

TNFSF8 binds TNFRSF8

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11/05/2024

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

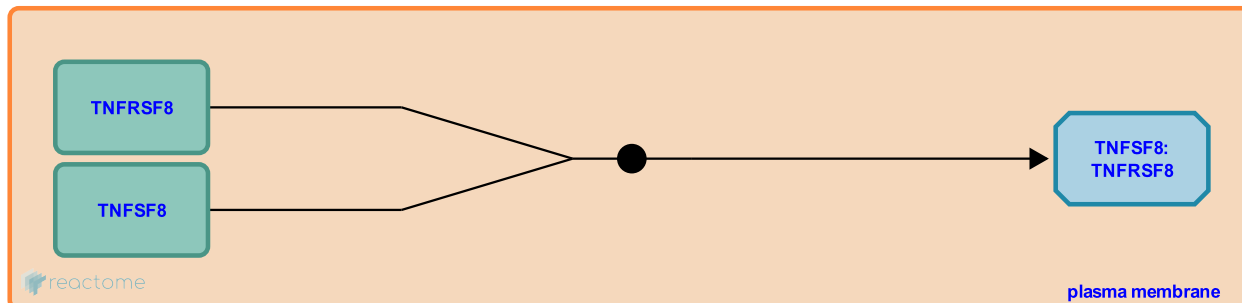
This document contains 1 reaction ([see Table of Contents](#))

TNFSF8 binds TNFRSF8 [↗](#)

Stable identifier: R-HSA-8856189

Type: binding

Compartments: plasma membrane



Tumor necrosis factor receptor superfamily 8 (TNFRSF8, CD30) and its ligand TNFSF8 (CD30 ligand, CD30L, CD153) are interacting cell-surface glycoproteins. TNFRSF8 is expressed on activated CD4 and CD8 T cells and B cells. It is a marker for Hodgkin's syndrome. TNFRSF8 signaling regulates lymphocyte survival (Blazar et al. 2004) and peripheral T cell responses, controlling T cell survival and down-regulating cytolytic capacity (Duckett et al. 1997, Kurts et al. 1999, Telford et al. 1997).

Literature references

Goodwin, RG., Wiley, SR., Smith, CA. (1996). Reverse signaling via CD30 ligand. *J. Immunol.*, 157, 3635-9. [↗](#)

Editions

2015-05-12	Reviewed	Ware, CF., Virgen-Slane, R.
2016-05-19	Authored, Edited	Garapati, P V.