

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
K2NA63	K2NA63_TRYCR	Trypanosoma cruzi marinkellei	NaN	19.946178	NaN	NaN	30984116	MPLALYKLLNMPMPWEETRYVNV VYHMGVLTLYDDTPTVAEQLYLAQ WGSMTWRMRSHKVELQQEGGAFR RMIHKSNENEPPIEYGDYIMDREPP EAVHDELDEEDSAIIDWFYDPFPRL VHPNQIRGPRRPNGYYSINVVECLF RSASPILPTLDDRNYLWDLKSFYT AKAMHLAIPRAPKFEVPPAVCEEDQ DWTEFNDRRIIHRDDPRRPRFTML TERQIAFPFLYGSVVEAVTVAPYHYP AEIRVENDDPALPCFSWNPINPIKA LKRNHAEVTATTTGVLCSVALQHVQ HEEELVKTEEGICPVQLPTNFAPFLE DLPLEDADTKQAMMLAFAPAPYNRF EGEMKRRVDIPVAEHWCDDPPTLVT GDTRDKTLRSYTQLLKHVAKNLRR NRLQARKRHRENTEDVLEPSRRLDE LGRLKFFQKTKVDWMEALQVMRQ GHNMLVQLINVKCLPYVHIDYNFEA KPTRTLTTKEIKKSRLGPAFHILIRELL GFMKQLIDMHAMYRLGKTDAFOLA DATHYLFSHLGRLTGYYRYKLRAMR QIKRTRDLKHVLYSKFNVGEVLRGP GCGFWAPAWRVVWFFLRGMTPLLQ RYLGNLTDRLRGRESKGYDGGKRI TRQRVETDKDVNIKEAFRRELEML PEDVRADVIRTMDQHMNEAFRHW AGLQWVSPGLARPLTELVNKYVCLR AEEYIRVTQYQRKRINEGDTVQKQAF MKNLGRRLTRLKLMEEQERQRAYLE GRDALVITPEEAKEIYRMMANWLT RGFKKIEFPKVSRAELRLLLESLNR LRDQHNIANRLTQAQREEQARIEEA FNSPHETLSKIIDCLARVRRFKNVEV EYMDTFSTLYPIYVNVVPEKLVDSFL DQYLWYEAMDQQLFPNWKPSD MEPVPVLLYKWCQGINDSPLGWDV TRDESTVLLHANLEDSFYDNVDWN LFRPPLLEMVMDKTLVEYIVSRHDVV VEFKDMSYQCRKGLLRGFMFSSFLS QYWGLVVDVLLVGTQRSQEIAGPAR RPNPFMTFMRDPLLATSHPIRGYCR YKNEVYVLLKYTKIEADDVRRRYLDE TKHDPERRSLNASVYGFKNASQWP RDARMRLFLNDVNLARAVLWEFRG RLPPSIAEMTESNTFVSVYSKDNPNL LFDMGGSVRILPVCRTTEEVLENE STWNLQHAKSKDVTARAFLQVAPD HVNHIRNKARRAIMMVGSSFTQSIA AKWNALVTEIVPYREAILGTDLSLQK VLARAEHRMQSRVMMALNSRSKAR FPPAMFYAPTDLGGGLMGLSVGHS LI PARDLIYSRTTSTGVQFFYSGLTNAD DIPIPNVLYQYTPWETEVRRESKAWT EFSVRDREKAAGTRLSLDDIESIIN KGIPRIRVLF SRHAKLFQFDKGFRCR MEFQRFSLSGYLNKWWFHPHEDG NICGGVLEKYRVDHIALGGVEAILEH SLFKGTGFPSWEGIEFNRSGGFENS KKDSKLAKQQRAGLANVNRFRAL WWCPTINRADVQAGFESKIDTTGVF MCGKLETIKKSLIKIFSGSLWEKCHG AVVNDIASKMKDAMADLDAASVTLQ QQHPQKSYTYTSSAPDVMVNSNR WPVTAKPTVLSDEAGDEYRSHLTSK FWIDVQLRWGNYDSHNIAEYTRKKF YEYSSAKMYPFPAGIVGVDLAYNC HSAFGYWIPQLKPLMVKLSAIMR H NIALNTRDRMKRELQLFSSAPTEA GLSVTNIAELFSEGMRWIVDDSAT YVTSEOPTAEGGRKFRSENGAVLLF EPTTGQLKLSIVHKS VFAGQKRRTKL AREKAAEEIASWLRSTPATQRP GKII VTRSRFQTLHNMLVLDYPNIIIGQS DLNLSIPMVLRRSRLVDLRISATESK	None	None	None	None	None	None	None		

