

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	entry
Q96RKO	CIC_HUMAN	Homo sapiens	Protein capicua homolog	39.564278	S12;S13;S16;S530;S534;S535;S538;S541;S542;S543;S566;T583;S649;S665;S734;T738;T752;T831;T880;S891;T967;S972;T973;S975;S982;T985;S991;S1001;T1002;T1143;T1149;S1154	S776;S780;S1055;S1082;S1186;S1271;S1340;S1345;S1405;S1609;S1663;S1648;T2200;S2203;S2260;S2282;S2287;S2291;S2298;S2306;T2307;S2311;S2318;S2504	40136647;35132862;35289036;32574038;30059200;41350704;39302247;28657654;27655845;40307207;23301498;38665916;35254053;33214551;34019948;31492838;29237092;39534244;37340703;20305658;35138101;39531497;30397120;21740066;34725712;32119511	MKPMKKAAGTGLSGPGSGSKSPATR AKALRRRGAGEGDKPEEEDDEAQQP QPQSGPEEAEEEGEEEAERGPGAEG PPELHPGDPAAPGAEDPKGDGEAG RWEPSLSRKATTFKSRAPKKKYVEE HGAGSSGVAGAPEERVRTPEEASGL GVPPRPPTSTRSSSTDTASEHSADLE DEPAEACGPGWPVPGSTSGSYDLRO LRSQRLARRGDGLFLPAVVRQVRR SQDLGVQFPGDRLTFYEGVPGAGV DVLADATPPGALVVGTAVCTCEP GVAAYREGVVVEVATKPAAYKVRLS GPSSQPLGSLPQPPQLHREPEE AVWVARSRLRLRPWPEPTMLRKP PTGPEEEQAEPCATLPPCPAALDPKQ PEDAEVSKISFGGNLGTCEEGEEK HPPALGTPALLPLPPQLSPPKSP AFVGPGRPGEQSPSCQEGSGGSR SSVASLEKGTAPAAARATPLTAAQK YKGDVVCTPSGIRKFKNGKQWRRL CSRDCMKESSRRGYCSRHLMSRT KEMEGLADSGPGGAGRPAVAARE GSTFDWGDSTRDSEASSVAARGD SRPRLVAPADLSRFDFDECEAAVML VSLGSSRSSTPSFSPVSTQSPFPAP SPSPSPLGFRPANFSPINASPIQRT AVRSRHLASATPKAGVLTTPDLGPH PPPAPRRHSSGILTFQTNLFTVPI SPGRRKTELLPHGALGAPGAGGG AAPDFPKSDSLDSGVDSVSHPTTPST PAGFRAVSPAVPFSRSRQPSPLLLL PPAGLTSDPGSPVRRVPAVQRDSPI VRNPVPLPSKFPGEVGTAGEVRAG GPRGCRETPVPPGVASGKPLPPP LPAPVITVPAAPTAVAQMPAFGL ASSPFQPVAFHPSAALLPVLVPSY TSHPAKKEVIMGRPGTVWTVNVEPR SVAVFPWHSVLPFLAPSQDPSPVQ SEAQQPASHPVASNQSKPAESA AHERPPGGTGSADPERPPGATCPES PGPGPHPLGVVESGKGPPTTEEE ASGPPGEPRLDSETESDHDDAFSL MSPEIQLPLPPGKRRTQSLALPKER DSSSEKDRSPNKREKDHIRRP AFMIFSKRHRALVHQHNPQDNRT VSKILGEWWYALGPKEKQYHDLAF QVKEAHFKAHPDWKCNDKRRKSS SEAKPTSLGLAGGHKETRERSMSET GTAAPGVSELLSVAQTLSSD APGSSSCGAERLHTVGGPGSAR FVSHSGVHSLDGGGEVDSQALQELTQ MVSGPASYSYGPSTQYGA PGEAGALAAATGRPPLPTRASRSOR AASEDMTSDERMVICEEGDDVI ADDGFGTTDIDLKCKERVTDSESGD SSGEDPEGKNGFGRKVFVIRSSFT HCRPPLDPEPPGPPDPPVAFGKGYG SAPSSASSPASSASAATSFLGSG TFKAQESGQGSTAGPLRPPPPGAGG PATPSKATRFPLMDPATFRKRPE GGLEPPGPSVIAAPPSSGGNQLTLV LPPNKEEQEGGARVPSAPAPSLAY GAPAAPLSRPAATMVTNVVRVPSST PVPIASKFPPTSGRAEASPNDTAGAR TEMGTGSRVPGGSLGSLVSDKK SAAATSPAPHLVAGPLLTGTVGKAPAT VTNLLVGTGYPGAPAPPVQVIAQGA PGGGTTAGSGAGAGSGPNPVPPLGI LQPGALGKAGGITVQYILPTLPQQL QVAPAPAPAGTKAAAPSGPAPTST RFTLPPGTSTNGKVLAAATAPTPGIPIL QSVPSAPPKQSVSPVQAPPVGGSA QLLPGKVLVPLAAPSMSVRRGGGAGQ PLPLVSPFVSPVQNGAQPSSKIIQLT PVPVSTPSGLVPLSPATLPGPTSQP QKVLPSSTRITYVQSGGHALPLGT SPASSQAGTVTSYGTSSVALGFTSL GPSGPAFVQPLLSAGAPLLAPGQV GVSPVPSQLPPACAAPGGPVITAFY SGSPAPTSSAPLAQPSQAPPVLYTV	True	False	2.21	4.89	2.04	1

