CD4 binds Interleukin-16

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05/05/2024

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. ↗

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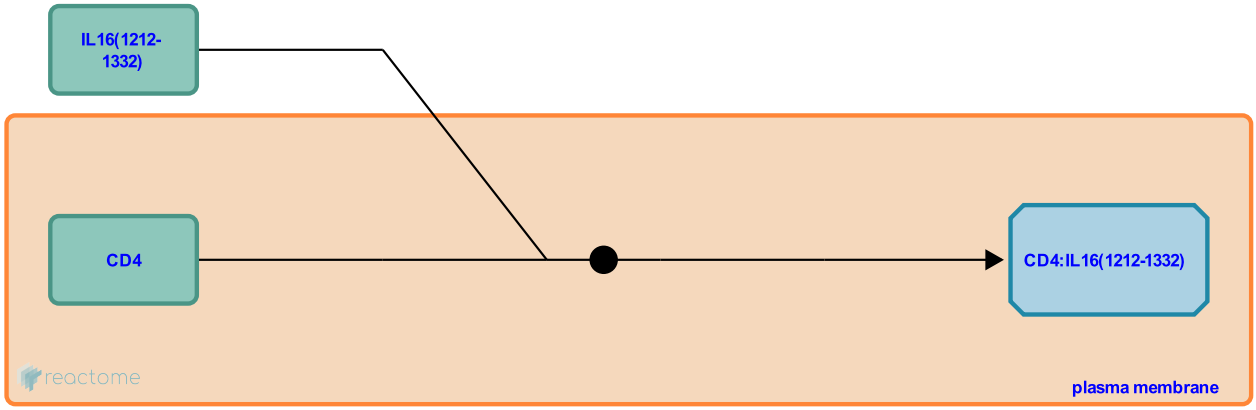
Stable identifier: R-HSA-449087

Type: binding

Compartments: extracellular region, plasma membrane



CD4 is a receptor for Interleukin-16 (IL16), explaining how IL16 acts as a chemoattractant for a variety of CD4+ immune cells (Cruikshank et al. 2000, Cruikshank & Little 2008). Signaling mediated by CD4 requires the amino acid sequence W345 to S350, located in the proximal end of the D4 domain. CD4 does not appear to require a co-receptor for IL16. Data from CD4 knockout mice suggests that there may be an additional IL16 receptor (Mathy et al. 2000).

Literature references

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Editions

2014-06-04	Authored	Jupe, S.
2016-01-28	Edited	Jupe, S.
2016-01-28	Reviewed	Meldal, BH.