



Full wwPDB EM Map Validation Report ⓘ

Dec 9, 2020 – 12:27 pm GMT

EMDB ID : EMD-5042
Title : Lumazine synthase structure : Structural survey of large protein complexes in Desulfovibrio vulgaris Hildenborough (DvH)
Authors : , Han.B-G.; , Dong.M.; , Liu.H.; , Camp.L.; , Geller.J.; , Singer.M.; , Hazen.TC.; , Choi.M.; , Witkowska.HE.; , Ball.DA.; , Typke.D.; , Downing.KH.; , Shatsky.M.; , Brenner.SE.; , Chandonia.J-M.; , Biggin.MD.; , Glaeser.RM.
Deposited on : 2009-01-08
Resolution : 15.00 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	3174	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	JEOL 4000EX	Depositor
Voltage (kV)	400	Depositor
Electron dose ($e^-/\text{\AA}^2$)	17	Depositor
Minimum defocus (nm)	0.6	Depositor
Maximum defocus (nm)	2.0	Depositor
Magnification	40000.0	Depositor
Image detector	KODAK SO-163 FILM	Depositor