



wwPDB EM Validation Summary Report ⓘ

Apr 16, 2024 – 02:19 pm BST

PDB ID : 5L3P
EMDB ID : EMD-4001
Title : Cryo-EM structure of stringent response factor RelA bound to ErmCL-stalled ribosome complex
Authors : Arenz, S.; Wilson, D.N.
Deposited on : 2016-05-24
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

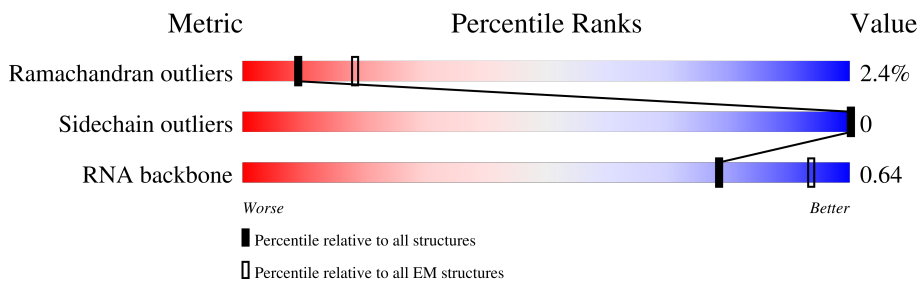
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



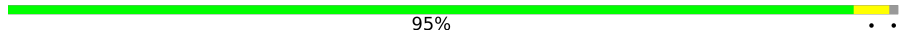

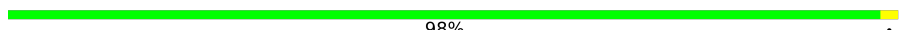

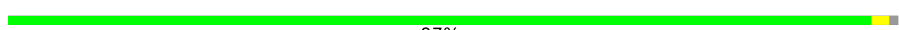





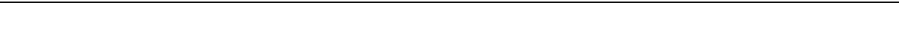

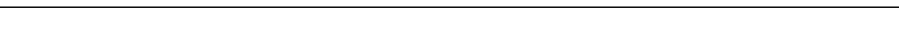
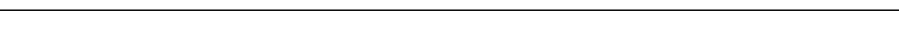
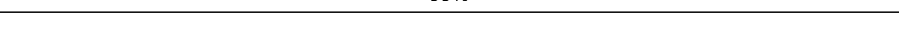
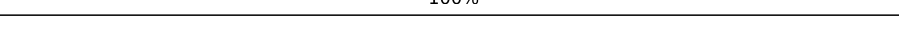
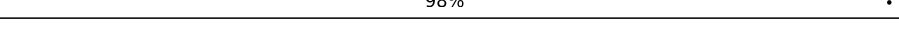
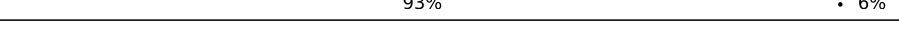
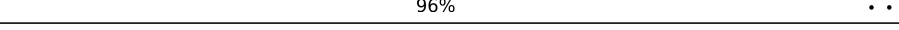

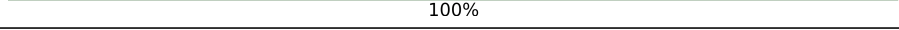
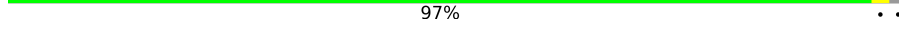
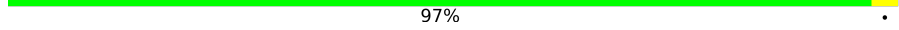


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	2903	84% 15%
2	B	120	88% 12%
3	D	273	99% .
4	E	209	99% .
5	F	201	98% .
6	G	179	97% ..
7	H	177	98% ..
8	I	149	97% .
9	N	142	99% .

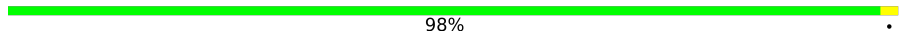



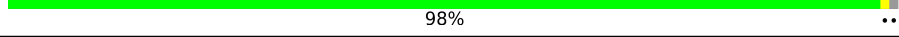
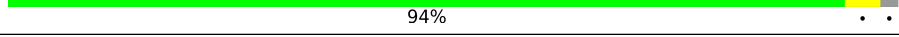


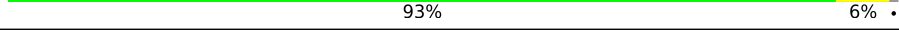
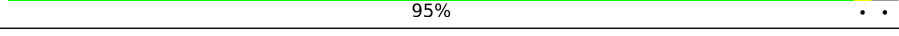
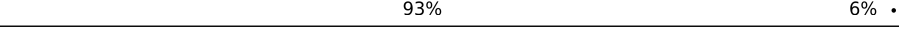
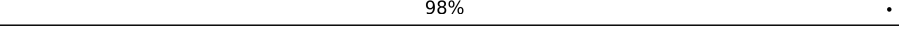
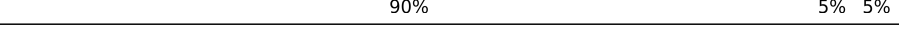
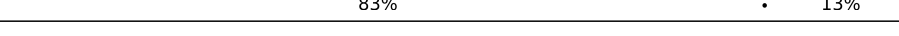
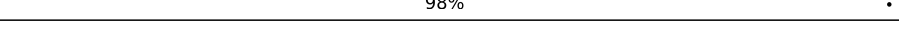

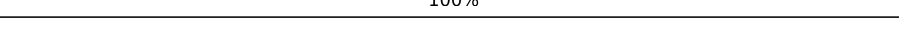
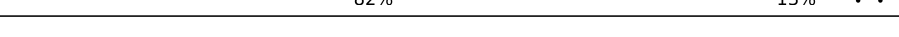
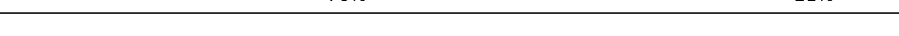

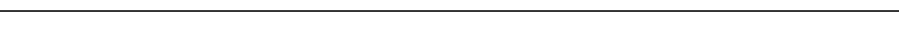

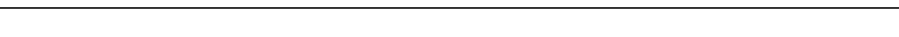
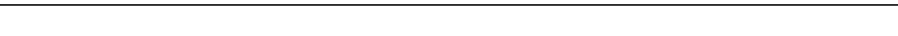
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Mol	Chain	Length	Quality of chain
10	O	123	95% 
11	P	144	95% 
12	Q	136	98% 
13	R	127	92% 
14	S	117	97% 
15	T	115	99% 
16	U	118	99% 
17	V	103	96% 
18	W	110	100% 
19	X	100	91% 
20	Y	104	96% 
21	Z	94	100% 
22	0	85	87% 
23	1	78	99% 
24	2	63	100% 
25	3	59	98% 
26	4	70	93% 
27	5	57	96% 
28	6	55	89% 
29	7	46	100% 
30	8	65	97% 
31	9	38	97% 
32	a	1539	88% 
33	b	240	89% 
34	c	233	88% 

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Mol	Chain	Length	Quality of chain
35	d	206	 98%
36	e	167	 90% 6%
37	f	135	 71% 26%
38	g	179	 81% 16%
39	h	130	 98%
40	i	130	 94%
41	j	103	 89% 6% 5%
42	k	129	 87% 10%
43	l	124	 93% 6%
44	m	118	 95%
45	o	89	 93% 6%
46	p	82	 98%
47	q	84	 90% 5% 5%
48	r	75	 83% 13%
49	t	87	 98%
50	u	71	 85% 7% 8%
51	v	6	 100%
52	x	77	 82% 13%
53	J	165	 76% 21%
54	K	142	 94% 5%
55	n	102	 95%
56	s	92	 85% 14%
57	z	819	 65% 33%
58	y	73	 59% 33% 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	2MG	A	1835	X	-	-	-
1	PSU	A	1911	X	-	-	-
1	3TD	A	1915	X	-	-	-
1	PSU	A	1917	X	-	-	-
1	5MU	A	1939	X	-	-	-
1	7MG	A	2069	X	-	-	-
1	OMG	A	2251	X	-	-	-
1	2MG	A	2445	X	-	-	-
1	H2U	A	2449	X	-	-	-
1	PSU	A	2457	X	-	-	-
1	OMC	A	2498	X	-	-	-
1	2MA	A	2503	X	-	-	-
1	PSU	A	2504	X	-	-	-
1	OMU	A	2552	X	-	-	-
1	PSU	A	2580	X	-	-	-
1	PSU	A	2604	X	-	-	-
1	PSU	A	2605	X	-	-	-
1	PSU	A	746	X	-	-	-
1	PSU	A	955	X	-	-	-
32	2MG	a	1207	X	-	-	-
32	4OC	a	1402	X	-	-	-
32	UR3	a	1498	X	-	-	-
32	2MG	a	1516	X	-	-	-
32	MA6	a	1518	X	-	-	-
32	MA6	a	1519	X	-	-	-
32	PSU	a	516	X	-	-	-
32	7MG	a	527	X	-	-	-
32	2MG	a	966	X	-	-	-
52	H2U	x	20	X	-	-	-
52	5MU	x	54	X	-	-	-
52	PSU	x	55	X	-	-	-
52	4SU	x	8	X	-	-	-
58	H2U	y	16	X	-	-	-
58	H2U	y	17	X	-	-	-
58	H2U	y	20	X	-	-	-
58	7MG	y	46	X	-	-	-
58	5MU	y	54	X	-	-	-
58	PSU	y	55	X	-	-	-

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 149606 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
			Total	C	N	O	P		
1	A	2890	62057	27688	11422	20057	2890	0	0

There is a discrepancy between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	120	A	U	conflict	GB 999944586

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	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	G	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	H	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	I	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

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

- Molecule 11 is a protein called 50S ribosomal protein L15.

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

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

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

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

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

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	Y	102	779	492	146	141		0	0

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	0	75	575	356	116	102	1	0	0

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	1	77	625	388	129	106	2	0	0

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	2	63	509	313	99	95	2	0	0

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	3	58	449	281	87	79	2	0	0

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	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	6	50	Total	C	N	O	0	0
			409	263	75	71		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	7	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	8	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	9	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1539	Total	C	N	O	P	0	0
			33029	14738	6052	10700	1539		

- Molecule 33 is a protein called 30S ribosomal protein S2.

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

- Molecule 34 is a protein called 30S ribosomal protein S3.

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

- Molecule 35 is a protein called 30S ribosomal protein S4.

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

- Molecule 36 is a protein called 30S ribosomal protein S5.

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

- Molecule 37 is a protein called 30S ribosomal protein S6.

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

- Molecule 38 is a protein called 30S ribosomal protein S7.

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

- Molecule 39 is a protein called 30S ribosomal protein S8.

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

- Molecule 40 is a protein called 30S ribosomal protein S9.

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

- Molecule 41 is a protein called 30S ribosomal protein S10.

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

- Molecule 42 is a protein called 30S ribosomal protein S11.

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

- Molecule 43 is a protein called 30S ribosomal protein S12.

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

- Molecule 44 is a protein called 30S ribosomal protein S13.

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

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

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

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

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

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

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

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

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

- Molecule 49 is a protein called 30S ribosomal protein S20.

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

- Molecule 50 is a protein called 30S ribosomal protein S21.

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

- Molecule 51 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	6	Total	C	N	O	P	0	0
			129	58	24	41	6		

- Molecule 52 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	x	77	Total	C	N	O	P	S	0	0
			1644	733	297	536	77	1		

- Molecule 53 is a protein called 50S ribosomal protein L10.

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

- Molecule 54 is a protein called 50S ribosomal protein L11.

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

- Molecule 55 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	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 56 is a protein called 30S ribosomal protein S19.

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

- Molecule 57 is a protein called GTP pyrophosphokinase,GTP pyrophosphokinase,GTP pyrophosphokinase.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	z	545	Total	C	N	O	0	0
			2255	1165	545	545		

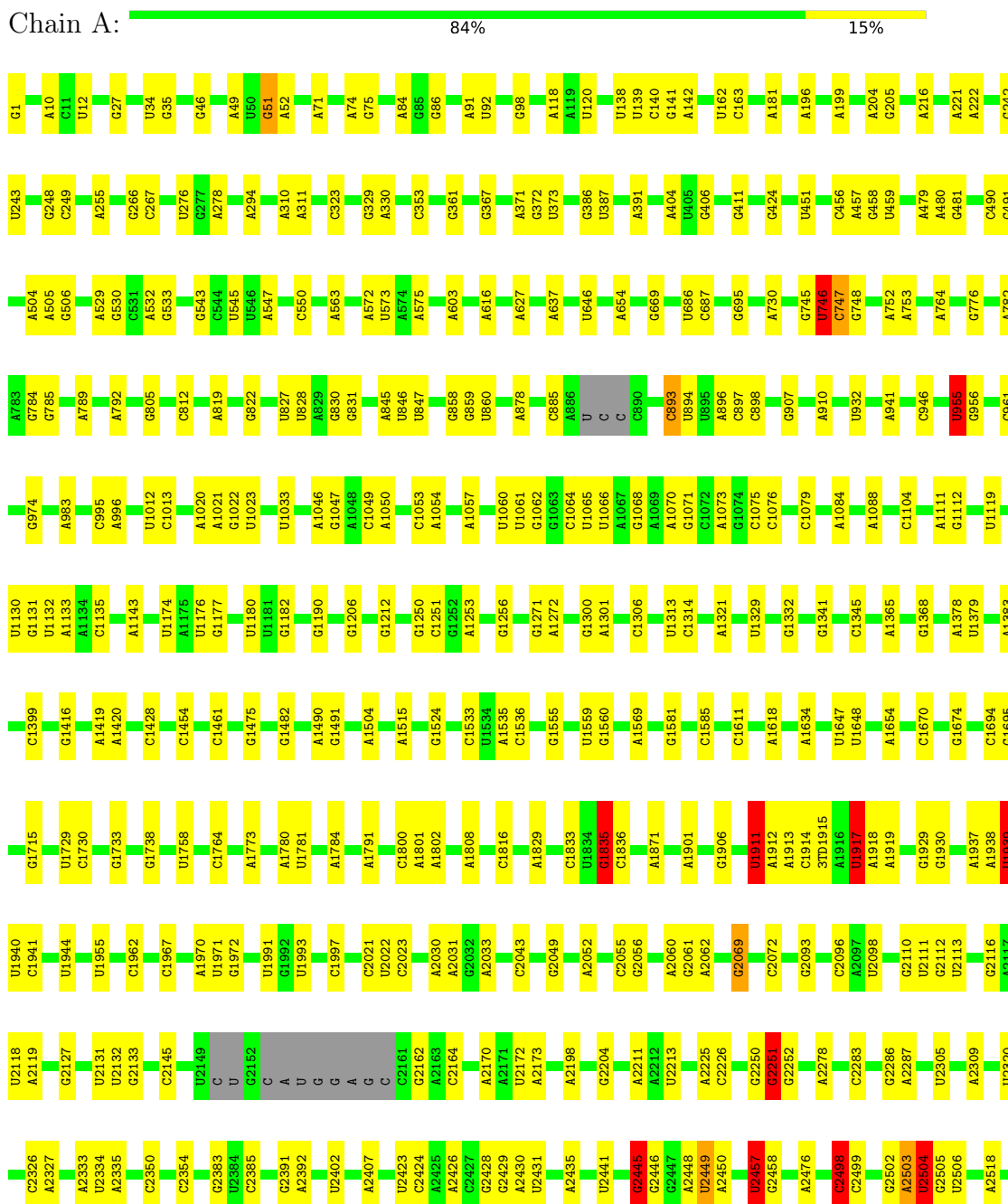
- Molecule 58 is a RNA chain called deacylated A/R-tRNA.

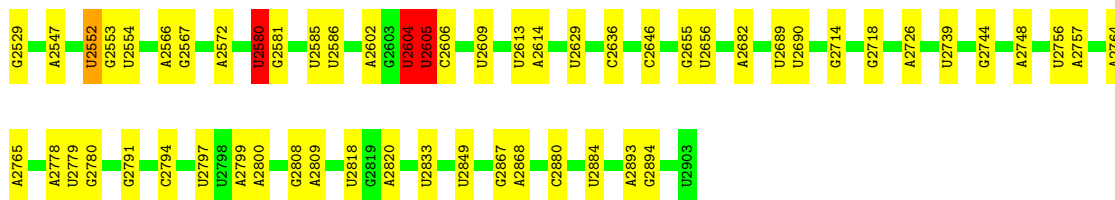
Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	73	Total	C	N	O	P	0	0
			1581	709	280	519	73		

3 Residue-property plots

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





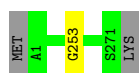
- Molecule 2: 5S ribosomal RNA

Chain B: 88% 12%



- Molecule 3: 50S ribosomal protein L2

Chain D: 99%



- Molecule 4: 50S ribosomal protein L3

Chain E: 99%



- Molecule 5: 50S ribosomal protein L4

Chain F: 98%



- Molecule 6: 50S ribosomal protein L5

Chain G: 97%



- Molecule 7: 50S ribosomal protein L6

Chain H: 98%



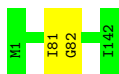
- Molecule 8: 50S ribosomal protein L9

Chain I:  97%



- Molecule 9: 50S ribosomal protein L13

Chain N:  99%



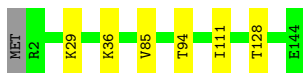
- Molecule 10: 50S ribosomal protein L14

Chain O:  95%



- Molecule 11: 50S ribosomal protein L15

Chain P:  95%



- Molecule 12: 50S ribosomal protein L16

Chain Q:  98%



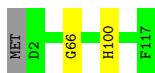
- Molecule 13: 50S ribosomal protein L17

Chain R:  92% 6%



- Molecule 14: 50S ribosomal protein L18

Chain S:  97%



- Molecule 15: 50S ribosomal protein L19

Chain T:  99%



- Molecule 16: 50S ribosomal protein L20

Chain U:  99%



- Molecule 17: 50S ribosomal protein L21

Chain V:  96%



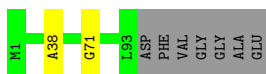
- Molecule 18: 50S ribosomal protein L22

Chain W:  100%

There are no outlier residues recorded for this chain.

- Molecule 19: 50S ribosomal protein L23

Chain X:  91% 7%



- Molecule 20: 50S ribosomal protein L24

Chain Y:  96%




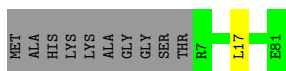
- Molecule 21: 50S ribosomal protein L25

Chain Z:  100%

There are no outlier residues recorded for this chain.

- Molecule 22: 50S ribosomal protein L27

Chain 0:  87% 12%



- Molecule 23: 50S ribosomal protein L28

Chain 1: 99%



- Molecule 24: 50S ribosomal protein L29

Chain 2: 100%

There are no outlier residues recorded for this chain.

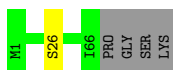
- Molecule 25: 50S ribosomal protein L30

Chain 3: 98%



- Molecule 26: 50S ribosomal protein L31

Chain 4: 93% • 6%



- Molecule 27: 50S ribosomal protein L32

Chain 5: 96% ••



- Molecule 28: 50S ribosomal protein L33

Chain 6: 89% • 9%



- Molecule 29: 50S ribosomal protein L34

Chain 7: 100%

There are no outlier residues recorded for this chain.


- Molecule 30: 50S ribosomal protein L35

- Molecule 35: 30S ribosomal protein S4

Chain d:  98%



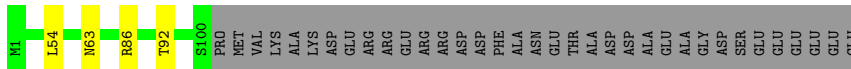
- Molecule 36: 30S ribosomal protein S5

Chain e:  90% 6%




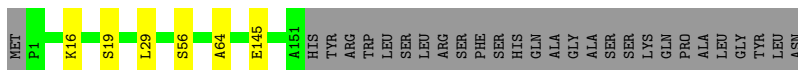
- Molecule 37: 30S ribosomal protein S6

Chain f:  71% 26%



- Molecule 38: 30S ribosomal protein S7

Chain g:  81% 16%



- Molecule 39: 30S ribosomal protein S8

Chain h:  98%




- Molecule 40: 30S ribosomal protein S9

Chain i:  94%




- Molecule 41: 30S ribosomal protein S10

Chain j:  89% 6% 5%



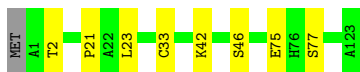
- Molecule 42: 30S ribosomal protein S11

Chain k:  87% 10%



- Molecule 43: 30S ribosomal protein S12

Chain l:  93% 6%



- Molecule 44: 30S ribosomal protein S13

Chain m:  95%



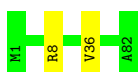
- Molecule 45: 30S ribosomal protein S15

Chain o:  93% 6%




- Molecule 46: 30S ribosomal protein S16

Chain p:  98%




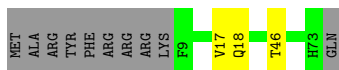
- Molecule 47: 30S ribosomal protein S17

Chain q:  90% 5% 5%



- Molecule 48: 30S ribosomal protein S18

Chain r:  83% 13%




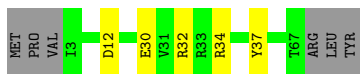
- Molecule 49: 30S ribosomal protein S20

Chain t:  98%



- Molecule 50: 30S ribosomal protein S21

Chain u:  85% 7% 8%




- Molecule 51: mRNA

Chain v:  100%


There are no outlier residues recorded for this chain.

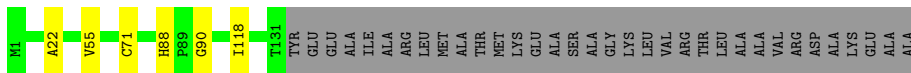
- Molecule 52: P-site tRNA

Chain x:  82% 13%



- Molecule 53: 50S ribosomal protein L10

Chain J:  76% 21%



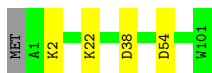
- Molecule 54: 50S ribosomal protein L11

Chain K:  94% 5%




- Molecule 55: 30S ribosomal protein S14

Chain n:  95%



- Molecule 56: 30S ribosomal protein S19

Chain s:  85% 14%

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24749	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (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: OMC, 2MG, 6MZ, OMU, 7MG, H2U, 5MC, UR3, 4SU, 1MG, 5MU, PSU, 3TD, 2MA, OMG, 4OC, YG, MA6

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.12	1/68920 (0.0%)	0.67	20/107498 (0.0%)
2	B	0.23	1/2876 (0.0%)	0.65	0/4483
3	D	0.20	0/2121	0.39	0/2852
4	E	0.21	0/1586	0.38	0/2134
5	F	0.20	0/1571	0.37	0/2113
6	G	0.21	0/1434	0.40	0/1926
7	H	0.20	0/1343	0.37	0/1816
8	I	0.21	0/1122	0.38	0/1515
9	N	0.21	0/1152	0.39	0/1551
10	O	0.20	0/947	0.40	0/1268
11	P	0.20	0/1054	0.39	0/1403
12	Q	0.21	0/1093	0.41	0/1460
13	R	0.21	0/973	0.39	0/1301
14	S	0.20	0/902	0.35	0/1209
15	T	0.20	0/929	0.41	0/1242
16	U	0.21	0/960	0.35	0/1278
17	V	0.21	0/829	0.38	0/1107
18	W	0.19	0/864	0.39	0/1156
19	X	0.20	0/744	0.39	0/994
20	Y	0.21	0/787	0.37	0/1051
21	Z	0.20	0/766	0.36	0/1025
22	0	0.20	0/582	0.35	0/769
23	1	0.19	0/635	0.36	0/848
24	2	0.21	0/510	0.36	0/677
25	3	0.21	0/453	0.41	0/605
26	4	0.21	0/531	0.40	0/709
27	5	0.19	0/450	0.36	0/599
28	6	0.21	0/416	0.41	0/554
29	7	0.20	0/380	0.36	0/498
30	8	0.21	0/513	0.42	0/676
31	9	0.19	0/303	0.38	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	a	0.13	1/36701 (0.0%)	0.66	5/57246 (0.0%)
33	b	0.21	0/1735	0.39	0/2338
34	c	0.21	0/1651	0.41	0/2225
35	d	0.21	0/1665	0.38	0/2227
36	e	0.22	0/1154	0.41	0/1554
37	f	0.21	0/835	0.39	0/1128
38	g	0.20	0/1195	0.39	0/1602
39	h	0.21	0/989	0.40	0/1326
40	i	0.21	0/1034	0.40	0/1375
41	j	0.21	0/796	0.42	0/1077
42	k	0.20	0/885	0.39	0/1195
43	l	0.21	0/969	0.42	0/1300
44	m	0.20	0/892	0.41	0/1193
45	o	0.20	0/722	0.35	0/964
46	p	0.20	0/659	0.35	0/884
47	q	0.22	0/657	0.43	0/881
48	r	0.20	0/511	0.40	0/689
49	t	0.20	0/671	0.34	0/888
50	u	0.21	0/500	0.38	0/668
51	v	0.10	0/144	0.64	0/222
52	x	0.27	1/1747 (0.1%)	0.64	0/2721
53	J	0.22	0/1001	0.43	0/1350
54	K	0.21	0/1046	0.41	0/1410
55	n	0.20	0/811	0.37	0/1081
56	s	0.20	0/652	0.37	0/877
57	z	0.16	0/1874	0.32	0/2332
58	y	0.29	1/1585 (0.1%)	0.66	0/2469
All	All	0.16	5/160827 (0.0%)	0.60	25/239936 (0.0%)

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
1	A	35	0
32	a	17	0
52	x	9	0
58	y	9	0
All	All	70	0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	U	OP3-P	-10.62	1.48	1.61
58	y	1	G	OP3-P	-10.62	1.48	1.61
52	x	1	C	OP3-P	-10.58	1.48	1.61
32	a	2	A	OP3-P	-10.57	1.48	1.61
1	A	1	G	OP3-P	-10.54	1.48	1.61

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1049	C	C2-N3-C4	18.01	128.91	119.90
1	A	1050	A	N1-C2-N3	16.54	137.57	129.30
1	A	1073	A	N1-C2-N3	16.48	137.54	129.30
1	A	1050	A	C2-N3-C4	12.07	116.63	110.60
1	A	1073	A	C2-N3-C4	11.70	116.45	110.60

5 of 70 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	746	PSU	C4',C2'
1	A	955	PSU	C4',C2'
1	A	1835	2MG	C2',C3'
1	A	1911	PSU	C4',C2'
1	A	1915	3TD	C4'

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	
3	D	269/273 (98%)	243 (90%)	25 (9%)	1 (0%)	34	69
4	E	207/209 (99%)	187 (90%)	17 (8%)	3 (1%)	11	45
5	F	199/201 (99%)	184 (92%)	11 (6%)	4 (2%)	7	39
6	G	175/179 (98%)	154 (88%)	18 (10%)	3 (2%)	9	42
7	H	174/177 (98%)	149 (86%)	23 (13%)	2 (1%)	14	50
8	I	147/149 (99%)	129 (88%)	14 (10%)	4 (3%)	5	33
9	N	140/142 (99%)	130 (93%)	8 (6%)	2 (1%)	11	45
10	O	120/123 (98%)	108 (90%)	7 (6%)	5 (4%)	3	25
11	P	141/144 (98%)	122 (86%)	13 (9%)	6 (4%)	2	24
12	Q	134/136 (98%)	123 (92%)	8 (6%)	3 (2%)	6	37
13	R	118/127 (93%)	103 (87%)	12 (10%)	3 (2%)	5	35
14	S	114/117 (97%)	106 (93%)	6 (5%)	2 (2%)	8	41
15	T	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
16	U	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
17	V	101/103 (98%)	91 (90%)	6 (6%)	4 (4%)	3	26
18	W	108/110 (98%)	94 (87%)	14 (13%)	0	100	100
19	X	91/100 (91%)	81 (89%)	8 (9%)	2 (2%)	6	37
20	Y	100/104 (96%)	87 (87%)	11 (11%)	2 (2%)	7	39
21	Z	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
22	0	73/85 (86%)	68 (93%)	4 (6%)	1 (1%)	11	45
23	1	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
24	2	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
25	3	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
26	4	64/70 (91%)	56 (88%)	7 (11%)	1 (2%)	9	43
27	5	54/57 (95%)	51 (94%)	2 (4%)	1 (2%)	8	40
28	6	48/55 (87%)	43 (90%)	4 (8%)	1 (2%)	7	38
29	7	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
30	8	62/65 (95%)	58 (94%)	3 (5%)	1 (2%)	9	43
31	9	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	5	33
33	b	216/240 (90%)	187 (87%)	25 (12%)	4 (2%)	8	40
34	c	204/233 (88%)	188 (92%)	14 (7%)	2 (1%)	15	51
35	d	203/206 (98%)	180 (89%)	19 (9%)	4 (2%)	7	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	e	155/167 (93%)	132 (85%)	17 (11%)	6 (4%)	3	27
37	f	98/135 (73%)	85 (87%)	9 (9%)	4 (4%)	3	26
38	g	149/179 (83%)	130 (87%)	13 (9%)	6 (4%)	3	26
39	h	127/130 (98%)	115 (91%)	11 (9%)	1 (1%)	19	56
40	i	125/130 (96%)	107 (86%)	13 (10%)	5 (4%)	3	26
41	j	96/103 (93%)	79 (82%)	11 (12%)	6 (6%)	1	17
42	k	114/129 (88%)	99 (87%)	11 (10%)	4 (4%)	3	30
43	l	121/124 (98%)	104 (86%)	9 (7%)	8 (7%)	1	16
44	m	112/118 (95%)	103 (92%)	7 (6%)	2 (2%)	8	41
45	o	86/89 (97%)	76 (88%)	5 (6%)	5 (6%)	1	19
46	p	80/82 (98%)	71 (89%)	7 (9%)	2 (2%)	5	35
47	q	78/84 (93%)	65 (83%)	9 (12%)	4 (5%)	2	21
48	r	63/75 (84%)	56 (89%)	4 (6%)	3 (5%)	2	22
49	t	83/87 (95%)	80 (96%)	3 (4%)	0	100	100
50	u	63/71 (89%)	48 (76%)	10 (16%)	5 (8%)	1	12
53	J	129/165 (78%)	102 (79%)	21 (16%)	6 (5%)	2	23
54	K	139/142 (98%)	118 (85%)	14 (10%)	7 (5%)	2	22
55	n	99/102 (97%)	87 (88%)	8 (8%)	4 (4%)	3	26
56	s	77/92 (84%)	71 (92%)	5 (6%)	1 (1%)	12	47
57	z	458/819 (56%)	423 (92%)	24 (5%)	11 (2%)	6	35
All	All	6305/7039 (90%)	5637 (89%)	516 (8%)	152 (2%)	9	35

5 of 152 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	N	81	ILE
11	P	128	THR
34	c	96	VAL
34	c	156	LEU
36	e	122	VAL

5.3.2 Protein sidechains [i](#)

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	D	216/218 (99%)	216 (100%)	0	100	100
4	E	164/164 (100%)	164 (100%)	0	100	100
5	F	165/165 (100%)	165 (100%)	0	100	100
6	G	148/150 (99%)	148 (100%)	0	100	100
7	H	137/138 (99%)	137 (100%)	0	100	100
8	I	114/114 (100%)	114 (100%)	0	100	100
9	N	116/116 (100%)	116 (100%)	0	100	100
10	O	103/104 (99%)	103 (100%)	0	100	100
11	P	102/103 (99%)	102 (100%)	0	100	100
12	Q	109/109 (100%)	109 (100%)	0	100	100
13	R	100/103 (97%)	100 (100%)	0	100	100
14	S	86/87 (99%)	86 (100%)	0	100	100
15	T	99/100 (99%)	99 (100%)	0	100	100
16	U	89/90 (99%)	89 (100%)	0	100	100
17	V	84/84 (100%)	84 (100%)	0	100	100
18	W	93/93 (100%)	93 (100%)	0	100	100
19	X	80/84 (95%)	80 (100%)	0	100	100
20	Y	83/85 (98%)	83 (100%)	0	100	100
21	Z	78/78 (100%)	78 (100%)	0	100	100
22	0	57/63 (90%)	57 (100%)	0	100	100
23	1	67/68 (98%)	67 (100%)	0	100	100
24	2	55/55 (100%)	55 (100%)	0	100	100
25	3	48/49 (98%)	48 (100%)	0	100	100
26	4	59/62 (95%)	59 (100%)	0	100	100
27	5	47/48 (98%)	47 (100%)	0	100	100
28	6	45/49 (92%)	45 (100%)	0	100	100
29	7	38/38 (100%)	38 (100%)	0	100	100
30	8	51/52 (98%)	51 (100%)	0	100	100
31	9	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	b	180/198 (91%)	180 (100%)	0	100	100
34	c	170/190 (90%)	170 (100%)	0	100	100
35	d	172/173 (99%)	172 (100%)	0	100	100
36	e	114/126 (90%)	114 (100%)	0	100	100
37	f	87/116 (75%)	87 (100%)	0	100	100
38	g	124/147 (84%)	124 (100%)	0	100	100
39	h	104/105 (99%)	104 (100%)	0	100	100
40	i	105/107 (98%)	105 (100%)	0	100	100
41	j	86/90 (96%)	86 (100%)	0	100	100
42	k	89/99 (90%)	89 (100%)	0	100	100
43	l	103/104 (99%)	103 (100%)	0	100	100
44	m	92/96 (96%)	92 (100%)	0	100	100
45	o	76/77 (99%)	76 (100%)	0	100	100
46	p	65/65 (100%)	65 (100%)	0	100	100
47	q	74/78 (95%)	74 (100%)	0	100	100
48	r	48/65 (74%)	48 (100%)	0	100	100
49	t	65/66 (98%)	65 (100%)	0	100	100
50	u	44/61 (72%)	44 (100%)	0	100	100
53	J	100/123 (81%)	100 (100%)	0	100	100
54	K	109/110 (99%)	109 (100%)	0	100	100
55	n	79/84 (94%)	79 (100%)	0	100	100
56	s	70/79 (89%)	70 (100%)	0	100	100
All	All	4823/5062 (95%)	4823 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
33	b	41	ASN
39	h	3	GLN
53	J	4	ASN
35	d	119	HIS
37	f	11	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2881/2903 (99%)	415 (14%)	43 (1%)
2	B	119/120 (99%)	13 (10%)	2 (1%)
32	a	1535/1539 (99%)	176 (11%)	0
51	v	5/6 (83%)	0	0
52	x	76/77 (98%)	13 (17%)	0
58	y	72/73 (98%)	28 (38%)	0
All	All	4688/4718 (99%)	645 (13%)	45 (0%)

5 of 645 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	12	U
1	A	27	G
1	A	34	U
1	A	35	G

5 of 45 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2286	G
1	A	2498	OMC
1	A	2326	C
1	A	2445	2MG
1	A	2566	A

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

46 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	$\# Z > 2$
58	PSU	y	55	58	18,21,22	1.81	4 (22%)	22,30,33	2.09	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	MA6	a	1518	32	18,26,27	0.75	0	19,38,41	1.24	3 (15%)
58	YG	y	37	1,58	31,42,43	1.40	3 (9%)	33,62,65	2.22	11 (33%)
32	2MG	a	1207	32	18,26,27	2.66	4 (22%)	16,38,41	1.47	3 (18%)
32	UR3	a	1498	32	19,22,23	2.03	4 (21%)	26,32,35	1.61	4 (15%)
52	5MU	x	54	52	19,22,23	2.12	5 (26%)	28,32,35	4.12	11 (39%)
1	PSU	A	1911	1	18,21,22	1.72	3 (16%)	22,30,33	2.13	5 (22%)
32	2MG	a	966	32	18,26,27	2.64	4 (22%)	16,38,41	1.48	3 (18%)
58	H2U	y	16	58	18,21,22	3.12	5 (27%)	21,30,33	1.90	5 (23%)
1	6MZ	A	2030	1	18,25,26	0.79	1 (5%)	16,36,39	2.21	4 (25%)
1	1MG	A	745	1	18,26,27	3.01	3 (16%)	19,39,42	1.31	2 (10%)
58	H2U	y	17	58	18,21,22	3.11	5 (27%)	21,30,33	1.94	5 (23%)
52	4SU	x	8	52	18,21,22	2.36	4 (22%)	26,30,33	2.42	7 (26%)
32	5MC	a	1407	32	18,22,23	1.70	3 (16%)	26,32,35	1.23	2 (7%)
32	PSU	a	516	32	18,21,22	1.73	3 (16%)	22,30,33	2.14	4 (18%)
1	OMG	A	2251	52,1	18,26,27	2.88	4 (22%)	19,38,41	1.31	3 (15%)
1	5MU	A	1939	1	19,22,23	2.16	5 (26%)	28,32,35	4.15	11 (39%)
1	PSU	A	2504	1	18,21,22	1.71	3 (16%)	22,30,33	2.10	5 (22%)
1	OMC	A	2498	1	19,22,23	1.41	3 (15%)	26,31,34	0.89	2 (7%)
32	4OC	a	1402	32	20,23,24	2.60	4 (20%)	26,32,35	1.02	3 (11%)
1	6MZ	A	1618	1	18,25,26	0.81	1 (5%)	16,36,39	2.17	4 (25%)
1	PSU	A	746	1	18,21,22	1.67	3 (16%)	22,30,33	2.07	4 (18%)
32	7MG	a	527	32	22,26,27	4.93	3 (13%)	29,39,42	2.50	9 (31%)
32	2MG	a	1516	32	18,26,27	2.65	4 (22%)	16,38,41	1.55	3 (18%)
1	5MC	A	747	1	18,22,23	1.69	3 (16%)	26,32,35	1.24	2 (7%)
58	5MU	y	54	58	19,22,23	2.16	5 (26%)	28,32,35	4.21	11 (39%)
1	PSU	A	2457	1	18,21,22	1.74	4 (22%)	22,30,33	2.13	5 (22%)
52	H2U	x	20	52	18,21,22	3.10	5 (27%)	21,30,33	1.82	5 (23%)
52	PSU	x	55	52	18,21,22	1.82	3 (16%)	22,30,33	2.06	5 (22%)
1	7MG	A	2069	1	22,26,27	4.96	4 (18%)	29,39,42	2.59	9 (31%)
1	H2U	A	2449	1	18,21,22	3.10	5 (27%)	21,30,33	1.83	5 (23%)
1	2MA	A	2503	1	17,25,26	1.10	1 (5%)	17,37,40	1.18	2 (11%)
1	PSU	A	1917	1	18,21,22	1.83	4 (22%)	22,30,33	2.10	5 (22%)
1	OMU	A	2552	1	19,22,23	2.66	7 (36%)	26,31,34	1.94	7 (26%)
32	5MC	a	967	32	18,22,23	1.72	3 (16%)	26,32,35	1.26	3 (11%)
1	2MG	A	1835	1	18,26,27	2.63	4 (22%)	16,38,41	1.53	3 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	H2U	y	20	58	18,21,22	3.10	5 (27%)	21,30,33	1.80	5 (23%)
1	PSU	A	2580	1	18,21,22	1.84	4 (22%)	22,30,33	2.13	5 (22%)
1	5MC	A	1962	1	18,22,23	1.69	3 (16%)	26,32,35	1.23	3 (11%)
58	7MG	y	46	58	22,26,27	4.94	3 (13%)	29,39,42	2.37	9 (31%)
1	3TD	A	1915	1	18,22,23	2.85	5 (27%)	22,32,35	2.08	4 (18%)
1	PSU	A	2605	1	18,21,22	1.81	4 (22%)	22,30,33	2.09	5 (22%)
1	PSU	A	955	1	18,21,22	1.77	4 (22%)	22,30,33	2.12	5 (22%)
32	MA6	a	1519	32	18,26,27	0.70	0	19,38,41	1.38	3 (15%)
1	PSU	A	2604	1	18,21,22	1.68	3 (16%)	22,30,33	2.10	5 (22%)
1	2MG	A	2445	1	18,26,27	2.64	4 (22%)	16,38,41	1.47	3 (18%)

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
58	PSU	y	55	58	2/2/5/5	4/7/25/26	0/2/2/2
32	MA6	a	1518	32	2/2/6/6	6/7/29/30	0/3/3/3
58	YG	y	37	1,58	-	1/20/42/43	0/3/4/4
32	2MG	a	1207	32	2/2/5/6	2/5/27/28	0/3/3/3
32	UR3	a	1498	32	2/2/5/5	5/7/25/26	0/2/2/2
52	5MU	x	54	52	3/3/5/5	3/7/25/26	0/2/2/2
1	PSU	A	1911	1	2/2/5/5	3/7/25/26	0/2/2/2
32	2MG	a	966	32	2/2/5/6	3/5/27/28	0/3/3/3
58	H2U	y	16	58	1/1/8/9	3/7/38/39	0/2/2/2
1	6MZ	A	2030	1	-	3/5/27/28	0/3/3/3
1	1MG	A	745	1	-	0/3/25/26	0/3/3/3
58	H2U	y	17	58	1/1/8/9	3/7/38/39	0/2/2/2
52	4SU	x	8	52	3/3/5/5	3/7/25/26	0/2/2/2
32	5MC	a	1407	32	-	4/7/25/26	0/2/2/2
32	PSU	a	516	32	2/2/5/5	3/7/25/26	0/2/2/2
1	OMG	A	2251	52,1	2/2/5/5	4/5/27/28	0/3/3/3
1	5MU	A	1939	1	3/3/5/5	1/7/25/26	0/2/2/2
1	PSU	A	2504	1	2/2/5/5	3/7/25/26	0/2/2/2
1	OMC	A	2498	1	2/2/5/5	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	4OC	a	1402	32	2/2/5/6	3/9/29/30	0/2/2/2
1	6MZ	A	1618	1	-	2/5/27/28	0/3/3/3
1	PSU	A	746	1	2/2/5/5	2/7/25/26	0/2/2/2
32	7MG	a	527	32	1/1/7/7	4/7/37/38	0/3/3/3
32	2MG	a	1516	32	2/2/5/6	5/5/27/28	0/3/3/3
1	5MC	A	747	1	-	6/7/25/26	0/2/2/2
58	5MU	y	54	58	3/3/5/5	3/7/25/26	0/2/2/2
1	PSU	A	2457	1	2/2/5/5	3/7/25/26	0/2/2/2
52	H2U	x	20	52	1/1/8/9	5/7/38/39	0/2/2/2
52	PSU	x	55	52	2/2/5/5	5/7/25/26	0/2/2/2
1	7MG	A	2069	1	1/1/7/7	3/7/37/38	0/3/3/3
1	H2U	A	2449	1	1/1/8/9	4/7/38/39	0/2/2/2
1	2MA	A	2503	1	2/2/5/5	2/3/25/26	0/3/3/3
1	PSU	A	1917	1	2/2/5/5	3/7/25/26	0/2/2/2
1	OMU	A	2552	1	1/1/5/5	5/9/27/28	0/2/2/2
32	5MC	a	967	32	-	5/7/25/26	0/2/2/2
1	2MG	A	1835	1	2/2/5/6	2/5/27/28	0/3/3/3
58	H2U	y	20	58	1/1/8/9	5/7/38/39	0/2/2/2
1	PSU	A	2580	1	2/2/5/5	3/7/25/26	0/2/2/2
1	5MC	A	1962	1	-	3/7/25/26	0/2/2/2
58	7MG	y	46	58	1/1/7/7	3/7/37/38	0/3/3/3
1	3TD	A	1915	1	1/1/5/5	6/7/25/26	0/2/2/2
1	PSU	A	2605	1	2/2/5/5	2/7/25/26	0/2/2/2
1	PSU	A	955	1	2/2/5/5	3/7/25/26	0/2/2/2
32	MA6	a	1519	32	2/2/6/6	3/7/29/30	0/3/3/3
1	PSU	A	2604	1	2/2/5/5	3/7/25/26	0/2/2/2
1	2MG	A	2445	1	2/2/5/6	1/5/27/28	0/3/3/3

The worst 5 of 164 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	y	46	7MG	C8-N9	-20.28	1.34	1.46
1	A	2069	7MG	C8-N9	-20.26	1.34	1.46
32	a	527	7MG	C8-N9	-20.21	1.34	1.46
1	A	2251	OMG	O6-C6	10.20	1.44	1.23
1	A	745	1MG	O6-C6	10.10	1.42	1.22

The worst 5 of 227 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	y	54	5MU	C4-N3-C2	-9.33	115.27	127.35
52	x	54	5MU	C4-N3-C2	-9.15	115.50	127.35
52	x	54	5MU	C5M-C5-C4	9.09	128.78	118.77
58	y	54	5MU	C5M-C5-C4	9.07	128.75	118.77
1	A	1939	5MU	C4-N3-C2	-9.04	115.65	127.35

5 of 70 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	746	PSU	C4'
1	A	746	PSU	C2'
1	A	955	PSU	C4'
1	A	955	PSU	C2'
1	A	1835	2MG	C2'

5 of 149 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	746	PSU	C3'-C4'-C5'-O5'
1	A	747	5MC	C3'-C4'-C5'-O5'
1	A	747	5MC	C2'-C1'-N1-C2
1	A	747	5MC	C2'-C1'-N1-C6
1	A	955	PSU	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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
57	<i>z</i>	6

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	<i>z</i>	517:UNK	C	518:UNK	N	39.33
1	<i>z</i>	561:UNK	C	663:ALA	N	37.34
1	<i>z</i>	493:UNK	C	494:UNK	N	34.24
1	<i>z</i>	547:UNK	C	548:UNK	N	30.19
1	<i>z</i>	526:UNK	C	527:UNK	N	18.32

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-4001. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis

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

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

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

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.