

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
O60449	LY75_HUMAN	Homo sapiens	Lymphocyte antigen 75	26.21016	T732	T933;S1703;S1719	29351928	MRTGWATPRRPAGLLMLLFWFFDL AEPSTGRAANDPFTIVHGNTGKCIKPV YGVWVADDCDEDEDKLVKVVWSQHR LFHLHSQKCLGLDITKSVNELRMFS CDSSAMLWVKCEHHSLYGAARYRL ALKDGHGTAISNASDVVKKGGSEES LCDQPYHEIYTRDGNYSYGRPCEFPFL IDGTWHHDCILDEHDHSGPWCAATL NYEYDRKWGICLKPENGCEDNWEK NEQFGSCYQFNTQTALSWKEAYVSC QNOGADLLSINSAAELTYLKEKEGIA KIFWIGLNQLYSARGWEWSDHKPL NFLNWDPRPSAPTIGGSSCARMDA ESGLWQSFSCAEQLPYVCRKPLNNT VELTDVWVWYSDTRCDAGWLPNNGF CYLLVNESNSWDKAHAKCAFSSDL ISIHSLADVEVVTKLHNEDIKEEVW IGLKNINIPTLFQWSDGTEVTLTYWD ENEPNVPYNKTPNCVSYLGEIGQW KVQSCEEKLYVCKRKGKELNDASS DKMCPPEDEGWKRHGETCYKIYEDE VPPFGTNCNLTTSRFEQEYLNLMK KYDKSLRKYFWTGLRDVDSCEYIN WATVGGRRRAVTFSNWNFLPASP GGCVAMSTGKSVGKWEVKDCRSFK ALSICKKMSGPLGPEEASPKPDDPCP EGWQSFPAASLSCYKVFHAERIVRKR NWEEAERFCQALGAHLSSFSHVDEI KEFLHFLTDQFSGQHWLWIGLNKR SPDLQGSWQWSDRTPVSTHMPNEF QQDYDIRDCAAVKVFHRPWRRGWH FYDDREFIYLRPFACDTKLEWVCQIP KGRTPKTPDWYNPDRAIHPPLIIE GSEYWFVADLHLNVEAVLYCASNH SFLATITTFVGLKAIKNIANISGDGQ KWWIRISEWPIDDHFTYSRYPWHRF PVTFGECELYMSAKTWLIDLKPTD CSTKLPFICEKYNVSSLEKYSPPSAA KVQCSEQWIPFQNKCFKIKPVSLLTF SQASDTCHSYGGTLPVLSQIEQDFI TSLLPDMEATLWIGLRWTAYEKINK WTDNRELTYSNFHPLLVSGRLRIPE NFFEEESRYHCALILNLQKSPFTGT WNFTSCSERHFVSLCQKYSEVKSRO TLQNASETVKYLNLYKIIPKTLTWH SAKRECLKSNMQLVSTDPYQQAFL SVQALLHNSSLWIGLFSQDDELNFG WSDGKRLHFSRWAETNGLEDCVV LDTDGFWKTVDNDNQGAICYYSG NETEKEVKPVDVSKCPSVLPNTPWI PFQNCYNFIITKNRHMATTQDEVH TKCQKLNPKSHILSIRDEKENNFVLE QLLYFNYMASWVMLGITYRNKSLM WFDKTPLSYTHWRAGRPTIKNEKFL AGLSTDGFWDIQTFFKVIEEAVYFHQ HSILACKIEMVDYKEYNTTLPOFM PYEDGIYSVIQKVTWYEALNMCOSQ SGGHLASVHNQNGQLFLEDIVKRD GFPLWVGLSSHDSSESSFEWSDGS TFDYIPWKGOTSPGNCVLLDPKGTW KHEKCNVSKDGAICYKPTKSKLSR LTYSSRCPAAKENGSRWIQYKGCY KSDQALHSFSEAKKLC SKHDHSATI VSIKDEDEKFNRLMRENNITMR VWLGLSQHSVDQSWSWLDGSEVTF VKWENKSKSGVGRCSMLIASNETW KKVECEHGFGRVCKVPLGPDYTAI AIIVATLSILVLMGGLIWFLFQRHRL HLAGFSSVRYAQGVNEIMLPSFH D	False	True	2.101	2.204	1.493	1.816	1.239	4.482	4.523