



## Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 09:57 PM UTC

PDB ID : 3IZL / pdb\_00003izl  
EMDB ID : EMD-5248  
Title : Mm-cpn rls deltalid with ATP and AlFx  
Authors : Douglas, N.R.; Reissmann, S.; Zhang, J.; Chen, B.; Jakana, J.; Kumar, R.;  
Chiu, W.; Frydman, J.  
Deposited on : 2010-10-29  
Resolution : 6.20 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](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  
MolProbity : **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

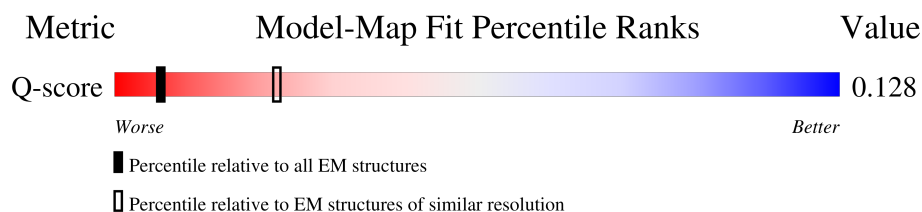
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 6.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



| Metric  | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|---------|-----------------------------|----------------------------------------------------------|
| Q-score | 25397                       | 537 ( 5.70 - 6.70 )                                      |

ENTRY-COMPOSITION INFOmissingINFO

SEQUENCE-PLOTS INFOmissingINFO

## 2 Experimental information

| Property                             | Value                          | Source    |
|--------------------------------------|--------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                | Depositor |
| Imposed symmetry                     | POINT, D8                      | Depositor |
| Number of particles used             | Not provided                   |           |
| Resolution determination method      | FSC 0.5 CUT-OFF                | Depositor |
| CTF correction method                | Not provided                   |           |
| Microscope                           | JEOL 3200FSC                   | Depositor |
| Voltage (kV)                         | 200                            | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | Not provided                   |           |
| Minimum defocus (nm)                 | Not provided                   |           |
| Maximum defocus (nm)                 | Not provided                   |           |
| Magnification                        | Not provided                   |           |
| Image detector                       | GATAN ULTRASCAN 4000 (4k x 4k) | Depositor |
| Maximum map value                    | 1.140                          | Depositor |
| Minimum map value                    | -0.491                         | Depositor |
| Average map value                    | 0.020                          | Depositor |
| Map value standard deviation         | 0.094                          | Depositor |
| Recommended contour level            | 0.38                           | Depositor |
| Map size ( $\text{\AA}$ )            | 266.0, 266.0, 266.0            | wwPDB     |
| Map dimensions                       | 200, 200, 200                  | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0               | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 1.33, 1.33, 1.33               | 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](#)

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

### 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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 3.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

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

There are no ligands in this entry.

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

There are no such residues in this entry.

### 3.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 4 Map visualisation

This section contains visualisations of the EMDB entry EMD-5248. 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.

### 4.1 Orthogonal projections

This section was not generated.

### 4.2 Central slices

This section was not generated.

### 4.3 Largest variance slices

This section was not generated.

### 4.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

### 4.5 Orthogonal surface views

This section was not generated.

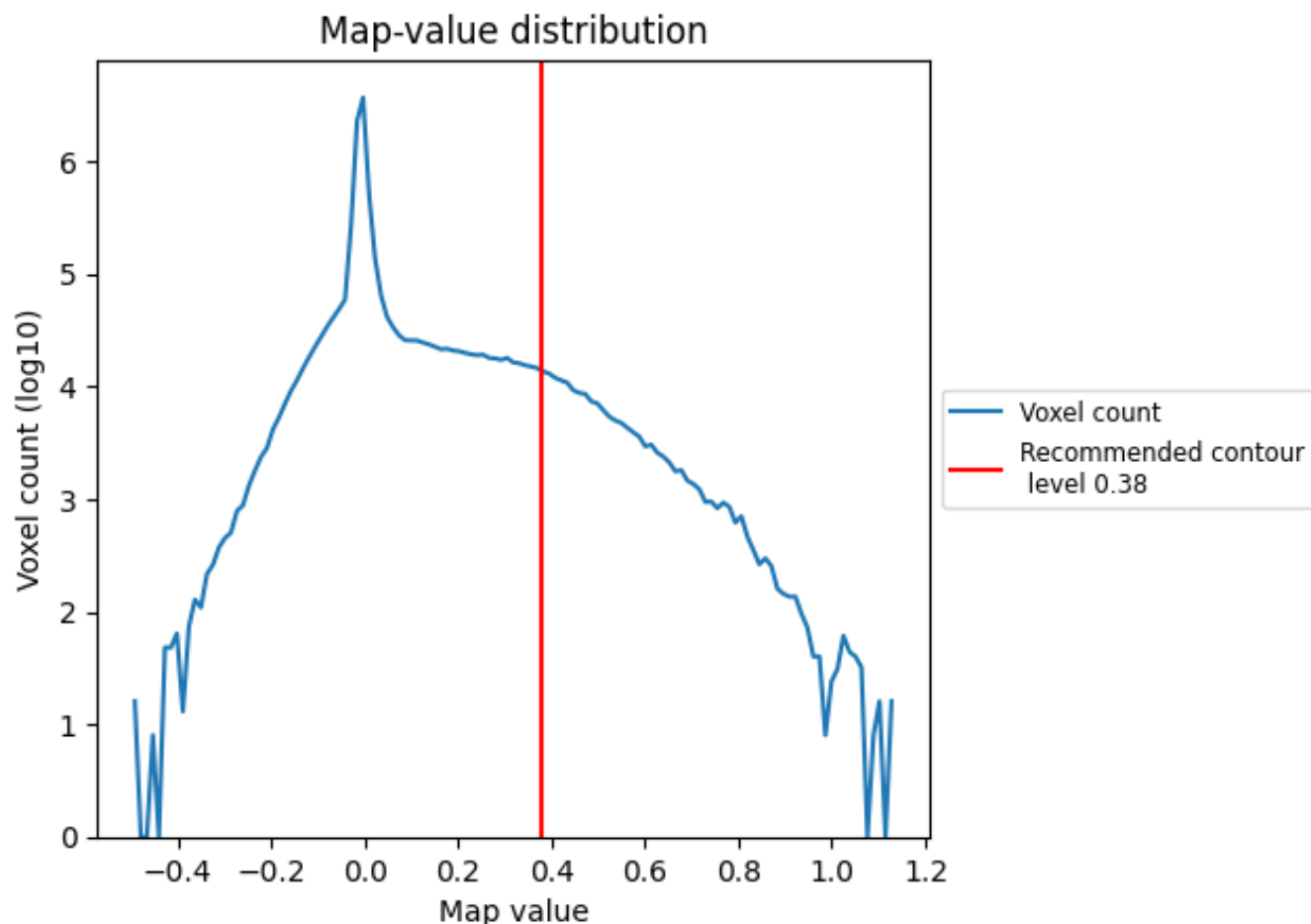
### 4.6 Mask visualisation

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

## 5 Map analysis [i](#)

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

### 5.1 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.

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

This section was not generated.

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

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

## 6 Fourier-Shell correlation

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

## 7 Map-model fit

This section contains information regarding the fit between EMDB map EMD-5248 and PDB model 3IZL. Per-residue inclusion information can be found in section ?? on page ??.

### 7.1 Map-model overlay

This section was not generated.

### 7.2 Q-score mapped to coordinate model

This section was not generated.

### 7.3 Atom inclusion mapped to coordinate model

This section was not generated.

### 7.4 Atom inclusion versus contour level

This section was not generated.

### 7.5 Map-model fit summary

This section was not generated.