

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	pl m
Q4AC94	C2CD3_HUMAN	Homo sapiens	C2 domain-containing protein 3	15.664604	T57;T708;S715	S466;S728;S1891;S2114;S2132	30379171;37217939;38253038	MKQRKGGSSGSRGRKKRGLSDISP STSLPLVVEGQLRCFLKLTVNRVWIK IAKPPTCVLVRVVRWWGETSDGTLFC PRDALQTEPKAVRRTTTRYAIRCGPKQ FTSYLTDMAVLVLEVITKLDGLPIGR VQINGLAQLSPTHQINGFFTVSSTS KKLGELQVSLALEPLSETYDSYHPLP TTDMTENVLLSKQGFRENTEPSSIQ FQVPSRPRDIHTIKIDGKELAANSSR STTPRGKDHVCFEAENPDTIKDSSFQ LQHSLNSGQSLESVTLKGRAPRKQM SLLNSSEFQPIRTVAKSHSDSCILS SNNLPTKDLLSALLEQGNKLRNAM VISAMKSSPETSMLLDQVHPPINED SLRASTQIRAFSRNRFKDIEDHLLP STENTFWRHDTKADTRAIQLLGSA ELSQGNFWDGLGSPDPSPGSDVY CISELNDPQYDQSLLENLFYAPKSD TSISDFLSEEDDIVSKKISQSTALAR SSKVLSSDHKLKRSAGKRNRLV EQQMLSETPEDAQMTLSVDRLALL GRTHSVRIIETMGVPPDSPQMPGK KSYAGPPPKVTTAKKRTFFVEYHFPV GFSEGLGKTALITEVVRASSKITD GKVKFQQRFFVFPVQFGGPMIEHWW NSNLTFQIYVKKTPQKKPEVIGSVL SLRAVIQSELLSFSQDLPVQENGO SPFGPLKVTMELITDNKDFGINTKL SGNTHYTPLCAPTSPNKALPELNQD MTCTKNPQNLNQIHEETAKKAQNL VLPNRKSPSPVAPHPSTFVATPASH NLVNQTNQTTKESALLLHVLLMVPD GKDFISGESEKQSPCNVYLNCKLFS TEEVTRSVIAWGTTQPVFNFVQVIPV SLSSKYLRLKNNVMVIETWNKVRV PGQDKLLGLVKPLPHQFYMVSKDAK ISRLLDAQYPVAVDSYMPVIDVFS GHQNGSLRVFLAMGSSNQIMALQR LKNEEGLTLPFSPRPAHFLDQPTAAS VAMAEDRGNGLMEHCFEIHIEVMK GLAPLQATVWGEADCYVQYFFVQVH SQSSVLKGFLENGITLKPFRATT LCVPDPFNFSEHHHSLLLPAEVPVQ RLLLSAFSAQGLVPGGGVQFEIWC YYYPNVDRQKAVAGKTLPLSRICAMV TTQHREDDVGIQTFNLPLTPRIENRKE LRNQSSGLLDVGLRYRRSPRTAEGV LAARTVSVQIIRACGLQAAAKALAE REPALQFSATVGVNASVTTHLSFLP QGEQRRTHPVACSFCEPFSHHVEFT CNLVTQHCSGEACFLAELEFAEVIF AVYHENTKASDIIIESCKEYLLGVV KVPTKELLIKRSGITGWYPILPEDGG LPHGLELMQKIVGGLELSISFTHRG DRERVLEAAEHLGWSFENS�KDFVR MDEGEFATVTIPTRLWLPPIHCVLLA GHNHIIHKNTCYLRYKFDHEAFWT PLKKPKESVNKKQIMVTFKASKRAE VTRGPSLLWYFREERLEIQVWRAYG NDSVERPHQTDWIGSAYVDLARLG ERSARTLTVSGVYPLFGRNASNLSG AALRVHVLSLSSHLEPTHELDMS DCSSHSESEQLPRRNDEVQLSPPEV ISCHQKSPASTQVPCSTTAEVRLTQ EGPADLDGTFVAVSILVERAMHLSLK GSPLTERKVSIPSCCVSFAADESSP VYTQVVENTDSPIWNFQQQSRLSKE LLLDPOQTLVFKVWHKGDEERVIGF ASVDLSPLLSGFQFVCGWYNITDFS GECQGIKAVVSPLESLIHFKEERQA RRGVETSKSLIPIYSPFSPASDTYAA FSSHMARQTLDLQLAHASSKELDFSS PGRSDTTRSQASRHEEHVQNIIRRFH ESLHLQGEAPLPCDDKLTTSPLSSQT SILTSLRKNLSELDQIQRYFRQKLT PFLPLSPQTQTAISQHQESCRDHLGP GASSLDPGSQCILEKSSNLVLQVSSL ITDLQITITRDSQAALSSHRARSRSNK ATLTPDAQDTEALQERCCTMPDEPLV RAPDKGTDSPSPPLEETSNGRML	None	None	None	None	None	None	N	

									HESLRHAVPITRMQSEDETEAGPAY					
									SDEDEEDIIIEPRTLNEITTVDKTS					
									WSSVISDTSEVISQPDEVQREGPSC					
									PSPGFPCREELMVKSSFLSSPERAV					
									NPHLPRQGSPSQSLVACECEASKAR					
									VGGESASANPOPIPCPTLSGAQSQSST					
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									ATSELGDSADSFKKLPLNLASQSRR					
									ENHKGPPIDSSDIRQRQVTTGSETST					
									KQSLLLPGPIVVPNFFLPQOLEASL					
									RMLLSATLPPAATTDQDKSEATRG					
									ALSQRPCRPRPNSLPLNLPEEETLRI					
									ARIFSSQYSQKD					