



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 11:19 am GMT

EMDB ID : EMD-21013  
Title : Cryo-EM reconstruction of the thermophilic bacteriophage P74-26 small terminase, asymmetric I  
Authors : , Hayes.JA.; , Hilbert.BJ.; , Gaubitz.C.; , Stone.NP.; , Kelch.BA.  
Deposited on : 2019-11-20  
Resolution : 4.40 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	POINT, C1	Depositor
Number of images used	152315	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50.0	Depositor
Minimum defocus (nm)	1.4	Depositor
Maximum defocus (nm)	2.6	Depositor
Magnification	130000.0	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor