



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 01:34 pm GMT

EMDB ID : EMD-8558  
Title : Negative stain reconstruction of Cas1-Cas2/3 complex of type I-F CRISPR system from *Pseudomonas aeruginosa* (PA14)  
Authors : , Chowdhury.S.; , Lander.GC.; , Rollins.MF.; , Carter.J.; , Golden.MS.; , Wilkinson.RA.; , Bondy-Denomy.J.; , Wiedenheft.B.  
Deposited on : 2017-01-13  
Resolution : 15.60 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	POINT, C1	Depositor
Number of images used	26403	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Ctffind4 was used for determining the CTF of each micrograph. Phases of each micrographs were flipped before particle extraction.	Depositor
Microscope	FEI TECNAI SPIRIT	Depositor
Voltage (kV)	120	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30.0	Depositor
Minimum defocus (nm)	0.99	Depositor
Maximum defocus (nm)	0.99	Depositor
Magnification	52000.	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor