RUNX3 translocates to the nucleus

Chuang, LS., Ito, Y., Orlic-Milacic, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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

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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. ↗

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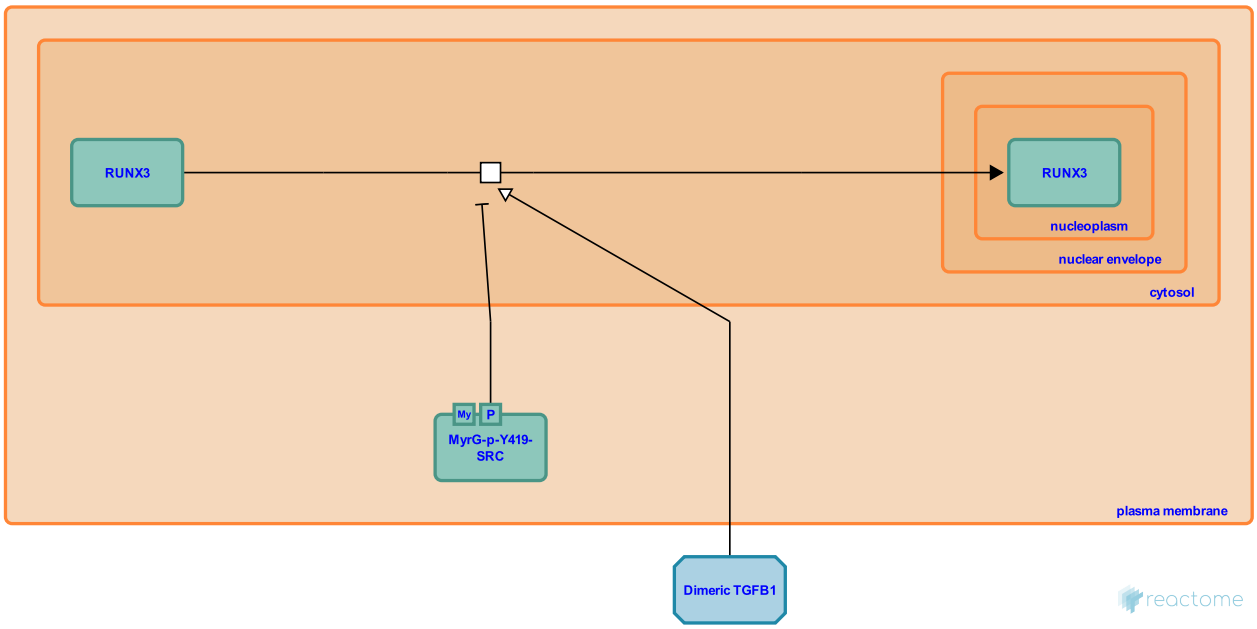
Stable identifier: R-HSA-8937814

Type: transition

Compartments: cytosol, nucleoplasm



Translocation of RUNX3 from the cytosol to the nucleus is stimulated by TGF-beta (TGFB1) treatment (Ito et al. 2005) and inhibited by SRC-mediated phosphorylation of RUNX3 on multiple tyrosine residues (Goh et al. 2010).

Literature references

Goh, YM., Cinghu, S., Hong, ET., Lee, YS., Kim, JH., Jang, JW. et al. (2010). Src kinase phosphorylates RUNX3 at tyrosine residues and localizes the protein in the cytoplasm. *J. Biol. Chem., 285*, 10122-9. ↗

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Editions

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