

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
K2MEB2	K2MEB2_TRYCR	Trypanosoma cruzi marinkellei	SEC7 domain-containing protein	19.946178	NaN	NaN	30984116	MTWRYDEVLDACGKALIEERSARIR SLLNVVVKDLTKIKSIANETSGQKLH AANGEAFKKAENSKGFEESTLSHLG FVTQVVLMECNGNRFSSKGLTAVLE FATVLLNSGLIPTSLLSIPPEISITKSP SGGAGEFFSKLLGGGAAANRHCVQF ASIESPTAQSEFKNGAVNVFAAVVE GVLAVARHIQGRDNDQLLFTLVTA LQASAVPCSGRAGLSEKPRDDYNNY FLAVRGDMLLHVIGELFGVFKRNNL ILPLVEGTSALNCIAKALSKAIEYET TEVIEETAIVNTIGESYQKDASRILEY CCSLTRSSPSTSPRPQGNIAHISV PNEASIMLLTALGIHLHLTVNGGPTF RNSTVILSAVKSRIPTLSTALLKDL DAFRLSVNVLLTCAMNFGHLMVNE TKTIFRYLFFRVLESKTSSTLQKSIVV EAFHRYIEEPQNLIALFLNYDCNTSS QSVYEQMIGYLAALSLPFGMKMDAV SDRNEAISGRIVLDFPIPESLQRSALS TLLVAYSNRQWIERFECQDTISFAN SSNFNSSSGVSEFAKHLEKRVDPQG EMVVSQSVGKENDQFVHALRIKDAF RKFIYLMNDVKDSKAAIEFLIREPLLI PNKIEETNHEESMEGNEAIGSGM SKCSETASETHFKNCDNSEEKVNSK AEMIAFFLKEKEDYIDKLVLEGEYFAK SFGDPQRRMIFVKWVERHSFAGMT LDAALRLFLGGFKLLGEAEVVDKTM EIFAAQYCRENPTAFRSANTAFILSF SICMLNTDAHSPHVKNKMTLDEFT RNNRGIDEGDDVDFSLKGIYERIVV NEIKLRPSRFVSSASNSGITGRNNSL SSNRISGLFESIPILKRFAPVARRIT DTVMIPLDVAGNMLFNTLQRKKEEI YQAEALRNALKDVIEALDTANALKSKF VEATRIENAIIPMWGITVDYLIRCLLC AFESFFSVAEATALPSNAQGCCHDPT QRYIDIAENREYFDNLLRGLVNTVRV CCDFGNISQAEGLIERLFEFLTQLSNI VVLSEQPIPCVSLLLNGISKPRIELKT ILDFLVNGASLTTRGWCVAYTGISL LELIFNGLEGTWKSQRRKPPLECSG KSLPVTRFGKVDIPTSFDKNSVQKR IALEALRCFSSVDVWLERLFDATEY PSQTQVFMNALVSVCEKELISLRTF SLTKLLDFTVCASFSSRMQWRDLW NNANKVFTLAGTMTFEIASLSLGG RIALTYLMREELLYSFOKEVLMFP ESILMGNQDVNIRQKVIETIAEIIIEFR ASRLASGWNVVSILSHCAVIPEVVK SAWDLSEGVTSHALMKDCFRDLI FCLTSFACNNVDEEVALLSISYLRVC GHWLQFLEPPEDIRDASAVAWEA GRFGADNEANAQQLIVGVPRTLS MVPITSQQPLEKPTTSLVKTNYHLW MSILEGMFPILVHPSVRVRAHVICS LWALIEQYAIATNIQESLFTGILRP VLCNLLMHAPVDQETVIDPVYKLL TLLSLKSMFLACRLHSHLLKLACET FVTICTTPVSLHVAQGLVDVILRICV DLEPRGYVHRLGLSETASELWVTRL LHELFGIGYDVIHFKRTTGWSELHH AIAVTPRIDFDLNIKEEVRNNIINTV LTSVLDGIHQVLFAMNRCSLQEEYL RLFKAMRRAYLVIALFCADSTGKVF PRLLTGFSSSLVIPEQQLLIPYLCVLI EFVFALRSNTPTIAETQALQEAAMKL MCETIRKSREFCIHSQAEHIAALES GTREEVTVPLKKHGRRTFVDVFRSG RAPLNCRAQHISQTVPERVLNEWRY LTHTLGLRYAFTVDGVTARCIPEVCL HELILLPSELEEQLVEPFICSCWEE LDVGTPLLRVSVISQTLRVLERKRGL LHA	None	None	None	None	None	None	None		