Phospho FT reduces D accumulation at the plasma membrane

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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

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. ↗

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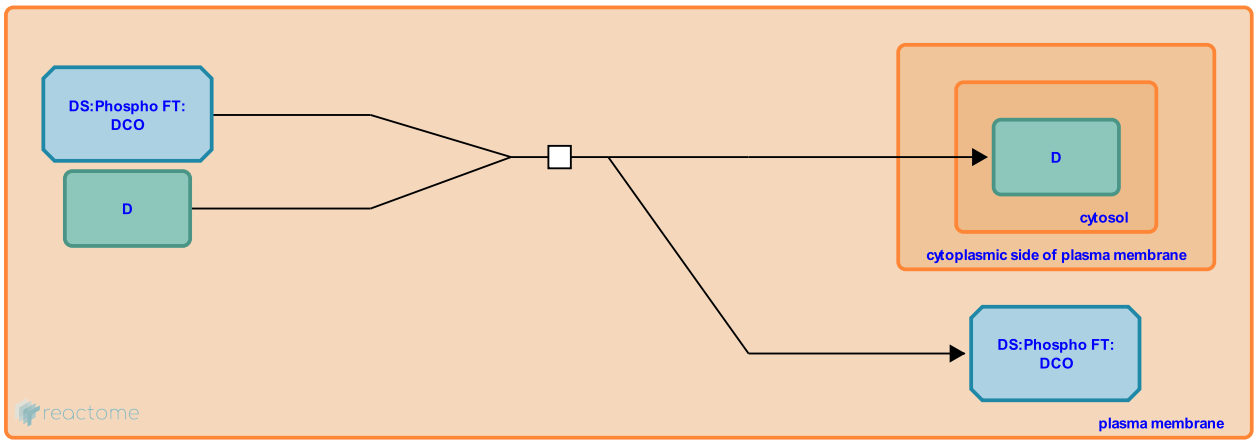
Stable identifier: R-DME-390116

Type: transition

Compartments: cytosol, plasma membrane



There are observations that Fat (FT), Dachsous (DS), and Four-jointed (FJ) modulate the subcellular localisation of Dachs (D). In the absence of FT, D accumulates at the plasma membrane. These suggest a simple model whereby signalling through FT regulates the stability of the serine/threonine kinase, Warts (WTS), by reducing protein levels of D at the plasma membrane so it fails to interact with WTS.

Literature references

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Editions

2009-01-23	Authored, Edited	Williams, MG.
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