



wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 01:12 pm GMT

EMDB ID : EMD-7067
Title : Cryo-EM structure of dimeric F1FO yeast mitochondrial ATP synthase with C2 symmetry
Authors : , Guo.H.; , Bueler.SA.; , Rubinstein.JL.
Deposited on : 2017-10-07
Resolution : 7.40 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

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	POINT, C2	Depositor
Number of images used	79942	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	36.0	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	34483.0	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor