	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	O76904	O76904_DROME	Drosophila melanogaster	NaN	28.06426	S1186;T1193	NaN	40245499	MLIWHLLLWPALIASAPPRPLTDQK AEVAKLRSELEKALEHDDGGAPPGV VVAPTWTQQAGQMPLGKTSKVVVD HSSLSSASAIRQEIQQAVAHQGQNQ EVLQLEALLKARGSSKESTAQVSTSR QEVLGATVQEANVVESHSTSQTVDL EQLQRLELSKRRTRDMLVLGRIEEL LNYSMPTDVDRWLTLQANGSVFLV GQQQEGLLVLSEEFTPLQSYVHPFPI TAMLGTDRWNRRVHMQEGLLVMA SQDQLIWLRLEPSLGLKPIWHWTIG SHVTKIRAFNMEGQDYLALVANHTL NIYVYDLEAEEFWIAQRVQMAETISN LAILDTGRELLLAVGQWDEVLIYACT SKGQPLHLRQQVAAPEVAGVTAFQ MGGRSYLALGGIMPQILVYVQGQLV PRTILGQNFGFVDHYLPIPVRSYRDD LLLLVQHRVVFDTHSLLVLEVLVWN GEAFEAGLPPPCGTAYGAGCMLDQD REAGISGAVLLRRSTNQPPLVVVPRK EAPTGIFVLETQLLARNSETQDLLEI RQFMQDWVHEQEELIQLAEELLAE KSESQYIEELSTPLVVSEGGTVEELF VNEARWTGADAVVDVSSLLQQILLL DGEMSSRRSKRQPETLFNFHYEQLE VEAVDSVELNLEKLNHETFYIRNGS LDLHLGTLNVQQLELLEAPKLELVP VHGAESYKILKMATDLDSIFINEME WDKLLQDLVWRHQPLKLSQLHVEG PVIFEDVLSLHSLNDLSFPGDYLWS QGNETSVVQAPKEFTQTLSANAVDT TGTINAVYPHDVITLSDSQEWPGLVT FSHLEVSEELELNGSAQGRQFEEAP LNPTLLESRVISADCHFEQLLVRGPL RLLGKVDNDSFGSLLGDLVQRSPNS AQELQISGQKRVDQLLLPVDAHIAD NQLSGIFLNDFVTKHTPQTLSNLSQ LGGYVYFHQLELGKESSYDGVRLEE LLSKSLRLDSPFPLSSPHTRLRFVGH APNFTRLQVENTLNKVPLSSGYQLL HEPLHLGRANFSRLMAGQAQVNYD VSGNGLLNGRSLIRILQEQPRTWSG EVHVQELILPQGVQANQLQGIKADL LLDFLQQLDELPLLILQGRIQVERIAV NGSVQAAETLNMQPFHELQRQVVW LDRQNELGTRWVLKESPQFQQNLQ VLGSFNERLLPELLDDIVLRSDAHEV LIEGTKSFLAPVNTKELHLAALNGIP FNHMANKLSPLHLTGNVRIQGRIFV EDLQLNGQVNGDPDIPADLQKLLR WDPNAGGFVHRGVVELPKKELERL VVLGHLKNRSREPVQELFDQLVFKQ QRGIHLHGHKTFTGRLRIEDGAHIKF FNGRNLEQFLENLIYVDSQGEIRLET PVRFAADVKMDHLEADRLVLSGELL NGCNVSQWLRDTIRVDRDFQQPEIA FAKGSLDGNFLEVEELNEVNLSLVV TRFTEQQLSDPLEADDLLLDGQLVV RGTVNGYNLPEEYANTLMINPLREQ QVDTPLLLSNIFVTGPLEVTAPVHGL NISDVAILGEDPVLLQSPLYFDTLHA PFLRAQQNINGFDFRAWYGGSLWA RGREQQEISGNWRVKKLQVKQGDE LRPRRQTAEESYREFCEGLVRILLPY KVQKLRRRFDLNQERDQENIRRVFA LEAPGGISYLLINERGCWTRIHRWN GSLFDRSGAFKSGPVDEAVALRVGN TSSNQDFAFMTSYELQDDQNEPSL NCSAVKPILLSWNLNKTKSTTEHME LSADTLRNLKDQYEQLKNQPLPNPS YQQAFKYLQRPSIKSQLGSQWQENK HELSPSEMARMRRRLLDTLEFRLQA EVNITQLSIPESDLFDEHLVEDFLEL MRQLRTLRRRLDTETLPLPNTPARV LAARSAQLIWPTLQELREVSSGNDS SFQEQVLEQTLLDVLMLANEENGS GDDEKLHAVIQRLRNLKGELQGQEE	False	True	False	False	0.375	0.469	False	5.0	1.777

								DDEGPAASYSDRNEQRLPLPEVDWR PIQTLRLAVGPANRPRLLYARLTVVT PTDGPPPTTPSTAPAAHIQLHHANGS LFQTLAGEHGARHLTSLRVRDETLL AFMEGCCRIRVLIYRGVQGFVDFVR FPAPAQEAKSGDGEVLQLLSLRLPL NRPPGAMYLLAVVQARRVTFYEVVV AGLLEPWLQCP									