



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 12:30 pm GMT

EMDB ID : EMD-5157  
Title : 8.4 angstrom cryo-electron structure of the recombinant *Acidianus tengchongensis* chaperonin beta-ATP  
Authors : , Huo.Y.; , Hu.Z.; , Zhang.K.; , Wang.L.; , Zhai.Y.; , Zhou.Q.; , Lander.G.; , Zhu.J.; , He.Y.; , Pang.X.; , Xu.W.; , Bartlam.M.; , Dong.Z.; , Sun.F.  
Deposited on : 2009-12-17  
Resolution : 8.40 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.

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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	70000	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	120	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	1.0	Depositor
Maximum defocus (nm)	4.0	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor