Autophosphorylation of KIT

Garapati, P V., Rönnstrand, L.
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: 78

This document contains 1 reaction (see Table of Contents)
Autophosphorylation of KIT

Stable identifier: R-HSA-205289

Type: transition

Compartments: plasma membrane, cytosol, extracellular region

The cytoplasmic domain of KIT contains a bipartite kinase domain separated by 77 residues. The first part of the catalytic domain contains the ATP binding region while the second part contains an activation loop. Both parts of the domain have a number of possible autophosphorylation sites. In contrast to many other tyrosine kinases, autophosphorylation of the activation loop does not seem to be involved in the activation of the kinase activity nor it is required for full kinase activity (DiNitto et al. 2010). Instead, phosphorylation sites in the juxtamembrane region are important for activation of the kinase activity. The dimerized KIT acts as both enzyme and substrate for itself and autophosphorylates these specific tyrosine residues with in the kinases domains in trans as well as tyrosine residues outside the kinase domain. The resulting phosphotyrosine residues serve as docking sites for a number of signal transduction molecules containing Src-homology 2 (SH2) and phosphotyrosine-binding (PTB) domains. A majority of the autophosphorylation sites reside outside the kinase domain.

Literature references


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