



## Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 03:50 AM UTC

PDB ID : 3JAG / pdb\_00003jag  
EMDB ID : EMD-3038  
Title : Structure of a mammalian ribosomal termination complex with ABCE1, eRF1(AAQ), and the UAA stop codon  
Authors : Brown, A.; Shao, S.; Murray, J.; Hegde, R.S.; Ramakrishnan, V.  
Deposited on : 2015-06-10  
Resolution : 3.65 Å(reported)  
Based on initial models : 3J7P, 3BK7, 1DT9, 4V51, 3J92

This is a Full wwPDB EM Validation 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 : 0.0.1.dev132  
Mogul : **FAILED**  
MolProbity : **FAILED**  
Buster-report : **FAILED**  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.8.1  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

PERCENTILES INFOmissingINFO

ENTRY-COMPOSITION INFOmissingINFO

SEQUENCE-PLOTS INFOmissingINFO

# 1 Experimental information

| Property                             | Value                            | Source    |
|--------------------------------------|----------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                  | Depositor |
| Imposed symmetry                     | POINT, C1                        | Depositor |
| Number of particles used             | 49979                            | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                | Depositor |
| CTF correction method                | Not provided                     |           |
| Microscope                           | FEI TITAN KRIOS, FEI TITAN KRIOS | Depositor |
| Voltage (kV)                         | 300, 300                         | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 30                               | Depositor |
| Minimum defocus (nm)                 | 2000, 2000                       | Depositor |
| Maximum defocus (nm)                 | 3600, 3600                       | Depositor |
| Magnification                        | 104478, 104478                   | Depositor |
| Image detector                       | FEI FALCON II (4k x 4k)          | Depositor |
| Maximum map value                    | 0.759                            | Depositor |
| Minimum map value                    | -0.468                           | Depositor |
| Average map value                    | 0.001                            | Depositor |
| Map value standard deviation         | 0.022                            | Depositor |
| Recommended contour level            | 0.07                             | Depositor |
| Map size ( $\text{\AA}$ )            | 562.8, 562.8, 562.8              | wwPDB     |
| Map dimensions                       | 420, 420, 420                    | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0                 | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 1.3399999, 1.3399999, 1.3399999  | Depositor |

## 2 Model quality [i](#)

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

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

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

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

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

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

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

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

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

#### 2.3.3 RNA [i](#)

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

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

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

### 2.5 Carbohydrates [i](#)

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

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

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

## 2.7 Other polymers ⓘ

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

POLYMER-BREAKS INFOmissingINFO

### 3 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-3038. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

#### 3.1 Orthogonal projections ⓘ

This section was not generated.

#### 3.2 Central slices ⓘ

This section was not generated.

#### 3.3 Largest variance slices ⓘ

This section was not generated.

#### 3.4 Orthogonal standard-deviation projections (False-color) ⓘ

This section was not generated.

#### 3.5 Orthogonal surface views ⓘ

This section was not generated.

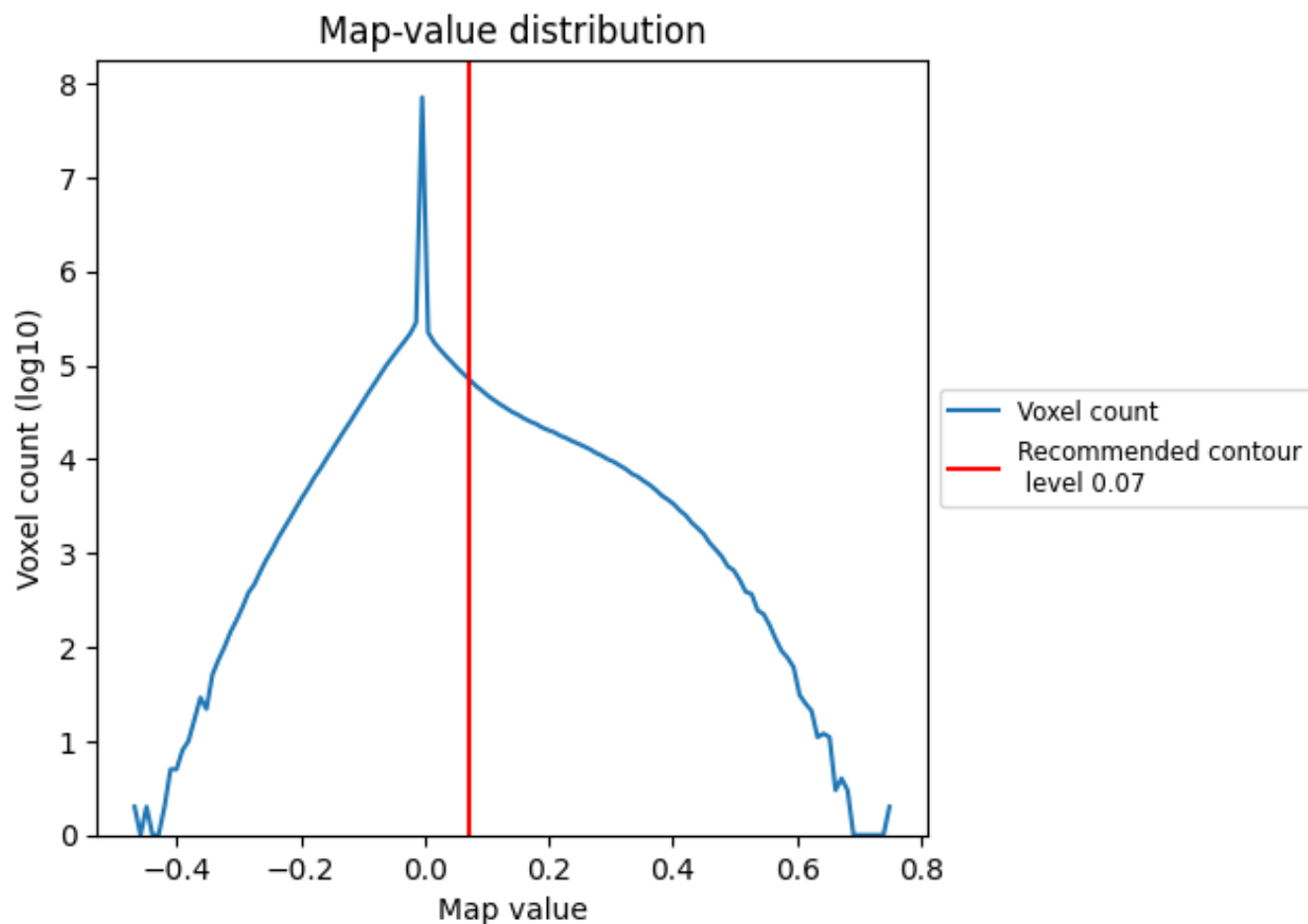
#### 3.6 Mask visualisation ⓘ

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

## 4 Map analysis [i](#)

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

### 4.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

### 4.2 Volume estimate versus contour level [i](#)

This section was not generated.

### 4.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum could not be displayed.

## 5 Fourier-Shell correlation ⓘ

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



## 6 Map-model fit

This section contains information regarding the fit between EMDB map EMD-3038 and PDB model 3JAG. Per-residue inclusion information can be found in section ?? on page ??.

### 6.1 Map-model overlay

This section was not generated.

### 6.2 Q-score mapped to coordinate model

This section was not generated.

### 6.3 Atom inclusion mapped to coordinate model

This section was not generated.

### 6.4 Atom inclusion versus contour level

This section was not generated.

### 6.5 Map-model fit summary

This section was not generated.