



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 02:16 AM UTC

PDB ID : 4V4A / pdb_00004v4a
Title : Crystal Structure of the Wild Type 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 : 9.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

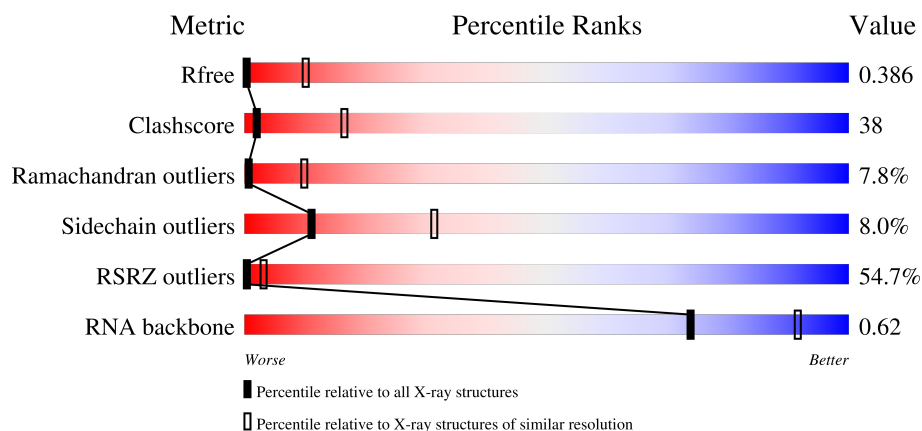
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 9.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1168 (11.50-4.00)
Clashscore	190562	1001 (11.50-4.06)
Ramachandran outliers	187476	1055 (11.50-4.00)
Sidechain outliers	187428	1018 (11.50-4.00)
RSRZ outliers	180081	1162 (11.50-4.00)
RNA backbone	3983	1057 (11.50-3.10)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1537	25% 23% 57% 15% 5%
2	AB	234	29% 26% 56% 16% .
3	AC	206	53% 28% 51% 18% .
4	AD	208	53% 34% 56% 10%

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Mol	Chain	Length	Quality of chain
5	AE	150	
6	AF	101	
7	AG	155	
8	AH	138	
9	AI	127	
10	AJ	98	
11	AK	119	
12	AL	124	
13	AM	125	
14	AN	60	
15	AO	88	
16	AP	83	
17	AQ	104	
18	AR	73	
19	AS	80	
20	AT	99	
21	B0	2887	
22	B9	118	
23	BA	270	
24	BB	205	
25	BC	197	
26	BD	178	
27	BE	177	
28	BF	52	
29	BG	143	

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Mol	Chain	Length	Quality of chain
30	BH	143	92% 100%
31	BI	132	96% 99%
32	BJ	141	79% 99%
33	BK	124	97% 100%
34	BL	114	97% 99%
35	BM	111	98% 100%
36	BN	125	94% 100%
37	BO	117	75% 100%
38	BP	100	64% 100%
39	BQ	130	92% 100%
40	BR	93	90% 100%
41	BS	113	99% 100%
42	BT	173	91% 100%
43	BU	86	92% 100%
44	BV	16	100%
45	BW	65	94% 100%
46	BX	55	89% 100%
47	BY	73	85% 100%
48	BZ	58	91% 100%
49	B1	53	98% 100%
50	B2	46	74% 100%
51	B3	63	51% 100%
52	B4	35	86% 100%
53	B5	217	90% 96%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 118711 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	1533	Total	C	N	O	P	0	0	0
			32939	14664	6099	10643	1533			

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

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

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

- Molecule 7 is a protein called 30S ribosomal protein S7.

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

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

- Molecule 11 is a protein called 30S ribosomal protein S11.

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

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

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

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

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

- Molecule 19 is a protein called 30S ribosomal protein S19.

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

- Molecule 20 is a protein called 30S ribosomal protein S20.

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

- Molecule 21 is a RNA chain called 23S RIBOSOMAL RNA.

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

- Molecule 22 is a RNA chain called 5S RIBOSOMAL RNA.

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

- Molecule 23 is a protein called 50S ribosomal protein L2.

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

- Molecule 24 is a protein called 50S ribosomal protein L3.

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

- Molecule 25 is a protein called 50S ribosomal protein L4.

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

- Molecule 26 is a protein called 50S ribosomal protein L5.

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

- Molecule 27 is a protein called 50S ribosomal protein L6.

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

- Molecule 28 is a protein called 50S ribosomal protein L9.

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

- Molecule 29 is a protein called 50S ribosomal protein L11.

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

- Molecule 30 is a protein called 50S ribosomal protein L13.

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

- Molecule 31 is a protein called 50S ribosomal protein L14.

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

- Molecule 32 is a protein called 50S ribosomal protein L15.

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

- Molecule 33 is a protein called 50S ribosomal protein L16.

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

- Molecule 34 is a protein called 50S ribosomal protein L17.

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

- Molecule 35 is a protein called 50S ribosomal protein L18.

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

- Molecule 36 is a protein called 50S ribosomal protein L19.

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

- Molecule 37 is a protein called 50S ribosomal protein L20.

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

- Molecule 38 is a protein called 50S ribosomal protein L21.

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

- Molecule 39 is a protein called 50S ribosomal protein L22.

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

- Molecule 40 is a protein called 50S ribosomal protein L23.

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

- Molecule 41 is a protein called 50S ribosomal protein L24.

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

- Molecule 42 is a protein called general stress protein Ctc.

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

- Molecule 43 is a protein called 50S ribosomal protein L27.

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

- Molecule 44 is a protein called 50S RIBOSOMAL PROTEIN L28.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

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

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

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

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

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

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L35.

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

- Molecule 52 is a protein called 50S ribosomal protein L36.

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

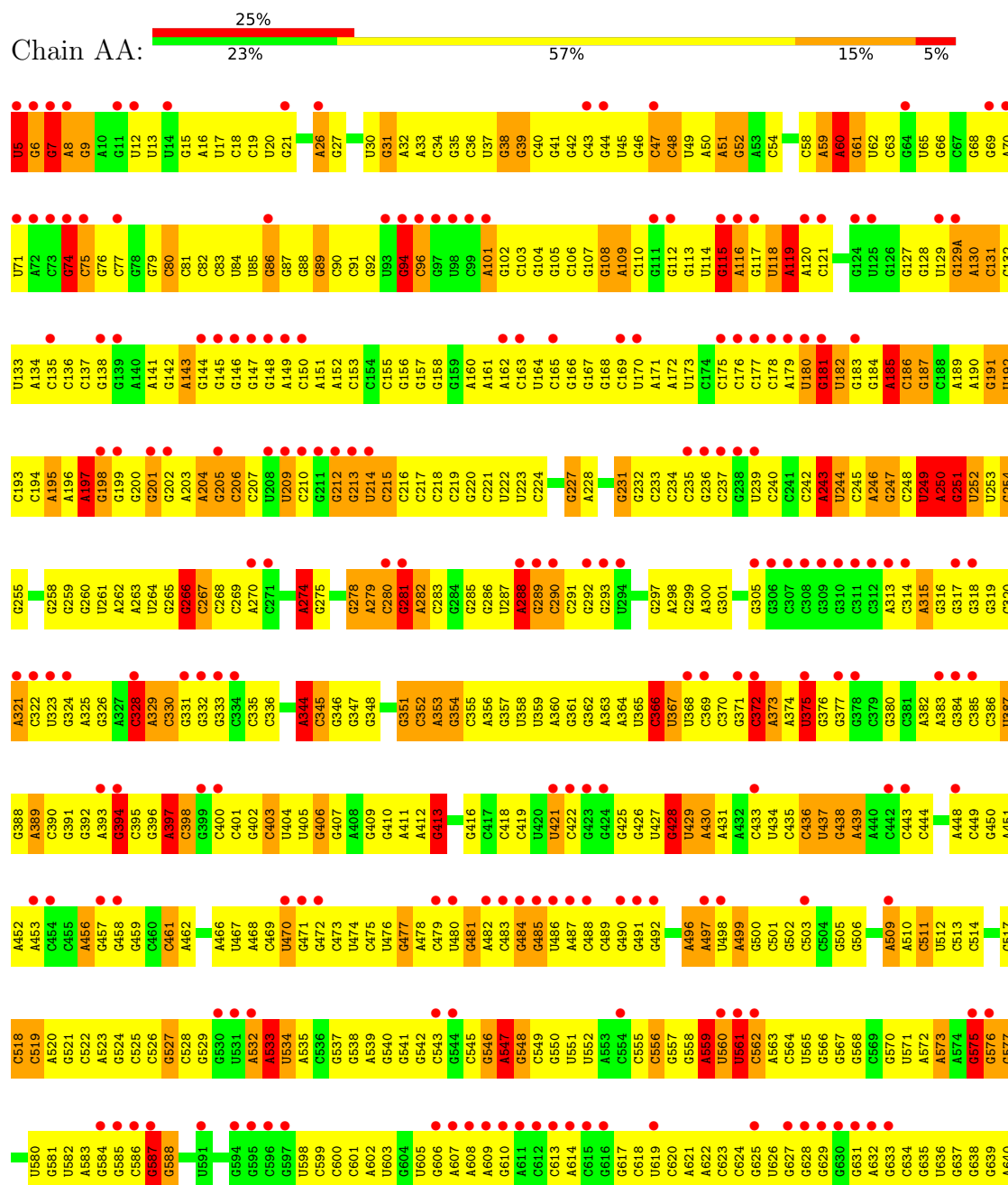
- Molecule 53 is a protein called 50S ribosomal protein L1P.

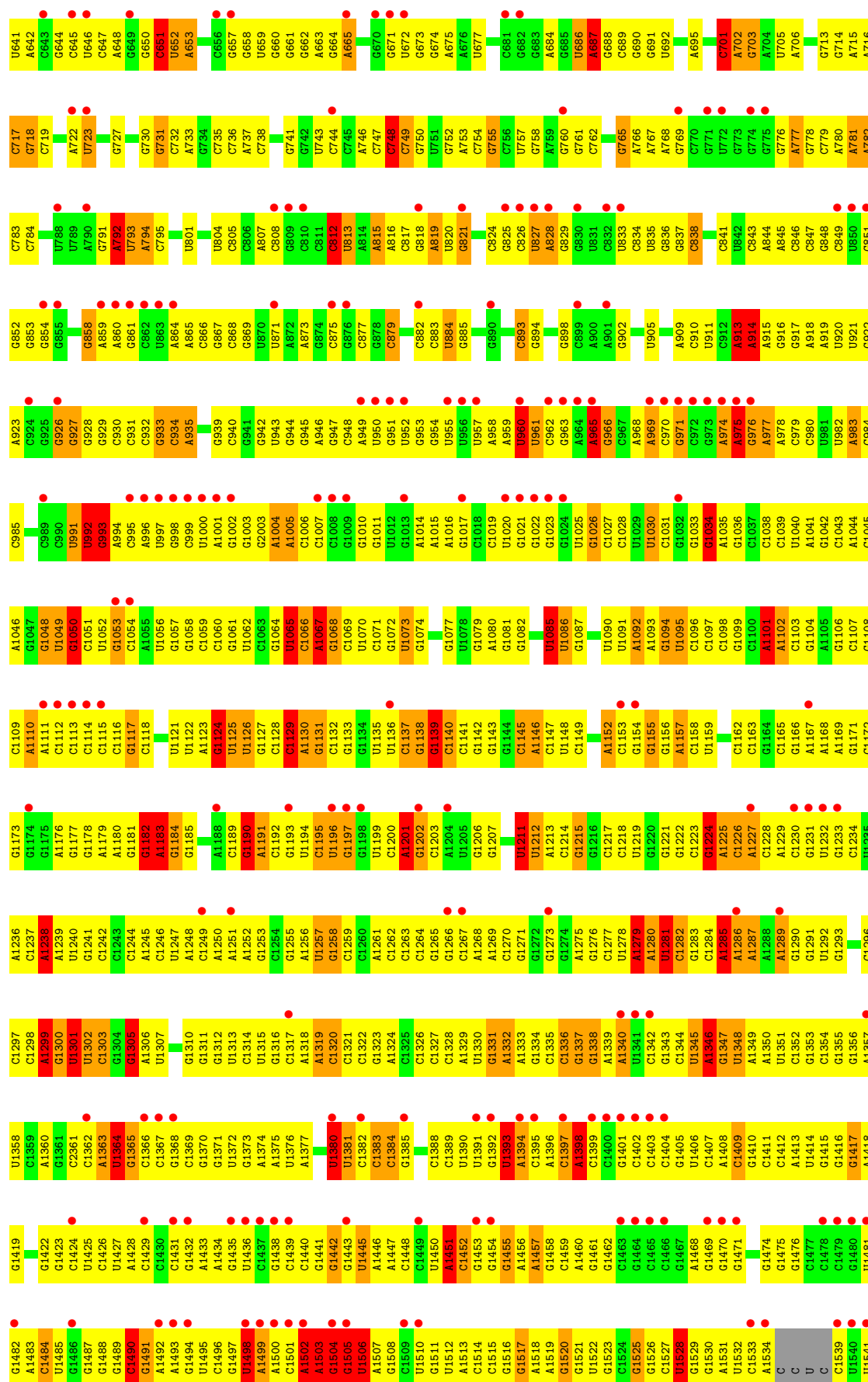
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
53	B5	217	Total C 217 217	0	0	217

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

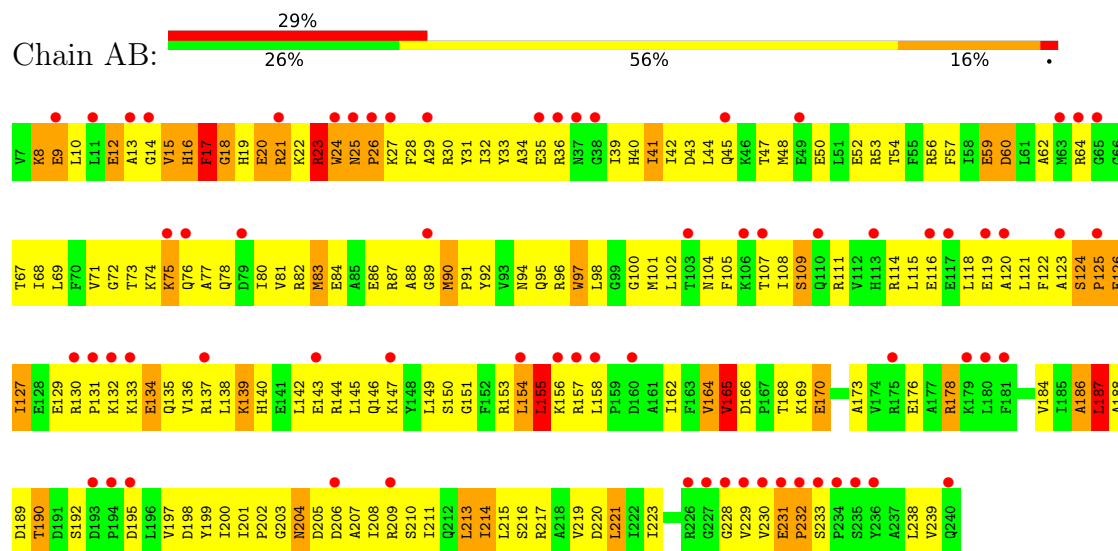
• Molecule 1: 16S RIBOSOMAL RNA



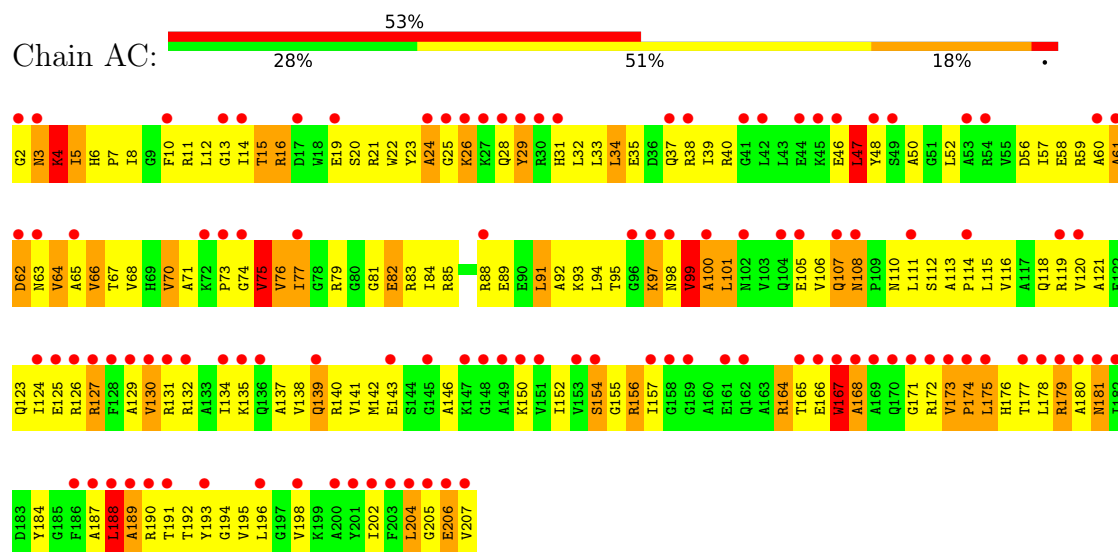


U1542
C1543
U1544

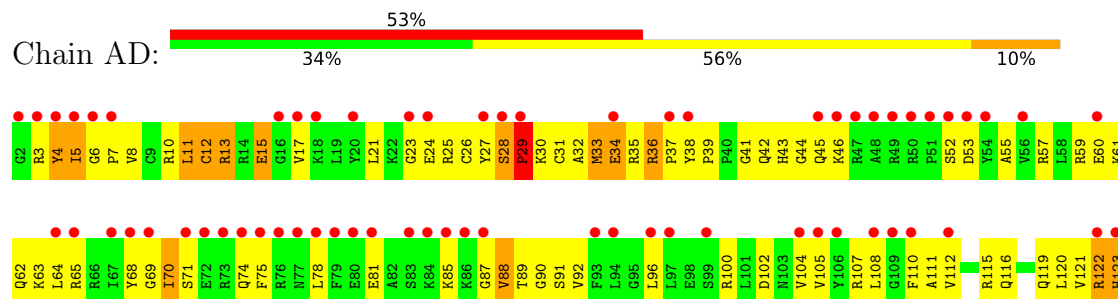
• Molecule 2: 30S ribosomal protein S2

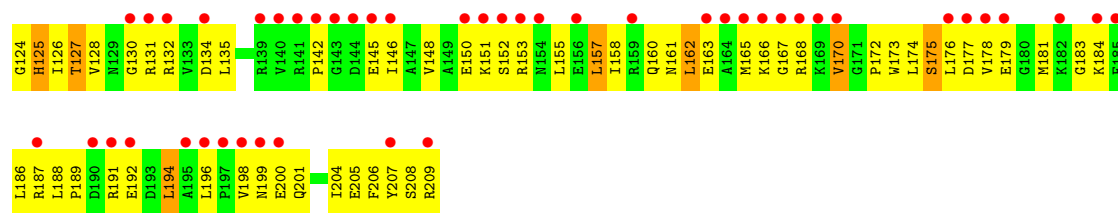


• Molecule 3: 30S ribosomal protein S3

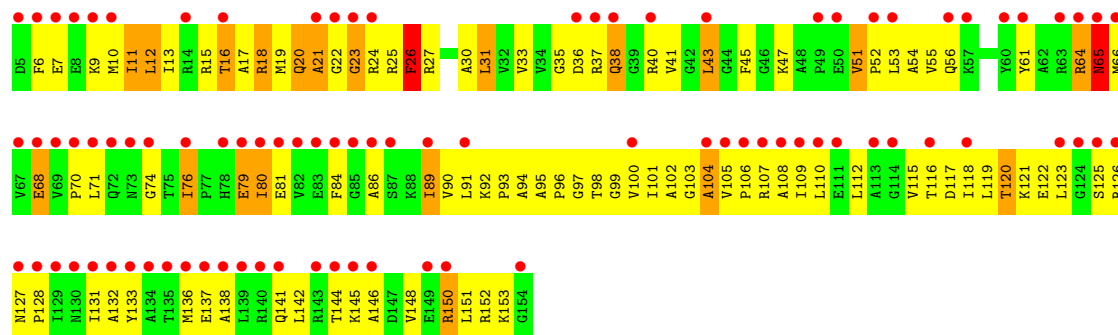


• Molecule 4: 30S ribosomal protein S4

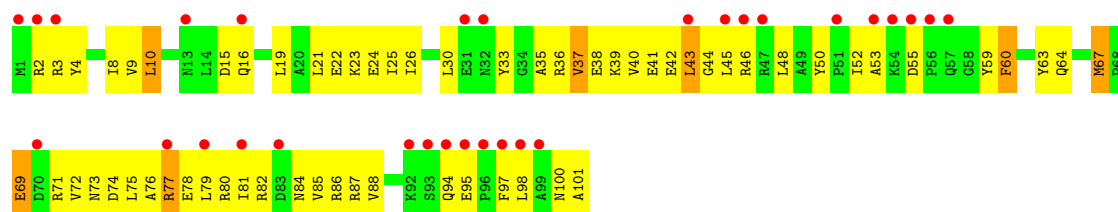




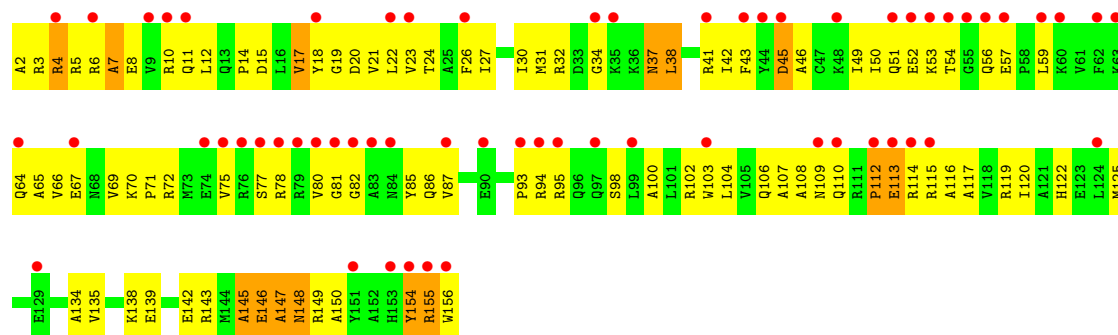
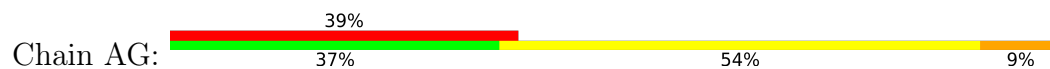
• Molecule 5: 30S ribosomal protein S5



• Molecule 6: 30S ribosomal protein S6

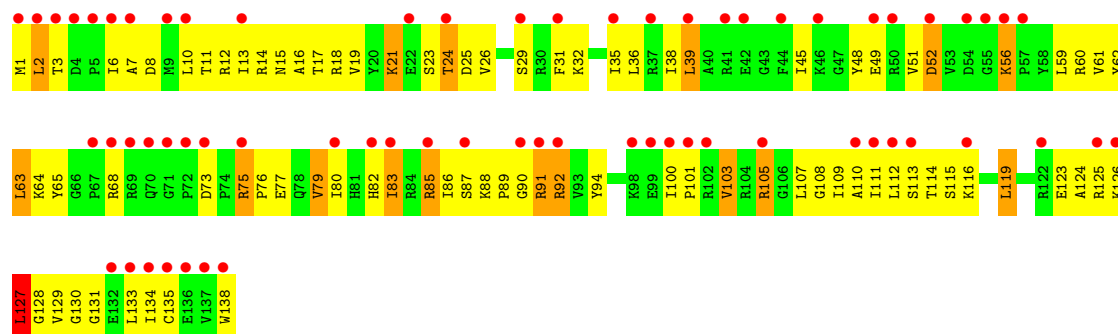


• Molecule 7: 30S ribosomal protein S7

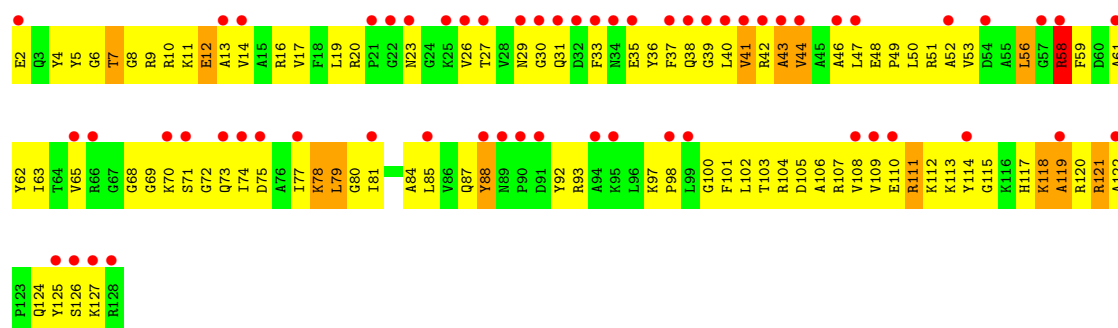


• Molecule 8: 30S ribosomal protein S8

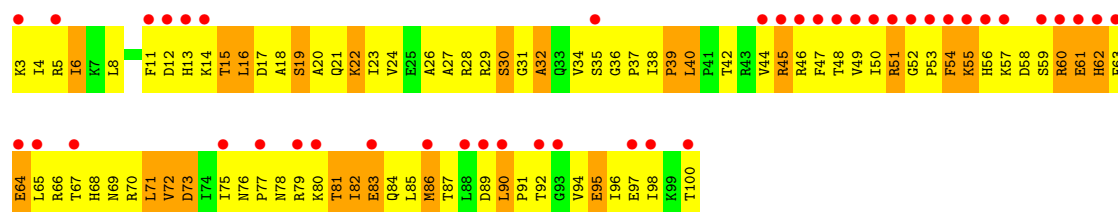
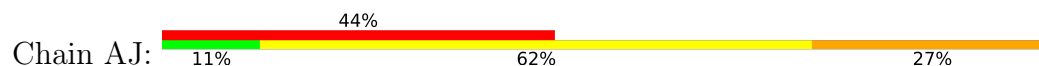




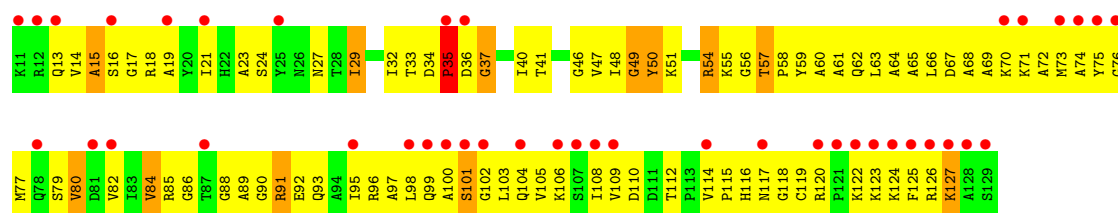
• Molecule 9: 30S ribosomal protein S9



• Molecule 10: 30S ribosomal protein S10

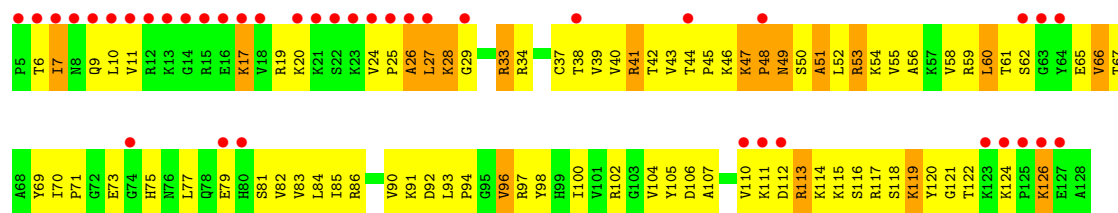


• Molecule 11: 30S ribosomal protein S11

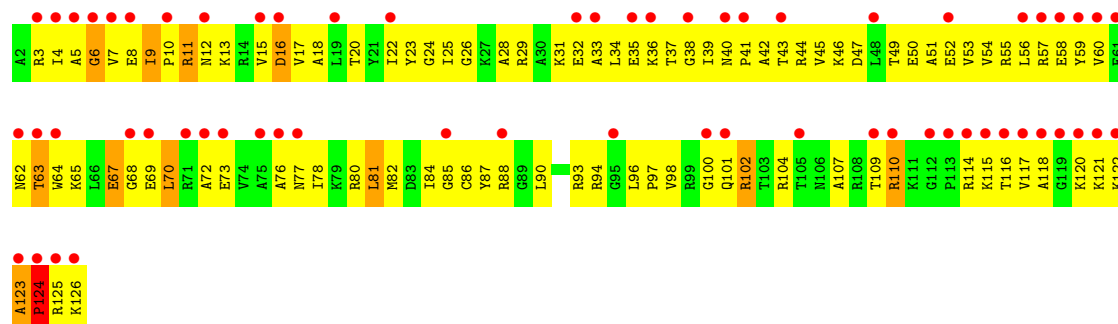


• Molecule 12: 30S ribosomal protein S12

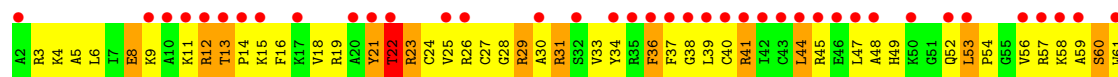




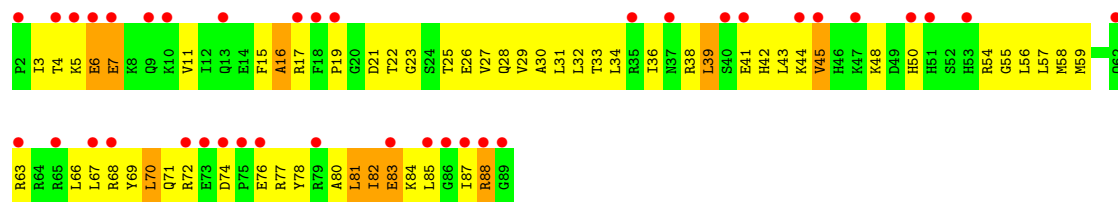
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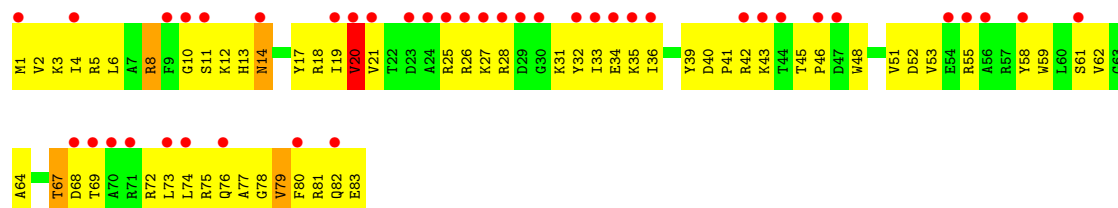
• Molecule 14: 30S ribosomal protein S14



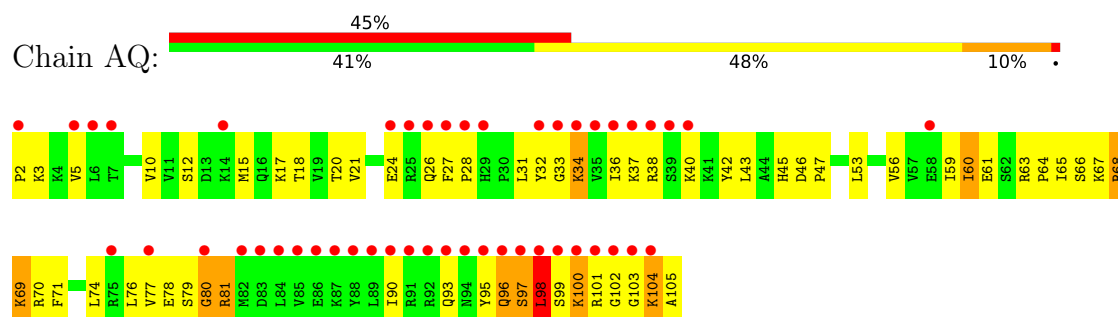
• Molecule 15: 30S ribosomal protein S15



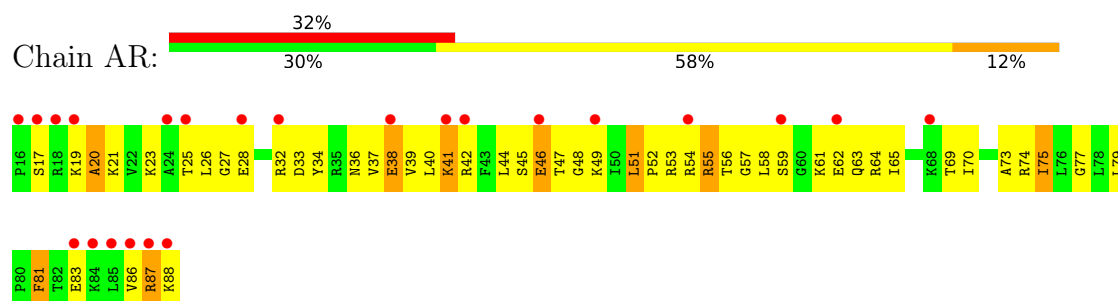
• Molecule 16: 30S ribosomal protein S16



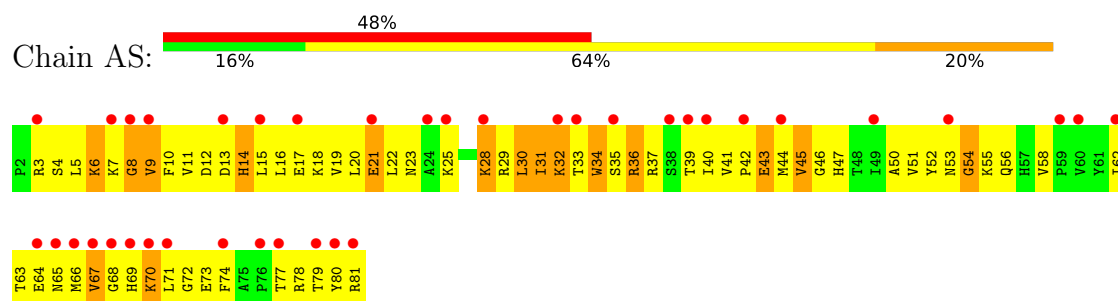
- Molecule 17: 30S ribosomal protein S17



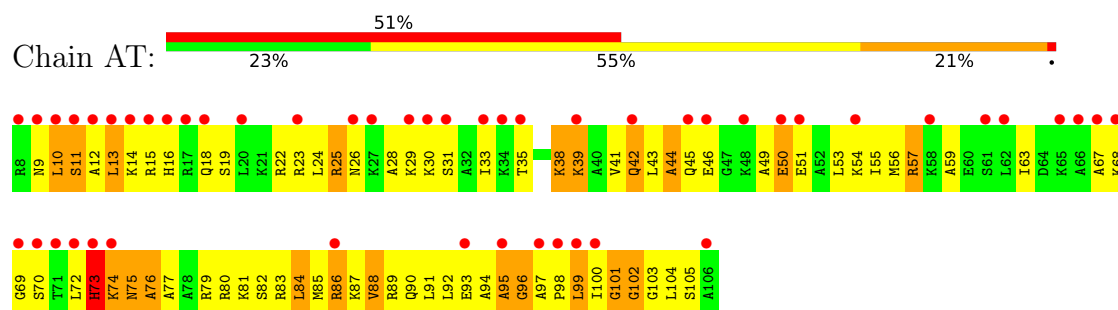
- Molecule 18: 30S ribosomal protein S18



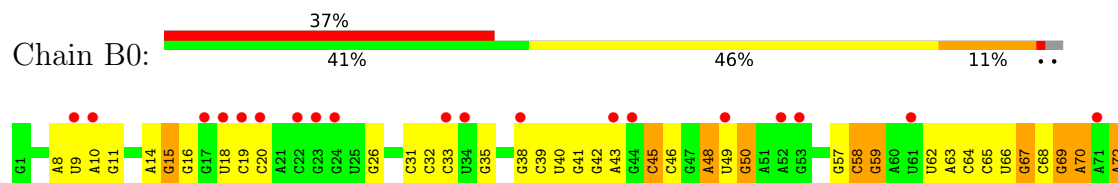
- Molecule 19: 30S ribosomal protein S19

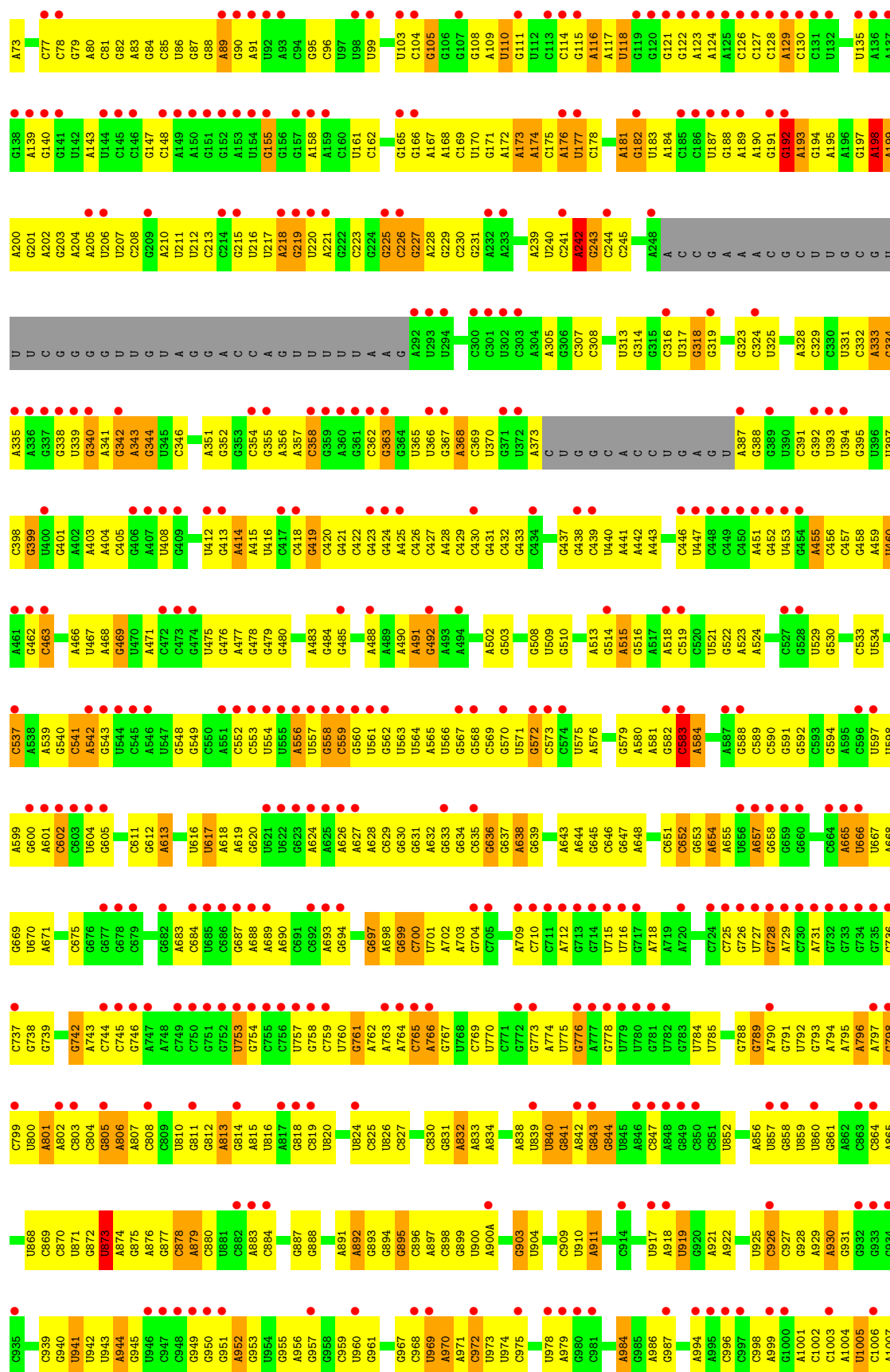


- Molecule 20: 30S ribosomal protein S20



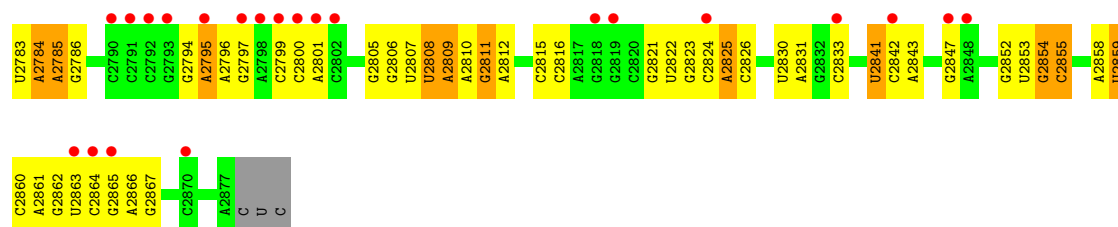
- Molecule 21: 23S RIBOSOMAL RNA



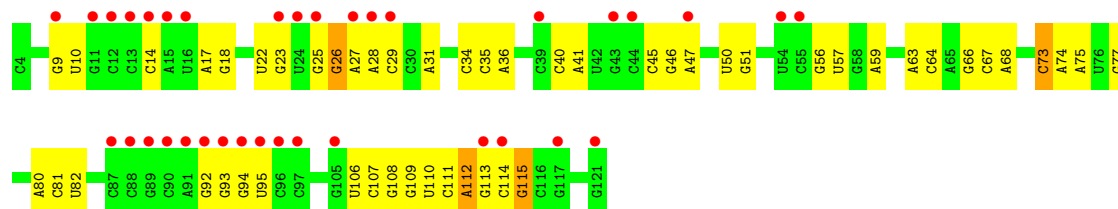


A1851	A1782	A1714	A1654	A1586	A1507	C1442	A1367	G1298	A1226	G1147	A1078	G1008
G1852	G1783	A1715	C1655	A1587	G1508	G1443	G1568	G1301	C1230	G1148	G1079	G1014
G1853	C1784	G1716	U1656	U1591	A1509	C1444	A1372	U1307	G1233	G1149	A1080	U1015
G1854	A1785	A1717	A1657	U1592	U1513	A1445	G1373	C1308	A1234	C1151	A1081	G1082
U1855	C1786	G1718	A1658	U1596	C1514	U1447	G1374	G1309	C1235	C1152	G1083	C1017
A3865	A1787	A1719	G1659	A1597	U1515	A1448	A1377	C1310	A1153	A1154	A1084	U1018
A3866	C1788	G1720	G1660	C1598	U1516	C1449	A1378	G1311	A1155	C1087	A1020	U1019
G3867	U1789	G1721	C1661	G1599	A1517	G1450	A1379	G1312	U1156	C1088	A1021	A1022
G3868	C1791	G1722	C1662	G1599	C1518	C1451	A1380	U1313	C1164	C1089	U1023	G1024
G3869	C1792	C1723	G1664	U1601	G1519	A1452	G1381	A1314	A1165	U1092	A1025	A1026
C3870	A1793	G1725	G1665	U1602	G1520	A1453	A1386	A1315	A1166	U1093	A1027	U1028
A3871	A1794	C1726	G1666	A1603	C1524	U1454	G1387	G1316	A1167	C1094	A1029	U1030
A3872	C1727	G1727	A1667	A1604	U1527	C1455	G1388	A1317	A1168	A1095	U1031	A1032
A3873	A1728	A1728	G1668	A1605	G1527	A1456	G1389	A1318	A1169	A1096	U1033	G1033
C3874	C1729	A1729	A1669	A1605	C1528	A1457	G1390	G1319	C1178	A1097	U1034	U1035
A3875	G1730	G1730	A1670	U1609	C1529	U1458	G1391	A1320	A1179	G1098	U1036	U1037
A3876	C1731	G1731	A1671	G1609	U1530	U1459	G1392	A1321	A1180	A1099	U1038	U1039
A3877	U1732	U1732	A1672	U1610	C1531	A1464	G1393	G1322	C1181	G1100	U1040	U1041
G1861	U1733	C1673	C1673	U1611	C1532	G1465	G1394	U1325	C1182	U1101	G1042	G1043
G1862	C1734	A1674	C1674	U1612	A1532	C1466	G1395	G1326	C1183	G1109	G1044	G1045
U1863	G1735	A1675	C1675	G1613	G1533	U1467	A1396	U1326	C1184	G1110	U1046	U1047
G1864	C1736	U1676	U1676	C1614	A1534	A1468	G1397	U1327	C1185	G1111	U1048	U1049
G1865	G1737	C1677	C1677	C1615	G1535	U1469	A1398	G1328	C1186	G1112	U1050	U1051
G1866	G1678	C1678	C1678	G1616	G1536	U1470	G1399	U1329	C1187	G1113	U1052	U1053
A1867	U1679	U1679	U1679	G1617	U1537	G1471	G1401	U1330	A1188	G1114	U1054	U1055
A1868	A1680	U1680	U1680	U1618	C1542	C1472	G1402	G1331	C1189	G1115	U1056	U1057
A1869	A1681	C1681	C1681	C1621	G1543	U1473	G1403	G1332	C1190	G1116	U1058	U1059
A1870	G1682	C1682	C1682	G1622	A1544	A1474	G1404	G1333	C1191	G1117	U1060	U1061
G1871	C1683	G1683	G1683	G1623	G1545	U1475	U1409	A1334	G1192	G1118	U1062	U1063
G1872	G1684	A1684	A1684	A1624	C1552	G1476	U1410	A1335	C1193	G1119	U1064	U1065
G1873	A1685	A1685	A1685	A1625	G1553	C1479	C1411	G1336	U1194	G1120	U1066	U1067
G1874	A1686	C1686	C1686	A1626	U1561	G1480	G1414	G1337	G1204	G1121	U1068	U1069
G1875	U1687	U1687	U1687	G1627	G1562	U1481	C1415	G1338	G1205	G1122	U1070	U1071
G1876	U1688	U1688	U1688	A1628	U1563	G1482	A1416	G1339	G1206	G1123	U1072	U1073
G1877	U1689	U1689	U1689	C1628	U1564	U1483	C1417	U1340	G1207	G1124	U1074	U1075
G1878	G1690	U1690	G1691	G1629	U1565	G1484	G1418	G1341	G1208	G1125	U1076	U1077
U1881	G1691	C1691	C1692	A1630	G1566	U1485	G1419	C1342	G1209	G1126	U1078	U1079
G1882	C1692	A1693	A1693	C1631	G1567	G1486	A1420	C1343	G1210	G1127	U1080	U1081
A1883	U1693	C1694	C1694	A1632	U1568	U1487	U1424	C1344	G1211	G1128	U1082	U1083
A1884	A1694	C1695	C1695	A1633	A1569	U1488	G1425	G1345	G1212	G1129	U1084	U1085
A1885	U1695	C1696	C1696	A1634	U1570	U1489	G1426	G1350	G1213	G1130	U1086	U1087
G1886	C1696	U1697	U1697	G1635	C1571	G1490	G1427	G1351	G1214	G1131	U1088	U1089
G1887	U1697	C1698	C1698	G1636	U1572	U1491	G1428	G1352	G1215	G1132	U1090	U1091
C1888	U1698	A1699	A1699	U1637	G1573	G1492	G1429	G1353	G1216	G1133	U1092	U1093
G1889	A1699	C1700	C1700	U1638	U1574	A1493	U1430	A1354	G1217	G1134	U1094	U1095
G1890	C1701	C1701	C1701	U1639	G1575	G1494	U1431	G1355	G1218	G1135	U1096	U1097
C1891	C1702	G1702	G1703	C1641	C1576	U1495	U1432	U1357	G1219	G1136	U1098	U1099
G1892	U1703	U1703	U1704	G1642	U1577	G1496	G1433	G1358	G1220	G1137	U1100	U1101
G1893	G1704	U1705	U1705	A1643	G1578	U1497	G1434	C1359	G1221	G1138	U1102	U1103
U1894	A1706	A1706	A1706	G1644	U1579	U1498	A1433	G1360	G1222	G1139	U1104	U1105
A1895	U1707	A1707	A1707	U1645	U1579	U1500	G1436	G1361	G1223	G1140	U1106	U1107
A1896	A1774	A1774	A1774	G1646	C1580	G1501	A1437	G1362	G1224	G1141	U1108	U1109
U1900	A1776	A1776	A1776	U1647	C1581	G1502	G1438	G1363	G1225	G1142	U1110	U1111
A1901	A1777	U1777	U1777	C1648	A1582	G1503	G1439	C1364	G1226	G1143	U1112	U1113
A1902	U1778	U1778	U1778	A1649	U1583	G1504	U1441	U1365	G1227	G1144	U1114	U1115
U1903	C1779	C1779	C1779	A1650	G1584	U1505	A1441	A1366	G1228	G1145	U1116	U1117
G1904	G1711	G1711	G1711	U1651	C1585	G1506			G1229	G1146	U1118	U1119
G1905	G1712	G1712	G1712								U1120	U1121
U1906	G1713	G1713	G1713								U1121	U1122

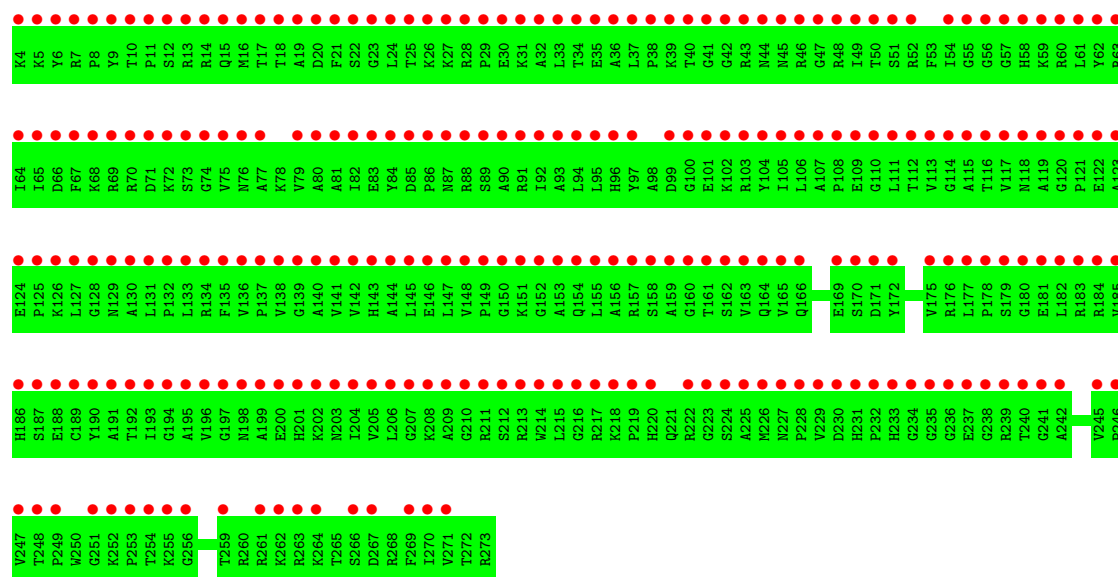




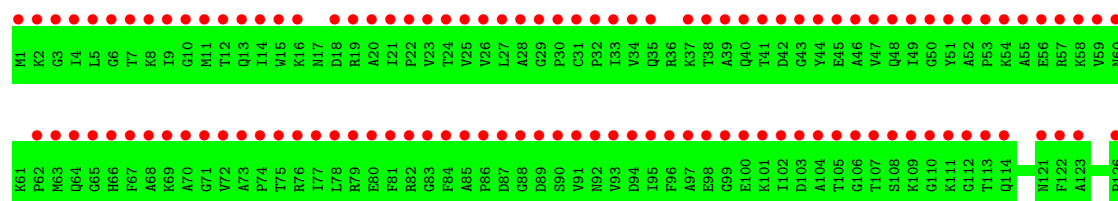
• Molecule 22: 5S RIBOSOMAL RNA

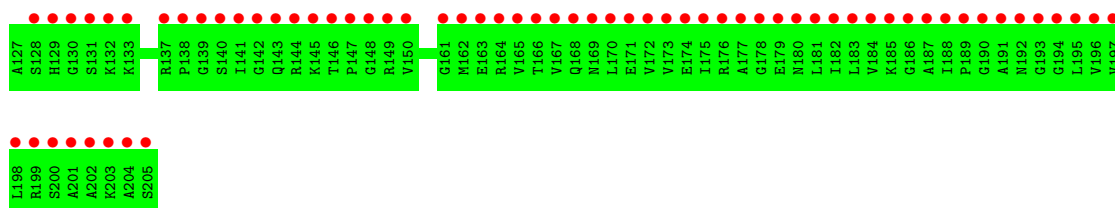


• Molecule 23: 50S ribosomal protein L2

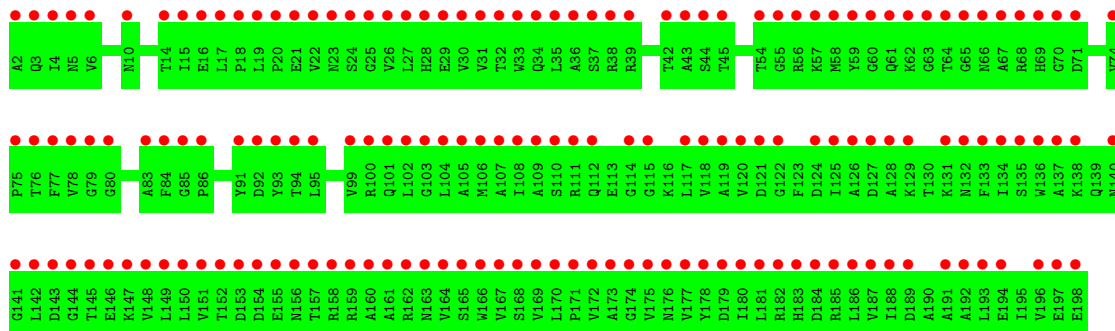
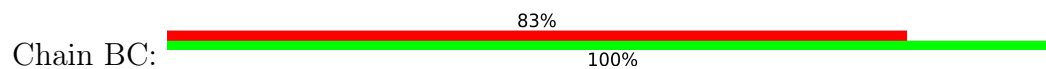


• Molecule 24: 50S ribosomal protein L3

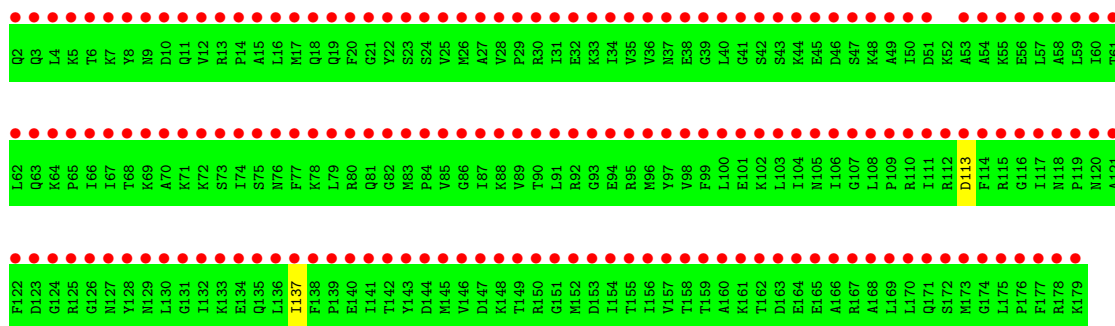




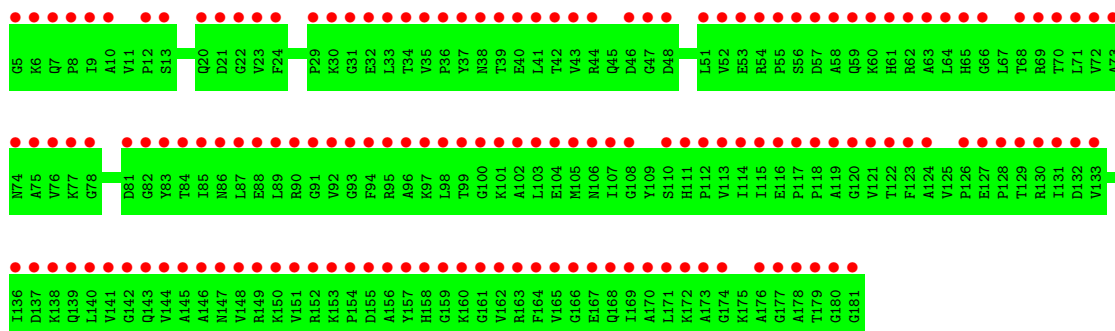
• Molecule 25: 50S ribosomal protein L4



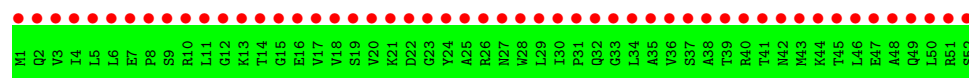
• Molecule 26: 50S ribosomal protein L5



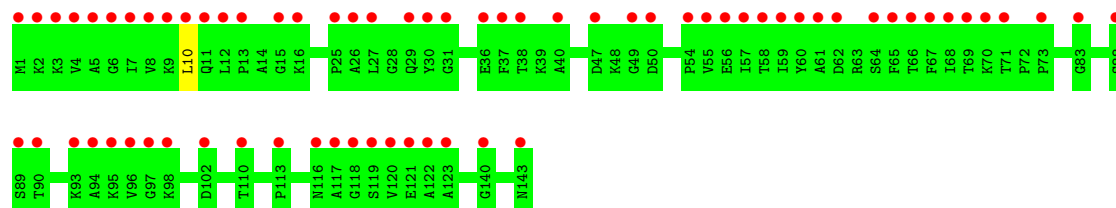
• Molecule 27: 50S ribosomal protein L6



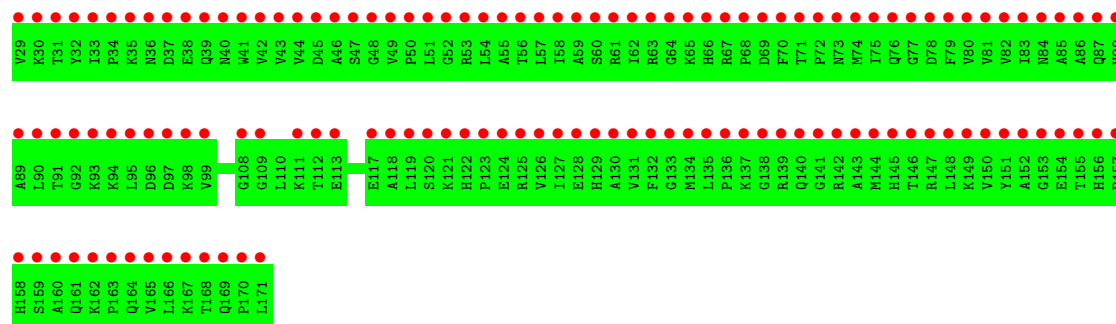
- Molecule 28: 50S ribosomal protein L9



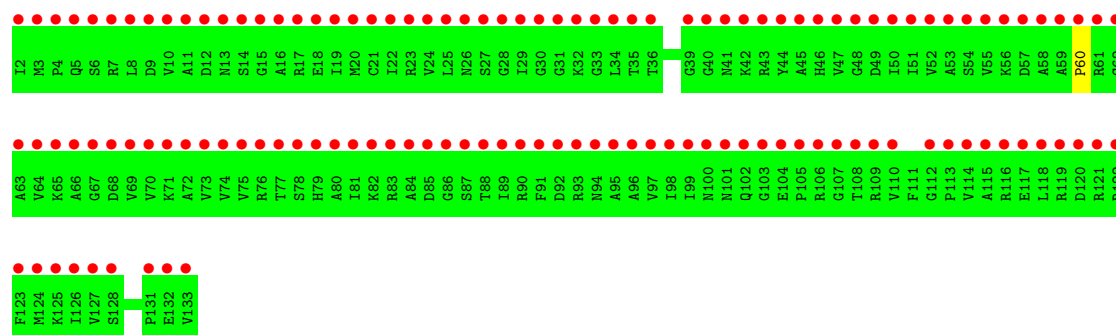
- Molecule 29: 50S ribosomal protein L11



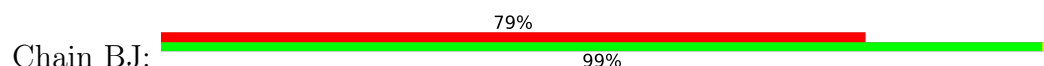
- Molecule 30: 50S ribosomal protein L13

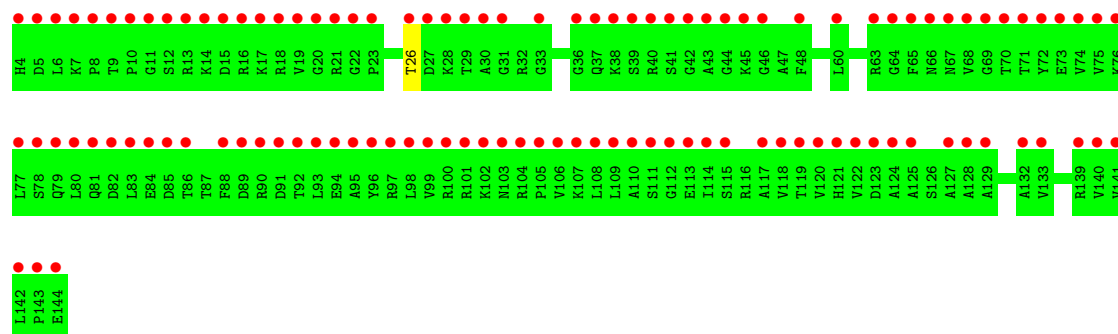


- Molecule 31: 50S ribosomal protein L14

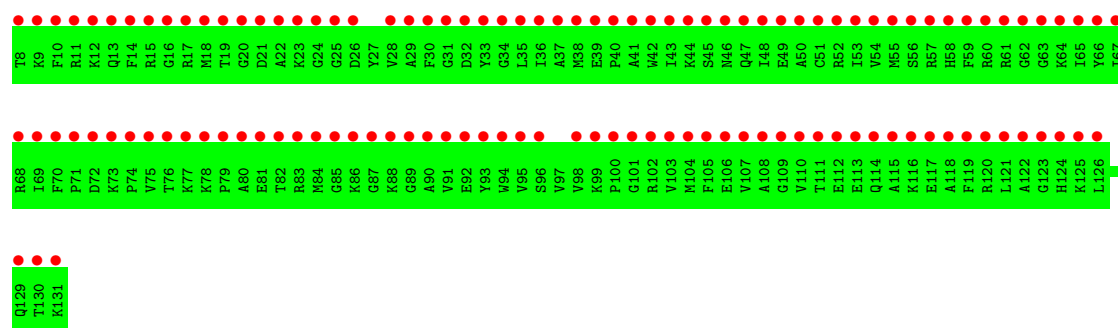


- Molecule 32: 50S ribosomal protein L15

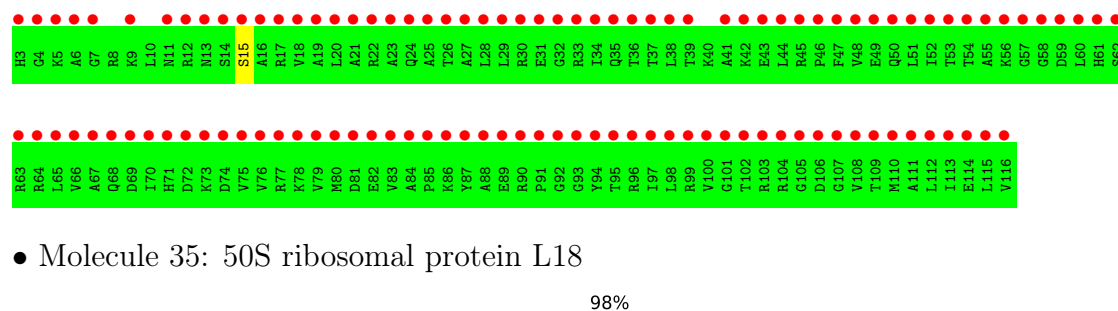




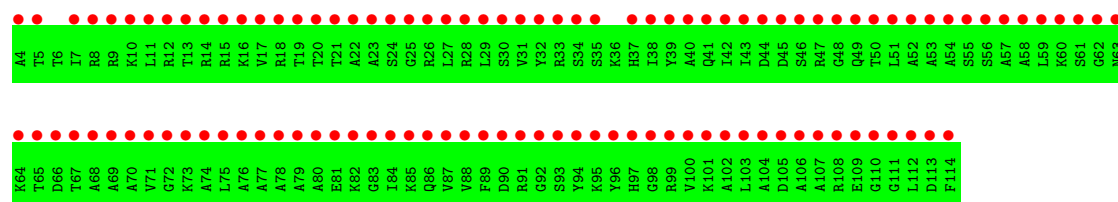
● Molecule 33: 50S ribosomal protein L16



● Molecule 34: 50S ribosomal protein L17

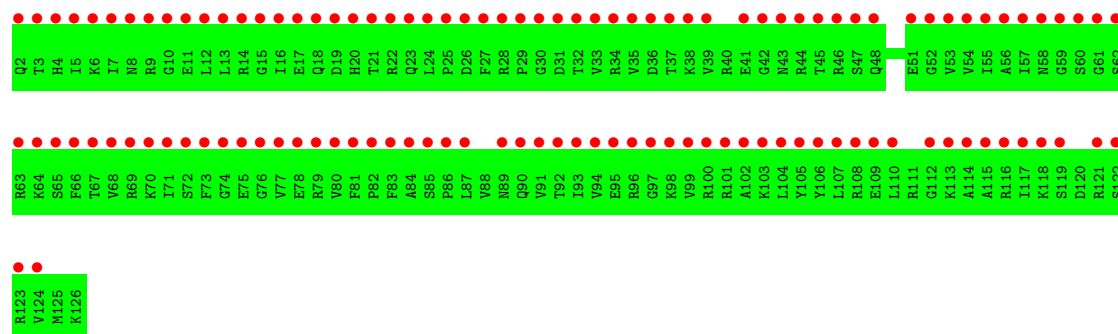


● Molecule 35: 50S ribosomal protein L18

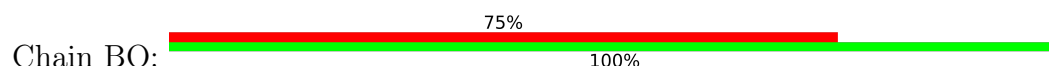


● Molecule 36: 50S ribosomal protein L19





● Molecule 37: 50S ribosomal protein L20



● Molecule 38: 50S ribosomal protein L21

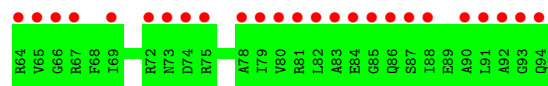
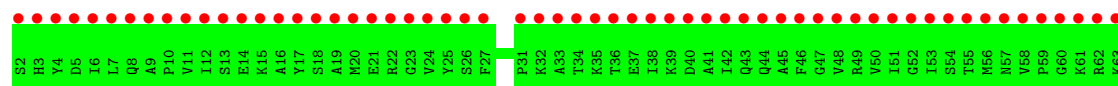


● Molecule 39: 50S ribosomal protein L22

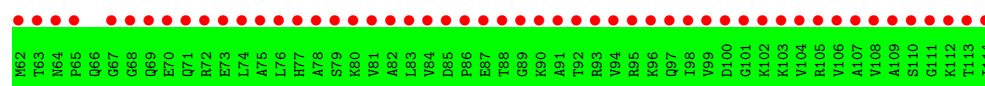
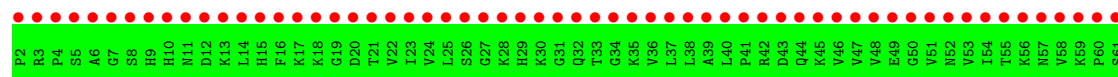


● Molecule 40: 50S ribosomal protein L23

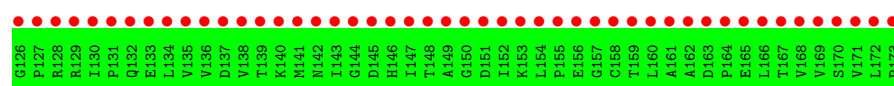
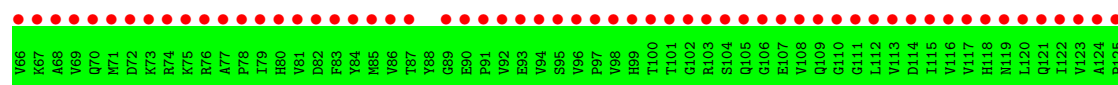
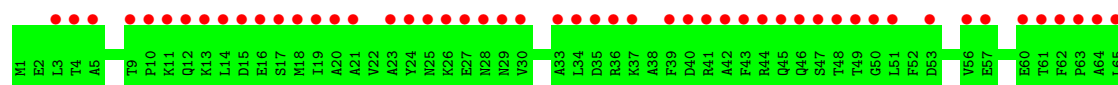




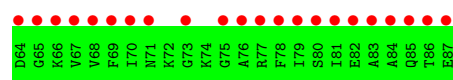
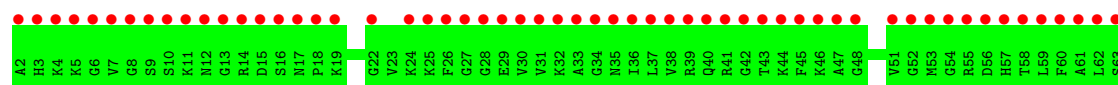
● Molecule 41: 50S ribosomal protein L24



● Molecule 42: general stress protein Ctc



● Molecule 43: 50S ribosomal protein L27

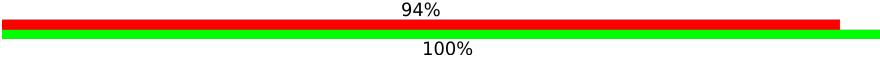


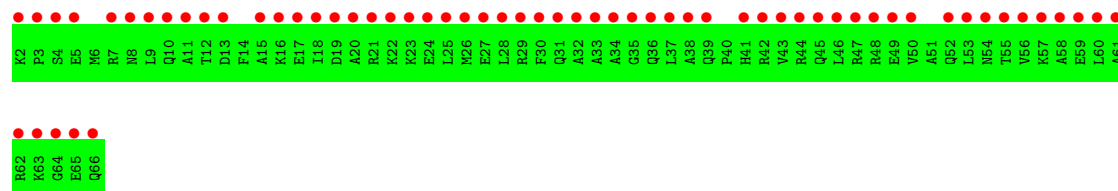
● Molecule 44: 50S RIBOSOMAL PROTEIN L28



There are no outlier residues recorded for this chain.

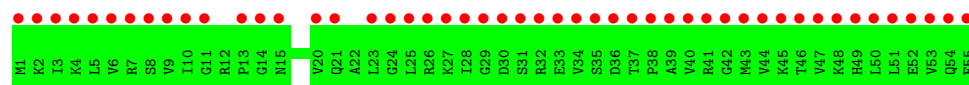
● Molecule 45: 50S ribosomal protein L29

Chain BW: 



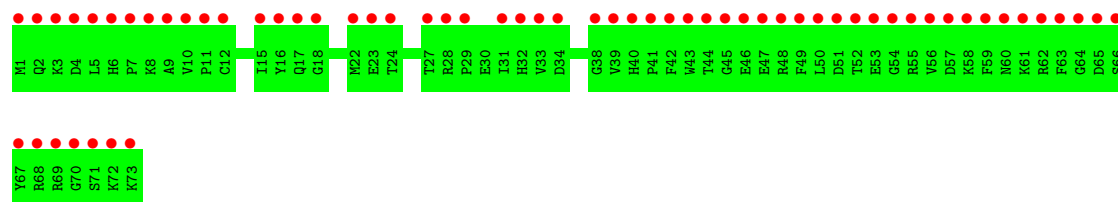
- Molecule 46: 50S ribosomal protein L30

Chain BX: 



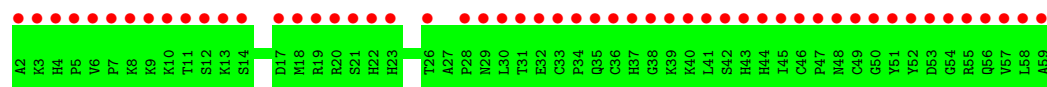
- Molecule 47: 50S ribosomal protein L31

Chain BY: 



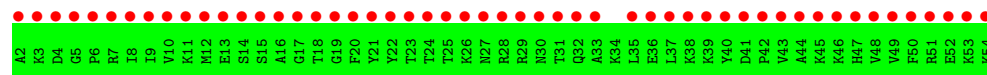
- Molecule 48: 50S ribosomal protein L32

Chain BZ: 



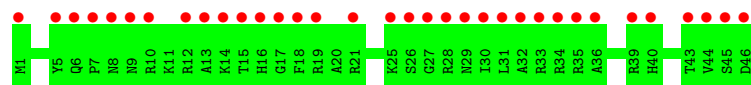
- Molecule 49: 50S ribosomal protein L33

Chain B1: 

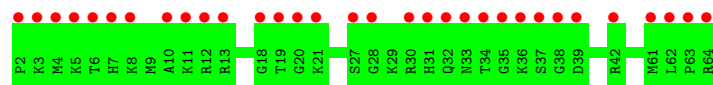


- Molecule 50: 50S ribosomal protein L34

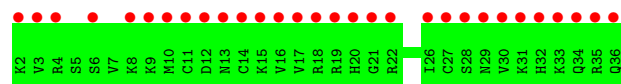
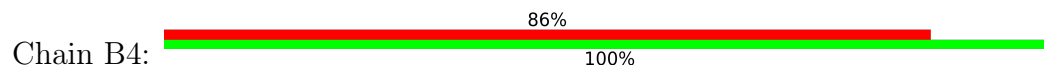
Chain B2: 



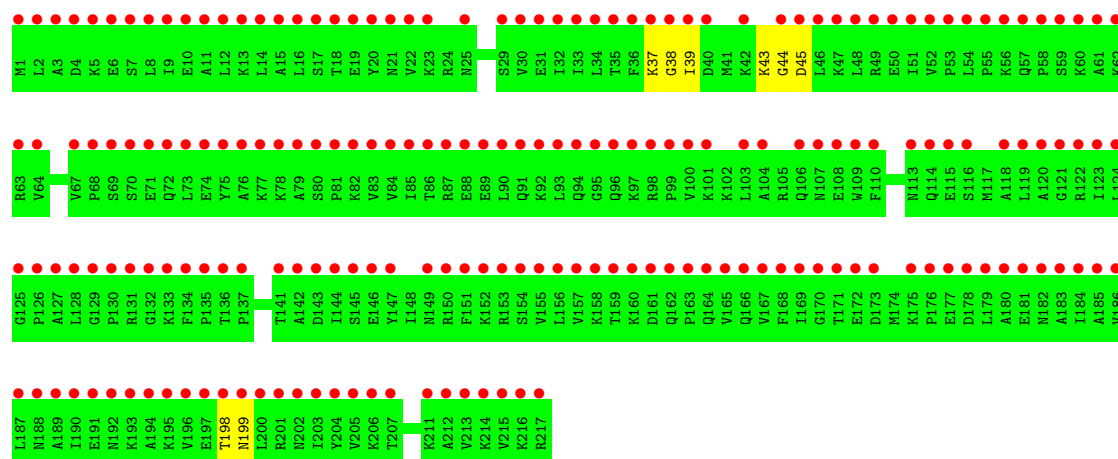
- Molecule 51: 50S ribosomal protein L35



- Molecule 52: 50S ribosomal protein L36



- Molecule 53: 50S ribosomal protein L1P



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	683.89Å 683.89Å 386.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.00 – 9.50 70.00 – 9.50	Depositor EDS
% Data completeness (in resolution range)	92.1 (70.00-9.50) 86.8 (70.00-9.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.49 (at 9.99Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.389 , 0.407 0.370 , 0.386	Depositor DCC
R_{free} test set	1282 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	437.2	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.00 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	118711	wwPDB-VP
Average B, all atoms (Å ²)	680.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	1.35	73/36823 (0.2%)	1.17	295/57351 (0.5%)
2	AB	0.45	0/1935	1.07	13/2609 (0.5%)
3	AC	0.44	0/1636	1.01	9/2205 (0.4%)
4	AD	0.44	0/1732	0.95	7/2318 (0.3%)
5	AE	0.63	0/1162	1.19	10/1564 (0.6%)
6	AF	0.41	0/855	0.95	3/1154 (0.3%)
7	AG	0.42	0/1275	1.00	7/1709 (0.4%)
8	AH	0.58	0/1135	1.13	8/1527 (0.5%)
9	AI	0.41	0/1028	0.95	5/1378 (0.4%)
10	AJ	0.43	0/807	1.08	6/1085 (0.6%)
11	AK	0.51	0/899	1.07	4/1213 (0.3%)
12	AL	0.52	0/985	1.08	4/1317 (0.3%)
13	AM	0.45	0/1006	0.99	2/1344 (0.1%)
14	AN	0.44	0/500	1.21	7/664 (1.1%)
15	AO	0.47	0/744	0.95	3/992 (0.3%)
16	AP	0.51	0/716	1.17	8/963 (0.8%)
17	AQ	0.54	0/869	1.07	1/1159 (0.1%)
18	AR	0.43	0/602	0.96	4/799 (0.5%)
19	AS	0.43	0/661	1.09	6/890 (0.7%)
20	AT	0.51	0/764	1.12	7/1006 (0.7%)
21	B0	0.44	15/67885 (0.0%)	0.65	63/105852 (0.1%)
22	B9	0.57	1/2815 (0.0%)	0.67	3/4384 (0.1%)
All	All	0.82	89/126834 (0.1%)	0.89	475/193483 (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.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	2	40
21	B0	0	5
All	All	2	45

The worst 5 of 89 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	59	A	O3'-P	-96.68	0.16	1.61
1	AA	1398	A	O3'-P	-69.11	0.57	1.61
1	AA	214	U	O3'-P	-58.74	0.73	1.61
1	AA	394	G	O3'-P	-57.14	0.75	1.61
1	AA	1505	G	O3'-P	-56.83	0.76	1.61

The worst 5 of 475 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	B0	1856	U	O3'-P-O5'	-61.52	11.72	104.00
1	AA	59	A	P-O3'-C3'	-46.98	49.73	120.20
1	AA	351	G	O3'-P-O5'	42.09	167.14	104.00
1	AA	274	A	O3'-P-O5'	-36.25	49.62	104.00
1	AA	1409	C	O3'-P-O5'	-34.78	51.83	104.00

All (2) chirality outliers are listed below:

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

5 of 45 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 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	32939	0	16652	3456	1
2	AB	1900	0	1951	227	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	AC	1612	0	1675	298	0
4	AD	1702	0	1767	228	2
5	AE	1146	0	1207	260	0
6	AF	842	0	855	77	2
7	AG	1256	0	1296	143	2
8	AH	1115	0	1177	128	0
9	AI	1010	0	1043	188	0
10	AJ	794	0	839	209	2
11	AK	884	0	904	87	0
12	AL	970	0	1056	154	0
13	AM	996	0	1068	185	0
14	AN	491	0	529	156	0
15	AO	733	0	770	63	0
16	AP	700	0	720	81	0
17	AQ	856	0	925	244	0
18	AR	596	0	668	77	0
19	AS	647	0	673	159	0
20	AT	762	0	853	291	0
21	B0	60636	0	30557	1715	1
22	B9	2519	0	1287	43	0
23	BA	270	0	0	0	0
24	BB	205	0	0	0	0
25	BC	197	0	0	0	0
26	BD	178	0	0	4	0
27	BE	177	0	0	0	0
28	BF	52	0	0	0	0
29	BG	143	0	0	1	0
30	BH	143	0	0	0	0
31	BI	132	0	0	2	0
32	BJ	141	0	0	1	0
33	BK	124	0	0	0	0
34	BL	114	0	0	1	0
35	BM	111	0	0	0	0
36	BN	125	0	0	0	0
37	BO	117	0	0	0	0
38	BP	100	0	0	0	0
39	BQ	130	0	0	0	0
40	BR	93	0	0	0	0
41	BS	113	0	0	0	0
42	BT	173	0	0	0	0
43	BU	86	0	0	0	0
44	BV	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	BW	65	0	0	0	0
46	BX	55	0	0	0	0
47	BY	73	0	0	0	0
48	BZ	58	0	0	0	0
49	B1	53	0	0	0	0
50	B2	46	0	0	0	0
51	B3	63	0	0	0	0
52	B4	35	0	0	0	0
53	B5	217	0	0	22	0
All	All	118711	0	68472	7084	5

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 38.

The worst 5 of 7084 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1278:U:H5''	1:AA:1279:A:P	1.31	1.68
1:AA:1458:G:C8	1:AA:1459:C:H2'	1.27	1.63
1:AA:191:G:C6	1:AA:192:U:C2	1.90	1.60
1:AA:1475:G:H5''	21:B0:1706:A:C4'	1.13	1.60
1:AA:1475:G:C5'	21:B0:1706:A:H4'	1.32	1.59

All (5) 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	Interatomic distance (Å)	Clash overlap (Å)
4:AD:172:PRO:O	6:AF:15:ASP:CB[3_555]	1.83	0.37
1:AA:416:G:OP1	21:B0:3140:G:O2'[3_555]	1.99	0.21
7:AG:51:GLN:NE2	10:AJ:87:THR:OG1[4_555]	2.08	0.12
4:AD:186:LEU:CD1	6:AF:15:ASP:OD2[3_555]	2.14	0.06
7:AG:57:GLU:OE2	10:AJ:89:ASP:OD1[4_555]	2.14	0.06

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 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	
2	AB	232/234 (99%)	174 (75%)	34 (15%)	24 (10%)	0	6
3	AC	204/206 (99%)	135 (66%)	40 (20%)	29 (14%)	0	3
4	AD	206/208 (99%)	166 (81%)	31 (15%)	9 (4%)	2	17
5	AE	148/150 (99%)	130 (88%)	13 (9%)	5 (3%)	3	21
6	AF	99/101 (98%)	79 (80%)	19 (19%)	1 (1%)	12	49
7	AG	153/155 (99%)	127 (83%)	16 (10%)	10 (6%)	1	12
8	AH	136/138 (99%)	125 (92%)	7 (5%)	4 (3%)	3	23
9	AI	125/127 (98%)	88 (70%)	27 (22%)	10 (8%)	1	9
10	AJ	96/98 (98%)	59 (62%)	20 (21%)	17 (18%)	0	2
11	AK	117/119 (98%)	88 (75%)	20 (17%)	9 (8%)	1	10
12	AL	120/124 (97%)	96 (80%)	15 (12%)	9 (8%)	1	10
13	AM	121/125 (97%)	87 (72%)	26 (22%)	8 (7%)	1	12
14	AN	58/60 (97%)	40 (69%)	11 (19%)	7 (12%)	0	4
15	AO	86/88 (98%)	70 (81%)	11 (13%)	5 (6%)	1	14
16	AP	81/83 (98%)	65 (80%)	15 (18%)	1 (1%)	10	44
17	AQ	102/104 (98%)	84 (82%)	10 (10%)	8 (8%)	1	10
18	AR	71/73 (97%)	62 (87%)	7 (10%)	2 (3%)	4	24
19	AS	78/80 (98%)	48 (62%)	19 (24%)	11 (14%)	0	3
20	AT	97/99 (98%)	65 (67%)	20 (21%)	12 (12%)	0	4
All	All	2330/2372 (98%)	1788 (77%)	361 (16%)	181 (8%)	1	10

5 of 181 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	8	LYS
2	AB	9	GLU
2	AB	15	VAL
2	AB	16	HIS
2	AB	17	PHE

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	
2	AB	202/202 (100%)	184 (91%)	18 (9%)	9	28
3	AC	160/160 (100%)	142 (89%)	18 (11%)	5	19
4	AD	180/180 (100%)	169 (94%)	11 (6%)	17	38
5	AE	115/115 (100%)	98 (85%)	17 (15%)	3	13
6	AF	90/90 (100%)	86 (96%)	4 (4%)	25	47
7	AG	126/126 (100%)	120 (95%)	6 (5%)	23	44
8	AH	119/119 (100%)	107 (90%)	12 (10%)	7	23
9	AI	98/98 (100%)	90 (92%)	8 (8%)	10	31
10	AJ	88/88 (100%)	79 (90%)	9 (10%)	7	23
11	AK	90/90 (100%)	83 (92%)	7 (8%)	11	32
12	AL	104/104 (100%)	95 (91%)	9 (9%)	9	29
13	AM	100/100 (100%)	93 (93%)	7 (7%)	14	35
14	AN	49/49 (100%)	47 (96%)	2 (4%)	27	49
15	AO	79/79 (100%)	72 (91%)	7 (9%)	9	28
16	AP	72/72 (100%)	67 (93%)	5 (7%)	14	36
17	AQ	96/96 (100%)	90 (94%)	6 (6%)	16	37
18	AR	64/64 (100%)	60 (94%)	4 (6%)	16	37
19	AS	71/71 (100%)	70 (99%)	1 (1%)	59	72
20	AT	76/76 (100%)	68 (90%)	8 (10%)	6	21
All	All	1979/1979 (100%)	1820 (92%)	159 (8%)	11	31

5 of 159 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	AL	81	SER
17	AQ	68	ARG
13	AM	9	ILE
15	AO	39	LEU

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Mol	Chain	Res	Type
19	AS	43	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
14	AN	49	HIS
15	AO	37	ASN
19	AS	56	GLN
5	AE	38	GLN
5	AE	20	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1522/1537 (99%)	236 (15%)	88 (5%)
21	B0	2815/2887 (97%)	440 (15%)	55 (1%)
22	B9	117/118 (99%)	10 (8%)	0
All	All	4454/4542 (98%)	686 (15%)	143 (3%)

5 of 686 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	8	A
1	AA	9	G
1	AA	31	G
1	AA	32	A

5 of 143 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	B0	1519	G
21	B0	1664	G
21	B0	3146	A
1	AA	792	A
1	AA	748	C

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 oligosaccharides 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
1	AA	106
21	B0	31
22	B9	2
13	AM	1
12	AL	1

The worst 5 of 141 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	9.14
1	AA	1458:G	O3'	1459:C	P	8.01
1	B0	1888:C	O3'	1889:G	P	6.96
1	AA	1459:C	O3'	1460:A	P	6.03
1	B0	3180:U	O3'	3181:C	P	5.42

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	1533/1537 (99%)	1.43	391 (25%) 1 8	207, 548, 819, 940	0
2	AB	234/234 (100%)	1.50	67 (28%) 1 7	754, 754, 754, 754	0
3	AC	206/206 (100%)	2.81	110 (53%) 0 3	378, 378, 378, 378	0
4	AD	208/208 (100%)	2.96	111 (53%) 0 3	709, 709, 709, 709	0
5	AE	150/150 (100%)	3.30	89 (59%) 0 2	756, 756, 756, 756	0
6	AF	101/101 (100%)	1.44	30 (29%) 1 7	748, 748, 748, 748	0
7	AG	155/155 (100%)	1.93	61 (39%) 1 5	374, 374, 374, 374	0
8	AH	138/138 (100%)	2.82	65 (47%) 0 4	856, 856, 856, 856	0
9	AI	127/127 (100%)	2.24	59 (46%) 0 4	439, 439, 439, 439	0
10	AJ	98/98 (100%)	3.00	43 (43%) 0 4	430, 430, 430, 430	0
11	AK	119/119 (100%)	2.12	42 (35%) 1 6	652, 652, 652, 652	0
12	AL	124/124 (100%)	1.94	40 (32%) 1 6	423, 541, 541, 541	0
13	AM	125/125 (100%)	2.40	62 (49%) 0 3	378, 572, 572, 572	0
14	AN	60/60 (100%)	4.09	39 (65%) 0 2	378, 378, 378, 378	0
15	AO	88/88 (100%)	2.08	38 (43%) 0 4	740, 740, 740, 740	0
16	AP	83/83 (100%)	2.39	41 (49%) 0 3	781, 781, 781, 781	0
17	AQ	104/104 (100%)	1.91	47 (45%) 0 4	857, 857, 857, 857	0
18	AR	73/73 (100%)	1.50	23 (31%) 1 6	748, 748, 748, 748	0
19	AS	80/80 (100%)	2.38	38 (47%) 0 4	633, 633, 633, 633	0
20	AT	99/99 (100%)	2.37	50 (50%) 0 3	940, 940, 940, 940	0
21	B0	2825/2887 (97%)	2.03	1080 (38%) 1 5	462, 737, 737, 940	0
22	B9	118/118 (100%)	1.74	35 (29%) 1 7	772, 938, 938, 938	0
23	BA	270/270 (100%)	8.12	252 (93%) 0 1	737, 737, 737, 737	0
24	BB	205/205 (100%)	7.27	180 (87%) 0 1	737, 737, 737, 737	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
25	BC	197/197 (100%)	7.86	163 (82%)	0	1	737, 737, 737, 737	0
26	BD	178/178 (100%)	9.94	177 (99%)	0	1	938, 938, 938, 938	0
27	BE	177/177 (100%)	7.15	155 (87%)	0	1	737, 737, 737, 737	0
28	BF	52/52 (100%)	9.12	52 (100%)	0	1	737, 737, 737, 737	0
29	BG	143/143 (100%)	4.35	69 (48%)	0	3	907, 907, 907, 907	0
30	BH	143/143 (100%)	6.73	131 (91%)	0	1	737, 737, 737, 737	0
31	BI	132/132 (100%)	10.34	127 (96%)	0	1	737, 737, 737, 737	0
32	BJ	141/141 (100%)	6.64	112 (79%)	0	1	737, 737, 737, 737	0
33	BK	124/124 (100%)	7.95	120 (96%)	0	1	737, 737, 737, 737	0
34	BL	114/114 (100%)	9.53	111 (97%)	0	1	737, 737, 737, 737	0
35	BM	111/111 (100%)	11.03	109 (98%)	0	1	938, 938, 938, 938	0
36	BN	125/125 (100%)	7.04	117 (93%)	0	1	737, 737, 737, 737	0
37	BO	117/117 (100%)	4.31	88 (75%)	0	2	737, 737, 737, 737	0
38	BP	100/100 (100%)	4.54	64 (64%)	0	2	737, 737, 737, 737	0
39	BQ	130/130 (100%)	7.19	119 (91%)	0	1	737, 737, 737, 737	0
40	BR	93/93 (100%)	7.99	84 (90%)	0	1	737, 737, 737, 737	0
41	BS	113/113 (100%)	9.26	112 (99%)	0	1	737, 737, 737, 737	0
42	BT	173/173 (100%)	15.01	158 (91%)	0	1	737, 772, 772, 772	0
43	BU	86/86 (100%)	9.01	79 (91%)	0	1	737, 737, 737, 737	0
44	BV	0/16	-	-	-	-	-	-
45	BW	65/65 (100%)	7.82	61 (93%)	0	1	737, 737, 737, 737	0
46	BX	55/55 (100%)	6.25	49 (89%)	0	1	737, 737, 737, 737	0
47	BY	73/73 (100%)	7.54	62 (84%)	0	1	737, 737, 737, 737	0
48	BZ	58/58 (100%)	6.92	53 (91%)	0	1	737, 737, 737, 737	0
49	B1	53/53 (100%)	9.08	52 (98%)	0	1	737, 737, 737, 737	0
50	B2	46/46 (100%)	3.95	34 (73%)	0	2	737, 737, 737, 737	0
51	B3	63/63 (100%)	3.01	32 (50%)	0	3	737, 737, 737, 737	0
52	B4	35/35 (100%)	4.10	30 (85%)	0	1	737, 737, 737, 737	0
53	B5	213/217 (98%)	8.93	196 (92%)	0	1	940, 940, 940, 940	0
All	All	10433/10519 (99%)	4.05	5709 (54%)	0	3	207, 737, 938, 940	0

The worst 5 of 5709 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
42	BT	137	ASP	89.0
42	BT	136	VAL	85.9
42	BT	138	VAL	78.6
42	BT	103	ARG	64.3
42	BT	101	THR	59.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.