



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:53 pm GMT

EMDB ID : EMD-6292  
Title : An EM structure of the helicase-loader complex in *G. kaustophilus* suggesting an early stage conformation in Gram-positive bacteria  
Authors : , Lin.Y-C.; , Vankadari.N.; , Hsiao.C-D.  
Deposited on : 2015-03-09  
Resolution : 19.00 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	10214	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	CTFFIND3	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	25	Depositor
Minimum defocus (nm)	0.6	Depositor
Maximum defocus (nm)	1.4	Depositor
Magnification	85658.0	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor