

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O14497	ARI1A_HUMAN	Homo sapiens	AT-rich interactive domain-containing protein 1A	24.267324	S58;S128;S129;T238;S241;S249;S254;S255;S256;S258;S260;S261;S264;S265;S637;S711;S764;S1090;S1091;S1180;S1235;S1242;T1888;S2262	S58;S79;S233;T286;S301;S363;S382;S604;S696;S698;S702;S730;S764;S772;S1184;S1235;S1604;S1751;S1754;T1888;S1929;S1944	33214551;35254053;30379171;29351928;38253038;35132862;30059200;31492838;32119511;35138101;34019948;27655845;23301498;21740066;20305658	MAAQVAPAAAASSLGNPPPPPPSELK KAEQQQREAGGEAAAAAARERGE MKAQAAGQEGEAVGPPQPLGKELQ DGAESNGGGGGGAGSGGGGPAEP DLKNSNGNAGPRPALNNNLTEPPG GGGGSSDGVGAPPHSAAAALPPPA YGFQPYGRSPSAVAAAAAVFHQQ HGGQQSPGLAALQSGGGGGLEPYA GPQQNSHDHGFPNHQYNSYYPNRS AYPPPAPAYALSSPRGGTPGSGAAAA AGSKPPSSSASASSSSSFAQQRFG AMGGGGPSAAGGTPQPTATPTLNQ LLTSPSSARGYQGYPGGDYSGGPQD GGAGKGPADMASQCWGAIAAAAAA AAASGGAQQRSHHAPMSPGSSGGG GQPLARTPQPSSPMDQMGKMRPQP YGGTNPYSQQQPPSPGQQGHGYP GQPYGSQTPQRYPMTMQGRAQSAM GGLSYTQQIPPYQQGQPSGYQQGQ TPYYNQSPHPQQQPPYSQQPPSQ TPHAQPSYQQPQSQPPQLQSSQPP YSQQSPQPPHQSPAPYPSQQSTTQ QHPQSQPPYSQPQAQSPYQQQPQ QPAPSTLSQAAYPQPSQSSQQT YSQQRFPFPQELSQDSFGSQASSAP SMTSSKGGQEDMNLSLQSRPSSLP DLSGSIDDLPMTGTEGALSPGVSTSGI SSSQGEQSNPAQSPFSPHTSPHLPGI RGPSPPVGSASVAQSRSGPLSPAA VPGNQMPRRPPSGQSDSIMHPSMN QSSIAQDRGYMQRNPQMPQYSSPO PGSALSPRQPSGGQIHTGMGSYQQN SMGSYGPQGGQYGPQGGYPRQPNY NALPNANYPSAGMAGGINPMGAGG QMHGQPGIPPYGTLPPGRMSHASM GNRPYGNMANMPPQVSGMCPFP GGMNRKTQETAAMHVAANSIQNR PPGYPNMNQGGMMGTGPPYQGIN SMAGMINPQGPYSMGGTMANNSA GMAASPEMMGLGDVCLTPATKMN NKADGTPKTESKSKSSSSTTNEKI TKLYELGGEPERKMWVDLYLAFTEE KAMGMTNLPAVGRKPLDLYRLVSV KEIGGLTQVNKNKKWRELATNLNV GTSSSAASSLKKQYIQCLYAFECKIE RGEDPPPDIFAAADSKKSQPKIQQPS PAGSGSMQGPQTPQSTSSMAEGG DLKPPTPASTPHSQIPPLPGMSRSNS VGIQDAFNDGSDSTFQKRNSMTPNP GYQPSMNTSDMMGRMSYEPNKDP YGSMRKAPGSDPFMSSGQGNPMMG GDPYSRAAGPGLGNVAMGPRQHYP YGGPYDRVRTEPGIGPEGNMSTGAP QPNLMPSNPDSCMYSPSRYPQQQ QQQQQRHDSYGNQFSTQGTSPGSP FPSQQTMYQQQQQNYKRPMDGTY GPPAKRHEGEMYSVPYSTGQQQPQ QQQLPPAQQPASQQQAAQPSPPQ DVYNYGNAYPATATAATERRPAGG PQNQFPFQFGRDRVSAPPGTNAQQ NMPPQMMGGPIQASAEVAQQGTM WQGRNDMTYNYANRQSTGSAPQGP AYHGVRNTRDEMLHTDQRANHEGS

WPSHGTRQPPYGPSAPVPPMTRPPP  
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GDTTEHIQTHFESKTELLPSRPHAPC  
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MMRRAARALLALAKVDENHSEFTL  
YESRLDISVPLMNSLVSQVICDVL  
FLIGQS