



wwPDB EM Validation Summary Report ⓘ

Nov 2, 2024 – 04:18 pm GMT

PDB ID : 6S13
EMDB ID : EMD-10079
Title : Erythromycin Resistant Staphylococcus aureus 70S ribosome (delta R88 A89 uL22).
Authors : Halfon, Y.; Matozv, D.; Eyal, Z.; Bashan, A.; Zimmerman, E.; Kjeldgaard, J.; Ingmer, H.; Yonath, A.
Deposited on : 2019-06-18
Resolution : 3.58 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

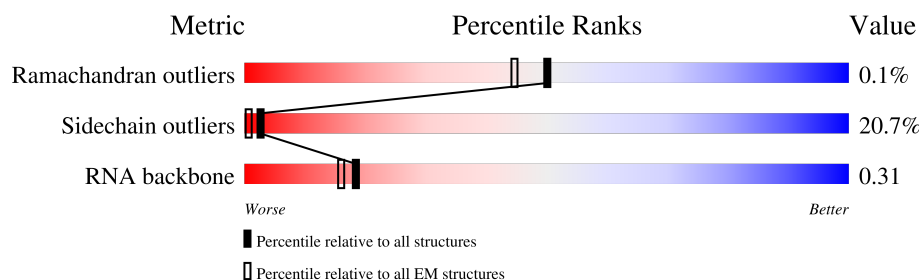
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.58 Å.

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














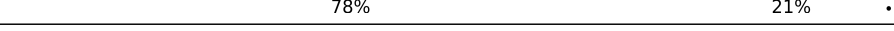



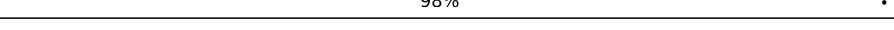



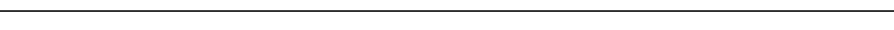

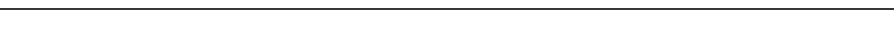
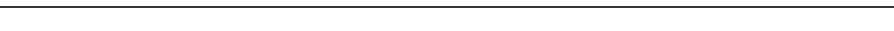


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	2905	
2	B	115	
3	C	274	
4	D	215	
5	E	206	
6	F	175	
7	G	175	
8	H	145	
9	I	122	










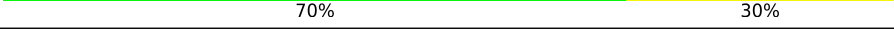



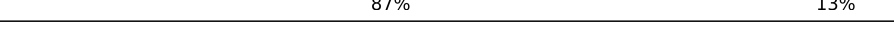




Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
10	J	146	 91% 9%
11	K	137	 86% 14%
12	L	120	 88% 12%
13	M	119	 79% 20% .
14	N	114	 88% 12%
15	O	116	 89% 11%
16	P	102	 78% 22%
17	Q	110	 73% 27%
18	R	89	 82% 18%
19	S	103	 79% 20% .
20	T	94	 81% 19%
21	U	82	 78% 21% .
22	V	58	 81% 19%
23	W	67	 88% 12%
24	X	58	 86% 14%
25	Y	59	 98% .
26	Z	48	 75% 23% .
27	1	47	 74% 26%
28	2	43	 91% 9%
29	3	64	 88% 12%
30	4	37	 76% 19% 5%
31	a	1539	 35% 54% 10%
32	b	226	 84% 15% .
33	c	202	 86% 13%
34	d	198	 81% 17% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
35	e	156	 87% 13%
36	f	95	 81% 19%
37	g	152	 76% 22% ..
38	h	131	 82% 18% .
39	i	127	 85% 15%
40	j	97	 82% 14% .
41	k	114	 77% 21% .
42	l	135	 75% 22% .
43	m	104	 87% 12% .
44	n	60	 70% 30%
45	o	88	 76% 22% .
46	p	89	 81% 19%
47	q	80	 78% 18% 5%
48	r	54	 87% 13%
49	s	80	 74% 24% .
50	t	81	 84% 16%
51	u	52	 75% 23% .
52	v	162	 78% 21% .

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 233957 atoms, of which 93218 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2905	Total	C	H	N	O	P	0	0
			93564	27803	31287	11387	20182	2905		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	115	Total	C	H	N	O	P	0	0
			3685	1094	1240	436	801	114		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	274	Total	C	H	N	O	S	0	0
			4291	1301	2201	415	369	5		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	215	Total	C	H	N	O	S	0	0
			3294	1018	1667	299	305	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	206	Total	C	H	N	O	S	0	0
			3192	986	1620	288	296	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	175	Total	C	H	N	O	S	0	0
			2667	837	1342	227	255	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	175	Total	C	H	N	O	S	0	0
			2488	790	1225	239	231	3		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	145	Total	C	H	N	O	S	0	0
			2277	714	1134	208	218	3		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	122	Total	C	H	N	O	S	0	0
			1899	572	981	174	168	4		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	146	Total	C	H	N	O	S	0	0
			2211	674	1125	214	197	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	137	Total	C	H	N	O	S	0	0
			2194	689	1123	203	175	4		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	120	Total	C	H	N	O	S	0	0
			1915	576	983	182	173	1		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	119	Total	C	H	N	O	S	0	0
			1816	557	925	174	159	1		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	114	Total	C	H	N	O	0	0
			1826	563	937	175	151		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	116	Total	C	H	N	O	S	0	0
			1956	593	1014	189	156	4		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	102	Total	C	H	N	O	S	0	0
			1620	503	830	142	144	1		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	110	Total	C	H	N	O	S	0	0
			1724	523	887	158	153	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	?	-	ARG	deletion	UNP A0A077UKF9
Q	?	-	ALA	deletion	UNP A0A077UKF9

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	89	Total	C	H	N	O	S	0	0
			1463	453	748	127	131	4		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	S	103	Total	C	H	N	O	S	0	0
			1579	486	809	142	141	1		

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	94	Total	C	H	N	O	0	0
			1488	463	766	130	129		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	82	Total	C	H	N	O	0	0
			1265	385	643	122	115		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	58	Total	C	H	N	O	0	0
			911	277	466	96	72		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	67	Total	C	H	N	O	0	0
			1104	333	563	102	106		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	58	Total	C	H	N	O	0	0
			940	280	491	85	84		

- Molecule 25 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Y	59	Total	C	H	N	O	S	0	0
			613	225	243	68	76	1		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
26	Z	48	Total	C	H	N	O	S	0	0
			718	222	358	77	59	2		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	1	47	Total	C	H	N	O	S	0	0
			784	238	394	78	70	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	2	43	Total	C	H	N	O	S	0	0
			782	225	415	89	52	1		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	3	64	Total	C	H	N	O	S	0	0
			1107	324	586	113	82	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	4	37	Total	C	H	N	O	S	0	0
			635	186	340	60	44	5		

- Molecule 31 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	a	1539	Total	C	H	N	O	P	0	0
			49563	14719	16594	6017	10694	1539		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	b	226	Total	C	H	N	O	S	0	0
			3705	1159	1886	317	335	8		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	c	202	Total	C	H	N	O	S	0	0
			2965	945	1464	284	271	1		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	d	198	Total	C	H	N	O	S	0	0
			2946	952	1449	275	268	2		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	e	156	Total	C	H	N	O	S	0	0
			2347	723	1202	211	209	2		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	f	95	Total	C	H	N	O	S	0	0
			1553	493	775	138	145	2		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	g	152	Total	C	H	N	O	S	0	0
			2326	722	1165	218	217	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	h	131	Total	C	H	N	O	S	0	0
			2103	650	1077	183	189	4		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	i	127	Total	C	H	N	O	S	0	0
			1812	576	890	179	166	1		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	j	97	Total	C	H	N	O	S	0	0
			1527	475	775	140	136	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	k	114	Total	C	H	N	O	S	0	0
			1594	498	784	151	159	2		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	l	135	Total	C	H	N	O	S	0	0
			2128	646	1091	211	178	2		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	m	104	Total	C	H	N	O	S	0	0
			1401	453	674	139	135			

- Molecule 44 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	n	60	Total	C	H	N	O	S	0	0
			979	307	492	98	77	5		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	o	88	Total	C	H	N	O	S	0	0
			1475	448	752	150	124	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	p	89	Total	C	H	N	O	S	0	0
			1403	436	709	128	129	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	q	80	Total	C	H	N	O	S	0	0
			1237	392	616	112	117			

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	r	54	Total	C	H	N	O	S	0	0
			927	284	482	86	73	2		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	s	80	Total	C	H	N	O	S	0	0
			1262	410	626	113	111	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	t	81	Total	C	H	N	O	S	0	0
			1207	358	616	117	115	1		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	52	Total	C	H	N	O		
			807	249	407	79	72	0	0

- Molecule 52 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	162	Total	C	H	N	O	S	0	0
			2682	835	1349	242	254	2		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	?	-	GLU	deletion	UNP W8USK0
v	?	-	VAL	deletion	UNP W8USK0
v	?	-	PHE	deletion	UNP W8USK0
v	?	-	VAL	deletion	UNP W8USK0
v	?	-	ALA	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0
v	?	-	LEU	deletion	UNP W8USK0
v	?	-	GLN	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0
v	?	-	MET	deletion	UNP W8USK0
v	?	-	GLN	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0

Continued on next page...

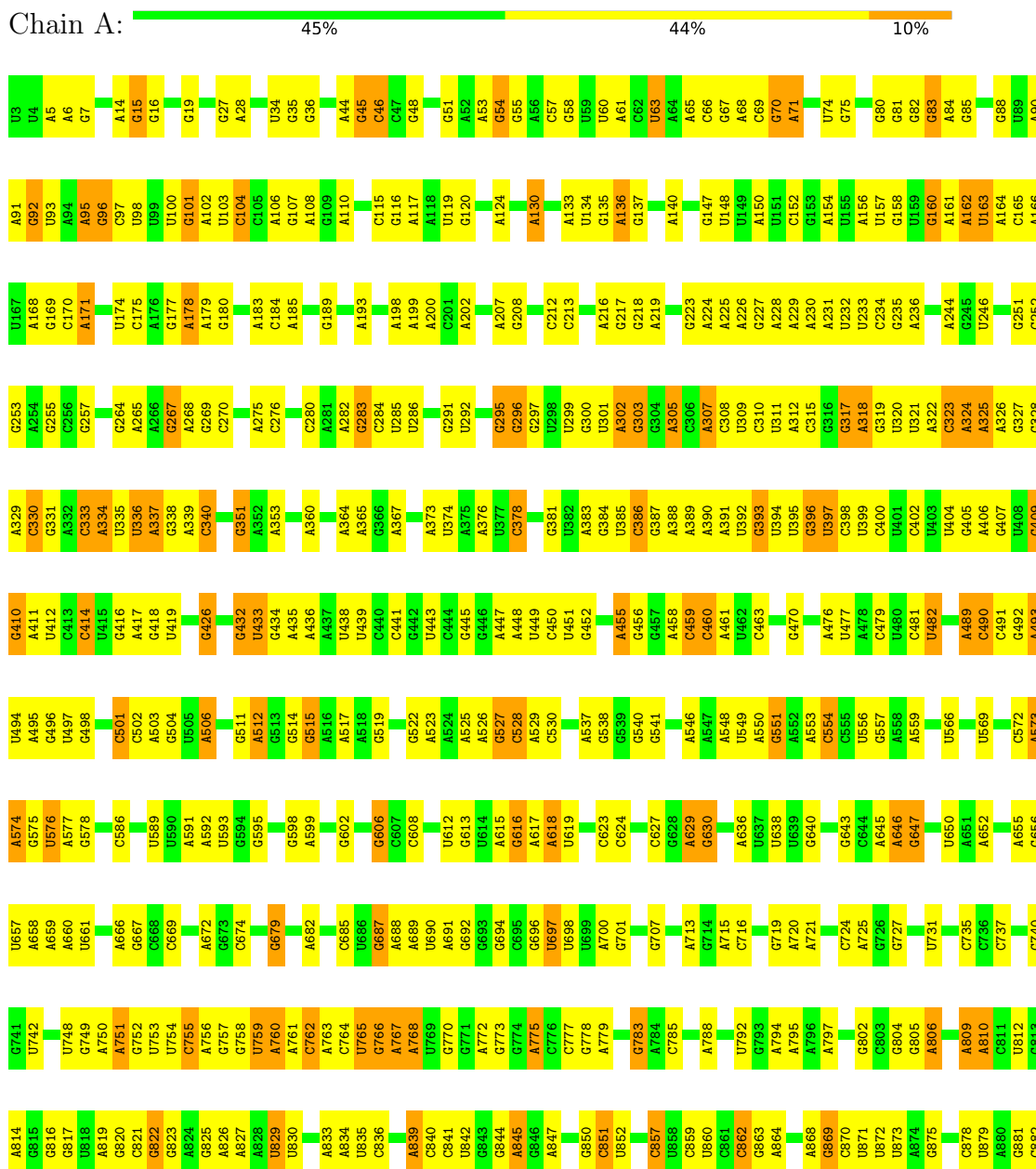
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
v	?	-	THR	deletion	UNP W8USK0
v	?	-	GLN	deletion	UNP W8USK0
v	?	-	VAL	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ASN	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ALA	deletion	UNP W8USK0
v	?	-	TYR	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ASP	deletion	UNP W8USK0
v	?	-	ASN	deletion	UNP W8USK0
v	?	-	GLU	deletion	UNP W8USK0

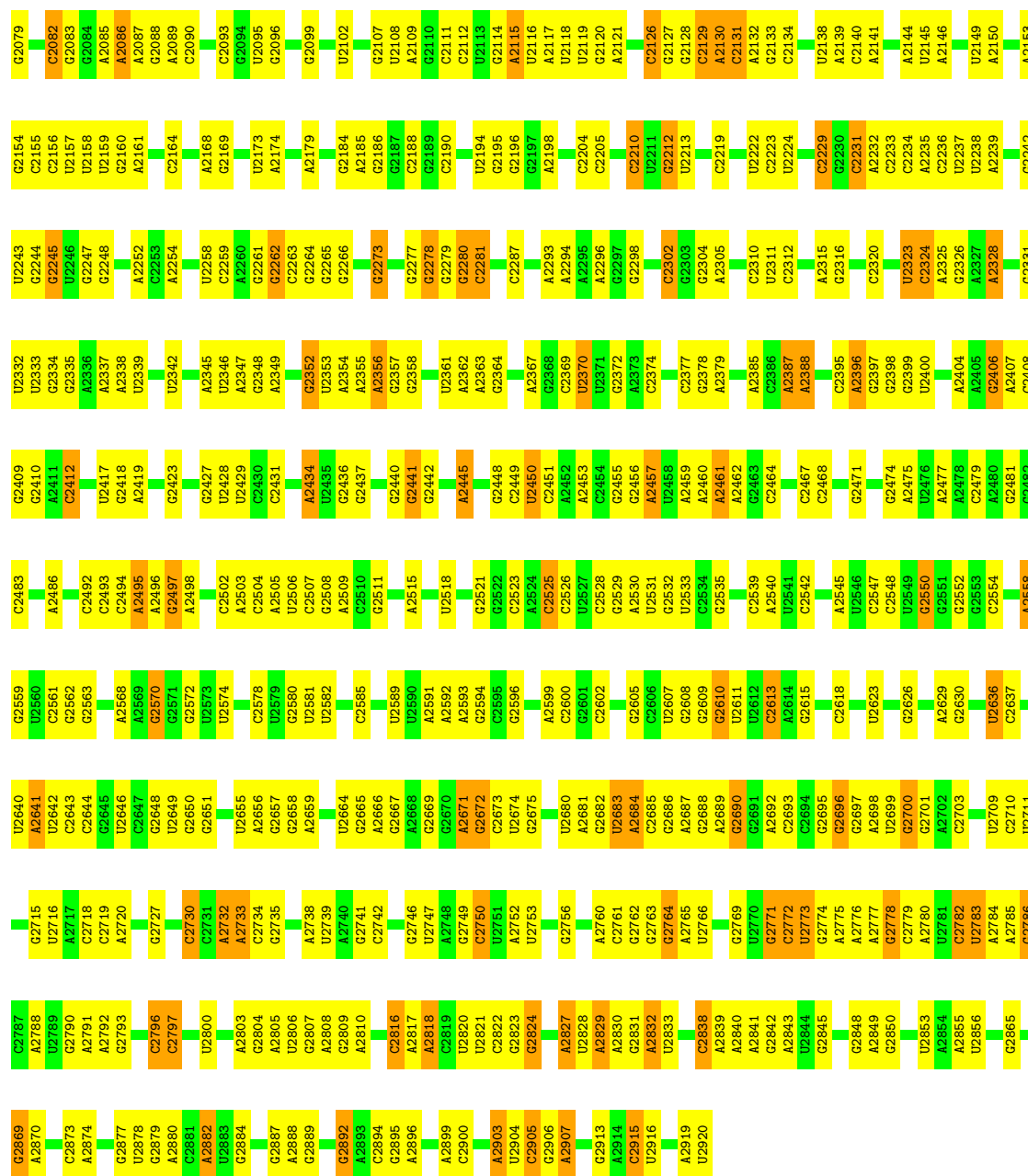
3 Residue-property plots [i](#)

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. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 23S ribosomal RNA

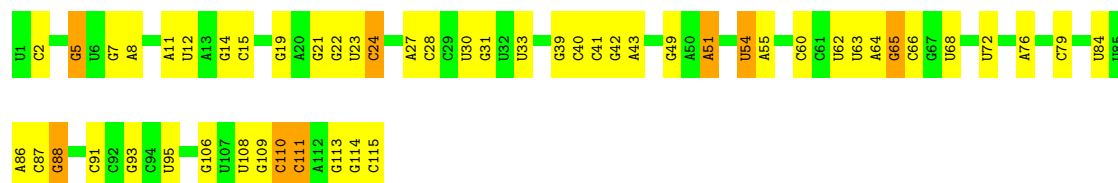


C1994	A1911	G1839	C1766	A1666	U1582	G1514	U1451	C1370	G1276	A1190	U1121	A1044	G965	A886
G1995	A1912	G1841	C1768	G1675	G1583	G1515	C1462	C1379	C1279	U1191	A1122	A1045	G970	A887
A1996	U1913	A1842	G1781	A1678	G1584	A1517	U1455	G1376	G1283	A1192	A1124	G1046	U971	G888
A1997	G1914	U1843	A1771	A1679	G1585	U1518	U1456	U1378	A1284	A1195	U1126	C1061	A972	A891
G1999	G1915	A1846	A1772	A1679	G1586	U1519	U1457	A1379	A1285	A1196	U1127	A1052	A973	U896
C2001	A1916	U1847	A1773	A1682	U1594	A1520	U1458	U1380	A1286	G1197	U1128	A1053	A974	A897
G2002	C1919	A1848	A1775	C1682	U1595	A1521	A1459	U1381	G1287	G1198	A1129	A1054	U974	U898
A2008	A1926	G1850	A1776	G1686	G1596	G1526	U1460	C1382	U1288	A1199	G1130	A1055	A977	U899
U2009	A1927	G1851	G1780	G1687	G1599	A1527	U1462	C1383	G1289	A1200	G1131	U1056	U977	U899
G2012	A1928	G1852	C1781	G1687	U1600	G1528	A1463	C1384	G1290	A1201	G1132	U1057	G983	G900
G2014	C1929	C1853	A1782	A1690	U1601	U1529	U1464	U1386	A1292	G1207	G1135	U1060	A982	A902
U2018	G1932	U1854	G1783	G1691	U1602	G1533	G1465	U1389	U1293	A1208	U1138	G1069	A986	G901
G2019	G1933	G1855	U1784	C1692	U1603	A1534	G1466	G1294	G1294	U1209	U1139	A1070	U987	G902
C2023	G1933	A1856	G1785	A1694	C1604	G1535	G1467	A1390	C1296	U1210	A1140	G1078	A988	G904
A2024	U1938	C1857	G1790	A1698	C1606	C1536	G1469	A1391	G1297	U1212	U1141	G1080	A908	A911
G2027	G1938	G1858	G1791	A1698	C1607	A1537	G1470	G1392	G1298	C1213	U1141	G1086	G990	C912
A2028	G1945	G1862	C1792	U1701	C1608	A1538	A1471	C1400	G1304	U1215	G1143	G1076	G997	U913
G2029	A1946	G1866	C1793	A1708	G1613	A1539	C1472	A1401	G1307	U1216	G1143	A1077	G997	G914
C2036	U1950	G1866	C1794	A1709	A1616	C1541	G1475	C1403	G1307	U1217	G1146	G1078	U1001	U915
G2044	A1954	U1871	A1795	A1709	A1616	C1542	A1476	A1404	C1308	C1222	C1148	G1080	A1003	U916
A2045	G1955	A1875	C1796	A1709	A1616	C1542	U1477	G1405	G1309	G1225	C1148	G1081	A1004	U917
G2047	G1956	G1876	C1797	A1709	A1616	C1542	A1478	G1406	A1310	G1226	C1148	G1082	A1005	G918
A2049	G1957	G1877	C1798	A1709	A1616	C1542	A1479	G1407	A1311	U1227	C1148	G1083	A1006	A920
C2051	U1966	U1878	C1799	A1709	A1616	C1542	G1480	G1408	A1312	U1228	C1148	G1086	C1008	G922
G2052	G1967	G1879	C1800	A1709	A1616	C1542	A1481	U1409	G1316	G1229	C1148	G1088	C1015	A923
A2056	U1967	A1880	G1803	A1709	A1616	C1542	U1482	U1410	G1320	A1230	C1148	G1089	G1016	G925
G2057	G1968	A1881	G1804	A1709	A1616	C1542	A1483	G1411	G1326	A1231	C1148	G1090	A1017	G926
A2058	C1969	U1882	C1805	A1709	A1616	C1542	G1484	G1412	U1330	G1232	C1148	G1091	A1018	G927
G2060	G1970	A1883	G1806	A1709	A1616	C1542	A1485	U1416	G1336	A1233	C1148	G1092	A1019	C928
U2061	U1971	G1884	C1807	A1709	A1616	C1542	A1486	U1430	G1340	G1234	C1148	A1094	G1020	U940
C2063	G1972	U1885	C1808	A1709	A1616	C1542	U1487	U1431	G1342	G1245	C1148	A1095	G1021	A941
A2064	U1973	A1886	C1809	A1709	A1616	C1542	A1488	U1432	G1342	G1248	C1148	G1099	A1024	C942
G2070	G1974	G1887	C1810	A1709	A1616	C1542	A1489	U1433	G1342	U1249	C1148	G1100	A1025	C943
C2071	C1975	U1888	C1811	A1709	A1616	C1542	A1490	U1434	G1342	G1253	C1148	G1101	A1026	G944
G2072	G1976	A1889	C1812	A1709	A1616	C1542	A1491	U1435	G1342	G1258	C1148	A1101	A1027	A946
C2073	U1977	G1890	C1813	A1709	A1616	C1542	A1492	U1436	G1342	G1261	C1148	U1105	G1028	A946
G2074	G1978	U1891	C1814	A1709	A1616	C1542	A1493	U1437	G1342	U1262	C1148	U1106	C1029	U947
A2075	U1979	A1892	C1815	A1709	A1616	C1542	A1494	U1438	G1342	G1265	C1148	G1107	C1030	U948
G2076	C1979	G1893	C1816	A1709	A1616	C1542	A1495	U1439	G1342	G1266	C1148	G1108	C1031	C949
C2077	U1980	A1894	C1817	A1709	A1616	C1542	A1496	U1440	G1342	G1267	C1148	G1109	A1032	A950
G2078	G1981	G1895	C1818	A1709	A1616	C1542	A1497	U1441	G1342	U1268	C1148	U1110	G1033	G951
A2079	C1982	U1896	C1819	A1709	A1616	C1542	A1498	U1442	G1342	G1269	C1148	U1111	A1034	A952
G2080	A1983	G1897	C1820	A1709	A1616	C1542	A1499	U1443	G1342	G1270	C1148	A1111	C1035	A955
C2081	C1984	U1898	C1821	A1709	A1616	C1542	A1500	U1444	G1342	U1271	C1148	A1112	C1036	A956
G2082	G1985	A1899	C1822	A1709	A1616	C1542	A1501	U1445	G1342	G1272	C1148	A1113	A1037	A957
A2083	U1986	G1899	C1823	A1709	A1616	C1542	A1502	U1446	G1342	U1273	C1148	A1114	C1038	C957
C2084	C1987	U1900	C1824	A1709	A1616	C1542	A1503	U1447	G1342	G1274	C1148	A1115	C1039	U958
G2085	G1988	A1901	C1825	A1709	A1616	C1542	A1504	U1448	G1342	U1275	C1148	A1116	A1040	C959
A2086	U1989	G1902	C1826	A1709	A1616	C1542	A1505	U1449	G1342	G1276	C1148	A1117	A1041	C960
C2087	C1990	U1903	C1827	A1709	A1616	C1542	A1506	U1450	G1342	U1277	C1148	A1118	G1042	G961
G2088	G1991	A1904	C1828	A1709	A1616	C1542	A1507	U1451	G1342	G1278	C1148	A1119	C1043	A962
A2089	U1992	G1905	C1829	A1709	A1616	C1542	A1508	U1452	G1342	U1279	C1148	A1120	A1044	
C2090	C1993	U1906	C1830	A1709	A1616	C1542	A1509	U1453	G1342	U1280	C1148			
G2091	G1994	A1907	C1831	A1709	A1616	C1542	A1510	U1454	G1342	U1281	C1148			
A2092	U1995	G1908	C1832	A1709	A1616	C1542	A1511	U1455	G1342	U1282	C1148			
C2093	C1996	U1909	C1833	A1709	A1616	C1542	A1512	U1456	G1342	U1283	C1148			
A2094	G1997	A1910	C1834	A1709	A1616	C1542	A1513	U1457	G1342	U1284	C1148			
G2095	U1998	G1911	C1835	A1709	A1616	C1542	A1514	U1458	G1342	U1285	C1148			
C2096	C1999	U1912	C1836	A1709	A1616	C1542	A1515	U1459	G1342	U1286	C1148			
A2097	G2000	A1913	C1837	A1709	A1616	C1542	A1516	U1460	G1342	U1287	C1148			
G2098	U2001	G1914	C1838	A1709	A1616	C1542	A1517	U1461	G1342	U1288	C1148			
A2099	C2002	A1915	C1839	A1709	A1616	C1542	A1518	U1462	G1342	U1289	C1148			
G2100	G2003	G1916	C1840	A1709	A1616	C1542	A1519	U1463	G1342	U1290	C1148			
C2101	U2004	U1917	C1841	A1709	A1616	C1542	A1520	U1464	G1342	U1291	C1148			
A2102	G2005	A1918	C1842	A1709	A1616	C1542	A1521	U1465	G1342	U1292	C1148			
C2103	C2006	G1919	C1843	A1709	A1616	C1542	A1522	U1466	G1342	U1293	C1148			
A2104	U2007	U1920	C1844	A1709	A1616	C1542	A1523	U1467	G1342	U1294	C1148			
G2105	G2008	A1921	C1845	A1709	A1616	C1542	A1524	U1468	G1342	U1295	C1148			
C2106	U2009	G1922	C1846	A1709	A1616	C1542	A1525	U1469	G1342	U1296	C1148			
A2107	C2010	U1923	C1847	A1709	A1616	C1542	A1526	U1470	G1342	U1297	C1148			
G2108	G2011	A1924	C1848	A1709	A1616	C1542	A1527	U1471	G1342	U1298	C1148			
C2109	U2012	U1925	C1849	A1709	A1616	C1542	A1528	U1472	G1342	U1299	C1148			
A2110	C2013	G1926	C1850	A1709	A1616	C1542	A1529	U1473	G1342	U1300	C1148			
G2111	U2014	A1927	C1851	A1709	A1616	C1542	A1530	U1474	G1342	U1301	C1148			
C2112	C2015	U1928	C1852	A1709	A1616	C1542	A1531	U1475	G1342	U1302	C1148			
A2113	G2016	G1929	C1853	A1709	A1616	C1542	A1532	U1476	G1342	U1303	C1148			
C2114	U2017	C1930	C1854	A1709	A1616	C1542	A1533	U1477	G1342	U1304	C1148			
G2115	G2018	U1931	C1855	A1709	A1616	C1542	A1534	U1478	G1342	U1305	C1148			
A2116	C2019	A1932	C1856	A1709	A1616	C1542	A1535	U1479	G1342	U1306	C1148			
G2117	U2020	G1933	C1857	A1709	A1616	C1542	A1536	U1480	G1342	U1307	C1148			
C2118	C2021	U1934	C1858	A1709	A1616	C1542	A1537	U1481	G1342	U1308	C1148			
A2119	G2022	A1935	C1859	A1709	A1616	C1542	A1538	U1482	G1342	U1309	C1148			
G2120	U2023	U1936	C1860	A1709	A1616	C1542	A1539	U1483	G1342	U1310	C1148			
C2121	C2024	G1937	C1861	A1709	A1616	C1542	A1540	U1484	G1342	U1311	C1148			
A2122	U2025	A1938	C1862	A1709	A1616	C1542	A1541	U1485	G1342	U1312	C1148			
G2123	G2026	U1939	C1863	A1709	A1616	C1542	A1542	U1486	G1342	U1313	C1148			
C2124	C2027	U1940	C1864	A1709	A1616	C1542	A1543	U1487	G1342	U1314	C1148			
A2125	U2028	A1941	C1865	A1709	A1616	C1542	A1544	U1488	G1342	U1315	C1148			
G2126	G2029	G1942	C1866	A1709	A1616	C1542	A1545	U1489	G1342	U1316	C1148			
C2127	C2030	U1943	C1867	A1709	A1616	C1542	A1546	U1490	G1342	U1317	C1148			
A2128	U2031	A1944	C1868	A1709	A1616	C1542	A1547	U1491	G1342	U1318	C1148			
G2129	G203													



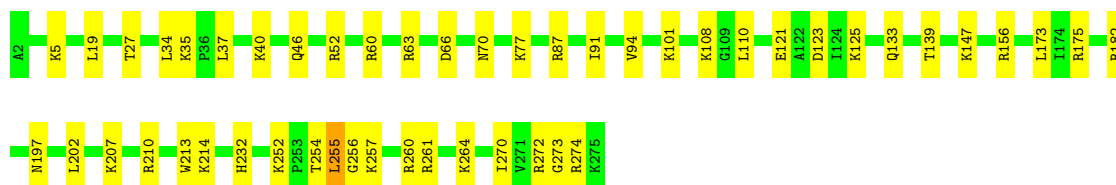
• Molecule 2: 5S ribosomal RNA

Chain B: 55% 38% 7%



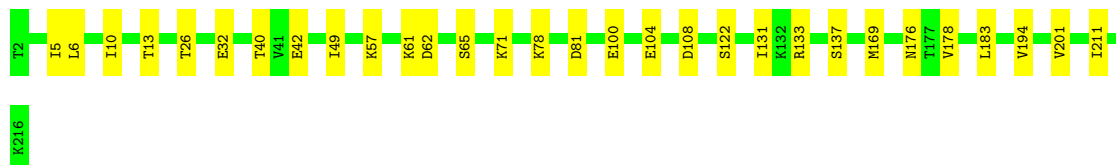
• Molecule 3: 50S ribosomal protein L2

Chain C: 82% 18%



- Molecule 4: 50S ribosomal protein L3

Chain D: 86% 14%



- Molecule 5: 50S ribosomal protein L4

Chain E: 79% 20%



- Molecule 6: 50S ribosomal protein L5

Chain F: 85% 15%



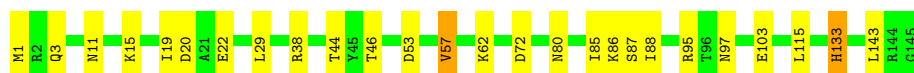
- Molecule 7: 50S ribosomal protein L6

Chain G: 87% 13%




- Molecule 8: 50S ribosomal protein L13

Chain H: 82% 17%



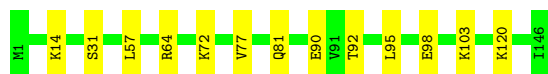
- Molecule 9: 50S ribosomal protein L14

Chain I:  83% 17%




- Molecule 10: 50S ribosomal protein L15

Chain J:  91% 9%




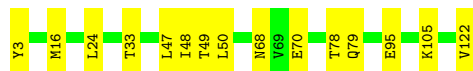
- Molecule 11: 50S ribosomal protein L16

Chain K:  86% 14%




- Molecule 12: 50S ribosomal protein L17

Chain L:  88% 12%



- Molecule 13: 50S ribosomal protein L18

Chain M:  79% 20%



- Molecule 14: 50S ribosomal protein L19

Chain N:  88% 12%




- Molecule 15: 50S ribosomal protein L20

Chain O:  89% 11%



- Molecule 16: 50S ribosomal protein L21

Chain P:  78% 22%




- Molecule 17: 50S ribosomal protein L22

Chain Q:  73% 27%




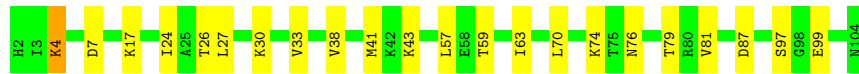
- Molecule 18: 50S ribosomal protein L23

Chain R:  82% 18%




- Molecule 19: 50S ribosomal protein L24

Chain S:  79% 20%




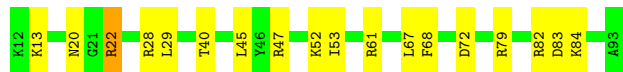
- Molecule 20: 50S ribosomal protein L25

Chain T:  81% 19%




- Molecule 21: 50S ribosomal protein L27

Chain U:  78% 21%




- Molecule 22: 50S ribosomal protein L28

Chain V:  81% 19%




- Molecule 23: 50S ribosomal protein L29

Chain W:  88% 12%



- Molecule 24: 50S ribosomal protein L30

Chain X:  86% 14%



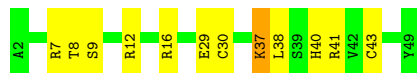
- Molecule 25: 50S ribosomal protein L31 type B

Chain Y:  98% .



- Molecule 26: 50S ribosomal protein L32

Chain Z:  75% 23% .




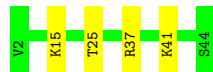
- Molecule 27: 50S ribosomal protein L33

Chain 1:  74% 26%




- Molecule 28: 50S ribosomal protein L34

Chain 2:  91% 9%




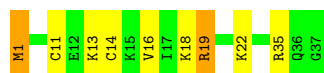
- Molecule 29: 50S ribosomal protein L35

Chain 3:  88% 12%



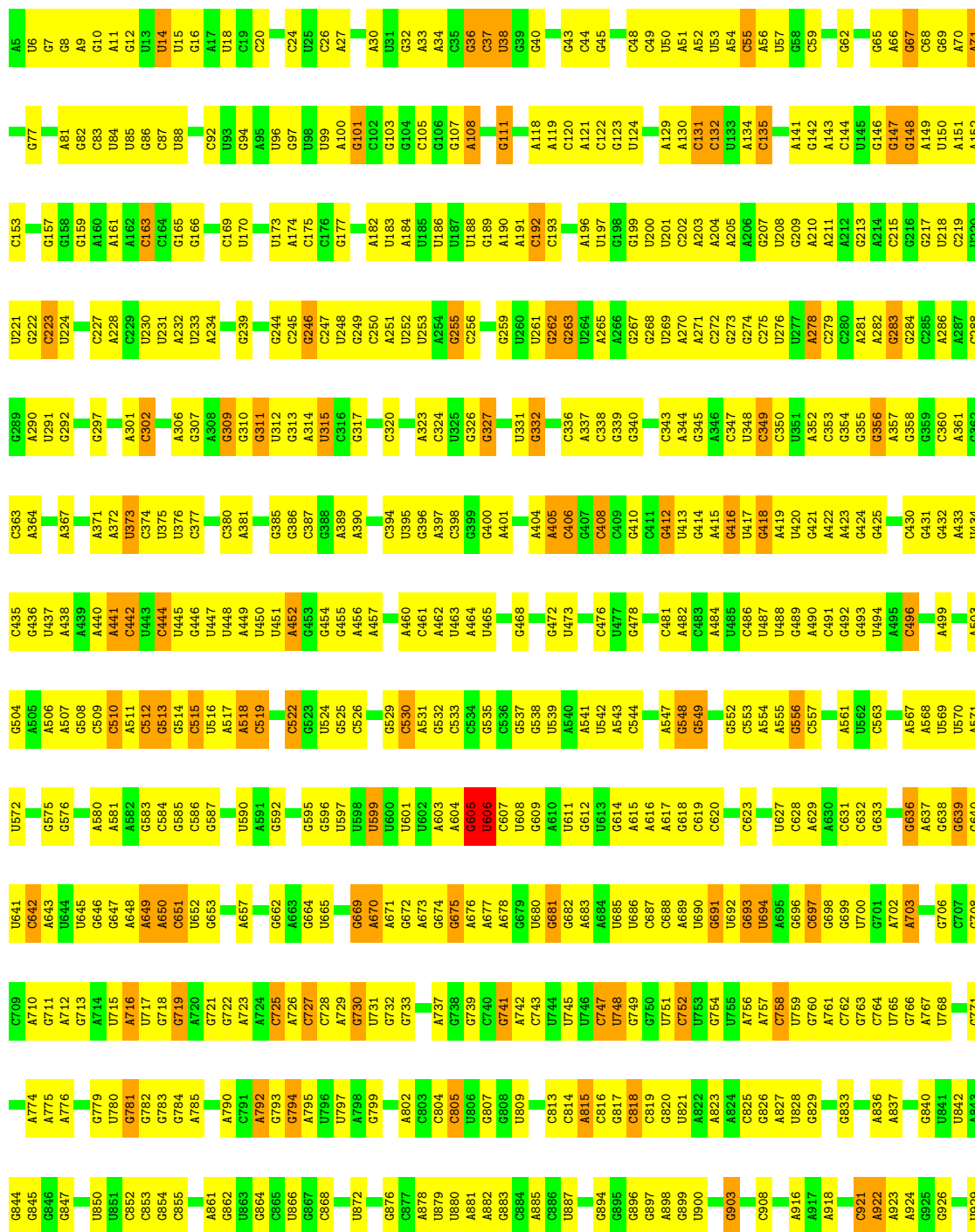
- Molecule 30: 50S ribosomal protein L36

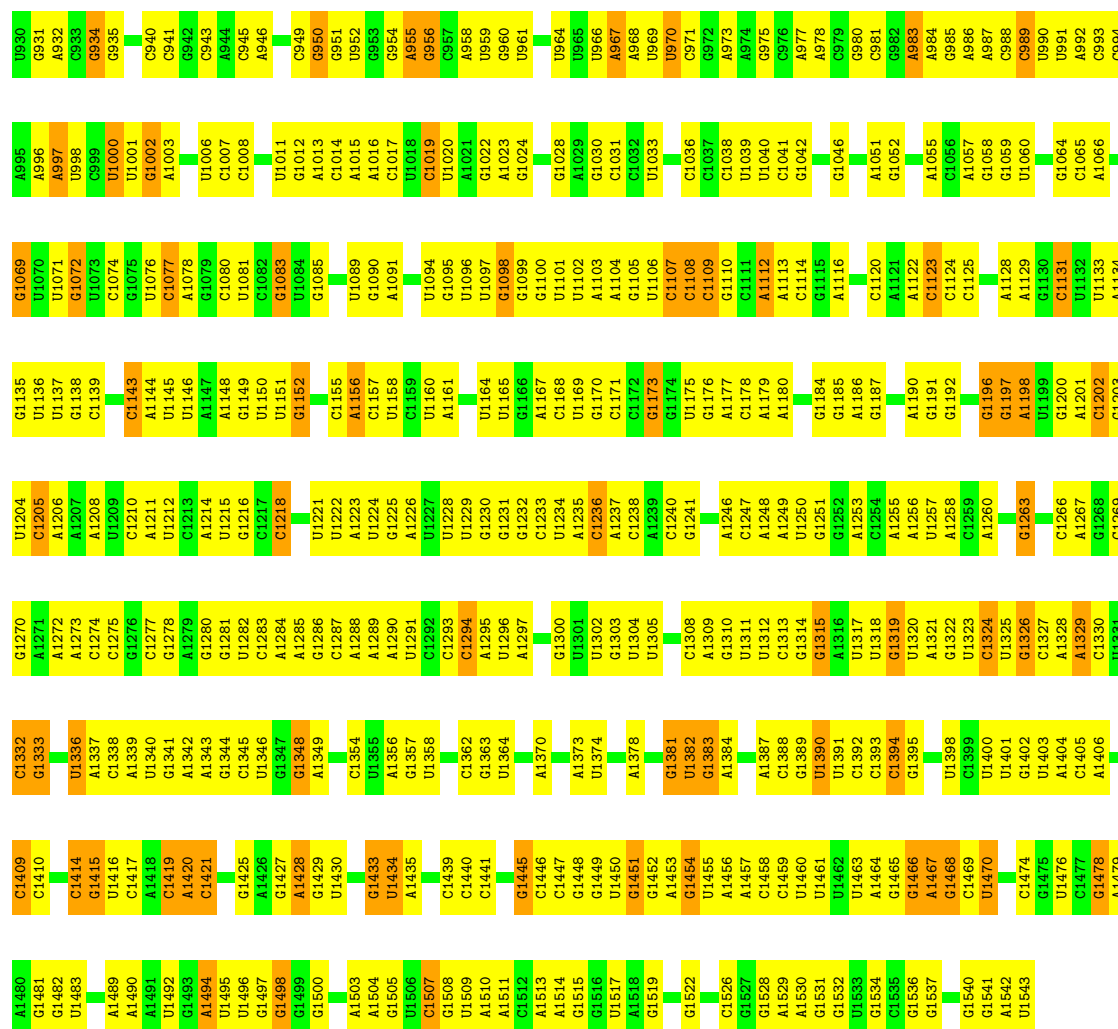
Chain 4:  76% 19% 5%



● Molecule 31: 16S ribosomal RNA

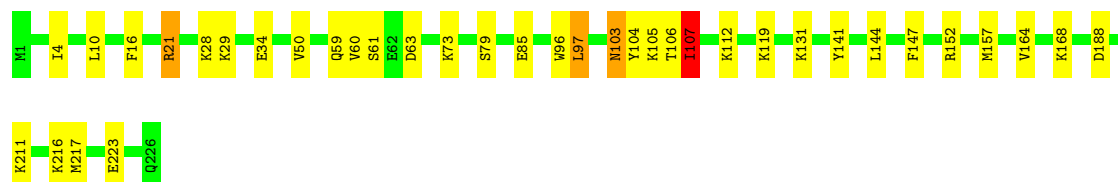
Chain a:  35% 54% 10%





• Molecule 32: 30S ribosomal protein S2

Chain b: 84% 15%



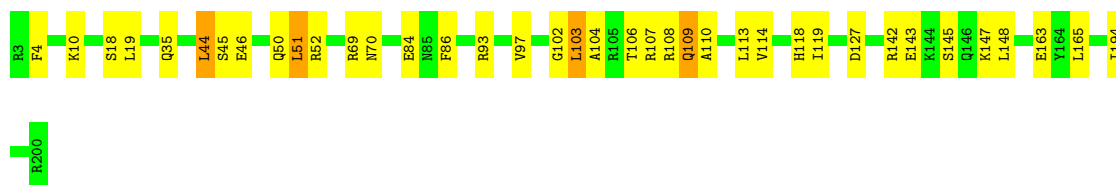
• Molecule 33: 30S ribosomal protein S3

Chain c: 86% 13%



• Molecule 34: 30S ribosomal protein S4

Chain d: 81% 17%



- Molecule 35: 30S ribosomal protein S5

Chain e: 87% 13%



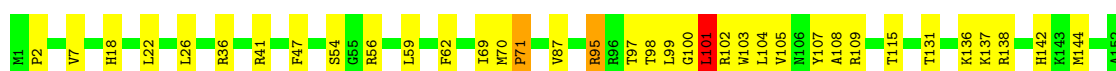
- Molecule 36: 30S ribosomal protein S6

Chain f: 81% 19%



- Molecule 37: 30S ribosomal protein S7

Chain g: 76% 22% ..



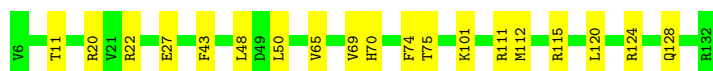
- Molecule 38: 30S ribosomal protein S8

Chain h: 82% 18%



- Molecule 39: 30S ribosomal protein S9

Chain i: 85% 15%




- Molecule 40: 30S ribosomal protein S10

Chain j: 82% 14%



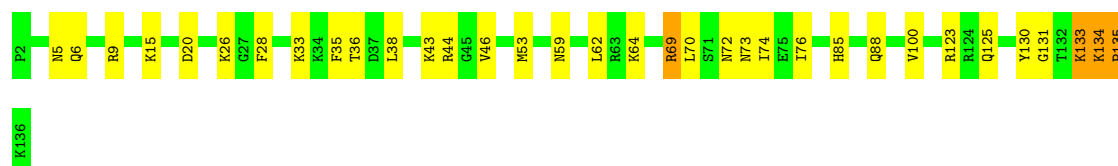
- Molecule 41: 30S ribosomal protein S11

Chain k:  77% 21%



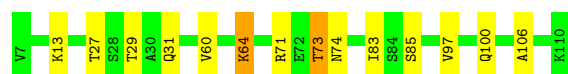
- Molecule 42: 30S ribosomal protein S12

Chain l:  75% 22%



- Molecule 43: 30S ribosomal protein S13

Chain m:  87% 12%




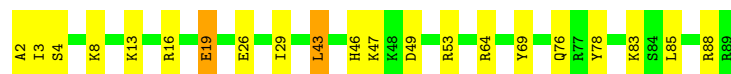
- Molecule 44: 30S ribosomal protein S14 type Z

Chain n:  70% 30%




- Molecule 45: 30S ribosomal protein S15

Chain o:  76% 22%




- Molecule 46: 30S ribosomal protein S16

Chain p:  81% 19%


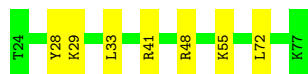


- Molecule 47: 30S ribosomal protein S17

Chain q:  78% 18% 5%




• Molecule 48: 30S ribosomal protein S18

Chain r:  87% 13%


• Molecule 49: 30S ribosomal protein S19

Chain s:  74% 24% .


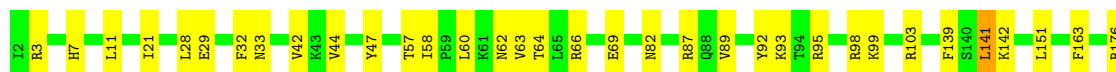
• Molecule 50: 30S ribosomal protein S20

Chain t:  84% 16%

• Molecule 51: 30S ribosomal protein S21

Chain u:  75% 23% .

• Molecule 52: Ribosome hibernation promoting factor

Chain v:  78% 21% .

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	145897	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.076	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.69	183/69739 (0.3%)	1.60	1291/108751 (1.2%)
2	B	1.04	0/2733	1.42	26/4257 (0.6%)
3	C	0.61	0/2125	0.82	2/2853 (0.1%)
4	D	0.70	0/1651	0.70	1/2215 (0.0%)
5	E	0.69	1/1595 (0.1%)	0.74	0/2154
6	F	0.37	0/1339	0.66	0/1805
7	G	0.38	0/1281	0.66	0/1736
8	H	0.66	0/1165	0.71	0/1570
9	I	0.65	0/925	0.80	0/1242
10	J	0.62	0/1100	0.71	0/1467
11	K	2.44	1/1095 (0.1%)	0.78	1/1472 (0.1%)
12	L	0.59	0/936	0.79	0/1253
13	M	0.45	0/900	0.70	0/1205
14	N	0.65	0/901	0.74	0/1209
15	O	0.71	0/954	0.76	0/1264
16	P	0.72	0/800	0.76	0/1070
17	Q	0.65	0/845	0.80	0/1140
18	R	0.60	0/723	0.68	0/966
19	S	0.49	0/779	0.69	0/1043
20	T	0.39	0/730	0.64	0/981
21	U	0.66	0/628	0.81	1/833 (0.1%)
22	V	0.49	0/451	0.76	0/603
23	W	0.45	0/542	0.73	0/722
24	X	0.64	0/451	0.71	0/606
25	Y	0.31	0/378	0.57	0/521
26	Z	0.63	0/366	0.85	0/489
27	1	0.44	0/395	0.77	0/530
28	2	0.78	0/371	0.81	0/484
29	3	0.60	0/526	0.83	1/690 (0.1%)
30	4	0.50	0/298	0.88	1/392 (0.3%)
31	a	2.36	45/36913 (0.1%)	1.54	698/57564 (1.2%)
32	b	1.12	1/1846 (0.1%)	0.63	1/2477 (0.0%)
33	c	0.29	0/1523	0.65	0/2062
34	d	0.31	0/1526	0.69	1/2063 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	e	0.32	0/1159	0.63	0/1566
36	f	0.36	0/789	0.66	0/1060
37	g	0.39	0/1175	0.87	2/1584 (0.1%)
38	h	1.16	4/1037 (0.4%)	0.96	7/1392 (0.5%)
39	i	0.34	0/937	0.71	0/1269
40	j	0.33	0/764	0.76	0/1034
41	k	0.34	0/824	0.75	1/1119 (0.1%)
42	l	6.63	7/1054 (0.7%)	0.87	4/1415 (0.3%)
43	m	0.32	0/732	0.71	0/991
44	n	6.34	3/497 (0.6%)	1.03	4/662 (0.6%)
45	o	0.33	0/732	0.72	1/979 (0.1%)
46	p	0.33	0/705	0.65	0/952
47	q	0.35	0/629	0.81	1/849 (0.1%)
48	r	0.35	0/452	0.72	0/604
49	s	6.45	8/654 (1.2%)	1.28	11/879 (1.3%)
50	t	0.37	0/591	0.73	0/793
51	u	0.45	0/403	0.83	1/535 (0.2%)
52	v	0.33	0/1350	0.72	1/1812 (0.1%)
All	All	1.85	253/153014 (0.2%)	1.41	2057/229184 (0.9%)

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
3	C	0	5
5	E	0	1
6	F	0	2
7	G	0	1
8	H	0	4
11	K	0	3
12	L	0	1
13	M	0	1
16	P	0	2
19	S	0	1
26	Z	0	2
30	4	0	2
31	a	0	2
32	b	0	4
33	c	0	1
34	d	0	7

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
37	g	0	10
39	i	0	1
40	j	0	4
41	k	0	5
42	l	0	2
43	m	0	5
44	n	0	4
45	o	0	4
47	q	0	5
49	s	0	3
50	t	0	1
51	u	0	3
52	v	0	3
All	All	0	89

The worst 5 of 253 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	n	16	TYR	CB-CG	140.63	3.62	1.51
1	A	333	C	N1-C6	139.55	2.20	1.37
31	a	606	U	C2-N3	135.46	2.32	1.37
31	a	605	G	N3-C4	131.79	2.27	1.35
31	a	605	G	C2-N3	128.80	2.35	1.32

The worst 5 of 2057 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	393	G	C8-N9-C4	-101.80	65.68	106.40
1	A	393	G	N7-C8-N9	65.13	145.66	113.10
1	A	393	G	N9-C4-C5	52.43	126.37	105.40
1	A	393	G	N3-C4-C5	-40.30	108.45	128.60
31	a	605	G	C2-N3-C4	36.17	129.98	111.90

There are no chirality outliers.

5 of 89 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	173	LEU	Peptide
3	C	255	LEU	Peptide
3	C	257	LYS	Peptide
3	C	273	GLY	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
3	C	40	LYS	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	272/274 (99%)	215 (79%)	57 (21%)	0	100	100
4	D	213/215 (99%)	166 (78%)	47 (22%)	0	100	100
5	E	204/206 (99%)	175 (86%)	29 (14%)	0	100	100
6	F	173/175 (99%)	141 (82%)	32 (18%)	0	100	100
7	G	173/175 (99%)	140 (81%)	33 (19%)	0	100	100
8	H	143/145 (99%)	118 (82%)	25 (18%)	0	100	100
9	I	120/122 (98%)	104 (87%)	16 (13%)	0	100	100
10	J	144/146 (99%)	124 (86%)	20 (14%)	0	100	100
11	K	135/137 (98%)	113 (84%)	22 (16%)	0	100	100
12	L	118/120 (98%)	101 (86%)	17 (14%)	0	100	100
13	M	117/119 (98%)	98 (84%)	19 (16%)	0	100	100
14	N	112/114 (98%)	94 (84%)	18 (16%)	0	100	100
15	O	114/116 (98%)	105 (92%)	9 (8%)	0	100	100
16	P	100/102 (98%)	85 (85%)	15 (15%)	0	100	100
17	Q	108/110 (98%)	90 (83%)	17 (16%)	1 (1%)	14	48
18	R	87/89 (98%)	70 (80%)	17 (20%)	0	100	100
19	S	101/103 (98%)	82 (81%)	19 (19%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
21	U	80/82 (98%)	70 (88%)	10 (12%)	0	100	100
22	V	56/58 (97%)	46 (82%)	10 (18%)	0	100	100
23	W	65/67 (97%)	58 (89%)	7 (11%)	0	100	100
24	X	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
25	Y	57/59 (97%)	48 (84%)	9 (16%)	0	100	100
26	Z	46/48 (96%)	29 (63%)	17 (37%)	0	100	100
27	1	45/47 (96%)	37 (82%)	8 (18%)	0	100	100
28	2	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
29	3	62/64 (97%)	50 (81%)	12 (19%)	0	100	100
30	4	35/37 (95%)	21 (60%)	14 (40%)	0	100	100
32	b	224/226 (99%)	193 (86%)	31 (14%)	0	100	100
33	c	200/202 (99%)	161 (80%)	39 (20%)	0	100	100
34	d	196/198 (99%)	136 (69%)	59 (30%)	1 (0%)	25	59
35	e	154/156 (99%)	133 (86%)	21 (14%)	0	100	100
36	f	93/95 (98%)	75 (81%)	18 (19%)	0	100	100
37	g	149/152 (98%)	99 (66%)	50 (34%)	0	100	100
38	h	127/131 (97%)	98 (77%)	29 (23%)	0	100	100
39	i	125/127 (98%)	86 (69%)	39 (31%)	0	100	100
40	j	95/97 (98%)	59 (62%)	35 (37%)	1 (1%)	12	45
41	k	112/114 (98%)	81 (72%)	31 (28%)	0	100	100
42	l	133/135 (98%)	102 (77%)	29 (22%)	2 (2%)	8	39
43	m	100/104 (96%)	62 (62%)	38 (38%)	0	100	100
44	n	58/60 (97%)	36 (62%)	22 (38%)	0	100	100
45	o	86/88 (98%)	71 (83%)	15 (17%)	0	100	100
46	p	87/89 (98%)	68 (78%)	19 (22%)	0	100	100
47	q	78/80 (98%)	51 (65%)	27 (35%)	0	100	100
48	r	52/54 (96%)	43 (83%)	9 (17%)	0	100	100
49	s	78/80 (98%)	58 (74%)	20 (26%)	0	100	100
50	t	79/81 (98%)	59 (75%)	20 (25%)	0	100	100
51	u	50/52 (96%)	32 (64%)	18 (36%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	v	158/162 (98%)	117 (74%)	41 (26%)	0	100	100
All	All	5503/5608 (98%)	4369 (79%)	1129 (20%)	5 (0%)	50	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	l	131	GLY
34	d	110	ALA
40	j	7	ARG
17	Q	87	PRO
42	l	135	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	220/221 (100%)	177 (80%)	43 (20%)	1	7
4	D	173/173 (100%)	144 (83%)	29 (17%)	1	11
5	E	168/168 (100%)	126 (75%)	42 (25%)	0	3
6	F	141/154 (92%)	116 (82%)	25 (18%)	1	9
7	G	124/153 (81%)	101 (82%)	23 (18%)	1	8
8	H	122/123 (99%)	98 (80%)	24 (20%)	1	7
9	I	100/100 (100%)	79 (79%)	21 (21%)	1	6
10	J	109/112 (97%)	96 (88%)	13 (12%)	4	22
11	K	108/114 (95%)	93 (86%)	15 (14%)	3	17
12	L	96/101 (95%)	82 (85%)	14 (15%)	2	16
13	M	86/95 (90%)	61 (71%)	25 (29%)	0	2
14	N	93/100 (93%)	79 (85%)	14 (15%)	2	15
15	O	96/96 (100%)	83 (86%)	13 (14%)	3	18
16	P	84/86 (98%)	64 (76%)	20 (24%)	0	4

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	Q	88/90 (98%)	59 (67%)	29 (33%)	0	1
18	R	78/80 (98%)	62 (80%)	16 (20%)	1	6
19	S	81/88 (92%)	59 (73%)	22 (27%)	0	3
20	T	78/82 (95%)	60 (77%)	18 (23%)	0	4
21	U	63/64 (98%)	45 (71%)	18 (29%)	0	2
22	V	44/49 (90%)	33 (75%)	11 (25%)	0	3
23	W	58/60 (97%)	50 (86%)	8 (14%)	3	17
24	X	52/52 (100%)	44 (85%)	8 (15%)	2	14
25	Y	23/56 (41%)	22 (96%)	1 (4%)	25	54
26	Z	35/44 (80%)	24 (69%)	11 (31%)	0	2
27	1	44/45 (98%)	32 (73%)	12 (27%)	0	2
28	2	39/39 (100%)	35 (90%)	4 (10%)	6	27
29	3	55/55 (100%)	48 (87%)	7 (13%)	3	19
30	4	35/35 (100%)	27 (77%)	8 (23%)	0	4
32	b	196/196 (100%)	160 (82%)	36 (18%)	1	8
33	c	138/164 (84%)	110 (80%)	28 (20%)	1	6
34	d	147/174 (84%)	114 (78%)	33 (22%)	1	5
35	e	118/122 (97%)	97 (82%)	21 (18%)	1	9
36	f	80/83 (96%)	62 (78%)	18 (22%)	1	5
37	g	118/128 (92%)	90 (76%)	28 (24%)	0	4
38	h	111/112 (99%)	88 (79%)	23 (21%)	1	6
39	i	86/105 (82%)	68 (79%)	18 (21%)	1	6
40	j	81/87 (93%)	66 (82%)	15 (18%)	1	8
41	k	82/90 (91%)	60 (73%)	22 (27%)	0	3
42	l	111/117 (95%)	80 (72%)	31 (28%)	0	2
43	m	62/92 (67%)	51 (82%)	11 (18%)	1	9
44	n	48/52 (92%)	35 (73%)	13 (27%)	0	3
45	o	77/80 (96%)	59 (77%)	18 (23%)	0	4
46	p	73/75 (97%)	56 (77%)	17 (23%)	0	4
47	q	65/75 (87%)	49 (75%)	16 (25%)	0	4
48	r	48/49 (98%)	41 (85%)	7 (15%)	2	16

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	s	67/70 (96%)	50 (75%)	17 (25%)	0	3
50	t	61/67 (91%)	49 (80%)	12 (20%)	1	7
51	u	40/48 (83%)	29 (72%)	11 (28%)	0	2
52	v	147/147 (100%)	115 (78%)	32 (22%)	1	5
All	All	4449/4768 (93%)	3528 (79%)	921 (21%)	3	6

5 of 921 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	l	5	VAL
51	u	38	TYR
34	d	103	LEU
50	t	79	MET
45	o	43	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
41	k	119	ASN
52	v	49	ASN
43	m	31	GLN
46	p	62	ASN
10	J	81	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2896/2905 (99%)	1223 (42%)	55 (1%)
2	B	114/115 (99%)	44 (38%)	0
31	a	1537/1539 (99%)	918 (59%)	0
All	All	4547/4559 (99%)	2185 (48%)	55 (1%)

5 of 2185 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	A
1	A	6	A
1	A	15	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	28	A
1	A	34	U

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1108	C
1	A	1520	A
1	A	2816	C
1	A	2450	U
1	A	1190	A

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

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

5.5 Carbohydrates [i](#)

There are no 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	A	8
31	a	2
52	v	1
43	m	1
37	g	1

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
38	h	1
5	E	1

The worst 5 of 15 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	v	106:GLN	C	131:ILE	N	30.98
1	A	2207:U	O3'	2208:A	P	12.82
1	A	1939:A	O3'	1944:U	P	12.52
1	a	465:U	O3'	466:G	P	11.00
1	A	929:C	O3'	937:G	P	9.63

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10079. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.