

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	29.375916	S826;T834	S156;S689;S692;S813;S818;S820;S858;S862;S916;S921;S930;S1059;T1061;T1066;S1110;T1237;S1239;S1270	28657654;29351928	MVQKKKFCPRLLDYLIVGARHPSS DSVAQTPELLRRYPLEDHTEFFLPDP VVFQCPEGCLSVRQRRMSLRDDTS FVFTLTKDGTGVTRYGICVNFYRSFQ KRISKEKGEAGSRRGKEGTHATCA SEEGGTESSESGSSLQPLSADSTPDV NQSPRGKRRAKAGSRSRNSTLTSLC VLSHYPPFFSTFRECLYTLKRLVDCCS ERLLGKKLGIPRGVQRTMWRIFTG SLLVEEKSSALLHDLREIEAWYRLL RSPVPVSGQKRVIEVLPQELQPALT FALPDPDSRFTLVDFPLHLPLELLGVD ACLQVLTCLLEHKVVLQSRDYNALS MSVMAFVAMIYPLEYMFVPIPLLPTC MASAEQLLLAPTYIIGVPASFFLYKL DFKMPDDVWLVLDLSNRVIAPNA EVLPIPEPESELEKHLKQALASMS LNTQPILNLEKFHEGQEIPLLGRPS NDLQSTPSTEFNPLIYGNDDVSDV ATRVAMVRFNSANVLQGFQMHTR TLRLFPRPVAFQAGSFLASRPRQTP FAEKLARTQAVEYFGEWILNPTNYA FORIHNNMFDPALIGDKPKWYAHQ LQPIHYRVYDSSQLAEALSVPPEPD SDSEPTDDSGSDSMYDSSSSYSS LGFVSEMMKCDINGDTPNVPLT HAALGDASEVEIDELQNKAEAEPPG PDSSENQENPLRSSSSTASSPST VIHGANSEPADSTEMDDKAAVGVSK PLPSVPPSIGKSNVDRRQAEIGESV RRRIYDNPYFEPQYGFPEEDEDQ GESYTPRFSQHVSIGNRAQKLLRPNS LRLASDSDAESDRASSPNSTVSNT STEGFGGIMSFASSLYRNHSTSFSL NLTLPTKGAREKATPFPSLKVFLNT LMEIVTEAGPGSGEGNRRALVDQKS SVIKHSPTVKREPPSPQGRSSNSSEN QQFLKEVHVSVDGQGVGLNMKK VRRLESEQLRVFVLSKLNRMVQSE DDARQDIIPDVEISRKYKGMILLK CTVLSLEQSYAHAGLGGMASIFGLL EIAQTHYYSKEPKRKRSPTESVNTP VGKDPGLAGRDPKAMAQLRVPQL GPRAPSATGKGPKELDTRSLKEENFI ASIELWNKHQEVKKQKALEKORPEV IKPVFDLGETEEKKSQISADSGVSLT SSSQRTDQDSVIGVSPAVMIRSSSQD SEVSTVVSNSSETLGADSDLSSNA GDGPGGEGSVHLASSRGTLSDEIE TNSATSTIFGKAHSLKPSIKELAGS PIRTSEVVSQRVLYEGLLGRDKGS MWDQLEDAAMETFSISKERSTLWD QMQFWEDAFLDVAMLEREGMGMD QGPOEMIDRYLSLGEHDKRLEDDE DRLLATLLHNLISYMLLMKVNKNDI RKKVRRMLMGKSHIGLVYSQQINEVL DQLANLNGRDLISWSSGSRHMKKQ TFVVHAGTDTNGDIFFMEVCDCCVV LRSNIGTVYERWYKLNMTYCPK TKVLCWRRNGSETQLNKFYTKKCR ELYVCVKDSMERAARQOSIKPGPE LGGEFPVQDLKTGEGLLQVTLEGI NLKFMHNQVFIELNHIKKNVTRGV FVLEEFVPEIKEVVSHKYKTPMAHEI CYSVLCVSYVAHVHSEEDLRTPPR PVSS	True	True	4.627	2.197	1.744	1.405	1.756	4.673