



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 01:12 PM UTC

PDB ID : 7V74 / pdb_00007v74
EMDB ID : EMD-31758
Title : Thermostabilized human prestin in complex with sulfate
Authors : Futamata, H.; Fukuda, M.; Yamashita, K.; Nishizawa, T.; Nureki, O.
Deposited on : 2021-08-21
Resolution : 3.63 Å(reported)
Based on initial model : 5DA0

This is a Full wwPDB EM Validation 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
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, C2	Depositor
Number of particles used	249144	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 ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.296	Depositor
Minimum map value	-0.225	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0359	Depositor
Map size (Å)	192.56058, 192.56058, 192.56058	wwPDB
Map dimensions	174, 174, 174	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.10667, 1.10667, 1.10667	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 [i](#)

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

2.8 Polymer linkage issues

There are no chain breaks in this entry.

3 Map visualisation

This section contains visualisations of the EMDB entry EMD-31758. 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.

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.

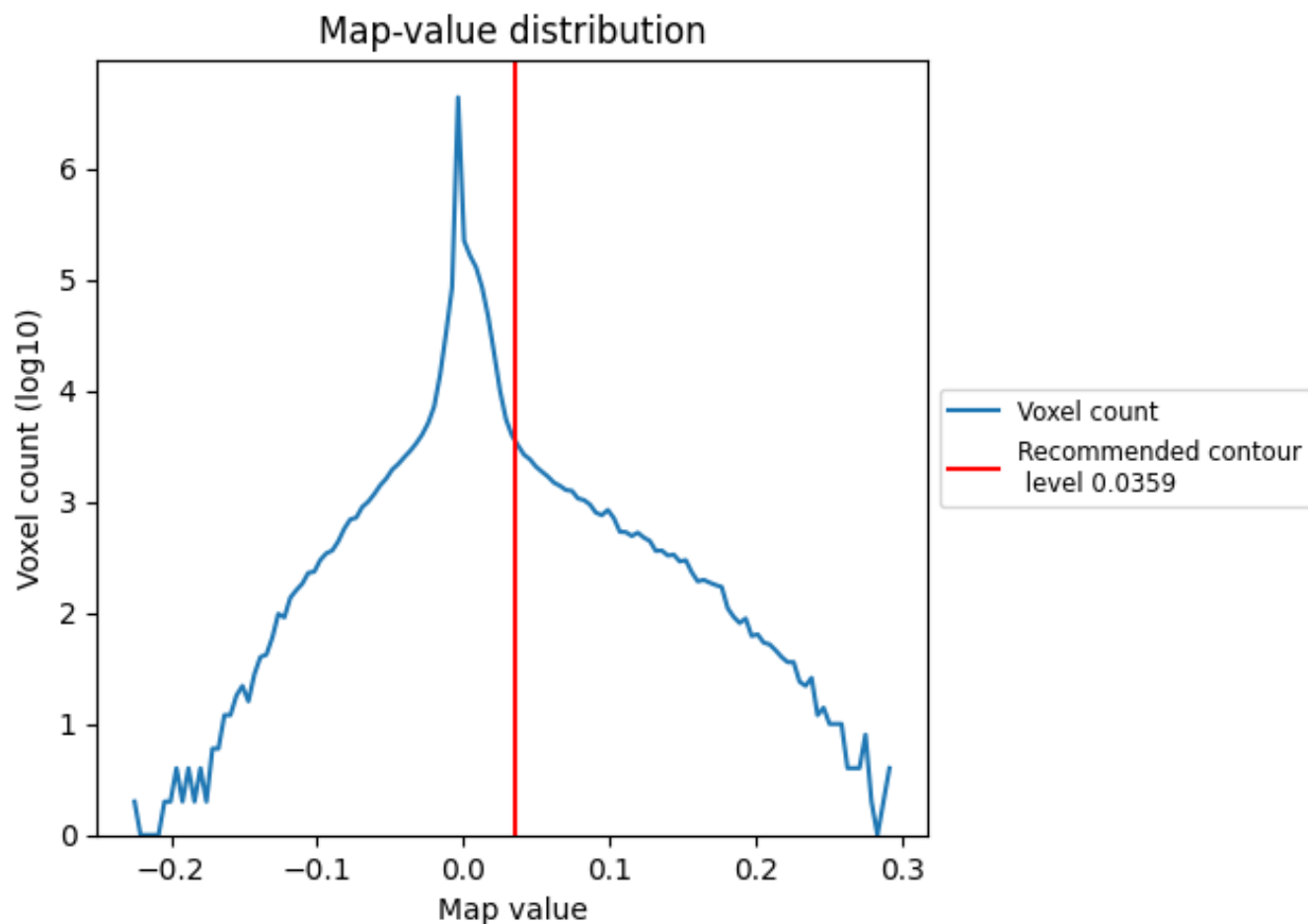
3.6 Mask visualisation

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-31758 and PDB model 7V74. 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.