

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q00174	LAMA_DROME	Drosophila melanogaster	Laminin subunit alpha	30.404062	NaN	NaN	33925313;28604694	MGHGVASIGALLVILAIISYQAEITP PYFNLATGRKIYATATCGQDIDGPEL YCKLVGANTEHDHIDYSVIQGVQVCD YCDPTVPERNHPPENAIIDGTEAWW QSPPLSRGMKFNEVNLTFINFEQEFH VAYLFIRMGNSPRPGLWTLEKSTDY GKTWTPWQHFSDFTPADCEYFGKD TYKPIRDRDDVICTEYSKIVPLENGE IPVMLLNERPSTNYFNSTVLQEWL RATNVIRILLRTRKLLGHLMSVARQ DPTVTRRYFYIKDISIGGRMCNNGH ADTCDVKDPKSPVRLACRCQHHTC GIQCNECCPGFEQKKWRQNTNARP FNCEPCNCHGHSNECKYDEEVNRK GLSLDIHGHYDGGGVQCNCQHNTV GINCNKCKPKYRPGKHWNEDV CSPQCQDYFFSTGHCEEETGNCECR AAFQPPSCDSCAYGYGYPNCRECE CNLNGTNGYHCEAESGQOCCKIN FAGAYCKQCAEGYGFPECKACECN KIGSITNDCNVTTGECKCLTNFGGD NCERCKHGYFNYPCTSYCDNDQ TESEICNKQSGQCICREGFGGPRCD QCLPGFYNYPDCKPCNCSSTGSSAIT CDNTGKCNCLNMFAGKQCTLCTAG YYSYDCLPCHCDSHGSQGVSCNSD GQCLCQPNFDGRQCDSCKEGFYFN PSCEDCNCDPAGVIDKFAAGCSVPV GELCKKERVTGRICNECKPLYWNL NISNTEGCEICDCWTDGTISALDICT SKSGQCPCKPHTQGRRCQECRDGT FDLDSASLFGCKDCSCDVGGSWQ VCDKISGQCKCHPRITGLACTQPLTT HFFPTLHQFYEYEDGSLPSGTQVR YDYDEAAFPGFSSKGYVFNIAIOND VRNEVNVFKSSLYRIVLRYVNPNAE NVTATISVSDNPLEVDQHVKVLLQ PTSEPQFVTVAGPLGVKPSAIVLDPG RYVFTTKANKNVMLDYFVLLPAAYY EAGILTRHISNPCELGNMELCRHYK YASVEVFSPAATPFVIGENSKPTNPV ETYTDPEHLQIVSHVGDIPVLSGSQN ELHYIVDVPRSGRYFVIDYISDRNFP DSYYINLKLKDNPDSETSVLLYPLY STICRTSVNEDGMEKSFYINKEDLO PVIISADIEDGSRFPIISVTAIPVDQWS IDYINPSPVCVIHDQCATPKFRSVP DSKKIEFETDHEDRATNKPPYASLD ERVKLVHLSQNEATVIESKVDATK PNLFVILVKYQPSHPKYQVYYTLTA GKNQYDGKFDIQHCPSSSGCRGVIR PAGEFSFEIDDEFKFTITDRSQSVW LDYLVVPLKQYNDLLVEETFQDT KEFIQNCGHDFHITHNASDFCKKS VFSLTADYNSGALPCNCDYAGSTSF ECHPFGGQCQCKPNVIERTCGACRS RYYGFPDCKPCKPNSAMCEPTTGE CMCPPNVIGDLCEKCAPNTYGFHQV IGCEECACNPMGIANGNSQCDFN GTCECRQNIAGRACDVCNNGYFNFP HCEQCSCHKPGTELEVCDKIDGACF CKKNVVGRDCDQCVDTYNLQESN PDGCTTCFCFGKTSRCD SAYLRVYN VSLKHSVITTFEFHEESIKFDMWPV PADEILLNETTLKADFTLREVNDERP AYFGVLDYLLNQNNHISAYGGDLAY TLHFTSGFDGKYIVAPDVLFSHNA LVHTSYEQPSRNEPFTNRVNVESN FQISGKPVSRADFMMVLRDLKVIFI RANYWEQTLVTHLSDVYLLTADEDA DGTGEYQFLAVERCSCPPGYSGHSC EDCAPGYRDPSPGYGGYCIPECN GHSETCDCATGICSKCQHGTEGDHC ERCVSGYGNATNGTPGDMICACP LPFDSNNFATSEISESGDQIHCECK PGYTGRPCESCANGFYGEPESIGQV CKPCECSGNINPEDQGSCTDRTGEC LRCLNNTFGAACNLCPAGFYGDAIK	None	None	None	None	None	None	None		

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