

UniprotKB ID	Entry name	organism	full name	oglcnaicscore	oglcnaicsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9VXY2	MADD_DROME	Drosophila melanogaster	MAP kinase-activating death domain protein	25.496522	NaN	NaN	33925313	MSDQKASLCPRLVDYMAIVGAHTT PPMPKGLQGLKAPPVQVDPDLLRRYP PSDHADFPPLDMVYFCQPEGCTSV GPRRTGSAIRDMTSFVFALTDKDSG KTRYGICVNFYRPIERPSSAAGSAGA GNDRPGNGGPGGGHGGAGGGAGG GGRGRRSSAFRRSWRKSMESS DSAFSSDYRSNVAPSDSDRELTSRR DSDQQLRSHSHSHHQPHHPSASPA VPKGLMAPSADSESGGSHSPSPRA SRKRTKLRNQLSTSLCIHSHHPFFT FRECLFILKKLIDACNESSPKRVGA SQKINRDNVVTVLTGHVSDATPSIV LHDVREIETWILRLLSTVPVPGSTR VEVEVLSPTVHEPLLFALPDHTRFSL VDFPLHLPLELLGVETCLKVWTLIM QENKVLQSRDYNALSMVMFAVVT MLYPLEYMFVPVILLPTCLSCAEQLL LAPTPFVIGVPASFLVYKKNFRLPDDI WVVDLSTKLTPTGGYEEIPLPEP EGTILKNHLKQALTSMTATNTAVSS QQLLPSVRDSLQEPPLLGVSQVRLPL QTPPHSAQASQORNSMAQGTISSRQ PSPMNSPALNPFVYGTVDVSDVAT RVAMVRRFFNAQNTLANFAEHTRTL RLYPRPVVAFQINSFLRSRPRASQFL NQFARTQAVEFLAEWVSLTPTNVAFL RVQTGVMDPMQVGDKPKWFAHALT PIRFSVWDDGSSSLNGLRSLKOLEC QPTDESGDSEADSSSSSYSSLSDF VSEMASSDLSPSLHDVFGSYNRPHV VPOTLSSNLDPALVYHPPSKLQYPEG IADAVASKEEEDERADSPVSSSSSR SDLSSPSFNRDSEFDQPKGGQTLG STTVGSGAAAPSFELATPLAMRLEAT IKMASIEQESDVTSTATGKTIAAGSK LQRHPSDESERPEKKIPPLTPPVKQ PGVSNILARTGSSGSSSSSPGRQSSQ SSLFENFASHAKELVRETTQSSQE GLLAHVDKFTLHAKKAAGEASKQAL EVSKQAAGVSKNTLEDLTYVGKSTL GDLTKTAKEAATKGIKIEHSAGG AGPPPKSPGSQLATHKQVQSGGGQ GGNNFFSAIGTDFNGLASSTSTMFS GMFGKKSQKQVPVQKQPNVSAG KAKSGINFDFPGRKGLVERTPLIKH SGPRQTQEELTRQQNQERSHNAE NQTFLDVNTQVLAGEGVGWLKLN RFKKLMEDESYRTLVLKLNKTLTK KIAPDDHIDDVCTKPVWKGMLKCI QAIAAGLDVTFANFGLGGMASVFQL MEVAHTHYWSKEINEGSDMSSLL SSHAASPMGSRNLRSPSPNGSHS ALGSEWASPQESRKSTQLAHGGPG GSHSGAPINRRLSSADSODGQSTTE MFKDMLSQKRSALKNMLTSFDSDT TTSKDSKSSGNLWSGKSTLSAGFR YTGGLINTSSSPDSDPRVYLFEG LGKDRNLNWNQMWFVEDAFDAV SQERDMIGMDQPIEMMERYKSL ESERKREHDEDRLLSTMLYNTAI LVMLNVAKDEIRRKIRLLGKSHIGL VYSQEVHNVDQINNNGNDIDLK LGSRLLRQSFVHQGTDVNGPLRF MEVRDDGLVLRVSDGTIVERWWE RLVNMTYSPKTKLLCWRNGGQT QLHKYYTRCKELYNCIEMERGG TPTNVPGLGGEFPVQDMNTGEGLL QVCLEGVGLLFSNSKFFVRLDHIRK CFTQKGGIFVLEEYKPNKTRNLIQRKY QSSMSDQICYSVLCVFSYVAGQDQ KKNPVVITPQIQDIHAQQKQKHQQQ QQHQQPQQQPHQTTTQONQPTA VASAVPTTAPAGOVNPNRMTAKSQ AGSISIRHTVPMQKPTITMSTVQQA RMPAQVATASVPVTPVPPPTAPPTS	None	None	None	None	None	None	None		

