



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 01:52 pm GMT

EMDB ID : EMD-9352  
Title : Cryo-EM structure of singly-bound SNF2h-nucleosome complex at 3.4 Å  
Authors : , Armache.J-P.; , Gamarra.N.; , Johnson.SL.; , Wu.S.; , Leonard.JD.; ,  
Narlikar.GJ.; , Cheng.Y.  
Deposited on : 2018-12-16  
Resolution : 3.39 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	43165	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	41.0	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor