	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi appara
	M9PEI7	M9PEI7_DROME	Drosophila melanogaster	NaN	49.61447	T2934;T6853;T7172;T7602;T8132;T9725	NaN	40245499;11955;14157;12594	MKIFLPLVTWIVLLLSSAVHSQYSQQ PQPFKTNLRANSRFRGEVFYLNLEN GYFGCQVNESTEYLQLFNLSKLCDG TQDCFLGADELSKELKCTNDCDKDG TKCTHGACLNGVCHCNDGYGGCNC VDKDENECKQRPCDVFAHCTNTLG SFTCTCFPGYRGNGFHCEDIDECQD PAIAARCVENAECCNLPAHFLCKCK DGYEGDGEVLCTDVDECRNPENCG PNALCTNTPGNYTCSCPDGYVGNNP YREGCQDVDECSYPNVCGPGAICTN LEGSYRCDCPPGYDGDGRSESGCVD QDECARTPCGRNADCLNTDGSFRC LCPDGYSGDPMNGCEDVDECATNN PCGLGAECVNLGGSFQCRCPSGFVL EHDPHADQLPQPLNTQQLGYGPGAT DIAPYQRTSGAGLACLDIDECNQPD GVAKCGTNAKCINFPGSYRCLCPSG FQGQGYLHCENINECQDNPCGENAI CTDTVGSFVCTCKPDYTGDPFRGCV DIDECTALDKPCGQHAVCENTVPGY NCKCPQGYDGKPDPKVACEQVDVNI LCSSNFDCTNNAECIENQCFCLDGF EPIGSSCVDIDECRTHAEVCGPHAQ CLNTPGSYGCECEAGYVGSPPRMAC KQPCEDVRCGAHAYCKPDQNEAYC VCEDGWTYNPSDVAAGCVDIDECDV MHGPFGSCGQNATCTNSAGGFTCA CPPGFSGDPHSKCVDVDECRTGASK CGAGAECVNVPGGGYTCRCPGNTIA DPDPSVRCVPIVSCSANEDCPGNSIC DATKRCLCPEPNIGNDCRHPCEALN CGAHAQCMLANGQAQCLCAPGYTG NSALAGGCNDIDECRANPCAEKAIC SNTAGGYLCQCPGGSSGDPYREGCI TSKTVGCSDANPCATGETCVQDSYT GNSVCICRQGYERNSENGQCQDVD ECSVQRGKPACGLNALCKNLPGSYE CRCPQGHNGNPFIMCEICNTPECQC QSPYKLVGNSCVLSGCSSGQACPSG AECISIAGGVSYCACPKGYQTQPDGS CVDVDECEERGAQLCAFGAQCVNK PGSYSCHCPEGYQGDAYNGLCALAQ RKCAADRECAANEKCIQPGECVCPP PYFLDPQDNNKCKSPCERFPCGINA KCTPSDPPQCMCEAGFKGDPLLGCT DEDECSHLPCAYGAYCVNKKGGYQC VCPKDYTGDPYKSGCIFESGTPKSKC LSNDDCASNLACLEGSCVSPCSSLL CGSNAYCETEQHAGWCRCRVGYVK NGDGDCVSQCQDVICGDGALCIPTS EGPTCKCPQGQLGNPFPGGSCSTDQ CSAARPCGERQICINGRCKERCEGV VCGIGATCDRNNGKCICEPNFVGNP DLICMPPIEQAKCSPGCGENAHCEY GLGQSRCACNPGTFGNPYEGCGAQ SKNVCQPNSCGPNAECRAVGNHIS CLCPQGFSGNPYIGCQDVDECANKP CGLNAACLNRAGGFECLCLSGHAG NPYSSCQPIESKFCQDANKCQCNER VECPEGYSCQKGQCKNLCSQASCGP RAICDAGNCICPMGYIGDPHDQVHG CSIRGQCGNDADCLHSEICFQLGKG LRKCVDACSKIQCGPNALCVSEDHR SSCICSDGFFGNPSNLQVGCQPERT VPEEEDKCKSDQDCSRGYGCQASV NGIKECINLCSNVVCGPNELCKINPA GHAICNCAESYVWNPVVSSCEKPSL PDCTSDANCPDASACRPDVLGVLKC VAICDAFTCPANSVCVARQHQGRCD CLNGFVGNPNDRNGCQPAQKHHC RNHAECQESEACIKDESTQTLGCRP ACDTVKCGPRAVCVTNNHQAQCQC PPGPFAGDPYDPFNGCQSVPCVYNH DCPPSQMCNRMTHTCFDVCDEESC GDNAICLAEDHRAVCQCPPGFKGDP LPEVACTKQGGCAAGTCHPSAICEV TPEGPVCKCPPLFVGDAKSGGCRPD GQCPNGDADCPANTICAGGVCQNP CDNACGSNAECKVINRKPVCSCPLR	NaN	NaN	NaN	NaN	NaN	NaN	NaN

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									VCDQETCALNAICVGRRHQPQCECR PGYQGNPHVQCDIPVKTPKPQCIQD ADCPSKLACINERCADPCATPHVCT PQQTCTVLDTLPKRAMACKCPGDTV TDISRNCVPITVPKVISGCQHNSECA NTEVCSNGNCLDACRLERCGVNAQ CTARDHYAQCNCPKGFQGNPRIECY TTEVDVPRIPNPGCSRNDDCPRDQI CRNEICISPCAADDCGIGAYCHVQQR KAICRCPPGYTGNPQERCLPPSDVIL VGCKSSTDCPSNEACINTQCASPCN CGPNAECTVKNHHPICYCKPGFSGN AQFGCAPIGCRSDDECSGDKQCVNR ECINPCLASDPCALNAECYGRNHRA NCRCPVGLEGDPFVRCLRLECHSDY DCASNLACVSNECVSPCGQRNPCA QNAICQALQHRAVCRCPDQLPLGNP YAYCEPRPVEPVCRDDGDCPSKLACI DDKCQDPCSVLSPCHPTAQCSVLNS VPVRTMVCECAEYEVPDASGACRK MMPPRLPGCESDQDCPDQEACIHA QCRNPCNCGTNAVCQVTQHRAVCS CQDGFEGNPYASCRSIGCRVDGECD SGKACINGDCINPCLINDPCGPNAE CYVQSNRAQCRCLSGYRGNPYERCR VIGCSSNNDCPTDKTCQNEQCVNPC VYHNPCAPRAECRAQNHLAVCRCP VDFLGNPYVDCRPPPQPICQLDTDC PGRQACINEQCVDPCVVLEPCQRPAI CEVTPTSPVRTMLCICPDGYVSRGK GGCKPTPGIKEVGGCISDSDCPTDKS CLNSVCRDPCNCGLNAECRIKDHKP VCTCRQGFEGNPEFECSKIECSINSD CPGTHVCRNQLCIPACQGEQCGSNA QCLAIEHRAVCECIPGHGGNARIACT PLGCRSDDECPTDKACVNGKCNDP CTTTALCAQDELCKVYHHRPQCACP PGTVPGKNGCESERHIPICISDADCP SQKACLRGECVNPCNATQPCGVNA FCSVRDTLPVRTMICECLEGYTGNP AVQCDKRSLCVIEKGFVRDVDGQCV CPPGTALDIYEYCTPCREEQGFRIDE SGHCVCALERGMVIDERGRCTCPID LGYRLTPRGECQPEEPPECTSNDQC ADNRFCNLDTKTCEDPCLTKVCGVN AFCNAVNHRAQCQCITGYTGNPDL HCNHTNFRTDFPRPDMVVSCLADG VQVEIHITEPGFNGVLYVKGHSKDE ECRRVVNLAGETVPRTEIFRVHFGS CGMQAVKDVASFVLVIQKHPKLVTY KAQAYNIKCVYQTGEKNVTLGFNVS MLTTAGTIANTGPPPICQMRIITNEG EEINSAEIGDNLKLQVDVEPATIYGG FARSCIAKTMEDNVQNEYLVTDENG CATDTSIFGNWEYNPDTNSLLASFN AFKFPSSDNIRFQCNIRVCFGRCQPV NCGGYNAFGRRRRSIADNSTDATAI ATNSGVEGQLREEITISSNAILTFEK RSGQGLNDANIKPAAQRVEDICVSM VGLIIALVITALLALVAVAVAVSCWL MAYRRRPKTIAPLPHPPEFPNPLFSN PDAVPEPTPDYIS							