



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 02:01 pm GMT

EMDB ID : EMD-9619  
Title : Cryo-EM structure of DNA-full Medusavirus  
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Deposited on : 2018-08-15  
Resolution : 31.80 Å(reported)

This is a wwPDB EM Map Validation Summary 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	2880	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	JEOL 2200FS	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20.0	Depositor
Minimum defocus (nm)	1.5783	Depositor
Maximum defocus (nm)	4.9672	Depositor
Magnification	27862.	Depositor
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor