

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ext reg
P42356	PI4KA_HUMAN	Homo sapiens	Phosphatidylinositol 4-kinase alpha	22.903221	S553	S230;S256;S257;S259;S260;S262;S265;S429;T1154;S1436	38253038	MAAAPARGGGGGGGGGGCSGSGS SASRCFYFNTVLSLARS LAVQRPASL EKVQKLLCMCPVDFHGFQDERRR DAVIALGIFLIESDLQHKDCVVPYLLR LLKGLPKVYVVEESTARKGRGALPV AESFSFCLVTLSDVAYRDP SLRDEI LEVLLQVLHVLLGMCQALEIQDKEY LCKYAIPLIGISRAFGRYSNMEESL LSKLFPKIPPHSLRVLEELEGVRRRS FNDFRSILPSNLLTVCQEGTLKRKTS SVSSISQVSPERGMPPSPGGSFAFH YFEASCLPDGTALEPEYFSTISSSFS VSPLFNGVTYKEFNIPLEMLRELLNL VKKIVEAVLKS LDAIVASVMEANPS ADLYYTSFSDPLYLTMFKMLRDTLYY MKDLPTS FVKEIHDFVLEQFNTSQG ELQKILHDADRIHNELSPLKLRCA NAACVDLMVWAVKDEQGAENLCIK LSEKLSKTSKSVIIAHLPLLICLQGG LGRLCERFPVVVH SVTPSLRDFLVIP SPVLV KLYKYSQYHTVAGNDKISV TNEHSESTLNVMSGKKSQPSMYEQ LRDIAIDNICRCLKAGLTVDPVIVEAF LASLSNRLYISQESDKDAHLIPDHTI RALGHIAVALRDTPKVMEPIQLQQ KFCQPPSLDVLIDQLGCLVITGNQ YIYQEVWNL FQQISVKASSVVYSATK DYKDHG YRHCSLAVINALANIAANIQ DEHLVDELLMNLEL FVQLGLEGR ASERASEKGPALKASSAGNLGVLP VIAVLRRLPPIKEAKPRLQKLRDFD WLYSVLMGF AVEGSLWPEEWYEG VCEIATKSPLLTFPSKEPLRSVLQYN SAMKNDTVTPAELSELRSTIINLLDP PPEVSALINKLDFAMSTYLLSVYRLE YMRVLRSTDPDRFQVMFCYFEDKAI QKDKSGMMQCVIAVADKVFDAFLN MMADKAKTKENEEERHAQFLLV NFNHIIHKRIRRVADKYL SGLVDKFP HLLWSGTVLKTMLDILQTL SLSLSA DIHKDQPYDIPDAPYRITV PDTYEAR ESIVKDF AARCGMILQEAMKWAPT TKSHLQEYLNKHQNWVWV SGLSQHTG LAMATESILHFAGYNKQNTTLGATQ LSERPACVKKDYSNF MASLNLNRNY AGEVYGMIRFSGTTGQMSDLNKMM VODLHSALDRSH PQHYTQAMFKLT AMLISSKDCDPOLLHHL CWGPLRM FNEHGMETALACWEWLLAGKDGVE VPFMREMAGAWHMTVEQKFGLFSA EIKEADPLAASEASQPKCPPEVTPH YIWIDFLVQRFEIAKYCSSDQVEIFSS LLQRSMSL NIGGAKGSMNRHVA AIG PRFKLLTGLSLLHADVVP NATIRNV LREKIYSTAFDYFSCPPKFTQGEKR LREDISIMIKFWTAMFSDKKYLTASQ LVPPDNQDTRS NLDITVGSRQATQ GWINTYPLSSGMSTISKKSGMSKKT NRGSQLHKYMKRRRTLLLSLLATEIE RLITWYNPLSAPELELDQAGENSVA NWRSKYISLSEKQWKD NVNLAWSIS PYLAVQLPARFKNTEAIGNEVTRLVR LDPGAVSDVPEAIKFLVTWHTIDADA PELSHVLCWAPTDPPTGLSYFSSMY PPHPLTAQYGVKVLRSFPPDAILFYIP QIVQALRYDKMGYVREYILWAASKS QLLAHQFIWNMKTNIYLD EEGHQK DPDIGDLLDQLVEEITGSLSGPAKDF YQREFDFFNKITNVAIHKPYKGD RKKACLSALSEVKVQPGCYLPSNPE AIVLDIDYKSGTPMQSAAKAPYLAKF KVKRCGVSELEKEGLRCRSDSEDEC STQEADGQKISWQAAIFKVGDDCRQ DMLALQIIDL FKNIFQLVGLDLFVFP YRVVATAPGCGVIECIPDCTSRDQLG RQDFGMYDYFTRQY GDESTLAFQQ ARYNFIRSM AAYSLLLFLLOIKDRHN GNIMLDKKGHIIHDFGFMFESSPG GNLWEPDIKLTDEMVMIMGGKME ATPFKWFMEMCVRGYLAVRPMYMDA	True	True	4.526	3.367	1.601	2.063	2.109	5.0	4.28

