	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	extracellular region
0	B1ATC3	B1ATC3_MOUSE	Mus musculus	NaN	25.775171	NaN	NaN	34678516	MEEKKKKKQEDKKKKEGAQKKAAD QKTKVPELTKTCSSQPQPAGTSPSTS TSTISSGSNGKRASACGQQPAASRYL PREVPPRFRQQEQKQLLKRGQPLPT GGLTSLNSAQAAGPAGASPPPLPGA GAQQHPSKLQQDLGHSGLVDHYEN SHWGQHPSYRSEANCSWDKVIIDRT EPEVWPSIPVTETESASECPTDTDSA SNCGSENSSMATGSAQSSFPSHLKK TNGSHGTNGALVQSPSNQSALGAG GTNGNGGVARVWGVATSSSSGLAH CSVGGGDGKMDNMIGDGRSQNCW GASNSNAGINLNLNPNANPAAWPV LGHEGTVATGNPSSICSPVSAIGQN MGSQNGNPVGALGAWGNLLPQESA EPQTSTSQNVSFSVQPQNLNTDGPN NTNPMNSSPNPINAMQTNGLPNW GMAVGMGAIIPPHLQGLPGANGSSV SQGSGSGGEGMGSSVWGLSPGNPA TGSTNCGFSQGNGDTVNSALSAKQ NGSSSAVQKEGNGGNAWDSGPPAG PGILAWGRGSGTNGIGNIHSGAWGH PSRSSSNGVNGEWGKPPNQHSSSDI SGKGSTGWDSASAASQTPALQPGSE HMNSWAKATSSGTTASEGSSDGSG NHNEGSTGREGTGEGRRRDKGVLD QGHIQLPRNDLDPRVLSNSGWGQT PVKQNTAWEFEESPRSERKNDNGT EAWGSIATQPSNSGGKTDGSIMNST NTSSVSGWVSSPPAAVPANTSWGDS NNKAPSGPGVWGDSISSTAVNNAAA TKSGHAWSGTVNQEDKSPTWGEPQ KPKSQNWGDGQRANPAWSTGAGD WADSSSVLGHLGDGKKNGSGWDAD GNRSGSGWNDATRCGTSGWGSGT NAKVNPGTNWGESLKPGPQQNWA HKPQDNNVSNWGGAASVKQTGTG WIGGPLPVKQKDSSEATGWEEPSPP SIRRKMEIDDGTSAWGDPSTYNNKT VNMWDRNNPVIQSSTTAPATPTTPT SSSTTHRAETPPSHQAGTQLNRSPL LGPVSSGWGEMPSVHSKAENSWGE PSSPCTLVDNGTAAWGKPPSSGSGW DHPAEPVVPFGRASAPAAAPALCKP ASKSMQEGWGSGADEMNLGTSQW EDEDGDMWNNAASQESSSSCSSW GNTSKKGLQKGMKTPGKQDEAWIM SRLIKQLTDMGFPREPAEEALKSNS MNLDQAMSALLEKKVDMDKRGLG MTDYNGMVTKPLGCRPPISKESSMD RPTFLDKLTLSFSNQDGGLVEEPTTS PFLPSPSLKLPLSNSALPSQALGGVA SGLGMQNLNSSRQIPSGNLGVFGN SGAAQARTMQQPPVQPLNSSQPSLR AQVPQFLSPQVQAQLLQFAAKNIGL SPALLTSPINPQHMTMLNQLYQLQL AYQRLQIQQQMLQAQRNVSGPMRQ QEQQVARTITNLQQQIQQHQRQLAQ ALLVKQPPPPPPPPHLSLHPSAGKSG MESFPPPPQAPGLPDLQTKEQQSSP NTFAPYPLAGLNPNMNVNSIDMSS GLSVKDPSQSQSRLPQWTHPNSMG NLSSAASPLDQNPSKHGAIPGGLSIG PPGKSSIDDSYGRYDLIQNSESPASP PVAVPHSWSRAKSDSDKISNGSSIS WPPEFHPGVPWKGLQNIDPENDPD VTPGSVPTGPTINTTIQDVNRYLLKS GGKLSDIKSTWSSGPASHTQASLSH ELWKVPRNTTAPTRPPPGLANPKPS STWGTSPLGWTSSYSSGSAWSTDTS GRTSSWLVLRNLTPQIDGSTLRTLCL QHGPLITFHLNLTQGNAVVRYSSKE EAAKAQKSLHMCVLGNTTILAEFAG EEEVNRFLAQGQALPPTSSWQSSSG	None	None	None	None	None	None	None	None	None

									GSQPRLGTSGSTHGLVRSDTAHWN TPCLSGKGSSELLWGGVPQYSSSLW GPPSAEDARVIGSPTPLNTLLPGDLL SGESI									