	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	B3DN78	B3DN78_DROME	Drosophila melanogaster	Laminin A chain	28.06426	T2198;S2473	NaN	40245499	MGHGVASIGALLVILAISYCQAELTP PYFNLATGRKIYATATCGQDTDGPEL YCKLVGANTEHDHIDYSVIQGQVCD YCDPTVPERNHPPENAIDGTEAWW QSPPLSRGMKFNEVNLTINFEQEFH VAYLFIRMGNSPRPGLWTLEKSTDY GKTWTPWQHFSDTPADCETYFGKD TYKPITRDDDVICTTEYSKIVPLENGE IPVMLLNERPSSTNYFNSTVLQEWT RATNVRIRLLRTKNLLGHLMSVARQ DPTVTRRYFYSIKDISIGGRCMCNGH ADTCDVKDPKSPVRILACRCQHHTC GIQCNECCPGFEQKKWRQNTNARP FNCEPCNCHGHSNECKYDEEVNRK GLSLDIHGHYDGGGVCQNCQHNTV GINCNKCKPKYYRPKGKHWNETDV CSPCQCDYFFSTGHCEEETGNCECR AAFQPPSCDSCAYGYYGYPNCRECE CNLNGTNGYHCEAESGQQCPCKIN FAGAYCKQCAEGYYGFPECKACECN KIGSITNDCNVTTGECKCLTNFGGD NCERCKHGYFNYPTCSYCDCDNQG TESEICNKQSGQCICREGFGGPRCD QCLPGFYNYPDCKPCNCSSTGSSAIT CDNTGKCNCLNNFAGKQCTLCTAG YYSYPDCLPCHCDSHGSQGVSCNSD GQCLCQPNFDGRQCDSCKEGFYNF PSCEDCNCDPAGVIDKFAGCGSVPV GELCKCKERVTGRICNECKPLYWNL NISNTEGCEICDCWTDGTISALDTCT SKSGQCPCKPHTQGRRCQECRDGT FDLDSASLFGCKDCSCDVGGSWQS VCDKISGQCKCHPRITGLACTQPLTT HFFPTLHQFQYEYEDGSLPSGTQVR YDYDEAAFPGFSSKGYVVFNAIQND VRNEVNVFKSSLYRIVLRYVNPNAE NVTATISVTSDNPLEVDQHVKVLLQ PTSEPQFVTVAGPLGVKPSAIVLDPG RYVFTTKANKNVMLDYFVLLPAAYY EAGILTRHISNPCELGNMELCRHYK YASVEVFSPAATPFVIGENSKPTNPV ETYTDPEHLQIVSHVGDIPVLSGSQN ELHYIVDVPRSGRYIFVIDYISDRNFP DSYYINLKLKDNPDSETSVLLYPCLY STICRTSVNEDGMEKSFYINKEDLQ PVIISADIEDGSRFPIISVTAIPVDQWS IDYINPSPVCVIHDQQCATPKFRSVP DSKKIEFETDHEDRIATNKPPYASLD ERVKLVHLDSQNEATIVIESKVDATK PNLFVILVKYYQPSHPKYQVYYTLTA GKNQYDGKFDIQHCPSSSGCRGVIR PAGEGSFEIDDEFKFTITTDRSQSVW LDYLVVVPLKQYNDDLLVEETFDQT KEFIQNCGHDHFHITHNASDFCKKS VFSLTADYNSGALPCNCDYAGSTSF ECHPFGGQCQCKPNVIERTCGACRS RYYGFPDCKPCKCPNSAMCEPTTGE CMCPPNVIGDLCEKCAPNTYGFHQV IGCEECACNPMGIANGNSQCDLFN GTCECRQNIEGRACDVCSNGYFNFP HCEQCSCHKPGTELEVCDKIDGACF CKKNVVGRDCDQCVDGTYNLQESN PDGCTTCFCFGKTSRCDSAYLRVYN VSLLKHVSITTPEFHEESIKFDMWPV PADEILLNETTLKADFTLREVNDERP AYFGVLDYLLNQNNHISAYGGDLAY TLHFTSGFDGKYIVAPDVILFSEHNA LVHTSYEQPSRNEPFTNRVNIVESN FQTISGKPVSRADFMMVLRDLKVIFI RANYWEQTLVTHLSDVYLTLADEDA DGTGEYQFLAVERCSCPPGYSGHSC EDCAPGYYRDPSGPYGGYCIPCECN GHSETCDCATGICSKCQHGTEGDHC ERCVSGYYGNATNGTPGDCMICACP LPFDSNNFATSCEISESGDQIHCECK PGYTGPRCESCANGFYGEPESIGEVC KPCECSGNINPEDQGSCDTRTGECL	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	None

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