



## Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:53 pm GMT

EMDB ID : EMD-6334  
Title : Negative stain 3D reconstruction of the yeast 26S proteasome in ATPgS in the presence of wild-type Ubp6 protein  
Authors : , Bashore.C.; , Dambacher.CM.; , Matyskiela.M.; , Lander.GC.; , Martin.A.  
Deposited on : 2015-05-05  
Resolution : 25.20 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](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.

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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	9000	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	Phase flipping of whole micrographs	Depositor
Microscope	FEI TECNAI SPIRIT	Depositor
Voltage (kV)	120	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	0.5	Depositor
Maximum defocus (nm)	1.5	Depositor
Magnification	52000.0	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor