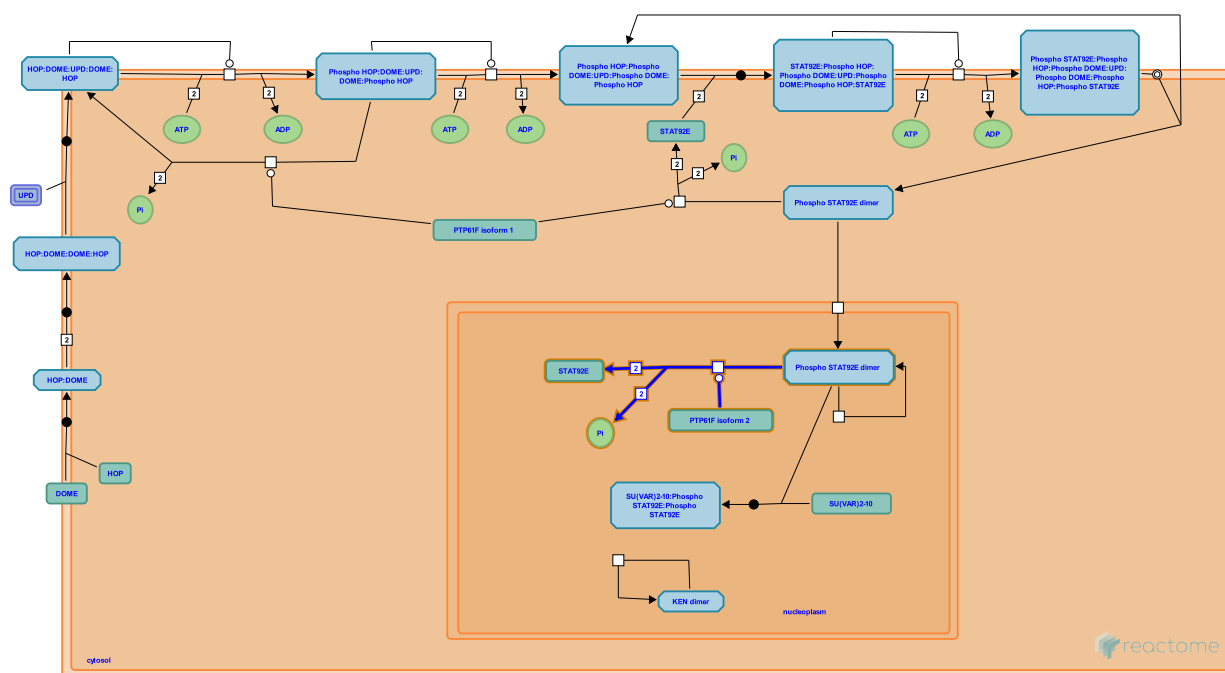


STAT92E dimer dephosphorylated in the nucleus and transported to the cytosol



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](https://reactome.org/About-Reactome).

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.

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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. [↗](#)

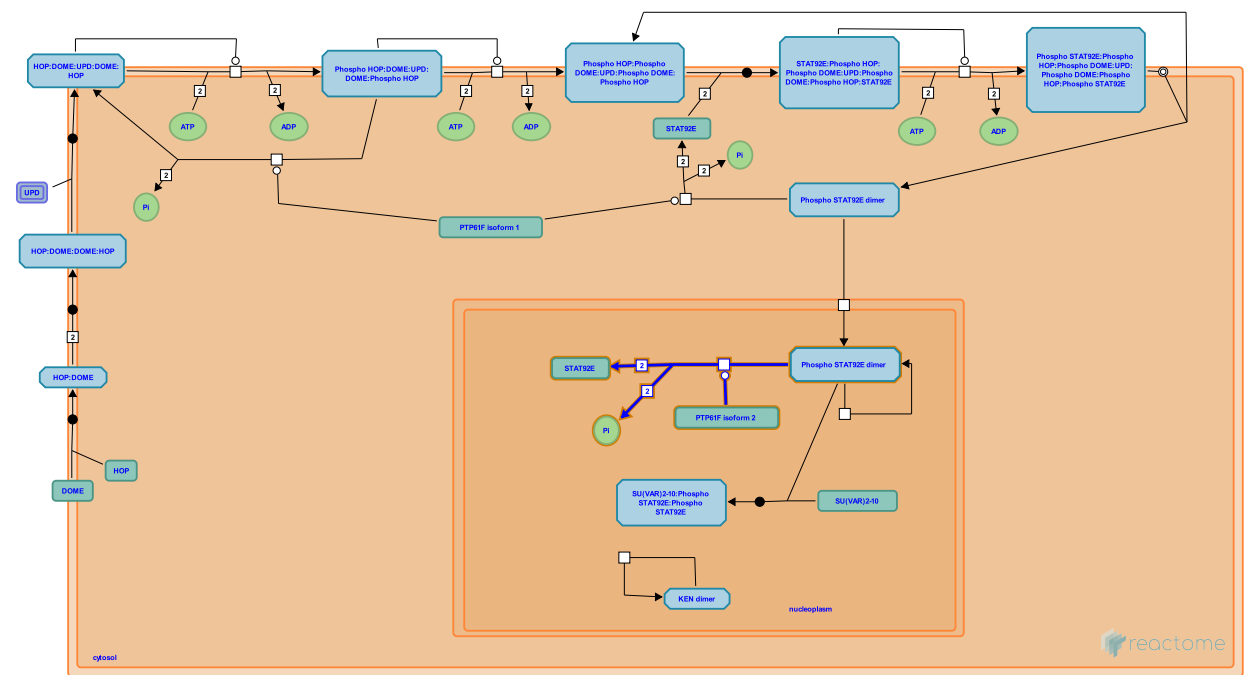
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

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

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

Stable identifier: R-DME-210693



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.

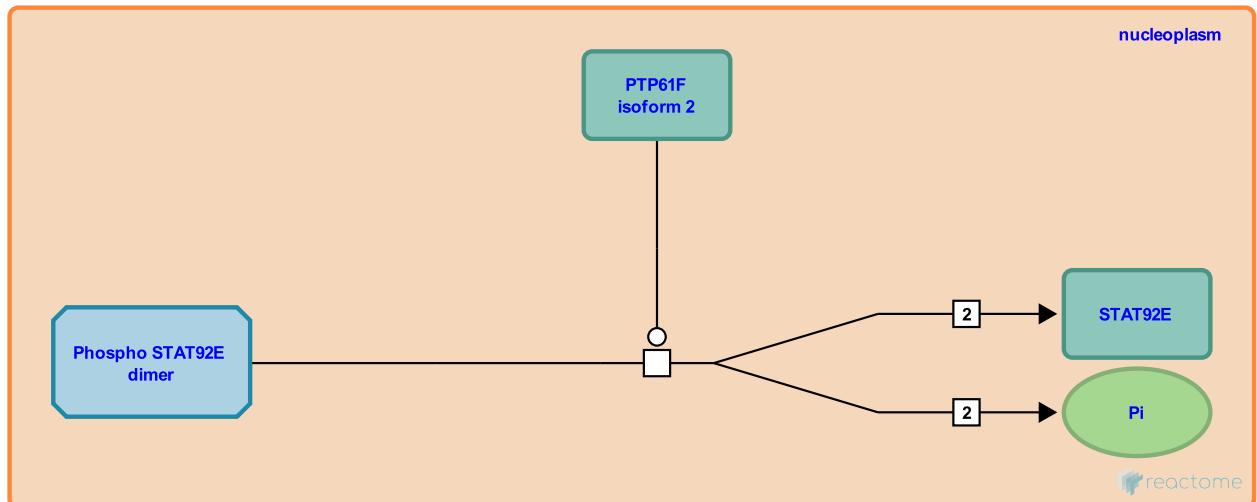
Phosphorylated STAT92E dimer is dephosphorylated by PTP61F isoform 2 ↗

Location: STAT92E dimer dephosphorylated in the nucleus and transported to the cytosol

Stable identifier: R-DME-210694

Type: transition

Compartments: nucleoplasm



An alternative spliced form of the protein tyrosine phosphatase, PTP61FC (PTP61F isoform 2) is active in the nucleus and dephosphorylates the phosphorylated STAT92E dimer on Tyr711 resulting in its dissociation.

Literature references

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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