

| UniprotKB ID | Entry name | organism     | full name                 | oglcnacscore | oglcnac sites         | phosphorylation sites        | PMIDS   | sequence   |
|--------------|------------|--------------|---------------------------|--------------|-----------------------|------------------------------|---|--|
| Q13315       | ATM_HUMAN  | Homo sapiens | Serine-protein kinase ATM | 27.791549    | S601;S941;S1731;T2608 | S367;S1893;S1981;S1983;S2996 | 22759405;37217939;30059200;27655845;34105348;29351928 | MSLVLNDLLICCRQLEHDRATERKK<br>EVEKFKRLIRDPETIKHLDRHSDSKQ<br>GKYLNWDAVFRFLQKYIQKETECLRI<br>AKPNVASTQASRQKKMQEISSLVK<br>YFIKCANRRAPRLKQCQELLYIMDTV<br>KDSSNGAIYGADCSNILLKDILSVRK<br>YWCEISQQWLELFSVYFRLYLKPS<br>QDVHRVLVARIHAVTKGCCSQTGD<br>LNSKFLDFFSKAIQCARQEKSSSGL<br>NHILAALTIFLKTAVNFRIRVCELG<br>DEILPTLLYIWTQHRLNDSLKEVIEL<br>FQLQYIHHPKGAKTQEKGAYESTK<br>WRSILYNLYDLLVNEISHIGSRGKYS<br>SGFRNIAVKENLIELMADICHQVFN<br>EDTRSLEISQSYTTTQRESSDYSVPC<br>KRKKIELGWEVIKDHLOKSONDFDL<br>VPWLQIATQLISKYPASLPNCELSPL<br>LMILSQLLPQQRHGERTPYVLRCLT<br>EVALCQDKRSNLESSQKSDLLKLWN<br>KIWCITFRGISSEQIQAENFLLGAI<br>QGSLEVDREFWKLFTGSACRPSCP<br>AVCCLTLALTTIVPGTVKMGIEQN<br>MCEVNRSFSLKESIMKWLLFYQLEG<br>DLENSTEVPPILHSNPHLVLEKILV<br>SLTMKNCKAAMNFFQSVPECEHHQ<br>KDKEELSFSEVEELFLQTTFDKMDF<br>LTIVRECGIEKHQSSIGFSVHQNKE<br>SLDRCLLGLSEQLLNYSSEITNSET<br>LVRCRLLVGVLGCCYMGVIAEEE<br>AYKSELFQKAKSLMQCAGESITLTK<br>NKTNEEFRIGSLRNMMQLCTRCLS<br>NCTKKSPNKIASGFFLRLLTSKLMN<br>DIADICKSLASFIKKPFDRGEVESME<br>DDTNGNLMEVEDQSSMNLFNNDYPD<br>SSVSDANEPGESQSTIGAINPLAEY<br>LSKQDLLFLDMLKFLCLCVTTAQTN<br>TVSFRAADIRKLLMLIDSSTLEPTK<br>SLHLHMYLMLLKEPLGEEYPLPME<br>DVLELLKPLSNVCSLYRRDQDVCKTI<br>LNHVLVHVKNLQSNMDSSENTRDA<br>QGQFLTIVGAFWHLTKERKYIFSVR<br>MALVNLKTLLEADPYSKWAILNVM<br>GKDFPVNEVFTQFLADNHHQVRML<br>AAESINRLFQDTKGDSSRLLKALPLK<br>LQQTAFENAYLKAQEGMREMSHSA<br>ENPETLDEIYNRKSULLTIAVVLSCS<br>PICEKQALFALCKSVKENGLEPHLVK<br>KVLEKVSETFGYRRLEDFMASHLDY<br>LVLEWLNLDTEYNLSSFPFILLNYT<br>NIEDFYRSCYKVLIPHLVIRSHFDEV<br>KSIANQIQEDWKSLLTDCFPKILVNI<br>LPYFAYEGTRDSGMAQQRETATKVY<br>DMLKSENLLGKQIDHLFISNLPEIVV<br>ELLMTLHEPANSSASQSTDLCDFSG<br>DLDPAPNPPHFP SHVIKATFAYISNC<br>HKTKLSILEILSKSPDSYQKILLAIC |

EQAETNNVYKKHRILKIYHLFVSLL  
LKDIKSGLGGAWAFVLRDVIYTLIHYI  
NQRPSCIMDVSLRSFSLCCDLLSQV  
CQTAVTYCKDALENHLHVIVGTLIPL  
VYEQVEVQKQVLDLLKYLVIDNKDN  
ENLYITIKLLDPFPHVVFKDLRITQ  
QKIKYSRGPFSLLEEINHFLSVSVYD  
ALPLTRLEGLKDLRRQLELHKDQMV  
DIMRASQDNPDGIMVKLVNLLQL  
SKMAINHTGEKEVLEAVGSCLEVG  
PIDFSTAIQHSKDASYTKALKLFEDK  
ELQWTFIMLTYNNTLVEDCVKVR  
AAVTKLKNILATKTGHSFWEIYKMTT  
DPMLAYLQPFRTSRKKFLEVPRFDK  
ENPFEGLDINLWIPLSENHDIWIKT  
LTCAFLDSGGTKCEILQLLKPMCEV  
KTDFCQTVLPYLIHDILLQDTNESWR  
NLLSTHVQGGFTSCLRHSQTSRST  
TPANLDSESEHFFRCCLDKKSQRTM  
LAVVDYMRRQKRPSSGTIFNDAFWL  
DLNYLEVAKVAQSCAAHFTALLYAEI  
YADKKSMDDEKRSALAFEEGSQSTT  
ISSLSEKSKEETGISLQDILLEIYRSIG  
EPDSLYGCGGGKMLQPITRLRITYEH  
EAMWKGALVITYDLETAIPSTRQAGI  
IQALQNLGLCHILSVYLGKLDYENKD  
WCPELEELHYQAAWRNMQWDHCT  
SVSKEVEGTSYHESLYNALQSLRDR  
EFSTFYESLKYARVKEVEEMCKRSL  
ESVYSLYPTLSRLQAIGELESIGELFS  
RSVTHRQLSEVIKWQKHSQLLKDS  
DFSFQEPIMALRTVILEILMEKEMD  
NSQRECIKDILTKHLVELSILARTFK  
NTQLPERAIFQIKQYNSVSCGVSEW  
QLEEAQVFWAKKEQSLALSILKQMI  
KKLDASCAANNPSLKLTYTECLRVC  
GNWLAETCLENPAVIMQTYLEKAVE  
VAGNYDGESSDELNRNGMKMAFLSL  
ARFSDTQYQRIENYMKSEFENKQA  
LLKRAKEEVGLLREHKIQTNRVTVKV  
QRELEDELALRALKEDRKRFLCKA  
VENYINCLLSGEEHDMWVFRCLCSL  
WLENSGVSEVNGMMKRDGMKIPTY  
KFLPLMYQLAARMGTKMMGGGLGFH  
EVLNNLISRISMDHPHHTLFILALA  
NANRDEFLTKEVARRSRITKNVPK  
QSSQLDEDRTEAANRIICTIRSRRPQ  
MVRSVEALCDAYIILANLDATQWKT  
QRKGINIPADQPITKLNLEDVVVPT  
MEIKVDHTGEYGNLVTIQSFKAEFR  
LAGGVNLPKIIDCVGSDGKERRQLV  
KGRDDLQDAVMQVVFQMCNTLL  
QRNTETRKRKLTICTYKVVPLSQRS  
VLEWCTGTVPIGEFLVNNEDGAHKR  
YRPNDFSAFQCQKKMMEVQKKSFE  
EKYEVFMDVCQNFQPVFRYFCMEK  
FLDPAIWFEKRLAYTRSVATSSIVGYI  
LGLGDRHVQNILINEQSAELVHIDLG  
VAFEQKILPTPETVPFRLTRDIVDG

