AAMP binds to TBXA2R

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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: 83

This document contains 1 reaction (see Table of Contents)
AAMP binds to TBXA2R

**Stable identifier:** R-HSA-9674529

**Type:** binding

**Compartments:** cytosol, plasma membrane

AAMP (Angio-associated migratory cell protein) binds to both the TP-alpha and TP-beta isoforms which arise due to differential splicing of a primary RNA transcript encoded by the TBXA2R (thromboxane A2 receptor) gene. Their association with AAMP is dependent on common (residues 312-328) and unique (residues 366-392 of TP-beta) sequences within the variant carboxyl-terminal domains of TP-alpha and TP-beta. Stimulation of the TPs with U46619, a stable mimetic of thromboxane (TX) A2, leads to a transient dissociation of AAMP from both the TP-alpha and TP-beta isoforms, coinciding with a transient redistribution of AAMP from its localization in an intracellular fibrous network. Down-regulation of AAMP reduces coronary artery smooth muscle migration, an effect that is further enhanced in the presence of U46619, while VEGF-mediated migration is not affected. AAMP and TXA2 can independently activate RHOA signaling. (Reid et al. 2011).

**Literature references**


**Editions**

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