

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	23.836362	S58;S128;S129;T238;S241;S249;S254;S255;S256;S258;S260;S261;S264;S265;S711;S764;S1090;S1091;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	31492838;32119511;29351928;34019948;21740066;27655845;35254053;35132862;35138101;30059200;23301498;20305658;30379171;33214551	MAAQVAPAAAASSLGNPPPPPPSELK KAEQQQREAGGEAAAAAARERGE MKAQAAGQEGGPAVGPQPPLGKELQ DGAESNGGGGGGAGSGGGGPGAEP DLKNSNGNAGPRPALNNNLTEPPG GGGGSSDGVGAPPHSAAAALPPPA YGFQPYGRSPSAVAAAAAVFHQQ HGGQQSPGLAALQSGGGGGLEPYA GPQQNSHDHGFPNHQYNSYYPNRS AYPPPAPAYALSSPRGGTPGSGAAAA AGSKPPSSSASASSSSSFAQQRFG AMGGGGPSAAGGTPQPTATPTLNQ LLTSPSSARGYQGYPGGDYSGGPQD GGAGKGPADMASQCWGAIAAAAAA AAASGGAQQRSHHAPMSPGSSGGG GQPLARTPQPSSPMDQMGKMRPQP YGGTNPYSQQQPPSPGQQGHGYP GQPYGSQTPQRYPMTMQGRAQSAM GGLSYTQQIPPYGQQGSPGYQQGQ TPYYNQSPHPQQQPPYSQQPPSQ TPHAQPSYQQPQSQPQLQSSQPP YSQQSPQPPHQSPAPYPSQQSTTQ QHPQSQPPYSQPQAQSPYQQQQPQ QPAPSTLSQAAYPQPQSQQSQQTA YSQQRFPQPQELSQDSFGSQASSAP SMTSSKGGQEDMNLSQLSRPSSLP DLSGSIDDLPMTGTEGALSPGVSTSGI SSSQGEQSNPAQSPFSPHTSPHLPGI RGPSPPVGSASVAQSRSGPLSPAA VPGNQMPRRPPSGQSDSIMHPSMN QSSIAQDRGYMQRNPQMPQYSSPO PGSALSPRQPSGGQIHTGMGSYQQN SMGSYGPQGGQYGPQGGYPRQPNY NALPNANYPSAGMAGGINPMGAGG QMHGQPGIPPYGTLPPGRMSHASM GNRPYGNMANMPPQVSGMCPFP GGMNRKTQETAAMHVAANSIQNR PPGYPNMNQGGMMGTGPPYGGGIN SMAGMINPQGPYSMGGTMANNNSA GMAASPEMMGLGDVCLTPATKMN NKADGTPKTESKSKSSSSTTNEKI TKLYELGGEPERKMWVDLYLAFTEE KAMGMTNLPAVGRKPLDLYRLYVSV KEIGGLTQVNKNKKWRELATNLNV GTSSSAASSLKKQYIQCLYAFECKIE RGEDPPPDIFAADSKKSQPKIQQPS PAGSGSMQGPQTPQSTSSMAEGG DLKPPTPASTPHSQIPPLPGMSRSNS VGIQDAFNDGSDSTFQKRNSMTPNP GYQPSMNTSDMMGRMSYEPNKDP YGSMRKAPGSDPFMSSGQGPNGGM GDPYSRAAGPGLGNVAMGPRQHYP YGGPYDRVTEPGIGPEGNMSTGAP QPNLMPSNPDSCMYSPSRYPQQQ QQQQQRHDSYGNQFSTQGTSPGSP FPSQQTMYQQQQQNYKRPMDGTY GPPAKRHEGEMYSVPYSTGQQQPQ QQQLPPAQQPASQQQAAQPSPPQ DVYNQYGNAYPATATAATERRPAGG PQNQFPFQFGRDRVSAPPGTNAQQ NMPPQMMGGPIQASAEVAQQGTM WQGRNDMTYNYANRQSTGSAPQGP AYHGVRNTRDEMLHTDQRANHEGS

