



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jan 22, 2018 – 06:38 PM EST

PDB ID : 6ENF
EMDB ID: : EMD-3898
Title : Cryo-EM structure of a polyproline-stalled ribosome in the absence of EF-P
Authors : Huter, P.; Arenz, S.; Wilson, D.N.
Deposited on : 2017-10-04
Resolution : 3.20 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-20030736

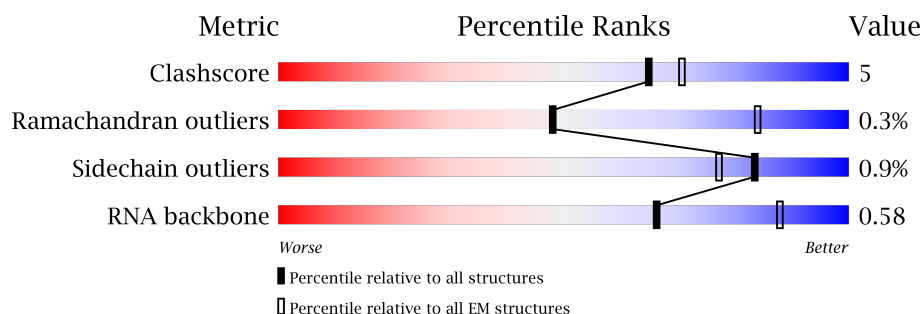
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



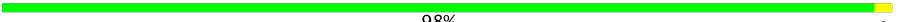
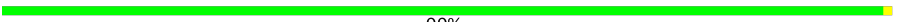
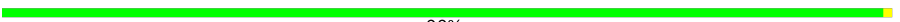






















Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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	1539	81% 18% .
2	b	218	98% .
3	c	206	100%
4	d	205	98% .
5	e	157	99% .
6	f	100	99% .
7	g	151	99% .
8	h	129	99% .













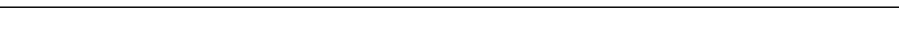


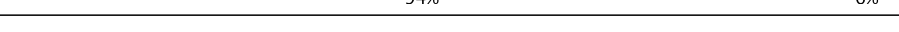
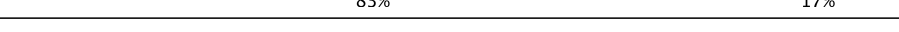


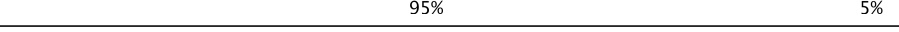
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Mol	Chain	Length	Quality of chain
9	i	127	 98% .
10	j	98	 99% .
11	k	116	 99% .
12	l	123	 98% .
13	m	114	 97% ..
14	n	101	 100%
15	o	88	 100%
16	p	82	 99% .
17	q	80	 98% .
18	r	65	 100%
19	s	79	 100%
20	t	85	 100%
21	u	65	 100%
22	v	3	 33% 67%
23	A	2903	 63% 29% . .
24	B	120	 64% 31% . .
25	C	271	 85% 15%
26	D	209	 88% 11%
27	E	201	 88% 12%
28	F	177	 85% 15%
29	G	176	 88% 12% .
30	J	142	 87% 13%
31	K	122	 80% 20%
32	L	143	 82% 17% .
33	M	136	 86% 13% .

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Mol	Chain	Length	Quality of chain
34	N	120	 85% 14% .
35	O	116	 92% 8%
36	P	114	 82% 18%
37	Q	117	 91% 9%
38	R	103	 88% 12%
39	S	110	 91% 9%
40	T	93	 87% 13%
41	U	102	 92% 8%
42	V	94	 84% 16%
43	W	78	 41% 40% 15% .
44	X	77	 91% 9%
45	Y	63	 94% 6%
46	Z	58	 86% 14%
47	0	56	 82% 18%
48	1	50	 94% 6%
49	2	46	 83% 17%
50	3	64	 83% 13% . .
51	4	38	 82% 18%
52	6	66	 95% 5%
53	x	77	 61% 32% 6%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 140797 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 16S ribosomal RNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	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 15 is a protein called 30S ribosomal protein S15.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 21 is a protein called 30S ribosomal protein S21.

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

- Molecule 22 is a RNA chain called RNA (5'-R(P*CP*CP*G)-3'), mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	v	3	Total	C	N	O	P	0	0
			63	28	11	21	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	2807	Total	C	N	O	P	0	0
			60275	26888	11109	19471	2807		

There are 3 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
A	2069	A	G	conflict	GB 802133627

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	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 1213441078

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 42 is a protein called 50S ribosomal protein L25.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	W	78	Total	C	N	O	S	0	0
			592	365	119	107	1		

- Molecule 44 is a protein called 50S ribosomal protein L28.

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

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

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

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

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

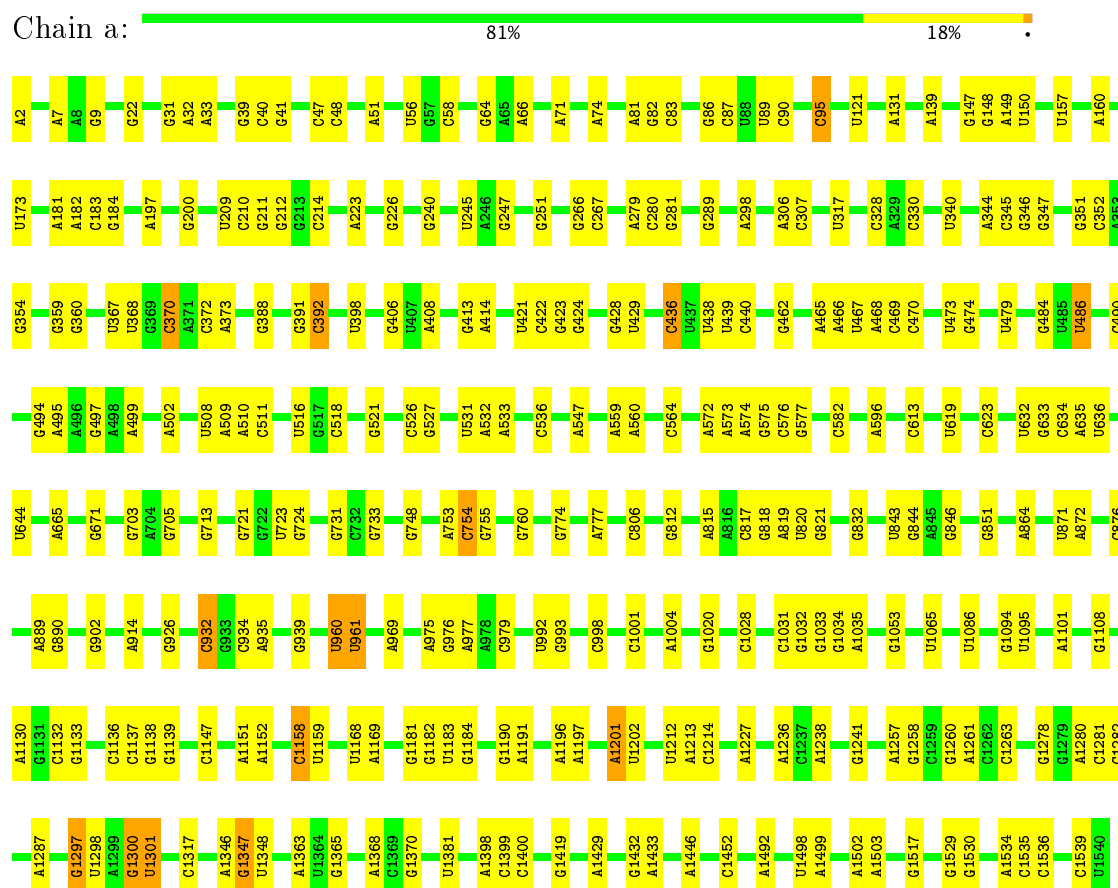
- Molecule 53 is a RNA chain called proline tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		

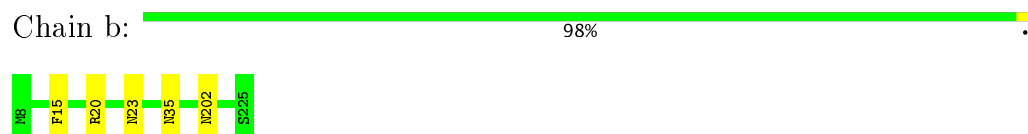
3 Residue-property plots

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: 16S ribosomal RNA



• Molecule 2: 30S ribosomal protein S2



• Molecule 3: 30S ribosomal protein S3



There are no outlier residues recorded for this chain.

- Molecule 4: 30S ribosomal protein S4

Chain d:  98%



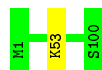
- Molecule 5: 30S ribosomal protein S5

Chain e:  99%



- Molecule 6: 30S ribosomal protein S6

Chain f:  99%



- Molecule 7: 30S ribosomal protein S7

Chain g:  99%



- Molecule 8: 30S ribosomal protein S8

Chain h:  99%



- Molecule 9: 30S ribosomal protein S9

Chain i:  98%



- Molecule 10: 30S ribosomal protein S10

Chain j:  99%



- Molecule 11: 30S ribosomal protein S11

Chain k:  99%



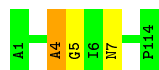
- Molecule 12: 30S ribosomal protein S12

Chain l:  98%



- Molecule 13: 30S ribosomal protein S13

Chain m:  97%



- Molecule 14: 30S ribosomal protein S14

Chain n:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: 30S ribosomal protein S15

Chain o:  100%

There are no outlier residues recorded for this chain.

- Molecule 16: 30S ribosomal protein S16

Chain p:  99%



- Molecule 17: 30S ribosomal protein S17

Chain q:  98%



- Molecule 18: 30S ribosomal protein S18

Chain r:  100%

There are no outlier residues recorded for this chain.

- Molecule 19: 30S ribosomal protein S19

Chain s:  100%

There are no outlier residues recorded for this chain.

- Molecule 20: 30S ribosomal protein S20

Chain t:  100%

There are no outlier residues recorded for this chain.

- Molecule 21: 30S ribosomal protein S21

Chain u:  100%

There are no outlier residues recorded for this chain.

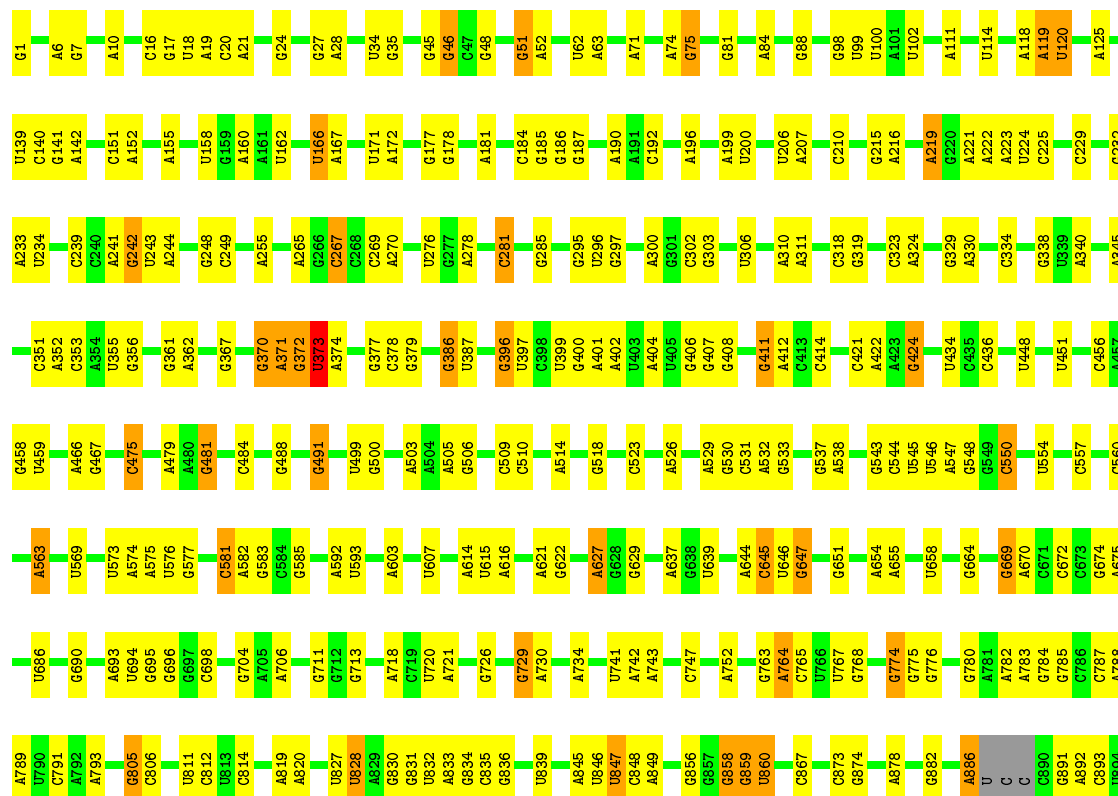
- Molecule 22: RNA (5'-R(P*CP*CP*G)-3'), mRNA

Chain v:  33% 67%

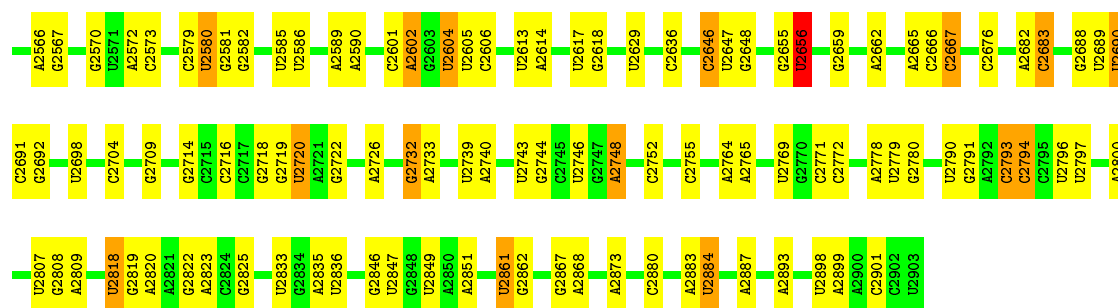
 G16
 C17
 G18

- Molecule 23: 23S ribosomal RNA

Chain A:  63% 29%

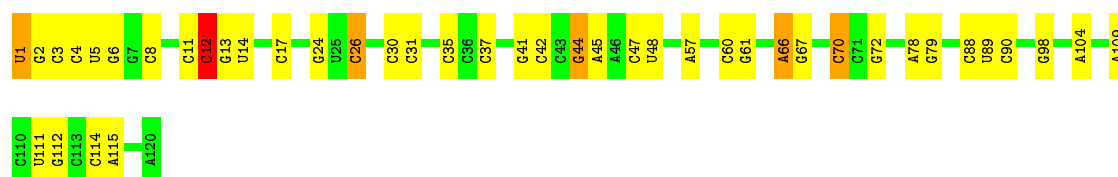


C2456	A2327	G2234	A	C	A2020	A1901	U1796	G1667	U1554	C1417	U1316	C1211	U1097	A1014	U895
U2457	G2328	G2238	C	C	U2021	A1901	G1797	C1668	G1555	G1418	G1317	G1211	A1098	A1014	A896
A2459	G2329	G2239	U	U	U2022	G1906	G1799	A1669	C1558	A1420	G1320	C1211	G1102	A1020	C897
U2460	U2245	U2245	G	G	G2024	U1911	A1800	U1671	U1559	A1421	A1321	C1221	A1103	G1021	C902
C2467	G2246	G2246	A	A	C2025	A1912	A1801	A1672	G1560	G1422	A1322	U1222	C1104	U1023	
U2474	A2247	A2247	A	G	A1913	A1913	A1802	G1673	C1565	C1428	G1324	U1224	G1106	G1026	G907
C2475	G2280	G2280	U	G	A2030	C1914	A1806	C1675	C1569	G1430	U1325	G1225	A1111	A1027	A909
C2476	G2251	G2251	A	U	A2033	U1915	G1807	G1681	A1570	A1431	U1326		A1111	A1028	A910
U2477	C2347	C2347	C	A	G2032	A1916	A1808		A1571	G1432			G1112		
A2478	C2350	C2354	C	G	U2034	U1917	A1809	G1687	A1572	A1433	U1329	A1247	G1115	A1032	C915
G2481	C2358	C2358	C	A	G2036	A1928	U1812	C1694	U1578	A1434	G1341	G1248	G1122	G1034	U919
G2494	A2286	A2286	C	U	A2037	G1929	A1816	G1695	A1579	C1437				G1035	G924
C2498	G2271	G2271	U	G	G2038	G1930	G1817	G1696		U1443	U1344	C1251	G1125	G1036	A925
G2502	A2273	A2273	U	G	U2039	U1931	U1818	A1701	A1583	U1443	U1345	G1252		A1040	U931
A2503	G2277	G2277	A	G	C2040	A1936	G1826	G1707	C1584	G1444	C1348	A1253	A1129	C1045	U934
U2504	A2369	A2369	U	A	C2043	A1937	U1827	G1707	C1585	A1254	C1349	U1254	G1130	A1046	C935
G2505	G2277	G2277	U	G	G2047	U1939	A1828	G1710	U1589	C1450	U1352	G1256	U1132	G1047	A936
U2506	A2278	A2278	G	A	G2048	U1940	A1829	A1711	A1591	A1453	A1353	C1257	A1134	A1048	
C2507	G2279	G2279	U	G	C1941	C1941	C1830		C1592	C1454	A1354	U1258	G1135	C1049	A941
G2508	C2283	C2283	U	C	A2052	U1942	G1833	G1715	A1593	C1461	G1355			G1056	
A2513	G2286	G2286	G	U	C2055	U1943	A1834	U1729	A1597	C1461	G1356	U1263	G1139	U1058	C946
U2514	A2287	A2287	U	U	G2056	U1944	A1835	C1730	A1598	G1475	G1357	A1264	G1140	U1059	C948
C2515	C2385	C2385	U	G	U1955	U1956	C1837	G1731	A1603	G1482	C1363	C1270	C1153	U1060	G949
A2516	A2288	A2288	U	A	C2060	U1956	G1839	C1732	C1607	A1490	G1364	G1271	U1061	U1061	
G2517	U2291	U2291	G	G	A2062	C1961	A1735	A1735	A1608	G1491	A1365	A1272	U1159	G1063	G954
U2518	G2293	G2293	A	U	C2063	G1964	G1847	G1738	C1611	U1497	G1368			C1064	U955
U2519	A2294	A2294	U	C	U2068	C1965	A1848		C1612	U1497		A1275	U1065	U1065	
C2520	G2295	G2295	G	G	A2069	A1966	G1857	A1744	C1613	A1504	A1373	G1278	C1167	U1066	C961
G2526	U2296	U2296	U	G	G2070	C1967	A1858	A1745	G1613	A1504	A1373	G1279	A1169	U1067	G962
A2529	G2297	G2297	U	A	A2071	U1970	U1859	A1759	G1622	C1507	A1378	G1279	C1170	G1068	G966
C2530	U2299	U2299	C	C	C2072	A1970	U1864	A1754	C1508	A1503	U1379	G1283	C1171	A1070	A973
G2535	C2300	C2300	G	G	U2076	G1972	U1865	A1755	U1629	A1509	G1380	G1283	C1172	G1071	G974
C2536	U2305	U2305	C	C	C2081	A1977	A1866	G1756			A1383	A1286	A1175	C1072	
C2537	G2428	G2428	U	C	A2082	A1977	G1869	A1757	U1636	A1515	C1386	A1287	U1176	C1076	A983
C2539	G2429	G2429	A	G	U2213	G1983	A1870	U1758	A1637	G1516	C1387	G1288	G1177	G1078	A984
C2540	A2430	A2430	U	U	U2086	C1986	A1871	A1759	C1638	G1524	A1387		G1178	U1078	C985
A2547	A2435	C2313	C	C	G2087	C1986	A1872	G1763	C1644	A1528	A1385	U1294	G1179	C1079	C986
U2552	U2441	A2314	U	G	A2088	A1987	G1873	C1764	G1645	A1528	U1181	G1300	U1180	A1084	C987
C2553	G2442	G2315	C	C	C2093	U1991	G1875	A1773	C1646	G1529	C1398	A1301	G1182	A1085	C994
U2554	C2443	G2316	U	A	A2094	G1992	A1870	C1774	U1647	G1530	C1399			A1086	C995
U2555	G2444	U2320	G	U	C2095	U1993	G1878		U1648	C1531	G1305	C1306	G1187	G1087	A996
C2556	G2445	U2321	U	U	A	U1996	G1879		A1532	A1532	U1409		U1188	A1088	
G2559	G2446	C2322	G	A	U	C1996	U1879	U1779	G1651	C1533	G1410	G1310	A1189	A1089	U999
A2448	A2447	G2323	C	G	A	C1997	U1880	A1780	A1652	U1534	U1412	U1311	G1191	A1090	A1000
U2560	G2448	U2324	G	U	C	G2004	A1884	A1784	G1653	C1536	C1414	U1313	G1191	A1091	A1009
U2561	U2449	G2325	C	A	U	G2004	A1885	A1785	G1659	C1543	U1415	U1314	A1204	G1092	
C2562	C2326	C2326	C	C	A2006	C2006	C1892	A1786	C1686		G1315	C1314	A1205	G1093	U1012
U2563															A1008



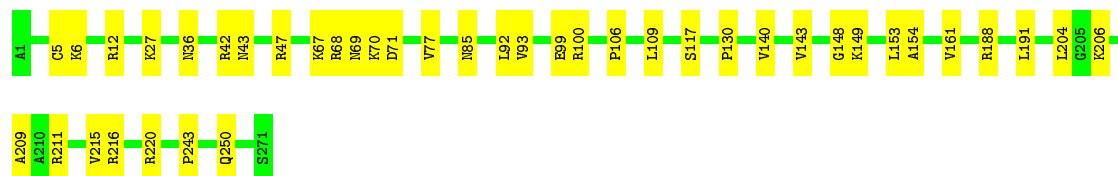
- Molecule 24: 5S ribosomal RNA

Chain B: 64% 31%



- Molecule 25: 50S ribosomal protein L2

Chain C: 85% 15%



- Molecule 26: 50S ribosomal protein L3

Chain D: 88% 11%



- Molecule 27: 50S ribosomal protein L4

Chain E: 88% 12%




- Molecule 28: 50S ribosomal protein L5

Chain F: 85% 15%




- Molecule 29: 50S ribosomal protein L6

Chain G:  88% 12%




- Molecule 30: 50S ribosomal protein L13

Chain J:  87% 13%




- Molecule 31: 50S ribosomal protein L14

Chain K:  80% 20%




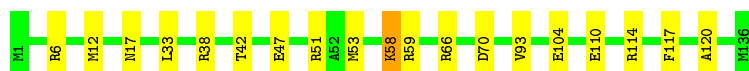
- Molecule 32: 50S ribosomal protein L15

Chain L:  82% 17%




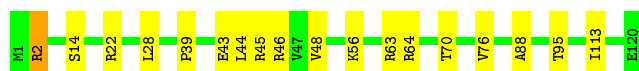
- Molecule 33: 50S ribosomal protein L16

Chain M:  86% 13%



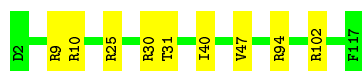
- Molecule 34: 50S ribosomal protein L17

Chain N:  85% 14%




- Molecule 35: 50S ribosomal protein L18

Chain O:  92% 8%



- Molecule 36: 50S ribosomal protein L19

Chain P:  82% 18%



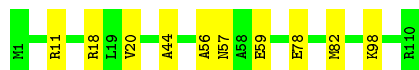
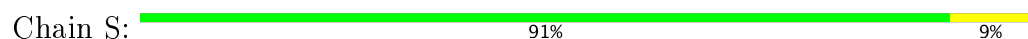
- Molecule 37: 50S ribosomal protein L20



- Molecule 38: 50S ribosomal protein L21



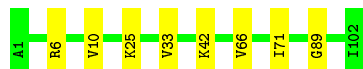
- Molecule 39: 50S ribosomal protein L22



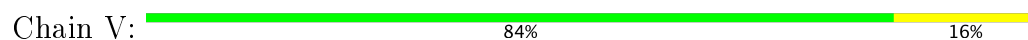
- Molecule 40: 50S ribosomal protein L23



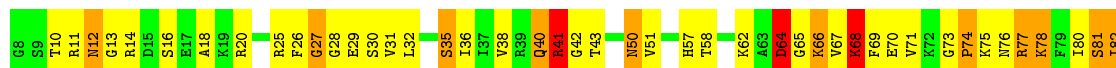
- Molecule 41: 50S ribosomal protein L24



- Molecule 42: 50S ribosomal protein L25



- Molecule 43: 50S ribosomal protein L27





- Molecule 44: 50S ribosomal protein L28

Chain X: 91% 9%



- Molecule 45: 50S ribosomal protein L29

Chain Y: 94% 6%



- Molecule 46: 50S ribosomal protein L30

Chain Z: 86% 14%



- Molecule 47: 50S ribosomal protein L32

Chain 0: 82% 18%



- Molecule 48: 50S ribosomal protein L33

Chain 1: 94% 6%



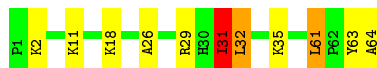
- Molecule 49: 50S ribosomal protein L34

Chain 2: 83% 17%




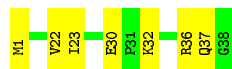
- Molecule 50: 50S ribosomal protein L35

Chain 3: 83% 13% ..



- Molecule 51: 50S ribosomal protein L36

Chain 4:  82% 18%



- Molecule 52: 50S ribosomal protein L31

Chain 6:  95% 5%



- Molecule 53: proline tRNA

Chain x:  61% 32% 6%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	75089	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	0.29	1/36967 (0.0%)	0.99	74/57666 (0.1%)
10	j	0.25	0/796	0.59	0/1077
11	k	0.27	0/885	0.52	0/1195
12	l	0.29	0/969	0.59	0/1300
13	m	0.24	0/892	0.54	0/1193
14	n	0.24	0/811	0.50	0/1081
15	o	0.24	0/722	0.51	0/964
16	p	0.26	0/659	0.52	0/884
17	q	0.28	0/657	0.56	0/881
18	r	0.23	0/511	0.49	0/689
19	s	0.26	0/652	0.50	0/877
2	b	0.27	0/1735	0.51	0/2338
20	t	0.26	0/671	0.45	0/888
21	u	0.30	0/500	0.59	0/668
22	v	0.33	0/69	1.11	0/105
23	A	0.30	1/67511 (0.0%)	1.00	224/105319 (0.2%)
24	B	0.36	1/2876 (0.0%)	1.07	18/4483 (0.4%)
25	C	0.26	0/2121	0.52	1/2852 (0.0%)
26	D	0.26	0/1586	0.51	0/2134
27	E	0.25	0/1571	0.46	0/2113
28	F	0.27	0/1434	0.51	0/1926
29	G	0.25	0/1343	0.47	0/1816
3	c	0.26	0/1651	0.51	0/2225
30	J	0.25	0/1152	0.46	0/1551
31	K	0.26	0/947	0.51	0/1268
32	L	0.26	0/1054	0.55	0/1403
33	M	0.27	0/1093	0.55	1/1460 (0.1%)
34	N	0.25	0/973	0.53	0/1301
35	O	0.24	0/902	0.45	0/1209
36	P	0.25	0/929	0.50	1/1242 (0.1%)
37	Q	0.25	0/960	0.42	0/1278
38	R	0.25	0/829	0.52	0/1107
39	S	0.24	0/864	0.50	0/1156
4	d	0.26	0/1665	0.55	1/2227 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
40	T	0.24	0/744	0.49	0/994
41	U	0.26	0/787	0.51	0/1051
42	V	0.25	0/766	0.49	0/1025
43	W	0.58	0/599	0.81	0/792
44	X	0.24	0/635	0.45	0/848
45	Y	0.23	0/510	0.45	0/677
46	Z	0.22	0/453	0.47	0/605
47	0	0.23	0/450	0.48	0/599
48	1	0.25	0/416	0.48	0/554
49	2	0.25	0/380	0.46	0/498
5	e	0.28	0/1154	0.57	0/1554
50	3	0.28	0/513	0.65	2/676 (0.3%)
51	4	0.26	0/303	0.51	0/397
52	6	0.26	0/531	0.48	0/709
53	x	0.38	0/1839	1.10	19/2866 (0.7%)
6	f	0.26	0/835	0.55	0/1128
7	g	0.26	0/1195	0.53	0/1602
8	h	0.26	0/989	0.54	1/1326 (0.1%)
9	i	0.27	0/1034	0.56	0/1375
All	All	0.29	3/153090 (0.0%)	0.90	342/229152 (0.1%)

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
10	j	0	1
12	l	0	1
13	m	0	1
17	q	0	1
2	b	0	1
28	F	0	2
29	G	0	2
33	M	0	1
38	R	0	1
5	e	0	1
6	f	0	1
7	g	0	1
All	All	0	14

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	B	1	U	OP3-P	-10.59	1.48	1.61
23	A	1	G	OP3-P	-10.59	1.48	1.61
1	a	2	A	OP3-P	-10.49	1.48	1.61

The worst 5 of 342 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	1507	C	N3-C2-O2	-11.99	113.51	121.90
1	a	582	C	N1-C2-O2	11.45	125.77	118.90
23	A	1507	C	N1-C2-O2	11.15	125.59	118.90
1	a	582	C	N3-C2-O2	-10.34	114.66	121.90
23	A	1914	C	N1-C2-O2	9.72	124.73	118.90

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	b	15	PHE	Peptide
5	e	121	ASN	Peptide
6	f	53	LYS	Peptide
7	g	28	ILE	Peptide
10	j	57	VAL	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	33016	0	16617	0	0
2	b	1704	0	1732	0	0
3	c	1624	0	1699	0	0
4	d	1643	0	1710	0	0
5	e	1141	0	1170	0	0
6	f	817	0	808	0	0
7	g	1181	0	1240	0	0
8	h	979	0	1034	0	0
9	i	1022	0	1070	0	0
10	j	786	0	828	0	0
11	k	869	0	878	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	l	955	0	1019	0	0
13	m	883	0	944	0	0
14	n	799	0	841	0	0
15	o	714	0	737	0	0
16	p	649	0	666	0	0
17	q	648	0	691	0	0
18	r	504	0	502	0	0
19	s	637	0	665	0	0
20	t	665	0	714	0	0
21	u	495	0	486	0	0
22	v	63	0	34	0	0
23	A	60275	0	30318	357	0
24	B	2572	0	1301	20	0
25	C	2082	0	2156	27	0
26	D	1565	0	1616	17	0
27	E	1552	0	1619	16	0
28	F	1410	0	1447	19	0
29	G	1323	0	1374	12	0
30	J	1129	0	1162	14	0
31	K	938	0	1012	15	0
32	L	1045	0	1117	19	0
33	M	1074	0	1157	8	0
34	N	960	0	1000	12	0
35	O	892	0	923	8	0
36	P	917	0	965	13	0
37	Q	947	0	1022	11	0
38	R	816	0	839	8	0
39	S	857	0	922	8	0
40	T	738	0	807	8	0
41	U	779	0	834	4	0
42	V	753	0	780	8	0
43	W	592	0	607	58	0
44	X	625	0	655	4	0
45	Y	509	0	543	3	0
46	Z	449	0	491	4	0
47	0	444	0	461	7	0
48	1	409	0	440	2	0
49	2	377	0	418	6	0
50	3	504	0	574	9	0
51	4	302	0	343	7	0
52	6	522	0	522	3	0
53	x	1646	0	832	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	140797	0	94342	596	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 5.

The worst 5 of 596 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)
43:W:25:ARG:HD3	43:W:29:GLU:OE2	1.51	1.09
43:W:40:GLN:NE2	43:W:57:HIS:O	1.86	1.07
43:W:77:ARG:O	43:W:78:LYS:C	1.92	1.05
43:W:66:LYS:O	43:W:82:ILE:HD13	1.62	0.98
24:B:72:G:H21	24:B:104:A:H62	1.14	0.93

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	
2	b	216/218 (99%)	200 (93%)	16 (7%)	0	100	100
3	c	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
4	d	203/205 (99%)	185 (91%)	18 (9%)	0	100	100
5	e	155/157 (99%)	137 (88%)	18 (12%)	0	100	100
6	f	98/100 (98%)	82 (84%)	16 (16%)	0	100	100
7	g	149/151 (99%)	135 (91%)	14 (9%)	0	100	100
8	h	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
9	i	125/127 (98%)	108 (86%)	17 (14%)	0	100	100
10	j	96/98 (98%)	84 (88%)	12 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	k	114/116 (98%)	98 (86%)	16 (14%)	0	100	100
12	l	121/123 (98%)	99 (82%)	21 (17%)	1 (1%)	22	65
13	m	112/114 (98%)	102 (91%)	8 (7%)	2 (2%)	10	47
14	n	99/101 (98%)	90 (91%)	9 (9%)	0	100	100
15	o	86/88 (98%)	80 (93%)	6 (7%)	0	100	100
16	p	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
17	q	78/80 (98%)	68 (87%)	9 (12%)	1 (1%)	14	55
18	r	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
19	s	77/79 (98%)	73 (95%)	4 (5%)	0	100	100
20	t	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
21	u	63/65 (97%)	50 (79%)	13 (21%)	0	100	100
25	C	269/271 (99%)	255 (95%)	14 (5%)	0	100	100
26	D	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
27	E	199/201 (99%)	185 (93%)	14 (7%)	0	100	100
28	F	175/177 (99%)	165 (94%)	10 (6%)	0	100	100
29	G	174/176 (99%)	162 (93%)	11 (6%)	1 (1%)	28	72
30	J	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
31	K	120/122 (98%)	107 (89%)	13 (11%)	0	100	100
32	L	141/143 (99%)	124 (88%)	17 (12%)	0	100	100
33	M	134/136 (98%)	128 (96%)	4 (3%)	2 (2%)	12	51
34	N	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
35	O	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
36	P	112/114 (98%)	106 (95%)	6 (5%)	0	100	100
37	Q	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
38	R	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
39	S	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
40	T	91/93 (98%)	81 (89%)	10 (11%)	0	100	100
41	U	100/102 (98%)	83 (83%)	16 (16%)	1 (1%)	18	61
42	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
43	W	76/78 (97%)	55 (72%)	13 (17%)	8 (10%)	0	3
44	X	75/77 (97%)	73 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	Y	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
46	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
47	0	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
48	1	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
49	2	44/46 (96%)	44 (100%)	0	0	100	100
50	3	62/64 (97%)	53 (86%)	7 (11%)	2 (3%)	5	30
51	4	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
52	6	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
All	All	5435/5531 (98%)	4983 (92%)	434 (8%)	18 (0%)	48	81

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	W	27	GLY
50	3	31	ILE
12	l	102	ASP
17	q	70	LYS
33	M	59	ARG

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
2	b	180/180 (100%)	176 (98%)	4 (2%)	57	85
3	c	170/170 (100%)	170 (100%)	0	100	100
4	d	172/172 (100%)	169 (98%)	3 (2%)	66	88
5	e	114/119 (96%)	113 (99%)	1 (1%)	82	94
6	f	87/87 (100%)	87 (100%)	0	100	100
7	g	124/124 (100%)	123 (99%)	1 (1%)	85	95
8	h	104/104 (100%)	104 (100%)	0	100	100
9	i	105/105 (100%)	103 (98%)	2 (2%)	62	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	j	86/86 (100%)	86 (100%)	0	100	100
11	k	89/89 (100%)	88 (99%)	1 (1%)	78	92
12	l	103/103 (100%)	102 (99%)	1 (1%)	80	93
13	m	92/92 (100%)	91 (99%)	1 (1%)	78	92
14	n	79/83 (95%)	79 (100%)	0	100	100
15	o	76/76 (100%)	76 (100%)	0	100	100
16	p	65/65 (100%)	64 (98%)	1 (2%)	70	90
17	q	74/74 (100%)	74 (100%)	0	100	100
18	r	48/56 (86%)	48 (100%)	0	100	100
19	s	70/70 (100%)	70 (100%)	0	100	100
20	t	65/65 (100%)	65 (100%)	0	100	100
21	u	44/55 (80%)	44 (100%)	0	100	100
25	C	216/216 (100%)	214 (99%)	2 (1%)	82	94
26	D	164/164 (100%)	163 (99%)	1 (1%)	89	96
27	E	165/165 (100%)	164 (99%)	1 (1%)	89	96
28	F	148/148 (100%)	148 (100%)	0	100	100
29	G	137/137 (100%)	137 (100%)	0	100	100
30	J	116/116 (100%)	116 (100%)	0	100	100
31	K	103/103 (100%)	103 (100%)	0	100	100
32	L	102/102 (100%)	101 (99%)	1 (1%)	80	93
33	M	109/109 (100%)	108 (99%)	1 (1%)	82	94
34	N	100/100 (100%)	99 (99%)	1 (1%)	80	93
35	O	86/86 (100%)	86 (100%)	0	100	100
36	P	99/99 (100%)	99 (100%)	0	100	100
37	Q	89/89 (100%)	89 (100%)	0	100	100
38	R	84/84 (100%)	83 (99%)	1 (1%)	75	91
39	S	93/93 (100%)	92 (99%)	1 (1%)	78	92
40	T	80/80 (100%)	80 (100%)	0	100	100
41	U	83/83 (100%)	83 (100%)	0	100	100
42	V	78/78 (100%)	78 (100%)	0	100	100
43	W	59/59 (100%)	43 (73%)	16 (27%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	X	67/67 (100%)	66 (98%)	1 (2%)	70	90
45	Y	55/55 (100%)	55 (100%)	0	100	100
46	Z	48/48 (100%)	48 (100%)	0	100	100
47	0	47/47 (100%)	47 (100%)	0	100	100
48	1	45/45 (100%)	45 (100%)	0	100	100
49	2	38/38 (100%)	38 (100%)	0	100	100
50	3	51/51 (100%)	51 (100%)	0	100	100
51	4	34/34 (100%)	34 (100%)	0	100	100
52	6	59/59 (100%)	59 (100%)	0	100	100
All	All	4502/4530 (99%)	4461 (99%)	41 (1%)	83	94

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	E	156	ASN
38	R	43	ASN
43	W	81	SER
32	L	27	LEU
33	M	6	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
25	C	36	ASN
26	D	49	GLN
43	W	40	GLN
25	C	114	GLN
26	D	150	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1538/1539 (99%)	267 (17%)	0
22	v	2/3 (66%)	2 (100%)	0
23	A	2804/2903 (96%)	477 (17%)	19 (0%)
24	B	119/120 (99%)	15 (12%)	1 (0%)
53	x	76/77 (98%)	24 (31%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4539/4642 (97%)	785 (17%)	20 (0%)

5 of 785 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	7	A
1	a	9	G
1	a	22	G
1	a	31	G
1	a	32	A

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	A	1300	G
23	A	1378	A
23	A	2326	C
23	A	1182	G
23	A	1190	G

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](#)

There are no chain breaks in this entry.