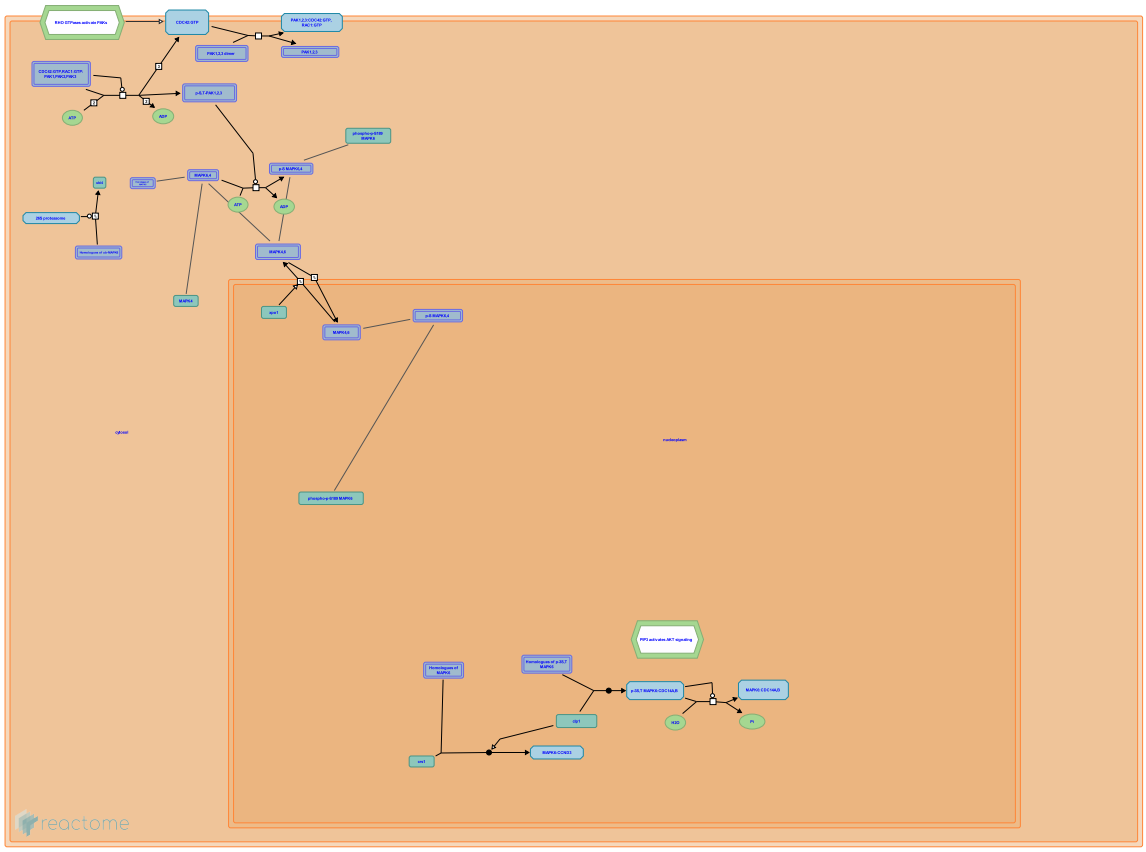
MAPK6/MAPK4 signaling



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

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. ↗

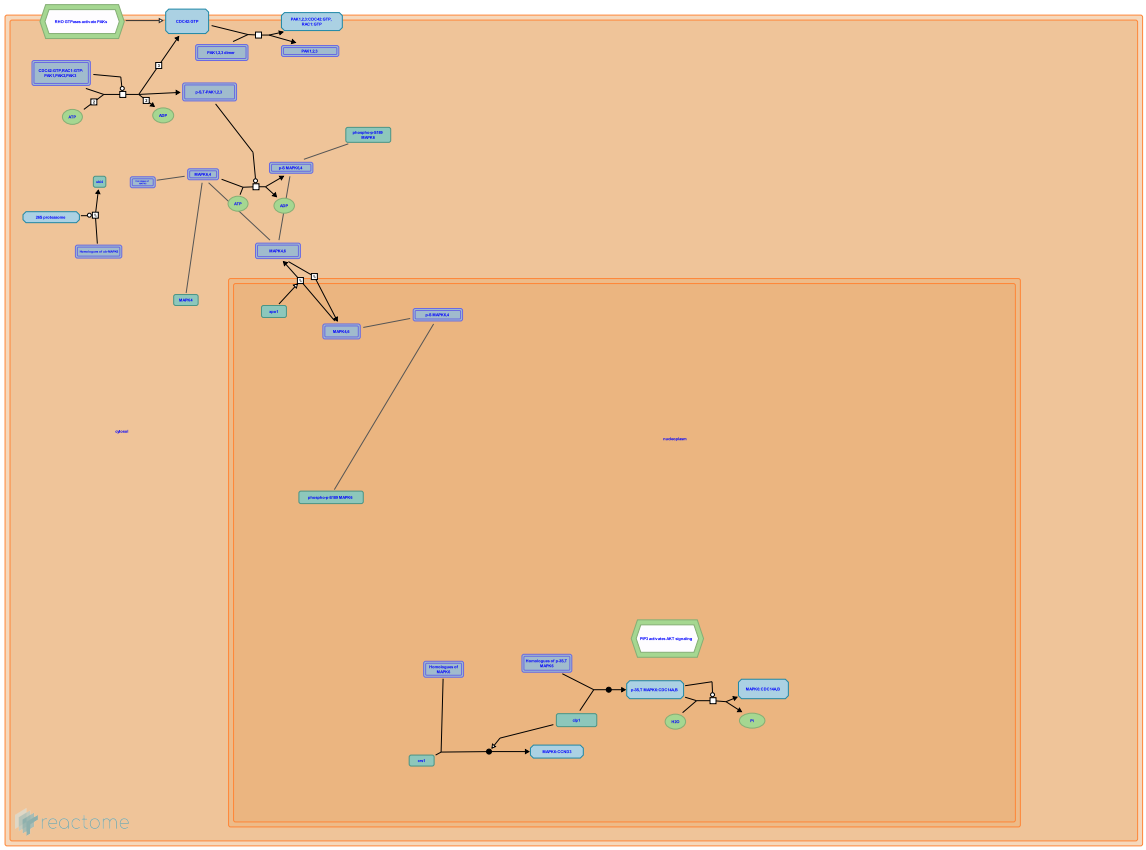
Reactome database release: 88

This document contains 1 pathway and 9 reactions (see Table of Contents)

MAPK6/MAPK4 signaling ↗

Stable identifier: R-SPO-5687128

Inferred from: MAPK6/MAPK4 signaling (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Activation of PAKs by RAC1 and CDC42 ↗

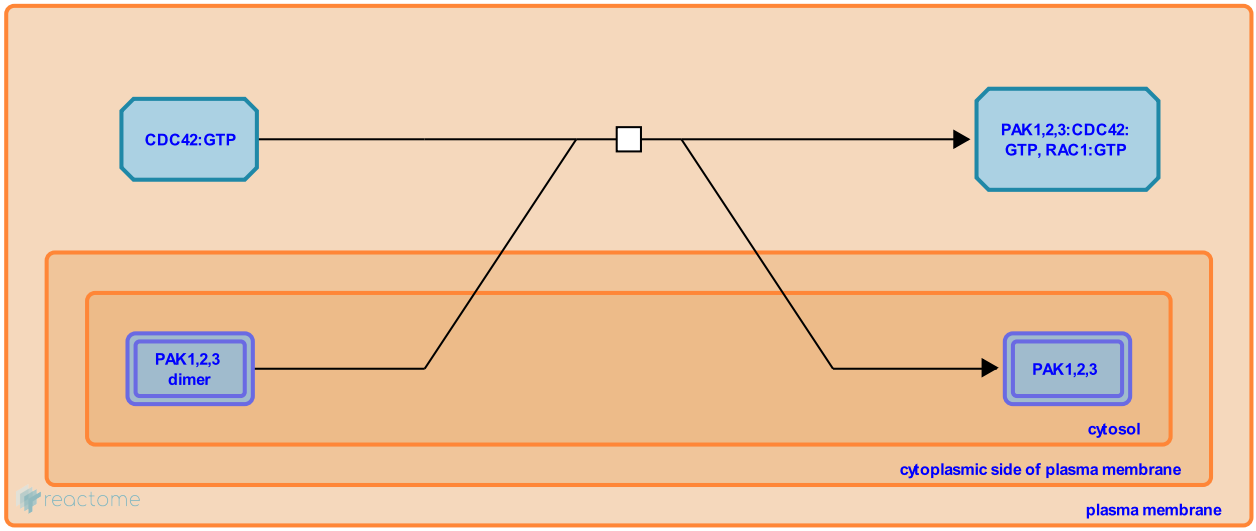
Location: MAPK6/MAPK4 signaling

Stable identifier: R-SPO-389788

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Activation of PAKs by RAC1 and CDC42 (Homo sapiens)



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Autophosphorylation of PAK1,2,3 ↗

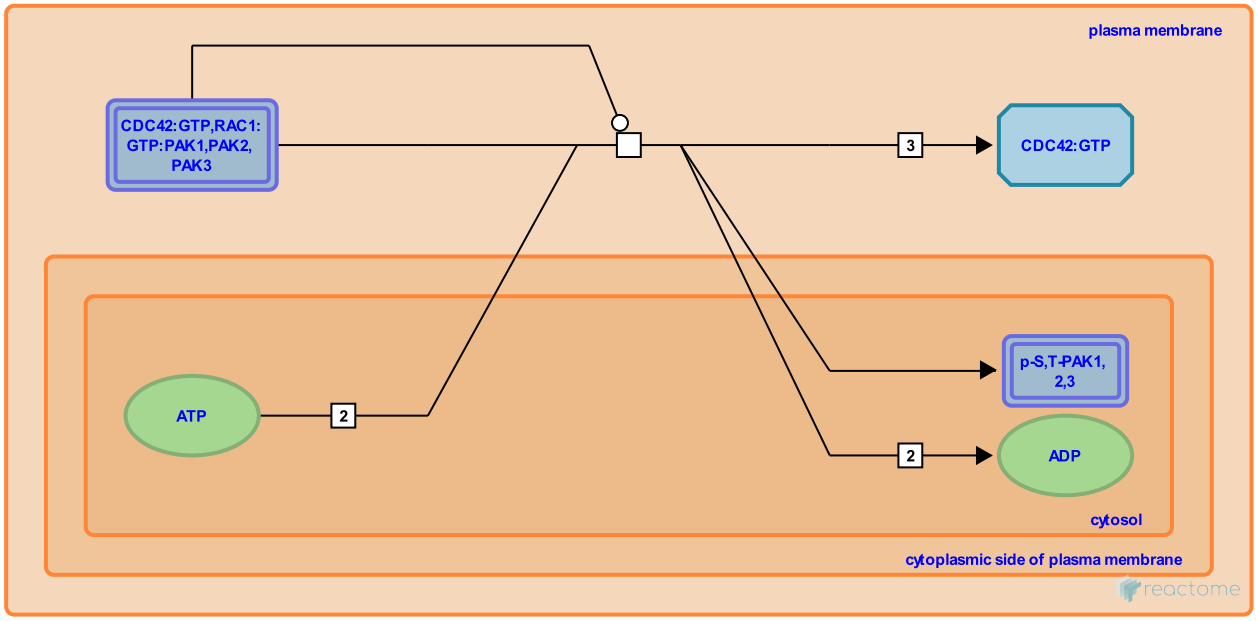
Location: MAPK6/MAPK4 signaling

Stable identifier: R-SPO-5627775

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Autophosphorylation of PAK1,2,3 (Homo sapiens)



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Followed by: PAK1,2,3 phosphorylates MAPK6,4

PAK1,2,3 phosphorylates MAPK6,4 ↗

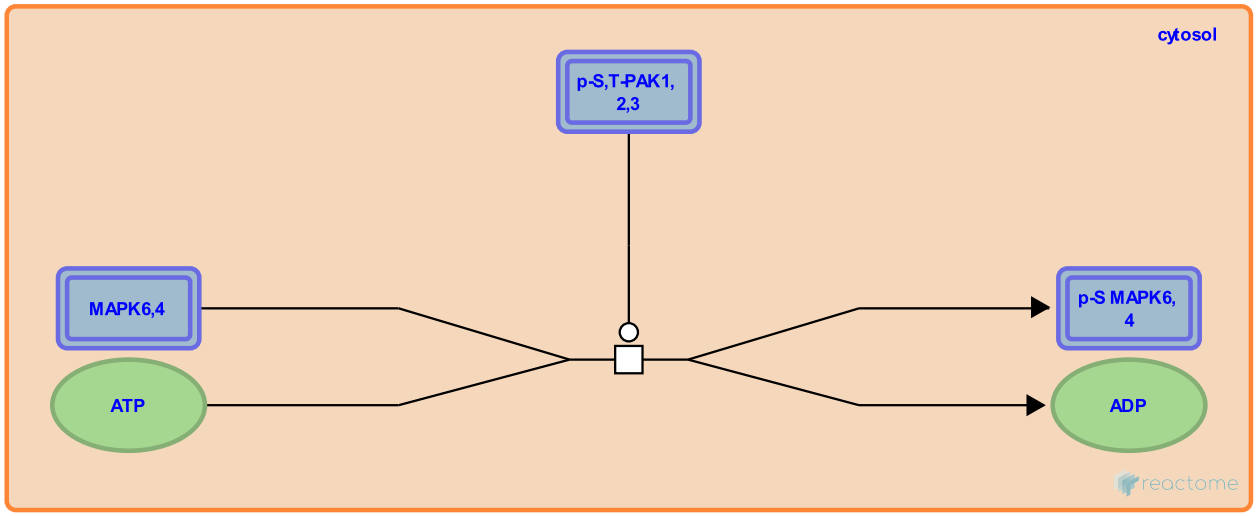
Location: MAPK6/MAPK4 signaling

Stable identifier: R-SPO-5687086

Type: transition

Compartments: cytosol

Inferred from: PAK1,2,3 phosphorylates MAPK6,4 (Homo sapiens)



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Preceded by: Autophosphorylation of PAK1,2,3

MAPK4,6 translocate to nucleus ↗

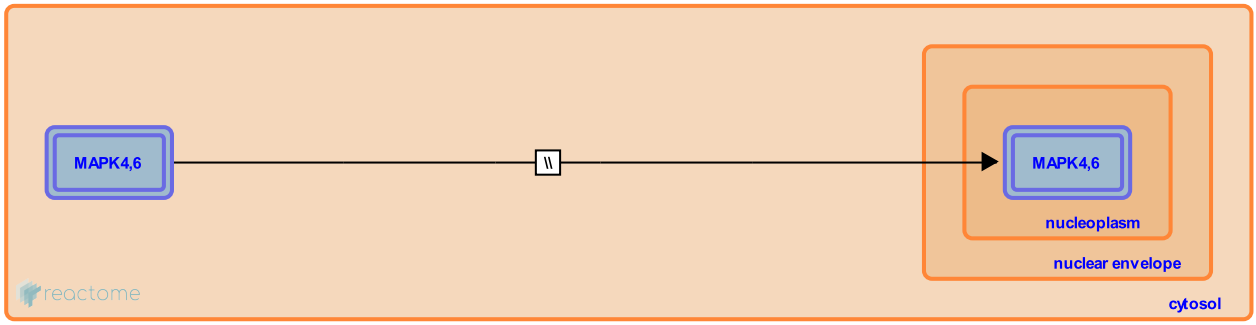
Location: MAPK6/MAPK4 signaling

Stable identifier: R-SPO-5687107

Type: omitted

Compartments: cytosol

Inferred from: MAPK4,6 translocate to nucleus (Homo sapiens)



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MAPK4,6 translocate to the cytoplasm ↗

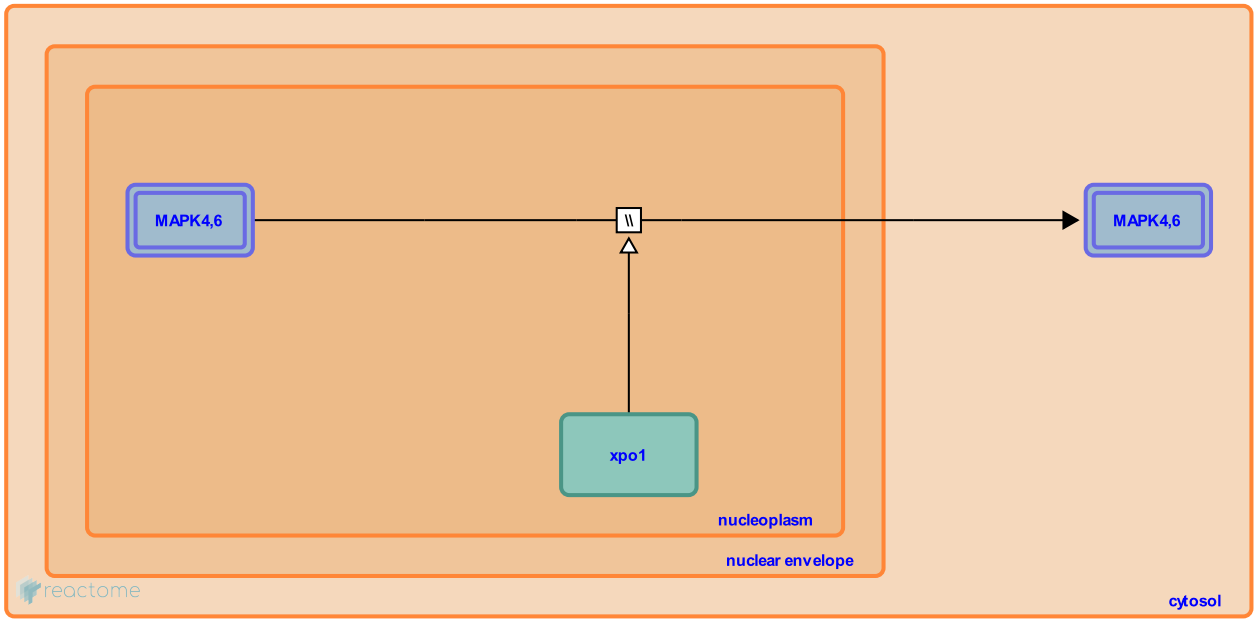
Location: MAPK6/MAPK4 signaling

Stable identifier: R-SPO-5687109

Type: omitted

Compartments: nucleoplasm

Inferred from: MAPK4,6 translocate to the cytoplasm (Homo sapiens)



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MAPK6 is degraded by the 26S proteasome ↗

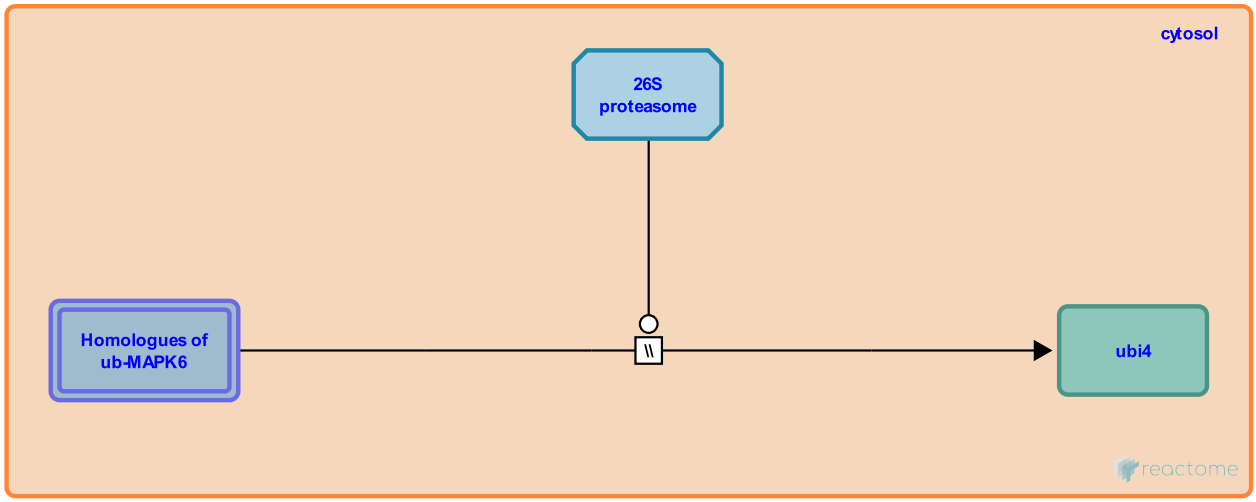
Location: MAPK6/MAPK4 signaling

Stable identifier: R-SPO-5687112

Type: omitted

Compartments: cytosol

Inferred from: MAPK6 is degraded by the 26S proteasome (Homo sapiens)



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CDC14A,B bind MAPK6 ↗

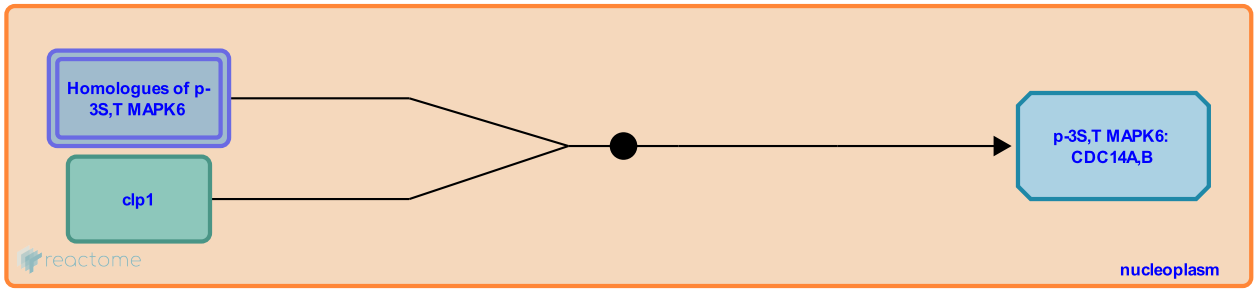
Location: MAPK6/MAPK4 signaling

Stable identifier: R-SPO-5692749

Type: binding

Compartments: nucleoplasm

Inferred from: CDC14A,B bind MAPK6 (Homo sapiens)



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CDC14A,B dephosphorylate p-3S,T MAPK6 ↗

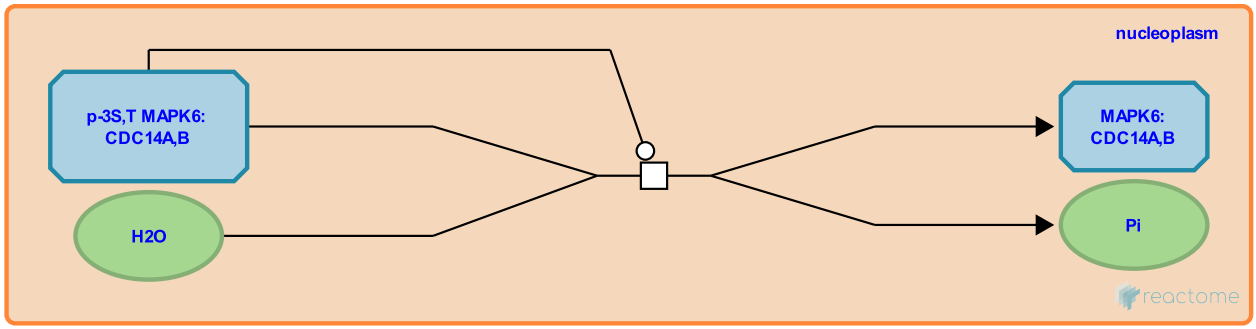
Location: MAPK6/MAPK4 signaling

Stable identifier: R-SPO-5692754

Type: transition

Compartments: nucleoplasm

Inferred from: CDC14A,B dephosphorylate p-3S,T MAPK6 (Homo sapiens)



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MAPK6 binds CCND3 ↗

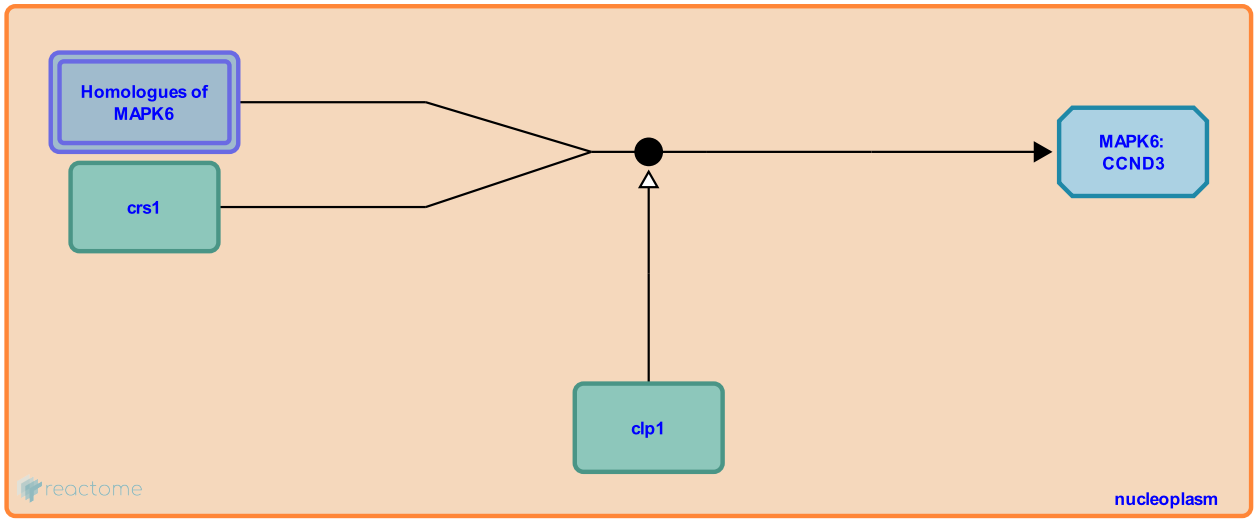
Location: MAPK6/MAPK4 signaling

Stable identifier: R-SPO-5692764

Type: binding

Compartments: nucleoplasm

Inferred from: MAPK6 binds CCND3 (Homo sapiens)



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