

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
A2A690	TANC2_MOUSE	Mus musculus	Protein TANC2	21.40691	S1943	S169;S238;S294;S400;S1446;S1462;S1534;S1549;S1583;S1726;S1828;S1831	22645316;34678516;35822049	MFRNSLKMLLTGGKSSRKNRSSDG GSEPPDRRQSSVDSRQSRSGQGGI STESDCAFEPDYAVPPLPVSEGDVEQ ELGPPPSVDEAANTLMTRLGFLLEGE KVTEVQPSDQYSMEVQDENQTSAIT QRISPCSTLTSSTASPPASSPCSTLPP VSTNAAAKDCSYGAVTSPTSTLESRD SGIIATLTNYSNMERTKYVGEKSKE LGSGGNLKPWQSQKSSMDSCLYRV DENMAASTYSLNKIPERNLETVLSQ SVQSIPLYLMRPNSVAATSSAHLED LAYLDEQRHTPLRTSLRMPRQSLSG ARTQQDLRVRFPYRPPDISLKPLLF EVPSITTESVVFGRDWWVFHEIDAQLQ SSNASVNQGVVIVGNIGFGKTAISR LVALSCHGTRMRQIASDSPHASPXH VDANRELPLTQAPSAHSSITSGSCPG TPEMRRRQEEAMRRLASQVVAYHY CQADNAYTCLVPEFVHNVAALLCRS PQLTAYREQLLREPHLQSMLESLRSC VQDPMAFRRGVLEPLENLHKERKI PDEDFIILIDGLNEAEFHKPDYGDITV SFLSKMIGNFPSWLKLVTVRTSLQE ITKLLPFHRIFLDRLEENEIDQDLQ AYILHRIHSSSEIQNNISLNGKMDNT TFGKLSHLKTLTSLQSYLYLKLTFDL IEKGYLVLKSSSYKVVPSLSEVYLLQ CNMKFPTQSSFDRVMPLLNVAVASL HPLTDEHIFQAINAGSIEGTLEWEDF QQRMENLSMFLIKRRDMTRMFVHP SFREWLIWREEGKTKFLCDPRSGH TLAFAWFSRQEGKLNRRQQTIELGHH ILKAHIFKGLSKKVGVSSEIQLGLWIS YSTEGLSMALASLRNLYTPNIKVSRL LILGGANINYRTEVLNNAIPILCVQSH LGYTEMVALLLEFGANVDASSEGL TPLGYAAAAGFLSIVVLLCKKRAKVD HLDKNGQCALVHAALRGHLEVVKF LIQCDWTMAGQQQGVFKKSHAIQQ ALIAAASMGYTEIVSYLLDLPEKDEE EVERAQINSFDSLWGETALTAAGR GKLDVCRLLLEQGAAVAQPNRRGAV PLFSTVRQGHWQIVDLLLLTHGADV MADKQGRTPLMMAASEGHLGTVDF LLAQGASIALMDKEGLTALSWACKL GHLSVVRSLVDNGAATDHADKNGR TPLDLAAFYGDAEVVQFLVDHGAMI EHVDYSGMRPLDRAVGCNRTSVVV TLLKKGAKIGPATWAMATSKPDIMII LLSKLMEEGDMFYKKGKVKKEAAQR YQYALKKFPREGFGEDLKTRELKV

								SLLLNL SRCRRKMNDFGMAEEFAT KALELKP KSYEAYARARAKRSSRQF AAALEDLKEAIKLC PNNREIQRLLM RVEEECRMQQQQQQPPPPPPQP PQELPEEETEPEPQHEDIYSVQDIFE EEYLEQDVENV SIGLQTEARPSQGLP VIQSPSSPAHRDSAYISSSPLGSHQ VDFRSNSSV GSPTRQGYQSTSPAL SPTHQNSHYRSP PHTSPA HQGASY RFSPPPVG GQSKEYSP PPSPLRRGP QYRASPPAESMSVYRSQSGSPVRYQ QETNVSQ L PGRPKSPLSKMAQRPYQ MPQLPVAVPQQGLRLQPAKAQIVRS NQPSSAVHSSTVIPTGAYGQVAHSM ASKYQSSQ GDMGVSQSRLVYQGSIG GIVGDGRP VQH VQASLSAGAICQHG GLTKEDLPQR PSSAYRGGMRYSQTP QIGRSQSAS YYPVCHSKLDLERSSSQ LGSPDVSHLIRRPISVNPNEIKPHPP TPRPLLHSQ SVGLRFSPSSNSISSTS NLTPTRFPSSSIQQMEIPLKPAYDRS CDELSPVSPTQGGYPSEPTRSRTPF MGIIDKTARTQ QYPHLHQQRNRTWA VSSVDTVLSPTSPGNLPQPEFSFSPPS SISNIAFYNKTNNAQNGHLEDDYY SPHGMLANGSRGDLLERSVQASSYP DVKVARTLPVAQAYQDNLYRQLSRD SRQGQTSPIKPKRPFVESNV
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