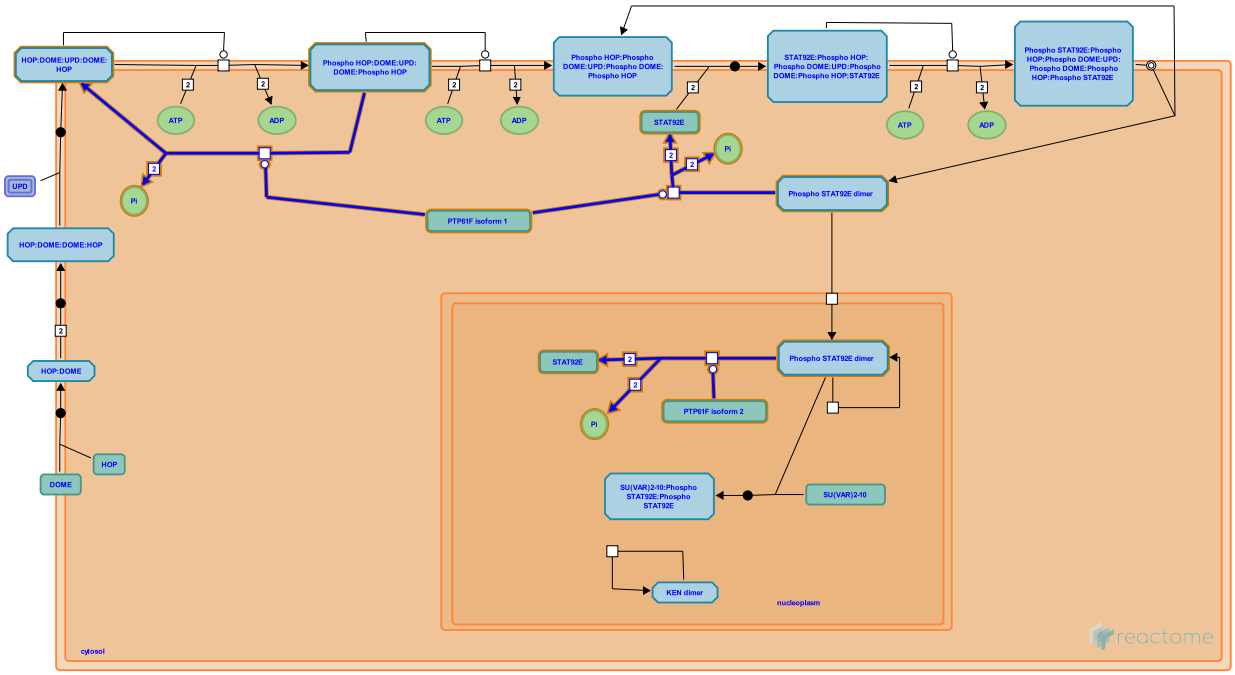
Dephosphorylation by PTP61F phosphatases



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17/05/2024

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.
The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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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. ↗

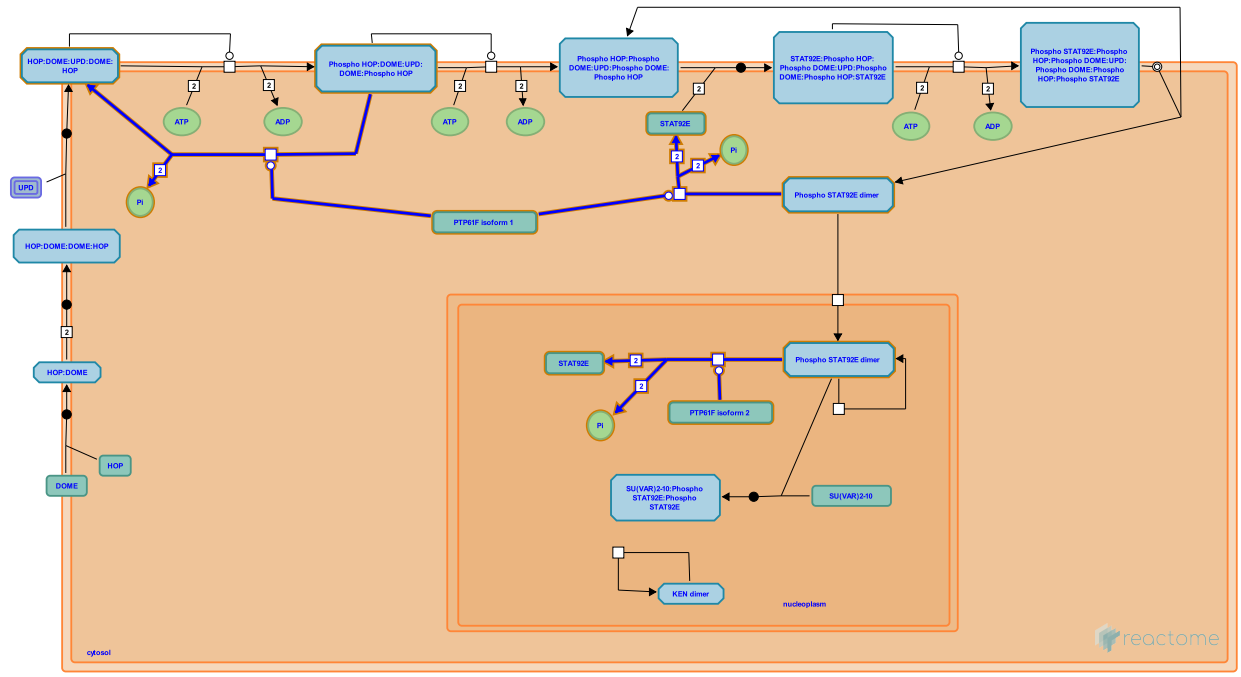
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

Dephosphorylation by PTP61F phosphatases ↗

Stable identifier: R-DME-210688



Spatzle (SPZ) dimer binding leads to Toll (TL) receptor homodimerisation and activation.

Literature references

Arbouzova, NI., Zeidler, MP. (2006). JAK/STAT signalling in Drosophila: insights into conserved regulatory and cellular functions. *Development, 133*, 2605-16. ↗

Editions

2006-11-02	Authored	Williams, MG.
2008-01-15	Edited	Williams, MG.
2008-01-16	Reviewed	Perrimon, N.

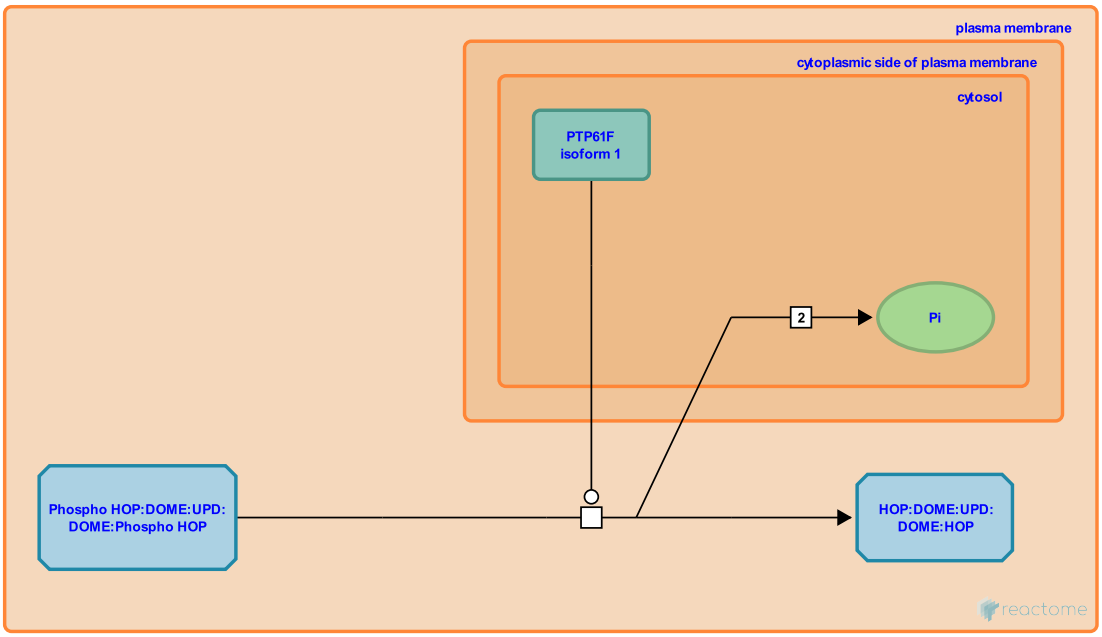
Phosphorylated HOP is dephosphorylated by PTP61F isoform 1 ↗

Location: Dephosphorylation by PTP61F phosphatases

Stable identifier: R-DME-210662

Type: transition

Compartments: plasma membrane, cytosol



The Janus tyrosine kinase, Hopscotch (HOP) is dephosphorylated in the cytosol by the protein tyrosine phosphatase, PTP61F isoform 1.

Literature references

Baeg, GH., Zhou, R., Perrimon, N. (2005). Genome-wide RNAi analysis of JAK/STAT signaling components in Drosophila. *Genes Dev, 19*, 1861-70. ↗

Kuttenkeuler, D., Boutros, M., Zeidler, MP., Müller, P., Gesellchen, V. (2005). Identification of JAK/STAT signalling components by genome-wide RNA interference. *Nature, 436*, 871-5. ↗

Dixon, JE., McLaughlin, S. (1993). Alternative splicing gives rise to a nuclear protein tyrosine phosphatase in Drosophila. *J Biol Chem, 268*, 6839-42. ↗

Editions

2006-11-02	Authored	Williams, MG.
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Phosphorylated STAT92E dimer is dephosphorylated by PTP61F isoform 1 ↗

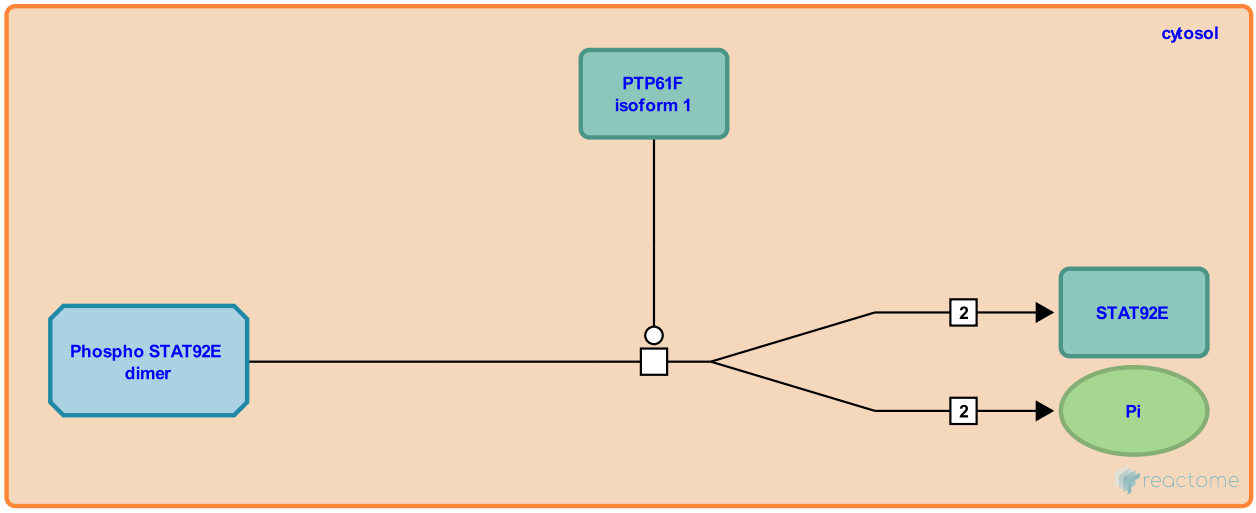
Location: Dephosphorylation by PTP61F phosphatases

Stable identifier: R-DME-210646

Type: transition

Compartments: cytosol

Inferred from: Phosphorylated STAT5A dimer is dephosphorylated by PTP1B (Mus musculus)



In the cytosol, phosphorylated STAT92E dimer is dephosphorylated on Tyr711 by the protein tyrosine phosphatase, PTP61F isoform 1.

Literature references

Baeg, GH., Zhou, R., Perrimon, N. (2005). Genome-wide RNAi analysis of JAK/STAT signaling components in Drosophila. *Genes Dev, 19*, 1861-70. ↗

Kuttenkeuler, D., Boutros, M., Zeidler, MP., Müller, P., Gesellchen, V. (2005). Identification of JAK/STAT signalling components by genome-wide RNA interference. *Nature, 436*, 871-5. ↗

Dixon, JE., McLaughlin, S. (1993). Alternative splicing gives rise to a nuclear protein tyrosine phosphatase in Drosophila. *J Biol Chem, 268*, 6839-42. ↗

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STAT92E dimer dephosphorylated in the nucleus and transported to the cytosol ↗

Location: Dephosphorylation by PTP61F phosphatases

Stable identifier: R-DME-210693

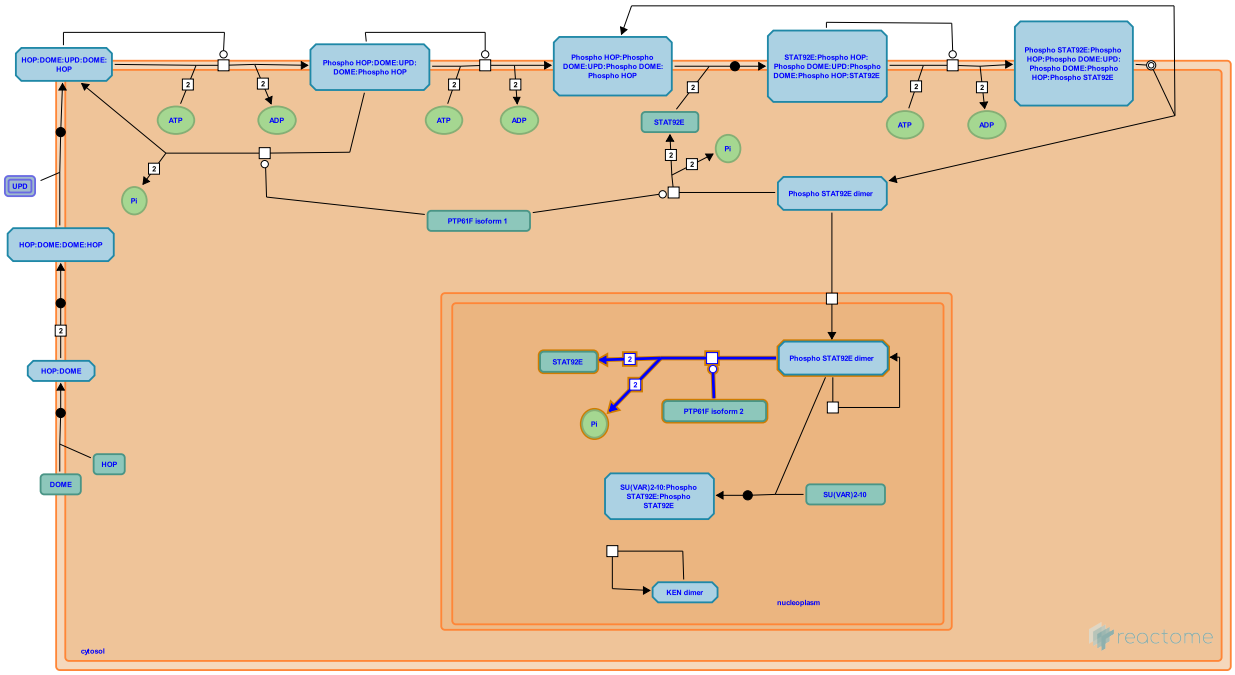

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Table of Contents