



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 02:04 pm GMT

EMDB ID : EMD-9233
Title : T20S proteasome
Authors : , Eng.ET.; , Kopylov.M.; , Jordan.KJ.; , Rice.WJ.; , Carragher.BO.; , Potter.CS.
Deposited on : 2018-10-18
Resolution : 2.10 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	POINT, D7	Depositor
Number of images used	127570	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	CTF amplitude correction was performed following 3D reconstruction.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	62.59	Depositor
Minimum defocus (nm)	0.2	Depositor
Maximum defocus (nm)	3.02	Depositor
Magnification	75574.	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor