p-6Y-VEGFR2 binds SH2D2A

Ballmer-Hofer, K., Berger, P., Garapati, P V., Welsh, M.
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.

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Literature references


Reactome database release: 74

This document contains 1 reaction (see Table of Contents)
p-6Y-VEGFR2 binds SH2D2A

Stable identifier: R-HSA-4420143

Type: binding

Compartments: plasma membrane, cytosol

Two-hybrid mapping showed that tyrosine 951 (Y951) serves as the binding site for T-cell specific adapter molecule (TSAD/SH2 domain-containing protein 2A (SH2D2A)), also referred as VEGF-receptor-associated protein (VRAP) (Wu et al. 2000). SH2D2A mediates vasular permeability downstream of VEGFR2 by forming a complex with c-SRC (Sun et al. 2012). Site-directed mutation of Y951 to phenylalanine (Y951F) in the VEGFR2, or siRNA mediated silencing of SH2D2A expression, prevented VEGFA mediated cytoskeletal reorganisation and migration but not mitogenicity (Matsumoto et al. 2005).

Literature references


Editions

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<th>Action</th>
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