



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 11:13 am GMT

EMDB ID : EMD-21001
Title : Cryo-EM structure of porcine ATP synthase reconstituted in small unilamellar vesicles_I
Authors : , Mnatsakanyan.N.; , Llaguno.MC.; , Yang.Y.; , Yan.Y.; , Weber.J.; , Sigworth.FJ.; , Jonas.EA.
Deposited on : 2019-11-19
Resolution : 19.00 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	7795	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	1.871	Depositor
Maximum defocus (nm)	4.219	Depositor
Magnification	47620.0	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor