



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2025 – 05:30 pm GMT

PDB ID : 7AC7
EMDB ID : EMD-11713
Title : Structure of accomodated trans-translation complex on E. Coli stalled ribosome.
Authors : Guyomar, C.; D'Urso, G.; Chat, S.; Giudice, E.; Gillet, R.
Deposited on : 2020-09-10
Resolution : 3.08 Å(reported)
Based on initial model : 4YBB

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : **FAILED**
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41

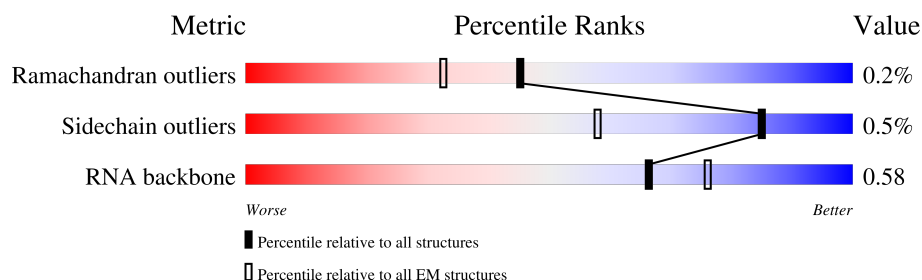
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.08 Å.

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


















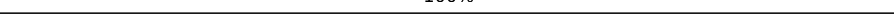
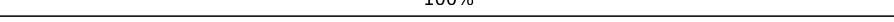
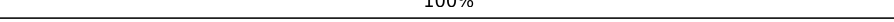
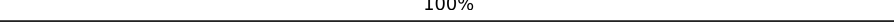
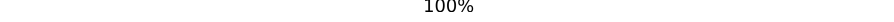

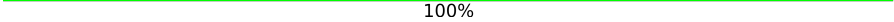
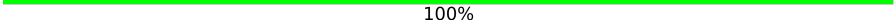

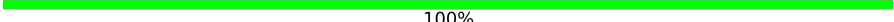
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	1	2903	
2	2	1540	
3	3	120	
4	4	363	
5	5	147	
6	7	76	
7	8	15	
8	A	84	
9	B	271	















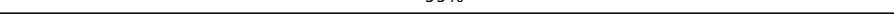
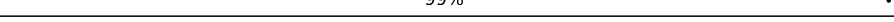
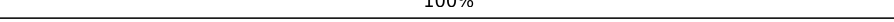
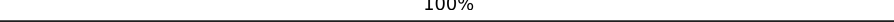
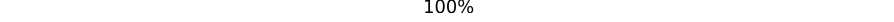
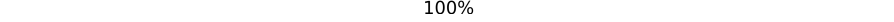
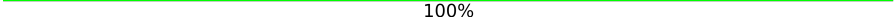
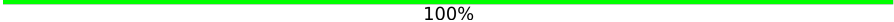

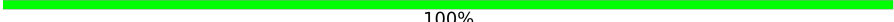
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Mol	Chain	Length	Quality of chain
10	C	209	 100%
11	D	201	 100%
12	E	177	 100%
13	F	175	 97%
14	G	149	 99%
15	H	130	 92% 8%
16	J	141	 100%
17	K	123	 100%
18	L	144	 100%
19	M	136	 99%
20	N	119	 100%
21	O	115	 100%
22	P	114	 100%
23	Q	117	 100%
24	R	103	 100%
25	S	109	 100%
26	T	94	 100%
27	U	103	 100%
28	V	94	 100%
29	W	2	 50% 50%
30	X	77	 100%
31	Y	58	 100%
32	Z	56	 100%
33	a	66	 100%
34	b	54	 100%

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Mol	Chain	Length	Quality of chain
35	c	52	 100%
36	d	46	 100%
37	e	64	 95% 5%
38	f	37	 100%
39	g	225	 100%
40	h	208	 100%
41	i	205	 100%
42	j	156	 100%
43	k	104	 100%
44	l	151	 100%
45	m	129	 100%
46	n	126	 98% .
47	o	99	 100%
48	p	117	 99% .
49	q	123	 99% .
50	r	115	 100%
51	s	100	 100%
52	t	87	 100%
53	u	81	 100%
54	v	80	 100%
55	w	65	 100%
56	x	82	 100%
57	y	85	 100%
58	z	70	 100%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 154883 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	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1540	Total	C	N	O	P	0	0
			33049	14747	6057	10705	1540		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called transfer-messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	363	Total	C	N	O	P	0	0
			7759	3466	1410	2520	363		

- Molecule 5 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	147	Total	C	N	O	S	0	0
			1191	753	223	211	4		

- Molecule 6 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	7	76	Total	C	N	O	P	S	0	0
			1635	735	291	532	75	2		

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	8	15	Total	C	N	O	P	0	0
			324	145	60	105	14		

- Molecule 8 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 10 is a protein called 50S ribosomal protein L3.

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

- Molecule 11 is a protein called 50S ribosomal protein L4.

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

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 14 is a protein called 50S ribosomal protein L9.

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

- Molecule 15 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	130	Total	C	N	O	S	0	0
			980	620	174	182	4		

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	141	Total	C	N	O	S	0	0
			1121	709	211	198	3		

- Molecule 17 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 19 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 20 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	O	115	Total	C	N	O	0	0
			884	548	177	159		

- Molecule 22 is a protein called 50S ribosomal protein L19.

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

- Molecule 23 is a protein called 50S ribosomal protein L20.

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

- Molecule 24 is a protein called 50S ribosomal protein L21.

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

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	109	Total	C	N	O	S	0	0
			849	527	165	155	2		

- Molecule 26 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	U	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 28 is a protein called 50S ribosomal protein L25.

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

- Molecule 29 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	W	2	Total	C	N	O	0	0
			16	12	2	2		

- Molecule 30 is a protein called 50S ribosomal protein L28.

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

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	58	Total	C	N	O	S	0	0
			477	294	93	89	1		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	56	Total	C	N	O	S	0	0
			434	272	84	76	2		

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

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

- Molecule 34 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	54	Total	C	N	O	S	0	0
			429	260	91	77	1		

- Molecule 35 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 36 is a protein called 50S ribosomal protein L34.

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

- Molecule 37 is a protein called 50S ribosomal protein L35.

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

- Molecule 38 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	37	Total	C	N	O	S	0	0
			297	183	64	46	4		

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 40 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 41 is a protein called 30S ribosomal protein S4.

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

- Molecule 42 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 43 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 44 is a protein called 30S ribosomal protein S7.

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

- Molecule 45 is a protein called 30S ribosomal protein S8.

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

- Molecule 46 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	126	Total	C	N	O	S	0	0
			1010	628	202	177	3		

- Molecule 47 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 48 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 49 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 50 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 51 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 52 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	87	Total	C	N	O	S	0	0
			708	436	143	128	1		

- Molecule 53 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 54 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 55 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 56 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 57 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

- Molecule 58 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 59 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	1	303	Total	Mg	0
			303	303	
59	2	118	Total	Mg	0
			118	118	
59	3	9	Total	Mg	0
			9	9	
59	7	1	Total	Mg	0
			1	1	
59	B	2	Total	Mg	0
			2	2	
59	C	1	Total	Mg	0
			1	1	
59	D	1	Total	Mg	0
			1	1	
59	L	1	Total	Mg	0
			1	1	
59	Q	2	Total	Mg	0
			2	2	
59	Z	1	Total	Mg	0
			1	1	
59	b	2	Total	Mg	0
			2	2	

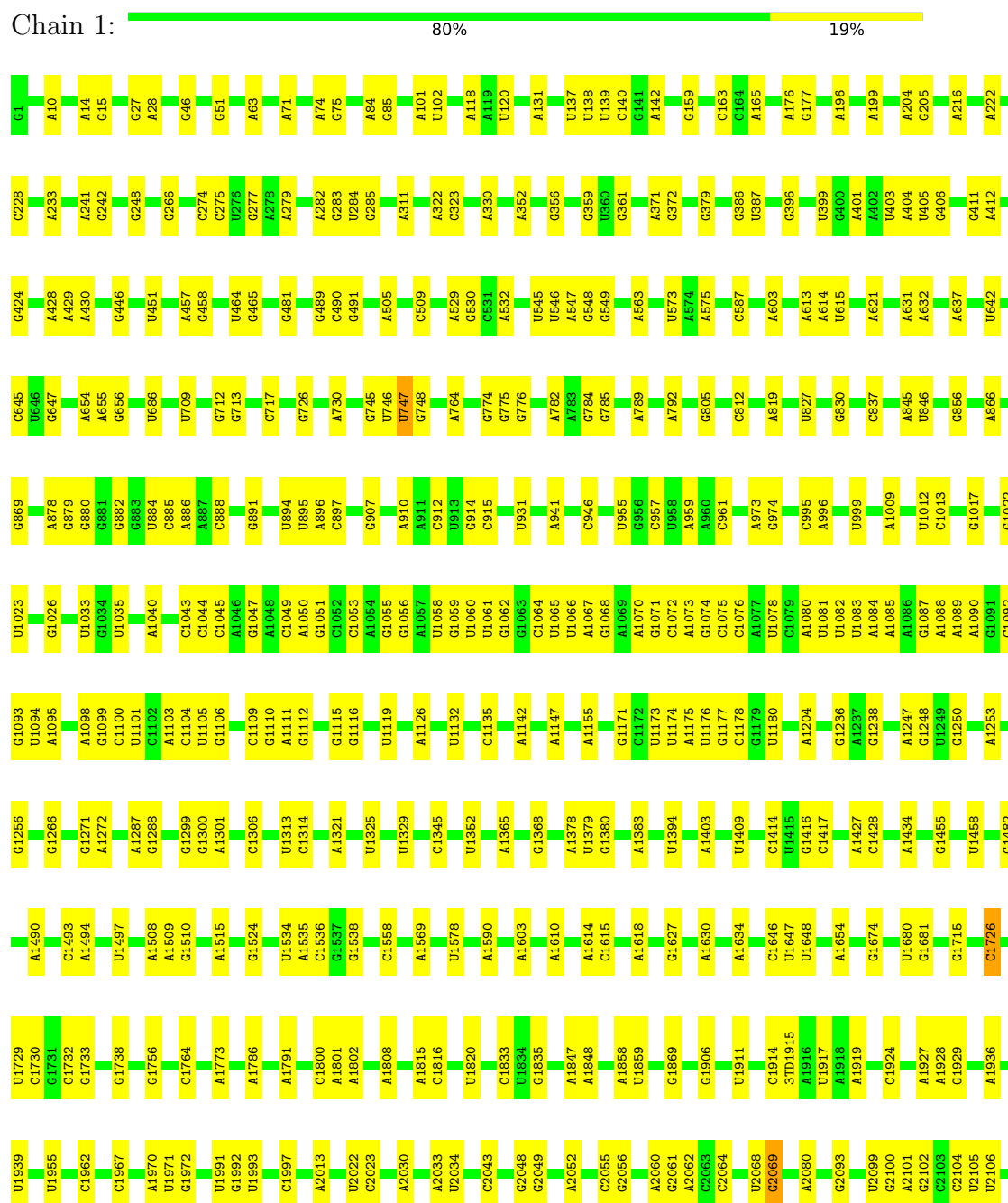
- Molecule 60 is ZINC ION (three-letter code: ZN) (formula: Zn).

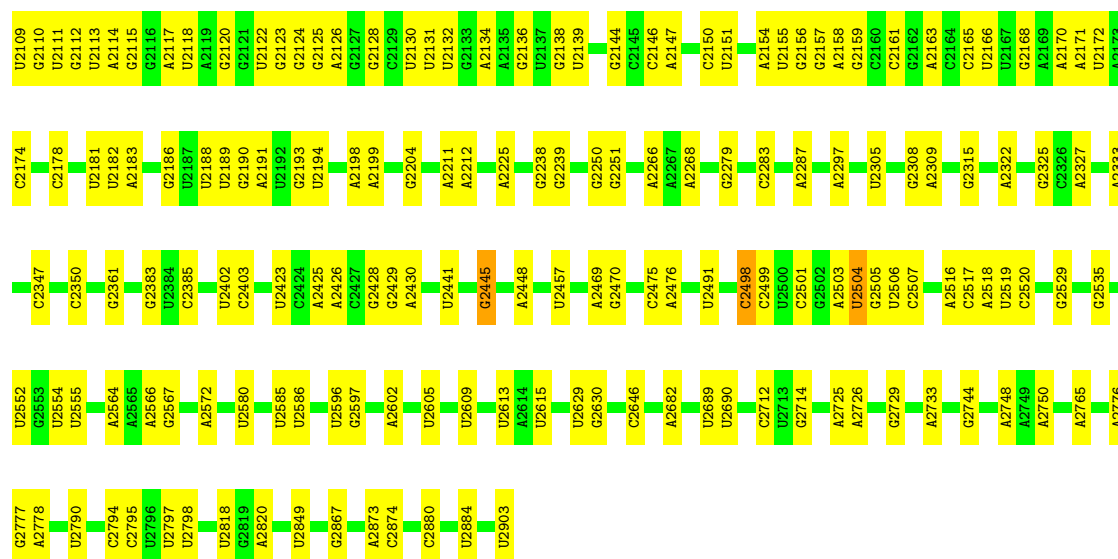
Mol	Chain	Residues	Atoms		AltConf
60	a	1	Total 1	Zn 1	0
60	f	1	Total 1	Zn 1	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

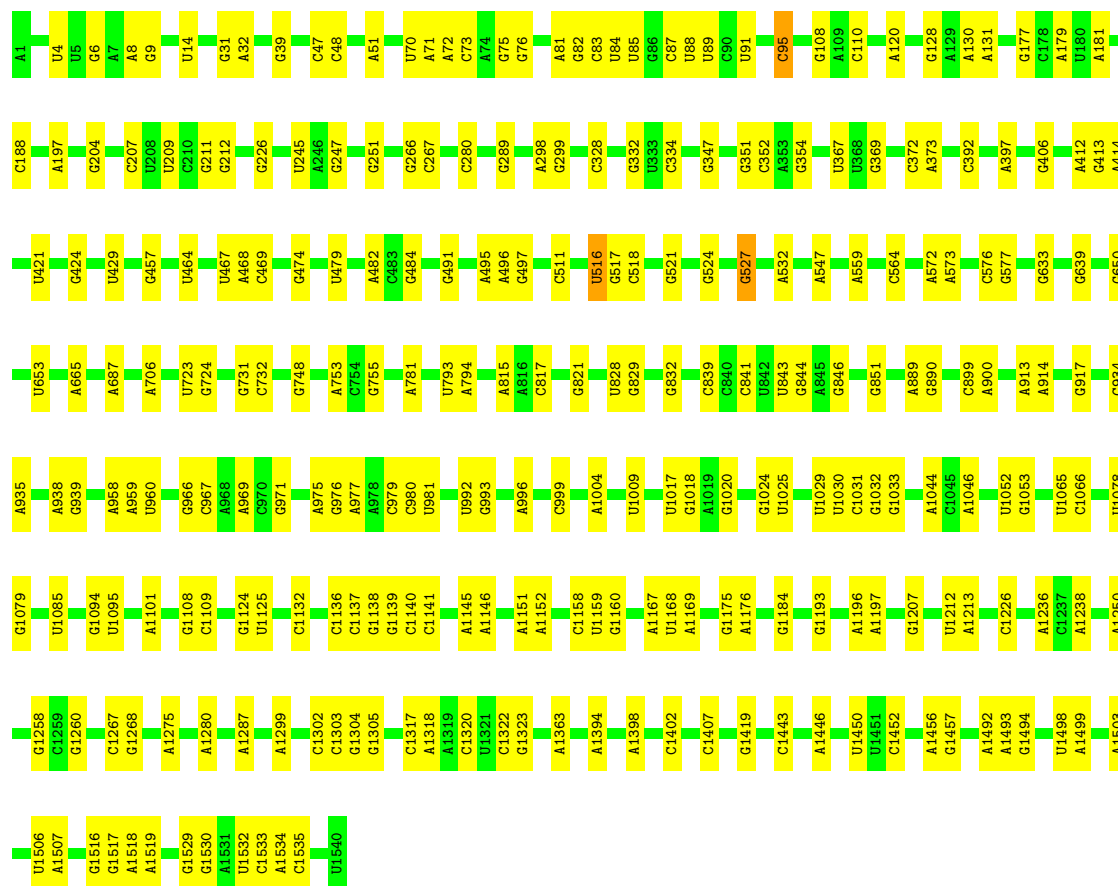
• Molecule 1: 23S ribosomal RNA





• Molecule 2: 16S ribosomal RNA

Chain 2: 83% 17%



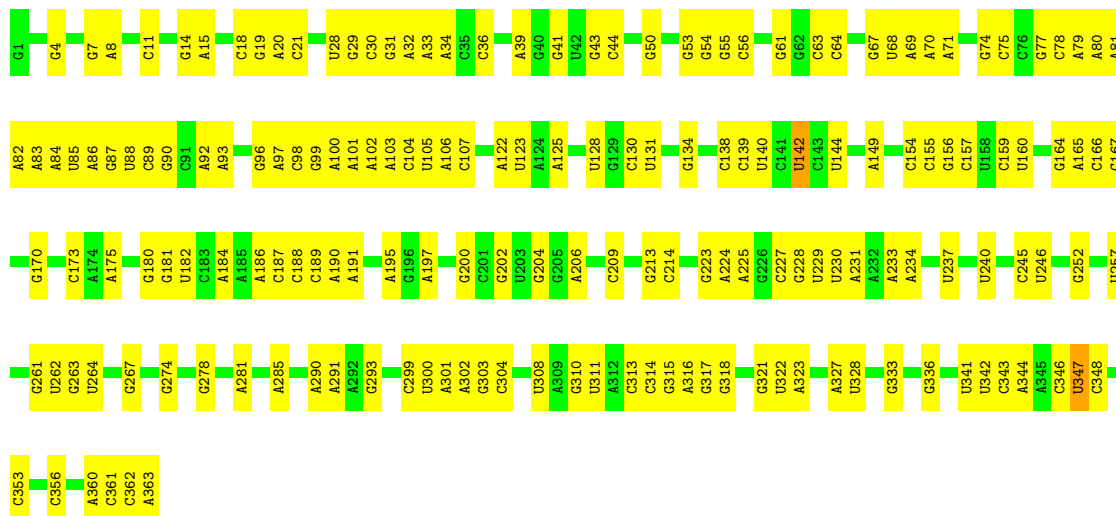
• Molecule 3: 5S ribosomal RNA

Chain 3: 89% 11%



• Molecule 4: transfer-messenger RNA (tmRNA)

Chain 4: 52% 47%



• Molecule 5: SsrA-binding protein

Chain 5: 90% 10%



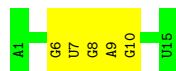
• Molecule 6: tRNA-Phe

Chain 7: 74% 24%



• Molecule 7: mRNA

Chain 8: 67% 33%



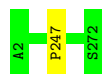
• Molecule 8: 50S ribosomal protein L27

Chain A: 96%



- Molecule 9: 50S ribosomal protein L2

Chain B:  100%



- Molecule 10: 50S ribosomal protein L3

Chain C:  100%

There are no outlier residues recorded for this chain.

- Molecule 11: 50S ribosomal protein L4

Chain D:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: 50S ribosomal protein L5

Chain E:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: 50S ribosomal protein L6

Chain F:  97%



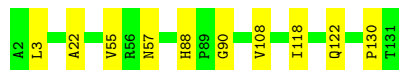
- Molecule 14: 50S ribosomal protein L9

Chain G:  99%



- Molecule 15: 50S ribosomal protein L10

Chain H:  92%



- Molecule 16: 50S ribosomal protein L13

Chain J:  100%

There are no outlier residues recorded for this chain.

- Molecule 17: 50S ribosomal protein L14

Chain K:  100%

There are no outlier residues recorded for this chain.

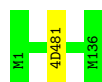
- Molecule 18: 50S ribosomal protein L15

Chain L:  100%

There are no outlier residues recorded for this chain.

- Molecule 19: 50S ribosomal protein L16

Chain M:  99%



- Molecule 20: 50S ribosomal protein L17

Chain N:  100%

There are no outlier residues recorded for this chain.

- Molecule 21: 50S ribosomal protein L18

Chain O:  100%

There are no outlier residues recorded for this chain.

- Molecule 22: 50S ribosomal protein L19

Chain P:  100%

There are no outlier residues recorded for this chain.

- Molecule 23: 50S ribosomal protein L20

Chain Q:  100%

There are no outlier residues recorded for this chain.

- Molecule 24: 50S ribosomal protein L21

Chain R:  100%

There are no outlier residues recorded for this chain.

- Molecule 25: 50S ribosomal protein L22

Chain S:  100%

There are no outlier residues recorded for this chain.

- Molecule 26: 50S ribosomal protein L23

Chain T:  100%

There are no outlier residues recorded for this chain.

- Molecule 27: 50S ribosomal protein L24

Chain U:  100%

There are no outlier residues recorded for this chain.

- Molecule 28: 50S ribosomal protein L25

Chain V:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: Nascent peptide

Chain W:  50% 50%



- Molecule 30: 50S ribosomal protein L28

Chain X:  100%

There are no outlier residues recorded for this chain.

- Molecule 31: 50S ribosomal protein L29

Chain Y:  100%

There are no outlier residues recorded for this chain.

- Molecule 32: 50S ribosomal protein L30

Chain Z:  100%

There are no outlier residues recorded for this chain.

- Molecule 33: 50S ribosomal protein L31

Chain a:  100%

There are no outlier residues recorded for this chain.

- Molecule 34: 50S ribosomal protein L32

Chain b:  100%

There are no outlier residues recorded for this chain.

- Molecule 35: 50S ribosomal protein L33

Chain c:  100%

There are no outlier residues recorded for this chain.

- Molecule 36: 50S ribosomal protein L34

Chain d:  100%

There are no outlier residues recorded for this chain.

- Molecule 37: 50S ribosomal protein L35

Chain e:  95% 5%



- Molecule 38: 50S ribosomal protein L36

Chain f:  100%

There are no outlier residues recorded for this chain.

- Molecule 39: 30S ribosomal protein S2

Chain g:  100%

There are no outlier residues recorded for this chain.

- Molecule 40: 30S ribosomal protein S3

Chain h:  100%



- Molecule 41: 30S ribosomal protein S4

Chain i:  100%


There are no outlier residues recorded for this chain.

- Molecule 42: 30S ribosomal protein S5

Chain j:  100%

There are no outlier residues recorded for this chain.

- Molecule 43: 30S ribosomal protein S6

Chain k:  100%

There are no outlier residues recorded for this chain.

- Molecule 44: 30S ribosomal protein S7

Chain l:  100%

There are no outlier residues recorded for this chain.

- Molecule 45: 30S ribosomal protein S8

Chain m:  100%

There are no outlier residues recorded for this chain.

- Molecule 46: 30S ribosomal protein S9

Chain n:  98%



- Molecule 47: 30S ribosomal protein S10

Chain o:  100%

There are no outlier residues recorded for this chain.

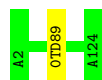
- Molecule 48: 30S ribosomal protein S11

Chain p:  99%



- Molecule 49: 30S ribosomal protein S12

Chain q:  99%



- Molecule 50: 30S ribosomal protein S13

Chain r:  100%

There are no outlier residues recorded for this chain.

- Molecule 51: 30S ribosomal protein S14

Chain s:  100%

There are no outlier residues recorded for this chain.

- Molecule 52: 30S ribosomal protein S15

Chain t:  100%

There are no outlier residues recorded for this chain.

- Molecule 53: 30S ribosomal protein S16

Chain u:  100%

There are no outlier residues recorded for this chain.

- Molecule 54: 30S ribosomal protein S17

Chain v:  100%

There are no outlier residues recorded for this chain.

- Molecule 55: 30S ribosomal protein S18

Chain w:  100%

There are no outlier residues recorded for this chain.

- Molecule 56: 30S ribosomal protein S19

Chain x:  100%

There are no outlier residues recorded for this chain.

- Molecule 57: 30S ribosomal protein S20

Chain y:  100%

There are no outlier residues recorded for this chain.

- Molecule 58: 30S ribosomal protein S21

Chain z:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36069	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29	Depositor
Minimum defocus (nm)	-700	Depositor
Maximum defocus (nm)	-2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 BASE (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, UR3, 4OC, 5MC, PSU, 0TD, MG, 2MG, MIA, 4D4, OMU, 2MA, 1MG, 6MZ, MA6, 3AU, OMC, 3TD, 4SU, ZN, H2U, G7M, OMG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.17	0/69286	0.74	5/108087 (0.0%)
2	2	0.17	0/36722	0.75	3/57278 (0.0%)
3	3	0.16	0/2872	0.75	0/4478
4	4	0.21	1/8615 (0.0%)	0.78	4/13430 (0.0%)
5	5	0.33	0/1213	0.64	1/1630 (0.1%)
6	7	0.18	0/1580	0.74	0/2459
7	8	0.20	0/363	0.76	0/566
8	A	0.26	0/642	0.45	0/848
9	B	0.27	1/2122 (0.0%)	0.44	0/2852
10	C	0.24	0/1586	0.45	0/2134
11	D	0.23	0/1571	0.40	0/2113
12	E	0.24	0/1435	0.43	0/1926
13	F	0.32	1/1333 (0.1%)	0.47	0/1805
14	G	0.34	1/1122 (0.1%)	0.52	2/1515 (0.1%)
15	H	0.25	0/993	0.45	0/1340
16	J	0.23	0/1144	0.41	0/1541
17	K	0.23	0/955	0.45	0/1279
18	L	0.24	0/1062	0.44	0/1413
19	M	0.25	0/1081	0.42	0/1443
20	N	0.23	0/964	0.41	0/1289
21	O	0.23	0/894	0.40	0/1198
22	P	0.23	0/929	0.44	0/1242
23	Q	0.23	0/960	0.34	0/1278
24	R	0.24	0/829	0.45	0/1107
25	S	0.23	0/856	0.44	0/1146
26	T	0.23	0/752	0.43	0/1005
27	U	0.24	0/796	0.42	0/1062
28	V	0.23	0/766	0.41	0/1025
29	W	1.13	0/16	1.22	0/20
30	X	0.23	0/635	0.47	0/848
31	Y	0.22	0/478	0.36	0/637

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Z	0.22	0/438	0.42	0/587
33	a	0.23	0/531	0.44	0/709
34	b	0.22	0/435	0.43	0/581
35	c	0.23	0/433	0.48	0/576
36	d	0.23	0/380	0.41	0/498
37	e	0.28	0/513	0.54	0/676
38	f	0.23	0/298	0.45	0/392
39	g	0.24	0/1791	0.39	0/2413
40	h	0.23	0/1663	0.41	0/2241
41	i	0.23	0/1665	0.42	0/2227
42	j	0.24	0/1165	0.43	0/1568
43	k	0.27	0/867	0.45	0/1171
44	l	0.23	0/1195	0.39	0/1602
45	m	0.24	0/989	0.46	0/1326
46	n	0.26	0/1022	0.47	0/1361
47	o	0.24	0/800	0.46	0/1082
48	p	0.36	1/893 (0.1%)	0.48	1/1205 (0.1%)
49	q	0.23	0/960	0.45	0/1286
50	r	0.23	0/900	0.43	0/1204
51	s	0.23	0/817	0.37	0/1088
52	t	0.22	0/716	0.36	0/956
53	u	0.23	0/653	0.43	0/877
54	v	0.22	0/658	0.45	0/881
55	w	0.23	0/544	0.39	0/731
56	x	0.23	0/675	0.44	0/908
57	y	0.24	0/670	0.35	0/888
58	z	0.23	0/597	0.41	0/792
All	All	0.20	5/166840 (0.0%)	0.68	16/249820 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	p	117	PRO	N-CD	-8.10	1.36	1.47
14	G	38	PRO	N-CD	-8.02	1.36	1.47
13	F	12	PRO	N-CD	-6.70	1.38	1.47
4	4	363	A	C3'-O3'	6.41	1.51	1.42
9	B	247	PRO	N-CD	-5.83	1.39	1.47

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1313	U	C2-N1-C1'	5.87	124.75	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	5	112	VAL	N-CA-CB	-5.82	98.71	111.50
1	1	837	C	N3-C2-O2	-5.63	117.96	121.90
4	4	142	U	N3-C4-O4	-5.62	115.47	119.40
2	2	979	C	C2-N1-C1'	5.56	124.92	118.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	5	145/147 (99%)	114 (79%)	29 (20%)	2 (1%)	9	32
8	A	82/84 (98%)	80 (98%)	2 (2%)	0	100	100
9	B	269/271 (99%)	266 (99%)	3 (1%)	0	100	100
10	C	207/209 (99%)	204 (99%)	3 (1%)	0	100	100
11	D	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
12	E	175/177 (99%)	168 (96%)	7 (4%)	0	100	100
13	F	173/175 (99%)	165 (95%)	8 (5%)	0	100	100
14	G	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
15	H	128/130 (98%)	98 (77%)	23 (18%)	7 (6%)	1	8
16	J	139/141 (99%)	138 (99%)	1 (1%)	0	100	100
17	K	121/123 (98%)	120 (99%)	1 (1%)	0	100	100
18	L	142/144 (99%)	137 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	M	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
20	N	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
21	O	113/115 (98%)	111 (98%)	2 (2%)	0	100	100
22	P	112/114 (98%)	112 (100%)	0	0	100	100
23	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
24	R	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
25	S	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
26	T	92/94 (98%)	92 (100%)	0	0	100	100
27	U	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
28	V	92/94 (98%)	92 (100%)	0	0	100	100
30	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
31	Y	56/58 (97%)	56 (100%)	0	0	100	100
32	Z	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
33	a	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
34	b	52/54 (96%)	52 (100%)	0	0	100	100
35	c	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
36	d	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
37	e	62/64 (97%)	57 (92%)	2 (3%)	3 (5%)	2	10
38	f	35/37 (95%)	35 (100%)	0	0	100	100
39	g	223/225 (99%)	219 (98%)	4 (2%)	0	100	100
40	h	206/208 (99%)	202 (98%)	4 (2%)	0	100	100
41	i	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
42	j	154/156 (99%)	147 (96%)	7 (4%)	0	100	100
43	k	102/104 (98%)	102 (100%)	0	0	100	100
44	l	149/151 (99%)	147 (99%)	2 (1%)	0	100	100
45	m	127/129 (98%)	127 (100%)	0	0	100	100
46	n	124/126 (98%)	120 (97%)	4 (3%)	0	100	100
47	o	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
48	p	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
49	q	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
50	r	113/115 (98%)	111 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	s	98/100 (98%)	98 (100%)	0	0	100	100
52	t	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
53	u	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
54	v	78/80 (98%)	72 (92%)	6 (8%)	0	100	100
55	w	63/65 (97%)	63 (100%)	0	0	100	100
56	x	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
57	y	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
58	z	68/70 (97%)	68 (100%)	0	0	100	100
All	All	5869/5973 (98%)	5678 (97%)	179 (3%)	12 (0%)	45	72

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	e	32	ILE
15	H	55	VAL
15	H	88	HIS
15	H	118	ILE
37	e	33	LEU

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	
5	5	123/123 (100%)	112 (91%)	11 (9%)	8	27
8	A	62/62 (100%)	59 (95%)	3 (5%)	21	49
9	B	216/216 (100%)	216 (100%)	0	100	100
10	C	164/164 (100%)	164 (100%)	0	100	100
11	D	165/165 (100%)	165 (100%)	0	100	100
12	E	148/148 (100%)	148 (100%)	0	100	100
13	F	136/136 (100%)	132 (97%)	4 (3%)	37	62
14	G	114/114 (100%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	H	99/99 (100%)	96 (97%)	3 (3%)	36	62
16	J	115/115 (100%)	115 (100%)	0	100	100
17	K	104/104 (100%)	104 (100%)	0	100	100
18	L	103/103 (100%)	103 (100%)	0	100	100
19	M	108/108 (100%)	108 (100%)	0	100	100
20	N	99/99 (100%)	99 (100%)	0	100	100
21	O	85/85 (100%)	85 (100%)	0	100	100
22	P	99/99 (100%)	99 (100%)	0	100	100
23	Q	89/89 (100%)	89 (100%)	0	100	100
24	R	84/84 (100%)	84 (100%)	0	100	100
25	S	92/92 (100%)	92 (100%)	0	100	100
26	T	81/81 (100%)	81 (100%)	0	100	100
27	U	84/84 (100%)	84 (100%)	0	100	100
28	V	78/78 (100%)	78 (100%)	0	100	100
29	W	1/1 (100%)	0	1 (100%)	0	0
30	X	67/67 (100%)	67 (100%)	0	100	100
31	Y	53/53 (100%)	53 (100%)	0	100	100
32	Z	47/47 (100%)	47 (100%)	0	100	100
33	a	59/59 (100%)	59 (100%)	0	100	100
34	b	46/46 (100%)	46 (100%)	0	100	100
35	c	47/47 (100%)	47 (100%)	0	100	100
36	d	38/38 (100%)	38 (100%)	0	100	100
37	e	51/51 (100%)	51 (100%)	0	100	100
38	f	34/34 (100%)	34 (100%)	0	100	100
39	g	187/187 (100%)	187 (100%)	0	100	100
40	h	171/171 (100%)	170 (99%)	1 (1%)	84	90
41	i	172/172 (100%)	172 (100%)	0	100	100
42	j	119/119 (100%)	119 (100%)	0	100	100
43	k	91/91 (100%)	91 (100%)	0	100	100
44	l	124/124 (100%)	124 (100%)	0	100	100
45	m	104/104 (100%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	n	104/104 (100%)	102 (98%)	2 (2%)	52	72
47	o	86/86 (100%)	86 (100%)	0	100	100
48	p	90/90 (100%)	90 (100%)	0	100	100
49	q	102/102 (100%)	102 (100%)	0	100	100
50	r	93/93 (100%)	93 (100%)	0	100	100
51	s	83/83 (100%)	83 (100%)	0	100	100
52	t	75/75 (100%)	75 (100%)	0	100	100
53	u	65/65 (100%)	65 (100%)	0	100	100
54	v	74/74 (100%)	74 (100%)	0	100	100
55	w	56/56 (100%)	56 (100%)	0	100	100
56	x	72/72 (100%)	72 (100%)	0	100	100
57	y	65/65 (100%)	65 (100%)	0	100	100
58	z	60/60 (100%)	60 (100%)	0	100	100
All	All	4884/4884 (100%)	4859 (100%)	25 (0%)	85	91

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	F	148	LEU
13	F	153	ARG
46	n	107	ASP
13	F	152	ARG
15	H	3	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
43	k	58	HIS
50	r	100	GLN
57	y	55	GLN
56	x	14	HIS
34	b	42	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2898/2903 (99%)	535 (18%)	25 (0%)
2	2	1535/1540 (99%)	244 (15%)	13 (0%)
3	3	119/120 (99%)	13 (10%)	0
4	4	362/363 (99%)	164 (45%)	14 (3%)
6	7	73/76 (96%)	12 (16%)	2 (2%)
7	8	14/15 (93%)	4 (28%)	2 (14%)
All	All	5001/5017 (99%)	972 (19%)	56 (1%)

5 of 972 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	14	A
1	1	15	G
1	1	27	G
1	1	28	A

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	938	A
7	8	9	A
2	2	1303	C
7	8	7	U
4	4	314	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

48 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	PSU	1	1911	1	18,21,22	1.10	1 (5%)	22,30,33	1.76	4 (18%)
1	5MU	1	747	1	19,22,23	4.90	7 (36%)	28,32,35	3.62	8 (28%)
1	6MZ	1	1618	1	18,25,26	2.10	3 (16%)	16,36,39	2.06	4 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	1	2504	1	18,21,22	1.08	1 (5%)	22,30,33	1.76	4 (18%)
4	PSU	4	342	4	18,21,22	1.11	1 (5%)	22,30,33	1.74	4 (18%)
2	MA6	2	1519	2	18,26,27	1.08	2 (11%)	19,38,41	4.39	3 (15%)
6	3AU	7	47	6	24,28,29	3.03	9 (37%)	33,40,43	1.30	3 (9%)
2	PSU	2	516	2	18,21,22	1.07	1 (5%)	22,30,33	1.69	5 (22%)
2	MA6	2	1518	2	18,26,27	1.05	2 (11%)	19,38,41	4.41	3 (15%)
2	5MC	2	967	2	18,22,23	3.60	7 (38%)	26,32,35	0.98	1 (3%)
1	2MA	1	2503	59,1	19,25,26	3.31	5 (26%)	21,37,40	1.69	2 (9%)
6	H2U	7	16	6	18,21,22	1.22	3 (16%)	21,30,33	1.79	3 (14%)
1	PSU	1	955	1	18,21,22	1.07	1 (5%)	22,30,33	1.75	4 (18%)
49	0TD	q	89	49	7,9,10	1.43	0	6,11,13	1.98	2 (33%)
1	PSU	1	2457	1	18,21,22	1.04	1 (5%)	22,30,33	1.71	3 (13%)
2	5MC	2	1407	2	18,22,23	3.62	7 (38%)	26,32,35	1.00	2 (7%)
4	5MU	4	341	4	19,22,23	4.89	7 (36%)	28,32,35	3.56	9 (32%)
6	H2U	7	20	6	18,21,22	1.10	2 (11%)	21,30,33	2.54	2 (9%)
1	PSU	1	1917	1	18,21,22	1.11	1 (5%)	22,30,33	1.77	4 (18%)
2	G7M	2	527	2	20,26,27	2.34	7 (35%)	17,39,42	1.06	1 (5%)
6	PSU	7	55	6	18,21,22	1.10	1 (5%)	22,30,33	1.73	4 (18%)
1	1MG	1	745	1	18,26,27	2.69	6 (33%)	19,39,42	1.44	3 (15%)
1	OMC	1	2498	59,1	19,22,23	3.05	8 (42%)	26,31,34	0.77	0
6	5MU	7	54	6	19,22,23	4.88	7 (36%)	28,32,35	3.56	9 (32%)
1	PSU	1	746	59,1	18,21,22	1.10	1 (5%)	22,30,33	1.79	5 (22%)
1	PSU	1	2580	1	18,21,22	1.07	1 (5%)	22,30,33	1.65	4 (18%)
1	PSU	1	2605	1	18,21,22	1.10	1 (5%)	22,30,33	1.76	4 (18%)
1	5MC	1	1962	1	18,22,23	3.61	7 (38%)	26,32,35	1.04	2 (7%)
1	5MU	1	1939	1	19,22,23	4.87	7 (36%)	28,32,35	3.63	9 (32%)
2	4OC	2	1402	2	20,23,24	3.28	9 (45%)	26,32,35	0.91	1 (3%)
2	2MG	2	1207	2	18,26,27	2.79	6 (33%)	16,38,41	1.32	3 (18%)
2	2MG	2	966	2	18,26,27	2.80	6 (33%)	16,38,41	1.44	3 (18%)
1	G7M	1	2069	1	20,26,27	2.33	7 (35%)	17,39,42	1.07	1 (5%)
6	4SU	7	8	6	18,21,22	3.74	8 (44%)	26,30,33	2.20	4 (15%)
1	OMG	1	2251	6,1	18,26,27	2.65	8 (44%)	19,38,41	1.51	4 (21%)
1	OMU	1	2552	1	19,22,23	3.21	7 (36%)	26,31,34	1.67	5 (19%)
1	2MG	1	1835	1	18,26,27	2.77	6 (33%)	16,38,41	1.36	3 (18%)
4	PSU	4	347	4	18,21,22	1.12	1 (5%)	22,30,33	1.75	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	3TD	1	1915	1	18,22,23	4.33	7 (38%)	22,32,35	1.60	3 (13%)
6	MIA	7	37	6	24,31,32	2.61	4 (16%)	26,44,47	3.13	8 (30%)
2	2MG	2	1516	2	18,26,27	2.79	6 (33%)	16,38,41	1.35	3 (18%)
6	PSU	7	39	6	18,21,22	1.08	1 (5%)	22,30,33	1.70	4 (18%)
1	6MZ	1	2030	1	18,25,26	2.05	3 (16%)	16,36,39	2.28	3 (18%)
6	G7M	7	46	6	20,26,27	4.14	10 (50%)	17,39,42	0.98	1 (5%)
6	PSU	7	32	6	18,21,22	1.07	1 (5%)	22,30,33	1.74	4 (18%)
1	2MG	1	2445	1	18,26,27	2.76	6 (33%)	16,38,41	1.37	4 (25%)
19	4D4	M	81	19	9,11,12	2.05	2 (22%)	8,13,15	1.84	3 (37%)
2	UR3	2	1498	2	19,22,23	2.99	6 (31%)	26,32,35	1.31	1 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	3/5/27/28	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
4	PSU	4	342	4	-	1/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	2/7/29/30	0/3/3/3
6	3AU	7	47	6	-	2/16/34/35	0/2/2/2
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/7/29/30	0/3/3/3
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	2MA	1	2503	59,1	-	2/3/25/26	0/3/3/3
6	H2U	7	16	6	-	1/7/38/39	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
49	0TD	q	89	49	-	4/7/12/14	-
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
4	5MU	4	341	4	-	0/7/25/26	0/2/2/2
6	H2U	7	20	6	-	6/7/38/39	0/2/2/2
1	PSU	1	1917	1	-	2/7/25/26	0/2/2/2
2	G7M	2	527	2	-	3/3/25/26	0/3/3/3
6	PSU	7	55	6	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	1MG	1	745	1	-	0/3/25/26	0/3/3/3
1	OMC	1	2498	59,1	-	2/9/27/28	0/2/2/2
6	5MU	7	54	6	-	2/7/25/26	0/2/2/2
1	PSU	1	746	59,1	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	3/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	2MG	2	1207	2	-	0/5/27/28	0/3/3/3
2	2MG	2	966	2	-	0/5/27/28	0/3/3/3
1	G7M	1	2069	1	-	2/3/25/26	0/3/3/3
6	4SU	7	8	6	-	0/7/25/26	0/2/2/2
1	OMG	1	2251	6,1	-	0/5/27/28	0/3/3/3
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
1	2MG	1	1835	1	-	2/5/27/28	0/3/3/3
4	PSU	4	347	4	-	2/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2
6	MIA	7	37	6	-	5/11/33/34	0/3/3/3
2	2MG	2	1516	2	-	0/5/27/28	0/3/3/3
6	PSU	7	39	6	-	0/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	2/5/27/28	0/3/3/3
6	G7M	7	46	6	-	3/3/25/26	0/3/3/3
6	PSU	7	32	6	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/5/27/28	0/3/3/3
19	4D4	M	81	19	-	5/11/12/14	-
2	UR3	2	1498	2	-	2/7/25/26	0/2/2/2

The worst 5 of 211 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	12.55	1.49	1.35
1	1	747	5MU	C2-N1	11.45	1.56	1.38
6	7	54	5MU	C2-N1	11.29	1.56	1.38
4	4	341	5MU	C2-N1	11.23	1.56	1.38
1	1	1939	5MU	C2-N1	11.12	1.56	1.38

The worst 5 of 173 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1518	MA6	C1'-N9-C4	14.05	151.33	126.64
2	2	1519	MA6	C1'-N9-C4	13.76	150.82	126.64
1	1	1939	5MU	C5-C4-N3	12.03	125.58	115.31
1	1	747	5MU	C5-C4-N3	11.95	125.52	115.31
6	7	54	5MU	C5-C4-N3	11.93	125.50	115.31

There are no chirality outliers.

5 of 67 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	M	81	4D4	C-CA-CB-OB
19	M	81	4D4	C-CA-CB-CG
19	M	81	4D4	N-CA-CB-OB
19	M	81	4D4	N-CA-CB-CG
49	q	89	0TD	SB-CB-CG-OD2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 443 ligands modelled in this entry, 443 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.