



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:06 PM BST

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 PDB ID : 3JAJ

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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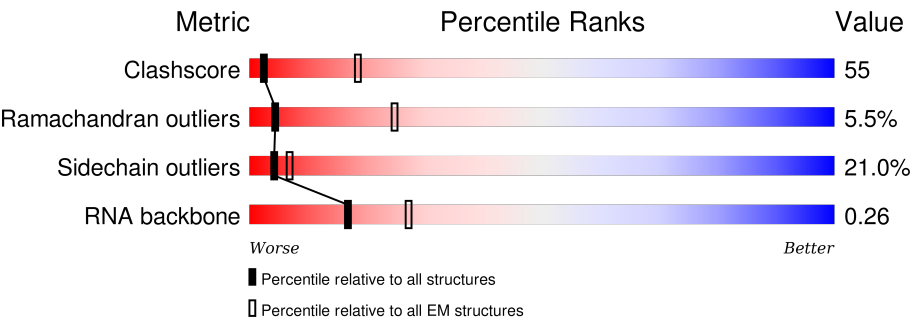
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.75 Å.

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














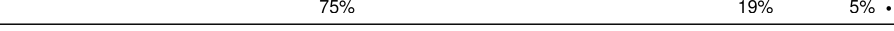







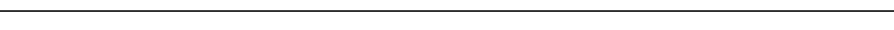

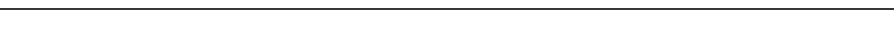
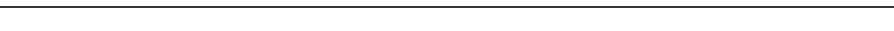


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	244	57% 25% 13% 5%
2	D	292	52% 30% 13% 5%
3	G	238	58% 29% 10% .
4	H	190	63% 25% 6% 6%
5	J	170	60% 31% 6% .
6	L	210	60% 27% 10% .
7	M	138	57% 33% 8% .
8	N	203	50% 33% 11% 6%


















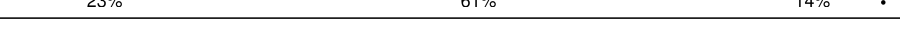







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Mol	Chain	Length	Quality of chain
9	O	201	
10	Q	187	
11	R	180	
12	S	175	
13	T	159	
14	U	99	
15	V	131	
16	X	119	
17	Y	134	
18	Z	135	
19	a	147	
20	b	75	
21	c	94	
22	d	107	
23	e	128	
24	f	109	
25	g	114	
26	h	122	
27	i	102	
28	k	69	
29	l	50	
30	m	52	
31	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	 77% 17% • •
85	Sf	71	 56% 30% 10% •
86	Sg	313	 83% 15% •
87	S1	74	 58% 26% 15% •
88	S4	76	 71% 25% •

## 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	g	1	Total	Mg	0
			1	1	
89	D	1	Total	Mg	0
			1	1	
89	S2	36	Total	Mg	0
			36	36	
89	V	1	Total	Mg	0
			1	1	
89	7	5	Total	Mg	0
			5	5	
89	5	116	Total	Mg	0
			116	116	

*Continued on next page...*

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Mol	Chain	Residues	Atoms		AltConf
89	8	6	Total 6	Mg 6	0

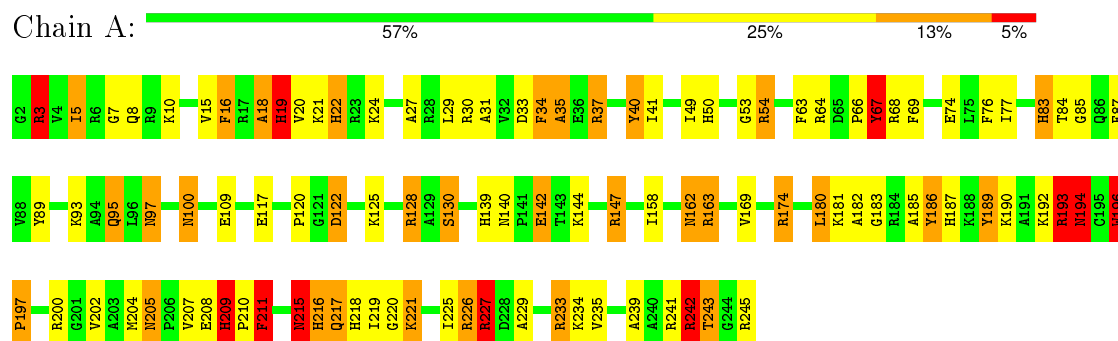
- Molecule 90 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

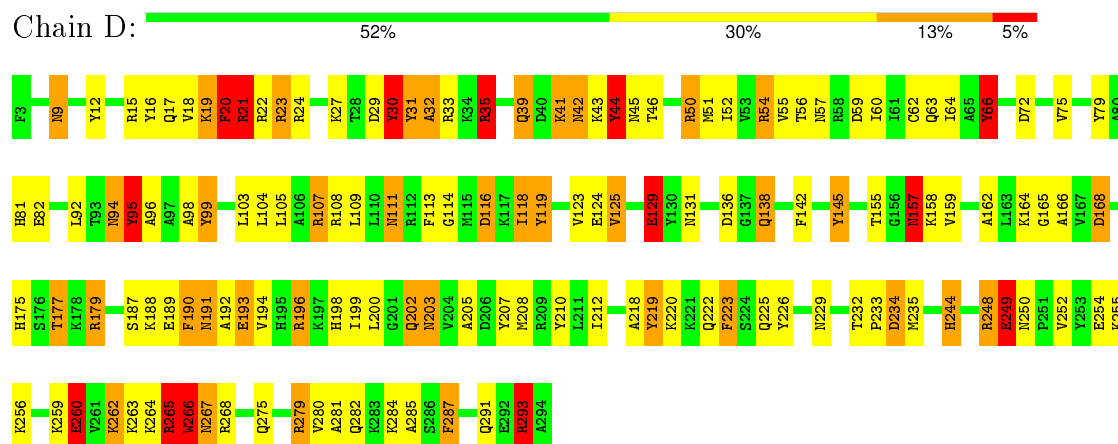
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

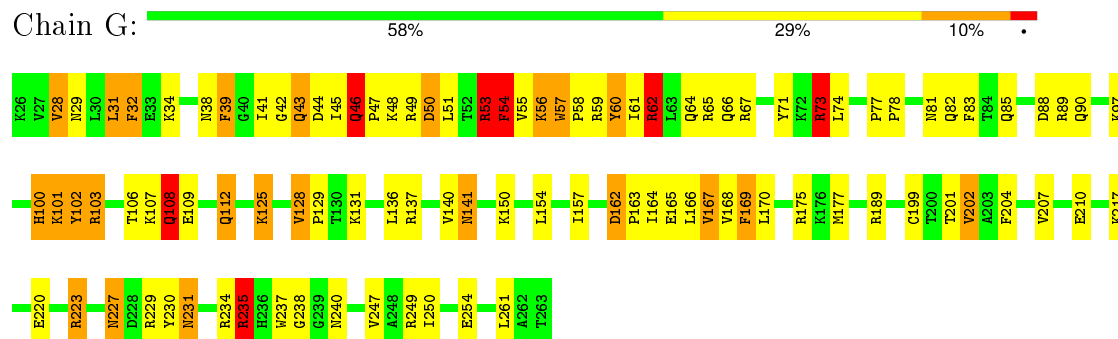
#### • Molecule 1: Ribosomal protein uL2



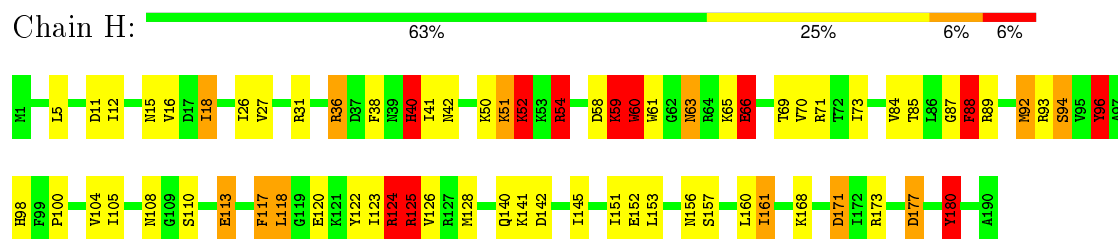
#### • Molecule 2: Ribosomal protein uL18



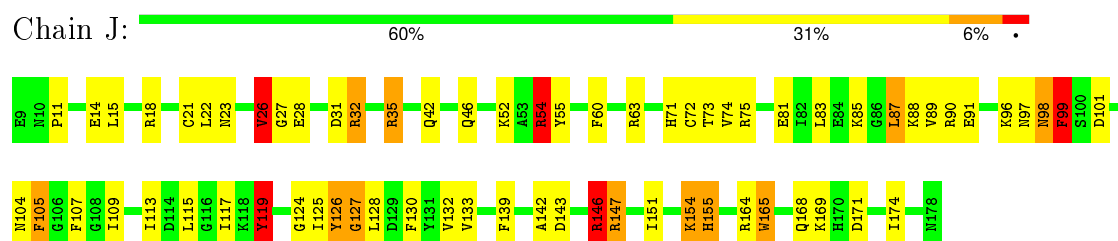
#### • Molecule 3: Ribosomal protein eL8



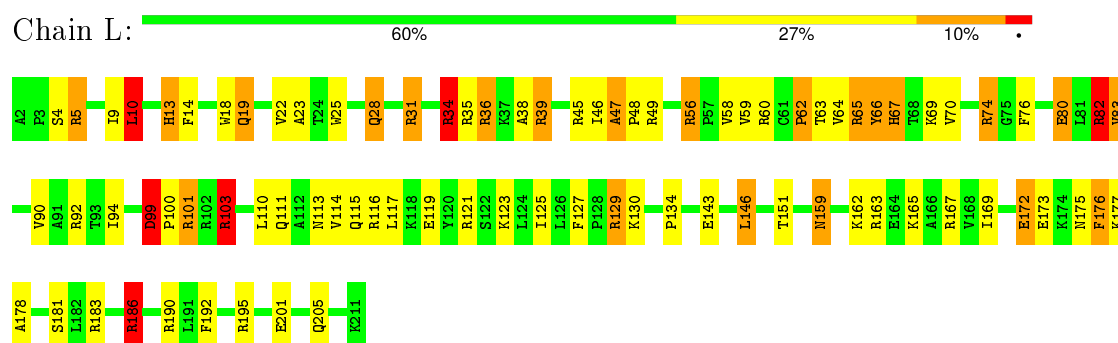
- Molecule 4: Ribosomal protein uL6



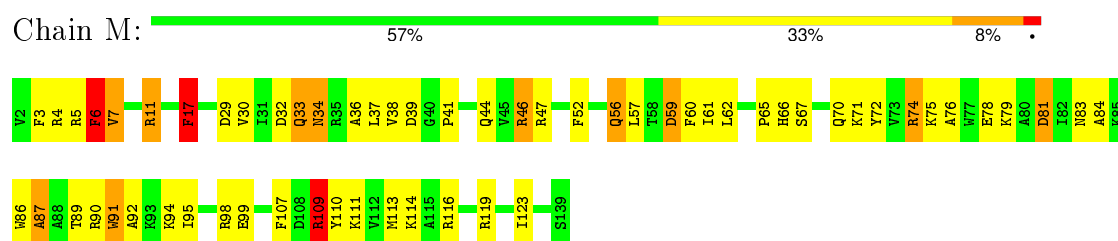
- Molecule 5: Ribosomal protein uL5



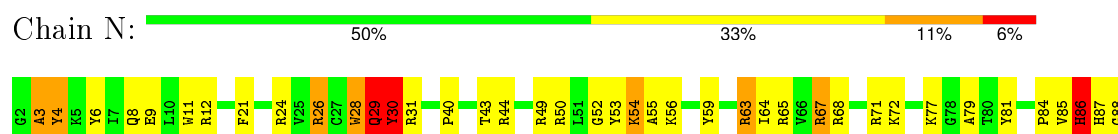
- Molecule 6: Ribosomal protein eL13

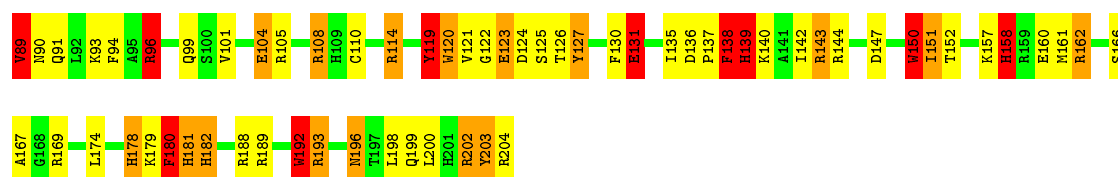


- Molecule 7: Ribosomal protein eL14

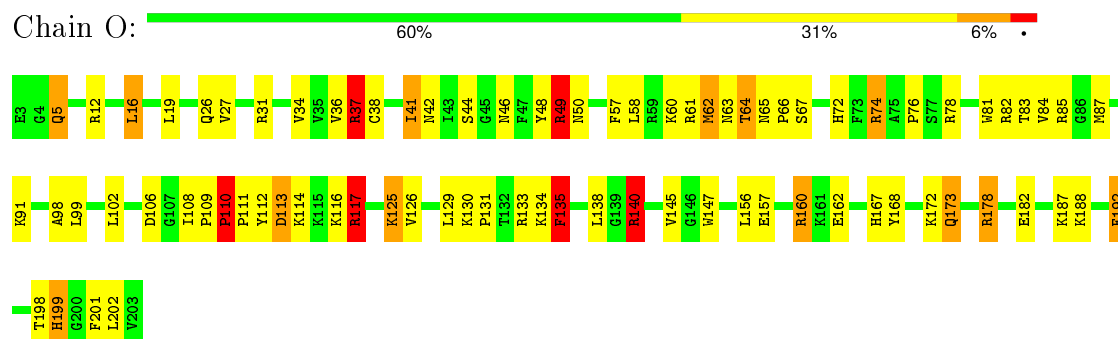


- Molecule 8: Ribosomal protein eL15

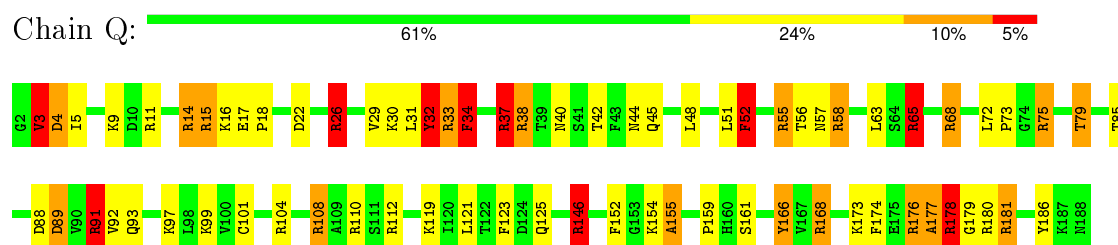




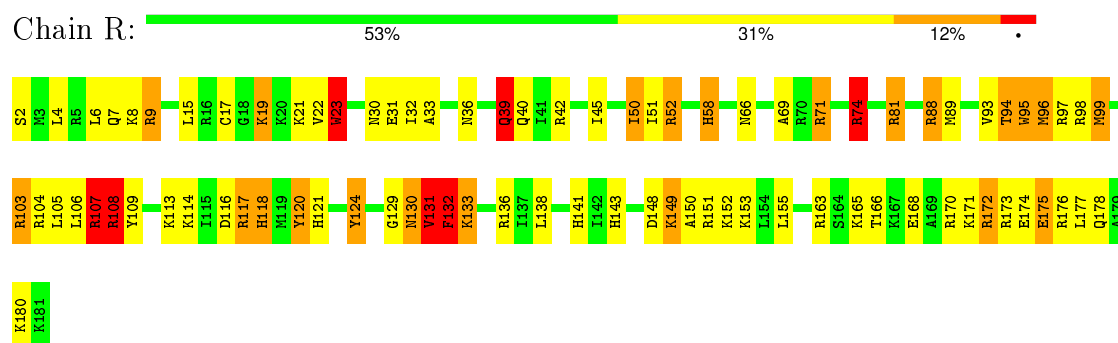
• Molecule 9: Ribosomal protein uL13



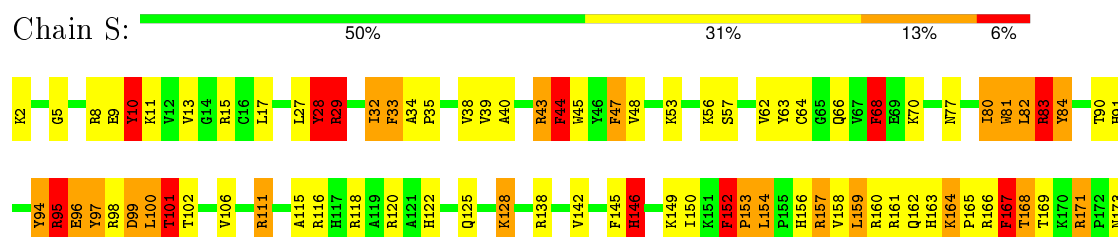
• Molecule 10: Ribosomal protein eL18



• Molecule 11: Ribosomal protein eL19

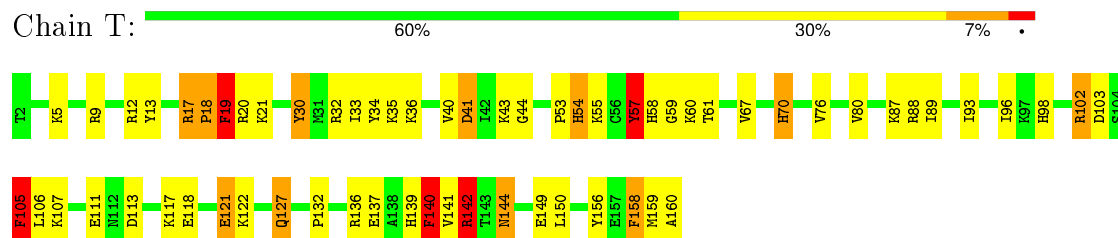


• Molecule 12: Ribosomal protein eL20

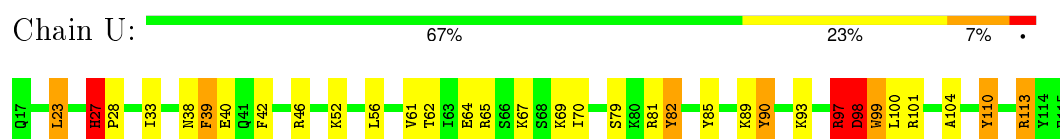


T174  
F175  
F176

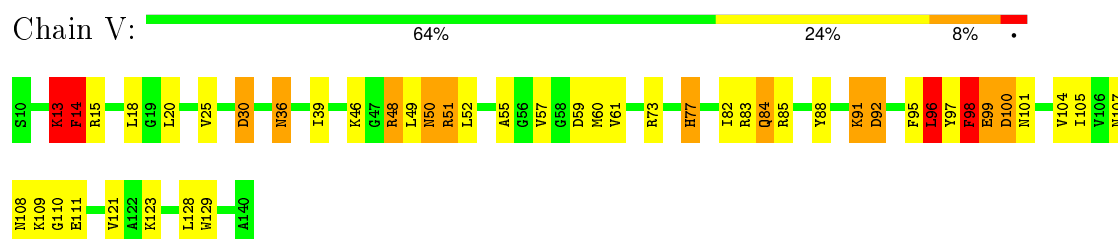
• Molecule 13: Ribosomal protein eL21



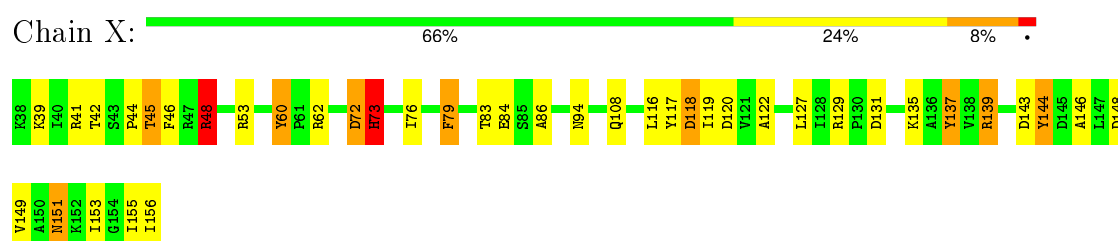
• Molecule 14: Ribosomal protein eL22



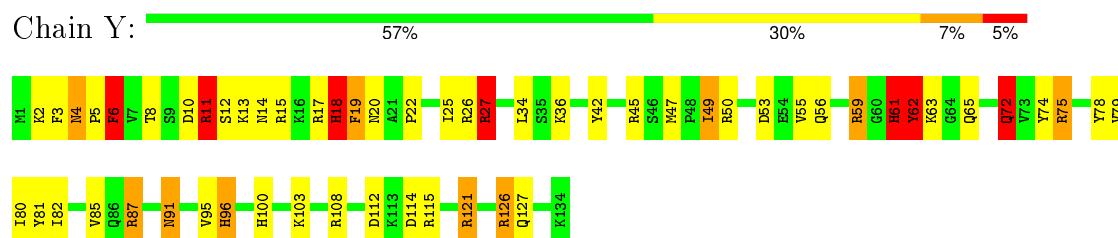
• Molecule 15: Ribosomal protein uL14



• Molecule 16: Ribosomal protein uL23

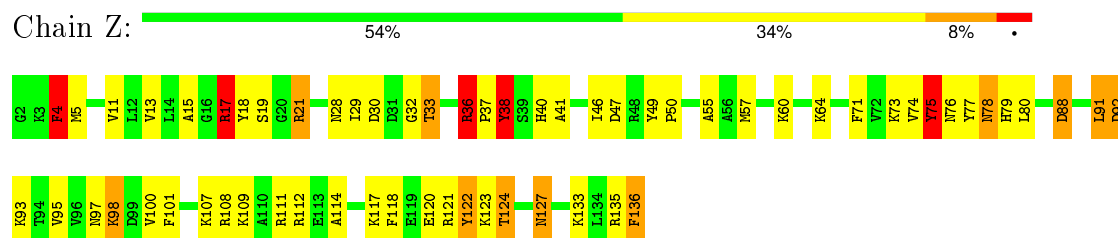


• Molecule 17: Ribosomal protein uL24

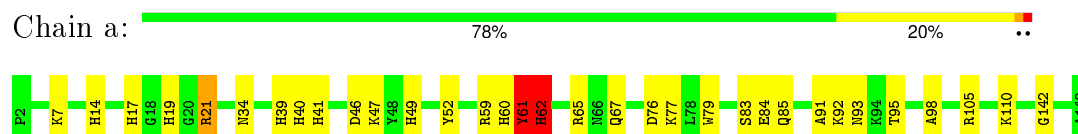


• Molecule 18: Ribosomal protein eL27

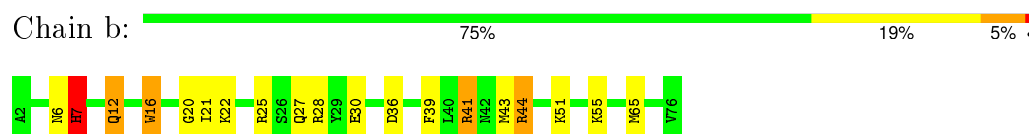




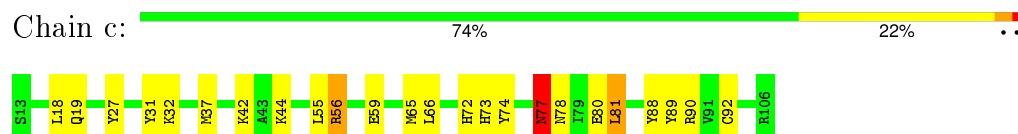
- Molecule 19: Ribosomal protein uL15



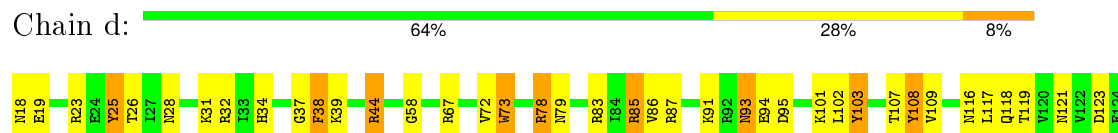
- Molecule 20: Ribosomal protein eL29



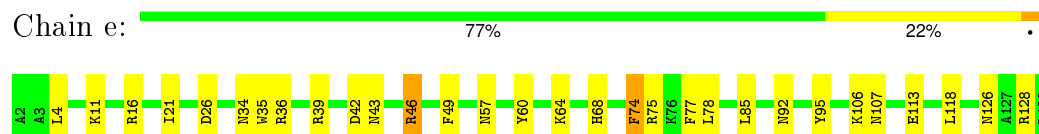
- Molecule 21: Ribosomal protein eL30



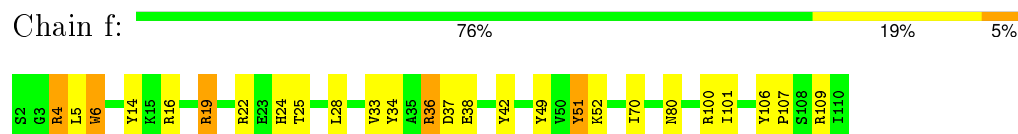
- Molecule 22: Ribosomal protein eL31




- Molecule 23: Ribosomal protein eL32



- Molecule 24: Ribosomal protein eL33




- Molecule 25: Ribosomal protein eL34

Chain g:  79% 17%



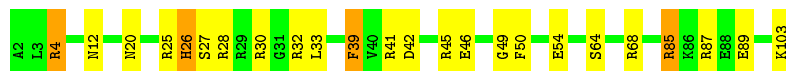
- Molecule 26: Ribosomal protein uL29

Chain h:  84% 11%



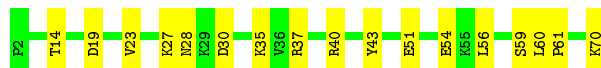
- Molecule 27: Ribosomal protein eL36

Chain i:  76% 20%




- Molecule 28: Ribosomal protein eL38

Chain k:  75% 25%



- Molecule 29: Ribosomal protein eL39

Chain l:  78% 20%



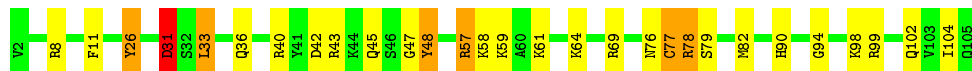
- Molecule 30: Ribosomal protein eL40

Chain m:  71% 25%



- Molecule 31: Ribosomal protein eL42

Chain o:  72% 21% 6%



- Molecule 32: 28S ribosomal RNA

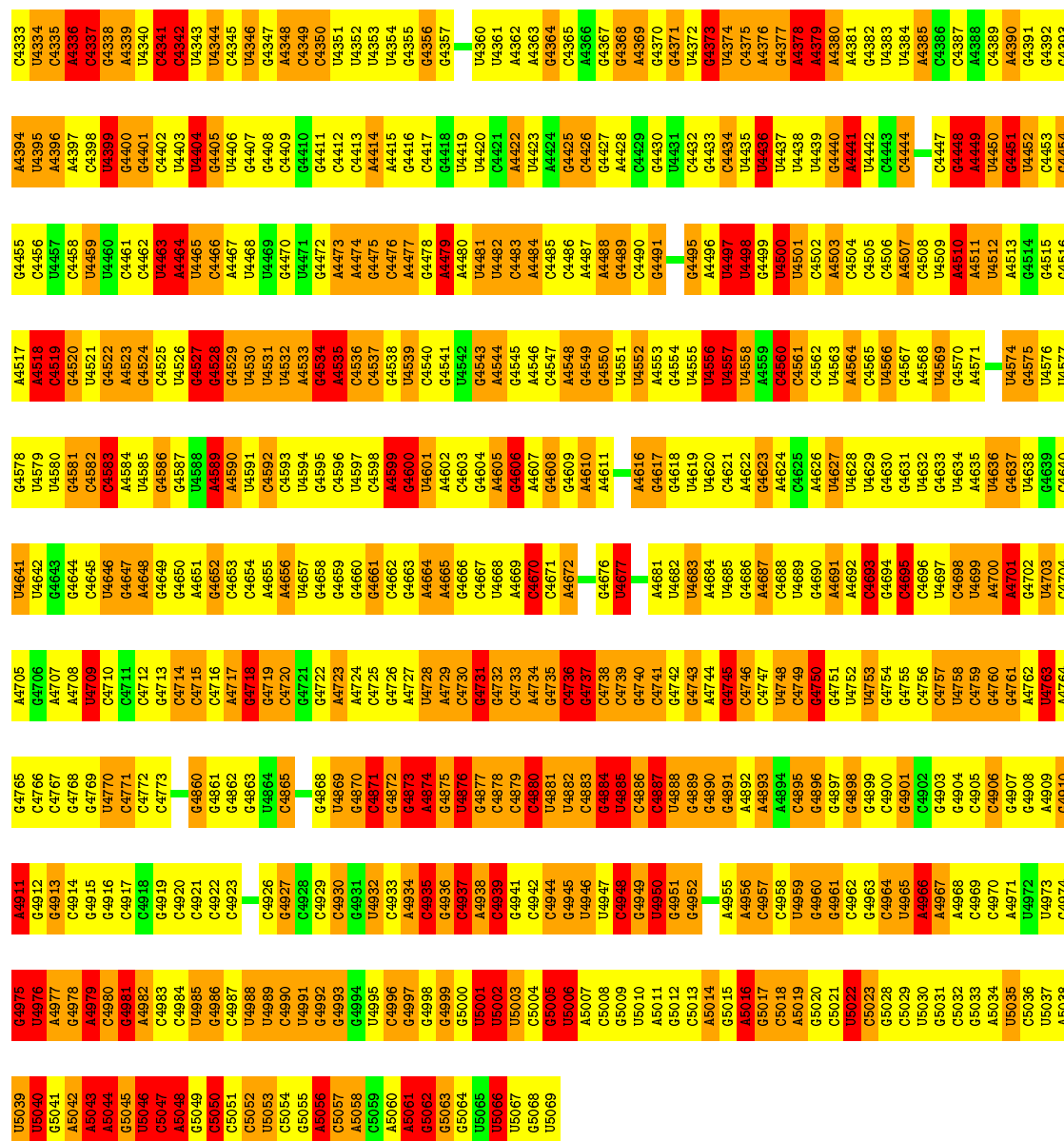
Chain 5:  7% 44% 36% 13%


**WORLDWIDE PDB**  
 PROTEIN DATA BANK  

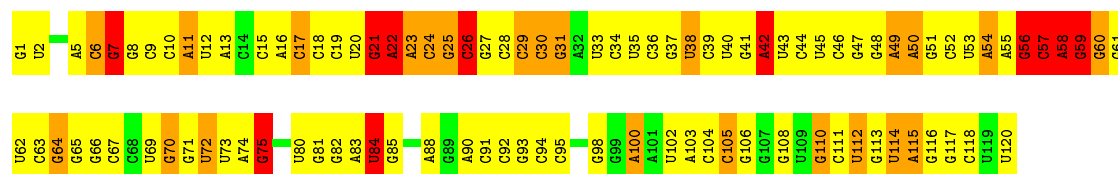
**EMDataBank**  
 Unified Data Resource for 3DEM

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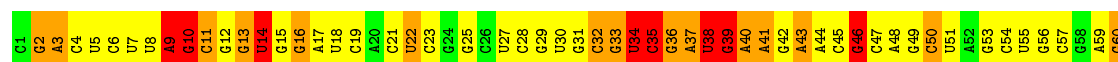


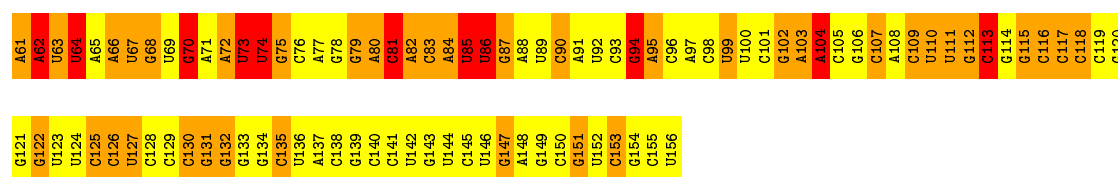
Chain 7: 16% 56% 19% 9%



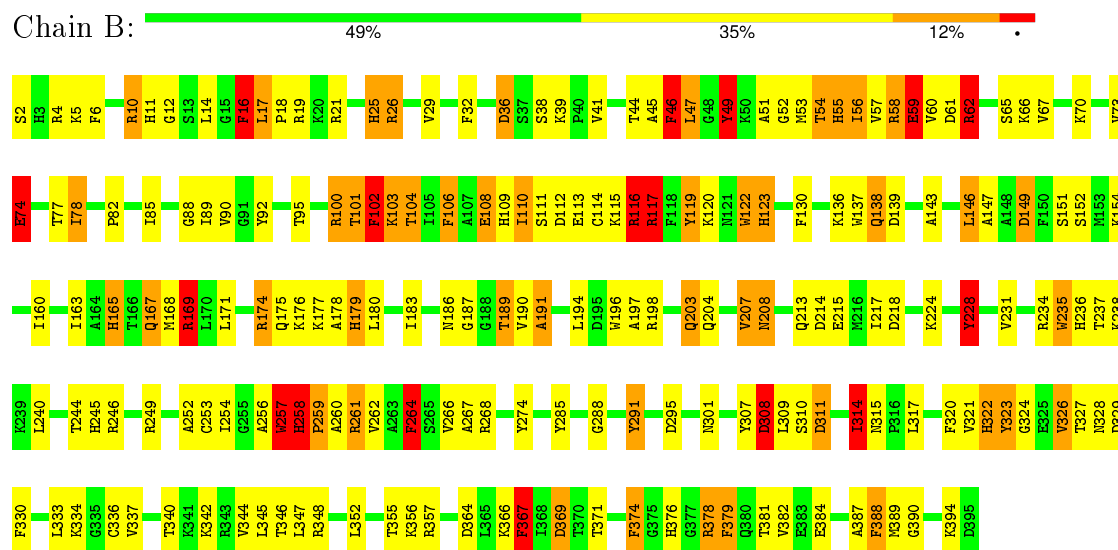
• Molecule 34: 5.8S ribosomal RNA

Chain 8: 50% 34% 12%

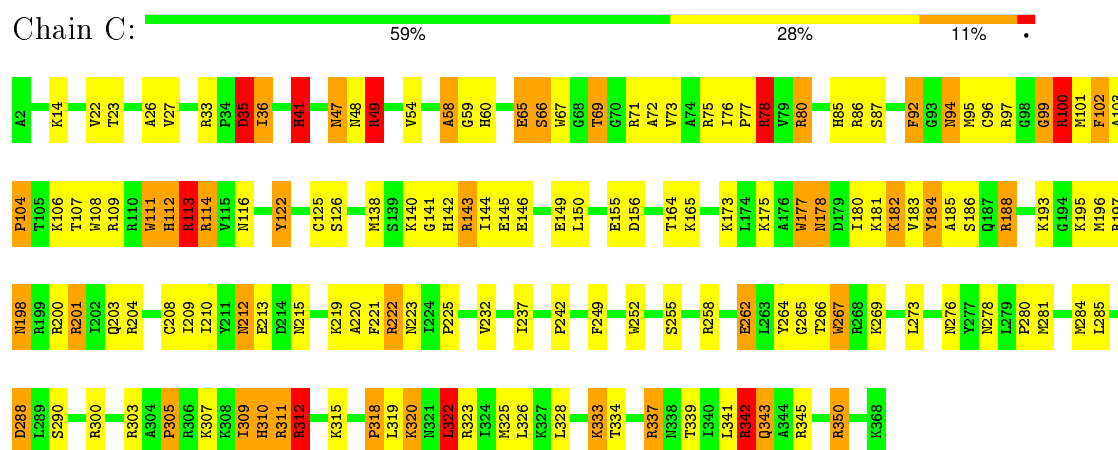




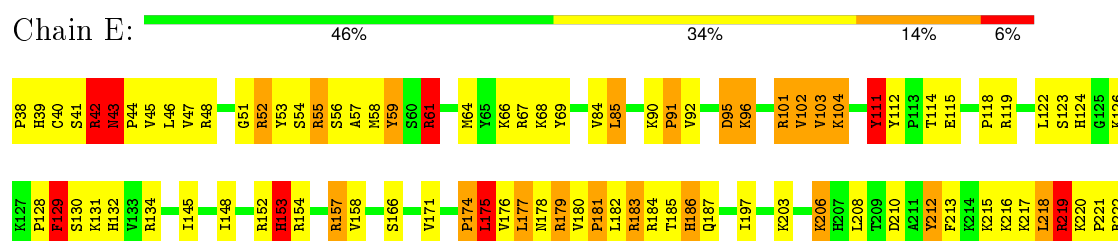
### • Molecule 35: Ribosomal protein uL3

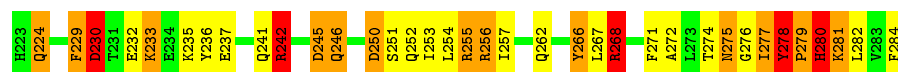


### • Molecule 36: Ribosomal protein uL4



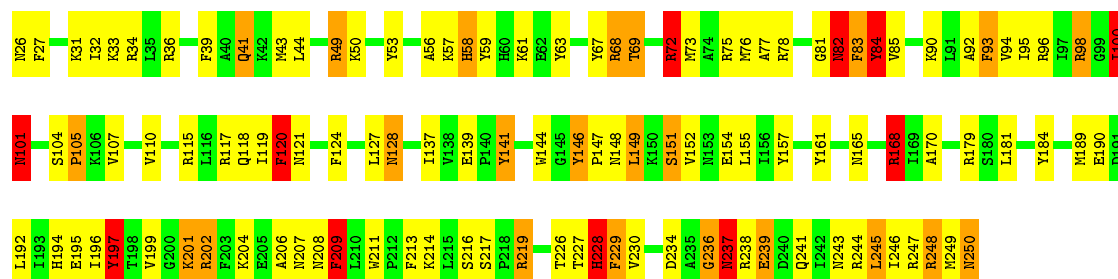
### • Molecule 37: Ribosomal protein eL6





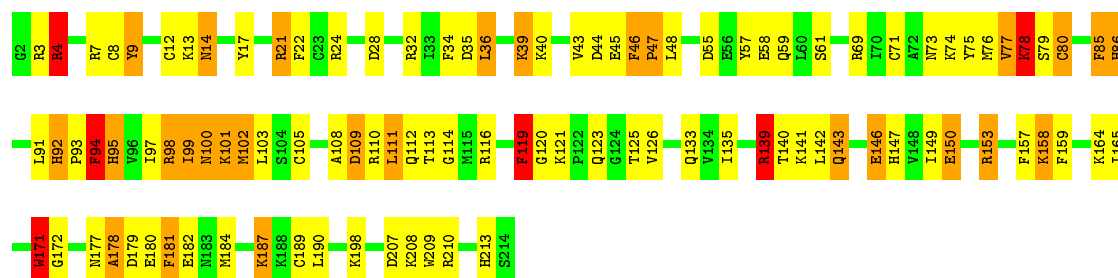
• Molecule 38: Ribosomal protein uL30

Chain F: 48% 36% 10% 5%



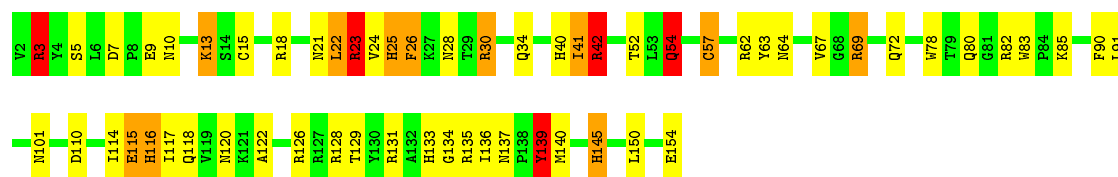
• Molecule 39: Ribosomal protein uL16

Chain I: 51% 33% 13% .



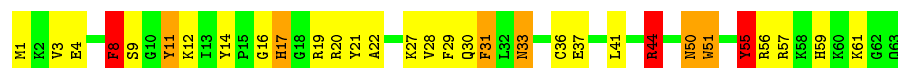
• Molecule 40: Ribosomal protein uL22

Chain P: 61% 28% 7% .



• Molecule 41: Ribosomal protein eL24

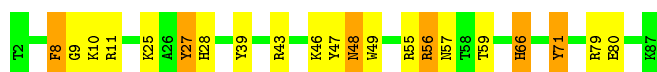
Chain W: 51% 35% 10% 5%



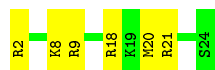
• Molecule 42: Ribosomal protein eL37

Chain j: 76% 17% 7%

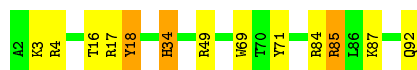
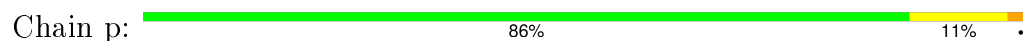




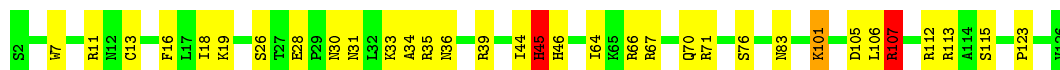
- Molecule 43: Ribosomal protein eL41



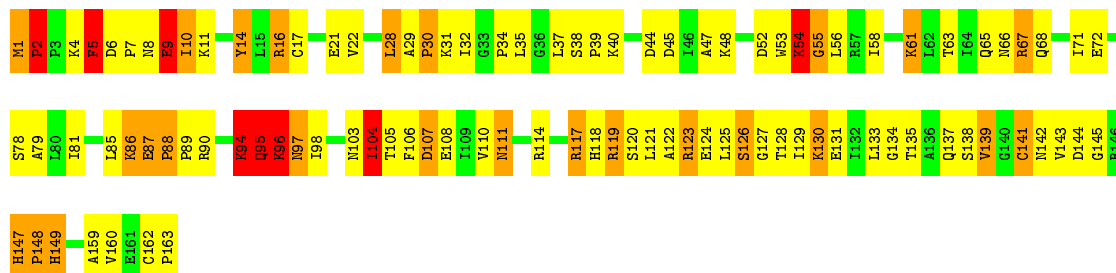
- Molecule 44: Ribosomal protein eL43



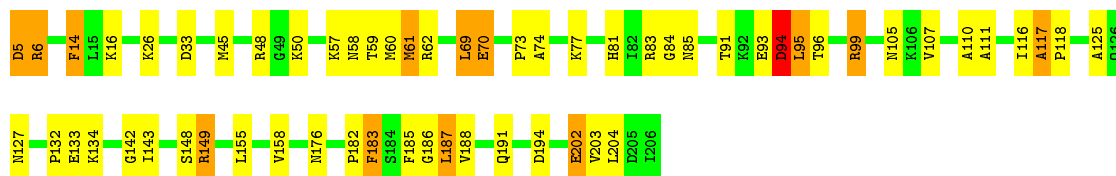
- Molecule 45: Ribosomal protein eL28



- Molecule 46: Ribosomal protein uL11

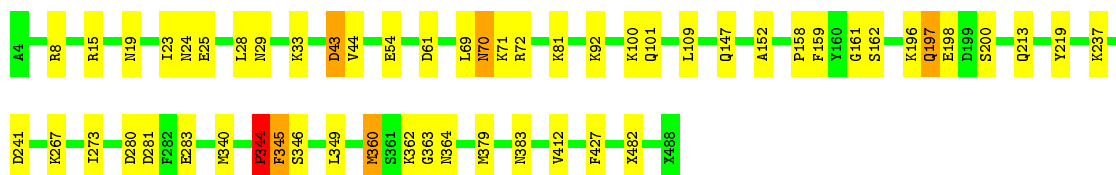


- Molecule 47: Ribosomal protein uL10



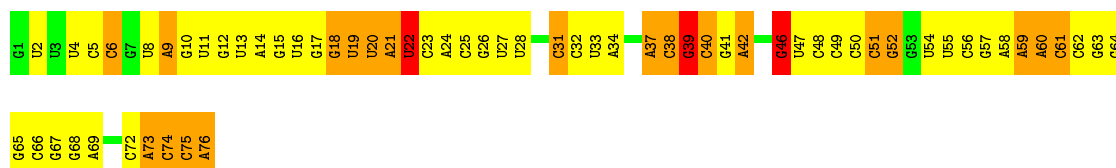
- Molecule 48: SRP54





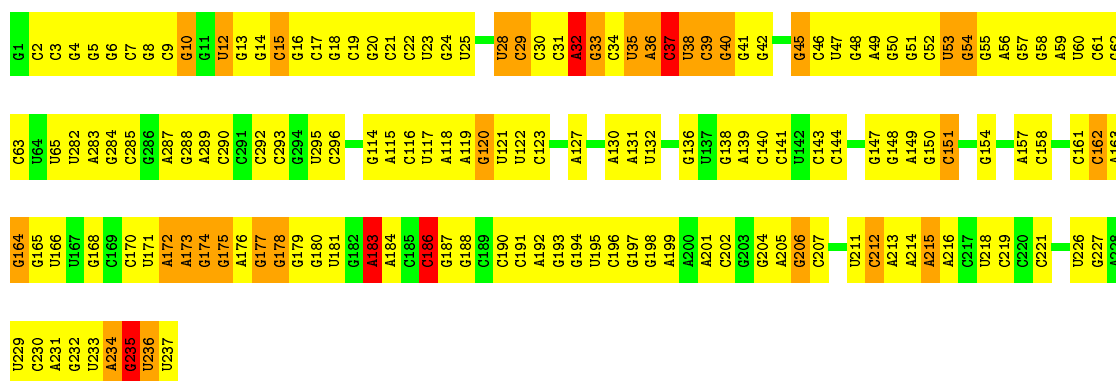
• Molecule 49: Val tRNA

Chain 3: 17% 53% 26% .



• Molecule 50: SRP 7S RNA

Chain 4: 23% 61% 14% .



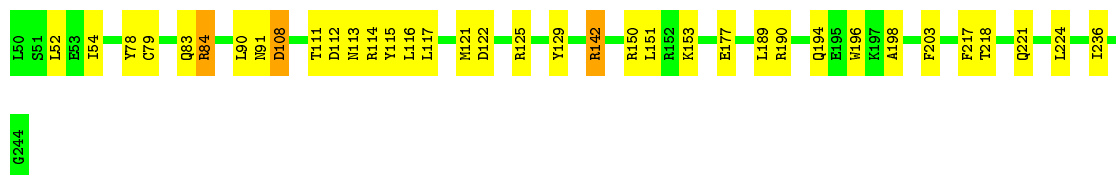
• Molecule 51: SRP19

Chain 9: 65% 35%



• Molecule 52: SRP68

Chain 6: 80% 18% .

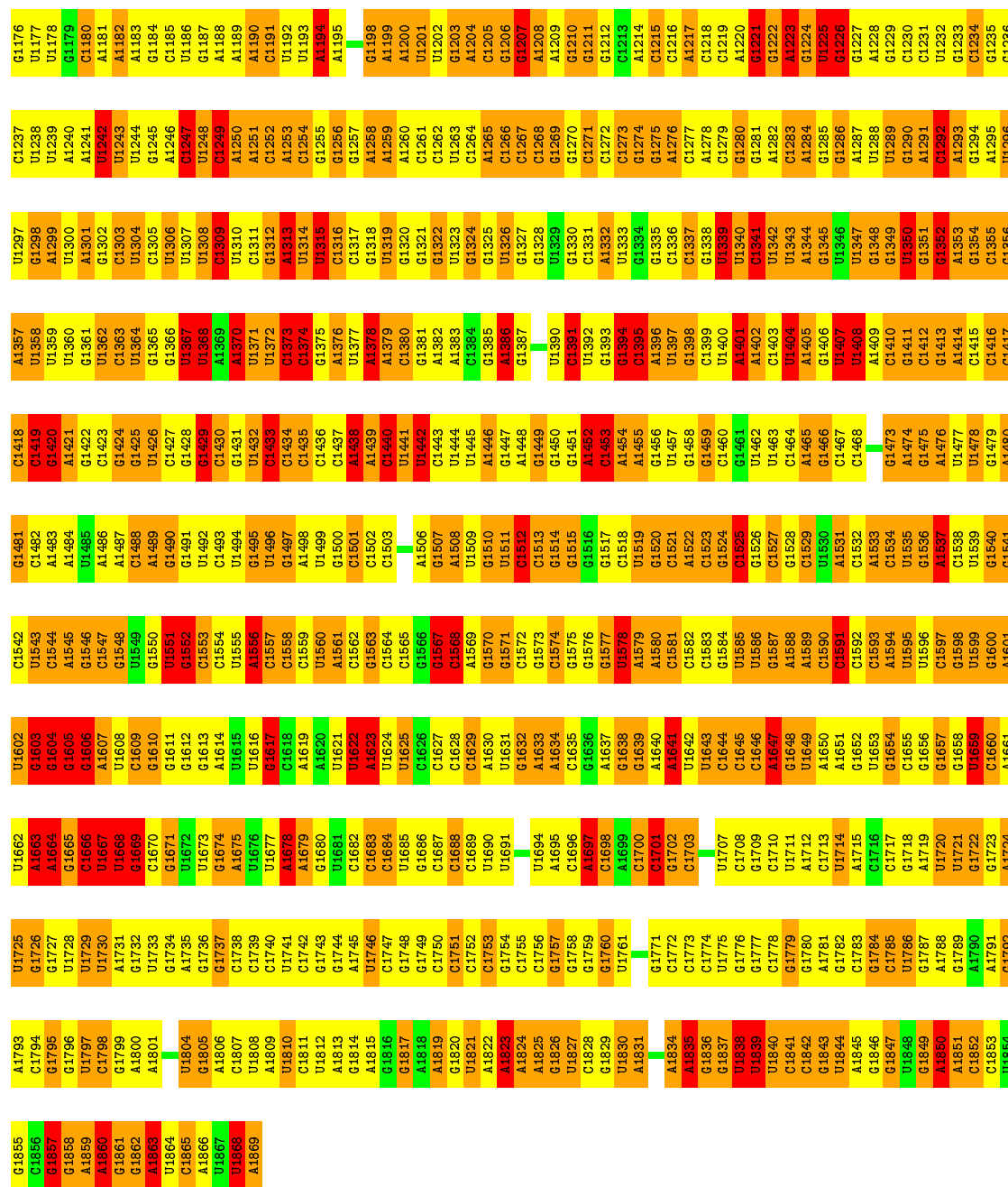


• Molecule 53: 18S ribosomal RNA

Chain S2: 8% 42% 39% 11%

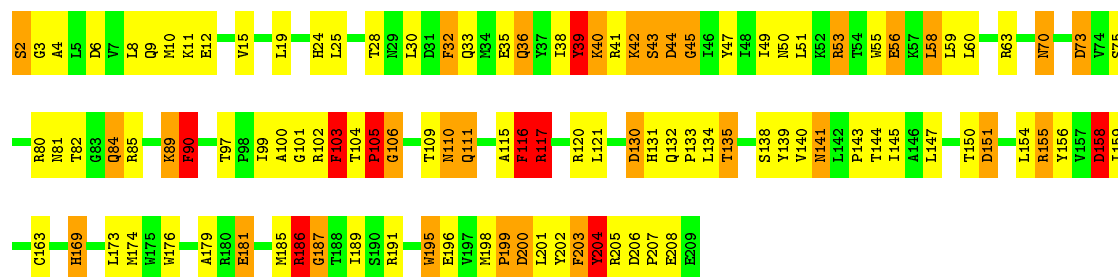


C1116	A1055	G993	G933	G873	A813	C887	U627	C568	G504	G444	C382	C321	C196	C125	U63	U1
C1117	U1056	C994	G934	G874	U814	U888	A628	C569	G505	A445	G383	C322	G200	G126	A64	A2
C1118	C1057	G995	G935	A875	U815	U889	A629	A569	G506	G446	U384	C323	G201	C127	G65	C3
A1119	A1058	G996	G936	A876	A816	G890	U630	C570	G507	A447	U385	C324	G202	C128	G66	C4
U1120	G1059	A997	G937	G877	A817	G891	U631	U571	G508	A448	C386	C325	G203	C129	G67	U5
G1121	A1060	A998	A938	G878	A818	G892	C632	U572	G509	A449	C387	C326	G204	C130	A68	G6
A1122	U1061	G999	U939	C979	A819	A893	C633	U573	G510	C450	U388	G327	G205	C131	G69	
C1123	A1062	C1000	U940	G880	U820	G894	A634	A574	U511	G451	A389	U328	G206	C132	G70	U9
C1124	C1063	U1001	C941	G881	G821	C895	G635	A575	G512	G452	U393	G329	G207	C133	G71	G10
C1125	G1064	U1002	G942	U882	U822	G896	C636	A576	G513	C453	G394	G332	G208	C134	C72	A11
C1126	G1065	U1003	G943	U883	U823	G897	U637	U577	G514	U454	G395	G333	G209	C135	C73	U12
C1127	U1066	U1004	A944	C884	C824	G898	C638	G578	A516	A455	G396	G334	A209	C136	G74	C13
C1128	C1067	U1005	A945	U885	A825	C730	C639	C579	C517	C456	U396	G335	U210	C137	G75	G14
C1129	G1068	C1006	U946	A886	A826	G731	A640	U580	G518	C457	G397	G336	G211	C138	U76	U15
G1130	U1069	C1007	G947	U887	A827	U732	A641	U581	G519	A458	A398	C337	G212	C139	A77	G16
C1131	A1070	U1008	C948	U888	G828	C733	U642	C582	A520	C459	C399	C338	G213	C140	A78	C17
C1132	G1071	A1009	G949	U889	C829	C734	A643	C583	A521	U460	C400	G339	U214	C141	A79	C18
A1133	U1072	G1010	C950	U890	A830	C735	G644	G584	A522	U461	A401	A340	G215	C142	G80	A19
G1134	U1073	A1011	C951	G891	G831	C736	C645	C585	A523	C462	C402	C341	G216	C143	U81	G20
C1135	C1074		G952	U892	G832	G737	U646	G586	U524	C463	C403	C342	A217	C144	G82	U21
U1136	U1075	U1015	C953	U893	C833	C738	U647	A597	U525	A464	G404	G343	U218	C145	A83	A22
U1137	G1076	U1016	U954	G894	C834	C739	A648	G588	A526	A465	G405	A344	U219	C146	A84	G23
C1138	A1077	U1017	A955	G895	C835	G744	U649	G589	C527	G466	U406	U344	U220	C147	A85	C24
G1139	C1078	U1018	G956	U896	G836	C745	A650	A590	A528	G467	G407	U345	A221	C148	C86	
G1140	C1079	C1019	A957	U897	A837	C746	U651	U591	A529	A468	A408	C346	U222	C149	U87	U26
G1141	A1080	U1020	G958	U898	G838	U747	U652	C592	U530	A469	C409	G347	C223	C150	G88	A27
G1142	U1081	U1021	G959	U899	C839	C748	A653	C593	A531	G470	G410	A348	A224	C151	C89	U28
A1143	A1082	U1022	U960	C900	C840	U749	A654	A594	C532	G471	G411	A349	G289	C152	G90	G29
A1144	A1083	A1023	G961	G901	G841	C750	A655	U595	A533	C472	G412	C350	U290	C153	A91	C30
A1145	A1084	A1024	A962	G902	C842	G751	G656	U596	G534	A473	G413	C351	U291	C154	A92	U31
G1146	C1085	U1025	A963	A903	C843	G752	U657	G597	G535	G474	A414	U352	G292	C155	U93	U32
C1147	G1086	C1026	A964	A904	U844	C753	U658	G598	A536	C475	A415	C353	A293	C156	G94	G33
A1148	A1087	U1027	U965	C905	G845	C754	G659	A599	C537	A476	U416	U354	C294	C157	C98	
A1149	U1088	U1028	U966	U906	G846	G755	U660	G600	U538	G477	G417	C356	U295	C158	A99	C37
A1150	G1089	G1029	C967	G907	A847	G756	U661	G601	C539	G478	A418	C357	U296	C159	U100	A38
G1151		A1030	U968	A908	U848	G757	G662	G602	U540	C479	G419	C358	A297	C160	U101	A39
U1152	C1092	A1031	U969	G909	A849	G758	C663	C603	U541	G490	G420	C359	C298	C161	U102	A40
C1153	A1093	C1032	G970	G910	C850	C790	A664	A604	U542	C481	G421	U359	C299	C162	A103	G41
U1154	C1094	G1033	G971	C911	C851	C791	G665	A605	G543	G482	U422	A360	A299	C163	A104	A42
U1155	U1095	A1034	A972	C912	G852	C792	U666	G606	G544	C483	U423	U361	U300	C164	A105	U43
U1156	G1096	A1035	C973	A913	C853	G793	U667	U607	U545	A484	C424	C362	A301	C165	C106	U44
G1157	G1097	A1036	C974	U914	A854	A794	A668	C608	G546	A485	G425	A363	A302	C166	U107	A45
G1158	C1098	G1037	G975	G915	G855	A795	A669	U609	C547	U486	A426	C364	C303	C167	A108	A46
U1159	G1099	U1038	C976	A916	C856	C796	A670	G610	C548	U487	U427	C365	C304	C168	U109	G47
U1160	A1100	C1039	C977	U917	U857	C797	A671	G611	C549	U488	U428	U366	U305	C169	U110	C48
U1161	U1011	G1040	G978	U918	A858	A798	A672	U612	C550	A489	C429	U367	C306	C170	C49	
C1162	G1102	G1041	C979	U919	G859	U799	G673	G613	U551	C490	C430	U368	G307	C171	U111	C49
C1163	C1103	A1042	A980	A920	G860	C793	C674	C614	G552	C491	G431	C369	G308	C172	U112	A50
G1164	G1104	G1043	A981	G921	U861	U801	U675	C615	U553	C492	G432	G370	G309	C173	G113	U51
C1165	G1105	G1044	G982	A922	A862	A802	C676	A616	A554	A493	A433	A371	C310	C174	G114	G52
G1166	C1106	U1045	A983	G923	U863	C903	G677	G617	A555	C494	G434	U372	C311	C175	U115	G53
G1167	G1107	U1046	C984	G924	A864	U803	U678	C618	U556	U495	A435	G373	G312	C176	U116	A54
G1168	C1108	C1047	G985	G925	A865	U804	A679	A619	U557	C496	G436	G374	A313	C177	C117	U55
G1169	G1109	G1048	G986	A926	U866	U806	G680	G620	G558	C497	G437	U375	U314	C178	C118	G56
A1170	U1110	A1049	A987	C927	G867	G807	U681	C621	G559	C498	G438	A376	G315	C179	U119	U57
G1171	U1111	U1050	C988	G928	G868	A808	U682	C622	A560	G499	A439	G377	G316	C180	U120	C58
U1172	U1112	G1051	C989	G929	A869	A809	G683	G623	A561	A500	G440	U378	C317	C181	U121	U59
A1173	A1113	A1052	A990	C930	A870	A810	G684	G624	U562	C501	C441	C379	A318	C182	G122	A60
U1174	U1114	C1053	G991	C931	U871	A811	A685	G625	G563	C502	C442	G380	C319	C183	G123	A61
G1175	U1115	G1054	A992	G932	A872	A812	U686	G626	A564	C503	U443	C381	G320	C184	U124	G62

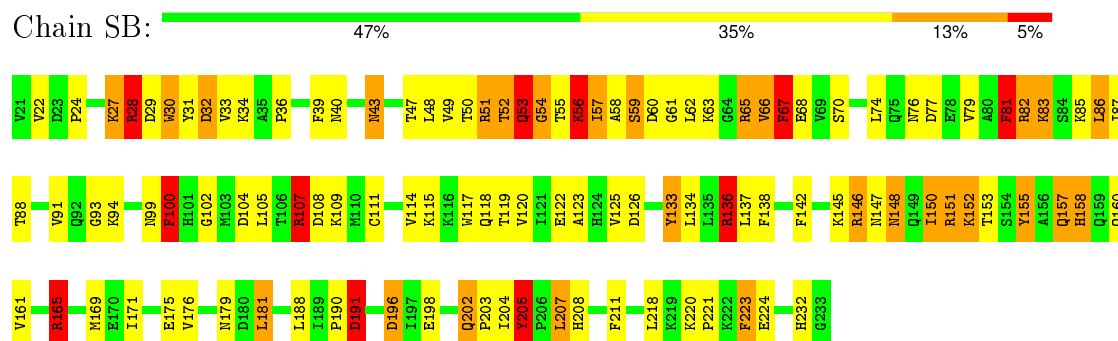


• Molecule 54: Ribosomal protein uS2

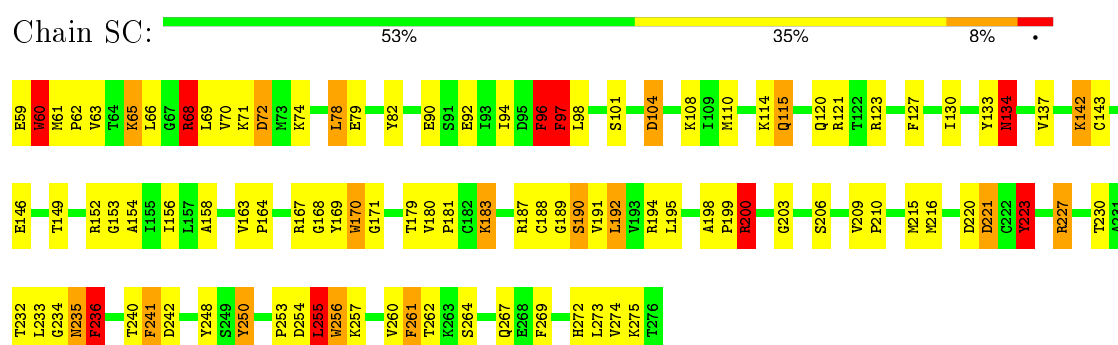
Chain SA:  47%  35%  14% •



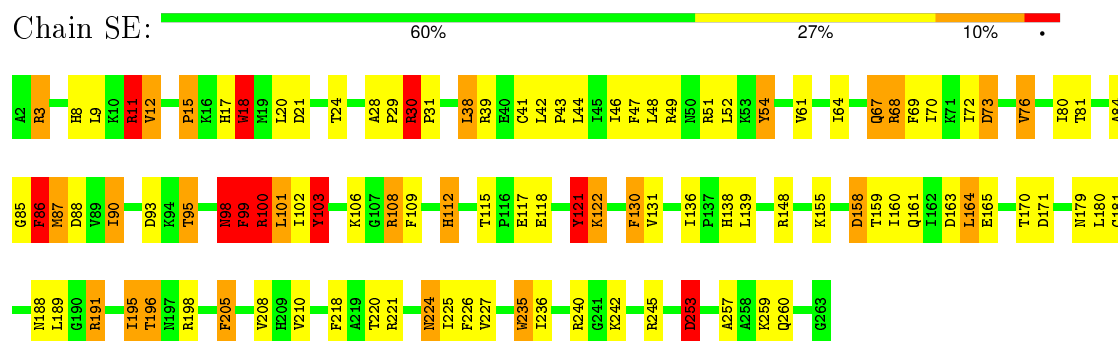
- Molecule 55: Ribosomal protein eS1



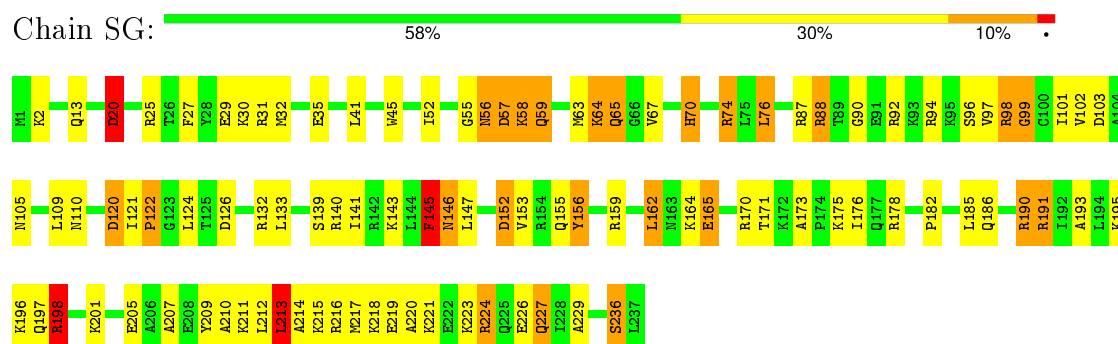
- Molecule 56: Ribosomal protein uS5



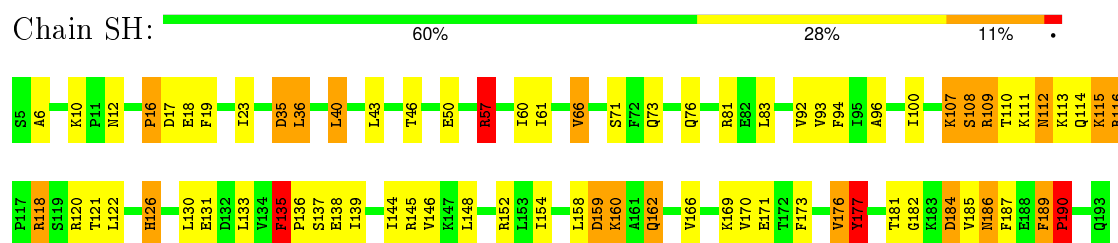
- Molecule 57: Ribosomal protein eS4



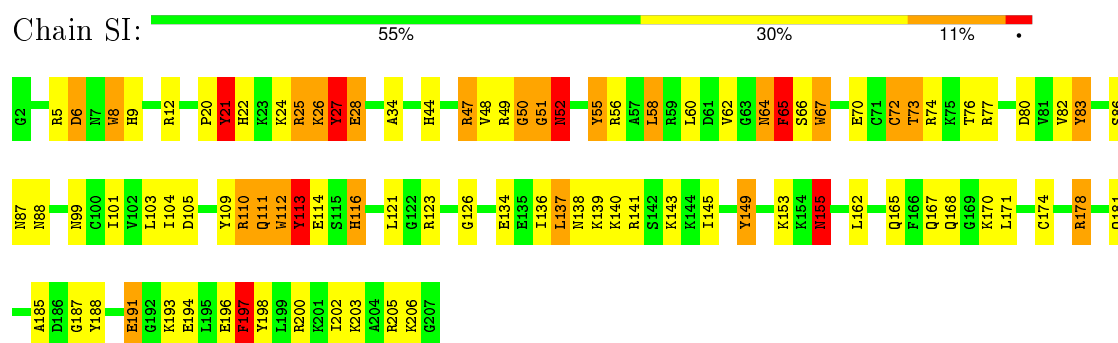
- Molecule 58: Ribosomal protein eS6



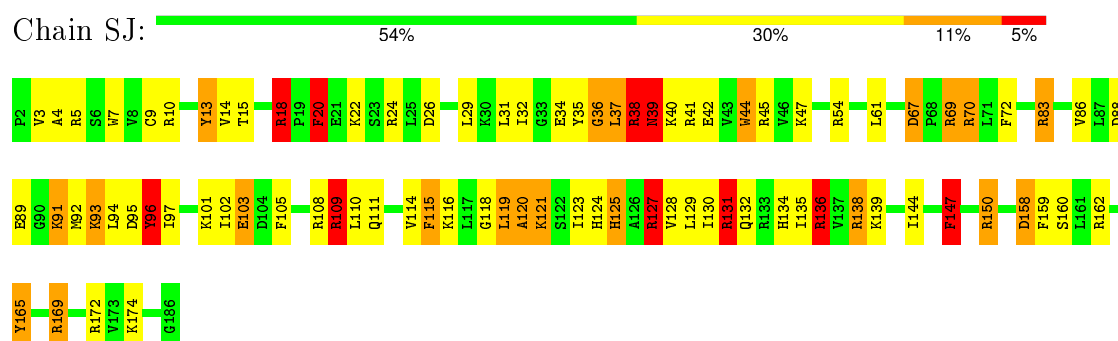
- Molecule 59: Ribosomal protein eS7



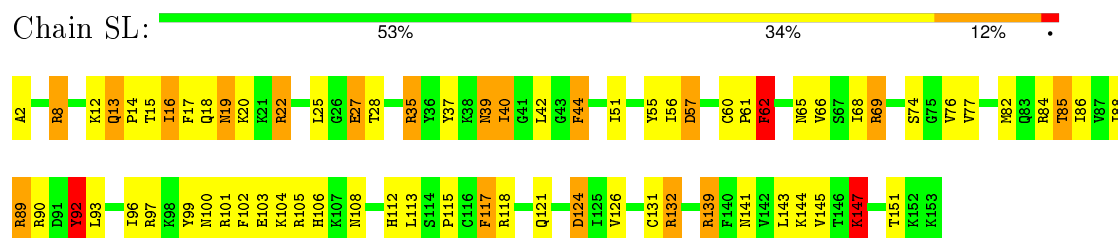
- Molecule 60: Ribosomal protein eS8



- Molecule 61: Ribosomal protein uS4

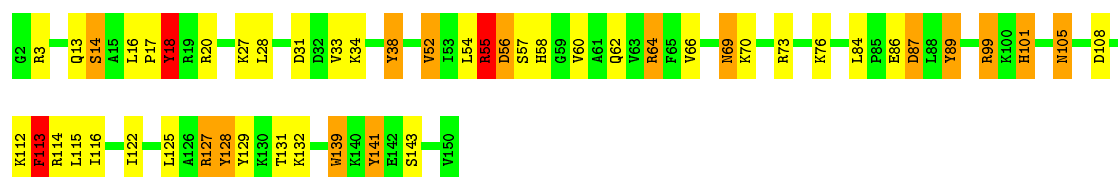


- Molecule 62: Ribosomal protein uS17



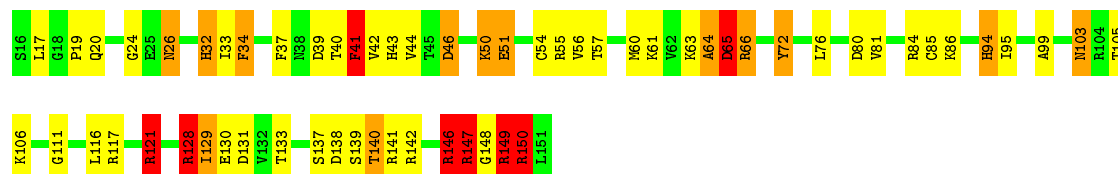
- Molecule 63: Ribosomal protein uS15





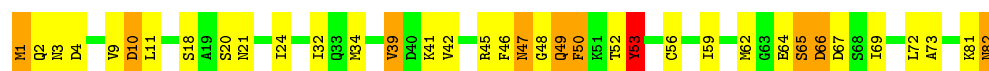
• Molecule 64: Ribosomal protein uS11

Chain SO: 55% 29% 10% 6%



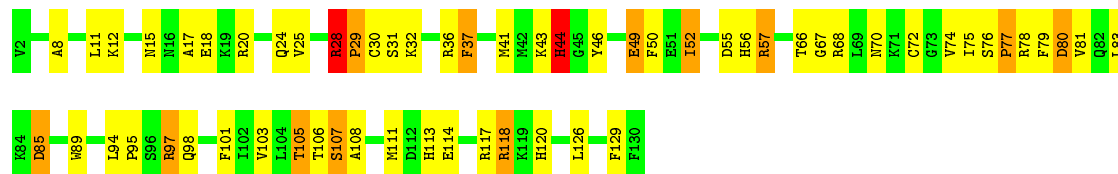
• Molecule 65: Ribosomal protein eS21

Chain SV: 56% 32% 11%



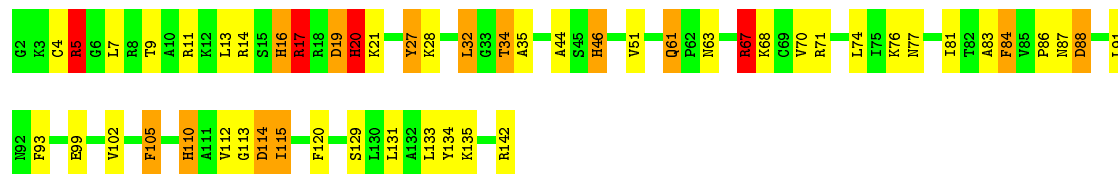
• Molecule 66: Ribosomal protein uS8

Chain SW: 53% 36% 9%



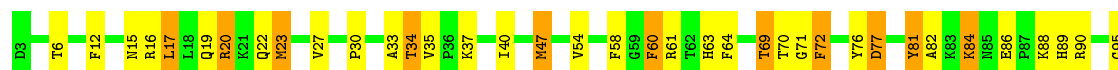
• Molecule 67: Ribosomal protein uS12

Chain SX: 63% 25% 9%



• Molecule 68: Ribosomal protein eS24

Chain SY: 62% 26% 12%





- Molecule 69: Ribosomal protein eS26

Chain Sa: 77% 16% 7%



- Molecule 70: Ribosomal protein eS27

Chain Sb: 73% 25% 2%



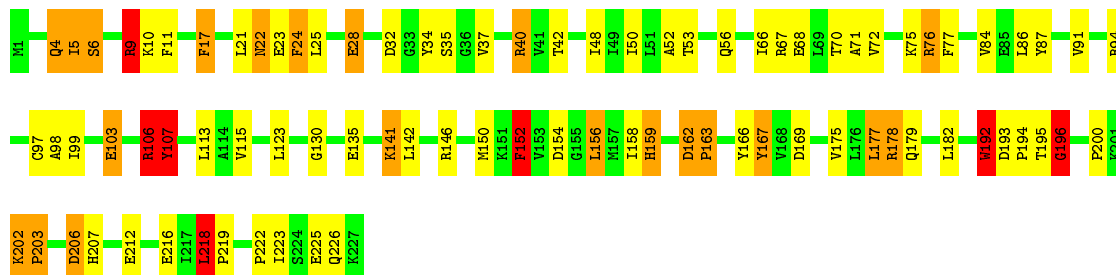
- Molecule 71: Ribosomal protein eS30

Chain Se: 77% 18% 5%



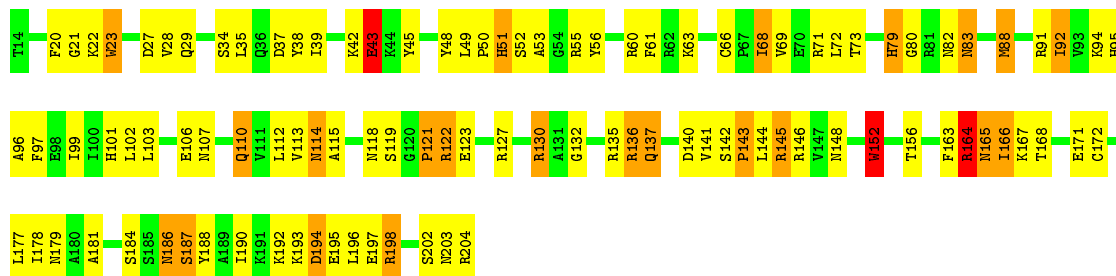
- Molecule 72: Ribosomal protein uS3

Chain SD: 62% 26% 9%



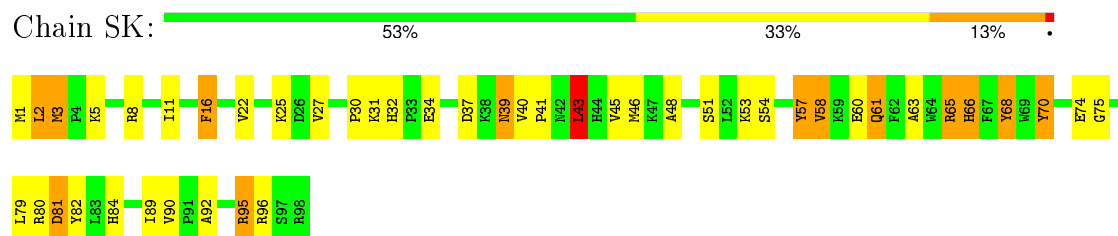
- Molecule 73: Ribosomal protein uS7

Chain SF: 47% 40% 12%

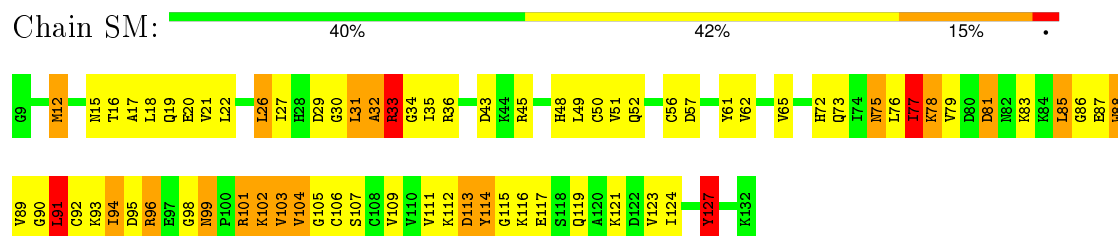


- Molecule 74: Ribosomal protein eS10

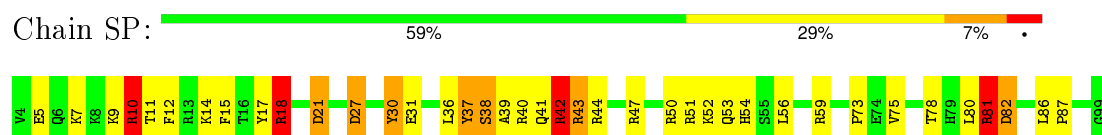




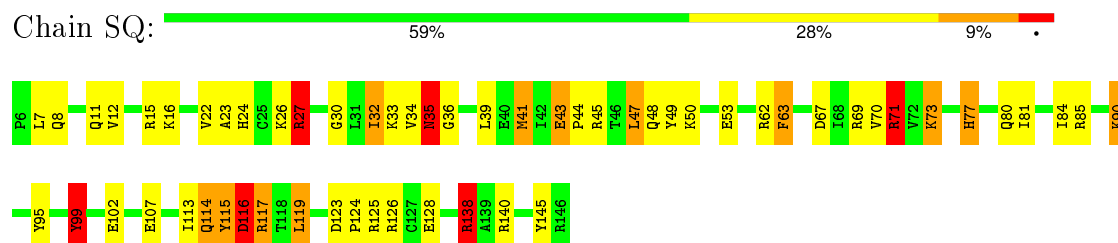
- Molecule 75: Ribosomal protein eS12



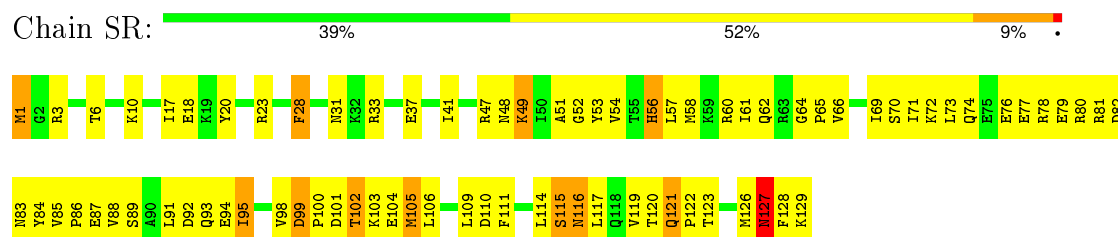
- Molecule 76: Ribosomal protein uS19



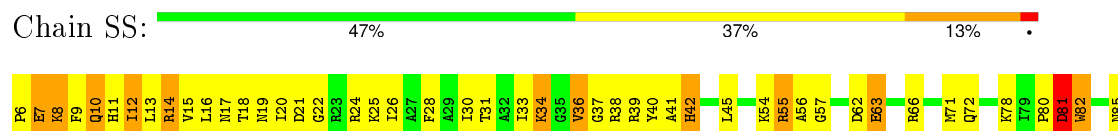
- Molecule 77: Ribosomal protein uS9



- Molecule 78: Ribosomal protein eS17



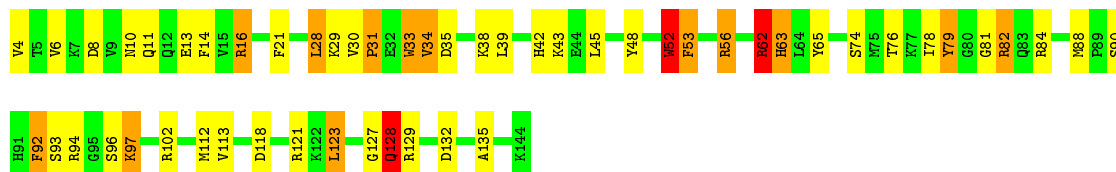
- Molecule 79: Ribosomal protein uS13





- Molecule 80: Ribosomal protein eS19

Chain ST: 62% 26% 9%



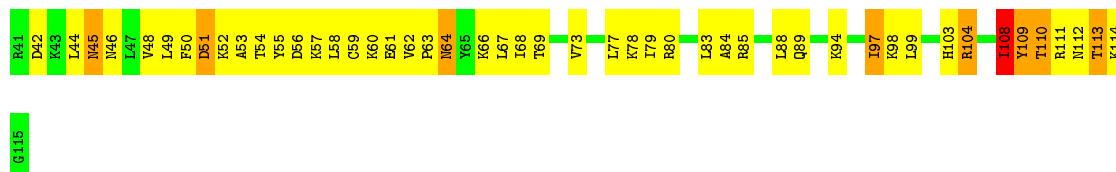
- Molecule 81: Ribosomal protein uS10

Chain SU: 66% 28% 6%



- Molecule 82: Ribosomal protein es25

Chain SZ: 36% 52% 11%



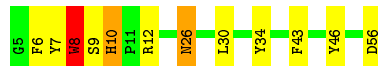
- Molecule 83: Ribosomal protein eS28

Chain Sc: 84% 13%



- Molecule 84: Ribosomal protein uS14

Chain Sd: 77% 17%




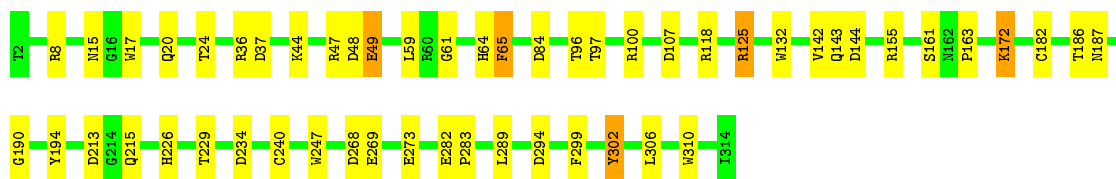
- Molecule 85: Ribosomal protein eS31

Chain Sf: 56% 30% 10%



- Molecule 86: Ribosomal protein RACK1

Chain Sg:  83% 15% •



• Molecule 87: SRP9

Chain S1:  58% 26% 15% •



• Molecule 88: SRP14

Chain S4:  71% 25% •



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	27627	Depositor
Resolution determination method	FSC 0.143	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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	A	0.70	1/1906 (0.1%)	1.25	18/2556 (0.7%)
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%)
2	D	0.67	2/2426 (0.1%)	1.17	24/3252 (0.7%)
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%)
3	G	0.78	8/1944 (0.4%)	1.10	14/2618 (0.5%)
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%)
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%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	I	0.59	1/1753 (0.1%)	1.05	8/2343 (0.3%)
4	H	0.77	2/1537 (0.1%)	1.10	10/2066 (0.5%)
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%)
5	J	0.69	2/1382 (0.1%)	1.09	15/1849 (0.8%)
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%)
6	L	0.68	3/1734 (0.2%)	1.05	7/2318 (0.3%)
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%)
7	M	0.62	1/1152 (0.1%)	1.10	6/1539 (0.4%)
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%)
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%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  > 2	RMSZ	# Z  > 2
78	SR	0.50	0/1060	0.73	0/1421
79	SS	0.46	0/1157	1.00	5/1548 (0.3%)
8	N	0.72	3/1746 (0.2%)	1.25	11/2338 (0.5%)
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
9	O	0.63	2/1684 (0.1%)	1.08	11/2251 (0.5%)
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
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
2	D	0	9
20	b	0	2
21	c	0	1
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
3	G	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
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
4	H	0	2
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
5	J	0	2
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
6	L	0	4
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
7	M	0	3
70	Sb	0	1
72	SD	0	3
73	SF	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
74	SK	0	1
75	SM	0	2
76	SP	0	3
77	SQ	0	1
79	SS	0	1
8	N	0	9
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
9	O	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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1868	0	1959	128	0
2	D	2380	0	2412	118	0
3	G	1912	0	2059	94	0
4	H	1518	0	1601	68	0
5	J	1359	0	1390	56	0
6	L	1703	0	1818	61	0
7	M	1131	0	1209	55	0
8	N	1701	0	1749	105	0
9	O	1651	0	1786	64	0
10	Q	1506	0	1623	65	0
11	R	1508	0	1664	117	0
12	S	1454	0	1496	114	0
13	T	1298	0	1366	52	0
14	U	808	0	831	15	0
15	V	979	0	1039	43	0
16	X	976	0	1053	36	0
17	Y	1115	0	1205	49	0
18	Z	1107	0	1182	49	0
19	a	1163	0	1211	0	0
20	b	610	0	650	0	0
21	c	732	0	769	0	0
22	d	888	0	930	0	0
23	e	1053	0	1147	0	0
24	f	876	0	912	0	0
25	g	906	0	1002	0	0
26	h	1015	0	1150	0	0
27	i	832	0	917	0	0
28	k	569	0	637	0	0
29	l	444	0	483	0	0
30	m	429	0	466	0	0
31	o	851	0	923	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	5	78406	0	39609	10744	0
33	7	2558	0	1296	323	0
34	8	3314	0	1683	553	0
35	B	3147	0	3280	197	0
36	C	2919	0	3100	118	0
37	E	1904	0	2055	111	0
38	F	1870	0	1996	128	0
39	I	1713	0	1752	122	0
40	P	1242	0	1269	60	0
41	W	528	0	541	53	0
42	j	706	0	742	0	0
43	n	222	0	258	0	0
44	p	708	0	760	0	0
45	r	1001	0	1062	0	0
46	K	1238	0	1293	97	0
47	q	1556	0	1612	0	0
48	z	3241	0	3210	0	0
49	3	1616	0	824	166	0
50	4	4551	0	2299	273	0
51	9	844	0	861	25	0
52	6	1497	0	1504	26	0
53	S2	36900	0	18593	5084	0
54	SA	1642	0	1646	166	0
55	SB	1725	0	1794	153	0
56	SC	1690	0	1777	73	0
57	SE	2076	0	2177	69	0
58	SG	1923	0	2089	72	0
59	SH	1521	0	1615	93	0
60	SI	1686	0	1772	83	0
61	SJ	1525	0	1640	62	0
62	SL	1238	0	1313	64	0
63	SN	1202	0	1289	50	0
64	SO	1016	0	1037	43	0
65	SV	625	0	628	17	0
66	SW	1034	0	1080	47	0
67	SX	1099	0	1166	42	0
68	SY	1023	0	1090	37	0
69	Sa	781	0	832	0	0
70	Sb	651	0	672	0	0
71	Se	452	0	494	0	0
72	SD	1765	0	1865	68	0
73	SF	1509	0	1563	86	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
74	SK	827	0	854	28	0
75	SM	960	0	989	63	0
76	SP	805	0	861	18	0
77	SQ	1124	0	1193	38	0
78	SR	1047	0	1101	214	0
79	SS	1139	0	1190	136	0
80	ST	1101	0	1135	58	0
81	SU	818	0	883	21	0
82	SZ	598	0	655	123	0
83	Sc	506	0	531	0	0
84	Sd	434	0	427	0	0
85	Sf	581	0	599	0	0
86	Sg	2436	0	2393	0	0
87	S1	608	0	617	28	0
88	S4	604	0	638	13	0
89	5	116	0	0	0	0
89	7	5	0	0	0	0
89	8	6	0	0	0	0
89	D	1	0	0	0	0
89	S2	36	0	0	1	0
89	V	1	0	0	0	0
89	g	1	0	0	0	0
90	Sa	1	0	0	0	0
90	j	1	0	0	0	0
90	m	1	0	0	0	0
90	o	1	0	0	0	0
All	All	227964	0	169843	19897	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 55.

The worst 5 of 19897 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5:294:G:C5'	32:5:296:A:H4'	1.20	1.68
49:3:31:C:H4'	53:S2:1640:A:C2	1.31	1.65
11:R:166:THR:HG21	53:S2:872:A:C3'	1.21	1.64
11:R:172:ARG:HG2	53:S2:909:G:P	1.35	1.61
39:I:101:LYS:HE2	39:I:121:LYS:CG	1.28	1.60

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	242/244 (99%)	194 (80%)	38 (16%)	10 (4%)	3	37
2	D	290/292 (99%)	228 (79%)	41 (14%)	21 (7%)	1	22
3	G	236/238 (99%)	188 (80%)	41 (17%)	7 (3%)	5	46
4	H	188/190 (99%)	162 (86%)	20 (11%)	6 (3%)	5	44
5	J	168/170 (99%)	126 (75%)	33 (20%)	9 (5%)	2	30
6	L	208/210 (99%)	166 (80%)	29 (14%)	13 (6%)	2	26
7	M	136/138 (99%)	111 (82%)	21 (15%)	4 (3%)	6	46
8	N	201/203 (99%)	159 (79%)	31 (15%)	11 (6%)	2	30
9	O	199/201 (99%)	177 (89%)	19 (10%)	3 (2%)	13	59
10	Q	185/187 (99%)	154 (83%)	24 (13%)	7 (4%)	4	39
11	R	178/180 (99%)	148 (83%)	23 (13%)	7 (4%)	4	38
12	S	173/175 (99%)	139 (80%)	27 (16%)	7 (4%)	4	38
13	T	157/159 (99%)	132 (84%)	20 (13%)	5 (3%)	5	44
14	U	97/99 (98%)	80 (82%)	14 (14%)	3 (3%)	5	45
15	V	129/131 (98%)	110 (85%)	14 (11%)	5 (4%)	4	38
16	X	117/119 (98%)	102 (87%)	12 (10%)	3 (3%)	7	48
17	Y	132/134 (98%)	105 (80%)	21 (16%)	6 (4%)	3	34
18	Z	133/135 (98%)	111 (84%)	15 (11%)	7 (5%)	2	30
19	a	145/147 (99%)	114 (79%)	24 (17%)	7 (5%)	3	33
20	b	73/75 (97%)	60 (82%)	10 (14%)	3 (4%)	3	37
21	c	92/94 (98%)	78 (85%)	10 (11%)	4 (4%)	3	36
22	d	105/107 (98%)	85 (81%)	16 (15%)	4 (4%)	4	39
23	e	126/128 (98%)	110 (87%)	14 (11%)	2 (2%)	12	58
24	f	107/109 (98%)	89 (83%)	11 (10%)	7 (6%)	1	26
25	g	112/114 (98%)	100 (89%)	10 (9%)	2 (2%)	11	56

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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	SN	147/149 (99%)	115 (78%)	28 (19%)	4 (3%)	6	48
64	SO	134/136 (98%)	99 (74%)	21 (16%)	14 (10%)	1	12
65	SV	80/82 (98%)	58 (72%)	15 (19%)	7 (9%)	1	16
66	SW	127/129 (98%)	108 (85%)	16 (13%)	3 (2%)	7	50
67	SX	139/141 (99%)	109 (78%)	26 (19%)	4 (3%)	6	46
68	SY	124/126 (98%)	101 (82%)	16 (13%)	7 (6%)	2	29
69	Sa	96/98 (98%)	69 (72%)	18 (19%)	9 (9%)	1	15
70	Sb	81/83 (98%)	61 (75%)	16 (20%)	4 (5%)	3	32
71	Se	55/57 (96%)	41 (74%)	12 (22%)	2 (4%)	4	41
72	SD	225/227 (99%)	174 (77%)	41 (18%)	10 (4%)	3	35
73	SF	189/191 (99%)	146 (77%)	33 (18%)	10 (5%)	2	30
74	SK	96/98 (98%)	58 (60%)	26 (27%)	12 (12%)	0	8
75	SM	122/124 (98%)	78 (64%)	24 (20%)	20 (16%)	0	5
76	SP	94/96 (98%)	67 (71%)	17 (18%)	10 (11%)	0	11
77	SQ	139/141 (99%)	111 (80%)	20 (14%)	8 (6%)	2	28
78	SR	127/129 (98%)	111 (87%)	11 (9%)	5 (4%)	4	38
79	SS	135/137 (98%)	114 (84%)	12 (9%)	9 (7%)	1	25
80	ST	139/141 (99%)	115 (83%)	18 (13%)	6 (4%)	3	36
81	SU	102/104 (98%)	83 (81%)	13 (13%)	6 (6%)	2	28
82	SZ	73/75 (97%)	59 (81%)	9 (12%)	5 (7%)	1	24
83	Sc	60/64 (94%)	47 (78%)	12 (20%)	1 (2%)	11	57
84	Sd	50/52 (96%)	36 (72%)	11 (22%)	3 (6%)	2	27
85	Sf	69/71 (97%)	42 (61%)	15 (22%)	12 (17%)	0	4
86	Sg	311/313 (99%)	240 (77%)	56 (18%)	15 (5%)	3	33
87	S1	72/74 (97%)	61 (85%)	6 (8%)	5 (7%)	1	24
88	S4	72/76 (95%)	68 (94%)	4 (6%)	0	100	100
All	All	12314/12513 (98%)	9837 (80%)	1799 (15%)	678 (6%)	4	30

5 of 678 Ramachandran outliers are listed below:

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

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

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	187/187 (100%)	137 (73%)	50 (27%)	0	5
2	D	246/247 (100%)	183 (74%)	63 (26%)	0	6
3	G	204/206 (99%)	150 (74%)	54 (26%)	0	5
4	H	169/169 (100%)	131 (78%)	38 (22%)	1	9
5	J	143/143 (100%)	108 (76%)	35 (24%)	1	7
6	L	176/176 (100%)	133 (76%)	43 (24%)	1	7
7	M	116/116 (100%)	88 (76%)	28 (24%)	1	7
8	N	171/171 (100%)	126 (74%)	45 (26%)	0	5
9	O	172/172 (100%)	138 (80%)	34 (20%)	1	12
10	Q	163/163 (100%)	126 (77%)	37 (23%)	1	8
11	R	159/159 (100%)	120 (76%)	39 (24%)	1	7
12	S	156/156 (100%)	124 (80%)	32 (20%)	1	11
13	T	139/139 (100%)	105 (76%)	34 (24%)	1	7
14	U	89/89 (100%)	65 (73%)	24 (27%)	0	5
15	V	101/101 (100%)	78 (77%)	23 (23%)	1	8
16	X	107/107 (100%)	89 (83%)	18 (17%)	2	19
17	Y	124/124 (100%)	94 (76%)	30 (24%)	1	7
18	Z	117/117 (100%)	93 (80%)	24 (20%)	1	11
19	a	119/119 (100%)	99 (83%)	20 (17%)	2	19
20	b	63/63 (100%)	48 (76%)	15 (24%)	1	7
21	c	79/79 (100%)	59 (75%)	20 (25%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	d	98/98 (100%)	65 (66%)	33 (34%)	0	2
23	e	114/114 (100%)	91 (80%)	23 (20%)	1	12
24	f	88/88 (100%)	73 (83%)	15 (17%)	2	19
25	g	98/98 (100%)	78 (80%)	20 (20%)	1	11
26	h	109/109 (100%)	91 (84%)	18 (16%)	3	20
27	i	86/86 (100%)	69 (80%)	17 (20%)	1	12
28	k	64/64 (100%)	51 (80%)	13 (20%)	1	11
29	l	47/47 (100%)	37 (79%)	10 (21%)	1	10
30	m	48/48 (100%)	33 (69%)	15 (31%)	0	3
31	o	92/92 (100%)	70 (76%)	22 (24%)	1	7
35	B	335/335 (100%)	260 (78%)	75 (22%)	1	9
36	C	305/305 (100%)	233 (76%)	72 (24%)	1	7
37	E	209/209 (100%)	163 (78%)	46 (22%)	1	9
38	F	194/194 (100%)	142 (73%)	52 (27%)	0	5
39	I	180/180 (100%)	126 (70%)	54 (30%)	0	4
40	P	134/134 (100%)	108 (81%)	26 (19%)	2	13
41	W	55/55 (100%)	38 (69%)	17 (31%)	0	3
42	j	73/73 (100%)	60 (82%)	13 (18%)	2	17
43	n	22/22 (100%)	16 (73%)	6 (27%)	0	5
44	p	74/74 (100%)	62 (84%)	12 (16%)	3	21
45	r	109/109 (100%)	83 (76%)	26 (24%)	1	7
46	K	136/136 (100%)	118 (87%)	18 (13%)	5	31
47	q	170/170 (100%)	134 (79%)	36 (21%)	1	10
48	z	340/340 (100%)	318 (94%)	22 (6%)	21	63
51	9	92/94 (98%)	88 (96%)	4 (4%)	35	74
52	6	157/157 (100%)	151 (96%)	6 (4%)	40	76
54	SA	174/174 (100%)	132 (76%)	42 (24%)	1	7
55	SB	194/194 (100%)	155 (80%)	39 (20%)	1	12
56	SC	184/184 (100%)	141 (77%)	43 (23%)	1	7
57	SE	224/224 (100%)	172 (77%)	52 (23%)	1	8
58	SG	207/207 (100%)	166 (80%)	41 (20%)	1	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	SH	169/169 (100%)	145 (86%)	24 (14%)	4	29
60	SI	178/178 (100%)	144 (81%)	34 (19%)	2	13
61	SJ	161/161 (100%)	117 (73%)	44 (27%)	0	5
62	SL	136/136 (100%)	104 (76%)	32 (24%)	1	7
63	SN	130/130 (100%)	103 (79%)	27 (21%)	1	11
64	SO	106/106 (100%)	74 (70%)	32 (30%)	0	4
65	SV	66/66 (100%)	50 (76%)	16 (24%)	1	7
66	SW	112/112 (100%)	90 (80%)	22 (20%)	1	13
67	SX	113/113 (100%)	95 (84%)	18 (16%)	3	23
68	SY	108/108 (100%)	85 (79%)	23 (21%)	1	10
69	Sa	85/85 (100%)	72 (85%)	13 (15%)	3	25
70	Sb	75/75 (100%)	58 (77%)	17 (23%)	1	8
71	Se	46/46 (100%)	35 (76%)	11 (24%)	1	7
72	SD	190/190 (100%)	149 (78%)	41 (22%)	1	9
73	SF	161/161 (100%)	123 (76%)	38 (24%)	1	7
74	SK	89/89 (100%)	68 (76%)	21 (24%)	1	7
75	SM	104/104 (100%)	74 (71%)	30 (29%)	0	4
76	SP	88/88 (100%)	70 (80%)	18 (20%)	1	11
77	SQ	117/117 (100%)	91 (78%)	26 (22%)	1	9
78	SR	117/117 (100%)	102 (87%)	15 (13%)	5	32
79	SS	119/119 (100%)	96 (81%)	23 (19%)	2	13
80	ST	112/112 (100%)	87 (78%)	25 (22%)	1	9
81	SU	94/94 (100%)	82 (87%)	12 (13%)	5	32
82	SZ	66/66 (100%)	57 (86%)	9 (14%)	5	30
83	Sc	57/57 (100%)	47 (82%)	10 (18%)	2	18
84	Sd	45/45 (100%)	36 (80%)	9 (20%)	1	12
85	Sf	64/64 (100%)	45 (70%)	19 (30%)	0	4
86	Sg	272/272 (100%)	235 (86%)	37 (14%)	5	30
87	S1	67/67 (100%)	59 (88%)	8 (12%)	6	35
88	S4	69/69 (100%)	60 (87%)	9 (13%)	5	32
All	All	10728/10733 (100%)	8471 (79%)	2257 (21%)	4	10

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

Mol	Chain	Res	Type
36	C	276	ASN
44	p	87	LYS
78	SR	31	ASN
37	E	112	TYR
39	I	28	ASP

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

Mol	Chain	Res	Type
36	C	343	GLN
45	r	12	ASN
79	SS	120	HIS
37	E	246	GLN
39	I	213	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
32	5	3667	C

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Mol	Chain	Res	Type
32	5	4450	U
53	S2	1433	C
32	5	3773	U
32	5	4118	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 carbohydrates 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](#)

There are no chain breaks in this entry.