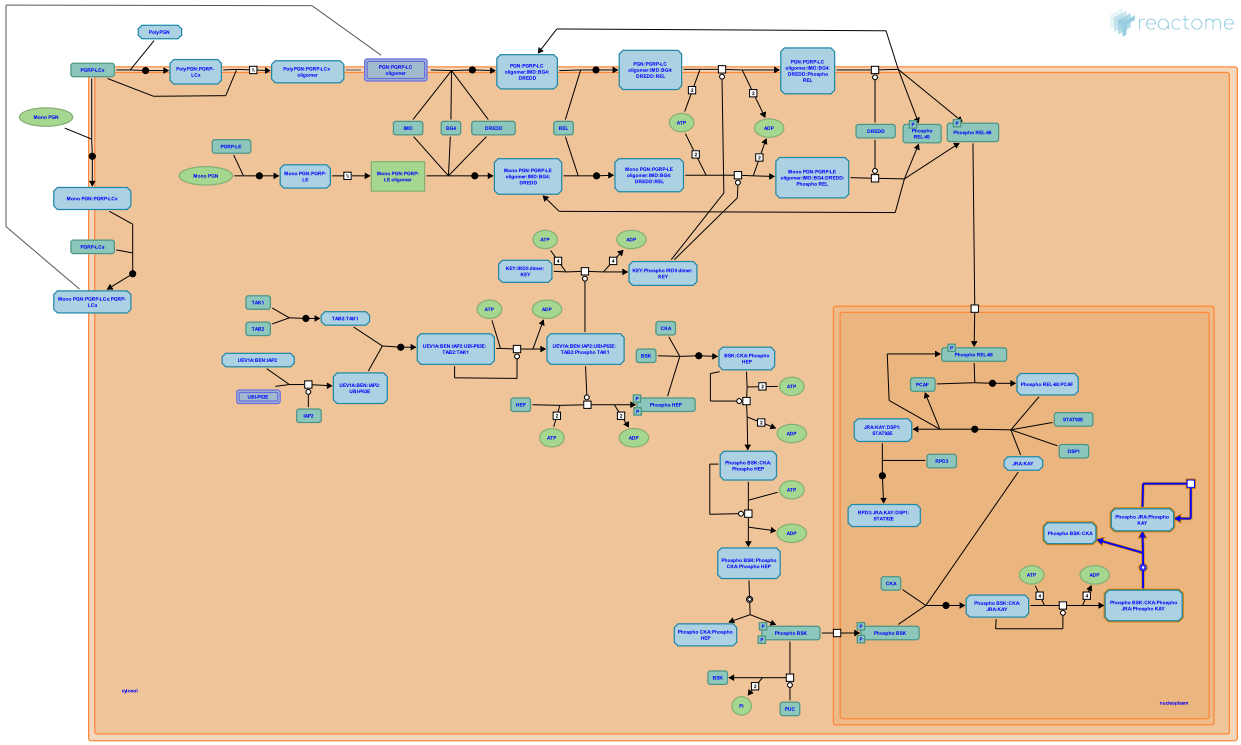
Transcriptional activtion by AP-1 transcription factor



Lemaitre, B., Silverman, N., Williams, MG.

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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.

18/05/2024

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).

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. ↗

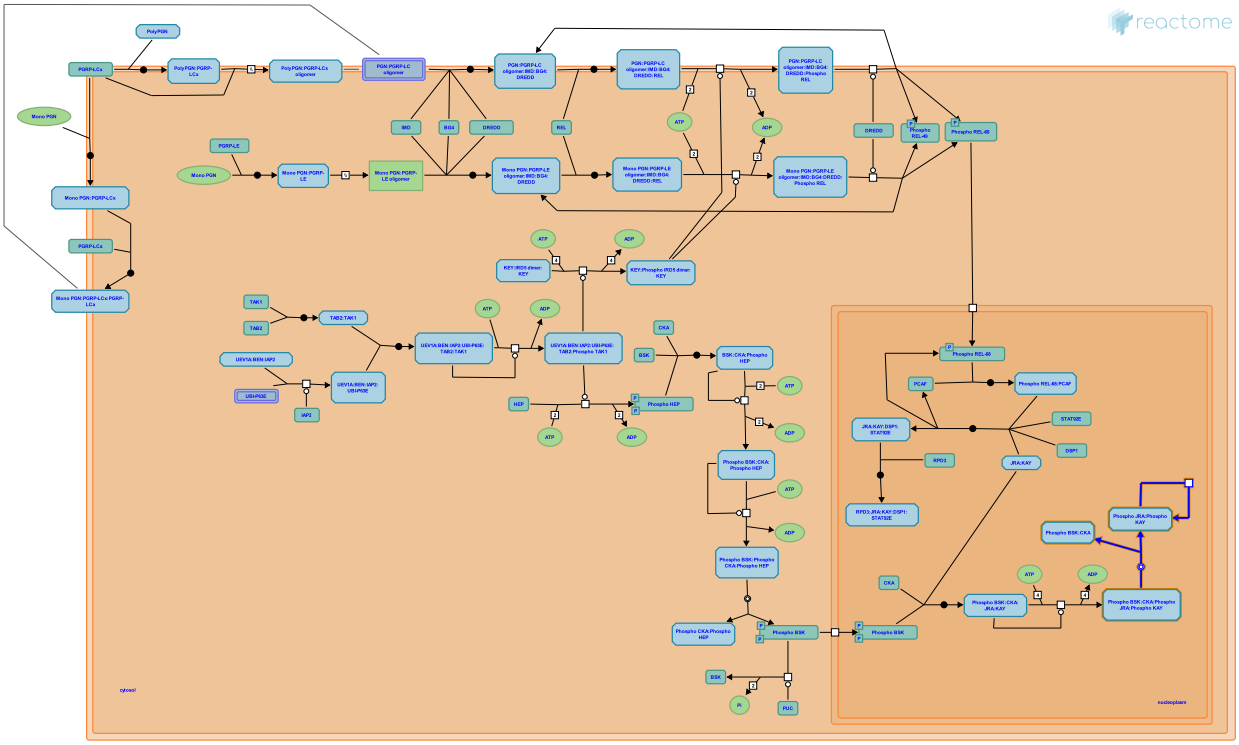
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

Transcriptional activtion by AP-1 transcription factor ↗

Stable identifier: R-DME-209425



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

Literature references

Leclerc, V., Reichhart, JM. (2004). The immune response of Drosophila melanogaster. *Immunol Rev, 198*, 59-71. ↗

Editions

2007-07-11	Authored	Williams, MG.
2007-07-12	Edited	Williams, MG.
2008-06-20	Reviewed	Lemaitre, B., Silverman, N.

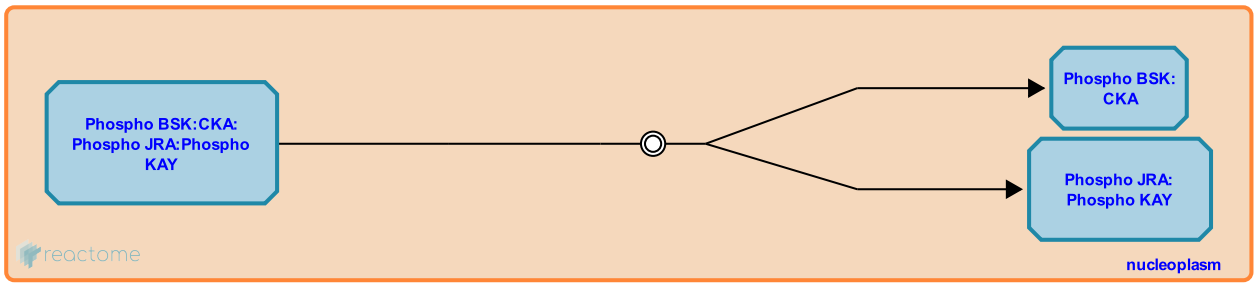
Phosphorylated AP-1, Phospho JRA:Phospho KAY dissociates from CKA ↗

Location: Transcriptional activtion by AP-1 transcription factor

Stable identifier: R-DME-209193

Type: dissociation

Compartments: nucleoplasm



The phosphorylated AP-1 transcription factor, JRA:KAY dissociates from the scaffolding protein CKA.

Followed by: Phosphorylated AP-1, Phospho JRA:Phospho KAY binds to a target gene and activates transcription

Literature references

Marinissen, MJ., Hou, SX., Chen, X., Chen, HW., Oh, SW., Gutkind, JS. et al. (2002). CKA, a novel multidomain protein, regulates the JUN N-terminal kinase signal transduction pathway in Drosophila. *Mol Cell Biol, 22*, 1792-803. ↗

Editions

2007-07-11	Authored	Williams, MG.
2008-06-20	Reviewed	Lemaitre, B., Silverman, N.
2014-05-20	Edited	Williams, MG.

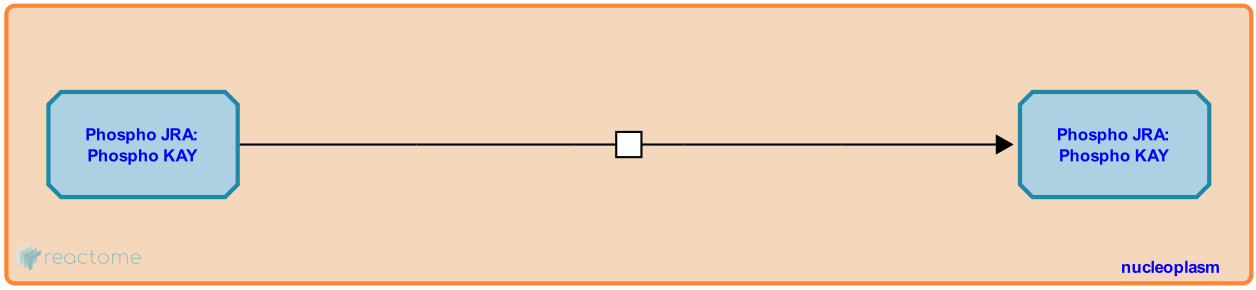
Phosphorylated AP-1, Phospho JRA:Phospho KAY binds to a target gene and activates transcription ↗

Location: Transcriptional activtion by AP-1 transcription factor

Stable identifier: R-DME-209358

Type: transition

Compartments: nucleoplasm



The phosphorylated AP-1 transcription factor binds to its target genes and activates transcription. One of its target genes encodes the phosphatase Puckered (PUC) which acts as a negative regulator of the pathway as part of a negative feedback loop.

In the eye, another transcriptional target, arising from the Frizzled (FZ):Dishevelled (DSH) complex activation in R3 cells, is for the Notch (N) receptor ligand Delta (DL). This will subsequently bind to its receptor N in the neighbouring R4 cell.

Preceded by: Phosphorylated AP-1, Phospho JRA:Phospho KAY dissociates from CKA

Literature references

Paricio, N., Mlodzik, M., Weber, U. (2000). Jun mediates Frizzled-induced R3/R4 cell fate distinction and planar polarity determination in the Drosophila eye. *Development, 127*, 3619-29. ↗

Marinissen, MJ., Hou, SX., Chen, X., Chen, HW., Oh, SW., Gutkind, JS. et al. (2002). CKA, a novel multidomain protein, regulates the JUN N-terminal kinase signal transduction pathway in Drosophila. *Mol Cell Biol, 22*, 1792-803. ↗

Glover, JN., Harrison, SC. (1995). Crystal structure of the heterodimeric bZIP transcription factor c-Fos-c-Jun bound to DNA. *Nature, 373*, 257-61. ↗

Struhl, G., Tomlinson, A. (1999). Decoding vectorial information from a gradient: sequential roles of the receptors Frizzled and Notch in establishing planar polarity in the Drosophila eye. *Development, 126*, 5725-38. ↗

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Editions

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2008-06-20	Reviewed	Lemaitre, B., Silverman, N.
2014-05-20	Edited	Williams, MG.

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