



## wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Feb 13, 2019 – 10:57 AM EST

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 : 2017-05-22  
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](mailto: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.

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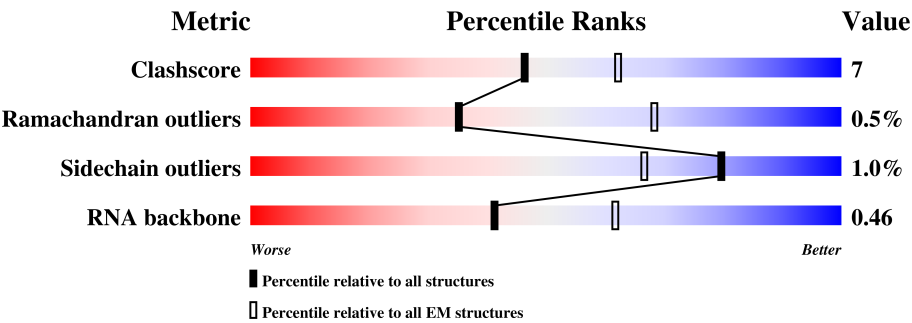
MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20031633

# 1 Overall quality at a glance i

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	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

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  $\geq 3$ , 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	
2	B	120	
3	C	271	
4	D	209	
5	E	201	
6	F	177	
7	G	176	
8	H	149	

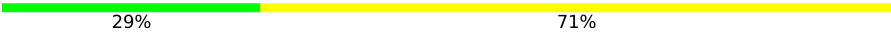

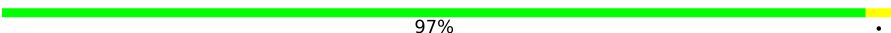
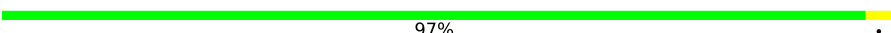
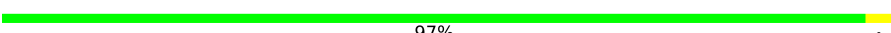
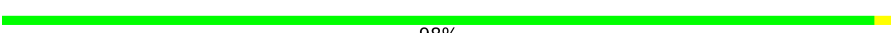
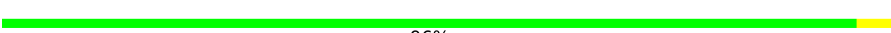






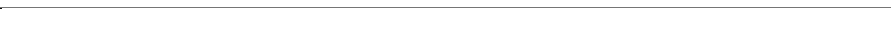

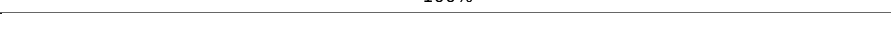
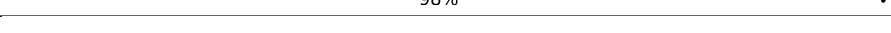
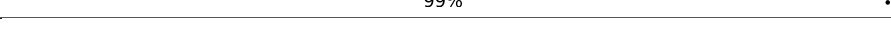
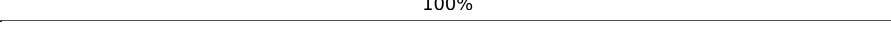
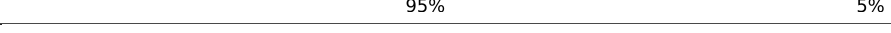
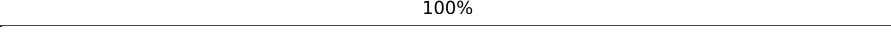
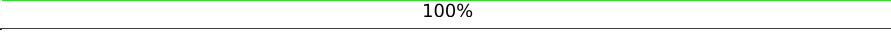
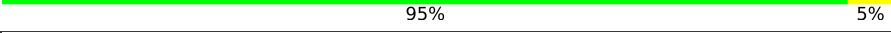
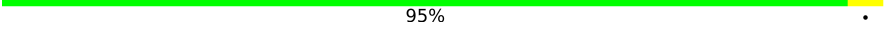

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Mol	Chain	Length	Quality of chain	
9	I	141	80%	20%
10	J	142	82%	18%
11	K	122	81%	19%
12	L	143	84%	15%
13	M	136	80%	19%
14	N	120	79%	21%
15	O	116	79%	21%
16	P	114	81%	19%
17	Q	117	84%	15%
18	R	103	78%	21%
19	S	110	84%	16%
20	T	93	81%	19%
21	U	102	83%	17%
22	V	94	81%	19%
23	W	75	89%	9%
24	X	77	73%	27%
25	Y	63	79%	21%
26	Z	58	81%	19%
27	0	56	84%	16%
28	1	50	84%	16%
29	2	46	74%	26%
30	3	64	72%	27%
31	4	38	82%	18%
32	5	131	72%	27%
33	6	66	85%	15%

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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		

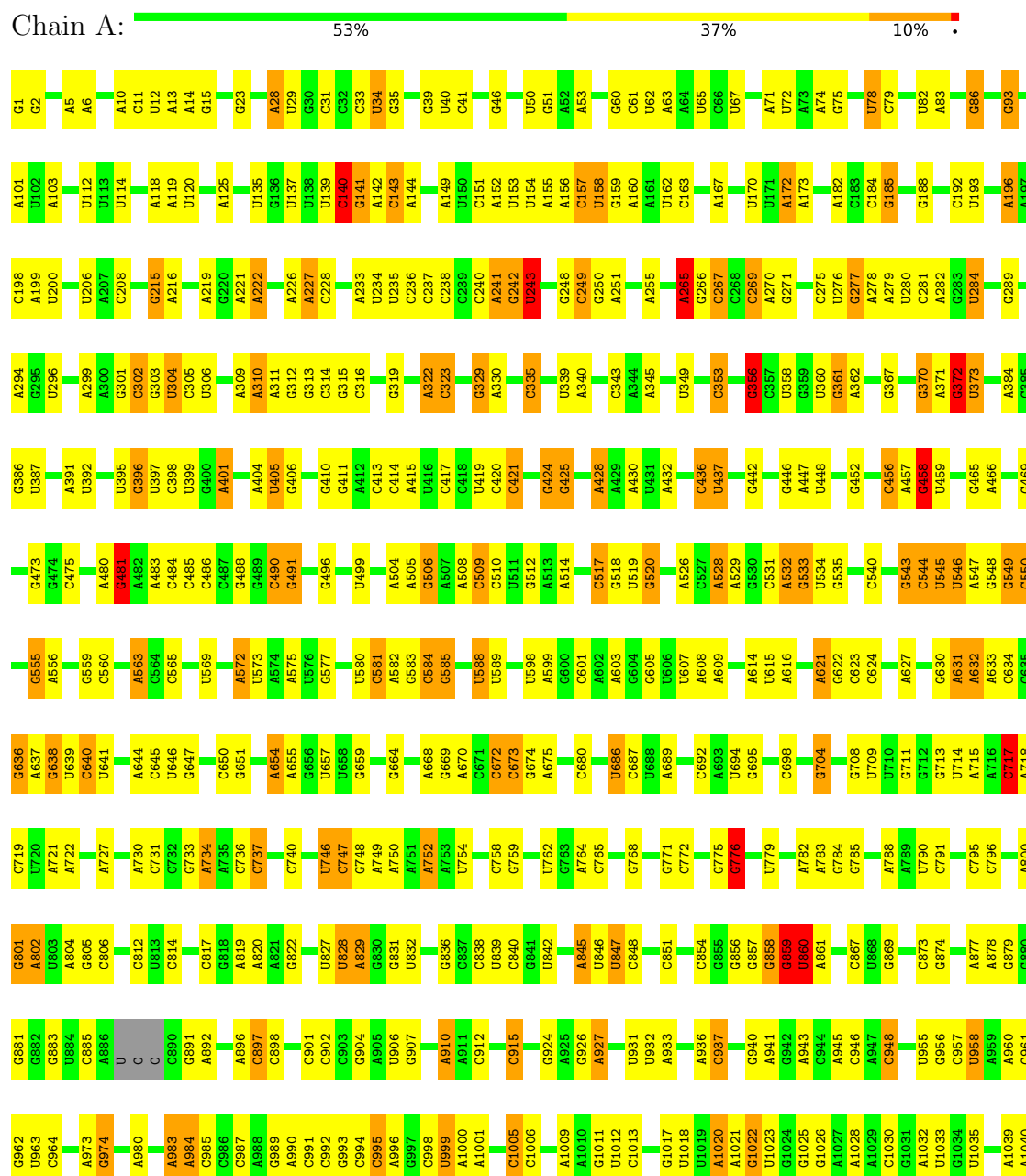
There is a discrepancy between the modelled and reference sequences:

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

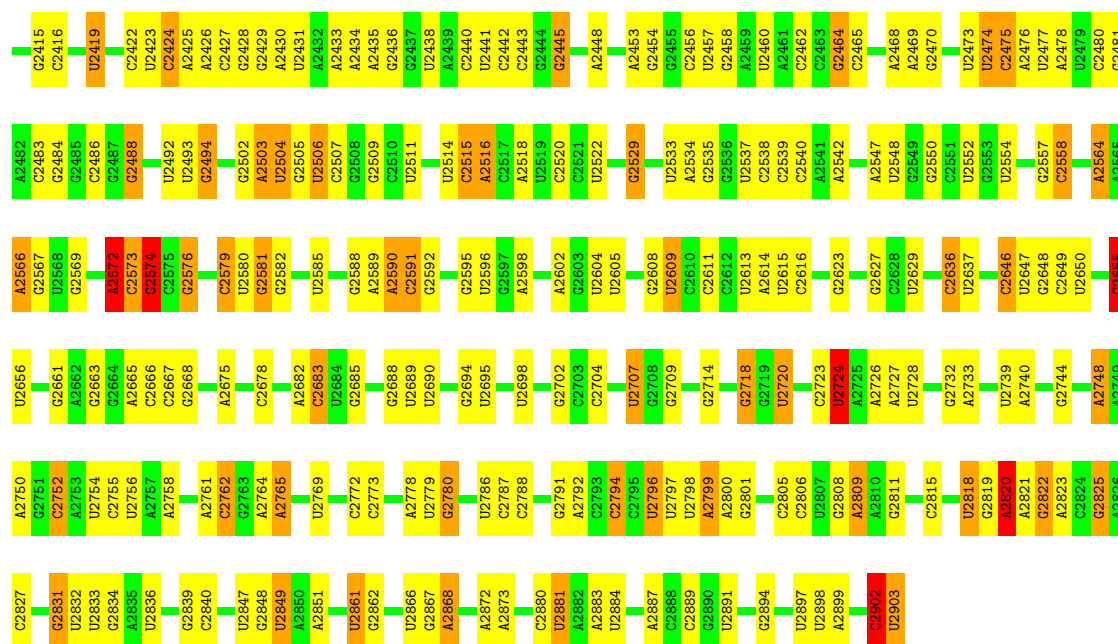
### 3 Residue-property plots

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

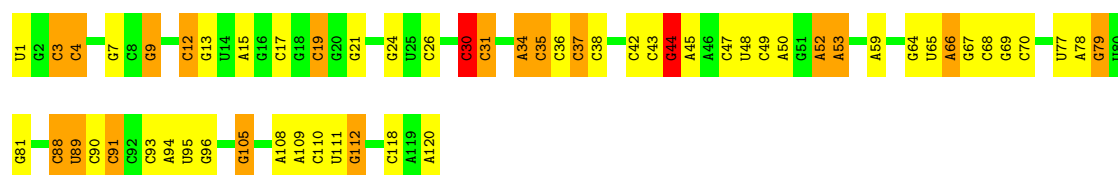


C2326	C2327	A2328	U2329	C2160	U2085	C2006	A1912	U1818	G1738	C1646	C1550	G1455	C1370	G1292	A1189	G1106	A1044
A2327	A2328	U2329	U2223	C2161	U2086	C2007	A1913	C1822	A1739	U1647	G1555	U1458	G1371	C1293	G1190	G1107	C1045
U2328	U2329	A2330	G2234	C2162	G2087	C2008	C1914	G1826	C1752	G1648	G1556	G1459	A1372	U1294	G1197	U1108	A1046
G2330	G2331	C2332	G2235	C2163	A2092	A2013	U1916	U1827	A1753	G1649	C1557	U1460	G1374	C1295	U1198	G1110	G1047
A2333	A2334	U2335	G2236	U2167	G2093	A2014	U1917	U1828	A1755	G1652	C1558	C1461	U1375	G1296	U1199	A1111	A1048
U2334	U2335	A2336	U2244	G2168	A2095	U2016	A1919	U1829	G1756	G1653	U1559	C1462	U1376	G1300	U1203	G1112	C1049
G2337	G2338	U2339	U2245	A2170	C2096	A2017	C1920	C1836	A1757	C1656	G1561	U1466	A1378	G1301	U1113	U1113	A1050
C2342	C2343	U2344	U2248	A2171	U2099	A2020	U1923	G1842	A1759	C1657	U1562	U1467	G1380	A1301	A1204	C1114	C1053
U2343	U2344	G2251	U2249	A2172	G2100	C2021	C1924	C1843	C1761	C1658	U1563	U1467	G1381	C1305	G1205	G1115	A1054
G2345	G2346	C2254	G2250	C2174	A2101	C2023	A1927	G1847	A1762	G1663	C1564	G1475	A1382	C1306	C1207	C1117	A1057
A2347	A2348	C2255	C2256	C2175	G2102	G2024	U1928	A1848	C1763	A1668	U1567	G1482	A1385	G1311	C1211	U1119	U1068
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C2350	C2351	U2352	U2260	C2177	C2104	U2026	G1930	C1853	U1769	C1670	A1569	U1486	A1387	C1314	G1215	G1122	U1061
C2354	C2355	U2356	U2261	C2178	U2105	G2029	C1934	U1854	G1770	G1674	C1574	A1490	A1392	C1315	G1216	G1123	G1062
A2357	A2358	U2359	U2262	C2179	G2107	A2030	G1935	U1855	C1771	C1675	U1578	G1491	A1393	U1316	C1221	G1124	G1063
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C2504	C2505	U2506	U2303	U2223	C2144	C2085	U1995	U1914	U1816	U1739	G1635	U1546	U1461	G1380	A1287	U1195	
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C2516	C2517	U2518	U2307	U2227	C2148	C2089	U1999	U1918	U1820	U1743	G1639	U1550	U1465	G1384	A1291	U1199	
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A2525	A2526	U2527	U2310	U2230	C2150	C2092	U2002	U1921	U1823	U1746	G1642	U1553	U1468	G1387	A1294	U1202	
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G2546	G2547	U2548	U2317	U2237	C2157	C2099	U2009	U1928	U1830	U1753	G1649	U1560	U1475	G1394	A1301	U1209	
A2549	A2550	U2551	U2318	U2238	C2158	C2100	U2010	U1929	U1831	U1754	G1650	U1561	U1476	G1395	A1302	U1210	
C2																	



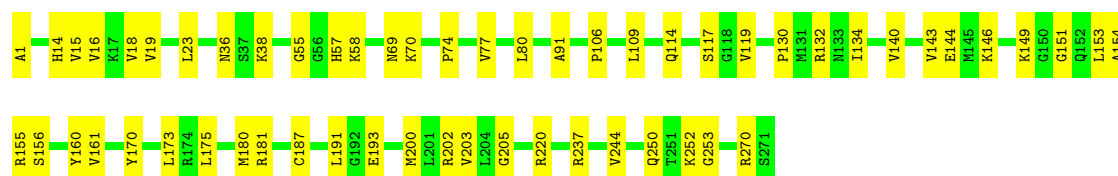
• Molecule 2: 5S ribosomal RNA

Chain B: 52% 32% 15%



• Molecule 3: 50S ribosomal protein L2

Chain C: 79% 21%



• Molecule 4: 50S ribosomal protein L3

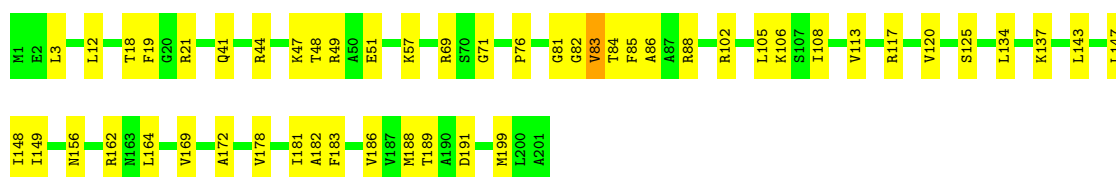
Chain D: 86% 14%



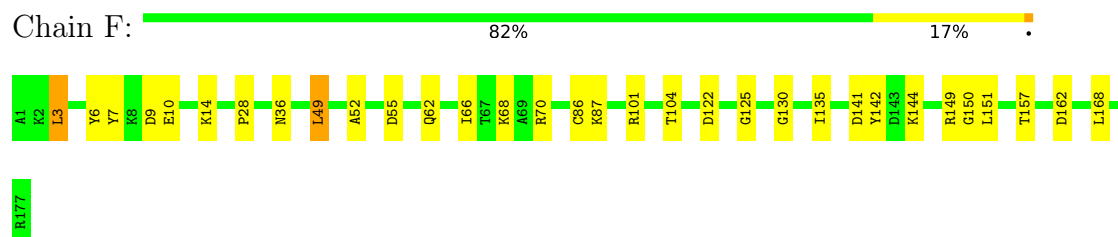
• Molecule 5: 50S ribosomal protein L4

Chain E: 75% 24%

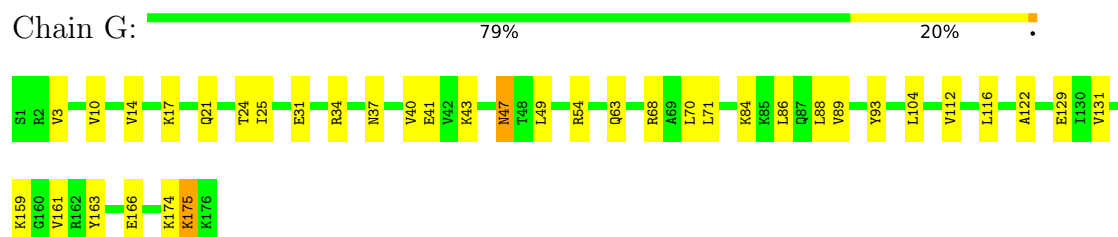




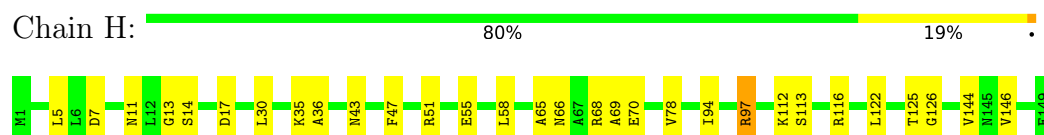
- Molecule 6: 50S ribosomal protein L5



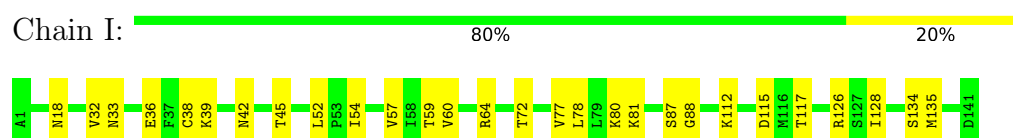
- Molecule 7: 50S ribosomal protein L6



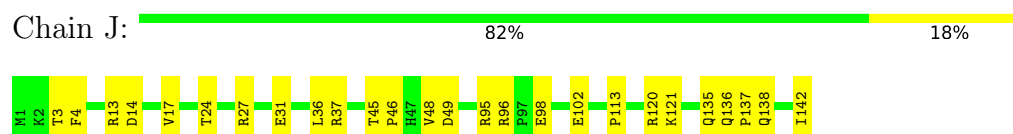
- Molecule 8: 50S ribosomal protein L9



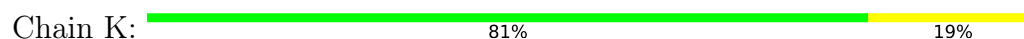
- Molecule 9: 50S ribosomal protein L11



- Molecule 10: 50S ribosomal protein L13



- Molecule 11: 50S ribosomal protein L14





- 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%



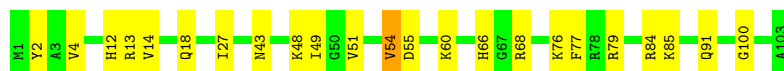
- Molecule 17: 50S ribosomal protein L20

Chain Q: 84% 15%

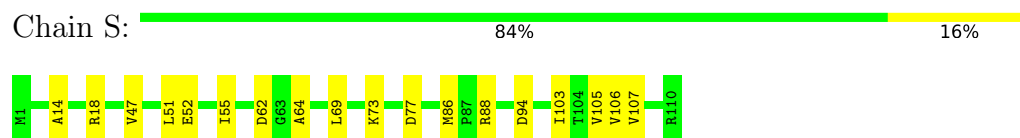


- Molecule 18: 50S ribosomal protein L21

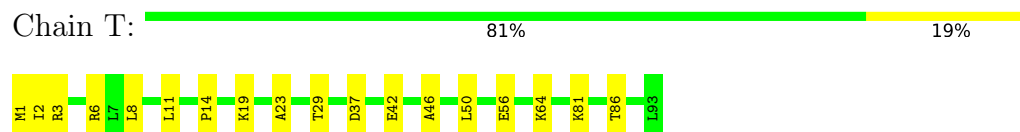
Chain R: 78% 21%



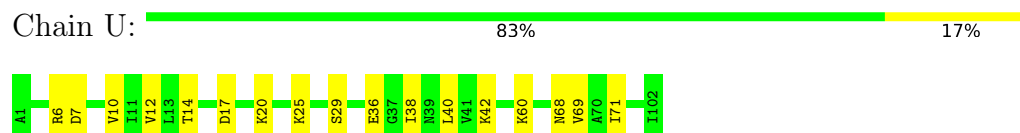
- Molecule 19: 50S ribosomal protein L22



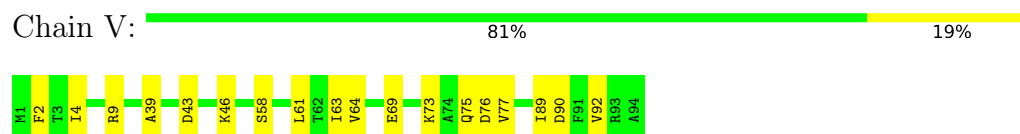
- Molecule 20: 50S ribosomal protein L23



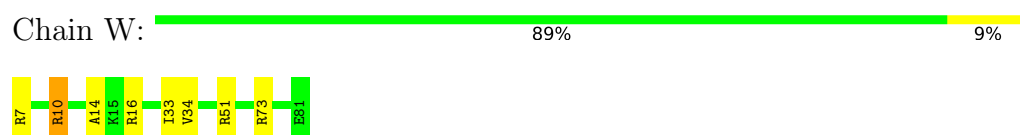
- Molecule 21: 50S ribosomal protein L24



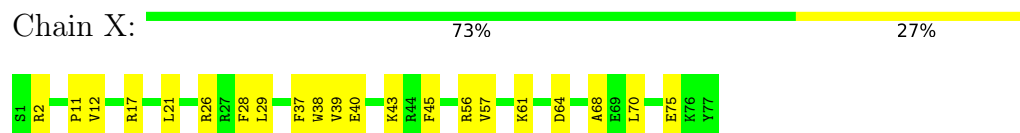
- Molecule 22: 50S ribosomal protein L25



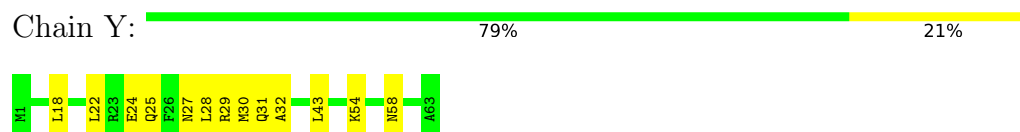
- Molecule 23: 50S ribosomal protein L27




- 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% .



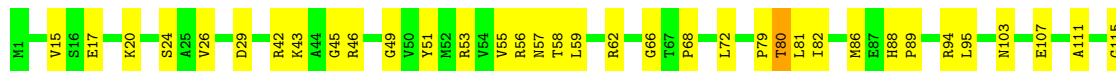
- Molecule 31: 50S ribosomal protein L36

Chain 4:  82% 18%




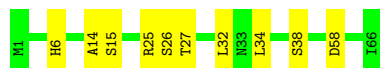
- Molecule 32: 50S ribosomal protein L10

Chain 5:  72% 27% .



- Molecule 33: 50S ribosomal protein L31

Chain 6:  85% 15%



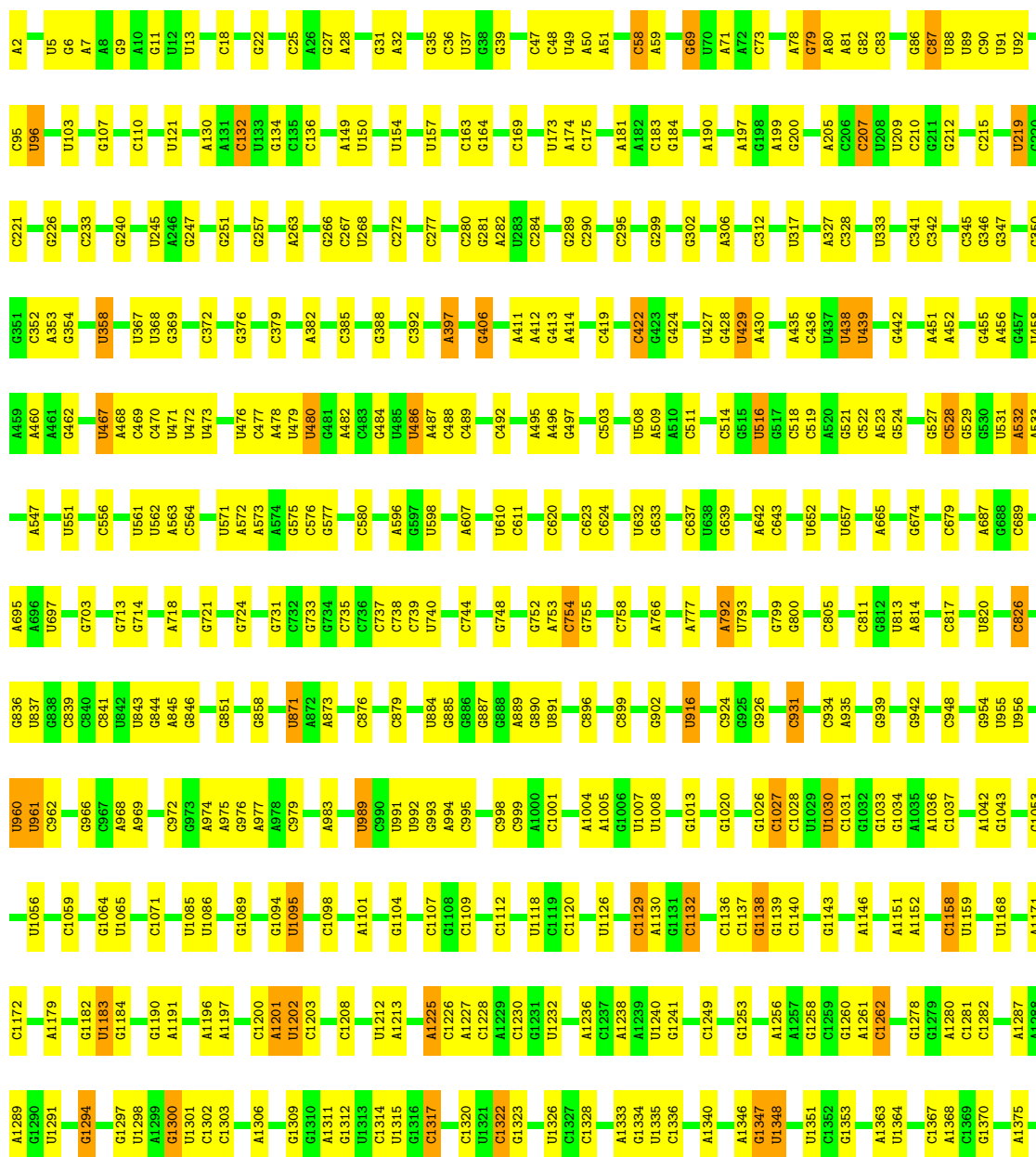
- Molecule 34: mRNA

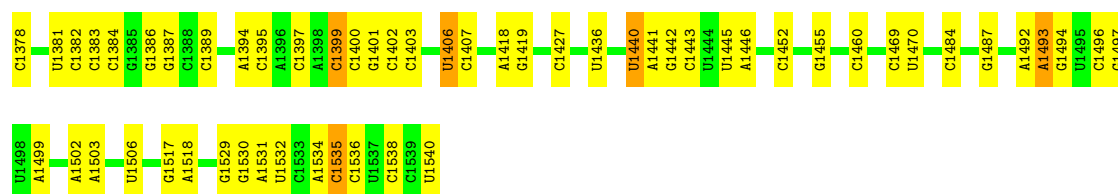
Chain 7:  29% 71%



- 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% .



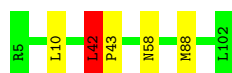
- Molecule 43: 30S ribosomal protein S9

Chain i:  98% .



- Molecule 44: 30S ribosomal protein S10

Chain j:  95% . .



- Molecule 45: 30S ribosomal protein S11

Chain k:  98% .



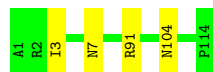
- Molecule 46: 30S ribosomal protein S12

Chain l:  98% .



- Molecule 47: 30S ribosomal protein S13

Chain m:  96% .



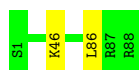
- Molecule 48: 30S ribosomal protein S14

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

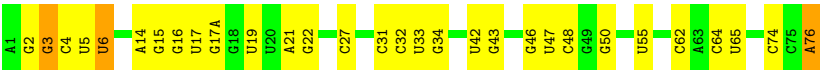
Chain v: 95%



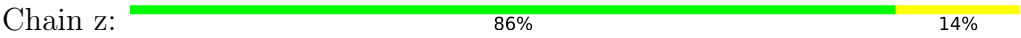
- Molecule 57: P-site Ile-tRNA

Chain x: 61% 35%





● Molecule 58: Apidaecin



## 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

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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%)	31	69
6	F	175/177 (99%)	159 (91%)	16 (9%)	0	100	100
7	G	174/176 (99%)	159 (91%)	14 (8%)	1 (1%)	27	66
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%)	21	60
12	L	141/143 (99%)	117 (83%)	23 (16%)	1 (1%)	24	63
13	M	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	11	46
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

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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%)	17	56
19	S	108/110 (98%)	101 (94%)	6 (6%)	1 (1%)	19	58
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%)	21	60
33	6	64/66 (97%)	53 (83%)	11 (17%)	0	100	100
36	b	216/218 (99%)	177 (82%)	37 (17%)	2 (1%)	19	58
37	c	204/206 (99%)	183 (90%)	18 (9%)	3 (2%)	11	46
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%)	17	56
41	g	149/151 (99%)	134 (90%)	14 (9%)	1 (1%)	24	63
42	h	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	21	60
43	i	125/127 (98%)	105 (84%)	19 (15%)	1 (1%)	21	60
44	j	96/98 (98%)	79 (82%)	15 (16%)	2 (2%)	8	40
45	k	114/116 (98%)	91 (80%)	23 (20%)	0	100	100
46	l	121/123 (98%)	94 (78%)	26 (22%)	1 (1%)	21	60
47	m	112/114 (98%)	98 (88%)	13 (12%)	1 (1%)	19	58
48	n	99/101 (98%)	88 (89%)	11 (11%)	0	100	100
49	o	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	14	51

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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%)	4	31
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	21
56	v	240/242 (99%)	213 (89%)	24 (10%)	3 (1%)	13	50
58	z	12/14 (86%)	10 (83%)	1 (8%)	1 (8%)	1	9
All	All	6099/6205 (98%)	5361 (88%)	706 (12%)	32 (0%)	35	69

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%)	81	91
4	D	164/164 (100%)	162 (99%)	2 (1%)	74	88
5	E	165/165 (100%)	163 (99%)	2 (1%)	74	88
6	F	148/148 (100%)	148 (100%)	0	100	100
7	G	137/137 (100%)	135 (98%)	2 (2%)	67	86
8	H	114/114 (100%)	114 (100%)	0	100	100
9	I	109/109 (100%)	107 (98%)	2 (2%)	62	83
10	J	116/116 (100%)	116 (100%)	0	100	100

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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%)	78	89
13	M	109/109 (100%)	108 (99%)	1 (1%)	81	91
14	N	100/100 (100%)	99 (99%)	1 (1%)	78	89
15	O	86/86 (100%)	86 (100%)	0	100	100
16	P	99/99 (100%)	98 (99%)	1 (1%)	78	89
17	Q	89/89 (100%)	88 (99%)	1 (1%)	76	89
18	R	84/84 (100%)	83 (99%)	1 (1%)	74	88
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%)	62	83
24	X	67/67 (100%)	66 (98%)	1 (2%)	67	86
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%)	55	81
37	c	170/170 (100%)	167 (98%)	3 (2%)	62	83
38	d	172/172 (100%)	167 (97%)	5 (3%)	45	76
39	e	114/119 (96%)	112 (98%)	2 (2%)	62	83
40	f	87/87 (100%)	86 (99%)	1 (1%)	76	89
41	g	124/124 (100%)	124 (100%)	0	100	100
42	h	104/104 (100%)	103 (99%)	1 (1%)	78	89
43	i	105/105 (100%)	104 (99%)	1 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	j	86/86 (100%)	84 (98%)	2 (2%)	53	80
45	k	89/89 (100%)	87 (98%)	2 (2%)	55	81
46	l	103/103 (100%)	103 (100%)	0	100	100
47	m	92/92 (100%)	89 (97%)	3 (3%)	41	73
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%)	67	86
51	q	74/74 (100%)	74 (100%)	0	100	100
52	r	48/56 (86%)	47 (98%)	1 (2%)	56	82
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%)	43	75
58	z	14/14 (100%)	13 (93%)	1 (7%)	16	50
All	All	5032/5060 (99%)	4981 (99%)	51 (1%)	80	89

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 ⓘ

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

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