



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2025 – 02:19 pm GMT

PDB ID : 9FBV
EMDB ID : EMD-50296
Title : 70S Escherichia coli ribosome with P-site initiator tRNA.
Authors : Koller, T.O.; Wilson, D.N.
Deposited on : 2024-05-14
Resolution : 2.40 Å (reported)
Based on initial model : 7K00

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:

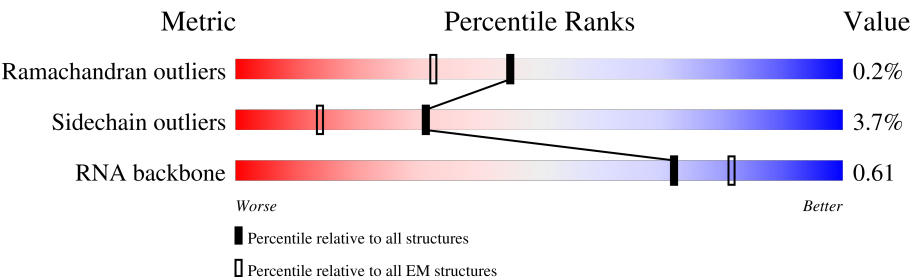
EMDB validation analysis : **FAILED**
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)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

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



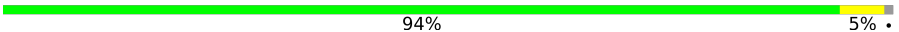

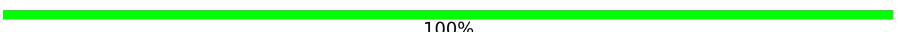
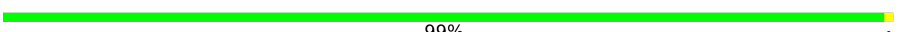
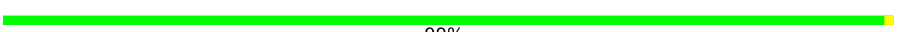







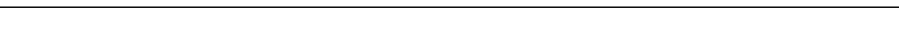

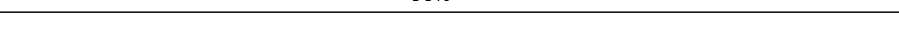
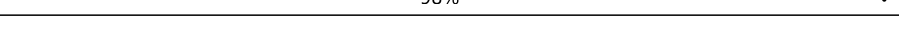
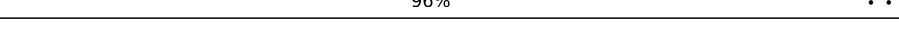

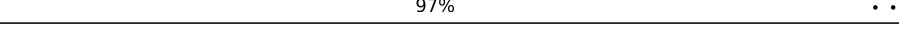
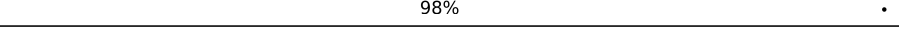


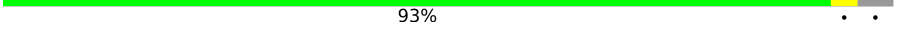


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	55	
2	1	46	
3	2	65	
4	3	38	
5	b	120	
6	c	273	
7	d	209	
8	e	201	
9	f	179	


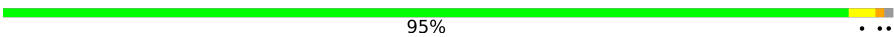



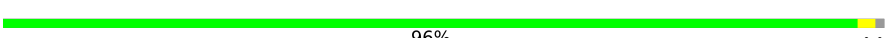




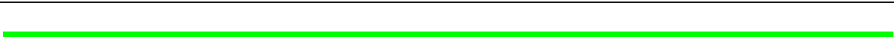


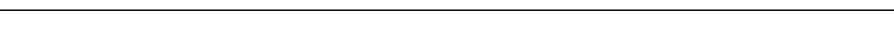
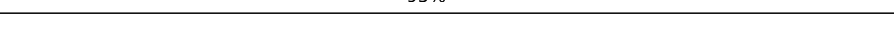
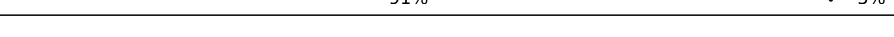
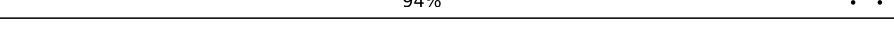
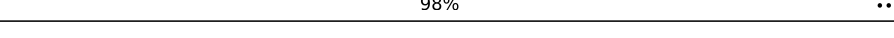

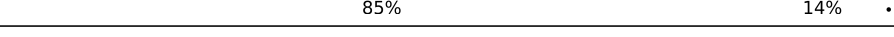
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Mol	Chain	Length	Quality of chain
10	g	177	 94% 5%
11	h	149	 26% 72%
12	i	142	 100%
13	k	144	 99%
14	l	136	 99%
15	m	127	 92% 7%
16	n	117	 97% ..
17	o	115	 99% .
18	p	118	 97% ..
19	q	103	 98% .
20	r	110	 99% .
21	s	100	 89% 7%
22	t	104	 89% 9% .
23	u	94	 96% .
24	v	85	 98% .
25	w	78	 96% ..
26	x	63	 92% 6% .
27	y	59	 97% ..
28	z	57	 98% .
29	4	70	 80% 6% 14%
30	a	2903	 83% 11% 5%
31	j	123	 93% . .
32	B	241	 89% . 7%
33	D	206	 87% 12%
34	E	167	 92% . 7%

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Mol	Chain	Length	Quality of chain
35	F	135	
36	H	130	
37	K	129	
38	L	124	
39	O	89	
40	P	82	
41	Q	84	
42	R	75	
43	T	87	
44	U	71	
45	X	3	
46	C	233	
47	G	179	
48	I	130	
49	J	103	
50	M	118	
51	N	101	
52	S	92	
53	A	1534	
54	Z	77	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 140031 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 Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

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

- Molecule 4 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 6 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 7 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 8 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 10 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 11 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 12 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
l	82	MS6	MET	variant	UNP P0ADY7

- Molecule 15 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 16 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 17 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 18 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 19 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 20 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 21 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 22 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	v	83	Total	C	N	O	S	0	0
			629	388	128	112	1		

- Molecule 25 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 28 is a protein called Large ribosomal subunit protein bL32.

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

- Molecule 29 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 30 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	2753	Total	C	N	O	P	0	0
			59130	26384	10897	19096	2753		

- Molecule 31 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	118	Total	C	N	O	S	0	0
			901	567	170	158	6		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 33 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 34 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 35 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 36 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 37 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	variant	UNP P0A7R9

- Molecule 38 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 39 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 40 is a protein called 30S ribosomal protein S16.

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

- Molecule 41 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 42 is a protein called Small ribosomal subunit protein bS18.

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

- Molecule 43 is a protein called 30S ribosomal protein S20.

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

- Molecule 44 is a protein called Small ribosomal subunit protein bS21.

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

- Molecule 45 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	X	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

- Molecule 46 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 47 is a protein called 30S ribosomal protein S7.

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

- Molecule 48 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 49 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 50 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 52 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	1519	Total	C	N	O	P	0	0
			32608	14548	5986	10555	1519		

- Molecule 54 is a RNA chain called fMet-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Z	73	Total	C	N	O	P	0	0
			1563	696	286	508	73		

- Molecule 55 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	3	1	Total	Zn	0
			1	1	
55	4	1	Total	Zn	0
			1	1	

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	b	5	Total	Mg	0
			5	5	
56	c	1	Total	Mg	0
			1	1	
56	d	1	Total	Mg	0
			1	1	
56	k	1	Total	Mg	0
			1	1	
56	p	1	Total	Mg	0
			1	1	
56	z	1	Total	Mg	0
			1	1	
56	a	205	Total	Mg	0
			205	205	
56	A	91	Total	Mg	0
			91	91	

- Molecule 57 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
57	d	1	Total	K	0
			1	1	
57	a	1	Total	K	0
			1	1	
57	A	1	Total	K	0
			1	1	


- Molecule 58 is water.

Mol	Chain	Residues	Atoms		AltConf
58	a	1	Total 1	O 1	0
58	X	7	Total 7	O 7	0
58	A	28	Total 28	O 28	0
58	Z	3	Total 3	O 3	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.

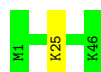
- Molecule 1: Large ribosomal subunit protein bL33

Chain 0: 



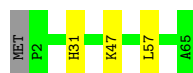
- Molecule 2: Large ribosomal subunit protein bL34

Chain 1: 



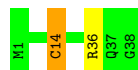
- Molecule 3: Large ribosomal subunit protein bL35

Chain 2: 




- Molecule 4: Large ribosomal subunit protein bL36A

Chain 3: 



- Molecule 5: 5S ribosomal RNA

Chain b: 



- Molecule 6: Large ribosomal subunit protein uL2

Chain c: 



- Molecule 7: Large ribosomal subunit protein uL3

Chain d: 100%

There are no outlier residues recorded for this chain.

- Molecule 8: Large ribosomal subunit protein uL4

Chain e: 98%



- Molecule 9: Large ribosomal subunit protein uL5

Chain f: 96%



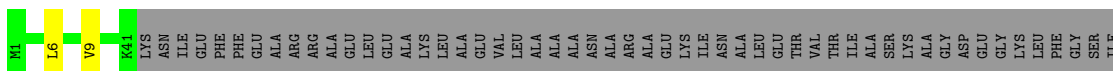
- Molecule 10: Large ribosomal subunit protein uL6

Chain g: 94%



- Molecule 11: Large ribosomal subunit protein bL9

Chain h: 26%



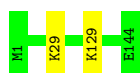
- Molecule 12: Large ribosomal subunit protein uL13

Chain i: 100%

There are no outlier residues recorded for this chain.

- Molecule 13: 50S ribosomal protein L15

Chain k: 99%



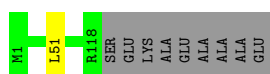
- Molecule 14: Large ribosomal subunit protein uL16

Chain l: 99%



- Molecule 15: Large ribosomal subunit protein bL17

Chain m: 92% 7%



- Molecule 16: Large ribosomal subunit protein uL18

Chain n: 97%



- Molecule 17: Large ribosomal subunit protein bL19

Chain o: 99%



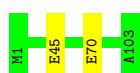
- Molecule 18: Large ribosomal subunit protein bL20

Chain p: 97%



- Molecule 19: Large ribosomal subunit protein bL21

Chain q: 98%



- Molecule 20: Large ribosomal subunit protein uL22

Chain r: 99%



- Molecule 21: Large ribosomal subunit protein uL23

Chain s: 89% 7%



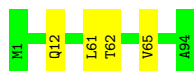
- Molecule 22: Large ribosomal subunit protein uL24

Chain t: 89% 9%



- Molecule 23: 50S ribosomal protein L25

Chain u: 96%



- Molecule 24: Large ribosomal subunit protein bL27

Chain v: 98%



- Molecule 25: Large ribosomal subunit protein bL28

Chain w: 96%



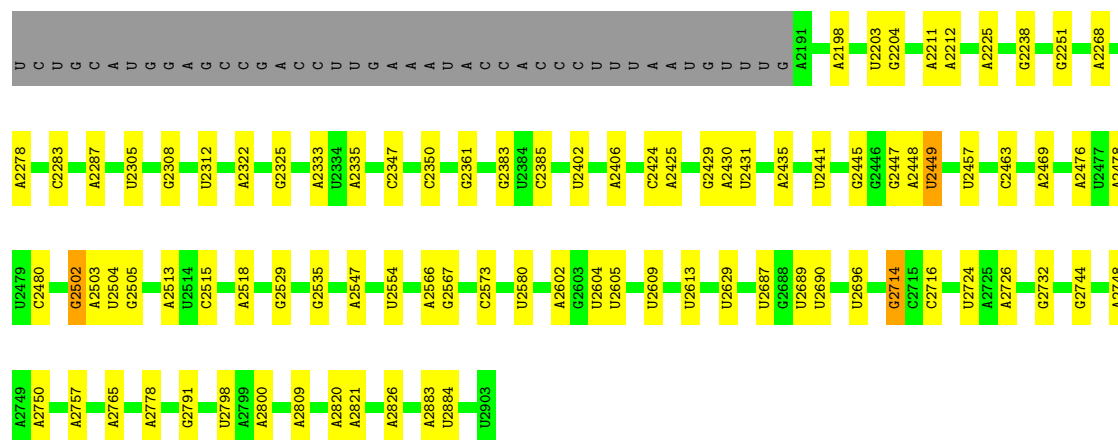
- Molecule 26: Large ribosomal subunit protein uL29

Chain x: 92% 6%



- Molecule 27: Large ribosomal subunit protein uL30

Chain y: 97%



- Molecule 31: Large ribosomal subunit protein uL14

Chain j: 93%



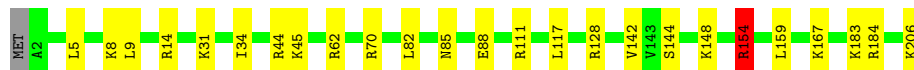
- Molecule 32: 30S ribosomal protein S2

Chain B: 89%



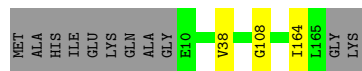
- Molecule 33: Small ribosomal subunit protein uS4

Chain D: 87%



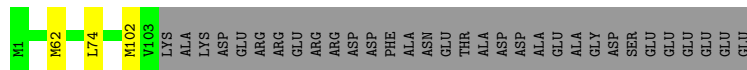
- Molecule 34: Small ribosomal subunit protein uS5

Chain E: 92%



- Molecule 35: 30S ribosomal protein S6, fully modified isoform

Chain F: 74%




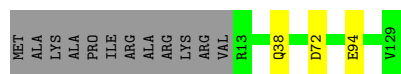
- Molecule 36: Small ribosomal subunit protein uS8

Chain H:  95% . .




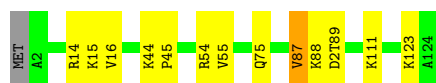
- Molecule 37: Small ribosomal subunit protein uS11

Chain K:  88% . 9%



- Molecule 38: Small ribosomal subunit protein uS12

Chain L:  89% 10% . .



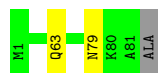
- Molecule 39: Small ribosomal subunit protein uS15

Chain O:  99% .



- Molecule 40: 30S ribosomal protein S16

Chain P:  96% . .




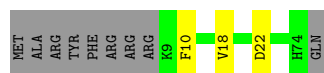
- Molecule 41: Small ribosomal subunit protein uS17

Chain Q:  92% . 6%



- Molecule 42: Small ribosomal subunit protein bS18

Chain R:  84% . 12%



- Molecule 43: 30S ribosomal protein S20

Chain T:  98% ..



- Molecule 44: Small ribosomal subunit protein bS21

Chain U:  93% 6% .




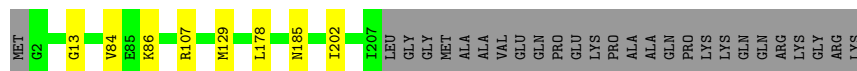
- Molecule 45: messenger RNA

Chain X:  100%


There are no outlier residues recorded for this chain.

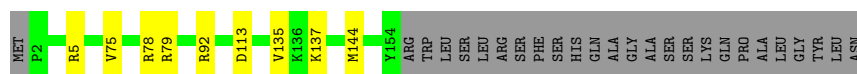
- Molecule 46: Small ribosomal subunit protein uS3

Chain C:  85% . 12%



- Molecule 47: 30S ribosomal protein S7

Chain G:  80% 5% 15%




- Molecule 48: Small ribosomal subunit protein uS9

Chain I:  95% . .



- Molecule 49: Small ribosomal subunit protein uS10

Chain J:  91% . 5%



- Molecule 50: Small ribosomal subunit protein uS13

Chain M:  94% . .



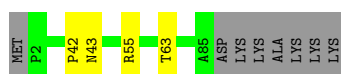
- Molecule 51: Small ribosomal subunit protein uS14

Chain N: 98%



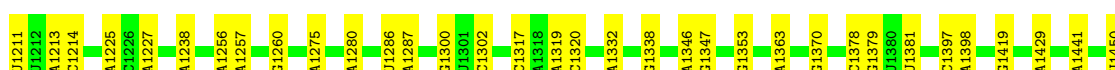
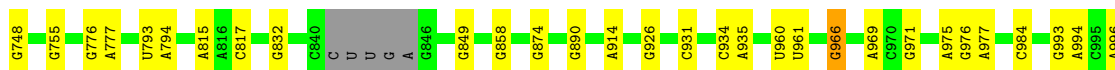
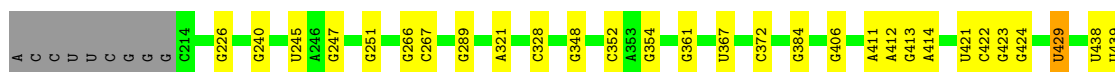
- Molecule 52: Small ribosomal subunit protein uS19

Chain S: 87%



- Molecule 53: 16S ribosomal RNA

Chain A: 85%



- Molecule 54: fMet-tRNA

Chain Z: 77%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	84771	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	900	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, MG, PSU, OMG, MS6, H2U, G7M, 3TD, 6MZ, 2MG, D2T, ZN, 1MG, IAS, MEQ, 5MC, OMU, 4D4, OMC, 4OC, 2MA, K, UR3

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	0.38	0/424	0.64	0/565
2	1	0.45	0/380	0.74	0/498
3	2	0.45	0/513	0.67	0/676
4	3	0.41	0/303	0.77	1/397 (0.3%)
5	b	0.52	0/2850	0.94	0/4444
6	c	0.43	0/2121	0.68	0/2852
7	d	0.41	0/1576	0.64	0/2119
8	e	0.39	0/1571	0.62	0/2113
9	f	0.35	0/1434	0.61	0/1926
10	g	0.36	0/1343	0.64	0/1816
11	h	0.37	0/306	0.64	0/413
12	i	0.38	0/1152	0.63	0/1551
13	k	0.45	0/1062	0.63	0/1413
14	l	0.37	0/1073	0.64	0/1433
15	m	0.41	0/958	0.68	0/1281
16	n	0.37	0/902	0.63	0/1209
17	o	0.39	0/929	0.65	0/1242
18	p	0.43	0/960	0.68	0/1278
19	q	0.40	0/829	0.65	0/1107
20	r	0.40	0/864	0.65	0/1156
21	s	0.36	0/744	0.59	0/994
22	t	0.36	0/787	0.64	0/1051
23	u	0.37	0/766	0.62	0/1025
24	v	0.43	0/637	0.61	0/841
25	w	0.40	0/635	0.67	0/848
26	x	0.34	0/502	0.58	0/667
27	y	0.36	0/453	0.62	0/605
28	z	0.42	0/450	0.67	0/599
29	4	0.40	0/488	0.61	0/649
30	a	0.60	0/65651	1.00	46/102413 (0.0%)
31	j	0.41	0/909	0.65	0/1217

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	B	0.35	0/1784	0.61	0/2403
33	D	0.37	0/1665	0.72	1/2227 (0.0%)
34	E	0.37	0/1165	0.61	0/1568
35	F	0.35	0/858	0.65	0/1160
36	H	0.36	0/989	0.63	0/1326
37	K	0.39	0/884	0.63	0/1191
38	L	0.41	1/960 (0.1%)	0.72	0/1286
39	O	0.37	0/722	0.61	0/964
40	P	0.35	0/653	0.68	0/877
41	Q	0.35	0/650	0.66	0/871
42	R	0.38	0/553	0.64	0/742
43	T	0.35	0/676	0.58	0/895
44	U	0.38	0/597	0.75	0/792
45	X	0.52	0/72	0.81	0/110
46	C	0.36	0/1651	0.61	0/2225
47	G	0.37	0/1219	0.62	0/1635
48	I	0.38	0/1034	0.66	0/1375
49	J	0.36	0/796	0.67	0/1077
50	M	0.36	0/900	0.65	0/1204
51	N	0.37	0/817	0.65	0/1088
52	S	0.39	0/685	0.61	0/922
53	A	0.53	0/36287	0.94	4/56602 (0.0%)
54	Z	0.59	0/1746	0.95	0/2719
All	All	0.53	1/150935 (0.0%)	0.90	52/225657 (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
25	w	0	1
30	a	0	5
32	B	0	1
33	D	0	1
34	E	0	1
36	H	0	1
38	L	0	1
46	C	0	1
51	N	0	1
All	All	0	13

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	L	87	VAL	C-N	5.24	1.46	1.34

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	2056	G	O5'-P-OP1	-8.52	98.03	105.70
30	a	1790	C	O5'-P-OP2	-8.06	98.45	105.70
30	a	1261	C	O5'-P-OP2	-8.05	98.45	105.70
30	a	2687	U	O5'-P-OP2	-7.42	99.02	105.70
30	a	1965	C	O5'-P-OP2	-7.16	99.26	105.70

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	a	1253	A	Sidechain
30	a	395	U	Sidechain
30	a	512	G	Sidechain
30	a	956	G	Sidechain
25	w	16	ASN	Peptide

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	
1	0	49/55 (89%)	47 (96%)	2 (4%)	0	100	100
2	1	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
3	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	3	36/38 (95%)	36 (100%)	0	0	100	100
6	c	269/273 (98%)	262 (97%)	7 (3%)	0	100	100
7	d	206/209 (99%)	201 (98%)	5 (2%)	0	100	100
8	e	199/201 (99%)	194 (98%)	4 (2%)	1 (0%)	25	38
9	f	175/179 (98%)	169 (97%)	6 (3%)	0	100	100
10	g	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
11	h	39/149 (26%)	36 (92%)	3 (8%)	0	100	100
12	i	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
13	k	142/144 (99%)	136 (96%)	5 (4%)	1 (1%)	19	29
14	l	132/136 (97%)	128 (97%)	4 (3%)	0	100	100
15	m	116/127 (91%)	111 (96%)	5 (4%)	0	100	100
16	n	114/117 (97%)	106 (93%)	7 (6%)	1 (1%)	14	22
17	o	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
18	p	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
19	q	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	13	20
20	r	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
21	s	91/100 (91%)	89 (98%)	2 (2%)	0	100	100
22	t	100/104 (96%)	96 (96%)	3 (3%)	1 (1%)	13	20
23	u	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
24	v	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
25	w	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
26	x	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
27	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
28	z	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
29	4	56/70 (80%)	52 (93%)	4 (7%)	0	100	100
31	j	114/123 (93%)	108 (95%)	5 (4%)	1 (1%)	14	22
32	B	222/241 (92%)	210 (95%)	12 (5%)	0	100	100
33	D	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
34	E	154/167 (92%)	150 (97%)	4 (3%)	0	100	100
35	F	101/135 (75%)	96 (95%)	5 (5%)	0	100	100
36	H	127/130 (98%)	122 (96%)	4 (3%)	1 (1%)	16	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	K	113/129 (88%)	108 (96%)	5 (4%)	0	100	100
38	L	120/124 (97%)	110 (92%)	9 (8%)	1 (1%)	16	26
39	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
40	P	79/82 (96%)	72 (91%)	7 (9%)	0	100	100
41	Q	77/84 (92%)	76 (99%)	1 (1%)	0	100	100
42	R	64/75 (85%)	60 (94%)	3 (5%)	1 (2%)	8	11
43	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
44	U	68/71 (96%)	66 (97%)	1 (2%)	1 (2%)	8	12
46	C	204/233 (88%)	192 (94%)	12 (6%)	0	100	100
47	G	151/179 (84%)	145 (96%)	6 (4%)	0	100	100
48	I	125/130 (96%)	115 (92%)	10 (8%)	0	100	100
49	J	96/103 (93%)	91 (95%)	4 (4%)	1 (1%)	13	20
50	M	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
51	N	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
52	S	82/92 (89%)	78 (95%)	4 (5%)	0	100	100
All	All	5479/5913 (93%)	5271 (96%)	197 (4%)	11 (0%)	45	59

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	n	88	LYS
49	J	57	VAL
19	q	45	GLU
13	k	29	LYS
36	H	66	PHE

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	46/49 (94%)	43 (94%)	3 (6%)	14	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	1	38/38 (100%)	37 (97%)	1 (3%)	41	62
3	2	51/52 (98%)	48 (94%)	3 (6%)	16	28
4	3	34/34 (100%)	32 (94%)	2 (6%)	16	28
6	c	216/218 (99%)	214 (99%)	2 (1%)	75	88
7	d	163/163 (100%)	163 (100%)	0	100	100
8	e	165/165 (100%)	162 (98%)	3 (2%)	54	73
9	f	148/150 (99%)	142 (96%)	6 (4%)	26	44
10	g	137/138 (99%)	128 (93%)	9 (7%)	14	23
11	h	32/114 (28%)	30 (94%)	2 (6%)	15	25
12	i	116/116 (100%)	116 (100%)	0	100	100
13	k	103/103 (100%)	102 (99%)	1 (1%)	73	86
14	l	107/107 (100%)	105 (98%)	2 (2%)	52	72
15	m	98/103 (95%)	97 (99%)	1 (1%)	73	86
16	n	86/87 (99%)	84 (98%)	2 (2%)	45	66
17	o	99/100 (99%)	99 (100%)	0	100	100
18	p	89/90 (99%)	87 (98%)	2 (2%)	47	67
19	q	84/84 (100%)	83 (99%)	1 (1%)	67	82
20	r	93/93 (100%)	92 (99%)	1 (1%)	70	84
21	s	80/84 (95%)	76 (95%)	4 (5%)	20	36
22	t	83/85 (98%)	75 (90%)	8 (10%)	7	10
23	u	78/78 (100%)	74 (95%)	4 (5%)	20	35
24	v	62/63 (98%)	62 (100%)	0	100	100
25	w	67/68 (98%)	66 (98%)	1 (2%)	60	77
26	x	54/55 (98%)	50 (93%)	4 (7%)	11	19
27	y	48/49 (98%)	47 (98%)	1 (2%)	48	69
28	z	47/48 (98%)	47 (100%)	0	100	100
29	4	55/62 (89%)	51 (93%)	4 (7%)	11	20
31	j	99/104 (95%)	96 (97%)	3 (3%)	36	57
32	B	186/199 (94%)	177 (95%)	9 (5%)	21	37
33	D	172/173 (99%)	147 (86%)	25 (14%)	2	3
34	E	119/126 (94%)	117 (98%)	2 (2%)	56	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	F	90/116 (78%)	87 (97%)	3 (3%)	33	53
36	H	104/105 (99%)	100 (96%)	4 (4%)	28	47
37	K	89/98 (91%)	86 (97%)	3 (3%)	32	52
38	L	102/103 (99%)	92 (90%)	10 (10%)	6	10
39	O	76/77 (99%)	76 (100%)	0	100	100
40	P	65/65 (100%)	63 (97%)	2 (3%)	35	56
41	Q	73/78 (94%)	71 (97%)	2 (3%)	40	60
42	R	57/65 (88%)	55 (96%)	2 (4%)	31	51
43	T	65/66 (98%)	64 (98%)	1 (2%)	60	77
44	U	60/61 (98%)	57 (95%)	3 (5%)	20	36
46	C	170/190 (90%)	163 (96%)	7 (4%)	26	44
47	G	126/147 (86%)	117 (93%)	9 (7%)	12	20
48	I	105/107 (98%)	101 (96%)	4 (4%)	28	47
49	J	86/90 (96%)	83 (96%)	3 (4%)	31	51
50	M	93/96 (97%)	89 (96%)	4 (4%)	25	42
51	N	83/84 (99%)	83 (100%)	0	100	100
52	S	72/79 (91%)	68 (94%)	4 (6%)	17	30
All	All	4571/4825 (95%)	4404 (96%)	167 (4%)	31	48

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	K	94	GLU
47	G	5	ARG
38	L	54	ARG
42	R	10	PHE
47	G	137	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
37	K	81	ASN
46	C	100	GLN
37	K	109	ASN
43	T	68	HIS

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Mol	Chain	Res	Type
46	C	140	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	a	2745/2903 (94%)	285 (10%)	0
45	X	2/3 (66%)	0	0
5	b	118/120 (98%)	12 (10%)	0
53	A	1515/1534 (98%)	192 (12%)	25 (1%)
54	Z	71/77 (92%)	14 (19%)	3 (4%)
All	All	4451/4637 (95%)	503 (11%)	28 (0%)

5 of 503 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	b	34	A
5	b	35	C
5	b	36	C
5	b	37	C
5	b	44	G

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	A	1026	G
54	Z	47	U
53	A	1124	G
53	A	1505	G
53	A	1045	C

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

37 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
7	MEQ	d	150	7	8,9,10	0.43	0	5,10,12	0.97	0
30	5MU	a	747	30	19,22,23	0.35	0	28,32,35	0.39	0
30	PSU	a	2604	30	18,21,22	0.89	1 (5%)	22,30,33	0.93	1 (4%)
30	5MC	a	1962	30	18,22,23	0.33	0	26,32,35	0.59	0
30	2MG	a	1835	30	18,26,27	1.14	2 (11%)	16,38,41	0.70	0
30	PSU	a	746	56,30	18,21,22	0.93	1 (5%)	22,30,33	0.67	0
30	PSU	a	2504	57,30	18,21,22	0.95	1 (5%)	22,30,33	0.71	0
30	6MZ	a	1618	30	18,25,26	0.83	0	16,36,39	0.79	0
53	5MC	A	967	53	18,22,23	0.38	0	26,32,35	0.59	0
30	1MG	a	745	30	18,26,27	1.11	2 (11%)	19,39,42	0.52	0
14	4D4	l	81	14	9,11,12	0.66	0	8,13,15	0.69	0
30	5MU	a	1939	30	19,22,23	0.39	0	28,32,35	0.44	0
53	2MG	A	966	53	18,26,27	1.03	2 (11%)	16,38,41	0.63	0
53	UR3	A	1498	53,57	19,22,23	0.41	0	26,32,35	0.75	1 (3%)
30	PSU	a	1911	30	18,21,22	0.91	1 (5%)	22,30,33	0.63	0
53	2MG	A	1516	53	18,26,27	0.98	2 (11%)	16,38,41	0.90	0
30	PSU	a	955	30	18,21,22	0.83	1 (5%)	22,30,33	0.73	0
53	4OC	A	1402	53	20,23,24	0.40	0	26,32,35	0.57	0
53	5MC	A	1407	53	18,22,23	0.36	0	26,32,35	0.66	0
53	G7M	A	527	53	20,26,27	1.11	3 (15%)	17,39,42	0.50	0
30	2MG	a	2445	30	18,26,27	1.14	2 (11%)	16,38,41	0.75	1 (6%)
30	2MA	a	2503	56,30	19,25,26	1.24	3 (15%)	21,37,40	1.78	4 (19%)
30	H2U	a	2449	30	18,21,22	0.59	0	21,30,33	1.10	3 (14%)
30	6MZ	a	2030	30	18,25,26	0.75	0	16,36,39	0.83	1 (6%)
37	IAS	K	119	37	6,7,8	0.86	0	6,8,10	0.99	0
30	OMG	a	2251	30,54	18,26,27	1.05	3 (16%)	19,38,41	0.72	0
53	PSU	A	516	53,56	18,21,22	0.90	1 (5%)	22,30,33	0.59	0
30	PSU	a	2457	30	18,21,22	1.05	1 (5%)	22,30,33	0.63	0
30	PSU	a	2580	30	18,21,22	0.94	1 (5%)	22,30,33	0.81	1 (4%)
30	OMU	a	2552	30	19,22,23	0.36	0	26,31,34	0.52	0
53	2MG	A	1207	53	18,26,27	1.09	2 (11%)	16,38,41	0.73	0
30	3TD	a	1915	30	18,22,23	1.07	1 (5%)	22,32,35	0.61	0
30	PSU	a	1917	30	18,21,22	0.96	1 (5%)	22,30,33	0.60	0
30	OMC	a	2498	56,30	19,22,23	0.50	0	26,31,34	0.54	0
30	PSU	a	2605	30	18,21,22	0.94	1 (5%)	22,30,33	0.80	1 (4%)
38	D2T	L	89	38	7,9,10	0.94	0	6,11,13	1.55	2 (33%)
30	G7M	a	2069	30	20,26,27	1.29	3 (15%)	17,39,42	0.68	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
7	MEQ	d	150	7	-	2/8/9/11	-
30	5MU	a	747	30	-	1/7/25/26	0/2/2/2
30	PSU	a	2604	30	-	0/7/25/26	0/2/2/2
30	5MC	a	1962	30	-	2/7/25/26	0/2/2/2
30	2MG	a	1835	30	-	0/5/27/28	0/3/3/3
30	PSU	a	746	56,30	-	1/7/25/26	0/2/2/2
30	PSU	a	2504	57,30	-	0/7/25/26	0/2/2/2
30	6MZ	a	1618	30	-	0/5/27/28	0/3/3/3
53	5MC	A	967	53	-	0/7/25/26	0/2/2/2
30	1MG	a	745	30	-	0/3/25/26	0/3/3/3
14	4D4	l	81	14	-	1/11/12/14	-
30	5MU	a	1939	30	-	0/7/25/26	0/2/2/2
53	2MG	A	966	53	-	0/5/27/28	0/3/3/3
53	UR3	A	1498	53,57	-	0/7/25/26	0/2/2/2
30	PSU	a	1911	30	-	0/7/25/26	0/2/2/2
53	2MG	A	1516	53	-	0/5/27/28	0/3/3/3
30	PSU	a	955	30	-	0/7/25/26	0/2/2/2
53	4OC	A	1402	53	-	0/9/29/30	0/2/2/2
53	5MC	A	1407	53	-	0/7/25/26	0/2/2/2
53	G7M	A	527	53	-	1/3/25/26	0/3/3/3
30	2MG	a	2445	30	-	1/5/27/28	0/3/3/3
30	2MA	a	2503	56,30	-	1/3/25/26	0/3/3/3
30	H2U	a	2449	30	-	0/7/38/39	0/2/2/2
30	6MZ	a	2030	30	-	2/5/27/28	0/3/3/3
37	IAS	K	119	37	-	0/7/7/8	-
30	OMG	a	2251	30,54	-	1/5/27/28	0/3/3/3
53	PSU	A	516	53,56	-	0/7/25/26	0/2/2/2
30	PSU	a	2457	30	-	0/7/25/26	0/2/2/2
30	PSU	a	2580	30	-	0/7/25/26	0/2/2/2
30	OMU	a	2552	30	-	0/9/27/28	0/2/2/2
53	2MG	A	1207	53	-	0/5/27/28	0/3/3/3
30	3TD	a	1915	30	-	2/7/25/26	0/2/2/2
30	PSU	a	1917	30	-	0/7/25/26	0/2/2/2
30	OMC	a	2498	56,30	-	0/9/27/28	0/2/2/2
30	PSU	a	2605	30	-	0/7/25/26	0/2/2/2
38	D2T	L	89	38	-	2/7/12/14	-
30	G7M	a	2069	30	-	2/3/25/26	0/3/3/3

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2457	PSU	C6-C5	4.05	1.40	1.35
30	a	1915	3TD	C6-C5	4.01	1.40	1.35
30	a	1911	PSU	C6-C5	3.58	1.39	1.35
30	a	1917	PSU	C6-C5	3.57	1.39	1.35
30	a	2605	PSU	C6-C5	3.43	1.39	1.35

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	2503	2MA	C5-C6-N1	-5.73	117.25	121.01
30	a	2503	2MA	C5-C6-N6	3.78	126.10	120.35
30	a	2449	H2U	C4-N3-C2	-2.99	123.31	125.79
30	a	2449	H2U	O2-C2-N1	-2.49	119.98	123.11
30	a	2449	H2U	N3-C2-N1	2.45	119.24	116.65

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
38	L	89	D2T	SB-CB-CG-OD2
30	a	746	PSU	O4'-C1'-C5-C6
30	a	1915	3TD	C3'-C4'-C5'-O5'
30	a	1915	3TD	O4'-C4'-C5'-O5'
30	a	2251	OMG	C1'-C2'-O2'-CM2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 311 ligands modelled in this entry, 311 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.