



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Dec 8, 2019 – 09:07 PM EST

PDB ID : 4D5Y
EMDB ID: : EMD-2810
Title : Cryo-EM structures of ribosomal 80S complexes with termination factors and cricket paralysis virus IRES reveal the IRES in the translocated state
Authors : Muhs, M.; Hilal, T.; Mielke, T.; Skabkin, M.A.; Sanbonmatsu, K.Y.; Pestova, T.V.; Spahn, C.M.T.
Deposited on : 2014-11-07
Resolution : 9.00 Å(reported)
Based on PDB ID : 4CXD

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

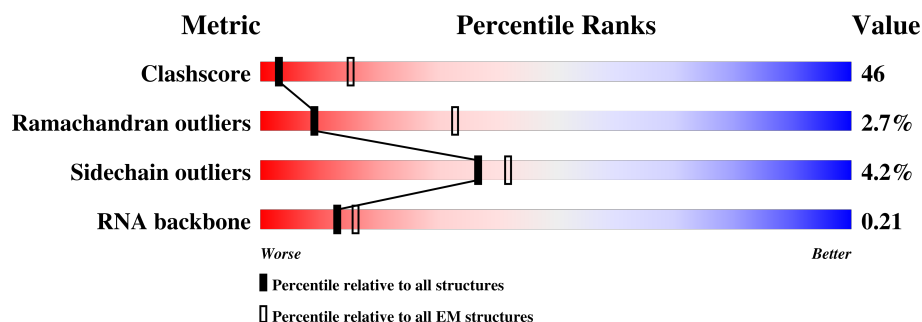
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 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.






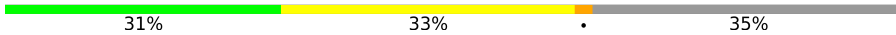


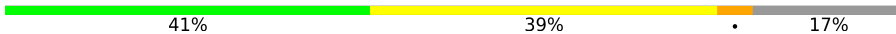










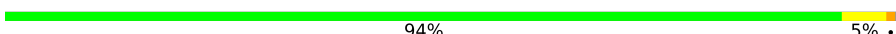






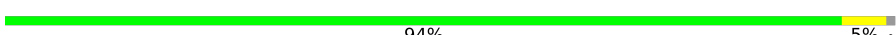
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	257	57% 38% . .
2	B	403	57% 36% 5% .
3	C	427	45% 35% 5% . 15%
4	D	297	55% 40% . .
5	E	288	23% 28% . 45%
6	F	248	52% 40% . 6%
7	G	266	50% 35% . . 12%
8	H	192	56% 41% .



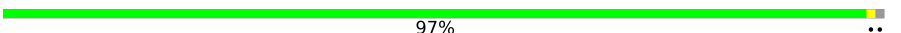


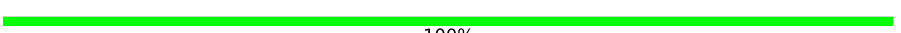







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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	215	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	159	
28	c	115	
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	

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Mol	Chain	Length	Quality of chain
34	i	105	 83% 8% • 8%
35	j	97	 84% • 12%
36	k	70	 97% ••
37	l	51	 94% ••
38	m	128	 38% • 59%
39	n	25	 100%
40	o	106	 93% 7%
41	p	92	 93% 5% •
42	t	137	 86% 7% • 5%
43	u	210	 92% 8%
44	2	5025	 7% 28% 36% • 28%
45	3	194	 7% 38% 35% • 19%
46	4	119	 13% 34% 52% •

2 Entry composition

There are 46 unique types of molecules in this entry. The entry contains 136495 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S RIBOSOMAL PROTEIN UL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	247	Total	C	N	O	S	0	1
			1888	1183	388	311	6		

- Molecule 2 is a protein called 60S RIBOSOMAL PROTEIN UL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	396	Total	C	N	O	S	0	1
			3190	2030	601	545	14		

- Molecule 3 is a protein called 60S RIBOSOMAL PROTEIN UL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	364	Total	C	N	O	S	0	1
			2889	1817	578	480	14		

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN UL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	290	Total	C	N	O	S	0	0
			2361	1489	431	427	14		

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN EL6.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	158	Total	C	N	O	0	0
			1286	834	238	214		

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN UL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	234	Total	C	N	O	S	0	0
			1949	1252	376	312	9		

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN EL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	235	Total	C	N	O	S	0	1
			1881	1197	363	317	4		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN UL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	192	Total	C	N	O	S	0	0
			1535	965	286	278	6		

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN UL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	196	Total	C	N	O	S	0	0
			1604	1022	308	262	12		

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN UL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN EL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	200	Total	C	N	O	S	0	1
			1617	1013	335	265	4		

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN EL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	140	Total	C	N	O	S	0	1
			1139	730	219	183	7		

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN EL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	204	Total	C	N	O	S	0	0
			1708	1077	360	266	5		

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN UL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	196	Total	C	N	O	S	0	1
			1607	1034	316	252	5		

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN UL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	1
			1234	771	241	213	9		

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN EL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	184	Total	C	N	O	S	0	0
			1493	933	311	244	5		

- Molecule 17 is a protein called 60S RIBOSOMAL PROTEIN UL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	183	Total	C	N	O	S	0	1
			1526	943	331	242	10		

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN EL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	173	Total	C	N	O	S	0	0
			1438	916	280	232	10		

- Molecule 19 is a protein called 60S RIBOSOMAL PROTEIN EL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1297	823	252	216	6		

- Molecule 20 is a protein called 60S RIBOSOMAL PROTEIN EL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	102	Total	C	N	O	S	0	1
			827	529	146	150	2		

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN UL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	128	Total	C	N	O	S	0	0
			963	610	181	167	5		

- Molecule 22 is a protein called 60S RIBOSOMAL PROTEIN EL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	64	Total	C	N	O	S	0	1
			529	337	104	85	3		

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN UL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	119	Total	C	N	O	S	0	0
			975	624	183	167	1		

- Molecule 24 is a protein called 60S RIBOSOMAL PROTEIN UL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	128	Total	C	N	O	S	0	1
			1065	668	217	177	3		

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN EL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	136	Total	C	N	O	S	0	0
			1114	719	209	182	4		

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN UL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1161	736	237	185	3		

- Molecule 27 is a protein called 60S RIBOSOMAL PROTEIN EL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	69	Total	C	N	O	S	0	1
			560	344	123	90	3		

- Molecule 28 is a protein called 60S RIBOSOMAL PROTEIN EL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	104	Total	C	N	O	S	0	1
			802	508	142	145	7		

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN EL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	109	Total	C	N	O	S	0	0
			904	570	174	158	2		

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN EL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	1
			1053	664	219	165	5		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN EL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	107	Total	C	N	O	S	0	0
			865	550	172	140	3		

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN EL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	115	Total	C	N	O	S	0	1
			907	566	188	147	6		

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN UL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1014	641	205	167	1		

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN EL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	97	Total	C	N	O	S	0	1
			783	488	168	122	5		

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN EL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	85	Total	C	N	O	S	0	1
			690	423	153	109	5		

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN EL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			568	366	103	98	1		

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN EL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			443	281	98	63	1		

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN EL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			428	266	90	66	6		

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN EL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN EL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	106	Total	C	N	O	S	0	0
			870	547	176	140	7		

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN EL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			707	445	136	119	7		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN EL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	t	130	Total	C	N	O	S	0	1
			1043	646	220	172	5		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN UL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	u	210	Total	C	N	O	S	0	0
			1621	990	278	347	6		

- Molecule 44 is a RNA chain called 28S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2	3616	Total	C	N	O	P	0	0
			77488	34508	14153	25212	3615		

- Molecule 45 is a RNA chain called 5.8S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	3	157	Total	C	N	O	P	0	0
			3334	1489	587	1102	156		

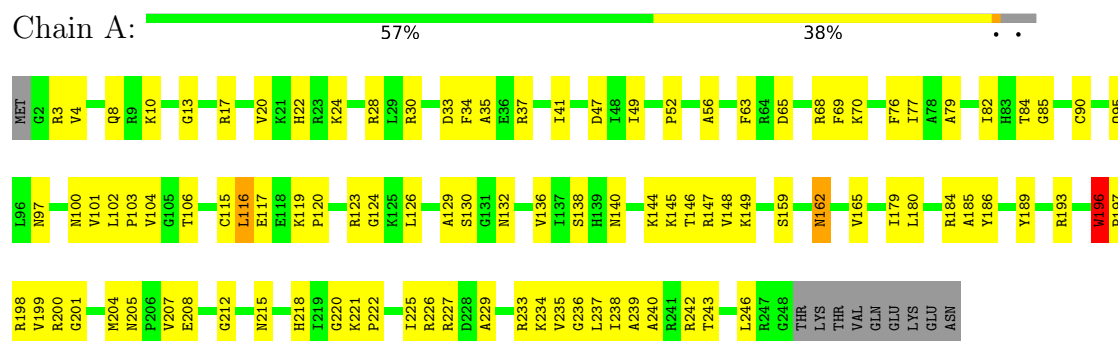
- Molecule 46 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	4	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

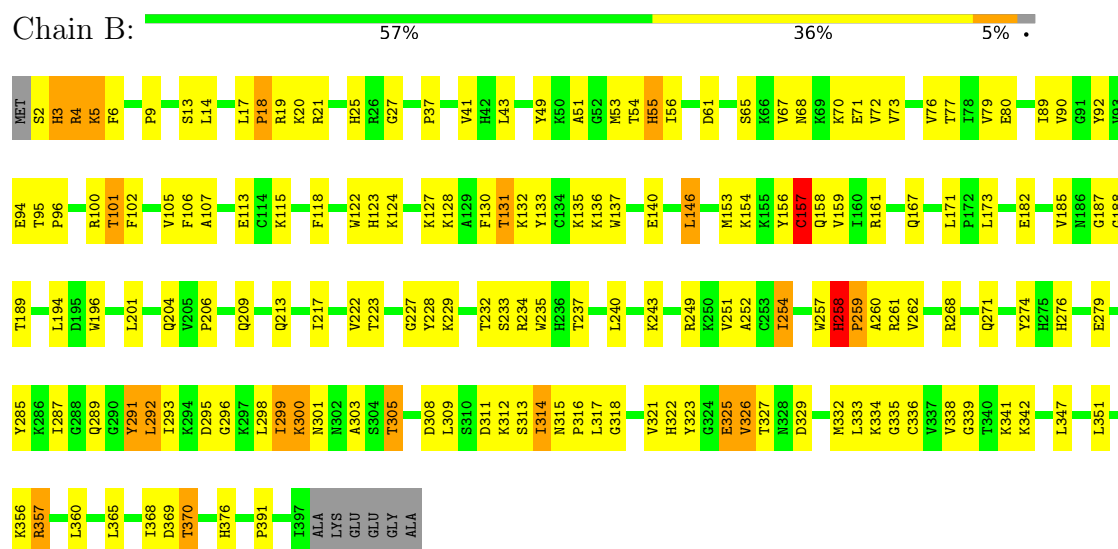
3 Residue-property plots

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.

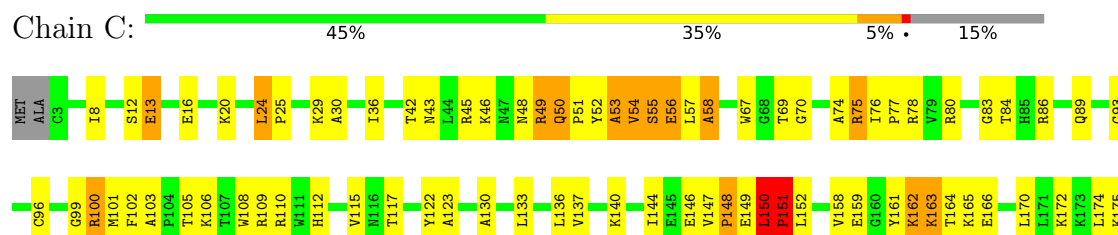
• Molecule 1: 60S RIBOSOMAL PROTEIN UL2

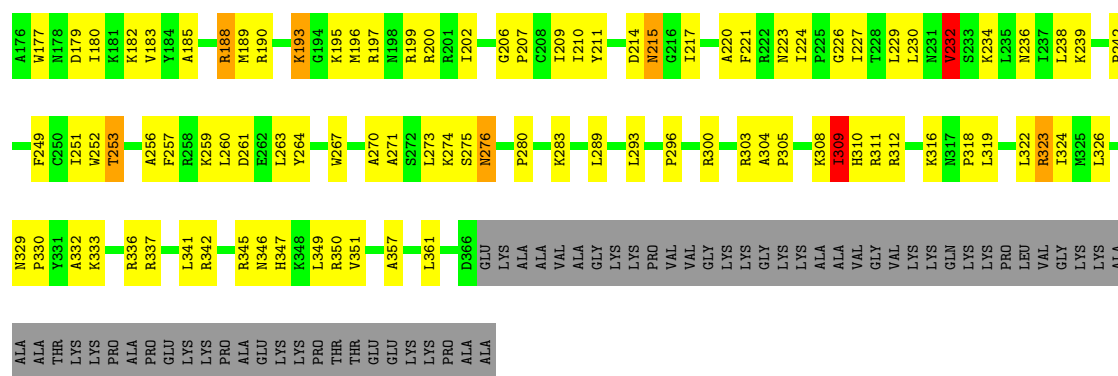


• Molecule 2: 60S RIBOSOMAL PROTEIN UL3

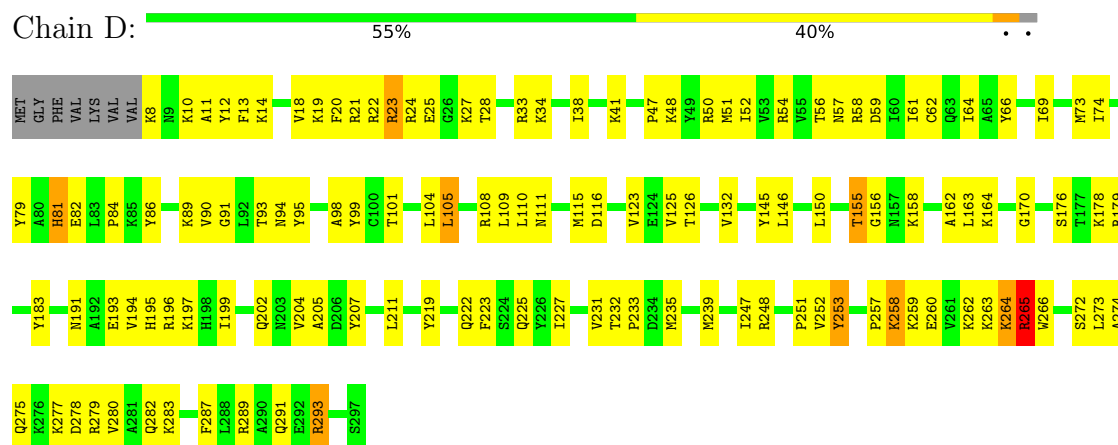


• Molecule 3: 60S RIBOSOMAL PROTEIN UL4

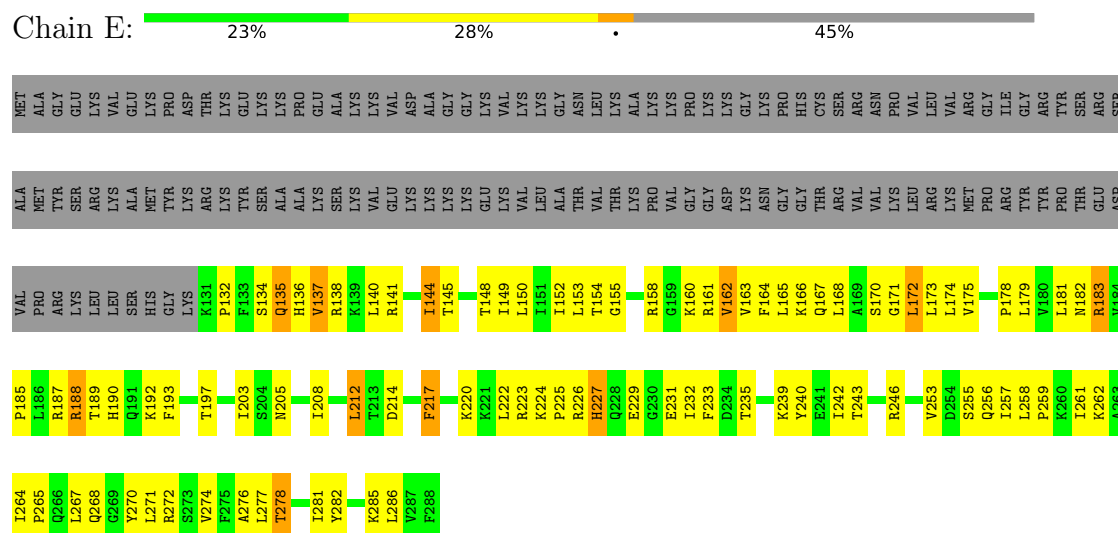




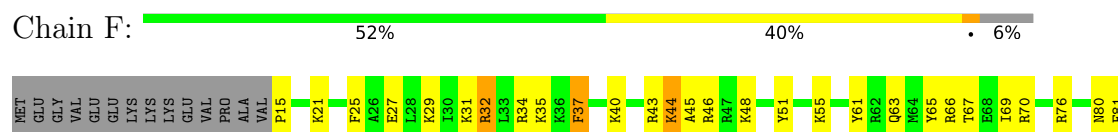
• Molecule 4: 60S RIBOSOMAL PROTEIN UL18

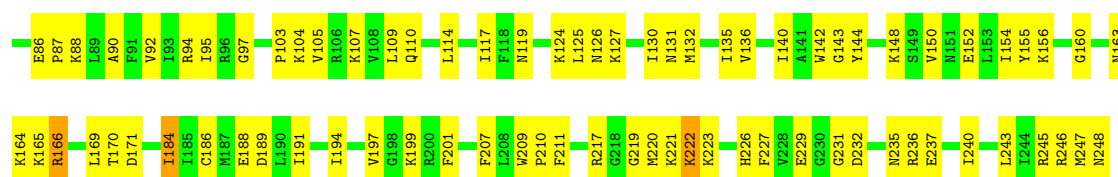


• Molecule 5: 60S RIBOSOMAL PROTEIN EL6

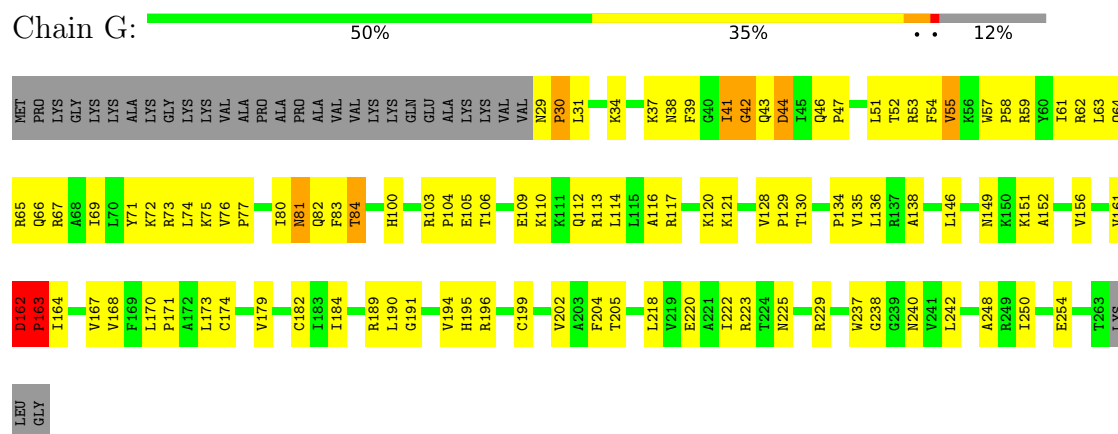


• Molecule 6: 60S RIBOSOMAL PROTEIN UL30

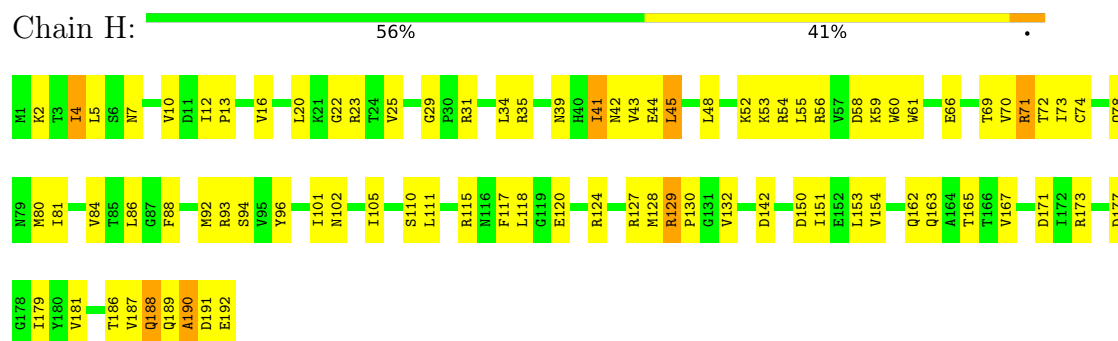




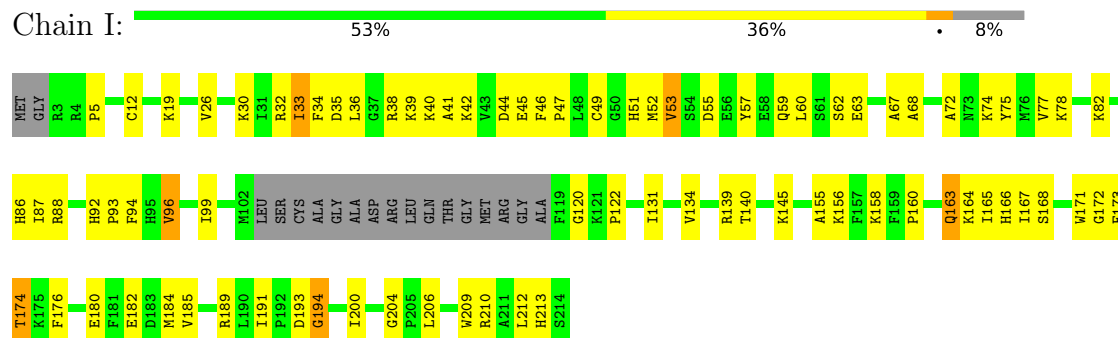
• Molecule 7: 60S RIBOSOMAL PROTEIN EL8



• Molecule 8: 60S RIBOSOMAL PROTEIN UL6

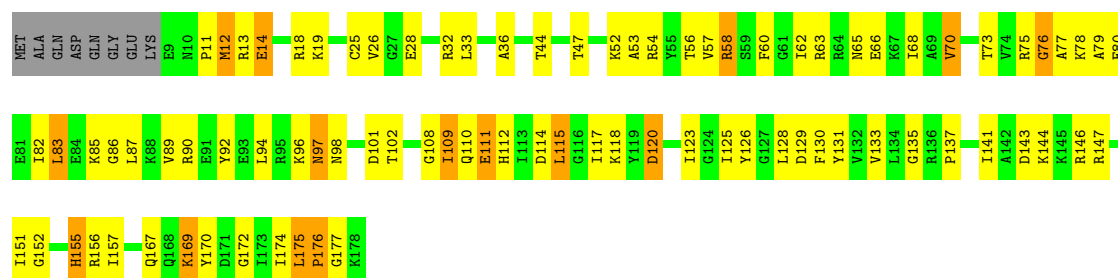


• Molecule 9: 60S RIBOSOMAL PROTEIN UL16



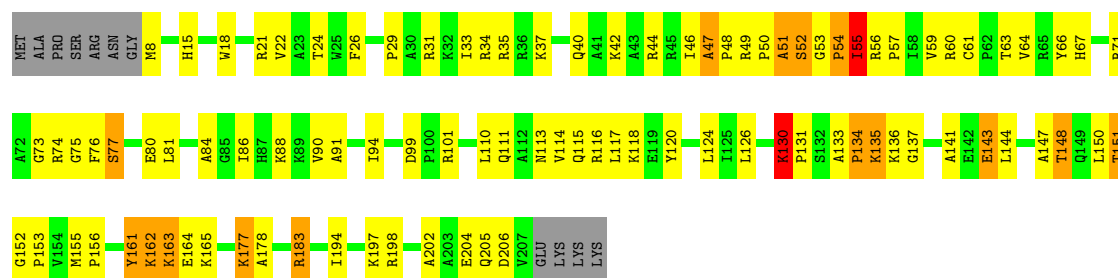
• Molecule 10: 60S RIBOSOMAL PROTEIN UL5





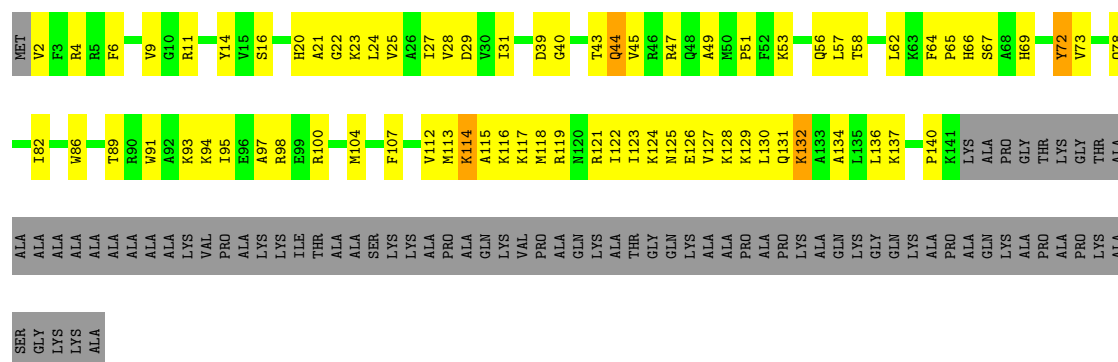
• Molecule 11: 60S RIBOSOMAL PROTEIN EL13

Chain L: 50% 37% 7% 5%



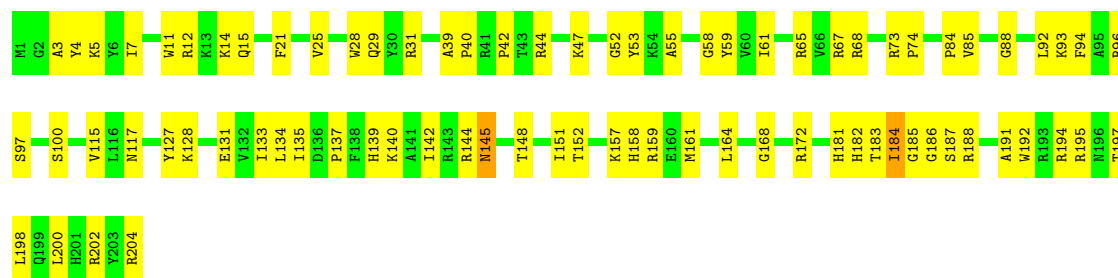
• Molecule 12: 60S RIBOSOMAL PROTEIN EL14

Chain M: 31% 33% 35%



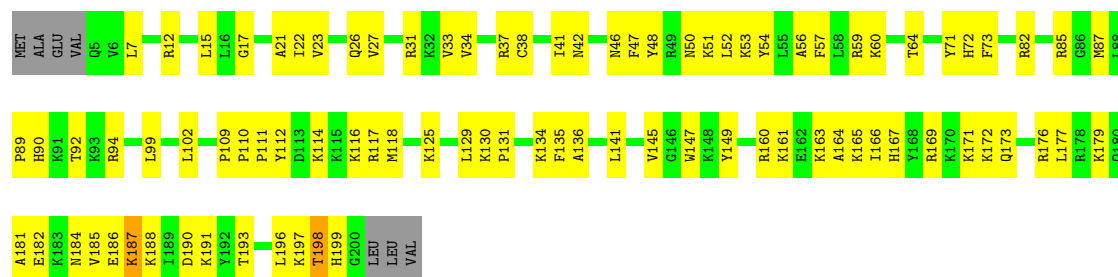
• Molecule 13: 60S RIBOSOMAL PROTEIN EL15

Chain N: 61% 38%



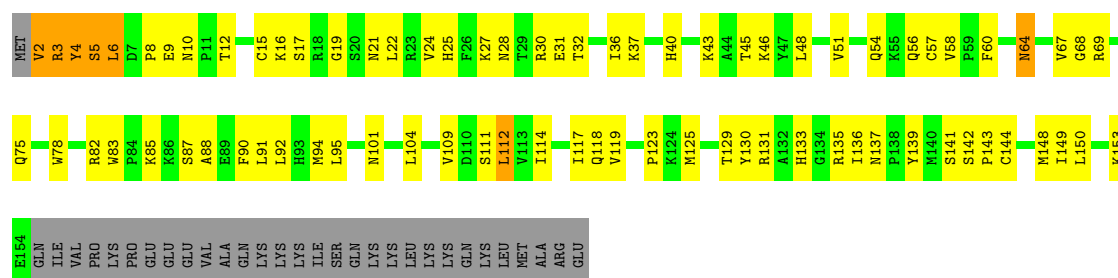
• Molecule 14: 60S RIBOSOMAL PROTEIN UL13

Chain O: 



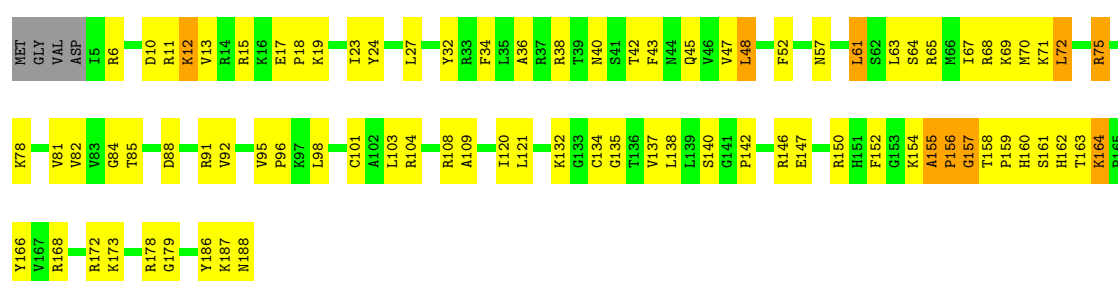
• Molecule 15: 60S RIBOSOMAL PROTEIN UL22

Chain P: 



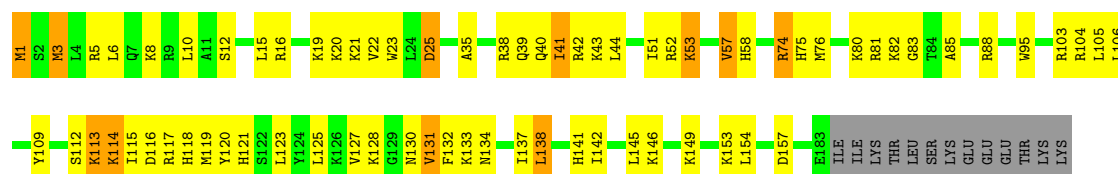
• Molecule 16: 60S RIBOSOMAL PROTEIN EL18

Chain Q: 



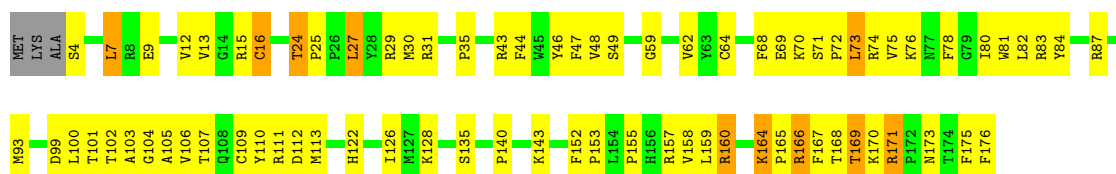
• Molecule 17: 60S RIBOSOMAL PROTEIN UL19

Chain R: 



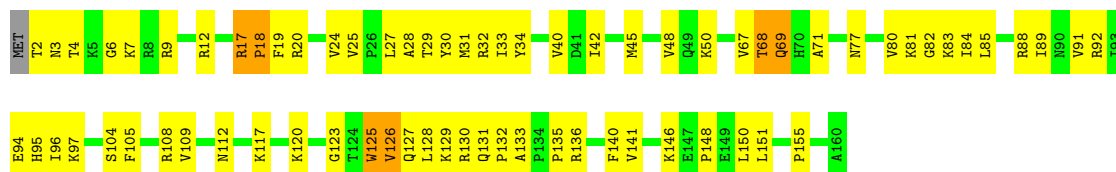
• Molecule 18: 60S RIBOSOMAL PROTEIN EL20

Chain S: 



• Molecule 19: 60S RIBOSOMAL PROTEIN EL21

Chain T: 55% 41% . .



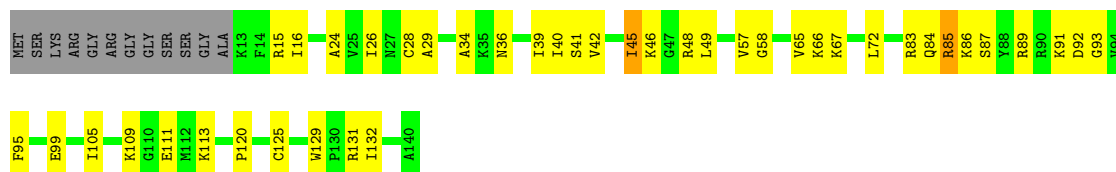
• Molecule 20: 60S RIBOSOMAL PROTEIN EL22

Chain U: 53% 26% . 20%



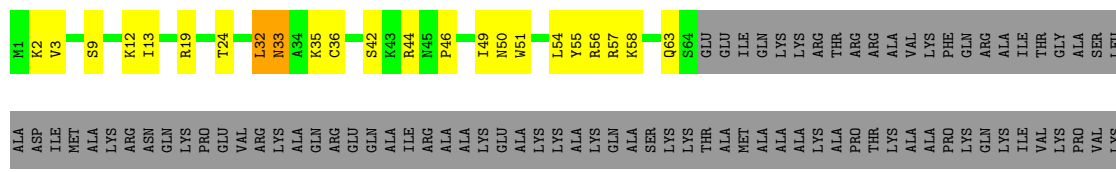
• Molecule 21: 60S RIBOSOMAL PROTEIN UL14

Chain V: 61% 29% . 9%



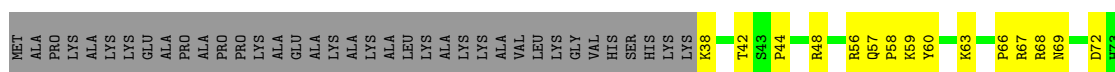
• Molecule 22: 60S RIBOSOMAL PROTEIN EL24

Chain W: 26% 13% . 59%



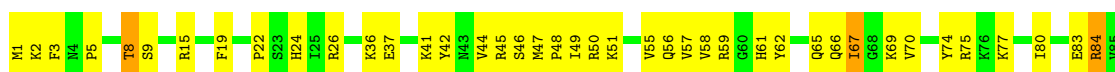
• Molecule 23: 60S RIBOSOMAL PROTEIN UL23

Chain X: 46% 30% 24%



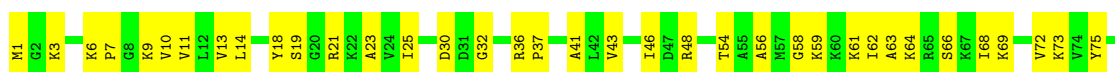
• Molecule 24: 60S RIBOSOMAL PROTEIN UL24

Chain Y:  42% 42% 0 12%



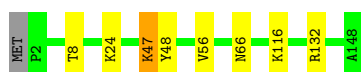
• Molecule 25: 60S RIBOSOMAL PROTEIN EL27

Chain Z:  54% 45%



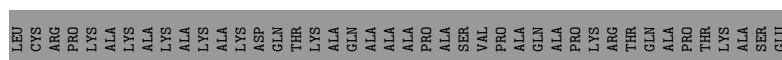
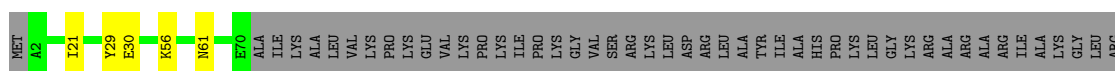
• Molecule 26: 60S RIBOSOMAL PROTEIN UL15

Chain a: 94% 5% ..

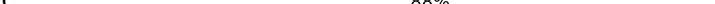


• Molecule 27: 60S RIBOSOMAL PROTEIN EL29

Chain b:  40% 5% 55%



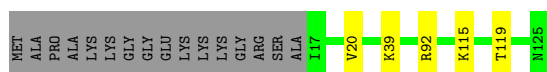
• Molecule 28: 60S RIBOSOMAL PROTEIN EL30

Chain c:  88% • 10%



• Molecule 29: 60S RIBOSOMAL PROTEIN EL31

Chain d: 83% • 13%



- Molecule 30: 60S RIBOSOMAL PROTEIN EL32

Chain e: 90% • 5%



- Molecule 31: 60S RIBOSOMAL PROTEIN EL33

Chain f: 86% 10% ••



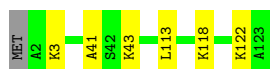
- Molecule 32: 60S RIBOSOMAL PROTEIN EL34

Chain g: 87% 10% ••



- Molecule 33: 60S RIBOSOMAL PROTEIN UL29

Chain h: 94% • 5%



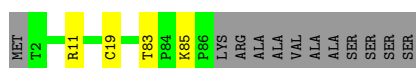
- Molecule 34: 60S RIBOSOMAL PROTEIN EL36

Chain i: 83% 8% • 8%



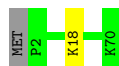
- Molecule 35: 60S RIBOSOMAL PROTEIN EL37

Chain j: 84% • 12%



- Molecule 36: 60S RIBOSOMAL PROTEIN EL38

Chain k: 97% ••



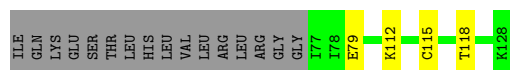
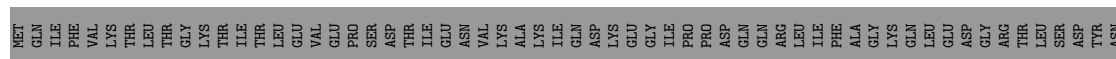
- Molecule 37: 60S RIBOSOMAL PROTEIN EL39

Chain l:  94%



- Molecule 38: 60S RIBOSOMAL PROTEIN EL40

Chain m:  38% 59%



- Molecule 39: 60S RIBOSOMAL PROTEIN EL41

Chain n:  100%

There are no outlier residues recorded for this chain.

- Molecule 40: 60S RIBOSOMAL PROTEIN EL44

Chain o:  93% 7%




- Molecule 41: 60S RIBOSOMAL PROTEIN EL43

Chain p:  93% 5%



- Molecule 42: 60S RIBOSOMAL PROTEIN EL28

Chain t:  86% 7% 5%

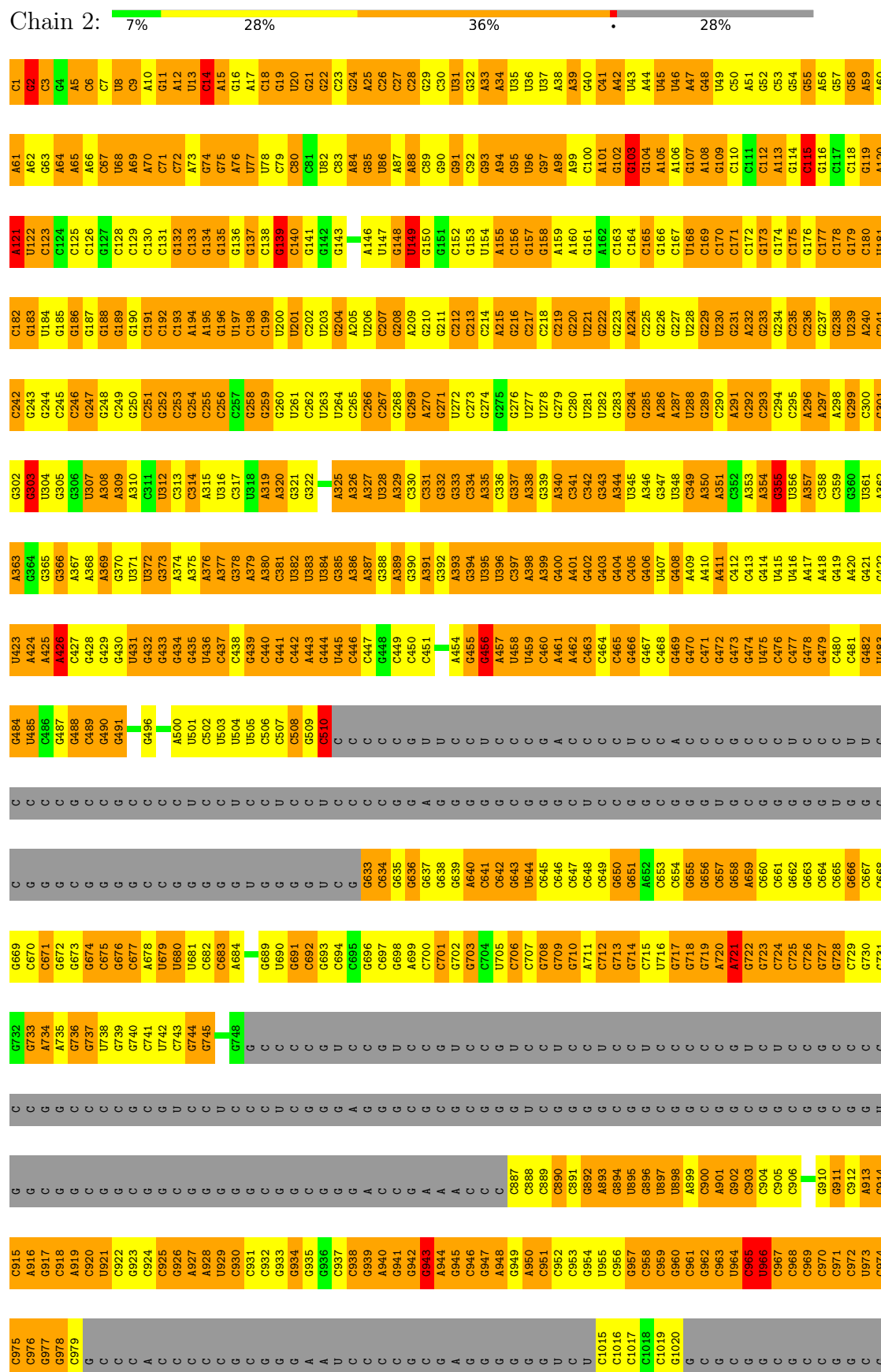


- Molecule 43: 60S RIBOSOMAL PROTEIN UL1

Chain u:  92% 8%



- Molecule 44: 28S Ribosomal RNA



G	C1893	G1829	C1769	U1707	A1647	C1586	C1525	G1463	C1402	G1341	C1279	C1219	G1158	C1096
C	C1894	U1830	C1770	A1648	G1587	A1526	C1464	U1403	G1342	C1280	C1221	G1159	C1097	
C	A1895	C1771	U1709	C1649	U1588		C1404	C1281	C1343	C1281	C1221	C1160	C	
U	G1896	G1832	A1772	U1650	C1589		G1529	G1405	U1344	U1282	G1222	C1161	G	
U	G1897	G1833	C1710	U1651	C1590		G1530	G1406		A1283	C1223	C1162	C	
C	C1898	C1834	G1712	U1652	G1591	G1531	G1531	A1407	C1347	C1284	G1224	C1163	G	
G	C1899	C1835	U1775	C1653	A1592	A1532	A1532	U1408	A1348	C1285	G1225	A1164	C	
A	G1900	A1836	G1776	C1654	C1593	C1533	A1533	U1409	C1349	C1286	G1226	G1165	C	
A	A1901	C1837	G1777	A1715	C1655	C1594	G1534	A1410	C1350	A1287	U1227	U1166	C	
C	C1902	U1838	G1778	U1656	C1595	C1535	U1473	C1411	A1351	C1288	C1228	G1167	C	
U	G1903	U1839	A1779	C1657	G1596	C1536	G1474		A1352	C1289	C1229			
U	C1904	U1840	G1718	A1658	G1597	A1537	G1475		A1353	C1290	C1230			
G	U1905		C1719	G1659	C1598	C1538	A1476		G1354	C1291	C1231	C1170	C	
G	A1906	U1844	C1762	G1720	U1599	U1589	G1477	G1415	C1355	A1292	C1232	C1171	C	
A	A1907	A1845	A1783	A1661	A1600		C1478	G1416	C1356	C1293	G	C1172	C	
U	U1908	A1846	A1784	U1662		G1540	A1478	C1417	C1357	C1294	A	G1174	C	
U	C1909	G1847	G1785	A1663		A1541	C1480	U1418	C1358	C1295	A	G1175	G	
C	A1910	C1848	C1786	G1664		A1542	G1481	C1419	C1359	G1296	G	G1176	G	
C	G1911	A1849	C1787	G1665		A1543	C1421	U1420	C1360	U1297	A	C1177	C	
G	A1912	C1850	C1788	U1727	U1666	C1544	A1482	C1422	U1361	C1298	G1238	G1178	G	
C	C1913	G1851	G1789	A1728	G1667	C1545	A1483	C1423	G1362	C1299	G1239	G1179	A	
U	C1914	A1852	G1790	G1668	G1608	U1546	G1484	A1423	G1363	U1300	C1240	G1180	C	
C	A1915	C1853	C1791	C1669	A1609	C1547	G1485	G1424	C1364	G1301	G1241	U1181	G	
A	C1916	U1854	U1792	G1731	A1610	U1548	C1486	U1425	C1365	A1242	G1242	C1182	G	
A	G1917	G1855	C1793	G1732	A1611	G1549	A1487	C1426	G1366	A1302	C1243	G1183	G	
G	C1918	C1856	U1733	C1672	A1612	U1551	C1488	C1427	C1367	A1303	A1243	G1184	C	
G	A1919	C1857	G1794	C1673	A1613	G1552	U1490	C1428	A1367	A1304	C1244	C1185	G	
A	C1920	G1858	U1796	C1674	C1614	G1553	G1491	C1430	U1368	C1305	G1245	G1186	G	
U	C1921	C1859	G1797	U1735	U1615	U1554	U1492	G1431	C1369	G1246	C1247	C1187	G	
U	A1922	G1860	G1798	G1737	C	A1616	U1493	A1432	G1370	C1247		G1188	G	
G	C1923	G1861	C1799	G1738	C	G1617	A1494	C1433	A1371	G1308		G1189	U	
G	A1924	C1862	G1800	C1739	A1618	U1557	A1495	G1434	A1372	A1249	G1250	U1189	C	
U	U1925		G1801	G1740	C	U1558	C1496	G1435	C1373	A1251	C1250	C1190	C	
U	C1926	G1865	A1802	G1741	A	C1559	G1497	U1436	G1374	A1313	C1251	G1191	C	
A	U1927	A1866	G1803	C1742	G	G1620	C1558	G1437	U1375	A1314	C1252	G1192	C	
C	C1928	U1867	A1804	G1743	C	A1822	U1561	A1438	G1376	G1315	G1253	G1193	C	
A	G1929	G1868	A1744	C	C1823	A1562	C1500	C1439	A1377	G1316	A1254	C1194	C	
A	C1930	A1869	A1745	G	A1624	G1563	G1501	C1440	A1378	C1195	C1255	C1196	G	
C	U1931	A1870	C1807	A1746	C1625	C1564	A1502	A1441	G1380	U1318	G1257	G1197	C	
C	U1932	G1871	C1808	C1747	U1626	G1565	A1503	C1442	C1381	C1320	G1258	G1198	C	
U	C1933	C1872	G1809	G1748	C	C1627	A1504	C1443	C1382	U1321	A1259	G1199	C	
A	A1934	G1873	G1810	A1749	C	U1828	U1567	G1444	G1383	A1322	C1260	G1200	G	
C	U1935	A1874	C1811	U1750	A	A1629	C1568	G1445	G1384	A1323	G1261	G1201	C	
C	A1936	C1875	U1812	C1751	C	G1630	C1569	C1446	C1385	C1324	G1262	A1202	C	
			G1813	U1752	C	G1631	G1508	C1447	C1386	A1325	G1263	G1203	C	
			G1814	C1753	C	A1632	U1571	G1509	C1387	C1326	G1264	G1204	C	
			A1815	A1754	C	G1633	A1572	G1449	G1388	G1327	U1265	U1205	C	
			C1816	A1755	C	C1634	C1573	U1450	C1389	U1328	G1266	U1206	C	
			G	C	G	U1635	G1574	C1451	U1390	G1329	G1267	C1207	C	
			C1817	U1757	G	G1636	U1575	C1452	C1391	C1330	G1268	U1208	C	
			G1818	C1758	C	G1637	G1576	C1453	C1392	G1331	C1269	C1209	C	
			C1819	U1759	A	U1638	A1516	C1454	C1393	G1332	G1270	C1147	C	
			A1820	A1760	C	U1639	A1578	C1455	C1394	G1333	G1271	C1211	C	
			C	U1761	G	C1640	G1579	C1456	G1395	A1334	C1272	G1149	C	
			C1701	C1762	C	A1641	U1580	C1457	C1396	G1273	G1213	G1150	C	
			A1702	U1763	C	C1642	U1581	C1458	C1397	A1274	C1214		C	
			G1703	C1643	C	U1643	C1582	C1459	C1398	G1275	G1215	G1154	C	
			U1704	C1644	C	C1645	G1583	C1460	C1399	G1276	C1216	A1155	C	
			U1705	C1645	C	U1646	G1584	G1461	A1400	U1277	C1217	U1094	C	
			C1706	C1646	C	U1647	G1585	C1462	A1401	C1280	C1218	U1157	C	
			U1707	C1647	C	U1648	G1586	G1463	A1402	C1281	C1219	C1158	C	
			C1708	C1648	C	U1649	G1587	G1464	A1403	C1282	C1220	C1159	C	
			U1709	C1649	C	U1650	G1588	G1465	C1404	C1283	C1221	C1160	C	
			U1710	U1650	C	U1651	G1589	G1466	U1344	U1282	G1222	C1161	G	
			C1711	U1651	C	G1590	C1590	G1467		A1283	C1223	C1162	C	
			G1712	U1652	C	G1591	G1531	A1407	C1347	C1284	G1224	C1163	G	
			U1652	C1653	C	A1592	A1532	U1408	A1348	C1285	G1225	A1164	C	
			G1713	C1653	C	C1593	C1533	U1409	C1349	C1286	G1226	G1165	C	
			A1714	C1654	C	U1594	G1534	A1410	C1350	A1287	U1227	U1166	C	
			A1715	C1655	C	C1595	C1535	C1411	A1351	C1288	C1228	G1167	C	
			U1656	C1596	C	G1596	C1536		A1352	C1289	C1229			
			G1717	C1657	C	G1597	A1537		A1353	C1290	C1230			
			A1718	A1658	C	C1598	C1538		G1354	C1291	C1231	C1170	C	
			C1719	G1659	C	U1599	U1589		C1355	A1292	C1232	C1171	C	
			G1720	A1660	C	A1600			C1356	C1293	G	C1172	C	
			A1721	A1661	C		G1540	C1417	C1357	C1294	A	G1174	C	
			U1662		C		A1541	U1418	C1358	C1295	A	G1175	G	
			A1663		C		A1542	C1419	C1359	G1296	G	G1176	G	
			G1664		C		A1543	U1420	C1360	U1297	A	C1177	C	
			C1665		C		C1544	C1421	U1361	C1298	G1238	G1178	G	
			U1666		C		A1482	C1422	G1361	C1299	G1239	G1179	A	
			G1667		C		C1545	A1423	G1362	C1299	G1240	G1180	C	
			U1668		C		G1608	G1424	C1363	U1300	C1241	U1181	G	
			G1669		C		A1609	U1425	C1364	G1301	G1242	C1182	G	
			C1670		C		A1610	C1426	G1365	A1302	C1243	G1183	G	
			G1671		C		A1611	C1427	C1366	A1303	A1243	G1184	C	
			C1672		C		A1612	U1428	A1367	A1304	C1244	C1185	G	
			U1673		C		A1613	U1429	A1368	C1305	G1245	G1186	G	
			C1674		C		C1614	G1430	U1369	G1246	C1247	C1187	G	
			U1735		C		U1615	U1431	G1370	C1247		G1188	G	
			G1736		C		A1616	U1432	A1371	G1308		G1189	U	
			C1737		C		G1617	C1433	A1372	A1249	G1250	U1189	C	
			G1738		C		U1557	G1434	C1373	A1251	C1250	C1190	C	
			C1739		C		C1558	G1435	G1374	A1313	C1251	G1191	C	
			G1740		C		G1620	U1436	U1375	A1314	C1252	G1192	C	
			A1741		C		C1559	G1437	G1376	G1315	G1253	G1193	C	
			C1742		C		U1561	A1438	A1377	G1316	A1254	C1194	C	
			G1743		C		C1822	C1439	A1378	C1195	C1255	C1196	G	
			A1744		C		G1623	U1562	C1379	G1318	G1256	C1197	C	
			C1745		C		A1624	G1501	A1441	G1380	U1318	G1257	G1197	C
			G1746		C		C1625	A1502	C1442	C1381	C1320	G1198	C	
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			G1748		C		C1627	A1504	G1444	G1383	A1322	C1260	G1200	C
			A1749		C		U1828	U1567	G1445	G1384	A1323	G1261	G1201	C
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			C1751		C		A1632	G1570	G1449	G1388	G1327	U1265	U1205	C
			U1752		C		G1633	A1572	U1450	C1389	U1328	G1266	U1206	C
			C1753		C		C1634	C1573	C1451	U1390	G1329	G1267	C1207	C
			A1754		C		U1635	G1574	C1452	C1391	C1330	G1268	U1208	C
			G		C		G1636	U1575	C1453	C1392	G1331	C1269	C1209	C
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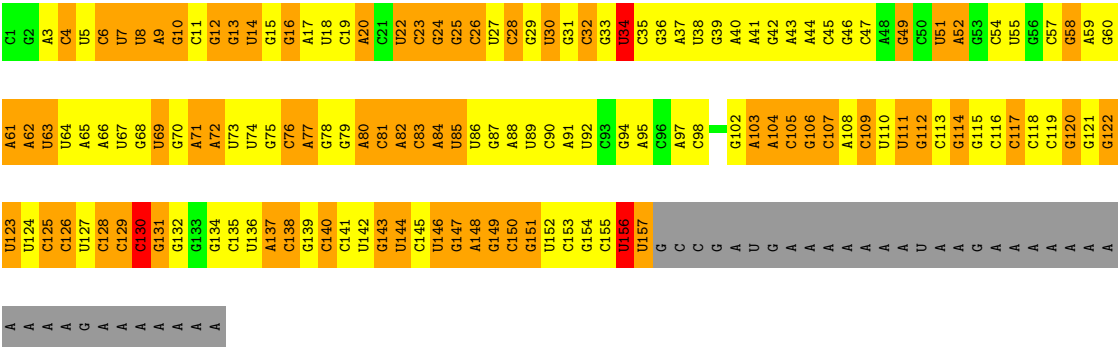
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A5017	G4948	C4883	G4823	C	A4703	U4642	C4581	A4519	U4457	U4397	G4337	A4277	A4215	G4151
G5018	G4949	C4884	G4824	C	G4704	A4643	C4582	C4520	U4458	U4398	A4338	C4278	A4216	C4152
G5019	G4950	C4885	G4825	U	G4705	U4644	G4583	C4521	U4459	U4399	A4339	C4279	G4217	C4153
U5020	G4951	U4886	G4826	C	C4706	U4645	C4584	U4522	U4460	G4400	A4340	U4280	C4218	U4154
U5021	G4952	U4887	G4827	C	U4707	C4646	C4585	U4523	U4461	A4401	A4341	U4281	C4219	G4155
U5022	U4953	C4888	G4828	A	C4708	A4647	A4586	A4524	G4462	U4402	G4342	G4282	U4220	G4156
G	U4954	C4889	G4829	C	G4709	C4648	U4587	C4525	G4465	C4403	U4343	A4283	C4221	G4157
U	U4955	G4890	G4830	G	G4710	U4649	U4588	U4526	C4466	U4404	U4344	A4284	C4222	G4158
C	U4956	G4891	U4831	C	U4711	G4650	U4589	G4527	U4467	U4405	A4345	A4285	C4223	C4159
	U4957	C4892	G4832	G	U4712	U4651	G4590	A4528	C4468	U4406	A4346	G4286	G4224	G4160
	U4958	G4893	C4833	C	U4713	U4652	U4591	U4529	U4469	C4407	C4347	C4287	U4225	G4161
	U4959	C4894	U4834	C	G4714	U4653	G4592	G4530	U4470	G4408	A4348	G4288	G4226	U4162
	U4960	G4895	C4835	C	G4715	G4654	U4593	A4531	A4471	A4409	C4349	G4289	G4227	A4163
	U4961	G4896	U4836	C	C4716	C4655	G4594	U4532	U4472	U4410	A4350	G4290	A4228	A4164
	U4962	G4897	U4837	G	U4717	U4656	U4595	G4533	U4473	G4411	G4351	G4291	G4229	A4165
	U4963	C4898	U4838	C	U4718	U4657	A4596	C4534	U4474	U4412	G4352	C4292	C4230	C4166
	C4968	C4899	G4839	C	G4719	U4658	G4597	U4535	G4475	C4413	C4353	C4293	C4231	C4167
	A4969	G4900	U4840	C	C4720	A4660	U4598	U4536	G4476	G4414	A4354	U4294	G4232	U4168
	G4970	U4901	C4841	C	A4721	A4661	G4599	U4537	A4477	G4415	U4355	C4295	A4233	G4169
	G4971	U4902	C4842	G	U4722	G4662	C4600	U4538	U4478	C4416	A4356	A4296	A4234	U4170
	G4972	C4903	U4843	G	A4723	U4663	U4601	U4539	C4479	U4417	C4357	G4297	G4235	
	A4973	G4904	G4844	G	G4724	C4664	U4602	U4540	G4480	C4418	C4358	G4298	G4236	A4173
	U4974	U4905	G4845	A	C4725	A4665	G4603	U4541	U4481	U4419	G4359	U4299	G4237	A4174
	G4975	G4906	G4846	G	C4726	G4666	G4604	C4542	G4482	U4420	G4360	U4300	C4238	A4175
	C4976	U4907	A4847	G	G4727	A4667	C4605	C4543	A4483	C4421	G4361	C4301	A4239	G4176
	U4977	G4908	A4848	G	U4728	U4668	U4606	A4544	G4484	C4422	C4362	C4302	A4240	G4177
	G4978	U4909	U4849	C	U4729	U4669	G4607	U4545	U4485	U4423	U4363	U4303	A4241	U4178
	C4979	A4910	G4850	C	C4730	C4670	U4608	G4546	U4486	A4424	U4364	U4304	A4179	A4180
	U4980	U4911	C4851	C	G4731	C4671	G4609	G4547	U4487	U4425	C4365	C4305	A4181	
	C4981	G4912	G4852	G	C4732	C4672	G4610	U4548	G4488	C4426	U4366	U4306	U4245	
	G4982	U4913	G4853	U	C4733	G4673	A4611	A4549	G4489	A4427	G4367	U4307	C4246	G4182
	U4983	G4914	U4854	G	C4734	C4674	G4612	U4550	U4490	U4428	A4368	A4308	C4247	C4183
	C4984	U4915	C4855	C	G4735	C4675	C4613	U4551	U4491	U4429	C4369	C4309	C4248	A4184
	U4985	U4916	G4856	C	C4736	C4676	G4614	C4552	U4492	G4430	C4370	C4310	U4249	G4185
	G4986	C4917	C4857	C	C4737	A4677	A4615		A4493	U4431	G4371	U4311	U4250	G4186
	C4987	A4918	G4858	C	U4738	G4678	U4616	C4556	G4494	G4432	C4372	U4312	G4251	U4187
	U4988	U4919	G4859	C	G4739	G4679	U4617	U4557	U4495	A4433	C4373	U4313	A4252	G4188
	G4989	C4920	C4860	C	U4740	C4680	G4618	C4558	C4496	A4434	A4374	U4314	U4253	U4189
	U4990	U4921	U4861	G	C4741	G4681		A4559	U4497	G4435	A4375	G4315	U4254	C4190
	U4991	G4922	G4862	G	C4742	A4682	G4621	U4561	G4498	A4437	G4376	G4316	U4255	C4191
	U4992	U4923	U4863	C	G4743	A4683	G4622	A4562	U4499	C4438	C4377	U4317	U4256	U4192
	C4993	A4924	C4864	G	C4744	C4684	G4623	C4563	G4500	G4439	C4378	U4318	U4257	A4193
	U4994	U4925	A4865	C	G4745	G4685	A4624	C4564	U4501	A4439	U4379	U4319	A4258	A4194
	U4995	G4926	U4866	C	C4746	A4686	A4625	G4565	U4502	A4440	U4380	U4320	U4259	G4195
	G4996	U4927	C4867	C	U4747	C4687	A4626	A4566	U4441	U4441	C4381	U4321	U4260	G4196
	U4997	U4928	G4868	C	G4748	A4688	G4627	U4567	U4442	A4382	A4322	U4261	U4262	C4197
	A4998	C4929	C4869	C	G4749	C4689	A4628	G4568	C4443	U4383	G4323	U4263	G4263	G4198
	G5000	U4930	G4870	C	C4750	G4690	G4629	A4569	G4444	A4384	C4324	C4263	A4267	A4203
	U4999	C4931	U4871	C	G	G4691	C4630	C4569	C4445	G4390	C4325	A4264	G4269	A4204
	C5001	G4932	G4872	G	G	C4692	C4631	A4570	C4446	C4386	A4326	G4265	C4201	
	U5002	A4933	C4873	C	G	A4693	U4632	A4571	A4447	G4387	G4327	U4266	U4202	U4202
	C5003	U4934	G4874	C	C	C4694	C4633	C4572	A4448	A4388	G4328	A4267	C4203	
	G5004	A4935	C4875	C	C	G4695	C4634	C4573	G4449	C4389	A4329	C4268	A4204	
	C5005	U4936	G4876	C	G	C4696	U4635	G4574	C4450	G4390	G4330	A4269	G4209	
	U4999	C4937	C4877	C	C	G4697	C4636	C4575	G4451	U4391	C4331	A4270	G4209	
	C5006	U4938	G4878	C	C	C4698	U4637	A4576	U4452	U4452	U4332	A4271	G4210	
	U5007	C4939	C4879	C	C	G4699	G4638	G4577	U4453	G4393	G4333	A4272	A4211	
	C5008	U4940	U4880	C	C	C4700	C4639	G4578	U4454	C4394	U4334	A4273	A4212	
	U5009	G4941	G4881	C	C	G4701	G4640	U4579	U4517	U4455	U4335	A4273	A4213	
	C5010	C4942	C4882	C	C									
	G5011	U4943	C4883	C	C									
	U5012	U4944	C4884	C	C									
	A5013	C4945	C4885	C	C									
	C5014	U4946	C4886	C	C									

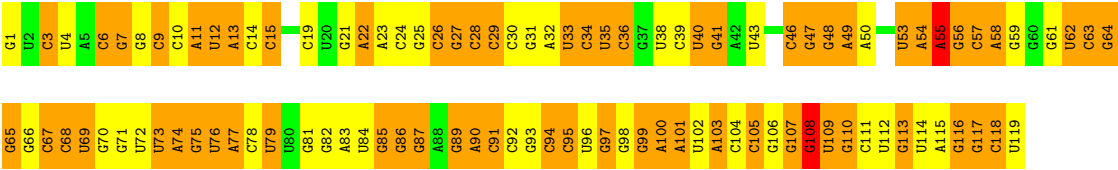
● Molecule 45: 5.8S Ribosomal RNA

Chain 3: 7% 38% 35% 19%



● Molecule 46: 5S Ribosomal RNA

Chain 4: 13% 34% 52% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	109596	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.44	0/1926	0.67	0/2583
10	J	0.49	0/1385	0.71	0/1852
11	L	0.53	2/1647 (0.1%)	0.73	3/2205 (0.1%)
12	M	0.49	0/1162	0.70	0/1556
13	N	0.43	0/1753	0.65	0/2348
14	O	0.44	0/1639	0.69	0/2193
15	P	0.44	0/1260	0.70	0/1691
16	Q	0.45	0/1517	0.74	0/2026
17	R	0.41	0/1542	0.64	0/2037
18	S	0.45	0/1478	0.73	0/1985
19	T	0.46	0/1325	0.72	0/1770
2	B	0.45	0/3258	0.73	2/4361 (0.0%)
20	U	0.47	0/841	0.71	0/1128
21	V	0.43	0/977	0.63	0/1312
22	W	0.43	0/542	0.59	0/722
23	X	0.41	0/992	0.67	0/1334
24	Y	0.47	0/1082	0.72	1/1441 (0.1%)
25	Z	0.47	0/1137	0.79	0/1517
26	a	0.45	0/1190	0.71	0/1591
27	b	0.45	0/570	0.72	0/752
28	c	0.46	0/813	0.70	0/1091
29	d	0.45	0/919	0.67	0/1238
3	C	0.47	0/2943	0.73	1/3953 (0.0%)
30	e	0.45	0/1071	0.68	0/1428
31	f	0.50	0/884	0.81	0/1185
32	g	0.48	0/917	0.74	0/1222
33	h	0.38	0/1022	0.64	0/1351
34	i	0.43	0/793	0.75	0/1048
35	j	0.49	0/704	0.76	0/931
36	k	0.43	0/574	0.73	0/761
37	l	0.40	0/453	0.61	0/599
38	m	0.42	0/434	0.70	0/575
39	n	0.40	0/240	0.50	0/305
4	D	0.49	1/2406 (0.0%)	0.70	1/3221 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	o	0.46	0/884	0.74	0/1166
41	p	0.40	0/717	0.61	0/953
42	t	0.48	0/1058	0.75	0/1416
43	u	0.45	0/1638	0.69	1/2222 (0.0%)
44	2	0.41	22/86672 (0.0%)	0.81	41/135198 (0.0%)
45	3	0.36	0/3723	0.79	1/5800 (0.0%)
46	4	0.38	0/2836	0.82	3/4421 (0.1%)
5	E	0.52	0/1311	0.73	0/1763
6	F	0.45	0/1985	0.68	0/2644
7	G	0.46	0/1914	0.72	0/2578
8	H	0.43	0/1554	0.69	0/2089
9	I	0.42	0/1642	0.67	0/2194
All	All	0.43	25/147330 (0.0%)	0.77	54/217756 (0.0%)

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
44	2	0	34
45	3	0	2
All	All	0	36

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	1701	C	C5'-C4'	18.32	1.73	1.51
44	2	1673	C	C3'-O3'	15.33	1.63	1.42
44	2	1701	C	O5'-C5'	14.40	1.67	1.44
44	2	1673	C	O3'-P	14.19	1.78	1.61
44	2	1701	C	P-O5'	13.52	1.73	1.59

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1701	C	O4'-C4'-C3'	-15.18	88.82	104.00
2	B	258	HIS	C-N-CD	-13.98	89.84	120.60
44	2	1701	C	O4'-C1'-N1	12.32	118.06	108.20
44	2	1701	C	C4'-C3'-O3'	12.21	137.41	113.00
44	2	1701	C	C2'-C3'-O3'	-10.63	86.10	109.50

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
44	2	1	C	Sidechain
44	2	115	C	Sidechain
44	2	121	A	Sidechain
44	2	149	U	Sidechain
44	2	2	G	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1888	0	1983	135	0
2	B	3190	0	3327	164	0
3	C	2889	0	3064	277	0
4	D	2361	0	2385	157	0
5	E	1286	0	1398	171	0
6	F	1949	0	2093	134	0
7	G	1881	0	2018	136	0
8	H	1535	0	1611	94	0
9	I	1604	0	1652	60	0
10	J	1362	0	1399	89	0
11	L	1617	0	1725	120	0
12	M	1139	0	1204	134	0
13	N	1708	0	1761	97	0
14	O	1607	0	1745	127	0
15	P	1234	0	1263	91	0
16	Q	1493	0	1612	119	0
17	R	1526	0	1682	75	0
18	S	1438	0	1472	85	0
19	T	1297	0	1366	115	0
20	U	827	0	852	29	0
21	V	963	0	1026	42	0
22	W	529	0	541	27	0
23	X	975	0	1053	64	0
24	Y	1065	0	1145	102	0
25	Z	1114	0	1194	62	0
26	a	1161	0	1213	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	b	560	0	590	0	0
28	c	802	0	845	0	0
29	d	904	0	947	0	0
30	e	1053	0	1144	0	0
31	f	865	0	904	0	0
32	g	907	0	1002	0	0
33	h	1014	0	1148	0	0
34	i	783	0	862	0	0
35	j	690	0	719	0	0
36	k	568	0	637	0	0
37	l	443	0	483	0	0
38	m	428	0	466	0	0
39	n	239	0	289	0	0
40	o	870	0	943	0	0
41	p	707	0	760	0	0
42	t	1043	0	1120	0	0
43	u	1621	0	1555	0	0
44	2	77488	0	39153	7457	0
45	3	3334	0	1693	312	0
46	4	2538	0	1286	274	0
All	All	136495	0	98330	9533	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 46.

The worst 5 of 9533 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)
44:2:1673:C:C3'	44:2:1673:C:O3'	1.63	1.46
44:2:1701:C:C5'	44:2:1701:C:O5'	1.67	1.39
44:2:3910:G:O2'	44:2:3911:A:H5'	1.22	1.34
1:A:196:TRP:HB3	1:A:197:PRO:CD	1.62	1.25
20:U:29:VAL:O	44:2:4022:C:O2'	186.30	1.23

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	14	56
2	B	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	4	32
3	C	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	3	29
4	D	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	10	49
5	E	156/288 (54%)	141 (90%)	8 (5%)	7 (4%)	3	28
6	F	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	10	49
7	G	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	3	30
8	H	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	11	50
9	I	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	11	50
10	J	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	18
11	L	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	2	24
12	M	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	12	52
13	N	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	11	51
14	O	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	11	51
15	P	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	8	45
16	Q	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	4	33
17	R	181/196 (92%)	174 (96%)	4 (2%)	3 (2%)	10	49
18	S	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	4	32
19	T	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	9	45
20	U	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
21	V	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	11	50
22	W	62/157 (40%)	61 (98%)	1 (2%)	0	100	100
23	X	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
24	Y	126/145 (87%)	119 (94%)	4 (3%)	3 (2%)	6	40
25	Z	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	5	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	4	33
27	b	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	2	22
28	c	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	8	45
29	d	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	19	61
30	e	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	6	40
31	f	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	2	26
32	g	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	4	32
33	h	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	6	39
34	i	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	1	21
35	j	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	6	40
36	k	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	11	51
37	l	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	8	43
38	m	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	8	45
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	9	45
41	p	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	4	33
42	t	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	2	24
43	u	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	12	52
All	All	6479/7422 (87%)	6102 (94%)	200 (3%)	177 (3%)	9	38

5 of 177 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	LYS
1	A	196	TRP
2	B	4	ARG
2	B	5	LYS
2	B	157	CYS

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	189/199 (95%)	184 (97%)	5 (3%)	49	73
2	B	344/349 (99%)	326 (95%)	18 (5%)	25	56
3	C	302/348 (87%)	284 (94%)	18 (6%)	21	52
4	D	244/250 (98%)	237 (97%)	7 (3%)	45	70
5	E	143/252 (57%)	135 (94%)	8 (6%)	23	54
6	F	203/215 (94%)	196 (97%)	7 (3%)	40	66
7	G	199/223 (89%)	192 (96%)	7 (4%)	39	66
8	H	171/171 (100%)	164 (96%)	7 (4%)	33	62
9	I	170/181 (94%)	161 (95%)	9 (5%)	25	56
10	J	143/149 (96%)	137 (96%)	6 (4%)	32	61
11	L	167/177 (94%)	156 (93%)	11 (7%)	18	48
12	M	118/161 (73%)	114 (97%)	4 (3%)	40	66
13	N	172/172 (100%)	170 (99%)	2 (1%)	74	87
14	O	168/174 (97%)	166 (99%)	2 (1%)	74	87
15	P	133/163 (82%)	126 (95%)	7 (5%)	25	56
16	Q	162/165 (98%)	157 (97%)	5 (3%)	43	69
17	R	161/175 (92%)	150 (93%)	11 (7%)	17	48
18	S	155/157 (99%)	148 (96%)	7 (4%)	30	60
19	T	139/140 (99%)	134 (96%)	5 (4%)	38	65
20	U	91/115 (79%)	88 (97%)	3 (3%)	41	67
21	V	100/107 (94%)	99 (99%)	1 (1%)	78	89
22	W	55/126 (44%)	52 (94%)	3 (6%)	24	55
23	X	107/133 (80%)	105 (98%)	2 (2%)	60	80
24	Y	119/135 (88%)	115 (97%)	4 (3%)	40	66
25	Z	118/118 (100%)	112 (95%)	6 (5%)	26	57
26	a	120/121 (99%)	116 (97%)	4 (3%)	41	67
27	b	58/126 (46%)	57 (98%)	1 (2%)	63	83
28	c	88/97 (91%)	87 (99%)	1 (1%)	76	88
29	d	100/110 (91%)	96 (96%)	4 (4%)	34	62
30	e	115/121 (95%)	112 (97%)	3 (3%)	49	73
31	f	87/89 (98%)	79 (91%)	8 (9%)	10	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	g	98/100 (98%)	88 (90%)	10 (10%)	8	30
33	h	109/110 (99%)	106 (97%)	3 (3%)	47	71
34	i	82/89 (92%)	76 (93%)	6 (7%)	15	46
35	j	71/80 (89%)	69 (97%)	2 (3%)	47	71
36	k	64/65 (98%)	64 (100%)	0	100	100
37	l	47/48 (98%)	46 (98%)	1 (2%)	56	78
38	m	48/116 (41%)	45 (94%)	3 (6%)	20	50
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	94/94 (100%)	89 (95%)	5 (5%)	25	56
41	p	74/75 (99%)	72 (97%)	2 (3%)	48	72
42	t	113/121 (93%)	106 (94%)	7 (6%)	20	51
43	u	177/177 (100%)	163 (92%)	14 (8%)	13	43
All	All	5642/6318 (89%)	5403 (96%)	239 (4%)	37	61

5 of 239 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	N	31	ARG
17	R	138	LEU
42	t	20	ARG
15	P	2	VAL
16	Q	75	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 125 such sidechains are listed below:

Mol	Chain	Res	Type
14	O	180	GLN
18	S	117	HIS
38	m	87	GLN
15	P	54	GLN
16	Q	162	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	2	3605/5025 (71%)	2046 (56%)	325 (9%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	3	156/194 (80%)	81 (51%)	6 (3%)
46	4	118/119 (99%)	68 (57%)	9 (7%)
All	All	3879/5338 (72%)	2195 (56%)	340 (8%)

5 of 2195 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	2	2	G
44	2	3	C
44	2	5	A
44	2	6	C
44	2	8	U

5 of 340 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	2	2006	C
44	2	2561	G
44	2	4867	G
44	2	2034	G
44	2	2371	G

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](#)

There are no ligands in this entry.

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.