



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:37 pm GMT

EMDB ID : EMD-5626
Title : Molecular Architecture of the ATP-Dependent Chromatin Remodeling Complex SWR1 by 3 Dimensional Electron Microscopy
Authors : , Nguyen.VQ.; , Ranjan.A.; , Stengel.F.; , Wei.D.; , Aebersold.R.; , Wu.C.; , Leschziner.AE.
Deposited on : 2013-04-05
Resolution : 28.00 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMMapValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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	18000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	CTFTILT (Grigorieff) for initial model; EMAN2 for projection-matching refinement	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	0.5	Depositor
Maximum defocus (nm)	2.0	Depositor
Magnification	87000.0	Depositor
Image detector	Not provided	Depositor