

UniprotKB ID	Entry name	organism	full name	oglcna score	oglcna sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi appara
Q9NYQ7	CEL3_HUMAN	Homo sapiens	Cadherin EGF LAG seven-pass G-type receptor 3	29.523143	S3064;S3286;T3287;S3300;S3308	T2126;T3051;S3097	35254053;38253038;29237092	MMARRPPWRGLGGRSTPILLLLLLL LFPLSQEELGGGGHGWDPGLAATT GPAHIGGGALALCPESGVRDGG PGLGVREPIFVGLRGRRSARNRSG PPEQPNEELGIEHGVQPLGSRERET GQGGSVLYWRPEVSSCGRTGPLQR GSLSPGALSSGVPGSGNSSPLPSDFL IRHHGPKPVSSQRNAGTGSRRKRVGT ARCCGELWATGSKGQGERATTSGAE RTAPRRNCLPGASGSGPELDSAPRT ARTAPASGSAPRESRTAPEPAPKRM RSRGLFRCRFLPQRPGPRPPLPARP EARKVTSANRARFRRAANRHPQFPQ YNYQTLVPENEAAGTAVLRVVAQDP DAGEAGRLVYSLAALMNSRSLELFSI DPOSGLIRTAALDRESMERHYLRV TAQDHGSPRLSATTMVAVTVADRND HSPVFEQAQYRETLRENVEEGYPII QLRATDGDAPPNANLRYRFVGPAA RAAAAAAFEIDPRSGLISTSGVDRE HMESYELVVEASDQGOEPGRSATV RVHITVLDENDNAPOFSEKRYVAQV REDVRPHTVLRVTATDRDKDANGL VHYNIISGNSRGHFAIDSLTGEIQVV APLDFEAEREYALRIRAQDAGRPPLS NNTGLASIQVVDINDHIPIFVSTPFQ VSVLENAPLGHSVIHQAVDADHGE NARLEYSLTGVPDTPFVINSATGW VSVSGPLDRESVEHYFFGVEARDHG SPPLSASASVTVLDVNDNRPEFT MKEYHLRLNEDAAGTVSVSVTAVD RDANSASISYQITGGNTRNRFAISTQG GVGLVTLALPLDYKQERYFKLVLTAS DRALHDHCYVHINITDANTHRPVFQ SAHYSVSVNEDRPMGSTIVVISASDD DVGENARITYLLEDNLPQFRIDADSG AITLQAPLDYEDQVYTLAITARDNGI PQKADTTYEVVMVNDVNDNAPQFV ASHYTGTVSEDAPPFTSVLQISATDR DAHANGRVQYTFONGEDGDGDFTI EPTSGIVRTVRRLDREAVSVYELTAY AVDRGVPLRTPVSIQVMVQDVNDN APVFPAAEFVVRVKENSIVGSVAQI TAVDPDEGPNAHIMYQIVEGNIPELF QMDIFSGELTALIDLYEARQEVVIV VQATSAPLVSRAVHVRLVDQNDNS PVLNNFQILFNYYVSNRSDTFPSGII GRIPAYDPDVSDFLHLYSFERGNELQ LLVVNQTSGELRLSRKLDNNRPLVA SMLVTVTDGLHSVTAQCVRVVIITE ELLANSLTVRLENMWQERFLSPLL RFLEGVAALVATPAEDVFIFINQNDT DVGTVLNVFSALAPRGAGAGAAG PWFSSSEELQEQLYVRAALAARSL DVLPFDDNVCLREPCENYMKCVSVL RFDSSAPFLASASTLFRPIQPIAGLRC RCPFGFTGDFCETELDLCSNPCR GGACARREGGYTCVCRPRFTGEDCE LDTEAGRCVPGVCRNGTCTDAPN GGFRCQCAGGAFEGPRCEVAARSF PPSSFVFRGLRQRFHLLTSLSFAT VQSGLLFYNGRLNEKHDFLALFLV AGQVRLTYSTGESNTVVSPTVPGLS DGQVHTVHLRYNKPRTDALGGAQ GPSKDKVAVLSVDDCDVAVALQFGA EIGNYSCAAAGVQTSKSKSLDLTGPL LLGGVPLPENFPVSHKDFIGCMRD LHIDGRRVDMAAFVANNGTMAGCQ AKLHFCDSGPKNSGFCSERWGSF SCDCPVGFGGKDCQLTMAHPHHFR GNGTLSWNFGSDMAVSPWYGLA FRTRATQGVLMQVQAGPHSTLLCQL DRGLLSVTVTRGSGRASHLLLDQVT VSDGRWHDRLRLELQEEPGRRGH VLMVSLDFSLFQDTMAVSGSELQGLK VKQLHVGGLPPGSAEEAPQGLVCCI QGVWLGSTPSGSPALLPPSHRVNAE PGCVVTNACASGCPPHADCRDLW QTFSTCQPGYYGPGCVDAALLNPC QNQGSCHRLPGAPHGYTCDVCGGY	False	True	0.995	1.519	0.988	0.827	0.896

FGHHCHEHRMDQQCPRGWWSPTC  
GPCNCDVHKGFDPNCNKTNGQCH  
CKEFHYRPRGSDSCLPCDCYPVGS  
SRSCAPHSGQCPCRPALGROCNCS  
DSPFAEVTASGCRVLYDACPKSLRS  
GVWWPQTKFGLATVPCPRGALGA  
AVRLCDEAQGWLEPDLFNCTSPA  
ELSLLLDGLELNKTALDTMEAKKLA  
QRLREVTGHTDDHYFSQDVRVTARLL  
AHLAFESHQQGFGLTATQDAHFN  
ENLLWAGSALLAPETGDLWAALGO  
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NMELTYLNPMLVTPNIMLSIDRME  
HPSSPRGARRYPRYHSNLFQDA  
WDPHTHVLLPSQSPRPSPEVLPTS  
SSIENSTTSSVPPAPPEPEPGISIII  
LLVYRTLGGLLPAQFQAERRGARLP  
QNPVMNSPVVSVAVFHGRNFLRGIL  
ESPISLEFRLLQTANRSKAICVQWDP  
PGLAEQHGVTARDCELVHRNGSH  
ARCRCRTGTGVLMDASPRERLEG  
DLELLAVFTHVVAVSVAALVLTAAI  
LLSLRSLKSNVRGIHANVAAALGVAE  
LLFLLGIHRTNQLVCTAVAILLHYF  
FLSTFAWLFVQGLHLYRMQVEPRN  
VDRGAMRFYHALGWVPAVLLGLA  
VGLDPEGYGNPDFCWISVHEPLIWS  
FAGPVVLVIVMNGTMFLLAARTSCS  
TGQREAKKTSALTLRSSFLLLLVSA  
SWLFGLLAVNHSILAFHYLHAGLCG  
LQGLAVLLFCVLNADARAAMPA  
CLGRKAAPFEARPAAPGLGPGAYNNT  
ALFEESGLIRITLGASTVSSVSSARSG  
RTQDQDSQRGRSYLRDNVLRHGS  
AADHTDHSLSLAHAGPTDLVAMFH  
RDAGADSDSDSLSLEEERSLSIPSS  
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PCALQTWGSEERLGLDTSKDAANN  
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RPLDSLRSNSREQLDQVPSRHPS  
REALGPLQLLRAREDSVSGPSHGP  
STEQLDILSSILASFNSALSSVQSSS  
TPLGPHTTATPSATASVLGPSTPRSA  
TSHSISELSPDSEVRSEGH