	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extrac region
0	O08873	MADD_RAT	Rattus norvegicus	MAP kinase-activating death domain protein	32.913164	NaN	S155;S688;S691;S778;S812;S817;S819;S857;S861;S895;S900;S909;S1038;T1040;T1045;S1089;T1194;S1196;S1225	17496889;19322778	MVQKKFCPRLLDYLVIVGARHPSSD SVAQTPELLRRYPLEDHPEFPLPPDV VFFCQPEGCLSVRQRRMSLRDDTSF VFTLTDKDTGVTRYGICVNFYRSFQK RMPKEKAEGGAGPRGKEGAHAPCA SEEAATESSESGSTLQPPSADSTPDV NQSPRGKRRAKAGNRSRNSTLTSLC VLSHYPFFSTFRECLYTLKRLVDCCS ERLLGKKPGIPRGVQRDTMWRIFTG SLLVEEKSSALLHDLREIEAWIYRLL RSPVPVSGQKRVDIEVLPQEVQQALT FALPDPSRFTLVDFPLHLPLELLGVD ACLQVLTCILLEHKVVLQSRDYNALS MSVMAFVAMIYPLEYMFPVIPLLPTC MASAEQLLLAPTPYIIGVPASFFLYKL DFKMPDDVWLVDLDSNRVIAPTNA EVLPILPEPESLELKKHLKQALASMS LNTQPILNLEKFHEGQETPLLLGRFS NDLQSTPSTEFNPLIYGNDVDSVDV ATRVAMVRFFNSANVLQGFQMHTR TLRLFPRPVVAFQAGSFLASRPRQTP FAEKLARTQAVEYFGEWILNPSNYA FQRIHNNTFDPALIGDKPKWYAHQL QPIHYRVYDSNSQLAEALSVPPERDS ESDPTDDSGSDSMDYDDSSSSYSSL GDFVSEMMKCDINGDTPNVDPLTH AALGDASEVEIDELQPQKEGEEPGP DSENSQENLPLRSSSSTTASSSPSTI VHGAHSEPADSTEVGDKAATGISKP LPPVPPSICKSTVDRRQTETGEGSVC QRTYDHPYFEPQYGSPAEEDDDEQG ESYTPRFSQHASGSRAQKLLRPNSL KLASDSDAESDSRASSPNSTVSNNS TEGFGGIMSFASSLYRNHSTSFSLS NLTLPTKGAREKTTPFPSLKGNRRAL VDQKSSVIKHSPTVKREPPSPQGRSS NSSENQQFLKEVVHSVLDGQGVGW LNMKKVRRLLESEQLRVFVLSKLSR AVQSEDDARQDVIQDVEISRKVYKG MLDLLKCTVLSLEQSYAHAGLGGMA SIFGLLEIAQTHYYSKEPDKRKRSPT ENVNTPVGKDPGLAGRGDPKAMAQ LRVPQLGPRAPSATGRGPKELDTRSL KEENFVASVGPEVIKPVFDLGETEEK KSQISADSGVSLASASQRTDQDSVIG VSPAVMIRSSSQDSEVSNSSGETLG ADSDLSSNAGDGPGGEGSAHLASSR ATLSDSEIETNSATSTIFGKAHSLKP KEKPASSPVRSSEDVSQRVYLYEGLL GRDKGSMWDQLEDAAMETFSISKE RSTLWDQMQFWEDAFLDAVMLERE GMGMDQGPQEMIDRYLSLGEHDRK RLEDDEDRLLATLLHNLISYMLLMK VNKNDIRKKVRRLMGKSHVGLVYSQ QINEVLDQLTNLNGRDLSIRSSGSR HMKKQTFVVHAGTDTNGDIFFMEV CDDCVVLRSNIGTVYERWWYEKLIN MTYCPKTKVLCLWRRNGSETQLNK FYTKKCRELYYCVKDSMERAAARQQ SIKPGPELGGEFPVQDMKTGEGGLL QVTLEGINLKFMHNQVFIELNHIKK CNTVRGVFVLEEFVPEIKEVVSHKYK TPMAHEICYSVLCLFSYVAAVRSSEE DLRTPPRPVSS	None	None	None	None	None	None	None	None	None