Dimerization of DAP12

Garapati, P V., Lanier, LL.

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

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. ↗

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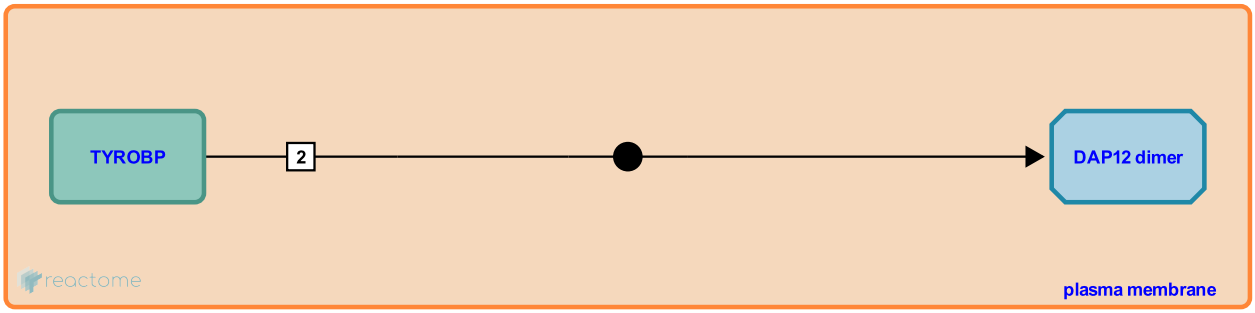
Stable identifier: R-HSA-2130151

Type: binding

Compartments: plasma membrane



DAP12 is expressed as a disulfide-bonded homodimer on NK cells, myeloid cells and a subset of T cells. Cystine-7 in the extracellular domain is involved in the interchain disulphide bond (numbering according to Lanier et al. 1998).

Literature references

Call, ME., Wucherpfennig, KW., Chou, JJ. (2010). The structural basis for intramembrane assembly of an activating immunoreceptor complex. *Nat Immunol, 11*, 1023-9. ↗

Feng, J., Call, ME., Wucherpfennig, KW. (2006). The assembly of diverse immune receptors is focused on a polar membrane-embedded interaction site. *PLoS Biol, 4*, e142. ↗

Lanier, LL., Corliss, BC., Wu, J., Leong, C., Phillips, JH. (1998). Immunoreceptor DAP12 bearing a tyrosine-based activation motif is involved in activating NK cells. *Nature, 391*, 703-7. ↗

Editions

2012-05-25	Authored, Edited	Garapati, P V.
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