

| UniprotKB ID | Entry name  | organism     | full name               | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS                               | sequence   | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasma membrane | ext reg |
|--------------|-------------|--------------|-------------------------|--------------|---------------|-----------------------|-------------------------------------|--|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|---------|
| Q61001       | LAMA5_MOUSE | Mus musculus | Laminin subunit alpha-5 | 36.427457    | T102;S2140    | NaN                   | 22517741;30059200;37507081;35822049 | MAKRRGGQLCAGSAPGALGPRSPAPR<br>PLLLLLAGLALVGEARTPGDGFSLH<br>PPYFNLAEGARITASATCGEEAPTRS<br>VSRPTEDLYCKLVGGPVAGGDPNQ<br>IQGQYCDICTAANSNKAHPVSNDAI<br>GTERWWQSPPLSRGLEYNVNVTL<br>DLGQVFHVAYVLKIFANSRPRDLV<br>LERSTDFGHYQVWQFFASSKRDCL<br>ERFGPRTLERITQDDVICTTEYSRIV<br>PLENGEIVVSLVNGRPGALNFSYSPL<br>LRDFTKATNIRLRFRLRNTLLGHLM<br>GKALRDPTVTRRYYSIKDISIGRVC<br>CHGHADVCDADPLDPFRLOCACQ<br>HNTCGGSCDRCCPGFNQOPWPKPAT<br>TDSANECQSCNCHGHAYDCYDPE<br>VDRRNASQNDNVYQGGGVCLDCQ<br>HHTTGINCERCLPGFFRAPDQPLDS<br>PHVCRPCDCESDFTDGTCEDLTGRC<br>YCRNFTGELCAACAEGYDFPHCY<br>PLPSFPHNDTREQVLPAGOIVNDCD<br>NAAGTOGNACRKPRLGRCVCKPN<br>FRGAHCELCAFGFHGPSCHPCQCSS<br>PGVANSLCDPESGQCMCRTEGEGD<br>RCDHICALGYFHFPLCQLCGSPAGT<br>LPEGCDEAGRCQCRPGFDGPHCDR<br>CLPGYHGYPDCHACACDPRGALDQ<br>QCGVGGGLCHCRPGYTGATCOECSPG<br>FYGFSPCHCHCSADGSLHTTCDPTT<br>GQCRCRPRVTGLHCDMCVPGAYNF<br>PYCEAGSCHPAGLAPANPALPETQA<br>PCMCRAHVEGSPCDRCRPGYWGSL<br>ASNPEGCTRCSCDPRGLGGVTECQ<br>GNGQCFCKAHVCGKCAACKDGGF<br>GLDYADYFGCRSCRCVGGALGQG<br>CEPKTGACRCRPNTOGPTCSEPAKD<br>HYLDLHHMRLEEEAATPEGHAV<br>RFGFNPLEFENFSWRGYAHMMAIQ<br>PRIVARLNVSPDLFRLVFRVYNRGS<br>TSVNGQISVREEGLSSCTNCTEQS<br>QPVAFPSTPAFVTVPQRGFGEFV<br>LNPGIWALLVEAEGVLLDYVLLPST<br>YYEALLQHRVTEACTYRPSALHSTE<br>NCLVYAHLPDGFPSAAGTEALCRH<br>DNSLPRPCPTEQLSPSHPLATCFGS<br>DVIQLEMAVPPQGVVLYVEYVGE<br>DSHQEMGVAVHTPQRAFPQGVNL<br>HPCPYSSLCRSPARDTQHLLAIFYLD<br>SEASIRLTAQAHHFLHSVTLVPVEE<br>FSTEFVEPRVFCVSSHGTFNPSSAA<br>CLASRFKPPQPIHKDCQVLPPLPDL<br>PLTQSQELSPGAPPEGPQPRPPTAVD<br>PNAEPTLLRHPQGTVVFTTQVPTLG<br>RYAFLHGYQPVHPSFVPEVLLNGG<br>RIWQGHANASFCPHGYGCRTLVLC<br>GOTMLDVTDNELTVTVRVPEGRWL<br>WLDYVLIVPEDAYSSSYLQEEPLDKS<br>YDFISHCATQGYHISPSSSPFCRNA<br>ATLSLFFYNNGALPCGCHEVGAVSP<br>TCEPFGGQPCRGHVIGRDCSRCAT<br>GYWGFNCRPCDCGARLCELTGQ<br>CICPRTVPPDCLVCQPSFGCHPLV<br>GCEECSGPGVQELTDPTCDMDS<br>GQCRCRPNVAGRCDTCAPGFYGY<br>SCRPCDCHEAGTMASVCDPLTGQC<br>HCKENVQGSRCDCQCRVGTFLDAA<br>NPKGCTRCFCGATERCGNSNLAR<br>HEFVDMEGWVLLSSDRQVVPHEHR<br>PEIELLHADLRSVADTFSELYWQAPP<br>SYLGDVRSYGGTLHYELHSETQRG<br>DIFIPYERPDVVLQGNQMSIAFLE<br>AYPPGQVHRGQLQVLEGNFRHLET<br>HNPPVSREELMMVLAGLEQLQIRALF<br>SQTSSSVLRRVVLEVASEAGRGP<br>SNVELCMCPANYRGDSCQECAPGY<br>YRDTKGLFLGRVPCQCHGHSRDL<br>PGSGICVGCQHNTGDCERCRCRPGF<br>VSSDPSNPASPCVSCPCPLAVPSNN<br>FADGCVLRNRTQCLCRPGYAGASC<br>ERCAPGFFGNPLVLGSSCQPCDCSG<br>NGDPNMFSDCDPLTGACRGLRHT | False         | True          | 1.531   | 1.748   | 2.052         | 1.217                 | 0.556           | 3.469           | 4.4     |

TGPHCERCAPGFYGNALLPGNCTRC  
DCSPCGTETCDPQSGRCLCKAGVTG  
QRCDRCLLEGYFGFEQCGCRPCAC  
GPAAKGSECHPQSGQCHCQPGTTG  
POCLECAPGYWGLPEKGCRRQCPC  
RGHCDPHTGHCTCPPGLSGERCDT  
CSQQHQVPVPGKPGGHHIHCVEVD  
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LRSPPGPRYQAAQQLQTLQEQSISLQ  
QDTERLGSQATGVQGGQAGLLDTE  
STLGRAQKLLSVRAVGRALNELAS  
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ATHIRDQLAQYESGLMDLREALNQA  
VNTTREAEEELNSRNQERLKEALQW  
KQELSQDNATLKATLQAASLILGHVS  
ELLQIDQAKEDLEHLAASLDGAWT  
PLLKRMQAFSPASSKVDLVEAAEAH  
AQKLNQLAINLSGIIILGINQDRFIORA  
VEASNAYSSILQAVQAAEDAAGQAL  
RQASRTWEMVVQRGLAAGARQLLA  
NSSALEETILGHQGRLLAAGRLQA  
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MLAMDTSETSEKIAHAKAVAAEALS  
TATHVQSXLQGMQKNVERWQSQLG  
GLQGQDLSQVERDASSVSTLEKTL  
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VRVERATVFSVDQDNMLEMADAYY  
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CIKGKALGKYVDLKRLLNTGISFGC  
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APITEVVYSGGFRGTQDNLLYYRT  
SPDGPYQVSLREGHVTLRFMNQEVE  
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VDDQLQLVKSHERTTPMLQLQPEEP  
SRLLGGLPVSGETFHNFSGCISNVFV  
QRLRGPQRVFDLHQNMGSVNVSVG  
CTPAQLIETSRAQAQVSRRSRQPSQ  
DLACTTPWLPGTIQDAYQFGGPLPSY  
LQFVGISPSHRNRLHLSMLVRPHAA  
SQGLLLSTAPMSGRSPSLVFLNHG  
HFVAQTEGPGPRLQVOSRQHSRAG  
QWHRVSVRWGMQIQIQLVVDGSQT  
WSOKALHHRVPRAERPOPYYTLVSGG  
LPASSYSSKLPVSVGFSGLKQLD  
KRPLRTPQMVGVTPCVSGPLEDGL  
FFPQSEGVTLELPKAKMPYVLELE  
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LCDGRWHRVAVIMGRDTRLEVDT  
QSNHTTCRLPESLAGSPALLHLGSL  
PKSSTARPELPAIRGCLRKLLINGAP  
VNVASVQIQGAVGMRGCPSTLAL  
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