



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:52 PM BST

PDB ID : 4V4W
EMDB ID: : EMD-1143
Title : Structure of a SecM-stalled E. coli ribosome complex obtained by fitting atomic models for RNA and protein components into cryo-EM map EMD-1143
Authors : Mitra, K.; Frank, J.
Deposited on : 2006-05-09
Resolution : 15.00 Å(reported)

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. A user guide is available at <http://wwpdb.org/validation/2016/EMValidationReportHelp>

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

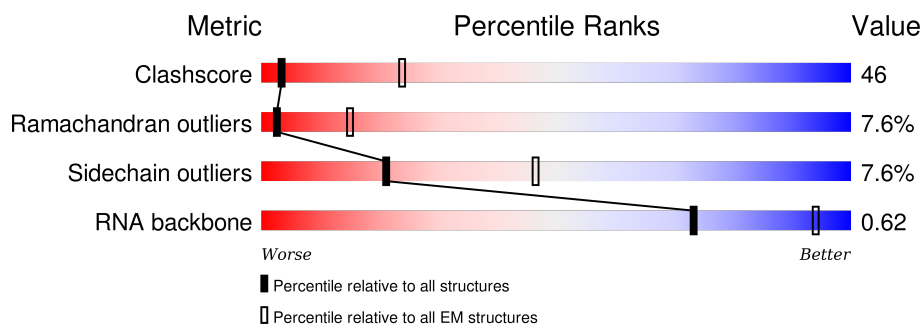
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 15.00 Å.

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



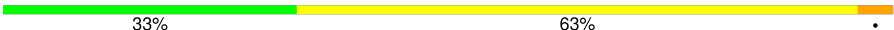


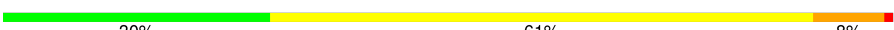
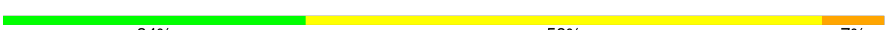
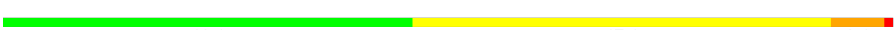




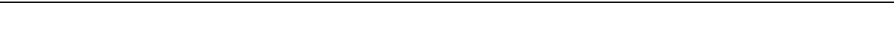

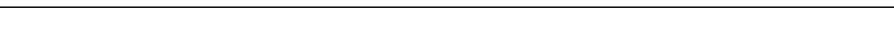
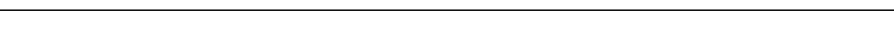


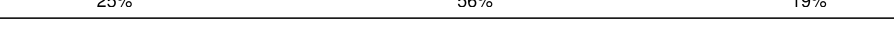






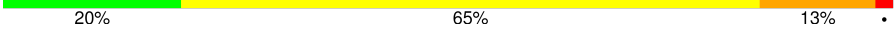
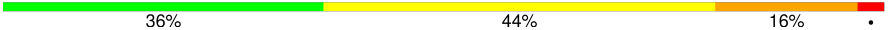
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	AA	1488	<div> <div>28%</div> <div>53%</div> <div>18%</div> <div>.</div> </div>
2	AU	76	<div> <div>28%</div> <div>58%</div> <div>14%</div> </div>
2	AV	76	<div> <div>30%</div> <div>58%</div> <div>12%</div> </div>
2	AW	76	<div> <div>26%</div> <div>59%</div> <div>14%</div> </div>
3	AB	236	<div> <div>44%</div> <div>51%</div> <div>.</div> </div>
4	AC	206	<div> <div>40%</div> <div>54%</div> <div>5%</div> </div>
5	AD	204	<div> <div>41%</div> <div>57%</div> <div>.</div> </div>
6	AE	148	<div> <div>40%</div> <div>57%</div> <div>.</div> </div>



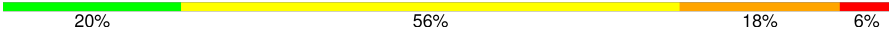

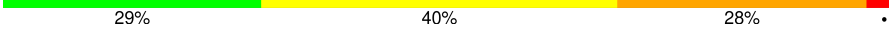





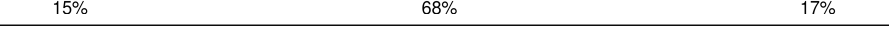
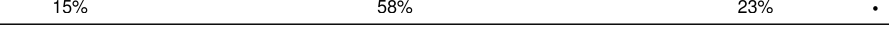


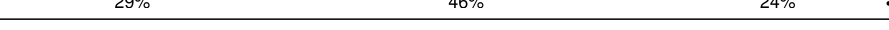




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Mol	Chain	Length	Quality of chain
7	AF	95	
8	AG	137	
9	AH	127	
10	AI	126	
11	AJ	96	
12	AK	116	
13	AL	101	
14	AM	115	
15	AN	61	
16	AO	86	
17	AP	78	
18	AQ	79	
19	AR	69	
20	AS	87	
21	AT	83	
22	B0	2740	
23	B9	108	
24	B2	222	
25	B3	119	
25	B5	119	
26	BA	227	
27	BB	209	
28	BC	198	
29	BD	177	
30	BE	167	

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Mol	Chain	Length	Quality of chain
31	BF	149	
32	BG	139	
33	BH	142	
34	BI	122	
35	BJ	140	
36	BK	131	
37	BL	114	
38	BM	113	
39	BN	114	
40	BO	115	
41	BQ	106	
42	BR	92	
43	BS	99	
44	BT	94	
45	BU	84	
46	BW	60	
47	BX	56	
48	BZ	29	
49	B1	52	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 141668 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1488	Total	C	N	O	P	0	0
			31924	14238	5854	10345	1487		

- Molecule 2 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AU	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		
2	AV	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		
2	AW	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		

- Molecule 3 is a protein called 30S ribosomal subunit protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	236	Total	C	N	O	S	0	0
			1847	1165	328	346	8		

- Molecule 4 is a protein called 30S ribosomal subunit protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AC	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 5 is a protein called 30S ribosomal subunit protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AD	204	Total	C	N	O	S	0	0
			1638	1023	314	297	4		

- Molecule 6 is a protein called 30S ribosomal subunit protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AE	148	Total	C	N	O	S	0	0
			1093	679	208	200	6		

- Molecule 7 is a protein called 30S ribosomal subunit protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AF	95	Total	C	N	O	S	0	0
			784	495	143	140	6		

- Molecule 8 is a protein called 30S ribosomal subunit protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AG	137	Total	C	N	O	S	0	0
			1079	671	204	200	4		

- Molecule 9 is a protein called 30S ribosomal subunit protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AH	127	Total	C	N	O	S	0	0
			968	610	171	181	6		

- Molecule 10 is a protein called 30S ribosomal subunit protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AI	126	Total	C	N	O	S	0	0
			1014	630	204	177	3		

- Molecule 11 is a protein called 30S ribosomal subunit protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AJ	96	Total	C	N	O	S	0	0
			773	484	148	140	1		

- Molecule 12 is a protein called 30S ribosomal subunit protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AK	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 13 is a protein called 30S ribosomal subunit protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AL	101	Total	C	N	O	S	0	0
			787	486	159	138	4		

- Molecule 14 is a protein called 30S ribosomal subunit protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AM	115	Total	C	N	O	S	0	0
			892	552	179	158	3		

- Molecule 15 is a protein called 30S ribosomal subunit protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AN	61	Total	C	N	O	S	0	0
			500	310	108	80	2		

- Molecule 16 is a protein called 30S ribosomal subunit protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AO	86	Total	C	N	O	S	0	0
			697	430	139	127	1		

- Molecule 17 is a protein called 30S ribosomal subunit protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AP	78	Total	C	N	O	S	0	0
			622	390	122	109	1		

- Molecule 18 is a protein called 30S ribosomal subunit protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AQ	79	Total	C	N	O	S	0	0
			640	405	119	113	3		

- Molecule 19 is a protein called 30S ribosomal subunit protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AR	69	Total	C	N	O	S	0	0
			576	362	112	101	1		

- Molecule 20 is a protein called 30S ribosomal subunit protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AS	87	Total	C	N	O	S	0	0
			695	443	132	118	2		

- Molecule 21 is a protein called 30S ribosomal subunit protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AT	83	Total	C	N	O	S	0	0
			649	401	134	111	3		

- Molecule 22 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	B0	2740	Total	C	N	O	P	0	0
			58824	26239	10826	19019	2740		

- Molecule 23 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	B9	108	Total	C	N	O	P	0	0
			2310	1030	423	750	107		

- Molecule 24 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B2	222	Total	C	N	O	S	0	0
			1652	1031	301	314	6		

- Molecule 25 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B3	119	Total	C	N	O	S	0	0
			845	531	137	174	3		
25	B5	119	Total	C	N	O	S	0	0
			845	531	137	174	3		

- Molecule 26 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BA	227	Total	C	N	O	S	0	0
			1733	1064	352	311	6		

- Molecule 27 is a protein called 50S ribosomal protein L3.

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

- Molecule 28 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BC	198	Total	C	N	O	S	0	0
			1531	960	280	287	4		

- Molecule 29 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BD	177	Total	C	N	O	S	0	0
			1415	902	250	257	6		

- Molecule 30 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BE	167	Total	C	N	O	S	0	0
			1253	789	228	234	2		

- Molecule 31 is a protein called 50S ribosomal protein L9.

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

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BG	139	Total	C	N	O	S	0	0
			1019	644	177	192	6		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BH	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BI	122	Total	C	N	O	S	0	0
			939	588	180	166	5		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BJ	140	Total	C	N	O	S	0	0
			1017	632	200	184	1		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BK	131	Total	C	N	O	S	0	0
			1036	661	200	171	4		

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BL	114	Total	C	N	O	S	0	0
			908	564	184	156	4		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	BM	113	Total	C	N	O	0	0
			864	534	174	156		

- Molecule 39 is a protein called 50S ribosomal protein L19.

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

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	BO	115	Total	C	N	O	0	0
			937	598	190	149		

- Molecule 41 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BQ	106	Total	C	N	O	S	0	0
			825	512	162	149	2		

- Molecule 42 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BR	92	Total	C	N	O	S	0	0
			717	455	132	129	1		

- Molecule 43 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BS	99	Total	C	N	O	S	0	0
			762	480	143	139			

- Molecule 44 is a protein called 50S ribosomal protein L25.

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

- Molecule 45 is a protein called 50S ribosomal protein L27.

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

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BW	60	Total	C	N	O	S	0	0
			495	305	96	92	2		

- Molecule 47 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BX	56	Total	C	N	O	S	0	0
			435	272	84	77	2		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	BZ	29	Total	C	N	O	0	0
			234	145	47	42		

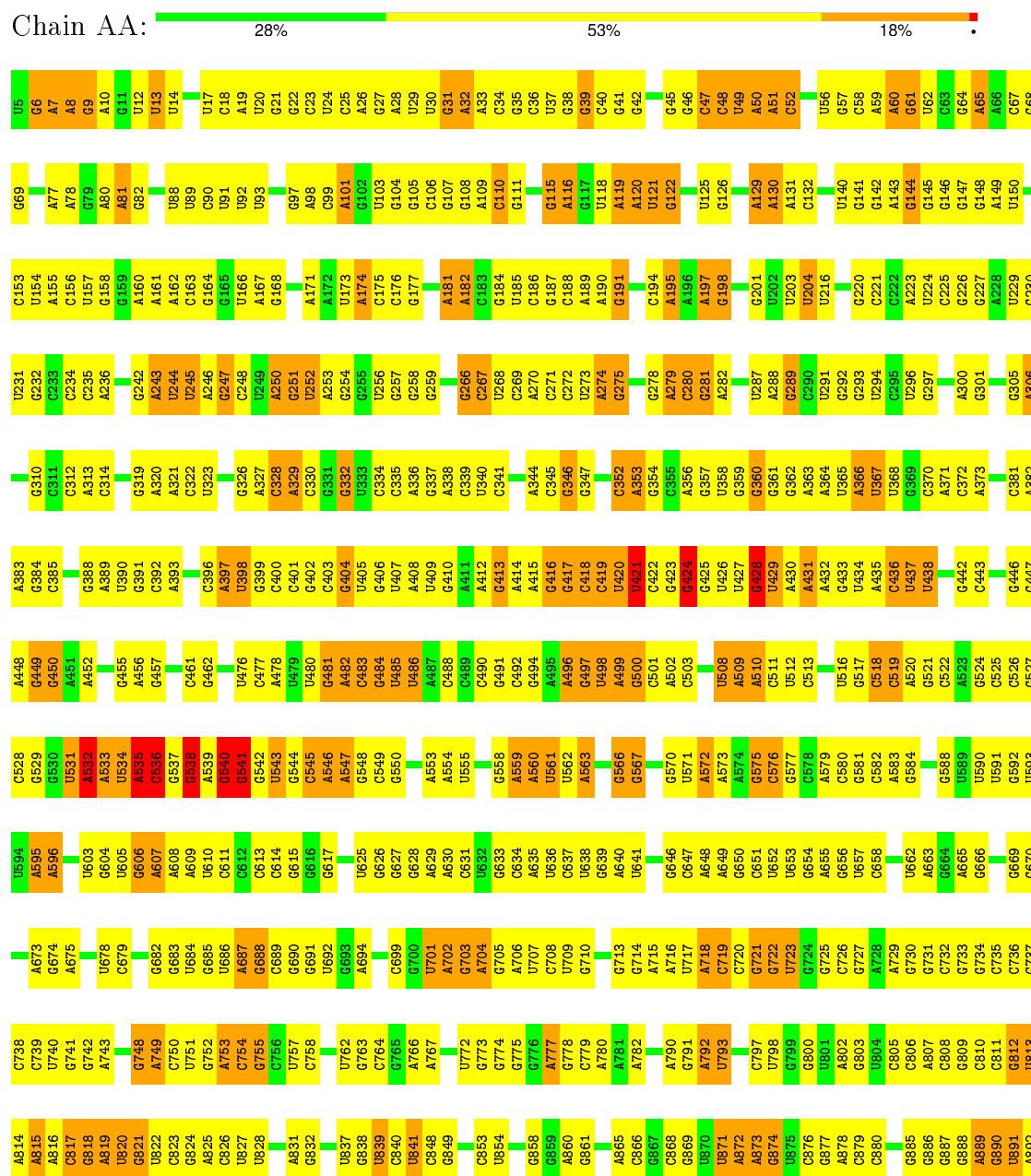
- Molecule 49 is a protein called 50S ribosomal protein L33.

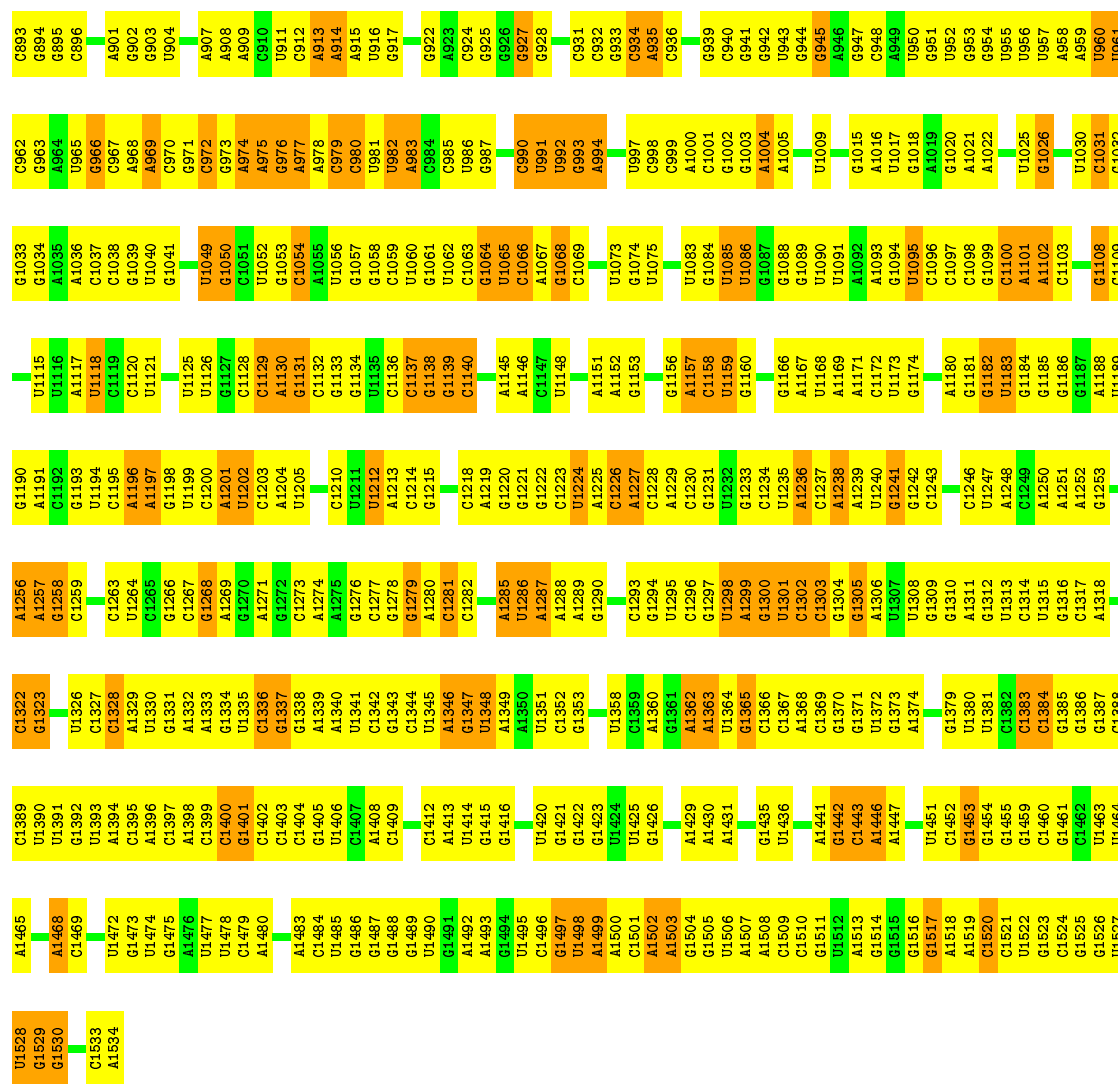
Mol	Chain	Residues	Atoms				AltConf	Trace
49	B1	52	Total	C	N	O	0	0
			424	272	78	74		

3 Residue-property plots

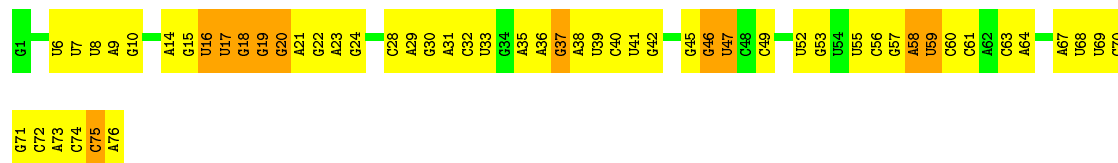
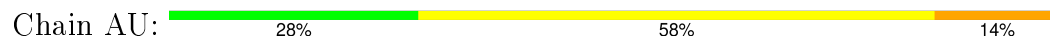
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric 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: 16S ribosomal RNA

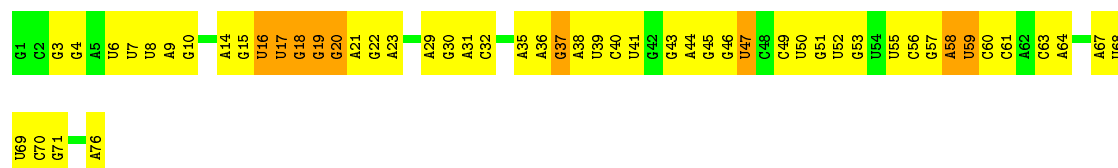




• Molecule 2: tRNA

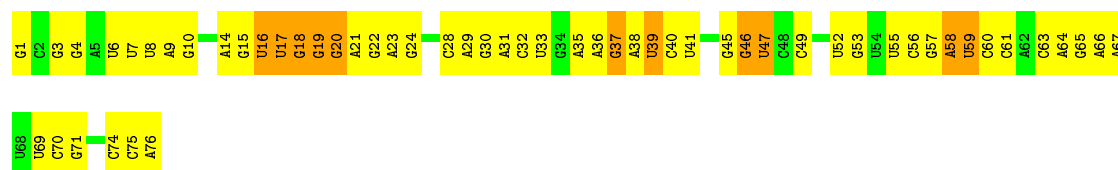


• Molecule 2: tRNA



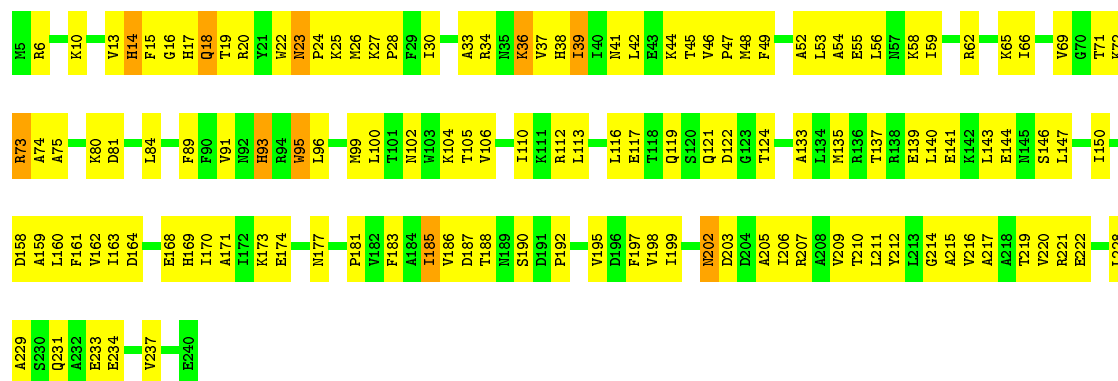
- Molecule 2: tRNA

Chain AW: 



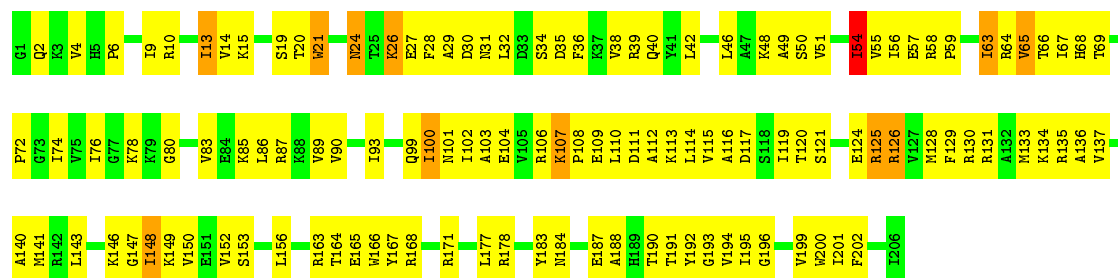
- Molecule 3: 30S ribosomal subunit protein S2

Chain AB: 



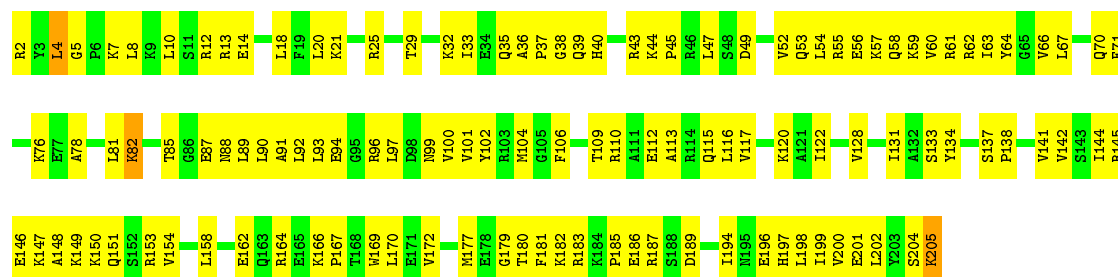
- Molecule 4: 30S ribosomal subunit protein S3

Chain AC: 



- Molecule 5: 30S ribosomal subunit protein S4

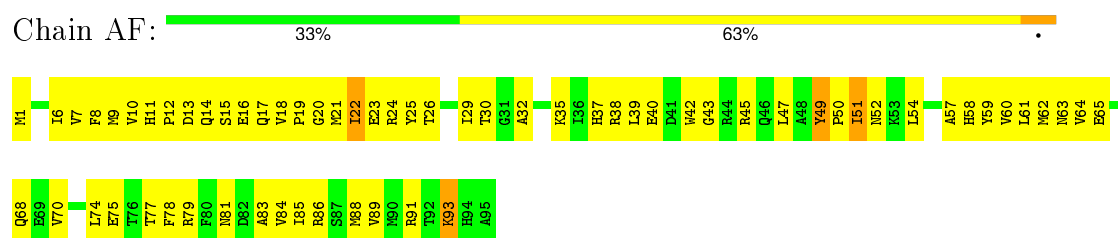
Chain AD: 



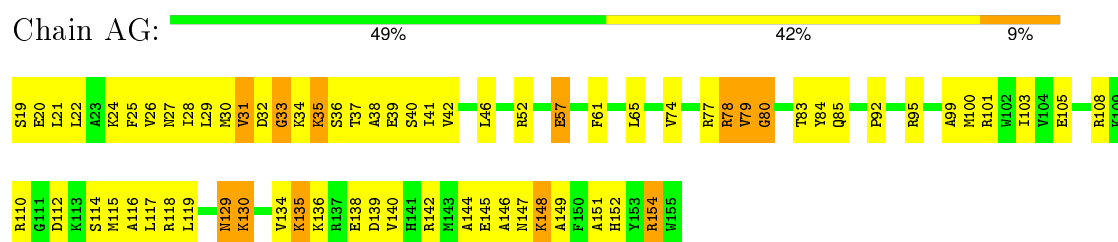
- Molecule 6: 30S ribosomal subunit protein S5



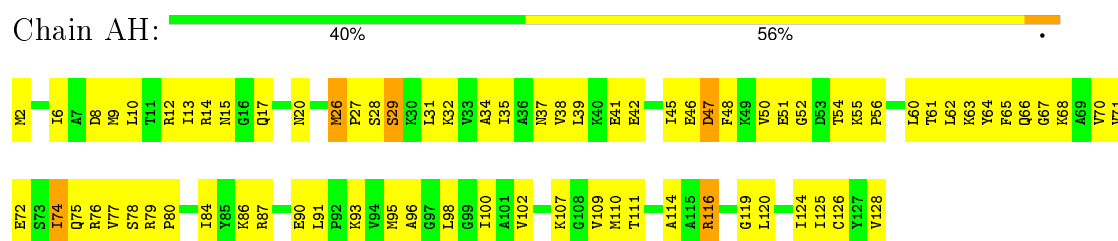
- Molecule 7: 30S ribosomal subunit protein S6



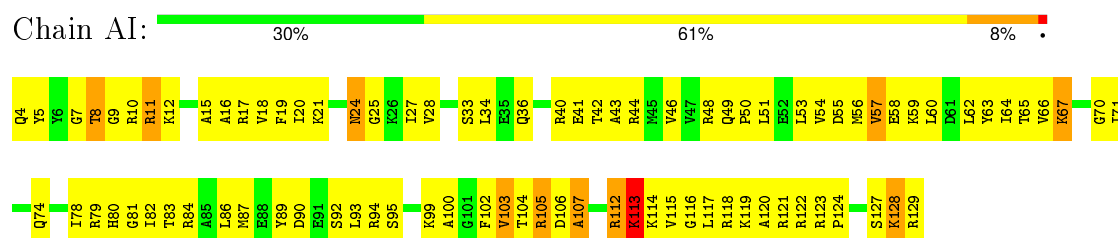
- Molecule 8: 30S ribosomal subunit protein S7



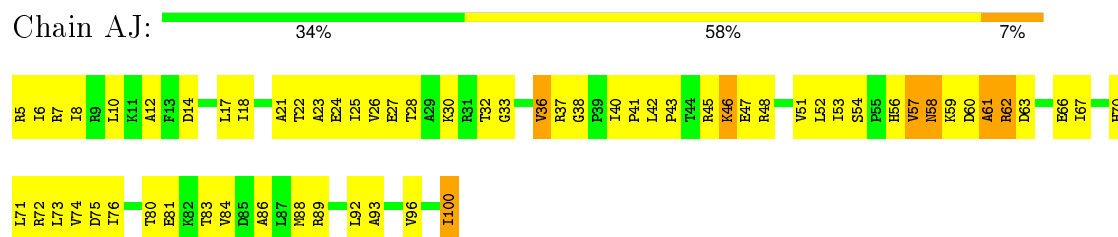
- Molecule 9: 30S ribosomal subunit protein S8



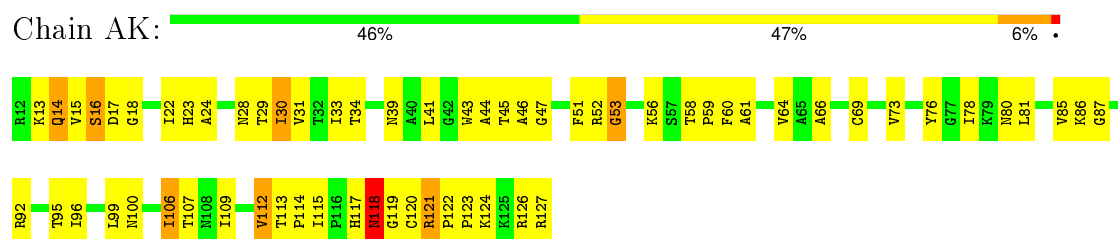
- Molecule 10: 30S ribosomal subunit protein S9



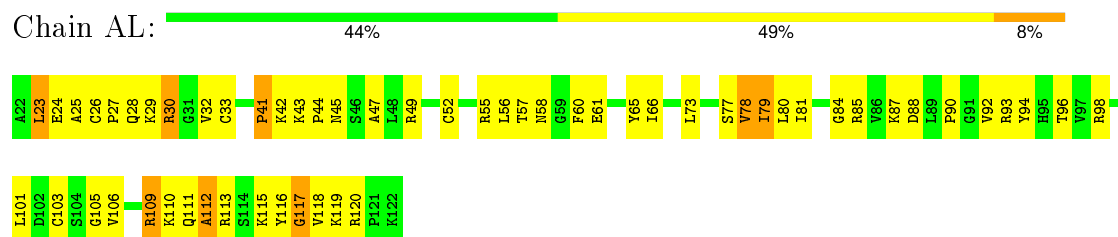
- Molecule 11: 30S ribosomal subunit protein S10



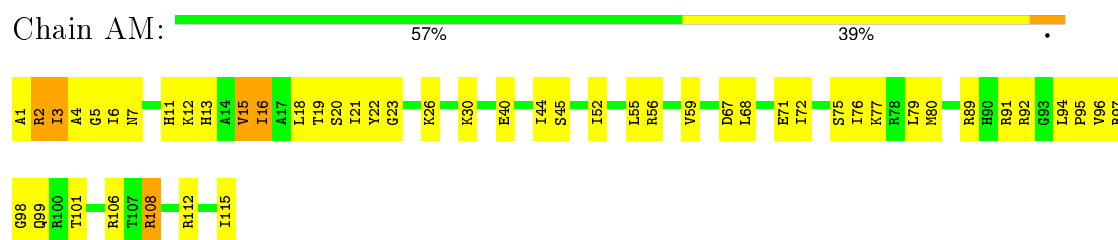
- Molecule 12: 30S ribosomal subunit protein S11



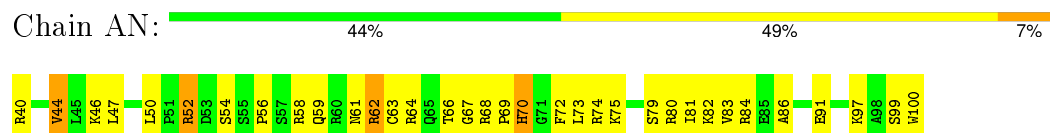
- Molecule 13: 30S ribosomal subunit protein S12



- Molecule 14: 30S ribosomal subunit protein S13

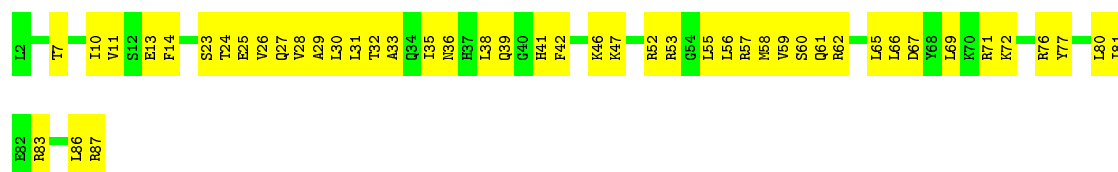


- Molecule 15: 30S ribosomal subunit protein S14



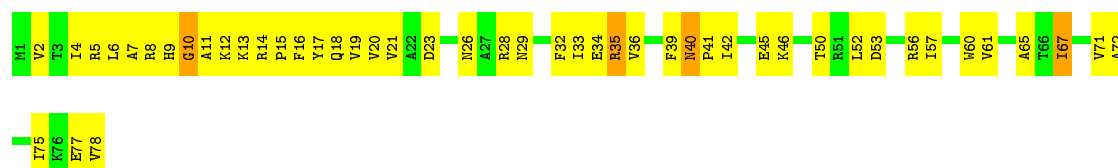
- Molecule 16: 30S ribosomal subunit protein S15





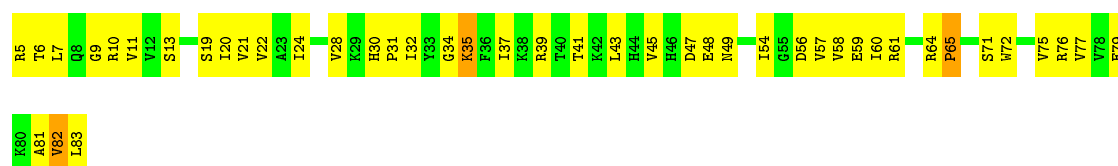
- Molecule 17: 30S ribosomal subunit protein S16

Chain AP: 38% 56% 5%



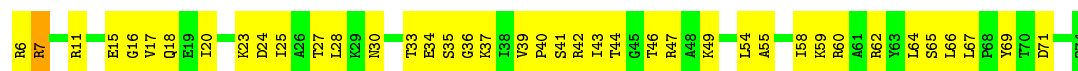
- Molecule 18: 30S ribosomal subunit protein S17

Chain AQ: 44% 52% .



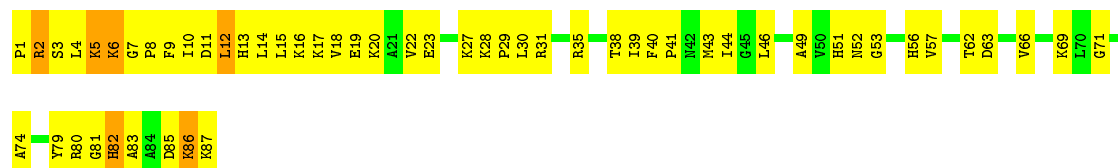
- Molecule 19: 30S ribosomal subunit protein S18

Chain AR: 42% 57% .



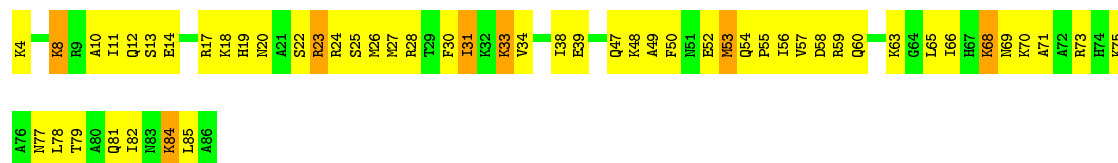
- Molecule 20: 30S ribosomal subunit protein S19

Chain AS: 37% 56% 7%



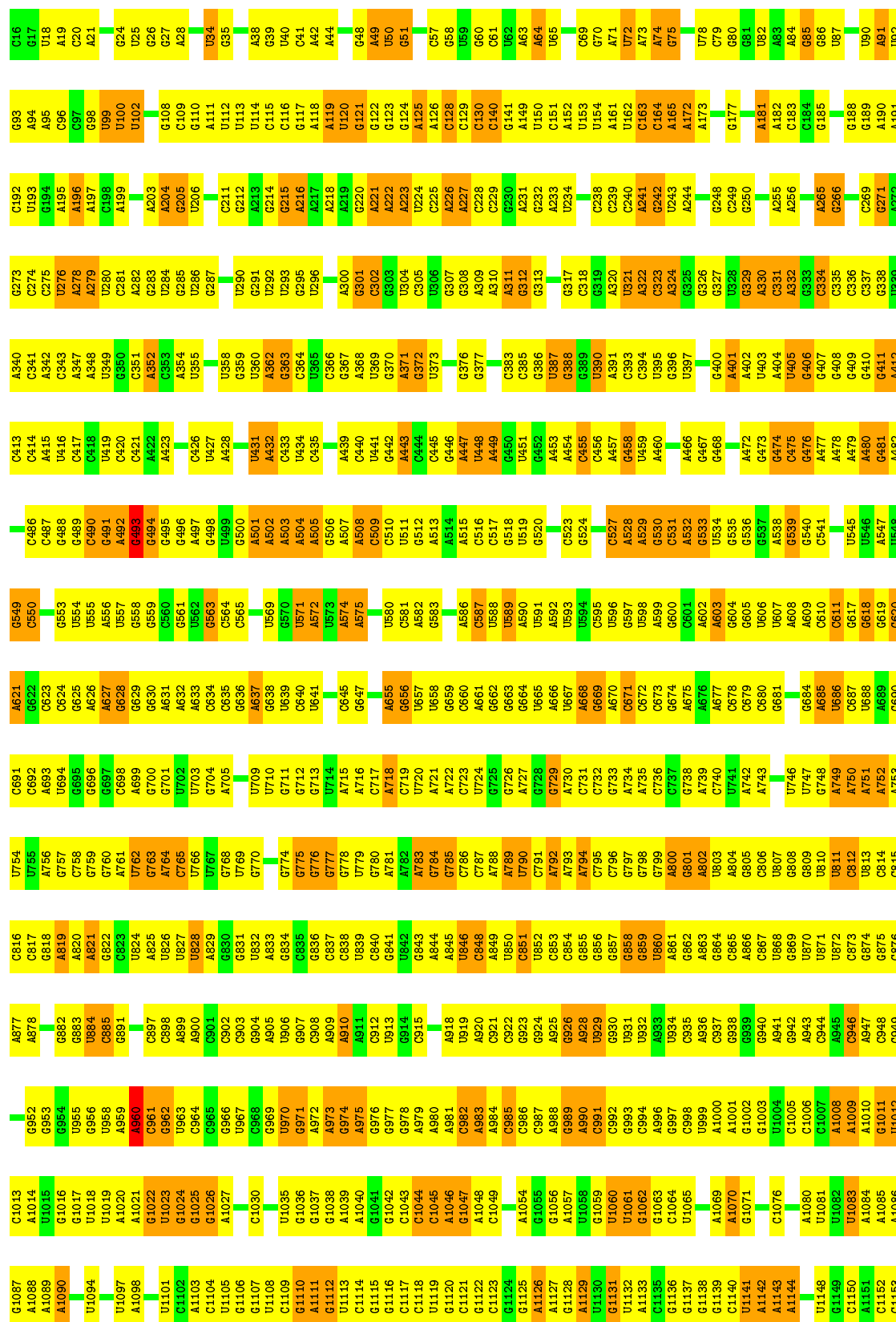
- Molecule 21: 30S ribosomal subunit protein S20

Chain AT: 36% 55% 8%



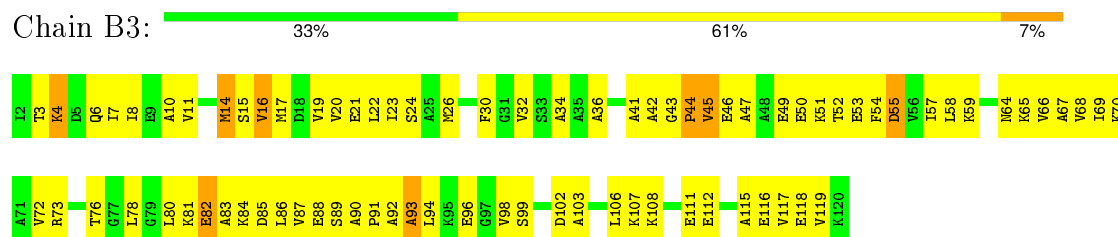
● Molecule 22: 23S ribosomal RNA

Chain B0:  25% 56% 19%

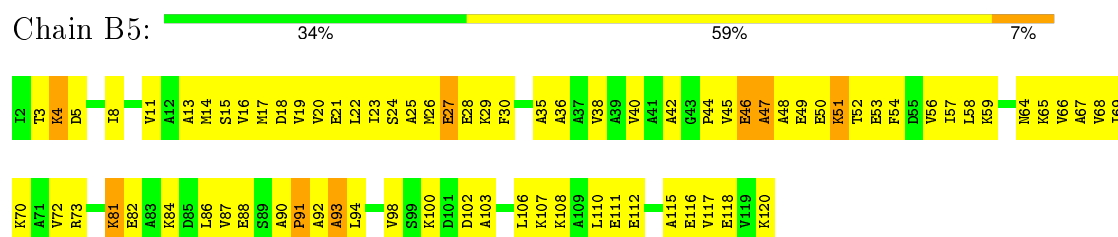


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G2223	C2146	A2014	G1946	C1798	G1697	A1632	C1565	U1489	A1423	G1356	G1288	G1225	A1155
A2224	A2017	A2015	G1948	A1789	A1698	A1633	A1566	A1490	G1424	A1566	C1289	A1226	A1156
G2225	C2148	U2016	G1949	C1790	A1699	A1634	G1567	A1491	G1425	G1368	C1290	G1227	G1157
G2226	U2149	G1945	A1872	A1791	A1700	A1635	G1568	A1492	G1426	A1359	C1291	G1228	U1158
A2227	C2150	A2020	A1953	A1794	A1701	A1636	A1569	A1493	A1427	G1360	G1292	G1229	U1159
G2228	U2151	C2021	G1954	A1795	G1702	A1637	A1570	A1494	C1428	C1361	C1293	A1230	G1160
G2229	G2152	U2022	U1955	C1796	G1703	A1638	A1571	A1495	G1429	G1295	U1231	G1232	C1161
G2230	C2153	C2023	U1956	C1798	G1704	A1639	A1572	A1496	G1430	G1364	C1295	G1233	C1164
G2231	A2154	G2024	U1957	A1797	A1705	A1640	G1573	A1497	A1431	A1365	G1296	U1234	A1165
G2232	U2155	C2025	C1958	U1798	C1706	G1642	C1574	C1498	G1432	A1366	C1297	U1235	G1166
G2233	C2156	A2026	G1959	G1799	G1707	G1643	U1575	A1499	A1433	A1367	C1298	G1235	G1167
G2234	G2157	A2027	A1889	C1800	C1708	C1644	U1576	A1500	A1434	G1368	G1299	G1236	C1168
G2235	A2158	A2028	A1890	A1801	U1709	G1645	C1577	C1501	G1435	G1369	G1300	A1237	G1168
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G2237	C2160	A2033	C1963	A1803	A1711	U1647	A1579	G1503	C1437	C1371	A1302	G1239	C1170
G2238	C2161	U2034	G1964	A1804	U1712	G1648	A1580	U1438	U1438	G1375	U1240	U1241	G1171
G2239	G2162	G2035	C1965	C1805	U1716	A1650	A1581	A1439	U1440	C1376	A1241	U1242	A1175
U2240	C2163	C2036	A1966	A1806	C1732	A1651	C1582	C1508	U1441	G1377	U1243	U1244	U1176
A2241	C2164	A2037	G1967	G1811	C1733	A1652	G1583	G1511	U1442	G1380	C1306	C1245	C1177
G2242	U2165	G2038	G1968	U1812	U1742	G1653	A1587	C1512	U1443	G1381	G1310	G1246	C1178
U2243	U2166	U2039	A1969	G1813	G1743	A1654	A1588	U1514	U1444	G1382	U1312	A1247	U1181
U2244	U2167	G2040	A1970	G1814	G1743	A1655	A1589	G1517	U1445	G1383	U1313	G1248	U1182
U2245	G2168	U2041	A1971	A1815	A1746	A1656	A1590	C1524	A1449	A1384	C1314	U1249	U1183
G2246	A2169	A2042	G1972	G1816	U1747	A1657	C1591	C1525	C1452	A1385	C1315	G1250	U1184
A2247	A2170	C2043	G1973	G1817	C1748	G1658	A1591	G1526	U1453	G1388	U1316	G1251	G1185
C2248	A2171	G2044	G1974	U1818	A1749	G1659	U1592	G1527	A1454	G1389	U1317	G1252	G1186
U2249	U2172	C2045	G1975	U1819	G1750	G1660	G1593	A1528	U1455	U1390	C1320	A1254	G1187
G2250	C2165	G2046	U1976	U1820	A1755	G1661	C1594	G1529	U1456	U1391	A1321	U1255	G1190
G2251	C2166	C2047	A1977	A1821	G1756	U1662	C1595	C1530	G1457	A1392	A1322	G1256	G1191
G2252	A2176	G2048	U1978	C1822	A1757	G1663	A1598	U1531	C1458	A1393	C1323	C1257	A1193
G2253	C2175	U2049	G1980	G1823	U1758	A1664	U1599	U1532	U1396	U1397	G1324	G1258	A1194
G2254	C2176	C2050	A1981	U1824	A1759	G1665	C1600	C1533	U1397	C1398	U1325	G1259	G1195
G2255	C2177	A2051	U1982	G1825	C1760	G1666	G1601	U1398	U1462	C1399	U1326	A1260	C1196
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A2267	U2194	A2063	A1997	G1836	C1771	A1677	C1612	U1548	U1475	U1411	U1340	A1272	C1211
A2268	U2195	C2063	G1998	C1837	A1772	A1678	G1613	A1549	A1477	G1412	A1342	A1273	G1212
G2269	C2196	C2064	A1998	G1838	A1773	A1679	A1614	A1549	G1478	G1413	A1343	A1274	A1213
G2270	U2197	C2065	C1999	G1839	A1774	A1680	C1615	A1550	U1479	U1414	U1344	A1275	G1214
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A2272	A2199	G2067	C2001	U1841	U1776	G1683	A1617	A1552	C1481	G1416	G1346	G1277	G1216
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A2279	A2211	U2074	C1941	G1849	U1784	U1692	G1627	U1565	U1488	U1354	G1290	G1290	U1224
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A2281	C2214	U2076	C1943	G1851	A1786	U1694	G1629	U1567	U1490	U1356	G1292	G1292	U1226
G2282	C2215	U2077	U1944	A1853	U1786	U1695	G1630	U1568	U1491	U1357	G1293	G1293	U1227
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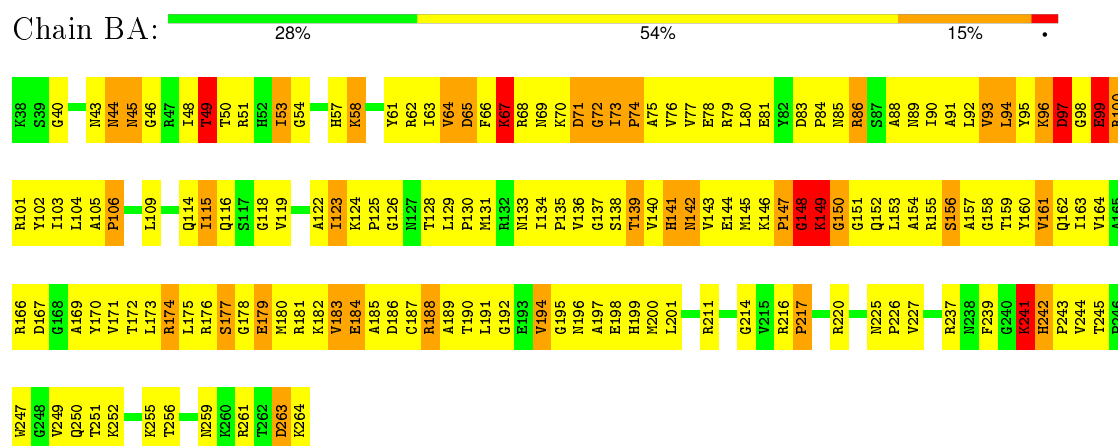
- Molecule 25: 50S ribosomal protein L7/L12



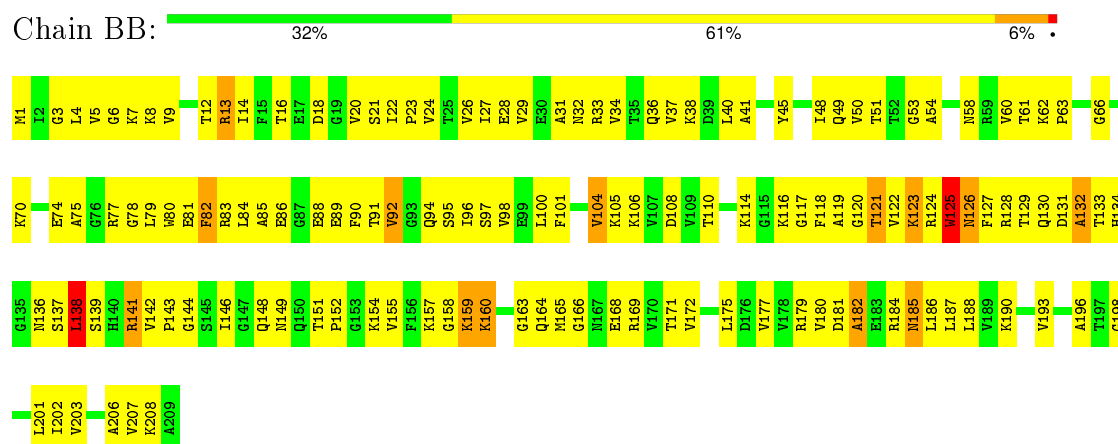
- Molecule 25: 50S ribosomal protein L7/L12



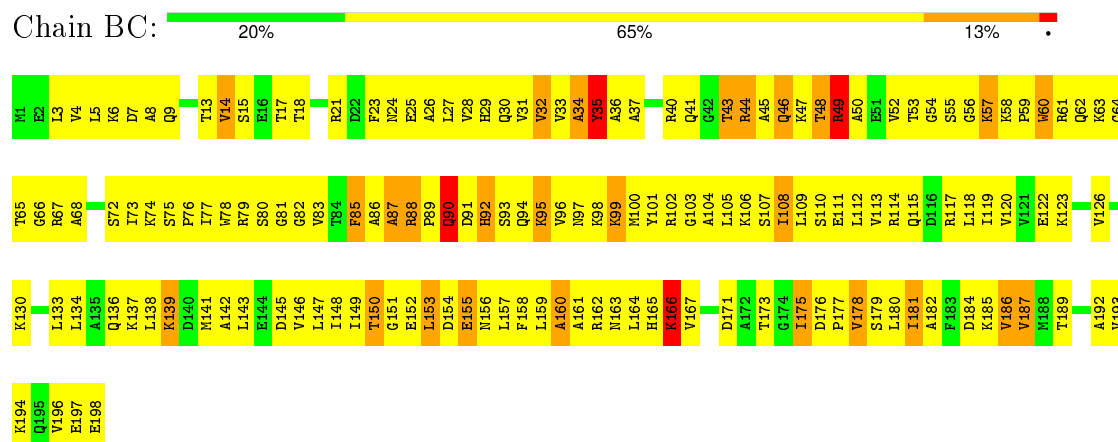
- Molecule 26: 50S ribosomal protein L2



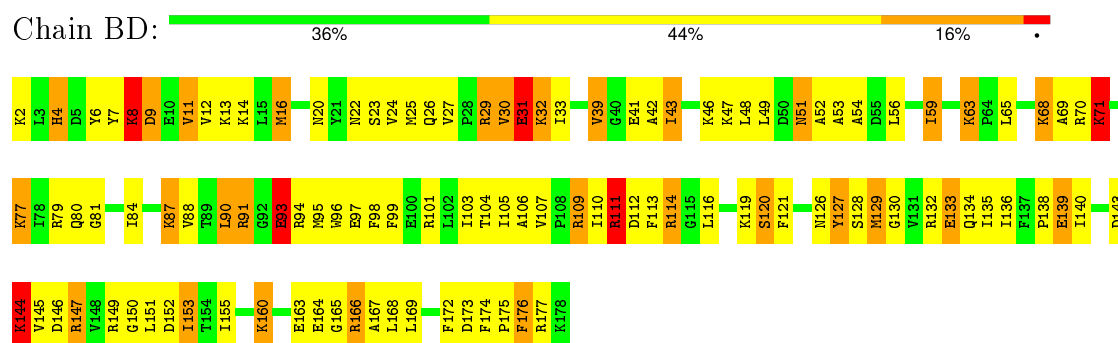
- Molecule 27: 50S ribosomal protein L3



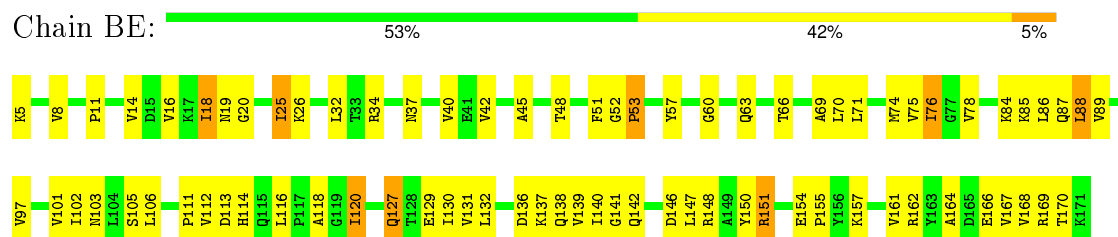
- Molecule 28: 50S ribosomal protein L4



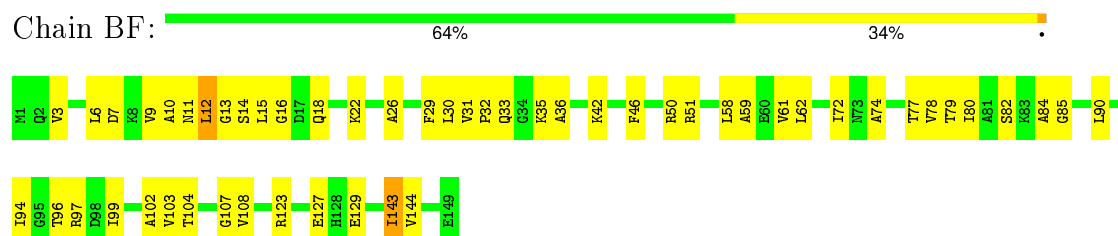
- Molecule 29: 50S ribosomal protein L5



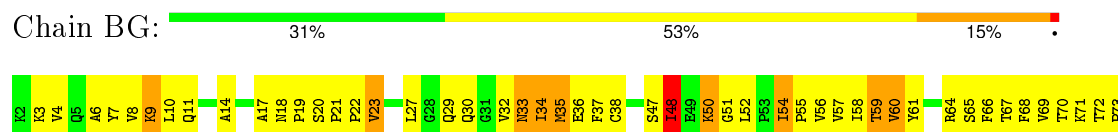
- Molecule 30: 50S ribosomal protein L6



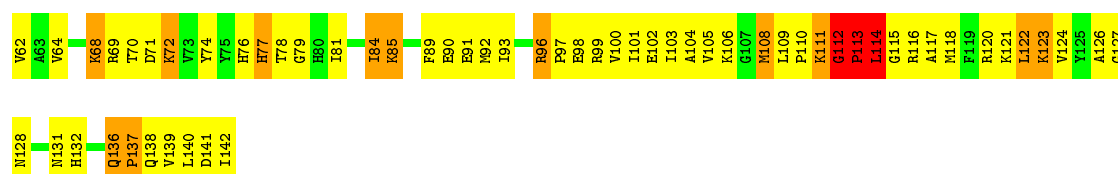
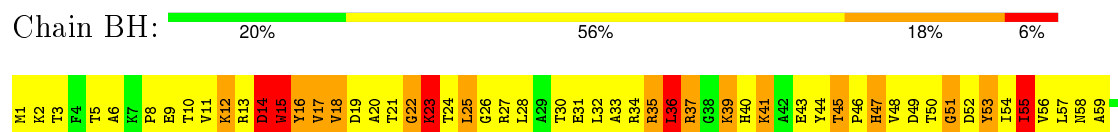
- Molecule 31: 50S ribosomal protein L9



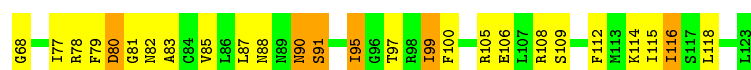
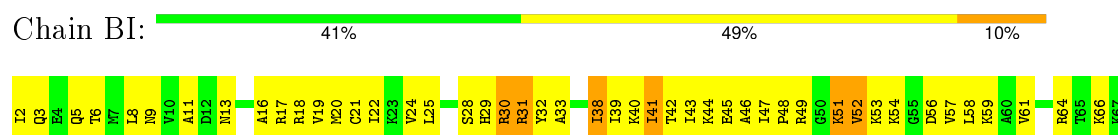
- Molecule 32: 50S ribosomal protein L11



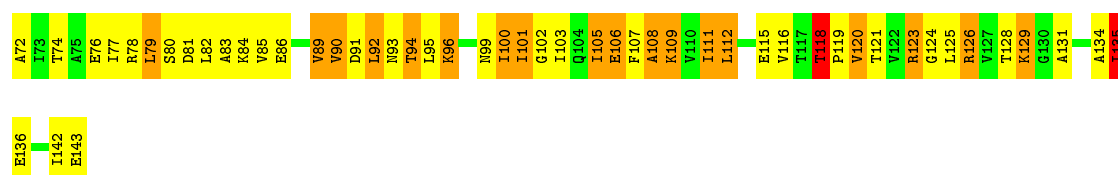
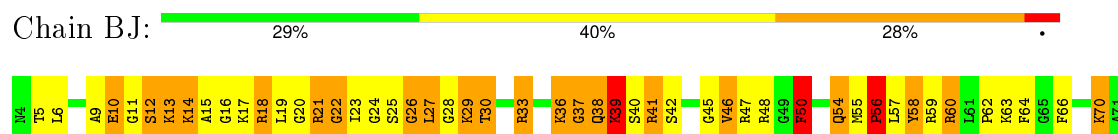
- Molecule 33: 50S ribosomal protein L13



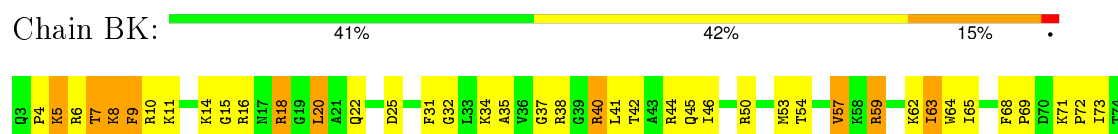
- Molecule 34: 50S ribosomal protein L14



- Molecule 35: 50S ribosomal protein L15



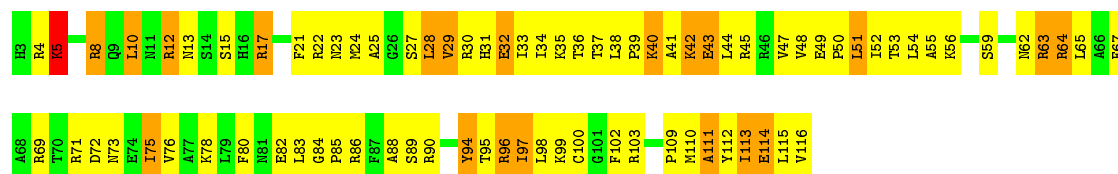
- Molecule 36: 50S ribosomal protein L16





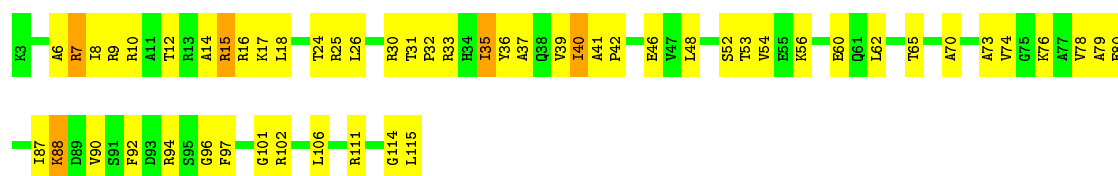
• Molecule 37: 50S ribosomal protein L17

Chain BL: 29% 53% 18%



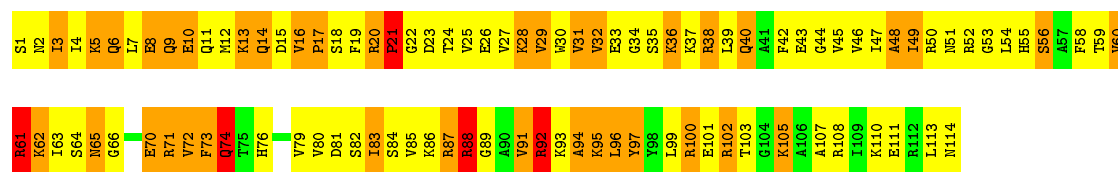
• Molecule 38: 50S ribosomal protein L18

Chain BM: 52% 43%



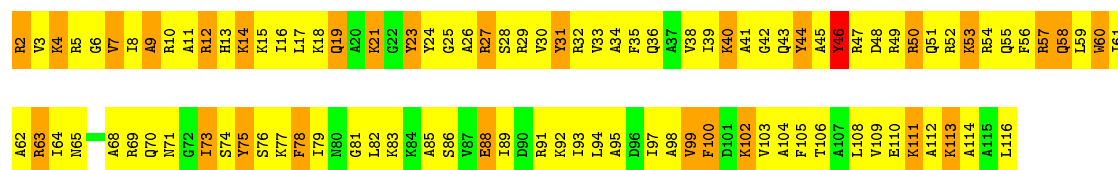
• Molecule 39: 50S ribosomal protein L19

Chain BN: 12% 50% 33%



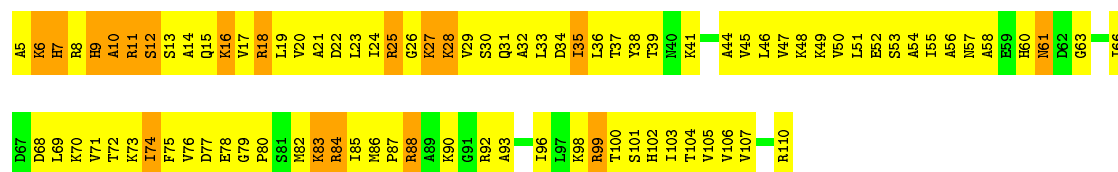
• Molecule 40: 50S ribosomal protein L20

Chain BO: 12% 63% 24%




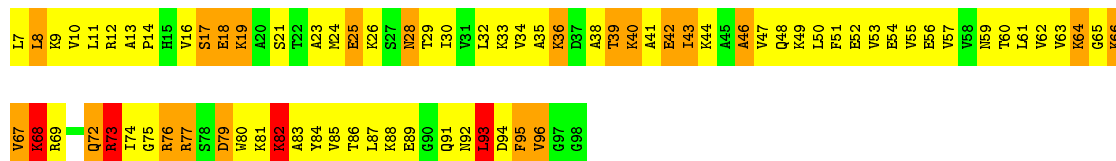
• Molecule 41: 50S ribosomal protein L22

Chain BQ: 15% 68% 17%



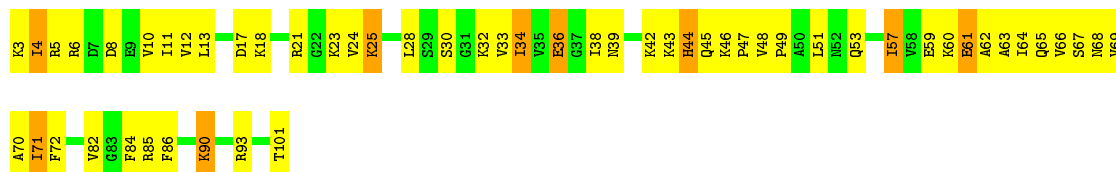
- Molecule 42: 50S ribosomal protein L23

Chain BR: 



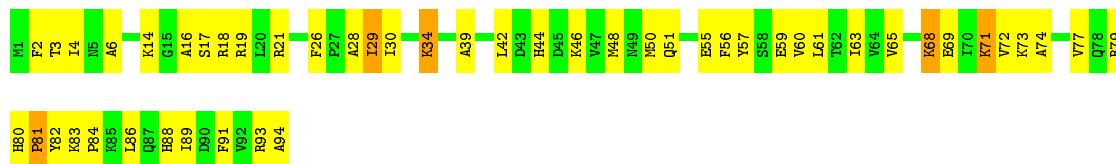
- Molecule 43: 50S ribosomal protein L24

Chain BS: 



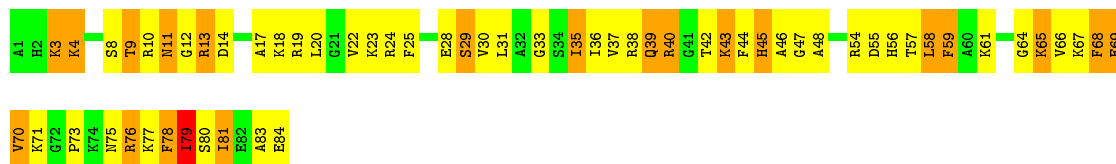
- Molecule 44: 50S ribosomal protein L25

Chain BT: 

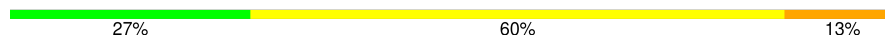


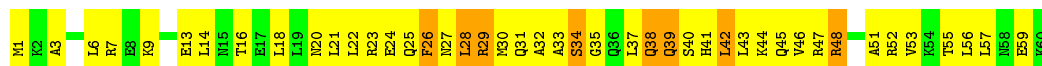
- Molecule 45: 50S ribosomal protein L27

Chain BU: 



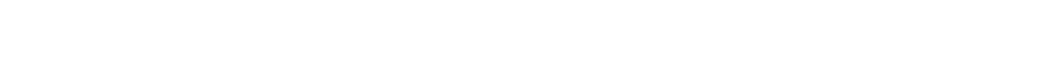
- Molecule 46: 50S ribosomal protein L29

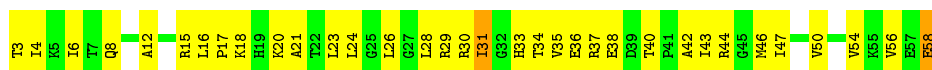
Chain BW: 



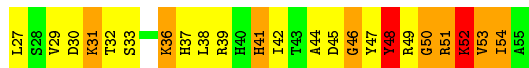
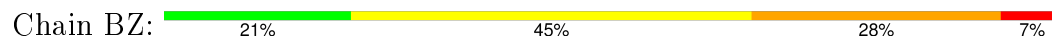
- Molecule 47: 50S ribosomal protein L30

Chain BX: 





- Molecule 48: 50S ribosomal protein L32



- Molecule 49: 50S ribosomal protein L33



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF correction of 3D-maps by Wiener filtration	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1100	Depositor
Minimum defocus (nm)	1.5	Depositor
Maximum defocus (nm)	4.3	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO163 film	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	AA	0.67	96/35745 (0.3%)	0.93	170/55764 (0.3%)
10	AI	0.24	0/1026	0.44	0/1364
11	AJ	0.23	0/783	0.46	0/1058
12	AK	0.24	0/886	0.44	0/1195
13	AL	0.22	0/799	0.44	0/1070
14	AM	0.21	0/900	0.43	0/1201
15	AN	0.25	0/510	0.39	0/679
16	AO	0.23	0/705	0.42	0/942
17	AP	0.26	0/632	0.44	0/848
18	AQ	0.24	0/649	0.45	0/870
19	AR	0.25	0/585	0.39	0/782
2	AU	0.17	0/1814	0.65	0/2827
2	AV	0.17	0/1814	0.64	0/2827
2	AW	0.18	0/1814	0.63	0/2827
20	AS	0.25	0/712	0.46	0/955
21	AT	0.24	0/655	0.38	0/866
22	B0	0.40	23/65882 (0.0%)	0.67	20/102783 (0.0%)
23	B9	0.20	0/2583	0.64	0/4028
24	B2	0.22	0/1665	0.44	0/2240
25	B3	0.22	0/842	0.43	0/1123
25	B5	0.22	0/844	0.46	0/1129
26	BA	0.72	4/1758 (0.2%)	0.65	2/2353 (0.1%)
27	BB	0.56	1/1582 (0.1%)	0.61	1/2122 (0.0%)
28	BC	0.25	0/1549	0.52	0/2082
29	BD	0.26	0/1438	0.46	0/1927
3	AB	0.25	0/1877	0.40	0/2523
30	BE	0.23	0/1273	0.43	0/1725
31	BF	0.24	0/1120	0.43	0/1509
32	BG	0.25	0/1032	0.54	0/1388
33	BH	0.27	0/1152	0.62	1/1551 (0.1%)
34	BI	0.23	0/948	0.45	0/1269
35	BJ	0.25	0/1025	0.56	0/1363
36	BK	0.27	0/1055	0.48	0/1409
37	BL	0.26	0/920	0.61	0/1229

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
38	BM	0.22	0/873	0.40	0/1170
39	BN	0.25	0/929	0.51	0/1242
4	AC	0.23	0/1652	0.42	0/2225
40	BO	1.30	6/949 (0.6%)	3.57	8/1261 (0.6%)
41	BQ	0.23	0/832	0.58	0/1113
42	BR	0.24	0/720	0.54	0/956
43	BS	0.25	0/769	0.42	0/1023
44	BT	0.25	0/766	0.41	0/1025
45	BU	0.27	0/642	0.50	0/848
46	BW	0.24	0/496	0.50	0/658
47	BX	0.23	0/439	0.45	0/587
48	BZ	0.24	0/238	0.45	0/316
49	B1	0.27	0/431	0.46	0/572
5	AD	0.22	0/1660	0.40	0/2220
6	AE	0.23	0/1106	0.42	0/1488
7	AF	0.24	0/802	0.45	0/1081
8	AG	0.23	0/1093	0.42	0/1467
9	AH	0.23	0/978	0.43	0/1311
All	All	0.46	130/153949 (0.1%)	0.75	202/230391 (0.1%)

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	AA	1	3
22	B0	5	4
All	All	6	7

The worst 5 of 130 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	B0	1996	C	N1-C2	33.93	1.74	1.40
22	B0	1579	A	N1-C2	27.63	1.59	1.34
22	B0	1421	G	N1-C2	25.25	1.57	1.37
1	AA	545	C	O3'-P	24.31	1.90	1.61
1	AA	536	C	N1-C6	24.27	1.51	1.37

The worst 5 of 202 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	BO	100	PHE	CZ-CE2-CD2	-69.61	36.57	120.10
40	BO	100	PHE	CD1-CE1-CZ	-69.56	36.62	120.10
40	BO	100	PHE	CE1-CZ-CE2	-53.35	23.98	120.00
40	BO	100	PHE	CG-CD1-CE1	-32.88	84.64	120.80
40	BO	100	PHE	CG-CD2-CE2	-32.87	84.64	120.80

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	428	G	C1'
22	B0	1593	G	C1'
22	B0	1653	G	C1'
22	B0	2143	C	C1'
22	B0	2250	G	C1'

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	538	G	Sidechain
1	AA	540	G	Sidechain
1	AA	541	G	Sidechain
22	B0	1418	G	Sidechain
22	B0	1579	A	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	AA	31924	0	16066	1600	0
2	AU	1622	0	821	102	0
2	AV	1622	0	821	75	0
2	AW	1622	0	821	80	0
3	AB	1847	0	1855	120	0
4	AC	1625	0	1699	164	0
5	AD	1638	0	1702	185	0
6	AE	1093	0	1132	117	0
7	AF	784	0	776	100	0
8	AG	1079	0	1108	91	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	AH	968	0	1021	96	0
10	AI	1014	0	1064	153	0
11	AJ	773	0	812	71	0
12	AK	870	0	878	98	0
13	AL	787	0	825	81	0
14	AM	892	0	954	65	0
15	AN	500	0	526	51	0
16	AO	697	0	716	72	0
17	AP	622	0	637	77	0
18	AQ	640	0	678	49	0
19	AR	576	0	599	55	0
20	AS	695	0	725	118	0
21	AT	649	0	697	67	0
22	B0	58824	0	29589	3943	0
23	B9	2310	0	1173	79	0
24	B2	1652	0	1730	181	0
25	B3	845	0	876	139	0
25	B5	845	0	878	133	0
26	BA	1733	0	1764	643	0
27	BB	1565	0	1612	264	0
28	BC	1531	0	1593	499	0
29	BD	1415	0	1451	166	0
30	BE	1253	0	1289	87	0
31	BF	1111	0	1146	48	0
32	BG	1019	0	1076	134	0
33	BH	1129	0	1162	273	0
34	BI	939	0	1011	95	0
35	BJ	1017	0	1086	283	0
36	BK	1036	0	1109	154	0
37	BL	908	0	946	174	0
38	BM	864	0	902	60	0
39	BN	917	0	965	236	0
40	BO	937	0	1008	249	0
41	BQ	825	0	886	220	0
42	BR	717	0	770	187	0
43	BS	762	0	809	72	0
44	BT	753	0	780	45	0
45	BU	634	0	656	172	0
46	BW	495	0	530	76	0
47	BX	435	0	470	41	0
48	BZ	234	0	235	43	0
49	B1	424	0	461	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	141668	0	94896	10859	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 46.

The worst 5 of 10859 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)
22:B0:1579:A:C2	26:BA:67:LYS:CA	1.76	1.66
22:B0:1996:C:C2	27:BB:138:LEU:CA	1.77	1.62
22:B0:1579:A:C4	26:BA:67:LYS:CA	1.86	1.52
22:B0:1579:A:C4	26:BA:67:LYS:HA	1.38	1.52
22:B0:1421:G:N1	26:BA:149:LYS:CA	1.71	1.51

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AB	230/236 (98%)	193 (84%)	28 (12%)	9 (4%)	4	36
4	AC	204/206 (99%)	160 (78%)	34 (17%)	10 (5%)	3	31
5	AD	202/204 (99%)	177 (88%)	22 (11%)	3 (2%)	13	57
6	AE	146/148 (99%)	135 (92%)	10 (7%)	1 (1%)	26	71
7	AF	93/95 (98%)	81 (87%)	10 (11%)	2 (2%)	8	49
8	AG	135/137 (98%)	114 (84%)	13 (10%)	8 (6%)	2	27
9	AH	125/127 (98%)	113 (90%)	9 (7%)	3 (2%)	7	47
10	AI	124/126 (98%)	93 (75%)	20 (16%)	11 (9%)	1	17
11	AJ	94/96 (98%)	73 (78%)	15 (16%)	6 (6%)	2	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	AK	114/116 (98%)	91 (80%)	14 (12%)	9 (8%)	1	19
13	AL	99/101 (98%)	75 (76%)	19 (19%)	5 (5%)	2	30
14	AM	111/115 (96%)	90 (81%)	18 (16%)	3 (3%)	6	45
15	AN	59/61 (97%)	50 (85%)	5 (8%)	4 (7%)	1	23
16	AO	84/86 (98%)	76 (90%)	8 (10%)	0	100	100
17	AP	76/78 (97%)	62 (82%)	13 (17%)	1 (1%)	15	60
18	AQ	77/79 (98%)	65 (84%)	10 (13%)	2 (3%)	7	45
19	AR	67/69 (97%)	62 (92%)	5 (8%)	0	100	100
20	AS	85/87 (98%)	69 (81%)	12 (14%)	4 (5%)	3	32
21	AT	81/83 (98%)	68 (84%)	11 (14%)	2 (2%)	7	46
24	B2	216/222 (97%)	183 (85%)	27 (12%)	6 (3%)	6	44
25	B3	108/119 (91%)	84 (78%)	18 (17%)	6 (6%)	2	28
25	B5	112/119 (94%)	89 (80%)	16 (14%)	7 (6%)	2	25
26	BA	215/227 (95%)	128 (60%)	56 (26%)	31 (14%)	0	6
27	BB	199/209 (95%)	148 (74%)	37 (19%)	14 (7%)	1	22
28	BC	194/198 (98%)	124 (64%)	45 (23%)	25 (13%)	0	7
29	BD	173/177 (98%)	96 (56%)	54 (31%)	23 (13%)	0	7
30	BE	165/167 (99%)	141 (86%)	22 (13%)	2 (1%)	16	61
31	BF	143/149 (96%)	121 (85%)	16 (11%)	6 (4%)	3	34
32	BG	135/139 (97%)	85 (63%)	33 (24%)	17 (13%)	0	8
33	BH	140/142 (99%)	77 (55%)	41 (29%)	22 (16%)	0	5
34	BI	120/122 (98%)	93 (78%)	20 (17%)	7 (6%)	2	27
35	BJ	136/140 (97%)	69 (51%)	37 (27%)	30 (22%)	0	2
36	BK	129/131 (98%)	93 (72%)	24 (19%)	12 (9%)	1	16
37	BL	110/114 (96%)	67 (61%)	32 (29%)	11 (10%)	1	14
38	BM	111/113 (98%)	90 (81%)	16 (14%)	5 (4%)	3	33
39	BN	112/114 (98%)	50 (45%)	35 (31%)	27 (24%)	0	2
40	BO	111/115 (96%)	59 (53%)	39 (35%)	13 (12%)	0	9
41	BQ	104/106 (98%)	68 (65%)	29 (28%)	7 (7%)	1	24
42	BR	83/92 (90%)	39 (47%)	25 (30%)	19 (23%)	0	2
43	BS	95/99 (96%)	69 (73%)	21 (22%)	5 (5%)	2	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	BT	92/94 (98%)	76 (83%)	13 (14%)	3 (3%)	5	40
45	BU	82/84 (98%)	43 (52%)	23 (28%)	16 (20%)	0	3
46	BW	58/60 (97%)	49 (84%)	5 (9%)	4 (7%)	1	23
47	BX	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
48	BZ	27/29 (93%)	11 (41%)	6 (22%)	10 (37%)	0	0
49	B1	50/52 (96%)	27 (54%)	19 (38%)	4 (8%)	1	19
All	All	5480/5639 (97%)	4077 (74%)	988 (18%)	415 (8%)	2	20

5 of 415 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AB	14	HIS
3	AB	93	HIS
4	AC	126	ARG
4	AC	178	ARG
8	AG	31	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AB	195/195 (100%)	190 (97%)	5 (3%)	54	80
4	AC	170/170 (100%)	164 (96%)	6 (4%)	43	74
5	AD	172/172 (100%)	170 (99%)	2 (1%)	78	90
6	AE	112/112 (100%)	108 (96%)	4 (4%)	42	74
7	AF	83/83 (100%)	80 (96%)	3 (4%)	42	74
8	AG	112/112 (100%)	108 (96%)	4 (4%)	42	74
9	AH	103/103 (100%)	100 (97%)	3 (3%)	50	78
10	AI	104/104 (100%)	100 (96%)	4 (4%)	40	73
11	AJ	84/84 (100%)	80 (95%)	4 (5%)	31	67
12	AK	89/89 (100%)	86 (97%)	3 (3%)	44	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	AL	85/85 (100%)	82 (96%)	3 (4%)	43	74
14	AM	93/93 (100%)	90 (97%)	3 (3%)	46	76
15	AN	52/52 (100%)	51 (98%)	1 (2%)	65	86
16	AO	74/74 (100%)	74 (100%)	0	100	100
17	AP	63/63 (100%)	60 (95%)	3 (5%)	31	67
18	AQ	73/73 (100%)	72 (99%)	1 (1%)	74	89
19	AR	60/60 (100%)	59 (98%)	1 (2%)	68	87
20	AS	75/75 (100%)	73 (97%)	2 (3%)	52	79
21	AT	63/63 (100%)	56 (89%)	7 (11%)	8	34
24	B2	172/172 (100%)	166 (96%)	6 (4%)	43	74
25	B3	83/83 (100%)	81 (98%)	2 (2%)	57	82
25	B5	83/83 (100%)	80 (96%)	3 (4%)	42	74
26	BA	176/176 (100%)	159 (90%)	17 (10%)	10	40
27	BB	164/164 (100%)	160 (98%)	4 (2%)	57	82
28	BC	163/163 (100%)	152 (93%)	11 (7%)	20	57
29	BD	149/149 (100%)	124 (83%)	25 (17%)	2	19
30	BE	130/130 (100%)	123 (95%)	7 (5%)	27	64
31	BF	114/114 (100%)	112 (98%)	2 (2%)	66	87
32	BG	108/108 (100%)	91 (84%)	17 (16%)	3	21
33	BH	116/116 (100%)	94 (81%)	22 (19%)	2	13
34	BI	103/103 (100%)	97 (94%)	6 (6%)	25	61
35	BJ	99/99 (100%)	74 (75%)	25 (25%)	1	6
36	BK	104/104 (100%)	90 (86%)	14 (14%)	5	27
37	BL	94/94 (100%)	80 (85%)	14 (15%)	4	23
38	BM	83/83 (100%)	78 (94%)	5 (6%)	24	60
39	BN	99/99 (100%)	74 (75%)	25 (25%)	1	6
40	BO	89/89 (100%)	70 (79%)	19 (21%)	1	9
41	BQ	89/89 (100%)	76 (85%)	13 (15%)	4	24
42	BR	77/77 (100%)	65 (84%)	12 (16%)	3	21
43	BS	82/82 (100%)	77 (94%)	5 (6%)	23	60
44	BT	78/78 (100%)	75 (96%)	3 (4%)	40	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
45	BU	62/62 (100%)	52 (84%)	10 (16%)	3 20
46	BW	55/55 (100%)	50 (91%)	5 (9%)	12 43
47	BX	47/47 (100%)	45 (96%)	2 (4%)	35 70
48	BZ	24/24 (100%)	18 (75%)	6 (25%)	1 6
49	B1	46/46 (100%)	37 (80%)	9 (20%)	1 12
All	All	4551/4551 (100%)	4203 (92%)	348 (8%)	21 53

5 of 348 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	BH	23	LYS
35	BJ	79	LEU
45	BU	45	HIS
33	BH	41	LYS
34	BI	41	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 139 such sidechains are listed below:

Mol	Chain	Res	Type
21	AT	54	GLN
27	BB	36	GLN
44	BT	44	HIS
24	B2	56	GLN
26	BA	52	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1487/1488 (99%)	248 (16%)	71 (4%)
2	AU	75/76 (98%)	13 (17%)	5 (6%)
2	AV	75/76 (98%)	10 (13%)	4 (5%)
2	AW	75/76 (98%)	13 (17%)	5 (6%)
22	B0	2739/2740 (99%)	541 (19%)	131 (4%)
23	B9	107/108 (99%)	20 (18%)	2 (1%)
All	All	4558/4564 (99%)	845 (18%)	218 (4%)

5 of 845 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	8	A
1	AA	9	G
1	AA	13	U
1	AA	31	G

5 of 218 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	B0	387	U
22	B0	926	G
22	B0	2458	G
22	B0	501	A
22	B0	655	A

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
25	B3	6
26	BA	5
25	B5	4

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Mol	Chain	Number of breaks
27	BB	4
42	BR	4
3	AB	2
31	BF	2
24	B2	2
40	BO	1
37	BL	1
29	BD	1
43	BS	1
35	BJ	1
32	BG	1
28	BC	1
14	AM	1

The worst 5 of 37 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B5	52:THR	C	53:GLU	N	10.02
1	BA	60:ALA	C	61:TYR	N	9.99
1	B5	50:GLU	C	51:LYS	N	9.70
1	BB	167:ASN	C	168:GLU	N	8.31
1	BC	96:VAL	C	97:ASN	N	7.51