



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:33 pm GMT

EMDB ID : EMD-5174  
Title : Structure of 70S ribosome in the 100S ribosome in the hibernation stage  
Authors : , Kato.T.; , Yoshida.H.; , Miyata.T.; , Maki.Y.; , Wada.A.; , Namba.K.  
Deposited on : 2010-03-10  
Resolution : 18.00 Å(reported)

This is a Full wwPDB EM Map 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.

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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) : 2.13

# 1 Experimental information

Property	Value	Source
EM reconstruction method	singleParticle	Depositor
Imposed symmetry	Not Provided	Depositor
Number of images used	17461	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	1.25	Depositor
Maximum defocus (nm)	3.5	Depositor
Magnification	88760.0	Depositor
Image detector	TVIPS TEMCAM-F415 (4k x 4k)	Depositor