

UniprotKB ID	Entry name	organism	full name	oglcnaScore	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q19853	Q19853_CAEL	Caenorhabditis elegans	EGF-like domain-containing protein	25.808555	T91	NaN	31682414	MRSWVLLAALAVICLGAPELSHKER IRKVLKSWNPANSNQLFHPVSEQKI QFDEQSDLFVDTHHISKRSIAEPHVF AGMATRGCNKPGYTGATCOYPLCSA RNPYPIDNKSDDISIDATNLANCSQ TYVVVVDETMRNKIEVETESPLNPT FYLQSESGDLIFPDTDRKTVTSYVAT YETLAPGQYLLGPRADSGDEFCTMM MTAHTNIQVTGGFTSGDQPERSDYP TLKFAYFDTESAVVLHAOGLHFPGOI QAIGFTGAENHISRYPMATRFNCTY PYILERYTCRKIGNNDIGHNLLQVEG MSDNGYVFRRLPYQCILPPVSTTTV PAPITTAAPLTTCQNGGQVLKDSG SPYCYCFGLYGRDCSQMLCANGGF LPTPTSEHCECEPFGTFHFCQNVIC PGASGIDFNAENPTVTLVIRSRSQLS DVIQQATNSVSRIVDELSAEPGYLTN FIVVLFDNAKLLVNQRYDSWDAAMV DLLKAINSAPSDGGCDDVVFSAVAS ALLSYPNTKSPYYITDANPNPSTEK QTIVHLESYWRAPVYFYVQPAIGSG CNTSPDSAGYRDMVMAAMSSGNT FYFNNRTTISNFFYVHMYNTLFRSQ LALSGDYSHCANQNIYKSAVDVTA DQVVVATGSNLKLVQVTTPTGAHPD FFVAFNDGVNIWTSNQIFAGQWFF NLVSDSPNSACTFKVYQKKYNLGG MSQYNPDYDIFWSFATLTSAGV RQPVAGFDASPVFHVSNYPEFISMD RVHANLQIYAIRDGVQTEVYVSSGM YRDACEFHFFPPFICNVPDEVLYFN FFARDNNDMALQRAGTMLCSAVHP TPPPQHCCQNGGVMNPTNTTCFCT POFTGTYCQIVCYNGGTVSGGQCV CPPGYAGESCEVPRCIETGPNPEFIR YGVDMVFAVEITQQLASIVMLDNN FQEILRDVQMQRGWRNRFVLVGF NSTWGGPIAQSPSNLTAIAALHNL ATNVPSDNGCSVKLWDALNHAIFAR DLVPGSFIEIFQTTPEYELDQRSLGLF YDMSRAMDISLYGFLTAKPTLLPAGF VCNATQVNYVLFQGMVTSSTGQTYI LQALEISNAIRLPIQFNSNGQVTINGN NDCRHEDGLTTYFPVDAYTQTIQLTV FGYGTTIQVYNGVLAEALELFYD DYTGQSVYEIRQACDNGWESFGQYC VKFLTVDNLDLSMPQARNFCASAGG YLADDLGDKNFYSSIAANTQFWI GLFKNSDGGQFYWDRGOGINPDLN QPITYWANGEPSNDPTRQCVYFDGR SGDKSKVWTTDTCATPRPFICQKHR YSDHKNPTIGDADLPAGDWWYKIK TNPTNSNPPYCSSLVSRVQSSLQIVSG FATKIGDDNPQIDPIQDFSSNRLITYV HSVDNENRVPIMTDAILWDFYNGTF YNGLYQARFGCQYGWVSDFFPCP NSDNQNNFVGLHVGEDFNTFQ RLTFGHCSPATIVCGNGGIRQNGQCI CTDYWTGSRCTVPCVNGGTKNSDE ATCTCPDGYAGLNCQFEVCQPKVPQ IFTDDTKLLFVVEVTRQNSDTVNQL IANLKNIVTSATNFAPFWSFYGLVT FDTTGRTFEKYNYYTIDALITDLTAQS TAISTDGACSMPLYGLVLAHLEHDN VISIPNSEIFLVAAGPSDLNKYGEA MNSLFNTEAHLHYIVSKSANCPTE GVNNVQDMTWLGYGSSGNILFTDS SNIVSLMNSYLPSTLYGASILQDPTGP ANYSCTDGSPLPWFVPVDSNTTFIYVT TSSEFGSLSVKDPLQAHNVAPAYN VNSQKQFYKIEVDRLGGIWTQLVQPP GLCLAHIYSTGGARVYTKFSLPNPVG GKEDPLGAHQDGRFVQPVSGFDNV AVFHIAGKPMQRGQLQYVEIFDIGQ VTVTNVLRSLEYRREGCSYEEYSDLF TCSGDMIAVFIHGVDYEQKFRRQQ	None	None	None	None	None	None	None		

