribosomal protein uS15

Chain SN:  77% 19% . .



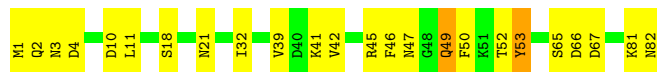
- Molecule 64: Ribosomal protein uS11

Chain SO:  69% 24% 6% .




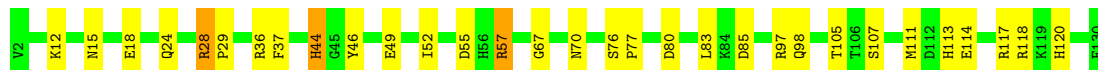
- Molecule 65: Ribosomal protein eS21

Chain SV:  71% 27% .




- Molecule 66: Ribosomal protein uS8

Chain SW:  76% 22% .




- Molecule 67: Ribosomal protein uS12

Chain SX:  82% 15% .

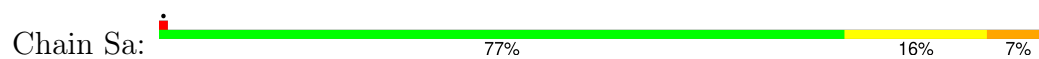


- Molecule 68: Ribosomal protein eS24

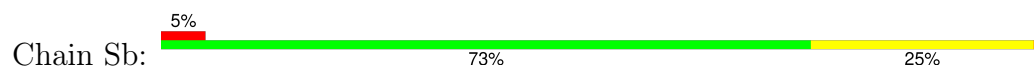
Chain SY:  77% 21% .



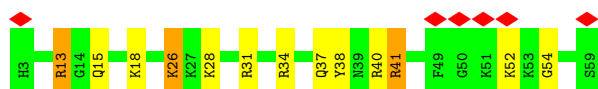
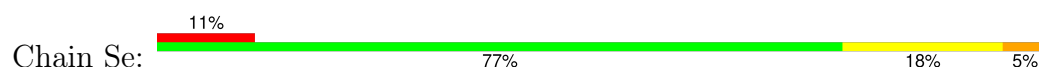
- Molecule 69: Ribosomal protein eS26



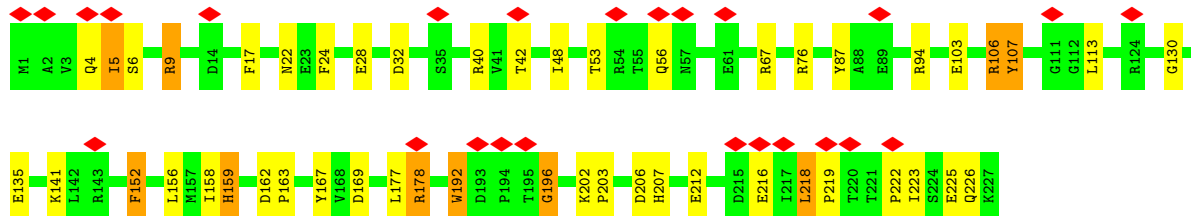
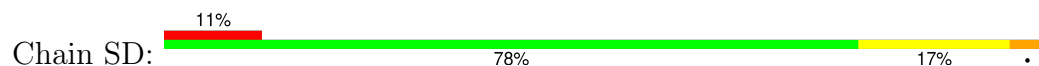
- Molecule 70: Ribosomal protein eS27



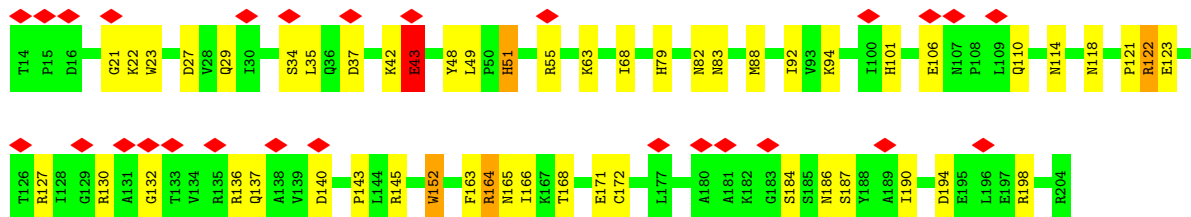
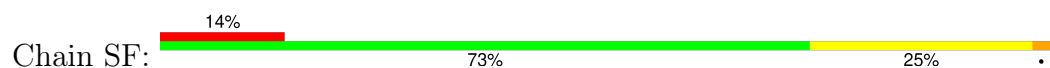
- Molecule 71: Ribosomal protein eS30



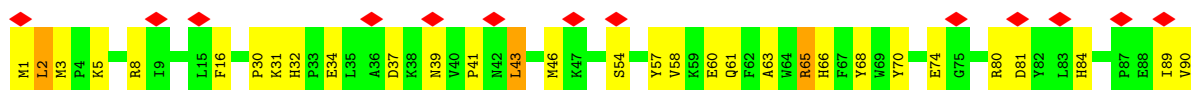
- Molecule 72: Ribosomal protein uS3



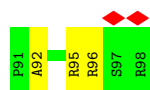
- Molecule 73: Ribosomal protein uS7



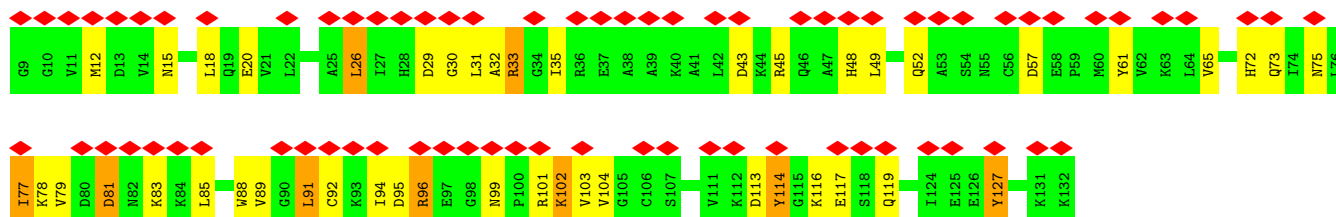
- Molecule 74: Ribosomal protein eS10



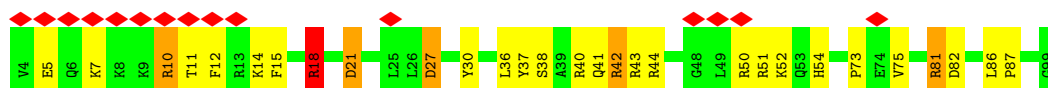




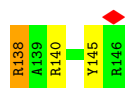
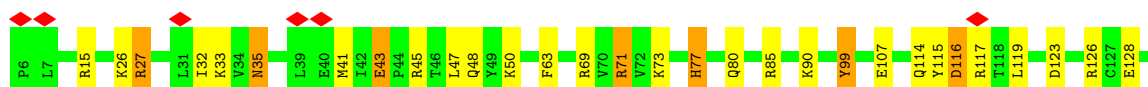
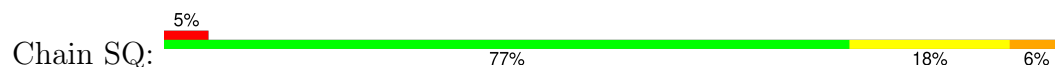
- Molecule 75: Ribosomal protein eS12



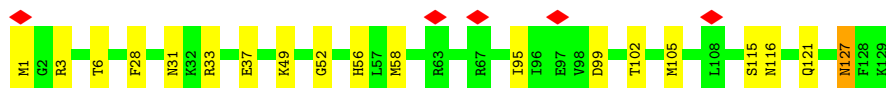
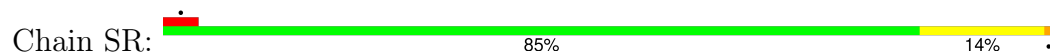
- Molecule 76: Ribosomal protein uS19



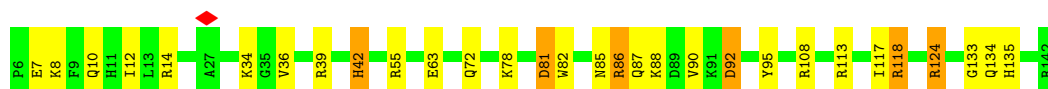
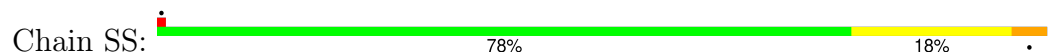
- Molecule 77: Ribosomal protein uS9




- Molecule 78: Ribosomal protein eS17

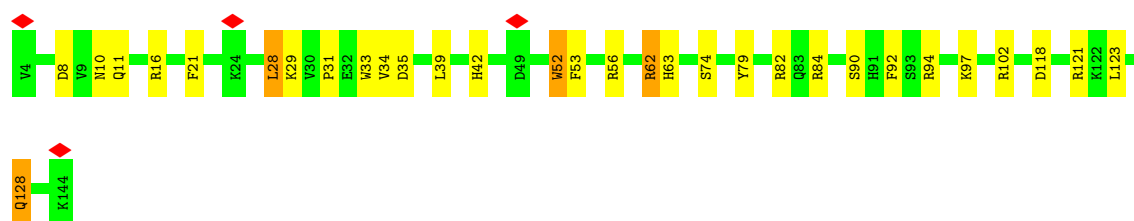


- Molecule 79: Ribosomal protein uS13




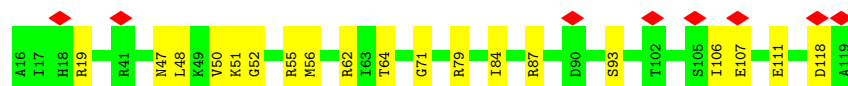
- Molecule 80: Ribosomal protein eS19

Chain ST:  78% 19%




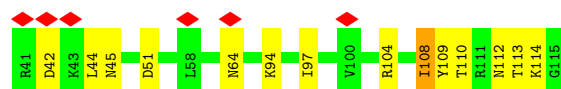
- Molecule 81: Ribosomal protein uS10

Chain SU:  82% 18% 8%




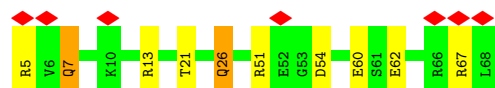
- Molecule 82: Ribosomal protein es25

Chain SZ:  81% 17% 8%




- Molecule 83: Ribosomal protein eS28

Chain Sc:  84% 12% 11%



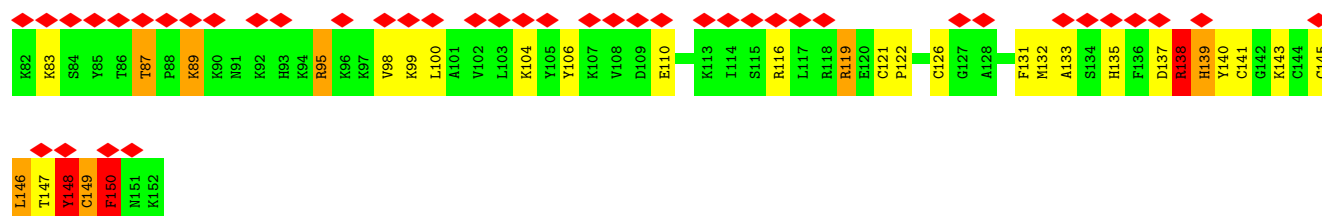
- Molecule 84: Ribosomal protein uS14

Chain Sd:  77% 17% 6%

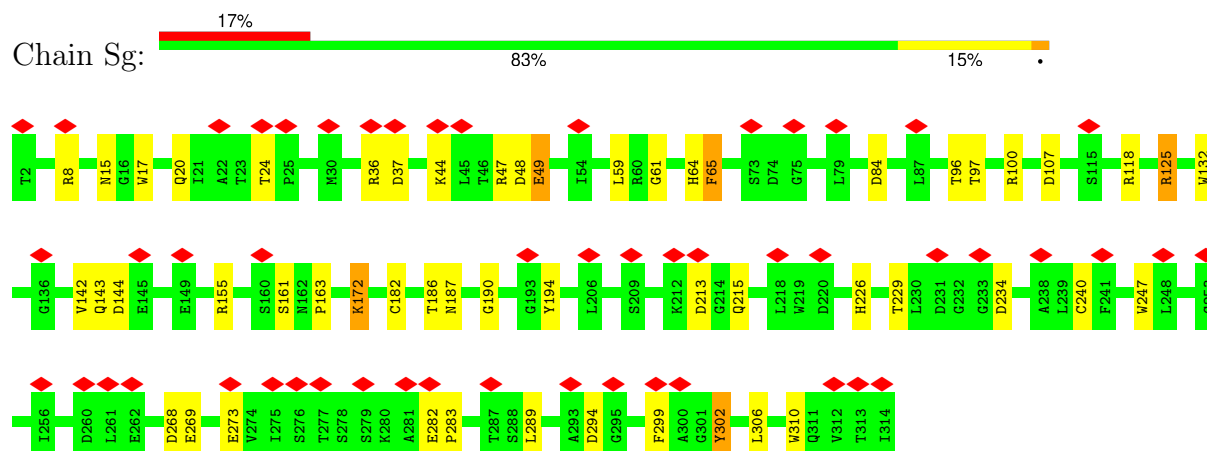


- Molecule 85: Ribosomal protein eS31

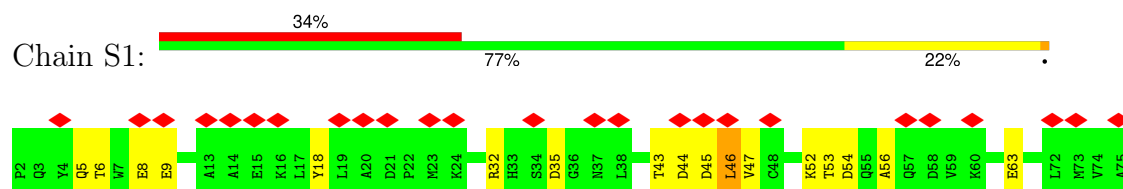
Chain Sf:  56% 30% 10% 4%



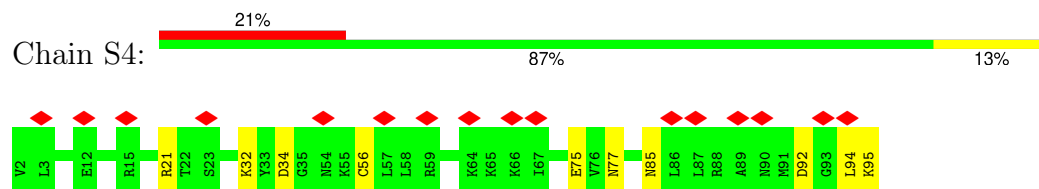
- Molecule 86: Ribosomal protein RACK1



- Molecule 87: SRP9



- Molecule 88: SRP14



## 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: MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.70	1/1906 (0.1%)	1.25	18/2556 (0.7%)
2	D	0.67	2/2426 (0.1%)	1.17	24/3252 (0.7%)
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	0.62	1/1152 (0.1%)	1.10	6/1539 (0.4%)
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	5/1770 (0.3%)
14	U	0.61	1/822 (0.1%)	0.99	1/1103 (0.1%)
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	1/903 (0.1%)	1.28	10/1216 (0.8%)
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	802/136805 (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	39/5766 (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	1.18	3/720 (0.4%)
42	j	0.83	1/721 (0.1%)	1.30	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	8/3171 (0.3%)	0.95	11/4257 (0.3%)
49	3	1.56	2/1804 (0.1%)	1.07	7/2805 (0.2%)
50	4	0.77	1/5090 (0.0%)	1.05	13/7936 (0.2%)
51	9	0.35	0/858	0.58	0/1156
52	6	0.30	0/1521	0.49	0/2039
53	S2	0.60	27/41241 (0.1%)	1.15	363/64249 (0.6%)
54	SA	0.63	1/1679 (0.1%)	1.05	10/2283 (0.4%)
55	SB	0.74	6/1753 (0.3%)	1.12	14/2350 (0.6%)
56	SC	0.69	1/1726 (0.1%)	1.05	14/2332 (0.6%)
57	SE	0.64	3/2118 (0.1%)	1.09	15/2849 (0.5%)
58	SG	0.69	4/1946 (0.2%)	1.05	8/2590 (0.3%)
59	SH	0.51	0/1544	0.94	5/2068 (0.2%)
60	SI	0.76	3/1715 (0.2%)	1.11	12/2287 (0.5%)
61	SJ	0.59	1/1550 (0.1%)	1.20	12/2069 (0.6%)
62	SL	0.66	1/1259 (0.1%)	1.05	4/1684 (0.2%)
63	SN	0.60	0/1226	1.05	7/1649 (0.4%)
64	SO	0.61	0/1029	1.23	13/1380 (0.9%)
65	SV	0.54	0/631	0.93	0/844
66	SW	0.64	1/1051 (0.1%)	1.03	6/1406 (0.4%)
67	SX	0.60	0/1118	1.06	10/1493 (0.7%)
68	SY	0.55	0/1040	0.94	0/1382
69	Sa	0.71	1/794 (0.1%)	1.16	6/1065 (0.6%)
70	Sb	0.48	0/665	0.90	1/891 (0.1%)
71	Se	0.50	0/458	0.97	3/602 (0.5%)
72	SD	0.60	1/1793 (0.1%)	1.01	5/2414 (0.2%)
73	SF	0.62	2/1531 (0.1%)	1.00	6/2059 (0.3%)
74	SK	0.58	0/851	1.01	5/1147 (0.4%)
75	SM	0.69	0/970	1.05	6/1300 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	SP	0.88	2/816 (0.2%)	1.19	10/1084 (0.9%)
77	SQ	0.51	0/1142	1.08	12/1528 (0.8%)
78	SR	0.50	0/1060	0.73	0/1421
79	SS	0.46	0/1157	1.00	5/1548 (0.3%)
80	ST	0.61	1/1119 (0.1%)	1.05	3/1499 (0.2%)
81	SU	0.52	0/828	0.91	0/1112
82	SZ	0.47	0/604	0.84	0/810
83	Sc	0.57	2/507 (0.4%)	0.75	0/677
84	Sd	0.66	0/445	1.12	2/589 (0.3%)
85	Sf	0.96	3/593 (0.5%)	1.61	15/786 (1.9%)
86	Sg	0.56	0/2493	0.85	3/3394 (0.1%)
87	S1	1.04	4/619 (0.6%)	0.90	1/832 (0.1%)
88	S4	0.88	2/608 (0.3%)	0.77	0/809
All	All	0.65	184/244482 (0.1%)	1.12	1884/358687 (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
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 184 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	3	31	C	O3'-P	-62.25	0.86	1.61
50	4	183	A	O3'-P	-44.21	1.08	1.61
32	5	1823	G	O3'-P	35.64	2.04	1.61
48	z	340	MET	C-N	22.91	1.86	1.34
48	z	345	PHE	C-N	-18.41	0.91	1.34

The worst 5 of 1884 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	3	38	C	P-O3'-C3'	-20.62	94.95	119.70
48	z	340	MET	O-C-N	19.47	153.86	122.70
49	3	31	C	O3'-P-O5'	-18.73	68.41	104.00
48	z	340	MET	C-N-CA	-18.61	75.16	121.70
85	Sf	146	LEU	CA-CB-CG	16.38	152.97	115.30

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 [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%)	2	21
2	D	290/292 (99%)	228 (79%)	41 (14%)	21 (7%)	1	13
3	G	236/238 (99%)	188 (80%)	41 (17%)	7 (3%)	3	27
4	H	188/190 (99%)	162 (86%)	20 (11%)	6 (3%)	3	26
5	J	168/170 (99%)	126 (75%)	33 (20%)	9 (5%)	1	17
6	L	208/210 (99%)	166 (80%)	29 (14%)	13 (6%)	1	15
7	M	136/138 (99%)	111 (82%)	21 (15%)	4 (3%)	3	27
8	N	201/203 (99%)	159 (79%)	31 (15%)	11 (6%)	1	17
9	O	199/201 (99%)	177 (89%)	19 (10%)	3 (2%)	8	38
10	Q	185/187 (99%)	154 (83%)	24 (13%)	7 (4%)	2	23
11	R	178/180 (99%)	148 (83%)	23 (13%)	7 (4%)	2	22
12	S	173/175 (99%)	139 (80%)	27 (16%)	7 (4%)	2	22
13	T	157/159 (99%)	132 (84%)	20 (13%)	5 (3%)	3	26
14	U	97/99 (98%)	80 (82%)	14 (14%)	3 (3%)	3	27
15	V	129/131 (98%)	110 (85%)	14 (11%)	5 (4%)	2	22
16	X	117/119 (98%)	102 (87%)	12 (10%)	3 (3%)	4	29
17	Y	132/134 (98%)	105 (80%)	21 (16%)	6 (4%)	2	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	Z	133/135 (98%)	111 (84%)	15 (11%)	7 (5%)	1	18
19	a	145/147 (99%)	114 (79%)	24 (17%)	7 (5%)	2	19
20	b	73/75 (97%)	60 (82%)	10 (14%)	3 (4%)	2	21
21	c	92/94 (98%)	78 (85%)	10 (11%)	4 (4%)	2	20
22	d	105/107 (98%)	85 (81%)	16 (15%)	4 (4%)	2	23
23	e	126/128 (98%)	110 (87%)	14 (11%)	2 (2%)	8	37
24	f	107/109 (98%)	89 (83%)	11 (10%)	7 (6%)	1	15
25	g	112/114 (98%)	100 (89%)	10 (9%)	2 (2%)	7	35
26	h	120/122 (98%)	97 (81%)	21 (18%)	2 (2%)	7	36
27	i	100/102 (98%)	85 (85%)	13 (13%)	2 (2%)	6	34
28	k	67/69 (97%)	53 (79%)	11 (16%)	3 (4%)	2	20
29	l	48/50 (96%)	42 (88%)	5 (10%)	1 (2%)	5	33
30	m	50/52 (96%)	44 (88%)	6 (12%)	0	100	100
31	o	102/104 (98%)	79 (78%)	17 (17%)	6 (6%)	1	16
35	B	392/394 (100%)	309 (79%)	54 (14%)	29 (7%)	1	12
36	C	365/367 (100%)	292 (80%)	55 (15%)	18 (5%)	2	18
37	E	232/236 (98%)	144 (62%)	55 (24%)	33 (14%)	0	3
38	F	223/225 (99%)	180 (81%)	35 (16%)	8 (4%)	3	24
39	I	211/213 (99%)	170 (81%)	28 (13%)	13 (6%)	1	15
40	P	151/153 (99%)	134 (89%)	15 (10%)	2 (1%)	10	41
41	W	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
42	j	84/86 (98%)	64 (76%)	18 (21%)	2 (2%)	5	30
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	16
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	18
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	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	26
57	SE	260/262 (99%)	198 (76%)	44 (17%)	18 (7%)	1	13
58	SG	235/237 (99%)	195 (83%)	32 (14%)	8 (3%)	3	25
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	20
61	SJ	183/185 (99%)	134 (73%)	34 (19%)	15 (8%)	1	10
62	SL	150/152 (99%)	122 (81%)	22 (15%)	6 (4%)	2	22
63	SN	147/149 (99%)	115 (78%)	28 (19%)	4 (3%)	4	29
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	9
66	SW	127/129 (98%)	108 (85%)	16 (13%)	3 (2%)	5	30
67	SX	139/141 (99%)	109 (78%)	26 (19%)	4 (3%)	3	27
68	SY	124/126 (98%)	101 (82%)	16 (13%)	7 (6%)	1	17
69	Sa	96/98 (98%)	69 (72%)	18 (19%)	9 (9%)	0	8
70	Sb	81/83 (98%)	61 (75%)	16 (20%)	4 (5%)	2	18
71	Se	55/57 (96%)	41 (74%)	12 (22%)	2 (4%)	3	24
72	SD	225/227 (99%)	174 (77%)	41 (18%)	10 (4%)	2	20
73	SF	189/191 (99%)	146 (77%)	33 (18%)	10 (5%)	1	18
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	16
78	SR	127/129 (98%)	111 (87%)	11 (9%)	5 (4%)	2	22
79	SS	135/137 (98%)	114 (84%)	12 (9%)	9 (7%)	1	14
80	ST	139/141 (99%)	115 (83%)	18 (13%)	6 (4%)	2	20
81	SU	102/104 (98%)	83 (81%)	13 (13%)	6 (6%)	1	16
82	SZ	73/75 (97%)	59 (81%)	9 (12%)	5 (7%)	1	14
83	Sc	60/64 (94%)	47 (78%)	12 (20%)	1 (2%)	7	36
84	Sd	50/52 (96%)	36 (72%)	11 (22%)	3 (6%)	1	15
85	Sf	69/71 (97%)	42 (61%)	15 (22%)	12 (17%)	0	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
86	Sg	311/313 (99%)	240 (77%)	56 (18%)	15 (5%)	2	19
87	S1	72/74 (97%)	61 (85%)	6 (8%)	5 (7%)	1	13
88	S4	72/76 (95%)	68 (94%)	4 (6%)	0	100	100
All	All	12314/12513 (98%)	9837 (80%)	1799 (15%)	678 (6%)	2	17

5 of 678 Ramachandran outliers are listed below:

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

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	187/187 (100%)	137 (73%)	50 (27%)	0	3
2	D	246/247 (100%)	183 (74%)	63 (26%)	0	3
3	G	204/206 (99%)	150 (74%)	54 (26%)	0	3
4	H	169/169 (100%)	131 (78%)	38 (22%)	1	5
5	J	143/143 (100%)	108 (76%)	35 (24%)	0	4
6	L	176/176 (100%)	133 (76%)	43 (24%)	0	4
7	M	116/116 (100%)	88 (76%)	28 (24%)	0	4
8	N	171/171 (100%)	126 (74%)	45 (26%)	0	3
9	O	172/172 (100%)	138 (80%)	34 (20%)	1	7
10	Q	163/163 (100%)	126 (77%)	37 (23%)	0	5
11	R	159/159 (100%)	120 (76%)	39 (24%)	0	4
12	S	156/156 (100%)	124 (80%)	32 (20%)	1	6
13	T	139/139 (100%)	105 (76%)	34 (24%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	U	89/89 (100%)	65 (73%)	24 (27%)	0	2
15	V	101/101 (100%)	78 (77%)	23 (23%)	0	5
16	X	107/107 (100%)	89 (83%)	18 (17%)	1	11
17	Y	124/124 (100%)	94 (76%)	30 (24%)	0	4
18	Z	117/117 (100%)	93 (80%)	24 (20%)	1	6
19	a	119/119 (100%)	99 (83%)	20 (17%)	1	11
20	b	63/63 (100%)	48 (76%)	15 (24%)	0	4
21	c	79/79 (100%)	59 (75%)	20 (25%)	0	3
22	d	98/98 (100%)	65 (66%)	33 (34%)	0	1
23	e	114/114 (100%)	91 (80%)	23 (20%)	1	6
24	f	88/88 (100%)	73 (83%)	15 (17%)	1	11
25	g	98/98 (100%)	78 (80%)	20 (20%)	1	6
26	h	109/109 (100%)	91 (84%)	18 (16%)	2	12
27	i	86/86 (100%)	69 (80%)	17 (20%)	1	7
28	k	64/64 (100%)	51 (80%)	13 (20%)	1	6
29	l	47/47 (100%)	37 (79%)	10 (21%)	1	6
30	m	48/48 (100%)	33 (69%)	15 (31%)	0	1
31	o	92/92 (100%)	70 (76%)	22 (24%)	0	4
35	B	335/335 (100%)	260 (78%)	75 (22%)	1	5
36	C	305/305 (100%)	233 (76%)	72 (24%)	0	4
37	E	209/209 (100%)	163 (78%)	46 (22%)	1	5
38	F	194/194 (100%)	142 (73%)	52 (27%)	0	2
39	I	180/180 (100%)	126 (70%)	54 (30%)	0	2
40	P	134/134 (100%)	108 (81%)	26 (19%)	1	7
41	W	55/55 (100%)	38 (69%)	17 (31%)	0	1
42	j	73/73 (100%)	60 (82%)	13 (18%)	1	9
43	n	22/22 (100%)	16 (73%)	6 (27%)	0	2
44	p	74/74 (100%)	62 (84%)	12 (16%)	2	12
45	r	109/109 (100%)	83 (76%)	26 (24%)	0	4
46	K	136/136 (100%)	118 (87%)	18 (13%)	3	18
47	q	170/170 (100%)	134 (79%)	36 (21%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	z	340/340 (100%)	318 (94%)	22 (6%)	14	41
51	9	92/94 (98%)	88 (96%)	4 (4%)	25	50
52	6	157/157 (100%)	151 (96%)	6 (4%)	28	53
54	SA	174/174 (100%)	132 (76%)	42 (24%)	0	4
55	SB	194/194 (100%)	155 (80%)	39 (20%)	1	7
56	SC	184/184 (100%)	141 (77%)	43 (23%)	0	4
57	SE	224/224 (100%)	172 (77%)	52 (23%)	0	5
58	SG	207/207 (100%)	166 (80%)	41 (20%)	1	7
59	SH	169/169 (100%)	145 (86%)	24 (14%)	2	17
60	SI	178/178 (100%)	144 (81%)	34 (19%)	1	7
61	SJ	161/161 (100%)	117 (73%)	44 (27%)	0	2
62	SL	136/136 (100%)	104 (76%)	32 (24%)	0	4
63	SN	130/130 (100%)	103 (79%)	27 (21%)	1	6
64	SO	106/106 (100%)	74 (70%)	32 (30%)	0	2
65	SV	66/66 (100%)	50 (76%)	16 (24%)	0	4
66	SW	112/112 (100%)	90 (80%)	22 (20%)	1	7
67	SX	113/113 (100%)	95 (84%)	18 (16%)	2	13
68	SY	108/108 (100%)	85 (79%)	23 (21%)	1	6
69	Sa	85/85 (100%)	72 (85%)	13 (15%)	2	14
70	Sb	75/75 (100%)	58 (77%)	17 (23%)	0	5
71	Se	46/46 (100%)	35 (76%)	11 (24%)	0	4
72	SD	190/190 (100%)	149 (78%)	41 (22%)	1	5
73	SF	161/161 (100%)	123 (76%)	38 (24%)	0	4
74	SK	89/89 (100%)	68 (76%)	21 (24%)	0	4
75	SM	104/104 (100%)	74 (71%)	30 (29%)	0	2
76	SP	88/88 (100%)	70 (80%)	18 (20%)	1	6
77	SQ	117/117 (100%)	91 (78%)	26 (22%)	1	5
78	SR	117/117 (100%)	102 (87%)	15 (13%)	3	19
79	SS	119/119 (100%)	96 (81%)	23 (19%)	1	7
80	ST	112/112 (100%)	87 (78%)	25 (22%)	1	5
81	SU	94/94 (100%)	82 (87%)	12 (13%)	3	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
82	SZ	66/66 (100%)	57 (86%)	9 (14%)	3	17
83	Sc	57/57 (100%)	47 (82%)	10 (18%)	1	10
84	Sd	45/45 (100%)	36 (80%)	9 (20%)	1	7
85	Sf	64/64 (100%)	45 (70%)	19 (30%)	0	2
86	Sg	272/272 (100%)	235 (86%)	37 (14%)	3	17
87	S1	67/67 (100%)	59 (88%)	8 (12%)	4	20
88	S4	69/69 (100%)	60 (87%)	9 (13%)	3	18
All	All	10728/10733 (100%)	8471 (79%)	2257 (21%)	2	6

5 of 2257 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
68	SY	61	ARG
72	SD	4	GLN
68	SY	47	MET
77	SQ	145	TYR
25	g	3	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 271 such sidechains are listed below:

Mol	Chain	Res	Type
73	SF	203	ASN
75	SM	99	ASN
83	Sc	45	ASN
30	m	87	GLN
26	h	98	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	5	3642/3658 (99%)	1674 (45%)	665 (18%)
33	7	119/120 (99%)	38 (31%)	13 (10%)
34	8	155/156 (99%)	63 (40%)	29 (18%)
49	3	73/76 (96%)	27 (36%)	5 (6%)
50	4	197/206 (95%)	43 (21%)	10 (5%)
53	S2	1714/1742 (98%)	830 (48%)	303 (17%)
All	All	5900/5958 (99%)	2675 (45%)	1025 (17%)



5 of 2675 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
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 ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	5	16
53	S2	6
48	z	5
50	4	3
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

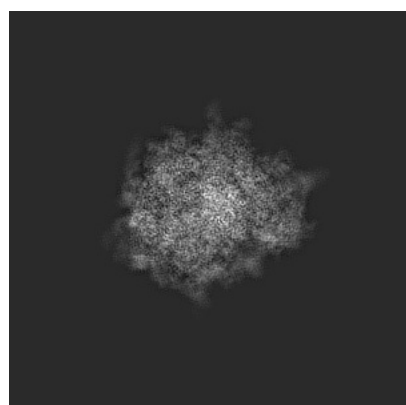
## 6 Map visualisation [i](#)

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.

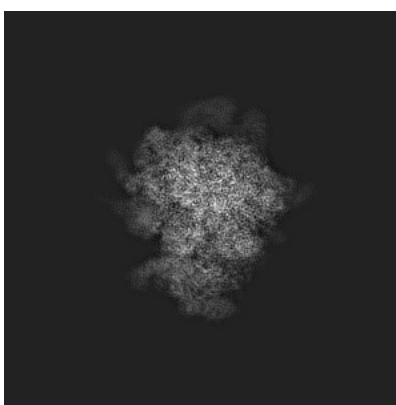
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

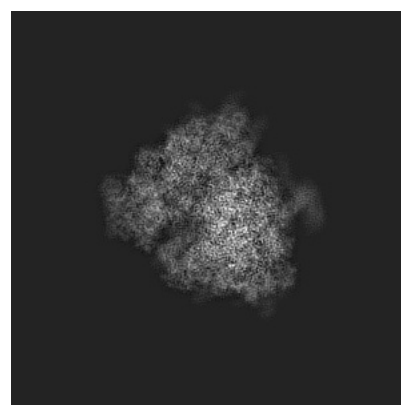
#### 6.1.1 Primary map



X



Y

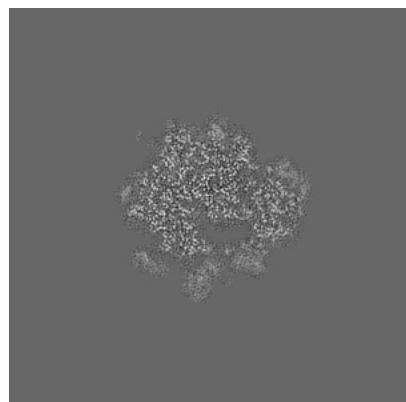


Z

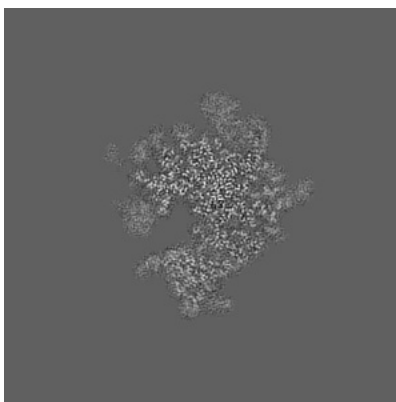
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

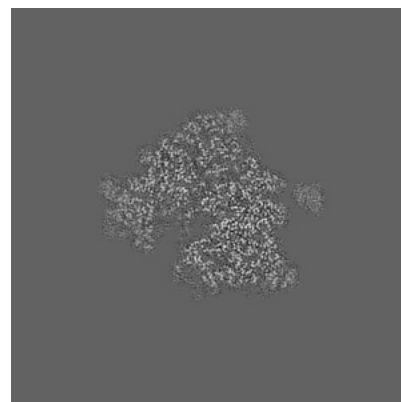
#### 6.2.1 Primary map



X Index: 210



Y Index: 210

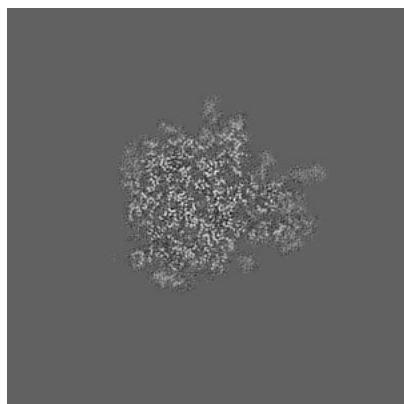


Z Index: 210

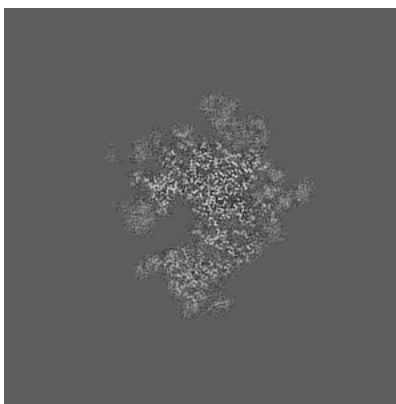
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

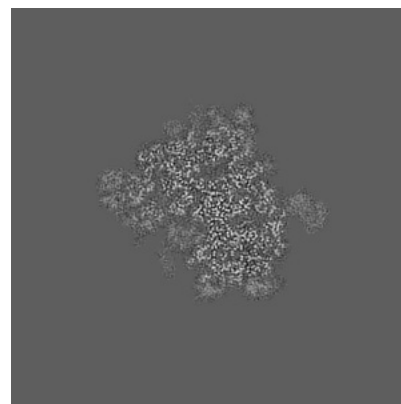
### 6.3.1 Primary map



X Index: 230



Y Index: 211

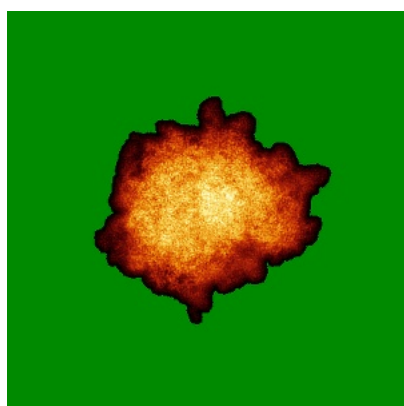


Z Index: 227

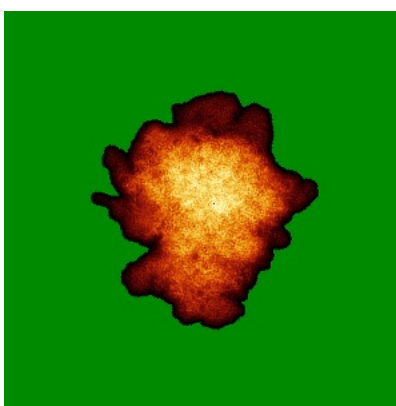
The images above show the largest variance slices of the map in three orthogonal directions.

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

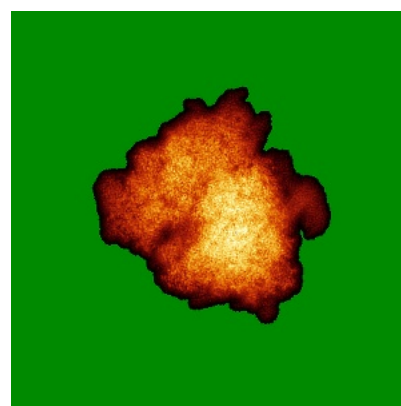
### 6.4.1 Primary map



X



Y

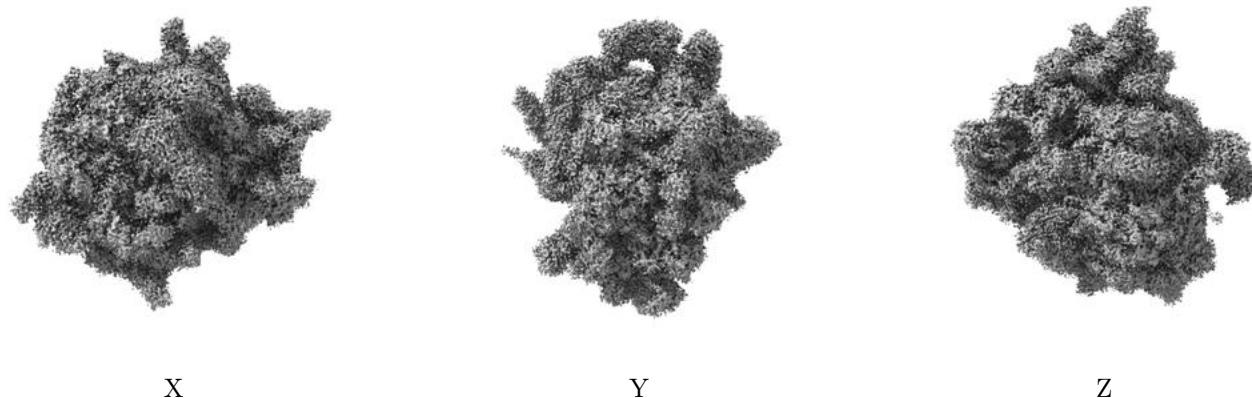


Z

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.

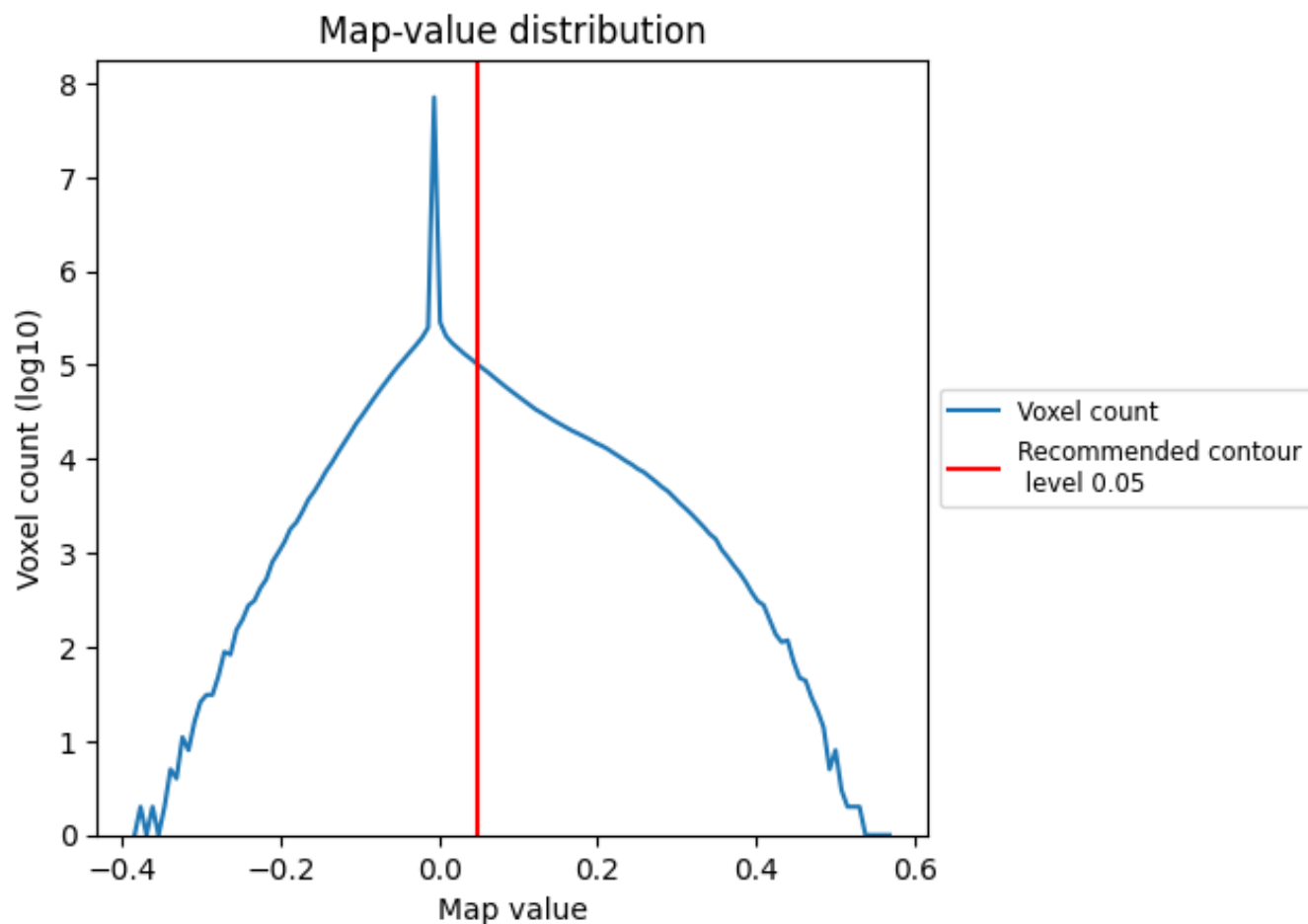
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

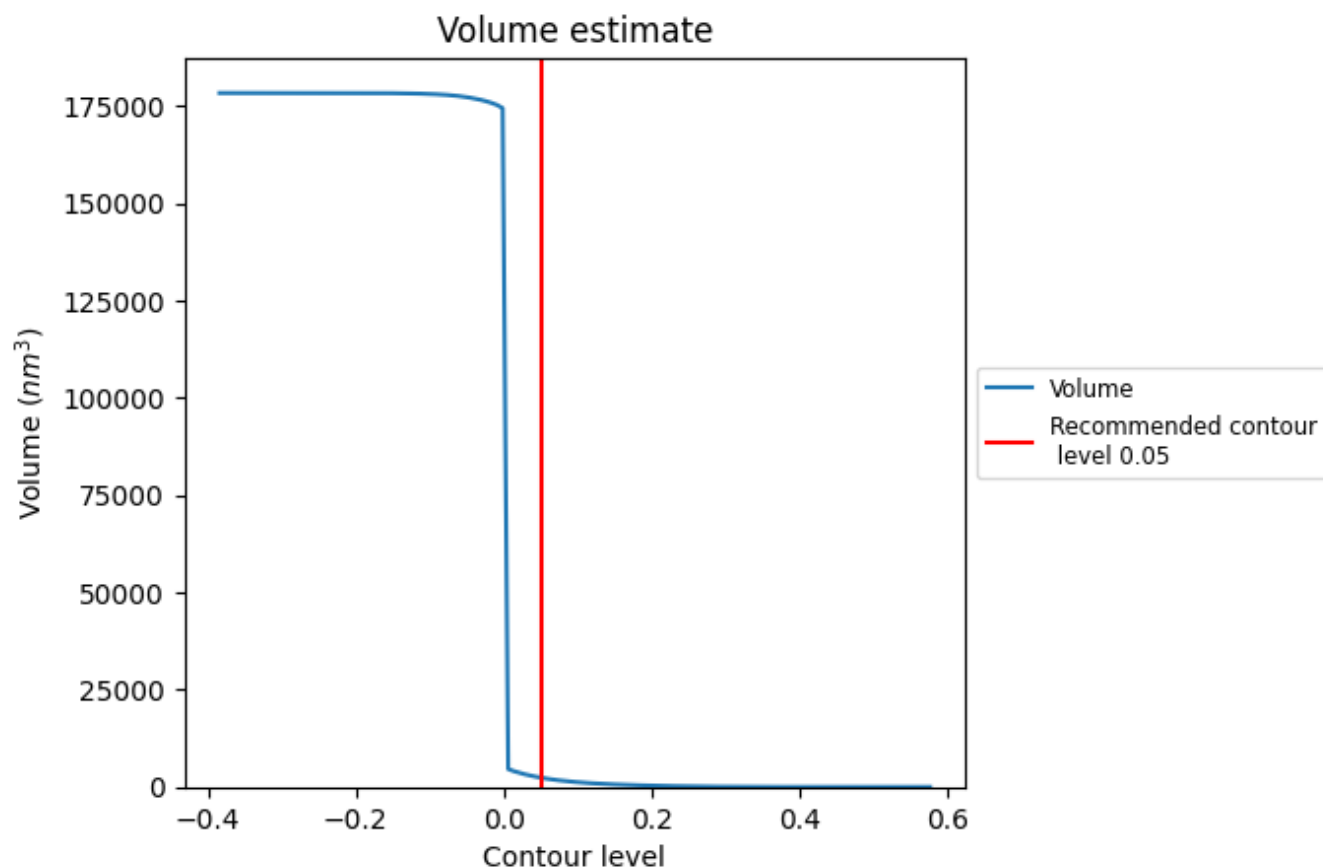
This section contains the results of statistical analysis of the map.

### 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.

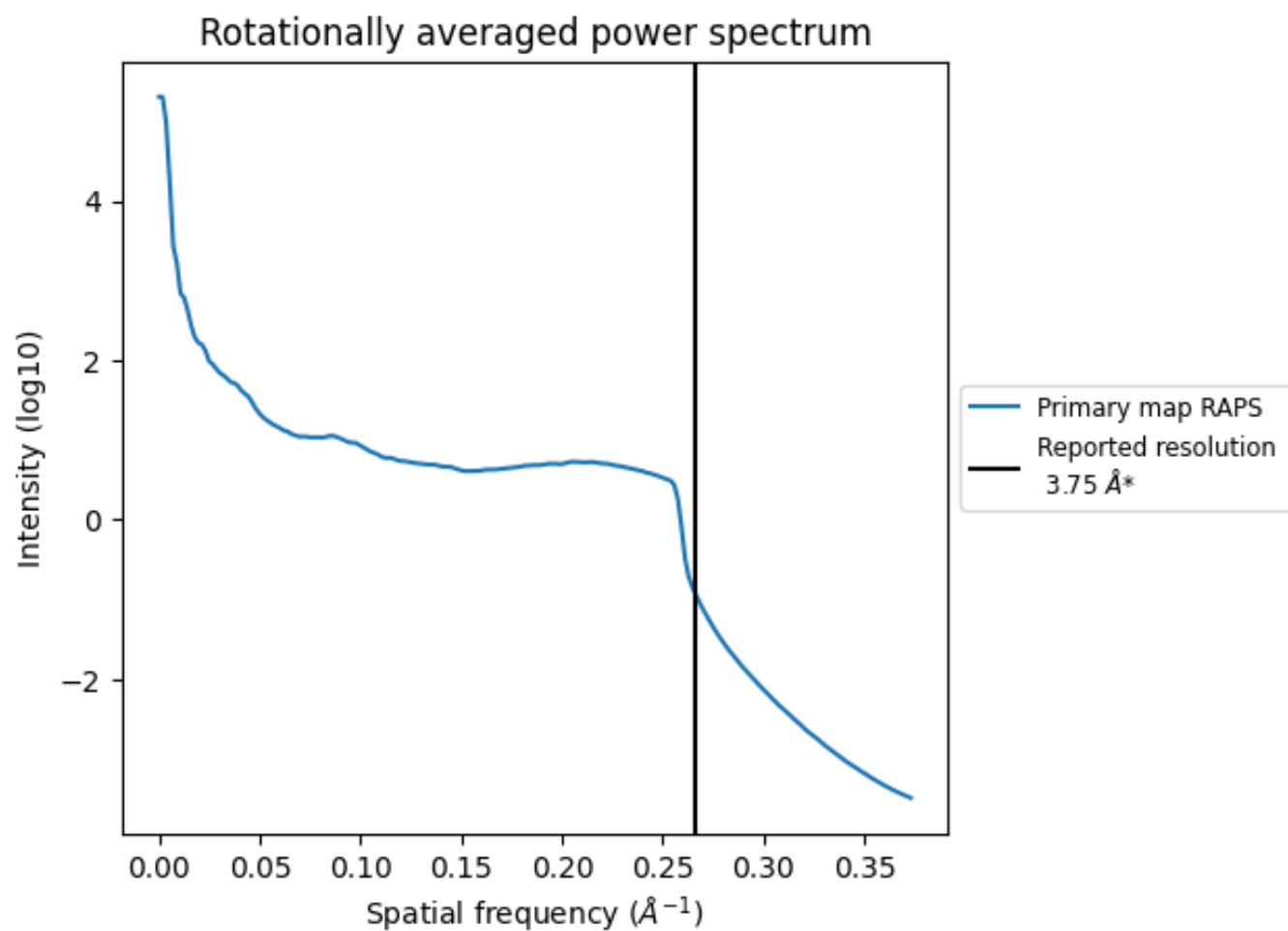
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2397 nm<sup>3</sup>; 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 ⓘ



\*Reported resolution corresponds to spatial frequency of 0.267 Å<sup>-1</sup>



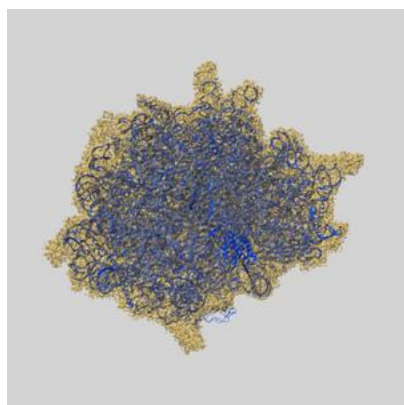
## 8 Fourier-Shell correlation

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

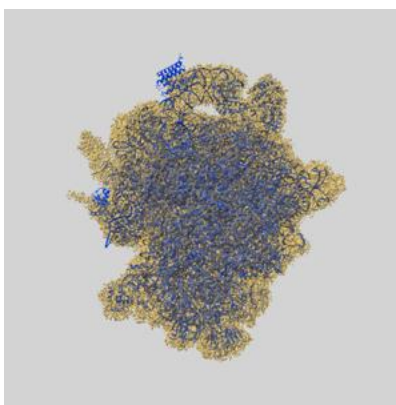
## 9 Map-model fit [i](#)

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](#).

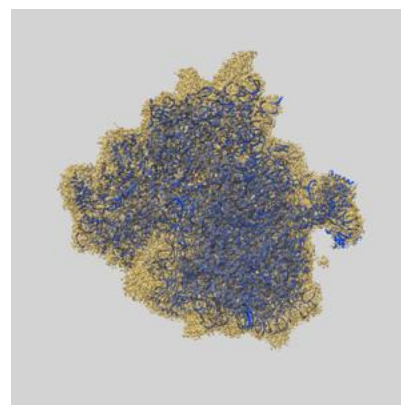
### 9.1 Map-model overlay [i](#)



X



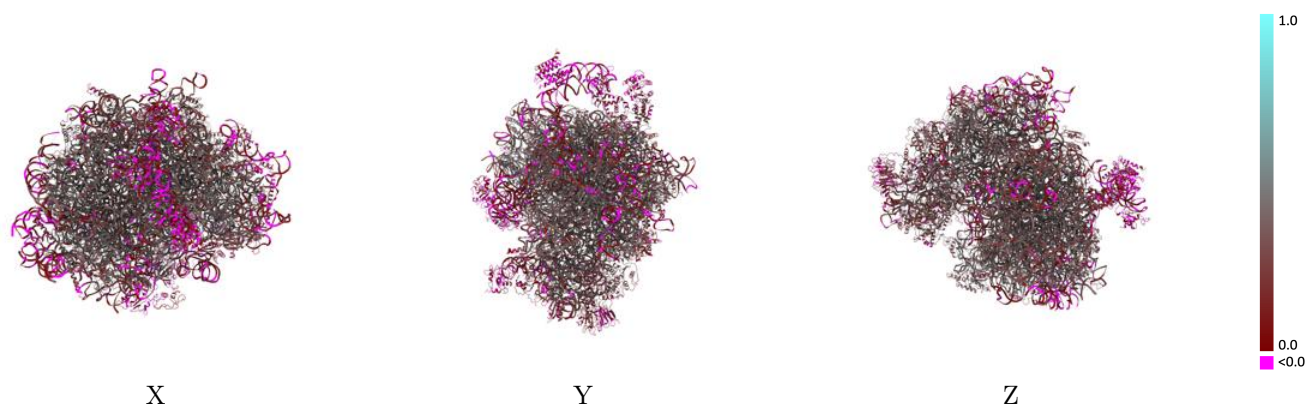
Y



Z

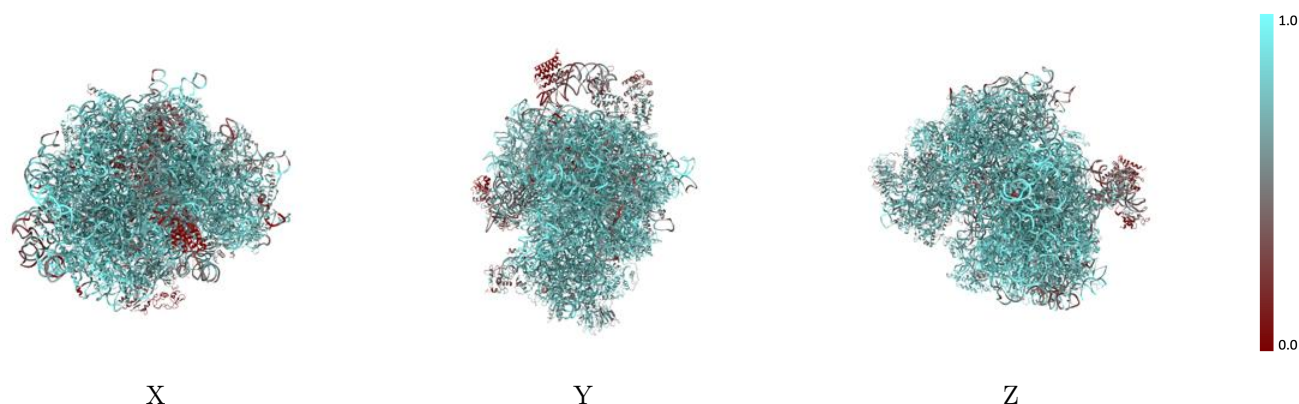
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



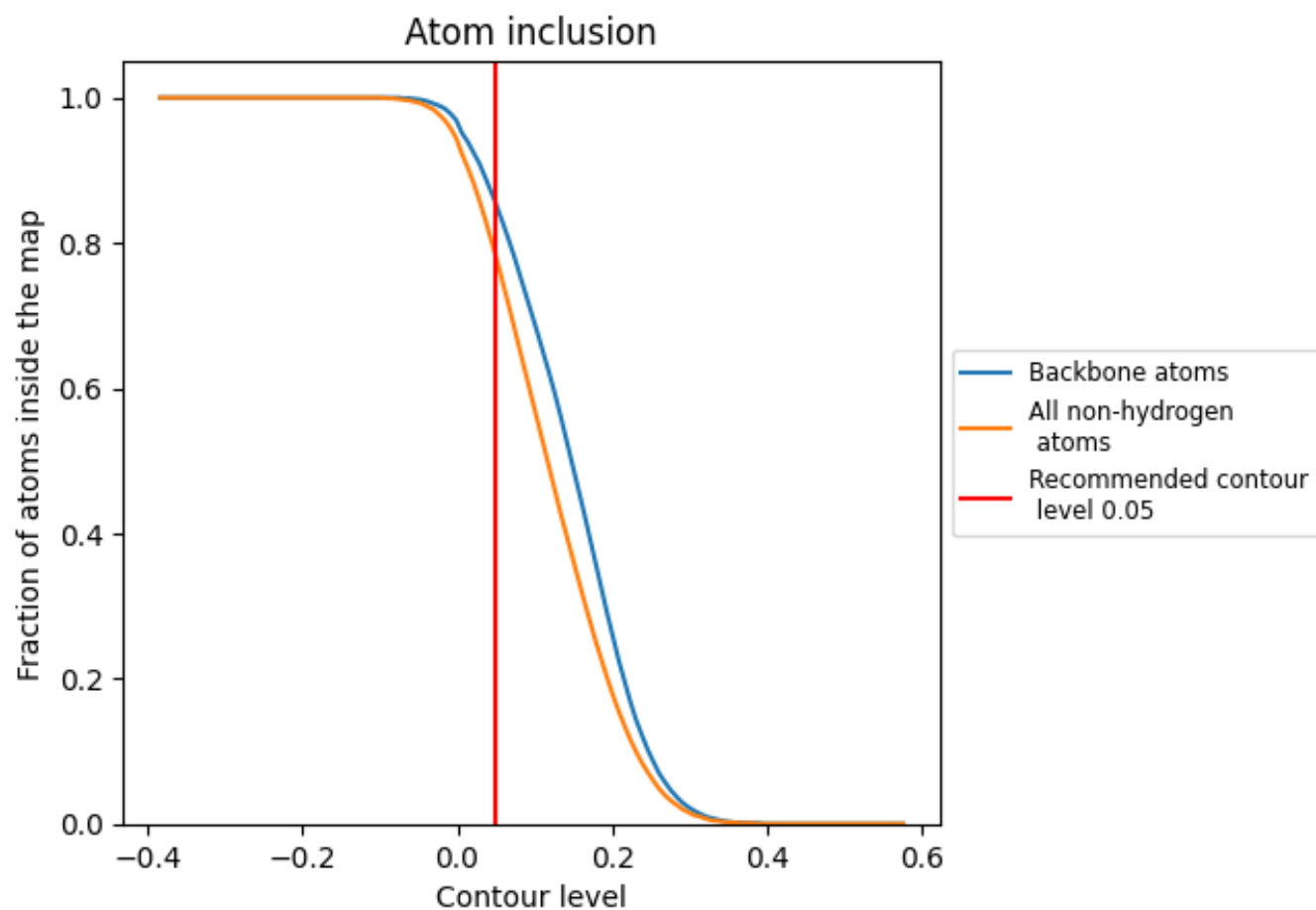
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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