



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Sep 10, 2019 – 09:57 AM EDT

PDB ID : 6PPK  
EMDB ID: : EMD-20441  
Title : RbgA+45SRbgA complex  
Authors : Ortega, J.  
Deposited on : 2019-07-07  
Resolution : 4.40 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

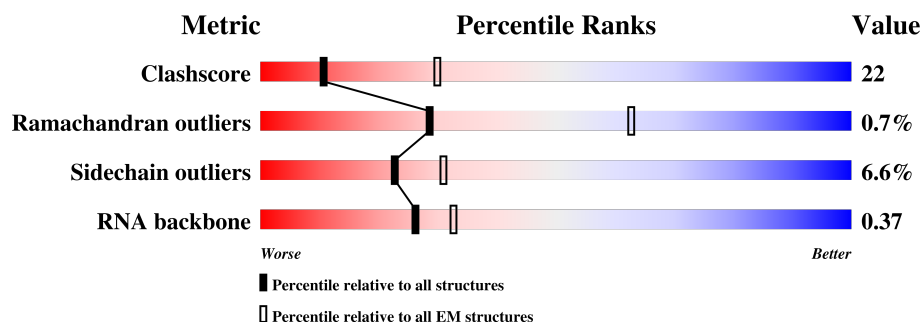
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.40 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.




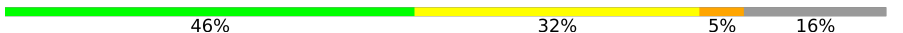











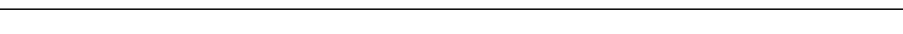
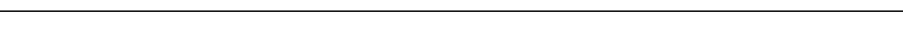
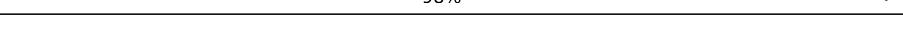
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

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  $\geq 3$ , 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	2927	32% 42% 16% • 9%
2	B	119	31% 44% 18% • 6%
3	C	277	56% 35% • 6%
4	D	209	47% 45% 6% •
5	E	207	61% 33% • 5%
6	F	179	31% 39% 7% 22%
7	G	179	41% 18% • 39%
8	J	145	48% 45% • •

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Mol	Chain	Length	Quality of chain
9	K	122	
10	L	146	
11	N	120	
12	O	120	
13	P	115	
14	Q	118	
15	R	102	
16	S	113	
17	T	95	
18	U	103	
19	V	94	
20	Z	59	
21	b	59	
22	Y	66	
23	d	44	
24	W	282	

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
25	GNP	W	301	-	-	X	-

## 2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 80451 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2658	Total	C	N	O	P	0	0
			57112	25477	10569	18408	2658		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	260	Total	C	N	O	S	0	0
			2010	1253	392	359	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	197	Total	C	N	O	S	0	0
			1511	951	280	278	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	139	Total	C	N	O	S	0	0
			1090	694	190	199	7		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	109	Total	C	N	O	S	0	0
			829	518	153	157	1		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	141	Total	C	N	O	S	0	0
			1119	708	205	201	5		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	122	Total	C	N	O	S	0	0
			904	561	171	171	1		

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	118	Total	C	N	O	S	0	0
			947	580	185	178	4		

- Molecule 12 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	O	100	Total	C	N	O	0	0
			775	483	154	138		

- Molecule 13 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	P	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 14 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 15 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	100	Total	C	N	O	S	0	0
			781	498	138	145			

- Molecule 16 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	90	Total	C	N	O	S	0	0
			724	452	133	136	3		

- Molecule 18 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	U	91	Total	C	N	O	S	0	0
			691	438	129	121	3		

- Molecule 19 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	V	78	Total	C	N	O	S	0	0
			604	375	118	111			

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	b	53	Total	C	N	O	S	0	0
			418	258	84	69	7		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

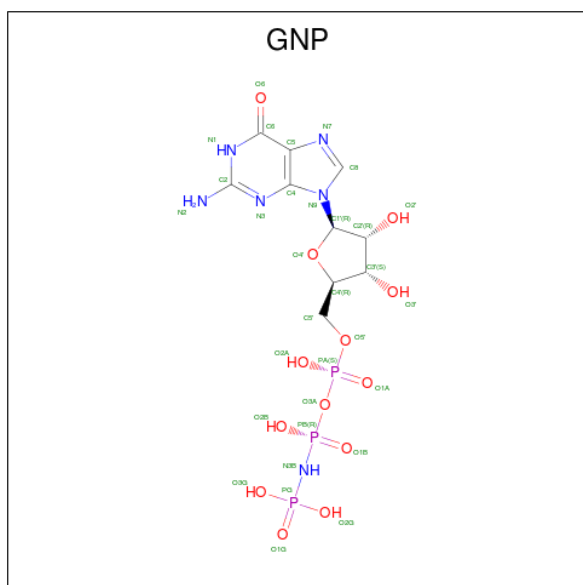
- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	43	Total	C	N	O	S	0	0
			359	217	88	53	1		

- Molecule 24 is a protein called Ribosome biogenesis GTPase A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	252	Total	C	N	O	S	0	0
			1958	1250	343	359	6		

- Molecule 25 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula:  $C_{10}H_{17}N_6O_{13}P_3$ ) (labeled as "Ligand of Interest" by author).

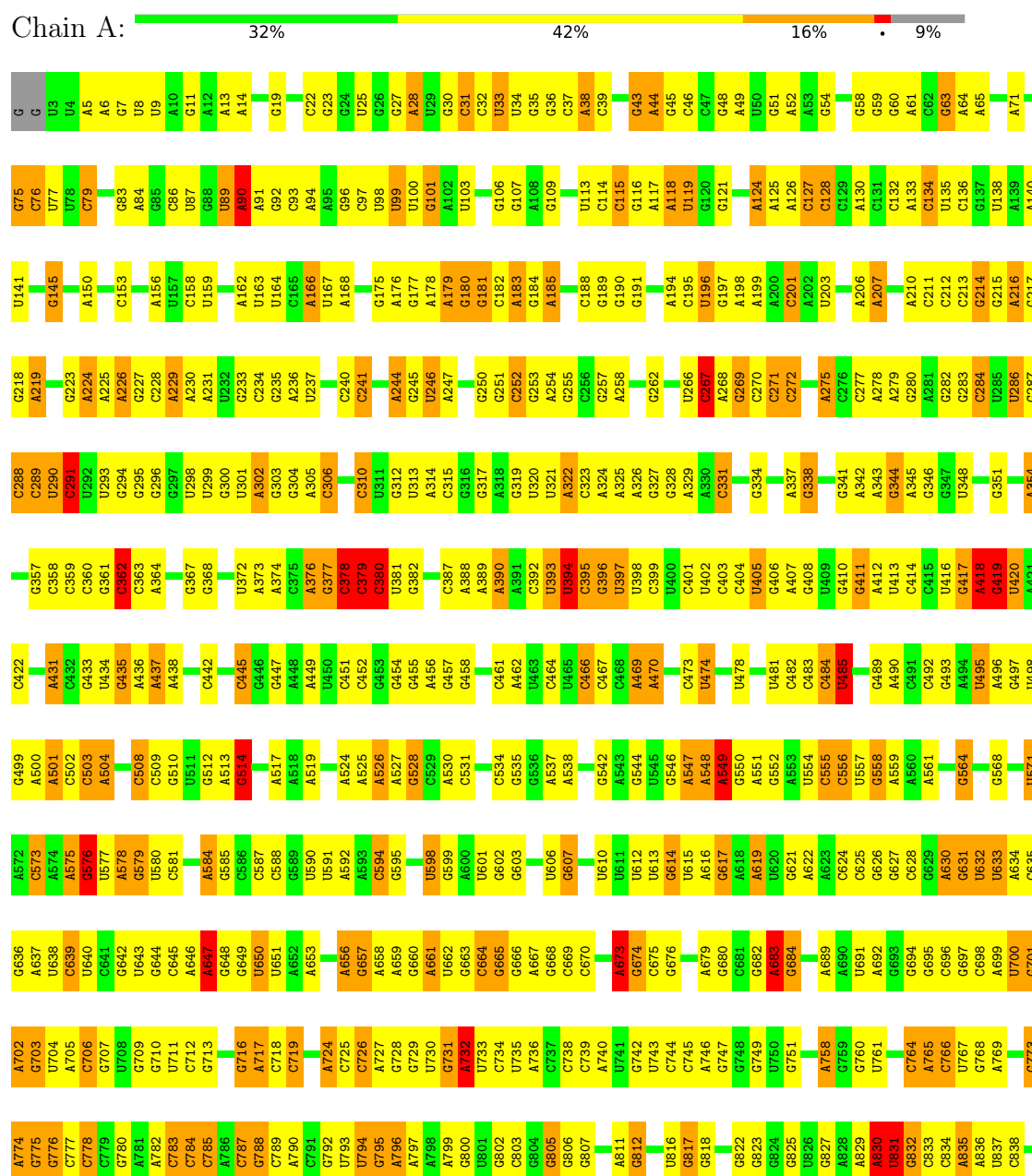


Mol	Chain	Residues	Atoms					AltConf
25	W	1	Total	C	N	O	P	0
			32	10	6	13	3	

### 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.

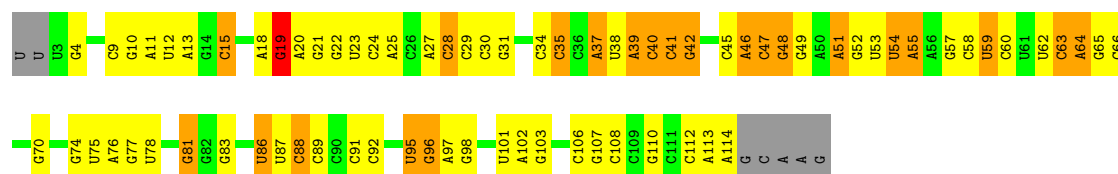
#### • Molecule 1: 23S rRNA



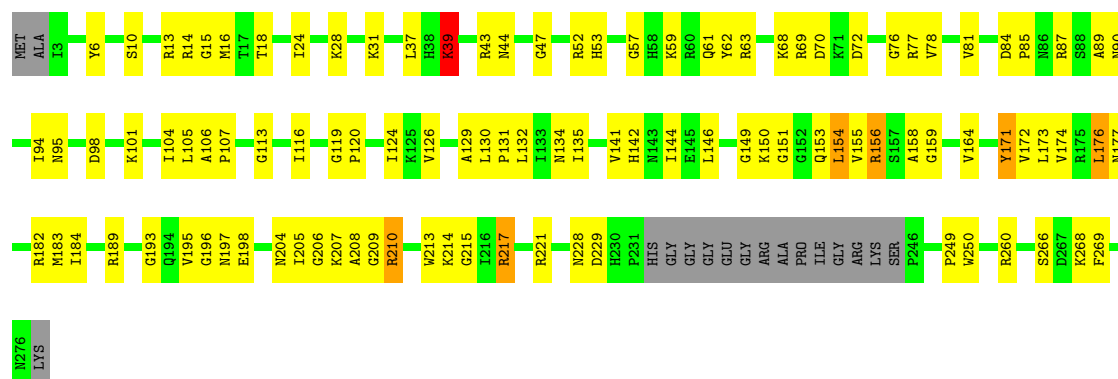


G	A1832	G1763	G1675	G1616	C1552	G1481	U1418	C1343	G1272	G1200	A1132	U1060	G985	U918	C842
U	G1833	U1764	A1679	A1617	A1553	G1482	G1419	C1344	G1275	A1201	G1133	A1061	G986	U919	C843
A	C1834	G1765	C1683	A1618	U1554	U1489	G1420	U1345	G1276	A1202	A1134	G1063	G987	G920	
A	C1835		C1683	A1619	U1555	U1490	A1421	A1346	G1277	G1203	G1135	U1062	G988	G921	A847
G	G1836	A1768	U1684	A1620	A1556		G1422	U1350	A1277	C1204	U	A1066	U989	U924	G852
C	G1837	U1685	U1685	A1621	U1557	C1483	A1423	U1351	A1278	U1205	G	A1067	C990	G	G853
G	A1838	A1686	G1557	G1622	G1558	C1494	A1424	U1352	A1279	G1206	C	G1068	A991	A925	C853
A		C1622	G1558			C1495	A1426	C1353	G1280	C1207	U	U1069	G992	G926	U854
A						G1496	G1427	C1354	G1281	G1208	A	G1070	G993	G928	G855
A						G1497		C1355	G1285	G1209	A	G1071	C997	G928	U857
G						G1497		U1355	A1286	G1211	U	A1072	G998	G928	U858
G						U1500	G1431	G1356	U1287	G1212	A	A1073	A999	G930	U859
G						U1501	A1430	G1359	G1288	G1213	G1145	A1074	G1000	C	U860
G						G1502	A1432	A1360	U1289	U1214	C1146		U1001	C	U861
G						G1503	A1433	A1361		U1215	U1079	G1080	G1002	C	U862
G						A1504	U1435	G1362	A1293	G1216	C1148	U1081	A1003	A	
U						A1505	U1436	G1363	A1294	U	U1081	U1082	U1004	C	A866
U						U1505	A1437	C1364	U1295	C	U1150		A1005	C	
U						A1506	C1438	U1365	G1296	U1151	C1155	G1093	A1006	G	U869
U						U1507	U1439	C1366	C1297	G1220	U1090	U1090	G1007	G	
A						C1508	G1440	G1367	G1298	A1221	U1091	A1091	A1008	G	C872
A						C1509	U1441	U1368	G1299	A1222	U1152	A1092	U1017	U	U873
C						G1510	A1442	C1369	U1307	C1223	U1153	G1098	A1019	U	U874
C						C1511	U1443	C1370	A1301		G1155	A1094	A1020	A	U881
C						G1512	C1444	G1371	A1302		U1157	G1095	U1016	C	A882
C						U1513	A1445	C1372		G1227	A1157	C1095	U1016	C	U886
C						C1514	U1446	C1372	A1305	G1228	G1158	A1096	G1017	C	C887
C						A1515	C1447	G1376	G1306	G1231	U1159	A1097	G1018	G	C888
C						A1516	U1448	G1377	U1307	A1247	U1159	A1097	G1018	G	A889
C						A1517	C1449	G1377	A1308	G1232	A1161	C1099	A1019	U	U890
C						U1518	U1450	U1380	G1309	A1233	U1162	G1102	A1020	U	U891
C						C1519	U1451	A1381	G1310		U1163	G1103	G1023	U950	U892
C						A1520	C1452	A1382	C1311	G1236	C1164	A1103	G1024	C951	U893
C						G1521	C1453	U1383	A1312		G1168	U1104	A1025	U954	U894
C						U1522	C1455	A1384	U1241	U1240	A1172	U1107	A1026	U955	U895
C						U1523	U1456	G1385	A1314	C1242	A1173	G1108	A1027	A956	G890
C						A1524	U1457	G1386	G1315	A1243	A1173	C	A1028	A957	G891
C						G1525	U1458	G1387	A1316	A1244	A1174	C	G1029	A958	U892
C						U1526	U1459	A1388	G1317	G1245	A1175	U	G1030	C959	U893
C						C1527	G1460	C1389	G1317	G1246	U1176	U	C1031	C959	A894
C						U1528	A1461	C1390	U1321	G1247	U1177	A	C1032	G963	G895
C						G1529	G1462	U1391	G1322	C1248	U1178	A	C1033	A964	A896
C						U1530	C1463		A1323	U1249	A1179	G	A1034	G967	G897
C							U1464	C1395	G1324	G1250	C1180	A	A1035	U972	U898
C						U1535	A1465	C1396	A1325	U1251	C1181	G	A1036	C968	U899
C						A1536	U1466	G1397	A1326	G1252	G1182	C	C1038	C969	
C						G1537	A1466	A1398	U1327		G1183	A1116	G1038	A970	G903
C						U1538	G1469			G1257	G1184	G1117	A1042	A971	G906
C						C1539	U1470	A1404	U1332	A1258	G1185	C	G1043	U972	U907
C						A1540	G1471	A1405	C1333	G1259	G1185	C	C1044	G973	A908
C						U1541	U1472	A1406	C1334		A1188	A	U1045	A974	A909
C						A1542	C1472	A1406	A1335	C1262	A1189	C	A1046	C975	G909
C						U1543	C1474	G1410	C1336	G1263	A1190	C	A	U976	A910
C						C1544	U1475	G1411	C1337	G1264	U1193	A	A1054	U977	G911
C						U1545	C1476	U1412	G1338		A1194	A	A1055	A978	G912
C						G1546	A1477	G1413	A1339	G1267	U1127	U1128	A1056	G981	A913
C							U1478	G1414	A1340	G1268	U1129	U1129	A1057	C981	C914
C						C1550	G1479	G1414	A1341	A1269	C1198	A1130	U1058	G984	A917
C						U1551	A1480	A1417	G1342		C1199	A1131	A1059		

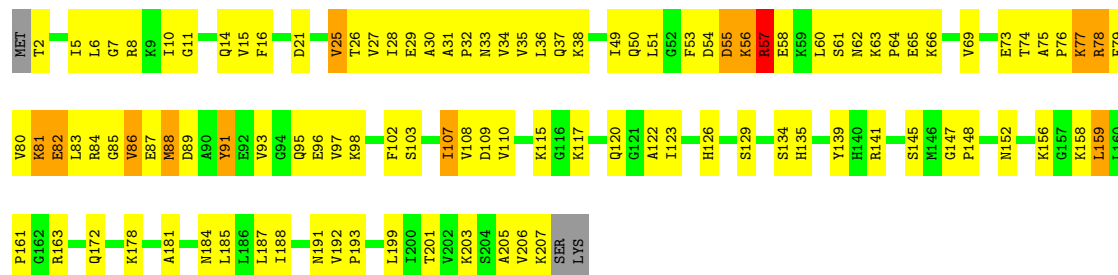
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G2847	G2848	A2778	C2710	U2642	G2572	U2448	A2363	A2297	C2230	C2166	A2100	C2025	U
A2849	A2849	G2780	C2711	A2643	G2573	U2449	A2364	A2298	C2231	C2167	U2103	A2026	A
G2850	G2850	C2781	C2712	U2644	U2574	G2450	A2365	G2299	G2232	G2168	U2104	C2027	G
A2851	A2851	C2782	C2713	G2647	U2575	C2451	G2366	G2300	C2233	C2169	U2105	C2028	C
G2852	G2852	U2783	C2714	U2648	U2576	C2452	C2367	U2301	C2234	A2170	A2106	G2029	G
C2853	C2853	U2784	C2715	U2649	G2577	U2453	A2368	A2302	G2235	C2171	C	A2030	A
A2854	A2854	U2785	C2716	G2650	G2578	C2454	G2370	A2303	U2240	C	G2109	A2031	A
G2855	G2855	U2786	C2717	U2651	A2579	A2455	A2371	C2304	A2241	G	C2110	A2032	A
A2856	A2856	U2787	C2718	C2652	C2580	A2456	U2372	A2307	U2242	C	A2111	C2035	U
U2857	U2857	U2788	C2719	G2653	U2581	G2457	G2373	G2308	C2243	A	G2112	C2038	U
U2858	U2858	U2789	C2720	C2654	G2582	G2458	A2374	G2309	G2244	G2177	C2113	G2039	C
G2859	G2859	U2790	C2721	U2655	U2583	U2459	A2375	C2310	G2245	C2178	G2116	U2040	U
U2860	U2860	U2791	C2722	G2656	U2584	A2460	G2376	C2311	C2246	U2179	U2120	G2041	G
U2861	U2861	U2792	C2723	A2658	G2585	U2461	G2377	C2312	C2247	U2180	G2117	A2049	U
U2865	U2865	U2793	C2724	U2659	C2586	A2462	G2378	C2313	G2248	U2181	U2121	C2052	G
U2866	U2866	U2794	C2725	G2660	A2593	A2463	G2379	C2314	G2249	G2182	U2122	A2055	U
U2867	U2867	U2795	C2726	A2661	A2594	A2464	G2380	A2315	U2250	U2183	G2123	U2065	G
U2868	U2868	U2796	C2727	A2662	A2595	A2465	C2381	A2316	C2251	G2184	A2124	U2066	U
U2870	U2870	U2797	C2728	U2663	G2596	C2466	C2382	A2317	G2252	U2185	G2125	C2067	C
U2871	U2871	U2798	C2729	U2664	C2597	C2467	A2387	G2318	G2253	G2186	U2126	C2068	C
U2872	U2872	U2799	C2730	U2665	G2598	C2468	U2392	G2319	A2254	A2187	G2127	C2069	C
U2873	U2873	U2800	C2731	U2666	U2599	C2469	U2393	G2320	C2255	G2188	U2128	A2069	A
U2874	U2874	C2800	C2732	U2667	U2600	C2470	C2383	U2321	U2256	G2189	U2129	A2060	G
U2883	U2883	A2803	U2733	G2668	A2601	C2471	C2384	C2322	U2257	C2190	G2130	G2072	U
U2886	U2886	A2804	U2734	U2669	G2602	C2472	C2385	C2323	U2258	A2191	G2131	C2073	C
U2887	U2887	A2805	U2735	U2670	A2603	C2473	C2386	C2324	U2259	G2192	U2132	C2074	C
U2888	U2888	A2806	U2736	U2671	G2604	C2474	C2387	G2325	U2260	U2193	G2133	C2075	C
U2889	U2889	A2807	U2737	U2672	C2605	C2475	C2388	C2326	U2261	G2194	U2134	C2076	C
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U2891	U2891	A2809	U2739	U2674	G2607	C2477	C2390	C2328	U2263	U2196	U2136	C2078	C
U2892	U2892	A2810	U2740	U2675	U2608	C2478	C2391	U2329	U2264	U2197	U2137	C2079	C
U2893	U2893	A2811	U2741	U2676	G2609	C2479	C2392	U2330	U2265	U2198	U2138	C2080	C
U2894	U2894	A2812	U2742	U2677	U2610	C2480	C2393	U2331	U2266	U2199	U2139	C2081	C
U2895	U2895	U2813	U2743	U2678	G2611	C2481	C2394	U2332	U2267	U2200	U2140	C2082	C
U2896	U2896	C2814	U2744	U2679	G	C2482	C2395	U2333	U2268	U2201	U2141	C2083	C
U2897	U2897	C2815	U2745	U2680	U	C2483	C2396	U2334	U2269	U2202	U2142	C2084	C
U2898	U2898	C2816	U2746	U2681	U	C2484	C2397	U2335	U2270	U2203	U2143	C2085	C
U2899	U2899	C2817	U2747	U2682	C2615	C2485	C2398	U2336	U2271	U2204	U2144	C2086	C
U2900	U2900	C2818	U2748	U2683	A2616	C2486	C2399	U2337	U2272	U2205	U2145	C2087	C
U2901	U2901	C2819	U2749	U2684	G2617	C2487	C2400	U2338	U2273	U2206	U2146	C2088	C
U2902	U2902	C2820	U2750	U2685	A2618	C2488	C2401	U2339	U2274	U2207	U2147	C2089	C
U2903	U2903	C2821	U2751	U2686	G2619	C2489	C2402	U2340	U2275	U2208	U2148	C2090	C
U2904	U2904	C2822	U2752	U2687	U2620	C2490	C2403	U2341	U2276	U2209	U2149	C2091	C
U2905	U2905	C2823	U2753	U2688	A2619	C2491	C2404	U2342	U2277	U2210	U2150	C2092	C
U2906	U2906	C2824	U2754	U2689	G2621	C2492	C2405	U2343	U2278	U2211	U2151	C2093	C
U2907	U2907	C2825	U2755	U2690	G2622	C2493	C2406	U2344	U2279	U2212	U2152	C2094	C
U2908	U2908	C2826	U2756	U2691	U2623	C2494	C2407	U2345	U2280	U2213	U2153	C2095	C
U2909	U2909	C2827	U2757	U2692	A2620	C2495	C2408	U2346	U2281	U2214	U2154	C2096	C
U2910	U2910	C2828	U2758	U2693	G2624	C2496	C2409	U2347	U2282	U2215	U2155	C2097	C
U2911	U2911	C2829	U2759	U2694	U2625	C2497	C2410	U2348	U2283	U2216	U2156	C2098	C
U2912	U2912	C2830	U2760	U2695	A2621	C2498	C2411	U2349	U2284	U2217	U2157	C2099	C
U2913	U2913	C2831	U2761	U2696	G2626	C2499	C2412	U2350	U2285	U2218	U2158	C2100	C
U2914	U2914	C2832	U2762	U2697	U2626	C2500	C2413	U2351	U2286	U2219	U2159	C2101	C
U2915	U2915	C2833	U2763	U2698	A2622	C2501	C2414	U2352	U2287	U2220	U2160	C2102	C
U2916	U2916	C2834	U2764	U2699	U2627	C2502	C2415	U2353	U2288	U2221	U2161	C2103	C
U2917	U2917	C2835	U2765	U2700	G2628	C2503	C2416	U2354	U2289	U2222	U2162	C2104	C
U2918	U2918	C2836	U2766	U2701	U2629	C2504	C2417	U2355	U2290	U2223	U2163	C2105	C
U2919	U2919	C2837	U2767	U2702	A2623	C2505	C2418	U2356	U2291	U2224	U2164	C2106	C
U2920	U2920	C2838	U2768	U2703	G2629	C2506	C2419	U2357	U2292	U2225	U2165	C2107	C
U2921	U2921	C2839	U2769	U2704	U2630	C2507	C2420	U2358	U2293	U2226	U2166	C2108	C
U2922	U2922	C2840	U2770	U2705	G2631	C2508	C2421	U2359	U2294	U2227	U2167	C2109	C
U2923	U2923	C2841	U2771	U2706	U2632	C2509	C2422	U2360	U2295	U2228	U2168	C2110	C
U2924	U2924	C2842	U2772	U2707	A2634	C2510	C2423	U2361	U2296	U2229	U2169	C2111	C
U2925	U2925	C2843	U2773	U2708	G2635	C2511	C2424	U2362	U2297	U2230	U2170	C2112	C
U2926	U2926	C2844	U2774	U2709	U2636	C2512	C2425	U2363	U2298	U2231	U2171	C2113	C
U2927	U2927	C2845	U2775	U2710	G2637	C2513	C2426	U2364	U2299	U2232	U2172	C2114	C
U2928	U2928	C2846	U2776	U2711	U2638	C2514	C2427	U2365	U2300	U2233	U2173	C2115	C
U2929	U2929	C2847	U2777	U2712	U2639	C2515	C2428	U2366	U2301	U2234	U2174	C2116	C
U2930	U2930	C2848	U2778	U2713	G2640	C2516	C2429	U2367	U2302	U2235	U2175	C2117	C
U2931	U2931	C2849	U2779	U2714	U2641	C2517	C2430	U2368	U2303	U2236	U2176	C2118	C
U2932	U2932	C2850	U2780	U2715	G2642	C2518	C2431	U2369	U2304	U2237	U2177	C2119	C
U2933	U2933	C2851	U2781	U2716	U2643	C2519	C2432	U2370	U2305	U2238	U2178	C2120	C
U2934	U2934	C2852	U2782	U2717	G2644	C2520	C2433	U2371	U2306	U2239	U2179	C2121	C
U2935	U2935	C2853	U2783	U2718	U2645	C2521	C2434	U2372	U2307	U2240	U2180	C2122	C
U2936	U2936	C2854	U2784	U2719	G2646	C2522	C2435	U2373	U2308	U2241	U2181	C2123	C
U2937	U2937	C2855	U2785	U2720	U2647	C2523	C2436	U2374	U2309	U2242	U2182	C2124	C
U2938	U2938	C2856	U2786	U2721	U2648	C2524	C2437	U2375	U2310	U2243	U2183	C2125	C
U2939	U2939	C2857	U2787	U2722	U2649	C2525	C2438	U2376	U2311	U2244	U2184	C2126	C
U2940	U2940	C2858	U2788	U2723	U2650	C2526	C2439	U2377	U2312	U2245	U2185	C2127	C
U2941	U2941	C2859	U2789	U2724	U2651	C2527	C2440	U2378	U2313	U2246	U2186	C2128	C
U2942	U2942	C2860	U2790	U2725	U2652	C2528	C2441	U2379	U2314	U2247	U2187	C2129	C
U2943	U2943	C2861	U2791	U2726	U2653	C2529	C2442	U2380	U2315	U2248	U2188	C2130	C
U2944	U2944	C2862	U2792	U2727	U2654	C2530	C2443	U2381	U2316	U2249	U2189	C2131	C
U2945	U2945	C2863	U2793	U2728	U2655	C2531	C2444	U2382	U2317	U2250	U2190	C2132	C
U2946	U2946	C2864	U2794	U2729	U2656	C2532	C2445	U2383	U2318	U2251	U2191	C2133	C
U2947	U2947	C2865	U2795	U2730	U2657	C2533	C2446	U2384	U2319	U2252	U2192	C2134	C
U2948	U2948	C2866	U2796	U2731	U2658	C2534	C2447	U2385	U2320	U2253	U2193	C2135	C
U2949	U2949	C2867	U2797	U2732	U2659	C2535	C2448	U2386	U2321	U2254	U2194	C2136	C
U2950	U2950	C2868	U2798	U2733	U2660	C2536	C2449	U2387	U2322	U2255	U219		



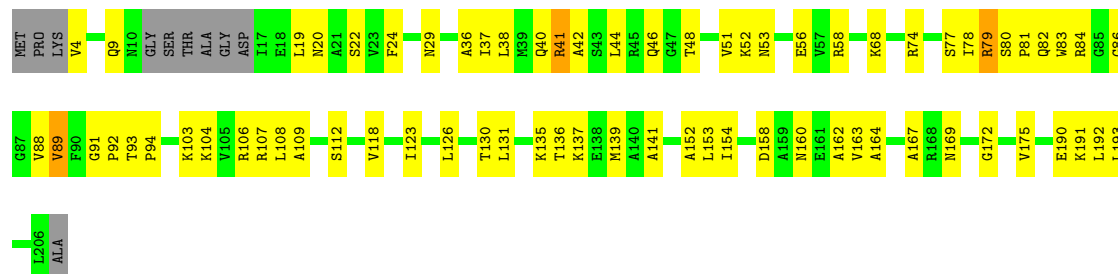
- Molecule 3: 50S ribosomal protein L2



- Molecule 4: 50S ribosomal protein L3

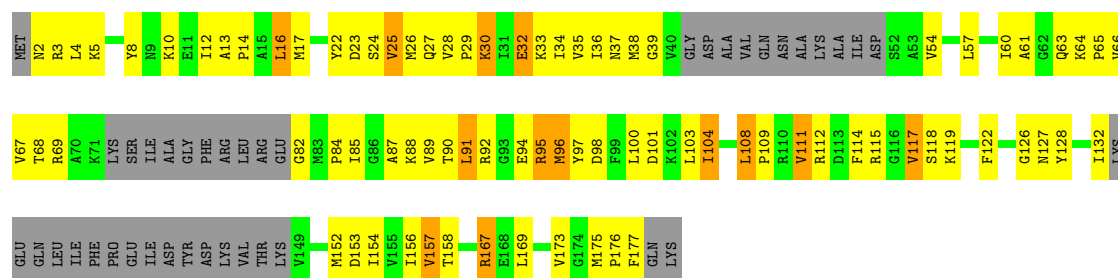


- Molecule 5: 50S ribosomal protein L4



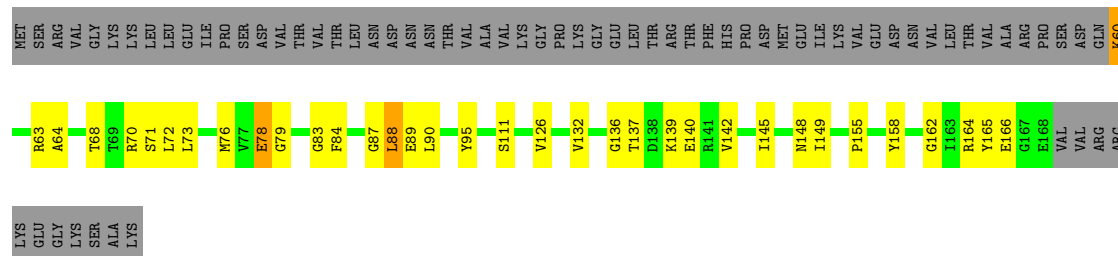
- Molecule 6: 50S ribosomal protein L5





• Molecule 7: 50S ribosomal protein L6

Chain G: 41% 18% 39%



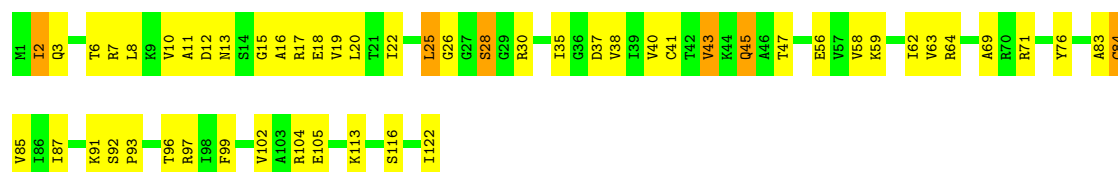
• Molecule 8: 50S ribosomal protein L13

Chain J: 48% 45% 7%



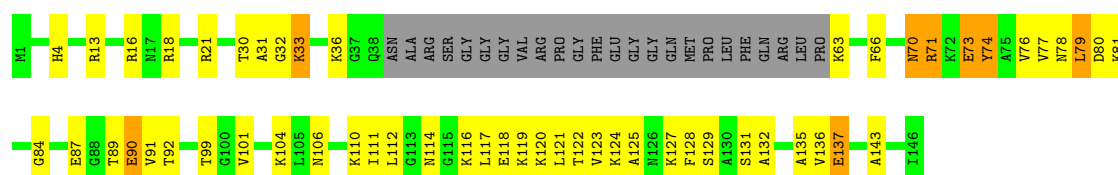
• Molecule 9: 50S ribosomal protein L14

Chain K: 57% 39% 5%

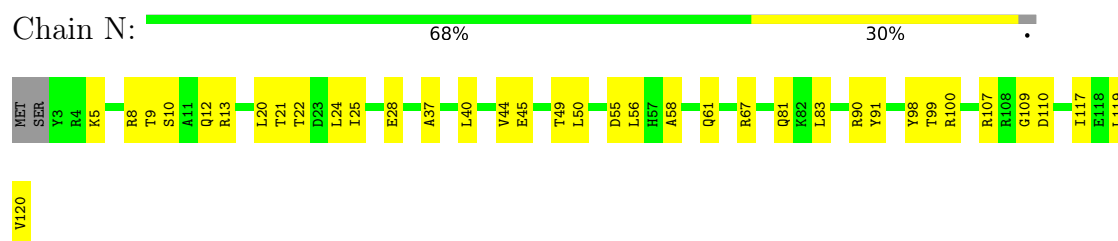


• Molecule 10: 50S ribosomal protein L15

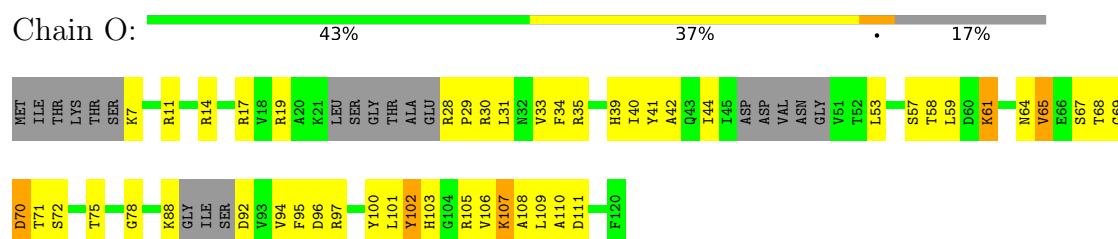
Chain L: 46% 32% 5% 16%



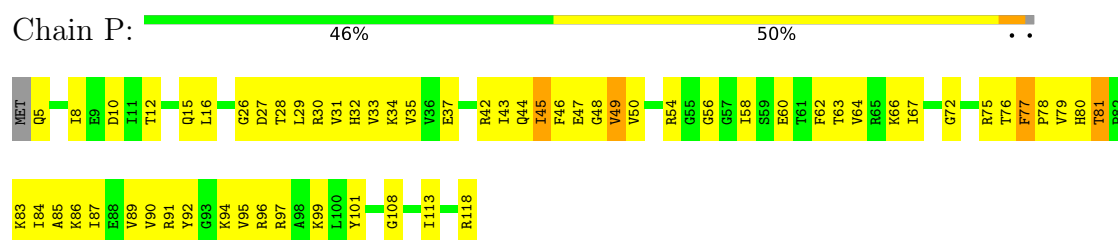
- Molecule 11: 50S ribosomal protein L17



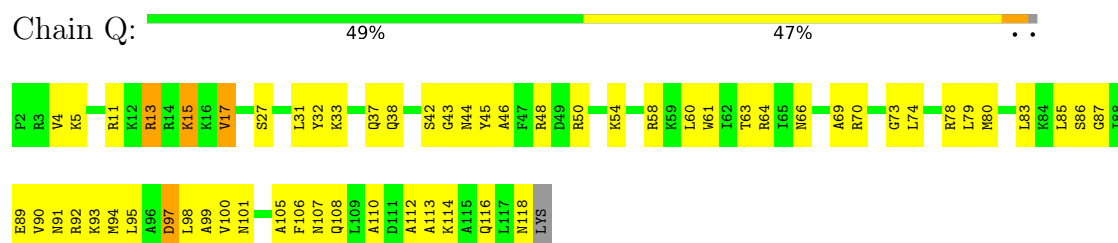
- Molecule 12: 50S ribosomal protein L18



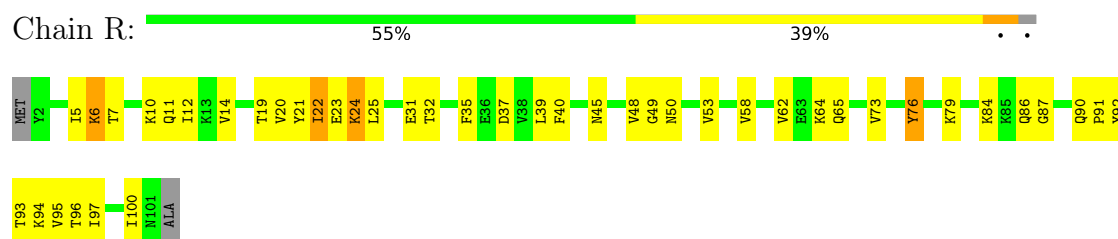
- Molecule 13: 50S ribosomal protein L19



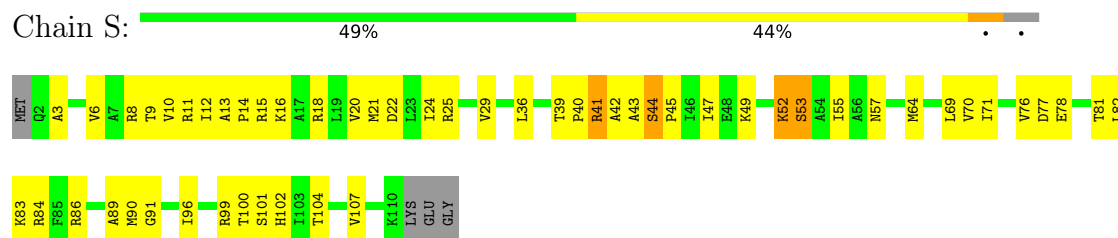
- Molecule 14: 50S ribosomal protein L20



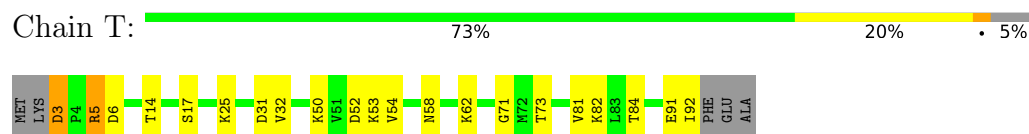
- Molecule 15: 50S ribosomal protein L21



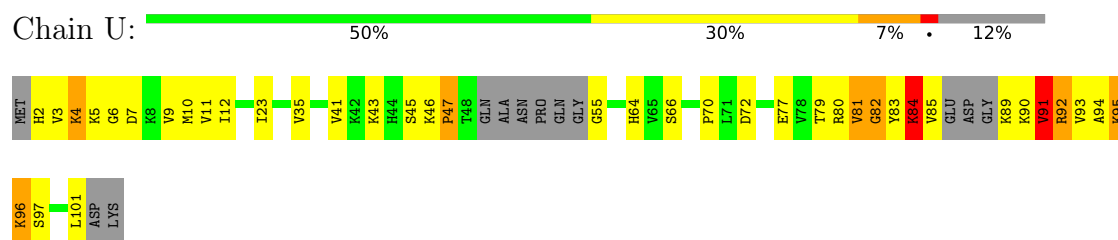
- Molecule 16: 50S ribosomal protein L22



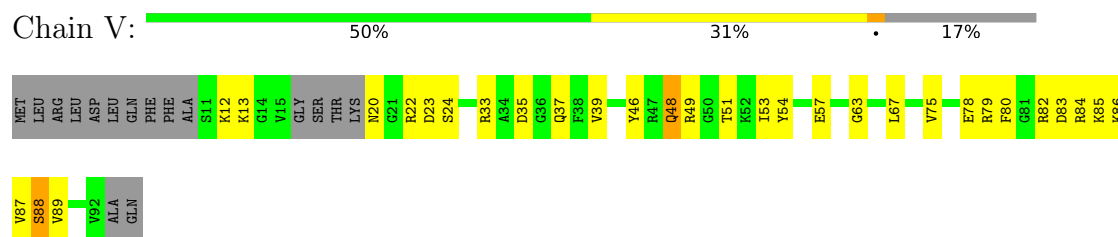
- Molecule 17: 50S ribosomal protein L23



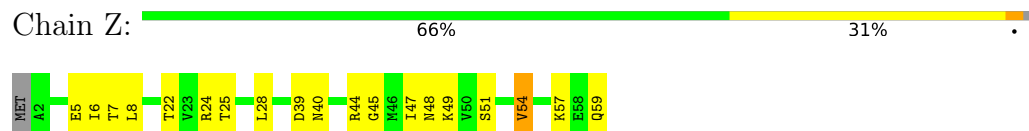
- Molecule 18: 50S ribosomal protein L24



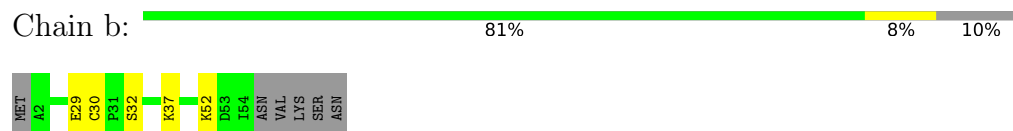
- Molecule 19: 50S ribosomal protein L27




- Molecule 20: 50S ribosomal protein L30



- Molecule 21: 50S ribosomal protein L32



- Molecule 22: 50S ribosomal protein L29

Chain Y:  58% 41%



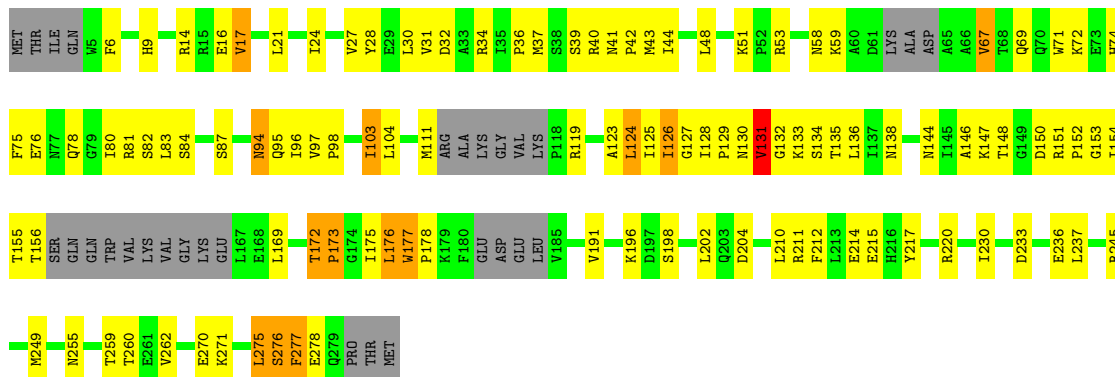
- Molecule 23: 50S ribosomal protein L34

Chain d:  98%



- Molecule 24: Ribosome biogenesis GTPase A

Chain W:  50% 34% 5% 11%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	81392	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	43	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (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: GNP

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	1.04	14/63968 (0.0%)	1.25	497/99771 (0.5%)
10	L	0.33	0/910	0.47	0/1210
11	N	0.44	0/954	0.61	0/1276
12	O	0.26	0/781	0.48	0/1042
13	P	0.37	0/949	0.62	1/1269 (0.1%)
14	Q	0.51	0/952	0.56	0/1266
15	R	0.48	1/792 (0.1%)	0.56	0/1063
16	S	0.43	0/851	0.54	0/1146
17	T	0.46	0/730	0.60	0/974
18	U	0.34	0/698	0.60	2/929 (0.2%)
19	V	0.40	0/611	0.77	3/810 (0.4%)
2	B	0.62	0/2678	1.18	21/4174 (0.5%)
20	Z	0.33	0/457	0.50	0/613
21	b	0.40	0/425	0.59	0/563
22	Y	0.35	0/531	0.51	0/707
23	d	0.54	0/362	0.56	0/473
24	W	0.29	0/1987	0.51	0/2680
3	C	0.41	0/2044	0.59	1/2741 (0.0%)
4	D	0.38	0/1591	0.59	2/2132 (0.1%)
5	E	0.43	0/1528	0.59	0/2061
6	F	0.21	0/1102	0.37	0/1476
7	G	0.30	0/841	0.54	1/1130 (0.1%)
8	J	0.36	0/1142	0.52	0/1537
9	K	0.38	0/927	0.81	7/1245 (0.6%)
All	All	0.91	15/87811 (0.0%)	1.14	535/132288 (0.4%)

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
5	E	0	1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	A	N9-C4	-6.73	1.33	1.37
1	A	830	A	N9-C4	-6.22	1.34	1.37
1	A	630	A	N9-C4	-6.14	1.34	1.37
1	A	2860	A	N9-C4	-5.97	1.34	1.37
1	A	1679	A	N9-C4	-5.71	1.34	1.37

The worst 5 of 535 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	K	2	ILE	CB-CA-C	12.98	137.56	111.60
19	V	82	ARG	CB-CA-C	11.91	134.21	110.40
1	A	1352	U	C2-N1-C1'	11.62	131.65	117.70
1	A	2825	C	C2-N1-C1'	11.49	131.44	118.80
1	A	2825	C	N1-C2-O2	11.39	125.73	118.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	41	ARG	Peptide

## 5.2 Too-close contacts [i](#)

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	57112	0	28735	1143	0
2	B	2395	0	1212	66	0
3	C	2010	0	2100	138	0
4	D	1569	0	1635	190	0
5	E	1511	0	1598	59	0
6	F	1090	0	1136	203	0
7	G	829	0	851	51	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	J	1119	0	1159	94	0
9	K	920	0	977	75	0
10	L	904	0	957	77	0
11	N	947	0	978	33	0
12	O	775	0	807	79	0
13	P	936	0	1008	92	0
14	Q	940	0	1005	76	0
15	R	781	0	820	66	0
16	S	842	0	899	71	0
17	T	724	0	768	15	0
18	U	691	0	755	87	0
19	V	604	0	614	59	0
20	Z	455	0	491	19	0
21	b	418	0	439	0	0
22	Y	530	0	568	34	0
23	d	359	0	398	0	0
24	W	1958	0	1979	203	0
25	W	32	0	13	10	0
All	All	80451	0	51902	2529	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 22.

The worst 5 of 2529 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)
10:L:117:LEU:CD2	10:L:136:VAL:HA	1.29	1.58
6:F:122:PHE:CE2	6:F:167:ARG:NH2	1.69	1.57
8:J:26:LEU:HA	8:J:29:LEU:CD1	1.40	1.50
13:P:33:VAL:HG21	13:P:77:PHE:CZ	1.48	1.47
24:W:81:ARG:NH1	24:W:103:ILE:CG1	1.79	1.45

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	C	256/277 (92%)	230 (90%)	24 (9%)	2 (1%)	21	64
4	D	204/209 (98%)	176 (86%)	27 (13%)	1 (0%)	31	73
5	E	193/207 (93%)	167 (86%)	26 (14%)	0	100	100
6	F	131/179 (73%)	114 (87%)	14 (11%)	3 (2%)	7	42
7	G	107/179 (60%)	93 (87%)	14 (13%)	0	100	100
8	J	139/145 (96%)	122 (88%)	17 (12%)	0	100	100
9	K	120/122 (98%)	100 (83%)	20 (17%)	0	100	100
10	L	118/146 (81%)	101 (86%)	16 (14%)	1 (1%)	21	64
11	N	116/120 (97%)	108 (93%)	8 (7%)	0	100	100
12	O	92/120 (77%)	84 (91%)	8 (9%)	0	100	100
13	P	112/115 (97%)	98 (88%)	13 (12%)	1 (1%)	19	60
14	Q	115/118 (98%)	105 (91%)	10 (9%)	0	100	100
15	R	98/102 (96%)	82 (84%)	15 (15%)	1 (1%)	17	58
16	S	107/113 (95%)	97 (91%)	9 (8%)	1 (1%)	19	60
17	T	88/95 (93%)	77 (88%)	11 (12%)	0	100	100
18	U	85/103 (82%)	62 (73%)	19 (22%)	4 (5%)	2	27
19	V	74/94 (79%)	67 (90%)	7 (10%)	0	100	100
20	Z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
21	b	51/59 (86%)	42 (82%)	9 (18%)	0	100	100
22	Y	63/66 (96%)	55 (87%)	8 (13%)	0	100	100
23	d	41/44 (93%)	38 (93%)	3 (7%)	0	100	100
24	W	242/282 (86%)	213 (88%)	26 (11%)	3 (1%)	14	55
All	All	2608/2954 (88%)	2283 (88%)	308 (12%)	17 (1%)	28	66

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	R	24	LYS
16	S	90	MET
18	U	82	GLY
24	W	172	THR
3	C	215	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
3	C	215/225 (96%)	209 (97%)	6 (3%)	47 71
4	D	167/170 (98%)	150 (90%)	17 (10%)	8 32
5	E	164/170 (96%)	162 (99%)	2 (1%)	74 87
6	F	120/154 (78%)	106 (88%)	14 (12%)	6 27
7	G	88/151 (58%)	82 (93%)	6 (7%)	17 49
8	J	120/123 (98%)	112 (93%)	8 (7%)	18 50
9	K	101/101 (100%)	98 (97%)	3 (3%)	44 69
10	L	93/110 (84%)	75 (81%)	18 (19%)	1 10
11	N	98/100 (98%)	98 (100%)	0	100 100
12	O	77/93 (83%)	68 (88%)	9 (12%)	6 27
13	P	99/100 (99%)	94 (95%)	5 (5%)	26 58
14	Q	96/97 (99%)	89 (93%)	7 (7%)	15 47
15	R	83/84 (99%)	80 (96%)	3 (4%)	38 66
16	S	90/93 (97%)	85 (94%)	5 (6%)	23 56
17	T	81/85 (95%)	78 (96%)	3 (4%)	37 66
18	U	78/87 (90%)	65 (83%)	13 (17%)	2 16
19	V	61/74 (82%)	59 (97%)	2 (3%)	41 68
20	Z	52/53 (98%)	50 (96%)	2 (4%)	36 65
21	b	47/53 (89%)	42 (89%)	5 (11%)	7 30
22	Y	56/57 (98%)	54 (96%)	2 (4%)	38 66
23	d	38/39 (97%)	38 (100%)	0	100 100
24	W	205/244 (84%)	188 (92%)	17 (8%)	12 43
All	All	2229/2463 (90%)	2082 (93%)	147 (7%)	23 50

5 of 147 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	L	87	GLU
12	O	107	LYS
24	W	94	ASN
10	L	90	GLU
12	O	7	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
13	P	44	GLN
14	Q	44	ASN
24	W	9	HIS
14	Q	37	GLN
14	Q	107	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2643/2927 (90%)	955 (36%)	55 (2%)
2	B	111/119 (93%)	38 (34%)	3 (2%)
All	All	2754/3046 (90%)	993 (36%)	58 (2%)

5 of 993 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	9	U
1	A	11	G
1	A	13	A
1	A	23	G

5 of 58 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1103	A
1	A	1339	A
1	A	2812	A
1	A	1107	U
1	A	1250	G

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
25	GNP	W	301	-	28,34,34	2.63	8 (28%)	30,54,54	1.36	3 (10%)

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
25	GNP	W	301	-	-	3/16/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	W	301	GNP	C4-N9	-10.31	1.34	1.47
25	W	301	GNP	PG-N3B	4.57	1.75	1.63
25	W	301	GNP	PB-N3B	4.54	1.75	1.63
25	W	301	GNP	C8-N9	-2.87	1.35	1.45
25	W	301	GNP	C5-C6	-2.43	1.48	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	W	301	GNP	PA-O3A-PB	-3.44	120.41	132.46
25	W	301	GNP	C4-C5-N7	3.12	106.60	102.46
25	W	301	GNP	C3'-C2'-C1'	2.49	106.16	101.44

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	W	301	GNP	PG-N3B-PB-O1B
25	W	301	GNP	PA-O3A-PB-O2B
25	W	301	GNP	C2'-C1'-N9-C4

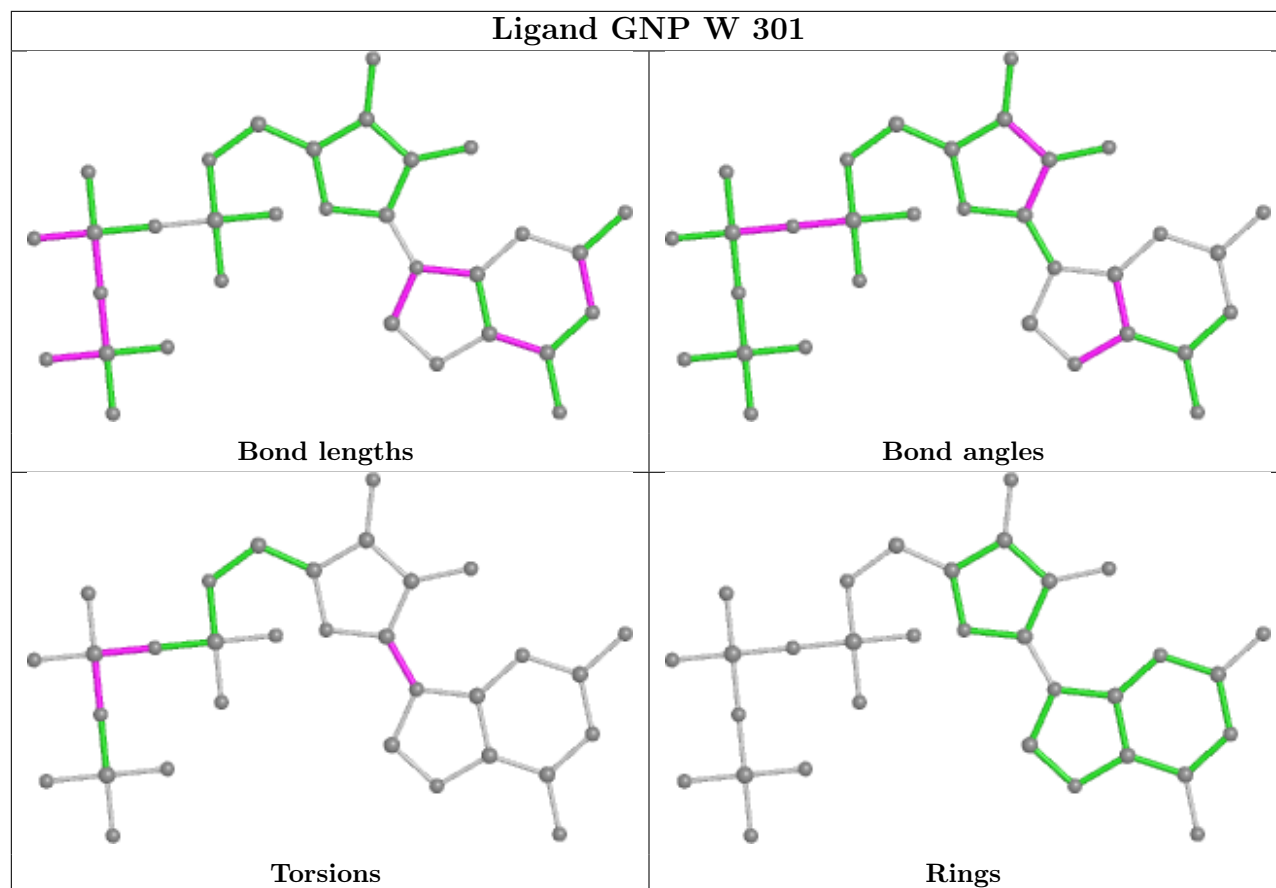
There are no ring outliers.

1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	W	301	GNP	10	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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.