```
froKCNQ1 MSS------- EQPAWTFGLF TPDQN----- -KQAP--LEM NEN--AINSL YEAIP----- LPQDGSSNGQ RQEDRQANSF 58
humKCNQ1 MAAASSPPRA ERKRWGWGRL PGARRGSAGL AKKCPFSLEL AEGGPAGGAL YAPIA----- --P-GA-PGP APP---ASPA 68
mouKCNQ1 MDTASSPPSA ERKRAGWSRL LGARRGSA-V VKKCPFSLEL AEGGPEGSTV YAPIA----- --PTGA-PGL APP--MSTPV 69
chiKCNQ1 M-SSSSPPGE HRSR-SLGRL SLPRKGSMTP GKK-PSSLEL AESVP--NAH YAPLPEAQGG QPPAGSGPGA ARE--RPPHV 73
fisKCNQ1 M---TSPAHS TATEASW--- ---TAGAADL --QMTEALHL RNDGVRFPS- ---------- ---------- ------SVPV 42

froKCNQ1 ELKRETLVAT DPPRPTINLD PRVSIYSGRR PLLSRTNIQG RVYNFLERPT GWKCFVYHFT VFLIVLICLI FSVLSTIQQY 138
humKCNQ1 APAAPPVASD LGPRPPVSLD PRVSIYSTRR PVLARTHVQG RVYNFLERPT GWKCFVYHFA VFLIVLVCLI FSVLSTIEQY 148
mouKCNQ1 SPA--PAPAD LGPRPRVSLD PRVSIYSARR PLLARTHIQG RVYNFLERPT GWKCFVYHFT VFLIVLVCLI FSVLSTIEQY 147
chiKCNQ1 RSEVVVVGAE -SARPPVSLD PRVSIYSLRK PLLSRSNIQG RVYNFLERPT GWKCFVYHFT VFLIVLICLI FSVLSTIEQY 152
fisKCNQ1 DPAV------ ITQHPPSHLH PRMSVYSATR PTLSRSFLQG RVYNFLERPT GWKCFVYHFT VFLIVLSCLI LSVLSTIDEY 116

froKCNQ1 NNLATETLFW MEIVLVVFFG AEYVVRLWSA GCRSKYVGVW GRLRFARKPI SVIDLIVVVA SVIVLCVGSN GQVFATSAIR 218
humKCNQ1 AALATGTLFW MEIVLVVFFG TEYVVRLWSA GCRSKYVGLW GRLRFARKPI SIIDLIVVVA SMVVLCVGSK GQVFATSAIR 228
mouKCNQ1 AALATGTLFW MEIVLVVFFG TEYVVRLWSA GCRSKYVGIW GRLRFARKPI SIIDLIVVVA SMVVLCVGSK GQVFATSAIR 227
chiKCNQ1 AALATGTLFW MEIVLVVFFG TEYVVRLWSA GCRSKYVGIW GRLRFARKPI SIIDLIVVVA SMIVLCVGSK GQVFATSAIR 232
fisKCNQ1 QALANKTLFW MELVLVMFFG VEYVVRLWSA GCRSKYVGIL GRLRFARKPI SVIDLIVVVA SIIVLAFGSN GQVFATSAVR 196

froKCNQ1 GIRFLQILRM LHVDRQGGTW RLLGSVVFIH RQELITTLYI GFLGLIFSSY FVYLAEKDAI DSSGEYQFGS YADALWWGVV 298
humKCNQ1 GIRFLQILRM LHVDRQGGTW RLLGSVVFIH RQELITTLYI GFLGLIFSSY FVYLAEKDAV NESGRVEFGS YADALWWGVV 308
mouKCNQ1 GIRFLQILRM LHVDRQGGTW RLLGSVVFIH RQELITTLYI GFLGLIFSSY FVYLAEKDAV NESGRIEFGS YADALWWGVV 307
chiKCNQ1 GIRFLQILRM LHVDRQGGTW RLLGSVVFIH RQELITTLYI GFLGLIFSSY FVYLAEKDAV NDSGETEFGS YADALWWGVV 312
fisKCNQ1 GVRFLQILRM LHVDRQGGTW RLLGSVVFIH RQELITTLYI GFLGLIFSSY FVYLAEKDAV DDHGNSGFGS YADALWWGVV 276

froKCNQ1 TVTTIGYGDK VPQTWIGKTI ASCFSVFAIS FFALPAGILG SGFALKVQQK QRQKHFNRQI PAAASLIQTA WRCYAAENPD 378
humKCNQ1 TVTTIGYGDK VPQTWVGKTI ASCFSVFAIS FFALPAGILG SGFALKVQQK QRQKHFNRQI PAAASLIQTA WRCYAAENPD 388
mouKCNQ1 TVTTIGYGDK VPQTWVGKTI ASCFSVFAIS FFALPAGILG SGFALKVQQK QRQKHFNRQI PAAASLIQTA WRCYAAENPD 387
chiKCNQ1 TVTTIGYGDK VPQTWIGKTI ASCFSVFAIS FFALPAGILG SGFALKVQQK QRQKHFNRQI PAAASLIQTA WRCYAAENPD 392
fisKCNQ1 TVTTIGYGDK VPQTWIGKTI ASCFSVFAIS FFALPAGILG SGFALKVQQK QRQKHFNRQI PAAASLIQAS WRCFALLNPD 356

froKCNQ1 SATWKIYIRK QSRNHHLMSP SPKPKKSAMV KKKKIRTERD EGST--DKML NIPHITYDHV AD-------- ---------- 438
humKCNQ1 SSTWKIYIRK APRSHTLLSP SPKPKKSVVV KKKKFKLDKD NGVTPGEKML TVPHITCDP- PE-------- ---------- 449
mouKCNQ1 SATWKIYVRK PARSHTLLSP SPKPKKSVMV KKKKFKLDKD NGMSPGEKMF NVPHITYDP- PE-------- ---------- 448
chiKCNQ1 SSTWKIYIRR PARNYHLLSP SPKPKKSVMV KKKKFKLDKD NGPSSPDKML TVPHITYDHV TD-------- ---------- 454
fisKCNQ1 SATYKLFVKR -----NLSSS GSSPKLKVKM RRKMKISDRN NGQNSP---- AVPSITYDSF DDGRDSRQET LTSLQQSVIS 427

froKCNQ1 ---------D RKNDGYSVES YENTVRKP-- FGFLDPSTGP FI-RTSSFTD DLDMEGDT-- LLTPITHISE LKEHHRAAIK 504
humKCNQ1 ---------E RRLDHFSVDG YDSSVRKS-- PTLLEVSMPH FM-RTNSFAE DLDLEGET-- LLTPITHISQ LREHHRATIK 515
mouKCNQ1 ---------D RRPDHFSIDG YDSSVRKS-- PTLLEVSTPH FL-RTNSFAE DLDLEGET-- LLTPITHVSQ LRDHHRATIK 514
chiKCNQ1 ---------D KKPD-FCFDT YENSVKKS-- PTFLDVNTGP FI-RTNSFAD ELDLEGET-- LLTPITHISQ LREHHRAAIK 519
fisKCNQ1 DGTNTTRRYE RAPSWNSLSS FQFSTPPATK PGVFEVSSRP TLQRSSSIAD DMETEPEREI VLIPVAHVSQ LRDSHRAAIR 507

froKCNQ1 VIRRMQYFVA KKKFQQARKP YDVRDVIEQY SQGHLNLMVR IKELQRRLDQ SLGKPSLFLS VSDKVKDKGI NTIGSRLNRV 584
humKCNQ1 VIRRMQYFVA KKKFQQARKP YDVRDVIEQY SQGHLNLMVR IKELQRRLDQ SIGKPSLFIS VSEKSKDRGS NTIGARLNRV 595
mouKCNQ1 VIRRMQYFVA KKKFQQARKP YDVRDVIEQY SQGHLNLMVR IKELQRRLDQ SIGKPSLFIP ISEKSKDRGS NTIGARLNRV 594
chiKCNQ1 VIRRMQYFVA KKKFQQARKP YDVRDVIEQY SQGHLNLMVR IKELQRRLDQ SIGKPSLFIS VSEKSKDRGN NTIGARLNRV 599
fisKCNQ1 VIQRMYYFVA RKKFQQARKP YDVRDVIEQY SQGHLNLMVR IKELQRRLDH SLGKQSLFQT SSERLKDKGT NTIGSRLNRM 587

froKCNQ1 EDKVTQMDHK LNLITDMLHH LLTNQ----- --------QG SQSIRTPHRS NSLNSENHPS RNTLPTYEQL NVPRMTQDNI 651
humKCNQ1 EDKVTQLDQR LALITDMLHQ LLSLHGGSTP GSGGPPREGG AHITQPCGSG GSVDPELFLP SNTLPTYEQL TVPRRGPDEG 675
mouKCNQ1 EDKVTQLDQR LVIITDMLHQ LLSMQ----- -QGGPTCNSR SQVVAS-NEG GSINPELFLP SNSLPTYEQL TVPQTGPDEG 667
chiKCNQ1 EDKVTQMDQK LNLITEMLHR LVSSHQRD-- -QGNNRSSQR ---------G NSVNSDLFIP NNTLPTYEQL TVPERNEDDI 667
fisKCNQ1 DEKITHMDRT LNSIAESLNL MLARERRGDL ARGKEQRSTM RRQSAT---- --------FS LSVLDSSEQL STT-TAIHED 654

froKCNQ1 S 652
humKCNQ1 S 676
mouKCNQ1 S 668
chiKCNQ1 S 668
fisKCNQ1 S 655
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S0 S1 S2 S2-3 linker S3 S4 S4-5 linker S5 pore S6 HA HB HC

conservation

Low High

▲ missense long QT mutaions

○ CaM interaction residues

Potential ATP binding residues