



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:40 pm GMT

EMDB ID : EMD-5717  
Title : The structure of Sinorhizobium meliloti phage phiM12, a novel T=19 icosahedral phage that is the founder of a new group of T4-like phages  
Authors : , Stroupe.ME.; , Brewer.TE.; , Sousa.DR.; , Jones.KM.  
Deposited on : 2013-07-11  
Resolution : 13.00 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	2038	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	120	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	15	Depositor
Minimum defocus (nm)	1.5	Depositor
Maximum defocus (nm)	3.5	Depositor
Magnification	65555.0	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor