



wwPDB X-ray Structure Validation Summary Report i

Jun 16, 2014 – 06:14 PM BST

PDB ID : 4V49
Title : Crystal Structure of a Streptomycin Dependent Ribosome from E. Coli 70S Ribosome.
Authors : Vila-Sanjurjo, A.; Ridgeway, W.K.; Seymaner, V.; Zhang, W.; Santoso, S.; Yu, K.; Cate, J.H.D.
Deposited on : 2003-06-13
Resolution : 8.70 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

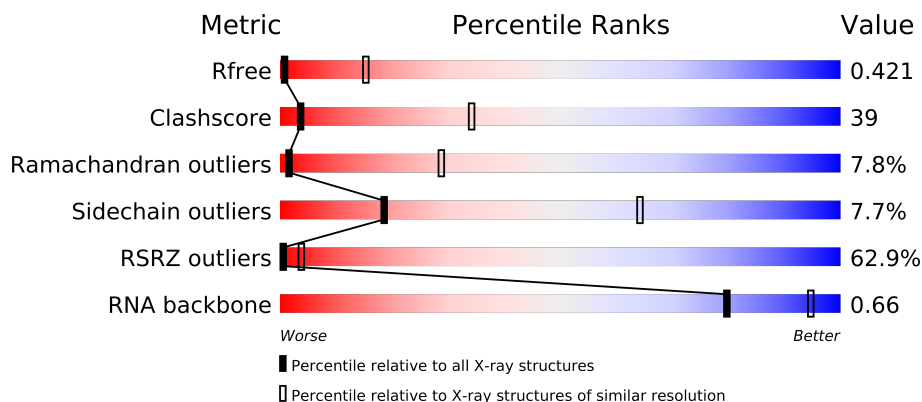
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1323
EDS : stable23397
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23397

1 Overall quality at a glance

The reported resolution of this entry is 8.70 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1106 (11.50-3.50)
Clashscore	79885	1008 (12.70-3.54)
Ramachandran outliers	78287	1303 (12.70-3.50)
Sidechain outliers	78261	1277 (12.70-3.50)
RSRZ outliers	66119	1105 (11.50-3.50)
RNA backbone	1838	1055 (11.50-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	AA	1527	
2	AV	76	
2	AW	76	
3	AU	18	
4	AB	234	
5	AC	206	
6	AD	208	
7	AE	150	
8	AF	101	
9	AG	155	
10	AH	138	
11	AI	127	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
12	AJ	98	
13	AK	119	
14	AL	124	
15	AM	125	
16	AN	60	
17	AO	88	
18	AP	83	
19	AQ	104	
20	AR	73	
21	AS	80	
22	AT	99	
23	B0	2887	
24	B9	118	
25	BA	270	
26	BB	205	
27	BC	197	
28	BD	178	
29	BE	177	
30	BF	52	
31	BG	143	
32	BH	143	
33	BI	132	
34	BJ	141	
35	BK	124	
36	BL	114	
37	BM	111	
38	BN	125	
39	BO	117	
40	BP	100	
41	BQ	130	
42	BR	93	
43	BS	113	
44	BT	173	
45	BU	86	
46	BV	16	
47	BW	65	
48	BX	55	
49	BY	73	
50	BZ	58	
51	B1	53	
52	B2	46	
53	B3	63	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	B4	35	
55	B5	217	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 122017 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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					ZeroOcc	AltConf	Trace
1	AA	1527	Total	C	N	O	P	0	0	0
			32819	14610	6085	10597	1527			

- Molecule 2 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AV	76	Total	C	N	O	P	0	0	0
			1625	725	293	531	76			
2	AW	76	Total	C	N	O	P	0	0	0
			1625	725	293	531	76			

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AU	9	Total	C	N	O	P	0	0	0
			176	81	24	62	9			

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AB	234	Total	C	N	O	S	0	0	0
			1900	1213	341	341	5			

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AC	206	Total	C	N	O	S	0	0	0
			1612	1016	314	281	1			

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AD	208	Total	C	N	O	S	0	0	0
			1702	1066	339	290	7			

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AE	150	Total	C	N	O	S	0	0	0
			1146	724	217	201	4			

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AF	101	Total	C	N	O	S	0	0	0
			842	531	155	153	3			

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AG	155	Total	C	N	O	S	0	0	0
			1256	781	252	217	6			

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AH	138	Total	C	N	O	S	0	0	0
			1115	705	215	192	3			

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AI	127	Total	C	N	O		0	0	0
			1010	639	198	173				

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AJ	98	Total	C	N	O	S	0	0	0
			794	499	156	138	1			

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AK	119	Total	C	N	O	S	0	0	0
			884	549	168	164	3			

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AL	124	Total	C	N	O	S	0	0	0
			970	611	195	163	1			

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AM	125	Total	C	N	O	S	0	0	0
			996	617	207	170	2			

- Molecule 16 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AN	60	Total	C	N	O	S	0	0	0
			491	312	104	71	4			

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AO	88	Total	C	N	O	S	0	0	0
			733	459	147	125	2			

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	AP	83	Total	C	N	O	S	0	0	0
			700	443	139	117	1			

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AQ	104	Total	C	N	O	S	0	0	0
			856	547	161	146	2			

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	AR	73	Total	C	N	O	0	0	0
			596	380	118	98			

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AS	80	Total	C	N	O	S	0	0	0
			647	414	119	112	2			

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AT	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			

- Molecule 23 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	B0	2825	Total	C	N	O	P	0	0	0
			60636	27047	11191	19573	2825			

- Molecule 24 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	B9	118	Total	C	N	O	P	0	0	0
			2519	1124	464	813	118			

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
25	BA	270	Total C	0	0	270
			270 270			

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
26	BB	205	Total C	0	0	205
			205 205			

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
27	BC	197	Total C 197 197	0	0	197

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
28	BD	178	Total C 178 178	0	0	178

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
29	BE	177	Total C 177 177	0	0	177

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
30	BF	52	Total C 52 52	0	0	52

- Molecule 31 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
31	BG	143	Total C 143 143	0	0	143

- Molecule 32 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
32	BH	143	Total C 143 143	0	0	143

- Molecule 33 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
33	BI	132	Total C 132 132	0	0	132

- Molecule 34 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
34	BJ	141	Total	C	0	0	141
			141	141			

- Molecule 35 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
35	BK	124	Total	C	0	0	124
			124	124			

- Molecule 36 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
36	BL	114	Total	C	0	0	114
			114	114			

- Molecule 37 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
37	BM	111	Total	C	0	0	111
			111	111			

- Molecule 38 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
38	BN	125	Total	C	0	0	125
			125	125			

- Molecule 39 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
39	BO	117	Total	C	0	0	117
			117	117			

- Molecule 40 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
40	BP	100	Total	C	0	0	100
			100	100			

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
41	BQ	130	Total C 130 130	0	0	130

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
42	BR	93	Total C 93 93	0	0	93

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
43	BS	113	Total C 113 113	0	0	113

- Molecule 44 is a protein called general stress protein Ctc.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
44	BT	173	Total C 173 173	0	0	173

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
45	BU	86	Total C 86 86	0	0	86

- Molecule 46 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
46	BV	16	Total C 16 16	0	0	16

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
47	BW	65	Total C 65 65	0	0	65

- Molecule 48 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
48	BX	55	Total C 55 55	0	0	55

- Molecule 49 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
49	BY	73	Total C 73 73	0	0	73

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
50	BZ	58	Total C 58 58	0	0	58

- Molecule 51 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
51	B1	53	Total C 53 53	0	0	53

- Molecule 52 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
52	B2	46	Total C 46 46	0	0	46

- Molecule 53 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
53	B3	63	Total C 63 63	0	0	63

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
54	B4	35	Total C 35 35	0	0	35

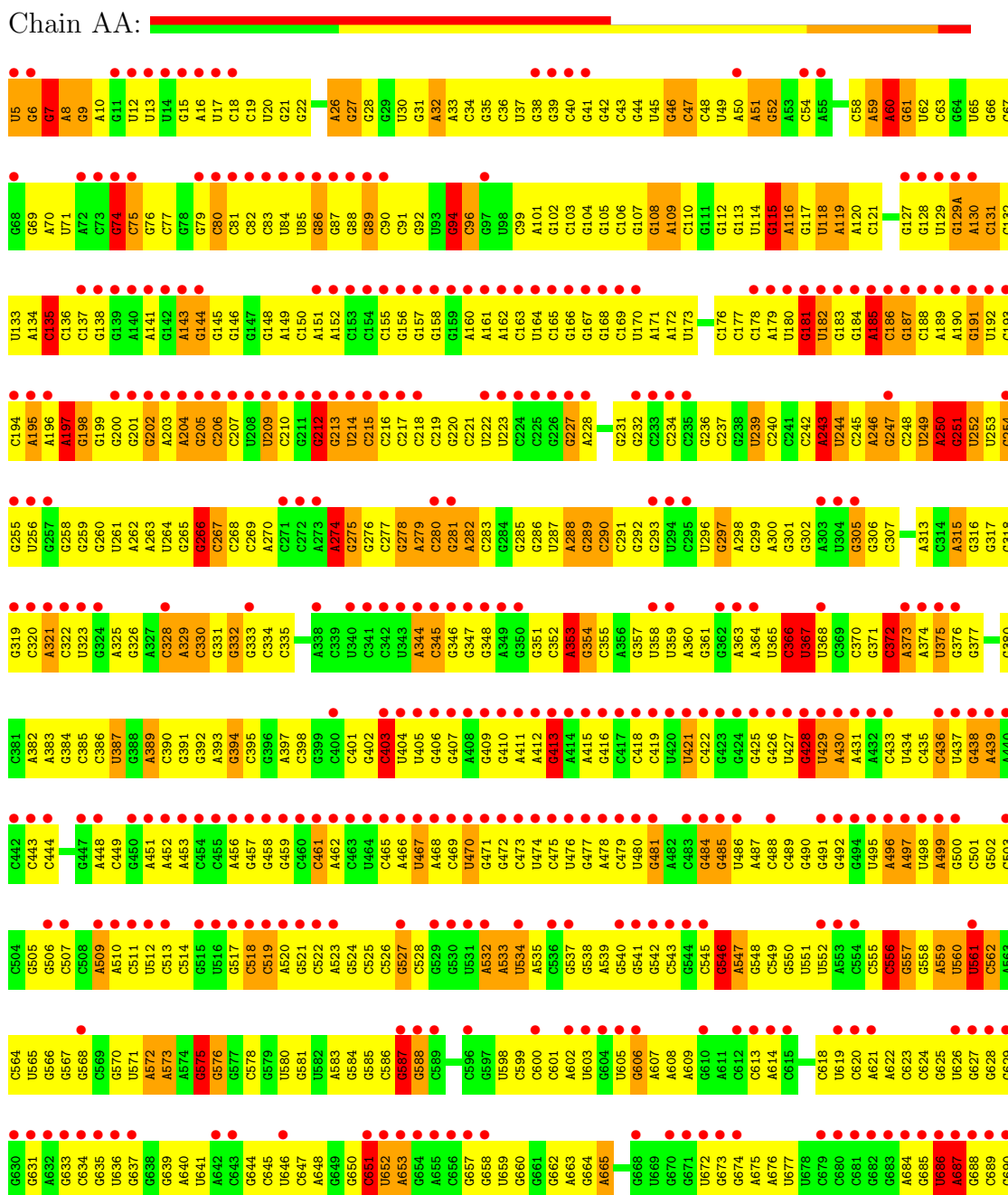
- Molecule 55 is a protein called 50S ribosomal protein L1P.

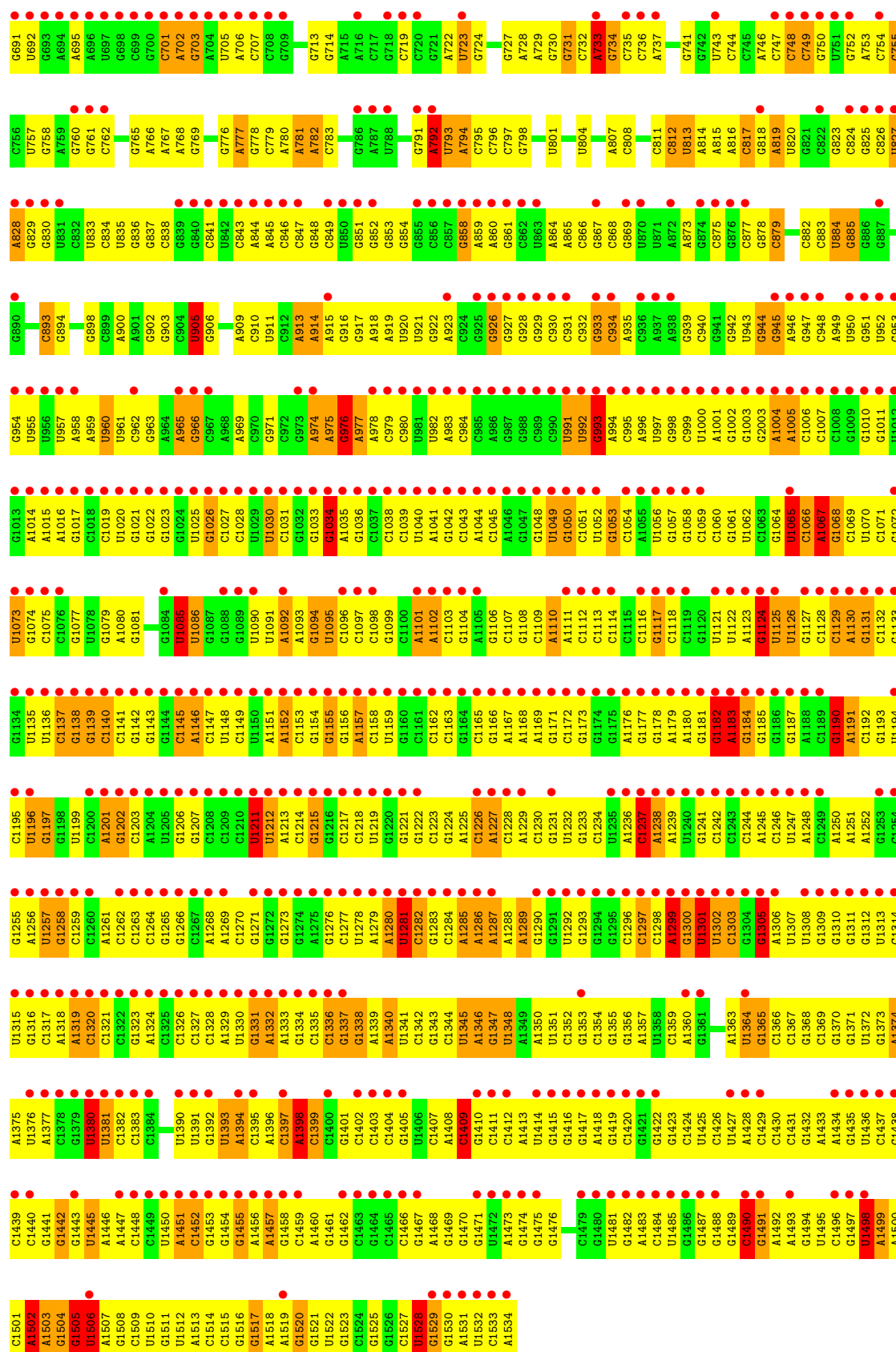
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
55	B5	217	Total 217	C 217	0	0	217

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

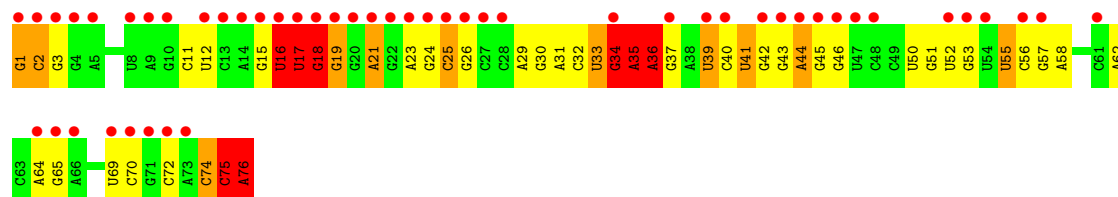
• Molecule 1: 16S RIBOSOMAL RNA





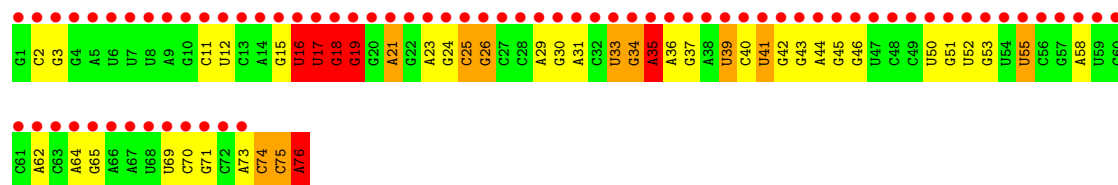
• Molecule 2: tRNA-Phe

Chain AV:



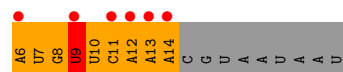
- Molecule 2: tRNA-Phe

Chain AW:



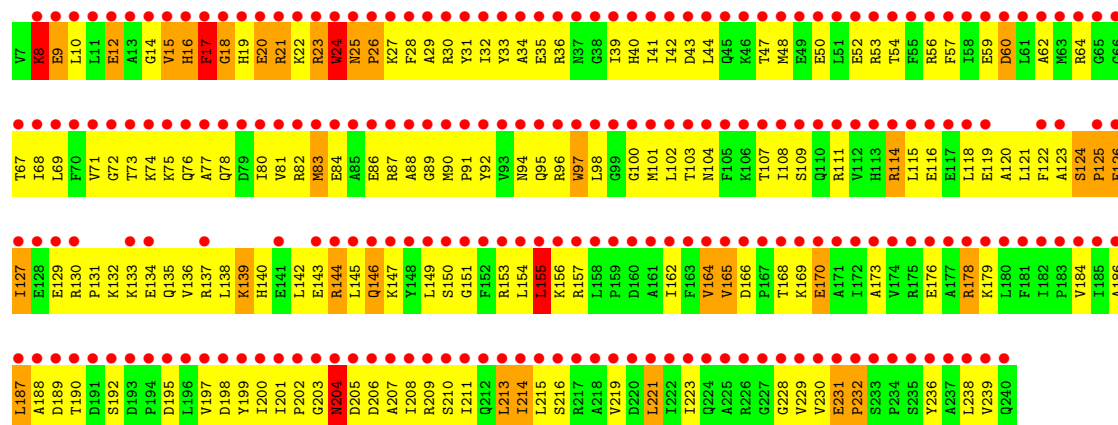
- Molecule 3: mRNA

Chain AU:



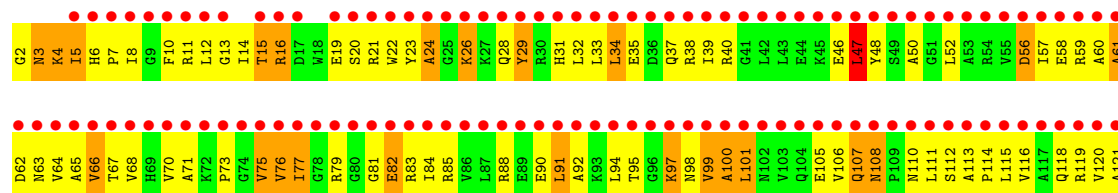
- Molecule 4: 30S ribosomal protein S2

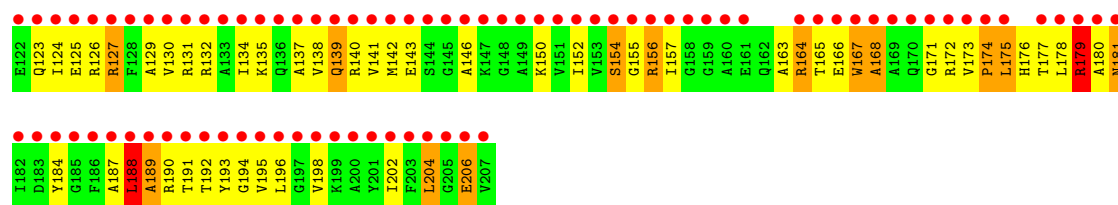
Chain AB:



- Molecule 5: 30S ribosomal protein S3

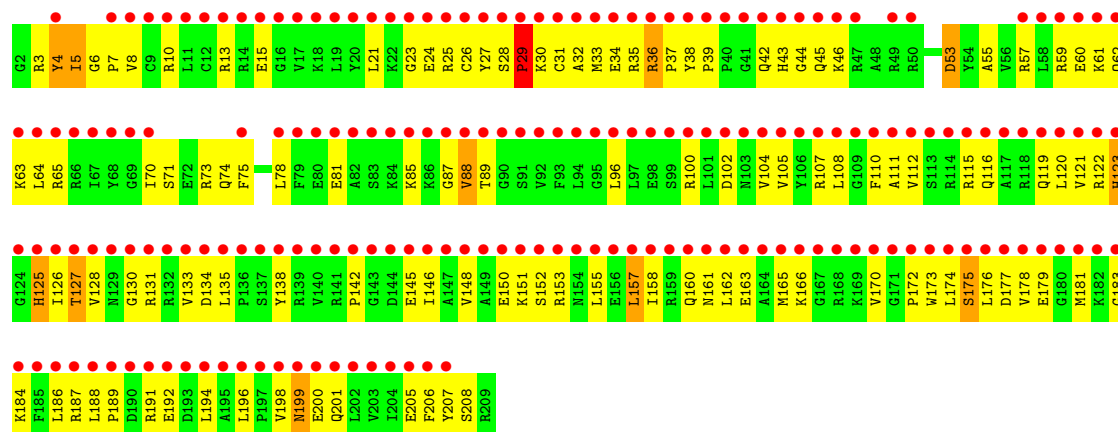
Chain AC:





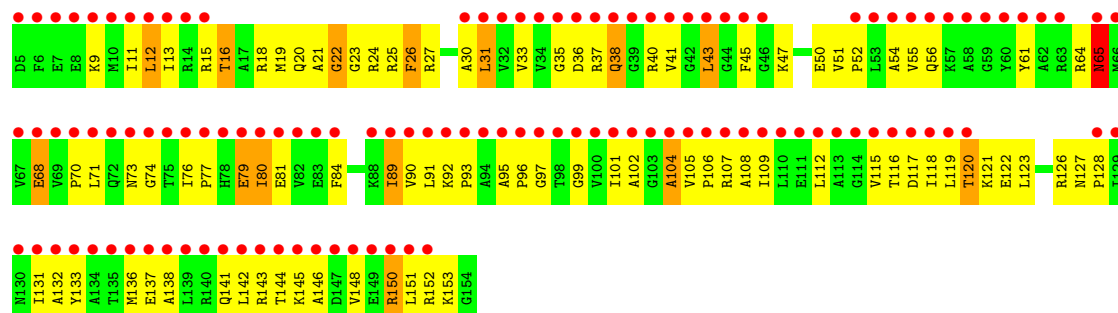
• Molecule 6: 30S ribosomal protein S4

Chain AD:



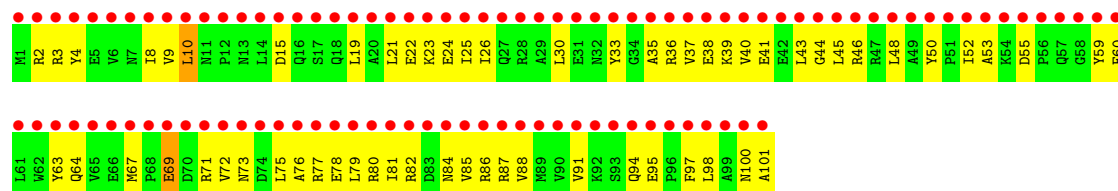
• Molecule 7: 30S ribosomal protein S5

Chain AE:



• Molecule 8: 30S ribosomal protein S6

Chain AF:



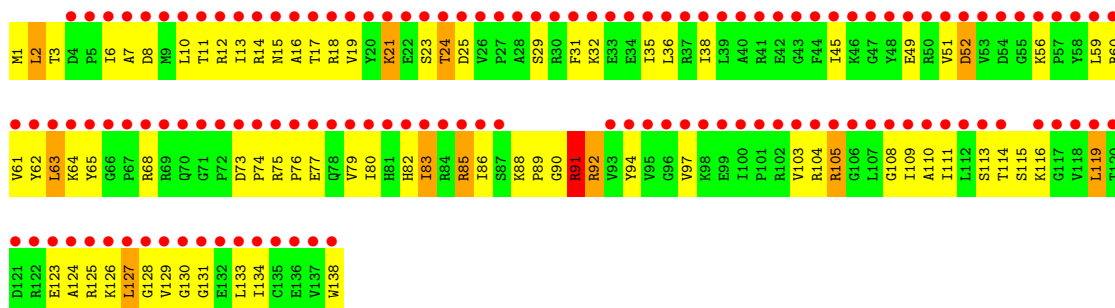
• Molecule 9: 30S ribosomal protein S7

Chain AG:



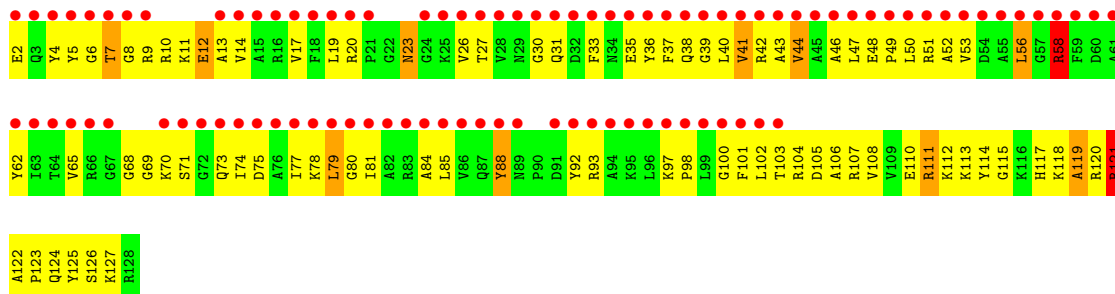
• Molecule 10: 30S ribosomal protein S8

Chain AH:



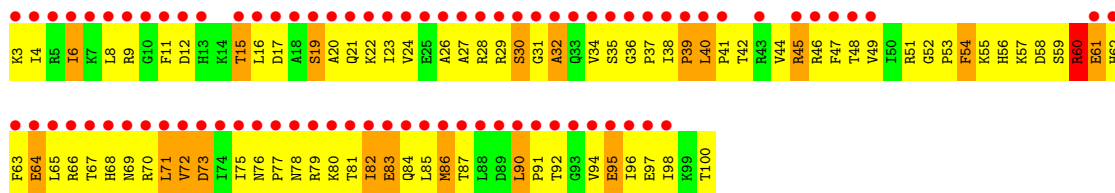
• Molecule 11: 30S ribosomal protein S9

Chain AI:



• Molecule 12: 30S ribosomal protein S10

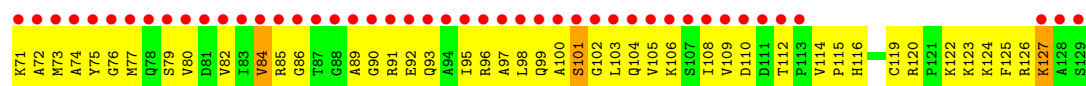
Chain AJ:



• Molecule 13: 30S ribosomal protein S11

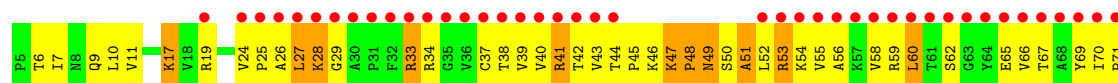
Chain AK:





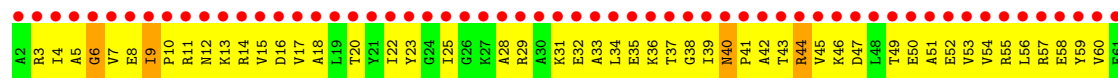
• Molecule 14: 30S ribosomal protein S12

Chain AL:



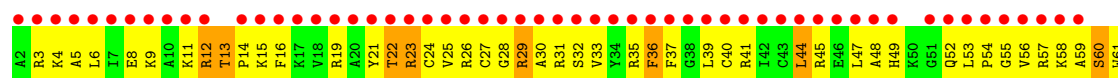
• Molecule 15: 30S ribosomal protein S13

Chain AM:



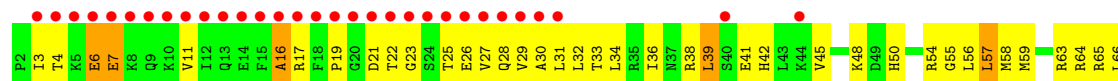
• Molecule 16: 30S ribosomal protein S14

Chain AN:



• Molecule 17: 30S ribosomal protein S15

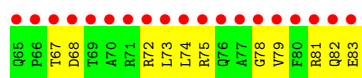
Chain AO:



• Molecule 18: 30S ribosomal protein S16

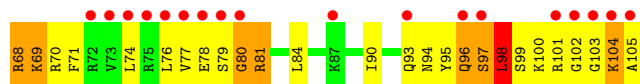
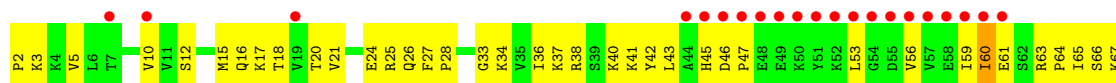
Chain AP:





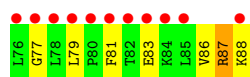
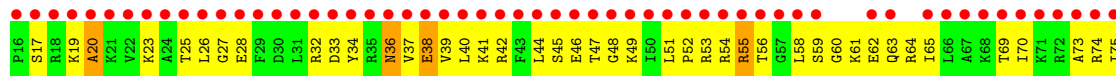
• Molecule 19: 30S ribosomal protein S17

Chain AQ:



• Molecule 20: 30S ribosomal protein S18

Chain AR:



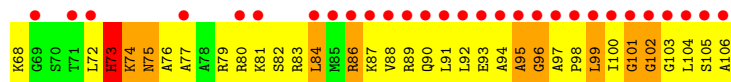
• Molecule 21: 30S ribosomal protein S19

Chain AS:



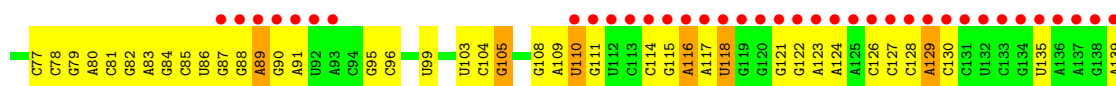
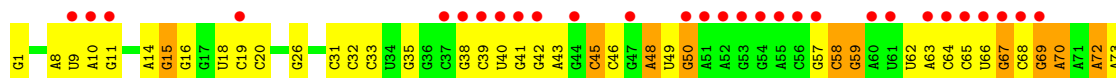
• Molecule 22: 30S ribosomal protein S20

Chain AT:



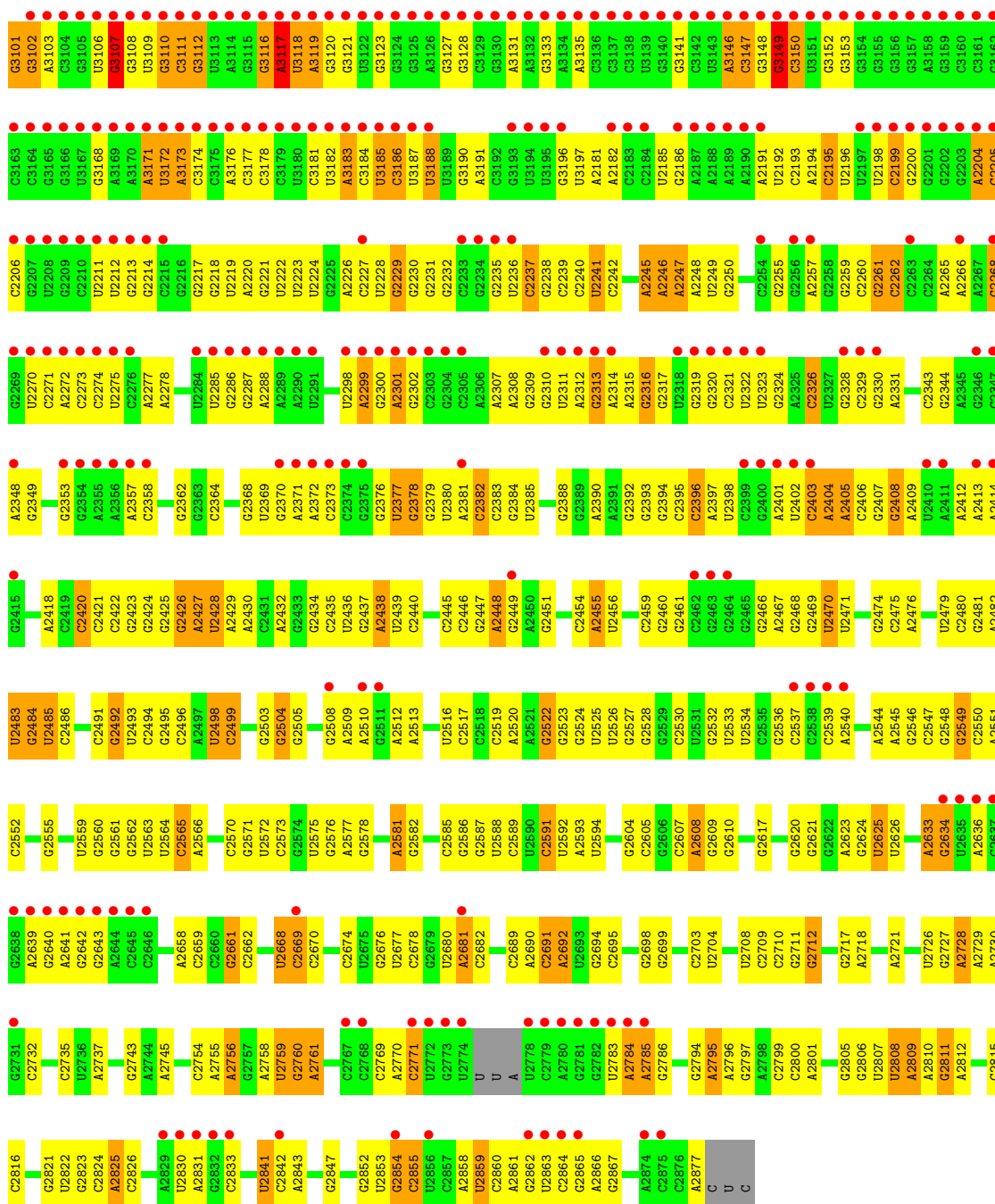
• Molecule 23: 23S RIBOSOMAL RNA

Chain B0:



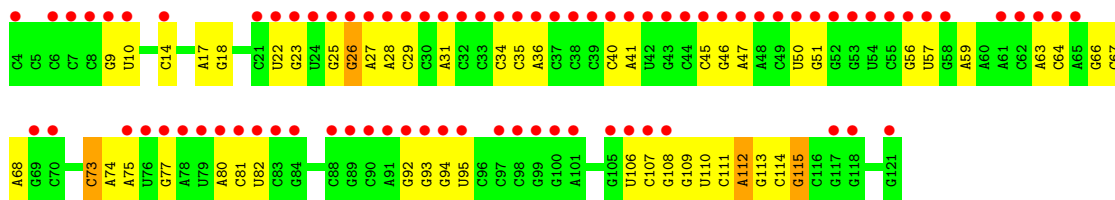


G2021	A1949	A1884	C1829	G1749	A1605	G1542	U1482	C1418	C1347	A1282	G1204	A1140
C2022	C1950	C1885	C1830	A1750	C1606	G1543	G1483	G1419	C1348	C1283	G1205	U1141
C2023	G1951	A1886	G1831	A1754	U1607	A1544	G1484	U1421	A1349	A1284	G1206	G1142
U2024	A1952	G1887	G1832	G1755	U1608	G1545	U1485	U1421	G1350	A1285	G1207	
A2025	A1953	C1888	G1833	G1756	G1609	G1546	A1486	A1422	G1351	U1286		G1145
C2026	G1954	G1889	G1834	G1757	A1610	U1547	C1487	A1423	G1352	U1287	C1210	G1146
C2027	G1955	G1890	G1835	G1760	U1611	U1548	G1488	U1424	A1353	A1288	G1211	G1147
C2028	G1956	G1891	G1836	G1761	U1612	U1549	G1489	U1425	A1354	A1289	G1148	
G2029	C1957	C1892	A1840	G1762	G1613	C1550	U1490	U1426	A1355	A1290	G1149	
U2030	G1958	G1841	G1842	G1763	C1614	U1551	C1491	G1427	G1356	G1291	C1214	
A2031	A1895	G1843	G1844	G1764	C1615	C1552	A1492	G1428	U1357	A1292	U1217	U1151
G2032	A1961	C1897	C1844	G1765	C1616	G1553	A1493	A1429	G1358	A1293	U1218	G1152
C2033	G1962	C1898	C1845	U1766	U1617	U1554	G1494	A1430	G1359	A1294	C1219	
A2034	G1963	U1899	A1846	U1770	U1618	A1555	G1495	U1431	G1360	U1295	G1220	A1154
G2035	A1964	A1899	G1847	A1771	A1619	A1556	G1496	U1432	G1361	G1296	G1221	G1155
G2036	U1965	A1900	G1848	C1772	C1620	U1557	C1497	A1433	A1362	A1297	G1222	U1156
A2037	C1966	A1901	U1849	C1773	G1621	C1558	G1498			G1298	G1223	G1157
G2038	A2037	A1902	G1850	A1774	C1622	U1559	A1499	G1436	U1365	A1299	A1224	U1158
C2039	G1970		G1851	A1775	C1623	A1560	U1500	A1437	A1366	A1300	G1225	U1159
A2040	C1971	G1905	A1851	A1776	A1624	A1561	C1501		G1367	A1301	A1226	
G2041	G1972	U1906	G1852	U1777	A1625	U1562	U1502	A1441	G1368	C1302		
A2042	C1973	C1907	C1853	A1778	A1626	U1563	G1503	A1442	G1373	U1307	U1232	C1164
G2043	U1974	C1908	G1854	U1779	A1627	U1564	G1504	G1443	G1374	A1233	U1233	C1165
A2044	G1975	U1909	G1855	C1779	C1627	G1565	U1505	A1444		G1308	A1234	A1166
G2045	U1976	A1910	U1856	A1780	A1632	G1566	C1506	A1445	C1380	C1310	G1235	G1168
C2046	C1977	A1911	A3865		C1633	A1567	A1507	U1446	G1381	G1311	G1236	G1169
C2047	U1978	G1912	A3866	A1785	A1634	A1568	U1508	U1447		U1309	G1237	U1170
C2048	C1979	G1913	G3867	G1786	U1635	A1569	A1509	U1448	G1386	A1314		A1171
C2049	U1980	U1914	U3868	G1787	A1715	C1570	A1510	G1450	G1387	U1313	G1248	U1172
G2050	A1981	A1915	G3869	U1788	G1640	G1571	A1512	C1451	C1388	A1315	G1249	G1173
U2051	C1982	G1916	C3870	U1789	C1641	C1572	U1513	U1452	G1389	G1316	A1250	G1174
G2052	G1983	G1917	A3871	G1790	G1642	C1573	U1514	U1453	G1390	A1251	G1251	A1175
		G1918	A3872	G1791	A1643	A1574	U1515	U1454	A1391	A1317	C1252	U1176
		A1919	G3873	G1792	G1644	C1575	U1516	U1455	U1392	A1318	C1253	U1177
		A1920	C3874	A1793	G1645	G1576	A1517	C1456	G1393	C1319	G1254	
		A1921	A3875	A1794	C1648	C1577	G1518	A1457	G1394	G1322	A1180	
		U1922	A3876		A1649	U1578	G1519	A1458	A1395	G1323	C1181	
		U1923	A3877	A1799	U1651	G1579	G1520	U1459	C1396	U1257	C1182	
		C1924	G1861	A1800		C1580	U1521	G1460	A1397	G1258	C1183	
		C1925	C1726	C1801	U1651	C1581	C1522	C1461	G1398	A1259	G1184	
		U1926	C1727	A1802	A1654	A1582	A1523	C1462	C1399	C1327	U1261	
		U1927	G1871	A1802	C1655	A1583	A1524	A1463	G1400	C1328	U1262	
		U1928	G1865	G1805	U1656	G1584	A1525	A1464	G1401	U1329	G1263	
		G1929	A1867	G1806	A1657	A1585	U1526	G1465	G1402	G1330	G1264	
		C1930	A1868	A1807	A1658	A1586	G1527	C1466	U1403	G1331	G1265	
		G1931	A1869	C1808	G1659	C1587	G1528	U1467	C1404	G1332	G1266	
		G1932	U1870	G1809	G1660	C1588	C1529	U1468	A1405	G1333	A1267	
		G1933	G1871	U1810	C1661	U1591	U1530	A1469	A1406	A1334	U1268	
		U1934	A1872	A1811	G1662	U1592	C1531	G1470	G1407	A1335	G1269	
		A1935	A1873	U1812	C1663	U1593	A1532	G1471	U1408	U1336	U1194	
			G1874	A1813	G1664	A1595	G1533	G1472	U1409	G1337	U1195	
		U1938	C1875		C1665	A1596	G1534	U1473	U1410	G1338	G1272	
		U1939	G1876	G1818	G1666	A1597	C1535	U1474	C1411	G1339	U1197	
			C1877	U1819	A1667	C1598	U1536	U1475	G1412	G1341	G1273	
		A1943	G1878	G1820	G1668	U1599	G1537	G1476	U1413	U1342	C1274	
		C1944	A1879	A1821	A1669	U1600	U1538		U1414	C1343	U1198	
		G1945	G1880		G1670	U1601	A1538		G1414	G1344	G1200	
		C1946	U1881	C1825	A1671	G1602	U1539	G1479	C1415	A1278	G1279	
			G1882	U1826	A1672	A1603	C1540	G1480	A1416	U1280	U1202	
			A1883		C1673	A1604	G1541	U1481	C1417	C1346	A1203	



• Molecule 24: 5S RIBOSOMAL RNA

Chain B9:



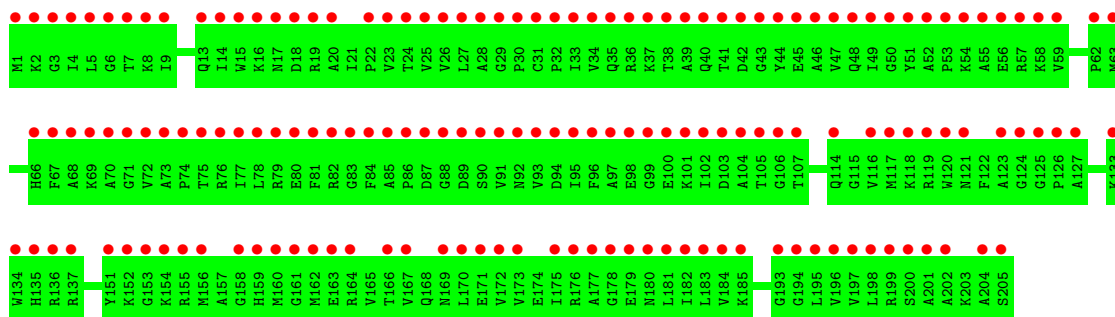
• Molecule 25: 50S ribosomal protein L2

Chain BA:



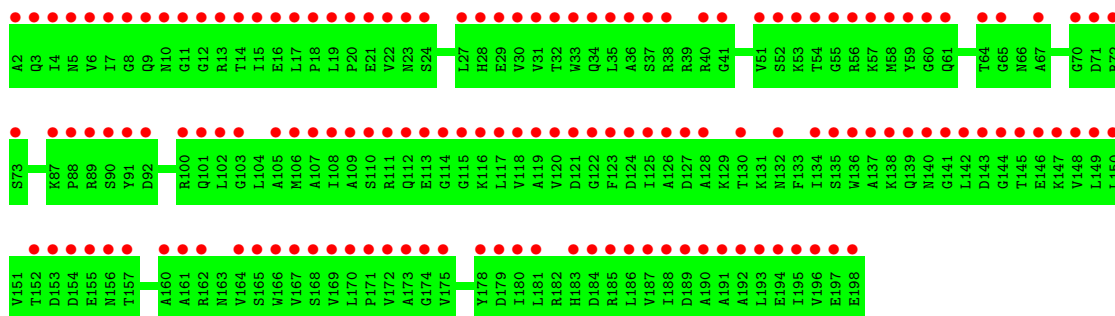
- Molecule 26: 50S ribosomal protein L3

Chain BB:



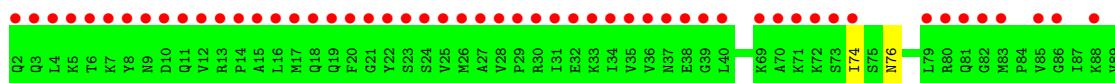
- Molecule 27: 50S ribosomal protein L4

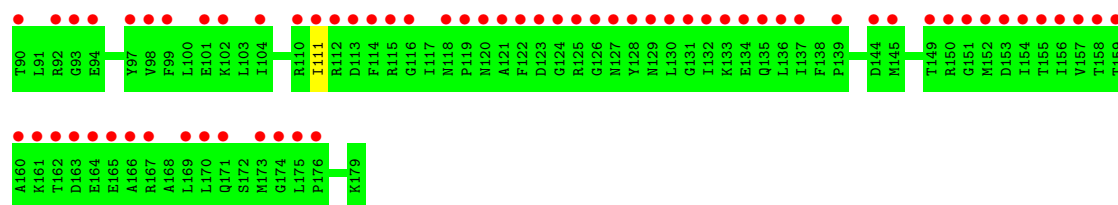
Chain BC:



- Molecule 28: 50S ribosomal protein L5

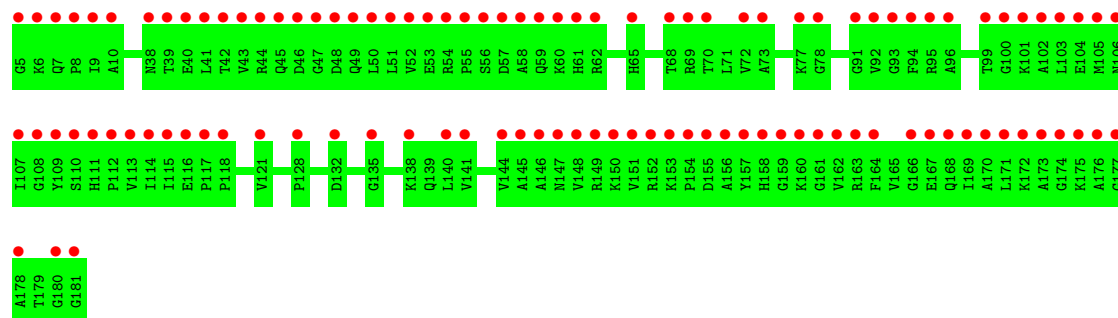
Chain BD:





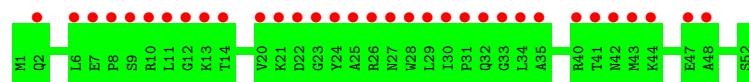
- Molecule 29: 50S ribosomal protein L6

Chain BE:



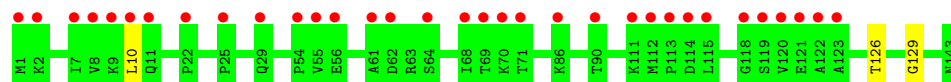
- Molecule 30: 50S ribosomal protein L9

Chain BF:



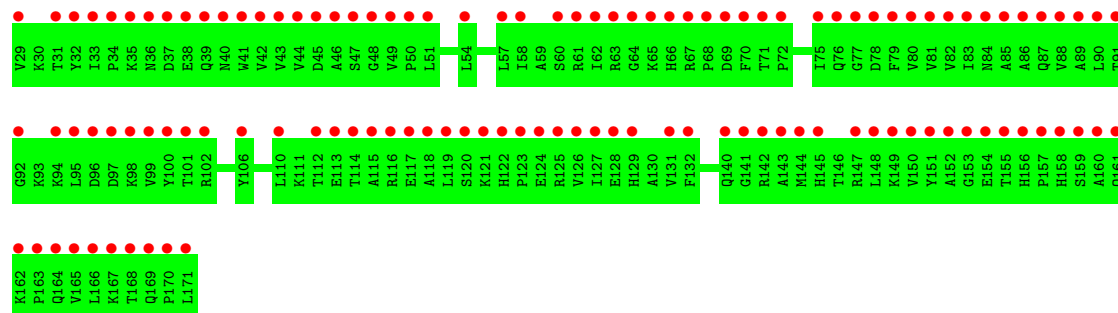
- Molecule 31: 50S ribosomal protein L11

Chain BG:



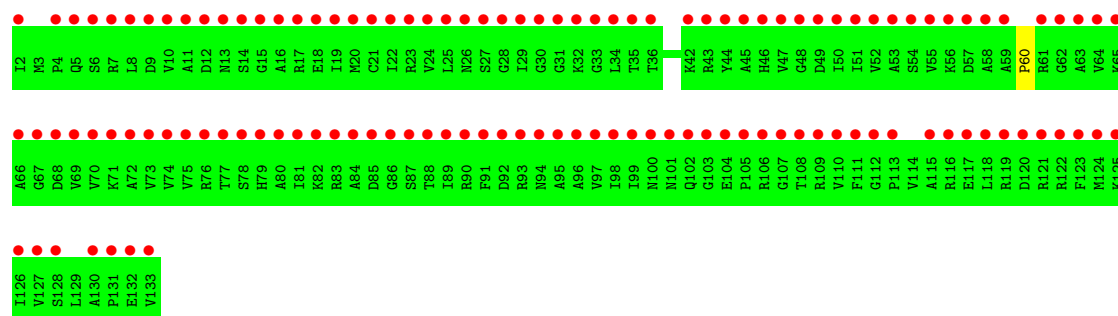
- Molecule 32: 50S ribosomal protein L13

Chain BH:



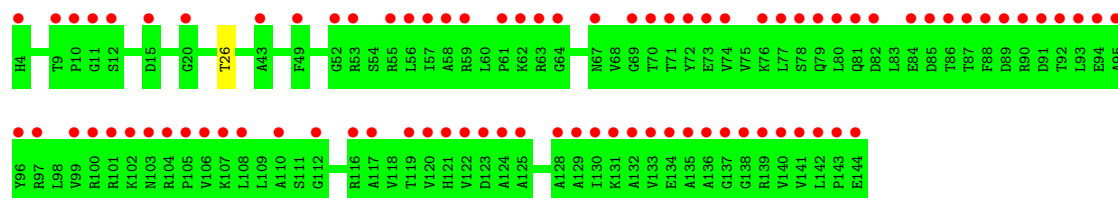
- Molecule 33: 50S ribosomal protein L14

Chain BI:



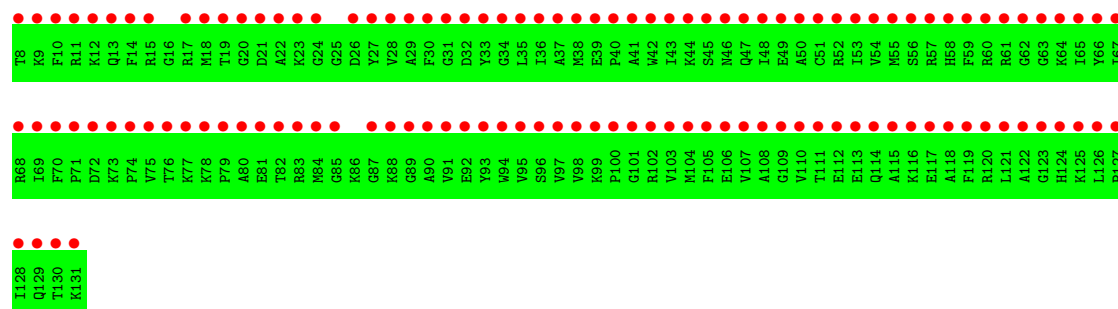
- Molecule 34: 50S ribosomal protein L15

Chain BJ:



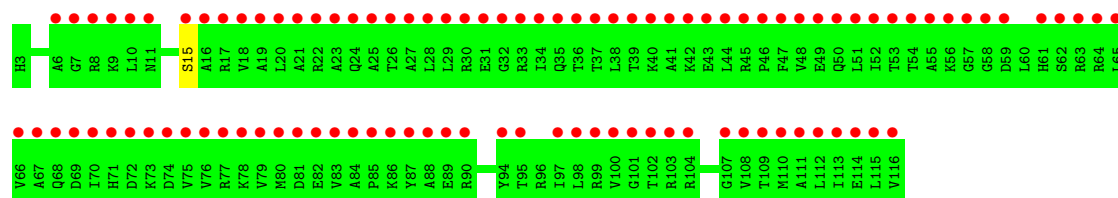
- Molecule 35: 50S ribosomal protein L16

Chain BK:



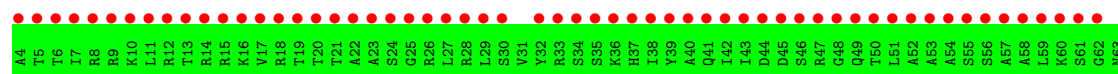
- Molecule 36: 50S ribosomal protein L17

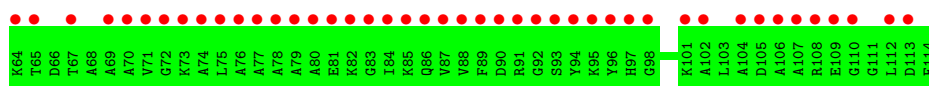
Chain BL:



- Molecule 37: 50S ribosomal protein L18

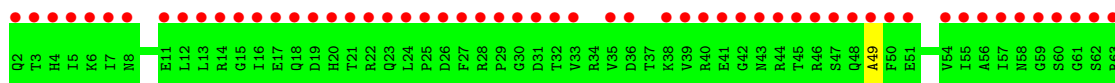
Chain BM:





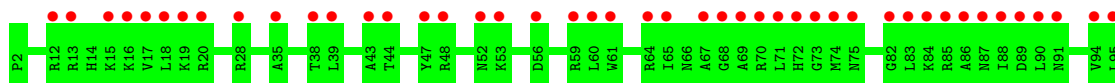
- Molecule 38: 50S ribosomal protein L19

Chain BN:



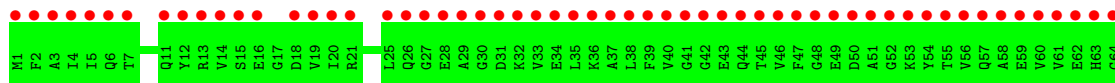
- Molecule 39: 50S ribosomal protein L20

Chain BO:



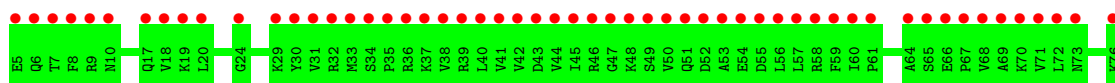
- Molecule 40: 50S ribosomal protein L21

Chain BP:



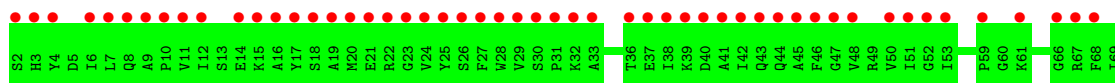
- Molecule 41: 50S ribosomal protein L22

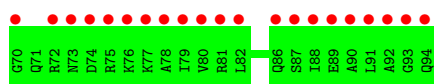
Chain BQ:



- Molecule 42: 50S ribosomal protein L23

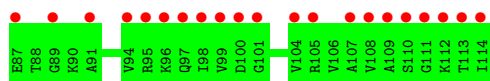
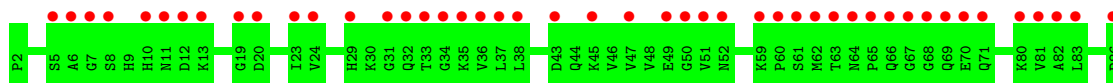
Chain BR:





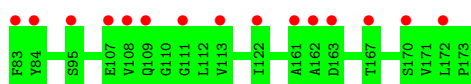
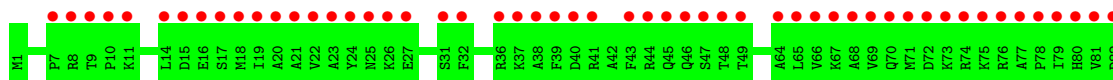
- Molecule 43: 50S ribosomal protein L24

Chain BS:



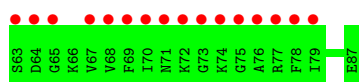
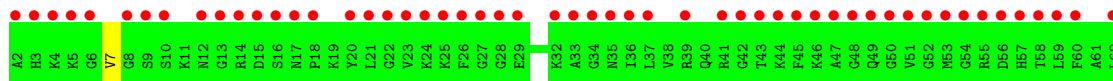
- Molecule 44: general stress protein Ctc

Chain BT:



- Molecule 45: 50S ribosomal protein L27

Chain BU:



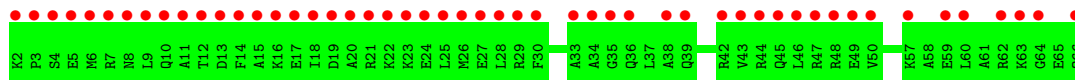
- Molecule 46: 50S RIBOSOMAL PROTEIN L28

Chain BV:

There are no outlier residues recorded for this chain.

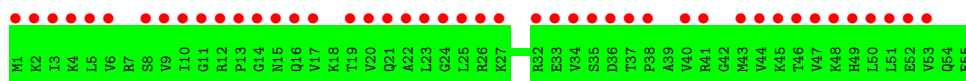
- Molecule 47: 50S ribosomal protein L29

Chain BW:



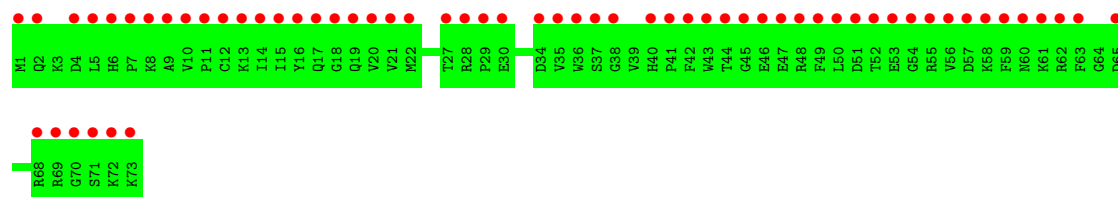
- Molecule 48: 50S ribosomal protein L30

Chain BX:



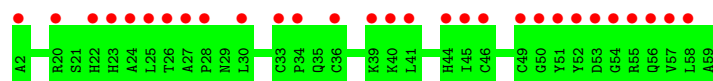
- Molecule 49: 50S ribosomal protein L31

Chain BY: 



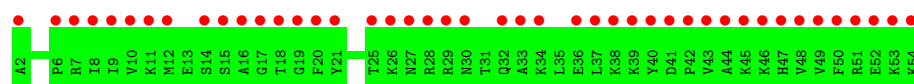
- Molecule 50: 50S ribosomal protein L32

Chain BZ: 



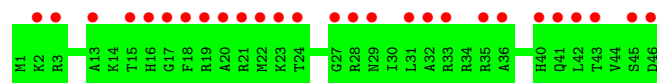
- Molecule 51: 50S ribosomal protein L33

Chain B1: 



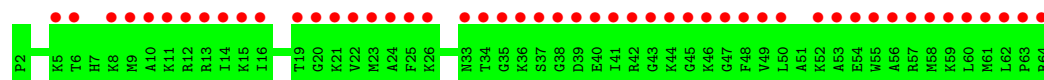
- Molecule 52: 50S ribosomal protein L34

Chain B2: 



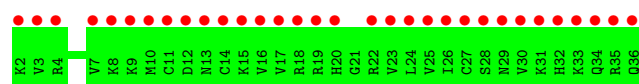
- Molecule 53: 50S ribosomal protein L35

Chain B3: 



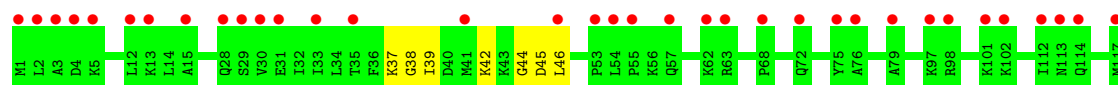
- Molecule 54: 50S ribosomal protein L36

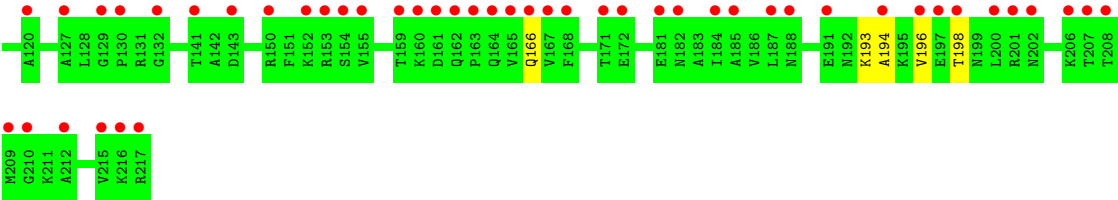
Chain B4: 



- Molecule 55: 50S ribosomal protein L1P

Chain B5: 





4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	682.32Å 682.32Å 386.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.00 – 8.70 241.24 – 8.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (70.00-8.70) 93.0 (241.24-8.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.97 (at 8.45Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.394 , 0.415 0.385 , 0.421	Depositor DCC
R_{free} test set	1778 reflections (5.17%)	DCC
Wilson B-factor (Å ²)	443.4	Xtriage
Anisotropy	0.381	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	-0.32 , 3000.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 37559 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	122017	wwPDB-VP
Average B, all atoms (Å ²)	641.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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 >5	RMSZ	# Z >5
1	AA	1.53	69/36688 (0.2%)	1.32	264/57135 (0.5%)
2	AV	2.23	23/1817 (1.3%)	1.84	42/2831 (1.5%)
2	AW	1.75	19/1816 (1.0%)	1.94	32/2827 (1.1%)
3	AU	45.18	35/188 (18.6%)	20.47	49/274 (17.9%)
4	AB	0.37	0/1935	0.68	1/2609 (0.0%)
5	AC	0.38	0/1636	0.66	0/2205
6	AD	0.37	0/1732	0.63	0/2318
7	AE	0.48	0/1162	0.79	0/1564
8	AF	0.34	0/855	0.63	0/1154
9	AG	0.35	0/1275	0.62	0/1709
10	AH	0.44	0/1135	0.74	0/1527
11	AI	0.36	0/1028	0.62	0/1378
12	AJ	0.36	0/807	0.71	0/1085
13	AK	0.39	0/899	0.70	0/1213
14	AL	0.70	1/986 (0.1%)	0.76	1/1320 (0.1%)
15	AM	0.44	1/1007 (0.1%)	1.11	3/1347 (0.2%)
16	AN	0.40	0/500	0.78	0/664
17	AO	0.36	0/744	0.63	1/992 (0.1%)
18	AP	0.43	0/716	0.76	0/963
19	AQ	0.44	0/869	0.75	0/1159
20	AR	0.36	0/602	0.63	0/799
21	AS	0.35	0/661	0.72	1/890 (0.1%)
22	AT	0.39	0/764	0.73	0/1006
23	B0	0.49	17/67885 (0.0%)	0.75	49/105852 (0.0%)
24	B9	0.68	1/2815 (0.0%)	0.76	3/4384 (0.1%)
All	All	1.97	166/130522 (0.1%)	1.25	446/199205 (0.2%)

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

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
-----	-------	---------------------	---------------------

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	2	40
2	AV	0	7
2	AW	0	7
23	B0	0	5
All	All	2	59

The worst 5 of 166 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	AU	14	A	C6-N6	279.73	3.57	1.33
3	AU	13	A	C6-N6	279.69	3.57	1.33
3	AU	6	A	C6-N6	279.55	3.57	1.33
3	AU	12	A	C6-N6	279.29	3.57	1.33
3	AU	8	G	C6-O6	259.50	3.57	1.24

The worst 5 of 446 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	AU	8	G	C5-C6-O6	-177.72	21.96	128.60
3	AU	6	A	C5-C6-N6	-127.11	22.02	123.70
3	AU	14	A	C5-C6-N6	-127.08	22.03	123.70
3	AU	12	A	C5-C6-N6	-127.07	22.05	123.70
3	AU	13	A	C5-C6-N6	-127.04	22.07	123.70

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	181	G	C3'
1	AA	1528	U	C3'

5 of 59 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	12	U	Sidechain
1	AA	187	G	Sidechain
1	AA	191	G	Sidechain
1	AA	197	A	Sidechain
1	AA	231	G	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32819	0	16577	3629	5
2	AV	1625	0	821	141	0
2	AW	1625	0	819	141	0
3	AU	176	0	79	11	0
4	AB	1900	0	1951	231	0
5	AC	1612	0	1676	292	0
6	AD	1702	0	1767	227	4
7	AE	1146	0	1207	233	0
8	AF	842	0	857	81	4
9	AG	1256	0	1294	119	0
10	AH	1115	0	1177	122	0
11	AI	1010	0	1043	172	0
12	AJ	794	0	838	216	0
13	AK	884	0	903	187	0
14	AL	970	0	1055	157	0
15	AM	996	0	1071	145	0
16	AN	491	0	531	160	0
17	AO	733	0	771	55	0
18	AP	700	0	720	96	0
19	AQ	856	0	926	355	0
20	AR	596	0	667	83	0
21	AS	647	0	673	129	0
22	AT	762	0	848	259	0
23	B0	60636	0	30552	1930	8
24	B9	2519	0	1287	43	0
25	BA	270	0	0	0	0
26	BB	205	0	0	0	0
27	BC	197	0	0	0	0
28	BD	178	0	0	12	0
29	BE	177	0	0	0	0
30	BF	52	0	0	0	0
31	BG	143	0	0	7	0
32	BH	143	0	0	0	0
33	BI	132	0	0	3	0
34	BJ	141	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	BK	124	0	0	0	0
36	BL	114	0	0	1	0
37	BM	111	0	0	0	0
38	BN	125	0	0	1	0
39	BO	117	0	0	0	0
40	BP	100	0	0	0	0
41	BQ	130	0	0	0	0
42	BR	93	0	0	0	0
43	BS	113	0	0	0	0
44	BT	173	0	0	0	0
45	BU	86	0	0	1	0
46	BV	16	0	0	0	0
47	BW	65	0	0	0	0
48	BX	55	0	0	0	0
49	BY	73	0	0	0	0
50	BZ	58	0	0	0	0
51	B1	53	0	0	0	0
52	B2	46	0	0	0	0
53	B3	63	0	0	0	0
54	B4	35	0	0	0	0
55	B5	217	0	0	36	0
All	All	122017	0	70110	7429	12

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 39.

The worst 5 of 7429 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:293:G:H4'	1:AA:609:A:C2	1.16	1.69
1:AA:675:A:H1'	13:AK:116:HIS:CD2	1.26	1.66
1:AA:21:G:C1'	1:AA:914:A:H62	1.08	1.65
6:AD:88:VAL:CA	7:AE:97:GLY:HA3	1.24	1.64
23:B0:3128:G:H4'	23:B0:3174:C:C4'	1.23	1.64

The worst 5 of 12 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:AD:172:PRO:O	8:AF:15:ASP:CB[3_555]	1.18	1.02
1:AA:416:G:C4'	23:B0:3153:G:O2'[3_555]	1.79	0.41
1:AA:416:G:O2'	23:B0:3153:G:O2'[3_555]	1.87	0.33
6:AD:172:PRO:O	8:AF:15:ASP:CA[3_555]	1.87	0.33

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:AD:186:LEU:CD1	8:AF:15:ASP:OD2[3.555]	1.91	0.29

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	AB	232/234 (99%)	174 (75%)	34 (15%)	24 (10%)	1	19
5	AC	204/206 (99%)	135 (66%)	40 (20%)	29 (14%)	0	11
6	AD	206/208 (99%)	166 (81%)	31 (15%)	9 (4%)	4	47
7	AE	148/150 (99%)	130 (88%)	13 (9%)	5 (3%)	6	55
8	AF	99/101 (98%)	79 (80%)	19 (19%)	1 (1%)	22	80
9	AG	153/155 (99%)	127 (83%)	16 (10%)	10 (6%)	2	35
10	AH	136/138 (99%)	125 (92%)	7 (5%)	4 (3%)	7	58
11	AI	125/127 (98%)	89 (71%)	26 (21%)	10 (8%)	1	28
12	AJ	96/98 (98%)	59 (62%)	20 (21%)	17 (18%)	0	6
13	AK	117/119 (98%)	88 (75%)	20 (17%)	9 (8%)	1	29
14	AL	122/124 (98%)	98 (80%)	15 (12%)	9 (7%)	2	31
15	AM	123/125 (98%)	88 (72%)	27 (22%)	8 (6%)	2	35
16	AN	58/60 (97%)	40 (69%)	11 (19%)	7 (12%)	1	14
17	AO	86/88 (98%)	70 (81%)	11 (13%)	5 (6%)	3	38
18	AP	81/83 (98%)	65 (80%)	15 (18%)	1 (1%)	19	77
19	AQ	102/104 (98%)	84 (82%)	10 (10%)	8 (8%)	1	29
20	AR	71/73 (97%)	62 (87%)	7 (10%)	2 (3%)	8	59
21	AS	78/80 (98%)	48 (62%)	19 (24%)	11 (14%)	0	11
22	AT	97/99 (98%)	65 (67%)	20 (21%)	12 (12%)	1	14
All	All	2334/2372 (98%)	1792 (77%)	361 (16%)	181 (8%)	1	29

5 of 181 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AB	9	GLU
4	AB	15	VAL
4	AB	16	HIS
4	AB	17	PHE
4	AB	21	ARG

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 X-ray entries followed by that with respect to entries of similar resolution. 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	AB	202/202 (100%)	180 (89%)	22 (11%)	9	46
5	AC	160/160 (100%)	142 (89%)	18 (11%)	9	43
6	AD	180/180 (100%)	172 (96%)	8 (4%)	39	82
7	AE	115/115 (100%)	100 (87%)	15 (13%)	6	36
8	AF	90/90 (100%)	88 (98%)	2 (2%)	64	91
9	AG	126/126 (100%)	122 (97%)	4 (3%)	51	87
10	AH	119/119 (100%)	109 (92%)	10 (8%)	16	60
11	AI	98/98 (100%)	90 (92%)	8 (8%)	17	61
12	AJ	88/88 (100%)	79 (90%)	9 (10%)	11	49
13	AK	90/90 (100%)	84 (93%)	6 (7%)	23	70
14	AL	104/104 (100%)	96 (92%)	8 (8%)	18	64
15	AM	100/100 (100%)	90 (90%)	10 (10%)	11	50
16	AN	49/49 (100%)	47 (96%)	2 (4%)	41	83
17	AO	79/79 (100%)	72 (91%)	7 (9%)	14	57
18	AP	72/72 (100%)	67 (93%)	5 (7%)	22	68
19	AQ	96/96 (100%)	90 (94%)	6 (6%)	25	72
20	AR	64/64 (100%)	61 (95%)	3 (5%)	36	80
21	AS	71/71 (100%)	68 (96%)	3 (4%)	40	82
22	AT	76/76 (100%)	69 (91%)	7 (9%)	13	55
All	All	1979/1979 (100%)	1826 (92%)	153 (8%)	18	64

5 of 153 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	AH	2	LEU
11	AI	111	ARG
20	AR	38	GLU
10	AH	52	ASP
10	AH	105	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
8	AF	73	ASN
11	AI	23	ASN
21	AS	14	HIS
9	AG	37	ASN
12	AJ	62	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1479/1527 (96%)	217 (14%)	92 (6%)
2	AV	75/76 (98%)	13 (17%)	3 (4%)
2	AW	74/76 (97%)	13 (17%)	3 (4%)
23	B0	2802/2887 (97%)	430 (15%)	56 (1%)
24	B9	116/118 (98%)	10 (8%)	0
3	AU	8/18 (44%)	1 (12%)	0
All	All	4554/4702 (96%)	684 (15%)	154 (3%)

5 of 684 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	8	A
1	AA	9	G
1	AA	27	G
1	AA	31	G

5 of 154 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	1201	A
1	AA	1451	A
23	B0	3149	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AA	1226	C
1	AA	1302	U

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 ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	84
23	B0	25
24	B9	2
2	AV	2
2	AW	1
3	AU	1
14	AL	1

The worst 5 of 116 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	1443:G	O3'	1445:U	P	10.46
1	AA	1459:C	O3'	1460:A	P	10.16
1	AA	1458:G	O3'	1459:C	P	8.01
1	B0	1888:C	O3'	1889:G	P	6.63

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B0	3180:U	O3'	3181:C	P	5.39

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1527/1527 (100%)	3.45	862 (56%) 0 4	341, 531, 705, 847	0
2	AV	76/76 (100%)	2.52	50 (65%) 0 4	379, 379, 379, 379	0
2	AW	76/76 (100%)	7.35	73 (96%) 0 2	510, 510, 510, 510	76 (100%)
3	AU	9/18 (50%)	3.17	6 (66%) 0 4	379, 379, 379, 379	0
4	AB	234/234 (100%)	9.97	222 (94%) 0 2	496, 496, 496, 496	0
5	AC	206/206 (100%)	5.59	198 (96%) 0 2	264, 264, 264, 264	0
6	AD	208/208 (100%)	7.25	189 (90%) 0 2	479, 479, 479, 479	0
7	AE	150/150 (100%)	6.82	118 (78%) 0 3	669, 669, 669, 669	0
8	AF	101/101 (100%)	7.67	101 (100%) 0 1	640, 640, 640, 640	0
9	AG	155/155 (100%)	7.17	145 (93%) 0 2	406, 406, 406, 406	0
10	AH	138/138 (100%)	8.39	129 (93%) 0 2	647, 647, 647, 647	0
11	AI	127/127 (100%)	4.11	94 (74%) 0 3	426, 426, 426, 426	0
12	AJ	98/98 (100%)	5.30	82 (83%) 0 3	507, 507, 507, 507	0
13	AK	119/119 (100%)	10.98	106 (89%) 0 2	510, 510, 510, 510	0
14	AL	124/124 (100%)	4.78	91 (73%) 0 3	367, 367, 384, 384	0
15	AM	125/125 (100%)	6.58	114 (91%) 0 2	349, 454, 454, 454	0
16	AN	60/60 (100%)	5.18	56 (93%) 0 2	264, 264, 264, 264	0
17	AO	88/88 (100%)	2.65	48 (54%) 0 4	572, 572, 572, 572	0
18	AP	83/83 (100%)	6.29	61 (73%) 0 3	662, 662, 662, 662	0
19	AQ	104/104 (100%)	1.98	39 (37%) 1 5	670, 670, 670, 670	0
20	AR	73/73 (100%)	7.47	68 (93%) 0 2	640, 640, 640, 640	0
21	AS	80/80 (100%)	8.57	75 (93%) 0 2	545, 545, 545, 545	0
22	AT	99/99 (100%)	6.92	75 (75%) 0 3	744, 744, 744, 744	0
23	B0	2825/2887 (97%)	2.26	1035 (36%) 1 5	517, 737, 737, 936	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
24	B9	118/118 (100%)	4.22	82 (69%)	0	3	772, 938, 938, 938	0
25	BA	270/270 (100%)	6.75	238 (88%)	0	3	737, 737, 737, 737	0
26	BB	205/205 (100%)	4.50	159 (77%)	0	3	737, 737, 737, 737	0
27	BC	197/197 (100%)	2.92	149 (75%)	0	3	737, 737, 737, 737	0
28	BD	178/178 (100%)	5.39	119 (66%)	0	4	938, 938, 938, 938	0
29	BE	177/177 (100%)	4.17	108 (61%)	0	4	737, 737, 737, 737	0
30	BF	52/52 (100%)	4.17	33 (63%)	0	4	737, 737, 737, 737	0
31	BG	143/143 (100%)	1.66	33 (23%)	1	6	907, 907, 907, 907	0
32	BH	143/143 (100%)	4.60	118 (82%)	0	3	737, 737, 737, 737	0
33	BI	132/132 (100%)	6.42	123 (93%)	0	2	737, 737, 737, 737	0
34	BJ	141/141 (100%)	3.30	86 (60%)	0	4	737, 737, 737, 737	0
35	BK	124/124 (100%)	6.71	121 (97%)	0	2	737, 737, 737, 737	0
36	BL	114/114 (100%)	4.01	101 (88%)	0	3	737, 737, 737, 737	0
37	BM	111/111 (100%)	8.08	102 (91%)	0	2	938, 938, 938, 938	0
38	BN	125/125 (100%)	6.06	111 (88%)	0	3	737, 737, 737, 737	0
39	BO	117/117 (100%)	2.65	67 (57%)	0	4	737, 737, 737, 737	0
40	BP	100/100 (100%)	3.57	84 (84%)	0	3	737, 737, 737, 737	0
41	BQ	130/130 (100%)	2.97	96 (73%)	0	3	737, 737, 737, 737	0
42	BR	93/93 (100%)	2.92	73 (78%)	0	3	737, 737, 737, 737	0
43	BS	113/113 (100%)	2.36	67 (59%)	0	4	737, 737, 737, 737	0
44	BT	173/173 (100%)	2.73	68 (39%)	1	4	737, 772, 772, 772	0
45	BU	86/86 (100%)	4.94	69 (80%)	0	3	737, 737, 737, 737	0
46	BV	0/16	-	-	-	-	-	-
47	BW	65/65 (100%)	3.41	51 (78%)	0	3	737, 737, 737, 737	0
48	BX	55/55 (100%)	3.68	45 (81%)	0	3	737, 737, 737, 737	0
49	BY	73/73 (100%)	5.41	61 (83%)	0	3	737, 737, 737, 737	0
50	BZ	58/58 (100%)	2.48	29 (50%)	0	4	737, 737, 737, 737	0
51	B1	53/53 (100%)	5.89	44 (83%)	0	3	737, 737, 737, 737	0
52	B2	46/46 (100%)	2.52	27 (58%)	0	4	737, 737, 737, 737	0
53	B3	63/63 (100%)	4.39	50 (79%)	0	3	737, 737, 737, 737	0
54	B4	35/35 (100%)	5.39	32 (91%)	0	2	737, 737, 737, 737	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
55	B5	217/217 (100%)	2.56	82 (37%) 1 4	940, 940, 940, 940	0
All	All	10592/10679 (99%)	4.18	6665 (62%) 0 4	264, 737, 938, 940	76 (0%)

The worst 5 of 6665 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
23	B0	3156	G	39.3
23	B0	3134	A	38.2
23	B0	3158	A	37.2
23	B0	3157	G	35.0
1	AA	208	U	34.6

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.