Antigen processing by cathepsin S in endosoytic vesicle

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.

30/04/2024

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. ↗

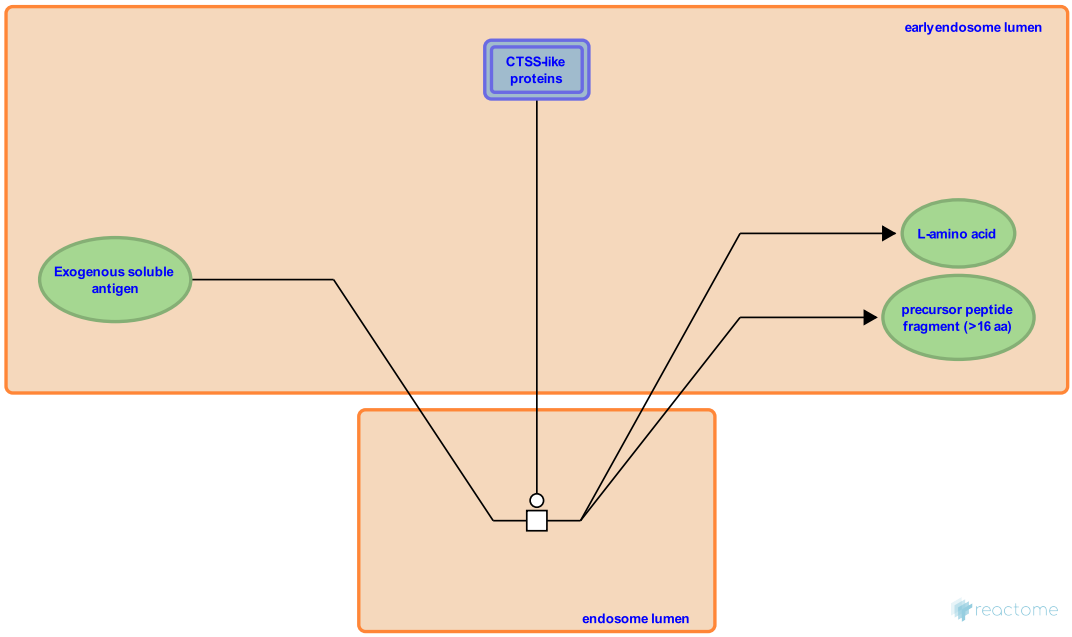
Antigen processing by cathepsin S in endosoytic vesicle ↗

Stable identifier: R-HSA-1236948

Type: transition

Compartments: endosome lumen

Inferred from: Processing of ovalbumin by cathepsin S (Gallus gallus)



Endocytic compartments contain many cysteine proteases such as cathepsin S that can generate cross-presented peptides. Cathepsins may participate in the generation of MHC class II-presentated peptides (Villadangos et al. 1999). Shen et al. (2004) demonstrated that cathepsin S contributes to TAP-independent cross-presentation in vivo, showing that ovalbumin was cross-presented by denritic cells (DCs) through both TAP-dependent and TAP-independent pathways. The TAP-independent pathway was sensitive to the cystine protease inhibitor leupeptin, but not to proteasome inhibitors. Further experiments with knockout mice showed that cathepsin S contributed to cross-presentation. DCs lacking cathepsin S lack the TAP-independent pathway (Khor et al. 2008, Shen et al. 2004).

Editions

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