



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:37 PM BST

PDB ID : 5ADY
EMDB ID: : EMD-3133
Title : Cryo-EM structures of the 50S ribosome subunit bound with HflX
Authors : Zhang, Y.; Mandava, C.S.; Cao, W.; Li, X.; Zhang, D.; Li, N.; Zhang, Y.;
Zhang, X.; Qin, Y.; Mi, K.; Lei, J.; Sanyal, S.; Gao, N.
Deposited on : 2015-08-25
Resolution : 4.50 Å(reported)
Based on PDB ID : 3FIK

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

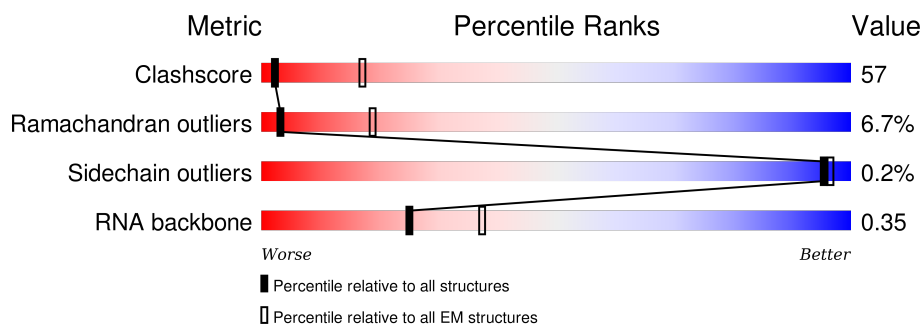
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 Å.

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





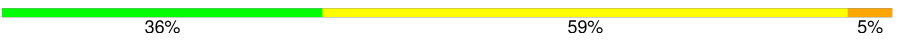
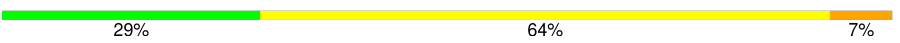


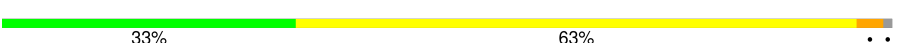
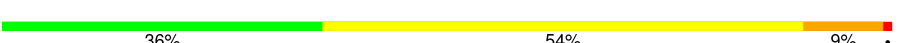
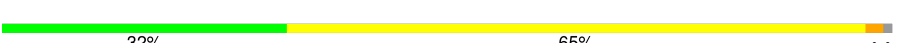

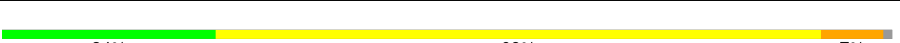
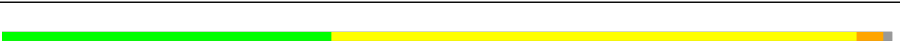
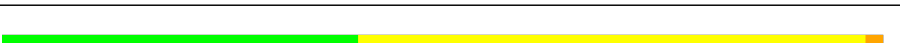
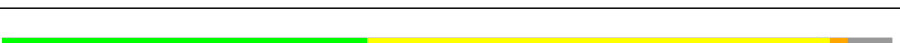
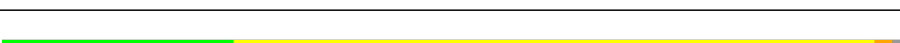

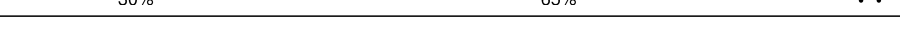
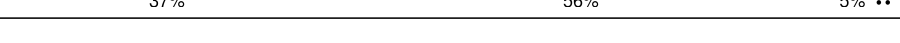





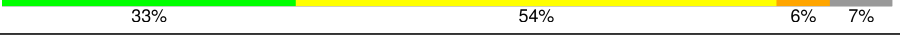

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	0	57	<div> <div>25%</div> <div>72%</div> <div>..</div> </div>
2	1	55	<div> <div>42%</div> <div>51%</div> <div>7%</div> </div>
3	2	46	<div> <div>39%</div> <div>54%</div> <div>7%</div> </div>
4	3	65	<div> <div>51%</div> <div>48%</div> <div>.</div> </div>
5	4	38	<div> <div>34%</div> <div>58%</div> <div>8%</div> </div>
6	5	234	<div> <div>39%</div> <div>56%</div> <div>.</div> </div>
7	6	426	<div> <div>30%</div> <div>65%</div> <div>.</div> </div>
8	7	165	<div> <div>38%</div> <div>55%</div> <div>6%</div> </div>

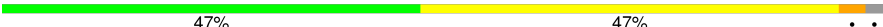
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Mol	Chain	Length	Quality of chain
9	A	120	
10	B	2903	
11	C	273	
12	D	209	
13	E	201	
14	F	179	
15	G	177	
16	H	149	
17	I	142	
18	J	142	
19	K	123	
20	L	144	
21	M	136	
22	N	127	
23	O	117	
24	P	115	
25	Q	118	
26	R	103	
27	S	110	
28	T	100	
29	U	104	
30	V	94	
31	W	85	
32	X	78	
33	Y	63	

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Mol	Chain	Length	Quality of chain
34	Z	59	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	GNP	6	527	-	-	X	-

2 Entry composition [i](#)

There are 36 unique types of molecules in this entry. The entry contains 97364 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 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 2 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	51	Total	C	N	O	0	1
			410	263	76	71		

- Molecule 3 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 7 is a protein called GTPASE HFLX.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	426	Total	C	N	O	S	0	0
			3403	2129	624	641	9		

- Molecule 8 is a protein called 50S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	164	Total	C	N	O	S	0	1
			1231	775	220	229	7		

- Molecule 9 is a RNA chain called 5S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

- Molecule 10 is a RNA chain called 23S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	264	C	G	CONFLICT	GB 731469900
B	542	C	U	CONFLICT	GB 731469900
B	846	U	C	CONFLICT	GB 731469900
B	1211	C	U	CONFLICT	GB 731469900
B	1220	G	A	CONFLICT	GB 731469900
B	1229	C	U	CONFLICT	GB 731469900
B	1723	G	A	CONFLICT	GB 731469900
B	1725	U	C	CONFLICT	GB 731469900
B	1726	C	G	CONFLICT	GB 731469900
B	1727	C	A	CONFLICT	GB 731469900
B	1730	C	U	CONFLICT	GB 731469900
B	1733	G	U	CONFLICT	GB 731469900
B	1734	G	C	CONFLICT	GB 731469900
B	1735	A	G	CONFLICT	GB 731469900
B	2794	C	U	CONFLICT	GB 731469900
B	2796	U	C	CONFLICT	GB 731469900
B	2799	A	G	CONFLICT	GB 731469900

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2802	G	A	CONFLICT	GB 731469900

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	272	Total	C	N	O	S	0	1
			2083	1288	424	364	7		

- Molecule 12 is a protein called 50S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 13 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 14 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 15 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 16 is a protein called 50S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 17 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 18 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 19 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	122	Total	C	N	O	S	0	1
			931	582	180	164	5		

- Molecule 20 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 21 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 22 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	121	Total	C	N	O	S	0	1
			961	593	197	166	5		

- Molecule 23 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 24 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	94	Total	C	N	O	S	0	1
			739	466	140	131	2		

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	103	Total	C	N	O	S	0	1
			780	492	147	141			

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

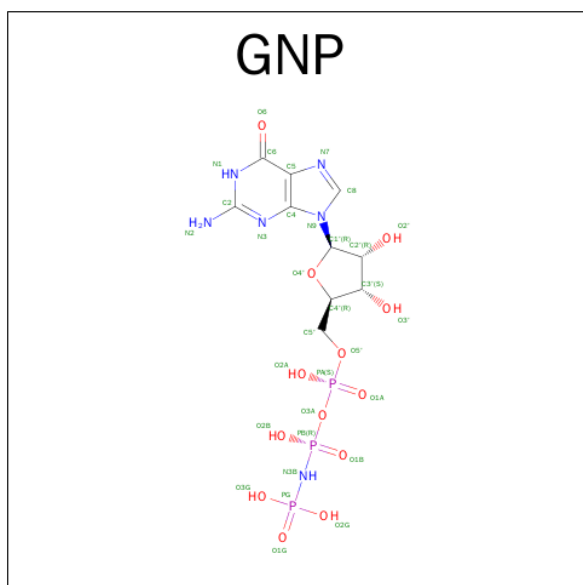
- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 35 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



- Molecule 36 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

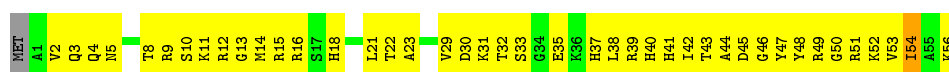
Mol	Chain	Residues	Atoms		AltConf
36	6	1	Total	Mg	0
			1	1	

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: 50S RIBOSOMAL PROTEIN L32

Chain 0: 



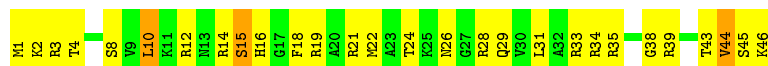
• Molecule 2: 50S RIBOSOMAL PROTEIN L33

Chain 1: 



• Molecule 3: 50S RIBOSOMAL PROTEIN L34

Chain 2: 



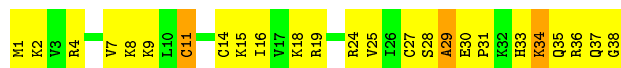
• Molecule 4: 50S RIBOSOMAL PROTEIN L35

Chain 3: 



• Molecule 5: 50S RIBOSOMAL PROTEIN L36

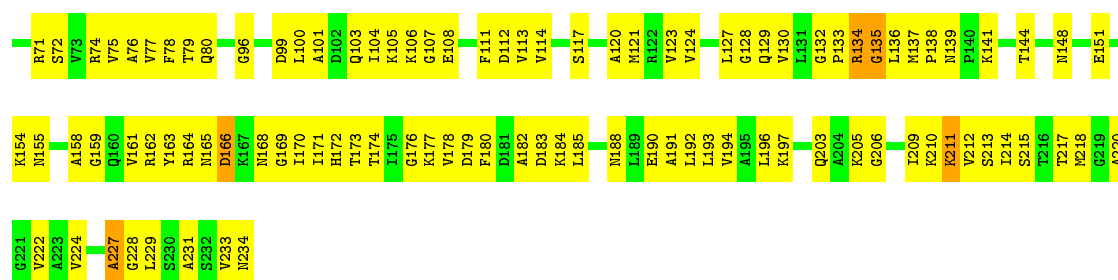
Chain 4: 



• Molecule 6: 50S RIBOSOMAL PROTEIN L1

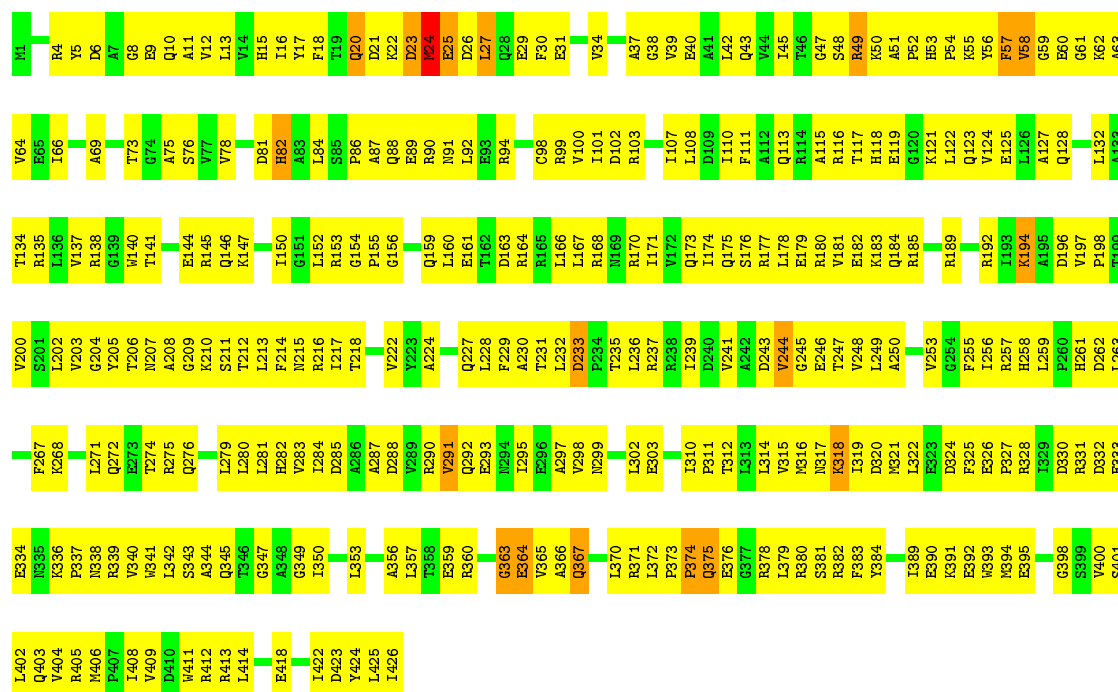
Chain 5: 





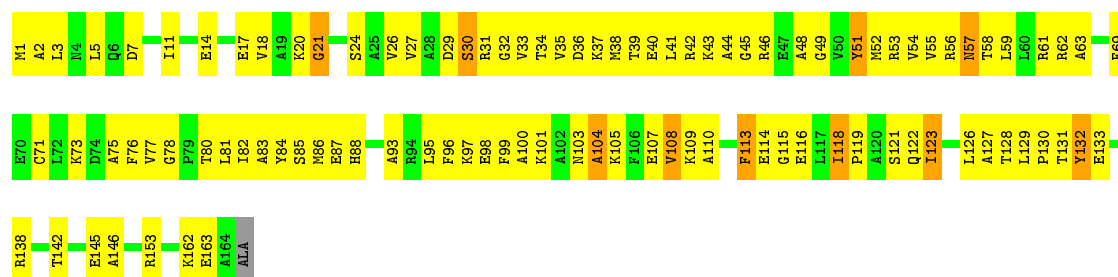
• Molecule 7: GTPASE HFLX

Chain 6: 30% 65% .



• Molecule 8: 50S RIBOSOMAL PROTEIN L10

Chain 7: 38% 55% 6% .



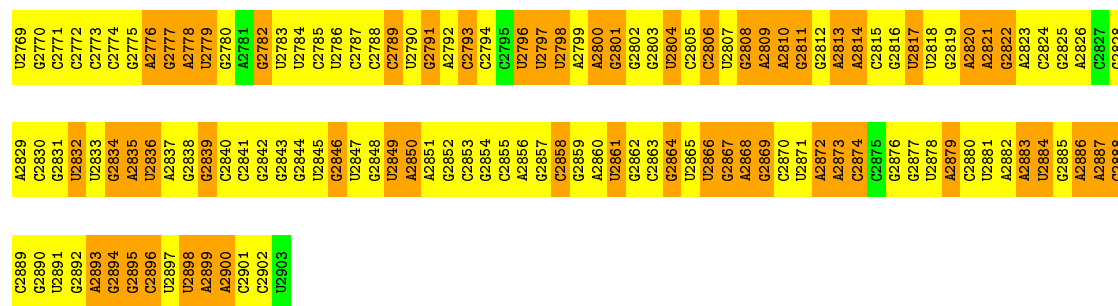
• Molecule 9: 5S RRNA

Chain A: 62% 32% . .

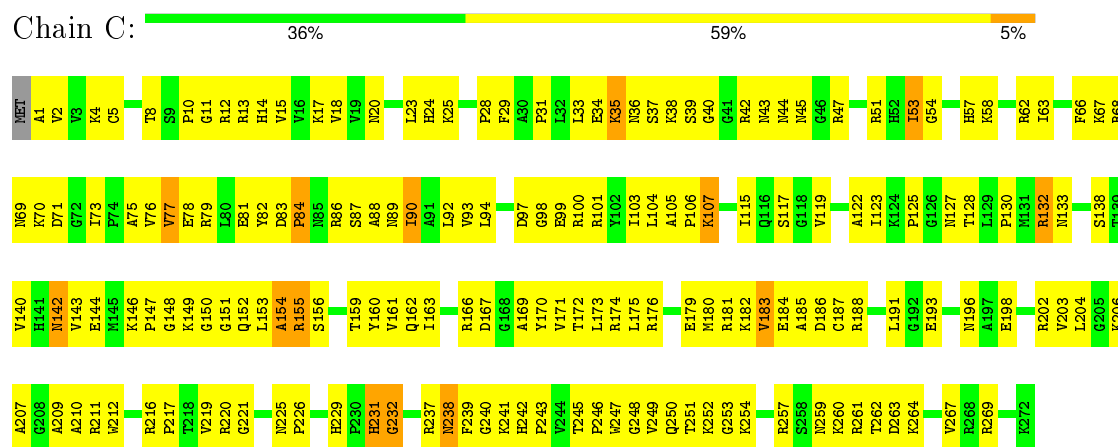


C1748	U1688	G1568	C1446	U1325	A1264	A1144	A1084	U1023	U963	C903	G843
A1749	A1689	A1569	C1447	U1326	A1265	C1145	A1085	G1024	C964	G904	A844
G1750	A1690	A1570	G1448	U1327	A1266	C1146	A1086	G1025	C965	A905	A845
U1751	G1691	A1571	A1449	A1328	U1267	U1147	G1087	G1026	G966	U906	U846
G1752	A1692	A1572	C1450	U1329	A1268	U1148	A1088	A1027	U967	G907	U847
G1753	G1693	G1573	G1451	U1330	A1269	G1149	A1089	A1028	C968	C908	C848
A1754	C1694	C1574	A1452	G1331	G1270	C1150	A1090	A1029	G969	A909	A849
A1755	G1695	C1575	A1453	G1332	G1271	A1151	G1091	C1030	U970	A910	A850
G1756	G1696	U1576	A1454	G1333	A1272	C1152	G1092	G1031	G971	A911	U851
A1757	G1697	C1577	G1455	U1334	A1273	C1153	G1093	A1032	A972	C912	U852
U1758	A1698	A1578	G1456	G1335	A1274	G1154	U1094	U1033	A973	U913	C853
A1759	G1699	G1579	A1457	A1336	A1275	A1155	A1095	G1034	G974	G914	C854
C1760	A1700	U1580	U1458	U1337	A1276	A1156	A1096	U1035	A975	C915	C855
C1761	A1701	G1581	G1459	G1338	G1277	G1157	U1097	G1036	G976	G916	G856
A1762	G1702	C1582	U1460	G1339	G1278	C1158	A1098	G1037	G977	A917	G857
G1763	G1703	U1583	C1461	U1340	G1279	U1159	U1099	G1038	G978	A918	G858
C1764	C1704	A1584	A1462	G1341	G1280	G1160	A1100	A1039	A979	U919	G859
U1765	A1705	A1585	C1463	A1342	G1281	C1161	U1101	A1040	A980	A920	U860
C1766	C1706	C1586	G1464	G1343	U1282	G1162	C1102	G1041	A981	C921	A861
G1767	U1647	U1587	G1465	C1344	G1283	G1163	A1103	G1042	G982	C922	G862
C1768	U1648	G1588	U1466	U1345	U1284	C1164	A983	C1043	A983	G923	A863
U1769	G1649	U1589	U1467	G1346	A1287	A1165	U1105	C1044	A984	G924	G864
G1770	A1650	A1590	U1468	A1347	A1288	G1166	U1106	C1045	C985	A925	C865
A1771	G1651	A1591	A1469	C1348	G1289	C1167	G1107	A1046	C986	G926	A866
C1772	A1652	C1592	A1470	U1409	G1290	G1168	U1108	G1047	C987	A927	C867
A1773	G1653	C1593	C1471	G1410	C1291	A1169	C1109	A1048	A988	A928	U868
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U1775	A1655	C1595	G1473	U1412	G1293	G1171	A1111	A1050	A990	G930	U870
G1776	C1656	A1596	A1474	A1413	C1294	C1172	G1112	G1051	C991	U931	U871
U1777	U1657	U1597	G1475	G1414	U1295	U1173	U1113	G1052	C992	U932	U872
C1778	G1658	A1598	U1476	G1415	C1296	U1174	C1114	A1054	G993	A933	C873
U1779	U1659	U1599	A1477	C1416	G1297	A1175	G1115	G1055	C994	U934	G874
A1780	G1660	C1600	U1478	C1417	C1297	U1176	G1116	G1056	C995	C935	G875
U1781	U1661	G1601	G1479	A1418	C1298	C1177	A996	A1057	A996	A936	C876
U1782	U1662	U1602	A1480	A1419	G1299	G1178	U1058	U1058	G997	A877	A877
A1783	G1663	A1603	U1481	A1420	G1300	G1179	G1059	G1059	C998	G938	A878
A1784	A1664	C1604	G1482	G1421	G1301	U1180	U1120	U1060	U999	G939	G879
A1785	U1665	C1605	G1483	G1422	A1302	U1181	C1121	U1061	A1000	G940	G880
U1786	G1666	C1606	U1486	G1424	G1303	G1182	G1122	G1062	A1001	A941	G881
A1787	U1667	G1607	A1487	G1425	A1304	U1183	C1123	G1063	G1002	G942	G882
C1788	A1668	A1608	U1488	G1426	C1305	U1184	G1124	G1064	G1003	A943	G883
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C1790	G1670	C1610	U1489	G1428	A1307	G1186	A1126	U1066	G1005	A945	C885
A1791	U1671	A1611	A1490	C1429	A1308	G1187	A1127	A1067	G1006	C946	A886
G1792	A1672	C1612	G1491	G1430	G1309	U1188	G1128	G1068	C1007	A947	U887
C1793	G1673	A1613	G1492	A1431	G1310	A1189	A1129	A1069	A1008	C948	C888
A1794	A1674	U1554	C1493	G1432	G1311	G1190	A1070	A1070	A1009	G949	C889
U1795	C1675	G1555	A1494	A1433	U1312	G1191	G1071	G1071	G950	G950	G890
G1796	A1676	C1556	A1495	A1434	G1313	G1192	U1132	C1072	G1010	C951	G891
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A1799	U1679	U1559	G1498	C1437	U1316	G1195	C1135	A1014	A1014	G954	U894
C1800	G1680	G1560	C1499	U1438	G1317	C1196	G1136	C1075	U1015	U955	U895
A1801	U1681	C1561	G1500	A1439	U1318	G1197	G1137	A1076	G1016	G956	A896
A1802	G1682	U1562	A1501	U1440	C1319	U1198	G1138	U1078	G1017	C957	C897
C1803	U1683	C1563	G1502	G1441	C1320	U1199	G1139	C1079	U1018	U958	C898
A1804	G1684	C1564	A1503	U1442	A1321	C1200	C1140	A1080	U1019	A959	A899
A1805	C1685	C1565	A1504	U1443	A1322	G1201	A1141	U1081	A1020	A960	A900
G1806	G1686	U1505	U1504	G1444	C1323	G1202	A1142	U1082	A1021	C961	C901
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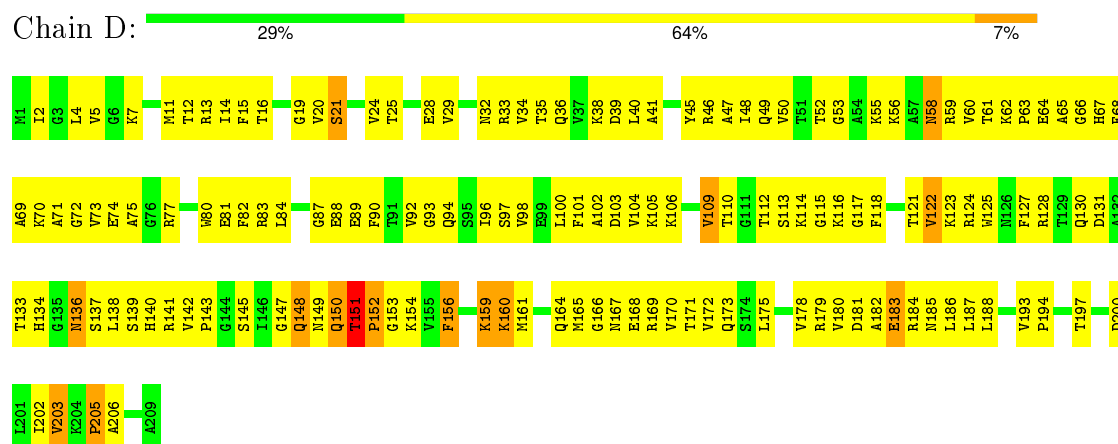
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A2711	C2651	A2590	A2531	G2470	A2411	G2351	G2291	U2231	U2111	A2051	U1991	U1931	A1871	G1811
G2712	C2652	G2591	G2532	A2471	A2412	G2352	U2292	G2232	G2112	G2052	G1992	A1932	A1872	U1812
G2713	U2653	G2592	U2533	G2472	G2413	G2353	G2293	U2233	U2113	G2053	U1993	G1933	G1873	G1813
G2714	A2654	U2593	G2534	U2473	G2414	G2354	G2294	G2234	A2114	A2054	C1994	C1934	C1874	G1814
G2715	G2655	G2594	A2534	U2474	G2415	G2355	G2295	G2235	G2115	C2055	U1995	G1935	C1875	G1815
G2716	U2656	G2595	G2535	C2475	G2416	G2356	U2296	G2236	G2116	G2056	A1936	A1936	A1876	A1816
C2717	A2657	U2596	U2536	A2476	A2417	G2357	G2297	G2237	A2117	G2057	C1997	A1937	A1877	G1817
G2718	C2658	G2597	U2537	U2477	C2418	G2358	A2298	G2238	U2118	A2058	A1998	A1938	A1878	U1818
G2719	G2659	A2598	G2538	A2478	A2419	G2359	U2299	G2239	A2119	A2059	G1999	U1939	C1878	U1819
A2720	A2660	G2599	C2539	U2479	U2419	G2360	U2299	G2240	G2120	C2000	C2000	U1940	U1880	U1820
U2721	G2661	A2600	C2540	C2480	C2420	G2361	C2300	U2240	G2120	A2060	C2001	C1941	U1881	A1821
G2722	A2662	C2601	A2541	G2481	G2421	G2362	C2301	A2241	G2121	G2061	C2002	C1942	C1882	A1822
C2723	G2663	A2602	G2542	A2482	C2422	U2362	U2302	G2242	U2122	A2062	G2003	C1943	U1883	G1823
G2724	G2664	G2603	G2543	C2483	U2423	G2363	G2303	G2243	G2123	C2063	A2003	U1944	G1884	G1824
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G2726	C2666	G2605	G2545	A2485	A2425	G2365	U2305	U2245	G2125	C2065	A2006	U1946	U1886	G1826
A2727	C2667	U2606	U2546	C2486	A2426	G2366	C2306	G2246	A2126	C2066	C2007	C1947	C1887	U1827
G2728	G2668	G2607	A2547	G2487	C2427	G2367	G2307	A2247	G2127	U2067	U2008	G1948	G1888	G1828
G2729	G2669	U2608	U2548	G2488	G2428	G2368	G2308	C2248	G2128	U2068	C2009	G1949	A1889	A1829
A2730	A2670	G2609	G2549	U2489	G2429	A2369	A2309	U2249	C2129	G2069	A2009	G1950	A1890	C1830
G2731	G2671	C2610	G2550	G2490	A2430	G2370	C2310	G2250	U2130	A2070	G2010	G1951	G1891	G1831
U2732	U2672	U2611	C2551	U2491	U2431	G2371	A2311	G2251	U2131	A2071	U2011	U1952	C1892	C1832
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A2734	G2674	A2613	G2553	U2493	A2433	G2373	C2313	G2253	G2133	C2073	A2013	A1954	C1894	U1834
G2735	A2675	U2614	U2554	G2494	A2434	G2374	A2314	C2254	A2134	U2074	A2014	G1955	U1895	G1835
U2736	G2676	G2615	U2555	G2495	A2435	G2375	G2315	G2255	U2135	U2075	A2015	U1956	G1896	C1836
G2737	G2677	U2617	G2556	A2496	G2436	A2376	G2316	G2256	G2136	U2076	U2016	C1957	G1897	C1837
G2738	C2678	G2618	G2557	U2497	G2437	A2377	A2317	U2257	U2137	C2077	G2017	C1958	U1898	C1838
U2739	A2679	U2619	C2558	U2498	U2438	G2378	G2318	G2258	G2138	C2078	G2018	G1959	A1899	G1839
U2740	G2680	C2620	C2559	C2499	A2439	G2379	G2319	U2259	U2139	U2079	A2019	G1960	A1900	G1840
A2741	U2681	U2621	A2560	U2500	C2440	C2380	U2320	C2260	G2140	A2080	A2020	C1961	A1901	U1841
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U2743	C2683	G2623	U2562	G2502	C2442	G2382	A2322	G2262	A2142	A2082	U2022	G1963	G1903	C1843
G2744	U2684	G2624	G2563	U2503	C2443	G2383	G2323	C2263	C2143	G2083	C2023	U1964	G1904	C1844
C2745	G2685	G2625	A2564	U2504	G2444	U2384	U2324	C2264	G2144	C2084	G2024	C1965	C1905	G1845
U2746	G2686	C2626	A2565	G2505	G2445	C2385	G2325	U2265	C2145	U2085	C2025	C1966	G1906	G1846
G2747	U2687	G2627	A2566	U2506	G2446	A2386	C2326	A2266	C2146	U2086	U2026	A1967	G1907	A1847
A2748	G2688	C2628	G2567	C2507	G2447	U2387	A2327	A2267	A2147	A2087	G2027	C1967	C1908	A1848
U2749	U2689	G2629	U2568	G2508	A2448	A2388	A2328	A2268	G2148	C2088	U2028	G1968	C1909	G1849
A2750	G2690	G2630	G2569	G2509	U2449	G2389	U2329	G2269	U2149	C2089	G2029	A1969	G1910	G1850
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G2755	U2695	G2635	G2574	U2514	G2454	C2394	U2334	A2274	A2154	A2094	U2034	C1974	U1915	U1855
U2756	U2696	G2636	C2575	G2515	G2455	G2395	A2335	C2275	U2155	A2095	G2035	G1975	U1916	U1856
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G2762	C2702	G2642	G2581	C2521	A2461	A2401	G2341	A2281	C2161	A2101	U2041	A1981	U1922	G1862
C2703	G2703	G2643	U2522	G2522	C2462	U2402	C2342	G2282	G2162	G2102	A2042	U1982	G1923	G1863
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A2766	U2706	G2646	G2585	G2525	C2465	G2405	G2345	G2285	U2166	U2106	C2045	C1985	U1926	A1866
G2767	U2707	U2647	U2586	G2526	C2466	A2406	A2346	G2286	U2167	U2107	C1986	A1987	A1927	G1867
U2768	G2708	G2648	A2587	C2527	C2467	A2407	C2347	A2287	U2167	G2107	C2047			



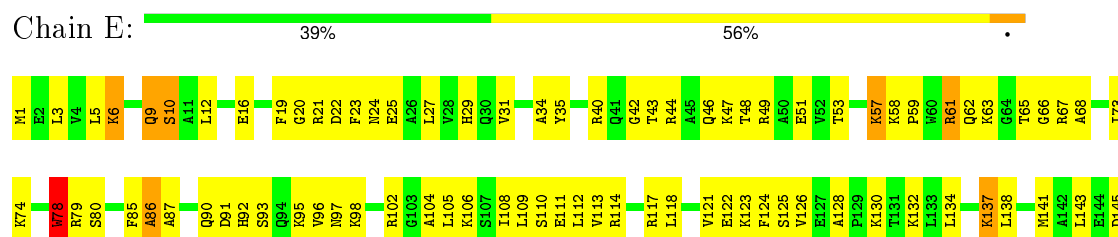
• Molecule 11: 50S RIBOSOMAL PROTEIN L2



• Molecule 12: 50S RIBOSOMAL PROTEIN L3



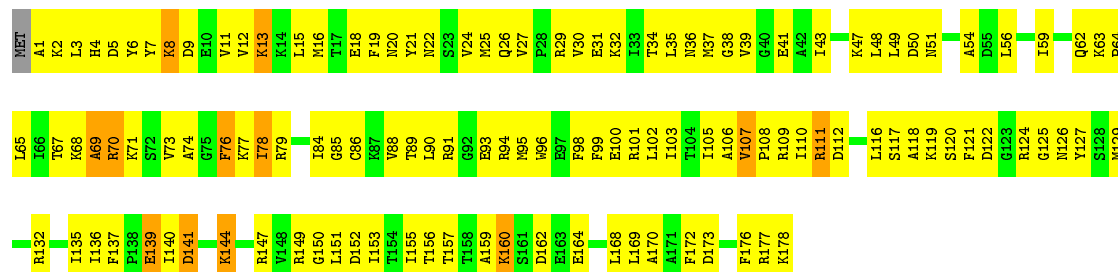
• Molecule 13: 50S RIBOSOMAL PROTEIN L4





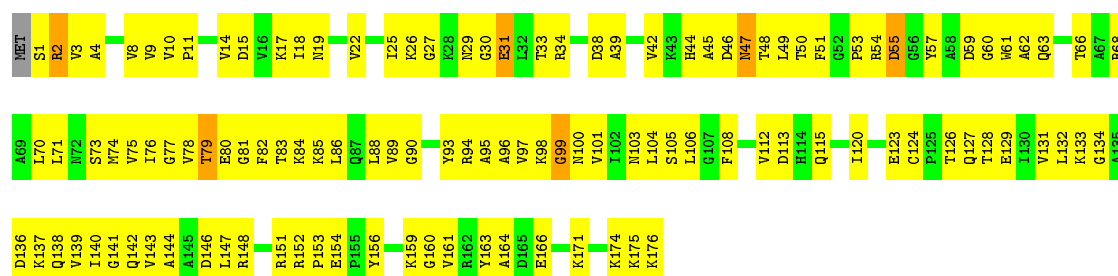
• Molecule 14: 50S RIBOSOMAL PROTEIN L5

Chain F: 30% 63% 7%



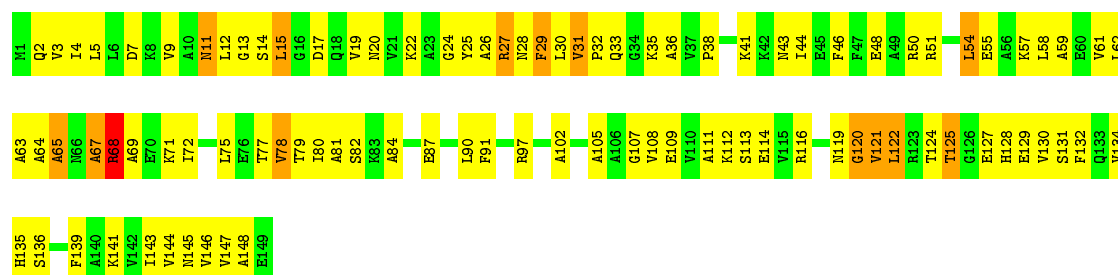
• Molecule 15: 50S RIBOSOMAL PROTEIN L6

Chain G: 33% 63%



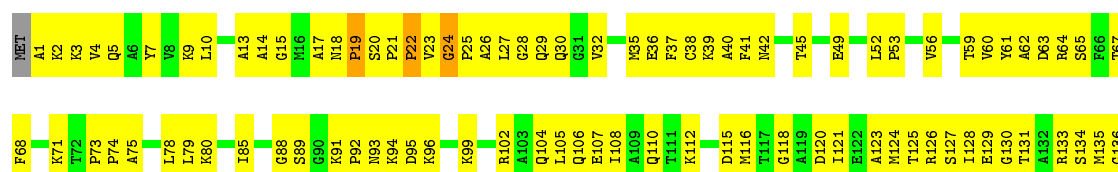
• Molecule 16: 50S RIBOSOMAL PROTEIN L9

Chain H: 36% 54% 9%



• Molecule 17: 50S RIBOSOMAL PROTEIN L11

Chain I: 32% 65%



L137
V138
V139
E140
D141

• Molecule 18: 50S RIBOSOMAL PROTEIN L13

Chain J: 27% 65% 7%

M1 P8 V11 K12 R13 R14 V15 V16 V17 V18 D19 D20 A20 T21 G22 G23 K24 T24 L25 G26 R27 L28 A29 A30 E31 L32 L33 A34 R35 L36 R37 G38 R39 H40 K41 A42 E43 Y44 T46 P46 H47 V48 D49 T50 G51 D52 Y53 I54 L57 N58 A59 D60 K61 V62 A63 V64 T65 G66 N67

H131 H132 Q138 V139 L140 D141 I142

• Molecule 19: 50S RIBOSOMAL PROTEIN L14

Chain K: 24% 68% 7%

MET I1 Q2 E3 Q4 T5 M6 L7 A10 N12 N13 G14 A15 R16 R17 V18 H19 C20 I21 C22 L24 G25 G26 S27 P37 E38 R39 V100 I101 E102 I103 A104 V105 K106 G107 M108 L109 P110 K111 G112 P113 L114 G115 R116 M117 F118 F119 A120 L121 L122 K123 A126 G127 N128 E129 H130

R63 T64 K65 K66 G67 V68 R69 R70 P71 D72 G73 S74 W75 I76 R77 F78 D79 A82 C83 V84 L85 L86 L87 N88 N89 S90 E91 Q92 P93 I94 G95 T96 R97 I98 F99 G100 P101 V102 T103 E104 E105 L106 E109 K110 F111 P112 M113 I114 I115 S116 A118 P119 E120 V121 L122

• Molecule 20: 50S RIBOSOMAL PROTEIN L15

Chain L: 37% 59% ..

MET R2 L3 S7 P8 S12 K13 R21 G22 I23 L27 G28 K29 R33 K36 G37 Q38 K39 S40 R41 S42 G43 G44 G45 V46 R47 R48 G49 F50 E51 G52 G53 Q54 M55 Y58 R59 R60 R63 F66 T67 S68 R69 K70 A71 T74 T75 E76 I77 R78 L79

S80 D81 L82 A83 K84 V85 E86 G87 G88 V89 V90 D91 L95 K96 A97 A98 N99 I100 I101 G102 I105 E106 F107 A108 K109 V110 I111 G112 A113 G114 E115 V116 T117 T118 P119 V120 T121 V122 R123 G124 L125 R126 V127 T128 K129 G130 A131 R132 A133 A134 I135 E136 A137 A138 G139 G140 K141 I142

E143 E144

• Molecule 21: 50S RIBOSOMAL PROTEIN L16

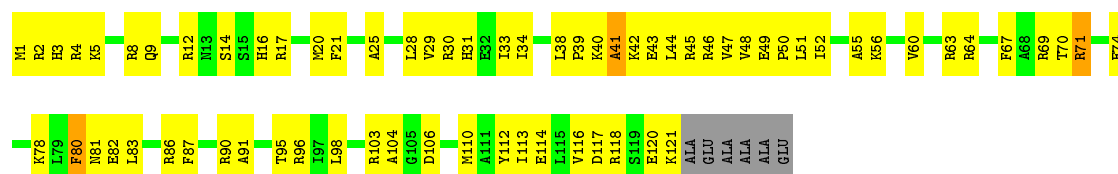
Chain M: 40% 57% .

M1 R6 T7 R8 R9 R10 K11 M12 H13 N17 N18 A21 Q22 F28 G29 S30 F31 G32 L33 K34 A35 R38 G39 R40 L41 T42 Q45 I46 E47 A48 A49 R50 R51 A52 M53 T54 R55 A56 V57 R58 K62 T63 T64 T65 T66 V67 P69 P72 I73 T74 E75

K76 F77 L78 A79 V80 R81 M82 G83 K84 G85 G87 E90 Y91 A94 L95 T96 Q97 P98 G99 K100 V101 L102 I103 E104 M105 D106 E110 E111 L112 A113 E114 E115 A116 F117 A118 L119 A120 A121 A122 K123 L124 P125 I126 T132 K133 T134 T135 M136

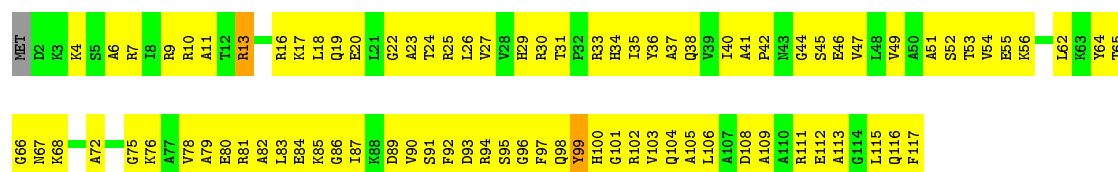
• Molecule 22: 50S RIBOSOMAL PROTEIN L17

Chain N: 41% 52% . 5%



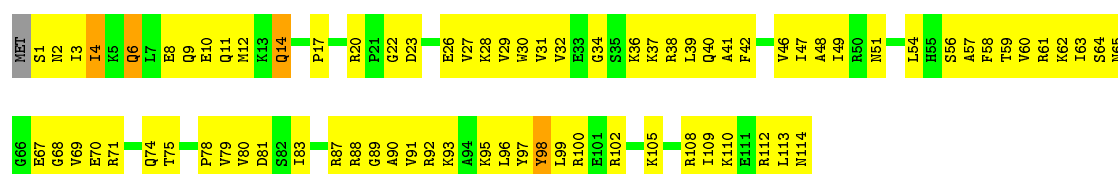
• Molecule 23: 50S RIBOSOMAL PROTEIN L18

Chain O: 26% 72%



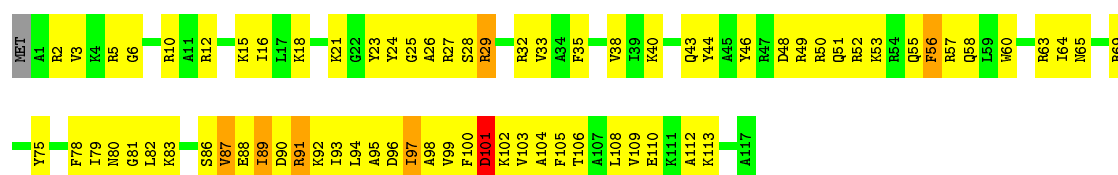
• Molecule 24: 50S RIBOSOMAL PROTEIN L19

Chain P: 30% 65%



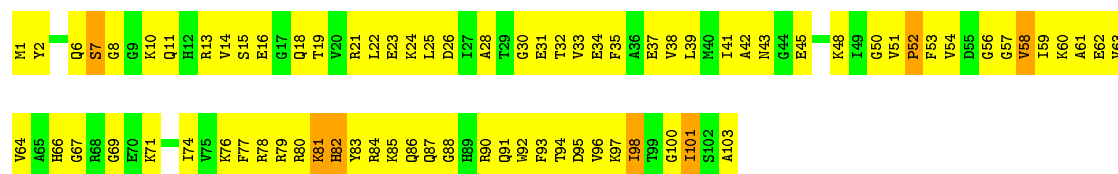
• Molecule 25: 50S RIBOSOMAL PROTEIN L20

Chain Q: 37% 56% 5%



• Molecule 26: 50S RIBOSOMAL PROTEIN L21

Chain R: 24% 69% 7%



• Molecule 27: 50S RIBOSOMAL PROTEIN L22

Chain S: 36% 59% 5%

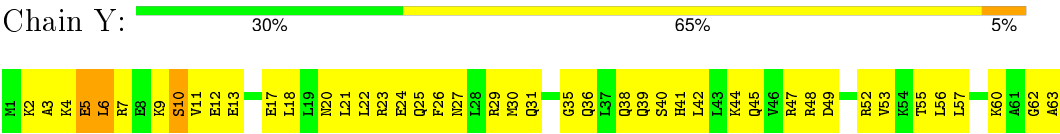




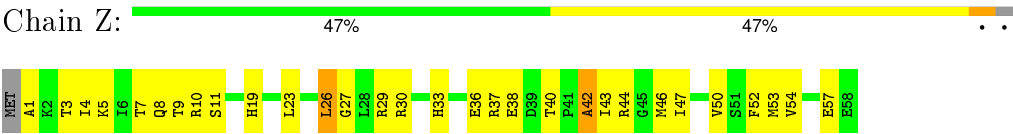
• Molecule 28: 50S RIBOSOMAL PROTEIN L23



● Molecule 33: 50S RIBOSOMAL PROTEIN L29



● Molecule 34: 50S RIBOSOMAL PROTEIN L30



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	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	OTHER	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	75000	Depositor
Image detector	FEI EAGLE 4K X 4K CCD	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GNP, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	0	0.65	0/450	0.77	0/599
10	B	1.18	47/69796 (0.1%)	1.22	227/108888 (0.2%)
11	C	0.63	0/2122	0.72	0/2854
12	D	0.66	0/1586	0.75	0/2134
13	E	0.58	0/1571	0.73	0/2113
14	F	0.46	0/1444	0.69	0/1937
15	G	0.57	0/1343	0.71	0/1816
16	H	0.46	0/1122	0.64	0/1515
17	I	0.41	0/1046	0.64	0/1410
18	J	0.64	0/1152	0.75	0/1551
19	K	0.60	0/940	0.75	0/1260
2	1	0.57	0/417	0.68	0/556
20	L	0.58	0/1054	0.79	1/1403 (0.1%)
21	M	0.68	0/1093	0.71	0/1460
22	N	0.66	0/974	0.74	0/1303
23	O	0.54	0/902	0.70	0/1209
24	P	0.61	0/929	0.71	0/1242
25	Q	0.78	0/960	0.77	0/1278
26	R	0.64	0/829	0.71	0/1107
27	S	0.66	0/864	0.84	0/1156
28	T	0.61	0/745	0.77	0/996
29	U	0.53	0/788	0.72	0/1053
3	2	0.69	0/380	0.78	0/498
30	V	0.60	0/766	0.72	0/1025
31	W	0.64	0/603	0.80	0/797
32	X	0.62	0/635	0.71	0/848
33	Y	0.53	0/510	0.68	0/677
34	Z	0.60	0/453	0.77	1/605 (0.2%)
4	3	0.64	0/513	0.76	0/676
5	4	0.65	0/303	0.77	0/397
6	5	0.35	0/1748	0.64	1/2355 (0.0%)
7	6	0.55	0/3456	0.76	1/4675 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
8	7	0.39	0/1245	0.63	0/1677
9	A	1.01	0/2800	1.16	6/4367 (0.1%)
All	All	1.03	47/105539 (0.0%)	1.10	237/157437 (0.2%)

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
13	E	0	1
14	F	0	1
24	P	0	1
25	Q	0	1
6	5	0	1
All	All	0	5

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	788	A	N9-C4	-8.84	1.32	1.37
10	B	118	A	N9-C4	-7.60	1.33	1.37
10	B	677	A	N9-C4	-6.86	1.33	1.37
10	B	1142	A	N9-C4	-6.60	1.33	1.37
10	B	1254	A	N9-C4	-6.54	1.33	1.37

The worst 5 of 237 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	828	U	C2-N1-C1'	8.23	127.58	117.70
10	B	205	G	C2-N3-C4	-8.04	107.88	111.90
10	B	1816	C	C2-N1-C1'	8.01	127.61	118.80
10	B	544	C	C2-N1-C1'	7.58	127.14	118.80
10	B	1238	G	N3-C4-C5	7.58	132.39	128.60

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	5	59	VAL	Peptide
13	E	59	PRO	Peptide

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Mol	Chain	Res	Type	Group
14	F	76	PHE	Peptide
24	P	14	GLN	Peptide
25	Q	101	ASP	Peptide

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	0	444	0	461	53	0
2	1	410	0	440	42	0
3	2	377	0	418	42	0
4	3	504	0	574	60	0
5	4	302	0	343	35	0
6	5	1733	0	1823	197	0
7	6	3403	0	3433	387	0
8	7	1231	0	1282	124	0
9	A	2504	0	1271	249	0
10	B	62317	0	31345	6160	0
11	C	2083	0	2157	244	0
12	D	1565	0	1616	238	0
13	E	1552	0	1619	130	0
14	F	1420	0	1460	169	0
15	G	1323	0	1374	136	0
16	H	1111	0	1148	188	0
17	I	1032	0	1088	142	0
18	J	1129	0	1162	144	0
19	K	931	0	1003	116	0
20	L	1045	0	1117	121	0
21	M	1074	0	1157	105	0
22	N	961	0	1000	107	0
23	O	892	0	923	130	0
24	P	917	0	965	101	0
25	Q	947	0	1022	143	0
26	R	816	0	839	106	0
27	S	857	0	922	100	0
28	T	739	0	807	74	0
29	U	780	0	834	89	0
30	V	753	0	780	60	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	W	596	0	610	94	0
32	X	625	0	655	92	0
33	Y	509	0	543	52	0
34	Z	449	0	491	26	0
35	6	32	0	13	23	0
36	6	1	0	0	0	0
All	All	97364	0	66695	9059	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 57.

The worst 5 of 9059 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)
16:H:68:ARG:HG3	16:H:132:PHE:CD2	1.40	1.55
16:H:68:ARG:HG3	16:H:132:PHE:CE2	1.37	1.53
16:H:68:ARG:HD2	16:H:132:PHE:CE1	1.43	1.52
16:H:68:ARG:CG	16:H:132:PHE:CZ	2.00	1.43
7:6:24:MET:HE3	7:6:257:ARG:NH2	1.28	1.43

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	
1	0	54/57 (95%)	45 (83%)	5 (9%)	4 (7%)	1	21
2	1	49/55 (89%)	45 (92%)	4 (8%)	0	100	100
3	2	44/46 (96%)	35 (80%)	6 (14%)	3 (7%)	1	24
4	3	62/65 (95%)	58 (94%)	4 (6%)	0	100	100
5	4	36/38 (95%)	26 (72%)	5 (14%)	5 (14%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	5	232/234 (99%)	190 (82%)	27 (12%)	15 (6%)	1	26
7	6	424/426 (100%)	364 (86%)	39 (9%)	21 (5%)	3	31
8	7	162/165 (98%)	128 (79%)	23 (14%)	11 (7%)	1	24
11	C	270/273 (99%)	219 (81%)	34 (13%)	17 (6%)	2	26
12	D	207/209 (99%)	166 (80%)	20 (10%)	21 (10%)	1	13
13	E	199/201 (99%)	160 (80%)	21 (11%)	18 (9%)	1	16
14	F	176/179 (98%)	131 (74%)	30 (17%)	15 (8%)	1	17
15	G	174/177 (98%)	142 (82%)	21 (12%)	11 (6%)	2	26
16	H	147/149 (99%)	97 (66%)	29 (20%)	21 (14%)	0	6
17	I	139/142 (98%)	122 (88%)	13 (9%)	4 (3%)	6	45
18	J	140/142 (99%)	109 (78%)	19 (14%)	12 (9%)	1	17
19	K	120/123 (98%)	96 (80%)	14 (12%)	10 (8%)	1	18
20	L	141/144 (98%)	113 (80%)	20 (14%)	8 (6%)	2	28
21	M	134/136 (98%)	113 (84%)	13 (10%)	8 (6%)	2	27
22	N	119/127 (94%)	96 (81%)	18 (15%)	5 (4%)	3	35
23	O	114/117 (97%)	105 (92%)	6 (5%)	3 (3%)	7	47
24	P	112/115 (97%)	89 (80%)	18 (16%)	5 (4%)	3	33
25	Q	115/118 (98%)	102 (89%)	7 (6%)	6 (5%)	2	30
26	R	101/103 (98%)	78 (77%)	13 (13%)	10 (10%)	1	14
27	S	108/110 (98%)	93 (86%)	8 (7%)	7 (6%)	1	26
28	T	92/100 (92%)	73 (79%)	13 (14%)	6 (6%)	1	26
29	U	101/104 (97%)	79 (78%)	14 (14%)	8 (8%)	1	19
30	V	92/94 (98%)	81 (88%)	10 (11%)	1 (1%)	17	64
31	W	77/85 (91%)	58 (75%)	12 (16%)	7 (9%)	1	16
32	X	75/78 (96%)	61 (81%)	9 (12%)	5 (7%)	1	24
33	Y	61/63 (97%)	49 (80%)	6 (10%)	6 (10%)	1	14
34	Z	56/59 (95%)	51 (91%)	3 (5%)	2 (4%)	4	40
All	All	4133/4234 (98%)	3374 (82%)	484 (12%)	275 (7%)	3	24

5 of 275 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	4	11	CYS

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Mol	Chain	Res	Type
5	4	34	LYS
6	5	38	PHE
6	5	39	VAL
6	5	135	GLY

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	0	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
6	5	181/181 (100%)	179 (99%)	2 (1%)	80	90
7	6	364/364 (100%)	363 (100%)	1 (0%)	94	96
8	7	123/123 (100%)	123 (100%)	0	100	100
11	C	216/218 (99%)	216 (100%)	0	100	100
12	D	164/164 (100%)	163 (99%)	1 (1%)	90	95
13	E	165/165 (100%)	164 (99%)	1 (1%)	90	95
14	F	149/150 (99%)	149 (100%)	0	100	100
15	G	137/138 (99%)	137 (100%)	0	100	100
16	H	114/114 (100%)	113 (99%)	1 (1%)	84	92
17	I	109/110 (99%)	109 (100%)	0	100	100
18	J	116/116 (100%)	116 (100%)	0	100	100
19	K	102/104 (98%)	102 (100%)	0	100	100
20	L	102/103 (99%)	102 (100%)	0	100	100
21	M	109/109 (100%)	109 (100%)	0	100	100
22	N	100/103 (97%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	O	86/87 (99%)	86 (100%)	0	100	100
24	P	99/100 (99%)	99 (100%)	0	100	100
25	Q	89/90 (99%)	88 (99%)	1 (1%)	80	90
26	R	84/84 (100%)	84 (100%)	0	100	100
27	S	93/93 (100%)	93 (100%)	0	100	100
28	T	80/84 (95%)	80 (100%)	0	100	100
29	U	83/85 (98%)	83 (100%)	0	100	100
30	V	78/78 (100%)	78 (100%)	0	100	100
31	W	59/63 (94%)	59 (100%)	0	100	100
32	X	67/68 (98%)	67 (100%)	0	100	100
33	Y	55/55 (100%)	55 (100%)	0	100	100
34	Z	48/49 (98%)	48 (100%)	0	100	100
All	All	3387/3419 (99%)	3380 (100%)	7 (0%)	95	97

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	D	151	THR
25	Q	56	PHE
13	E	78	TRP
6	5	38	PHE
16	H	68	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
15	G	115	GLN
21	M	17	ASN
32	X	15	ASN
16	H	33	GLN
18	J	40	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	2902/2903 (99%)	1015 (34%)	56 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	A	116/120 (96%)	35 (30%)	2 (1%)
All	All	3018/3023 (99%)	1050 (34%)	58 (1%)

5 of 1050 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	7	G
9	A	11	C
9	A	13	G
9	A	14	U
9	A	15	A

5 of 58 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	B	1267	U
10	B	1652	A
10	B	2688	G
10	B	1321	A
10	B	1395	A

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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
35	GNP	6	527	36	29,34,34	2.14	9 (31%)	29,54,54	2.81	10 (34%)

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
35	GNP	6	527	36	-	0/13/38/38	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	6	527	GNP	PB-O3A	-7.21	1.50	1.59
35	6	527	GNP	PB-O2B	-3.48	1.47	1.56
35	6	527	GNP	C8-N7	-2.45	1.29	1.34
35	6	527	GNP	PG-O3G	-2.27	1.50	1.56
35	6	527	GNP	PG-O2G	-2.20	1.50	1.56

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	6	527	GNP	C5-C6-N1	-8.92	111.86	123.52
35	6	527	GNP	PA-O3A-PB	-4.95	114.77	132.71
35	6	527	GNP	O3G-PG-O1G	-3.22	105.11	113.58
35	6	527	GNP	C2'-C1'-N9	-3.05	105.29	113.47
35	6	527	GNP	C2'-C3'-C4'	-2.81	96.89	102.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	6	527	GNP	23	0

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.