

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
P50851	LRBA_HUMAN	Homo sapiens	Lipopolysaccharide-responsive and beige-like anchor protein	18.535991	S1233;S2518;T2540	S10;S979;S1003;S1100;S1135;S1139;S1233;S1247;S1261;S1488;S1498;S1605;S1767;S1770;S2064;S2496	23301498;29351928;35132862;28510447;32119511	MASEDNRVSPSPPTGDDGGGGGRE ETPTEGGALSLKPLGPIRGIRMKFAV LTGLVEVGEVSNRDIIVTFVNLVVG GQFDLEMNFIIQEGESINCMVDLLE KCDITCQAEVWSMFTAILKKSIRNLQ VCTEVGLVEKVLGKIEKVDNMIADLL VDMLGVLASYNLTVRELKLFSSKLQ GDKGRWPPHAGKLLSVLKHMPQKY GPDAFFNFPGKSAAAIALPPIAKWPY QNGFTFHTWLRMDPVNNINVDKDK PYLYCFRTSKGLGYSAHFVGGCLIVT SIKSKGKGFQHCVKFDFKPKQKWMY VTIVHIYNRWKNSSELRCYVNGELAS YGEITWFVNTSDTFDKCFLGSSETA DANRVFCGQMTAVYLFSEALNAAQI FAIYQLGLGYKGTFFKAESDLFLAE HHKLLLYDGKLSAIAFTYNPRATDA QLCLESSPKDNPSIFVHSPHALMLQ DVKAVLTHSIQSAMHSIGGVQVLF LFAQLDYRQYLSDEIDLTCSTLLAFI MELLKNSIAMQEQLACKGFLVIGY SLEKSSKSHVSRVLELCLAFSKYLS NLQNGMPLLKQLCDHVLLNPAIWIH TPAKVQLMLYTYLSTEFITVNIYNTI RRVGTVLLIMHTLKYYYWAVNPQDR SGITPKGLDGPRPNQKEMLSLRAFL LMFIKQLVMKDSGVKEDELQAILNY LLTMHEDDNLMDVLQLLVALMSEH PNSMIPAFDQRNGLRVYKLLASKSE GIRVQALKAMGYFLKHLAPKRKAEV MLGHGLFSLLAERLMLQTNLITMTT YNVLFELIEQIGTQVIHKQHPDPDS SVKIQNPQILKVIATLLRNSPQCPES MEVRRRAFLSDMIKLFNNSRENRRSL LQCSVWQEWMLSLCYFNPKNSDEQ KITEMVYAIFRILLYHAVKYEWGGWR VWVDTLSTHSKVTFEIHKENLANIF REQQKVDDEEIGLCSSTSVQAASGIR RDINVSVGSQPDTKDSPVCPHFIT NGNENSSIEKTSSLESASNIELQTTN TSYEEMKAEQENQELPDEGTLEETL TNETRNADDLEVSSDIEAVAISNS FITGKDSMTVSEVTASISSPEEDA SEMPEFLDKSIVEEEEEDDYVELKV EGSPTEEANLPTELQDNLSPAASE AGEKLDMFGNDDKLIFQEGKPVTEK QTDTETQDSKDSGIQMTASGSSAM SPETTQSIAVESDLGQMLEEGKKA TNLTRETCLINDCHGSVSEASSEKI AKLDVSNVATDTERLELKASPNVEA PQPHRHVLEISRQHEQPGGIAPDA VNGQRRDRSRSTVFRIFEFNWSQMH QRLLTDLLFSIETDIQMWRSHSTKT MDFVNSSDNVIFVHNTIHLISQVMD NMVMACGGILPLLSAATSATHELEN IEPTQGLSIEASVTFLQRLISLVDLIF ASSLGFTIEIAEKSMSSGGILRQCLR LVCAVAVRNCLEQQHSQKTRGD KALKPMHSLIPLGKSAKSPVDIVTG GISPVRDLDRLLQDMDINRLRAVVF

RDIEDSKQAQFLALAVVYFISVLMVS
KYRDILEPQNERHSQSCTETGSENE
NVSLSEITPAAFSTLTTASVEESESTS
SARRRDSGIGEETATGLGSHVEVTP
HTAPPGVSAGPDAISEVLSTLSLEVN
KSPETKNDRGNDLDTKATPSVSVSK
NVNVKDILRSLVNIPADGVTVDPALL
PPACLGALGDLSVEQPVQFRSFDRS
VIVAAKKSAVSPSTFNNTSIPNAVSUV
SSVDSAQASDMGGESPGSRSSNAKL
PSVPTVDSVSQDPVSNMSITERLEH
ALEKAAPLLREIFVDFAPFLSRTLLG
SHGQELLIEGTSLVCMKSSSSVVELV
MLLCSQEWQNSIQKNAGLAFIELVN
EGRLLSQTMKDHLVRVANEAEFILS
RQRAEDIHRHAEFESLCAQYSADKR
EDEKMCDDLIRAAKYRDHVTATQLI
QKIINILTDKHGAWGNSAVSRPLEF
WRLDYWEDDLRRRRRFVRNPLGST
HPEATLKTAVEHVCIFKLRENSKAT
DEDILAKGKQSIRSQALGNQNSENEI
LLEGDDDTLSSVDEKDLNLAGPVS
LSTPAQLVAPSVVVKGLSVTSSELY
FEVDEEDPNFKKIDPKILAYTEGLHG
KWLFTIERSIFSRRYLLQNTALEIFM
ANRVAVMFNFPDPATVKKVVNYLPR
VGVGTSFGLPQTRRISLASPRQLFKA
SNMTQRWQHREISNFEYLMFLNTI
AGRSYNDLNQYPVFPWVITNYESEE
LDLTLPTNFRDLSKPIGALNPKRAAF
FAERYESWEDDQVPKFHYGTHYSTA
SFVLAWLLRIEPTTYFLNLQGGKFD
HADRTFSSISRAWRNSQRDTSDIKE
LIPEFYLPPEMFVNFNNYNLGVMD
GTVVSDVELPPWAKTSEEFVHINRL
ALESEFVSCQLHQWIDLIFGYKQQG
PEAVRALNVFYLYTYEGAVNLNSITD
PVLREAVEAQIRSFQTPSQLLIEPH
PPRGSAMQVSPLMFTDKAQQDVIM
VLKFPSPVTHVAANTQPGLATPA
VITVTANRLFVANKWHNLPAHQGAV
QDQPYQLPVEIDPLIASNTGMHRRQI
TDLLDQSIQVHSQCFVITSDNRYILV
CGFWDKSFVYSTDTGRLIQVVFHGH
WDVVTCLARSESYIGGCYILSGSRD
ATLLWYWNGKCSGIGDNPGETAA
PRAILTGHDYEVTC AAVCAELGLVLS
GSQEGPCLIHSMNGDLLRTLEGPEN
CLKPKLIQASREGHCVIFYENGLFCT
FSVNGKLQATMETDDNIRAIQLSRD
GQYLLTGGDRGVVVVRQVSDLKQLF
AYPGCDAGIRAMALS YDQRCIISGMA
SGSIVLFYNDFNRRWHHEYQTRY