



## wwPDB EM Validation Summary Report ⓘ

May 27, 2024 – 06:26 PM EDT

PDB ID : 5K7R  
EMDB ID : EMD-8220  
Title : MicroED structure of trypsin at 1.7 Å resolution  
Authors : de la Cruz, M.J.; Hattne, J.; Shi, D.; Seidler, P.; Rodriguez, J.; Reyes, F.E.;  
Sawaya, M.R.; Cascio, D.; Eisenberg, D.; Gonen, T.  
Deposited on : 2016-05-26  
Resolution : 1.70 Å(reported)  
Based on initial model : 2PTN

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : **FAILED**  
MolProbity : **FAILED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON CRYSTALLOGRAPHY*

The reported resolution of this entry is 1.70 Å.

There are no overall percentile quality scores available for this entry.

ENTRY-COMPOSITION INFOmissingINFO

SEQUENCE-PLOTS INFOmissingINFO

## 2 Experimental information

Property	Value	Source
EM reconstruction method	CRYSTALLOGRAPHY	Depositor
Imposed symmetry	3D CRYSTAL, $a=53.12$ Å, $b=56.08$ Å, $c=64.38$ Å, $\alpha=90^\circ$ , $\beta=90^\circ$ , $\gamma=90^\circ$ , space group=P 21 21 21	Depositor
Number of images used	Not provided	
Resolution determination method	DIFFRACTION PATTERN/LAYERLINES	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	0.004	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor

## 3 Model quality [i](#)

### 3.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 3.2 Too-close contacts [i](#)

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### 3.3 Torsion angles [i](#)

#### 3.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 3.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 3.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 3.4 Non-standard residues in protein, DNA, RNA chains [i](#)

validation-pack failed to run properly - this section is therefore empty.

### 3.5 Carbohydrates [i](#)

validation-pack failed to run properly - this section is therefore empty.

### 3.6 Ligand geometry [i](#)

validation-pack failed to run properly - this section is therefore empty.

### 3.7 Other polymers [i](#)

validation-pack failed to run properly - this section is therefore empty.

### 3.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.