

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membra
Q61001	LAMA5_MOUSE	Mus musculus	Laminin subunit alpha-5	46.289916	T102;S2140;T2427	NaN	22517741;40885482;37507081;35822049;40021952;30059200	MAKRGGQLCAGSAPGALGPRSPAPR PLLLLLAGLALVGEARTPGGDFSLH PPYFNLAEGARITASATCGEEAPTRS VSRPTEDLYCKLVGGPVAGGDPNQT IQGQYCDICTAANSNKAHPVSNDAID GTERWWQSPPLSRGLEYNVNVTL DLGOVFHVAYVLKIFANSRPRDLWV LERSTDFGHTYQPWQFFASSKRDCLE ERFGPRTLERITQDDVICTEYSRIV PLENGEIVVSLVNGRPGALNFSYSPL LRDFTKATNIRLRLRNTLLGLHLM GKALRDPVTRRYYYSIKDISIGGRCV CHGHADVCDAKDPLDPFRLQCACQ HNTCGGSCDRCCPGFNQFPWKPAT TDSANECQSCNCHGHAYDCYDPE VDRRNASQNDNVYOGGGVCLDCQ HHTTGINCERCLPGFFRAPDQPLDS PHVCRPCDCESDFDTGTCEDLTGRC YCRPNFTGELCAACAEGYTDFPHCY PLPSFPHNDTREQVLPAGQIVNCDC NAAGTQGNACRDKPRLGRCVCKPN FRGAHCELCAPGFHGPSCHPCQCSS PGVANSLCDPESGQCMCRTGFEGD RCDHICALGYFHFPLCQLCGCSPAGT LPEGCDEAGRCQCRPGFDGPHCDR CLPGYHGYPDCHACACDPRGALDQ QCGVGGGLCHCRPGYTGATCQECSPG FYGFSPCIPCHCSADGSLHTTCDPTT GQCRCRPRVTGLHCDMCPVGYNF PYCEAGSCHPAGLAPANPALPETQA PCMCRAHVEGSPCDRCKPGYWGLS ASNPEGCTRCSCDPRGTLGGVTECQ GNGQCFCKAHVCGKTCACCKDGF GLDYADYFGRCRCRDVGGALGQG CEPKTGACRCRPNTOGPTCSEPAKD HYLPDLHMRLEEEAATPEGHAV RFGFNPLEFENFSWRGYAHMMAIQ PRIVARLNVTSDFLFRVFRYVNRGS TSVNGQISVREEGKLSSCTNCTEQS QPVAFPSTPEAFVTVPRGFGPEFV LNPGIWALLVEAEGVLLDYVLLPST YYEALLQHRVTEACTYRPSALHSTE NCLVYAHPLDGFPSAAGTEALCRH DNSLPRPCPTEQLSPSHPLATCFGS DVDIQLEMVAVPQPGQYVVEVYGE DSHQEMGVAVHTPQRAPQGGVNLN HPCPYSSLCRSPARDTQHHLAIFYLD SEASIRLTAEQAHFHLSVTLVPVEE FSTEFVPRVFCVSSHGTFFNPSSAA CLASRFPKPPQPIILKDCQVLPPLDL PLTQSQELSPGAPPEGPQPRPPTAVD PNAEPTLLRHPQGTVVFTTQVPTLG RYAFLHGYQPVHPSFPVEVLINGG RIWQHANASFCPHGYGCRTLVLCE GQTMLDVTDNELTVTVRVEGRWL WLDYVVLIVPEDAYSSSYLQEEPLDKS YDFISHCATQGYHISPSSSSPFCRNA ATSLSLFYNNGALPCGCHEVGAVSP TCEPFGQCPCRGHVIGRDCSRCAT GYWGFNCRPCDCGARLCELTGQ CICPPRTVPPDCLVCQPPQSFQGHPLV GCEECSGPGVQELTDPCTDMDS GQCRCPNVAGRRCDTCAPGFYGY SCRPCDHEAGTMASVCDPLTGQC HCKENVQGSRCDCQCRVGTFFSLDAA NPKGCTRCFCGATERCNGSNLAR HEFVDMEGWVLLSSDRQVVPHEHR PEIELLHADLRVADTFSELYWQAPP SYLGDVSSYGGTLHYELHSETORG DIFIPYERPDVVLQGNQMSIAFLEL AYPPGQVHRGQLQVLEGNFRHLET HNPVSRREELMMVLAGLEQLQIRALF SQTSSSVSLRRVVLEVAEAGRPPA SNVELCMCPANYRGDSCQECAPGY YRDTKGLFLGRCVPCQCHGHSRDL PGSGICVGCQHNTGDCQCRCPGF VSSDPSNPASPCVSCPCPLAVPSNN FADGCVLRNGRTQCLCRPGYAGASC ERCAPGFFGNPLVLGSSCQPCDCSG NGDPNMFISDCDPLTGACRGLRHT	False	True	1.531	1.746	2.051	1.216	0.556	3.469

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