



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:15 PM BST

PDB ID : 4V7H
EMDB ID: : EMD-1345
Title : Structure of the 80S rRNA and proteins and P/E tRNA for eukaryotic ribosome based on cryo-EM map of *Thermomyces lanuginosus* ribosome at 8.9Å resolution
Authors : Taylor, D.J.; Devkota, B.; Huang, A.D.; Topf, M.; Narayanan, E.; Sali, A.; Harvey, S.C.; Frank, J.
Deposited on : 2009-09-22
Resolution : 8.90 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

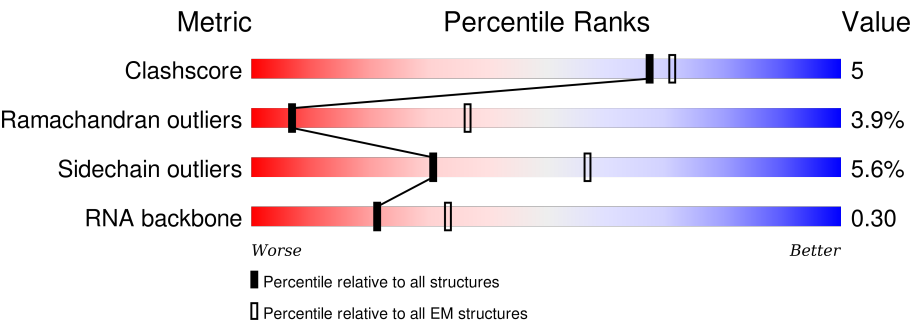
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

1 Overall quality at a glance i

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

The reported resolution of this entry is 8.90 Å.

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




























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

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 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	AA	1761	<div><div>72%</div><div>24%</div><div>.</div></div>
2	AB	193	<div><div>97%</div><div>.</div></div>
3	AC	188	<div><div>93%</div><div>7%</div><div>.</div></div>
4	AD	158	<div><div>65%</div><div>12%</div><div>.</div><div>22%</div></div>
5	AE	162	<div><div>93%</div><div>6%</div><div>.</div></div>
6	AG	186	<div><div>91%</div><div>8%</div><div>.</div></div>
7	AH	125	<div><div>89%</div><div>7%</div><div>.</div><div>.</div></div>
8	AI	138	<div><div>83%</div><div>11%</div><div>.</div><div>.</div></div>


















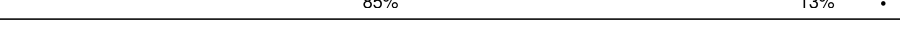


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Mol	Chain	Length	Quality of chain
9	AJ	96	
10	AK	125	
11	AL	118	
12	AM	130	
13	AN	50	
14	AO	84	
15	AQ	80	
16	AS	71	
17	AR	313	
18	AT	141	
19	A7	76	
20	B0	109	
21	B1	48	
22	B2	98	
23	B8	118	
24	B9	72	
25	BA	213	
26	BB	243	
27	BC	362	
28	BD	257	
29	BE	237	
30	BF	213	
31	BG	113	
32	BH	179	
33	BI	165	

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Mol	Chain	Length	Quality of chain
34	BJ	151	 89% 10% .
35	BK	138	 89% 10% .
36	BL	192	 90% 9% .
37	BM	178	 77% 19% . .
38	BN	150	 93% 7%
39	BO	121	 94% 5% .
40	BP	176	 83% 16% .
41	BQ	116	 91% 9%
42	BR	131	 86% 13% .
43	BS	45	 82% 16% .
44	BT	80	 86% 13% .
45	BU	116	 95% . .
46	BV	142	 83% 15% .
47	BW	79	 91% 6% .
48	BX	86	 86% 14%
49	BY	52	 90% 8% .
50	BZ	92	 85% 13% .
51	B3	113	 . 60% 36%
52	B4	157	 . 60% 36% .
53	B5	3170	 . 65% 31% .

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 165754 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1761	Total	C	N	O	P	0	3
			37458	16745	6626	12327	1760		

- Molecule 2 is a protein called 40S ribosomal protein S0(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	193	Total	C	N	O	S	0	0
			1500	958	269	271	2		

- Molecule 3 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	188	Total	C	N	O	S	0	0
			1469	929	271	263	6		

- Molecule 4 is a protein called 40S ribosomal protein S9(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	124	Total	C	N	O	S	0	0
			1018	647	189	181	1		

- Molecule 5 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	162	Total	C	N	O	S	0	0
			1207	765	222	218	2		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AG	186	Total	C	N	O	S	0	0
			1456	908	277	268	3		

- Molecule 7 is a protein called 40S ribosomal protein S22(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AH	125	Total	C	N	O	S	0	0
			992	634	181	174	3		

- Molecule 8 is a protein called 40S ribosomal protein S16(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AI	138	Total	C	N	O	S	0	0
			1087	695	200	192			

- Molecule 9 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AJ	96	Total	C	N	O	S	0	0
			771	487	140	143	1		

- Molecule 10 is a protein called 40S ribosomal protein S14(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	125	Total	C	N	O	S	0	0
			924	566	179	176	3		

- Molecule 11 is a protein called 40S ribosomal protein S23(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	118	Total	C	N	O	S	0	0
			906	579	166	159	2		

- Molecule 12 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AM	130	Total	C	N	O	S	0	0
			1077	669	217	189	2		

- Molecule 13 is a protein called 40S ribosomal protein S29(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AN	50	Total	C	N	O	S	0	0
			417	258	87	68	4		

- Molecule 14 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AO	84	Total	C	N	O	S	0	0
			694	446	129	118	1		

- Molecule 15 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AQ	80	Total	C	N	O	S	0	0
			643	410	127	104	2		

- Molecule 16 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AS	71	Total	C	N	O	S	0	0
			548	348	101	93	6		

- Molecule 17 is a protein called RACK1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AR	313	Total	C	N	O	S	0	0
			2410	1526	413	463	8		

- Molecule 18 is a protein called s19e protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AT	141	Total	C	N	O	S	0	0
			1102	687	206	207	2		

- Molecule 19 is a RNA chain called P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	A7	76	Total	C	N	O	P	0	0
			1648	746	294	533	75		

- Molecule 20 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	B0	109	Total	C	N	O	S	0	0
			881	555	176	149	1		

- Molecule 21 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	B1	48	Total	C	N	O	S	0	0
			424	263	95	64	2		

- Molecule 22 is a protein called 60S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	B2	98	Total	C	N	O	S	0	0
			752	484	125	142	1		

- Molecule 23 is a protein called 60S ribosomal protein LP0.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	B8	118	Total	C	N	O	S	0	0
			947	609	167	168	3		

- Molecule 24 is a protein called 60S ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B9	72	Total	C	N	O	S	0	0
			539	332	104	98	5		

- Molecule 25 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BA	213	Total	C	N	O	S	0	0
			1683	1074	294	306	9		

- Molecule 26 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BB	243	Total	C	N	O	S	0	0
			1848	1150	374	323	1		

- Molecule 27 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BC	362	Total	C	N	O	S	0	0
			2887	1833	545	502	7		

- Molecule 28 is a protein called 60S ribosomal protein L4(B).

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BD	257	Total	C	N	O	S	0	0
			1950	1226	375	346	3		

- Molecule 29 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BE	237	Total	C	N	O	S	0	0
			1913	1210	329	372	2		

- Molecule 30 is a protein called 60S ribosomal protein L7(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BF	213	Total	C	N	O	S	0	0
			1561	1010	281	269	1		

- Molecule 31 is a protein called 60S ribosomal protein L8(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BG	113	Total	C	N	O	S	0	0
			844	540	144	158	2		

- Molecule 32 is a protein called 60S ribosomal protein L9(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BH	179	Total	C	N	O	S	0	0
			1418	896	260	259	3		

- Molecule 33 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BI	165	Total	C	N	O	S	0	0
			1326	834	257	228	7		

- Molecule 34 is a protein called 60S ribosomal protein L11(B).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BJ	151	Total	C	N	O	S	0	0
			1195	744	229	218	4		

- Molecule 35 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BK	138	Total	C	N	O	S	0	0
			1038	651	190	195	2		

- Molecule 36 is a protein called 60S ribosomal protein L15(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BL	192	Total	C	N	O	S	0	0
			1618	1011	340	266	1		

- Molecule 37 is a protein called 60S ribosomal protein L16(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BM	178	Total	C	N	O	S	0	0
			1317	845	254	217	1		

- Molecule 38 is a protein called 60S ribosomal protein L17(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BN	150	Total	C	N	O		0	0
			1189	742	230	217			

- Molecule 39 is a protein called 60S ribosomal protein L18(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BO	121	Total	C	N	O	S	0	0
			931	598	170	162	1		

- Molecule 40 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BP	176	Total	C	N	O		0	0
			1317	816	277	224			

- Molecule 41 is a protein called 60S ribosomal protein L21(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BQ	116	Total	C	N	O	S	0	0
			893	564	173	153	3		

- Molecule 42 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BR	131	Total	C	N	O	S	0	0
			977	614	183	173	7		

- Molecule 43 is a protein called 60S ribosomal protein L24(A).

Mol	Chain	Residues	Atoms				AltConf	Trace
43	BS	45	Total	C	N	O	0	0
			371	238	73	60		

- Molecule 44 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BT	80	Total	C	N	O	S	0	0
			642	411	108	121	2		

- Molecule 45 is a protein called 60S ribosomal protein L26(A).

Mol	Chain	Residues	Atoms				AltConf	Trace
45	BU	116	Total	C	N	O	0	0
			916	576	179	161		

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BV	142	Total	C	N	O	S	0	0
			1123	717	218	185	3		

- Molecule 47 is a protein called 60S ribosomal protein L31(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	79	Total	C	N	O	S	0	0
			663	415	135	112	1		

- Molecule 48 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BX	86	Total	C	N	O	S	0	0
			605	379	111	114	1		

- Molecule 49 is a protein called 60S ribosomal protein L37(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BY	52	Total	C	N	O	S	0	0
			403	245	85	69	4		

- Molecule 50 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BZ	92	Total	C	N	O	S	0	0
			749	472	151	121	5		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B3	113	Total	C	N	O	P	0	0
			2403	1075	429	787	112		

- Molecule 52 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B4	157	Total	C	N	O	P	0	0
			3329	1490	581	1102	156		

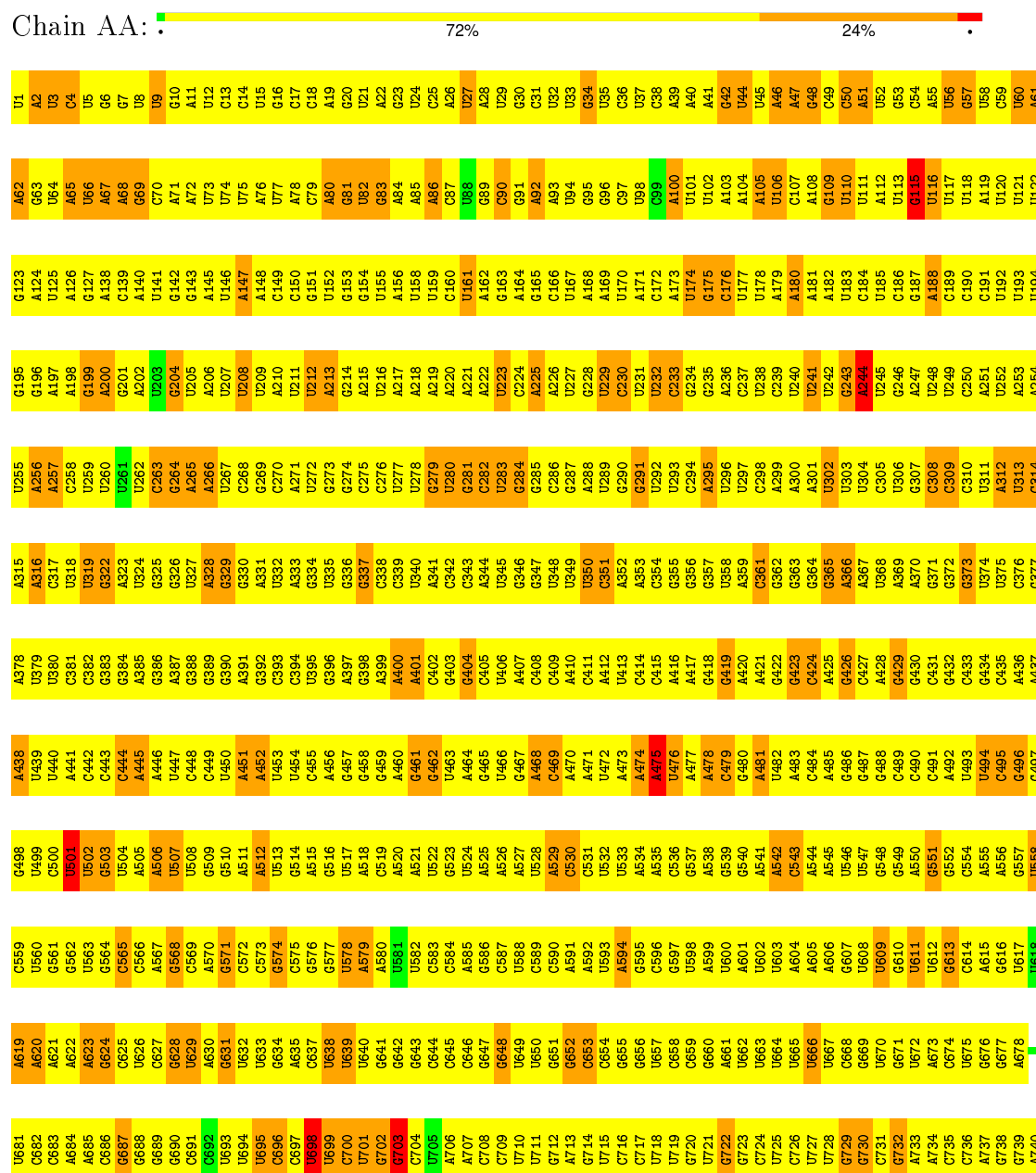
- Molecule 53 is a RNA chain called 26S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B5	3170	Total	C	N	O	P	0	0
			67775	30273	12178	22155	3169		

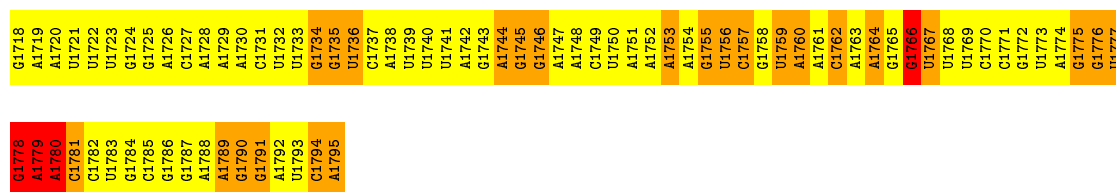
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 18S rRNA

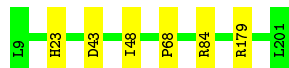


A1653	A1598	G1538	G1478	G1415	G1355	U1295	A1234	C1174	A1113	G1048	U988	A928	G868	A804	C741
U1659	G1599	G1539	C1479	G1416	C1356	G1296	U1235	G1175	U1114	U1049	C989	A929	G869	U805	U742
G1660	C1600	G1540	C1480	C1417	C1357	G1297	U1236	C1176	G1115	G1050	G990	U930	C870	A806	U743
G1661	U1601	A1481	A1481	A1418	U1358	U1298	G1237	C1177	G1116	U1051	A991	U931	G871	A807	U744
G1662	G1602	U1542	G1482	A1419	U1359	U1299	A1238	U1178	U1117	U1052	A992	A932	G872	U808	A746
G1663	G1603	A1543	C1483	U1420	U1360	U1300	G1239	A1179	C1118	U1053	G993	C933	U873	A809	C747
U1664	G1604	A1421	G1484	A1421	C1361	G1301	A1240	A1180	G1119	U1054	A994	U934	C874	G810	U748
A1665	G1605	A1422	A1485	A1422	C1362	U1302	G1241	U1181	C1120	U1055	U995	C935	C875	A811	U749
G1666	G1606	G1346	G1486	C1423	U1363	C1303	C1242	U1182	A1121	U1056	G996	C936	G876	A812	U750
U1667	U1607	C1547	U1487	A1424	G1364	U1304	U1243	U1183	A1122	G1057	A997	G937	G877	U813	G751
G1668	G1608	A1548	G1488	G1425	G1365	G1305	C1244	U1184	G1123	A1058	U998	A938	G878	A814	A752
A1669	A1609	U1549	U1489	G1426	U1366	C1306	U1245	A1185	G1124	A1059	C999	A939	G879	G815	A753
G1670	U1610	U1550	U1490	U1427	U1367	U1307	U1246	C1186	C1125	U1060	U1000	A940	C880	G816	A754
G1671	G1611	G1551	A1491	C1428	A1368	U1308	U1247	U1187	U1126	G1061	G1001	G941	A881	A817	A755
C1672	A1612	U1552	C1492	U1429	U1369	A1309	C1248	C1188	G1127	A1062	G1002	C942	U882	C818	A756
C1673	C1613	A1553	C1493	A1430	C1370	A1310	U1249	A1189	A1128	C1063	U1003	A943	C883	U820	A757
U1674	G1614	A1554	U1494	U1431	C1371	U1311	U1250	A1190	A1129	C1064	A1004	U944	G884	U821	U758
C1675	U1615	U1555	U1495	A1433	A1372	G1312	G1251	C1191	A1130	A1066	C1005	U945	G885	U822	U759
A1676	C1616	U1556	G1496	U1434	C1373	G1313	A1252	A1192	C1131	C1067	C1006	U946	U886	G823	A760
G1677	C1617	A1557	G1497	G1435	U1374	C1314	U1253	C1193	U1132	U1068	G1007	G947	U887	G824	G761
G1678	U1618	U1558	C1498	G1436	U1375	G1315	U1254	G1194	U1133	C1069	U1008	C948	U888	U825	A762
A1679	U1619	U1559	C1499	G1437	C1376	A1316	U1255	G1195	A1134	G1070	C1009	C949	U889	U826	G763
U1680	G1620	G1560	G1500	C1438	U1377	U1317	U1256	G1196	A1135	G1071	C1010	A950	C890	C827	U764
C1681	C1621	C1561	A1501	U1439	U1378	A1318	G1257	G1197	A1136	U1072	U1011	A951	A891	U828	G765
U1682	U1622	U1562	G1502	U1440	A1379	A1319	U1258	A1198	G1137	A1073	A1012	G952	A892	A829	U766
C1683	C1623	C1563	A1503	A1443	G1380	C1320	G1259	A1199	G1138	C1074	G1013	G953	U893	U830	U767
C1684	U1624	U1564	G1504	A1444	A1381	G1321	G1260	A1200	A1139	C1075	U1014	A954	U894	U831	C768
U1685	U1625	U1565	G1505	G1445	G1382	A1322	G1261	C1201	A1140	U1076	C1015	C955	G895	U832	A769
A1686	U1626	C1566	U1506	G1446	G1383	A1323	U1262	U1202	U1141	U1077	U1016	G956	U896	U833	A770
G1687	G1627	A1567	C1507	U1447	G1384	C1324	G1263	C1203	U1142	A1078	U1017	U957	C897	G834	A771
G1688	U1628	A1568	U1508	U1448	A1385	G1325	G1264	A1204	G1143	C1079	A1018	U958	G898	U835	G772
A1689	A1629	C1569	U1509	C1449	C1386	A1326	U1265	C1205	A1144	G1080	A1019	U959	A899	U836	C773
G1690	C1630	G1570	G1510	U1450	U1387	G1327	G1266	C1206	C1145	A1081	C1020	U960	G900	G837	A774
A1691	A1631	A1571	G1511	G1451	A1388	A1328	G1267	A1207	G1146	G1082	C1021	C961	U901	G838	G775
A1692	C1632	G1572	U1512	G1452	U1389	C1329	U1268	G1208	G1147	A1083	A1022	A962	U902	U839	G776
G1693	A1633	G1573	A1513	G1453	C1390	U1330	G1269	G1209	A1148	A1084	U1023	G963	G903	U840	C777
C1634	C1634	A1574	A1514	G1454	G1391	U1331	C1270	U1210	A1149	A1085	A1024	U964	A904	U841	G778
G1695	C1635	A1575	U1515	C1455	G1392	U1332	A1271	C1211	G1150	U1086	A1025	A965	A905	C842	U779
G1696	G1636	U1576	C1516	G1456	U1393	A1333	U1272	C1212	G1151	C1087	A1026	A966	A906	U843	A780
G1697	C1637	U1577	U1517	C1457	U1394	A1334	G1273	A1213	G1152	A1088	C1027	U967	U907	A844	U781
A1698	C1638	C1578	U1518	A1458	U1395	C1335	G1274	G1214	C1153	A1089	U1028	C968	U908	G845	U782
A1699	G1639	C1579	G1519	U1459	C1396	C1336	C1275	A1215	A1154	A1090	A1029	A969	C909	G846	G783
U1700	G1640	U1580	U1520	G1460	A1397	U1337	C1276	C1216	C1155	G1091	U1030	A970	U910	A847	C784
C1701	U1641	A1581	G1521	C1461	A1398	A1338	G1277	A1217	C1156	U1092	G1031	G971	U911	C848	U785
U1702	C1642	G1582	A1522	G1462	G1399	C1339	U1278	C1218	C1158	C1093	C1032	A972	G912	C849	C786
C1703	G1643	U1583	A1523	G1463	C1400	U1340	U1279	A1219	U1159	G1098	C1033	A973	G913	U850	G787
G1704	C1644	A1584	A1524	G1464	C1401	A1341	U1280	A1220	A1160	G1099	G1034	C974	A914	U851	A788
A1705	U1645	C1585	C1525	G1465	G1402	A1342	C1281	U1221	G1161	U1100	A1035	G975	U915	C852	A789
U1706	A1646	G1586	U1526	U1466	A1403	A1343	U1282	A1222	G1162	U1101	G1036	A976	U916	G853	U790
G1707	G1647	C1587	C1527	A1467	U1404	U1344	A1284	A1223	A1163	C1102	U1037	A977	U917	U854	A791
U1708	U1648	G1588	C1528	C1468	G1405	A1345	G1285	G1224	G1164	U1103	A1038	A978	A918	A855	U792
C1709	A1649	U1589	G1529	A1469	G1406	G1346	U1286	G1225	U1165	G1104	G1039	G979	U919	A856	A796
A1710	U1650	A1590	U1530	C1470	A1407	G1347	U1287	A1226	G1166	G1105	A1040	U980	U920	U857	A797
G1711	C1651	A1591	C1531	U1471	A1408	G1348	G1288	U1227	G1167	G1106	U1041	U981	G921	G858	G797
A1712	G1652	G1592	G1532	G1472	G1409	G1349	G1289	U1228	A1168	G1107	C1042	A982	A922	A859	C798
G1713	A1653	U1593	U1533	A1473	U1410	G1350	U1290	G1229	G1169	G1108	G1043	G983	A923	U860	A799
C1714	U1654	C1594	G1534	C1474	U1411	G1351	G1291	A1230	C1170	G1109	G1044	G984	G924	U864	U800
G1715	U1655	A1595	U1535	G1475	U1412	C1352	G1292	C1231	C1171	A1110	U1045	G985	A925	A865	G801
G1716	G1656	U1596	U1536	G1476	G1413	A1293	A1293	C1232	U1172	G1111	U1046	G986	C926	G866	G802
A1717	A1657	C1597	G1537	A1477	A1414	A1354	G1294	G1233	G1173	U1112	G1047	A987	U927	G867	A803



- Molecule 2: 40S ribosomal protein S0(A)

Chain AB: 97%



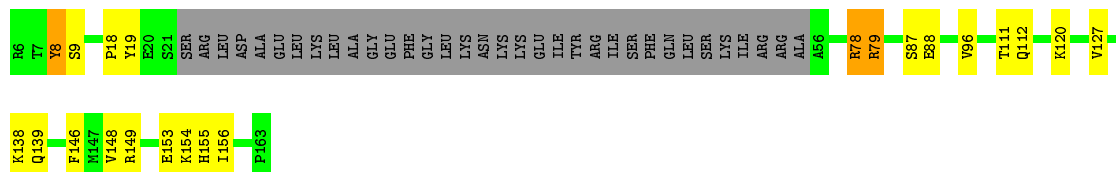
- Molecule 3: 40S ribosomal protein S3

Chain AC: 93%



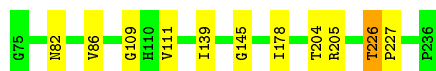
- Molecule 4: 40S ribosomal protein S9(A)

Chain AD: 65%



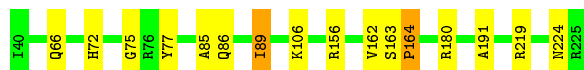
- Molecule 5: 40S ribosomal protein S2

Chain AE: 93%



- Molecule 6: 40S ribosomal protein S5

Chain AG: 91%

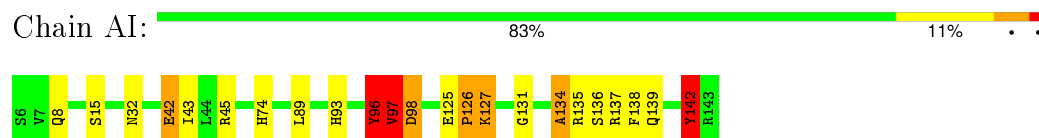


- Molecule 7: 40S ribosomal protein S22(A)

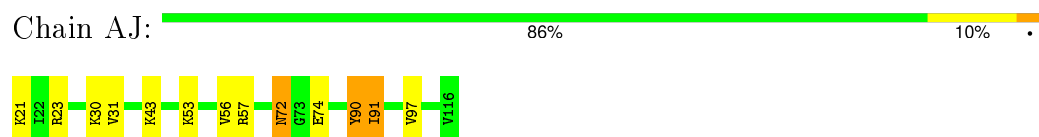
Chain AH: 89%



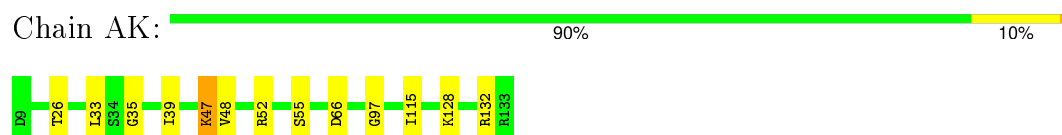
- Molecule 8: 40S ribosomal protein S16(A)



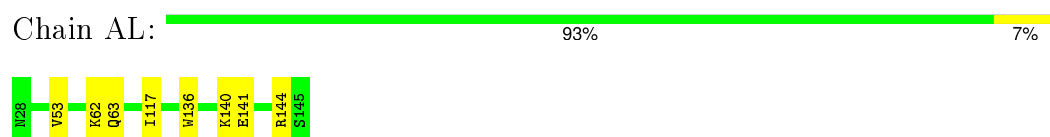
- Molecule 9: 40S ribosomal protein S20



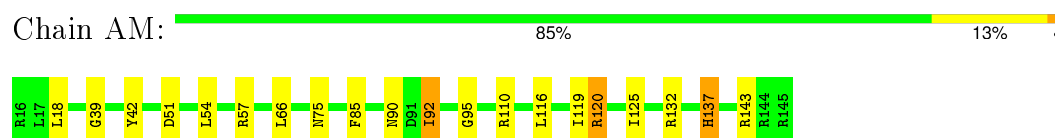
- Molecule 10: 40S ribosomal protein S14(A)



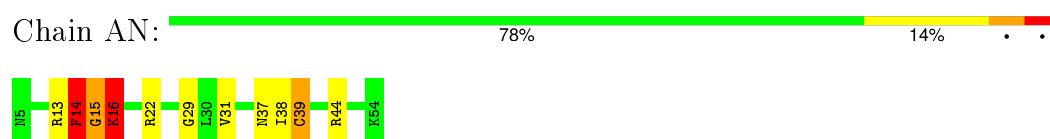
- Molecule 11: 40S ribosomal protein S23(A)



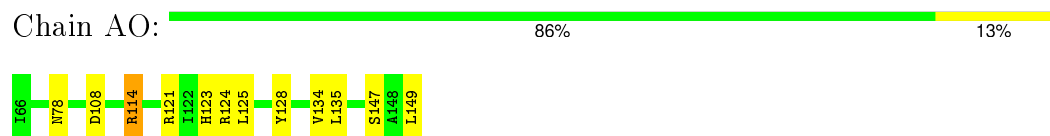
- Molecule 12: 40S ribosomal protein S18



- Molecule 13: 40S ribosomal protein S29(A)



- Molecule 14: 40S ribosomal protein S13



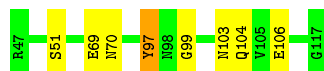
- Molecule 15: 40S ribosomal protein S11

Chain AQ:  93% 6%

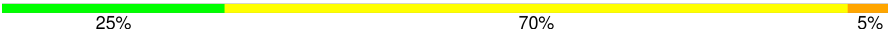


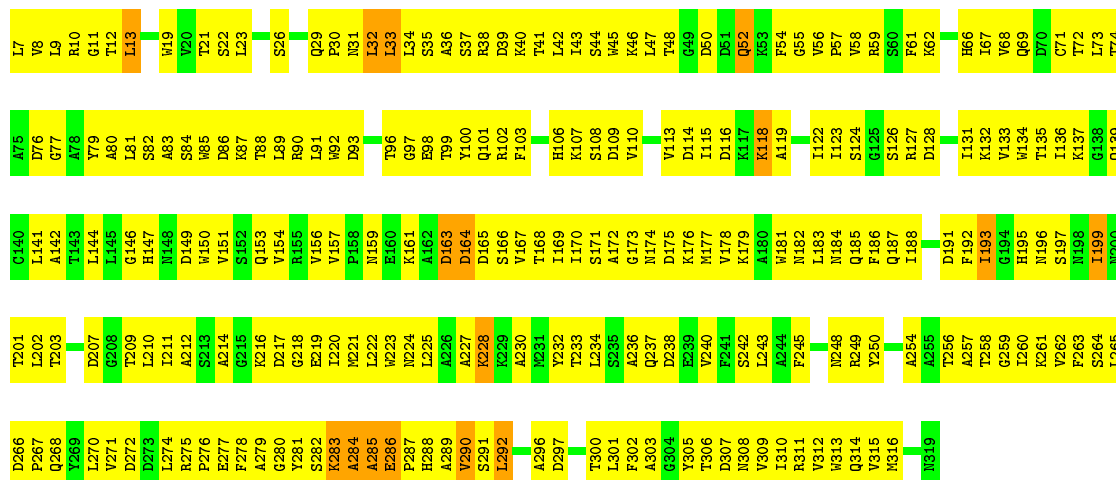
- Molecule 16: 40S ribosomal protein S15

Chain AS:  89% 10%




- Molecule 17: RACK1 protein

Chain AR:  25% 70% 5%



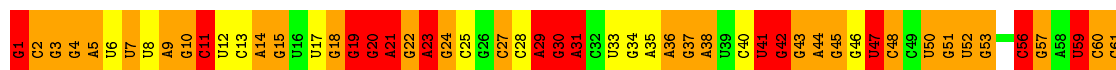
- Molecule 18: s19e protein

Chain AT:  82% 15%




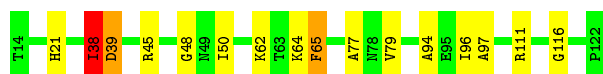
- Molecule 19: P/E tRNA

Chain A7:  11% 21% 42% 26%



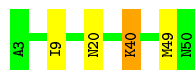
- Molecule 20: 60S ribosomal protein L32

Chain B0:  85% 12%



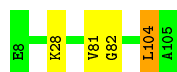
- Molecule 21: 60S ribosomal protein L39

Chain B1: 92% 6% •



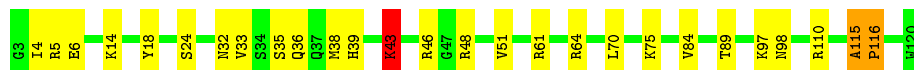
- Molecule 22: 60S ribosomal protein L30e

Chain B2: 96% ••



- Molecule 23: 60S ribosomal protein LP0

Chain B8: 77% 20% ••



- Molecule 24: 60S ribosomal protein L43

Chain B9: 82% 14% •



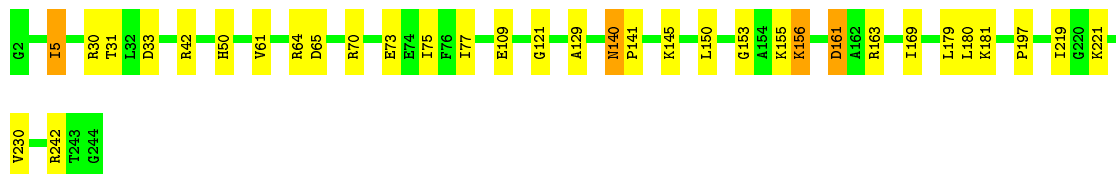
- Molecule 25: 60S ribosomal protein L1

Chain BA: 91% 8% •



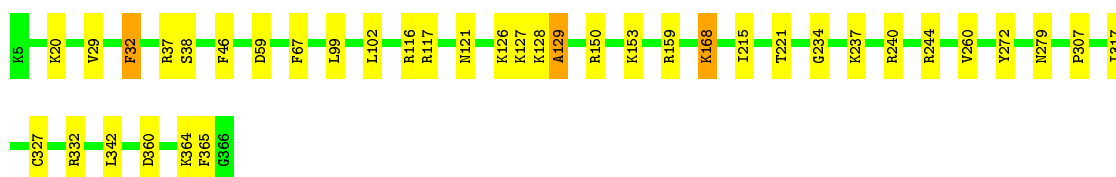
- Molecule 26: 60S ribosomal protein L2

Chain BB: 86% 12% •



- Molecule 27: 60S ribosomal protein L3

Chain BC: 90% 10% •



- Molecule 28: 60S ribosomal protein L4(B)

Chain BD: 91% 8% .



- Molecule 29: 60S ribosomal protein L5

Chain BE: 86% 13% .



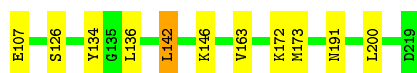
- Molecule 30: 60S ribosomal protein L7(A)

Chain BF: 93% 6% .



- Molecule 31: 60S ribosomal protein L8(A)

Chain BG: 90% 9% .



- Molecule 32: 60S ribosomal protein L9(A)

Chain BH: 88% 11% .



- Molecule 33: 60S ribosomal protein L10

Chain BI: 88% 9% .



- Molecule 34: 60S ribosomal protein L11(B)

Chain BJ: 89% 10% .



- Molecule 35: 60S ribosomal protein L12

Chain BK: 89% 10% .



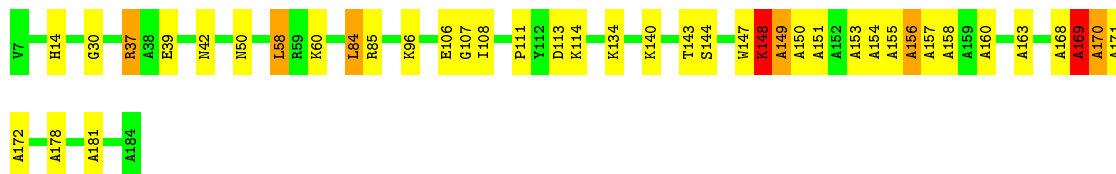
- Molecule 36: 60S ribosomal protein L15(A)

Chain BL: 90% 9% .



- Molecule 37: 60S ribosomal protein L16(A)

Chain BM: 77% 19% . .



- Molecule 38: 60S ribosomal protein L17(A)

Chain BN: 93% 7%



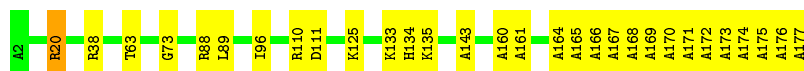
- Molecule 39: 60S ribosomal protein L18(A)

Chain BO: 94% 5% .



- Molecule 40: 60S ribosomal protein L19

Chain BP: 83% 16% .



- Molecule 41: 60S ribosomal protein L21(A)

Chain BQ: 91% 9%



- Molecule 42: 60S ribosomal protein L23

Chain BR: 86% 13% .



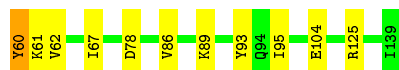
- Molecule 43: 60S ribosomal protein L24(A)

Chain BS: 82% 16% .



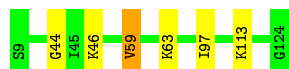
- Molecule 44: 60S ribosomal protein L25

Chain BT: 86% 13% .



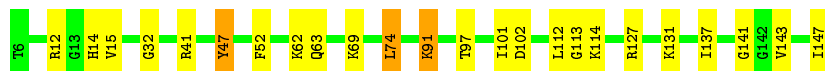
- Molecule 45: 60S ribosomal protein L26(A)

Chain BU: 95% . .



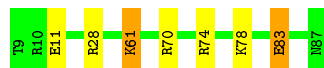
- Molecule 46: 60S ribosomal protein L28

Chain BV: 83% 15% .



- Molecule 47: 60S ribosomal protein L31(A)

Chain BW: 91% 6% .

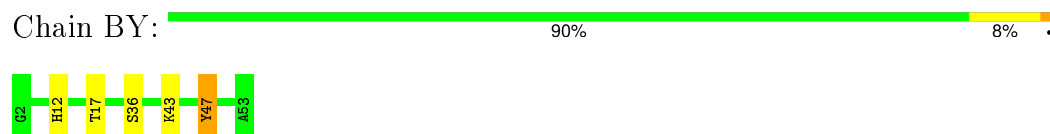


- Molecule 48: 60S ribosomal protein L35

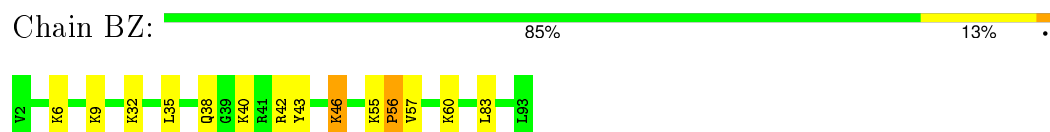
Chain BX: 86% 14%



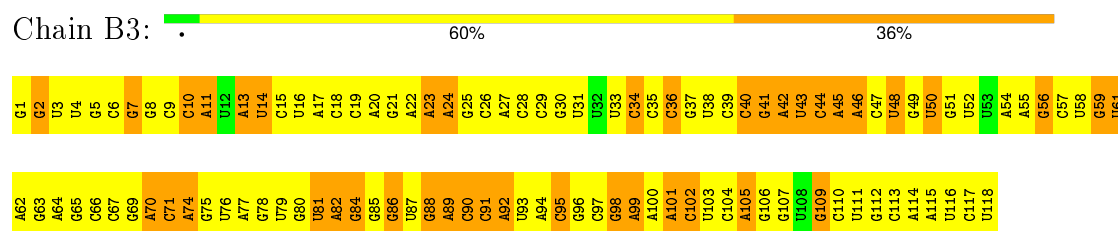
- Molecule 49: 60S ribosomal protein L37(A)



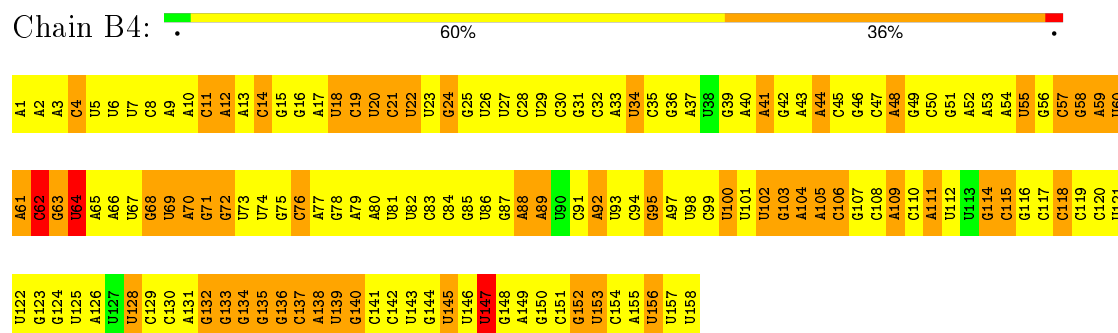
- Molecule 50: 60S ribosomal protein L42



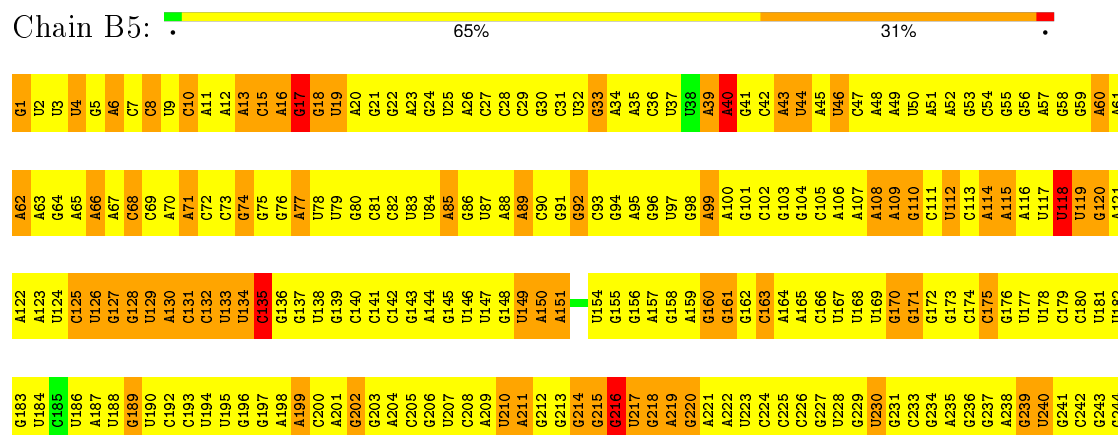
- Molecule 51: 5S ribosomal RNA



- Molecule 52: 5.8S ribosomal RNA



- Molecule 53: 26S ribosomal RNA



A1231	A1165	A1105	U1044	A974	A914	G853	C793	G733	U669	G609	U549	C489	C427	A367	A306	U245
C1232	G1166	G1106	G1045	G975	A915	G854	U794	C734	C670	G610	A550	A490	A428	A368	A307	U246
G1233	U1167	C1107	A1046	C976	G916	U855	G795	A735	U671	A611	A551	C491	U429	A369	A308	C247
G1234	U1168	U1108	A1047	U977	A917	G856	U796	A736	A672	U612	G552	U492	U430	U370	U310	U248
U1235	A1169	U1109	C1048	C978	C918	G857	U797	G737	U673	G613	U553	G493	U431	G371	U311	U249
G1236	A1170	U1110	U1049	G979	U919	A858	G798	A738	U674	G614	A554	G494	G432	A372	C312	U250
C1237	G1171	U1111	U050	U986	A920	G859	G799	G739	C675	U615	U555	G495	A433	A373	A313	C251
C1238	U1172	A1112	U1051	U987	A921	C860	G800	G740	A676	G616	U556	C496	U434	A374	U314	U252
U1239	U1173	U1113	U1052	U988	U922	C861	A801	U741	A677	G617	A557	C497	U435	A375	C315	A253
A1240	A1174	U1114	A1053	U989	C923	U862	C802	G742	U678	C618	U558	A498	A438	A376	U316	A254
C1175	C1175	A1115	A1054	A990	G924	C863	C803	G743	U679	A619	A559	G499	C439	A377	U317	A255
G1242	G1176	G1116	U1055	U991	A925	G864	C804	U744	A680	U620	G560	C500	A440	A378	A318	G256
G1243	G1177	U1117	U1056	G992	A926	U865	G805	G745	U681	A621	C561	C501	U441	C379	A319	U257
A1244	G1178	C1118	A1057	A993	C927	A866	A806	A746	U682	A622	C562	U502	G442	U380	G320	G258
A1245	A1179	C1119	U1058	G994	C928	G867	A807	A747	U683	U623	U563	C503	G443	U381	C321	C259
G1246	A1180	A1120	G1059	G995	A929	C868	U808	U748	G684	G624	U564	C504	U444	U382	U322	C260
U1247	U1181	U1121	U1060	U996	U930	G869	G809	G749	G685	G625	U565	G505	G445	G383	G323	U261
U1248	A1182	U1122	A1061	A997	G931	G870	A810	G750	G688	U626	G566	U506	U446	A384	A324	U262
G1249	C1183	U1123	A1062	A998	U932	U871	U811	A751	U689	U627	G567	U507	U447	A385	A325	C263
G1250	A1184	U1124	G1063	G999	A933	U872	G812	C752	A690	A628	U568	U508	U448	A386	U326	G264
A1251	C1185	U1125	A1064	C1000	G934	U874	G813	C753	A691	U629	U569	U509	U449	A387	A327	A265
A1252	G1186	G1126	A1065	A1002	U935	G875	U814	G754	A692	A630	U570	C510	G450	A388	U328	A266
U1253	C1187	G1127	A1066	A1003	A936	A876	G815	A755	C695	U631	A571	G511	U451	A389	U329	G267
G1254	U1188	U1128	U1067	U1004	G937	C877	A816	U756	C696	G632	A572	U512	G452	G390	G330	A268
C1255	C1189	A1129	C1068	G1005	G938	G878	A817	C757	A697	C633	C573	G513	C453	A391	G331	G269
G1256	A1190	A1130	C1069	A1006	U939	U879	C818	C758	U698	C634	U574	G514	C454	G392	C332	U270
C1257	U1191	G1131	U1070	A1007	G940	G880	U819	U759	A699	G635	C575	C515	C455	U393	G333	C271
U1258	C1192	C1132	U1071	U1008	G941	C881	A820	G760	C700	G636	C576	A516	U456	A394	C340	C272
A1259	U1193	A1133	U1072	A1009	U942	A882	A821	A761	C697	C637	C577	G517	U457	A395	G335	A273
A1260	A1200	G1134	U1073	G1010	U943	A883	G822	U762	C702	G638	A578	G518	U458	A396	A336	G274
G1261	C1201	A1135	U1074	A1011	C944	A884	C823	G763	G703	G639	G579	A519	U459	A397	G337	U275
A1262	A1202	A1136	A1075	G1012	C945	U885	C824	U764	U704	U640	C580	U520	C460	A398	A338	U276
A1263	C1203	C1137	C1076	G1013	U946	C886	U825	C765	A705	C641	U581	A521	U461	A399	C339	G277
G1264	A1204	U1138	U1077	U1014	G947	G887	A826	U766	U706	U642	G582	A522	C462	A400	C340	U278
U1265	A1205	G1139	U1078	C1017	C948	A888	A827	U767	G707	U643	G583	A523	C463	U401	G341	U279
G1266	G1206	G1140	A1079	G1018	C949	U889	U828	C768	A709	A644	A584	C524	U464	A402	A342	U280
U1267	C1207	C1141	U1080	G1019	G950	C890	U829	G769	A709	A645	A585	C525	U465	A403	U343	G281
U1268	U1208	G1142	U1081	G1020	A951	G891	A830	G770	A710	A646	C586	C526	U466	G404	A344	G282
U1269	G1209	A1143	U1082	G1021	A952	U892	G831	A771	A711	A647	U587	A527	U467	U405	G345	G283
A1270	U1210	U1144	G1083	U1022	G953	C893	G832	U772	G712	C648	G588	U528	G468	G406	C346	A284
A1271	U1211	G1145	A1084	C1023	U954	G894	U834	G773	U713	C649	A589	A529	G469	A407	G347	A285
C1272	A1212	C1146	A1085	G1024	U955	A895	U834	G774	G714	C650	G590	G530	G470	A408	A348	U286
G1273	G1213	G1147	C1086	A1025	U956	A896	G835	A775	A715	G651	U591	G531	U471	A409	A349	G287
A1274	U1214	G1148	G1087	A1026	C957	U897	A836	U776	G716	G652	G592	A532	A472	U410	C350	C288
C1275	U1215	G1149	U1088	A1027	C958	U898	A837	U777	C717	A653	A593	A533	G473	U411	A351	A289
U1276	C1216	A1150	G1089	G1029	C959	U899	G838	U778	G718	C654	A594	U534	G474	G412	A352	G290
C1277	A1217	G1090	G1090	A1030	U960	C899	C839	G779	U719	C655	A595	G535	G475	U413	G353	C291
A1278	U1218	U1152	A1091	C1031	C961	G901	C840	A780	A720	U656	U596	U536	G476	U414	U354	U292
G1279	G1219	A1153	C1092	C1032	A962	G902	A841	G781	G721	A657	G597	A537	A477	G415	A355	C293
C1280	U1220	C1154	A1093	U1033	G963	U903	G842	U782	G722	G658	A598	G538	A478	A416	C356	U294
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C1282	G1222	U1095	U1095	G1035	A965	U905	G844	A784	U724	A660	G600	U540	C480	A418	G358	A296
G1283	A1223	G1157	U1096	A1036	U966	A906	G845	G785	G725	U661	U601	U541	U481	G419	U359	G297
C1284	C1224	G1097	C1037	G907	A967	G907	A846	A786	G726	U662	A602	G542	C482	G420	G360	U298
G1285	A1225	A1159	A1098	C1038	G968	G908	A847	G787	G727	G663	A603	C543	G483	G421	A361	G299
A1286	G1226	C1160	A1099	U1039	C969	G909	A848	G788	G728	U664	G604	C544	C484	A422	U362	G300
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U1288	C1228	U1162	G1101	U1041	G971	C911	U850	U790	C730	A666	C606	C546	U486	G424	G364	U302
G1289	U1229	A1163	A1102	U1042	C972	G912	U851	A791	C671	C667	A607	G547	U487	G425	A365	G303
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A3399	G3342	C3220	G3220	C3159	C3099	U3038	U2978	G2918	U2858	C2798	U2735	A2674	U2613	U2553	C2492
G3343	U3281	U3281	C3221	U3160	U3100	C3039	U2979	A2919	U2859	A2799	A2736	C2675	G2614	U2554	U2493
A3344	U3282	U3222	U3222	C3161	G3101	U3040	U2980	U2920	U2860	G2800	C2737	A2676	G2615	G2555	G2494
G3345	A3223	G3102	G3102	C3162	A3041	U3041	U2981	U2921	U2861	A2801	A2738	G2677	C2616	U2556	G2495
U3346	G3284	U3284	G3224	A3163	A3103	U3042	A2982	G2922	U2862	A2802	A2739	A2678	U2617	G2557	G2496

4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO163 FILM	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, 5MU, OMG, H2U, YYG, 2MG, 5MC, 1MA, M2G, 7MG, PSU

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	AA	1.91	76/41893 (0.2%)	2.21	3096/65278 (4.7%)
10	AK	0.93	0/935	1.07	0/1257
11	AL	0.88	0/920	0.98	0/1226
12	AM	0.94	0/1094	1.08	2/1468 (0.1%)
13	AN	3.66	2/427 (0.5%)	1.42	4/567 (0.7%)
14	AO	0.92	0/707	1.04	0/950
15	AQ	0.96	0/656	1.04	0/885
16	AS	0.90	0/559	1.02	2/748 (0.3%)
17	AR	0.91	1/2463 (0.0%)	1.24	7/3350 (0.2%)
18	AT	0.96	2/1118 (0.2%)	1.10	6/1498 (0.4%)
19	A7	3.12	162/1483 (10.9%)	3.79	362/2311 (15.7%)
2	AB	0.87	0/1535	0.91	0/2097
20	B0	0.91	0/898	1.03	0/1201
21	B1	1.04	0/431	1.09	0/570
22	B2	0.85	0/760	0.89	0/1020
23	B8	0.94	0/965	1.09	4/1298 (0.3%)
24	B9	0.94	0/546	1.14	3/729 (0.4%)
25	BA	0.84	0/1709	0.97	0/2295
26	BB	0.95	0/1882	1.06	1/2528 (0.0%)
27	BC	0.91	0/2953	1.05	3/3974 (0.1%)
28	BD	0.89	0/1987	0.98	4/2690 (0.1%)
29	BE	0.94	0/1956	1.11	8/2646 (0.3%)
3	AC	0.94	0/1488	1.00	0/1996
30	BF	0.85	0/1593	0.98	2/2160 (0.1%)
31	BG	0.80	0/853	1.01	0/1153
32	BH	0.89	0/1437	1.06	0/1935
33	BI	0.96	0/1352	1.12	3/1815 (0.2%)
34	BJ	0.97	0/1212	1.03	0/1622
35	BK	1.98	6/1049 (0.6%)	1.04	1/1408 (0.1%)
36	BL	1.01	0/1652	1.03	1/2211 (0.0%)
37	BM	0.97	2/1341 (0.1%)	1.33	6/1808 (0.3%)
38	BN	0.93	0/1212	1.03	4/1631 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	BO	0.92	0/943	0.97	0/1274
4	AD	0.93	0/1035	1.13	5/1390 (0.4%)
40	BP	0.94	0/1334	0.98	0/1791
41	BQ	0.91	0/909	0.98	1/1216 (0.1%)
42	BR	0.92	0/992	1.13	2/1333 (0.2%)
43	BS	1.03	0/380	1.12	2/504 (0.4%)
44	BT	0.85	0/649	1.00	2/873 (0.2%)
45	BU	0.93	0/927	0.96	0/1237
46	BV	0.88	0/1152	1.07	2/1542 (0.1%)
47	BW	0.99	0/673	1.06	0/894
48	BX	0.82	0/607	1.03	2/818 (0.2%)
49	BY	0.95	0/413	1.10	2/548 (0.4%)
5	AE	0.86	0/1227	0.99	0/1663
50	BZ	0.91	0/761	1.12	3/1006 (0.3%)
51	B3	1.34	1/2686 (0.0%)	2.18	192/4184 (4.6%)
52	B4	1.35	0/3719	2.19	267/5791 (4.6%)
53	B5	1.35	3/75857 (0.0%)	2.17	5569/118271 (4.7%)
6	AG	0.91	0/1472	0.98	1/1982 (0.1%)
7	AH	0.95	2/1008 (0.2%)	1.17	2/1351 (0.1%)
8	AI	2.93	6/1106 (0.5%)	1.15	5/1481 (0.3%)
9	AJ	0.85	0/781	1.04	2/1053 (0.2%)
All	All	1.46	263/179697 (0.1%)	1.97	9578/268527 (3.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	2	28
10	AK	0	4
12	AM	0	3
13	AN	0	2
14	AO	0	4
19	A7	0	44
2	AB	0	1
20	B0	0	1
23	B8	0	3
24	B9	0	3
26	BB	1	4
27	BC	0	1
28	BD	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
29	BE	1	7
30	BF	1	0
31	BG	2	2
32	BH	0	3
33	BI	0	2
34	BJ	0	3
35	BK	0	2
36	BL	1	7
37	BM	0	5
38	BN	0	2
39	BO	0	1
4	AD	0	3
40	BP	0	4
42	BR	0	3
43	BS	0	1
44	BT	0	1
45	BU	0	1
46	BV	0	3
47	BW	0	2
48	BX	2	1
49	BY	0	1
5	AE	0	1
50	BZ	0	5
51	B3	1	0
52	B4	0	6
53	B5	33	112
7	AH	1	0
8	AI	0	3
9	AJ	0	3
All	All	45	285

The worst 5 of 263 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	856	A	N3-C4	94.83	1.91	1.34
1	AA	856	A	C5-C4	83.45	1.97	1.38
1	AA	1200	A	N3-C4	80.10	1.82	1.34
1	AA	501	U	C2-N3	76.02	1.91	1.37
1	AA	856	A	C6-N1	74.78	1.87	1.35

The worst 5 of 9578 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1545	A	O5'-P-OP1	-67.13	30.14	110.70
1	AA	864	U	P-O3'-C3'	-44.04	66.85	119.70
1	AA	1516	C	O5'-P-OP2	-30.31	74.33	110.70
1	AA	1213	A	O5'-P-OP1	-23.91	82.01	110.70
1	AA	1519	G	O3'-P-O5'	23.73	149.08	104.00

5 of 45 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	109	G	C3'
1	AA	933	C	C2'
7	AH	34	ILE	CB
26	BB	161	ASP	CA
29	BE	216	GLU	CA

5 of 285 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	225	A	Sidechain
1	AA	244	A	Sidechain
1	AA	474	A	Sidechain
1	AA	475	A	Sidechain
1	AA	80	A	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	AA	37458	0	18828	602	0
2	AB	1500	0	1524	1	0
3	AC	1469	0	1534	1	0
4	AD	1018	0	1067	1	0
5	AE	1207	0	1274	0	0
6	AG	1456	0	1523	2	0
7	AH	992	0	1027	39	0
8	AI	1087	0	1145	19	0
9	AJ	771	0	829	2	0
10	AK	924	0	949	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	AL	906	0	970	1	0
12	AM	1077	0	1107	19	0
13	AN	417	0	408	22	0
14	AO	694	0	740	13	0
15	AQ	643	0	688	2	0
16	AS	548	0	574	3	0
17	AR	2410	0	2367	538	0
18	AT	1102	0	1112	38	0
19	A7	1648	0	830	56	0
20	B0	881	0	926	1	0
21	B1	424	0	459	1	0
22	B2	752	0	803	1	0
23	B8	947	0	972	19	0
24	B9	539	0	555	1	0
25	BA	1683	0	1772	3	0
26	BB	1848	0	1908	16	0
27	BC	2887	0	2964	3	0
28	BD	1950	0	2019	3	0
29	BE	1913	0	1842	1	0
30	BF	1561	0	1633	1	0
31	BG	844	0	909	0	0
32	BH	1418	0	1483	4	0
33	BI	1326	0	1368	2	0
34	BJ	1195	0	1230	15	0
35	BK	1038	0	1110	23	0
36	BL	1618	0	1673	1	0
37	BM	1317	0	1407	63	0
38	BN	1189	0	1201	0	0
39	BO	931	0	1010	0	0
40	BP	1317	0	1389	113	0
41	BQ	893	0	924	0	0
42	BR	977	0	1026	15	0
43	BS	371	0	382	1	0
44	BT	642	0	679	0	0
45	BU	916	0	996	0	0
46	BV	1123	0	1160	2	0
47	BW	663	0	700	0	0
48	BX	605	0	661	1	0
49	BY	403	0	398	0	0
50	BZ	749	0	815	0	0
51	B3	2403	0	1219	0	0
52	B4	3329	0	1685	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	B5	67775	0	34047	227	0
All	All	165754	0	111821	1335	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 5.

The worst 5 of 1335 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)
35:BK:121:PHE:CZ	35:BK:121:PHE:CE1	1.78	1.71
35:BK:121:PHE:CE2	35:BK:121:PHE:CZ	1.79	1.69
35:BK:121:PHE:CE2	35:BK:121:PHE:CD2	1.76	1.69
35:BK:121:PHE:CD1	35:BK:121:PHE:CE1	1.80	1.69
35:BK:121:PHE:CG	35:BK:121:PHE:CD2	1.82	1.68

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	191/193 (99%)	173 (91%)	16 (8%)	2 (1%)	19	65
3	AC	186/188 (99%)	148 (80%)	28 (15%)	10 (5%)	2	29
4	AD	120/158 (76%)	97 (81%)	16 (13%)	7 (6%)	2	27
5	AE	160/162 (99%)	141 (88%)	13 (8%)	6 (4%)	4	37
6	AG	184/186 (99%)	156 (85%)	20 (11%)	8 (4%)	3	34
7	AH	121/125 (97%)	105 (87%)	11 (9%)	5 (4%)	3	35
8	AI	136/138 (99%)	106 (78%)	21 (15%)	9 (7%)	1	24
9	AJ	94/96 (98%)	77 (82%)	14 (15%)	3 (3%)	5	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	AK	123/125 (98%)	99 (80%)	20 (16%)	4 (3%)	5	40
11	AL	116/118 (98%)	89 (77%)	25 (22%)	2 (2%)	11	55
12	AM	128/130 (98%)	103 (80%)	20 (16%)	5 (4%)	4	36
13	AN	48/50 (96%)	36 (75%)	8 (17%)	4 (8%)	1	18
14	AO	82/84 (98%)	68 (83%)	11 (13%)	3 (4%)	4	38
15	AQ	78/80 (98%)	66 (85%)	11 (14%)	1 (1%)	15	60
16	AS	69/71 (97%)	54 (78%)	12 (17%)	3 (4%)	3	34
17	AR	311/313 (99%)	282 (91%)	28 (9%)	1 (0%)	46	83
18	AT	137/141 (97%)	110 (80%)	21 (15%)	6 (4%)	3	33
20	B0	107/109 (98%)	75 (70%)	20 (19%)	12 (11%)	0	11
21	B1	46/48 (96%)	36 (78%)	9 (20%)	1 (2%)	8	49
22	B2	96/98 (98%)	87 (91%)	7 (7%)	2 (2%)	9	50
23	B8	116/118 (98%)	85 (73%)	25 (22%)	6 (5%)	2	30
24	B9	70/72 (97%)	48 (69%)	16 (23%)	6 (9%)	1	17
25	BA	211/213 (99%)	172 (82%)	30 (14%)	9 (4%)	3	34
26	BB	241/243 (99%)	174 (72%)	53 (22%)	14 (6%)	2	27
27	BC	360/362 (99%)	279 (78%)	68 (19%)	13 (4%)	4	38
28	BD	255/257 (99%)	208 (82%)	41 (16%)	6 (2%)	7	47
29	BE	235/237 (99%)	175 (74%)	47 (20%)	13 (6%)	2	29
30	BF	211/213 (99%)	150 (71%)	55 (26%)	6 (3%)	6	44
31	BG	111/113 (98%)	88 (79%)	20 (18%)	3 (3%)	6	45
32	BH	177/179 (99%)	146 (82%)	25 (14%)	6 (3%)	5	40
33	BI	163/165 (99%)	123 (76%)	31 (19%)	9 (6%)	2	29
34	BJ	149/151 (99%)	112 (75%)	33 (22%)	4 (3%)	6	45
35	BK	136/138 (99%)	107 (79%)	22 (16%)	7 (5%)	2	30
36	BL	190/192 (99%)	156 (82%)	29 (15%)	5 (3%)	7	45
37	BM	176/178 (99%)	134 (76%)	34 (19%)	8 (4%)	3	33
38	BN	148/150 (99%)	122 (82%)	23 (16%)	3 (2%)	9	51
39	BO	119/121 (98%)	92 (77%)	23 (19%)	4 (3%)	5	40
40	BP	174/176 (99%)	155 (89%)	15 (9%)	4 (2%)	8	48
41	BQ	114/116 (98%)	94 (82%)	16 (14%)	4 (4%)	4	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	BR	129/131 (98%)	96 (74%)	28 (22%)	5 (4%)	4	36
43	BS	43/45 (96%)	33 (77%)	10 (23%)	0	100	100
44	BT	78/80 (98%)	59 (76%)	16 (20%)	3 (4%)	4	37
45	BU	114/116 (98%)	95 (83%)	15 (13%)	4 (4%)	4	39
46	BV	140/142 (99%)	98 (70%)	31 (22%)	11 (8%)	1	19
47	BW	77/79 (98%)	58 (75%)	16 (21%)	3 (4%)	4	36
48	BX	84/86 (98%)	63 (75%)	14 (17%)	7 (8%)	1	18
49	BY	50/52 (96%)	39 (78%)	10 (20%)	1 (2%)	9	51
50	BZ	90/92 (98%)	68 (76%)	18 (20%)	4 (4%)	3	33
All	All	6694/6830 (98%)	5337 (80%)	1095 (16%)	262 (4%)	7	36

5 of 262 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	81	PRO
3	AC	179	GLN
4	AD	96	VAL
5	AE	86	VAL
5	AE	226	THR

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	
2	AB	161/161 (100%)	160 (99%)	1 (1%)	90	95
3	AC	152/152 (100%)	149 (98%)	3 (2%)	63	85
4	AD	113/142 (80%)	103 (91%)	10 (9%)	12	45
5	AE	127/127 (100%)	122 (96%)	5 (4%)	39	72
6	AG	155/155 (100%)	150 (97%)	5 (3%)	46	76
7	AH	106/106 (100%)	100 (94%)	6 (6%)	25	62
8	AI	115/115 (100%)	107 (93%)	8 (7%)	19	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AJ	90/90 (100%)	86 (96%)	4 (4%)	35	69
10	AK	95/95 (100%)	88 (93%)	7 (7%)	17	54
11	AL	98/98 (100%)	94 (96%)	4 (4%)	37	71
12	AM	115/115 (100%)	107 (93%)	8 (7%)	19	56
13	AN	45/45 (100%)	40 (89%)	5 (11%)	8	34
14	AO	74/74 (100%)	70 (95%)	4 (5%)	27	64
15	AQ	71/71 (100%)	68 (96%)	3 (4%)	36	70
16	AS	57/57 (100%)	56 (98%)	1 (2%)	66	87
17	AR	257/257 (100%)	246 (96%)	11 (4%)	35	70
18	AT	114/114 (100%)	102 (90%)	12 (10%)	8	36
20	B0	94/94 (100%)	89 (95%)	5 (5%)	28	64
21	B1	44/44 (100%)	41 (93%)	3 (7%)	20	57
22	B2	82/82 (100%)	80 (98%)	2 (2%)	57	82
23	B8	100/100 (100%)	87 (87%)	13 (13%)	5	28
24	B9	55/55 (100%)	52 (94%)	3 (6%)	27	63
25	BA	194/194 (100%)	183 (94%)	11 (6%)	25	62
26	BB	186/186 (100%)	176 (95%)	10 (5%)	27	64
27	BC	302/302 (100%)	282 (93%)	20 (7%)	21	57
28	BD	199/199 (100%)	188 (94%)	11 (6%)	27	63
29	BE	199/199 (100%)	187 (94%)	12 (6%)	24	60
30	BF	143/143 (100%)	135 (94%)	8 (6%)	26	62
31	BG	89/89 (100%)	82 (92%)	7 (8%)	15	51
32	BH	160/160 (100%)	151 (94%)	9 (6%)	26	62
33	BI	141/141 (100%)	134 (95%)	7 (5%)	30	66
34	BJ	129/129 (100%)	120 (93%)	9 (7%)	19	56
35	BK	112/112 (100%)	107 (96%)	5 (4%)	34	69
36	BL	164/164 (100%)	157 (96%)	7 (4%)	35	70
37	BM	119/119 (100%)	108 (91%)	11 (9%)	11	43
38	BN	122/122 (100%)	118 (97%)	4 (3%)	45	76
39	BO	99/99 (100%)	96 (97%)	3 (3%)	48	77
40	BP	118/118 (100%)	113 (96%)	5 (4%)	36	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	BQ	87/87 (100%)	81 (93%)	6 (7%)	19	56
42	BR	102/102 (100%)	96 (94%)	6 (6%)	24	61
43	BS	38/38 (100%)	32 (84%)	6 (16%)	3	21
44	BT	71/71 (100%)	64 (90%)	7 (10%)	10	39
45	BU	100/100 (100%)	98 (98%)	2 (2%)	63	85
46	BV	113/113 (100%)	103 (91%)	10 (9%)	12	45
47	BW	69/69 (100%)	65 (94%)	4 (6%)	25	61
48	BX	55/55 (100%)	53 (96%)	2 (4%)	42	74
49	BY	42/42 (100%)	39 (93%)	3 (7%)	18	55
50	BZ	81/81 (100%)	76 (94%)	5 (6%)	23	60
All	All	5554/5583 (100%)	5241 (94%)	313 (6%)	31	62

5 of 313 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	BB	155	LYS
29	BE	23	ARG
46	BV	47	TYR
27	BC	32	PHE
27	BC	244	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
27	BC	173	GLN
30	BF	112	ASN
46	BV	39	HIS
27	BC	313	HIS
30	BF	194	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1757/1761 (99%)	380 (21%)	79 (4%)
19	A7	75/76 (98%)	8 (10%)	3 (4%)
51	B3	112/113 (99%)	40 (35%)	4 (3%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	B4	156/157 (99%)	55 (35%)	10 (6%)
53	B5	3169/3170 (99%)	942 (29%)	139 (4%)
All	All	5269/5277 (99%)	1425 (27%)	235 (4%)

5 of 1425 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	A
1	AA	3	U
1	AA	4	C
1	AA	9	U
1	AA	27	U

5 of 235 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	B5	277	G
53	B5	914	A
53	B5	3077	A
53	B5	372	A
53	B5	638	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

14 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	2MG	A7	10	19	18,26,27	1.88	8 (44%)	21,38,41	2.83	10 (47%)
19	H2U	A7	16	19	17,21,22	1.89	3 (17%)	23,30,33	2.37	9 (39%)
19	H2U	A7	17	19	17,21,22	2.68	7 (41%)	23,30,33	2.71	6 (26%)
19	M2G	A7	26	19	18,27,28	1.81	4 (22%)	22,40,43	2.92	9 (40%)
19	OMC	A7	32	19	15,22,23	1.73	3 (20%)	20,31,34	2.07	5 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	OMG	A7	34	19	18,26,27	1.67	3 (16%)	21,38,41	2.98	3 (14%)
19	YYG	A7	37	19	28,42,43	1.74	7 (25%)	28,62,65	2.82	13 (46%)
19	PSU	A7	39	19	15,21,22	1.84	7 (46%)	16,30,33	2.59	4 (25%)
19	5MC	A7	40	19	14,22,23	2.38	4 (28%)	17,32,35	2.07	4 (23%)
19	7MG	A7	46	19	20,26,27	1.68	5 (25%)	23,39,42	2.56	7 (30%)
19	5MC	A7	49	19	14,22,23	1.77	2 (14%)	17,32,35	2.25	5 (29%)
19	5MU	A7	54	19	13,22,23	0.96	0	16,32,35	4.68	6 (37%)
19	PSU	A7	55	19	15,21,22	1.65	2 (13%)	16,30,33	3.69	4 (25%)
19	1MA	A7	58	19	15,25,26	0.91	1 (6%)	15,37,40	2.61	4 (26%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	2MG	A7	10	19	-	0/5/27/28	0/3/3/3
19	H2U	A7	16	19	-	0/7/38/39	0/2/2/2
19	H2U	A7	17	19	-	0/7/38/39	0/2/2/2
19	M2G	A7	26	19	-	0/7/29/30	0/3/3/3
19	OMC	A7	32	19	-	0/5/27/28	0/2/2/2
19	OMG	A7	34	19	-	0/5/27/28	0/3/3/3
19	YYG	A7	37	19	-	0/20/42/43	0/4/4/4
19	PSU	A7	39	19	-	0/7/25/26	0/2/2/2
19	5MC	A7	40	19	-	0/3/25/26	0/2/2/2
19	7MG	A7	46	19	-	0/7/37/38	0/3/3/3
19	5MC	A7	49	19	-	0/3/25/26	0/2/2/2
19	5MU	A7	54	19	-	0/3/25/26	0/2/2/2
19	PSU	A7	55	19	-	0/7/25/26	0/2/2/2
19	1MA	A7	58	19	-	0/3/25/26	0/3/3/3

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	A7	17	H2U	C4-N3	-6.07	1.28	1.37
19	A7	17	H2U	C2-N3	-5.93	1.26	1.38
19	A7	55	PSU	C6-C5	-4.48	1.32	1.38
19	A7	40	5MC	C2'-C1'	-4.37	1.46	1.53
19	A7	40	5MC	C4-N3	-4.26	1.28	1.35

The worst 5 of 89 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	A7	54	5MU	C5-C4-N3	-12.29	115.03	125.35
19	A7	34	OMG	C5-C6-N1	-10.12	110.29	123.52
19	A7	26	M2G	C5-C6-N1	-8.97	111.80	123.52
19	A7	46	7MG	C5-C6-N1	-7.67	111.97	123.39
19	A7	58	1MA	C1'-N9-C4	-7.61	118.31	126.81

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	A7	10	2MG	1	0
19	A7	37	YYG	1	0
19	A7	40	5MC	3	0

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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	AH	1
18	AT	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AH	32:LYS	C	33:VAL	N	2.59
1	AT	78:LYS	C	79:LEU	N	2.49