

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q0VGY8	TANC1_MOUSE	Mus musculus	Protein TANC1	22.019087	S202	S60;S63;S64;S204;S267;S462;S1436;S1463;S1665;S1673;S1674	22645316;34418053	MLKAVLKKSREGGKGSKKEAGGDF GSETPALSSSGDSPVNSLSTTEDTYR VSLAKGVSMSPSSPLLPROSLLTQS RSNKKSPGPVRKPKYVESPRVPGDP VMIPFGEGSKPSEPSATEAKADNEP SCSPAAQELLTRLGFLLEGIPSATH ITIEDKNEAMCTALSQGISPCSTLTS STASPSTDSPCSTLNSCVSKTAASKS PCETISSPSTLESKDSGIIATITSSSE NDDRSGSSLEWNRDGLRLGVQKG VLHRRADNCSPVAEEETTGAESV LPKAEPSAGDGPVYPQSSGSLIMPR PNSVAATSSTKLEDLSYLDGQRNAP LRTSIRLPWHNTAGGRAPEVKARFA PYKPQEILLKPLLFEVPSITTDVSVFG RDWLFHQIEENLRNTELAENRGAV VVGSVGFGKTAISKLVALSCHGSRM RQIASSSPSLSPKSSDPTQDLPGTPL LSPSSSTSALSVRTTPAGPGTADSQR PREDAVKYLASKVVAYHYCQADNTY TCLVPEFVHSIAALLCRSHQLAAYRD LLIKEPQLQSMLSLRSCVQDPVAAFK RGVLEPLTSLRNEQKIPEEEYIILIDG LNEAEFHKPDYGDTLSSFITKIIPKFP TWLKLIVTVRANFQEIISALPFVKLSL DDFPDNKDIHSDLHAYVQHRVHSS QDILSNISLNGKADAALISKVSSHLLV LRLSGSYLYLKLTLDLFQRGHLVIKS ASYKVPVSLSELYLLQCNMFMFTQ SAFDRALPILNVALASLHPMTDEQIF QAINAGHIQGEQGWFDFQQRMEAL SCFLIKRRDKTRMFCHPSFREWLWV RADGESTAFLCEPRNGHALLAFMFS RQESKLNRRQTMELGHHILKAHIFK GLSKKTGVSSSHLQALWIGYSTEGLS AALASLRNLYTPNVKVSRLILGGAN VNYRTEVLNNAIPILCVQSHLGHEEV VTLLLEFGACLDGMSSENGMNALCY AAAAGHMKLVCLLIKKGARVDHLDK KGQCALVHSALRGHSDILQYLLNCE WSAGPPQPGLRKSQALQALQALAAA SMGHSSVVQSLLGMAEEHEIEVNG TDTLWGETALTAAGRKVEICELL ERGAAVSRANRRGVPLFCAARQGH WQVVRLLDRGCDVNLSDKQGRTP LMVASCEGHLSTVEFLLSKGAALSS LDKEGLSALSWACLKGHRAVVQYLV EEGAEIDQTDKNGRTPLDLAAFYGD AETVLYLVEKGAVIEHVDHSGMRPL

										DRAIGCRNTAVVVTLLRKGAKLGNA AWAMATSKPDILIILLQKLVEEGNV MYKKGKMKEEAAQRYQYALRKFPRE GLGEDMRPFNELRVSLYLNLRCRR KTNDFGLAEFASKALELKPKSYEAF YARARAKRNSRQFLAALADLQEAVK LCPNNQEIKRLLARVEEICKQLQRN QQQKQQGPPAPANDSDNEEDAPA SSLKDFPIEEAEEEDTSSQEEISP TPRSQPPPSVSPYIRNLQEGLQSKG RSASPQSRAGISKSLRETVAQSGLV MQPTKQAQIVKTNQHLGSGQSSMR NSSTKIQVSSQNPPSPMPGRVSAA PAVSRNQHLEGTGPFTAGTGCGHFG DRLGASQSLQLQRSESGTAYPLPSK VKAERLLAHASVAVDMAPPNQQGP VSCSDVRHPASLSSSGSSGSPSSSIK MSSSTSSLTSSSSVSDGFKVQGPDS RIRDKGTQVQGGTAEHRPRNTPFM GIMDKTARFQQSNPPNRSWHCPV AEGLLTNTATAAGLQSNSEKPTLKP GGYCSQAKPCSVPLSMGVHNGAQ VKELEENKCQIPALCQDNRITKGPV HLYPEGVSKQPLHVSTEAHRSHLTS AKPKRSFIESNV
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