



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2025 – 06:04 pm GMT

PDB ID : 8PKL
EMDB ID : EMD-17743
Title : Escherichia coli paused disome complex (leading 70S non-rotated closed PRE state)
Authors : Fluegel, T.; Schacherl, M.
Deposited on : 2023-06-26
Resolution : 3.09 Å(reported)
Based on initial model : 7N1P

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

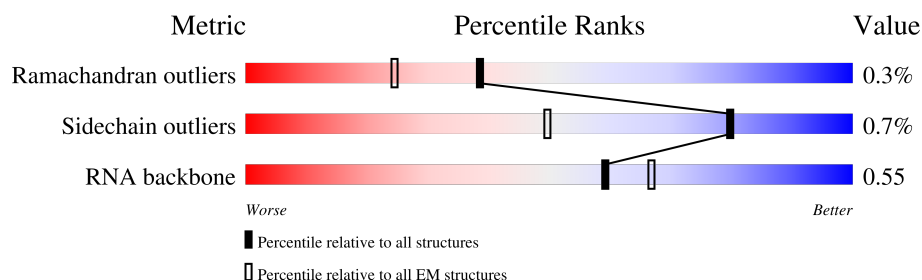
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.09 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.






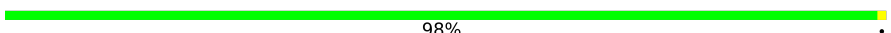
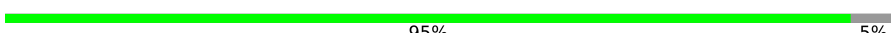










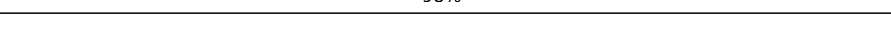
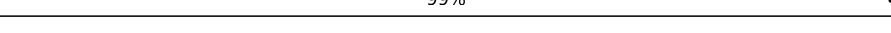
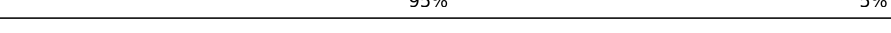


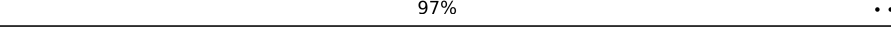
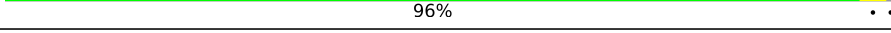



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	0	38	100%
2	1	78	96% ..
3	2	63	100%
4	3	59	98% .
5	4	70	93% . .
6	5	57	98% .
7	6	65	98% .
8	7	2921	81% 17% ..
9	8	120	85% 14% .


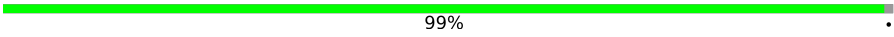
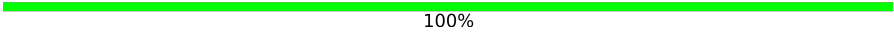

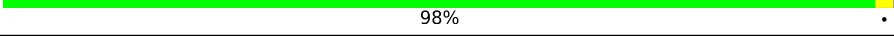
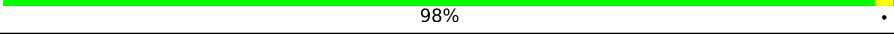
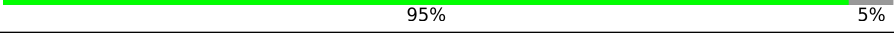
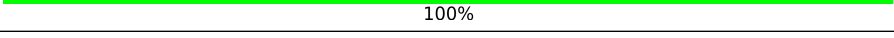
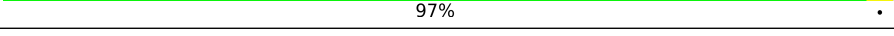

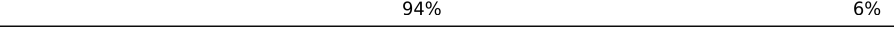
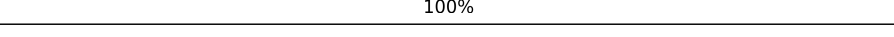
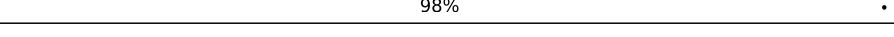
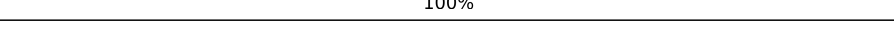
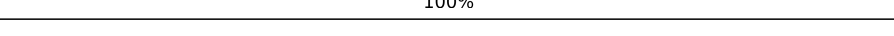
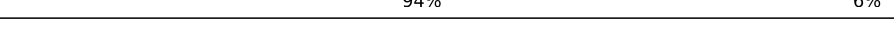
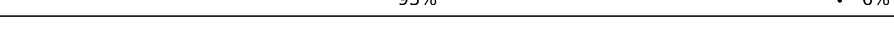
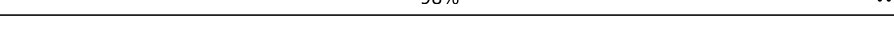
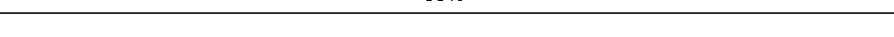






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Mol	Chain	Length	Quality of chain
10	A	1535	
11	B	241	
12	C	233	
13	D	206	
14	E	167	
15	F	135	
16	G	179	
17	H	130	
18	I	130	
19	J	103	
20	K	129	
21	L	124	
22	M	118	
23	N	101	
24	O	89	
25	P	82	
26	Q	84	
27	R	75	
28	S	92	
29	T	87	
30	U	71	
31	V	24	
32	W	76	
33	X	77	
34	Y	76	

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Mol	Chain	Length	Quality of chain
35	a	234	 57%43%
36	b	273	 99%.
37	c	209	 100%
38	d	201	 100%
39	e	179	 98%..
40	f	177	 98%..
41	g	55	 95%5%
42	h	136	 100%
43	i	149	 97%. .
44	j	165	 82%18%
45	k	142	 94%6%
46	l	46	 100%
47	m	142	 98%.
48	n	123	 100%
49	o	144	 100%
50	p	36	 94%6%
51	q	127	 93%. 6%
52	r	117	 98%..
53	s	115	 99%.
54	t	118	 99%.
55	u	103	 100%
56	v	110	 99%.
57	w	100	 92%. 7%
58	x	104	 97%..
59	y	94	 100%

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Mol	Chain	Length	Quality of chain
60	z	85	<div><div></div><div>99%</div><div>.</div></div>

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 151734 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 protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 2 is a protein called 50S ribosomal protein L28.

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

- Molecule 3 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 4 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 5 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	68	Total	C	N	O	S	0	0
			533	330	101	96	6		

- Molecule 6 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	2904	Total	C	N	O	P	0	0
			62355	27824	11468	20159	2904		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

- Molecule 10 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	1535	Total	C	N	O	P	0	0
			32950	14703	6044	10668	1535		

- Molecule 11 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	227	Total	C	N	O	S	0	0
			1776	1123	318	327	8		

- Molecule 12 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	212	Total	C	N	O	S	0	0
			1658	1049	311	294	4		

- Molecule 13 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 14 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	158	Total	C	N	O	S	0	0
			1166	725	220	215	6		

- Molecule 15 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 16 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 17 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 19 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J	100	Total	C	N	O	S	0	0
			803	502	154	146	1		

- Molecule 20 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	K	118	Total	C	N	O	S	0	0
			884	545	175	161	3		

- Molecule 21 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 22 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	M	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 23 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 24 is a protein called 30S ribosomal protein S15.

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

- Molecule 25 is a protein called 30S ribosomal protein S16.

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

- Molecule 26 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 27 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 28 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 29 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	70	Total	C	N	O	S	0	0
			584	363	122	98	1		

- Molecule 31 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	V	24	Total	C	N	O	P	0	0
			516	231	99	162	24		

- Molecule 32 is a RNA chain called tRNA-Trp (P-site).

Mol	Chain	Residues	Atoms					AltConf	Trace	
32	W	76	Total	C	N	O	P	S	0	0
			1630	730	286	536	76	2		

- Molecule 33 is a RNA chain called tRNA-Arg (E-site).

Mol	Chain	Residues	Atoms						AltConf	Trace
33	X	77	Total	C	N	O	P	S	0	0
			1654	740	297	538	77	2		

- Molecule 34 is a RNA chain called tRNA-Ala (A-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Y	76	Total	C	N	O	P	0	0
			1628	726	293	533	76		

- Molecule 35 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 36 is a protein called 50S ribosomal protein L2.

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

- Molecule 37 is a protein called 50S ribosomal protein L3.

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

- Molecule 38 is a protein called 50S ribosomal protein L4.

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

- Molecule 39 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 40 is a protein called 50S ribosomal protein L6.

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

- Molecule 41 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	g	52	Total	C	N	O	0	0
			427	275	78	74		

- Molecule 42 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	136	Total	C	N	O	S	1	0
			1085	692	209	178	6		

- Molecule 43 is a protein called 50S ribosomal protein L9.

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

- Molecule 44 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	135	Total	C	N	O	S	0	0
			1023	648	179	192	4		

- Molecule 45 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

- Molecule 46 is a protein called 50S ribosomal protein L34.

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

- Molecule 47 is a protein called 50S ribosomal protein L13.

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

- Molecule 48 is a protein called 50S ribosomal protein L14.

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

- Molecule 49 is a protein called 50S ribosomal protein L15.

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

- Molecule 50 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	p	36	Total	C	N	O	0	0
			206	125	44	37		

- Molecule 51 is a protein called 50S ribosomal protein L17.

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

- Molecule 52 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	r	116	Total	C	N	O	0	0
			891	552	178	161		

- Molecule 53 is a protein called 50S ribosomal protein L19.

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

- Molecule 54 is a protein called 50S ribosomal protein L20.

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

- Molecule 55 is a protein called 50S ribosomal protein L21.

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

- Molecule 56 is a protein called 50S ribosomal protein L22.

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

- Molecule 57 is a protein called 50S ribosomal protein L23.

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

- Molecule 58 is a protein called 50S ribosomal protein L24.

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

- Molecule 59 is a protein called 50S ribosomal protein L25.

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

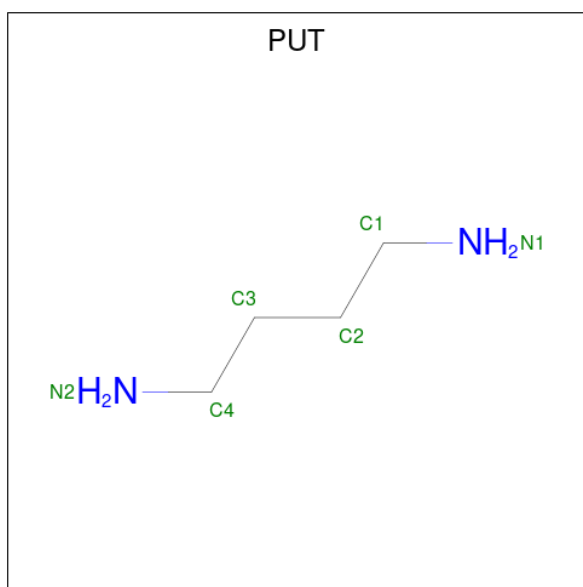
- Molecule 60 is a protein called 50S ribosomal protein L27.

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

- Molecule 61 is ZINC ION (three-letter code: ZN) (formula: Zn).

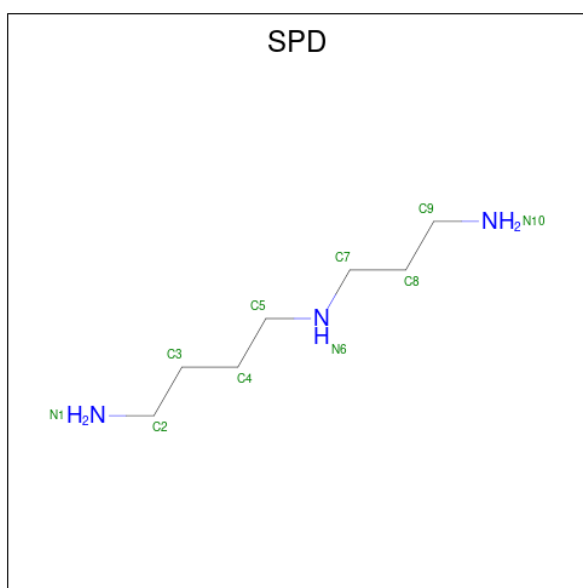
Mol	Chain	Residues	Atoms		AltConf
61	0	1	Total	Zn	0
			1	1	
61	4	1	Total	Zn	0
			1	1	

- Molecule 62 is 1,4-DIAMINOBUTANE (three-letter code: PUT) (formula: C₄H₁₂N₂).



Mol	Chain	Residues	Atoms			AltConf
62	7	1	Total	C	N	0
			6	4	2	
62	7	1	Total	C	N	0
			6	4	2	

- Molecule 63 is SPERMIDINE (three-letter code: SPD) (formula: C₇H₁₉N₃).

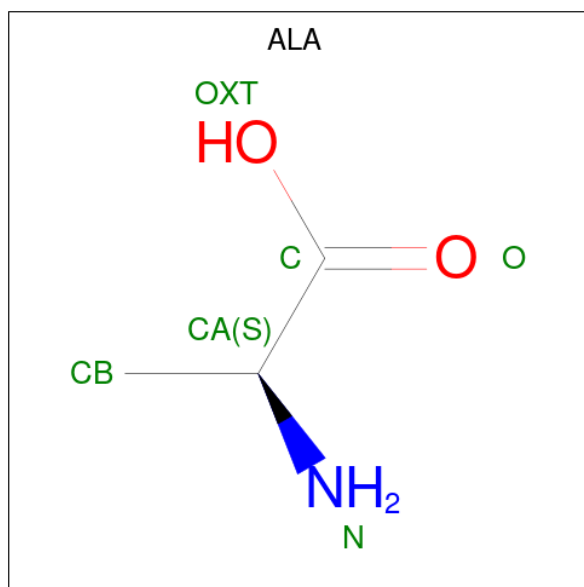


Mol	Chain	Residues	Atoms			AltConf
63	7	1	Total	C	N	0
			10	7	3	

- Molecule 64 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
64	7	257	Total	Mg	0
			257	257	
64	A	23	Total	Mg	0
			23	23	
64	I	1	Total	Mg	0
			1	1	
64	V	1	Total	Mg	0
			1	1	
64	X	1	Total	Mg	0
			1	1	
64	Y	1	Total	Mg	0
			1	1	
64	b	1	Total	Mg	0
			1	1	
64	q	1	Total	Mg	0
			1	1	
64	r	1	Total	Mg	0
			1	1	

- Molecule 65 is ALANINE (three-letter code: ALA) (formula: $C_3H_7NO_2$).



Mol	Chain	Residues	Atoms				AltConf
65	Y	1	Total	C	N	O	0
			5	3	1	1	

- Molecule 66 is water.

Mol	Chain	Residues	Atoms		AltConf
66	7	12	Total 12	O 12	0
66	x	1	Total 1	O 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: 50S ribosomal protein L36

Chain 0:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: 50S ribosomal protein L28

Chain 1:  96%



- Molecule 3: 50S ribosomal protein L29

Chain 2:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: 50S ribosomal protein L30

Chain 3:  98%



- Molecule 5: Large ribosomal subunit protein bL31A

Chain 4:  93%



- Molecule 6: 50S ribosomal protein L32

Chain 5:  98%




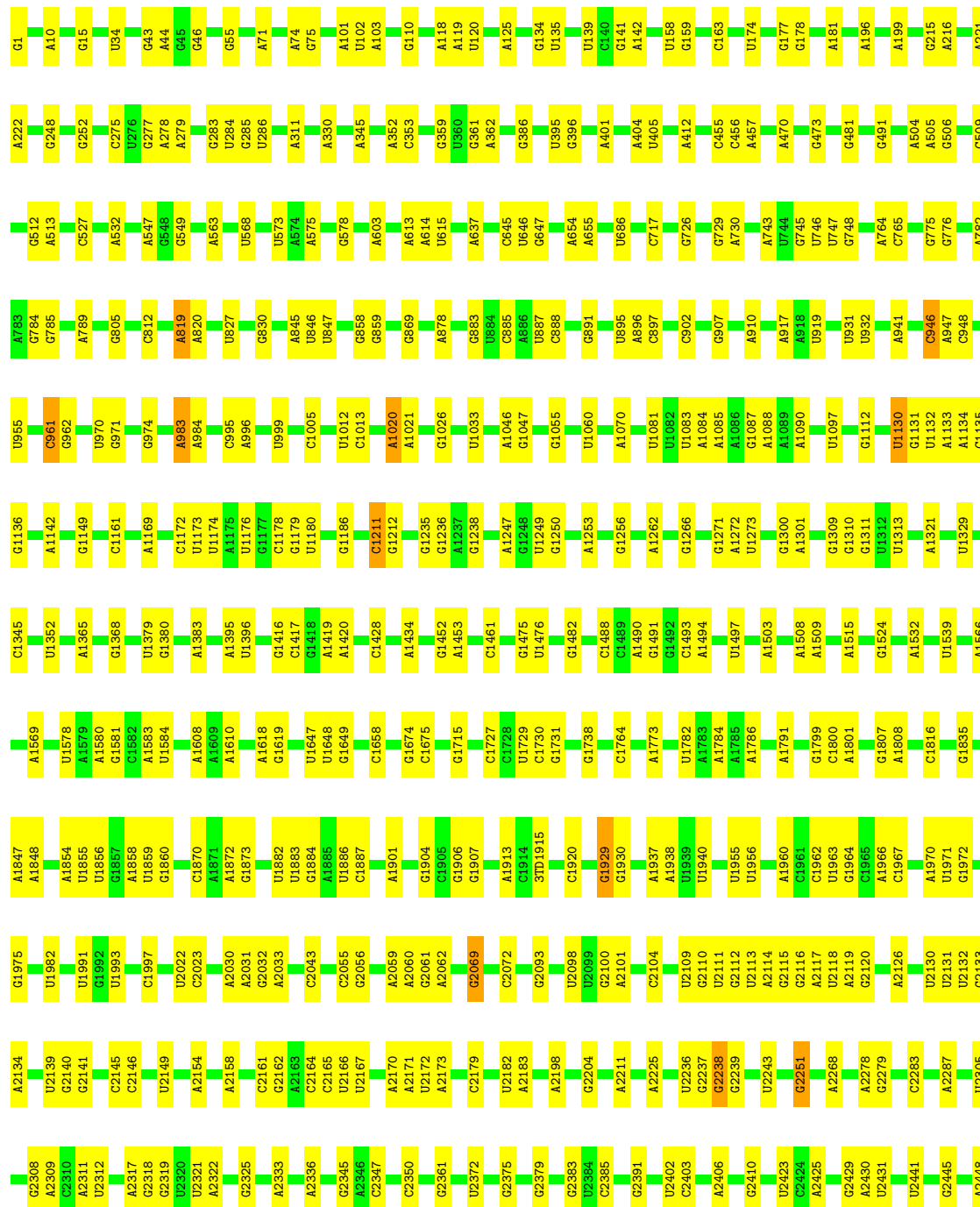
- Molecule 7: 50S ribosomal protein L35

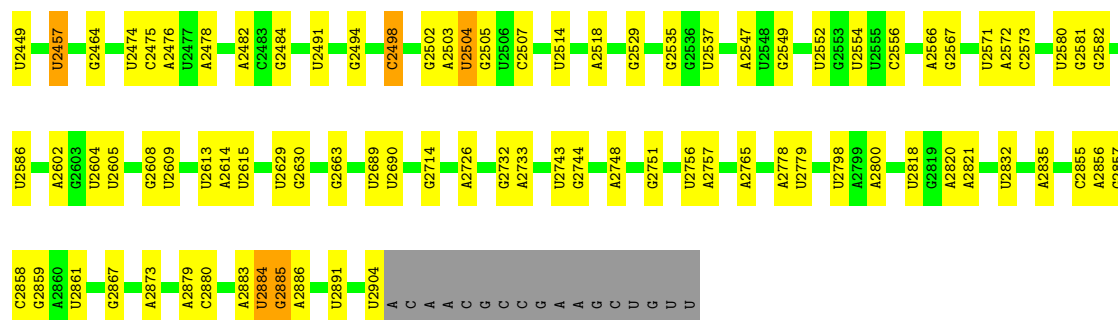
Chain 6:  98%



- Molecule 8: 23S ribosomal RNA

Chain 7:  81% 17%





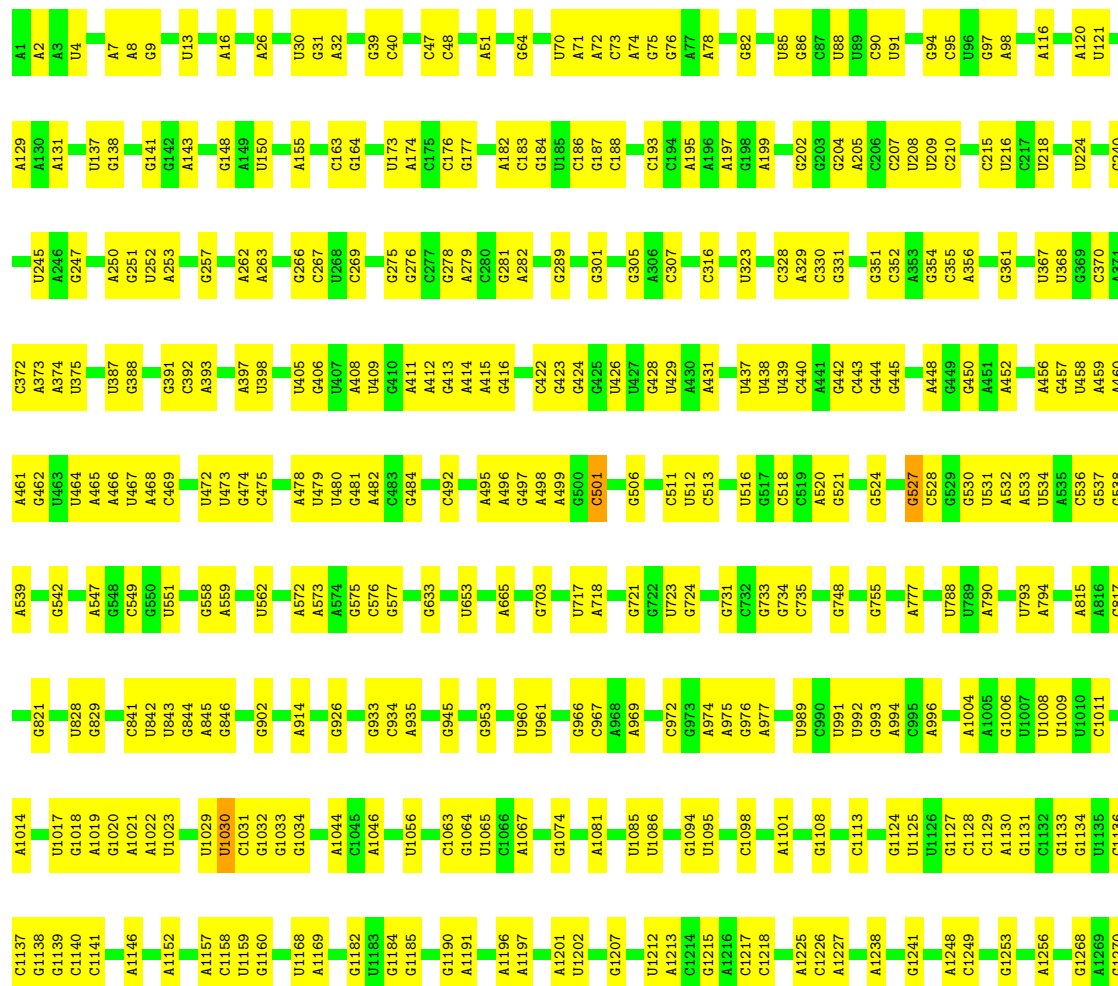
• Molecule 9: 5S ribosomal RNA

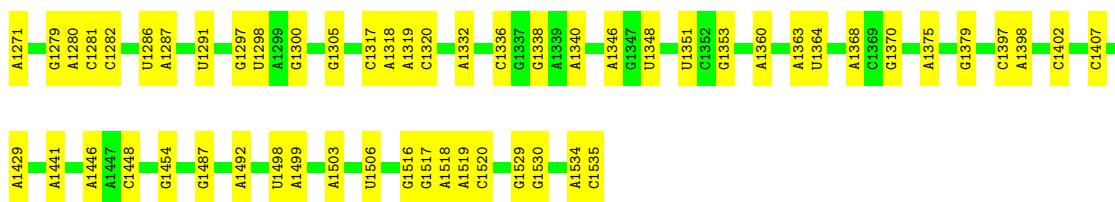
Chain 8: 85% 14%



• Molecule 10: 16S ribosomal RNA

Chain A: 73% 26%





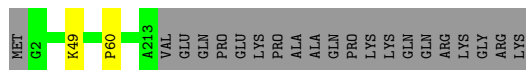
- Molecule 11: Small ribosomal subunit protein uS2

Chain B: 90% 6%



- Molecule 12: Small ribosomal subunit protein uS3

Chain C: 90% 9%



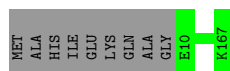
- Molecule 13: Small ribosomal subunit protein uS4

Chain D: 98%



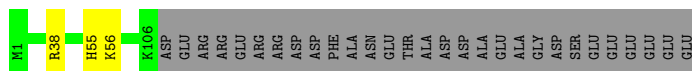
- Molecule 14: Small ribosomal subunit protein uS5

Chain E: 95% 5%



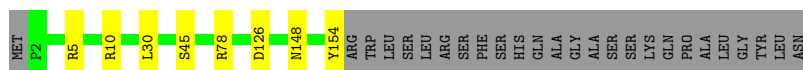
- Molecule 15: 30S ribosomal protein S6

Chain F: 76% 21%



- Molecule 16: 30S ribosomal protein S7

Chain G: 81% 15%



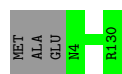
- Molecule 17: Small ribosomal subunit protein uS8

Chain H:  99%



- Molecule 18: Small ribosomal subunit protein uS9

Chain I:  98%



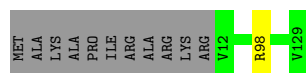
- Molecule 19: 30S ribosomal protein S10

Chain J:  94%



- Molecule 20: Small ribosomal subunit protein uS11

Chain K:  91%



- Molecule 21: Small ribosomal subunit protein uS12

Chain L:  99%



- Molecule 22: Small ribosomal subunit protein uS13

Chain M:  99%



- Molecule 23: Small ribosomal subunit protein uS14

Chain N:  98%



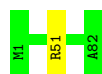
- Molecule 24: 30S ribosomal protein S15

Chain O:  98% ..



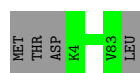
- Molecule 25: 30S ribosomal protein S16

Chain P:  99% .




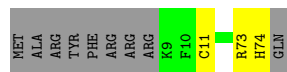
- Molecule 26: Small ribosomal subunit protein uS17

Chain Q:  95% 5%




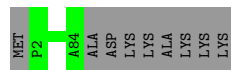
- Molecule 27: Small ribosomal subunit protein bS18

Chain R:  84% . 12%



- Molecule 28: Small ribosomal subunit protein uS19

Chain S:  90% 10%



- Molecule 29: Small ribosomal subunit protein bS20

Chain T:  97% ..



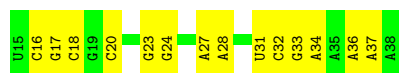
- Molecule 30: 30S ribosomal protein S21

Chain U:  96% ..



- Molecule 31: mRNA

Chain V:  42% 58%



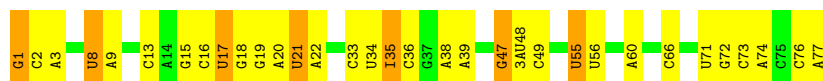
- Molecule 32: tRNA-Trp (P-site)

Chain W:  61% 32% 8%



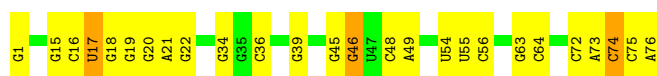
- Molecule 33: tRNA-Arg (E-site)

Chain X:  57% 34% 9%



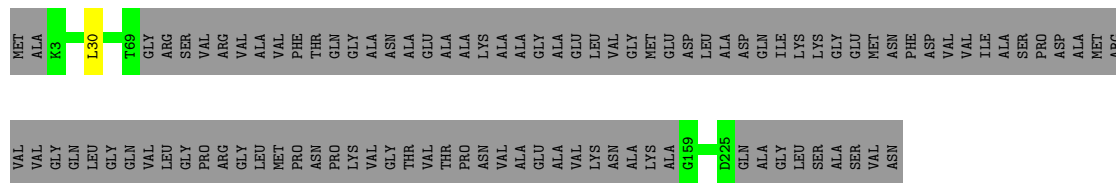
- Molecule 34: tRNA-Ala (A-site)

Chain Y:  66% 30% 4%



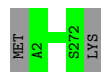
- Molecule 35: Large ribosomal subunit protein uL1

Chain a:  57% 43%



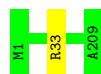
- Molecule 36: 50S ribosomal protein L2

Chain b:  99% 1%



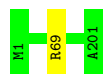
- Molecule 37: 50S ribosomal protein L3

Chain c:  100%



- Molecule 38: 50S ribosomal protein L4

Chain d:  100%



- Molecule 39: 50S ribosomal protein L5

Chain e:  98%



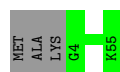
- Molecule 40: 50S ribosomal protein L6

Chain f:  98%



- Molecule 41: 50S ribosomal protein L33

Chain g:  95%



- Molecule 42: 50S ribosomal protein L16

Chain h:  100%


There are no outlier residues recorded for this chain.

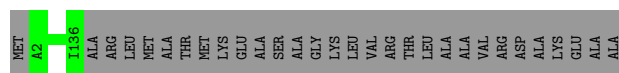
- Molecule 43: 50S ribosomal protein L9

Chain i:  97%



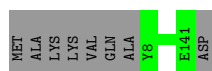
- Molecule 44: Large ribosomal subunit protein uL10

Chain j:  82%



- Molecule 45: 50S ribosomal protein L11

Chain k:  94% 6%



- Molecule 46: 50S ribosomal protein L34

Chain l:  100%

There are no outlier residues recorded for this chain.

- Molecule 47: 50S ribosomal protein L13

Chain m:  98%



- Molecule 48: 50S ribosomal protein L14

Chain n:  100%

There are no outlier residues recorded for this chain.

- Molecule 49: 50S ribosomal protein L15

Chain o:  100%

There are no outlier residues recorded for this chain.

- Molecule 50: Nascent peptide

Chain p:  94% 6%



- Molecule 51: 50S ribosomal protein L17

Chain q:  93% 6%



- Molecule 52: 50S ribosomal protein L18

Chain r:  98%



- Molecule 53: 50S ribosomal protein L19

Chain s:  99%



- Molecule 54: 50S ribosomal protein L20

Chain t:  99%



- Molecule 55: 50S ribosomal protein L21

Chain u:  100%

There are no outlier residues recorded for this chain.

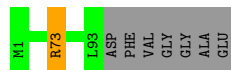
- Molecule 56: 50S ribosomal protein L22

Chain v:  99%



- Molecule 57: 50S ribosomal protein L23

Chain w:  92% 7%



- Molecule 58: 50S ribosomal protein L24

Chain x:  97%



- Molecule 59: 50S ribosomal protein L25

Chain y:  100%

There are no outlier residues recorded for this chain.

- Molecule 60: 50S ribosomal protein L27

Chain z:  99%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34905	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k 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: 5MC, 4OC, H2U, 1MG, MG, 2MA, 3TD, MIA, PSU, 3AU, 6MZ, OMC, PUT, G7M, MA6, ZN, 2MG, UR3, OMU, OMG, SPD, 5MU, RSP, 4SU

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	0	0.24	0/303	0.58	0/397
2	1	0.24	0/635	0.60	0/848
3	2	0.24	0/510	0.52	0/677
4	3	0.28	0/453	0.60	0/605
5	4	0.29	0/543	0.59	0/726
6	5	0.25	0/450	0.58	0/599
7	6	0.24	0/513	0.57	0/676
8	7	0.23	1/69306 (0.0%)	0.72	51/108116 (0.0%)
9	8	0.25	1/2876 (0.0%)	0.70	2/4483 (0.0%)
10	A	0.21	0/36637	0.74	5/57149 (0.0%)
11	B	0.25	0/1807	0.50	0/2435
12	C	0.25	0/1685	0.56	0/2270
13	D	0.24	0/1665	0.55	0/2227
14	E	0.26	0/1179	0.52	0/1584
15	F	0.25	0/881	0.50	0/1189
16	G	0.25	0/1219	0.51	0/1635
17	H	0.25	0/989	0.55	0/1326
18	I	0.25	0/1034	0.59	0/1375
19	J	0.25	0/813	0.62	0/1100
20	K	0.26	0/900	0.57	0/1215
21	L	0.28	0/969	0.61	0/1300
22	M	0.24	0/919	0.59	0/1226
23	N	0.25	0/817	0.59	0/1088
24	O	0.23	0/722	0.59	0/964
25	P	0.25	0/659	0.61	0/884
26	Q	0.26	0/657	0.59	0/881
27	R	0.29	0/553	0.59	0/742
28	S	0.26	0/680	0.53	0/915
29	T	0.24	0/676	0.51	0/895
30	U	0.26	0/592	0.58	0/785
31	V	0.28	0/578	0.80	0/899

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	W	0.35	1/1604 (0.1%)	0.78	0/2496
33	X	0.47	3/1628 (0.2%)	0.79	0/2526
34	Y	0.35	1/1725 (0.1%)	0.78	2/2687 (0.1%)
35	a	0.26	0/1033	0.48	0/1387
36	b	0.26	0/2121	0.60	0/2852
37	c	0.27	0/1586	0.56	0/2134
38	d	0.24	0/1571	0.51	0/2113
39	e	0.28	0/1444	0.54	0/1937
40	f	0.31	0/1343	0.54	0/1816
41	g	0.25	0/434	0.52	0/576
42	h	0.25	0/1104	0.58	0/1474
43	i	0.25	0/1122	0.50	0/1515
44	j	0.25	0/1037	0.51	0/1400
45	k	0.26	0/993	0.53	0/1341
46	l	0.24	0/380	0.64	0/498
47	m	0.28	0/1152	0.52	0/1551
48	n	0.27	0/955	0.63	0/1279
49	o	0.26	0/1062	0.61	0/1413
50	p	0.64	0/57	0.90	0/76
51	q	0.28	0/973	0.59	0/1301
52	r	0.25	0/901	0.60	0/1209
53	s	0.25	0/929	0.56	0/1242
54	t	0.26	0/960	0.52	0/1278
55	u	0.27	0/829	0.56	0/1107
56	v	0.24	0/864	0.57	0/1156
57	w	0.30	0/744	0.52	0/994
58	x	0.26	0/787	0.53	0/1051
59	y	0.25	0/766	0.52	0/1025
60	z	0.26	0/642	0.56	0/848
All	All	0.24	7/162966 (0.0%)	0.69	60/243493 (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
5	4	0	1
13	D	0	1
16	G	0	1
19	J	0	2
20	K	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	O	0	1
25	P	0	1
27	R	0	1
29	T	0	2
30	U	0	1
38	d	0	1
39	e	0	1
40	f	0	1
47	m	0	1
57	w	0	1
All	All	0	17

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	W	1	A	OP3-P	-10.67	1.48	1.61
33	X	1	G	OP3-P	-10.63	1.48	1.61
8	7	1	G	OP3-P	-10.60	1.48	1.61
9	8	1	U	OP3-P	-10.59	1.48	1.61
34	Y	1	G	OP3-P	-10.55	1.48	1.61

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	7	1860	G	P-O3'-C3'	-11.62	105.76	119.70
8	7	1856	U	P-O3'-C3'	-11.23	106.22	119.70
8	7	2237	G	P-O3'-C3'	-10.79	106.75	119.70
8	7	1859	U	P-O3'-C3'	-10.24	107.42	119.70
8	7	2885	G	P-O3'-C3'	-9.97	107.73	119.70

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	4	25	ARG	Sidechain
13	D	104	ARG	Sidechain
16	G	78	ARG	Sidechain
19	J	37	ARG	Sidechain
19	J	48	ARG	Sidechain

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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	
1	0	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
2	1	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
3	2	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
4	3	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
5	4	66/70 (94%)	56 (85%)	9 (14%)	1 (2%)	8	33
6	5	54/57 (95%)	54 (100%)	0	0	100	100
7	6	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
11	B	225/241 (93%)	189 (84%)	29 (13%)	7 (3%)	3	19
12	C	210/233 (90%)	186 (89%)	23 (11%)	1 (0%)	25	58
13	D	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
14	E	156/167 (93%)	152 (97%)	4 (3%)	0	100	100
15	F	104/135 (77%)	84 (81%)	19 (18%)	1 (1%)	13	42
16	G	151/179 (84%)	140 (93%)	10 (7%)	1 (1%)	19	51
17	H	127/130 (98%)	127 (100%)	0	0	100	100
18	I	125/130 (96%)	117 (94%)	8 (6%)	0	100	100
19	J	98/103 (95%)	89 (91%)	8 (8%)	1 (1%)	13	42
20	K	116/129 (90%)	102 (88%)	14 (12%)	0	100	100
21	L	121/124 (98%)	116 (96%)	5 (4%)	0	100	100
22	M	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
23	N	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
24	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	P	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
26	Q	78/84 (93%)	77 (99%)	1 (1%)	0	100	100
27	R	64/75 (85%)	52 (81%)	12 (19%)	0	100	100
28	S	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
29	T	84/87 (97%)	84 (100%)	0	0	100	100
30	U	68/71 (96%)	64 (94%)	3 (4%)	1 (2%)	8	33
35	a	130/234 (56%)	123 (95%)	7 (5%)	0	100	100
36	b	269/273 (98%)	265 (98%)	4 (2%)	0	100	100
37	c	207/209 (99%)	202 (98%)	5 (2%)	0	100	100
38	d	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
39	e	176/179 (98%)	170 (97%)	6 (3%)	0	100	100
40	f	174/177 (98%)	170 (98%)	4 (2%)	0	100	100
41	g	50/55 (91%)	50 (100%)	0	0	100	100
42	h	135/136 (99%)	135 (100%)	0	0	100	100
43	i	147/149 (99%)	122 (83%)	25 (17%)	0	100	100
44	j	133/165 (81%)	122 (92%)	11 (8%)	0	100	100
45	k	132/142 (93%)	123 (93%)	9 (7%)	0	100	100
46	l	44/46 (96%)	44 (100%)	0	0	100	100
47	m	140/142 (99%)	137 (98%)	2 (1%)	1 (1%)	19	51
48	n	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
49	o	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
50	p	5/36 (14%)	2 (40%)	2 (40%)	1 (20%)	0	0
51	q	118/127 (93%)	115 (98%)	3 (2%)	0	100	100
52	r	114/117 (97%)	110 (96%)	3 (3%)	1 (1%)	14	45
53	s	112/115 (97%)	111 (99%)	1 (1%)	0	100	100
54	t	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
55	u	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
56	v	108/110 (98%)	99 (92%)	8 (7%)	1 (1%)	14	45
57	w	91/100 (91%)	89 (98%)	2 (2%)	0	100	100
58	x	100/104 (96%)	94 (94%)	6 (6%)	0	100	100
59	y	92/94 (98%)	92 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	z	82/85 (96%)	79 (96%)	3 (4%)	0	100	100
All	All	6037/6490 (93%)	5723 (95%)	297 (5%)	17 (0%)	38	68

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	U	64	ASN
11	B	117	LEU
11	B	118	GLU
15	F	38	ARG
19	J	94	ALA

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	
1	0	34/34 (100%)	34 (100%)	0	100	100
2	1	67/68 (98%)	65 (97%)	2 (3%)	36	64
3	2	55/55 (100%)	55 (100%)	0	100	100
4	3	48/49 (98%)	48 (100%)	0	100	100
5	4	60/62 (97%)	59 (98%)	1 (2%)	56	78
6	5	47/48 (98%)	47 (100%)	0	100	100
7	6	51/52 (98%)	51 (100%)	0	100	100
11	B	189/199 (95%)	186 (98%)	3 (2%)	58	79
12	C	172/190 (90%)	171 (99%)	1 (1%)	84	91
13	D	172/173 (99%)	170 (99%)	2 (1%)	67	83
14	E	120/126 (95%)	120 (100%)	0	100	100
15	F	92/116 (79%)	90 (98%)	2 (2%)	47	71
16	G	126/147 (86%)	120 (95%)	6 (5%)	21	51
17	H	104/105 (99%)	104 (100%)	0	100	100
18	I	105/107 (98%)	105 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	J	88/90 (98%)	88 (100%)	0	100	100
20	K	91/99 (92%)	91 (100%)	0	100	100
21	L	103/104 (99%)	103 (100%)	0	100	100
22	M	95/96 (99%)	95 (100%)	0	100	100
23	N	83/84 (99%)	82 (99%)	1 (1%)	67	83
24	O	76/77 (99%)	76 (100%)	0	100	100
25	P	65/65 (100%)	65 (100%)	0	100	100
26	Q	74/78 (95%)	74 (100%)	0	100	100
27	R	57/65 (88%)	55 (96%)	2 (4%)	31	61
28	S	72/79 (91%)	72 (100%)	0	100	100
29	T	65/66 (98%)	65 (100%)	0	100	100
30	U	59/61 (97%)	59 (100%)	0	100	100
35	a	110/181 (61%)	109 (99%)	1 (1%)	75	88
36	b	216/218 (99%)	216 (100%)	0	100	100
37	c	164/164 (100%)	163 (99%)	1 (1%)	84	91
38	d	165/165 (100%)	165 (100%)	0	100	100
39	e	149/150 (99%)	147 (99%)	2 (1%)	65	82
40	f	137/138 (99%)	135 (98%)	2 (2%)	60	80
41	g	47/49 (96%)	47 (100%)	0	100	100
42	h	110/109 (101%)	110 (100%)	0	100	100
43	i	114/114 (100%)	110 (96%)	4 (4%)	31	61
44	j	103/123 (84%)	103 (100%)	0	100	100
45	k	104/110 (94%)	104 (100%)	0	100	100
46	l	38/38 (100%)	38 (100%)	0	100	100
47	m	116/116 (100%)	115 (99%)	1 (1%)	75	88
48	n	104/104 (100%)	104 (100%)	0	100	100
49	o	103/103 (100%)	103 (100%)	0	100	100
50	p	5/5 (100%)	4 (80%)	1 (20%)	1	4
51	q	100/103 (97%)	98 (98%)	2 (2%)	50	74
52	r	86/87 (99%)	86 (100%)	0	100	100
53	s	99/100 (99%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	t	89/90 (99%)	89 (100%)	0	100	100
55	u	84/84 (100%)	84 (100%)	0	100	100
56	v	93/93 (100%)	93 (100%)	0	100	100
57	w	80/84 (95%)	79 (99%)	1 (1%)	65	82
58	x	83/85 (98%)	82 (99%)	1 (1%)	67	83
59	y	78/78 (100%)	78 (100%)	0	100	100
60	z	62/63 (98%)	62 (100%)	0	100	100
All	All	5009/5249 (95%)	4973 (99%)	36 (1%)	80	90

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	i	91	PHE
58	x	6	ARG
43	i	114	GLU
51	q	2	ARG
16	G	30	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
55	u	6	GLN
53	s	10	GLN
40	f	101	ASN
38	d	115	GLN
40	f	115	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	1531/1535 (99%)	392 (25%)	30 (1%)
31	V	23/24 (95%)	13 (56%)	3 (13%)
32	W	74/76 (97%)	24 (32%)	4 (5%)
33	X	74/77 (96%)	27 (36%)	6 (8%)
34	Y	75/76 (98%)	22 (29%)	2 (2%)
8	7	2899/2921 (99%)	457 (15%)	31 (1%)
9	8	119/120 (99%)	14 (11%)	3 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4795/4829 (99%)	949 (19%)	79 (1%)

5 of 949 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	10	A
8	7	15	G
8	7	34	U
8	7	44	A
8	7	46	G

5 of 79 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	1168	U
33	X	1	G
10	A	1201	A
31	V	17	G
33	X	47	G7M

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

54 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
8	2MA	7	2503	8,64	19,25,26	3.57	6 (31%)	21,37,40	3.54	4 (19%)
10	2MG	A	1207	10	18,26,27	2.85	7 (38%)	16,38,41	1.35	3 (18%)
8	PSU	7	2504	8	18,21,22	4.67	8 (44%)	22,30,33	1.84	5 (22%)
33	4SU	X	8	33	18,21,22	3.79	7 (38%)	26,30,33	2.26	4 (15%)
8	PSU	7	2457	8	18,21,22	4.62	8 (44%)	22,30,33	1.94	5 (22%)
8	5MU	7	747	8	19,22,23	0.23	0	28,32,35	0.34	0
8	OMC	7	2498	8,64	19,22,23	3.24	8 (42%)	26,31,34	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	G7M	Y	46	34	20,26,27	2.81	8 (40%)	17,39,42	1.09	1 (5%)
8	PSU	7	746	8,64	18,21,22	4.67	9 (50%)	22,30,33	1.78	5 (22%)
8	OMG	7	2251	8,32	18,26,27	2.82	7 (38%)	19,38,41	1.51	4 (21%)
33	PSU	X	56	33	18,21,22	4.69	8 (44%)	22,30,33	1.81	5 (22%)
8	6MZ	7	2030	8	18,25,26	2.08	4 (22%)	16,36,39	2.23	3 (18%)
10	2MG	A	1516	10	18,26,27	2.84	7 (38%)	16,38,41	1.38	3 (18%)
33	3AU	X	48	33	24,28,29	2.84	7 (29%)	33,40,43	1.30	3 (9%)
34	H2U	Y	17	34	18,21,22	3.09	5 (27%)	21,30,33	2.03	5 (23%)
32	H2U	W	16	32	18,21,22	3.07	5 (27%)	21,30,33	1.94	5 (23%)
10	G7M	A	527	10	20,26,27	2.80	8 (40%)	17,39,42	1.04	1 (5%)
8	PSU	7	2605	8	18,21,22	4.65	8 (44%)	22,30,33	1.80	5 (22%)
33	G7M	X	47	33	20,26,27	2.83	7 (35%)	17,39,42	1.26	1 (5%)
33	RSP	X	33	33	17,21,22	4.13	7 (41%)	22,30,33	0.82	0
8	2MG	7	1835	8	18,26,27	1.03	2 (11%)	16,38,41	0.84	0
33	5MU	X	55	33	19,22,23	7.20	7 (36%)	28,32,35	3.32	10 (35%)
10	UR3	A	1498	10	19,22,23	2.76	8 (42%)	26,32,35	1.32	2 (7%)
10	2MG	A	966	10	18,26,27	2.85	7 (38%)	16,38,41	1.36	3 (18%)
8	OMU	7	2552	8	19,22,23	3.20	8 (42%)	26,31,34	1.71	5 (19%)
10	MA6	A	1518	10	18,26,27	1.05	2 (11%)	19,38,41	3.38	3 (15%)
32	PSU	W	32	32	18,21,22	4.66	8 (44%)	22,30,33	1.87	5 (22%)
8	1MG	7	745	8	18,26,27	2.74	6 (33%)	19,39,42	1.46	3 (15%)
8	PSU	7	2604	8	18,21,22	4.63	8 (44%)	22,30,33	1.85	5 (22%)
10	4OC	A	1402	10	20,23,24	3.24	8 (40%)	26,32,35	0.90	1 (3%)
32	4SU	W	8	32	18,21,22	3.79	7 (38%)	26,30,33	2.25	5 (19%)
8	2MG	7	2445	8	18,26,27	2.81	7 (38%)	16,38,41	1.41	4 (25%)
33	H2U	X	21	33	18,21,22	3.09	5 (27%)	21,30,33	1.99	5 (23%)
8	PSU	7	955	8	18,21,22	4.63	8 (44%)	22,30,33	1.87	5 (22%)
10	5MC	A	967	10	18,22,23	4.04	7 (38%)	26,32,35	1.01	2 (7%)
32	H2U	W	17	32	18,21,22	3.08	5 (27%)	21,30,33	2.00	5 (23%)
33	2MA	X	38	33	19,25,26	3.67	6 (31%)	21,37,40	3.82	3 (14%)
32	MIA	W	37	32	24,31,32	2.33	3 (12%)	26,44,47	2.62	7 (26%)
10	5MC	A	1407	10	18,22,23	4.04	7 (38%)	26,32,35	1.00	2 (7%)
32	H2U	W	20	32	18,21,22	3.06	5 (27%)	21,30,33	2.01	5 (23%)
32	G7M	W	46	32	20,26,27	2.81	7 (35%)	17,39,42	1.13	1 (5%)
34	PSU	Y	55	34	18,21,22	4.66	8 (44%)	22,30,33	1.87	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	H2U	7	2449	8	18,21,22	3.02	5 (27%)	21,30,33	2.04	5 (23%)
33	H2U	X	17	33	18,21,22	3.10	5 (27%)	21,30,33	1.95	4 (19%)
34	5MU	Y	54	34	19,22,23	0.27	0	28,32,35	0.29	0
32	PSU	W	55	32	18,21,22	4.68	8 (44%)	22,30,33	1.84	5 (22%)
8	3TD	7	1915	8	19,22,23	4.04	7 (36%)	21,32,35	1.72	2 (9%)
8	6MZ	7	1618	8	18,25,26	2.02	3 (16%)	16,36,39	2.23	4 (25%)
8	G7M	7	2069	8	20,26,27	2.77	8 (40%)	17,39,42	1.06	1 (5%)
10	MA6	A	1519	10	18,26,27	1.06	2 (11%)	19,38,41	3.44	3 (15%)
32	5MU	W	54	32	19,22,23	7.19	7 (36%)	28,32,35	3.31	9 (32%)
8	5MC	7	1962	8	18,22,23	4.03	7 (38%)	26,32,35	1.03	2 (7%)
8	PSU	7	2580	8	18,21,22	4.62	9 (50%)	22,30,33	1.89	6 (27%)
8	5MU	7	1939	8	19,22,23	0.27	0	28,32,35	0.27	0

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
8	2MA	7	2503	8,64	-	0/3/25/26	0/3/3/3
10	2MG	A	1207	10	-	0/5/27/28	0/3/3/3
8	PSU	7	2504	8	-	0/7/25/26	0/2/2/2
33	4SU	X	8	33	-	2/7/25/26	0/2/2/2
8	PSU	7	2457	8	-	1/7/25/26	0/2/2/2
8	5MU	7	747	8	-	1/7/25/26	0/2/2/2
8	OMC	7	2498	8,64	-	2/9/27/28	0/2/2/2
34	G7M	Y	46	34	-	2/3/25/26	0/3/3/3
8	PSU	7	746	8,64	-	1/7/25/26	0/2/2/2
8	OMG	7	2251	8,32	-	3/5/27/28	0/3/3/3
33	PSU	X	56	33	-	1/7/25/26	0/2/2/2
8	6MZ	7	2030	8	-	3/5/27/28	0/3/3/3
10	2MG	A	1516	10	-	0/5/27/28	0/3/3/3
33	3AU	X	48	33	-	4/16/34/35	0/2/2/2
34	H2U	Y	17	34	-	7/7/38/39	0/2/2/2
32	H2U	W	16	32	-	1/7/38/39	0/2/2/2
10	G7M	A	527	10	-	2/3/25/26	0/3/3/3
8	PSU	7	2605	8	-	0/7/25/26	0/2/2/2
33	G7M	X	47	33	-	3/3/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	RSP	X	33	33	-	1/7/25/26	0/2/2/2
8	2MG	7	1835	8	-	0/5/27/28	0/3/3/3
33	5MU	X	55	33	-	2/7/25/26	0/2/2/2
10	UR3	A	1498	10	-	2/7/25/26	0/2/2/2
10	2MG	A	966	10	-	0/5/27/28	0/3/3/3
8	OMU	7	2552	8	-	0/9/27/28	0/2/2/2
10	MA6	A	1518	10	-	0/7/29/30	0/3/3/3
32	PSU	W	32	32	-	0/7/25/26	0/2/2/2
8	1MG	7	745	8	-	0/3/25/26	0/3/3/3
8	PSU	7	2604	8	-	0/7/25/26	0/2/2/2
10	4OC	A	1402	10	-	0/9/29/30	0/2/2/2
32	4SU	W	8	32	-	2/7/25/26	0/2/2/2
8	2MG	7	2445	8	-	0/5/27/28	0/3/3/3
33	H2U	X	21	33	-	2/7/38/39	0/2/2/2
8	PSU	7	955	8	-	0/7/25/26	0/2/2/2
10	5MC	A	967	10	-	0/7/25/26	0/2/2/2
32	H2U	W	17	32	-	2/7/38/39	0/2/2/2
33	2MA	X	38	33	-	3/3/25/26	0/3/3/3
32	MIA	W	37	32	-	3/11/33/34	0/3/3/3
10	5MC	A	1407	10	-	0/7/25/26	0/2/2/2
32	H2U	W	20	32	-	1/7/38/39	0/2/2/2
32	G7M	W	46	32	-	3/3/25/26	0/3/3/3
34	PSU	Y	55	34	-	0/7/25/26	0/2/2/2
8	H2U	7	2449	8	-	0/7/38/39	0/2/2/2
33	H2U	X	17	33	-	5/7/38/39	0/2/2/2
34	5MU	Y	54	34	-	2/7/25/26	0/2/2/2
32	PSU	W	55	32	-	0/7/25/26	0/2/2/2
8	3TD	7	1915	8	-	2/7/25/26	0/2/2/2
8	6MZ	7	1618	8	-	4/5/27/28	0/3/3/3
8	G7M	7	2069	8	-	3/3/25/26	0/3/3/3
10	MA6	A	1519	10	-	3/7/29/30	0/3/3/3
32	5MU	W	54	32	-	2/7/25/26	0/2/2/2
8	5MC	7	1962	8	-	0/7/25/26	0/2/2/2
8	PSU	7	2580	8	-	0/7/25/26	0/2/2/2
8	5MU	7	1939	8	-	0/7/25/26	0/2/2/2

The worst 5 of 334 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	X	55	5MU	C4-C5	21.25	1.80	1.44
32	W	54	5MU	C4-C5	21.10	1.79	1.44
32	W	54	5MU	C6-N1	15.74	1.64	1.38
33	X	55	5MU	C6-N1	15.72	1.64	1.38
8	7	1915	3TD	C6-C5	12.53	1.49	1.35

The worst 5 of 189 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	X	38	2MA	C1'-N9-C4	15.64	154.12	126.64
8	7	2503	2MA	C1'-N9-C4	14.16	151.52	126.64
10	A	1519	MA6	N1-C6-N6	-12.74	103.65	117.06
10	A	1518	MA6	N1-C6-N6	-12.24	104.17	117.06
32	W	54	5MU	C5-C4-N3	10.12	123.95	115.31

There are no chirality outliers.

5 of 75 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	527	G7M	O4'-C4'-C5'-O5'
10	A	527	G7M	C3'-C4'-C5'-O5'
34	Y	17	H2U	O4'-C4'-C5'-O5'
34	Y	17	H2U	C3'-C4'-C5'-O5'
34	Y	17	H2U	O4'-C1'-N1-C6

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 293 ligands modelled in this entry, 289 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
62	PUT	7	3001	-	5,5,5	0.25	0	4,4,4	0.52	0
62	PUT	7	3002	-	5,5,5	0.25	0	4,4,4	0.54	0
63	SPD	7	3003	-	9,9,9	0.32	0	8,8,8	0.85	0
65	ALA	Y	102	34	3,4,5	1.17	1 (33%)	2,4,6	3.11	1 (50%)

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
62	PUT	7	3001	-	-	1/3/3/3	-
62	PUT	7	3002	-	-	0/3/3/3	-
63	SPD	7	3003	-	-	0/7/7/7	-
65	ALA	Y	102	34	-	0/0/2/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	Y	102	ALA	O-C	2.01	1.27	1.19

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	Y	102	ALA	O-C-CA	-4.39	110.38	124.28

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	7	3001	PUT	C1-C2-C3-C4

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 [i](#)

There are no chain breaks in this entry.