TRAIL-mediated dimerization of procaspase-8

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02/05/2024

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. ↗

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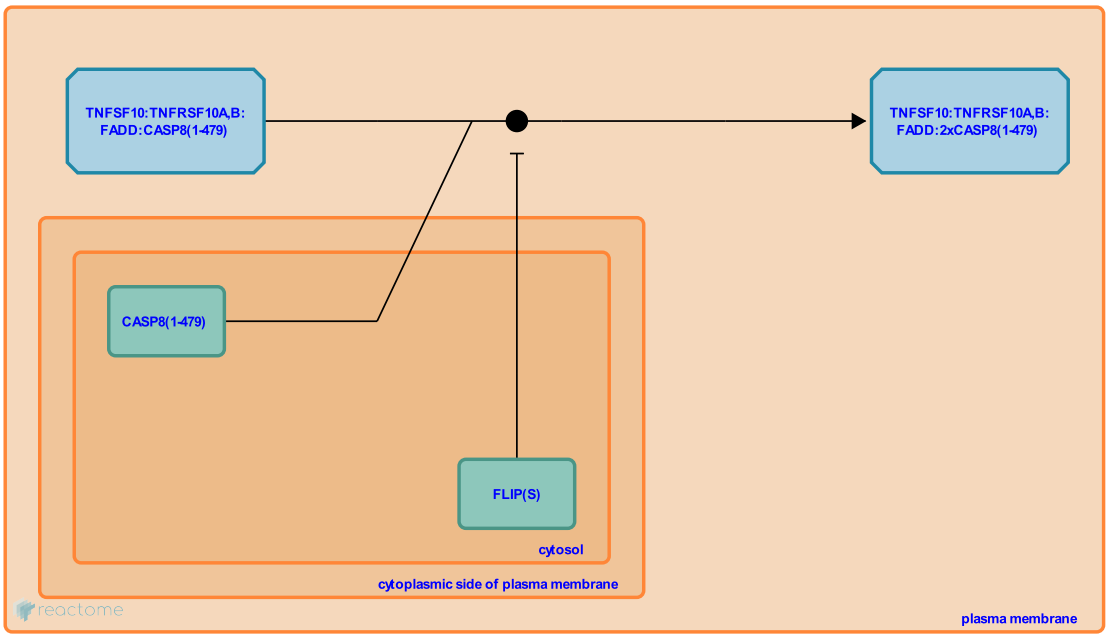
Stable identifier: R-HSA-141156

Type: binding

Compartments: plasma membrane, cytosol



Monomeric caspase-8 zymogens undergo dimerization and subsequent conformational changes at the TRAIL:TRAIL receptor-2:FADD receptor complex leading to the formation of the catalytically active form of procaspase-8.

Literature references

Juo, P., Blenis, J., Weigand, MA., Sprick, MR., Rauch, CT., Rieser, E. et al. (2000). FADD/MORT1 and caspase-8 are recruited to TRAIL receptors 1 and 2 and are essential for apoptosis mediated by TRAIL receptor 2. *Immunity, 12*, 599-609. ↗

Sperandio, S., Shin, H., Ricci, JE., Scott, FL., Renatus, M., Sutherlin, DP. et al. (2003). A unified model for apical caspase activation. *Mol Cell, 11*, 529-41. ↗

Editions

2012-11-19	Reviewed	Gillespie, ME.
2013-05-18	Edited	Shamovsky, V.
2013-05-22	Reviewed	Salvesen, GS., Pop, C.