



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:39 pm GMT

EMDB ID : EMD-5713
Title : Electron microscopy of negatively-stained gp12 tubular protein of T7 bacteriophage
Authors : , Cuervo.A.; , Pulido-Cid.M.; , Chagoyen.M.; , Arranz.R.; , Gonzalez-Garcia.VA.; , Garcia-Doval.C.; , Caston.JR.; , Valpuesta.JM.; , van.Raaij.MJ.; , Martin-Benito.J.; , Carrascosa.JL.
Deposited on : 2013-07-02
Resolution : 26.00 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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	640	Depositor
Resolution determination method	FSC 0.33 CUT-OFF	Depositor
CTF correction method	each micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	1.5	Depositor
Maximum defocus (nm)	3.5	Depositor
Magnification	108696.0	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor