



Full wwPDB EM Map Validation Report ⓘ

Dec 7, 2020 – 04:25 pm GMT

EMDB ID : EMD-0684
Title : Cryo-EM structure of the catalytic activated yeast spliceosome (B* complex) assembled on ACT1 pre-mRNA at 2.9 angstrom resolution
Authors : Wan, R.; Bai, R.; Yan, C.; Lei, J.; Shi, Y.
Deposited on : 2019-01-13
Resolution : 2.90 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	SINGLE PARTICLE	Depositor
Imposed symmetry	Not Provided	Depositor
Number of particles used	555036	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 ($e^-/\text{\AA}^2$)	49.3	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor