

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q80T79	CSMD3_MOUSE	Mus musculus	CUB and sushi domain-containing protein 3	24.474581	NaN	NaN	33300544	MKGSRKGESRAKESKPREPGTRRCA KCGRLDFILKKMGKSGFTFWNLV FLLTLSCVKGFIYTCGGTLKGLNGTI ESPGFPYGYPNGANCTWVIAEERN RIQIVFQSFALIEEEYDYLSDYDGHPH PTNFRTRLTGFFHLPPTSTKSVFSL RLTSDFAVSAHGFKVYEEELQSSSC GNPGVPPKGVLYGTRFDVGDKIRYS CVTGYILDGHPQLTCIANSVNTASW DFPVPICRAEDACGGTMRGSSGISS PGFPNEYHNADCTWIVAEPGDTI SLIFTDFQMEEKYDYLEIEGSEPPTI WLSGMNIPPIISNKNWLRHLHFVTD SNHRYRGSAPYQSSPLTLTASIGE LEEHIRTATGAIDVASTPADVTVSSV TAVTSHRLEEQRVQVRSLSDSGLD PNTPEDQLSPHQADTQSTSRPRNA EQIERTKELAVVTHRKKKIDFKSRG FKLFPKDNSNKFSLLEGGIKTAS NLCDDPGEPENGKRFSGDFSLGSTV QFSCDEEDYVLQGAKSITCQRIAEVFA AWSDRHPVCKVKTCGSNLQGPSGT FTSPNFPFOYDSNAQCWVITAVNT NKVIQINFEEFDLEIGYDTLTIGDGG EVGDPRTLQVLTGSFVPLIVSMRS QMWLHLQTDSEVGSVGFKNYKEI EKESCGDPGTPLYGIREGDGFSNRD VLRFCQFGFELIGEKSIVCQENNQ WSANIPICIFPCLSNFTAPMGTVLSP DYPEGYGNLNCIWTIISDPGSRIHL SFNDFDLESQFDFLAVKDGSDSPDSP ILGTFTGAEVPSHLTNSHILRLEFQ ADHSMGRGFNITYNTFGHNECPD PGIPINARRFGDNFQLGSSISVICEE GFIKTQGTETITCILMDGKVMWSGPI PRCGAPCGGHFSAPSGVILSPGWPG YYKDSLNCWEVIEAEPGHSIKITFER FQTELNVDVLEVHDGPNLLSPLLGS YNGTQVPPQLFSSSNFYLLFTTNDNS RSNNGFKIHYESVTVNTYSCLDPGIP VHRRRYGHDFSIGSTVSFSCDPGYR LSHEEPLLCEKNHWSHPLPTCDA LCGGDVRGPGSTILSPGYPEFYNSL NCTWTVDVTHGKGVQFNHFTFHLE DHHDYLLITENGSTQPLARLTGSEL PSTINAGLYGNFRAQLRFISDFISISYE GFNITFSEYNLEPCEDPGIQYGSRV GFSFGVGDTLTFSCSLGYRLEGSSEI ICLGGRRVWSAPLPRCVAECCGASA TNNEGILLSPNYPLNYENNHECIYSL QVQAGKGINISARTFHLAQGDVLKIY DGKDKTTHLLGAFTGASMRGLTSS TSNQLWLEFNSDSEGTDEGFQLVYT SFELSHCEDPGIPQFGYKISDQGHFA GSTIHYGCNPGYTLHGSSLLKCMTE RRAWDYPLPSCIAECGGRFKGESSG RILSPGYPPFYDNLRCMWMIEVDP GNIVSLQFLAFDTEASHDILRVWDG PPENEMLLKEVSGSLIPDGIHSTLNI VTIQFDTDFYISKSGFAIQFSSSVATA CRDPGVPMNGTRNGDGREPGDTVV FQCDPGYELQGGQERITCIQVENRYF WQSPPPVCIAPCGGNLTGSSGFILSP NFPHPYPHSRDCDWTISVNTDYVIS LAFISFISIEPNYDFLYYDGPDSNSPL IGSFQDSKLPERIESSNTMHLAFRS DGSVSYTGHFLEYKAKLRESCFDPG NIMNGTRLGMDYKLGSTVYTYCDAG YVLQGYSTLTCIMGDDGRPGWNRVL PSCHAPCGSRSTGSEGTVLSPNYPK NYSVDHNCVYSIAVPKEFVVFQGFV FFQTSLHDVVEVFDGPTQQSPLLSS LSGSHSGESLPLSSGNQITIRFTSVG PITAKGFHFVYQAVPRTSSTQCSSVP EPRFGRRIGNDFAVGSLVLFECNPG	None	None	None	None	None	None	None		

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