

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane
Q8WXG6	MADD_HUMAN	Homo sapiens	MAP kinase-activating death domain protein	40.896779	S826;T834	S156;S689;S692;S813;S818;S820;S858;S862;S916;S921;S930;S1059;T1061;T1066;S1110;T1237;S1239;S1270	29351928;40914422;28657654	MVQKKKFCPRLLDYLIVIGARHPSS DSVAQTPELLRRYPLEDHTEFPLPPD VVFQCQPEGCLSVRQRMSLRDSTS FVFTLTDKDTGVTRYGICVNFYRSFQ KRISKEKGEKGAGSRGKEGTHATCA SEEGTESSESGLQPLSADSTPDV NQSPRGKRRKAGSRSRNSTLTLSC VLSHYPPFFSTFRECLYTLKRLVDCCS ERLLGKKGIPRGVQRTMWRIFTG SLLVEEKSSALLHDLREIEAWIYRLL RSPVPVSGQKRVDIEVLPQELQPALT FALPDPSPRFTLVDFPLHLPLELLGVD ACLQVLTCILLEHKVVLQSRDYNALS MSVMAFVAMIYPLEYMFVPIPLPTC MASAEQLLLAPTYIIGVPA SFFLYKLL DFKMPDDVWLVDLDSNRVIAPTNA EVLPIPEPESELEKHLKQALASMS LNTQPILNLEKFHEGQEIPLLGRPS NDLQSTPSTEFNPLYGNDVDSVDV ATRVAMVRFNSANVLQGFQMHTR TLRLFRPVVAFQAGSFLASRPQTP FAEKLARTQAVEYFGEWILNPTNYA FORIHNNMFDPALIGDKPKWYAHQ LQPIHYRVYDSNSQLAEALSVPPERD SDSEPTDSDSGSDSMDYDSSSSYSS LGDVFSEMMKCDINGDTPNVDPALT HAALGDASEVEIDELQNKAEAEPPG PDESENQENPLRSSSTTASSSPST VIHGANSEPADSTEMDDKAAVGVSK PLPSVPPSIGKSNVDRRQAEIGEGSV RRRIYDNPYFEPQYGFPEEDEDQ GESYTPRFHQVSGNRAQKLLRPNS LRLASDSDAESDRASSPNSTVSN STEGFGGIMSFASSLYRNHSTSFSL NLTLPTKGAREKATPFFSLKVFGLNT LMEIVTEAGPGSGEGNRRLVLDQKS SVIKHSPTVKREPPSPQGRSSNSEN QQFLKEVVHSLVDGQGVGWLNMKK VRRLESEQLRVFVLSKLNRMVQSE DDARQDIIIPDVEISRKVYKMLDLLK CTVLSLEQSYAHAGLGGMASIFGLL EIAQTHYYSKEPDKRKRSPTESVNT VGKDPGLAGRGDPKAMAQLRVPQL GPRAPSATGKGPKELDTRSLKEENFI ASIELWNKHQEVKKQKALEKQRPEV IKPVFDLGETEEKKSQISADSGVSLT SSSQRTDQDSVIGVSPAVMIRSSSQD SEVSTVSNSSGETLGADSDLSSNA GDGPGGEGSVHLASSRGTLSDEIE TNSATSTIFGKAHSLKPSIKELAGS PIRTSEVSRVYLYEGLLGRDKGS MWDQLEDAAMETFSISKERSTLWD QMWFVEDAFLDVMLEREGMGMD QGPQEMIDRYLSLGEHDRKRELDDE DRLLATLLHNLSYMLLMKVNKNDI RKKVRRMLMGKSHIGLVYSQQINEVL DQLANLNGRDLISWSSGRHMKKQ TFVVHAGTDTNGDIFFMEVCDCCVV LRSNIGTVYERWWYEKLINMTYCPK TKVLCLWRRNGSETQLNKFYTKKCR ELYCVKDSMERAARQOSIKPGPE LGGEFPVQDLKTGEGGLOVLEGI NLKFMHNQVFIELNHIKCNVTRGV FVLEEFVPEIKVVSFKYKTPMAHEI CYSVLCVFSYVAAVHSSEEDLRTPPR PVSS	True	True	4.627	2.191	1.746	1.401	1.754	4.627