



wwPDB EM Map Validation Summary Report ⓘ

Dec 9, 2020 – 12:30 pm GMT

EMDB ID : EMD-30362
Title : 2.05 angstrom resolution structure determination of sulfur oxygenase reductase using 200kV cryo-EM
Authors : , Moriya.T.; , Naruhiko.A.; , Sato.Y.; , Arakawa.T.; , Kawasaki.M.; , Yamada.C.; , Fushinobu.S.; , Senda.T.
Deposited on : 2020-07-02
Resolution : 2.05 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	POINT, O	Depositor
Number of images used	71358	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	0.3	Depositor
Maximum defocus (nm)	1.5	Depositor
Magnification	150000.0	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor