



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:32 PM BST

PDB ID : 3J7Q  
EMDB ID: : EMD-2650  
Title : Structure of the idle mammalian ribosome-Sec61 complex  
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.  
Deposited on : 2014-08-01  
Resolution : 3.50 Å(reported)  
Based on PDB ID : 3J3B, 3J3F

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
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>

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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) : trunk27241

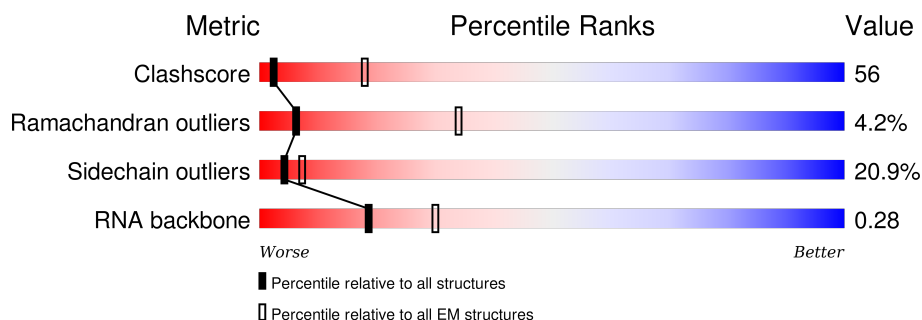
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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.









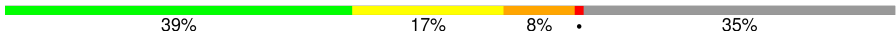





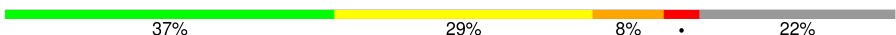












Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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  $\geq 3$ , 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	5	3722	8% 43% 34% 12% •
2	7	120	18% 56% 21% 5%
3	8	156	7% 53% 26% 13%
4	A	257	50% 28% 12% 6% 5%
5	B	394	48% 34% 13% 5%
6	C	367	55% 31% 11% •
7	D	297	46% 35% 12% 5% •
8	E	236	47% 27% 19% 7%

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Mol	Chain	Length	Quality of chain
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	L	211	
15	M	213	
16	N	204	
17	O	204	
18	P	153	
19	Q	188	
20	R	196	
21	S	224	
22	T	160	
23	U	128	
24	V	140	
25	W	157	
26	X	156	
27	Y	145	
28	Z	136	
29	a	148	
30	b	160	
31	c	115	
32	d	125	
33	e	135	

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Mol	Chain	Length	Quality of chain
34	f	110	 78%15%5% ..
35	g	117	 77%19% ..
36	h	123	 80%12%6% ..
37	i	105	 76%17% ..
38	j	86	 73%21%6%
39	k	70	 71%27% ..
40	l	51	 76%20% ..
41	m	128	 31%8%59% .
42	n	25	 72%20%8%
43	o	106	 69%23%6% ..
44	p	91	 82%15% ..
45	r	125	 73%23% ..
46	1	476	 60%19%18% .
47	2	68	 71%18%9% .
48	3	36	 94%6%

## 2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 140540 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 5 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 6 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 7 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 8 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 9 is a protein called Ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

- Molecule 11 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 13 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 14 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 15 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 16 is a protein called Ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 18 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 20 is a protein called Ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 21 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 22 is a protein called Ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 24 is a protein called Ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called Ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 27 is a protein called Ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called Ribosomal protein eL27.



Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 30 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 32 is a protein called Ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called Ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called Ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 37 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 39 is a protein called Ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 43 is a protein called Ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 44 is a protein called Ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 46 is a protein called Sec61 alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1	392	Total	C	N	O	S	0	0
			3051	2007	493	532	19		

- Molecule 47 is a protein called Sec61 gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 48 is a protein called Sec61 beta subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	3	36	Total	C	N	O	0	0
			180	108	36	36		

- Molecule 49 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
49	8	4	Total 4	Mg 4	0
49	7	5	Total 5	Mg 5	0
49	P	1	Total 1	Mg 1	0
49	V	1	Total 1	Mg 1	0
49	5	119	Total 119	Mg 119	0

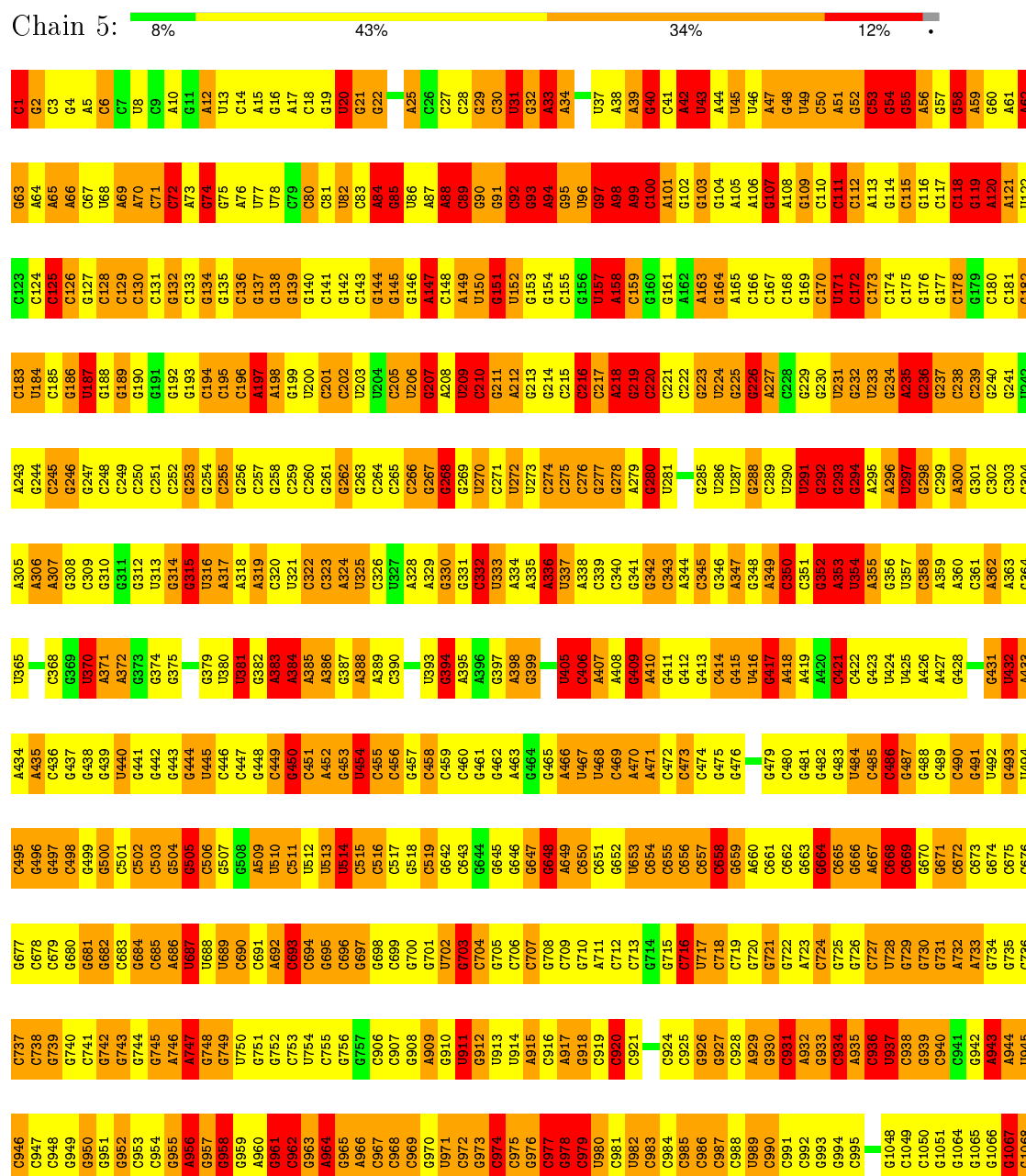
- Molecule 50 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
50	o	1	Total 1	Zn 1	0
50	j	1	Total 1	Zn 1	0
50	m	1	Total 1	Zn 1	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 errors 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: 28S ribosomal RNA

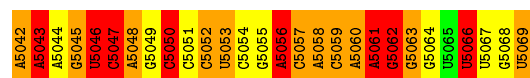


U2080	A2017	A1956	C1894	G1833	C1772	C1692	A1632	G1570	G1506	U1465	G1385	C1325	C1264	G1195	G1069
C2081	C2018	U1959	G1895	U1834	U1773	U1693	G1633	G1571	C1507	C1446	C1386	A1326	G1265	G1196	G1070
G2082	C2019	U1959	A1896	G1835	C1774	C1694	A1634	U1572	A1508	C1447	C1387	C1327	G1266	C1197	C1071
C2083	U2020	A1960	A1897	G1836	A1775	U1695	G1635	U1573	C1509	G1448	A1388	G1328	C1267	G1198	C1072
G2084	G2021	U1961	G1898	A1837	A1776	C1696	U1636	U1574	G1510	C1449	G1389	G1329	G1268	G1199	G1073
G2085	C2022	A1962	G1899	A1838	C1777	G1697	A1637	U1575	U1511	C1450	G1390	A1330	G1269	G1200	G1074
G2086	G2023	C1983	C1900	U1839	C1778	C1698	A1638	U1576	G1512	G1451	A1391	C1331	A1270	U1201	G1075
C2087	A2024	A1964	C1901	G1840	U1779	A1699	U1639	G1577	U1513	A1452	A1392	C1332	G1271	C1202	C1076
C2088	A2025	G1965	G1902	C	C1718	C1718	G1640	U1578	U1514	G1453	C1393	A1333	C1272	G1203	C1077
G2089	U2026	C1966	G1903	G1842	U1780	C1719	A1641	C1579	U1515	G1454	G1394	A1334	G1273	C1204	A1078
U2090	U2027	A1967	U1781	A1843	U1782	A1720	A1642	C1580	G1516	G1455	U1395	A1335	A1274	G1205	A1079
C2091	U2028	G1968	C1783	G1844	U1783	G1721	A1643	G1581	G1517	C1456	G1396	G1336	G1275	C1206	G1080
G2092	U2029	A1969	U1784	U1845	U1784	C1722	C1644	U1582	A1518	G1457	A1397	A1337	C1276	C1207	C1081
A2093	A2033	A1970	C1785	G1846	C1785	A1723	C1645	A1583	C1519	C1458	A1398	G1338	G1277	G1208	C1082
G2094	G2034	G1971	A1786	C1847	G1724	U1725	A1646	C1584	C1520	A1459	G1399	A1339	C1278	U1209	U1083
A2095	C2035	G1972	A1787	G1848	U1726	U1726	U1647	C1585	C1521	C1460	G1400	C1340	A1279	C1210	C1084
G2096	C2036	G1973	U1788	U1849	C1648	U1648	G1649	G1586	A1522	C1461	C1401	U1341	G1280	C1211	C1085
U2097	U2037	U1974	C1789	A1850	U1727	U1727	U1649	G1587	A1523	C1462	C1402	A1342	G1281	G1212	C1086
G2098	U2038	G1975	G1851	G1851	U1728	U1728	A1650	U1588	A1524	C1463	G1403	A1343	G1282	G1213	A1087
G2099	G2039	G1976	U1791	U1852	U1729	U1730	G1651	C1589	A1525	C1464	G1404	C1344	G1283	C1214	C1088
A2100	A2040	U1977	U1792	G1853	U1731	U1731	G1652	C1590	U1526	C1465	G1405	A1345	G1284	C1215	C1089
C2101	A2041	C1978	A1794	G1854	G1733	G1733	A1653	U1591	U1528	C1466	C1406	C1346	U1285	C1216	C1090
G2102	A2042	A1979	A1795	G1855	G1734	G1734	G1654	A1599	G1529	C1467	G1407	G1347	C1286	G1217	C1091
G2103	A2043	U1980	U1796	C1856	U1735	U1735	G1655	G1594	G1530	C1468	G1408	C1348	G1287	G1218	G1092
G2104	U2044	G1981	G1797	C1857	U1736	U1736	U1656	G1595	G1531	C1469	G1409	G1349	G1288	G1219	C1093
A2105	G2045	G1982	G1798	A1858	A1736	A1736	G1657	U1596	A1534	U1471	U1410	C1350	C1289	G1220	G1094
G2106	G2046	A1983	G1922	C1859	U1737	U1737	G1658	U1597	C1535	C1472	C1411	G1351	G1290	G1221	A1095
A2107	A2047	U1984	A1923	U1860	G1739	G1739	U1659	C1598	U1538	C1473	G1412	C1352	G1291	A1222	C1096
G2108	U2048	G1985	C1924	U1861	C1740	C1740	G1660	A1599	G1539	C1474	C1413	G1353	C1292	G1232	C1097
G2109	G2049	U1986	G1925	C1856	G1741	G1741	C1661	A1600	C1540	G1475	C1414	A1354	G1293	G1233	G1098
G2110	U2050	C1987	C1926	G1864	A1742	A1742	C1662	A1601	C1541	C1476	G1415	G1355	A1294	G1234	C1099
G2111	C2051	G1988	U1927	G1865	A1743	A1743	C1663	U1602	C1542	C1477	G1416	U1356	C1295	G1235	U1100
C2112	G2052	G1989	C1928	U1866	U1744	U1744	C1664	C1603	U1543	C1478	C1417	C1357	C1296	G1236	C1167
G2113	C2053	A1990	A1929	A1867	G1745	G1745	C1665	G1479	G1544	C1480	G1418	G1358	C1297	C1237	G1168
G2114	U2054	A1991	U1930	C1868	A1746	A1746	C1666	G1544	G1544	G1481	G1419	G1359	C1298	A1238	G1169
G2115	G2055	U1992	C1931	G1869	U1747	U1747	G1667	G1545	C1545	C1482	A1420	G1360	G1299	C1239	G1170
C2116	G2056	C1993	A1932	C1870	U1748	U1748	A1668	C1546	G1546	G1483	G1421	G1361	G1300	G1240	G1171
G2117	A2057	C1994	G1933	A1871	A1749	A1749	A1669	U1609	A1547	C1483	G1422	G1362	C1301	G1241	C1172
G2118	G2058	G1995	A1934	C1872	G1750	G1750	G1670	C1610	G1548	C1484	U1423	C1363	U1302	G1242	G1173
C2119	C2059	C1996	C1935	A1873	A1751	A1751	U1671	C1611	G1549	C1485	G1424	U1364	A1303	G1243	G1174
G2120	G2060	U1997	G1936	A1874	G1752	G1752	U1672	C1612	C1550	C1486	G1425	C1365	A1304	G1244	A1175
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G2122	C2062	A1999	G1938	U1876	G1754	G1754	C1674	C1614	G1552	G1488	A1427	C1367	C1306	G1246	U1177
G2123	G2063	G2000	A1939	G1877	C1755	C1755	C1675	C1615	A1553	G1489	U1428	A1368	A1307	U1247	U1178
C2124	G2064	G2001	G1940	C1878	U1756	U1756	C1676	U1616	A1554	G1490	C1429	A1369	C1308	U1248	U1179
C2125	G2065	A2002	A1941	C1879	U1757	U1757	U1677	G1617	G1555	A1491	C1430	G1370	C1309	C1249	C1180
G2126	C2066	G2003	A1942	G1880	G1758	G1758	C1678	C1618	C1556	G1492	C1431	A1371	C1310	C1250	C1181
C2127	C2067	U2004	A1943	C1881	G1759	G1759	A1679	C1619	C1557	U1493	G1432	A1372	C1311	C1251	C1182
G2128	C2068	G2005	A1944	U1882	G1760	G1760	G1680	U1620	A1558	U1494	A1433	A1373	A1312	C1252	C1183
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C2131	A2071	U2008	U1947	G1885	G1763	G1763	U1683	A1623	G1561	A1497	C1436	C1376	C1315	A1255	U1186
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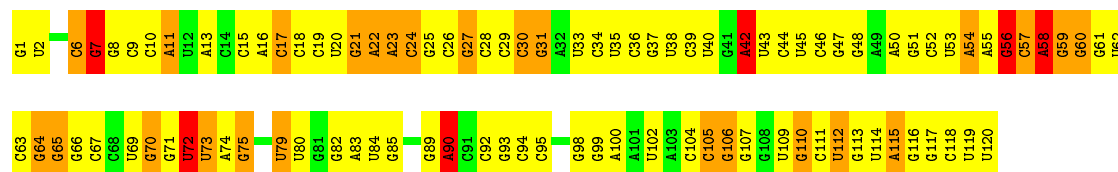




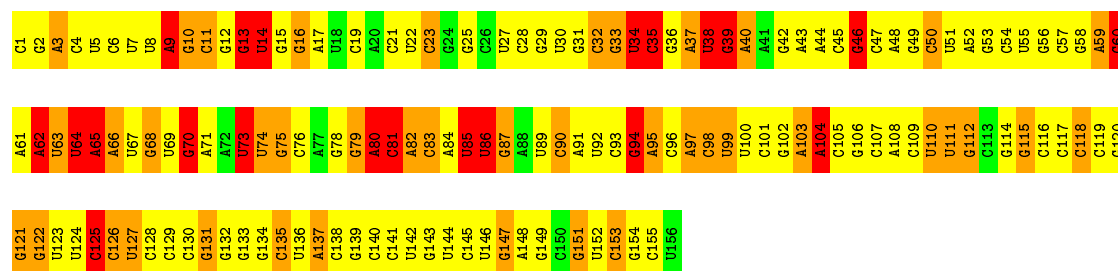
- Molecule 2: 5S ribosomal RNA

Chain 7: 18% 56% 21% 5%



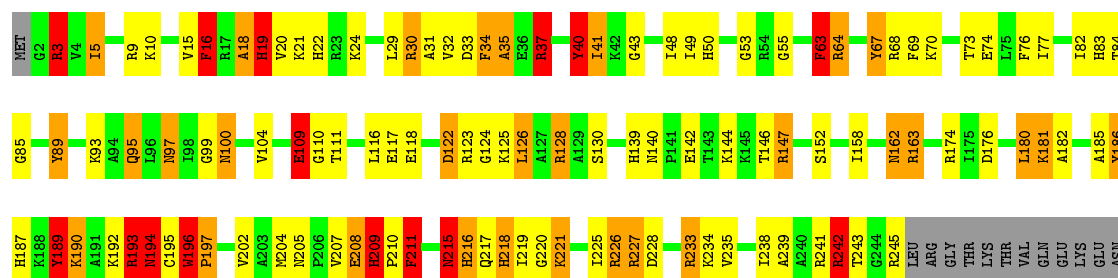
- Molecule 3: 5.8S ribosomal RNA

Chain 8: 7% 53% 26% 13%



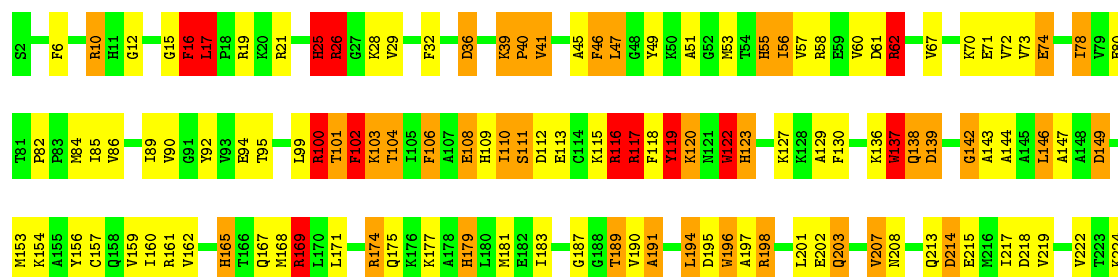
- Molecule 4: Ribosomal protein uL2

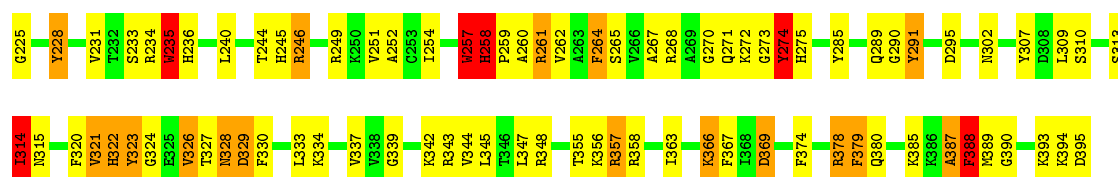
Chain A: 50% 28% 12% 6% 5%



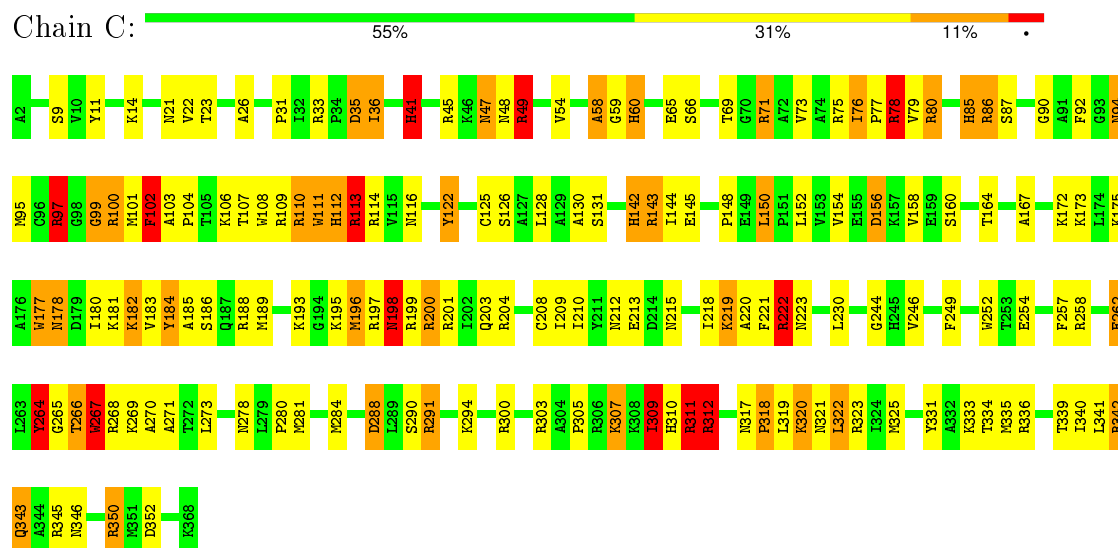
- Molecule 5: Ribosomal protein uL3

Chain B: 48% 34% 13% 5%

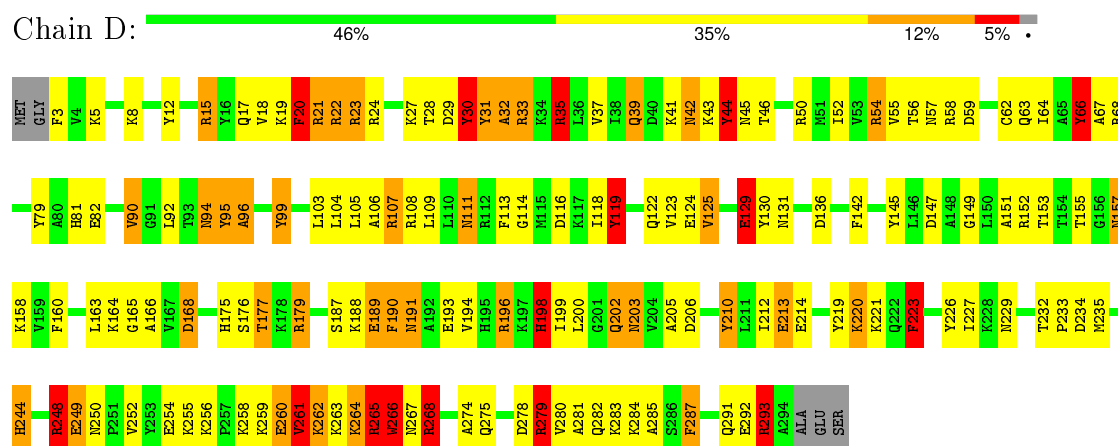




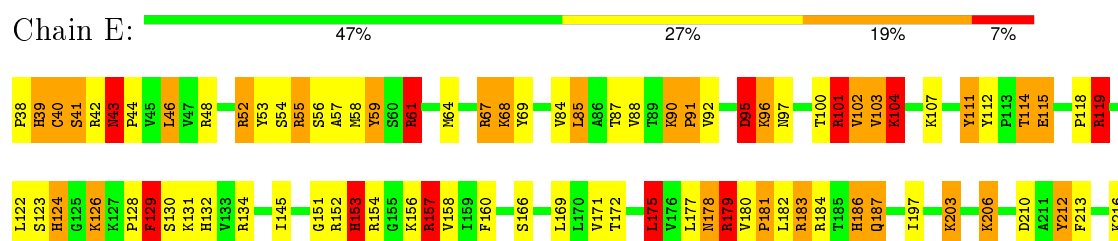
• Molecule 6: Ribosomal protein uL4



• Molecule 7: Ribosomal protein uL18



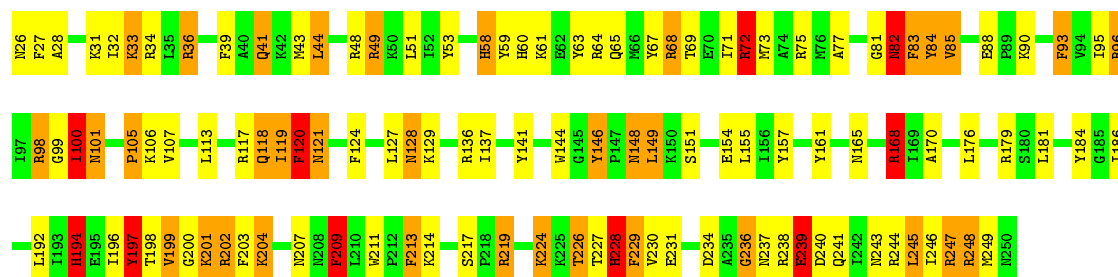
• Molecule 8: Ribosomal protein eL6





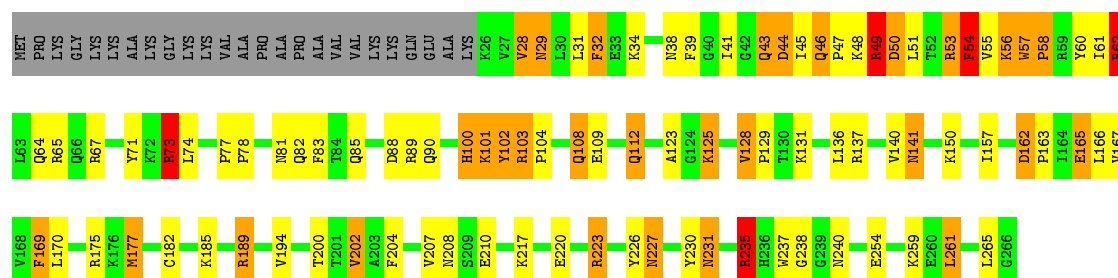
• Molecule 9: Ribosomal protein uL30

Chain F: 48% 32% 16%



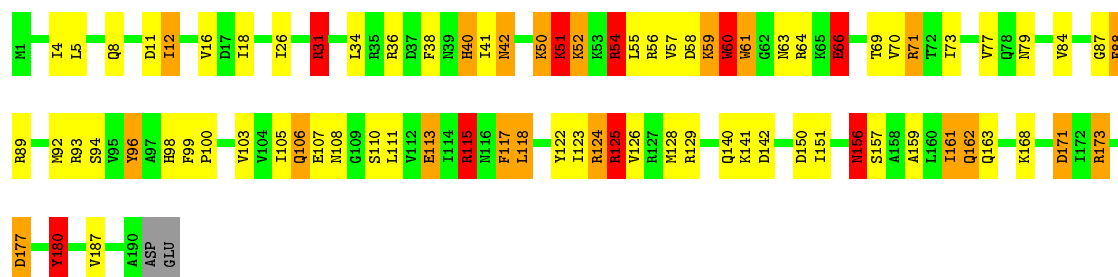
• Molecule 10: Ribosomal protein eL8

Chain G: 55% 22% 11% 9%



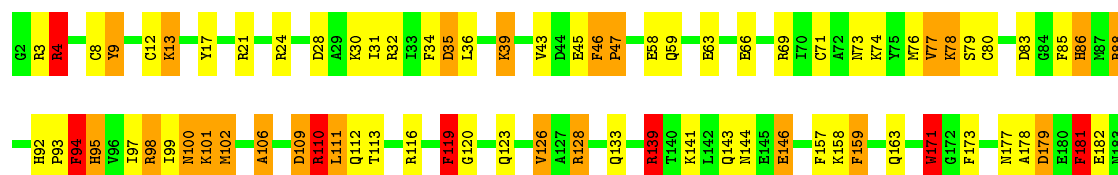
• Molecule 11: Ribosomal protein uL6

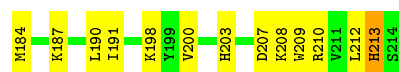
Chain H: 57% 27% 10% 5%



• Molecule 12: Ribosomal protein uL16

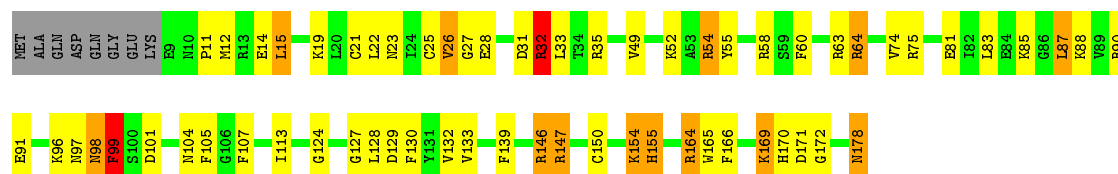
Chain I: 58% 28% 11%





• Molecule 13: Ribosomal protein uL5

Chain J: 60% 27% 7% . .



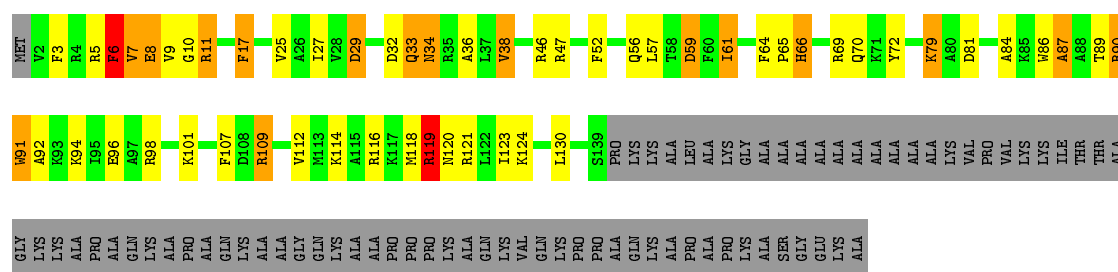
• Molecule 14: Ribosomal protein eL13

Chain L: 54% 33% 8% 5%



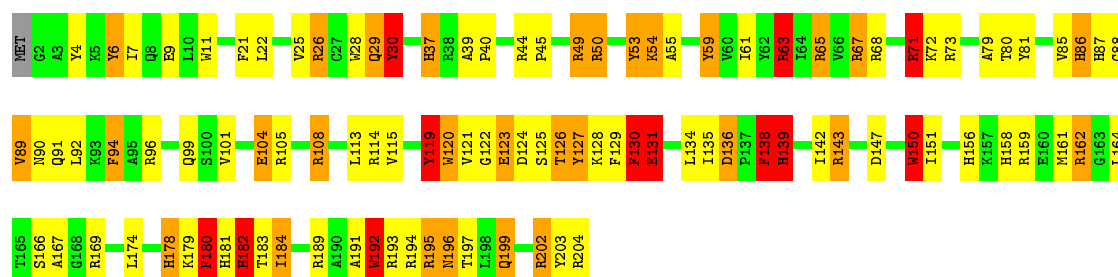
• Molecule 15: Ribosomal protein eL14

Chain M: 39% 17% 8% . 35%

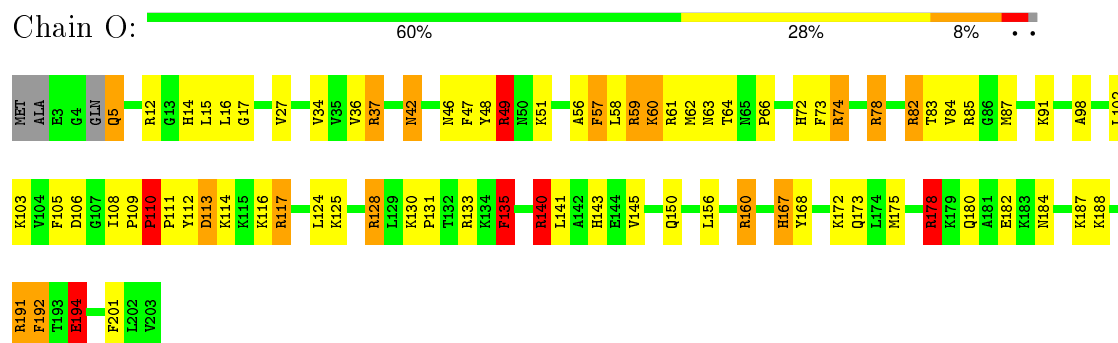


• Molecule 16: Ribosomal protein eL15

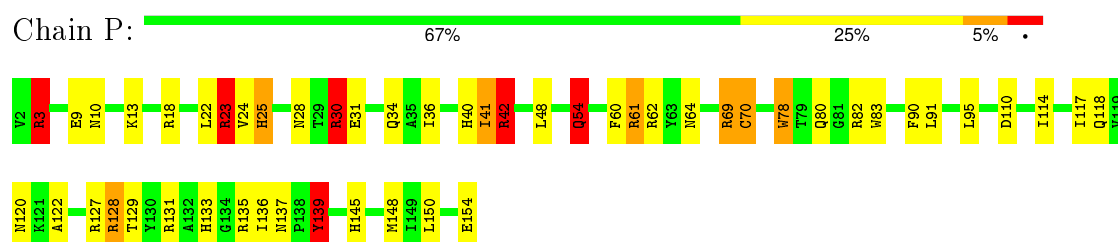
Chain N: 49% 31% 14% 6%



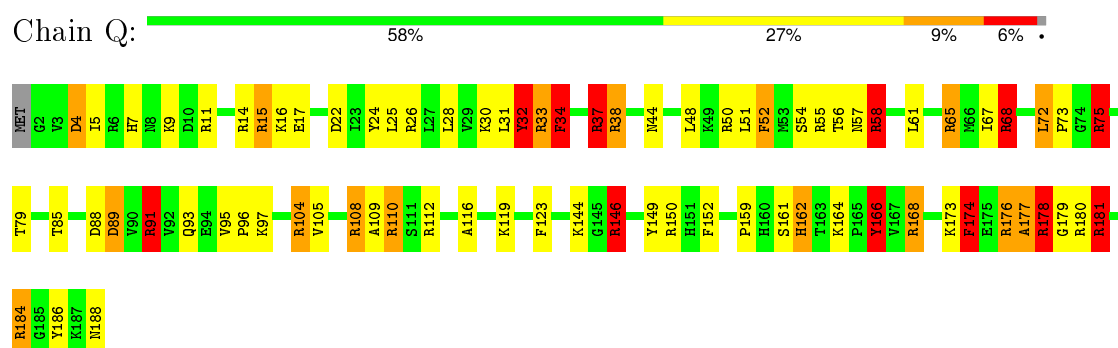
- Molecule 17: Ribosomal protein uL13



- Molecule 18: Ribosomal protein uL22



- Molecule 19: Ribosomal protein eL18



- Molecule 20: Ribosomal protein eL19

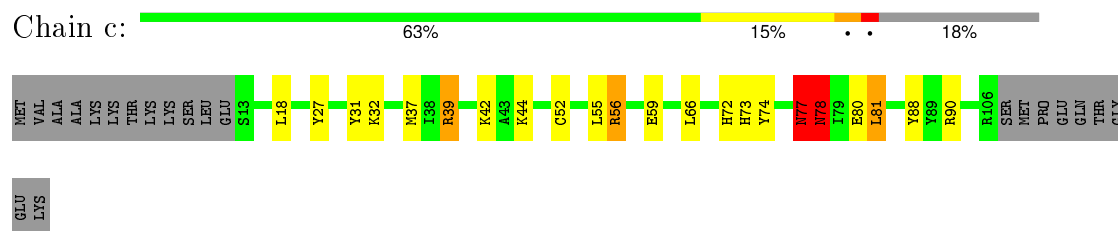


- Molecule 21: Ribosomal protein eL20

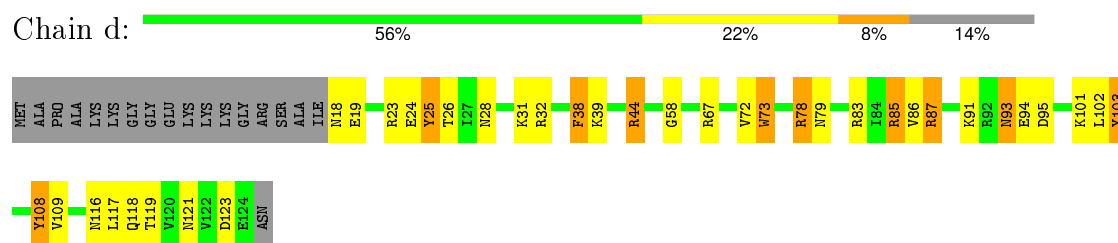




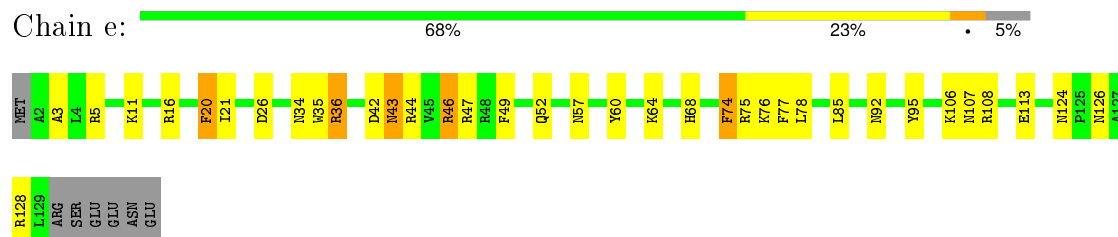
- Molecule 31: Ribosomal protein eL30



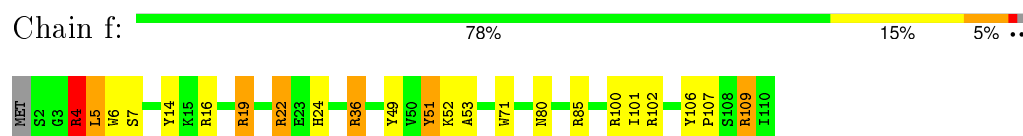
- Molecule 32: Ribosomal protein eL31



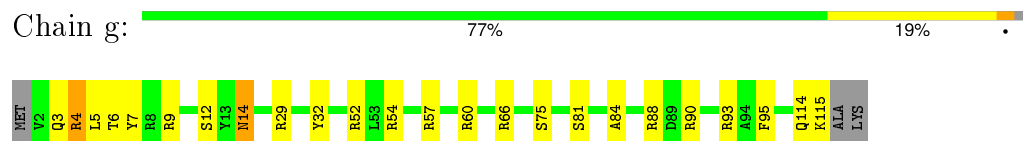
- Molecule 33: Ribosomal protein eL32



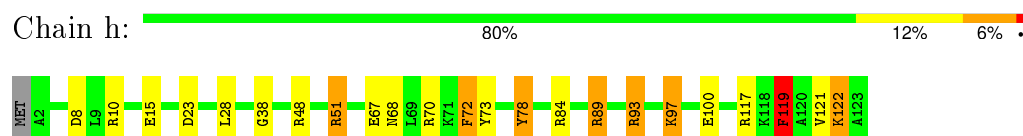
- Molecule 34: Ribosomal protein eL33



- Molecule 35: Ribosomal protein eL34



- Molecule 36: Ribosomal protein uL29



- Molecule 37: Ribosomal protein eL36

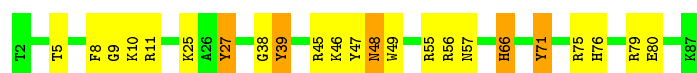


Chain i:  76% 17% . .



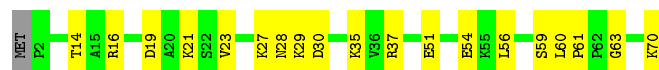
- Molecule 38: Ribosomal protein eL37

Chain j:  73% 21% 6%



- Molecule 39: Ribosomal protein eL38

Chain k:  71% 27% .



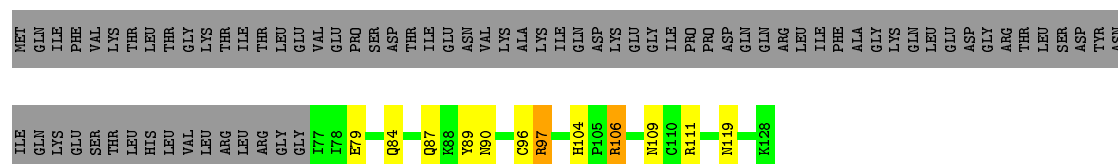
- Molecule 40: Ribosomal protein eL39

Chain l:  76% 20% . .



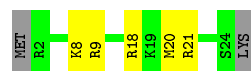
- Molecule 41: Ribosomal protein eL40

Chain m:  31% 8% 59%



- Molecule 42: Ribosomal protein eL41

Chain n:  72% 20% 8%




- Molecule 43: Ribosomal protein eL42

Chain o:  69% 23% 6% . .



- Molecule 44: Ribosomal protein eL43

Chain p:  82% 15%



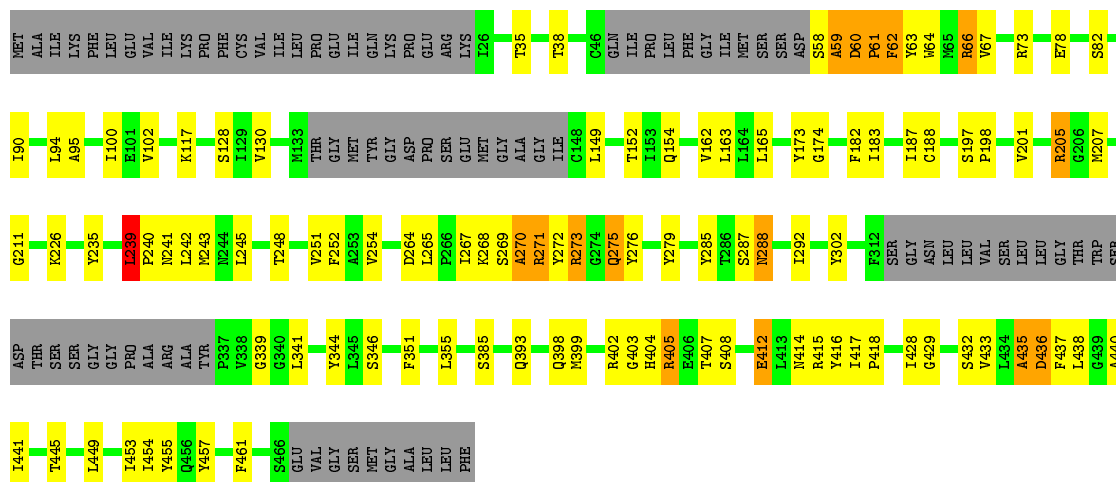
- Molecule 45: Ribosomal protein eL28

Chain r:  73% 23%



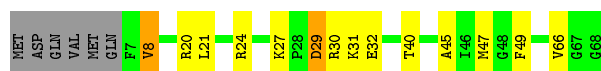
- Molecule 46: Sec61 alpha subunit

Chain 1:  60% 19% 18%



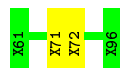
- Molecule 47: Sec61 gamma subunit

Chain 2:  71% 18% 9%



- Molecule 48: Sec61 beta subunit

Chain 3:  94% 6%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	80019	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	27	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	5	0.64	80/87792 (0.1%)	1.13	742/136945 (0.5%)
10	G	0.76	4/1966 (0.2%)	1.09	14/2645 (0.5%)
11	H	0.77	3/1537 (0.2%)	1.17	10/2066 (0.5%)
12	I	0.66	1/1753 (0.1%)	1.11	12/2343 (0.5%)
13	J	0.63	1/1382 (0.1%)	1.04	11/1849 (0.6%)
14	L	0.71	2/1734 (0.1%)	1.12	15/2318 (0.6%)
15	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
16	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
17	O	0.72	3/1684 (0.2%)	1.11	12/2251 (0.5%)
18	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
19	Q	0.69	0/1530	1.35	31/2041 (1.5%)
2	7	0.54	1/2858 (0.0%)	0.96	9/4455 (0.2%)
20	R	0.79	3/1524 (0.2%)	1.27	21/2013 (1.0%)
21	S	0.95	8/1493 (0.5%)	1.30	19/2002 (0.9%)
22	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
23	U	0.63	1/822 (0.1%)	1.03	2/1103 (0.2%)
24	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
25	W	0.71	0/541	1.23	5/720 (0.7%)
26	X	0.64	0/993	1.09	10/1334 (0.7%)
27	Y	0.72	0/1132	1.24	19/1504 (1.3%)
28	Z	0.63	0/1130	1.11	8/1507 (0.5%)
29	a	0.93	6/1192 (0.5%)	1.37	17/1591 (1.1%)
3	8	0.68	3/3701 (0.1%)	1.20	42/5766 (0.7%)
30	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
31	c	0.70	0/742	1.14	5/996 (0.5%)
32	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)
33	e	0.90	3/1071 (0.3%)	1.23	15/1429 (1.0%)
34	f	1.02	2/895 (0.2%)	1.34	17/1198 (1.4%)
35	g	0.65	0/916	1.08	5/1220 (0.4%)
36	h	0.63	0/1023	1.21	13/1350 (1.0%)
37	i	0.63	0/843	1.19	8/1115 (0.7%)
38	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	k	0.59	0/575	0.97	1/761 (0.1%)
4	A	0.80	3/1906 (0.2%)	1.26	21/2556 (0.8%)
40	l	0.68	0/454	1.07	3/599 (0.5%)
41	m	0.57	0/435	1.02	3/575 (0.5%)
42	n	0.48	0/223	1.02	0/284
43	o	0.64	0/864	1.27	9/1140 (0.8%)
44	p	0.64	1/718 (0.1%)	1.00	3/953 (0.3%)
45	r	0.68	0/1017	1.12	8/1365 (0.6%)
46	1	0.45	0/3114	0.63	0/4218
47	2	0.47	0/504	0.71	1/673 (0.1%)
5	B	0.81	8/3214 (0.2%)	1.16	26/4308 (0.6%)
6	C	0.73	4/2973 (0.1%)	1.12	18/3990 (0.5%)
7	D	0.73	2/2426 (0.1%)	1.23	27/3252 (0.8%)
8	E	0.73	5/1941 (0.3%)	1.21	20/2601 (0.8%)
9	F	0.80	2/1905 (0.1%)	1.27	26/2539 (1.0%)
All	All	0.68	165/151252 (0.1%)	1.14	1311/223243 (0.6%)

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
1	5	1	158
10	G	0	3
11	H	0	3
12	I	0	5
13	J	0	2
14	L	0	5
15	M	0	4
16	N	0	11
17	O	0	3
18	P	0	1
19	Q	0	5
2	7	0	2
20	R	0	6
21	S	0	11
22	T	0	2
23	U	0	2
24	V	0	3
25	W	0	1
26	X	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
27	Y	0	4
29	a	0	9
3	8	0	11
30	b	0	1
31	c	0	2
32	d	0	4
33	e	0	4
34	f	0	2
35	g	0	1
36	h	0	3
37	i	0	3
38	j	0	4
39	k	0	1
4	A	0	6
43	o	0	6
44	p	0	1
45	r	0	5
46	1	0	1
47	2	0	1
5	B	0	13
6	C	0	5
7	D	0	8
8	E	0	12
9	F	0	5
All	All	1	340

The worst 5 of 165 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1823	G	O3'-P	41.48	2.10	1.61
10	G	109	GLU	CD-OE2	16.17	1.43	1.25
11	H	66	GLU	CD-OE1	15.86	1.43	1.25
34	f	6	TRP	CB-CG	-15.77	1.21	1.50
30	b	16	TRP	CB-CG	-13.52	1.25	1.50

The worst 5 of 1311 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	8	60	G	N9-C1'-C2'	16.16	135.01	114.00
38	j	11	ARG	NE-CZ-NH2	-13.83	113.38	120.30
19	Q	37	ARG	NE-CZ-NH2	12.90	126.75	120.30
1	5	92	C	N1-C1'-C2'	-12.62	97.59	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	I	139	ARG	CG-CD-NE	12.29	137.61	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1992	U	C1'

5 of 340 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	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	5	78486	0	39661	10163	0
2	7	2558	0	1296	307	0
3	8	3314	0	1683	481	0
4	A	1868	0	1959	156	0
5	B	3147	0	3280	217	0
6	C	2919	0	3100	162	0
7	D	2380	0	2412	171	0
8	E	1904	0	2055	132	0
9	F	1870	0	1996	174	0
10	G	1934	0	2086	102	0
11	H	1518	0	1601	84	0
12	I	1713	0	1752	88	0
13	J	1359	0	1390	63	0
14	L	1703	0	1818	87	0
15	M	1131	0	1209	68	0
16	N	1701	0	1749	116	0
17	O	1651	0	1786	86	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	P	1242	0	1269	56	0
19	Q	1506	0	1623	74	0
20	R	1508	0	1664	98	0
21	S	1454	0	1496	120	0
22	T	1298	0	1366	74	0
23	U	808	0	831	25	0
24	V	979	0	1039	51	0
25	W	528	0	541	52	0
26	X	976	0	1053	64	0
27	Y	1115	0	1205	60	0
28	Z	1107	0	1182	49	0
29	a	1163	0	1211	0	0
30	b	610	0	650	0	0
31	c	732	0	769	0	0
32	d	888	0	930	0	0
33	e	1053	0	1147	0	0
34	f	876	0	912	0	0
35	g	906	0	1002	0	0
36	h	1015	0	1149	0	0
37	i	832	0	917	0	0
38	j	706	0	743	0	0
39	k	569	0	637	0	0
40	l	444	0	483	0	0
41	m	429	0	466	0	0
42	n	222	0	264	0	0
43	o	851	0	922	0	0
44	p	708	0	760	0	0
45	r	1001	0	1062	0	0
46	1	3051	0	3158	175	0
47	2	494	0	527	23	0
48	3	180	0	40	1	0
49	5	119	0	0	0	0
49	7	5	0	0	0	0
49	8	4	0	0	0	0
49	P	1	0	0	0	0
49	V	1	0	0	0	0
50	j	1	0	0	0	0
50	m	1	0	0	0	0
50	o	1	0	0	0	0
All	All	140540	0	101851	12655	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 56.



The worst 5 of 12655 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)
1:5:100:C:C5	1:5:101:A:C8	2.00	1.49
1:5:1174:G:N2	1:5:1175:A:N7	1.67	1.41
1:5:2526:C:C5	46:1:405:ARG:CZ	2.04	1.41
1:5:1266:G:N2	1:5:2111:G:N3	1.67	1.39
1:5:2361:G:O6	18:P:25:HIS:CD2	1.74	1.38

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	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	4	36
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	1	13
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	3	33
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	15
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	5
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	3	30
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	6	42
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	9	50
12	I	211/213 (99%)	168 (80%)	30 (14%)	13 (6%)	2	21
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	3	28
14	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	2	25
15	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	13	56
16	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	5	42
17	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	13	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	15	60
19	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	6	44
20	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	8	49
21	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	11	54
22	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	10	51
23	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	9	50
24	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	8	48
25	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	12	55
26	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	11	54
27	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	3	30
28	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	4	35
29	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	2	24
30	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	2	24
31	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	3	31
32	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	4	35
33	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	24	70
34	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	3	29
35	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	11	53
36	h	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	7	46
37	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	9	51
38	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	3	28
39	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	15
40	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	3	32
41	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	n	21/25 (84%)	21 (100%)	0	0	100	100
43	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	2	22
44	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	17	63
45	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	3	27
46	1	384/476 (81%)	325 (85%)	42 (11%)	17 (4%)	3	30
47	2	60/68 (88%)	51 (85%)	6 (10%)	3 (5%)	3	27
All	All	6815/7604 (90%)	5717 (84%)	811 (12%)	287 (4%)	6	32

5 of 287 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	108	GLU

### 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	187/199 (94%)	139 (74%)	48 (26%)	0	4
5	B	335/335 (100%)	265 (79%)	70 (21%)	1	8
6	C	305/305 (100%)	239 (78%)	66 (22%)	1	7
7	D	246/250 (98%)	178 (72%)	68 (28%)	0	3
8	E	209/209 (100%)	157 (75%)	52 (25%)	1	5
9	F	194/194 (100%)	145 (75%)	49 (25%)	1	4
10	G	206/226 (91%)	158 (77%)	48 (23%)	1	5
11	H	169/171 (99%)	125 (74%)	44 (26%)	0	4
12	I	180/180 (100%)	136 (76%)	44 (24%)	1	5
13	J	143/149 (96%)	115 (80%)	28 (20%)	1	9
14	L	176/177 (99%)	135 (77%)	41 (23%)	1	5
15	M	116/160 (72%)	95 (82%)	21 (18%)	2	12
16	N	171/172 (99%)	129 (75%)	42 (25%)	1	5
17	O	172/174 (99%)	146 (85%)	26 (15%)	3	21
18	P	134/134 (100%)	112 (84%)	22 (16%)	3	17
19	Q	163/164 (99%)	132 (81%)	31 (19%)	2	10
20	R	159/175 (91%)	120 (76%)	39 (24%)	1	5
21	S	156/192 (81%)	121 (78%)	35 (22%)	1	6
22	T	139/140 (99%)	112 (81%)	27 (19%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	U	89/114 (78%)	67 (75%)	22 (25%)	1	5
24	V	101/107 (94%)	77 (76%)	24 (24%)	1	5
25	W	55/126 (44%)	42 (76%)	13 (24%)	1	5
26	X	107/133 (80%)	89 (83%)	18 (17%)	2	15
27	Y	124/135 (92%)	96 (77%)	28 (23%)	1	6
28	Z	117/118 (99%)	94 (80%)	23 (20%)	1	9
29	a	119/120 (99%)	102 (86%)	17 (14%)	4	24
30	b	63/123 (51%)	45 (71%)	18 (29%)	0	3
31	c	79/97 (81%)	60 (76%)	19 (24%)	1	5
32	d	98/110 (89%)	66 (67%)	32 (33%)	0	2
33	e	114/121 (94%)	89 (78%)	25 (22%)	1	7
34	f	88/89 (99%)	73 (83%)	15 (17%)	2	15
35	g	98/100 (98%)	79 (81%)	19 (19%)	2	10
36	h	109/110 (99%)	92 (84%)	17 (16%)	3	20
37	i	86/89 (97%)	71 (83%)	15 (17%)	2	14
38	j	73/73 (100%)	60 (82%)	13 (18%)	2	13
39	k	64/65 (98%)	52 (81%)	12 (19%)	2	11
40	l	47/48 (98%)	39 (83%)	8 (17%)	2	15
41	m	48/116 (41%)	36 (75%)	12 (25%)	1	4
42	n	22/24 (92%)	17 (77%)	5 (23%)	1	6
43	o	92/94 (98%)	70 (76%)	22 (24%)	1	5
44	p	74/74 (100%)	61 (82%)	13 (18%)	2	13
45	r	109/109 (100%)	85 (78%)	24 (22%)	1	7
46	1	330/398 (83%)	309 (94%)	21 (6%)	22	62
47	2	53/59 (90%)	50 (94%)	3 (6%)	25	66
All	All	5919/6458 (92%)	4680 (79%)	1239 (21%)	4	8

5 of 1239 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	M	17	PHE
19	Q	119	LYS
41	m	97	ARG

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Mol	Chain	Res	Type
15	M	91	TRP
17	O	62	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 188 such sidechains are listed below:

Mol	Chain	Res	Type
16	N	178	HIS
20	R	66	ASN
45	r	6	GLN
16	N	182	HIS
18	P	54	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3647/3722 (97%)	1611 (44%)	629 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
All	All	3921/3998 (98%)	1703 (43%)	660 (16%)

5 of 1703 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C
1	5	8	U
1	5	12	A

5 of 660 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	2114	G
1	5	2554	U
1	5	4938	A
1	5	2248	C
1	5	2347	A

## 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 ⓘ

Of 133 ligands modelled in this entry, 133 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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.