

# CD209 activate GTPase RAS

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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. [↗](#)

Reactome database release: 88

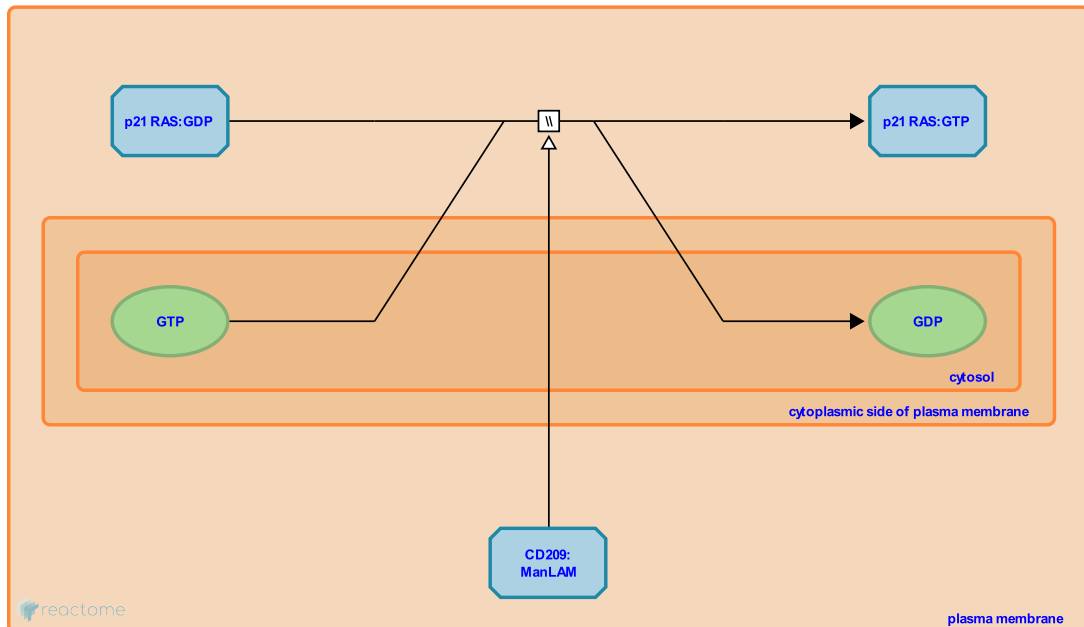
This document contains 1 reaction ([see Table of Contents](#))

## CD209 activate GTPase RAS [↗](#)

**Stable identifier:** R-HSA-5621573

**Type:** omitted

**Compartments:** plasma membrane, cytosol



Both CLEC7A (Dectin-1) and CD209 (DC-SIGN) modulates Toll-like receptor signalling by activating RAF1 which in turn induces the phosphorylation of p65 (RELA) subunit leading to the modification of p50/p65 NF- $\kappa$ B dimer (Gringhuis et al. 2007 & 2009). Gringhuis et al. demonstrated that CD209 (DC-SIGN) stimulated by ManLAM (lipoarabinomannan) activates the small GTPase RAS. Immunoblotting detected active RAS in dendritic cells when induced by ManLAM (Gringhuis et al. 2007). RAF1 is recruited to the membrane through an interaction with the active form of RAS.

### Literature references

Litjens, M., Geijtenbeek, TB., Gringhuis, SI., van Kooyk, Y., den Dunnen, J., van Het Hof, B. (2007). C-type lectin DC-SIGN modulates Toll-like receptor signaling via Raf-1 kinase-dependent acetylation of transcription factor NF- $\kappa$ B. *Immunity*, 26, 605-16. [↗](#)

### Editions

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