

Interaction of exogenous soluble antigen with its corresponding receptor

Desjardins, M., English, L., Garapati, P V.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

15/05/2024

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](#))

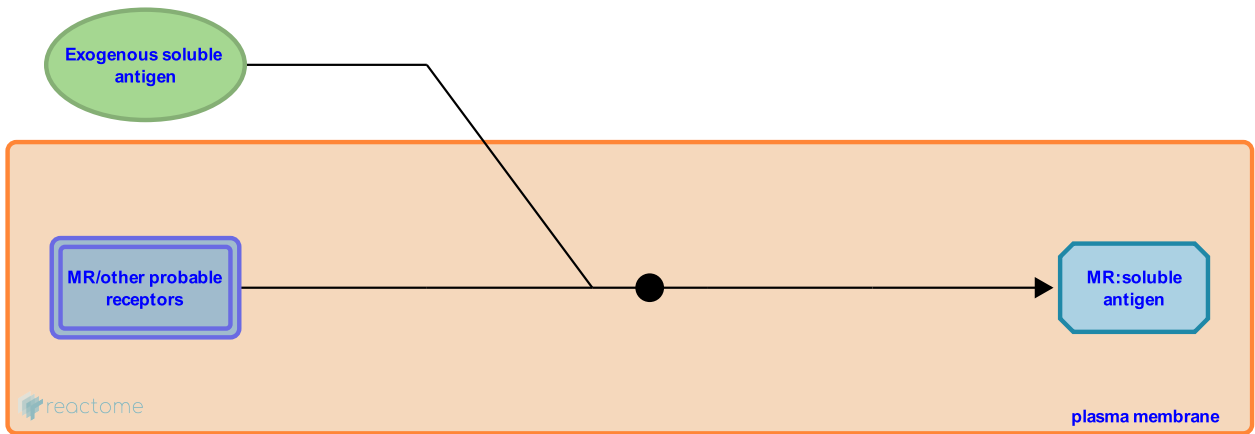
Interaction of exogenous soluble antigen with its corresponding receptor ↗

Stable identifier: R-HSA-1236939

Type: binding

Compartment: plasma membrane, extracellular region

Inferred from: [Interaction of soluble ovalbumin with mannose receptor \(Gallus gallus\)](#)



Soluble antigens are presented to dendritic cells (DCs) in some cases by receptor mediated endocytosis or fluid-phase endocytosis. Burgdorf et al. (2008) suggest that there are two different endocytic compartments for antigen processing: one dedicated to MHC class I (early endosomes) and the other one for MHC class II presentation (lysosomes). Sorting of cargo into these different compartments occurs at the plasma membrane and is likely to depend on the type of endocytic receptor the cargo is interacting with (Burgdorf et al. 2008, Zhuang et al. 2006). The mannose receptor (MR) is the best studied receptor that targets soluble antigens to early endosomes but not to lysosomes (Burgdorf et al. 2006). Antigens taken up by the MR are targeted towards a mildly acidic stable early endosomal compartment for exclusive presentation on MHC I molecules (Burgdorf et al. 2008).

Editions

| | | |
|------------|------------------|-----------------------------|
| 2011-03-28 | Authored, Edited | Garapati, P V. |
| 2011-05-13 | Reviewed | Desjardins, M., English, L. |