

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
B1AUX2	B1AUX2_MOUSE	Mus musculus	NaN	24.791867	NaN	NaN	34678516;37507081	MASAVSPANLPAVLLQPRWKRVVG WSGVPVRRPHGHRAVAIKELIVVFG GGNEGIVDELHVYNTATNQWFIPAV RGDIPPGCAAYGFVCDGTRLLVFGG MVEYKYSNDLYELQASRWKRL KAKTPKNGPPPAPRLGHSFSLVGNK CYLFGGLANSEDPKNNIPRYLNDL YILELRPGSGVVAWDIPITYGLPPPR ESHTAVVYTEKDNKSKLVYGGMS GCRLGDLWTLDIETLTWNKPSLSGV APLPRSLHSATTIGNKMYVFGGWVP LVMDDVKVATHEKEWKCTNTLACL NLDTMAWETILMDTLEDNIPRARAG HCAVAINTRLYIWSGRDGYRKAWNN QVCKDLWYLETEKPPPARVQLVR ANTNSLEVSWGAVATADSYLLQLQK YDIPATAATATSPTPNPVPSPANPP KSPAPAAAAPAVQPLTQVGITLVPQA ATAPPSTTTIQVLPVPGSSISVPTAA RTQGVPAVLKVTGPOATTGTPLVTM RPASQAGKAPVTVTSLPASVRMVVP TQSAQGTVIGSNPQMSGMAALAAA AATQKIPSSAPTIVLSPAGTTIVKTV AVTPGTTLPATVKVASSPVMVSNPA TRMLKTAQAQVTSVSSAANTSTRPI ITVHKSGTVVAQQAQVVITVGGV TKTITLVKSPISVPGGSALISNLGKVM SVVQTKPVQTSAVTQASTGPVTQII QTKGPLPAGTILKLVTSADGKPTTIT TTQASGAGTKPTILGISSVSPSTTKPG TTTTIKTIPMSAITQAGATGVTSSPGI KSPITHTTKVMTSGTGAPAKIITAVPK IATGHGQQQVTVVLKGAQPGQPTI LRTVPMGGVRLVTPVTVSAVKPAVTT LVVKGTTGVTLGTVTGTVSTSLAGA GAHSTSASLATPITTLGTIATLSSQVI NPTAITVSAAQTTLTAAGGLTPTIT MQPVSQPTQVTLITAPSGVEAQPVH DLPVSILASPTTEQPTATVTHADSGQG DVQPGTVTLVCSNPPCETHETGTTN TATTTVANLGGHPQPTQVQFVCDR QETAASLVTSAVGQQNGNVVRVCS NPPCETHETGTTNTATTATSNMAGO HGCSNPPCETHETGTTSTATTAMSS MGTGQQRDRRTTNTPTVVRITVAP GALERVQGTVKPQCQTQQTNMTT TMTVQATGAPCSAGPLLRPSVALES GSHSPAFLVQLALPSVRVGLSGPSSK DMPTGRQPETYHTYTTNTPTTTRSI MVAGELGAARVPTSTYESLQASSP SSTMTMTALEALLCPSATVTQVCSN PPCETHETGTTNTATTSNAGSAQRV CSNPPCETHETGTTHTATTATSNNGG AGQPEGGQPPASGHPCETHQTSTG TTMSVSVGLIPDATSSHGTLESGL VVAVPTVTSQAGSTLLASFPTQRVCS NPPCETHETGTTHTATTVTSNMSSN QDPPPAASDQGEVASTQGDSTNITS ASAITTSVSTLPRAVTTVQSTPVPG PSVFNISLTTETPGALNSEVPIPATI TVTIANTEETSDMPFSAVDILQPPEEL QVSPGPRQLPPRQLQSASTPLMG ESTEVLASQTPELQAAVDLSSTGDP SSGQEPITSAVVATVVVQPPPTQSE VDQLSLPQELMAEAQAGTTLMVTG LTPPEELAVTAAAAAAAQAAATEEAQA LAIQAVLQAAQAVMAGTGEPMDTS EAAAAVTQAEGLHLSAEGQEQATT IPIVLTQOELALVQQQQQLQEAQA QAQQQHHLPTALAPADSLNDPSIE SNCLNELASAVPSTVALLPSTATESL APSNTFVAPQPVVASPAKMQAAATL TEVANGIESLGVKPDLPSPSKAPVK KENQWFDVGVKGTSMVTHYFLPP DDAVQSDDDSGTVPDYNQLKKQEL QPGTAYKFRVAGINACGRGPFSEISA FKTCLPGFPGAPCAIKISKSPDGAHL	None	None	None	None	None	None	None		

