



wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 12:30 pm GMT

EMDB ID : EMD-5294
Title : 3D reconstruction of frozen hydrated HIV-1 integrase dimer in complex with two Fabs.
Authors : , Wu.S.; , Avila-Sakar.A.; , Kim.J.; , Booth.DS.; , Greenberg.CH.; , Rossi.A.; , Liao.M.; , Alian.A.; , Griner.SL.; , Juge.N.; , Mergel.CM.; , Chaparro-Riggers.J.; , Strop.P.; , Tampe.R.; , Edwards.RH.; , Stroud.RM.; , Craik.CS.; , Cheng.Y.
Deposited on : 2011-05-22
Resolution : 9.60 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

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	14000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	2.0	Depositor
Maximum defocus (nm)	5.0	Depositor
Magnification	80000.0	Depositor
Image detector	TVIPS TEMCAM-F816 (8k x 8k)	Depositor