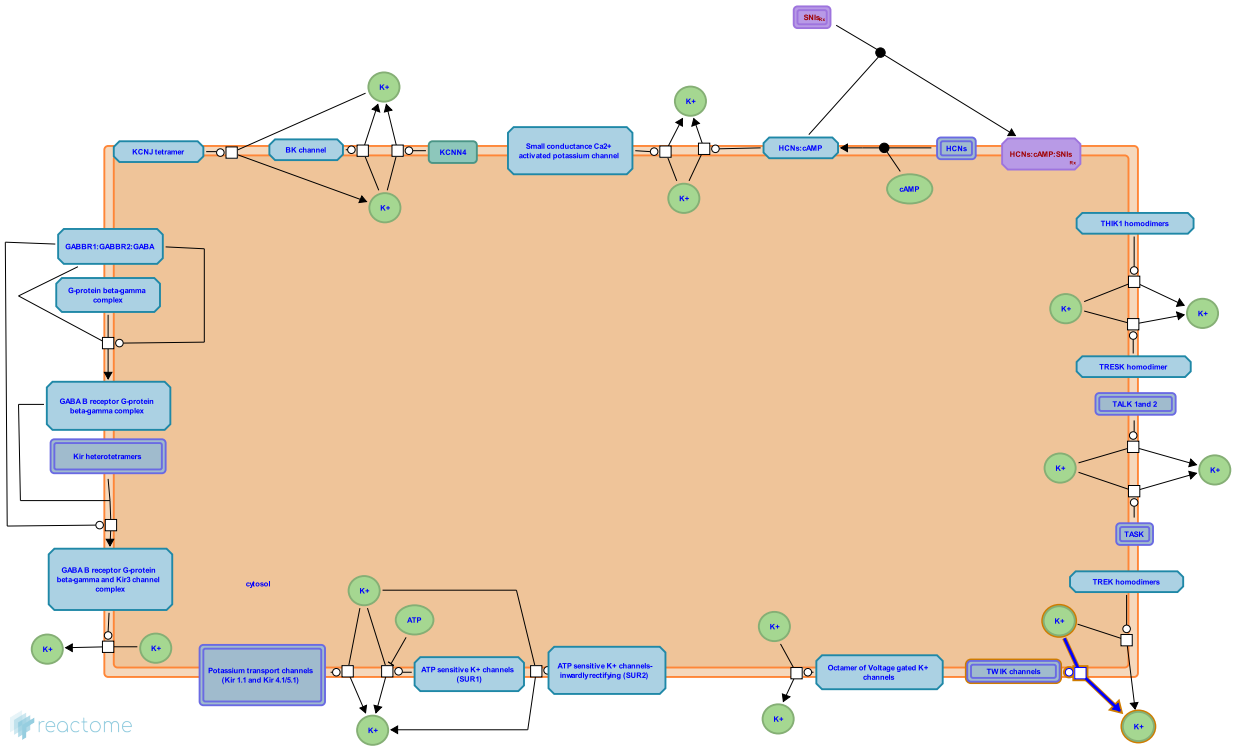
Tandem of pore domain in a weak inwardly rectifying K+ channels (TWIK)



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

20/05/2024

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. ↗

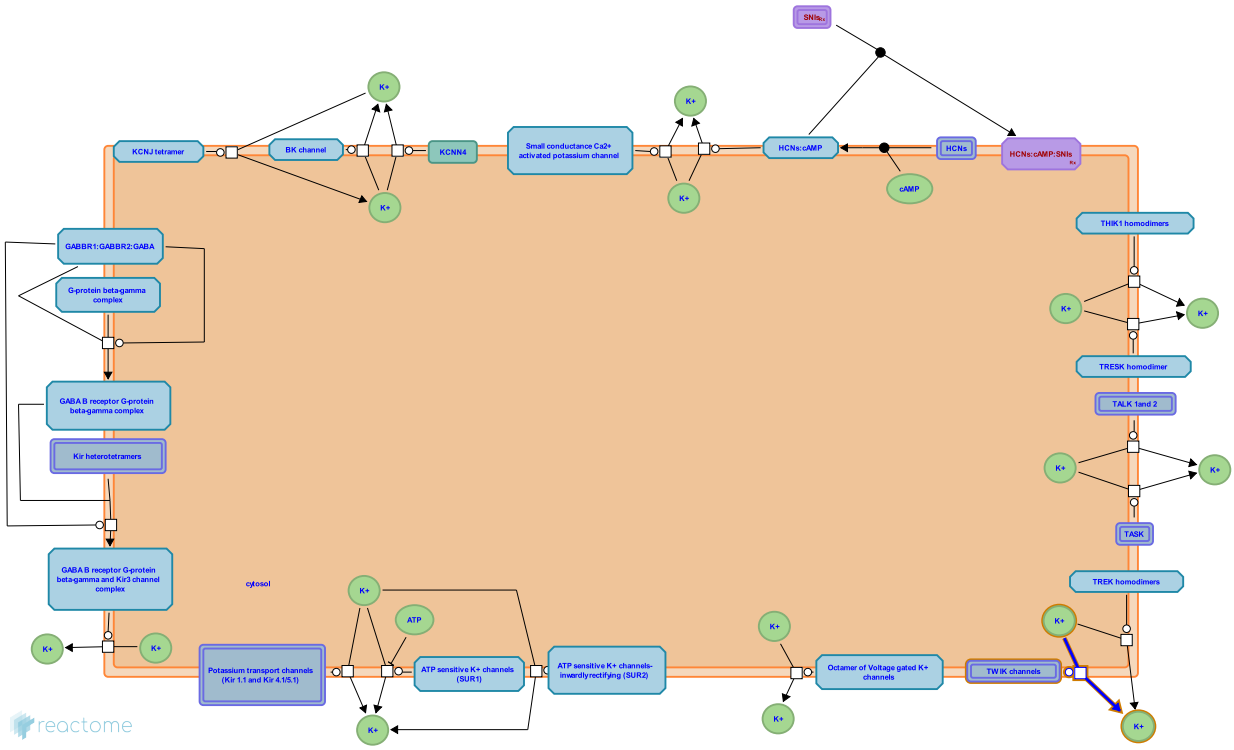
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Tandem of pore domain in a weak inwardly rectifying K+ channels (TWIK) ↗

Stable identifier: R-HSA-1299308

Compartments: plasma membrane, cytosol, extracellular region



TWIK channels exhibit very low current and comprise of TWIK1, TWIK2 and KCNK7 members. TWIK current may be low due to rapid recycling of the channels from the plasma membrane.

Literature references

Feliciangeli, S., Barhanin, J., Warth, R., Bendahhou, S., Tardy, MP., Chatelain, FC. et al. (2010). Potassium channel silencing by constitutive endocytosis and intracellular sequestration. *J Biol Chem, 285*, 4798-805. ↗

Editions

2010-09-23	Reviewed	Jassal, B.
2011-05-23	Authored, Edited	Mahajan, SS.

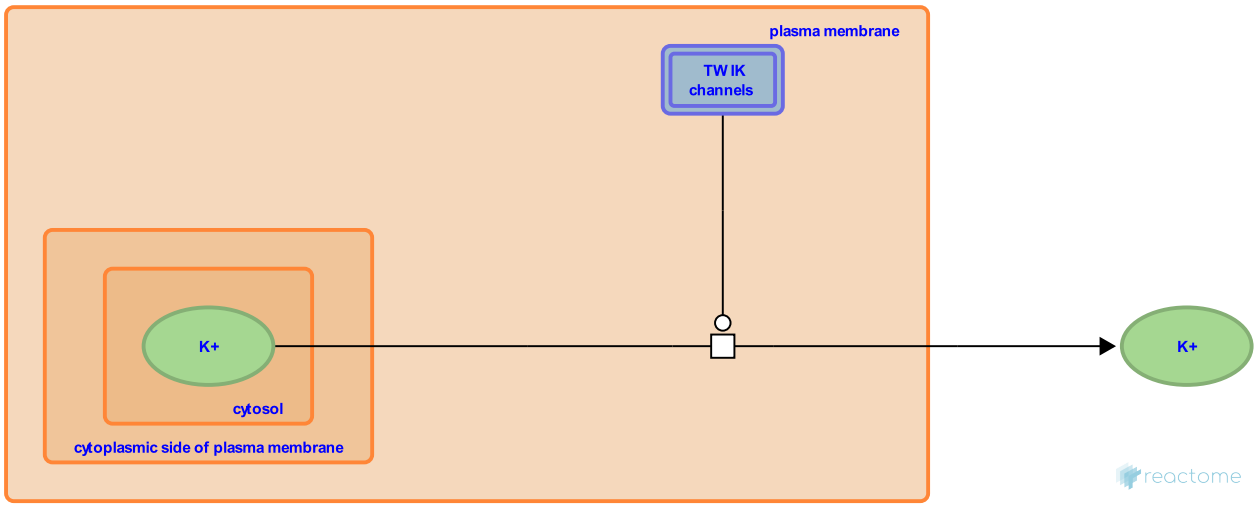
Activation of tandem pore domain in a weak inwardly rectifying K+ channels ↗

Location: Tandem of pore domain in a weak inwardly rectifying K+ channels (TWIK)

Stable identifier: R-HSA-1299304

Type: transition

Compartments: plasma membrane, extracellular region, cytosol



Activation of TWIK channels results in low outward K+ currents.

Literature references

Feliciangeli, S., Barhanin, J., Warth, R., Bendahhou, S., Tardy, MP., Chatelain, FC. et al. (2010). Potassium channel silencing by constitutive endocytosis and intracellular sequestration. *J Biol Chem, 285*, 4798-805. ↗

Editions

2010-09-23	Reviewed	Jassal, B.
2011-05-22	Authored	Mahajan, SS.
2011-05-23	Edited	Mahajan, SS.

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