



Full wwPDB EM Validation 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 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 : **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.