Cube Biotech

# Potassium voltage-gated channel subfamily A member 3

**Organism:** Homo sapiens (Human) | **Gene names:** KCNA3, HGK5

**Entry:** P22001

**Mass:** 63.842 Da

**Transmembrane:** 6

**Subcellular location:** Cell membrane {ECO:0000250}, Multi-pass membrane protein.

**Cofactor:** -

**Extinction coefficient:** 0.753

**Isoelectric Point:** 5.61

**PubMed ID:** 7829094, 16710414, 15489334, 1986382, 1373731, 1547020

**Family:** -

**Function:**

Mediates the voltage-dependent potassium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a potassium-selective channel through which potassium ions may pass in accordance with their electrochemical gradient.

**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 | | |

**Involvement in disease:**

-

**Binding site:**

-

**Tissue specificity:**

-

**3D (X-ray crystallography):**

X-ray crystallography (1); Electron microscopy (2)

**Pharmaceutical use:**

-

**AS sequence:**

MDERLSLLRSPPPPSARHRAHPPQRPASSGGAHTLVNHGYAEPAAGRELPPDMTVVPGDHLLEPEVADGGGAPPQGGCGGG
GCDRYEPLPPSLPAAGEQDCCGERVVINISGLRFETQLKTLCQFPETLLGDPKRRMRYFDPLRNEYFFDRNRPSFDAILYYYQSG
GRIRRPVNVPIDIFSEEIRFYQLGEEAMEKFREDEGFLREEERPLPRRDFQRQVWLLFEYPESSGPARGIAIVSVLVILISIVIFCLET
LPEFRDEKDYPASTSQDSFEAAGNSTSGSRAGASSFSDPFFVVETLCIIWFSFELLVRFFACPSKATFSRNIMNLIDIVAIIPYFITLG
TELAERQGNGQQAMSLAILRVIRLVRVFRIFKLSRHSKGLQILGQTLKASMRELGLLIFFLFIGVILFSSAVYFAEADDPTSGFSSIPD
AFWWAVVTMTTVGYGDMHPVTIGGKIVGSLCAIAGVLTIALPVPVIVSNFNYFYHRETEGEEQSQYMHVGSCQHLSSSAEELRK
ARSNSTLSKSEYMVIEEGGMNHSAFPQTPFKTGNSTATCTTNNNPNSCVNIKKIFTDV

**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)