AKAP9:KCNQ1 tetramer:KCNE dimer transports K+ from cytosol to extracellular region

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19/05/2024

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. ↗

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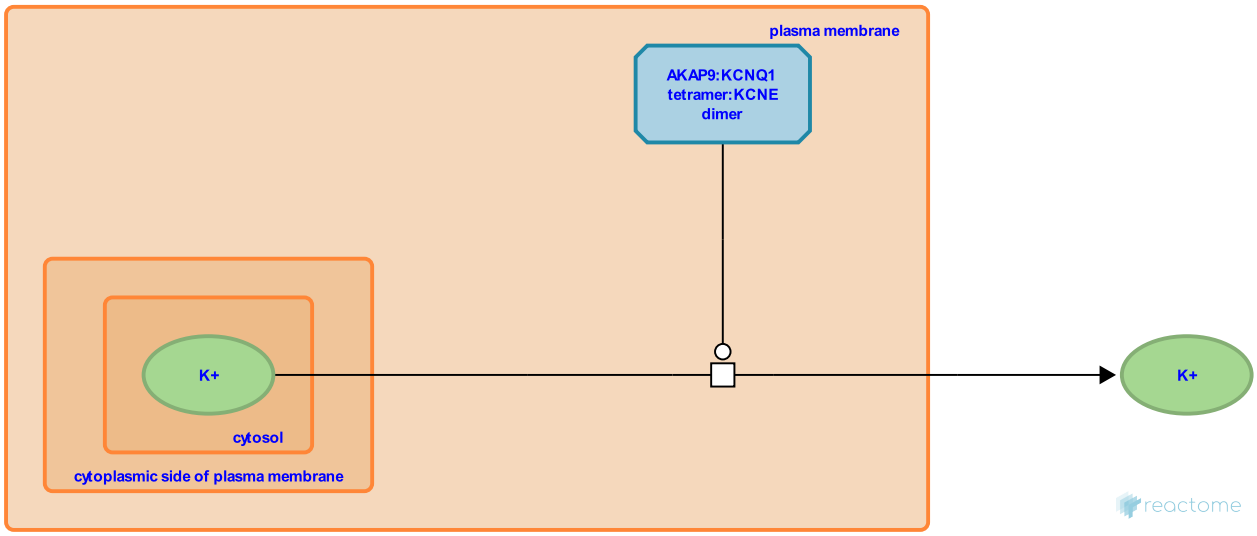
Stable identifier: R-HSA-5577050

Type: transition

Compartments: cytosol, extracellular region, plasma membrane



Two potassium currents, I_{Ks} and I_{Kr}, provide the principal repolarising currents in cardiac myocytes for the termination of action potentials. Potassium voltage-gated channel subfamily KQT member 1 (KCNQ1 aka Kv7.1) is the pore-forming alpha subunit of a complex also containing an ancillary protein from potassium voltage-gated channel subfamily E members (KCNE) that assemble as a beta subunit. The stoichiometry is believed to be 4 KCNQ1 subunits to 2 KCNE subunits (Plant et al. 2014). A-kinase anchor protein 9 (AKAP9) is an essential anchoring protein that binds to KCNQ1. Defects in KCNQ1 that disrupt this binding can result in type 1 long-QT syndrome (LQT1), a hereditary, potentially lethal arrhythmia syndrome (Chen et al. 2007). The AKAP9:KCNQ1:KCNE complex creates the slowly activating delayed rectifier cardiac potassium current I_{Ks} by the efflux of K+ from cardiac cells (Schroeder et al. 2000).

Literature references

Tester, DJ., Sampson, KJ., Chen, L., Kass, RS., Marquardt, ML., Ackerman, MJ. (2007). Mutation of an A-kinase-anchoring protein causes long-QT syndrome. *Proc. Natl. Acad. Sci. U.S.A., 104*, 20990-5. ↗

Goldstein, SA., Dai, H., Xiong, D., Plant, LD. (2014). Individual IKs channels at the surface of mammalian cells contain two KCNE1 accessory subunits. *Proc. Natl. Acad. Sci. U.S.A., 111*, E1438-46. ↗

Greger, R., Jentsch, TJ., Bleich, M., Schroeder, BC., Warth, R., Fehr, S. et al. (2000). A constitutively open potassium channel formed by KCNQ1 and KCNE3. *Nature, 403*, 196-9. ↗

Editions

2014-06-05	Authored, Edited	Jassal, B.
2015-11-09	Reviewed	Colotti, G.