



Full wwPDB EM Map Validation Report ⓘ

Dec 7, 2020 – 05:51 pm GMT

EMDB ID : EMD-0898
Title : The cryo-EM structure of coxsackievirus A16 mature virion in complex with Fabs 18A7, 14B10 and NA9D7
Authors : He, M.Z.; Xu, L.F.; Zheng, Q.B.; Zhu, R.; Yin, Z.C.; Cheng, T.; Li, S.W.
Deposited on : 2019-12-10
Resolution : 3.78 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	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, 1	Depositor
Number of particles used	27819	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor