



## wwPDB EM Validation Summary Report ⓘ

Jun 7, 2021 – 01:19 pm BST

EMDB ID : EMD-12620  
Title : Focused refinement of the core RNA polymerase II pre-initiation complex in a consensus CC state (without ADP-BeF3)  
Authors : Aibara, S.; Schilbach, S.; Cramer, P.  
Deposited on : 2021-03-16  
Resolution : 2.40 Å(reported)

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/EMMapValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

EMDB validation analysis : 0.0.0.dev75  
Validation Pipeline (wwPDB-VP) : 2.19

# 1 Experimental information

| Property                             | Value                         | Source    |
|--------------------------------------|-------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE               | Depositor |
| Imposed symmetry                     | Not Provided                  |           |
| Number of particles used             | 271685                        | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF             | Depositor |
| CTF correction method                | Not provided                  |           |
| Microscope                           | FEI TITAN KRIOS               | Depositor |
| Voltage (kV)                         | 300                           | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 41.1                          | Depositor |
| Minimum defocus (nm)                 | Not provided                  |           |
| Maximum defocus (nm)                 | Not provided                  |           |
| Magnification                        | Not provided                  |           |
| Image detector                       | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |

## 2 Map visualisation

This section contains visualisations of the EMDB entry EMD-12620. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 2.1 Orthogonal projections

This section was not generated.

### 2.2 Central slices

This section was not generated.

### 2.3 Largest variance slices

This section was not generated.

### 2.4 Orthogonal surface views

This section was not generated.

### 2.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

### 3 Map analysis

This section contains the results of statistical analysis of the map.

#### 3.1 Map-value distribution

This section was not generated.

#### 3.2 Volume estimate versus contour level

This section was not generated.

#### 3.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 4 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.