



## Full wwPDB EM Validation Report ⓘ

Feb 25, 2024 – 11:22 AM EST

EMDB ID : EMD-21995  
Title : 1.8 Angstrom resolution structure of b-galactosidase with a 200 kV cryoARM electron microscope  
Authors : Merk, A.; Fukumura, T.  
Deposited on : 2020-05-19  
Resolution : 1.80 Å(reported)

This is a Full wwPDB EM 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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) : 2.36

# 1 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	257202	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	JEOL CRYO ARM 200	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40.0	Depositor
Minimum defocus (nm)	-0.8	Depositor
Maximum defocus (nm)	-0.9500000000000001	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor