



Full wwPDB EM Validation Report ⓘ

Oct 6, 2024 – 04:20 am BST

EMDB ID : EMD-11617
Title : Cryo-EM structure of the SARS-CoV-2 spike protein bound to neutralizing
sybodies (Sb23) 2-up conformation
Authors : Hallberg, B.M.; Das, H.
Deposited on : 2020-08-16
Resolution : 2.94 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) : 2.39

1 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	Not Provided	
Number of particles used	69567	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	0.3	Depositor
Maximum defocus (nm)	1.1	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor