

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extr regi
E9Q3L2	PI4KA_MOUSE	Mus musculus	Phosphatidylinositol 4-kinase alpha	24.474581	NaN	S233;S259;S260;S262;S263;S265;S268;S432;S1439	33300544	MAAAGARGGGGGGGGGGGSSGS SSSSTRGRFYFNTVLSLARS LAVQRPASLEKVQKLLCMCPVDFH GIFQLDERRRDAVIALGIFL IESDLQHKDCVVPYLLRLLR GLPKVYVVEESTARKGRG NLPVAESFSFCLVTLSDVACR DPSLRDEILEAILQVLHVLG MCGALEIQEKEYLCKYAI PCLIGISRSFGRYNSSE SLLSKLFPKVSPhSLRIP EEELEGVRRRSFNDFRSIL PSNLLTVCQEGTLKRR TSSVSSISQVSPERGIP PPSPPGGSAFHYFEASCL PDGTALEPEYFSTISS FSISPLFNGITYKEFCIP LEMLRELLNLVKKIVEE PVLKSLDAIVAGVMEAN PSADLYYTFSDPLYLTM FKMRLRDTLYYMKDLPT SFVKEIHDFVLEQFNMS QGELQKILHDADRIHSE MSPLKLRCCANAACVDL MVWAVKDEQGAENLCI KLSEKLQSKTSSKVIIA HLLPICLQGLGRLCER FVSVHVTPLSRDFLVI PSPVLVKLYKHSQYHT VAGSDIKISVTNEHSE STLNVLPGKKNQPSMY EQLRDAIDNICRCLKAG LTVDPVIVEAFLASLN RLYISQESDKDAHLIP DHTIRALGHIAVALRDT PKVMEPIQLIQKQFCQ PPSPLDVLIIDQLGCL VITGNQYIQEVWNL FQQISVKASSVVSAT KDYKDHGYRHC SLAVINALANIAANI QEEHLVDELLMNLLE FVLQGLEGRASERASE KGPALKASSAGNLG VLIPIVIAVLRRLRPP IKAERLQKLFDRF WLYSVLMGFAVEG SGLWPEEWYEG VCEIATKSPLLT FPSKEPLRSVLQYN SAMKNDVT PAELSELRSTI NLLDPPEVSALIN KLD FAMSTYLLSVYR LEYMRVLRSTDP DRFQVMFCYFED KAIQDKKSGMMQ CVIADKVFDAFLN MMAEKAKTKENE EELERHAQFLLV NFNHIIHKRIR RVADKYL SGLVDFKFP HLLWSGT VLVKMLDILQ TLSLSLSA DIHKDQ PYYDIPDAPYRIT VPDTYEAR ESIVKDF AARCGMILQ EAMKWAPT VTKSHLQ EYLNKHQ NVWSGLSQHT G LAMATESIL HFAGYNKQNT TLGATQL TERPACV KKDYSNFMAS LNLNRNY AGEVHGMIR FSGATGQMS DLNKM MVQDLTAL DSHPHOHT QAMFKLT AMLISSKDC DPQLLHHL CWGPLRM FNEHGMETA LACWEWLLAG KNGVEV PFMREMAGA WHMTVEQK GLFSVETKEAD PLAASEASQ RPCPEVTP HYIWD FLVQRFEIA KYCSSDQ VEIIFS SLLQRSMS LNI GGARGSMNR HVAAI GPRFKLL TLGLSLL HADVV PNATIRN VLREKI YSTAFDY FSCPPK FPTQGEK RLRE DISIMIK FWTAMFSD KKYLTAS QLVPPD NQDTRS NLDITVGS RQQAT QGWINTY PLSSGM STISKK SGMSKK TNRGSQL HKYMKRR TLLSLL LATEI ERLITWY NPLSAPE LE LDQAGENS V ANWRSKY ISLSEK QWKDN VNLAW SI SPYLAVOL PARFKNTE AIGNEV TRLV RLD PGAVSDV PEAIKFLV TWHTIDAD APELSH VLCWAPT DPPTGLS YFSM YPPHPL TAQYGV KVLRSF PPDAILFYI PQIVQAL RYDKMGY VREILWAA AK SLLAHQ FIWNMKT NIYLD DEEGHQ KDPDIG DLEQLVE EITGSL SGP AKDFYQRE FDFFNK ITNVS AIKPY PKGDERKKA CLSAL SEVKVQ PGCYL PSNPEATV LDIDYK SGT PMQSA AKAPY LAK FKVKRC GVSELE KEGLQ CRS DAEDE CFSQEA DGKKIC WQAAI FKVGD DDCR QDMLAL QIIDL FKNIF QLVGLD LDFV PYRVVAT APGCGV IECPD CTSRD QL GROTD FGM YDYFTR OYGD DESTLAF Q QARYNF FIRS MAAYS LLLFLL QIKDRH NGNIML DKKG HIIHID FGF MFESS P GGNLG WEPDI KLTDE MVMIM GGKMEATP FKF WMEMC VRGYL AVR PYMD	False	False	2.759	3.189	1.403	1.737	1.886	4.339	1.26

