



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 12:28 pm GMT

EMDB ID : EMD-5213  
Title : Molecular architecture of the yeast TRAPP<sup>II</sup> tethering complex - form1  
Authors : , Yip.CK.; , Berscheminski.J.; , Walz.T.  
Deposited on : 2010-07-16  
Resolution : 32.00 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	1993	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	1.8	Depositor
Maximum defocus (nm)	2.5	Depositor
Magnification	51159.0	Depositor
Image detector	KODAK SO-163 FILM	Depositor