



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 11:12 AM UTC

PDB ID : 8U81 / pdb_00008u81
EMDB ID : EMD-41996
Title : KCTD5/Cullin3/Gbeta1gamma2 Complex: State A From Composite RE-
LION Multi-body Refinement Map
Authors : Kuntz, D.A.; Nguyen, D.M.; Narayanan, N.; Prive, G.G.
Deposited on : 2023-09-15
Resolution : 3.82 Å (reported)
Based on initial models : 4EOZ, 3DRX, 6VMS

This is a wwPDB EM Validation Summary 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/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>.

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

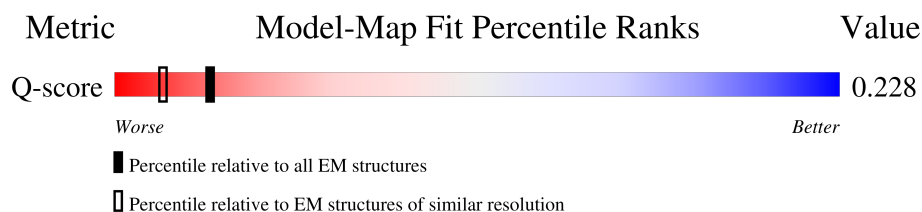
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.82 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 (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	9152 (3.32 - 4.32)

ENTRY-COMPOSITION INFOmissingINFO

SEQUENCE-PLOTS INFOmissingINFO

2 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48895	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.35	Depositor
Minimum defocus (nm)	250	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	25.614	Depositor
Minimum map value	-6.558	Depositor
Average map value	-0.007	Depositor
Map value standard deviation	1.074	Depositor
Recommended contour level	1.6	Depositor
Map size ($\text{\AA}$)	333.72, 333.72, 333.72	wwPDB
Map dimensions	324, 324, 324	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.03, 1.03, 1.03	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-41996. 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.

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.

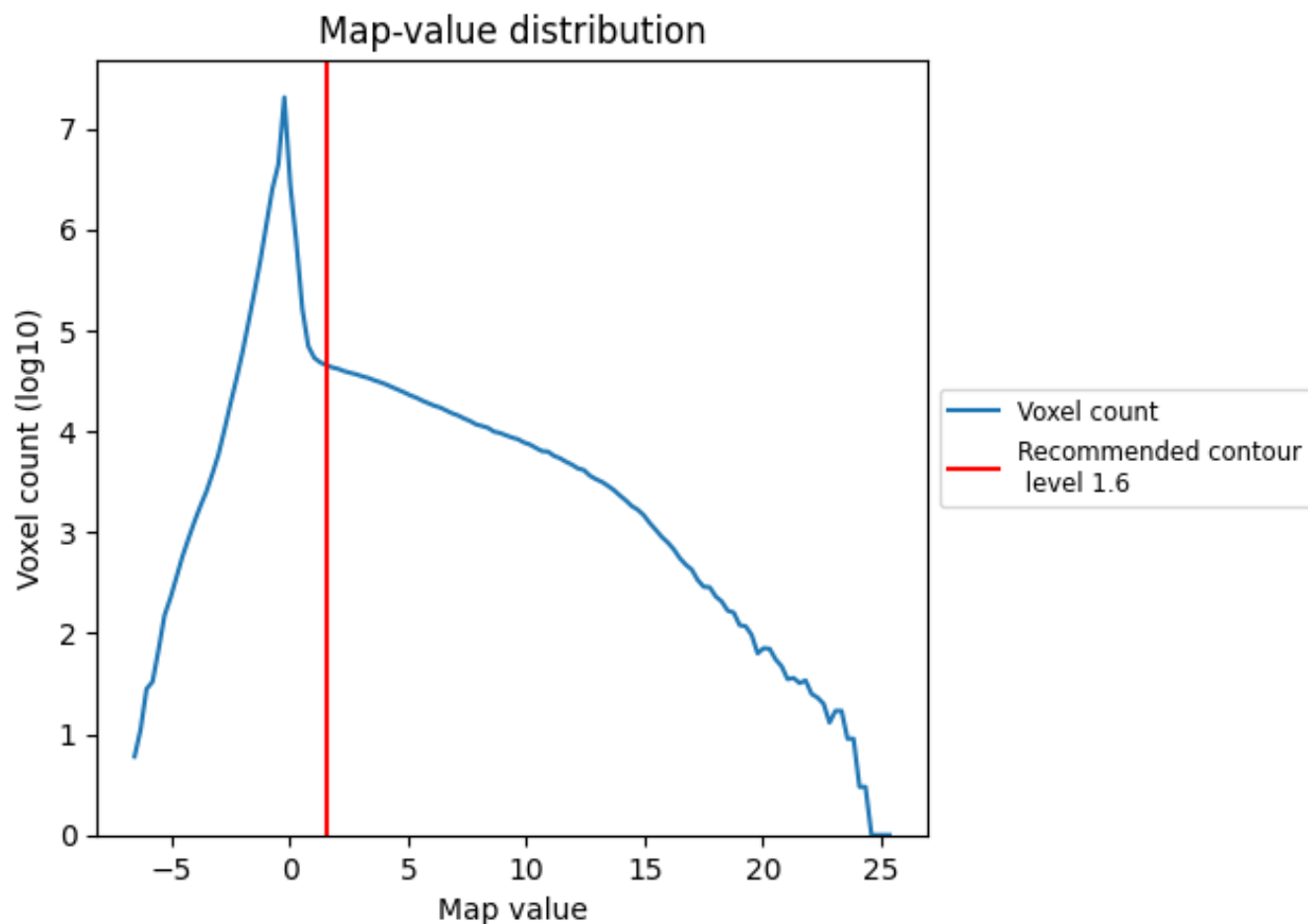
4.6 Mask visualisation

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-41996 and PDB model 8U81. 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.