

KCNA5 Rabbit pAb

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Catalog # AP52165

Product Information

Application	WB
Primary Accession	P22460
Reactivity	Human
Predicted	Rat, Pig, Dog, Mouse, Rabbit, Chicken
Host	Rabbit
Clonality	Polyclonal
Calculated MW	67228
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human KCNA5
Epitope Specificity	551-613/613
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SUBCELLULAR LOCATION	Membrane; Multi-pass membrane protein.
DISEASE	Familial atrial fibrillation 7 (ATFB7) [MIM:612240]: A familial form of atrial fibrillation, a common sustained cardiac rhythm disturbance. Atrial fibrillation is characterized by disorganized atrial electrical activity and ineffective atrial contraction promoting blood stasis in the atria and reduces ventricular filling. It can result in palpitations, syncope, thromboembolic stroke, and congestive heart failure. Note=The disease is caused by mutations affecting the gene represented in this entry.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	Potassium channels represent the most complex class of voltage-gated ion channels from both functional and structural standpoints. Their diverse functions include regulating neurotransmitter release, heart rate, insulin secretion, neuronal excitability, epithelial electrolyte transport, smooth muscle contraction, and cell volume. Four sequence-related potassium channel genes - shaker, shaw, shab, and shal - have been identified in Drosophila, and each has been shown to have human homolog(s). This gene encodes a member of the potassium channel, voltage-gated, shaker-related subfamily. This member contains six membrane-spanning domains with a shaker-type repeat in the fourth segment. It belongs to the delayed rectifier class, the function of which could restore the resting membrane potential of beta cells after depolarization and thereby contribute to the regulation of insulin secretion. This gene is intronless, and the gene is clustered with genes KCNA1 and KCNA6 on chromosome 12.

Additional Information

Gene ID 3741

Other Names	Potassium voltage-gated channel subfamily A member 5, HPCN1, Voltage-gated potassium channel HK2, Voltage-gated potassium channel subunit Kv1.5, KCNA5
Dilution	WB=1:500-2000,ELISA=1:5000-10000
Storage	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

Protein Information

Name	KCNA5
Function	Voltage-gated potassium channel that mediates transmembrane potassium transport in excitable membranes. Forms tetrameric potassium- selective channels through which potassium ions pass in accordance with their electrochemical gradient. The channel alternates between opened and closed conformations in response to the voltage difference across the membrane. Can form functional homotetrameric channels and heterotetrameric channels that contain variable proportions of KCNA1, KCNA2, KCNA4, KCNA5, and possibly other family members as well; channel properties depend on the type of alpha subunits that are part of the channel (PubMed: 12130714). Channel properties are modulated by cytoplasmic beta subunits that regulate the subcellular location of the alpha subunits and promote rapid inactivation (PubMed: 12130714). Homotetrameric channels display rapid activation and slow inactivation (PubMed: 12130714 , PubMed: 8505626). Required for normal electrical conduction including formation of the infranodal ventricular conduction system and normal action potential configuration, as a result of its interaction with XIRP2 (By similarity). May play a role in regulating the secretion of insulin in normal pancreatic islets.
Cellular Location	Cell membrane; Multi-pass membrane protein
Tissue Location	Pancreatic islets and insulinoma.

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References

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Philipson L.H.,et al.Proc. Natl. Acad. Sci. U.S.A. 88:53-57(1991).
Curran M.E.,et al.Genomics 12:729-737(1992).
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