

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
O88278	CELR3_RAT	Rattus norvegicus	Cadherin EGF LAG seven-pass G-type receptor 3	23.439218	NaN	T2117;T3050;S3098	38843836	MARRPLWWGLPGPSTPLLLLLFSL FPSSREEMGGGGDQGWDPGVATAT GPRAQIGSGAVALCPESPGVWEDGD PGLGVREPVMKLRVGRQNRNGR GAPEQPNREPVVQALGSREQEAGQG SGYLLCWHPEISSCGRTGHLRRGSL PLDALSPGDSDLRNSSPHPSELLAQ PDSRPVAFQRNGRRSIRKRVETFR CCGKLWEPGHKQGERSATSTVDR GPLRRDCLPGSLGSLGEDSAPRAV RTAPAPGSAPHE SRTAPERMRSRGL FRRGFLFERPGPRPPGFFTGAEEKRI LSTNQARRAANRHPOFPQYNYQT LVPENEAAGTAVLRVVAQDDPDPGEA GRLVYSLAALMNSRSELEFSIDPQSG LIRTAALDRESMERHYLRVTAQDH GSPRLSATTMVAVTVADRNDHAPVF EQAQYRETLRENVEEGYPILQLRATD GDAPPANLRYRFVGSAAARTAAAA AFEIDPRSGLISTSGRVDREHMESYE LVVEASDQGEPEGPRSATVRVHITVL DENDNAPQFSEKRYVAQVREDVRP HTVVLRVTATDKDKDANGLVHYNIS GNSRGHFAIDSLTGEIQVMAPLDFE AEREYALRIRAQDAGRPPLSNNTGL ASIQVVDINDHSPFVSTPFFQVSVLE NAPLGHSVIHQAVDADHGENSRLE YSLTGVASDTPFVINSATGWVSVSGP LDRESVEHYFFGVEARDHGSPLSA SASVTVTLDVNDNRPEFTMKEYHL RLNEDAAVGTSVVSVTAVDRDANSA ISYQITGNGTRNRFAISTQGGMGLVT LALPLDYKQERYFKLVTASDRALHD HCYVHINITDANTHRPVFQSAHYSV SMNEDRPVGSVVVISASDDDDVGEN ARITYLLEDNLPQFRIDADSGAITLQA PLDYEDQVYTLAITARDNGIPQKAD TTYVEVMVNDVNDNAPQFVASHYT GLVSEDAPPFTSVLQISATDRDAHAN GRVQYTFQNGEDGDFTIEPTSGI VRTVRRLDREAVPVYELTAYAVDRG VPPLRTPVSIQVTVQDVNDNAPVFPA EEFEVRVKENSIVGSVVAQITAVDPD DGNNAHIMYQIVEGNIPELFQMDIFS GELTALIDLDEARQYEVVIVVQATSA PLVSRATVHVRLVDQNDNSPVLNMF QILFNMYVSNRSDTFPSGIIRIPAYD PDVSDHLFYSFERGNELQLLVNVQT SGELRLSRKLDNNRPLVASMLVTVT DGLHSVTAQCVLRVVIITEELLANSL TVRLENMWQERFLSPLLGHFLEGV AAVLATPTEDVFIFNIQNDTDVGGTV LNVFSALAPRGAGAGAAGPWFSSSE ELQEQLYVRRRAALARSLLDVLFPD DNVCLREPCENYMKCVSVLRFDSSA PFLASASTLFRPIQIAGLRRCRCPGPF TGDFCETELDLCYSNPCRNGGACAR REGGYTCVCRPRFTGEDCELDTEAG RCVPGVCRNGGTCTNAPNGGFRCQ CPAGGAFEGPRCEVAARSFPPSSFV MFRGLRQRHLLTSLSFATVQPSGL LFYNGRLNEKHDFLALELVAGQVRL TYSTGESSTVVSPTVPGGLSDGQWH TVHLRYYNKPRTDALGGAQGPSKDK VAVLSVDDCNVAVALRFGAEIGNYS CAAAGVQTSKKSLDLTGPLLLGGVP NLPENFPVSRKDFIGCMRDLHIDGR RVDMAAFVANNGTAGCQAKSHFC ASGPCKNGGLCSERWGGFSCDCPV GFGGKDCRLTMAHPYHFQNGTSL WDFGNDMPVSPWYLGSLFRTRAT KGVLMQVQLGPHSVLLCKLDQGLLS VTLSTRASGHAVHLLDQMTVSDGR WHDLRLELQEEPPGRRGHIFMVS LDFTLFQDTMAMGSELEGLKVKHL	False	True	False	1.236	0.718	0.512	0.567	5.0	1.232

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TEQLDILSSILASFNSSALSSVQSS
PSGPHTTATPSATASALGPSTPRSAT
SHSISELSPDSEVPRSEGH