



Full wwPDB EM Validation Report ⓘ

Mar 19, 2025 – 12:03 am GMT

EMDB ID : EMD-52431
Title : CryoEM structure of cyclised H-pilus
Authors : Ishimoto, N.; Beis, K.
Deposited on : 2024-12-26
Resolution : 2.24 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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) : 2.41

1 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=28.93°, rise=12.14 Å, axial sym=C5	Depositor
Number of segments used	123942	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	50.0	Depositor
Minimum defocus (nm)	0.8	Depositor
Maximum defocus (nm)	1.8	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor