



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 01:04 pm GMT

EMDB ID : EMD-6464
Title : Reconstruction of the T20S proteasome at 2.8 Angstrom resolution using optimal exposure filtering
Authors : , Grant.T.; , Grigorieff.N.
Deposited on : 2015-09-10
Resolution : 2.80 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	49954	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	CTF parameters provided by Campbell et al.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	0.9	Depositor
Maximum defocus (nm)	2.4	Depositor
Magnification	37313.0	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor