



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:32 PM UTC

PDB ID : 8C9A / pdb_00008c9a
EMDB ID : EMD-16507
Title : Cryo-EM captures early ribosome assembly in action
Authors : Lauer, S.; Nikolay, R.; Qin, B.
Deposited on : 2023-01-21
Resolution : 4.86 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

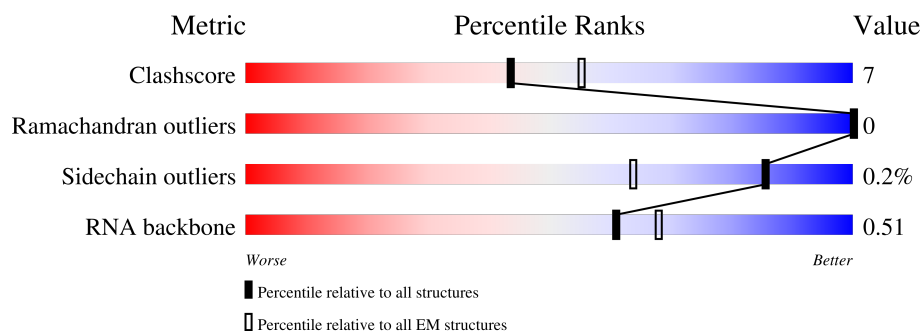
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.86 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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

Mol	Chain	Length	Quality of chain
1	A	2904	
2	2	46	
3	E	201	
4	S	110	
5	U	104	
6	Y	63	
7	T	100	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 18059 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	650	Total	C	N	O	P	0	0
			13953	6230	2588	4485	650		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	35	Total	C	N	O	S	0	0
			286	171	73	41	1		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	147	Total	C	N	O	S	0	0
			1137	721	196	216	4		

- Molecule 4 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S	94	Total	C	N	O	S	0	0
			726	451	136	138	1		

- Molecule 5 is a protein called 50S ribosomal protein L24.

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

- Molecule 6 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Y	60	Total	C	N	O	S	0	0
			494	305	96	91	2		

- Molecule 7 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	T	87	684	435	123	124	2	0	0



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A U G U G U C G C C U C A A U C C A C C A C C U C C U G G G C C U
U A A A A G C G G U U A C C G A G A A C C G G G U U G G U A A C C G
G G C C G C U G G A A C A A C G G G G G U U G G U A C C A A G G G U
C U G G U G U C G A G G U U G U G C C A A G A A C C G G A C C A C C
U G C C U G A A A G C A U C C U A A G C A A C C C C U C C A A C C G
G U C C C U G A A A A A C C G U U G A C A A G C A A C C C C U U A C
C G U U G U G A G C A A C C G G U A A G C A A C C C U U A A C C U U
C G U U G U G A G C A A C C G G U A A G C A A C C C U U

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- Molecule 2: 50S ribosomal protein L34

Chain 2:  61% 15% 24%

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MET LYS ARG THR PHE GLN PRO SER VAL L10 R14 R21 L31 R34 R39 A40 R41 L42 T43 V44 SER LYS

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- Molecule 3: 50S ribosomal protein L4

Chain E:  61% 12% 27%

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MET GLU LEU V4 L12 F19 V31 G42 THR ARG ALA GLN LYS THR ARG ALA GLU VAL THR GLY SER GLY LYS LYS PRO TRP ARG GLN LYS GLY THR GLY ARG ALA ARG SER GLY SER ILE LYS SER PRO ILE TRP ARG SER GLY VAL PHE ALA ARG GLN
ASP HIS SER Q94 N97 R102 G103 A104 L109 V113 L118 K132 Q136 R137 L138 K139 E144 L147 I148 I149 T150 N163 D168 V169 A172 D191 A192 L200 A201

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- Molecule 4: 50S ribosomal protein L22

Chain S:  67% 18% 15%

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MET E2 A5 K6 V17 I24 I24 L33 I37 K49 K54 A58 D62 T72 K73 I74 F75 V76 D77 E78 K82 LYS ARG ILE MET PRO ARG ALA LYS GLY ARG ALA ASP ARG ILE LEU K98 I103 T104 V105 V106 D109 R110

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- Molecule 5: 50S ribosomal protein L24

Chain U:  81% 17% .

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MET A1 I4 V12 L13 T14 V35 I38 E61 I64 Q65 V66 V69 T76 G77 K78 R81 E87 V92 R93 K96 S97 N98 I102 LYS

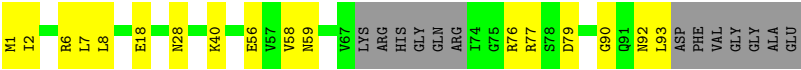
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- Molecule 6: 50S ribosomal protein L29

Chain Y:  67% 29% 5%



● Molecule 7: 50S ribosomal protein L23



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23547	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	62	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.07	0/15628	0.21	2/24363 (0.0%)
2	2	0.08	0/287	0.19	0/376
3	E	0.07	0/1146	0.21	0/1542
4	S	0.07	0/731	0.21	0/980
5	U	0.10	0/787	0.22	0/1051
6	Y	0.11	0/495	0.23	0/658
7	T	0.10	0/688	0.21	0/920
All	All	0.07	0/19762	0.21	2/29890 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	624	C	OP1-P-O3'	-8.90	81.29	108.00
1	A	624	C	OP2-P-O3'	-7.97	84.09	108.00

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	13953	0	7022	116	0
2	2	286	0	317	8	0
3	E	1137	0	1191	20	0
4	S	726	0	765	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	U	779	0	834	16	0
6	Y	494	0	530	13	0
7	T	684	0	749	13	0
All	All	18059	0	11408	182	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 7.

The worst 5 of 182 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)
1:A:395:U:O2'	1:A:396:G:N7	2.03	0.90
1:A:255:A:O2'	1:A:256:A:O4'	1.92	0.86
1:A:234:U:O4	1:A:263:G:N2	2.10	0.84
1:A:18:U:O4	1:A:19:A:N6	2.10	0.84
1:A:69:C:O2	1:A:73:A:O2'	1.95	0.83

There are no symmetry-related clashes.

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	
2	2	33/46 (72%)	33 (100%)	0	0	100	100
3	E	143/201 (71%)	141 (99%)	2 (1%)	0	100	100
4	S	90/110 (82%)	89 (99%)	1 (1%)	0	100	100
5	U	100/104 (96%)	94 (94%)	6 (6%)	0	100	100
6	Y	58/63 (92%)	54 (93%)	4 (7%)	0	100	100
7	T	83/100 (83%)	78 (94%)	5 (6%)	0	100	100
All	All	507/624 (81%)	489 (96%)	18 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	2	27/38 (71%)	27 (100%)	0	100	100
3	E	123/165 (74%)	123 (100%)	0	100	100
4	S	80/93 (86%)	80 (100%)	0	100	100
5	U	83/85 (98%)	82 (99%)	1 (1%)	63	73
6	Y	55/55 (100%)	55 (100%)	0	100	100
7	T	75/84 (89%)	75 (100%)	0	100	100
All	All	443/520 (85%)	442 (100%)	1 (0%)	85	86

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	U	98	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	E	136	GLN
4	S	60	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	644/2904 (22%)	111 (17%)	7 (1%)

5 of 111 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	19	A

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Mol	Chain	Res	Type
1	A	27	G
1	A	33	C
1	A	45	G
1	A	46	G

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	271	G
1	A	410	G
1	A	501	A
1	A	428	A
1	A	148	U

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 oligosaccharides 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.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-16507. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

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

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.