	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	extracellu region
0	P11046	LAMB1_DROME	Drosophila melanogaster	Laminin subunit beta-1	30.60235	T197;T234;T1702	NaN	33925313;40245499	MLELRLIVVIVLALLSWQWDPVDSQ RPPQHGRRDRPKYPPNKFIKTHPCE RSSCYPATGNLLIGRENRLTASSTCG LHSPERFCILSHLQDKKCFLCDTRE ETKHDPYKNHRIGQIIYKTKPGTNIP TWWQSENGKENATIQLDLEAEFHF THLIITFTTFRPAAMYIERSFDFGQT WHIYRYFAYDCKESFPGVPTVLENIT DVMCTSRYSNVEPSRNGEVIFRVLP PNINVTDPYAEHVQNQLKMTNLRIQ MTKLHKLGDNLLDSRLENEEKYYYG ISNMVVRGSCSCYGHASQCLPLDPA FSQADNEDGMVHGRCECTHNTKG MNCEECEDFFNDLPWKPAFGKKTN ACKKCECNDHAVSCHFDEAVFTAS GFVSGGVCDNCLHNTRGQHCEEC MPYFYRDPEQDITSERVCQPCDCDP QGSSDDGICDSLNELEEGAVAGACH CKAFVTGRRCNQCKDGYWNLQSDN PEGCEPCTCNPLGTLNNSGCVMRT GECKCKKYVTGKDCNQCMPETYGL SESPEGCSLCNCDAGGSYDNYCDVI SGQCRCRPHMTGRSCSQPKQNYFIP LLPEVHEAEVVDECISYGANGNCSL VAETPDGSFTGIGFTRVPENSELVFT VGDIPRSMPYDAVIRYQSTSRGDWE NAFITLVRPDQVDPEGGCGELAAAT SSETRIPFSLPDRSRQVVALNEVCLE AGKVYKFRIYFERKRHDVDSPTATIL VDSLTLIPRIDVTPIFQGSVLADIRKK DYEKYNCKSSLYDMNYKSDPKCQN LDNILSVFVHDGASMCNCNPTGSLS KVCESNGGYCQCKPNVVGRQCDQC APGTYGFGPEGCKACDCNSIGSKDK YCDLITGQCQCVPNTYGRECNQCQP GYWNFPECRVCQCNGHAATCDPIQ GTCIDCQDSTTGYSCDSCLDGYYGN PLFGSEIGCRPCRCPETVASGLAHAD GCSLDTRNNNMLCHCQEGYSGSRC EICADNFFGNPDNGGTCSKCECSN NVDLYDTGNCDRQTGACLKCLYQTT GDHCELCKDGFFGDALQQNCQQCE CDFLGTNNTIAHCDRFTGQCPCLPN VQGVRCDQCAENHWKIASGEGCES CNCDPIGALHEQCNSYTGQCQCKPG FGGRACNQCQAHYWGNPNEKCQP CECDQFGAADFQCDRETGNCVCHE GIGGYKCNECARGYIGQFPHCSPCG ECFNNWDLILSALEDATTATILRAKE IKQVGATGAYTSEFSELDKKLQHIRN LLQNTSVSLVDIEKLDYETQSLRDQL QASHGRLSETEQNLDDIYNSLSLSG VELESLQNHSRLVQQLSKELKENGI QLQESNIEGALNLTRHAYERVSNLS TLKDEANELASNTDRNCKRVENLS NKIQAEADDLANNNKLIEDYRAELT SLTSQIPELNNQVCGKPGDPCDSLC GGAGCGHCGGFLSCEHGAKTHSEE ALKVAKDAETAITSKKDQADQTIRAL TQAKLNASEAYEKAKRGFEQSERYL NQTNANIKLAENLFIALNNFQENKT ASPSESKELAQKTLDLDLKLEPEEIE TLGDQINRAVSSLKNVEAIIYRTKPD LDRVNNLQSIANATKEKADKILDSA NSVVESLAAADESQGKAKDAIQQAN SNIELAGQDLEKIDEETYSAEAPANN TAQQVEKLAKKVQKLQNNIMKNDR DAKEITKEAGSVKLEAMRARGEANN LQSATSATNQTLTDRASRSENARER AKQLLQRASKLTVDTNAKLKDLNDL QTVYLNKNQQLLRLQAEIGPLNKEL NEHLIHIKERGSHYRQCYT	False	False	False	False	False	0.938	False	0.404	3.788