	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	V5DHX4	V5DHX4_TRYCR	Trypanosoma cruzi Dm28c	NaN	19.946178	NaN	NaN	30984116	MLTRYTEAKAKTPFFNTQLCAQGRRGSTDGLLLTIGDITVPVPENLSHPENVKWLLPGIVGCGADTDKPDNSDDNSTGNMVEKGFQLHGGNAFFQLNDSTTRGYLRWMCQKEQLRQDMCLVGEPGPAMRWLVQMYSYLVRREMQCVSLNRDTTESDLGQRREIRNGTLVYDDQCVVVAAREGQLLLLEGLEKVERNVLPVINNLLENREMHLENGMMLIHPERYDRLLQELLSAKKRRYEHGSSDIKNGEKMSSHDAMTHAAAHEELRRMGFIRVSEHFRVVGITVPVPPYDGNPLDPPLRSRFQCLYVNIPLPGLAATKNMTASASVRGGYATGAAESLLKLRTIIDEVNASTKDFIVGGTQAGNSGEPSNHHHNDNSSGIGGVASTVRGLQTIGSYELAVLSRQRQLFPDISLGEILPRAFPWMLYAQQTATSGIAHIEEAARCRREYERLLGACNIGFPLYECRHSSIDKDGDAIGNNHEDGVYAGEEDATSSRASVGILSTRGHARMSQTLREKLAAQRRRSSRGGTEKSTEEPEVSRRPEDFNDVLSIENIHVAETNCGAVVGDACIASREKGGIYRLPICMGETAMHTANGETTNSFLVAARCPTPCNVFTTAHHHVLQSMLQLHIAGQHILLLGPTGCGKTTLLREFAQLIGYRMETMYLYADMTNKDLFQRRTTDSSTGDTTWENSALVEAALRGRIAVLDGIDKLPHGMLASLQHLLVDGNSSLYDGTILRSQREYEILKQKLMATDLEMQARRIFPVHPAFRVVATARSTSSAGSSGGGGKANQSRWRVTHEVTSLFGLVMMPATTQTILHAVLSRAASTELETWRNEMSSLTESDGGAMAERSLETIKRDVDRLLRLRDALERLQETEPKVPQLSLRQLLHLIRFRVRHPDDFTPGVESTLLLPLMNTLTAKQVRQAMHSCGFQGVSDREEKQKQEQRHHGTRKGTETVADLSEGRRGKRHDVLTEVSALKNTNAITECQGCGFMRVFAVHGRPVFCSSRVYSEEERAMVPYVPYFHSNPVHESIIAWLAKQYAVGNNILLIGNQGVGKNKVVDAFLARIGVPRQYIQLHRDTTVGTLTINPTVEGGRVIWSDSPLVKAVERGYCLVVDEIDKAPVEVVQVLKGLVEDHEMRLRDGRQIRGPRARVVAADSDPKVEANVIAMHPDFRIIVLANPPGFPFHGNDFYRECGDLFASYVMGNPDALSQLRVLKAYGPNLPDTLLVRLISAFQTLQKSFEEGHLTYPFSLRELIAVVKHMAAFPHDGIYDALNNVFNFDARNENTLHLVRQVMHLHLSPLVSAGGMRRLLPLRAGQSLPLHVSPQSLQVPATAPLKLSTMPSVSDATLLPVRFLTDADCDKPDIAQSVPTWCEQYKESEFAAVVPNVESEGFTEWLAAPDIPFLRSGDVVVGIAPVEADVDMGALITLAVLFLREEATNDTSNNNSTRIKRLLLAMVAPPSVASFGMVTMRRSHLSLGQIQFFDLTRFFPAADFSSSSSALAPSLHAFNAEPHSSFLVTATQAGWLNDAFGAPIPLVAVVDAQSGLVLLINTTAAAVQSCDVSPRQQGEEEECTRGAVLPVRIAPPSCEPSLCLCSLRPLSGIVAMTRPRSPELFVWMNGQRIVVTLPAASIDKLQFVTDNLAMVSLRVGETVSNCLLKMAVSADGQAKASLLHLPDGISGDIVGFAGNQATALPSDHALLQPLKLEELKGAVVVPGFSETNRGDVVYMTLDEYSPAKRMWSVRLFTDADAAAAVCTGSLRVSHPNHQLLATEWSSAEHRGRIVAVDFQQHMVRRFAPPPTASSSSSLSSSQAPGMPLFALNEGTGVALWYDNTAQRLLVADVVEERVQKRYRNWSTLLEGSVKQIGNVASTTRQPLS	None	None	None	None	None	None	None	None	None

									MTYSKPRAKPSGTLKHGKEDDEEHHGGNTYAGGTGGTDTAGLGGIVGPYRLDKGWPVHQVSPEEKQRVPPHIIEEAKRMGKAALEERLREIGMSAKEYEQYRALQERVQAPVALLRSVLSGLKAAEGERTWLRGQTDGIWDDSKIVEGIVGERNIYKRREESTETNLFQSKHKKRLLFVLDVSASMYRFEGMDHRLTKLLESTVMVMEAFAGFEEKIDYAMVGHNGDSACIELVSFGHSPANQKARMEVCQRMVAHAQYCWSGDNTVEAMRQSIDLVTAEKGDAYLVFVISDANLPRYGIQPSELSAIMRSHKEVLMFCIFIATLGEQASNLQAEMPPGHGFECLDTQALPHILKQIFFSVNLL									