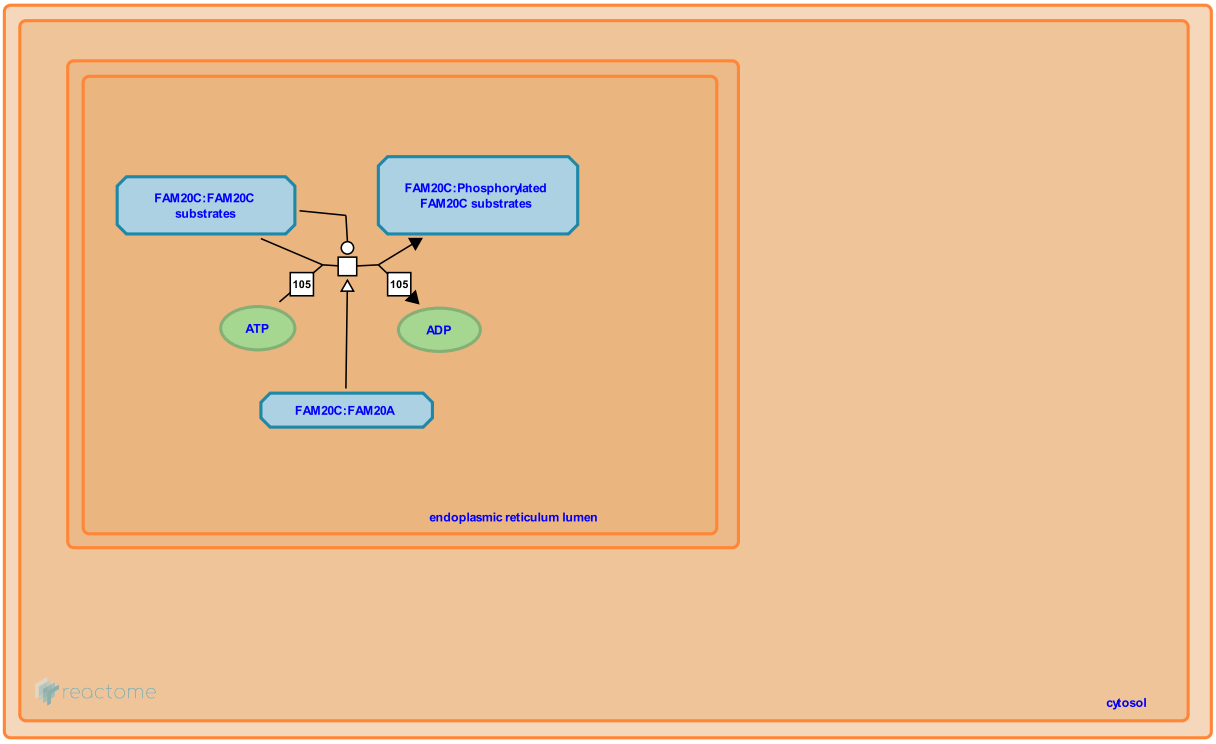
Post-translational protein phosphorylation



Jupe, S., Wiley, SE.

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

13/05/2024

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. ↗

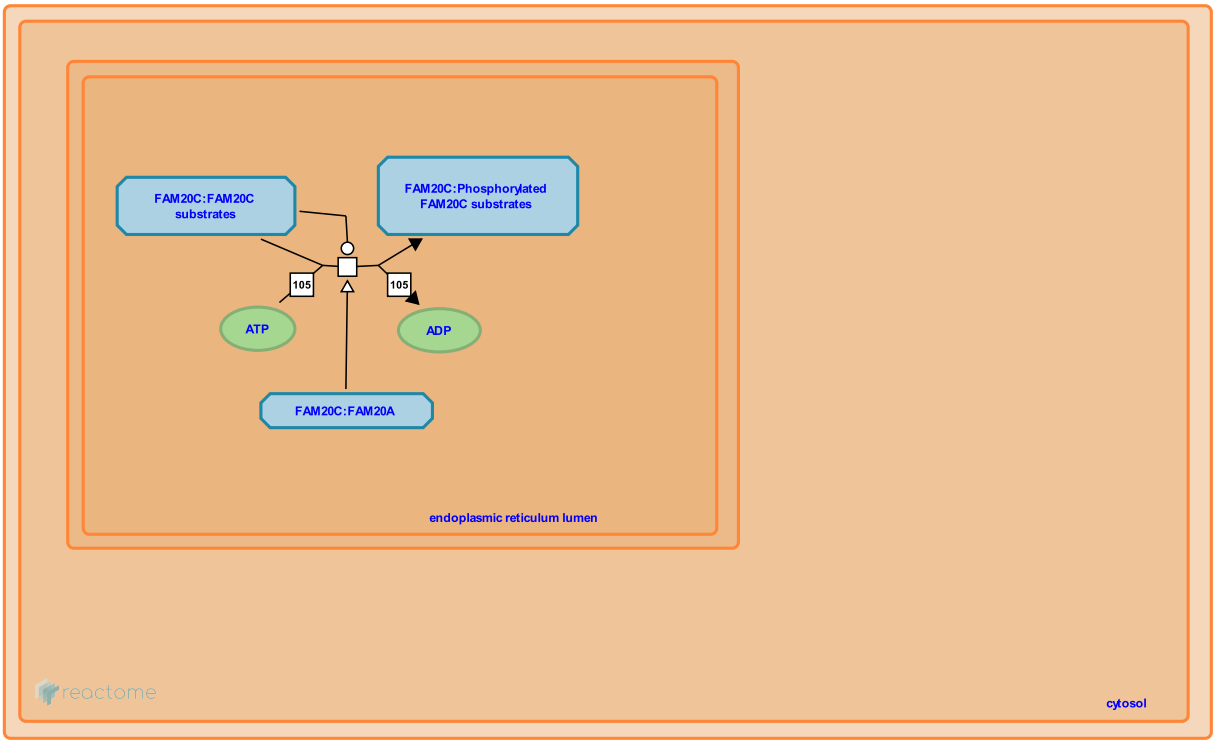
Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

Post-translational protein phosphorylation ↗

Stable identifier: R-HSA-8957275



Secretory pathway kinases phosphorylate a diverse array of substrates involved in many physiological processes.

Literature references

Kinch, LN., Tagliabracci, VS., Sreelatha, A. (2015). The secretory pathway kinases. *Biochim. Biophys. Acta, 1854*, 1687-93. ↗

Editions

2016-12-08	Authored	Jupe, S.
2017-01-23	Reviewed	Wiley, SE.
2017-01-24	Edited	Jupe, S.

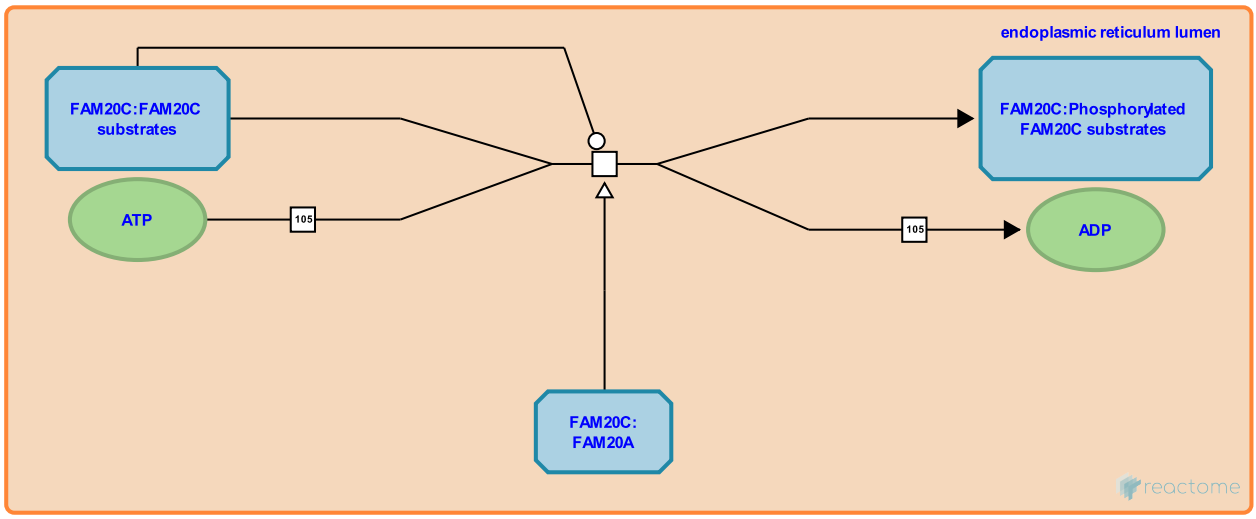
FAM20C phosphorylates FAM20C substrates ↗

Location: Post-translational protein phosphorylation

Stable identifier: R-HSA-8952289

Type: transition

Compartments: endoplasmic reticulum lumen



Extracellular serine/threonine protein kinase FAM20C is an extracellular kinase that can phosphorylate a broad range of secreted protein. FAM20C is bound and allosterically activated by the pseudokinase FAM20A (Tagliabracchi et al. 2012, 2015, Cui et al. 2015).
Loss of function mutations in Fam20C cause Raine Syndrome, an osteosclerotic bone dysplasia (Faundes et al. 2014).

Literature references

Grishin, N., Engel, JL., Cui, J., Nguyen, KB., Wiley, SE., Kinch, LN. et al. (2015). A Single Kinase Generates the Majority of the Secreted Phosphoproteome. *Cell, 161*, 1619-32. ↗

Editions

2016-12-14	Authored	Jupe, S.
2017-01-19	Edited	Jupe, S.
2017-01-23	Reviewed	Wiley, SE.

Table of Contents