



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:28 pm GMT

EMDB ID : EMD-5141
Title : Ab initio reconstruction of the E. coli 70S ribosome complex (70S-fMet-tRNA^{fMet}-Phe-tRNA^{Phe}-EF-Tu-GDP-kirromycin) via the asymmetric random-model method.
Authors : , Sanz.E.; , Stewart.AB.; , Belnap.DM.
Deposited on : 2009-11-21
Resolution : 23.00 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	10000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Phase-flipped per micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	1.6	Depositor
Maximum defocus (nm)	4.0	Depositor
Magnification	50000.0	Depositor
Image detector	GENERIC FILM	Depositor