DAP12 interacts with NKG2C

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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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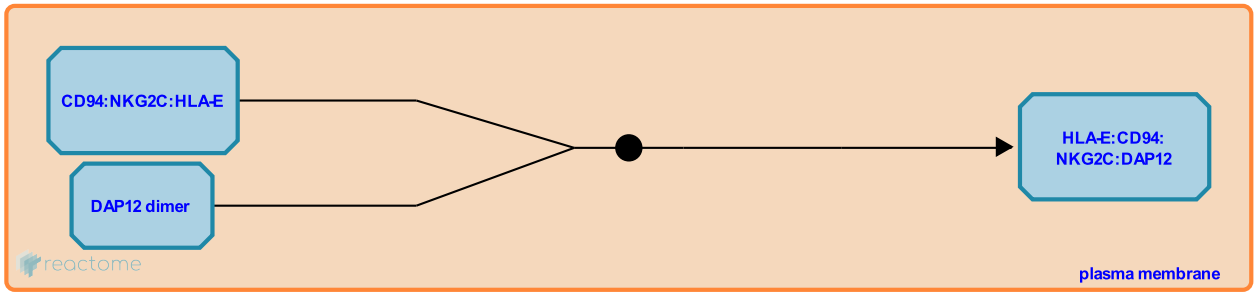
Stable identifier: R-HSA-2172126

Type: binding

Compartments: plasma membrane



NKG2C, a C-type lectin-like surface receptor, is a member of the NKG2 family and forms heterodimers with CD94 that is expressed on NK cells and a subset of T cells. The CD94/NKG2C killer lectin-like receptor (KLR) perform an important role in immunosurveillance by binding to HLA-E complexes that present peptides derived from the signal sequences of other HLA class I molecules (A, B, C, G), thereby monitoring MHC class I expression. It has been proposed that the activating receptor CD94/NKG2C may contribute with other NK stimulatory molecules (like NKp46, NKp44 and NKp30 and NKG2D) to trigger effector functions when the control exerted by inhibitory receptors is overcome (Guma et al. 2005). NKG2C/CD94 associates with the ITAM-containing adapter protein DAP12 and this leads to cell activation and cytotoxic function. The charged residues in the transmembrane domains of DAP12 and NKG2C are necessary for this interaction (Lanier et al. 1998). NK cells expressing the CD94/NKG2C receptor are preferentially expanded during cytomegalovirus infection in humans (Lopez-Verges et al. 2011)

Literature references

Lanier, LL., Phillips, JH., Corliss, B., Wu, J. (1998). Association of DAP12 with activating CD94/NKG2C NK cell receptors. *Immunity, 8*, 693-701. ↗

Busch, LK., García, P., Bellosillo, B., Gumá, M., López-Botet, M., Salazar-Fontana, LI. et al. (2005). The CD94/NKG2C killer lectin-like receptor constitutes an alternative activation pathway for a subset of CD8+ T cells. *Eur. J. Immunol., 35*, 2071-80. ↗

Editions

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