



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 12:42 pm GMT

EMDB ID : EMD-5476  
Title : Structure of the vacuolar-type ATPase from *Saccharomyces cerevisiae* at 11 Angstrom resolution  
Authors : , Benlekbir.S.; , Bueler.SA.; , Rubinstein.JL.  
Deposited on : 2012-08-22  
Resolution : 11.00 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.

---

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	34448	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	12	Depositor
Minimum defocus (nm)	3.0	Depositor
Maximum defocus (nm)	5.0	Depositor
Magnification	50000.0	Depositor
Image detector	KODAK SO-163 FILM	Depositor