

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
P25391	LAMA1_HUMAN	Homo sapiens	Laminin subunit alpha-1	15.760109	NaN	NaN	34019948;37217939	MRGGVLLVLLLCVAAQCQRGLFPA ILNLSNAHISTNATCGEKPEMFC KLVEHVPGRPVRNPQCRICDGNAN PRERHPISHAIDGTNNWWWQSPSIQ GREYHWVTITLDRQVFQVAVIIKA ANAPRPGNWILERSLDGTTFFSPWQY YAVSDSECLSRYNITPRRGPTTYRAD DEVICTSYYSRLVPLEHGEIHTSLING RPSADDLSPKLEFTSARYIRLRQRI RTLNADLMTLSHREPKELDPVITRR YYYSIKDISVGGMCICYGHASSCPWD ETTKKLQCCQCEHNTCGESCNRCCP GYHQQPWRPGTVSSGNTCEACNCH NKAKDCYYDESVAKQKSLNTAGQF RGGGVCINCLQNTMGINCETCIDGY YRPHKVSPEDEPCRPCNCDPVGSL SSVICDDLHSLHNGKQPGQCPCCK EGYTGEKCDRCQLGYKDYPTCVSCG CNPVGSASDEPCTGPCVCKENVEGK ACDRCKPGFYNLKEKNPRGCSECF FGVSDVCSSLSWPVGQVNSMSGWL VTDLISPRKIPSQDQALGGRHQVSI NTAVMORLAPKYWAPEAYLGNKL TAFGGFLKYTVSYDIPVETVDSNLMS HADVIKGNGLTLSTQAEGLSLQPYE EYLNVVRLVPENFQDFHSKRQIDRD QLMTVLANVTHLLIRANYSKAMAL YRLESVSLDIASSNAIDLVAADVEH CECPQGYTGTSCESCLSGYRVDGIL FGGICQPCECHGAAECNVHGVGIC CAHNTTGvhCEQCLPGFYGEPSRGT PGDCQPCACPLTIASNNFSPCTHLN DGDEVVCDWCAPGYSGAWCERCAD GYYGNPTVPGESCVPDCSGNVDP EAGHCDSVTGECLKCLGNTDGAHC ERCADGFYGDVA TAKNCRACECHV KGSHSVCHLETGLCDCKPNVTGQ QCDQCLHGYGLDSGHGCRPCNCS VAGSVSDGCTDEGQCHCVPGVAGK RCDRCAHGFYAYQDGSCTPCDPHT QNTCDPETGECVCPHTQGVKCEEC EDGHVWGYDAEVGQACNCSLVGST HHRCDVVTGHCQCKSKFGGRACDQ CSLGYRDFPDCVPCDCLRGTSGDA CNLEQGLCGVEETGACPCKENVF GPQCNECREGTFALRADNPLGCSPC FCGSLSHLCSLEEDYVRTPVTLGSD QPLL RVVSQSNLRGTTEGVYQAPD FLLDAATVROHIRAEPFYWRPQOF QGDQLMAYGGKLYSVAFYSLDGVG TSNFEPQVLKGGRIKQVIYMDAPA PENGVRQEQEVAMRENFWKYFNSV SEKPVTRDFMSVLSDIEYLIKASYG QGLQQRISDISMEVGRKAELHPE EEVASLLENCVCPGTVGFSCQDCA PGYHRGKLPAGSDRGRPLVAPCVP CSCNNHSDTCDPNTGKCLNCGDNT AGDHCDVCTSGYKVTGSASDCAL CACPHSPASFSPTCVLEGDHDFRC DACLLGYEGKHCERCSSSYGNPQT PGCSCQKDCNPHGCVHGD CDRTS GQCVCR LGASGLRCDECEPRHILME TDCVSCDDECVGVLNLDLDEIGDAV LSLNLGTIIPVYGILSNLENTTKYLQ ESLLKENMQKDLGKIKLEGVAEETD NLQKCLRMLASTQKVNATERIFK ESQDLAIAIERLQMSITEIMEKTLN QTLDEDFLLPNSTLQNMQNGTSL LEIMQIRDFTLHQNATLELKAAD LLSQIQENYQKPLEEVLKEAASHV LSKHNNELKAAEALVREAEAKMQE SNHLLLMVNANLREFSDKKLHVQE EQNLTSSELIVQGRGLIDAAAQTDV QDALEHLEDHQDKLLWSAKIRHHI DDLVMHMSQRNAVLDVYRAEDHAA EFORLADVLYSGLNIRNVSLNATSA AVVHYNIQSLIESEELARDAHRTVT ETSLLSESLVSNKAAVQRSSRFLKE	False	True	2.515	1.918	1.446	1.257	0.899	2.522	5.0

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KGAKTKELATSASQSAVSTLRDVGAL
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PGTES