



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 12:51 pm GMT

EMDB ID : EMD-6101  
Title : CryoEM reveals different coronin binding modes for ADP- and ADP-BeFx-actin filaments  
Authors : , Ge.P.; , Durer.ZAO.; , Kudryashov.D.; , Zhou.ZH.; , Reisler.E.  
Deposited on : 2014-09-20  
Resolution : 8.60 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	helical	Depositor
Imposed symmetry	HELICAL, twist=166.3°, rise=28.23 Å, axial sym=C1	Depositor
Number of images used	Not provided	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	120	Depositor
Electron dose ( $e^-/\text{Å}^2$ )	25	Depositor
Minimum defocus (nm)	2.0	Depositor
Maximum defocus (nm)	4.0	Depositor
Magnification	104384.0	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor