



wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 12:47 pm GMT

EMDB ID : EMD-6044
Title : Ribosome conformation along minimum free-energy trajectory
Authors : , Dashti.A.; , Schwander.P.; , Langlois.R.; , Fung.R.; , Li.W.; , Hosseinizadeh.A.; , Liao.HY.; , Pallesen.J.; , Sharma.G.; , Stupina.VA.; , Simon.AE.; , Dinman.J.; , Frank.J.; , Ourmazd.A.
Deposited on : 2014-08-22
Resolution : 20.00 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

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	849914	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	80000.0	Depositor
Image detector	TVIPS TEMCAM-F415 (4k x 4k)	Depositor