



## wwPDB EM Validation Summary Report ⓘ

Oct 22, 2024 – 02:19 PM EDT

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

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:

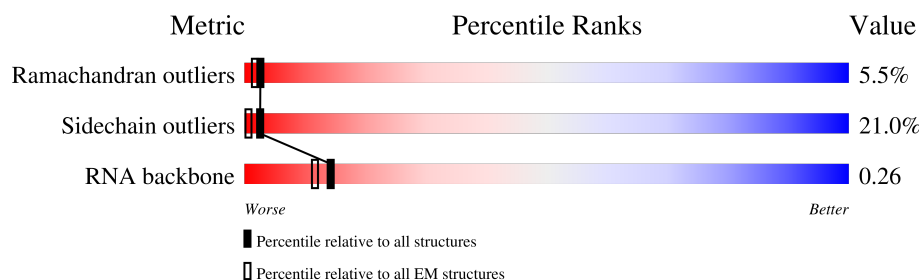
EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP)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









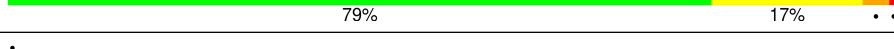
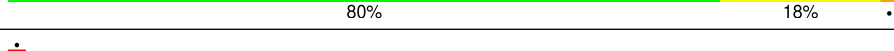
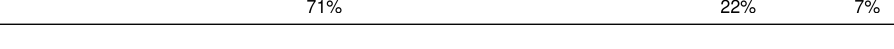
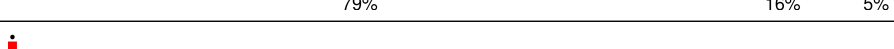
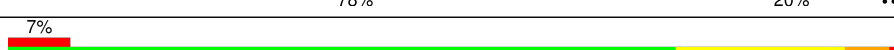

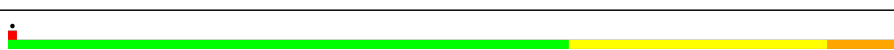

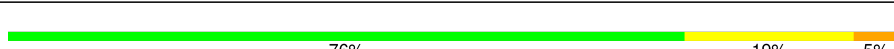





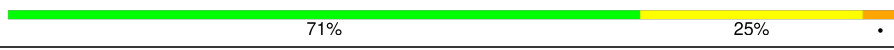
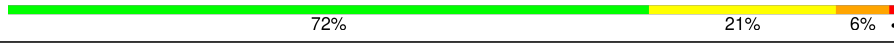
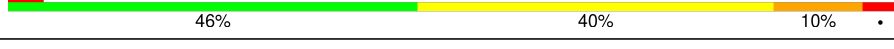


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	







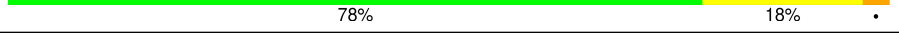




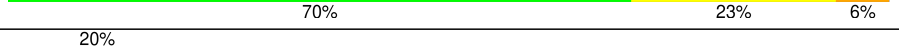



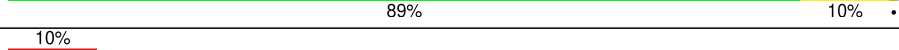



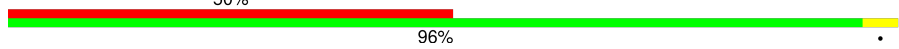

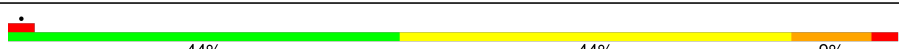


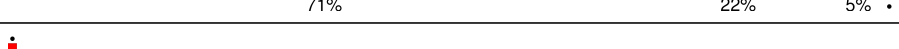
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Mol	Chain	Length	Quality of chain
9	O	201	
10	Q	187	
11	R	180	
12	S	175	
13	T	159	
14	U	99	
15	V	131	
16	X	119	
17	Y	134	
18	Z	135	
19	a	147	
20	b	75	
21	c	94	
22	d	107	
23	e	128	
24	f	109	
25	g	114	
26	h	122	
27	i	102	
28	k	69	
29	l	50	
30	m	52	
31	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	2	31	
50	3	76	
51	4	206	
52	9	105	
53	6	179	
54	S2	1742	
55	SA	208	
56	SB	213	
57	SC	218	
58	SE	262	




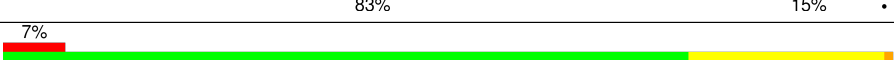
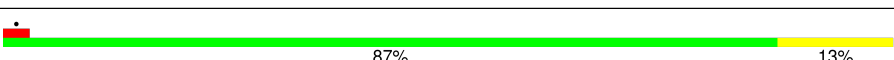

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Mol	Chain	Length	Quality of chain
59	SG	237	
60	SH	189	
61	SI	206	
62	SJ	185	
63	SL	152	
64	SN	149	
65	SO	136	
66	SV	82	
67	SW	129	
68	SX	141	
69	SY	126	
70	Sa	98	
71	Sb	83	
72	Se	57	
73	SD	227	
74	SF	191	
75	SK	98	
76	SM	124	
77	SP	96	
78	SQ	141	
79	SR	129	
80	SS	137	
81	ST	141	
82	SU	104	
83	SZ	75	

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Mol	Chain	Length	Quality of chain
84	Sc	64	
85	Sd	52	
86	Sf	71	
87	Sg	313	
88	S1	74	
89	S4	76	

## 2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 228197 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein uL2.

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

- Molecule 2 is a protein called Ribosomal protein uL18.

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

- Molecule 3 is a protein called Ribosomal protein eL8.

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

- Molecule 4 is a protein called Ribosomal protein uL6.

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

- Molecule 5 is a protein called Ribosomal protein uL5.

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

- Molecule 6 is a protein called Ribosomal protein eL13.

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

- Molecule 7 is a protein called Ribosomal protein eL14.

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

- Molecule 8 is a protein called Ribosomal protein eL15.

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

- Molecule 9 is a protein called Ribosomal protein uL13.

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

- Molecule 10 is a protein called Ribosomal protein eL18.

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

- Molecule 11 is a protein called Ribosomal protein eL19.

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

- Molecule 12 is a protein called Ribosomal protein eL20.

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

- Molecule 13 is a protein called Ribosomal protein eL21.

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

- Molecule 14 is a protein called Ribosomal protein eL22.



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

- Molecule 15 is a protein called Ribosomal protein uL14.

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

- Molecule 16 is a protein called Ribosomal protein uL23.

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

- Molecule 17 is a protein called Ribosomal protein uL24.

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

- Molecule 18 is a protein called Ribosomal protein eL27.

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

- Molecule 19 is a protein called Ribosomal protein uL15.

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

- Molecule 20 is a protein called Ribosomal protein eL29.

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

- Molecule 21 is a protein called Ribosomal protein eL30.

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

- Molecule 22 is a protein called Ribosomal protein eL31.

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

- Molecule 23 is a protein called Ribosomal protein eL32.

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

- Molecule 24 is a protein called Ribosomal protein eL33.

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

- Molecule 25 is a protein called Ribosomal protein eL34.

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

- Molecule 26 is a protein called Ribosomal protein uL29.

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

- Molecule 27 is a protein called Ribosomal protein eL36.

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

- Molecule 28 is a protein called Ribosomal protein eL38.

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

- Molecule 29 is a protein called Ribosomal protein eL39.

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

- Molecule 30 is a protein called Ribosomal protein eL40.

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

- Molecule 31 is a protein called Ribosomal protein eL42.

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

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

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

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

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

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

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

- Molecule 35 is a protein called Ribosomal protein uL3.

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

- Molecule 36 is a protein called Ribosomal protein uL4.

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

- Molecule 37 is a protein called Ribosomal protein eL6.

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

- Molecule 38 is a protein called Ribosomal protein uL30.

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

- Molecule 39 is a protein called Ribosomal protein uL16.

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

- Molecule 40 is a protein called Ribosomal protein uL22.

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

- Molecule 41 is a protein called Ribosomal protein eL24.

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

- Molecule 42 is a protein called Ribosomal protein eL37.

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

- Molecule 43 is a protein called Ribosomal protein eL41.

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

- Molecule 44 is a protein called Ribosomal protein eL43.

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

- Molecule 45 is a protein called Ribosomal protein eL28.

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

- Molecule 46 is a protein called Ribosomal protein uL11.

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

- Molecule 47 is a protein called Ribosomal protein uL10.

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

- Molecule 48 is a protein called SRP54.

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

- Molecule 49 is a protein called Nascent chain.

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

- Molecule 50 is a RNA chain called Val tRNA.

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

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

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

- Molecule 52 is a protein called SRP19.

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

- Molecule 53 is a protein called SRP68.

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

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

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

- Molecule 55 is a protein called Ribosomal protein uS2.

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

- Molecule 56 is a protein called Ribosomal protein eS1.

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

- Molecule 57 is a protein called Ribosomal protein uS5.

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

- Molecule 58 is a protein called Ribosomal protein eS4.

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

- Molecule 59 is a protein called Ribosomal protein eS6.

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

- Molecule 60 is a protein called Ribosomal protein eS7.

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

- Molecule 61 is a protein called Ribosomal protein eS8.

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

- Molecule 62 is a protein called Ribosomal protein uS4.

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

- Molecule 63 is a protein called Ribosomal protein uS17.

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

- Molecule 64 is a protein called Ribosomal protein uS15.

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

- Molecule 65 is a protein called Ribosomal protein uS11.

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

- Molecule 66 is a protein called Ribosomal protein eS21.

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

- Molecule 67 is a protein called Ribosomal protein uS8.

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

- Molecule 68 is a protein called Ribosomal protein uS12.

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

- Molecule 69 is a protein called Ribosomal protein eS24.

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

- Molecule 70 is a protein called Ribosomal protein eS26.



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

- Molecule 71 is a protein called Ribosomal protein eS27.

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

- Molecule 72 is a protein called Ribosomal protein eS30.

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

- Molecule 73 is a protein called Ribosomal protein uS3.

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

- Molecule 74 is a protein called Ribosomal protein uS7.

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

- Molecule 75 is a protein called Ribosomal protein eS10.

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

- Molecule 76 is a protein called Ribosomal protein eS12.

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

- Molecule 77 is a protein called Ribosomal protein uS19.

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

- Molecule 78 is a protein called Ribosomal protein uS9.

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

- Molecule 79 is a protein called Ribosomal protein eS17.

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

- Molecule 80 is a protein called Ribosomal protein uS13.

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

- Molecule 81 is a protein called Ribosomal protein eS19.

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

- Molecule 82 is a protein called Ribosomal protein uS10.

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

- Molecule 83 is a protein called Ribosomal protein es25.

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

- Molecule 84 is a protein called Ribosomal protein eS28.

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

- Molecule 85 is a protein called Ribosomal protein uS14.

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

- Molecule 86 is a protein called Ribosomal protein eS31.

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

- Molecule 87 is a protein called Ribosomal protein RACK1.

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

- Molecule 88 is a protein called SRP9.

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

- Molecule 89 is a protein called SRP14.

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

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

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

*Continued on next page...*

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

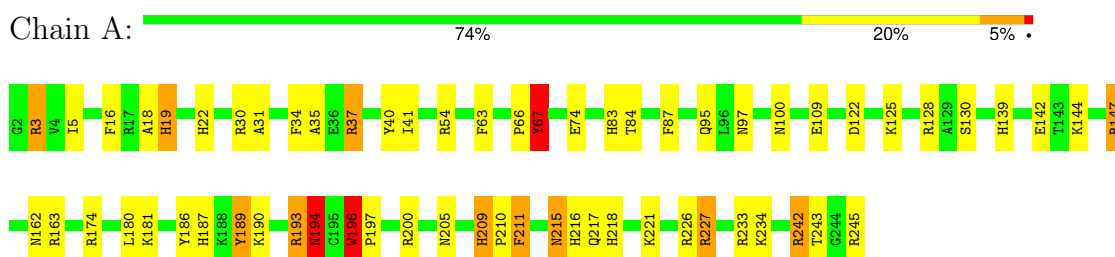
- Molecule 91 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

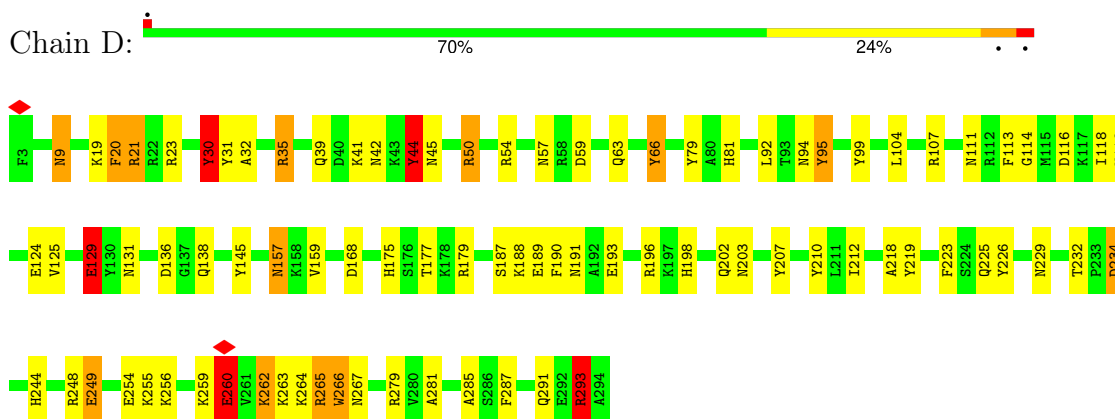
### 3 Residue-property plots [i](#)

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

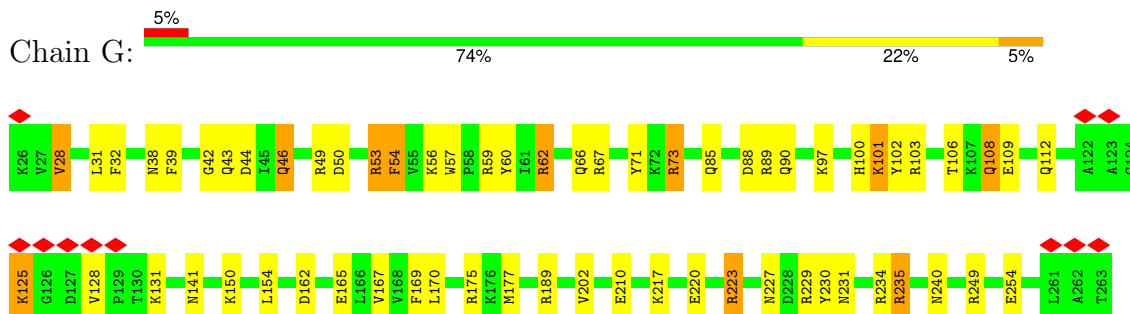
- Molecule 1: Ribosomal protein uL2




- Molecule 2: Ribosomal protein uL18

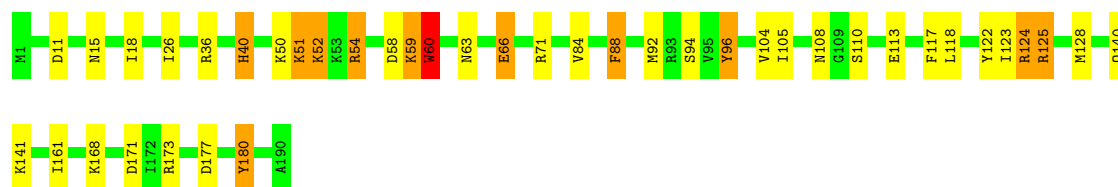


- Molecule 3: Ribosomal protein eL8



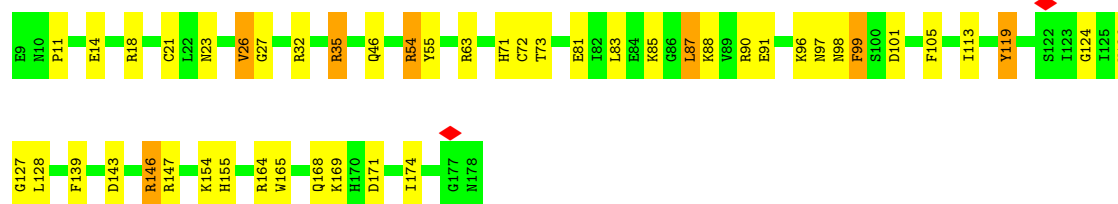
- Molecule 4: Ribosomal protein uL6

Chain H:  78% 15% 6% •



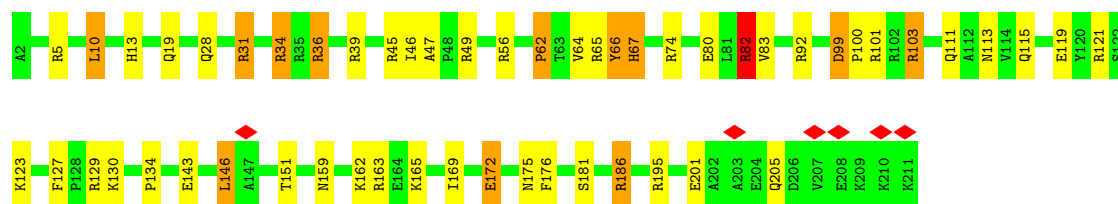
- Molecule 5: Ribosomal protein uL5

Chain J:  72% 24% •



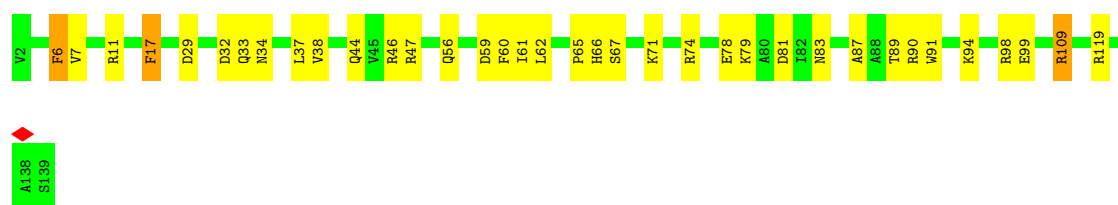
- Molecule 6: Ribosomal protein eL13

Chain L:  74% 20% 6% •



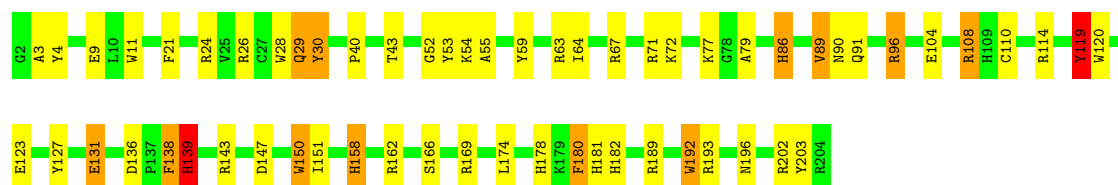
- Molecule 7: Ribosomal protein eL14

Chain M:  74% 24% •

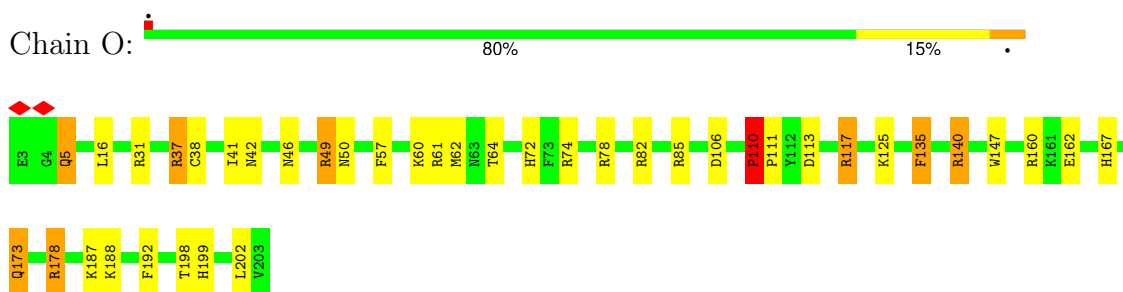


- Molecule 8: Ribosomal protein eL15

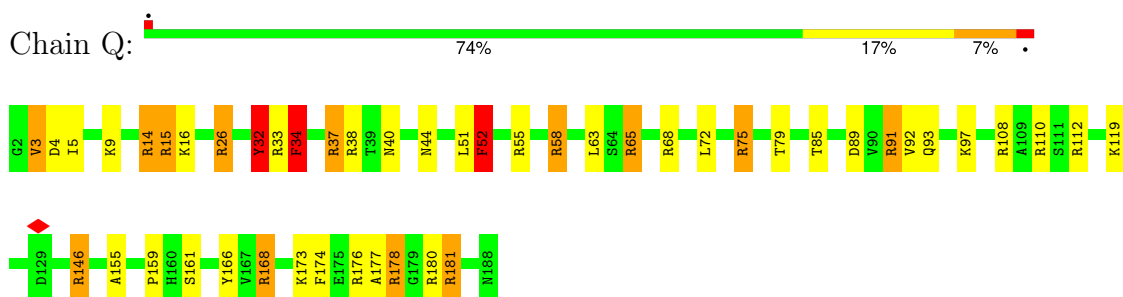
Chain N:  70% 23% 6% •



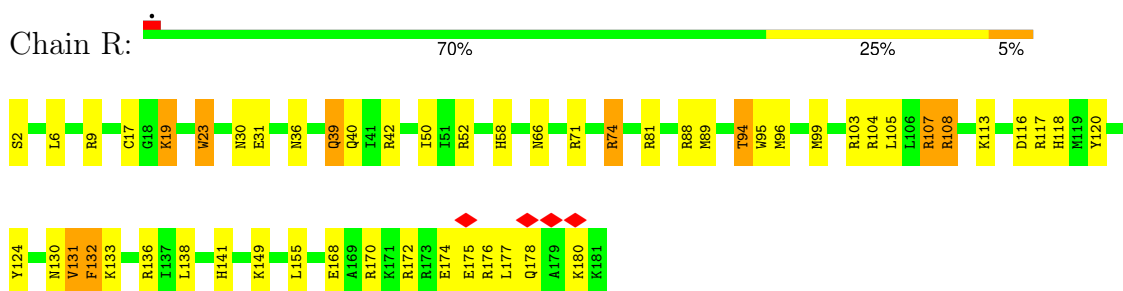
- Molecule 9: Ribosomal protein uL13



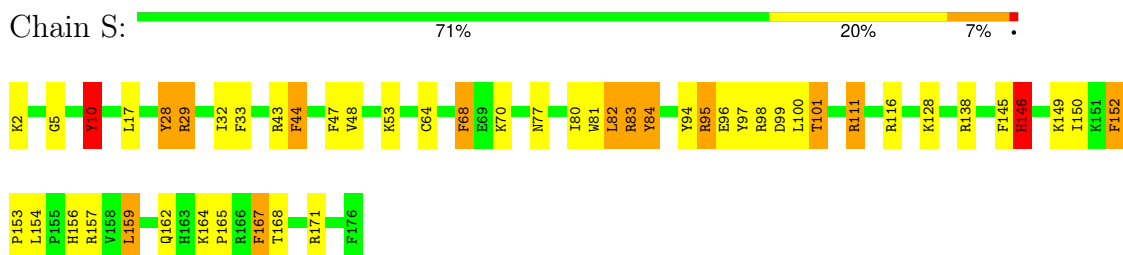
- Molecule 10: Ribosomal protein eL18



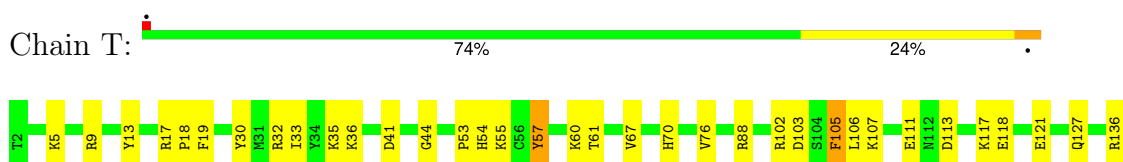
- Molecule 11: Ribosomal protein eL19

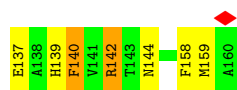


- Molecule 12: Ribosomal protein eL20



- Molecule 13: Ribosomal protein eL21





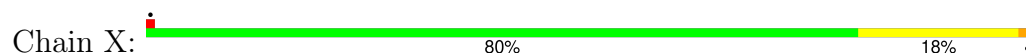
- Molecule 14: Ribosomal protein eL22



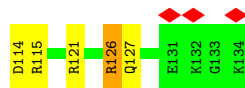
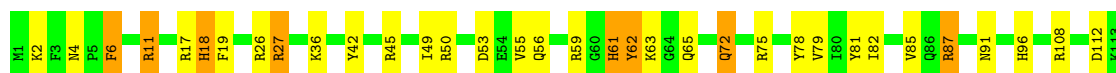
- Molecule 15: Ribosomal protein uL14



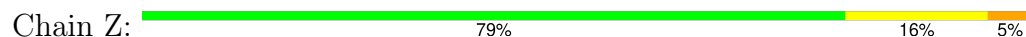
- Molecule 16: Ribosomal protein uL23



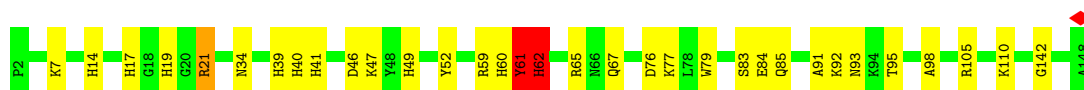
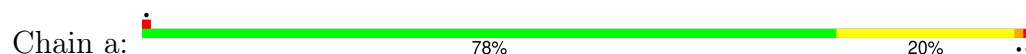
- Molecule 17: Ribosomal protein uL24



- Molecule 18: Ribosomal protein eL27

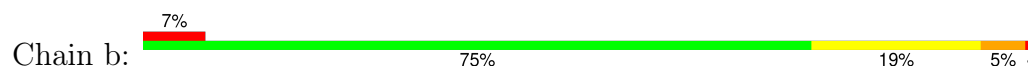


- Molecule 19: Ribosomal protein uL15





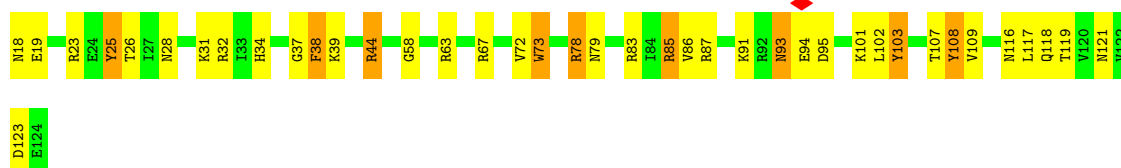
- Molecule 20: Ribosomal protein eL29



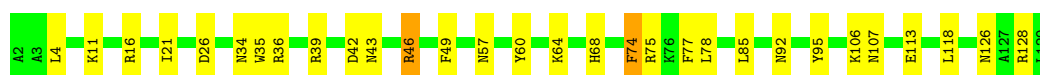
- Molecule 21: Ribosomal protein eL30



- Molecule 22: Ribosomal protein eL31



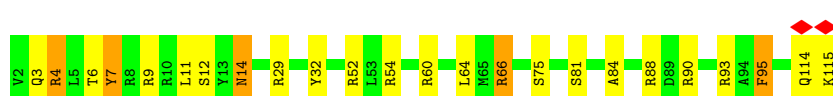
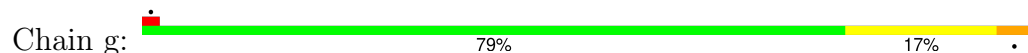
- Molecule 23: Ribosomal protein eL32



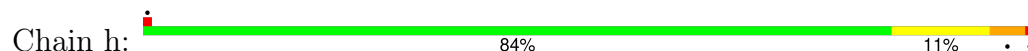
- Molecule 24: Ribosomal protein eL33



- Molecule 25: Ribosomal protein eL34



- Molecule 26: Ribosomal protein uL29

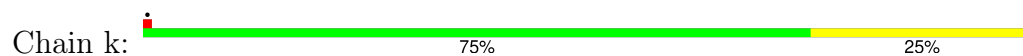




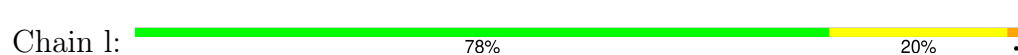
- Molecule 27: Ribosomal protein eL36



- Molecule 28: Ribosomal protein eL38



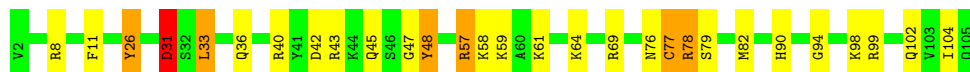
- Molecule 29: Ribosomal protein eL39



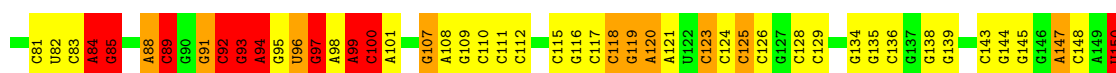
- Molecule 30: Ribosomal protein eL40



- Molecule 31: Ribosomal protein eL42



- Molecule 32: 28S ribosomal RNA





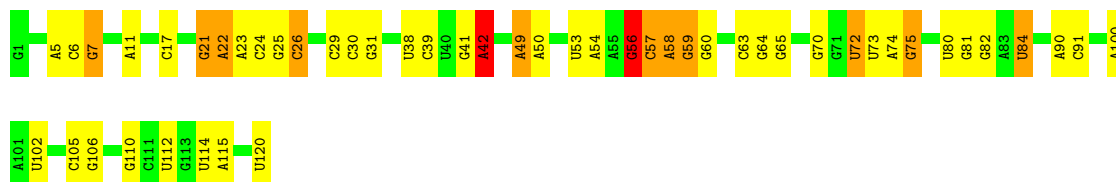
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U2873	G2795	G2710	G2618	G2523	G2443	A2360	G2278	G2106	G2034	G1961	G1890	G1803	C1732
U2874	G2796	G2711	G2619	G2524	C2446	C2361	A2279	C2107	C2035	C1962	A1891	A1804	G1733
C2875	A2798	C2713	G2620	C2526	U2447	U2362	G2280	G2108	C2036	C1963	C1892	A1805	G1734
	G2799	C2716	A2623	G2528	A2448	G2364	G2282	G2109	U2037	A1964	C1893	C1808	U1735
A2879	C2802		C2627	A2529	A2449	C2365	G2283	C2110	G2039		C1894		A1736
U2880	A2806	G2721	A2531	C2530	A2451	A2366	G2288	G2112	A2040	A1967	A1897	G1815	C1740
G2889	A2807	G2722	U2630	C2532	U2454	A2367	C2289	G2113	U2044	C1971	C1898	C1816	G1741
G2896		A2725	U2631	C2533	G2455	A2368	G2299	G2114	G1974	U1974	G1899	G1817	A1742
G2897		G2726	U2632	C2534	G2456	A2370	G2300	G2115	G1975	C1900	C1900	G1818	
G2898			G2638	G2535		U2371	G2301	C2116	G1976	G1902	G1902	G1819	G1745
G2899			U2639	A2536	G2459	U2372		G2117	U2048	G1903	G1903	G1821	A1746
G2900			G2640	A2537	A2460	G2378	U2305	G2118	G2052	A1907	C1897	G1822	
G2901			G2643	G2544	G2463	A2382	G2306	G2119	C2053		C1898	G1823	G1750
G2902			G2648	U2545	C2464	C2383	G2307	G2120	U2054	G1910	C1899	G1827	A1751
G2903			G2649	G2546	C2465	G2384	G2308	G2121	G2055	G1911	G1911	C1828	G1752
U2904			G2650	C2547	G2466	U2389	G2309	G2122	G2056	G1912	G1912	G1829	G1753
C2905			G2653	G2548	U2467	G2390	C2310	G2123	A2057	C1913	C1913	G1830	U1754
			G2658	G2549	U2468	G2391	C2311	G2124	C2058	G1916	G1916	G1832	U1755
			A2659	G2550	G2470	G2392	G2312	C2125	C2059	U1917	U1917	G1833	U1757
			A2660	G2551	G2471	G2393	G2313	G2126		U1918	U1918	G1834	G1758
			U2661	G2552	A2472	G2394	G2314	C2127		G1919	G1919	G1835	G1759
			G2662	G2553	A2473	C2395	G2315	G2128		C1920	C1920	G1836	G1760
			G2663	G2554	A2474	G2396	G2316	C2129		G1921	G1921		
			G2664	G2555	G2475	G2397	G2317	G2130		G1922	G1922	A1843	C1762
			U2665	C2560	G2476	U2398	G2320	C2244		A1923	A1923		C1763
			U2666	C2563		G2399	G2321	G2245		G1924	G1924	C1847	G1764
			C2667	C2566	G2479	A2403	G2322	C2246		G1925	G1925	C1848	A1765
			C2670	G2566	G2487	G2406	G2323	C2247		C1928	C1928	U1849	A1766
			G2673	C2571	C2488	U2407	G2324	C2248		G1930	G1930	A1850	A1767
			A2674	C2572	C2489	U2408	C2325	C2249		U1931	U1931	G1851	C1768
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			A2678	C2577		A2417	U2329	G2252		A1934	A1934	G1854	U1771
			G2683	U2580	C2499	C2422	G2330	G2253		G1935	G1935	G1855	C1772
			C2684	A2581	G2502	G2423	G2331	G2254		C1936	C1936	G1864	U1773
			G2685	C2582	G2503	G2424	G2332	G2255		G1937	G1937	G1865	C1774
			G2686	C2583	C2504	U2425	G2333	C2256		A1938	A1938	U1866	A1775
			U2687	G2586	G2505	U2426	G2334	C2257		U1939	U1939	A1867	A1776
			G2688	A2587	G2506	G2427	G2335	C2258		G1940	G1940	A1868	C1777
			C2689	U2588	A2507	A2428	G2336	C2259		A1941	A1941	G1869	C1778
			G2694	C2589	U2509	U2429	G2337	G2260		G1945	G1945		U1779
			A2695	G2597	G2510		G2338	G2261		U1946	U1946	G1876	A1780
			A2696	C2597	A2511	U2432	G2339	G2262		A1947	A1947	U1877	U1781
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			C2704	G2601	A2513	G2434	G2342	G2264		A2009	A2009	A1787	A1787
			G2706	G2602	G2514	G2435	G2343	C2265		A2010	A2010	G1880	A1788
			U2787	A3624	G2515	U2436	U2344	G2266		G2011	G2011	C1881	C1789
			U2788	G2623	G2516	A2437		U2267		A2011	A2011	U1948	U1790
			G3625	C3626	G2517	A2438		G2268		C2014	C2014	U1949	U1882
			G3626	C3627	A2518	G2439		U2269		G1951	G1951	G1950	U1791
			G3627		U2708	U2440		C2016		G1952	G1952	C1883	U1792
						C2441		A2100		A1956	A1956	G1885	A1793
								G2102				G1886	U1793
								C2101				G1887	G1797
								G2270				A1888	G1798
								C2271					G1799
								G2272					U1800
								G2273					
								G2274					
								G2275					
								A2276					





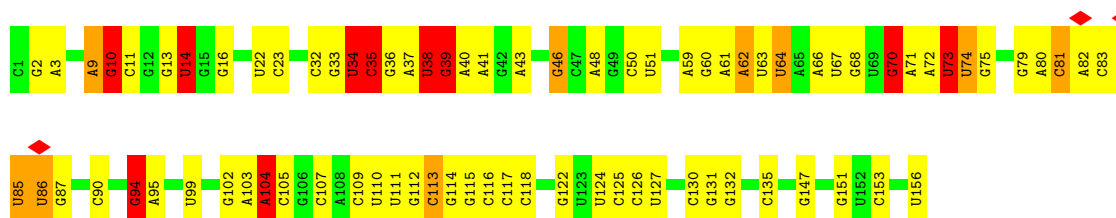
• Molecule 33: 5S ribosomal RNA

Chain 7: 58% 31% 9%



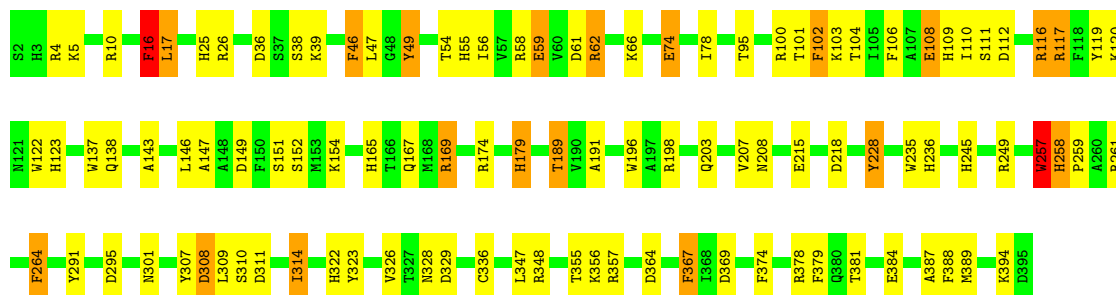
• Molecule 34: 5.8S ribosomal RNA

Chain 8: 48% 40% 6% 6%



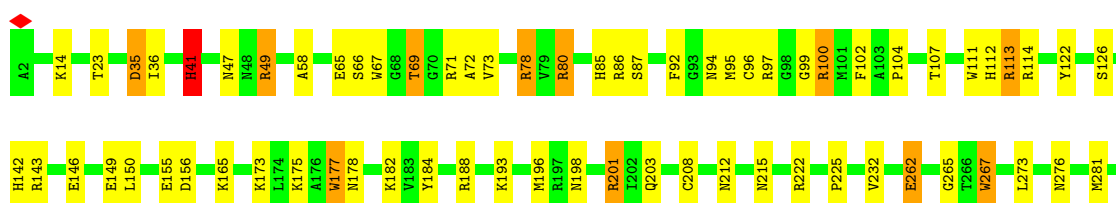
• Molecule 35: Ribosomal protein uL3

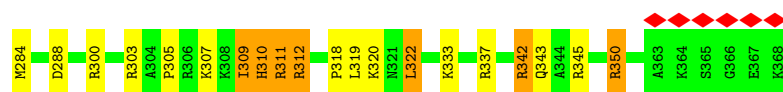
Chain B: 73% 22% 5%



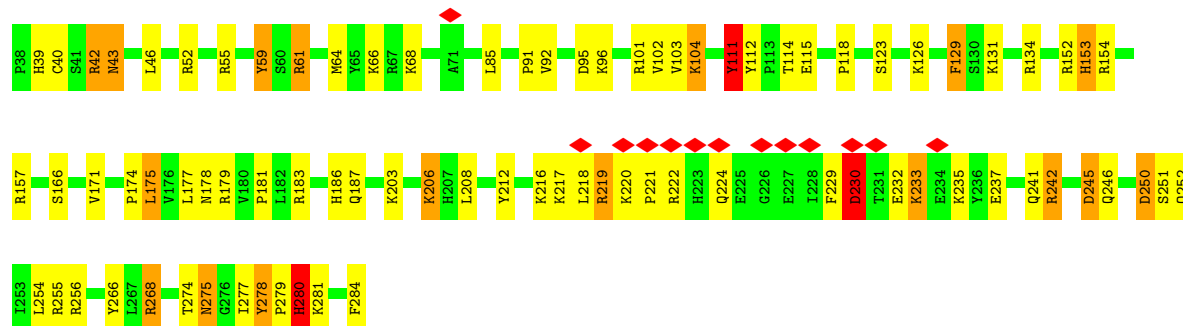
• Molecule 36: Ribosomal protein uL4

Chain C: 76% 19% 5%

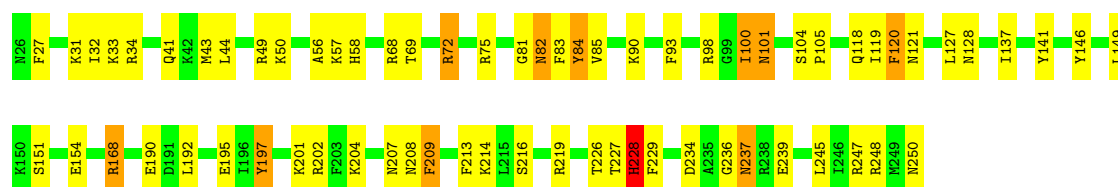




• Molecule 37: Ribosomal protein eL6



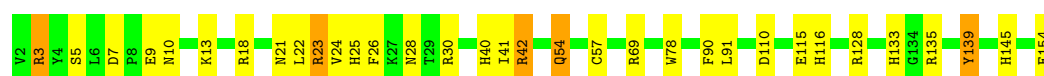
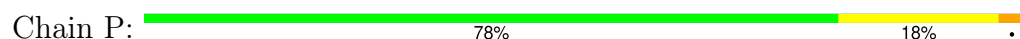
• Molecule 38: Ribosomal protein uL30



• Molecule 39: Ribosomal protein uL16



• Molecule 40: Ribosomal protein uL22



• Molecule 41: Ribosomal protein eL24

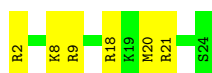




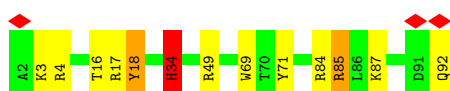
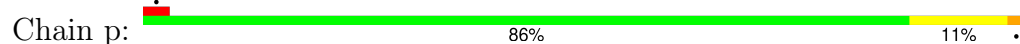
- Molecule 42: Ribosomal protein eL37



- Molecule 43: Ribosomal protein eL41



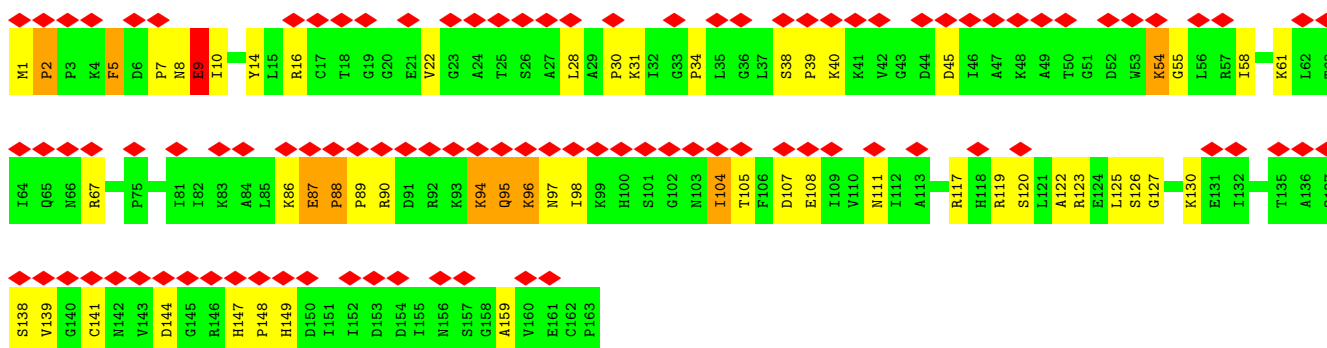
- Molecule 44: Ribosomal protein eL43



- Molecule 45: Ribosomal protein eL28



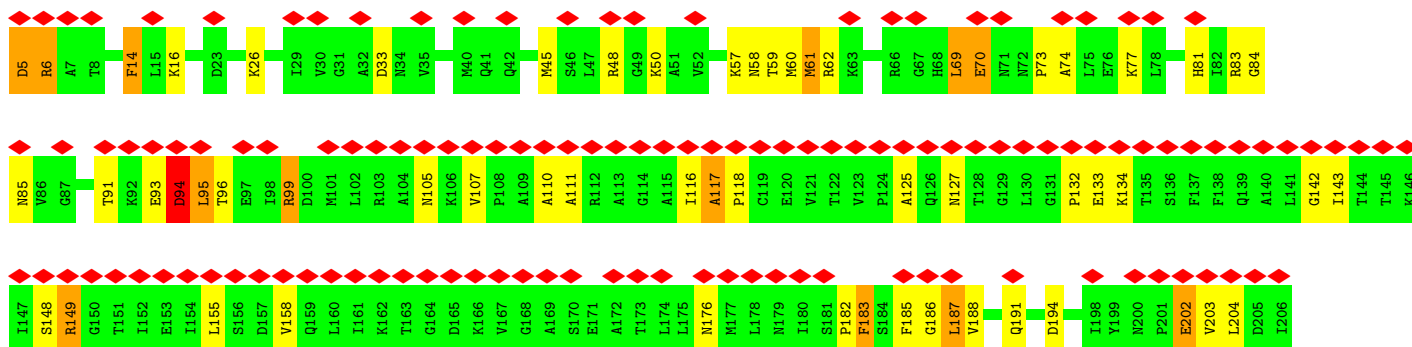
- Molecule 46: Ribosomal protein uL11



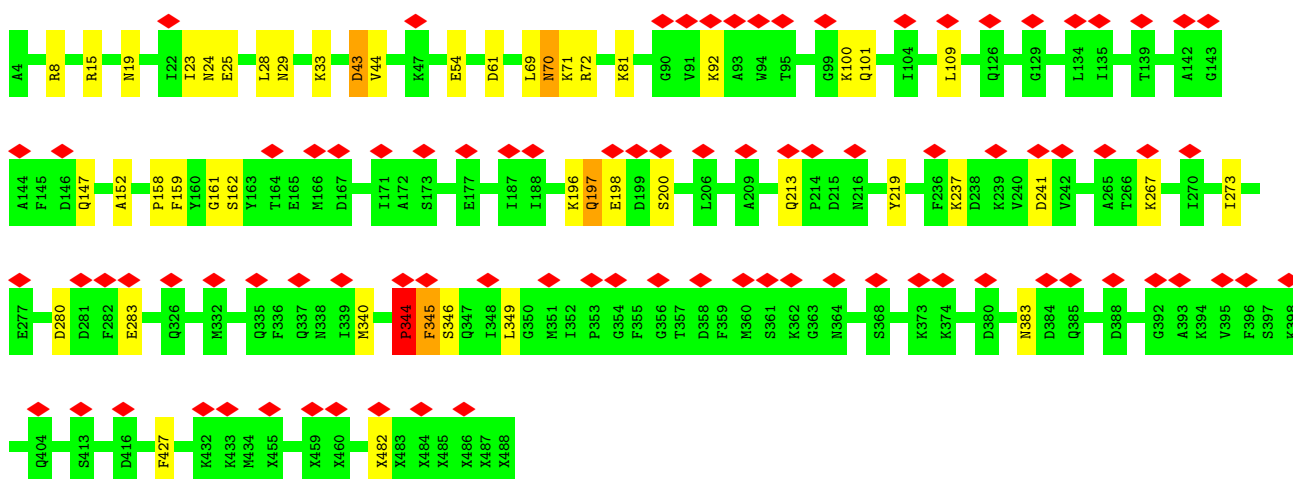
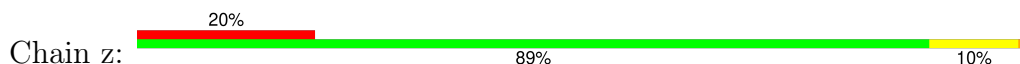
- Molecule 47: Ribosomal protein uL10



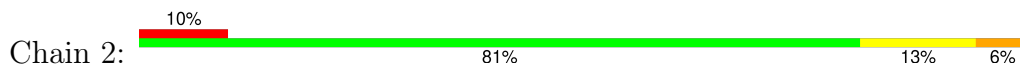




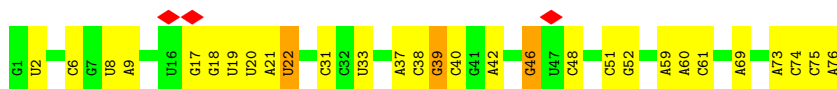
• Molecule 48: SRP54



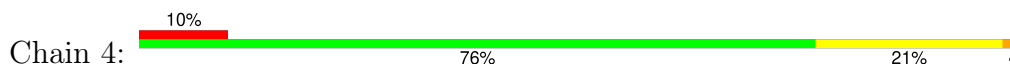
• Molecule 49: Nascent chain

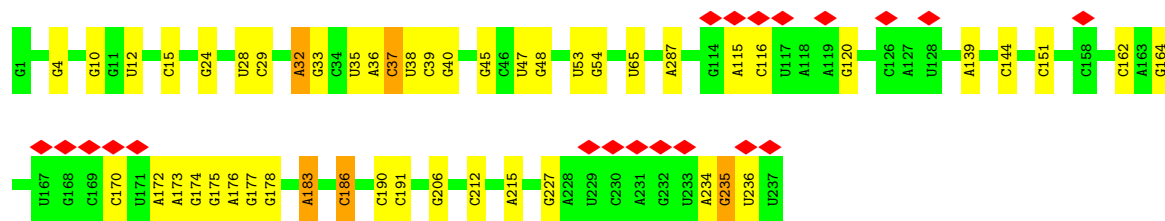


• Molecule 50: Val tRNA

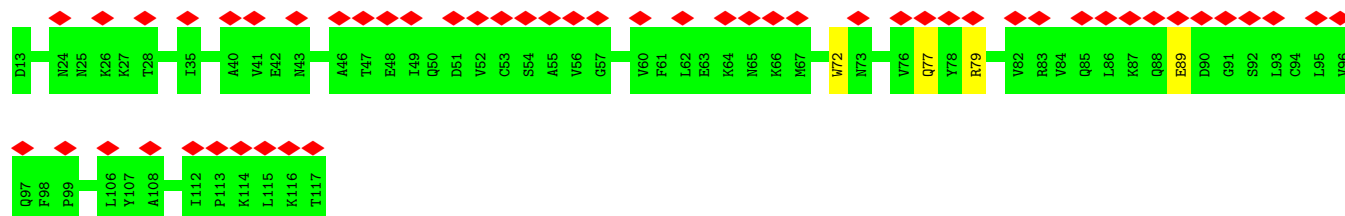


• Molecule 51: SRP 7S RNA

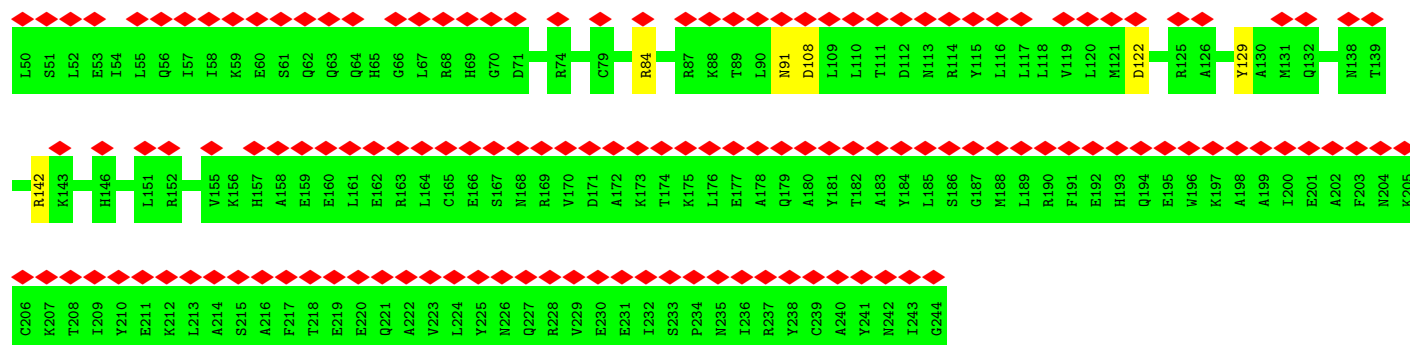
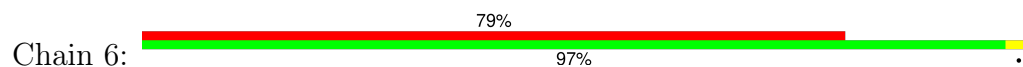




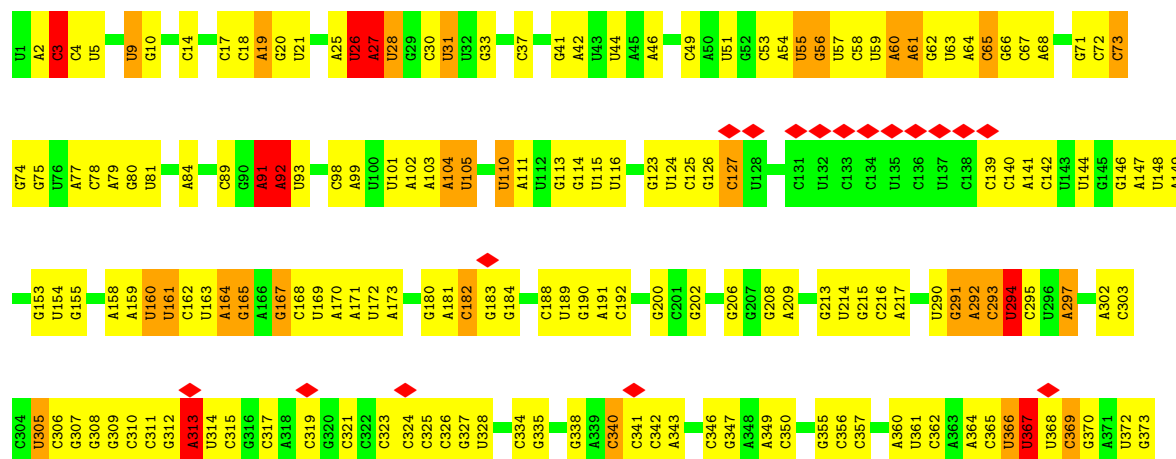
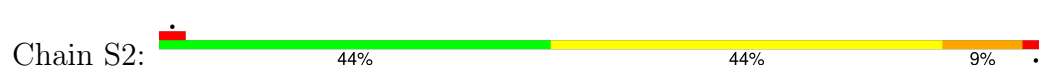
• Molecule 52: SRP19



• Molecule 53: SRP68



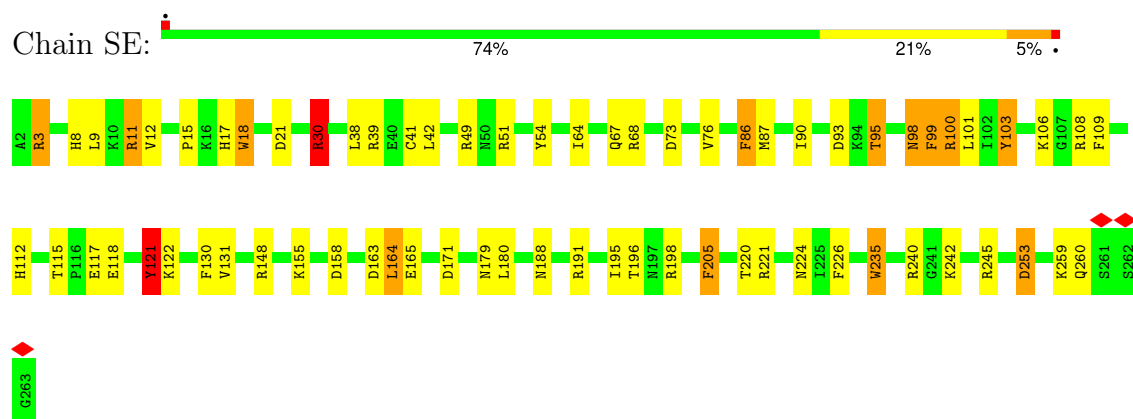
• Molecule 54: 18S ribosomal RNA



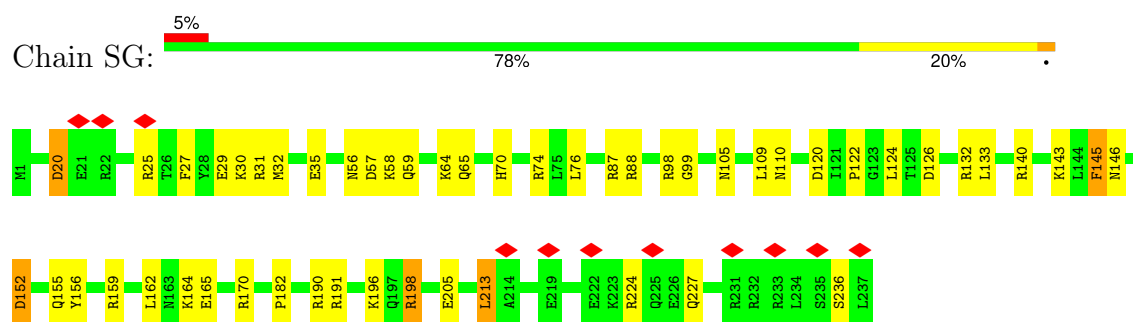




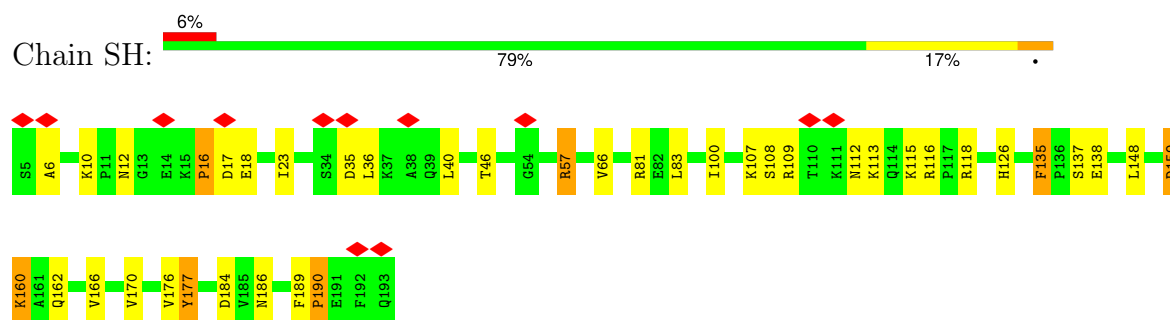
- Molecule 58: Ribosomal protein eS4



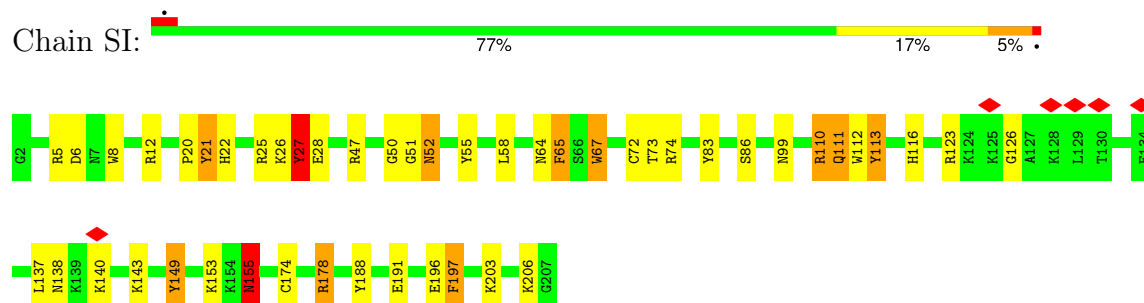
- Molecule 59: Ribosomal protein eS6



- Molecule 60: Ribosomal protein eS7

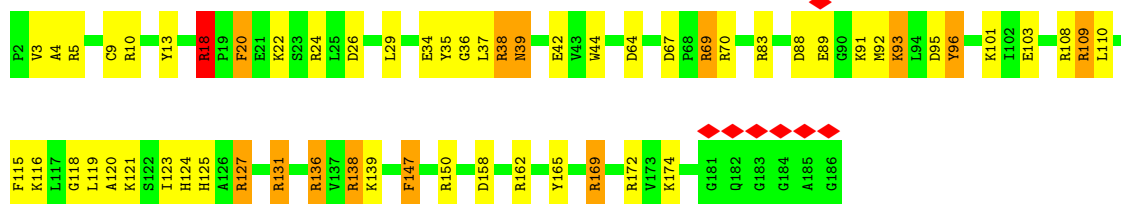


- Molecule 61: Ribosomal protein eS8




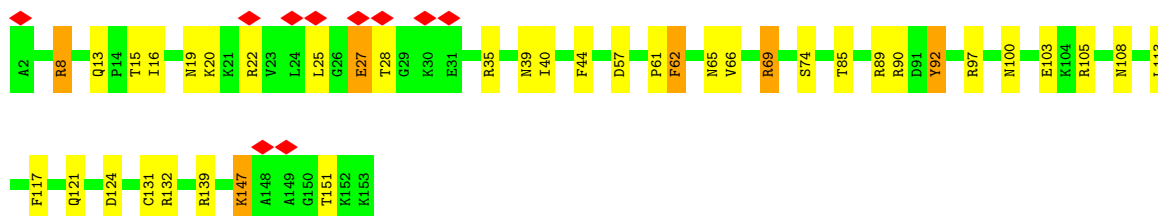
- Molecule 62: Ribosomal protein uS4

Chain SJ: 




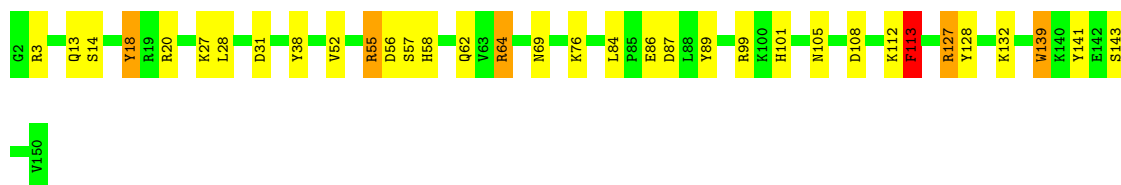
- Molecule 63: Ribosomal protein uS17

Chain SL: 



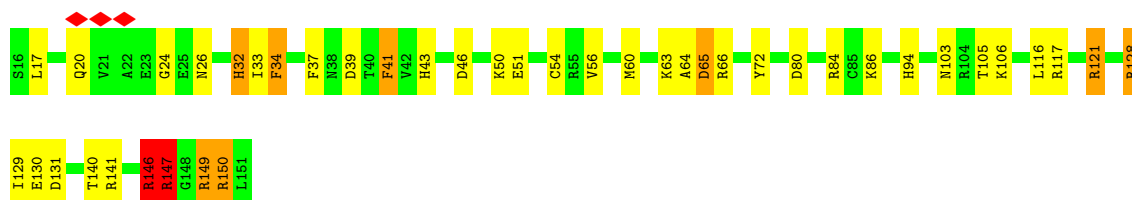
- Molecule 64: Ribosomal protein uS15

Chain SN: 



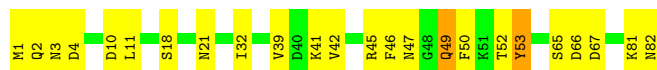
- Molecule 65: Ribosomal protein uS11

Chain SO: 




- Molecule 66: Ribosomal protein eS21

Chain SV: 




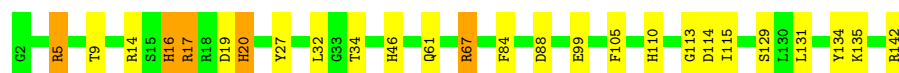
- Molecule 67: Ribosomal protein uS8

Chain SW:  76% 22%




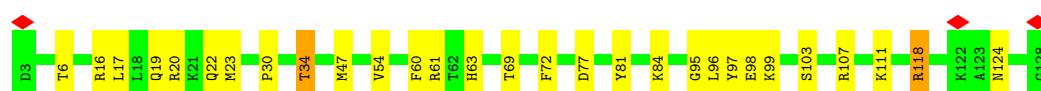
- Molecule 68: Ribosomal protein uS12

Chain SX:  82% 15%




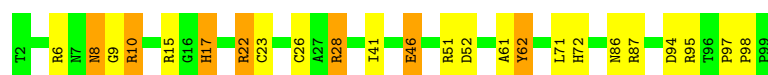
- Molecule 69: Ribosomal protein eS24

Chain SY:  77% 21%




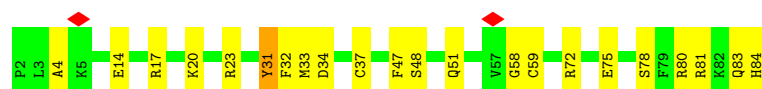
- Molecule 70: Ribosomal protein eS26

Chain Sa:  76% 17% 7%




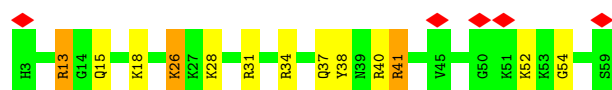
- Molecule 71: Ribosomal protein eS27

Chain Sb:  73% 25%




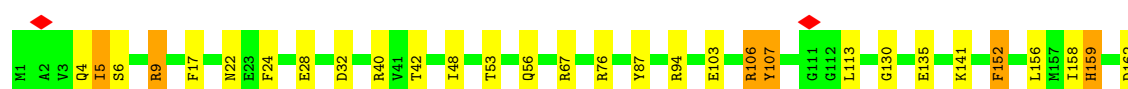
- Molecule 72: Ribosomal protein eS30

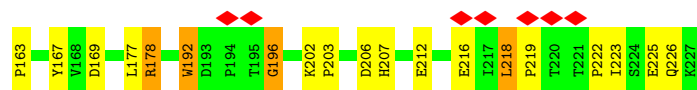
Chain Se:  9% 77% 18% 5%



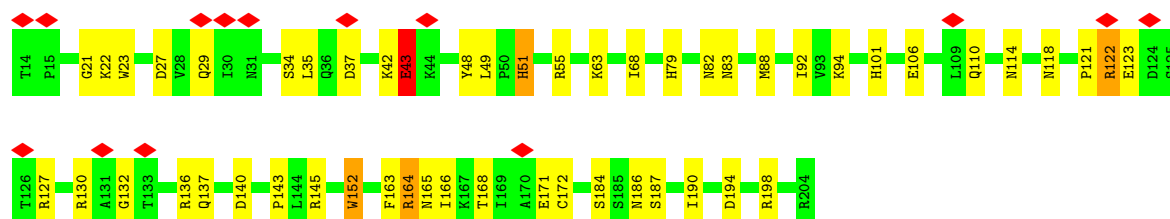
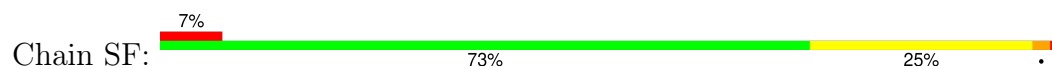
- Molecule 73: Ribosomal protein uS3

Chain SD:  78% 17%

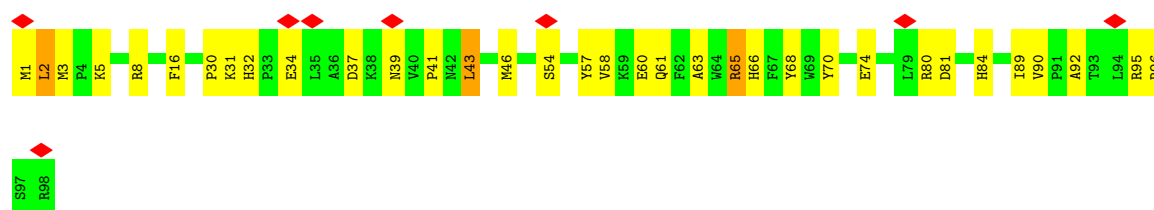




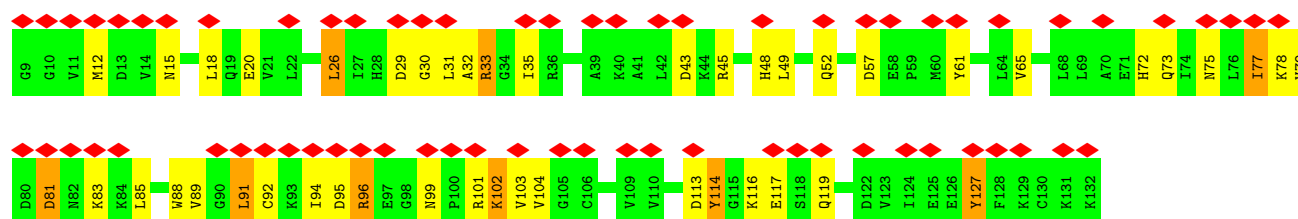
- Molecule 74: Ribosomal protein uS7



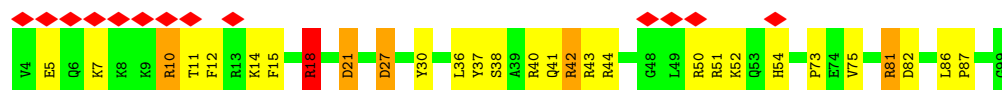
- Molecule 75: Ribosomal protein eS10



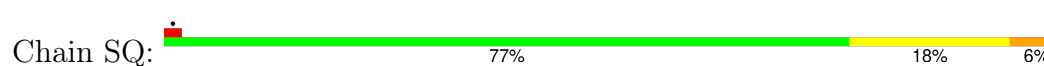
- Molecule 76: Ribosomal protein eS12



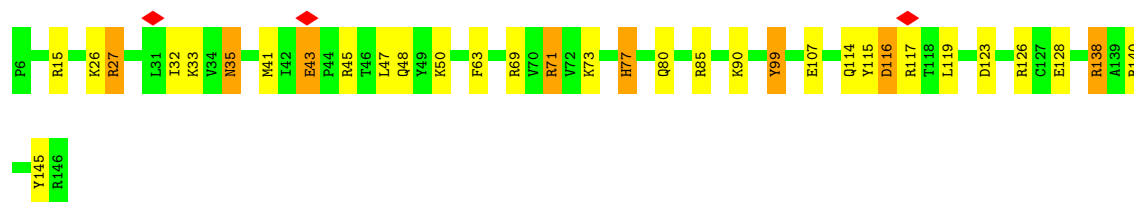
- Molecule 77: Ribosomal protein uS19



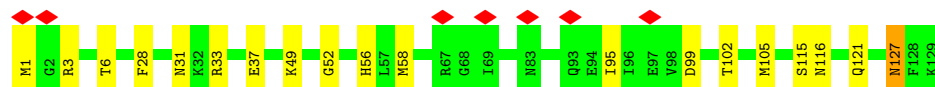
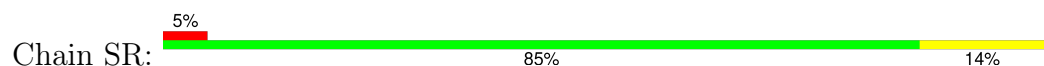
- Molecule 78: Ribosomal protein uS9



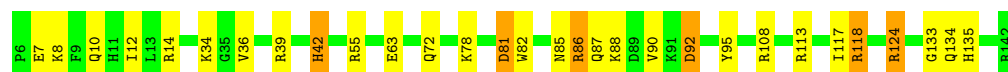
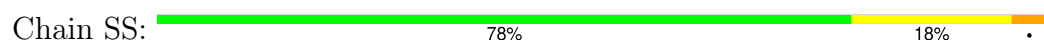




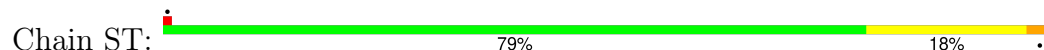
- Molecule 79: Ribosomal protein eS17



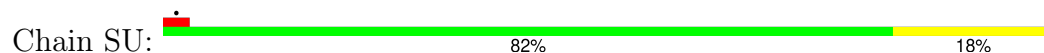
- Molecule 80: Ribosomal protein uS13



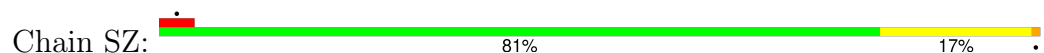
- Molecule 81: Ribosomal protein eS19



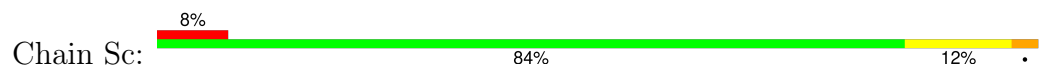
- Molecule 82: Ribosomal protein uS10

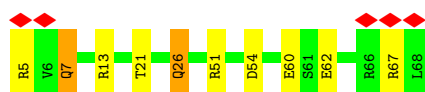


- Molecule 83: Ribosomal protein es25

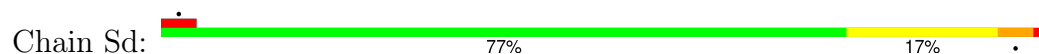


- Molecule 84: Ribosomal protein eS28

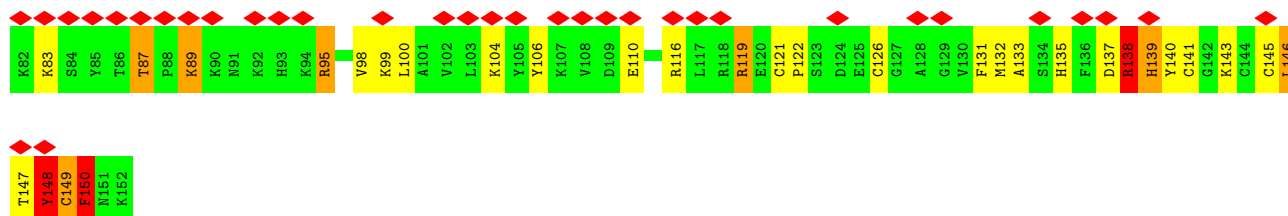




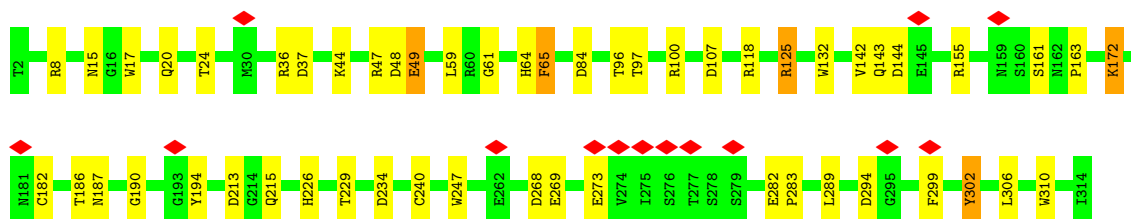
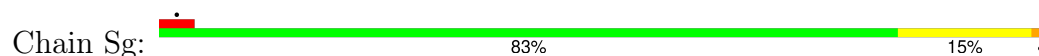
- Molecule 85: Ribosomal protein uS14



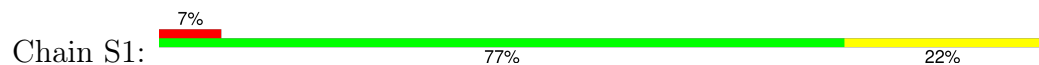
- Molecule 86: Ribosomal protein eS31



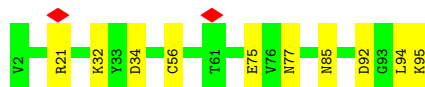
- Molecule 87: Ribosomal protein RACK1



- Molecule 88: SRP9



- Molecule 89: SRP14



## 4 Experimental information

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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

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

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

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

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

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

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

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

The worst 5 of 183 bond length outliers are listed below:

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

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

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

There are no chirality outliers.

5 of 529 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	18	ALA	Peptide

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

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	242/244 (99%)	194 (80%)	38 (16%)	10 (4%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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%)	350 (88%)	31 (8%)	18 (4%)	2	20
49	2	27/31 (87%)	15 (56%)	9 (33%)	3 (11%)	0	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	9	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
53	6	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
55	SA	206/208 (99%)	163 (79%)	30 (15%)	13 (6%)	1	15
56	SB	211/213 (99%)	154 (73%)	36 (17%)	21 (10%)	0	7
57	SC	216/218 (99%)	182 (84%)	27 (12%)	7 (3%)	3	26
58	SE	260/262 (99%)	198 (76%)	44 (17%)	18 (7%)	1	13
59	SG	235/237 (99%)	195 (83%)	32 (14%)	8 (3%)	3	25
60	SH	187/189 (99%)	141 (75%)	29 (16%)	17 (9%)	0	8
61	SI	204/206 (99%)	165 (81%)	30 (15%)	9 (4%)	2	20
62	SJ	183/185 (99%)	133 (73%)	35 (19%)	15 (8%)	1	10
63	SL	150/152 (99%)	122 (81%)	22 (15%)	6 (4%)	2	22
64	SN	147/149 (99%)	115 (78%)	28 (19%)	4 (3%)	4	29
65	SO	134/136 (98%)	99 (74%)	21 (16%)	14 (10%)	0	6
66	SV	80/82 (98%)	58 (72%)	15 (19%)	7 (9%)	0	9
67	SW	127/129 (98%)	108 (85%)	16 (13%)	3 (2%)	5	30
68	SX	139/141 (99%)	109 (78%)	26 (19%)	4 (3%)	3	27
69	SY	124/126 (98%)	101 (82%)	16 (13%)	7 (6%)	1	17
70	Sa	96/98 (98%)	69 (72%)	18 (19%)	9 (9%)	0	8
71	Sb	81/83 (98%)	61 (75%)	16 (20%)	4 (5%)	2	18
72	Se	55/57 (96%)	41 (74%)	12 (22%)	2 (4%)	3	24
73	SD	225/227 (99%)	174 (77%)	41 (18%)	10 (4%)	2	20
74	SF	189/191 (99%)	145 (77%)	34 (18%)	10 (5%)	1	18
75	SK	96/98 (98%)	58 (60%)	26 (27%)	12 (12%)	0	4
76	SM	122/124 (98%)	78 (64%)	24 (20%)	20 (16%)	0	2
77	SP	94/96 (98%)	67 (71%)	17 (18%)	10 (11%)	0	6
78	SQ	139/141 (99%)	111 (80%)	20 (14%)	8 (6%)	1	16
79	SR	127/129 (98%)	111 (87%)	11 (9%)	5 (4%)	2	22
80	SS	135/137 (98%)	114 (84%)	12 (9%)	9 (7%)	1	14
81	ST	139/141 (99%)	115 (83%)	18 (13%)	6 (4%)	2	20
82	SU	102/104 (98%)	83 (81%)	13 (13%)	6 (6%)	1	16
83	SZ	73/75 (97%)	59 (81%)	9 (12%)	5 (7%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
84	Sc	60/64 (94%)	47 (78%)	12 (20%)	1 (2%)	7	36
85	Sd	50/52 (96%)	36 (72%)	11 (22%)	3 (6%)	1	15
86	Sf	69/71 (97%)	42 (61%)	15 (22%)	12 (17%)	0	2
87	Sg	311/313 (99%)	240 (77%)	56 (18%)	15 (5%)	2	19
88	S1	72/74 (97%)	61 (85%)	6 (8%)	5 (7%)	1	13
89	S4	72/76 (95%)	68 (94%)	4 (6%)	0	100	100
All	All	12341/12544 (98%)	9853 (80%)	1811 (15%)	677 (6%)	2	17

5 of 677 Ramachandran outliers are listed below:

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

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	187/187 (100%)	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%)	87 (75%)	29 (25%)	0	3
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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%)	88 (82%)	19 (18%)	1	9
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%)	68 (79%)	18 (21%)	1	6
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%)	141 (73%)	53 (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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
48	z	340/340 (100%)	321 (94%)	19 (6%)	17	45
49	2	29/29 (100%)	26 (90%)	3 (10%)	6	25
52	9	92/94 (98%)	88 (96%)	4 (4%)	25	50
53	6	157/157 (100%)	151 (96%)	6 (4%)	28	53
55	SA	174/174 (100%)	132 (76%)	42 (24%)	0	4
56	SB	194/194 (100%)	155 (80%)	39 (20%)	1	7
57	SC	184/184 (100%)	141 (77%)	43 (23%)	0	4
58	SE	224/224 (100%)	172 (77%)	52 (23%)	0	5
59	SG	207/207 (100%)	166 (80%)	41 (20%)	1	7
60	SH	169/169 (100%)	145 (86%)	24 (14%)	2	17
61	SI	178/178 (100%)	144 (81%)	34 (19%)	1	7
62	SJ	161/161 (100%)	116 (72%)	45 (28%)	0	2
63	SL	136/136 (100%)	104 (76%)	32 (24%)	0	4
64	SN	130/130 (100%)	103 (79%)	27 (21%)	1	6
65	SO	106/106 (100%)	74 (70%)	32 (30%)	0	2
66	SV	66/66 (100%)	50 (76%)	16 (24%)	0	4
67	SW	112/112 (100%)	90 (80%)	22 (20%)	1	7
68	SX	113/113 (100%)	95 (84%)	18 (16%)	2	13
69	SY	108/108 (100%)	85 (79%)	23 (21%)	1	6
70	Sa	85/85 (100%)	71 (84%)	14 (16%)	2	12
71	Sb	75/75 (100%)	58 (77%)	17 (23%)	0	5
72	Se	46/46 (100%)	35 (76%)	11 (24%)	0	4
73	SD	190/190 (100%)	149 (78%)	41 (22%)	1	5
74	SF	161/161 (100%)	123 (76%)	38 (24%)	0	4
75	SK	89/89 (100%)	68 (76%)	21 (24%)	0	4
76	SM	104/104 (100%)	74 (71%)	30 (29%)	0	2
77	SP	88/88 (100%)	70 (80%)	18 (20%)	1	6
78	SQ	117/117 (100%)	91 (78%)	26 (22%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
79	SR	117/117 (100%)	102 (87%)	15 (13%)	3	19
80	SS	119/119 (100%)	96 (81%)	23 (19%)	1	7
81	ST	112/112 (100%)	88 (79%)	24 (21%)	1	6
82	SU	94/94 (100%)	82 (87%)	12 (13%)	3	19
83	SZ	66/66 (100%)	57 (86%)	9 (14%)	3	17
84	Sc	57/57 (100%)	47 (82%)	10 (18%)	1	10
85	Sd	45/45 (100%)	36 (80%)	9 (20%)	1	7
86	Sf	64/64 (100%)	45 (70%)	19 (30%)	0	2
87	Sg	272/272 (100%)	235 (86%)	37 (14%)	3	17
88	S1	67/67 (100%)	59 (88%)	8 (12%)	4	20
89	S4	69/69 (100%)	60 (87%)	9 (13%)	3	18
All	All	10757/10762 (100%)	8495 (79%)	2262 (21%)	2	6

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

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

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

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

### 5.3.3 RNA ⓘ

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

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

5 of 2678 RNA backbone outliers are listed below:

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

5 of 1029 RNA pucker outliers are listed below:

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

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

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

## 5.5 Carbohydrates [i](#)

There are no 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
54	S2	6
48	z	5
51	4	3
50	3	3
46	K	2
49	2	1
37	E	1
89	S4	1
53	6	1
84	Sc	1
11	R	1

The worst 5 of 41 chain breaks are listed below:

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

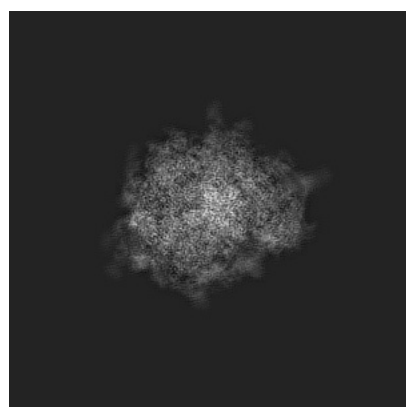
## 6 Map visualisation [i](#)

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

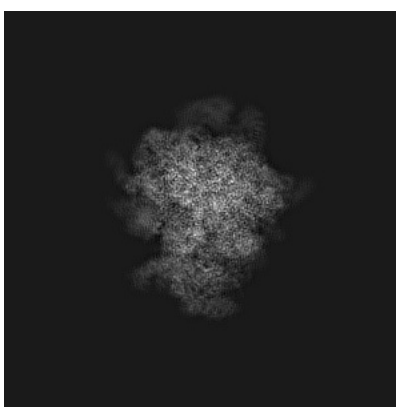
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

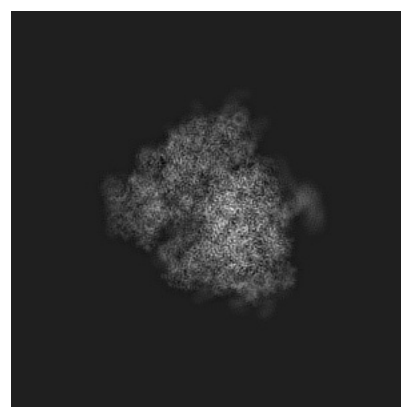
#### 6.1.1 Primary map



X



Y

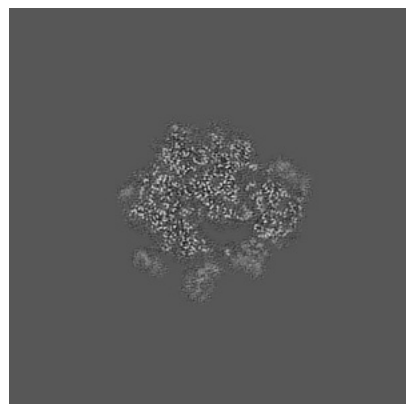


Z

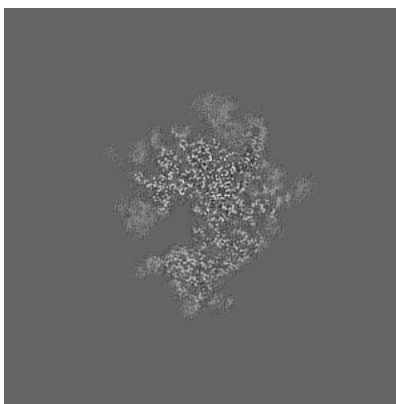
The images above show the map projected in three orthogonal directions.

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

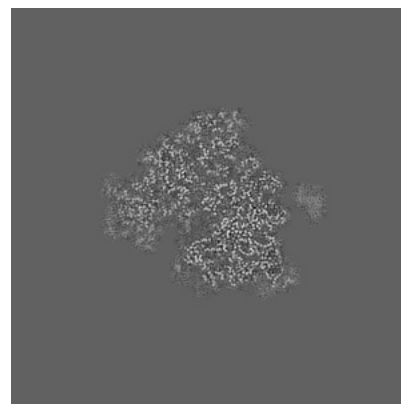
#### 6.2.1 Primary map



X Index: 210



Y Index: 210

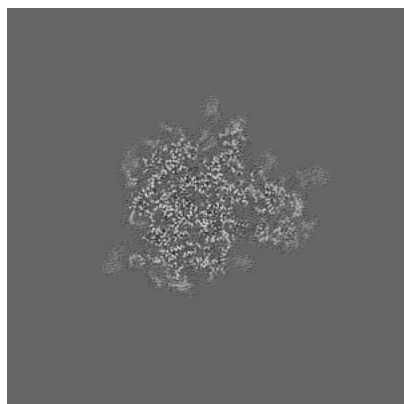


Z Index: 210

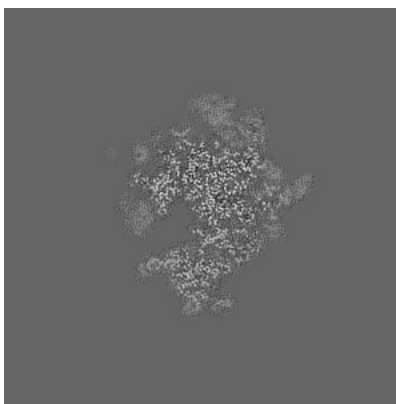
The images above show central slices of the map in three orthogonal directions.

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

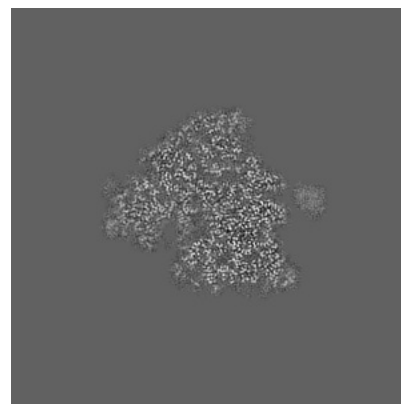
### 6.3.1 Primary map



X Index: 234



Y Index: 212

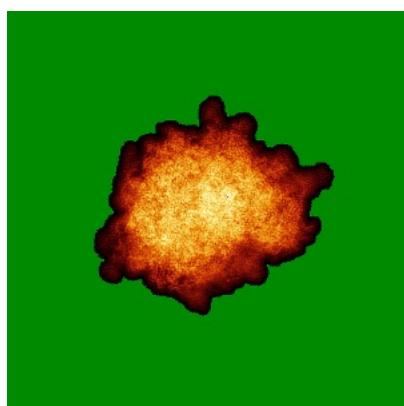


Z Index: 208

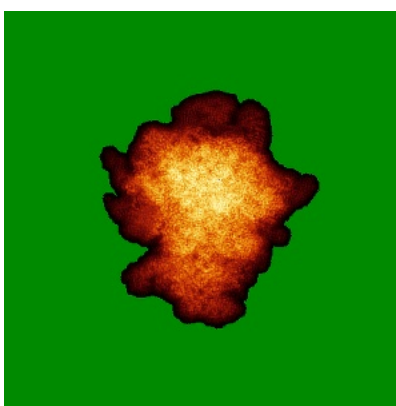
The images above show the largest variance slices of the map in three orthogonal directions.

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

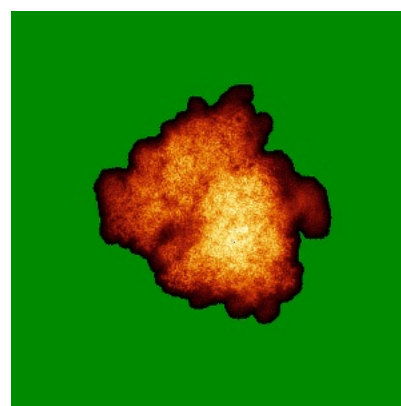
### 6.4.1 Primary map



X



Y

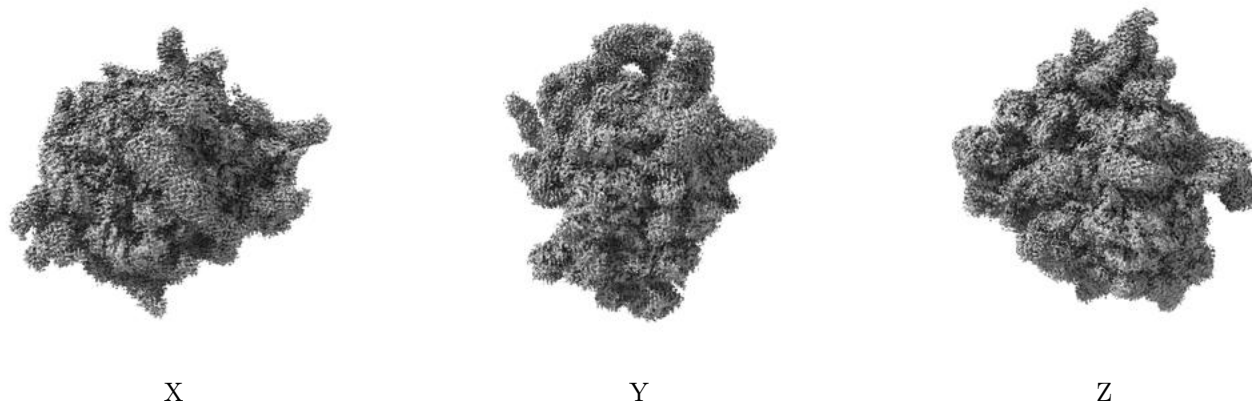


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



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

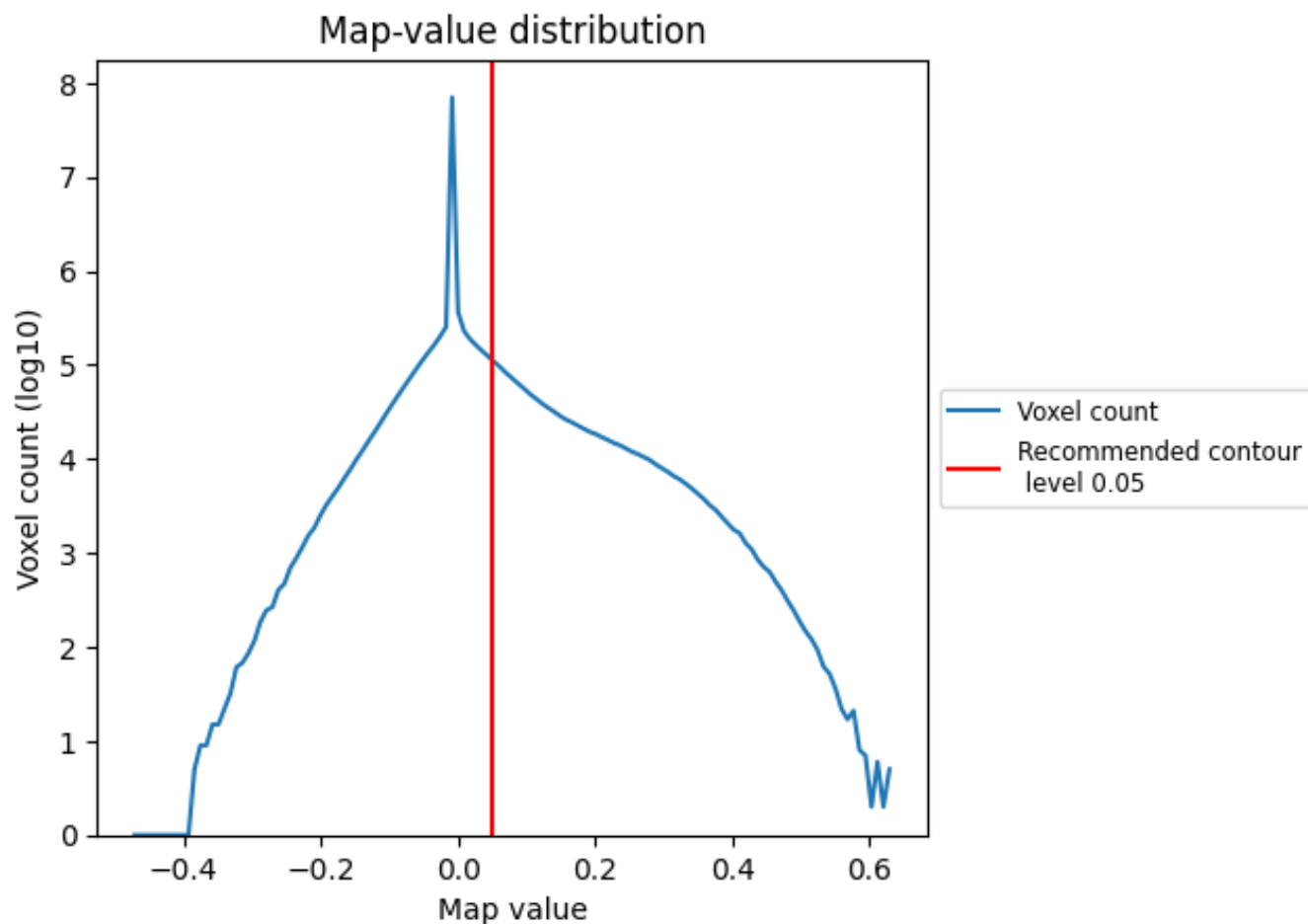
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

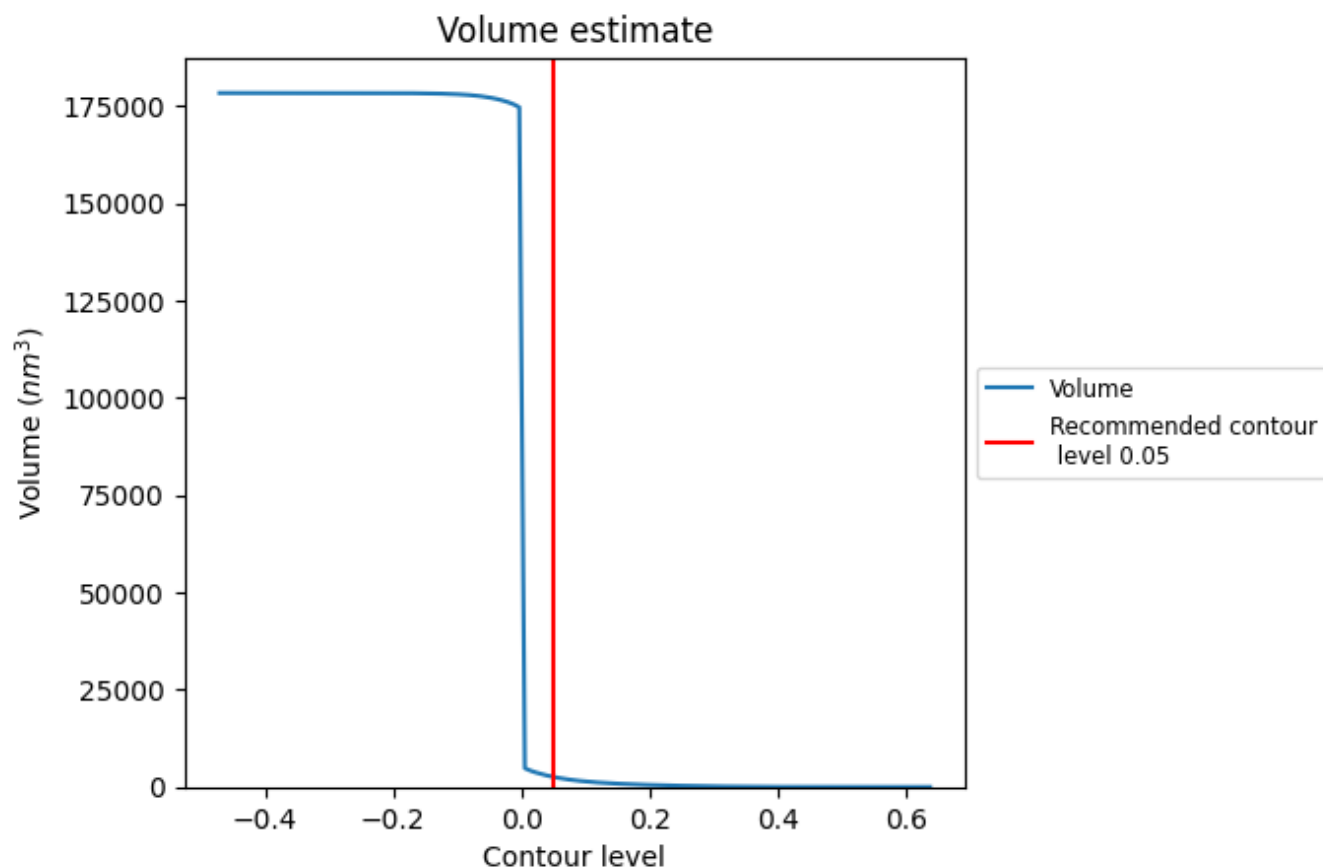
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

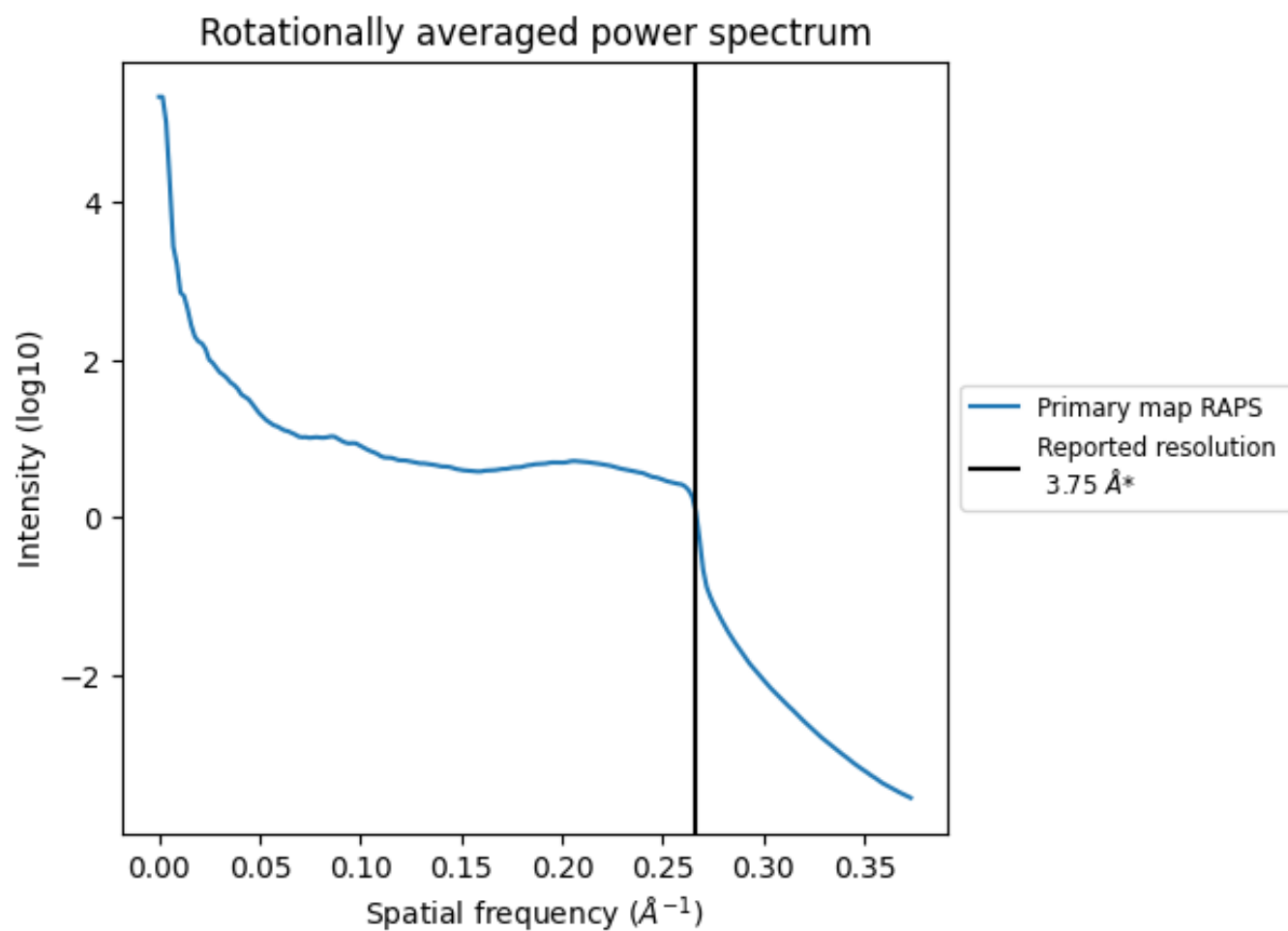
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2578  $\text{nm}^3$ ; this corresponds to an approximate mass of 2329 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ



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

## 8 Fourier-Shell correlation

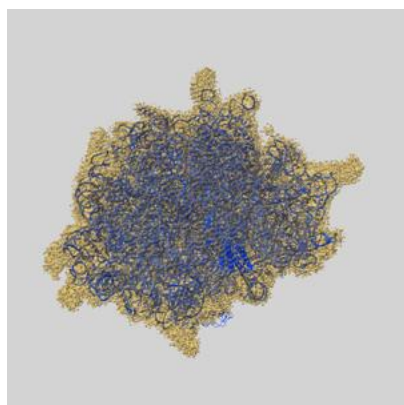
This section was not generated. No FSC curve or half-maps provided.



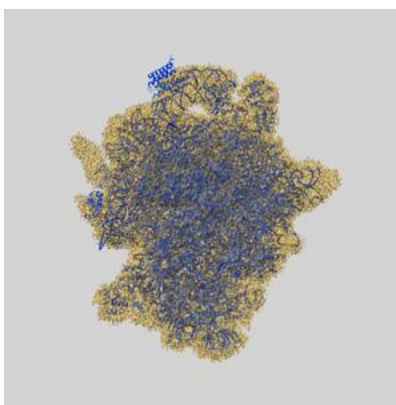
## 9 Map-model fit [i](#)

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

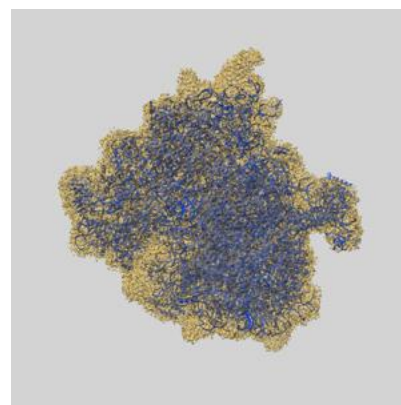
### 9.1 Map-model overlay [i](#)



X



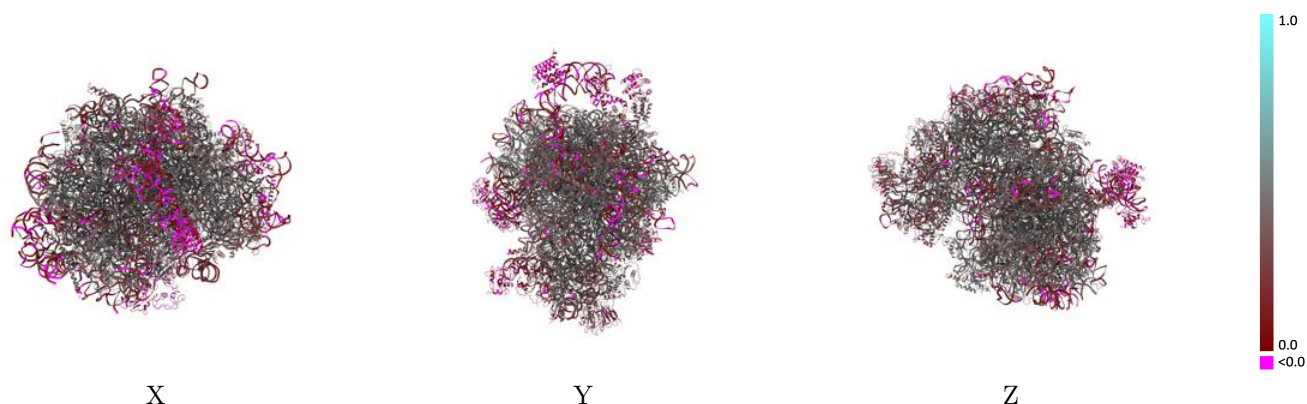
Y



Z

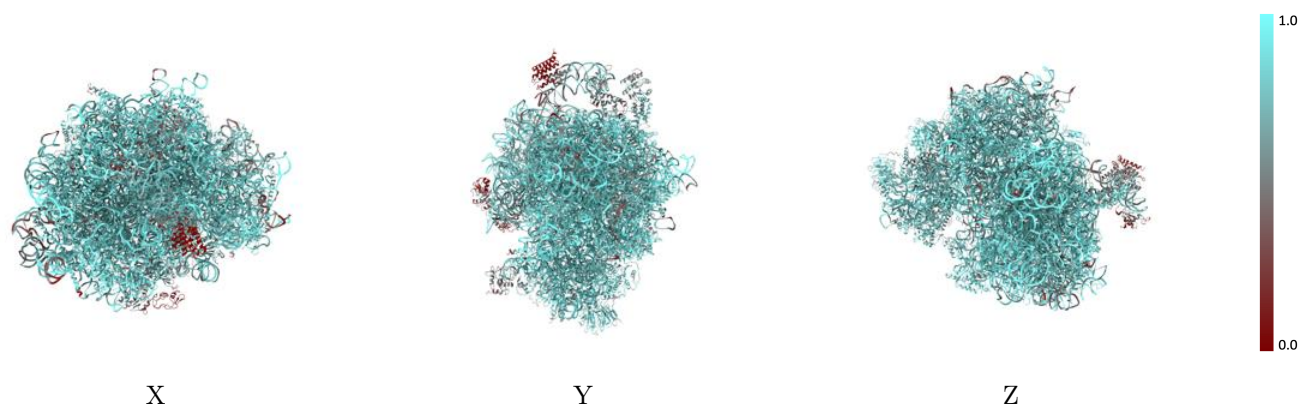
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



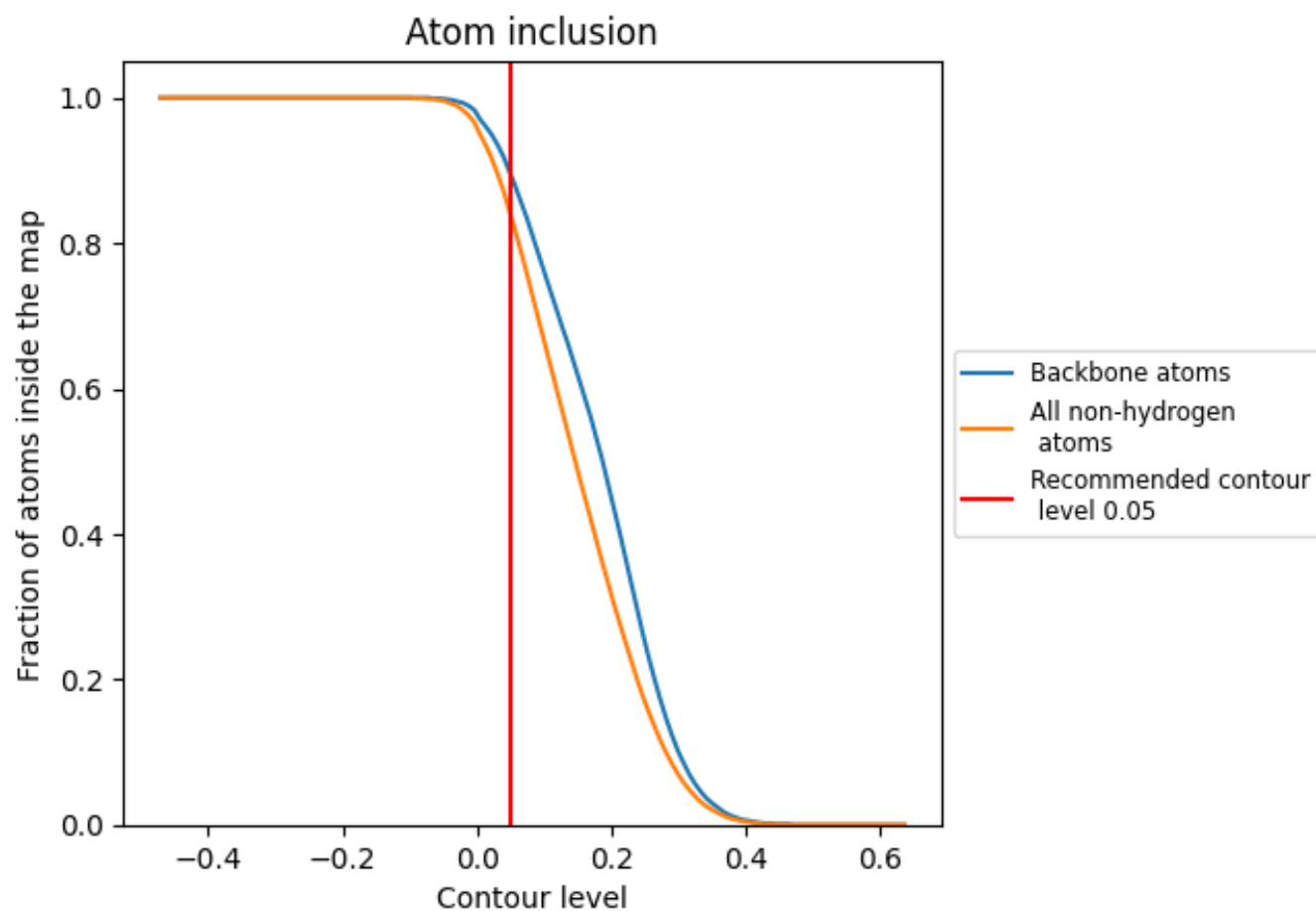
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ





















































































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

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





























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

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