



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 01:21 pm GMT

EMDB ID : EMD-5494
Title : Cryo-EM structure of short shafted adenovirus type 5 complexed with factor X
Authors : , Doronin.K.; , Flatt.JW.; , Di.Paolo.NC.; , Khare.R.; , Kalyuzhniy.O.; , Accchione.M.; , Sumida.JP.; , Ohto.U.; , Shimizu.T.; , Akashi-Takamura.S.; , Miyake.K.; , MacDonald.JW.; , Bammler.TK.; , Beyer.RP.; , Farin.FM.; , Stewart.PL.; , Shayakhmetov.DM.
Deposited on : 2012-09-10
Resolution : 11.10 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	520	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	0.5	Depositor
Maximum defocus (nm)	2.1	Depositor
Magnification	400000.0	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor