



## wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:10 pm GMT

PDB ID : 3J7P  
EMDB ID: : EMD-2646  
Title : Structure of the 80S mammalian ribosome bound to eEF2  
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.  
Deposited on : 2014-08-01  
Resolution : 3.50 Å(reported)  
Based on PDB ID : 3J3B, 3J3A, 3J3F, 3J3D

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report  
for a publicly released PDB/EMDB entry.

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>  
with specific help available everywhere you see the ⓘ symbol.

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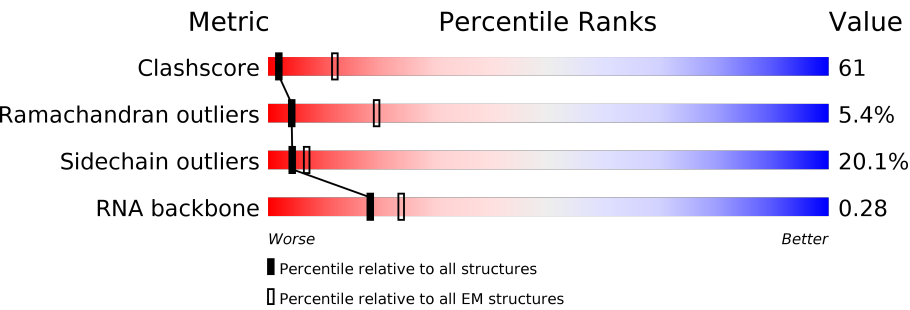
MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc29047

# 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 3.50 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	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	3664	9% 46% 34% 11%
2	7	120	18% 57% 22% .
3	8	156	8% 54% 25% 13%
4	A	257	49% 28% 12% 6% 5%
5	B	394	48% 34% 14% 5%
6	C	367	55% 31% 11% .
7	D	297	45% 35% 13% 5% .
8	E	236	47% 27% 19% 6%









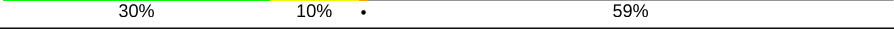


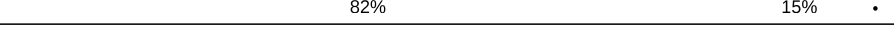

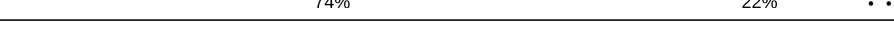
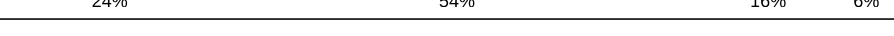

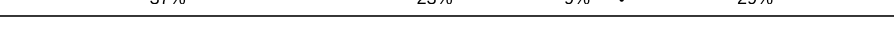

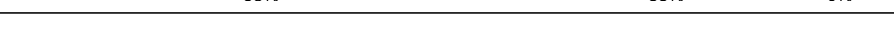
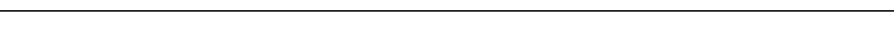

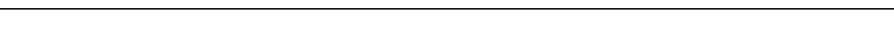
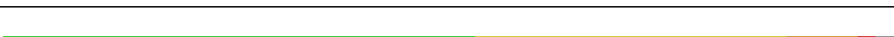
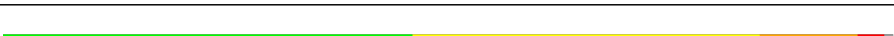

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Mol	Chain	Length	Quality of chain
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	K	163	
15	L	211	
16	M	213	
17	N	204	
18	O	204	
19	P	153	
20	Q	188	
21	R	196	
22	S	224	
23	T	160	
24	U	128	
25	V	140	
26	W	157	
27	X	156	
28	Y	145	
29	Z	136	
30	a	148	
31	b	160	
32	c	115	
33	d	125	


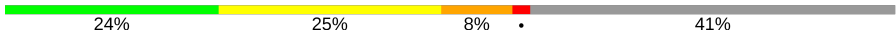

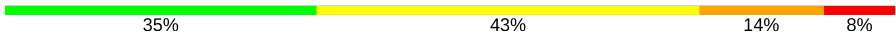


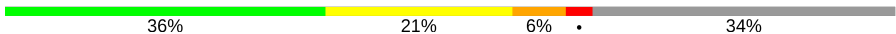

















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Mol	Chain	Length	Quality of chain
34	e	135	
35	f	110	
36	g	117	
37	h	123	
38	i	105	
39	j	86	
40	k	70	
41	l	51	
42	m	128	
43	n	25	
44	o	106	
45	p	91	
46	q	202	
47	r	125	
48	4	856	
49	S2	1742	
50	SA	295	
51	SB	264	
52	SC	218	
53	SD	243	
54	SE	263	
55	SF	204	
56	SG	249	
57	SH	194	
58	SI	208	

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

## 2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 221686 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	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- 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 uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	151	Total	C	N	O	S	0	0
			1140	708	215	213	4		

- Molecule 15 is a protein called Ribosomal protein eL13.

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

- Molecule 16 is a protein called Ribosomal protein eL14.

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

- Molecule 17 is a protein called Ribosomal protein eL15.

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

- Molecule 18 is a protein called Ribosomal protein uL13.

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

- Molecule 19 is a protein called Ribosomal protein uL22.

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

- Molecule 20 is a protein called Ribosomal protein eL18.

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

- Molecule 21 is a protein called Ribosomal protein eL19.



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

- Molecule 22 is a protein called Ribosomal protein eL20.

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

- Molecule 23 is a protein called Ribosomal protein eL21.

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

- Molecule 24 is a protein called Ribosomal protein eL22.

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

- Molecule 25 is a protein called Ribosomal protein uL14.

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

- Molecule 26 is a protein called Ribosomal protein eL24.

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

- Molecule 27 is a protein called Ribosomal protein uL23.

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

- Molecule 28 is a protein called Ribosomal protein uL24.

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

- Molecule 29 is a protein called Ribosomal protein eL27.

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

- Molecule 30 is a protein called Ribosomal protein uL15.

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

- Molecule 31 is a protein called Ribosomal protein eL29.

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

- Molecule 32 is a protein called Ribosomal protein eL30.

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

- Molecule 33 is a protein called Ribosomal protein eL31.

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

- Molecule 34 is a protein called Ribosomal protein eL32.

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

- Molecule 35 is a protein called Ribosomal protein eL33.

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

- Molecule 36 is a protein called Ribosomal protein eL34.

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

- Molecule 37 is a protein called Ribosomal protein uL29.

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

- Molecule 38 is a protein called Ribosomal protein eL36.

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

- Molecule 39 is a protein called Ribosomal protein eL37.

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

- Molecule 40 is a protein called Ribosomal protein eL38.

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

- Molecule 41 is a protein called Ribosomal protein eL39.

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

- Molecule 42 is a protein called Ribosomal protein eL40.

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

- 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 eL42.

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

- Molecule 45 is a protein called Ribosomal protein eL43.

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

- Molecule 46 is a protein called Ribosomal protein uL10.

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

- Molecule 47 is a protein called Ribosomal protein eL28.

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

- Molecule 48 is a protein called Eukaryotic elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	4	856	Total	C	N	O	S	0	0
			6673	4234	1148	1247	44		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 50 is a protein called Ribosomal protein uS2.

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

- Molecule 51 is a protein called Ribosomal protein eS1.

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

- Molecule 52 is a protein called Ribosomal protein uS5.

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

- Molecule 53 is a protein called Ribosomal protein uS3.

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

- Molecule 54 is a protein called Ribosomal protein eS4.

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

- Molecule 55 is a protein called Ribosomal protein uS7.

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

- Molecule 56 is a protein called Ribosomal protein eS6.

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

- Molecule 57 is a protein called Ribosomal protein eS7.

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

- Molecule 58 is a protein called Ribosomal protein eS8.

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

- Molecule 59 is a protein called Ribosomal protein uS4.

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

- Molecule 60 is a protein called Ribosomal protein eS10.

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

- Molecule 61 is a protein called Ribosomal protein uS17.

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

- Molecule 62 is a protein called Ribosomal protein eS12.

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

- Molecule 63 is a protein called Ribosomal protein uS15.

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

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

- Molecule 66 is a protein called Ribosomal protein uS9.

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

- Molecule 67 is a protein called Ribosomal protein eS17.

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

- Molecule 68 is a protein called Ribosomal protein uS13.

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

- Molecule 69 is a protein called Ribosomal protein eS19.

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

- Molecule 70 is a protein called Ribosomal protein uS10.

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

- Molecule 71 is a protein called Ribosomal protein eS21.

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

- Molecule 72 is a protein called Ribosomal protein uS8.

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

- Molecule 73 is a protein called Ribosomal protein uS12.

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

- Molecule 74 is a protein called Ribosomal protein eS24.

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

- Molecule 75 is a protein called Ribosomal protein es25.

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

- Molecule 76 is a protein called Ribosomal protein eS26.

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

- Molecule 77 is a protein called Ribosomal protein eS27.



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

- Molecule 78 is a protein called Ribosomal protein eS28.

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

- Molecule 79 is a protein called Ribosomal protein uS14.

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

- Molecule 80 is a protein called Ribosomal protein eS30.

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

- Molecule 81 is a protein called Ribosomal protein eS31.

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

- Molecule 82 is a protein called Ribosomal protein RACK1.

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

- Molecule 83 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

*Continued on next page...*

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Mol	Chain	Residues	Atoms		AltConf
83	m	1	Total 1	Zn 1	0

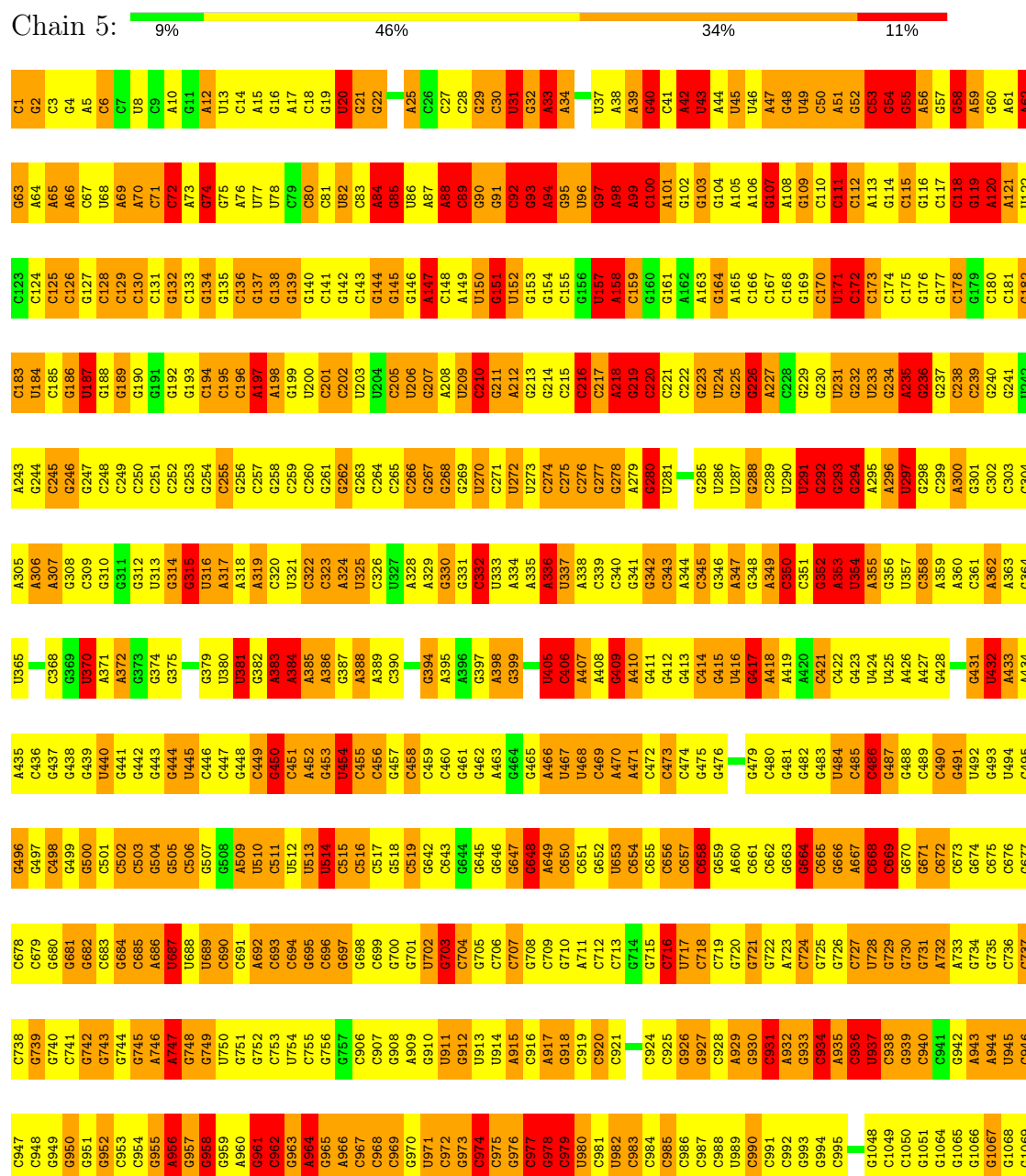
- Molecule 84 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	P	1	Total 1	Mg 1	0
84	S2	36	Total 36	Mg 36	0
84	V	1	Total 1	Mg 1	0
84	7	5	Total 5	Mg 5	0
84	4	1	Total 1	Mg 1	0
84	5	118	Total 118	Mg 118	0
84	8	4	Total 4	Mg 4	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 the various outlier classes 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



G2079	G2080	G2081	A2017	G1957	G1895	U1834	U1773	G1633	G1571	G1507	C1446	C1385	A1326	G1265	G1196	G1070
U2080	C2081	G2082	C2018	A1958	A1896	G1835	C1774	A1634	U1572	A1508	C1447	A1387	C1327	G1266	C1197	C1071
C2083	G2084	C2085	U2020	A1959	A1897	G1836	A1776	G1635	G1573	C1509	U1449	U1389	G1328	G1267	G1198	G1072
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G2089	G2090	G2091	C2022	A1961	C1899	A1838	C1777	A1637	U1575	U1511	C1451	A1391	A1331	G1269	G1200	G1074
G2092	G2093	G2094	C2023	C1963	C1901	G1840	U1779	U1638	U1576	G1512	C1452	A1392	C1332	A1270	U1201	G1075
G2095	G2096	G2097	G2024	A1964	G1902	C	A1780	U1639	G1577	U1513	C1453	G1393	A1333	G1271	G1202	G1076
G2098	G2099	G2100	A2025	G1965	G1903	G1842	A1781	C1640	U1578	U1514	G1454	G1394	A1334	C1272	G1203	C1077
G2101	G2102	G2103	A2026	A1966	U1906	A1843	U1782	G1641	C1579	A1515	G1455	A1334	A1335	G1273	G1204	A1078
G2104	G2105	G2106	G2027	A1967	U1907	G1844	C1783	A1642	C1580	G1516	C1456	G1336	G1336	A1274	G1205	C1079
G2107	G2108	G2109	C2028	G1968	A1908	U1845	U1784	C1644	U1581	G1517	C1457	G1337	G1337	G1275	G1206	C1080
G2110	G2111	G2112	G2029	G1969	A1909	G1846	C1785	C1645	U1582	A1518	C1458	A1338	G1338	G1276	G1207	C1081
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G2119	G2120	G2121	A2034	G1972	G1911	A1849	A1788	C1648	C1586	G1521	C1461	G1400	U1341	A1279	C1210	C1084
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G2125	G2126	G2127	C2036	G1974	C1913	G1851	U1790	A1650	A1523	A1524	C1463	G1402	A1342	G1281	G1212	C1086
G2128	G2129	G2130	G2037	G1975	U1916	U1852	U1791	G1651	C1589	A1525	C1464	G1403	A1343	G1282	G1213	A1087
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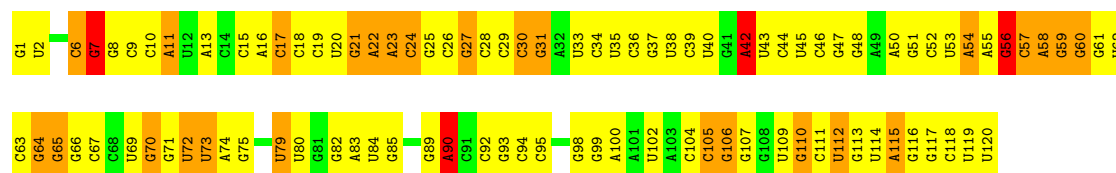
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PROTEIN DATA BANK

 **EMDataBank**  
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C5018	G4949	G4750	U4690	C4750	U4688	U4629	A4504	U4505	U4441	A4380	G4316	G4254	C4191	U4070	U4070
U5019	U4950	A4751	G4691	U4751	U4689	G4630	C4506	C4505	U4442	A4381	A4317	A4255	A4192	U4071	U4071
C5020	C4951	C4752	A4692	C4752	U4690	U4631	U4507		U4443	G4382	C4319	A4256	C4193	C4072	C4072
G5021	G4952	U4753	U4693	A4753	U4691	U4632	G4507	C4506	C4444	U4383			U4194	A4073	A4073
U5022	U4953	G4754	C4694	C4754	U4692	U4633	A4508	A4507		U4384	G4320	C4258	C4195	C4074	C4074
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G5024	G4955	U4756	U4696	C4756	C4695	U4635	A4510	C4509	G4448	A4386	G4322	U4260	G4197	G4076	G4076
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C5034	C4965	C4766				G4644	U4580	C4518	C4458	U4395	C4332	G4272	C4207	G4086	G4086
G5035	G4966	A4767	U4706	A4767	U4705	C4645	U4581	G4520	U4459	A4396	C4333	G4273	U4208	G4087	G4087
C5036	U4967	C4768	U4707	C4768	A4706	U4646	C4582	U4521	U4460	A4397	U4334	A4274	G4209	C4088	C4088
U5037	C4968	U4769	U4708	A4769	A4707	G4647	C4583	G4522	C4461	C4398	A4335	G4275	U4210	G4089	G4089
C5038	G4969	C4770	C4710	C4770	C4708	U4648	A4584	A4523	C4462	U4399	A4336	G4276	C4211	G4090	G4090
A5039	U4970	C4771	U4711	C4771	C4710	G4649	U4585	G4524	U4463	C4400	C4337	G4277	A4212	G4091	G4091
G5040	C4971	C4772	U4712	C4772	U4711	G4650	U4586	U4464	U4464	G4401	G4338	C4278	A4213	G4092	G4092
U5041	U4972	C4773	G4713	A4773	C4712	A4651	G4587		U4465	C4402	A4339	A4279	A4214	G4093	G4093
C5042	C4973	C4774	C4714	C4774	C4713	G4652		G4528	C4466	U4403	U4340	A4280	C4215	G4154	G4154

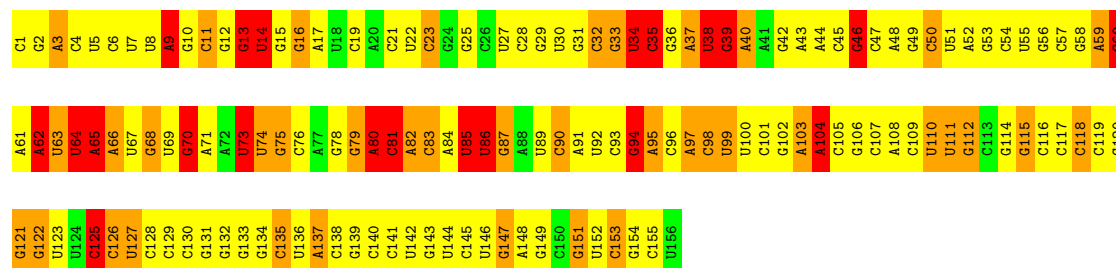
- Molecule 2: 5S ribosomal RNA

Chain 7: 



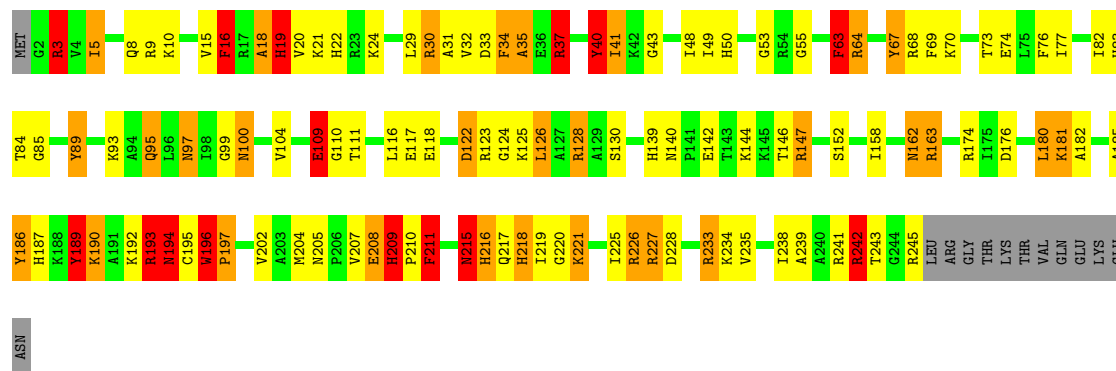
- Molecule 3: 5.8S ribosomal RNA

Chain 8: 



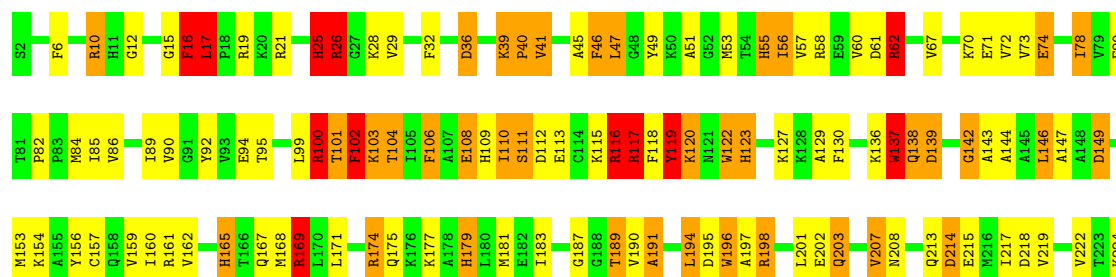
- Molecule 4: Ribosomal protein uL2

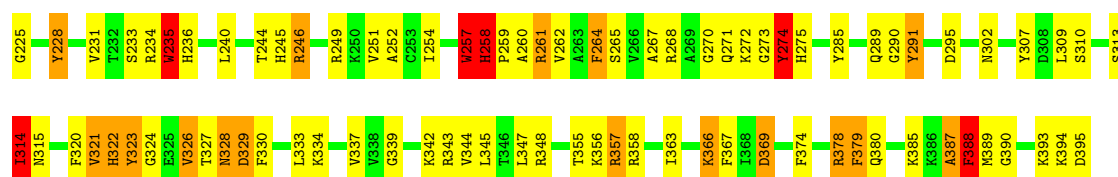
Chain A: 



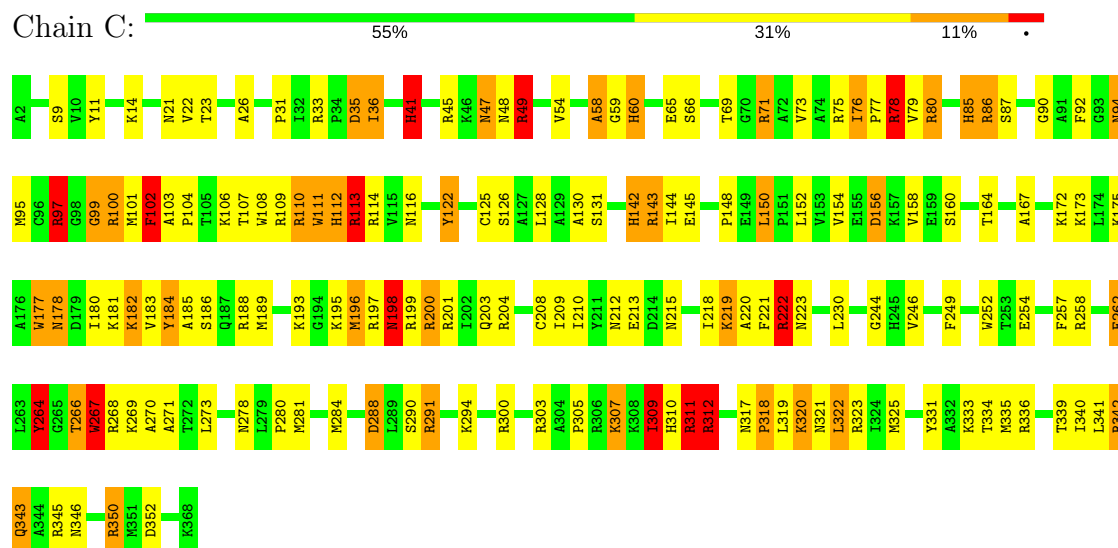
- Molecule 5: Ribosomal protein uL3

Chain B: 

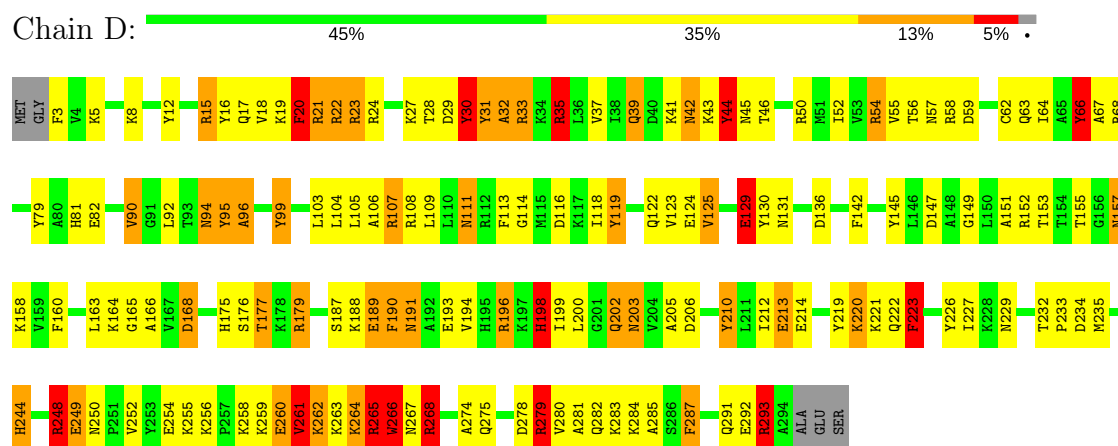




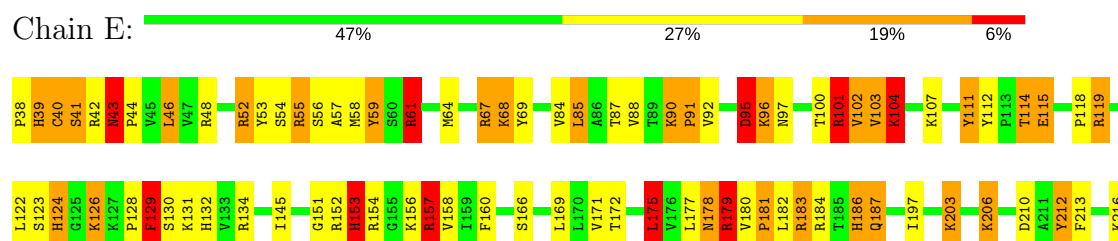
### • Molecule 6: Ribosomal protein uL4



### • Molecule 7: Ribosomal protein uL18



### • Molecule 8: Ribosomal protein eL6

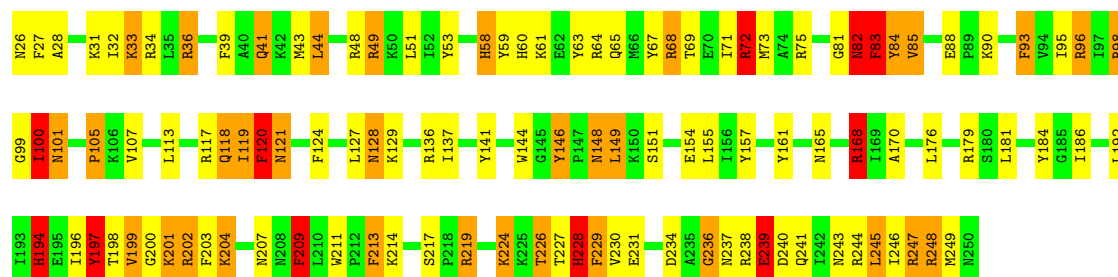






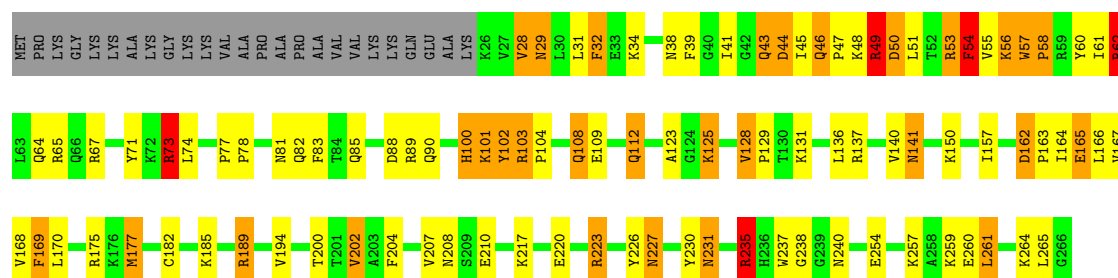
• Molecule 9: Ribosomal protein uL30

Chain F: 49% 31% 15% 5%



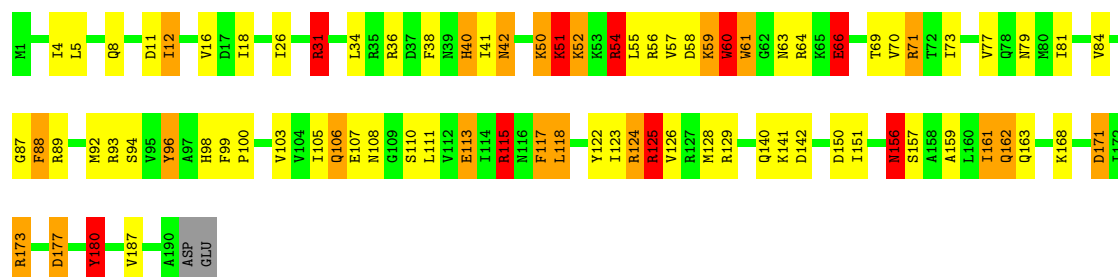
• Molecule 10: Ribosomal protein eL8

Chain G: 53% 24% 11% 9%



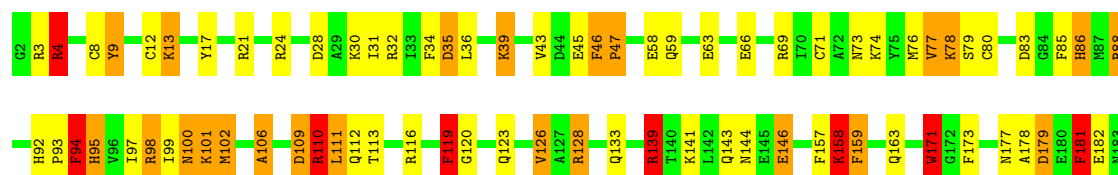
• Molecule 11: Ribosomal protein uL6

Chain H: 56% 28% 10% 5%



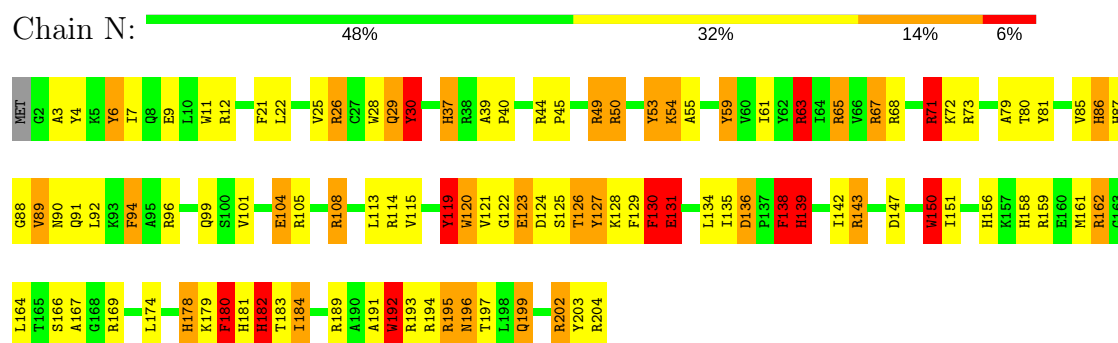
• Molecule 12: Ribosomal protein uL16

Chain I: 58% 27% 11%

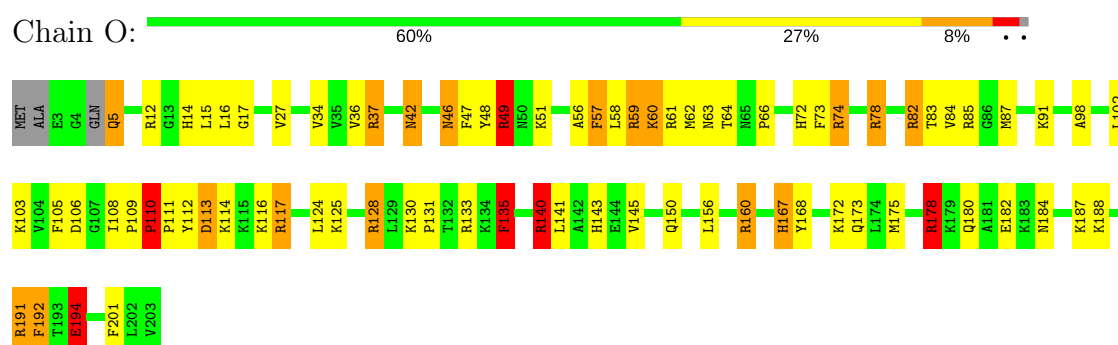




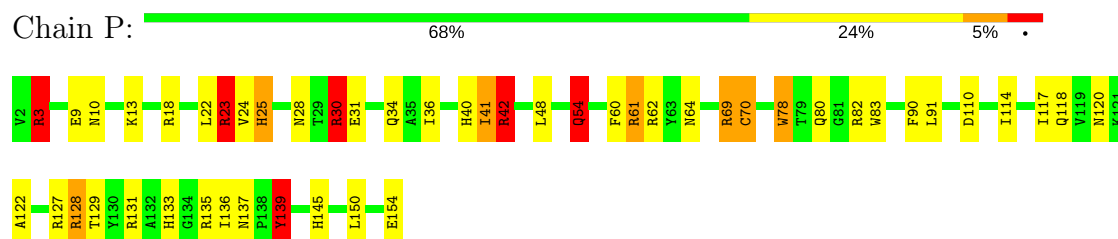
- Molecule 17: Ribosomal protein eL15



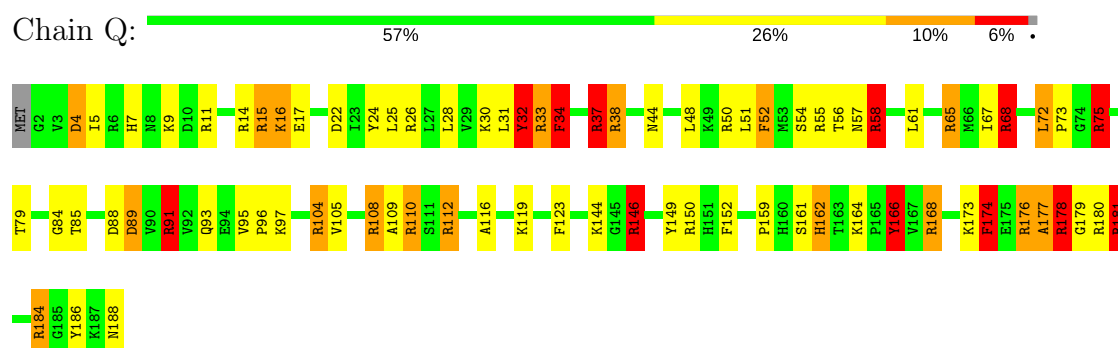
- Molecule 18: Ribosomal protein uL13



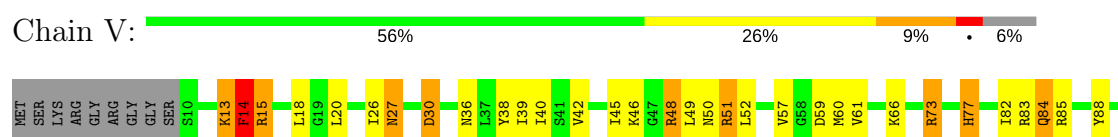
- Molecule 19: Ribosomal protein uL22



- Molecule 20: Ribosomal protein eL18



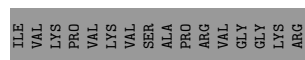
- Molecule 21: Ribosomal protein eL19





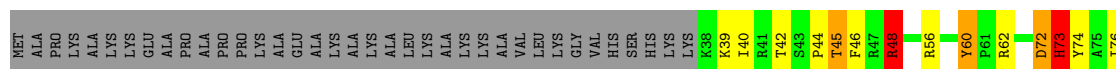
• Molecule 26: Ribosomal protein eL24

Chain W: 24% 10% 60%



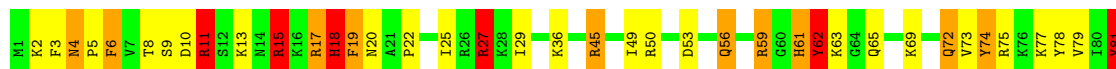
• Molecule 27: Ribosomal protein uL23

Chain X: 48% 20% 6% 24%



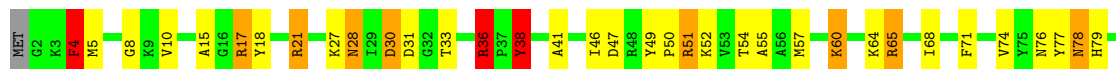
• Molecule 28: Ribosomal protein uL24

Chain Y: 52% 25% 10% 5% 8%



• Molecule 29: Ribosomal protein eL27

Chain Z: 55% 32% 10%




• Molecule 30: Ribosomal protein uL15

Chain a: 77% 17%




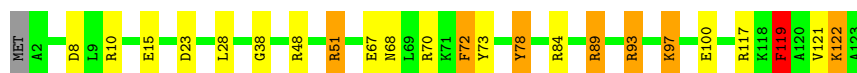


Chain g:  77% 19% . .



- Molecule 37: Ribosomal protein uL29

Chain h:  80% 12% 6% ..



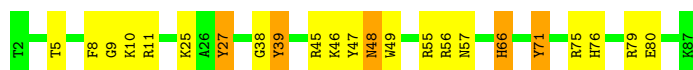
- Molecule 38: Ribosomal protein eL36

Chain i:  76% 17% . .



- Molecule 39: Ribosomal protein eL37

Chain j:  73% 21% 6%



- Molecule 40: Ribosomal protein eL38

Chain k:  71% 27%



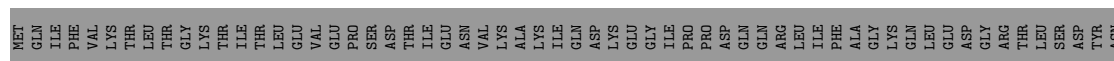
- Molecule 41: Ribosomal protein eL39

Chain l:  76% 18% . .



- Molecule 42: Ribosomal protein eL40

Chain m:  30% 10% 59%



- Molecule 43: Ribosomal protein eL41

Chain n: 




- Molecule 44: Ribosomal protein eL42

Chain o: 



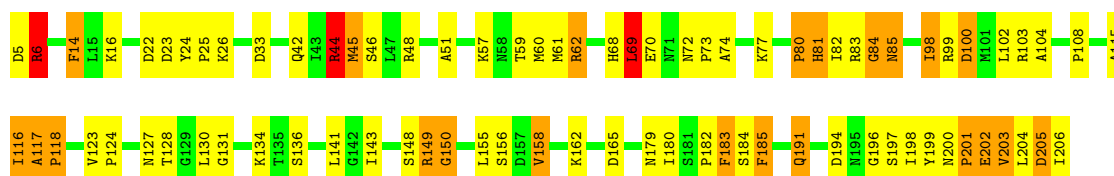
- Molecule 45: Ribosomal protein eL43

Chain p: 



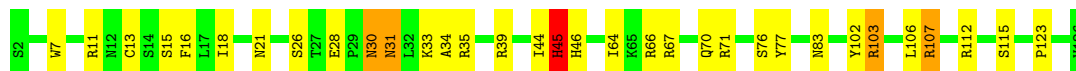
- Molecule 46: Ribosomal protein uL10

Chain q: 



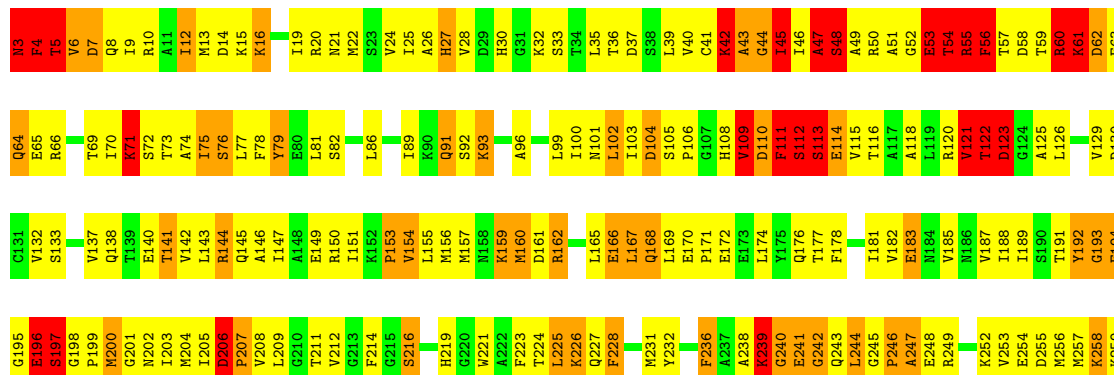
- Molecule 47: Ribosomal protein eL28

Chain r: 

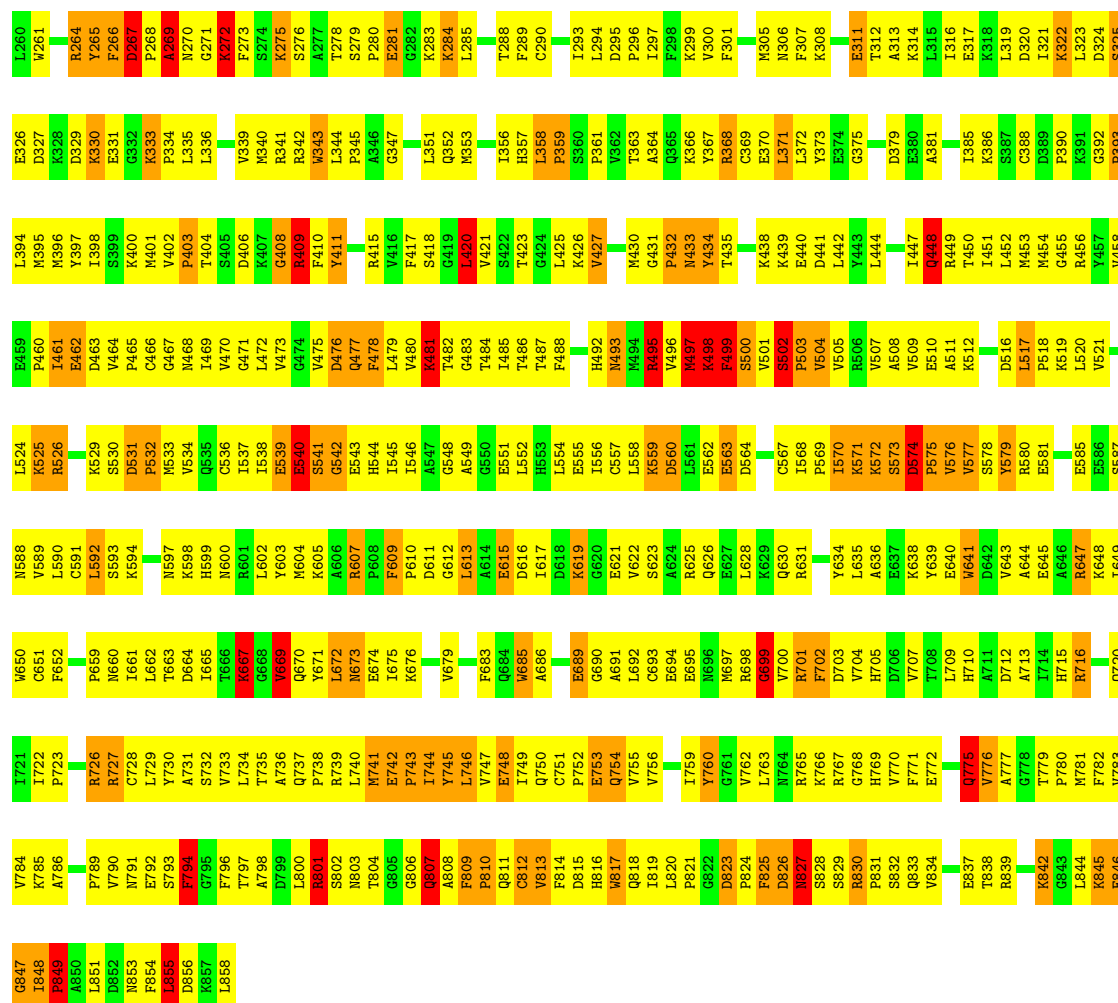


- Molecule 48: Eukaryotic elongation factor 2

Chain 4: 

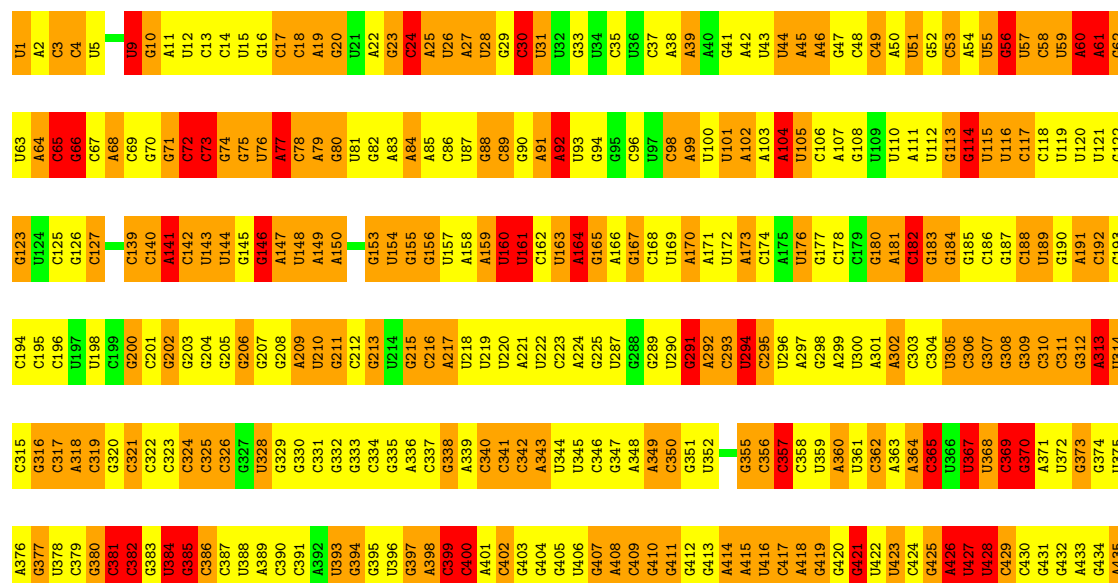




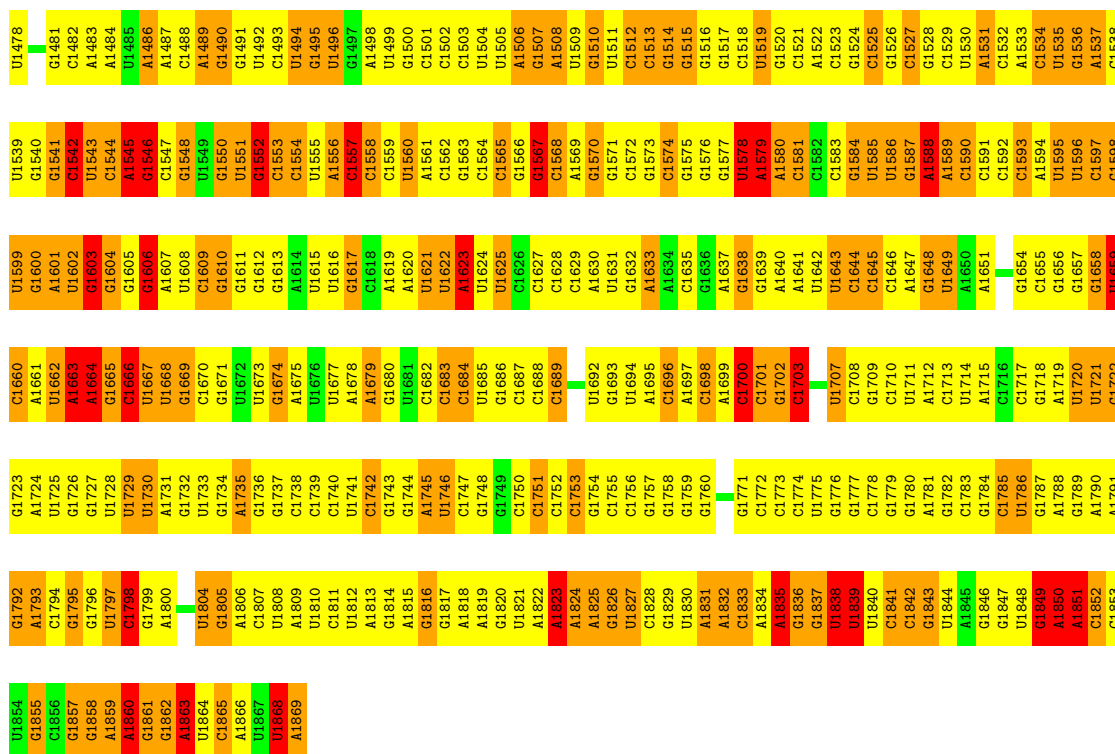


• Molecule 49: 18S ribosomal RNA

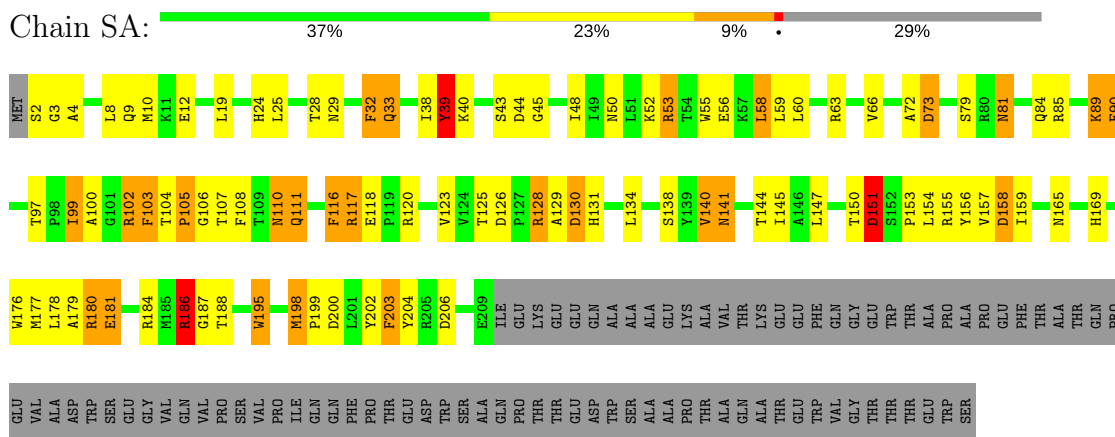
Chain S2: 8% 46% 37% 9%



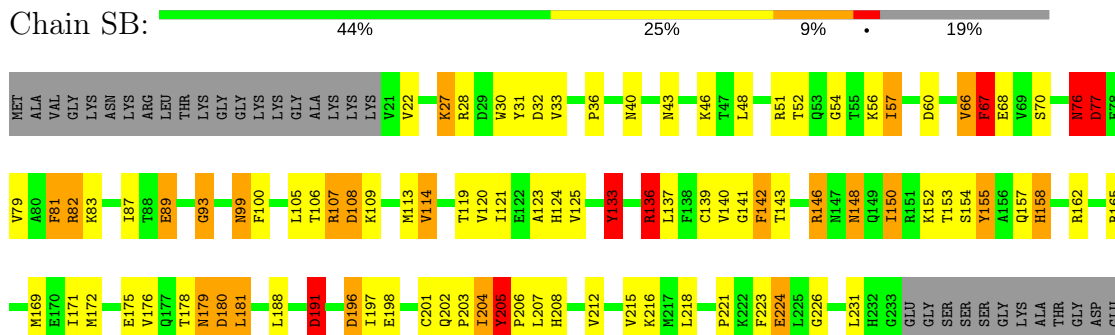
C1416	C1352	A1291	C1231	C1109	A1049	A987	C927	G867	U806	A679	A619	U557	C497	G436
C1417	A1353	C1292	U1232	G1110	A1050	C988	G928	G868	G807		G620	U558	C498	G437
C1418	G1354	A1293	G1233	U1111	G1051	C989	G929	A869	A808	U682	G621	G559	C499	G438
C1419	C1355	A1173	C1234	U1112	A1052	A990	G930	A870	A809		G622	A860	A500	A439
G1420	G1356	U1295	G1235	A1113	C1053	G991	C931	U871	G684	G684	G623	C501	C501	C440
G1421	A1357	U1296	G1236	U1114	G1054	A992	G932	A872	A811	A685	G624	U562	C502	C441
G1422	U1358	U1297	C1237	U1115	A1055	G993	G933	G873	A812	U686	G625	G563	C503	C442
C1423		G1298	U1238	C1116	U1056	C994	G934	G874	A813	C587	G626	A564	G504	U443
C1424	U1362	A1299	U1239	C1117	C1057	G995	G935	A975	U814		U627		G505	U444
G1425	C1363	U1300	A1240	C1118	A1058	A996	G936	C976	U815	U688	A628	C567	G506	A445
G1426	U1364	A1301	C1180	A1119	G1059	A997	C937	C977	A816	U689	A629	G569	G507	A446
C1427	G1365	G1302	U1242	U1120	A1060	A998	A938	G878	G817	G691	U630	A569	A508	A447
G1428	C1366	C1303	U1243	G1121	U1061	G999	U939	C879	A818	G692	U631	C570	G509	A448
G1429	U1367	U1304	U1244	A1122	A1062	C1000	U940	G880	G819	A693	C632	U571	G510	A449
C1430	U1368	C1305	G1245	C1123	C1063	A1001	C941	G881	U820		C633	U572	U511	C450
G1431	U1369	U1306	A1246	C1124	C1064	U1002	G942	U882	C694	C695	G634	U573	A512	G451
C1432	A1370	U1307	C1247	C1125	G1065	U1003	U943	G883	U822	G696	G635	A574	G513	G452
C1433	U1371	U1308	U1248	G1126	U1066	U1004	A944	C884	U823	G697	G636	A575	U514	G453
C1434	U1372	C1309	C1249	C1127	C1067	G1005	U945	U885	C824	G698	U637	A576	G515	U454
C1435	C1373	U1310	A1250	C1128	G1068	C1006	U946	A886	A825	C730	C638	U577	A516	A455
C1436	C1374	A1251	A1251	G1129	U1069	C1007	G947	U887	A826	G731	C639	C578	C517	C456
C1437	G1375	C1312	C1252	G1130	U1070	U1008	C948	U888	A827	U732	A640	C579	G518	C457
A1438	A1376	A1313	A1253	G1131	G1071	U1009	G949	U889	G828	C733	A641	U580	A519	A458
A1439	U1377	U1314	C1254	C1132	U1072	C950	C950	U890	C829	C734	U642	U581	A520	C459
C1440	A1378	U1315	G1255	A1133	U1073	U1013	C951	G891	A830	C735	A643	C582	A521	A460
U1441	A1379	C1316	G1256	G1134	C1074	U1014	G952	U892	G831	C736	G644	C583	A522	U461
C1442	C1380	C1317	G1257	C1135	C1075	U1015	C953	U893	C833	G737	C645	C584	A523	C462
C1443	G1381	G1318	A1258	U1136	G1076	U1016	U954	G894	C834		C646	C585	U524	C463
A1446	A1382	U1319	A1259	U1137	A1077	A955	U955	G895	C835	C739	U647	A525	A464	A464
G1447	C1383	G1320	A1260	C1138	C1078	U1018	G956	U896	C836	G744	A648	A526	A465	A465
A1448	G1384	G1321	C1261	U1139	C1079	C1019	A957	U897	G836	C745	U649	C527	G466	G466
G1449	C1385	G1322	C1262	G1140	A1080	A1020	C958	U898	A837	C746	A650	A590	A598	A467
G1450	A1386	U1323	U1263	G1141	U1081	U1021	G959	U899	G838	U747	U651	U591	A468	A468
G1451	A1387	G1324	C1264	C1142	A1082	U1022	U960	C900	C839	C748	U652	C592	U530	A469
A1452	A1388	G1325	A1265	A1143	A1083	A1023	G961	G901	C840	U749	A653	C593	A531	G470
U1452		U1326	C1266	A1144	A1084	A1024	A962	G902	G841	C750	A654	A594	C532	G471
G1453	U1327	G1327	C1267	A1145	C1085	U1025	A963	A903	C842	G751	A655	U595	A533	C472
A1454			C1268	C1146	G1086	C1026	A964	A904	C843	G752	G656	U596	G534	A473
G1455	G1330	G1330	G1269	C1147	A1087	A1027	U965	C905	U844	C753	U657	G597	G535	G474
G1456	C1331	C1331	G1270	A1148	U1088	A1028	U966	U906	G845	C785	U658	G598	A536	C475
U1457	A1396	G1211	C1271	A1149	C1089	G1029	C967	G907	G846	C786	G659	A599	C537	A476
G1458	U1397	G1333	C1272	A1150	C1090	A1030	U968	A908	A847	G787	C660	G600	U638	G477
G1459	G1398	G1334	G1273	G1151	C1091	A1031	U969	G909	U848	G788	U661	G601	C539	G478
C1460	C1399	G1335	G1274	U1152	G1092	C1032	G970	G910	A849	G789	G662	G602	U540	C479
G1461	U1400	C1336	G1275	C1153	A1093	G1033	G971	C911	C850	C790	C663	C603	U541	G480
U1462	A1401	C1337	A1276	U1154	C1094	A1034	A972	C912	C851	C791	A664	A604	U542	C481
U1463	A1402	G1338	C1277	U1155	U1095	A1035	C973	A913	G852	C792	G665	A605	C543	G482
C1464	C1403	U1339	A1278	U1156	G1096	A1036	C974	U914	C853	G793	U666	G606	G544	C483
A1465	U1404	U1340	C1279	G1157	G1097	G1037	G975	G915	A854	A794	U667	U607	A545	A484
A1405	A1405	C1341	G1280	G1158	C1098	U1038	G976	A916	G855	A795	A668	C608	G546	
G1406	G1406	U1342	G1281	G1159	G1099	C1039	C977	U917	C856	C796	A669	U609	G547	U487
U1407	U1407	U1343	A1282	U1160	A1100	G1040	C978	U918	U857	C797	A670	G610	C548	U488
U1408	U1408	A1344	C1283	U1161	U1101	G1041	C979	A919	A858	A798	A671	G611	C549	A489
A1409	G1345	G1345	A1284	C1162	G1102	A1042	A980	A920	G859	U799	A672	U612	C550	C490
C1410	C1410	U1346	G1285	C1163	G1103	G1043	A981	G921	G860	U800	G673	G613	U551	C491
G1411	U1347	G1286	G1286	G1164	G1104	G1044	G982	A922	A861	U801	G674	C514	G552	C492
C1412	C1412	A1287	A1287	G1165	G1105	U1045	A983	G923	A862	A802	U675	C515	U553	A493
G1413	G1413	U1288	U1288	G1166	C1106	U1046	C984	G924	C903	C903	C676	A616	A554	C494
A1414	A1414	U1289	U1289	G1167	G1107	U1047	G985	G925	U804	U804	C677	G617	A555	U495
U1477	C1415	G1351	G1290	C1168	G1108	G1048	G986	A926	A864	U805	U678	C618	U556	C496



- Molecule 50: Ribosomal protein uS2



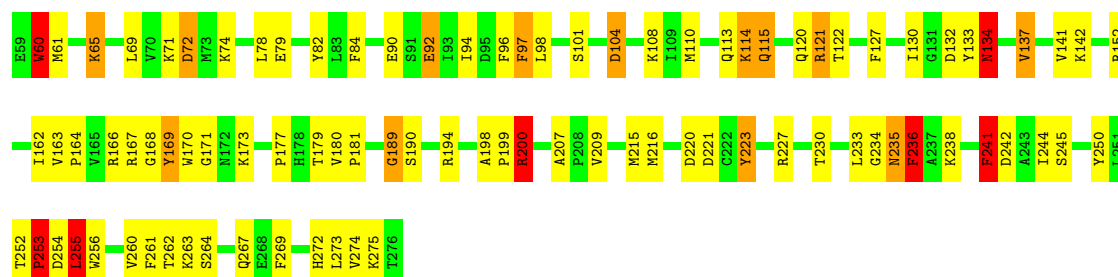
- Molecule 51: Ribosomal protein eS1



THR  
GLY  
ALA  
LYS  
VAL  
GLU  
ARG  
ALA  
ASP  
GLY  
TYR  
GLU  
PRO  
PRO  
VAL  
GLN  
GLU  
SER  
VAL

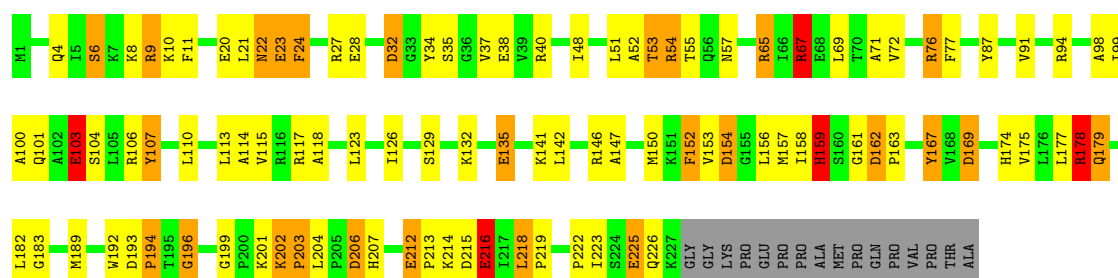
• Molecule 52: Ribosomal protein uS5

Chain SC:  58% 33% 6%



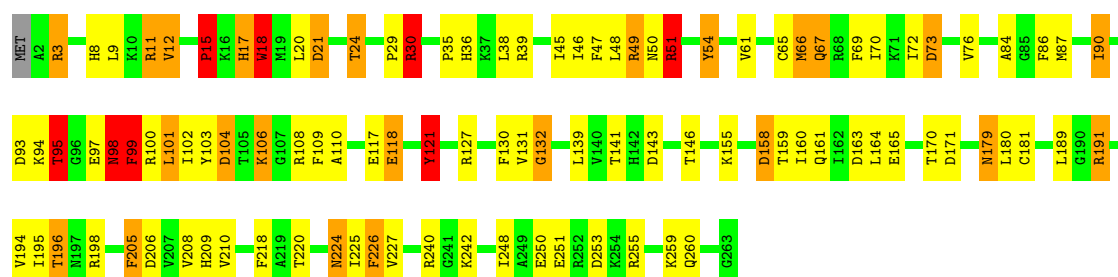
• Molecule 53: Ribosomal protein uS3

Chain SD:  51% 29% 11% 7%



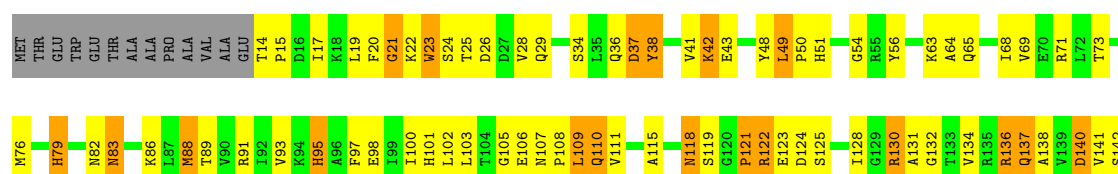
• Molecule 54: Ribosomal protein eS4

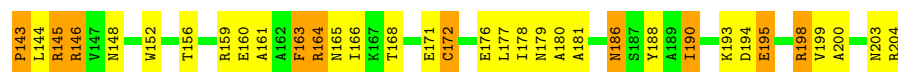
Chain SE:  60% 27% 9%



• Molecule 55: Ribosomal protein uS7

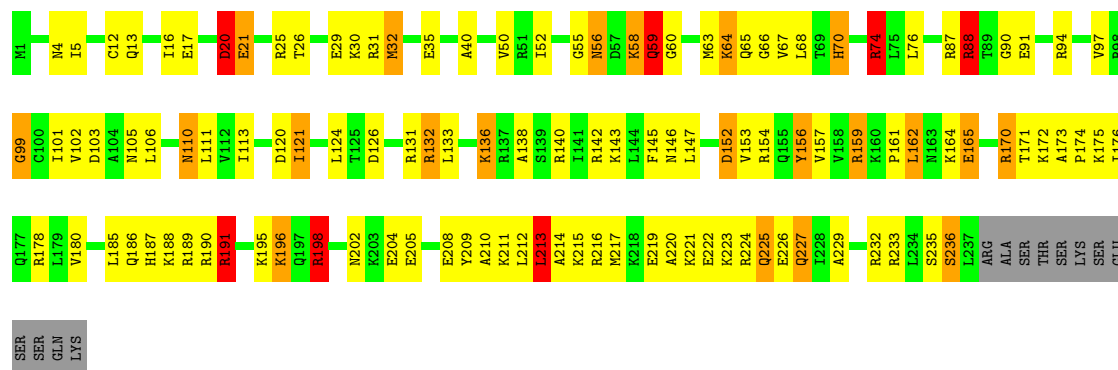
Chain SF:  40% 39% 14% 6%





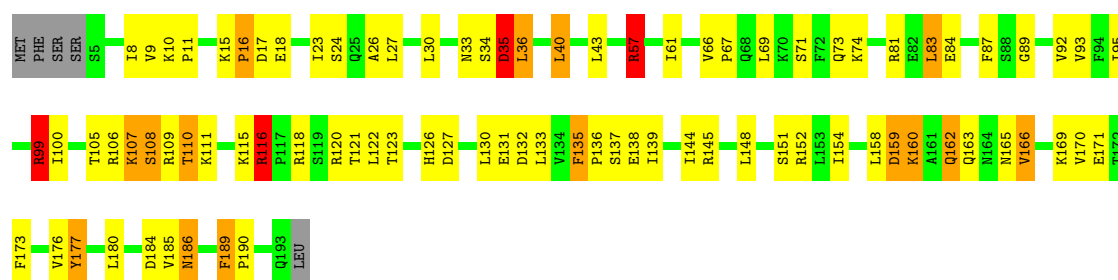
• Molecule 56: Ribosomal protein eS6

Chain SG: 48% 36% 8% 5%



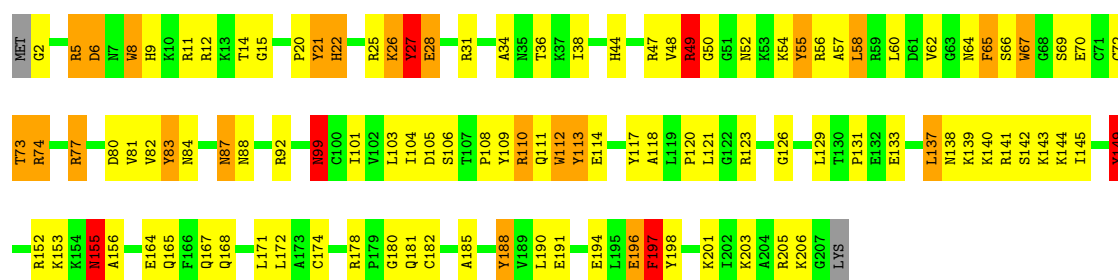
• Molecule 57: Ribosomal protein eS7

Chain SH: 53% 35% 8% . .



• Molecule 58: Ribosomal protein eS8

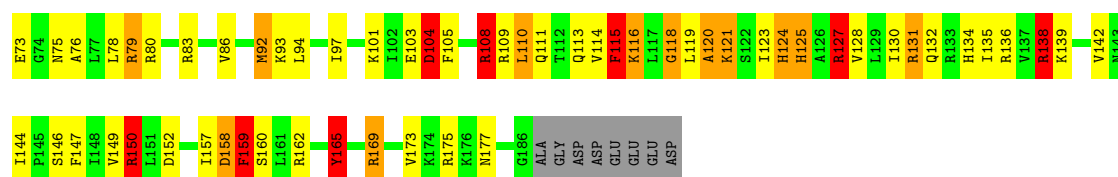
Chain SI: 46% 39% 11% . .



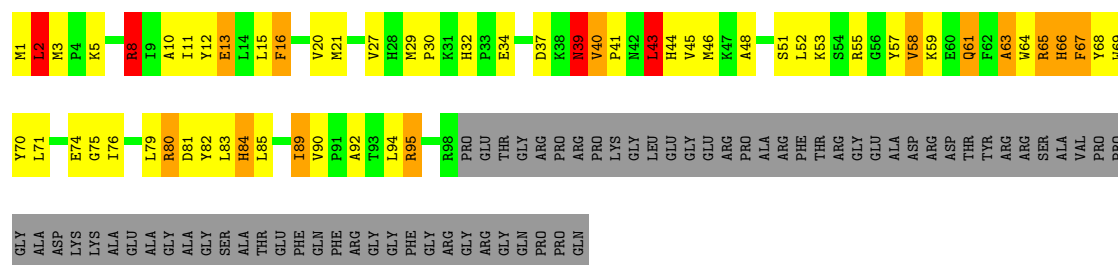
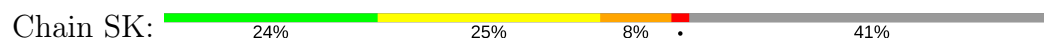
• Molecule 59: Ribosomal protein uS4

Chain SJ: 45% 33% 10% 7% 5%

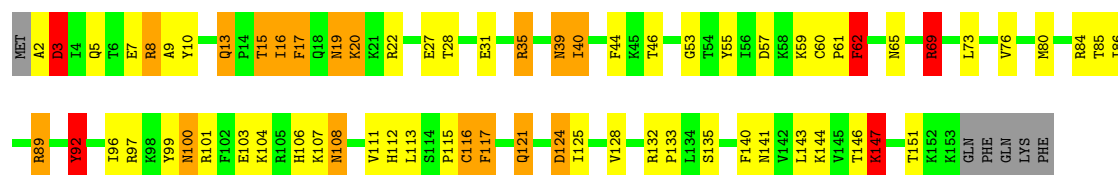




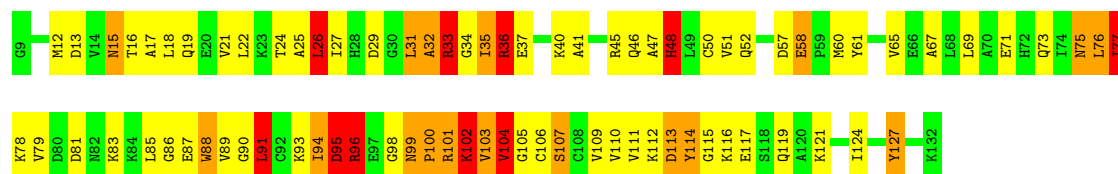
- Molecule 60: Ribosomal protein eS10



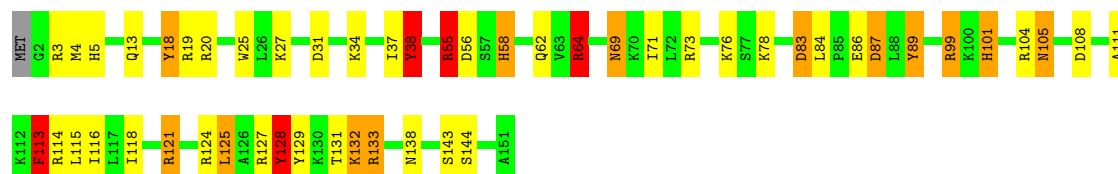
- Molecule 61: Ribosomal protein uS17



- Molecule 62: Ribosomal protein eS12

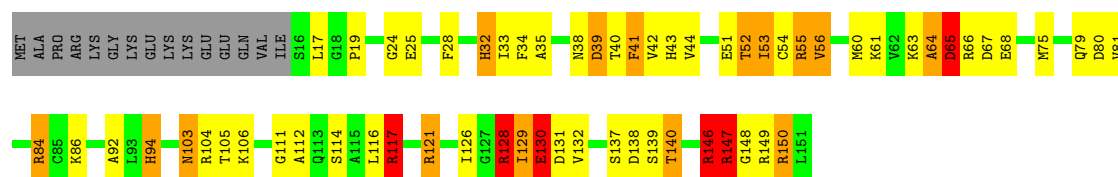


- Molecule 63: Ribosomal protein uS15

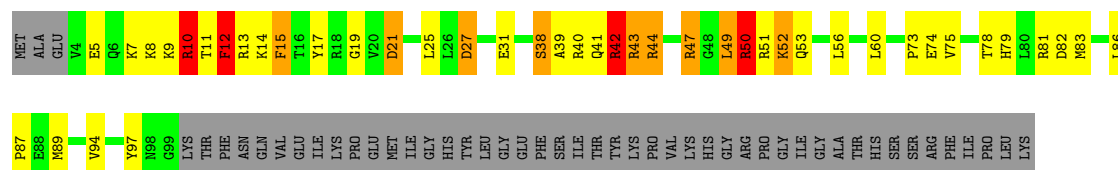


- Molecule 64: Ribosomal protein uS11

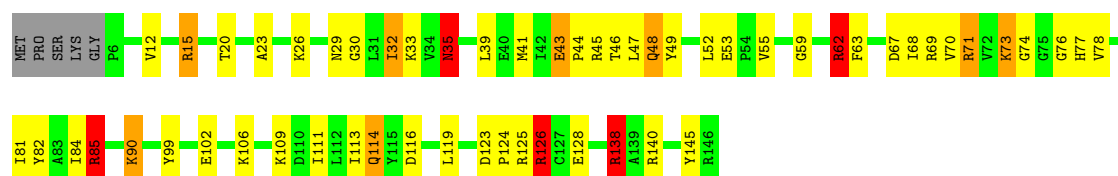




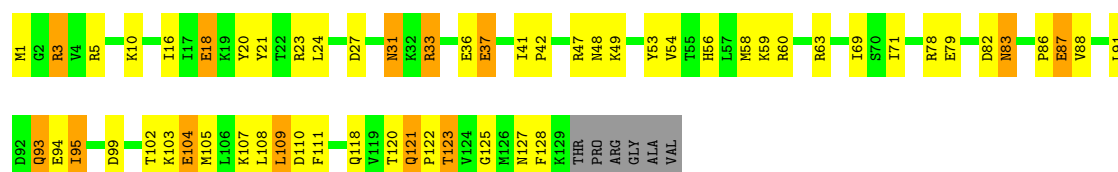
• Molecule 65: Ribosomal protein uS19



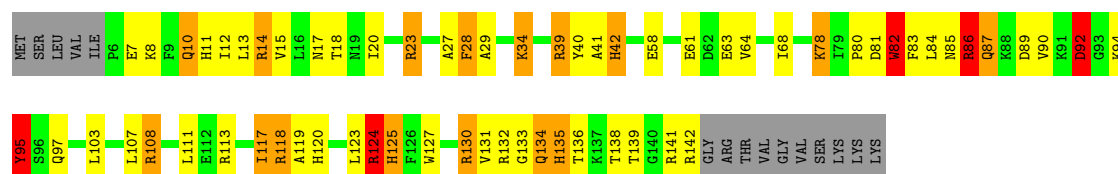
• Molecule 66: Ribosomal protein uS9



• Molecule 67: Ribosomal protein eS17



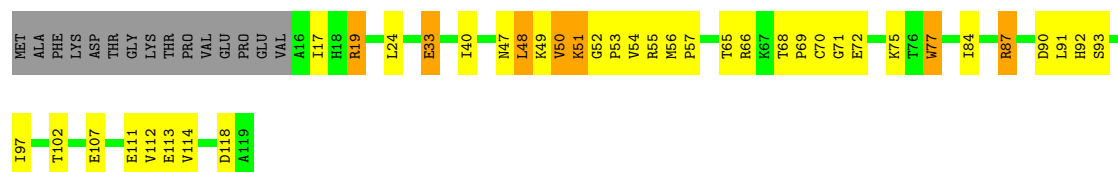
• Molecule 68: Ribosomal protein uS13



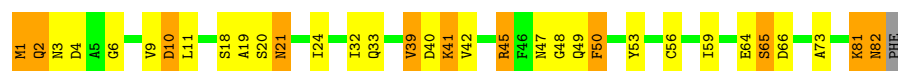
• Molecule 69: Ribosomal protein eS19



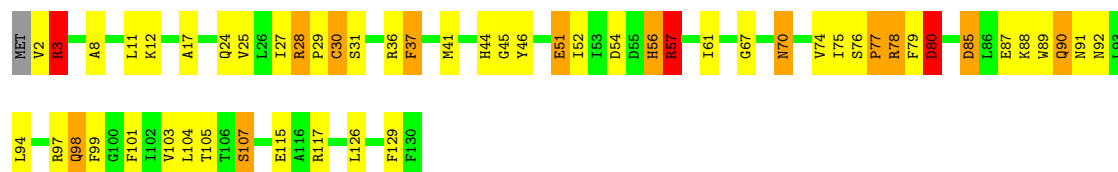
- Molecule 70: Ribosomal protein uS10



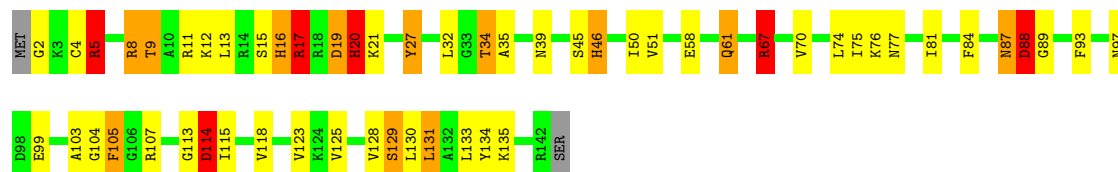
- Molecule 71: Ribosomal protein eS21



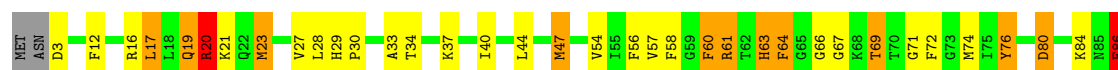
- Molecule 72: Ribosomal protein uS8



- Molecule 73: Ribosomal protein uS12

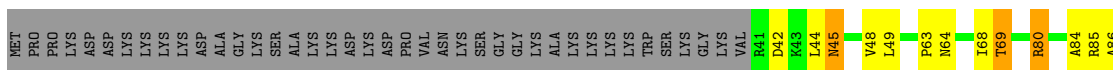


- Molecule 74: Ribosomal protein eS24





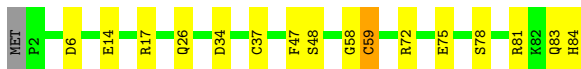
- Molecule 75: Ribosomal protein es25



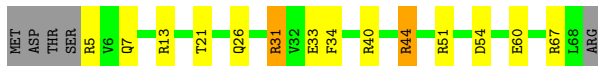
- Molecule 76: Ribosomal protein eS26



- Molecule 77: Ribosomal protein eS27



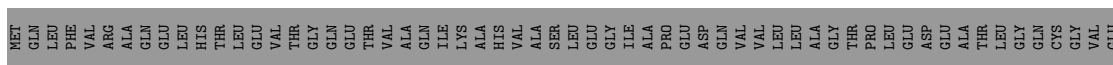
- Molecule 78: Ribosomal protein eS28



- Molecule 79: Ribosomal protein uS14

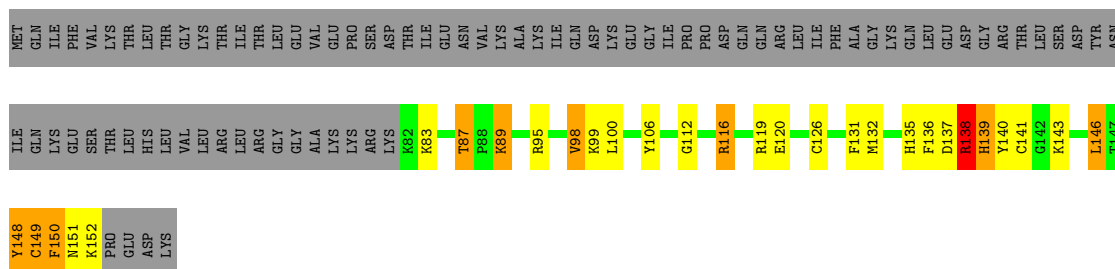


- Molecule 80: Ribosomal protein eS30



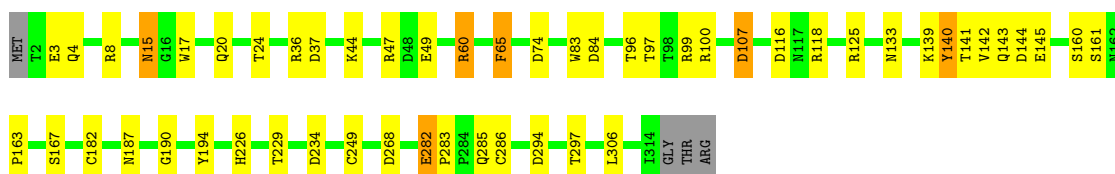
- Molecule 81: Ribosomal protein eS31

Chain Sf:



- Molecule 82: Ribosomal protein RACK1

Chain Sg:



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	36667	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	104478	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	0.64	75/87792 (0.1%)	1.12	729/136945 (0.5%)
10	G	0.76	4/1966 (0.2%)	1.09	14/2645 (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	12/2343 (0.5%)
13	J	0.63	1/1382 (0.1%)	1.04	12/1849 (0.6%)
14	K	1.04	11/1154 (1.0%)	1.78	54/1555 (3.5%)
15	L	0.70	2/1734 (0.1%)	1.12	15/2318 (0.6%)
16	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
17	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
18	O	0.72	3/1684 (0.2%)	1.10	12/2251 (0.5%)
19	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
2	7	0.54	1/2858 (0.0%)	0.96	9/4455 (0.2%)
20	Q	0.69	0/1530	1.35	31/2041 (1.5%)
21	R	0.79	3/1524 (0.2%)	1.27	20/2013 (1.0%)
22	S	0.95	8/1493 (0.5%)	1.30	19/2002 (0.9%)
23	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
24	U	0.63	1/822 (0.1%)	1.03	3/1103 (0.3%)
25	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
26	W	0.71	0/541	1.23	5/720 (0.7%)
27	X	0.64	0/993	1.09	10/1334 (0.7%)
28	Y	0.72	0/1132	1.24	19/1504 (1.3%)
29	Z	0.63	0/1130	1.11	10/1507 (0.7%)
3	8	0.68	3/3701 (0.1%)	1.19	42/5766 (0.7%)
30	a	0.93	6/1192 (0.5%)	1.37	17/1591 (1.1%)
31	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
32	c	0.70	0/742	1.14	5/996 (0.5%)
33	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)
34	e	0.90	3/1071 (0.3%)	1.23	15/1429 (1.0%)
35	f	1.01	2/895 (0.2%)	1.34	17/1198 (1.4%)
36	g	0.65	0/916	1.08	5/1220 (0.4%)
37	h	0.63	0/1023	1.21	14/1350 (1.0%)
38	i	0.63	0/843	1.20	8/1115 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)
4	A	0.80	3/1906 (0.2%)	1.26	21/2556 (0.8%)
40	k	0.59	0/575	0.97	1/761 (0.1%)
41	l	0.70	0/454	1.14	4/599 (0.7%)
42	m	0.55	0/435	0.95	1/575 (0.2%)
43	n	0.49	0/223	1.01	0/284
44	o	0.64	0/864	1.27	8/1140 (0.7%)
45	p	0.64	1/718 (0.1%)	1.01	3/953 (0.3%)
46	q	0.81	7/1580 (0.4%)	1.35	37/2133 (1.7%)
47	r	0.68	0/1017	1.12	8/1365 (0.6%)
48	4	0.99	20/6804 (0.3%)	1.41	93/9189 (1.0%)
49	S2	0.65	37/41243 (0.1%)	1.14	330/64257 (0.5%)
5	B	0.81	8/3214 (0.2%)	1.16	25/4308 (0.6%)
50	SA	0.94	4/1679 (0.2%)	1.06	6/2283 (0.3%)
51	SB	0.89	6/1753 (0.3%)	1.15	14/2350 (0.6%)
52	SC	0.99	8/1726 (0.5%)	1.11	9/2332 (0.4%)
53	SD	1.39	12/1793 (0.7%)	1.10	9/2414 (0.4%)
54	SE	0.83	8/2118 (0.4%)	0.98	7/2849 (0.2%)
55	SF	0.74	1/1531 (0.1%)	1.08	9/2059 (0.4%)
56	SG	0.97	9/1946 (0.5%)	1.03	9/2590 (0.3%)
57	SH	0.73	2/1544 (0.1%)	1.02	8/2068 (0.4%)
58	SI	0.97	8/1715 (0.5%)	1.12	12/2287 (0.5%)
59	SJ	1.07	12/1550 (0.8%)	1.28	16/2069 (0.8%)
6	C	0.73	3/2973 (0.1%)	1.12	18/3990 (0.5%)
60	SK	0.75	1/851 (0.1%)	1.00	3/1147 (0.3%)
61	SL	0.85	5/1259 (0.4%)	1.09	7/1684 (0.4%)
62	SM	2.22	2/970 (0.2%)	1.21	8/1300 (0.6%)
63	SN	0.82	4/1232 (0.3%)	1.15	10/1656 (0.6%)
64	SO	1.18	7/1029 (0.7%)	1.38	12/1380 (0.9%)
65	SP	1.52	6/816 (0.7%)	1.29	8/1084 (0.7%)
66	SQ	0.72	2/1142 (0.2%)	1.01	8/1528 (0.5%)
67	SR	0.81	5/1060 (0.5%)	1.02	2/1421 (0.1%)
68	SS	0.66	1/1157 (0.1%)	1.18	13/1548 (0.8%)
69	ST	0.67	2/1119 (0.2%)	1.08	7/1499 (0.5%)
7	D	0.73	2/2426 (0.1%)	1.23	26/3252 (0.8%)
70	SU	0.94	4/828 (0.5%)	0.96	1/1112 (0.1%)
71	SV	0.73	0/631	0.97	0/844
72	SW	1.06	6/1051 (0.6%)	1.22	5/1406 (0.4%)
73	SX	0.99	6/1118 (0.5%)	1.12	12/1493 (0.8%)
74	SY	1.63	5/1040 (0.5%)	1.11	9/1382 (0.7%)
75	SZ	0.56	0/604	0.87	0/810
76	Sa	0.81	1/794 (0.1%)	1.25	5/1065 (0.5%)
77	Sb	0.59	0/665	0.90	0/891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
78	Sc	0.68	0/508	1.13	4/680 (0.6%)
79	Sd	0.79	0/445	1.12	1/589 (0.2%)
8	E	0.73	5/1941 (0.3%)	1.21	20/2601 (0.8%)
80	Se	0.72	1/458 (0.2%)	1.16	5/602 (0.8%)
81	Sf	1.08	6/593 (1.0%)	1.57	12/786 (1.5%)
82	Sg	0.80	11/2493 (0.4%)	0.89	8/3394 (0.2%)
9	F	0.80	2/1905 (0.1%)	1.27	27/2539 (1.1%)
All	All	0.75	379/237633 (0.2%)	1.15	2051/348088 (0.6%)

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	0	154
10	G	0	3
11	H	0	3
12	I	0	4
13	J	0	2
14	K	0	5
15	L	0	5
16	M	0	4
17	N	0	11
18	O	0	3
19	P	0	1
2	7	0	2
20	Q	0	5
21	R	0	6
22	S	0	11
23	T	0	2
24	U	0	2
25	V	0	3
26	W	0	1
27	X	0	1
28	Y	0	4
3	8	0	11
30	a	0	9
31	b	0	1
32	c	0	2
33	d	0	4
34	e	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
35	f	0	2
36	g	0	1
37	h	0	3
38	i	0	3
39	j	0	4
4	A	0	6
40	k	0	1
44	o	0	6
45	p	0	1
46	q	0	7
47	r	0	5
48	4	0	40
49	S2	1	66
5	B	0	13
50	SA	0	2
51	SB	0	4
52	SC	0	4
53	SD	0	3
54	SE	0	2
55	SF	0	1
57	SH	0	1
58	SI	0	6
59	SJ	0	2
6	C	0	5
60	SK	0	1
61	SL	0	4
62	SM	0	3
63	SN	0	1
64	SO	0	1
65	SP	0	1
66	SQ	0	1
67	SR	0	2
7	D	0	8
70	SU	0	1
71	SV	0	2
72	SW	0	2
73	SX	0	2
74	SY	0	1
75	SZ	0	1
76	Sa	0	1
77	Sb	0	1
79	Sd	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	E	0	12
81	Sf	0	4
9	F	0	5
All	All	1	507

The worst 5 of 379 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	SM	58	GLU	CD-OE1	64.43	1.96	1.25
53	SD	216	GLU	CD-OE1	43.67	1.73	1.25
1	5	1823	G	O3'-P	41.55	2.11	1.61
74	SY	86	GLU	CD-OE2	39.60	1.69	1.25
65	SP	21	ASP	CG-OD1	30.90	1.96	1.25

The worst 5 of 2051 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	4	699	GLY	CA-C-N	-32.10	46.58	117.20
48	4	699	GLY	C-N-CA	-28.33	50.88	121.70
48	4	768	GLY	O-C-N	21.39	156.93	122.70
72	SW	117	ARG	NE-CZ-NH2	-20.64	109.98	120.30
46	q	205	ASP	CA-C-N	-20.22	72.71	117.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
49	S2	1109	C	C1'

5 of 507 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	78486	0	39660	10326	0
2	7	2558	0	1296	309	0
3	8	3314	0	1683	481	0
4	A	1868	0	1959	159	0
5	B	3147	0	3280	216	0
6	C	2919	0	3100	160	0
7	D	2380	0	2412	174	0
8	E	1904	0	2055	132	0
9	F	1870	0	1996	174	0
10	G	1934	0	2086	132	0
11	H	1518	0	1601	87	0
12	I	1713	0	1752	106	0
13	J	1359	0	1389	73	0
14	K	1140	0	1189	583	0
15	L	1703	0	1818	75	0
16	M	1131	0	1209	68	0
17	N	1701	0	1749	118	0
18	O	1651	0	1786	87	0
19	P	1242	0	1269	54	0
20	Q	1506	0	1623	80	0
21	R	1508	0	1664	104	0
22	S	1454	0	1496	121	0
23	T	1298	0	1366	75	0
24	U	808	0	831	25	0
25	V	979	0	1039	53	0
26	W	528	0	541	52	0
27	X	976	0	1053	37	0
28	Y	1115	0	1205	62	0
29	Z	1107	0	1182	49	0
30	a	1163	0	1211	0	0
31	b	610	0	650	0	0
32	c	732	0	769	0	0
33	d	888	0	930	0	0
34	e	1053	0	1147	0	0
35	f	876	0	912	0	0
36	g	906	0	1002	0	0
37	h	1015	0	1149	0	0
38	i	832	0	917	0	0
39	j	706	0	743	0	0
40	k	569	0	637	0	0
41	l	444	0	483	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	m	429	0	466	0	0
43	n	222	0	261	0	0
44	o	851	0	922	0	0
45	p	708	0	760	0	0
46	q	1556	0	1604	0	0
47	r	1001	0	1062	0	0
48	4	6673	0	6737	2045	0
49	S2	36900	0	18598	5189	0
50	SA	1642	0	1646	99	0
51	SB	1725	0	1797	76	0
52	SC	1690	0	1777	66	0
53	SD	1765	0	1865	95	0
54	SE	2076	0	2177	74	0
55	SF	1509	0	1563	61	0
56	SG	1923	0	2089	97	0
57	SH	1521	0	1616	90	0
58	SI	1686	0	1772	102	0
59	SJ	1525	0	1640	95	0
60	SK	827	0	854	50	0
61	SL	1238	0	1315	57	0
62	SM	960	0	989	108	0
63	SN	1208	0	1294	55	0
64	SO	1016	0	1039	58	0
65	SP	805	0	861	25	0
66	SQ	1124	0	1193	47	0
67	SR	1047	0	1103	43	0
68	SS	1139	0	1191	76	0
69	ST	1101	0	1135	69	0
70	SU	818	0	883	25	0
71	SV	625	0	628	19	0
72	SW	1034	0	1080	48	0
73	SX	1099	0	1166	64	0
74	SY	1023	0	1090	54	0
75	SZ	598	0	656	16	0
76	Sa	781	0	830	0	0
77	Sb	651	0	672	0	0
78	Sc	506	0	536	0	0
79	Sd	434	0	427	0	0
80	Se	452	0	494	0	0
81	Sf	581	0	599	0	0
82	Sg	2436	0	2393	0	0
83	Sa	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	j	1	0	0	0	0
83	m	1	0	0	0	0
83	o	1	0	0	0	0
84	4	1	0	0	0	0
84	5	118	0	0	0	0
84	7	5	0	0	0	0
84	8	4	0	0	0	0
84	P	1	0	0	0	0
84	S2	36	0	0	0	0
84	V	1	0	0	0	0
All	All	221686	0	166619	21521	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 61.

The worst 5 of 21521 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:4:753:GLU:HA	48:4:782:PHE:CE1	1.25	1.71
48:4:236:PHE:CE2	48:4:273:PHE:CZ	1.79	1.71
10:G:261:LEU:CD2	10:G:264:LYS:HE2	1.21	1.66
1:5:4413:C:H4'	12:I:157:PHE:CE2	1.13	1.65
48:4:751:CYS:CB	48:4:755:VAL:HB	1.23	1.64

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	32
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	3	29
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	13
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	4
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	3	27
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	5	38
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	8	45
12	I	211/213 (99%)	166 (79%)	31 (15%)	14 (7%)	1	17
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	2	25
14	K	147/163 (90%)	83 (56%)	31 (21%)	33 (22%)	0	1
15	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	2	22
16	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	12	52
17	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	5	37
18	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	12	52
19	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	14	55
20	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	6	40
21	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	8	44
22	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	11	49
23	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	9	47
24	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	8	45
25	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	7	43
26	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	11	50
27	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	11	49
28	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	3	27
29	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	4	31
30	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	2	22
31	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	2	22
32	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	3	28
33	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	4	31
34	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	22	65
35	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	3	26
36	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	10	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	h	120/123 (98%)	102 (85%)	15 (12%)	3 (2%)	6	41
38	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	9	46
39	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	2	25
40	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	13
41	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	3	28
42	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
43	n	21/25 (84%)	21 (100%)	0	0	100	100
44	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	2	20
45	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	17	59
46	q	200/202 (99%)	133 (66%)	27 (14%)	40 (20%)	0	1
47	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	2	24
48	4	854/856 (100%)	754 (88%)	58 (7%)	42 (5%)	2	24
50	SA	206/295 (70%)	176 (85%)	24 (12%)	6 (3%)	5	38
51	SB	211/264 (80%)	170 (81%)	27 (13%)	14 (7%)	1	17
52	SC	216/218 (99%)	189 (88%)	19 (9%)	8 (4%)	4	32
53	SD	225/243 (93%)	170 (76%)	44 (20%)	11 (5%)	2	24
54	SE	260/263 (99%)	202 (78%)	41 (16%)	17 (6%)	1	18
55	SF	189/204 (93%)	160 (85%)	19 (10%)	10 (5%)	2	22
56	SG	235/249 (94%)	194 (83%)	35 (15%)	6 (3%)	6	40
57	SH	187/194 (96%)	143 (76%)	29 (16%)	15 (8%)	1	12
58	SI	204/208 (98%)	176 (86%)	21 (10%)	7 (3%)	4	35
59	SJ	183/194 (94%)	145 (79%)	24 (13%)	14 (8%)	1	13
60	SK	96/165 (58%)	60 (62%)	26 (27%)	10 (10%)	0	7
61	SL	150/158 (95%)	122 (81%)	21 (14%)	7 (5%)	3	26
62	SM	122/124 (98%)	77 (63%)	25 (20%)	20 (16%)	0	2
63	SN	148/151 (98%)	115 (78%)	28 (19%)	5 (3%)	4	35
64	SO	134/151 (89%)	102 (76%)	18 (13%)	14 (10%)	0	7
65	SP	94/145 (65%)	65 (69%)	18 (19%)	11 (12%)	0	6
66	SQ	139/146 (95%)	112 (81%)	21 (15%)	6 (4%)	3	28
67	SR	127/135 (94%)	95 (75%)	24 (19%)	8 (6%)	1	18
68	SS	135/152 (89%)	104 (77%)	23 (17%)	8 (6%)	2	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	ST	139/145 (96%)	116 (84%)	17 (12%)	6 (4%)	3	28
70	SU	102/119 (86%)	80 (78%)	18 (18%)	4 (4%)	3	31
71	SV	80/83 (96%)	63 (79%)	10 (12%)	7 (9%)	1	10
72	SW	127/130 (98%)	112 (88%)	11 (9%)	4 (3%)	5	37
73	SX	139/143 (97%)	116 (84%)	18 (13%)	5 (4%)	4	33
74	SY	124/132 (94%)	92 (74%)	23 (18%)	9 (7%)	1	14
75	SZ	73/125 (58%)	54 (74%)	13 (18%)	6 (8%)	1	11
76	Sa	96/115 (84%)	74 (77%)	15 (16%)	7 (7%)	1	14
77	Sb	81/84 (96%)	61 (75%)	15 (18%)	5 (6%)	2	19
78	Sc	62/69 (90%)	46 (74%)	16 (26%)	0	100	100
79	Sd	50/56 (89%)	38 (76%)	9 (18%)	3 (6%)	2	19
80	Se	55/133 (41%)	40 (73%)	14 (26%)	1 (2%)	10	48
81	Sf	69/156 (44%)	39 (56%)	21 (30%)	9 (13%)	0	5
82	Sg	311/317 (98%)	250 (80%)	45 (14%)	16 (5%)	2	23
All	All	12341/13747 (90%)	10066 (82%)	1613 (13%)	662 (5%)	4	22

5 of 662 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	108	GLU

### 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	4
5	B	335/335 (100%)	265 (79%)	70 (21%)	1	7

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	h	109/110 (99%)	92 (84%)	17 (16%)	3	18
38	i	86/89 (97%)	71 (83%)	15 (17%)	2	13
39	j	73/73 (100%)	60 (82%)	13 (18%)	2	12
40	k	64/65 (98%)	52 (81%)	12 (19%)	2	9
41	l	47/48 (98%)	39 (83%)	8 (17%)	2	14
42	m	48/116 (41%)	34 (71%)	14 (29%)	0	3
43	n	22/24 (92%)	17 (77%)	5 (23%)	1	5
44	o	92/94 (98%)	70 (76%)	22 (24%)	1	4
45	p	74/74 (100%)	61 (82%)	13 (18%)	2	12
46	q	170/170 (100%)	133 (78%)	37 (22%)	1	6
47	r	109/109 (100%)	86 (79%)	23 (21%)	1	7
48	4	728/728 (100%)	586 (80%)	142 (20%)	1	8
50	SA	174/245 (71%)	141 (81%)	33 (19%)	2	9
51	SB	194/231 (84%)	164 (84%)	30 (16%)	3	18
52	SC	184/184 (100%)	148 (80%)	36 (20%)	1	8
53	SD	190/202 (94%)	163 (86%)	27 (14%)	4	22
54	SE	224/225 (100%)	180 (80%)	44 (20%)	1	8
55	SF	161/170 (95%)	128 (80%)	33 (20%)	1	7
56	SG	207/218 (95%)	171 (83%)	36 (17%)	2	13
57	SH	169/174 (97%)	149 (88%)	20 (12%)	6	29
58	SI	178/180 (99%)	148 (83%)	30 (17%)	2	14
59	SJ	161/168 (96%)	128 (80%)	33 (20%)	1	7
60	SK	89/136 (65%)	68 (76%)	21 (24%)	1	4
61	SL	136/142 (96%)	116 (85%)	20 (15%)	3	20
62	SM	104/104 (100%)	76 (73%)	28 (27%)	0	3
63	SN	130/131 (99%)	101 (78%)	29 (22%)	1	5
64	SO	106/119 (89%)	83 (78%)	23 (22%)	1	6
65	SP	88/130 (68%)	73 (83%)	15 (17%)	2	14
66	SQ	117/121 (97%)	100 (86%)	17 (14%)	4	21
67	SR	117/121 (97%)	102 (87%)	15 (13%)	5	25
68	SS	119/132 (90%)	97 (82%)	22 (18%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	ST	112/115 (97%)	89 (80%)	23 (20%)	1	7
70	SU	94/107 (88%)	84 (89%)	10 (11%)	8	35
71	SV	66/67 (98%)	53 (80%)	13 (20%)	1	8
72	SW	112/113 (99%)	93 (83%)	19 (17%)	2	14
73	SX	113/115 (98%)	97 (86%)	16 (14%)	4	22
74	SY	108/114 (95%)	86 (80%)	22 (20%)	1	7
75	SZ	66/103 (64%)	55 (83%)	11 (17%)	2	14
76	Sa	85/98 (87%)	76 (89%)	9 (11%)	8	35
77	Sb	75/76 (99%)	64 (85%)	11 (15%)	3	20
78	Sc	57/62 (92%)	43 (75%)	14 (25%)	1	4
79	Sd	45/48 (94%)	35 (78%)	10 (22%)	1	6
80	Se	46/105 (44%)	35 (76%)	11 (24%)	1	4
81	Sf	64/140 (46%)	45 (70%)	19 (30%)	0	3
82	Sg	272/275 (99%)	242 (89%)	30 (11%)	7	33
All	All	10721/11706 (92%)	8570 (80%)	2151 (20%)	4	8

5 of 2151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	b	7	HIS
44	o	99	ARG
72	SW	56	HIS
32	c	66	LEU
36	g	66	ARG

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

Mol	Chain	Res	Type
30	a	66	ASN
42	m	109	ASN
72	SW	82	GLN
31	b	12	GLN
34	e	126	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3645/3664 (99%)	1616 (44%)	0
2	7	119/120 (99%)	31 (26%)	0
3	8	155/156 (99%)	61 (39%)	0
49	S2	1716/1742 (98%)	745 (43%)	0
All	All	5635/5682 (99%)	2453 (43%)	0

5 of 2453 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

There are no RNA pucker outliers to report.

## 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 ⓘ

There are no chain breaks in this entry.