| | 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 | extracellu region |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Q5EAK6 | ATM_DROME | Drosophila melanogaster | Serine/threonine-protein kinase ATM | 28.06426 | S2;T913;T2175;T2180 | NaN | 40245499 | MSALLNEIQRILGDLQSGKAASRNK<br>GIQQLDEKLSSCREDLDKLFLSKTSD<br>ISWTTIFEASKEALFKQAGNLEDVNE<br>KVFKTLAGKNYLYDNVLEKITQFNLE<br>AGSQTSGNGHFLAKTSIFSAFEDGIK<br>MRVVVKYFGDRILSLLEKGIYSSVSY<br>VRDLKINEYSRILSYLFELNVDMDEV<br>LRTRILKCITRTVSLAKDRVQLHVDL<br>VEYLPELSSFALSAFGARKTEIVRVYL<br>IFASELAVNYNHQLNVHMQEILPKL<br>CEYHDEDAFRDDTRNLFFQCVSKSL<br>HSMYLKMDMCDFNTLGVPVHEKW<br>PQTLLRLKTIVNVEIRKNSWARCKN<br>ALLSNNKFSDPFIKMSALAMYIVLW<br>HLETKKADENGEGDAPKKIPKPADK<br>METIFSLIDKKENTFNDVWLAIFTEI<br>LQLSSVILNVANYQMALTTVAEIMQ<br>MYGNAKNLRNLRLCLAHLLTKEQE<br>LLHSKSIREDFLGELWSQMANQLIS<br>ETTTNSEEIKEKQLVLQMLIRHNKL<br>NQKLSSTLLNNIISNEMLKRNECLA<br>TIREIFIHADKCGQDKASADLEPIIAW<br>AYGSADRFIAAQMIHNIDSIDAQLQA<br>DTFAISIINFLDVQQLRQISQSEHIVP<br>STERNLLAYKYNEQLICFDKDYATPF<br>ESITHIQSETKNCLIQSNYDCLMRGL<br>NFEIAKENKPAAIIKNLNSLLKLICT<br>MERLLHYKVFDADTYTGCPLIKRIGL<br>YLSHIEFQLKANGAEILDKSDLPEILR<br>LEIYVLDVFRTNLVLLDYLERQPIEM<br>LVEFVGAALKLHSMQRERSVDADH<br>GTITRLCLNILAGLCAYNSHRDEAFE<br>HIVKVTMRWHPQDVLIVTKMLCSCQ<br>TISEASSSWLVSKLKTLFQQHHQDA<br>ELMDKVVQHMPTIFYFVRHKENHL<br>DDMLMALNSLLRIAIKKSYTSNLTAK<br>IVRCVGLIAQRCPDIYLLENFAVICKS<br>TAKFITMPTLEVRFATLFTFTILLESN<br>CVTSDAIGHSRTHWDFCQELYESIE<br>FKKLTYNNEDAIQNSNALIVQMLIAI<br>FLRSSFHQEIALKELLHHCALRRLTE<br>REFISLQSMSSCHRQTVRDLIRPFAA<br>ILLHHWSSKRWPISKFPYFLCYSTKS<br>EFRKTHASEIMAYTFLYGKTEDIERC<br>SKSISEELALPILASFLLIKNSSCSES<br>EGQNFKEHLQLLSENLSYSQLNATD<br>VDLDLDILCYVISMLHDPQEMMRLF<br>GSLAICNRTASWYSLSGESLFKCLN<br>FHIDPEMRPSMDSRIQSMTTLQTKH<br>SRVLVDIFGRLKTNCYSASFSSQALH<br>DFFLYCEVADAVYDAARKNETIVTQC<br>SFFVRDIWFFVVRLLIHTKFIRVQMA<br>ALTFLELLLNKHNFRLDDYQNHFGD<br>IAKLLSNFQLCCEAKEVREKTMSIV<br>MYILESKKGHINLNSFLEETTDCEFL<br>KPLREDCKSSQPNIDRADVANYLRS<br>FLLSPTPERLRDLRTYIAEHKDKVQE<br>HEKLLFGVINKLIQMTRDAHNKTTSI<br>DSLKCLAQIGPLKISTVSYYFQTDFEA<br>FEKSNGEPMEAFLGVVCHSLDTSLF<br>QFDPKTHEGLVSVAIQVVNSKPGSNI<br>MERYKNLRIFADKSTASTFLHSNKQI<br>RRIDWLSILKATKSLSYEPWMCAFV<br>SKVFQMCGWLGFDKLAATSFAFAKT<br>CLLPFIKLLLENSLEHVESLSQMLDY<br>FFEGFTSSTAPNSQEIFRNKRAIKKF<br>LHICEYIRIFNNWTIPINLSNVVMAS<br>NHCQAYFLSIMYLELWACSESPKSK<br>ADFLDNECFQDGAKKAYESIGCLDAI<br>PGFVNPMRSRLDFLGHGSNLSTILL<br>ESDHLDRASGQLCIDIMKGNGLWSF<br>AKLQQHQNIEPDYEIFWRLGQWDSL<br>TDPKHQQNQTVVRTSLDLEQEFKR<br>HHFVALRSIGQREEENSLSAIEQAYS<br>CVRDILMEISVECLQSVYKYLTWLCS<br>LQQAEDFCQIQFGTQLDPASTTKIFR<br>KWQTELELKYGNFSCKEYVIAHQIAL<br>LKLAGTRASRRMSEFYQKDPISTYL<br>MKGIEECKSAGKLNLAAKYTATLRE<br>LPNIRESIKISVLLEDAEINLKMGNQ | True | False | 3.539 | 5.0 | 3.105 | 1.905 | 1.191 | 2.109 | 2.086 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | QIAKAILDYVTNNNEFVYCVQRVPAL<br>RMQGEFLLDCNAETLSWVQSHKFN<br>NSLKLIDDFVQHRQTLSEKYRDIFD<br>WHQLDAYASKQRTAAYATIAKYADR<br>EYQQLHDYRHSQEYQTLKDIIEQNR<br>QTAEKVTQRENQDRRVISVQMKRYA<br>SLDEQQLNQIEEKLTEYLRLALTNY<br>MAYCRLDSGFSSAAIYRIISLWFTNA<br>TSKQCQECIKDEILTVPSYKFICAAN<br>QLTARLNSKNTSLLKGLTDLLVQCG<br>KDHPYHTFYQLYPLVFAHLDGENSN<br>TERSGIARKIIAMICEKNGTAGECSK<br>QLESLLPALITFANEGKTNDNRPVS<br>DSVRNKQFDKVRRWRNLNAVHCPT<br>LELPVMPSKEYSIISVVKWTNETTQC<br>GGLNAPVKIMCVCSDGKIRAQLVKG<br>KDDLRQDAVMQQVFGIVNELLNQD<br>SEFIERKLKLRTYKVTPLSMRSGILE<br>WCTNSVPVGHYLVVEGKGGAHARY<br>RPNDWNNNKCRKLSSDHLKSPKET<br>RYAIYKKICENIKPVFHYFLLEKFPIP<br>GVWFERRLAYTNSVATTSMVGYVLG<br>LGDRHTQNILVDQQTAEVIHIDFGIA<br>FEQGKIQTTPETVPFRLTRDFVAPM<br>GICGTKGVFAKSCEATMHILRRYKSV<br>FTTILEVLLYDPLFIWGVLKKKQSPQ<br>QSGEESVNLVAQRALLLVQNKLDGR<br>EAGTMGDSNVEAQVERLINEATLPS<br>NLCMLFPGWDPHL | | | | | | | | | |