

# 2xPDXK:2xZn<sup>2+</sup> phosphorylates PXL

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## Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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## Literature references

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 74

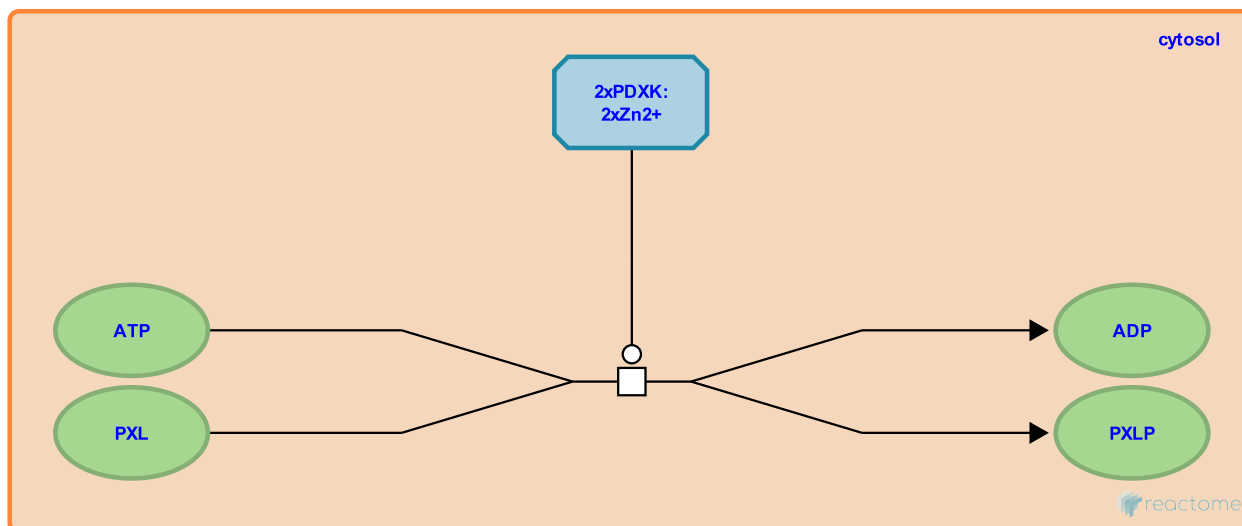
This document contains 1 reaction ([see Table of Contents](#))

## 2xPDXK:2xZn2+ phosphorylates PXL ↗

**Stable identifier:** R-HSA-964970

**Type:** transition

**Compartments:** cytosol



Pyridoxal kinase (PDXK) catalyzes the ATP-dependent phosphorylation of pyridoxal (PXL) to form pyridoxal 5'-phosphate (PXL P) (Lee et al. 2000, di Salvo et al. 2004).

### Literature references

Lee, HS., Moon, BJ., Choi, SY., Kwon, OS. (2000). Human pyridoxal kinase: overexpression and properties of the recombinant enzyme. *Mol Cells*, 10, 452-9. ↗

di Salvo, ML., Hunt, S., Schirch, V. (2004). Expression, purification, and kinetic constants for human and Escherichia coli pyridoxal kinases. *Protein Expr Purif*, 36, 300-6. ↗

### Editions

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