



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jun 5, 2017 – 06:53 PM EDT

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
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029077

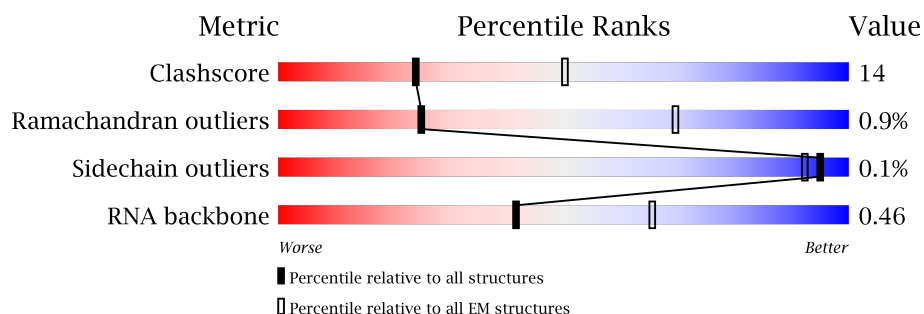
1 Overall quality at a glance

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.






















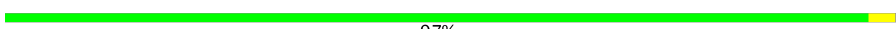
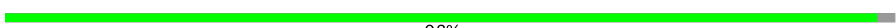

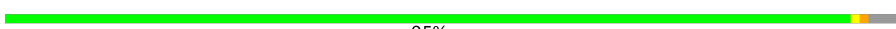
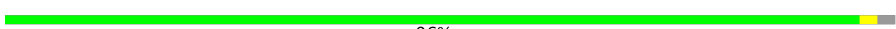

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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

Mol	Chain	Length	Quality of chain
1	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		

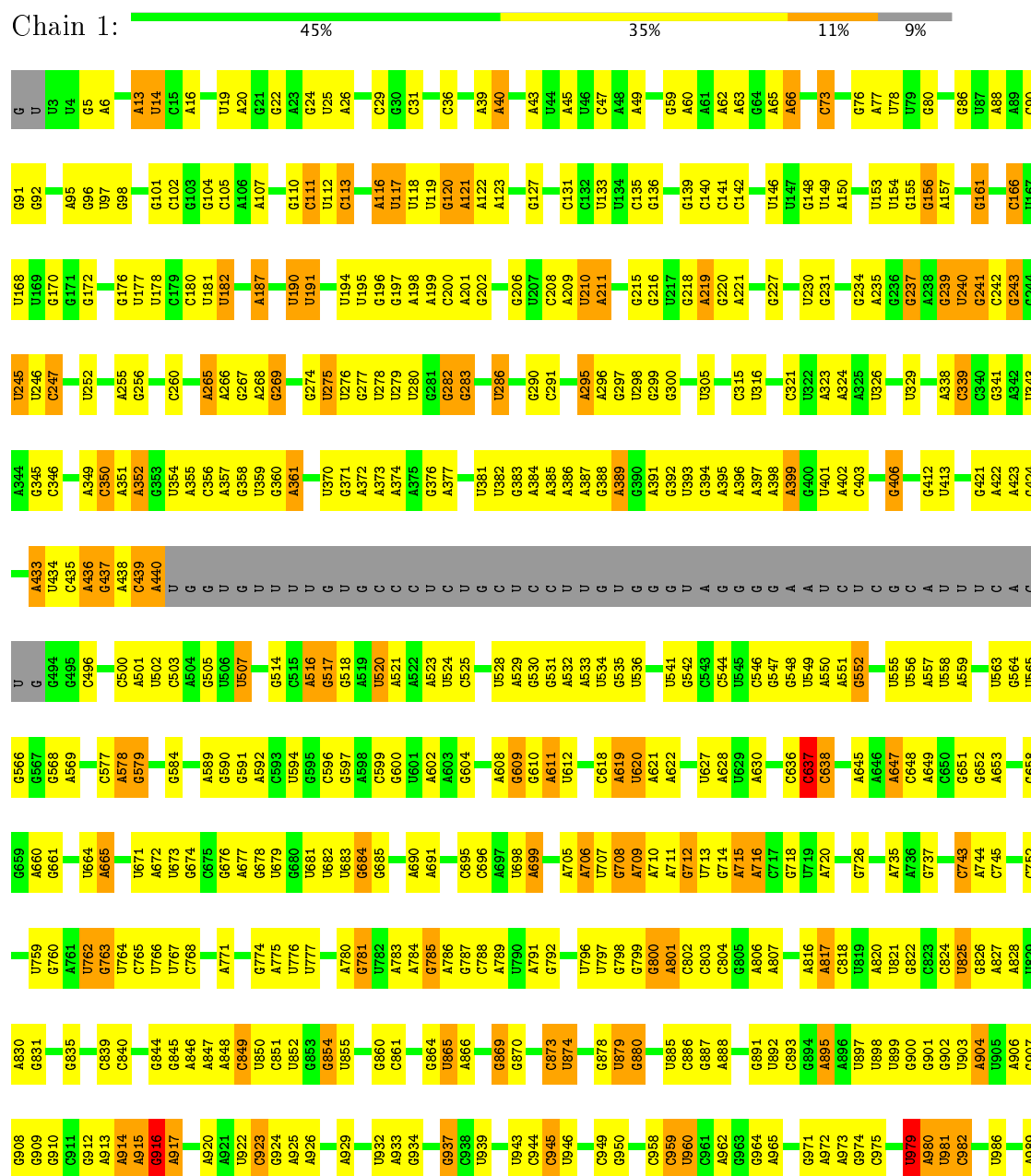
- Molecule 44 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

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

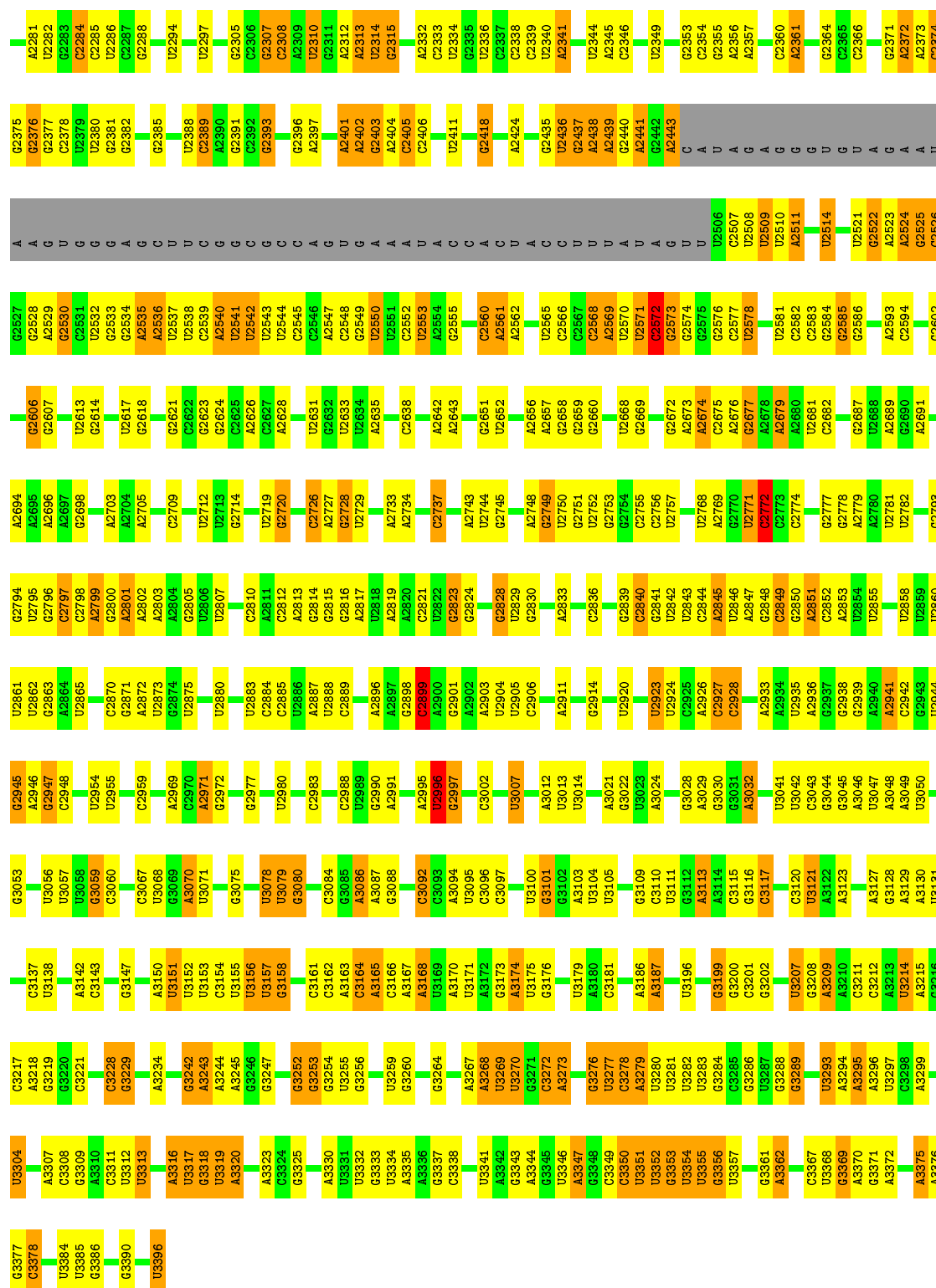
3 Residue-property plots [i](#)

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.

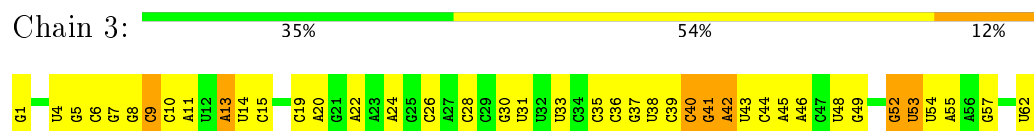
• Molecule 1: 25S ribosomal RNA

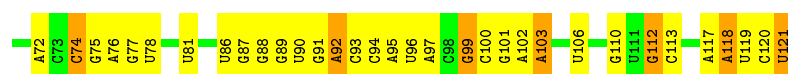


C2192	U2109	G	A1910	U1820	U1724	C1628	U1553	G1466	U1356	A1278	G1213	A1129	U1051	U990
U2193	G2110	U	G1914	U1821	C1725	U1629	U1554	A1466	G1357	C1279	U2144	A1130	U1052	G991
G2194	G2111	A	G1915	G1830	U1732	U1630	U1555	A1467	C1358	G1280	U2145	G1131		A992
C2195	U2112	G	A1916	U1831	U1737	A1631	A1557	A1468	C1359	G1281	C1216		A1055	G993
G2196	A2113	C	U1917	U1832	U1738	A1632		U1469	G1362	G1282	U2117	G1134	U1056	G994
C2197	C2114	U	U1920	A1835	C1738	G1635	G1560	U1470	A1363	C1283	U2118	A1135	U1057	
U2205	G2115	G				U1636	G1561	U1471		C1284	C1219			A997
G2206	A2116	G				U1637	U1562	U1472		G1285	U2220	A1143	U1060	A998
A2207	G2117	C	C1926	G1838	A1741	A1637	G1563	G1473	A1366	A1286	A1221	U1144	A1061	C
C2208	C2118	C	G1927	A1839	U1742	U1638	U1564	A1474	G1367	A1287	G1222	G1145	A1062	G
U2209	A2119	U	G1928	U1840	C1743	C1639	U1565	A1475	U1368	U1288	A1223	G1146	G1063	A
G2210	G2120	U	G1929	A1841	A1749	G1640	G1565	G1476		G1289	G1224	G1147	A1064	A
	A2121	U	A1930	A1842	U1750	U1641	A1566	A1477	G1380		A1225	G1148	A1065	A
G2122	C2122	G	U1931		G1751	A1642	U1567		A1381	C1292	G1226	G1149		U
G2123	G2123	U	C1932	C1846	C1759	G1643	U1568	G1480	G1382	U1293		A1150	C1069	G
U2214	A2124	A	A1933	A1847	U1760	G1646	U1569	A1481	G1383	A1294	C1228	U1151	A1061	C
A2215		G	G1934	G1848	C1761	A1647	U1570	A1482	U1384	G1295	G1230	G1152	U1071	U
G2216	A2131	U	G1935	C1849	C1762	A1648	A1571	G1483	C1385		A1231	A1153	G1072	U
		U		A1850	U1772	G1662	U1572	U1484	A1386	A1302		A1154	U1073	A
G2134		C	G1940		U1763	U1649		G1485		A1303	C1232	C1155	U1074	G
		U		C1854	U1764		A1575		A1390	A1304		C1156	U1075	A
U2137		G	A1946	A1858	C1657	C1658	G1576	G1488	C1391	U1305	U1235	C1157	U1078	G
U2224		C	G1947	A1859	U1658	U1659	G1577	A1489	G1392	G1306	G1236	A1158	U1079	G
U2225		U	G1948	G1860	U1659	C1660	C1578		A1393	G1307	G1237	A1159	A1080	U
C2226	U2140	G	G1949	U1861	G1769	G1661	C1579	G1493	A1394	A1308	C1238		A1081	U
A2228	A2141	C	U1950	G1862	G1770	G1662	A1580	U1494	G1395	U1309	C1239	G1166	U1082	C
U2229	C2143	A	C1951	G1863	U1771	G1663	C1581	U1495		G1310	U1241	U1167	U1083	G
A2144	A2145	G	G1952	G1864	C1772		A1583		A1399	G1242	U1242	U1168	G1084	C
C2237	C2146	C	G1953	A1865	G1775	G1666		G1500	G1400	G1313	G1243	A1169		G
		U					G1586	A1503	G1404	C1316	A1244	C1175	G1087	G
U2241	A2147	C	U1955	A1866	G1778	U1672	A1587	A1504		A1317	A1245	C1176		U
	U2148	U	A	G1867	C1779	G1672	A1588		A1407	A1318	G1246	G1177	G1090	C
A2244	G2150	G	G	G1868	G1780	G1677	A1589	C1508		G1321	U1247	A1178		G
G2249		C	U	U1871	G1784	A1679	G1590	U1511	G1417	U1322	G1249	A1179	A1093	A
G2250	G2155	C	A	C1872	U1785	G1680			A1419	G1250	G1250	U1181	U1095	A
G2251		U	G	U1873			A1593		G1420	A1326	A1251	A1182	U1096	U
A2252	C2163	U	G	A1874					G1421	C1327	U1253		G1097	G
G2253		C			C1792	A1683	C1596	U1522		G1328		G1186	A1098	A
U2254	A2166	G	C	U1880	C1793	U1687	A1602	U1523	U1427	U1329	C1257	C1187	A1099	C
A2255	G2167	C	C	A1881	G1794	U1688	A1603	U1526		A1330	U1258	U1100	G1101	U
A2256	A2168	U	U	U	U1795	U1689	G1604	C1527	A1433	U1331	A1259	A1102	A1103	U
C2257	G2169	C	G	A1884	G1796	U1689	A1605		G1434	A1332	A1260	U1191	A1104	G
U2258	U2170	A	U	U1885	A1797	C1693	U1606	C1531	A1435	C1333	A1261	C1192	G1103	A
A2259	G2171	A	G	A1886	U1801	U1694	U1607	C1532	C1437	U1334	G1262	A1193	G1104	C
U2260	A2172	U	C	A1887	C1802	U1695	C1608	U1533	U1438		A1263	A1195	G1106	C
G2261		U	U	U1890	A1806	U1702	C1609	A1534		A1337	G1264	C1196	C1107	U
A2262	U2175	A	G	A1891	G1807	U1703	G1610	A1535	U1445	C1342	U1265	A1200	U1108	A
	G2176	C	C			A1704	G1611		A1446	A1343	G1266	G1201	U1109	U
C2265	G2177	G	A	A1895	A1810	U1705	G1617	G1541	G1447			C1201	U1110	U
U2266	A2178	U	G			G1705	G1618	G1542	U1448	U1348	U1269	A1202	U1111	C
C2267	G2180	C	C	G1899	A1813	C1709	A1619	G1543	A1449	G1349	A1270	A1203	A1112	U
U2269		C	A	A1900	C1710	C1710	U1620	G1547	G1450	A1350	A1271			C
G2185	U2186	U	G	A1901	U1815	A1621	A1621	C1548	C1451	U1351	C1272	U1208	G1117	A
A2270		U	U	G1902	A1816	U1817	U1817	U1549	A1452	A1352	A1273	G1209		A
C2271	G2187	U	G		G1817	U1721	U1818	C1550	A1453	U1353	A1274	U1210	U1125	A
G2272	A2188	G	G	G1906	U1722	U1722	U1818	C1551	A1454	G1354	C1275	U1211	G1126	C
G2273	U2189	U	U		U1819	A1723	U1626	G1552	U1455	A1355		A1212		U
A2275		C	C	A1909										

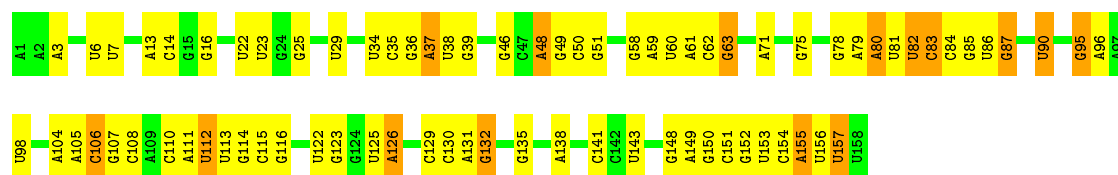


• Molecule 2: 5S ribosomal RNA

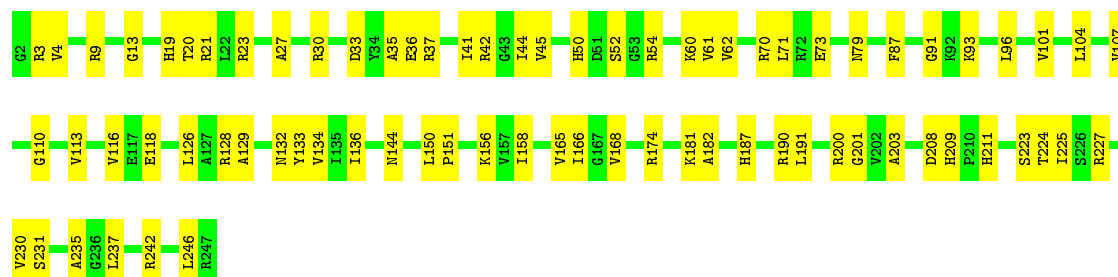




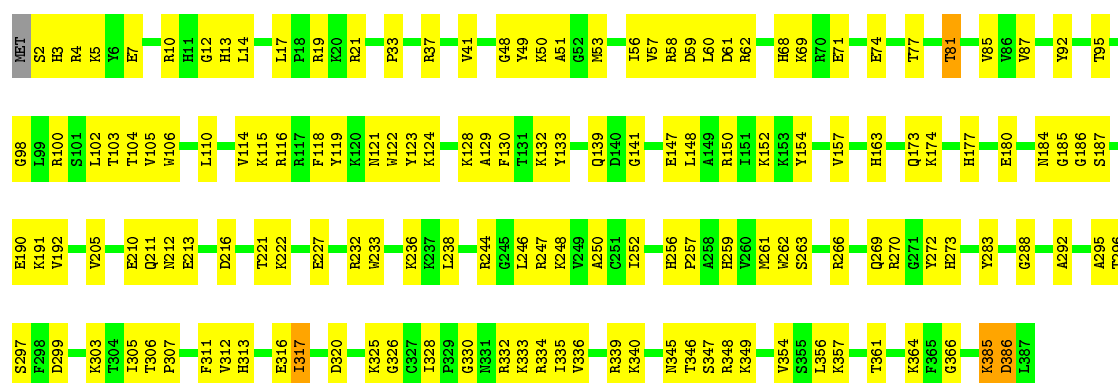
• Molecule 3: 5.8S ribosomal RNA



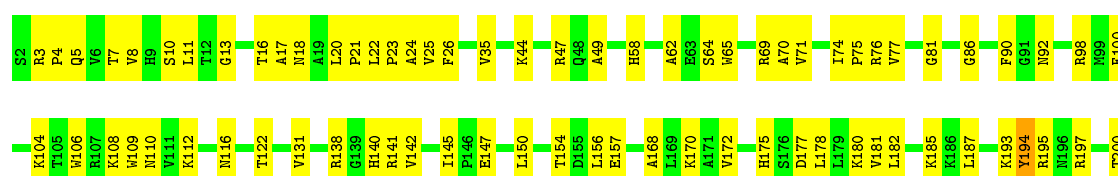
• Molecule 4: 60S ribosomal protein L2-A

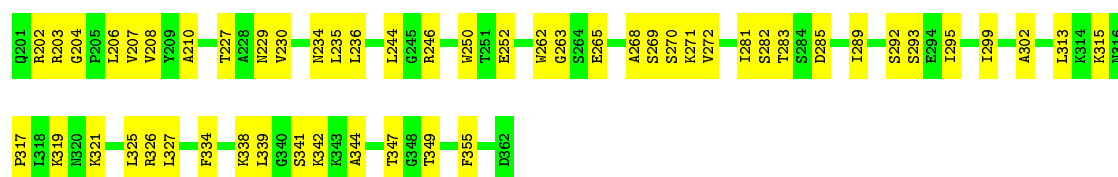


• Molecule 5: 60S ribosomal protein L3



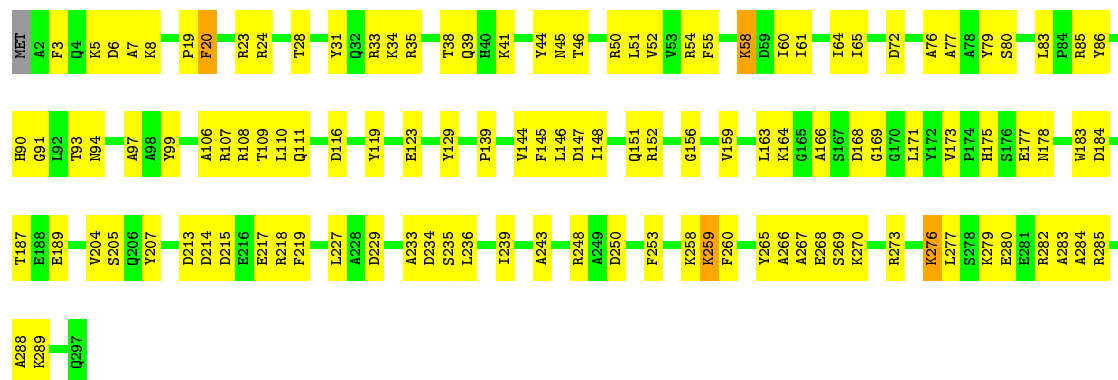
• Molecule 6: 60S ribosomal protein L4-A





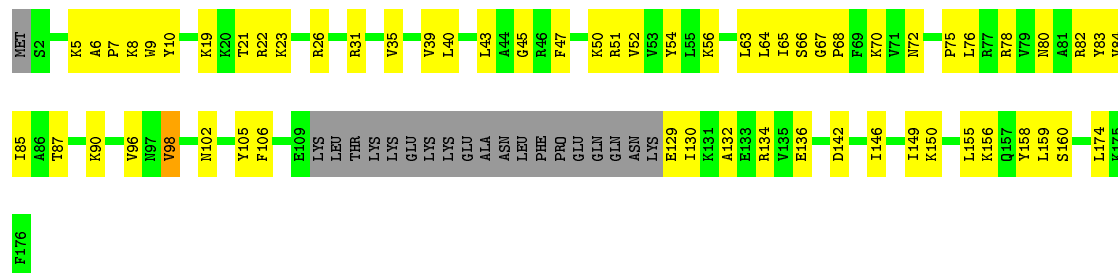
- Molecule 7: 60S ribosomal protein L5

Chain D: 60% 38%



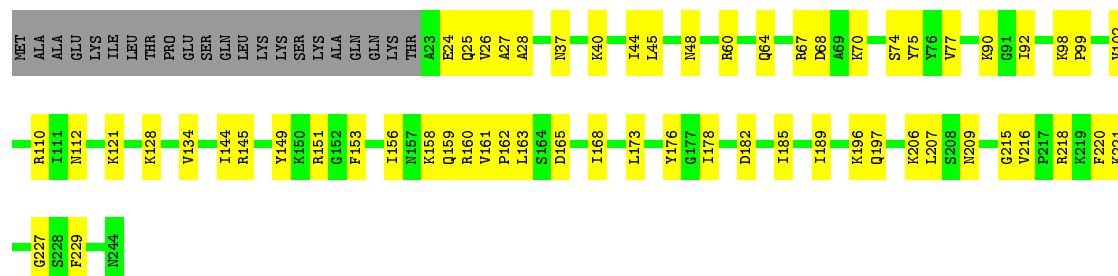
- Molecule 8: 60S ribosomal protein L6-A

Chain E:  54% 34% 11%



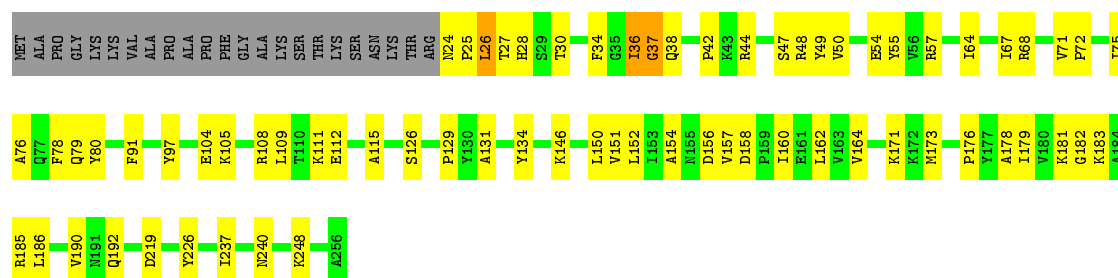
- Molecule 9: 60S ribosomal protein L7-A

Chain F:  66% 25% 9%



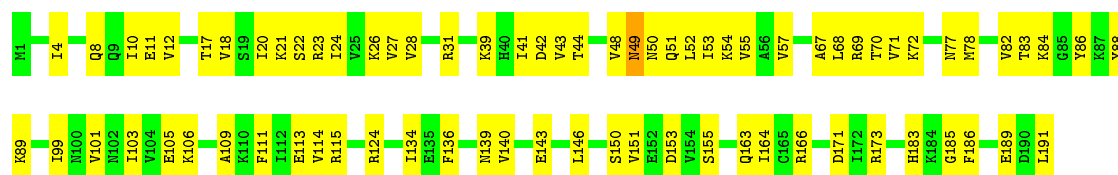
- Molecule 10: 60S ribosomal protein L8-A

Chain G: 64% 26% 9%



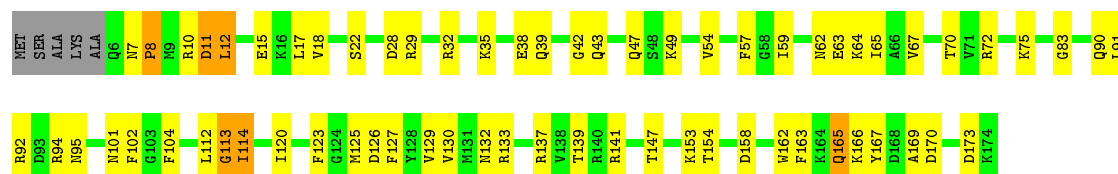
- Molecule 11: 60S ribosomal protein L9-A

Chain H: 61% 39%



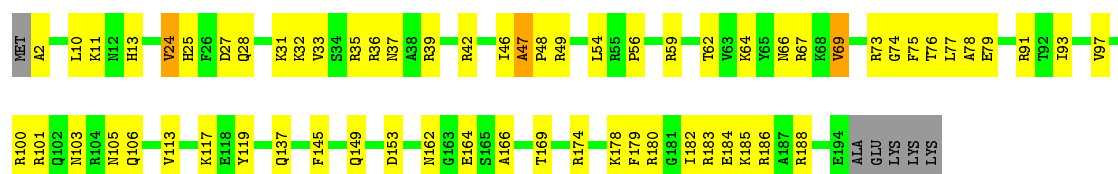
- Molecule 12: 60S ribosomal protein L11-A

Chain J: 59% 34%



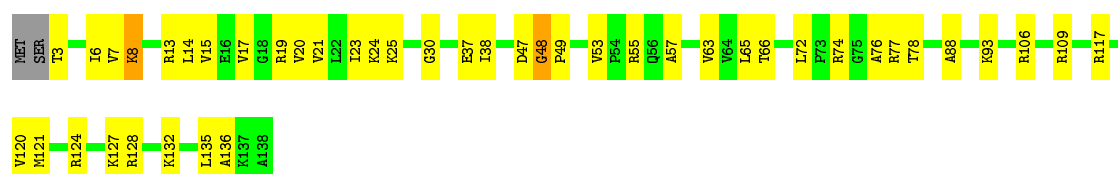
- Molecule 13: 60S ribosomal protein L13-A

Chain L: 65% 31%

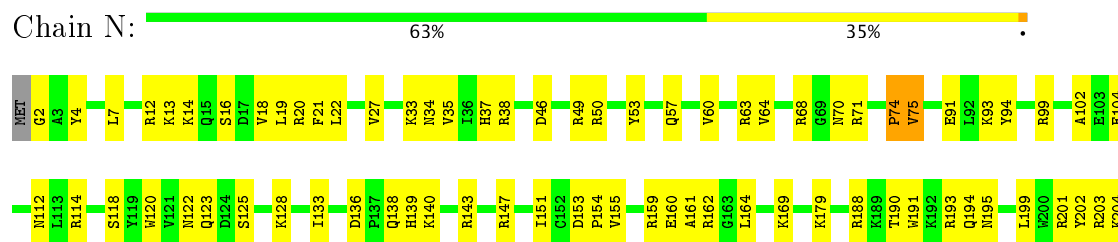


- Molecule 14: 60S ribosomal protein L14-A

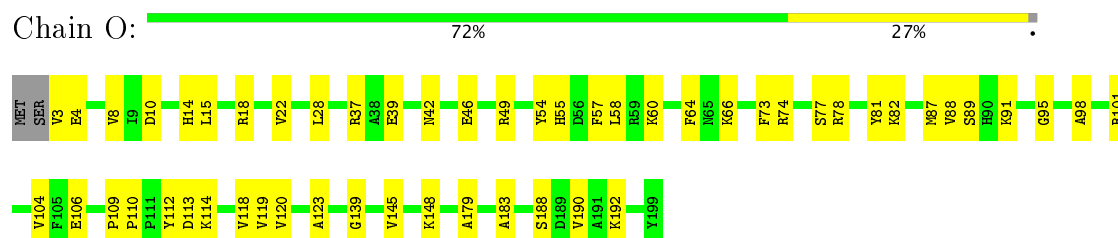
Chain M: 67% 30%



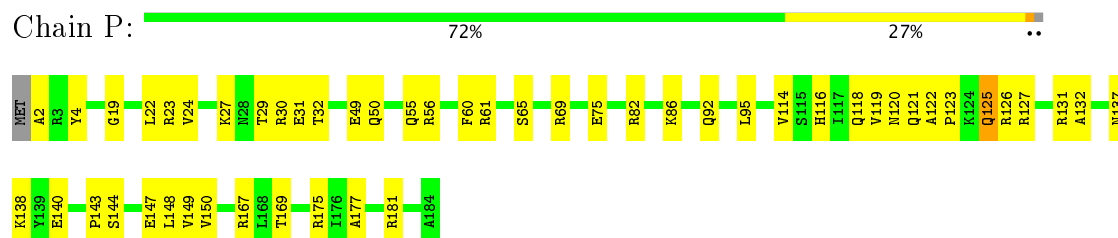
- Molecule 15: 60S ribosomal protein L15-A



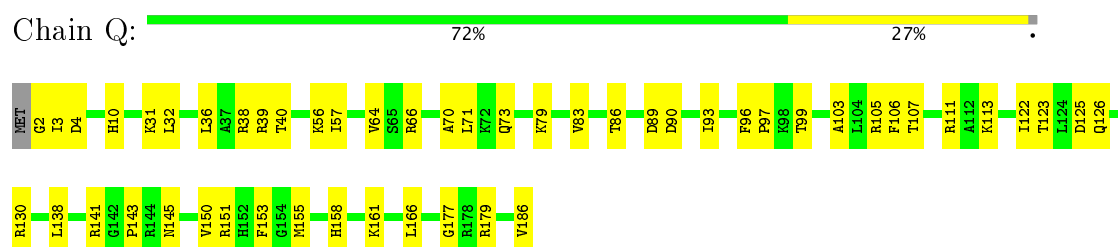
- Molecule 16: 60S ribosomal protein L16-A



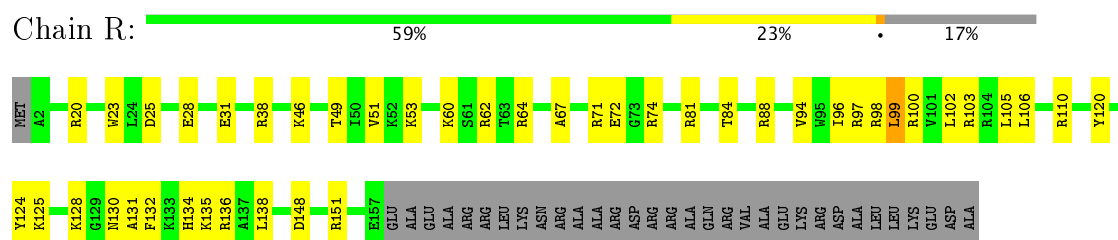
- Molecule 17: 60S ribosomal protein L17-A



- Molecule 18: 60S ribosomal protein L18-A

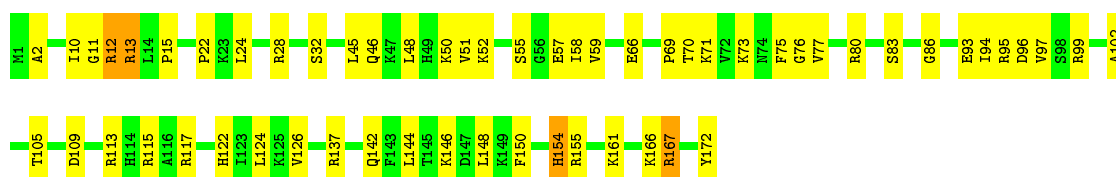


- Molecule 19: 60S ribosomal protein L19-A



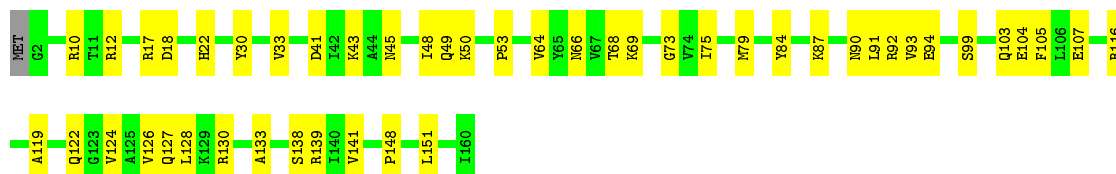
- Molecule 20: 60S ribosomal protein L20-A





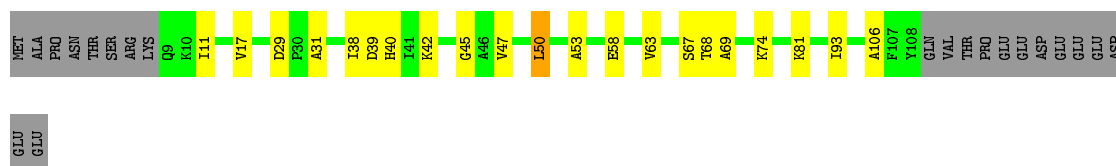
• Molecule 21: 60S ribosomal protein L21-A

Chain T: 70% 29%



• Molecule 22: 60S ribosomal protein L22-A

Chain U: 65% 17% 17%



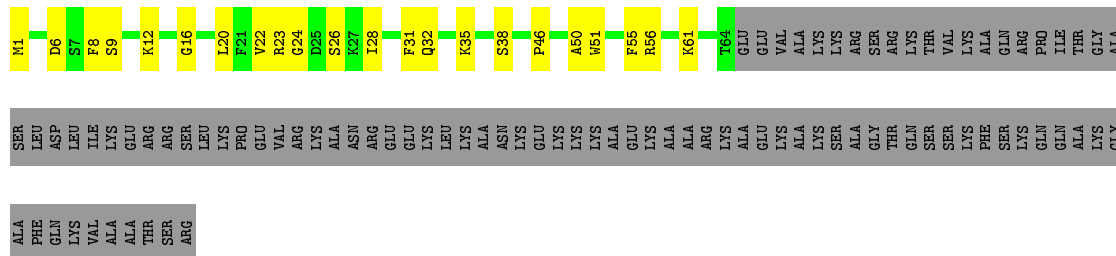
• Molecule 23: 60S ribosomal protein L23-A

Chain V: 74% 26%



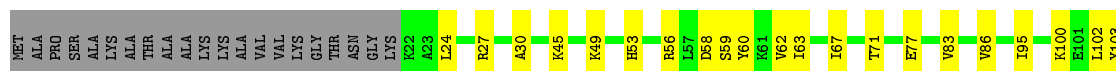
• Molecule 24: 60S ribosomal protein L24-A

Chain W: 27% 14% 59%



• Molecule 25: 60S ribosomal protein L25

Chain X: 63% 22% 15%





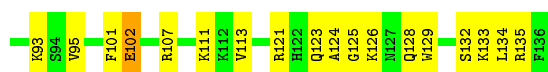
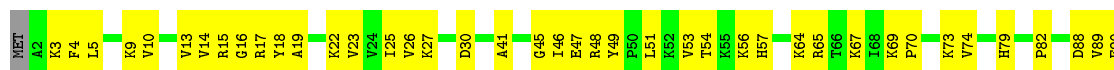
- Molecule 26: 60S ribosomal protein L26-A

Chain Y: 72% 26% ..



- Molecule 27: 60S ribosomal protein L27-A

Chain Z: 56% 43% ..



- Molecule 28: 60S ribosomal protein L28

Chain a: 97% ..



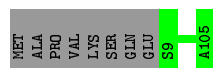
- Molecule 29: 60S ribosomal protein L29

Chain b: 98% .



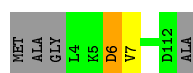
- Molecule 30: 60S ribosomal protein L30

Chain c: 92% 8%



- Molecule 31: 60S ribosomal protein L31-A

Chain d: 95% ..



- Molecule 32: 60S ribosomal protein L32

Chain e: 96% ..



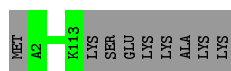
- Molecule 33: 60S ribosomal protein L33-A

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%



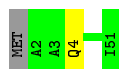
- Molecule 38: 60S ribosomal protein L38

Chain k: 99%




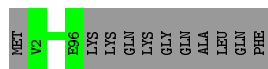
- Molecule 39: 60S ribosomal protein L39

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% .

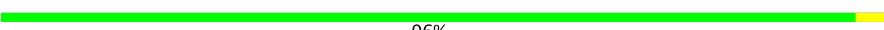


- Molecule 43: Eukaryotic translation initiation factor 6

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%)	32	70
6	C	359/361 (99%)	329 (92%)	29 (8%)	1 (0%)	44	78
7	D	294/297 (99%)	267 (91%)	24 (8%)	3 (1%)	18	55
8	E	152/176 (86%)	143 (94%)	6 (4%)	3 (2%)	9	35
9	F	220/244 (90%)	205 (93%)	15 (7%)	0	100	100
10	G	231/256 (90%)	208 (90%)	20 (9%)	3 (1%)	14	47
11	H	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	32	70
12	J	167/174 (96%)	144 (86%)	18 (11%)	5 (3%)	5	26
13	L	191/199 (96%)	172 (90%)	16 (8%)	3 (2%)	11	42
14	M	134/138 (97%)	123 (92%)	9 (7%)	2 (2%)	12	44
15	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	18	55
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%)	28	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	S	170/172 (99%)	157 (92%)	10 (6%)	3 (2%)	10	39
21	T	157/160 (98%)	148 (94%)	8 (5%)	1 (1%)	28	66
22	U	98/121 (81%)	86 (88%)	11 (11%)	1 (1%)	18	55
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%)	7	32
28	a	146/149 (98%)	131 (90%)	11 (8%)	4 (3%)	6	28
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%)	9	37
32	e	125/130 (96%)	117 (94%)	7 (6%)	1 (1%)	22	60
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%)	20	58
36	i	97/100 (97%)	82 (84%)	13 (13%)	2 (2%)	8	34
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	28
43	y	225/227 (99%)	220 (98%)	4 (2%)	1 (0%)	38	73
44	z	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	4	22
All	All	6348/6731 (94%)	5900 (93%)	394 (6%)	54 (1%)	25	58

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%)	91	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%)	89	95
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%)	80	92
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.