

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
V5DUQ0	V5DUQ0_TRYCR	Trypanosoma cruzi Dm28c	DUF2428 domain-containing protein	19.946178	NaN	NaN	30984116	<p> MQKLLFLGNVFFVFAYMSFDYHYH FIYFCLYVRVSCFOQLLAAPRRRTTQ MSEYSTAMRMQQRHRTTEIYPLPE CVLTELTSGIPIICKASTSLOPFAPKA ASIVCREVENMTSVTSSEHRVRCISQ ITGVLENTFMAQRSVTECRVFLRK LAAHFVFPMLHCAVRYLHRAALATL LRTVYVIDELETFCFAAFTAAHIRC WGSGETSERRPTIFGDNAAVLRSEA TLGFKDSVMSWINCIDSTTVVAMP LFPVFASTFFDVLPLLGESLQWV LNASVKCREVGIGNATNGTILGEDL AYVRYGIRVITYTHKFLHLLQDVVW NGDRTHCHLKEDVGKLFSSAVLM LSSPVFPKDVNLGAGLLVSSLLTLRA CVPWLLLEVCRQCGTLDPPTAAAAA KPGVTRIAYTLESLLQSDVRECVELI CSDDHRRARERPAALCALRNILGA LTNNGRFALLKGLLAHLSTPIHGNV DSLGIKLPITPLAGAGTSVEALEV HDIIMPAAEAYCSALQAPDTRFMAIQ TIDSVVRHISSVLNCAEVLHPPSE NETRRGNVRENVQWPHGGKLLTE PKRGLMALCARNAKLTRLNHATE IIMGWDDNTLQVTGPLYDAYNEIL SVHAALRCAALFPSTFETHVLDEDI FDTAEALRRILCIPNERRGKYHALLG ILSVLPVQFSLVKKNFQETASISE VQGLCCFSRMLLSGACNHKVGNI GDVFAKAASLIRHSDNADAHREFLF MQGIIDPLVKSLVSGYAAPPHLSEA ACVSNIVTHMIMPCLKSEEVFIPILLS QLTQALEGKHNSRVNQSVVEIHR ARVVGKDIGAYLQPKSQTFQAILASL QVHETELRYTALGLCVLSTKKAETVK AWQCRMMEWYISTNMYCGGDSVA MRNLLEVYKWMRRLVDSYGNQN NKQKGMAGSETAEQYKELVVDHC VRMVGCLVPOIGENANWCRNLSLE RRVAAMSTYSCLLRNAEFLSEEDV RNLKEQLFPVALIEGLECLSEGWE KARLSAYSILIIYCNHVPDAIFSHRHL GDPTAASAAKAEELLRARTFRKSEGE VLWYVLATHFTPAAKQAAAENPSHE CEKVRDVECEMKLLKEKLSLRLAL GAKGACEFLQLHPLHGHSCLVALLS NAWEIKRDFHLLYEACNLLCCSA VLQTCSSLVGGEPVNSVDDGDVEVD CRGHVFEKDGSYTEDKMRTVVNNT WLSIRTAASAVERVMNLAKVEDLSL PVVREICVYLIESLLRTHKNGVMRKY REALKTVAALLRSRDVAFHSLPRE MLDFLLGPDGVTSSRVARMLRRSQ GLPHAILAVLEADPTVPVFLFPRAM KLLLRVAKGAHVGGDDCQHHLTEE KCRSQRNALNVLKIFIFENKIFASRS VADLEAAFWIAAEGFDDPSWGIRNS SLMLFSAVLPREFVGEHPSTGSGVGN TSLHDIAVRAPRGVAFAYEELVKSST TPVPSLGVFLLQMLSMVTPDPPHL FTNATTSQIADADVSSRIVRAIML CGSSKNLMVRAASAVALTSLVPTSH LETLAEIISNLFQPKNGLNAVHGAL LHLQGFHTFYVGTLLRRNMRKKAMN SSATATVAFVLRNLVVEGLGAPSLAV SSSKLYQACVHCPTIAVTFSLASDA LYYIQSFGLCADNTAPIVNLMRFGVA VYGAVCAPTRSFELARHDHAAVCE NGALFALLVVRLLSLSKEEAEGTEEE NDKLLSFNGNAQVWDTLSQVFTSE SGEYLISCLMYHVSHHTAEKRWPPE ESERTMRQFTLRLHCDPVNAALWM LLRDLSEDSLLQRLPCTRIHMSVH LEYLVLLGNDGGPRSETCEALCKAL EENLLCRMDPQSKRPLQNTVQSW AIRFLGRCCVRHGASSVTLRLILEHY </p>	None	None	None	None	None	None	None	None	

