2nd transmembrane region

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hKCNK18  115 STVGYGYIYPVTRLGKYLCMLYALFGIPLMFLVLTDTGDILATILSTSY-NRFRKFPFFT
hKCNK1   116 STTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIR----
hKCNK2   156 TTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGI-AKVEDT----
hKCNK3    92 TTIGYGHAAPSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVRYLL-HRAKKG----
hKCNK4   102 TTIGYGNVALRTDAGRLFCIFYALVGIPLFGILLAGVGDRLGSSLRHGI-GHIEAI----
hKCNK5    97 TTIGYGNVAPKTPAGRLFCVFYGLFGVPLCLTWISALGKFFGGRAKRLG-QF--------
hKCNK6   105 TTVGYGYTTPLTDAGKAFSIAFALLGVPTTMLLLTASAQRLSLLLTHVPLSWLSMR----
hKCNK7   104 TTTGYGHMAPLSPGGKAFCMVYAALGLPASLALVATLRHCLLPVLSRPR-AWVAVH----
hKCNK9    92 TTIGYGHAAPGTDAGKAFCMFYAVLGIPLTLVMFQSLGERMNTFVRYLL-KRIKKC----
hKCNK10  166 TTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSI-ARVEKV----
hKCNK12  128 STIGFGMTTPATVGGKAFLIAYGLFGCAGTILFFNLFLERIISLLAFIM-RACRER----
hKCNK13  109 STIGFGMTTPATVGGKIFLIFYGLVGCSSTILFFNLFLERLITIIAYIM-KSCHQR----
hKCNK15   92 TTIGYGHAAPGTDSGKVFCMFYALLGIPLTLVTFQSLGERLNAVVRRLL-LAAKCC----
hKCNK16  107 TTIGYGNLAPSTEAGQVFCVFYALLGIPLNVIFLNHLGTGLRAHLAAI--ER--------
hKCNK17  115 TTIGYGNLSPNTMAARLFCIFFALVGIPLNLVVLNRLGHLMQQGVNHWA-SR--------
```

4th transmembrane region

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hKCNK18  333 H--------PNFF---LFFSIYIIVGMEIVFIAFKLVQNRLID--I--------YKNV--
hKCNK1   235 EGY-NQKFRELYK---IGITCYLLLGLIAMLVVLETFCELHELKKFRKMFYV--------
hKCNK2   276 GS--DIEYLDFYK---PVVWFWILVGLAYFAAVLSMIGDWLRV--I--------SKKT--
hKCNK3   209 QKDQALQTQPQYV---AFSFVYILTGLTVIGAFLNLVVLRFMT--M--------NAED--
hKCNK4   222 ADP-RQ-DSPAYQ---PLVWFWILLGLAYFASVLTTIGNWLRV--V--------SRRT--
hKCNK5   213 VNP-SANYHALYR---YFVELWIYLGLAWLSLFVNWKVSMFVE--VHKAIKKRR------
hKCNK6   224 EAP-GQPYRALYK---VLVTVYLFLGLVAMVLVLQTFRHVSDLHGLTELILLPP---P--
hKCNK7   222 RGR-SLHP-VIYHLGQLALLGYLLLGLLAMLLAVETFSELPQVRAMGKFF-RPSGP----
hKCNK9   209 QTKGALQKKPLYV---AFSFMYILVGLTVIGAFLNLVVLRFLT--M--------NSED--
hKCNK10  286 GNA-GINYREWYK---PLVWFWILVGLAYFAAVLSMIGDWLRV--L--------SKKT--
hKCNK12  266 QHA-AYRNQGLYR---LGNFLFILLGVCCIYSLFNVISILIKQ--VLNWMLRKLSCRC--
hKCNK13  247 QNA-HYESQGLYR---FANFVFILMGVCCIYSLFNVISILIKQ--SLNWILRKMDSGC--
hKCNK15  209 QSGEALQRKLPYV---AFSFLYILLGLTVIGAFLNLVVLRFLV--A--------SADW--
hKCNK16  222 TDP-SKHYISVYR---SLAAIWILLGLAWLALILPLGPLLLHR--CCQLWLLSLRQGC--
hKCNK17  231 MNP-SQRYPLWYK---NMVSLWILFGMAWLALIIKLILSQLET----------PGRVCSC
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