



## wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 01:07 pm GMT

EMDB ID : EMD-7032  
Title : Global architecture of the HIV-1 reverse transcriptase initiation complex  
Authors : , Larsen.KP.; , Mathiharan.YK.; , Chen.DH.; , Puglisi.JD.; , Skiniotis.G.; ,  
Puglisi.EV.  
Deposited on : 2017-09-18  
Resolution : 8.00 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.

---

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	21520	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	70.0	Depositor
Minimum defocus (nm)	1.3	Depositor
Maximum defocus (nm)	2.5	Depositor
Magnification	50000.0	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor