



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:37 AM UTC

PDB ID : 7WYW / pdb_00007wyw
EMDB ID : EMD-32896
Title : Cryo-EM structure of Na⁺,K⁺-ATPase in the E2P state formed by inorganic phosphate
Authors : Kanai, R.; Cornelius, F.; Vilsen, B.; Toyoshima, C.
Deposited on : 2022-02-16
Resolution : 3.80 Å(reported)
Based on initial model : 7D91

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
Mogul : **FAILED**
MolProbity : **FAILED**
Buster-report : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
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	46883	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	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.

SUGAR-GEOMETRY INFOmissingINFO

2.5 Ligand geometry [i](#)

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

2.6 Other polymers [i](#)

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

2.7 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

3 Map visualisation

This section contains visualisations of the EMDB entry EMD-32896. 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 ⓘ

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

4.1 Map-value distribution ⓘ

This section was not generated.

4.2 Volume estimate versus contour level ⓘ

This section was not generated.

4.3 Rotationally averaged power spectrum ⓘ

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

5 Fourier-Shell correlation ⓘ

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

6 Map-model fit

This section was not generated.