

Degradation of MHC I Complex

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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

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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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- 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: 70

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

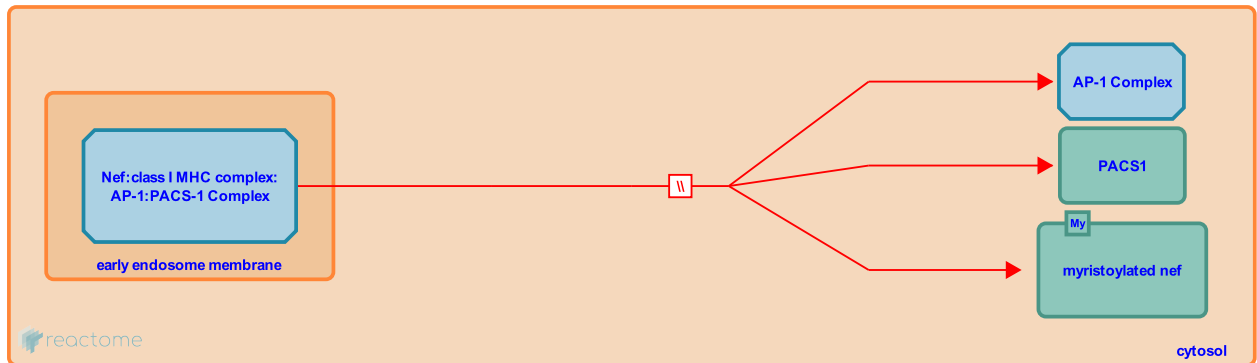
Degradation of MHC I Complex ↗

Stable identifier: R-HSA-182263

Type: omitted

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease



Once the complex of Nef, major histocompatibility complex class I molecules, PACS-1 and AP-1 arrives at the endosome, the MHC I complex is targeted for degradation.

Literature references

Roeth, JF., Williams, M., Kasper, MR., Filzen, TM., Collins, KL. (2004). HIV-1 Nef disrupts MHC-I trafficking by recruiting AP-1 to the MHC-I cytoplasmic tail. *J Cell Biol*, 167, 903-13. ↗

Editions

2007-07-25	Authored	Gillespie, ME.
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