



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Jul 11, 2018 – 03:39 PM EDT

PDB ID : 2RDO
EMDB ID: : EMD-1430
Title : 50S subunit with EF-G(GDPNP) and RRF bound
Authors : Gao, N.; Zavialov, A.V.; Ehrenberg, M.; Frank, J.
Deposited on : 2007-09-24
Resolution : 9.10 Å(reported)
Based on PDB ID : 2AW4, 1EK8

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB 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.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031172

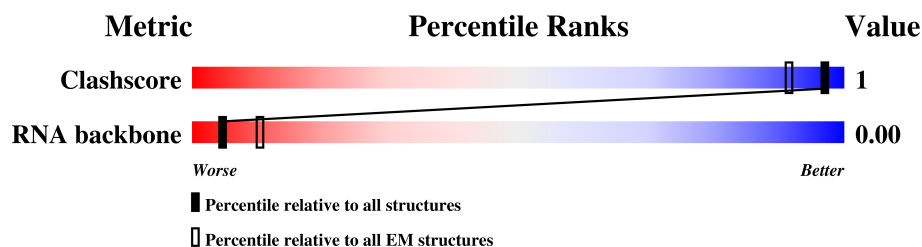
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.10 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.



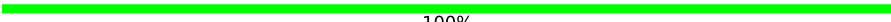
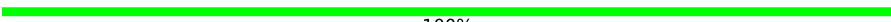













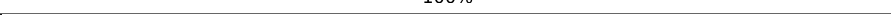
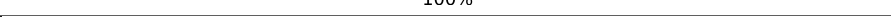
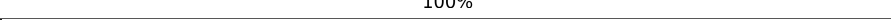
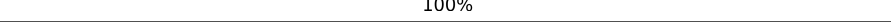
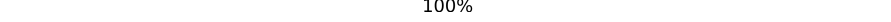
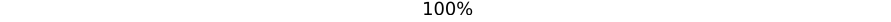
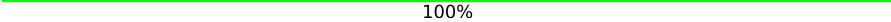
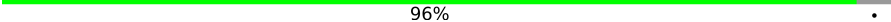
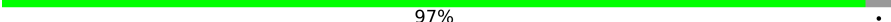
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
RNA backbone	3747	458

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

Mol	Chain	Length	Quality of chain
1	A	120	98% .
2	B	2904	98% .
3	V	94	100%
4	C	272	97% ..
5	D	209	100%
6	E	201	100%
7	F	178	100%
8	G	176	99% .
9	J	142	99% .
10	K	123	98% .

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Mol	Chain	Length	Quality of chain
11	L	144	 100%
12	M	136	 100%
13	N	127	 100%
14	O	117	 100%
15	P	114	 100%
16	Q	117	 100%
17	R	103	 98% .
18	S	110	 100%
19	T	100	 99% .
20	U	103	 99% .
21	W	84	 100%
22	X	63	 100%
23	Y	58	 100%
24	Z	70	 100%
25	0	56	 100%
26	1	54	 100%
27	2	46	 100%
28	3	64	 100%
29	4	38	 100%
30	I	141	 100%
31	H	149	 100%
32	9	233	 96% .
33	7	704	 97% .
34	8	185	 100%

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 7428 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	A	117	Total	P	0	117
			117	117		

- Molecule 2 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
2	B	2841	Total	P	0	2841
			2841	2841		

- Molecule 3 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	V	94	Total	C	0	94
			94	94		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	C	267	Total	C	0	267
			267	267		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms		AltConf	Trace
5	D	209	Total	C	0	209
			209	209		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms		AltConf	Trace
6	E	201	Total	C	0	201
			201	201		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms		AltConf	Trace
7	F	178	Total	C	0	178
			178	178		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms		AltConf	Trace
8	G	176	Total	C	0	176
			176	176		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
9	J	140	Total	C	0	140
			140	140		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
10	K	121	Total	C	0	121
			121	121		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
11	L	144	Total	C	0	144
			144	144		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
12	M	136	Total	C	0	136
			136	136		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
13	N	127	Total	C	0	127
			127	127		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
14	O	117	Total	C	0	117
			117	117		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
15	P	114	Total	C	0	114
			114	114		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
16	Q	117	Total	C	0	117
			117	117		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
17	R	103	Total	C	0	103
			103	103		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
18	S	110	Total	C	0	110
			110	110		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
19	T	99	Total	C	0	99
			99	99		

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

Mol	Chain	Residues	Atoms		AltConf	Trace
20	U	102	Total	C	0	102
			102	102		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms		AltConf	Trace
21	W	84	Total	C	0	84
			84	84		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms		AltConf	Trace
22	X	63	Total	C	0	63
			63	63		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms		AltConf	Trace
23	Y	58	Total	C	0	58
			58	58		

- Molecule 24 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms		AltConf	Trace
24	Z	70	Total	C	0	70
			70	70		

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms		AltConf	Trace
25	0	56	Total	C	0	56
			56	56		

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms		AltConf	Trace
26	1	54	Total	C	0	54
			54	54		

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms		AltConf	Trace
27	2	46	Total	C	0	46
			46	46		

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms		AltConf	Trace
28	3	64	Total	C	0	64
			64	64		

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms		AltConf	Trace
29	4	38	Total	C	0	38
			38	38		

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms		AltConf	Trace
30	I	141	Total	C	0	141
			141	141		

- Molecule 31 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms		AltConf	Trace
31	H	149	Total	C	0	149
			149	149		

- Molecule 32 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms		AltConf	Trace
32	9	223	Total	C	0	223
			223	223		

- Molecule 33 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms		AltConf	Trace
33	7	684	Total	C	0	684
			684	684		

- Molecule 34 is a protein called Ribosome recycling factor.

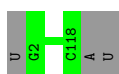
Mol	Chain	Residues	Atoms		AltConf	Trace
34	8	185	Total	C	0	185
			185	185		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

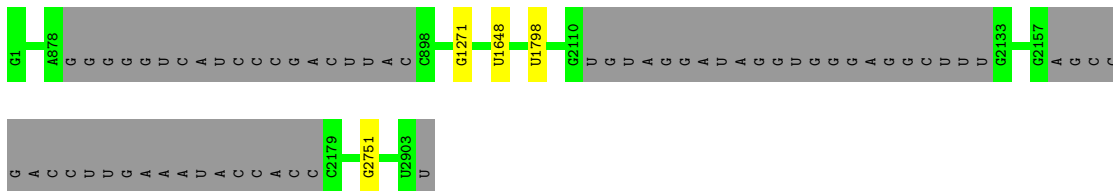
- Molecule 1: 5S RIBOSOMAL RNA

Chain A:  98%



- Molecule 2: 23S RIBOSOMAL RNA

Chain B:  98%



- Molecule 3: 50S ribosomal protein L25

Chain V:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: 50S ribosomal protein L2

Chain C:  97%



- Molecule 5: 50S ribosomal protein L3

Chain D:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: 50S ribosomal protein L4

Chain E:  100%

There are no outlier residues recorded for this chain.

- Molecule 7: 50S ribosomal protein L5

Chain F:  100%

There are no outlier residues recorded for this chain.

- Molecule 8: 50S ribosomal protein L6

Chain G:  99%



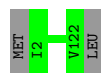
- Molecule 9: 50S ribosomal protein L13

Chain J:  99%



- Molecule 10: 50S ribosomal protein L14

Chain K:  98%



- Molecule 11: 50S ribosomal protein L15

Chain L:  100%

There are no outlier residues recorded for this chain.

- Molecule 12: 50S ribosomal protein L16

Chain M:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: 50S ribosomal protein L17

Chain N:  100%

There are no outlier residues recorded for this chain.

- Molecule 14: 50S ribosomal protein L18

Chain O:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: 50S ribosomal protein L19

Chain P:  100%

There are no outlier residues recorded for this chain.

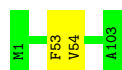
- Molecule 16: 50S ribosomal protein L20

Chain Q:  100%

There are no outlier residues recorded for this chain.

- Molecule 17: 50S ribosomal protein L21

Chain R:  98%



- Molecule 18: 50S ribosomal protein L22

Chain S:  100%

There are no outlier residues recorded for this chain.

- Molecule 19: 50S ribosomal protein L23

Chain T:  99%



- Molecule 20: 50S ribosomal protein L24

Chain U:  99%



- Molecule 21: 50S ribosomal protein L27

Chain W:  100%

There are no outlier residues recorded for this chain.

- Molecule 22: 50S ribosomal protein L29

Chain X:  100%

There are no outlier residues recorded for this chain.

- Molecule 23: 50S ribosomal protein L30

Chain Y:  100%

There are no outlier residues recorded for this chain.

- Molecule 24: 50S ribosomal protein L31

Chain Z:  100%

There are no outlier residues recorded for this chain.

- Molecule 25: 50S ribosomal protein L32

Chain 0:  100%

There are no outlier residues recorded for this chain.

- Molecule 26: 50S ribosomal protein L33

Chain 1:  100%

There are no outlier residues recorded for this chain.

- Molecule 27: 50S ribosomal protein L34

Chain 2:  100%

There are no outlier residues recorded for this chain.

- Molecule 28: 50S ribosomal protein L35

Chain 3:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: 50S ribosomal protein L36

Chain 4:  100%

There are no outlier residues recorded for this chain.

- Molecule 30: 50S ribosomal protein L11

Chain I:  100%

There are no outlier residues recorded for this chain.

- Molecule 31: 50S ribosomal protein L9

Chain H:  100%

There are no outlier residues recorded for this chain.

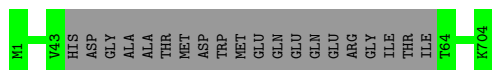
- Molecule 32: 50S ribosomal protein L1

Chain 9:  96%



- Molecule 33: Elongation factor G

Chain 7: 97% .



- Molecule 34: Ribosome recycling factor

Chain 8: 100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	113355	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF correction of 3D maps by Wiener filtration	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	4900	Depositor
Magnification	49700	Depositor
Image detector	KODAK SO-163 FILM	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	117	0	0	0	0
2	B	2841	0	0	3	0
3	V	94	0	0	0	0
4	C	267	0	0	2	0
5	D	209	0	0	0	0
6	E	201	0	0	0	0
7	F	178	0	0	0	0
8	G	176	0	0	1	0
9	J	140	0	0	0	0
10	K	121	0	0	0	0
11	L	144	0	0	0	0
12	M	136	0	0	0	0
13	N	127	0	0	0	0
14	O	117	0	0	0	0
15	P	114	0	0	0	0
16	Q	117	0	0	0	0
17	R	103	0	0	1	0
18	S	110	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	T	99	0	0	0	0
20	U	102	0	0	0	0
21	W	84	0	0	0	0
22	X	63	0	0	0	0
23	Y	58	0	0	0	0
24	Z	70	0	0	0	0
25	0	56	0	0	0	0
26	1	54	0	0	0	0
27	2	46	0	0	0	0
28	3	64	0	0	0	0
29	4	38	0	0	0	0
30	I	141	0	0	0	0
31	H	149	0	0	0	0
32	9	223	0	0	0	0
33	7	684	0	0	0	0
34	8	185	0	0	0	0
All	All	7428	0	0	5	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (5) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1798:U:P	4:C:253:GLY:CA	2.73	0.76
2:B:1271:G:P	2:B:1648:U:P	2.90	0.70
4:C:6:LYS:CA	4:C:7:PRO:CA	2.86	0.53
2:B:2751:G:P	8:G:1:SER:CA	3.03	0.47
17:R:53:PHE:CA	17:R:54:VAL:CA	2.96	0.43

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	0/120	-	-
2	B	0/2904	-	-
All	All	0/3024	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.