



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Aug 17, 2017 – 03:06 PM EDT

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 : unknown
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

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

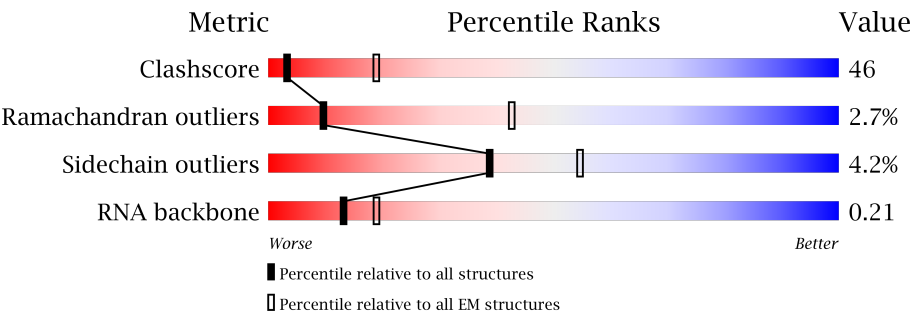
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

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 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.






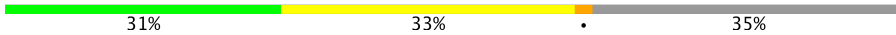


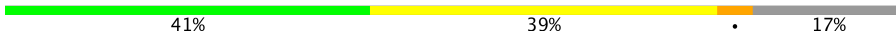










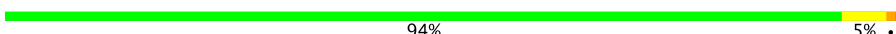






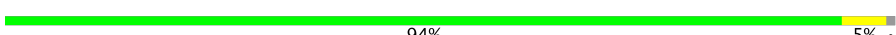
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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 ≥ 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	<div><div>57%</div><div>38%</div><div>• •</div></div>
2	B	403	<div><div>57%</div><div>36%</div><div>5% •</div></div>
3	C	427	<div><div>45%</div><div>35%</div><div>5% • 15%</div></div>
4	D	297	<div><div>55%</div><div>40%</div><div>• •</div></div>
5	E	288	<div><div>23%</div><div>28%</div><div>• 45%</div></div>
6	F	248	<div><div>52%</div><div>40%</div><div>• 6%</div></div>
7	G	266	<div><div>50%</div><div>35%</div><div>• • 12%</div></div>
8	H	192	<div><div>56%</div><div>41%</div><div>•</div></div>



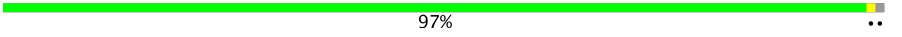
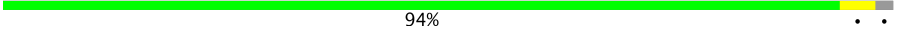

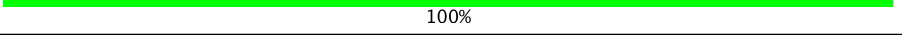
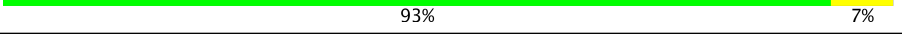
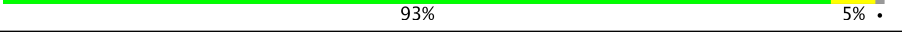
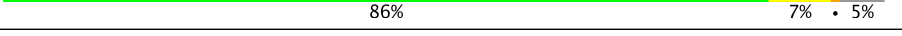
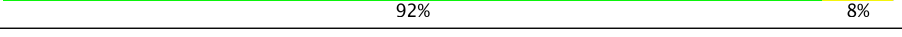
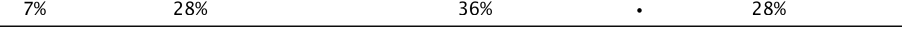


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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	215	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	159	
28	c	115	
29	d	125	
30	e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

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		

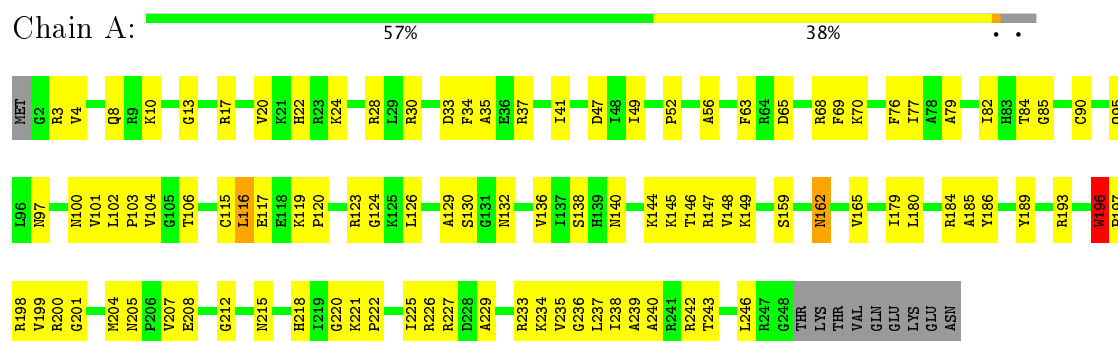
- Molecule 46 is a RNA chain called 5S Ribosomal RNA.

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

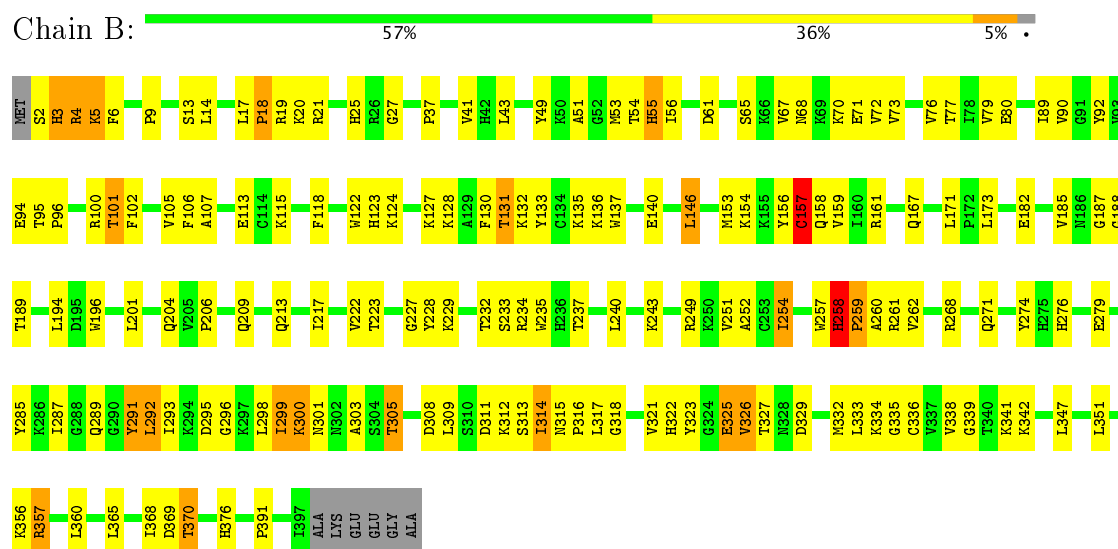
3 Residue-property plots

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.

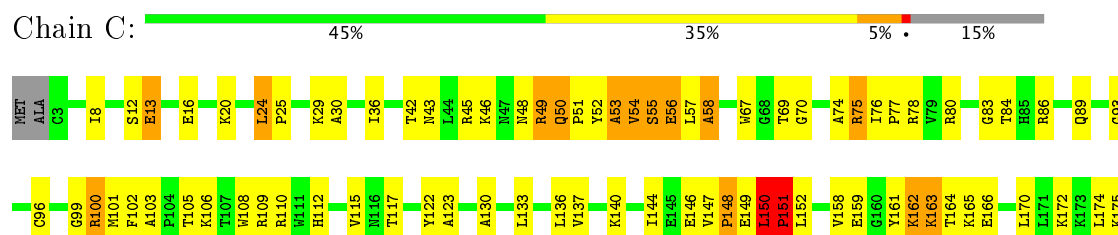
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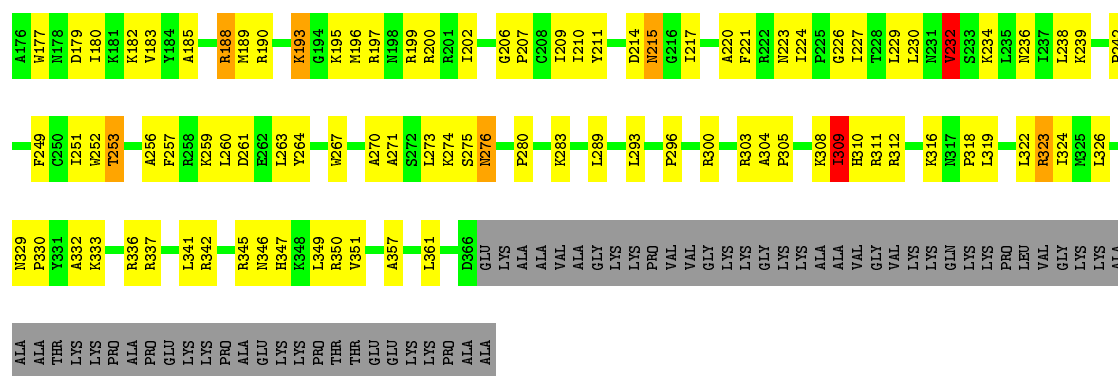


• Molecule 2: 60S RIBOSOMAL PROTEIN UL3

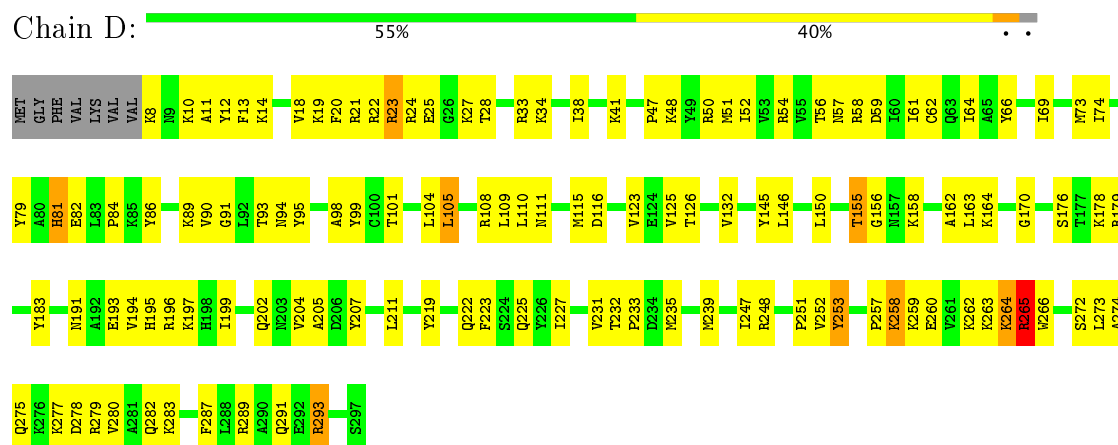


• Molecule 3: 60S RIBOSOMAL PROTEIN UL4

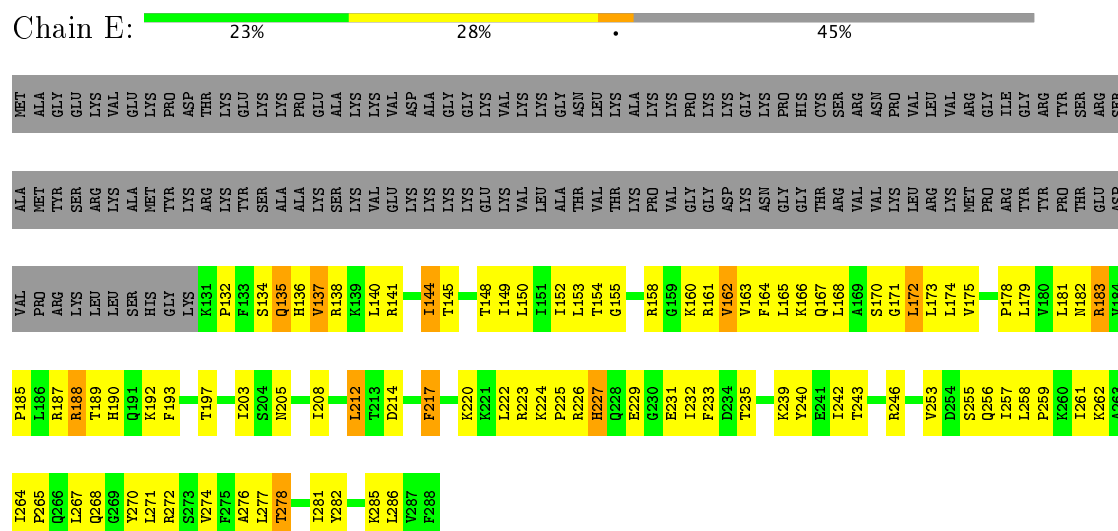




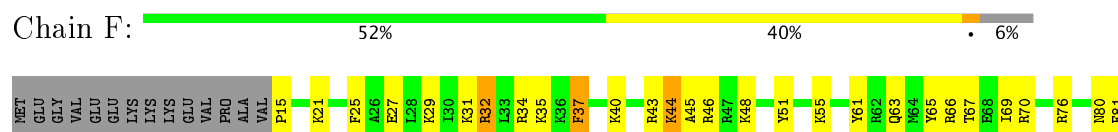
• Molecule 4: 60S RIBOSOMAL PROTEIN UL18

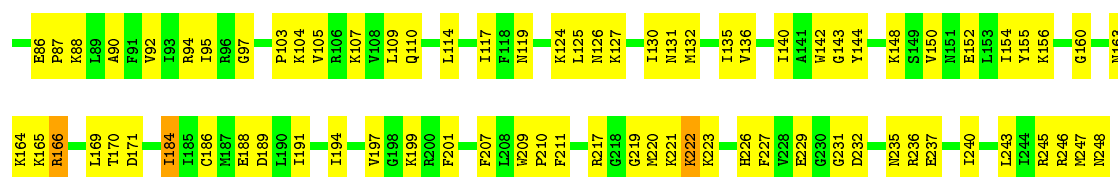


• Molecule 5: 60S RIBOSOMAL PROTEIN UL6

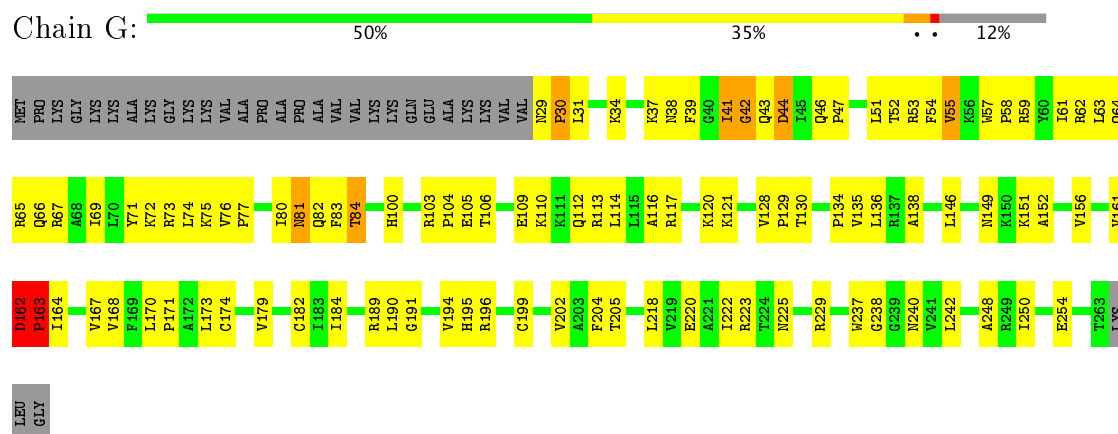


• Molecule 6: 60S RIBOSOMAL PROTEIN UL30

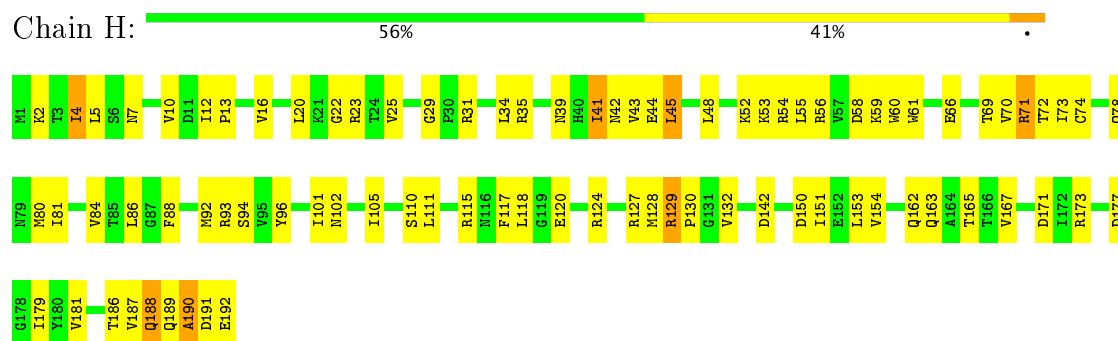




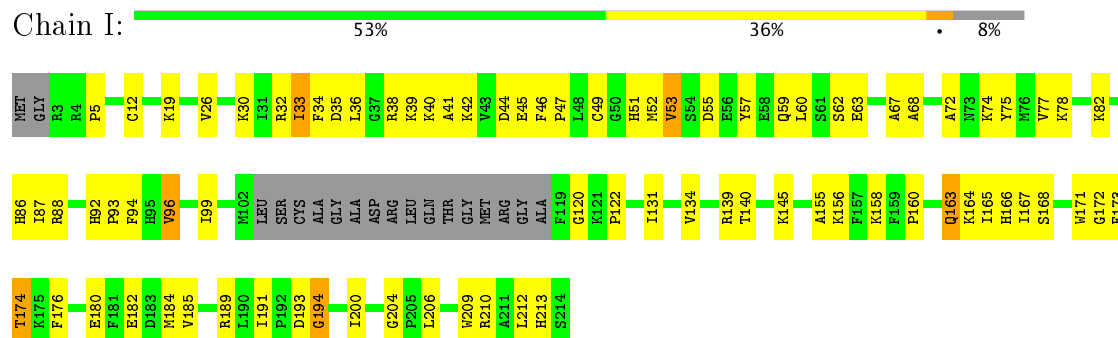
• Molecule 7: 60S RIBOSOMAL PROTEIN EL8



• Molecule 8: 60S RIBOSOMAL PROTEIN UL6

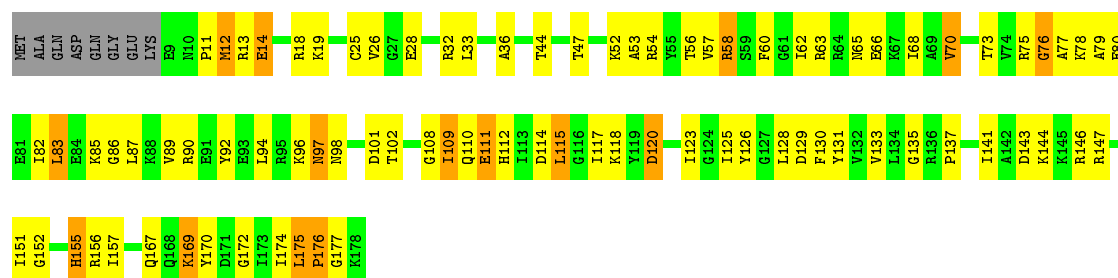


• Molecule 9: 60S RIBOSOMAL PROTEIN UL16

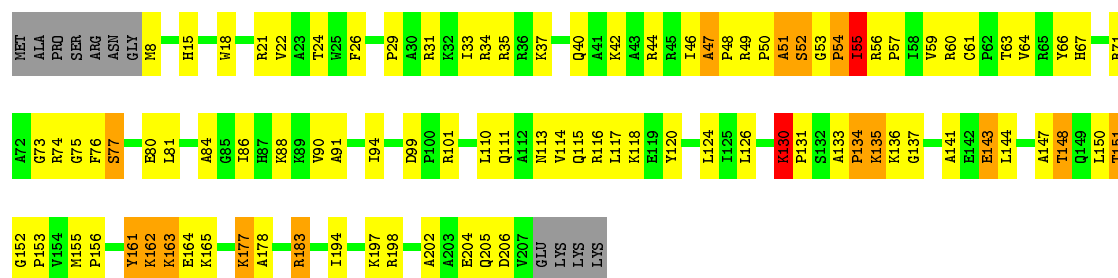


• Molecule 10: 60S RIBOSOMAL PROTEIN UL5

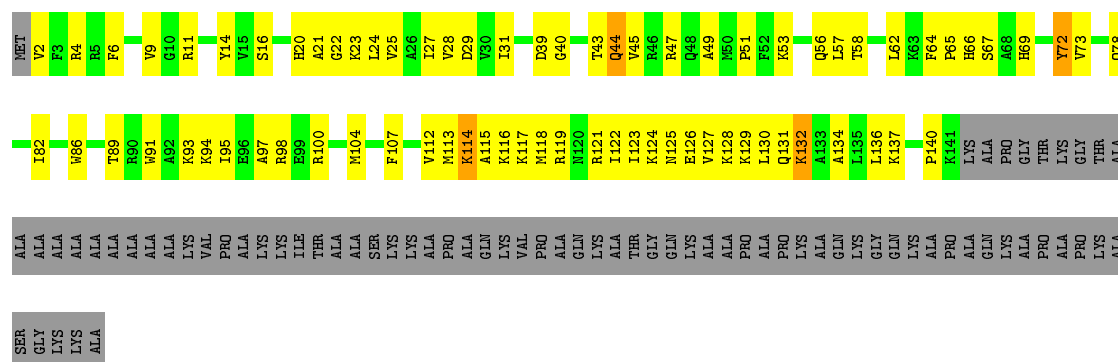




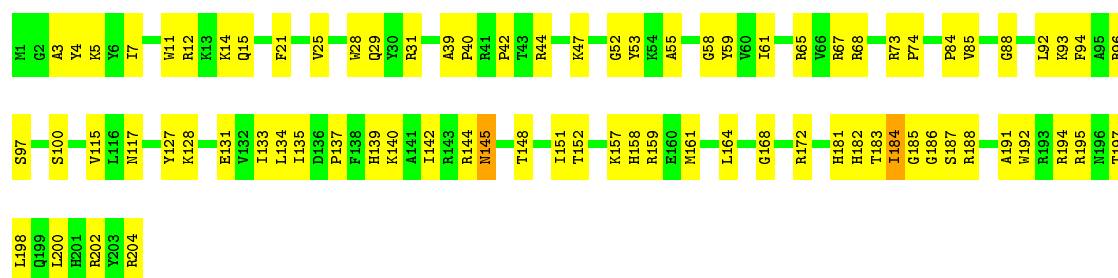
- Molecule 11: 60S RIBOSOMAL PROTEIN EL13



• Molecule 12: 60S RIBOSOMAL PROTEIN EL14

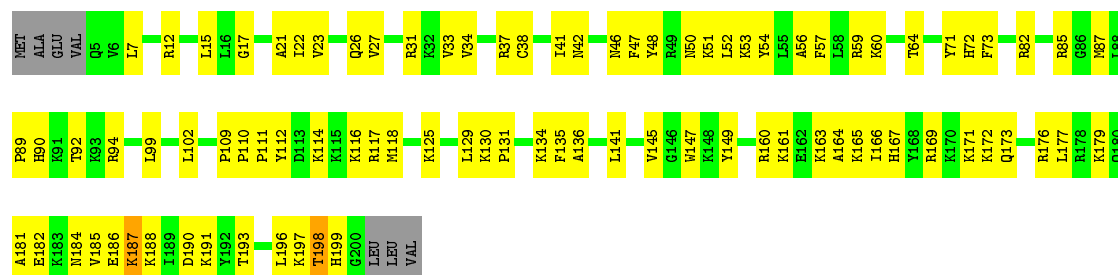


• Molecule 13: 60S RIBOSOMAL PROTEIN EL15



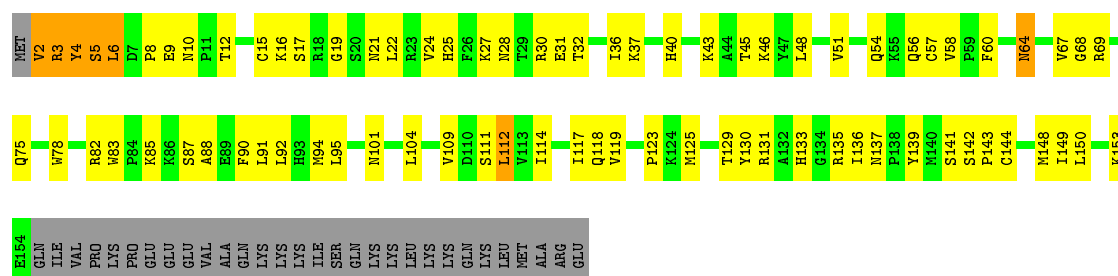
- Molecule 14: 60S RIBOSOMAL PROTEIN UL13

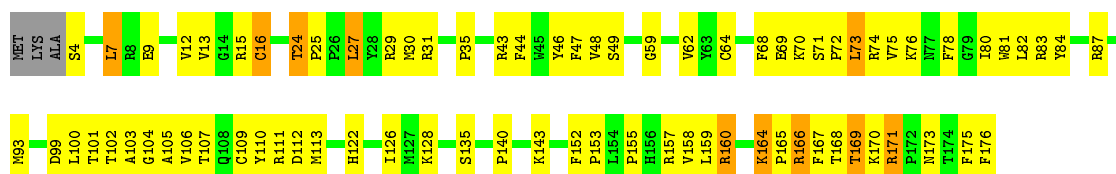
Chain O: 



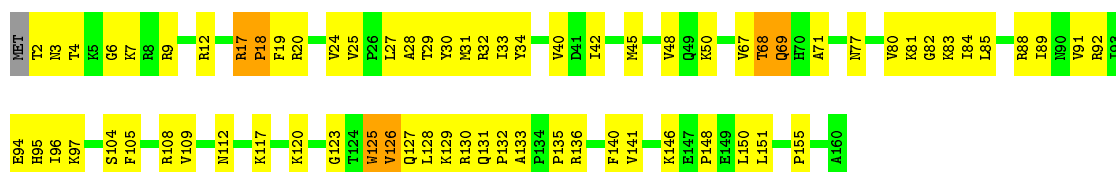
• Molecule 15: 60S RIBOSOMAL PROTEIN UL22

Chain P: 

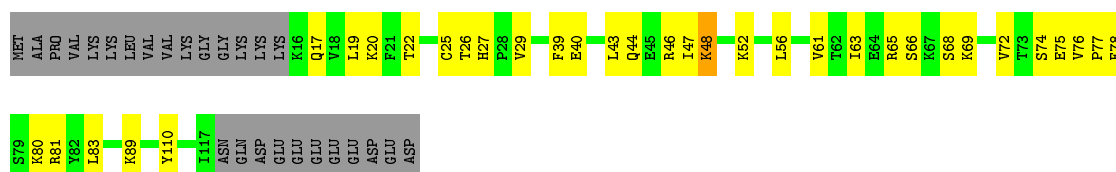




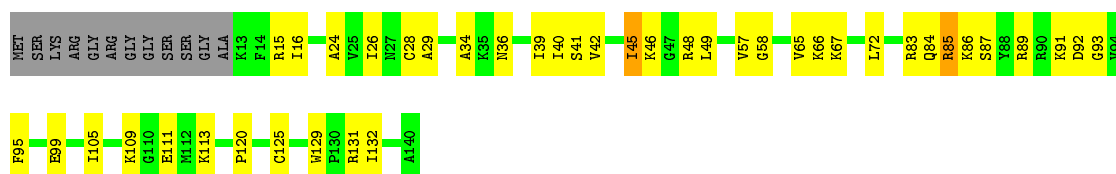
• Molecule 19: 60S RIBOSOMAL PROTEIN EL21



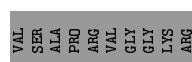
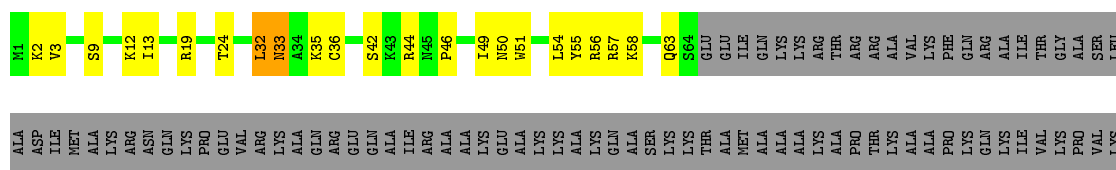
• Molecule 20: 60S RIBOSOMAL PROTEIN EL22



• Molecule 21: 60S RIBOSOMAL PROTEIN UL14

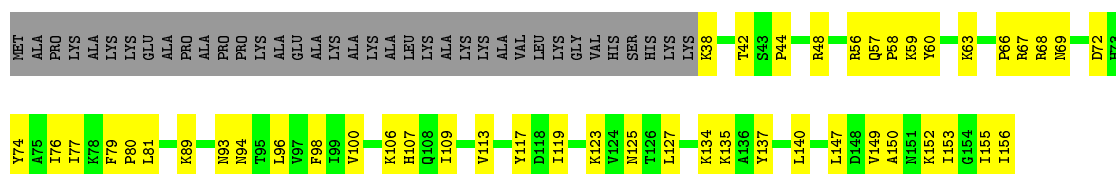


• Molecule 22: 60S RIBOSOMAL PROTEIN EL24

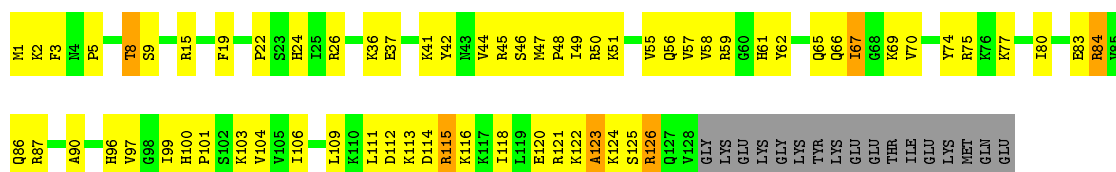


• Molecule 23: 60S RIBOSOMAL PROTEIN UL23

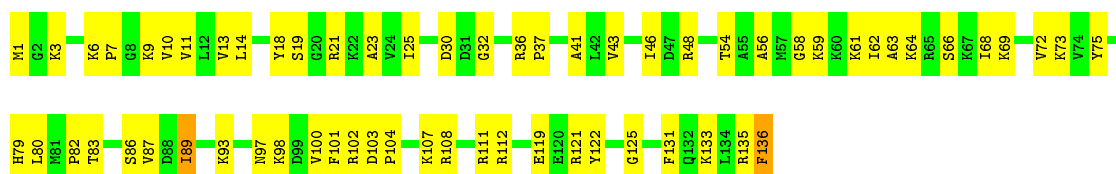




• Molecule 24: 60S RIBOSOMAL PROTEIN UL24



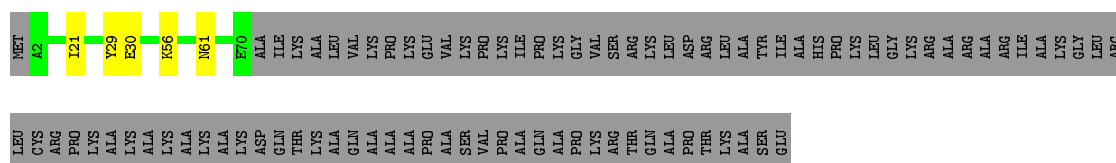
• Molecule 25: 60S RIBOSOMAL PROTEIN EL27



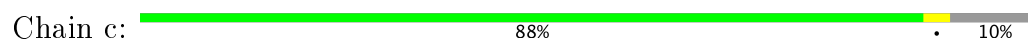
• Molecule 26: 60S RIBOSOMAL PROTEIN UL15



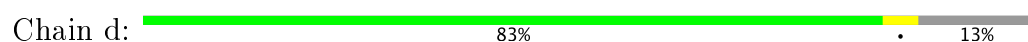
• Molecule 27: 60S RIBOSOMAL PROTEIN EL29

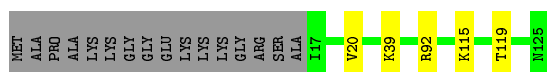


• Molecule 28: 60S RIBOSOMAL PROTEIN EL30



• Molecule 29: 60S RIBOSOMAL PROTEIN EL31





- Molecule 30: 60S RIBOSOMAL PROTEIN EL32

Chain e: 90% 5%



- Molecule 31: 60S RIBOSOMAL PROTEIN EL33

Chain f: 86% 10% ..



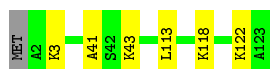
- Molecule 32: 60S RIBOSOMAL PROTEIN EL34

Chain g: 87% 10% ..



- Molecule 33: 60S RIBOSOMAL PROTEIN UL29

Chain h: 94% 5% ..



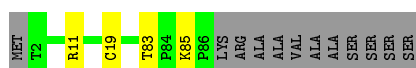
- Molecule 34: 60S RIBOSOMAL PROTEIN EL36

Chain i: 83% 8% 8%



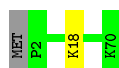
- Molecule 35: 60S RIBOSOMAL PROTEIN EL37

Chain j: 84% 12%



- Molecule 36: 60S RIBOSOMAL PROTEIN EL38

Chain k: 97% ..



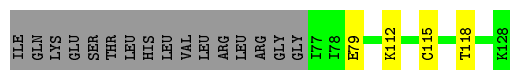
- Molecule 37: 60S RIBOSOMAL PROTEIN EL39

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%

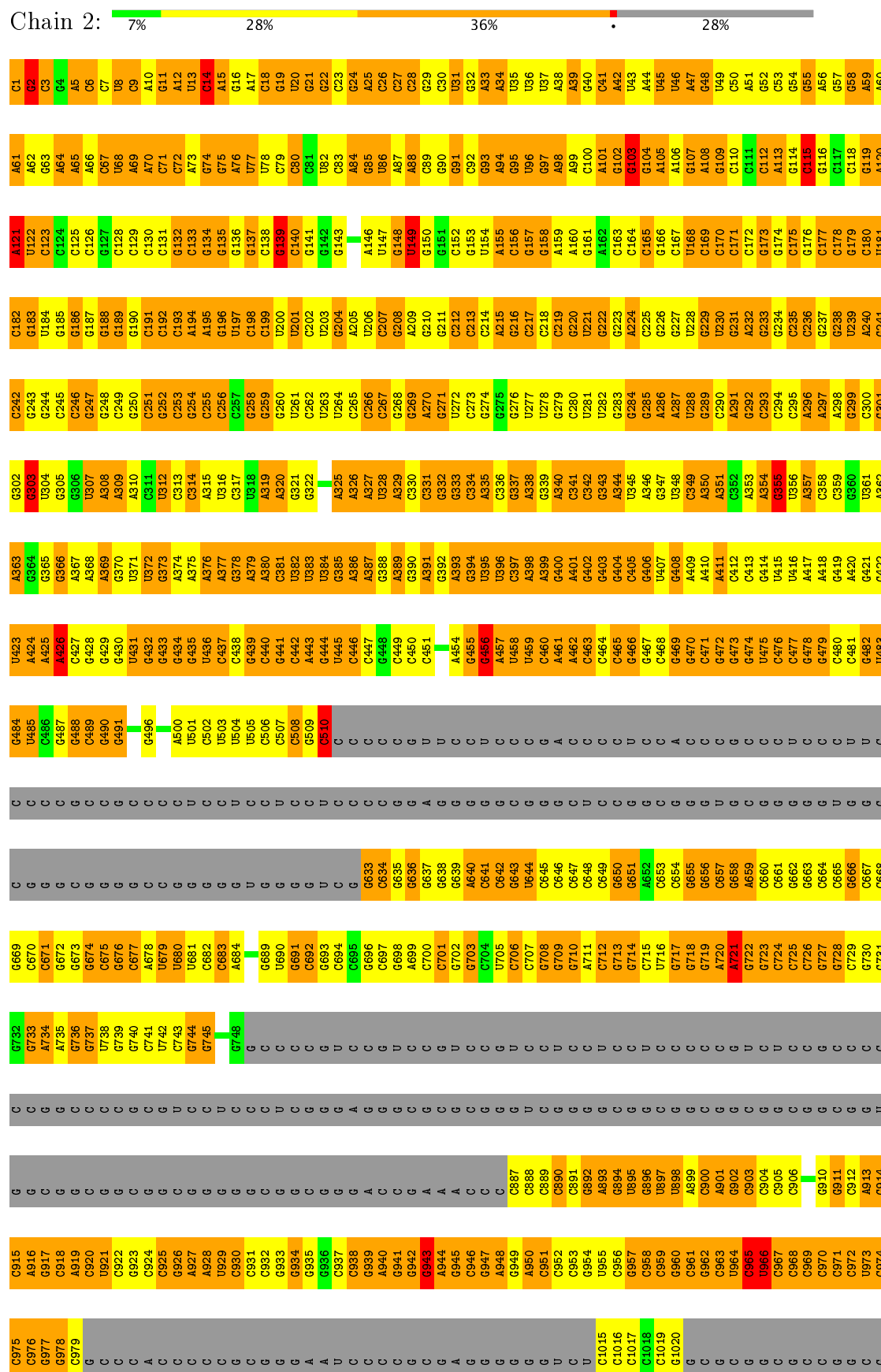


- Molecule 43: 60S RIBOSOMAL PROTEIN UL1

Chain u:  92% 8%



- Molecule 44: 28S Ribosomal RNA



G	C1893	G1829	U1769	A1647	C1586	C1525	G1463	G1402	G1341	G1279	C1219	G1158	C1096	U
C	G1894	U1830	U1770	A1648	G1587	A1526	C1464	U1403	G1342	G1280	G1220	U1159	C1097	C
A	G1895	G1831	U1709	G1649	G1588	G1529	C1465	G1404	U1343	G1281	G1221	C1160	C	U
C	G1896	A1772	C1710	U1650	C1589	G1530	G1466	G1405	U1344	U1282	G1222	C1161	C	C
U	G1897	G1833	A1773	U1651	G1590	C1531	G1467	G1406	G1345	A1283	G1223	C1162	C	C
U	G1898	G1834	G1712	U1652	G1591	G1532	G1468	A1407	C1347	C1284	G1224	C1163	C	U
G	G1899	U1775	G1713	C1653	A1592	A1532	G1469	U1408	A1348	C1285	G1225	A1164	C	U
A	G1900	G1776	U1714	C1654	A1593	A1533	G1470	C1409	C1349	C1286	G1226	G1165	C	G
A	G1901	G1777	A1715	C1655	C1594	G1534	G1471	C1410	G1350	U1287	G1227	U1166	C	U
U	G1902	G1778	A1716	U1656	U1595	C1535	U1473	C1411	A1351	C1288	G1228	G1167	C	G1044
U	G1903	U1779	A1717	C1657	G1596	C1536	G1474	G1412	A1352	C1289	G1229	C	C	G1045
G	U1840	U1781	G1718	A1658	G1597	A1537	G1475	G1413	A1353	C1290	G1230	G1170	C	G1046
C	G1905	A1780	G1719	G1659	G1598	G1538	A1476	G1414	G1354	G1291	G1231	C1171	C	G1047
G	G1906	G1782	G1720	G1660	U1599	A1539	G1477	G1415	C1355	A1292	C1232	C1172	C	G1048
A	A1845	A1783	A1721	A1661	A1600	G1540	G1478	G1416	C1356	G1293	G	C1173	C	G1049
A	U1808	A1784	G1724	U1662	G1603	G1541	A1479	C1417	C1357	C1294	A	C1174	C	G1050
U	G1898	G1785	A1725	G1663	G1604	A1542	U1480	U1418	C1358	G1295	A	G1175	C	C1051
C	A1910	C1786	U1726	C1665	G1605	A1543	G1481	C1419	C1359	G1296	G	G1176	C	C1052
C	A1849	C1787	U1727	U1666	G1606	A1544	A1482	U1420	G1360	U1297	A	C1177	C	G1053
C	G1856	C1788	G1728	U1667	C1607	C1545	G1483	C1422	G1361	C1298	G1238	G1178	C	G1054
G	C1913	G1789	A1728	G1668	G1608	U1546	C1484	A1423	G1362	U1299	G1239	G1179	A	G1055
C	G1914	G1790	G1729	G1669	G1609	U1547	G1485	G1424	G1363	U1300	G1240	C1180	C	C1056
U	A1915	C1791	A1730	C1669	A1609	U1548	C1486	U1425	C1364	G1301	G1241	G1181	C	C1057
A	C1916	U1792	G1731	G1670	A1610	G1549	A1487	C1426	G1365	A1302	G1242	G1182	C	A1058
A	G1917	C1793	G1732	G1671	A1611	G1550	C1488	C1427	C1366	A1303	A1243	G1183	C	C1059
G	G1918	G1794	U1733	U1672	G1612	U1551	G1489	G1428	A1367	A1304	C1244	C1184	C	C1060
A	A1920	C1795	U1735	C1673	A1613	G1552	U1490	C1429	U1368	C1305	G1245	G1185	C	C1061
G	G1858	G1796	U1736	C	G1614	G1553	G1491	C1430	C1369	A1306	G1246	C1186	C	C1062
U	C1859	G1797	U1736	C	U1615	A1554	U1492	G1431	G1370	C1307	G1247	C1187	C	U1063
U	U1860	G1798	G1737	C	A1616	G1555	U1493	A1432	A1371	G1248	G1248	C1188	C	G1064
U	G1861	C1799	G1738	C	A1617	G1556	A1494	G1433	A1372	U1189	G1249	U1189	U	C1065
U	C1862	G1800	G1738	A	A1618	U1557	G1495	G1434	G1373	A1250	G1250	G1190	C	C1066
U	U1925	U1801	G1740	G	C1619	U1558	G1496	G1435	G1374	G1251	G1251	G1191	C	A1067
A	G1865	G1802	C1741	A	A1620	C1559	U1497	G1436	U1375	C1252	G1252	G1192	C	C1068
A	U1927	A1866	C1742	C	A1621	G1560	C1498	C1437	G1376	G1253	G1253	G1193	C	G1069
C	G1867	A1804	G1743	C	C1622	U1561	C1499	A1438	A1377	A1254	G1254	C1194	C	G1070
A	G1868	G1805	A1744	C	G1623	A1562	U1561	C1439	A1378	G1255	G1255	C1195	C	C1071
A	A1869	C1806	A1745	G	C1624	G1563	U1501	C1440	G1379	C1256	G1256	C1196	C	
U	C1870	A1807	U1746	A	A1625	C1564	A1502	A1441	G1380	U1319	G1257	G1197	C	G1074
U	G1871	G1808	C1747	C	U1626	G1565	A1503	C1442	C1381	C1320	G1258	G1198	C	A1075
C	G1872	C1873	G1748	G	C1627	G1566	A1504	C1443	C1382	U1321	G1259	G1199	G1136	C1076
A	A1874	A1810	A1749	A	A1629	U1567	G1505	G1444	G1383	A1322	G1260	G1201	G1137	C1077
A	U1935	G1811	U1750	C	G1630	C1568	A1506	G1445	G1384	A1323	G1261	G1202	U1138	G1078
C	G1875	U1812	C1751	C	G1631	C1569	U1507	C1446	C1385	C1324	G1262	A1202	U1139	G1079
C	C1997	G1813	U1752	C	U1632	U1570	G1508	C1447	C1386	A1325	G1263	G1203	C1140	U1080
G	G1939	G1814	C1753	C	A1632	G1571	U1510	C1448	C1387	C1326	G1264	G1204	G1141	U1081
C2000	A1940	A1815	A1754	C	G1633	A1572	G1514	G1449	G1388	G1270	G1265	U1205	G1142	U1082
C2001	G2002	A1816	A1755	C	C1634	C1573	U1515	U1450	C1389	U1206	U1265	U1206	G1143	C1083
A2003	A1942	G1817	G1756	C	U1635	G1574	C1514	C1451	U1390	G1328	C1266	C1207	G1144	C1084
A2004	G1943	G1818	C1757	C	G1636	U1575	U1514	U1452	C1391	G1329	G1267	U1208	G1145	C1085
U2005	C1944	C1819	U1758	C	G1637	G1576	U1515	C1453	C1392	G1331	C1269	C1209	G1146	A1086
C2006	U1883	G1820	A1759	A	U1638	C1577	A1516	G1454	C1393	G1332	G1270	U1210	G1147	C1087
A2007	G	A1821	U1760	C	G1639	A1578	U1517	C1455	C1394	G1333	G1271	C1211	G1148	C1088
C2008	A2008	G1822	U1761	G	C1640	U1578	G1518	C1456	A1334	G1395	C1272	G1212	G1149	C1089
C2009	A	U1823	G1762	C	A1641	A1580	C1519	C1457	G1396	G1335	G1273	G1213	G1150	C1090
U2010	C	G1824	U1763	C	U1642	U1581	C1520	G1458	C1397	U1336	A1274	G1214	G	U1091
A2011	G	C1825	U1766	C	U1643	C1582	U1521	C1459	C1398	C1337	C1275	G1215	G1154	C1092
G2012	U	A1826	U1767	C	C1644	G1583	G1522	C1460	G1399	G1338	G1276	C1216	A1155	C1093
C2013	U	U1827	U1705	C	G1645	G1584	G1523	G1461	A1400	G1339	U1277	C1217	C1156	U1094
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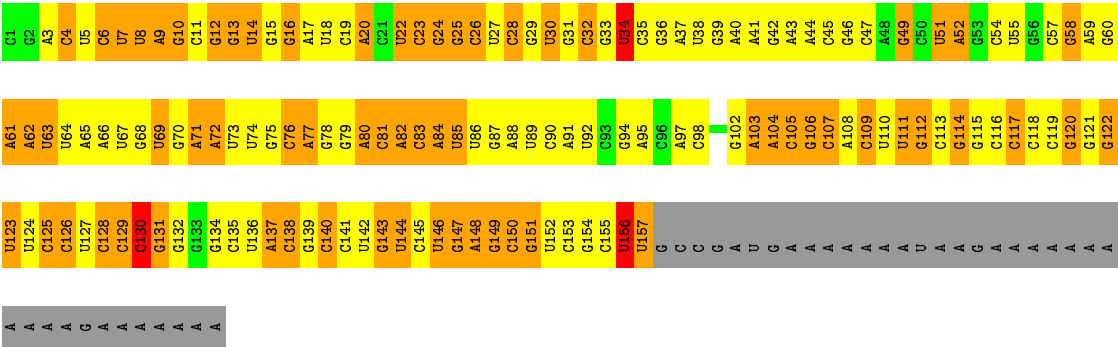
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C	C	G2749	C2688	G2627	C2564	A2504	C2440	A2380	G2319	U2257	U	C	C	G2017
C	C	G2750	G2689	C2628	C2565	A2504	C2441	A2381	C2320	A2258	C	G	A	A2018
C	C	G2751	C2690	G2629	C2566	G2505	C2442	G2382	U2321	G2259	C	G	C	A2019
C	C	C2752	G2691	C2630	G2567	A2506	G2443	G2383	G2322	G2260	U	C	C	A2020
C	G	G2753	G2692	C2631	A2568	U2507	U2444	C2384	C2323	A2261	C	G	G	A2021
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C	C	G2755	G2694	G2633	U2634	C2509	C2446	C2386	G2325	G2263	C	C	A	G2023
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C	C	G2823	C2757	C2696	G2635	C2572	G2448	C2388	U2327	C2265	C	G	C	A2025
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C	U	G2825	U2759	C2698	A2637	G2574	U2450	C2390	U2329	G2267	C	G	G	G2027
C	C	A2826	A2760	G2699	A2575	A2514	G2451	U2330	U2330	C2268	A	C	C	C2028
C	C	A2827	C2761	G2700	G2639	G2576	G2452	U2392	G2331	U2269	C	C	C	G2029
C	A	G2828	C2762	G2701	G2640	A2577	G2453	G2393	G2332	G2270	C	G	G	G2030
C	C	U2829	C2763	A2702	G2641	A2578	G2454	A2394	U2333	C2271	C	G	C	G2031
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C	C	G2833	U2767	C2706	G2645	G2582	G2458	G2398	A2337	G2275	C	U	G	A2035
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C	C	G2788	C2726	U2664	U2602	A2541	G2479	U2417	A2356	G2294	C	C	C	G2054
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C	U	C2791	G2729	C2667	U2605	G2544	C2482	U2420	A2359	G2297	C	U	G	G2057
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C	C	G2861	A2734	C2672	C2611	C2549	G2487	G2425	U2363	G2303	C	C	C	C2062
C	C	A2862	G2735	A2673	C2550	A2488	A2488	A2426	A2366	G2304	C	U	C	G2063
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C	C	A2802	U2738	C2676	U2614	G2553	G2491	G2429	C2369	G2307	C	G	A	A
C	C	U2803	G2739	G2677	U2615	C2554	G2492	A2430	C2370	A2308	C	G	C	G2046
C	U	G2866	C2740	U2678	U2616	G2555	G2493	U2431	G2371	G2309	C	G	C	U2047
C	A	C2867	U2740	U2678	U2617	G2556	A2494	G2432	G2371	G2310	C	G	C	G2048
C	C	U2868	A2741	C2681	U2557	C2549	G2495	A2433	A2373	C2311	C	U	C	G2049
C	C	G2869	A2742	C2682	C2681	G2558	G2496	G2434	C2374	G2312	C	C	C	A
C	C	U2870	A2743	G2682	G2620	A2588	C2497	G2435	U2375	G2313	U	C	C	G2050
C	C	C2807	U2744	G2683	G2621	C2589	C2497	C2435	U2376	G2314	C	C	C	G2051
C	C	A2872	C2745	U2684	C2684	C2590	G2498	G2436	C2376	C2315	C	C	C	A
C	A	C2873	U2746	C2685	A2592	C2584	C2499	A2427	G2377	C2315	C	C	C	A

U4087	U4026	C	C3904	G3842	G3778	C3718	G3655	G3594	U	G	C	G	C	U
G4088	C4027	C	A3905	G3843	C3779	G3719	A3656	G3595	U	C	G	G	C	C
G4089	U4028	C	G3906	G3844	G3780	G3720	A3657	G3596	C	A	G	C	G	G
C4090	G4029	G	G3907	A3845	C3781	C3721	G3658	G3597	C	G	G	C	G	U
G4091	A4030	G	G3908	A3846	A3782	G3722	U3659	A3598	C	G	C	C	A	C
C4092	U4031	G	U3909	C3847	U3783	G3723	G3660	A3599	G	G	C	C	G	C
C4093	C4032	A	G3910	G3848	A3784	G3724	A3661	U3600	G	G	G	G	C	C
A4094	U4033	G	G3911	G3849	A3785	A3725	U3662	G3602	G	C	C	C	G	C
A4095	U4034	G	G3912	G3850	A3786	G3726	G3663	C3603	C	C	C	C	A	C
	U4035	G	G3913	C3851	U3787	U3727	U3664	G3603	C	C	C	C	C	C
	U4036	C	G3914	U3852	G3788	A3728	C3665	A3604	G	G	C	C	C	C
	U4037	C	G3915	U3853	G3789	A3729	U3666	C3605	C	C	C	C	C	C
	U4038	C		G3854	A3790	C3730	G3667	U3606	C	A	G	C	C	C
	U4039	C	U3919	G3855	U3791	U3731	C3668	G3607	U	U	G	G	A	C
G4102	C4040	C	G3920	C3856	G3792	A3732	C3669	C3608	C	G	C	G	C	C
C4103	A4041	G	A3921	G3857	U3793	U3733	G3670	U3609	C	C	C	C	C	C
A4104	C4042	G	G3922	G3858		G3734	A3671	U3610	G	G	C	C	U	G
C4105	U4043	G	A3923	A3859	G3796	A3735	G3672	A3611	C	C	G	C	G	C
G4106	G4044	C	G3924	A3860	A3797	C3736	G3673	A3612	C	G	C	C	C	C
A4107	U4045	C	G3925		G3798	U3737	G3674	U3613	U	C	C	C	G	G
C4108	C4046	G	U3926	A3863	A3799	C3738	C3675	U3614	C	G	C	A	G	A
U4109	C4047	G	G3927	G3864	U3800	U3739	U3676	A3615	G	C	C	C	C	C
		G	U3928	G3865	U3801	C3740	C3677	A3616	G	C	G	C	G	C
G4110		U	A3929	G3866	C3802	U3741	U3678	A3617	C	C	C	C	C	C
C4111	G4050	C	G3930	G3867	C3803	G3742	G3679	A3618	G	C	C	G	A	C
G4112	U4051	C	A3931	G3868	C3804	A3743	A3680	C3619	U	G	C	C	C	C
C4113	A4052	G	G3932	G3869	A3805	A3744	A3681	A3620	C	C	G	C	C	C
	C4053	C	U3933	A3870	C3806	G3745	U3682	A3621	G	U	C	G	U	C
A4117	G4054	C	A3934	A3871	U3807	G3746	G3683	A3622	C	C	C	C	C	C
C4118	U4055	G	A3935	A3872	G3808	U3747	U3684	G3623	C	C	C	C	C	C
U4119	C4056	C	G3936	G3873	U3809	A3748	C3685	C3624	C	C	C	C	C	C
C4120	G4057	C	U3937	A3874	C3810	G3749	A3686	A3625	C	C	C	C	C	C
U4121	U4058	C	G3938	G3875	C3811	C3750	A3687	U3626	C	C	G	G	C	C
C4122	G4059	C	G3939	A3876	G3812	G3751	A3688	C3627	C	C	C	C	C	C
U4123	G4060	U	G3940	A3877		A3752	G3689	G3628	C	C	C	C	A	G
G4124	G4061	C	A3941	C3878	A3814	A3753	U3690	A3568	C	U	G	C	C	C
C4125	C4062	C		C3879	C3815		G3691	G3569	C	C	C	C	C	C
G4126	G4063	G4002	G3942	C3879		A3754	G3692	G3630	C	C	G	C	U	C
C4127	C4064	G4003	G3943	C3880	C3819	U3755	A3692	C3571	C	C	C	C	C	C
G4128	G4065	G4004	C3944	U3881	U3820	G3756	A3693	A3632	G	C	C	C	U	G
C4129	A4066	C4005	G3945	A3882	A3821	C3757	G3694	G3633	C	C	C	C	C	C
U4130	G4067	C4006	C3946	U3883	U3822	G3758	A3695	G3634	C	C	C	C	C	C
C4131	C4068	G4007	C	U3884	C3823	U3759	A3696	C3635	G	G	C	C	G	G
U4132	C4069	C		G3885	C3824	C3760	A3697	C3636	U	U	G	A	G	G
C4133	G4070	C	G	A3886	A3825	U3698	U3698	U3576	C	C	C	C	C	C
U4134	C4071	C	G	G3887	G3826	G3762	C3700	G3579	C	C	C	C	A	G
C4135	A4072	G4011	C	G3888	C3827	U3763	G3706	A3579	C	C	C	C	G	G
G4136	G4073	C	U3889	U3883	G3828	A3764	A3701	A3580	C	C	C	C	A	G
U4137	C4074	G4012	C	G3890	A3829	U3765	C3702	C3642	C	G	C	C	C	C
G4075	G4075	G4014	C	G3891	A3830	C3766	U3703	G3643	C	C	C	C	C	C
C4076	C4076	A4015	C	A3892	A3831	U3767	G3704	G3644	C	C	C	C	C	C
U4077	C4077	A4016	C	G3893	C3832	A3768	A3705	G3645	G	C	C	C	C	A
U4117	U4078	U4017	C	U3894	C3833	A3769	A3706	U3646	C	C	C	C	G	G
C4142	U4079	A4018	C	G3895	A3834	U3770		G3647	G	C	C	C	G	C
U4080	C4019	C	U3896	U3896	C3835	U3771	C3740	U3648	G	G	G	C	G	G
C4020	G4081	G	A3897	A3897	A3836	A3772		U3649	C	C	C	C	A	C
G4082	U4021	C	G3898	G3898	C3837	G3773	G3743	G3589	C	C	C	C	C	C
C4083	C4022	U	U3899	C3838	C3838	G3774	A3651	A3590	C	C	C	C	U	G
U4084	U4023	G	C3900	G3839	C3839	G3775	A3745	C3652	C	C	C	C	G	G
U4148	C4085	U	U3900	G3900	A3840	A3776	A3716	G3653	C	C	C	C	U	C
C4086		C		C3903	A3841	A3772	A3717	C3654	C	C	C	C	A	C

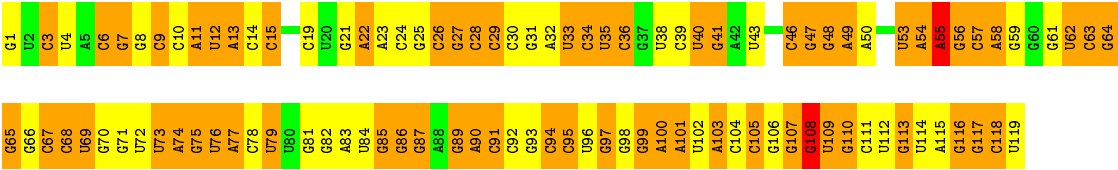
A5015	G4947	G4882	G4822	G4702	A4641	U4580	A4456	U4396	A4336	G4276	G4214	U4150
A5016	G4948	C4883	G4823	A4703	U4642	C4581	U4457	U4397	G4337	A4277	A4215	G4151
G5017	G4949	C	U4824	C4704	A4643	G4582	U4458	A4338	A4339	C4278	A4216	A4152
G5018	G4950	U	G4825	C4705	A4644	G4583	U4459	U4339	U4339	C4279	A4217	C4153
G5019	G4951	C	G4826	C4706	U4645	A4584	U4460	G4400	A4340	G4280	C4218	U4154
U5020	G4952	C	G4827	U4707	C4646	C4585	U4461	A4401	A4341	U4281	G4219	G4155
U5021	G4953	C	G4828	C4708	A4647	U4586	U4462	U4402	G4342	G4282	U4220	G4156
U5022	U4954	A	G4829	G4709	U4648	C4587	U4463	C4403	U4343	A4283	C4221	G4157
G	U4955	C	G4830	G4710	U4649	U4588	C4466	C4404	U4344	A4284	C4222	G4158
U	U4956	C	G4831	U4711	G4650	U4589	A4467	U4405	A4345	G4285	G4223	C4159
C	U4957	C	U4832	U4712	A4651	A4590	C4468	U4406	C4346	G4286	G4224	G4160
	U4958	G	U4833	U4713	G4652	U4591	U4469	C4407	C4347	G4287	U4225	G4161
	U4959	C	G4834	G4714	U4653	G4592	U4470	G4408	A4348	G4288	G4226	U4162
	U4960	C	U4835	G4715	G4654	U4593	A4471	A4409	C4349	G4289	G4227	A4163
	U4961	C	C4836	C4716	C4655	G4594	U4472	U4410	A4350	G4290	A4228	A4164
	U4962	C	U4837	U4717	U4656	U4595	U4473	G4411	G4351	G4291	A4229	A4165
	U4963	C	U4838	C4718	U4657	U4596	G4474	U4412	G4352	C4292	G4230	A4166
	C4968	C	G4839	G4719	C4658	U4597	G4475	C4413	G4353	C4293	C4231	C4167
A4969	G4969	C	U4840	C4720	U4659	U4598	G4476	G4414	A4354	U4294	G4232	U4168
G4970	G4970	C	U4841	A4721	A4660	U4599	A4477	G4415	A4355	C4295	A4233	G4169
U4971	U4971	C	C4842	G4722	U4661	C4600	U4478	C4416	A4356	A4234	U4170	
U4972	G4972	G	G4843	U4723	G4662	U4601	U4479	U4417	A4357	G4297	G4235	
C4973	C4973	G	U4844	G4724	U4663	U4602	G4480	C4418	C4358	G4298	G4236	
A4974	A4974	A	G4845	C4725	A4664	G4603	U4481	U4419	U4359	U4299	G4237	A4173
G4975	G4975	C	G4846	C4726	G4665	C4604	G4482	U4420	G4360	U4300	C4238	A4174
U4976	C4976	C	U4847	G4727	A4666	C4605	A4483	C4421	G4361	A4239	A4239	G4175
U4977	U4977	G	A4848	G4728	U4667	U4606	G4484	C4422	C4362	C4302	A4240	G4176
G4978	G4978	C	U4849	U4729	U4668	G4607	U4485	U4423	C4363	U4303	A4241	U4177
C4979	C4979	C	U4850	C4730	U4669	A4608	U4486	A4424	U4364	U4304	A4242	A4178
U4980	U4980	C	G4851	C4731	C4670	G4609	G4487	U4425	G4365	C4305	A4180	A4179
U4981	A4911	C	G4852	C4732	C4671	U4610	G4488	C4426	U4366	U4306	G4243	A4181
C4982		G	G4853	G4733	C4672	G4611	G4489	A4427	G4367	C4307	C4246	G4182
G4983		U	U4854	C4734	U4673	A4612	U4490	U4428	A4368	U4308	G4247	C4183
C4984		G	C4855	G4735	C4674	U4613	U4491	U4429	C4369	A4309	C4248	A4184
U4985	U4920	C	G4856	C4736	C4675	C4614	U4492	G4430	G4370	C4310	U4249	G4185
G4986	U4921	C	C4857	C4737	A4676	A4615	U4493	U4431	G4371	U4311	U4250	G4186
C4987	A4921	C	G4858	U4738	A4677	G4616	G4494	G4432	C4372	U4312	G4251	U4187
U4988	A4922	C	G4859	G4739	U4678	A4617	U4495	A4433	C4373	U4313	A4252	G4188
A4989	A4923	C	C4860	U4740	G4679	U4618	C4496	A4434	A4374	U4314	U4253	U4189
U4990	C4924	C	G4861	C4741	C4680	G4619	C4497	G4435	A4375	G4315	U4254	C4190
	C4925	C	G4862	U4742	A4681	U4620	U4498	A4436	G4376	G4317	U4255	C4191
U4995	U4926	C	G4863	C4743	U4682	G4621	U4499	A4437	G4377	U4318	U4256	U4192
G4996	U4927	C	U4864	G4744	A4683	G4622	G4500	G4438	G4378	U4319	G4257	A4193
A4997		C	A4865	C4745	G4684	G4623	G4501	A4439	G4379	U4320	U4258	A4194
U4998		C	G4866	G4746	U4685	A4624	U4502	A4440	U4380	U4321	U4260	G4196
A4999		C	A4867	C4747	A4686	G4625	U4503	U4441	C4381	U4322	U4261	C4197
G5000		C	U4868	G4748	U4687	G4626	A4504	U4442	A4382	A4323	U4262	G4198
U5001		C	G4869	G4749	C4688	U4627	G4505	C4443	U4383	U4324	C4263	A4199
C5002		C	G4870	C4750	G4689	A4629	A4506	G4444	A4384	G4324	G4264	G4200
A5003		C	G4871	G	G4690	C4630	C4507	C4445	G4385	C4325	G4265	C4201
G5004		C	G4872	G	C4691	C4631	U4508	C4446	C4386	A4326	U4266	U4202
C5005		C	C4873	G	A4692	A4632	G4509	A4447	G4387	G4327	G4267	C4203
C5006		C	G4874	C	C4693	G4633	U4510	A4448	A4388	G4328	A4267	G4204
C5007		C	G4875	C	C4694	C4634	U4511	G4449	C4389	A4329	C4268	A4204
U5008		C	U4940	C	G4695	G4635	U4512	G4450	G4390	G4330	G4269	
C5009		C	G4876	C	G4696	U4636	A4513	C4451	U4391	G4331	A4270	G4209
G5010		C	C4877	C	C4697	G4637	U4514	U4452	C4392	U4332	A4271	G4210
C5011		C	G4878	C	C4698	U4638	U4515	U4453	G4393	G4333	A4272	A4211
U5012		C	U4879	C	G4699	G4639	U4516	U4454	C4394	U4334	A4273	C4212
C5013		C	U4880	C	C4700	G4640	U4517	U4455	U4395	C4335		A4213
A5014		C	C4881	C	G4701							

• Molecule 45: 5.8S Ribosomal RNA

Chain 3: 7% 38% 35% 19%



● Molecule 46: 5S Ribosomal RNA



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%)	15	57
2	B	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	4	33
3	C	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	3	30
4	D	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	11	50
5	E	156/288 (54%)	141 (90%)	8 (5%)	7 (4%)	3	29
6	F	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	11	50
7	G	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	3	31
8	H	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	11	51
9	I	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	11	51
10	J	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	19
11	L	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	2	25
12	M	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	13	54
13	N	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	12	53
14	O	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	12	53
15	P	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	9	46
16	Q	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	4	35
17	R	181/196 (92%)	174 (96%)	4 (2%)	3 (2%)	11	50
18	S	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	4	34
19	T	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	9	47
20	U	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
21	V	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	11	51
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%)	7	42
25	Z	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	5	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	4	35
27	b	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	2	23
28	c	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	9	46
29	d	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	20	63
30	e	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	7	42
31	f	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	2	28
32	g	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	4	34
33	h	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	6	41
34	i	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	1	22
35	j	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	7	42
36	k	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	12	53
37	l	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	8	45
38	m	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	9	46
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	9	47
41	p	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	4	35
42	t	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	2	25
43	u	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	13	54
All	All	6479/7422 (87%)	6102 (94%)	200 (3%)	177 (3%)	10	40

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%)	51	75
2	B	344/349 (99%)	326 (95%)	18 (5%)	27	59
3	C	302/348 (87%)	284 (94%)	18 (6%)	22	55
4	D	244/250 (98%)	237 (97%)	7 (3%)	48	73
5	E	143/252 (57%)	135 (94%)	8 (6%)	25	57
6	F	203/215 (94%)	196 (97%)	7 (3%)	42	69
7	G	199/223 (89%)	192 (96%)	7 (4%)	41	69
8	H	171/171 (100%)	164 (96%)	7 (4%)	35	65
9	I	170/181 (94%)	161 (95%)	9 (5%)	26	59
10	J	143/149 (96%)	137 (96%)	6 (4%)	34	64
11	L	167/177 (94%)	156 (93%)	11 (7%)	19	52
12	M	118/161 (73%)	114 (97%)	4 (3%)	42	69
13	N	172/172 (100%)	170 (99%)	2 (1%)	75	88
14	O	168/174 (97%)	166 (99%)	2 (1%)	75	88
15	P	133/163 (82%)	126 (95%)	7 (5%)	26	59
16	Q	162/165 (98%)	157 (97%)	5 (3%)	45	71
17	R	161/175 (92%)	150 (93%)	11 (7%)	18	51
18	S	155/157 (99%)	148 (96%)	7 (4%)	32	63
19	T	139/140 (99%)	134 (96%)	5 (4%)	40	68
20	U	91/115 (79%)	88 (97%)	3 (3%)	43	70
21	V	100/107 (94%)	99 (99%)	1 (1%)	80	90
22	W	55/126 (44%)	52 (94%)	3 (6%)	25	58
23	X	107/133 (80%)	105 (98%)	2 (2%)	62	82
24	Y	119/135 (88%)	115 (97%)	4 (3%)	42	69
25	Z	118/118 (100%)	112 (95%)	6 (5%)	28	60
26	a	120/121 (99%)	116 (97%)	4 (3%)	43	70
27	b	58/126 (46%)	57 (98%)	1 (2%)	66	84
28	c	88/97 (91%)	87 (99%)	1 (1%)	78	89
29	d	100/110 (91%)	96 (96%)	4 (4%)	36	65
30	e	115/121 (95%)	112 (97%)	3 (3%)	51	75
31	f	87/89 (98%)	79 (91%)	8 (9%)	11	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	g	98/100 (98%)	88 (90%)	10 (10%)	8	33
33	h	109/110 (99%)	106 (97%)	3 (3%)	49	74
34	i	82/89 (92%)	76 (93%)	6 (7%)	16	49
35	j	71/80 (89%)	69 (97%)	2 (3%)	49	74
36	k	64/65 (98%)	64 (100%)	0	100	100
37	l	47/48 (98%)	46 (98%)	1 (2%)	59	80
38	m	48/116 (41%)	45 (94%)	3 (6%)	21	53
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	94/94 (100%)	89 (95%)	5 (5%)	26	59
41	p	74/75 (99%)	72 (97%)	2 (3%)	50	74
42	t	113/121 (93%)	106 (94%)	7 (6%)	21	54
43	u	177/177 (100%)	163 (92%)	14 (8%)	14	45
All	All	5642/6318 (89%)	5403 (96%)	239 (4%)	39	64

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.