NTRK3 dimers trans-autophosphorylate

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03/05/2024

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

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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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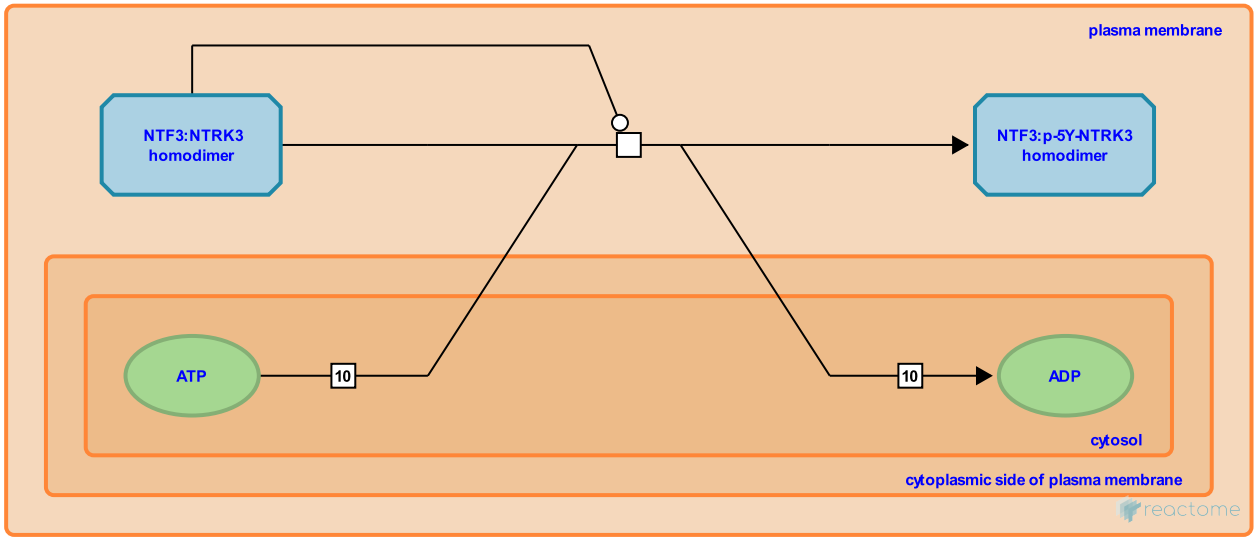
Stable identifier: R-HSA-9034714

Type: transition

Compartments: plasma membrane, cytosol



NTRK3 (TRKC), activated by NTF3 binding, trans-autophosphorylates on tyrosine residues in the intracellular domain (Urfer et al. 1995, Yuen and Mobley 1999, Huang and Reichardt 2001). Tyrosine residue Y516 of NTRK3 was directly shown to be autophosphorylated (Werner et al. 2014), while tyrosine residues Y705, Y709, Y710 and Y834 are predicted to be phosphorylated based on sequence similarity with NTRK2 (TRKB).

Literature references

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Editions

2018-01-02	Authored	Orlic-Milacic, M.
2018-05-09	Edited	Orlic-Milacic, M.
2018-05-09	Reviewed	Tsoulfas, P.