Trimming of N-ter extended precursor fragments by cytosolic aminopeptidases

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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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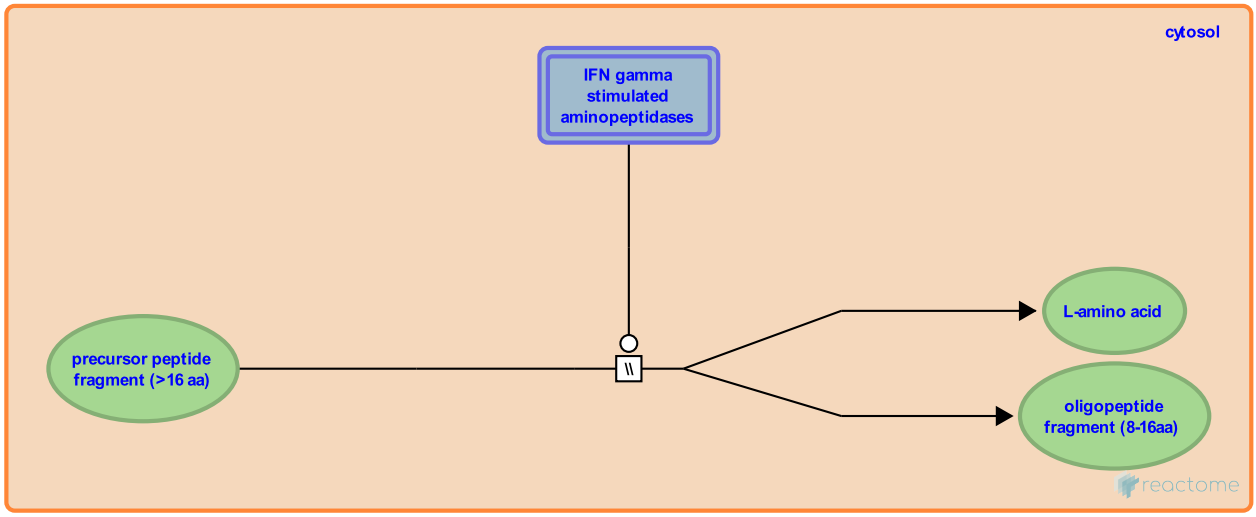
Stable identifier: R-HSA-983162

Type: omitted

Compartments: cytosol



Some peptides generated by the 26S proteasome are too long to bind to MHC class I molecules. These N-terminal extended precursor peptides may be trimmed by cytosolic aminopeptidases, such as Tripeptidyl peptidase II (TPP2), puromycin-sensitive aminopeptidase (PSA), bleomycin hydrolase (BH), and leucine aminopeptidase (LAP).

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Editions

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