

# PP1 binds to phosphorylated TIM in complex with PER

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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: 88

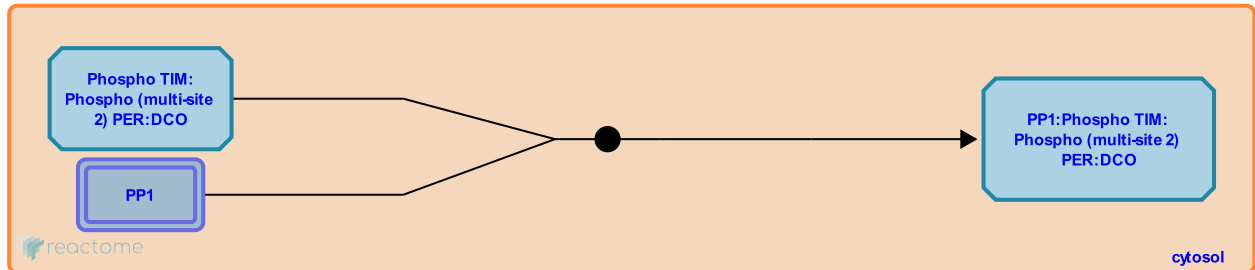
This document contains 1 reaction ([see Table of Contents](#))

## PP1 binds to phosphorylated TIM in complex with PER [↗](#)

**Stable identifier:** R-DME-538824

**Type:** binding

**Compartments:** cytosol



The protein phosphatase, PP1, binds to Timeless (TIM). The interaction is probably via the RVXF, PP1-binding motif in TIM. This binding motif appears to be absent in the protein Period (PER). The catalytic unit of PP1 could be either of the 4 isoforms which exist in fly: flapwing (FLW), Protein phosphatase 1 at 13C (PP1-13C), Protein phosphatase 1 at 87B (PP1-87B), Protein phosphatase 1alpha at 96A (PP1alpha-96A).

### Literature references

Fang, Y., Sehgal, A., Sathyanarayanan, S. (2007). Post-translational regulation of the *Drosophila* circadian clock requires protein phosphatase 1 (PP1). *Genes Dev*, 21, 1506-18. [↗](#)

### Editions

2010-03-08	Authored	Williams, MG.
2010-07-06	Reviewed	Edery, I.
2014-05-20	Edited	Williams, MG.