



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 02:00 pm GMT

EMDB ID : EMD-9704
Title : Cryo-EM structure of the HCV IRES dependently initiated CMV-stalled 80S ribosome, rotated (Structure v)
Authors : , Yokoyama.T.; , Shigematsu.H.; , Shirouzu.M.; , Imataka.H.; , Ito.T.
Deposited on : 2018-11-02
Resolution : 4.60 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

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	POINT, C1	Depositor
Number of images used	23546	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	33557.	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor