



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:54 pm GMT

EMDB ID : EMD-5200
Title : 5.4-Angstrom cryoEM structure of the Bordetella Bacteriophage capsid
Authors : , Jin.L.; , Hodes.A.; , Hui.WH.; , Zhang.X.; , Zhang.X.; , Yu.X.; , Miller.JF.;
 , Zhou.ZH.
Deposited on : 2010-05-13
Resolution : 5.40 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	18524	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	0.5	Depositor
Maximum defocus (nm)	1.72	Depositor
Magnification	97940.0	Depositor
Image detector	GENERIC TVIPS	Depositor