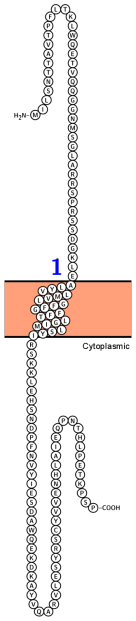
Potassium voltage-gated channel subfamily E member 1

Organism: Homo sapiens (Human) | **Gene names:** KCNE1



Entry: P15382

Mass: 14.675 Da

Transmembrane: 1

Subcellular location: Cell membrane {ECO:0000269|PubMed:19219384}, Single-pass type I membrane protein {ECO:0000305}. Apical cell membrane {ECO:0000250|UniProtKB:P15383}. Membrane raft {ECO:0000269|PubMed:20533308}. Note=Colocalizes with KCNB1 at the plasma membrane (By similarity). Targets to the membrane raft when associated with KCNQ1 (PubMed:20533308). {ECO:0000250|UniProtKB:P15383, ECO:0000269|PubMed:20533308}.

Cofactor: -

Extinction coefficient: 1.359

Isoelectric Point: 6.83

PubMed ID: 2730656, 7828904, 15489334, 9312006, 9230439, 11874988, 19219384, 20533308, 21676880, 21669976, 26307551, 18611041, 8899564, 9328483, 9354783, 9354802, 9445165, 10400998, 10973849, 11692163, 15051636, 16414944, 16823764, 19716085, 25037568

Family: -

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Function:

Ancillary protein that assembles as a beta subunit with a voltage-gated potassium channel complex of pore-forming alpha subunits. Modulates the gating kinetics and enhances stability of the channel complex. Assembled with KCNB1 modulates the gating characteristics of the delayed rectifier voltage-dependent potassium channel KCNB1 (PubMed:19219384). Assembled with KCNQ1/KVLQT1 is proposed to form the slowly activating delayed rectifier cardiac potassium (IKs) channel. The outward current reaches its steady state only after 50 seconds. Assembled with KCNH2/HERG may modulate the rapidly activating component of the delayed rectifying potassium current in heart (IKr). {ECO:0000269|PubMed:19219384}.

Data from experiment(s): Hek293 membrane pellets

DIBMA 10	No data	DIBMA 12	No data
DIBMA Glycerol	No data	DIBMA Glucosamine	No data
Amphipol 17	No data	Amphipol 18	No data
AASTY 6-45	No data	AASTY 11-45	No data
AASTY 6-50	No data	AASTY 11-50	No data
AASTY 6- 55	No data	AASTY 11- 55	No data
SMALP 502-E	No data	SMALP 140-I	No data
SMALP 300	No data	SMALP 200	No data
SMALP 140	No data	DDM	No data
DM	No data	LMNG	No data
Fos-12	No data	Digitonin-A	No data
RIPA	No data		

Data from experiment(s): Hek293 membrane pellets 1 %

DIBMA 10	No data	DIBMA 12	No data
DIBMA Glycerol	No data	DIBMA Glucosamine	No data
Amphipol 17	No data	Amphipol 18	No data
AASTY 6-45	No data	AASTY 11-45	No data
AASTY 6-50	No data	AASTY 11-50	No data
AASTY 6- 55	No data	AASTY 11- 55	No data
SMALP 502-E	No data	SMALP 140-I	No data
SMALP 300	No data	SMALP 200	No data
SMALP 140	No data	DDM	No data
DM	No data	LMNG	No data
Fos-12	No data	Digitonin-A	No data
RIPA	No data		

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Involvement in disease:

Jervell and Lange-Nielsen syndrome 2 (JLNS2) [MIM:612347]: An autosomal recessive disorder characterized by congenital deafness, prolongation of the QT interval, syncopal attacks due to ventricular arrhythmias, and a high risk of sudden death. {ECO:0000269|PubMed:10400998, ECO:0000269|PubMed:21676880, ECO:0000269|PubMed:9328483, ECO:0000269|PubMed:9354783}. Note=The disease is caused by variants affecting the gene represented in this entry.; Long QT syndrome 5 (LQT5) [MIM:613695]: A heart disorder characterized by a prolonged QT interval on the ECG and polymorphic ventricular arrhythmias. They cause syncope and sudden death in response to exercise or emotional stress, and can present with a sentinel event of sudden cardiac death in infancy. {ECO:0000269|PubMed:10400998, ECO:0000269|PubMed:10973849, ECO:0000269|PubMed:11692163, ECO:0000269|PubMed:16414944, ECO:0000269|PubMed:19716085, ECO:0000269|PubMed:25037568, ECO:0000269|PubMed:9354802, ECO:0000269|PubMed:9445165}. Note=The disease is caused by variants affecting the gene represented in this entry.

Binding site:

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Tissue specificity:

Expressed in lung, kidney, testis, ovaries, small intestine, peripheral blood leukocytes. Expressed in the heart (PubMed:19219384). Not detected in pancreas, spleen, prostate and colon. Restrictively localized in the apical membrane portion of epithelial cells. {ECO:0000269|PubMed:19219384, ECO:0000269|PubMed:9312006}.

3D (X-ray crystallography):

NMR spectroscopy (1)

Pharmaceutical use:

-

AS sequence:

MILSNTTAVTPFLTKLWQETVQQGGNMSGLARRSPRSSDGKLEALYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESD AWQEKDKAYVQARVLESYRSCYVVENHLAIEQPNTHLPETKPSP

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Creditnotes:

The protein visualizations are generated with the help of Protter:
Omasits, U., Ahrens, C.H., MÃ¼ller, S., Wollscheid, B. “Protter: interactive protein feature visualization and integration with experimental proteomic data”. *Bioinformatics*. 2014 Mar 15; **30**(6):884-6. doi: 10.1093/bioinformatics/btt607.

IP and extinction coefficients are gathered from Protparam by ExPASy:
Gasteiger, E., Hoogland, C., Gattiker, A., Duvaud, S., Wilkins, M.R., Appel, R.D., Bairoch, A. “Protein Identification and Analysis Tools on the ExPASy Server”. (In) *John M. Walker (ed): The Proteomics Protocols Handbook*, Humana Press (2005). pp. 571-607

The basic knowledge is found on UniProt:
The UniProt Consortium. “UniProt: the universal protein knowledgebase in 2021”. *Nucleic Acids Res*. **49**:D1 (2021)