Initial activation of proMMP9 by MMPs

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04/05/2024

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. ↗

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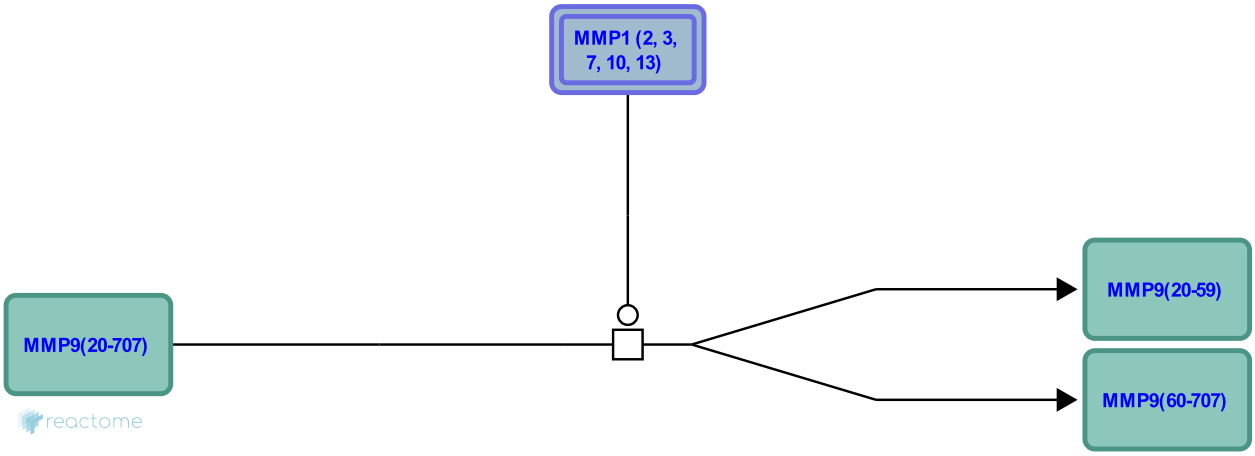
Stable identifier: R-HSA-1592436

Type: transition

Compartments: extracellular region



MMP1 (Sang et al. 1995), MMP2 (Fridman et al. 1995), MMP3 (Goldberg et al. 1992, Ogata et al. 1992, Okada et al. 1992), MMP7 (Imai et al. 1995, Sang et al. 1995), MMP10 (Nakamura et al. 1998) and MMP13 (Knauper et al. 1997) activate MMP9 by a stepwise mechanism but the second cleavage is apparently not an autocatalytic event as is the case for MMP1 (Okada et al. 1992). The first site is the Glu59-Met60 bond, generating an inactive 85-86 kDa intermediate (O'Connell et al. 1994), followed by cleavage of the Arg106-Phe107 peptide bond producing the fullly active 82 kDa form of MMP9 (Okada et al. 1992, Fridman et al. 1995).

Literature references

Nagase, H., Ogata, Y., Enghild, JJ. (1992). Matrix metalloproteinase 3 (stromelysin) activates the precursor for the human matrix metalloproteinase 9. *J Biol Chem, 267*, 3581-4.

Smith, B., López-Otin, C., Knäuper, V., Murphy, G. (1997). Activation of progelatinase B (proMMP-9) by active collagenase-3 (MMP-13). *Eur J Biochem, 248*, 369-73.

Fujii, Y., Okada, Y., Nakamura, H., Ohuchi, E., Yamamoto, E. (1998). Activation of the precursor of human stromelysin 2 and its interactions with other matrix metalloproteinases. *Eur J Biochem, 253*, 67-75.

Marmer, BL., Genrich, LT., Strongin, A., Goldberg, GI., Collier, IE. (1992). Interaction of 92-kDa type IV collagenase with the tissue inhibitor of metalloproteinases prevents dimerization, complex formation with interstitial collagenase, and activation of the proenzyme with stromelysin. *J Biol Chem, 267*, 4583-91.

Sang, QX., Van Wart, HE., Birkedal-Hansen, H. (1995). Proteolytic and non-proteolytic activation of human neutrophil progelatinase B. *Biochim Biophys Acta, 1251*, 99-108.

Editions

2011-09-09	Authored	Jupe, S.
2012-02-21	Edited	Jupe, S.
2012-02-28	Reviewed	Overall, CM., Butler, GS.