

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
V5B673	V5B673_TRYCR	Trypanosoma cruzi Dm28c	NaN	19.946178	NaN	NaN	30984116	MGRLSNAVAESCVAVTEKALKRRLG ITANRAHQSERTVEFAFTASKDRLG EISSALFKEFVQAACGSEQGRTKLGS VDVSVDAQKGLQSVLFTDVVCVHNF RFDELPPDSPAITVAEATYFRYLAK HSDAQAYAVTEFPKCLAAGGGPRLD VIIAGYVLFSLSDDGDEVKLRMYIK NIDEVLGTMCTSSFASVTLPHSWSN LDQLEPHQLVDLLEETQLAISDFWT DSAQDTRARSQVIFLMTTIGSELREY FSKKTAAAGGVFGDSKSAATEMALSC CDDWVNMCRNLTTIDWGAVWGGR FEDLQLRVVCDRLRVVASLRDLVGE MVELLNASGELHFLRKETLWEAME SIDIFQTTAAVEKQWDAALSAFYRRL EPVEHRCAAALRDFFGERNLAPQT ILNEVVKFRQLIRRPVVAKELVSERD ALLAKLNERLQIRLEFEHRSESTED DLFLEDEDRRCTGRFMPGVVNNM IWLRLRGRVEEMIKMCKSLLDLQ NAREFVLAADTLEEIGDYELELYKH WAMDVEDNSHALILDANAPLMDID ANGRVEVNYPERLVQLIREVRFRLG GLRITGEIQRMVVDQGVCFYRNGVSL KQIASTYNSMTKDIIPCTRAMLLEPA LFFENITASGDRKLTWRNVEDAER FIGKLRITASQSLTDANRRLHRLHKEI EAIVVVLFVSDLLRSRERWMGKVHT IREKMEMSGFKNMENWKLFWDVQ LYKAMEYQYQLGLESLHEVVAEMKA DIVYDQETGLAALRPSLEVIRGQYYQ RIKDFMTFPLGFRGCGENEFFKEMP ARNERGIFAVMQHAAQLFKKVQOEL KRFHPLLIIGQCGRNGNPSLEEIVGK TLTEVQHWEQGIRLLKQKGEINGE ELFIKCGCITLCTASIKGTVEDHLYKL SEVLRVTLRRSAENHLRRIDAYLVEV SGSLDSTLTKLDEIGAANVHHAYLVE QRPAMEVEFYHFYKNMMLLQSMAN RAGLDFAKTRDEWDRVMRRLDSE SEMEEQMDKLGVIIEESVKSQK LERFTNQWHELKPKNADSPNAVQF VKDQKEKFKALETEGEECVQCKYF QLEEPDIEPLHDLGRDIEEYALMWS MVGTFNEELGVLRAEPWALRAKLY RFDDLKVVWQEKLEIPNNPITVQIR TLSDSWSRCAPLKFVVRGDFGFTPGH WVELFRLLGTPNATQDTLQFGDILD RYENILRHEMELKKLHSAQGEAQI REALDVRSWGTVNAKFTLCAHPERP GVMILITEWKDLSALSDNQALLSM KESPYFSIFASDANKWEERLACLDE YLRSMNQIQRKWVYLEPIFRRGALP QEQERFARIDKEYLQVMHTIAKDSRI VPLATHKEYKEVLRNVLEQLDRCQR ALNQYLEAKRDSFPRFYFISDDDLLE VLAQSRNPLVIQSHLKKLFMGHGV RFDTQKEHILQIHSLEGETVQLEFPV RITDEVEEWLSKLDVAMKDTLRVHL VRCLEKLDIGAYATQILCTAGMIDFT KKTEEAIRESKVGGLLKLANLQSQL RDLTYTGGSSDVVVVLLKSLIMDLI HNIEVVDTLIRNGVEKETDWLWRKQ LRYLDHNNNCVLRMVDAEFNYSY EYQGNAPKLVHTPLTDRCYLTLTQG MQLGYGGNYPGAGTGKTESVKALG NAMGRQVLVFNCDGIDFKSMGRIF TGLVKCGAWGCFDEFNRLKVDQLS AVSQMIQVIOEALKNGESHCHLLGR DIDVNPAGIFVTMNPAGKRYGGRS KLPDNLKQLFRSVAMSAPDNELIME TILFSEGFENATELAKRTVEVFLAA GLLSYQQHYDWGLRAMKSVMLGG SLIHQYLMDRVGGKVKLTPQDVLQK ECEILKSLRVNTLSKLTFFEDAILFNN	None	None	None	None	None	None	None		

LIADVFPGVPIKEIDYTELHPAIVESIK  
ELKQLQFVESQVQKILQLYEALKQRM  
GVVLVGPGGSGKSTLLRVLRRALQR  
LGVSVPLYVMNPKAMPRTQLLGHM  
DNDTREWFDGVLTEAAKKVVKEEN  
DVRSWIVCDGDIDPEWIESLNSVLD  
DNKLLTMPNGVRIQFGDNVSFLFET  
HSLEFASPATVSRMGIYLSSEEDVNP  
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VMRAWTKPLRPGVYRPFILVGPEGC  
GKTMILLTNLFAGISGTRVATVNCSA  
QTEAIHVIOKQKQTCQMFNTNQGRV  
LRPKEAERLVLLKDMNLPKPKDKYG  
TVQLHSLLQQLILYSGFYDLDLEWIT  
VERVQIVGSMNPPGSMGRYPVAPRF  
LAIVSVLCMSYPSRESMQIYSEFFNI  
MIQSHKLFELPGKGAADIARIMTIV  
YETIAIRCTVDVSSHIFTPRDVTKW  
ALNLLNYSVDIPDAIGYEGRRIFIDR  
LVSPDERTKFAKLIYDNLIFLVGHRA  
GITEKETTYVSWMDVASSRVKNLM  
PPAWMN