



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Sep 10, 2017 – 05:14 AM EDT

PDB ID : 5O2R
EMDB ID: : EMD-3730
Title : Cryo-EM structure of the proline-rich antimicrobial peptide Api137 bound to the terminating ribosome
Authors : Graf, M.; Berninghausen, O.; Beckmann, R.; Wilson, D.N.
Deposited on : unknown
Resolution : 3.40 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

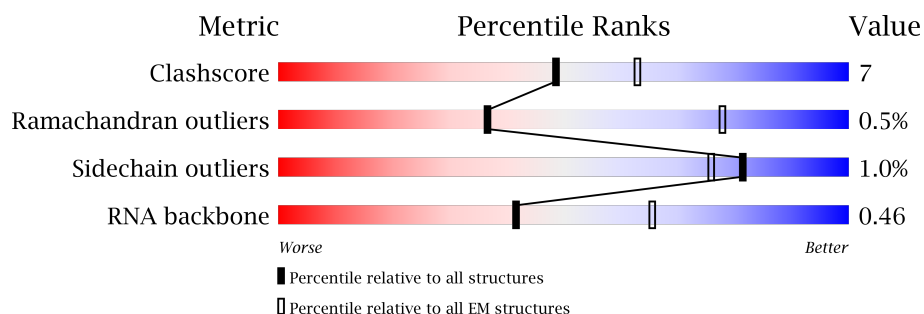
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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




























Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	2903	53% 37% 10% .
2	B	120	52% 32% 15% .
3	C	271	79% 21%
4	D	209	86% 14%
5	E	201	75% 24%
6	F	177	82% 17% .
7	G	176	79% 20% .
8	H	149	80% 19% .

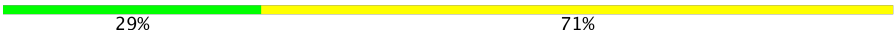

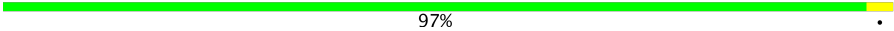
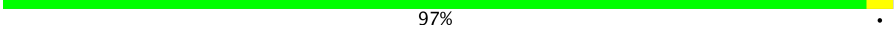
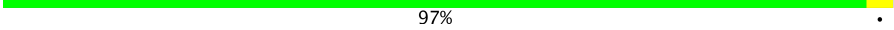
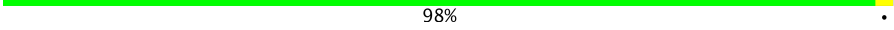
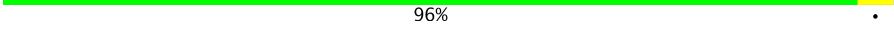
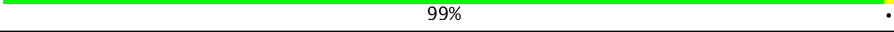
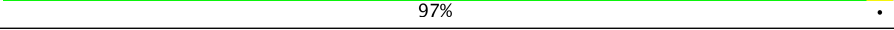
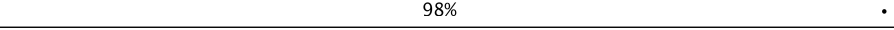
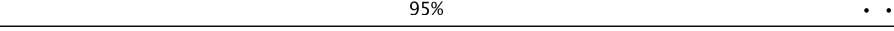
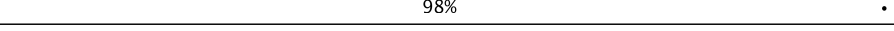
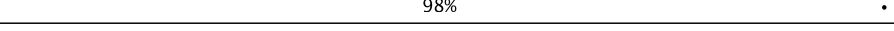
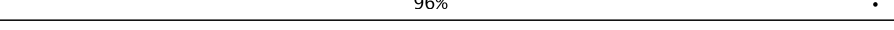
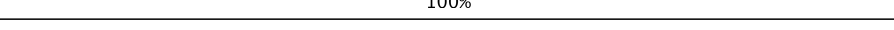
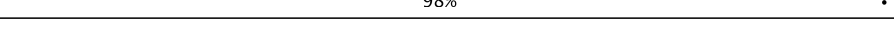
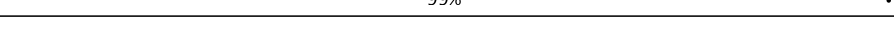
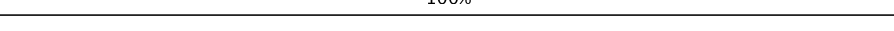
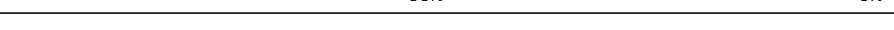
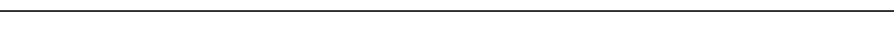

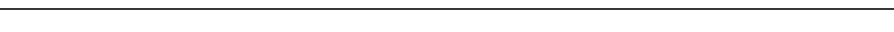
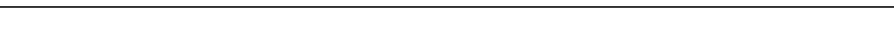


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain	
9	I	141		
10	J	142		
11	K	122		
12	L	143		.
13	M	136		.
14	N	120		
15	O	116		
16	P	114		
17	Q	117		.
18	R	103		.
19	S	110		
20	T	93		
21	U	102		
22	V	94		
23	W	75		.
24	X	77		
25	Y	63		
26	Z	58		
27	0	56		
28	1	50		
29	2	46		
30	3	64		.
31	4	38		
32	5	131		.
33	6	66		

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	7	7	 29% 71%
35	a	1539	 68% 29% .
36	b	218	 97% .
37	c	206	 97% .
38	d	205	 97% .
39	e	157	 98% .
40	f	100	 96% .
41	g	151	 99% .
42	h	129	 97% .
43	i	127	 98% .
44	j	98	 95% . .
45	k	116	 98% .
46	l	123	 98% .
47	m	114	 96% .
48	n	101	 100%
49	o	88	 98% .
50	p	82	 99% .
51	q	80	 100%
52	r	65	 95% 5%
53	s	79	 100%
54	t	85	 100%
55	u	65	 95% 5%
56	v	242	 95% .
57	x	77	 61% 35% .
58	z	14	 86% 14%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 147985 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2900	Total	C	N	O	P	0	0
			62262	27774	11460	20128	2900		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	747	C	U	conflict	GB 802133627
A	1847	G	A	conflict	GB 802133627

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	120	A	U	conflict	GB 1150448909

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 8 is a protein called 50S ribosomal protein L9.

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

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

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

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 16 is a protein called 50S ribosomal protein L19.

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

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	102	Total	C	N	O		0	0
			779	492	146	141			

- Molecule 22 is a protein called 50S ribosomal protein L25.

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

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 34 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	7	7	Total	C	N	O	P	0	0
			149	67	27	48	7		

- Molecule 35 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	1539	Total	C	N	O	P	0	0
			33016	14725	6052	10700	1539		

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 38 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 42 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 43 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 44 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 46 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 48 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP P0AG59

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 50 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 51 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	r	65	Total	C	N	O	0	0
			504	317	96	91		

- Molecule 53 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 55 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	u	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

- Molecule 56 is a protein called Peptide chain release factor RF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	v	242	Total	C	N	O	S	0	0
			1880	1151	359	362	8		

- Molecule 57 is a RNA chain called P-site Ile-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	77	Total	C	N	O	P	0	0
			1647	734	296	540	77		

- Molecule 58 is a protein called Apidaecin.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	z	14	Total	C	N	O	0	0
			120	80	25	15		

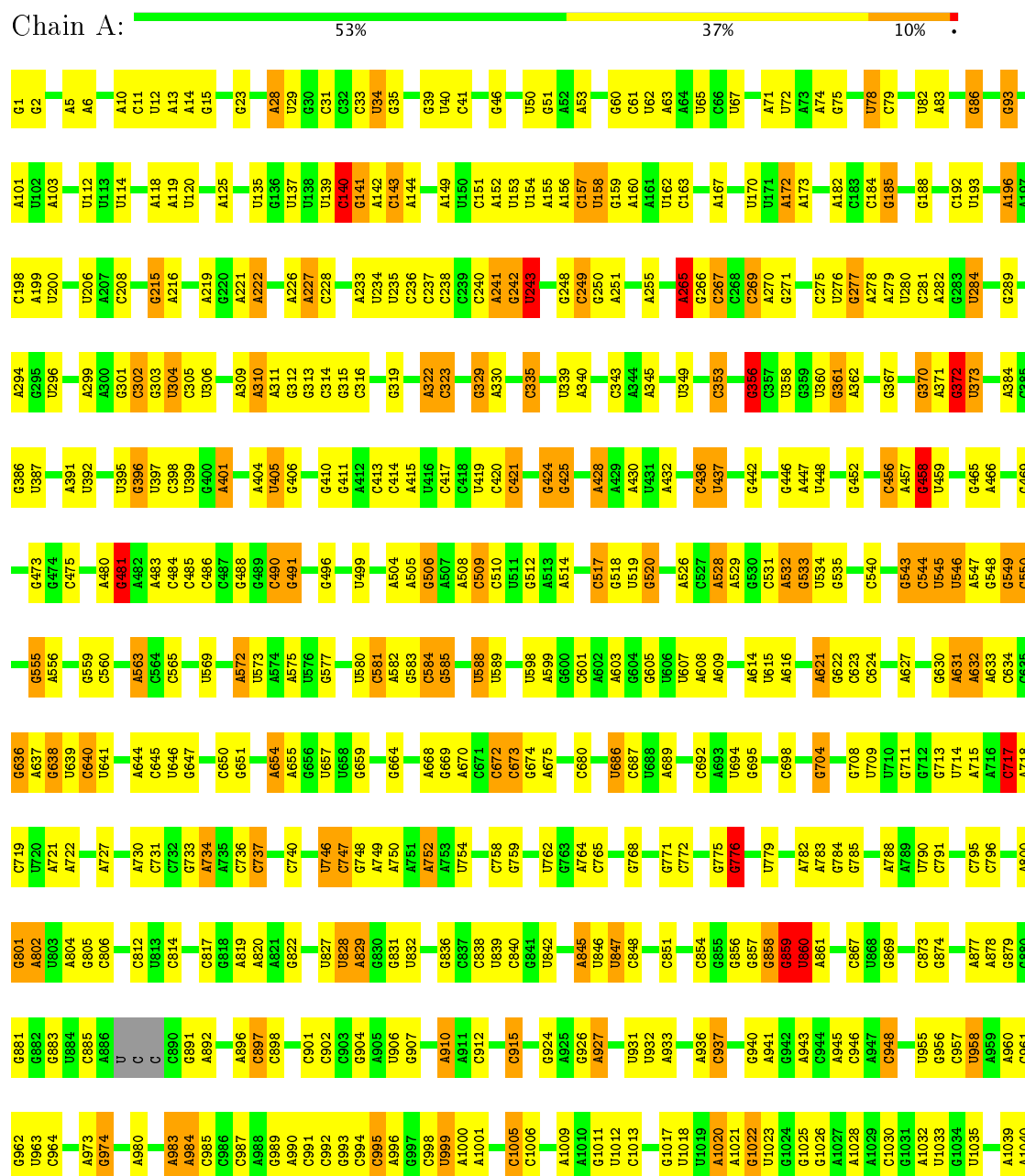
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	10	ARG	GLN	conflict	UNP Q8WSY8

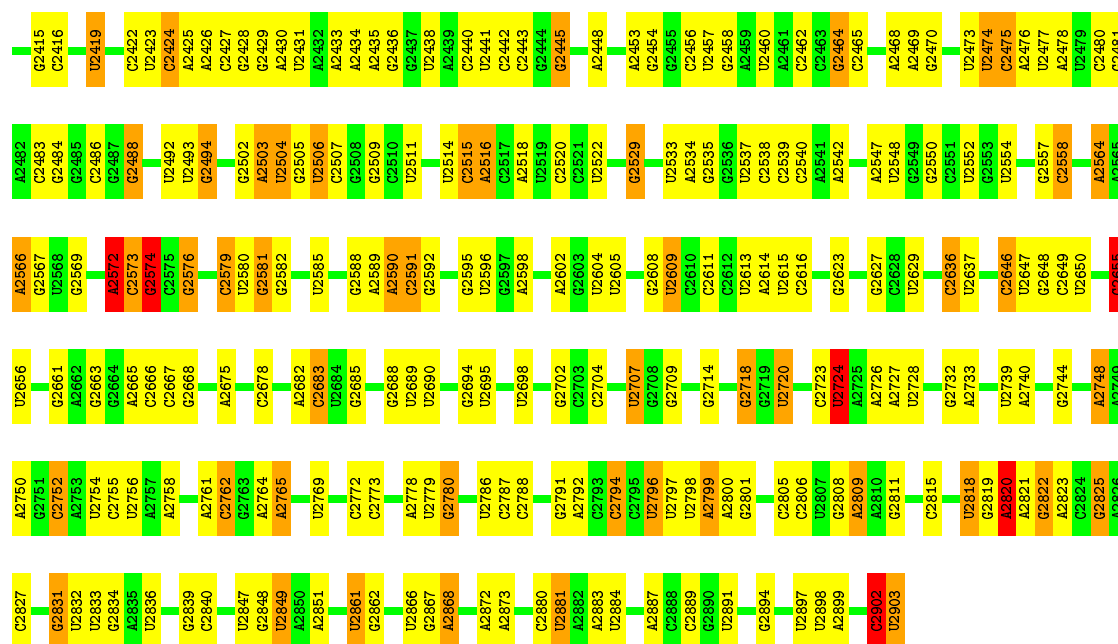
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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

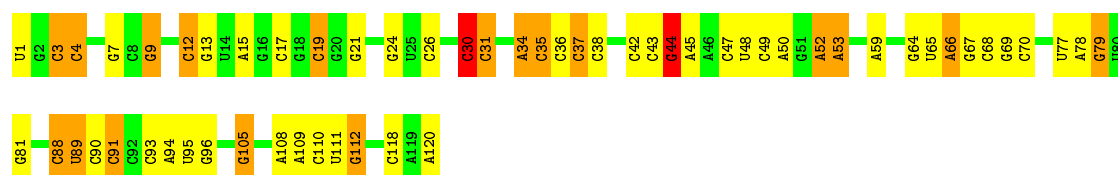


C2326	U2229	C2160	U2085	C2006	A1912	U1818	G1738	C1646	C1550	G1485	C1370	G1292	A1183	G1106	C1044
A2327	U2293	C2161	U2086	U2007	A1913	C1822	A1739	U1647	G1555	U1458	G1371	C1293	G1190	G1107	C1045
U2328	U2234	A2162	G2087	C1914	A1914	C1752	C1752	G1648	C1556	G1459	A1372	U1294	G1197	U1108	A1046
G2330	G2235	C2164	A2088	U1915	A1916	G1826	A1764	G1649	C1557	U1460	G1374	C1295	U1198	G1110	G1047
G2331	G2235	C2165	U2092	A2013	A1917	G1827	A1765	G1652	C1558	C1461	U1375	G1296	U1199	A1111	A1048
G2332	G2238	U2166	G2093	A2014	A1918	G1828	G1756	G1653	U1559	C1462			U1112	C1112	C1049
G2333	G2239	U2167	A2094	A2015	A1919	G1829	A1757	C1656	G1560		A1378	G1300	U1203	U1113	A1050
U2334	U2244	G2168	A2095	U2016	A1920	C1836	A1758	C1657	U1561	U1466	U1379	G1301	A1204	G1114	C1053
A2335	U2244	A2169	C2096	U2017	U1923	C1836	A1759	C1658	U1562	U1467	G1380	C1305	A1205	G1115	A1054
A2336	U2244	A2170	C2096	U2018	U1924	C1842	C1760	C1659	U1563			C1306	C1207	C1117	
G2337	C2248	A2171	U2099	A2020	C1924	G1843	C1761	G1663	C1564	G1475	A1382	G1311	C1208	U1119	A1057
C2342	U2249	U2172	G2100	C2021	C1924	C1843	A1762		C1565	G1482	A1385	U1312	C1211	U1120	U1056
U2343	G2250	A2173	A2101	C2023	A1927	G1847	C1763	A1668	A1566	G1483	C1386	U1313	G1212	G1121	G1059
U2344	G2251	C2174	C2102	G2024	A1928	C1848	C1764	A1669	G1567		A1387	C1314	G1212	U1061	U1061
G2345	C2254	C2175	C2103	C2025	A1929	C1849		C1670	G1568	U1498		C1315	G1215	G1122	G1062
A2346		A2176	C2104	U2026	G1930		U1769		A1569		A1392			C1123	G1063
G2347	C2258	C2177	U2105	U2027		A1853	G1776		C1574	A1490	A1393	U1316	G1216	G1124	C1064
C2350	U2259	C2178	U2106	G2029	C1934	A1854	G1770	G1674		A1491	U1394	U1317	C1221	A1127	U1065
C2351	C2260	C2179	A2107	A2030	G1935	U1855	C1771	C1675	U1578		U1395	U1318	U1222		U1066
C2354	C2264	A2184	U2108	A2031	A1936	G1856	A1772			A1494	U1396	C1319	G1223	U1130	A1067
G2357	U2265	G2185	G2032	A1937	A1937	G1857	A1773	A1679	U1584	A1495	U1397	C1320	U1224	G1131	G1068
A2358	A2267	G2186	U2111	A1938	A1938		C1774	G1680	C1585		C1398	A1321	G1225	U1132	A1069
G2359		U2188	G2112	U1940	U1940	G1860	U1775	G1681	A1586	A1504	C1399	A1322	A1226		A1070
G2360	C2267	U2189	U2113	C1941	C1941	U1865	G1776	G1682	G1587	A1505	U1400	C1323			
G2361	A2273	G2115	C2043	U1943	U1943	G1869	U1779	A1689	C1592	U1506	G1401	G1324	U1231	C1135	G1071
G2362	G2279	A2116	C2044	U1944	U1944	A1870	U1781	A1690	A1593	U1507	U1402	U1325	C1232	G1072	C1072
C2364		U2192	G2045	G1945	G1945	A1871	U1782	G1693	U1594	A1508		U1326	C1233	G1139	A1073
G2365	C2283	U2195	C2046	U1946	U1946	A1872	U1783	C1694	C1595	G1510	U1409	G1331	G1236	A1142	G1074
A2377	A2284		C2047	C1947	C1947	G1873	A1784	G1695			C1414	G1332	A1237	A1143	C1076
C2380	C2285	A2198	U2052	G1954	G1954	C1874	A1785	G1696	U1602	U1513	U1415	G1333			A1077
G2383	G2286	G2200	G2123	U1955	U1955	U1880	A1786	G1697	A1603	G1514	G1416	U1340	A1244	G1149	U1078
C2385	A2287	G2201	G2124	A1966	A1966	A1881	A1787	A1698	C1604	A1515		A1341	A1247	A1151	C1079
	U2291	U2292	G2125	U1967	C1967	U1882	C1788	G1699	G1605	G1516	A1419	A1342	G1248	G1152	A1081
G2391	U2293	U2293	G2126	G1964	G1964	U1883	A1791	G1707	C1606	G1517	G1421	G1343	U1249	C1153	U1082
U2393	C2300	C2206	U2130	C1965	C1965	U1884			C1607	G1521	G1422	U1344	G1250	G1154	U1083
G2394	G2304	G2207	U2132	A1970	U1971	U1886	U1796	G1714	A1608	U1522	G1423	C1345		A1155	A1084
C2395	U2305	C2208	U2133	A1971	G1972	U1887	G1797	G1715	C1611	U1523	G1424	C1348	A1253	G1157	A1085
		U2210	G2136	U1972	G1973	U1888	U1798	G1716	G1612	G1524	A1427	C1349	U1254	G1162	A1086
U2402	G2308	A2211	U2137	C2066	C2066	G1889	U1799	G1720	G1613	G1529	C1428	C1350	G1256		G1087
C2403	U2310	G2212	G2138	G2067	G1974	C1892	G1799	G1721	G1619	U1530	U1432	U1352	C1257	G1171	A1088
G2405	A2314	C2214	U2139	C2068	C1978	U1893	A1801	G1724	G1622	C1531	G1433	U1356	A1264	G1172	A1089
A2407	U2320	G2224	G2140	U2069	A1978	C1894	A1802	U1725	U1624	U1534	A1434	G1355	A1265	G1173	A1090
G2409	U2321	A2225	U2148	G2078	C1994	U1895	C1804	G1726	U1624	U1535	G1437	G1356	G1266	U1174	C1092
A2411	U2324	C2226	G2157	U2079	C1997	G1897	G1728	C1727	G1627	G1537	U1438	G1360	U1267	A1175	G1093
A2412	G2325	G2228	G2159	A1998	A1998	U1900	U1729	G1730	G1631	U1541	U1443	G1361	A1269	U1176	U1094
						A1901	A1808	G1731	G1631	U1542	U1444	C1363	C1270	G1177	A1095
						C1902	A1809	G1732	A1634	U1545	G1445	G1364	C1271	G1178	A1096
						G1906	A1810	G1733	C1638	G1546	C1446	A1365	A1272	G1179	A1097
						G1907	U1812	G1734	C1644	C1547	C1447	A1366	A1273	U1180	A1098
						U1911	U1816	G1736	C1644	C1548	G1448	A1367	A1274	U1181	U1101
							C1816	U1736	C1644	C1548	G1448	A1368	A1275	G1182	C1102
							G1817	G1737	G1645	A1549	C1454	G1369	G1288	U1183	C1103
														U1188	A1105



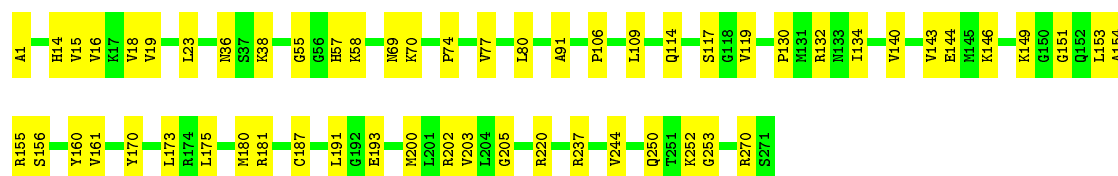
- Molecule 2: 5S ribosomal RNA

Chain B: 52% 32% 15%



- Molecule 3: 50S ribosomal protein L2

Chain C: 79% 21%



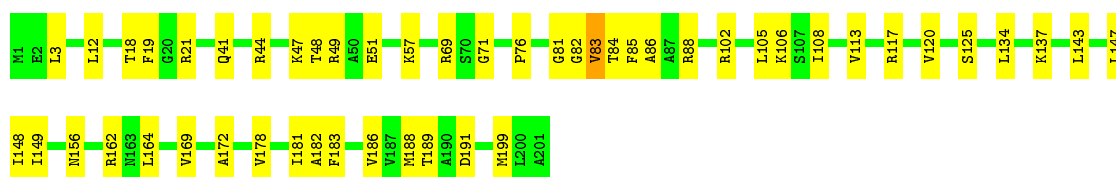
- Molecule 4: 50S ribosomal protein L3

Chain D: 86% 14%



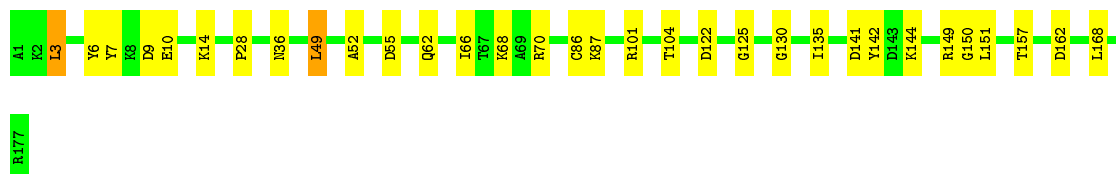
- Molecule 5: 50S ribosomal protein L4

Chain E: 75% 24%



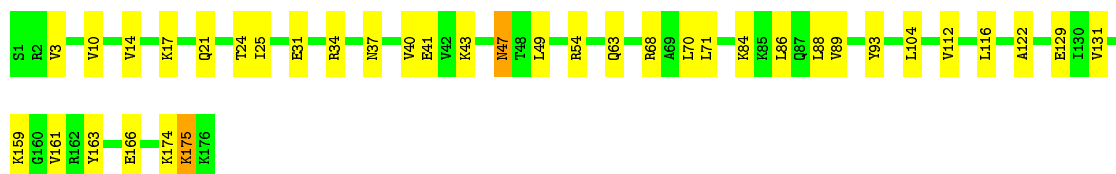
- Molecule 6: 50S ribosomal protein L5

Chain F: 82% 17%



- Molecule 7: 50S ribosomal protein L6

Chain G: 79% 20%



- Molecule 8: 50S ribosomal protein L9

Chain H: 80% 19%



- Molecule 9: 50S ribosomal protein L11

Chain I: 80% 20%



- Molecule 10: 50S ribosomal protein L13

Chain J: 82% 18%



- Molecule 11: 50S ribosomal protein L14

Chain K: 81% 19%



- Molecule 12: 50S ribosomal protein L15

Chain L: 84% 15%



- Molecule 13: 50S ribosomal protein L16

Chain M: 80% 19%



- Molecule 14: 50S ribosomal protein L17

Chain N: 79% 21%



- Molecule 15: 50S ribosomal protein L18

Chain O: 79% 21%



- Molecule 16: 50S ribosomal protein L19

Chain P: 81% 19%



- Molecule 17: 50S ribosomal protein L20

Chain Q: 84% 15%

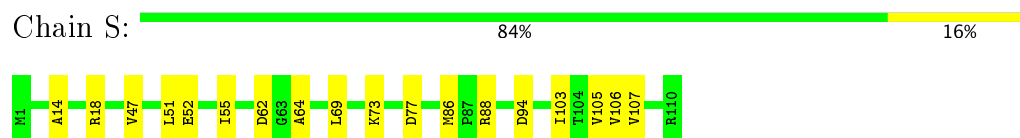


- Molecule 18: 50S ribosomal protein L21

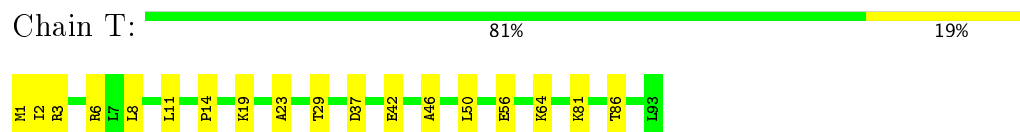
Chain R: 78% 21%



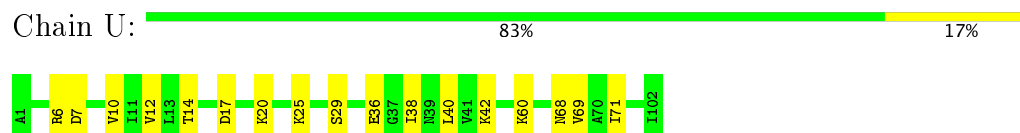
- Molecule 19: 50S ribosomal protein L22



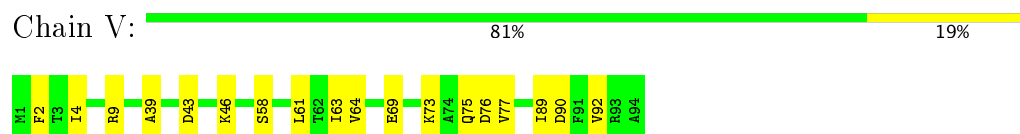
- Molecule 20: 50S ribosomal protein L23



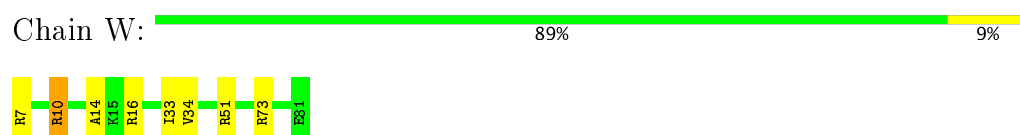
- Molecule 21: 50S ribosomal protein L24



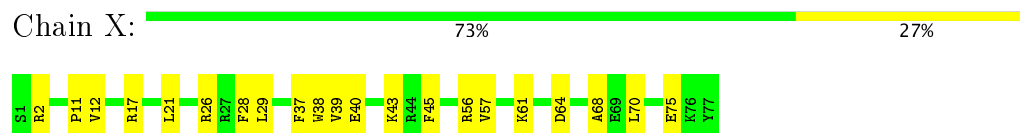
- Molecule 22: 50S ribosomal protein L25



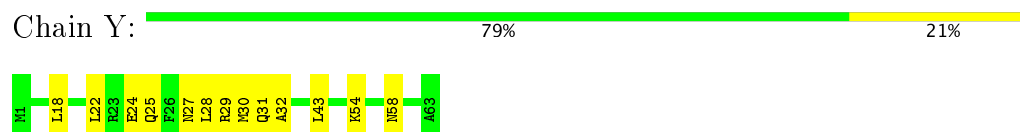
- Molecule 23: 50S ribosomal protein L27




- Molecule 24: 50S ribosomal protein L28



- Molecule 25: 50S ribosomal protein L29




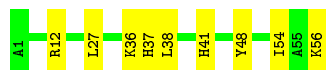
- Molecule 26: 50S ribosomal protein L30

Chain Z:  81% 19%




- Molecule 27: 50S ribosomal protein L32

Chain 0:  84% 16%



- Molecule 28: 50S ribosomal protein L33

Chain 1:  84% 16%



- Molecule 29: 50S ribosomal protein L34

Chain 2:  74% 26%




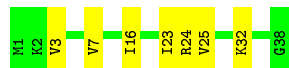
- Molecule 30: 50S ribosomal protein L35

Chain 3:  72% 27% .



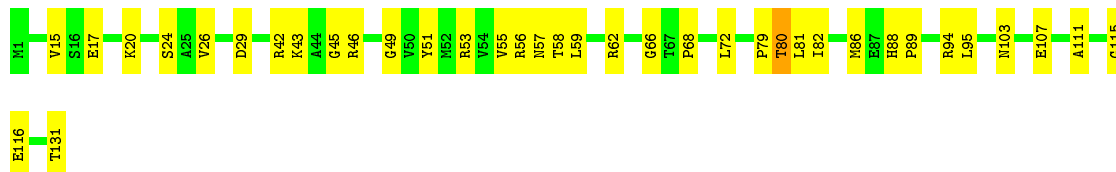
- Molecule 31: 50S ribosomal protein L36

Chain 4:  82% 18%




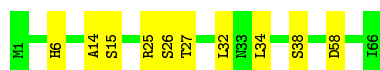
- Molecule 32: 50S ribosomal protein L10

Chain 5:  72% 27% .



- Molecule 33: 50S ribosomal protein L31

Chain 6:  85% 15%



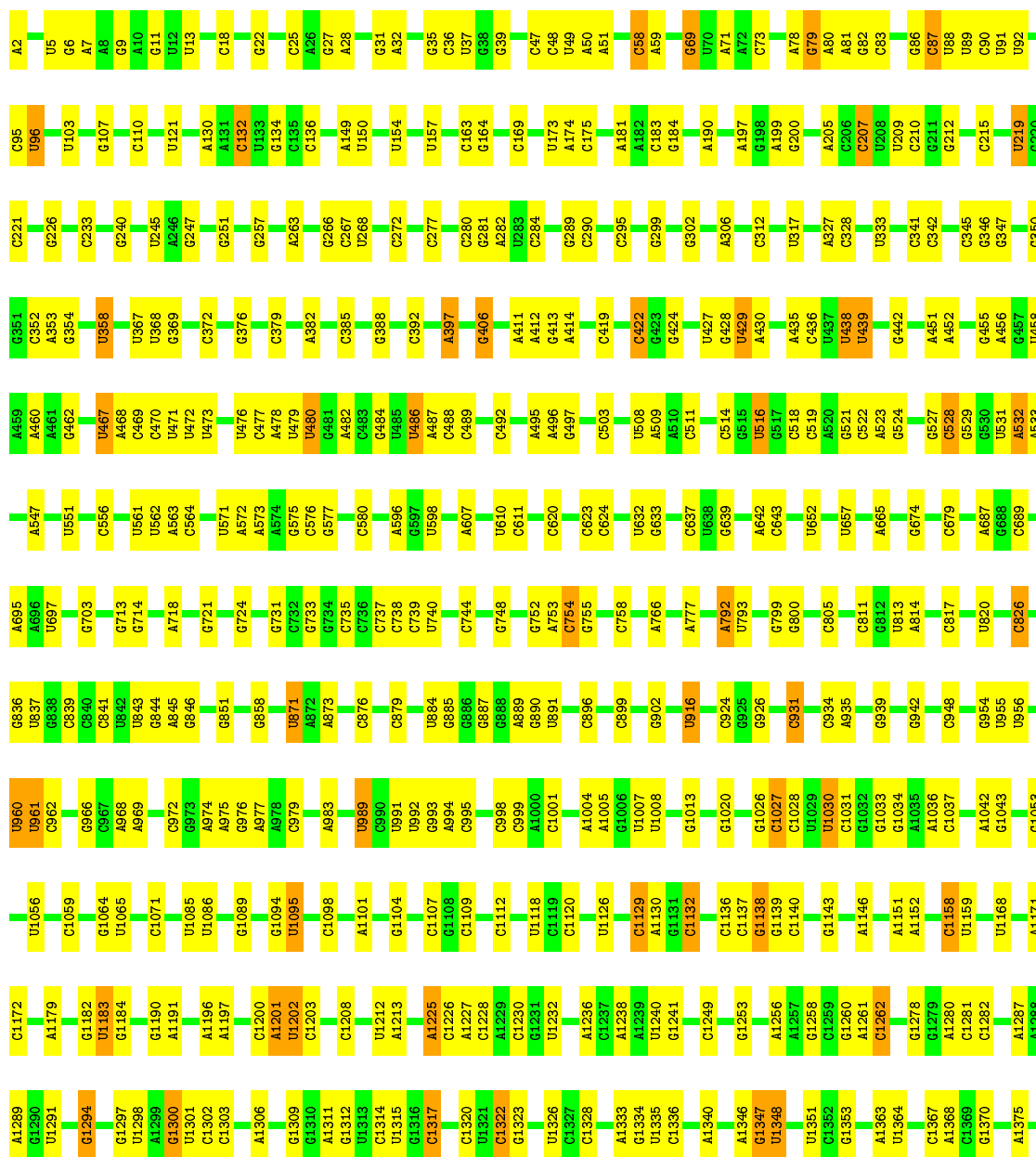
- Molecule 34: mRNA

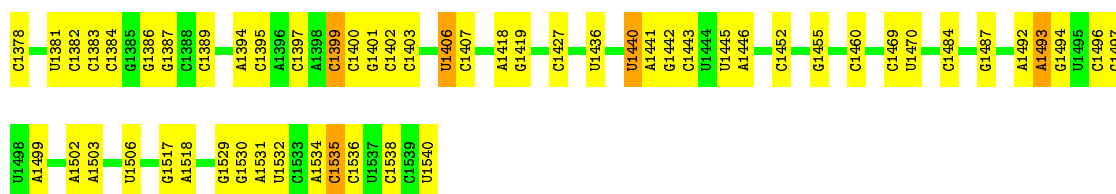
Chain 7:  29% 71%



- Molecule 35: 16S ribosomal RNA

Chain a:  68% 29% .





- Molecule 36: 30S ribosomal protein S2

Chain b:  97%



- Molecule 37: 30S ribosomal protein S3

Chain c:  97%



- Molecule 38: 30S ribosomal protein S4

Chain d:  97%



- Molecule 39: 30S ribosomal protein S5

Chain e:  98%



- Molecule 40: 30S ribosomal protein S6

Chain f:  96%



- Molecule 41: 30S ribosomal protein S7

Chain g:  99%



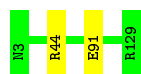
- Molecule 42: 30S ribosomal protein S8

Chain h:  97% .



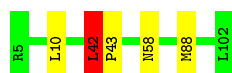
- Molecule 43: 30S ribosomal protein S9

Chain i:  98% .



- Molecule 44: 30S ribosomal protein S10

Chain j:  95% . .



- Molecule 45: 30S ribosomal protein S11

Chain k:  98% .



- Molecule 46: 30S ribosomal protein S12

Chain l:  98% .



- Molecule 47: 30S ribosomal protein S13

Chain m:  96% .



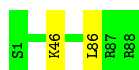
- Molecule 48: 30S ribosomal protein S14

Chain n:  100%

There are no outlier residues recorded for this chain.

- Molecule 49: 30S ribosomal protein S15

Chain o:  98% .



- Molecule 50: 30S ribosomal protein S16

Chain p: 99%



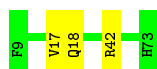
- Molecule 51: 30S ribosomal protein S17

Chain q: 100%

There are no outlier residues recorded for this chain.

- Molecule 52: 30S ribosomal protein S18

Chain r: 95% 5%



- Molecule 53: 30S ribosomal protein S19

Chain s: 100%

There are no outlier residues recorded for this chain.

- Molecule 54: 30S ribosomal protein S20

Chain t: 100%

There are no outlier residues recorded for this chain.

- Molecule 55: 30S ribosomal protein S21

Chain u: 95% 5%



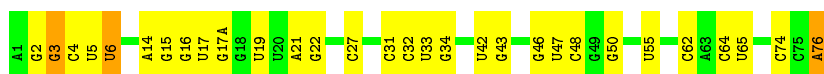
- Molecule 56: Peptide chain release factor RF1

Chain v: 95%




- Molecule 57: P-site Ile-tRNA

Chain x: 61% 35%



- Molecule 58: Apidaecin

Chain z:  86% 14%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	36826	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON II (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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	1.25	33/69734 (0.0%)	1.36	809/108788 (0.7%)
10	J	0.57	0/1152	0.63	0/1551
11	K	0.59	0/947	0.76	0/1268
12	L	0.62	1/1054 (0.1%)	0.79	0/1403
13	M	0.62	0/1093	0.71	1/1460 (0.1%)
14	N	0.58	0/973	0.74	0/1301
15	O	0.56	0/902	0.67	0/1209
16	P	0.60	0/929	0.68	1/1242 (0.1%)
17	Q	0.72	0/960	0.66	0/1278
18	R	0.58	0/829	0.72	0/1107
19	S	0.58	0/864	0.70	0/1156
2	B	1.04	1/2876 (0.0%)	1.47	56/4483 (1.2%)
20	T	0.53	0/744	0.65	0/994
21	U	0.47	0/787	0.66	0/1051
22	V	0.55	0/766	0.65	0/1025
23	W	0.65	0/582	0.63	0/769
24	X	0.53	0/635	0.65	0/848
25	Y	0.41	0/510	0.66	0/677
26	Z	0.53	0/453	0.65	0/605
27	0	0.57	0/450	0.65	0/599
28	1	0.55	0/416	0.66	0/554
29	2	0.62	0/380	0.74	0/498
3	C	0.62	0/2121	0.69	0/2852
30	3	0.63	0/513	0.78	1/676 (0.1%)
31	4	0.65	0/303	0.59	0/397
32	5	0.39	0/1001	0.81	1/1350 (0.1%)
33	6	0.40	0/531	0.63	0/709
34	7	1.17	0/166	1.09	0/256
35	a	1.17	5/36967 (0.0%)	1.33	366/57666 (0.6%)
36	b	0.44	0/1735	0.71	0/2338
37	c	0.54	0/1651	0.79	2/2225 (0.1%)
38	d	0.51	0/1665	0.75	3/2227 (0.1%)
39	e	0.59	0/1154	0.76	1/1554 (0.1%)
4	D	0.63	0/1586	0.69	1/2134 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	f	0.48	0/835	0.81	2/1128 (0.2%)
41	g	0.46	0/1195	0.68	0/1602
42	h	0.54	0/989	0.78	2/1326 (0.2%)
43	i	0.53	0/1034	0.70	0/1375
44	j	0.50	0/796	0.93	3/1077 (0.3%)
45	k	0.51	0/885	0.69	0/1195
46	l	0.63	0/969	0.77	2/1300 (0.2%)
47	m	0.49	0/892	0.74	0/1193
48	n	0.52	0/811	0.63	0/1081
49	o	0.48	0/722	0.68	1/964 (0.1%)
5	E	0.61	1/1571 (0.1%)	0.68	1/2113 (0.0%)
50	p	0.54	0/659	0.71	0/884
51	q	0.57	0/657	0.73	0/881
52	r	0.53	0/511	0.69	0/689
53	s	0.52	0/652	0.69	0/877
54	t	0.48	0/671	0.66	0/888
55	u	0.43	0/500	0.82	0/668
56	v	0.53	0/1910	0.75	2/2573 (0.1%)
57	x	1.03	0/1841	1.38	26/2869 (0.9%)
58	z	0.40	0/127	0.81	0/175
6	F	0.51	0/1434	0.74	3/1926 (0.2%)
7	G	0.47	0/1343	0.65	0/1816
8	H	0.36	0/1122	0.60	1/1515 (0.1%)
9	I	0.35	0/1046	0.67	0/1410
All	All	1.06	41/160601 (0.0%)	1.21	1285/239775 (0.5%)

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
56	v	0	1

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	G	OP3-P	-11.16	1.47	1.61
35	a	2	A	OP3-P	-10.97	1.48	1.61
2	B	1	U	OP3-P	-10.32	1.48	1.61
1	A	1142	A	N9-C4	-7.34	1.33	1.37
5	E	85	PHE	CA-CB	-7.07	1.38	1.53

The worst 5 of 1285 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	j	42	LEU	C-N-CD	-15.77	85.92	120.60
37	c	96	VAL	C-N-CD	-15.69	86.08	120.60
35	a	516	U	N3-C2-O2	-13.84	112.52	122.20
1	A	1917	U	N3-C2-O2	-13.13	113.01	122.20
1	A	2072	C	C6-N1-C2	-13.04	115.08	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
56	v	303	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	A	62262	0	31312	463	0
2	B	2572	0	1302	16	0
3	C	2082	0	2157	40	0
4	D	1565	0	1616	22	0
5	E	1552	0	1619	37	0
6	F	1410	0	1447	23	0
7	G	1323	0	1374	22	0
8	H	1111	0	1148	19	0
9	I	1032	0	1088	14	0
10	J	1129	0	1162	21	0
11	K	938	0	1012	17	0
12	L	1045	0	1116	17	0
13	M	1074	0	1157	19	0
14	N	960	0	1000	15	0
15	O	892	0	923	17	0
16	P	917	0	965	20	0
17	Q	947	0	1022	17	0
18	R	816	0	839	20	0
19	S	857	0	922	12	0
20	T	738	0	807	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	U	779	0	834	13	0
22	V	753	0	780	10	0
23	W	575	0	592	5	0
24	X	625	0	655	11	0
25	Y	509	0	543	14	0
26	Z	449	0	491	7	0
27	0	444	0	461	6	0
28	1	409	0	440	5	0
29	2	377	0	418	9	0
30	3	504	0	574	13	0
31	4	302	0	343	5	0
32	5	988	0	1025	29	0
33	6	522	0	522	8	0
34	7	149	0	76	3	0
35	a	33016	0	16617	0	0
36	b	1704	0	1732	0	0
37	c	1624	0	1699	0	0
38	d	1643	0	1710	0	0
39	e	1141	0	1170	0	0
40	f	817	0	808	0	0
41	g	1181	0	1240	0	0
42	h	979	0	1034	0	0
43	i	1022	0	1070	0	0
44	j	786	0	828	0	0
45	k	869	0	878	0	0
46	l	955	0	1018	0	0
47	m	883	0	944	0	0
48	n	799	0	841	0	0
49	o	714	0	737	0	0
50	p	649	0	666	0	0
51	q	648	0	691	0	0
52	r	504	0	501	0	0
53	s	637	0	665	0	0
54	t	665	0	714	0	0
55	u	495	0	486	0	0
56	v	1880	0	1841	0	0
57	x	1647	0	831	0	0
58	z	120	0	128	0	0
All	All	147985	0	100591	828	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 828 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:A:2312:U:O2	6:F:36:ASN:ND2	1.78	1.16
1:A:280:U:H2'	1:A:281:C:H6	1.11	1.14
1:A:1432:G:O5'	16:P:105:LYS:HG2	54.54	1.07
1:A:306:U:H3	1:A:310:A:N6	1.57	1.02
1:A:280:U:H2'	1:A:281:C:C6	1.96	1.01

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	269/271 (99%)	242 (90%)	27 (10%)	0	100	100
4	D	207/209 (99%)	182 (88%)	25 (12%)	0	100	100
5	E	199/201 (99%)	182 (92%)	16 (8%)	1 (0%)	32	71
6	F	175/177 (99%)	159 (91%)	16 (9%)	0	100	100
7	G	174/176 (99%)	159 (91%)	14 (8%)	1 (1%)	28	68
8	H	147/149 (99%)	127 (86%)	20 (14%)	0	100	100
9	I	139/141 (99%)	114 (82%)	25 (18%)	0	100	100
10	J	140/142 (99%)	129 (92%)	11 (8%)	0	100	100
11	K	120/122 (98%)	103 (86%)	16 (13%)	1 (1%)	22	62
12	L	141/143 (99%)	117 (83%)	23 (16%)	1 (1%)	25	65
13	M	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	12	49
14	N	118/120 (98%)	105 (89%)	13 (11%)	0	100	100
15	O	114/116 (98%)	104 (91%)	10 (9%)	0	100	100
16	P	112/114 (98%)	102 (91%)	10 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
18	R	101/103 (98%)	87 (86%)	13 (13%)	1 (1%)	18	59
19	S	108/110 (98%)	101 (94%)	6 (6%)	1 (1%)	20	61
20	T	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
21	U	100/102 (98%)	84 (84%)	16 (16%)	0	100	100
22	V	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
23	W	73/75 (97%)	66 (90%)	7 (10%)	0	100	100
24	X	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
25	Y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
26	Z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
27	0	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
28	1	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
29	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
30	3	62/64 (97%)	54 (87%)	8 (13%)	0	100	100
31	4	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
32	5	129/131 (98%)	101 (78%)	27 (21%)	1 (1%)	22	62
33	6	64/66 (97%)	53 (83%)	11 (17%)	0	100	100
36	b	216/218 (99%)	177 (82%)	37 (17%)	2 (1%)	20	61
37	c	204/206 (99%)	183 (90%)	18 (9%)	3 (2%)	12	49
38	d	203/205 (99%)	180 (89%)	23 (11%)	0	100	100
39	e	155/157 (99%)	136 (88%)	19 (12%)	0	100	100
40	f	98/100 (98%)	82 (84%)	15 (15%)	1 (1%)	18	59
41	g	149/151 (99%)	134 (90%)	14 (9%)	1 (1%)	25	65
42	h	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	22	62
43	i	125/127 (98%)	105 (84%)	19 (15%)	1 (1%)	22	62
44	j	96/98 (98%)	79 (82%)	15 (16%)	2 (2%)	8	43
45	k	114/116 (98%)	91 (80%)	23 (20%)	0	100	100
46	l	121/123 (98%)	94 (78%)	26 (22%)	1 (1%)	22	62
47	m	112/114 (98%)	98 (88%)	13 (12%)	1 (1%)	20	61
48	n	99/101 (98%)	88 (89%)	11 (11%)	0	100	100
49	o	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	15	54

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	p	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
51	q	78/80 (98%)	62 (80%)	16 (20%)	0	100	100
52	r	63/65 (97%)	50 (79%)	11 (18%)	2 (3%)	5	34
53	s	77/79 (98%)	69 (90%)	8 (10%)	0	100	100
54	t	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
55	u	63/65 (97%)	43 (68%)	17 (27%)	3 (5%)	2	23
56	v	240/242 (99%)	213 (89%)	24 (10%)	3 (1%)	14	53
58	z	12/14 (86%)	10 (83%)	1 (8%)	1 (8%)	1	10
All	All	6099/6205 (98%)	5361 (88%)	706 (12%)	32 (0%)	37	71

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	G	175	LYS
18	R	54	VAL
32	5	80	THR
36	b	19	THR
37	c	96	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	216/216 (100%)	214 (99%)	2 (1%)	82	92
4	D	164/164 (100%)	162 (99%)	2 (1%)	75	89
5	E	165/165 (100%)	163 (99%)	2 (1%)	75	89
6	F	148/148 (100%)	148 (100%)	0	100	100
7	G	137/137 (100%)	135 (98%)	2 (2%)	70	87
8	H	114/114 (100%)	114 (100%)	0	100	100
9	I	109/109 (100%)	107 (98%)	2 (2%)	64	85
10	J	116/116 (100%)	116 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	K	103/103 (100%)	103 (100%)	0	100	100
12	L	102/102 (100%)	101 (99%)	1 (1%)	80	91
13	M	109/109 (100%)	108 (99%)	1 (1%)	82	92
14	N	100/100 (100%)	99 (99%)	1 (1%)	80	91
15	O	86/86 (100%)	86 (100%)	0	100	100
16	P	99/99 (100%)	98 (99%)	1 (1%)	80	91
17	Q	89/89 (100%)	88 (99%)	1 (1%)	78	90
18	R	84/84 (100%)	83 (99%)	1 (1%)	75	89
19	S	93/93 (100%)	93 (100%)	0	100	100
20	T	80/80 (100%)	80 (100%)	0	100	100
21	U	83/83 (100%)	83 (100%)	0	100	100
22	V	78/78 (100%)	78 (100%)	0	100	100
23	W	57/57 (100%)	56 (98%)	1 (2%)	64	85
24	X	67/67 (100%)	66 (98%)	1 (2%)	70	87
25	Y	55/55 (100%)	55 (100%)	0	100	100
26	Z	48/48 (100%)	48 (100%)	0	100	100
27	0	47/47 (100%)	47 (100%)	0	100	100
28	1	45/45 (100%)	45 (100%)	0	100	100
29	2	38/38 (100%)	38 (100%)	0	100	100
30	3	51/51 (100%)	51 (100%)	0	100	100
31	4	34/34 (100%)	34 (100%)	0	100	100
32	5	100/100 (100%)	100 (100%)	0	100	100
33	6	59/59 (100%)	59 (100%)	0	100	100
36	b	180/180 (100%)	176 (98%)	4 (2%)	57	83
37	c	170/170 (100%)	167 (98%)	3 (2%)	64	85
38	d	172/172 (100%)	167 (97%)	5 (3%)	48	78
39	e	114/119 (96%)	112 (98%)	2 (2%)	64	85
40	f	87/87 (100%)	86 (99%)	1 (1%)	78	90
41	g	124/124 (100%)	124 (100%)	0	100	100
42	h	104/104 (100%)	103 (99%)	1 (1%)	80	91
43	i	105/105 (100%)	104 (99%)	1 (1%)	80	91

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	j	86/86 (100%)	84 (98%)	2 (2%)	56	82
45	k	89/89 (100%)	87 (98%)	2 (2%)	57	83
46	l	103/103 (100%)	103 (100%)	0	100	100
47	m	92/92 (100%)	89 (97%)	3 (3%)	43	76
48	n	79/83 (95%)	79 (100%)	0	100	100
49	o	76/76 (100%)	76 (100%)	0	100	100
50	p	65/65 (100%)	64 (98%)	1 (2%)	70	87
51	q	74/74 (100%)	74 (100%)	0	100	100
52	r	48/56 (86%)	47 (98%)	1 (2%)	59	83
53	s	70/70 (100%)	70 (100%)	0	100	100
54	t	65/65 (100%)	65 (100%)	0	100	100
55	u	44/55 (80%)	44 (100%)	0	100	100
56	v	195/195 (100%)	189 (97%)	6 (3%)	45	77
58	z	14/14 (100%)	13 (93%)	1 (7%)	17	54
All	All	5032/5060 (99%)	4981 (99%)	51 (1%)	81	91

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	c	64	ARG
38	d	183	ARG
56	v	322	ILE
38	d	7	LYS
38	d	190	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
30	3	42	HIS
36	b	121	GLN
51	q	30	HIS
31	4	35	GLN
36	b	18	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2898/2903 (99%)	681 (23%)	27 (0%)
2	B	119/120 (99%)	30 (25%)	5 (4%)
34	7	6/7 (85%)	4 (66%)	0
35	a	1538/1539 (99%)	345 (22%)	0
57	x	76/77 (98%)	21 (27%)	0
All	All	4637/4646 (99%)	1081 (23%)	32 (0%)

5 of 1081 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	G
1	A	10	A
1	A	12	U
1	A	14	A
1	A	23	G

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1182	G
1	A	1378	A
2	B	52	A
1	A	1300	G
1	A	1399	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	L	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L	60:ARG	C	61:LEU	N	1.18