Transport of Antigen peptide in to ER

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05/05/2024

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

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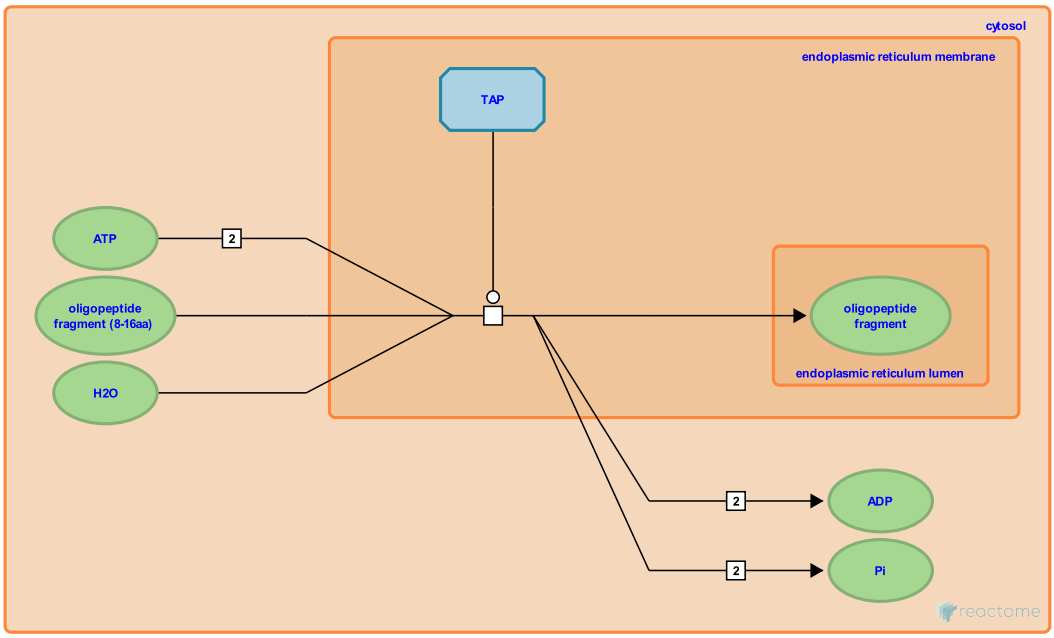
Stable identifier: R-HSA-983144

Type: transition

Compartments: endoplasmic reticulum lumen, cytosol, endoplasmic reticulum membrane



Ttransporter associated with antigen processing (TAP) is a heterodimeric complex, composed of TAP1 and TAP2 proteins, members of the ATP-binding cassette (ABC) superfamily. TAP consists of two transmembrane domains (TMDs) and two cytosolic nucleotide-binding domains. Peptide binding to the cytosolic-facing cavity formed by the TMDs causes it to undergo a conformational change that induces ATP hydrolysis, forcing the opening of a pore and translocation of the peptide into the ER lumen. TAP transports peptides in the range of 8-16 amino acids into the ER, which is the peptide length typically generated by the immunoproteasome.

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Editions

2010-10-29	Authored, Edited	Garapati, P V.
2011-02-11	Reviewed	Elliott, T.