HGFAC cleaves pro-HGF to form HGF dimer

Birchmeier, W., D'Eustachio, P., Heynen, G., Jassal, B., Orlic-Milacic, M.

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

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. ↗

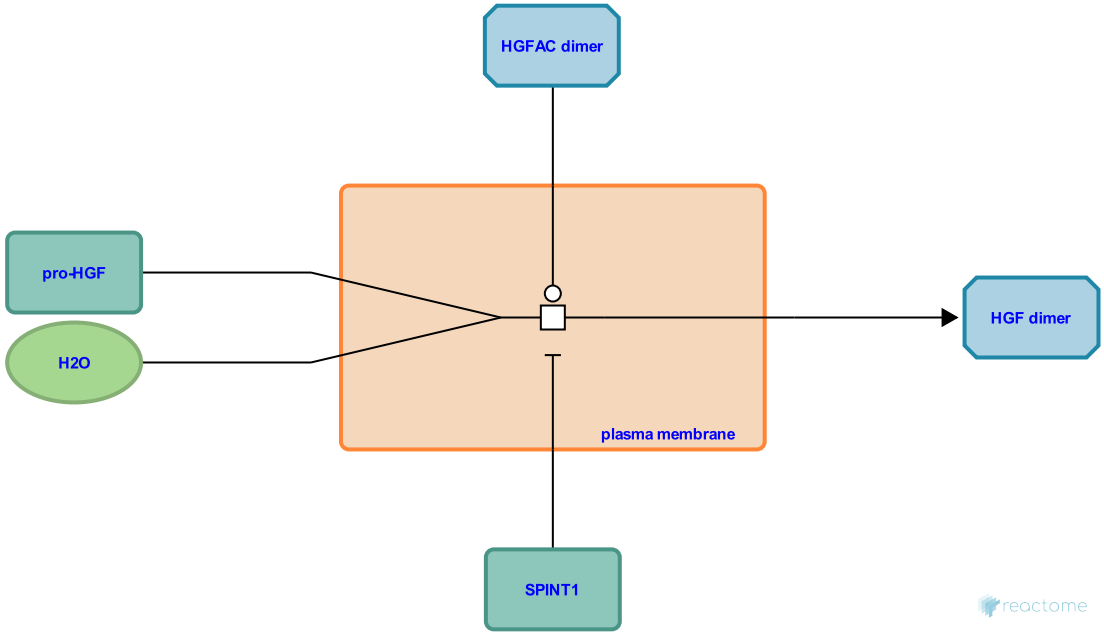
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

HGFAC cleaves pro-HGF to form HGF dimer ↗

Stable identifier: R-HSA-6800299

Type: transition

Compartments: extracellular region, plasma membrane



HGF is a pleiotropic factor and activates hepatocyte growth factor receptor (MET), a proto-oncogenic receptor tyrosine kinase. HGF is secreted into the extracellular matrix as an inactive single chain precursor (pro-HGF (32-728)) and requires cleavage at Arg494–Val495 to form the biologically active alpha-beta heterodimer. Hepatocyte growth factor activator (HGFAC, commonly known as HGFA) is a serine protease that converts HGF into its active form (Shia et al. 2005). The Kunitz-type protease inhibitor 1 (SPINT1, aka HAI1) is an inhibitor of HGFAC activity (Shia et al. 2005).

Literature references

Kirchhofer, D., Shia, S., Corpuz, RT., Stamos, J., Santell, L., Fan, B. et al. (2005). Conformational lability in serine protease active sites: structures of hepatocyte growth factor activator (HGFA) alone and with the inhibitory domain from HGFA inhibitor-1B. *J. Mol. Biol., 346*, 1335-49. ↗

Editions

2015-09-29	Authored, Edited	Jassal, B.
2016-01-11	Reviewed	D'Eustachio, P.
2016-07-11	Reviewed	Birchmeier, W., Heynen, G.
2016-07-19	Edited	Orlic-Milacic, M.