

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
Q924A2-2	CIC_MOUSE	Mus musculus	Protein capicua homolog	38.223321	NaN	S774;S778;S1053;S1080;S1184;S1269;S1338;S1343;S1403;S1604;S1625;S1644;T2192;S2195;S2253;S2275;S2280;S2284;S2291;S2299;T2300;S2304;S2311;S2497	40997131	MKPMKKACPLAGSASGSKSPPATR AKALRRRGAGEGDKPEEEEEQAQPE QAGPEEAEEGEEEEAEERDPGAEQTH PELQPNPTPLGLTEDPKGDGEAGR WEPSSLRKTATFKSRAPKKKYVEEH GTGNVGVVGAPEERERTPEDASALG VPPRPPTSTRSSSTDTASEHSADLED EPPEACGPGWPSTGTSEGYDLRQL RSQRVLARRGDGLFLPAVVRQVRRS QDLGVQFPDRLTFYEGVPGGGVD VVLVDVTPPGALMVGTAVCTCPEPG VAAAYREGVVVEVATKPAAYKVRLLSPG PSSHAGPPGTLPOAQQLHREPEEA VWVTRSSLRLLRPPWEPGALLRKHP AGPEEEQAEPGALPPCPSSVEPKQP EDAEVSNISFGSNLGRCEEGEEKH PPSLGTPVLLPLPPQLLSPPPKSPAF GGGRPSEQPSPCQEGSQGSRSSS VASLEKGAAPAAARTPLTAAQKY KKGDVVCTPNGIRKFKNGKQWRRR CSRDGCMKESQRRGYCSRHLSMRT KEMEGLADSGPGGTGRPAGVAARE GSTEFDWGDSTRDSEASSVAARGD SRPRLVAPADLSRFEFDECEAAVML VSLGSSRSGTSPFSFVSTQSPFSPAP SPSPSLPFGFRPANFSPINASPVIQRT AVRSRHLSASTPKAGVLTTPDLGPHP PPPAPRERHSSGILPTFQTNLFTTVP SPGRRKTELLPHPGTLGASGAGGGG AAPDFPKSDSLDSGVDVSVSHTPPST PAGFRAVSPAVFSSRSRQPSPLLLL PPAGLTSDPGFSVRRVPAVORDSPVI VRNPDVPLPSKFPGEVGTAGEARAG GPGRSECRETVPVPGVASGKPLPPPL PAPVPITVPPAAPTAVAQPMPTLGLA SSPFQPVAFHPSAALLPVLVSSYP SHPAPKKEVIMGRPGTVWTVNVEPRS VAVFPWHSVFLAPSQDPSPVQPS EAQPPASHPVASNQSKEPAESAAVA HEQPPGGTGGADPGRPPGAVCPESP GPGPPLTLGVDPGKSLPPTTEEAP GPPGEPRLDSETESDHDDAFLSIMS PEIQLPLPPGKRRQSLSALPKERDS SSEKDRSPNKREKDHIRRPMAF MIFSKRHRALVHQRHPNQDNRTVS KILGEWWYALGPKEKQKYHDLAFQV KEAHFKAHPDWKWCNKDRKKSSE AKPASLGLAGGHKETREERSMSETGT AAAPGVSELLSVAAQTLSSDTKVP GSGPCGAERLHAVGAPGSARPRAFS HSGVHSLDGGVEVDSQALQELTQMV SGPASYSGPKSPQYGAAGSFAAPGE GGTLATSGRPPLPSRASRSQRAASE DMTSDEERMVICEEEDDDVIADDS FGTTDIDLKCKERVTDSESGDSSGE DPEGKGFGRKVFSPVIRSSFTHCR PTLDPEPPGPPDPPAAFSKGYGTPPS SSSSPASTSVSVTSFSLGSGTFKTQ ESGQGSTAVPLRPPPGAGGPATPSK ATRFPPDTSATFRKRKRPESVGSLEAP GPSVIAAPPSSGGNLLQTLVLPSSKE DREGTRVPSAPAPLAYGAPAAPLCR PAATMVTNVVRPVSSSTPVIASKPFP TSGRAEASSNDIAGARTEMGTGSRV PGGSPMGVSLVYSDKKSAAAATSPA PHLVAGPLLGTVGKAPATVTNLLVGT PGYGAPASPAVQFIAQAGPAGSATPAG SGASTGSGPNPVPVPLGILQFGALGKA GGITQVQYILPTLPQQLQVAPAPAPA PGTKAAAPSGPAPTTISIRFTLPPGTST NGKVLAAAPTAGIPILQSVPSAPPPK AQSVSPVQATPSGSAQLLPGKVLVLP LAAPSMVSRGGGAGQPLPLVSSPFS VPVQNGAQQPSKIIQLTPVPVSTPSG LVPLSPATMPGPTSQPKVLLPSST RITYVQSAGGHTLPLGTSSACSQTGT VTSYGTSSVALGFTSLGSPGPAFVQ PLLSGQAPLLAPGQVGVSPVPSQPLP PACTASGGPVITAFYGPSPAPTSAPL	True	False	1.246	4.206	1.447	0.906	False	1.267	1.234

