

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9JKK8	ATR_MOUSE	Mus musculus	Serine/threonine-protein kinase ATR	25.590209	NaN	S431;S438;S439	35822049	MGDGHLELASMPALRELGSATPEE YNTVVQKPRQILCQFIDRLITDVENVV ALELVKKTDAQPTSMVLLDFIQHIM KSSPLMFVNVNGSQGONEAKDSCIE FSHWIITRLLRIAATPSCMHLHKKIC EVICSLFLFKSKNPAIFGVLTRRELLY LFEDLIYLHKRNAVGEVMEWPVVVS RFLSRLDEHMGCLQPAPLQFMNVQ NVEFIEVTLLMVLIIHVPTVFFRROE LLWQIGCALLEHGSFKIRSLAISLLT ELFELGGLPAQPASTFFSLFLELLQH LVGMDADQLKLYEPLSKLLKTLFP FEAEAYRNIEPVYLVNVLLEKLSVMFE DRVLMRLKSDLLKAALCHLLQYFLT FVPAGYESALQVRKVYVTNICRALVD ALGVQKHVGYLLGPFYAALKMESKE IIERIQCCQAQENLSGNNDEVSPKR RKLSSLSYKPKSRQPEEIIHVDMD KKSILWNVLKQKAESLQISLECGTLK NSVAELEGITVVLQTLALCTVHCSH QDMDGHNVDHQHKYKKPPVVVT WMSLDFYTKVLKSCRSLLESVQKLE LELVIDSMVRICDALMYMQVKSFFK DHVLEELCGMLSLPWYSYSDDNSL KMTTFATNLLPLSQRVWDSYSPQAQ SKCVFLLTLFPRRIFLEWRTAVYNW ALKSSHEVIRASCVKGFFILLHQONS CNQIPKMLVDRVKDDSDMVKKEFA SVLGQLVCTLHGMFYLSSSVEPCFE HMDLFSKNLKATSOHECSSSQVKA STCKPFLFLLTKNTPSPVKLAFIDNL HHLCKHLDFQEDEREVKAVLGTLL NLMEDPKDVRIAFSGNIKYLESLN SEDFVKELFVLRMKEAYTHAQIAR NNEKDTLILTTGDIGRAAKGDLIPP ALLHLLHCLLSKASVSGAAYTEIRA LVAAKSVKLQNFSSQYKPKICQFLVE SLHSSQMTALPSAPCQSSEIRKQDV AHHREMANTLSEIANVDFPDLNR FLTRTLOVLLPDLAAKASPAASALIRT LGKQLNVSRRILINNFYIFSHLVC SCSKDELERALHYLKNETEIELGSL RODFQGLHNEILLRIGEHYQQVFN GLSILASFASDDPYQGPRDITSPEL MADYLOPKLLGILAFFNMQLSSSV GIEDKMMALTSMLMMLMGPXHV SSVRVKMMTTLRTGLRFKDDFPELC CRAWDCFVRCLDHAYLGPLLSHVIV ALLPLIHMOPKETA AIFHYLIENRDA VQDFLHEIYFLPDHPELEKIKAVLOE YRKETSETDLQTLQLSMKAIQHE NVDVRIHALTSLKETLYKNQEKLIKY ATDSEVPEVISQLVTVILKGCQDAN SQARLLCGECLGELGAIDPCRLDFST TETQKDFTFVTGVEDLSFAYGLLM ELTRAYLAYADNSRAQDSAAAYIQEL LSYDCREMQSNPGYQLWKRFPPE HVREILEPHLNTRYKSSQKSTDWSG VTKPIYLSKLGNNFAEWSSSWAGYLI TKVRDNLASKIFTCCSMMKHDFKV TIYLLPHILVYVLLGCNQEDQQEVYA EIMAVLKHDEQHAISTQDSASDLCO LSTQTVFVLDHLTQWARHKFQALN AEKLAQNKPKGVSNVNFEDYQSVTR FLDLIPQDTLAVASFRSKAYTRAVMH FESFITEKKQNIQKHLGFLQKLYAA MHEPDGVAGVS AIRKAEP SLKEQILE HESIGLLRDATA CYDRAIQLEPDQIIH YHGVMKSMGLGQLSTVITQVNGVH ANRSEWTDENLYRVEAAWKLSQW DLVENYLAADGKSTTWSVRLGQLL SAKKRDTTTFYDTLKLVRAEQIVPLS AASFERSYQRYEFIVRLHMLCEL EHSLKPLFRKSPGDSNEDSLNWG ARLEMTQNSYRAKEPILALRRALLSL NKRDPYNEMVGECLWQSARVARKA	None	None	None	None	None	None	None		

GHHQTAYNALLNAGESRLAELYVER
AKWLWSKGDVHQALIVLQKGVELCF
PENKSPSESKHMLIHGRATLLVGRF
MEETANFESNAVMMKKYKDVTLFLPE
WEDGHFYLAKEYDKLMPMVTDNK
MEKQGD LIRYIVLHFGRSLQYGNQFI
YQSMPRMLSLWLDGAKAYEWEKG
GRSDRLQMRNDLAKINSVLTEHTN
RLAPYQELTAFSQLISRICSHSDEVF
VVLMEIIAKVFLAYPQQAMWMMTA
VSKSSYPMRVNRCKEILTKAIHMKK
SLEKFGDATTRLTDKLELCNKSV
GSNSTLSMSTHFKMLKRLVEDPTFS
EILPLQSVMIPTLPSVLGAHANHDP
FPGHWAYLAGFDDVEILSSLQKPK
KISLKGSDGKFYIMMCKPKDDLKRD
CRLMEFNLSLINKSLRKDAESRRREL
HIRTYAVIPLNDECGIIEWVNNTAGL
RPILTKIYKEKGVYMTGKELROCMLP
KSAALSEKLVFQELLPRHPPVFHE
WFLRTFPDPTSWYSSRSAYCRSTAV
MSMVGYILGLGDRHGENILFDSFTG
ECVHVDFNCLFNKGETFEVPEIVPF
RLTHNMVNGMGPMTGELFRRAC
EVTLRLMRDQREPLMSVLKTFHDP
LVEGSKPVKGHSKAPLNETGEVVNE
KAKTHVLDIEQRLQGVIKTRNRVTGL
PLSIEGHVHYLIQEATDENLLCQMYL
GWTPYM