

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
K2N6M0	K2N6M0_TRYCR	Trypanosoma cruzi marinkellei	C-type lectin domain-containing protein	19.946178	NaN	NaN	30984116	MSSFFFLPQSMKALHRRCAQTGEVL WVTLPLLLLVAWATCCCVAVTAQGT SPSPFCPIGWALWPMFEKARDGVS SDDATVWCVPQKVRVAPAEVTEAC AHIFDLRPPRGWSEANRELIPQPFVS HSHEQNLWLQELLSPPFGDLGELVA LGGAAAGFGDIFWWDGMNNVNGVP SYTNFAPSTDWQTHSGCIAMQRDG VWRLVDCKTPQMPFVCAFOWNALN ETNTSSNDGDNSSDGGADATTNSS TGDNPVDVQPTRPPVQPPPECLD GWSSYKDKCYRLYAEIDGGERGMN QQAARFCQSIHPHVTTLAVLNAEE NAFLGRLVQDSARDHNYDLAQMEV FIGGIFTARGSVGVWYEDALWYGER DYMLSFPSSPTWPTAKNNLYFNWG VGEPSMSFGCVAVDNNGTWRAVDS RLSLPFVCAYLNDGSKPEVPTAPE SDSASSSVDTGSNTTAPTPTPHQSDL CSDDWVYFAPTNRFCRVLTDRAVSA ADLEQSCGRLLFASDDTIHAATIKS VEESAFVGRVLAEAGLQRLVGVSYI ERGMHGLYLDGTSAWESTLAESLW AVGQPSRDSGCVLDDHTGAWYFPC GTPANAYACAYSAGAVIAPTSTPAPT DVPTTTTTSTSAPEKWPLETRIA SLSGAVHLVVAAGTVGTYTVAGSGG RTDGLLLMFAPDLSEIVAKVGWDEH VKVSPCLWGYKKQEYIFAVMQGVVT VFHPNETMRGRVCSDDGVHYVPA GNITFEVLDVALRGFIPFSSSQEAE EAQGGGSSNESSVIGGNDISFVTRA VGIRLWSSEALQFLFHRRPLGTRAAI CRLRFSSSPDCTSGRYVLFGESLAVV ERERGRGLITYQLANVVPSNGSGLD RLHDPAEDEEQPATEFFVCAAAASIN ALPPQSPNSSASVWSEGNYSYDRSYS SISDTDVLYENEMERNSTSFVSVDG QPMWLYTLIPHLRVHVTTPHVAVRG MWALPPSGFDTSCGVFKPSSFGPSVK TLFLLQFSSPVVFDGEGLEREGMALL LSQKPGNCQRHQPTARSADSSLP PALDTMVAVSTVFFSSRALNGSSVA EQSRVAFMQLNLNHTGMWGTNFT EKRQTWHLCFAYTPLSRFVPLTGFKI IVSRARISLTATHEGYGGDVSSGSDN SSQLNLGVGFSGLLILWGLDVHMMW SPSTISMAEIAFAHSPPGNARFADPT LQCTNTSLFYRQSRSGIFNPQSATN NDLRSSRNFGVTLTEQQQRAAVV VPPGFLNEETTRRMRLCLSVLPFQ NNRRVFIPTSATVDVYPIEVHFIGPYA VRFPIATTDPLTVVEVSENVNELVL PLFGYGLSDYMMLFLSEKPCLSLFD AGETHEEASEACVDCISRMNFTIMR PYDVPPNYRQSNSSRSAAVSGDFFIT LNETHTASEVADRVFGRAREPLFLC LYAPGTRRAVYPLRFKVVRRPYIKSI RSIGAAPLQGEATVVLYASFVDLV VEGFLHEGAAAFVPAVDCSNGTSF LWRSVPVTSAVPSMVIKGDMSGYSV SSKSFSSRYVSLTSTSSWFLSLT QAHTARIGAVEPTDDVIDRFQWCVR YRDADADVDSASDATAPAAAAAED ANSWRRGFVPTGIPYRLVIPRVDGFL FGNSTEKHKRRRTRHPTLGPWERLQ IVGPLIDHTFALGNPLFMFLAEDVVP CKKLKKYFINTNSFDRFITAVNGYAI LPKLLNNTGLFKLCASAIHPERQSSE EGTEAALQFFELKGLRIELVGPVYSV FSLNRTDYVTVEQGGQWTLPIGGSG LSNMVLRFRPIGANCSTPMPDFLD DVIVRNLFEELEKLGALATLFRPDGG DVKRRTDSHYVLERDLIRGLSVQEY MLCFKPRSTPWSMSSDILLNVREH VRRPSRYSYFNADGSEDVVAATALPP	None	None	None	None	None	None	None		

TKIALEWLTNERDTTNIVGAAGREVA  
VALWCRGGKANTSAVVPCGNWRR  
VMFVRPIDDGSDPCFTDFEAIQLDVV  
RGPVYVLDGILTIPRAVSRNVSFYFN  
ATQPWILCLETAPERWRKSIHPLLQL  
QFTTIVVPVGRHFDDASNTTATFF  
GRMGDADISDDRTDLEGNRTLILYV  
EDTSRIFYLNQYGIQRFMRFGSH  
CEEDVLAVDSEGNRSRAELVAVQVE  
LNNTLLYEPLILEDDHGVFLFPSTH  
FANLEARTPMCLSTNGGTSYVKTNL  
SLAILPSRLRRDLPADESHISELAFR  
RTLIVPRMSKGTVSIAELNAHDDNE  
PNSTNYRTDSGGAFVAVTRVLFSSA  
CHNSREGLPIIVVIVPNILTLTEAHR  
VATKGRHLICVQMPREDESSGGSDGG  
NVSDDEDGRTHALAFPTGFFQVLD  
VTVTSVSLHRAIPSDVAEQNGIRHLV  
FCRGNESMTLLVTIESGMEGKETND  
NFDSVDAYSVEEQYINMLNVPGALS  
FFRLAKFRLGRPCNVLDQPEAATV  
TSLSNLTATFANNKVRIWTEGSDA  
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VDGGRHYMSVGISYISVSWAPTLRV  
RLSMGEEEEAEKGMRNQSGFSSMY  
VFEQTNHFGRLLVDARYSTDSSFRD  
TPLIRYLNQFTTDALWSGFLQGVGF  
VSSGELYLPALTIGDAPNESELLFFIN  
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PTTLQVHVSQSTGWLLPIASPCGRSI  
QAGVIVRFVDGNVRSCTPEVDHAY  
VMDAFIMKPREWMGKGVTPILTTL  
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DDVRISFVPVMDVQGPVAVCGTLW  
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RLQSMELFPVTPRTLYHVCYSVDGGI  
SFHPAGDAPPFLQLTILPPTILGLGTE  
NEQRLYNRGGLTTLALRLRLLELD  
SSTPSSDPSMRVTFFAERPPSYH  
HPSLCFIGNGIGTGNGREATGALGA  
LAVAVLRTDLFGEVCNGANLTSVIRA  
GDSESSNPLALPVFLVDVTGCLWD  
PAATTGGTVGADGSRNLTGGGCDGA  
VLRDDWLNNTATLRRAGGLGATSLL  
KGSSSTEYLRRLSTSYLLCTSVDGV  
LFYSANFLLRNESQGDVRESTFSSSL  
ATAVPRESAVPLKNVSRPLVLRVDP  
NINGSYYTRDLAVILQLVVRPRLATV  
PTTLELETSTESLVRFRQRAVAELHI  
DPAIVVRLSNRRMVLPPRAENATV  
SIKYVTYTLSSLTDARVLDGSVEE  
MGTLTPPELLRYANLLRNNDTQT  
SLLSTLLPPAVSVAGLTVRAPYVNF  
TFGTGVDLHAALLQSHSHELKGPFE  
EKMWRARFAAVPHATLVAEIPDDV  
TKRSKGLKWWLVSLLLSIVFVIG  
SIFFYRRYLRRLSTKAQQEERRRR  
MGVEA