	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellula region
0	Q96L96	ALPK3_HUMAN	Homo sapiens	Alpha-protein kinase 3	20.532046	S42;S238	S228;S1222	36240223;37217939;38253038	MGSRRAPSRGWGAGGRSGAGGDGE DDGPVWIPSPASRSYLLSVRPETSLS SNRLSHPSSGRSTFCSIIAQLTEETQ PLFETTLKSRSVSEDSDVRFTCIVTG YPEPEVTWYKDDTELDRYCGLPKYEI THQGNRHTLQLYRCREEDAAIYQAS AQNSKGIVSCSGVLEVGTMTEYKIH QRWFAKLKRKAAAKLREIEQSWKHE KAVPGEVDTLRKLSPDRFQRKRRLS GAQAPGPSVPTREPEGGTLAAWQEG ETETAQHSGLGLINSFASGEVTTNG EAAPENGEDGEHGLLTYICDAMELG PQRALKEESGAKKKKKDEESKQGLR KPELEKAAQSRRSSENCIPSSDEPDS CGTQGPVGVEQVQTQPRGRAARGP GSSGTDSTRKPASAVGTPDKAQKAP GPGPGQEVYFSLKDMYLENTQAVRP LGEEGPQTLSVRAPGESPKGKAPLR ARSEGVPGAPGQPTHSLTPQPTRPF NRKRFAPPKPKGEATTDSKPISSLSQ APECGAQSLGKAPPQASVQVPTPPA RRRHGTRDSTLQGQAGHRTPGEVLE CQTTTAPTMSASSSSDVASIGVSTSG SQGIIEPMDMETQEDGRTSANQRTG SKKNVQADGKIQVDGRTRGDGTQTA QRTRADRKTQVDAGTQESKRPQSDR SAQKGMMTQGRAETQLETTQAGEKI QEDRKAQADKGTQEDRRMQGEKG MQGEKGTQSEGSAPTAMEGQSEQE VATSLGPPSRTPKLPPTAGPRAPLNI ECFVQTPEGSCFPKKPGCLPRSEEA VVTASRNHEQTVLGPLSGNLMLPAQ PPHEGSVEQVGGERCRGPQSSGPVE AKQEDSPFQCPKEERPGGVPCMDQ GGCPLAGLSQEVPTMPSLPGTGLTA SPKAGPCSTPTSQHGSTATFLPSEDQ VLMSSAPTLHLGLGTPTQSHPPETM ATSSEGACAQVPDVEGRTPGPRSCD PGLIDSLKNYLLLLLKLSSTETSGAG GESQVGAATGGLVPSATLTPTVEVA GLSPRTSRRILERVENNHLVQSAQT LLLSPCTSRRLTGLLDREVQAGRQAL AAARGSWGPGPSSLTVPAIVVDEED PGLASEGASEGEGEVSPEGPGLLGA SQESSMAGRLGEAGGQAAPGQGPS AESIAQEPSQEEKFPGEALTGLPAAT PEELALGARRKRFLPKVRAAGDGEA TTPEERESPTVSPRGPRKSLVPGSPG TPGRERRSPTQGRKASMLEVPRAEE ELAAGDLGPSPKAGGLDTEVALDEG KQETLAKPRKAKDLLKAPQVIRKIRV EQFPDASGSLKLWCQFFNILSDSVL TWAKDQRPVGEVGRSAGDEGPAAL AIVQASPVDCGVYRCTIHNEHGSAST DFCLSPEVLSGFISREEGEVGEEIEM TPMVFAKGLADSGCWGDKLFGRLV SEELRGGGYGCGLRKASQAKVIYGL EPIFESGRTCIIKVSSLLVFGPSSETS LVGRNYDVTIQGCKIQNMSREYCKIF AAEARAAPGFGEVPEIIPLYLIYRPAN NIPYATLEEDLGKPLESYCSREWGC AEAPTASGSSEAMQKCQTFQHWLY QWTNGSFLVTDLAGVDWKMTDVQI ATKLRGYQGLKESCFPALLDRFASS HQCNAYCELLGLTPLKGPEAAHPQA KAKGSKSPSAGRKGSQLSPQPQKKG LPSPQGTRKSAPSSKATPQASEPVTT QLLGQPPTQEEGSKAQGMR	None	None	None	None	None	None	None	None	None