



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:05 PM BST

PDB ID : 3J7R  
EMDB ID: : EMD-2644  
Title : Structure of the translating mammalian ribosome-Sec61 complex  
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.  
Deposited on : 2014-08-01  
Resolution : 3.90 Å(reported)  
Based on PDB ID : 3J3B, 3J3A, 3J3F, 3J3D

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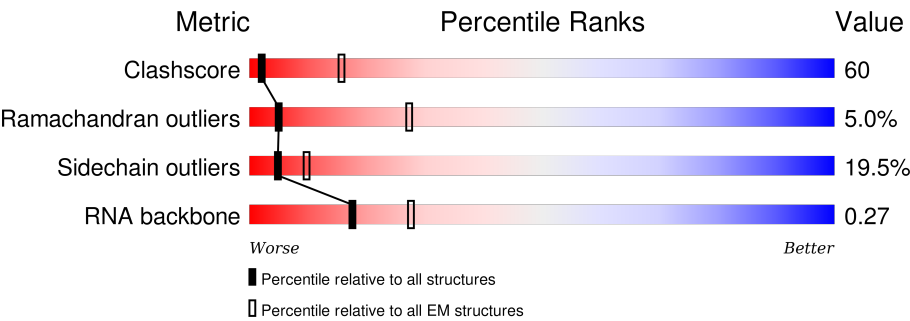
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

# 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 3.90 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	5	3722	<div><div>8%</div><div>44%</div><div>35%</div><div>12%</div></div>
2	7	120	<div><div>18%</div><div>56%</div><div>21%</div><div>5%</div></div>
3	8	156	<div><div>7%</div><div>53%</div><div>26%</div><div>13%</div></div>
4	A	257	<div><div>49%</div><div>29%</div><div>12%</div><div>6%</div><div>5%</div></div>
5	B	394	<div><div>48%</div><div>34%</div><div>13%</div><div>5%</div></div>
6	C	367	<div><div>55%</div><div>31%</div><div>11%</div><div>.</div></div>
7	D	297	<div><div>46%</div><div>35%</div><div>12%</div><div>5%</div><div>.</div></div>
8	E	236	<div><div>47%</div><div>27%</div><div>19%</div><div>7%</div></div>

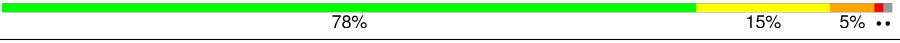










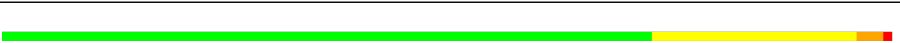




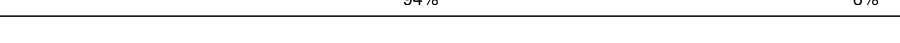
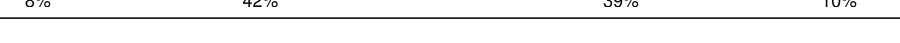
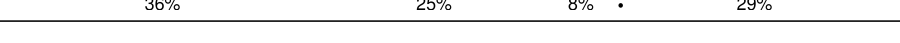
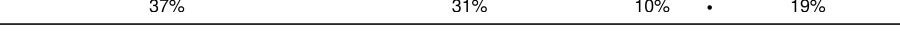



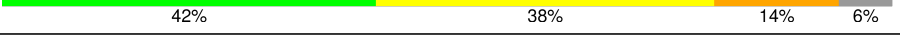

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Mol	Chain	Length	Quality of chain
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	L	211	
15	M	213	
16	N	204	
17	O	204	
18	P	153	
19	Q	188	
20	R	196	
21	S	224	
22	T	160	
23	U	128	
24	V	140	
25	W	157	
26	X	156	
27	Y	145	
28	Z	136	
29	a	148	
30	b	160	
31	c	115	
32	d	125	
33	e	135	


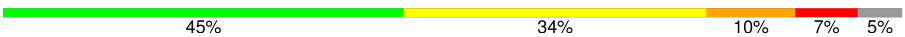
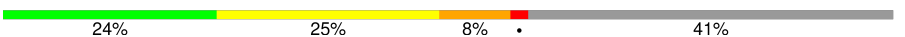



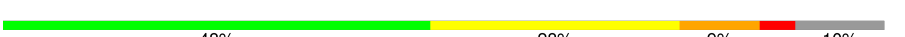
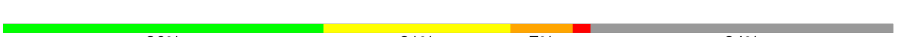


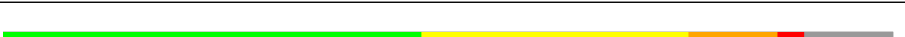


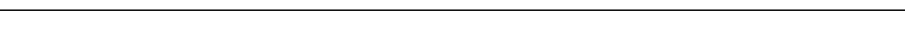
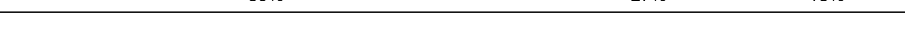
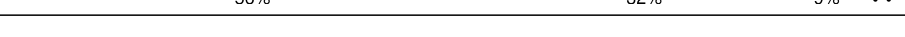



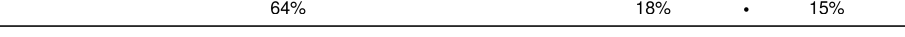





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Mol	Chain	Length	Quality of chain
34	f	110	
35	g	117	
36	h	123	
37	i	105	
38	j	86	
39	k	70	
40	l	51	
41	m	128	
42	n	25	
43	o	106	
44	p	91	
45	r	125	
46	z	217	
47	1	393	
48	2	68	
49	3	36	
50	S2	1742	
51	SA	295	
52	SB	264	
53	SC	218	
54	SD	243	
55	SE	263	
56	SF	204	
57	SG	249	
58	SH	194	

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Mol	Chain	Length	Quality of chain
59	SI	208	
60	SJ	194	
61	SK	165	
62	SL	158	
63	SM	124	
64	SN	151	
65	SO	151	
66	SP	145	
67	SQ	146	
68	SR	135	
69	SS	152	
70	ST	145	
71	SU	119	
72	SV	83	
73	SW	130	
74	SX	143	
75	SY	132	
76	SZ	125	
77	Sa	115	
78	Sb	84	
79	Sc	69	
80	Sd	56	
81	Se	133	
82	Sf	156	
83	Sg	317	

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Mol	Chain	Length	Quality of chain
84	S4	10	<div><div></div><div>10%</div><div></div><div>90%</div><div></div></div>
85	S5	74	<div><div></div><div>39%</div><div></div><div>59%</div><div></div><div></div></div>
86	S6	76	<div><div></div><div>29%</div><div></div><div>68%</div><div></div><div></div></div>

## 2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 222336 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 RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3720	Total	C	N	O	P	0	0
			79736	35504	14597	25916	3719		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

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

- Molecule 5 is a protein called Ribosomal protein uL3.

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

- Molecule 6 is a protein called Ribosomal protein uL4.

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

- Molecule 7 is a protein called Ribosomal protein uL18.

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

- Molecule 8 is a protein called Ribosomal protein eL6.

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

- Molecule 9 is a protein called Ribosomal protein uL30.

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

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

- Molecule 11 is a protein called Ribosomal protein uL6.

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

- Molecule 12 is a protein called Ribosomal protein uL16.

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

- Molecule 13 is a protein called Ribosomal protein uL5.

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

- Molecule 14 is a protein called Ribosomal protein eL13.

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

- Molecule 15 is a protein called Ribosomal protein eL14.

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

- Molecule 16 is a protein called Ribosomal protein eL15.

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

- Molecule 17 is a protein called Ribosomal protein uL13.

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

- Molecule 18 is a protein called Ribosomal protein uL22.

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

- Molecule 19 is a protein called Ribosomal protein eL18.

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

- Molecule 20 is a protein called Ribosomal protein eL19.

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

- Molecule 21 is a protein called Ribosomal protein eL20.

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

- Molecule 22 is a protein called Ribosomal protein eL21.

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

- Molecule 23 is a protein called Ribosomal protein eL22.

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

- Molecule 24 is a protein called Ribosomal protein uL14.

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

- Molecule 25 is a protein called Ribosomal protein eL24.

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

- Molecule 26 is a protein called Ribosomal protein uL23.

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

- Molecule 27 is a protein called Ribosomal protein uL24.

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

- Molecule 28 is a protein called Ribosomal protein eL27.

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

- Molecule 29 is a protein called Ribosomal protein uL15.

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

- Molecule 30 is a protein called Ribosomal protein eL29.

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

- Molecule 31 is a protein called Ribosomal protein eL30.

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

- Molecule 32 is a protein called Ribosomal protein eL31.

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

- Molecule 33 is a protein called Ribosomal protein eL32.

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

- Molecule 34 is a protein called Ribosomal protein eL33.

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

- Molecule 35 is a protein called Ribosomal protein eL34.

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

- Molecule 36 is a protein called Ribosomal protein uL29.

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

- Molecule 37 is a protein called Ribosomal protein eL36.

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

- Molecule 38 is a protein called Ribosomal protein eL37.

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

- Molecule 39 is a protein called Ribosomal protein eL38.

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

- Molecule 40 is a protein called Ribosomal protein eL39.

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

- Molecule 41 is a protein called Ribosomal protein eL40.

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

- Molecule 42 is a protein called Ribosomal protein eL41.

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

- Molecule 43 is a protein called Ribosomal protein eL42.

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

- 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 uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	z	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a protein called Sec61 alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	1	375	Total	C	N	O	S	0	0
			2914	1919	469	508	18		

- Molecule 48 is a protein called Sec61 gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 49 is a protein called Sec61 beta subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	3	36	Total	C	N	O	0	0
			180	108	36	36		

- Molecule 50 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 51 is a protein called Ribosomal protein uS2.

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

- Molecule 52 is a protein called Ribosomal protein eS1.

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

- Molecule 53 is a protein called Ribosomal protein uS5.

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

- Molecule 54 is a protein called Ribosomal protein uS3.

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

- Molecule 55 is a protein called Ribosomal protein eS4.

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

- Molecule 56 is a protein called Ribosomal protein uS7.

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

- Molecule 57 is a protein called Ribosomal protein eS6.

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

- Molecule 58 is a protein called Ribosomal protein eS7.

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

- Molecule 59 is a protein called Ribosomal protein eS8.

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

- Molecule 60 is a protein called Ribosomal protein uS4.

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

- Molecule 61 is a protein called Ribosomal protein eS10.

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

- Molecule 62 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SL	156	Total	C	N	O	S	0	0
			1276	813	239	218	6		

- Molecule 63 is a protein called Ribosomal protein eS12.

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

- Molecule 64 is a protein called Ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	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 uS19.

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

- Molecule 67 is a protein called Ribosomal protein uS9.

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

- Molecule 68 is a protein called Ribosomal protein eS17.

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

- Molecule 69 is a protein called Ribosomal protein uS13.

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

- Molecule 70 is a protein called Ribosomal protein eS19.

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

- Molecule 71 is a protein called Ribosomal protein uS10.

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

- Molecule 72 is a protein called Ribosomal protein eS21.

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

- Molecule 73 is a protein called Ribosomal protein uS8.

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

- Molecule 74 is a protein called Ribosomal protein uS12.

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

- Molecule 75 is a protein called Ribosomal protein eS24.

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

- Molecule 76 is a protein called Ribosomal protein es25.

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

- Molecule 77 is a protein called Ribosomal protein eS26.

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

- Molecule 78 is a protein called Ribosomal protein eS27.

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

- Molecule 79 is a protein called Ribosomal protein eS28.

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

- Molecule 80 is a protein called Ribosomal protein uS14.

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

- Molecule 81 is a protein called Ribosomal protein eS30.

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

- Molecule 82 is a protein called Ribosomal protein eS31.

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

- Molecule 83 is a protein called Ribosomal protein RACK1.

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

- Molecule 84 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
84	S4	10	Total	C	N	O	P	
			201	91	23	78	9	
							0	0

- Molecule 85 is a RNA chain called A/P tRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	S5	74	Total	C	N	O	P	
			1579	705	285	516	73	
							0	0

- Molecule 86 is a RNA chain called P/E tRNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
86	S6	76	Total	C	N	O	P	
			1622	723	291	532	76	
							0	0

- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

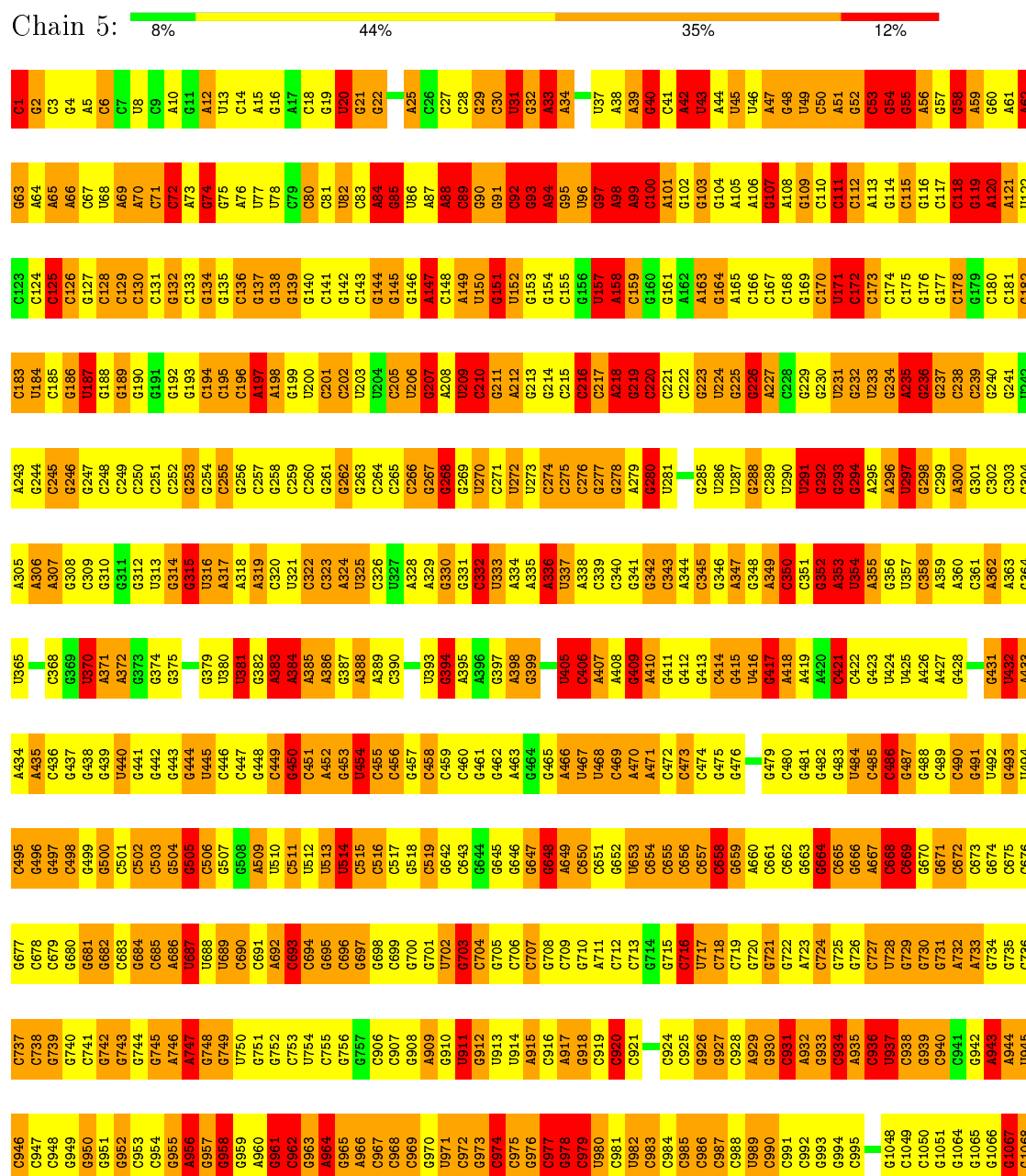
- Molecule 88 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
88	P	1	Total	Mg	
			1	1	0
88	S2	36	Total	Mg	
			36	36	0
88	V	1	Total	Mg	
			1	1	0
88	7	5	Total	Mg	
			5	5	0
88	5	120	Total	Mg	
			120	120	0
88	8	3	Total	Mg	
			3	3	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.

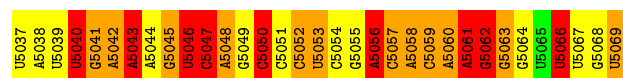
#### • Molecule 1: 28S ribosomal RNA






C3854	C3794	A3733	C3673	U3613	U2874	A2807	A2744	G2679	G2618	G2557	G2496	U2486	U2371	C2310	C2250
C3855	A3795	U3734	G3674	G3614	C2875	G2808	A2745	G2682	G2619	C2558	C2497	C2437	U2372	C2311	G2251
A3856	G3796	G3735	G3675	G3615	G2876	G2809	A2746	G2683	G2620	C2559	C2498	A2438	C2373	C2312	G2252
C3857	C3797	A3736	G3676	U3616	G2877	G2811	U2747	A2621	A2621	C2560	C2499	C2439		A2313	A2253
C3858	U3798	A3737	G3677	G3617	G2878	A2812	C2748	C2684	G2622	C2561	G2502	C2440	A2376	G2314	G2254
G3859	G3799	G3738	G3678	C3618	A2879	A2813	C2749	C2685	A2623	C2562	G2503	C2441	C2377	G2315	G2255
A3860	A3800	C3739	U3679	G3619	U2880	C2814	G2751	G2686	G2624	C2563	G2504	G2442	C2378	C2316	G2256
A3611	U3801	G3740	U3680	G3620	C2881	C2815	G2752	U2687		G2564	C2505	G2443		C2317	G2257
A3862	U3802	C3741	A3621	G3621	G2884	G2816	G2753	G2688	C2627	U2444	C2506	A2444	A2382	G2318	C2258
C3863	A3803	G3742	A3622	C3622		C2817	G2754	C2689	U2628	U2565	C2507	C2445	C2383	C2319	G2259
C3864	C3804	G3743	C3623	C3623	G2888	C2818	A2755	C2690	C2629	C2566	A2507	C2446	U2384	G2320	C2260
A3865	U3805	G3744	G3624	A3624	G2889	G2819	G2756	U2691	U2630	C2568	U2508	U2447	U2385	G2321	G2261
C3866	G3806	U3745	C3625	G3625	C2890	U2820	G2757	U2692	U2631	C2569	C2509	G2448	U2386	G2322	G2262
A3867	A3807	A3746	G3626	G3626	U2891	U2821	G2758	G2693	U2632	U2570	G2510	A2449		C2323	A2263
G3868	C3808	A3747	A3627	G3627	C2892	G2822	G2759	G2694	U2633	C2571	A2511	G2450	A2389	C2324	G2264
C3869	G3809	A3748	U3688	G3628		C2823	G2760	A2695	C2634	C2572	A2512	A2451	C2390	C2325	G2265
A3870	C3810	C3749	G3689	A3629	A2895	G2824	U2761	A2696	U2635	A2573	A2513	G2452	G2391	C2326	C2266
G3871	G3811	G3750	U3690	A3630	G2896	A2825	G2762	C2697	U2636	G2574	G2514	A2453	C2392	G2327	U2267
A3872	C3812	G3751	G3691	U3631	G2897	U2826	U2763	G2698	U2637	U2575	G2515	U2454	C2393	G2328	A2268
G3873	A3813	C3752	A3692	C3632	G2898	G2827	A2764	C2699	U2638	G2576	G2516	G2455	G2394	U2329	C2269
C3874	U3814	G3753	G3693	C3633	C2899	G2828	A2765	G2700	U2639	G2577	A2517	G2456	G2395	G2330	G2270
A3875	G3815	G3754	U3694	A3634	U2900	G2829	A2766	U2701	G2640	G2578	G2518	G2457	A2396	C2331	C2271
A3876	A3816	G3755	U3695	A3635		G2830	U2767	C2702	A2641	G2579	U2519	C2458	C2397	A2332	C2272
C3877	A3817	A3756	C3696	G3636		G2831	C2768	G2703	A2642	U2580	C2520	G2459	U2398	G2333	G2273
G3878	U3818	G3757	U3697	U3637	U2904	C2832	U2769	G2704	G2643	A2581	G2521	A2460	G2399	C2334	C2274
A3879	G3819	U3758	G3698	G3638	C2905	A2833	C2770	G2705	G2644	A2582	G2522	G2461	G2400	C2335	G2275
G3880	G3820	A3759	C3699	U3639	G2907	G2834	G2771	G2706	G2645	C2583	G2523	G2462	A2401	G2336	A2276
C3881	A3821	A3760	C3700	U3640	U2908	A2835	C2772	U2707	G2646	G2584	G2524	G2463	G2402	G2337	C2277
U3882	G3822	C3761	A3701	U3641	C2909	A2836	G2773	U2708	A2647	C2585	U2525	G2464	A2403	C2338	G2278
C3883	G3823	U3762	A3702	A3642	G2910	U2837	G2774	U2709	G2648	C2586	C2526	G2465	A2404	C2339	A2279
U3884	A3824	A3763	G3703	G3643	U3643	G2838	C2775	G2710	G2649	U2587	G2527	G2466	G2405	G2340	G2280
A3825	A3825	U3764	U3704	U3644	C3584	U2839	G2776	G2711	G2650	C2588	G2528	U2467	G2406	A2341	U2281
G3886	C3826	G3765	G3705	U3645	C3585	U2840	G2777	G2712	C2651	C2589	A2529	U2468	G2407	G2342	A2282
C3887	G3827	A3766	C3706	A3646	C3586	G2841	C2779	G2713	G2652	C2590	U2530	C2469	U2408	G2343	G2283
G3888	A3828	C3767	U3707	A3647	C3587	G2842		G2714	C2653	A2591	C2531	C2470	U2409	U2344	G2284
C3889	G3829	U3768	C3708	A3648	C3588	U2843	U2782	G2715	C2654	U2592	C2532	G2471	C2410	G2345	A2285
A3890	A3830	C3769	U3709	A3649	C3589	A2844	A2783	G2716	C2655	C2593	G2533	A2472	C2411	G2346	G2286
U3891	U3831	U3770	G3710	C3650	G3590		C2784		U2656	C2594	C2534	A2473	A2412	A2347	G2287
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A3894	C3834	U3773	G3713	A3653	C3593	A2850	A2787	G2722	A2659	C2597	U2537	G2476	U2415	U2350	C2290
G3895	G3835	A3774	G3714	G3654	C3594	G2851	U2788	G2723	A2660	U2598	U2538	A2477	G2416	C2351	G2291
C3896	A3836	U3775	U3715	C3655	U3595	U2852	A2789	G2724	U2661	C2599	C2539	C2478	A2417	U2352	C2292
G3897	C3837	G3776	C3716	A3656	A3596	C2853	U2790	A2725	G2662	A2600	C2540	G2479	A2418	U2353	U2293
G3898	U3838	G3777	A3717	U3657	G3597	G2854	C2791	G2726	G2663	A2601	G2541	G2480	C2419	G2354	G2294
G3899	G3839	U3778	A3718	C3658	C3598	G2855	C2792	G2727	G2664	G2602	G2542	G2481	A2420		G2295
G3900	U3840	A3779	A3719	G3659	A3599	C2856	G2793	U2728	U2665	C2603	A2543	C2482	G2421	G2296	G2296
A3901	C3841	G3780	G3720	C3660	C3600	A2857	C2794	G2729	U2666	C2604	C2544	C2483	C2422	C2297	G2297
A3902	C3842	C3781	U3721	G3661	C3601	A2858	A2795		C2667	G2605	U2545	A2484	A2423	U2359	U2298
A3903	C3843	G3782	G3722	A3662	C3602	G2859	G2796	G2733	G2668	G2606	G2546	U2485	G2424	A2360	G2299
G3904	U3844	A3783	A3723	A3663	G3603	C2860	C2797	U2734	C2669	C2607	G2547	G2486	U2425	G2361	A2300
A3905	A3845	A3784	A3724	G3664	A3604	G2861	U2798	G2735	C2670	C2548	U2426	U2426	U2426	U2362	G2301
A3906	C3846	A3785	G3725	C3665	C3605	G2862	G2799	G2736	C2671	G2549	C2427	A2488	A2428	A2363	C2302
G3907	C3847	U3786		G3666	U3606	G2863	G2800	C2737	C2672	C2550	C2489	A2429	A2429	C2364	C2303
U3848	U3848	C3789	A3728	C3667	U3607	C2866	U2801	U2738	G2673	A2551	U2490	C2491		C2365	U2304
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C3910	C3850	U3790	U3729	G3669	G3609	U2867	U2803	U2740	G2675	C2614	A2553	C2492	U2432	A2367	G2306
C3911	U3851	C3791	U3730	C3670	A3610	C2872	C2804	U2741	A2676	G2493	U2554	G2493	G2433	A2368	A2307
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							A2806	A2743	A2678	G2617	G2556		U2495		G2309

U4976	C4914	C4771	C4710	A4648	A4584	G4524	U4463	G4400	C4337	G4277	A4213	G4151	G4091	C3975	U3914
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A4978	G4916	C4773	C4712	G4650	G4586	U4526	U4465	U4403	A4339	A4279	A4215	G4153	G4093	C3977	G3916
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G4981	C4919	C4776	C4715	G4653	A4589	G4529	U4468	G4406	C4342	A4282	U4218	G4156	G4096	G4036	G3919
A4982	G4920	C4777	C4716	C4654	U4590	U4530	U4469	U4407	U4343	G4283	U4219	A4157	G4097	G4037	U3920
C4983	C4921	G4778	G4717	A4655	U4591	U4531	G4470	G4408	U4344	C4284	A4220	A4158	A4098	C4038	U3921
C4984	C4922	G4779	C4718	A4656	C4592	U4532	U4471	G4409	C4345	U4285	A4221		G4099	G4039	G3922
U4985	U4985	C4780	C4719	G4657	U4593	A4533	G4472	U4410	U4346	C4286	C4222	C4161	C4100	C4040	A3923
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U4989	G4927	G4784	A4723	G4661		C4537	C4476	C4414	C4350	U4290	G4226	C4165	G4104	U4044	U3927
C4990	C4928	C4662	A4724	G4662	A4599	G4538	A4477	A4414	U4351	G4291	U4227	C4166	A4105	G4045	A3928
U4991	C4929	G4663	C4725	G4663	G4600	U4539	G4478	A4415	U4352	A4292	G4228	G4167	G4106	A4046	G3929
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	C4934	U4668	C4730	U4668	A4605	A4544	C4483	U4420		G4297	U4233	A4172	C4111	C4051	G3935
	C4935	G4669	G4732	G4669	G4606	G4545	A4484	C4421	U4360	A4298	A4234	G4173	C4112	C4052	A3936
	G4936	C4670	C4733	C4670	A4607	A4546	C4485	A4422	U4361	U4299	A4234	U4174	U4113	A4053	C3937
	C4937	C4671	G4734	C4671	G4608	C4547	C4486	U4423	A4362	U4300	G4235	G4175	C4114	C4054	G3938
	U4938	G4672	G4735	G4672	G4609	A4548	A4487	A4424	A4363	U4301	G4236	C4176	G4115	U4055	G3939
	C4939	U4673	C4736		A4610	G4549	A4488	G4425	G4364	U4302	C4237	C4177	C4116	A4056	U3940
		G4675	G4737		C4615	U4550	C4489	G4426		C4303	G4238	A4178	U4117	C4057	
	U5003	C4676	C4738	C4676	G4616	U4551	U4490	G4427	C4367	A4304	A4239	G4179	U4118	U4058	A3942
	C5004	G4677	C4739	G4677	A4617	U4552	G4491	A4428	G4368	G4305	G4240	U4180	C4119	C4059	A3943
	U5005	C4678	G4740	C4678	G4618	A4553	U4492	C4429	A4369	U4306	C4241	U4181	U4120	U4060	G3944
	G5006	G4679	C4741	G4679	U4619	U4554			G4370	A4307	U4242	G4182	G4121	G4061	A3945
	A5007	U4680	G4742	G4680	U4620	U4555			G4371	C4308	C4243	G4183	C4122	U4062	G3946
	C5008	C4681	G4743	U4681	U4621	U4556	U4495	G4433	U4372	G4309		G4184	C4123	U4063	A3947
	G5009	U4682	C4744	U4682	C4621	U4557	U4497	U4435	U4373	A4310	G4248	A4185	C4124	G4064	C3948
	U5010	G4683	G4745	U4683	A4622	U4558	U4498	U4436	U4374	A4311	A4249	A4186	C4125	G4065	
	A5011	U4684	C4746	U4684	G4623	A4559	G4499	U4437	C4375	U4312	G4250	G4187	C4126	U4066	A3949
	C5012	G4685	C4747	U4685	A4624	C4560	U4500	U4438	A4376	A4313	A4251	U4188	A4127	U4067	U3950
	G5013	U4686	U4748	G4686	C4625	C4561	U4501	U4439	G4377	C4314	C4252	U4189	A4128	G4068	G3951
	A5014	C4687	C4749	C4687	U4626	U4562	C4502	G4440	A4378	A4315	A4253	U4190	G4129	U4069	A3952
	G5015	G4688	G4750	U4688	U4627	U4563	A4503	U4441	A4379	G4316	G4254	C4191	C4130	U4070	G3953
	U5016	U4689	C4751	U4689	U4628	A4564	C4504	U4442	A4380	A4317	A4255	A4192	G4131	U4071	A3954
	C5017	G4690	U4752	G4690	U4629	C4565	C4505	C4443	A4381	C4318	A4256	C4193	C4132	G3955	G3956
	G5018	U4691	U4753	G4691	G4630	U4566	C4506	C4444	G4382	C4319	A4257	U4194	C4133	C4072	G3957
	A5019	C4692	G4754	G4692	G4631	G4567	A4507		U4383	G4320	C4258	G4195	C4134	A4073	U3957
	C5020	G4693	G4755	C4693	U4632	U4568	C4508	C4447	U4384	U4321	C4259	G4196	G4135	U4074	G3958
	U5021	U4694	C4756	U4694	U4633	U4569	U4509	G4448	A4385	G4322	U4260	G4197	G4136	U4075	U3959
	G5022	C4695	C4757	C4695	U4634	G4570	A4510	A4449	C4386	A4323	C4261	G4198	C4137	G4076	A3960
	C5023	U4696	U4758	U4696	A4635	A4571	A4511	U4450	C4387	A4324		G4199	C4138	A4077	G3961
	U5024	G4697	C4759	G4697	U4636	U4572	U4512	G4451	A4388	A4325	G4201	G4200	G4139	C4078	A3962
	C5025	U4698	G4760	G4698	G4637	G4573	A4513	U4452	C4389	A4326	G4266	G4202	C4140	C4080	A3963
	U5026	C4699	G4761	U4699	U4638	U4574	G4514	C4453	A4390	C4327	U4267	U4203	G4141	A3965	U3964
	G5027	U4699	A4762	U4699	U4639	G4575	G4515	G4454	A4391	G4328	A4268	A4203	C4142	G4081	A3966
	C5028	G4700	C4763	U4700	C4640	U4576	G4516	G4455	G4392	G4329	G4269	C4204	G4143	U4083	A3967
	U5029	U4701	G4702	U4701	U4641	U4577	A4517	C4456	G4393	G4330	C4270	A4205	C4144	G4084	U3968
	C5030	C4703	G4703	U4703	U4642	U4578	A4518	U4457	A4394	G4331	A4271	C4206	C4145	A4085	G3969
	G5031	U4704	C4704	G4643	U4579	U4579	C4519	U4458	U4395	C4332	G4272	C4207	G4146	G4086	G3970
	C5032	C4705	C4705	G4644	U4580	U4580	G4520	U4459	A4396	C4333	A4273	U4208	G4147	G4087	G3971
	U5033	A4707	G4707	U4707	C4645	G4581	U4521	U4460	A4397	U4334	G4274	U4209	C4148	G4088	A3972
	A5034	G4708	C4708	U4708	U4646	C4582	G4522	C4461	C4398	A4335	G4275	U4210	C4149	G4089	G3973
	C5036	U4709	U4709	G4647	G4647	C4583	A4523	C4462	U4399	A4336		C4211	G4150	G4090	G3974



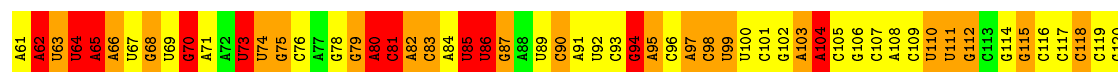
• Molecule 2: 5S ribosomal RNA

Chain 7: 18% 56% 21% 5%



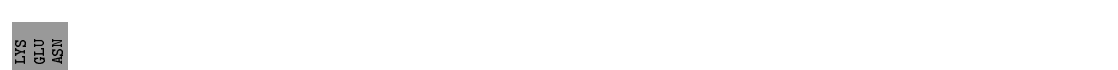
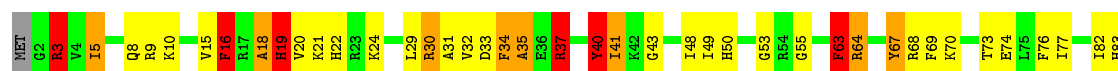
• Molecule 3: 5.8S ribosomal RNA

Chain 8: 7% 53% 26% 13%



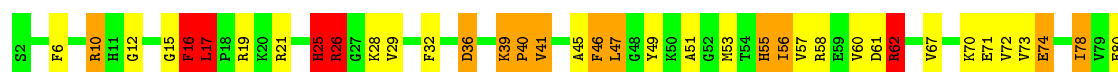
• Molecule 4: Ribosomal protein uL2

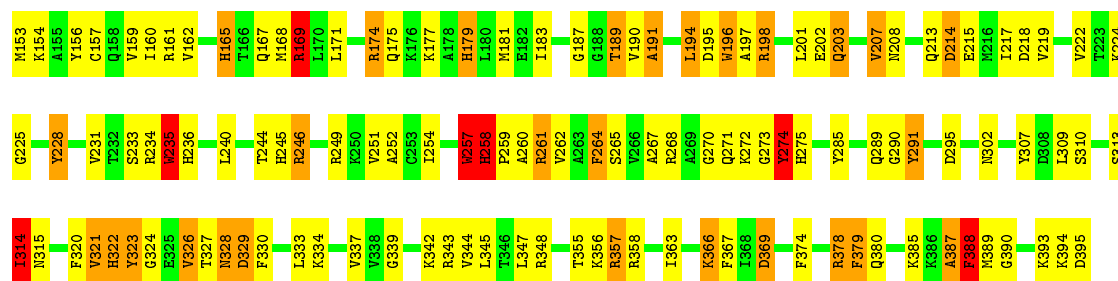
Chain A: 49% 29% 12% 6% 5%



• Molecule 5: Ribosomal protein uL3

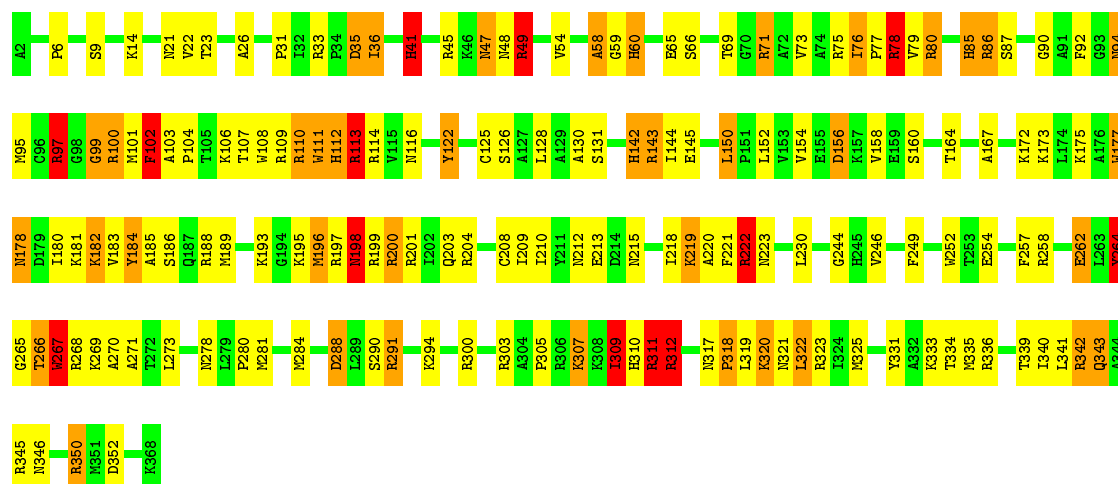
Chain B: 48% 34% 13% 5%





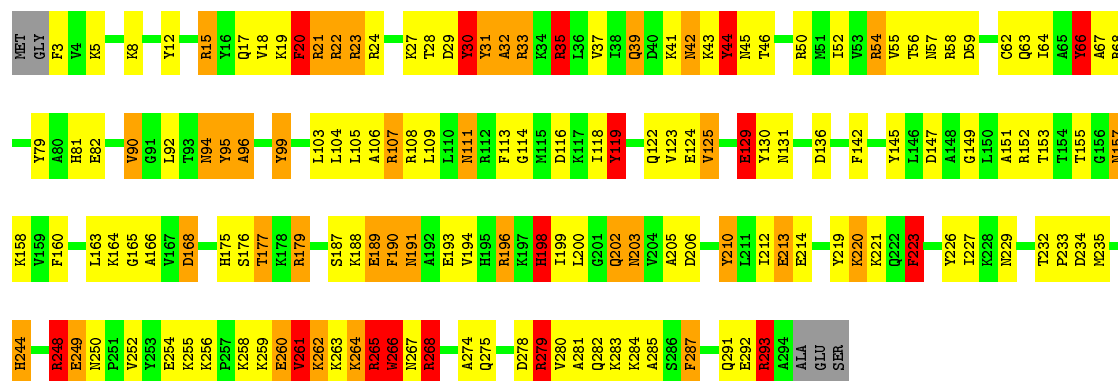
• Molecule 6: Ribosomal protein uL4

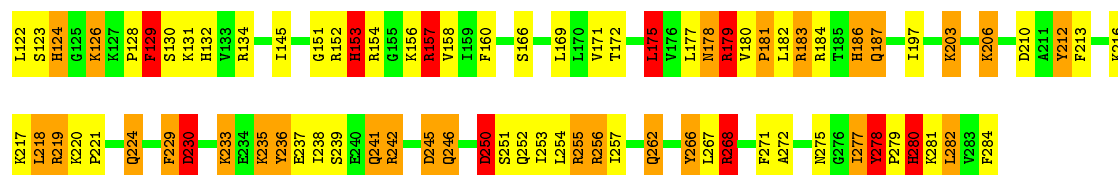
Chain C: 55% 31% 11%



• Molecule 7: Ribosomal protein uL18

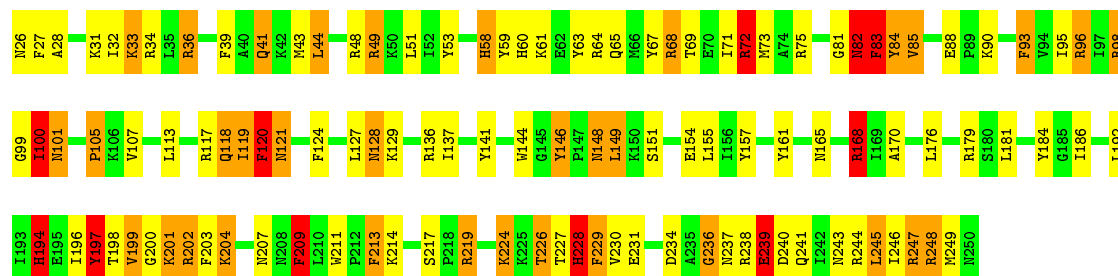
Chain D: 46% 35% 12% 5%





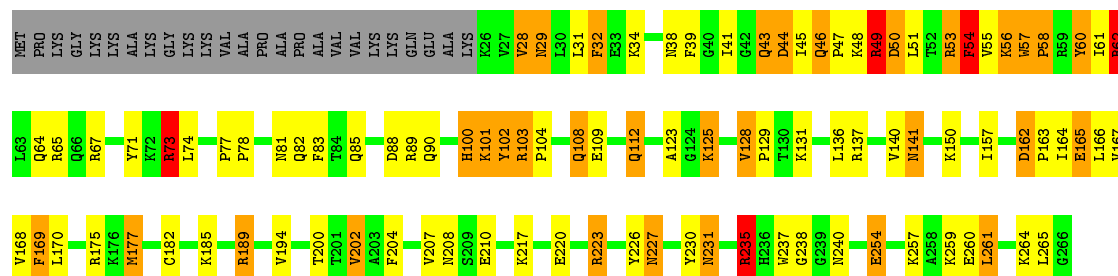
• Molecule 9: Ribosomal protein uL30

Chain F: 49% 31% 15% 5%



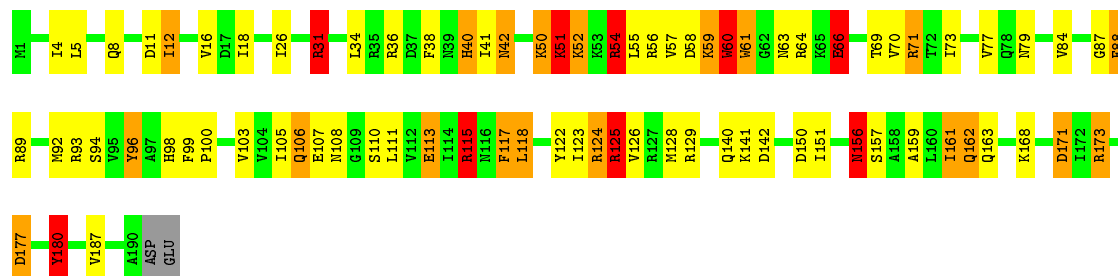
• Molecule 10: Ribosomal protein eL8

Chain G: 53% 23% 12% 9%



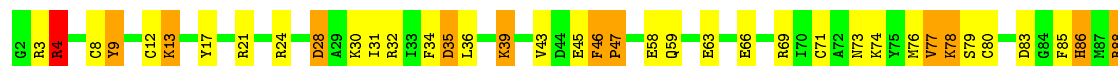
• Molecule 11: Ribosomal protein uL6

Chain H: 57% 27% 10% 5%



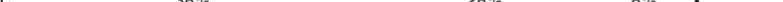
• Molecule 12: Ribosomal protein uL16

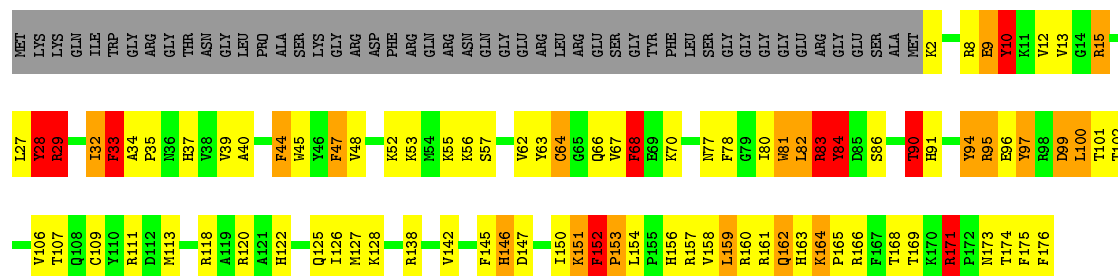
Chain I: 57% 28% 12%

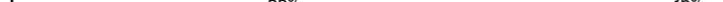


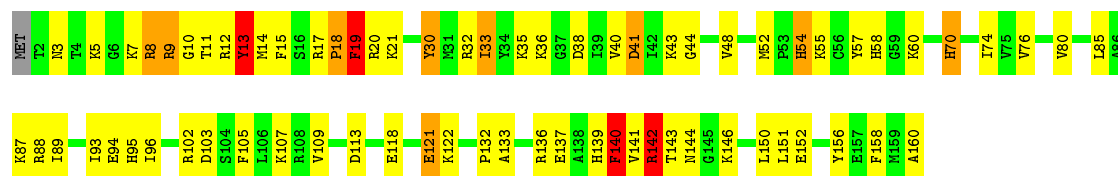


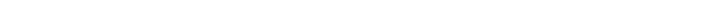


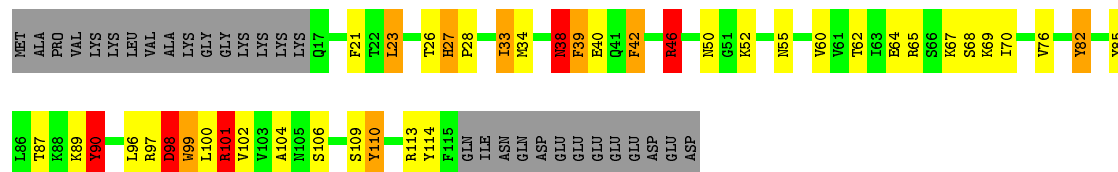
Chain S: 

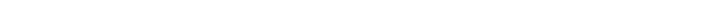


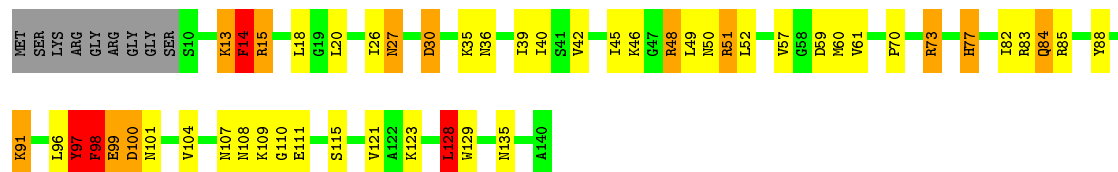
Chain T:  55% 36% 6% 3%

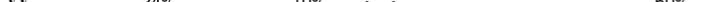


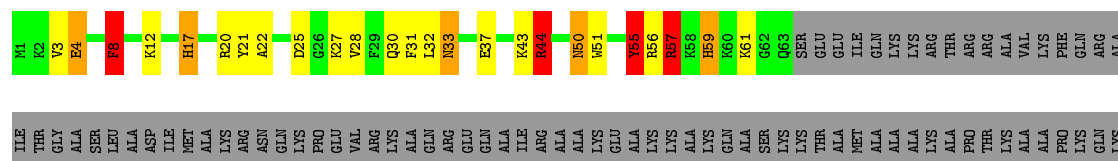
Chain U: 



Chain V:  57% 25% 9% • 6%

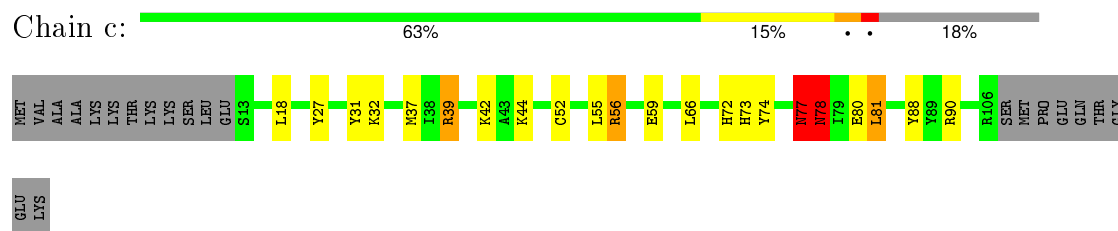


Chain W:  24% 10% . . 60%

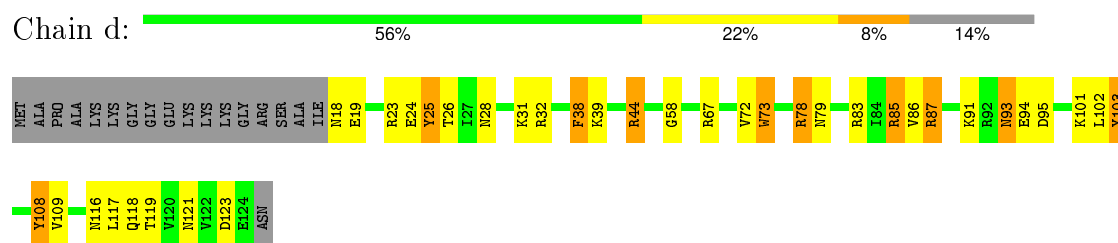




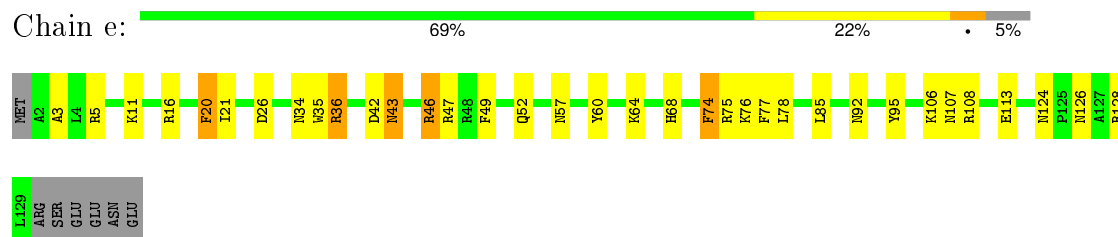
- Molecule 31: Ribosomal protein eL30



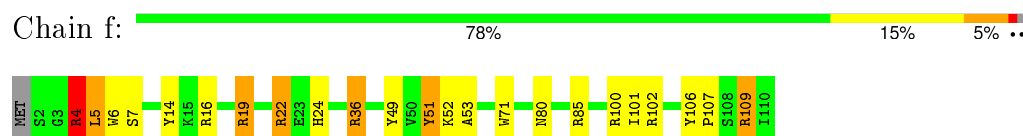
- Molecule 32: Ribosomal protein eL31



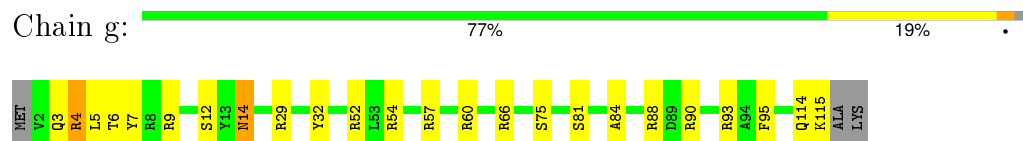
- Molecule 33: Ribosomal protein eL32



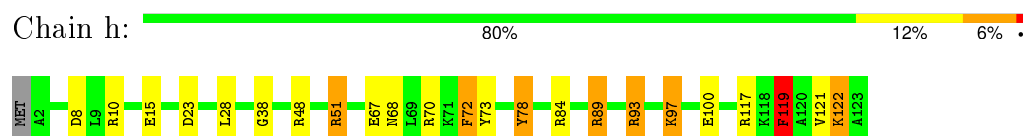
- Molecule 34: Ribosomal protein eL33



- Molecule 35: Ribosomal protein eL34



- Molecule 36: Ribosomal protein uL29



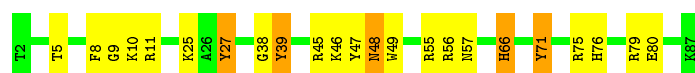
- Molecule 37: Ribosomal protein eL36

Chain i:  76% 17% . .



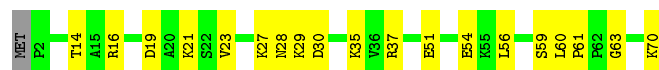
- Molecule 38: Ribosomal protein eL37

Chain j:  73% 21% 6%



- Molecule 39: Ribosomal protein eL38

Chain k:  71% 27% .



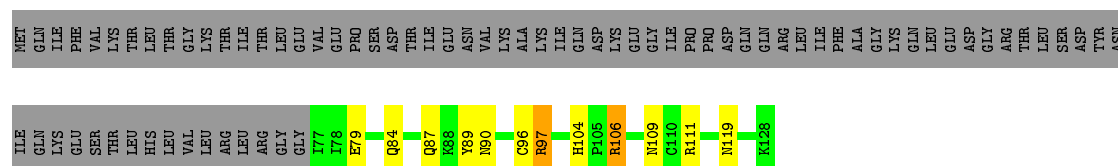
- Molecule 40: Ribosomal protein eL39

Chain l:  76% 20% . .



- Molecule 41: Ribosomal protein eL40

Chain m:  31% 8% . 59%



- Molecule 42: Ribosomal protein eL41

Chain n:  72% 20% 8%




- Molecule 43: Ribosomal protein eL42

Chain o:  69% 23% 6% . .



- Molecule 44: Ribosomal protein eL43

Chain p:  82% 15%




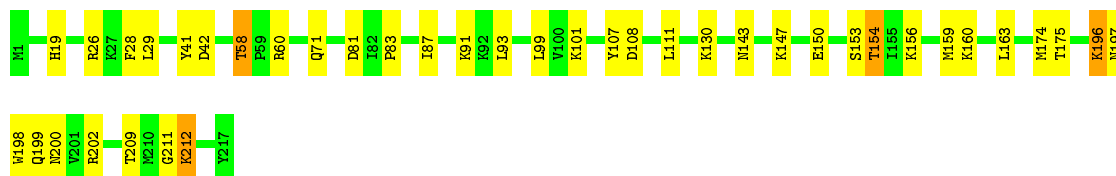
- Molecule 45: Ribosomal protein eL28

Chain r:  73% 23%



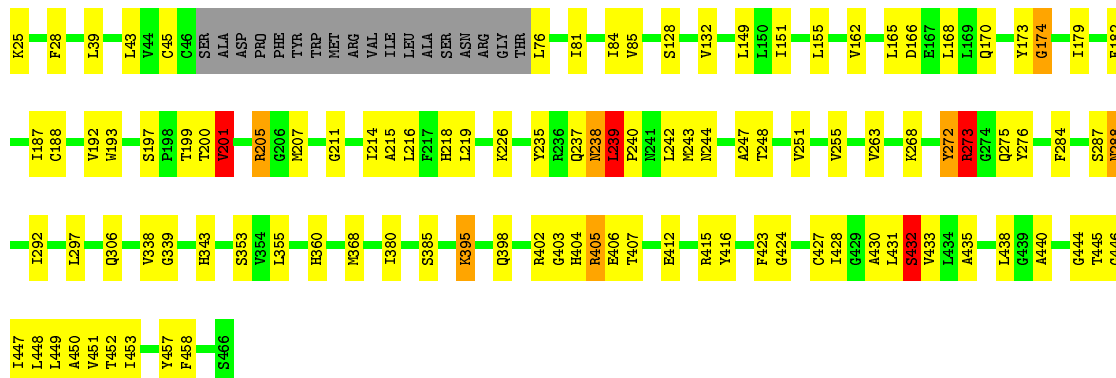
- Molecule 46: Ribosomal protein uL1

Chain z:  82% 17%



- Molecule 47: Sec61 alpha subunit

Chain 1:  68% 24% 5%



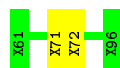
- Molecule 48: Sec61 gamma subunit

Chain 2:  68% 21% 9%



- Molecule 49: Sec61 beta subunit

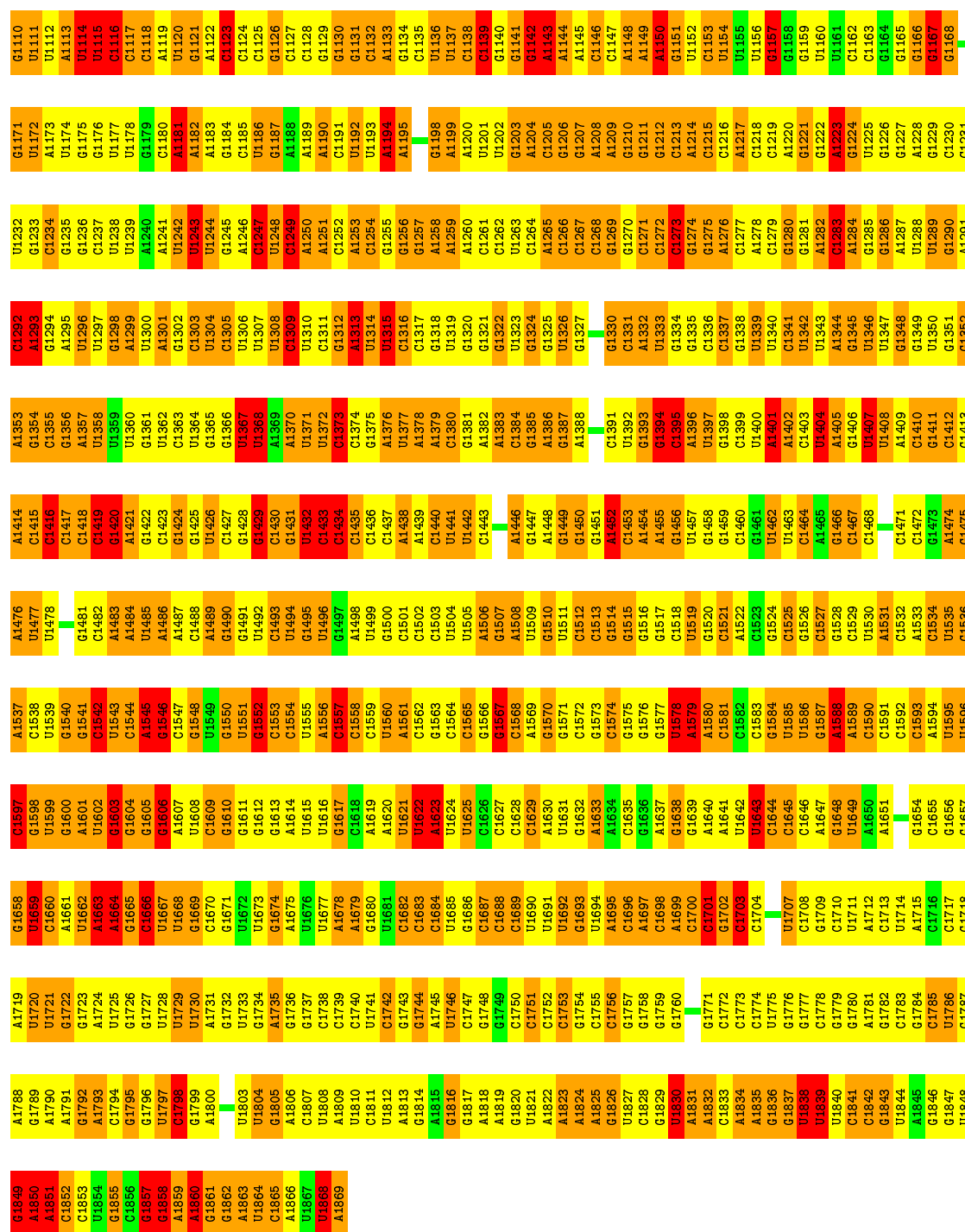
Chain 3:  94% 6%



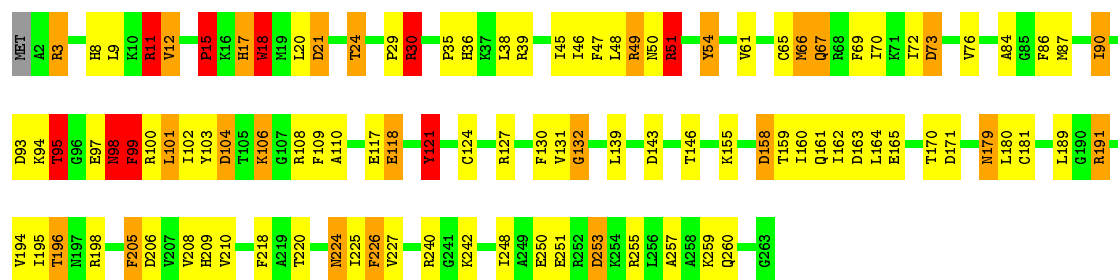
• Molecule 50: 18S ribosomal RNA

Chain S2: 

A1050	C988	G928	G868	G807	A679	A619	U557	C497	G436	A376	C315	C194	G123	U63	U1
G1051	C989	G929	A869	A808		G620	G558	G498	G437	G377	G316	C195	U124	A64	A2
A1052	C990	C930	A870	C621	G663	G621	G559	G499	G438	U378	G317	C196	C125	C65	C3
C1053	G991	C931	U871	A810	G684	G622	A500	A501	A439	C379	A318	U197	G126	G66	C4
G1054	G992	G932	U872	A811	A685	G623	A561	C501	C440	G380	C319	U198	C127	G67	U5
A1055	G993	G933	G873	A812	U686	G624	U562	C502	C441	C381	G320	C199		A68	
U1056	C994	G934	A874	A813		G625	G563	C503	C442	C382	G321	G200	C139	G69	U9
U1057	C995	G935	G875	A814	U688	G626	A564	C504	U443	G383	G322	C201	G70	G10	
A1058	G996	G936	C876	U815	U689	U627		G505	G444	U384	G323	G202	A141	G71	A11
G1059	A997	C937	C877	U816	G690	A628	C567	G506	A445	G385	G324	G203	C142	G72	A12
A1060	A998	A938	C878	U817	G691	A629	C568	G507	G446	C386	G325	G204	U143	C73	A13
U1061	G999	U939	C879	U818	G692	U630	A569	A508	A447	C387	G326	G205	U144	C74	A14
A1062	A1000	U940	G880	G819	A693	U631	C570	G509	A448	U388	G327	G206	G145	G75	U15
C1063	A1001	C941	G881	U820	G694	C632	U571	G510	A449	A389	U328	G207	G146	U76	G16
C1064	U1002	G942	U882	G821	C695	C633	U572	U511	C450	C390	G329	G208	A147	A77	C17
G1065	U1003	U943	U883	U822	G696	A634	U573	A512	G451	C391	G330	A209	U148	C78	A18
U1066	A1004	A944	C884	U823	U824	G635	A574	G513	G452	A392	C331	U210	U149	A79	A19
C1067	G1005	U945	U885	C824	G698	C836	A575	U514	C453	U393	G332	G211	A150	G80	G20
G1068	C1006	U946	A886	A825	C730	U637	A576	G515	U454	G394	G333	C212		U81	U21
U1069	C1007	G947	U887	A826	G731	C638	U577	A516	A455	G395	C334	G213	G153	G82	A22
A1070	A1008	C948	U888	A827	U732	C639	C578	C517	C456	U396	G335	U214	U154	A83	G23
G1071		G949	U889	G828	C733	A640	C579	G518	G457	G397	A336	G215	G155	A84	C24
U1072	A1012	C950	U890	G829	C734	A641	U580	A519	A458	A398	C337	C216	G156	A85	A25
U1073	U1013	C951	G891	A830	C735	U642	U581	A520	C459	C399	G338	U217	G157	C86	U26
C1074	G1014	G952	U892	G831	C736	A643	C582	A521	A460	C400	A339	U218	A158	U87	A27
G1075	U1015	C953	U893	G832	G737	G644	C583	A522	U461	A401	C340	U219	U159	G88	U28
U1076	U1016	U954	G894	C833	C738	C645	G584	A523	C462	C402	C341	U220	U160	C89	G29
A1077	U1017	A955	U895	C834	C739	G646	C585	U524	C463	G403	C342	A221	U161	G90	C30
C1078	U1018	G956	U896	G835	C744	U647		A525	A464	G404	A343	U222	C162	A91	U31
U1079	C1019	A957	U897	G836	C745	U648	G588	A526	A465	G405	U344	C223	U163	A92	U32
A1080	A1020	G958	U898	A837	C746	U649	G589	C527	G466	U406	U345	A224	A164	G93	U33
U1081	U1021	C959	U899	G838	U747	A650	A590	A528	G467	G407	C346	G225	G165	U94	C34
A1082	U1022	U960	C900	C839	C748	U651	U591	A529	A468	A408	G347	U287	G166	G95	C35
C1083	A1023	G961	G901	C840	U749	U652	C592	U530	A469	A409	A348	G288	G167	C96	U36
A1084	A1024	A962	G902	G841	C750	A653	C593	A531	G470	G410	A349	G289	C168	U97	C37
U1085	U1025	A963	A903	C842	C751	A654	A594	C532	G471	G411	C350	U290	U169	C98	A38
G1086	C1026	A964	A904	C843	G752	A655	A595	C533	C472	G412	G351	C291	A170	C98	A39
A1087	U1027	U965	C905	U844	C753	G656	U596	G534	A473	G413	U352		U100	A99	
U1088	A1028	U966	U906	G845	C755	U657	G597	G535	G474	A414	C393	U172	A171	U01	G41
G1089	G1029	C967	G907	G846	C756	U658	G598	A536	C475	A415	G355	C295	A173	A102	A42
A1090	A1030	U968	A908	A847	G757	G659	A599	C537	A476	U416	C356	C296	C174	A103	U43
C1091	A1031	U969	G909	U848	G758	C860	G600	U538	G477	C417	C357	U296	A175	A104	U44
G1092	C1032	G970	G910	A849	G759	U661	G601	C539	G478	A418	C358	A297	U176	U05	
A1093	G1033	C971	C911	C850	C790	G662	G602	U540	C479	G419	U359	G298	G177	C106	A45
U1094	A1034	A972	C912	G851	C791	C663	C603	U541	C480	A420	A360	G107	A107	G47	
C1095	A1035	C973	A913	G852	C792	U664	A604	U542	C481	G421	U361	U300	C179	G108	C48
G1096	A1036	C974	U914	C853	G793	G665	A605	C543	G482	U422	C362	A301	G180	U109	C49
C1097	G1037	C975	G915	A854	A794	U666	G606	C544	C483	U423	A363	A302	A181	U110	A50
U1098	U1038	G976	A916	G855	A795	U667	U607	A545	A484	C424	C364	C303	C382	U111	U51
G1099	C1039	C977	U917	C856	G796	A668	C608	G546		G425	C365	C304	G183	U112	G52
A1100	G1040	G978	U918	U857	C797	A669	U609	G547	U487	A426	U366	U305	G184	C53	
U1101	G1041	C979	A919	A858	A798	A670	G610	C548	U488	U427	U367	C306	G185	G114	A54
G1102	A1042	A980	A920	G859	U799	U671	G611	C549	A489	U428	U368	G307	C186	U115	U55
C1103	G1043	A981	G921	G860	U800	A672	U612	C550	C490	C429	C369	G308	G187	U116	G56
U1104	U1044	G982	A922	A861	U801	G673	G613	U551	C491	C430	G370	C309	C188	C117	U57
G1105	C1045	C983	G923	A862	C802	G674	C614	G552	C492	G431	A371	C310	U189	C118	C58
C1106	U1046	C984	G924	U863	U803	U675	C615	U553	A493	G432	U372	G311	G190	U120	A59
G1107	U1047	G985	G925	A864	U804	C676	A616	U554	C494	G433	G373	C312	A191	U121	U60
A1108	G1048	G986	A926	C867	U805	G677	G617	A555	U495	G434	G374	A313	C192	U121	A61
C1109	U1049	A987	C927	U868	U806	U678		U556	U496	A435	U375	U214	C193	C122	G62

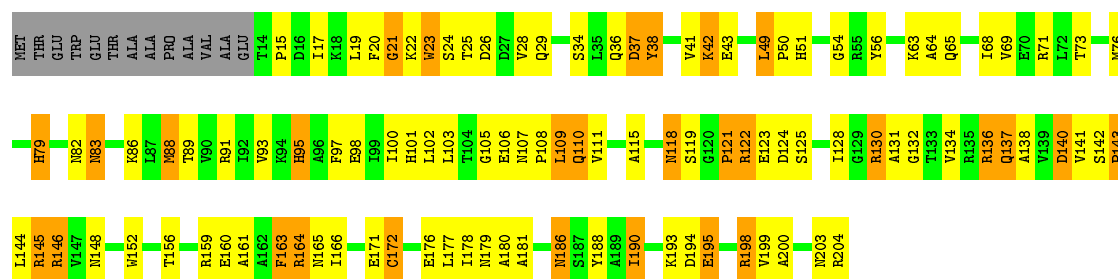






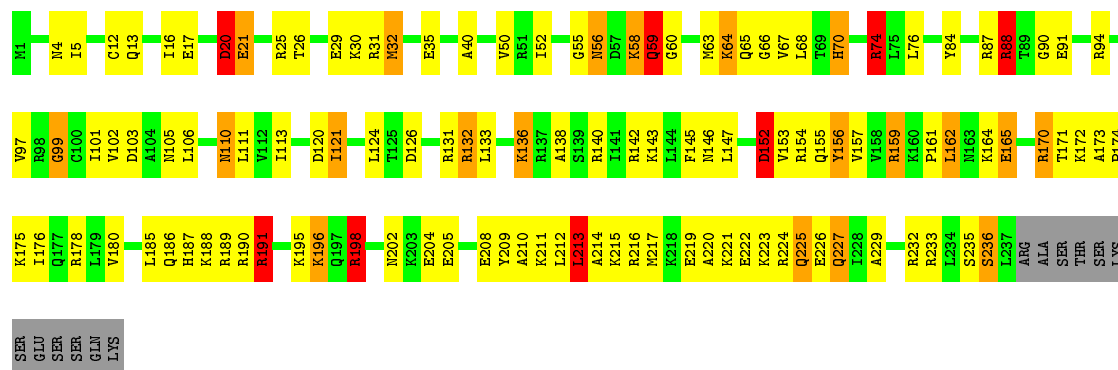
• Molecule 56: Ribosomal protein uS7

Chain SF:



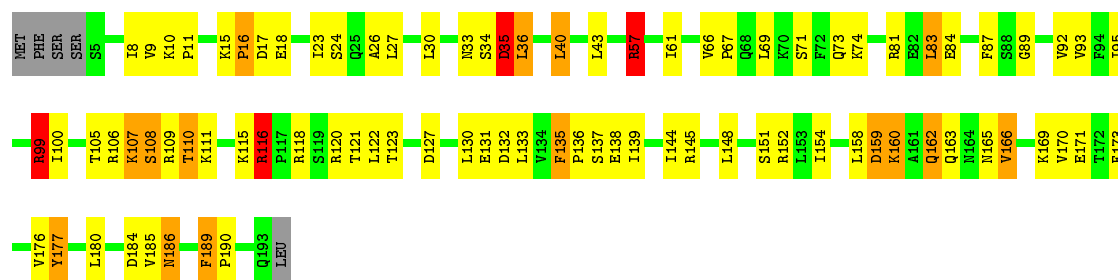
• Molecule 57: Ribosomal protein eS6

Chain SG:



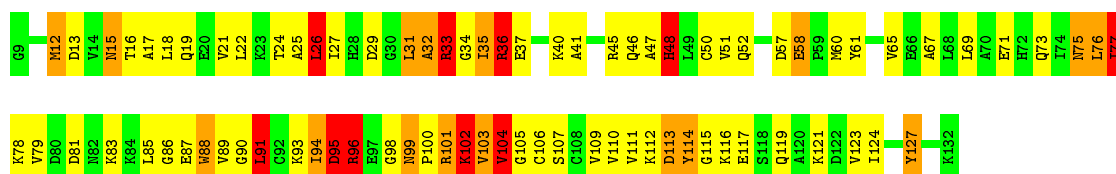
• Molecule 58: Ribosomal protein eS7

Chain SH:



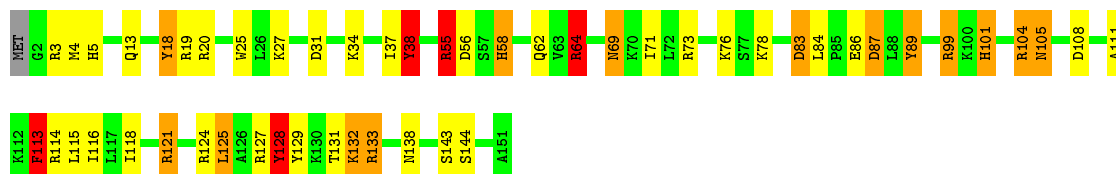
• Molecule 59: Ribosomal protein eS8





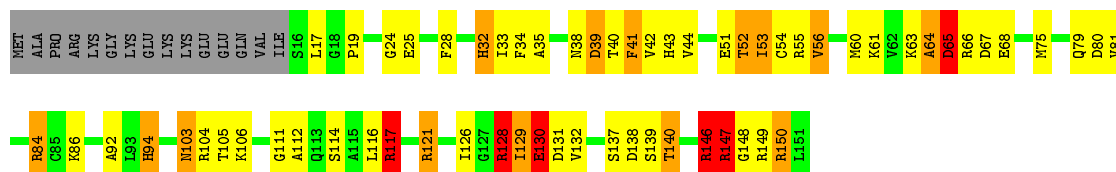
• Molecule 64: Ribosomal protein uS15

Chain SN: 66% 21% 9% . .



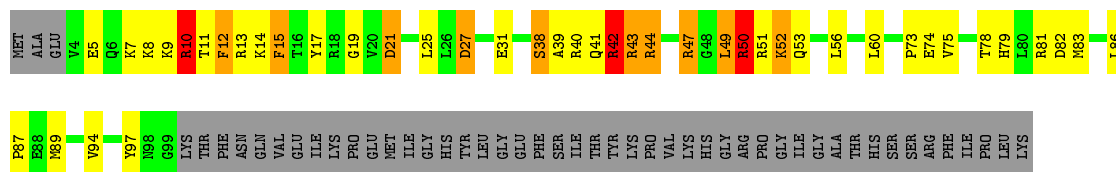
• Molecule 65: Ribosomal protein uS11

Chain SO: 48% 28% 9% . 10%



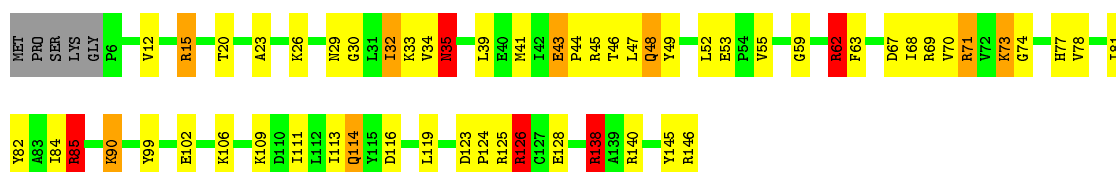
• Molecule 66: Ribosomal protein uS19

Chain SP: 36% 21% 7% . 34%



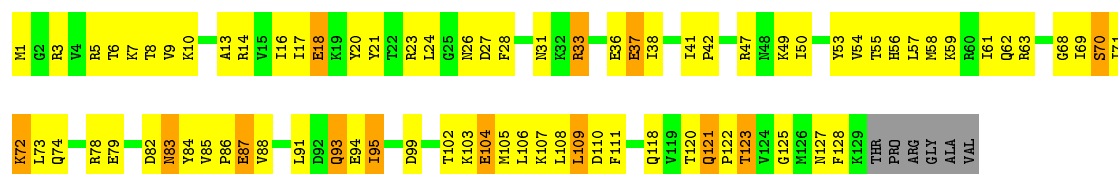
• Molecule 67: Ribosomal protein uS9

Chain SQ: 57% 31% 5% . .

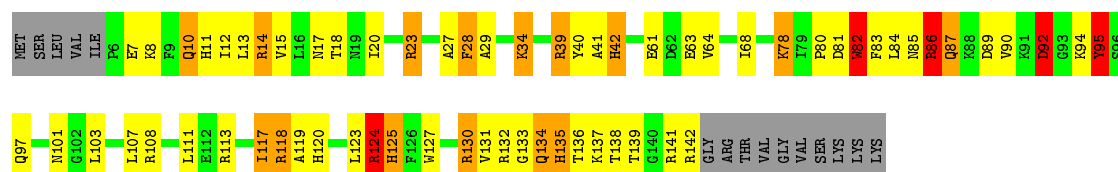


• Molecule 68: Ribosomal protein eS17

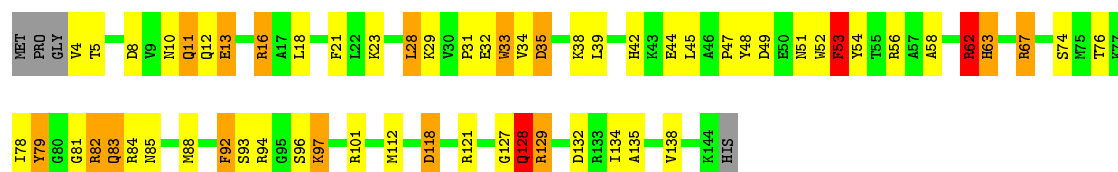
Chain SR: 37% 49% 10% .



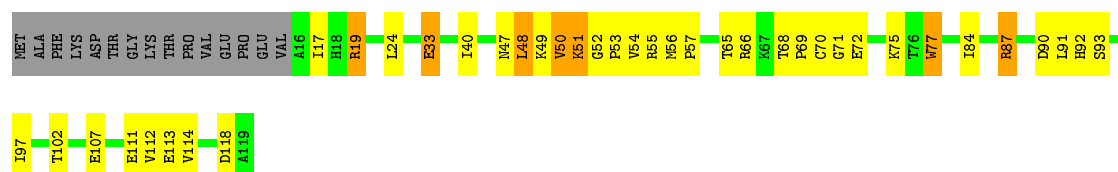
• Molecule 69: Ribosomal protein uS13



• Molecule 70: Ribosomal protein eS19



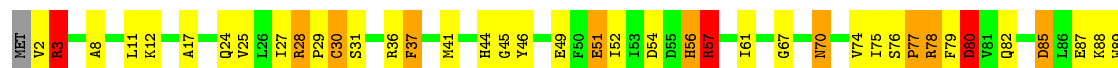
• Molecule 71: Ribosomal protein uS10



• Molecule 72: Ribosomal protein eS21



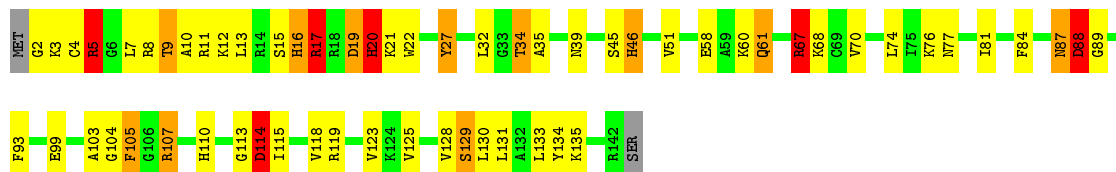
• Molecule 73: Ribosomal protein uS8





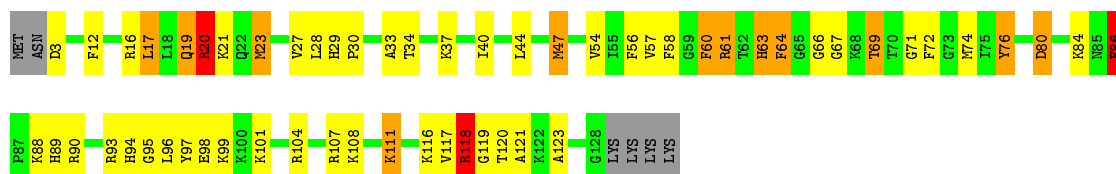
- Molecule 74: Ribosomal protein uS12

Chain SX: 56% 31% 8% 5%



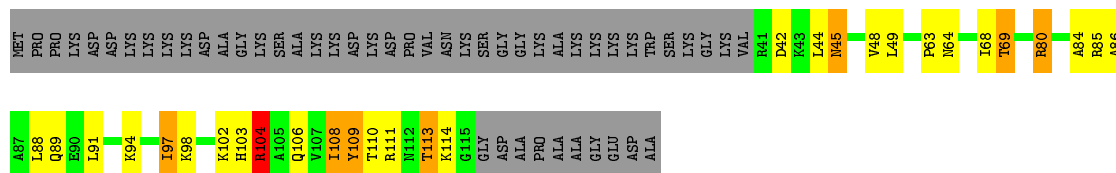
- Molecule 75: Ribosomal protein eS24

Chain SY: 52% 33% 9% 5%



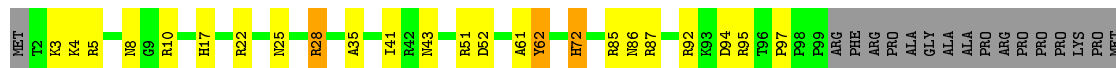
- Molecule 76: Ribosomal protein es25

Chain SZ: 37% 17% 6% 40%



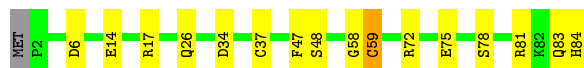
- Molecule 77: Ribosomal protein eS26

Chain Sa: 64% 18% 15%



- Molecule 78: Ribosomal protein eS27

Chain Sb: 80% 18% 2%



- Molecule 79: Ribosomal protein eS28

Chain Sc: 72% 17% 7%



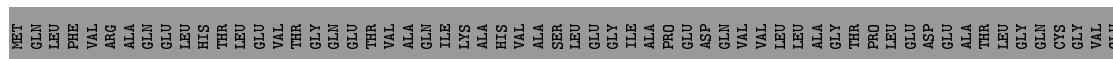
- Molecule 80: Ribosomal protein uS14

Chain Sd: 71% 18% 7%



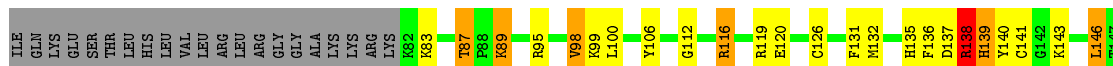
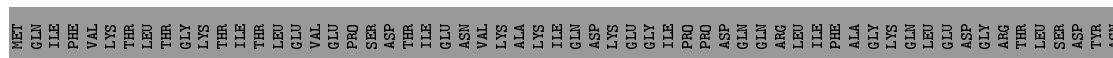
- Molecule 81: Ribosomal protein eS30

Chain Se: 32% 9% 57%



- Molecule 82: Ribosomal protein eS31

Chain Sf: 27% 12% 6% 54%



- Molecule 83: Ribosomal protein RACK1

Chain Sg: 82% 15% 2%



- Molecule 84: Messenger RNA

Chain S4: 10% 90%



- Molecule 85: A/P tRNA

Chain S5: 

39%

59%

G1	C2	C3	C4	G5	G6	A7	U8	A9	G10	C11	C12	C13	A14	G15	G18	G19	U20	A21	G22	A23	G24	C25	A26	G27	G28	G29	G30	A31	U32	U33	G34	A35	A36	A37	A38	U39	C40	C41	C42	C43	C44	U45	G46	C47	C48	C49	U50	U51	G52	G53	U54	U55	C56	G57	A58	U59	C60	C61	C62
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G63	A64	G65	U66	C67	G68	G69	G70	G71	C72	A73	C74	C75	A76
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● Molecule 86: P/E tRNA

Chain S6: 

29%

68%

U1	G2	C3	C4	G5	G6	G7	U8	A9	G10	C11	G12	C13	C14	G15	A16	A17	G18	G19	U20	A21	G22	A23	G24	C25	A26	G27	G28	G29	G30	A31	U32	U33	G34	A35	A36	A37	A38	U39	C40	C41	C42	C43	C44	G45	G46	U47	C48	C49	U50	U51	G52	G53	U54	U55	C56	G57	A58	U59	U60
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C61	C62	G63	A64	G65	U66	C67	C68	G69	G70	G71	C72	A73	C74	C75	A76
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## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	14723	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)	2500	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	5	0.70	83/89191 (0.1%)	1.13	754/139124 (0.5%)
10	G	0.76	4/1966 (0.2%)	1.09	13/2645 (0.5%)
11	H	0.77	3/1537 (0.2%)	1.17	10/2066 (0.5%)
12	I	0.66	1/1753 (0.1%)	1.11	13/2343 (0.6%)
13	J	0.63	1/1382 (0.1%)	1.04	10/1849 (0.5%)
14	L	0.71	2/1734 (0.1%)	1.12	16/2318 (0.7%)
15	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
16	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
17	O	0.72	3/1684 (0.2%)	1.11	12/2251 (0.5%)
18	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
19	Q	0.69	0/1530	1.35	31/2041 (1.5%)
2	7	0.54	1/2858 (0.0%)	0.96	9/4455 (0.2%)
20	R	0.79	3/1524 (0.2%)	1.27	20/2013 (1.0%)
21	S	0.95	8/1493 (0.5%)	1.30	20/2002 (1.0%)
22	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
23	U	0.63	1/822 (0.1%)	1.03	3/1103 (0.3%)
24	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
25	W	0.72	0/541	1.23	5/720 (0.7%)
26	X	0.64	0/993	1.09	10/1334 (0.7%)
27	Y	0.72	0/1132	1.24	20/1504 (1.3%)
28	Z	0.63	0/1130	1.11	9/1507 (0.6%)
29	a	0.93	6/1192 (0.5%)	1.37	16/1591 (1.0%)
3	8	0.68	3/3701 (0.1%)	1.20	42/5766 (0.7%)
30	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
31	c	0.70	0/742	1.14	5/996 (0.5%)
32	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)
33	e	0.90	3/1071 (0.3%)	1.23	14/1429 (1.0%)
34	f	1.02	2/895 (0.2%)	1.34	17/1198 (1.4%)
35	g	0.65	0/916	1.08	5/1220 (0.4%)
36	h	0.63	0/1023	1.21	13/1350 (1.0%)
37	i	0.63	0/843	1.19	8/1115 (0.7%)
38	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	k	0.59	0/575	0.98	1/761 (0.1%)
4	A	0.80	3/1906 (0.2%)	1.26	21/2556 (0.8%)
40	l	0.68	0/454	1.07	3/599 (0.5%)
41	m	0.57	0/435	1.02	3/575 (0.5%)
42	n	0.49	0/223	1.02	0/284
43	o	0.64	0/864	1.27	9/1140 (0.8%)
44	p	0.64	1/718 (0.1%)	1.00	3/953 (0.3%)
45	r	0.68	0/1017	1.12	8/1365 (0.6%)
46	z	0.46	0/1768	0.73	0/2368
47	1	0.59	2/2969 (0.1%)	0.72	3/4014 (0.1%)
48	2	0.46	0/504	0.62	0/673
5	B	0.81	8/3214 (0.2%)	1.16	26/4308 (0.6%)
50	S2	0.68	37/41243 (0.1%)	1.12	315/64257 (0.5%)
51	SA	0.94	4/1679 (0.2%)	1.06	6/2283 (0.3%)
52	SB	1.42	7/1752 (0.4%)	1.63	20/2347 (0.9%)
53	SC	0.98	8/1726 (0.5%)	1.09	9/2332 (0.4%)
54	SD	1.39	12/1793 (0.7%)	1.08	9/2414 (0.4%)
55	SE	0.83	8/2118 (0.4%)	0.98	8/2849 (0.3%)
56	SF	0.74	1/1531 (0.1%)	1.08	11/2059 (0.5%)
57	SG	0.97	10/1946 (0.5%)	1.03	9/2590 (0.3%)
58	SH	0.73	2/1544 (0.1%)	1.02	8/2068 (0.4%)
59	SI	0.97	8/1715 (0.5%)	1.12	10/2287 (0.4%)
6	C	0.73	4/2973 (0.1%)	1.12	18/3990 (0.5%)
60	SJ	1.07	12/1550 (0.8%)	1.28	16/2069 (0.8%)
61	SK	0.75	1/851 (0.1%)	1.00	3/1147 (0.3%)
62	SL	0.85	5/1298 (0.4%)	1.08	7/1735 (0.4%)
63	SM	2.22	2/970 (0.2%)	1.21	8/1300 (0.6%)
64	SN	0.82	4/1232 (0.3%)	1.15	10/1656 (0.6%)
65	SO	1.18	7/1029 (0.7%)	1.38	11/1380 (0.8%)
66	SP	1.52	6/816 (0.7%)	1.29	8/1084 (0.7%)
67	SQ	0.72	2/1142 (0.2%)	1.01	8/1528 (0.5%)
68	SR	0.82	5/1060 (0.5%)	1.08	5/1421 (0.4%)
69	SS	0.66	1/1157 (0.1%)	1.18	13/1548 (0.8%)
7	D	0.73	2/2426 (0.1%)	1.23	27/3252 (0.8%)
70	ST	0.67	2/1119 (0.2%)	1.08	7/1499 (0.5%)
71	SU	0.94	4/828 (0.5%)	0.96	1/1112 (0.1%)
72	SV	0.73	0/631	0.97	0/844
73	SW	1.06	7/1051 (0.7%)	1.22	5/1406 (0.4%)
74	SX	0.95	6/1118 (0.5%)	1.10	11/1493 (0.7%)
75	SY	1.64	5/1040 (0.5%)	1.11	9/1382 (0.7%)
76	SZ	0.56	0/604	0.87	0/810
77	Sa	0.81	1/794 (0.1%)	1.20	4/1065 (0.4%)
78	Sb	0.59	0/665	0.90	0/891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
79	Sc	0.68	0/508	1.13	4/680 (0.6%)
8	E	0.73	5/1941 (0.3%)	1.21	20/2601 (0.8%)
80	Sd	0.79	0/445	1.12	1/589 (0.2%)
81	Se	0.72	1/458 (0.2%)	1.17	5/602 (0.8%)
82	Sf	1.08	6/593 (1.0%)	1.57	12/786 (1.5%)
83	Sg	0.80	11/2493 (0.4%)	0.89	8/3394 (0.2%)
84	S4	0.23	0/219	0.63	0/337
85	S5	1.22	1/1762 (0.1%)	0.80	2/2739 (0.1%)
86	S6	0.31	1/1812 (0.1%)	1.00	5/2823 (0.2%)
9	F	0.80	2/1905 (0.1%)	1.27	27/2539 (1.1%)
All	All	0.77	357/238566 (0.1%)	1.13	1895/350392 (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	5	1	157
10	G	0	3
11	H	0	3
12	I	0	5
13	J	0	2
14	L	0	5
15	M	0	4
16	N	0	10
17	O	0	3
18	P	0	1
19	Q	0	5
2	7	0	2
20	R	0	6
21	S	0	11
22	T	0	2
23	U	0	2
24	V	0	3
25	W	0	1
26	X	0	1
27	Y	0	4
29	a	0	9
3	8	0	11
30	b	0	1
31	c	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
32	d	0	4
33	e	0	4
34	f	0	2
35	g	0	1
36	h	0	3
37	i	0	3
38	j	0	4
39	k	0	1
4	A	0	6
43	o	0	6
44	p	0	1
45	r	0	5
47	l	0	3
5	B	0	13
50	S2	1	62
51	SA	0	2
52	SB	0	5
53	SC	0	4
54	SD	0	2
55	SE	0	2
56	SF	0	1
58	SH	0	1
59	SI	0	6
6	C	0	5
60	SJ	0	2
61	SK	0	1
62	SL	0	4
63	SM	0	1
64	SN	0	1
65	SO	0	1
66	SP	0	1
67	SQ	0	1
68	SR	0	2
7	D	0	8
71	SU	0	1
72	SV	0	2
73	SW	0	2
74	SX	0	2
75	SY	0	1
76	SZ	0	1
77	Sa	0	1
78	Sb	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	E	0	12
80	Sd	0	2
82	Sf	0	4
9	F	0	5
All	All	2	455

The worst 5 of 357 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	2037	C	O3'-P	-68.26	0.79	1.61
63	SM	58	GLU	CD-OE1	64.53	1.96	1.25
85	S5	47	U	O3'-P	-49.36	1.01	1.61
52	SB	145	LYS	C-N	-44.69	0.31	1.34
54	SD	216	GLU	CD-OE1	43.79	1.73	1.25

The worst 5 of 1895 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	SB	145	LYS	CA-C-N	-33.88	42.66	117.20
1	5	4116	C	P-O3'-C3'	33.09	159.40	119.70
52	SB	145	LYS	O-C-N	-27.76	78.29	122.70
1	5	4116	C	O3'-P-O5'	-27.74	51.30	104.00
86	S6	55	U	OP2-P-O3'	27.36	165.39	105.20

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1992	U	C1'
50	S2	1109	C	C1'

5 of 455 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	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	5	79736	0	40287	10586	0
2	7	2558	0	1296	304	0
3	8	3314	0	1683	486	0
4	A	1868	0	1959	160	0
5	B	3147	0	3280	213	0
6	C	2919	0	3100	160	0
7	D	2380	0	2412	171	0
8	E	1904	0	2055	132	0
9	F	1870	0	1996	171	0
10	G	1934	0	2086	143	0
11	H	1518	0	1601	85	0
12	I	1713	0	1751	89	0
13	J	1359	0	1390	76	0
14	L	1703	0	1818	88	0
15	M	1131	0	1209	70	0
16	N	1701	0	1749	119	0
17	O	1651	0	1786	89	0
18	P	1242	0	1269	55	0
19	Q	1506	0	1623	73	0
20	R	1508	0	1664	111	0
21	S	1454	0	1496	116	0
22	T	1298	0	1366	73	0
23	U	808	0	831	26	0
24	V	979	0	1039	58	0
25	W	528	0	541	52	0
26	X	976	0	1053	50	0
27	Y	1115	0	1205	60	0
28	Z	1107	0	1182	49	0
29	a	1163	0	1211	0	0
30	b	610	0	650	0	0
31	c	732	0	769	0	0
32	d	888	0	930	0	0
33	e	1053	0	1147	0	0
34	f	876	0	912	0	0
35	g	906	0	1001	0	0
36	h	1015	0	1149	0	0
37	i	832	0	917	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	j	706	0	743	0	0
39	k	569	0	637	0	0
40	l	444	0	483	0	0
41	m	429	0	466	0	0
42	n	222	0	262	0	0
43	o	851	0	922	0	0
44	p	708	0	760	0	0
45	r	1001	0	1062	0	0
46	z	1741	0	1848	0	0
47	1	2914	0	3025	205	0
48	2	494	0	527	17	0
49	3	180	0	41	1	0
50	S2	36900	0	18591	5686	0
51	SA	1642	0	1646	147	0
52	SB	1725	0	1794	230	0
53	SC	1690	0	1777	88	0
54	SD	1765	0	1863	116	0
55	SE	2076	0	2177	76	0
56	SF	1509	0	1563	61	0
57	SG	1923	0	2089	98	0
58	SH	1521	0	1616	90	0
59	SI	1686	0	1772	95	0
60	SJ	1525	0	1640	95	0
61	SK	827	0	854	48	0
62	SL	1276	0	1353	86	0
63	SM	960	0	989	108	0
64	SN	1208	0	1294	58	0
65	SO	1016	0	1039	57	0
66	SP	805	0	861	23	0
67	SQ	1124	0	1193	51	0
68	SR	1047	0	1103	164	0
69	SS	1139	0	1189	81	0
70	ST	1101	0	1135	68	0
71	SU	818	0	883	27	0
72	SV	625	0	628	21	0
73	SW	1034	0	1080	50	0
74	SX	1099	0	1159	132	0
75	SY	1023	0	1090	57	0
76	SZ	598	0	656	16	0
77	Sa	781	0	828	0	0
78	Sb	651	0	672	0	0
79	Sc	506	0	536	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	Sd	434	0	427	0	0
81	Se	452	0	494	0	0
82	Sf	581	0	599	0	0
83	Sg	2436	0	2393	0	0
84	S4	201	0	101	75	0
85	S5	1579	0	797	465	0
86	S6	1622	0	815	641	0
87	Sa	1	0	0	0	0
87	j	1	0	0	0	0
87	m	1	0	0	0	0
87	o	1	0	0	0	0
88	5	120	0	0	0	0
88	7	5	0	0	0	0
88	8	3	0	0	0	0
88	P	1	0	0	0	0
88	S2	36	0	0	0	0
88	V	1	0	0	0	0
All	All	222336	0	164885	21260	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 60.

The worst 5 of 21260 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)
50:S2:460:A:C2	50:S2:461:U:C5	1.85	1.62
52:SB:97:LEU:CB	52:SB:228:LEU:HD11	1.27	1.61
50:S2:1640:A:H4'	86:S6:41:C:C1'	1.31	1.58
1:5:1560:A:C2	1:5:1561:G:C5	1.92	1.54
60:SJ:59:GLU:CG	60:SJ:59:GLU:CD	1.75	1.53

There are no symmetry-related clashes.

## 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	
4	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	4	39
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	1	17
6	C	365/367 (100%)	304 (83%)	45 (12%)	16 (4%)	3	34
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	20
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	6
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	3	33
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	6	45
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	9	51
12	I	211/213 (99%)	168 (80%)	30 (14%)	13 (6%)	2	27
13	J	168/178 (94%)	136 (81%)	24 (14%)	8 (5%)	3	32
14	L	208/211 (99%)	171 (82%)	26 (12%)	11 (5%)	2	30
15	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	13	57
16	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	5	44
17	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	13	57
18	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	15	59
19	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	6	46
20	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	8	50
21	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	11	55
22	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	10	53
23	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	9	51
24	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	8	50
25	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	12	56
26	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	11	55
27	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	3	33
28	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	4	38
29	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	2	30
30	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	2	30
31	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	3	35
32	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	4	38
33	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	24	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	3	33
35	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	11	54
36	h	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	7	48
37	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	9	52
38	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	3	32
39	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	21
40	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	3	35
41	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	n	21/25 (84%)	21 (100%)	0	0	100	100
43	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	2	28
44	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	17	63
45	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	3	32
46	z	213/217 (98%)	166 (78%)	29 (14%)	18 (8%)	1	17
47	1	363/393 (92%)	312 (86%)	36 (10%)	15 (4%)	3	36
48	2	60/68 (88%)	49 (82%)	7 (12%)	4 (7%)	1	25
51	SA	206/295 (70%)	176 (85%)	24 (12%)	6 (3%)	6	45
52	SB	209/264 (79%)	168 (80%)	26 (12%)	15 (7%)	1	22
53	SC	216/218 (99%)	188 (87%)	20 (9%)	8 (4%)	4	39
54	SD	225/243 (93%)	170 (76%)	44 (20%)	11 (5%)	3	32
55	SE	260/263 (99%)	202 (78%)	41 (16%)	17 (6%)	1	26
56	SF	189/204 (93%)	160 (85%)	19 (10%)	10 (5%)	2	30
57	SG	235/249 (94%)	194 (83%)	35 (15%)	6 (3%)	7	47
58	SH	187/194 (96%)	143 (76%)	29 (16%)	15 (8%)	1	19
59	SI	204/208 (98%)	176 (86%)	21 (10%)	7 (3%)	5	42
60	SJ	183/194 (94%)	145 (79%)	24 (13%)	14 (8%)	1	20
61	SK	96/165 (58%)	60 (62%)	26 (27%)	10 (10%)	1	12
62	SL	154/158 (98%)	124 (80%)	23 (15%)	7 (4%)	3	33
63	SM	122/124 (98%)	77 (63%)	25 (20%)	20 (16%)	0	5
64	SN	148/151 (98%)	115 (78%)	28 (19%)	5 (3%)	5	42
65	SO	134/151 (89%)	102 (76%)	18 (13%)	14 (10%)	1	12
66	SP	94/145 (65%)	65 (69%)	18 (19%)	11 (12%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	SQ	139/146 (95%)	112 (81%)	21 (15%)	6 (4%)	3	35
68	SR	127/135 (94%)	95 (75%)	22 (17%)	10 (8%)	1	19
69	SS	135/152 (89%)	104 (77%)	23 (17%)	8 (6%)	2	28
70	ST	139/145 (96%)	116 (84%)	17 (12%)	6 (4%)	3	35
71	SU	102/119 (86%)	80 (78%)	18 (18%)	4 (4%)	4	37
72	SV	80/83 (96%)	63 (79%)	10 (12%)	7 (9%)	1	17
73	SW	127/130 (98%)	112 (88%)	11 (9%)	4 (3%)	5	44
74	SX	139/143 (97%)	115 (83%)	19 (14%)	5 (4%)	4	40
75	SY	124/132 (94%)	92 (74%)	23 (18%)	9 (7%)	1	22
76	SZ	73/125 (58%)	54 (74%)	13 (18%)	6 (8%)	1	18
77	Sa	96/115 (84%)	71 (74%)	17 (18%)	8 (8%)	1	18
78	Sb	81/84 (96%)	61 (75%)	15 (18%)	5 (6%)	2	27
79	Sc	62/69 (90%)	46 (74%)	16 (26%)	0	100	100
80	Sd	50/56 (89%)	38 (76%)	9 (18%)	3 (6%)	2	27
81	Se	55/133 (41%)	40 (73%)	14 (26%)	1 (2%)	11	54
82	Sf	69/156 (44%)	39 (56%)	21 (30%)	9 (13%)	0	7
83	Sg	311/317 (98%)	250 (80%)	45 (14%)	16 (5%)	2	31
All	All	11778/13204 (89%)	9619 (82%)	1571 (13%)	588 (5%)	5	31

5 of 588 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	47	LEU

### 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	
4	A	187/199 (94%)	139 (74%)	48 (26%)	0	6
5	B	335/335 (100%)	265 (79%)	70 (21%)	1	11
6	C	305/305 (100%)	239 (78%)	66 (22%)	1	10
7	D	246/250 (98%)	178 (72%)	68 (28%)	0	5
8	E	209/209 (100%)	157 (75%)	52 (25%)	1	7
9	F	194/194 (100%)	145 (75%)	49 (25%)	1	7
10	G	206/226 (91%)	158 (77%)	48 (23%)	1	8
11	H	169/171 (99%)	125 (74%)	44 (26%)	0	6
12	I	180/180 (100%)	136 (76%)	44 (24%)	1	7
13	J	143/149 (96%)	115 (80%)	28 (20%)	1	14
14	L	176/177 (99%)	135 (77%)	41 (23%)	1	8
15	M	116/160 (72%)	95 (82%)	21 (18%)	2	16
16	N	171/172 (99%)	129 (75%)	42 (25%)	1	7
17	O	172/174 (99%)	146 (85%)	26 (15%)	3	25
18	P	134/134 (100%)	112 (84%)	22 (16%)	3	21
19	Q	163/164 (99%)	132 (81%)	31 (19%)	2	14
20	R	159/175 (91%)	120 (76%)	39 (24%)	1	7
21	S	156/192 (81%)	121 (78%)	35 (22%)	1	9
22	T	139/140 (99%)	112 (81%)	27 (19%)	2	14
23	U	89/114 (78%)	67 (75%)	22 (25%)	1	7
24	V	101/107 (94%)	77 (76%)	24 (24%)	1	7
25	W	55/126 (44%)	42 (76%)	13 (24%)	1	8
26	X	107/133 (80%)	89 (83%)	18 (17%)	2	20
27	Y	124/135 (92%)	96 (77%)	28 (23%)	1	9
28	Z	117/118 (99%)	93 (80%)	24 (20%)	1	12
29	a	119/120 (99%)	102 (86%)	17 (14%)	4	28
30	b	63/123 (51%)	45 (71%)	18 (29%)	0	4
31	c	79/97 (81%)	60 (76%)	19 (24%)	1	7
32	d	98/110 (89%)	66 (67%)	32 (33%)	0	3
33	e	114/121 (94%)	89 (78%)	25 (22%)	1	10
34	f	88/89 (99%)	73 (83%)	15 (17%)	2	20
35	g	98/100 (98%)	79 (81%)	19 (19%)	2	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	h	109/110 (99%)	92 (84%)	17 (16%)	3	24
37	i	86/89 (97%)	71 (83%)	15 (17%)	2	18
38	j	73/73 (100%)	60 (82%)	13 (18%)	2	18
39	k	64/65 (98%)	52 (81%)	12 (19%)	2	15
40	l	47/48 (98%)	39 (83%)	8 (17%)	2	20
41	m	48/116 (41%)	36 (75%)	12 (25%)	1	7
42	n	22/24 (92%)	17 (77%)	5 (23%)	1	9
43	o	92/94 (98%)	70 (76%)	22 (24%)	1	7
44	p	74/74 (100%)	61 (82%)	13 (18%)	2	18
45	r	109/109 (100%)	85 (78%)	24 (22%)	1	10
46	z	195/196 (100%)	169 (87%)	26 (13%)	5	30
47	1	316/331 (96%)	300 (95%)	16 (5%)	29	68
48	2	53/59 (90%)	49 (92%)	4 (8%)	17	56
51	SA	174/245 (71%)	141 (81%)	33 (19%)	2	14
52	SB	194/231 (84%)	164 (84%)	30 (16%)	3	24
53	SC	184/184 (100%)	148 (80%)	36 (20%)	1	14
54	SD	190/202 (94%)	163 (86%)	27 (14%)	4	28
55	SE	224/225 (100%)	180 (80%)	44 (20%)	1	14
56	SF	161/170 (95%)	129 (80%)	32 (20%)	1	13
57	SG	207/218 (95%)	171 (83%)	36 (17%)	2	18
58	SH	169/174 (97%)	149 (88%)	20 (12%)	6	35
59	SI	178/180 (99%)	148 (83%)	30 (17%)	2	20
60	SJ	161/168 (96%)	128 (80%)	33 (20%)	1	12
61	SK	89/136 (65%)	68 (76%)	21 (24%)	1	8
62	SL	140/142 (99%)	118 (84%)	22 (16%)	3	24
63	SM	104/104 (100%)	76 (73%)	28 (27%)	0	5
64	SN	130/131 (99%)	101 (78%)	29 (22%)	1	9
65	SO	106/119 (89%)	83 (78%)	23 (22%)	1	10
66	SP	88/130 (68%)	73 (83%)	15 (17%)	2	20
67	SQ	117/121 (97%)	100 (86%)	17 (14%)	4	27
68	SR	117/121 (97%)	102 (87%)	15 (13%)	5	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	SS	119/132 (90%)	97 (82%)	22 (18%)	2	16
70	ST	112/115 (97%)	89 (80%)	23 (20%)	1	12
71	SU	94/107 (88%)	84 (89%)	10 (11%)	8	39
72	SV	66/67 (98%)	53 (80%)	13 (20%)	1	13
73	SW	112/113 (99%)	93 (83%)	19 (17%)	2	20
74	SX	113/115 (98%)	98 (87%)	15 (13%)	5	30
75	SY	108/114 (95%)	86 (80%)	22 (20%)	1	12
76	SZ	66/103 (64%)	54 (82%)	12 (18%)	2	16
77	Sa	85/98 (87%)	70 (82%)	15 (18%)	2	18
78	Sb	75/76 (99%)	64 (85%)	11 (15%)	4	26
79	Sc	57/62 (92%)	43 (75%)	14 (25%)	1	7
80	Sd	45/48 (94%)	35 (78%)	10 (22%)	1	9
81	Se	46/105 (44%)	35 (76%)	11 (24%)	1	7
82	Sf	64/140 (46%)	45 (70%)	19 (30%)	0	4
83	Sg	272/275 (99%)	242 (89%)	30 (11%)	8	38
All	All	10267/11258 (91%)	8268 (80%)	1999 (20%)	5	14

5 of 1999 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	Y	126	ARG
38	j	79	ARG
74	SX	67	ARG
29	a	7	LYS
32	d	123	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 278 such sidechains are listed below:

Mol	Chain	Res	Type
27	Y	56	GLN
35	g	18	ASN
73	SW	98	GLN
27	Y	127	GLN
31	c	19	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3703/3722 (99%)	1640 (44%)	636 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
50	S2	1717/1742 (98%)	771 (44%)	273 (15%)
84	S4	9/10 (90%)	9 (100%)	0
85	S5	71/74 (95%)	47 (66%)	10 (14%)
86	S6	75/76 (98%)	53 (70%)	8 (10%)
All	All	5849/5900 (99%)	2612 (44%)	958 (16%)

5 of 2612 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C
1	5	8	U
1	5	12	A

5 of 958 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3667	C
1	5	4349	C
50	S2	1494	U
1	5	3736	A
1	5	4096	C

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 170 ligands modelled in this entry, 170 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.