

| 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 |
|--------------|------------|--------------|--|--------------|---------------|-----------------------|----------|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|----------------------|
| O75197       | LRP5_HUMAN | Homo sapiens | Low-density lipoprotein receptor-related protein 5 | 22.903221    | T1122         | NaN                   | 38253038 | MEAAPPGPPWPLLLLLLLLLLALCGCP<br>APAAASPLLLFANRRDVRLVDAGGV<br>KLESTIVVSGLEDAAAVDFQFSKGA<br>YWTDVSEAIKQTYLNQTGAAVQNV<br>VISGLVSPDGLACDWVVGKKLYWTD<br>ETNRIEVANLNGTSRKVLFWQDLQ<br>PRAIALDPAHGYMYWTDWGETPRIE<br>RAGMDGSTRKIIVDSDIYWPNGLTID<br>LEEKLYWADAKLSFIHRANLDGSF<br>RQKVVEGSLTHPFALTLSGDTLYWT<br>DWQTRSIHACNKRTGGKRKEILSAL<br>YSPMDIQVLSQERQPPFFHTRCEDN<br>GGCSHLCLLSPSEPFYTCACPTGVQL<br>QDNGRTCKAGAEVLLARRTLRR<br>ISLDTPDFTDIVLQVDDIRHAIIDYD<br>PLEGYVYWTDDVRAIRRAYLDGSG<br>AQTLVNTEINPDGIAVDWVARNLY<br>WTDGTDRIEVTRLNGTSRKILVSED<br>LDEPRAIALHPVMGLMYWTDWGEN<br>PKIECANLDGQERRVLVNASLGWPN<br>GLALDLQEGKLYWGDAKTDKIEVIN<br>VDGTRRRTLLEDKLPHFGLLLGDF<br>IYWTDWQRRSIEVHKVKASRDVID<br>QLPDLMLKAVNVAKVGTNPCAD<br>RNGGCSHLCCFFPHATRCCGPIGLE<br>LLSDMKTICVPEAFLVFTSRAAIHRIS<br>LETNNNDVAIPLTGVEASALDFDV<br>SNNHIYWTDVSLKTISSAFMNGSSV<br>EHVVEFLDYPEGMAVDWMGKNLY<br>WADTGTNRIEVARLDGQFRQVLVW<br>RDLNPRSLALDPTKGIYWTEWGG<br>KPRIVRAFMDGTNCMTLVVKVGRA<br>NDLTIDYADQRLYWTDLDTNMISS<br>NMLGQERVVIADDLPHPFGLTYQSD<br>YIYWTDWNLHSIERADKTSGRNRTLI<br>QGHLDVMDILVFHSSRQDGLNDC<br>MHNNGQCGQLCLAIPEGGHRCCAS<br>HYTLDPSSRNCSPTTFLFSQKSAI<br>SRMIPDDQHSPDLILPLHGLRNVKAI<br>DYDPLDKFIYWVDGRQNIKRAKDDG<br>TQPFVLTSLSQGNPDRQPHDLSIDI<br>YSRTLFWTCEATNTINVHRLSGEAM<br>GVVLRGDRDKPRAIVNAERGLYF<br>TNMQDRAAKIERAALDGTREVLFT<br>TGLIRPVALVDNLTGKLFVVDADL<br>KRIESCDLSGANRLTLEDANIVQPLG<br>LTILGKHLIYWDROQQMIERVEKTT<br>GDKRTRIQGRVAHLTGIHAVEEVSLE<br>EFSAHPCARDNGGCSHICIAKGDGT<br>PRCSCPVHLLQNLCTGEPPTCSP<br>DQFACATGEIDCIPGAWRCDGFPEC<br>DDQSDEEGCPVCSAAQFPCARGQCV<br>DLRLRCDGEADCQDRSDEADCDAIC<br>LPNQFRCASGQCVLIKQCDSFPDC<br>IDGSDELMCEITKPPSDDSPAHSSAI<br>GPVIGIILSLFVMGGVYFVCORVVCQ<br>RYAGANGPPHEVYSGTPTHVPLNFI<br>APGGSQHGPFTGIACGKSMSSVSL<br>MGGRGGVPLYDRNHVTGASSSSSS<br>TKATLYPILNPPSPATDPSLYNMD<br>MFYSSNIPATARYRPIIRGMAPPTT<br>PCSTDVCDSDYSASRWKASKYYLDL<br>NSDSDPYPPPTPHSQYLSAEDSCPP<br>SPATERSYFHLFPPPPSPCTDSS | False         | True          | 2.551   | 3.788   | 2.141         | 4.229                 | 1.725           | 4.811           | 2.977                |

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