

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
O75096	LRP4_HUMAN	Homo sapiens	Low-density lipoprotein receptor-related protein 4	26.21016	T604	NaN	29351928	MRRQWGALLGALLCAHGLASSPE CACGRSHFTCAVSALGECTCIPAQW QCDDGNDNDCGDHSDDEGCILPTCSPL DFHCDNGKCIIRRSWVCDGDNDCED DSDEQDCPPRECEDEFPCQNGYCI RSLWHCDGDNDCGDNDSDEQCDMR KCSDKFEFRCSGSCIAEHWYCDGDT DCKDGSDEENCPSAVPAPPNLEEF QCAYGRCLDIYHCDGDDDCGDWSD ESDCSSHQPCRSGEFMCDSGLCINA GWRCDGDADCDQSDERNCTTSM CTAEQFRCHSGRCVRLSWRCGDGED DCADNSDEENCENTGSPQCALDQF LCWNGRCIGQRKLCNGVNDCCGDN DESPQONCRPRTGEENCNVNNGGC AQKQCMVARGAVQCTCHTGYRLTED GHTCQDVNECAEEGYCSOGCTNSE GAFQWCWETGYELRPDRRCKALGP EPVLLFANRIDIRQVLPHRSEYTL NNLENAIALDFHHRRELVFWSVTL DRILRANLNGSNVEEVVSTGLESPG GLAVDWVHDKLYWTDSGTSRIEVAN LDGAHRKVLLWQNLEKPRAIALHP MEGTIYWDWGNTPRIEASSMDGS GRRRIADTHLFWPNGLTIDYAGRRM YWVDAKHHVIERANLDGSHRKAVIS QGLPHFAITVFEDSLYWDWHTKS INSANKFTGKNQEIIRNKLHFPMDI HTLHPQRQPAGKNRCGDNNGGCTH LCLPSGQNYTCACPTGFRKISSHACA QSLDKFLLFARRMDIRISFDTEDLS DDVIPLADVRSVAALDWDSDRDHVV WTDVSTDTISRAKWDGTGQEVVVD SLESPAGLADWVTKLYWTDAGTD RIEVANTDGS MRTVLIWENLDRPRD IVVEPMGGYMYWTDWGASPKIERA GMDASGRQVISSNLTWPNGLAIDY GSQRLYWADAGMKTIEFAGLDGSKR KVLIGSQLPHPFGLTYGERIYWDW QTKSIQADRLTGLDRETLQENLEN LMDIHVFHRRRPPVSTPCAMENGG CSHLCLRSPNPSGFSCTCPTGINLLS DGKTCSPGMNSFLIFARRIDIRMVSL DIPYFADVVPINITMKNTAIGVDPQ EGKVYWDSTLHRISANLDGSQHE DIITGLQTTDGLAVDAIGRKVYWTD TGTNRIEVGNLDGSMRKVLVWQNL DSPRAIVLYHEMGFMYWTDWGENA KLESGMDGSDRAVLINNNLWPN GLTVDKASSQLLWADAHTERIAAD LNGANRHTLVSPVQHPYGLTLLDSYI YWTDWQTRSIIHRADKGTGSNVILVR SNLPLGLMDMQAVDRAQPLGFNCKG SRNGGCSHLCLPRPSGFSCACPTGI QLKGDGKTCDPSPETYLLFSSRGSIR RISLDTSDHTDVHVPPELNNVISLD YDSVDGKVYYTDVFLDVIRRADLNG SNMETVIGRGLKTTDGLAVDWVAR NLYWTDTGRNTIEASRLDGSCRKVI NNSLDEPRAIAVFPKGYLFWTDWG HIAKIERANLDGSEKVLINTDLGWP NGLTLDYDTRRIYVWDAHLDRIESA DLNGLRQVLVSHVSHPFALTQQDR WYIYWDWQTKSIQRVDKYSGRNKET VLANVEGLMDIIVVSPQRGTGTNAC GVNNGGCTHLCFARASDFVCACPD EPDSRPCSLVPLVPPAPRATGMSE KSPVLPNTPTTLYSSTRTRTSLEE VEGRCSERDARLGLCARSNDVPA PGEGLHISYAIGLLSILLIVVIAAL MLYRHKKSKFTDPGMGNLTYSNPS YRTSTQEVKIEAIPKAMYNLQCYKK EGGPDHNYTKEKIKIVEGICLLSGDD AEWDDLKQLRSSRGGLLRDHVCMK TDTVSIQASSGSLDDTETEQLLQEEQ	False	True	2.527	2.542	2.474	1.128	1.346	4.729	2.671

