	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	p n
0	O35161	CELR1_MOUSE	Mus musculus	Cadherin EGF LAG seven-pass G-type receptor 1	28.302299	S307;S2773;T2774;T2780;T2781	S2776;S2779;S2886;S2888	30016717;34418053	MAPSSPRVLPALVLLAAAALPALELG AAAWELRVPGGARAFALGPGWSYRL DTTRTPRELLDVSREGPAAGRRLGL GAGTLGCARLAGRLLPLQVRLVARG APTAPSLVLRARAYGARCGVRLLRRS ARGAELRSPAVRSVPGLGDALCFPA AGGGAASLTSVLEAITNFPACSCPPV AGTGCRRGPICLRPGGSAELRLVCAL GRAAGAVWVELVIEATSGTPSESPSV SPSLLNLSQPRAGVVRRSRRGTGSS TSPQFPLPSYQVSVPENEPAGTAVIE LRAHDPDEGDAGRLSYQMEALFDE RSNGYFLIDAATGAVTTARSLDRETK DTHVLKVSAVDHGSPRRSAATYLTV TVSDTNDHSPVFEQSEYRERIRENL EVGYEVLTIRATDGDAPSNANMRYR LLEGAGGVFEIDARSGVVRTRAVVD REEAAEYQLLVEANDQGRNPGPLSA SATVHIVVEDENDNYPQFSEKRYVV QVPEDVAVNTAVLRVQATDRDQGQ NAAIHYSIVSGNLKGQFYLHSLSGSL DVINPLDFEAIREYTLRIKAQDGGRP PLINSSGLVSVQVLDVNDNAPIFVSS PFQAAVLENVPLGHSVLHIQAVDAD AGENARLQYRLVDTASTIVGGSSVDS ENPASAPDFPFQIHNSSGWITVCAE LDREEVEHYSFGVEAVDHGSPAMSS SASVSITVLDVNDNDPMFTQPVYEL RLNEDAAVGSSVLTLRARDRDANSV ITYQLTGGNTRNRFALSSQSGGGLIT LALPLDYKQERQYVLAVTASDGTRS HTAQVFINVTDANTHRPVFQSSHYT VSVSEDRPVGTSIATISATDEDTGEN ARITYVLEDPVPQFRIDPDTGTIYTMT ELDYEDQAAYTLAITAQDNGIPQKSD TTSLEILILDANDNAPRFLRDFYQGS VFEDAPPSTSVLQVSATDRDSGPNG RLLYTFQGGDDGDGDFYIEPTSGVIR TQRRLDRENVAVYNLWALAVDRGSP NPLSASVGIQVSVLDINDNPPVFEKD ELELFVEENSPVGSVVARIRANDPD EGPNAQIMYQIVEGNVPEVFQLDLL SGDLRALVELDFEVRRDYMLVVQAT SAPLVSRATVHIRLLDQNDNPPELPD FQILFNNYVTNKSNSFPSGVIGRIPA HDPDLSDSLNYTFLQGNELSLLLLD PATGELQLSRDLDNNRPLEALMEVS VSDGIHSVTALCTLRVTIITDDMLTN SITVRLENMSQEKFLSPLLSLFVEGV ATVLSTTKDDIFVFNIQNDTDVSSNI LNVTFSALLPGGTRGRFFPSEDLQE QIYLNRTLLTTISAQRVLPFDDNICLR EPCENYMKCVSVLRFDSSAPFISSTT VLFRPIHPITGLRCRCPPGFTGDYCE TEIDLCYSNPCGANGRCRSREGGYT CECFEDFTGEHCQVNVRSGRCASG VCKNGGTCVNLLIGGFHCVCPPGEY EHPYCEVSTRSFPPQSFVTFRGLRQ RFHFTVSLAFATQDRNALLLYNGRF NEKHDFIALEIVEEQLQLTFSAGETT TTVTPQVPGGVSDGRWHSVLVQYYN KPNIGHLGLPHGPSGEKVAVVTVDD CDAAVAVHFGSYVGNYSCAAQGTQS GSKKSLDLTGPLLLGGVPNLPEDFPV HSRQFVGCMRNLSIDGRIVDMAAFI ANNGTRAGCASQRNFCDGTSCQNG GTCVNRWNTYLCECPLRFGGKNCE QAMPHPQRFTGESVVLWSDLDITIS VPWYLGLMFRTRKEDGVLMEATAG TSSRLHLQILNSYIRFEVSYGPSDVA SMQLSKSRITDGGWHHLLIELRSAK EGKDIKYLAVMTLDYGMDQSTVQIG NQLPGLKMRTIVIGGVTEDKVSVRH GFRGCMQGVRMGETSTNIATLNMN DALKVRVKDGCDVEDPCASSPCPPH SHCRDTWDSYSCICDRGYFGKKCVD ACLLNPCKHVAACVRSPNTPRGYSC ECGPGHYGQYCENKVDLPCPKGWW GNPVCGPCHCAVSQGFDPDCNKTN GQCQCKENYYKPPAQDACLPCDCFP	False	True	1.352	3.019	1.103	1.121	1.099	5

									HGSHSRACDMDTGQCACKPGVIGR QCNRCDNPFAEVTSLGCEVIYNGCP RAFEAGIWWPQTKFGQPAAVPCPKG SVGNAVRHCSGEKGWLPPELFNCT SGSFVDLKALNEKLNRNETRMDGN RSLRLAKALRNATQGNSTLFGNDVR TAYQLLARILQHESRQQGFDLAATR EANFHEDVVHTGSALLAPATEASWE QIQRSEAGAAQLLRHFEAYFSNVAR NVKRTYLRPFVIVTANMILAVDIFDK LNFTGAQVPRFEDIQEELPRELESSV SFPADTFKPPEKKEGPVVRLTNRRTT PLTAQPEPRAERETSSSRRRRHPDE PGQFAVALVVIYRTLGQLLPEHYDPD HRSLRLPNRPVINTPVVSAMVYSEG TPLPSSLQRPILVEFSLLETEERSKPV CVFWNHSLDTGGTGGWSAKGCELL SRNRTHVTCQCSHSASCAVLMDISR REHGEVLPLKIITYAALSLSLVALLVA FVLLSLVRTLRSNLHSIHKNLITALF FSQLIFMVGINQTENPFLCTVVAILL HYVSMGTFAWTLVENLHVYRMLTE VRNIDTGPMRFYHVVGWGIPAIVTG LAVGLDPQGYGNPDFCWLSLQDTLI WSFAGPVGTVIIINTVIFVLSAKVSCQ RKHHYYERKGVVSMLRTAFLLLLLV TATWLLGLLAVNSDTLSFHYLFAAF SCLQGIFVLLFHCVAHREVRKHLRA VLAGKKLQLDDSATTRATLLTRSLN CNNTYSEGPDMLRTALGESTASLDS TTRDEGVQKLSVSSGPARGNHGEPD ASFIPRNSKKAHGPDSDSDSELSLD EHSSSYASSHTSDSEDDGGEAEDK WNPAGGPAHSTPKADALANHVPAG WPDESLAGSDSEELDTEPHLKVETK VSVELHRQAQGNHCGDRPSDPESG VLAKPVAVLSSQPQEQRKGILKNKVT YPPPLPEQPLKSRLREKLADCEQSPT SSRTSSLGSGDGVHATDCVITIKTPR REPGREHLNGVAMNVRTGSAQANG SDSEKP							