Collagen type VI degradation by MMP2,9,11

Jupe, S., Sorsa, T.

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

01/05/2024

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. ↗

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. ↗

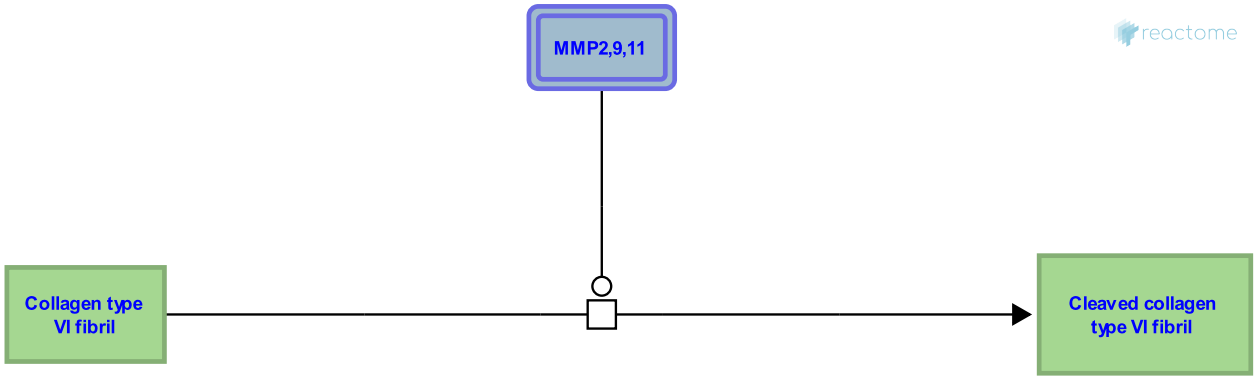
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Collagen type VI degradation by MMP2,9,11 ↗

Stable identifier: R-HSA-1564112

Type: transition

Compartments: extracellular region



Type VI collagen aggregates into distinctive microfibrils known as beaded filaments that form an independent microfibrillar network in virtually all connective tissues except for bone (von der Mark et al. 1984). It plays a role in the maintenance of tissue integrity since it participates in both cell-matrix and matrix-matrix interactions, interacting with many other ECM proteins including fibronectin (Chang et al. 1997), type IV collagen (Kuo et al. 1997), type II collagen, decorin and biglycan (Bidanset et al. 1992). Collagen type VI has been described as a connecting protein (Gelse et al. 2003).

Collagen type VI is resistant to digestion by many MMPs but is cleaved by MMP2 (Myint et al. 1996, Veidal et al. 2011), MMP9 (Veidal et al. 2011) and MMP11 (Motrescu et al. 2008).

Literature references

Stoll, I., Etique, N., Motrescu, ER., Tomasetto, C., Blaise, S., Chenard, MP. et al. (2008). Matrix metalloproteinase-11/stromelysin-3 exhibits collagenolytic function against collagen VI under normal and malignant conditions. *Oncogene, 27*, 6347-55. ↗

Veidal, SS., Leeming, DJ., Nawrocki, A., Zheng, Q., Karsdal, MA., Larsen, MR. et al. (2011). MMP mediated degradation of type VI collagen is highly associated with liver fibrosis--identification and validation of a novel biochemical marker assay. *PLoS One, 6*, e24753. ↗

Editions

2011-07-12	Authored	Jupe, S.
2012-10-08	Reviewed	Sorsa, T.
2012-11-12	Edited	Jupe, S.