

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
Q924A2	CIC_MOUSE	Mus musculus	Protein capicua homolog	17.741191	S772	S774;S778;S1053;S1080;S1184;S1269;S1338;S1343;S1403;S1604;S1625;S1644;T2192;S2195;S2253;S2275;S2280;S2284;S2291;S2299;T2300;S2304;S2311;S2497	35822049;34678516;29187734	MKPMKKACPLAGSASGSKSPATR AKALRRRGAGEGDKPEEEEEAQPQE QAGPEEAEEGEEEAERDPGAEGTH PELQPNPTPLGLTEDPKGDGEAGR WEP SLRKTATFKSRAPKKKYVEEH GTGNVGVVGAPEERERTPEDASALG VPPRPPTSTRSSSTDTASEHSADLED EPPEACGPGWPSTGTSEGYDLRQL RSQRVLARRGDGLFLPAVVRQVRRS QDLGVQFPGDRALTFYEGVPGGGVD VVLDTVPPPGALMVGTAVCTCVEPG VAAYREGVVVEVATKPAAYKVRLSPG PSSHAGPPGTLPAQQT LHREPEEA VWVTRSSLRLLRPPWEPGALLRKHP AGPEEEQAEPGPALPPCPSSVEPKQP EDAEVSNISFGSNLGRCEEGEEKH PPSLGTPVLLPLPPPQLLSPPPKSPAF GGPGRPSEQSPCQEGSQGGSRSSS VASLEKGAAPAARARTPLTAAQQKY KKGDVVCTPNGIRKKFNGKQWRRL CSR DGCMKESQRRGYCSRHLSMRT KEMEGLADSGPGGTGRPAGVAARE GST EFDWGD ETSRDSEASSVAARGD SRPRLVAPADLSRFEFDECEAAVML VSLGSSRSGTPSFSPVSTQSPFSPAP SPSPSPLFGFRPANFSPINASPVIQRT AVRSRHLSASTPKAGVLTTPDLGPHP PPPAPRERHSSGILPTFQTNLTFTVPI SPGRRKTELLPHPGTLGASGAGGGG AAPDFPKSDSLDSGVDSVSHTPTPST PAGFRAVSPAVPFSRSRQPSPLLLLP PPAGLTSDPGPSVRRVPAVQRDSPVI VRNPDVPLPSKFPGVGTAGEARAG GPGRSCRETPVPPGVASGKPLPPPL PAPVPITVPPAAPTAVAQPMPTLGLA SSPFQPVAFHPSPAALLPVLVPSSYP SHPAPKKEVIMGRPGTVWTVNVEPRS VAVFPWHS LVPFLAPSQDPDSVQPS EAQQPASHPVASNQSKEPAESAAVA HEQPPGGTGGADPGRPPGAVCPESP GPGPPLTLGGVDPGKSLPPTTEEEAP GPPGEPRLDSETESDHDDAFLSIMS PEIQLPLPPGKRRTQLSALPKERDS SSEKDG RSPNKREKDHIRPMNAF MIFSKRHRALVHQRHPNQDNRTVS KILGEWYALGPKEKQKYHDLAFQV KEAHFKAHPDWKWCNKDRKKSSE AKPASLGLAGGHKETRERSMSETGT AAPGVSEL SVAAQTLLSSDTKVP GSGPCGAERLHAVGAPGSARPRAFS HSGVHSLDGGEVDSQALQELTQMV

SGPASYSGPKPSPQYGAPGSFAAPGE  
GGTLATSGRPPLLPSRASRSQRAASE  
DMTSDEERMVICEEGDDDDVIADDS  
FGTTDIDLKCKERVTDSESGDSSGE  
DPEGNKGFGRKVFSPVIRSSFTHCR  
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ATRFPPTDSATFRRKRPEVGSLEAP  
GPSVIAAPPSGGNLLQTLVLPSSKE  
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TSGRAEASSNDIAGARTEMGTGSRV  
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LVPPLSPATMPGPTSQPQKVLLPSST  
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VTSYGPTSSVALGFTSLGSPGPAFVQ  
PLLSGQAPLLAPGQVGVSPVSPQLP  
PACTASGGPVITAFYPGSPAPTSAPL  
GPPSQAPPSLVYTVATSTTPPAATILP  
KGPPASATATPAPTSPPFSATGSMTY  
SLVAPKAQRPSPKAPQKVKAASIPV  
GSFESGTTGRPGSTPRQSSDSGVAR  
EPAAPESELEGQPTPPAPPPPTETWP  
PTARSSPPPLPAEERPGTKGPETAS  
KFPSSSSDWRVPGLGLESRGEPPTP  
PSPAPATGPSGSSGSSEGSSGRAAG  
DTPERKEVTSSGKKMKVRPPPLKKT  
FDSVDKVLSEVDFEERFAELPEFRPE  
EVLPSPTLQSLATSPRILGSYRKKR  
KNSTDLDAPEDPTSPKRKMRRRSS  
CSSEPNTPKSAKCEGDIFTFDRTGTE  
TEDVLGELEYEKVPYSSLRRTLDQRR  
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YADIFPSKVCLQLKIREVRQKIMQAA  
TPTEQPPGAEAPLPGPPPTGMAATPV  
PTPSPAGGPDPTSPGSDSGTAQVAPP  
LPPPEPGPGQPGWEGAPQSPPPS  
GPSTAATGR