

| UniprotKB ID | Entry name  | organism     | full name                              | oglcnacscore | oglcnac sites                       | phosphorylation sites | PMIDS                               | sequence   | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum |
|--------------|-------------|--------------|--|--------------|-------------------------------------|-----------------------|-------------------------------------|--|---------------|---------------|---------|---------|---------------|-----------------------|
| O95490       | AGRL2_HUMAN | Homo sapiens | Adhesion G protein-coupled receptor L2 | 27.293837    | T1160;S1161;T1194;S1201;S1211;T1218 | S1374;S1409;S1430     | 40914422;23301498;34019948;38253038 | MVSSGCRMRLWFIHVISFLPNTGEF<br>SRAALPFGLVRRRELSCEGYSIDLRCP<br>GSDVIMIESANYGRTDDKICDADPFQ<br>MENTDCYLPDAFKIMTQRCNNRTQ<br>CIVVTGSDVFPDPCPGTYKYLEVQYE<br>CVPYIFVCPGTLKAIVDSPCIYEAQK<br>AGAWCKDPLQAADKIYFMPWTPYRT<br>DTLIEYASLEDFONSROTTTYKLPNR<br>VDGTGFVVYDGAFFNKERTRNIVK<br>FDLRTRIKSGEAIHNYANYHDTSPYR<br>WGGKTDIDLAVDENGLWVIYATEQN<br>NGMIVISQLNPHYTLRFEATWETVYD<br>KRAASNAFMICGVLYVVRVYQDNE<br>SETGKNSIDYINTRLNRGEYVDVPP<br>PNQYQYIAAVDYNPRDNQLYVWNN<br>NFILRYSLEFGPPDPAQVPTTAVTITS<br>SAELFKTIISTTSTTSQKGPMSITVAG<br>SQEGSKGTKPPPAAVSTTKIPPITNIFP<br>LPERFCEALDSKGIKWPTQQRGMM<br>VERPCPKGTRGTASYLCMISTGTWN<br>PKGPDLSNCTSHWVNQLAQKIRSGE<br>NAASLANELAKHTKGPVFAADVSS<br>VRLMEQLVDILDAQLQELKPSEKDS<br>AGRSYNKLQKREKTCRAYLKAIVDTV<br>DNLLRPEALESWKHMNSSEQAHTA<br>TMLLDTLEEGAFVLADNLLLEPTRVS<br>MPTENIVLEVAVLSTEGIQDFKPL<br>GIKAGAGSSIQLSANTVKQNSRNGLA<br>KLVFIYRSLGQFLSTENATIKLGADF<br>IGRNSTIAVNSHVIVSVSINKESSRVYL<br>TDPVLFITLPHIDPDNYFNANCSFWN<br>YSERTMMGYWSTQGCKLVDTNKTR<br>TTCACSHLTNFAILMAHREIAYKDG<br>VHELLLTITWVGIVISLVCLAICIFTF<br>CFFRQLQSDRNTIHKNLINLFAIEF<br>IFLIGIDKTKYAIACPIFAGLLHFFFLA<br>AFAWMCLEGVQLYMLLVEVFSEYS<br>RKYYVYVAGYLPATVVGVAADYK<br>SYGTEKACWLHVDNYFIWFSFIGPVT<br>FIILLNIIFLVITLCKMVKHSNTLKPDP<br>SSRLENIKSWVLGAFALLCLLGLTW<br>SFGLLFINEETIVMAYLFTIFNAFOG<br>VFIFIFHCALQKVRKEYGKCFRHSY<br>CCGGLPTESPHSSVKASTTRTSARYS<br>SGTQSRIRRMWVNDTVRKQSESSFIS<br>GDINSTSTLNQGMTGNLLTNPLLR<br>PHGTNNPYNTLLAETVVCNAPSAPV<br>FNSPGHSLNNARDTSAMDTPPLNG<br>NFNNSYSLHKGDYNDVSVQVDCGL<br>SLNDTAFEKMHISELVHNNLRGSSK<br>THNLETLVPKPVIGSSSEDDAIVA<br>DASSLMHSDNPGLELHHKLEAPLI<br>PORTHSLLYQPQKKVKSEGTDVYS<br>QLTAAEDHLQSPNRDSLYTSMPNL<br>RDSYPPESSPDMEDLSPSRRENE<br>DIYKSMPNLGAGHQLQMCYQISRG<br>NSDGYIIPINKEGCIPEGDVREGQMQ<br>LVTSL | False         | True          | 1.481   | 1.8     | 1.103         | 1.54                  |