

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	go ap
O15230	LAMA5_HUMAN	Homo sapiens	Laminin subunit alpha-5	25.108844	T97;S245;T2021;S2138;S2211;S2217;T2425;T3116	NaN	28657654;37340703;34019948;23271734;37217939	MAKRLCAGSALCVRGPRGPAPLLLV GLALLGAARAREEAGGGFSLHPPYF NLAEGARIAASATCGEEAPARGSPRP TEDLYCKLVGGPVAGGDPNQITRGG YCDICTAANSNKAHPASNAIDGTER WWQSPPLSRGLEYNEVNVTLDLGQ VFHVAVVLIKFANSRPRDLWVWLS MDFGRTYQPWQFFASSKRDCLERF GPOTLERITRDDAAICTTEYSRIVPLE NGEIVVSLVNGRPGAMNFSYSPLLR EFTKATNVRLRFLRTNTLLGHLMGK ALRDPVTRRRYYYSIKDISIGRCVCH GHADACDAKDPDTPFRLQCTCQHN TCGGTCDRCCPGFNQPPWKPATAN SANECQSCNCYGHATDCYYDPEVD RRRASQSLDGTQGGGVCIDCQHHT TGVNCERCLPGFYRSPNHPLDSPHV CRRNCESDFDTGTCEDLTGRCYCR PNFSGERCVDCAEGFTGFPPSCYPTP SSSNDTREQVLPAGQIVNCDCSAAG TQGNACKRDPVGRCLCKPNFQGT HCELCAPGFYGGCQPCQCSSPGVA DDRCDDPTGQCRVRGFEFATCDR CAPGYFHFPLCQLCGCSPAGTLPEG CDEAGRCLCQPEFAGPHCDRCRPGY HGFPNCQACTCDPRGALDQLCGAG GLCRCRPGYGTACQECSPGFHGF SCVPCCHSAEGLHAACDPRSGQCS CRPRVTGLRCDTCVPGAYNFPYCEA GSCHPAGLAPVDPALPEAQVPCMC AHVEGPSCDRCKPGFVGLSPSNPE GCTRCSCDLRGTGGVAECQPGTGQ CFCKPHVCGQACASCKDGFGLDQ ADYFGCRSCRDIGGALGQSCPEPT GVCRCRPNTQGPTCSEPARDHYPD LHHLRLEEEAATPEGHAVRFGFNP LEFENFSWRGYAQMAPPVQPRIVARL NLTSPLDFWLVRVYVNRGAMSVSG RVSVREEGRSATCANCTAQSQPVAF PPSTEPAFITVPQRFGEFVFLNPGT WALRVEAEGVLLDYVLLPSAYYEA LLQLRVTEACTYRPSAQSGDNCLL YTHLPLDGFPSAAGLEALCRQDNSL PRPCPTEQLSPSHPLITCTGSDVDV QLQVAVPQPGRYALVVEYANEDARQ EVGVAVHTPQRAFQOGLLSLHPCLY STLCRGTARDTQDHLAVFHLDEAS VRLTAEQARFFLHGVTLVPIEEFSPE FVEPRVSCISSHGAFGNPNSAACLP FPKPPQIHLRDCQVIPLPPGLPLTHA QDLTPAMSPAGPRPRPPTAVDPAE PTLLREPQATVVFTTHVPTLGRYAFL LHGYQPAHPTFPVEVLINAGRWWQ HANAFPCPHGYGCRTLVVCEGQALL DVTHSELTVTRVPKGRWLWLDYVL VVPENVYSFGYLRPEPLDKSYDFISH CAAQGYHISPSSSSLFCRNAASLSL FYNGARPCGCHEVGATGPTCEPFG GQCPCHAHVIGRDCSRCATGYWGF PNCRPCDCGARLCELTGQCICPPR TIPPDCLLCQPQTFGCHPLVGECEC NCSGPGIQELDPTCDTDSGQCKCR PNVTGRRCDTCSPGFHGYPRCRPCD CHEAGTAPGVCDPLTGQCYCKENVQ GPKCDQCSLGTFSLDAANPKGCTRC FCFGATERCRSSSYTRQEFVDMEG WVLLSTDROVVPHERQPGTEMLRA DLRHVPEAVPEAFPELYWQAPPSYL GDRVSSYGGTLRYELHSETQRGDVF VPMESRPDVVLQGNQMSITFLEPAY PTPGHVHRGQLQVLEGNFRHTTETR NTVSREELMMVLASLEQLQIRALFS QISSAVFLRRVALEVASPAGQ GALAS NVELCLCPASYRGDSCQECAPGFYR DVKGLFLGRVCPCQCHGHSRDLCP GSGVCVDCQHNTGAHCERCQAGF VSSRDDPSAPCVSCPCPLSVSPNNF AEGCVLRGGRTQCLCKPGYAGASCE RCAPGFFGNPLVLGSSCQPCDCSGN GDPNLLFSDCDPLTGACRGLRHTT	True	True	1.505	4.548	1.624	1.293	0.6

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