	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	extra regio
0	Q9ESE1	LRBA_MOUSE	Mus musculus	Lipopolysaccharide-responsive and beige-like anchor protein	24.474581	NaN	S10;S979;S1003;S1097;S1132;S1136;S1219;S1221;S1228;S1244;S1258;S1487;S1497;S1608;S1770;S1773;S2057;S2489	33300544	MASEDNRAPSRPPTGDDGGGGGKE ETPTEGGALSLKPGLPIRGIRMKFAV LTGLVEVGEVSNRDIVETVFNLLVG GQFDLEMNFIIQEGESIMCMVELLE KCDVTCQAEVWSMFTAILKKSIRNL QVCTEVGLVEKVLGKIEKVDSMIADL LVDMLGVLASYNLTVRELKLFFSKL QGDKGQWPPHAGKLLSVLKHMPQK YGPDAFFNFPGKSAAAIALPPIARWP YQNGFTFHTWLRMDPVNNINVDKD KPYLYCFRTSKGLGYSAHFVGGCLII TSIKSKGKGFQHCVKFDFKPQKWY MVTIVHIYNRWKNSELRCYVNGELA SYGEITWFVNTSDTFDKCFLGSSETA DANRVFCGQMTAVYLFSDALNAAQI FAIYQLGLGYKGTFKFKAESDLFLAE HHKLLLYDGKLSSAIAFMYNPRATD AQLCLESSPKDNPSIFVHSPHALML QDVKAVLTHSIQSAMHSIGGVQVLF PLFAQLDYKQYLSDEVDLTICTTLLA FIMELLKNSIAMQEQMLACKGFLVI GYSLEKSSKSHVSRAVLELCLAFSKY LSNLQNGMPLLKQLCDHILLNPAV WIHTPAKVQLMLYTYLSTEFIGTVNI YNTIRRVGTVLLIMHTLKYYYWAVNP QDRSGITPKGLDGPRPNQKEILSLRA FLLMFIKQLVMKDSGVKEDELQAIL NYLLTMHEDDNLMDVLQLLVALMA EHPNSMIPAFDQRNGLRVIYKLLAS KSEGIRVQALKALGYFLKHLAPKRKA EVMLGHGLFSLLAERLMLQTNLITM TMYNVLFEILIEQICTQVIHKQHPDP DSTVKIQNPQILKVIATLLRNSPQCP ESMEVRRAFLSDMIKLFNNSRENR RSLLQCSVWQEWMLSLCYFNPKNS DEQKITEMVYAIFRILLYHAVKYEWG GWRVWVDTLSITHSKVTFEIHKENL ANIFREEQRKGDEETGPCSSSLVPE GTGATRGVDVSVGSQHEDRKDSPIS PHFTRNSDENSSIGRASSIDSASNTE LQTHDMSSDEKKVERENQELLDQA TVEETATNGAKDDLETSSDAAEPVTI NSNSLEPGKDTVTISEVSASISSPSE EDAAEMPELLEKSGVEEKEDDDYVE LKVEGSPTEEAGLPTELQGEGLSVAA SGGREEPDMCGHGCEVQVEAPITKI HNDPETTDSEDSRFPTVATAGSLAT SSEVPVPQATVQSDSHEMLDGGMK ATNLAGETESVSDCADNVSEAPATS EQKITKLDVSSVASDTERFELKASTS TEAPQPQRHGLEISRQQEQTAQGTA PDAVDQQRRDSRSTMFRIPEFKWSQ MHQRLLTDLLFSIETDIQMWRSHST KTVMDFVNSSDNVIFVHNTIHLISQ VMDNMVMACGGILPLLSAATSATH ELENIEPTQGLSIEASVTFLQRLISLV DVLIFASSLGFTEIEAEKNMSSGGIL RQCLRLVCAVAVRNCLECQQHSQL KARGDTAKSSKTIHSLIPMGKSAAKS PVDIVTGGISSVRDLDRLPARTWTLI GLRAVVFRDIEDSKQAQFLALAVVYF ISVLMVSKYRDILEPQDERHSQSLKE TSSDNGNASLPDAENTPAEFSSLTL SSVEESLEGTSCTRRRDSGLGEETAS GLGSGLSVASPAAPLGVSAGPDAISE VLCTLSLEVNKSQETRIDGGNELDR KVTPSVPVSKNVNVKDILRSLVNMP ADGVTVDPALLPPACLGALGDLSVD PPMQFRSFDRSVIIATKKSSVLPSAL TTSAPSSAVSVVSSVDPTHASDTGGE SPGSRSPKCKTALSCKQLAPSHKTPA AHMSITERLEHALEKAAPLLREIFVD FAPFLSRTLLGSHGQELLIEGTSLVC MKSSSSVVELVMLLCSQEWQNSIQ KNAGLAFIELVNEGRLLSQTMKDHL VRVANEAEFILSRQRAEDIHRHAEF ESLCAQYSADKREEEKMCDHLIRAA KYRDHVTATQLIQKIINLLTDKHGAW GSSAVSRPREFWRLDYWEDDLRRR RRFVRNPLGSTHPEATLKTAVEHAA	None	None	None	None	None	None	None	None	None

									DEDILAKGKQSIKSQALGNQNSENE ALLEGDDDTLSSVDEKDLENLAGPV SLSTPAQLVAPSVVVKGTLSVTSSEL YFEVDEEDPNFKKIDPKILAYTEGLH GKWLFTEIRSIFSRRYLLQNTALEIF MANRVAVMFNFPDPATVKKVVNYL PRVGVGTSFGLPQTRRISLATPRQLF KASNMTQRWQHREISNFEYLMFLN TIAGRSYNDLNQYPVFPWVITNYESE ELDLTLPSNFRDLSKPIGALNPKRAA FFAERFESWEDDQVPKFHYGTHYST ASFVLAWLLRIEPFTTYFLNLQGGKF DHADRTFSSVSRAWRNSQRDTSDIK ELIPEFYYLPEMFVNFNNYNLGVMD DGTVVSDVELPPWAKTSEEFVRINR LALESEFVSCQLHQWIDLIFGYKQQ GPEAVRALNVFYYLTYEGAVNLNSIT DPVLREAVEAQIRSFGQTPSQLLIEP HPPRGSAMQASPLMFTDQAQQDVI MVLKFPSNSPVTHVAANTQPGLAM PAVITVTANRLFAVNKWHNLPAHQG AVQDQPYQLPVEIDPLIACGTGTHRR QVTDLLDQSIQVHSQCFVITSDNRYI LVCGFWDKSFRVYSTDTGKLIQVVF GHWDVVTCLARSESYIGGNCYILSG SRDATLLLWYWNGKSSGIGDNPGG ETATPRAILTGHDYEITCAAVCAELG LVLSGSQEGPCLIHSMNGDLLRTLE GPENCLKPKLIQASREGHCVIFYENG CFCTFSVNGKLQATVETDDHIRAIQL SRDGQYLLTGGDNGVVIVRQVSDLK QLFAYPGCDAGIRAMALSFDQRCIIS GMASGSIVLFYNDFNRWHHEYQTR Y								