	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	K7SWG8	K7SWG8_TRYCR	Trypanosoma cruzi	ATP pyrophosphate-lyase	19.946178	NaN	NaN	30984116	MVTGWAVMLAAVRQGPVLNKETGC CGGIPLLGWRLSTYALYLVLLLLLLP QSGVGQAACPEIEVKVLTLNVTDLP MPAYLTESLYYGFVAALWSRNYVVG DNVRVTLINKSTTIAESGKAVEEAFQ ANPDIFILAVSMGDATLHYYLTVIRN REIVSFAPFTGSTVVRGWDPYLYFVR ADPLAELFALIRYALTFLRVRRLGFM YLEGVFFGDYEYEATKNVMTRFGYN LSGVFAVKSSLTHEAESSVFDAAWE AFANTLPQAVIVFGAPIKDTAKFIQR MLTDNRTAGAYLLAPSAVQEITVET WRSAVAGGIKFVSGQVITTGTNPVAR DIQYAAIRRFQDVMRRFMENFLPES SSIRKNFPDDDIEGEIMVAGWIAGEI LSQTLSSREWAKNRDAYLASLYNQR RYMVDNLVIGDYGGSCQGVAESEGA MCYCNQGGRTVYMKKFVDGHRAEP LVDGTISFWTWQCSPSEAVIVPPLNG FAIAMRDNPLAIFALRAFGVGARAAV VNNSLIKRFAFTVQVVNSTVDGAAA ALVSELKVKLVDVVTGVVTKGMLEV EDVAFINPMYLQPRIGGFRKNVIRLL PTLEQQFFVIAEYLGNMSDGSVHAVI RGDDGATMAEVLRLSLETFGGSLLS TRLLAGGDKMADYLPEEGDVFVVGI SADDVGAIAQHVVSHDGVRVFVVFL EFSMLYPEFVAAFRDGAGADRVVFA TNLPHWNDNKTTSVTAQKFNAAVP DVNKRTPLAMMGFTTGLLVVTVRSR MEKVSVELFENFFFSNVAVRVDDM LYGPFIDGNACPVTQSGAGCGRNYG ATQISVWSLARALDPAVPVLSHAVTP SMEYRMPVASGLTARQLIGVIVGCV FAALLIIALILLLLHFCRDSRDNENAP KERTDPVTLVFTDIESSTALWAACPE AMPDAVATHHRLIRSLIAKHHCYEV KTIGDSFMIACKSVFAAVQLVRELQQ MFLQQDWGTSVIDDAYHKFEEDRA EDDEEYVPPTARLDDAVYRQYWNGL RVRIGVHTGLCDIRRDDVTKGYDYYG GTSNMAARTESVGNGGQVLLTRAAY MSLSTAEREQVEVTALGGVALRGVP VPVEMYQLDAVPGRTFAALRLDREM PDLDDGSDFESSEDVSMYSARTGTA QAVVSVLTVTYGTLAPRQRLKALMP LCERWNVRFPRRPSFLQDEEYCRLV IDRLAVKMSSVMERKGQLGMDQN MSFTLSATAPGAHDPASGTWGRRG GEQVHARRFREAASQSNSVEVHAFT ADEPRFSTDDSIITVRARRFR	None	None	None	None	None	None	None	None	None