



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 10, 2017 – 05:01 PM EDT

PDB ID : 5O60
EMDB ID: : EMD-3750
Title : Structure of the 50S large ribosomal subunit from Mycobacterium smegmatis
Authors : Hentschel, J.; Burnside, C.; Mignot, I.; Leibundgut, M.; Boehringer, D.; Ban, N.
Deposited on : unknown
Resolution : 3.20 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

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

A user guide is available at

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

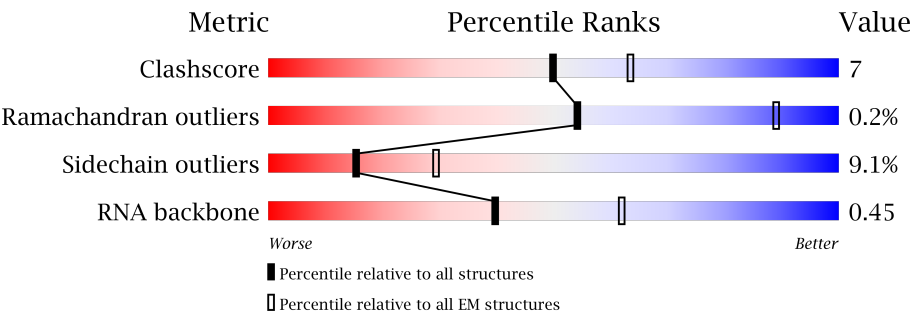
MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 Å.

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




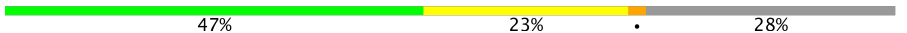























Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	3	24	58% 38% .
2	A	3120	59% 32% 9% .
3	B	118	63% 29% 8%
4	C	278	67% 28% ..
5	D	217	69% 24% 6% .
6	E	215	76% 20% ..
7	F	187	70% 24% ..
8	G	179	70% 23% 5% .

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Mol	Chain	Length	Quality of chain
9	H	151	
10	I	175	
11	J	142	
12	K	147	
13	L	122	
14	M	147	
15	N	138	
16	O	199	
17	P	127	
18	Q	113	
19	R	129	
20	S	103	
21	T	153	
22	U	100	
23	V	105	
24	W	215	
25	X	88	
26	Y	64	
27	Z	77	
28	a	61	
29	b	57	
30	c	55	
31	d	47	
32	e	64	
33	f	37	

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Mol	Chain	Length	Quality of chain
34	g	75	<div><div></div><div>59%</div><div>5%</div><div>36%</div></div>
35	2	3	<div><div></div><div>100%</div></div>

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 98153 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 bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	23	Total	C	N	O	0	0
			189	111	50	28		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	124	Total	C	N	O	S	0	0
			988	613	203	172			

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	100	Total	C	N	O	S	0	0
			754	478	137	139			

- Molecule 21 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	e	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 34 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 35 is a RNA chain called tRNA CCA-end acetylated (Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

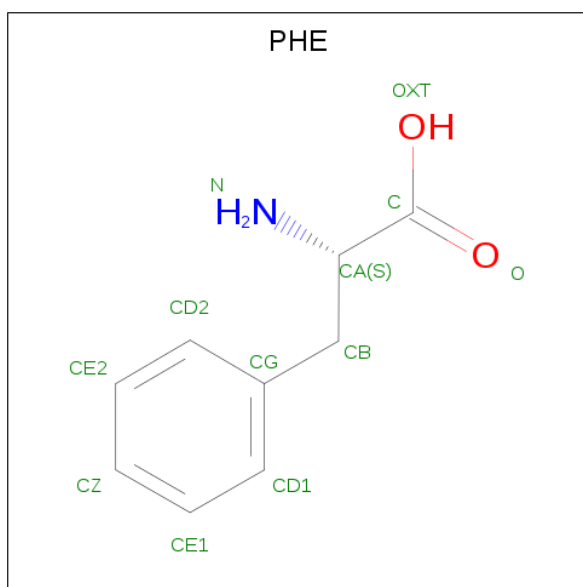
- Molecule 36 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	D	1	Total	Mg	0
			1	1	
36	B	9	Total	Mg	0
			9	9	
36	C	4	Total	Mg	0
			4	4	
36	c	1	Total	Mg	0
			1	1	
36	A	388	Total	Mg	0
			388	388	
36	T	1	Total	Mg	0
			1	1	
36	N	2	Total	Mg	0
			2	2	
36	2	1	Total	Mg	0
			1	1	
36	F	1	Total	Mg	0
			1	1	

- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	g	1	Total	Zn	0
			1	1	
37	Y	1	Total	Zn	0
			1	1	
37	c	1	Total	Zn	0
			1	1	
37	f	1	Total	Zn	0
			1	1	

- Molecule 38 is PHENYLALANINE (three-letter code: PHE) (formula: C₉H₁₁NO₂).



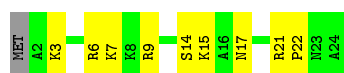
Mol	Chain	Residues	Atoms				AltConf
38	2	1	Total	C	N	O	0
			11	9	1	1	

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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

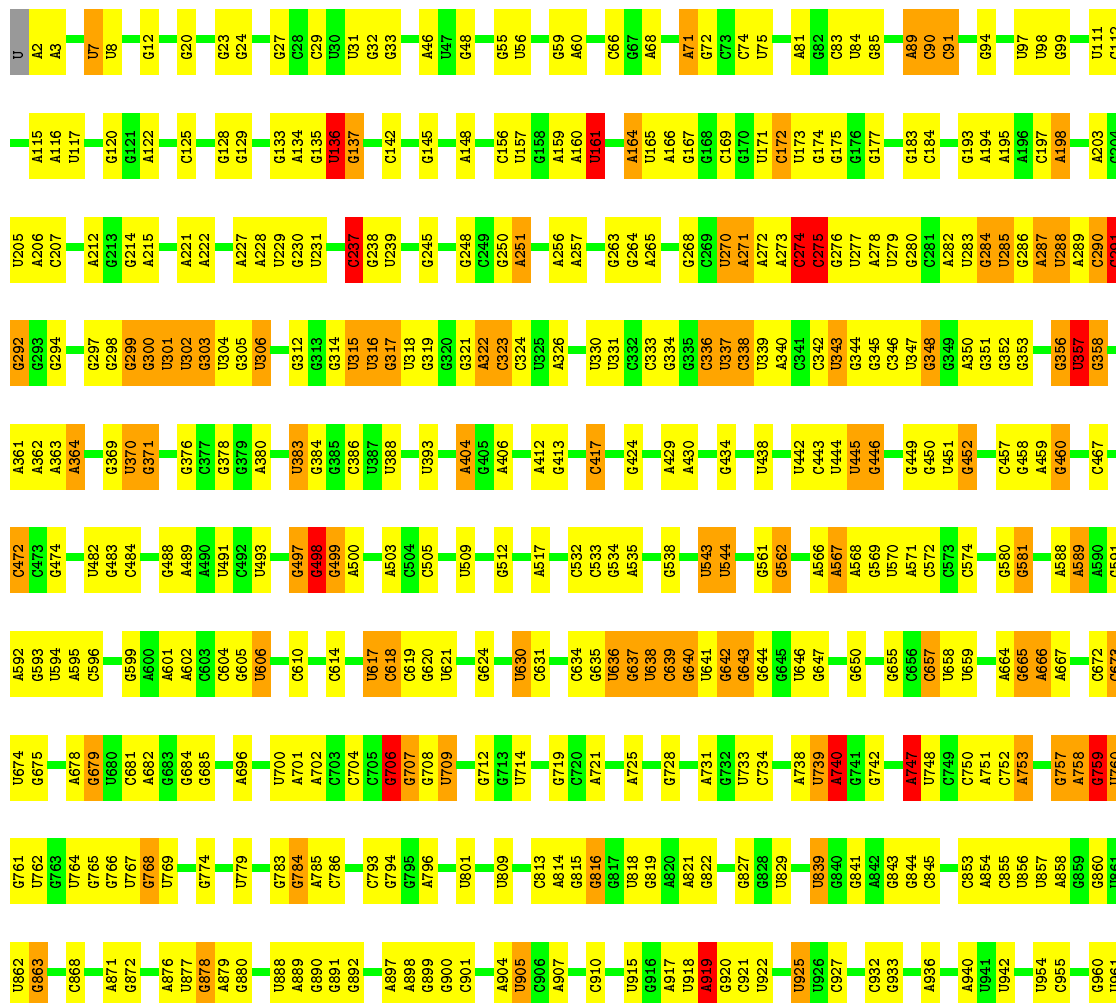
- Molecule 1: 50S ribosomal protein bL37

Chain 3: 

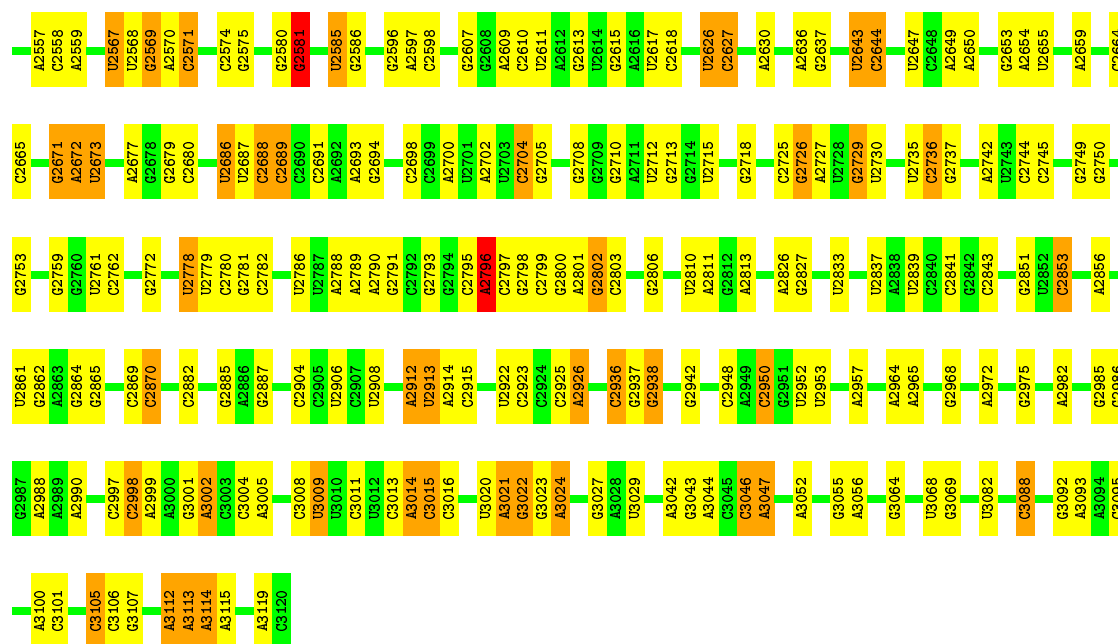


- Molecule 2: 23S rRNA

Chain A: 

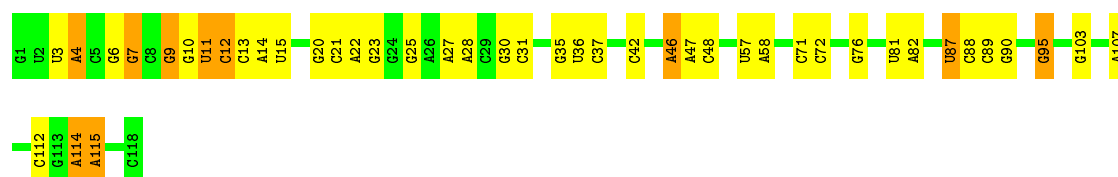


C2455	C2456	G2379	C2399	G2196	A2084	G1967	G1840	A1731	G1637	U1540	G1443	G1343	G1238	U1153	A1047	U962
G2457	U2457	G2380	A2300	A2201	C2085	C1973	G1845	U1732	G1638	G1541	G1447	G1344	C1239	U1158	A1048	U965
G2458	G2459	A2381	C2304	C2206	C2087	A1974	G1855	C1733	G1639	A1542	C1457	G1345	G1240	U1163	G1049	U966
U2460	U2363	C2382	A2306	C2206	C2088	A1975	C1856	A1737	A1640	U1544	G1454	U1346	A1244	A1163	A1058	G971
G2461	G2384	C2383	G2309	U2215	C2089	A1976	U1857	G1738	G1641	C1545	U1455	U1164	U1245	A1164	G1063	A972
G2462	G2463	G2385	G2310	U2217	U2091	C1977	G1862	G1746	G1642	U1546	U1457	G1353	A1247	G1165	G1070	G973
U2467	U2467	U2387	G2316	A2221	U2092	U1981	C1863	G1756	G1647	G1550	G1458	G1359	U1250	A1168	U1075	U975
G2476	G2476	U2388	G2316	A2222	G2093	A1990	U1863	G1757	U1551	U1552	U1459	A1362	A1251	G1173	A1076	A976
G2483	G2483	U2389	G2320	C2223	G2095	G1993	U1864	G1765	G1649	C1553	G1461	U1363	G1252	G1174	A1077	G977
A2491	A2492	U2390	G2320	C2223	G2096	G1993	U1865	G1766	G1650	U1554	G1462	U1362	C1253	A1175	G1078	G979
A2492	A2492	U2391	G2320	C2223	G2096	G1993	U1866	G1767	A1655	A1555	G1462	U1365	G1254	G1176	C980	C980
A2493	A2493	U2392	U2325	U2226	A2106	U1999	U1867	U1757	A1656	A1556	G1465	A1368	G1257	G1177	U981	A982
A2494	A2494	U2393	U2326	A2227	G2107	A2000	U1868	G1758	A1657	A1557	U1467	A1369	U1259	U1178	U1083	A982
A2495	A2495	U2394	U2327	A2227	A2108	G2007	U1869	A1759	U1659	A1564	U1468	U1370	G1260	G1180	G1085	G986
A2502	A2502	U2395	U2328	A2227	U2111	A2008	U1870	G1761	A1660	A1565	A1469	G1371	A1261	U1184	U1088	G990
G2503	G2503	U2396	U2329	A2227	U2112	G2009	U1871	A1764	U1665	A1566	A1469	G1371	A1261	U1185	C991	C991
G2504	G2504	U2397	U2330	A2227	U2113	G2010	U1872	A1765	U1666	A1567	A1469	G1371	A1261	A1186	C992	C992
G2505	G2505	U2398	U2331	A2227	U2114	G2011	U1873	U1767	U1667	A1568	A1469	G1371	A1261	A1187	G1091	G993
G2506	G2506	U2399	U2332	A2227	U2115	G2012	U1874	U1767	U1668	A1569	A1469	G1371	A1261	A1188	G1092	G994
G2507	G2507	U2400	U2333	A2227	U2116	G2013	U1875	A1767	U1669	A1570	A1469	G1371	A1261	A1189	U995	U995
G2508	G2508	U2401	U2334	A2227	U2117	G2014	U1876	A1768	U1670	A1571	A1469	G1371	A1261	A1190	G1096	G996
G2509	G2509	U2402	U2335	A2227	U2118	G2015	U1877	U1768	U1671	A1572	A1469	G1371	A1261	A1191	G997	G997
A2510	A2510	U2403	U2336	A2227	U2119	G2016	U1878	U1769	U1672	A1573	A1469	G1371	A1261	A1192	A1099	C999
A2511	A2511	U2404	U2337	A2227	U2120	G2017	U1879	A1770	U1673	A1574	A1469	G1371	A1261	A1193	C1000	C1000
A2512	A2512	U2405	U2338	A2227	U2121	G2018	U1880	U1771	U1674	A1575	A1469	G1371	A1261	A1194	C1001	C1001
U2515	U2515	U2406	U2339	A2227	U2122	G2019	U1881	U1772	U1675	A1576	A1469	G1371	A1261	A1195	C1002	C1002
U2516	U2516	U2407	U2340	A2227	U2123	G2020	U1882	U1773	U1676	A1577	A1469	G1371	A1261	A1196	A1106	A1106
C2517	C2517	U2408	U2341	A2227	U2124	G2021	U1883	U1774	U1677	A1578	A1469	G1371	A1261	A1197	G1107	C1003
C2521	C2521	U2409	U2342	A2227	U2125	G2022	U1884	U1775	U1678	A1579	A1469	G1371	A1261	A1198	A1108	C1004
G2527	G2527	U2410	U2343	A2227	U2126	G2023	U1885	U1776	U1679	A1580	A1469	G1371	A1261	A1199	C1005	G1005
A2528	A2528	U2411	U2344	A2227	U2127	G2024	U1886	U1777	U1680	A1581	A1469	G1371	A1261	A1200	C1006	G1006
A2529	A2529	U2412	U2345	A2227	U2128	G2025	U1887	U1778	U1681	A1582	A1469	G1371	A1261	A1201	G1114	G1114
G2532	G2532	U2413	U2346	A2227	U2129	G2026	U1888	U1779	U1682	A1583	A1469	G1371	A1261	A1202	C1007	G1007
A2533	A2533	U2414	U2347	A2227	U2130	G2027	U1889	U1780	U1683	A1584	A1469	G1371	A1261	A1203	U1009	U1009
A2534	A2534	U2415	U2348	A2227	U2131	G2028	U1890	U1781	U1684	A1585	A1469	G1371	A1261	A1204	A1010	A1010
U2536	U2536	U2416	U2349	A2227	U2132	G2029	U1891	U1782	U1685	A1586	A1469	G1371	A1261	A1205	A1011	A1011
U2543	U2543	U2417	U2350	A2227	U2133	G2030	U1892	U1783	U1686	A1587	A1469	G1371	A1261	A1206	C1012	C1012
U2544	U2544	U2418	U2351	A2227	U2134	G2031	U1893	U1784	U1687	A1588	A1469	G1371	A1261	A1207	U1013	U1013
U2545	U2545	U2419	U2352	A2227	U2135	G2032	U1894	U1785	U1688	A1589	A1469	G1371	A1261	A1208	G1014	G1014
G2549	G2549	U2420	U2353	A2227	U2136	G2033	U1895	U1786	U1689	A1590	A1469	G1371	A1261	A1209	C1022	C1022
U2550	U2550	U2421	U2354	A2227	U2137	G2034	U1896	U1787	U1690	A1591	A1469	G1371	A1261	A1210	A1025	A1025
A2551	A2551	U2422	U2355	A2227	U2138	G2035	U1897	U1788	U1691	A1592	A1469	G1371	A1261	A1211	C1030	C1030
A2552	A2552	U2423	U2356	A2227	U2139	G2036	U1898	U1789	U1692	A1593	A1469	G1371	A1261	A1212	G1031	G1031
G2553	G2553	U2424	U2357	A2227	U2140	G2037	U1899	U1790	U1693	A1594	A1469	G1371	A1261	A1213	A1032	A1032
U2554	U2554	U2425	U2358	A2227	U2141	G2038	U1900	U1791	U1694	A1595	A1469	G1371	A1261	A1214	A1033	A1033
U2555	U2555	U2426	U2359	A2227	U2142	G2039	U1901	U1792	U1695	A1596	A1469	G1371	A1261	A1215	A1146	A1146
U2556	U2556	U2427	U2360	A2227	U2143	G2040	U1902	U1793	U1696	A1597	A1469	G1371	A1261	A1216	C1037	C1037
A2557	A2557	U2428	U2361	A2227	U2144	G2041	U1903	U1794	U1697	A1598	A1469	G1371	A1261	A1217	U1044	U1044
G2558	G2558	U2429	U2362	A2227	U2145	G2042	U1904	U1795	U1698	A1599	A1469	G1371	A1261	A1218	C1045	C1045
G2559	G2559	U2430	U2363	A2227	U2146	G2043	U1905	U1796	U1699	A1600	A1469	G1371	A1261	A1219	C1046	C1046
U2560	U2560	U2431	U2364	A2227	U2147	G2044	U1906	U1797	U1700	A1601	A1469	G1371	A1261	A1220		
U2561	U2561	U2432	U2365	A2227	U2148	G2045	U1907	U1798	U1701	A1602	A1469	G1371	A1261	A1221		
U2562	U2562	U2433	U2366	A2227	U2149	G2046	U1908	U1799	U1702	A1603	A1469	G1371	A1261	A1222		
U2563	U2563	U2434	U2367	A2227	U2150	G2047	U1909	U1800	U1703	A1604	A1469	G1371	A1261	A1223		
U2564	U2564	U2435	U2368	A2227	U2151	G2048	U1910	U1801	U1704	A1605	A1469	G1371	A1261	A1224		
U2565	U2565	U2436	U2369	A2227	U2152	G2049	U1911	U1802	U1705	A1606	A1469	G1371	A1261	A1225		
U2566	U2566	U2437	U2370	A2227	U2153	G2050	U1912	U1803	U1706	A1607	A1469	G1371	A1261	A1226		
U2567	U2567	U2438	U2371	A2227	U2154	G2051	U1913	U1804	U1707	A1608	A1469	G1371	A1261	A1227		
U2568	U2568	U2439	U2372	A2227	U2155	G2052	U1914	U1805	U1708	A1609	A1469	G1371	A1261	A1228		
U2569	U2569	U2440	U2373	A2227	U2156	G2053	U1915	U1806	U1709	A1610	A1469	G1371	A1261	A1229		
U2570	U2570	U2441	U2374	A2227	U2157	G2054	U1916	U1807	U1710	A1611	A1469	G1371	A1261	A1230		
U2571	U2571	U2442	U2375	A2227	U2158	G2055	U1917	U1808	U1711	A1612	A1469	G1371	A1261	A1231		
U2572	U2572	U2443	U2376	A2227	U2159	G2056	U1918	U1809	U1712	A1613	A1469	G1371	A1261	A1232		
U2573	U2573	U2444	U2377	A2227	U2160	G2057	U1919	U1810	U1713	A1614	A1469	G1371	A1261	A1233		
U2574	U2574	U2445	U2378	A2227	U2161	G2058	U1920	U1811	U1714	A1615	A1469	G1371	A1261	A1234		
U2575	U2575	U2446	U2379	A2227	U2162	G2059	U1921	U1812	U1715	A1616	A1469	G1371	A1261	A1235		
U2576	U2576	U2447	U2380	A2227	U2163	G2060	U1922	U1813	U1716	A1617	A1469	G1371	A1261	A1236		
U2577	U2577	U2448	U2381	A2227	U2164	G2061	U1923	U1814	U1717	A1618	A1469	G1371	A1261	A1237		
U2578	U2578	U2449	U2382	A2227	U2165	G2062	U1924	U1815	U1718	A1619	A1469	G1371	A1261	A1238		
U2579	U2579	U2450	U2383	A2227	U2166	G2063	U1925	U1816	U1719	A1620	A1469	G1371	A1261	A1239		
U2580	U2580	U2451	U2384	A2227	U2167	G2064	U1926	U1817	U1720	A1621	A1469	G1371	A1261	A1240		
U2581	U2581	U2452	U2385	A2227	U2168	G2065	U1927	U1818	U1721	A1622	A1469	G1371	A1261	A1241		
U2582	U2582	U2453	U2386	A2227	U2169	G2066	U1928	U1819	U1722	A1623	A1469	G1371	A1261	A1242		
U2583	U2583	U2454	U2387	A2227	U2170	G2067	U1929	U1820	U1723	A1624	A1469	G1371	A1261	A1243		
U2584	U2584	U2455	U2388	A2227	U2171	G2068	U1930	U1821	U1724	A1625	A1469	G1371	A1261	A1244		
U2585	U2585	U2456	U2389	A2227	U2172	G2069	U1931	U1822	U1725	A1626	A1469	G1371	A1261	A1245		
U2586	U2586	U2457	U2390	A2227	U2173	G2070	U1932	U1823	U1							



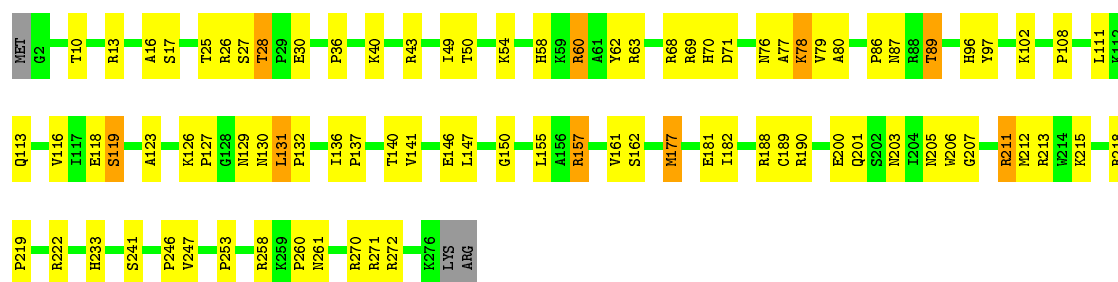
• Molecule 3: 5S rRNA

Chain B: 63% 29% 8%



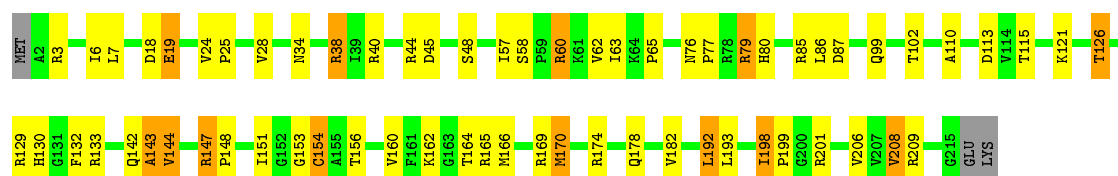
• Molecule 4: 50S ribosomal protein L2

Chain C: 67% 28% 5%

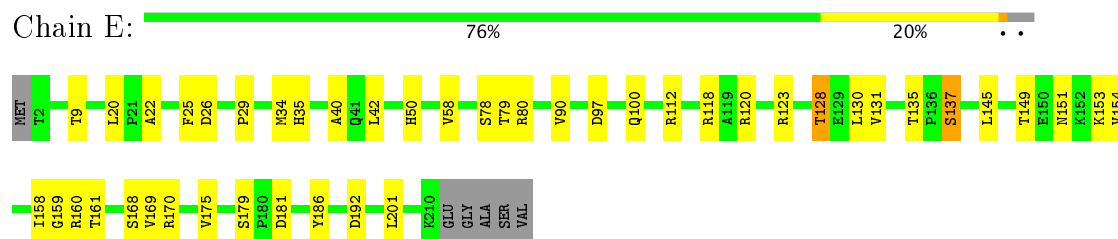


• Molecule 5: 50S ribosomal protein L3

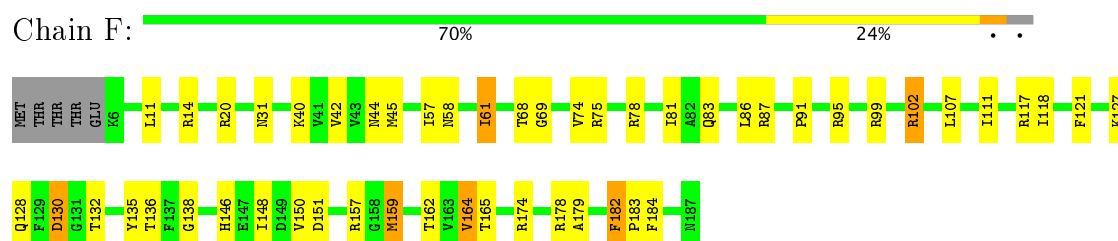
Chain D: 69% 24% 6%



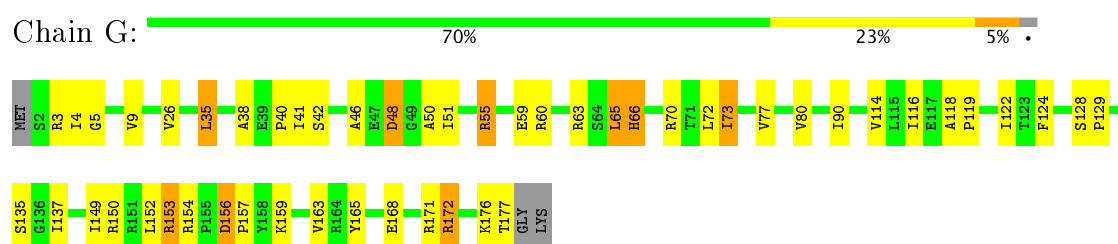
- Molecule 6: 50S ribosomal protein L4



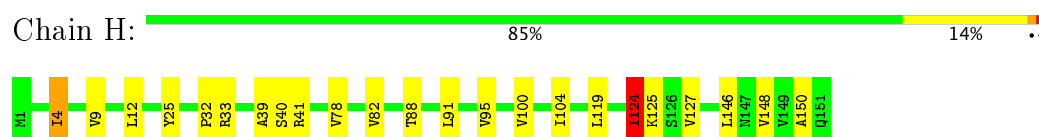
- Molecule 7: 50S ribosomal protein L5



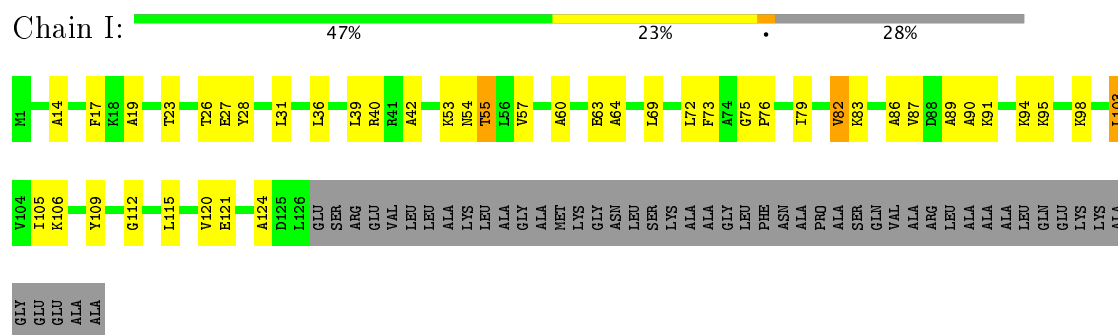
- Molecule 8: 50S ribosomal protein L6



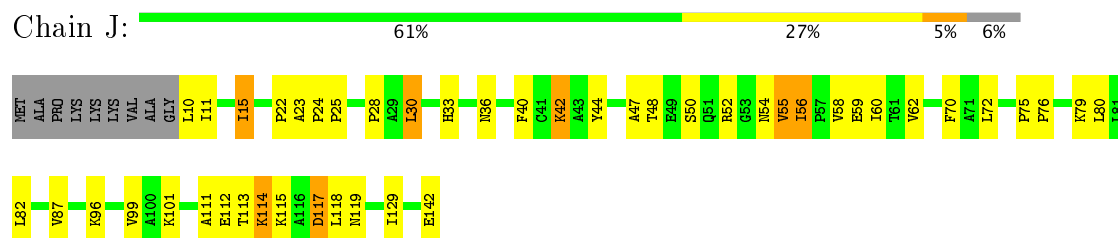
- Molecule 9: 50S ribosomal protein L9



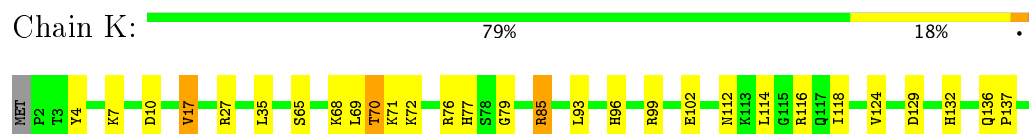
- Molecule 10: 50S ribosomal protein L10



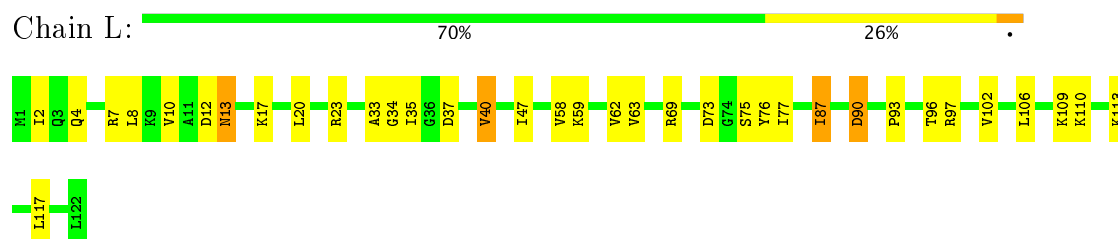
- Molecule 11: 50S ribosomal protein L11



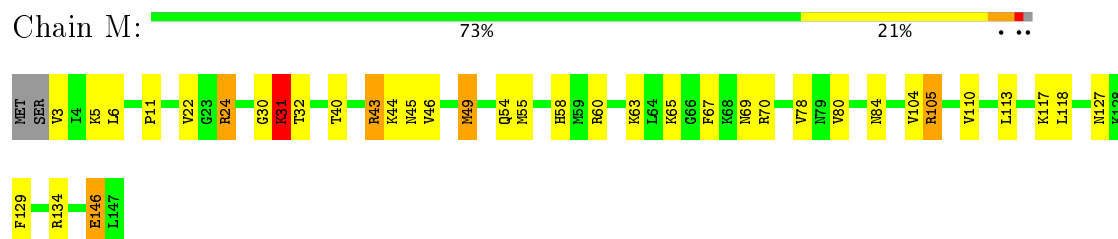
- Molecule 12: 50S ribosomal protein L13



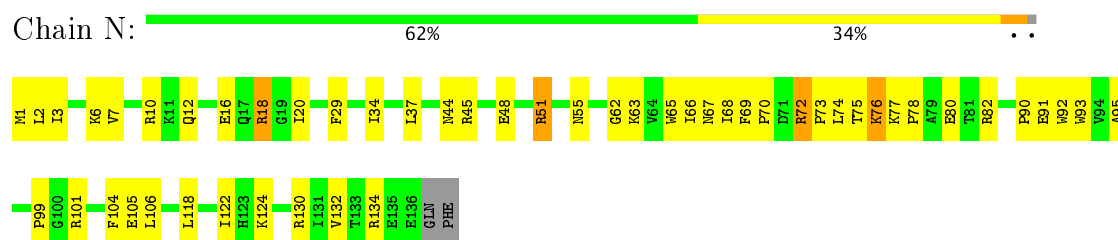
- Molecule 13: 50S ribosomal protein L14



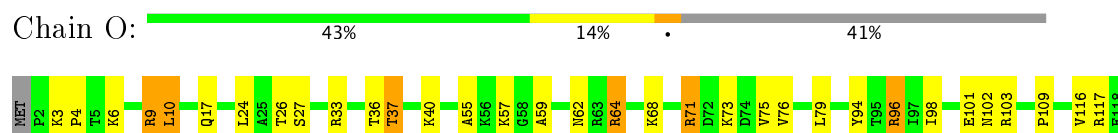
- Molecule 14: 50S ribosomal protein L15

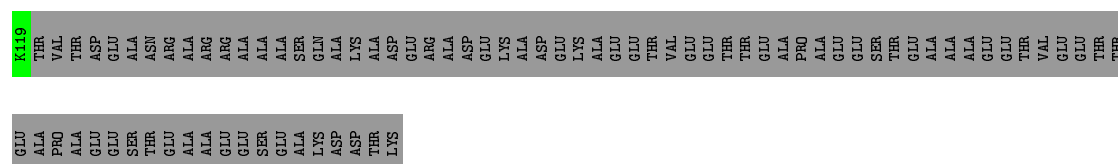


- Molecule 15: 50S ribosomal protein L16

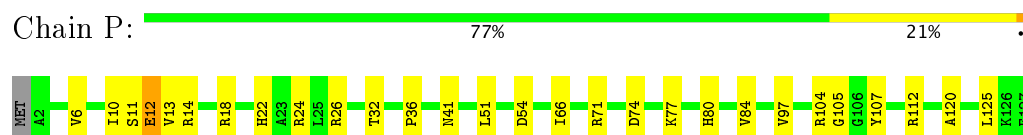


- Molecule 16: 50S ribosomal protein L17

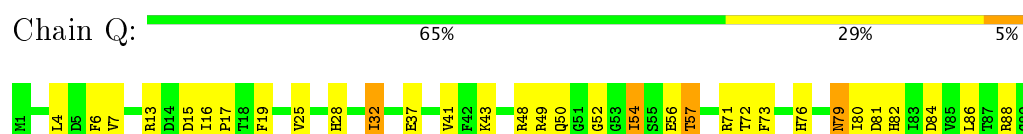




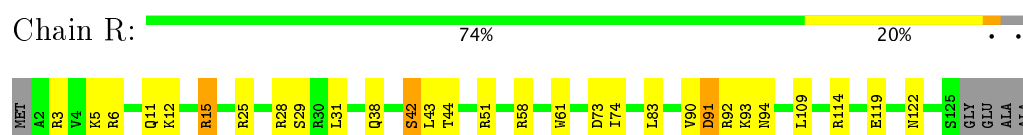
- Molecule 17: 50S ribosomal protein L18



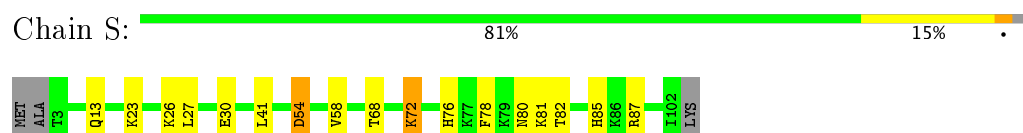
- Molecule 18: 50S ribosomal protein L19



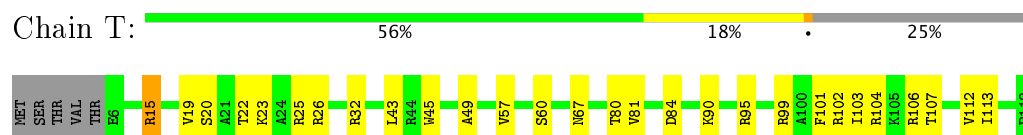
- Molecule 19: 50S ribosomal protein L20



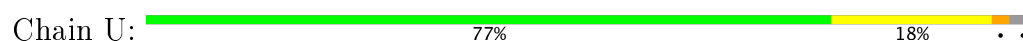
- Molecule 20: 50S ribosomal protein L21

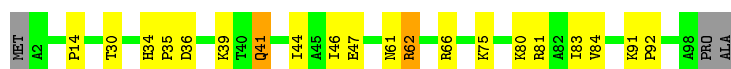


- Molecule 21: 50S ribosomal protein L22



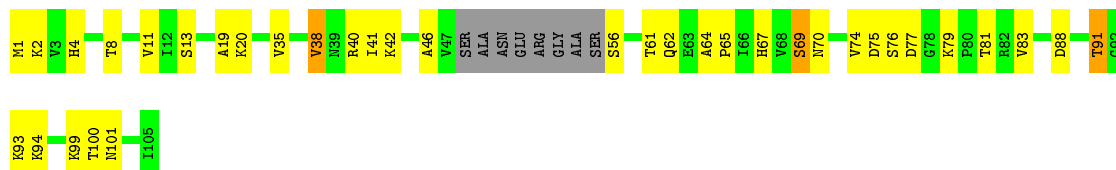
- Molecule 22: 50S ribosomal protein L23





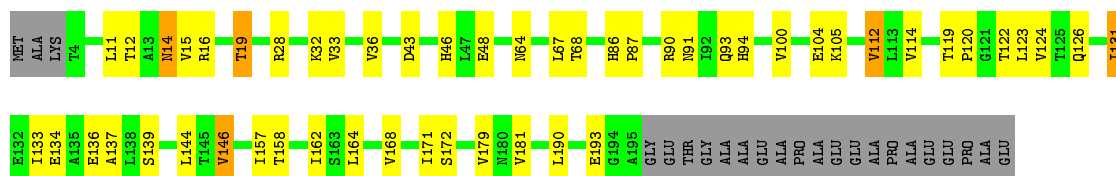
- Molecule 23: 50S ribosomal protein L24

Chain V: 58% 31% 8%



- Molecule 24: 50S ribosomal protein L25

Chain W: 65% 22% 11%



- Molecule 25: 50S ribosomal protein L27

Chain X: 68% 20% 10%



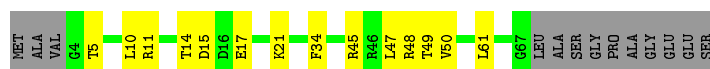
- Molecule 26: 50S ribosomal protein L28

Chain Y: 70% 23% 5%



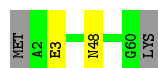
- Molecule 27: 50S ribosomal protein L29

Chain Z: 65% 18% 17%




- Molecule 28: 50S ribosomal protein L30

Chain a: 93% 5% 2%




- Molecule 29: 50S ribosomal protein L32

Chain b:  86% 9% 5%



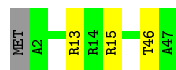
- Molecule 30: 50S ribosomal protein L33 1

Chain c:  80% 9% 11%




- Molecule 31: 50S ribosomal protein L34

Chain d:  91% 6% •



- Molecule 32: 50S ribosomal protein L35

Chain e:  89% 9% •



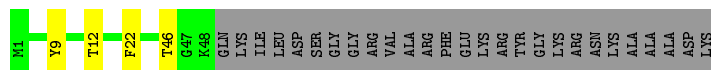
- Molecule 33: 50S ribosomal protein L36

Chain f:  95% 5%



- Molecule 34: 50S ribosomal protein L31

Chain g:  59% 5% 36%



- Molecule 35: tRNA CCA-end acetylated (Phe)

Chain 2:  100%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	224584	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction in Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	100719	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 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	3	0.56	0/191	0.60	0/247
10	I	0.41	0/925	0.54	0/1246
11	J	0.42	0/1006	0.57	0/1364
12	K	0.50	0/1157	0.63	0/1567
13	L	0.52	0/946	0.66	0/1268
14	M	0.51	0/1091	0.71	0/1457
15	N	0.54	0/1118	0.64	0/1506
16	O	0.52	0/945	0.73	0/1267
17	P	0.37	0/966	0.55	0/1298
18	Q	0.50	0/921	0.65	0/1236
19	R	0.63	0/1000	0.67	0/1341
2	A	0.83	29/75001 (0.0%)	1.19	238/117027 (0.2%)
20	S	0.48	0/764	0.65	0/1030
21	T	0.57	0/887	0.69	0/1204
22	U	0.49	0/766	0.57	0/1030
23	V	0.55	1/738 (0.1%)	0.62	0/987
24	W	0.42	0/1443	0.61	0/1970
25	X	0.56	0/595	0.63	0/798
26	Y	0.64	0/478	0.75	1/641 (0.2%)
27	Z	0.44	0/534	0.57	0/713
28	a	0.53	0/477	0.64	0/640
29	b	0.51	0/427	0.67	0/572
3	B	0.53	0/2821	1.04	4/4396 (0.1%)
30	c	0.45	0/413	0.57	0/553
31	d	0.54	0/380	0.70	0/500
32	e	0.51	0/507	0.69	0/672
33	f	0.58	0/303	0.66	0/401
34	g	0.36	0/372	0.50	0/503
35	2	0.65	0/68	1.16	0/103
4	C	0.54	0/2153	0.67	0/2895
5	D	0.55	0/1609	0.71	0/2165
6	E	0.47	0/1592	0.61	0/2153

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
7	F	0.35	0/1467	0.53	0/1973
8	G	0.36	0/1369	0.52	0/1848
9	H	0.33	0/1027	0.52	0/1398
All	All	0.75	30/106457 (0.0%)	1.08	243/159969 (0.2%)

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	936	A	N9-C4	-8.24	1.32	1.37
2	A	889	A	N3-C4	-7.64	1.30	1.34
23	V	56	SER	CB-OG	7.10	1.51	1.42
2	A	889	A	N9-C4	-6.90	1.33	1.37
2	A	1630	U	C1'-N1	6.59	1.58	1.48

The worst 5 of 243 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	975	U	C5-C4-O4	-10.81	119.42	125.90
2	A	981	U	C5-C6-N1	10.39	127.89	122.70
2	A	975	U	N3-C4-O4	8.32	125.22	119.40
2	A	2245	C	N1-C2-O2	8.12	123.77	118.90
2	A	1403	C	C4-C5-C6	8.06	121.43	117.40

There are no chirality outliers.

There are no planarity outliers.

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	3	189	0	205	6	0
2	A	66981	0	33699	519	0
3	B	2522	0	1285	20	0
4	C	2110	0	2165	65	0
5	D	1587	0	1630	44	0
6	E	1569	0	1607	26	0
7	F	1445	0	1476	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	G	1348	0	1399	33	0
9	H	1018	0	988	14	0
10	I	918	0	959	36	0
11	J	990	0	1021	28	0
12	K	1130	0	1167	29	0
13	L	938	0	1000	22	0
14	M	1078	0	1151	41	0
15	N	1092	0	1128	44	0
16	O	928	0	972	25	0
17	P	956	0	991	16	0
18	Q	907	0	938	30	0
19	R	988	0	1038	25	0
20	S	754	0	802	13	0
21	T	873	0	909	19	0
22	U	756	0	802	14	0
23	V	732	0	782	23	0
24	W	1428	0	1443	31	0
25	X	586	0	601	14	0
26	Y	470	0	480	14	0
27	Z	531	0	541	15	0
28	a	474	0	500	0	0
29	b	423	0	463	0	0
30	c	405	0	407	0	0
31	d	377	0	411	0	0
32	e	502	0	541	0	0
33	f	299	0	321	0	0
34	g	364	0	348	0	0
35	2	62	0	33	1	0
36	2	1	0	0	0	0
36	A	388	0	0	0	0
36	B	9	0	0	0	0
36	C	4	0	0	0	0
36	D	1	0	0	0	0
36	F	1	0	0	0	0
36	N	2	0	0	0	0
36	T	1	0	0	0	0
36	c	1	0	0	0	0
37	Y	1	0	0	0	0
37	c	1	0	0	0	0
37	f	1	0	0	0	0
37	g	1	0	0	0	0
38	2	11	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	98153	0	64211	1039	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 7.

The worst 5 of 1039 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)
2:A:2422:A:O2'	26:Y:63:ARG:NH1	1.74	1.20
2:A:142:C:H5''	22:U:41:GLN:HE21	1.27	0.99
2:A:301:U:H5'	2:A:302:U:H5''	1.47	0.96
2:A:2772:G:H1'	13:L:23:ARG:HH12	1.31	0.95
2:A:164:A:H4'	26:Y:41:ARG:HH12	1.31	0.95

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	3	21/24 (88%)	21 (100%)	0	0	100	100
4	C	273/278 (98%)	259 (95%)	14 (5%)	0	100	100
5	D	212/217 (98%)	199 (94%)	12 (6%)	1 (0%)	32	74
6	E	207/215 (96%)	201 (97%)	5 (2%)	1 (0%)	32	74
7	F	180/187 (96%)	164 (91%)	15 (8%)	1 (1%)	28	72
8	G	174/179 (97%)	166 (95%)	7 (4%)	1 (1%)	28	72
9	H	149/151 (99%)	140 (94%)	8 (5%)	1 (1%)	25	68
10	I	124/175 (71%)	117 (94%)	7 (6%)	0	100	100
11	J	131/142 (92%)	124 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	K	144/147 (98%)	138 (96%)	6 (4%)	0	100	100
13	L	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
14	M	143/147 (97%)	135 (94%)	7 (5%)	1 (1%)	25	68
15	N	134/138 (97%)	124 (92%)	10 (8%)	0	100	100
16	O	116/199 (58%)	111 (96%)	5 (4%)	0	100	100
17	P	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
18	Q	111/113 (98%)	106 (96%)	5 (4%)	0	100	100
19	R	122/129 (95%)	116 (95%)	6 (5%)	0	100	100
20	S	98/103 (95%)	96 (98%)	2 (2%)	0	100	100
21	T	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
22	U	95/100 (95%)	91 (96%)	4 (4%)	0	100	100
23	V	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
24	W	190/215 (88%)	186 (98%)	4 (2%)	0	100	100
25	X	77/88 (88%)	73 (95%)	4 (5%)	0	100	100
26	Y	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
27	Z	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
28	a	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
29	b	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
30	c	47/55 (86%)	44 (94%)	2 (4%)	1 (2%)	8	42
31	d	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
32	e	61/64 (95%)	61 (100%)	0	0	100	100
33	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
34	g	46/75 (61%)	46 (100%)	0	0	100	100
All	All	3615/3991 (91%)	3457 (96%)	151 (4%)	7 (0%)	54	86

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	c	7	VAL
5	D	143	ALA
14	M	31	LYS
8	G	66	HIS
6	E	90	VAL

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	3	18/19 (95%)	16 (89%)	2 (11%)	7	30
4	C	215/218 (99%)	193 (90%)	22 (10%)	8	34
5	D	160/163 (98%)	132 (82%)	28 (18%)	2	11
6	E	169/173 (98%)	153 (90%)	16 (10%)	10	37
7	F	151/156 (97%)	135 (89%)	16 (11%)	8	32
8	G	148/150 (99%)	131 (88%)	17 (12%)	6	28
9	H	90/116 (78%)	85 (94%)	5 (6%)	25	64
10	I	89/120 (74%)	84 (94%)	5 (6%)	25	64
11	J	102/108 (94%)	88 (86%)	14 (14%)	4	19
12	K	119/120 (99%)	113 (95%)	6 (5%)	28	67
13	L	100/100 (100%)	90 (90%)	10 (10%)	9	35
14	M	112/114 (98%)	102 (91%)	10 (9%)	11	41
15	N	114/116 (98%)	104 (91%)	10 (9%)	12	42
16	O	97/158 (61%)	88 (91%)	9 (9%)	10	38
17	P	93/94 (99%)	86 (92%)	7 (8%)	16	52
18	Q	100/100 (100%)	92 (92%)	8 (8%)	14	49
19	R	97/99 (98%)	91 (94%)	6 (6%)	21	60
20	S	81/83 (98%)	74 (91%)	7 (9%)	12	43
21	T	90/117 (77%)	81 (90%)	9 (10%)	9	35
22	U	83/85 (98%)	80 (96%)	3 (4%)	40	76
23	V	81/86 (94%)	76 (94%)	5 (6%)	21	60
24	W	155/168 (92%)	139 (90%)	16 (10%)	8	33
25	X	58/63 (92%)	54 (93%)	4 (7%)	18	55
26	Y	50/51 (98%)	44 (88%)	6 (12%)	6	26
27	Z	58/66 (88%)	58 (100%)	0	100	100
28	a	52/54 (96%)	50 (96%)	2 (4%)	38	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	b	43/46 (94%)	38 (88%)	5 (12%)	6	27
30	c	47/52 (90%)	43 (92%)	4 (8%)	12	44
31	d	35/36 (97%)	32 (91%)	3 (9%)	12	43
32	e	53/54 (98%)	47 (89%)	6 (11%)	7	29
33	f	35/35 (100%)	33 (94%)	2 (6%)	24	63
34	g	43/63 (68%)	39 (91%)	4 (9%)	10	38
All	All	2938/3183 (92%)	2671 (91%)	267 (9%)	15	39

5 of 267 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	J	99	VAL
14	M	105	ARG
29	b	14	ARG
11	J	119	ASN
13	L	58	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
15	N	123	HIS
18	Q	79	ASN
30	c	48	HIS
16	O	17	GLN
17	P	53	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	3118/3120 (99%)	784 (25%)	30 (0%)
3	B	117/118 (99%)	28 (23%)	2 (1%)
35	2	2/3 (66%)	2 (100%)	0
All	All	3237/3241 (99%)	814 (25%)	32 (0%)

5 of 814 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A	7	U

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Mol	Chain	Res	Type
2	A	12	G
2	A	20	G
2	A	29	C
2	A	31	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	1084	U
2	A	1344	A
2	A	3113	A
2	A	1231	U
2	A	1368	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 413 ligands modelled in this entry, 412 are 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	$\# Z > 2$
38	PHE	2	1002	35	11,11,12	0.78	0	12,13,15	0.71	0

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
38	PHE	2	1002	35	-	0/4/6/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.