

Collagen type I degradation by MMP15

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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. [↗](#)
- 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. [↗](#)
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Reactome database release: 88

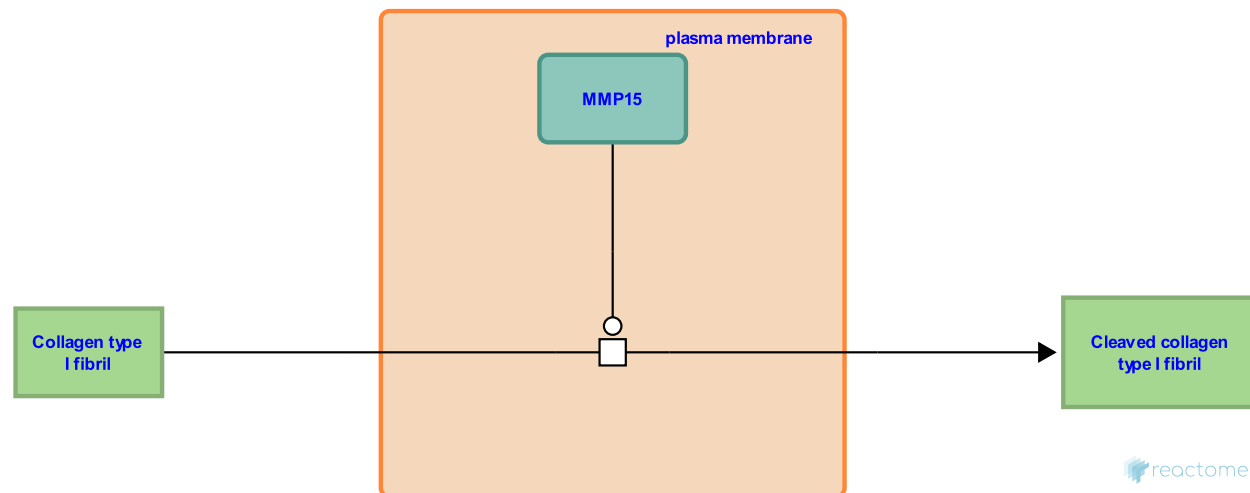
This document contains 1 reaction ([see Table of Contents](#))

Collagen type I degradation by MMP15 [↗](#)

Stable identifier: R-HSA-2473596

Type: transition

Compartments: plasma membrane



The membrane-type MMP MMP15 (MT2-MMP) is a fibrillar collagenase able to degrade collagen type I (Morrison and Overall 2006) and believed able to degrade types II and III (Somerville et al. 2003).

Literature references

Overall, CM., Morrison, CJ. (2006). TIMP independence of matrix metalloproteinase (MMP)-2 activation by membrane type 2 (MT2)-MMP is determined by contributions of both the MT2-MMP catalytic and hemopexin C domains. *J Biol Chem*, 281, 26528-39. [↗](#)

Editions

2011-07-12	Authored	Jupe, S.
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