



## Full wwPDB EM Validation Report ⓘ

Mar 6, 2025 – 02:55 pm GMT

EMDB ID : EMD-10907  
Title : Structure of the P+9 ArfB-ribosome complex with P/E hybrid tRNA in the post-hydrolysis state  
Authors : Chan, K.-H.; Petrychenko, V.  
Deposited on : 2020-04-23  
Resolution : 3.20 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

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>.

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

EMDB validation analysis : **FAILED**  
Validation Pipeline (wwPDB-VP) : 2.41

# 1 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23340	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50.0	Depositor
Minimum defocus (nm)	0.2	Depositor
Maximum defocus (nm)	0.0025	Depositor
Magnification	59000.0	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor