

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
V5BNT6	V5BNT6_TRYCR	Trypanosoma cruzi Dm28c	NaN	19.946178	NaN	NaN	30984116	MITLHFKNKNNNNNEKEWRRRKE MSESHSMLEPMEAAGAGTRTDCL LTGAMPSTAVICMTSVGEEPGDAS GMTADDDSFPSVAQTSKGLDLFSTN WATASLRSGSSPSPNTVHFPPKPKS ELTKEDFAMPEAVTQRAGFHGGIWR RIQSFSPRQGGYRDLNALSVDLAT MDLERLKKSFLAHAQLFRSDLLEM YKVTGNVAREMRHAERQTEROQRK KQIHRTNPRRTTDSAKLSATALSDLE EGLGGESVASIAEESTTNGLLTESVL FRKEYSSKTRLLCIWLYDRLMEQQ LCDFRNSSSSMKCDTLGGHTNLVA RSFLGSGTKMMMLKLRGPPTPQKL FGFDIFDELSDRLRERDPSSMLAA NMSMDNLPPLPVFVYVFSRAVFRA CYLDRFPKGSFIFSSSSVSPLLTAV NNTSQPGTGTADAARKESTRLAFSA GYSRDDMVQEVSVLLEECRHVVMR FFELFDREQRGFITWSSFTDLLMER VEVQHRLMVVKENSEADVQSDAKV FDEYVLEPPFSPVIRQLGYLGAVTEVR HSHSAIVEGQHDFAVWDSFYSGLI WRKLLVRSADVLFSHRQCAPDEWD AERWAAAADSARNLQQQRKFNRRRI LRHEEGYKHKDMSQLKTMKKSRTG EKGVNAEDNNLSGGTGDGRIDRR AKPSIESALQLYNVSPPELPTYVTLH NDLLLRFNIEQHIWVPEISITVST ETITSMEWCPSSPEGDPTMNWYMF LGTRSGVVFKVDLREILRKLPLKKNV GGDFMTTGAATSTVCEKLGPIYLQ RNKIHEEFVTSLSLTPGILLSASLD GTVVLSRASNMTSLRSFRLMDDSGV RYACMTPLRNIIVTLSATNHLIHWGN TNQVSYLDLYDPISPHYFPIISVKVDE SLGQLISVDSSGYAKVWVSLRNLTK MSFYAVSGAVFSAFRHMYTVENAV QQNGYRLFVDVEKEKKRFRPQGDA SAOHGTPAILQTTLSTVEAAMNAKN FYPARYVAYDSLKRFLVSGAKNNV VCVVFVSLGALKAHSSPICHVSVCE NRWVLSASIADCRLWSYKCALCLG LKANSLEFAMVRMAPVFDASTKFS TSAELEAVSGETDCHKLDACKQPLP TVSEVINAVGARAVAQRMERSAKCL SKRMASPEDEMRRTAMLSRLGKNVN GGTSLNTIGNTTIGTATTVSTVIGSTG GAGSGSGGRVGGMGFSGGTTEND LVKSQGTLYRILCVHIDIQEHFIFYAL NNGDIRVHRTNSGQLSKTLVTMPPS TDLILAAVIQYRHIFTSNRRPTDRGYS TITEGIETASGVAGAQRVHEIAFILH RLHHERKIKLQEGESTSIHKEAIGM MTRRDVKELGVMYADGVIRFFPLIG GSVHAHRRIIPEFLVSRATSYMQLER NLQRRMATPSHDLISOASDMEETHK QQLNFIVEADAVSFVAVSETLEFICL VQVNGRISIMDMKTQTGAVVQVFTV SGELSAVSFLGAYPCLVVAETOGTVS FFLVKGAAMLNLLDFYKSLVLHRR HQRGRNSLLFVDKHPVNDIDKYSN GSTLRMWWFCVPGTPTALHFDPIYG ALYIGTRQGYFSSYLVRNLIVAFDLH PIINVSRAKSLDPPMTSTRQFHDS NEPRLNVLVFFGITPDCVMRYLET ERPSSATLGRELKHTANSTGYSVSW RGADSPLLSSAPRAKPNISSPADNVR GDRGAAMARFWKGSLSWIFEACKP LFFPASSNMSARQFPETANLPFDILT VTSELLVGAAILRHALLIMSMMSD FSSMRKPSMANAGESFTSFASSTCH HYAAVSLTSLDIRHIRQIVEEIRYRN GSVGTGTERQDSPTS DGLPGGFREV EEEFDFDMVRDINSYLPGTIADNWW	None	None	None	None	None	None	None		

