Activation of ZAP-70

Garapati, P V., Rudd, C.E.., Trowsdale, J., de Bono, B.

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. ↗

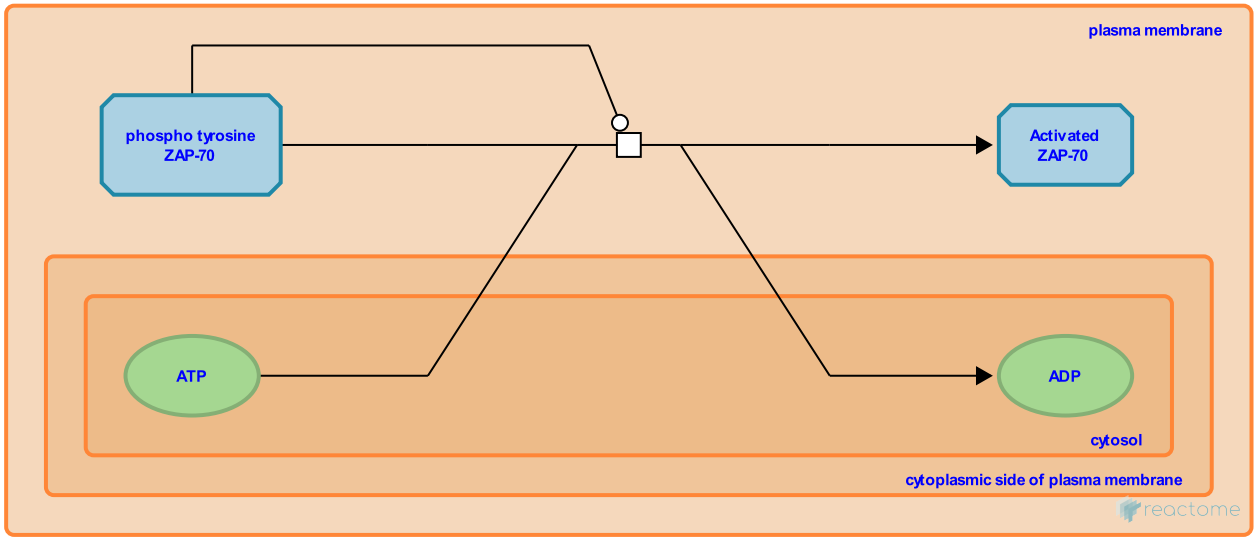
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Activation of ZAP-70

Stable identifier: R-HSA-202174

Type: transition

Compartments: cytosol, plasma membrane



Later ZAP-70 undergoes trans-autophosphorylation at Y315 and Y319. These sites appear to be positive regulatory sites. ZAP-70 achieve its full activation after the trans-autophosphorylation. Activated ZAP-70 phosphorylates T-cell-specific adaptors, such as LAT and SLP-76 leading to the recruitment and activation of other kinase families and enzymes, resulting in secondary messenger generation and culminating in T cell activation.

Literature references

Chu, DH., Morita, CT., Weiss, A. (1998). The Syk family of protein tyrosine kinases in T-cell activation and development. *Immunol Rev, 165*, 167-80.

van Oers, NS., Weiss, A. (1995). The Syk/ZAP-70 protein tyrosine kinase connection to antigen receptor signalling processes. *Semin Immunol, 7*, 227-36.

Editions

2008-01-24	Authored	de Bono, B., Garapati, P V., Rudd, C.E..
2008-02-26	Reviewed	Trowsdale, J.