

Dual-specific AKAPs bind type I and II PKA regulatory subunits

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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

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

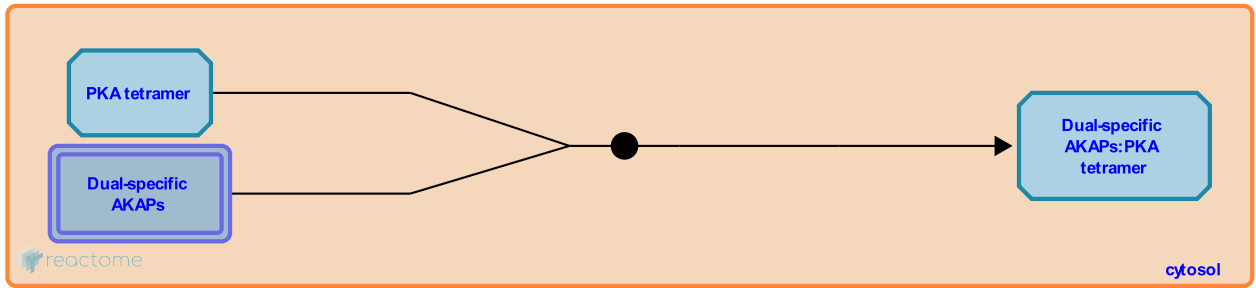
This document contains 1 reaction ([see Table of Contents](#))

Dual-specific AKAPs bind type I and II PKA regulatory subunits ↗

Stable identifier: R-HSA-992708

Type: binding

Compartments: cytosol



Protein kinase A (PKA) refers to a family of multimeric enzyme complexes whose activity is dependent on the level of cyclic AMP (cAMP), hence PKA is also known as cAMP-dependent protein kinase (EC 2.7.11.11). PKA has several functions in the cell, including regulation of glycogen, sugar, and lipid metabolism. PKA is a holoenzyme complex consisting of two regulatory and two catalytic subunits. When cAMP levels are low the holoenzyme remains intact and is inactive. When the concentration of cAMP rises (e.g. as a result of adenylate cyclase activation by G protein-coupled receptors coupled to Gs, or inhibition of phosphodiesterases that degrade cAMP) cAMP binds to two binding sites on the regulatory subunits, leading to the release and activation of the catalytic subunits. The regulatory subunits of PKA are also important for localizing the kinase inside the cell. A-kinase anchor proteins (AKAPs) bind to the regulatory subunits and to cytoskeletal structures or membranes, anchoring the enzyme complex to a particular subcellular compartment. Dual-specificity A kinase-anchoring proteins (AKAP1/D-AKAP1) and (AKAP10/D-AKAP2) interact with the type I and type II regulatory subunits of PKA (Huang et al. 1997). AKAP10 additionally has two regulator of G-protein signaling (RGS) domains, giving it the potential to coordinate a signaling complex that links cAMP signaling with G-protein-coupled receptor (GPCR) signaling (Burns-Hamuro et al. 2004).

Literature references

Taylor, SS., Weiner, JA., Chun, J., Durick, K., Huang, LJ. (1997). D-AKAP2, a novel protein kinase A anchoring protein with a putative RGS domain. *Proc Natl Acad Sci U S A*, 94, 11184-9. ↗

Taylor, SS., Weiner, JA., Chun, J., Durick, K., Huang, LJ. (1997). Identification of a novel protein kinase A anchoring protein that binds both type I and type II regulatory subunits. *J Biol Chem*, 272, 8057-64. ↗

Editions

2010-10-29	Authored	Akkerman, JW.
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