

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q7Z407	CSMD3_HUMAN	Homo sapiens	CUB and sushi domain-containing protein 3	18.9764	T410;S411;T2911	NaN	37217939;38253038	MKGIRKGESRAKESKPWEPGKRRCA KCGRDLFILMKMGKSGFTFWNLV FLLTVSCVKGFYITCGGTLKGLNGTI ESPGFPYGYPNGANCTWVIIAEERN RIQIVFQSFALLEEYDYLSDYDGHPH PTNFRTRLTGPHLPPVSTKSVFSL RLTSDFAVSAHGFKVYEEELQSSSC GNPGVPPKGVLYGTRFDVGDKIRYS CVTYILDGHPQLTCIANSVNTASW DFPVPICRAEDACGGTMRGSSGISS PSFPNEYHNNADCTWTIVAEPGDTI SLIFTDFQMEEKYDYLEIEGSEPTI WLSGMNIPPIISNKNWLRHLHFVTD SNHRYRGFSAPYQGSSTLTHTTSTG ELEEHNRITTTGAIIVASTPADVTVSS VTAVTIHRLSEEQRVQVTSLRNSGL DPNTSKDGLSPHPADTQSTRRRPRH AEQIERTKELAVVTHRKKAIIDFKSR GFKLFPKDNNSNKFSLNEGGIKTAS NLCPPDPEPENKRGSDFSLGSTV QFSCDEYVLQGAKSITCQRIAEVFA AWSDRHPVCKVKTCGSNLQGPSGT FTSPNFPFQYDSNAQCVWVITAVNT NKVIQINFEEFDLEIGYDTLTIGDGG EVGDPRTVLQVLTGSFVPLIVSMSS QMWLHLQTDSEVSGVGFKNYKEI EKESCGDPGTPLYGIREGDGFSNRD VLRFCQGFELIGEKSIVCQENNO WSANIPICIFPCLSNFTAPMGTVLS DYPEGYGNLNCIWTIISDPGSRHIL SFNDFDLESQDFLAVKDGDSPESPI LGTFTGAEVPSHLTNSHILRLEFQA DHSMSGRGFNITYNTFGHNECPDP GIPINARRFGDNFQLGSSISVICEEG FIKTQGTETITCILMDGKVMWSGLIP KCGAPCGGHFSAPSGVILSPGWPGY YKDSLNCWEVIEAEPGHSKITFERF QTELNVDVLEVHDGPNLLSPLLGSY NGTQVPQFLFSSNFYLLFTDINSR SNNGFKIHYESVTNTYSCLDPGIPV HGRRYGHDFSIGSTVSFSCDSGYRL SHEEPLLECKNHWWSHPLPTCDAL CGGDVRGPGSTILSPGYPEFYNSLN CTWTVDVTHGKGVQFNHFTFHLED HHDYLLITENGSTQPLARLTGSDLP PTINAGLYGNFRAQLRFISDFISYE GFNITFSEYNLEPCEDPGIPQYGSRI GFNFGIGDTLTFSCSSGYRLEGTSEII CLGGRRVWSAPLPRCVAECGASAT NNEGILLSPNYPLNYENNHECIYSIQ VQAGKGINISARTFHQAQGDVLKIYD GKDKTTHLLGAFTGASMRGLTSSST SNQLWLEFNSDTEGTDEGFQLVYTS FELSHCEDPGIPQFGYKISDQGHFA GSTIYGCNPGYTLHGSSLLKCMGTGE RRAWDYPLPSCIAECGRFKGESSG RILSPGYPPYDNNLRMWMIEVDP GNIVSLQFLAFDTEASHDILRVWDG PPENDMLLKEISGSLIPEGIHSTLNIV TIQFDTFYISKSGFAIQFSSSVATAC RDPGVPMPNGTRNGDREPQDVTVF QCDPGYELQGEERITCIQVENRYFW QPSPPVCIAPCGGNLTGSSGFILSPN FPHYPHSRDCDWITVNVADYVISLA FISFSIEPNYDFLYYDGPDSNSPLIG SFQDSKLPRIESSNTMHLAFRSD GSVSYTGPHLEYKAKLRESCFDPGNI MNGTRLGMDYKLGSTVYYCDAGY VLQGYSTLTCIMGDDGRPGWNRALP SCHAPGSRSTGSEGTVLSPNYPKN YSVGHNCVYIAVPKEFVVFQVVF QTSLHDVVEYDGPQSSLLSLS GSHSGESLPLSSGNQITIRFTSVGPIT AKGFHFVYQAVPRTSSTQCSSVPEP RFGRRIGNEFAVGSSVLFDCNPGYIL HGSIAIRCETVPNSLAQWNSLPTCI VPCGGILTKRGTILSPGYPEPYDNN LNCVWKITVEGAGIQVQVVSFATE HNWDSLDFYDGGDNNAPRLGYSYG TTIPHLLNSTSNLNLNFQSDISVSA	False	True	1.255	1.878	1.467	0.846	0.646	4.711	1.435

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