	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	extracellular region
0	Q9P281	BAHC1_HUMAN	Homo sapiens	BAH and coiled-coil domain-containing protein 1	21.722709	S686	S2274	30379171;31492838	MDGRDFAPPPHLLSERGSLGHRSAA AAARLAPAGPAAQPPAHFQPGKYFP SPLPMASHTASSRLMGSSPASSFMG SFLTSSLGSAASTHPSGPSSSPPEQA YRGSHPTTSQIWFSHSHEAPGYPRF SGSLASTFLPVSHLDHHGNSNVLYG QHRFYGTQKDNFYLRNLPPQPTLLP ANHNFPSVARAAPAHPMGSCSRDR DRGEAGSLQKGPKDFDRFLVGKELG REKAGKAAEGKERPAAEEDGGKER HKLVLPVPADGHCREGGPAPRGACE GRPKHLTSCLLNTKVLNGEMGRAAL ASCAGGMLGRPGTGVVTSGRCAKEA AGPPEPGPAFSECLERRQMLHHTAS YAGPPPPLSTAAGSFPCLQLHGGPD GLCPLQDKAPRDLKASGPTFVPSVG HLADKGRPFQAAEACAVAGEGKDR HLEGTMAPDHAAPYGVSYAHLKAEG KGERRPGGFEAALNPRLKGLDYLSS AGPEASFPGLPKSGLDKSGYFELPTS SQDCARPGHQDPLGGKAPQACCTL DKTVGKEAPAGPPGAQKVARIRHQQ HLMAAEVEQGGIGAEAKRKSLELAS LGYSGPHLPPWGVQAGQGTAMAISE ERKAGAYLDPFGSGLQQAALLPQEL PAPPDEVSAMKNLLKYSSQALVVGQ KAPLVGLGGLKASCIQQEAKFLSSKG PGQSERPDCARSREHDTTHGDGEV RQPPVGIAVALARQKDTVSRSEAAYG TNTARQGRAAPAFKGGGGPRSTHAL DLEAEEERTRLCDDRLGLASRELLL QDSKDRVEFARIHPPSSCPGDLAPH LMMQSGQLGGDPAPHTHPHPPWLP RTRSPSLWMGGHSYGLGHPALHQN LPPGFPASVAGPVPSVFPLPQDAPTQ LVILPSEPTPHSAPHALADVMDQASL WPPMYGGRGPASHMQHPGQLPVYS RPQLLRQQELYALQQQRAAQFQRKP EDQHLDLEEPAQEKAPKSTHKPVAL TPTAPGAPSPAAGPTKLPPCCHPPDP KPPASSPTPPPRPSAPCTLNVCPASS PGPGSRVRSAEEKNGEGQQSTADIIT SEPVARAHSVAHAGLEFLASNDPST SASQSFGITDLPPGYLRPMAGLGFSL PSDVHSSNLEDPETMQTTAPGAQPE PTRTFLPGEPPPCSPRSLEEPGLLSG AREATQDLAATPYPTERGPQGKAAD PSPLEGLQELQCAALLEAGGPEATG QAHSTQGGAREERSREEGEQGPSS GASSQVLEQRAGSPGALEDEGEQPA PEEDELEEDELGQQSMEDSEEDCG GAPDNSHPPRALPGLDALVAATINL GDLPSDSPPDPQPPAASGPPSTVPLP HSSGIHGIALLSELADLAIQRQRSER TVPEEEEDVLAFNLQHLATLATAWS LVEAAGLDSSTAPAQPPTANPCSGP RLTPRMQILQRKDTWTPKTKPVCPL KAAIDRLDTQEVGMRVRLAELQRRY KEKQRELARLQRKHDHERDESSRSP ARRGPGRPRKRKHSSSLPAPRPTGP LPRSDGKKVKAVRTSLGLLCAELRG GSGGEPAKKRSKLERSVYAGLQTAS VEKAQCKKSSCQGGLAPSVAHRVAQ LKPKVKSKGLPTGLSSFQQKEATPG GRIREKLSRAKSAKVSGATRHPQPK GHGSRETPRCPAQPSVAASQEAGSG YDSEDCEGLLGTEAPPREAGLLLHT GASVAVLGPSPSSVVKMEANQKAKK KKERQGLLGACRLSSPESEVKIKRRS VKAKVGTTLERAPGQRPPGALGKKK AKGKAKGSLRAEPGATPSRDALFNP SRAFACREEGSQLASERLKRATRKG TVLQPVLRRKNGALSITLATRNAKAI LGKGRKLSKVKHKAGKQGKGRAVS RLLESFAVEEDFEFDDNSSFSEEEE DEEEEEEDSGPLSAEQSAALARSCAI HKEDLRDGLPVLIPKEDSLLYAGSVR TLQPPDIYSIVIEGERGNRQRIYSLEQ LLQEAVLDVRPQSSRYLPPGTRVCAY	None	None	None	None	None	None	None	None	None

								WSQKSRCLYPGNVVRGASGDEDED LDSVVVEFDDGDTGHIAVSNVRLLP PDFKIQCTEPSPALLVSSSCRRTKKV SSEAPPPSEAATPSLSPKAQDGPEAL KTPGKKSISKDKAGKAELLTSGAKSP TGASDHFLGRRGSPLLSWSAVAQTK RKAVAAASKGPGVLQNLFQLNGSSK KLRAREALFPVHSVATPIFGNGFRAD SFSSLASSYAPFVGGTGPGLPRGAHK LLRAKKAERVEAEKGGRRRAGGEFL VKLDHEGVTSPKNKTCKALLMGDK DFSPKLGRPLPSPSYVHPALVGKDKK GRAPIPPLPMGLALRKYAGQAEFPLP YDSDCHSSFSDEDEDGPGLAAGVPS RFLARLSVSSSSSGSSTSSSSGSVST SSLCSSDNEDSSYSSDDEDPALLLQ TCLTHPVPTLLAQPEALRSKGSGPH AHAQRCFLSRATVAGTGAGSGPSSS SKSKLKRKEALSFSKAKELSRRQRPP SVENRPKISAFLPARQLWKWSGNPT QRRGMKGKARKLFYKAIVRGEETLR VGDCAVFLSAGRPNLPYIGRIESMW ESWGSNMVVKVKWFYHPEETKLGK RQCDGKNALYQSCHEDENDVQTIS HKCQVVAREQYEQMARSRKCQDRQ DLYYLAGTYDPTTGRLVTADGVPILC								