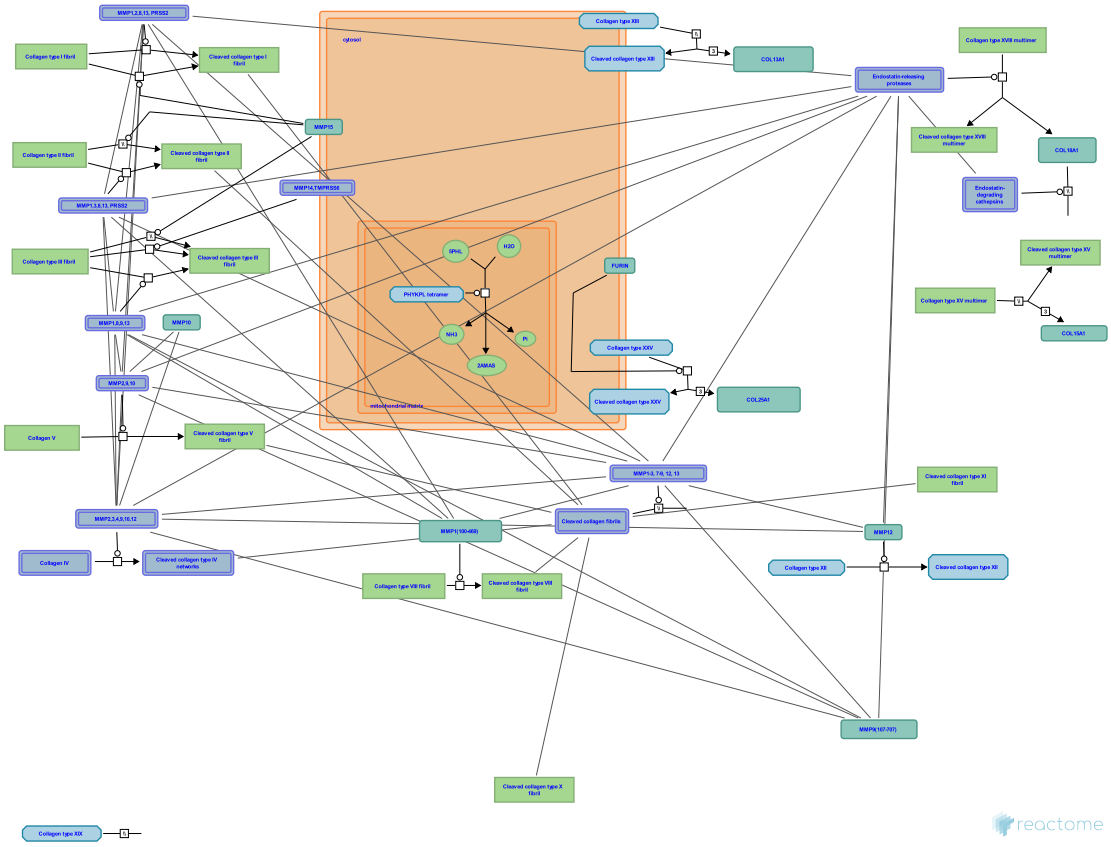
Collagen degradation



European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

03/05/2024

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

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. ↗

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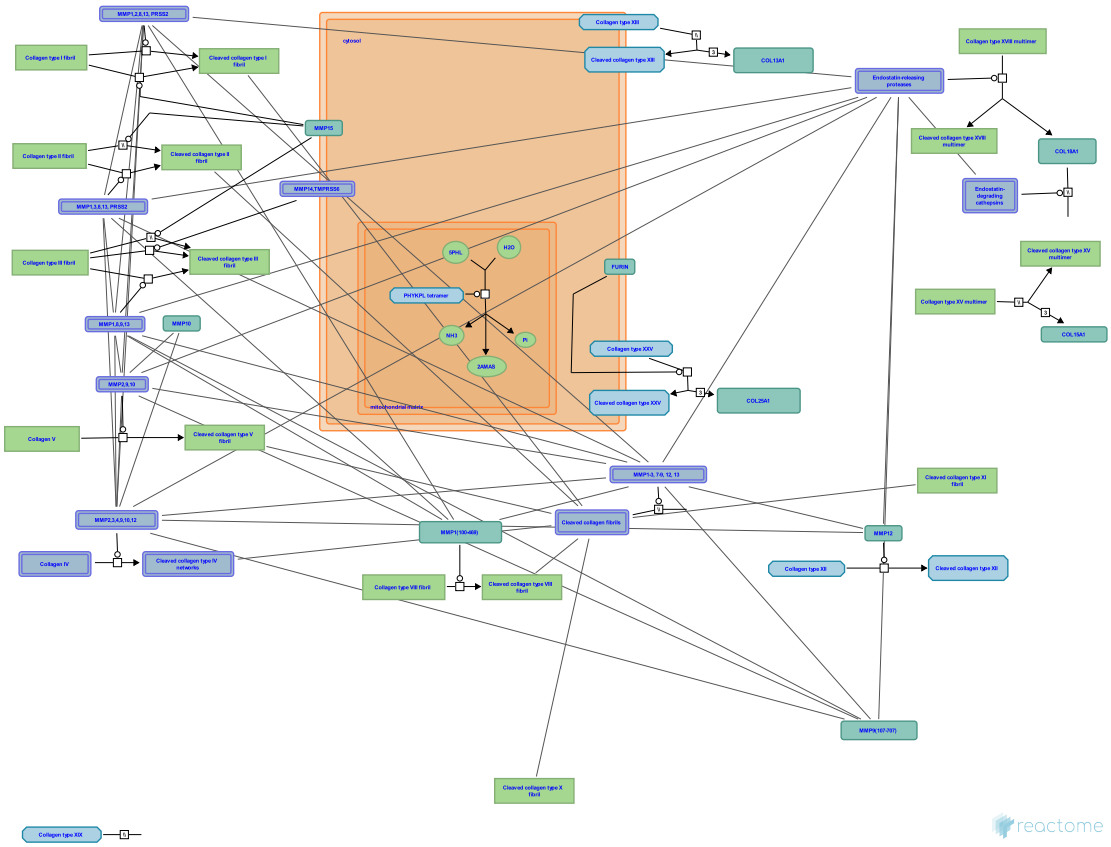
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Collagen degradation ↗

Stable identifier: R-CFA-1442490

Inferred from: Collagen degradation (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Collagen type I degradation by MMP1,2,8,13, PRSS2 ↗

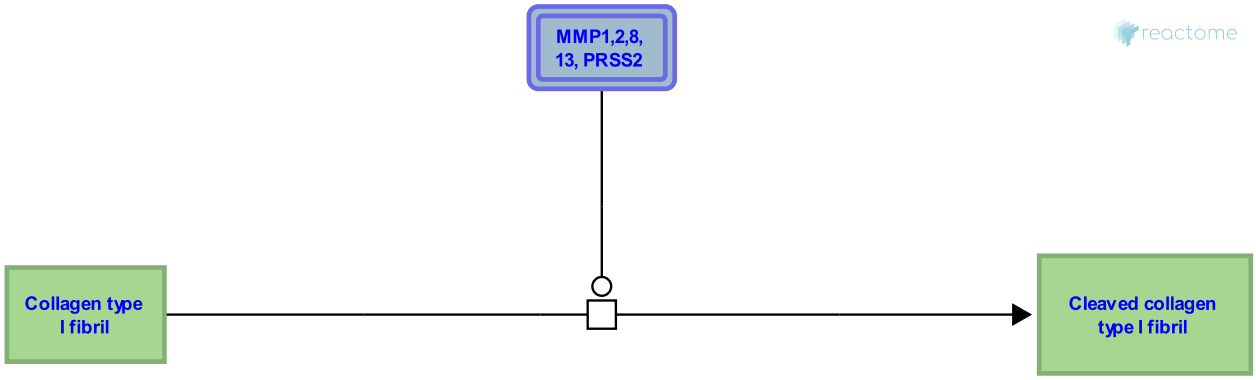
Location: Collagen degradation

Stable identifier: R-CFA-1454822

Type: transition

Compartments: extracellular region

Inferred from: Collagen type I degradation by MMP1,2,8,13, PRSS2 (Homo sapiens)



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Followed by: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13

Collagen type I degradation by MMP15 ↗

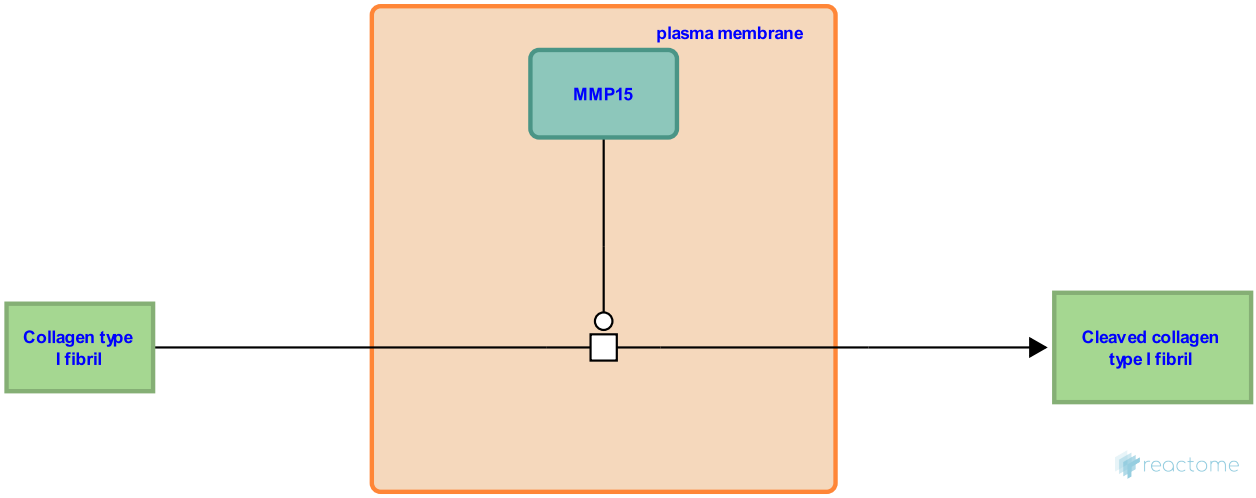
Location: Collagen degradation

Stable identifier: R-CFA-2473596

Type: transition

Compartments: plasma membrane

Inferred from: Collagen type I degradation by MMP15 (Homo sapiens)



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Followed by: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13

Collagen type II degradation by MMP1,3,8,13,PRSS2 ↗

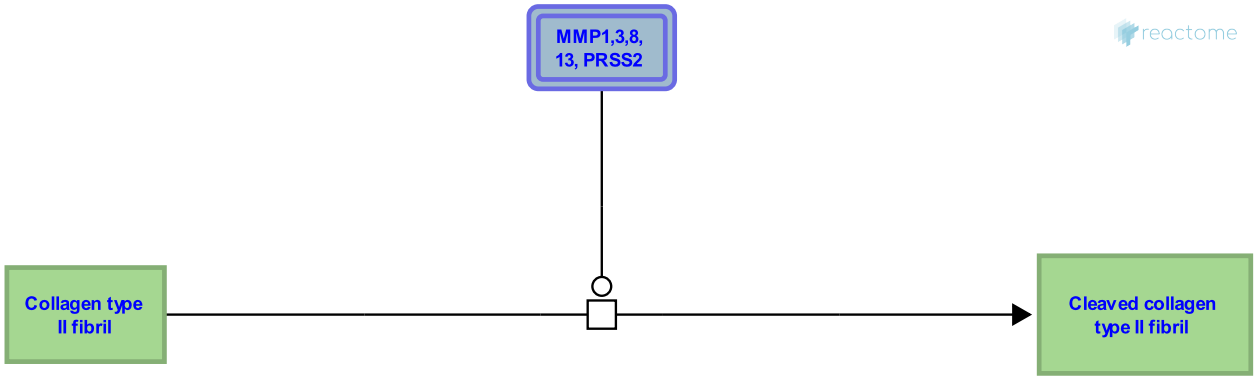
Location: Collagen degradation

Stable identifier: R-CFA-1474197

Type: transition

Compartments: extracellular region

Inferred from: Collagen type II degradation by MMP1,3,8,13,PRSS2 (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13

Collagen type II degradation by MMP15 ↗

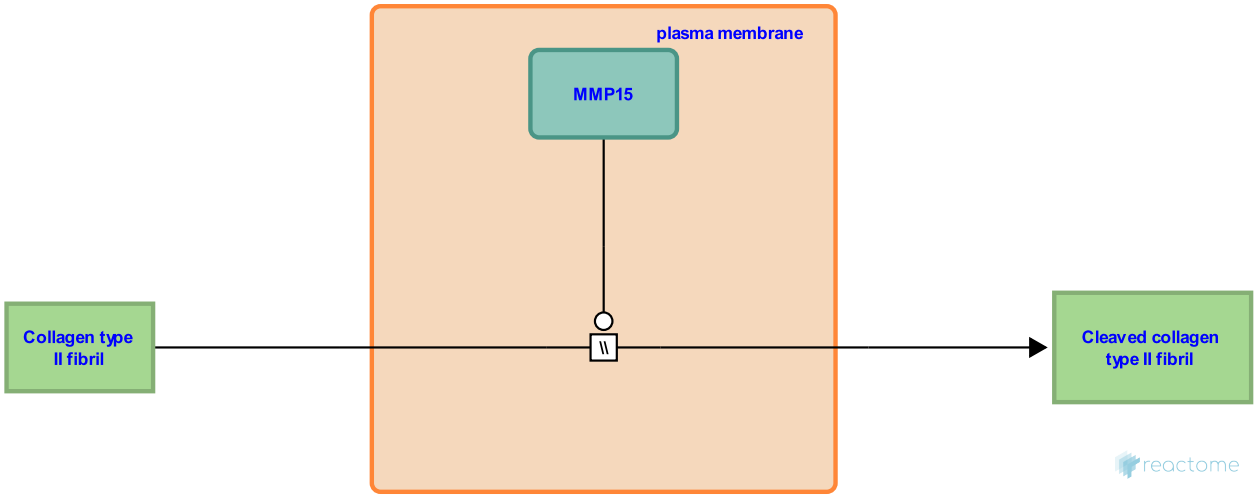
Location: Collagen degradation

Stable identifier: R-CFA-2473594

Type: omitted

Compartments: plasma membrane

Inferred from: Collagen type II degradation by MMP15 (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Collagen type III degradation by MMP1,8,9,13 ↗

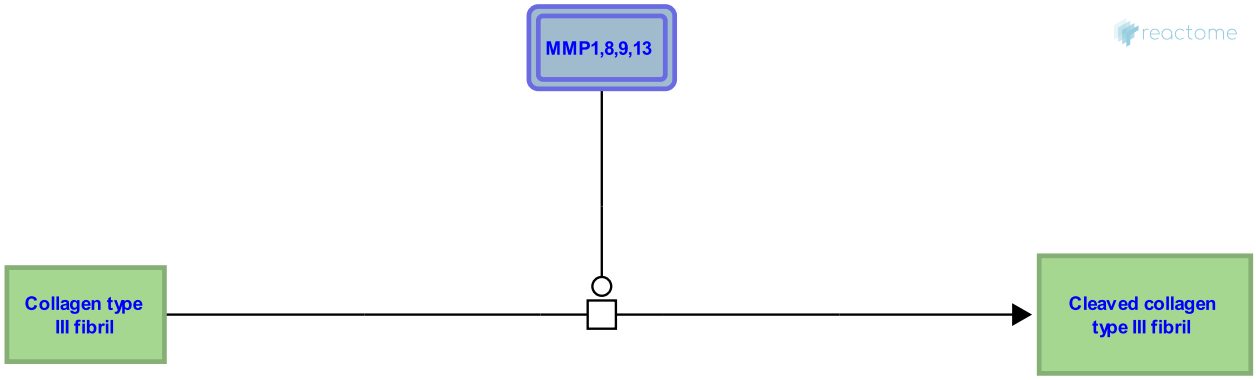
Location: Collagen degradation

Stable identifier: R-CFA-1474213

Type: transition

Compartments: extracellular region

Inferred from: Collagen type III degradation by MMP1,8,9,13 (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13

Collagen type III degradation by MMP14 ↗

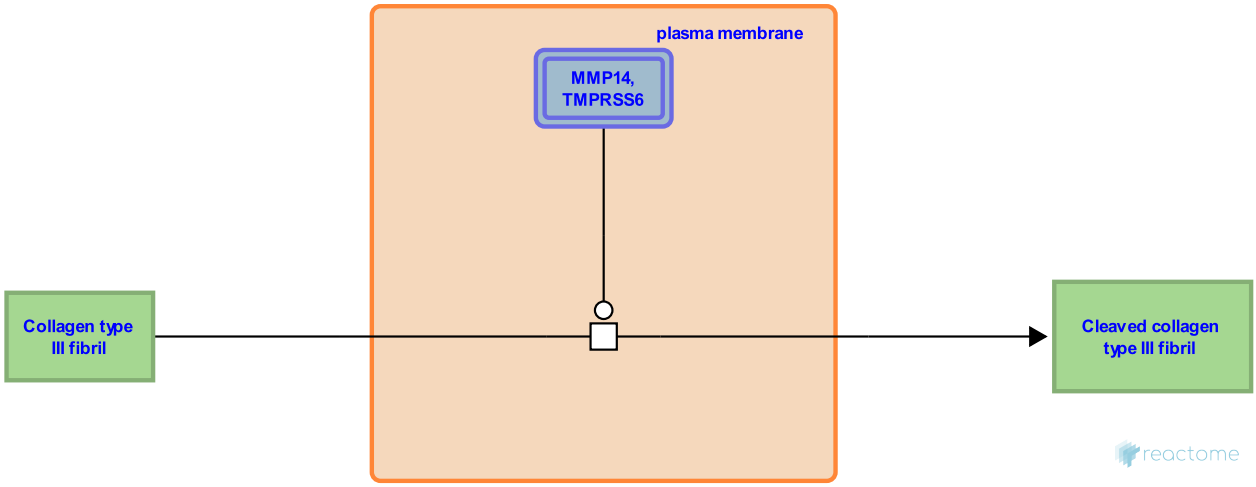
Location: Collagen degradation

Stable identifier: R-CFA-1474210

Type: transition

Compartments: plasma membrane, extracellular region

Inferred from: Collagen type III degradation by MMP14 (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

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Followed by: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13

Collagen type III degradation by MMP15 ↗

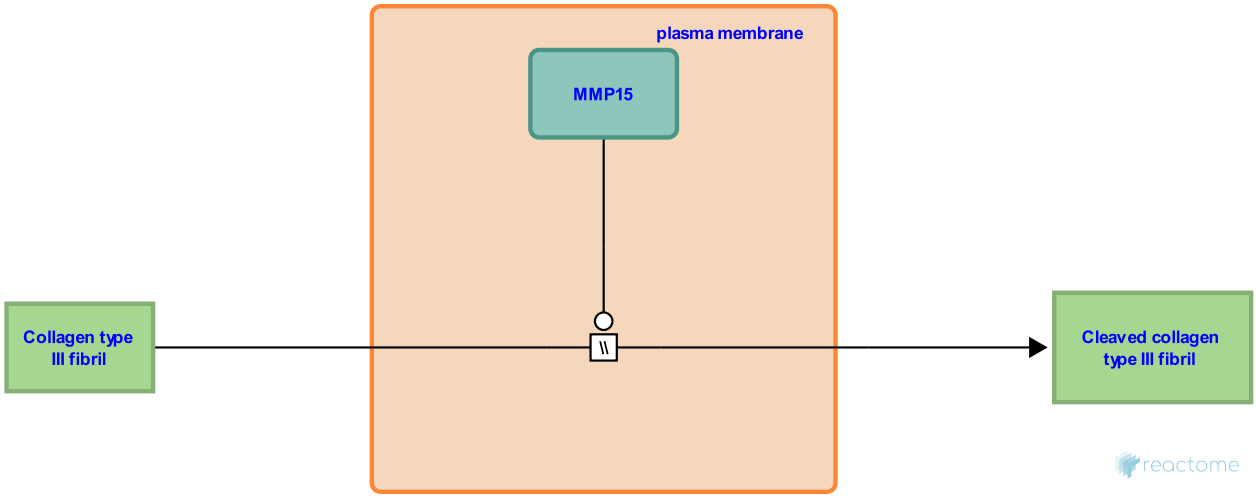
Location: Collagen degradation

Stable identifier: R-CFA-2473584

Type: omitted

Compartments: plasma membrane, extracellular region

Inferred from: Collagen type III degradation by MMP15 (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Collagen type IV degradation by MMP2,3,4,9,10,12 ↗

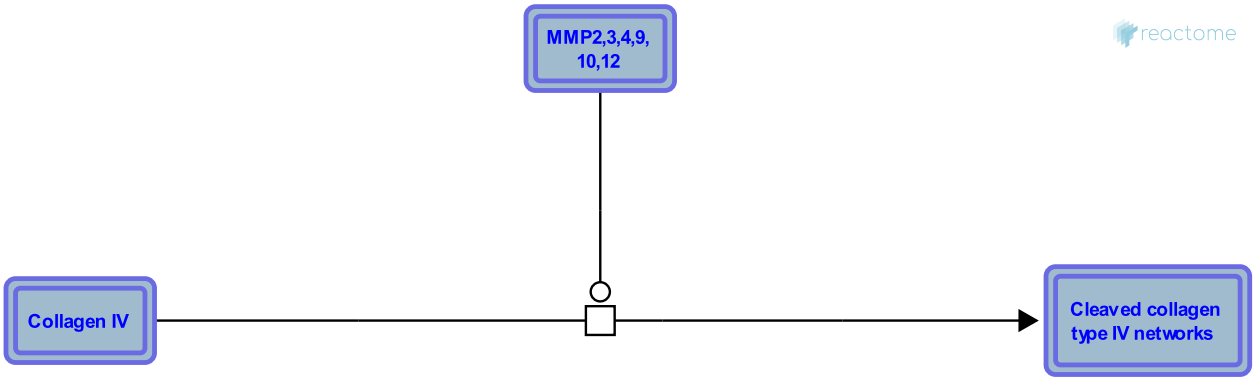
Location: Collagen degradation

Stable identifier: R-CFA-1564142

Type: transition

Compartments: extracellular region

Inferred from: Collagen type IV degradation by MMP2,3,4,9,10,12 (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13

Collagen type V degradation by MMP2,9,10 ↗

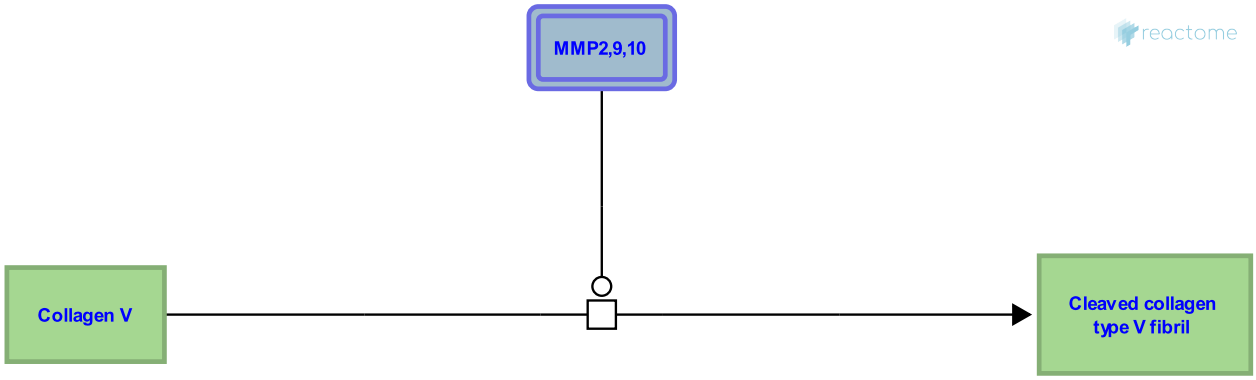
Location: Collagen degradation

Stable identifier: R-CFA-1564164

Type: transition

Compartments: extracellular region

Inferred from: Collagen type V degradation by MMP2,9,10 (Homo sapiens)



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The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13

Collagen type VIII degradation by MMP1 ↗

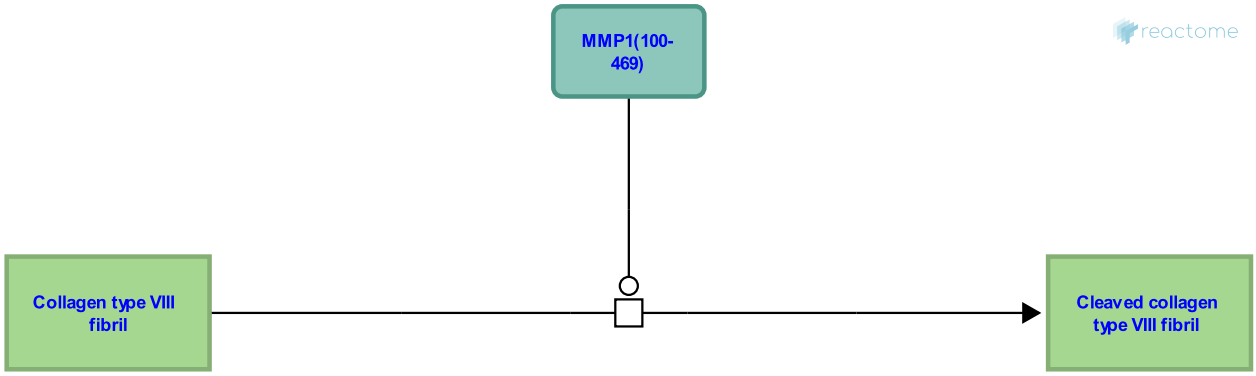
Location: Collagen degradation

Stable identifier: R-CFA-1564169

Type: transition

Compartments: extracellular region

Inferred from: Collagen type VIII degradation by MMP1 (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13

Collagen type XII degradation by MMP12 ↗

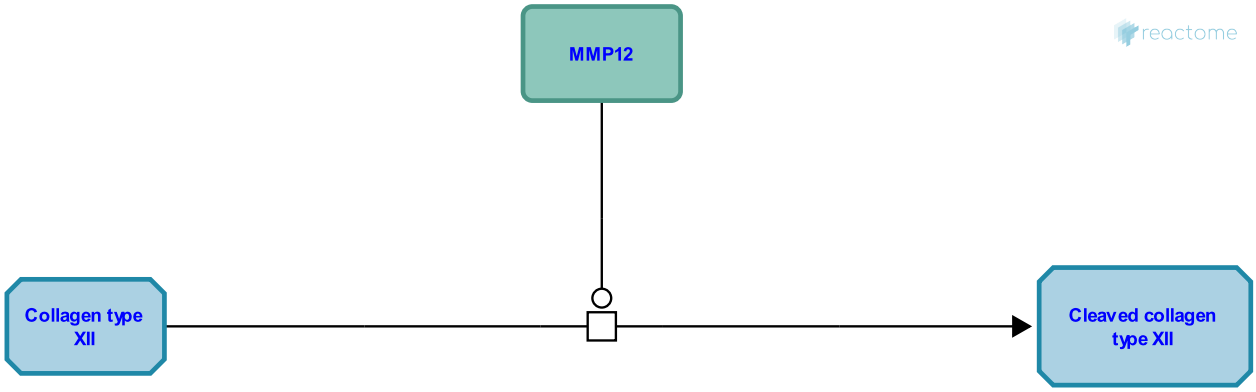
Location: Collagen degradation

Stable identifier: R-CFA-2168046

Type: transition

Compartments: extracellular region

Inferred from: Collagen type XII degradation by MMP12 (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13

Collagen type XV restin release ↗

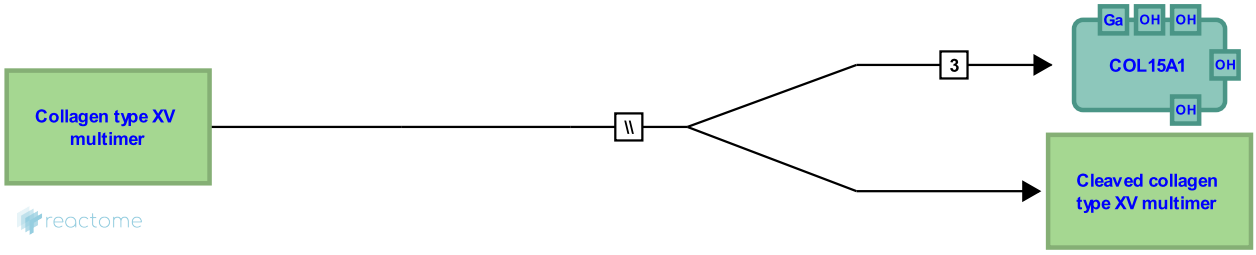
Location: Collagen degradation

Stable identifier: R-CFA-2168038

Type: omitted

Compartments: extracellular region

Inferred from: Collagen type XV restin release (Homo sapiens)



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The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Collagen type XVIII endostatin release ↗

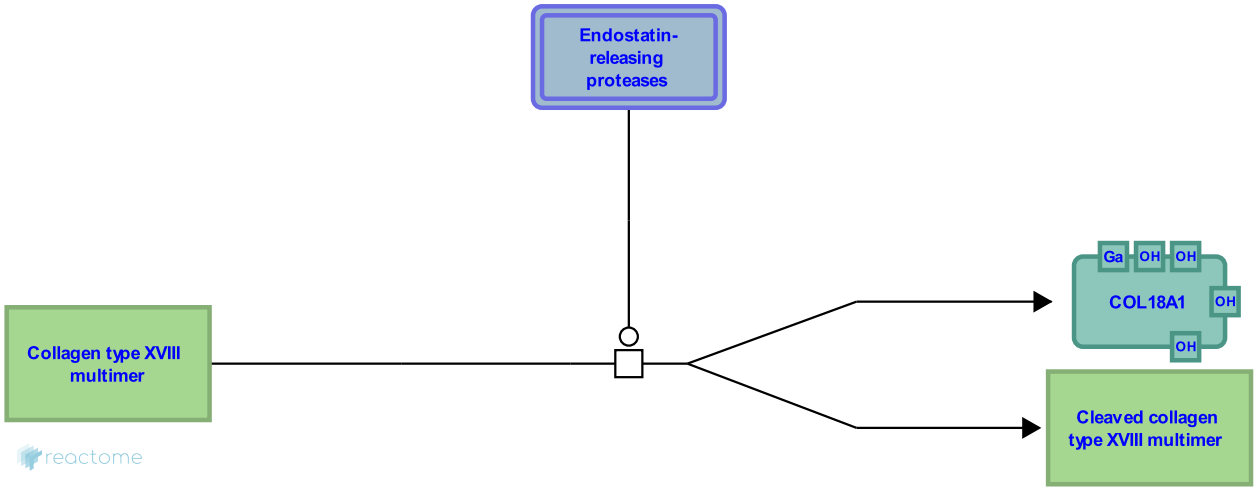
Location: Collagen degradation

Stable identifier: R-CFA-2168923

Type: transition

Compartments: extracellular region

Inferred from: Collagen type XVIII endostatin release (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Endostatin degradation by cathepsins ↗

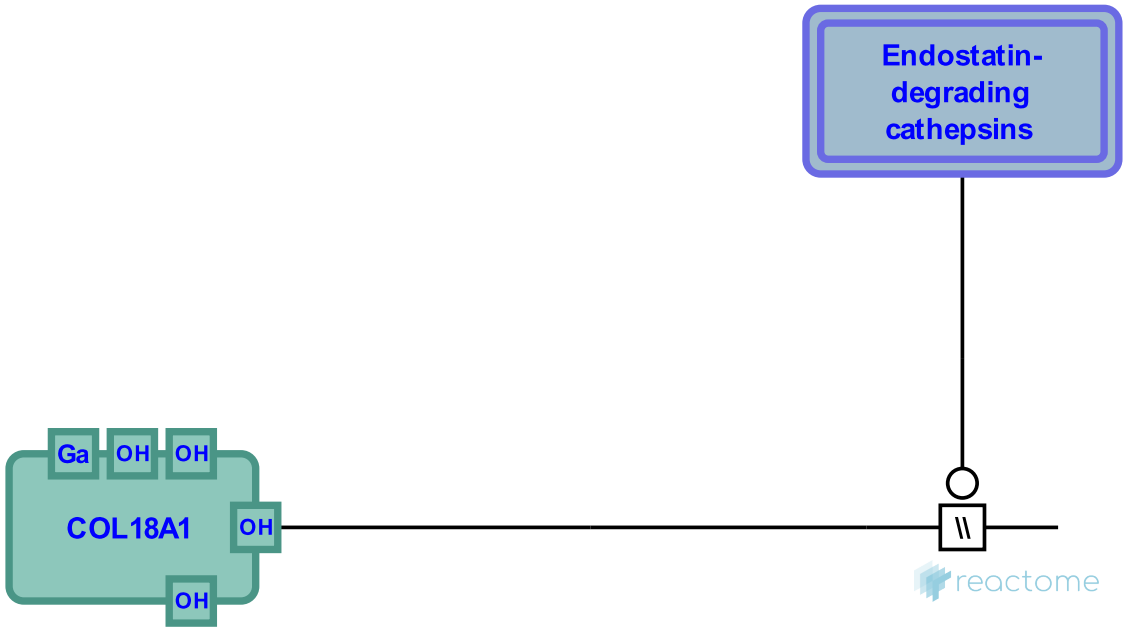
Location: Collagen degradation

Stable identifier: R-CFA-2471621

Type: omitted

Compartments: extracellular region

Inferred from: Endostatin degradation by cathepsins (Homo sapiens)



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The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Collagen type XIX degradation ↗

Location: Collagen degradation

Stable identifier: R-CFA-2172433

Type: omitted

Compartments: extracellular region

Inferred from: Collagen type XIX degradation (Homo sapiens)

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

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Collagen type XIII ectodomain shedding ↗

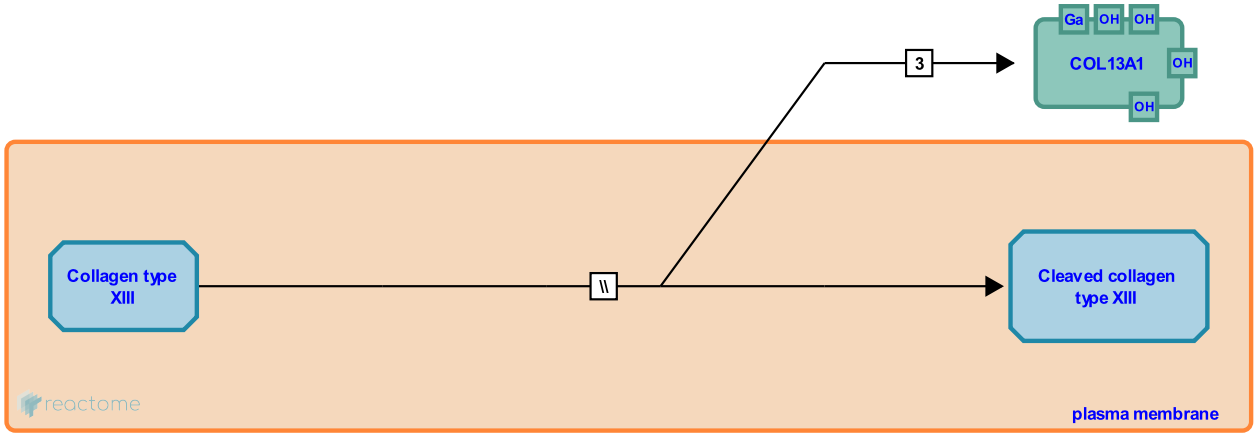
Location: Collagen degradation

Stable identifier: R-CFA-2167942

Type: omitted

Compartments: plasma membrane

Inferred from: Collagen type XIII ectodomain shedding (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Collagen type XXV ectomain shedding ↗

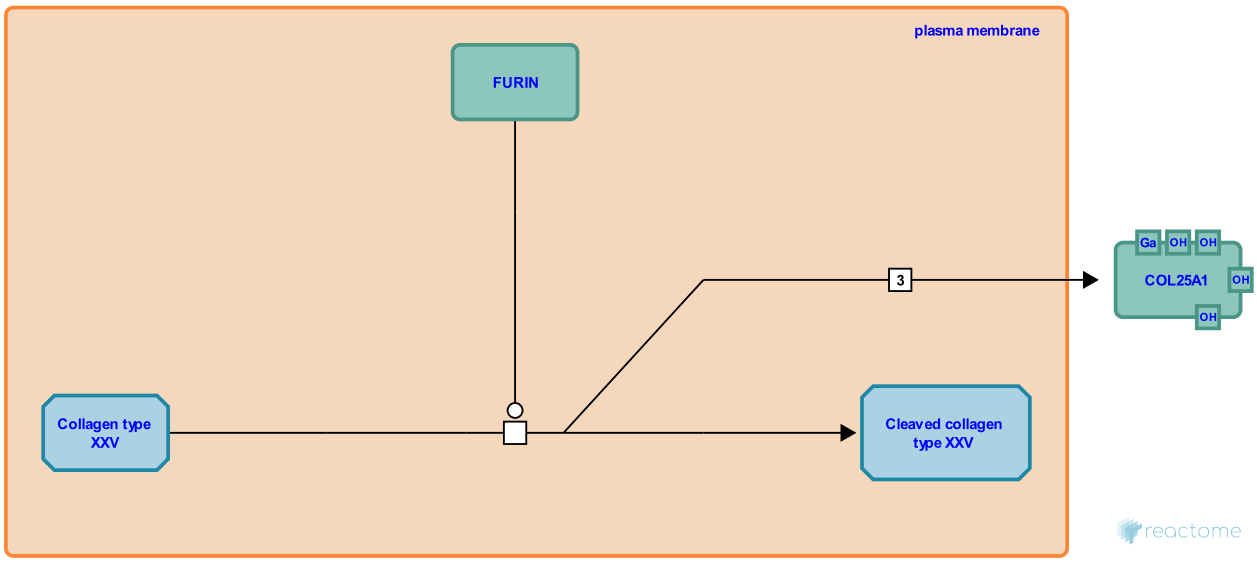
Location: Collagen degradation

Stable identifier: R-CFA-2471842

Type: transition

Compartments: plasma membrane

Inferred from: Collagen type XXV ectomain shedding (Homo sapiens)



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Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13 ↗

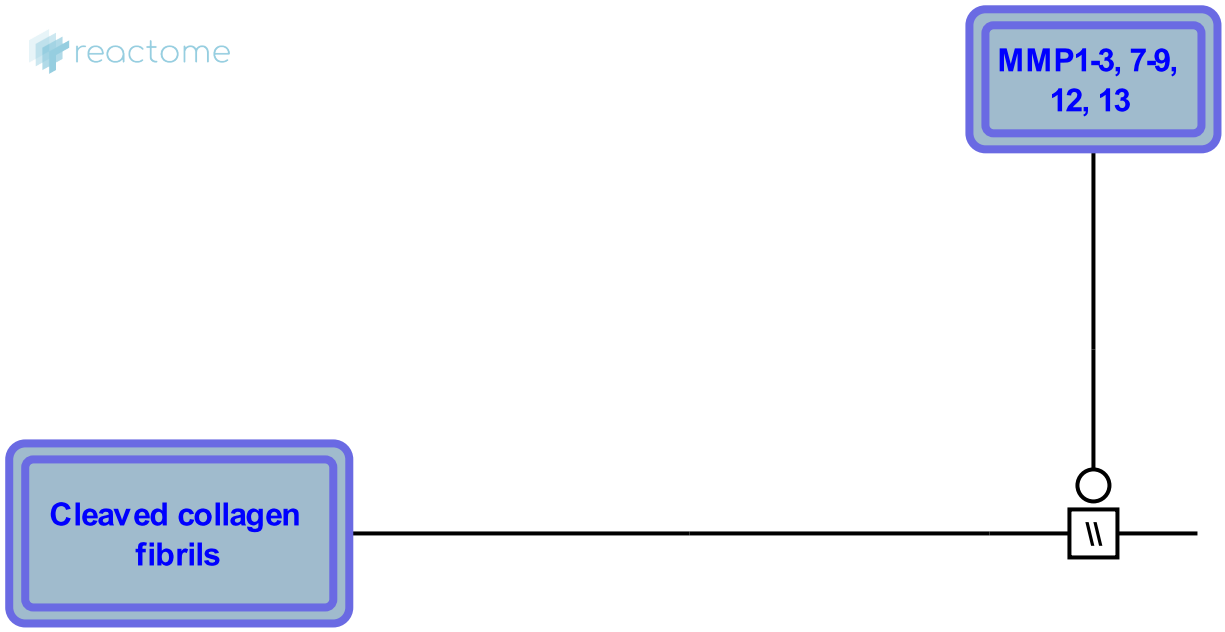
Location: Collagen degradation

Stable identifier: R-CFA-1454757

Type: omitted

Compartments: extracellular region

Inferred from: Gelatin degradation by MMP1, 2, 3, 7, 8, 9, 12, 13 (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Collagen type III degradation by MMP1,8,9,13, Collagen type VIII degradation by MMP1, Collagen type IV degradation by MMP2,3,4,9,10,12, Collagen type I degradation by MMP1,2,8,13, PRSS2, Collagen type III degradation by MMP14, Collagen type II degradation by MMP1,3,8,13,PRSS2, Collagen type XII degradation by MMP12, Collagen type V degradation by MMP2,9,10, Collagen type I degradation by MMP15

PXLP-K278-PHYKPL tetramer hydrolyses 5PHL ↗

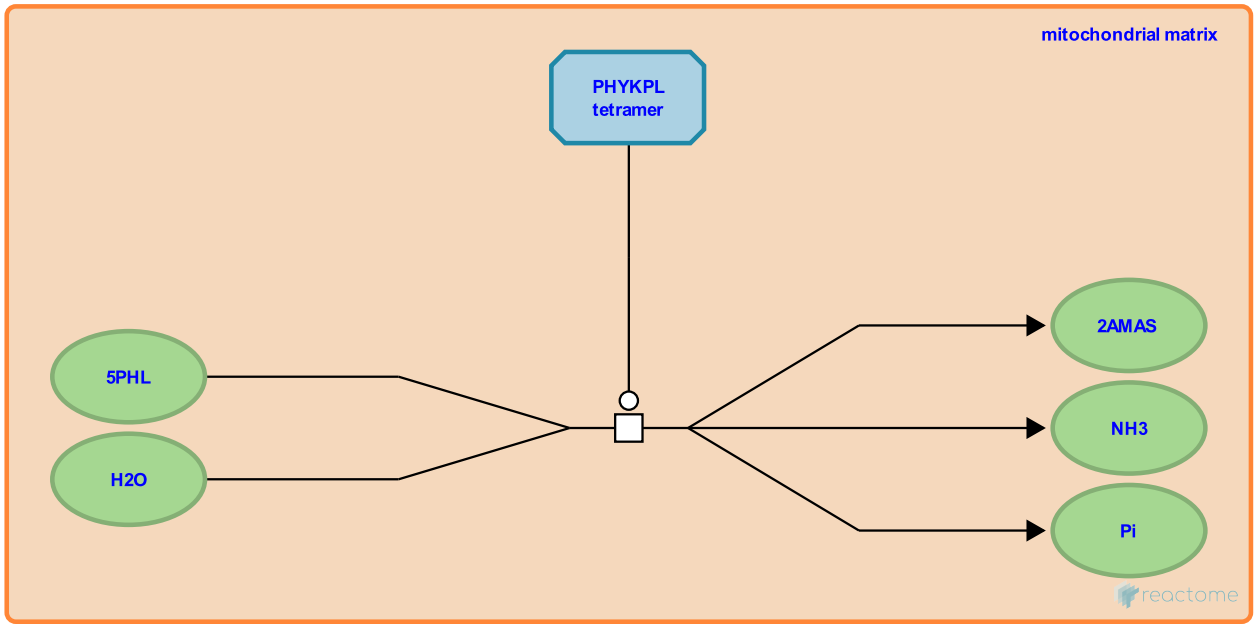
Location: Collagen degradation

Stable identifier: R-CFA-5696408

Type: transition

Compartments: mitochondrial matrix

Inferred from: PXLP-K278-PHYKPL tetramer hydrolyses 5PHL (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

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