



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jan 17, 2017 – 05:52 PM EST

PDB ID : 5H4P
EMDB ID: : EMD-9569
Title : Structural snapshot of cytoplasmic pre-60S ribosomal particles bound with Nmd3, Lsg1, Tif6 and Reh1
Authors : Ma, C.; Wu, S.; Li, N.; Chen, Y.; Yan, K.; Li, Z.; Zheng, L.; Lei, J.; Woolford, J.L.; Gao, N.
Deposited on : 2016-11-01
Resolution : 3.07 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 : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

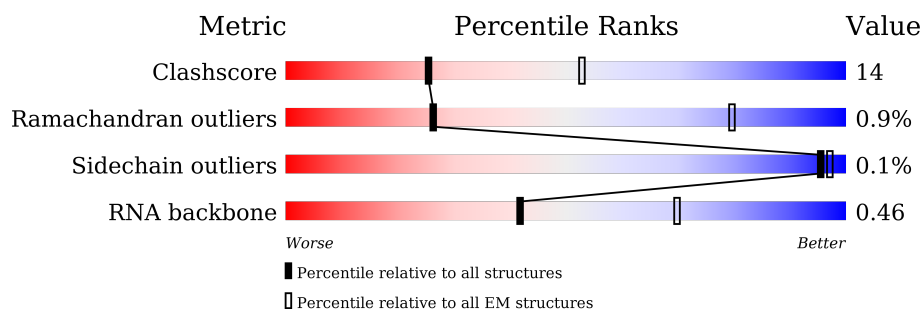
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.07 Å.

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






















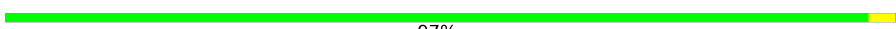
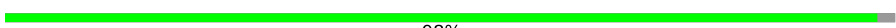

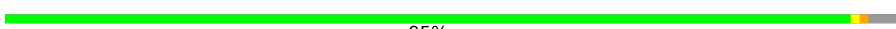


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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

Mol	Chain	Length	Quality of chain
1	1	3396	45% 35% 11% 9%
2	3	121	35% 54% 12%
3	4	158	51% 39% 9%
4	A	246	69% 31%
5	B	387	61% 38% .
6	C	361	65% 35%
7	D	297	60% 38% .
8	E	176	54% 34% . 11%

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Mol	Chain	Length	Quality of chain
9	F	244	
10	G	256	
11	H	191	
12	J	174	
13	L	199	
14	M	138	
15	N	204	
16	O	199	
17	P	184	
18	Q	186	
19	R	189	
20	S	172	
21	T	160	
22	U	121	
23	V	137	
24	W	155	
25	X	142	
26	Y	127	
27	Z	136	
28	a	149	
29	b	59	
30	c	105	
31	d	113	
32	e	130	
33	f	107	

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Mol	Chain	Length	Quality of chain
34	g	121	 93% 7%
35	h	120	 97% ..
36	i	100	 97% ..
37	j	88	 99% .
38	k	78	 99% .
39	l	51	 96% ..
40	o	106	 90% 10%
41	p	92	 99% .
42	w	248	 96% .
43	y	227	 99% .
44	z	56	 96% .

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 122929 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 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3091	Total	C	N	O	P	0	0
			66124	29535	11927	21571	3091		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 12 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	183	Total	C	N	O	S	0	0
			1442	896	287	259			

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	156	Total	C	N	O	S	0	0
			1258	781	265	212			

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 21 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 24 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	64	Total	C	N	O	S	0	0
			528	340	103	84	1		

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 26 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 27 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 34 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 35 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 36 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 37 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	77	Total	C	N	O		0	0
			612	391	115	106			

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 40 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	95	Total	C	N	O	S	0	0
			765	481	154	125	5		

- Molecule 41 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 42 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	w	248	Total	C	N	O	S	0	0
			1894	1208	318	361	7		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	y	227	Total	C	N	O	S	0	0
			1699	1054	296	342	7		

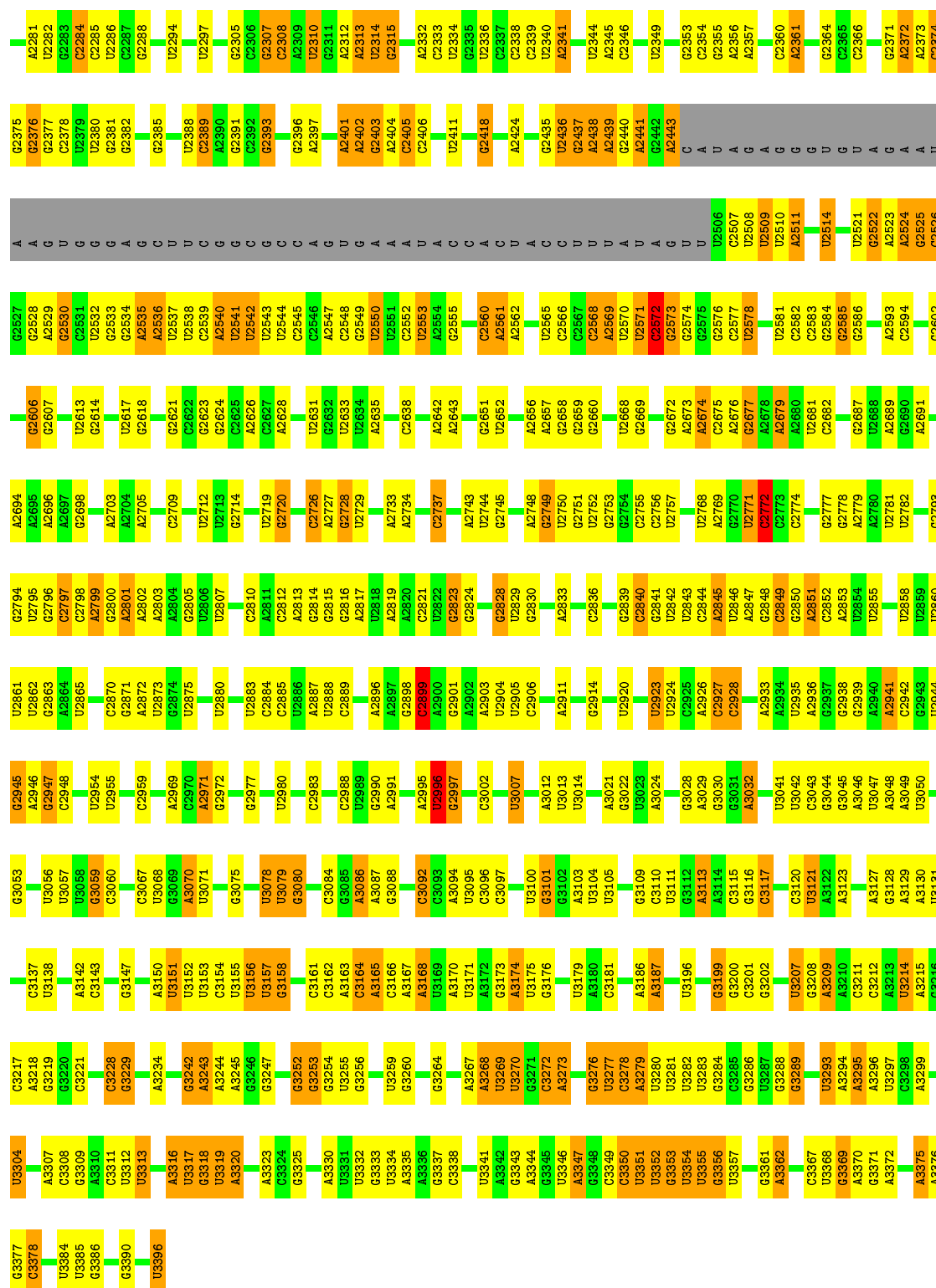
- Molecule 44 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	56	Total	C	N	O	S	0	0
			469	289	92	85	3		

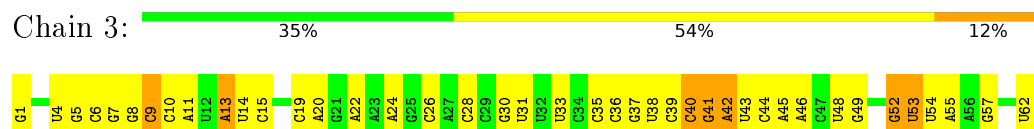
- Molecule 1: 25S ribosomal RNA

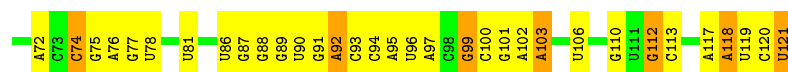


C2192	U2109	G	A1910	U1820	U1724	C1628	U1553	G1466	U1356	A1278	G1213	A1129	U1051	U990
U2193	G2110	U	G1914	U1821	C1725	U1629	U1554	A1466	G1357	C1279	U2144	A1130	U1052	G991
G2194	G2111	A	U1915	G1830	U1732	U1630	U1555	A1467	C1358	G1280	U2145	G1131	U1053	A992
C2195	U2112	G	A1916	U1831	U1737	A1631	A1557	A1468	C1359	G1281	C1216	G1134	A1055	G993
G2196	A2113	C	U1917	U1832	U1738	A1632	U1558	U1469	G1362	G1282	U2117	A1135	U1056	G994
C2197	C2114	U	U1918	A1835	C1739	G1635	G1560	U1470	A1363	G1283	U2118	G1136	U1057	A997
U2205	G2115	G	U1919	U1836	U1740	G1636	G1561	U1471	U1364	C1284	C1219	A1143	U1060	A998
G2206	A2116	C	C1926	G1838	A1741	U1637	G1562	U1472	A1366	G1285	U2220	U1144	A1061	G999
A2207	G2117	G	G1927	A1839	U1742	U1638	U1563	G1473	G1367	A1286	A1221	U1145	A1062	C
C2208	A2118	C	G1928	U1840	U1743	C1639	U1564	A1474	U1288	G1287	A1222	G1146	G1063	A
U2209	G2119	U	G1929	A1841	A1749	G1640	G1565	A1475	U1368	G1288	A1223	G1147	A1064	A
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C2212	G2121	G	A1931	U1843	G1751	A1642	U1567	U1477	A1381	C1292	G1226	G1149	U1069	U
G2213	U2122	U	U1932	C1846	C1759	U1643	U1568	G1480	G1382	U1293	U1227	A1150	C1069	G
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C2215	A2131	G	G1934	G1848	C1761	A1647	U1570	A1482	U1384	G1295	G1229	G1152	U1071	U
U2216	U2132	U	G1935	C1849	C1762	G1648	A1571	G1483	C1385	G1296	G1230	A1153	G1072	U
G2217	G2133	C	U1940	A1850	U1763	A1649	U1572	U1484	A1386	A1302	A1231	A1154	U1073	A
C2218	U2134	U	U1941	C1854	U1764	U1649	A1573	G1485	A1390	A1303	C1232	C1155	U1074	G
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G2220	G2136	C	G1943	A1856	U1765	U1659	G1576	A1488	G1392	U1305	U1236	G1157	U1078	G
A2221	U2137	U	G1944	A1857	G1766	U1660	G1577	A1489	A1407	G1306	G1237	A1158	U1079	G
C2222	U2138	C	U1945	U1858	G1767	U1661	C1578	G1493	A1394	G1307	G1238	A1159	A1080	U
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G2224	U2140	G	U1947	A1860	G1769	G1663	A1580	U1495	A1399	U1309	U1240	U1167	U1082	C
C2225	C2142	A	C1948	G1861	G1770	U1664	C1581	U1496	G1400	G1313	U1241	U1168	G1083	C
U2226	A2143	U	G1949	U1862	U1771	G1665	A1582	G1500	G1401	G1242	A1242	A1169	A1084	G
G2227	U2144	C	U1950	G1863	C1772	U1666	A1583	G1501	G1402	C1314	G1243	C1175	G1087	G
C2228	A2145	U	A1951	A1864	G1773	C1667	G1584	A1503	G1403	C1315	A1244	C1176	U1088	U
U2229	G2146	G	U1952	U1865	U1774	U1668	A1585	A1504	A1407	A1316	A1245	G1177	G1090	C
C2230	U2147	C	C1953	G1866	G1775	U1669	G1586	U1508	G1408	A1317	A1246	G1178	A1093	A
A2231	A2148	U	U1954	A1867	G1776	U1670	A1587	C1508	G1409	U1322	U1247	A1179	U1094	A
G2232	U2149	G	A1955	G1868	C1777	G1671	U1588	U1511	A1418	G1321	G1248	U1181	U1095	A
C2233	G2150	C	U1956	U1869	G1778	U1672	G1590	U1512	A1419	U1323	G1249	A1182	U1096	U
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G2235	C2152	C	C1958	U1871	G1780	G1674	G1592	U1514	G1421	C1327	U1252	G1186	A1099	A
A2236	U2153	G	U1959	G1872	G1781	U1675	C1596	U1515	U1427	U1328	U1253	C1187	U1100	C
C2237	G2154	U	U1960	A1873	U1782	U1676	A1602	U1516	G1433	A1330	C1257	U1188	G1101	U
U2238	A2155	C	A1961	U1874	U1783	U1677	G1604	C1517	G1434	U1331	U1258	U1191	A1102	U
G2239	U2156	G	U1962	G1875	G1784	U1678	A1605	C1518	A1435	A1332	A1259	C1192	A1103	G
C2240	C2157	C	C1963	U1876	U1785	U1679	U1606	C1519	U1436	C1333	A1260	A1193	G1104	A
U2241	U2158	U	U1964	A1877	G1786	U1680	U1607	C1520	C1437	U1334	G1261	G1194	A1105	C
A2242	G2159	C	U1965	G1878	U1787	G1681	C1608	U1533	U1438	A1337	G1262	A1195	G1106	C
C2243	U2160	U	U1966	U1879	U1788	U1682	C1609	A1534	U1439	G1342	U1263	C1196	U1108	U
U2244	G2161	G	U1967	A1880	A1806	U1683	G1610	A1535	U1445	C1343	U1264	A1200	U1109	A
C2245	A2162	C	A1968	U1881	G1807	U1684	G1611	G1541	A1446	A1343	U1265	G1201	U1110	U
G2246	U2163	U	U1969	G1882	U1808	U1685	G1612	G1542	G1447	U1348	G1266	C1202	U1111	C
A2247	C2164	C	C1970	U1883	U1789	U1686	A1603	G1543	U1448	U1349	U1267	A1203	A1112	U
C2248	U2165	G	U1971	A1884	U1790	U1687	G1604	G1544	U1449	G1350	U1268	A1204	G1113	C
U2249	G2166	U	U1972	G1885	U1791	U1688	A1605	U1545	G1450	A1351	C1269	U1208	G1114	A
C2250	A2167	C	U1973	U1886	U1792	U1689	U1606	C1546	U1451	U1352	A1270	G1209	U1115	A
G2251	U2168	U	U1974	A1887	U1793	U1690	U1607	C1547	U1452	U1353	A1271	U1210	U1116	C
A2252	C2169	C	U1975	G1888	U1794	U1691	C1608	U1548	A1453	A1354	C1272	G1211	G1117	A
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A2255	U2172	C	U1978	U1891	A1807	U1694	G1611	C1551	U1456	A1357	A1275	U1214	G1120	C
C2256	C2173	U	A1979	A1892	U1809	U1695	G1612	C1552	U1457	U1358	U1276	U1215	G1121	U
G2257	U2174	U	U1980	U1893	U1810	U1696	G1613	C1553	U1458	A1359	U1277	U1216	G1122	A
C2258	A2175	C	U1981	U1894	U1811	U1697	G1614	C1554	U1459	U1360	U1278	U1217	G1123	C
U2259	U2176	U	U1982	A1895	U1812	U1698	G1615	C1555	U1460	U1361	U1279	U1218	G1124	A
C2260	G2177	C	C1983	U1896	U1813	U1699	G1616	C1556	U1461	U1362	U1280	U1219	G1125	C
U2261	A2178	G	U1984	U1897	U1814	U1700	G1617	C1557	U1462	U1363	U1281	U1220	G1126	U
C2262	C2179	U	A1985	A1898	U1815	U1701	G1618	C1558	U1463	U1364	U1282	U1221	G1127	A
G2263	U2180	C	U1986	G1899	U1816	U1702	G1619	C1559	U1464	U1365	U1283	U1222	G1128	C
A2264	G2181	U	C1987	U1900	U1817	U1703	G1620	C1560	U1465	U1366	U1284	U1223	G1129	A
C2265	U2182	C	U1988	A1901	U1818	U1704	G1621	C1561	U1466	U1367	U1285	U1224	G1130	U
U2266	A2183	G	U1989	G1902	U1819	U1705	G1622	C1562	U1467	U1368	U1286	U1225	G1131	C
C2267	C2184	U	U1990	U1903	U1820	U1706	G1623	C1563	U1468	U1369	U1287	U1226	G1132	A
U2268	U2185	U	A1991	U1904	U1821	U1707	G1624	C1564	U1469	U1370	U1288	U1227	G1133	U
C2269	G2186	C	U1992	U1905	U1822	U1708	G1625	C1565	U1470	U1371	U1289	U1228	G1134	C
A2270	U2187	C	U1993	U1906	U1823	U1709	G1626	C1566	U1471	U1372	U1290	U1229	G1135	A
C2271	C2187	U	U1994	U1907	U1824	U1710	G1627	C1567	U1472	U1373	U1291	U1230	G1136	U
G2272	U2188	G	U1995	U1908	U1825	U1711	G1628	C1568	U1473	U1374	U1292	U1231	G1137	C
C2273	A2189	C	U1996	U1909	U1826	U1712	G1629	C1569	U1474	U1375	U1293	U1232	G1138	A
U2274	U2190	U	U1997	U1910	U1827	U1713	G1630	C1570	U1475	U1376	U1294	U1233	G1139	U
A2275	C2191	C	U1998	U1911	U1828	U1714	G1631	C1571	U1476	U1377	U1295	U1234	G1140	C

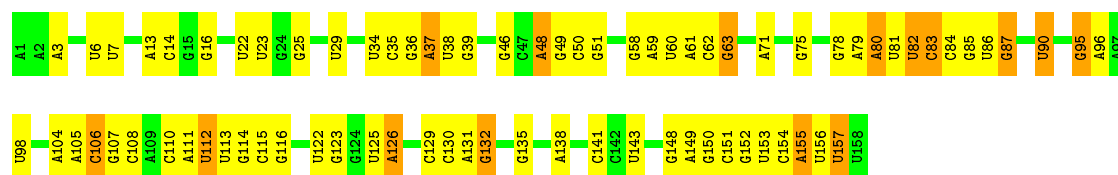


• Molecule 2: 5S ribosomal RNA

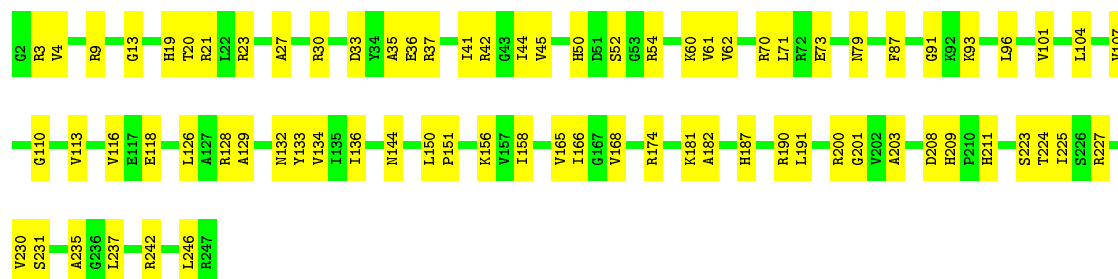




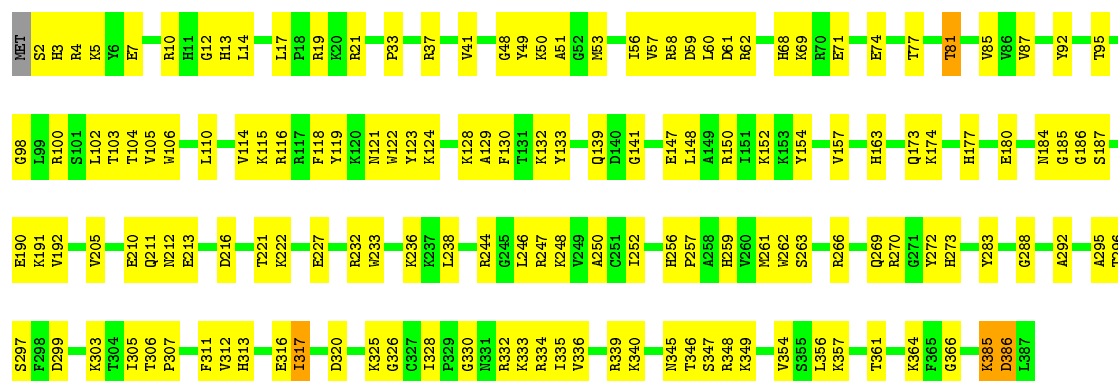
• Molecule 3: 5.8S ribosomal RNA



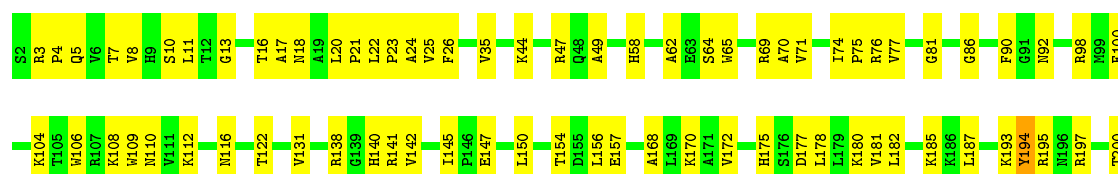
• Molecule 4: 60S ribosomal protein L2-A

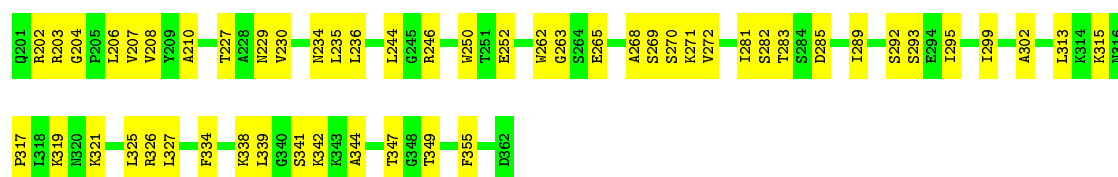


• Molecule 5: 60S ribosomal protein L3



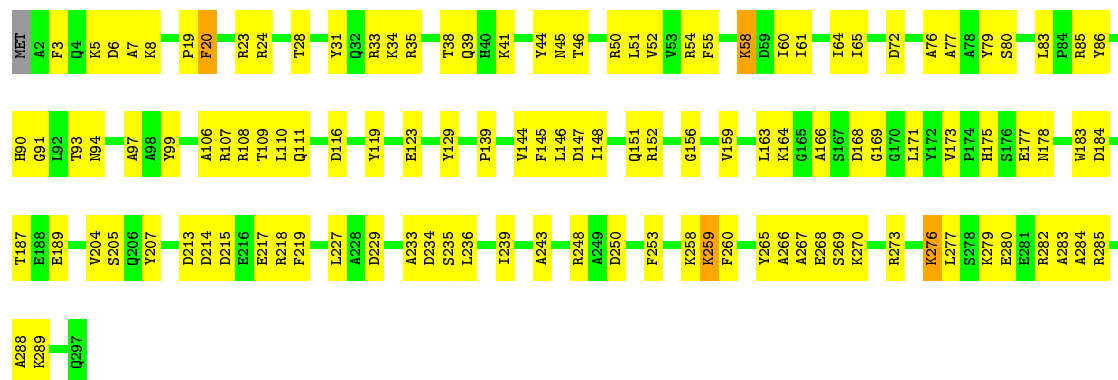
• Molecule 6: 60S ribosomal protein L4-A





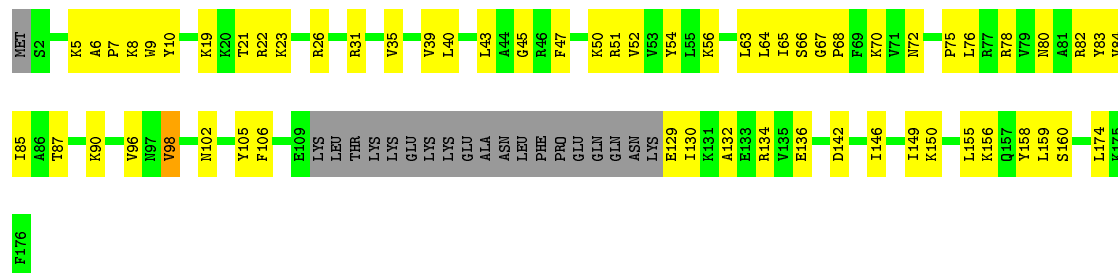
- Molecule 7: 60S ribosomal protein L5

Chain D: 60% 38%



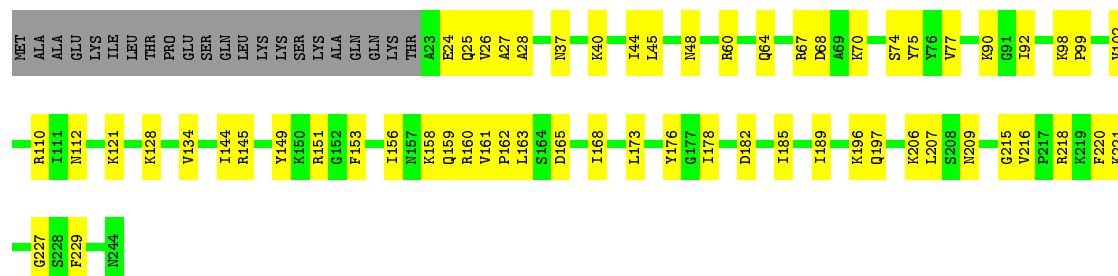
- Molecule 8: 60S ribosomal protein L6-A

Chain E:  54% 34% 11%



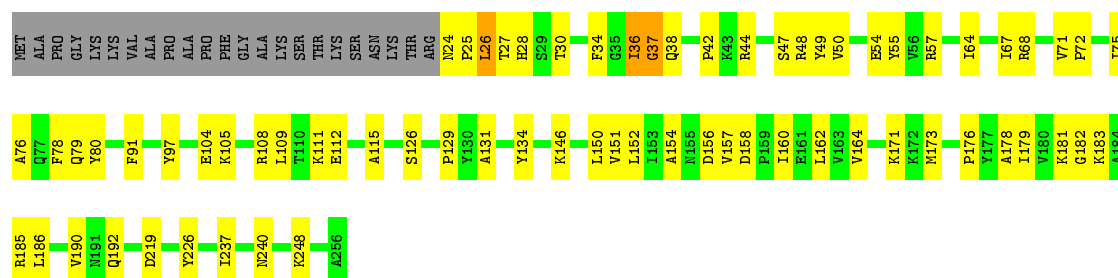
- Molecule 9: 60S ribosomal protein L7-A

Chain F:  66% 25% 9%



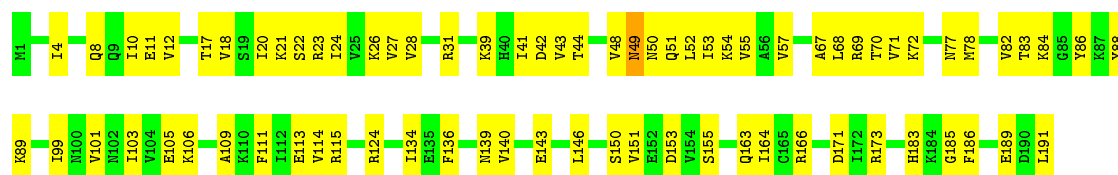
- Molecule 10: 60S ribosomal protein L8-A

Chain G:  64% 26% 9%



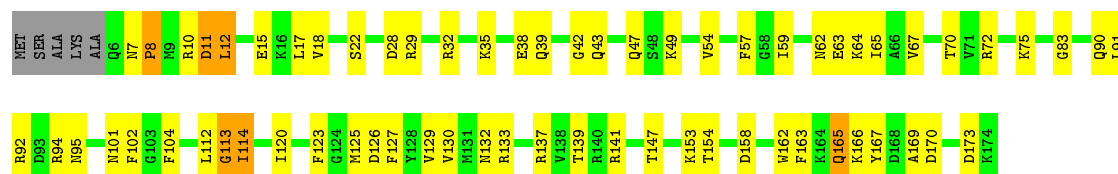
- Molecule 11: 60S ribosomal protein L9-A

Chain H: 61% 39%



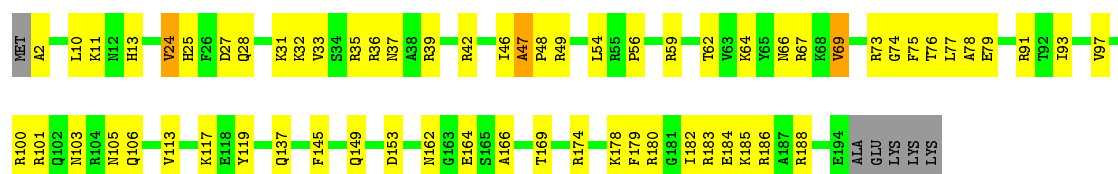
- Molecule 12: 60S ribosomal protein L11-A

Chain J: 59% 34%



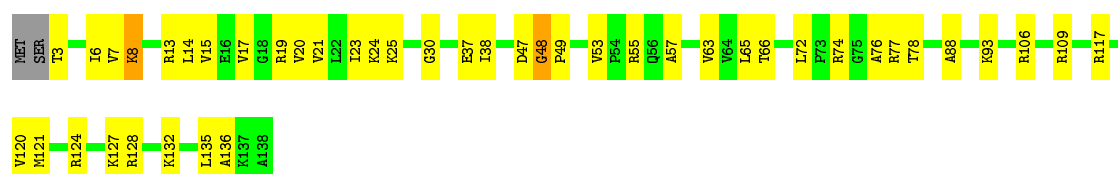
- Molecule 13: 60S ribosomal protein L13-A

Chain L: 65% 31%



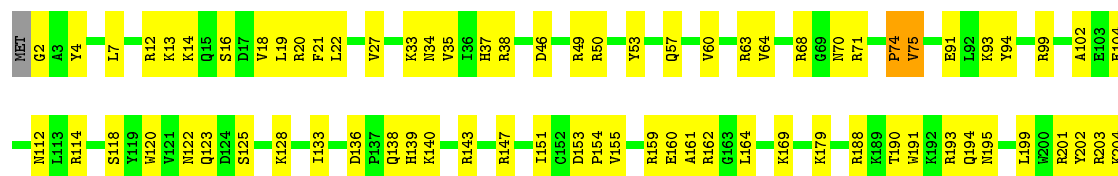
- Molecule 14: 60S ribosomal protein L14-A

Chain M: 67% 30%



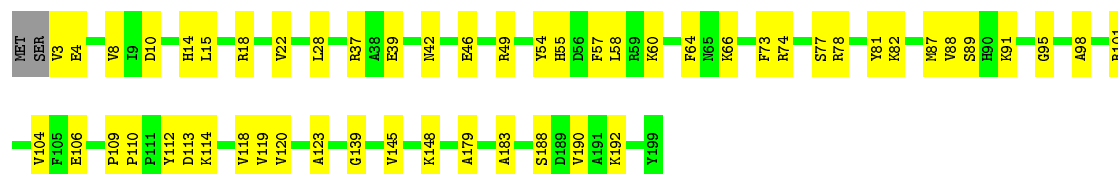
- Molecule 15: 60S ribosomal protein L15-A

Chain N:  63% 35% .



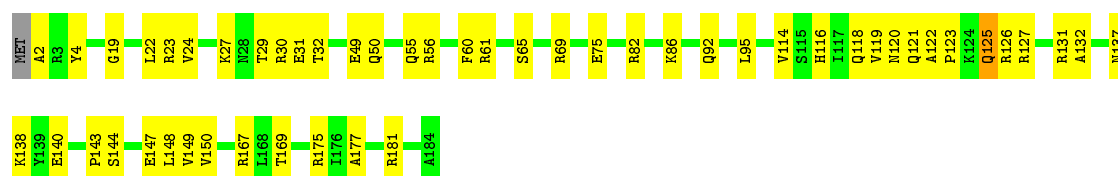
- Molecule 16: 60S ribosomal protein L16-A

Chain O:  72% 27% .



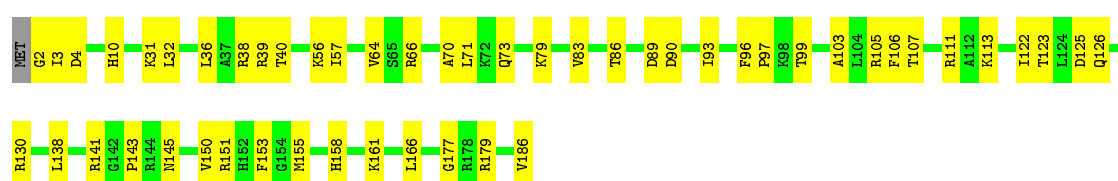
- Molecule 17: 60S ribosomal protein L17-A

Chain P:  72% 27% ..



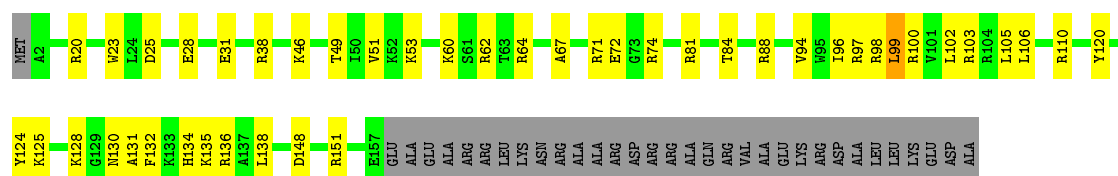
- Molecule 18: 60S ribosomal protein L18-A

Chain Q:  72% 27% .



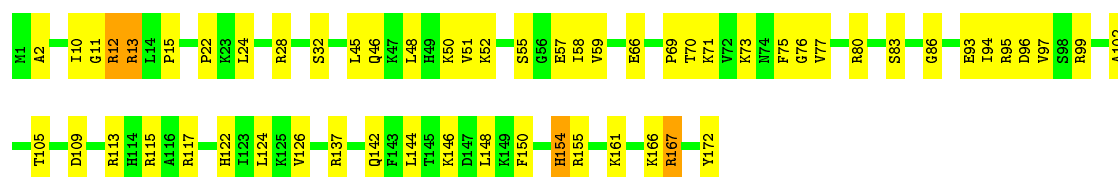
- Molecule 19: 60S ribosomal protein L19-A

Chain R:  59% 23% 17% .



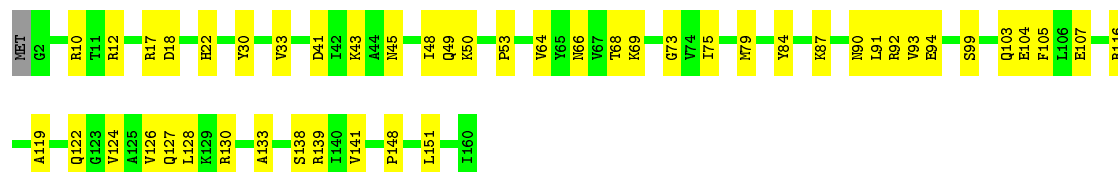
- Molecule 20: 60S ribosomal protein L20-A

Chain S:  66% 31% .



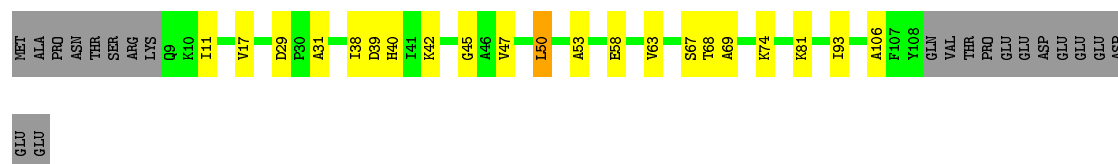
• Molecule 21: 60S ribosomal protein L21-A

Chain T: 70% 29%



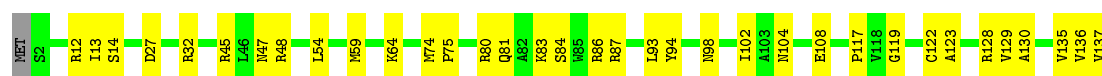
• Molecule 22: 60S ribosomal protein L22-A

Chain U: 65% 17% 17%



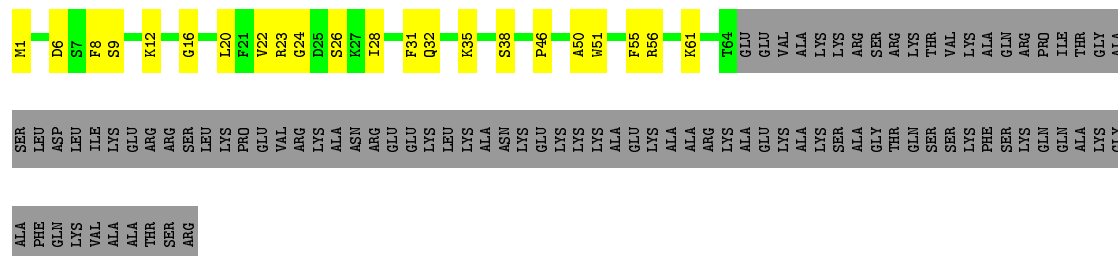
• Molecule 23: 60S ribosomal protein L23-A

Chain V: 74% 26%



• Molecule 24: 60S ribosomal protein L24-A

Chain W: 27% 14% 59%



• Molecule 25: 60S ribosomal protein L25

Chain X: 63% 22% 15%





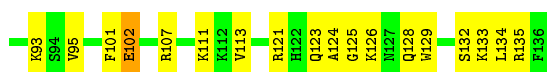
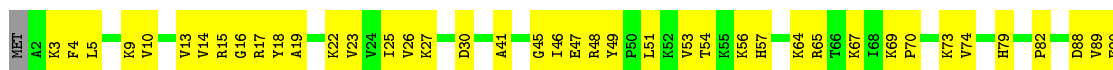
- Molecule 26: 60S ribosomal protein L26-A

Chain Y: 72% 26% ..



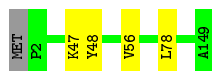
- Molecule 27: 60S ribosomal protein L27-A

Chain Z: 56% 43% ..



- Molecule 28: 60S ribosomal protein L28

Chain a: 97% ..



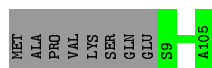
- Molecule 29: 60S ribosomal protein L29

Chain b: 98% .



- Molecule 30: 60S ribosomal protein L30

Chain c: 92% 8% .



- Molecule 31: 60S ribosomal protein L31-A

Chain d: 95% ..



- Molecule 32: 60S ribosomal protein L32

Chain e: 96% ..



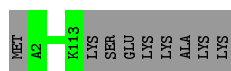
- Molecule 33: 60S ribosomal protein L33-A

Chain f: 99%



- Molecule 34: 60S ribosomal protein L34-A

Chain g: 93% 7%



- Molecule 35: 60S ribosomal protein L35-A

Chain h: 97% ..



- Molecule 36: 60S ribosomal protein L36-A

Chain i: 97% ..



- Molecule 37: 60S ribosomal protein L37-A

Chain j: 99%



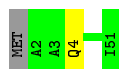
- Molecule 38: 60S ribosomal protein L38

Chain k: 99%




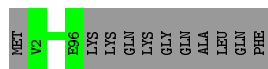
- Molecule 39: 60S ribosomal protein L39

Chain l: 96% ..



- Molecule 40: 60S ribosomal protein L42-A

Chain o:  90% 10%



- Molecule 41: 60S ribosomal protein L43-A

Chain p:  99% .



- Molecule 42: 60S ribosomal export protein NMD3

Chain w:  96% .



- Molecule 43: Eukaryotic translation initiation factor 6

Chain y:  99% .



- Molecule 44: Cytoplasmic 60S subunit biogenesis factor REH1

Chain z:  96% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	84240	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z > 2	RMSZ	# Z > 2
1	1	0.88	0/74017	0.89	34/115398 (0.0%)
10	G	0.43	0/1836	0.59	0/2481
11	H	0.40	0/1539	0.57	0/2073
12	J	0.34	0/1374	0.55	0/1842
13	L	0.44	0/1568	0.63	0/2106
14	M	0.43	0/1068	0.55	0/1438
15	N	0.52	0/1757	0.63	0/2354
16	O	0.51	1/1585 (0.1%)	0.58	0/2128
17	P	0.48	0/1465	0.61	0/1968
18	Q	0.44	0/1465	0.62	0/1965
19	R	0.42	0/1275	0.57	1/1702 (0.1%)
2	3	0.73	0/2883	0.83	0/4491
20	S	0.48	0/1481	0.57	0/1990
21	T	0.44	0/1300	0.56	0/1743
22	U	0.40	0/812	0.58	0/1099
23	V	0.46	0/1018	0.64	0/1369
24	W	0.44	0/540	0.56	0/717
25	X	0.46	0/979	0.61	0/1321
26	Y	0.42	0/1004	0.62	1/1341 (0.1%)
27	Z	0.46	0/1118	0.60	0/1497
28	a	0.46	0/1204	0.63	0/1612
29	b	0.35	0/473	0.50	0/629
3	4	0.94	0/3746	0.86	0/5832
30	c	0.46	0/751	0.53	0/1008
31	d	0.47	0/890	0.55	0/1196
32	e	0.45	0/1041	0.58	0/1394
33	f	0.52	0/868	0.56	0/1168
34	g	0.48	0/890	0.57	0/1189
35	h	0.40	0/978	0.55	1/1301 (0.1%)
36	i	0.40	0/778	0.61	0/1034
37	j	0.48	0/696	0.62	0/923
38	k	0.38	0/618	0.58	0/826
39	l	0.47	0/443	0.58	0/588
4	A	0.50	0/1908	0.61	0/2564

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	o	0.46	0/777	0.61	0/1028
41	p	0.53	0/701	0.58	0/934
42	w	0.51	2/1931 (0.1%)	0.64	2/2629 (0.1%)
43	y	0.38	0/1720	0.56	0/2341
44	z	0.37	0/472	0.56	0/626
5	B	0.52	0/3146	0.61	0/4228
6	C	0.46	0/2800	0.61	0/3790
7	D	0.39	0/2425	0.55	0/3271
8	E	0.41	0/1260	0.57	0/1694
9	F	0.46	0/1821	0.57	0/2451
All	All	0.74	3/132421 (0.0%)	0.79	39/195279 (0.0%)

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	G	0	1
11	H	0	1
12	J	0	1
13	L	0	1
14	M	0	1
16	O	0	2
17	P	0	1
20	S	0	2
22	U	0	1
27	Z	0	1
31	d	0	1
32	e	0	1
35	h	0	1
39	l	0	1
42	w	0	1
43	y	0	1
5	B	0	2
7	D	0	1
All	All	0	21

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	w	186	ASP	C-N	11.11	1.59	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	w	165	VAL	C-N	7.19	1.48	1.34
16	O	74	ARG	C-N	-5.12	1.22	1.34

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2572	C	N1-C2-O2	8.73	124.14	118.90
42	w	165	VAL	O-C-N	8.29	136.85	121.10
1	1	2572	C	C2-N1-C1'	7.83	127.42	118.80
1	1	1269	U	C2-N1-C1'	7.74	126.99	117.70
26	Y	126	LEU	CA-CB-CG	6.84	131.03	115.30

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	B	385	LYS	Peptide
5	B	81	THR	Peptide
7	D	58	LYS	Peptide
10	G	30	THR	Peptide
11	H	49	ASN	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	66124	0	33228	1119	0
2	3	2579	0	1304	72	0
3	4	3353	0	1695	47	0
4	A	1874	0	1943	73	0
5	B	3075	0	3142	128	0
6	C	2748	0	2859	112	0
7	D	2375	0	2325	103	0
8	E	1239	0	1326	57	0
9	F	1784	0	1862	60	0
10	G	1804	0	1877	60	0
11	H	1518	0	1587	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	J	1353	0	1383	60	0
13	L	1543	0	1608	58	0
14	M	1053	0	1149	45	0
15	N	1720	0	1779	85	0
16	O	1555	0	1659	38	0
17	P	1442	0	1485	44	0
18	Q	1441	0	1543	59	0
19	R	1258	0	1342	47	0
20	S	1445	0	1487	61	0
21	T	1276	0	1323	45	0
22	U	796	0	812	13	0
23	V	1003	0	1048	31	0
24	W	528	0	558	19	0
25	X	964	0	1025	27	0
26	Y	993	0	1081	27	0
27	Z	1092	0	1155	51	0
28	a	1173	0	1215	0	0
29	b	462	0	491	0	0
30	c	743	0	797	0	0
31	d	876	0	912	0	0
32	e	1020	0	1090	0	0
33	f	850	0	880	0	0
34	g	880	0	945	0	0
35	h	969	0	1078	0	0
36	i	771	0	849	0	0
37	j	681	0	687	0	0
38	k	612	0	682	0	0
39	l	436	0	475	0	0
40	o	765	0	827	0	0
41	p	694	0	738	0	0
42	w	1894	0	1846	0	0
43	y	1699	0	1680	0	0
44	z	469	0	492	0	0
All	All	122929	0	89269	2151	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 14.

The worst 5 of 2151 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)
1:1:3151:U:OP2	5:B:132:LYS:NZ	1.71	1.22
1:1:912:G:OP2	4:A:9:ARG:NH1	1.74	1.20
1:1:1724:U:OP2	19:R:128:LYS:NZ	1.78	1.16
1:1:1135:A:OP2	5:B:5:LYS:NZ	51.85	1.15
1:1:2436:U:H2'	1:1:2437:G:H5''	1.26	1.14

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	
4	A	244/246 (99%)	236 (97%)	8 (3%)	0	100	100
5	B	384/387 (99%)	357 (93%)	25 (6%)	2 (0%)	34	72
6	C	359/361 (99%)	329 (92%)	29 (8%)	1 (0%)	46	80
7	D	294/297 (99%)	267 (91%)	24 (8%)	3 (1%)	19	58
8	E	152/176 (86%)	143 (94%)	6 (4%)	3 (2%)	9	38
9	F	220/244 (90%)	205 (93%)	15 (7%)	0	100	100
10	G	231/256 (90%)	208 (90%)	20 (9%)	3 (1%)	15	50
11	H	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	34	72
12	J	167/174 (96%)	144 (86%)	18 (11%)	5 (3%)	5	28
13	L	191/199 (96%)	172 (90%)	16 (8%)	3 (2%)	12	44
14	M	134/138 (97%)	123 (92%)	9 (7%)	2 (2%)	13	47
15	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	19	58
16	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
17	P	181/184 (98%)	178 (98%)	3 (2%)	0	100	100
18	Q	183/186 (98%)	172 (94%)	11 (6%)	0	100	100
19	R	154/189 (82%)	147 (96%)	6 (4%)	1 (1%)	30	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	S	170/172 (99%)	157 (92%)	10 (6%)	3 (2%)	11	42
21	T	157/160 (98%)	148 (94%)	8 (5%)	1 (1%)	30	68
22	U	98/121 (81%)	86 (88%)	11 (11%)	1 (1%)	19	58
23	V	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
24	W	62/155 (40%)	60 (97%)	2 (3%)	0	100	100
25	X	119/142 (84%)	113 (95%)	6 (5%)	0	100	100
26	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
27	Z	133/136 (98%)	124 (93%)	6 (4%)	3 (2%)	8	35
28	a	146/149 (98%)	131 (90%)	11 (8%)	4 (3%)	6	31
29	b	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
30	c	95/105 (90%)	92 (97%)	3 (3%)	0	100	100
31	d	107/113 (95%)	101 (94%)	4 (4%)	2 (2%)	10	40
32	e	125/130 (96%)	117 (94%)	7 (6%)	1 (1%)	24	63
33	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
34	g	110/121 (91%)	105 (96%)	5 (4%)	0	100	100
35	h	117/120 (98%)	110 (94%)	6 (5%)	1 (1%)	21	61
36	i	97/100 (97%)	82 (84%)	13 (13%)	2 (2%)	9	37
37	j	85/88 (97%)	77 (91%)	8 (9%)	0	100	100
38	k	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
39	l	48/51 (94%)	43 (90%)	5 (10%)	0	100	100
40	o	93/106 (88%)	84 (90%)	9 (10%)	0	100	100
41	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
42	w	246/248 (99%)	220 (89%)	19 (8%)	7 (3%)	6	30
43	y	225/227 (99%)	220 (98%)	4 (2%)	1 (0%)	39	75
44	z	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	4	24
All	All	6348/6731 (94%)	5900 (93%)	394 (6%)	54 (1%)	26	61

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	98	VAL
10	G	36	ILE
28	a	78	LEU

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Mol	Chain	Res	Type
32	e	123	LYS
42	w	328	ILE

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	
4	A	189/189 (100%)	189 (100%)	0	100	100
5	B	318/323 (98%)	317 (100%)	1 (0%)	94	97
6	C	288/288 (100%)	287 (100%)	1 (0%)	94	97
7	D	244/245 (100%)	244 (100%)	0	100	100
8	E	134/153 (88%)	134 (100%)	0	100	100
9	F	186/205 (91%)	186 (100%)	0	100	100
10	G	187/208 (90%)	186 (100%)	1 (0%)	92	96
11	H	171/171 (100%)	171 (100%)	0	100	100
12	J	147/150 (98%)	147 (100%)	0	100	100
13	L	154/159 (97%)	153 (99%)	1 (1%)	90	96
14	M	107/109 (98%)	107 (100%)	0	100	100
15	N	175/176 (99%)	175 (100%)	0	100	100
16	O	160/162 (99%)	160 (100%)	0	100	100
17	P	145/146 (99%)	145 (100%)	0	100	100
18	Q	150/151 (99%)	150 (100%)	0	100	100
19	R	129/154 (84%)	129 (100%)	0	100	100
20	S	156/156 (100%)	156 (100%)	0	100	100
21	T	136/137 (99%)	136 (100%)	0	100	100
22	U	87/107 (81%)	87 (100%)	0	100	100
23	V	104/105 (99%)	104 (100%)	0	100	100
24	W	56/129 (43%)	56 (100%)	0	100	100
25	X	104/118 (88%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	Y	109/110 (99%)	109 (100%)	0	100	100
27	Z	115/116 (99%)	115 (100%)	0	100	100
28	a	118/119 (99%)	118 (100%)	0	100	100
29	b	46/47 (98%)	46 (100%)	0	100	100
30	c	81/88 (92%)	81 (100%)	0	100	100
31	d	92/97 (95%)	92 (100%)	0	100	100
32	e	109/111 (98%)	109 (100%)	0	100	100
33	f	90/91 (99%)	90 (100%)	0	100	100
34	g	95/103 (92%)	95 (100%)	0	100	100
35	h	104/105 (99%)	104 (100%)	0	100	100
36	i	81/82 (99%)	81 (100%)	0	100	100
37	j	70/71 (99%)	70 (100%)	0	100	100
38	k	68/69 (99%)	68 (100%)	0	100	100
39	l	45/46 (98%)	45 (100%)	0	100	100
40	o	82/91 (90%)	82 (100%)	0	100	100
41	p	71/72 (99%)	71 (100%)	0	100	100
42	w	205/221 (93%)	203 (99%)	2 (1%)	82	93
43	y	189/194 (97%)	189 (100%)	0	100	100
44	z	51/51 (100%)	51 (100%)	0	100	100
All	All	5348/5625 (95%)	5342 (100%)	6 (0%)	95	98

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	G	26	LEU
42	w	330	ARG
13	L	24	VAL
6	C	194	TYR
42	w	328	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
20	S	154	HIS

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Mol	Chain	Res	Type
26	Y	4	GLN
43	y	86	ASN
21	T	58	GLN
23	V	98	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3086/3396 (90%)	747 (24%)	47 (1%)
2	3	120/121 (99%)	20 (16%)	1 (0%)
3	4	157/158 (99%)	39 (24%)	2 (1%)
All	All	3363/3675 (91%)	806 (23%)	50 (1%)

5 of 806 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	6	A
1	1	14	U
1	1	22	G
1	1	24	G

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1607	U
1	1	2209	U
1	1	3353	G
1	1	1815	U
1	1	2101	C

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.