



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

Mar 2, 2017 – 11:27 am GMT

PDB ID : 3BBX  
EMDB ID: : EMD-1455  
Title : The Hsp15 protein fitted into the low resolution Cryo-EM map of the 50S.nc-tRNA.Hsp15 complex  
Authors : Jiang, L.; Abrahams, J.P.  
Deposited on : 2007-11-11  
Resolution : 10.00 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  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
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) : recalc29047

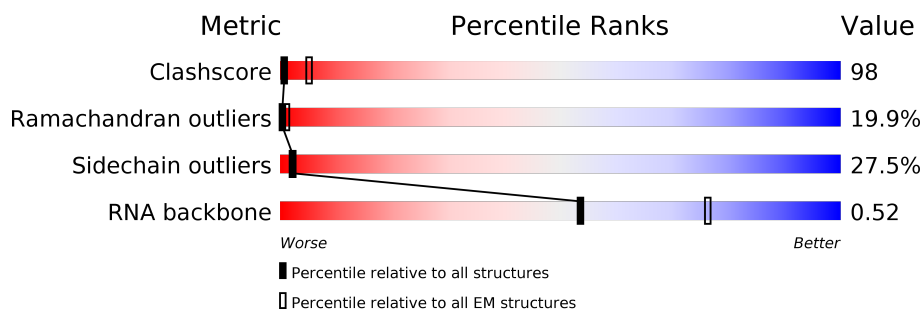
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 10.00 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.







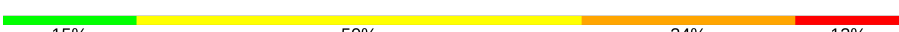
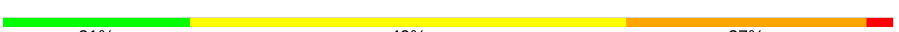
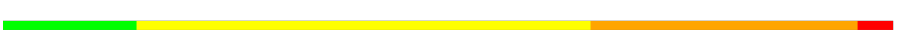







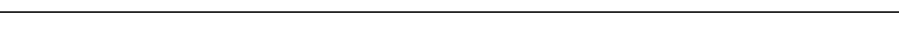

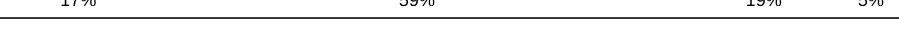

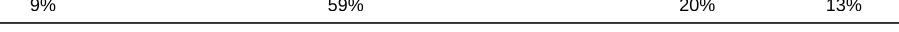



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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  $\geq 3$ , 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	120	22% 63% 13% .
2	B	2904	20% 66% 13% .
3	V	94	27% 56% 16% .
4	C	273	13% 41% 37% 8% .
5	D	209	10% 53% 33% .
6	E	201	12% 55% 28% 5% .
7	F	178	19% 52% 27% .
8	G	176	24% 57% 16% .

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Mol	Chain	Length	Quality of chain
9	H	149	
10	J	142	
11	K	123	
12	L	144	
13	M	136	
14	N	127	
15	O	117	
16	P	114	
17	Q	117	
18	R	103	
19	S	110	
20	T	100	
21	U	103	
22	W	84	
23	X	63	
24	Y	58	
25	Z	70	
26	0	56	
27	1	54	
28	2	46	
29	3	64	
30	4	38	

## 2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 89335 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	117	Total	C	N	O	P	0	0
			2507	1116	459	815	117		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	2902	Total	C	N	O	P	0	61
			61056	27210	11229	19715	2902		

- Molecule 3 is a protein called 50S ribosomal protein L25.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	178	Total	C	N	O	S	0	0
			1420	905	251	258	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
			1323	832	243	246	2		

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

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

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	140	Total	C	N	O	S	0	0
			1112	704	210	194	4		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

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

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

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

- Molecule 17 is a protein called 50S ribosomal protein L20.

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

- Molecule 18 is a protein called 50S ribosomal protein L21.

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

- Molecule 19 is a protein called 50S ribosomal protein L22.

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

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	99	Total	C	N	O	S	0	0
			777	491	145	139	2		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	W	84	Total	C	N	O	S	0
			634	391	129	113	1	0

- Molecule 23 is a protein called 50S ribosomal protein L29.

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

- Molecule 24 is a protein called 50S ribosomal protein L30.

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

- Molecule 25 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Z	70	Total	C	N	O	S	0
			549	339	104	100	6	0

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	0	56	Total	C	N	O	S	0
			444	269	94	80	1	0

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	1	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 31 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
31	Q	2	Total	Mg	0
			2	2	
31	E	3	Total	Mg	0
			3	3	
31	B	92	Total	Mg	0
			92	92	
31	C	1	Total	Mg	0
			1	1	
31	T	2	Total	Mg	0
			2	2	
31	U	1	Total	Mg	0
			1	1	
31	2	3	Total	Mg	0
			3	3	
31	L	4	Total	Mg	0
			4	4	
31	S	2	Total	Mg	0
			2	2	

- Molecule 32 is water.

Mol	Chain	Residues	Atoms		AltConf
32	B	443	Total	O	0
			443	443	

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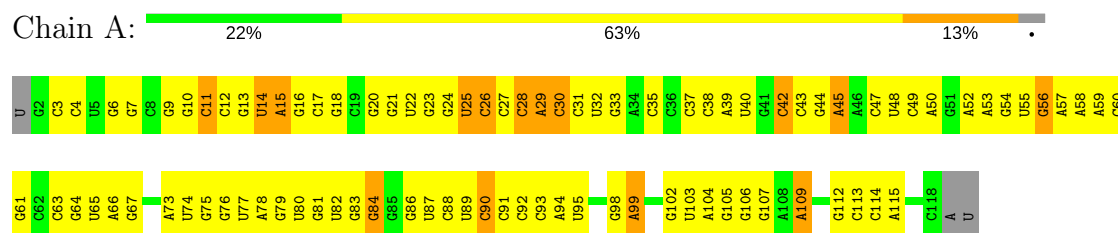
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Mol	Chain	Residues	Atoms		AltConf
32	C	1	Total 1	O 1	0
32	D	1	Total 1	O 1	0
32	E	18	Total 18	O 18	0
32	L	8	Total 8	O 8	0
32	Q	7	Total 7	O 7	0
32	S	7	Total 7	O 7	0
32	T	5	Total 5	O 5	0
32	U	5	Total 5	O 5	0
32	2	11	Total 11	O 11	0

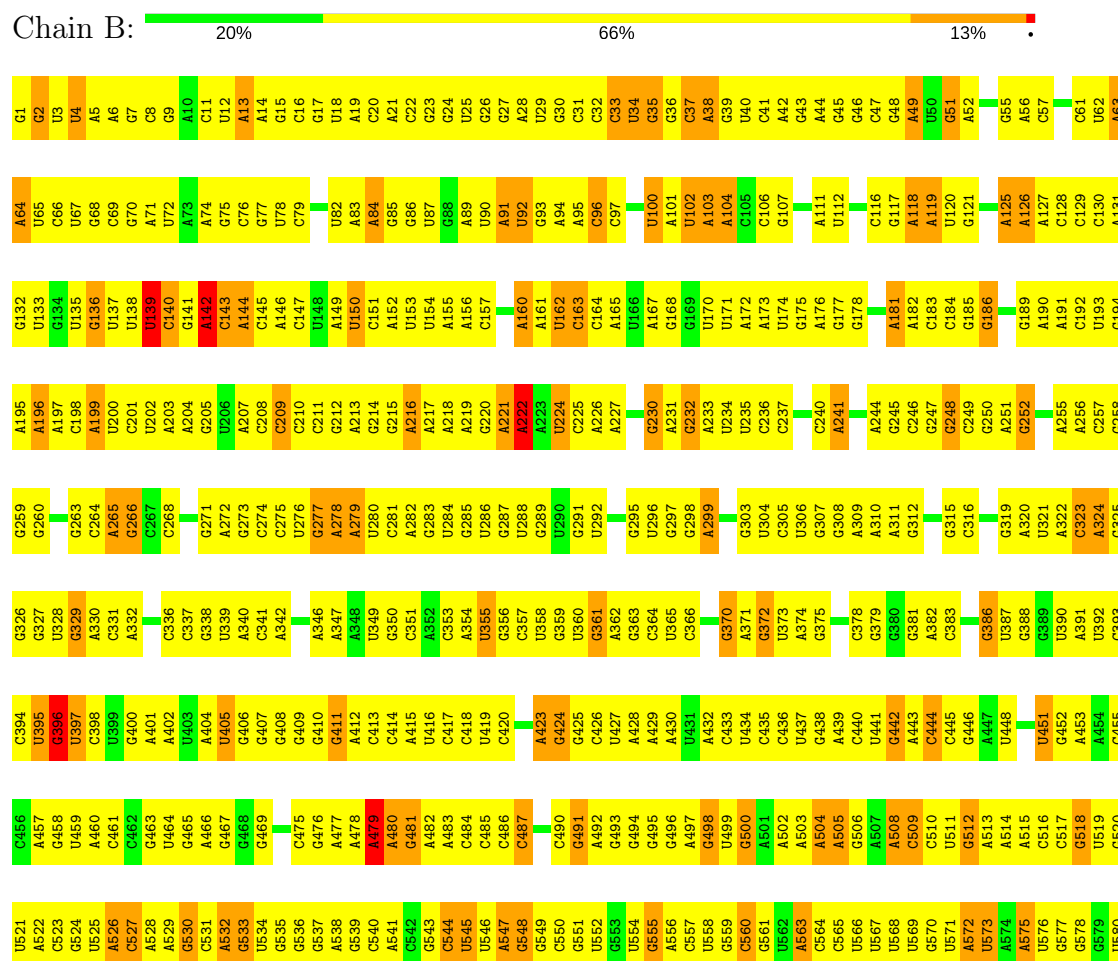
### 3 Residue-property plots

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: 5S ribosomal RNA

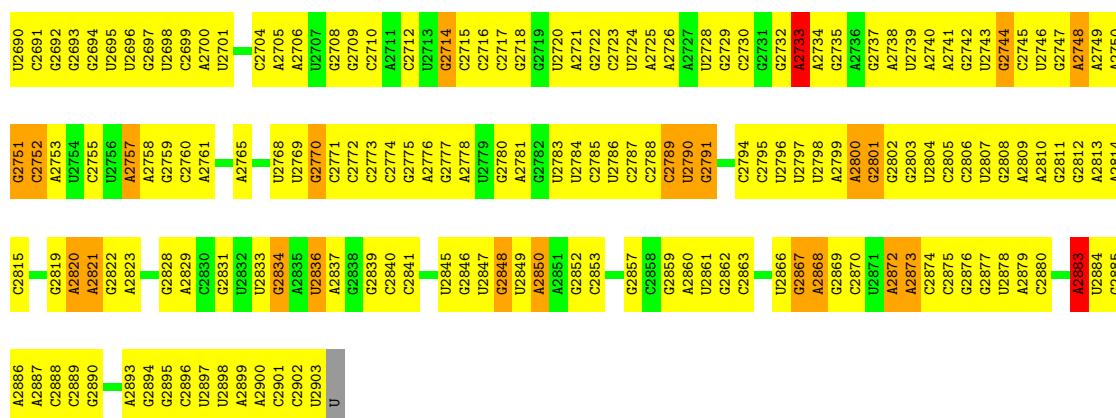


#### • Molecule 2: 23S ribosomal RNA

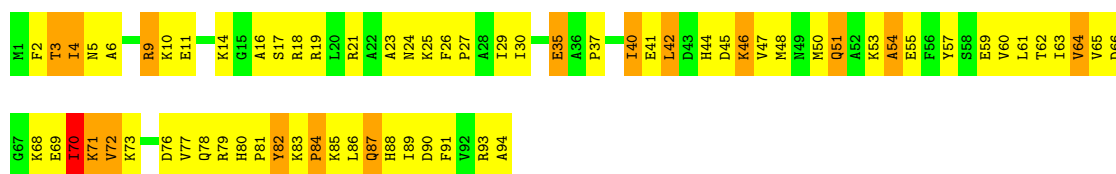


C1493	C1428	A1365	C1288	U1173	C1043	G978	A918	A844	A781	U709	A644	C581
A1494	G1429	A1366	G1239	U1174	C1044	A979	U919	A845	A782	U710	C645	A582
A1495	G1430	A1367	U1240	U1175	C1045	A980	A920	U846	A783	G711	U646	G583
A1496	G1368	A1301	A1241	U1176	A1046	A981	C921	U847	G784	G712		G584
	A1431	G1369	C1243	G1177	G1047	G982	G922	C848	G785	G713		G585
G1501	A1433	C1370	G1303	C1178	A1048	A983	G923	C849	G786		G649	
A1502	A1434	C1371	A1304	G1179	C1049	A984	G924	U850	C787	A716	C650	A586
		C1305	G1245	U1180	A1050	G985	A925	U851	G788		G551	C587
	C1437	A1372	A1246	U1181	G1051	C986	G926	U852	A718	C717	U652	U588
A1504	U1438	G1374	A1247	G1182	C1052	G987	A927	U853	G789	A719	U653	U589
A1505	A1439	U1375	G1248	U1183	C1053	A988	A928	C854	G791	U720	A655	U591
A1506	U1440	C1376	U1249	U1184	A1054	G989	G929	U855	A792	A721	G656	A592
C1507	U1313	U1313	G1250	G1185	G1055	A990	G930	U856	A793	A722	U657	U593
A1508	G1441	G1377										
A1509	U1442	A1378	C1251	U1188	A1057	C991	U931	U857	A794		U658	U594
G1510	U1443	U1316	G1252	U1189	A1057	C992	U932	U858	C795	G726	U659	C595
G1511	G1317	A1253	A1253	A1126	G993	A933	A933	U859	G796	A727	C660	U596
	U1318	G1381	A1254	G1190	U1060	C994	U934	U860	G797	G728	A661	G597
C1512	G1445	G1381	U1255	G1191	U1061	C995	C935	A861	G798	G729	G662	U598
U1513	C1446	G1382	G1256	G1192	G1062	A996	A936	C862				
U1514	C1447	A1383	C1320	G1193	G1063	G997	C937	U863	G799	A730	G663	A599
A1515	G1448	A1384	A1321	U1194	C1064	C998	G938	A864				
	U1449	A1385	A1322	A1195	U1065	C999	G939	C865				
C1516	G1449	C1386	U1258	A1196	U1065	U999	G939					
C1517	A1450	A1387	C1323	G1196	U1065	A1000	G940	U869	A804	A734	U667	U606
	G1451	U1325	A1260	C1261	A1133	A1001	A941	U870	A805	A735	A668	U607
	A1452	U1326	A1262	U1198	A1069	G1002	G942	U871	G805	C736	G669	A608
G1524	A1453	U1327	U1263	U1199	A1070		A943	U872	C906	A737	A670	A609
A1525	G1454	U1391	A1264	C1200	G1071	C1005	C944	U873	U807	G738		C610
C1526	U1455	A1392	G1264	U1201	C1072	A945	C945	C874	G808	C672	C673	C611
U1527	U1456	U1329	A1265	G1198	C1073	C1007	C946	G874	G809			G612
A1528	U1457	U1330	G1266	G1202	C1076	A1008	A947	C875	U810	A742	G674	A613
C1529	U1458	G1331	U1267	U1203	C1077	A1009	C948	C876	U811	A743	A675	A614
U1530	U1459	A1395	A1268	A1204	U1077	A1009	G949	A877	C912	U744		U615
C1531	U1460	U1396	G1332	A1205	U1078	A1010	G949	C878	U813	G745	C680	A616
A1532	C1461	C1398	G1333	G1206	A1143	C1079	G950	U879	C814	U746		G617
C1533	C1462	C1399	C1270	C1207	A1080	U1012	C951	C87				
U1534	C1463	U1400	A1336	A1272	U1081	C1013	G952	G890	C615	U747	G681	G618
A1535	G1464	U1401	U1337	U1273	U1082	A1014	G953	C881	C616	G748	G682	G619
	A1465	U1402	G1338	C1274	U1083	U1015	G954	G882	C617	A749	U683	G620
C1536			G1338	G1275	U1083	U1015	G954					
C1537		A1403	G1339	G1212	A1084	G1016	U955	U895	C618	A750	G684	A621
G1538	A1469	C1404	A1276	U1151	A1085	G1017	G956	A819	G619	A751	A685	G622
C1539	A1470	U1405	G1277	G1215	A1086	U1018	C957	U	U886	A752	U686	C623
A1540	G1471	U1406	C1341	U1216	G1087	U1018	G958	A896	C624	A753	C687	G624
		U1405	A1342	U1217	A1088	C1153	U959	C897	G625			
		G1407		G1279	A1088	A1020	A899	C898	G626	U754	U688	
			C1345	G1280	A1089	A1021	A960	C898	G627	U755	U689	
U1474	G1475	U1408	G1346	G1281	A1090	G1022	C961	A900	G628	U756	A690	A627
G1475	G1476	U1409	G1410	U1219	A1091	U1023	G962		G629			
A1544	A1477	G1410	C1282	G1220	G1091	G1024	U963	A900	G630	C757		
A1545	A1477	U1411	C1348	C1221	C1158	G1024	U963		A693			
G1546	G1478	U1412	A1284	U1222	U1159	G1025	C964	C903	U827			
		A1413	C1350	G1223	C1160		C965	A904	U828	C765	G695	A631
				U1224	C1161		G966	A905		U766		
A1548	C1480	C1351	A1285	G1224	A1098	A1028	U967		G632			
A1549	U1481	U1415	A1287	G1225	G1099	C1030	C968	C908	U831	G770	G698	A633
C1550	G1482	A1416	A1353	A1226	C1100	G1030	U968	U909	G832	G771	A699	C634
A1551	A1483	C1417	A1354	G1228	C1164	G1031	G969	A910	A833	G772	G700	G635
		G1418	G1355	C1290	A1165	A1032	U970	A910	G834	C773		A636
A1552			C1291			U1033	G971	A911	C935	U773	G701	A637
A1553	U1485	A1419		C1229	C1104			C912		G774	U702	G638
U1554	U1486	A1420	G1292	A1230	U1105	A972	U972	U912	U839	G775	U703	A639
			C1293	U1231	G1168		A973	U913	G640	G776		C640
A1556	C1488	G1424	C1361	G1232	A1169	A1039	G974	C915	G841	G777	A705	U641
C1557	U1489	G1425	C1362	U1295	C1170	A1040	A975	C915				
C1558		G1426	G1296	C1296	G1171	C1109	G976	A916	U842			U642
		C1363	G1296	U1236	G1172	C1110	C977					
U1559		A1427		A1297	C1173	C1110						

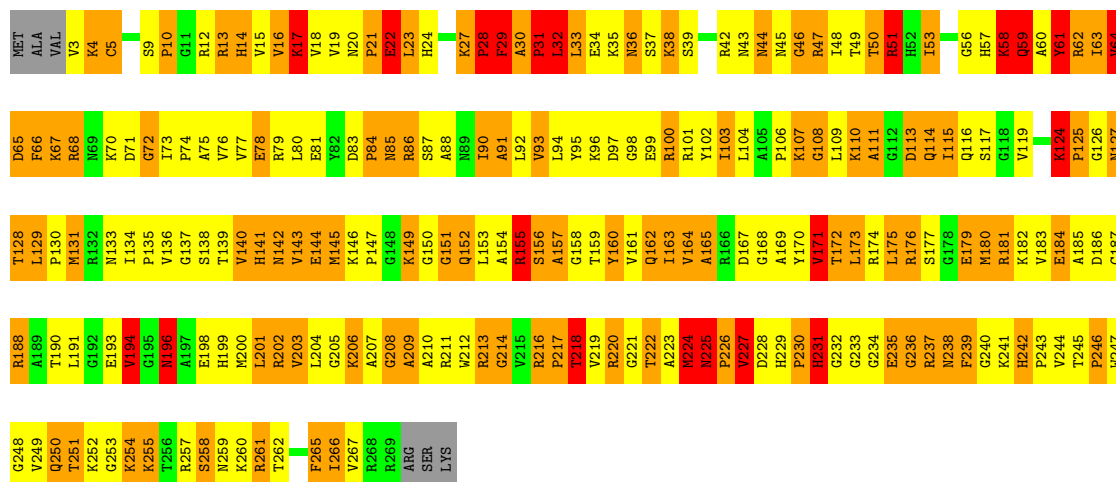
C2633	A2565	U2504	G2304	U2244	U2076	A2015	G1954	U1883	A1815	G1753	C1691	
G2630	A2566	G2505	U2305	U2245	A2077	U2016	U1955	G1884	C1816	A1754	U1692	U1629
G2631	G2370	U2506	G2306	G2246	A2078	G2017	U1956	U1885	G1817	A1755	U1693	A1630
A2632	U2568	G2507	G2307	A2247	U2079	G2018	C1957	U1886	U1818	G1756	C1694	
G2633	G2508	U2509	G2308	C2248	A2080	A2019	C1958	G1887	A1819	A1757	U1695	G1633
A2634	G2570	C2510	A2309	U2249	U2081	A2020	G1959	U1888	U1820	U1758		A1634
A2635	U2571	C2511	C2310	G2250	A2082	C2021	A1960	A1889	A1821	A1759		A1635
G2636	A2572	U2512	A2311	G2251	G2083	U2022	C1961	A1890	C1822	C1760		U1636
U2637	C2573	C2513	U2312	G2252	C2084	C2023	C1962	G1891	G1823		A1700	A1637
G2638	G2574	A2513	C2313	G2253	U2085	G2024	U1963		U1824	C1764	G1702	
A2639	C2575	U2514	A2314	C2254	U2086	C2025	G1964	U1898	U1825	U1765		C1638
G2640	G2576	C2515	G2315	G2255	G2087	G2026	C1965	A1900	G1826	C1704		C1639
A2641	A2577	U2516	G2316	G2256	U2088	G2027	U1966	A1901	U1827	G1767	A1705	A1640
G2642	G2578	C2517	A2317	U2257	C2089	U2028	C1967	A1902	G1828	C1768		G1642
G2643	U2579	A2518	G2318	C2258	A2090	G2029	U1968	U1903	A1829	U1769	G1707	
G2644	G2580	C2519	U2319	U2259	U2091	A2030	A1969	G1904	C1830	G1770	U1708	
G2645	C2581	U2520	U2320	C2260	U2092	A2031	A1970	U1905	G1831	C1771	U1709	
G2646	G2582	C2521	U2321	C2261	A2093	G2032	U1971	C1906	C1832	A1772	G1710	
G2647	U2583	U2522	A2322	C2262	A2094	A2033	G1972		C1833	C1773	U1711	
U2648	G2584	G2523	G2323	U2263	A2095	U2034	C1973	U1909	C1838	C1774		G1649
G2649	U2585	U2524	U2324	C2264	C2096	G2035	C1974	U1910	U1775	U1775	U1713	
U2650	G2586	G2525	G2325	U2265	U2097	C2036	U1975		G1839	U1776	U1714	
G2651	A2587	U2526	C2326	A2266	U2098	A2037	U1976	A1913	U1777		G1715	A1652
C2652	G2588	C2527	A2327	A2267	U2099	G2038	A1977	C1842	U1778	U1778	U1716	
G2653	A2589	U2528	A2328	U2268	G2100	U2039	A1978	C1843	U1779	U1779	A1717	A1654
A2654	U2590	G2529	U2329	G2269	A2101	G2040	U1979	C1844	A1780			A1655
	C2591	C2530	G2330	A2270	C2102	U2041	G1980	U1917	G1845	U1781	G1719	C1656
	G2592	U2531	U2331	G2271	C2103	A2042	A1981	U1918	U1846	U1782	U1720	U1657
	U2593	G2532	C2332	A2272	C2104	C2043	U1982	A1919	A1847	U1783	G1721	C1658
	G2594	C2533	A2333	U2273	U2105	G2044	G1983	C1920	A1784	A1784	A1722	C1659
	U2595	U2401	U2334	A2274	U2106	C2045	G1984	G1921	A1785		G1723	G1660
	G2596	U2402	A2335	C2275		G2046	C1985	G1922	A1786		G1724	G1661
	C2597		A2336	G2276	G2133	C2047	C1986	U1923	A1787		G1725	U1662
		G2405	G2337	G2277	U2137	G2048	A1987	C1924	C1788		G1726	G1663
	A2600	A2407	C2338	A2278	G2138	G2049	G1988	A1854	A1789		G1727	A1664
	C2601	U2408	C2339	G2279	U2139	C2050	G1989	U1855	C1790		G1728	A1665
	A2602	G2409	A2340	G2280	G2140	A2051	C1990	U1856	A1791		U1729	G1666
	G2603		G2341	A2281	G2141	C2052	U1991	G1857	G1792		G1730	G1667
	U2604	U2410	U2342	G2282	G2142	G2053	C1992	A1858	C1793		G1731	A1668
	G2605	A2411	G2343	C2283	A2142	A2054	U1993		A1794		G1732	A1669
	C2606	G2412	A2344	G2284	C2143	C2055	C1994	G1863	C1795		G1733	C1670
	G2607	G2413	A2345	A2285	G2144	G2056	U1995	U1864	U1796		U1671	
	U2608	U2414	C2346	G2286	C2145	G2057	C1996	U1865	G1797		A1735	A1672
	G2609	G2415	C2347	A2287	C2146		C1997	U1866	U1798		U1736	G1673
	C2610	C2416	G2348	G2288	A2147	A2060	A1998	G1867	G1799		G1737	G1674
	G2611	U2417	G2349	A2289	U2148	G2061	C1999	C1868	C1800			C1675
	C2612	A2418	C2350	G2290	U2149	A2062	C2000	G1869	A1801		G1738	A1676
	U2613	U2419	A2351	U2291	C2150	C2063	C2001	A1870	A1802		G1740	A1677
		C2420	G2352	U2292	U2151	C2064	G2002	A1871	A1803		C1741	A1678
	U2617	U2421	C2353	G2293	C2152	C2065	A2003	A1872	C1804		U1742	
	G2618	C2422	G2354	G2294	C2153	C2066	G2004	G1873	A1805		G1743	G1681
	C2619	U2423	U2355	C2295	A2154	G2067	A2005	C1874	C1806		U1744	U1682
	U2620	A2424	A2356	U2296	U2155	U2068	C2006	G1875	G1807		U1745	U1683
	G2621	U2425	C2357	A2297	G2156	G2069	U2007	A1876	A1808		A1746	G1684
	U2622	G2426	G2358	U2298	G2157	A2070	C2008	A1877	A1809		U1747	C1685
	G2623	C2427	G2359	U2299	C2158	A2071	C2009	G1878	A1810		G1748	C1686
	U2624	U2428	C2360	C2300	C2177	C2072		C1879	G1811		A1749	G1687
	G2625	C2429	G2361	U2301	C2178	C2073	G2012	U1880	U1812		G1750	A1688
	U2626	U2430	C2362	C2302	C2179	U2074	A2013	A1881	U1813		U1751	A1689
	C2627	U2431	G2363	U2303	C2180	U2075	A2014	U1882	U1814		C1752	A1690



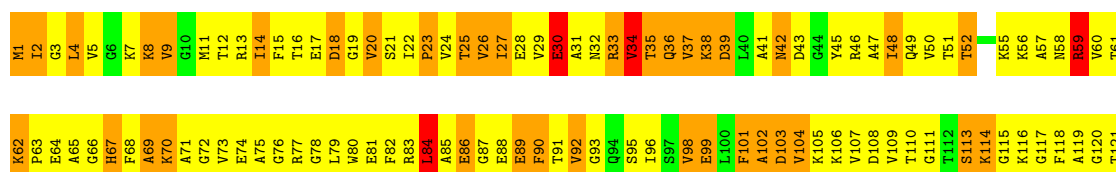
### • Molecule 3: 50S ribosomal protein L25

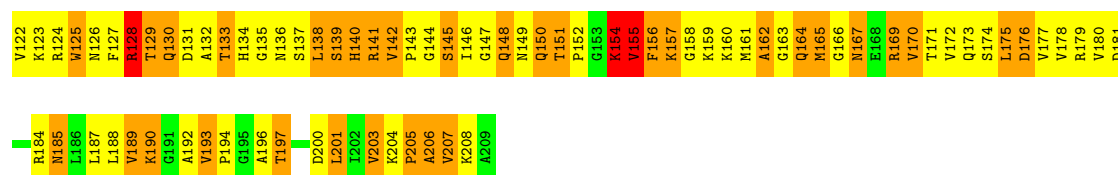


### • Molecule 4: 50S ribosomal protein L2



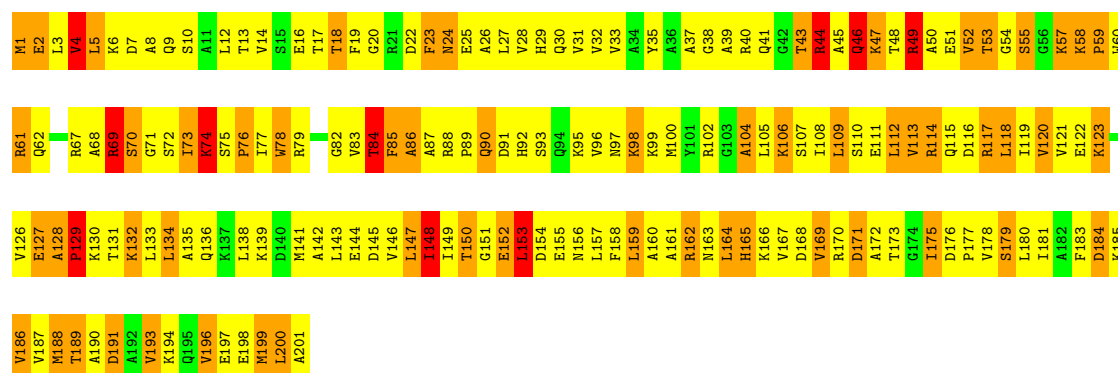
### • Molecule 5: 50S ribosomal protein L3





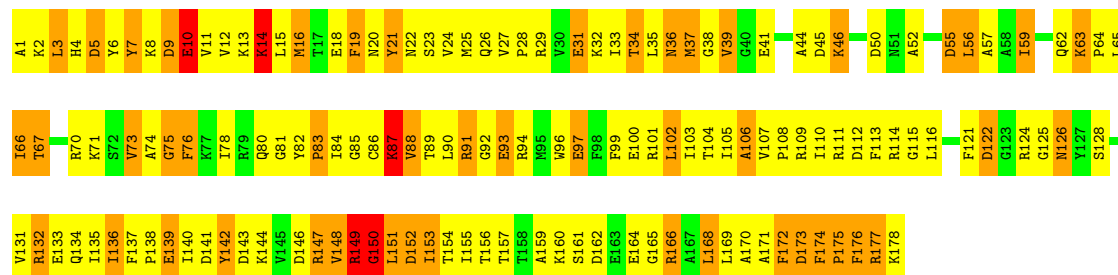
• Molecule 6: 50S ribosomal protein L4

Chain E: 12% 55% 28% 5%



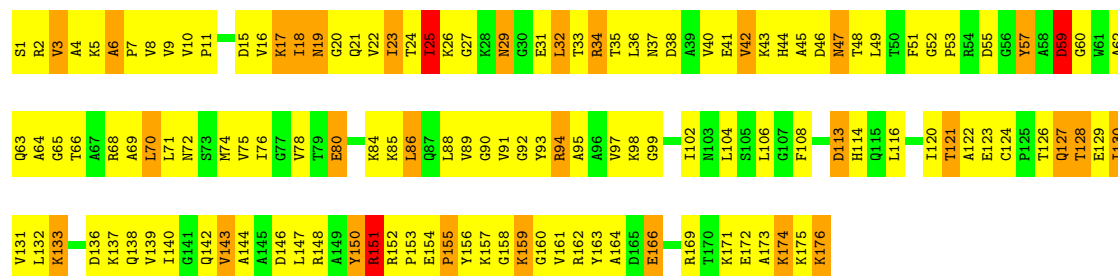
• Molecule 7: 50S ribosomal protein L5

Chain F: 19% 52% 27%



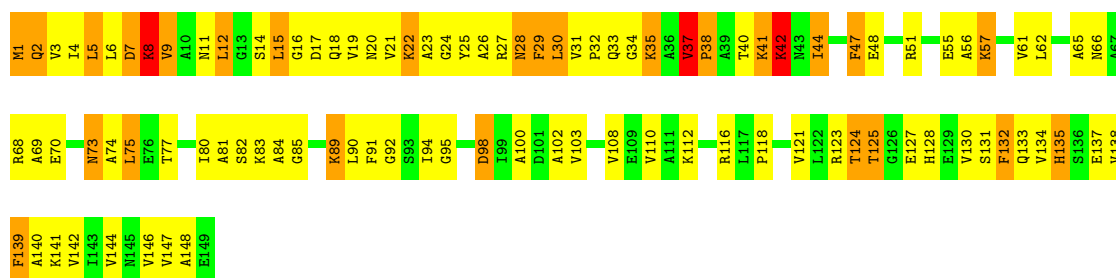
• Molecule 8: 50S ribosomal protein L6

Chain G: 24% 57% 16%



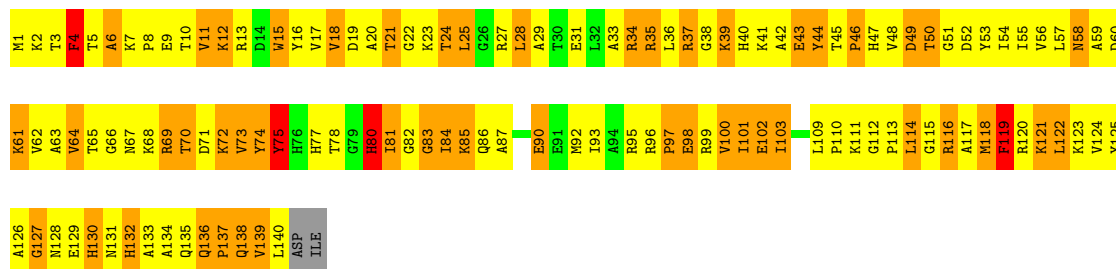
• Molecule 9: 50S ribosomal protein L9

Chain H: 34% 47% 17%



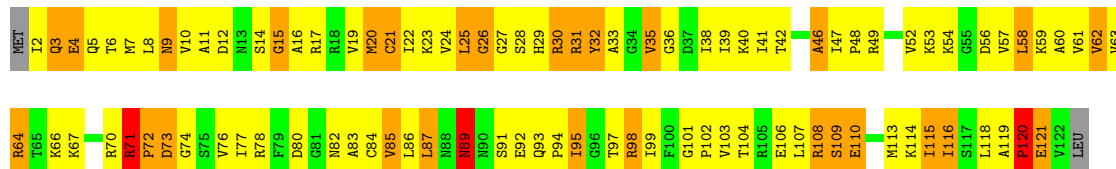
• Molecule 10: 50S ribosomal protein L13

Chain J: 11% 51% 35%



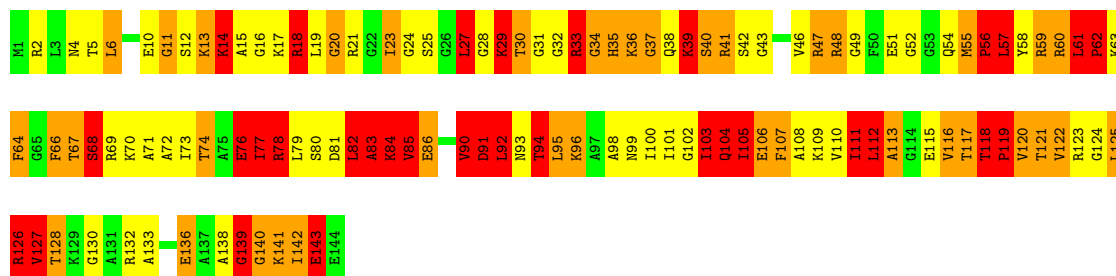
• Molecule 11: 50S ribosomal protein L14

Chain K: 20% 53% 23%



• Molecule 12: 50S ribosomal protein L15

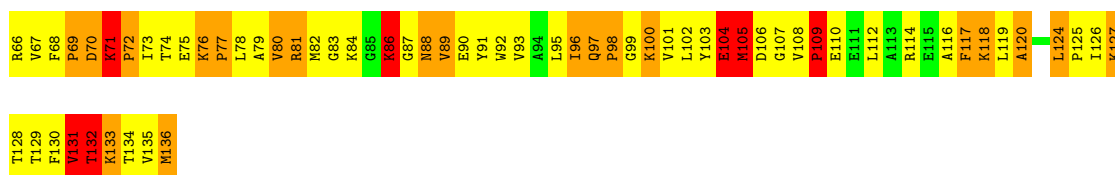
Chain L: 17% 34% 26% 23%



• Molecule 13: 50S ribosomal protein L16

Chain M: 15% 50% 24% 12%





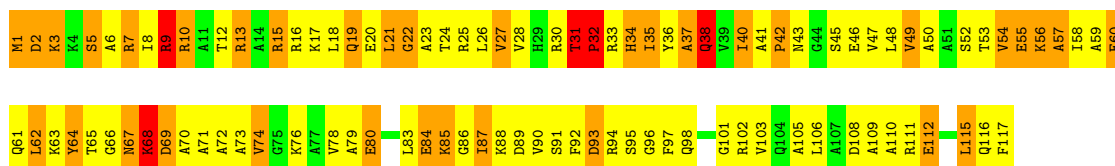
• Molecule 14: 50S ribosomal protein L17

Chain N: 21% 49% 27%



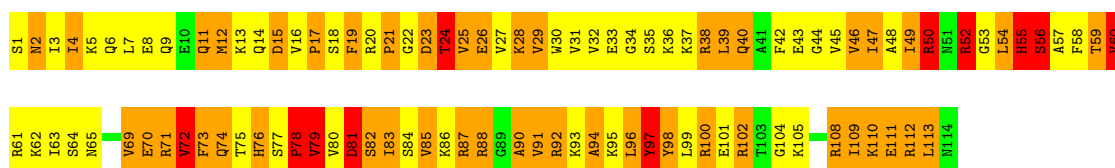
• Molecule 15: 50S ribosomal protein L18

Chain O: 15% 51% 30%



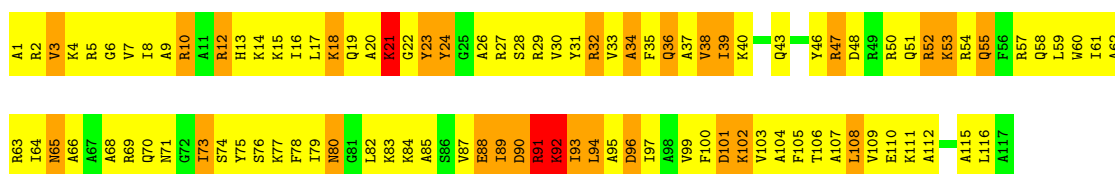
• Molecule 16: 50S ribosomal protein L19

Chain P: 10% 40% 40% 10%



• Molecule 17: 50S ribosomal protein L20

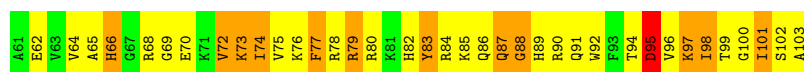
Chain Q: 14% 61% 23%



• Molecule 18: 50S ribosomal protein L21

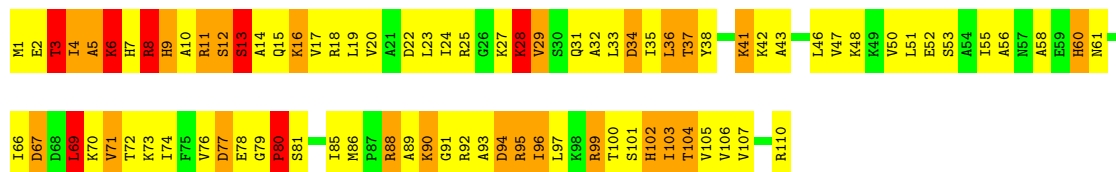
Chain R: 13% 52% 31%





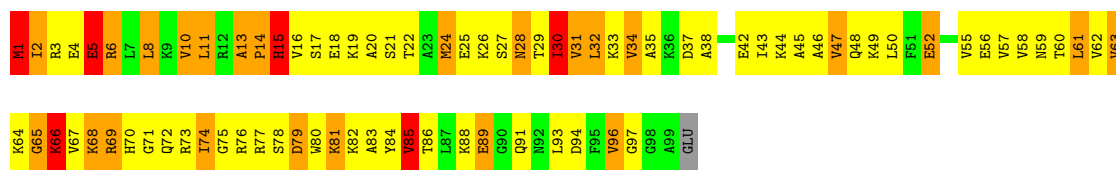
• Molecule 19: 50S ribosomal protein L22

Chain S: 22% 50% 22% 6%



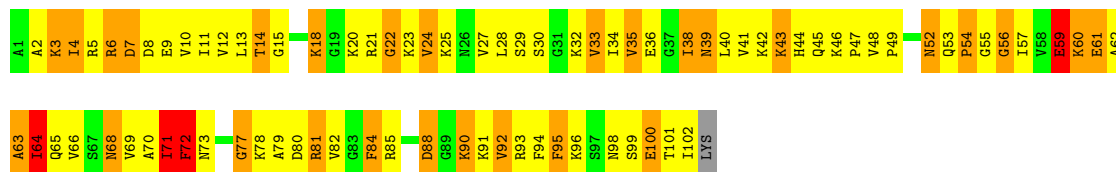
• Molecule 20: 50S ribosomal protein L23

Chain T: 17% 52% 24% 6%



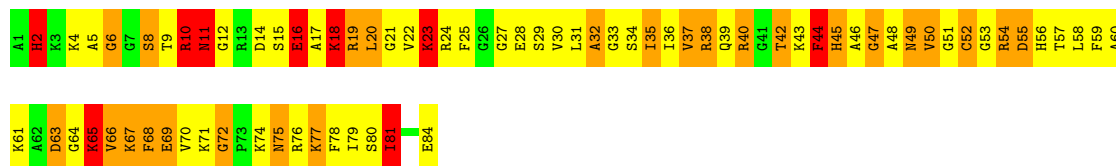
• Molecule 21: 50S ribosomal protein L24

Chain U: 18% 50% 27%



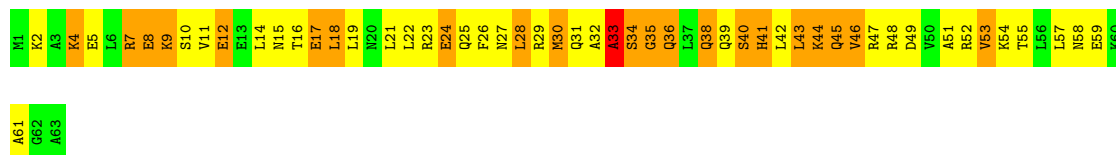
• Molecule 22: 50S ribosomal protein L27

Chain W: 12% 48% 30% 11%



• Molecule 23: 50S ribosomal protein L29

Chain X: 17% 48% 33%




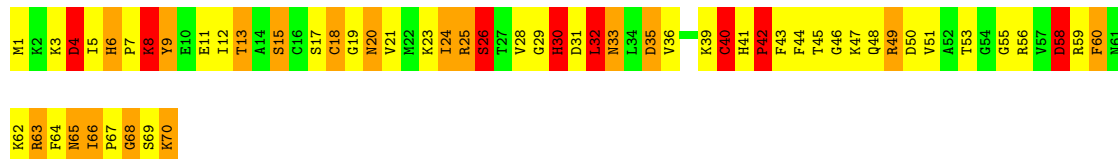
- Molecule 24: 50S ribosomal protein L30

Chain Y: 




- Molecule 25: 50S ribosomal protein L31

Chain Z: 

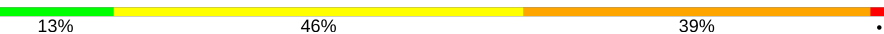


- Molecule 26: 50S ribosomal protein L32

Chain 0: 




- Molecule 27: 50S ribosomal protein L33

Chain 1: 




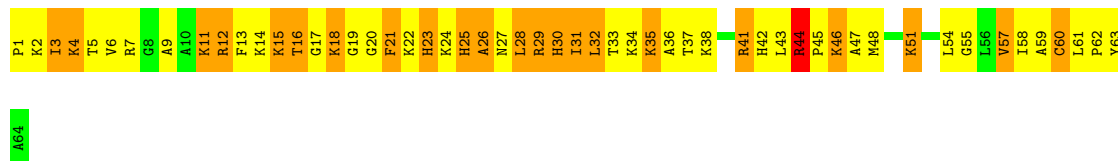
- Molecule 28: 50S ribosomal protein L34

Chain 2: 



- Molecule 29: 50S ribosomal protein L35

Chain 3: 



- Molecule 30: 50S ribosomal protein L36

Chain 4: 

M1	K2	V3	R4	A5	S6	V7	K8	K9	L10	C11	R12	M13	C14	R15	I16	V17	K18	R19	D20	G21	V22	I23	R24	V25	I26	C27	S28	A29	E30	P31	K32	H33	K34	Q35	R36	Q37	G38
----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



## 4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF correction of each particle	Depositor
Microscope	FEI Tecnai F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	1.5	Depositor
Maximum defocus (nm)	3.5	Depositor
Magnification	50000	Depositor
Image detector	Kodak SO-163 film	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	A	0.29	0/2801	0.75	0/4363
10	J	0.41	1/1135 (0.1%)	0.72	3/1529 (0.2%)
11	K	0.35	0/939	1.00	2/1258 (0.2%)
12	L	0.70	0/1062	1.60	30/1413 (2.1%)
13	M	0.48	0/1093	1.03	8/1460 (0.5%)
14	N	0.38	0/1021	0.92	7/1364 (0.5%)
15	O	0.30	0/910	0.67	0/1219
16	P	0.55	0/929	1.40	16/1242 (1.3%)
17	Q	0.41	0/960	0.86	2/1278 (0.2%)
18	R	1.06	6/829 (0.7%)	1.42	14/1107 (1.3%)
19	S	0.28	0/864	0.69	1/1156 (0.1%)
2	B	0.45	23/68281 (0.0%)	0.93	94/106437 (0.1%)
20	T	0.39	0/784	0.78	4/1048 (0.4%)
21	U	0.33	0/787	0.74	0/1051
22	W	0.37	0/642	0.96	5/848 (0.6%)
23	X	0.30	0/510	0.80	1/677 (0.1%)
24	Y	0.31	0/453	0.64	0/605
25	Z	0.48	0/559	1.04	5/745 (0.7%)
26	0	0.53	1/450 (0.2%)	1.15	7/599 (1.2%)
27	1	0.36	0/448	0.71	0/594
28	2	0.33	0/380	0.64	0/498
29	3	0.48	0/513	0.96	1/676 (0.1%)
3	V	0.31	0/766	0.53	0/1025
30	4	0.40	0/303	0.73	0/397
4	C	0.40	0/2092	0.88	7/2813 (0.2%)
5	D	0.40	0/1586	0.80	2/2134 (0.1%)
6	E	0.45	1/1571 (0.1%)	0.88	6/2113 (0.3%)
7	F	0.34	0/1444	0.87	5/1937 (0.3%)
8	G	0.31	0/1343	0.70	0/1816
9	H	1.99	0/1121	0.83	1/1512 (0.1%)
All	All	0.49	32/96576 (0.0%)	0.92	221/144914 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	J	0	2
12	L	0	1
16	P	0	1
17	Q	0	1
18	R	0	1
2	B	0	61
4	C	0	3
All	All	0	70

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2789	C	O3'-P	44.85	2.15	1.61
2	B	2390	U	O3'-P	-27.39	1.28	1.61
2	B	2626	C	O3'-P	23.56	1.89	1.61
2	B	2582	G	O3'-P	21.37	1.86	1.61
2	B	1417	C	O3'-P	-19.51	1.37	1.61

The worst 5 of 221 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1250	G	P-O3'-C3'	-66.83	39.50	119.70
2	B	2582	G	P-O3'-C3'	-54.08	54.80	119.70
2	B	1250	G	O3'-P-O5'	-47.15	14.41	104.00
2	B	1417	C	O3'-P-O5'	-41.83	24.52	104.00
2	B	1580	A	O3'-P-O5'	-38.06	31.68	104.00

There are no chirality outliers.

5 of 70 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	136	G	Sidechain
2	B	139	U	Sidechain
2	B	142	A	Sidechain
2	B	143	C	Sidechain
2	B	51	G	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	2507	0	1261	547	0
2	B	61056	0	30280	9648	0
3	V	753	0	777	235	0
4	C	2053	0	2111	760	0
5	D	1565	0	1597	807	0
6	E	1552	0	1611	578	0
7	F	1420	0	1451	471	0
8	G	1323	0	1367	217	0
9	H	1111	0	1146	140	0
10	J	1112	0	1141	313	0
11	K	930	0	997	291	0
12	L	1053	0	1114	673	0
13	M	1074	0	1136	507	0
14	N	1008	0	1040	285	0
15	O	900	0	927	259	0
16	P	917	0	958	316	0
17	Q	947	0	1016	425	0
18	R	816	0	830	336	0
19	S	857	0	915	293	0
20	T	777	0	832	278	0
21	U	779	0	832	210	0
22	W	634	0	654	294	0
23	X	509	0	528	238	0
24	Y	449	0	487	170	0
25	Z	549	0	546	175	0
26	0	444	0	444	324	0
27	1	441	0	485	153	0
28	2	377	0	408	327	0
29	3	504	0	563	259	0
30	4	302	0	336	147	0
31	2	3	0	0	0	0
31	B	92	0	0	0	0
31	C	1	0	0	0	0
31	E	3	0	0	0	0
31	L	4	0	0	0	0
31	Q	2	0	0	0	0
31	S	2	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	T	2	0	0	0	0
31	U	1	0	0	0	0
32	2	11	0	0	8	0
32	B	443	0	0	273	0
32	C	1	0	0	1	0
32	D	1	0	0	0	0
32	E	18	0	0	5	0
32	L	8	0	0	7	0
32	Q	7	0	0	2	0
32	S	7	0	0	0	0
32	T	5	0	0	16	0
32	U	5	0	0	6	0
All	All	89335	0	57790	14330	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 98.

The worst 5 of 14330 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:B:1417:C:C5	2:B:1418:G:C5	1.77	1.72
2:B:827:U:P	2:B:2446:G:H5'	1.30	1.69
2:B:5:A:C2	2:B:2899:A:C5	1.79	1.68
1:A:57:A:C4	7:F:12:VAL:HG13	1.19	1.68
2:B:2848:G:C8	16:P:96:LEU:HD23	1.24	1.67

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	
3	V	92/94 (98%)	62 (67%)	21 (23%)	9 (10%)	1	13
4	C	265/273 (97%)	103 (39%)	82 (31%)	80 (30%)	0	0
5	D	207/209 (99%)	90 (44%)	69 (33%)	48 (23%)	0	2
6	E	199/201 (99%)	99 (50%)	60 (30%)	40 (20%)	0	2
7	F	176/178 (99%)	95 (54%)	48 (27%)	33 (19%)	0	3
8	G	174/176 (99%)	118 (68%)	39 (22%)	17 (10%)	1	13
9	H	145/149 (97%)	86 (59%)	43 (30%)	16 (11%)	0	10
10	J	138/142 (97%)	69 (50%)	40 (29%)	29 (21%)	0	2
11	K	119/123 (97%)	71 (60%)	32 (27%)	16 (13%)	0	6
12	L	142/144 (99%)	60 (42%)	40 (28%)	42 (30%)	0	0
13	M	134/136 (98%)	69 (52%)	37 (28%)	28 (21%)	0	2
14	N	125/127 (98%)	73 (58%)	35 (28%)	17 (14%)	0	6
15	O	115/117 (98%)	64 (56%)	26 (23%)	25 (22%)	0	2
16	P	112/114 (98%)	39 (35%)	36 (32%)	37 (33%)	0	0
17	Q	115/117 (98%)	81 (70%)	22 (19%)	12 (10%)	0	10
18	R	101/103 (98%)	44 (44%)	31 (31%)	26 (26%)	0	1
19	S	108/110 (98%)	63 (58%)	27 (25%)	18 (17%)	0	4
20	T	97/100 (97%)	42 (43%)	40 (41%)	15 (16%)	0	4
21	U	100/103 (97%)	33 (33%)	46 (46%)	21 (21%)	0	2
22	W	82/84 (98%)	29 (35%)	26 (32%)	27 (33%)	0	0
23	X	61/63 (97%)	28 (46%)	21 (34%)	12 (20%)	0	2
24	Y	56/58 (97%)	29 (52%)	17 (30%)	10 (18%)	0	3
25	Z	68/70 (97%)	29 (43%)	26 (38%)	13 (19%)	0	3
26	0	54/56 (96%)	30 (56%)	15 (28%)	9 (17%)	0	4
27	1	52/54 (96%)	19 (36%)	23 (44%)	10 (19%)	0	3
28	2	44/46 (96%)	23 (52%)	14 (32%)	7 (16%)	0	4
29	3	62/64 (97%)	30 (48%)	25 (40%)	7 (11%)	0	8
30	4	36/38 (95%)	18 (50%)	9 (25%)	9 (25%)	0	1
All	All	3179/3249 (98%)	1596 (50%)	950 (30%)	633 (20%)	0	2

5 of 633 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	C	21	PRO
4	C	22	GLU
4	C	28	PRO
4	C	29	PHE
4	C	31	PRO

### 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	V	78/78 (100%)	66 (85%)	12 (15%)	3	19
4	C	213/218 (98%)	144 (68%)	69 (32%)	0	2
5	D	164/164 (100%)	112 (68%)	52 (32%)	0	2
6	E	165/165 (100%)	115 (70%)	50 (30%)	0	2
7	F	149/149 (100%)	118 (79%)	31 (21%)	1	8
8	G	137/137 (100%)	105 (77%)	32 (23%)	1	5
9	H	114/114 (100%)	83 (73%)	31 (27%)	0	4
10	J	114/116 (98%)	84 (74%)	30 (26%)	0	4
11	K	102/104 (98%)	78 (76%)	24 (24%)	1	5
12	L	103/103 (100%)	61 (59%)	42 (41%)	0	0
13	M	109/109 (100%)	77 (71%)	32 (29%)	0	3
14	N	103/103 (100%)	78 (76%)	25 (24%)	1	5
15	O	87/87 (100%)	58 (67%)	29 (33%)	0	2
16	P	99/99 (100%)	77 (78%)	22 (22%)	1	7
17	Q	89/89 (100%)	66 (74%)	23 (26%)	0	4
18	R	84/84 (100%)	68 (81%)	16 (19%)	2	11
19	S	93/93 (100%)	72 (77%)	21 (23%)	1	7
20	T	83/84 (99%)	60 (72%)	23 (28%)	0	3
21	U	83/84 (99%)	62 (75%)	21 (25%)	0	5
22	W	62/62 (100%)	46 (74%)	16 (26%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	X	55/55 (100%)	40 (73%)	15 (27%)	0	4
24	Y	48/48 (100%)	36 (75%)	12 (25%)	1	5
25	Z	62/62 (100%)	44 (71%)	18 (29%)	0	3
26	0	47/47 (100%)	31 (66%)	16 (34%)	0	1
27	1	48/48 (100%)	33 (69%)	15 (31%)	0	2
28	2	38/38 (100%)	27 (71%)	11 (29%)	0	3
29	3	51/51 (100%)	33 (65%)	18 (35%)	0	1
30	4	34/34 (100%)	21 (62%)	13 (38%)	0	0
All	All	2614/2625 (100%)	1895 (72%)	719 (28%)	2	4

5 of 719 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	K	98	ARG
13	M	132	THR
27	1	6	GLU
12	L	18	ARG
12	L	115	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
10	J	135	GLN
14	N	9	GLN
25	Z	65	ASN
10	J	136	GLN
11	K	88	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	114/120 (95%)	22 (19%)	0
2	B	2804/2904 (96%)	445 (15%)	0
All	All	2918/3024 (96%)	467 (16%)	0

5 of 467 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	C
1	A	12	C
1	A	13	G
1	A	14	U
1	A	15	A

There are no RNA pucker outliers to report.

## 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 110 ligands modelled in this entry, 110 are monoatomic - leaving 0 for Mogul analysis.

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.