



## Full wwPDB EM Map Validation 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 Full wwPDB EM Map 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.

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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	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