



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:58 pm GMT

EMDB ID : EMD-6422
Title : CryoEM structure of GroEL
Authors : , Roh.SH.; , Hryc.C.; , Chiu.W.
Deposited on : 2015-08-10
Resolution : 4.10 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	Not Provided	Depositor
Number of images used	40000	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	particle-based	Depositor
Microscope	JEOL 3200FS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	0.5	Depositor
Maximum defocus (nm)	3.0	Depositor
Magnification	59800.0	Depositor
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor