IER3 recruits MAPKs to PP2A-B56-beta,gamma

Orlic-Milacic, M., Porteu, F.

02/05/2024

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. ↗
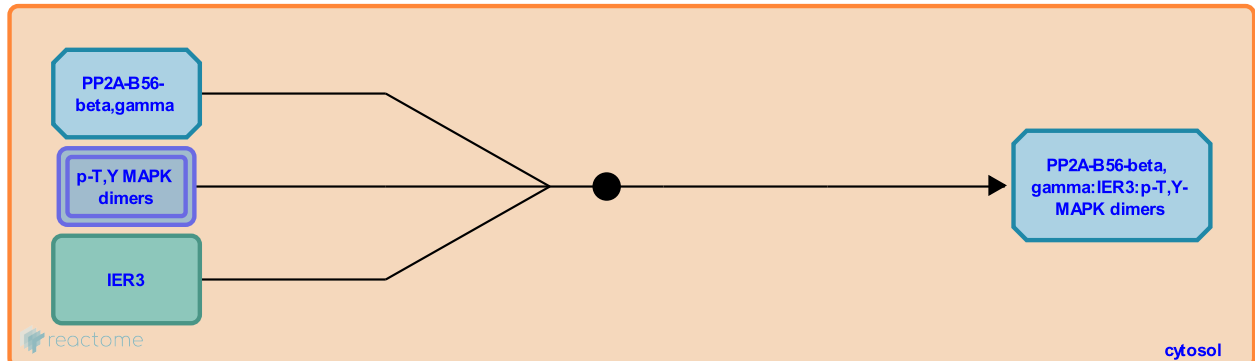
Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

IER3 recruits MAPKs to PP2A-B56-beta,gamma ↗

Stable identifier: R-HSA-6811472

Type: binding

Compartments: cytosol

IER3 (IEX-1) recruits both an activated MAPK (MAPK1 (ERK2) or MAPK3 (ERK1)) and the protein phosphatase 2A (PP2A) complex containing regulatory subunits B56-beta (PPP2R5B) or B56-gamma (PPP2R5C), through an interaction with the B56 subunit, forming a tripartite complex (Letourneux et al. 2006, Rocher et al. 2007).

Literature references

Rocher, G., Porteu, F., Letourneux, C. (2006). B56-containing PP2A dephosphorylate ERK and their activity is controlled by the early gene IEX-1 and ERK. *EMBO J, 25*, 727-38. ↗

Rocher, G., Letourneux, C., Porteu, F., Lenormand, P. (2007). Inhibition of B56-containing protein phosphatase 2As by the early response gene IEX-1 leads to control of Akt activity. *J. Biol. Chem., 282*, 5468-77. ↗

Editions

2015-12-22	Authored, Edited	Orlic-Milacic, M.
2016-02-08	Reviewed	Porteu, F.