



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:42 PM BST

PDB ID : 3J8G
EMDB ID: : EMD-6149
Title : Electron cryo-microscopy structure of EngA bound with the 50S ribosomal subunit
Authors : Zhang, X.; Yan, K.; Zhang, Y.; Li, N.; Ma, C.; Li, Z.; Zhang, Y.; Feng, B.; Liu, J.; Sun, Y.; Xu, Y.; Lei, J.; Gao, N.
Deposited on : 2014-10-24
Resolution : 5.00 Å(reported)
Based on PDB ID : 2WWQ, 2HJG

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>

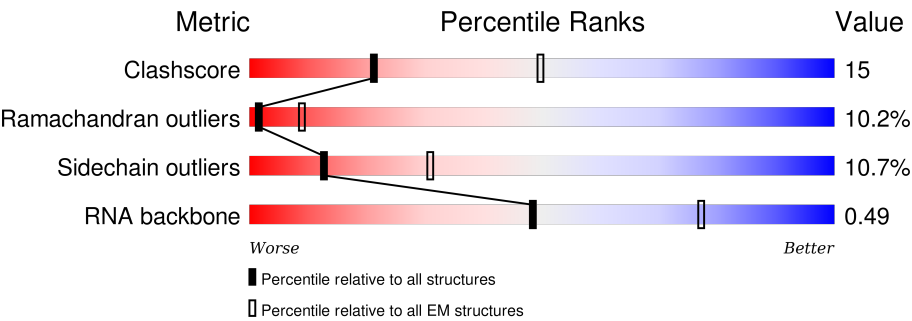
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

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 5.00 Å.

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









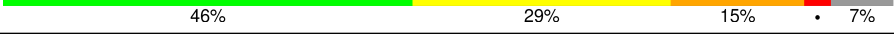

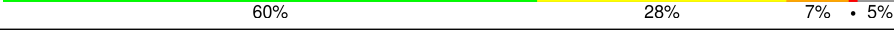
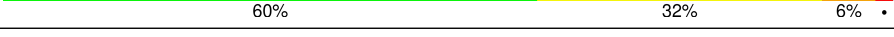
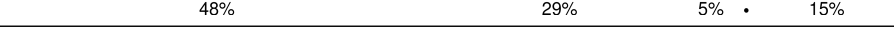

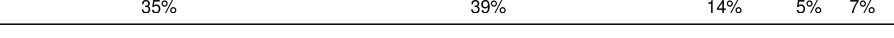
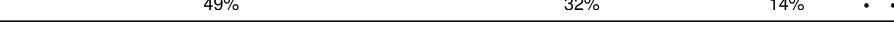
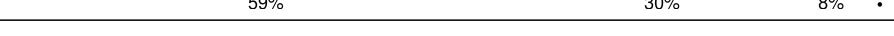


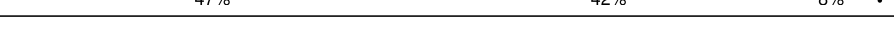
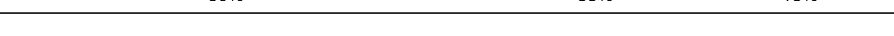

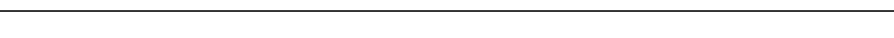

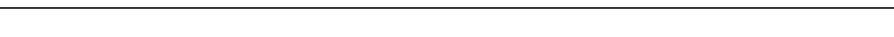
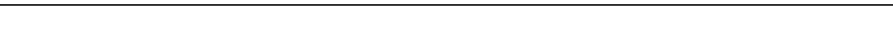
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	A	117	13% 42% 44% .
2	B	2903	11% 38% 50% .
3	0	78	58% 23% 15% ..
4	K	123	56% 33% 7% ..
5	L	144	57% 22% 16% ..
6	1	63	68% 24% 5% .
7	M	136	54% 34% 12%
8	N	127	53% 33% 6% . 6%

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Mol	Chain	Length	Quality of chain
9	O	117	
10	P	115	
11	Q	118	
12	R	103	
13	S	110	
14	D	209	
15	T	100	
16	2	59	
17	U	104	
18	W	94	
19	X	490	
20	E	201	
21	Y	85	
22	3	57	
23	5	234	
24	6	46	
25	7	65	
26	8	38	
27	C	273	
28	F	179	
29	G	177	
30	H	149	
31	I	142	
32	J	142	

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 94855 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 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	115	Total	C	N	O	P	0	0
			2455	1097	451	795	112		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	2874	Total	C	N	O	P	0	0
			61689	27523	11353	19941	2872		

- Molecule 3 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 4 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	121	Total	C	N	O	S	0	0
			931	582	179	164	6		

- Molecule 5 is a protein called 50S ribosomal protein L15.

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

- Molecule 6 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 7 is a protein called 50S ribosomal protein L16.

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

- Molecule 8 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 9 is a protein called 50S ribosomal protein L18.

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

- Molecule 10 is a protein called 50S ribosomal protein L19.

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

- Molecule 11 is a protein called 50S ribosomal protein L20.

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

- Molecule 12 is a protein called 50S ribosomal protein L21.

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

- Molecule 13 is a protein called 50S ribosomal protein L22.

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

- Molecule 14 is a protein called 50S ribosomal protein L3.

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

- Molecule 15 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 16 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	99	Total	C	N	O	S	0	0
			755	479	140	136			

- Molecule 18 is a protein called 50S ribosomal protein L25.

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

- Molecule 19 is a protein called GTPase Der.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	418	Total	C	N	O	S	0	0
			3280	2074	582	610	14		

- Molecule 20 is a protein called 50S ribosomal protein L4.

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

- Molecule 21 is a protein called 50S ribosomal protein L27.

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

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 23 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	5	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 26 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 28 is a protein called 50S ribosomal protein L5.

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

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	175	Total	C	N	O	S	0	0
			1316	827	242	245	2		

- Molecule 30 is a protein called 50S ribosomal protein L9.

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

- Molecule 31 is a protein called 50S ribosomal protein L11.

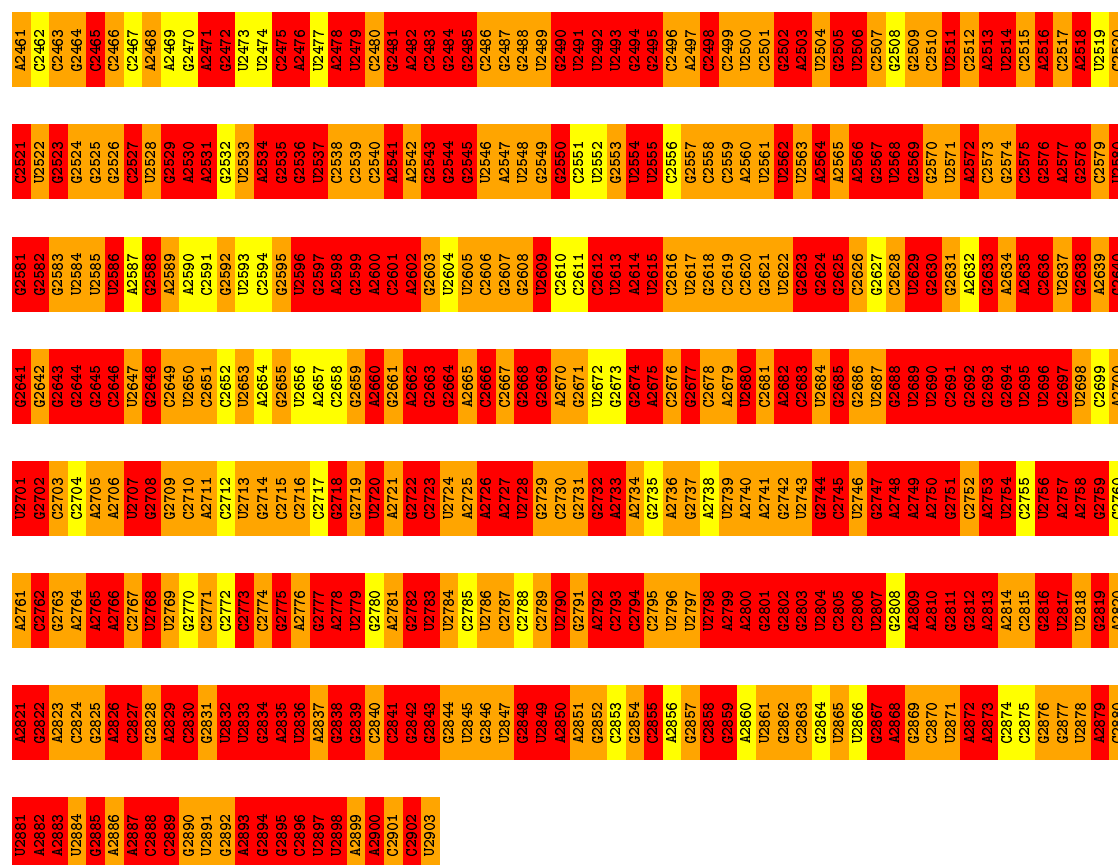
Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 32 is a protein called 50S ribosomal protein L13.

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

G1441	G1381	A1321	G1261	U1201	U1141	U1081	A1021	C961	C901	G841	A781	A721	A661	C601	A541
G1442	G1382	A1322	A1262	G1202	A1142	U1082	G1022	G962	C902	U842	A782	A722	G662	A602	C542
G1443	A1383	A1323	U1263	U1203	A1143	U1083	U1023	G963	C903	G843	A783	G723	G663	A603	G543
G1444	A1384	G1324	A1264	U1204	A1144	A1084	G1024	C964	C904	A844	G784	U724	G664	G604	C544
G1445	A1385	U1325	A1265	A1205	C1145	A1085	G1025	G965	A905	A845	G785	G725	U665	G605	U545
G1446	G1386	U1326	G1266	G1206	C1146	A1086	G1026	G966	U906	U846	G786	G726	G666	U606	U546
G1447	A1387	U1327	U1267	G1207	A1147	G1087	A1027	U967	G907	U847	G787	A727	U667	U607	A547
G1448	G1388	A1328	A1268	C1208	U1148	A1088	G1028	C968	C908	A848	A788	G728	A668	A608	G548
G1449	G1389	U1329	A1269	U1209	G1149	A1089	A1029	G969	A909	A849	A789	G729	G669	A609	G549
G1450	U1390	C1270	C1270	G1210	A1150	A1090	C1030	U970	A910	U850	A790	A730	A670	C610	C550
G1451	U1391	G1271	A1271	G1211	A1151	A1091	G1031	G971	A911	C851	G791	C731	C671	C611	G551
G1452	A1392	G1332	A1272	G1212	C1152	A1092	A1032	A972	C912	U852	A792	G732	G672	G612	U552
G1453	A1393	U1273	A1273	A1213	C1153	G1093	U1033	A973	C913	C853	A793	G733	G673	A613	G553
G1454	U1394	G1334	A1274	A1214	G1154	U1094	G1034	G974	G914	C854	A794	A734	G674	A614	U554
G1455	G1395	C1335	A1275	G1215	A1155	A1095	U1035	A975	C915	G855	C795	A735	A675	U615	G555
G1456	A1396	A1336	A1276	G1216	A1156	A1096	G1036	G976	C916	G856	C796	G736	A676	A616	A556
G1457	U1397	G1337	G1277	U1217	G1157	A1097	G1037	G977	A917	G857	G797	G737	A677	G617	C557
G1458	G1398	G1338	G1278	G1218	C1158	A1098	G1038	G978	A918	G858	G798	G738	G678	G618	U558
G1459	C1399	G1339	G1279	U1219	U1159	G1099	A1039	A979	U919	G859	G799	A739	G679	G619	G559
G1460	U1400	U1340	G1280	G1220	G1160	C1100	A1040	A980	A920	U860	A800	C740	G680	G620	C560
G1461	G1401	G1341	U1281	C1221	C1161	U1101	G1041	A981	C921	A861	G801	U741	G681	A621	G561
G1462	U1402	G1342	U1282	U1222	G1162	C1102	G1042	C982	C922	G862	A802	A742	G682	G622	U562
G1463	G1343	G1283	G1283	G1223	G1163	A1103	C1043	A983	C923	A863	U803	A743	U683	C623	A563
G1464	A1404	G1344	A1284	U1224	C1164	G1104	C1044	A984	G924	G864	A804	U744	G684	C624	C564
G1465	U1405	C1345	A1285	G1225	A1165	U1105	C1045	C985	A925	G865	G805	G745	A685	G625	C565
U1466	U1406	G1346	A1286	A1226	G1166	G1106	A1046	C986	G926	A866	C806	U746	U686	A826	U566
G1467	G1407	A1347	A1287	G1227	C1167	G1107	G1047	G987	A927	C867	U807	U747	G687	A627	U567
U1468	G1408	C1348	G1288	G1228	G1168	U1108	A1048	A988	A928	U868	G808	G748	U688	G628	U568
A1469	U1409	C1349	C1289	G1229	A1169	C1109	C1049	G989	U929	U869	G809	A749	A689	G629	U569
A1470	G1410	C1350	C1290	A1230	G1170	G1110	A1050	A990	G930	U870	U810	A750	G690	G630	A570
G1471	U1411	C1351	G1291	U1231	G1171	A1111	G1051	C991	U931	U871	U811	A751	C691	A631	U571
G1472	U1412	U1352	G1292	G1232	C1172	G1112	C1052	C992	U932	U872	G812	A752	G692	A832	A572
G1473	A1413	A1353	G1293	C1233	U1173	U1113	G1053	G993	A933	C873	U813	A753	A693	A633	U573
U1474	G1414	U1354	U1294	C1234	U1174	C1114	A1054	C994	U934	G874	C814	U754	G694	C634	A574
G1475	U1415	G1355	C1295	G1235	A1175	G1115	G1055	C995	C935	G875	C815	U755	G695	C635	A575
U1476	G1416	G1356	G1296	G1236	U1176	G1116	G1056	A996	A936	C876	C816	A756	G696	G636	U576
G1477	C1417	C1357	G1297	A1237	G1177	C1117	A1057	G997	C937	A877	C817	G757	G697	A637	U577
G1478	G1418	G1358	G1298	G1238	C1178	C1118	U1058	C998	G938	A878	G818	C758	G698	G638	G578
G1479	A1419	A1359	G1299	G1239	G1179	U1119	G1059	G999	G939	G879	A819	G759	A699	U639	G579
U1480	A1420	G1360	G1300	U1240	U1180	G1120	U1060	A1000	G940	G880	A820	G760	G700	C640	U580
U1481	G1421	G1361	A1301	A1241	U1181	C1121	U1061	A1001	A941	G881	A821	A761	G701	U641	C581
G1482	G1422	C1362	A1302	U1242	G1182	G1122	G1062	G1002	G942	G882	G822	U762	U702	U642	A582
G1483	G1423	G1363	G1303	C1243	U1183	C1123	G1063	G1003	A943	G883	C823	G763	U703	A643	G583
U1484	G1424	G1364	A1304	A1244	U1184	G1124	C1064	U1004	C944	U884	U824	A764	G704	A644	C584
U1485	G1425	A1365	C1305	G1245	G1185	G1125	U1065	C1005	A945	C885	A825	C765	A705	C645	G585
G1486	G1426	A1366	C1306	A1246	G1186	A1126	U1066	C1006	C946	A886	U826	U766	A706	U646	A586
U1487	A1427	A1367	G1307	A1247	G1187	A1127	A1067	C1007	A947	U887	U827	U767	G707	G647	C587
C1488	C1428	G1368	A1308	G1248	U1188	G1128	G1068	A1008	C948	C888	A828	G768	G708	G648	U588
C1489	G1429	G1369	G1309	U1249	A1189	A1129	A1069	A1009	G949	C889	A829	U769	U709	G649	U589
A1490	G1430	C1370	G1310	G1250	G1190	U1130	A1070	A1010	G950	C890	G830	G770	U710	C650	A590
G1491	A1431	G1371	G1311	C1251	G1191	G1131	G1071	G1011	C951	G891	G831	G771	G711	G651	U591
G1492	G1432	U1372	U1312	G1252	G1192	U1132	C1072	A892	G952	A892	U832	G772	G712	U652	A592
C1493	A1433	A1373	G1313	A1253	G1193	A1133	A1073	C1013	G953	C893	A833	U773	G713	U653	U593
A1494	A1434	G1374	C1314	A1254	A1194	A1134	G1074	A1014	G954	U894	G834	G774	U714	A654	U594
A1495	G1435	U1375	C1315	U1255	G1195	C1135	C1075	U1015	U955	U895	C835	G775	A715	A655	C595
G1496	G1436	G1376	U1316	G1256	C1196	G1136	C1076	A896	G956	A896	G836	G776	A716	G656	U596
U1497	C1437	G1377	G1317	C1257	G1197	G1137	A1077	G1017	C957	C897	G837	G777	G717	U657	G597
G1498	U1438	A1378	U1318	U1258	U1198	G1138	U1078	U1018	U958	C898	C838	G778	A718	U658	U598
C1499	A1439	G1379	C1319	G1259	U1199	G1139	C1079	A899	G959	A899	U839	U779	C719	A659	U599
G1500	U1440	G1380	C1320	A1260	C1200	C1140	A1080	A1020	A960		C840	G780	U720	C660	

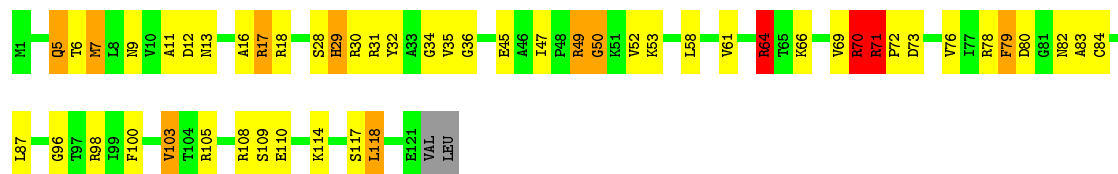
U2401	G2341	A2281	G2221	C2161	A2101	U2041	A1981	G1921	G	A1801	C1741	G1681	U1621	C1561	G1501
U2402	G2342	G2282	C2222	G2162	G2102	A2042	U1982	G1922	G	A1802	U1742	G1682	G1622	U1562	A1502
C2403	U2343	A2163	G2223	A2163	C2103	C2043	G1983	G1923	U	A1803	G1743	G1683	G1623	U1563	A1503
U2404	U2344	G2283	G2224	C2164	C2104	C2044	G1984	C1924	U	C1804	A1744	G1684	U1624	C1564	A1504
G2405	G2345	C2165	A2225	C2165	U2105	C2045	C1985	C1925	U	A1805	A1745	C1565	C1625	C1505	U1505
A2406	A2346	G2286	C2226	U2166	U2106	G2046	C1986	U1926	A	C1806	A1746	C1686	A1626	A1566	U1506
G2407	C2347	A2287	A2227	U2167	G2107	C2047	A1987	A1927	C	G1807	U1747	G1687	G1627	G1567	C1507
U2408	U2348	G2288	G2228	G2168	A2108	G2048	G1988	A1928	C	A1808	C1748	U1688	G1628	G1568	A1508
G2409	G2349	A2289	U2229	A2169	U2109	G2049	G1989	G1929	G	A1809	A1749	U1689	U1629	A1569	A1509
G2410	C2350	G2290	G2230	A2170	G2110	C2050	C1990	G1930	C	A1810	G1750	A1570	A1630	A1570	G1510
A2411	G2351	U2291	U2231	A2171	U2111	A2051	C1991	G1931	A	G1811	U1751	C1691	G1631	A1571	G1511
A2412	A2352	G2292	C2232	U2172	G2112	A2052	G1992	A1932	A	U1812	C1752	U1692	A1632	A1572	C1512
G2413	G2353	C2173	U2233	A2173	U2113	C2053	U1993	G1933	G	G1813	G1753	U1693	G1633	G1573	U1513
G2414	C2354	G2294	G2234	C2174	A2114	A2054	C1994	C1934	C	G1814	A1754	C1694	A1634	C1574	G1514
G2415	G2355	C2295	G2235	C2175	G2115	C2055	U1995	G1935	A	A1815	A1755	G1695	A1635	C1575	A1515
C2416	U2356	U2296	U2236	A2176	G2116	G2056	C1996	A1936	G	A1816	G1756	U1696	U1636	U1576	G1516
C2417	G2357	A2297	G2237	C2177	A2117	G2057	C1997	A1937	A	G1817	A1757	G1697	A1637	C1577	G1517
A2418	A2358	G2298	G2238	U2178	U2118	A2058	A1998	A1938	G	U1818	U1758	U1698	C1638	U1578	C1518
U2419	C2359	U2299	U2239	C2179	A2119	A2059	C1999	U1939	C	A1819	A1759	G1699	C1639	A1579	G1519
C2420	G2360	U2300	U2240	U2180	G2120	A2060	C2000	U1940	U	U1820	C1760	A1700	A1640	U1580	U1520
G2421	G2361	U2181	A2241	U2181	G2121	G2061	C2001	C1941	C	A1821	C1761	A1581	A1641	G1581	G1521
C2422	C2362	U2302	G2242	U2182	U2122	A2062	G2002	C1942	U	G1822	A1762	G1702	G1642	C1582	A1522
G2423	G2363	A2183	U2243	A2183	G2123	C2063	A2003	U1943	U	G1823	G1763	G1703	G1643	A1583	U1523
C2424	C2364	U2184	U2244	A2184	G2124	C2064	G2004	U1944	G	G1824	C1764	C1704	C1644	G1524	G1524
A2425	G2365	U2185	U2245	G2125	G2125	C2065	A2005	G1945	A1885	U1825	U1765	A1705	G1645	C1585	A1525
A2426	A2366	G2186	G2246	A2126	A2126	C2066	C2006	U1946	U1886	G1826	G1766	C1706	C1646	A1586	C1526
C2427	C2367	U2187	A2247	G2127	G2127	G2067	U2007	C1947	G1887	U1827	G1767	G1707	U1647	G1587	G1527
G2428	C2368	U2188	C2248	G2128	C2128	U2068	C2008	G1948	G1888	G1828	U1648	C1588	U1648	A1528	A1528
G2429	A2369	U2189	U2249	G2129	C2129	G2069	A2009	G1949	A1889	U1829	U1769	U1589	G1649	U1589	G1529
A2430	G2370	G2190	U2250	U2130	U2130	A2070	G2010	G1950	A1890	G1830	G1770	A1590	A1650	G1530	G1530
U2431	G2371	A2191	G2251	U2131	U2131	A2071	U2011	U1951	G1891	G1831	C1771	A1591	G1651	C1531	C1531
A2432	U2372	U2192	G2252	U2132	C2072	C2072	G2012	A1952	C1892	G1832	A1772	U1712	A1652	C1532	A1532
G2433	G2373	G2193	G2253	C2073	A2013	C2073	A2013	A1953	G1893	C1833	A1773	A1713	G1653	C1533	G1533
A2434	C2374	U2194	U2254	A2134	U2074	G2074	A2014	G1954	C1894	G1834	C1774	U1714	A1654	U1534	U1534
A2435	G2375	U2195	G2255	A2135	A2135	U2075	A2015	U1955	C1895	G1835	U1775	G1715	A1655	C1535	A1535
G2436	G2376	C2196	G2256	G2136	U2076	A2076	U2016	U1956	G1896	C1836	G1776	U1716	C1656	C1536	C1536
G2437	A2377	U2197	U2257	U2137	A2077	G2077	U2017	C1957	G1897	C1837	U1777	A1717	U1657	A1597	G1537
U2438	A2378	A2198	C2258	G2138	G2138	C2078	G2018	C1958	U1898	C1838	U1778	G1718	C1658	A1598	G1538
A2439	G2379	A2199	U2259	U2139	U2139	U2079	A2019	G1959	A1899	G1839	U1779	G1719	G1659	U1599	U1539
C2440	C2380	C2200	C2260	G2140	G2140	A2080	A2020	A1960	A1900	G1840	A1780	U1720	G1660	C1600	G1540
U2441	A2381	G2201	C2261	G2141	G2141	U2081	C2021	C1961	A1901	U1841	U1781	G1721	G1661	G1601	C1541
C2442	G2382	U2202	U2262	A2142	A2142	A2082	U2022	C1962	C1902	G1842	U1782	A1722	U1662	U1602	U1542
G2443	G2383	C2203	C2263	C2143	C2143	G2083	C2023	U1963	G1903	C1843	A1783	G1723	G1663	A1603	G1543
U2444	U2384	G2204	G2264	G2144	G2144	C2084	G2024	G1964	G1904	C1844	A1784	G1724	A1664	C1604	A1544
G2445	C2385	A2205	U2265	C2145	C2145	U2085	C2025	C1965	C1905	G1845	A1785	U1725	A1665	C1605	A1545
G2446	A2386	C2206	A2266	C2146	C2146	U2086	U2026	A1966	G1906	G1846	A1786	C1726	G1666	C1606	G1546
G2447	U2387	C2207	A2267	A2147	A2147	G2087	G2027	C1967	G1907	G1847	A1787	C1727	G1667	C1607	C1547
A2448	A2388	C2208	A2268	G2148	G2148	U2088	U2028	G1968	C1908	G1848	A1788	C1728	A1668	A1608	A1548
U2449	G2389	G2209	C2269	U2149	U2149	C2089	G2029	A1969	C1909	G1849	A1789	U1729	A1669	A1609	A1549
A2450	U2390	U2210	A2270	C2150	C2150	A2090	A2030	A1970	G1910	G1850	C1790	G1730	C1670	A1610	C1550
U2451	G2391	A2211	G2271	U2151	U2151	C2091	A2031	U1971	U1911	U1851	A1791	G1731	U1671	C1611	A1551
C2452	A2392	A2212	U2272	G2152	G2152	U2092	G2032	C1972	A1912	U1852	A1792	C1732	A1672	C1612	A1552
A2453	U2393	U2213	C2273	C2153	C2153	G2093	A2033	G1973	A1913	U1853	C1793	G1733	G1673	G1613	U1553
C2454	C2394	C2214	A2274	A2154	A2154	A2094	U2034	C1974	C1914	A1854	A1794	G1734	A1674	A1614	U1554
G2455	G2395	C2215	U2275	U2155	U2155	G2095	G2035	G1975	U1915	U1855	C1795	A1735	C1675	C1615	G1555
A2456	G2396	A2216	G2276	G2156	G2156	C2096	C2036	U1976	A1916	U1856	U1796	U1736	A1676	C1556	C1556
G2457	G2397	G2217	G2277	G2157	G2157	A2097	A2037	A1977	U1917	U1857	G1797	G1737	A1677	C1557	C1557
G2458	U2398	G2218	A2278	A2158	A2158	U2098	G2038	A1978	A1918	U1858	U1798	G1738	A1678	A1618	U1558
A2459	C2399	U2219	G2279	C2159	C2159	U2099	U2039	A1979	A1919	U1859	A1799	G1739	A1679	A1619	C1559
U2460	G2400	U2220	G2280	C2160	C2160	G2100	G2040	G1980	C1920	G	C1800	G1740	U1680	G1620	G1560



• Molecule 3: 50S ribosomal protein L28



• Molecule 4: 50S ribosomal protein L14



• Molecule 5: 50S ribosomal protein L15





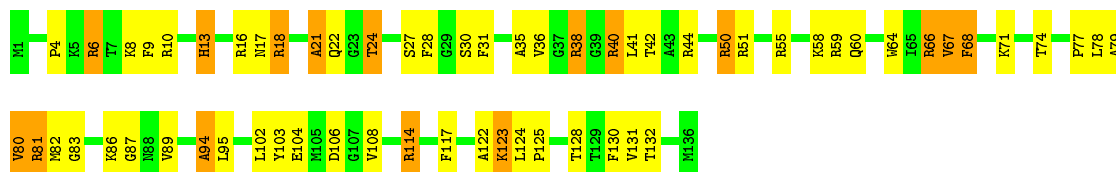
- Molecule 6: 50S ribosomal protein L29

Chain 1: 68% 24% 5%



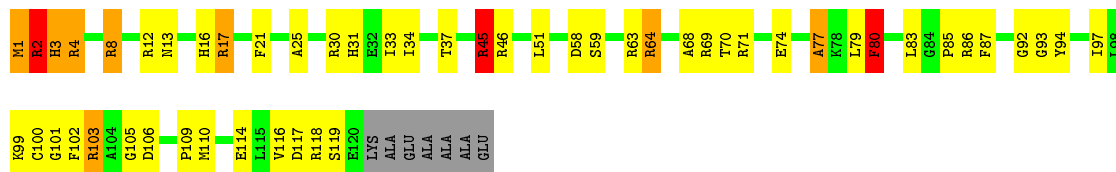
- Molecule 7: 50S ribosomal protein L16

Chain M: 54% 34% 12%



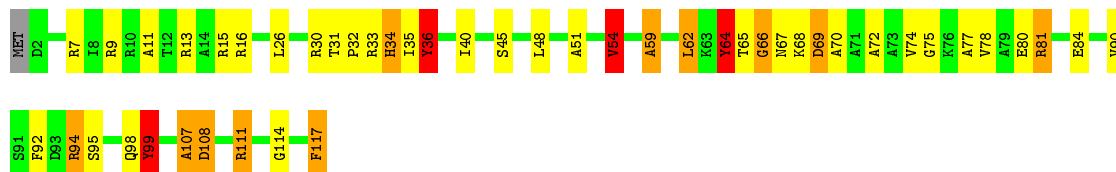
- Molecule 8: 50S ribosomal protein L17

Chain N: 53% 33% 6% 6%



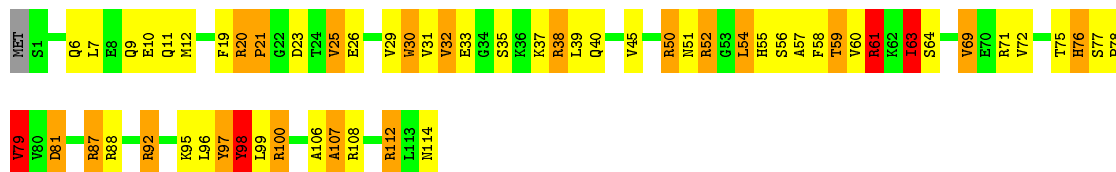
- Molecule 9: 50S ribosomal protein L18

Chain O: 59% 27% 9% 2%



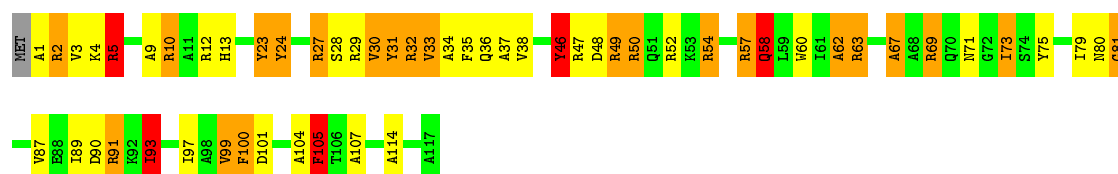
- Molecule 10: 50S ribosomal protein L19

Chain P: 48% 31% 17% 2%



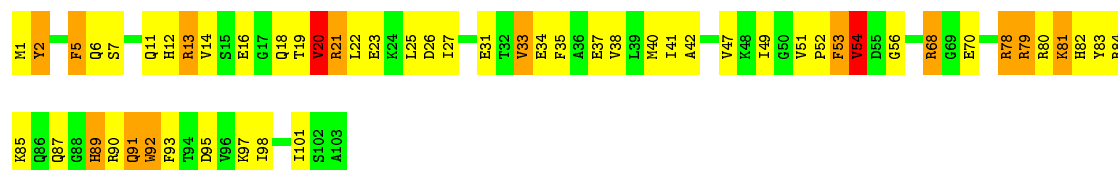
- Molecule 11: 50S ribosomal protein L20

Chain Q: 



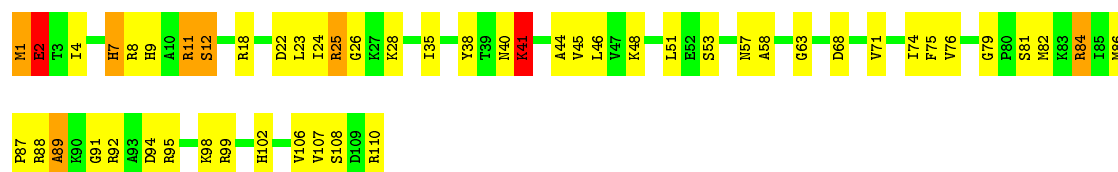
- Molecule 12: 50S ribosomal protein L21

Chain R: 



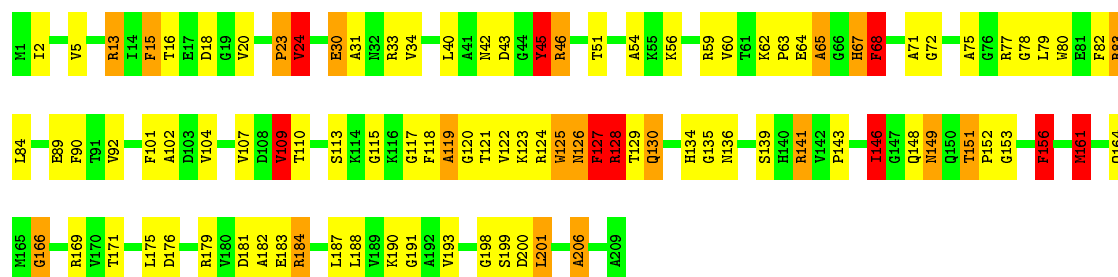
- Molecule 13: 50S ribosomal protein L22

Chain S: 



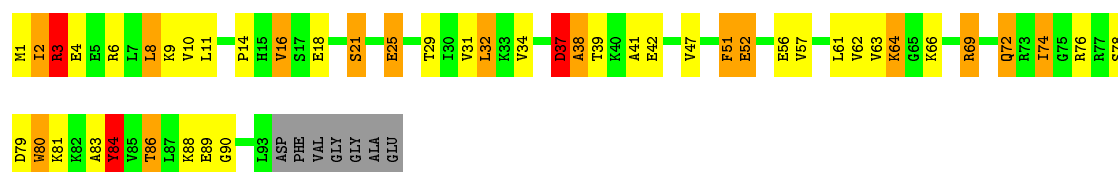
- Molecule 14: 50S ribosomal protein L3

Chain D: 

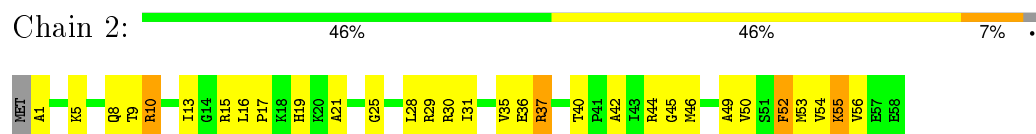


- Molecule 15: 50S ribosomal protein L23

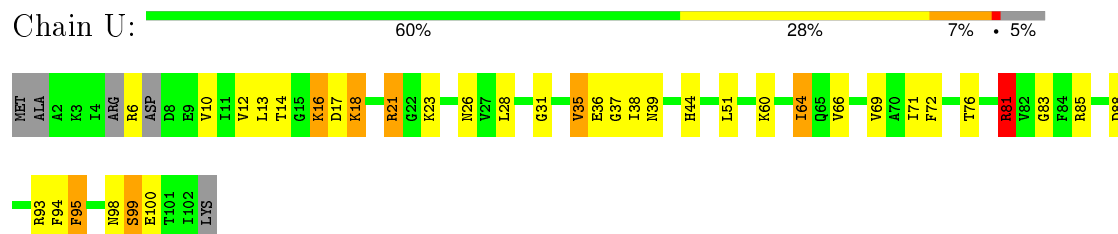
Chain T: 



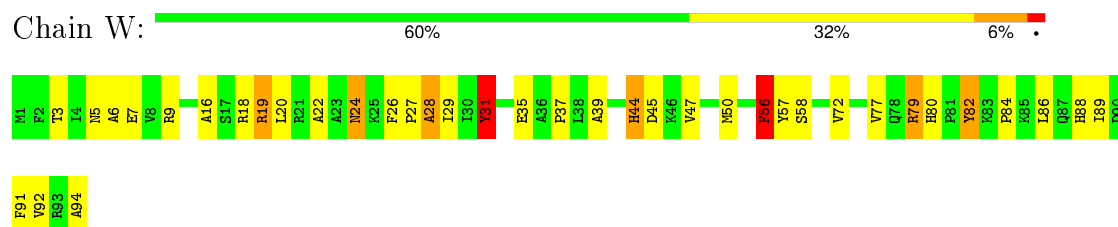
- Molecule 16: 50S ribosomal protein L30



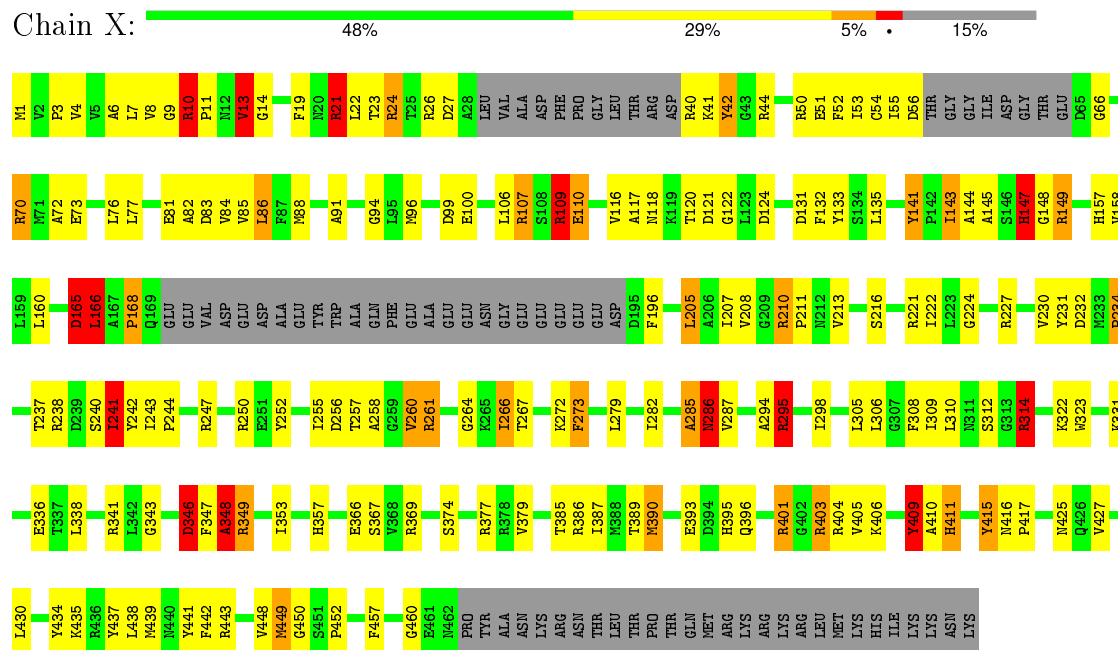
- Molecule 17: 50S ribosomal protein L24



- Molecule 18: 50S ribosomal protein L25

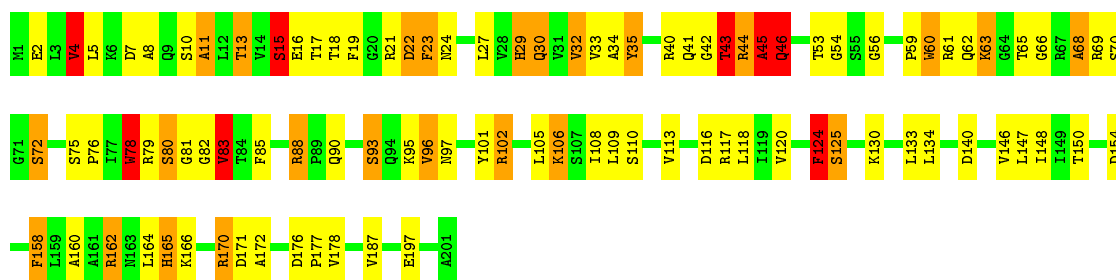


- Molecule 19: GTPase Der



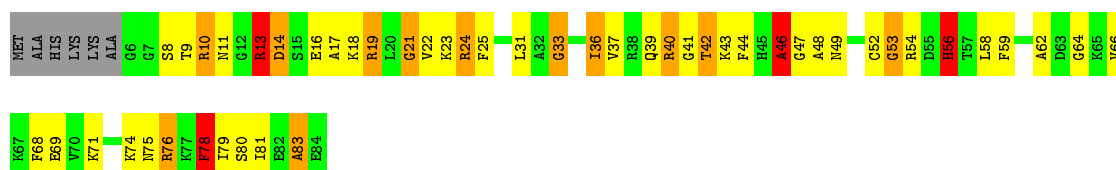
- Molecule 20: 50S ribosomal protein L4





- Molecule 21: 50S ribosomal protein L27

Chain Y:



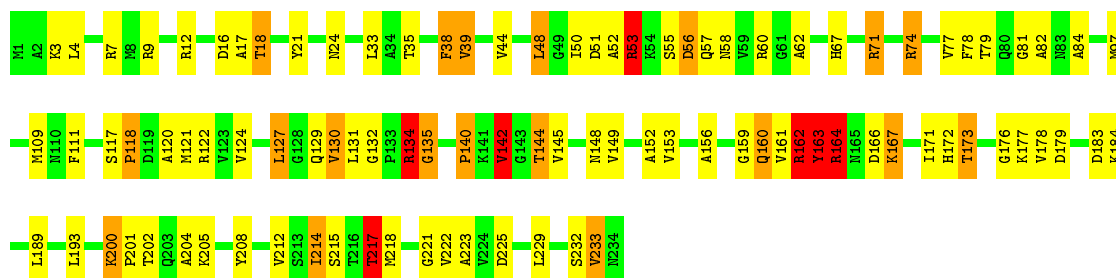
- Molecule 22: 50S ribosomal protein L32

Chain 3:



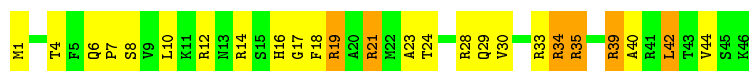
- Molecule 23: 50S ribosomal protein L1

Chain 5:



- Molecule 24: 50S ribosomal protein L34

Chain 6:



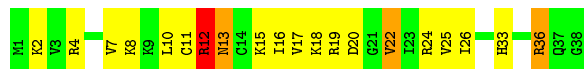
- Molecule 25: 50S ribosomal protein L35

Chain 7:



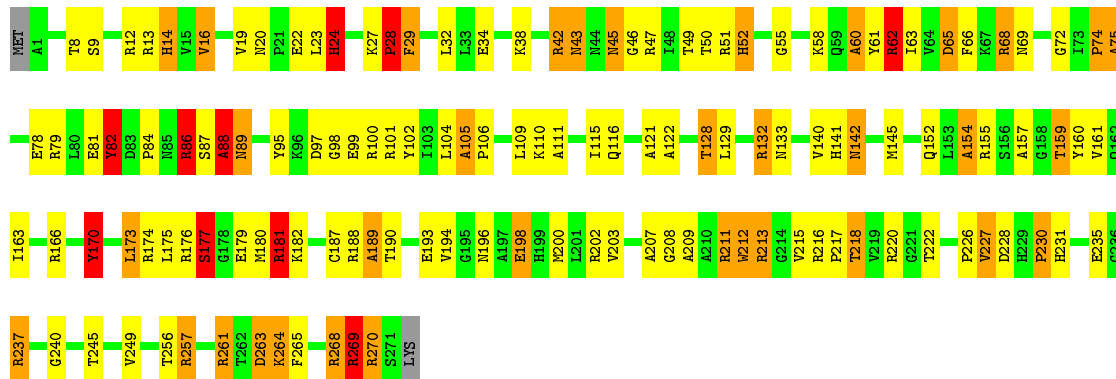
- Molecule 26: 50S ribosomal protein L36

Chain 8: 



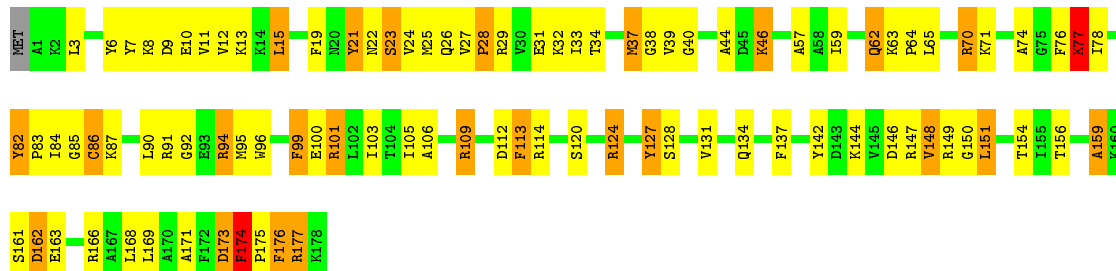
- Molecule 27: 50S ribosomal protein L2

Chain C: 



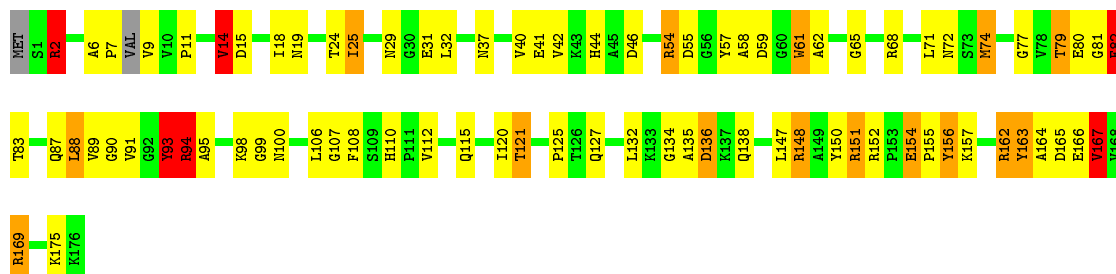
- Molecule 28: 50S ribosomal protein L5

Chain F: 

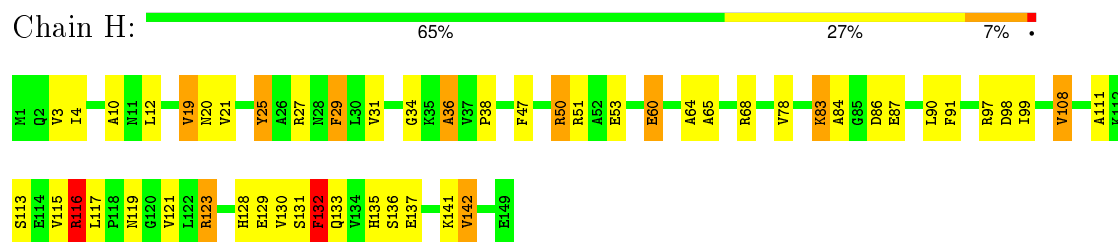


- Molecule 29: 50S ribosomal protein L6

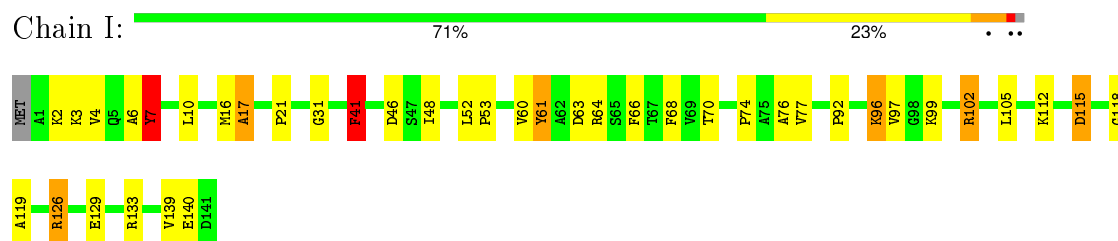
Chain G: 



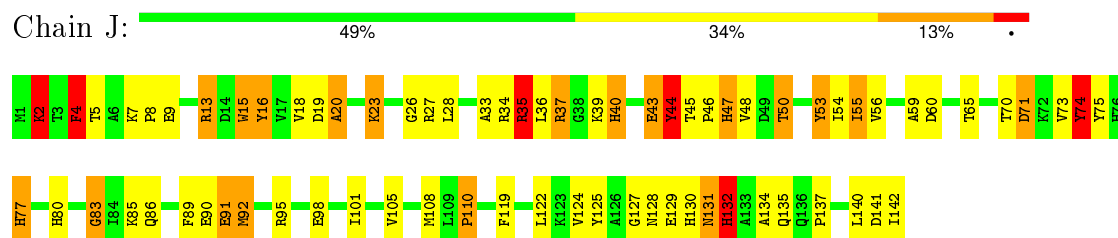
- Molecule 30: 50S ribosomal protein L9



- Molecule 31: 50S ribosomal protein L11



- Molecule 32: 50S ribosomal protein L13



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	189614	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI EAGLE 4k*4k CCD	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	A	3.57	414/2744 (15.1%)	3.75	637/4276 (14.9%)
10	P	1.83	13/929 (1.4%)	2.13	26/1242 (2.1%)
11	Q	1.81	9/960 (0.9%)	2.35	47/1278 (3.7%)
12	R	1.75	4/829 (0.5%)	2.09	26/1107 (2.3%)
13	S	1.83	9/864 (1.0%)	2.06	22/1156 (1.9%)
14	D	1.81	19/1586 (1.2%)	2.12	48/2134 (2.2%)
15	T	1.88	7/744 (0.9%)	2.05	24/994 (2.4%)
16	2	1.84	8/453 (1.8%)	2.15	14/605 (2.3%)
17	U	1.71	2/761 (0.3%)	1.94	13/1013 (1.3%)
18	W	1.74	5/766 (0.7%)	2.12	22/1025 (2.1%)
19	X	1.73	26/3334 (0.8%)	2.01	98/4502 (2.2%)
2	B	3.66	11120/69092 (16.1%)	3.80	17069/107787 (15.8%)
20	E	1.83	25/1571 (1.6%)	2.01	44/2113 (2.1%)
21	Y	1.84	8/603 (1.3%)	2.19	20/797 (2.5%)
22	3	1.85	2/450 (0.4%)	2.17	18/599 (3.0%)
23	5	1.68	18/1748 (1.0%)	1.99	52/2355 (2.2%)
24	6	1.97	5/380 (1.3%)	2.15	17/498 (3.4%)
25	7	1.82	6/513 (1.2%)	2.15	14/676 (2.1%)
26	8	1.72	3/303 (1.0%)	2.04	3/397 (0.8%)
27	C	1.87	34/2121 (1.6%)	2.07	66/2852 (2.3%)
28	F	1.75	16/1444 (1.1%)	2.21	59/1937 (3.0%)
29	G	1.77	12/1335 (0.9%)	2.13	40/1803 (2.2%)
3	0	1.89	7/635 (1.1%)	2.19	18/848 (2.1%)
30	H	1.71	8/1122 (0.7%)	1.87	17/1515 (1.1%)
31	I	1.65	5/1046 (0.5%)	1.92	28/1410 (2.0%)
32	J	1.79	12/1152 (1.0%)	2.02	36/1551 (2.3%)
4	K	1.72	6/940 (0.6%)	2.04	23/1258 (1.8%)
5	L	1.89	18/1054 (1.7%)	2.13	35/1403 (2.5%)
6	1	1.66	2/510 (0.4%)	1.81	4/677 (0.6%)
7	M	1.78	7/1093 (0.6%)	2.07	34/1460 (2.3%)
8	N	1.83	10/973 (1.0%)	2.11	35/1301 (2.7%)
9	O	1.84	12/902 (1.3%)	2.08	26/1209 (2.2%)
All	All	3.21	11852/102957 (11.5%)	3.42	18635/153778 (12.1%)

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	A	0	69
10	P	0	7
11	Q	0	11
12	R	0	8
13	S	0	3
14	D	0	11
15	T	0	3
16	2	0	4
17	U	0	4
18	W	0	2
19	X	0	25
2	B	0	1764
20	E	0	7
21	Y	0	6
22	3	0	4
23	5	0	7
24	6	0	3
25	7	0	3
26	8	0	1
27	C	0	11
28	F	0	6
29	G	0	9
3	0	0	5
30	H	0	9
31	I	0	3
32	J	0	9
4	K	0	4
5	L	0	10
6	1	0	6
7	M	0	9
8	N	0	4
9	O	0	5
All	All	0	2032

The worst 5 of 11852 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	159	G	N7-C5	-23.28	1.25	1.39
2	B	1674	G	N7-C5	-21.28	1.26	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	770	G	N7-C5	-20.77	1.26	1.39
2	B	1626	A	N7-C5	-20.30	1.27	1.39
2	B	1641	A	N7-C5	-19.84	1.27	1.39

The worst 5 of 18635 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1784	A	N1-C6-N6	27.35	135.01	118.60
2	B	319	G	N1-C6-O6	25.96	135.47	119.90
2	B	332	A	N1-C6-N6	25.93	134.16	118.60
2	B	909	A	N1-C6-N6	25.56	133.93	118.60
2	B	2270	A	N1-C6-N6	25.05	133.63	118.60

There are no chirality outliers.

5 of 2032 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2	G	Sidechain
1	A	4	C	Sidechain
1	A	5	U	Sidechain
1	A	7	G	Sidechain
1	A	8	C	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2455	0	1253	65	0
2	B	61689	0	30889	2037	0
3	O	625	0	655	7	0
4	K	931	0	1003	12	0
5	L	1045	0	1117	16	0
6	1	509	0	543	8	0
7	M	1074	0	1157	17	0
8	N	960	0	1000	14	0
9	O	892	0	923	10	0
10	P	917	0	965	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	Q	947	0	1022	16	0
12	R	816	0	839	13	0
13	S	857	0	922	18	0
14	D	1565	0	1616	24	0
15	T	738	0	807	9	0
16	2	449	0	491	4	0
17	U	755	0	807	6	0
18	W	753	0	780	11	0
19	X	3280	0	3334	47	0
20	E	1552	0	1619	27	0
21	Y	596	0	610	14	0
22	3	444	0	461	7	0
23	5	1733	0	1824	19	0
24	6	377	0	418	4	0
25	7	504	0	574	8	0
26	8	302	0	343	8	0
27	C	2082	0	2157	31	0
28	F	1420	0	1460	18	0
29	G	1316	0	1364	15	0
30	H	1111	0	1148	13	0
31	I	1032	0	1088	3	0
32	J	1129	0	1162	30	0
All	All	94855	0	64351	2462	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 15.

The worst 5 of 2462 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)
19:X:347:PHE:CD2	19:X:449:MET:CG	2.00	1.45
19:X:347:PHE:CD2	19:X:449:MET:HG2	1.49	1.26
19:X:347:PHE:CD2	19:X:449:MET:HG3	1.84	0.97
19:X:449:MET:CE	19:X:449:MET:HA	1.97	0.94
19:X:347:PHE:HD2	19:X:449:MET:HG2	0.77	0.90

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	0	75/78 (96%)	54 (72%)	11 (15%)	10 (13%)	0	7
4	K	119/123 (97%)	84 (71%)	21 (18%)	14 (12%)	0	9
5	L	141/144 (98%)	108 (77%)	23 (16%)	10 (7%)	1	22
6	1	61/63 (97%)	49 (80%)	12 (20%)	0	100	100
7	M	134/136 (98%)	97 (72%)	18 (13%)	19 (14%)	0	6
8	N	118/127 (93%)	91 (77%)	20 (17%)	7 (6%)	2	27
9	O	114/117 (97%)	96 (84%)	12 (10%)	6 (5%)	2	30
10	P	112/115 (97%)	81 (72%)	18 (16%)	13 (12%)	0	9
11	Q	115/118 (98%)	87 (76%)	17 (15%)	11 (10%)	1	14
12	R	101/103 (98%)	71 (70%)	23 (23%)	7 (7%)	1	23
13	S	108/110 (98%)	83 (77%)	16 (15%)	9 (8%)	1	18
14	D	207/209 (99%)	143 (69%)	42 (20%)	22 (11%)	0	11
15	T	91/100 (91%)	58 (64%)	17 (19%)	16 (18%)	0	4
16	2	56/59 (95%)	46 (82%)	7 (12%)	3 (5%)	2	29
17	U	94/104 (90%)	66 (70%)	16 (17%)	12 (13%)	0	8
18	W	92/94 (98%)	77 (84%)	10 (11%)	5 (5%)	2	29
19	X	410/490 (84%)	329 (80%)	46 (11%)	35 (8%)	1	17
20	E	199/201 (99%)	145 (73%)	28 (14%)	26 (13%)	0	7
21	Y	77/85 (91%)	43 (56%)	15 (20%)	19 (25%)	0	1
22	3	54/57 (95%)	36 (67%)	10 (18%)	8 (15%)	0	5
23	5	232/234 (99%)	185 (80%)	23 (10%)	24 (10%)	1	12
24	6	44/46 (96%)	33 (75%)	7 (16%)	4 (9%)	1	16
25	7	62/65 (95%)	44 (71%)	11 (18%)	7 (11%)	0	10
26	8	36/38 (95%)	26 (72%)	6 (17%)	4 (11%)	0	11
27	C	269/273 (98%)	201 (75%)	35 (13%)	33 (12%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	F	176/179 (98%)	119 (68%)	41 (23%)	16 (9%)	1	16
29	G	171/177 (97%)	128 (75%)	26 (15%)	17 (10%)	1	13
30	H	147/149 (99%)	109 (74%)	25 (17%)	13 (9%)	1	16
31	I	139/142 (98%)	114 (82%)	16 (12%)	9 (6%)	1	25
32	J	140/142 (99%)	102 (73%)	21 (15%)	17 (12%)	0	8
All	All	3894/4078 (96%)	2905 (75%)	593 (15%)	396 (10%)	1	13

5 of 396 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	0	15	ASN
3	0	28	PHE
3	0	70	LEU
5	L	29	LYS
5	L	41	ARG

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	
3	0	67/68 (98%)	62 (92%)	5 (8%)	17	55
4	K	102/104 (98%)	92 (90%)	10 (10%)	10	42
5	L	102/103 (99%)	89 (87%)	13 (13%)	5	30
6	1	55/55 (100%)	50 (91%)	5 (9%)	12	46
7	M	109/109 (100%)	105 (96%)	4 (4%)	41	74
8	N	100/103 (97%)	93 (93%)	7 (7%)	19	58
9	O	86/87 (99%)	73 (85%)	13 (15%)	3	24
10	P	99/100 (99%)	87 (88%)	12 (12%)	6	32
11	Q	89/90 (99%)	81 (91%)	8 (9%)	12	46
12	R	84/84 (100%)	69 (82%)	15 (18%)	2	16
13	S	93/93 (100%)	88 (95%)	5 (5%)	27	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	D	164/164 (100%)	143 (87%)	21 (13%)	5	30
15	T	80/84 (95%)	69 (86%)	11 (14%)	4	28
16	2	48/49 (98%)	44 (92%)	4 (8%)	14	51
17	U	81/85 (95%)	72 (89%)	9 (11%)	8	36
18	W	78/78 (100%)	71 (91%)	7 (9%)	12	46
19	X	357/419 (85%)	324 (91%)	33 (9%)	11	45
20	E	165/165 (100%)	152 (92%)	13 (8%)	15	53
21	Y	59/63 (94%)	55 (93%)	4 (7%)	20	59
22	3	47/48 (98%)	40 (85%)	7 (15%)	4	25
23	5	181/181 (100%)	158 (87%)	23 (13%)	5	30
24	6	38/38 (100%)	35 (92%)	3 (8%)	15	53
25	7	51/52 (98%)	44 (86%)	7 (14%)	4	28
26	8	34/34 (100%)	31 (91%)	3 (9%)	12	47
27	C	216/218 (99%)	190 (88%)	26 (12%)	6	32
28	F	149/150 (99%)	131 (88%)	18 (12%)	6	32
29	G	136/138 (99%)	115 (85%)	21 (15%)	3	23
30	H	114/114 (100%)	105 (92%)	9 (8%)	15	53
31	I	109/110 (99%)	100 (92%)	9 (8%)	14	51
32	J	116/116 (100%)	99 (85%)	17 (15%)	4	25
All	All	3209/3302 (97%)	2867 (89%)	342 (11%)	13	38

5 of 342 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	X	56	ASP
20	E	83	VAL
31	I	4	VAL
19	X	106	LEU
19	X	295	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
18	W	51	GLN

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Mol	Chain	Res	Type
21	Y	39	GLN
32	J	40	HIS
19	X	147	HIS
19	X	357	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	112/117 (95%)	20 (17%)	4 (3%)
2	B	2873/2903 (98%)	580 (20%)	122 (4%)
All	All	2985/3020 (98%)	600 (20%)	126 (4%)

5 of 600 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	13	G
1	A	14	U
1	A	15	A
1	A	16	G

5 of 126 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	1272	A
2	B	1714	U
2	B	2576	G
2	B	1312	U
2	B	1428	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

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](#)

There are no chain breaks in this entry.