

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	pl m
Q924A2	CIC_MOUSE	Mus musculus	Protein capicua homolog	38.223321	S772;S1638;T1643;S1851;S1852;S1855;T1872;S1877;T1878;S1880;S1896;S2044	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	MKPMKKACPLAGSASGSKSPATR AKALRRRGAGEGDKPEEEEEAQPE QAGPEEAEEGEEEAERDPGAEGTH PELQPNPTPLGLEDPKGDGEAGR WEPSSLRKTATFKSRAPKKKYVEEH GTGNVGVVGAPEERERTPEDASALG VPPRPPTSTRSSSTDTASEHSADLED EPPEACGPGWPSTGTSEGYDLRQL RSQRVLARRGDGLFLPAVVRQVRRS QDLGVQFPGDRALTFYEGVPGGGVD VVLVDVTPPPGALMVGTAVCTCVEPG VAAYREGVVVAVATKPAAYKVRVLSG PSSHAGPPGTLRQAQQLHREPEEA VWVTRSSLRLLRPPWEPGALLRKHP AGPEEEQAEPCGALPPCPSVPEKQP EDAESVNSIFGSNLGTRCEEKKEKH PPSLGTPVLLPLPPQLLSPPKSPAF GGPGRPSEQPSPCQEGSQGGRSSSS VASLEKGAAPAAARARTPLTAAQOKY KKGDVVCTPNGIRKFKNGKQWRRL CSRDCMKESQRRGYCSRHLSMRT KEMEGLADSGPGGTGRPAGVAARE GSTFDWGDSTRDSEASSVAARGD SRPRLVAPADLSRFEFDECEAAVML VSLGSSRSGTSPSPVSTQSPFPAP SPSPPLFGFRPANFSPINASPVIQRT AVRSRHLASSTPKAGVLTPPDLGPHP PPPAPRERHSSGILPTFTQNLTFIVPI SPGRRKTELLPHPGTLGASGAGGGG AAPDFPKSDSLDSGVDSVSHPTPST PAGFRAVSPAVPFRSRQPSPLLLL PPAGLTSDDPGPSVRRVPAVQRDSPVI VRNPDVPLPSKFPGEVGTAGEARAG GPGRSCRETPVPPGVASGKPLPPPL PAPVPIVPPAAPTAVAQPMPTLGLA SSPFQPVAFHPSAALLPVLVPSVYP SHPAPKKEVIMGRPGTVWTVNVEPRS VAVFPWHSVLPFLAPSQDPSPVQPS EAQQPASHPVASNQSKPEAESAAVA HEQPPGGTGGADPGRPPGAVCPESP GPGPPLTLGGVDPGKSLPPTTEEEAP GPPGEPRLDSETESDHDADFLSIMS PEIQLPLPPGKRRTQSLALPKERDS SSEKDGSRPNKREKDHIRPMNAF MIFSKRHRALVHQHRPNQDNRTVS KILGEWWYALGPKEKQKYHDLAFVQ KEAHFKAHPDWKWCNKDRKSSSE AKPASLGLAGGHKETRERSMSETGT AAAPGVSELLSVAQTLSSDTKVP GSGPCGAERLHAVGAPGARPRAFS HSGVHSLDGGEVDSQALQELTQMV SGPASYSKPKSPQYVAPGSAAPGE GGTLATSGRPPLPSRASRSQRAASE DMTSDDEERMVICEEGDDVDIADDS FGTTDIDLKCKERVTDSESGDSSGE DPEGNKGFRKVFSPVIRSSFTCHR PTLDPEPPGPPDPAAFSKGYGTPPS SSSSPASTSVSVSTFSLGSGTFFKTQ ESGQGSTAVPLRPPPPGAGPATPSK ATRFPPDTSATFRKRKRPESVGSLEAP GPSVIAAPPSSGGNLLQTLVLPSSKE DREGTRVPSAPAPPLAYGAPAAPLCR PAATMVTNVVRPVSTPVPIASKPFP TSGRAEASSNDIAGARTEMGTGSRV PGGSPMGVSLVYSDKKSAAAATSPA PHLVAGPLLVGTVGKAPATVNTLLVGT PGYGAPASPAVQFIAQGAPGSATPAG SGASTGSGPNPVLGILQPGALGKA GGITQVQYILPTLPOQLQVAPAPAPA PGTKAAAPSGPAPTTSIRFTLPPGTST NGKVLAAAPTAGIPILQSVSPAPPK AQSVSPVQATPSGSSAQLLPGKVLVP LAAPMSVVRGGGAGQPLPLVSSPFS VPVQNGAQQPSKIIQLTPVPVSTPSG LVPLSPATMPGPTSQPQVLLPSSST RITYVQSAGGHTLPLGTSSACSQTGT VTSYGTSSVALGFTSLGPSGPAFVQ PLLSGQAPLLAPGQVGVSPVSPQLP PACTASGGPVITAFYGPSAPTSAPL GPPSQAPPSLVYVATSTTPPAATILP	True	False	1.246	4.206	1.447	0.906	False	1.7

KGPPASATATPAPTSPFPSATGSMTY
SLVAPKAQRPSKAPQKVKAASIPV
GSFESGTTGRPGSTPRQSSDSGVAR
EPAAPESELEGGQTPPAPPPPTETWP
PTARSSPPPLPAEERPGTKGPETAS
KFPSSSSDWRVPGLGLESRGEPPTP
PSPAPATGPSGSSGSSEGSRAAG
DTPERKEVTSSGKMKVRPPPKKT
FDSVDKVLSEVDFEERFAELPEFRPE
EVLPSPTLQSLATSPRILGSYRKKR
KNSTDLDAPEDPTSPKRKMRRRSS
CSSEPNTPKSAKCEGDIFTDRGTGTE
TEDVLGELEYKVPYSSLRRTLDQRR
ALVMQLFQDHGFFPSAQATAAFQAR
YADIFPSKVCLQLKIREVRQKIMQAA
TPTEQPPGAEAPLPGPPPTGMAATPV
PTPSPAGGPDPTSPGSDSGTAQVAPP
LPPPEPGPGQGWEGAPQSPPPS
GPSTAATGR