

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9HCU4	CEL2_HUMAN	Homo sapiens	Cadherin EGF LAG seven-pass G-type receptor 2	12.395336	S2072	NaN	32574038;35289036;35138101	MRSPATGVPLPTPPPLLLLLLLLLLPP PLLGDQVGPCRSLGSRGRGSSGACA PMGWLCPPSSASNLWLYTSRCRDAG TELTGHLVPHHDGLRVWCPESEAH PLPPAPEGCPWSCRLLGIGGHLSPQ GKLTLP EEHPCLKAPRLRCQSCCLA QAPGLRAGERSPEESLGRRKRNVN TAPQFQPPSYQATVPENQPAGTPVA SLRAIDPDEGEAGRLEYTMDALFDS RSNQFFSLDPVTGAVTTAEELDRET KSTHVFRVTAQDHGMPRRSALATLT ILVTDTNDHDPVFEQQEYKESLREN LEVGYEVLTVRATDGDAPPNANILYR LLEGSGGSPSEVFEIDPRSGVIRTRG PVDREEVESYQLTVEASDQGRDPGP RSTTAAVFLSVEDDNDNAPQFSEKR YVVQVREDVTPGAPVLRVTASDRDK GSNAVVHYSIMSGNARGQFYLDAQT GALDVVSPLDYETTKEYTLRVRAQD GGRPPLSNVSGLVTVQVLDINDNAPI FVSTPFQATVLESVPLGYLVLVHVQAI DADAGDNARLEYRLAGVGHDFPFTI NNGTGWISVAAELDREEVDFYSFGV EARDHGTPALTASASVSVTVLDVND NNPTFTQPEYTVRLNEDAAVGTSVV TVSAVDRDAH SVITYQITSGNTRNRF SITSQSGGLVSLALPLDYKLERQYV LAVTASDGTRQDTAQIVNVNTDANT HRPVFQSSH YTVNVNEDRPAGTTVV LISATDED TGENARITYFMEDSIPQF RIDADTGAVTTQ AELDYEDQVSYTLA ITARDNGIPQKSDTTYLEILVNDVND NAPQFLRDSYQGSVYEDVPPFTSVL QISATDRDSGLNGRVFYTFQGGDDG DGD FIVESTSGIVRTLRRLDRENVAQ YVLRAYAVDKGMPPPARTPMEVTVTV LDVNDNPPVFEQDEFDVFVEENSPI GLAVARVTATDPDEGTNAQIMYQIV EGNIPEVFQLDIFSGELTALVDLDYE DRPEYVLVIQATSAPLVSRATVHVRL LDRNDNPPVLGNFEILFN NYVTNRS SSFPGGAIGRVPAHDPDISDSLTYSF ERGNELSLVLLNASTGELKLSRALD NNRPLEAIMSVLVSDGVHSVTAQCA LRVTIITDEMLTHSITLRLEDMSPER FLSPLLGLFIQAVAATLATPPDHVVV FNVQRDTDAPGGHILNVSLSVGQPP GPGGGPPFLPSEDLQERLYLNRSLLT AISAQRVLPFDDNICLREPCENYMR

CVSVLRFDSSAPFIASSSVLFRPIHPV  
GGLRCRCPPGFTGDYCETEVDLCYS  
RPCGPHGRCSREGGYTCLCRDGYT  
GEHCEVSARSGRCTPGVCKNGGTC  
VNLLVGGFKDCDCPSGDFEKPYCQVT  
TRSFPAHSFITFRGLRQRFHFTLALS  
FATKERDGLLLYNGRFNEKHDFVAL  
EVIQEQVQLTFSAGESTTTVSPFVPG  
GVSDGQWHTVQLKYYNKPLLQGTG  
LPQGPSEQKVAVVTVDGCDTGVALR  
FGSVLGNYSCAAQGTQGGSKKSLDL  
TGPLLLGGVPDLPEFVVRMRQFVG  
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PGCPAKKNVCDSENTCHNGGTCVNQ  
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LMFRTRQADGVLLQAITRGRSTITLQ  
LREGHVMLSVEGTGLQASSLRLEPG  
RANDGDWHHAQLALGASGGPGHAI  
LSFDYGQORAEGNLGPRHLHGLHS  
NITVGGIPGPAGGVARGFRGCLQGV  
RVSDTPEGVNSLDP SHGESINVEQG  
CSLPDPCDSNPCPANSYCSNDWDSY  
SCSCDPGYYGDNCTNVCDLNPCEH  
QSVCTRKPSAPHGYTCECPPNYLGP  
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CDVSKGFDPCNKTSGECHCKENH  
YRPPGSPTCLLCDCYPTGSLSRVCDP  
EDGQCPCPKGVIGRQCDCRDNPF AE  
VTTNGCEVNYDSCPRAIEAGIWWPR  
TRFGLPAAAPCPKGSFGTAVRHCDE  
HRGWLPPNLFNCTSITFSELKGF AE  
RLQRNESGLDSGRSQQLALLLRNAT  
QHTAGYFGSDVKVAYQLATRLLAHE  
STQRGFGLSATQDVHFTENLLRVGS  
ALLDTANKRHWELIQQTEGGTAWLL  
QHYEAYASALAQNMRHTYLSPTIV  
TPNIVISVVRDKGNFAGAKLPRYEA  
LRGEQPPDLETTVILPESVFRETTPV  
VRPAGPGEAQEPEELARRRRHPEL  
SQGEAVASVIIYRTLAGLLPHNYDPD  
KRSLRVPKRPIINTPVVSISVHDDEEL  
LPRALDKPVTVQFRLLETEERTKPIC  
VFWNHSILVSGTGGWSARGCEVVF  
RNESHVSCQCNHMTSFAVLMDVSR  
RENGEILPLKTLTYVALGVTLAALLLT  
FFFLTLLRILRSNQHGIRRNLTAALG  
LAQLVFLGINQADLPFACTVIAILLH  
FLYLCTFSWALLEALHLYRALTEVRD  
VNTGPMRFYYMLGWGVPAFITGLAV  
GLDPEGYGNPDFCWLSIYDTLIWSF  
AGPVAFVSMVFLYILAAARASCAAQ

