



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2025 – 06:35 pm GMT

PDB ID : 9GHF
EMDB ID : EMD-51355
Title : Staphylococcus aureus FusB bound to the large subunit of the Escherichia coli 70S ribosome (FusB-70S:LSU)
Authors : Gonzalez-Lopez, A.; Selmer, M.
Deposited on : 2024-08-15
Resolution : 2.40 Å (reported)
Based on initial models : 9GHE, 8P2H

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:

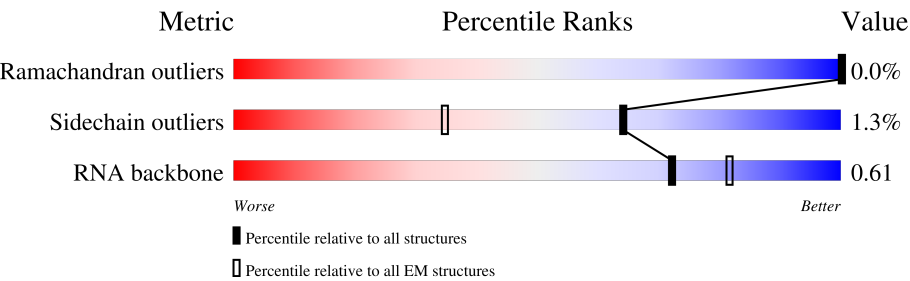
EMDB validation analysis : **FAILED**
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)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



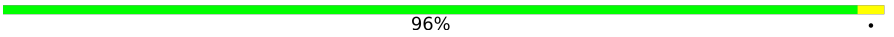



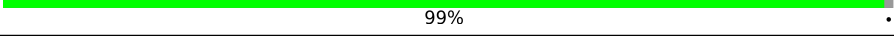
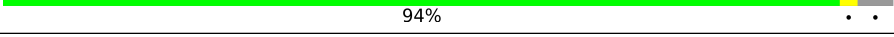


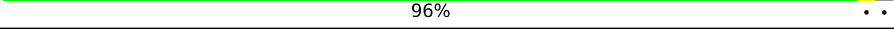
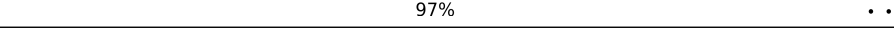
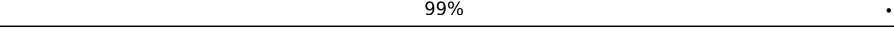
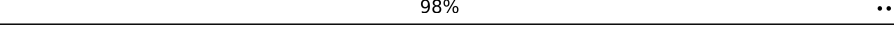
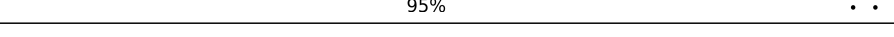
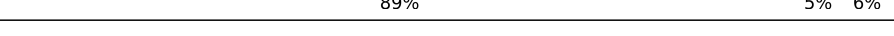


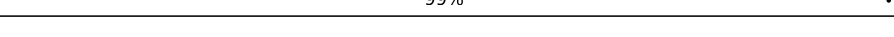

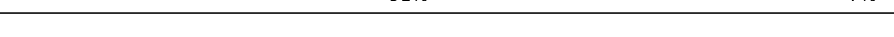






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	<div><div>89%</div><div>9%</div><div></div><div></div></div>
2	1	46	<div><div>98%</div><div></div><div></div><div></div></div>
3	2	65	<div><div>95%</div><div></div><div></div><div></div></div>
4	3	38	<div><div>100%</div><div></div><div></div><div></div></div>
5	4	70	<div><div>84%</div><div></div><div></div><div></div></div>
6	9	24	<div><div>25%</div><div>17%</div><div>58%</div><div></div></div>
7	A	1554	<div><div>84%</div><div>14%</div><div></div><div></div></div>
8	B	241	<div><div>88%</div><div>8%</div><div></div><div></div></div>
9	C	233	<div><div>88%</div><div>12%</div><div></div><div></div></div>

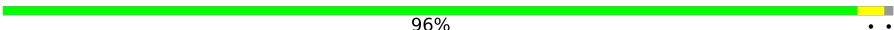
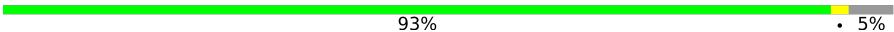

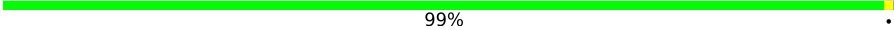
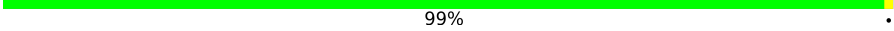
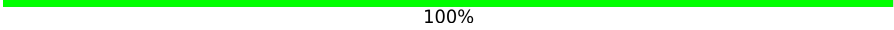
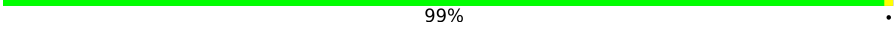
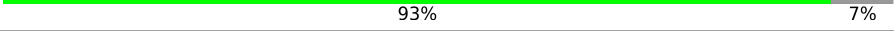
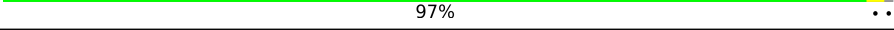
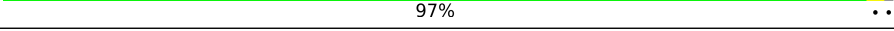
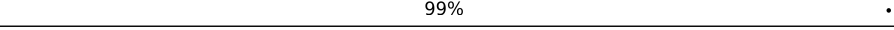
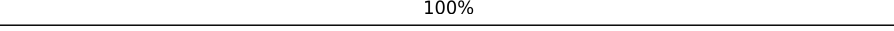
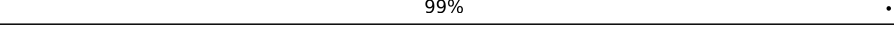
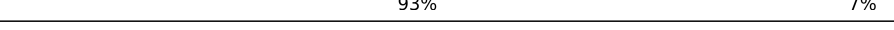

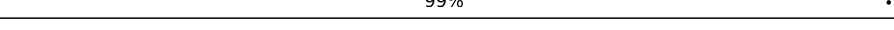

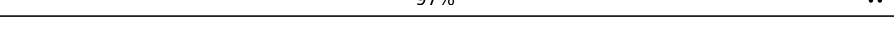
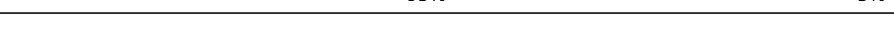


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Mol	Chain	Length	Quality of chain
10	D	206	 96% .
11	E	167	 90% . 8%
12	F	135	 75% 25%
13	G	179	 80% . 16%
14	H	130	 99% .
15	I	130	 94% . .
16	J	103	 90% . 7%
17	K	129	 91% 9%
18	L	124	 96% . .
19	M	118	 97% . .
20	N	101	 99% .
21	O	89	 98% . .
22	P	82	 95% . .
23	Q	84	 89% 5% 6%
24	R	75	 84% . 15%
25	S	92	 91% 9%
26	T	87	 99% .
27	U	71	 76% . 23%
28	V	213	 91% . 7%
29	Z	77	 70% 29% .
30	a	2930	 83% 11% 5%
31	b	119	 92% 8%
32	c	273	 99% . .
33	d	209	 99% .
34	e	201	 100%

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Mol	Chain	Length	Quality of chain
35	f	179	 96% ..
36	g	177	 93% • 5%
37	h	149	 26% • 72%
38	i	142	 99% ..
39	j	123	 99% •
40	k	144	 100%
41	l	136	 99% •
42	m	127	 93% 7%
43	n	117	 97% ..
44	o	115	 97% ..
45	p	118	 99% •
46	q	103	 100%
47	r	110	 99% •
48	s	100	 93% 7%
49	t	104	 88% • 11%
50	u	94	 99% •
51	v	85	 88% 12%
52	w	78	 97% ..
53	x	63	 95% 5%
54	y	59	 98% •
55	z	57	 95% 5%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 141978 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 L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	50	Total	C	N	O	0	0
			413	267	75	71		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	45	Total	C	N	O	S	0	0
			367	222	88	55	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

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 50S ribosomal protein L36.

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 protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 6 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	9	10	Total	C	N	O	P	0	0
			218	98	45	65	10		

- Molecule 7 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	1514	Total	C	N	O	P	0	0
			32500	14503	5963	10520	1514		

- Molecule 8 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	222	Total	C	N	O	S	0	0
			1737	1099	312	318	8		

- Molecule 9 is a protein called 30S ribosomal protein S3.

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

- Molecule 10 is a protein called 30S ribosomal protein S4.

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

- Molecule 11 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	154	Total	C	N	O	S	0	0
			1135	706	215	208	6		

- Molecule 12 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	101	Total	C	N	O	S	0	0
			824	520	149	149	6		

- Molecule 13 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	150	Total	C	N	O	S	0	0
			1176	732	226	214	4		

- Molecule 14 is a protein called 30S ribosomal protein S8.

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

- Molecule 15 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	125	Total	C	N	O	S	0	0
			1001	622	200	176	3		

- Molecule 16 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	96	Total	C	N	O	S	0	0
			775	487	148	139	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	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	modified residue	UNP P0A7R9

- Molecule 18 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	121	Total	C	N	O	S	0	0
			942	582	193	162	5		

- Molecule 19 is a protein called 30S ribosomal protein S13.

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

- Molecule 20 is a protein called 30S ribosomal protein S14.

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

- Molecule 21 is a protein called 30S ribosomal protein S15.

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

- Molecule 22 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	79	Total	C	N	O	S	0	0
			629	394	124	110	1		

- Molecule 23 is a protein called 30S ribosomal protein S17.

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

- Molecule 24 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	64	Total	C	N	O	S	0	0
			524	330	99	94	1		

- Molecule 25 is a protein called 30S ribosomal protein S19.

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

- Molecule 26 is a protein called 30S ribosomal protein S20.

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

- Molecule 27 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	55	Total	C	N	O	S	0	0
			460	287	95	77	1		

- Molecule 28 is a protein called Far1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	198	Total	C	N	O	S	1	0
			1659	1075	271	306	7		

- Molecule 29 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	2782	Total	C	N	O	P	0	0
			59756	26665	11017	19292	2782		

- Molecule 31 is a RNA chain called 5S rRNA.

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

- Molecule 32 is a protein called 50S ribosomal protein L2.

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

- Molecule 33 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	207	Total	C	N	O	S	0	0
			1552	972	286	291	3		

- Molecule 34 is a protein called 50S ribosomal protein L4.

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

- Molecule 35 is a protein called 50S ribosomal protein L5.

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

- Molecule 36 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	168	Total	C	N	O	S	0	0
			1255	791	228	234	2		

- Molecule 37 is a protein called 50S ribosomal protein L9.

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

- Molecule 38 is a protein called 50S ribosomal protein L13.

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

- Molecule 39 is a protein called 50S ribosomal protein L14.

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

- Molecule 40 is a protein called 50S ribosomal protein L15.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	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	modified residue	UNP P0ADY7

- Molecule 42 is a protein called 50S ribosomal protein L17.

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

- Molecule 43 is a protein called 50S ribosomal protein L18.

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

- Molecule 44 is a protein called 50S ribosomal protein L19.

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

- Molecule 45 is a protein called 50S ribosomal protein L20.

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

- Molecule 46 is a protein called 50S ribosomal protein L21.

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

- Molecule 47 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	109	Total	C	N	O	S	0	0
			845	526	162	154	3		

- Molecule 48 is a protein called 50S ribosomal protein L23.

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

- Molecule 49 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	93	Total	C	N	O	S	0	0
			717	452	135	130			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	93	Total	C	N	O	S	0	0
			745	474	136	133	2		

- Molecule 51 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	75	Total	C	N	O	S	0	0
			569	353	113	102	1		

- Molecule 52 is a protein called 50S ribosomal protein L28.

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

- Molecule 53 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	60	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 54 is a protein called 50S ribosomal protein L30.

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

- Molecule 55 is a protein called 50S ribosomal protein L32.

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

- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total	Zn	0
			1	1	
56	4	1	Total	Zn	0
			1	1	
56	V	1	Total	Zn	0
			1	1	

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

Mol	Chain	Residues	Atoms		AltConf
57	A	32	Total	K	0
			32	32	
57	F	1	Total	K	0
			1	1	
57	a	75	Total	K	0
			75	75	
57	c	3	Total	K	0
			3	3	
57	e	1	Total	K	0
			1	1	

- Molecule 58 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	A	55	Total	Mg	0
			55	55	
58	a	241	Total	Mg	0
			241	241	
58	b	3	Total	Mg	0
			3	3	

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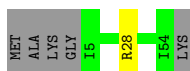
Mol	Chain	Residues	Atoms		AltConf
58	c	2	Total 2	Mg 2	0
58	d	1	Total 1	Mg 1	0
58	z	1	Total 1	Mg 1	0

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 L33

Chain 0:  89% 9%



- Molecule 2: 50S ribosomal protein L34

Chain 1:  98%



- Molecule 3: 50S ribosomal protein L35

Chain 2:  95%




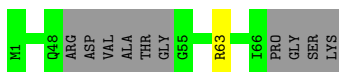
- Molecule 4: 50S ribosomal protein L36

Chain 3:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: 50S ribosomal protein L31

Chain 4:  84% 14%

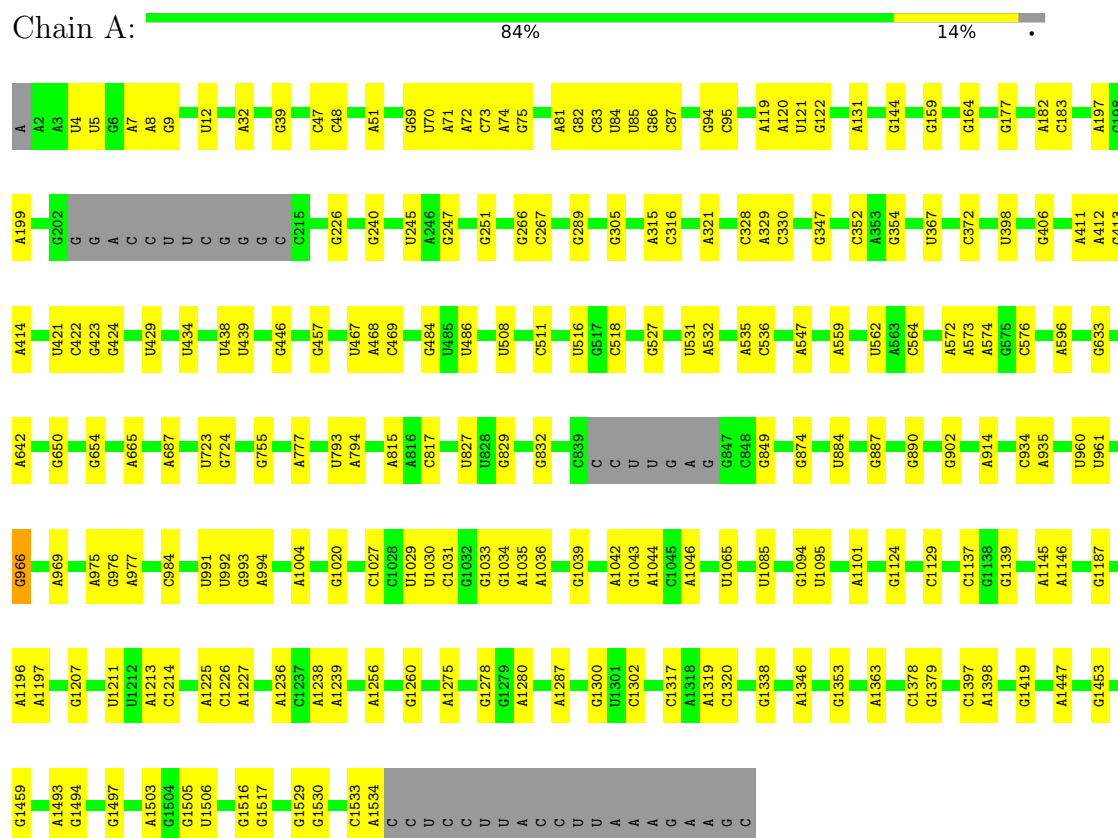


- Molecule 6: mRNA

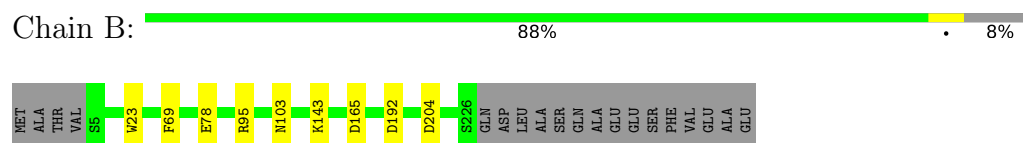
Chain 9:  25% 17% 58%



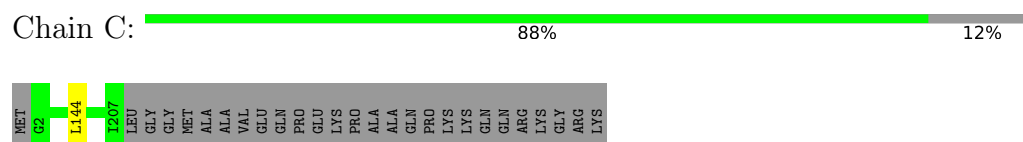
- Molecule 7: 16S rRNA



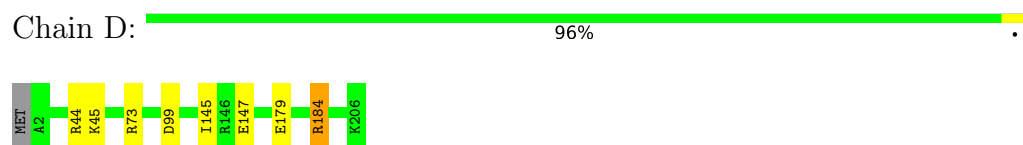
- Molecule 8: 30S ribosomal protein S2




- Molecule 9: 30S ribosomal protein S3



- Molecule 10: 30S ribosomal protein S4



- Molecule 11: 30S ribosomal protein S5

Chain E:  90% • 8%


MET
ALA
HIS
ILE
GLU
LYS
GLN
ALA
GLY
GLU
L11
N77
E101
N148
L164
LEU
GLY
LYS

- Molecule 12: 30S ribosomal protein S6

Chain F:  75% 25%

M1
P101
MET
VAL
LYS
ALA
LYS
ASP
GLU
GLU
ARG
ARG
GLU
ARG
ASP
ASP
PHE
ALA
ASN
GLU
THR
ALA
ASP
ASP
ALA
GLU
GLY
ASP
SER
GLU
GLU
GLU
GLU
GLU

- Molecule 13: 30S ribosomal protein S7

Chain G:  80% • 16%

MET
P2
E63
V75
R78
R111
V135
D140
F151
ALA
HIS
TYR
ARG
TRP
LEU
SER
LEU
SER
ARG
SER
PHE
SER
HIS
GLN
ALA
GLY
ALA
SER
SER
LYS
GLN
PRO
ALA
LEU
GLY
TYR
LEU
ASN

- Molecule 14: 30S ribosomal protein S8

Chain H:  99% •


MET
S2
A130

- Molecule 15: 30S ribosomal protein S9

Chain I:  94% • •

MET
ALA
GLN
R4
R41
E42
R123
S128
LYS
ARG

- Molecule 16: 30S ribosomal protein S10

Chain J:  90% • 7%

MET
GLN
ASN
GLN
R5
R31
THR
GLY
A34
V57
R62
D75
L102
GLY

- Molecule 17: Small ribosomal subunit protein uS11

Chain K:  91% 9%

MET
ALA
LYS
PRO
ILE
ARG
ALA
ARG
LYS
ARG
VAL
R13
V129

- Molecule 18: 30S ribosomal protein S12

Chain L:  96% ..



- Molecule 19: 30S ribosomal protein S13

Chain M:  97% ..



- Molecule 20: 30S ribosomal protein S14

Chain N:  99% .



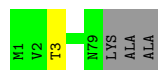
- Molecule 21: 30S ribosomal protein S15

Chain O:  98% ..




- Molecule 22: 30S ribosomal protein S16

Chain P:  95% ..




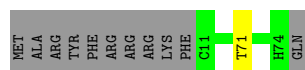
- Molecule 23: 30S ribosomal protein S17

Chain Q:  89% 5% 6%




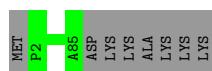
- Molecule 24: 30S ribosomal protein S18

Chain R:  84% . 15%



- Molecule 25: 30S ribosomal protein S19

Chain S:  91% 9%




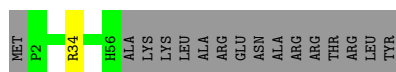
- Molecule 26: 30S ribosomal protein S20

Chain T:  99%



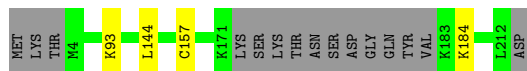
- Molecule 27: 30S ribosomal protein S21

Chain U:  76% 23%



- Molecule 28: Far1

Chain V:  91% 7%




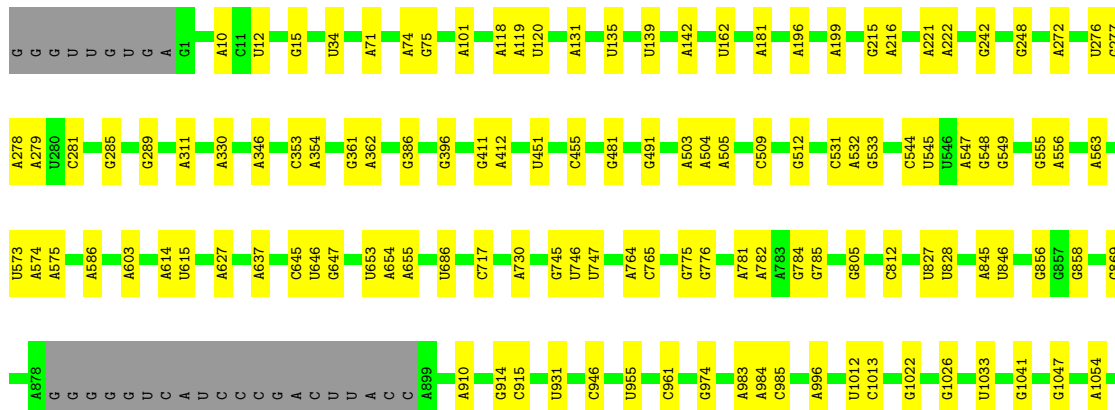
- Molecule 29: tRNA

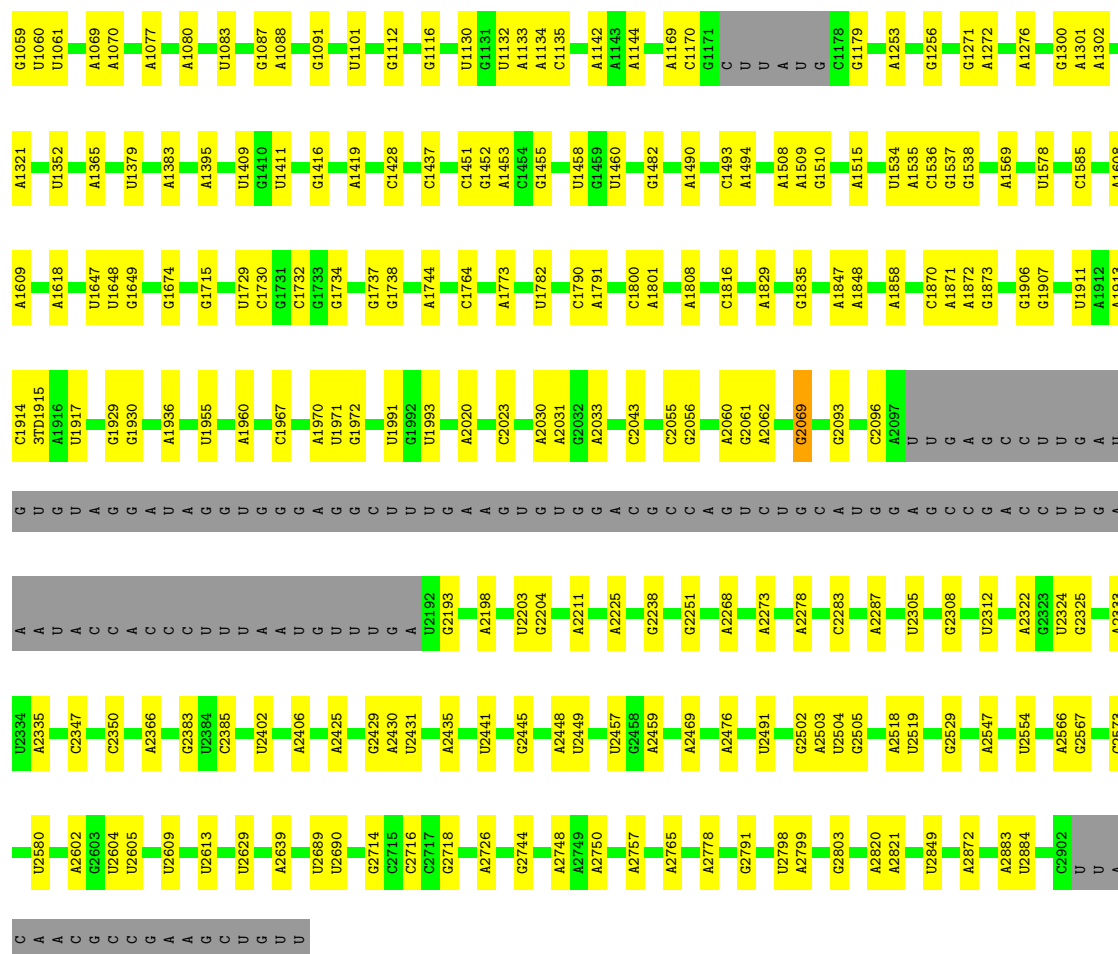
Chain Z:  70% 29%



- Molecule 30: 23S rRNA

Chain a:  83% 11% 5%





• Molecule 31: 5S rRNA

Chain b: 92% 8%



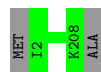
• Molecule 32: 50S ribosomal protein L2

Chain c: 99% 1%



• Molecule 33: 50S ribosomal protein L3

Chain d: 99% 1%



• Molecule 34: 50S ribosomal protein L4

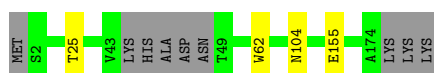
- Molecule 35: 50S ribosomal protein L5

Chain f: 96%



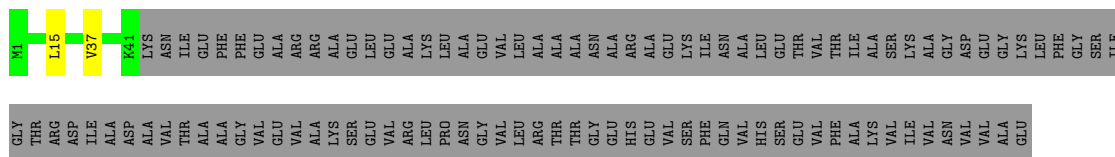
- Molecule 36: 50S ribosomal protein L6

Chain g: 93% • 5%



- Molecule 37: 50S ribosomal protein L9

Chain h:  26% . 72%



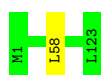
- Molecule 38: 50S ribosomal protein L13

Chain i: 99%



- Molecule 39: 50S ribosomal protein L14

Chain j: 99%



- Molecule 40: 50S ribosomal protein L15

Chain k: 100%

There are no outlier residues recorded for this chain.

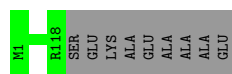
- Molecule 41: Large ribosomal subunit protein uL16

Chain l:  99% .



- Molecule 42: 50S ribosomal protein L17

Chain m:  93% 7%



- Molecule 43: 50S ribosomal protein L18

Chain n:  97% ..



- Molecule 44: 50S ribosomal protein L19

Chain o:  97% ..



- Molecule 45: 50S ribosomal protein L20

Chain p:  99% .



- Molecule 46: 50S ribosomal protein L21

Chain q:  100%

There are no outlier residues recorded for this chain.

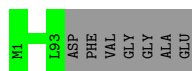
- Molecule 47: 50S ribosomal protein L22

Chain r:  99% .



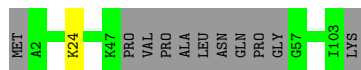
- Molecule 48: 50S ribosomal protein L23

Chain s:  93% 7%



- Molecule 49: 50S ribosomal protein L24

Chain t: 88% 11%



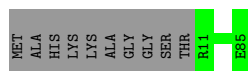
- Molecule 50: 50S ribosomal protein L25

Chain u: 99%



- Molecule 51: 50S ribosomal protein L27

Chain v: 88% 12%



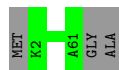
- Molecule 52: 50S ribosomal protein L28

Chain w: 97%



- Molecule 53: 50S ribosomal protein L29

Chain x: 95% 5%



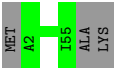
- Molecule 54: 50S ribosomal protein L30

Chain y: 98%



- Molecule 55: 50S ribosomal protein L32

Chain z: 95% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29766	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.47	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	130000	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: D2T, 5MU, 6MZ, IAS, 4D4, OMG, ZN, 1MG, PSU, 5MC, MEQ, 3TD, H2U, MA6, K, UR3, MG, 2MG, 4OC, OMC, 2MA, MS6, OMU, G7M

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	0.31	0/420	0.54	0/560
2	1	0.29	0/370	0.60	0/487
3	2	0.32	0/513	0.56	0/676
4	3	0.29	0/303	0.56	0/397
5	4	0.32	0/488	0.56	0/649
6	9	0.46	0/245	0.90	0/380
7	A	0.42	0/36110	0.89	0/56322
8	B	0.29	0/1768	0.54	0/2381
9	C	0.28	0/1651	0.53	0/2225
10	D	0.29	0/1665	0.54	0/2227
11	E	0.29	0/1148	0.53	0/1545
12	F	0.28	0/843	0.51	0/1140
13	G	0.29	0/1190	0.53	0/1595
14	H	0.29	0/989	0.54	0/1326
15	I	0.29	0/1013	0.56	0/1350
16	J	0.28	0/784	0.59	0/1059
17	K	0.30	0/884	0.54	0/1191
18	L	0.29	0/945	0.60	0/1268
19	M	0.29	0/900	0.53	0/1204
20	N	0.30	0/817	0.52	0/1088
21	O	0.29	0/722	0.51	0/964
22	P	0.28	0/639	0.57	0/859
23	Q	0.28	0/650	0.54	0/871
24	R	0.29	0/532	0.54	0/715
25	S	0.32	0/685	0.54	0/922
26	T	0.28	0/676	0.49	0/895
27	U	0.31	0/467	0.62	0/620
28	V	0.29	0/1693	0.47	0/2274
29	Z	0.46	0/1813	0.88	0/2825
30	a	0.41	0/66355	0.89	6/103511 (0.0%)
31	b	0.43	0/2850	0.90	0/4444

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	c	0.29	0/2121	0.57	0/2852
33	d	0.29	0/1562	0.53	0/2102
34	e	0.28	0/1571	0.52	0/2113
35	f	0.29	0/1434	0.54	0/1926
36	g	0.29	0/1273	0.54	0/1725
37	h	0.30	0/306	0.56	0/413
38	i	0.28	0/1144	0.52	0/1541
39	j	0.28	0/955	0.56	0/1279
40	k	0.31	0/1062	0.53	0/1413
41	l	0.30	0/1073	0.55	0/1433
42	m	0.28	0/958	0.54	0/1281
43	n	0.29	0/902	0.56	0/1209
44	o	0.29	0/929	0.54	0/1242
45	p	0.28	0/960	0.54	0/1278
46	q	0.30	0/829	0.57	0/1107
47	r	0.28	0/852	0.54	0/1142
48	s	0.27	0/744	0.55	0/994
49	t	0.30	0/721	0.55	0/956
50	u	0.29	0/758	0.53	0/1015
51	v	0.32	0/576	0.55	0/762
52	w	0.29	0/635	0.56	0/848
53	x	0.27	0/492	0.50	0/655
54	y	0.29	0/453	0.51	0/605
55	z	0.30	0/435	0.55	0/581
All	All	0.38	0/152873	0.81	6/228442 (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
3	2	0	1
10	D	0	2
13	G	0	1
15	I	0	1
16	J	0	1
21	O	0	1
23	Q	0	1
27	U	0	1
52	w	0	1
All	All	0	10

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	512	G	O4'-C1'-N9	6.35	113.28	108.20
30	a	1936	A	O4'-C1'-N9	5.47	112.58	108.20
30	a	242	G	C3'-C2'-C1'	-5.34	97.23	101.50
30	a	781	A	O3'-P-O5'	-5.30	93.94	104.00
30	a	1790	C	O5'-P-OP2	-5.15	101.06	105.70

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2	13	ARG	Sidechain
10	D	184	ARG	Sidechain
10	D	73	ARG	Sidechain
13	G	111	ARG	Sidechain
15	I	41	ARG	Sidechain

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	48/55 (87%)	48 (100%)	0	0	100	100
2	1	43/46 (94%)	43 (100%)	0	0	100	100
3	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	36 (100%)	0	0	100	100
5	4	56/70 (80%)	55 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	B	220/241 (91%)	214 (97%)	5 (2%)	1 (0%)	25	38
9	C	204/233 (88%)	199 (98%)	5 (2%)	0	100	100
10	D	203/206 (98%)	202 (100%)	1 (0%)	0	100	100
11	E	152/167 (91%)	150 (99%)	2 (1%)	0	100	100
12	F	99/135 (73%)	99 (100%)	0	0	100	100
13	G	148/179 (83%)	147 (99%)	1 (1%)	0	100	100
14	H	127/130 (98%)	127 (100%)	0	0	100	100
15	I	123/130 (95%)	120 (98%)	3 (2%)	0	100	100
16	J	92/103 (89%)	88 (96%)	3 (3%)	1 (1%)	12	18
17	K	113/129 (88%)	111 (98%)	2 (2%)	0	100	100
18	L	118/124 (95%)	114 (97%)	4 (3%)	0	100	100
19	M	113/118 (96%)	111 (98%)	2 (2%)	0	100	100
20	N	98/101 (97%)	98 (100%)	0	0	100	100
21	O	86/89 (97%)	86 (100%)	0	0	100	100
22	P	77/82 (94%)	75 (97%)	2 (3%)	0	100	100
23	Q	77/84 (92%)	77 (100%)	0	0	100	100
24	R	62/75 (83%)	62 (100%)	0	0	100	100
25	S	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
26	T	84/87 (97%)	84 (100%)	0	0	100	100
27	U	53/71 (75%)	53 (100%)	0	0	100	100
28	V	195/213 (92%)	192 (98%)	3 (2%)	0	100	100
32	c	269/273 (98%)	263 (98%)	6 (2%)	0	100	100
33	d	204/209 (98%)	200 (98%)	4 (2%)	0	100	100
34	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
35	f	175/179 (98%)	173 (99%)	2 (1%)	0	100	100
36	g	164/177 (93%)	163 (99%)	1 (1%)	0	100	100
37	h	39/149 (26%)	37 (95%)	2 (5%)	0	100	100
38	i	139/142 (98%)	139 (100%)	0	0	100	100
39	j	121/123 (98%)	120 (99%)	1 (1%)	0	100	100
40	k	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
41	l	132/136 (97%)	130 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	m	116/127 (91%)	114 (98%)	2 (2%)	0	100	100
43	n	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
44	o	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
45	p	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
46	q	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
47	r	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
48	s	91/100 (91%)	90 (99%)	1 (1%)	0	100	100
49	t	89/104 (86%)	89 (100%)	0	0	100	100
50	u	91/94 (97%)	91 (100%)	0	0	100	100
51	v	73/85 (86%)	72 (99%)	1 (1%)	0	100	100
52	w	75/78 (96%)	75 (100%)	0	0	100	100
53	x	58/63 (92%)	58 (100%)	0	0	100	100
54	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
55	z	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
All	All	5605/6126 (92%)	5529 (99%)	74 (1%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	J	57	VAL
8	B	165	ASP

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%)	45 (98%)	1 (2%)	47	67
2	1	37/38 (97%)	37 (100%)	0	100	100
3	2	51/52 (98%)	50 (98%)	1 (2%)	50	70
4	3	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	4	55/62 (89%)	54 (98%)	1 (2%)	54	73
8	B	184/199 (92%)	176 (96%)	8 (4%)	25	42
9	C	170/190 (90%)	169 (99%)	1 (1%)	84	92
10	D	172/173 (99%)	165 (96%)	7 (4%)	26	44
11	E	117/126 (93%)	114 (97%)	3 (3%)	41	62
12	F	88/116 (76%)	88 (100%)	0	100	100
13	G	124/147 (84%)	119 (96%)	5 (4%)	27	45
14	H	104/105 (99%)	104 (100%)	0	100	100
15	I	103/107 (96%)	101 (98%)	2 (2%)	52	72
16	J	85/90 (94%)	84 (99%)	1 (1%)	67	82
17	K	89/98 (91%)	89 (100%)	0	100	100
18	L	101/103 (98%)	100 (99%)	1 (1%)	73	86
19	M	93/96 (97%)	92 (99%)	1 (1%)	70	84
20	N	83/84 (99%)	83 (100%)	0	100	100
21	O	76/77 (99%)	76 (100%)	0	100	100
22	P	64/65 (98%)	63 (98%)	1 (2%)	58	76
23	Q	73/78 (94%)	70 (96%)	3 (4%)	26	44
24	R	55/65 (85%)	54 (98%)	1 (2%)	54	73
25	S	72/79 (91%)	72 (100%)	0	100	100
26	T	65/66 (98%)	65 (100%)	0	100	100
27	U	48/61 (79%)	48 (100%)	0	100	100
28	V	191/204 (94%)	187 (98%)	4 (2%)	48	69
32	c	216/218 (99%)	214 (99%)	2 (1%)	75	88
33	d	162/163 (99%)	162 (100%)	0	100	100
34	e	165/165 (100%)	165 (100%)	0	100	100
35	f	148/150 (99%)	142 (96%)	6 (4%)	26	44
36	g	130/138 (94%)	126 (97%)	4 (3%)	35	56
37	h	32/114 (28%)	30 (94%)	2 (6%)	15	25
38	i	115/116 (99%)	114 (99%)	1 (1%)	75	88
39	j	104/104 (100%)	103 (99%)	1 (1%)	73	86
40	k	103/103 (100%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	l	107/107 (100%)	106 (99%)	1 (1%)	75	88
42	m	98/103 (95%)	98 (100%)	0	100	100
43	n	86/87 (99%)	84 (98%)	2 (2%)	45	66
44	o	99/100 (99%)	97 (98%)	2 (2%)	50	70
45	p	89/90 (99%)	89 (100%)	0	100	100
46	q	84/84 (100%)	84 (100%)	0	100	100
47	r	92/93 (99%)	92 (100%)	0	100	100
48	s	80/84 (95%)	80 (100%)	0	100	100
49	t	76/85 (89%)	75 (99%)	1 (1%)	65	81
50	u	77/78 (99%)	77 (100%)	0	100	100
51	v	56/63 (89%)	56 (100%)	0	100	100
52	w	67/68 (98%)	67 (100%)	0	100	100
53	x	54/55 (98%)	54 (100%)	0	100	100
54	y	48/49 (98%)	48 (100%)	0	100	100
55	z	46/48 (96%)	46 (100%)	0	100	100
All	All	4714/5029 (94%)	4651 (99%)	63 (1%)	64	81

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	I	123	ARG
38	i	95	ARG
23	Q	52	GLU
37	h	37	VAL
43	n	56	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
28	V	92	GLN
50	u	12	GLN
28	V	128	ASN
43	n	116	GLN
55	z	6	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	Z	75/77 (97%)	22 (29%)	2 (2%)
30	a	2774/2930 (94%)	313 (11%)	0
31	b	118/119 (99%)	9 (7%)	0
6	9	9/24 (37%)	4 (44%)	1 (11%)
7	A	1508/1554 (97%)	183 (12%)	44 (2%)
All	All	4484/4704 (95%)	531 (11%)	47 (1%)

5 of 531 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	9	19	G
6	9	20	C
6	9	21	A
6	9	22	A
7	A	4	U

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	1094	G
7	A	1225	A
7	A	1124	G
7	A	1187	G
7	A	1275	A

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

39 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
33	MEQ	d	150	33	8,9,10	0.42	0	5,10,12	0.60	0
30	2MA	a	2503	57,30,58	19,25,26	1.03	2 (10%)	21,37,40	1.82	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
30	PSU	a	2604	30	18,21,22	0.89	1 (5%)	22,30,33	0.82	1 (4%)
7	MA6	A	1518	7	18,26,27	0.76	0	19,38,41	0.47	0
7	2MG	A	1516	7	18,26,27	1.03	2 (11%)	16,38,41	0.79	0
7	4OC	A	1402	7	20,23,24	0.37	0	26,32,35	0.43	0
30	PSU	a	2457	30	18,21,22	0.88	1 (5%)	22,30,33	0.65	0
30	PSU	a	2580	57,30	18,21,22	0.92	1 (5%)	22,30,33	0.73	1 (4%)
30	G7M	a	2069	30	20,26,27	1.13	3 (15%)	17,39,42	0.48	0
7	5MC	A	967	7	18,22,23	0.32	0	26,32,35	0.51	0
7	2MG	A	966	7	18,26,27	1.01	2 (11%)	16,38,41	0.77	0
7	5MC	A	1407	7	18,22,23	0.32	0	26,32,35	0.57	0
30	6MZ	a	2030	30	18,25,26	0.67	0	16,36,39	0.78	1 (6%)
30	2MG	a	2445	30	18,26,27	1.06	2 (11%)	16,38,41	0.71	0
30	H2U	a	2449	30	18,21,22	0.56	0	21,30,33	0.78	1 (4%)
30	5MU	a	747	30	19,22,23	0.25	0	28,32,35	0.31	0
30	PSU	a	746	30,58	18,21,22	0.90	1 (5%)	22,30,33	0.62	0
30	6MZ	a	1618	30	18,25,26	0.67	0	16,36,39	0.72	1 (6%)
7	PSU	A	516	7,58	18,21,22	0.91	1 (5%)	22,30,33	0.64	0
30	OMU	a	2552	30	19,22,23	0.20	0	26,31,34	0.41	0
30	1MG	a	745	30	18,26,27	0.99	2 (11%)	19,39,42	0.51	0
30	PSU	a	955	30	18,21,22	0.89	1 (5%)	22,30,33	0.65	0
30	PSU	a	1917	30	18,21,22	0.91	1 (5%)	22,30,33	0.55	0
30	OMG	a	2251	57,30,29	18,26,27	1.01	2 (11%)	19,38,41	0.78	0
7	2MG	A	1207	57,7	18,26,27	1.02	2 (11%)	16,38,41	0.76	0
30	PSU	a	2504	57,30	18,21,22	0.91	1 (5%)	22,30,33	0.69	0
41	4D4	l	81	41	9,11,12	0.48	0	8,13,15	0.71	0
30	3TD	a	1915	30	18,22,23	0.96	1 (5%)	22,32,35	0.63	0
30	5MC	a	1962	30	18,22,23	0.31	0	26,32,35	0.50	0
30	PSU	a	1911	30	18,21,22	0.88	1 (5%)	22,30,33	0.69	0
30	2MG	a	1835	30	18,26,27	1.01	2 (11%)	16,38,41	0.67	0
7	G7M	A	527	7	20,26,27	1.12	2 (10%)	17,39,42	0.48	0
7	UR3	A	1498	7	19,22,23	0.25	0	26,32,35	0.63	0
30	5MU	a	1939	57,30	19,22,23	0.30	0	28,32,35	0.35	0
30	OMC	a	2498	30,58	19,22,23	0.28	0	26,31,34	0.45	0
30	PSU	a	2605	30	18,21,22	0.95	1 (5%)	22,30,33	0.69	0
17	IAS	K	119	17	6,7,8	0.91	0	6,8,10	1.01	0
7	MA6	A	1519	7	18,26,27	0.73	0	19,38,41	0.56	0
18	D2T	L	89	18	7,9,10	0.95	0	6,11,13	2.54	4 (66%)

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
33	MEQ	d	150	33	-	2/8/9/11	-
30	2MA	a	2503	57,30,58	-	2/3/25/26	0/3/3/3
30	PSU	a	2604	30	-	0/7/25/26	0/2/2/2
7	MA6	A	1518	7	-	0/7/29/30	0/3/3/3
7	2MG	A	1516	7	-	0/5/27/28	0/3/3/3
7	4OC	A	1402	7	-	0/9/29/30	0/2/2/2
30	PSU	a	2457	30	-	0/7/25/26	0/2/2/2
30	PSU	a	2580	57,30	-	0/7/25/26	0/2/2/2
30	G7M	a	2069	30	-	2/3/25/26	0/3/3/3
7	5MC	A	967	7	-	0/7/25/26	0/2/2/2
7	2MG	A	966	7	-	0/5/27/28	0/3/3/3
7	5MC	A	1407	7	-	0/7/25/26	0/2/2/2
30	6MZ	a	2030	30	-	2/5/27/28	0/3/3/3
30	2MG	a	2445	30	-	0/5/27/28	0/3/3/3
30	H2U	a	2449	30	-	0/7/38/39	0/2/2/2
30	5MU	a	747	30	-	0/7/25/26	0/2/2/2
30	PSU	a	746	30,58	-	4/7/25/26	0/2/2/2
30	6MZ	a	1618	30	-	0/5/27/28	0/3/3/3
7	PSU	A	516	7,58	-	0/7/25/26	0/2/2/2
30	OMU	a	2552	30	-	0/9/27/28	0/2/2/2
30	1MG	a	745	30	-	0/3/25/26	0/3/3/3
30	PSU	a	955	30	-	0/7/25/26	0/2/2/2
30	PSU	a	1917	30	-	0/7/25/26	0/2/2/2
30	OMG	a	2251	57,30,29	-	1/5/27/28	0/3/3/3
7	2MG	A	1207	57,7	-	0/5/27/28	0/3/3/3
30	PSU	a	2504	57,30	-	0/7/25/26	0/2/2/2
41	4D4	l	81	41	-	2/11/12/14	-
30	3TD	a	1915	30	-	2/7/25/26	0/2/2/2
30	5MC	a	1962	30	-	2/7/25/26	0/2/2/2
30	PSU	a	1911	30	-	2/7/25/26	0/2/2/2
30	2MG	a	1835	30	-	0/5/27/28	0/3/3/3
7	G7M	A	527	7	-	1/3/25/26	0/3/3/3
7	UR3	A	1498	7	-	0/7/25/26	0/2/2/2
30	5MU	a	1939	57,30	-	0/7/25/26	0/2/2/2
30	OMC	a	2498	30,58	-	0/9/27/28	0/2/2/2
30	PSU	a	2605	30	-	0/7/25/26	0/2/2/2
17	IAS	K	119	17	-	1/7/7/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MA6	A	1519	7	-	0/7/29/30	0/3/3/3
18	D2T	L	89	18	-	2/7/12/14	-

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2605	PSU	C6-C5	3.72	1.39	1.35
30	a	2504	PSU	C6-C5	3.61	1.39	1.35
30	a	1915	3TD	C6-C5	3.60	1.39	1.35
7	A	516	PSU	C6-C5	3.58	1.39	1.35
30	a	1917	PSU	C6-C5	3.57	1.39	1.35

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	2503	2MA	C5-C6-N1	-5.58	117.35	121.01
18	L	89	D2T	CB-CA-N	4.81	119.34	109.10
30	a	2503	2MA	C5-C6-N6	4.26	126.82	120.35
30	a	2503	2MA	CM2-C2-N1	2.59	121.19	117.15
18	L	89	D2T	OD1-CG-CB	-2.55	117.11	122.44

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
30	a	746	PSU	C2'-C1'-C5-C4
30	a	746	PSU	C2'-C1'-C5-C6
30	a	746	PSU	O4'-C1'-C5-C6
30	a	1911	PSU	O4'-C1'-C5-C4
30	a	1911	PSU	O4'-C1'-C5-C6

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 418 ligands modelled in this entry, 418 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.