



Full wwPDB EM Validation Report ⓘ

Nov 13, 2022 – 03:32 PM EST

EMDB ID : EMD-22094
Title : CryoEM structure of the holo-SrpI encapsulin complex from *Synechococcus elongatus* PCC 7942
Authors : LaFrance, B.J.; Nichols, R.J.; Phillips, N.R.; Oltrogge, L.M.; Valentin-Alvarado, L.E.; Bischoff, A.J.; Savage, D.F.; Nogales, E.
Deposited on : 2020-06-01
Resolution : 2.20 Å(reported)

This is a Full wwPDB EM 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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) : 2.31.2

1 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	11980	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	CTF refinement was performed in Relion/3.1	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35.0	Depositor
Minimum defocus (nm)	1.0	Depositor
Maximum defocus (nm)	2.8000000000000003	Depositor
Magnification	64000.0	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor